MYC shapes the composition of RNA polymerase II through direct recruitment of transcription elongation factors

MYC beeinflusst die Zusammensetzung der RNA-Polymerase II durch die direkte Rekrutierung von Transkriptions-Elongationsfaktoren

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SUMMARY

The transcription factor MYC is a onco-protein, found to be deregulated in many human cancers. High MYC levels correlate with an aggressive tumor outcome and poor survival rates. Despite MYC being discovered as an oncogene already in the 1970s, how MYC regulates transcription of its target genes, which are involved in cellular growth and proliferation, is not fully understood yet.

In this study, the question how MYC influences factors interacting with the RNA polymerase II ensuring productive transcription of its target genes was addressed using quantitative mass spectrometry. By comparing the interactome of RNA polymerase II under varying MYC levels, several potential factors involved in transcriptional elongation were identified. Furthermore, the question which of those factors interact with MYC was answered by employing quantitative mass spectrometry of MYC itself. Thereby, the direct interaction of MYC with the transcription elongation factor SPT5, a subunit of the DRB-sensitivity inducing factor, was discovered and analyzed in greater detail. SPT5 was shown to be recruited to chromatin by MYC. In addition, the interaction site of MYC on SPT5 was narrowed down to its evolutionary conserved NGN-domain, which is the known binding site for SPT4, the earlier characterized second subunit of the DRB-sensitivity inducing factor. This finding suggests a model in which MYC and SPT4 compete for binding the NGN-domain of SPT5.

Investigations of the SPT5-interacting region on MYC showed binding of SPT5 to MYC’s N-terminus including MYC-boxes 0, I and II.

In order to analyze proteins interacting specifically with the N-terminal region of MYC, a truncated MYC-mutant was used for quantitative mass spectrometric analysis uncovering reduced binding for several proteins including the well-known interactor TRRAP and TRRAP-associated complexes.

Summarized, the interactome of MYC as well as the interactome of the RNA polymerase II were determined in two different cancer cell lines comprising a starting point for further projects investigating MYC’s biology and function as well as the transcription process in cancer cells, which could uncover vulnerabilities for cancer treatment. Furthermore, the uncovered direct interaction of MYC with SPT5 offers a new point of action in targeting MYC-dependent cancers.

ZUSAMMENFASSUNG

Bei dem Transkriptionsfaktor MYC handelt es sich um ein Onkoprotein, welches in einer Vielzahl der menschlichen Krebserkrankungen in erhöhter Konzentration vorliegt, was wiederum mit einem schweren Krankheitsverlauf einhergeht. Bereits in den 1970iger Jahren wurde das Protein MYC als ein Onkoprotein identifiziert, aber wie es die Transkription seiner großen Bandbreite an Zielgenen, welche für Zellwachstum und -proliferation verantwortlich sind, reguliert, ist bisher noch nicht eindeutig geklärt.

In dieser Arbeit wurde die zentrale Frage untersucht, wie MYC die Proteine beeinflusst, die mit der RNA-Polymerase II interagieren, um dadurch eine schnelle und produktive Transkription seiner Zielgene zu ermöglichen. Hierfür wurden mittels der Durchführung massenspektrometrischer Untersuchungen Proteine, die in der An- und Abwesenheit von MYC mit der RNA-Polymerase II interagieren, identifiziert, was eine MYC-bedingte Änderung einiger Elongationsfaktoren im Interaktom der RNA-Polymerase II aufzeigte. Des Weiteren wurden ebenfalls unter Zuhilfenahme massenspektrometrischer Analysen Proteine bestimmt, die mit MYC selbst interagieren. Hierdurch konnte die bisher unbeschriebene, direkte Interaktion zwischen MYC und SPT5, der großen Untereinheit des DRB-*sensitivity inducing factors*, aufgedeckt und näher analysiert werden. Es konnte gezeigt werden, dass MYC SPT5 zum Chromatin rekrutiert. Weiter konnte nachgewiesen werden, dass MYC mit der evolutionär konservierten NGN-Domäne von SPT5 interagiert, an welche auch SPT4, die zweite Untereinheit des DRB-*sensitivity inducing factors*, bindet. Dies resultiert in dem Modell, dass MYC mit SPT4 um die Bindestelle auf SPT5 konkurriert und durch dieses ersetzt werden kann. Die Nähere Untersuchung der Bindestelle von SPT5 auf MYC zeigte eine Binderegion im N-terminalen Bereich von MYC auf, der die MYC-Boxen 0, I und II miteinschließt.

Um Proteine zu identifiziert, die selektiv mit dem N-terminalen Bereich von MYC interagieren, wurde die quantitative Massenspektrometrie auf eine N-terminal trunkierten Mutante von MYC angewendet. Es konnten einige Proteine identifiziert werden, die selektiv den N-terminalen Bereich von MYC binden, darunter auch der bekannte Interaktor TRRAP, sowie TRRAP-assoziierte Komplexe.

Zusammenfassend wurden im Laufe dieser Arbeit Datensätze generiert, die das Interaktom von MYC, sowie das Interaktom der RNA-Polymerase II in zwei verschiedenen Krebszelllinien umfassen, und als Grundlage für weitere Projekte dienen, die sich mit der Biologie und

Funktionsweise des MYC Proteins sowie dem Transkriptionsprozess in Krebszellen befassen, was in der Entdeckung neuer therapeutischer Angriffspunkte in Krebszellen resultieren könnte. Einen solchen therapeutischen Angriffspunkt könnte im Speziellen die hier beschriebene direkte Interaktion zwischen MYC und SPT5 darstellen.

1 INTRODUCTION

1.1 The oncogenic transcription factor MYC

The proto-oncogene c-MYC was first described by Sheiness and Bishop in 1979 as a homologue of the viral v-MYC causing myelocytomatosis (Sheiness and Bishop 1979; Vennstrom et al. 1982). Besides c-MYC (hereafter referred to as MYC), the MYC family comprises two more proteins namely NMYC and LMYC, expressed in different tissues (Kohl et al. 1983; Legouy et al. 1987; Nau et al. 1985; Schwab et al. 1983). NMYC was discovered as being expressed in neuronal tissue during neuronal development but is not expressed in adults. Exceptionally, high NMYC levels are found in neuroblastoma, which is a neuronal tumor developed during early childhood, and are linked to lower survival rates (Brodeur et al. 1984; Kohl et al. 1983; Schwab et al. 1983). LMYC is expressed in lung tissue and upregulated in non-small cell lung cancer (Legouy et al. 1987; Nau et al. 1985).

MYC is widely expressed during development and in adults in proliferating tissue upon external growth stimuli. High MYC expression was observed for many different human cancers, like colorectal and pancreatic cancer, or B- and T-cell lymphoma (Dang 2012; Vita and Henriksson 2006).

As a transcription factor, MYC regulates cellular growth and proliferation (Dang et al. 2006; Trumpp et al. 2001) and plays an indispensable role in embryonic development as homozygous deletion of MYC or NMYC result in an embryonic lethal phenotype in mice (Davis et al. 1993; Dubois et al. 2008; Trumpp et al. 2001).

The fact that MYC is so frequently deregulated in many different human cancer types, which goes hand in hand with aggressiveness of the tumor, underlines the importance of finding strategies to target the MYC protein for targeted cancer treatment.

Hence, the question what are characteristics of cancer and how cancer formation occurs will be addressed in the following paragraphs to understand the mechanisms underlying MYC deregulation.

1.2 Hallmarks of cancer

According to the World Health Organization, 9.8 million people have died from cancer worldwide only in 2018, making about 17% of all deaths, with the highest death rate resulting from lung, colorectal, stomach, liver, and breast cancer (status: 12.09.2018; https://www.who.int/news-room/fact-sheets/detail/cancer). These numbers highlight the importance of better understanding the biological mechanisms underlying tumor formation and progression and of using this knowledge to find new strategies for targeted cancer treatment.

Basic characteristics of cancer were described earlier by Hanahan and Weinberg as initial six hallmarks of cancer as the sustainment of proliferative signaling, the evasion of growth suppressors, and the resistance to cell death, as well as the induction of angiogenesis, the activation of invasion and metastasis, and the replicative immortality (Hanahan and Weinberg 2000). Recently, the deregulation of cellular energetics, genome instability and mutations, as well as the avoidance of immune destruction and tumor-promoting inflammation were added to the hallmarks of cancer (Hanahan and Weinberg 2011).

Having identified these common hallmarks of cancer opens action points for the therapeutic targeting of many different cancer types (Hanahan and Weinberg 2011). Furthermore, it also clarifies why certain proteins function as oncogenes or tumor suppressors - their functions promote or avoid one or several of these hallmarks of cancer, and so does MYC.

1.3 MYC target genes

The transcription factor MYC regulates genes playing a role in several of the described cancer hallmarks: MYC influences cellular growth via a crosstalk with the mTOR pathway, which results in enhanced eIF4E expression, the limiting factor for translation initiation (Lin et al. 2008). eIF4E was shown to be necessary for cancer cell growth, especially in MYC-driven lymphomas (Pourdehnad et al. 2013), highlighting a function of MYC in linking high transcription levels to high translation levels via an increase in mRNA capping (Elkon et al. 2015; Lombardi et al. 2016).

In addition to translation initiation factors, MYC directly promotes transcription of ribosomal proteins and ribosome biogenesis factors, which leads to an increased availability of the translation machinery. This is confirmed by the finding that MYC high affinity target genes encode for proteins functioning in ribosome structure and biogenesis, cellular biosynthetic processes, translation, and RNA binding (Lorenzin et al. 2016).

At first, E-boxes (CACGAG) were identified as MYC binding sites on chromatin. However, MYC was shown to bind to almost all open promoters, as determined by RNA polymerase II (RNAPII) occupancy and histone marks (Blackwell et al. 1990; Blackwell et al. 1993; Blackwood and Eisenman 1991; Guccione et al. 2006; Walz et al. 2014).

There are two opposing models explaining how MYC influences transcription: the "general amplifier" model postulates that MYC acts as a general promoter of transcription resulting in the global upregulation of all genes actively transcribed within the corresponding cell type (Lin et al. 2012; Nie et al. 2012), while the second model hypothesizes that MYC acts as the regulator of a specific set of genes namely MYC target genes (Horiuchi et al. 2012; Kawauchi et al. 2012; Kress, Sabo, and Amati 2015; Muhar et al. 2018; Pelizzola et al. 2015; Sabo et al. 2014). So how MYC exactly regulates the transcriptome of a cell is still under debate, but that MYC has a strong impact on transcription mainly by RNAPII is commonly acknowledged and was globally analyzed (Rahl et al. 2010; Rahl and Young 2014; Walz et al. 2014).

Besides its function in cellular growth, MYC was shown to influence the cellular metabolism, the cell cycle, and signal transduction. MYC was determined as one of the initial factors needed for the generation of induced pluripotent stem cells (iPS) (Takahashi and Yamanaka 2006), emphasizing a crucial role in stem cell maintenance and cell differentiation. Furthermore, MYC upregulation also influences cell adhesion, genomic stability, apoptosis and angiogenesis (Adhikary and Eilers 2005; Arnold and Watt 2001; Baudino et al. 2002; Cole and Cowling 2008; Dang 2012; Eilers and Eisenman 2008; Felsher and Bishop 1999b; Frye et al. 2003; Iritani and Eisenman 1999; Johnston et al. 1999; Mai et al. 1999; Meyer and Penn 2008). Comparing data obtained from tissue cell culture with *in vivo* studies suggests, that MYC also plays a role in tumor recognition and infiltration by the immune system (Schlee et al. 2007; Swaminathan et al. 2020).

Summarizing what is known about target genes of MYC, it becomes obvious that MYC and MYC target genes play a role in many of the above-mentioned hallmarks of cancer (Dang et al. 2006; Dang 2012; Gabay, Li, and Felsher 2014; Rahl and Young 2014; Vita and Henriksson 2006).

So, it is known that MYC influences transcription of RNAPII, but what the mechanistical details are and which proteins are involved in addition, had not been investigated on a global scale so far. Through its target genes and its high transcriptional amplification, MYC could be linked to several hallmarks of cancer, characteristics which make up a tumor. But what mechanistic events are necessary for tumor formation leading to these hallmarks and how does MYC get deregulated?

1.4 The biology of tumor formation

Cancer occurs from transformed cells in which tumor suppressors have become unfunctional and proto-oncogenes have become activated. The most prominent and most studied example for a tumor suppressor is p53, also named “the guardian of the genome”. Upon DNA damage p53 is expressed and in turn induces expression of p21, which leads to a cell cycle arrest (el-Deiry et al. 1993; Xiong et al. 1993), a crucial step enabling correct DNA repair and thus avoiding spreading of DNA mutations through cell division. If the DNA damage burden is too high or unrepairable, high p53 expression levels induce apoptosis. In many human cancers the p53 gene has been found to be mutated resulting in a non-functional p53 protein (Olivier, Hollstein, and Hainaut 2010). Consequently, DNA mutations are not repaired, which can promote tumorigenesis. So, inactivation of p53 is a mechanism to escape apoptosis, including MYC-induced apoptosis, and goes along with high mutational burden, both described as hallmarks of cancer.

Many tumors are characterized by the activation of the proto-oncogenes Ras and Raf, both belonging to the MAP-kinase pathway. The MAP-kinase pathway is stimulated by external growth stimuli and downstream transcription factors are activated resulting in cellular growth, proliferation, and differentiation. Mutations of the proteins Ras and Raf result in constitutive hyper activation of the MAP-kinase pathway. For example, deregulation of the MAP-kinase pathway through the BRAF V600E mutation is currently treated with a combinatorial treatment inhibiting several components of the deregulated signaling cascade, namely BRAF itself, the EGF receptor (EGFR) and the kinase MEK, also important within the MAP-kinase pathway and downstream of BRAF within the signaling cascade (Corcoran et al. 2018; Ducreux et al. 2019; Kopetz et al. 2019; Lee et al. 2019; Ursem, Atreya, and Van Loon 2018). This combinatorial treatment aims to reduce the occurrence of mutations, which would circumvent the treatment. This is one example for targeted therapy based on mutations found in the patient in contrast to chemotherapy, which targets fast dividing cells independent of their mutational status.

These were two examples for a tumor suppressor and a proto-oncogene, respectively, leading to tumor formation, and which therapies are currently used for treatment. So how could this be applied to the proto-oncogene MYC in particular?

1.5 MYC upregulation in cancer

As mentioned above, very high MYC levels are characteristic for many different tumors and several mechanisms leading to MYC upregulation have been described (Schaub et al. 2018).
One mechanism is disturbing MYC's protein stability control by mutations within the MYC protein itself. MYC is a very unstable protein with a half-life of only 20 min and tightly regulated through degradation via the ubiquitin-proteasome system. However, certain mutations of know phosphorylation sites, recognized by ubiquitin transferring ligases, are described to affect MYC's half-life. Namely mutations in Threonine 58 (T58) and Serine 62 (S62) affect MYC protein stability by priming MYC for degradation by the ubiquitin-proteasome system. S62 gets phosphorylated by ERK downstream of the Ras/Raf/MAPK signaling cascade and MYC-pS62 first of all leads to protein stabilization upon mitotic growth stimuli leading to cell cycle entry and mitosis. MYC-pS62 is primed for further phosphorylation at T58 by GSK3β (glycogen synthase kinase 3) (Gregory and Hann 2000; Gregory, Qi, and Hann 2003; Lutterbach and Hann 1994). MYC-pT58-pS62 is recognized by PIN1 (prolyl isomerase) recruiting PP2A (protein phosphatase 2A), which de-phosphorylates MYC at S62 (Yeh et al. 2004). MYC-pT58 is finally recognized by the E3-ligase FBXW7 (F-box/WD repeat containing 7) leading to MYC's ubiquitination and its proteasomal degradation (Welcker, Orian, Grim, et al. 2004). Counteractors of FBXW7 are USP28 and USP36, which facilitate the de-ubiquitination of MYC (Diefenbacher et al. 2014; Popov, Herold, et al. 2007; Popov, Wanzel, et al. 2007; Sun, He, et al. 2015).
To escape this tight regulation, cancer cells often exhibit a mutation in T58 (Bahram et al. 2000; Bhatia et al. 1993; Hemann et al. 2005) or an inactivating mutation in the E3-ligase FBXW7 (Akhoondi et al. 2007; Welcker, Orian, Grim, et al. 2004; Welcker, Orian, Jin, et al. 2004; Yada et al. 2004). Like this, the MYC protein cannot be targeted for degradation by the ubiquitin-proteasome system anymore resulting in higher MYC protein levels within the cell.

Despite expectations of an oncogene found to be upregulated in the majority of human cancers, the MYC protein is rarely found to be mutated. On contrary, chromosomal translocation, gene amplification, or mutations in upstream pathways are frequently described for MYC.
The first mechanism leading to high MYC protein levels was discovered in Burkitt's lymphoma: here the *MYC* gene gets activated by chromosomal translocation (Dalla-Favera et al. 1982; Neel et al. 1982; Taub et al. 1982). Through this translocation, the *MYC* gene becomes

regulated by the IgG promoter, highly expressed in B-cells and resulting in very high MYC expression, which itself is sufficient for tumor formation in this type of cancer (Felsher and Bishop 1999a).

The second and most common mechanism for MYC upregulation in solid tumors is gene amplification: cancer cells often harbor karyotypical abnormalities, including several copies of the *MYC* gene originally located on chromosome 8 (Meyer and Penn 2008; Vita and Henriksson 2006). Amplifications of the *MYC* gene were found in several solid tumor entities, like leukemia (Collins and Groudine 1982; Dalla-Favera, Wong-Staal, and Gallo 1982), colorectal carcinoma (Alitalo et al. 1983; Finley et al. 1989), osteosarcoma (Squire et al. 2003), or breast carcinomas (Blancato et al. 2004; Chrzan et al. 2001; Escot et al. 1986; Singhi et al. 2012), and correlate with MYC protein overexpression (Blancato et al. 2004).

The third mechanism in how MYC gets upregulated is the secondary upregulation through deregulated, upstream signaling pathways like the MAP-kinase pathway or the WNT pathway (He et al. 1998; Myant and Sansom 2011; Tuupanen et al. 2009; Yochum, Cleland, and Goodman 2008). The WNT-β-catenin pathway is constantly activated in the majority of colorectal cancers (CRCs) leading to the accumulation of β-catenin (Ahmed et al. 2013; Reya and Clevers 2005; Sebio, Kahn, and Lenz 2014; Wanitsuwan et al. 2008), which results in increased MYC expression (He et al. 1998).

The fact that tumors employ so many mechanisms to upregulate MYC, suggests selective advantages for tumor cells expressing high MYC levels and opens the question if high MYC expression is necessary for the tumor to grow or in other words if targeting MYC is a promising strategy for cancer treatment and might lead to tumor growth arrest or even regression.

1.6 MYC addiction of tumors

As so many tumors show MYC upregulation, the dependency of tumors on high MYC levels (MYC addiction) was investigated in several cancer models (Felsher 2010). Upon MYC depletion in mice, no tumor formation occurred anymore even after the constant activation of the WNT pathway in a colorectal cancer model, highlighting MYC in being essential in upregulating most of downstream WNT target genes (Sansom et al. 2007; Athineos and Sansom 2010). Also in pancreatic cancer it was shown that synergistic inhibition of ERK1/2 and ERK5 results in a strong decrease in MYC protein levels and in inhibition of tumor growth (Vaseva et al. 2018).

In a mouse model, in which human MYC expression is under the control of a Tet-Off-System (EµSR-tTA), constant overexpression of MYC in hematopoietic cells resulted in the formation of T-cell lymphomas and acute myeloid leukemia, which regressed when MYC expression was switched off (Felsher and Bishop 1999a). Further investigations showed that MYC activation lead to chromosomal instability and that tumor regression after MYC inactivation was due to increased apoptosis as well as cell differentiation (Marinkovic et al. 2004). In another study, the same mouse model was used to investigate MYC-dependent osteosarcoma formation (Jain et al. 2002). Temporary inactivation of the MYC transgene resulted in a decreased proliferation rate and in the differentiation of immature osteoblasts. Upon reactivation of MYC expression these cells underwent apoptosis (Jain et al. 2002).

In summary, these studies highlight that MYC overexpression is crucial for tumor formation, as shown for colorectal cancer, pancreatic cancer, T-cell lymphoma, as well as osteosarcoma. But more importantly, even the temporal loss of MYC *in vivo* leads to proliferation arrest of the tumor, followed by either differentiation or apoptosis of the tumor cells. These data provide clear evidence for MYC being a bona fide cancer target.

Identification of different target gene sets being regulated by different MYC levels as determined by different promoter affinities (Lorenzin et al. 2016) and the fact that mice with heterozygous loss of the *MYC* gene are viable (Trumpp et al. 2001) suggest that there is a therapeutic window for targeting oncogenic MYC. This hypothesis was promoted by the development of Omo-MYC. Omo-MYC is a protein consisting of the C-terminal part of MYC (Soucek et al. 2002; Soucek, Nasi, and Evan 2004; Soucek et al. 2008). Like this, Omo-MYC is still able to bind MYC's partner protein the MYC-associated factor X (MAX) and thus, it competes with endogenous MYC for MAX binding (Jung et al. 2017; Savino et al. 2011). Without MAX, MYC cannot bind to promoters of its target genes nor stimulate their transcription. Furthermore, Omo-MYC was shown to form homodimers, which occupy MYC binding sites on chromatin but do not activate MYC target gene transcription, since Omo-MYC is lacking the transactivation domain (TAD). Heterodimers between MYC and Omo-MYC have not been observed. Adding Omo-MYC to cancer cells resulted in significant lowering of MYC's oncogenic function, as well as lower proliferation rates of tumor cells. The potential of Omo-MYC was also studied *in vivo*: the treatment of mice suffering from different tumor entities, including adenocarcinoma, glioblastoma and pancreatic tumors, with Omo-MYC resulted in significant tumor growth arrest, lessened tumor volume and prolonged survival

(Annibali et al. 2014; Beaulieu et al. 2019; Sodir et al. 2011; Soucek et al. 2008; Soucek et al. 2013). Furthermore, it highlighted that MYC inhibition within an adult mouse does not impair its well-being.

A central point of MYC's oncogenic function is in promoting transcription of its target genes related to cellular growth and proliferation. Therefore, MYC interacts with and activates the transcription machinery. To elucidate, how MYC can influence target gene expression, its basic structural components need to be discussed.

1.7 MYC domain structure and DNA binding

The MYC family proteins share conserved sequences named as MYC-boxes 0-IV (MB0-IV), illustrated in Figure 1.1. These conserved MBs as well as the overall comparable domain architecture between the three MYC family members suggest overlapping functions, indicated by the alternative expression pattern within different cell types. Therefore, identifying MYC interacting proteins critical for the modulation of the transcription machinery would most likely be applicable for all MYC family members. Especially finding interaction partners of MYC binding to conserved MBs would suggest similar binding to NMYC and LMYC. Some interaction partners had already been described for MYC, but only few are structurally resolved and there are only few analyses performed to identify MYC interacting proteins on a global scale.

MBI and MBII comprise the N-terminal TAD important for MYC's function in cellular transformation and the induction of apoptosis (Cowling and Cole 2006; Kato et al. 1990; Stone et al. 1987; Bar-Ner et al. 1992). In between MBIIIa and MBIIIb a so-called PEST-domain enriched for proline (P), glutamic acid (E), serine (S), and threonine (T), important for MYC protein stability and degradation has been identified. PEST-domains are known to destabilize proteins and for example the green fluorescent protein (GFP) fused with a PEST-domain has a shorter half-life than the wildtype form (Gregory and Hann 2000; Herbst et al. 2004; Salghetti, Kim, and Tansey 1999). MBIIIa is absent in LMYC and was found to bind to histone deacetylases (HDACs) (Herbst et al. 2004; Herbst et al. 2005; Kurland and Tansey 2008). WDR5 is a transcription factor, which was shown to recruit MYC to its target genes by interacting with MBIIIb (Thomas, Wang, et al. 2015; Thomas et al. 2019; Thomas et al. 2020) (see section 1.12). Within MBIV there is the nuclear localization signal (NLS) ensuring MYC being transported into the nucleus (Dang and Lee 1988).

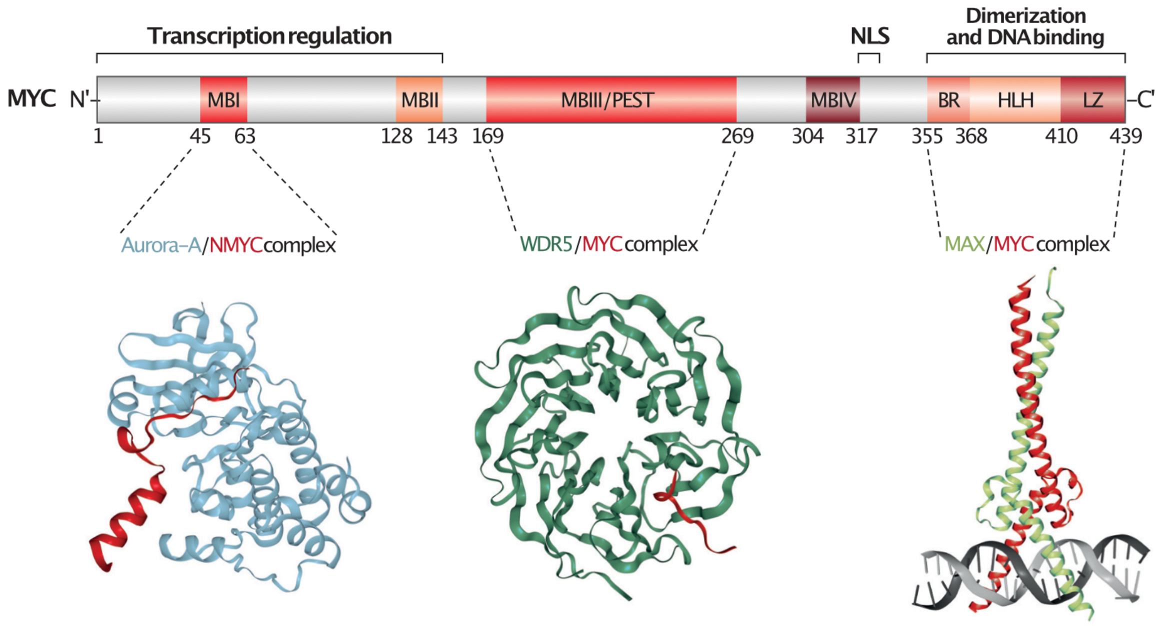


Figure 1.1: MYC domain structure

Top: MYC protein is shown with conserved MYC boxes (MB) highlighted in red colours. Numbers below indicate amino acids of human c-MYC. MB0, which is located N-terminally of MBI, is not annotated. Below: three protein structures have been resolved in complex with MYC, namely AURKA, WDR5, and MAX.

From (Wolf and Eilers 2020).

The C-terminal region of MYC comprising the basic region (bR) and the helix-loop-helix leucin zipper (HLH-LZ) binds to MAX and forms an α-helix structure (Figure 1.1) (Blackwood and Eisenman 1991; Dang, McGuire, et al. 1989; Dang, van Dam, et al. 1989; Ferre-D'Amare et al. 1993; Ferre-D'Amare et al. 1994; Murre, McCaw, and Baltimore 1989; Murre et al. 1989; Nair and Burley 2003). The MYC-MAX heterodimer binds to chromatin and MAX was shown to be necessary for MYC's binding to DNA (Amati et al. 1992; Amati, Brooks, et al. 1993; Amati, Littlewood, et al. 1993; Blackwood and Eisenman 1991; Blackwood et al. 1991; Kretzner, Blackwood, and Eisenman 1992b, 1992a; Littlewood et al. 1992).

The C-terminal part of MYC is also involved in binding the MYC-interacting zinc finger 1 (MIZ1) (Peukert et al. 1997; Schneider et al. 1997). Binding of MIZ1 to the MYC-MAX heterodimer is linked to transcriptional repression by MYC (Herold et al. 2002; Walz et al. 2014; Wiese et al. 2013; Wiese et al. 2015; Wolf et al. 2013). The MIZ1-MYC-MAX complex was shown to recruit histone methyltransferases (HMTs) and HDACs, both favoring closing of the chromatin structure and repression of transcription at these loci (Brenner et al. 2005; Kurland and Tansey 2008).

To find out, how MYC can interact with the transcription machinery, details of the transcription cycle and the involved proteins will be described.

1.8 Basic mechanisms of transcription

MYC is involved in the transcriptional regulation of genes transcribed by all three RNA polymerases (Arabi et al. 2005; Dang 2012; Felton-Edkins et al. 2003; Gomez-Roman et al. 2003; Grandori et al. 2005; Luscher and Vervoorts 2012; Steiger et al. 2008; van Riggelen, Yetil, and Felsher 2010). But besides effects on RNAPI and RNAPIII, MYC most importantly affects transcription by RNAPII. There are several publications in how MYC affects the different steps of the transcriptional process of RNAPII, which will be discussed in the following paragraphs.

Transcription of messenger RNAs (mRNAs) encoding for proteins is carried out by RNAPII. RNAPII consists of 12 subunits namely RPB1-12 encoded by *POLR2A-L* (Figure 1.2.A and B). Only the complete assembled holoenzyme gets transported into the nucleus, the place of mRNA generation (Wild and Cramer 2012). The two largest subunits, RPB1 and RPB2, form a cleft-like structure around the DNA comprising the active center.

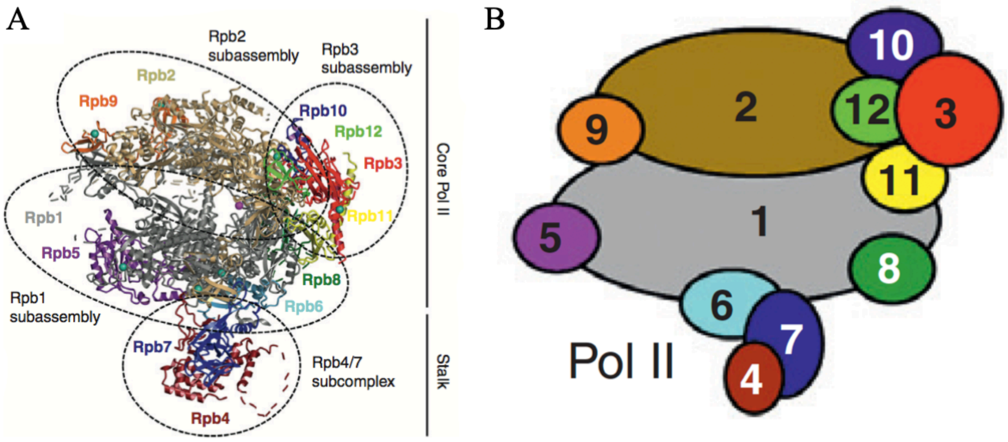


Figure 1.2: RNA polymerase II composition and chromatin association.
***A**. Crystal structure of the RNAPII complex (Wild and Cramer 2012).*
***B**. Schematic overview of the RNAPII subunits (Wild and Cramer 2012).*

Depending on the transcriptional state, RNAPII interacts with different proteins, named as initiation, elongation, and termination factors. Their association with RNAPII is predominantly mediated by the action of several transcription-related kinases and phosphatases acting on RNAPII itself as well as on the associated factors. RPB1 has an extended, unstructured C-terminal domain (CTD) consisting of 52 repeats of the heptapeptide YSPTSPS in humans, which gets phosphorylated by specific kinases shaping a platform for the interaction with various factors (Figure 1.3.A) (Buratowski 2009; Cheung and Cramer 2012; Feaver, Gileadi, and Kornberg 1991; Harlen and Churchman 2017a; Heidemann et al. 2013; Jonkers and Lis 2015; Lee and Greenleaf 1989; Payne and Dahmus 1993; Shandilya and Roberts 2012; Spencer and Groudine 1990; Svejstrup 2004; Zhang and Corden 1991a, 1991b).

The transcription cycle is depicted in Figure 1.3.B. First, unphosphorylated RNAPII is recruited to the open promoter by general transcription factors (GTFs) forming the pre-initiation complex (PIC). One of those factors, the general transcription factor II H (GTFIIH), harbors a helicase activity needed for scanning for the transcriptional start site (TSS), as well as the kinase subunit CDK7 responsible for the phosphorylation of the serine residue at position five in the heptapeptide (Ser5) of the RNAPII CTD. Phosphorylated Ser5 (pSer5) is used as a marker for initiating RNAPII (Figure 1.3.A) (Buratowski 1993; Drapkin et al. 1994; Ebmeier et al. 2017; Flores, Lu, and Reinberg 1992; Greber et al. 2017; Greber and Nogales 2019; Kolesnikova, Radu, and Poterszman 2019; Lu et al. 1992; Malik, Molina, and Xue 2017; Parvin and Sharp 1993; Peissert et al. 2020; Rimel and Taatjes 2018; Roy et al. 1994; Schaeffer et al. 1993).

For promoter escape, the GTFs are released and replaced by different factors. As shown by crystal structures, factor II F (GTFIIF) gets replaced by the negative elongation factor (NELF), and factor II E (GTFIIE) by the DRB-sensitivity inducing factor (DSIF), consisting of SPT4 and SPT5. This constitution of RNAPII associated factors results in a promoter-proximal pausing 60-100 nucleotides (nt) downstream of the TSS (Adelman and Lis 2012; Marshall and Price 1995). In profiles of RNAPII chromatin immunoprecipitation followed by deep sequencing (ChIPseq), through which the genome-wide position of a DNA-bound protein of interest is annotated, promoter proximal pausing is visible as a peak shortly after the TSS (compare Figure 1.3.A) (Core et al. 2012).

Promoter-proximal pausing gets released by the positive elongation factor b (P-TEFb), consisting of cyclin T1 or T2 and the kinase CDK9 (Marshall and Price 1995; Marshall et al. 1996; Peterlin and Price 2006; Svejstrup 2004). CDK9 does not only phosphorylate the Ser2 residue of the CTD (pSer2), a mark for elongating RNAPII (Figure 1.3.A), but also NELF and the SPT5 subunit of DSIF. Phosphorylation of NELF results in its dissociation from RNAPII, liberating binding surface on RNAPII, which enables the recruitment of elongation factors, for example the polymerase-associated factor complex (PAFC) and the elongation factor SPT6 (Bernecky, Plitzko, and Cramer 2017; Ehara et al. 2017; Farnung, Vos, and Cramer 2018;

Peterlin and Price 2006; Vos, Farnung, Boehning, et al. 2018; Vos, Farnung, Urlaub, et al. 2018; Wada, Takagi, Yamaguchi, Watanabe, et al. 1998). In contrast to NELF, the phosphorylation of SPT5 does not release it from RNAPII, but provokes structural changes converting DSIF into a positive elongation factor staying attached to RNAPII (Peterlin and Price 2006).

During the elongation phase, the factor GTFIIS suppresses backtracking of RNAPII and the so-called facilitates chromatin transcription (FACT) complex, consisting of SPT16 and SSRP1, conveys removal of nucleosomes (Campbell et al. 2019; Dutta et al. 2015; Ehara et al. 2017; Elmendorf et al. 2001; Farnung, Vos, and Cramer 2018; Feng et al. 2016; Labhart and Morgan 1998; Marciano et al. 2018; Pavri et al. 2006; Sheridan et al. 2019; Xu et al. 2017; Zatreanu et al. 2019).

Once the poly adenylation site (PAS) is passed, the association of RNAPII to chromatin is loosened and transcription rate is slowed down. Polyadenylation and cleavage specificity factors (CPSFs) lead to cleavage of the nascent mRNA. There are two models of transcriptional termination discussed in the field: the torpedo model and the allosteric model. According to the torpedo model, the exoribonuclease XRN2 degrades extruding nascent RNA from the uncapped 5’end after cleavage by the CPSFs. Once XRN2 reaches RNAPII, RNAPII is released from chromatin (Fong et al. 2015). According to the allosteric model, weakened interaction between RNAPII and the PAS as well as conformational changes within RNAPII lead to its falling off the gene (Zhang, Rigo, and Martinson 2015).

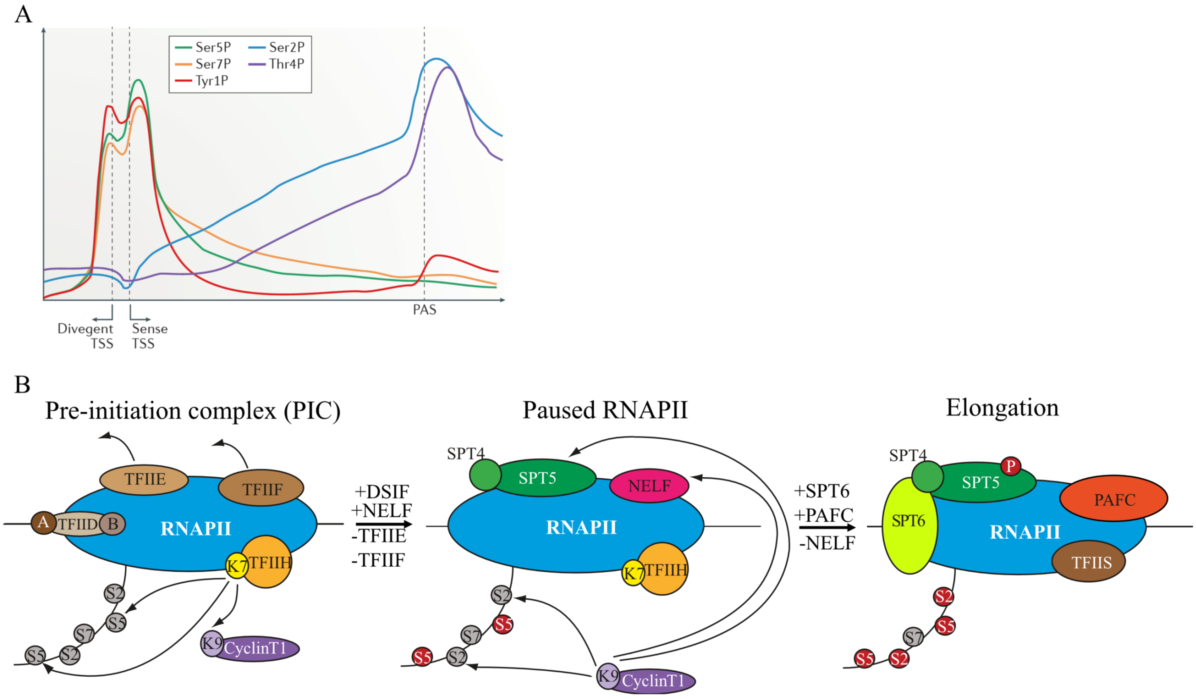


Figure 1.3: The transcription cycle.

***A**. RNAPII occupancy on chromatin at different regions within the gene. Different colour depicts different phosphorylation status of the CTD of RNAPII (Harlen and Churchman 2017a).*

***B**. Schematic overview of the transcription cycle. RNAPII (blue) gets recruited to the promoter in an unphosphorylated state by general transcription factors (shades of brown). They built up the so-called pre-initiation complex (PIC). The kinase subunit CDK7 (yellow) of TFIIH phosphorylates Ser5 of the CTD of RNAPII. Upon promoter escape, the general TFs are released from RNAPII and DSIF (green) and NELF (pink) bind to RNAPII resulting in promoter-proximal pausing of RNAPII. Pausing is released by phosphorylation of SPT5, NELF and Ser2 (CTD) by the CDK9 subunit of P-TEFb (purple). The release of NELF enables binding of the PAFC (orange), SPT6 (light green), and TFIIS (brown). Phosphorylation events are depicted in red. The termination process is not shown. To reduce complexity only selected factors and RNAPII-interactors are depicted.*

TSS: transcriptional start site; PAS: poly adenylation site

1.9 The role of SPT5 within the transcription cycle

In this study, the elongation factor SPT5, the large subunit of DSIF, was identified as a novel interactor of MYC. Therefore, its biological function within the transcription cycle will be illustrated in greater detail:

DSIF was discovered as a complex of the two proteins SPT4 and SPT5 in humans in 1998 (Wada, Takagi, Yamaguchi, Ferdous, et al. 1998). At that moment, *SPT* genes were known to affect Ty-mediated repression in *Saccharomyces cerevisiae* (Winston et al. 1984). SPT4 is a zinc finger protein of 14 kDa and the small subunit of DSIF (Hartzog et al. 1996; Malone, Fassler, and Winston 1993). SPT5, the large subunit of DSIF with 130 kDa in size, is conserved in all kingdoms of life (Swanson, Malone, and Winston 1991). It has an N-terminal acidic region followed by the conserved NGN-domain, which is evolutionary related to the bacterial NusG protein and necessary for the binding of SPT4 (Hartzog and Winston 1997). The NGN-SPT4 interaction has been structurally resolved (Wenzel et al. 2009) (see also Figure 1.4.A and B). Furthermore, SPT5 harbors five KOW (Kyprides, Ouzounis, Woese) domains, whose structures are resolved in complex with RNAPII (Bernecky, Plitzko, and Cramer 2017; Ehara et al. 2017; Guo et al. 2008; Yamaguchi et al. 1999) (Figure 1.4.A and C). The C-terminal repeat region (CTR) is unstructured and a target for phosphorylation by transcription-related kinases.

First, DSIF was described as a pausing factor since it was found to be associated to promoter proximal paused RNAPII. Later SPT5 was found to be a target of CDK9 and to stay attached to RNAPII during elongation (Wada, Takagi, Yamaguchi, Watanabe, et al. 1998). Structural insights into the transcription machinery could uncover structures from the paused RNAPII complex with DSIF and NELF being bound (Vos, Farnung, Urlaub, et al. 2018), as well as an elongating RNAPII complex together with DSIF, SPT6, and the PAFC (Vos, Farnung, Boehning, et al. 2018). These visualized structural changes within the SPT5 protein upon its phosphorylation within the CTR by CDK9 and revealed SPT5 functioning in the stabilization of the closed conformation of elongating RNAPII as well as in re-winding the downstream DNA and in keeping the non-template DNA strand away from the actively transcribing center within RNAPII. SPT5 seems to be necessary for the elongating RNAPII, maintaining its structure and efficiency.

Furthermore, the unstructured CTR of SPT5 comes into close proximity to the exiting nascent mRNA and functions as a platform recruiting mRNA-processing factors, like for example the human capping enzyme (MCE) or splicing factors (Cortazar et al. 2019).

Recently, a function of SPT5 in transcriptional termination was uncovered. At the transcription end site (TES) SPT5 gets de-phosphorylated by the protein phosphatase 1 (PP1) resulting in RNAPII slowing down its transcription rate. The decelerated RNAPII can then be easily caught by the exoribonuclease XRN2, facilitating transcriptional termination and the release of

RNAPII from chromatin in the so called “sitting duck torpedo model” (Cortazar et al. 2019; Parua et al. 2018). Hence, SPT5 plays an essential role in the transcription cycle: not only as initially discovered in promoter-proximal pausing, but also in efficient transcriptional elongation, mRNA maturation, as well as transcription termination.

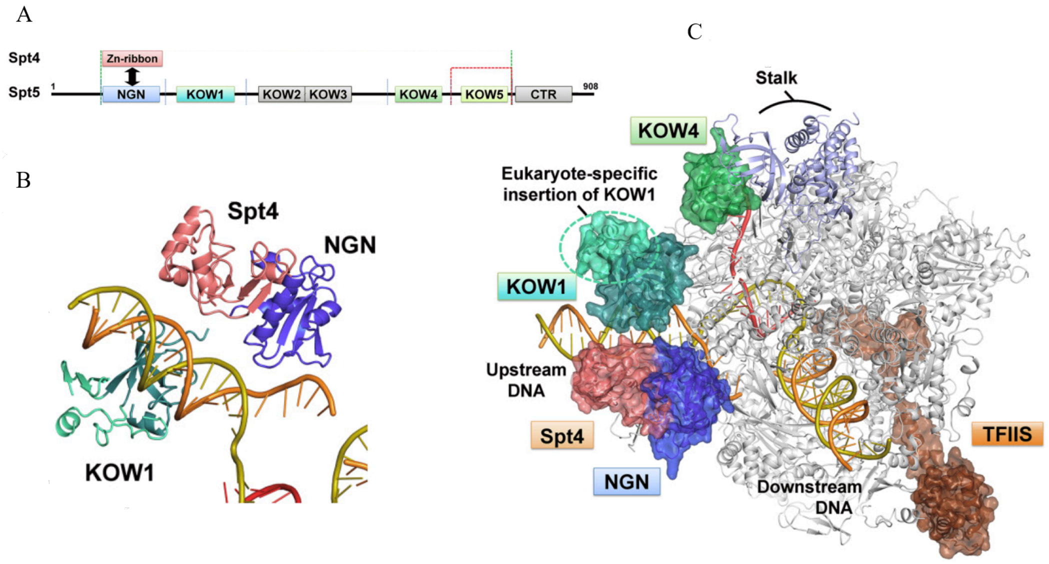


Figure 1.4: Domains and structure of SPT4 and SPT5.

***A**. Schematic depiction of the domains of SPT4 and SPT5.*

***B**. Structure of SPT4 (red) in complex with the conserved NGN-domain of SPT5 (blue) close to DNA (orange and yellow). KOW1 domain of SPT5 is shown in green.*

***C**. Structure of SPT4 (red) and SPT5 (blue and green) bound to RNAPII (grey). TFIIS is shown in brown. DNA is shown in yellow and orange and RNA in red.*

Adapted from (Ehara et al. 2017).

1.10 MYC influences the transcriptional process

Despite MYC has been identified as a proto-oncogene already in the 1970s and since then numerous studies had been performed on MYC, it is still not fully understood yet, how it mechanistically regulates the transcription of its target genes. Several studies have been published highlighting MYC’s impact on different stages of the transcriptional cycle and its interaction with various transcription-related proteins. Therefore, it seems that MYC can influence the transcriptional process at several distinct steps.

1.10.1 MYC and chromatin opening

The transactivating domain of MYC was shown to interact with a variety of different proteins linked to MYC’s transforming activity, for example the Transformation/Transcription Domain

Associated Protein (TRRAP) (Bouchard et al. 2001; McMahon, Wood, and Cole 2000). TRRAP is a large, multidomain protein with a size of approximately 440 kDa. It belongs to the phosphoinositide 3-kinase-related kinase family (PIKK) and is a component of many different chromatin remodelling complexes, including the NuA4, the STAGA and a SWR1-like complex (Allard et al. 1999; Brand et al. 1999; Cai et al. 2003; Doyon and Cote 2004; Doyon et al. 2004; Elias-Villalobos, Fort, and Helmlinger 2019; Martinez et al. 2001; Sharov et al. 2017; Vassilev et al. 1998; Zhang et al. 2014). TRRAP functions as an adapter protein to recruit histone acetyltransferases (HATs) to chromatin, to open up chromatin and facilitate transcription, or to enable DNA repair. Furthermore, it was shown to play an important role in glioblastoma (Wurdak et al. 2010).

TRRAP was shown to interact with MYC, more precisely with MBII (Buchel et al. 2017; Feris, Hinds, and Cole 2019; Frank et al. 2003; Kalkat et al. 2018; Liu et al. 2003; McMahon et al. 1998; McMahon, Wood, and Cole 2000; Nikiforov et al. 2002; Park et al. 2001; Park, Wood, and Cole 2002; Tu et al. 2015). Like this, MYC recruits HATs to chromatin via TRRAP to open up chromatin and facilitate transcription of its target genes (Bouchard et al. 2001; Frank et al. 2003; McMahon, Wood, and Cole 2000; Wood et al. 2000).

Via TRRAP GCN5 (*KAT2A*), a component of the STAGA co-activator complex, is recruited, which acetylates histone H3 at several positions (K9/K14/K18) (Knoepfler et al. 2006; Liu et al. 2003; McMahon, Wood, and Cole 2000). TIP60 (*KAT5*) as well as TIP48 (*RUVBL2*), TIP49 (*RUVBL1*) and BAF53 (*ACTL6A*) are components of the NuA4 complex also recruited by TRRAP. They acetylate histone H4 at lysines K5, K8 and K12 (Frank et al. 2003; Martinato et al. 2008). The acetylases p300 (*EP300*) and CBP (*CREBBP*) are also known to be recruited by MYC and to activate transcription (Vervoorts et al. 2003).

The SWI/SNF (SWItch/Sucrose NonFermentable) complex is a chromatin remodeling complex, implicated in the regulation of chromatin looping and chromatin accessibility (Hodges et al. 2018; Kim, Bresnick, and Bultman 2009; Kim et al. 2009; Ni et al. 2008). There are several SWI/SNF complexes varying in their protein constitution. All complexes have a molecular weight of close to 2 MDa and consist of at least 10 protein subunits. Each complex contains one subunit with a AAATPase function encoded by *SMARCA2* (BRM) or *SMARCA4* (BRG1) (He, Liu, and Tang 2012; Zinzalla 2016).

Components of the SWI/SNF complex are often mutated in human cancers (Biegel, Busse, and Weissman 2014; Kadoch et al. 2013; Shain and Pollack 2013; Zinzalla 2016). The SWI/SNF complex was first described as a tumor suppressor, but now the SWI/SNF complex was also found to promote some cancer types after gain-of-function mutations, highlighting it as a putative target in cancer therapy (Biegel, Busse, and Weissman 2014; Zinzalla 2016). In particular, it seems that upon mutation or loss of one subunit, tumors become dependent on the other subunits of the SWI/SNF complex (Hoffman et al. 2014; Kadoch et al. 2013; Roberts et al. 2002; Wang et al. 2009).

Already in 1999 Cheng and colleagues identified a direct interaction of MYC with the SWI/SNF complex via the subunit INI1 (BAF47) encoded by the *SMARCB1* gene *in vitro* and *in vivo* (Cheng et al. 1999). This interaction was not mediated by MYC's TAD domain, but by its bR-HLH-LZ region, which is known to bind MAX and is important for DNA binding of MYC (Cheng et al. 1999; Sammak et al. 2019; Stojanova et al. 2016). Here opposing studies exist claiming either that there is no interference of the MYC-INI1 interaction with the MYC-MAX interaction (Stojanova et al. 2016) or a competition of INI1 and MAX for MYC binding, resulting in abolished DNA binding for the MYC-INI1 complex (Sammak et al. 2019).

INI1 was described as a tumor suppressor and found to be deleted in different cancer types (Biegel et al. 1999; Biegel, Busse, and Weissman 2014; Grand et al. 1999; Kadoch et al. 2013; Klochendler-Yeivin et al. 2000; Roberts et al. 2002; Versteege et al. 1998; Wilson and Roberts 2011). MYC and INI1 were shown to have common binding sites on chromatin with the major proportion being within promoter regions. The common target genes of MYC and INI1 have functions in translation. Upon INI1 overexpression an opposing effect on MYC's function in transcription regulation and cellular transformation was observed resulting in lower cell proliferation rates (Stojanova et al. 2016). This suggests an antagonistic effect of MYC and INI1 on MYC-regulated genes (Kadoch et al. 2013; Weissmiller et al. 2019).

In contrast to the tumor suppressive outcome of the INI1-MYC interaction, a tumor promoting function was proposed for BRG1 in upregulating MYC expression in leukemia (Shi et al. 2013). However, others reported an antagonistic function of BRG1 and MYC on target gene expression in different cancer entities (Medina et al. 2008; Pal et al. 2003; Romero et al. 2012). This could be due to different compositions of the SWI/SNF complexes involved or to a different mutational background and dissimilar cellular cancer systems used in these divergent studies.

Furthermore, several components of the SWI/SNF complex have been identified in interactomic studies of MYC (Dingar et al. 2018; Kalkat et al. 2018; Koch et al. 2007; Tu et al. 2015).

1.10.2 *MYC and transcriptional initiation*

To investigate the impact of MYC on transcription, the distribution and density of RNAPII within the gene can be analyzed by ChIPseq and different phases of the transcription cycle are analyzed using antibodies specific to a certain phosphorylation status of RNAPII (see section 1.8). But since an increase in RNAPII ChIPseq signal within the gene body can be the result of an increase in initiation or an increase in RNAPII pause release (Ehrensberger, Kelly, and Svejstrup 2013), also nascent RNA needs to be taken into consideration (de Pretis et al. 2017). De Pretis and colleagues re-analyzed data from previously published RNAPII ChIPseq experiments upon acute manipulation of MYC protein levels (de Pretis et al. 2017; Kress et al. 2016; Lin et al. 2012; Nie et al. 2012; Sabo et al. 2014; Walz et al. 2014). They could confirm a positive correlation of MYC occupancy and transcriptional output for MYC activated genes and showed that MYC influences the recruitment and loading of RNAPII on MYC target genes as well as pause release (de Pretis et al. 2017).

One proposed mechanism how MYC affects initiation of transcription is via the mediator complex. MYC was shown to interact with the mediator complex, namely with MED1 and CDK8 (Adhikary and Eilers 2005; Bouchard et al. 2004; Eberhardy and Farnham 2001, 2002). The mediator complex, a huge complex of up to 26 subunits and more than 1 MDa in size, was discovered in yeast (Flanagan et al. 1991; Kelleher, Flanagan, and Kornberg 1990). It mediates the effects of transcriptional activators and repressors by forming a loop between enhancers, the transcriptional promoter, and several components of the PIC (Uthe, Vanselow, and Schlosser 2017), thereby majorly affecting transcriptional initiation of RNAPII.

Additionally, an interaction of MYC (MB0) with GTFIIF was reported (Kalkat et al. 2018). GTFIIF is a component of the PIC and involved in RNAPII recruitment and initiation (see Figure 1.3).

1.10.3 *MYC and transcriptional pause release*

The lab of Richard Young performed RNAPII chromatin immunoprecipitation followed by genome-wide sequencing and calculated the traveling ratio (TR), defined as the amount of RNAPII at promoter proximal pausing sites divided by the amount of RNAPII within the gene body (Rahl et al. 2010). Using a MYC/MAX inhibitor, which prevents MYC from binding to DNA (Yin et al. 2003), they were the first to describe global MYC-dependent changes of RNAPII behavior on chromatin and upon inhibition of MYC an increase in TR was observed, suggesting that MYC facilitates RNAPII promoter proximal pause release most likely by the recruitment of P-TEFb (Rahl et al. 2010). Furthermore, direct interaction of MYC with CyclinT1 and CDK9 (P-TEFb) was shown in *in vitro* assays and in cell extracts (Eberhardy and Farnham 2001, 2002; Gargano et al. 2007; Kalkat et al. 2018; Kanazawa et al. 2003; Rahl et al. 2010). Like this MYC would reduce RNAPII pausing on all transcribed genes by recruiting P-TEFb (Lin et al. 2012; Nie et al. 2012; Rahl et al. 2010; Rahl and Young 2014). However, as discussed above, this change in TR could not only be the result of effects on pause release, but moreover on RNAPII elongation speed, processivity, or a sign of premature termination (de Pretis et al. 2017; Ehrensberger, Kelly, and Svejstrup 2013).

Another mechanism was proposed through which MYC facilitates RNAPII initiation and pause release at once by recruiting P-TEFb through GTFIIF (Kalkat et al. 2018).

Reported recruitment of the initiation factor GTFIIH (CDK7) or the pause release factor P-TEFb (CDK9) can lead to an increase in CTD phosphorylation of RNAPII at MYC target genes (Bouchard et al. 2004; Cowling and Cole 2007; Eberhardy and Farnham 2001). Similar to MYC, NMYC is reported to positively affect RNAPII promoter escape and pause release (Buchel et al. 2017).

1.10.4 MYC and transcriptional elongation

Several studies linked MYC to RNAPII elongation.

NMYC was recently shown to clear stalled RNAPII complexes at the promoter by recruiting BRCA1 in a USP11-dependent manner (Herold et al. 2019). In addition, NMYC suppressed transcriptional termination at premature PASs (Herold et al. 2019), which was also observed for MYC (Chiu et al. 2018).

Based on the interaction of MYC with the PAFC, which is shown to be favorized when MYC was phosphorylated at T58 and S62 and stabilized by proteasomal inhibition, Jaenicke and colleagues proposed a model, in which the turnover of MYC is necessary for its promoting role in transcription and for the transfer of the PAFC on the elongating RNAPII (Jaenicke et al. 2016). Furthermore, Gerlach et al. could show a PAFC-dependent recruitment of MYC to chromatin and vice versa in Drosophila (Gerlach et al. 2017).

Related to MYC effecting not only transcription initiation, but also elongation, its impact on co-transcriptional pre-mRNA splicing via NUAK1 regulating PP1 activity was observed resulting in MYC-driven tumors being dependent on NUAK1 kinase activity (Cossa et al. 2020).

These publications demonstrated a role of MYC in several steps within the transcriptional cycle of RNAPII. However, there has been no systemic investigation yet, for which of these steps MYC is critical, a question which can be addressed by global studies of the RNAPII interactome and how it is shaped by MYC.

So far, this general impact of MYC on transcription led to the application of general transcriptional inhibitors for the treatment of MYC-dependent cancers. However, using transcriptional inhibitors is rather unspecific and more specific MYC inhibitors are needed for cancer therapy.

1.11 Targeting MYC

MYC is known as being "undruggable" and there is no therapy available for directly targeting MYC so far. This is due to the fact that the MYC protein is mostly unstructured and does not possess any binding pocket as enzymes do. In this aspect, the identification of an interactor could provide structural insights, helpful for drug design.

The interaction of MYC and MAX, necessary for DNA binding, is structurally resolved but difficult to disrupt by a small molecule due to the large interface in between the two proteins (Clausen et al. 2010; Guo et al. 2009; Fletcher and Prochownik 2015; Nair and Burley 2003; Wolf and Eilers 2020). So far, one inhibitor, 10058-F4, is reported to be able to displace MYC from chromatin (Nie et al. 2012; Yin et al. 2003; Zirath et al. 2013). Another option being investigated is the stabilization of MAX homodimers also resulting in lower MYC-occupancy on chromatin (Jiang et al. 2009; Struntz et al. 2019).

Hence, in addition to targeting MYC's DNA-binding, other strategies are examined for indirect MYC targeting. This includes targeting its protein stability, as well as its transcriptional and translational regulation (Wolf and Eilers 2020).

Since MYC upregulates transcription, general transcription inhibitors, like for example THZ1 inhibiting CDK7 or Flavopiridol inhibiting CDK9, show effects in the therapy of MYC amplified tumors by not only decreasing MYC's transcriptional levels, but also decreasing its effect in amplifying transcription (Chipumuro et al. 2014; Christensen et al. 2014; Kwiatkowski et al. 2014; Walsby et al. 2011). These broad, unspecific transcriptional inhibitors have severe side effects. Therefore, it is of primary importance to further characterize MYC's function and to understand how it influences the composition of the transcription machinery.

One more specific transcriptional inhibitor going into the direction of targeted cancer therapy is JQ-1. JQ-1 is a small molecule binding acetylated histones, thereby masking them for the binding by the bromodomain-containing protein 4 (BRD4) (Delmore et al. 2011; Filippakopoulos et al. 2010). BRD4 binds super-enhancers and as MYC expression is under the regulation of such a super-enhancer, JQ-1 also reduces MYC expression (Delmore et al. 2011; Loven et al. 2013). Therefore, JQ-1 is tested for cancer treatment to inhibit transcriptional activation, also in MYC deregulated cancer backgrounds (Cheng et al. 2013; Dawson et al. 2011; Filippakopoulos and Knapp 2014; Henssen et al. 2013; Mertz et al. 2011; Ott et al. 2012; Zuber et al. 2011), but one clinical study using a BET inhibitor already had to be prematurely terminated facing intolerable toxicity (Postel-Vinay et al. 2019).

For the specific reduction of MYC mRNA levels, the usage of antisense oligonucleotides (Giles et al. 1999a, 1999b; Spiller et al. 1998) or siRNAs (Li et al. 2013; Sklar et al. 1991) was investigated, but faced the problem of compound applicability and stability.

Instead of targeting the MYC protein itself, another possibility is to target its function via targeting interacting proteins necessary for MYC's function, like for example WDR5 (see section 1.12).

So, the idea arose to further explore MYC interacting proteins and to find MYC interactors, which could be targeted for cancer therapy instead of directly targeting MYC.

1.12 MYC interactomic studies

Several MYC interacting proteins had been identified so far and few attempts had been made to determine MYC interacting proteins on a global scale to further elucidate the mechanisms underlying MYC's function in the cell (Buchel et al. 2017; Heidelberger et al. 2018; Kalkat et al. 2018; Koch et al. 2007).

Koch and colleagues employed TAP/MudPIT (combination of tandem affinity purification (TAP) with the mass spectral multidimensional protein identification technology (MudPIT)) in DLD1 and HEK293T cells and identified 221 MYC-associated proteins. One of these 221 proteins is FBX29 (*FBXW8*), which was shown to exhibit a negative effect on MYC protein stability. FBX29, as well as the proteins SV40 Large T Antigen (T-ag), DBC1 (*CCAR2*), MCM7, and Mi2β/CHD4 were found to interact either with MBII alone or with MBII in combination with the bR-HLH-LZ region (Koch et al. 2007).

In Büchel et al., based on HA-IP from SH-EP cells engeneered to express HA-tagged NMYC, the PAFC as well as alternating complexes of Aurora kinase A (AURKA) or RAD21, TFIIIC,

and TOP2A are identified and shown to influence the transcription machinery to prevent transcription replication conflicts during the S phase of the cell cycle (Buchel et al. 2017).
In yet another study the ATPase VCP (p97) was identified by SILAC (Stable Isotope Labeling by/with Amino acids in Cell culture) mass spectrometry from U2OS cells expressing GFP-MYC. VCP was demonstrated to facilitate MYC's turnover through the ubiquitin-proteasome system together with HUWE1 (Heidelberger et al. 2018). The E3-ligase HUWE1 (HECTH9) had previously been reported to influence MYC's protein stability and biological activity as well as SCF^{SKP2} (Adhikary et al. 2005; Kim et al. 2003; Peter et al. 2014).
Recently, Kalkat et al. have used proximity-based biotin labelling of MYC-interacting proteins, which allows labelling of proteins in close proximity to MYC within the living cell, in which full-length MYC or MB-deletion mutants were transiently expressed (Kalkat et al. 2018). The results confirmed TRRAP interacting with MBII as previously suggested (Nikiforov et al. 2002), but also identified the general transcription factor GTFIIF binding directly to MB0 and proposed the recruitment of P-TEFb by MYC via GTFIIF (Kalkat et al. 2018).

Some interactors had been identified independent of a cell-wide study and characterized in further detail. One of those is WDR5, which was discovered as a component of the MLL complex responsible for histone H3 methylation (Gori, Divieti, and Demay 2001; Gori, Friedman, and Demay 2006; Guarnaccia and Tansey 2018; Lu et al. 2018). Later it was shown to also belong to the NSL complex involved in histone acetylation (Zhao et al. 2013) as well as to the NuRD (nucleosome remodeling and deacetylase) complex (Bode et al. 2016).
WDR5 is overexpressed in many different cancers (Aho et al. 2019; Neilsen et al. 2018) and depletion in colorectal cancer cells resulted in reduced cell viability and increased sensitivity towards DNA damaging agents. According to these findings, WDR5 itself might serve as a target for cancer treatment, especially in combination with DNA damage inducing therapy (Carugo et al. 2016; Neilsen et al. 2018). Directly targeting the MLL complex using WIN (WDR5 interaction) site inhibitors has been discussed for the treatment of leukemia (Aho et al. 2019; Lu et al. 2018).
Interestingly, WDR5 is reported to interact with several transcription factors, including MYC (Ang et al. 2011; Hayashida 2015; Malek et al. 2017; Schneider and Saur 2016; Thomas, Wang, et al. 2015; Ullius et al. 2014; Wu et al. 2011). The interaction site has been mapped to MBIIIb and a part of MYC's structure in complex with WDR5 could be resolved (Thomas, Wang, et al. 2015) (Figure 1.1). The interaction with WDR5 is conserved for NMYC and LMYC (Sun,

Bell, et al. 2015; Thomas, Wang, et al. 2015). MYC and WDR5 share common binding sites on chromatin with the main proportion comprising promoter regions and by mathematical modeling WDR5 could be assigned as one determinant for MYC's affinity towards DNA binding sites (Lorenzin et al. 2016; Thomas, Wang, et al. 2015). Indeed, treatment with an inhibitor blocking WDR5 binding to chromatin also reduced MYC binding to chromatin and decreased expression of MYC target genes (Aho et al. 2019; Thomas et al. 2019; Thomas et al. 2020). These results indicate a WDR5-dependent recruitment of MYC to its DNA-binding sites and highlight the possibility to treat MYC-dependent tumors indirectly via a MYC-interacting protein, which is necessary for MYC's oncogenic function (Carugo et al. 2016; Chacon Simon et al. 2020; Schneider and Saur 2016; Thomas, Foshage, et al. 2015; Thomas, Wang, et al. 2015; Thomas et al. 2019; Thomas et al. 2020).

Another protein shown to interact with MYC via the conserved MBII is ZNF281 as originally identified by Koch and colleagues (Koch et al. 2007). *ZNF281* encodes for a zinc finger protein also called ZBP-99 or ZFP281. It is a transcription factor and has recently been described as an onco-protein in various different tumor entities and could serve as a prognostic marker. ZNF281 binds GC-rich sequences within many promoters also bound by MYC (Luo et al. 2019).

A third interesting interaction partner of MYC is Aurora kinase A (AURKA), which binds MYC and NMYC preventing them from getting ubiquitinated by the E3-ligase FBXW7 and therefore leading to their protein stabilization (Dauch et al. 2016; Otto et al. 2009; Richards et al. 2016). Targeting AURKA independently of its kinase function showed positive therapeutic effects on tumor growth in NMYC-driven cancers, which led to testing AURKA-inhibitors in clinical trials (Beltran et al. 2011; Brockmann et al. 2013; Gustafson et al. 2014; Otto et al. 2009). Targeting MYC via AURKA might also be possible in c-MYC-driven tumors (Dauch et al. 2016). An interaction with similar outcome has been reported for AURKB, another family member of the Aurora kinase family, and c-MYC (Jiang et al. 2020). AURKB phosphorylates c-MYC at Ser67, which is not conserved in NMYC and which leads to stabilization of the c-MYC protein since the phosphorylation of Thr58 and Ser62, leading to its ubiquitination and subsequent degradation, is impaired. The usage of AURKB inhibitors *in vivo* showed regression in tumors with functional FBXW7 (Jiang et al. 2020).

These examples demonstrate that there is a possibility to target MYC indirectly through an interacting protein necessary for MYC's oncogenic function as shown for WDR5 or AURKA. These two proteins are involved in MYC protein stability or chromatin recruitment, but are not linked to the transcriptional machinery nor do they affect transcription by RNAPII.

To sum up, there had been few attempts in creating a cell-wide picture of MYC-interacting proteins. The performed interactomic studies so far were either based on NMYC or in the presence of a proteasomal inhibitor or without taking into consideration that MYC is strongly bound to chromatin. Using a strategy based on the extraction of chromatin-bound proteins might result in the identification of proteins important for MYC's function on chromatin, which might be also exploited for targeting MYC's transforming ability.

1.13 Objective of the project

The onco-protein MYC is deregulated in the majority of human cancers and high MYC levels are associated with aggressiveness of the tumor. However, no treatment therapies are available for directly targeting the MYC protein. Therefore, it is important to understand MYC's function in greater detail and to identify novel interaction partners to uncover possible points of action for cancer therapy.

The central question of this study was to determine how MYC influences the transcriptional machinery and what other proteins are involved in this mechanism in a global, unbiased way. Since transcription is a chromatin-associated process, the extraction of chromatin-bound proteins from DNA without disrupting protein-protein interactions needed to be implemented. Subsequent quantitative mass spectrometry was performed in order to analyze proteins common in their binding to RNAPII and MYC. Furthermore, different cancer cell lines have been used to study the composition of the transcriptional apparatus in the background of varying MYC levels.

In this thesis following objectives were pursued: first, establishment of a native purification strategy suitable for further validation of protein-protein interactions by quantitative mass spectrometry; second, validation of potential protein candidates resulting from the quantitative mass spectrometry analysis; third, further characterization of the nature of the interaction between MYC and a protein of interest validated beforehand; fourth, investigating the mechanism underlying this interaction and its link to transcriptional regulation.

2 MATERIALS

2.1 Mammalian cell lines, culturing medium and antibiotics

2.1.1 Cell lines

Cell lines were routinely screened for mycoplasma contamination and found negative.

Cell line	**Specification**
HEK293T	Human embryonic kidney cell line, adherent, female (ATCC)
U2OS	Human osteosarcoma cell line, adherent, female (ATCC)
U2OS MYC-Tet-On (W11 clone)	Derived from U2OS single cell clone harboring MYC-Tet-On system (Walz et al. 2014)
T-lymphoma MYC-Tet-Off	Murine T-lymphoma cell line, suspension cells, female, harboring MYC-Tet-Off system (van Riggelen et al. 2010)

2.1.2 Cultivation media and supplements

HEK293T, U2OS (culturing medium)	Dulbecco's Modified eagle's Medium (DMEM; Thermo Fisher Scientific) 10% (v/v) Fetal bovine serum (FBS; Capricorn Scientific GmbH) 1% (v/v) penicillin/streptomycin (Sigma)
T-lymphoma (culturing medium)	RPMI 1640 Medium (RPMI; Thermo Fisher Scientific) 10% (v/v) FBS 1% (v/v) penicillin/streptomycin (Sigma) 1% MEM non-essential amino acids (Thermo Fisher Scientific) 1% L-Glutamine (Thermo Fisher Scientific) 50 µM β-mercaptoethanol (Sigma)
Transfection Medium	Dulbecco's Modified eagle's Medium (DMEM) 2% (v/v) FBS
Freezing Medium	50% (v/v) FBS 40% (v/v) culturing medium 10% (v/v) DMSO

2.1.3 Antibiotics and inhibitors

Item	**Final concentration**	**Company**
5,6-Dichlorobenzimidazole 1-β-D-ribofuranoside (DRB)	100 µM	Sigma
Doxycycline	1 µg/ml	Sigma
Flavopiridol	100 nM	Sigma
Puromycine	2 µg/ml	InvivoGen

2.2 Bacterial strains, culture medium and supplements

2.2.1 Bacterial strains

XL1 blue	Escherichia coli, genotype: recA1, endA1, gyrA96, thi-1, hsdR17, supE44, relA1, lac [F´ proAB lacIqZΔM15 Tn10(Tetr)]; used for amplification of plasmid DNA

2.2.2 Culturing medium and antibiotics

LB medium	10% (w/v) Trypton/Pepton (Roth) 0.5% (w/v) Yeast extract (Roth) 1% (w/v) NaCl (Roth)
LB agar	LB medium supplemented with 1.2% (w/v) Agar-Agar (Roth) Agar was melted by heating and cooled down before addition of antibiotics
Antibiotics (for selection)	100 µg/ml Ampicillin (Roth), final concentration 100 µg/ml Carbenicillin (Roth), final concentration 30 µg/ml Kanamycin (Roth), final concentration

2.3 Stock Solutions and buffers

All buffers and solutions were prepared in Millipore water and stored at RT unless otherwise stated.

All chemicals and solutions were purchased from Roth or Sigma in highest purity levels.

Name	**Ingredients**
Ammonium persulfate (APS, 10%)	5 g APS dissolved in 50 ml water, aliquoted and stored at -20 °C
Ampicillin stock solution (100 mg/ml)	10 g Ampicillin in 100 ml water, sterile filtered, aliquoted and stored at -20 °C
BCA Solution A	1% (w/v) BCA-N_2 2% (w/v) Na_2CO_3
BCA Solution B	4% (w/v) $CuSO_4$
BisTris Buffer 3.5x	1.25 M Bis-Tris, pH 6.7 Stored at 4 °C
BisTris stacking gel	4% (v/v) acrylamide / bisacrylamide 1 x Bis-Tris Buffer 0.05% (v/v) APS 0.01% (v/v) TEMED
BisTris separation gel	8-12% (v/v) acrylamide / bisacrylamide 1 x Bis-Tris Buffer 0.05% (v/v) APS 0.01% (v/v) TEMED
Blocking Solution Fuji	5% (w/v) milk powder in TBS-T filtrated (paper-filter), stored at -20 °C
Blocking Solution and primary Antibody dilution buffer LI-COR	Odyssey Blocking Buffer in TBS (LI-COR Biosciences, #927-50000), stored at 4 °C diluted 1:5 in TBS as working solution
Bradford reagent	0.01% (w/v) Coomassie Brilliant Blue G250 8.5% phosphoric acid 4.75% ethanol filtrated (paper-filter) and stored at 4 °C (dark)
BSA/PBS	5 mg/ml BSA in PBS sterile filtered (0.2 µm), stored at 4 °C
CDK7 Buffer	20 mM HEPES, pH 7.4 100 mM NaCl 3 mM $MgCl_2$ 4% (v/v) glycerol sterile filtered (0.2 µm), stored at 4 °C freshly added: 1mM DTT 1mM ATP

Name	**Ingredients**
ChIP Elution Buffer	1% SDS 0.1 M $NaHCO_3$
ChIP Lysis Buffer I	5 mM PIPES, pH 8.0 85 mM KCl 0.5% NP-40 10 mM Glycine stored at 4 °C
ChIP Lysis Buffer II	10 mM Tris/HCl, pH 7.5 150 mM NaCl 1 mM EDTA 1% NP-40 1% Deoxycholic acid sodium salt 0.1% SDS stored at 4 °C
ChIP Wash Buffer I	20 mM Tris/HCl, pH 8.1 150 mM NaCl 2 mM EDTA 0.1% SDS 1% Triton-X-100 stored at 4 °C
ChIP Wash Buffer II	20 mM Tris/HCl, pH 8.1 500 mM NaCl 2 mM EDTA 0.1% SDS 1% Triton-X-100 stored at 4 °C
ChIP Wash Buffer III	10 mM Tris/HCl, pH 8.1 150 mM LiCl 1 mM EDTA 1% NP-40 1% Deoxycholic acid sodium salt stored at 4 °C
Crystal Violet Solution	0.1% (w/v) crystal violet 20% (v/v) ethanol
Deoxynucleotide triphosphate (dNTP) mix (10 mM)	50 µl per dNTP (100 mM), fill up to 500 µl with water, stored at -20 °C

Name	Ingredients
DNA loading buffer (6x)	10 mM EDTA, pH 8.0 0.2% (w/v) Orange G (Thermo Fisher Scientific) 40% (w/v) sucrose
Doxycycline 1 mg/ml	50 mg Doxycycline in 50 ml ethanol aliquoted and stored at -20 °C
Gel Fixation Solution	40% (v/v) methanol 10% (v/v) acetic acid
Gel Washing Solution	50% (v/v) ethanol
Gel Reducing Solution 100x (20 g/l)	1 g sodium thiosulfate in 50 ml water sterile filtered (0.2 µm)
Gel Silver Solution 100x (200 g/l)	10 g silver nitrate in 50 ml water sterile filtered (0.2 µm)
Gel Developing Solution (27.5 g/l)	13.75 g sodium carbonate in 500 ml water sterile filtered (0.2 µm) 0.2% (v/v) formaldehyde (fresh)
Gel Stopping Solution	10% (v/v) acetic acid
Glycine stock solution (ChIP)	1 M glycine in water sterile filtered (0.2 µm)
HEGN Buffer	40 mM HEPES, pH 7.8 140 mM KCl 20% (v/v) glycerol 0.4 mM EDTA 0.2% (v/v) NP-40 sterile filtered (0.2 µm) stored at 4°C
High Salt Wash Buffer	50 mM Tris, pH8.0 1 M NaCl 20 mM Imidazole, pH 8.0 10% glycerol freshly added: 0.5 mM DTT
IP Buffer	20 mM HEPES, pH 7.9 200 mM NaCl 0.2% NP-40 0.5 mM EDTA 10% Glycerol stored at 4 °C

Name	Ingredients
Kanamycin stock solution (30 mg/ml)	3 g Kanamycin in 100 ml water, sterile filtered, aliquoted and stored at -20 °C
Laemmli Sample Buffer 6x	12% (w/v) SDS 60‰ (w/v) bromphenol blue 47% (v/v) glycerol 60 mM Tris/HCl, pH 6.8 9.3% (w/v) DTT Aliquoted and stored at -20 °C
LDS Sample Buffer 1x	4x LDS sample buffer (Thermo Fisher Scientific, NP0007) diluted with water
Miniprep Solution 1	1% SDS 200 mM NaOH
Miniprep Solution 2	11.5% (v/v) acetic acid 3 M CH_3COOK stored at 4 °C
MOPS running buffer 20x	1 M MOPS 1 M Tris base 20 mM EDTA 2% (w/v) SDS stored at 4 °C
MOPS running buffer 1x	1x MOPS running buffer 5 mM sodium bisulfite stored at 4 °C
MS Cytoplasmic Lysis Buffer	10 mM HEPES, pH 7.9 0.34 M sucrose 3 mM $CaCl_2$ 2 mM $Mg(CH_3COO)_2$ 0.1 mM EDTA 0.5% NP-40 sterile filtered (0.2 µm), stored at 4 °C
MS IP Washing Buffer	20 mM HEPES, pH 7.9 150 mM KCl 0.5 mM EDTA 10% glycerol sterile filtered (0.2 µm), stored at 4 °C

Name	**Ingredients**
MS Nuclear Lysis Buffer	20 mM HEPES, pH 7.9 3 mM EDTA 10% glycerol 150 mM CH_3COOK 1.5 mM $MgCl_2$ sterile filtered (0.2 µm), stored at 4 °C
MS Nuclease Incubation Buffer	150 mM HEPES, pH 7.9 1.5 mM $MgCl_2$ 150 mM CH_3COOK sterile filtered (0.2 µm), stored at 4 °C
MS Nuclei Washing Buffer	10 mM HEPES, pH 7.9 0.34 M Sucrose 3 mM $CaCl_2$ 2 mM $Mg(CH_3COO)_2$ 0.1 mM EDTA sterile filtered (0.2 µm), stored at 4 °C
MYC Lysis Buffer (MS)	20 mM HEPES, pH 7.9 180 mM NaCl 1.5 mM $MgCl_2$ 10% glycerol 0.2% NP-40 sterile filtered (0.2 µm), stored at 4 °C
NETN Buffer	20 mM Tris, pH 8.0 100 mM NaCl 1 mM EDTA 0.5% NP-40 sterile filtered (0.2 µm), stored at 4 °C
Phosphatase inhibitor	Ser/Thr phosphatase inhibitor (Sigma, #P0044) Tyr phosphatase inhibitor (Sigma, #P5726) stored at -20°C; used 1:1000
Phosphate-buffered saline (PBS) 1x	137 mM NaCl 2.7 mM KCl 10.1 mM Na_2HPO_4 1.76 mM KH_2PO_4 autoclaved

Name	**Ingredients**
Polybrene (Hexadimethrinbromide, 4 mg/ml)	200 mg polybrene in 50 ml water sterile filtered (0.2 µm), aliquoted and stored at -20 °C
Polyethylenimin (PEI)	0.09% PEI 6 mM HCl sterile filtered (0.2 µm), stored at 4 °C (dark)
Primary Antibody dilution buffer for Fuji immunoblot	5% BSA 0.02% NaN_3 in TBS-T
Protease inhibitor	protease inhibitor cocktail (Sigma, #P8340), aliquoted and stored at -20°C; used 1:1000
Proteinase K	10 mg/ml (Roth) in water aliquoted and stored at -20 °C
Pull down Buffer	20 mM HEPES, pH 7.5 100 mM NaCl 3 mM $MgCl_2$ 4% (v/v) glycerol sterile filtered (0.2 µm), stored at 4 °C freshly added: 1 mM DTT
Purification Buffer I	20 mM HEPES, pH7.4 500 mM NaCl 10% glycerol freshly added: 1 mM DTT
Purification Buffer II	50 mM Tris, pH8.0 500 mM NaCl 20 mM Imidazole, pH8.0 10% glycerol freshly added: 0.5 mM DTT, protease inhibitors
Reducing Solution 200x	1 M sodium bisulfite stored at 4 °C
RNase A (10 mg/ml)	100 mg RNase A (Roth) in 27 µl 3 M sodium acetate, pH 5.2 add 9 ml ddH2O; 450 µl aliquots, boiled for 30 min at 100°C to inactivate DNases add 50 µl 1M Tris, pH 7.4 per aliquot stored at -20°C

Name	Ingredients
TAE 50x	2 M Tris, pH 8.0 5.7% (v/v) acetic acide 50 mM EDTA, pH 8.0
Tris-buffered saline (TBS) 20x	500 mM Tris, pH 7.4 2.8 M NaCl
TBS-T	1 x TBS 0.2% (v/v) Tween-20
TE	10 mM Tris pH 7.4 1 mM EDTA pH 8.0
Transfer Buffer 20x	500 mM Bis-Tris 500 mM Bicine 20.5 mM EDTA 0.1 mM Chlorobutanol stored at 4 °C
Transfer Buffer 1x	1x transfer Buffer 40% (v/v) methanol stored at 4 °C

2.4 Purchased Chemicals and Solutions

Compound	Company
Dimethyl pimelimidate dihydrochloride (DMP)	Sigma
Dithiothreitol	Invitrogen
Ethanolamine	Sigma
Ethidiumbromide	Roth
GlycoBlue Coprecipitant	Life Technologies
Imidazole	Roth
Immobilon Western HRP Substrate	Millipore
Instant Blue	Expedeon
IPTG	Roth
Lipofectamine 2000 transfection reagent	Invitrogen
OptiMEM	Thermo Fisher Scientific
Phenol/Chloroform mixture	Invitrogen
Protamine sulfate salt	Sigma
Rotiphorese Gel 30	Roth
Rox	Thermo Fisher Scientific
Sodium dihydrogen phosphate	Roth
Triethanolamine (TEA)	Roth

Trypsin	Sigma

2.5 Standards, enzymes, kits and beads

2.5.1 DNA and protein standards

Gene Ruler™ 1 kb Plus DNA Ladder	Thermo Fisher Scientific
PageRule™ Prestained Protein Ladder (10-180 kDa)	Thermo Fisher Scientific
Colour Prestained Protein Standard, Broad Range (11-245 kDa)	New England Biolabs
HiMark™ Pre-Stained Protein Standard (31-460 kDa)	Life technologies

2.5.2 Enzymes

ABsolute QPCR SYBR Green Mix (no ROX)	Thermo Fisher Scientific
Benzonase nuclease purity >99%, 25 U/µl	Merck Millipore
Phusion	Thermo Fisher Scientific
PowerUP SYBR Green Master Mix	Thermo Fisher Scientific
T4 DNA Ligase	Thermo Fisher Scientific
Restriction enzymes:	
AgeI-HF	New England Biolabs
EcoRI-HF	New England Biolabs
HindIII-HF	New England Biolabs
KpnI-HF	New England Biolabs
NotI-HF	New England Biolabs
SpeI	New England Biolabs
XhoI	New England Biolabs

2.5.3 Kits

CloneJET PCR Cloning Kit	Thermo Fisher Scientific
Experion DNA 1 K Analysis Kit	BioRad
GeneJET Gel Extraction Kit	Thermo Fisher Scientific
NEBNext ChIPseq Library Prep Master Mix Set for Illumina	New England Biolabs
NEBNext Multiplex Oligos for Illumina	New England Biolabs
NGS Fragment High Sensitivity Analysis Kit (1-6,000 bp)	Advanced Analytical
PureLink HiPure Plasmid Maxiprep Kit	Invitrogen
QIAquick Gel Extraction Kit	Qiagen
QIAquick MinElute DNA Purification Kit	Qiagen
QIAquick PCR Purification Kit	Qiagen

Quant-iT PicoGreen dsDNA Assay Kit	Thermo Fisher Scientific

2.5.4 Beads

Item	**Company**
Agencourt AMPure XP Beads	Beckman Coulter
Dynabeads Protein A for Immunoprecipitation	Life Technologies GmbH
Dynabeads Protein G for Immunoprecipitation	Life Technologies GmbH
Pierce Anti-HA Magnetic beads	Thermo Fisher Scientific

2.6 Nucleic acids (Oligonucleotides)

2.6.1 Primers

All oligonucleotides were purchased from Sigma in 0.025 µmol scale and DST purity (desalted) unless otherwise stated. Primers were solubilized in water at 100 µM and working stock was diluted in water to 10 µM. Primers were stored at -20 °C. (F/fwd=forward, R/rev=reverse)

2.6.1.1 Primers for cloning protein coding sequences

Name	**Sequence 5´-3´**
EW_1669_KpnI-HA-SPT4_f	CGGGTACCATGTACCCATACGATGTTCCAGATTACGCCGCCCTGGAGACGGTGCC
EW_1296_KpnI-FLAG_fwd	GGGGTACCATGGATTACAAGGATGACG
EW_1297_SPT4-NotI_rev	ATAGTTTAGCGGCCGCCTAGGTCTTTATA
EW_1238_HA-SPT5_KpnI_f	CGGGGTACCATGTACCCATACGATGTTCC
EW_1239_SPT5_NotI_r	ATAGTTTAGCGGCCGCTCAGGCTTCCAGGAG
EW_1219_SPT5_D1_D2_D3_f	CGGGGTACCATGGATTACAAGGAT
EW_1220_SPT5_D1_r	ATAGTTTAGCGGCCGCTCAGGCCACCTCCTTCAC
EW_1221_SPT5_D2_r	ATAGTTTAGCGGCCGCTCACACCTTCAGCTCATG
EW_1222_SPT5_D3_r	ATAGTTTAGCGGCCGCTCAACGGTCCACAGAGAT
EW_1223_SPT5_D4_f	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCGAGTATGCTTTCGATGATGA

EW_1224_SPT5_D5_f	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCCGGCTCACCACGGTGGGCTC
EW_1225_SPT5_D4_D5_r	ATAGTTTAGCGGCCGCTCAGGCTTCCAGGAGCTTCC
EW_1258_SPT5_D6_f	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCATGAGCAGGGGCCGGGGCCG
EW_1259_SPT5_D7_f	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCGCTGTGGCCTTGGACTCAGA
EW_1275_Flag-Spt5-dN175-F	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCGATCCCAATCTGTGGACTG
EW_1276_Flag-Spt5-dN	ATAGTTTAGCGGCCGCTCAGGCTTCCAGGAGCTT
EW_1277_Flag-Spt5-dN271	CGGGGTACCATGGATTACAAGGATGACGACGATAAGGGTGGAGGCGGTAGCAACCTGAAACCAAAGTCCTG
EW_1318_deltaNGN-rev-NEW	TGGTTTCAGGTTGGCCTTGACTCCTGGGAG
EW_1319_deltaNGN-fwd-NEW	CTCCCAGGAGTCAAGGCCAACCTGAAACCA
EW_1478_Hind-NGN-Fwd	CCAAGCTTATGGATCCCAATCTGTGGACTG
EW_1479_NGN-Hind-Rev	GGAAGCTTCACCTCCTTCACCACTTT
EW_1435_HindIII-tGFP-fwd2	CCAAGCTTATGGAGAGCGACGAGAGC
EW_1436_tGFP-EcoRI-rev2	CGGAATTCTTCTTCACCGGCATCTGC
EW_1439_KpnI-SPT5-fwd2	CGGGTACCATGTCGGACAGCGAGGA
EW_1440_SPT5-EcoRI-rev2	CGGAATTCGGCTTCCAGGAGCTTCCC
EW_1478_Hind-NGN-Fwd	CCAAGCTTATGGATCCCAATCTGTGGACTG
EW_1479_NGN-Hind-Rev	GGAAGCTTCACCTCCTTCACCACTTT
EW-781_Myc-WT-F	GTACCGGTATGCCCCTCAACGTTAGCTT
EW-782_Myc-WT-R	GGACTAGTTTAGGCGTAATCTGGAACATCG
EW_1226_c-Myc_HA_f	GTACCGGTATGCCCCTCA
EW_1227_c-Myc_HA_r	GGACTAGTTTAGGCGTAATCTGG
EW_1228_c-Myc_MB1-del_HA_r	AGCGGCGGCTCGCCGGGGGCTGC
EW_1229_c-Myc_MB1-del_HA_f	GCCCCCGGCGAGCCGCCGCTCCG
EW_1230_c-Myc_MB2-del_HA_r	CTGAGACGAGGTTTTTGATGAAGGTCTCGTCGT

EW_1231_c-Myc_MB2-del_HA_f	CATCAAAAACCTCGTCTCAGAGAAGCTGG
EW_1232_c-Myc_MB3a-del_HA_r	TGCTGTCGTTCTCTGAGGCGGCGGC
EW_1233_c-Myc_MB3a-del_HA_f	CGCCTCAGAGAACGACAGCAGCTCGC
EW_1234_c-Myc_MB3b-del_HA_r	GCCTCTTTTCTTCTTGTTCCTCCTCAGAGTC
EW_1235_c-Myc_MB3b-del_HA_f	GGAACAAGAAGAAAAGAGGCAGGCTCCTG
EW_1236_c-Myc_MB4-del_HA_r	CAGGATAGTCGGAGACGTGGCACCTCT
EW_1237_c-Myc_MB4-del_HA_f	CCACGTCTCCGACTATCCTGCTGCCAAGAG
EW_1299_MYC_AGEI_S6E-F	GTACCGGTATGCCCCTCAACGTTGAGTTCAC
EW_1300_MYC_AGEI_S6D_F	GTACCGGTATGCCCCTCAACGTTGACTTCAC
EW_1670_MYCdelta44-Age-F	GTACCGGTATGCCCAGCGAGGATATCTGG
EW_1993_MYC-d68-123-rev	GATGTTTTTGATGAAGGAGCGGCGGCTAGG
EW_1994_MYC-d68-123-fwd	CCTAGCCGCCGCTCCTTCATCAAAAACATC

2.6.1.2 Primers for cloning shRNAs

Primers EW_880 and EW_881 were ordered in 0.05 µmol scale.

Name	**Sequence 5´-3´**
EW_1054_hSPT5_mirE_1	TGCTTGCTGTTGACAGTGAGCGCAAGAAGCTGTTTGGTCTAAAATAGTGAAGCCACAGATGTATTTTAGACCAAACAGCTTCTTTTGCCTACTGCCTCGGA
EW_1055_hSPT5_mirE_2	TGCTGTTGACAGTGAGCGCCCCAATCTGTGGACTGTCAAATAGTGAAGCCACAGATGTATTTGACAGTCCACAGATTGGGATGCCTACTGCCTCGGA
EW_1056_hSPT5_mirE_3	TGCTGTTGACAGTGAGCGAAGGGACCAGCGAGAAGAAGAATAGTGAAGCCACAGATGTATTCTTCTTCTCGCTGGTCCCTCTGCCTACTGCCTCGGA
EW_1057_hSPT5_mirE_4	TGCTGTTGACAGTGAGCGCTCTGTGGACTGTCAAATGTAATAGTGAAGCCACAGATGTATTACATTTGACAGTCCACAGATTGCCTACTGCCTCGGA
EW_1058_hSPT5_mirE_5	TGCTGTTGACAGTGAGCGCCCATGTGAAAGACATCGTTAATAGTGAAGCCACAGATGTATTAACGATGTCTTTCACATGGATGCCTACTGCCTCGGA

EW_880_mirE_XhoI_PCR_f	TACAATACTCGAGAAGGTATATTGCTGTTGACAGTGAGCG
EW_881_mirE_EcoRI_PCR_r	TTAGATGAATTCTAGCCCCTTGAAGTCCGAGGCAGTAGGCA

2.6.1.3 *Primers for ChIP qPCR*

Primer-specific product was monitored by performing a melting curve.

Target	**Forward sequence (5´-3´)**	**Reverse sequence (5´-3´)**
Control Region	TTTTCTCACATTGCCCCTGT	TCAATGCTGTACCAGGCAAA
ACTB TSS	CGTTCCGAAAGTTGCCTTTT	GCCGCTGGGTTTTATAGGG
NCL TSS	TACTGGGCAGGCTCAGTCTT	GAAGATCCCGGAGCACGTA

2.6.1.4 *Primers for Sanger sequencing*

Sanger sequencing was performed by LGC Genomics.

Name	**Sequence 5´-3´**
EW_859_SFFV_seq	CTTCTGCTTCCCGAGCTCTA
EW_1067_SUPT5H_F_2_JH	CAGAACACCATCTCCCTG
EW_1068_SUPT5H_F_3_JH	AGAGACAGCATCAGGTGT
EW_1069_SUPT5H_F_4_JH	ATGACCTCGACCTATGG
EW_1302_pCMV3_Flag-tag_F	AGCTGTCAGGCTTGAGATCC
CMV-F	GCAAATGGGCGGTAGGCGT
IRESHygRn	CAGACCTTGCATTCCTTTGG
pcDNA3.1-R	TAGAAGGCACAGTCGAGGCT
pJET1.2-F	CGACTCACTATAGGGAGAGCGGC
pJET1.2-R	AAGAACATCGATTTTCCATGGCAG
SV40	CACTGCATTCTAGTTGTGGTT
T7prom	TAATACGACTCACTATAGGG
T7term	GCTAGTTATTGCTCAGCGG

2.6.2 *siRNAs*

SiRNAs were purchased from Dharmacon as smart pools out of 4 different siRNA sequences.

Target	**Ordering number**
ON-TARGETplus Non-targeting Pool	D-001810-10

ON-TARGETplus Human MYC (4609) siRNA - SMARTpool	L-003282-02

2.6.3 Plasmids

2.6.3.1 Empty vectors

Name	**Specification**
pCDNA3	Cloning vector (Invitrogen) Mammalian expression Ampicillin resistance CMV promoter
pCMV3	Cloning vector (ABclonal) Mammalian expression KpnI and NotI restriction sites Kanamycin resistance CMV promoter
pGIPZ	lentiviral expression plasmid, for shRNAs Mammalian expression XhoI and EcoRI restriction sites Ampicillin resistance Puromycin resistance CMV promoter (Fellmann et al. 2013)
pIND11	lentiviral expression plasmid, for shRNAs, Doxycycline-inducible XhoI and EcoRI restriction sites Ampicillin resistance TRE promoter Constitutive GFP expression Inducible RFP expression (Fellmann et al. 2013)
pLT3	lentiviral expression plasmid, for shRNAs, Doxycycline-inducible XhoI and EcoRI restriction sites Ampicillin resistance Puromycin resistance TRE3G promoter Inducible GFP expression (Fellmann et al. 2013)

pRRL-SFFV-IRES-puro	Addgene #12252 3rd generation lentiviral backbone cloning vector Mammalian expression AgeI and SpeI restriction sites Ampicillin resistance Puromycin resistance SFFV promoter

2.6.3.2 Packaging vectors for lentivirus production

Name	**Specification**
pMD2.G	Trono Laboratory plasmid for lentivirus production Addgene #12259 VSV-G envelope expressing plasmid
psPAX2	Trono Laboratory plasmid for lentivirus production Addgene #12260 2nd generation lentiviral packaging plasmid

2.6.3.3 Plasmids available in the Department of Biochemistry and Molecular Biology

Name	**Specification**
pRRL-MYC-WT-HA	lentiviral expression plasmid, SFFV-promoter, full-length wildtype MYC(1-439) with C-terminal HA-tag
pRRL-MYC-ΔN1-HA	lentiviral expression plasmid, SFFV-promoter, truncated MYC(63-439) with C-terminal HA-tag
pRRL-MYC-ΔN2-HA	lentiviral expression plasmid, SFFV-promoter, truncated MYC(143-439) with C-terminal HA-tag
pRRL-MYC-ΔN3-HA	lentiviral expression plasmid, SFFV-promoter, truncated MYC(269-439) with C-terminal HA-tag
pRRL-MYC-ΔN4-HA	lentiviral expression plasmid, SFFV-Promoter, truncated MYC(317-439) with C-terminal HA-tag
pCDNA3-MYC-HA	eukaryotic expression plasmid, CMV-promoter, full-length wildtype MYC(1-439) with C-terminal HA-tag
pCDNA3-GFP	eukaryotic expression plasmid, CMV-promoter, GFP expression, used to control and adjust transient transfection levels

pGFP-Lenti	transfection and infection control, strong GFP expression
pUHD Myc WT	eukaryotic expression plasmid, CMV-promoter, MYC WT
pUHD Myc T58A	eukaryotic expression plasmid, CMV-promoter, MYC MUT with T58 to A58
pUHD Myc S62A	eukaryotic expression plasmid, CMV-promoter, MYC MUT with T62 to A62
pUHD Myc T58A/S62A	Eukaryotic expression plasmid, CMV-promoter, MYC MUT with T58 and S62 to A58 and A62
pK10R7Sumo-3C-optSPT4_optSPT5	*E. coli* expression plasmid, expression of full-length SPT4 and SPT5, codon optimized for *E. coli* expression (Vos, Farnung, Urlaub, et al. 2018)

2.6.3.4 Plasmids purchased from ABclonal

Name	**Specification**
pCMV3-N-FLAG-SPT5	ABclonal; eukaryotic expression plasmid, CMV-promoter, full-length wildtype SPT5 with N-terminal FLAG-tag

2.6.3.5 Plasmids generated in this study

Name	**Specification**
pRRL-RPB3-HA	lentiviral expression plasmid, SFFV-promoter, full-length wildtype RPB3 with C-terminal HA-tag
pCMV3-N-FLAG-SPT5_D1	eukaryotic expression plasmid, CMV-promoter, SPT5(1-271) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5_D2	eukaryotic expression plasmid, CMV-promoter, SPT5(1-513) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5_D3	eukaryotic expression plasmid, CMV-promoter, SPT5(1-747) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5_D4	eukaryotic expression plasmid, CMV-promoter, SPT5(837-1087) with N-terminal FLAG-tag

pCMV3-N-FLAG-SPT5_D5	eukaryotic expression plasmid, CMV-promoter, SPT5(749-1087) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5_D6	eukaryotic expression plasmid, CMV-promoter, SPT5(694-1087) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5_D7	eukaryotic expression plasmid, CMV-promoter, SPT5(263-1087) with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT5-ΔNGN	eukaryotic expression plasmid, CMV-promoter, SPT5 lacking aa 175-270 with N-terminal FLAG-tag
pCMV3-N-FLAG-SPT4	eukaryotic expression plasmid, CMV-promoter, full-length wildtype SPT4 with N-terminal FLAG-tag
pCDNA3-His-FLAG-entry vector	eukaryotic expression plasmid, CMV-promoter, multiple cloning site in front of C-terminal His-FLAG-tag, entry vector for subsequent cloning
pCDNA3-SPT5-WT-His-FLAG	eukaryotic expression plasmid, CMV-promoter, SPT5-WT with C-terminal His-FLAG-tag
pCDNA3-SPT5-ΔNGN -His-FLAG	eukaryotic expression plasmid, CMV-promoter, SPT5 lacking aa 175-270 with C-terminal His-FLAG-tag
pCDNA3-NGN-tGFP-His-FLAG	eukaryotic expression plasmid, CMV-promoter, SPT5 (175-270) with C-terminal tGFP-His-FLAG-tag
pCDNA3-tGFP-His-FLAG	eukaryotic expression plasmid, CMV-promoter, tGFP with C-terminal His-FLAG-tag
pRRL-puro-MYC-Δ44-HA	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 1-44 with C-terminal HA-tag
pRRL-puro-MYC-Δ(68-123)-HA	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 68-123 with C-terminal HA-tag
pRRL-MYC-ΔMBI	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 45-63 with C-terminal HA-tag

pRRL-MYC-ΔMBII	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 128-143 with C-terminal HA-tag
pRRL-MYC-ΔMBIII	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 188-199 and 258-267 with C-terminal HA-tag
pRRL-MYC-ΔMBIV	lentiviral expression plasmid, SFFV-promoter, MYC deleted for aa 304-317 with C-terminal HA-tag (116 Ile→Val)
pRRL-MYC-S6E-HA	lentiviral expression plasmid, SFFV-promoter, MYC MUT with S6 to E6
pRRL-MYC-S6D-HA	lentiviral expression plasmid, SFFV-promoter, MYC MUT with S6 to D6
pGIPZ-hSPT5-mirE1	lentiviral expression plasmid, shRNA mirE1 against human SPT5
pGIPZ-hSPT5-mirE2	lentiviral expression plasmid, shRNA mirE2 against human SPT5
pGIPZ-hSPT5-mirE3	lentiviral expression plasmid, shRNA mirE3 against human SPT5
pGIPZ-hSPT5-mirE4	lentiviral expression plasmid, shRNA mirE4 against human SPT5
pGIPZ-hSPT5-mirE5	lentiviral expression plasmid, shRNA mirE5 against human SPT5
pIND11-h-SPT5-mirE1	lentiviral expression plasmid, shRNA mirE1 against human SPT5, Doxycycline-inducible
pIND11-h-SPT5-mirE2	lentiviral expression plasmid, shRNA mirE2 against human SPT5, Doxycycline-inducible
pLT3-h-SPT5-mirE3	lentiviral expression plasmid, shRNA mirE3 against human SPT5, Doxycycline-inducible
pLT3-h-SPT5-mirE4	lentiviral expression plasmid, shRNA mirE4 against human SPT5, Doxycycline-inducible
pLT3-h-SPT5-mirE5	lentiviral expression plasmid, shRNA mirE5 against human SPT5, Doxycycline-inducible
pet22 Twin Strep h-c-MYC	*E. coli* expression plasmid, expression of full-length MYC with Strep-tag (Maren Bleckmann, Rudolf Virchow Center, Würzburg)

2.7 Proteins

Protein (Tag)	**Expression organism**	**Source**
CDK7	Insect cells	(Boehning et al. 2018)
DSIF (His)	*E. coli*	(Vos, Farnung, Urlaub, et al. 2018)
GST-CTD and GST-pCTD	*E. coli*	Robert Düster, research group of Matthias Geyer, University of Bonn
MYC (MBP)	Insect cells	Robert Düster, research group of Matthias Geyer, University of Bonn
MYC (Strep)	*E. coli*	Maren Bleckmann, Rudolf Virchow Center, Würzburg
SPT5 + MBP-SPT4 (co-expressed)	*E. coli*	Lars Schönemann, Rudolf Virchow Center, Würzburg

2.8 Antibodies

2.8.1 Primary Antibodies

(IB: immunoblot; IP: immunoprecipitation; ChIP: chromatin immunoprecipitation)

Target	**Company**	**Ordering number**	**Application**
CDK2	Cell Signaling	2546S	IB
CDK7	Santa Cruz	sc-56284	IB
FLAG-Tag	Sigma	F3165-1MG	IB, IP
GST-Tag	Sigma	GE27-4577-01	IB, IP
HA-Tag	Santa Cruz	sc-805X	IB, IP
IgG from mouse serum	Sigma	I5381	IP, ChIP
IgG from rabbit serum	Sigma	I5006	IP, ChIP
MYC	Abcam	ab32072	IB, IP
RNAPII RPB1 total	Santa Cruz	sc-899X	IB, IP
RNAPII RPB1 total	Santa Cruz	sc-17798	IB, IP, ChIP, ChIPseq
RNAPII RPB1 unphosphorylated	Abcam	ab817	IB
RNAPII RPB1 pSer2	Abcam	ab24758	IB
RNAPII RPB1 pSer2	Abcam	ab5095	IB, ChIP, ChIPseq

Target	Company	Ordering number	Application
RNAPII RPB1 pSer5	Biolegend	MMS-128P	IB
RNAPII RPB2	Santa Cruz	sc-166803	IB
SPT4	Santa Cruz	sc-515238X	IB
SPT5	Santa Cruz	sc-133217X	IP, ChIP, ChIPseq
SPT5	Abcam	ab126592	IB
SPT6	Novus Biologicals	NB100-2582	IB
Tubulin A	Santa Cruz	sc-12462-R	IB
Vinculin	Sigma	V9131-.5ML	IB

2.8.2 Secondary Antibodies

Target	Company	Ordering number	Application
anti-mouse IgG-HRP	GE Healthcare	NA934V	IB
anti-rabbit IgG-HRP	GE Healthcare	NA931V	IB
anti-goat IgG-HRP	Santa Cruz	sc-2020	IB
anti-rabbit IgG light chain HRP	Abcam	ab99697	IB
anti-mouse 800 CW	LI-COR Biosciences	926-32212	IB
anti-rabbit 680 RD	LI-COR Biosciences	926-68073	IB
TrueBlot anti-mouse	Biomol	18-8817-33	IB
TrueBlot anti-rabbit	Biomol	18-8816-33	IB

2.9 Consumables

Consumables, including disposable plastic items as for example reaction tubes and falcons, cell culture dishes, plastic pipets, cryotubes, syringes, cuvettes were purchased from the companies Eppendorf, Greiner, Falcon, Nunc, Sarstedt, Applied Biosystems, Beckman Coulter, and VWR.

2.9.1 Membranes and equipment

2.9.1.1 Membranes

Membrane for immunoblotting	Company
Immobilon-P Membrane, PVDF	Merck
Immobilon-FL Membrane, PVDF	Merck
Whatman filter paper	Sigma

2.9.1.2 Equipment

Item	**Type**	**Company**
Automated Electrophoresis	Experion Fragment Analyzer	Bio-Rad Advanced Analytical
Cell counter	Casy cell counter	Innovatis
Centrifuges	5417R / 5424 / 5430 Multifuge 1S-R Avanti J-26 XP Magafuge 40R Galaxy MiniStar	Eppendorf Heraeus Beckman Coulter Heraeus VWR
Centrifuge adapters	Adapters for 3x 1.5 ml tubes to fit in a 50 ml bucket (JA25.50) Adapters for 2x 1.5 ml tubes to fit in a 50 ml bucket (JA25.50)	Beckman Coulter Beranek Laborgeräte
Flow cytometer	BD FACS Aria III	BD Biosciences
Freezing container	Mr. Frosty	Thermo Fisher Scientific
Glass syringe	20 µl and 50 µl	Hamilton
Heating Block	Dry Bath Heating System, Dual Block, Digital Dry Block Heating TBD-100	Starlab Biosan
Image Reader	Las-4000 mini Odyssey CLx	Fujifilm LI-COR Biosciences
Immunoblot transfer chamber	PerfectBlue Tank Electro Blotter Web S	Peqlab
Incubator for cells	BBD 6220	Heraeus
Mass spectrometer (nanoLC-MS/MS)	Orbitrap Fusion mass spectrometer	Thermo Fisher Scientific
Microscopes	DMI6000 B Axio Vert.A1 Axiovert 40CFL	Leica Zeiss Zeiss
PCR thermal cycler	C1000 Thermal Cycler Mastercycler pro S	Bio-Rad Eppendorf
Photometer	Multiscan Ascent Infinite 200 PRO NanoDrop 1000 Bio Photometer	Thermo Labsystems Lifesciences Tecan Thermo Fisher Scientific Eppendorf
Power supply	Power Pac Consort EV231/EV243	Bio-Rad Roth

Item	**Type**	**Company**
Quantitative RT-PCR machine	StepOne plus	Applied Biosystem
Sonifier	Digital Sonifier W-250 D	Branson
SDS-PAGE system	Mini–PROTEAN Tetra Cell	Bio-Rad
Sequencer	NextSeq 500	Illumina
Sterile bench	HeraSafe Laminair HB2448S	Heraeus Heraeus
Thermoshaker	Thermomixer comfort Star Lab	Eppendorf Star Labs
UV fluorescent table	Maxi UV fluorescent table	Peqlab
Vortex mixer	Vortex-Genie 2	Scientific Industries
Water bath	Julabo ED-5M water bath Memmert water bath	Julabo Memmert
Water purification system	Millipore Milli-Q Integral 15	Millipore

2.9.2 Software and online programs

Software	**Source**
Affinity Designer v1.7.3	Pantone LLC
ApE plasmid editor v2.0.61	M. Wayne Davis
BD FACSDiva v6.1.2	BD Biosciences
BedTools v2.26.0	(Quinlan 2014)
BioVenn	https://www.biovenn.nl/ (Hulsen, de Vlieg, and Alkema 2008)
Bowtie v1.2. and v2.27.0	(Langmead et al. 2009)
David	https://david.ncifcrf.gov/
EndNote X9.3.2	Clarivate Analytics, Michael O. McCracken
Expasy Translation Tool	https://web.expasy.org/translate/
Fragment Analyzer	Applied Biosciences
ImageJ v1.52q	Wayne Rasband
ImageStudio Lite v5.2.5	LI-COR Biosciences
Integrated Genome Browser v9.1.0	Freese et al., 2016 BioViz
LAS-4000 mini 2.1	Fujifilm
Max Quant v1.5.3.12	(Cox and Mann 2008)
Multi Gauge	Fujifilm
Multiscan Ascent	Thermo Fisher Scientific
NanoDrop 1000 3.8.1	Thermo Fisher Scientific

Software	**Source**
NgsPlot v2.61	(Shen et al. 2014)
Office	Microsoft
R v3.4.4	https://www.r-project.org/
Samtools v1.3	http://samtools.sourceforge.net
SnapGene Viewer v5.0.7	GSL Biotech LLC.
StepOne Software v2.3	Applied Biosysems
SplashRNA	http://splashrna.mskcc.org/ (Pelossof et al. 2017)
Spotfire	TIBCO Software
Tecan i-control	Tecan Trading AG
T_m Calculator	https://www.thermofisher.com/de/de/home/brands/thermo-scientific/molecular-biology/molecular-biology-learning-center/molecular-biology-resource-library/thermo-scientific-web-tools/tm-calculator.html (Thermo Fisher Scientific)
UCSC Genome Browser	https://genome.ucsc.edu/

3 METHODS

3.1 Cell biology

Cells were cultured in incubators set to 37 °C with 5% CO_2 and 95% relative humidity.

3.1.1 Culturing

Human U2OS, U2OS$^{MYC\text{-}Tet\text{-}On}$ and HEK293T cells were cultured in DMEM medium containing 10% FBS and 1% penicillin/streptomycin solution (P/S). Murine T-lymphoma$^{MYC\text{-}Tet\text{-}Off}$ cells were grown in RPMI medium supplemented with 10% FBS, 1% P/S, 1% glutamine solution, 1% MEM non-essential amino acids, and 50 µM β-mercaptoethanol.

3.1.2 Thawing

Cells were rapidly thawed in a water bath and immediately transferred into 10 ml of the corresponding culturing medium. Cells were pelleted at 209 g for 4 min to remove residual DMSO, resuspended in fresh medium and transferred into a suitable cell culture dish or flask.

3.1.3 Passaging

For passaging suspension cells (T-lymphoma cells), cells were distributed equally within the plate or flask by gentle pipetting up and down and transferred into a fresh plate or flask containing fresh culturing medium.

Adherent cells were washed with sterile PBS and detached using trypsin-EDTA solution. Trypsin was removed by centrifugation prior to seeding or cell counting.

3.1.4 Counting

The number of detached cells was determined using the Casy cell counting machine according to the Manufacturer’s instructions.

3.1.5 Freezing

After trypsinization and pelleting, cells were resuspended in freezing medium containing 50% FBS, 10% DMSO and 40% corresponding culturing medium. A volume of 1 ml corresponding to cells from one 10 cm dish or one third of a 15 cm dish was aliquoted per cryotube. Gradual freezing of the cell suspension was ensured using a freezing box filled with 100% isopropanol and incubating at -80 °C overnight. Frozen cells were stored at -80 °C for short term or in liquid nitrogen for long term storage.

3.1.6 Transient transfection for protein expression using PEI

For protein overexpression, HEK293T cells were transiently transfected with the corresponding plasmids. 24 hrs before transfection, 3.5×10^6 HEK293T cells were seeded per 10 cm dish. For transfection, two mixtures were prepared: the PEI- and the DNA-mixture. The PEI-mixture consisted of 25 µl PEI in 250 µl OptiMEM per 10 cm dish and for the DNA-mixture a total of 10 µg DNA were added to 250 µl OptiMEM per dish. Both mixtures were vortexed briefly and spun down. After incubation for 5 min at RT, the DNA-mixture was added dropwise to the PEI-mixture followed by pipetting up and down several times. The transfection mixture was incubated for another 20 min at RT. Meanwhile, cells were washed once with sterile PBS and 5 ml of transfection medium (DMEM with 2% FBS) were added per plate. Finally, the transfection mixture was added dropwise onto the plate and mixed by gentle swirling. After 17 hrs cells were washed once with sterile PBS and culturing medium was added. Cells were harvested 24 hrs post-transfection.

3.1.7 Transfection for lentivirus production using PEI

PEI transfection was used for virus production (see section 3.1.6). In contrast to the transfection for protein expression, 5×10^6 HEK293T cells were seeded per 10 cm dish the day before transfection. The PEI-mixture consists of 30 µl PEI in 500 µl OptiMEM per dish. For the DNA-mixture, the two packaging plasmids PAX2 (10 µg) and pMD2G (2.5 µg), required for the functional production of virus particles, were added to 10 µg of the plasmid of interest in 500 µl OptiMEM per 10 cm dish. In addition, simple CMV-GFP expressing lentiviral plasmid was used as a positive control for transfection and later infection of cells. The transfection was carried out as described above (see section 3.1.6). As soon as the transfection mixture was added to the cells, they were transferred to a biosafety level 2 laboratory. 8 hrs post-transfection, transfection medium was removed, cells were washed once with sterile PBS and culturing medium was added with 6 ml over day and 8 ml overnight. Virus-containing supernatant was harvested twice a day for a total of three times, pooled and stored at 4 °C until the last harvest. GFP expression in control cells as well as cell morphology were consistently checked as a method control. Virus-containing supernatant was passed through a 0.45 µm membrane filter to remove remaining cells. Subsequently, the virus was used for infection or aliquoted, flash frozen in liquid nitrogen and stored at -80 °C.

3.1.8 Lentiviral infections

Viral infections were carried out in a biosafety level 2 laboratory using fresh virus or virus subjected to a single freeze-thaw cycle. To estimate virus production and infection efficiency, virus encoding GFP was used alongside the experiment as a positive control. Adherent cells were seeded the day before infection and suspension cells immediately before infection (see Table 3.1). Equal volumes of culturing medium and virus were added to the cells (see Table 3.1), as well as polybrene (1:500 for U2OS and HEK293T cells) or proteamine sulfate (1:1000 for T-lymphoma cells). The day after infection, culturing medium was added or a second infection was carried out by adding additional virus and culturing medium, but no polybrene nor proteamine sulfate. The second day after infection, cells were split in half; one half was left untreated and the other half was treated with antibiotics for the selection of infected cells (Puromycin, 1:5000). For cells infected with virus encoding for pInd-plasmids, selection by FACS sorting was carried out (see chapter 3.1.12).

Table 3.1: Overview of cell number and virus volume used for lentiviral infection of various cell lines.

Cell line	**Cell number**	**ml medium**	**ml virus-containing supernatant**
T-lymphoma cells	1x10^6 cells / ml	3 ml per 10 cm dish containing cells	3 ml per 10 cm dish
U2OS cells	6x10^5 cells / 10 cm dish	3 ml per 10 cm dish	3 ml per 10 cm dish
HEK293T cells	3.5x10^6 cells / 10 cm dish	3 ml per 10 cm dish	3 ml per 10 cm dish

3.1.9 Transfection with siRNAs using Lipofectamine RNAiMAX

2 x10^6 U2OS cells were seeded per 15 cm dish 24 hrs prior to transfection. For transfection, two mixtures were generated per dish: 16 µl siRNA and 16 µl Lipofectamine RNAiMAX Transfection Reagent were added to separate tubes of 1.15 ml OptiMEM each. Both mixtures were homogenized by brief vortexing, spun down and incubated for 5 min at RT. Then, the siRNA-containing mixture was added dropwise to the Lipofectamine mixture, homogenized by pipetting up and down several times and incubated for another 20 min at RT. Meanwhile, the cells were washed once with sterile PBS and 10 ml transfection medium (DMEM with 2% FBS) were added. Finally, the transfection mixture was added dropwise to the plate and distributed

by gentle shaking. 17 hrs post-transfections, cells were washed once with sterile PBS and 15 ml culturing medium were added. 24 hrs post-transfection, cells were split and then harvested 48 hrs or 72 hrs post-transfection according to the experimental design.

3.1.10 Cell culture manipulations and inhibitor treatments

The Tet-On system for MYC overexpression in U2OS cells or the Tet-Off system for MYC depletion in T-lymphoma cells were induced by applying Doxycycline at a final concentration of 1 µg/ml for 18 hrs. Equal volume of diluent (ethanol) was used as a control. The same Doxycycline concentration was used for the induction of shRNA expression from the pInd11 or pLT3 vector backbones, but the treatment was performed for 48 hrs with Doxycycline being replaced after 24 hrs.

Transcriptional inhibition with DRB was performed for 4 hrs at 100 µM and with the CDK9-inhibitor Flavopiridol for 3 hrs at 100 nM. The solvent DMSO served as a control for the treatment with transcriptional inhibitors.

3.1.11 Crystal violet staining

Cells were fixed by adding formaldehyde to a final concentration of 1% and incubating for 10 min at RT. Cells were washed with Millipore water and incubated with Crystal Violet Solution for 1 hr at RT. The remaining crystal violet solution was removed and cells were washed with Millipore water. Cells were dried by turning the plate upside down and photographed.

3.1.12 GFP- and RFP-based FACS sorting for the selection of infected cells

RFP expression in pIND11-infected cells (constitutive expression of GFP) was induced by 4 hrs of treatment with Doxycycline (1 µg/ml), which was then removed. The next day, cells were trypsinized, centrifuged, and cells resuspended in sterile PBS containing 2% FBS. To avoid cell clusters, cells were pushed through a 35 µm cell strainer. Cells were sorted according to high GFP and RFP expression using a BD FACS Aria III cell sorter (BD Biosciences). For parameter settings, non-infected parental cells were used, as well as non-induced infected cells only expressing GFP.

3.2 Molecular biology

3.2.1 Transformation of bacterial cells

Chemically competent XL1 blue *E. coli* were thawed on ice and 50 µl of bacterial suspension were mixed with plasmid DNA. For re-transformation of existing plasmids 0.5 µg of plasmid DNA, and during cloning procedure 10 µl of a 20 µl ligation reaction (see section 3.2.4) were used. Bacteria were incubated with the plasmid DNA for 30 min on ice. Heat shock was performed at 42 °C for 45 sec and bacteria were cooled down on ice for another 3 min. 500 µl LB medium were added and bacteria incubated at 37 °C with shaking. After 45 min, the resistance gene was expressed by the transformed bacteria and bacterial solution was centrifuged for 2 min at 845 g. Pellet was resuspended in 100 µl LB medium and bacteria were streaked onto a LB-agar plate supplemented with Carbenicillin (for Ampicillin resistance) or Kanamycin according to the transformed plasmid backbone.

3.2.2 Analytical preparation of plasmid DNA from E. coli (Miniprep)

One single colony from a LB-agar plate was picked using a plastic pipette tip and transferred into 3 ml LB medium supplemented with the corresponding antibiotics for selection. The bacterial culture was grown overnight at 37 °C with 200 rpm shaking or at 30 °C for lentiviral plasmids, which tend to religate. The next day, 1 ml of bacterial culture was pelleted at 845 g for 5 min and the pellet was resuspended in 300 µl LB medium. 300 µl Miniprep Solution 1 was added, solutions were homogenized by inverting the tube and lysis was performed for 5 min at RT. Lysis was stopped by the addition of 300 µl Miniprep Solution 2, inversion of the tube for homogenization and incubation for another 5 min at RT. Cell debris were pelleted at 15871 g for 5 min (RT) and 800 µl DNA-containing supernatant transferred into a fresh tube. DNA was precipitated by adding 600 µl 100% isopropanol followed by intense vortexing and centrifugation at 20442 g for 10 min in a centrifuge pre-cooled to 4 °C. DNA pellet was washed twice with 1 ml ice cold 70% ethanol. Ethanol was removed completely and DNA pellet was dried for 10 min at RT with the tube's lid open. The DNA pellet was resuspended in 50 µl TE-buffer containing 0.1 mg RNase A per ml. DNA was analyzed by analytical restriction digest (see 3.2.7) for the presence of the insert DNA before subsequent preparative DNA purification (Maxiprep, see 3.2.3).

3.2.3 Preparative DNA purification from E. coli (Maxiprep)

For preparative DNA purification 200 ml bacterial overnight culture were harvested by centrifuging at 9605 g for 30 min (JLA16.250 rotor, Beckman Coulter). The bacterial pellet could be stored at -20 °C prior to DNA purification. DNA purification was carried out using the PureLink HiPure Plasmid Maxiprep Kit according to the manufacturer's instructions.
DNA concentration was determined by UV/VIS spectrophotometry using the NanoDrop 1000 and purity was determined by monitoring the ratio of absorbance at 260/280 nm, which should be in the range of 1.8 to 2.0. The DNA concentration was adjusted to 1 mg/ml.

3.2.4 Ligation

Ligation was carried out in a reaction volume of 20 µl using the T4 DNA ligase. Digested vector DNA and insert DNA were used in 1:3 molar ratio with 200 ng of vector DNA. Ligation was performed at 16 °C overnight or at RT for 2 hrs.

3.2.5 Oligo design

mRNA sequence of protein of interest was downloaded from the UCSC website according to the human hg19 genome. Favoured restriction enzyme sites and protein tags were added according to the experimental needs. Two corresponding oligos were adjusted in length and melting temperature using T_m Calculator. Primer oligos were purchased from Sigma.

3.2.6 Polymerase chain reaction (PCR) for DNA amplification for cloning

Phusion polymerase was used for PCR amplification of insert DNA. Primer oligos were designed as explained above (see section 3.2.5). A two-step protocol was run to ensure binding of whole primer sequence once restriction sites and protein tag sequences had been added to the template. The PCR reaction was pipetted as mentioned in Table 3.2 and the general PCR program is mentioned in Table 3.3. Annealing temperature of primer oligos was calculated using the T_m Calculator.

Table 3.2: PCR reaction mixture.

Component	**Final amount**
Template DNA	100 ng
5x Phusion HF buffer or GC buffer	1x
DMSO	Up to 6% (v/v)
dNTPs	200 µM
Primer 1	500 nM
Primer 2	500 nM
Phusion polymerase	1 U
Water	Fill up to 50 µl

Table 3.3: PCR program.

Step	**Temperature**	**Time**
Initial denaturation	98 °C	30 sec
4 cycles	98 °C 55-70 °C (depending on oligo primers) 72 °C	10 sec 10 sec 30 sec per kb
28 cycles	98 °C 55-70 °C (depending on oligo primers) 72 °C	10 sec 10 sec 30 sec per kb
Final extension	72 °C	5 min
Hold	4 °C	∞

3.2.7 Restriction digest

Restriction digest was performed using two different restriction enzymes. Enzymes from NEB were used, which could be added simultaneously to the reaction, since the provided cut smart buffer was optimized for all restriction enzymes used here. For a preparative digestion, e.g. of a PCR product or a vector backbone, 2 µl of restriction enzymes were used in a reaction volume of 50 µl and incubated for 4 hrs at 37 °C. Wherever applicable, restriction enzymes were heat inactivated as described in the manufacturer's instructions. Restriction digest was always followed by a gel purification clean-up to prevent unprecise cutting by the enzyme (see sections 3.2.9 and 3.2.10). For an analytical restriction digest, e.g. of miniprep DNA, 0.5 µl restriction enzymes were used in a reaction volume of 20 µl and incubated for at least 2 hrs at 37 °C. Analytical digest was visualized on an agarose gel (see section 3.2.9).

3.2.8 Cloning of shRNAs

shRNAs against a protein of interest were selected based on published data (Fellmann et al. 2013; Pelossof et al. 2017) (splash algorithm). Five shRNAs were selected per protein of interest and ordered as dissolved DNA oligo from Sigma in HPLC quality. 10 ng DNA oligos were inserted for PCR amplification to generate overhangs for corresponding restriction enzymes (Table 3.4 and Table 3.5).

Table 3.4: shRNA-PCR reaction mixture

Component	**Final amount**
Template shRNA oligo	10 ng
5x Phusion HF buffer	1x
DMSO	5% (v/v)
dNTPs	200 µM
Primer 1	500 nM
Primer 2	500 nM
Phusion polymerase	1 U
Water	Fill up to 50 µl

Table 3.5: shRNA-PCR program.

Step	**Temperature**	**Time**
Initial denaturation	98 °C	2 min
20 cycles	98 °C 62 °C 72 °C	25 sec 25 sec 20 sec
Final extension	72 °C	5 min
Hold	4 °C	∞

The PCR product was checked on a 3% agarose gel (see section 3.2.9 below) and DNA was purified by chloroform-phenol extraction (see section 3.2.14). DNA was digested with XhoI and EcoRI-HF simultaneously for 3 hrs and gel purified (see section 3.2.10). Cloning procedure was performed as usual.

3.2.9 Agarose gel electrophoresis

Agarose gel electrophoresis was performed to visualize DNA fragments. Depending on the fragment size, 0.8, 1.0, 2.0 or 3.0% agarose gels were used. The corresponding amount of agarose was melted in 180 ml of 1x TAE buffer. After cooling down, 3.6 µl Ethidium bromide were added and the solution was poured into a tray with a comb. Agarose gel electrophoresis was performed at 160 V for 1.5 hrs.

3.2.10 DNA gel extraction

After restriction digest, enzymes had to be removed from the reaction and proper restriction digest had to be proven. Therefore, DNA was visualized and purified via agarose gel electrophoresis (see section 3.2.9). Subsequently, the desired DNA band was cut out from the gel using UV-light visualization. DNA was purified using the GeneJET Gel Extraction Kit according to the manufacturer's instructions and eluted in nuclease-free water.

3.2.11 Generation of DNA inserts by DNA-block synthesis

Insert DNA fragments, which could not be generated by PCR, were purchased from the IDT company as gblock with 5´-phosphorylation. The synthesized DNA was inserted by blunt-end ligation into the pJET vector (CloneJET PCR Cloning Kit) according to the manufacturer's instructions.

3.2.12 Bioanalyzer/Fragment Analyzer

DNA library prior to sequencing (see section 3.3.15) was analyzed on Bioanalyzer using the Experion Automated Electrophoresis System chips or on Fragment Analyzer using the NGS Fragment High Sensitivity Analysis Kit (1-6,000 bp).

3.2.13 Quantitative real-time PCR (qPCR)

qPCR was used to determine chromatin IP efficiency. The qPCR was performed in a 96-well format and technical triplicates were made per DNA and oligo primer pair combination. Each oligo primer pair was diluted to 10 µM in water within one tube. The SYBR Green-primer mixture was prepared by calculating 4.5 µl SYBR Green and 0.5 µl oligo primer pair (10 µM) dilution per well. 5 µl of this SYBR Green-primer mixture and 5 µl of DNA were added per well. The plate was sealed with foil and shortly spun down. List of qPCR oligo primers can be found in materials (section 2.6.1.3). The qPCR was performed in a quantitative RT-PCR machine (StepOnePlus Real-Time PCR System) with the following program:

Table 3.6: qPCR program.

Step	Cycles	Temperature	Time
Initial denaturation	1	50 °C 95 °C	2 min 2 min
Denaturation	40	95 °C	3 sec
Annealing and extension		60 °C	30 sec
Melting curve	1	95 °C 60 °C rise to 95 °C with +0.3°C 95 °C	15 sec 1 min 15 sec

ChIP efficiency was calculated by the enrichment over input (1%). In addition, the fold enrichment over an IgG control (IP with beads coupled to unspecific IgG antibody, see ChIP protocol section 3.3.13) and a primer pair corresponding to a negative region not found in the human or murine genome were used to check antibody specificity.

To calculate the enrichment of each sample, the CT value (cycle threshold) of each sample was subtracted from the input: $\Delta CT = CT_{Input} - CT_{ChIP}$.

Relative expression was calculated as: 2^ΔCT

Average CT value and standard deviation were calculated from technical triplicates using Microsoft Excel functions.

3.2.14 DNA isolation by chloroform-phenol extraction and ethanol precipitation

The appropriate amount of the corresponding buffer was added to each sample to a final volume of 300 µl. The same amount of Phenol/Chloroform mixture was added and the resulting mixture was vortexed intensively for 15 sec and put on a rotating wheel for 5 min. Phases were separated by centrifugation at 20817 g for 5 min. The upper clear phase containing DNA was transferred into a fresh tube. For DNA precipitation, 1 ml ice-cold 100% ethanol was added along with 30 µl sodium acetate and 1 µl GlycoBlue Coprecipitant for pellet visualization. Solutions were mixed by inverting the tube 8 times and DNA was precipitated for at least 30 min at -20 °C. DNA was pelleted by centrifugation for 20 min at 20817 g in a pre-cooled centrifuge (4 °C). DNA pellet was washed twice with 1 ml of 70% ice-cold ethanol. After completely removing the ethanol, the DNA pellet was dried for 10 min at RT with the tube’s lid open. DNA pellet was resuspended in an appropriate amount of TE buffer or water (e.g. 300 µl for ChIP (see section 3.3.13), 30 µl for ChIPseq (see section 3.3.14)).

3.3 Biochemistry

3.3.1 *Crosslinking of antibodies to magnetic beads*

Per 10 µl magnetic Dynabeads (Protein A : Protein G = 1:1) 1 µg of antibody was added. Antibody was coupled to the beads by incubating overnight at 4 °C on a rotating wheel in 700 µl BSA/PBS solution. Beads were washed three times with BSA/PBS, three times with 0.1 M sodium dihydrogen phosphate buffer (pH 8.0) and once with 0.2 mM triethanolamine (TEA, pH 8.2). Covalent crosslinking of the antibodies to the beads was performed for 45 min at RT on a rotating wheel with 10 mM dimethyl pimelimidate dihydrochloride (DMP) in TEA. Beads were washed once with 0.1 M ethanolamine (pH 8.0) and blocked for 1 hr in ethanolamine (RT, rotating wheel). Finally, the beads were washed three times with PBS and resuspended in the corresponding buffer depending on further applications.

3.3.2 *Whole cell extracts*

Whole cell extracts were generated by directly adding 1x Laemmli sample buffer to the cells and scraping them off the plate. For 6 cm dish 500 µl were used, for 10 cm 700 µl, and for 15 cm 1 ml. To reduce viscosity, 1 µl of Benzonase was added, followed by incubation for at least 30 min at RT on a rotating wheel. Samples were denatured by heating at 95 °C for 5 min and then stored at -20 °C.

3.3.3 *Protein purification of native chromatin-bound RNAPII complexes*

The purification of native RNAPII complexes was based on the protocol published in PNAS in 2008 (Aygun, Svejstrup, and Liu 2008).

Filtered tips were used and all buffers were sterile filtered, stored at 4 °C and freshly supplemented with protease and phosphatase inhibitors. All centrifugation steps were carried out in centrifuges pre-cooled to 4 °C.

Stable cell lines of U2OS and T-lymphoma cells were generated expressing the C-terminally HA-tagged RPB3 subunit (HA) of RNAPII or the corresponding empty vector (EV).

3.3.3.1 Cell harvest

For U2OS cells 2.5 x10^6 cells were seeded per 15 cm dish the day before harvest. 41 dishes were harvested per IP condition. Then, cells were washed twice with cold PBS and scraped off in 1 ml cold PBS containing phosphatase and protease inhibitors. Cells were pelleted at 209 g for 15 min. Cell pellet was flash frozen in liquid nitrogen and stored at -80 °C.

For T-lymphoma cells two days before harvest per condition 7x 15 cm dishes were generated with 25 ml of 1 x10^6 cells per ml. The day before harvest another 25 ml fresh medium were added per dish. Cells were collected by transferring 200 ml into one Beckman tube and centrifuging with 300 g for 20 min (JLA16.250, Beckman Coulter). Cell pellet was washed twice with cold PBS containing phosphatase and protease inhibitors. Cell pellet was flash frozen in liquid nitrogen and stored at -80 °C.

3.3.3.2 Cell fractionation

Per condition 5 ml of MS Cytoplasmic Lysis Buffer were added to the cell pellet and cell swelling was enhanced by pressing the solution through a 200 µl pipet tip. First lysis was performed for 20 min on rotating wheel at 4 °C. Nuclei were collected by centrifugation (3900 g, 20 min) and supernatant was collected containing the cytoplasmic fraction. Nuclei were washed once in MS Nuclei Washing Buffer and immediately spun down again. Second lysis was performed by addition of 5 ml of MS Nuclear Lysis Buffer and homogenization of the cells in a 7 ml glass homogenizer for 10 and 15 strokes for U2OS and T-lymphoma cells, respectively, followed by 20 min incubation on ice. Chromatin was pelleted in Corex glass tube at 20442 g for 30 min (JA25.50, Beckman Coulter) and supernatant was collected containing the nucleoplasmic fraction. To extract chromatin-bound proteins, 2 ml of MS Nuclease Incubation Buffer were added to the chromatin and homogenizer was used 30 strokes for U2OS and 45 strokes for T-lymphoma cells. Additionally, samples were sonicated using the Branson Digital Sonifier 4 times for 10 sec each with 45 sec pausing (amplitude 20%) in a maximum of 2 ml. Benzonase (100 U) were added per ml sample and nucleic acids were digested for 40 min at 16 °C with 14000 rpm shaking. Chromatin was pelleted in ultracentrifugation tubes (Beckmann Coulter) at 39191 g for 30 min (JA25.50, Beckman Coulter) in pre-cooled centrifugation adapters. Supernatant containing solubilized proteins was collected for further immunoprecipitation. To the pelleted chromatin 1x Laemmli sample buffer was added (same amount as supernatant) as well as 1 µl Benzonase to reduce viscosity and incubated on rotating wheel for at least 15 min (RT).

Successful fractionation as well as bait distribution was monitored by western blot analysis of the different fractions.

3.3.3.3 HA-Immunoprecipitation

Per IP condition 80 µl covalently coupled magnetic HA-beads were used and washed three times in MS Nuclease Incubation Buffer. Equal amount of lysate was used per condition and 1% input was kept for later analysis. Additionally, 150 U of Benzonase were added to the lysate per IP. IP was carried out for 3 hrs rotating in cold room (4 °C). Afterwards, beads were washed four times in MS IP Washing Buffer supplemented with 0.1% TritonX-100 with the fourth washing step being incubated for 5 min with rotation in cold room. Additional two washing steps were performed with MS IP Washing Buffer without the addition of TritonX-100 and solutions were transferred into fresh tubes within the last washing step. MS IP Washing Buffer was removed completely.

For elution 4x LDS Sample Buffer was diluted to 1x in Millipore water. 100 µl 1x LDS Sample Buffer were added to each sample and samples were eluted by incubation in thermo shaker at 37 °C for 30 min with 450 rpm shaking. Supernatant of elution 1 was collected and DTT was added to a final concentration of 50 mM before boiling at 95 °C for 5 min. Second elution was performed by adding another 100 µl 1x LDS Sample Buffer to the beads as well as DTT (final concentration 50 mM) and boiling at 95 °C for 7 min. Elutions were not combined, but elution 2 was used to visualize elution efficiency. Efficient immunoprecipitation of the bait, its associated proteins as well as elution efficiency were analyzed by PAGE followed by silver staining with 4.5% of elution 1 and 2. Finally, elution 1 was handed over to the research group of Andreas Schlosser (Rudolf Virchow Center, Würzburg) for label-free quantitative mass spectrometry (qMS, see section 3.3.3.4 below).

3.3.3.4 Sample preparation for label-free quantitative mass spectrometry

Sample preparation of eluted HA-immunoprecipitated material was mainly performed by the research group of Andreas Schlosser (Rudolf Virchow Center, Würzburg) and main steps are described here. For alkylation of proteins iodoacetamide was added to a final concentration of 120 mM and samples were incubated in the dark for 20 min. Proteins were precipitated by adding four volumes of pre-cooled 100% acetone, vortexing and incubating samples overnight at -20 °C. Samples were centrifuged with 16000 g for 20 min at 4 °C and protein pellet was washed three times with cold acetone. Pellet was dried and proteins were digested in 0.5% Sodium Deoxycholate (SDC) with 0.25 µg Lys C for 2 hrs at 30 °C and 0.25 µg Trypsin at 37 °C overnight with 600 rpm shaking. SDC extraction was performed twice using ethylacetate and 0.5% trifluoroacetic acid (TFA) by vortexing and shaking for 2 min and centrifuging at 16000 g for 2 min (Masuda, Tomita, and Ishihama 2008). Proteins were further purified via 3 discs of C18 Empore SPE Disks (3M) in a 200 µl pipet tip (Rappsilber, Ishihama, and Mann 2003). Then, StageTips were prewet in 50 µl methanol, washed in 50 µl 60% acetonitrile (ACN) and 0.3 % formic acid (FA) and conditioned twice with 50 µl 0.3% TFA. Samples were loaded after the addition of 100 µl 0.3% TFA to the StageTips. Three washes were performed using

2% ACN and 0.3% TFA. Elution was done twice in 20 µl 60% ACN and 0.3% FA and samples were dried overnight in Lyophylle. Proteins were resuspended in 24 µl 2% ACN and 0.1% FA by vortexing for 10 min and 2 min of sonication and transferred into HPLC vial.

Samples were measured by nanoLC-MS/MS in Orbitrap Fusion mass spectrometer (Thermo Fisher Scientific) at the research group of Andreas Schlosser.

For in gel digestion, samples were separated by SDS PAGE (NuPAGE system), gel lane was cut into pieces, destained (70 mM ammonium bicarbonate, 30 mM acetonitrile), equilibrated (100 mM ammonium bicarbonate, pH 7.8), dehydrated (100% acetonitrile), and dried by vacuum centrifugation before enzymatic digestion.

3.3.4 Protein purification of native chromatin-bound MYC

This protocol is adapted from Aygün et al. (Aygun, Svejstrup, and Liu 2008) and was optimized for natively solubilization of MYC and its interacting proteins.

U2OS cells and T-lymphoma cells were infected to express C-terminally HA-tagged c-MYC (HA) or with the corresponding empty vector (EV).

To avoid protein contaminations filtered tips were used and buffers were sterile filtered. All solutions were used cold and buffers were freshly supplemented with protease and phosphatase inhibitors.

3.3.4.1 Cell harvest

Cell seeding and harvest was performed as described for the purification of RNAPII complexes (section 3.3.3.1). The T-lymphoma cells harbour a MYC-Tet-Off system. To reduce competition of HA-tagged with endogenous MYC, T-lymphoma cells were treated with Doxycycline 16 hrs prior to harvest.

3.3.4.2 Protein isolation

Cell pellets were resuspended in 4 ml MYC Lysis Buffer and lysis was facilitated by using a 7 ml glass homogenizer for 10 strokes (U2OS cells) or 15 strokes (T-lymphoma cells) and by short sonication using the Branson Digital Sonifier: four repetitions of 10 sec sonication and 45 sec pausing with an amplitude of 20%. Sonication was performed in a maximum volume of 1 ml. To solubilize proteins from chromatin, 100 U Benzonase were added per ml lysate and incubated for 40 min on rotating wheel in cold room (4 °C). Samples were transferred into ultracentrifuge tubes (Beckman Coulter) and insoluble chromatin was pelleted at 39191 g for 30 min (JA25.50, Beckman Coulter) in pre-cooled centrifuge adapters. Supernatant was subsequently used for HA-immunoprecipitation and to chromatin pellet 1x Laemmli with 1 µl

Benzonase were added. Chromatin pellet was incubated on rotating wheel for at least 15 min (RT) to reduce viscosity. Solubilization of MYC was validated by western blot analysis.

3.3.4.3 HA-Immunoprecipitation

HA-Immunoprecipitation was performed as described for RNAPII complex purification for qMS. Eluted fractions were analyzed by PAGE followed by silver staining before proceeding with sample preparation for qMS (see sections 3.3.3.3 and 3.3.3.4).

3.3.5 Protein quantification by Bicinchoninic acid (BCA)

Protein amount in lysates was determined in technical triplicates. Assay was pipetted in a 96-well format. BCA solutions A and B were mixed in a ratio of 50:1. As standards BSA dilution row was used with concentrations of 0, 0.5, 1, 2, 4, 8, and 16 mg/ml. 1.5 µl of sample or BSA standard or lysis buffer were added per well. Finally, 150 µl of Solution A/B mixture were added per well using a multistep pipet. Reaction was performed at 37 °C for 15 min. Plate was mixed by shaking for 5 sec with 780 rpm and absorbance at 550 nm was measured using the Multiskan Ascent plate reader. Protein concentration of lysates was determined by subtracting the background value of the lysis buffer and then fitting the value to the standard curve generated using the BSA dilutions.

3.3.6 Protein quantification by Bradford

Bradford assay was performed in 96-well plate and each sample was measured in technical triplicates. Standard curve was generated by measuring BSA dilutions (0, 0.25, 0.5, 0.75, 1.0, 1.25, 1.5, 1.75, and 2.0 mg/ml). 1.5 µl of sample, BSA standard or lysis buffer were pipetted per well. 150 µl Bradford reagent were added per well using a multistep pipet. Additionally, 2 µl 150 mM NaCl were added. Plate was shaken for 5 sec with 780 rpm and absorbance at 630 nm was measured using the Multiskan Ascent plate reader. Standard curve was made from measurement of BSA dilutions. Background (lysis buffer) was subtracted from sample values and protein amount was calculated using to the standard curve.

3.3.7 Polyacrylamide Gel Electrophoresis (PAGE)

BisTris gels were casted using the BioRad gel casting system. Solutions were prepared from 3.5x BisTris buffer, Acrylamide and Millipore water. APS and TEMED were added just before pouring the mixture in the cast. For separation gel 8, 10 or 12% Acrylamide were used according to the size of the proteins of interest. Stacking gel was prepared with 4% Acrylamide.

Protein samples were supplemented with 6x Laemmli sample buffer to generate 1x Laemmli sample buffer concentration, boiled for 5 min at 95 °C and shortly spun down. Per gel pocket a maximum of 20 µl per sample were loaded. Equal amount of proteins was loaded using a 25 µl or 50 µl glass syringe (Hamilton). Additionally, a molecular weight marker was used at both sides of the gel. Usually the PageRuler Prestained Protein Ladder (10-180 kDa, Thermo Fisher Scientific) was used, but for proteins with a molecular weight exceeding 180 kDa the Colour Prestained Protein Standard Broad Range (11-245 kDa, New England Biolabs) or the HiMark Pre-Stained Protein Standard (31-460 kDa, life technologies) were utilized. Electrophoresis was performed in 1x MOPS running buffer supplemented with 1x reducing solution at 80 V until separation gel was reached and then voltage was increased to 120 V.

3.3.8 Immunoblot (Western Blot) – Fuji system

Western blot was performed in Peqlab wet blotting system filled with 1x transfer buffer. After separation of proteins by electrophoresis, they were transferred onto a PVDF membrane. Membrane was activated by incubating in methanol for 30 sec. The immunoblot was assembled as followed with all components being soaked in 1x transfer buffer: black side of cassette (minus pole), one sponge, 2 Whatman papers, gel, membrane, 3 Whatman papers, one sponge, red site of cassette (plus pole). Air bubbles were removed by gentle rolling over each layer of the sandwich. Transfer was performed for 3 hrs at 400 mA in cold room (4 °C). After transfer was completed, membrane was washed once in TBS-T before blocking it for 1 hr at RT in blocking solution. Later, blocked membrane was again rinsed briefly in TBS-T before incubating with primary antibody overnight at 4 °C. Next day, membrane was washed 6 times for 5 min each with TBS-T, incubated with HRP-labelled secondary antibody for 1 hr at RT (diluted 1:7500 in blocking solution; 1:3000 for TrueBlot antibodies) and again washed 6 times with TBS-T for 5 min each. Immobilon Western HRP Substrate was added according to the manufacturer’s instructions to visualize antibody by chemiluminescence and detected by LAS-4000 mini imager (Fujifilm). Proteins were quantified with normalization to a loading control using the ImageStudio Lite software (LI-COR).

3.3.9 Immunoblot (Western Blot) – LI-COR system

Immunoblot could also be performed using the LI-COR system, which detects a fluorescent labelled secondary antibody. Immunoblot was essentially performed as described above (section 3.3.8). Besides this, membrane was washed in TBS without the addition of Tween-20.

As blocking solution Odyssey Blocking Buffer (LI-COR) was diluted 5x in TBS. Primary and secondary (1:15000) antibodies were diluted in Odyssey Blocking Buffer in TBS (1:5, LI-COR). Western blot was imaged on Odyssey CLx (LI-COR) and proteins were quantified with ImageStudio Lite software (LI-COR).

3.3.10 Coomassie staining

After PAGE, gel was incubated in Instant blue solution for 1 hr at RT with gentle shaking. Instant blue was removed and gel was washed with Millipore water with gentle shaking until the background stain was low. Water was renewed several times. Stained gel was imaged.

3.3.11 Silver staining

After PAGE, gel was incubated in Gel Fixation Solution for 1 hr with gentle shaking. Afterwards, gel was washed three times for 20 min with Gel Washing Solution. Gel Reducing Solution was added for 1 min followed by three washing steps with Millipore water for 20 sec each. Gel was incubated with Gel Silver Solution for another 20 min. After two additional washing steps with Millipore water for 20 sec each, Gel Developing Solution was added and gel was incubated until protein bands reached the desired intensity. Finally, development was stopped in Gel Stopping Solution for 10 min. Gel was imaged and could be stored in Millipore water for few days.

3.3.12 Immunoprecipitation (IP)

Adherent cells were washed once with cold PBS and scrapped off in IP Buffer containing protease and phosphatase inhibitors. For 10 cm dish 700 µl IP Buffer and for 15 cm dish 1 ml IP Buffer were used. Suspension cells were pelleted (470 g, 10 min, 4 °C) and cell pellet was washed once in cold PBS containing protease and phosphatase inhibitors before IP Buffer containing protease and phosphatase inhibitors was added. Cell lysis was carried out for at least 30 min on rotating wheel in cold room. Cell debris were removed by centrifugation at 20817 g for 10 min (4 °C). Supernatant was flash frozen in liquid nitrogen and stored at -80 °C or directly utilized for immunoprecipitation (IP). Lysate obtained from equal number of cells seeded was used per IP. Otherwise, protein concentration of lysates was determined by BCA or Bradford assays (see sections 3.3.5 and 3.3.6) and equal amount of proteins were used per IP. Per condition 20 µl Dynabeads were used. For HA-tagged proteins covalently coupled beads were used. Otherwise, corresponding antibody was coupled to the beads the evening before IP. Per IP condition a 1:1 ration of Protein A and Protein G Dynabeads (Thermo Fisher Scientific) were washed three times with 5 g/L BSA in PBS (BSA/PBS). Overnight 2 µg corresponding antibody was coupled to 20 µl ProteinA/G Dynabeads in 700 µl BSA/PBS. Beads for several conditions were coupled in one reaction and distributed right before adding the lysate. Before IP, beads were washed two times in BSA/PBS and once in IP Buffer to remove uncoupled antibody. Lysate was added to the beads and incubated for 3 hrs on rotating wheel in cold room. Additionally, lysate corresponding to 0.5, 1.0, or 2.0% input according to the experimental design were taken before IP and used for comparison later. After incubation, beads were washed six times in IP Buffer with changing the reaction tube in the last washing step. Proteins bound to antibody-coupled Dynabeads were eluted by adding 2x Laemmli sample buffer and cooking the sample for 5 min at 95 °C. In this method, the antibody gets also eluted. Proteins bound to covalently coupled HA-beads were eluted by the addition of 1x LDS sample buffer to the beads and incubation for 30 min at 37 °C and 450 rpm shaking. Eluate was removed from the beads and DTT was added to the eluate to a final concentration of 50 mM prior to cooking at 95 °C for 5 min.

For immunoprecipitation of tagged proteins, a control IP was performed with lysates from cells not expressing the tagged protein.

For immunoprecipitation of endogenous proteins, a control IP was performed with Protein A/G Dynabeads coupled to unspecific IgG of corresponding species of the specific antibody (e.g. IgG rabbit for MYC IP with abcam Y69 antibody).

3.3.12.1 Incubation with CDK7

For the incubation with CDK7, proteins of interest were expressed in HEK293T cells and HA-IP was performed as described above. Washed but not eluted HA-beads after IP were split into two conditions. Beads were incubated in CDK7 buffer and active recombinant CDK7 complex (Mat1, CyclinH, CDK7), a gift from the Cramer laboratory (Boehning et al. 2018), was added to one condition (15 µM), and to the control no CDK7 complex was added. Samples were incubated at 30 °C for 1 hr. Beads were washed four times with changing the reaction tube in the last washing step. Proteins were eluted in 1x LDS buffer by incubating at 37 °C for 30 min with 450 rpm shaking. Finally, DTT was added to the eluate to a final concentration of 50 mM and samples were boiled for 5 min at 95 °C.

3.3.12.2 Incubation with recombinant CTD

GST-tagged CTD and pCTD (pSer5) pre-incubated with active CDK7 were a gift from Robert Düster, group of Matthias Geyer, University of Bonn. Proteins of interest were expressed after transient transfection in HEK293T cells and HA-IP was performed as described above. After incubation of lysate with HA-beads, HA-beads were washed and separated into seven conditions. To the control IP Buffer was added. Three conditions were incubated with increasing concentrations of GST-CTD and three conditions with increasing concentrations of GST-pCTD (0.1, 0.5, 1.0 µg). All conditions were incubated for 3 hrs at RT with rotation in the presence of phosphatase inhibitors. HA-beads were washed four times with changing the reaction tube in the last washing step. Immunoprecipitated proteins were eluted in 1x LDS buffer by incubation for 30 min in a thermo shaker set to 37 °C and 450 rpm. DTT was added to the eluates to a final concentration of 50 mM and samples were boiled for 5 min at 95 °C.

3.3.13 Chromatin immunoprecipitation (ChIP)

siRNA treated cells for MYC knockdown were harvested 48 hrs post transfection (see section 3.1.9).

Cells harbouring an inducible shRNA against SPT5 were harvested 48 hrs post shRNA induction by Doxycycline (see section 3.1.10).

One plate per condition was trypsinized and cell number was determined (see section 3.1.3 and 3.1.4) before starting ChIP procedure.

3.3.13.1 Crosslinking of proteins to DNA

First, proteins were crosslinked to DNA by adding formaldehyde to a final concentration of 1%, distributed by gentle swirling and incubated at RT for 10 min. Crosslinking was stopped by the addition of 125 mM glycine final concentration, mixed by gentle swirling and incubated for another 5 min at RT.

After crosslinking, all followings steps were performed on ice and with pre-cooled reagents.

3.3.13.2 Cell harvest

For adherent cells, medium was removed and cells were washed twice with cold PBS before scrapping them off in 1 ml of cold PBS containing protease and phosphatase inhibitors per 15 cm dish. Scraped cells were pelleted at 470 g for 15 min at 4 °C.

Suspension cells were pelleted at 470 g for 15 min in a pre-cooled centrifuge (4 °C) and cell pellet was washed twice in cold PBS containing protease and phosphatase inhibitors.

Cell pellet was flash frozen in liquid nitrogen and stored at -80 °C.

3.3.13.3 Chromatin preparation

Cell pellet was thawed and lysed in 1 ml ChIP Lysis Buffer I containing protease and phosphatase inhibitors per 10 x10^6 cells. For spike-in for later normalization, 10% of cells from a different species were used, e.g. murine T-lymphoma cells, which had been crosslinked as mentioned above (see section 3.3.13.1). Antibody to be used for IP later must be able to recognize the species of spiked-in cells. Cell lysis was performed for 20 min on ice and nuclei were collected by centrifugation (470 g, 15 min, 4 °C). Nuclei were lysed in 1.5 ml of ChIP Lysis Buffer II containing protease and phosphatase inhibitors for a maximum of 40 x10^6 cells. Lysis was carried out for 10 min on ice. Sonication was performed using Branson Digital Sonifier in cold room (4 °C). 1.5 ml of lysate was transferred in a 15 ml tube. Chromatin fractionation was performed as follows: intervals of 10 sec with 45 sec pausing and an amplitude of 25% for a total of 20 min. Aliquots of 25 µl were taken at the time points 0, 1 and 20 min of sonication and chromatin size was controlled on an agarose gel. Therefore, RNA was digested for 1 hr at 37 °C by adding 40 µg/ml RNase A along with 258,8 µl TE Buffer and 160 mM NaCl final concentration. Crosslink was reverted overnight at 65 °C with 650 rpm shaking. Proteins were digested by addition of 200 µg/ml Proteinase K and 4 mM EDTA and incubated for 2 hrs at 45 °C with 650 rpm shaking. Afterwards, DNA was isolated by chloroform-phenol extraction followed by ethanol precipitation (see section 3.2.14). DNA pellet was resuspended in 25 µl TE buffer and 10 µl were analyzed on a 2% agarose gel. Meanwhile, fragmented chromatin was stored on ice till fragment size had been determined to a size of 200 nt.

3.3.13.4 Immunoprecipitation (IP)

The day before IP, Dynabeads were coupled to the corresponding antibodies. Per IP condition, 15 µl Protein A and 15 µl Proteins G Dynabeads (Thermo Fisher Scientific) were mixed and washed three times with 1 ml BSA/PBS. For antibody coupling, 3 µg of corresponding antibody (or unspecific IgG as a control) were added to 30 µl Dynabeads in a total of 400 µl BSA/PBS and incubated overnight at 4 °C with rotation. If same antibody was needed for several conditions it was coupled at once and divided just before IP procedure.

The day of IP, beads were washed three times with 1 ml of BSA/PBS to remove unbound antibody and, if necessary, beads were divided according to different conditions. Fragmented chromatin, of which suitable size had been verified, was centrifuged for 20 min at 20817 g (4 °C). Chromatin corresponding to one 15 cm dish was added per IP condition. 1% input was kept for later enrichment calculation. IP was performed for 6 hrs in cold room on rotating wheel. After IP, beads were washed three times with ChIP Wash Buffer I, ChIP Wash Buffer II, ChIP Wash Buffer III with rotating incubation for 5 min each, and with TE Buffer with renewing the tube in the last washing step. TE Buffer was completely removed before elution was performed by incubating in 150 µl of freshly prepared ChIP Elution Buffer for 15 min at RT with rotation. Elution was performed twice in the volume of 150 µl each and the two eluted fractions were pooled resulting in 300 µl. 1% input sample was filled up to 300 µl with ChIP Elution Buffer. For eluted samples and 1% input samples RNA was digested and de-crosslinked by adding 14 µl of 1 M Tris-HCl buffer (pH 7.4), 11.2 µl of 5 M NaCl and 2 µl RNase A (10 mg/ml stock). Samples were incubated at 37 °C for 1 hr and overnight at 65 °C with 650 rpm shaking. Proteins were digested by adding 5 µl Proteinase K (20 mg/ml stock) and 3.5 µl of 0.5 M EDTA and incubating for 2 hrs at 45 °C and 650 rpm shaking. DNA was isolated by chloroform-phenol extraction and ethanol precipitation as described before (see section 3.2.14). DNA was resuspended in 300 µl water and IP efficiency was analyzed with quantitative real-time PCR (see section 3.2.13).

3.3.14 ChIPsequencing sample preparation

Samples for ChIPseq were prepared as described for ChIP (see section 3.3.13). Per IP a total of 100 µl Dynabeads were coupled to 15 µg antibody and chromatin corresponding to 50 x10^6 cells were used per IP. Isolated DNA was resuspended in 30 µl nuclease-free water. From this, 3 µl DNA were diluted to 130 µl and utilized for further analysis by quantitative real-time PCR (see section 3.2.13).

3.3.15 ChIPsequencing library preparation

ChIP quality was determined by qPCR as enrichment over input and over a negative region (see section 3.2.13). ChIP-DNA concentration was determined by Picogreen measurement (see section 3.3.16). Equal amount of DNA for input and ChIP samples were used for library preparation. Library preparation was performed using the NEBNext ChIPseq Library Prep Master Mix Set for Illumina and the NEBNext Multiplex Oligos for Illumina (New England Biolabs) according to the manufacturer's instructions for all samples along with a water control in addition to detect possible DNA contamination. After each enzymatic reaction a purification step via QIAquick PCR Purification Kit and QIAquick MinElute DNA Purification Kit (Qiagen) was inserted according to the manufacturer's instructions with elution in 0.3x EB Buffer. Adapters were diluted 1:30 in 0.3x EB Buffer prior to use. After Adapter ligation, size selection was performed by running a 2% agarose gel and DNA was cut out in between 200 – 250 bp and purified using the QIAquick Gel Extraction Kit according to the manufacturer's instructions. Number of PCR cycles was adjusted to starting material (17 cycles for siMYC experiment; 16 cycles for shSPT5 experiment). Quality and concentration of DNA library were verified by running on Bioanalyzer (BioRad) using the Experion Automated Electrophoresis

System chips or on Fragment Analyzer (Advanced Analytical) using the NGS Fragment High Sensitivity Analysis Kit (1-6,000 bp; Advanced Analytical). Equimolar concentrations of samples were mixed and this mix was again analyzed on Bioanalyzer or Fragment Analyzer prior to sequencing on NextSeq 500 sequencer (Illumina).

3.3.16 Picogreen

Picogreen measurement was used to quantify ChIP-DNA prior to library preparation and performed using the Quant-iT PicoGreen dsDNA Assay Kit (Thermo Fisher Scientific) according to the manufacturer's instructions. DNA standard curve was prepared using 0, 50, 250, 500, 1000, 2000 and 5000 pg of standard DNA. For every sample and DNA standard technical duplicates of 1 µl were measured. Input samples were pre-diluted 10-fold. For measurement Infinite 200 PRO NanoQuant Microplate Reader (Tecan) was used.

3.3.17 Purification of recombinant SPT4 and SPT5

Strep-MYC and His-DSIF (SPT4 and SPT5) were co-expressed and purified from *E. coli* by Maren Bleckmann, Core facility for protein purification, Rudolf Virchow Center Würzburg. Experimental details are described in brief. Bacteria were grown at 37 °C and protein expression was induced by the addition of 1 mM IPTG at an OD of 0.5. Bacteria were harvested 3 hrs post induction, pellet was resuspended in Purification Buffer I and flash frozen in liquid nitrogen. Cells were broken up by short sonication and lysates were cleared by centrifugation. Proteins were purified via His-Beads (IDA) followed by Streptavidin beads for 1 hr at 4 °C. For the elution from the His column 500 mM imidazole (pH8.0) were added to the Purification Buffer I.

His-DSIF (SPT4 and SPT5) was expressed and purified from *E. coli* by Lars Schönemann, Core facility for protein purification, Rudolf Virchow Center Würzburg. Bacteria were grown at 37 °C and protein expression was induced at an OD of 0.5 by the addition of 1 mM IPTG. After 3 hrs bacterial cells were harvested and pellet was frozen in liquid nitrogen. Pellet was resuspended in Purification Buffer II and cells were lyzed by short sonication. Lysates were cleared by centrifugation and His-tagged proteins were purified by Ni-NTA resin with incubation for 1 hr at 4°C. Column was washed twice with Purification Buffer II, twice with High Salt Wash Buffer, once with Purification Buffer II and eluted in 7 fractions in Purification Buffer II supplemented with 300 mM Imidazole (pH8.0).

3.3.18 Pull down with recombinant proteins

Protein G Dynabeads were coupled to MYC-specific antibody (Y69) for 3 hrs at 4 °C with rotation in Pull down Buffer containing 300 µg/ml BSA. 5 µl coupled beads were used per condition. Recombinant proteins were produced and purified by Robert Düster (MBP-MYC from insect cells, research group of Matthias Geyer, University of Bonn) and Lars Schönemann (SPT5 and SPT4 from *E. coli*, Protein core facility, Rudolf Virchow Center). 10 µg of bait protein and 10 µg of prey protein were incubated together for 3 hrs in Pull down Buffer (4 °C with rotation). Beads were washed thrice and added to the recombinant proteins and incubated for 1.5 hrs at 4 °C (with rotation). Beads were washed twice with Pull down Buffer, twice with NETN Buffer, and transferred into a new reaction tube in Pull down Buffer before eluting in 1.5x Laemmli Buffer and boiling at 95 °C for 5 min.

3.4 Data Analysis

3.4.1 Mass spectrometry data analysis

Data analysis from label-free quantitative mass spectrometry (qMS) was performed by Jens Vanselow, Stephanie Lamer and Andreas Schlosser (Rudolf Virchow Center, Würzburg). Additional p- and q-value calculations were performed by Apoorva Baluapuri (research group of Elmar Wolf, University of Würzburg). Main steps are described here. Raw qMS data files were analyzed with MaxQuant software (Cox and Mann 2008) and database search with Andromeda. The search was performed against the UniProt human reference proteome database (download date: 2016-12). The search was performed with tryptic cleavage specificity with 2 allowed miscleavages.

Protein identification was controlled with the false-discovery rate (<1% FDR on protein and peptide level). In addition to MaxQuant default settings (e.g. at least 1 razor/unique peptide for identification, 2 allowed miscleavages), the search was performed against following variable modifications: Protein N-terminal acetylation, Gln to pyro-Glu formation (N-term. Q) and oxidation (on Met). For protein quantitation, the LFQ intensities were used (Cox et al. 2014). Proteins with less than two identified razor/unique peptides were rejected. Missing LFQ intensities in the control samples were imputed with values close to the baseline if intensities in the corresponding IP samples were present. Data imputation was performed with values from a standard normal distribution with a mean of the 5% quantile of the combined LFQ intensities and a standard deviation of 0.1. To calculate significant enrichment within one experiment, proteins were sorted based on their intensity values and over all proteins a box plot was generated. The interquartile range (IQR) was determined. Proteins with enrichment values differing from the median of the boxplot by more than 1.5-fold of IQR were determined as significantly enriched and with more than 3-fold of IQR as highly significantly enriched.

Within replicates, missing log2 fold change values for individual samples were imputed via MICE package in R, and the p- and q-values were calculated using the linear method in the limma package in R. For RNAPII proteomic analysis, interacting proteins were defined by log2FC(HA/EV) > 2 and q-value < 0.1 and n>2. For MYC proteomic analysis, interacting proteins were defined by log2FC(HA/EV) > 1 and q-value < 0.1.

3.4.2 Next-generation sequencing

ChIPseq data analysis was performed by Apoorva Baluapuri (research group of Elmar Wolf, University of Würzburg). The main steps are described here. Base calling was performed with Illumina's CASAVA software and overall sequencing quality was tested using the FastQC script. Reads were mapped to the human genome (hg19) or the murine genome (mm10) with Bowtie2 with allowing one mismatch generating a SAM-file (Langmead et al. 2009). Normalization was done based on the scaling factor for each spiked-in ChIPseq dataset calculated (Orlando et al. 2014). SAM-files were sorted using SAMtools and converted into BAM-files. All samples were normalized to the sample with the smallest number of mapped reads; therefore, reads were randomized. Indexed BAI-files were created before conversion into bedgraph-files. BedGraphs were visualized in Integrated Genome Browser (IGB). Meta gene analysis was performed using NgsPlot software (Shen et al. 2014). For density plot generation the normalized BAM files were converted to BED files. Read densities were calculated using Bedtools *coveragebed*, binned and summarized using R.

4 RESULTS

4.1 Analyzing RNAPII-interacting proteins by mass spectrometry

The transcription factor MYC is known to influence transcription of RNAPII and to be bound to almost all open promoters. We hypothesize that MYC shapes the composition of the transcriptional machinery as shown for the loading of the PAFC (Jaenicke et al. 2016). To test this hypothesis on a global scale, we needed to purify native complexes of transcriptionally engaged RNAPII with transcription factors being bound. Proteins interacting with RNAPII were identified by subsequent quantitative mass spectrometry. Using a model system in which MYC expression can be manipulated allows the comparison of the RNAPII interactome determined from cells with different MYC levels.

4.1.1 Establishing a native purification protocol

4.1.1.1 Crosslinking of antibodies

The purification method of RNAPII and its interacting proteins used here was based on a method published in PNAS in 2008 (Aygun, Svejstrup, and Liu 2008). The authors showed that Benzonase treatment, which digests DNA and RNA, increases the solubilization of chromatin-bound factors and enables the native purification of transcription-engaged RNAPII complexes (Figure 4.1).

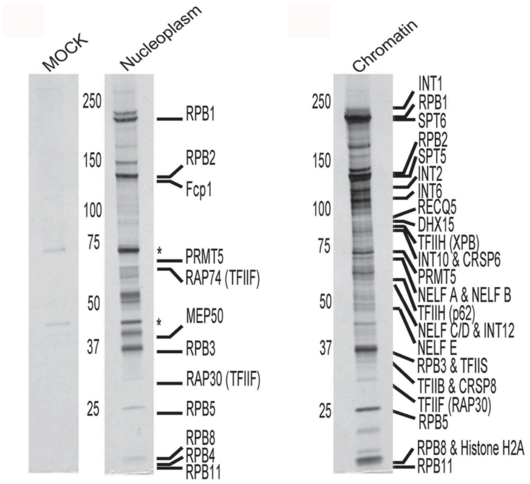


Figure 4.1: Purification method of native RNAPII complexes.

Silver gel staining of proteins found in RNAPII IP from HEK293T cells. Elutions from cell extracts without (left) and with (right) Benzonase treatment are shown.

Figure 1 A and B from (Aygun, Svejstrup, and Liu 2008).

I adapted this protocol for U2OS cells and a schematic overview is shown in Figure 4.2.A. In brief, cells were harvested, nuclei were isolated followed by isolation of the chromatin-bound fraction. Proteins were extracted from chromatin by mechanical force followed by extensive Benzonase treatment, resulting in the digestion of DNA and RNA and the release of bound proteins. Detailed method description can be found in section 3.3.3. To visualize the distribution of RNAPII throughout the different cellular fractions, I performed immunoblotting of the largest subunit of RNAPII (RPB1), irrespective of its CTD modification (total RNAPII, Figure 4.2.B). The “Extract” fraction indicates RNAPII protein, which could be solubilized from chromatin by Benzonase treatment, but there was still RNAPII detected in the “Chromatin” fraction, which could not be solubilized from chromatin.

To enrich for RNAPII and its interactors, immunoprecipitation (IP) using a RNAPII-specific antibody is needed. The “Extract” fraction was utilized as an input for IP. Subsequently, quantitative label-free mass spectrometry (qMS) was performed to identify RNAPII-bound proteins.

The usage of antibodies specific for certain phosphorylation statuses of the CTD of RNAPII for the IP step would enable to see changes in the RNAPII interactome in regard to defined steps within the transcription cycle. Two antibodies were used: IgG as a negative control and an antibody recognizing pSer5 modified CTD of RNAPII. Both antibodies were either crosslinked (CL) to the bead material using DMP (see section 3.3.1) to avoid contamination of the IP samples with eluted antibody, which would be detected by qMS, or only incubated with the beads without crosslinking. Therefore, input material was allocated into four conditions and incubated with IgG, IgG-CL, pSer5, or pSer5-CL beads. As shown in Figure 4.2.C the IgG control did not bind RNAPII. Both, pSer5 and pSer5-CL bound RNAPII, but a dramatic reduction in the affinity of the crosslinked antibody was observed compared to the non-crosslinked one. For all four conditions Elution1 was sufficient in releasing RNAPII complexes from the bead material. These results were confirmed by silver staining (Figure 4.2.D). We concluded that the DMP-crosslinking method either damaged the antibody or blocked its epitope as shown by severe reductions in IP efficiency, which made it unsuitable for our experimental set-up.

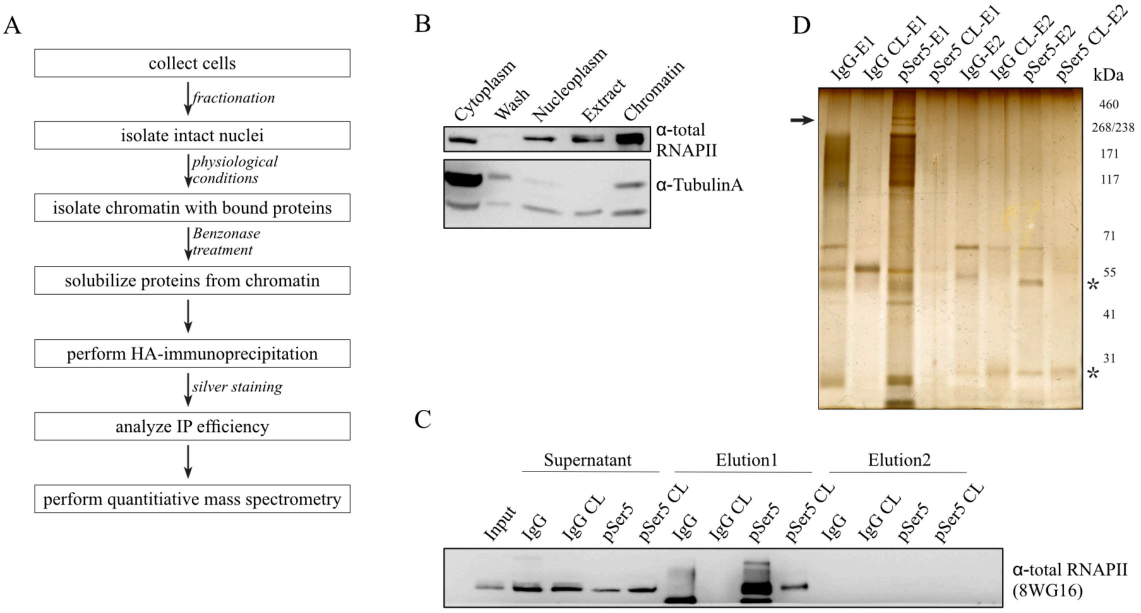


Figure 4.2: Purification method for native RNAPII complexes from U2OS cells.

***A**. Extraction strategy of native complexes of chromatin-bound, transcription-engaged RNAPII.*

***B**. Immunoblot of cell fractionation. Distribution of total RNAPII (RPB1 independent of its phosphorylation status) within the different fractions is shown. Tubulin A served as cytoplasmic marker. Extract fraction was used for subsequent immunoprecipitation.*

***C**. Immunoblot of total RNAPII (RPB1 independent of its phosphorylation status) from IP-experiment. Extract fraction from B was divided into four IP conditions: Immunoprecipitation of RNAPII by IgG control antibody or pSer5 RNAPII-specific antibody was determined as well as binding capacity of crosslinked (CL) versus non-crosslinked antibody. Elution1 was performed without DTT and Elution2 with DTT.*

***D**. Silver staining of PAGE gel with elution samples from C. IgG antibody was used as control. CL stands for crosslinked antibodies via DMP. The arrow indicates the two bands corresponding to hyper- and hypo-phosphorylated RPB1. * indicates antibody heavy and light chains eluted in Elution2 (E2). CL: crosslinked; E1: Elution1 (without DTT); E2: Elution2 (with DTT)*

4.1.1.2 Stable cell lines expressing fusion proteins

Since crosslinking of specific antibodies to the bead material led to a dramatic reduction in protein binding efficiency (Figure 4.2.C and D), a tag was introduced to enable the usage of commercially available covalently coupled beads for IP to avoid contamination of the eluted fraction with the antibody. I fused the third largest subunit of RNAPII, RPB3, to a C-terminal HA-tag and generated stable U2OS and T-lymphoma cell lines (shown for U2OS cells, Figure 4.3.A) by lentiviral transduction. C-terminally tagged RPB3 is known to be incorporated within a functional RNAPII complex (Aygun, Svejstrup, and Liu 2008). For all qMS experiments, HA-tagged protein expressing cells (HA) were compared to control cells not expressing an HA-tagged protein (empty vector, EV) to determine unspecific enrichment of proteins, for example by binding to the bead material or the antibody backbone.

As shown in Figure 4.3.B, the RNAPII complex was strongly enriched in the chromatin solubilized fraction (Extract), which was used for subsequent HA-IP, as shown for the largest subunits RPB1 and the bait RPB3 in both U2OS and T-lymphoma cells. Usage of covalently coupled HA-beads avoided contamination of the eluted fraction (E1) by the antibody. Efficiency and specificity of HA-IP and its elution were validated by silver staining of proteins (Figure 4.3.C). For Elution2 (E2) the harsher conditions resulted in remaining beads-bound proteins being eluted as well as the HA-antibody itself. Latter was visible by protein bands characteristic for antibody elution in E2 (marked with * in Figure 4.3.C). Further on, it could be shown that the main proportion of proteins was eluted within E1 elution. Hence, E1 was used for subsequent qMS, since E1 was sufficient in protein elution and like this contamination of the sample by the HA-antibody could be avoided.

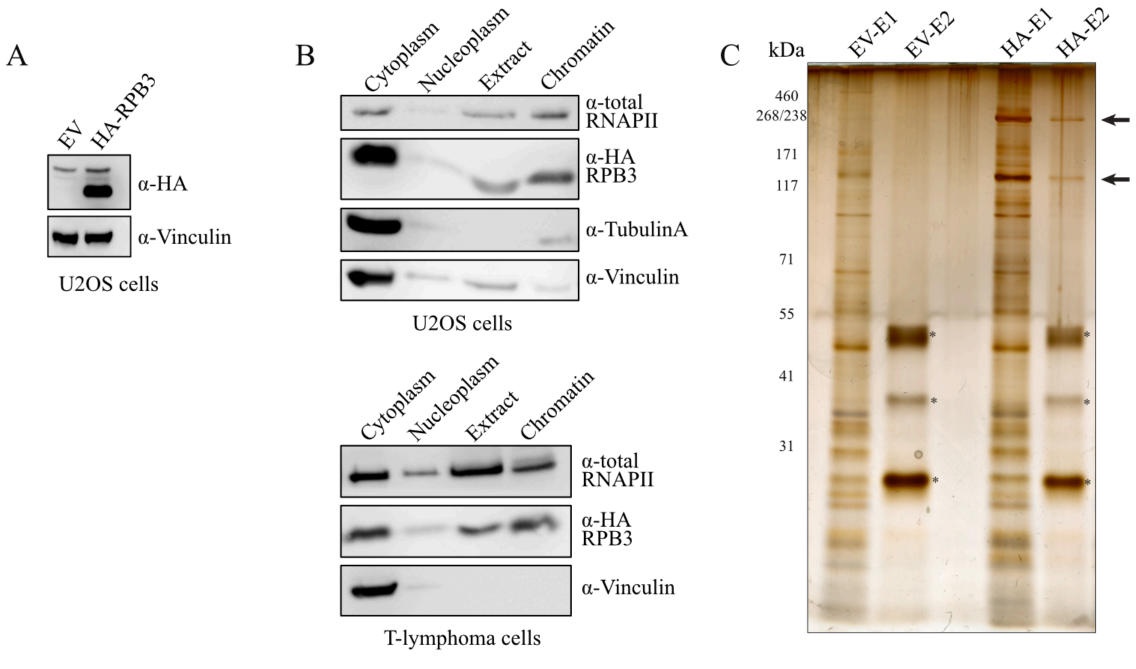


Figure 4.3: Extraction of HA-RPB3.

***A**. Western blot analysis of U2OS cells expressing HA-RPB3 or an empty vector (EV). Vinculin was used as a loading control.*

B**. Western blot analysis of extraction procedure. Cytoplasmic, nucleoplasmic, chromatin solubilized (Extract) and chromatin fractions were separated. Immunoblotting shows the distribution of total RNAPII (RPB1), HA-tagged RPB3 and one or two cytoplasmic markers (Tubulin A and Vinculin),* *respectively. Upper subfigure presents analysis performed in U2OS and lower in T-lymphoma cells.* ***C*. Silver stained PAGE. Elution1 (E1) and Elution2 (E2) are shown from HA-IP performed on Extract fraction from T-lymphoma cells expressing no HA-tagged protein (EV) or HA-RPB3. Arrows indicate bands corresponding to RPB1 and RPB2. * indicates the antibody being eluted in E2.*

4.1.1.3 Optimizing protein extraction from chromatin

The critical step within the extraction procedure is the release of proteins from chromatin, which is facilitated by Benzonase treatment. Benzonase has its optimal working temperature at 37 °C, however, proteases show highest enzymatic activity at 37 °C, too. Therefore, two different temperatures for Benzonase treatment were tested side by side: 16 and 4 °C. HA-RPB3 expressing T-lymphoma cells or EV control cells were harvested and fractionation was performed as described earlier. Chromatin fraction was divided and one half was incubated with Benzonase at 16 °C, the other at 4 °C. Distribution of RPB1 within the different fractions was monitored by immunoblotting and we concluded that the temperature did not influence the extraction efficacy since similar amounts of RPB1 were solubilized from chromatin (Figure 4.4.A).

Therefore, subsequent HA-IP was performed on the 4 °C samples and silver staining of elutions are shown in Figure 4.4.B. Similarly as depicted in Figure 4.3.C (16 °C), the bands corresponding to the antibody eluted in E2 are visible. In E1 from HA-cells there are two protein bands of comparable size to the 238/268 protein ladder bands, most likely corresponding to the hypo- and hyperphosphorylated RPB1. A protein band at approximately 120 kDa might be RPB2. All these bands are also very prominent in Figure 4.3.C. However, it becomes obvious when comparing Figure 4.4.B to Figure 4.3.C, that besides the three described protein bands only few additional protein bands were detected when Benzonase treatment was performed at 4 °C.

To see what proteins are found in the HA-IP of samples incubated at 16 °C or 4 °C with Benzonase, E1 of the HA-IPs was analyzed by label-free quantitative mass spectrometry (qMS) and samples were processed as described in the methods section 3.3.3.4. Upon the identification of charged, cleaved protein peptides by qMS, the abundance of proteins within the sample can be calculated as log10 intensity. Further on, the enrichment of each protein was calculated as the log2 fold change of a protein from HA-cells over EV-cells. Based on these values a significance for the protein enrichment can be calculated.

Reducing the Benzonase incubation temperature from 16 to 4 °C strongly decreased the amount of proteins found to be bound to RNAPII, despite RNAPII being solubilized to a similar extent and exhibiting similar enrichment values (compare Figure 4.4.C and D; for table with values see 7.3.1). When Benzonase treatment was performed at 4 °C only 16 proteins were found to be highly significantly enriched over the background (red), whereas Benzonase treatment at 16 °C resulted in 106 proteins with high confidence (red) and additional 66 proteins with lower confidence (green). Overall, 294 proteins had been identified by qMS in at 4°C treated samples and 1164 proteins in at 16 °C treated samples.

This led to the conclusion, that Benzonase treatment at 16 °C more efficiently released proteins from chromatin than at 4 °C as shown by an increasing number of proteins identified by qMS and especially by an increasing number of highly enriched proteins representing significant interactors of RNAPII (Figure 4.4). Subsequently, Benzonase treatment was performed at 16 °C for further experiments regarding RNAPII complexes.

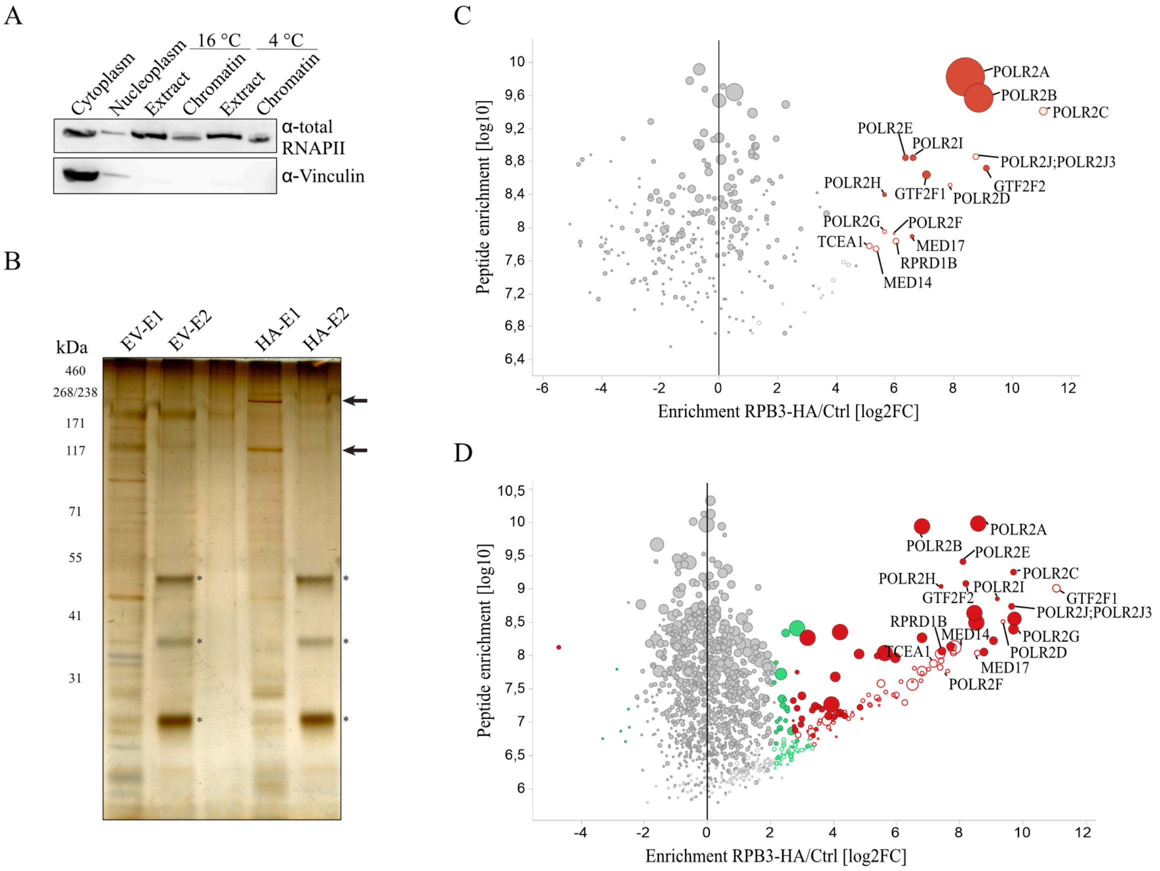


Figure 4.4: Optimizing protein extraction from chromatin.

A. Immunoblot for RPB1 within the different fractions from T-lymphoma cells. Cells were fractionated into Cytoplasm, Nucleoplasm, and chromatin-associated proteins. Chromatin fraction was equally splitted into two and protein extraction was performed upon incubation with Benzonase at 16 °C and 4 °C, respectively. Solubilized (Extract) and unsolubilized (Chromatin) RPB1 was stained using an antibody specific for RPB1 independent of its phosphorylation status (total RNAPII). Vinculin was used *as a marker for the cytoplasmic fraction.*

***B**. Silver stained PAGE of HA-IP elutions from T-lymphoma cells. Extract from A incubated with Benzonase at 4 °C was used for subsequent HA-IP. Elutions 1 (E1) and 2 (E2) from HA-RPB3 (HA) and EV control cells (EV) were analyzed by PAGE and proteins were stained by silver staining. . The arrows mark the protein bands with sizes corresponding to RPB1 and RPB2. * indicates the antibody being eluted in E2.*

***C**. and **D**. Enrichment plots showing the log2 fold change enrichment of proteins in HA-IP from HA-RPB3-expressing over EV T-lymphoma cells on the x-axis and log10 of protein intensity on the y-axis. Each circle represents a single identified protein. To calculate significant enrichment within one experiment, proteins were sorted based on their intensity values and over all proteins a box plot was generated (not shown) and the interquartile range (IQR) was determined. Proteins with enrichment values differing from the median of the boxplot (not shown) by more than 1.5-fold of IQR were determined as significantly enriched (green) and with more than 3-fold of IQR as highly significantly enriched (red). Open circles depict imputed values of proteins with zero peptides being detected in the control cells. The circle size represents the number of unique peptides identified for the corresponding protein.*

***C**. Enrichment plot for RNAPII protein complexes extracted with 4 °C Benzonase treatment. Highly significantly enriched proteins (based on protein distribution within the plot) are shown in red and labelled with the gene name. 16 proteins had been identified as highly significant interactors.*

***D**. Enrichment plot for RNAPII protein complexes extracted with 16 °C Benzonase treatment. Highly significantly enriched proteins (based on protein distribution within the plot) are shown in red and the ones significantly enriched as compared to the background (grey) in green. For better comparison, only the 16 proteins identified as significant interactors in C are labelled with their gene names. 106 proteins had been identified as highly significant interactors (red) and 66 proteins as significant interactors (green).*

4.1.2 RNAPII interactome – experimental setup

The experiments described so far resulted in an optimized protocol for the extraction and purification of native, chromatin-bound, and transcriptionally-engaged RNAPII complexes via the IP of HA-tagged RPB3 from U2OS and T-lymphoma cells as described in methods section 3.3.3.

For qMS experiments two cell systems were used: first, the human osteosarcoma U2OS cell line harboring a MYC-Tet-On system. U2OS cells express comparably low levels of MYC (Lorenzin et al. 2016). The addition of Doxycycline results in massive overexpression of MYC (Figure 4.5.A) (Lorenzin et al. 2016; Walz et al. 2014). Second, a murine T-lymphoma cell line engineered with a MYC-Tet-Off system (van Riggelen et al. 2010) was employed and in response to treatment with Doxycycline, MYC protein levels get depleted within 2 hrs, cells arrest in proliferation, and upon 2 days of continuous treatment cells undergo apoptosis (Figure 4.5.B and master thesis of Sarah Dötsch, 2017, research group of Elmar Wolf, University of Würzburg).

The aim was to investigate if the transcription factor and proto-oncogene MYC is able to introduce changes in the proteins bound to RNAPII. Therefore, series of experiments were performed in above described T-lymphoma$^{\text{MYC-Tet-Off}}$ and U2OS$^{\text{MYC-Tet-On}}$ cells, in which the RNAPII interactome could be investigated under varying MYC levels in the cells. MYC has earlier been described to influence P-TEFb recruitment to paused RNAPII to facilitate its pause release (see section 1.10.3) (Eberhardy and Farnham 2001, 2002; Rahl et al. 2010). To analyze, if MYC-mediated effects on the RNAPII interactome are CDK9-dependent, which is the kinase subunit of P-TEFb, the RNAPII interactome was in addition analyzed after the treatment with the CDK9-inhibitor Flavopiridol.

In summary, following qMS experiments have been performed for RNAPII in T-lymphoma$^{\text{MYC-Tet-Off}}$ cells (Figure 4.5.C, black): five from cells expressing MYC (Ethanol, MYC ON), four in cells depleted for MYC expression (Doxycycline, Tet-Off system, MYC OFF), three experiments from cells expressing MYC and treated with the CDK9-inhibitor Flavopiridol (MYC ON Flavo), and finally another three experiments from cells depleted of MYC expression (Doxycycline) and treated with the CDK9-inhibitor Flavopiridol (MYC OFF Flavo). Additionally, the RNAPII interactome was analyzed three times from U2OS$^{\text{MYC-Tet-On}}$ cells expressing normal MYC levels (MYC ON) and once expressing strongly elevated MYC levels (Doxycycline, MYC HIGH), as well as once after Flavopiridol treatment (MYC ON Flavo) and after the combination of MYC overexpression (Doxycycline) and Flavopiridol treatment (MYC HIGH Flavo) (Figure 4.5.C, grey).

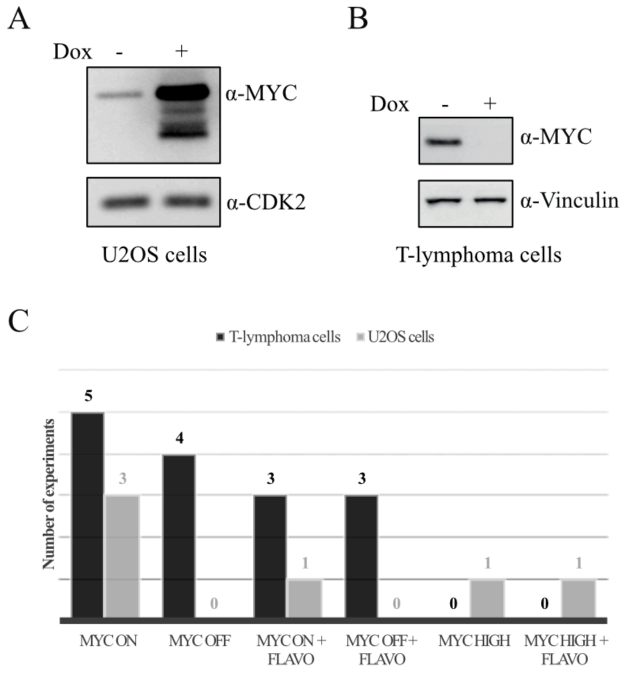


Figure 4.5: Overview of qMS experiments performed for HA-RPB3.

A. *Western blot analysis of MYC overexpression in U2OS cells upon Doxycycline treatment. CDK2 served as a loading control.*

B. *Western blot analysis of MYC depletion in T-lymphoma cells upon Doxycycline treatment. Vinculin was used as a loading control. This figure was published in a similar form in (Baluapuri et al. 2019).*

C. *Bar chart illustrating number of experiments performed in T-lymphoma (black) and U2OS (grey) cells. In T-lymphoma cells the MYC-Tet-Off system was used for MYC depletion (MYC ON and MYC OFF). In U2OS cells the MYC-Tet-On system was used to induce MYC overexpression (MYC ON and MYC HIGH). CDK9-dependency was analyzed by a combinatorial treatment of MYC manipulation and the CDK9-inhibitor Flavopiridol (Flavo).*

4.1.3 RNAPII interactome – from T-lymphoma cells

The Figure 4.6 depicts enrichment plots of three biological replicates from T-lymphoma cells illustrating proteins enriched in HA-RPB3 IP (for table with values see 7.3.2). For better comparison, 12 proteins comprising known RNAPII-interactors are labelled. As expected, most abundant proteins are RNAPII subunits as shown for the bait (*POLR2C*) and four additional subunits (*POLR2A*, *POLR2B*, *POLR2E*, and *POLR2H*). Furthermore, two subunits of the integrator (*INTS1* and *INTS4*) as well as one mediator subunit (*MED14*) are highlighted. Very abundantly, the initiation factor GFTIIF was detected (*GTF2F1* and *GTF2F2*). Representing elongation, the two elongation factors SPT5 (*SUPT5H*) and SPT6 (*SUPT6H*) are labelled.

When comparing the overall amount of proteins identified, it becomes obvious that within Rep2 (Figure 4.6.B) there were much less proteins identified than in Rep1 (Figure 4.6.A) or Rep3 (Figure 4.6.C) and when comparing the enrichment of single proteins within these three replicates, changes within their enrichment can be observed. For example, the three labelled subunits from the integrator and the mediator complex are more abundant in Rep1 (log2FC between 6 to 9) and Rep3 (log2FC between 6 to 8) than in Rep2 (log2FC 4 to 6). This results in a shift from highly significant RNAPII interactors to less significant interactors for MED14 and INTS1. Even more dramatic changes could be observed for the elongation factor SPT6, which is found not to be enriched within Rep3 over control cells.

Direct comparison of the labelled proteins within the three replicates, which are known interactors of RNAPII, demonstrates the necessity of replicates to get a reliable picture of proteins interacting with RNAPII by determining q-values as a reliability score of that interaction.

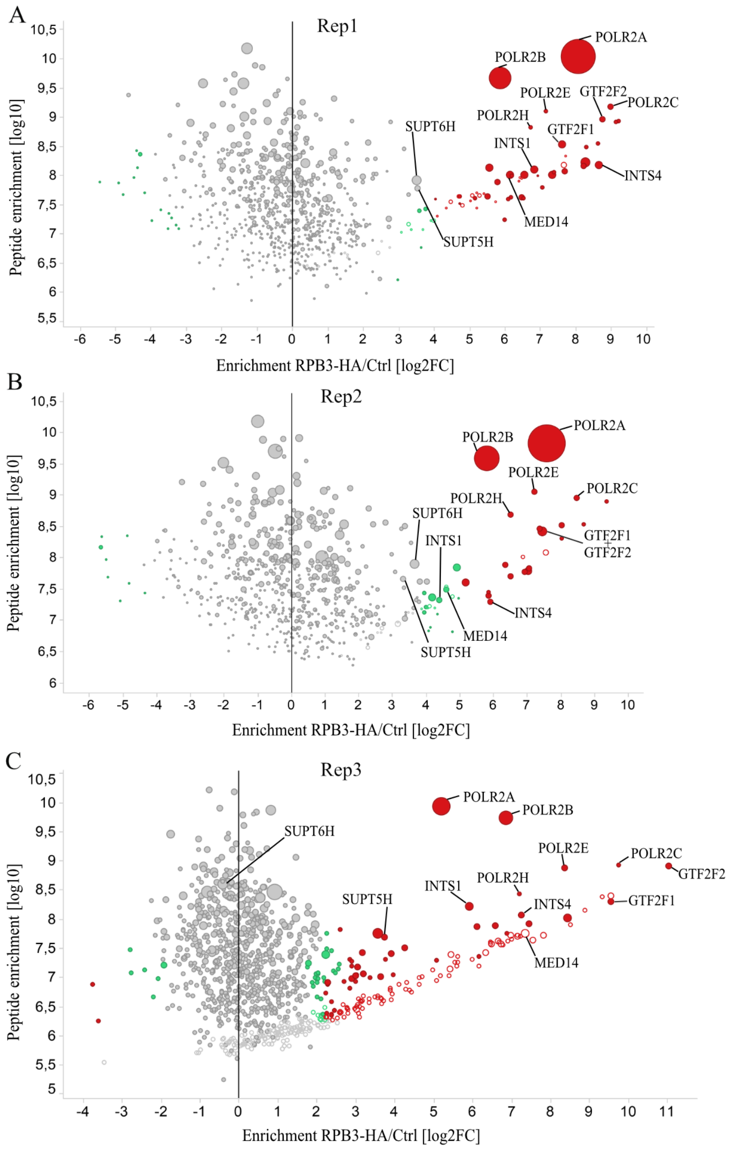


Figure 4.6: Enrichment plots of three biological replicates of RNAPII-interacting proteins from T-lymphoma cells.

Enrichment plots were generated as for the Figure 4.4. Overall protein intensity is shown on y-axis (log10) and fold change of HA-RPB3-expressing cells over EV control cells on x-axis (log2FC). Each circle represents one protein, while open circles indicate that the value of the EV control had to be imputed for fold change calculations. Circle size indicates the number of unique peptides identified for the very protein relative to the other proteins within the same plot. Coloring indicates a significance in the interaction based on the distribution of the proteins within each plot, with red showing highly significant interactors and green significant interactors. Same 12 proteins had been labelled for comparison.

***A**. Enrichment plot of the replicate 1 (Rep1) from T-lymphoma cells.*

***B**. Enrichment plot of the replicate 2 (Rep2) from T-lymphoma cells.*

***C**. Enrichment plot of the replicate 3 (Rep3) from T-lymphoma cells.*

The interactome of RNAPII from T-lymphoma cells (n=5) is shown in Figure 4.7.A and consists of proteins with known functions in all phases of the transcriptional cycle, enforcing solubilization of chromatin engaged, transcribing RNAPII complexes (for table with values see 7.3.3). Depending on the log2 fold change enrichment values in HA-RPB3- over EV-expressing cells (log2FC>2) as well as the q-value calculated from 5 experiments (q<0.1), 101 proteins were determined as significant interactors of RNAPII in T-lymphoma cells, which had to be identified in 3 out of 5 experiments (n>2). Four out of the 101 significant interactors did only match these cut-offs in the four experiments performed after MYC depletion (see section 4.1.5). Strongest enrichment is detected for the 11 out of 12 RNAPII subunits (red) including the bait RPB3 (*POLR2C*; log2FC=8.9). RPB10 (*POLR2L*) was not detected, which might be due to either its small size of only 8 kDa or to sample preparation.

Very prominently, subunits comprising the mediator complex (yellow) and subunits of the integrator complex (green) were identified, both known to interact with RNAPII. The mammalian mediator core complex comprises up to 26 subunits and a four subunits kinase module, which can reversibly associate with the core complex (Borggrefe et al. 2002). 24 subunits were significantly enriched in the RNAPII interactome belonging to mediator's middle, head, and tail regions. Subunits belonging to its kinase module were either not enriched or not identified at all. This goes in line with the finding that association of the kinase module with the core mediator results in conformational changes abolishing simultaneous binding to RNAPII (Tsai et al. 2013).

All 14 subunits of the integrator complex were found to be significantly enriched in the RNAPII interactome. The integrator was originally found to be involved in snRNA processing, but a role in the premature transcriptional termination is also discussed. The high abundance within the interactome suggests a more general role in RNAPII transcription than snRNA maturation. Highest enrichment was observed for subunits INTS4 and INTS6 with the log2FC of 7.8 and 7.4, respectively.

Identified general transcription factors comprising the PIC have been marked in purple colour. The two subunits of GTFIIF were prominently enriched in all replicates and in some even exhibiting as strong enrichment as the bait itself (GTF2F1 log2FC=8.2 and GTF2F2 log2FC=8.4).

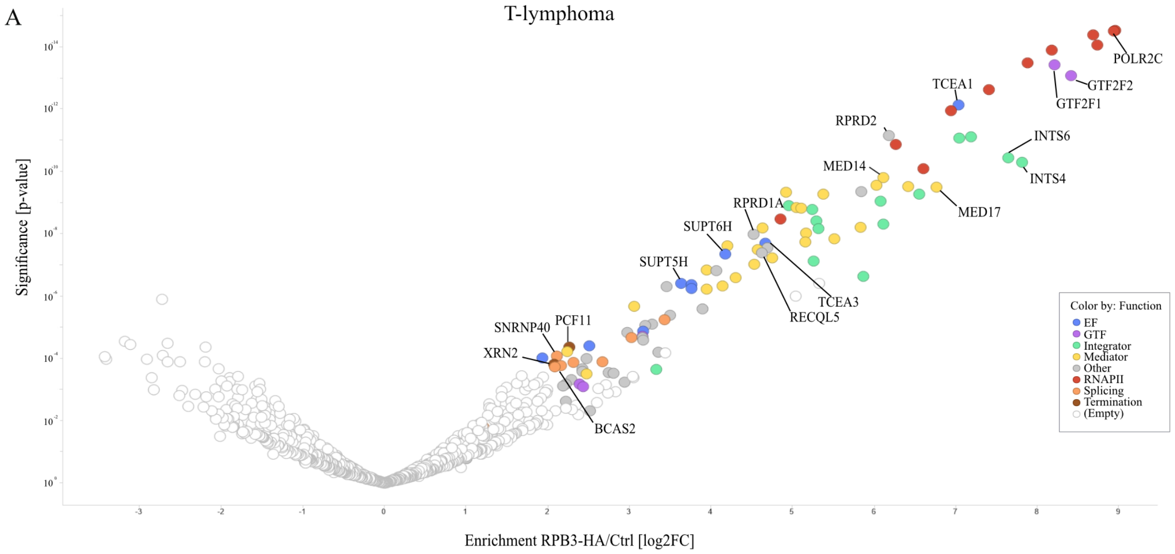
Highly enriched proteins involved in transcriptional elongation (blue) include SPT6 (*SUPT6H* log2FC=4.2), SPT5 (*SUPT5H* log2FC=3.6), TFIIS (TCEA1 log2FC=7.0 and TCEA3 log2FC=4.7), several components of the PAFC (CDC73 log2FC=3.8, PAF1 log2FC=3.8, and CTR9 log2FC=3.2), ELL (log2FC=2.5), and SCAF8 (log2FC=1.9).

Proteins playing a role in splicing, like components of the spliceosome or RNA-binding proteins facilitating splicing or alternative splicing, are depicted in orange. Among them, the strongest enrichment was found for the RNA-binding protein RBM22 (log2FC=3.0), a pre-mRNA splicing factor. Two other exemplary proteins of this category are BCAS2 (log2FC=2.2) and SNRNP40 (log2FC=2.1).

Proteins marked in brown have described functions in transcriptional termination and in T-lymphoma cells only two proteins exhibiting a function in transcriptional termination are found to be significantly enriched in the RNAPII interactome, namely PCF11 (log2FC=2.3) and XRN2 (log2FC=2.1).

Proteins not belonging to any of those functional groups are presented in grey colour. These include proteins with a role in mRNA export, as well as phosphatases, kinases, proteasomal subunits and proteins with no described function in transcription. Within this group of proteins, very strong enrichment was observed for phosphatases, including subunits of Protein Phosphatase 2 (PPP2R1A, log2FC=4.7 and PPP2CB, log2FC=4.1) and RPRD1A (log2FC=4.5) and RPRD1B (log2FC=5.8) implicated in de-phosphorylation of RNAPII's CTD. RECQL5, an ATP-dependent DNA helicase, previously identified as a RNAPII interactor (Aygun, Svejstrup, and Liu 2008), is also strongly enriched over control cells (log2FC=4.6).

Gene ontology term (GO-term) analysis using the DAVID software for the significant interactors emphasized proteins of nuclear localization and their involvement in transcription (Figure 4.7.B).



B

Gene ontology term	q-value
Nucleus	$1.4\text{x}10^{-37}$
Transcription	$4.9\text{x}10^{-24}$
RNA processing	$1.8\text{x}10^{-25}$
Transcription initiation from RNAPII promoter	$6.2\text{x}10^{-36}$

T-lymphoma cells

Figure 4.7: RNAPII interactome from T-lymphoma cells.

__A__. Volcano plot showing the RNAPII interactome. Each circle corresponds to one identified protein. Y-axis depicts the p-value calculated from 5 independent experiments. X-axis depicts the log2 fold change of the enrichment of a protein in HA-RPB3 expressing cells over control cells. Significant interactors were defined by the cut-offs of log2FC>2 and q-value<0.1 and n>2, resulting in 101 proteins significantly interacting with RNAPII. The function of these 101 proteins is indicated by different colouring (see legend). Exemplary proteins for each functional group are labelled by their gene name.

__B__. Gene ontology term analysis. Using the DAVID software, significantly interacting proteins of RNAPII as defined in A for T-lymphoma cells were analyzed regarding their functional annotation and the resulting enrichment in GO-terms is depicted in table format.

This figure was published in a similar form in (Baluapuri et al. 2019).

4.1.4 RNAPII interactome – cell line-dependent changes

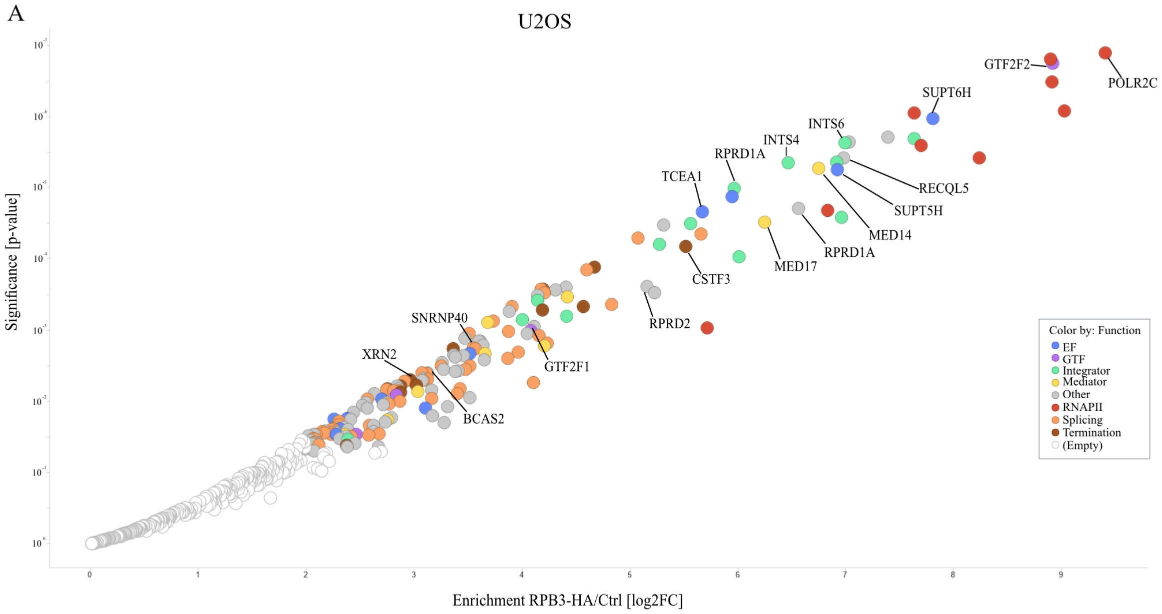
Results of qMS from U2OS cells (n=3) are shown in Figure 4.8.A (for table with values see 7.3.4). For U2OS cells only proteins exhibiting a positive enrichment in HA- over EV-cells were considered for p- and q-value calculations resulting in a different shape of the curve. We identified 154 proteins as significant interactors of RNAPII when same cut-offs are applied as for T-lymphoma cells. GO-term analysis by DAVID also confirmed that most of the identified significant interactors exhibit functions in transcription and are located in the nucleus (Figure 4.8.B).

To get an idea, on the one hand of consistent RNAPII interactors in both cell lines and on the other hand of divergent RNAPII interactors, I directly compared 101 proteins identified in T-lymphoma cells (black), and 154 proteins from U2OS cells (grey) (Figure 4.8.C). 57 proteins were found to be common in both interactomes (light grey). These are mainly RNAPII subunits, as well as mediator and integrator subunits and GTFIIF. Furthermore, they include well known RNAPII interactors, such as subunits of the PAFC, SPT5, SPT6, RECQL5 and XRN2.

The proteins significantly enriched only in T-lymphoma cells comprise more mediator subunits. This is due to the fact that these mediator subunits were identified in only one out of three qMS experiments from U2OS cells, although in this single experiment showing high enrichment over control cells. It is likely that the mediator complex got disrupted during the purification procedure prior to qMS in the other replicates. Other proteins showing enriched binding only in T-lymphoma cells are well known transcription-associated factors, such as GTFIIE, GTFIIH, VEZF1, SCAF8 or TRRAP.

For U2OS cells almost two third of the proteins defined as significant RNAPII interactors, were not defined as significant interactors in T-lymphoma cells. A closer look into these proteins revealed that most of these proteins indeed exhibit a function related to the transcriptional process and allow to conclude that this higher number of significant interactors was neither due to a higher unspecific binding nor to the enrichment of proteins not related to transcription. Among those proteins are especially the ones harboring a function in splicing, the regulation of alternative splicing or transcriptional termination, in particular proteins termed as cleavage and polyadenylation specificity factors (CPSFs). Furthermore, several SCAF proteins were identified, which contain a CTD-binding domain, but exhibit different functions. Lastly, analyses performed in U2OS cells detected other known transcription-related proteins, for example SSRP1, a subunit of the FACT complex, IWS1, an interactor of SPT6, the pausing factor NELFB and GTFIII (*GTF2I*).

A direct comparison of the interactomes resulting from T-lymphoma versus U2OS cells indicated a more complex interactome of RNAPII in U2OS cells.



B

Gene ontology term	q-value
Nucleoplasm	4.7×10^{-43}
Transcription	4.3×10^{-13}
RNA processing	1.6×10^{-75}
Transcription initiation from RNAPII promoter	3.4×10^{-15}

U2OS cells

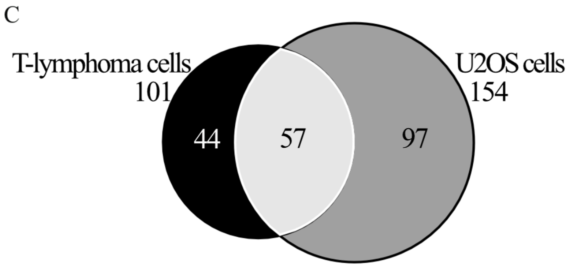


Figure 4.8: RNAPII interactome from U2OS cells and its overlap with T-lymphoma cells.

***A**. Volcano plot for the RNAPII interactome. P-value from three independent experiments was plotted over the log2 fold enrichment from HA-RPB3-expressing cells over EV control cells. Each circle displays an identified protein. Applying cut-offs of a q-value<0.1 and a log2FC>2 resulted in 154 proteins being significantly enriched in RNAPII binding. These 154 proteins were classified into functionally related group as indicated by different colouring (see legend). Exemplary proteins for each functional group are labelled with their gene name. For U2OS cells only proteins having a positive log2 FC over control cells were considered for p-value and q-value calculations and are depicted here.*

***B**. Gene ontology term analysis. Using the DAVID software, significantly interacting proteins of RNAPII as defined in A for U2OS cells were analyzed regarding their functional annotation and GO-terms are depicted in a table format.*

***C**. Venn diagram for significant RNAPII interactors for T-lymphoma and U2OS cells. In T-lymphoma cells 101 proteins were identified (Figure 4.7.A; black) and in U2OS cells 154 proteins (Figure 4.8.A; grey). 57 proteins were found to be significantly enriched in both cell lines (light grey).*

4.1.5 RNAPII interactome – MYC-dependent changes

MYC depletion in T-lymphoma cells (n=4, Figure 4.9; for table with values see 7.3.3) showed that the most abundant proteins identified by qMS were RNAPII subunits (red), similar to the control condition (Figure 4.7.A), indicating that MYC does not alter formation of the RNAPII holoenzyme itself. Subunits of the mediator (yellow) and the integrator (green) complex are identified as well. In addition, several proteins involved in transcription initiation (purple), elongation (blue), and termination (brown), as well as in mRNA splicing (orange), are detected.

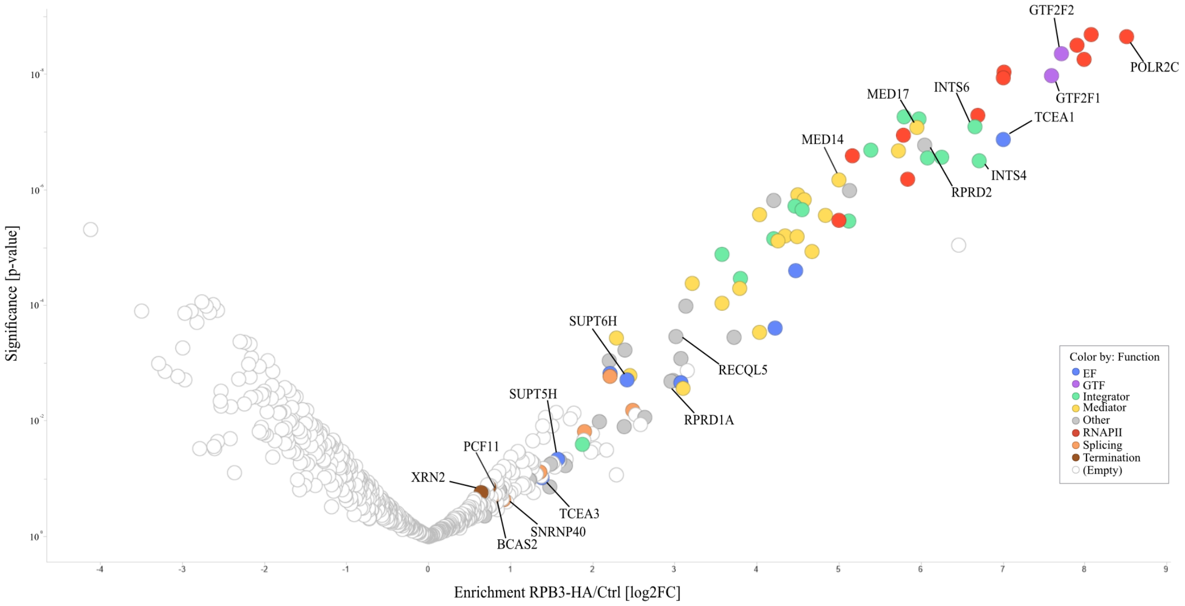


Figure 4.9: RNAPII interactome upon MYC depletion in T-lymphoma cells.

Volcano plot for the RNAPII interactome upon MYC depletion. P-values calculated from four independent experiments is plotted over the log2 fold change enrichment in cells expressing HA-RPB3 over EV control cells (Ctrl). Each circle represents one identified protein and the function of significantly enriched proteins (log2FC>2, q-value<0.1) is indicated by different colouring (see legend). Exemplary proteins for each functional group are labelled by the gene name.

To visualize MYC-dependent changes in the RNAPII interactome, log2 fold change of MYC-expressing cells (MYC ON) over cells depleted from MYC (MYC OFF) is shown in Figure 4.10.A (for table with values see 7.3.5). The proteins previously identified as significant RNAPII interactors (Figure 4.7.A) are shown in light grey. As expected, abundance of the RNAPII subunits was not affected by altered MYC levels. Only one protein was found to be significantly increased (p<0.05) in its interaction with RNAPII upon MYC depletion, VEZF1. VEZF1 is a transcription factor, associated with pausing of the elongating RNAPII and regulation of alternative splicing (Gowher et al. 2012).

Six RNAPII-interactors got significantly decreased in their binding to RNAPII upon MYC depletion ($p<0.05$), namely TCEA3, CCDC12, MED11, RPRD1A, ELL, and SPT5 (*SUPT5H*). Six more RNAPII interactors showed a decrease with less significance ($p<0.1$), namely MED18, RECQL5, EIF3A, PCF11, BCAS2, and INTS8, and SPT6 (*SUPT6H*) with p=0.107.
The strongest decrease was observed for TCEA3 (log2FC=3.4, p=0.0002), encoding TFIIS, a elongation factor helping in restarting of stalled RNAPII through the facilitation of mRNA cleavage by RNAPII (Dutta et al. 2015; Ehara et al. 2017; Elmendorf et al. 2001; Labhart and Morgan 1998; Sheridan et al. 2019; Xu et al. 2017; Zatreanu et al. 2019). However, the interaction of TCEA1, a paralog also encoding TFIIS (Labhart and Morgan 1998), with RNAPII was not influenced by MYC (log2FC=-0.3 and p=0.70). Divergent functions of TCEA3 and TCEA1 are already discussed with TCEA3 showing tumor suppressive functions and regulating differentiation of mouse embryonic fibroblasts (Kazim et al. 2020; Park et al. 2013). RECQL5 (log2FC=1.5, p=0.08) encodes a helicase inhibiting transcriptional elongation at DNA damage sites and blocks GTFIIS-binding to RNAPII (Aygun, Svejstrup, and Liu 2008; Aygun and Svejstrup 2010; Kassube et al. 2013; Saponaro et al. 2014).

As only two mediator subunits, MED11 (log2FC=2.2, p=0.01) and MED18 (log2FC=1.5, p=0.07), are decreased in RNAPII association upon MYC depletion in T-lymphoma cells, while the others are not affected suggests either a mediator complex-independent function of MED11 and MED18, or a false positive hit. Although MYC had previously been reported to facilitate binding of the mediator complex to some of its target genes (Adhikary and Eilers 2005; Bouchard et al. 2004) (see section 1.10.1), a general effect on all mediator subunits would have been expected. Similarly, for the integrator complex only one subunit, INTS8 (log2FC=1.2, p=0.09), showed decreased binding to RNAPII upon MYC depletion, however, there was no general effect observed on all integrator subunits.

Among the decreased interactors are three transcription elongation factors, SPT5 (log2FC=1.9, p=0.03), SPT6 (log2FC=1.3, p=0.107), and ELL (log2FC=1.7, p=0.02), and binding of SPT5 to RNAPII was affected most by MYC depletion. SPT5 is the large subunit of DSIF and its function in transcription is described in section 1.9. SPT6 was recently crystalized within the transcription elongation complex (Vos, Farnung, Boehning, et al. 2018). It binds to the linker region of the RPB1 subunit of RNAPII proximal to the CTD and additionally interacts with SPT5. SPT6 is a histone chaperone, interacting with SETD1A and SETD2, mediating histone repositioning and reassembly during transcription and therefore facilitates transcription elongation by RNAPII (Farnung, Vos, and Cramer 2018; Gopalakrishnan et al. 2019; Jeronimo, Poitras, and Robert 2019; Oqani et al. 2019; Vos, Farnung, Boehning, et al. 2018). ELL is an elongation factor and a component of the super elongation complex (SEC) facilitating pause release and transcriptional elongation of mRNAs, as well as the little elongation complex (LEC) facilitating snRNA transcription (Hu et al. 2013; Smith et al. 2011).

With PCF11 (lof2FC=1.3, p=0.08) one termination factor was found decreased in its interaction upon depletion of MYC. Three other proteins found to be decrease in RNAPII interaction upon MYC depletion are BCAS2 (log2FC=1.2, p=0.07), which is a component of the spliceosome (Zhang et al. 2018), RPRD1A (log2FC=1.8, p=0.01), which binds pSer2 and pSer7 CTD of RNAPII and facilitates Ser5 de-phosphorylation and was co-purified with RECQL5 earlier (Ali et al. 2019; Ni et al. 2011; Ni et al. 2014), and CCDC12 (log2FC=1.8, p=0.01), which might play a role in splicing, but was not studied in great detail so far.

Unexpectedly, with EIF3A (log2FC=1.3, p=0.08) a translation initiation factor was affected in its binding to RNAPII.

In summary, most of the proteins found to be decreased in their interaction with RNAPII upon MYC depletion are linked to transcriptional elongation, whereas the only protein found to show an increased interaction with RNAPII is linked to pausing of elongating RNAPII.

The decreased interaction with RNAPII upon MYC depletion in T-lymphoma cells was validated by immunoblotting, as exemplary shown for SPT5 and SPT6, and quantified from independent triplicate experiments with normalization to bait protein levels (RPB3-HA) (Figure 4.10.B). Of note, RPB2 protein levels were not affected by MYC depletion.

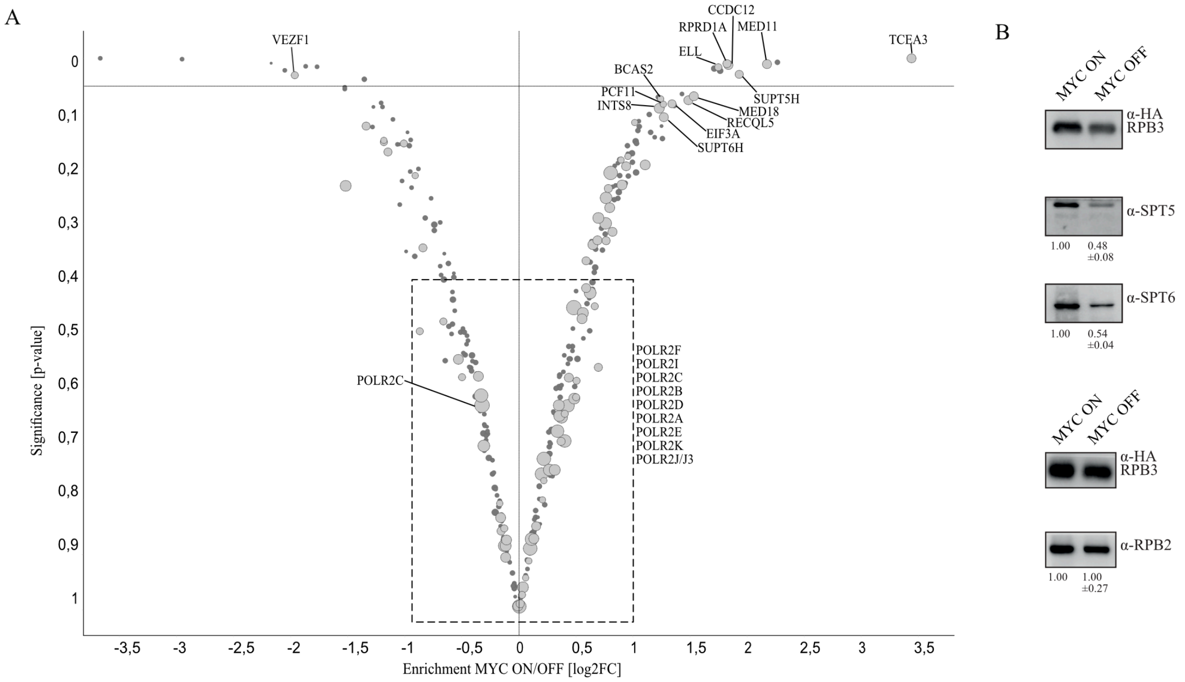


Figure 4.10: RNAPII interactome upon MYC depletion in T-lymphoma cells.
***A**. Volcano plot illustrating changes in the RNAPII interactome upon MYC depletion. X-axis depicts the log2 fold change enrichment of T-lymphoma cells expressing MYC (MYC ON) over cells depleted of MYC after Doxycycline treatment (MYC OFF) and y-axis shows the p-values calculated from four experiments with MYC ON and MYC OFF being processed side-by-side. Each circle represents one identified protein, while light grey colour designates a significant RNAPII-interactor. Proteins changing their abundance in the RNAPII interactome upon MYC depletion are labelled by gene names. Box indicates the location of several RNAPII-subunits within the plot. Only proteins identified in at least four out of eight conditions (four times in the presence of MYC and four times after MYC depletion) were considered. Circle size corresponds to the mean log2 fold change enrichment from MYC ON cells over EV control cells (x-axis in Figure 4.7.A).*
***B**. Immunoblots of HA-IP from T-lymphoma cells. RNAPII-interacting proteins were purified by fractionation followed by HA-IP for RPB3 as for qMS using T-lymphoma cells expressing MYC (MYC ON) or depleted of MYC by Doxycycline treatment (MYC OFF). Immunoblots were performed for IP efficiency (HA-antibody) and for co-IPed proteins (SPT5, SPT6, and RPB2). Co-IP efficiency was calculated from three independent experiments by determining the enrichment of the co-IPed protein over the IPed protein. The MYC ON condition was set to 1.*
This figure was published in a similar form in (Baluapuri et al. 2019).

4.1.6 RNAPII interactome – changes induced by MYC overexpression

In U2OS$^{\text{MYC-Tet-On}}$ cells the RNAPII interactome was analyzed once for changes in protein abundance after increased MYC expression upon Doxycycline treatment (Figure 4.11; for table with values see 7.3.6). A comparison between normal MYC levels and highly overexpressed MYC levels (MYC HIGH) did not reveal changes in the abundance of proteins belonging to RNAPII (red), the mediator (yellow) or the integrator (green) complex. Furthermore, general transcription factors (GTFs) did not change (e.g. GTF2F2, purple).

SPT5, SPT6, and ELL were the three elongation factors showing dependency on MYC in T-lymphoma cells. For SPT6 a small decrease in RNAPII binding could be observed upon MYC overexpression, from log2FC of 7.6 to 7.3. Similar effects were seen for SPT5 (log2FC of 3.9 for MYC ON and 3.4 for MYC HIGH). ELL, however, showed the opposite effect, shifting from log2FC of 4.2 in MYC ON to 4.4 in MYC HIGH. The negative trend for SPT5 and SPT6 could be explained by a phenomenon called “squelching”. “Squelching” describes the effect of very high MYC levels exceeding the levels of the binding partners. Like this, almost all of, for example, SPT5 would be bound by MYC, resulting in titrating away SPT5 from other binding partners, like in this case RNAPII. Additionally, in U2OS cells the second subunit of DSIF, SPT4, could be detected mirroring the effect of MYC overexpression on SPT5 with log2FC of 7.7 in MYC ON and 7.1 in MYC HIGH. TCEA3 was ot detected in U2OS cells.

As highlighted in Figure 4.11, the strongest increase in proteins binding to RNAPII in the MYC HIGH condition was observed for MYC itself. This is most likely due to the high abundance of MYC after Doxycycline-induced overexpression, resulting in residual MYC within the sample which is detected by qMS, as observed for very abundant proteins like ribosomal proteins or histones. The EV control was not treated with Doxycycline, so the background binding by MYC resulting from MYC overexpression could not be determined. Besides MYC, also MAX showed increased binding to RNAPII.

Replicates would be needed to confirm the trend observed for the elongation factors SPT5, SPT6, and ELL, and to allow calculations of the significant change in between the two conditions.

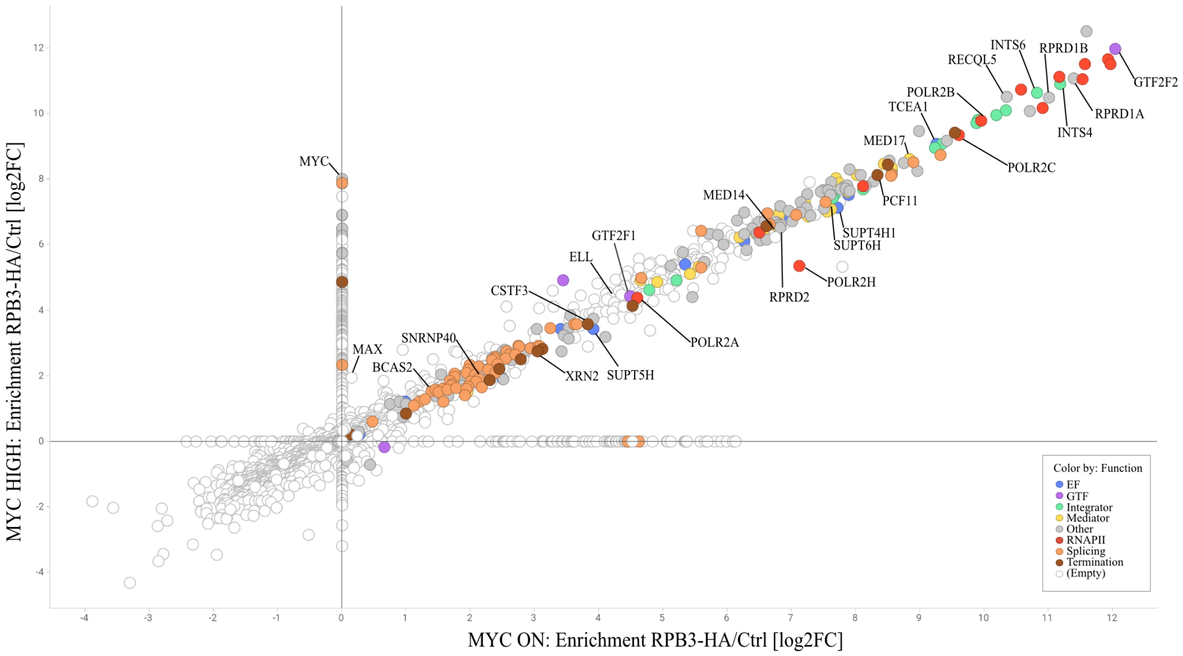


Figure 4.11: RNAPII interactome in U2OS cells with MYC ON versus MYC HIGH.

A diagram depicting RNAPII interactors from U2OS cells with normal MYC expression (MYC ON, x-axis) versus MYC overexpression (MYC HIGH, y-axis) upon Doxycycline treatment. Log2 fold change enrichment values from HA- over EV-cells from single experiments are shown. Each circle represents one protein. Some circles have been labelled with the corresponding gene name. Colouring indicates the function as specified in the figure inlay.

4.1.7 RNAPII interactome – changes upon CDK9-inhibition

The CDK9-inhibitor Flavopiridol was used, to see if the effects on the RNAPII interactome caused by MYC (see Figure 4.10 and Figure 4.11) could be explained solely by recruiting P-TEFb, as suggested earlier (see section 1.10.3), or if these are two distinct phenotypes, or if there is a cooperative effect.

In T-lymphoma cells upon Flavopiridol treatment (n=3), independent of the MYC status, proteins involved in transcriptional elongation (blue) and termination (brown) were found less bound to RNAPII. This was expected, since Flavopiridol inhibits CDK9 and therefore inhibits the transition of RNAPII into productive elongation (Figure 4.12; for table with values see 7.3.7). The specificity of Flavopiridol is under debate, as there are reports demonstrating additional inhibitory function towards CDK7 (Galbraith, Bender, and Espinosa 2019), which acts already at the step of promoter escape.

For direct visualization of the effect of MYC in the presence of Flavopiridol, values from cells treated with Flavopiridol in the presence or absence of MYC were plotted (Figure 4.12). The three proteins SPT6, TCEA3, and RECQL5 showed a strong decrease in RNAPII-binding upon MYC depletion also in the presence of Flavopiridol. For SPT6 a decrease in the log2 enrichment from 2.5 (MYC ON, Flavo) to 1.3 (MYC OFF, Flavo) was detected, for TCEA3 from 2.5 to 0.9, and for RECQL5 from 4.4 to 1.4. So, these three proteins interacted less with RNAPII upon MYC depletion, independently of CDK9-inhibition, suggesting a MYC-specific effect on their association with RNAPII. However, SPT6 and TCEA3 bind elongating RNAPII and the Flavopiridol treatment, which inhibits CDK9 activity, should prevent RNAPII from elongation. This suggests that either Flavopiridol treatment was not sufficient or CDK9 activity was recovered during sample preparation, as it was performed without the addition of Flavopiridol.

For the DSIF subunit SPT5, independent of the MYC status a general decrease in its interaction with RNAPII was observed upon Flavopiridol treatment and it did not match the previously defined cut-offs for a significant RNAPII-interactor anymore. As SPT5 is reported to be bound to RNAPII even before CDK9 activity is required, the observed decrease in SPT5-binding upon Flavopiridol treatment was surprising. Due to the low enrichment values, no conclusion could be drawn if the decrease observed upon MYC depletion is solely MYC-dependent or could also be partially mediated by CDK9.

Similarly, for the proteins BCAS2, ELL, CCDC12, PCF11, EIF3A, MED18, and MED11, which also showed MYC-dependent changes in their binding to RNAPII, no conclusion could be drawn since they were either very weakly or not at all identified in one or both conditions.

For RPRD1A upon MYC depletion in combination with Flavopiridol treatment a small decrease in RNAPII-binding was observed with a log2 fold change of 2.5 in MYC ON Flavo and 2.1 in MYC OFF Flavo. Since RPRD1A binds RNAPII with pSer2 and pSer7 CTD, less binding would be expected since Flavopiridol should abolish phosphorylation of Ser2 of the CTD-heptapeptides. INTS8, the one integrator subunit showing MYC-dependent changes, was also mildly decreased in RNAPII-binding upon MYC-depletion in the presence of Flavopiridol (log2FC=2.7 for MYC ON Flavo and log2FC=2.2 for MYC OFF Flavo).

In summary, for several of the proteins, which showed MYC-dependent RNAPII-binding before (see Figure 4.10), MYC-dependency was still oberserved even after CDK9-inhibition by Flavopiridol, like for TCEA3, SPT6, or RECQL5. However, many proteins showed a strong overall decrease in RNAPII-binding upon Flavopiridol treatment, which made the analysis of a MYC-dependent effect impossible.

Numerous proteins were identified as significant interactors in the combinatorial treatment with Flavopiridol and MYC depletion, which were not determined as significant in the MYC ON nor in the Flavopiridol-treated cells, including several proteasomal subunits. This suggests that RNAPII is targeted for protein degradation upon a severe transcriptional blockage induced by the combinatorial treatment.

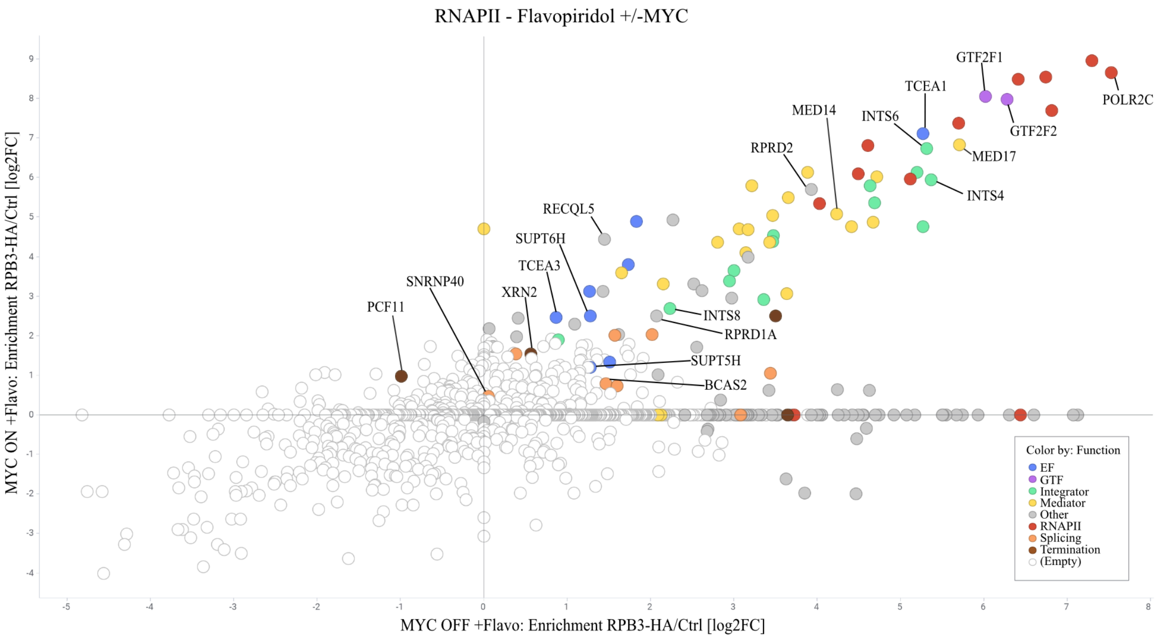


Figure 4.12: RNAPII interactome upon Flavopiridol treatment in T-lymphoma cells.

Volcano plot showing the RNAPII interactome upon Flavopiridol treatment in the presence and absence of MYC. Triplicate experiments were performed in T-lymphoma cells. For comparison, Flavopiridol-treated cells are depicted on the y-axis and Flavopiridol-treated cells in combination with MYC *depletion on the x-axis. Both axes depict log2 fold change of HA-RPB3-expressing cells over the EV control (Ctrl). Each circle represents one identified protein. 101 proteins previously described as significant RNAPII interactors in T-lymphoma cells are coloured according to their functions (see figure inlay). Same proteins as for previous figures are labelled by gene name.*

In U2OS cells one experiment was performed using Doxycycline and/or Flavopiridol and in the Figure 4.13 a direct comparison of MYC ON and MYC HIGH in the presence of Flavopiridol is shown (for table with values see 7.3.6). As observed in T-lymphoma cells (Figure 4.12), upon Flavopiridol treatment subunits of RNAPII (red), the mediator (yellow) and the integrator (green) complexes were not affected. However, in U2OS cells upon MYC overexpression a tendency to weakened RNAPII-binding in the MYC HIGH situation was observed before for the three elongation factors SPT5, SPT6, and ELL (Figure 4.11).

So, when U2OS cells were treated with Flavopiridol, for SPT6 the log2 fold change of 6.4 with normal MYC expression (MYC ON) reduced to 6.0 upon MYC overexpression (MYC HIGH). Similarly, SPT4, the small subunit of DSIF, showed a small decrease from 6.6 to 6.5 upon MYC overexpression in the presence of Flavopiridol, whereas for SPT5 no change was observed (log2FC=2.6). Of note, a log2 fold change of 2.6 measured for SPT5 shows it is much less enriched than SPT6 or SPT4 (log2FC above 6). When compared to unperturbed U2OS cells (MYC ON, log2FC=3.9), SPT5 enrichment in the RNAPII interactome was decreased after Flavopiridol treatment, which had already been observed in T-lymphoma cells (Figure 4.12).

Changes in BCAS2 and ELL could again not be evaluated since they were either only identified in one condition or with a very low enrichment. For MED11, although strong enrichment values were observed, there was no change from MYC ON to MYC HIGH upon Flavopiridol treatment (log2FC=8.0).

To confirm the effects observed for the elongation factors SPT6 and SPT4 and to elucidate the effects on ELL, which was not detected when MYC was overexpressed in combination with Flavopiridol treatment, more repetitions of the experiments are needed.

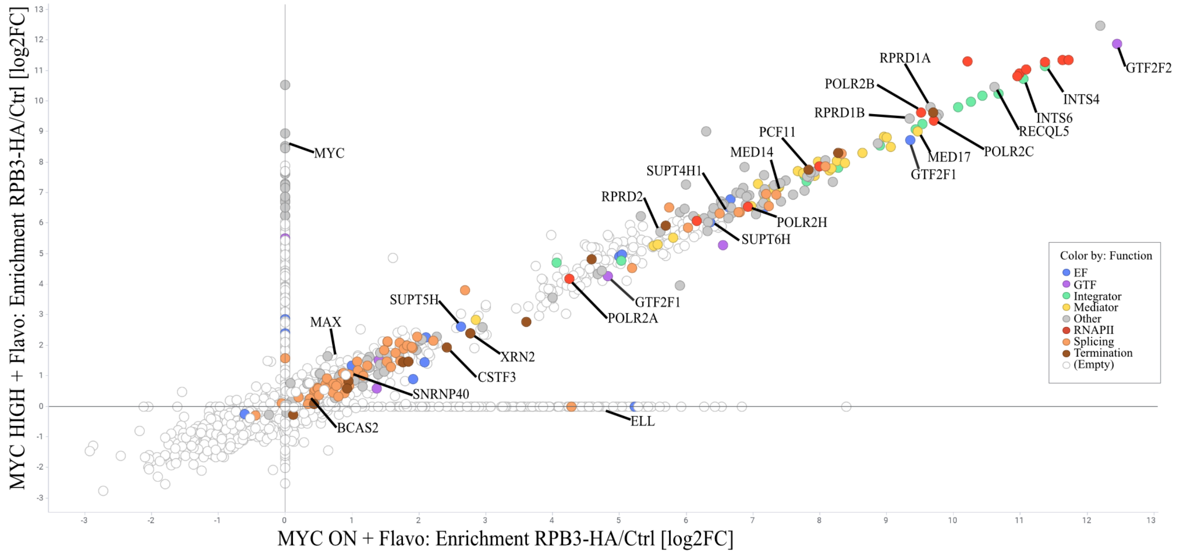


Figure 4.13: RNAPII interactome in U2OS cells upon Flavopiridol treatment.

Plot illustrating the comparison of RNAPII interactomic studies from U2OS cells for MYC ON versus MYC HIGH in the presence of Flavopiridol. X-axis shows U2OS cells treated with Flavopiridol and y-axis with Flavopiridol upon MYC overexpression. Both axes depict log2 fold change values of HA-RPB3-expressing cells over EV control cells (Ctrl). Each circle represents one protein and exemplary proteins are labelled by the corresponding gene name. Colouring corresponds to the protein's function (see figure inlay).

4.2 Analyzing MYC-interacting proteins by mass spectrometry

The results of the interactomic studies of RNAPII in cells expressing MYC or having it depleted, showed decreased binding for several proteins, which mainly function in transcriptional elongation, such as SPT5, SPT6, ELL, and TCEA3, upon MYC depletion. This suggests, that their binding to RNAPII might be mediated by their direct recruitment by MYC or through an indirect mechanism, for example through enhanced CDK9 action. CDK9 phosphorylates RNAPII at Ser2, which results in elongation-competent RNAPII with pSer2 being a docking site for various elongation factors. The first mechanism requires direct binding of MYC to the recruited elongation factor, which can be deciphered by a global analysis of MYC interacting proteins. For this purpose, I established a protocol for extracting MYC and its associated proteins from chromatin, which was followed by quantitative mass spectrometric analysis. Same cell lines were used as for the RNAPII interactomic studies to allow comparison.

4.2.1 *Optimizing conditions for MYC protein extraction from chromatin*

MYC is a very unstable protein and tends to form aggregates. As a transcription factor, it is strongly bound to chromatin together with its partner protein Max making it challenging to extract the MYC protein. Therefore, the purification procedure had to be adjusted compared to RNAPII extraction and previously published methods for solubilization of native MYC complexes. Hence, I established a one-step cell lysis procedure and optimized buffer conditions to solubilize MYC and to prevent protein aggregation (Figure 4.14.A and B). Furthermore, a Dounce homogenizer and short sonication were used to break up cellular plasma as well as nuclear membranes, followed by Benzonase treatment to extract proteins from chromatin (see methods section 3.3.4).

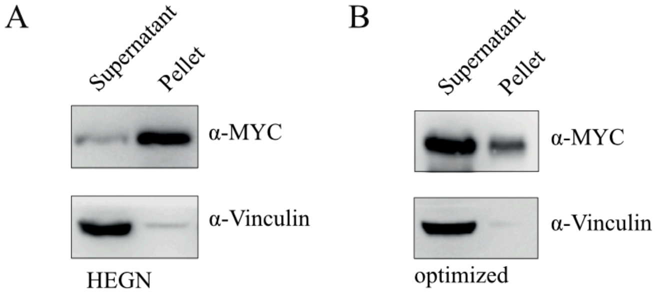


Figure 4.14: Optimization of the MYC protein solubilization.

A. *Immunoblot of MYC solubilization using HEGN buffer. Endogenous MYC protein was stained to show its solubilization (supernatant) from chromatin (pellet). Vinculin was used as a control for a non-chromatin bound protein.*

B. *Immunoblot of MYC solubilization using optimized conditions. Endogenous MYC protein was stained upon solubilization with an optimized buffer and extraction procedure including Benzonase treatment to resolve MYC (supernatant) from chromatin (pellet). Vinculin was used as a control for a non-chromatin bound protein.*

This figure was published in a similar form in (Baluapuri et al. 2019).

Similar to the method used for qMS analysis of RNAPII complexes, immunoprecipitation was used to enrich for MYC and its interacting proteins. Therefore, MYC was fused to a C-terminal HA-tag and stably expressed in U2OS (Figure 4.15.A) and T-lymphoma cells. Of note, in U2OS cells endogenous MYC can compete with HA-MYC for binding to interacting proteins. In case of T-lymphoma$^{\text{MYC-Tet-Off}}$ cells, endogenous MYC was depleted by Doxycycline treatment prior to protein extraction to reduce competition with untagged MYC (Figure 4.5.B). A direct comparison of immunoblots developed with the MYC-specific antibody and the HA-tag-specific antibody gives an estimation of MYC overexpression when compared to EV cells. As shown by western blotting (Figure 4.15.B), a main proportion of MYC could be gained (Extract fraction) and used for subsequent HA-IP.

In addition to the wildtype full-length HA-MYC, a N-terminally truncated MYC deleted of the first 63 amino acids, including MB0 and MBI, named MYC-dN1, was used for mass spectrometric analysis (see section 4.3) and its solubilization is shown here side-by-side to wildtype MYC (Figure 4.15.A and B). Note that MYC-dN1 is not recognized by the MYC-specific antibody used here, since the epitope recognized by this antibody is within the very N-terminus of the MYC protein and absent from the mutant.

The protein band with lower molecular weight detected in Figure 4.15.B is most likely a C-terminal-degradation product of the MYC protein, since it is detected by the antibody specifically recognizing MYC's N-terminus and not by the HA-specific antibody recognizing the C-terminal HA-tag. Furthermore, the intensity of the protein band with lower molecular weight mirrors the intensity of the full-length MYC protein band, so it is increased with overexpression of wildtype MYC.

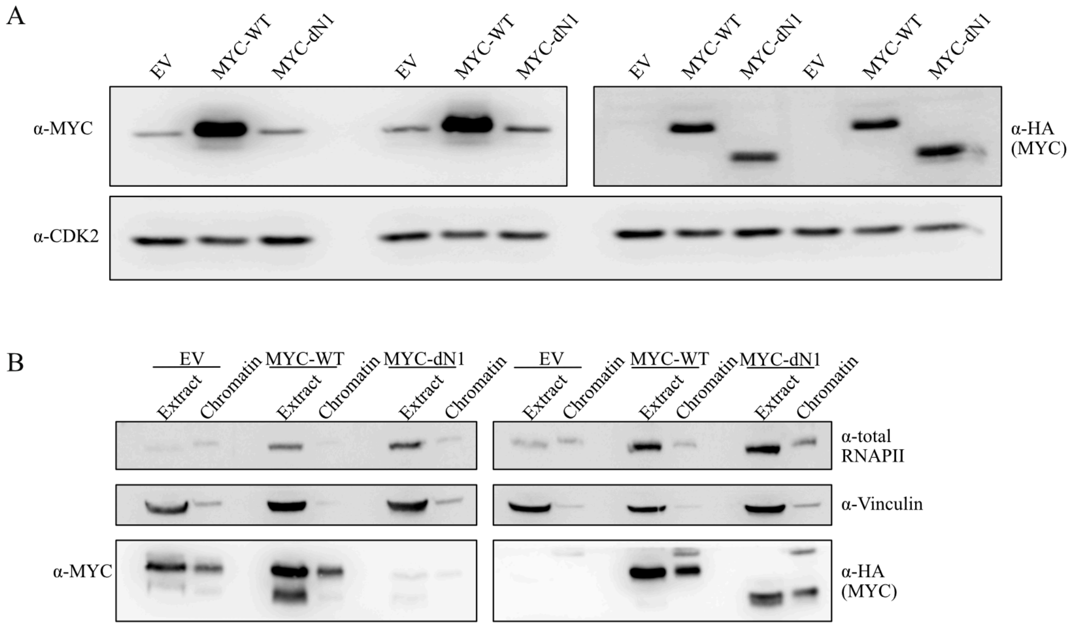


Figure 4.15: Stable expression and extraction of HA-MYC and HA-MYC-dN1 from U2OS cells.

***A**. Immunoblot for HA-MYC and HA-MYC-dN1 expression. Stable expression of HA-MYC or HA-MYC-dN1 (MYC64-439) in U2OS cells was validated by immunoblotting using a MYC-specific (left) or an HA-specific antibody (right). Cells expressing an empty vector were used as a control (EV). CDK2 was used as a loading control. Note that MYC-dN1 is not detected by the MYC-specific antibody (left), since the antibody recognizes an N-terminal epitope. Samples from one experiment were loaded twice next to each other.*

***B**. Immunoblot of HA-MYC and HA-MYC-dN1 solubilization. Extraction of chromatin-bound proteins* *from the stable U2OS cell lines from A using the conditions determined in Figure 4.14. Solubilization of MYC and MYC-dN1 was determined by a MYC-specific antibody (left) or an HA-specific antibody (right). Note that MYC-dN1 is not detected by the MYC-specific antibody, since the epitope is deleted within this mutant. Vinculin was used as a control for a protein not bound to chromatin. An antibody staining total RNAPII (RPB1 independent of its phosphorylation status) was used as a control for a chromatin-bound protein. The Extract fraction was used for further HA-IP followed by qMS. The Chromatin fraction depicts proteins, which could not be solubilized under the conditions used here.*

4.2.2 MYC interactome from T-lymphoma and U2OS cells

qMS was performed for three replicates from U2OS and three replicates from T-lymphoma cells. Exemplary single experiments are shown in the Figure 4.16.A for T-lymphoma and Figure 4.16.B for U2OS cells. Strongest enrichment and intensity were observed for the bait MYC itself, followed by its well-known and characterized interaction partner MAX (Figure 4.16.A and B; for table with values see 7.3.8). Additionally, TRRAP and HUWE1 were abundantly detected to bind MYC, in line with previous reports (section 1.10.1 and 1.12). Other previously described MYC-interacting proteins, such as ZNF281 (section 1.12) and p400 (*EP400*) (section 1.10.1), were detected, as well as ATAD3A, a mitochondrial protein not found to exhibit known functions related to MYC yet.

A comparison of the two plots allows following conclusions: first, MYC was successfully solubilized and well-known interactors were identified with high enrichment values; second, these interactors are reported to have functions related to transcription and chromatin remodelling, which underlines a high efficiency of the chromatin extraction method; third, several proteins previously unrelated to MYC are identified; fourth, the log2 enrichment values of most of the interactors are lower than 4 for both cell lines, making it difficult to distinguish them from background-binding; fifth, qMS performed from T-lymphoma and U2OS cells are similar for many proteins, but there are also differences observed.

One example of a dramatic change between cell systems is HUWE1. In U2OS cells, HUWE1 is less bound to MYC (log2FC<4 as compared to around 7 in T-lymphoma cells). Second, the circle size, which represents the number of unique peptides identified for that protein, is much lower in U2OS cells (number of unique peptides was 23) than in T-lymphoma cells (number of unique peptides was 71). This also points towards a lower enrichment of HUWE1 within the U2OS sample indicating weaker interaction with MYC in these cells.

However, repetitions of the experiments are required to distinguish real interactors from background-binding due to the overall low enrichment values and to discriminate experimental variances from cell type-dependent ones.

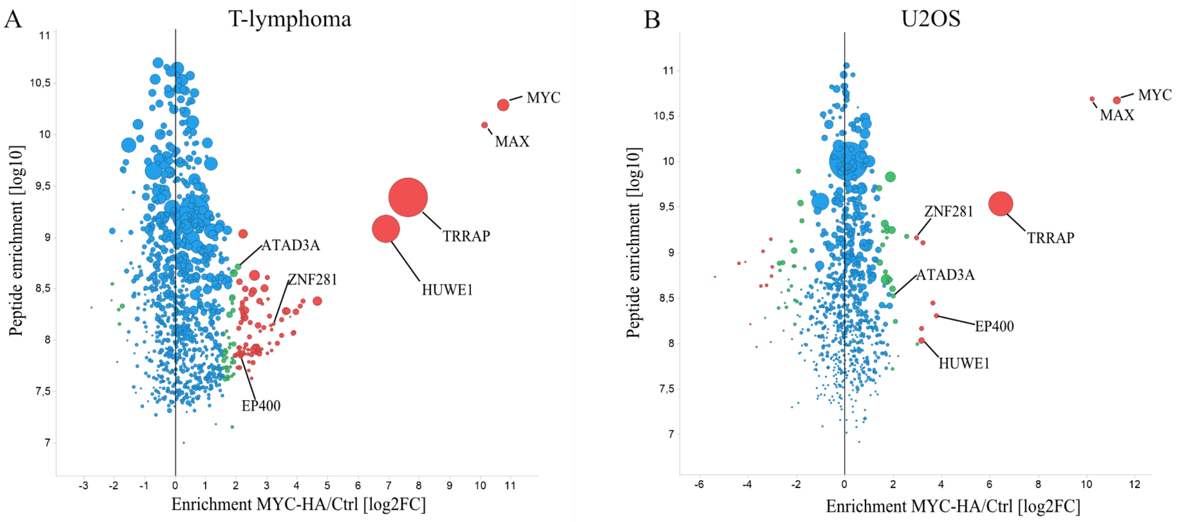


Figure 4.16: MYC interactomes from T-lymphoma and U2OS cells.

Enrichment plots for MYC protein complexes. X-axis shows log2 fold change enrichment of proteins in HA-IP from HA-MYC-expressing over EV cells (Ctrl). Y-axis depicts log10 of protein enrichment. Highly significantly enriched proteins (based on protein distribution within the plot) are shown in red and with less significance in green. Each circle represents one identified protein. Circle size is determined by the number of unique peptides identified per protein relative to the other proteins within one plot. For comparison same 7 proteins have been labelled with gene names.

***A**. Enrichment plot for MYC protein complexes from T-lymphoma cells. Endogenous MYC was depleted by Doxycycline treatment.*

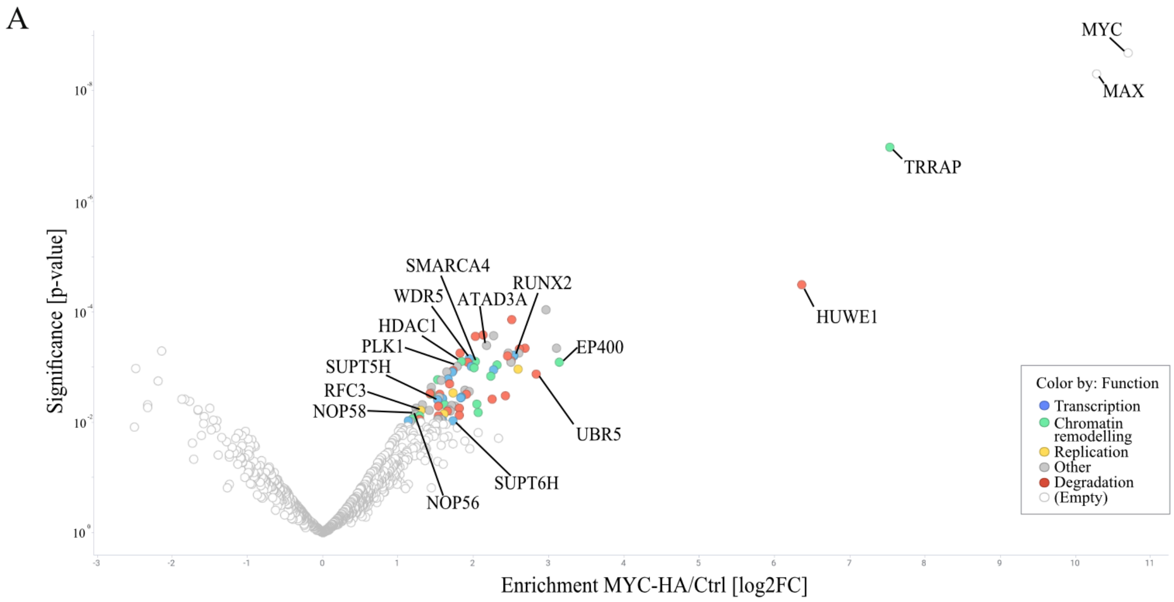
***B**. Enrichment plot for MYC protein complexes from U2OS cells.*

To uncover significant interactors of MYC, three replicates were combined and p-values were calculated as shown in Figure 4.17 and Figure 4.18 (for table with values see 7.3.9, 7.3.10, and 7.3.11). Protein enrichment was evaluated according to the cell line (Figure 4.18.A, T-lymphoma cells, and B, U2OS cells), or according to the qMS measurement timepoint (Figure 4.17.A, combination of experiments from T-lymphoma and U2OS cells (firstly performed experiments)). The interactome shown in Figure 4.17.A is published in (Baluapuri et al. 2019). According to the interactome shown in Figure 4.17.A (for table with values see 7.3.9), 88 proteins have been classified as significant MYC interactors setting thresholds to a log2 fold change enrichment >1 and a q-value <0.1 calculated from the three independent replicates. Within these 88 interactors, several previously known MYC interacting proteins were detected, such as MAX (log2FC=10.3 for Figure 4.17.A), the adaptor protein TRRAP (log2FC=7.5) as well as related HATs and HDACs including p400 (EP400; log2FC=3.1), HDAC1 (log2FC=1.8), GATAD2B (log2FC=1.6), ACTL6A (log2FC=2.0), RUVBL1 (log2FC=1.6), RUVBL2 (log2FC=1.5), DMAP1 (log2FC=2.3) (green, see section 1.10.1). Furthermore, the well-characterized MYC interactor WDR5 (log2FC=1.9) was also found significantly enriched (blue, see section 1.12). In line with the data for NMYC from Büchel and colleagues (Buchel et al. 2017), we detected an interaction with RAD21 (log2FC=1.6) and TOP2A (log2FC=2.0) for c-MYC. In our experiments, PLK1 (log2FC=1.8) another well-known MYC-interactor is identified. Our data confirmed interaction of MYC with several subunits of the chromatin remodeling SWI/SNF complex including SMARCA4 (log2FC=2.0), SMARCC1 (log2FC=2.0), and SMARCD2 (log2FC=2.1) (green, see section 1.10.1). The zinc finger protein ZNF281 (log2FC=2.5), which was recently shown to share chromatin binding sites with MYC (Koch et al. 2007; Luo et al. 2019), was also identified in our analysis (blue, see section 1.12).

Some identified MYC-interactors are reported to function in transcription, such as the elongation factors SPT5 (log2FC=1.5) and SPT6 (log2FC=1.7), the RNAPII subunit RPB2 (log2FC=1.6), the histone chaperone FACT (facilitates chromatin transcription) subunits SPT16 (log2FC=1.4) and SSRP1 (log2FC=1.3), and the poly(A)-binding protein PABPC4 (log2FC=2.5). Among the enriched proteins in the MYC interactome are also CBFB (log2FC=1.8) and RUNX2 (log2FC=2.3), which can form a heterodimer to control transcription of genes related to osteogenesis (Kundu et al. 2002; Yoshida et al. 2002). Our data show that EBP1 encoded by the *PA2G4* gene (log2FC=1.8) interacts with MYC, which plays a role in cellular growth, ribosomal rRNA maturation and assembly, as well as internal ribosomal entry site (IRES)- mediated translation initiation (Kowalinski et al. 2007; Squatrito et al. 2004; Squatrito et al. 2006). Interestingly, targeting NMYC through the NMYC-PA2G4 binding site has recently been reported (Koach et al. 2019). NOP56 (log2FC=1.2) and NOP58 (log2FC=1.2), known to function in ribosomal biogenesis and pre-rRNA processing, are also detected to be significantly enriched interacting partners of MYC.

Intriguingly, many proteasomal subunits were found to be significantly enriched in their association with MYC, which reflects the unstable nature of the MYC proteins. This was confirmed by GO-term analysis of the 88 MYC interactors (Figure 4.17.B) and goes along with the identification of several E3 ligases involved in targeting MYC for degradation through the ubiquitin-proteasome system, including HUWE1 (log2FC=6.4) and UBR5 (log2FC=2.4).

Other significantly enriched GO-term were Nucleoplasm, Regulation of mRNA stability and Poly(A) RNA binding, Positive regulation of RNAPII transcriptional PIC assembly and Transcription (Figure 4.17.B).



B

Gene ontology term	q-value
Nucleoplasm	3.8×10^{-32}
Regulation of mRNA stability	1.7×10^{-26}
Positive regulation of RNA-Pol II transcriptional pre-initiation complex assembly	1.3×10^{-8}
Poly(A) RNA binding	4.9×10^{-6}
Transcription	2.6×10^{-3}
Proteasome	2.3×10^{-37}

Figure 4.17: MYC interactome.

A. *Volcano plot of MYC interacting proteins of two experiments from T-lymphoma cells and one experiment from U2OS cells measured on the mass spectrometer the same day. Cut-offs (log2FC>1 and q-value<0.1) resulted in 88 significant MYC-interactors. These interactors are shown in different colours corresponding to the protein's function (see legend). Each dot represents one protein. Exemplary proteins are labelled by corresponding gene names. This interactome is published in (Baluapuri et al. 2019), since cell-type specific ones were not available by then.*

B. *Table of significantly enriched gene ontology (GO) terms. Using the DAVID software, enriched GO terms were determined based on the 88 significant MYC interactors from A.*

This figure was published in a similar form in (Baluapuri et al. 2019).

The MYC-interacting proteins showed overall weaker enrichment than for RNAPII-bound proteins. This may reflect their rather transient interaction. Triplicate experiments identified 95 significant MYC interactors (log2 fold change enrichment >1 and q-value <0.1) in T-lymphoma and 69 in U2OS cells (Figure 4.18.A and B; for table with values see 7.3.10 and 7.3.11). As U2OS cells still expressed endogenous MYC, it might have been competing with the HA-MYC for protein binding and resulted in the lower number of significant interactors when compared to T-lymphoma cells, in which endogenous MYC got depleted by the addition of Doxycycline. The overlap between the interactomes generated from the two different cell lines (Figure 4.18.A and B) is displayed in Figure 4.18.C. 27 proteins were commonly enriched in their interaction with MYC in both cell lines, corresponding to about 40% significant interactors in U2OS cells and less than 30% in T-lymphoma cells. Among those 27 proteins are known MYC interactors including TRRAP and proteins belonging to one of the TRRAP complexes, as well as p400 or WDR5. Aside HUWE1, several proteasomal subunits are found to be common MYC interactors in both cell lines, suggesting that MYC-targeting by the ubiquitin-proteasome system is a relevant mechanism of post-translational regulation. From the groups of proteins exhibiting functions in transcription, RPB2 and SPT16 were identified as significant interactors in both cell lines.

The two elongation factors SPT5 and SPT6, however, were identified as novel MYC interactors and found as significant in T-lymphoma cells only. That is also the case for the transcription factor RUNX2, subunits of the casein kinase 2 (*CSNK2A* and *CSNK2B*), as well as the two E3-ligases UBR5 and FBXW7.

In U2OS cells proteins being significantly enriched in MYC-binding included replication factors, namely RFC3 and RFC4, and proteins playing a role in ribosomal biogenesis (for example UTP15, UTP18, NOP56, NOP58).

To sum up, many proteins, in particular previously characterized MYC-interactors, are identified as significant interactors in both cell lines. Still, more than 50% of the significant interactors are not found to be significant in the other cell line. This can be explained by cell line-specific interactions, including differences in interaction intensities, as it is observed for proteins important for ribosomal biogenesis, very weakly identified in T-lymphoma cells. Cell line-dependent differences in protein expression levels might also contribute to the variance in the MYC interactomes.

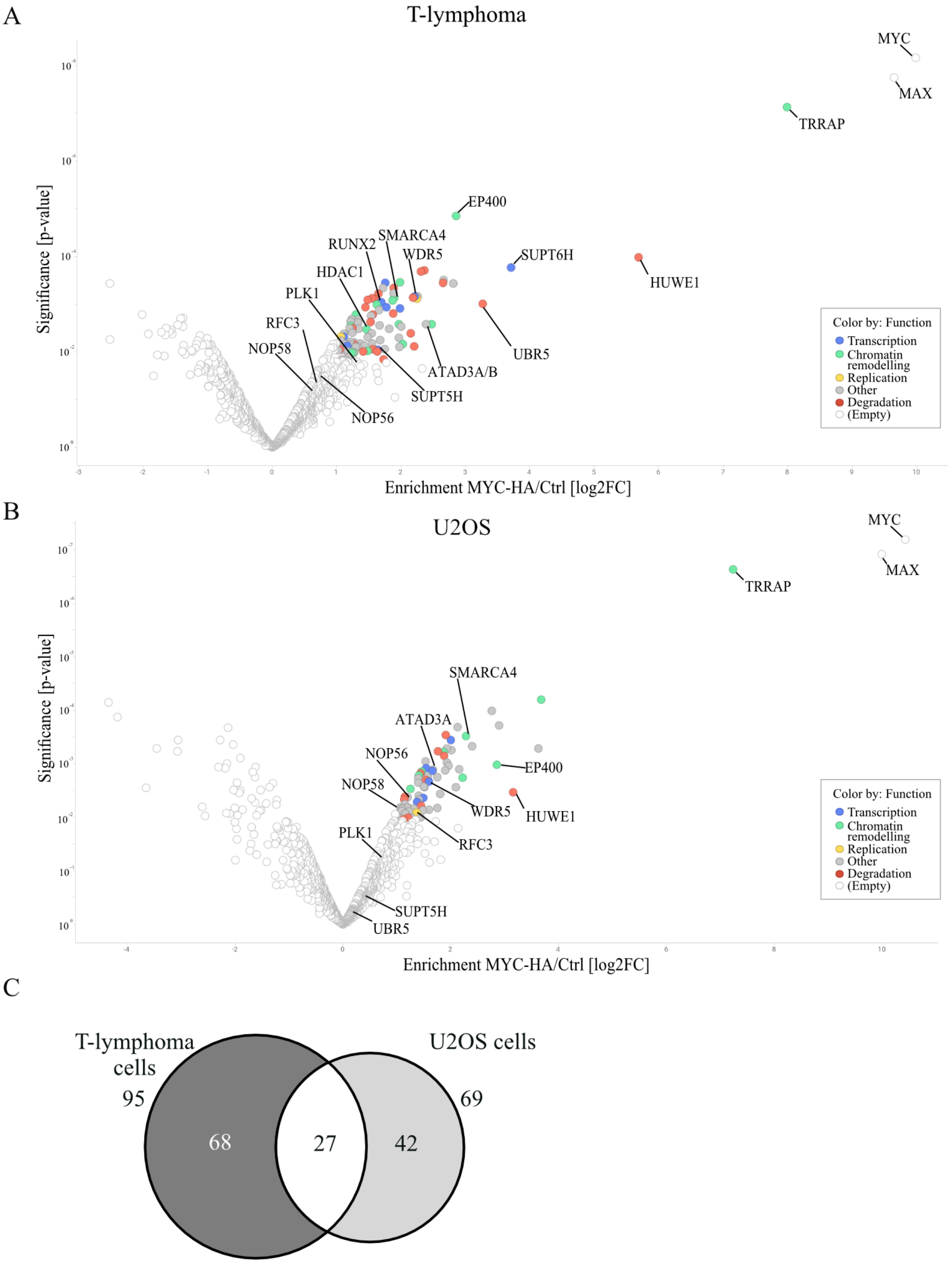


Figure 4.18: MYC interactome from T-lymphoma and U2OS cells.

A. Volcano plot of MYC interacting proteins from T-lymphoma cells. Three independent experiments were used for p- and q-value calculations. P-value is plotted over log2 fold change enrichment from HA-MYC expressing cells over EV control cells (Ctrl). Each circle represents one identified protein. Significant interactors are defined as proteins with q<0.1 and log2FC>1, resulting in 95 proteins which are highlighted in colours corresponding to their function. Same exemplary proteins are labelled by their gene name as in Figure 4.17.A.

***B**. Volcano plot of MYC interacting proteins from U2OS cells. Q- and p-values were calculated from triplicate experiments. The plot was generated as in A and 14 out of the 17 proteins highlighted in A are labelled. Cut-offs resulted in 69 proteins being significantly enriched.*
***C**. Venn diagram comparing significant MYC interacting proteins from experiments shown in A and B. Significant interactors determined from T-lymphoma (A) are shown in dark and from U2OS cells (B) in light grey.*

To further analyze the quality and reliability of the generated MYC interactome, the 88 proteins identified as significant MYC interactors based on Figure 4.17.A were compared to previously published MYC interactomes (Buchel et al. 2017; Kalkat et al. 2018; Koch et al. 2007; Heidelberger et al. 2018) (see Figure 5.1, section 5.2).

4.3 Interactomic studies for N-terminally truncated MYC

To identify candidates specifically binding the very N-terminal region of MYC, a MYC mutant (hereafter referred to as MYC-dN1), in which the first 63 amino acids (aa) including MB0 and MBI were deleted, was fused to a C-terminal HA-tag and expressed in U2OS and T-lymphoma cells upon lentiviral integration. HA-protein expression as well as solubilization from chromatin are shown in the Figure 4.15.A and B, respectively. qMS was performed as described above (section 3.3.4 and 3.4.1) and three independent experiments were combined for p-value calculation in T-lymphoma and U2OS cells, respectively (Figure 4.19.A and B; for table with values see 7.3.10 and 7.3.11). As already observed for MYC-WT, MYC-dN1 interactors had lower log2 fold change enrichment values as compared to RNAPII. Note that in U2OS cells MYC-dN1-HA had to compete with endogenous wildtype MYC still present within the cells.
Same proteins as for MYC-WT are labelled for comparison and colouring indicates the protein’s function as based on proteins classified as significant interactors for wildtype MYC (compare to Figure 4.18). These include MYC and MAX as well as the known interactors TRRAP and HUWE1 and the mitochondrial protein ATAD3A. A decrease in chromatin remodelling factors (green) in general can be noticed.

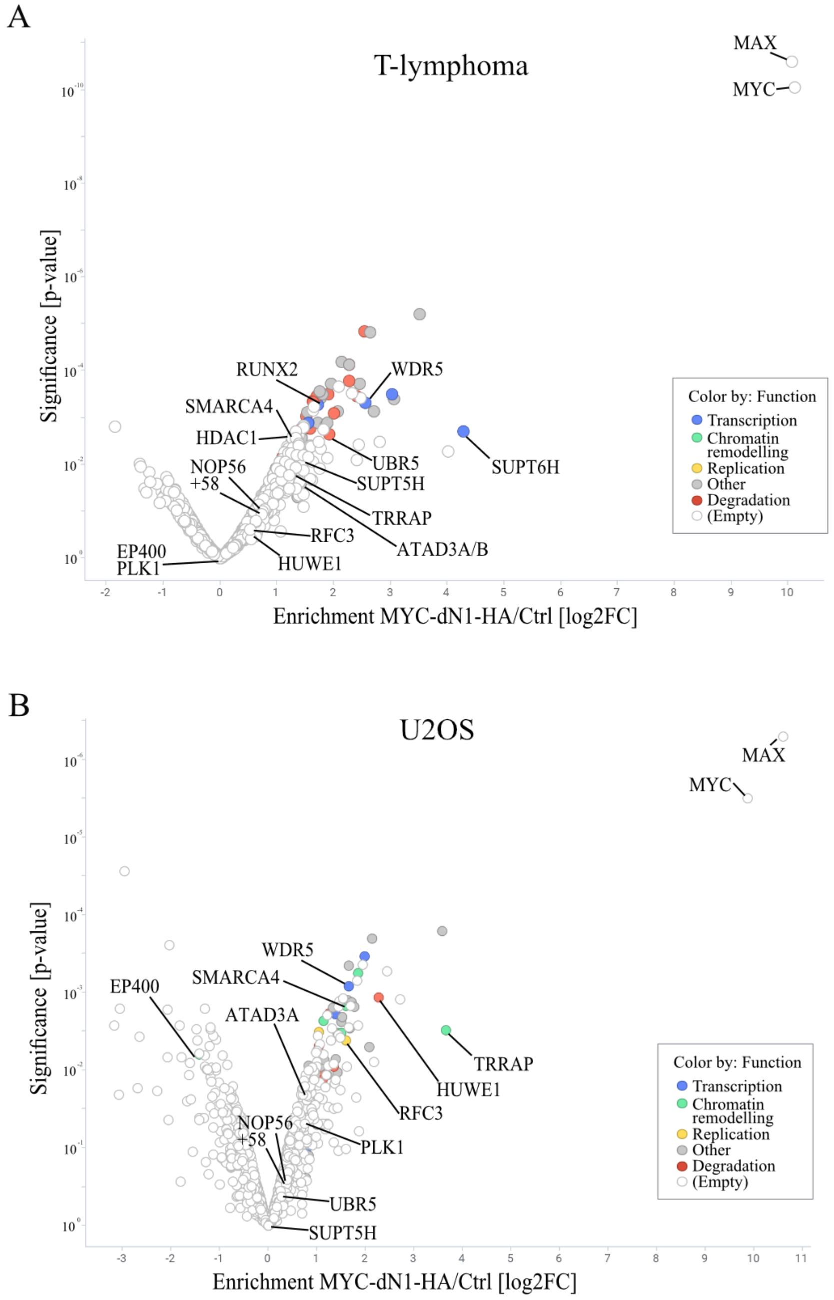


Figure 4.19: Interactome of MYC-dN1 (aa 64-439) from T-lymphoma and U2OS cells.

***A**. Volcano plot of the MYC-dN1 interactome from T-lymphoma cells. P-values calculated from three independent experiments are plotted over the log2 fold enrichment over EV control cells (Ctrl). Each circle depicts one identified protein. Colouring indicates the protein's function as annotated in the inlay and is based on the significant interactors for MYC-WT from T-lymphoma cells. Same proteins as for the MYC-WT interactome are labelled by the gene name (see Figure 4.18.A).*

***B**. Volcano plot of the MYC-dN1 interactome from U2OS cells. Triplicate experiments were performed from U2OS cells. The plot was generated as in A. Colouring represents the protein's function as indicated by the inlay and is based on the corresponding MYC-WT interactome from U2OS cells (see Figure 4.18.B). Same proteins as for the MYC-WT interactome are labelled by their gene name.*

A direct comparison of proteins enriched for MYC-dN1 over MYC-WT for T-lymphoma and U2OS cells, respectively, revealed several proteins with decreased binding to the N-terminally truncated MYC mutant (Figure 4.20.A and B; for table with values see 7.3.10 and 7.3.11). Among those is TRRAP, as well as TRRAP-associated factors. Interestingly, Kalkat and colleagues used MB-deletion mutants of MYC and after biotin labelling of proximal proteins, qMS analysis found TRRAP binding MBII, but not MBI. To analyze MBI-binding of TRRAP, Kalkat and colleagues used a Δ45-63 mutant, whereas here amino acids 1-63 got deleted. Different mutations can have different effects on the conformation of the further C-terminal MBII or TRRAP might have an additional binding site within the very N-terminal region, which is deleted in our study (aa1-44) (Kalkat et al. 2018).

Furthermore, the proteins HUWE1, UBR5, and FBXW7, all three E3-ligases mediating MYC's protein stability, were reduced in binding to MYC-dN1 compared to MYC-WT in T-lymphoma cells pointing towards an interaction site within the first 63 amino acids of MYC. FBXW7 is known to bind MYC in an MBI-phosphorylation-dependent manner (see section 1.12). In U2OS cells, however, the E3-ligases showed over all less enrichment and less proteasomal subunits were identified in the interactome of MYC-dN1 compared to MYC-WT. These observations did not result in higher stabilization of the MYC-dN1 protein compared to MYC-WT as determined by immunoblotting (see Figure 4.15).

My results identified SPT5 and SPT6 as MYC interactors for the first time. SPT6 showed a small increase in binding MYC-dN1 (log2FC=4.3) compared to MYC-WT (log2FC=3.7) in T-lymphoma cells. In U2OS cells, SPT6 was not detected, neither for MYC-WT nor for MYC-dN1. SPT5, however, showed a minor decrease in binding MYC-dN1 compared to MYC-WT with a log2FC enrichment of 1.6 for MYC-WT and 1.5 for MYC-dN1 in T-lymphoma cells, while in U2OS cells SPT5 showed a log2FC enrichment of 0.5 for MYC-WT and was not detected in the MYC-dN1 experiments. So, based on a decrease in log2FC, SPT5 might have a binding site within MYC's N-terminus, but as the interaction was not abolished with the N-terminal truncated MYC mutant, it implies it is not the only binding site.

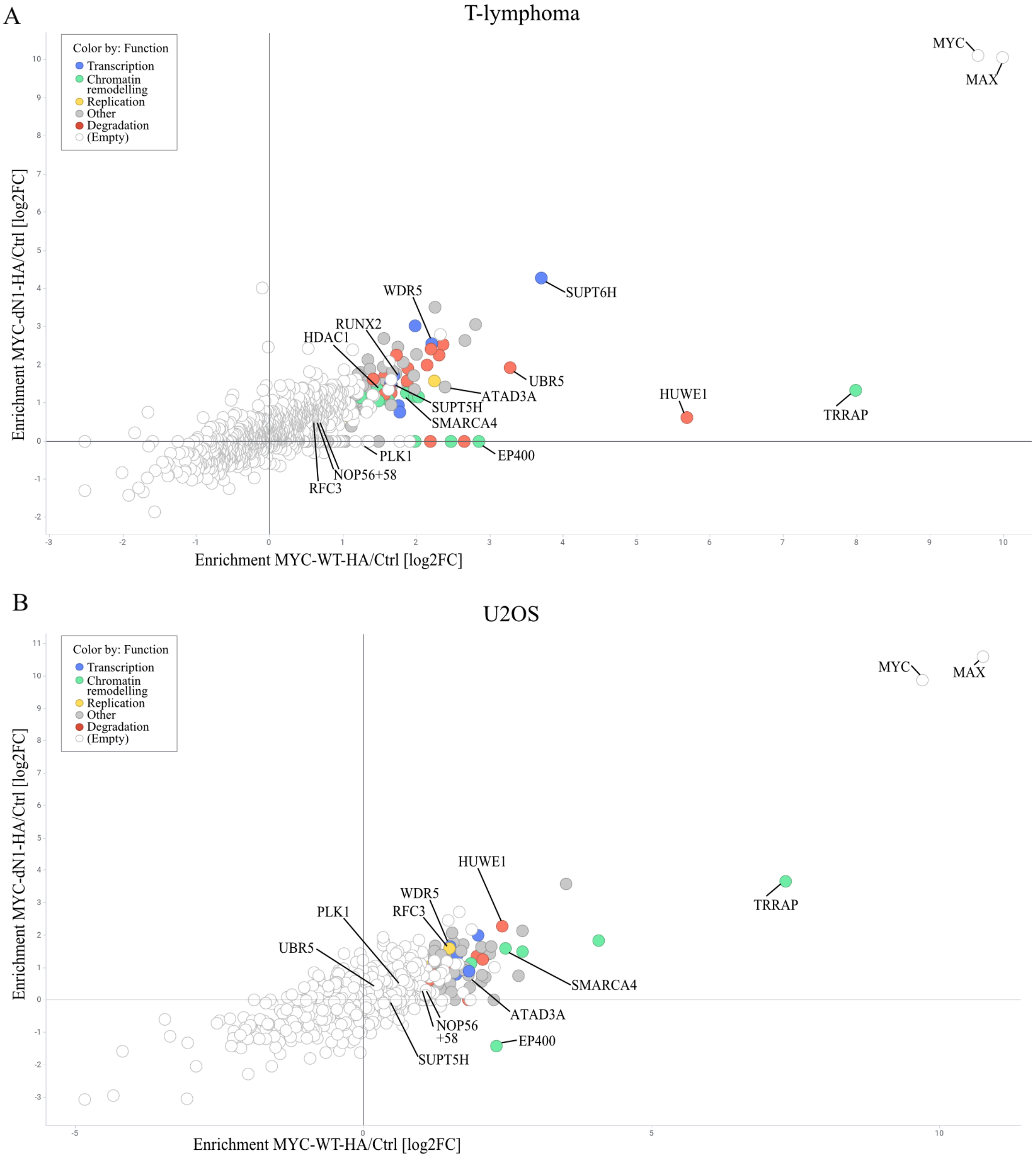


Figure 4.20: Comparison of the MYC-WT and MYC-dN1 interactomes in T-lymphoma and U2OS cells.

***A**. Plot comparing proteins enriched in the MYC-WT versus the MYC-dN1 interactomes from T-lymphoma cells. Triplicate experiments were performed for MYC-WT (see Figure 4.18.A) and MYC-dN1 (see Figure 4.19.A) interactors. Log2 fold change enrichments in HA-IP over EV cells (Ctrl) are depicted, with MYC-WT interactors on the x-axis and MYC-dN1 interactors on the y-axis. Each circle represents one identified protein and significant MYC-interactors as determined by log2FC and q-value cut-offs (see Figure 4.18) are highlighted by different colouring indicating their cellular function (see inlay). Same proteins are labelled by their gene names as in Figure 4.18.A and Figure 4.19.A.*

***B**. Plot comparing proteins enriched in the MYC-WT versus the MYC-dN1 interactomes from U2OS cells. The plot was generated as in panel A, but based on the interactomes from U2OS cells shown in in Figure 4.18.B and Figure 4.19.B.*

4.4 The overlap of the MYC and RNAPII interactomes

We hypothesized that there are proteins, which MYC directly transfers onto RNAPII to regulate productive transcription of its target genes. A candidate protein needs to fulfill certain criteria: first, it plays a role in promoting transcription and therefore is an interactor of RNAPII; second, changes in its association to RNAPII are MYC-dependent; third, for a direct handover by MYC, it is a component of the MYC interactome.

A comparison of significant interactors of RNAPII to the ones of MYC resulted in a restricted overlap with six common proteins, namely: SPT5, SPT6, POLR2B, TRRAP, PSMC5, and PSMD11 (Figure 4.21.A). Out of these six overlapping proteins, only the two elongation factors SPT5 and SPT6 fulfilled all requirements for a MYC-dependent hand over onto RNAPII: both proteins have known functions in transcriptional elongation, are found by qMS to interact with both, RNAPII and MYC, and their binding to RNAPII got negatively affected upon depletion of MYC. Since SPT5 showed slightly higher significance in the MYC qMS (see Figure 4.17) and, more importantly, a stronger dependency on MYC in the RNAPII qMS (Figure 4.10) than SPT6, SPT5 was selected for further studies. The enrichment values for SPT5 in the RNAPII interactomes as well as in the MYC interactomes are shown in Figure 4.21.B and Figure 4.21.C, respectively.

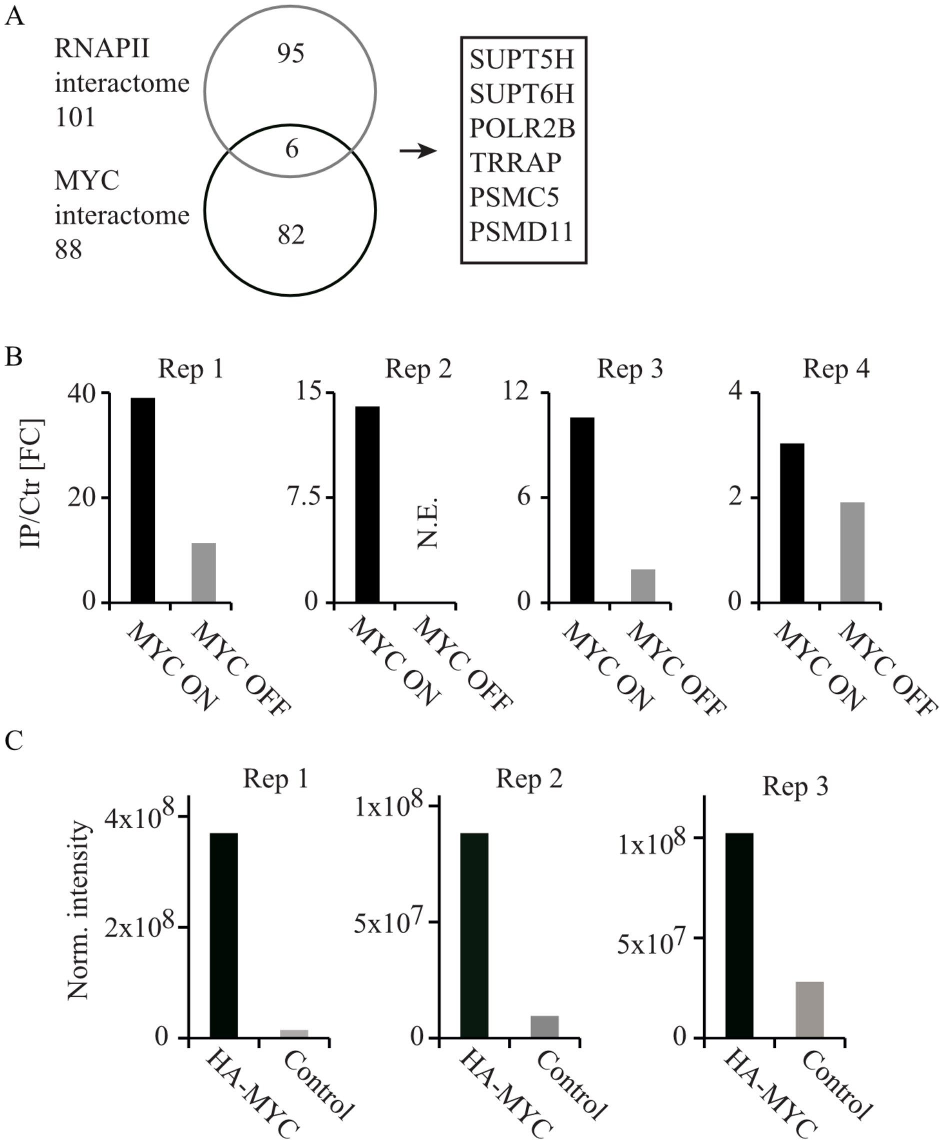


Figure 4.21: The overlap of significant RNAPII and MYC interactors and SPT5 enrichment values.

***A**. Venn diagram showing the overlap of the 101 proteins identified as significant RNAPII interactors (grey) and the 88 proteins identified as significant MYC interactors (black). The six common proteins are listed in the table on the right (gene names).*

***B**. Bar charts depicting enrichment values of SPT5 in the RNAPII interactome. Four replicates from T-lymphoma cells (underlying Figure 4.10.A) are shown expressing either normal MYC levels (MYC ON, black), or are depleted of MYC by Doxycycline treatment (MYC OFF, grey). Y-axis corresponds to the log2 fold change enrichment of SPT5 in HA-RPB3- over control EV-expressing cells as determined by qMS after HA-IP. N.E.: not enriched*

***C**. Bar charts displaying enrichment values for SPT5 in the MYC interactome. Normalized intensities are shown for SPT5 in HA-MYC- (black) or in EV-expressing control cells (grey). Values correspond to three replicates underlying Figure 4.17.A. The SPT5 enrichment was determined in HA-IP by qMS. This figure was published in a similar form in (Baluapuri et al. 2019).*

4.5 MYC-dependent recruitment of SPT5 to chromatin

That the handover of SPT5 from MYC to RNAPII happens on chromatin for transcribed MYC target genes and therefore influences SPT5 chromatin-binding was not formally proven so far. Therefore, to prove that SPT5 handover to processive RNAPII is a mechanism by which MYC regulates transcription of its target genes, chromatin immunoprecipitations followed by deep sequencing (ChIPseq) for SPT5 and RNAPII were performed.

U2OS cells expressing MYC (MYC ON, green) or depleted of MYC by siRNA treatment (MYC OFF, blue) were analyzed for SPT5 and RNAPII binding to chromatin. Briefly, proteins were crosslinked to DNA, chromatin was isolated and fractionated using sonication, and bound DNA was enriched by protein specific IP for SPT5, RNAPII, or unspecific IgG as a control. Enriched DNA was isolated, sequencing library was prepared, and DNA was sequenced using Illumina sequencing.

SiRNA-mediated knockdown of MYC was validated by immunoblotting (Figure 4.22.A). Genome browser tracks of several MYC-occupied genes showed a decrease in SPT5 occupancy throughout the gene, whereas total RNAPII was not affected (Figure 4.22.B). This finding was confirmed by the genome wide analysis showing a decrease in SPT5 binding to chromatin upon MYC knockdown, which was not caused by changes in RNAPII occupancy (Figure 4.22.C).

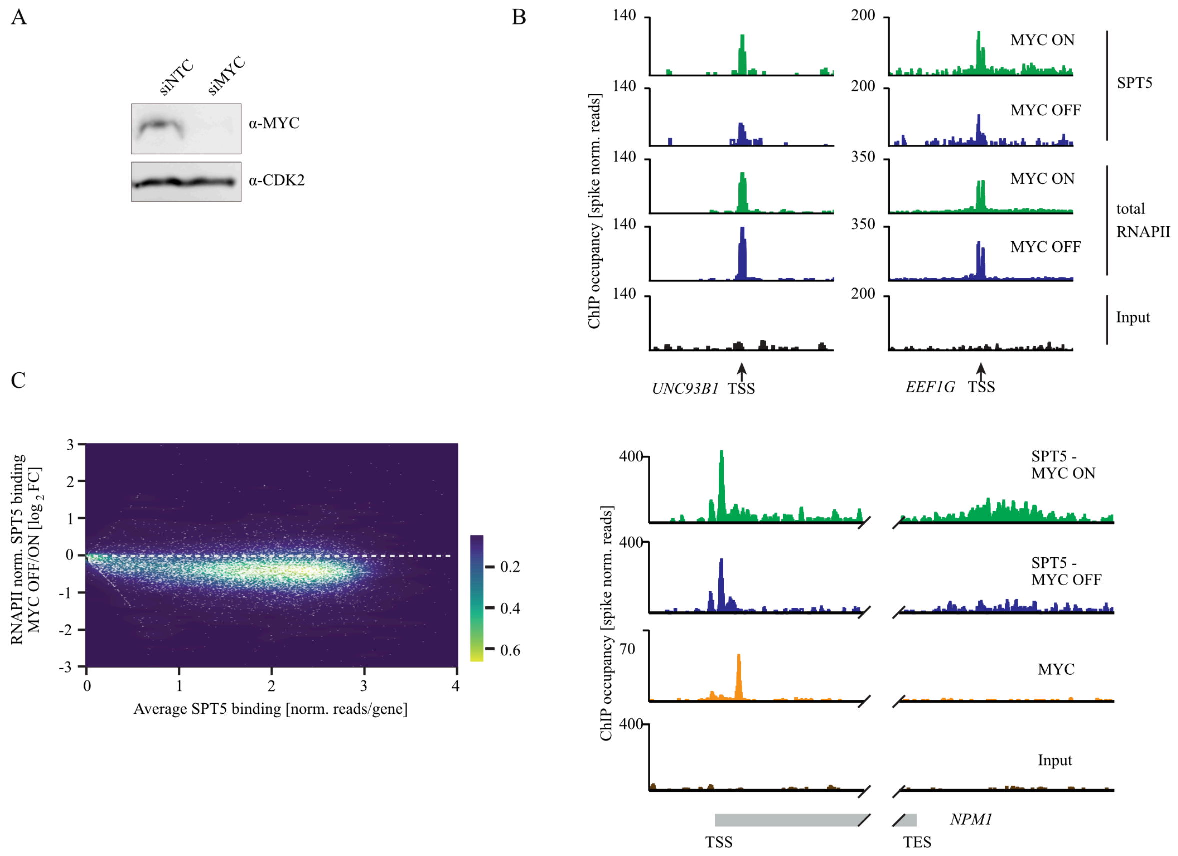


Figure 4.22: The MYC-dependent recruitment of SPT5 to chromatin.

***A**. Immunoblot of MYC levels after siRNA-mediated knockdown. Immunoblot from U2OS whole cell lysates treated with a non-targeting siRNA (siNTC, MYC ON) or an siRNA targeting MYC (siMYC, MYC OFF). CDK2 was used as a loading control.*

***B**. Genome browser tracks from SPT5 and total RNAPII ChIPseq from U2OS cells. ChIPseq against SPT5 and total RNAPII was performed from U2OS cells treated with control siNTC (MYC ON, green) or MYC-targeting siRNA (MYC OFF, blue) as validated in A. Genome browser tracks are shown for the genes* UNC93B1 *and* EEF1G *(top). Bottom shows the* NPM1 *gene. MYC ChIPseq profile was re-analyzed from published data (Lorenzin et al. 2016) and is shown in orange. Input is shown in black. ChIP was normalized to a murine spike-in control.*

***C**. Density plot showing SPT5 binding to chromatin normalized to RNAPII binding. Based on the ChIPseq experiment shown in B. Each white dot represents a single gene as exemplary shown in B. Colouring indicates SPT5 binding intensity. On the y-axis the change of SPT5 binding of MYC OFF / MYC ON is depicted as log2 fold change normalized to total RNAPII signal. On the x-axis overall SPT5 binding normalized to reads per gene is shown. ChIP was normalized to a murine spike-in control.*

TSS: transcription start site; TES: transcription end site; norm.: normalized.

This figure was published in a similar form in (Baluapuri et al. 2019).

ChIP qPCR of two MYC target genes confirmed a decrease in SPT5 occupancy upon MYC knockdown, whereas RNAPII levels, determined by an IP against total RNAPII independent of its CTD-phosphorylation status, were not affected (Figure 4.23).

The shown ChIPseq experiment (Figure 4.22) confirmed a MYC-dependent recruitment of SPT5 to RNAPII-transcribed genes.

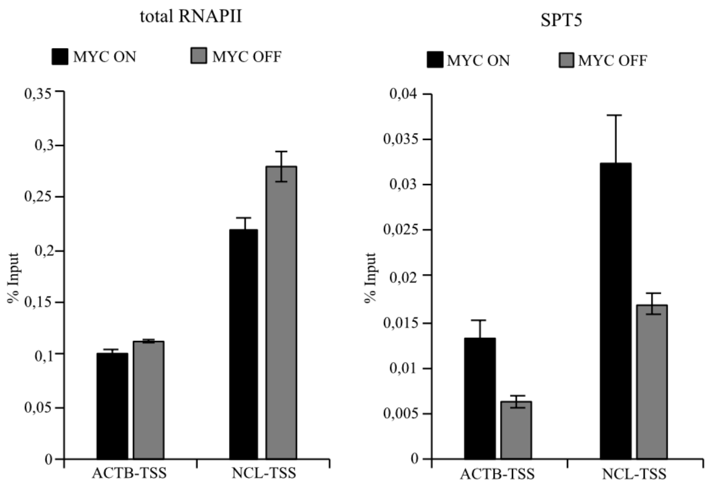


Figure 4.23: qPCR validation of RNAPII and SPT5 enrichment at MYC target gene promoters.
qPCR from ChIP experiments. ChIP experiment from U2OS cells treated with siNTC (MYC ON, black) or siMYC (MYC OFF, grey). Chromatin binding of total RNAPII (left) or SPT5 (right) was analyzed by qPCR with primers specific for the TSS of the ACTB *and the* NCL *genes, two MYC target genes. Error bars indicate standard deviation from technical triplicates. TSS: transcription start site*
This figure was published in a similar form in (Baluapuri et al. 2019).

4.6 Characterizations of the MYC-SPT5 interaction

In order to validate the interaction of SPT5 and MYC, co-IPs of endogenous proteins were performed in different cell lines using specific antibodies. Co-immunoprecipitation of SPT5 with MYC and vice versa, of MYC with SPT5 is shown for U2OS, T-lymphoma, and HEK293T cells (Figure 4.24.A-C, with A in U2OS cells, B in T-lymphoma cells, and C in HEK293T cells; A and C were performed by Bikash Adhikari, research group of Elmar Wolf, University of Würzburg).

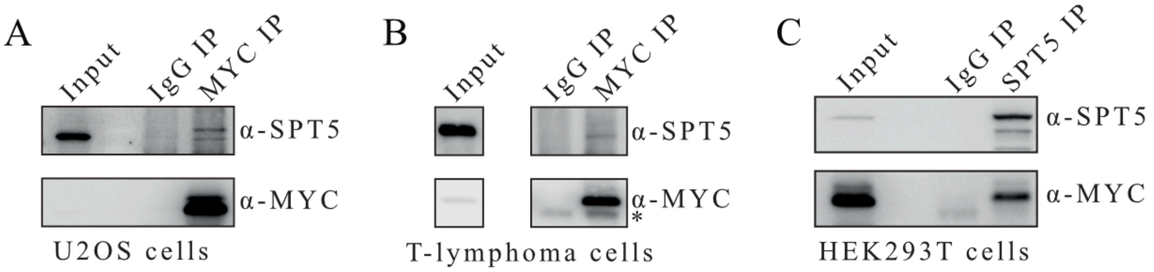


Figure 4.24: Co-IPs of endogenous proteins from different cell lines.

__A__. Western blot of an immunoprecipitation experiment from U2OS cells. Endogenous MYC was immunoprecipitated and SPT5 was visualized in co-IP. IgG-coupled beads were used as a control. This experiment was performed by Bikash Adhikari (research group of Elmar Wolf, University of Würzburg).

*__B__. Western blot of an immunoprecipitation experiment from T-lymphoma cells. IP was performed for endogenous MYC and SPT5 was stained in co-IP. IgG served as a control. * indicates the eluted antibody heavy chain.*

__C__. Western blot of an immunoprecipitation experiment from HEK293T cells. IP was performed for endogenous SPT5 and MYC was stained in co-IP. IgG was used as a control. This experiment was performed by Bikash Adhikari (research group of Elmar Wolf, University of Würzburg).

This figure was published in a similar form in (Baluapuri et al. 2019).

I have wondered if other proteins are required for the interaction of SPT5 and MYC. To address this question, tagged proteins were transiently expression in HEK293T cells. In case of a third protein involved in the MYC-SPT5 interaction, this might be a limitation in the overexpression system. Still, the SPT5-MYC interaction was confirmed (Figure 4.25.A and B).

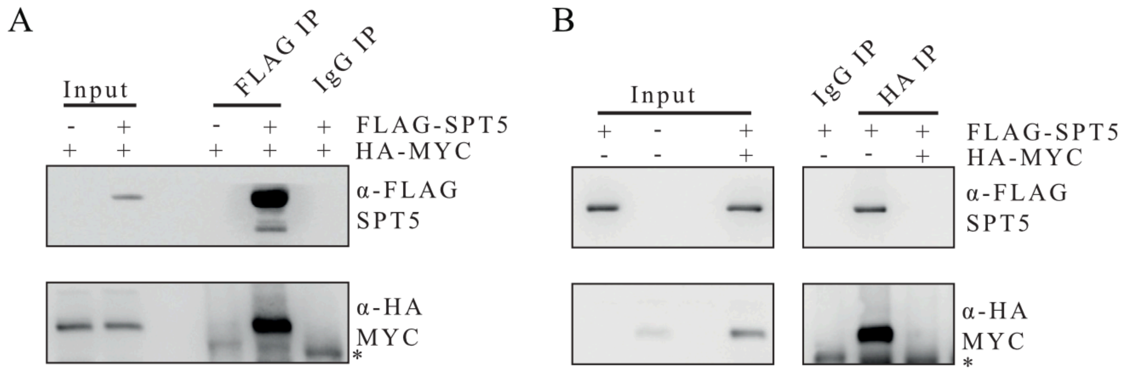


Figure 4.25: Co-IPs after protein overexpression in HEK293T cells.

*__A__. Western blot of an immunoprecipitation experiment from HEK293T cells. HA-MYC and FLAG-SPT5 were overexpressed by transient transfection. IP was performed against the FLAG-tag of SPT5 and SPT5 was visualized by FLAG immunoblotting. HA-MYC in co-IP was visualized by an HA immunoblot. Beads coupled to unspecific IgG served as a control as well as lysates expressing HA-MYC only followed by FLAG-IP. * indicates the antibody heavy chain.*

***B**. Western blot of an immunoprecipitation experiment from HEK293T cells. HA-MYC and FLAG-SPT5 were overexpressed by transient transfection. IP was performed against the HA-tagged MYC and MYC was visualized by HA immunoblotting. FLAG-SPT5 in co-IP was visualized by a FLAG immunoblot. Beads coupled to unspecific IgG served as control as well as lysates expressing FLAG-SPT5 only. * indicates the antibody heavy chain.*

This figure was published in a similar form in (Baluapuri et al. 2019).

Silver staining of co-IPs from HEK293T cells overexpressing tagged proteins showed a clear intense band for both proteins, but no other proteins were enriched in the IP condition when compared to a control condition pointing towards a direct interaction of both proteins (Figure 4.26.A and B). Identity of the protein bands labelled as FLAG-SPT5 and HA-MYC was confirmed by mass spectrometry.

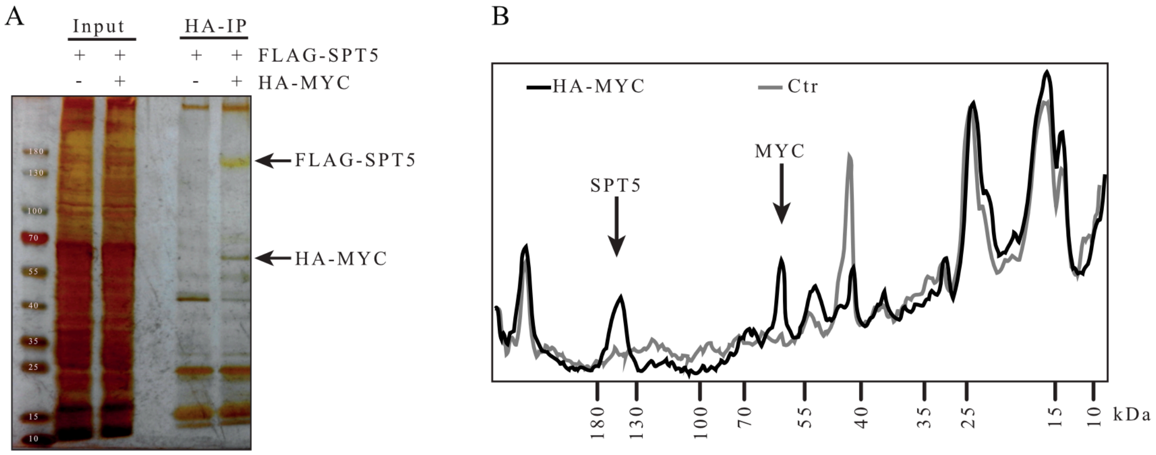


Figure 4.26: Interaction of MYC and SPT5 full-length proteins.

***A**. PAGE followed by silver staining of HA-IP from HEK293T cells. FLAG-SPT5 and HA-MYC were overexpressed by transient transfection. HA-IP was performed from cells expressing either FLAG-SPT5 alone (control) or in combination with HA-MYC. Input and samples eluted from HA-beads were loaded onto PAGE and gel was stained for proteins using the silver staining method. FLAG-SPT5 and HA-MYC are labelled with arrows as determined by MS from a corresponding Coomassie gel (not shown).*

***B**. Density blot from the elution lanes of the HA-IPs from the silver gel shown in A. The grey line corresponds to the control from HEK293T cells expressing FLAG-SPT5 only and the black line to the co-expression of FLAG-SPT5 with HA-MYC. Numbers below indicate the signal of the protein marker in kDa. Arrows indicate the intensities corresponding to FLAG-SPT5 or HA-MYC. Density blot was generated using the Image J software.*

This figure was published in a similar form in (Baluapuri et al. 2019).

The described setup of transiently overexpressing tagged proteins in HEK293T cells was applied in further interaction studies and allowed the usage of several truncated or deletion mutants of the SPT5 (N-FLAG-tag) and the MYC (C-HA-tag) protein, respectively, to narrow down the interaction sites on both proteins.

4.6.1 The N-terminal NGN-domain of SPT5 is necessary for MYC-binding

SPT5 is a protein of 130 kDa with several structured domains, which are associated with different functions. Therefore, identifying the interacting region of MYC on SPT5 could help in elucidating the mechanisms underlying their interaction.

Three SPT5 mutants lacking C-terminal regions and four lacking N-terminal regions were generated, resulting in a total of seven deletion mutants, numbered D1-D7, all harboring the N-terminal FLAG-tag (for a schema see Figure 4.27.A). SPT5-D1-D7 mutants were cloned by Ashwin Narain, research group of Elmar Wolf, University of Würzburg. These mutants were transiently overexpressed in HEK293T cells and their ability to co-IP with co-expressed HA-MYC (full-length) was analyzed by western blotting (Figure 4.27.B).

Expression of all SPT5-mutants could be confirmed by immunoblotting, with SPT5-D1 showing lower expression levels, likely due to detection limits according to its small size compared to the other mutants. The three mutants SPT5-D1, -D2, and -D3 comprising the N-terminal region of SPT5 were able to co-IP with HA-MYC, but the four mutants SPT5-D4-D7 covering the C-terminal domains of SPT5 failed to be co-IPed by MYC (Figure 4.27.B). This proved that a sequence in the very N-terminal part of SPT5 is necessary and sufficient for MYC-binding, since the SPT5-D1 mutant comprising amino acids 1 to 271 was tested positively in the experiments. Within this N-terminal region the NGN-domain is annotated, a NusG-like domain evolutionary conserved back to bacteria.

Thus, I cloned a mutant lacking only the NGN-domain (aa 175-270), referred to as SPT5-ΔNGN (Figure 4.27.A), and checked for MYC-binding in co-IPs (Figure 4.27.C). Indeed, SPT5-ΔNGN could not be co-IPed by HA-MYC, demonstrating that the NGN-domain of SPT5 is essential for MYC-binding. Reversely, expressing the NGN-domain itself, fused to GFP for size reasons, showed that this domain is sufficient for MYC-binding as illustrated by the co-IP experiment shown in Figure 4.27.D. Here, the GFP alone was used as a control and did not show MYC-binding capacities.

Furthermore, full-length SPT5 and SPT5-ΔNGN were analyzed in their binding to NMYC. NMYC-HA was immunoprecipitated and SPT5-binding was analyzed. Full-length SPT5 was able to bind NMYC, but not SPT5-ΔNGN (Figure 4.27.E). This points towards a conserved binding site on c-MYC and NMYC.

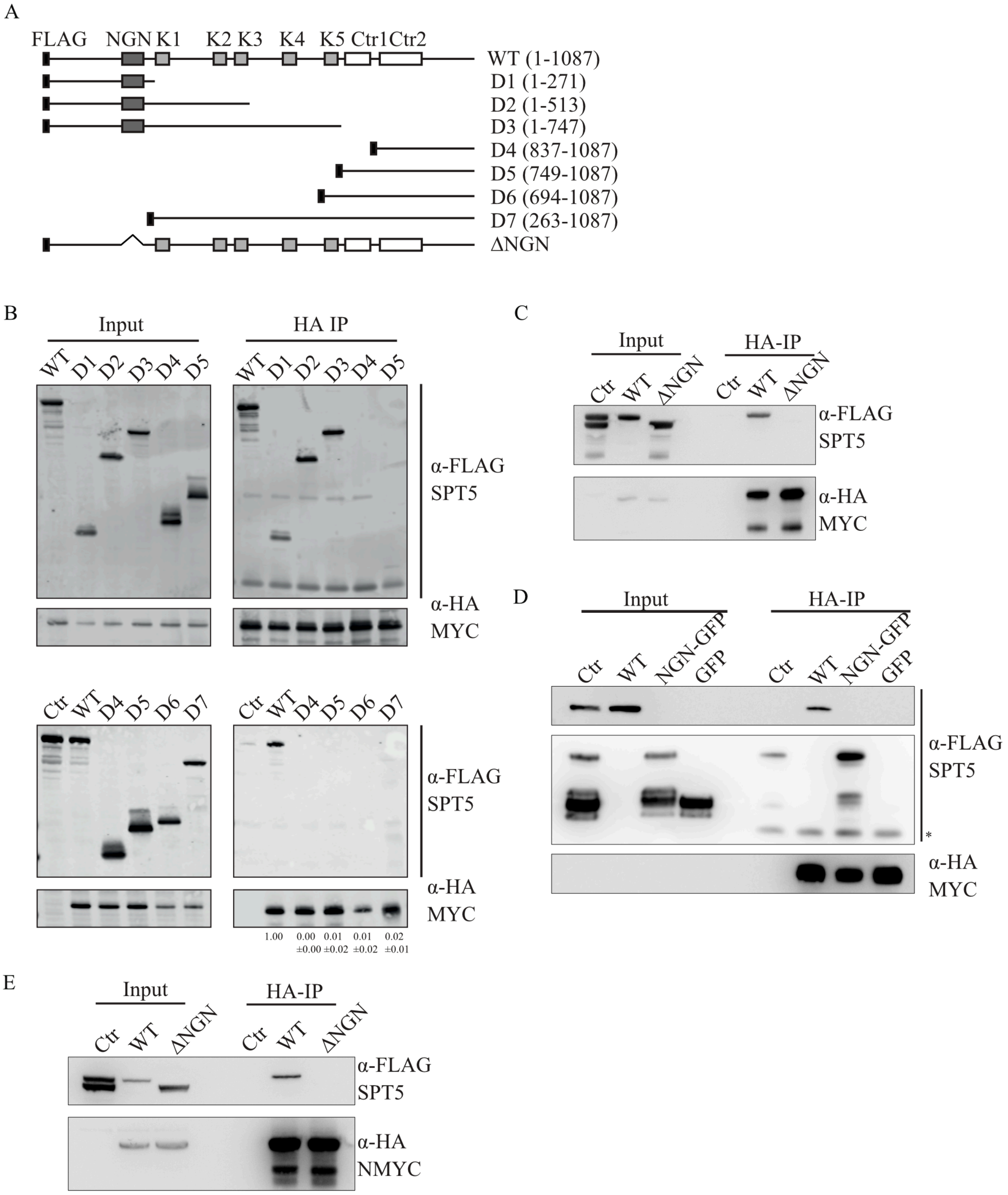


Figure 4.27: SPT5's NGN-domain is necessary and sufficient for MYC-binding.

A*. Schematic overview of the SPT5 domain structure and the generated SPT5 mutants. Numbers correspond to amino acids of human SPT5. All constructs have an N-terminal FLAG-tag (black). K: KOW domain; Ctr: C-terminal repeat region.*

B*. Western blot from a co-IP experiment from HEK293T cells. Full-length HA-MYC was co-expressed with full-length FLAG-SPT5 or its mutants D1 to D7. Immunoblots on the left show input levels and on the right IP against the HA-tag of MYC. HA-MYC was visualized by HA-antibody and FLAG-SPT5 and its mutants by FLAG-antibody. Upper panel shows the results for full-length SPT5 (WT) and the mutants*

D1 to D5. Lower panel shows full-length SPT5 (WT) and the mutants D4 to D7. As a control, full-length FLAG-SPT5 was expressed in HEK293T cells without HA-MYC (Ctr). Numbers below depict the quantification of immunoblots from three independent experiments calculated using the Studio Lite software (LI-COR).

***C**. Western blot from a co-IP experiment from HEK293T cells. FLAG-SPT5 full-length (WT) or FLAG-SPT5-ΔNGN were expressed in HEK293T cells (Ctr) or co-expressed with full-length HA-MYC using transient transfection. Input is shown on the left and HA-IP on the right. FLAG-SPT5 and SPT5-ΔNGN were detected using FLAG-antibody and HA-MYC using HA-antibody.*

***D**. Western blot from a co-IP experiment from HEK293T cells. IP was performed against HA-tag and MYC-HA was detected by HA-immunoblot. HA-MYC was co-expressed with full-length FLAG-SPT5 (WT), NGN-GFP-FLAG (NGN-GFP), or GFP-FLAG (GFP). Co-IP was determined by FLAG-immunoblot. As control (Ctr) a lysate from cells expressing FLAG-tagged proteins only and no HA-protein was used. * marks the antibody light chain.*

***E**. Western blot from a co-IP experiment from HEK293T cells. HA-tagged full-length NMYC and FLAG-tagged full-length SPT5 (WT) or SPT5-ΔNGN were expressed in HEK293T cells by transient transfection. IP was performed with an HA-specific antibody. Immunoblot was performed using HA- and FLAG-antibodies, respectively. A lysate from cells not expressing HA-NMYC was used as a control (Ctr).*

This figure was published in a similar form in (Baluapuri et al. 2019).

4.6.2 Mutually exclusive binding of MYC and SPT4 to SPT5

The NGN-domain of SPT5, shown in the previous set of experiments to be necessary for MYC binding, is known to interact with SPT4, the second subunit of DSIF. Thus, I analyzed a possible competitive or cooperative binding of SPT4 and MYC on SPT5. Surprisingly, transient overexpression of SPT4 together with SPT5 and MYC in HEK293T cells completely abolished coprecipitation of SPT5 by MYC (compare second to third lane in HA-IP, Figure 4.28). SPT4 itself was not co-IPed by MYC. These results strongly support the idea of mutually exclusive, competitive binding of MYC and SPT4 to the same region on SPT5.

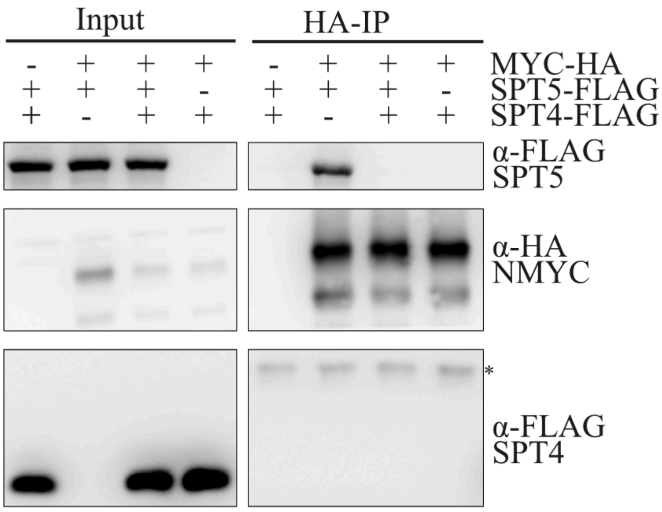


Figure 4.28: Mutual exclusive binding of MYC and SPT4 to SPT5.

*Western blot from a co-IP experiment from HEK293T cells. HA-MYC, FLAG-SPT5, and FLAG-SPT4 were expressed in the indicated combinations in HEK293T cells using transient transfection. IP was performed with HA-specific beads. Proteins were visualized using tag-specific antibodies. * marks the antibody light chain.*

4.6.3 SPT5 binds the N-terminal region of MYC

To narrow down the interaction site for SPT5 on MYC, a series of MYC mutants was generated. The mutants ΔMBI, ΔMBII, ΔMBIII, and ΔMBIV were deleted for the corresponding MYC-box (MB) (schema see Figure 4.29.A) and all of them contained a C-terminal HA-tag. MB-deletion mutants were cloned by Markus Vogt, research group of Elmar Wolf, University of Würzburg. Mutants were expressed in HEK293T cells and the ability of full-length, FLAG-tagged SPT5 to co-IP with these mutants was analyzed by western blot analysis (Figure 4.29.B). Deletion of MBI or MBII resulted in a decrease of the SPT5 coprecipitation by 30%, but binding was not abolished.

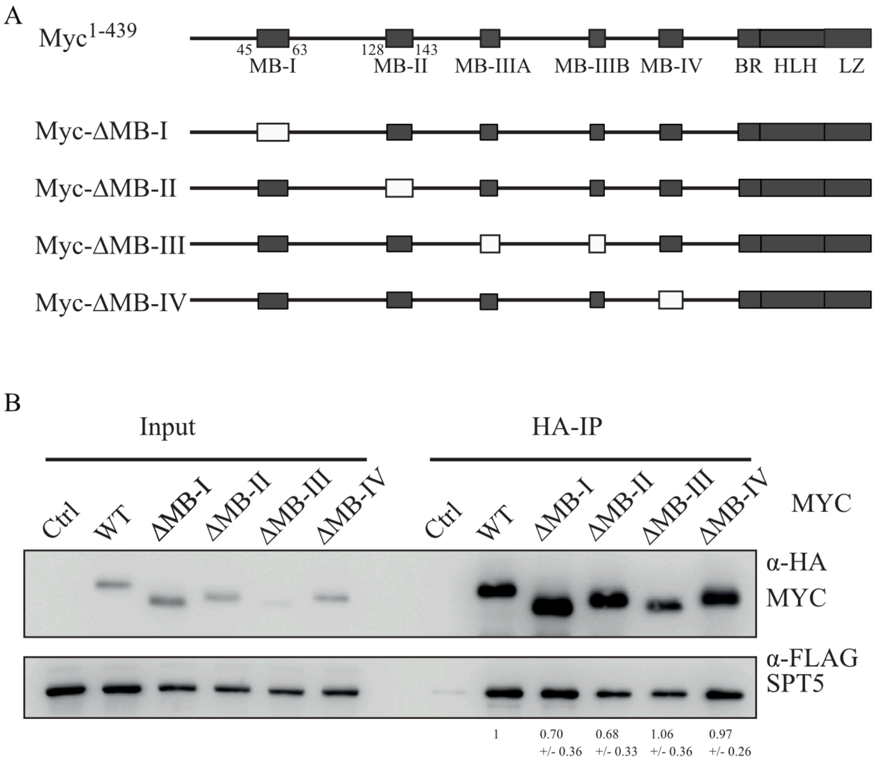


Figure 4.29: SPT5 showed decreased interaction for MYC deleted of MBI or MBII.

A. *Schema showing domains of MYC and different MYC mutants. All constructs were designed with a C-terminal HA-tag. White boxes indicate MB-deletions, while grey boxes indicate unperturbed domains. Numbers below indicate amino acid position.*

B. *Western Blot from a co-IP experiment in HEK293T cells. FLAG-SPT5 was co-expressed with full-length HA-MYC (WT) or mutants lacking one of the MYC boxes (MB). IP was performed with HA-specific beads. Proteins were visualized by tag-specific antibodies. Numbers below indicate quantification of immunoblots from three independent experiments calculated using the Studio Lite software (LI-COR). As control (Ctrl) a lysate from cells expressing FLAG-SPT5 only and no HA-protein was used.*

Two amino acids within MBI, Thr58 and Ser62, are known to get phosphorylated to control MYC's protein stability (see section 1.5). Therefore, I tested MYC mutants of either Thr58 or Ser62 or both amino acids, which abolish phosphorylation and mimic an unphosphorylated status (T58A, S62A, T58A/S62A). Full-length FLAG-SPT5 was co-expressed with MYC mutants in HEK293T cells and FLAG-IP was performed (Figure 4.30). As the binding capacity for SPT5 to all three mutants, T58A, S62A and T58A/S62A, was comparable as of the wild type MYC (MYC-WT), it is unlikely that SPT5-binding interferes with MYC's phosphorylation status neither at Thr58 nor at Ser62.

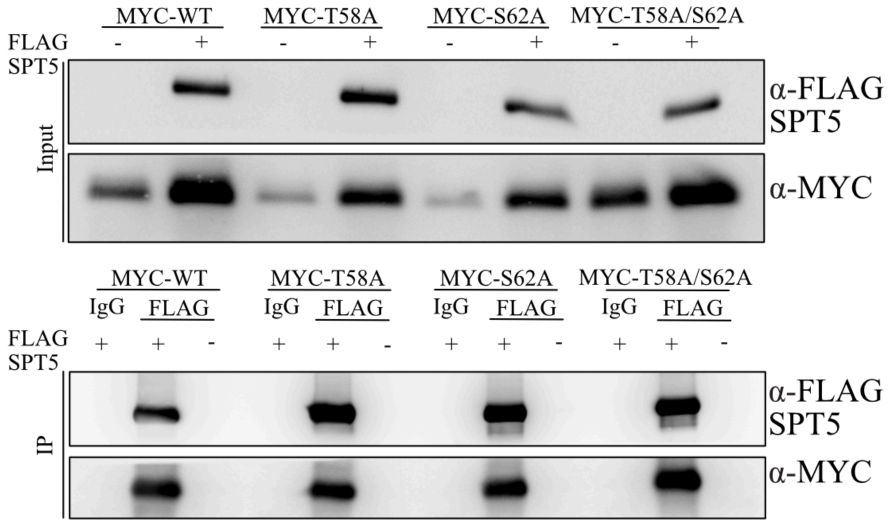


Figure 4.30: Co-IPs of MYC phospho-mutants with SPT5.

Western Blot from co-IP experiments from HEK293T cells. FLAG-SPT5 was expressed together with MYC-WT or the MYC mutants T58A, S62A, or T58A/S62A. Top blot shows input levels and bottom eluates from FLAG or IgG IPs. SPT5 was visualized by a FLAG-specific antibody, MYC by a MYC-specific antibody. IP specificity was controlled by the pulldown with unspecific IgG or by cell lysates expressing no FLAG-tagged protein.

For another series of mutants, truncated versions of MYC harboring a C-terminal HA-tag were generated (schema see Figure 4.31.A). MYC-ΔN1, -ΔN2, -ΔN3 and -ΔN4 were lacking the N-terminus including MBI, MBII, MBIII, and MBIV, respectively. These mutants were characterized earlier within the master thesis of Sarah Dötsch (2017, research group of Elmar Wolf, University of Würzburg) and particularly the MYC-ΔN1 mutant was used for the qMS studies described in results section 4.3. Overexpression of these four HA-tagged mutants resulted in varying expression levels, most likely due to a highly instable nature of the truncated proteins (Figure 4.31.B). The mutant MYC-ΔN2 (labelled as MYC144-439) was expressed in a comparable extend as the wild type (WT) form of MYC. The ability to co-IP full-length SPT5 strongly decreased to 14% for MYC-ΔN2 (MYC144-439) as compared to MYC-WT, but was not abolished (Figure 4.31.C).

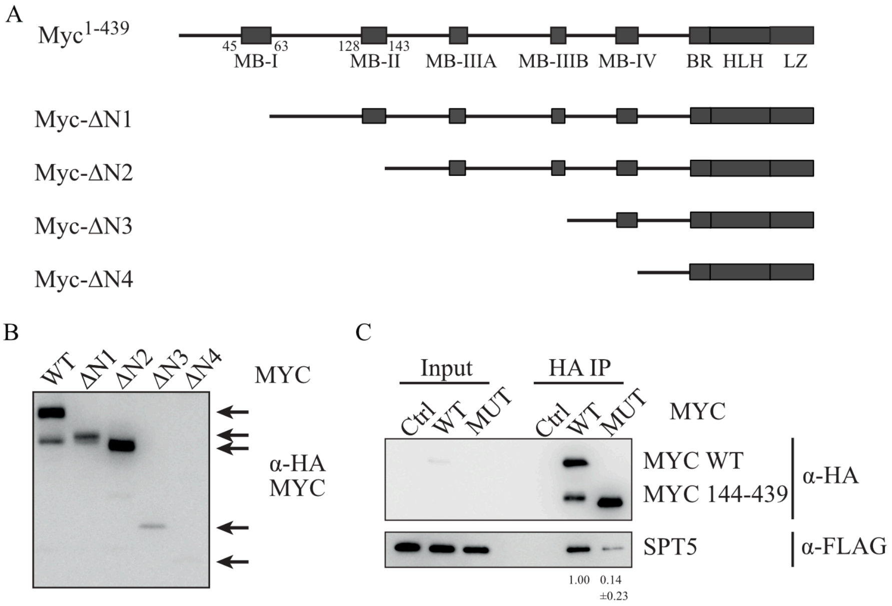


Figure 4.31: SPT5 showed decreased interaction with N-terminally truncated MYC.

A*. Schema showing domains of MYC and N-terminally truncated MYC mutants. All constructs were designed with a C-terminal HA-tag. Numbers below indicate amino acid position.*

B*. Western Blot from HA-MYC-mutants expressed in HEK293T cells. MYC mutants ΔN1 to ΔN4 were expressed in HEK293T cells using transient transfection and expression levels were analyzed by HA-immunoblotting. Same cell number was used per western blot sample. Arrows point at protein bands corresponding to the MYC mutants.*

C*. Western blot from a co-IP experiment from HEK293T cells. Full-length MYC-HA (WT) or the MYC-ΔN2 mutant lacking amino acids 1-143 (MYC144-439) were expressed by transient transfection in HEK293T cells together with full-length FLAG-SPT5. Lysates from cells expressing only FLAG-SPT5 were used as control (Ctrl). Proteins were detected by tag-specific antibodies. IP was performed against the HA-tag of MYC. Numbers below indicate the quantification calculated from three different experiments using the Studio Lite software (LI-COR).*

This figure was published in a similar form in (Baluapuri et al. 2019).

Deletion of the first 143 aa showed a strong decrease in SPT5 binding, while deletion of MBI or MBII only had minor effects (compare Figure 4.32.B and Figure 4.29.B). This inconsistency can be explained by either high binding affinity of MYC’s first 44 aa for SPT5 or of a region between MBI and MBII. To address this issue, I generated a MYC mutant lacking the first 44 aa (MYC-d(1-44)), which also includes MB0, and produced stable cell lines expressing it (Figure 4.32.A). However, MYC-d(1-44) was still able to bind to endogenous SPT5. Another MYC mutant lacking the region between MBI and MBII, MYC-d(68-123), similarly showed no reduction in SPT5-binding (Figure 4.32.B).

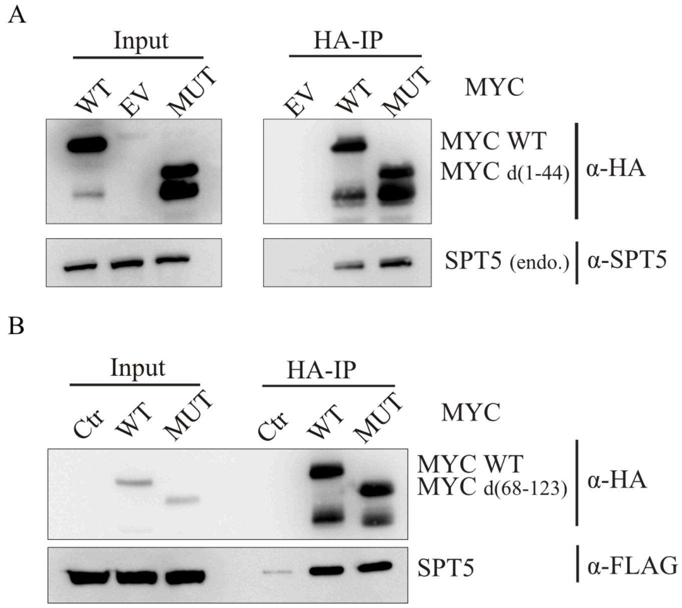


Figure 4.32: Co-IPs of SPT5 with MYC deletion mutants.
__A__. Western blot analysis of HA-IPs from HEK293T cells. Stable cell lines expressing HA-tagged MYC-WT, MYC-MUT deleted of the first 44 aa (MYC-d(1-44)), or the corresponding empty vector (EV) were generated and HA-IP was performed. MYC was stained using an HA-specific antibody. Endogenous (endo.) SPT5 was detected by an SPT5-antibody. Please note the difference in loading order for input (left) and IP (right).
__B__. Western blot analysis of HA-IPs from HEK293T cells. HA-tagged MYC-WT or MYC-MUT deleted of the spacer region in between MBI and MBII (MYC-d(68-123)) were expressed together with full-length FLAG-SPT5 in HEK293T cells by transient transfection. HA-IP was performed and cells expressing only FLAG-SPT5 served as a control (Ctr). MYC was visualized using an HA-specific antibody and SPT5 using a FLAG-specific antibody.

In summary, SPT5-binding to MYC was affected strongest by the deletion of aa 1-143 including MB0, MBI, and MBII, but was not abolished. Deletion of single elements within this region had only minor effects on SPT5 binding to MYC.

4.6.4 In vitro pulldowns with recombinant proteins show direct interaction

To prove a direct interaction of SPT5 and MYC, as indicated by silver staining of co-IPs from HEK293T cells (Figure 4.26.A and B), both proteins were expressed and purified from *E. coli* excluding any third mammalian protein, which could mediate their interaction. Since full-length MYC could not be purified from *E. coli* without losing most of it due to protein aggregation, in a first approach the full-length MYC fused to a Strep-tag was co-expressed and -purified with His-DSIF (SPT4 and SPT5) from *E. coli* (Maren Bleckmann, Core Facility Protein Expression, Rudolf Virchow Center, Würzburg). The SPT5-MYC complex was purified by Streptavidin-pulldown followed by His-pulldown (Figure 4.33.A). When the same pulldown strategy was employed on *E. coli* expressing His-DSIF only, almost no SPT5 could be detected (Figure 4.33.A).

This set of experiments demonstrated the direct interaction of MYC and SPT5. SPT4 was not detected, due to either technical reasons or to mutually exclusive binding of SPT4 and MYC on SPT5 as observed by exogenous co-IPs in HEK293T cells (Figure 4.28). To elucidate between those two possibilities, SPT5, SPT4, and MYC were expressed and purified separately and mixed only for the pulldown experiment. MBP-MYC was expressed and purified from insect cells by Robert Düster (research group of Matthias Geyer, University of Bonn), while SPT5-His and SPT4-MBP were expressed and purified from *E. coli* (Lars Schönemann, Core Facility Protein Expression, Rudolf Virchow Center, Würzburg). The pulldown of MYC by a MYC-specific antibody resulted in the pulldown of SPT5 as visualized by electrophoresis followed by Coomassie staining and immunoblotting (Figure 4.33.B and C). In the Figure 4.33.B MBP-SPT4 was found together with SPT5 when MYC was pulled down, inconsistently to the results from HEK293T cells presented in Figure 4.28. This can have several reasons: first, a post translational modification (PTM) can prevent simultaneous binding of SPT4 and MYC to SPT5; second, the presence of one or several other proteins in the cell lysate might block an interaction site now occupied by SPT4 or MYC; third, one or several of these three proteins (MYC, SPT4, SPT5) might not be folded correctly resulting in a decrease in sterically hindrance.

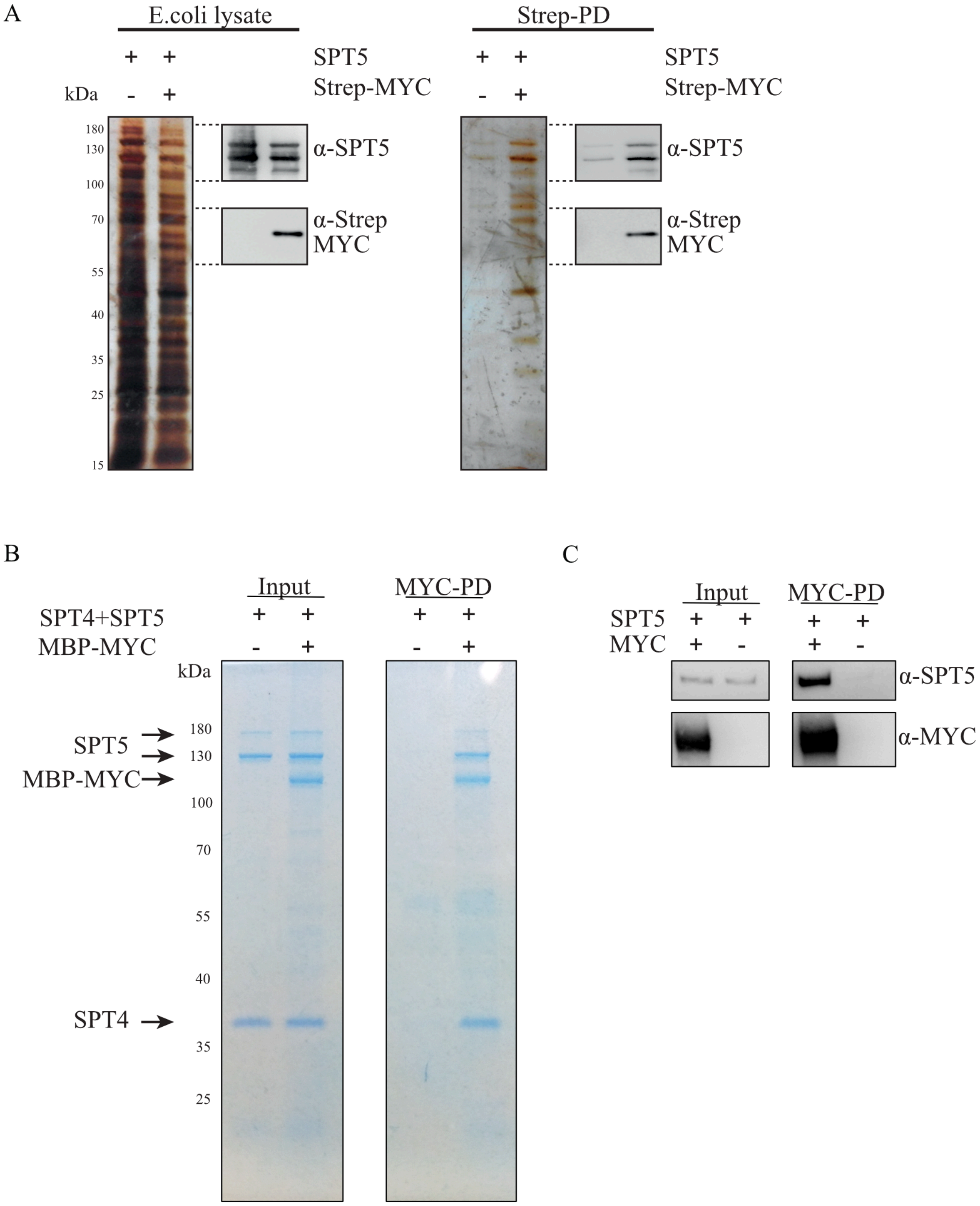


Figure 4.33: Direct interaction of recombinant proteins.

***A**. Silver stained-PAGE and immunoblot of SPT5 and MYC co-expressed in* E. coli. *His-DSIF (SPT5 and SPT4) alone or in combination with Strep-MYC were expressed in* E. coli *(input, left) by Maren Bleckmann, Rudolf Virchow Center, Würzburg. Immunoblotting was performed with SPT5-specific antibody and an antibody recognizing the Strep-tag for MYC detection. MYC was pulled down via the Strep-tag and co-precipitated SPT5 was analyzed. Strep = Streptavidin; PD: pulldown.*

***B**. Coomassie stained PAGE of MYC-pulldown of recombinant proteins. MBP-MYC was expressed and purified from insect cell by Robert Düster, research group of Matthias Geyer, University of Bonn. DSIF*

(MBP-SPT4 and SPT5) was expressed and purified from E. coli *by Lars Schönemann, Rudolf Virchow Center, Würzburg. Upon incubation of MBP-MYC with DSIF, MBP-MYC was pulled down using a MYC-specific antibody and eluted material was analyzed by Coomassie stained-PAGE. PD: pulldown* ***C****. Immunoblotting of MYC pulldown of recombinant proteins. Replicate experiment as the one shown in B. SPT5 and MYC were detected by protein-specific antibodies. PD: pulldown*

In summary, strongest defects in SPT5-binding were observed when the first 143 aa of MYC were deleted. However, even this MYC mutant interacted weakly with SPT5, suggesting several, non-overlapping binding sites for SPT5 on the MYC protein, most likely within MBI and MBII. Another weaker binding site may be more C-terminally located than MBII, since there was residual binding observed for MYC(144-439).

4.7 CDK7-mediated handover of SPT5 from MYC to RNAPII

The data obtained so far showed a MYC-dependent recruitment of SPT5 to chromatin and RNAPII. But the molecular mechanism underlying this transfer has not been elucidated so far. Transcription-related kinases are essential in the regulation of the different steps within the transcription cycle and are especially needed for overcoming transcriptional pausing and the formation of a productive elongation complex. Along this line, their implication in the handover of SPT5 onto RNAPII was investigated by employing endogenous co-IPs in the presence of inhibitors of different transcription-related kinases.

Upon the treatment of T-lymphoma cells with the pan kinase inhibitor DRB, MYC protein levels were strongly reduced. Interestingly, co-IP efficiency of SPT5 with residual MYC got increased as calculated as a fold change of SPT5 over MYC based on input and IP levels (Figure 4.34.A). Results from SPT5-MYC proximity ligation assays (PLAs), performed by Apoorva Baluapuri (research group of Elmar Wolf, University of Würzburg), in the presence of various transcriptional kinase inhibitors pointed towards the involvement of the CDK7 kinase activity during the transfer of SPT5 from MYC onto RNAPII (Baluapuri et al. 2019). To investigate how CDK7 is related to the handover in more detail, I overexpressed HA-MYC and FLAG-SPT5 in HEK293T cells and pulled on HA. I added recombinantly expressed, purified active CDK7 complex, gifted from the Cramer laboratory (Boehning et al. 2018), to the IPed complex, to analyze if CDK7 was able to disrupt the SPT5-MYC complex. As shown by the immunoblot in Figure 4.34.B, the addition of CDK7 did not affect the ability of MYC to co-IP SPT5. This shows, that neither MYC nor SPT5 are bound and phosphorylated by CDK7 in a way that disrupts the complex, but rather an additional protein is involved, like for example RNAPII or SPT4.

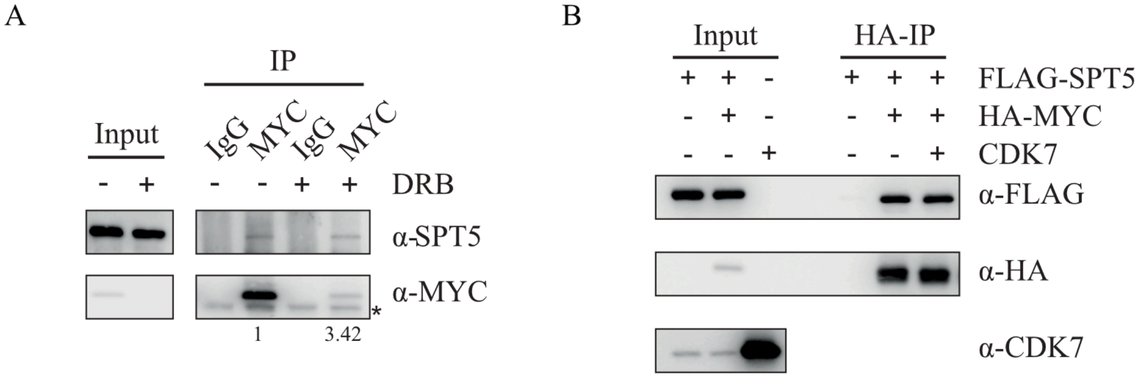


Figure 4.34: CDK7-involvement in the handover of SPT5 from MYC to RNAPII.

*A. Immunoblots of MYC-IP from T-lymphoma cells treated with the pan transcriptional kinase inhibitor DRB. DMSO was used as a control treatment. Endogenous MYC was precipitated by a MYC-specific antibody. Beads coupled to unspecific IgG were used as a precipitation control. Co-precipitation of endogenous SPT5 was analyzed by a specific antibody. Numbers below indicate protein levels calculated for co-IPed SPT5 based on the MYC-IP efficiency using the LI-COR software. IP-efficiency in the untreated cells was set to 1. Note that MYC levels were strongly reduced in T-lymphoma cells upon DRB treatment. * indicates the antibody heavy chain.*

B. Immunoblot of MYC-SPT5 co-IP in the presence of CDK7. HA-MYC and FLAG-SPT5 were transiently expressed in HEK293T cells and the HA-IP was performed. Cells expressing only FLAG-SPT5 were used as a control. Recombinant CDK7 (Boehning et al. 2018) was added and co-IP efficiency of SPT5 was analyzed. CDK7 was stained with a protein-specific antibody, also recognizing endogenous CDK7 in whole HEK293T cell lysate.

This figure was published in a similar form in (Baluapuri et al. 2019).

Furthermore, CDK7 is known to phosphorylate the CTD of RNAPII at Ser5, so I hypothesized that the phosphorylation status of the CTD is involved in the handover of SPT5 from MYC onto RNAPII. SPT5 is shown to interact with the RNAPII core complex rather than with its unstructured CTD, however, due to technical obstacles unstructured regions cannot be visualized by crystal structures. I incubated pre-formed complexes of SPT5 and MYC from HA-IP of HEK293T lysates with increasing concentrations of unphosphorylated CTD or with pCTD (GST-tag), which got phosphorylated by CDK7. Both CTD samples were kindly provided by the Geyer laboratory (Robert Düster, research group of Matthias Geyer, University of Bonn). Neither the unphosphorylated nor the phosphorylated CTD peptides disrupted the MYC-SPT5 complex, as shown by the immunoblotting in Figure 4.35.

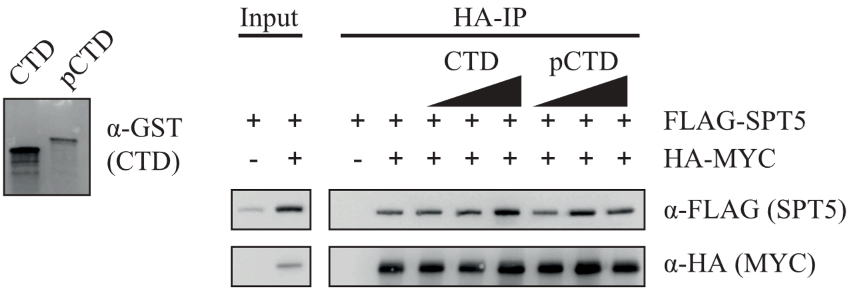


Figure 4.35: The RNAPII-CTD did not alter the MYC-SPT5 interaction.

Immunoblot of MYC-SPT5 co-IP in the presence of CDK7-phosphorylated pCTD. GST-tagged CTD of RPB1 was expressed and purified by Robert Düster, research group of Matthias Geyer, University of Bonn. CTD was incubated with active CDK7 to generate pSer5-CTD (pCTD). CTD and pCTD were stained with a GST-specific antibody (left). FLAG-SPT5 and HA-MYC were transiently expressed in HEK293T cells and HA-IP was performed. Cells expressing only FLAG-SPT5 were used as a control. Increasing amounts of CTD or pCTD were added and SPT5 binding to MYC was analyzed by tag-specific immunoblotting.

The handover can also be induced by reduced binding affinity of MYC for SPT5. A possible mechanism involving a kinase is a differential phosphorylation status of MYC. For that reason, we analyzed the phosphorylation status of MYC with and without CDK7 inhibition. Phosphoproteomics, performed by Nevenka Dudvarski Stankovic (research group of Elmar Wolf, University of Würzburg) and Andreas Schlosser (Rudolf Virchow Center, Würzburg), pointed towards a CDK7-induced phosphorylation of MYC at Ser6. Therefore, I tested co-IP efficiency in HEK293T cells of SPT5 with two phospho-mimetic MYC mutants: S6D and S6E cloned by Nevenka Dudvarski Stankovic (Figure 4.36). As analyzed by immunoblotting of FLAG-tagged SPT5 and HA-tagged MYC, mutating Ser6 of the MYC protein did not alter its interaction with SPT5.

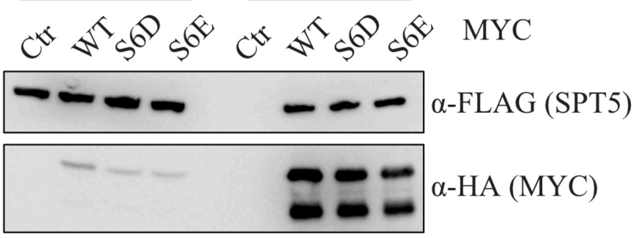


Figure 4.36: Co-IPs of SPT5 with MYC-S6 mutants.

Immunoblotting of co-IPs of MYC-mutants with SPT5. FLAG-SPT5 and HA-MYC were transiently *expressed in HEK293T cells. MYC wildtype (WT), or S6D- or S6E-mutants were used, all fused to an HA-tag. Control lysates did not contain any HA-tagged protein (Ctr). MYC-WT or -mutants were IPed using HA-specific beads and the ability of SPT5 to be co-IPed was analyzed by immunoblotting using a FLAG-specific antibody.*

Despite these efforts, a phosphorylation event on SPT5, MYC, or RNAPII critical for the handover of SPT5 was not identified. Still, an involvement of CDK7 within this transfer was confirmed by proximity-ligation assays (PLAs) performed by Apoorva Baluapuri, research group of Elmar Wolf. These assays showed that when CDK7 was inhibited the proximity between MYC-SPT5 was enhanced and RNAPII-SPT5 proximity was decreased. Inhibition of CDK9, which acts only after CDK7 within the transcription cycle, did not show an effect. Furthermore, additional siRNA-mediated knockdown of GTFIIE lowered the effect of CDK7 inhibition. This led to the conclusion that the transfer of SPT5 from MYC onto RNAPII is dependent on CDK7 and at least partially based on the release of GTFIIE from the RNAPII complex induced by CDK7 (Baluapuri et al. 2019).

4.8 ShRNA-mediated SPT5-knockdown decreased RNAPII levels in the gene body

MYC as an oncogenic transcription factor has global effects on RNAPII behavior. To see to what extent this is mediated by the recruitment of SPT5, RNAPII behavior was analyzed by ChIPseq after the knockdown of SPT5. To this end, five shRNA sequences targeting SPT5 mRNA for degradation (h-SPT5-mirE1-5) were cloned into a constitutive active vector backbone (pGIPZ) (see section 3.2.8), lentiviruses were generated and U2OS cells were transduced. Constitutive active shRNA expression against SPT5 resulted in rapid cell death as shown by crystal violet staining of U2OS cells (Figure 4.37.A), suggesting the essentiality of SPT5 and a need for an inducible, acute depletion system.

Thus, shRNAs were re-cloned into two different inducible vector backbones, one harboring GFP and RFP markers (pInd11) and the other a puromycin resistance gene (pLT3). Efficiency of shRNA-mediated knockdown of SPT5 was verified by western blotting after 24 and 48 hrs upon shRNA-induction by Doxycycline (Figure 4.37.B). The shRNAs h-SPT5-mirE1 and h-SPT5-mirE3 showed highest efficiency according to the SPT5 protein levels at 48 hrs post induction. The comparison to non-targeting shRNAs excluded a basal shRNA expression without the addition of Doxycycline, hence there was no leakiness of the plasmid.

Having h-SPT5-mirE1 and h-SPT5-mirE3 in two different vector backbones, cells were engineered to express both shRNAs after the addition of Doxycycline resulting in an even stronger SPT5 knockdown (Figure 4.37.C). MYC levels were not affected at this time point.

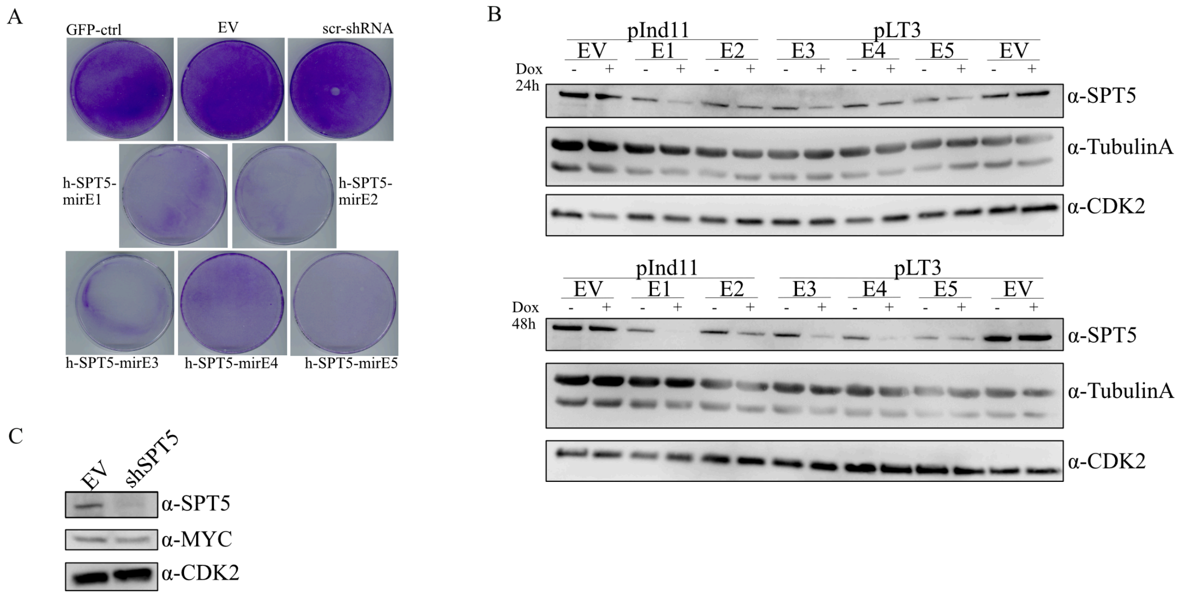


Figure 4.37: ShRNA-mediated knockdown of SPT5 in U2OS cells.

__A__. Crystal violet staining of U2OS cells. U2OS cells were infected to constitutively express shRNAs targeting SPT5 or a non-targeting shRNA (EV).

__B__. Immunoblotting of SPT5 levels after shRNA expression. U2OS cells were infected with inducible shRNA vectors against SPT5 or a non-targeting shRNA (EV). ShRNA expression was induced by Doxycycline for the indicated timeframes. SPT5 protein levels were analyzed by a protein-specific antibody and CDK2 and Tubulin A were used as loading controls.

__C__. Immunoblot of SPT5 levels after shRNA expression. U2OS cells were engineered to express a combination of two shRNAs targeting SPT5, E1 and E3 from B, or non-targeting control shRNAs (EV). ShRNA expression was induced by Doxycycline for 48 hrs and SPT5 protein levels were determined by a protein-specific antibody. CDK2 was used as a loading control. MYC levels were also analyzed.

A replicate of subfigure C was published in (Baluapuri et al. 2019).

To investigate the effect of the SPT5 knockdown on RNAPII function, ChIPseq was performed for total RNAPII and pSer2 RNAPII in U2OS cells expressing an shRNA targeting SPT5 or a control shRNA for 48 hrs (Figure 4.38.A). ChIPseq was normalized to a murine spike-in control and bioinformatic analysis of the ChIPseq experiment and generation of metagene plots was executed by Apoorva Baluapuri, research group of Elmar Wolf, University of Würzburg.

Metagene analysis for total RNAPII is shown in the Figure 4.38.B. Not much difference was observed neither at the TSS (transcriptional start site) nor in the gene body when comparing the control condition to the SPT5-knockdown. After the TES (transcriptional end site) there was more RNAPII signal in the control condition compared to cells expressing the shRNA targeting SPT5.

The metagene plot for pSer2 RNAPII is shown in the Figure 4.38.C. Here an increased signal at the TSS is shown for shSPT5-expressing cells, but a drop within the gene body was observed resulting in less signal at the TES upon knockdown of SPT5 (Figure 4.38.C). For better visualization, the ratio of the shSPT5 condition over the EV control condition was calculated and plotted for pSer2 RNAPII (Figure 4.38.D) underlining an increase at the TSS and a progressive decrease throughout the gene body with the strongest effect at the TES.

The difference at the TSS observed for total RNAPII (B) versus pSer2 RNAPII (C) can be explained by the fact that the antibody against total RNAPII recognizes unphosphorylated as well as phosphorylated RNAPII. That there is less pSer2 RNAPII in the control condition but same amount of total RNAPII at the TSS, could mean that the ratio changes from either unphosphorylated or pSer5 RNAPII in the control to pSer2 in the SPT5-knockdown cells. This could be a result of the usually fast release of pSer2 RNAPII into the gene body being slowed down or completely blocked upon SPT5-knockdown resulting in the increased pSer2 RNAPII signal observed at the TSS using the pSer2 RNAPII specific antibody.

The decrease of RNAPII signal within the gene body and at the TES, observed for both, total RNAPII and pSer2 RNAPII, might be due to a reduction in speed of RNAPII or it falling off the gene during the elongation process before the TES is reached. Which of these two scenarios is correct can only be determined by a time-resolved analysis of nascent transcription (Baluapuri et al. 2019; Ehrensberger, Kelly, and Svejstrup 2013). An analysis of nascent RNA production under varying MYC levels by Apoorva Baluapuri (research group of Elmar Wolf, University of Würzburg) showed a decrease in processivity comparing normal to low MYC levels in U2OS cells, which could be mediated by the recruitment of SPT5 by MYC (Baluapuri et al. 2019).

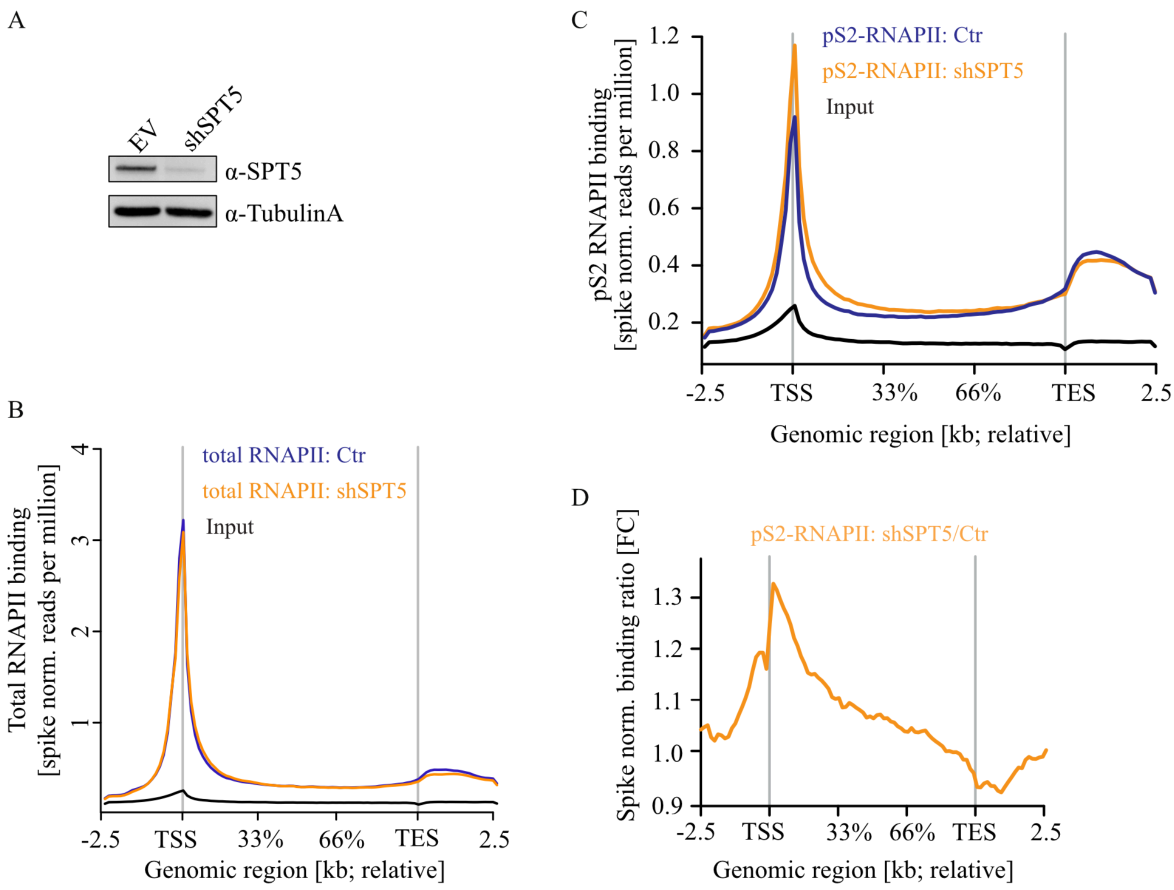


Figure 4.38: ChIPseq of total RNAPII and pSer2 RNAPII after shRNA-mediated SPT5-knockdown.

***A**. Immunoblotting of SPT5 levels from U2OS cells after the induction of an shRNA targeting SPT5 or a control shRNA (EV). SPT5 protein levels were visualized by a protein-specific antibody. Tubulin A was used as a loading control.*

***B** and **C**. Metagene analysis of spike-in normalized ChIPseq. Results from U2OS cells expressing a shRNA targeting SPT5 (orange) or non-targeting shRNA (Ctr, blue) are shown. ChIPseq was performed for total RNAPII (**B**) or pSer2 RNAPII (**C**) and binding to chromatin was visualized in a metagene plot for all active genes (n=27590) with all genes set to one length. Input is shown in black. ChIPseq was normalized to a murine spike-in control. Plots were generated by Apoorva Baluapuri, research group of Elmar Wolf, University of Würzburg.*

***D**. Metagene plot for the ratio of pSer2 RNAPII chromatin binding. Ratio was calculated for pSer2 RNAPII binding to chromatin in U2OS cells with shRNA-mediated knockdown of SPT5 over control cells as shown in C. All active genes (n=27590) were calculated to have the same length. ChIPseq was normalized to a murine spike-in control. The plot was generated by Apoorva Baluapuri, research group of Elmar Wolf, University of Würzburg.*

This figure was published in a similar form in (Baluapuri et al. 2019) including a replicate of A and B.

5 DISCUSSION

5.1 The perspective of the identified RNAPII interactome

In this study, I established a method for the native isolation of chromatin-bound protein complexes. The interactome of RNAPII captured proteins involved in all phases of the transcriptional cycle. For transcriptional initiation, GTFs and the mediator complex were identified. For transcriptional elongation, several elongation factors (DSIF, SPT6, PAFC), chromatin remodeling factors (FACT, SWI/SNF), as well as mRNA processing factors were detected, including the integrator complex, as well as subunits of the spliceosome or RNA binding proteins. For transcriptional termination, proteins belonging to the cleavage and polyadenylation machinery, the exoribonuclease XRN2 or polyA-binding proteins were discovered. The qMS results fit to previously performed RNAPII MS studies (Aygun, Svejstrup, and Liu 2008; Burriss and Mosley 2019; Harlen and Churchman 2017a, 2017b; Pineda et al. 2015) and cover well known and expected interacting proteins of RNAPII. Interestingly, there were also proteins found for the first time to interact with RNAPII and without a characterized role in the transcription process so far, like CCDC12, DDX42, or WDR92. Their impact on transcription ought to be further investigated and might provide more understanding of the fundamental process of transcription.

Along this line, it should be mentioned that cancer cells are considered to be more dependent on transcription than normal cells (Bradner, Hnisz, and Young 2017). This is supported by the fact that inhibitors for kinases with general functions in transcription, as for example SY-1365 and SY 5609 inhibiting CDK7 or BAY1143572 and BAY1251152 inhibiting CDK9, are used for cancer treatment in clinical studies (Galbraith, Bender, and Espinosa 2019) (SY 5609 in the study NCT04247126; SY-1365 in the study NCT03134638; BAY1143572 in the study NCT02745743; BAY1251152 in the study NCT02635672; source: https://clinicaltrials.gov/ct2/home). Among the newly-identified transcription regulators might be proteins essential for the transcription in cancer cells, which can be further exploited for the anticancer therapy.

5.2 Analyzing the MYC interactome

The MYC interactome resulted in 88 proteins being determined as MYC interacting proteins. Several well-characterized interactors of MYC were identified, as for example MAX, TRRAP, HUWE1, WDR5, RAD21, EP400, and TOP2A. Besides HUWE1, there were also other E3-ligases identified, like for example UBR5. Furthermore, a significant portion of the identified interactors comprises subunits of the proteasome, reflecting the instable nature of the MYC protein. The importance of the MYC protein's turnover for its function has been described in serveal studies (Adhikary et al. 2005; Diefenbacher et al. 2014; Jaenicke et al. 2016; Peter et al. 2014; Popov et al. 2010).

The MYC interactome also revealed proteins, which were not linked to MYC so far and many of them are involved in transcription, including other transcription factors, like for example RUNX2 or GATAD2B, as well as chromatin remodeling factors, like SPT6 or the FACT complex.

Three earlier performed systemic studies investigating MYC interacting proteins were used for comparing MYC-interacting proteins (Buchel et al. 2017; Heidelberger et al. 2018; Kalkat et al. 2018).

In the study performed by Büchel and colleagues, 292 proteins were identified as NMYC interactors (Buchel et al. 2017). Why there were three times more interactors identified in this published study compared to the study presented in this thesis, can be explained by several factors: in Büchel et al. mild lysis buffer followed by short sonication was used in SH-EP cells expressing HA-tagged NMYC. The experiment was performed once and thus no p- and q-values could be calculated. Milder total protein lysis and the lack of replicates can lead to the detection of proteins, not directly interacting with MYC. Further, the observed discrepancy can depend on different cell systems used and the expression of two different proteins, NMYC versus c-MYC.

In the study performed by Heidelberger et al., SILAC qMS from U2OS cells with GFP-based enrichment of GFP-MYC resulted in 503 significant interactors based on enrichment values and p-values. A high salt buffer was used (500 mM NaCl) and proteins were extracted from chromatin by short sonication (Heidelberger et al. 2018).

For both reports, as well as the study described in this thesis, an IP-based enrichment was used, which could lead to the detection of interactions that occurred post-lysis. Some interactors can also get lost during the IP-washing procedure. Another discrepancy might be due to differences in the solubilization of chromatin-bound proteins like for example the Benzonase treatment, which was performed within this thesis aside of a short sonication step common to all studies.

Recently, Kalkat et al. had used proximity-based biotin labelling of MYC-interacting proteins, which allowed labelling in the living cells (Kalkat et al. 2018). Here, full-length MYC was transiently expressed by the addition of tetracycline in the presence of biotin and the proteasomal inhibitor MG132. Proteins were solubilized from chromatin using short sonication and Benzonase treatment. Based on the streptavidin-pulldown of biotinylated proteins, the highest number of 613 MYC interactors was determined. Some of them might be very transient interactions, which are mostly lost during the extraction procedure of tagged MYC proteins, as used in the other studies, in contrast to labelling in living cells, as used in this study. Such high number of proteins detected as MYC interactors can also be an artefact of the labelling method, as additionally proteins which do not directly interact with MYC but via another protein got labelled. However, capturing of indirect MYC interactors is also a challenge of IP-based qMS identification. Treatment with the proteasomal inhibitor might also stabilize interactions, which usually promote proteasomal degradation of the MYC protein, and result in high MYC levels, which turnover is tightly regulated by the ubiquitin-proteasome system. The advantage of the biotin-labelling method is that post-lysis interactions and thus false-positive interactions are omitted as the biotin-labelling of nearby proteins is only carried out by living cells.

The highest similarity between the three studies and the 88 MYC-interacting proteins identified here can be found with the Heidelberger et al. dataset, likely due to fact that the cell system was same and the pulldown methodology was similar. 48 proteins are found to be common between the MYC interactome determined by Heidelberger and colleagues and me, with 22 also being identified by Kalkat and colleagues. Additional 10 proteins were found common in the here described interactome and in Kalkat et al.. Lowest overlap was observed with the NMYC interactome from Büchel and colleagues resulting in 21 commonly identified interactors. Only 7 proteins were identified in all four interactomic studies analyzed here, namely ATAD3A, EP400, MAX, PLK1, RUVBL1, RUVBL2, and UTP20.

The overlap between MYC interacting proteins found in all three datasets based on the here identified 88 interactors is shown in Figure 5.1 resulting in 64 out of 88 proteins being identified in at least two proteomic studies and assembling a highly confident MYC interactome.

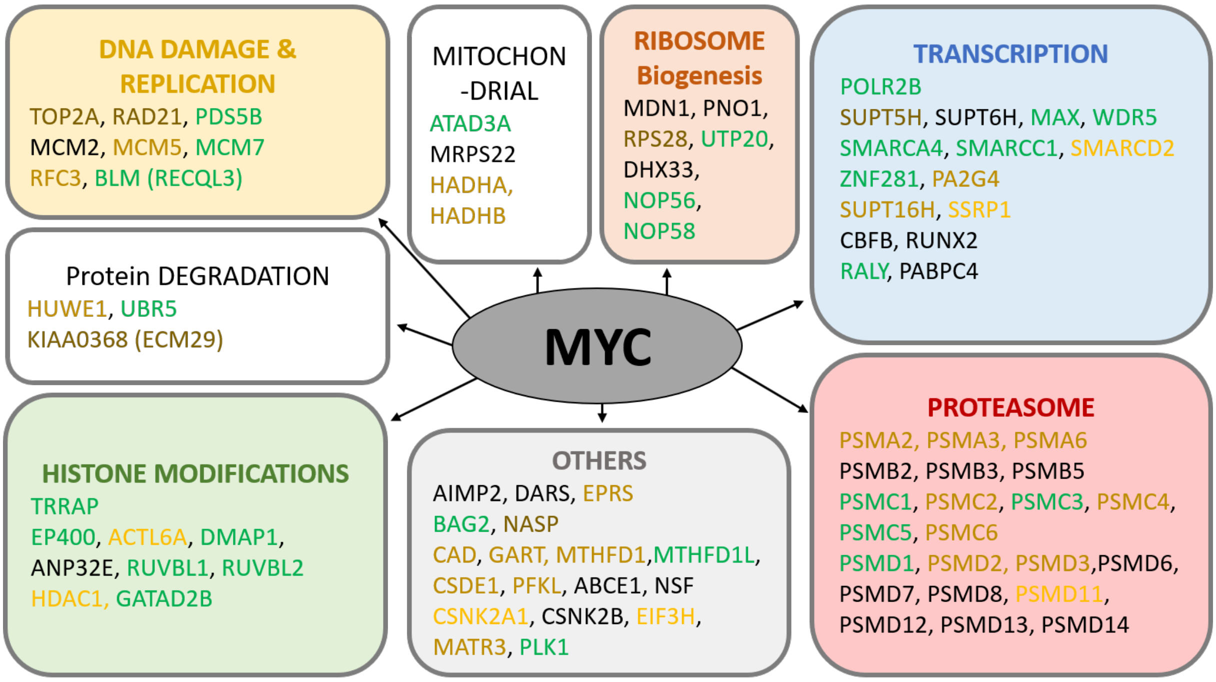


Figure 5.1: MYC interactors

Listed are the 88 proteins identified as significant MYC-interactors based on the interactomic data presented in this study. Proteins were grouped according to their function and background colouring is same as for qMS plots for MYC, with "Transcription" also including chromatin remodelling factors. MYC interactors were compared to three other MYC interactomic studies: (Buchel et al. 2017; Heidelberger et al. 2018; Kalkat et al. 2018). Proteins written in green were identified in at least two other interactomic studies, yellow or brown colour in one of the other studies (yellow overlaps with Kalkat et al., 2018; light brown with Heidelberger et al., 2018; dark brown with Buchel et al., 2017). Black proteins were identified only within this study.

The identification of MYC-interacting proteins opens the possibility to target the onco-protein MYC in many different ways: as highlighted in sections 1.5 and 1.11, MYC is deregulated in most of human cancers, but no clinical therapy is available for targeting MYC directly so far, but there are some promising approaches.

First, the structural insights into a protein directly binding to MYC helps to resolve an interacting part of MYC, which might be exploited for a drug design, like for PROTACs. PROTAC stands for "Proteolysis Targeting Chimeras". It brings the protein of interest in close proximity to an E3-ligase resulting in its ubiquitination and proteasomal degradation. The PROTAC consists of three moieties: one domain binding the E3-ligase, another binding the protein to be degraded, and a linker connecting both parts. So, identifying a peptide binding to MYC or resolving a part of MYC's structure can become the basis of such a PROTAC, which can trigger MYC's degradation via the ubiquitin-proteasome system.

Second, in case a protein interacting with MYC is necessary for MYC's transforming function, finding a molecule disrupting this protein-protein interface (PPI) will lead to a decreased or abolished oncogenic function of MYC. There are already some promising candidates like a small molecule disrupting the MYC-MAX interaction (Carabet et al. 2018; Carabet, Rennie, and Cherkasov 2018; Castell et al. 2018), or the Omo-MYC peptide, which competes with MYC for MAX binding and for DNA binding, shown to have therapeutic efficiency in mice (Beaulieu et al. 2019).

Third, inhibiting a protein MYC's transforming function is at least partially dependent on, indirectly leads to decreased or abolished oncogenic function of MYC. One example is WDR5. Thomas and colleagues developed a molecule blocking the DNA-binding capacity of WDR5. Since WDR5 is recruiting MYC to several of its target genes, this molecule was also inhibiting MYC's binding to DNA at WDR5-dependent loci and induced apoptosis of cancer cells *in vitro* and more importantly lowered tumor burden and increased survival of *in vivo* mouse models (Thomas et al. 2019; Thomas et al. 2020). Indirect targeting of MYC via AURKA inhibition is under investigation, as AURKA was shown to be important for MYC's oncogenic function and its protein stability (Beltran et al. 2011; Brockmann et al. 2013; Dauch et al. 2016; Gustafson et al. 2014; Otto et al. 2009).

Fourth, going into similar direct as inhibiting the function of a MYC-interacting protein, use of the PROTAC system against a MYC-interactor and thereby indirectly targeting MYC for proteasomal degradation might be possible. Since there is no molecule available binding MYC directly, a scenario could be possible in which the MYC-interactor is bound by the PROTAC leading to its ubiquitination and subsequent degradation. This could also have an impact on MYC's protein stability.

In the perspective evaluations of the proteins found to significantly interact with MYC in the study presented in my thesis, one approach will employ shRNA screens in cancer cells and compared to non-cancer cells. This is not only possible in cancer cells, but also in organoids derived from mice or patients. Moreover, implantation of cells, where the levels of a newly identified MYC interactor can be experimentally controlled, into mice will determine the protein's impact not only on tumor maintenance but also on tumor engraftment, depending on the experimental system and the timing of shRNA induction. *In vivo* models will additionally enable to measure the effect of immune cell invasion into the tumor and generally of tumor microenvironmental factors, which cannot be studied in cell culture or organoid culture models.

5.3 MYC facilitates the loading of elongation factors onto RNAPII

Using T-lymphoma cells harboring a MYC-Tet-Off system allowed the comparison of the RNAPII interactome under varying MYC levels but within the same cellular system. Most of the 101 proteins determined as significant RNAPII interactors from the total of nine HA immunoprecipitations, showed no significant change in their binding to RNAPII upon MYC depletion (Figure 4.10), including the RNAPII complex itself, as well as the integrator complex and the majority of the mediator complex.

Thirteen proteins were found to be decreased (six with $p<0.05$, six with $p<0.1$, and one with $p=0.107$) in their association to RNAPII upon MYC depletion, whereas only one protein showed increased binding. The fact that there are much more proteins being decreased in RNAPII-binding upon MYC depletion rather than increased is expected for an activating transcription factor, like MYC. The factors found to be negatively affected in their association to RNAPII by MYC depletion primarily belong to proteins involved in transcriptional elongation, namely SPT5, SPT6, ELL, and TFIIS.

If one or several of these elongation factors are not efficiently transferred onto RNAPII, defects in the elongation process are expected. This can turn out as a decrease in elongation speed, in particular when a factor critical for the elongating conformation of RNAPII is lost, like SPT5. The absence of elongation factors can result in pausing or stalling of RNAPII within the gene body, which is expected upon loss of TFIIS, as it helps stalled RNAPII to cleave nascent RNA and to get restarted. Similarly, the loss of ELL would lead to increased pausing and less elongating RNAPII, since P-TEFb important for pause release will be less recruited. As SPT5 and SPT6 are reported to be involved in the recruitment of additional RNA-processing factors, their loss would additionally affect RNA processing.

To elucidate the role of SPT6 in MYC-dependent transcriptional regulation, I performed first co-IPs of MYC and SPT6, which were successful but showed less enrichment of SPT6 in the co-IP than for SPT5 when comparing the co-IPed signal to the input signal. As described, SPT6 is an elongation factor and a histone chaperone and a decrease in RNAPII elongation rate can be expected upon SPT6 depletion, since histones cannot be properly removed. In this case, RNAPII will stall at histones, which will likely result in premature termination. Recently, SPT6 was implicated in R-loop formation via the termination of lncRNAs, related to DNA damage and DNA replication stress (Nojima et al. 2018). Further on, SPT6 was shown to suppress intergenic initiation events, therefore, lack of it might induce additional initiation events (Doris et al. 2018).

All these defects might result in premature termination of RNAPII and consequently, in an increase of immature transcripts.

5.3.1 MYC recruits SPT5 via its TAD

qMS data identified SPT5 as being recruited to RNAPII and chromatin by MYC. ChIPseq of SPT5 in U2OS cells expressing or depleted of MYC confirmed a clear decrease in SPT5 occupancy on chromatin after MYC depletion, suggesting that SPT5-loading onto RNAPII indeed happens on chromatin and in a MYC-dependent manner. Furthermore, experiments with recombinant proteins confirmed a direct interaction of MYC and SPT5.

The set-up of experiments with overexpressed, tagged, full-length or truncated versions of both proteins, MYC or SPT5, allowed mapping of the interaction sites within both proteins.

Although, several mutants of MYC with deletions of either the conserved MBs themselves or their combination with unstructured regions have been investigated for SPT5-binding, none of them fully abolished coprecipitation of SPT5. The strongest decrease in interaction with SPT5 was observed for MYC mutants depleted of the very N-terminal region including MB0, MBI and MBII (MYC-dN2; MYC-144-439). This was supported by the *in vitro* results gathered from experiments where recombinant proteins were used, in which MYC1-163 was sufficient to pull down full-length SPT5 (Baluapuri et al. 2019) (performed by Theresa Endres, research group of Martin Eilers, University of Würzburg). However, a MYC mutant depleted of amino acids 1-44 (MYC-d44) showed no effect on SPT5 binding, nor did the deletion of the unstructured region in between MBI and MBII (MYC-d(68-123)). These results suggest a major SPT5-binding site within the N-terminal conserved regions of MYC, in particular MBI and MBII, since NMYC showed an identical binding behavior, but moreover point to additional binding sites within more C-terminal regions of the MYC protein presumably resulting in the residual binding observed *in vivo* when whole cell lysates were used. Furthermore, the idea of MYC forming multimers should be taken into consideration. As full-length MYC was present in cells co-expressing the MYC mutants, it could mediate the residual binging through the formation of multimers between the MYC mutant and the endogenous full-length MYC, still able to bind SPT5.

5.3.2 MYC and SPT4 compete for binding to SPT5's NGN-domain

Further on, utilizing a variety of SPT5 deletion mutants, the MYC binding site on SPT5 was narrowed down to the highly conserved NGN-domain within the N-terminal part of SPT5. Co-IP experiments in HEK293T cells clearly showed the NGN-domain to be essential and sufficient for MYC-binding. The same binding behavior was observed for NMYC. It remains to map the interaction site within NGN-domain in greater detail using further mutants of the NGN-domain itself.

The NGN-domain is known to be bound by SPT4, the other subunit of DSIF (Wada, Takagi, Yamaguchi, Ferdous, et al. 1998). Co-expression of SPT4 in HEK293T cells resulted in an abolishment of the MYC-SPT5 interaction. Furthermore, SPT4 was not found to be able to bind MYC, nor trimeric complexes harboring MYC, SPT5 and SPT4 were identified in cell lysates. These findings strongly suggest mutually exclusive binding of MYC and SPT4 to the same domain on SPT5, namely the NGN-domain. Further experiments with recombinantly expressed and highly purified proteins are needed to identify the kinetics underlying this competitive behavior of MYC and SPT4 for SPT5-binding.

Especially the role of SPT4 within the handover has not been studied intensively yet, since there is no antibody available for ChIP or ChIPseq of SPT4. In addition, siRNA-mediated knockdown of SPT4 resulted in a strong decrease of SPT5 protein levels. Therefore, knock-in of a tag, which can be used for ChIP and ChIPseq, like an HA- or V5-tag, as well as an AID-tag, which mediates inducible, specific and fast degradation, into the endogenous locus of SPT4 will ensure progress in understanding the implications of SPT4. This tool will enable to: first, study the effect of acute SPT4 depletion on SPT5 loading onto RNAPII and on RNAPII transcriptional behavior; second, determine SPT4 binding to chromatin; third, identify SPT4 target genes by RNAseq after acute SPT4 depletion. These experiments would help in generating knowledge on SPT4, which is up to date only poorly investigated. This will also provide further insights in the handover of SPT5 from MYC onto RNAPII.

5.3.3 Model for the MYC-SPT5-SPT4 triangle

The findings from this study were summarized in the following model (Figure 5.2): the model proposes SPT4 and SPT5 not being bound in the nucleoplasm, but only on RNAPII at the chromatin. MYC binds SPT5 in the nucleoplasm and recruits it to its target genes where they form a trimeric complex with RNAPII. Trimeric complex formation is facilitated by CDK7, which phosphorylates GTFIIE and leads to its dissociation from RNAPII and enables SPT5 to bind to RNAPII (Baluapuri et al. 2019). The trimeric complex of MYC-SPT5-RNAPII is resolved by SPT4, which having higher affinity for SPT5 than MYC replaces MYC from SPT5. Like this, DSIF, the complex of SPT4 and SPT5, is loaded onto RNAPII and upon loading of NELF, the pausing complex, the substrate for P-TEFb, is assembled. As NELF was only sparsely found in the RNAPII interactome and not in the MYC interactome, it is speculative how MYC might be involved in NELF-loading. Of note, a direct interaction of MYC with GTFIIF was described, which was reported to get replaced by NELF (Kalkat et al. 2018). The link to previous observations of MYC interacting with P-TEFb and facilitating RNAPII promoter-proximal pause release can be made by MYC generating the substrate pausing complex for P-TEFb by recruiting SPT5.

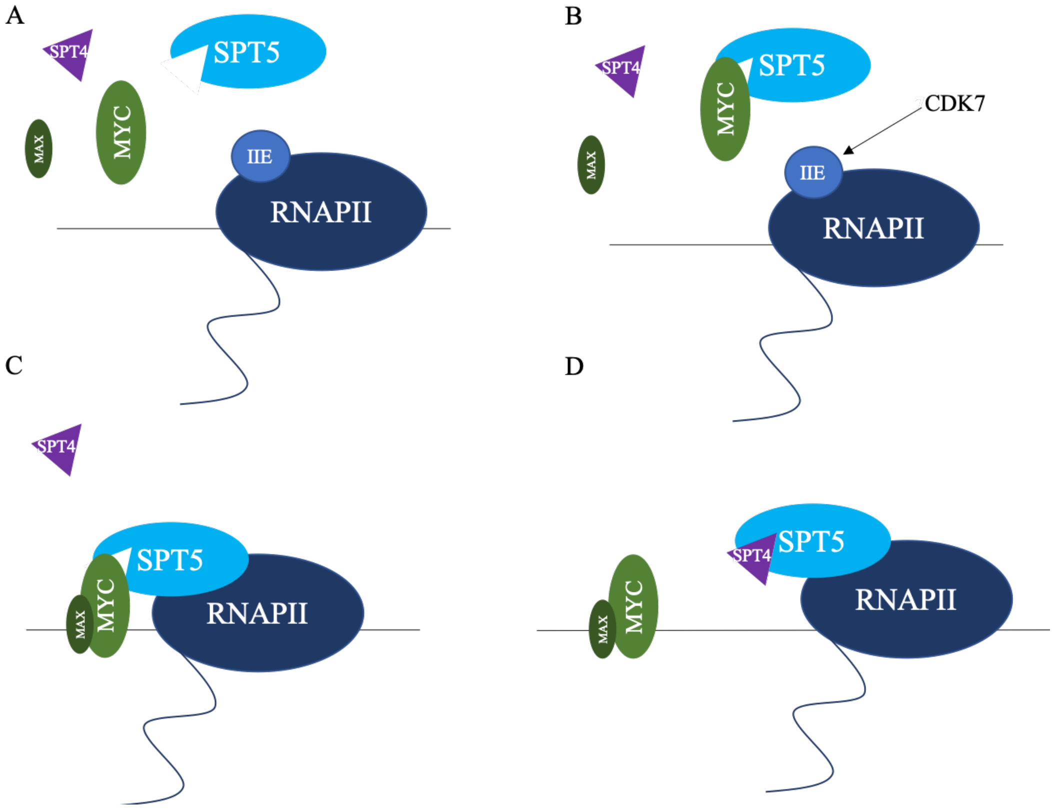


Figure 5.2: Proposed model for the handover of SPT5 onto RNAPII by MYC.

A. *SPT4 and SPT5 do not form a complex in the nucleoplasm.*

B. *MYC binds to SPT5 in the nucleoplasm independent of SPT4.*

C. *The MYC-MAX dimer recruits SPT5 to its target genes. A trimeric complex of MYC-SPT5-RNAPII is formed on chromatin. Trimeric complex formation is dependent on the action of CDK7 resulting in the release of GTFIIE blocking the binding site of SPT5 on RNAPII.*

D. *SPT4 replaces MYC from SPT5. RNAPII is loaded with DSIF (SPT4 and SPT5). Together with NELF the pausing complex is assembled, which is the substrate for P-TEFb action.*

The critical point here is that SPT4 and SPT5 do not form a complex in the cytoplasm, but only upon RNAPII-binding. This is against the current opinion from the literature, in which DSIF is always seen as a complex of SPT4 and SPT5. The separation of SPT4 and SPT5 in the nucleoplasm suggests the involvement of some other proteins. Several scenarios can be imagined: First, SPT4 and/or SPT5 can be bound to another protein, which is masking their interaction site. Second, stoichiometry of SPT4 and SPT5 can be different within the cell and an excess of SPT5 might result in SPT5 not being bound by SPT4. Third, SPT4 recognizes the structured NGN-domain of SPT5. In cases SPT5 is found in an interaction with another protein or the NGN-domain is only folded correctly upon SPT5 binding to RNAPII might impede SPT4 and SPT5 interaction in the nucleoplasm. Fourth, binding to RNAPII might not be possible for SPT4 and SPT5 at once, since the binding site of one of the proteins is occupied by another protein, like for example an initiation factor. This factor needs to be removed first in order to allow binding of the whole DSIF complex.

The NGN-domain, identified as a critical domain for MYC-binding, is evolutionary conserved and its structure has been elucidated. Further experiments using proteins recombinantly purified from *E. coli* or insect cells can provide structural insights into a purified MYC-peptide being bound to the NGN-domain. As illustrated above, structural knowledge on the MYC protein or the protein-protein interface is fundamental for structure-based drug design, as for example for PROTACs.

Structural insights can also reveal the mechanism underlying the MYC-SPT4 competition. Both proteins were shown to bind the same domain on SPT5 in a mutually exclusive way, which does not necessarily mean that both proteins bind to the same sites within the domain. Until now, in co-IP assays it was possible to disrupt the MYC-SPT5 interaction by SPT4, but not the other way around. This needs to be formalized performing binding-kinetic assays with highly purified proteins, but already points towards a stronger affinity of SPT4-SPT5 than MYC-SPT5. Hence, using a molecule based on the binding-involved SPT4-peptide could lead to a cell-wide abolishment of the MYC-SPT5 interaction, but binding of SPT4 to SPT5 would not be hindered, thus enabling SPT5 to pursue its functions in transcription. Like this, the recruitment of SPT5 to MYC target genes would be reduced, but the general function of SPT5 as a universal transcription elongation factor, which is also necessary for non-transformed cells (Yilmaz et al. 2018), would not be impaired.

Identifying critical residues on the NGN-domain important for MYC-binding is a subject of current investigations. Like this, a SPT5 mutant might be generated, which cannot bind to MYC anymore. This would enable further studies on the cellular consequences of disrupting the MYC-SPT5 interaction and clarify the potential of targeting this interaction for cancer treatment.

5.3.4 MYC influences the transcription machinery

With the SPT5-MYC interaction identified and characterized within this study, as well as its influence on transcription processivity and directionality (Baluapuri et al. 2019), an additional piece in the puzzle of how MYC influences and regulates the transcriptional process of its target genes and thereby, how oncogenic transformation of the cell can be driven by MYC, has been added. The MYC interactomic study performed here, as well as other interactomic studies also discussed within this thesis, revealed a large set of proteins interacting with MYC. It can be assumed, that the mechanism how MYC influences the transcriptional cycle within the cells is not a single step based on one protein-protein interaction, but rather MYC is a transcription factor interacting with several proteins harboring important and central roles within the transcription process, like it was shown for SPT5 in this thesis, but had also been shown for P-TEFb (Eberhardy and Farnham 2001, 2002; Gargano et al. 2007; Kalkat et al. 2018; Kanazawa et al. 2003; Rahl et al. 2010) and the PAFC (Jaenicke et al. 2016). Summarizing several interactomic and mechanistical studies, MYC seems to influence the transcriptional process at several steps. The question arises, if these mechanisms occur consecutively at each target gene or if various genes are regulated by MYC in different ways. In the first scenario, MYC would recruit several proteins one after another and hand them over to the transcribing RNAPII after previous steps have been completed. This would most likely be executed by several MYC molecules being loaded with different proteins. In the second scenario expression of several different genes would be regulated by the limitation of a certain factor, which is then brought in by MYC. But since the factors described as MYC interactors are playing a general role in transcription and are not important for only a subset of genes, this would require MYC to be able to sense which factor in particular is needed.

5.3.5 SPT5 and oncogenic MYC levels – protein squelching

High MYC levels as found in many different cancer types, seemed to result in a mechanism termed “squelching”. High MYC concentrations would titrate SPT5 away, since there is much more MYC in the cell compared to SPT5 and at one point, SPT5 becomes limiting (Baluapuri et al. 2019). This was supported by qMS performed for RNAPII interacting proteins in U2OS cells (MYC ON and MYC HIGH) resulting in a slight decrease for the interaction of SPT5 or also SPT6 (n=1). Like this SPT5 would be squelched away from genes, which are no MYC targets, and for example tumor suppressor genes could be lowered in their transcription levels. High SPT5 levels found in uterine, ovarian, and pancreatic carcinoma (Gao et al. 2013) could overcome sequestration by high MYC levels. Indeed, these cells showed a different gene signature, assuming high SPT5 levels helped cancer cells in overcoming MYC-induced apoptosis (Baluapuri et al. 2019).

First experiments in the model organism *Drosophila melanogaster* showed a clear genetic interaction between MYC and SPT5. In a MYC-dependent neuroblast type 2 tumor model, SPT5-depletion strongly reduced tumor mass and extended survival of the flies (personal communication from Peter Gallant, University of Würzburg).

These findings emphasize a critical role of SPT5 in MYC's oncogenic function and open up a new perspective for targeting MYC-driven cancers.

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7 APPENDIX

7.1 List of abbreviations

7.1.1 Prefixes

p	pico
n	nano
µ	micro
m	milli
c	centi
k	kilo

7.1.2 Units

A	Ampere
Da	Dalton
g	gram
hr	hour
l	liter
m	meter
min	minute
M	mol/l
OD	optical density
sec	second
U	Unit
v/v	volume per volume
w/v	weight per volume
°C	degree celcius

7.1.3 Proteins and biomolecules

α	anti
A	alanine, Ala
aa	amino acid
ATP	adenosine-triphosphate
AURKA	Aurora kinase A
AURKB	Aurora kinase B
BAF53	actin like 6A, INO80 complex subunit K, *ACTL6A*
bp	base pair(s)
bR	basic region
BRCA1	breast cancer 1, early-onset
BRD4	bromodomain-containing protein 4
BSA	bovine serum albumin
CBP	CREB binding protein, histone lysine acetyltransferase CREBBP
CDK	cycline-dependent kinase

CPSF	polyadenylation and cleavage specificity factor
CTD	C-terminal domain of RNA polymerase II
CTR	C-terminal repreat region of SPT5
D	asparic acid, Asp
DBC1	BMP/retinoic acid inducible neural specific 1, FAM5A
dNTPs	deoxynucleotide triphosphate (dATP, dCTP, dGTP, dTTP)
DSIF	DRB-sensitivity inducing factor
E	glutamic acid, Glu
E-box	enhancer box
EF	elongation factor
EGF	epidermal growth factor
EGFR	EGF receptor
ERK	extracellular signal-regulated kinase, mitogen-activated protein kinase
FACT	facilitates chromatin transcription
FBX29	F-box/WD repeat containing 8, *FBXW8*
FBXW7	F-box/WD repeat containing 7
G	glycine, Gly
GCN5	lysine acetyltransferase 2A, *KAT2A*
GFP	green fluorescent protein
GSK3β	glycogen synthase kinase 3
GST	glutathiome-S-transferase
GTF	general transcription factor
HDAC	histone deacetylase
HLH-LZ	helix-loop-helix leucin zipper
HMT	histone methyltransferase
HRP	horseradish peroxidase
HUWE1	HECT, UBA and WWE domain containing E3 ubiquitin protein ligase 1, HECTH9
IgG	immunoglobulin
INTS	integrator complex subunit
IWS1	Interacts with SUPT6H, CTD assembly factor 1
KOW	Kyprides, Ouzounis, Woese protein domain
LEC	little elongation complex
M	methionine, Met
MAP-kinase	mitogen-activated protein kinase
MAX	MYC-associated factor X
MB	MYC box
MBP	maltose-binding protein
MCE	human capping enzyme
MCM	minichromosome maintenance complex component
MED	mediator complex subunit
MEK	mitogen-activated protein kinase kinase, ERK activator kinase
Mi2β/CHD4	chromodomain helicase dna binding protein 4
MIZ1	MYC-interacting zinc finger 1
MLL	mixed lineage leukemia
mRNA	messenger RNA
MYC	MYC proto-oncogene, BHLH transcription factor
NELF	negative elongation factor
NLS	nuclear localization signal

nt	nucleotide(s)
NUAK1	NUAK family kinase 1
NuRD	nucleosome remodeling and deacetylase
p	phosphor
P	proline, Pro
p21	cyclin-dependent kinase inhibitor 1A, Cip1
p53	tumor protein p53
p97	valosin containing protein, VCP, CDC48
p300	histone acetyltransferase p300
PAFC	polymerase-associated factor complex
PAS	poly adenylation site
PIC	pre-initiation complex
PIKK	phosphoinositide 3-kinase-related kinase family
PIN1	prolyl isomerase
PP1	protein phosphatase 1
PP2A	protein phosphatase 2A
PPI	protein-protein interface
PROTAC	proteolysis targeting chimeras
P-TEFb	positive elongation factor b
PTM	post translational modification
Raf	rapidly accelerated fibrosarcoma, RAF proto-oncogene serine/threonine-protein kinase
RAD21	RAD21 cohesin complex component
Ras	rat sarcoma viral oncogene homolog
RNA	ribonucleic acid
RNAPII	RNA polymerase II
RPB1-12	RNA polymerase II subunit A-K
rRNA	ribosomal RNA
S	serine, Ser
SEC	super elongation complex
shRNA	short hairpin RNA
siRNA	small interfering RNA
SKP2	S-phase kinase-associated protein 2, E3 ubiquitin protein ligase, FBXL1
SMARCA2	SWI/SNF-related matrix-associated actin, BRM
SMARCA4	SWI/SNF-related matrix-associated actin, BRG1
SMARCB1	SWI/SNF-related matrix-associated actin, INI1, SNF5, BAF47
SPT4	suppressor of Ty 4 homolog 1, DRB-sensitivity inducing factor small subunit
SPT5	suppressor of Ty 5 homolog, DRB-sensitivity inducing factor large subunit
SPT6	suppressor of Ty 6 homolog, transcription elongation factor SPT6
SPT16	suppressor of Ty 16 homolog, facilitates chromatin transcription complex subunit SPT16
SSRP1	structure specific recognition protein 1, facilitates chromatin transcription complex subunit SSRP1
Strep	streptavidin
SWI/SNF	switch/sucrose nonfermentable
T	threonine, Thr
TAD	transactivation domain
T-ag	SV40 large T antigen

TES	transcriptional end site
TF	transcription factor
TIP48	RuvB like AAA ATPase 2, INO80 complex subunit J, *RUVBL2*
TIP49	RuvB like AAA ATPase 1, INO80 complex subunit H, *RUVBL1*
TIP60	lysine acetyltransferase 5, *KAT5*
TOP2A	DNA topoisomerase II alpha
TR	traveling ratio
tRNA	transfer RNA
TRRAP	transformation/transcription domain associated protein
TSS	transcriptional start site
Ub	ubiquitin
USP	ubiquitin-specific protease
V	valine, Val
WDR5	WD repeat domain 5
WIN	WDR5 interaction site
Xrn2	5'-3' exoribonuclease 2
Y	tyrosine, Tyr
ZNF281	zinc finger protein 281, ZBP99

7.1.4 Chemicals and Solutions

ACN	acetonitrile
APS	ammonium persulfate
BCA	bicinchoninic acid
DMEM	Dulbecco’s Modified Eagle’s Medium
DMP	dimethyl pimelimidate dihydrochloride
DMSO	dimethylsulfoxide
DOX	doxycycline
DRB	5,6-dichlorobenzimidazole 1-β-D-ribofuranoside
DTT	dithiothreitol
EDTA	ethylenediaminetetraacetic acid
FA	formic acid
FBS	fetal bovine serum
Flavo	Flavopiridol
HEPES	4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid
IPTG	isopropyl β- d-1-thiogalactopyranoside
LB	lysogeny broth
MOPS	3-(N-morpholino)propane-1-sulfonic acid
NP-40	nonidet P-40
P/S	penicillin/streptomycin solution
PBS	phosphate-buffered saline
PEI	polyethylenimine
PIPES	piperazine-N,N′-bis(2-ethanesulfonic acid)
PVDF	polyvinylidene difluoride
SDC	sodium deoxycholate
SDS	sodium dodecyl sulfate
TAE	Tris-acetat-EDTA
TBS	Tris-buffered saline
TBS-T	Tris-buffered saline with Tween-20

TE	Tris-EDTA
TEA	triethanolamine
TEMED	N,N,N′,N′-tetramethylethan-1,2-diamin
TFA	trifluoroacetic acid
Tris	Tris(hydroxymethyl)aminomethan

7.1.5 Further abbreviations

ChIP	chromatin immunoprecipitation
ChIP-seq	chromatin immunoprecipitation followed by deep-sequencing
CL	crosslinked using DMP
Co-IP	co-immunoprecipitation
CRC	colorectal cancer
CT	cycle threshold
Ctr	control
Ctrl	control
ds	double-stranded
DST	desalted
E1	Elution 1, no DTT
E2	Elution 2, with DTT and heating to 95 C for 5 min
ECL	enhanced chemiluminescence
E. coli	*Escherichia coli*
endo.	endogenous
EV	empty vector
F; fwd	forward
FACS	fluorescence-activated cell sorting
FC	fold change
FDR	false-discovery rate
FLAG	polypeptide protein tag (DYKDDDDK amino acid sequence)
g	rcf, relative centrifugal force
GO	gene ontology
HA	polypeptide protein tag, derived from Human influenza hemagglutinin protein
His-tag	hexahistidine tag
HPLC	high performance liquid chromatography
IB	immunoblot
IP	immunoiprecipitation
iPS	induced pluripotent stem cells
IQR	interquartile range
LC	liquid chromatography
LFQ	label-free quantification
MS	mass spectrometry
MUT	mutant
norm.	normalized
PAGE	polyacrylamide-gelelectrophoresis
PCR	polymerase chain reaction
PD	pulldown
qMS	quantitative label-free mass spectrometry
qPCR	quantitative real-time PCR

r; rev	reverse
Rep	replicate
RT	room temperature
rpm	rotations per minute
S phase	synthesis phase of the cell cycle
SILAC	Stable Isotope Labeling by/with Amino acids in Cell culture
TAP/MudPIT	combination of tandem affinity purification (TAP) with the mass spectral multidimensional protein identification technology (MudPIT)
Tet-On	tetracycline-controlled transcriptional activation technology
Tet-Off	tetracycline-controlled transcriptional repression technology
UV	ultraviolet
WT	wild type

7.2 Table of figures and tables

7.3 Additional tables for qMS data

7.3.1 Table with values corresponding to Figure 4.4

Table 7.1: Values corresponding to Figure 4.4.C. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant) and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
POLR2C	9,41	11,04	12	2
GTF2F2	8,72	9,10	11	2
POLR2B	9,58	8,83	58	2
POLR2J;POLR2J3	8,86	8,74	8	2
POLR2A	9,83	8,38	80	2
POLR2D	8,52	7,87	7	2
GTF2F1	8,64	7,05	12	2
POLR2I	8,85	6,60	8	2
MED17	7,90	6,56	6	2
POLR2E	8,85	6,34	9	2
RPRD1B	7,83	6,02	8	2
POLR2F	7,93	5,96	3	2
POLR2H	8,40	5,62	6	2
POLR2G	7,96	5,62	6	2
MED14	7,75	5,33	9	2
TCEA1	7,78	5,10	9	2
BTF3	7,54	4,64	2	0
IXL;MED29	7,55	4,39	5	0
RPRD2	7,59	4,23	6	0
MED8	7,37	3,87	4	0
MED1	7,22	3,83	3	0
NACA	8,17	3,65	8	0
MED27	7,19	3,51	3	0
PPP2CB	7,15	3,47	3	0
SRP14	8,26	3,43	3	0
MED22	7,27	3,39	3	0
RPL38	8,42	3,34	3	0
XRN2	7,30	3,19	3	0
INTS7	6,98	2,91	3	0
TUBA1B	7,99	2,77	7	0
TUBB	7,76	2,63	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NUDT21	7,59	2,58	3	0
SCAF4	7,68	2,52	3	0
DSG1	6,81	2,42	2	0
RPS7	9,49	2,26	12	0
MED19	7,65	2,23	4	0
INTS6	6,73	2,21	4	0
CALML5	7,08	2,16	3	0
RPS26;RPS26P11	8,62	2,11	6	0
GTF2B	7,85	1,98	6	0
RPS17	9,08	1,93	9	0
RPS23	8,30	1,84	5	0
EEF1A1;EEF1A1P5	8,53	1,81	7	0
PPP2R1A	7,29	1,77	6	0
RPS24	8,58	1,70	6	0
EIF2S2	7,78	1,69	7	0
SNRPD1	8,05	1,65	3	0
SNRNP27	7,58	1,63	5	0
FIP1L1	8,11	1,62	7	0
RPL23	8,13	1,61	4	0
HMGA1	8,44	1,60	1	0
ARL6IP4	7,35	1,56	2	0
FAU	8,41	1,51	3	0
MED20	6,85	1,36	4	0
UPF3B	7,42	1,34	2	0
RPS12	7,98	1,32	3	0
RPS14	8,59	1,28	9	0
RPS5	8,22	1,26	3	0
SNRPB2	8,86	1,26	8	0
RPL31	8,99	1,26	8	0
RPS11	8,98	1,22	11	0
RPS4X	8,99	1,22	14	0
ENO1	6,92	1,16	2	0
RPL26	9,09	1,14	8	0
MED23	6,73	1,13	3	0
U2AF2	8,89	1,13	12	0
RPS27A;UBB;UBC;UBA52	8,57	1,13	6	0
SNRPA1	9,39	1,13	16	0
RPL17;RPL17-C18orf32	8,91	1,09	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPS15A	8,13	1,08	5	0
INTS4	6,76	1,06	2	0
UTP14A	7,47	1,04	2	0
CPSF4	7,81	0,94	3	0
VEZF1	7,99	0,92	6	0
HNRNPH1	7,93	0,92	3	0
ZNF148	7,91	0,85	5	0
HP1BP3	8,02	0,80	3	0
SNRPC	6,88	0,79	2	0
TCF7	7,86	0,78	2	0
TCEB1	7,22	0,78	3	0
RPSA	7,68	0,74	5	0
RPS3	8,32	0,72	7	0
TUBB4B	7,63	0,72	5	0
SNRPD2	8,06	0,71	5	0
RBM39	8,67	0,71	11	0
WWP2	7,70	0,70	8	0
HIST1H2AC	9,51	0,68	6	0
CPSF6	8,22	0,65	8	0
SRP72	7,99	0,59	12	0
CXorf56	6,90	0,58	2	0
HMGA1	8,82	0,57	6	0
RPL11	7,72	0,57	2	0
RPS19	8,30	0,57	6	0
PRPF31	7,75	0,52	3	0
FRG1	8,25	0,52	10	0
KRT1	9,64	0,52	34	0
WBP11	8,43	0,51	8	0
RPS13	8,50	0,51	5	0
U2AF1	8,90	0,50	5	0
PUF60	8,09	0,45	9	0
RPL22	8,43	0,44	3	0
KLF13	8,32	0,42	5	0
SON	7,89	0,42	7	0
RPS8	8,61	0,40	10	0
EIF2S1	7,77	0,38	8	0
RPL36A;RPL36A-HNRNPH2	8,40	0,38	6	0
FAM32A	7,84	0,36	3	0
ATP5B	6,92	0,34	2	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
ASUN	6,73	0,32	3	0
KRR1	7,70	0,31	2	0
LBR	8,41	0,30	2	0
RPL30	9,00	0,29	7	0
HSPA8	8,49	0,28	14	0
WBSCR22	8,11	0,25	2	0
RPL22L1	8,30	0,22	2	0
SMAD3	7,13	0,22	2	0
PPIH	7,68	0,16	4	0
RBBP6	8,00	0,16	2	0
DDX41	8,27	0,16	13	0
CHAMP1	7,14	0,16	3	0
TCEB3	7,55	0,16	3	0
HIST1H2BC	9,71	0,13	9	0
SUB1	7,88	0,11	2	0
SP2	8,06	0,11	4	0
HCFC1	7,02	0,07	2	0
PRPF4	8,35	0,07	11	0
KRT2	8,82	0,06	18	0
PHF6	9,09	0,00	16	0
CTCF	9,54	0,00	27	0
GRB10	7,66	-0,04	2	0
MECP2	7,94	-0,06	4	0
RPS2	7,82	-0,07	3	0
RUVBL1	7,67	-0,08	6	0
HNRNPC	8,22	-0,13	4	0
S100A9	7,23	-0,14	1	0
CPSF3L	6,72	-0,14	2	0
RPS10;RPS10-NUDT3	8,35	-0,15	6	0
RPS3A	9,07	-0,19	11	0
PRPF4B	8,06	-0,19	4	0
SF3A3	7,39	-0,20	3	0
PRDX1	7,30	-0,20	2	0
EIF2S3;EIF2S3L	8,11	-0,27	8	0
DDX17	8,08	-0,29	9	0
RNPS1	7,39	-0,34	2	0
RPL24	8,38	-0,35	5	0
LUC7L2	8,68	-0,36	14	0
ARGLU1	8,76	-0,39	11	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SF3B4	7,16	-0,39	2	0
RPL5	8,21	-0,41	5	0
DDX27	7,21	-0,42	3	0
TCF7;TCF7L2	8,76	-0,43	5	0
RPL27A	8,16	-0,45	3	0
RPL23A	9,68	-0,50	11	0
MAZ	9,15	-0,52	12	0
CPSF2	7,59	-0,52	7	0
HIST1H1B	8,82	-0,53	4	0
PCBP2;Isoform	7,64	-0,58	3	0
PPP1CC	6,86	-0,59	2	0
HNRNPF	7,86	-0,59	3	0
RPS20	7,77	-0,63	3	0
PCBP1	8,20	-0,63	9	0
NPM1	8,96	-0,65	6	0
BUB3	7,48	-0,65	6	0
DDX5	9,01	-0,68	17	0
YBX1	9,92	-0,69	24	0
PRPF3	8,36	-0,70	12	0
DDX47	7,22	-0,70	2	0
RBM27	8,17	-0,71	6	0
RPL37A	8,00	-0,72	2	0
MFAP1	7,56	-0,76	5	0
RPS6	9,03	-0,80	11	0
H2AFY	7,70	-0,82	2	0
DIMT1	7,87	-0,82	3	0
FXR2	7,10	-0,83	3	0
SP3	8,17	-0,86	4	0
CREB1	7,92	-0,87	2	0
HNRNPM	8,17	-0,87	8	0
RPS16;ZNF90	7,82	-0,87	2	0
YARS	7,02	-0,91	3	0
ABCF1	7,45	-0,93	3	0
SF3B2	7,85	-0,93	5	0
HNRNPUL2;HNRNPUL2-BSCL2	8,48	-0,94	14	0
RPL13	7,69	-0,96	3	0
RBM8A	7,33	-1,00	2	0
HIST1H1E;HIST1H1D	9,78	-1,02	15	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
LUC7L	8,05	-1,03	5	0
H1F0	8,19	-1,04	3	0
RUVBL2	7,79	-1,05	6	0
SUPT5H	7,06	-1,08	2	0
IQGAP1	7,30	-1,12	3	0
RPL35	8,48	-1,20	3	0
TRA2B	7,34	-1,20	2	0
SLK	7,15	-1,23	4	0
ALYREF	8,13	-1,24	3	0
WDR33	7,59	-1,25	3	0
SP1	7,98	-1,27	4	0
HNRNPU	8,63	-1,28	9	0
RPS18	7,75	-1,28	5	0
HSP90AB1	7,93	-1,30	12	0
LYAR	8,49	-1,35	4	0
EFTUD2	7,91	-1,38	8	0
PRPF40A	7,85	-1,46	4	0
PSIP1	7,72	-1,47	3	0
ATP5A1	7,16	-1,50	5	0
PRPF19	7,86	-1,56	4	0
NHP2L1	7,81	-1,58	4	0
SRRM2	7,65	-1,60	4	0
DDX3X;DDX3Y	8,39	-1,60	10	0
NONO	7,86	-1,62	4	0
RAN	7,49	-1,63	3	0
ACTB	8,20	-1,63	8	0
PHB	6,56	-1,65	2	0
CHTOP	7,38	-1,66	2	0
PES1	7,52	-1,72	3	0
MAFK	7,97	-1,77	3	0
REXO4	7,89	-1,77	2	0
TOP1	8,30	-1,79	8	0
SFPQ	8,01	-1,80	5	0
SNRNP40	7,67	-1,84	3	0
PRPF8	7,97	-1,87	14	0
HSPD1	7,20	-1,90	3	0
POLDIP3	7,23	-1,90	3	0
SSB	7,92	-1,91	2	0
PATZ1	8,06	-1,91	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNIP1	7,85	-1,92	4	0
DYNLL1	7,32	-1,92	2	0
SF3A1	7,58	-1,92	4	0
HSPA5	7,08	-1,95	2	0
YBX3	8,22	-1,96	1	0
RBMX	8,33	-2,03	9	0
SRRM1	7,83	-2,03	3	0
SRSF2	7,72	-2,04	2	0
SNRNP70	7,63	-2,04	5	0
SF3B3	7,75	-2,05	6	0
ZNF787	8,02	-2,13	2	0
HNRNPL	8,44	-2,16	10	0
NO66	7,57	-2,17	2	0
SNW1	7,46	-2,18	4	0
RBBP4	7,74	-2,23	3	0
ERI1	7,84	-2,23	2	0
RPL19	8,80	-2,24	6	0
GLYR1	7,44	-2,25	2	0
SMC3	7,59	-2,26	2	0
SF3B1	7,96	-2,27	3	0
MAFG	8,39	-2,34	6	0
HNRNPK	8,35	-2,35	9	0
HNRNPA2B1	7,82	-2,35	5	0
HIST1H4A	9,28	-2,35	8	0
FIZ1	7,83	-2,35	2	0
DHX15	7,80	-2,39	5	0
LMNB1	7,88	-2,39	8	0
FTSJ3	8,19	-2,42	5	0
SRSF3	8,16	-2,43	2	0
RBM22	7,26	-2,44	2	0
CHERP	7,32	-2,47	2	0
DCAF13	8,05	-2,51	4	0
SUPT6H	7,38	-2,53	7	0
RBM25	7,86	-2,64	4	0
NAT10	7,35	-2,69	2	0
RPL8	8,49	-2,71	3	0
RPL27	8,60	-2,73	2	0
SMARCA5	7,97	-2,81	6	0
RPL6	8,29	-2,89	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RBM15	7,01	-2,90	2	0
RPL15	7,38	-2,90	2	0
PAF1	7,35	-2,96	4	0
RPL3	8,18	-2,98	2	0
CPSF1	7,57	-3,13	3	0
METAP1	7,70	-3,27	3	0
HIST1H3A;H3F3C	9,07	-3,28	4	0
CDC5L	8,00	-3,31	5	0
EIF4A3	7,67	-3,44	3	0
KIAA0020	8,25	-3,50	2	0
SRSF1	7,74	-3,66	2	0
DDX39B	8,02	-3,66	2	0
SLTM	7,48	-3,67	2	0
RPS25	8,80	-3,71	2	0
ZNF319	8,33	-3,74	2	0
MYH9	7,70	-3,79	5	0
MATR3	7,86	-3,85	2	0
VIM	7,45	-3,89	4	0
TARDBP	7,71	-3,89	2	0
U2SURP	7,82	-3,90	3	0
DDX39A	7,62	-3,92	2	0
SNRNP200	7,79	-4,02	4	0
ERH	7,88	-4,04	2	0
TP53BP1	7,14	-4,11	4	0
DDX21	8,88	-4,37	3	0
SMARCA4	7,22	-4,41	2	0
NCL	8,83	-4,68	5	0
PTBP1	7,83	-4,74	4	0
SRRT	7,78	-4,75	2	0
RPL7A	8,76	-4,81	4	0
RPS9	8,05	-5,09	3	0

Table 7.2: Values corresponding to Figure 4.4.D. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GTF2F1	9,02	11,07	24	2
POLR2G	8,42	9,75	9	2
INTS4	8,56	9,75	43	2
ASUN	8,41	9,72	32	2
POLR2C	9,27	9,72	16	2
POLR2J;POLR2J3	8,75	9,65	15	2
POLR2D	8,52	9,38	12	2
POLR2I	8,86	9,19	10	2
INTS9	8,23	9,07	24	2
INTS5	8,07	8,78	21	2
POLR2A	10,00	8,59	153	2
MED17	8,05	8,56	18	2
INTS1	8,51	8,53	58	2
INTS6	8,65	8,48	52	2
GTF2F2	9,10	8,19	18	2
POLR2E	9,42	8,11	13	2
MED14	8,13	7,82	46	2
CPSF3L	8,05	7,79	17	2
INTS7	8,14	7,78	22	2
INTS10	8,14	7,71	20	2
POLR2F	7,77	7,61	6	2
RPRD1B	8,08	7,43	21	2
VWA9	7,94	7,40	16	2
POLR2H	9,04	7,40	9	2
RECQL5	7,84	7,38	13	2
INTS2	8,03	7,36	31	2
TCEA1	7,89	7,16	24	2
MED8	7,81	7,00	11	2
MED1	7,78	6,81	30	2
PPP2R1A	8,28	6,80	32	2
MED27	7,75	6,80	12	2
POLR2B	9,96	6,79	104	2
INTS12	7,64	6,78	10	2
MED4	7,82	6,57	12	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
POLR2K	7,61	6,50	4	2
MED23	7,57	6,49	34	2
MED16	7,31	6,25	14	2
RPRD1A	7,62	6,13	10	2
MED24	7,42	5,98	18	2
POLR2L	7,37	5,97	3	2
INTS8	7,98	5,95	32	2
MED10	7,42	5,88	6	2
MED20	7,47	5,66	6	2
SUPT6H	8,05	5,64	64	2
RPRD2	7,59	5,51	22	2
MED11	7,26	5,45	4	2
IXL;MED29	7,35	5,44	6	2
MED15	7,38	5,37	14	2
PPP2CB	8,01	5,37	16	2
MED18	7,34	5,37	5	2
C7orf26	7,26	5,16	8	2
MED22	7,28	5,14	7	2
MED6	7,42	5,11	7	2
TCEA3	7,34	4,93	8	2
MED28	7,06	4,90	4	2
CDC73	7,24	4,83	19	2
SUPT5H	8,03	4,81	33	2
MED7	7,13	4,59	9	2
INIP	7,16	4,59	4	2
SCAF8	7,06	4,48	11	2
PPP2R1B	7,17	4,36	10	2
PAF1	7,10	4,35	19	2
CTR9	7,15	4,21	20	2
INTS3	8,37	4,19	52	2
THOC1	7,13	4,13	17	2
MED26	7,12	4,12	7	2
MED30	6,80	4,07	3	2
WWP2	7,69	4,05	31	2
MED31	7,14	4,01	4	2
EIF3A	7,09	4,01	16	2
PPP1R10	7,01	3,98	12	2
RPAP3	7,03	3,98	4	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TRRAP	7,27	3,92	73	2
PPIG	6,90	3,90	5	2
THOC2	7,11	3,85	20	2
LEO1	6,93	3,83	10	2
MED12;TNRC11	7,04	3,76	28	2
NUMA1	7,20	3,62	19	2
SAFB	7,04	3,55	6	2
YLPM1	6,99	3,54	6	2
SRSF10	7,25	3,54	11	2
NUP98	6,77	3,51	4	2
RPAP2	6,89	3,47	3	2
GTF2H2C;GTF2H2	6,91	3,43	7	2
MDN1	7,25	3,42	24	2
WTAP	6,68	3,39	11	2
TAF6	6,81	3,36	11	2
CSTF2	6,83	3,35	5	2
BCAS2	7,20	3,33	16	2
SETD2	6,86	3,30	21	2
WDR92;DKFZp434B156	6,82	3,28	3	2
YTHDC1	6,78	3,27	7	2
THOC6	6,94	3,26	8	2
LMNA	6,88	3,18	3	2
SNRNP200	8,28	3,16	96	2
CRNKL1	7,40	3,00	23	2
DDX42	7,06	2,99	13	2
KIAA1429	6,97	2,95	19	2
EIF3L	6,82	2,88	14	2
EWSR1	7,76	2,84	9	2
RBM17	7,23	2,84	14	2
TAF5	6,89	2,76	13	2
GTF2H4	6,95	2,74	10	2
DDX39A	7,03	2,70	4	2
PCF11	7,34	2,70	18	2
PLEC	8,13	-4,73	12	2
NELFB	6,62	3,33	7	1
MED25	6,65	3,24	4	1
NCOA5	6,66	3,24	8	1
CDK8	6,75	3,21	4	1

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
VIM	6,64	3,16	11	1
TTN	6,66	3,16	3	1
GPN1	6,61	3,07	4	1
PHF3	6,59	3,00	11	1
CCDC12	6,57	2,85	3	1
RNGTT	6,59	2,85	10	1
EIF3I	6,73	2,84	7	1
PRPF8	8,43	2,83	117	1
THOC7;NIF3L1BP1	6,66	2,78	9	1
ELL	6,68	2,78	9	1
PELP1	6,55	2,71	3	1
NELFE	6,73	2,69	5	1
SUPT4H1	6,64	2,67	1	1
RBM4	6,49	2,67	8	1
MNAT1	6,51	2,66	7	1
TAF1;TAF1L	6,59	2,64	15	1
CCNH	6,45	2,64	7	1
ARID1A	6,87	2,64	22	1
INCENP	6,44	2,63	4	1
PGAM5	6,64	2,62	4	1
BYSL	6,51	2,62	8	1
ZNF653	6,57	2,58	7	1
FEN1	6,55	2,56	5	1
NELFA	6,38	2,54	5	1
SERBP1	7,18	2,53	12	1
RBBP5	6,56	2,52	5	1
CDC40	7,22	2,50	17	1
BCLAF1	7,03	2,48	7	1
GTF2E1	6,54	2,47	5	1
TP53BP1	8,34	2,46	22	1
TAF15	7,34	2,43	6	1
CCT6A	6,69	2,42	6	1
CDKN2AIP	6,49	2,42	6	1
NELFCD;TH1L	6,66	2,41	7	1
ICE1	6,75	2,41	6	1
NCBP1	7,26	2,37	14	1
FUBP3	6,61	2,36	6	1
GNB2	6,54	2,35	3	1

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
XAB2	7,36	2,34	23	1
TCEA2	6,38	2,33	4	1
GTF2I	7,73	2,32	35	1
PSMD14	6,43	2,31	3	1
PABPC1	7,06	2,30	9	1
SRSF9	6,47	2,29	3	1
SF3B5	6,90	2,29	3	1
ERCC2	6,92	2,28	16	1
PPIE	6,49	2,28	4	1
FBXO11	6,48	2,24	3	1
RAB1B	6,51	2,24	3	1
TAF9	6,48	2,24	6	1
CDSN	6,48	2,21	3	1
MED19	7,02	2,21	6	1
RAE1	6,39	2,20	6	1
PHRF1	6,46	2,19	3	1
RAD50	6,39	2,18	9	1
HDAC2	6,69	2,18	6	1
SLU7	6,47	2,18	4	1
KHDRBS1	7,91	2,17	9	1
CCT7	6,86	2,16	12	1
TPI1	6,32	2,14	5	1
RNPS1	7,60	2,12	7	1
CCNL1	6,60	2,11	6	1
PRDM10	6,93	-2,48	5	1
AMY2B;AMY1A;AMY2A;AMY1B	7,21	-2,54	4	1
HSP90B1	6,73	-2,61	4	1
GFI1	6,88	-2,77	2	1
C19orf53	7,80	-2,89	3	1
MAFF	6,76	-3,35	2	1
PSPC1	6,18	2,35	4	0
RPL14	7,30	2,11	3	0
GTF2H1	6,42	2,06	9	0
ZRANB2	7,75	2,06	11	0
EIF3M	6,41	2,04	5	0
PSMD6	6,18	2,03	4	0
SRSF6	7,58	2,02	10	0
AP2B1	6,36	2,02	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CLP1	6,74	2,01	10	0
UBTF	7,85	2,01	31	0
ZNF646	6,18	2,00	3	0
RBM5	6,69	1,98	12	0
RBM10	7,11	1,98	14	0
TRA2B	7,63	1,98	11	0
CDK7	6,67	1,97	5	0
BLMH	6,36	1,97	4	0
WDR61	6,37	1,97	4	0
ZC3H11A	6,41	1,97	4	0
CCT4	6,86	1,93	13	0
SMARCD2	7,05	1,93	10	0
THOC5	6,92	1,93	9	0
SUGP1	6,47	1,93	5	0
DDX39B	7,75	1,92	19	0
ACIN1	7,63	1,92	18	0
DYNC1H1	6,39	1,91	22	0
PDCD4	6,40	1,90	3	0
DGCR6L;DGCR6	6,46	1,90	3	0
TAF4	6,30	1,90	7	0
SNRNP40	7,64	1,89	16	0
PNN	7,83	1,89	27	0
RBM14	8,01	1,88	20	0
GNAI3	6,80	1,87	9	0
SF3A1	7,90	1,86	33	0
IWS1	7,06	1,86	14	0
BHLHA15	6,40	1,85	4	0
RPL12	7,40	1,84	6	0
PLRG1	7,36	1,83	16	0
SYMPK	7,36	1,82	23	0
SMARCA2	6,27	1,81	3	0
RPL10	7,74	1,81	10	0
DDX26B	6,44	1,81	5	0
PPIL1	7,00	1,79	5	0
NOP16	6,33	1,79	4	0
WDR82	7,28	1,76	12	0
TRA2A	6,80	1,76	6	0
EIF4A3	8,17	1,76	23	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNW1	7,39	1,73	18	0
ISY1	6,61	1,71	5	0
ASH2L	6,38	1,70	5	0
NUP205	6,31	1,69	10	0
CHD4	7,95	1,68	68	0
CBX3	7,65	1,67	11	0
RPA1	6,31	1,67	4	0
WWP1	7,11	1,66	12	0
EIF3B	6,97	1,65	15	0
IMP3	6,82	1,64	2	0
EXOSC7	6,36	1,64	4	0
HNRNPH1	8,01	1,63	9	0
SETD1A	6,15	1,63	4	0
CWC15	7,15	1,63	7	0
MED13	6,29	1,63	7	0
ANP32E	6,53	1,63	3	0
CSNK2B;CSNK2B-LY6G5B-1181; CSNK2B-LY6G5B-991	7,12	1,61	4	0
GATAD2B	7,33	1,60	10	0
C17orf49;BAP18; RNASEK-C17orf49	6,47	1,60	4	0
NCL	9,04	1,60	16	0
CSNK2A2	6,67	1,59	7	0
THOC3	6,60	1,57	7	0
DKC1	7,23	1,56	6	0
FUS	7,52	1,56	8	0
CBX1	6,43	1,55	3	0
HNRNPF	8,06	1,55	13	0
SURF6	7,21	1,54	5	0
PSMC2	6,74	1,54	10	0
NUP85	6,11	1,53	7	0
NUP93	7,25	1,53	20	0
SCAF4	8,14	1,52	16	0
DYNLL1	7,97	1,51	6	0
RUVBL1	8,19	1,51	31	0
MYH9	7,09	1,51	30	0
CCT5	6,52	1,50	5	0
CHTOP	6,98	1,50	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PRPF19	8,13	1,50	13	0
RBM22	7,11	1,49	12	0
RIF1	6,11	1,49	4	0
CSTF1	7,48	1,49	13	0
CCT2	7,06	1,48	12	0
ERH	7,78	1,48	6	0
ILF2	7,34	1,47	12	0
UCHL5	6,40	1,47	4	0
SAP30BP	7,10	1,46	8	0
CMTR1	6,52	1,45	4	0
HSP90AA1	7,10	1,45	9	0
POLE	6,34	1,44	11	0
PRPS1;PRPS1L1	6,33	1,44	3	0
RPS2	7,92	1,44	12	0
ACTL6A	7,00	1,43	8	0
KDM1A	6,40	1,43	10	0
MAGOH;MAGOHB	7,17	1,43	5	0
CPSF3	7,96	1,43	21	0
CNOT8	6,20	1,42	3	0
RBBP7	7,40	1,41	6	0
EIF3H	6,69	1,39	4	0
HNRNPH2	6,55	1,37	3	0
EIF3F	6,79	1,37	5	0
CBFB	6,72	1,36	4	0
ETF1	6,33	1,35	5	0
DDX31	7,27	1,34	11	0
PSMC6	6,15	1,33	5	0
RPS8	8,66	1,32	19	0
HDGFRP2	7,17	1,32	7	0
TXNL1	6,65	1,32	2	0
CLTC	7,43	1,32	33	0
RPLP0;RPLP0P6	7,74	1,31	11	0
MTA1	6,24	1,30	4	0
AHCY	6,38	1,29	5	0
TFIP11	6,24	1,29	5	0
PPWD1	6,32	1,28	6	0
TOX4;TOX3	6,29	1,28	4	0
DGCR14	6,27	1,27	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CPSF2	8,06	1,26	31	0
C14orf166	6,61	1,26	6	0
SFSWAP	6,32	1,26	5	0
NSA2	7,52	1,26	8	0
CHD8	6,47	1,25	9	0
SUZ12	6,37	1,25	8	0
DHX16	7,14	1,25	15	0
DHX9	8,44	1,25	32	0
EIF3K	6,21	1,24	4	0
DHX15	8,18	1,24	38	0
RAD21	6,81	1,22	11	0
SFN	6,40	1,21	3	0
SF3A3	7,61	1,21	14	0
PELO	6,26	1,21	6	0
WDR48	6,03	1,20	4	0
MYEF2	6,35	1,20	3	0
CAD	6,27	1,18	5	0
CACTIN	6,26	1,18	5	0
CWC22	6,86	1,18	14	0
RTF1	6,94	1,18	14	0
HNRNPD	7,12	1,18	8	0
EIF3G	6,30	1,17	5	0
RPS12	7,71	1,16	7	0
IK	7,50	1,16	18	0
NUP155	6,52	1,15	8	0
HIST1H2AJ;HIST1H2AH;H2AFJ;HIST1H2AG	8,52	1,15	2	0
MBD2	6,17	1,15	6	0
EIF3E	6,89	1,14	10	0
XRN2	7,75	1,14	29	0
RBBP4	7,91	1,14	14	0
DHX38	6,22	1,14	8	0
PDCD11	6,41	1,13	2	0
RNPC3	6,45	1,13	6	0
NEDD8;NEDD8-MDP1	6,76	1,13	3	0
C17orf85	6,45	1,13	4	0
ZNF592	6,13	1,13	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TOE1	6,25	1,12	3	0
SNRPB;SNRPN	7,93	1,12	8	0
PPP1CA	7,72	1,11	17	0
MARK2	7,34	1,11	19	0
NCBP2	6,32	1,11	3	0
EPB41L4B	6,96	1,10	12	0
DNAJA2	7,34	1,09	10	0
HNRNPM	8,56	1,08	40	0
METAP1	8,30	1,07	13	0
CCT8	7,17	1,06	13	0
ATAD3A	6,28	1,05	6	0
SAP18	7,75	1,05	12	0
DPF2	6,75	1,05	4	0
PSMD3	6,53	1,05	6	0
PPP1CB	7,04	1,05	5	0
CTNNBL1	7,09	1,05	10	0
SIN3A	6,66	1,04	10	0
RUVBL2	8,17	1,04	32	0
CUL3	6,07	1,03	4	0
EDC4	6,18	1,03	4	0
RTCB	6,87	1,03	8	0
DDX50	7,47	1,02	13	0
TRIM28	7,44	1,02	19	0
AQR	7,48	1,01	32	0
GTF2E2	6,96	1,01	6	0
MBD3	6,31	1,01	3	0
RPS27	7,63	0,99	5	0
HNRNPR	7,43	0,98	17	0
NEDD4	6,26	0,98	3	0
SRSF5	7,14	0,97	5	0
SNRNP70	7,73	0,97	19	0
RPL4	8,05	0,97	20	0
ALDH18A1	6,71	0,96	7	0
RBM7	6,23	0,95	3	0
DNTTIP1	6,62	0,95	7	0
CPSF7	6,28	0,95	4	0
TMPO	7,17	0,94	8	0
MTA2	7,75	0,94	22	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HELLS	7,36	0,94	13	0
ZNF260	6,14	0,94	3	0
SSRP1	8,26	0,94	31	0
G3BP1	6,22	0,93	4	0
SF3B4	7,20	0,92	3	0
MFAP1	7,72	0,92	18	0
PRMT1	6,69	0,92	8	0
PABPN1	7,02	0,92	6	0
PSMC4	6,33	0,92	4	0
ZNF207	7,25	0,92	5	0
CASP14	6,56	0,92	7	0
STAG2	6,39	0,92	8	0
LRRC59	7,19	0,91	8	0
C9orf114	7,77	0,90	7	0
SMCHD1	6,70	0,90	12	0
UBAP2L	6,32	0,89	2	0
TARDBP	7,56	0,89	7	0
SF3B6	7,00	0,89	6	0
ZFR	6,48	0,89	7	0
JUP	7,57	0,88	22	0
NUSAP1	6,88	0,88	2	0
NOL12	7,11	0,87	4	0
RRP8	6,71	0,87	3	0
SYF2	6,57	0,87	3	0
ILF3	7,65	0,86	18	0
ZNF579	7,06	0,86	7	0
CHMP4B	6,18	0,86	3	0
HNRNPK	8,38	0,86	27	0
DUT	6,66	0,86	4	0
FCF1	7,52	0,85	12	0
CUL2	6,32	0,85	4	0
CALML5	7,18	0,85	8	0
PPIL3	6,31	0,85	4	0
EIF4A1	7,70	0,85	15	0
METTL17	7,03	0,84	1	0
DSG1	7,48	0,84	16	0
BUD31	6,74	0,83	7	0
CCNK	6,28	0,83	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RP9	7,08	0,83	5	0
EEF1D	6,65	0,83	3	0
DNAJC9	6,90	0,82	3	0
CCT3	7,22	0,82	14	0
HNRNPA0	6,93	0,82	4	0
SMU1	7,72	0,82	21	0
DDX23	7,82	0,82	37	0
GNB1	6,07	0,82	5	0
NVL	6,18	0,82	5	0
RPL15	8,21	0,81	13	0
CDC23	6,22	0,81	9	0
GNB2L1	7,34	0,81	13	0
CSNK2A1;CSNK2A3	7,59	0,80	16	0
SF3A2	7,39	0,80	11	0
SNRPC	7,13	0,80	6	0
RUNX2	6,55	0,78	4	0
GATAD2A	6,08	0,78	3	0
L3MBTL3	6,50	0,78	6	0
DNAJA1	7,75	0,77	14	0
SMARCB1	6,70	0,77	7	0
HCFC1	6,70	0,76	17	0
RPL13	7,96	0,76	8	0
PHB2	6,78	0,76	7	0
NPM1	9,07	0,76	21	0
GAPDH	7,50	0,76	15	0
EIF5A;EIF5AL1	7,06	0,75	5	0
RPS28	7,20	0,75	5	0
EIF4B	6,63	0,75	9	0
RPL6	8,39	0,74	13	0
RANBP2	6,14	0,74	6	0
PRPF38B	6,16	0,72	3	0
RBM6	6,26	0,72	3	0
SNRPG;SNRPGP15	6,85	0,72	3	0
ADNP	6,38	0,72	8	0
PRPF38A	7,02	0,71	10	0
RPL24	8,59	0,71	12	0
RBM8A	7,33	0,71	7	0
RPS24	8,69	0,71	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPLP2	7,54	0,70	7	0
CLASRP	5,96	0,70	3	0
HDAC1	7,40	0,70	14	0
EBNA1BP2	8,05	0,69	8	0
ARL6IP4	7,11	0,69	5	0
ZC3H18	7,15	0,69	10	0
CNOT1	6,11	0,68	6	0
BPTF	6,27	0,68	10	0
ZNF830	6,31	0,68	3	0
SRSF7	7,66	0,67	9	0
TUFM	6,53	0,67	5	0
CGGBP1	6,80	0,67	7	0
SRRT	7,91	0,67	32	0
ZC3H14	6,27	0,67	4	0
LMNB1	7,77	0,67	24	0
ARG1	6,89	0,67	9	0
RFC2	6,95	0,66	8	0
SLC25A5	7,52	0,66	12	0
CTNNB1	7,19	0,66	14	0
MCM3	7,42	0,65	21	0
ELAVL1	7,66	0,65	11	0
HNRNPA2B1	8,09	0,64	19	0
SRSF1	7,62	0,64	12	0
SRP68	8,10	0,64	26	0
EEF1G	6,86	0,63	6	0
ENO1	6,78	0,63	4	0
SF1	7,41	0,63	15	0
EXOSC1	6,29	0,63	2	0
PHF5A	6,99	0,63	6	0
GTF2B	8,41	0,63	20	0
CSTF3	7,56	0,63	18	0
RPL7	7,73	0,62	9	0
DDOST	6,27	0,62	3	0
RPL13A;RPL13a	7,39	0,62	4	0
RPS6	9,30	0,62	29	0
ERCC3	6,91	0,61	11	0
C11orf31;SELH	6,99	0,60	2	0
RFC3	7,18	0,60	13	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
TEX10	6,49	0,60	7	0
PYCR2	6,80	0,60	3	0
SERPINB3;SERPINB4	6,10	0,60	4	0
MATR3	8,07	0,59	32	0
HSP90AB1	8,31	0,59	31	0
AATF	6,67	0,58	2	0
NIP7	7,08	0,58	4	0
CHAMP1	6,71	0,57	1	0
VDAC1	6,77	0,57	5	0
PLK1	6,99	0,57	8	0
WDR12	6,71	0,56	3	0
RARS	5,92	0,56	4	0
WDR6	5,96	0,55	3	0
MEN1	6,48	0,55	6	0
PTBP1	7,85	0,55	9	0
HIST1H2AC	9,82	0,55	9	0
DDX55	8,32	0,54	18	0
RPS9	8,90	0,54	24	0
EFTUD2	8,20	0,54	51	0
SEH1L	6,54	0,54	7	0
CDK9	6,99	0,54	11	0
KIF2C	6,64	0,53	6	0
SP2	7,96	0,53	12	0
RAC1	6,45	0,53	3	0
CCDC59	7,76	0,53	2	0
PATZ1	8,47	0,53	30	0
RPS18	8,22	0,52	17	0
CBX5	6,84	0,52	4	0
NXF1	7,17	0,52	6	0
RPL32	8,13	0,52	13	0
HNRNPAB	7,25	0,51	7	0
RPS19BP1	7,55	0,51	6	0
BRIX1	7,97	0,50	11	0
PCNA	6,97	0,50	7	0
TXN	6,32	0,50	2	0
TCEB3	7,58	0,50	11	0
RRP7A;RRP7BP	7,42	0,49	8	0
UTP6	6,13	0,49	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NOB1	6,67	0,49	3	0
MAPK1	6,14	0,49	4	0
POGZ	6,63	0,49	8	0
FAU	8,20	0,48	4	0
STRAP	6,36	0,48	4	0
SAMD1	6,99	0,48	3	0
DDX21	9,25	0,48	29	0
RPL39P5;RPL39	8,54	0,48	3	0
RPF1	8,43	0,46	14	0
SCAF11	7,10	0,46	4	0
ZCCHC8	6,54	0,46	3	0
RPL10A	8,39	0,46	14	0
NONO	8,16	0,45	24	0
SARNP	6,60	0,44	2	0
PUS1	6,21	0,44	4	0
GNL3L	6,25	0,44	3	0
BRD4	6,18	0,43	3	0
HIST1H4A	9,96	0,43	20	0
SMARCE1	7,06	0,43	10	0
ABCE1	6,64	0,43	8	0
TUBB4B;TUBB4A	7,90	0,43	21	0
RPL35	8,96	0,43	7	0
ITCH	6,11	0,42	5	0
PPP1CC	7,19	0,42	3	0
FBXL6	7,25	0,41	2	0
TCP1	6,89	0,41	14	0
TRMT10C	7,17	0,41	4	0
DDX54	7,26	0,40	10	0
U2SURP	7,83	0,40	29	0
DRG1	6,66	0,40	6	0
CFL1	6,75	0,40	5	0
WRNIP1	6,03	0,39	3	0
UTP23	7,72	0,39	4	0
POLDIP3	7,31	0,38	9	0
TUBB	7,57	0,38	5	0
SMC5	6,03	0,37	3	0
RPL27A	8,20	0,37	4	0
MDH2	6,03	0,37	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TPR	6,65	0,36	9	0
RBMX2	6,72	0,35	3	0
SIRT7	8,26	0,35	10	0
CCAR1	6,98	0,35	7	0
UTP18	7,13	0,35	3	0
RPL7L1	7,45	0,34	5	0
PPAN-P2RY11;PPAN	7,08	0,34	5	0
FABP5	7,24	0,34	2	0
WDR46	8,14	0,34	13	0
TUBA1B	8,08	0,33	15	0
RPS3A	9,38	0,33	24	0
NAA40	6,87	0,33	5	0
DNAJB6;DNAJB7	5,81	0,32	2	0
VDAC2	7,14	0,31	6	0
RRP15	7,17	0,31	2	0
SNRPE	7,46	0,30	3	0
H2AFV;H2AFZ	8,27	0,30	3	0
TGM3	6,53	0,30	7	0
PCID2	6,36	0,29	4	0
POLR1D	6,94	0,29	4	0
EIF3C;EIF3CL	6,77	0,29	12	0
ZNF384	6,40	0,29	3	0
CWC25	6,77	0,29	2	0
ACTB	8,60	0,29	19	0
HNRNPLL;HNRPLL	6,41	0,28	6	0
HSPA5	7,69	0,28	23	0
RPL18A	7,75	0,27	9	0
RPL19	9,09	0,27	19	0
RPS13	8,84	0,26	14	0
NSF	6,38	0,26	5	0
ANAPC7	6,32	0,26	5	0
POLR1C	6,84	0,26	4	0
CSTA	6,73	0,25	4	0
EXOSC8	6,45	0,25	3	0
RBM25	7,94	0,25	33	0
RBM15B	6,12	0,25	3	0
SRSF3	8,22	0,25	11	0
HSPA8	8,69	0,24	40	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HNRNPA1; HNRNPA1L2	7,90	0,24	12	0
DIMT1	8,80	0,24	21	0
RPL5	8,57	0,24	22	0
EXOSC10	6,56	0,23	6	0
RQCD1	6,17	0,23	5	0
MCM4	7,48	0,23	22	0
NOP58	7,52	0,23	13	0
RPS16;ZNF90	8,06	0,23	12	0
NOP56	7,59	0,23	14	0
DDX3X;DDX3Y	8,61	0,23	39	0
RPS27L	6,98	0,23	2	0
RBM15	7,06	0,22	14	0
POP4	6,53	0,22	3	0
NO66	8,51	0,21	12	0
DDX17	8,11	0,21	23	0
GLYR1	8,18	0,21	22	0
RBM34	6,99	0,21	2	0
LUC7L3	7,34	0,21	13	0
BDH1	6,41	0,20	3	0
DSC1	7,14	0,20	7	0
DDX47	8,12	0,19	12	0
CTSD	6,05	0,19	4	0
AKAP17A	7,22	0,19	2	0
MCM5	7,51	0,18	17	0
DHX35	6,56	0,18	10	0
RALY	7,84	0,18	5	0
PCBP2	7,34	0,17	6	0
C3	6,44	0,17	3	0
CS	6,60	0,17	2	0
RPS4X	9,06	0,17	20	0
DCD	7,50	0,17	7	0
CBX8	6,44	0,17	7	0
UHRF1	7,18	0,16	5	0
ATP5B	7,84	0,16	17	0
DDX1	6,62	0,16	7	0
ASF1A	7,06	0,15	2	0
ZSCAN26;ZNF187	7,60	0,15	4	0
SYNCRIP	6,77	0,15	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NOLC1	8,05	0,15	5	0
BRD3	5,94	0,15	3	0
EXOSC2	6,69	0,15	8	0
HIST1H3A	9,45	0,15	14	0
DSP	7,81	0,15	55	0
MMTAG2	6,92	0,14	5	0
LUC7L2	8,67	0,14	18	0
PKP1	6,09	0,14	3	0
CDC5L	8,15	0,14	44	0
RPS5	8,40	0,13	14	0
SRRM2	7,65	0,13	18	0
HNRNPA3	8,49	0,13	26	0
MRPL22	6,98	0,12	5	0
PYCR1	6,98	0,12	4	0
HP1BP3	8,52	0,12	19	0
CDC2;CDK1	7,42	0,12	10	0
RPL37	8,19	0,12	7	0
FYTTD1	6,76	0,11	3	0
RBMX	8,67	0,11	32	0
NFYC	6,15	0,11	2	0
RPL17;RPL17-C18orf32	8,72	0,11	17	0
RASA1	6,83	0,11	10	0
RSL24D1	6,64	0,11	2	0
CDC2L1;CDK11B; CDK11A	7,88	0,11	22	0
GNL3	7,99	0,11	6	0
IMMT	6,78	0,10	9	0
PAXBP1	6,52	0,10	10	0
PA2G4	6,51	0,10	5	0
IGKV4-1	8,00	0,10	3	0
MRPL15	6,53	0,10	4	0
USP39	7,38	0,09	13	0
ACTR8	6,17	0,09	5	0
MINA	7,08	0,08	3	0
YBX1	10,33	0,08	33	0
MUTYH	6,55	0,07	3	0
HIST1H1E; HIST1H1D	10,14	0,07	29	0
KRR1	8,29	0,06	14	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
RFC5	7,16	0,06	9	0
NUDT21	7,86	0,06	11	0
DDX51	6,56	0,06	3	0
PWP2	5,89	0,06	2	0
CHERP	7,60	0,06	19	0
RPS23	7,99	0,06	8	0
SF3B2	8,23	0,05	29	0
RPL8	9,21	0,05	20	0
ATRX	6,39	0,05	5	0
KAT7	6,16	0,05	4	0
CCDC137	6,58	0,05	3	0
SHMT2	7,00	0,05	8	0
RANGAP1	6,72	0,04	5	0
RNF2	7,20	0,04	11	0
RCC2	8,54	0,04	21	0
CDC27	6,11	0,03	5	0
DDX24	6,32	0,03	3	0
SKP1	7,71	0,03	11	0
PKM	6,54	0,02	6	0
NRF1	6,28	0,02	3	0
MICU1	7,46	0,02	14	0
YEATS4	6,53	0,02	3	0
MYL12A;MYL12B; MYL9	6,52	0,01	2	0
TRAP1	6,17	0,01	3	0
NOL7	7,49	0,01	4	0
KPNA3	7,14	0,01	7	0
GTF3C4	5,98	0,01	4	0
CDK13	7,26	0,01	10	0
FRMD5	6,05	0,01	2	0
ATP5A1	7,82	0,01	17	0
GRB10	7,27	0,00	7	0
BUB3	7,96	0,00	12	0
RPS25	9,04	0,00	14	0
GTF3C3	6,08	0,00	5	0
DLAT	6,56	-0,01	4	0
MAT2A	6,79	-0,01	6	0
ZNF800	6,91	-0,01	5	0
EED	6,72	-0,02	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNRPD3	8,18	-0,02	5	0
BTF3	7,34	-0,02	2	0
SMARCD1	6,51	-0,02	5	0
NR2C2	6,36	-0,02	5	0
ALKBH5	6,70	-0,03	5	0
KRT1	9,98	-0,03	76	0
EXOSC4	6,73	-0,03	2	0
GNL2	7,78	-0,03	16	0
KIF2A	6,77	-0,03	11	0
MEAF6	6,53	-0,03	2	0
NOM1	6,90	-0,04	5	0
SCAF1	6,85	-0,04	7	0
KIF22	6,80	-0,04	7	0
CFAP20	7,70	-0,04	8	0
H2AFY	8,39	-0,04	12	0
RBX1	7,14	-0,05	3	0
RPS20	7,97	-0,05	7	0
DARS	6,76	-0,05	8	0
TRIP12	7,08	-0,05	22	0
SART1	7,96	-0,05	24	0
U2AF1	9,08	-0,06	13	0
FIP1L1	8,08	-0,06	12	0
HSPA9	7,49	-0,07	17	0
RPL7A	9,15	-0,07	25	0
UPF1	6,02	-0,07	6	0
FBL	8,17	-0,07	17	0
ATP5O	6,98	-0,07	2	0
PSMD2	6,84	-0,08	10	0
RPL29	8,05	-0,08	3	0
NFRKB	6,20	-0,08	5	0
TAF2	6,48	-0,08	7	0
CMAS	7,07	-0,08	6	0
RPL23	8,32	-0,08	7	0
ATF2	6,27	-0,09	3	0
ZNF512	6,66	-0,09	3	0
MARK3	6,17	-0,09	5	0
TEAD1;TEAD4; TEAD3	6,94	-0,09	7	0
EEF1A1; EEF1A1P5	8,53	-0,10	23	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
IKZF3	6,81	-0,10	3	0
RPS14	8,67	-0,10	11	0
MRPL9	7,57	-0,11	6	0
DCAF13	8,53	-0,11	15	0
EMG1	7,50	-0,11	9	0
CPSF4	7,81	-0,11	11	0
PPIB	7,28	-0,12	8	0
WDR33	8,01	-0,12	29	0
SMAD3	7,11	-0,12	9	0
HIST1H1B	9,54	-0,12	7	0
SSB	7,61	-0,13	6	0
TCEB2	6,94	-0,13	2	0
SAP30	6,53	-0,13	2	0
BOD1L1	6,84	-0,13	3	0
TOP2B	7,06	-0,13	19	0
RRS1	7,82	-0,13	11	0
WDR5	7,35	-0,13	9	0
SF3B3	8,29	-0,13	51	0
RFC4	7,26	-0,13	10	0
VDAC3	6,77	-0,14	5	0
RPS26;RPS26P11	8,18	-0,14	4	0
HIST1H2BC	10,13	-0,14	18	0
RPL34	7,74	-0,14	5	0
RPP30	7,46	-0,14	5	0
EIF6	7,33	-0,15	3	0
RBM39	8,68	-0,15	22	0
RPS15	8,49	-0,16	8	0
C19orf43	7,55	-0,16	8	0
DNTTIP2	6,45	-0,16	4	0
TCEB1	7,46	-0,17	5	0
PDS5A	7,46	-0,17	24	0
RPL26	9,19	-0,17	21	0
DDX41	8,46	-0,18	46	0
HADHB	6,74	-0,18	6	0
H1F0	8,81	-0,18	7	0
PHF2	7,02	-0,18	7	0
CBX4	6,10	-0,18	2	0
DDX56	7,92	-0,19	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
FBXO28	6,82	-0,19	9	0
RPL21	7,93	-0,19	10	0
RPS11	8,76	-0,19	21	0
EXOSC6	6,78	-0,20	4	0
ZNF668	6,40	-0,20	5	0
DEK	7,73	-0,21	7	0
HNRNPL	8,66	-0,21	18	0
DDX27	7,55	-0,21	15	0
NOP10	6,65	-0,21	4	0
SMC4	6,90	-0,21	11	0
SFPQ	8,43	-0,22	26	0
EPB41L5	6,81	-0,22	6	0
DLST	5,95	-0,22	2	0
CCNT1	6,10	-0,23	3	0
ZNF771	8,31	-0,23	15	0
PHB	6,89	-0,23	6	0
RCL1	6,85	-0,23	7	0
S100A8	6,58	-0,23	2	0
CUL1	8,31	-0,24	46	0
EXOSC9	6,47	-0,24	4	0
THRAP3	7,54	-0,25	10	0
TCF7;TCF7L2	8,57	-0,25	13	0
CKAP5	6,09	-0,25	4	0
RPS10;RPS10-NUDT3	8,63	-0,25	15	0
PSMD11	6,57	-0,25	4	0
SRSF2	7,68	-0,25	9	0
HNRNPDL	6,69	-0,27	3	0
RPS27A;UBB; UBC;UBA52	8,44	-0,27	9	0
CDC42	6,49	-0,27	2	0
SRP19	6,64	-0,27	6	0
RPL28	7,72	-0,28	6	0
FTSJ3	8,35	-0,28	22	0
HNRNPA3	7,83	-0,28	2	0
NHP2L1	7,59	-0,29	7	0
RPL31	8,93	-0,29	14	0
TCF7	7,98	-0,29	2	0
RRP36	6,98	-0,29	4	0
PLAG1	6,33	-0,29	4	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
DDX18	8,66	-0,29	13	0
HIRA	6,06	-0,30	3	0
IGKV2D-29; IGKV2D-26	7,85	-0,30	3	0
PPIL4	6,84	-0,30	5	0
FXR1	6,58	-0,30	5	0
DDX6	7,02	-0,30	5	0
RAN	7,75	-0,30	11	0
GATA3	6,73	-0,30	4	0
PRDX1	7,37	-0,31	6	0
SKIV2L2	7,63	-0,31	27	0
TFB1M	7,33	-0,31	6	0
EPB41	7,12	-0,31	12	0
SF3B1	8,53	-0,32	66	0
RPL36A;RPL36A-HNRNPH2	8,60	-0,32	15	0
KIAA0020	9,09	-0,33	18	0
DSC3	6,17	-0,34	4	0
ZBTB14	6,62	-0,35	3	0
ZFP3	6,45	-0,35	2	0
HNRNPUL2; HNRNPUL2-BSCL2	8,72	-0,35	37	0
RPP25L	6,58	-0,36	3	0
LIG1	5,89	-0,36	2	0
FBLL1	7,26	-0,38	2	0
UBA1	6,08	-0,38	4	0
PSMD13	6,64	-0,39	5	0
PQBP1	7,09	-0,39	3	0
RPL11	8,10	-0,40	8	0
SDAD1	7,61	-0,40	10	0
CPSF6	8,24	-0,40	12	0
RPL36	7,57	-0,40	5	0
RPS15A	8,62	-0,40	12	0
RPSA	7,75	-0,40	8	0
ARPC4;ARPC4-TTLL3	6,07	-0,40	2	0
ZSCAN25	6,80	-0,40	5	0
WDR43	6,91	-0,41	5	0
HSPD1	7,29	-0,41	14	0
FRG1	8,63	-0,41	16	0
POLR1B	6,65	-0,41	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MRPL48	7,61	-0,42	4	0
DDX10	7,52	-0,43	14	0
NACA	7,89	-0,43	4	0
CXorf56	7,19	-0,43	8	0
RBM42	7,07	-0,43	3	0
HSD17B10	6,83	-0,44	2	0
UTP3	7,62	-0,44	2	0
ZFP91;ZFP91-CNTF	7,98	-0,44	12	0
BRD2	7,56	-0,45	18	0
UPF3B	7,12	-0,45	6	0
SMARCA4	7,59	-0,46	30	0
CENPV	6,83	-0,46	3	0
U2AF2	9,11	-0,46	22	0
RAB7A	5,88	-0,46	4	0
EIF5B	6,92	-0,47	7	0
PURA	6,43	-0,47	4	0
RPL23A	10,02	-0,48	21	0
UBA52	7,34	-0,48	3	0
ZFP64	6,88	-0,48	6	0
MORF4L2	7,87	-0,48	10	0
ABCF2	7,36	-0,48	15	0
PCBP1	8,49	-0,48	15	0
CREB1	7,85	-0,49	5	0
PRPF6	7,78	-0,49	37	0
DMAP1	6,95	-0,49	9	0
ABT1	6,75	-0,50	3	0
REXO4	8,22	-0,50	8	0
LSM14B	7,28	-0,50	6	0
MRTO4	6,92	-0,51	3	0
TTF1	6,80	-0,51	2	0
DDB1	7,26	-0,51	17	0
EHMT1	5,98	-0,51	3	0
YY2	5,84	-0,51	2	0
PRDX2	6,00	-0,52	3	0
ZNF740	7,55	-0,52	8	0
EIF3D	7,18	-0,52	12	0
ANXA2;ANXA2P2	6,56	-0,52	5	0
KPNB1	7,16	-0,52	12	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GTPBP1	6,99	-0,53	8	0
MYO1G	6,58	-0,53	5	0
KPNA2	7,83	-0,53	10	0
UNG;DKFZp-781L1143	6,62	-0,53	2	0
TOP2A	8,13	-0,53	29	0
DDX52	7,45	-0,54	9	0
CCNL2	6,14	-0,54	4	0
LUC7L	8,08	-0,54	12	0
SRP72	8,47	-0,54	29	0
RPS17	8,57	-0,55	15	0
ZCCHC17	6,54	-0,55	3	0
STRBP	6,50	-0,56	3	0
HSPH1	6,22	-0,56	3	0
FAM133A	6,79	-0,56	2	0
ZBTB7A	6,62	-0,57	2	0
SBSN	6,47	-0,57	3	0
ZNF593	8,73	-0,57	4	0
NGDN	7,46	-0,57	5	0
RBPJ	7,36	-0,57	9	0
TBP;TBPL2	7,11	-0,58	4	0
HADHA	6,72	-0,58	2	0
DDX5	9,41	-0,58	46	0
VEZF1	7,47	-0,59	10	0
HNRNPU	7,34	-0,59	2	0
ZNF444	8,23	-0,59	6	0
RPL37A	8,16	-0,59	5	0
CHD1	6,67	-0,59	7	0
SERPINB12	6,66	-0,59	4	0
C11orf57	6,93	-0,59	3	0
USP7	6,70	-0,59	10	0
PRPF40A	7,84	-0,60	20	0
DHX33	6,74	-0,60	8	0
NOP2	7,89	-0,60	14	0
MAFG	8,58	-0,60	21	0
YARS	7,78	-0,60	20	0
DHX8	7,31	-0,60	26	0
MOGS	7,20	-0,61	5	0
CSNK1A1	7,27	-0,61	9	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RUNX3	6,10	-0,62	2	0
TSR1	8,06	-0,62	12	0
SMC3	7,78	-0,62	39	0
NEIL1	7,65	-0,62	5	0
WHSC1	6,77	-0,62	5	0
CAAP1	6,64	-0,62	2	0
RPS3	8,66	-0,63	24	0
DGKZ	6,21	-0,63	4	0
USP3	6,88	-0,63	7	0
CXXC1	6,67	-0,63	6	0
PWP1	7,57	-0,64	7	0
RCC1	8,37	-0,64	9	0
C9orf78	5,96	-0,65	3	0
DNAJB11	7,17	-0,65	8	0
RPL38	8,01	-0,66	6	0
BLM	7,48	-0,66	12	0
SNRNP27	7,18	-0,67	5	0
ZNF275	6,52	-0,67	4	0
TCEANC2	6,66	-0,67	2	0
HMGB2	7,23	-0,67	5	0
NFYA	6,57	-0,67	2	0
FAM76B	6,40	-0,68	3	0
ACO2	6,81	-0,68	3	0
BUD13	6,49	-0,69	4	0
SRSF11	6,70	-0,69	4	0
EEFSEC	6,35	-0,69	2	0
ZNF746	6,07	-0,70	3	0
SMNDC1	7,32	-0,70	7	0
LEF1	7,37	-0,70	4	0
DNMT1	7,43	-0,70	15	0
RBM28	7,63	-0,70	12	0
SRP14	7,83	-0,71	4	0
RPF2	8,03	-0,72	10	0
OGT	6,73	-0,73	14	0
MCM7	7,51	-0,73	12	0
RPL35A	7,47	-0,74	4	0
EZH2	6,44	-0,75	4	0
PHF6	9,37	-0,75	22	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PUF60	8,23	-0,75	22	0
EPB41L2	6,49	-0,75	4	0
RPS19	8,42	-0,75	14	0
KLF13	8,33	-0,75	16	0
DDX46	6,82	-0,75	7	0
SNRPB2	9,50	-0,75	13	0
RPUSD4	6,80	-0,75	6	0
SMARCC2	6,81	-0,75	7	0
ZNF281	7,90	-0,76	7	0
NSD1	7,03	-0,76	4	0
CMSS1	7,20	-0,76	3	0
HCFC2	6,08	-0,76	3	0
ZNF48	8,12	-0,76	10	0
XRCC1	6,11	-0,76	3	0
SNIP1	8,14	-0,77	11	0
MYL6	6,89	-0,77	3	0
PDS5B	7,16	-0,77	13	0
WBP11	8,52	-0,77	19	0
SNRPD2	8,00	-0,77	11	0
ARGLU1	8,41	-0,78	18	0
MIOS	6,01	-0,78	4	0
HOXC4	6,98	-0,79	7	0
ZSCAN21	6,63	-0,79	5	0
AUH	5,98	-0,79	3	0
MCM6	7,52	-0,80	16	0
LYAR	8,08	-0,80	5	0
EIF2S1	8,11	-0,80	20	0
LIG3	7,24	-0,81	3	0
ABCF1	8,05	-0,82	18	0
SREK1	6,68	-0,83	5	0
MAZ	9,04	-0,84	20	0
ZNF691	6,73	-0,85	4	0
ATF1	7,06	-0,85	3	0
VCP	6,36	-0,86	4	0
RPL18	7,10	-0,86	3	0
ZNF652	7,87	-0,86	15	0
NOL10	7,26	-0,86	11	0
RRP12	7,63	-0,86	14	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RASA2	6,55	-0,87	2	0
MAFK	8,34	-0,87	10	0
SNRNP35	6,39	-0,88	3	0
IMPDH2	6,53	-0,88	4	0
ALYREF	8,63	-0,89	9	0
HNRNPC	8,79	-0,89	13	0
CHD1L	6,07	-0,90	4	0
EEF2	7,60	-0,90	22	0
SNRPF	7,23	-0,90	2	0
RPS7	9,37	-0,90	25	0
HMGB1	7,82	-0,90	12	0
NMT1	6,32	-0,91	2	0
POLR1A	6,82	-0,91	12	0
RSBN1L	7,44	-0,91	10	0
TRMT1L	6,50	-0,92	3	0
PRPF31	7,99	-0,92	19	0
HNRNPU	8,96	-0,92	35	0
DDX49	7,36	-0,92	8	0
MRGBP	6,80	-0,93	3	0
SUPT16H	8,42	-0,93	55	0
PSIP1	8,12	-0,93	20	0
RPL27	9,25	-0,94	13	0
SMARCA5	8,21	-0,94	50	0
PPIH	7,80	-0,94	8	0
IQGAP1	7,89	-0,94	29	0
RBM26	7,29	-0,95	17	0
HMGA1	9,00	-0,95	8	0
NOP14	7,19	-0,96	6	0
DHX37	7,03	-0,96	8	0
MECP2	8,27	-0,96	18	0
PRPF4B	7,84	-0,96	22	0
SPTBN1	5,88	-0,96	3	0
PARP1	8,14	-0,97	20	0
AURKB	7,35	-0,97	9	0
LARP7	7,67	-0,97	7	0
MAK16	6,62	-0,97	2	0
SNRPA1	9,46	-0,98	31	0
AGO2	6,71	-0,98	11	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ZNF524	7,28	-0,99	3	0
RPL3	8,65	-1,00	20	0
NSUN5	7,99	-1,00	3	0
MPHOSPH10	7,12	-1,00	8	0
KRI1	6,87	-1,00	4	0
ARRB2	6,76	-1,01	2	0
CLK3	7,69	-1,02	13	0
IMP4	7,29	-1,02	6	0
LARP1	6,73	-1,02	3	0
ZNF787	8,25	-1,03	8	0
RBM19	6,06	-1,03	3	0
FAM32A	8,00	-1,04	9	0
SUB1	7,94	-1,04	5	0
YBX3	8,37	-1,05	6	0
DOT1L	6,98	-1,05	7	0
ZFP62	7,47	-1,06	6	0
ZRSR1;ZRSR2	6,04	-1,07	3	0
POP1	7,93	-1,07	10	0
RPL22	8,83	-1,10	9	0
MRPL40	7,01	-1,10	2	0
CPSF1	8,38	-1,11	40	0
FIZ1	8,34	-1,11	12	0
C4orf27	6,50	-1,11	3	0
DIEXF	7,02	-1,12	9	0
PRPF4	8,60	-1,12	30	0
WBSCR22	8,20	-1,13	2	0
VRK1	7,23	-1,13	6	0
MAP7	7,10	-1,13	6	0
RPL9	8,33	-1,14	10	0
TCF7	7,45	-1,14	2	0
SMARCC1	7,77	-1,15	27	0
POLR1E	7,11	-1,16	2	0
SND1	6,79	-1,16	7	0
NXT1	6,92	-1,16	2	0
HDGF	6,19	-1,17	2	0
GRWD1	8,46	-1,17	11	0
PES1	7,82	-1,18	9	0
PHF8	5,88	-1,22	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ZNHIT6	6,64	-1,22	2	0
BRD7	6,84	-1,22	4	0
ARPC1B	6,67	-1,22	4	0
FXR2	7,19	-1,23	11	0
RSBN1	7,73	-1,23	12	0
SRPK1	7,57	-1,23	11	0
NAP1L1	7,75	-1,23	9	0
ATP5C1	7,02	-1,24	4	0
POF1B	6,02	-1,24	3	0
ZNF319	8,43	-1,25	23	0
GTPBP4	7,45	-1,26	5	0
INO80	6,39	-1,28	7	0
SIM2	6,15	-1,29	3	0
ZNF865	7,07	-1,30	6	0
SNRPD1	8,33	-1,31	4	0
SRBD1	7,15	-1,32	13	0
BAP1	6,51	-1,33	2	0
MORF4L1	8,19	-1,33	17	0
MEPCE	7,66	-1,34	7	0
EIF2S3;EIF2S3L	8,43	-1,36	18	0
SRRM1	8,06	-1,38	10	0
ZNF148	7,73	-1,38	13	0
LBR	8,11	-1,39	1	0
RPL22L1	8,55	-1,39	2	0
EIF2S2	7,98	-1,39	18	0
ARHGEF2	6,35	-1,40	2	0
SP3	7,98	-1,41	12	0
PRPF3	8,71	-1,42	30	0
MRPL46	7,71	-1,42	2	0
FAM120A	7,14	-1,42	10	0
MCM2	7,57	-1,45	19	0
KIF4A;KIF4B	6,56	-1,45	4	0
THYN1	6,74	-1,46	2	0
RBM27	8,19	-1,51	24	0
HMGA1	8,47	-1,52	2	0
ESF1	6,67	-1,52	6	0
ZNF146	7,48	-1,53	9	0
SON	8,04	-1,54	22	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SMC1A	7,78	-1,55	38	0
KLF16	7,50	-1,57	1	0
UTP15	6,90	-1,58	2	0
SET;SETSIP	7,43	-1,61	3	0
CTCF	9,68	-1,62	45	0
ANAPC2	6,05	-1,64	3	0
RPL30	9,41	-1,64	11	0
NAT10	8,25	-1,64	34	0
PRDM15	7,19	-1,66	6	0
LYZ	6,84	-1,66	2	0
RBBP6	7,58	-1,67	9	0
TRMT112	8,36	-1,68	4	0
ERI1	8,14	-1,71	5	0
SRP9	7,31	-1,72	4	0
ZKSCAN1	6,82	-1,73	5	0
SLTM	7,86	-1,73	14	0
SLK	7,31	-1,73	5	0
DIAPH3	7,86	-1,75	7	0
UTP14A	7,07	-1,75	3	0
EIF1AX;EIF1AY	7,40	-1,78	3	0
PNO1	7,56	-1,81	6	0
NSUN2	8,19	-1,86	20	0
TGM1	5,81	-1,92	3	0
YY1	7,02	-1,92	3	0
SMC2	7,34	-1,95	9	0
ZFX;ZFY	7,47	-1,97	10	0
DHX30	6,29	-2,06	3	0
SP1	7,78	-2,08	8	0
BAZ1B	6,82	-2,11	2	0
TOP1	8,78	-2,12	31	0
HMGN2	7,36	-2,22	3	0
TMA16	7,25	-2,23	2	0
TCERG1	7,40	-2,26	7	0
MYBBP1A	8,80	-2,52	4	0

7.3.2 Table with values corresponding to Figure 4.6

Table 7.3: Values corresponding to Figure 4.6.A. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
POLR2J;POLR2J3	8,94	9,19	11	2
POLR2I	8,92	9,13	8	2
POLR2C	9,19	8,96	18	2
GTF2F2	8,97	8,74	15	2
INTS4	8,18	8,64	17	2
POLR2G	8,56	8,60	11	2
POLR2D	8,50	8,27	9	2
INTS6	8,23	8,26	19	2
MED17	8,17	8,20	12	2
POLR2A	10,05	8,05	116	2
POLR2F	8,35	7,70	4	2
INTS9	8,08	7,67	11	2
TCEA1	8,19	7,64	14	2
GTF2F1	8,54	7,60	18	2
MED8	8,07	7,37	7	2
ASUN	8,02	7,32	14	2
POLR2E	9,11	7,15	11	2
VWA9	7,81	7,05	7	2
MED21	7,99	6,90	3	2
INTS1	8,11	6,82	12	2
POLR2H	8,83	6,70	8	2
MED1	8,02	6,53	14	2
MED16	7,62	6,51	6	2
MED23	7,63	6,44	9	2
MED27	8,00	6,19	8	2
RPRD2	7,63	6,14	8	2
MED14	8,02	6,12	16	2
CPSF3L	7,60	6,08	9	2
INTS5	7,25	5,99	6	2
POLR2B	9,68	5,84	72	2
INTS7	7,89	5,77	13	2
INTS12	7,55	5,71	3	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PPP2R1A	8,13	5,54	17	2
RPRD1B	7,61	5,14	8	2
MED4	7,66	5,07	8	2
POLR2K	7,58	5,01	3	2
MED10	7,53	4,72	4	2
MED7	7,24	3,98	4	2
IXL;MED29	7,96	6,46	5	1
MED20	7,96	6,40	5	1
MED22	7,90	6,39	5	1
MED11	7,70	5,39	3	1
INTS2	7,66	5,28	7	1
MED15	7,50	4,78	4	1
INTS8	7,64	4,72	7	1
MED31	7,31	4,06	3	1
PPP2CB	7,12	2,70	6	1
SNRNP200	7,78	-0,06	7	1
NSUN2	8,10	-1,42	3	1
BRD2	7,47	-3,13	2	1
INTS10	7,64	5,49	8	0
MED6	7,45	5,20	2	0
MED18	7,71	5,18	2	0
MED24	7,64	4,69	2	0
RECQL5	7,56	4,45	3	0
RPAP2	7,44	4,33	1	0
MED19	7,60	4,03	3	0
MED30	7,24	3,90	3	0
BCLAF1	7,44	3,74	3	0
POLR2M;GCOM1;GCOM2	7,08	3,66	2	0
CDKN2AIP	6,77	3,63	2	0
TCEA3	7,40	3,55	3	0
SUPT5H	7,79	3,51	3	0
SUPT6H	7,93	3,49	12	0
RPRD1A	7,08	3,33	3	0
INTS3	7,69	3,26	7	0
MED25	7,18	3,26	1	0
RPL28	8,46	3,13	6	0
MED26	7,04	3,05	3	0
PSMD11	6,22	2,97	0	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPL6	8,92	2,76	10	0
EPRS	6,78	2,72	0	0
MYH9	7,27	2,71	7	0
SET;SETSIP	8,08	2,64	6	0
WDR92;DKFZp434B156	6,88	2,50	1	0
PSMC5	6,23	2,46	4	0
ELL	6,67	2,41	0	0
BTF3	8,03	2,35	4	0
SCAF4	8,30	2,34	7	0
THRAP3	8,03	2,28	4	0
PPP1R10	6,89	2,26	1	0
GTF2E1	6,36	2,24	0	0
VEZF1	7,95	2,24	6	0
SCAF8	7,18	2,17	5	0
SRRM1	8,57	2,13	12	0
ANP32B	7,52	2,11	2	0
RPL13	8,28	2,10	7	0
DYNC1H1	5,99	2,08	1	0
HSP90AA1	7,16	2,07	4	0
TRA2A	7,12	2,04	2	0
PSMC2	6,81	2,00	2	0
DENND2D	7,25	1,99	2	0
ZRANB2	7,90	1,97	7	0
U2SURP	7,99	1,96	7	0
CCT6A	7,14	1,92	1	0
SRSF11	7,16	1,85	3	0
PA2G4	6,95	1,81	3	0
ZCCHC17	6,96	1,79	2	0
CCT5	6,52	1,79	2	0
EPB41L4B	7,14	1,78	4	0
PKM	6,82	1,78	3	0
NMT1	6,89	1,77	1	0
SNRNP70	7,92	1,76	8	0
PPP2R1B	7,19	1,75	2	0
CHTOP	7,05	1,74	2	0
SRSF6	7,51	1,73	3	0
ZSCAN25	7,24	1,70	1	0
SYNCRIP	7,02	1,69	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
YTHDC1	6,87	1,69	1	0
SYMPK	7,34	1,67	1	0
RPL17;RPL17-C18orf32	8,94	1,66	10	0
CDC73	6,78	1,65	2	0
SERBP1	7,16	1,64	2	0
EEF1D	6,91	1,64	0	0
XRN2	7,60	1,63	5	0
PSMC6	6,45	1,63	1	0
PCF11	7,06	1,62	4	0
CPSF7	6,80	1,59	3	0
GTF2H2C;GTF2H2	6,58	1,59	1	0
SUB1	8,27	1,56	3	0
SETD2	6,61	1,55	1	0
TCF7	7,69	1,54	1	0
ICE1	6,65	1,53	0	0
PYCR2	7,02	1,53	0	0
CPSF6	8,56	1,52	5	0
RPS23	8,09	1,49	4	0
TPI1	6,37	1,48	0	0
CCT3	7,16	1,48	2	0
CFL1	6,85	1,48	2	0
THOC7;NIF3L1BP1	6,68	1,47	1	0
KHDRBS1	7,78	1,45	2	0
SCAF11	7,33	1,39	1	0
PAF1	6,67	1,37	1	0
CRNKL1	6,86	1,34	0	0
AHCY	6,24	1,33	0	0
SLK	7,83	1,32	4	0
PSMD2	6,93	1,32	3	0
SNRPG;SNRPGP15	7,19	1,32	2	0
RUVBL2	7,99	1,30	13	0
BCAS2	6,91	1,29	1	0
ZC3H18	7,41	1,28	4	0
TCP1	6,93	1,28	5	0
SRP14	8,10	1,28	3	0
GTF2E2	7,10	1,26	2	0
ZSCAN21	7,01	1,26	1	0
CDK13	8,05	1,25	9	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
PSMD6	6,31	1,24	0	0
ATAD3A	6,42	1,23	1	0
SCAF1	7,04	1,19	1	0
SRSF3	8,32	1,18	9	0
RPL8	9,33	1,17	18	0
ZNF260	6,41	1,17	0	0
SNRPC	7,23	1,17	2	0
PRDX1	7,54	1,17	3	0
PGAM5	6,68	1,16	0	0
EIF4B	6,77	1,16	0	0
RPL13A;RPL13a	7,55	1,15	2	0
HSP90AB1	8,40	1,14	23	0
ZNF197	6,84	1,14	0	0
MAGOH;MAGOHB	6,81	1,14	2	0
BUD31	6,84	1,13	0	0
SRSF10	6,74	1,13	1	0
SF3B4	7,22	1,12	3	0
PPIG	7,41	1,12	1	0
EBNA1BP2	8,08	1,11	4	0
CCT7	6,69	1,10	2	0
EEF1G	6,75	1,10	3	0
WWP2	8,11	1,10	9	0
SNRPE	7,32	1,09	2	0
PPAN-P2RY11;PPAN	7,24	1,09	1	0
SRSF9	7,03	1,08	0	0
CSTF2	7,23	1,07	2	0
EWSR1	7,17	1,07	1	0
PELO	6,55	1,07	2	0
PYCR1	7,14	1,06	2	0
RPS18	8,29	1,06	7	0
AP2M1	6,54	1,04	1	0
RPAP3	6,62	1,04	2	0
CHD1	6,94	1,03	0	0
CHAMP1	7,37	1,02	3	0
HSPA9	7,62	1,01	19	0
XAB2	6,65	1,01	0	0
RNPS1	7,45	0,99	4	0
FAM76B	6,72	0,98	0	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SFSWAP	7,06	0,97	2	0
CLTC	7,35	0,96	6	0
CAD	6,11	0,96	2	0
SF3A2	7,50	0,95	3	0
CDK7	6,48	0,92	0	0
CDC40	6,86	0,91	3	0
RPL12	7,22	0,91	3	0
EEF2	7,60	0,89	6	0
NACA	8,06	0,89	6	0
HNRNPF	7,86	0,89	4	0
RBBP6	7,85	0,88	3	0
SNRNP40	7,38	0,87	1	0
CHMP4B	6,69	0,85	0	0
RRP36	7,19	0,85	2	0
SAP30BP	7,05	0,83	1	0
HAUS8	7,40	0,83	1	0
RPL35A	7,48	0,83	2	0
SNRPF	7,15	0,82	1	0
HSD17B10	6,86	0,81	3	0
SAFB	7,31	0,81	1	0
EPB41	7,41	0,79	3	0
NCL	8,97	0,78	11	0
DUT	6,87	0,77	1	0
TUBB	7,36	0,77	3	0
EIF2S2	8,21	0,77	8	0
CCDC137	6,75	0,76	1	0
TFB1M	7,56	0,76	1	0
PHF5A	6,97	0,76	3	0
HNRNPAB	7,31	0,76	2	0
HDGFRP2	7,21	0,76	2	0
PPIL4	7,10	0,75	1	0
UTP14A	7,16	0,74	1	0
RPL14	7,03	0,74	1	0
TRA2B	7,34	0,74	4	0
CCT2	6,90	0,74	4	0
DDX54	7,71	0,73	1	0
ABCE1	6,77	0,73	3	0
GLUD1;GLUD2	6,45	0,73	1	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DCD	7,51	0,72	2	0
RPL32	8,17	0,71	6	0
RPS27	7,60	0,71	4	0
DDX46	7,03	0,70	3	0
EIF5B	7,22	0,70	1	0
RPL34	7,95	0,70	4	0
PNN	7,56	0,69	6	0
RPS28	7,15	0,69	1	0
PSMC3	6,47	0,68	2	0
RTCB	7,01	0,67	3	0
CUL2	6,41	0,67	1	0
ZBTB7A	6,76	0,67	1	0
RPS25	9,05	0,65	7	0
RPS12	7,62	0,64	2	0
EED	6,78	0,64	1	0
DDX27	7,60	0,63	3	0
CCT8	6,99	0,62	6	0
ATRX	6,50	0,62	1	0
PSMD1	5,90	0,61	1	0
PABPC4	6,29	0,59	1	0
SLC25A5	7,27	0,59	5	0
RPL4	7,99	0,59	7	0
HCFC1	6,97	0,58	3	0
RRS1	8,02	0,58	4	0
EIF3A	6,41	0,58	1	0
NOP16	6,30	0,58	1	0
IWS1	7,13	0,58	1	0
RBM17	6,99	0,56	2	0
TARDBP	7,50	0,56	3	0
SREK1	6,97	0,56	1	0
RTF1	7,00	0,54	1	0
NCBP1	6,74	0,54	1	0
LUC7L3	7,23	0,54	3	0
CWC25	6,96	0,53	1	0
INIP	6,65	0,53	0	0
EEF1A1;EEF1A1P5	8,48	0,53	10	0
G3BP1	6,43	0,52	0	0
SART1	7,85	0,52	3	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	6,90	0,51	0	0
BUB3	7,93	0,51	9	0
GRB10	7,35	0,50	4	0
SF3B5	6,89	0,50	1	0
SREK1IP1	7,33	0,50	3	0
DNAJA2	7,18	0,50	3	0
THOC2	6,38	0,50	2	0
HNRNPD	7,05	0,49	2	0
CCAR1	6,91	0,48	1	0
RBX1	6,96	0,48	2	0
PABPC1;PABPC3	6,91	0,48	5	0
GNB2L1	7,12	0,46	4	0
NXT1	6,74	0,46	1	0
RPS2	7,91	0,46	7	0
RBM26	7,66	0,45	4	0
YWHAZ	6,42	0,45	0	0
ZNF646	7,15	0,45	1	0
TAF15	6,99	0,45	0	0
CBX5	6,81	0,43	3	0
RASA2	6,62	0,43	0	0
ERH	7,55	0,42	3	0
SSB	7,71	0,42	3	0
NSD1	7,21	0,42	1	0
SMAD3	7,25	0,41	4	0
MAP7	7,07	0,41	1	0
MRPL40	6,93	0,40	1	0
RPS17	8,65	0,40	8	0
PCNP	6,47	0,40	0	0
RPL10	7,76	0,39	4	0
SUCLG1	6,40	0,38	0	0
ILF3	7,29	0,38	0	0
ATP5A1	7,14	0,38	6	0
LUC7L2	8,64	0,38	18	0
HNRNPLL;HNRPLL	6,65	0,36	1	0
RPS24	8,56	0,36	6	0
EIF5A;EIF5AL1	6,99	0,35	2	0
YARS	7,86	0,35	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HNRNPM	8,22	0,35	19	0
CMAS	7,08	0,34	3	0
FAM120A	7,38	0,34	1	0
GNAI3	6,54	0,34	0	0
HSPD1	7,37	0,33	5	0
KIF4A;KIF4B	6,44	0,33	1	0
RPLP0;RPLP0P6	7,55	0,33	5	0
SRSF2	7,88	0,33	6	0
PRPS1	6,45	0,32	1	0
DHX8	7,49	0,32	3	0
ZNF148	7,89	0,32	8	0
RPL31	9,02	0,31	7	0
SMNDC1	7,10	0,30	2	0
SRSF1	7,49	0,30	4	0
MED12;TNRC11	6,47	0,29	1	0
YBX3	8,43	0,29	2	0
KLF13	8,40	0,29	8	0
ENO1	6,75	0,28	3	0
MICU1	7,58	0,28	9	0
GATAD2B	6,83	0,27	2	0
RPS6	9,25	0,27	15	0
ARGLU1	8,41	0,26	8	0
SNRPD2	7,92	0,26	3	0
SRFBP1	7,33	0,26	1	0
KIF2C	6,62	0,25	1	0
SF3A1	7,68	0,25	3	0
RBM28	7,64	0,24	2	0
HNRNPH1	7,71	0,23	6	0
MPHOSPH10	7,37	0,23	0	0
PRPF40A	7,83	0,22	6	0
CHERP	7,41	0,21	0	0
RPL19	9,07	0,20	12	0
NPM1	9,00	0,20	9	0
CCT4	6,48	0,19	1	0
GTPBP1	6,83	0,19	1	0
PRPF8	7,94	0,18	13	0
KLF16	7,73	0,18	1	0
PLRG1	6,95	0,18	0	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EIF3I	6,67	0,18	1	0
SP3	8,09	0,17	6	0
EIF2S1	8,34	0,16	7	0
RPL27A	8,03	0,16	3	0
SRP72	8,09	0,16	14	0
CBFB	6,66	0,15	0	0
KIF2A	6,87	0,15	2	0
SNW1	7,08	0,15	3	0
WWP1	7,71	0,15	2	0
CAPRIN1	6,51	0,14	0	0
PRPF4B	8,05	0,14	7	0
CTR9	6,38	0,14	0	0
DDX39A	6,83	0,13	2	0
RPL5	8,83	0,12	10	0
POGZ	6,58	0,12	0	0
SMC4	6,80	0,12	0	0
ZNF800	7,71	0,11	1	0
RPL37A	8,28	0,11	4	0
CTNNB1	7,23	0,11	1	0
SRRM2	7,54	0,11	3	0
ZNF281	7,98	0,11	3	0
DYNLL1	7,57	0,11	2	0
SF1	7,19	0,10	2	0
RPL18	7,26	0,10	2	0
TAF6	6,32	0,09	1	0
H1F0	8,72	0,09	6	0
RBMX	8,31	0,08	8	0
HSPA5	7,68	0,07	8	0
PPP1CB	6,80	0,07	0	0
PSMC1	6,50	0,06	0	0
RPS5	8,46	0,06	8	0
HADHB	6,69	0,06	0	0
CGGBP1	6,82	0,06	0	0
ZFP91;ZFP91-CNTF	8,04	0,05	4	0
TCF7	7,81	0,05	3	0
UTP23	7,72	0,04	1	0
WBP11	8,49	0,04	9	0
U2AF1	9,02	0,03	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ZNF653	6,95	0,03	2	0
NOP58	7,25	0,03	2	0
RBM15	7,08	0,02	0	0
HSPA8	8,64	0,02	21	0
INCENP	6,93	0,02	0	0
KPNB1	6,77	0,02	2	0
DDB1	6,67	0,02	0	0
DNAJA1	7,41	0,01	3	0
RPS20	7,86	0,01	4	0
TCEB2	6,88	0,00	0	0
LRRC59	7,02	0,00	3	0
SRSF5	7,22	-0,02	1	0
RBM27	8,29	-0,03	7	0
RPS19	8,54	-0,03	11	0
RSBN1	7,87	-0,03	9	0
SON	7,90	-0,03	4	0
SRSF7	7,59	-0,04	2	0
CBX3	7,36	-0,04	4	0
PSMC4	6,55	-0,04	0	0
RPL36A;RPL36A-HNRNPH2	8,71	-0,04	7	0
RP9	6,89	-0,05	1	0
RBM10	6,46	-0,05	0	0
RPS13	8,73	-0,05	7	0
VDAC3	6,68	-0,05	1	0
TEX10	6,53	-0,05	0	0
CWC15	6,80	-0,06	0	0
HNRNPA3	7,59	-0,07	0	0
RPLP2	7,40	-0,07	4	0
ACTB	8,48	-0,07	19	0
HDAC1	7,21	-0,07	1	0
RPL18A	7,65	-0,07	5	0
MTHFD1	6,25	-0,08	1	0
LBR	8,20	-0,09	2	0
MAZ	9,11	-0,09	16	0
REXO4	8,18	-0,10	5	0
CDK9	6,77	-0,11	2	0
CAT	6,77	-0,11	0	0
KPNA4	6,83	-0,11	1	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HNRNPK	8,17	-0,12	8	0
UTP3	7,61	-0,12	1	0
SP1	7,91	-0,12	4	0
TCERG1	7,23	-0,12	1	0
RPS29	7,19	-0,12	0	0
ELAVL1	7,50	-0,13	4	0
LMNB1	7,58	-0,14	7	0
PUF60	8,35	-0,15	9	0
RPS26;RPS26P11	8,22	-0,15	5	0
LYAR	7,94	-0,15	2	0
RPL7	7,64	-0,16	1	0
HIST1H2AC	9,66	-0,16	8	0
EIF2S3;EIF2S3L	8,52	-0,16	15	0
SAP18	7,24	-0,18	5	0
RPL21	7,96	-0,19	4	0
RPL35	8,97	-0,19	5	0
HMGA1	9,07	-0,20	7	0
CMSS1	7,31	-0,20	1	0
RUVBL1	7,85	-0,20	12	0
RPL36	7,70	-0,21	1	0
WBSCR22	8,34	-0,21	2	0
MYL6	6,85	-0,21	1	0
ZNF740	7,47	-0,22	1	0
MRPL48	7,50	-0,22	2	0
TUBA1B	7,88	-0,22	12	0
PCBP2;Isoform	7,20	-0,22	4	0
MCM7	7,33	-0,22	0	0
NXF1	7,02	-0,23	1	0
TRMT10C	7,13	-0,23	4	0
ZNF691	6,73	-0,24	0	0
ERCC3	6,66	-0,24	2	0
RPS4X	8,92	-0,26	18	0
RPS15	8,53	-0,26	4	0
ZNF652	7,89	-0,27	2	0
DHX9	8,12	-0,27	12	0
RBM5	6,39	-0,27	0	0
PPP1CA	7,51	-0,27	4	0
RALY	7,63	-0,28	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SF3B6	6,80	-0,28	3	0
EIF1AX;EIF1AY	7,12	-0,28	2	0
RBM8A	7,07	-0,29	3	0
LUC7L	8,04	-0,29	7	0
SSRP1	8,09	-0,30	8	0
FAM207A	7,05	-0,30	0	0
HNRNPR	7,15	-0,30	2	0
ZNF771	8,28	-0,31	5	0
GNL3	8,00	-0,32	1	0
SKP1	7,69	-0,32	3	0
PRPF38A	6,86	-0,34	0	0
PARP1	7,95	-0,34	4	0
SRP9	7,39	-0,35	1	0
ZFP64	7,12	-0,35	1	0
RAB1A	6,14	-0,35	1	0
TPR	6,60	-0,36	3	0
RPS11	8,75	-0,37	11	0
NOP2	7,89	-0,37	1	0
PHGDH	6,60	-0,37	5	0
RUNX2	6,75	-0,37	0	0
AQR	6,95	-0,39	0	0
PSMD13	6,66	-0,40	0	0
C14orf166	6,38	-0,40	0	0
RASA1	6,96	-0,40	2	0
ARPC1B	6,78	-0,40	0	0
HMGB2	6,90	-0,41	0	0
ACO2	6,12	-0,41	0	0
HIST1H3A;H3F3C	9,46	-0,42	11	0
GTF2B	8,05	-0,42	13	0
RPS8	8,33	-0,43	12	0
RBM25	7,70	-0,43	3	0
PATZ1	8,32	-0,44	8	0
SMC2	7,17	-0,44	0	0
LEF1	7,38	-0,45	0	0
HNRNPA1;HNRNPA1L2	7,82	-0,45	1	0
SNRPB;SNRPN	7,63	-0,46	3	0
HNRNPA2B1	7,95	-0,46	5	0
EFTUD2	7,77	-0,47	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PURB	6,41	-0,47	0	0
DNAJB11	7,21	-0,47	3	0
SMC1A	7,46	-0,47	2	0
SRP68	7,90	-0,47	8	0
CCAR2	6,36	-0,48	1	0
EIF3D	7,11	-0,48	2	0
SNRPD3	7,67	-0,48	4	0
USP3	6,93	-0,48	1	0
RSBN1L	7,51	-0,49	0	0
HMGA1	8,40	-0,49	1	0
RPS7	9,39	-0,49	15	0
IMPDH2	6,64	-0,51	2	0
UTP15	6,85	-0,51	1	0
CTNNBL1	6,80	-0,51	0	0
NIP7	6,78	-0,51	0	0
MRPL9	7,27	-0,52	2	0
ALDH18A1	6,46	-0,52	1	0
HNRNPL	8,42	-0,53	13	0
RBM39	8,57	-0,53	20	0
ZBTB14	6,70	-0,54	2	0
RAN	7,45	-0,55	4	0
BRD7	6,77	-0,55	2	0
DHX15	7,94	-0,56	7	0
ZNF146	7,33	-0,57	0	0
PWP1	7,59	-0,57	1	0
EIF4A1	7,36	-0,58	8	0
TUBB2A	7,01	-0,58	1	0
RPS16;ZNF90	7,97	-0,58	6	0
UBA52	7,54	-0,58	0	0
ZNF207	7,10	-0,59	1	0
DDX17	7,91	-0,60	8	0
ARRB2	6,87	-0,60	0	0
WDR43	6,84	-0,60	0	0
PRDM10	6,94	-0,61	2	0
USP7	6,82	-0,61	1	0
PCBP1	8,36	-0,61	10	0
MRPL46	7,08	-0,62	1	0
PRPF6	7,40	-0,62	1	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TTN	6,97	-0,63	2	0
POLDIP3	7,12	-0,64	3	0
ZKSCAN1	6,94	-0,64	0	0
RPL37	7,92	-0,65	3	0
ACIN1	7,44	-0,66	1	0
METAP1	8,08	-0,67	5	0
UBTF	7,37	-0,69	2	0
ZNF865	7,13	-0,70	2	0
C19orf53	7,78	-0,70	2	0
EIF3E	6,64	-0,70	1	0
SF3A3	7,32	-0,70	4	0
U2AF2	8,93	-0,70	19	0
MATR3	7,55	-0,71	2	0
IK	7,01	-0,72	1	0
ZSCAN26;ZNF187	7,51	-0,72	2	0
WDR82	6,62	-0,72	0	0
FAM32A	8,03	-0,73	5	0
RPS3A	9,24	-0,73	11	0
EIF3F	6,52	-0,74	1	0
TRIM28	7,49	-0,74	3	0
ABCF2	7,20	-0,75	1	0
CFAP20	7,45	-0,77	2	0
HNRNPC	8,45	-0,77	11	0
EIF4A3	7,55	-0,78	0	0
SUPT16H	8,31	-0,79	11	0
PSIP1	8,14	-0,82	4	0
GNL2	7,72	-0,82	1	0
LSM14B	7,23	-0,82	2	0
RPL3	8,47	-0,83	6	0
RPS27A;UBB;UBC; UBA52	8,29	-0,83	6	0
GAPDH	7,14	-0,83	2	0
PRDM15	7,28	-0,83	2	0
SP2	7,80	-0,83	5	0
DKC1	6,62	-0,84	1	0
THOC5	6,38	-0,85	1	0
RPL23	8,27	-0,86	5	0
DNTTIP2	6,92	-0,86	0	0
CDC5L	7,96	-0,86	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RCC2	8,36	-0,87	10	0
NONO	7,99	-0,87	3	0
HIST1H2BC	9,86	-0,88	15	0
TUBB4B	7,66	-0,88	11	0
UHRF1	7,00	-0,88	0	0
RPL24	8,36	-0,91	8	0
PRPF31	8,07	-0,92	6	0
METTL17	6,93	-0,93	1	0
ZNF48	8,16	-0,93	6	0
MAT2A	6,67	-0,94	0	0
DDX23	7,42	-0,94	3	0
UTP18	7,04	-0,94	1	0
DDX6	7,04	-0,94	0	0
PRPF19	7,59	-0,95	5	0
NHP2L1	7,51	-0,95	4	0
RPS21	6,55	-0,95	0	0
PLEC	7,47	-0,96	0	0
WDR33	7,96	-0,98	5	0
GLYR1	7,97	-0,98	4	0
CHD4	7,56	-0,99	2	0
NOLC1	7,87	-0,99	1	0
FTSJ3	8,21	-1,01	7	0
SNRNP27	7,16	-1,02	2	0
MTA2	7,01	-1,04	2	0
FIP1L1	7,96	-1,06	4	0
RBBP4	7,58	-1,07	3	0
TCEB1	7,14	-1,07	1	0
CREB1	7,69	-1,07	2	0
RPL23A	9,89	-1,07	16	0
GTPBP4	7,30	-1,08	0	0
GTF2I	7,16	-1,09	4	0
MCM2	7,21	-1,09	4	0
PTBP1	7,49	-1,10	3	0
SLTM	7,79	-1,11	2	0
SMARCC1	7,41	-1,11	2	0
RPL7A	8,92	-1,12	14	0
RPL26	9,11	-1,12	9	0
NOP10	6,68	-1,13	0	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNRPD1	7,88	-1,14	2	0
ELF1;DKFZp686H0575	6,46	-1,14	0	0
NOP56	7,28	-1,15	3	0
RPF2	7,83	-1,16	2	0
UBA1	5,87	-1,16	5	0
RPSA	7,88	-1,17	4	0
VCP	6,26	-1,17	1	0
TRIP12	7,13	-1,18	1	0
ZNF579	7,02	-1,18	1	0
HELLS	6,85	-1,19	0	0
SMC3	7,58	-1,19	4	0
TOP2A	7,79	-1,19	6	0
TCF7;TCF7L2	8,43	-1,20	8	0
CPSF4	7,58	-1,20	2	0
DEK	7,48	-1,21	2	0
CSTF1	7,09	-1,22	0	0
MCM3	7,07	-1,22	2	0
DDX39B	7,30	-1,23	1	0
DDX55	8,07	-1,24	4	0
SMU1	7,37	-1,25	3	0
RPL38	7,66	-1,25	3	0
FXR1	6,43	-1,26	0	0
SND1	6,56	-1,26	2	0
HNRNPA3	8,16	-1,27	4	0
SHMT2	6,66	-1,28	0	0
NAP1L1	7,60	-1,28	3	0
DIMT1	8,56	-1,28	8	0
HNRNPUL2;HNRNPUL2-BSCL2	8,70	-1,29	19	0
YBX1	10,18	-1,29	26	0
NUMA1	6,57	-1,29	0	0
ZFX;ZFY	7,58	-1,29	9	0
DDX3X;DDX3Y	8,42	-1,31	12	0
NSUN5	7,81	-1,32	1	0
WDR5	7,16	-1,33	2	0
RPL15	7,89	-1,34	4	0
RPL39P5;RPL39	8,39	-1,35	1	0
ZNF524	7,26	-1,36	2	0
H2AFV;H2AFZ	7,93	-1,36	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SRRT	7,61	-1,37	5	0
DDX5	9,02	-1,37	22	0
DDX1	6,55	-1,37	0	0
RBBP7	6,98	-1,39	0	0
SFPQ	8,26	-1,41	6	0
CTCF	9,59	-1,41	32	0
MAFG	8,36	-1,41	7	0
KIAA0020	8,87	-1,43	5	0
VDAC2	6,72	-1,43	3	0
H2AFY	8,09	-1,45	7	0
ZNF787	8,05	-1,45	5	0
USP39	7,11	-1,45	0	0
BRIX1	7,80	-1,46	3	0
ERI1	8,36	-1,48	4	0
NUDT21	7,66	-1,50	4	0
CPSF2	7,76	-1,51	7	0
SF3B2	7,79	-1,51	2	0
RBPJ	7,17	-1,51	1	0
ZNF444	8,19	-1,51	0	0
ZNF319	8,54	-1,52	6	0
C19orf43	7,47	-1,53	0	0
DCAF13	8,36	-1,54	4	0
NSF	6,14	-1,55	0	0
MFAP1	7,47	-1,57	2	0
RBM14	7,47	-1,58	3	0
RRP12	7,04	-1,62	1	0
MINA	6,99	-1,62	1	0
FXR2	7,10	-1,65	1	0
HIST1H1E;HIST1H1D	9,74	-1,65	11	0
PES1	7,75	-1,66	3	0
RPL30	9,19	-1,67	7	0
SNRPA1	9,45	-1,67	19	0
RPS3	8,53	-1,67	12	0
MORF4L2	7,73	-1,69	2	0
SF3B3	8,11	-1,70	10	0
TMPO	6,95	-1,71	1	0
UPF3B	6,99	-1,72	1	0
SNIP1	7,89	-1,73	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPS15A	8,41	-1,73	4	0
HP1BP3	7,92	-1,76	4	0
HNRNPU	8,82	-1,76	16	0
PPIH	7,69	-1,77	1	0
RPL10A	7,96	-1,81	4	0
FIZ1	8,37	-1,84	5	0
C9orf114	7,41	-1,85	0	0
TOP2B	6,74	-1,85	1	0
MCM6	7,04	-1,85	2	0
NGDN	7,26	-1,86	0	0
S100A9	6,88	-1,86	0	0
TRMT112	8,44	-1,87	2	0
HIST1H4A	9,64	-1,92	14	0
NSA2	7,18	-1,92	1	0
EMG1	7,32	-1,93	1	0
FAU	8,30	-1,93	3	0
CPSF3	7,53	-1,94	3	0
ABCF1	7,77	-1,95	3	0
DDX50	6,58	-1,97	0	0
PHF6	9,23	-1,98	13	0
RPS10;RPS10-NUDT3	8,44	-1,99	5	0
SF3B1	8,17	-1,99	7	0
KRR1	8,12	-2,04	4	0
SRPK1	7,37	-2,05	1	0
NEIL1	7,34	-2,05	1	0
CUL1	8,25	-2,05	7	0
HSPH1	6,47	-2,06	1	0
HNRNPA0	6,93	-2,10	1	0
CAAP1	6,82	-2,10	0	0
RPL22L1	8,40	-2,11	2	0
CSNK2A1;CSNK2A3	7,11	-2,16	1	0
RNF2	6,76	-2,18	1	0
LARP7	7,53	-2,20	1	0
PSMD3	6,07	-2,25	1	0
DDX21	8,86	-2,25	10	0
MEPCE	7,49	-2,26	2	0
IQGAP1	7,68	-2,27	2	0
HMGN2	7,20	-2,30	0	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
RPS19BP1	7,29	-2,31	3	0
WDR46	7,76	-2,32	1	0
NAT10	7,77	-2,34	1	0
FCF1	7,14	-2,38	1	0
DARS	6,60	-2,39	1	0
TCEB3	7,41	-2,41	3	0
RPF1	7,71	-2,44	1	0
TOP1	8,71	-2,46	10	0
RPS9	8,64	-2,48	7	0
MAFK	8,07	-2,51	3	0
ZNF593	8,32	-2,51	1	0
SIRT7	8,01	-2,52	4	0
FBL	7,81	-2,53	4	0
KRT1	9,58	-2,54	22	0
NOP14	7,10	-2,58	1	0
MARK2	6,86	-2,61	0	0
CDC2L1;CDK11B;CDK11A	7,65	-2,61	1	0
CSTF3	7,33	-2,61	0	0
MCM5	7,25	-2,61	1	0
DDX41	8,19	-2,62	10	0
PRPF3	8,53	-2,62	6	0
RPL27	8,74	-2,63	5	0
DNMT1	7,34	-2,63	1	0
NUP93	6,83	-2,65	0	0
VIM	6,51	-2,65	1	0
RPS14	8,56	-2,66	6	0
RPL11	7,83	-2,74	2	0
FRG1	8,39	-2,76	7	0
PDS5B	6,80	-2,79	0	0
BLM	7,27	-2,81	0	0
CDC2;CDK1	7,15	-2,86	0	0
ALYREF	8,26	-2,87	2	0
KRT2	8,91	-2,89	7	0
POP1	7,63	-2,91	1	0
DDX56	7,74	-3,07	1	0
PRPF4	8,57	-3,08	10	0
CPSF1	8,30	-3,13	6	0
CSNK1A1	7,09	-3,22	1	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
SNRPB2	9,22	-3,24	9	0
MCM4	7,16	-3,29	0	0
RCC1	7,98	-3,29	2	0
CCDC59	7,47	-3,31	1	0
MECP2	8,15	-3,36	2	0
GRWD1	8,19	-3,37	4	0
SMARCA4	7,28	-3,42	3	0
RPL22	8,69	-3,47	2	0
TP53BP1	7,67	-3,48	1	0
SKIV2L2	7,36	-3,51	0	0
ATP5B	7,09	-3,52	7	0
SMARCA5	7,93	-3,61	5	0
HMGB1	7,42	-3,73	3	0
DIAPH3	8,37	-3,89	0	0
PDS5A	7,24	-3,99	0	0
MORF4L1	7,71	-4,19	3	0
DDX18	8,37	-4,32	2	0
RPL9	8,14	-4,40	1	0
MYBBP1A	8,44	-4,42	1	0
NO66	7,97	-4,49	2	0
HIST1H1B	9,38	-4,65	4	0
CLK3	7,68	-4,79	0	0
DDX47	7,89	-4,93	1	0
TSR1	7,89	-5,46	0	0

Table 7.4: Values corresponding to Figure 4.6.B. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
POLR2I	8,91	9,35	8	2
POLR2D	8,55	8,66	8	2
POLR2C	8,97	8,46	13	2
POLR2J;POLR2J3	8,52	8,03	10	2
POLR2G	8,31	8,00	9	2
POLR2A	9,84	7,58	114	2
TCEA1	8,09	7,54	14	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GTF2F1	8,42	7,43	22	2
GTF2F2	8,48	7,35	13	2
POLR2E	9,06	7,20	11	2
RPRD2	7,83	7,05	13	2
INTS6	7,79	7,02	21	2
INTS9	7,79	6,91	12	2
POLR2F	8,03	6,86	5	2
ASUN	7,71	6,50	15	2
POLR2H	8,70	6,49	10	2
RPRD1B	7,90	6,34	11	2
INTS4	7,30	5,91	11	2
MED17	7,40	5,85	11	2
CPSF3L	7,46	5,83	9	2
POLR2B	9,59	5,78	76	2
PAF1	7,61	5,17	16	2
MED21	7,35	4,96	2	1
VIM	7,84	4,89	18	1
INTS5	6,83	4,78	2	1
IXL;MED29	7,39	4,77	5	1
RECQL5	7,54	4,60	5	1
MED14	7,50	4,58	15	1
INTS1	7,33	4,38	11	1
MED8	7,10	4,32	3	1
MED22	7,21	4,24	4	1
CDC73	7,37	4,16	16	1
MED23	6,89	4,12	4	1
RPRD1A	7,23	4,09	6	1
MED16	6,84	4,05	3	1
MED20	7,21	4,03	4	1
MED1	7,22	3,99	6	1
TCEA3	7,45	3,94	5	1
INTS10	7,13	3,94	8	1
POLR2K	7,18	3,86	3	1
BRD2	7,44	-4,36	3	1
C19orf53	7,60	-4,84	1	1
DDX18	8,36	-4,88	3	1
PLEC	7,31	-5,09	4	1
MORF4L1	7,70	-5,45	3	1

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NSUN2	7,97	-5,51	4	1
TRMT112	8,35	-5,65	2	1
CUL1	8,17	-5,67	5	1
PPP2R1A	7,62	4,00	12	0
PABPC1;PABPC3	7,63	3,80	12	0
INTS8	7,31	3,77	6	0
BCLAF1	7,37	3,73	3	0
PPP2CB	7,33	3,70	7	0
SUPT6H	7,91	3,65	27	0
INTS7	7,21	3,63	8	0
MED11	7,12	3,60	3	0
CCDC12	6,66	3,56	4	0
RPS12	8,25	3,55	7	0
MED4	7,14	3,46	3	0
MED27	7,13	3,38	3	0
MED10	7,09	3,38	2	0
CTR9	7,04	3,36	12	0
RPS2	8,51	3,35	12	0
SERBP1	7,53	3,33	9	0
SUPT5H	7,67	3,29	12	0
RPS23	8,47	3,25	6	0
SETD2	6,95	3,16	11	0
MED15	6,98	3,15	4	0
SRSF6	7,78	3,07	6	0
RPS27	8,06	2,96	5	0
PABPC4	6,76	2,95	2	0
RPS16;ZNF90	8,57	2,78	15	0
CHTOP	7,24	2,73	3	0
RBM22	6,96	2,73	7	0
INTS2	6,88	2,69	6	0
MED7	6,82	2,65	3	0
PPIL1	7,03	2,60	4	0
MED30	6,81	2,56	3	0
SCAF8	7,22	2,56	5	0
XAB2	6,94	2,54	8	0
RPS28	7,50	2,53	7	0
EIF3B	7,10	2,49	7	0
RPS18	8,54	2,41	12	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RBM8A	7,54	2,39	4	0
EIF3I	7,07	2,38	3	0
SRSF10	6,96	2,36	4	0
EIF3A	6,74	2,35	10	0
PHF5A	7,27	2,34	4	0
RPS27L	7,43	2,30	2	0
RPS8	8,79	2,29	15	0
MYH9	7,10	2,28	16	0
BCAS2	7,07	2,26	4	0
MYEF2	6,63	2,26	2	0
ELL	6,58	2,25	5	0
RPL12	7,45	2,22	5	0
ERH	7,87	2,21	5	0
EIF3C;EIF3CL	7,14	2,20	8	0
G3BP1	6,72	2,19	3	0
SMARCB1	6,82	2,12	2	0
MED19	7,04	2,11	5	0
SCAF4	8,18	2,10	8	0
EIF4G1	6,98	2,09	5	0
CWC15	7,16	2,05	5	0
PHF3	6,70	2,04	3	0
PNN	7,77	1,97	12	0
EIF3F	6,94	1,94	5	0
RNPS1	7,61	1,94	6	0
CDC40	7,02	1,91	7	0
RBM10	6,78	1,89	5	0
RPL14	7,22	1,89	3	0
CAPRIN1	6,80	1,89	2	0
PCF11	7,07	1,87	4	0
PPIL3	6,38	1,84	2	0
SNRNP40	7,53	1,83	7	0
DDX39A	7,10	1,82	3	0
EIF3H	6,91	1,81	3	0
VWA9	6,29	1,81	3	0
SNW1	7,35	1,79	9	0
PABPN1	7,07	1,79	3	0
TRA2B	7,50	1,76	5	0
RPS21	6,95	1,75	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GRB10	7,55	1,74	5	0
NCL	9,12	1,74	11	0
RPS20	8,13	1,72	6	0
EIF3M	6,39	1,70	2	0
RPLP2	7,68	1,70	4	0
SNRPF	7,27	1,68	3	0
IWS1	7,30	1,67	8	0
ACO2	6,43	1,66	2	0
MATR3	7,90	1,65	14	0
NOLC1	8,25	1,65	6	0
SAP18	7,52	1,62	6	0
SNRPE	7,38	1,62	2	0
MTA2	7,38	1,60	6	0
EIF3E	6,98	1,60	3	0
HDLBP	6,64	1,56	2	0
RBMX	8,54	1,56	22	0
MAGOH;MAGOHB	6,84	1,55	4	0
THOC7;NIF3L1BP1	6,65	1,54	3	0
BUD31	6,88	1,54	4	0
CCAR1	7,07	1,53	3	0
DDX46	7,15	1,52	8	0
SRRT	7,98	1,48	18	0
RBM4	6,45	1,48	4	0
XRN2	7,52	1,46	6	0
RPS26;RPS26P11	8,46	1,45	5	0
CCT3	7,10	1,44	6	0
SAFB	7,39	1,43	4	0
GNL3L	6,43	1,42	2	0
BUD13	6,64	1,41	2	0
HNRNPM	8,37	1,41	23	0
SRSF1	7,64	1,38	9	0
TARDBP	7,61	1,36	6	0
GTF2I	7,49	1,36	12	0
SAP30BP	7,10	1,34	5	0
SYNCRIP	6,90	1,34	6	0
HNRNPH1	7,87	1,33	6	0
UBTF	7,65	1,33	10	0
SF1	7,36	1,31	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MFAP1	7,82	1,31	13	0
EWSR1	7,17	1,30	5	0
SRSF11	6,99	1,30	3	0
PCBP2;Isoform	7,41	1,29	4	0
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	7,00	1,29	2	0
RPS11	8,98	1,28	12	0
PRPF6	7,66	1,28	17	0
TUBB2A	7,27	1,28	3	0
EFTUD2	8,02	1,27	19	0
EIF4A3	7,83	1,27	10	0
THRAP3	7,75	1,26	5	0
RPL10	7,87	1,25	9	0
PKM	6,65	1,23	3	0
THOC2	6,47	1,21	2	0
GATAD2B	6,95	1,20	7	0
THOC3	6,66	1,19	3	0
PYCR1	7,12	1,19	3	0
RPS17	8,75	1,18	13	0
NCBP1	6,82	1,18	3	0
SNRPD3	7,89	1,17	3	0
LMNB1	7,76	1,15	14	0
YBX3	8,54	1,13	1	0
RUNX2	6,95	1,13	2	0
DDX17	8,14	1,13	13	0
RPS27A;UBB;UBC;UBA52	8,55	1,13	8	0
DDX42	6,70	1,13	4	0
SNRNP200	7,94	1,12	26	0
RPL28	7,93	1,10	6	0
ZC3H18	7,32	1,09	5	0
RANGAP1	6,73	1,09	2	0
ELAVL1	7,66	1,07	8	0
RPL31	9,11	1,07	8	0
PRPF19	7,85	1,05	9	0
RPLP0;RPLP0P6	7,64	1,04	4	0
KTN1	6,57	1,04	3	0
LUC7L3	7,27	1,03	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PPP1CB	6,92	1,03	3	0
DCD	7,52	1,01	2	0
RPS19	8,68	1,01	11	0
LYAR	8,09	1,00	4	0
PRPF38A	7,03	0,99	2	0
POLDIP3	7,33	0,99	7	0
CRNKL1	6,75	0,98	5	0
ARGLU1	8,49	0,98	8	0
SNRNP70	7,71	0,98	13	0
PRPF40A	7,92	0,97	15	0
RPS4X	9,08	0,96	16	0
SRRM2	7,64	0,96	9	0
PLRG1	7,04	0,95	5	0
ILF3	7,35	0,94	6	0
RPL24	8,59	0,94	9	0
CBX3	7,48	0,94	5	0
MYO1G	6,58	0,93	2	0
PPP1R10	6,55	0,91	5	0
PRPF8	8,02	0,90	35	0
EEF1G	6,67	0,88	4	0
CHERP	7,48	0,85	8	0
RPL23	8,48	0,85	8	0
RPL17;RPL17-C18orf32	8,72	0,83	13	0
HNRNPF	7,80	0,82	5	0
RUVBL2	7,85	0,81	14	0
YTHDC1	6,65	0,80	2	0
EIF4B	6,65	0,80	4	0
LRRC59	7,11	0,79	3	0
ETF1	6,42	0,79	2	0
TCF7	7,49	0,78	1	0
SRSF7	7,69	0,77	5	0
SREK1	6,97	0,77	5	0
RBM25	7,85	0,77	13	0
NOP10	6,90	0,76	2	0
SF3B6	6,93	0,75	3	0
RPL13	7,95	0,75	8	0
EEF1A1;EEF1A1P5	8,47	0,74	11	0
POGZ	6,64	0,73	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PHF2	6,94	0,73	2	0
HDGFRP2	7,16	0,72	4	0
RP9	6,98	0,70	2	0
KHDRBS1	7,59	0,69	2	0
SF3A1	7,71	0,69	10	0
RPS24	8,58	0,69	8	0
DNAJA2	7,17	0,68	6	0
HNRNPA3	7,67	0,67	2	0
ACIN1	7,59	0,65	4	0
RPS5	8,51	0,62	13	0
TCEB2	6,93	0,61	2	0
DDX39B	7,50	0,61	9	0
RPS13	8,80	0,61	9	0
ZRANB2	7,57	0,61	9	0
CSTF2	7,10	0,60	3	0
TCF7	7,86	0,60	2	0
DDX3X;DDX3Y	8,63	0,58	24	0
TUBA1B	7,96	0,57	9	0
RUVBL1	7,93	0,57	11	0
TRA2A	6,77	0,57	2	0
HNRNPDL	6,87	0,56	3	0
RPS15A	8,64	0,55	6	0
RBM17	6,95	0,55	5	0
NHP2L1	7,67	0,55	7	0
NXT1	6,72	0,53	2	0
UTP14A	7,08	0,53	3	0
KIF4A;KIF4B	6,43	0,51	3	0
SF3B4	7,07	0,51	3	0
TUBB4B	7,82	0,51	9	0
HAUS8	7,30	0,51	2	0
SNRPB;SNRPN	7,74	0,50	3	0
RBM15	7,12	0,50	8	0
CWC25	6,92	0,50	4	0
EIF6	7,30	0,48	3	0
HNRNPK	8,22	0,47	20	0
DNAJA1	7,44	0,47	6	0
NMT1	6,59	0,46	3	0
RPL38	7,84	0,45	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EDC4	6,51	0,42	5	0
HIST1H3A;H3F3C	9,55	0,42	9	0
IK	7,13	0,41	4	0
TCP1	6,73	0,41	6	0
RRP12	7,24	0,40	3	0
RAE1	6,47	0,39	2	0
UPF3B	7,20	0,38	4	0
PSMC3	6,38	0,38	2	0
RPL35A	7,36	0,36	3	0
PPIG	7,24	0,36	5	0
SNRNP27	7,30	0,35	4	0
HNRNPAB	7,21	0,35	3	0
RPL13A;RPL13a	7,36	0,34	2	0
RBBP7	7,15	0,33	2	0
INTS3	6,98	0,32	6	0
TRRAP	6,40	0,30	2	0
SF3A2	7,34	0,29	7	0
H1F0	8,72	0,29	7	0
DDX23	7,54	0,27	12	0
SMNDC1	7,06	0,25	6	0
RALY	7,67	0,24	3	0
PHGDH	6,65	0,23	2	0
LUC7L	8,08	0,23	5	0
CHD1	6,76	0,22	2	0
HCFC1	6,88	0,22	5	0
HNRNPL	8,49	0,22	15	0
LUC7L2	8,58	0,22	11	0
RPL36	7,73	0,22	4	0
HIST1H1E;HIST1H1D	9,91	0,21	20	0
MAP7	7,01	0,21	3	0
HELLS	6,99	0,20	3	0
EIF3D	7,17	0,20	6	0
PRDX1	7,33	0,20	2	0
SF3A3	7,41	0,20	10	0
RPS3	8,70	0,20	17	0
SON	7,90	0,20	9	0
PPP1CC	6,90	0,18	3	0
SNRPD2	7,88	0,17	5	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
PQBP1	7,06	0,17	2	0
SHMT2	6,79	0,16	2	0
DYNLL1	7,54	0,16	2	0
RBM14	7,63	0,16	8	0
RPS6	9,20	0,15	17	0
SRSF3	8,10	0,14	7	0
RPL4	7,88	0,14	6	0
AQR	6,99	0,13	5	0
RPS3A	9,32	0,13	18	0
CTNNBL1	6,85	0,12	4	0
DHX9	8,14	0,12	17	0
ACTB	8,48	0,11	11	0
KIF22	6,86	0,11	3	0
CPSF7	6,48	0,11	2	0
SF3B2	7,93	0,10	16	0
RPL34	7,82	0,09	4	0
HNRNPA1;HNRNPA1L2	7,86	0,08	5	0
FIP1L1	8,06	0,07	4	0
RPS14	8,77	0,07	8	0
MYL6	6,86	0,06	3	0
SRSF5	7,20	0,05	3	0
GTPBP4	7,40	0,05	5	0
RTF1	6,88	0,04	5	0
ACTL6A	6,73	0,04	4	0
EIF3L	6,60	0,03	2	0
HSPA9	7,42	0,03	11	0
NGDN	7,42	0,01	2	0
HNRNPR	7,16	0,01	7	0
KPNB1	6,73	-0,01	3	0
PCBP1	8,41	-0,01	12	0
SMARCC2	6,79	-0,03	2	0
RPS25	8,91	-0,04	8	0
NSD1	7,10	-0,04	1	0
RPL37A	8,23	-0,04	4	0
HSPA8	8,60	-0,04	23	0
ARL6IP4	7,06	-0,04	2	0
RBM39	8,60	-0,05	18	0
HNRNPA2B1	7,97	-0,05	11	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPL6	8,30	-0,05	6	0
CREB1	7,78	-0,06	3	0
CSTF1	7,19	-0,06	3	0
SMU1	7,47	-0,07	6	0
FAM76B	6,51	-0,08	3	0
CALML5	7,00	-0,09	4	0
DENND2D	6,82	-0,09	2	0
DRG1	6,52	-0,10	4	0
SRP72	8,02	-0,12	17	0
CDC5L	8,02	-0,13	13	0
RBBP4	7,66	-0,13	9	0
ABCE1	6,60	-0,14	3	0
RPL27A	7,95	-0,14	3	0
RPL36A;RPL36A-HNRNPH2	8,67	-0,14	8	0
BRD7	6,79	-0,15	4	0
UTP3	7,57	-0,16	2	0
HSP90AA1	6,70	-0,18	2	0
NUP93	7,00	-0,18	5	0
RPL22L1	8,55	-0,18	2	0
TMPO	7,07	-0,18	2	0
FAU	8,43	-0,19	4	0
RPL11	8,01	-0,20	5	0
DDX54	7,53	-0,20	2	0
NUMA1	6,65	-0,22	3	0
PPP2R1B	6,80	-0,22	4	0
PTBP1	7,56	-0,23	6	0
HIST1H2AC	9,62	-0,23	6	0
RPSA	7,95	-0,24	8	0
HDAC1	7,16	-0,25	4	0
HIST1H2BC	9,91	-0,27	15	0
TCEB1	7,20	-0,27	3	0
VEZF1	7,44	-0,28	5	0
PRPF4B	7,96	-0,28	10	0
NOL10	7,12	-0,28	3	0
SRP14	7,80	-0,29	3	0
WWP2	7,85	-0,29	11	0
NXF1	6,98	-0,29	3	0
FCF1	7,29	-0,29	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPL32	7,98	-0,30	5	0
U2SURP	7,53	-0,32	6	0
RPL39P5;RPL39	8,47	-0,32	1	0
HNRNPC	8,47	-0,32	9	0
SRSF2	7,75	-0,32	4	0
SSB	7,57	-0,34	3	0
NPM1	8,89	-0,34	11	0
SFSWAP	6,82	-0,34	3	0
SF3B3	8,21	-0,35	18	0
ATP5A1	7,00	-0,35	5	0
DDX5	9,09	-0,37	24	0
SLC25A5	7,10	-0,38	2	0
HIST1H4A	9,75	-0,38	14	0
RPL18A	7,58	-0,39	3	0
ZNF593	8,46	-0,39	2	0
KPNA2	7,34	-0,39	3	0
SFPQ	8,33	-0,40	15	0
HNRNPA3	8,22	-0,41	8	0
SART1	7,68	-0,41	11	0
DHX15	7,93	-0,41	14	0
POLR1A	6,91	-0,43	3	0
CPSF6	8,19	-0,43	7	0
PYCR2	6,65	-0,44	2	0
CPSF3	7,64	-0,44	8	0
CBX5	6,66	-0,45	3	0
GNL3	7,95	-0,45	1	0
EPB41	7,19	-0,47	2	0
PPP1CA	7,46	-0,47	9	0
SREK1IP1	7,16	-0,48	2	0
GTF2B	8,02	-0,48	11	0
KRT1	9,71	-0,49	41	0
SP1	7,83	-0,49	4	0
CWC22	6,58	-0,50	3	0
KLF13	8,27	-0,51	10	0
MEPCE	7,61	-0,52	4	0
PA2G4	6,51	-0,52	3	0
TUBB	7,14	-0,53	2	0
SUB1	7,89	-0,53	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
FAM120A	7,23	-0,54	7	0
BUB3	7,75	-0,54	8	0
FXR2	7,18	-0,56	4	0
SNIP1	7,97	-0,56	7	0
GLYR1	7,99	-0,56	7	0
KRT2	9,05	-0,56	26	0
SAMD1	6,86	-0,57	2	0
ZSCAN26;ZNF187	7,50	-0,58	3	0
NONO	8,00	-0,59	10	0
RBM27	8,19	-0,60	10	0
TCF7;TCF7L2	8,46	-0,60	6	0
PUF60	8,26	-0,61	17	0
U2AF2	8,92	-0,62	19	0
SP2	7,79	-0,62	5	0
GAPDH	7,13	-0,64	4	0
FTSJ3	8,22	-0,66	8	0
RPL35	8,88	-0,68	5	0
WTAP	6,58	-0,68	2	0
RBBP6	7,59	-0,70	5	0
SMAD3	7,07	-0,71	4	0
WBP11	8,37	-0,72	11	0
RTCB	6,78	-0,72	2	0
CTNNB1	7,10	-0,72	3	0
HSP90AB1	8,08	-0,75	14	0
CDC2L1;CDK11B;CDK11A	7,76	-0,75	9	0
LSM14B	7,21	-0,76	3	0
PARP1	7,87	-0,78	9	0
RBM28	7,48	-0,79	4	0
U2AF1	8,89	-0,79	10	0
RPL3	8,45	-0,80	12	0
HNRNPU	8,88	-0,81	17	0
REXO4	8,07	-0,84	4	0
RPL21	7,86	-0,85	3	0
RPL23A	9,89	-0,86	16	0
ZFP91;ZFP91-CNTF	7,90	-0,90	5	0
TCERG1	7,11	-0,90	3	0
SMC3	7,58	-0,91	11	0
DEK	7,49	-0,94	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MCM4	7,28	-0,94	5	0
DDX27	7,36	-0,95	2	0
RFC4	6,98	-0,96	2	0
HP1BP3	7,96	-0,96	7	0
RPS15	8,43	-0,97	6	0
H2AFV;H2AFZ	7,94	-0,98	2	0
ZNF281	7,83	-0,99	4	0
ALYREF	8,35	-1,00	7	0
RPL15	7,90	-1,01	3	0
SND1	6,56	-1,01	2	0
YBX1	10,19	-1,03	35	0
CPSF4	7,57	-1,04	4	0
RPL7A	8,91	-1,05	14	0
MCM3	7,06	-1,06	7	0
NOP14	7,18	-1,07	3	0
WDR46	7,83	-1,07	2	0
RPS7	9,31	-1,07	16	0
SMARCC1	7,40	-1,08	7	0
RPL8	8,97	-1,08	12	0
SYMPK	6,88	-1,09	3	0
DSP	6,93	-1,10	4	0
RBPJ	7,18	-1,10	4	0
RPL26	9,09	-1,11	14	0
HSPD1	7,17	-1,12	5	0
SF3B1	8,22	-1,13	22	0
WDR43	6,76	-1,13	2	0
NACA	7,75	-1,14	4	0
RPS9	8,71	-1,14	15	0
RPL19	8,89	-1,15	10	0
RPL22	8,79	-1,16	6	0
FAM32A	7,97	-1,16	5	0
DDX41	8,26	-1,16	16	0
DDX52	7,14	-1,16	4	0
HNRNPUL2;HNRNPUL2-BSCL2	8,69	-1,18	19	0
RPL7	7,51	-1,19	2	0
RRP36	6,89	-1,20	2	0
MCM7	7,20	-1,21	2	0
CPSF2	7,77	-1,21	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SRRM1	7,99	-1,22	5	0
TOP2A	7,77	-1,23	11	0
NOP56	7,26	-1,24	4	0
MCM2	7,18	-1,25	4	0
GNL2	7,66	-1,27	6	0
SMC4	6,62	-1,27	2	0
KPNA3	7,02	-1,29	3	0
JUP	7,12	-1,31	2	0
DIMT1	8,54	-1,33	13	0
ABCF2	7,13	-1,33	5	0
SMC2	7,06	-1,35	3	0
SP3	7,90	-1,36	4	0
TRIP12	7,09	-1,36	4	0
MCM6	7,05	-1,36	5	0
SSRP1	7,96	-1,37	11	0
DHX8	7,27	-1,37	6	0
ZNF148	7,67	-1,38	8	0
NOP58	7,07	-1,39	3	0
H2AFY	8,07	-1,39	8	0
TCEB3	7,46	-1,39	3	0
WBSCR22	8,19	-1,40	2	0
EBNA1BP2	7,71	-1,43	3	0
CHD4	7,50	-1,44	12	0
EIF4A1	7,26	-1,44	5	0
METAP1	7,99	-1,45	6	0
LEO1	7,19	-1,49	2	0
PRPF31	8,00	-1,51	7	0
SMC1A	7,34	-1,52	9	0
PPIH	7,69	-1,53	6	0
DCAF13	8,35	-1,55	8	0
EMG1	7,33	-1,56	3	0
RPL5	8,63	-1,58	10	0
NOP2	7,76	-1,58	3	0
PES1	7,73	-1,59	4	0
RPL10A	7,96	-1,60	5	0
SNRPD1	7,83	-1,60	2	0
DDX21	8,88	-1,60	13	0
WDR33	7,89	-1,62	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DNMT1	7,38	-1,63	4	0
RPL30	9,18	-1,65	8	0
POP1	7,68	-1,65	4	0
EEF2	7,25	-1,67	4	0
CSNK2A1;CSNK2A3	7,13	-1,68	3	0
RSBN1	7,68	-1,68	5	0
SRP68	7,77	-1,72	9	0
VRK1	7,02	-1,73	3	0
RNF2	6,77	-1,73	3	0
EIF2S3;EIF2S3L	8,35	-1,77	11	0
SUPT16H	8,21	-1,77	16	0
MAFG	8,33	-1,77	9	0
RPL27	8,77	-1,78	6	0
SMARCA4	7,33	-1,79	5	0
RCC2	8,27	-1,80	11	0
RRP7A;RRP7BP	7,18	-1,80	1	0
MAZ	8,92	-1,83	11	0
SLTM	7,72	-1,84	3	0
SNRPA1	9,42	-1,85	18	0
ZNF787	8,01	-1,86	4	0
FBL	7,84	-1,87	3	0
WDR82	6,51	-1,87	2	0
TOP2B	6,72	-1,87	2	0
ZNF524	7,21	-1,88	2	0
CSTF3	7,35	-1,90	4	0
MORF4L2	7,70	-1,93	5	0
ZNF771	8,11	-1,93	6	0
EIF2S1	8,11	-1,94	6	0
ILF2	6,95	-1,98	2	0
CTCF	9,53	-2,03	28	0
KIAA0020	8,82	-2,03	8	0
PSIP1	8,03	-2,03	7	0
RPL9	8,20	-2,03	4	0
RAN	7,32	-2,06	3	0
RPS10;RPS10-NUDT3	8,43	-2,06	9	0
C9orf114	7,39	-2,11	3	0
RPS19BP1	7,28	-2,15	2	0
MCM5	7,26	-2,15	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PRPF3	8,54	-2,16	15	0
GRWD1	8,22	-2,17	7	0
TRIM28	7,37	-2,18	4	0
WDR5	7,09	-2,21	5	0
CDK13	7,60	-2,24	2	0
FRG1	8,40	-2,26	8	0
NUDT21	7,60	-2,30	3	0
HIST1H1B	9,43	-2,33	6	0
ZFX;ZFY	7,50	-2,40	2	0
SLK	7,37	-2,40	2	0
DDX49	6,94	-2,40	2	0
EIF2S2	7,86	-2,41	5	0
MAFK	8,07	-2,41	5	0
DDX6	6,93	-2,44	2	0
KRR1	8,09	-2,45	5	0
TOP1	8,71	-2,45	14	0
HMGA1	8,86	-2,46	6	0
CSNK1A1	7,11	-2,46	2	0
ATP5B	7,12	-2,48	3	0
BTF3	7,33	-2,51	3	0
RRS1	7,69	-2,57	2	0
SMARCA5	7,96	-2,60	11	0
PRPF4	8,58	-2,62	15	0
PHF6	9,19	-2,64	15	0
SKIV2L2	7,38	-2,69	5	0
ZNF740	7,27	-2,69	3	0
TP53BP1	7,68	-2,75	5	0
CXorf56	7,08	-2,75	2	0
NSUN5	7,72	-2,77	3	0
WWP1	7,45	-2,79	5	0
MECP2	8,15	-2,86	6	0
DDX55	7,97	-2,87	4	0
ERI1	8,27	-2,97	3	0
NAP1L1	7,50	-2,99	2	0
LARP7	7,49	-3,01	2	0
MICU1	7,29	-3,12	2	0
TSR1	7,92	-3,14	2	0
HSPA5	7,42	-3,18	4	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
SNRPB2	9,21	-3,26	10	0
NO66	7,99	-3,33	1	0
YARS	7,55	-3,36	6	0
IQGAP1	7,64	-3,38	4	0
ABCF1	7,70	-3,48	3	0
DDX56	7,73	-3,49	2	0
FIZ1	8,30	-3,50	4	0
NAT10	7,73	-3,52	4	0
RCC1	7,97	-3,58	2	0
PATZ1	8,11	-3,59	6	0
IGKV2D-29;IGKV2D-26	7,83	-3,62	2	0
ZNF652	7,67	-3,71	4	0
ZNF319	8,44	-3,77	6	0
MYBBP1A	8,44	-3,81	4	0
C19orf43	7,37	-3,82	2	0
ZNF444	8,09	-3,92	3	0
CPSF1	8,28	-3,99	6	0
SIRT7	7,96	-4,07	3	0
DDX47	7,89	-4,40	2	0

Table 7.5: Values corresponding to Figure 4.6.C. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
GTF2F1	8,54	10,27	23	2
GTF2F2	8,98	10,17	18	2
POLR2J;POLR2J3	8,37	9,32	16	2
POLR2C	8,98	9,31	13	2
POLR2I	8,40	9,03	10	2
POLR2D	8,20	9,02	13	2
INTS6	8,10	8,68	41	2
POLR2E	9,06	8,39	16	2
INTS4	8,08	8,35	34	2
INTS3	8,02	7,71	31	2
POLR2G	7,88	7,62	10	2

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
ASUN	8,03	7,46	31	2
MED14	7,94	7,39	44	2
POLR2H	8,44	7,37	8	2
INTS2	7,74	7,33	19	2
INTS9	7,63	7,27	15	2
POLR2B	9,91	7,23	105	2
INTS5	7,73	7,12	14	2
INTS10	7,71	7,03	16	2
SON	7,54	7,00	14	2
RECQL5	7,80	6,95	11	2
RPRD2	7,70	6,93	20	2
POLR2F	7,63	6,85	5	2
INTS8	7,76	6,84	19	2
MED17	7,79	6,84	18	2
MED8	7,81	6,82	10	2
MED15	7,33	6,81	13	2
TCEA1	7,82	6,72	22	2
RPRD1B	7,93	6,69	16	2
MED1	7,79	6,67	34	2
TCEA3	7,83	6,46	12	2
MED4	7,63	6,35	11	2
INTS1	8,21	6,23	42	2
CPSF3L	7,56	6,22	12	2
INTS7	7,85	6,21	18	2
POLR2K	7,47	5,97	3	2
MED16	7,36	5,91	11	2
MED23	7,59	5,90	31	2
MED6	7,51	5,81	4	2
VWA9	7,43	5,69	13	2
INTS12	7,18	5,62	8	2
MED27	7,34	5,50	6	2
MED7	7,33	5,48	8	2
POLR2A	10,02	5,41	141	2
PPP2R1A	7,64	5,17	24	2
MED24	7,24	5,06	16	2
MED26	7,10	5,06	7	2
SRSF4	7,23	4,96	3	2
RPRD1A	7,22	4,73	9	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
IXL;MED29	7,06	4,61	6	2
FABP5	6,98	4,57	5	2
TRRAP	7,03	4,45	25	2
MED20	7,05	4,42	6	2
CALML5	7,11	4,40	5	2
MED18	7,07	4,35	6	2
THOC1	7,13	4,32	16	2
GATAD2B	7,80	4,17	10	2
NUP155	6,80	4,15	8	2
PHF2	6,84	4,08	9	2
MED25	6,83	4,07	6	2
SRSF5	6,91	4,03	5	2
XAB2	7,02	3,96	15	2
MED31	6,79	3,93	4	2
RPAP2	6,92	3,93	4	2
MED22	6,97	3,92	6	2
DSP	7,91	3,86	71	2
C7orf26	6,93	3,77	5	2
PGAM5	6,79	3,77	4	2
WDR82	7,19	3,75	8	2
GTF2E2	6,82	3,75	4	2
JUP	7,57	3,67	20	2
MED10	6,78	3,67	4	2
BCAS2	6,74	3,67	10	2
THOC5	7,10	3,66	10	2
SUPT5H	7,83	3,62	26	2
CSTA	6,87	3,60	4	2
DHX16	6,79	3,59	6	2
PPP2R1B	6,82	3,58	8	2
DSG1	7,40	3,56	17	2
JARID2	6,87	3,51	3	2
ISY1	6,71	3,47	7	2
DKFZp434B156;WDR92	6,77	3,46	4	2
C11orf31;SELH	6,82	3,40	3	2
PPP2CB	7,30	3,40	11	2
BCLAF1	7,34	3,38	9	2
MDN1	6,74	3,38	8	2
DKC1	7,20	3,32	12	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CRNKL1	7,18	3,25	18	2
PHF3	6,73	3,20	11	2
SERBP1	7,56	3,18	18	2
LYZ	7,11	3,11	4	2
MED12;TNRC11	6,79	3,09	14	2
DDX42	7,19	3,05	10	2
CASP14	6,71	3,03	10	2
EIF3A	7,58	2,99	46	2
HADHB	6,61	2,99	6	2
GPN1	6,63	2,93	3	2
UPF1	6,47	2,92	13	2
CDKN2AIP	6,61	2,90	5	2
IGHA1;IGHA2	6,63	2,90	5	2
EIF3G	6,62	2,86	7	2
KPNA3	6,65	2,84	7	2
GNB2	6,73	2,83	4	2
BPTF	6,64	2,79	8	2
PELP1	6,57	2,77	3	2
RPLP2	7,28	2,76	6	2
SNRPE	7,21	2,74	3	2
NCOA5	6,52	2,74	6	2
RBM22	6,94	2,69	12	2
SERPINB12	6,50	2,68	5	2
ERCC2	6,52	2,67	7	2
ANXA2;ANXA2P2	6,63	2,66	9	2
PRMT1	6,50	2,66	5	2
RAD50	6,39	2,65	4	2
RBM10	7,02	2,63	11	2
TAF15	7,56	2,61	5	2
VDAC1	6,39	2,56	4	2
CCT7	6,58	2,56	9	2
SCAF8	7,13	2,56	12	2
GNAI2	7,16	2,55	9	2
WDR3	6,68	2,53	3	2
CNOT1	6,45	2,52	20	2
SNRNP40	7,90	2,51	15	2
SHMT2	6,40	2,51	4	2
SFSWAP	6,37	2,49	4	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
THOC6	6,92	2,48	7	2
WTAP	6,52	2,47	4	2
EWSR1	7,55	2,46	7	2
STAG2	6,52	2,46	14	2
DDX50	6,97	2,46	9	2
CLP1	6,85	2,45	8	2
CCT6A	6,55	2,44	6	2
G3BP1	6,49	2,43	7	2
ZC3H11A	6,64	2,42	4	2
SBSN	6,51	2,40	3	2
SAP18	7,57	2,38	13	2
MED28	6,54	2,37	4	2
MAGOH;MAGOHB	6,90	2,34	7	2
EIF3L	7,08	2,34	16	2
KTN1	6,47	2,34	8	2
TGM3	6,45	2,32	10	2
MED30	6,50	2,29	3	2
RBM5	6,73	2,29	8	2
DARS	6,36	2,28	7	2
MED19	6,76	2,27	4	2
SRSF10	6,87	2,26	5	2
HSP90AA1	6,48	2,25	7	2
PRRC2C	7,07	2,24	15	2
CD2BP2	6,41	2,24	3	2
ANXA1	6,40	2,23	6	2
EIF3F	7,11	2,23	7	2
SNRPD3	7,75	2,22	5	2
EIF3E	7,22	2,21	14	2
EIF3I	7,19	2,18	9	2
PPP1R10	6,99	2,16	7	2
EIF3M	6,61	2,15	3	2
TRA2B	7,71	2,14	10	2
CHTOP	6,93	2,14	3	2
PLRG1	7,19	2,13	14	2
NUSAP1	6,95	2,13	2	2
ALDH18A1	7,01	2,11	13	2
SUZ12	6,34	2,11	6	2
ARID1A	6,57	2,09	13	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MTA1	6,36	2,08	6	2
C17orf85	6,39	2,07	7	2
SMARCB1	6,51	2,06	5	2
THOC3	6,96	2,05	6	2
NCBP1	7,21	2,03	11	2
GTF2E1	6,09	2,00	2	2
REXO1	6,35	1,99	5	2
PABPC1;PABPC3	7,29	1,97	13	2
EIF3C;EIF3CL	7,35	1,96	18	2
SRSF6	7,09	1,96	6	2
EIF4B	6,92	1,93	10	2
BUD13	6,71	1,91	7	2
HSPD1	7,02	1,86	14	2
ZFX;ZFY	7,30	-2,59	7	2
ZSCAN25	6,74	-3,23	2	2
RPS12	7,51	2,10	11	1
MATR3	7,87	2,05	22	1
PNN	7,88	2,04	23	1
PCF11	7,43	2,00	17	1
SRSF1	7,73	1,99	10	1
NOP58	7,53	1,96	10	1
XRN2	7,81	1,95	23	1
THOC7;NIF3L1BP1	6,51	1,93	5	1
RPS28	6,44	1,88	5	1
TCP1	6,60	1,85	10	1
CHD8	6,44	1,84	7	1
EIF4G2	6,37	1,83	9	1
GTF2H4	6,51	1,82	8	1
ATP5C1	6,42	1,75	3	1
RPL12	7,20	1,75	7	1
SF3B6	6,77	1,75	7	1
EIF3H	7,07	1,74	6	1
RPL14	7,20	1,74	3	1
KPNA4	6,36	1,72	4	1
RBM8A	7,12	1,71	6	1
CDC40	6,76	1,70	8	1
BYSL	6,91	1,69	10	1
SNW1	7,45	1,68	19	1

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CWC22	7,07	1,67	12	1
PAXBP1	6,36	1,67	5	1
CDK7	6,49	1,66	2	1
TMPO	6,83	1,66	8	1
RBM4	6,41	1,65	6	1
CSNK2A2	6,97	1,64	7	1
GAPDH	7,24	1,63	10	1
CCT2	6,49	1,62	6	1
PHB	6,80	1,62	6	1
SMARCD2	6,69	1,61	8	1
CBX3	7,41	1,61	12	1
FEN1	6,89	1,61	5	1
PBRM1	6,29	1,60	11	1
THOC2	7,19	1,60	29	1
RUNX2	6,41	1,59	3	1
PHB2	6,74	1,59	7	1
CWC15	7,20	1,58	6	1
PPIL1	6,73	1,58	6	1
PYCR2	6,73	1,58	4	1
TAF6	6,71	1,52	9	1
GTF2H2C;GTF2H2	6,56	1,52	5	1
ACTL6A	6,83	1,49	3	1
HDAC2	6,57	1,48	5	1
DRG1	6,85	1,47	8	1
DNAJA2	6,92	1,46	10	1
POGZ	6,41	1,46	7	1
CCT3	6,81	1,45	14	1
KIAA1429	6,87	1,44	23	1
EIF4G1	6,97	1,42	18	1
RTF1	7,16	1,40	16	1
PPP1CB	6,89	1,39	4	1
ATP5A1	6,93	1,38	10	1
MBD3	6,44	1,38	4	1
CAPRIN1	6,80	1,35	6	1
SND1	6,91	1,33	12	1
CENPV	7,11	1,32	3	1
VDAC2	6,77	1,32	3	1
RAD21	6,52	1,29	8	1

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ARG1	7,09	1,28	9	1
EIF3B	7,03	1,27	11	1
MRTO4	7,01	1,27	6	1
SF3B4	6,98	1,24	4	1
ETF1	6,47	1,24	7	1
RANGAP1	6,72	1,23	7	1
SLC25A5;SLC25A6	7,16	1,21	8	1
ATP5B	7,08	1,20	9	1
EPB41L5	6,78	-1,20	4	1
S100A8	6,47	-1,30	1	1
DENND2D	6,61	-1,35	2	1
FBXL6	7,04	-1,44	2	1
RBPJ	7,23	-1,49	8	1
DOT1L	6,69	-1,56	3	1
NOL12	6,94	-1,57	4	1
YY1	6,84	-1,58	2	1
POLR1A	7,39	-1,59	20	1
RPL7L1	7,40	-1,73	3	1
CMSS1	7,30	-1,76	2	1
SMCHD1	7,26	-1,76	14	1
MPHOSPH10	7,31	-1,83	4	1
PRDM10	6,67	-1,97	3	1
DNMT1	7,78	-2,13	12	1
CCT4	6,32	2,28	6	0
CUL3	6,28	2,27	7	0
ZNHIT6	6,31	2,20	3	0
SUGP1	6,31	2,17	5	0
G3BP2	6,29	2,12	3	0
EIF4A3	8,19	2,10	23	0
RPS2	8,20	2,07	13	0
UBTF	7,95	2,03	38	0
CBX8	6,32	1,95	5	0
MED13	6,27	1,93	6	0
HNRNPM	8,19	1,90	32	0
RPL38	7,82	1,88	5	0
CAT	6,21	1,84	6	0
SSRP1	8,34	1,84	35	0
PRPF19	7,87	1,82	13	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ICE1	6,26	1,82	4	0
LTV1	6,25	1,79	5	0
NOP56	7,50	1,76	15	0
RPLP0;RPLP0P6	7,80	1,69	6	0
CCAR2	6,25	1,68	3	0
TFIP11	6,29	1,68	5	0
LGALS7	6,25	1,68	5	0
SCAF4	8,17	1,66	13	0
DYNC1H1	6,22	1,61	10	0
RBBP5	6,31	1,60	3	0
EFTUD2	8,13	1,60	37	0
GTF2I	7,52	1,55	30	0
CCDC12	6,10	1,55	1	0
UBAP2L	6,27	1,52	5	0
SLU7	6,27	1,52	5	0
CSNK2A1;CSNK2A3	7,75	1,51	13	0
ERH	7,44	1,51	7	0
RNGTT	6,32	1,49	5	0
NCL	9,02	1,49	19	0
PRPF6	7,82	1,48	33	0
PRPF8	8,55	1,48	114	0
VDAC3	6,16	1,46	4	0
RNPS1	7,70	1,44	7	0
EIF3K	6,27	1,42	4	0
HSP90AB1	7,74	1,42	25	0
EIF4A1	7,64	1,42	16	0
RPS18	8,34	1,41	21	0
CSNK1D;CSNK1E	6,10	1,41	3	0
MTA2	7,44	1,41	18	0
HIST1H2AJ;HIST1H2AH; H2AFJ;HIST1H2AG	8,51	1,40	2	0
NUP93	7,42	1,40	21	0
AFF4	6,08	1,38	3	0
SETD2	6,32	1,38	5	0
DDOST	6,14	1,37	4	0
PKP1	6,23	1,36	5	0
TXN	6,25	1,36	5	0
AP2A1	6,30	1,36	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GATAD2A	6,18	1,33	3	0
SIN3A	6,14	1,33	3	0
EPRS	6,13	1,32	5	0
PTBP1	7,84	1,32	10	0
SRP14	7,75	1,30	4	0
DDX39B	8,08	1,29	21	0
RBM14	7,96	1,29	23	0
KHDRBS1	7,92	1,29	9	0
RPS8	8,62	1,28	18	0
GNL3L	6,24	1,27	3	0
HIST1H2AC	9,77	1,24	11	0
POLE	6,21	1,24	6	0
CDC5L	7,92	1,24	27	0
KIF4A	6,10	1,22	5	0
NOLC1	8,44	1,22	7	0
DSC1	7,26	1,22	9	0
UTP6	6,15	1,20	4	0
UPF2	6,17	1,19	7	0
RBBP4	7,87	1,18	12	0
PABPC4	6,15	1,18	3	0
RPL7	7,73	1,18	10	0
PRDX2	6,21	1,18	6	0
RUVBL2	7,90	1,17	28	0
CNOT8	6,10	1,17	3	0
C14orf166	6,42	1,16	6	0
PAF1	7,31	1,15	14	0
ACIN1	7,97	1,15	24	0
HELLS	7,29	1,14	11	0
RBM15	7,39	1,14	14	0
CTNNBL1	6,80	1,13	7	0
CDK9	6,87	1,12	11	0
ZRANB2	7,65	1,12	9	0
ZCCHC8	6,48	1,11	2	0
LIG1	5,95	1,11	4	0
ARHGEF2	6,15	1,11	3	0
NIPBL	6,11	1,10	4	0
GRB10	7,59	1,09	8	0
EEF1A1;EEF1A1P5	8,37	1,09	17	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
AQR	7,32	1,09	25	0
HSPB1	6,22	1,08	3	0
KRT1	10,12	1,07	73	0
SMARCD1	6,10	1,07	3	0
ADNP	6,23	1,07	6	0
RPS16;ZNF90	8,22	1,07	15	0
SRSF7	7,77	1,07	11	0
RBMX2	6,71	1,07	5	0
TUBB4B;TUBB4A	7,34	1,04	16	0
SNRNP70	7,84	1,04	21	0
PCNA	6,59	1,04	5	0
CDC73	7,31	1,04	20	0
RBMX	8,61	1,03	23	0
LRRC59	6,93	1,03	5	0
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	6,94	1,03	5	0
HNRNPA3	7,88	1,03	2	0
DSC3	6,01	1,03	3	0
POLR1C	7,01	1,02	4	0
CFAP20	7,57	1,01	9	0
MNAT1	6,36	1,01	4	0
ENO1	6,26	1,01	9	0
FBXO28	6,82	1,01	11	0
MRPL46	7,59	1,01	2	0
LMNB1	7,19	1,00	15	0
RPL23	8,07	1,00	10	0
SF3A2	7,48	1,00	12	0
NOP10	6,19	1,00	6	0
FUS	7,71	1,00	7	0
RPS13	8,71	0,99	13	0
TRA2A	6,15	0,98	3	0
RPS27	7,62	0,98	8	0
PWP1	7,27	0,98	2	0
WDR61	6,51	0,97	5	0
API5	6,64	0,97	6	0
WHSC1	6,49	0,96	4	0
ASCC3	5,93	0,96	8	0
SRRM2	7,86	0,96	14	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RBM17	7,31	0,95	13	0
EXOSC7	6,48	0,95	3	0
DMAP1	6,62	0,95	9	0
FNBP4	6,22	0,95	3	0
KAT7	6,17	0,95	5	0
RPL10	7,65	0,94	13	0
DCD	7,79	0,94	4	0
RFC5	7,02	0,93	8	0
NVL	6,27	0,93	5	0
CTSD	6,25	0,93	6	0
SMU1	7,57	0,93	16	0
ELL	6,32	0,93	3	0
CCT8	6,89	0,93	9	0
SNRPC	6,69	0,93	4	0
TUBB	7,11	0,92	5	0
ATRX	6,22	0,92	4	0
VRK1	7,26	0,92	6	0
PSMD2	6,19	0,92	4	0
TAF1;TAF1L	6,27	0,92	9	0
RBM6	6,40	0,92	6	0
HNRNPF	7,89	0,91	10	0
SYF2	6,50	0,91	3	0
DDX39A	7,21	0,91	9	0
WDR43	6,87	0,91	5	0
VCP	6,12	0,90	3	0
HNRNPK	8,36	0,90	28	0
TUBA1B	7,67	0,90	11	0
DHX30	6,34	0,90	9	0
SF3A3	7,60	0,89	12	0
SRSF11	6,35	0,89	3	0
DDX23	7,78	0,89	35	0
ACO2	6,13	0,89	3	0
RPS23	8,03	0,89	9	0
ARID2	6,32	0,88	7	0
CFL1	6,19	0,88	2	0
RBM25	7,92	0,88	30	0
UTP18	7,39	0,88	6	0
CHD4	7,95	0,87	55	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DHX15	8,27	0,87	39	0
RPS27L	7,06	0,87	3	0
NCCRP1	6,14	0,85	4	0
RPP40	7,05	0,85	2	0
EIF6	7,47	0,83	3	0
CDC27	6,01	0,83	4	0
ILF3	7,66	0,83	13	0
BLMH	6,77	0,82	7	0
RPL15	7,78	0,82	14	0
SF3A1	7,99	0,82	33	0
KIF2C	6,62	0,82	5	0
ANP32B	6,98	0,81	3	0
ACTB	8,48	0,81	19	0
SRRT	8,00	0,80	31	0
PSMD11	6,07	0,80	3	0
BUD31	6,38	0,80	6	0
IGKV2D-29;IGKV2D-26	8,14	0,80	3	0
HSPA9	7,13	0,80	12	0
HNRNPD	7,06	0,80	7	0
RUVBL1	7,93	0,79	26	0
RPS4X	9,24	0,79	26	0
TAF9	6,60	0,79	6	0
HNRNPH1	7,83	0,78	7	0
DDX17	8,24	0,78	22	0
ERCC3	6,88	0,78	8	0
RPS5	8,57	0,78	15	0
DHX9	8,44	0,77	33	0
RPS27A;UBB;UBC;UBA52	8,61	0,77	11	0
FBLL1	7,33	0,76	2	0
POLR1B	6,38	0,76	5	0
DHX33	6,27	0,76	4	0
LYAR	8,24	0,76	7	0
CTNNB1	7,01	0,76	13	0
HAL	6,02	0,75	4	0
CIRH1A	6,56	0,75	3	0
CCNT1	6,03	0,75	3	0
ZKSCAN1	6,65	0,75	2	0
SUPT16H	8,54	0,75	58	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ACTR8	6,08	0,74	4	0
PPP1CA	7,28	0,74	12	0
CSTF1	7,55	0,74	12	0
EIF3D	7,18	0,74	9	0
TARDBP	7,45	0,73	6	0
RNPC3	6,20	0,73	3	0
FBL	8,14	0,73	16	0
EXOSC1	6,22	0,73	3	0
ZNF197	6,50	0,72	2	0
SAFB	7,29	0,72	9	0
IK	7,23	0,72	12	0
DNAJA1	7,51	0,72	14	0
RAE1	6,65	0,72	8	0
RNF2	7,15	0,72	7	0
RPP30	7,45	0,71	5	0
PRPF38A	7,32	0,71	7	0
CHD1L	6,09	0,71	5	0
HDLBP	6,28	0,70	6	0
RPS3	9,18	0,70	25	0
AHCY	6,02	0,70	3	0
CCNL1	6,37	0,70	4	0
HIST1H4A	9,85	0,69	19	0
RPS10;RPS10-NUDT3	8,65	0,69	17	0
LSG1	6,15	0,69	4	0
WWP2	8,07	0,69	22	0
CHMP4B	6,65	0,69	3	0
DDX47	8,23	0,68	15	0
PCBP2;PCBP3	7,40	0,68	4	0
IWS1	7,47	0,68	9	0
AURKB	7,19	0,68	6	0
NOP16	6,52	0,67	4	0
PARP1	8,20	0,67	17	0
DYNLL1	7,77	0,67	7	0
FYTTD1	6,88	0,66	2	0
PCID2	6,42	0,65	4	0
RPL10A	8,17	0,65	14	0
MAPK1	6,02	0,64	3	0
EEF1G	6,66	0,64	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPL24	8,56	0,64	14	0
CDC42	6,05	0,63	2	0
LARP1	6,69	0,63	8	0
HNRNPA2B1	7,93	0,63	16	0
PYCR1	7,08	0,63	3	0
PPP1CC	6,95	0,63	2	0
ZC3H13	6,52	0,63	4	0
CCAR1	7,10	0,63	11	0
ZC3H14	6,34	0,62	6	0
POLDIP3	7,48	0,62	11	0
UTP15	6,93	0,62	6	0
HEATR1	6,08	0,62	3	0
RPL18A	7,42	0,62	7	0
SNRPB;SNRPN	8,00	0,61	7	0
YTHDF3	6,00	0,61	3	0
SRFBP1	6,90	0,61	2	0
SRP54	6,01	0,60	3	0
GTPBP4	7,58	0,60	14	0
PWP2	5,93	0,59	3	0
RPL35A	7,13	0,59	4	0
RPS29	6,73	0,59	1	0
MRPL40	6,83	0,58	2	0
HADHA	6,50	0,58	2	0
DDX6	7,15	0,58	9	0
PABPN1	6,93	0,58	3	0
WAPAL	6,15	0,57	3	0
CSTF3	7,73	0,57	22	0
BUB3	8,05	0,56	12	0
ANAPC7	6,16	0,56	5	0
DUT	6,08	0,56	3	0
RALY	7,79	0,56	5	0
FUBP3	6,11	0,56	3	0
OGT	6,40	0,55	7	0
EXOSC9	6,41	0,55	4	0
RPS15	8,41	0,55	8	0
EEF1D	6,59	0,55	4	0
ABCE1	6,45	0,55	7	0
SNRPF	6,97	0,55	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
YWHAE	6,49	0,54	3	0
DDX1	6,71	0,54	6	0
RPUSD4	6,71	0,53	5	0
PRPF18	6,01	0,53	3	0
ELAVL1	7,69	0,53	11	0
CPSF4	8,00	0,53	12	0
MCM7	7,45	0,53	12	0
THAP11	6,06	0,53	2	0
PHF5A	6,75	0,53	4	0
GNB2L1	6,93	0,52	11	0
HNRNPR	7,35	0,52	9	0
RPL4	7,93	0,52	18	0
HIST2H3A;HIST1H3A; *HIST3H3*	9,39	0,52	15	0
THRAP3	7,71	0,52	13	0
HNRNPA3	8,36	0,52	25	0
RPS19	8,52	0,51	15	0
MEN1	6,09	0,51	3	0
PLEC	7,49	0,51	11	0
LUC7L3	7,24	0,51	13	0
C1orf131	7,17	0,51	2	0
RPL6	8,29	0,51	10	0
ITCH	6,07	0,50	6	0
RFC2	7,03	0,50	5	0
DDX52	7,36	0,50	7	0
GTF2B	8,15	0,50	17	0
MRPL48	7,23	0,49	3	0
FXR1	6,58	0,49	5	0
SRBD1	7,06	0,49	10	0
SART1	7,98	0,48	20	0
BTF3	7,30	0,48	5	0
SMARCE1	6,88	0,48	7	0
EXOSC4	6,59	0,48	3	0
ANP32E	5,99	0,48	3	0
CHD1	6,72	0,47	14	0
RPS11	8,88	0,47	26	0
PURB	6,09	0,47	3	0
DHX35	6,53	0,46	7	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
RPL26	9,26	0,46	23	0
WRNIP1	6,00	0,46	4	0
TUFM	6,26	0,46	5	0
REXO4	8,15	0,46	7	0
SNRPD2	7,82	0,45	12	0
HDGFRP2	7,45	0,45	8	0
H1F0	8,67	0,45	8	0
BOD1L1	7,02	0,45	3	0
RCL1	6,99	0,45	6	0
DNAJB11	6,87	0,45	5	0
RFC3	7,08	0,45	9	0
SRP72	8,09	0,44	28	0
RRP12	7,26	0,44	11	0
DDX5	9,27	0,44	50	0
H2AFV;H2AFZ	8,03	0,44	3	0
TCEB2	6,81	0,43	5	0
HNRNPL	8,40	0,43	19	0
RFC4	7,18	0,43	7	0
NPM1	9,20	0,43	21	0
RPS20	7,77	0,42	6	0
ZNF207	7,22	0,42	3	0
SYNCRIP	6,70	0,42	7	0
WDR48	6,09	0,42	4	0
SEH1L	6,38	0,41	2	0
RAC1	6,23	0,41	5	0
MMTAG2	7,05	0,41	6	0
DIS3	6,08	0,40	4	0
SAP30BP	7,58	0,40	12	0
RPL37A	7,82	0,40	5	0
RPL13	7,78	0,40	10	0
RIOK2	6,33	0,40	4	0
MYO1G	6,26	0,40	5	0
CPSF7	6,51	0,40	4	0
WDR5	7,40	0,39	9	0
NONO	8,28	0,39	24	0
RPS15A	8,60	0,39	15	0
RPL9	8,47	0,39	12	0
RPP25L	6,54	0,38	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNRPD1	7,60	0,38	4	0
GTPBP1	6,85	0,38	7	0
CDC2L1;CDK11B;CDK11A	8,17	0,38	24	0
CMAS	7,19	0,37	8	0
NELFCD;TH1L	6,20	0,36	3	0
CHERP	7,54	0,36	15	0
DHX38	6,25	0,35	6	0
MTPAP	6,13	0,35	3	0
TRMT10C	7,15	0,33	4	0
YARS	7,52	0,33	20	0
MARK2	7,31	0,33	13	0
KDM1A	6,32	0,33	6	0
RPL19	8,75	0,32	19	0
USP39	7,24	0,31	9	0
EXOSC6	6,81	0,31	4	0
PA2G4	6,04	0,31	3	0
POLR1D	6,93	0,30	4	0
BCL7C;BCL7B	6,74	0,30	2	0
U2SURP	7,72	0,30	31	0
MYEF2	6,05	0,30	3	0
PPIH	7,81	0,29	12	0
HDAC1	7,29	0,29	12	0
AEBP2	6,17	0,29	2	0
ZC3H18	7,36	0,29	12	0
RBBP7	7,24	0,29	5	0
DDX41	8,43	0,29	46	0
CSNK1A1	7,26	0,29	10	0
RBMXL1	6,86	0,29	1	0
CDC2;CDK1	7,45	0,29	7	0
PSMC2	5,99	0,28	4	0
ABCF2	7,35	0,28	16	0
CDC20	6,10	0,27	3	0
PSMD3	6,22	0,27	5	0
RPL23A	9,87	0,27	26	0
RPL11	8,31	0,26	12	0
WDR46	7,95	0,25	9	0
KIF2A	6,82	0,25	6	0
TSR1	8,24	0,25	11	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HNRNPA1;HNRNPA1L2	7,99	0,24	9	0
STRBP	6,49	0,24	7	0
PPIB	6,81	0,24	5	0
C1QB	7,33	0,24	2	0
NUP107	6,66	0,24	3	0
SET;SETSIP	6,95	0,24	3	0
DDX21	9,13	0,24	26	0
RPS3A	9,64	0,24	26	0
RPL3	8,55	0,23	19	0
PRPF40A	7,74	0,23	17	0
KPNB1	6,72	0,23	6	0
BAZ1B	6,00	0,22	4	0
RBM42	6,92	0,22	3	0
RPL28	7,41	0,22	7	0
RBM15B	6,18	0,22	3	0
FIP1L1	8,16	0,21	13	0
PRMT5	6,04	0,21	4	0
BHLHA15	6,81	0,21	3	0
NUDT21	7,90	0,20	11	0
SF3B2	8,14	0,20	24	0
NAP1L1	7,66	0,19	9	0
RPS7	9,35	0,19	35	0
SRSF3	7,98	0,19	10	0
TRAP1	5,93	0,19	3	0
YLPM1	7,25	0,19	12	0
EPB41	7,38	0,18	11	0
TOP2B	7,14	0,18	27	0
NT5E	6,21	0,18	3	0
RPL21	7,68	0,18	9	0
SF1	7,31	0,18	8	0
UPF3B	7,37	0,17	7	0
CPSF6	8,00	0,17	20	0
HMGB2	7,03	0,17	4	0
MCM3	7,23	0,17	10	0
RCC1	8,19	0,17	8	0
TRIM28	7,32	0,16	16	0
THYN1	6,68	0,16	1	0
CGGBP1	6,63	0,16	3	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
RQCD1	6,21	0,16	3	0
SLTM	7,99	0,15	20	0
TCEANC2	6,45	0,14	3	0
LUC7L	8,53	0,14	21	0
MAP7	7,32	0,14	7	0
UTP14C	6,51	0,14	2	0
CLTC	7,64	0,13	40	0
MFAP1	7,93	0,13	17	0
RPL27A	8,00	0,13	4	0
NHP2L1	7,22	0,13	7	0
SMARCC1	7,62	0,13	30	0
METAP1	8,09	0,12	8	0
ZCCHC17	6,29	0,12	2	0
LUC7L2	8,44	0,12	15	0
ESF1	6,86	0,11	4	0
WDR12	6,34	0,11	3	0
PRDX1	6,86	0,11	4	0
EXOSC2	6,81	0,10	7	0
GLYR1	7,93	0,10	16	0
DDX3X;DDX3Y	8,67	0,10	35	0
ZNF593	8,61	0,10	4	0
MAT2A	6,70	0,10	4	0
AP2M1	6,39	0,09	3	0
ATP5O	6,44	0,09	2	0
RPS24	8,47	0,09	8	0
PRPF3	8,87	0,09	39	0
HNRNPA0	7,01	0,09	4	0
TAF5	6,88	0,09	9	0
USP10	5,87	0,09	3	0
SCAF11	7,47	0,08	6	0
RPS25	8,58	0,08	15	0
RPL29	8,03	0,08	3	0
CDCA8	6,85	0,08	2	0
SRPK1	7,55	0,07	10	0
MCM5	7,41	0,07	21	0
NXF1	7,40	0,07	4	0
PPIL3	5,95	0,07	3	0
LSM14B	7,29	0,07	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SRP68	7,86	0,07	24	0
SKIV2L2	7,62	0,06	23	0
FAM133A	7,14	0,06	3	0
C9orf114	7,65	0,06	8	0
KIF22	6,89	0,06	6	0
HBS1L	5,88	0,05	2	0
POP4	6,53	0,05	3	0
FXR2	7,45	0,05	14	0
RPL13A;RPL13a	6,98	0,05	3	0
RPS21	6,17	0,05	2	0
RAN	7,14	0,04	6	0
ARPC4;ARPC4-TTLL3	5,57	0,04	2	0
EMG1	7,59	0,04	8	0
SF3B1	8,51	0,04	56	0
RPL17;RPL17-C18orf32	8,74	0,04	20	0
H2AFY	8,43	0,04	11	0
HP1BP3	8,36	0,04	16	0
SKP1	7,38	0,04	8	0
PRRC2A	6,65	0,04	11	0
HIST1H1E;HIST1H1D	10,29	0,04	29	0
KPNA2	7,50	0,03	7	0
CSTF2	7,13	0,03	4	0
HNRNPLL;HNRPLL	6,28	0,03	5	0
SDAD1	7,65	0,02	9	0
NAT10	7,96	0,02	30	0
MEAF6	6,57	0,02	3	0
RRP15	7,19	0,02	2	0
SNIP1	8,18	0,02	10	0
TEAD1;TEAD4;TEAD3	6,87	0,01	2	0
NIP7	6,62	0,01	3	0
NO66	8,03	0,01	8	0
HNRNPAB	7,08	0,01	6	0
SMC4	6,85	0,01	10	0
FAM76B	7,09	0,01	6	0
RP9	7,20	0,01	5	0
CXorf56	7,58	0,00	8	0
YTHDC1	6,07	-0,01	3	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
DDX55	8,06	-0,01	16	0
FAM120A	7,12	-0,01	16	0
CCNK	6,57	-0,01	2	0
BRD2	7,64	-0,02	18	0
SCAF1	7,21	-0,03	2	0
RRP7A;RRP7BP	7,68	-0,03	8	0
VIM	6,74	-0,03	8	0
HSPA5	7,47	-0,03	21	0
RPF2	7,53	-0,04	7	0
NEDD8;NEDD8-MDP1	6,41	-0,04	1	0
HNRNPC	8,67	-0,05	14	0
KRI1	6,67	-0,05	2	0
MOGS	7,15	-0,06	5	0
CDK12	6,52	-0,06	5	0
METTL17	7,04	-0,06	2	0
POLE3	6,27	-0,06	2	0
RPL27	8,82	-0,06	13	0
TRMT1L	6,64	-0,06	3	0
AGO2	6,59	-0,06	7	0
FRG1	8,70	-0,07	18	0
YBX3	8,50	-0,07	7	0
DDX10	7,36	-0,07	12	0
EED	6,65	-0,07	7	0
SMARCA2	6,11	-0,07	4	0
RBX1	6,80	-0,07	3	0
HSPA8	8,53	-0,08	34	0
RTCB	6,83	-0,08	8	0
ALKBH5	6,73	-0,08	6	0
EME1	6,21	-0,08	3	0
MORF4L1	7,88	-0,08	15	0
HIST1H1B	9,58	-0,08	7	0
MCM4	7,28	-0,09	16	0
PLK1	6,92	-0,09	8	0
ABT1	6,95	-0,09	3	0
ARGLU1	8,71	-0,09	18	0
RPS14	8,63	-0,10	11	0
SAMD1	6,86	-0,10	2	0
ZNF146	7,43	-0,11	9	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
TOP2A	8,04	-0,11	40	0
IGKV4-1	7,88	-0,11	3	0
DCAF13	8,65	-0,11	15	0
RRP36	7,08	-0,12	3	0
DDX49	7,15	-0,12	8	0
SYMPK	7,58	-0,12	15	0
UHRF1	7,11	-0,12	6	0
SRSF2	7,88	-0,12	9	0
SF3B3	8,31	-0,12	43	0
C4orf27	6,51	-0,13	3	0
LEO1	7,36	-0,13	8	0
MCM2	7,37	-0,14	17	0
RSL24D1	6,75	-0,14	3	0
RPL22L1	8,48	-0,14	4	0
MRPL22	6,41	-0,15	3	0
PPIL4	6,86	-0,15	6	0
SNRPB2	9,33	-0,15	16	0
ARRB2;DKFZp686L 0365	6,72	-0,15	4	0
CHMP2A	5,87	-0,15	2	0
DNAJC9	6,96	-0,16	3	0
NOB1	6,87	-0,16	4	0
BARX1	6,36	-0,16	3	0
DDX46	6,73	-0,16	9	0
USP7	6,90	-0,16	17	0
TCEB3	7,75	-0,16	11	0
ALYREF	8,75	-0,16	8	0
STK19	6,51	-0,16	2	0
ILF2	7,29	-0,16	10	0
NUP205	7,20	-0,17	16	0
NAA40	6,76	-0,17	3	0
TP53BP1	8,92	-0,17	22	0
DDX31	6,89	-0,17	5	0
NUDT16L1	6,05	-0,18	3	0
ARL6IP4	7,22	-0,18	5	0
DHX8	7,39	-0,18	24	0
DEK	7,57	-0,18	8	0
ERI1	8,58	-0,18	8	0
CWC25	6,61	-0,18	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SMC2	7,29	-0,18	11	0
KIF20B	5,96	-0,18	4	0
C19orf43	7,68	-0,19	8	0
RPS17	8,68	-0,19	16	0
FLOT2	6,01	-0,19	6	0
NOL10	7,28	-0,20	12	0
DDX18	8,52	-0,20	12	0
SMARCC2	6,63	-0,20	5	0
CPSF2	8,17	-0,20	25	0
TCF7	7,89	-0,21	2	0
CAD	6,10	-0,21	3	0
EXOSC8	6,47	-0,21	2	0
CPSF3	8,15	-0,21	19	0
NGDN	7,56	-0,22	4	0
NSUN5	7,69	-0,22	3	0
RCC2	8,29	-0,22	22	0
SNRNP27	6,96	-0,23	4	0
NET1	5,44	-0,23	2	0
MRGBP	6,75	-0,23	3	0
RPS19BP1	7,34	-0,23	5	0
CTR9	7,53	-0,23	21	0
PPIG	6,77	-0,23	6	0
RPL8	8,95	-0,24	15	0
PNO1	7,59	-0,24	5	0
SMC5	5,94	-0,25	3	0
DDB1	6,58	-0,25	8	0
LIG3	7,32	-0,26	2	0
MUTYH	6,56	-0,26	4	0
EEF2	7,20	-0,28	13	0
CKAP5	6,49	-0,28	11	0
SFPQ	8,59	-0,28	26	0
WWP1	7,72	-0,28	14	0
POLR1E	7,11	-0,28	2	0
RPS26;RPS26P11	8,08	-0,28	4	0
RPL34	7,17	-0,28	4	0
ABCF1	7,92	-0,28	15	0
MORF4L2	7,84	-0,29	11	0
LARP7	7,69	-0,29	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EIF1AX;EIF1AY	6,76	-0,29	4	0
NOM1	6,68	-0,29	3	0
NCBP2	6,22	-0,30	3	0
RPL5	8,81	-0,30	23	0
SMNDC1	7,38	-0,30	5	0
MEPCE	7,66	-0,30	6	0
NOP14	7,16	-0,30	9	0
SIRT7	8,16	-0,30	10	0
RPL22	8,74	-0,31	9	0
HMGB1	7,69	-0,32	9	0
RPL32	7,80	-0,32	10	0
U2AF2	8,57	-0,32	22	0
FCF1	7,33	-0,33	10	0
DNAJC13	6,05	-0,33	6	0
HCFC1	6,77	-0,33	7	0
C11orf57	6,69	-0,34	2	0
RPS9	8,80	-0,35	23	0
HNRNPUL2;HNRNPUL2-BSCL2	8,86	-0,35	33	0
TCF7	7,55	-0,36	2	0
RPL7A	9,14	-0,36	23	0
MRPL9	7,29	-0,36	4	0
HIST1H2BD;HIST1H2BH; HIST2H2BF	9,93	-0,37	20	0
NACA	8,06	-0,37	7	0
EIF5A;EIF5A2	6,37	-0,37	3	0
ZNF444	8,06	-0,37	5	0
RSBN1	7,94	-0,37	12	0
RBM27	7,99	-0,37	20	0
SMC1A	7,59	-0,38	43	0
SMC3	7,67	-0,38	44	0
PRPF4	8,82	-0,38	34	0
ZNF771	8,32	-0,38	13	0
RPL39P5;RPL39	8,24	-0,39	3	0
PDS5B	7,02	-0,40	13	0
PRPF31	7,98	-0,40	16	0
SSB	7,82	-0,40	4	0
SNRPA1	9,58	-0,41	30	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RPL31	8,78	-0,41	13	0
MYH9	6,71	-0,42	15	0
PSIP1	6,23	-0,42	2	0
CXXC1	6,77	-0,42	9	0
RPF1	7,83	-0,43	9	0
ZNF787	8,21	-0,44	10	0
MCM6	7,24	-0,45	13	0
WBP11	8,10	-0,45	16	0
ZNF691	6,72	-0,46	3	0
HNRNPU	8,90	-0,47	38	0
NOP2	7,91	-0,48	11	0
CREB1	7,72	-0,48	5	0
IMP4	7,81	-0,48	9	0
PKM	6,35	-0,48	3	0
PPAN-P2RY11;PPAN	7,05	-0,48	2	0
EIF2S1	8,26	-0,48	18	0
RPL18	6,76	-0,49	1	0
SMAD3	7,00	-0,49	8	0
USP3	7,11	-0,50	9	0
KLF13	8,45	-0,50	16	0
ARPC1B	6,52	-0,51	5	0
PDS5A	7,41	-0,51	22	0
TCEB1	7,26	-0,51	4	0
MINA	7,05	-0,52	3	0
TBP;TBPL2	6,85	-0,53	3	0
PCBP1	8,39	-0,54	10	0
SNRNP35	6,63	-0,54	2	0
SP2	7,86	-0,54	11	0
ATF2	6,06	-0,54	2	0
RBM28	7,32	-0,55	6	0
TRIP12	7,53	-0,57	29	0
GRWD1	8,30	-0,57	9	0
EIF2S2	7,85	-0,57	19	0
EBNA1BP2	7,54	-0,57	5	0
TAF4	6,41	-0,58	5	0
GNL3	8,16	-0,58	4	0
EIF2S3;EIF2S3L	8,35	-0,58	19	0
SUPT6H	8,56	-0,58	66	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
YBX1	10,38	-0,59	32	0
RPL36	7,49	-0,60	7	0
DIEXF	7,29	-0,60	7	0
KRR1	8,16	-0,60	8	0
NSA2	7,03	-0,61	5	0
ATF1	6,92	-0,61	1	0
EPB41L4B	6,95	-0,62	6	0
WBSCR22	8,47	-0,62	2	0
NUP85	5,98	-0,63	3	0
PSIP1	8,27	-0,63	22	0
MAZ	9,14	-0,63	19	0
ANKRD17	5,91	-0,64	3	0
NOL7	7,53	-0,64	4	0
SMARCA5	8,10	-0,64	39	0
UBA52	7,31	-0,65	3	0
SBNO1	6,28	-0,66	5	0
FAU	8,18	-0,66	4	0
SNRNP200	8,52	-0,66	85	0
SRP19	6,12	-0,67	3	0
C3	6,76	-0,67	3	0
DHX37	7,14	-0,67	10	0
MAFK	8,13	-0,68	10	0
TRMT112	8,19	-0,68	3	0
HSD17B10	6,49	-0,68	3	0
RPS6	9,29	-0,68	25	0
MECP2	8,57	-0,69	20	0
TCERG1	7,06	-0,69	6	0
TOP1	8,98	-0,70	38	0
RPL30	9,19	-0,70	12	0
RPL36A;RPL36A-HNRNPH2	8,50	-0,71	16	0
RASA1	6,65	-0,71	5	0
POP1	7,81	-0,71	9	0
NEIL1	7,68	-0,72	4	0
SRRM1	7,81	-0,72	10	0
PURA	6,57	-0,72	2	0
UTP3	7,62	-0,72	7	0
RBM26	7,73	-0,73	22	0
ZSCAN26;ZNF187	7,59	-0,73	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SREK1	6,36	-0,73	4	0
PHF6	9,49	-0,74	25	0
AATF	6,33	-0,75	4	0
DIMT1	8,90	-0,75	20	0
TCF7;TCF7L2	8,79	-0,75	9	0
EXOSC10	6,46	-0,76	4	0
ZNF740	7,57	-0,77	7	0
FTSJ3	8,15	-0,78	18	0
ZFP62	7,62	-0,78	1	0
PUF60	8,20	-0,78	21	0
LEF1	7,45	-0,79	2	0
U2AF1	8,68	-0,79	11	0
RPSA	7,99	-0,81	10	0
WDR33	8,35	-0,82	33	0
KIAA0020	8,90	-0,82	14	0
RBM39	8,37	-0,84	14	0
RPL35	8,48	-0,84	7	0
RBM19	6,08	-0,84	3	0
NMT1	6,32	-0,85	2	0
MAFG	8,32	-0,86	18	0
GNL2	7,80	-0,86	14	0
CBFB	6,62	-0,86	4	0
HMMR	6,48	-0,87	2	0
PLAG1	6,14	-0,87	2	0
COPA	5,92	-0,89	3	0
CLK3	7,91	-0,90	14	0
UTP23	7,90	-0,91	3	0
IKZF3	6,78	-0,92	1	0
FAM32A	7,87	-0,92	7	0
ZBTB14	5,85	-0,92	2	0
IMP3	7,02	-0,92	2	0
RSBN1L	7,74	-0,93	8	0
POLRMT	6,62	-0,94	3	0
TAF2	6,95	-0,95	9	0
CUL1	8,39	-0,96	33	0
KLF16	7,66	-0,96	1	0
BRD3	6,61	-0,97	2	0
DIDO1	6,64	-0,98	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EIF5B	6,83	-0,98	5	0
SMARCA4	7,58	-0,98	28	0
MICU1	7,21	-0,99	10	0
DGKZ	6,24	-1,01	3	0
PES1	7,88	-1,01	7	0
ZFP91;ZFP91-CNTF	7,90	-1,02	8	0
BLM	7,34	-1,02	7	0
EP300	6,08	-1,03	2	0
ZNF524	7,17	-1,04	3	0
TCOF1	8,38	-1,07	1	0
NSUN2	8,08	-1,07	13	0
DDX56	8,03	-1,07	9	0
TPR	7,23	-1,08	20	0
RRS1	7,46	-1,10	6	0
RBBP6	7,75	-1,10	13	0
ZNF652	7,73	-1,10	15	0
IQGAP1	7,71	-1,11	25	0
LBR	7,47	-1,12	1	0
SMC6	5,81	-1,12	3	0
SRP9	7,06	-1,12	4	0
HMGA1	8,16	-1,13	1	0
UTP14A	6,87	-1,15	3	0
BRIX1	7,29	-1,16	4	0
ZFR	7,02	-1,16	3	0
CPSF1	8,56	-1,16	41	0
SUB1	7,41	-1,17	6	0
CCDC59	7,66	-1,18	1	0
SLK	7,42	-1,19	8	0
HMGN2	7,25	-1,20	2	0
HMGA1	8,85	-1,21	11	0
PATZ1	8,11	-1,27	19	0
ZNF281	7,57	-1,31	3	0
ZNF148	7,84	-1,32	12	0
DDX27	7,28	-1,33	8	0
RPL37	7,72	-1,37	5	0
FIZ1	8,33	-1,40	12	0
SP3	7,94	-1,40	5	0
NUMA1	7,91	-1,49	23	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
ZNF319	8,54	-1,53	22	0
PRPF4B	8,13	-1,58	25	0
CDK13	7,74	-1,58	22	0
CTCF	9,61	-1,63	37	0
VEZF1	7,52	-1,63	8	0
ZNF48	8,19	-1,63	8	0
DIAPH3	8,76	-1,82	8	0
SPTBN1	5,78	-1,83	3	0
C19orf53	7,48	-1,89	3	0
MYBBP1A	8,66	-1,93	5	0
SP1	7,89	-2,05	8	0

7.3.3 Table with values corresponding to Figure 4.7 and Figure 4.9

Table 7.6: Values corresponding to Figure 4.7 and Figure 4.9. Values are sorted according to mean log2FC and p-value of MYC ON. Genes marked in bold were determined as significant RNAPII interactors in T-lymphoma cells according to the cutoffs: log2FC>2, q-value<0.1 and n>=3.

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	n (exp) MYC ON	mean log2FC MYC OFF	p-vlaue MYC OFF	q-value MYC OFF	n (exp) MYC OFF	Function
POLR2I	8,95	2,98E-15	1,56E-12	5	8,08	2,03E-09	6,73E-07	4	RNAPII
POLR2C	8,94	3,10E-15	1,56E-12	5	8,51	2,21E-09	6,73E-07	4	RNAPII
POLR2D	8,69	4,21E-15	1,56E-12	5	7,90	3,14E-09	6,73E-07	4	RNAPII
POLR2J;POLR2J3	8,73	8,65E-15	2,41E-12	5	7,99	5,47E-09	7,05E-07	4	RNAPII
POLR2G	8,18	1,28E-14	2,86E-12	5	7,01	1,15E-08	9,22E-07	4	RNAPII
GTF2F1	8,21	3,88E-14	6,17E-12	5	7,71	4,31E-09	6,94E-07	4	GTF
POLR2A	7,88	3,33E-14	6,17E-12	5	7,02	9,07E-09	9,22E-07	4	RNAPII
GTF2F2	8,41	8,30E-14	1,16E-11	5	7,59	1,05E-08	9,22E-07	4	GTF
POLR2E	7,41	2,40E-13	2,97E-11	5	6,69	5,13E-08	3,45E-06	4	RNAPII
TCEA1	7,04	7,33E-13	8,17E-11	5	7,00	1,34E-07	5,74E-06	4	EF
POLR2H	6,94	1,13E-12	1,14E-10	5	5,78	1,13E-07	5,18E-06	4	RNAPII
ASUN	7,19	7,64E-12	6,55E-10	5	6,25	2,67E-07	8,42E-06	4	Integrator
RPRD2	6,18	7,09E-12	6,55E-10	5	6,04	1,66E-07	6,67E-06	4	Other
INTS9	7,04	8,38E-12	6,67E-10	5	5,97	5,90E-08	3,45E-06	4	Integrator
POLR2B	6,27	1,36E-11	1,01E-09	5	5,16	2,52E-07	8,42E-06	4	RNAPII
INTS6	7,65	3,64E-11	2,53E-09	5	6,66	8,00E-08	4,05E-06	4	Integrator
INTS4	7,81	5,17E-11	3,39E-09	5	6,71	3,13E-07	9,16E-06	4	Integrator
POLR2F	6,60	8,10E-11	5,01E-09	4	5,83	6,42E-07	1,80E-05	4	RNAPII

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
MED14	6,11	1,55E-10	9,08E-09	4	5,00	6,75E-07	1,81E-05	4	Mediator
MED16	6,03	2,73E-10	1,52E-08	4	4,57	1,48E-06	3,53E-05	4	Mediator
MED23	6,42	3,04E-10	1,61E-08	4	4,84	2,72E-06	5,47E-05	4	Mediator
MED17	6,77	3,25E-10	1,64E-08	5	5,95	8,17E-08	4,05E-06	4	Mediator
RPRD1B	5,84	4,38E-10	2,12E-08	5	5,13	1,02E-06	2,63E-05	4	Other
IXL;MED29	4,92	4,63E-10	2,15E-08	5	4,34	6,20E-06	1,11E-04	4	Mediator
INTS5	6,55	5,30E-10	2,27E-08	5	6,08	2,75E-07	8,42E-06	4	Integrator
MED1	5,38	5,30E-10	2,27E-08	5	4,26	7,49E-06	1,24E-04	4	Mediator
CPSF3L	6,08	9,04E-10	3,73E-08	5	5,79	5,36E-08	3,45E-06	4	Integrator
INTS8	4,95	1,23E-09	4,90E-08	5	3,58	1,31E-05	2,00E-04	4	Integrator
MED22	5,05	1,45E-09	5,56E-08	4	4,68	1,15E-05	1,80E-04	4	Mediator
MED20	5,11	1,54E-09	5,74E-08	4	4,49	6,40E-06	1,11E-04	4	Mediator
INTS12	5,24	1,66E-09	5,98E-08	4	4,55	2,20E-06	4,72E-05	4	Integrator
POLR2K	4,86	3,41E-09	1,19E-07	4	5,00	3,32E-06	6,46E-05	3	RNAPII
INTS7	5,29	3,93E-09	1,33E-07	5	4,47	1,89E-06	4,19E-05	4	Integrator
INTS1	6,11	4,99E-09	1,63E-07	5	5,12	3,41E-06	6,46E-05	4	Integrator
MED27	4,64	6,41E-09	1,98E-07	5	4,04	2,65E-06	5,47E-05	4	Mediator
MED21	5,84	6,38E-09	1,98E-07	3	4,04	2,94E-04	3,21E-03	2	Mediator
INTS10	5,32	6,98E-09	2,10E-07	5	3,80	3,42E-05	5,00E-04	4	Integrator
MED4	5,17	9,76E-09	2,86E-07	4	4,50	1,20E-06	2,97E-05	4	Mediator
RPRD1A	4,52	1,04E-08	2,98E-07	4	2,95	2,02E-03	1,50E-02	2	Other
MED8	5,52	1,45E-08	4,03E-07	5	5,72	2,12E-07	7,60E-06	4	Mediator
MED6	5,16	1,84E-08	4,99E-07	3				0	Mediator
TCEA3	4,67	2,03E-08	5,38E-07	4	1,38	9,69E-02	2,36E-01	2	EF
MED10	4,21	2,44E-08	6,32E-07	4	3,22	4,18E-05	5,98E-04	4	Mediator
PPP2R1A	4,69	2,78E-08	7,05E-07	5	4,21	1,54E-06	3,53E-05	4	Other
MED15	4,58	3,20E-08	7,93E-07	4	3,79	5,11E-05	7,15E-04	3	Mediator
RECQL5	4,62	4,07E-08	9,86E-07	5	3,01	3,48E-04	3,74E-03	3	Other
SUPT6H	4,17	4,61E-08	1,09E-06	5	2,42	1,92E-03	1,47E-02	4	EF
MED24	4,76	5,88E-08	1,37E-06	3				0	Mediator
INTS2	5,26	7,54E-08	1,72E-06	4	4,20	7,01E-06	1,19E-04	4	Integrator
MED18	4,54	9,71E-08	2,16E-06	3				0	Mediator
MED7	3,95	1,43E-07	3,13E-06	4	3,10	2,74E-03	1,94E-02	2	Mediator
PPP2CB	4,07	1,51E-07	3,23E-06	5	3,14	1,02E-04	1,28E-03	4	Other
VWA9	5,87	2,37E-07	4,98E-06	4	5,39	2,04E-07	7,60E-06	4	Integrator
MED11	4,30	2,54E-07	5,25E-06	3				0	Mediator
SUPT5H	3,63	3,91E-07	7,93E-06	5	1,57	4,55E-02	1,42E-01	3	EF
PAF1	3,76	4,33E-07	8,46E-06	5	4,48	2,51E-05	3,77E-04	3	EF

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
MED26	4,14	4,67E-07	8,97E-06	3	2,29	3,65E-04	3,79E-03	4	Mediator
BCLAF1	3,46	5,07E-07	9,57E-06	4	2,98	2,00E-03	1,49E-02	2	Other
CDC73	3,76	5,77E-07	1,07E-05	4	3,07	2,14E-03	1,57E-02	4	EF
MED31	3,95	6,12E-07	1,12E-05	3	3,58	9,08E-05	1,22E-03	3	Mediator
MED30	3,06	2,18E-06	3,79E-05	4				0	Mediator
DYNC1H1	3,90	2,60E-06	4,45E-05	3				0	Other
CDKN2AIP	3,50	4,12E-06	6,95E-05	3	3,07	8,33E-04	7,77E-03	3	Other
RBM22	3,43	5,73E-06	9,52E-05	3	1,35	7,66E-02	2,02E-01	2	Splicing
PSMD11	3,28	7,94E-06	1,30E-04	3				0	Other
WDR92;DKFZp434B156	3,19	8,83E-06	1,43E-04	3				0	Other
CTR9	3,17	1,36E-05	2,17E-04	5	4,22	2,44E-04	2,71E-03	2	EF
SERBP1	2,97	1,45E-05	2,28E-04	4	2,20	9,11E-04	8,26E-03	4	Other
GTF2E1	3,16	1,93E-05	2,99E-04	3				0	GTF
RPAP2	3,16	2,11E-05	3,22E-04	3	3,72	3,57E-04	3,77E-03	3	Other
XAB2	3,03	2,15E-05	3,24E-04	4	2,49	6,48E-03	3,80E-02	2	Splicing
CCDC12	3,17	2,60E-05	3,86E-04	3	1,23	1,04E-01	2,48E-01	2	Other
ELL	2,51	3,99E-05	5,62E-04	4				0	EF
PCF11	2,26	4,34E-05	6,05E-04	5	0,73	1,38E-01	2,95E-01	4	Termination
MED19	2,24	6,14E-05	8,34E-04	5	2,45	1,64E-03	1,34E-02	4	Mediator
EIF3A	3,36	6,34E-05	8,51E-04	4				0	Other
SNRNP40	2,11	8,57E-05	1,11E-03	5	0,76	2,33E-01	4,24E-01	3	Splicing
PPP1R10	2,48	1,03E-04	1,29E-03	4	1,66	5,94E-02	1,68E-01	2	Other
CRNKL1	2,67	1,29E-04	1,54E-03	4				0	Splicing
SRSF10	2,32	1,36E-04	1,58E-03	4				0	Splicing
XRN2	2,08	1,59E-04	1,83E-03	5	0,64	1,76E-01	3,50E-01	4	Termination
BCAS2	2,16	1,74E-04	1,98E-03	4	0,91	2,32E-01	4,23E-01	2	Splicing
SRSF6	2,09	1,88E-04	2,12E-03	4	1,90	1,51E-02	6,81E-02	4	Splicing
EIF3B	2,43	2,15E-04	2,39E-03	3	1,47	1,40E-01	2,99E-01	2	Other
INTS3	3,33	2,23E-04	2,44E-03	5	1,87	2,55E-02	9,57E-02	4	Integrator
EWSR1	2,43	2,60E-04	2,81E-03	4	0,86	1,55E-01	3,19E-01	3	Other
DDX42	2,75	2,90E-04	3,10E-03	3				0	Other
THOC2	2,80	2,98E-04	3,16E-03	4	2,64	8,66E-03	4,69E-02	2	Other
MED25	2,48	3,17E-04	3,33E-03	3				0	Mediator
NCBP1	2,29	4,93E-04	4,82E-03	4	2,08	1,03E-02	5,31E-02	3	Other
TRRAP	2,94	5,79E-04	5,51E-03	3				0	Other
PSMC5	2,22	6,68E-04	6,10E-03	3	1,60	4,84E-02	1,48E-01	2	Other

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
GTF2H2C; GTF2H2	2,39	6,76E-04	6,12E-03	3				0	GTF
RBM10	2,19	7,72E-04	6,69E-03	4	1,49	5,52E-02	1,59E-01	2	Other
TAF15	2,44	8,08E-04	6,92E-03	3				0	GTF
GNAI3	2,23	2,44E-03	1,70E-02	3				0	Other
DSP	2,52	4,98E-03	2,85E-02	3	0,68	4,39E-01	6,31E-01	3	Other
VEZF1	-0,06	9,15E-01	9,54E-01	5	2,39	5,96E-04	5,73E-03	4	Other
SCAF8	1,93	9,79E-05	1,24E-03	5	2,21	1,52E-03	1,26E-02	4	EF
ZRANB2	1,21	1,67E-02	6,95E-02	4	2,21	1,69E-03	1,34E-02	4	Splicing
VIM	1,01	1,69E-01	3,35E-01	5	2,38	1,26E-02	6,04E-02	3	Other
THOC1	5,32	4,00E-07	7,95E-06	2				0	
C7orf26	5,04	1,01E-06	1,82E-05	2				0	
THOC6	3,44	6,70E-05	8,89E-04	2				0	
GNAI2	3,05	4,12E-04	4,11E-03	2				0	
MED28	3,05	3,74E-04	3,86E-03	2				0	
ARID1A	2,83	1,21E-03	9,45E-03	2	2,58	1,13E-02	5,66E-02	2	
MDN1	2,74	1,28E-03	9,83E-03	2				0	
CLP1	2,71	6,90E-04	6,20E-03	2				0	
PHB	2,62	9,29E-04	7,84E-03	2				0	
GTF2H4	2,60	2,66E-03	1,83E-02	2				0	
INIP	2,38	6,38E-03	3,43E-02	2				0	
KIAA1429	2,35	3,16E-03	2,08E-02	2				0	
RPAP3	2,30	4,40E-03	2,67E-02	2				0	
SMARCD2	2,23	4,04E-03	2,48E-02	2				0	
NCOA5	2,10	4,86E-03	2,83E-02	2				0	
POLR2L				0	6,46	9,06E-06	1,46E-04	2	
SETD2	2,00	1,03E-03	8,29E-03	4	3,15	1,32E-03	1,14E-02	2	
WDR82	0,92	1,63E-01	3,29E-01	4	2,52	7,83E-03	4,27E-02	2	
NUMA1	1,50	3,67E-02	1,18E-01	4	2,28	8,50E-02	2,17E-01	2	
RBM5	1,32	3,19E-02	1,08E-01	3	2,16	3,21E-02	1,12E-01	2	
HIST2H2AC; HIST2H2AA3				0	2,03	3,01E-02	1,06E-01	2	
RTF1	0,57	1,61E-01	3,29E-01	5	1,99	1,67E-02	7,20E-02	3	
RBM17	1,33	4,45E-03	2,68E-02	5	1,97	3,43E-02	1,16E-01	2	
IMMT				0	1,89	2,12E-02	8,46E-02	2	
HDGFRP2	0,91	5,10E-02	1,48E-01	4	1,77	7,22E-03	3,97E-02	3	
FAM76B	0,19	7,12E-01	8,22E-01	4	1,73	9,05E-03	4,82E-02	3	
EIF3L	1,64	1,47E-02	6,37E-02	3	1,67	4,63E-02	1,43E-01	2	
EIF4B	1,44	6,30E-03	3,43E-02	4	1,58	5,16E-02	1,54E-01	2	
NCL	1,28	2,84E-03	1,91E-02	5	1,55	7,20E-03	3,97E-02	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
EIF3E	1,34	2,24E-02	8,87E-02	4	1,54	6,22E-02	1,73E-01	2	
HSD17B10	-0,16	7,87E-01	8,78E-01	3	1,51	5,36E-02	1,57E-01	2	
CDC42	-1,05	1,24E-01	2,75E-01	2	1,50	1,23E-02	6,00E-02	4	
RPS2	1,20	1,62E-02	6,79E-02	5	1,43	8,78E-03	4,71E-02	4	
EIF3I	1,64	4,79E-03	2,81E-02	4	1,40	6,63E-02	1,80E-01	3	
SRP14	0,07	8,69E-01	9,23E-01	5	1,40	1,91E-02	7,89E-02	4	
SAP18	1,72	1,03E-03	8,29E-03	5	1,39	1,22E-02	6,00E-02	4	
EIF3F	1,27	2,57E-02	9,77E-02	4	1,37	8,94E-02	2,25E-01	2	
RPS28	1,02	2,60E-02	9,79E-02	5	1,31	8,38E-02	2,15E-01	2	
PPIL1	1,89	2,07E-03	1,50E-02	3	1,28	5,43E-02	1,57E-01	3	
BUD13	0,40	4,86E-01	6,43E-01	3	1,28	1,71E-01	3,46E-01	2	
RPS12	1,74	2,62E-03	1,81E-02	4	1,27	2,23E-02	8,76E-02	4	
SAP30BP	1,56	3,00E-03	1,99E-02	4	1,26	6,42E-02	1,76E-01	3	
RPL12	1,77	7,68E-04	6,69E-03	4	1,26	5,27E-02	1,56E-01	3	
TCEB2	0,04	9,36E-01	9,65E-01	4	1,25	4,94E-02	1,51E-01	3	
MAGOH;MAGOHB	1,94	4,04E-04	4,10E-03	4	1,23	1,03E-01	2,47E-01	2	
IWS1	1,17	1,53E-02	6,54E-02	4	1,20	4,58E-02	1,43E-01	3	
POGZ	0,27	5,48E-01	7,06E-01	4	1,20	1,36E-01	2,93E-01	2	
ZNF197	0,50	4,69E-01	6,30E-01	2	1,17	1,42E-01	3,01E-01	2	
SLC25A5	0,33	4,84E-01	6,42E-01	4	1,17	7,89E-02	2,07E-01	3	
CHTOP	1,71	5,90E-04	5,57E-03	5	1,15	1,21E-01	2,78E-01	3	
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	1,05	2,58E-02	9,77E-02	4	1,14	1,26E-01	2,84E-01	2	
GRB10	0,27	5,54E-01	7,09E-01	5	1,14	5,05E-02	1,51E-01	4	
CDC40	1,58	4,62E-03	2,73E-02	4	1,10	3,57E-02	1,19E-01	4	
TRA2B	1,50	8,54E-04	7,26E-03	5	1,09	3,38E-02	1,15E-01	4	
CCT5	1,94	8,42E-03	4,26E-02	2	1,05	1,55E-01	3,19E-01	2	
CCT3	1,49	2,84E-03	1,91E-02	4	1,02	7,86E-02	2,07E-01	3	
SMARCB1	1,00	8,04E-02	2,05E-01	3	1,00	1,73E-01	3,48E-01	2	
SNRNP70	0,73	1,34E-01	2,87E-01	5	1,00	4,25E-02	1,35E-01	4	
CPSF7	0,53	2,75E-01	4,52E-01	4	0,98	6,27E-02	1,73E-01	4	
DKC1	1,83	1,48E-02	6,41E-02	3	0,98	1,91E-01	3,67E-01	2	
BTF3	-0,26	6,92E-01	8,09E-01	4	0,97	7,18E-02	1,91E-01	4	
CCT7	1,71	3,89E-03	2,42E-02	3	0,95	2,49E-01	4,42E-01	2	
RPL28	0,54	3,21E-01	4,95E-01	5	0,93	1,47E-01	3,08E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
RPS23	1,56	2,39E-03	1,69E-02	5	0,92	8,39E-02	2,15E-01	4	
IKZF5				0	0,91	1,25E-01	2,84E-01	3	
GATAD2B	1,34	9,20E-03	4,50E-02	4	0,91	6,02E-02	1,69E-01	4	
PABPC1;PABPC3	1,99	1,30E-03	9,91E-03	4	0,90	2,22E-01	4,12E-01	2	
SF3A1	0,64	1,58E-01	3,29E-01	5	0,89	1,41E-01	3,01E-01	3	
PHF5A	0,85	5,90E-02	1,64E-01	5	0,89	1,85E-01	3,60E-01	3	
TPR	0,32	5,51E-01	7,07E-01	3	0,87	1,85E-01	3,60E-01	3	
CCAR1	0,81	7,91E-02	2,03E-01	4	0,86	1,74E-01	3,48E-01	3	
ZC3H18	0,59	2,18E-01	3,96E-01	4	0,85	8,31E-02	2,15E-01	4	
SNRPE	1,43	1,11E-03	8,75E-03	5	0,85	7,39E-02	1,96E-01	4	
HADHB	0,01	9,91E-01	9,95E-01	3	0,84	1,85E-01	3,60E-01	3	
SCAF1	0,51	3,72E-01	5,40E-01	3	0,84	3,44E-01	5,38E-01	2	
SMAD3	-0,57	2,36E-01	4,14E-01	4	0,84	1,15E-01	2,68E-01	4	
TCF7	0,00	9,93E-01	9,96E-01	4	0,83	1,06E-01	2,51E-01	4	
EIF3G	0,96	1,59E-01	3,29E-01	2	0,82	2,56E-01	4,49E-01	2	
DCD	0,20	6,70E-01	7,94E-01	4	0,81	1,94E-01	3,68E-01	4	
CSTF2	0,11	8,12E-01	8,94E-01	4	0,81	1,89E-01	3,65E-01	3	
HNRNPM	0,90	3,11E-02	1,07E-01	5	0,80	9,16E-02	2,29E-01	4	
SREK1IP1	0,19	7,75E-01	8,68E-01	2	0,77	3,32E-01	5,26E-01	3	
RPL13	0,96	3,64E-02	1,18E-01	5	0,76	2,07E-01	3,89E-01	4	
SCAF4	1,44	4,92E-03	2,84E-02	5	0,75	1,30E-01	2,85E-01	4	
ZBTB14	-1,41	2,39E-02	9,30E-02	3	0,75	2,96E-01	4,96E-01	2	
GNB2	0,88	2,05E-01	3,79E-01	2	0,73	3,08E-01	5,09E-01	2	
ERH	1,44	1,70E-03	1,26E-02	5	0,72	1,86E-01	3,61E-01	4	
SF3A2	0,71	1,27E-01	2,77E-01	4	0,72	1,25E-01	2,84E-01	4	
PLRG1	1,51	5,75E-03	3,20E-02	4	0,69	3,46E-01	5,40E-01	2	
ATRX	0,08	8,78E-01	9,29E-01	3	0,68	3,41E-01	5,35E-01	2	
MAP7	-0,20	6,89E-01	8,07E-01	4	0,67	2,50E-01	4,43E-01	3	
THRAP3	0,66	2,45E-01	4,20E-01	4	0,67	2,82E-01	4,80E-01	4	
RPLP2	0,72	8,16E-02	2,07E-01	5	0,66	1,77E-01	3,53E-01	4	
RPS27	1,55	3,79E-03	2,37E-02	4	0,66	1,78E-01	3,53E-01	4	
SF3B4	0,82	4,82E-02	1,43E-01	5	0,64	1,79E-01	3,53E-01	4	
KHDRBS1	1,62	6,55E-04	6,03E-03	5	0,64	2,77E-01	4,77E-01	4	
EIF3C;EIF3CL	1,78	1,03E-02	4,95E-02	3	0,63	2,80E-01	4,78E-01	3	
PYCR2	0,56	2,46E-01	4,20E-01	4	0,63	3,12E-01	5,13E-01	3	
NXF1	0,02	9,61E-01	9,81E-01	4	0,62	2,95E-01	4,96E-01	3	
MYH9	1,70	5,42E-03	3,04E-02	4	0,62	2,72E-01	4,71E-01	4	
PABPN1	0,86	1,24E-01	2,75E-01	3	0,62	4,19E-01	6,12E-01	2	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
ATAD3A	1,01	1,43E-01	3,02E-01	2	0,60	4,13E-01	6,10E-01	2	
AQR	0,93	7,41E-02	1,98E-01	4	0,59	3,01E-01	5,01E-01	3	
CDK9	0,55	3,08E-01	4,82E-01	3	0,58	4,41E-01	6,32E-01	2	
PHF2	0,37	4,78E-01	6,37E-01	3	0,57	4,19E-01	6,12E-01	2	
SP2	-0,38	3,53E-01	5,22E-01	5	0,56	2,22E-01	4,12E-01	4	
HNRNPF	1,29	3,77E-03	2,37E-02	5	0,56	3,01E-01	5,01E-01	4	
CMAS	0,27	6,00E-01	7,43E-01	3	0,55	3,70E-01	5,60E-01	3	
NPM1	0,33	4,42E-01	6,11E-01	5	0,55	2,87E-01	4,86E-01	4	
PPP2R1B	1,41	1,21E-02	5,58E-02	4	0,55	3,26E-01	5,21E-01	3	
BUD31	0,84	7,72E-02	2,00E-01	4	0,55	3,84E-01	5,77E-01	3	
LUC7L3	0,89	5,10E-02	1,48E-01	4	0,55	2,49E-01	4,42E-01	4	
CGGBP1	0,09	8,66E-01	9,23E-01	3	0,54	4,45E-01	6,34E-01	2	
KIF4A;KIF4B	-0,02	9,61E-01	9,81E-01	4	0,53	4,19E-01	6,12E-01	3	
RPL35A	0,20	6,64E-01	7,91E-01	4	0,52	3,16E-01	5,16E-01	4	
TCEB1	-0,76	7,45E-02	1,98E-01	5	0,51	3,61E-01	5,50E-01	3	
ACTL6A	0,77	1,61E-01	3,29E-01	3	0,51	4,99E-01	6,69E-01	2	
EPB41L2				0	0,50	4,78E-01	6,55E-01	2	
PELO	0,52	3,39E-01	5,10E-01	3	0,49	4,81E-01	6,55E-01	2	
PRDM10	-2,48	1,10E-03	8,75E-03	3	0,49	3,05E-01	5,05E-01	4	
RUVBL2	1,31	3,95E-03	2,45E-02	5	0,48	3,30E-01	5,25E-01	4	
RNPS1	1,68	3,58E-04	3,73E-03	5	0,48	3,58E-01	5,49E-01	4	
SF3B6	0,53	2,40E-01	4,17E-01	4	0,48	3,64E-01	5,53E-01	4	
U2SURP	0,24	6,35E-01	7,73E-01	5	0,47	4,42E-01	6,32E-01	3	
EEF1G	1,06	2,41E-02	9,34E-02	4	0,47	5,09E-01	6,77E-01	2	
PSMC2	0,91	1,63E-01	3,29E-01	3	0,46	3,89E-01	5,84E-01	4	
EEF1A1;EEF1A1P5	0,56	1,72E-01	3,39E-01	5	0,45	3,60E-01	5,50E-01	4	
KPNA4	-0,32	5,54E-01	7,09E-01	3	0,45	5,41E-01	7,05E-01	2	
HIST1H2AC	0,54	1,81E-01	3,48E-01	5	0,44	4,29E-01	6,21E-01	4	
PYCR1	0,60	1,98E-01	3,70E-01	4	0,44	4,54E-01	6,44E-01	3	
GATA3				0	0,43	4,49E-01	6,38E-01	3	
UPF3B	-0,49	3,20E-01	4,93E-01	4	0,42	4,71E-01	6,55E-01	3	
EEF1D	0,92	1,06E-01	2,49E-01	3	0,41	5,56E-01	7,13E-01	2	
POLDIP3	0,34	4,56E-01	6,22E-01	4	0,41	4,07E-01	6,03E-01	4	
ABCE1	0,48	2,95E-01	4,70E-01	4	0,40	5,69E-01	7,24E-01	2	
SRSF5	-0,21	6,41E-01	7,76E-01	4	0,40	4,73E-01	6,55E-01	3	
CCT2	1,04	6,55E-02	1,77E-01	3	0,39	5,77E-01	7,31E-01	2	
RPL14	1,87	6,15E-04	5,76E-03	4	0,39	5,83E-01	7,36E-01	2	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
VDAC2	-0,22	6,91E-01	8,08E-01	3	0,39	5,86E-01	7,38E-01	2	
YTHDC1	0,78	2,32E-01	4,09E-01	4	0,38	7,21E-01	8,22E-01	2	
RPS18	1,15	1,36E-02	6,09E-02	5	0,37	4,62E-01	6,51E-01	4	
RBBP7	0,19	7,00E-01	8,13E-01	4	0,37	4,98E-01	6,69E-01	3	
SNRPD3	1,09	1,61E-02	6,79E-02	5	0,36	4,76E-01	6,55E-01	4	
SET;SETSIP	-0,62	4,67E-01	6,29E-01	3	0,36	5,60E-01	7,16E-01	4	
CREB1	-0,92	5,99E-02	1,65E-01	4	0,36	4,28E-01	6,21E-01	4	
SNW1	1,62	2,82E-03	1,91E-02	4	0,36	4,77E-01	6,55E-01	4	
SCAF11	0,99	4,40E-02	1,34E-01	4	0,36	6,16E-01	7,59E-01	2	
NKAP				0	0,36	6,03E-01	7,49E-01	2	
RPL17;RPL17-C18orf32	0,79	7,87E-02	2,02E-01	5	0,36	4,80E-01	6,55E-01	4	
PKM	0,06	9,21E-01	9,58E-01	4	0,35	4,95E-01	6,68E-01	4	
SRRM1	-1,23	5,89E-02	1,64E-01	5	0,35	5,28E-01	6,95E-01	4	
SNRPF	0,75	1,13E-01	2,60E-01	4	0,35	6,47E-01	7,84E-01	3	
SF1	0,31	4,61E-01	6,25E-01	5	0,35	4,75E-01	6,55E-01	4	
DSC1	1,38	4,97E-02	1,46E-01	2	0,35	6,18E-01	7,60E-01	2	
RPL6	0,13	8,13E-01	8,95E-01	5	0,35	5,26E-01	6,94E-01	4	
TRA2A	0,56	3,01E-01	4,77E-01	4	0,34	5,52E-01	7,10E-01	3	
CHERP	0,69	1,25E-01	2,77E-01	4	0,33	6,44E-01	7,83E-01	2	
MFAP1	-0,18	7,16E-01	8,24E-01	5	0,33	5,88E-01	7,39E-01	4	
RUVBL1	0,71	9,29E-02	2,26E-01	5	0,31	4,81E-01	6,55E-01	4	
HCFC1	-0,68	2,34E-01	4,11E-01	4	0,31	5,11E-01	6,78E-01	4	
HNRNPA3	0,51	2,65E-01	4,44E-01	4	0,30	6,79E-01	7,99E-01	2	
HSP90AA1	1,10	3,66E-02	1,18E-01	4	0,30	6,71E-01	7,95E-01	2	
CALML5	0,08	8,57E-01	9,19E-01	4	0,29	6,51E-01	7,87E-01	3	
PPP1CB	0,81	8,03E-02	2,05E-01	4	0,29	6,88E-01	8,04E-01	2	
HDAC1	0,59	2,11E-01	3,86E-01	4	0,29	7,17E-01	8,21E-01	2	
PRPF8	1,36	1,95E-02	7,88E-02	5	0,29	6,28E-01	7,69E-01	4	
ARGLU1	-0,15	7,32E-01	8,36E-01	5	0,28	7,18E-01	8,21E-01	4	
SRRM2	0,63	1,18E-01	2,65E-01	5	0,28	5,47E-01	7,07E-01	4	
TRMT10C	-0,05	9,23E-01	9,59E-01	3	0,27	7,30E-01	8,27E-01	2	
RPLP0;RPLP0P6	0,97	2,70E-02	9,99E-02	5	0,26	6,13E-01	7,58E-01	4	
SRSF2	-0,46	3,32E-01	5,06E-01	4	0,26	5,92E-01	7,41E-01	4	
CWC25	0,25	5,70E-01	7,18E-01	4	0,25	6,92E-01	8,06E-01	3	
SRSF3	0,36	4,37E-01	6,06E-01	4	0,25	6,13E-01	7,58E-01	4	
PRPF6	0,58	1,96E-01	3,67E-01	5	0,24	6,60E-01	7,89E-01	3	
ATP5A1	0,93	5,68E-02	1,61E-01	5	0,24	7,19E-01	8,21E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
TRIP12	-0,57	2,24E-01	4,01E-01	4	0,24	6,63E-01	7,89E-01	3	
NACA	-0,23	5,82E-01	7,29E-01	5	0,23	6,27E-01	7,69E-01	4	
SP3	-1,26	1,99E-02	7,96E-02	4	0,23	6,63E-01	7,89E-01	4	
SYNCRIP	0,79	1,14E-01	2,60E-01	4	0,22	6,62E-01	7,89E-01	4	
CCT8	1,13	4,10E-02	1,28E-01	3	0,22	7,51E-01	8,33E-01	3	
SSB	-0,71	1,88E-01	3,57E-01	4	0,22	7,01E-01	8,10E-01	4	
PNN	1,83	7,14E-04	6,37E-03	4	0,21	7,33E-01	8,28E-01	4	
EIF4A3	1,15	4,82E-02	1,43E-01	5	0,21	7,40E-01	8,28E-01	3	
TUBB	0,13	7,47E-01	8,43E-01	5	0,21	7,35E-01	8,28E-01	4	
EPB41L4B	1,25	3,13E-02	1,07E-01	3	0,21	7,23E-01	8,22E-01	4	
SMC4	0,08	8,59E-01	9,20E-01	4	0,20	8,01E-01	8,77E-01	2	
RPS27A;UBB; UBC;UBA52	0,39	3,57E-01	5,26E-01	5	0,19	6,81E-01	8,01E-01	4	
NOP58	0,12	8,02E-01	8,87E-01	5	0,18	7,40E-01	8,28E-01	3	
SRRT	0,13	7,74E-01	8,68E-01	5	0,18	7,72E-01	8,51E-01	4	
RPL13A;RPL13a	0,24	6,19E-01	7,58E-01	4	0,17	7,53E-01	8,35E-01	3	
PRDX1	-0,28	6,09E-01	7,53E-01	4	0,17	8,03E-01	8,77E-01	3	
RASA1	-0,89	1,10E-01	2,55E-01	3	0,16	8,32E-01	8,93E-01	2	
SMNDC1	0,21	6,25E-01	7,63E-01	4	0,16	8,22E-01	8,91E-01	2	
EPB41	-0,15	7,35E-01	8,38E-01	5	0,15	7,37E-01	8,28E-01	4	
GAPDH	0,09	8,42E-01	9,10E-01	4	0,15	7,39E-01	8,28E-01	4	
ELAVL1	0,51	2,57E-01	4,35E-01	4	0,15	7,50E-01	8,33E-01	4	
SRP72	0,09	8,20E-01	8,98E-01	5	0,14	7,50E-01	8,33E-01	4	
ALKBH5	-0,75	2,62E-01	4,42E-01	2	0,14	8,35E-01	8,93E-01	2	
CBX3	0,85	4,18E-02	1,29E-01	5	0,14	7,99E-01	8,77E-01	4	
CSNK2A1; CSNK2A3	0,13	8,22E-01	8,99E-01	4	0,14	8,61E-01	9,09E-01	3	
SLK	-1,25	4,94E-02	1,46E-01	4	0,13	8,22E-01	8,91E-01	4	
ACTB	0,17	6,69E-01	7,94E-01	5	0,13	7,89E-01	8,68E-01	4	
RBMX	0,74	8,94E-02	2,22E-01	5	0,12	8,18E-01	8,91E-01	4	
EIF6	0,32	5,55E-01	7,09E-01	3	0,12	8,54E-01	9,06E-01	3	
RBM8A	1,16	1,28E-02	5,82E-02	5	0,11	8,33E-01	8,93E-01	3	
ILF3	1,35	8,17E-03	4,17E-02	4	0,11	8,88E-01	9,35E-01	2	
RPL31	0,05	9,06E-01	9,52E-01	5	0,10	8,34E-01	8,93E-01	4	
ZNF148	-1,16	2,49E-02	9,63E-02	5	0,10	8,24E-01	8,91E-01	4	
RFC2	0,56	3,92E-01	5,64E-01	2	0,09	8,96E-01	9,40E-01	2	
U2AF1	-0,68	1,17E-01	2,65E-01	5	0,09	8,53E-01	9,06E-01	4	
SRSF1	0,69	9,05E-02	2,24E-01	5	0,08	8,51E-01	9,06E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
RPS5	0,41	3,02E-01	4,78E-01	5	0,08	8,61E-01	9,09E-01	4	
PPIL4	-0,09	8,69E-01	9,23E-01	3	0,07	9,18E-01	9,57E-01	2	
DUT	-0,23	6,99E-01	8,13E-01	3	0,05	9,43E-01	9,71E-01	3	
NSD1	-0,78	1,38E-01	2,92E-01	4	0,04	9,41E-01	9,71E-01	3	
HELLS	0,74	1,64E-01	3,29E-01	4	0,04	9,41E-01	9,71E-01	3	
HNRNPH1	1,09	1,43E-02	6,25E-02	5	0,02	9,58E-01	9,80E-01	4	
LYAR	-0,14	7,53E-01	8,47E-01	5	0,02	9,68E-01	9,86E-01	3	
TUBA1B	0,31	4,52E-01	6,19E-01	5	0,02	9,71E-01	9,87E-01	4	
ENO1	-0,42	4,13E-01	5,83E-01	4	0,02	9,82E-01	9,91E-01	2	
PCBP2;Isoform	0,70	9,92E-02	2,37E-01	5	0,02	9,80E-01	9,91E-01	3	
RNF2	-0,40	4,49E-01	6,16E-01	4	0,01	9,86E-01	9,91E-01	2	
ZSCAN26;ZNF187	-0,60	1,90E-01	3,58E-01	4	0,01	9,89E-01	9,91E-01	2	
LUC7L2	0,25	5,09E-01	6,66E-01	5	0,00	1,00E+00	1,00E+00	4	
CPSF6	0,06	8,99E-01	9,46E-01	5	-0,01	9,88E-01	9,91E-01	4	
MICU1	-1,18	3,60E-02	1,17E-01	4	-0,01	9,87E-01	9,91E-01	4	
PRPF19	1,06	2,67E-02	9,95E-02	5	-0,01	9,84E-01	9,91E-01	4	
KIF2A	0,03	9,60E-01	9,81E-01	3	-0,01	9,85E-01	9,91E-01	2	
RPS26;RPS26P11	0,35	4,09E-01	5,80E-01	5	-0,01	9,77E-01	9,91E-01	4	
DDX23	0,61	2,20E-01	3,97E-01	4	-0,02	9,76E-01	9,91E-01	3	
RPS16;ZNF90	1,08	2,96E-02	1,05E-01	5	-0,03	9,58E-01	9,80E-01	4	
HIST1H2BC	-0,15	6,99E-01	8,13E-01	5	-0,03	9,40E-01	9,71E-01	4	
TCERG1	-1,13	2,76E-02	1,00E-01	4	-0,04	9,60E-01	9,80E-01	2	
H2AFV;H2AFZ	-0,14	7,74E-01	8,68E-01	4	-0,04	9,54E-01	9,78E-01	4	
H1F0	-0,13	7,33E-01	8,37E-01	5	-0,04	9,48E-01	9,74E-01	4	
SART1	0,31	4,90E-01	6,46E-01	4	-0,04	9,45E-01	9,72E-01	3	
RPL38	0,12	8,01E-01	8,87E-01	4	-0,04	9,25E-01	9,61E-01	4	
RTCB	0,16	7,19E-01	8,25E-01	4	-0,06	9,12E-01	9,54E-01	4	
ZSCAN21	-1,00	1,59E-01	3,29E-01	3	-0,06	9,34E-01	9,68E-01	2	
HNRNPK	0,73	7,56E-02	1,99E-01	5	-0,06	8,92E-01	9,37E-01	4	
RPS17	0,43	3,58E-01	5,26E-01	5	-0,07	9,02E-01	9,45E-01	4	
TCF7;TCF7L2	-0,79	6,38E-02	1,73E-01	5	-0,08	8,70E-01	9,17E-01	4	
ZNF292				0	-0,08	9,20E-01	9,57E-01	3	
RPS8	1,27	6,62E-03	3,53E-02	5	-0,08	8,54E-01	9,06E-01	4	
UTP14A	-1,28	6,17E-02	1,69E-01	4	-0,09	9,19E-01	9,57E-01	3	
RPL34	-0,34	4,99E-01	6,55E-01	4	-0,11	8,58E-01	9,08E-01	4	
RPL24	0,48	2,39E-01	4,15E-01	5	-0,11	8,03E-01	8,77E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
RPS24	0,67	1,04E-01	2,46E-01	5	-0,12	8,23E-01	8,91E-01	4	
SNRPD2	0,30	4,43E-01	6,11E-01	5	-0,12	8,26E-01	8,91E-01	4	
TCP1	1,01	3,36E-02	1,12E-01	4	-0,12	8,36E-01	8,93E-01	3	
DDX46	-0,11	8,29E-01	9,03E-01	4	-0,13	8,24E-01	8,91E-01	4	
ARL6IP4	-0,20	7,00E-01	8,13E-01	3	-0,15	8,35E-01	8,93E-01	3	
PRPF4B	-1,03	2,73E-02	9,99E-02	5	-0,15	7,61E-01	8,42E-01	4	
KLF13	-0,26	5,28E-01	6,85E-01	5	-0,16	7,37E-01	8,28E-01	4	
ZNF865	-2,32	1,40E-03	1,06E-02	3	-0,16	7,64E-01	8,44E-01	3	
RPL10	0,73	1,09E-01	2,53E-01	4	-0,19	7,02E-01	8,10E-01	4	
TARDBP	0,43	2,97E-01	4,73E-01	5	-0,19	6,76E-01	7,97E-01	4	
LRRC59	0,43	3,43E-01	5,14E-01	4	-0,19	6,71E-01	7,95E-01	4	
PRPF38A	0,79	1,01E-01	2,40E-01	4	-0,19	7,24E-01	8,22E-01	3	
U2AF2	-0,55	2,04E-01	3,77E-01	5	-0,20	6,63E-01	7,89E-01	4	
RBM39	-0,47	3,15E-01	4,91E-01	5	-0,20	6,94E-01	8,07E-01	4	
H2AFY	-0,69	1,13E-01	2,60E-01	5	-0,20	6,89E-01	8,04E-01	4	
ZCCHC17	-0,19	7,79E-01	8,70E-01	3	-0,20	8,03E-01	8,77E-01	3	
SMC1A	-0,54	1,83E-01	3,50E-01	5	-0,21	7,08E-01	8,15E-01	3	
SUB1	-0,62	2,45E-01	4,20E-01	5	-0,22	7,00E-01	8,10E-01	4	
HSPA9	-0,08	8,48E-01	9,14E-01	5	-0,23	6,87E-01	8,04E-01	4	
LSM14B	-0,59	1,36E-01	2,90E-01	5	-0,25	6,55E-01	7,89E-01	3	
RPS11	0,09	8,20E-01	8,98E-01	5	-0,25	5,86E-01	7,38E-01	4	
RBM14	0,50	3,08E-01	4,82E-01	5	-0,25	6,35E-01	7,76E-01	4	
RBX1	0,52	3,29E-01	5,03E-01	3	-0,26	6,02E-01	7,49E-01	4	
RBBP4	0,30	4,78E-01	6,37E-01	5	-0,26	6,58E-01	7,89E-01	4	
CHMP4B	-0,17	7,78E-01	8,70E-01	3	-0,26	7,28E-01	8,26E-01	2	
LBR	-1,95	6,62E-03	3,53E-02	3	-0,26	6,54E-01	7,89E-01	3	
ACIN1	0,90	8,64E-02	2,16E-01	4	-0,26	6,72E-01	7,95E-01	3	
CMSS1	-1,19	4,48E-02	1,35E-01	3	-0,27	7,01E-01	8,10E-01	3	
BUB3	0,08	8,37E-01	9,07E-01	5	-0,27	5,66E-01	7,22E-01	4	
IK	0,69	1,67E-01	3,34E-01	4	-0,27	7,14E-01	8,20E-01	2	
WBP11	-1,02	4,35E-02	1,34E-01	5	-0,27	5,83E-01	7,36E-01	4	
RFC4	0,08	8,80E-01	9,30E-01	3	-0,28	7,06E-01	8,13E-01	2	
RPS20	0,58	2,13E-01	3,88E-01	4	-0,28	5,41E-01	7,05E-01	4	
HSPA8	0,01	9,83E-01	9,91E-01	5	-0,29	5,24E-01	6,94E-01	4	
CDC2L1;CDK11B; CDK11A	-0,39	4,61E-01	6,25E-01	4	-0,29	6,74E-01	7,97E-01	3	
SF3B5	0,58	2,83E-01	4,59E-01	3	-0,30	6,89E-01	8,04E-01	2	
DNAJA2	0,55	2,27E-01	4,04E-01	4	-0,31	5,29E-01	6,95E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
PDS5A	-1,68	9,64E-03	4,69E-02	3	-0,32	7,47E-01	8,33E-01	2	
SF3A3	0,66	1,79E-01	3,47E-01	4	-0,32	5,98E-01	7,46E-01	4	
GTPBP4	-0,34	4,75E-01	6,35E-01	4	-0,32	6,48E-01	7,85E-01	2	
CLTC	1,48	1,06E-02	5,04E-02	3	-0,32	6,03E-01	7,49E-01	3	
RBM25	0,29	4,88E-01	6,44E-01	5	-0,33	4,72E-01	6,55E-01	4	
SNRNP27	-0,68	1,48E-01	3,12E-01	4	-0,33	5,52E-01	7,10E-01	3	
EIF3D	0,08	8,62E-01	9,21E-01	4	-0,33	5,43E-01	7,06E-01	3	
HSP90AB1	-0,20	6,55E-01	7,86E-01	5	-0,34	5,01E-01	6,71E-01	4	
PRPF40A	-0,21	6,67E-01	7,93E-01	4	-0,34	5,05E-01	6,75E-01	4	
PPIH	-0,86	7,55E-02	1,99E-01	4	-0,35	5,33E-01	6,99E-01	3	
BOD1L1	0,70	2,90E-01	4,65E-01	2	-0,36	6,43E-01	7,83E-01	2	
RPL4	0,43	3,37E-01	5,09E-01	4	-0,36	4,56E-01	6,45E-01	4	
MCM7	0,02	9,64E-01	9,81E-01	4	-0,36	6,15E-01	7,59E-01	2	
DYNLL1	1,01	2,37E-02	9,27E-02	5	-0,37	5,07E-01	6,76E-01	4	
EIF2S2	-1,41	7,62E-03	3,97E-02	5	-0,37	4,33E-01	6,25E-01	4	
SRSF11	0,25	6,61E-01	7,90E-01	4	-0,37	6,39E-01	7,79E-01	3	
TCF7	-0,62	3,44E-01	5,15E-01	4	-0,38	5,62E-01	7,18E-01	3	
RBBP6	-1,10	6,63E-02	1,78E-01	4	-0,38	5,26E-01	6,94E-01	4	
RPS3	-0,41	3,51E-01	5,22E-01	5	-0,38	4,59E-01	6,49E-01	4	
HIST1H3A; H3F3C	0,07	8,51E-01	9,14E-01	5	-0,39	3,97E-01	5,94E-01	4	
UBTF	1,13	3,96E-02	1,25E-01	5	-0,40	5,70E-01	7,24E-01	2	
PCBP1	-0,37	3,34E-01	5,08E-01	5	-0,40	3,99E-01	5,94E-01	4	
FXR2	-0,72	1,67E-01	3,34E-01	4	-0,40	4,70E-01	6,55E-01	3	
EFTUD2	0,87	5,25E-02	1,50E-01	5	-0,41	4,39E-01	6,31E-01	4	
HSPD1	-0,26	5,67E-01	7,17E-01	4	-0,41	4,18E-01	6,12E-01	4	
PA2G4	0,08	8,77E-01	9,28E-01	4	-0,42	4,94E-01	6,68E-01	3	
CAPRIN1	1,23	3,38E-02	1,12E-01	3	-0,45	5,92E-01	7,41E-01	2	
RPS27L	0,61	3,04E-01	4,80E-01	3	-0,45	5,52E-01	7,10E-01	2	
DDX3X;DDX3Y	-0,02	9,59E-01	9,81E-01	5	-0,45	3,12E-01	5,13E-01	4	
SNRPD1	-0,36	3,78E-01	5,48E-01	5	-0,46	4,42E-01	6,32E-01	4	
RAN	-0,61	1,61E-01	3,29E-01	5	-0,47	4,96E-01	6,68E-01	3	
RPL23	0,19	6,38E-01	7,75E-01	5	-0,47	3,20E-01	5,19E-01	4	
RPL36A;RPL36A-HNRNPH2	-0,44	2,69E-01	4,47E-01	5	-0,47	3,98E-01	5,94E-01	4	
SF3B2	-0,22	6,05E-01	7,49E-01	5	-0,47	5,46E-01	7,07E-01	3	
DDX17	0,42	3,00E-01	4,76E-01	5	-0,47	3,20E-01	5,19E-01	4	
RPS3A	-0,17	6,55E-01	7,86E-01	5	-0,48	3,25E-01	5,21E-01	4	
ZNF740	-0,88	7,60E-02	1,99E-01	4	-0,48	3,82E-01	5,77E-01	3	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
DDX39B	1,07	5,24E-02	1,50E-01	5	-0,48	5,39E-01	7,05E-01	2	
DNAJA1	0,84	7,79E-02	2,01E-01	4	-0,49	3,26E-01	5,21E-01	4	
GTF2I	1,02	6,30E-02	1,72E-01	4	-0,49	3,98E-01	5,94E-01	4	
TFB1M	0,08	9,09E-01	9,52E-01	2	-0,50	4,79E-01	6,55E-01	2	
PUF60	-0,43	2,91E-01	4,65E-01	5	-0,50	2,73E-01	4,71E-01	4	
SRSF7	0,53	1,78E-01	3,46E-01	5	-0,50	2,80E-01	4,78E-01	4	
HP1BP3	0,01	9,82E-01	9,91E-01	5	-0,50	3,39E-01	5,34E-01	4	
MYL6	-0,49	2,87E-01	4,62E-01	4	-0,50	5,43E-01	7,06E-01	2	
PPIG	-0,39	4,73E-01	6,33E-01	4	-0,51	4,63E-01	6,51E-01	3	
RPL19	-0,23	5,56E-01	7,09E-01	5	-0,52	3,01E-01	5,01E-01	4	
RPS4X	0,39	3,19E-01	4,93E-01	5	-0,52	3,19E-01	5,19E-01	4	
NOLC1	0,53	2,42E-01	4,18E-01	5	-0,53	3,48E-01	5,41E-01	3	
RBM15	0,55	2,46E-01	4,20E-01	4	-0,54	3,32E-01	5,26E-01	3	
CCT4	1,21	3,81E-02	1,20E-01	3	-0,54	3,62E-01	5,51E-01	3	
RBPJ	-1,02	3,22E-02	1,09E-01	4	-0,55	3,52E-01	5,45E-01	3	
SON	-0,59	1,69E-01	3,35E-01	5	-0,55	3,54E-01	5,46E-01	4	
MPHOSPH10	-1,36	3,51E-02	1,14E-01	3	-0,56	4,96E-01	6,68E-01	3	
HIST1H1E; HIST1H1D	0,24	5,76E-01	7,24E-01	5	-0,56	2,59E-01	4,51E-01	4	
HSPA5	-0,53	3,06E-01	4,81E-01	4	-0,56	3,80E-01	5,74E-01	3	
HMGB1	-1,63	1,24E-02	5,67E-02	3	-0,56	4,67E-01	6,55E-01	2	
LUC7L	-0,33	4,03E-01	5,74E-01	5	-0,56	2,96E-01	4,96E-01	4	
RPS19	-0,05	9,09E-01	9,52E-01	5	-0,56	2,39E-01	4,31E-01	4	
KRT1	-0,31	4,85E-01	6,43E-01	5	-0,57	3,32E-01	5,26E-01	4	
ZNF653	-0,38	5,75E-01	7,23E-01	2	-0,57	4,29E-01	6,21E-01	2	
GTF2B	0,15	7,14E-01	8,24E-01	5	-0,57	2,80E-01	4,78E-01	4	
MAZ	-1,35	3,62E-03	2,31E-02	5	-0,58	2,09E-01	3,93E-01	4	
GLYR1	-0,48	2,30E-01	4,07E-01	5	-0,58	2,31E-01	4,22E-01	4	
HNRNPL	-0,41	2,98E-01	4,74E-01	5	-0,59	2,21E-01	4,12E-01	4	
CPSF3	0,12	8,20E-01	8,98E-01	4	-0,59	3,55E-01	5,47E-01	4	
MRPL9	-0,14	7,95E-01	8,82E-01	3	-0,61	2,94E-01	4,96E-01	3	
MCM3	-0,04	9,32E-01	9,63E-01	4	-0,62	3,14E-01	5,14E-01	4	
TUBB2A	-0,32	5,10E-01	6,67E-01	4	-0,62	2,71E-01	4,71E-01	3	
SNRPB;SNRPN	0,58	2,11E-01	3,86E-01	4	-0,62	2,44E-01	4,37E-01	4	
SMC3	-0,73	9,54E-02	2,30E-01	5	-0,62	2,55E-01	4,48E-01	4	
SP1	-1,73	6,80E-03	3,57E-02	4	-0,62	3,37E-01	5,32E-01	4	
DHX9	0,69	1,51E-01	3,16E-01	4	-0,64	2,37E-01	4,29E-01	4	
RPS7	-0,66	1,06E-01	2,49E-01	5	-0,64	1,95E-01	3,68E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
HNRNPC	-0,07	8,51E-01	9,14E-01	5	-0,64	1,69E-01	3,42E-01	4	
ZNF263				0	-0,66	4,07E-01	6,03E-01	2	
PPP1CA	-0,15	7,13E-01	8,24E-01	5	-0,66	2,56E-01	4,49E-01	4	
MCM4	-0,79	1,40E-01	2,97E-01	4	-0,68	2,46E-01	4,38E-01	3	
RPL7	0,05	9,11E-01	9,53E-01	4	-0,69	3,40E-01	5,34E-01	2	
PSMD2	-0,15	8,10E-01	8,94E-01	3	-0,69	2,43E-01	4,37E-01	3	
RSBN1	-0,88	9,21E-02	2,25E-01	4	-0,69	1,56E-01	3,20E-01	4	
PTBP1	0,27	5,28E-01	6,85E-01	5	-0,69	1,94E-01	3,68E-01	4	
RALY	0,14	7,47E-01	8,43E-01	4	-0,70	1,65E-01	3,36E-01	4	
LEO1	-0,81	1,31E-01	2,84E-01	3	-0,70	3,48E-01	5,41E-01	2	
CTCF	-1,58	7,75E-04	6,69E-03	5	-0,70	1,32E-01	2,89E-01	4	
WWP2	0,35	3,96E-01	5,68E-01	5	-0,71	1,82E-01	3,58E-01	4	
NEIL1	-0,64	2,51E-01	4,26E-01	3	-0,72	4,70E-01	6,55E-01	2	
GNB2L1	0,57	2,82E-01	4,58E-01	3	-0,72	1,55E-01	3,19E-01	4	
RPL21	-0,24	5,77E-01	7,24E-01	4	-0,72	2,26E-01	4,16E-01	3	
TBC1D10B				0	-0,73	4,89E-01	6,64E-01	2	
RPL18	-1,44	2,74E-02	9,99E-02	3	-0,73	4,76E-01	6,55E-01	3	
KTN1	0,64	3,34E-01	5,08E-01	2	-0,73	3,56E-01	5,47E-01	2	
TMPO	-0,45	3,37E-01	5,09E-01	4	-0,73	3,25E-01	5,21E-01	2	
RPS6	0,12	7,64E-01	8,58E-01	5	-0,74	1,34E-01	2,91E-01	4	
RPL11	-0,34	4,71E-01	6,32E-01	5	-0,74	1,20E-01	2,77E-01	4	
MCM2	-0,97	4,06E-02	1,27E-01	5	-0,75	1,14E-01	2,66E-01	4	
RSBN1L	-1,07	5,70E-02	1,61E-01	3	-0,76	2,24E-01	4,14E-01	3	
HNRNPA2B1	-0,02	9,64E-01	9,81E-01	4	-0,76	1,27E-01	2,85E-01	4	
EIF2S1	-1,40	6,37E-03	3,43E-02	5	-0,76	1,34E-01	2,91E-01	4	
ZNF787	-1,11	1,84E-02	7,63E-02	4	-0,76	1,48E-01	3,09E-01	4	
HMGN2	-2,08	9,90E-04	8,17E-03	3	-0,79	2,80E-01	4,78E-01	2	
ZNF281	-1,33	2,35E-02	9,22E-02	4	-0,79	2,44E-01	4,37E-01	4	
RBM28	-0,70	1,47E-01	3,09E-01	4	-0,79	1,81E-01	3,56E-01	4	
SNRNP200	1,02	9,17E-02	2,25E-01	5	-0,79	4,29E-01	6,21E-01	4	
CHD4	0,36	5,06E-01	6,63E-01	4	-0,81	3,22E-01	5,19E-01	4	
HIST1H4A	0,06	8,82E-01	9,32E-01	5	-0,81	1,19E-01	2,76E-01	4	
FRG1	-1,28	5,83E-03	3,23E-02	5	-0,81	9,39E-02	2,33E-01	4	
TRIM28	-0,80	9,11E-02	2,24E-01	4	-0,82	1,37E-01	2,95E-01	4	
RUNX2	-0,74	1,81E-01	3,48E-01	4	-0,83	3,21E-01	5,19E-01	2	
PSIP1	-1,09	1,06E-02	5,04E-02	5	-0,83	9,96E-02	2,40E-01	4	
PARP1	-0,09	8,44E-01	9,11E-01	4	-0,84	9,92E-02	2,40E-01	4	
DNAJB11	-1,04	6,47E-02	1,75E-01	3	-0,84	1,42E-01	3,01E-01	3	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
SSRP1	0,27	5,86E-01	7,31E-01	4	-0,84	1,93E-01	3,68E-01	4	
RPL32	0,33	4,21E-01	5,87E-01	5	-0,84	1,09E-01	2,55E-01	4	
TCEB3	-0,71	1,05E-01	2,49E-01	5	-0,84	2,27E-01	4,16E-01	4	
DHX8	-0,55	2,45E-01	4,20E-01	4	-0,86	1,72E-01	3,46E-01	3	
SMARCC1	-0,34	4,48E-01	6,16E-01	4	-0,86	1,08E-01	2,54E-01	4	
RPS13	0,35	3,64E-01	5,32E-01	5	-0,86	8,88E-02	2,24E-01	4	
MRPL48	-0,57	2,88E-01	4,63E-01	3	-0,87	1,32E-01	2,88E-01	3	
SMU1	0,36	4,62E-01	6,25E-01	4	-0,87	1,23E-01	2,82E-01	4	
LARP7	-1,47	4,55E-03	2,71E-02	4	-0,87	1,95E-01	3,68E-01	3	
MCM6	-0,48	3,18E-01	4,93E-01	4	-0,88	9,75E-02	2,37E-01	4	
NONO	-0,25	5,61E-01	7,14E-01	5	-0,88	1,53E-01	3,19E-01	3	
SNRPA1	-1,33	2,28E-03	1,61E-02	5	-0,88	9,21E-02	2,29E-01	4	
SNIP1	-0,94	3,53E-02	1,15E-01	5	-0,89	1,29E-01	2,85E-01	4	
RPL23A	-0,58	1,35E-01	2,88E-01	5	-0,89	6,16E-02	1,72E-01	4	
C19orf43	-1,05	5,52E-02	1,57E-01	4	-0,90	2,26E-01	4,16E-01	3	
TP53BP1	0,43	6,13E-01	7,56E-01	4	-0,91	4,16E-01	6,12E-01	3	
UPF1	0,94	3,17E-01	4,91E-01	2	-0,95	2,51E-01	4,43E-01	2	
RRP12	-0,03	9,42E-01	9,68E-01	4	-0,95	2,70E-01	4,70E-01	2	
FAM120A	-0,99	7,63E-02	1,99E-01	4	-0,95	2,14E-01	4,00E-01	2	
HNRNPAB	0,15	7,51E-01	8,46E-01	4	-0,96	8,09E-02	2,10E-01	4	
FIP1L1	-0,32	4,13E-01	5,83E-01	5	-0,96	6,18E-02	1,72E-01	4	
ZNF652	-1,42	9,13E-03	4,48E-02	4	-0,96	5,69E-02	1,63E-01	4	
FAM32A	-0,93	4,40E-02	1,34E-01	4	-0,98	6,72E-02	1,81E-01	4	
WWP1	-1,07	5,12E-02	1,48E-01	4	-0,98	1,29E-01	2,85E-01	4	
ZFP91;ZFP91-CNTF	-0,85	8,60E-02	2,15E-01	4	-0,99	5,93E-02	1,68E-01	4	
LMNB1	0,01	9,84E-01	9,91E-01	5	-1,00	1,43E-01	3,01E-01	4	
ZNF771	-0,61	1,89E-01	3,57E-01	4	-1,00	4,15E-02	1,33E-01	4	
ATP5B	-0,85	1,78E-01	3,46E-01	4	-1,00	2,39E-01	4,31E-01	3	
ZNF48	-1,60	7,77E-03	4,03E-02	3	-1,00	1,00E-01	2,41E-01	4	
EMG1	-0,84	7,61E-02	1,99E-01	4	-1,00	1,28E-01	2,85E-01	3	
SRP9	-1,88	5,38E-03	3,02E-02	3	-1,01	1,93E-01	3,68E-01	2	
RPL8	-0,34	4,67E-01	6,29E-01	5	-1,01	8,83E-02	2,24E-01	4	
CDC5L	-0,16	6,75E-01	7,97E-01	5	-1,02	8,53E-02	2,17E-01	4	
WDR33	-0,52	2,68E-01	4,46E-01	4	-1,02	5,34E-02	1,57E-01	4	
S100A9	-2,91	1,06E-04	1,31E-03	3	-1,02	1,93E-01	3,68E-01	2	
NOP56	0,08	8,70E-01	9,23E-01	4	-1,04	6,61E-02	1,80E-01	4	
SRP68	-0,73	1,36E-01	2,90E-01	5	-1,05	3,84E-02	1,26E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
SND1	-0,35	5,14E-01	6,71E-01	4	-1,05	1,55E-01	3,19E-01	2	
PHF6	-1,29	3,51E-03	2,28E-02	5	-1,05	4,15E-02	1,33E-01	4	
METAP1	-0,22	5,89E-01	7,33E-01	5	-1,06	4,44E-02	1,39E-01	4	
HNRNPUL2; HNRNPUL2-BSCL2	-0,87	3,06E-02	1,07E-01	5	-1,06	3,38E-02	1,15E-01	4	
RBM27	-0,91	5,13E-02	1,48E-01	5	-1,07	6,65E-02	1,80E-01	4	
DDX5	-0,05	9,08E-01	9,52E-01	5	-1,07	4,33E-02	1,37E-01	4	
MATR3	0,73	1,09E-01	2,53E-01	5	-1,08	6,90E-02	1,85E-01	3	
MECP2	-1,79	1,79E-03	1,31E-02	4	-1,08	9,51E-02	2,34E-01	4	
SF3B1	-0,40	4,15E-01	5,84E-01	4	-1,08	6,37E-02	1,75E-01	4	
ZFX;ZFY	-2,72	7,90E-05	1,04E-03	4	-1,10	5,85E-02	1,67E-01	4	
EEF2	-0,94	5,86E-02	1,64E-01	5	-1,11	3,91E-02	1,27E-01	4	
KRT2	-0,55	2,26E-01	4,03E-01	5	-1,12	1,20E-01	2,77E-01	4	
RPL26	-0,37	3,47E-01	5,18E-01	5	-1,14	2,73E-02	9,94E-02	4	
NUP93	0,31	6,02E-01	7,45E-01	4	-1,14	1,46E-01	3,08E-01	2	
TUBB4B	-0,64	1,56E-01	3,25E-01	5	-1,15	1,09E-01	2,55E-01	4	
RPL15	-0,33	4,86E-01	6,43E-01	4	-1,16	2,23E-02	8,76E-02	4	
WDR5	-0,53	2,79E-01	4,55E-01	4	-1,16	1,63E-01	3,33E-01	2	
HNRNPU	-0,93	2,89E-02	1,03E-01	5	-1,16	2,12E-02	8,46E-02	4	
SNRPG; SNRPGP15	0,04	9,40E-01	9,68E-01	3	-1,18	3,04E-01	5,05E-01	2	
RPL3	-0,71	7,44E-02	1,98E-01	5	-1,18	2,73E-02	9,94E-02	4	
HNRNPA0	-1,22	2,99E-02	1,05E-01	3	-1,19	1,28E-01	2,85E-01	2	
HNRNPR	0,33	4,62E-01	6,25E-01	4	-1,19	2,89E-02	1,04E-01	4	
SIRT7	-1,45	1,19E-02	5,52E-02	4	-1,20	5,38E-02	1,57E-01	3	
CPSF2	-0,26	5,64E-01	7,15E-01	5	-1,21	7,11E-02	1,90E-01	4	
HMGA1	-1,02	2,50E-02	9,63E-02	5	-1,21	2,91E-02	1,04E-01	4	
EIF2S3;EIF2S3L	-1,06	3,40E-02	1,12E-01	4	-1,22	2,39E-02	9,17E-02	4	
DHX15	0,45	3,53E-01	5,22E-01	4	-1,22	8,99E-02	2,25E-01	4	
RPL5	-0,81	5,64E-02	1,60E-01	5	-1,23	2,30E-02	8,92E-02	4	
SNRPB2	-1,80	9,71E-04	8,08E-03	5	-1,24	3,72E-02	1,22E-01	4	
NHP2L1	-0,04	9,31E-01	9,63E-01	5	-1,26	3,28E-02	1,13E-01	4	
NAP1L1	-1,13	2,74E-02	9,99E-02	4	-1,27	9,62E-02	2,36E-01	4	
RPL18A	0,01	9,86E-01	9,92E-01	4	-1,27	2,53E-02	9,51E-02	4	
SFPQ	-0,45	3,20E-01	4,94E-01	4	-1,28	5,03E-02	1,51E-01	4	
RPL35	-0,25	5,44E-01	7,02E-01	5	-1,28	4,72E-02	1,45E-01	4	
RPS14	-0,49	2,64E-01	4,43E-01	5	-1,30	1,48E-02	6,78E-02	4	
RPL10A	-0,19	7,05E-01	8,17E-01	4	-1,32	2,66E-02	9,90E-02	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
RPSA	-0,99	2,52E-02	9,67E-02	5	-1,32	1,63E-02	7,11E-02	4	
DDX41	-0,69	1,24E-01	2,75E-01	5	-1,33	1,76E-02	7,46E-02	4	
HMGA1	-0,83	9,26E-02	2,25E-01	4	-1,34	2,77E-02	1,00E-01	4	
RPS25	0,03	9,42E-01	9,68E-01	5	-1,35	4,09E-02	1,33E-01	4	
YBX3	0,16	7,03E-01	8,16E-01	5	-1,36	3,26E-02	1,13E-01	4	
CDK13	-1,46	2,88E-02	1,03E-01	4	-1,36	1,88E-02	7,85E-02	4	
REXO4	-0,64	1,64E-01	3,29E-01	4	-1,37	2,09E-02	8,46E-02	4	
RPL7A	-0,57	1,51E-01	3,16E-01	5	-1,38	1,37E-02	6,36E-02	4	
RPS10; RPS10-NUDT3	-0,75	8,75E-02	2,17E-01	5	-1,38	1,22E-02	6,00E-02	4	
RCC1	-1,42	1,56E-02	6,66E-02	4	-1,38	1,29E-01	2,85E-01	2	
ABCF2	-0,55	2,25E-01	4,02E-01	4	-1,39	3,65E-02	1,21E-01	3	
YARS	-0,87	9,86E-02	2,37E-01	4	-1,40	1,27E-02	6,05E-02	4	
ZNF319	-2,20	1,30E-04	1,54E-03	4	-1,43	1,25E-02	6,04E-02	4	
ZNF524	-1,74	1,02E-03	8,29E-03	4	-1,43	2,71E-02	9,94E-02	3	
RPL37A	-0,57	1,70E-01	3,36E-01	5	-1,44	1,71E-02	7,36E-02	4	
RPS9	-0,83	5,77E-02	1,62E-01	5	-1,44	1,10E-02	5,60E-02	4	
EIF4A1	0,42	4,23E-01	5,89E-01	4	-1,46	4,99E-02	1,51E-01	4	
CPSF4	-0,34	3,91E-01	5,63E-01	5	-1,48	5,56E-02	1,60E-01	3	
YBX1	-0,64	1,06E-01	2,49E-01	5	-1,49	6,57E-03	3,81E-02	4	
SLTM	-1,20	1,39E-02	6,15E-02	5	-1,50	9,47E-03	5,00E-02	4	
RRS1	-1,25	4,56E-02	1,37E-01	4	-1,50	9,54E-02	2,34E-01	3	
SUPT16H	-0,54	2,11E-01	3,86E-01	5	-1,51	1,12E-02	5,61E-02	4	
CFAP20	0,27	6,21E-01	7,59E-01	3	-1,51	1,29E-01	2,85E-01	2	
PRPF4	-1,90	4,13E-04	4,11E-03	5	-1,52	1,76E-02	7,46E-02	4	
RPL39P5;RPL39	-0,39	3,56E-01	5,24E-01	5	-1,53	2,32E-02	8,95E-02	4	
KPNA2	0,24	6,58E-01	7,86E-01	3	-1,53	5,02E-02	1,51E-01	2	
MAFG	-1,11	8,74E-03	4,38E-02	5	-1,54	6,35E-03	3,75E-02	4	
TOP1	-2,19	4,47E-05	6,15E-04	5	-1,56	1,90E-02	7,89E-02	4	
HNRNPA1; HNRNPA1L2	-0,01	9,74E-01	9,87E-01	4	-1,56	1,54E-02	6,84E-02	3	
RPS19BP1	-0,73	1,07E-01	2,50E-01	5	-1,56	5,21E-02	1,55E-01	2	
CHAMP1	-1,20	9,22E-02	2,25E-01	3	-1,57	1,57E-01	3,20E-01	2	
CSTF3	-0,48	3,75E-01	5,44E-01	4	-1,60	1,04E-01	2,48E-01	2	
HNRNPA3	-0,64	2,44E-01	4,20E-01	5	-1,60	1,37E-02	6,36E-02	4	
RRP36	-0,50	3,14E-01	4,91E-01	4	-1,61	3,67E-02	1,21E-01	3	
PRPF31	-0,98	1,89E-02	7,71E-02	5	-1,62	3,82E-03	2,46E-02	4	
IQGAP1	-1,89	5,48E-04	5,26E-03	4	-1,64	3,16E-02	1,11E-01	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
DDX27	-0,62	2,49E-01	4,24E-01	4	-1,65	3,50E-02	1,17E-01	3	
DDX55	-0,79	1,28E-01	2,79E-01	4	-1,65	3,77E-03	2,46E-02	4	
RPL27A	-0,32	5,14E-01	6,71E-01	5	-1,67	5,80E-03	3,46E-02	4	
FAU	-0,56	2,00E-01	3,70E-01	5	-1,67	1,10E-02	5,60E-02	4	
FBL	-0,63	2,30E-01	4,07E-01	4	-1,68	9,63E-03	5,04E-02	3	
PRPF3	-1,57	2,11E-03	1,51E-02	5	-1,70	3,33E-02	1,14E-01	4	
WBSCR22	-1,15	2,78E-02	1,00E-01	4	-1,70	2,98E-03	2,08E-02	4	
GNL2	-0,90	5,50E-02	1,57E-01	4	-1,70	1,03E-02	5,31E-02	3	
NUDT21	-0,61	2,20E-01	3,97E-01	4	-1,71	2,41E-02	9,19E-02	4	
EBNA1BP2	-0,44	4,55E-01	6,22E-01	4	-1,73	1,98E-02	8,13E-02	4	
DNMT1	-1,47	3,58E-03	2,29E-02	4	-1,74	1,51E-02	6,81E-02	3	
FTSJ3	-0,75	1,12E-01	2,57E-01	5	-1,75	1,33E-02	6,25E-02	4	
RCC2	-0,88	4,11E-02	1,28E-01	5	-1,76	2,64E-03	1,89E-02	4	
UBA52	-1,12	4,85E-02	1,43E-01	3	-1,76	2,47E-02	9,37E-02	3	
RPL22	-1,41	9,00E-03	4,47E-02	4	-1,76	6,97E-03	3,97E-02	4	
RPS15A	-0,63	1,68E-01	3,34E-01	5	-1,79	1,40E-02	6,43E-02	4	
SF3B3	-0,54	1,80E-01	3,47E-01	5	-1,81	7,03E-03	3,97E-02	4	
SKP1	-0,31	5,62E-01	7,14E-01	3	-1,82	7,22E-03	3,97E-02	3	
RPL22L1	-0,96	2,72E-02	9,99E-02	5	-1,84	3,23E-03	2,19E-02	4	
ZNF593	-0,67	1,30E-01	2,82E-01	5	-1,88	2,18E-02	8,65E-02	2	
PWP1	-0,63	2,32E-01	4,09E-01	3	-1,90	4,21E-02	1,34E-01	2	
DIMT1	-0,44	2,75E-01	4,52E-01	5	-1,90	1,38E-03	1,15E-02	4	
FIZ1	-2,03	2,17E-04	2,40E-03	4	-1,91	2,43E-03	1,76E-02	4	
RBM26	-0,97	1,26E-01	2,77E-01	3	-1,92	4,01E-03	2,53E-02	4	
RPS15	-0,17	6,63E-01	7,90E-01	5	-1,97	8,94E-04	8,22E-03	4	
ABCF1	-1,14	3,17E-02	1,08E-01	4	-1,97	6,91E-03	3,97E-02	4	
IMP4	-0,97	2,23E-01	4,00E-01	2	-1,98	1,77E-02	7,46E-02	2	
PES1	-1,53	6,55E-04	6,03E-03	5	-2,00	3,04E-03	2,08E-02	4	
RPL27	-0,90	4,34E-02	1,34E-01	5	-2,01	3,49E-03	2,32E-02	4	
IMPDH2	-1,63	3,77E-02	1,20E-01	2	-2,01	1,63E-02	7,11E-02	2	
NAT10	-1,20	2,82E-02	1,01E-01	4	-2,02	4,29E-03	2,68E-02	3	
ZNF444	-1,62	2,74E-03	1,87E-02	4	-2,04	3,42E-03	2,29E-02	3	
C9orf114	-0,70	1,71E-01	3,39E-01	4	-2,04	1,62E-02	7,11E-02	2	
BRD2	-1,70	4,47E-03	2,68E-02	4	-2,04	1,29E-02	6,10E-02	4	
SMARCA4	-1,51	2,12E-03	1,51E-02	5	-2,07	1,54E-02	6,84E-02	4	
PATZ1	-1,86	2,87E-03	1,92E-02	5	-2,07	1,14E-03	9,95E-03	4	
NO66	-1,20	4,42E-02	1,34E-01	5	-2,11	3,82E-03	2,46E-02	3	
SMARCA5	-1,80	3,90E-04	3,99E-03	5	-2,16	7,99E-04	7,56E-03	4	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
GNL3	-0,06	8,85E-01	9,33E-01	4	-2,17	3,90E-03	2,49E-02	3	
MAFK	-1,52	9,62E-04	8,06E-03	5	-2,18	1,72E-03	1,35E-02	4	
KIAA0020	-0,99	1,98E-02	7,96E-02	5	-2,18	4,68E-04	4,64E-03	4	
RPL30	-0,93	2,80E-02	1,00E-01	5	-2,19	1,03E-03	9,10E-03	4	
DDX21	-0,39	3,80E-01	5,49E-01	5	-2,25	4,38E-04	4,41E-03	4	
RPL9	-1,51	1,23E-02	5,67E-02	4	-2,25	5,01E-03	3,07E-02	3	
KRR1	-1,16	9,02E-03	4,47E-02	5	-2,30	4,16E-04	4,25E-03	4	
MYBBP1A	-2,73	1,26E-06	2,22E-05	5	-2,31	1,89E-03	1,46E-02	3	
DDX47	-1,79	1,28E-02	5,82E-02	4	-2,36	7,96E-02	2,08E-01	2	
TRMT112	-2,50	1,29E-04	1,54E-03	4	-2,41	5,61E-03	3,38E-02	3	
BRIX1	-1,74	2,62E-02	9,79E-02	3	-2,42	2,04E-02	8,31E-02	2	
RPL36	-0,51	2,72E-01	4,50E-01	4	-2,53	5,44E-03	3,30E-02	2	
RPL37	-0,10	8,54E-01	9,17E-01	3	-2,53	3,01E-03	2,08E-02	4	
C19orf53	-3,18	2,86E-05	4,19E-04	4	-2,54	4,46E-03	2,76E-02	4	
MORF4L1	-1,93	4,39E-03	2,67E-02	4	-2,57	2,24E-02	8,76E-02	2	
ERI1	-1,83	3,39E-03	2,22E-02	4	-2,58	1,21E-04	1,50E-03	4	
NUP205	-1,95	1,52E-02	6,52E-02	2	-2,61	2,98E-02	1,06E-01	2	
CLK3	-2,08	5,86E-03	3,23E-02	3	-2,62	2,73E-02	9,94E-02	2	
DCAF13	-0,79	5,92E-02	1,64E-01	5	-2,63	9,56E-05	1,26E-03	4	
GRWD1	-1,56	1,21E-03	9,45E-03	5	-2,67	1,33E-04	1,55E-03	4	
MORF4L2	-1,17	1,43E-02	6,25E-02	4	-2,71	1,01E-04	1,28E-03	4	
HIST1H1B	-1,24	2,77E-02	1,00E-01	5	-2,76	8,53E-05	1,17E-03	4	
DDX54	-0,18	7,50E-01	8,46E-01	3	-2,79	2,99E-02	1,06E-01	2	
ALYREF	-0,95	3,40E-02	1,12E-01	5	-2,83	1,96E-04	2,22E-03	4	
TOP2A	-0,43	2,90E-01	4,65E-01	5	-2,89	1,26E-04	1,50E-03	4	
SDAD1	-0,46	4,89E-01	6,45E-01	2	-2,97	1,96E-03	1,49E-02	2	
CUL1	-2,03	1,69E-03	1,26E-02	4	-2,98	1,35E-04	1,55E-03	4	
CPSF1	-2,00	5,35E-04	5,18E-03	4	-3,00	5,40E-04	5,27E-03	4	
DDX56	-1,39	1,46E-02	6,37E-02	4	-3,05	1,68E-03	1,34E-02	2	
NSUN5	-1,03	1,98E-02	7,96E-02	5	-3,22	1,37E-03	1,15E-02	2	
RPF2	-1,17	4,41E-02	1,34E-01	3	-3,29	9,96E-04	8,91E-03	2	
DDX18	-1,93	7,73E-04	6,69E-03	5	-3,50	1,25E-04	1,50E-03	3	
NSUN2	-2,66	3,34E-05	4,83E-04	5	-4,12	4,82E-06	8,87E-05	4	
DSG1	2,00	6,78E-03	3,57E-02	2				0	
EPRS	2,00	1,39E-02	6,16E-02	2				0	
PHF3	1,97	1,26E-03	9,74E-03	3				0	
THOC5	1,94	1,33E-02	6,03E-02	3				0	
TAF6	1,93	4,79E-03	2,81E-02	3				0	

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	n (exp) MYC ON	mean log2FC MYC OFF	p-vlaue MYC OFF	q-value MYC OFF	n (exp) MYC OFF	Function
EIF3M	1,92	1,86E-03	1,36E-02	3				0	
TPI1	1,88	2,45E-03	1,70E-02	3				0	
ISY1	1,88	1,04E-02	4,98E-02	2				0	
HDAC2	1,88	1,01E-02	4,87E-02	2				0	
CAD	1,86	1,38E-02	6,15E-02	3				0	
MED12;TNRC11	1,85	1,18E-02	5,50E-02	3				0	
ERCC2	1,83	1,34E-02	6,03E-02	2				0	
RNGTT	1,79	1,89E-02	7,71E-02	2				0	
PSMD14	1,77	1,42E-02	6,25E-02	2				0	
THOC3	1,74	5,35E-03	3,02E-02	3				0	
GPN1	1,69	1,80E-02	7,47E-02	2				0	
RAD21	1,69	2,12E-02	8,48E-02	2				0	
EIF3H	1,64	6,37E-03	3,43E-02	3				0	
NUSAP1	1,61	2,58E-02	9,77E-02	2				0	
CSNK2A2	1,60	2,62E-02	9,79E-02	2				0	
EIF4G1	1,59	2,60E-02	9,79E-02	2				0	
C17orf85	1,56	2,73E-02	9,99E-02	2				0	
MNAT1	1,55	3,10E-02	1,07E-01	2				0	
ALDH18A1	1,55	3,44E-02	1,14E-01	3				0	
PELP1	1,52	3,10E-02	1,07E-01	2				0	
PGAM5	1,52	8,36E-03	4,25E-02	3				0	
ANP32B	1,51	4,73E-02	1,42E-01	2				0	
FEN1	1,48	3,82E-02	1,20E-01	2				0	
AHCY	1,47	1,07E-02	5,05E-02	3				0	
MTA2	1,42	1,91E-02	7,77E-02	4				0	
MBD3	1,40	4,43E-02	1,34E-01	2				0	
CCT6A	1,40	1,85E-02	7,65E-02	3				0	
THOC7;NIF3L1BP1	1,38	5,01E-03	2,85E-02	4				0	
NELFCD;TH1L	1,38	6,38E-02	1,73E-01	2				0	
TBL3	1,36	5,79E-02	1,62E-01	2				0	
HIST1H2AJ;HIST1H2AH; H2AFJ;HIST1H2AG	1,36	4,97E-02	1,46E-01	2				0	
SYMPK	1,34	1,89E-02	7,71E-02	4				0	
SURF6	1,32	6,34E-02	1,73E-01	2				0	
STAG2	1,31	6,31E-02	1,72E-01	2				0	
DDX50	1,27	1,02E-01	2,43E-01	3				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
CASP14	1,25	7,80E-02	2,01E-01	2				0	
BPTF	1,23	9,14E-02	2,25E-01	2				0	
CDK7	1,23	3,15E-02	1,08E-01	3				0	
RBM4	1,22	2,96E-02	1,05E-01	3				0	
PSMD6	1,20	3,13E-02	1,07E-01	3				0	
FUS	1,19	8,32E-02	2,10E-01	2				0	
DDX39A	1,19	1,11E-02	5,22E-02	5				0	
FUBP3	1,19	1,18E-01	2,65E-01	2				0	
PSMD1	1,18	8,55E-02	2,15E-01	2				0	
DENND2D	1,18	1,17E-01	2,65E-01	2				0	
RAD50	1,17	8,69E-02	2,17E-01	2				0	
CWC15	1,15	2,13E-02	8,48E-02	4				0	
RFC5	1,14	9,41E-02	2,28E-01	2				0	
CCNL1	1,14	9,97E-02	2,38E-01	2				0	
TAF5	1,13	1,02E-01	2,43E-01	2				0	
SUZ12	1,13	9,88E-02	2,37E-01	2				0	
G3BP2	1,12	1,10E-01	2,54E-01	2				0	
TAF9	1,09	1,11E-01	2,57E-01	2				0	
NOP16	1,09	4,74E-02	1,42E-01	3				0	
BYSL	1,09	1,16E-01	2,63E-01	2				0	
CWC22	1,07	7,66E-02	1,99E-01	3				0	
G3BP1	1,06	3,70E-02	1,18E-01	4				0	
KDM1A	1,03	1,28E-01	2,79E-01	2				0	
C11orf31;SELH	1,03	1,27E-01	2,77E-01	2				0	
SUGP1	1,01	1,36E-01	2,90E-01	2				0	
ETF1	0,94	8,16E-02	2,07E-01	3				0	
ZC3H11A	0,94	1,62E-01	3,29E-01	2				0	
UBAP2L	0,91	1,76E-01	3,44E-01	2				0	
RFC3	0,91	1,77E-01	3,44E-01	2				0	
RBBP5	0,90	1,89E-01	3,57E-01	2				0	
HNRNPH2	0,90	1,81E-01	3,48E-01	2				0	
MYEF2	0,89	1,24E-01	2,75E-01	3				0	
ZNF260	0,88	2,00E-01	3,70E-01	2				0	
SMARCE1	0,87	1,06E-01	2,49E-01	3				0	
WDR61	0,86	1,99E-01	3,70E-01	2				0	
PDCD11	0,84	2,25E-01	4,02E-01	2				0	
SMCHD1	0,83	2,12E-01	3,86E-01	2				0	
PABPC4	0,83	1,25E-01	2,77E-01	4				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
SAFB	0,83	7,35E-02	1,96E-01	4				0	
HDLBP	0,82	2,32E-01	4,09E-01	2				0	
CFL1	0,80	1,56E-01	3,25E-01	3				0	
EXOSC7	0,79	2,35E-01	4,12E-01	2				0	
PHB2	0,79	2,38E-01	4,15E-01	2				0	
PSMC6	0,78	2,85E-01	4,60E-01	2				0	
DDX31	0,78	2,75E-01	4,52E-01	2				0	
DRG1	0,77	1,63E-01	3,29E-01	3				0	
DHX16	0,77	2,59E-01	4,37E-01	2				0	
HAUS8	0,77	2,51E-01	4,26E-01	2				0	
NUP85	0,77	2,79E-01	4,55E-01	2				0	
HNRNPD	0,74	1,64E-01	3,29E-01	3				0	
PPIB	0,74	2,89E-01	4,64E-01	2				0	
SYF2	0,71	2,83E-01	4,59E-01	2				0	
CBFB	0,70	1,94E-01	3,63E-01	3				0	
GNL3L	0,70	2,03E-01	3,76E-01	3				0	
RAE1	0,69	1,94E-01	3,63E-01	3				0	
ERCC3	0,69	2,06E-01	3,80E-01	3				0	
UTP6	0,68	3,07E-01	4,82E-01	2				0	
TFIP11	0,68	3,06E-01	4,81E-01	2				0	
CHD8	0,68	3,15E-01	4,91E-01	2				0	
RAC1	0,65	3,24E-01	4,97E-01	2				0	
MEAF6	0,65	2,91E-01	4,65E-01	3				0	
C14orf166	0,65	2,38E-01	4,15E-01	3				0	
TAF2	0,65	3,30E-01	5,04E-01	2				0	
ARG1	0,64	3,36E-01	5,09E-01	2				0	
SLU7	0,63	3,44E-01	5,15E-01	2				0	
PSMC3	0,63	3,42E-01	5,14E-01	2				0	
ACO2	0,63	1,85E-01	3,54E-01	4				0	
GTF2E2	0,62	2,64E-01	4,43E-01	3				0	
API5	0,61	3,68E-01	5,37E-01	2				0	
MTA1	0,60	3,62E-01	5,30E-01	2				0	
RBMX2	0,59	3,71E-01	5,39E-01	2				0	
POLE3	0,58	4,01E-01	5,72E-01	2				0	
CUL2	0,57	3,90E-01	5,62E-01	2				0	
PCNA	0,57	4,01E-01	5,72E-01	2				0	
POLR1C	0,56	4,03E-01	5,74E-01	2				0	
FBLL1	0,56	4,01E-01	5,72E-01	2				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
JUP	0,55	3,52E-01	5,22E-01	3				0	
PAXBP1	0,53	4,18E-01	5,86E-01	2				0	
PRMT1	0,53	4,21E-01	5,87E-01	2				0	
ICE1	0,53	4,14E-01	5,84E-01	3				0	
SNRPC	0,52	2,66E-01	4,46E-01	4				0	
PPIL3	0,52	3,70E-01	5,39E-01	3				0	
RANGAP1	0,52	3,37E-01	5,09E-01	3				0	
CBX5	0,51	2,74E-01	4,52E-01	4				0	
MRPL46	0,51	3,58E-01	5,26E-01	3				0	
CSTF1	0,50	3,28E-01	5,02E-01	4				0	
PPP1CC	0,49	3,60E-01	5,28E-01	3				0	
AURKB	0,47	4,71E-01	6,32E-01	2				0	
SEH1L	0,47	4,83E-01	6,42E-01	2				0	
NIP7	0,46	3,35E-01	5,08E-01	4				0	
NVL	0,43	5,27E-01	6,85E-01	2				0	
KIF2C	0,42	4,16E-01	5,84E-01	3				0	
RNPC3	0,39	5,56E-01	7,09E-01	2				0	
NXT1	0,38	4,63E-01	6,25E-01	3				0	
CSTA	0,38	5,71E-01	7,18E-01	2				0	
INCENP	0,38	5,64E-01	7,15E-01	2				0	
HNRNPLL; HNRPLL	0,35	5,00E-01	6,56E-01	3				0	
ZCCHC8	0,35	5,93E-01	7,37E-01	2				0	
CCDC137	0,34	6,17E-01	7,58E-01	2				0	
CUL3	0,34	6,14E-01	7,56E-01	2				0	
ZNF207	0,33	5,32E-01	6,89E-01	3				0	
TUFM	0,33	6,15E-01	7,57E-01	2				0	
UTP18	0,33	5,68E-01	7,18E-01	3				0	
CAT	0,32	5,54E-01	7,09E-01	3				0	
RAB1A	0,32	5,49E-01	7,06E-01	3				0	
PPAN-P2RY11;PPAN	0,31	5,69E-01	7,18E-01	3				0	
EIF3K	0,31	6,42E-01	7,76E-01	2				0	
PCID2	0,31	6,38E-01	7,75E-01	2				0	
EXOSC1	0,29	6,56E-01	7,86E-01	2				0	
TAF1;TAF1L	0,29	6,85E-01	8,05E-01	2				0	
CTNNBL1	0,28	5,40E-01	6,97E-01	4				0	
DDX10	0,28	6,75E-01	7,97E-01	2				0	
CTSD	0,27	6,87E-01	8,06E-01	2				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
WDR12	0,26	6,93E-01	8,10E-01	2				0	
DDB1	0,26	6,41E-01	7,76E-01	3				0	
EED	0,26	6,26E-01	7,63E-01	3				0	
MRPL40	0,26	6,26E-01	7,63E-01	3				0	
NOB1	0,26	6,95E-01	8,11E-01	2				0	
NEDD8;NEDD8-MDP1	0,25	7,25E-01	8,31E-01	2				0	
RCL1	0,25	7,11E-01	8,22E-01	2				0	
ZC3H14	0,24	7,08E-01	8,20E-01	2				0	
GTPBP1	0,24	6,37E-01	7,75E-01	3				0	
RP9	0,23	5,97E-01	7,42E-01	4				0	
TAF4	0,22	7,38E-01	8,40E-01	2				0	
CNOT1	0,22	7,52E-01	8,46E-01	2				0	
NUP155	0,20	7,23E-01	8,29E-01	3				0	
WTAP	0,19	6,79E-01	7,99E-01	4				0	
KPNB1	0,19	6,75E-01	7,97E-01	4				0	
AP2M1	0,18	7,45E-01	8,43E-01	3				0	
PWP2	0,18	7,88E-01	8,79E-01	2				0	
DNTTIP1	0,17	7,91E-01	8,81E-01	2				0	
MARK2	0,16	8,08E-01	8,93E-01	3				0	
NEDD4	0,15	8,19E-01	8,98E-01	2				0	
MTHFD1	0,14	8,25E-01	9,00E-01	2				0	
RBM6	0,14	8,32E-01	9,04E-01	2				0	
MRPL22	0,14	8,39E-01	9,09E-01	2				0	
LARP1	0,14	8,30E-01	9,03E-01	2				0	
KAT7	0,14	8,34E-01	9,04E-01	2				0	
DDOST	0,14	8,32E-01	9,04E-01	2				0	
ILF2	0,13	8,29E-01	9,03E-01	3				0	
PLK1	0,11	8,62E-01	9,21E-01	2				0	
CTNNB1	0,09	8,40E-01	9,09E-01	4				0	
DHX35	0,08	9,00E-01	9,47E-01	2				0	
SRFBP1	0,07	9,12E-01	9,53E-01	2				0	
IMP3	0,07	9,16E-01	9,54E-01	2				0	
DNAJB6;DNAJB7	0,06	9,24E-01	9,59E-01	2				0	
L3MBTL3	0,06	9,27E-01	9,60E-01	2				0	
CHD1	0,06	9,08E-01	9,52E-01	4				0	
MYO1G	0,04	9,40E-01	9,68E-01	3				0	
DPF2	0,03	9,61E-01	9,81E-01	2				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
POLR1D	0,03	9,62E-01	9,81E-01	2				0	
PHGDH	0,02	9,73E-01	9,87E-01	2				0	
DDX24	0,02	9,75E-01	9,87E-01	2				0	
USP39	0,02	9,71E-01	9,86E-01	3				0	
MMTAG2	0,01	9,84E-01	9,91E-01	2				0	
FBXO28	0,01	9,89E-01	9,94E-01	2				0	
EIF5A;EIF5AL1	0,00	9,98E-01	9,98E-01	3				0	
SMARCA2	0,00	9,97E-01	9,98E-01	2				0	
ARPC4;ARPC4-TTLL3	0,00	9,97E-01	9,98E-01	2				0	
TEAD1;TEAD4; TEAD3	-0,01	9,92E-01	9,95E-01	2				0	
NAA40	-0,02	9,77E-01	9,88E-01	2				0	
RBM15B	-0,02	9,76E-01	9,88E-01	2				0	
PRPS1	-0,02	9,71E-01	9,86E-01	2				0	
RPP30	-0,03	9,64E-01	9,81E-01	2				0	
RASA2	-0,03	9,63E-01	9,81E-01	2				0	
ZBTB7A	-0,04	9,50E-01	9,75E-01	2				0	
TGM3	-0,05	9,36E-01	9,65E-01	2				0	
SRBD1	-0,06	9,25E-01	9,59E-01	2				0	
SIN3A	-0,06	9,27E-01	9,60E-01	2				0	
RBM42	-0,07	9,16E-01	9,54E-01	2				0	
CCAR2	-0,07	9,15E-01	9,54E-01	2				0	
DDX52	-0,09	8,49E-01	9,14E-01	4				0	
METTL17	-0,09	8,67E-01	9,23E-01	3				0	
RRP7A;RRP7BP	-0,09	8,72E-01	9,24E-01	3				0	
YWHAZ	-0,10	8,86E-01	9,33E-01	2				0	
HNRNPDL	-0,11	8,72E-01	9,24E-01	2				0	
FYTTD1	-0,11	8,68E-01	9,23E-01	2				0	
POP4	-0,11	8,62E-01	9,21E-01	2				0	
WDR48	-0,12	8,51E-01	9,14E-01	2				0	
NSF	-0,13	8,19E-01	8,98E-01	3				0	
DMAP1	-0,14	8,32E-01	9,04E-01	2				0	
UHRF1	-0,14	7,89E-01	8,79E-01	3				0	
HADHA	-0,15	8,20E-01	8,98E-01	2				0	
EXOSC4	-0,16	8,11E-01	8,94E-01	2				0	
FCF1	-0,17	7,43E-01	8,42E-01	4				0	
C1QB	-0,17	7,96E-01	8,82E-01	2				0	

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	n (exp) MYC ON	mean log2FC MYC OFF	p-vlaue MYC OFF	q-value MYC OFF	n (exp) MYC OFF	Function
PSMC1	-0,17	7,95E-01	8,82E-01	2				0	
DNAJC9	-0,17	7,94E-01	8,82E-01	2				0	
KIF22	-0,18	7,30E-01	8,35E-01	3				0	
FABP5	-0,21	7,45E-01	8,43E-01	2				0	
EXOSC2	-0,22	7,40E-01	8,40E-01	2				0	
CBX8	-0,22	7,39E-01	8,40E-01	2				0	
RPS29	-0,22	6,76E-01	7,97E-01	3				0	
EXOSC9	-0,22	7,36E-01	8,38E-01	2				0	
CENPV	-0,22	7,43E-01	8,42E-01	2				0	
RPL29	-0,22	7,31E-01	8,36E-01	2				0	
NMT1	-0,24	6,87E-01	8,06E-01	4				0	
HMGB2	-0,24	6,52E-01	7,84E-01	3				0	
BCL7C	-0,24	7,18E-01	8,25E-01	2				0	
MAPK1	-0,24	7,16E-01	8,24E-01	2				0	
FXR1	-0,24	6,56E-01	7,86E-01	3				0	
VDAC1	-0,27	6,79E-01	7,99E-01	2				0	
WHSC1	-0,28	6,70E-01	7,94E-01	2				0	
PQBP1	-0,28	6,73E-01	7,97E-01	2				0	
WDR43	-0,28	5,33E-01	6,89E-01	4				0	
USP3	-0,29	5,98E-01	7,42E-01	3				0	
PSMD3	-0,29	6,14E-01	7,56E-01	3				0	
SRSF9	-0,30	6,19E-01	7,58E-01	3				0	
RPP40	-0,30	6,67E-01	7,93E-01	2				0	
SMC5	-0,30	6,48E-01	7,81E-01	2				0	
CDC27	-0,30	6,45E-01	7,77E-01	2				0	
TBP;TBPL2	-0,30	6,58E-01	7,86E-01	2				0	
IGKV4-1	-0,31	6,43E-01	7,76E-01	2				0	
NCBP2	-0,31	6,43E-01	7,76E-01	2				0	
ACTR8	-0,33	6,19E-01	7,58E-01	2				0	
TEX10	-0,35	5,24E-01	6,83E-01	3				0	
SHMT2	-0,35	4,49E-01	6,16E-01	4				0	
RRP15	-0,36	5,85E-01	7,30E-01	2				0	
ADNP	-0,36	5,88E-01	7,32E-01	2				0	
POLR1B	-0,36	5,79E-01	7,25E-01	2				0	
RPP25L	-0,37	5,83E-01	7,29E-01	2				0	
TOP2B	-0,37	4,66E-01	6,29E-01	4				0	
MUTYH	-0,37	5,69E-01	7,18E-01	2				0	
MAT2A	-0,38	4,72E-01	6,32E-01	3				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
POLR1A	-0,39	4,58E-01	6,23E-01	3				0	
LIG1	-0,39	5,59E-01	7,12E-01	2				0	
SUCLG1	-0,42	5,50E-01	7,07E-01	2				0	
NOL10	-0,43	4,16E-01	5,84E-01	3				0	
RPS21	-0,43	4,21E-01	5,87E-01	4				0	
DDX1	-0,43	4,27E-01	5,93E-01	3				0	
ANXA2;ANXA2P2	-0,43	5,30E-01	6,87E-01	2				0	
WDR46	-0,45	3,12E-01	4,88E-01	5				0	
RIF1	-0,46	4,88E-01	6,45E-01	2				0	
LYZ	-0,46	5,45E-01	7,02E-01	2				0	
RUNX3	-0,47	4,93E-01	6,48E-01	2				0	
RPF1	-0,48	4,17E-01	5,84E-01	4				0	
DDX49	-0,48	4,01E-01	5,72E-01	3				0	
RSL24D1	-0,48	4,63E-01	6,25E-01	2				0	
EDC4	-0,49	4,81E-01	6,40E-01	2				0	
UTP3	-0,49	2,77E-01	4,53E-01	4				0	
DHX38	-0,50	4,49E-01	6,16E-01	2				0	
FAM207A	-0,50	4,53E-01	6,19E-01	2				0	
MINA	-0,50	3,53E-01	5,22E-01	3				0	
GATAD2A	-0,51	4,46E-01	6,14E-01	2				0	
RQCD1	-0,51	4,41E-01	6,10E-01	2				0	
UTP23	-0,51	3,53E-01	5,22E-01	3				0	
MEN1	-0,51	4,58E-01	6,23E-01	2				0	
BLMH	-0,52	4,38E-01	6,07E-01	2				0	
TRAP1	-0,52	4,26E-01	5,92E-01	2				0	
DEK	-0,53	2,41E-01	4,18E-01	4				0	
DLAT	-0,53	4,21E-01	5,87E-01	2				0	
AATF	-0,54	4,51E-01	6,17E-01	2				0	
EXOSC6	-0,55	4,05E-01	5,75E-01	2				0	
NOP10	-0,55	2,44E-01	4,20E-01	4				0	
RARS	-0,56	4,12E-01	5,83E-01	2				0	
CBX4	-0,56	3,96E-01	5,68E-01	2				0	
PSPC1	-0,58	4,07E-01	5,78E-01	2				0	
EXOSC8	-0,59	3,83E-01	5,52E-01	2				0	
ZNF146	-0,59	2,68E-01	4,46E-01	3				0	
NGDN	-0,59	1,52E-01	3,17E-01	5				0	
SFSWAP	-0,60	2,74E-01	4,52E-01	4				0	
RPUSD4	-0,61	3,63E-01	5,31E-01	2				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
WRNIP1	-0,61	3,55E-01	5,23E-01	2				0	
SRP19	-0,62	3,53E-01	5,22E-01	2				0	
SMARCC2	-0,63	2,47E-01	4,21E-01	3				0	
PRDX2	-0,63	3,51E-01	5,22E-01	2				0	
ZNF512	-0,64	3,36E-01	5,09E-01	2				0	
BRD7	-0,64	2,43E-01	4,19E-01	3				0	
PSMD13	-0,64	2,28E-01	4,05E-01	3				0	
FBXL6	-0,65	3,45E-01	5,15E-01	2				0	
EXOSC10	-0,65	3,28E-01	5,02E-01	2				0	
ANAPC7	-0,65	3,25E-01	4,98E-01	2				0	
SAMD1	-0,66	3,17E-01	4,91E-01	2				0	
UTP15	-0,67	2,26E-01	4,03E-01	3				0	
YLPM1	-0,67	3,16E-01	4,91E-01	2				0	
APEX1	-0,67	3,81E-01	5,50E-01	2				0	
CDC2;CDK1	-0,68	2,63E-01	4,43E-01	3				0	
NOM1	-0,69	3,16E-01	4,91E-01	2				0	
BRD4	-0,69	2,99E-01	4,75E-01	2				0	
NOP2	-0,69	8,23E-02	2,08E-01	5				0	
DDX6	-0,70	1,74E-01	3,42E-01	4				0	
MCM5	-0,70	1,87E-01	3,56E-01	4				0	
SAP30	-0,71	2,86E-01	4,61E-01	2				0	
EPB41L5	-0,72	2,77E-01	4,53E-01	2				0	
SBSN	-0,72	2,82E-01	4,58E-01	2				0	
SREK1	-0,72	2,14E-01	3,89E-01	4				0	
USP7	-0,72	1,80E-01	3,47E-01	3				0	
VRK1	-0,73	1,89E-01	3,57E-01	3				0	
ZNF691	-0,73	1,77E-01	3,44E-01	3				0	
ZNF579	-0,74	2,69E-01	4,47E-01	2				0	
CCNK	-0,74	2,76E-01	4,53E-01	2				0	
GTF3C3	-0,74	2,68E-01	4,46E-01	2				0	
PSMC4	-0,74	2,91E-01	4,65E-01	2				0	
DHX33	-0,74	2,80E-01	4,55E-01	2				0	
SERPINB12	-0,74	2,67E-01	4,46E-01	2				0	
ABT1	-0,76	2,63E-01	4,43E-01	2				0	
ARRB2	-0,77	1,50E-01	3,16E-01	3				0	
STRBP	-0,78	2,48E-01	4,23E-01	2				0	
SRPK1	-0,80	1,59E-01	3,29E-01	3				0	
ARPC1B	-0,81	1,40E-01	2,96E-01	3				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
KPNA3	-0,81	1,31E-01	2,84E-01	3				0	
ATF2	-0,81	2,35E-01	4,12E-01	2				0	
UBA1	-0,82	2,21E-01	3,98E-01	2				0	
VDAC3	-0,82	1,63E-01	3,29E-01	3				0	
EIF5B	-0,82	1,91E-01	3,60E-01	3				0	
ATP5O	-0,83	2,38E-01	4,15E-01	2				0	
CXXC1	-0,84	2,16E-01	3,92E-01	2				0	
LEF1	-0,84	1,23E-01	2,75E-01	3				0	
MOGS	-0,84	2,08E-01	3,82E-01	2				0	
MIOS	-0,87	1,95E-01	3,66E-01	2				0	
DARS	-0,88	1,26E-01	2,77E-01	3				0	
POLE	-0,89	1,99E-01	3,70E-01	2				0	
C3	-0,89	2,07E-01	3,81E-01	2				0	
PDS5B	-0,89	1,37E-01	2,90E-01	3				0	
PURB	-0,90	1,91E-01	3,60E-01	2				0	
CDC23	-0,91	1,77E-01	3,44E-01	2				0	
KRI1	-0,91	1,77E-01	3,44E-01	2				0	
OGT	-0,91	1,75E-01	3,43E-01	2				0	
SMC2	-0,92	7,66E-02	1,99E-01	4				0	
NOL7	-0,92	1,73E-01	3,40E-01	2				0	
MED13	-0,93	1,69E-01	3,35E-01	2				0	
ZFR	-0,94	1,66E-01	3,33E-01	2				0	
EIF1AX;EIF1AY	-0,94	9,20E-02	2,25E-01	3				0	
SERPINB3; SERPINB4	-0,95	1,60E-01	3,29E-01	2				0	
SMARCD1	-0,95	1,63E-01	3,29E-01	2				0	
FAM133A	-0,95	1,62E-01	3,29E-01	2				0	
LGALS7	-0,95	1,61E-01	3,29E-01	2				0	
MEPCE	-0,96	4,99E-02	1,46E-01	4				0	
ZSCAN25	-0,96	2,19E-01	3,96E-01	3				0	
NOL12	-0,96	2,32E-01	4,09E-01	2				0	
TRMT1L	-0,97	1,86E-01	3,55E-01	2				0	
TTN	-0,98	7,54E-02	1,99E-01	3				0	
NSA2	-0,99	1,18E-01	2,65E-01	3				0	
EME1	-1,01	1,34E-01	2,88E-01	2				0	
LIG3	-1,03	1,29E-01	2,80E-01	2				0	
NFYA	-1,03	1,32E-01	2,84E-01	2				0	
DLST	-1,05	1,21E-01	2,72E-01	2				0	
ITCH	-1,07	1,15E-01	2,62E-01	2				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
ZFP64	-1,08	1,32E-01	2,84E-01	2				0	
BHLHA15	-1,09	1,22E-01	2,72E-01	2				0	
PSIP1	-1,13	9,84E-02	2,37E-01	2				0	
MRPL15	-1,15	1,11E-01	2,57E-01	2				0	
C11orf57	-1,17	8,99E-02	2,23E-01	2				0	
WDR3	-1,19	8,50E-02	2,14E-01	2				0	
ESF1	-1,20	1,14E-01	2,60E-01	2				0	
PURA	-1,22	7,53E-02	1,99E-01	2				0	
MBD2	-1,23	8,08E-02	2,06E-01	2				0	
AKAP17A	-1,24	9,48E-02	2,29E-01	2				0	
CXorf56	-1,24	3,48E-02	1,14E-01	3				0	
POLR1E	-1,25	7,31E-02	1,96E-01	2				0	
AGO2	-1,25	6,94E-02	1,86E-01	2				0	
IGKV2D-29; IGKV2D-26	-1,28	5,25E-02	1,50E-01	3				0	
C4orf27	-1,30	6,18E-02	1,69E-01	2				0	
ZFP62	-1,30	6,12E-02	1,69E-01	2				0	
RPL7L1	-1,33	8,11E-02	2,06E-01	2				0	
SNRNP35	-1,35	5,25E-02	1,50E-01	2				0	
KLF16	-1,35	3,73E-02	1,19E-01	3				0	
CCDC59	-1,36	3,67E-02	1,18E-01	3				0	
ZNF646	-1,36	1,18E-01	2,65E-01	2				0	
MRGBP	-1,38	4,78E-02	1,43E-01	2				0	
DIEXF	-1,40	5,77E-02	1,62E-01	2				0	
ARHGEF2	-1,43	5,41E-02	1,54E-01	2				0	
DNTTIP2	-1,43	4,81E-02	1,43E-01	2				0	
ATF1	-1,44	4,06E-02	1,27E-01	2				0	
ZNF275	-1,44	4,05E-02	1,27E-01	2				0	
POP1	-1,45	4,88E-03	2,83E-02	4				0	
CKAP5	-1,45	4,47E-02	1,35E-01	2				0	
VCP	-1,47	1,17E-02	5,49E-02	3				0	
CSNK1A1	-1,47	6,71E-03	3,56E-02	4				0	
DGKZ	-1,48	3,51E-02	1,14E-01	2				0	
MRTO4	-1,48	3,49E-02	1,14E-01	2				0	
UNG;DKFZp-781L1143	-1,49	3,38E-02	1,12E-01	2				0	
TXN	-1,50	3,31E-02	1,11E-01	2				0	
NOP14	-1,50	3,41E-03	2,22E-02	4				0	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**n (exp) MYC ON**	**mean log2FC MYC OFF**	**p-vlaue MYC OFF**	**q-value MYC OFF**	**n (exp) MYC OFF**	**Function**
SKIV2L2	-1,50	7,90E-03	4,07E-02	4				0	
DHX37	-1,51	3,22E-02	1,09E-01	2				0	
PNO1	-1,53	2,98E-02	1,05E-01	2				0	
HNRNPU	-1,53	3,11E-02	1,07E-01	2				0	
THYN1	-1,56	2,70E-02	9,99E-02	2				0	
PKP1	-1,58	2,78E-02	1,00E-01	2				0	
RBM34	-1,68	2,21E-02	8,77E-02	2				0	
PRDM15	-1,71	2,54E-02	9,71E-02	2				0	
ANP32E	-1,73	2,29E-02	9,00E-02	2				0	
BLM	-1,80	4,01E-03	2,47E-02	3				0	
IKZF3	-1,84	1,11E-02	5,22E-02	2				0	
ELF1;DKFZp-686H0575	-1,84	1,60E-02	6,77E-02	2				0	
TSR1	-1,85	7,29E-03	3,81E-02	4				0	
PLAG1	-1,85	1,58E-02	6,72E-02	2				0	
S100A8	-1,86	1,65E-02	6,93E-02	2				0	
DSC3	-1,91	8,86E-03	4,43E-02	2				0	
RBM19	-1,93	8,57E-03	4,32E-02	2				0	
DHX30	-1,96	1,38E-02	6,15E-02	2				0	
CHD1L	-1,98	8,17E-03	4,17E-02	2				0	
ZNF800	-2,02	3,28E-02	1,10E-01	2				0	
ZNHIT6	-2,03	6,28E-03	3,43E-02	2				0	
DOT1L	-2,06	9,11E-03	4,48E-02	2				0	
CAAP1	-2,12	4,96E-03	2,85E-02	2				0	
ZKSCAN1	-2,19	1,73E-03	1,28E-02	3				0	
ATP5C1	-2,22	3,66E-03	2,32E-02	2				0	
HSP90B1	-2,40	3,57E-03	2,29E-02	2				0	
CNOT8	-2,51	1,54E-03	1,16E-02	2				0	
PLEC	-2,65	1,32E-04	1,55E-03	4				0	
HSPH1	-2,83	1,03E-03	8,29E-03	2				0	
YY1	-2,85	4,24E-04	4,18E-03	2				0	
DIAPH3	-3,11	3,55E-05	5,08E-04	3				0	
SPTBN1	-3,41	1,07E-04	1,31E-03	2				0	
BAZ1B	-3,42	8,77E-05	1,12E-03	2				0	

7.3.4 Table with values corresponding to Figure 4.8

Table 7.7: Values corresponding to Figure 4.8. Values are sorted according to mean log2FC and p-value. Genes marked in bold were determined as significant RNAPII interactors in U2OS cells according to the cutoffs: log2FC>2 and q-value<0.1.

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
POLR2C	9,40	1,27E-07	3,00E-05	RNAPII
GTF2F2	8,92	1,77E-07	3,00E-05	GTF
POLR2H	8,90	1,55E-07	3,00E-05	RNAPII
POLR2B	8,91	3,28E-07	4,17E-05	RNAPII
POLR2D	9,02	8,23E-07	7,61E-05	RNAPII
POLR2I	7,63	8,97E-07	7,61E-05	RNAPII
SUPT6H	7,81	1,06E-06	7,69E-05	EF
INTS3	7,63	2,03E-06	1,07E-04	Integrator
RPRD1B	7,39	1,93E-06	1,07E-04	Other
PPP2R1A	7,03	2,27E-06	1,07E-04	Other
INTS6	6,99	2,31E-06	1,07E-04	Integrator
POLR2A	7,70	2,53E-06	1,07E-04	RNAPII
POLR2F	8,23	3,83E-06	1,39E-04	RNAPII
RECQL5	6,98	3,78E-06	1,39E-04	Other
INTS1	6,92	4,37E-06	1,41E-04	Integrator
INTS4	6,47	4,42E-06	1,41E-04	Integrator
SUPT5H	6,92	5,54E-06	1,57E-04	EF
MED14	6,75	5,28E-06	1,57E-04	Mediator
INTS5	5,97	1,01E-05	2,69E-04	Integrator
SCAF11	5,95	1,32E-05	3,36E-04	EF
RPRD1A	6,56	1,93E-05	4,67E-04	Other
POLR2G	6,83	2,09E-05	4,75E-04	RNAPII
TCEA1	5,67	2,15E-05	4,75E-04	EF
INTS9	6,96	2,60E-05	5,51E-04	Integrator
MED17	6,24	3,05E-05	6,21E-04	Mediator
ASUN	5,56	3,18E-05	6,23E-04	Integrator
SAFB2	5,31	3,32E-05	6,26E-04	Other
YTHDC1	5,65	4,48E-05	8,13E-04	Splicing
ZNF326	5,07	5,06E-05	8,88E-04	Splicing
INTS7	5,27	6,14E-05	1,04E-03	Integrator
CSTF3	5,52	6,62E-05	1,09E-03	Termination
INTS2	6,01	9,21E-05	1,46E-03	Integrator
CPSF3	4,67	1,30E-04	2,01E-03	Termination
NCBP1	4,59	1,42E-04	2,12E-03	Splicing

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
RPRD2	5,15	2,43E-04	3,50E-03	Other
C17orf85	4,41	2,48E-04	3,50E-03	Other
CCAR1	4,31	2,72E-04	3,54E-03	Other
CSTF2	4,19	2,65E-04	3,54E-03	Termination
CRNKL1	4,18	2,64E-04	3,54E-03	Splicing
WDR82	5,22	2,96E-04	3,68E-03	Other
CSTF1	4,21	2,95E-04	3,68E-03	Splicing
SAFB	4,14	3,27E-04	3,97E-03	Other
MED6	4,42	3,36E-04	3,98E-03	Mediator
INTS10	4,14	3,76E-04	4,35E-03	Integrator
KHSRP	4,83	4,29E-04	4,86E-03	Splicing
CPSF1	4,57	4,65E-04	5,07E-03	Termination
IK	3,90	4,68E-04	5,07E-03	Splicing
CPSF3L	4,19	5,20E-04	5,51E-03	Termination
PHF3	3,88	5,37E-04	5,58E-03	Other
INTS8	4,41	6,39E-04	6,50E-03	Integrator
INTS12	4,00	7,06E-04	7,05E-03	Integrator
RBM8A	3,73	7,36E-04	7,20E-03	Splicing
MED22	3,68	7,79E-04	7,48E-03	Mediator
PHRF1	4,11	8,89E-04	8,38E-03	Other
POLR2E	5,72	9,21E-04	8,52E-03	RNAPII
GTF2F1	4,08	1,02E-03	9,21E-03	GTF
CTNNBL1	3,87	1,03E-03	9,21E-03	Splicing
CSNK2A1;CSNK2A3	4,04	1,11E-03	9,58E-03	Other
TRA2A	3,51	1,10E-03	9,58E-03	Splicing
XAB2	4,16	1,18E-03	1,00E-02	Splicing
PGAM5	3,47	1,29E-03	1,08E-02	Other
ZC3H18	3,61	1,43E-03	1,16E-02	Other
CHERP	3,60	1,43E-03	1,16E-02	Other
SF3A2	4,23	1,53E-03	1,22E-02	Splicing
MED4	4,21	1,65E-03	1,28E-02	Mediator
SCAF1	3,63	1,63E-03	1,28E-02	Other
SNRNP40	3,55	1,77E-03	1,35E-02	Splicing
U2SURP	3,56	1,81E-03	1,35E-02	Splicing
TTF2	3,36	1,83E-03	1,35E-02	Termination
SF3A3	3,96	2,05E-03	1,49E-02	Splicing
MED8	3,65	2,14E-03	1,51E-02	Mediator
PAF1	3,51	2,12E-03	1,51E-02	EF
KIAA1429	3,46	2,27E-03	1,56E-02	Other

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
RBM15	3,37	2,24E-03	1,56E-02	Other
THOC1	3,38	2,37E-03	1,61E-02	Other
FUS	3,87	2,46E-03	1,65E-02	Splicing
SRRT	3,65	2,58E-03	1,71E-02	Other
APOBEC3B	3,26	2,85E-03	1,86E-02	Other
SNRNP70	3,52	3,19E-03	2,03E-02	Splicing
CWC15	3,25	3,17E-03	2,03E-02	Splicing
RBM12B	3,27	3,51E-03	2,21E-02	Other
RNPS1	3,48	3,57E-03	2,22E-02	Splicing
HNRNPUL1	3,41	3,67E-03	2,25E-02	Other
FUBP3	3,38	3,82E-03	2,32E-02	Other
THOC2	3,12	3,98E-03	2,36E-02	Other
BCAS2	3,11	4,04E-03	2,36E-02	Splicing
TRA2B	3,07	4,00E-03	2,36E-02	Splicing
RPS16;ZNF90	3,09	4,69E-03	2,71E-02	Other
CWC22	3,12	4,89E-03	2,79E-02	Splicing
SRSF9	3,08	5,05E-03	2,79E-02	Splicing
RBM10	3,07	5,05E-03	2,79E-02	Other
XRN2	2,96	4,98E-03	2,79E-02	Termination
SNRPA	2,91	5,21E-03	2,85E-02	Splicing
PRPF8	4,10	5,43E-03	2,94E-02	Splicing
CPSF2	3,02	5,87E-03	3,14E-02	Termination
WDR33	2,87	6,03E-03	3,20E-02	Termination
NELFB	2,84	6,12E-03	3,21E-02	Other
AQR	3,42	6,69E-03	3,41E-02	Splicing
ZCCHC8	2,85	6,65E-03	3,41E-02	Other
CPSF4	2,75	6,65E-03	3,41E-02	Termination
PPIL1	2,74	6,79E-03	3,42E-02	Splicing
PPP1R10	3,16	6,91E-03	3,45E-02	Other
SAP18	2,86	7,06E-03	3,47E-02	Splicing
ACIN1	2,80	7,08E-03	3,47E-02	Splicing
MED27	3,03	7,28E-03	3,53E-02	Mediator
SYMPK	2,87	7,42E-03	3,56E-02	Termination
NCBP2	3,40	7,78E-03	3,67E-02	Splicing
THOC5	2,63	7,76E-03	3,67E-02	Other
TAF15	2,83	8,12E-03	3,79E-02	GTF
TPM3;DKFZp686J1372	3,51	8,81E-03	4,08E-02	Other
PRPF19	3,16	9,02E-03	4,14E-02	Splicing
LEO1	2,70	9,20E-03	4,18E-02	EF

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
PHF5A	2,56	9,27E-03	4,18E-02	Splicing
CDC40	2,86	1,00E-02	4,47E-02	Splicing
AKAP8	2,75	1,04E-02	4,58E-02	Other
PSPC1	2,55	1,05E-02	4,60E-02	Other
SRSF10	2,77	1,07E-02	4,68E-02	Splicing
YLPM1	2,71	1,11E-02	4,79E-02	Other
ZC3H11A	2,52	1,14E-02	4,87E-02	Other
PPP2CB	3,31	1,18E-02	5,02E-02	Other
CMTR1	2,56	1,24E-02	5,22E-02	Other
CDC73	3,11	1,25E-02	5,23E-02	EF
VDAC1	2,43	1,42E-02	5,89E-02	Other
RPS2	3,17	1,59E-02	6,51E-02	Other
DHX30	2,79	1,68E-02	6,84E-02	Other
SSRP1	2,38	1,75E-02	7,06E-02	EF
BCLAF1	2,41	1,77E-02	7,08E-02	Other
SCAF4	2,26	1,78E-02	7,08E-02	EF
MED31	2,75	1,81E-02	7,14E-02	Mediator
PLRG1	2,30	1,89E-02	7,42E-02	Splicing
EIF3L	2,73	1,94E-02	7,54E-02	Other
NCOA5	3,28	1,96E-02	7,58E-02	Other
ERH	2,30	2,13E-02	8,15E-02	Splicing
RBM17	2,58	2,17E-02	8,26E-02	Splicing
RPS27	2,62	2,19E-02	8,26E-02	Other
ILF2	2,35	2,31E-02	8,64E-02	Other
CTR9	2,31	2,43E-02	8,97E-02	EF
SF3B1	2,25	2,43E-02	8,97E-02	Splicing
FUBP1	2,38	2,48E-02	9,08E-02	Other
PRPF38A	2,23	2,51E-02	9,11E-02	Splicing
FYTTD1	2,17	2,60E-02	9,40E-02	Other
SF1	2,15	2,63E-02	9,42E-02	Splicing
ALDH18A1	2,62	2,68E-02	9,53E-02	Other
PPP2R1B	2,27	2,72E-02	9,58E-02	Other
KHDRBS3	2,23	2,73E-02	9,58E-02	Splicing
MFAP1	2,67	2,86E-02	9,69E-02	Splicing
GTF2I	2,46	2,88E-02	9,69E-02	GTF
MED20	2,36	2,89E-02	9,69E-02	Mediator
HNRNPR	2,23	2,87E-02	9,69E-02	Splicing
KHDRBS1	2,17	2,78E-02	9,69E-02	Splicing
SNW1	2,09	2,87E-02	9,69E-02	Splicing

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	Function
POLDIP3	2,07	2,89E-02	9,69E-02	Other
IWS1	2,27	2,91E-02	9,70E-02	EF
PRPF38B	2,58	2,99E-02	9,89E-02	Splicing
ZC3H4	2,02	3,06E-02	1,01E-01	Other
SNRNP200	2,41	3,10E-02	1,01E-01	Splicing
PAXBP1	2,36	3,13E-02	1,02E-01	Other
HADHA	2,30	3,31E-02	1,06E-01	Other
CCAR2	2,06	3,33E-02	1,06E-01	Splicing
VWA9	2,39	3,38E-02	1,07E-01	Integrator
SRSF6	2,08	3,37E-02	1,07E-01	Splicing
PNN	2,04	3,53E-02	1,10E-01	Other
ILF3	2,10	3,78E-02	1,14E-01	Other
EWSR1	2,08	3,73E-02	1,14E-01	Other
SRSF7	2,07	3,78E-02	1,14E-01	Splicing
BUB3	2,03	3,84E-02	1,16E-01	Other
PPWD1	2,45	3,92E-02	1,17E-01	Other
DDX42	2,09	3,99E-02	1,18E-01	Other
MYEF2	2,05	4,00E-02	1,18E-01	Other
DHX16	2,12	4,07E-02	1,19E-01	Splicing
CPSF6	2,37	4,15E-02	1,21E-01	Termination
EIF3A	2,66	4,31E-02	1,25E-01	Other
NELFE	2,38	4,36E-02	1,25E-01	Other
DHX9	2,00	4,59E-02	1,31E-01	Other
ATAD3A	2,07	4,97E-02	1,38E-01	Other
RANGAP1	2,69	5,02E-02	1,39E-01	
C7orf26	2,19	5,29E-02	1,46E-01	
MED15	2,64	5,36E-02	1,46E-01	
EIF3C;EIF3CL	2,16	5,38E-02	1,46E-01	
PRMT1	2,16	6,08E-02	1,61E-01	
TFIP11	2,21	6,89E-02	1,76E-01	
DNAJC8	2,06	8,55E-02	2,00E-01	
RBM5	2,10	8,83E-02	2,04E-01	
RBM6	2,14	9,49E-02	2,14E-01	
NONO	1,99	3,76E-02	1,14E-01	
NHP2L1	1,98	4,44E-02	1,27E-01	
MCM5	1,98	3,71E-02	1,14E-01	
VDAC2	1,96	3,44E-02	1,08E-01	
RPS20	1,95	6,82E-02	1,76E-01	
RBM14	1,94	3,99E-02	1,18E-01	

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	Function
EIF3I	1,92	7,16E-02	1,80E-01	
SRSF1	1,91	4,81E-02	1,34E-01	
CHTOP	1,91	4,63E-02	1,31E-01	
SYNCRIP	1,90	5,99E-02	1,60E-01	
RPL11	1,89	7,59E-02	1,86E-01	
DHX15	1,88	5,38E-02	1,46E-01	
API5	1,87	6,84E-02	1,76E-01	
EFTUD2	1,85	6,76E-02	1,76E-01	
EIF4A3	1,85	6,77E-02	1,76E-01	
EIF3F	1,84	8,12E-02	1,94E-01	
MED23	1,84	4,71E-02	1,33E-01	
NUP93	1,83	9,46E-02	2,14E-01	
HNRNPH1	1,83	6,09E-02	1,61E-01	
DDX50	1,82	5,66E-02	1,52E-01	
MTA2	1,81	8,17E-02	1,94E-01	
ADAR	1,81	7,93E-02	1,91E-01	
HNRNPH3	1,79	1,01E-01	2,17E-01	
SPTBN1	1,78	9,89E-02	2,17E-01	
G3BP1	1,77	6,44E-02	1,69E-01	
RAD50	1,77	5,46E-02	1,47E-01	
SNRPD2	1,74	7,37E-02	1,83E-01	
SF3A1	1,74	7,73E-02	1,88E-01	
CLP1	1,74	6,94E-02	1,77E-01	
PELP1	1,74	7,16E-02	1,80E-01	
THRAP3	1,73	9,29E-02	2,12E-01	
HNRNPA3	1,73	9,11E-02	2,10E-01	
TPR	1,73	1,30E-01	2,42E-01	
SCAF8	1,72	1,03E-01	2,19E-01	
TARDBP	1,72	7,45E-02	1,84E-01	
TCERG1	1,72	7,06E-02	1,79E-01	
CSNK2A2	1,69	8,82E-02	2,04E-01	
CCT4	1,69	9,18E-02	2,10E-01	
SLU7	1,67	1,18E-01	2,34E-01	
RALY	1,67	7,53E-02	1,85E-01	
HDGFRP2	1,66	8,36E-02	1,97E-01	
FAM120A	1,66	2,26E-01	3,64E-01	
SMU1	1,65	1,01E-01	2,17E-01	
THOC6	1,64	7,94E-02	1,91E-01	
RCC2	1,63	1,04E-01	2,19E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
ZFR	1,63	1,24E-01	2,39E-01	
MCM7	1,63	8,56E-02	2,00E-01	
ERLIN1	1,62	1,21E-01	2,37E-01	
XRCC5	1,62	1,00E-01	2,17E-01	
EIF3E	1,61	1,13E-01	2,28E-01	
MCM2	1,61	7,25E-02	1,81E-01	
PRPF6	1,60	1,07E-01	2,22E-01	
RBFOX2;RBFOX1	1,59	9,86E-02	2,17E-01	
CCT3	1,59	8,04E-02	1,93E-01	
DDX23	1,59	8,23E-02	1,95E-01	
SF3B2	1,58	9,80E-02	2,17E-01	
PABPC1;PABPC3	1,57	1,05E-01	2,20E-01	
SKIV2L2	1,57	1,08E-01	2,23E-01	
PRPF40A	1,57	9,70E-02	2,17E-01	
CWC27	1,57	1,26E-01	2,40E-01	
PPIE	1,57	1,49E-01	2,67E-01	
PTBP1	1,56	9,35E-02	2,12E-01	
MED1	1,56	1,01E-01	2,17E-01	
MCM3	1,55	1,24E-01	2,39E-01	
LUC7L3	1,55	1,00E-01	2,17E-01	
LMNB2	1,54	1,52E-01	2,72E-01	
SFPQ	1,54	1,09E-01	2,23E-01	
SRSF5	1,53	1,28E-01	2,42E-01	
EIF4G1	1,52	1,23E-01	2,38E-01	
PPIB	1,52	9,82E-02	2,17E-01	
PRKDC	1,51	1,01E-01	2,17E-01	
RBMX	1,51	1,15E-01	2,31E-01	
HNRNPM	1,50	1,01E-01	2,17E-01	
CD2BP2	1,49	1,30E-01	2,42E-01	
SRSF4	1,49	1,03E-01	2,18E-01	
HNRNPA0	1,49	1,29E-01	2,42E-01	
SRRM2	1,48	1,02E-01	2,18E-01	
CKAP4	1,48	1,20E-01	2,36E-01	
DDX46	1,48	1,12E-01	2,28E-01	
PABPN1	1,47	1,42E-01	2,59E-01	
HNRNPDL	1,47	1,25E-01	2,40E-01	
HNRNPA2B1	1,46	1,55E-01	2,75E-01	
GPN1	1,46	1,79E-01	3,08E-01	
SRSF3	1,46	1,07E-01	2,22E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
EMD	1,46	1,12E-01	2,28E-01	
HNRNPF	1,46	1,17E-01	2,33E-01	
PHB2	1,45	1,05E-01	2,19E-01	
PPIG	1,45	1,19E-01	2,34E-01	
RBM25	1,42	1,26E-01	2,40E-01	
CLASRP	1,42	2,08E-01	3,41E-01	
RTCB	1,41	1,18E-01	2,34E-01	
HDAC1	1,41	1,37E-01	2,53E-01	
CPSF7	1,41	1,11E-01	2,26E-01	
NELFA	1,40	1,44E-01	2,63E-01	
NUP107	1,40	1,87E-01	3,17E-01	
SAP30BP	1,39	1,15E-01	2,31E-01	
ZNF207	1,38	1,29E-01	2,42E-01	
HSP90AB1	1,38	1,24E-01	2,39E-01	
CCT7	1,37	1,70E-01	2,98E-01	
PQBP1	1,37	1,32E-01	2,45E-01	
SCRIB	1,37	1,21E-01	2,37E-01	
HNRNPK	1,37	1,44E-01	2,63E-01	
DDX1	1,37	1,36E-01	2,52E-01	
MED16	1,35	1,40E-01	2,58E-01	
NUP133	1,35	2,74E-01	4,22E-01	
SREK1	1,32	1,47E-01	2,67E-01	
DDX26B	1,30	1,83E-01	3,12E-01	
RBM7	1,30	2,14E-01	3,48E-01	
SF3B6	1,30	1,55E-01	2,75E-01	
EIF3B	1,30	1,97E-01	3,30E-01	
DDX17	1,29	1,70E-01	2,98E-01	
ELAVL1	1,28	1,71E-01	2,98E-01	
THOC3	1,28	2,01E-01	3,33E-01	
SF3B3	1,28	2,05E-01	3,36E-01	
MED26	1,26	1,48E-01	2,67E-01	
PHB	1,26	1,57E-01	2,77E-01	
RPL18A	1,26	1,82E-01	3,11E-01	
WDR43	1,25	1,57E-01	2,77E-01	
SLTM	1,24	1,74E-01	3,02E-01	
NEXN	1,24	1,56E-01	2,76E-01	
CALD1	1,23	1,81E-01	3,11E-01	
DDX39B	1,23	1,90E-01	3,20E-01	
LRPPRC	1,23	2,02E-01	3,34E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
SUGP1	1,22	2,63E-01	4,10E-01	
PPP1CA	1,21	1,93E-01	3,24E-01	
TCP1	1,21	1,83E-01	3,12E-01	
MYH9	1,20	2,12E-01	3,44E-01	
UHRF1	1,18	1,77E-01	3,07E-01	
MATR3	1,16	2,01E-01	3,33E-01	
PPIH	1,16	2,04E-01	3,36E-01	
SYF2	1,16	2,86E-01	4,36E-01	
RFC5	1,15	1,89E-01	3,20E-01	
HNRNPAB	1,15	2,44E-01	3,85E-01	
TOE1	1,14	2,67E-01	4,13E-01	
NUP205	1,14	3,32E-01	4,95E-01	
RAE1	1,14	1,95E-01	3,26E-01	
RPL39P5;RPL39	1,13	2,44E-01	3,85E-01	
HNRNPC	1,12	2,31E-01	3,68E-01	
DDX3X;DDX3Y	1,12	2,52E-01	3,95E-01	
ACTL6A	1,11	2,36E-01	3,76E-01	
ISY1	1,11	2,45E-01	3,85E-01	
CCT8	1,10	2,10E-01	3,43E-01	
HNRNPLL;HNRPLL	1,10	2,51E-01	3,94E-01	
CHD4	1,10	2,82E-01	4,32E-01	
IMMT	1,08	2,22E-01	3,58E-01	
MED24	1,07	2,99E-01	4,54E-01	
UBTF	1,07	2,18E-01	3,53E-01	
DNAJA3	1,05	2,30E-01	3,68E-01	
TUBA1B	1,01	2,81E-01	4,32E-01	
RPL27A	1,01	2,55E-01	3,97E-01	
CCNB1	0,97	2,84E-01	4,34E-01	
RFC4	0,97	2,67E-01	4,13E-01	
NPM3	0,97	3,60E-01	5,25E-01	
HCFC1	0,97	3,20E-01	4,82E-01	
HNRNPU	0,93	3,25E-01	4,86E-01	
CKAP5	0,92	3,67E-01	5,28E-01	
ALKBH5	0,91	3,61E-01	5,25E-01	
CDC2;CDK1	0,90	3,81E-01	5,41E-01	
HNRNPL	0,90	3,21E-01	4,82E-01	
MYL6	0,90	3,17E-01	4,79E-01	
HNRNPA1;HNRNPA1L2	0,88	3,98E-01	5,59E-01	
HDAC2	0,88	3,12E-01	4,72E-01	

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	Function
RAD21	0,87	3,49E-01	5,13E-01	
RPLP0;RPLP0P6	0,86	3,43E-01	5,07E-01	
CCT6A	0,85	3,61E-01	5,25E-01	
RPL7	0,85	3,31E-01	4,93E-01	
RNF2	0,84	3,52E-01	5,17E-01	
HNRNPD	0,84	3,65E-01	5,28E-01	
CLK3	0,83	3,62E-01	5,25E-01	
DMAP1	0,82	3,34E-01	4,96E-01	
FXR1	0,82	3,69E-01	5,29E-01	
PRDX1	0,81	3,46E-01	5,10E-01	
CIRH1A	0,80	3,72E-01	5,30E-01	
SARNP	0,77	3,66E-01	5,28E-01	
MDN1	0,77	4,18E-01	5,80E-01	
MYH10	0,76	3,70E-01	5,29E-01	
NOP56	0,74	4,16E-01	5,78E-01	
NF2	0,74	3,88E-01	5,51E-01	
RRP36	0,73	4,04E-01	5,63E-01	
H2AFV;H2AFZ	0,73	3,94E-01	5,57E-01	
CYFIP1	0,73	4,42E-01	6,00E-01	
HADHB	0,73	4,00E-01	5,60E-01	
SCAI;C9orf126	0,73	4,34E-01	5,95E-01	
RAI14	0,73	3,96E-01	5,58E-01	
DKC1	0,72	4,22E-01	5,84E-01	
DHX8	0,72	4,33E-01	5,94E-01	
WWP2	0,72	4,24E-01	5,84E-01	
HIST1H4A	0,71	4,03E-01	5,63E-01	
NUP98	0,71	4,93E-01	6,43E-01	
FLNA	0,71	4,30E-01	5,91E-01	
GPKOW	0,70	4,46E-01	6,00E-01	
CLTA	0,69	5,09E-01	6,56E-01	
SRSF11	0,68	4,46E-01	6,00E-01	
NCL	0,67	4,78E-01	6,28E-01	
MPRIP	0,67	4,53E-01	6,05E-01	
EEF1D	0,67	5,79E-01	7,23E-01	
PDLIM4	0,67	4,45E-01	6,00E-01	
NXF1	0,66	4,37E-01	5,96E-01	
LMNB1	0,66	4,53E-01	6,05E-01	
RFC3	0,66	4,61E-01	6,14E-01	
RPL23	0,65	4,44E-01	6,00E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
AP2A1	0,65	4,66E-01	6,17E-01	
SUPT16H	0,65	4,98E-01	6,46E-01	
SMC3	0,65	5,06E-01	6,54E-01	
PINX1	0,64	4,53E-01	6,05E-01	
PRPF31	0,62	4,67E-01	6,17E-01	
FOSL2	0,62	4,63E-01	6,16E-01	
GNAI3	0,62	4,69E-01	6,18E-01	
SP110	0,62	5,43E-01	6,93E-01	
XRCC6	0,60	4,81E-01	6,31E-01	
SQSTM1	0,60	5,21E-01	6,69E-01	
USP39	0,59	4,88E-01	6,38E-01	
ANXA2;ANXA2P2	0,59	5,02E-01	6,50E-01	
SMARCD2	0,59	4,94E-01	6,43E-01	
CDKN2AIP	0,59	5,72E-01	7,17E-01	
POLR1A	0,57	5,54E-01	7,04E-01	
RCL1	0,56	5,30E-01	6,80E-01	
KPNA2	0,55	5,38E-01	6,88E-01	
WDR18	0,54	6,05E-01	7,46E-01	
RPL7L1	0,53	5,72E-01	7,17E-01	
FNBP4	0,52	6,65E-01	7,85E-01	
SRPK1	0,51	5,54E-01	7,04E-01	
DPF2	0,49	5,58E-01	7,06E-01	
POLR1C	0,49	5,59E-01	7,07E-01	
ZSCAN26;ZNF187	0,49	5,75E-01	7,20E-01	
HSPA1B;HSPA1A	0,48	5,72E-01	7,17E-01	
SRSF2	0,48	6,06E-01	7,46E-01	
SMARCA4	0,47	6,07E-01	7,46E-01	
EIF3D	0,46	6,23E-01	7,63E-01	
FBL	0,46	5,99E-01	7,42E-01	
RPL27	0,45	5,92E-01	7,37E-01	
KIAA1522	0,45	6,64E-01	7,85E-01	
FIZ1	0,44	5,99E-01	7,42E-01	
CAPRIN1	0,44	6,63E-01	7,85E-01	
DHX35	0,43	6,49E-01	7,76E-01	
LMNA	0,42	6,41E-01	7,73E-01	
HSPA8	0,42	6,27E-01	7,65E-01	
MYO1C	0,42	6,40E-01	7,73E-01	
ADNP	0,41	6,48E-01	7,76E-01	
SND1	0,41	6,57E-01	7,83E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
SMC1A	0,41	6,41E-01	7,73E-01	
H2AFY	0,41	6,22E-01	7,63E-01	
RIF1	0,41	6,28E-01	7,65E-01	
HSPA5	0,41	6,31E-01	7,66E-01	
AHNAK	0,40	6,61E-01	7,85E-01	
DDX41	0,40	6,48E-01	7,76E-01	
KIF2A	0,39	6,45E-01	7,76E-01	
DDX5	0,39	6,68E-01	7,88E-01	
RBMX2	0,38	6,72E-01	7,89E-01	
KPNB1	0,38	6,81E-01	7,95E-01	
MYO1B	0,37	6,73E-01	7,89E-01	
MPG	0,37	7,13E-01	8,17E-01	
SMARCB1	0,37	6,86E-01	7,99E-01	
FAM98B	0,37	6,74E-01	7,89E-01	
ZNF22	0,35	6,89E-01	7,99E-01	
U2AF1	0,34	6,89E-01	7,99E-01	
PPP1CB	0,33	7,05E-01	8,14E-01	
DDB1	0,32	7,07E-01	8,14E-01	
RPS9	0,32	7,05E-01	8,14E-01	
NUP155	0,32	7,17E-01	8,18E-01	
SMNDC1	0,32	7,13E-01	8,17E-01	
TUBB4B	0,32	7,46E-01	8,37E-01	
DNAJA1	0,32	7,32E-01	8,30E-01	
GTF3C4	0,31	7,47E-01	8,37E-01	
NUP88	0,31	7,15E-01	8,18E-01	
FLNC	0,31	7,30E-01	8,29E-01	
MYBBP1A	0,29	7,39E-01	8,34E-01	
DNAJC9	0,29	7,27E-01	8,28E-01	
HEATR1	0,28	7,92E-01	8,69E-01	
NMT1	0,28	7,41E-01	8,34E-01	
LIMA1	0,28	7,39E-01	8,34E-01	
PYCR1	0,27	7,56E-01	8,45E-01	
NOL6	0,27	7,86E-01	8,66E-01	
CAPZB	0,26	7,59E-01	8,45E-01	
PDS5B	0,26	7,58E-01	8,45E-01	
SMCHD1	0,26	7,60E-01	8,45E-01	
RPL28	0,26	7,62E-01	8,45E-01	
SMARCC1	0,26	7,71E-01	8,53E-01	
PWP1	0,25	7,92E-01	8,69E-01	

Gene name	mean log2FC MYC ON	p-vlaue MYC ON	q-value MYC ON	Function
ACTN4	0,25	7,77E-01	8,58E-01	
CLTC	0,22	8,20E-01	8,96E-01	
RBPJ	0,21	8,02E-01	8,78E-01	
MAPRE1	0,21	8,27E-01	9,00E-01	
TRIM28	0,20	8,31E-01	9,01E-01	
RPL22L1	0,19	8,27E-01	9,00E-01	
LRRC59	0,18	8,35E-01	9,04E-01	
RPS15A	0,17	8,39E-01	9,07E-01	
RPL7A	0,17	8,44E-01	9,10E-01	
UTP18	0,17	8,49E-01	9,12E-01	
BAZ1B	0,16	8,49E-01	9,12E-01	
GAPDH	0,16	8,72E-01	9,28E-01	
RNMT	0,14	8,71E-01	9,28E-01	
PRPF4	0,14	8,63E-01	9,25E-01	
RPS18	0,14	8,66E-01	9,26E-01	
H2AFY2	0,13	8,73E-01	9,28E-01	
EIF2B1	0,13	8,83E-01	9,33E-01	
NUMA1	0,13	9,00E-01	9,45E-01	
SPATS2L	0,13	8,80E-01	9,33E-01	
PLOD3	0,12	8,83E-01	9,33E-01	
WDR5	0,12	8,87E-01	9,35E-01	
POLR1B	0,12	8,92E-01	9,38E-01	
EPB41	0,11	9,02E-01	9,45E-01	
FLNB	0,10	9,11E-01	9,50E-01	
C8orf33	0,10	9,30E-01	9,62E-01	
RRS1	0,10	9,04E-01	9,45E-01	
CTNNA1	0,10	9,15E-01	9,51E-01	
DDOST	0,09	9,13E-01	9,50E-01	
ACTN1	0,08	9,27E-01	9,61E-01	
RPL36	0,06	9,47E-01	9,78E-01	
RPL24	0,05	9,50E-01	9,79E-01	
RPS19	0,04	9,63E-01	9,88E-01	
DNTTIP1	0,04	9,64E-01	9,88E-01	
PELO	0,04	9,64E-01	9,88E-01	
RPS5	0,03	9,69E-01	9,90E-01	
PPP1CC	0,03	9,72E-01	9,90E-01	
MRPL15	0,03	9,73E-01	9,90E-01	
HSPA9	0,02	9,76E-01	9,90E-01	
ACTB	0,02	9,77E-01	9,90E-01	

Gene name	**mean log2FC MYC ON**	**p-vlaue MYC ON**	**q-value MYC ON**	**Function**
ZNF524	0,02	9,81E-01	9,91E-01	
SFSWAP	0,02	9,78E-01	9,90E-01	
NOP58	0,02	9,86E-01	9,91E-01	
BMS1	0,01	9,89E-01	9,91E-01	
PLEC	0,01	9,89E-01	9,91E-01	
C11orf31;SELH	0,01	9,90E-01	9,91E-01	
DDX55	0,01	9,91E-01	9,91E-01	

7.3.5 Table with values corresponding to Figure 4.10

Table 7.8: Values corresponding to Figure 4.10. Values are sorted according to log2FC and p-value. Genes marked in bold showed MYC-dependent changes in RNAPII-binding in T-lymphoma cells and were described in more detail.

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
TCEA3	3,44	2,43E-04	1
CCDC12	1,83	9,36E-03	1
MED11	2,17	1,07E-02	1
RPRD1A	1,83	1,24E-02	1
ELL	1,75	1,58E-02	1
SUPT5H	1,93	2,93E-02	1
VEZF1	-1,96	3,05E-02	1
MED18	1,53	6,85E-02	1
BCAS2	1,24	7,35E-02	1
RECQL5	1,49	7,57E-02	1
EIF3A	1,34	8,25E-02	1
PCF11	1,27	8,36E-02	1
INTS8	1,23	9,08E-02	1
SUPT6H	1,27	1,07E-01	1
PSMC5	1,02	1,17E-01	1
RPAP2	-1,34	1,23E-01	1
SRSF10	-1,18	1,49E-01	1
CRNKL1	-1,18	1,52E-01	1
MED30	-1,01	1,54E-01	1
CTR9	-1,15	1,70E-01	1
SNRNP40	0,96	1,78E-01	1
XRN2	0,90	1,84E-01	1
INTS10	1,11	1,93E-01	1

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
MED26	0,94	1,96E-01	1
POLR2G	0,80	2,08E-01	1
ZRANB2	-0,91	2,13E-01	1
MED1	0,90	2,29E-01	1
VWA9	-1,52	2,32E-01	1
MED31	0,78	2,36E-01	1
POLR2H	0,77	2,53E-01	1
IXL;MED29	0,80	2,71E-01	1
POLR2B	0,70	2,89E-01	1
INTS9	0,76	2,99E-01	1
PPP2CB	0,82	3,15E-01	1
MED10	0,69	3,30E-01	1
CDKN2AIP	0,76	3,31E-01	1
INTS12	0,65	3,38E-01	1
MED7	-0,84	3,44E-01	1
BCLAF1	0,59	3,67E-01	1
MED27	0,59	4,16E-01	1
POLR2F	0,62	4,26E-01	1
EIF3B	0,66	4,49E-01	1
POLR2I	0,48	4,52E-01	1
MED16	0,56	4,62E-01	1
INTS7	0,55	4,73E-01	1
THOC2	-0,66	4,77E-01	1
VIM	-0,87	4,95E-01	1
MED8	-0,53	5,46E-01	1
INTS3	0,70	5,60E-01	1
MED6	-0,35	5,77E-01	1
MED25	-0,50	5,79E-01	1
PPP2R1A	0,44	5,79E-01	1
EWSR1	0,50	5,85E-01	1
GTF2F1	-0,33	6,11E-01	1
DSP	0,50	6,15E-01	1
INTS1	0,48	6,17E-01	1
MED14	0,35	6,29E-01	1
POLR2C	-0,32	6,29E-01	1
INTS6	0,43	6,30E-01	1
XAB2	0,40	6,45E-01	1
RPRD1B	0,35	6,48E-01	1

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
MED23	0,37	6,51E-01	1
ASUN	0,34	6,76E-01	1
INTS4	0,40	6,94E-01	1
CDC73	0,37	6,95E-01	1
TCEA1	-0,31	7,03E-01	1
POLR2D	0,22	7,26E-01	1
MED17	0,27	7,46E-01	1
MED21	0,32	7,47E-01	1
POLR2A	0,20	7,54E-01	1
RBM10	0,22	7,65E-01	1
SRSF6	0,21	8,00E-01	1
SCAF8	-0,17	8,07E-01	1
MED4	-0,16	8,33E-01	1
MED15	0,15	8,49E-01	1
SERBP1	-0,13	8,52E-01	1
PAF1	-0,15	8,57E-01	1
MED22	0,13	8,71E-01	1
POLR2E	0,11	8,72E-01	1
POLR2K	-0,11	8,73E-01	1
INTS5	-0,13	8,83E-01	1
CPSF3L	-0,11	8,84E-01	1
POLR2J;POLR2J3	0,10	8,89E-01	1
INTS2	-0,11	9,04E-01	1
MED19	0,09	9,11E-01	1
NCBP1	0,06	9,42E-01	1
RPRD2	0,04	9,59E-01	1
PPP1R10	0,03	9,73E-01	1
RBM22	0,01	9,89E-01	1
MED20	-0,01	9,93E-01	1
GTF2F2	0,01	9,93E-01	1
DDX39A	-6,23	5,17E-07	0
POLR2L	-3,67	1,02E-04	0
ACO2	-2,95	1,66E-03	0
PSMC2	2,26	7,09E-03	0
CDC42	-2,17	9,05E-03	0
RTF1	-1,87	1,48E-02	0
TCEB2	-1,77	1,51E-02	0
RPL14	1,71	1,82E-02	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
NXT1	-2,05	2,19E-02	0
MYH9	1,76	2,30E-02	0
HDGFRP2	-1,36	3,78E-02	0
SRP14	-1,53	5,28E-02	0
FAM76B	-1,53	5,55E-02	0
PELO	1,43	6,44E-02	0
EEF1G	1,22	7,03E-02	0
CGGBP1	-1,21	8,06E-02	0
PABPC4	1,36	8,54E-02	0
TCF7	-1,20	8,78E-02	0
MAP7	-1,28	8,83E-02	0
RPS8	1,23	9,23E-02	0
HNRNPH1	1,14	1,02E-01	0
IKZF5	-1,10	1,11E-01	0
DNAJA2	1,05	1,14E-01	0
DUT	1,25	1,23E-01	0
TCP1	1,05	1,24E-01	0
GRB10	-1,28	1,25E-01	0
DNAJA1	1,04	1,31E-01	0
EPB41L4B	1,15	1,34E-01	0
SP2	-0,97	1,34E-01	0
RPS27L	1,19	1,43E-01	0
GTF2I	1,26	1,46E-01	0
PHF2	-0,95	1,48E-01	0
RNPS1	1,02	1,50E-01	0
RBM8A	1,03	1,54E-01	0
SMAD3	-1,05	1,56E-01	0
HADHB	-1,06	1,56E-01	0
PRPF38A	0,95	1,58E-01	0
EIF3G	-0,96	1,58E-01	0
SNW1	0,99	1,73E-01	0
RPS20	0,95	1,73E-01	0
SMARCB1	0,88	1,83E-01	0
DYNLL1	1,00	1,88E-01	0
RPL4	0,87	1,90E-01	0
LRRC59	0,84	1,94E-01	0
ZNF197	-0,88	2,01E-01	0
CPSF7	-0,95	2,05E-01	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
PNN	1,03	2,07E-01	0
RPS27	0,88	2,13E-01	0
CCT4	0,96	2,13E-01	0
BUD13	-1,02	2,22E-01	0
ATAD3A	0,93	2,26E-01	0
RPS24	0,85	2,31E-01	0
SF3B5	0,82	2,33E-01	0
CSTF2	-0,94	2,34E-01	0
CHTOP	0,87	2,43E-01	0
PPP2R1B	0,87	2,54E-01	0
SF3A2	-0,77	2,54E-01	0
EFTUD2	0,84	2,56E-01	0
U2SURP	-1,04	2,65E-01	0
RPS28	0,81	2,72E-01	0
ERH	0,78	2,73E-01	0
CCAR1	-0,82	2,89E-01	0
SMNDC1	-0,69	2,98E-01	0
EIF3L	-0,74	3,01E-01	0
HNRNPF	0,72	3,08E-01	0
EIF4B	-0,74	3,12E-01	0
CLTC	0,76	3,19E-01	0
TRA2A	0,69	3,30E-01	0
RPL10	0,64	3,32E-01	0
RPS16;ZNF90	0,77	3,33E-01	0
ILF3	0,67	3,46E-01	0
PRPF19	0,73	3,48E-01	0
BTF3	-0,99	3,50E-01	0
HSD17B10	-0,65	3,54E-01	0
WDR82	-0,91	3,59E-01	0
RUVBL2	0,63	3,69E-01	0
RBM17	-0,62	3,72E-01	0
SNRNP70	-0,69	3,77E-01	0
KHDRBS1	0,67	3,79E-01	0
CCT8	0,66	3,88E-01	0
TRMT10C	-0,57	3,90E-01	0
SCAF1	-0,68	3,93E-01	0
SAFB	-0,57	3,97E-01	0
DKC1	-0,66	4,01E-01	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
RPS23	0,64	4,06E-01	0
PCBP2;Isoform	0,58	4,19E-01	0
DDX39B	0,65	4,19E-01	0
HNRNPK	0,50	4,22E-01	0
CWC25	-0,58	4,23E-01	0
PKM	0,62	4,35E-01	0
MAGOH;MAGOHB	-0,58	4,38E-01	0
SCAF4	0,60	4,45E-01	0
SNRPE	0,46	4,52E-01	0
HDAC1	-0,56	4,58E-01	0
RPL17;RPL17-C18orf32	0,54	4,60E-01	0
RBM5	-0,58	4,82E-01	0
MTA2	-0,61	4,86E-01	0
ABCE1	-0,49	4,90E-01	0
TARDBP	0,47	4,90E-01	0
ATP5A1	0,62	4,94E-01	0
PPP1CB	-0,48	4,97E-01	0
CCT2	-0,51	4,97E-01	0
SRRT	-0,59	5,00E-01	0
ZC3H18	-0,45	5,03E-01	0
RPS17	0,57	5,08E-01	0
PRPF6	-0,45	5,12E-01	0
TPR	-0,46	5,18E-01	0
BUD31	0,44	5,22E-01	0
CBX3	0,47	5,23E-01	0
RTCB	0,47	5,30E-01	0
POGZ	-0,49	5,35E-01	0
RPS2	-0,47	5,38E-01	0
SAP30BP	-0,41	5,39E-01	0
ELAVL1	0,40	5,39E-01	0
SYNCRIP	0,44	5,45E-01	0
RPAP3	0,51	5,45E-01	0
RPS18	0,45	5,45E-01	0
NUMA1	-0,65	5,48E-01	0
POLDIP3	-0,41	5,49E-01	0
NCL	-0,38	5,52E-01	0
DDX23	0,43	5,54E-01	0
SF3A1	-0,44	5,60E-01	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
EIF3E	-0,42	5,61E-01	0
EIF3F	-0,41	5,67E-01	0
SRSF3	0,39	5,69E-01	0
RP9	-0,37	5,72E-01	0
LUC7L3	0,36	5,74E-01	0
SRSF1	0,35	5,77E-01	0
RBX1	0,37	5,93E-01	0
PRPF8	0,49	5,95E-01	0
PPIL1	0,36	5,96E-01	0
CDK9	0,36	5,98E-01	0
THOC7; NIF3L1BP1	0,33	5,99E-01	0
EIF3I	-0,38	6,13E-01	0
SNRPD3	0,36	6,15E-01	0
DDX46	0,40	6,29E-01	0
RPL13	0,37	6,33E-01	0
PYCR2	-0,34	6,40E-01	0
SRRM2	0,30	6,40E-01	0
IK	0,37	6,42E-01	0
RPL24	0,31	6,43E-01	0
SRP72	-0,30	6,45E-01	0
TUBA1B	0,35	6,46E-01	0
PYCR1	-0,30	6,64E-01	0
RBBP7	-0,30	6,66E-01	0
KPNA4	-0,28	6,68E-01	0
EIF3C;EIF3CL	0,29	6,74E-01	0
GAPDH	-0,28	6,76E-01	0
TRA2B	0,26	6,78E-01	0
CCT7	-0,31	6,80E-01	0
CCT3	-0,28	6,81E-01	0
NXF1	-0,29	6,85E-01	0
HIST1H2AC	-0,29	6,92E-01	0
RFC2	0,27	6,96E-01	0
RPS26;RPS26P11	0,28	6,99E-01	0
RPLP0;RPLP0P6	0,27	7,04E-01	0
SREK1IP1	-0,30	7,12E-01	0
RBMX	0,27	7,17E-01	0
CDC40	0,27	7,18E-01	0
CCT5	-0,26	7,24E-01	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
RPLP2	-0,23	7,28E-01	0
HCFC1	-0,23	7,29E-01	0
SF3B6	-0,22	7,51E-01	0
EEF1D	-0,23	7,54E-01	0
ACIN1	0,22	7,56E-01	0
HSP90AA1	0,22	7,57E-01	0
THRAP3	0,28	7,57E-01	0
SRSF11	0,30	7,58E-01	0
SF3B4	0,18	7,75E-01	0
CSNK2B;CSNK2B-LY6G5B-1181; CSNK2B-LY6G5B-991	0,18	7,76E-01	0
SETD2	-0,21	7,79E-01	0
SF1	-0,20	7,81E-01	0
NPM1	-0,19	7,92E-01	0
SNRPD2	0,18	7,99E-01	0
SRSF5	-0,17	8,02E-01	0
SNRPC	-0,17	8,02E-01	0
YTHDC1	0,23	8,10E-01	0
PHF5A	-0,18	8,13E-01	0
IWS1	0,15	8,20E-01	0
ARID1A	-0,21	8,24E-01	0
KPNB1	-0,15	8,27E-01	0
RPL34	0,17	8,32E-01	0
ACTL6A	0,15	8,32E-01	0
SART1	-0,15	8,34E-01	0
RUVBL1	0,13	8,36E-01	0
H1F0	-0,15	8,40E-01	0
ZCCHC17	0,19	8,44E-01	0
CAPRIN1	0,16	8,45E-01	0
CMAS	-0,16	8,48E-01	0
DCD	-0,15	8,50E-01	0
HELLS	0,13	8,57E-01	0
AQR	0,13	8,58E-01	0
DSC1	0,11	8,61E-01	0
ATRX	0,12	8,62E-01	0
SYMPK	0,13	8,64E-01	0
CPSF6	-0,13	8,68E-01	0

Gene name	**log2FC MYC ON/OFF**	**p-vlaue MYC ON/OFF**	**RNAPII interactor (colour)**
RPS27A;UBB; UBC;UBA52	-0,11	8,69E-01	0
PABPC1; PABPC3	-0,13	8,73E-01	0
EEF1A1; EEF1A1P5	0,11	8,75E-01	0
GATA3	0,14	8,77E-01	0
SCAF11	0,10	8,79E-01	0
SAP18	-0,11	8,80E-01	0
UBTF	0,12	8,83E-01	0
RPL31	-0,10	8,84E-01	0
KIF4A;KIF4B	-0,10	8,88E-01	0
EIF6	-0,10	8,89E-01	0
RPL28	-0,13	8,89E-01	0
PRDX1	-0,10	8,94E-01	0
CALML5	0,10	8,97E-01	0
HNRNPA3	0,07	9,09E-01	0
RPL13A;RPL13a	0,07	9,11E-01	0
RPL35A	-0,08	9,13E-01	0
SNRPF	0,08	9,26E-01	0
PABPN1	-0,06	9,33E-01	0
CHERP	0,06	9,37E-01	0
RPS5	-0,04	9,52E-01	0
SLC25A5	-0,04	9,55E-01	0
GATAD2B	0,03	9,56E-01	0
CWC15	0,04	9,57E-01	0
RPL6	-0,05	9,57E-01	0
RPS12	-0,04	9,58E-01	0
TUBB	-0,04	9,61E-01	0
GNB2	-0,04	9,61E-01	0
PLRG1	0,03	9,61E-01	0
LUC7L2	0,03	9,63E-01	0
RPL12	0,03	9,64E-01	0
G3BP1	0,02	9,71E-01	0
NIP7	0,02	9,74E-01	0
SET;SETSIP	-0,03	9,76E-01	0
HNRNPM	0,02	9,77E-01	0
EIF4A3	0,01	9,95E-01	0
SSB	0,00	9,96E-01	0
ACTB	0,00	9,97E-01	0

7.3.6 Table with values corresponding to Figure 4.11 and Figure 4.13

Table 7.9: Values corresponding to Figure 4.11 and Figure 4.13. Values are sorted for log2FC in MYC ON in U2OS cells.

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
GTF2F2	12,04	11,96	12,45	11,88	GTF
POLR2I	11,97	11,52	11,72	11,33	RNAPII
POLR2D	11,93	11,66	11,63	11,34	RNAPII
HIST2H3A	11,59	12,51	12,20	12,47	Other
POLR2G	11,58	11,50	11,37	11,28	RNAPII
POLR2F	11,54	11,05	11,09	11,04	RNAPII
RPRD1A	11,39	11,08	9,65	9,79	Other
INTS4	11,18	10,91	11,37	11,14	Integrator
POLR2K	11,17	11,11	10,95	10,81	RNAPII
RPRD1B	11,01	10,49	9,34	9,42	Other
POLR2L	10,91	10,17	10,21	11,30	RNAPII
INTS6	10,83	10,63	11,05	10,72	Integrator
RANGAP1	10,71	10,08	0,00	10,54	Other
POLR2M;GCOM1;GCOM2	10,58	10,72	10,99	10,89	RNAPII
RECQL5	10,35	10,50	10,61	10,45	Other
INTS5	10,34	10,11	10,43	10,17	Integrator
INTS7	10,18	9,94	10,68	10,23	Integrator
POLR2B	9,95	9,78	9,51	9,62	RNAPII
INTS2	9,91	9,81	10,26	9,97	Integrator
INTS8	9,88	9,70	10,06	9,80	Integrator
POLR2C	9,61	9,33	9,70	9,35	RNAPII
CPSF3L	9,54	9,42	9,70	9,62	Termination
PPP2R1A	9,42	9,18	9,74	9,48	Other
INTS9	9,35	9,07	9,53	9,25	Integrator
SNRPF	9,32	8,74	8,33	8,27	Splicing
TCEA1	9,26	9,08	9,35	8,72	EF
ASUN	9,23	8,95	9,43	9,07	Integrator
RPAP2	8,98	9,47	9,78	9,57	Other
INIP	8,96	8,25	8,87	8,60	Other
WTAP	8,90	8,51	8,08	7,87	Splicing
MED17	8,83	8,61	9,46	9,00	Mediator
NCOA5	8,75	8,50	6,94	6,90	Other
INTS12	8,56	8,27	8,90	8,55	Integrator
MED1	8,56	8,35	9,00	8,82	Mediator

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
KHSRP	8,56	8,16	6,78	6,35	Splicing
SF3A2	8,55	8,10	7,35	6,93	Splicing
HNRNPH2	8,53	8,56	7,16	7,57	Other
TTF2	8,50	8,45	8,27	8,30	Termination
MED27	8,44	8,47	8,96	8,82	Mediator
PCF11	8,34	8,12	7,83	7,76	Termination
UPF1	8,28	7,92	7,86	7,67	Other
WDR82	8,15	7,79	7,05	6,30	Other
POLR2J	8,12	7,77	7,99	7,86	RNAPII
INTS3	8,11	7,70	8,27	7,81	Integrator
FUBP1	8,08	8,13	5,90	3,97	Other
MED8	8,02	8,12	9,06	8,50	Mediator
CMTR1	7,91	7,63	7,41	7,31	Other
MSH6	7,90	8,30	8,08	8,06	Other
CTR9	7,90	7,51	7,16	6,50	EF
MED21	7,88	7,61	8,63	8,29	Mediator
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B—991	7,87	7,80	7,77	7,06	Other
PPP2R1B	7,84	7,72	7,92	7,68	Other
PPP2CB	7,81	7,76	7,81	7,52	Other
GLUD1;GLUD2	7,80	5,32	0,00	0,00	
FAM120A	7,77	7,69	7,18	7,11	Other
RBM5	7,76	7,31	6,32	5,87	
MED11	7,74	7,87	7,97	8,02	Mediator
SUPT4H1	7,72	7,12	6,64	6,51	EF
MED23	7,69	8,02	8,25	8,03	Mediator
INTS10	7,66	7,52	7,77	7,55	Integrator
DDX26B	7,64	7,43	7,80	7,38	Integrator
C17orf85	7,62	7,90	7,15	6,97	Other
MED6	7,61	7,09	8,14	7,73	Mediator
DHX30	7,61	7,52	7,31	7,25	Other
SUPT6H	7,60	7,29	6,35	6,04	EF
MED10	7,60	7,55	8,37	7,97	Mediator
CTDP1	7,57	7,67	8,19	7,35	Other
MED9	7,55	7,01	8,17	7,80	Mediator
NCBP2	7,53	7,31	6,81	6,36	Splicing
NABP1	7,51	7,10	7,41	6,72	Other

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
TFIP11	7,49	7,66	6,38	6,30	Other
THOC1	7,45	7,60	6,89	6,60	Other
LSM8	7,36	6,92	5,73	5,31	
NELFE	7,29	6,89	7,60	6,93	Other
SETD2	7,28	7,91	4,38	3,82	
MED31	7,26	6,86	7,75	7,64	Mediator
GPN1	7,24	7,55	7,84	7,51	Other
MYL6	7,23	7,13	7,49	7,40	Other
MED24	7,21	7,30	7,92	7,55	Mediator
FAM208A	7,16	7,03	5,59	5,40	
PAXBP1	7,14	7,31	6,27	6,15	Other
NELFB	7,14	6,98	7,12	6,58	Other
PRMT1	7,13	7,02	6,17	5,63	
POLR2H	7,13	5,36	6,92	6,53	RNAPII
STRAP	7,07	6,91	7,23	6,56	Splicing
EIF3H	7,00	6,72	7,15	6,66	Other
IWS1	6,97	6,87	5,04	4,96	EF
MTA2	6,96	7,04	6,81	6,97	Other
TIAL1	6,87	6,60	5,23	4,80	
RPRD2	6,84	6,58	5,61	5,72	Other
LMNA	6,83	6,53	6,90	6,88	Other
NUP93	6,82	7,18	6,75	7,00	Other
MED20	6,82	6,94	7,67	7,70	Mediator
THOC5	6,80	6,61	6,32	6,04	Other
MED14	6,79	6,67	7,38	7,17	Mediator
MED7	6,78	6,58	7,39	7,21	Mediator
CWC27	6,77	6,91	5,86	6,07	
ZRANB2	6,76	6,70	6,56	6,62	Other
DNAJC8	6,76	6,47	6,47	5,85	
CCDC88B	6,75	6,23	6,42	0,00	
UBL5	6,67	6,30	0,00	0,00	
PPP1CB	6,66	6,63	6,50	6,31	Splicing
PRPF38B	6,63	6,97	6,02	5,84	Splicing
DIS3L2	6,62	6,34	6,41	6,22	
CPSF4	6,62	6,58	5,69	5,91	Termination
GEMIN4	6,61	6,22	5,97	5,79	
MED15	6,59	6,72	7,27	7,14	Mediator
PRKRA	6,59	6,74	6,67	6,52	Other

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
THOC7;NIF3L1BP1	6,57	6,83	5,90	5,63	
MED16	6,56	6,32	7,18	6,87	Mediator
CSNK2A2	6,52	6,31	6,12	5,90	
ERLIN1	6,51	6,13	6,54	6,60	Other
IXL;MED29	6,50	6,61	7,07	7,29	Mediator
POLR2E	6,50	6,37	6,16	6,06	RNAPII
NELFA	6,49	6,70	6,63	6,16	Other
TOE1	6,48	6,68	0,00	5,72	
ALDH18A1	6,47	6,36	5,97	6,48	Other
CBLL1	6,46	6,32	5,60	0,00	
MED18	6,45	6,34	7,18	6,72	Mediator
HEATR1	6,39	6,48	6,00	7,26	Other
ATR	6,30	6,79	0,00	0,00	
NELFCD;TH1L	6,30	5,84	6,32	5,75	Other
TCP1	6,28	5,70	6,53	5,90	
C7orf26	6,27	6,33	6,41	6,50	Other
EDC4	6,27	6,99	6,85	7,16	Other
EEF1D	6,26	6,11	6,66	6,79	EF
HNRNPK	6,26	6,17	5,71	5,63	
DAZAP1	6,19	5,79	5,96	5,62	
MED22	6,19	6,22	6,97	6,57	Mediator
NUP133	6,16	6,73	5,90	6,35	Other
GNAI3	6,13	0,00	5,70	5,77	
TPR	6,12	6,21	6,52	6,21	
SEC61B	6,09	0,00	4,67	0,00	
GPKOW	6,07	6,28	5,61	5,21	
CDKN2AIP	6,02	5,89	5,63	5,30	
EIF4G2	6,02	5,94	5,96	5,78	
SLC4A1AP	6,01	6,40	5,70	4,93	
SMARCB1	5,99	0,00	5,92	0,00	
ZC3H4	5,94	6,01	4,68	4,33	Other
LSM6	5,93	5,56	0,00	0,00	
SCAI;C9orf126	5,91	6,50	0,00	4,87	
DCD	5,90	0,00	8,40	0,00	
RPAP3	5,89	5,30	6,42	5,90	
MOV10	5,87	5,77	5,70	5,77	
RNGTT	5,85	6,30	6,70	6,35	Other
EIF3K	5,85	5,29	0,00	0,00	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
EIF2AK2	5,83	6,13	5,79	6,03	
MRPS26	5,80	0,00	6,53	0,00	
PCNP	5,79	4,96	4,78	4,80	
YTHDF2	5,78	6,04	6,11	5,82	
CD2BP2	5,77	6,31	5,23	5,61	
MDN1	5,72	6,32	6,10	6,22	Other
AKAP8L	5,70	5,93	4,51	5,24	
HECTD4	5,70	0,00	0,00	0,00	
COIL	5,68	5,58	5,19	5,41	
RECQL	5,65	0,00	6,03	6,06	
URI1	5,64	5,39	5,94	5,96	
PHRF1	5,64	5,48	4,74	4,44	Other
MSH2	5,63	6,14	6,03	6,09	
GEMIN5	5,62	6,29	0,00	0,00	
C15orf52	5,61	5,42	5,04	5,12	
CSTA	5,60	5,56	6,83	0,00	
HNRNPR	5,60	5,31	5,18	4,53	Splicing
RRP9	5,59	6,41	5,74	6,52	Splicing
PTCD3	5,58	0,00	5,43	0,00	
MED30	5,56	5,33	6,16	6,13	Mediator
PUM2	5,55	5,44	5,41	5,41	
FNBP4	5,53	5,55	4,48	4,63	
ZNF830	5,51	5,63	0,00	0,00	
TMEM214	5,49	5,13	5,01	4,67	
SART3	5,48	5,27	5,19	0,00	
CDC2;CDK1	5,48	5,86	5,91	6,10	
CCDC9	5,47	4,68	0,00	0,00	
NOLC1	5,47	6,42	0,00	5,24	
LSM4	5,47	5,72	0,00	0,00	
PHF3	5,45	4,40	1,81	2,00	Other
MAGEA11	5,44	5,55	5,06	5,21	
MED4	5,42	5,10	5,81	5,53	Mediator
ZMAT2	5,40	5,48	4,29	3,90	
PLOD1	5,39	5,50	5,68	5,32	
NKTR	5,38	5,42	0,00	5,21	
MRPS15	5,37	0,00	5,98	5,26	
MRPS31	5,35	0,00	5,88	5,18	
WDR61	5,35	5,41	4,99	4,90	EF

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
USP10	5,35	5,17	4,89	5,01	
MRPS16	5,34	0,00	0,00	0,00	
CBX5	5,34	0,00	5,20	5,20	
NOP10	5,34	5,37	0,00	5,43	
THOC3	5,33	5,62	0,00	0,00	
ERF	5,31	5,67	6,50	6,05	
PPWD1	5,31	5,77	0,00	3,57	Other
NUP155	5,27	5,23	0,00	5,21	
CELF1	5,27	5,79	0,00	0,00	
VWA9	5,21	4,91	4,06	4,71	Integrator
STAU2	5,20	4,89	5,06	5,11	
RAD50	5,19	5,12	5,33	5,45	
KPNA1;KPNA5	5,19	5,07	5,19	5,13	
RNPC3	5,17	4,43	3,29	0,00	
USP3	5,17	5,39	4,64	5,20	
GTF2E1	5,17	4,98	6,12	5,54	
PWP2	5,16	5,37	5,35	5,90	
NUP62	5,15	5,26	4,85	5,55	
FAM50A	5,14	4,82	0,00	0,00	
DGCR14	5,14	5,24	0,00	0,00	
DDX39A	5,12	5,36	0,00	6,26	Other
CLP1	5,12	0,00	0,00	0,00	
PFDN2	5,11	5,32	5,74	5,49	
PPP1R8	5,09	4,66	0,00	0,00	
EXOSC8	5,08	0,00	0,00	0,00	
PLEC	5,06	0,00	0,00	5,48	
UPF2	5,03	4,61	4,85	4,79	
PML	4,99	4,78	5,26	0,00	
FGF2	4,98	4,91	5,43	5,39	
PNISR	4,98	5,51	4,50	0,00	
KPNA3	4,96	5,16	4,84	5,57	
LSM12	4,92	4,64	5,49	5,24	
MED26	4,91	4,87	5,57	5,30	Mediator
KIN	4,90	4,95	0,00	0,00	
ZNF22	4,86	4,83	4,92	5,21	
NUP35	4,84	4,29	4,82	5,60	
TRIM25	4,84	0,00	0,00	4,96	
ZNF346	4,81	5,46	0,00	4,76	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
CCNL1	4,81	4,82	0,00	4,83	
KLHDC4;DKFZp434 G0522	4,81	5,03	5,19	4,96	
TRAM1	4,80	3,37	3,70	0,00	
INTS1	4,79	4,62	5,03	4,77	Integrator
RBM15B	4,79	5,39	4,69	0,00	
SRSF8	4,74	5,02	0,00	0,00	
UQCC2	4,74	4,51	4,75	4,11	
ATXN2	4,73	4,42	0,00	4,25	
CLPB	4,70	4,78	5,11	4,12	
WDR3	4,69	4,50	4,58	5,20	
ARID1A	4,68	0,00	4,67	4,84	
KIFC1	4,68	4,39	5,69	5,27	
XAB2	4,66	4,98	2,69	3,80	Splicing
DENR	4,65	0,00	5,65	4,99	
MED25	4,64	4,92	5,51	5,27	Mediator
PLOD3	4,63	4,53	4,77	4,69	
IGF2BP2	4,63	5,27	4,40	0,00	
DOCK7	4,63	4,79	4,65	4,65	
NUP160	4,62	5,57	3,98	5,60	
CCAR2	4,62	0,00	4,28	0,00	Splicing
POLR2A	4,60	4,37	4,25	4,18	RNAPII
C9orf78	4,59	4,22	0,00	0,00	
DNAJC10	4,59	4,91	4,68	5,16	
LEPRE1	4,58	4,03	0,00	3,68	
CACYBP	4,56	0,00	4,66	4,94	
UXT	4,55	4,11	0,00	4,89	
ORC3	4,53	4,42	3,84	4,18	
CPSF2	4,53	4,14	3,61	2,77	Termination
NDUFV3	4,52	0,00	0,00	0,00	
CCDC47	4,51	0,00	4,21	4,21	
MPHOSPH8	4,50	4,27	3,99	3,53	
GTF2F1	4,49	4,43	4,82	4,26	GTF
MRPL19	4,49	3,77	4,24	0,00	
CLTA	4,48	0,00	5,03	0,00	
PRCC	4,46	5,18	4,00	3,68	
PPIL2	4,45	0,00	0,00	0,00	
PARP2	4,42	0,00	0,00	0,00	
NUP85	4,42	5,04	0,00	5,18	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
FASTKD2	4,41	4,73	3,51	0,00	
EIF4E2	4,41	0,00	0,00	0,00	
ENAH	4,41	0,00	4,54	0,00	
RBM6	4,39	4,12	1,76	1,93	
SUN1	4,37	4,63	4,48	5,31	
PARD3	4,36	0,00	0,00	3,94	
ZC3H13	4,36	4,47	3,63	3,26	
CLASRP	4,32	4,57	3,84	3,25	
CBX2	4,31	0,00	0,00	3,78	
GPATCH11	4,28	4,09	0,00	0,00	
UBAP2L	4,27	0,00	4,31	4,30	
QKI	4,27	0,00	0,00	0,00	
WDR75	4,26	4,94	0,00	5,79	
TMEM201	4,24	4,23	0,00	4,44	
TBL2	4,22	3,74	0,00	0,00	
SLC2A1	4,22	0,00	0,00	0,00	
CGN	4,21	3,96	0,00	3,99	
SENP3;SENP3-EIF4A1	4,19	0,00	4,40	4,39	
ELL	4,18	4,39	4,75	0,00	
ZCCHC7	4,17	0,00	0,00	3,71	
SMCHD1	4,17	0,00	5,14	0,00	
VRK2	4,16	0,00	4,28	0,00	
GTF3C4	4,13	4,55	0,00	5,16	
USP7	4,13	4,32	0,00	0,00	
MAP4K4;MINK1	4,12	0,00	0,00	4,42	
TUBA3C;TUBA3E	4,12	4,50	5,50	5,22	
KIAA1671	4,12	3,97	0,00	4,69	
HNRNPUL1	4,10	3,19	2,95	2,59	Other
UTP6	4,09	0,00	0,00	4,08	
CYC1	4,00	3,95	0,00	0,00	
FAM208B	3,98	4,82	0,00	0,00	
KIRREL	3,97	0,00	0,00	0,00	
GIGYF2	3,95	4,04	3,97	3,85	
NKRF	3,93	4,34	0,00	0,00	
EIF3L	3,92	3,75	4,00	3,56	Other
SUPT5H	3,92	3,44	2,63	2,61	EF
PDRG1	3,91	3,91	4,41	3,93	
SRPK2	3,90	0,00	0,00	3,50	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SUPV3L1	3,85	3,88	3,87	3,88	
PTK2	3,85	0,00	4,54	0,00	
EIF3C;EIF3CL	3,83	2,90	3,90	3,41	
CSTF3	3,83	3,59	2,42	1,94	Termination
DRG1	3,83	3,59	3,96	0,00	
MRE11A	3,80	0,00	3,82	3,61	
PTBP2	3,79	0,00	0,00	0,00	
DHX36	3,79	3,88	0,00	0,00	
WWP2	3,75	0,00	3,81	0,00	
SNX8	3,71	4,44	4,20	3,04	
CSTF2T	3,70	3,52	0,00	0,00	
CWC22	3,65	3,59	1,48	1,84	Splicing
ESYT1	3,63	3,15	3,46	3,21	
APOBEC3C	3,63	3,86	0,00	0,00	
NUP214	3,62	3,88	3,85	4,13	
ZNF326	3,62	3,57	1,89	1,96	Splicing
FASN	3,62	0,00	5,19	5,72	
GPANK1	3,62	0,00	0,00	0,00	
DHX38	3,60	4,07	1,79	2,29	
AURKA	3,59	0,00	0,00	0,00	
CETN2	3,59	0,00	0,00	3,74	
PTDSS1	3,59	3,38	0,00	3,45	
NIPBL	3,59	3,34	0,00	3,71	
NEDD8;NEDD8-MDP1	3,57	0,00	0,00	0,00	
MYEF2	3,55	3,83	0,00	0,00	Other
MBD4	3,54	3,72	0,00	0,00	
FUBP3	3,53	3,14	2,04	2,18	Other
SAFB2	3,53	3,45	1,91	1,94	Other
USP36	3,52	0,00	0,00	0,00	
FARP1	3,50	0,00	5,08	0,00	
KIAA1429	3,46	3,24	2,27	2,28	Other
GTF3A	3,45	4,92	6,55	5,27	GTF
MRPL39	3,44	0,00	0,00	0,00	
COX7A2	3,42	0,00	3,94	3,86	
ZCCHC8	3,42	2,76	1,48	1,13	Other
SCAF11	3,41	3,44	2,10	2,26	EF
ASPM	3,36	0,00	0,00	0,00	
ASH2L	3,36	0,00	3,95	0,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SNAP29	3,30	4,12	4,96	4,72	
DDOST	3,28	4,59	4,32	3,70	
HEXIM1	3,28	0,00	0,00	0,00	
LYZ	3,27	0,00	0,00	0,00	
ITCH	3,26	0,00	0,00	3,09	
AQR	3,25	3,45	1,71	2,09	Splicing
WDR48	3,15	0,00	0,00	0,00	
GNAI2;GNAI1;GNAO1	3,13	0,00	0,00	0,00	
CPSF1	3,12	2,83	1,84	1,46	Termination
SOAT1	3,11	0,00	0,00	1,84	
FUS	3,09	2,90	1,72	1,49	Splicing
ZNF668	3,08	4,07	0,00	3,68	
CTNNBL1	3,06	2,91	-0,06	0,11	Splicing
XRN2	3,04	2,74	2,76	2,40	Termination
RBM12B	3,04	3,42	0,63	1,64	Other
MTHFD1L	3,01	3,13	0,00	2,93	
HLTF	2,98	3,32	3,79	2,98	
CTXN3	2,97	0,00	0,00	0,00	
TAF15	2,96	2,86	1,40	1,52	GTF
ERH	2,93	2,84	2,21	2,15	Splicing
ADAR	2,88	2,73	1,71	1,96	
RBM10	2,86	2,76	1,51	1,39	Other
HNRNPA2B1	2,83	2,49	2,11	1,81	
ZFR	2,83	2,61	1,50	1,23	
CSTF2	2,78	2,50	1,76	1,44	Termination
DDX20	2,78	2,34	1,03	0,00	
NCBP1	2,76	2,89	1,53	2,12	Splicing
EIF3M	2,75	2,72	2,97	2,35	
EIF3A	2,75	2,79	2,76	2,39	Other
SRSF7	2,75	2,92	1,97	2,28	Splicing
ZNF865	2,74	0,00	3,53	0,00	
SCAF8	2,73	2,44	1,66	1,41	
GPATCH8	2,70	2,08	0,93	0,71	
SRSF9	2,70	2,66	1,90	1,92	Splicing
PAF1	2,65	2,59	2,08	1,45	EF
AKAP8	2,64	2,48	0,52	1,07	Other
HNRNPA3	2,64	2,37	1,69	1,64	
TRMT2A	2,61	3,54	4,21	3,95	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
TRA2B	2,61	2,65	1,77	1,88	Splicing
SAFB	2,59	2,67	1,69	1,70	Other
EIF4A3	2,58	2,75	1,47	1,64	
RNPS1	2,57	2,76	1,52	2,11	Splicing
NDE1;NDEL1	2,56	4,11	0,00	4,62	
PTRH2	2,56	0,00	0,00	0,00	
SRSF10	2,55	2,53	1,82	2,00	Splicing
RBM15	2,55	2,70	1,25	1,62	Other
EHBP1	2,54	0,00	0,00	0,00	
YLPM1	2,53	2,79	0,56	0,88	Other
DDX51	2,53	0,00	3,00	3,33	
SNRPG;SNRPGP15	2,51	2,23	1,21	0,89	
PPP1R10	2,51	1,90	1,16	0,66	Other
MAG	2,51	0,00	0,00	0,00	
BCLAF1	2,50	2,72	1,41	1,76	Other
THRAP3	2,50	2,55	1,63	1,68	
LEO1	2,50	1,92	1,91	0,90	EF
ILF3	2,47	2,40	1,41	1,37	Other
DNAJC13	2,47	2,02	1,71	1,86	
HNRNPH3	2,47	2,33	1,78	1,64	
CPSF3	2,45	2,22	0,94	0,84	Termination
RBM7	2,44	1,97	0,52	0,62	
ICE1	2,43	0,00	0,00	0,00	
TRA2A	2,43	2,36	1,65	1,76	Splicing
HNRNPA1;HNRNPA1L2	2,43	2,13	1,74	1,50	
EIF4A1;EIF4A2	2,42	2,61	2,55	2,56	
EIF3F	2,40	2,79	2,27	2,06	
CENPF	2,40	0,00	0,00	3,01	
PPIE	2,39	2,55	1,16	0,98	
YTHDC1	2,39	2,59	1,08	1,47	Splicing
SNRNP200	2,38	2,54	1,23	1,34	Splicing
CSNK2A1;CSNK2A3	2,37	2,44	1,96	1,85	Other
RBMXL1	2,37	2,57	1,26	1,37	
SRSF1	2,35	2,45	1,45	1,63	
TRAF1	2,34	0,00	0,00	0,00	
PRPF8	2,34	2,48	1,09	1,17	Splicing
DHX9	2,33	2,54	1,25	1,27	Other
SRRT	2,32	2,10	1,39	1,05	Other

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
EIF3E	2,31	1,78	2,12	1,40	
WDR33	2,31	1,87	0,92	0,57	Termination
APOBEC3B	2,30	2,25	1,04	0,84	Other
SEPT10	2,30	2,87	3,01	2,34	
CTNNB1	2,30	1,78	1,95	2,40	
ARVCF	2,29	2,09	0,00	1,57	
SRSF6	2,27	2,18	1,52	1,47	Splicing
MYO1E;MYO1F	2,24	2,29	0,00	2,74	
PABPN1	2,23	2,07	1,26	1,25	
CHTOP	2,22	2,50	0,95	1,41	
NONO	2,22	2,31	0,50	1,09	
SF3B5	2,22	2,00	1,14	0,91	
MAGOHB	2,22	2,32	1,06	1,39	
ILF2	2,20	2,19	1,16	1,00	Other
SUGP2	2,19	2,56	1,11	0,78	
SNRPA	2,18	1,66	0,79	0,32	Splicing
EFTUD2	2,17	2,21	0,97	0,97	
SF3A1	2,15	1,72	0,85	0,47	
ZNF609	2,15	0,00	0,00	0,00	
ING2	2,15	2,09	2,04	0,00	
HNRNPA0	2,14	1,92	1,29	1,00	
DHX15	2,14	1,94	0,99	1,23	
CDC40	2,13	2,30	1,13	1,10	Splicing
EIF3I	2,12	2,14	2,23	2,03	
SNRNP40	2,12	1,91	0,95	1,04	Splicing
SF3B3	2,12	2,04	0,91	0,90	
MATR3	2,10	2,14	0,88	0,96	
SNRNP70	2,09	1,83	0,95	0,67	Splicing
PCID2	2,09	1,97	0,84	1,14	
SF3B1	2,07	2,01	0,72	0,75	Splicing
CCDC12	2,06	2,10	0,91	0,91	
DDX42	2,05	1,82	0,93	0,66	Other
CCT4	2,05	1,20	2,16	1,65	
ANXA1	2,05	2,44	2,83	1,90	
TARDBP	2,03	1,93	0,77	0,69	
THOC2	2,02	2,07	1,53	1,51	Other
RBMX	2,02	2,16	1,29	1,23	
RBM17	2,01	1,83	0,92	0,64	Splicing

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
BUD31	1,99	1,98	0,38	0,68	
PPIL1	1,99	2,34	0,43	0,51	Splicing
SNRPN;SNRPB	1,99	1,67	0,85	0,78	
PHF5A	1,97	1,68	0,88	0,43	Splicing
CRNKL1	1,96	2,20	0,60	0,72	Splicing
MED28	1,96	1,50	2,85	2,84	Mediator
PNN	1,95	1,85	0,82	1,05	Other
CSDE1	1,95	2,61	1,86	1,61	
API5	1,95	2,39	2,02	1,68	
SF3A3	1,94	1,60	0,71	0,46	Splicing
RBM8A	1,94	2,09	0,94	1,03	Splicing
SYNCRIP	1,92	1,83	1,33	1,10	
CSTF1	1,91	1,41	1,16	1,00	Splicing
CHERP	1,88	1,71	0,33	0,73	Other
SFPQ	1,86	1,96	0,23	0,57	
ZC3H18	1,85	1,69	0,72	0,74	Other
HDGFRP2	1,85	1,89	1,01	0,96	
BUB3	1,84	1,99	1,15	0,88	Other
PABPC1;PABPC3	1,82	1,54	1,63	1,52	
CAPRIN1	1,82	1,79	1,66	1,75	
SF3B2	1,82	1,62	0,51	0,35	
SMU1	1,81	1,83	0,65	0,63	
LSM2	1,81	1,58	0,44	0,31	
CDC73	1,81	1,76	0,94	0,76	EF
KDM1A	1,80	0,00	0,00	0,00	
ARMC5	1,79	2,73	1,96	0,00	
HNRNPC	1,79	1,77	1,10	1,15	
PKP2	1,78	1,97	0,00	1,13	
IK	1,77	1,63	0,49	0,37	Splicing
HNRNPAB	1,77	1,63	1,24	0,86	
STAG2	1,76	2,75	1,81	2,10	
SLU7	1,76	1,82	0,18	0,31	
DHX16	1,75	2,07	0,81	0,78	Splicing
PLRG1	1,75	1,97	0,73	0,67	Splicing
HNRNPDL	1,74	1,41	1,31	0,92	
PRPF6	1,73	1,63	0,66	0,55	
HNRNPH1	1,72	1,74	0,80	0,73	
ACIN1	1,72	1,75	0,86	1,09	Splicing

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SF1	1,71	1,70	0,77	0,74	Splicing
EIF4G1	1,70	1,55	1,59	1,36	
PTBP1	1,69	1,65	0,84	0,77	
DPY30	1,68	1,87	1,12	0,92	
DDX17	1,68	1,72	0,17	0,41	
CWC15	1,67	1,86	0,61	0,58	Splicing
HNRNPF	1,67	1,71	0,68	0,77	
LARP1	1,67	1,60	1,57	1,75	
NDUFS1	1,66	0,00	0,00	0,00	
PABPC4	1,66	0,94	1,13	1,57	
ATAD3A	1,66	1,38	2,01	2,14	Other
RALY	1,65	1,81	1,06	1,01	
VDAC3	1,65	0,69	2,14	1,74	
U2SURP	1,64	1,58	0,49	0,58	Splicing
SF3B4	1,63	1,75	0,81	0,65	
DDX3X;DDX3Y	1,62	1,93	0,64	0,83	
CCAR1	1,60	1,49	0,75	0,29	Other
ELAVL1	1,59	1,62	0,86	0,90	
KHDRBS3	1,59	1,21	0,76	0,67	Splicing
SUGP1	1,58	0,89	0,33	0,00	
ZC3H11A	1,57	1,44	0,80	0,97	Other
DDX6	1,57	1,20	1,62	1,31	
SNW1	1,57	1,59	0,20	0,31	Splicing
DDX39B	1,57	1,70	1,01	0,87	
THOC6	1,56	1,44	0,98	0,87	
SRSF5	1,56	1,33	1,29	1,05	
HNRNPU	1,55	1,45	0,75	0,80	
SCAF1	1,55	1,44	0,35	0,20	Other
KPNA4	1,55	2,18	1,33	1,91	
FYTTD1	1,54	2,04	-0,25	-0,28	Other
LUZP1	1,53	1,84	1,68	2,41	
ZC3H14	1,51	1,66	0,58	0,82	
PRPF38A	1,51	1,51	0,48	0,62	Splicing
PELP1	1,51	1,73	1,36	1,43	
RBM14	1,50	1,64	0,03	0,45	
PSPC1	1,47	1,39	0,61	0,60	Other
PRPF19	1,46	1,59	0,44	0,57	Splicing
SF3B6	1,43	1,24	0,41	0,33	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZNF134	1,42	2,50	1,12	2,53	
PPHLN1	1,41	1,62	0,31	0,52	
PRPF40A	1,40	1,32	0,42	0,38	
WDR18	1,40	1,42	1,43	1,50	
BCAS2	1,39	1,54	0,36	0,25	Splicing
NCL	1,39	1,80	1,67	1,45	
EIF3B	1,38	1,19	1,47	1,18	
RBM25	1,37	1,30	0,24	0,25	
RBFOX2;RBFOX1	1,36	1,08	0,34	0,34	
MRPL23	1,34	0,00	0,00	0,00	
HNRNPM	1,33	1,24	0,53	0,59	
TXLNA	1,33	1,09	2,03	1,69	
SRRM2	1,33	1,57	0,71	0,66	
NUP205	1,32	1,88	1,08	1,67	
SAP18	1,30	1,30	0,62	0,91	Splicing
AIFM1	1,29	0,58	1,46	0,88	
HNRNPD	1,29	0,72	0,80	0,27	
RANBP2	1,29	2,00	1,38	1,28	
VCL	1,27	0,00	0,00	0,00	
RBM22	1,23	1,39	0,28	0,38	
TEX10	1,21	1,38	0,89	1,24	
KHDRBS1	1,20	1,22	0,34	0,08	Splicing
GTF2E2	1,19	1,06	2,03	1,49	
SYF2	1,19	1,56	-0,11	0,45	
TUBB4B	1,18	0,96	2,20	2,01	
SLTM	1,18	1,15	-0,12	0,16	
ISY1	1,18	1,24	0,28	0,44	
SKIV2L2	1,17	0,98	0,24	0,48	
FMNL3	1,16	1,40	0,00	2,39	
STAU1	1,15	1,15	0,89	0,85	
SLC25A5	1,15	1,26	1,09	1,11	
CAV1	1,14	0,82	0,65	0,58	
NOL11	1,13	1,49	1,08	1,62	
ZNF207	1,12	1,12	0,34	0,18	
NOL9	1,12	1,34	1,14	1,36	
SIPA1L1	1,12	0,70	0,60	1,05	
C3orf38	1,12	0,00	0,00	0,00	
LAS1L	1,11	0,88	0,92	1,03	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SNRPD1	1,11	1,09	0,52	0,25	
G3BP2	1,10	1,04	0,98	0,94	
RBMX2	1,10	0,73	0,00	1,08	
G3BP1	1,10	0,95	1,51	1,23	
WDR36	1,09	1,47	0,68	1,80	
CEP135	1,07	1,67	1,46	2,12	
RBMS1	1,07	0,95	0,32	0,34	
HNRNPL	1,06	0,96	0,42	0,36	
SRSF3	1,06	0,91	0,37	0,33	
PPP1CA	1,05	1,00	0,28	0,54	
RPS12	1,03	1,03	1,75	2,48	
SNRPE	1,03	0,75	0,64	0,01	
DDX1	1,02	1,08	0,84	0,78	
CSNK1D;CSNK1E	1,00	0,92	0,55	0,80	
FAM83H	1,00	1,12	0,83	1,19	
VDAC1	1,00	1,13	1,23	1,50	Other
SYMPK	1,00	0,85	0,43	0,08	Termination
CSNK1A1;CSNK1A1L	1,00	0,88	0,64	0,69	
PRKDC	0,99	0,91	0,85	0,74	
SSRP1	0,99	1,21	1,00	1,33	EF
RPN2	0,98	1,16	0,93	1,50	
VDAC2	0,96	0,72	1,26	1,14	
PGAM5	0,95	0,76	0,82	0,75	Other
UBA52;UBB;RPS27A;UBC	0,94	2,80	1,61	4,86	
DDX50	0,94	0,96	0,24	0,26	
RTCB	0,93	0,89	0,89	0,71	
TUBA1A	0,93	0,81	2,04	1,93	
RPS21	0,92	0,39	1,44	1,24	
EEF1G	0,92	0,73	1,65	1,51	
RPGRIP1L	0,92	0,00	0,00	0,00	
RPLP2	0,91	0,73	1,46	1,26	
TUBA1B	0,90	0,80	2,10	1,99	
SUPT16H	0,90	0,86	0,30	0,84	
EIF3G	0,90	0,72	1,79	0,82	
EWSR1	0,89	1,22	0,08	0,76	Other
GNB2;GNB4	0,89	0,27	0,58	0,46	
MRPS22	0,89	-0,19	1,63	0,33	
ASPH	0,88	0,37	1,44	0,89	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
RBM4;RBM4B	0,88	0,60	0,22	0,29	
DDX46	0,87	0,86	0,01	-0,18	
TUBB	0,86	0,81	2,01	1,94	
SIX4	0,85	1,26	0,63	0,87	
CCT6A	0,85	0,92	1,25	0,75	
EIF4B	0,85	0,69	1,04	0,56	
C1QBP	0,84	0,17	0,91	0,18	
RPL12	0,84	0,32	1,35	1,47	
LUC7L3	0,84	1,22	0,34	0,38	
PDCD11	0,83	1,03	0,83	1,44	
CIRH1A	0,83	0,92	0,58	1,26	
NOL6	0,82	0,82	0,45	1,09	
PRC1	0,82	0,68	0,19	0,29	
CCT3	0,80	0,37	1,07	0,47	
MRPS35	0,79	0,00	1,56	0,76	
DDX23	0,78	0,57	-0,23	-0,34	
SQSTM1	0,78	0,00	1,09	0,81	
CYFIP1	0,78	0,69	1,05	1,36	
SNRPD2	0,78	0,54	0,15	-0,04	
ZNF638	0,77	0,80	-0,12	0,02	
CDK11B;CDC2L1;CDK11A	0,77	0,80	0,06	0,33	
TGM2	0,76	0,16	0,96	0,36	
CLTC	0,75	0,55	0,85	0,72	
ALKBH5	0,75	1,29	0,88	0,47	
POLDIP3	0,75	1,14	0,10	0,19	Other
BUD13	0,75	1,24	-0,49	-0,54	
RPLP0;RPLP0P6	0,74	0,59	1,28	1,11	
DDX5	0,74	0,72	-0,25	-0,25	
CTNND1	0,73	0,31	0,53	0,51	
DKC1	0,72	0,60	0,72	0,94	
PALLD	0,71	0,86	1,00	0,78	
ACTA1;ACTC1;ACTG2;ACTA2	0,71	1,28	0,15	0,71	
YWHAZ	0,70	0,84	1,07	1,05	
CKAP5	0,70	1,49	1,12	1,60	
YY1;YY2	0,70	0,93	0,88	1,09	
RPL4	0,68	0,49	0,90	0,73	
AP2S1	0,67	1,33	0,12	-1,15	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
PQBP1	0,67	0,46	-0,31	-0,32	
SRSF4	0,66	0,57	0,00	0,00	
GTF2I	0,66	-0,16	1,37	0,58	GTF
FXR1	0,65	0,70	0,68	0,44	
HDAC2	0,65	0,63	0,36	0,56	
AP2A1	0,65	0,33	0,46	0,56	
GPATCH1	0,65	1,49	0,09	0,31	
TCERG1	0,65	0,45	0,13	-0,16	
bK150C2.9;APOBEC3D	0,64	1,86	0,00	0,00	
PRDX5	0,64	0,00	0,00	0,00	
RCL1	0,64	0,34	0,51	1,07	
CHCHD3	0,64	0,21	0,56	0,38	
PARP14	0,63	0,00	0,92	0,59	
CCT8	0,63	-0,01	1,26	0,67	
TOP2A	0,61	0,49	0,17	0,93	
MYBBP1A	0,60	0,70	0,73	1,17	
DNAJA2	0,60	1,13	1,64	1,73	
NCKAP1	0,59	0,38	0,97	1,07	
TRIM28	0,59	0,53	0,72	0,12	
HNRNPLL;HNRPLL	0,59	0,69	0,60	0,04	
SMC3	0,58	0,99	0,73	0,50	
WDR43	0,58	0,64	0,70	1,00	
ALYREF	0,58	0,49	0,14	-0,04	
CBX3	0,58	0,75	0,32	1,25	
VAPA	0,58	0,08	0,59	0,64	
SSR4	0,57	0,07	0,19	0,75	
KRT18	0,56	0,37	0,57	0,80	
P4HB	0,56	0,00	0,00	0,00	
C14orf166	0,56	0,52	0,44	0,34	
EIF4E	0,55	0,51	1,22	0,42	
ARHGEF2	0,55	0,21	0,81	0,35	
BANF1	0,54	0,39	-0,27	1,49	
GTF3C1	0,54	0,44	0,93	1,10	
MRPS27	0,54	-0,88	1,05	-0,06	
MYH9	0,53	0,33	0,34	0,59	
BAG2	0,53	0,72	0,85	0,75	
HIST2H3PS2	0,51	0,44	0,36	0,43	
YTHDF1	0,51	0,98	0,94	0,70	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
NDUFA9	0,51	0,54	0,08	0,30	
DNAJA1	0,50	0,97	1,38	1,76	
RPN1	0,50	0,18	0,76	0,83	
PPIG	0,50	0,56	-0,08	0,38	
LMNB2	0,48	0,52	0,63	0,73	
MFAP1	0,48	0,61	-0,45	-0,30	Splicing
NUDT21	0,48	0,47	-0,11	-0,23	
FAM98A	0,47	0,75	0,39	0,06	
ABLIM1	0,46	0,09	-0,33	0,25	
CTSD	0,46	0,00	0,00	0,00	
DHX8	0,46	0,70	0,07	0,19	
ENY2	0,46	0,81	0,63	0,11	
RPL7	0,45	0,43	0,43	0,23	
PDLIM7	0,45	0,27	0,45	0,42	
GAPDH	0,44	0,61	0,44	0,21	
RPF2	0,44	0,63	0,28	0,48	
ORC2	0,44	0,47	0,44	0,61	
CHD4	0,44	0,39	0,38	0,46	
IMMT	0,43	0,15	0,52	0,47	
RPS27	0,43	-0,71	0,42	0,44	Other
PHB2	0,43	0,31	0,69	0,46	
NOC2L	0,43	0,43	0,60	1,29	
HCFC1	0,43	0,16	0,38	0,23	
SEPT2	0,43	0,62	1,14	0,96	
MCM2	0,43	-0,36	2,91	2,54	
SCRIB	0,42	0,08	0,11	0,45	
SAP30BP	0,41	0,53	0,06	0,01	
GRSF1	0,39	0,51	0,59	0,37	
MRPS6	0,39	0,00	1,80	0,07	
PHF8;PHF2	0,39	0,23	0,63	0,27	
SNRPD3	0,39	0,51	-0,22	1,47	
HSP90AB1	0,38	0,61	0,53	1,52	
MRPS34	0,38	-0,62	1,02	0,09	
NOSIP	0,38	0,49	0,58	-0,04	
PRPF18	0,37	0,56	0,00	0,00	
RPS27A	0,37	0,29	0,11	0,30	
CDK9	0,37	0,19	-0,16	-0,42	
SERBP1	0,37	0,09	1,08	0,89	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
AP2M1	0,36	-0,01	0,15	0,03	
MYO1B	0,35	-0,44	0,27	0,19	
SEPT7	0,35	0,47	1,15	0,65	
MAPRE1	0,35	0,41	1,15	0,57	
TBL3	0,35	0,89	-0,08	0,89	
RSF1	0,35	0,33	0,00	0,42	
KPNA2	0,35	0,70	0,39	0,74	
ZNF581	0,34	0,00	0,00	0,00	
PYCR2	0,34	-0,19	0,27	0,59	
EIF5B	0,34	0,43	0,88	0,72	
SRPK1	0,34	0,45	0,29	0,81	
EDF1	0,31	-0,21	1,16	0,10	
PPP1R12A	0,31	-0,18	0,10	-0,08	
RPS27L	0,30	0,68	0,56	0,65	
ADNP	0,30	0,28	0,21	0,27	
ACTL6A	0,30	-0,12	0,35	0,23	
MYO1C	0,30	-0,26	0,20	0,05	
HMGB1;HMGB1P1	0,28	0,91	1,72	1,39	
RPL15	0,28	0,06	0,52	0,50	
SCAF4	0,28	0,22	-0,61	-0,25	EF
RAD21	0,27	0,36	0,19	0,40	
MYL12A;MYL12B;MYL9	0,27	0,20	1,26	0,81	
RPS2	0,27	0,28	0,57	0,75	Other
FN1	0,26	0,60	0,13	0,81	
MRPS14	0,26	-1,20	0,92	-0,19	
RPS29	0,26	-0,23	0,52	0,63	
LMNB1	0,26	0,12	0,22	0,24	
SEPT11	0,26	0,32	0,82	0,84	
LARP4	0,25	0,54	0,29	0,43	
FRMD6	0,25	-0,64	-0,17	0,00	
SRPR	0,25	-0,33	0,15	-0,01	
EEF1A2	0,24	0,41	0,77	0,53	
POLR1A	0,24	-0,14	0,33	0,38	
MYH10	0,24	-0,04	0,12	0,48	
ACTN1	0,24	0,22	-0,03	0,26	
FEN1	0,23	0,32	0,79	0,82	
NUP98	0,22	0,55	0,00	0,65	
HSPA8	0,21	0,31	0,51	0,48	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
KIF2C	0,21	0,49	0,62	0,06	
SMARCA4	0,21	-0,05	-0,22	0,21	
FLNC	0,21	0,34	0,02	0,31	
HACD3	0,21	-0,07	0,25	1,05	
SRP9	0,20	-0,01	0,61	0,26	
GAR1	0,20	0,02	-0,04	0,13	
CDK2AP1;CDK2AP2	0,19	0,07	0,00	0,00	
CPSF7	0,19	0,39	-0,43	-0,67	
SON	0,18	0,20	-0,44	-0,30	
SPTBN1	0,18	-0,20	0,22	-0,03	
UBTF	0,18	0,07	0,28	0,46	
ZNF524	0,17	0,28	0,37	0,54	
PCBP2	0,17	0,11	-0,07	0,05	
AHNAK	0,16	-0,74	0,27	-0,24	
PHB	0,16	-0,28	-0,17	0,35	
RUVBL2	0,15	0,19	0,40	0,46	
FBL	0,15	0,17	0,25	0,86	
MCM3	0,15	-1,13	1,70	1,22	
NOP56	0,15	0,08	0,34	0,87	
SND1	0,15	0,54	0,83	0,76	
ERAL1	0,15	0,00	1,15	0,00	
MAX	0,15	1,94	0,70	1,67	
IQGAP1	0,14	0,06	0,80	0,45	
MEF2D	0,14	0,72	1,03	0,49	
SDF2L1	0,14	0,00	1,30	0,60	
HSPA1B;HSPA1A	0,13	0,89	0,50	1,05	
GPR125	0,13	0,64	0,00	0,00	
PPIL4	0,13	0,28	-0,53	-0,01	
CPSF6	0,13	0,22	0,11	-0,28	Termination
ZNF384;ZNF362	0,12	0,06	-0,05	0,19	
FLG	0,12	-0,62	0,36	-0,11	
DBN1	0,12	-0,22	0,20	0,02	
KRT80	0,11	-0,20	1,00	0,63	
CHD1	0,11	-0,05	0,00	0,04	
RPS20	0,11	0,02	0,51	0,48	
SEPT9	0,10	-0,02	0,62	0,41	
RAI14	0,10	-0,03	-0,30	-0,06	
KPNB1	0,10	0,29	0,05	0,15	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ERBB2IP	0,10	-0,23	0,02	-0,45	
RRBP1	0,10	-0,49	0,69	0,15	
DSC1	0,10	-0,40	0,22	-0,14	
PRDX1	0,10	-0,98	-0,27	-0,19	
NOC4L	0,09	0,30	0,03	0,35	
HIST1H4A	0,09	0,18	-0,03	0,21	
LRPPRC	0,09	-0,23	-0,34	-0,18	
HADHA	0,08	-0,59	0,03	0,06	Other
UTP15	0,08	0,33	0,12	0,66	
TUBG1;TUBG2	0,08	-0,37	0,85	0,27	
HSP90AB2P	0,08	0,00	0,00	1,20	
PLEKHG3	0,07	0,51	0,43	0,66	
HNRNPUL2;HNRNPUL2-BSCL2	0,07	0,17	-0,15	-0,16	
SRSF2	0,07	-0,09	-0,12	0,04	
Cxorf67	0,07	0,50	0,74	0,47	
hCG_1984214;MRPS17	0,07	-0,46	0,41	0,21	
HSPD1	0,06	-0,78	-0,10	-0,40	
CCT5	0,06	0,10	0,75	0,55	
PDLIM4	0,06	0,17	0,18	0,12	
MCM5	0,05	0,29	1,25	0,76	
DDX21	0,05	0,44	0,11	0,61	
MCM7	0,05	0,48	1,53	1,08	
ZNF800	0,05	0,13	0,33	0,18	
RPS16;ZNF90	0,05	0,08	0,44	0,16	Other
MRPL17	0,05	0,00	0,41	-0,09	
KRT8	0,04	0,18	0,29	0,19	
DYNLL1;DYNLL2	0,04	-0,14	0,33	-0,02	
SMC1A	0,04	0,00	0,16	0,40	
SERPINH1	0,04	-0,62	-0,03	-0,36	
SMARCD2	0,03	0,33	0,07	0,25	
DSG1	0,03	0,00	0,14	-0,54	
UHRF1	0,02	-0,17	-0,33	0,05	
SPECC1L;SPECC1L-ADORA2A	0,01	-0,01	0,07	0,09	
FLNA	0,00	-0,09	0,35	0,29	
MYC	0,00	8,01	0,00	8,51	Other
SNRPC	0,00	7,88	7,20	6,97	Splicing
LEF1	0,00	7,86	0,00	0,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
KMT2C	0,00	7,47	0,00	0,00	
CLK3	0,00	6,90	0,00	6,25	Other
CWC25	0,00	6,89	0,00	0,00	
RPLP1	0,00	6,50	6,88	7,84	Other
MYO5A	0,00	6,43	0,00	0,00	
FBLL1	0,00	6,40	0,00	0,00	
CUX2	0,00	6,38	0,00	0,00	
ZNF598	0,00	6,36	0,00	0,00	
BATF3	0,00	6,29	6,52	6,70	Other
FAM220BP	0,00	6,15	0,00	0,00	
NUP107	0,00	5,96	0,00	5,49	
RSRC2	0,00	5,76	0,00	0,00	
MAK16	0,00	5,74	5,32	6,22	Other
C2orf49	0,00	5,71	0,00	0,00	
PLK1	0,00	5,52	5,15	5,95	
UTP20	0,00	5,42	0,00	5,95	
GNPAT	0,00	5,41	0,00	0,00	
PELO	0,00	5,26	5,68	0,00	
KMT2D	0,00	5,23	0,00	0,00	
STARD9	0,00	5,20	0,00	0,00	
MLF2	0,00	5,14	0,00	0,00	
EXOSC4	0,00	4,95	0,00	0,00	
RGPD3;RGPD4;RGPD1;RGPD2	0,00	4,91	0,00	0,00	
EXOSC10	0,00	4,87	4,58	4,82	Termination
FLOT1	0,00	4,79	4,37	4,52	
NUP50	0,00	4,77	0,00	0,00	
PAPD5	0,00	4,72	4,73	4,96	
ZCCHC4	0,00	4,68	0,00	0,00	
GPN3	0,00	4,68	0,00	0,00	
ACTBL2	0,00	4,66	0,00	0,00	
NABP2	0,00	4,56	3,87	3,50	
POU2F1;POU2F2;POU2F3	0,00	4,55	4,98	0,00	
COLGALT1	0,00	4,53	5,33	5,07	
NUFIP1	0,00	4,52	0,00	0,00	
ATAD2	0,00	4,52	0,00	5,30	
PTBP3	0,00	4,50	0,00	0,00	
ZC3HAV1	0,00	4,49	4,64	5,09	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
RBPJ	0,00	4,48	0,00	0,00	
PDS5B	0,00	4,48	3,75	4,60	
ALKBH2	0,00	4,47	4,54	4,33	
S100A10	0,00	4,44	0,00	0,00	
NFYC	0,00	4,39	4,57	0,00	
UBAP2	0,00	4,39	0,00	0,00	
SMAD3	0,00	4,31	4,63	5,20	
ABCF2	0,00	4,29	4,70	0,00	
BAG3	0,00	4,29	0,00	0,00	
DLG1	0,00	4,28	4,08	3,77	
FAM58A	0,00	4,28	0,00	0,00	
CDC20	0,00	4,23	0,00	0,00	
CNTRL	0,00	4,22	0,00	0,00	
PICK1	0,00	4,15	0,00	0,00	
CASC3	0,00	4,13	0,00	0,00	
MB21D1	0,00	4,10	0,00	4,57	
SRP54	0,00	4,08	4,07	4,24	
AAAS	0,00	4,03	0,00	0,00	
YWHAB	0,00	4,00	0,00	4,22	
MSI2	0,00	3,92	0,00	3,40	
SEC24C	0,00	3,87	3,94	3,83	
CDK11A	0,00	3,85	0,00	0,00	
STOML2	0,00	3,85	0,00	3,99	
AP3B1	0,00	3,81	4,13	4,06	
TFAP4	0,00	3,80	0,00	4,03	
SSFA2	0,00	3,77	0,00	0,00	
EEF1B2	0,00	3,73	0,00	5,07	
REXO1	0,00	3,70	0,00	0,00	
SDE2	0,00	3,70	0,00	0,00	
MCM6	0,00	3,67	0,00	0,00	
OCIAD2	0,00	3,65	0,00	0,00	
SRBD1	0,00	3,65	0,00	0,00	
RPAP1	0,00	3,62	4,50	4,15	
CHMP4B	0,00	3,60	0,00	0,00	
C17orf49;BAP18	0,00	3,59	0,00	0,00	
SMARCD1	0,00	3,58	0,00	0,00	
CWF19L1	0,00	3,57	0,00	0,00	
FNDC3B	0,00	3,56	0,00	0,00	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
FLOT2	0,00	3,53	3,70	0,00	
PUM1	0,00	3,51	0,00	0,00	
RMDN3	0,00	3,51	3,57	0,00	
GTF2H4	0,00	3,50	4,47	4,25	
PURB	0,00	3,49	0,00	0,00	
NUPL1	0,00	3,49	0,00	0,00	
ACLY	0,00	3,49	0,00	3,70	
LENG8	0,00	3,48	0,00	0,00	
PRKRIP1	0,00	3,48	0,00	0,00	
HDLBP	0,00	3,42	4,51	4,06	
TCEA2	0,00	3,41	0,00	0,00	
MAN1B1	0,00	3,40	0,00	0,00	
POM121C;POM121	0,00	3,39	0,00	0,00	
SMPD4	0,00	3,36	0,00	3,26	
TRRAP	0,00	3,35	0,00	2,69	
WDR83	0,00	3,29	0,00	0,00	
MBNL1;MBLL;MBNL2	0,00	3,26	0,00	0,00	
KIF23	0,00	3,24	0,00	0,00	
CD44	0,00	3,22	0,00	0,00	
EMC7	0,00	3,21	0,00	0,00	
PAXIP1	0,00	3,15	0,00	0,00	
YWHAG	0,00	3,09	3,00	3,25	
AKAP1	0,00	3,08	0,00	0,00	
ZNF236	0,00	3,07	0,00	3,64	
NTPCR	0,00	3,04	0,00	0,00	
OVOL2	0,00	3,03	0,00	0,00	
RGPD5;RGPD8	0,00	3,02	0,00	0,00	
TIA1	0,00	3,01	0,00	0,00	
GCFC2	0,00	3,00	0,00	0,00	
ERLIN2	0,00	2,98	0,00	0,00	
EDC3	0,00	2,97	0,00	0,00	
EXOSC3	0,00	2,97	0,00	0,00	
RBPMS2	0,00	2,96	0,00	0,00	
YEATS4	0,00	2,95	0,00	0,00	
ATP6V0C	0,00	2,92	0,00	0,00	
YARS2	0,00	2,92	0,00	0,00	
DHX35	0,00	2,92	0,00	0,00	
DST	0,00	2,91	0,00	2,82	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
WIZ	0,00	2,88	0,00	0,00	
AURKC	0,00	2,80	0,00	3,91	
YWHAQ	0,00	2,80	4,17	4,47	
TIMM8A	0,00	2,73	0,00	0,00	
SSB	0,00	2,73	2,89	2,98	
SMG8	0,00	2,70	0,00	0,00	
STXBP1	0,00	2,69	0,00	0,00	
CDKN2AIPNL	0,00	2,55	0,00	0,00	
MRRF	0,00	2,55	0,00	0,00	
SPG11	0,00	2,52	0,00	0,00	
EPC1;EPC2	0,00	2,52	0,00	0,00	
XRCC1	0,00	2,52	0,00	0,00	
AGO2;AGO1;AGO3	0,00	2,50	0,00	0,00	
DHX57	0,00	2,48	0,00	0,00	
PPRC1	0,00	2,46	0,00	0,00	
LARP4B	0,00	2,41	0,00	0,00	
COPA	0,00	2,37	2,62	3,03	
KRT26	0,00	2,36	0,00	0,00	
NUP188	0,00	2,35	0,00	0,00	
PARP12	0,00	2,35	0,00	0,00	
AP2A2	0,00	2,32	0,00	0,00	
EPB41L1	0,00	2,32	0,00	0,00	
TRIM21	0,00	2,28	0,00	0,00	
PHC3;PHC2	0,00	2,18	0,00	0,00	
SMG9	0,00	2,17	0,00	0,00	
E2F6	0,00	2,13	0,00	0,00	
UGT8	0,00	2,09	0,00	2,15	
TRIM33	0,00	2,07	0,00	0,00	
DHX34	0,00	2,03	0,00	0,00	
FLII	0,00	2,03	0,00	0,00	
PDLIM3	0,00	1,94	0,00	0,00	
MRPL13	0,00	1,93	0,00	0,00	
NTHL1	0,00	1,93	0,00	0,00	
GTF3C5	0,00	1,93	0,00	0,00	
EIF2D	0,00	1,92	0,00	0,00	
FMR1	0,00	1,87	0,00	0,00	
CDC23	0,00	1,80	0,00	0,00	
NUDT16L1	0,00	1,75	0,00	0,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ATP5A1	0,00	1,64	0,00	0,00	
SUN2	0,00	1,56	0,00	0,00	
PHF14	0,00	1,54	0,00	0,00	
ZBTB11	0,00	1,43	0,00	0,00	
FOXRED1	0,00	1,27	0,00	0,00	
PATZ1	0,00	1,25	0,00	0,00	
KCNAB1	0,00	1,05	0,00	0,00	
RAE1	0,00	1,03	0,87	0,64	
EXOC1	0,00	1,01	0,00	0,00	
ODF2	0,00	0,90	0,00	0,00	
PTMS	0,00	0,89	0,00	0,00	
TFRC	0,00	0,85	0,00	0,00	
C12orf57	0,00	0,77	0,00	0,00	
NDNL2	0,00	0,65	0,00	0,00	
NIP7	0,00	0,56	0,00	0,68	
CLK4	0,00	0,25	0,00	0,00	
RNMT	0,00	0,09	-0,14	-0,42	
FAM98B	0,00	0,05	0,15	0,00	
AZGP1	0,00	0,03	0,81	0,00	
GATAD2B	0,00	0,02	-0,23	0,01	
MDK	0,00	0,00	6,30	9,00	Other
TMEM63A	0,00	0,00	6,27	0,00	
SMC4	0,00	0,00	5,78	5,50	
BTF3L4	0,00	0,00	5,68	5,57	
BCL7C	0,00	0,00	5,40	0,00	
SMC2	0,00	0,00	5,36	0,00	
CAD	0,00	0,00	5,34	4,68	
HOOK2	0,00	0,00	5,28	0,00	
EIF2A	0,00	0,00	5,27	0,00	
LASP1	0,00	0,00	5,26	0,00	
TAGLN2	0,00	0,00	5,21	4,79	
ZYX	0,00	0,00	5,21	0,00	
CEP131	0,00	0,00	5,14	5,12	
SAP30	0,00	0,00	5,06	5,40	
STK10	0,00	0,00	4,97	5,37	
TTN	0,00	0,00	4,94	0,00	
AGPS	0,00	0,00	4,90	0,00	
MCM4	0,00	0,00	4,84	4,79	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
MRPS24	0,00	0,00	4,79	0,00	
PIP	0,00	0,00	4,69	0,00	
TMED9	0,00	0,00	4,60	0,00	
ALB	0,00	0,00	4,58	0,00	
TUBA4A	0,00	0,00	4,55	4,51	
SET;SETSIP	0,00	0,00	4,48	0,00	
SSR1	0,00	0,00	4,44	4,35	
TRIM26	0,00	0,00	4,43	0,00	
AEN	0,00	0,00	4,39	0,00	
PPAN;PPAN-P2RY11	0,00	0,00	4,34	0,00	
FARSB	0,00	0,00	4,31	0,00	
EXOSC7	0,00	0,00	4,27	0,00	
OXSR1	0,00	0,00	4,24	0,00	
MRPL43	0,00	0,00	4,23	0,00	
LACTB	0,00	0,00	4,22	0,00	
TBX3;TBX2	0,00	0,00	4,12	0,00	
TROVE2	0,00	0,00	4,09	0,00	
TECR	0,00	0,00	4,08	0,00	
RBM19	0,00	0,00	4,07	4,87	
AP3D1	0,00	0,00	4,02	3,25	
TOR1AIP1	0,00	0,00	3,98	3,77	
CUL4A	0,00	0,00	3,94	0,00	
PURA	0,00	0,00	3,89	0,00	
LAMTOR1	0,00	0,00	3,85	0,00	
KRT13	0,00	0,00	3,85	0,00	
WIBG	0,00	0,00	3,81	0,00	
GSN	0,00	0,00	3,80	0,00	
ATP5J2-PTCD1;PTCD1	0,00	0,00	3,71	0,00	
PIH1D1	0,00	0,00	3,70	0,00	
STAG1;DKFZp781D1416	0,00	0,00	3,67	0,00	
OTUD6B	0,00	0,00	3,57	0,00	
DNAJB12	0,00	0,00	3,57	0,00	
CTTN	0,00	0,00	3,56	0,00	
PBRM1	0,00	0,00	3,56	0,00	
MALSU1	0,00	0,00	3,53	0,00	
PSMA7;PSMA8	0,00	0,00	3,44	0,00	
RBBP5	0,00	0,00	3,43	0,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
UTRN	0,00	0,00	3,40	0,00	
ABCE1	0,00	0,00	3,33	0,00	
TBC1D10B	0,00	0,00	3,31	0,00	
ZC3H7B	0,00	0,00	3,30	0,00	
MRPL21	0,00	0,00	3,28	0,00	
CCNK	0,00	0,00	3,27	0,00	
RANBP9	0,00	0,00	3,25	0,00	
FARSA	0,00	0,00	3,25	0,00	
EZR;RDX	0,00	0,00	3,23	0,00	
SS18	0,00	0,00	3,07	0,00	
FAM111B	0,00	0,00	3,07	0,00	
CDC27	0,00	0,00	3,07	0,00	
CLPX	0,00	0,00	3,02	0,00	
GGCT	0,00	0,00	3,00	0,00	
PLAGL1	0,00	0,00	2,94	0,00	
SEC23B	0,00	0,00	2,90	0,00	
ANXA7	0,00	0,00	2,87	0,00	
TRIM27	0,00	0,00	2,84	0,00	
MRPL28	0,00	0,00	2,83	0,00	
ITIH4	0,00	0,00	2,83	0,00	
KIDINS220	0,00	0,00	2,78	0,00	
SBNO1	0,00	0,00	2,78	0,00	
SIAE	0,00	0,00	2,77	0,00	
MYO1D	0,00	0,00	2,73	0,00	
VCP	0,00	0,00	2,72	0,00	
AMOTL2	0,00	0,00	2,62	0,00	
OGT	0,00	0,00	2,61	0,00	
ETF1	0,00	0,00	2,58	0,00	
C3orf17	0,00	0,00	2,57	0,00	
NXT1	0,00	0,00	2,54	0,00	
ARF1;ARF3	0,00	0,00	2,50	0,00	
NDUFA4	0,00	0,00	2,48	0,00	
SRCAP	0,00	0,00	2,42	0,00	
SENP2	0,00	0,00	2,30	0,00	
WRAP53	0,00	0,00	2,29	0,00	
TAF4	0,00	0,00	2,19	0,00	
INO80E	0,00	0,00	2,14	0,00	
LRPAP1	0,00	0,00	2,11	0,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
TBC1D10A	0,00	0,00	2,09	0,00	
WDR11	0,00	0,00	2,05	0,00	
ECH1	0,00	0,00	2,00	0,00	
MRPL37	0,00	0,00	1,88	0,00	
CCNT2	0,00	0,00	1,87	0,00	
SETD1A	0,00	0,00	1,82	0,00	
CNN3	0,00	0,00	1,77	0,00	
CDK5RAP1	0,00	0,00	1,71	0,00	
C5orf24	0,00	0,00	1,69	0,00	
ASF1B	0,00	0,00	1,62	0,00	
SNAP91;PICALM	0,00	0,00	1,57	0,00	
EIF2B3	0,00	0,00	1,45	0,00	
MRPL45	0,00	0,00	1,39	0,00	
ABCD3	0,00	0,00	1,29	0,00	
FAM91A1	0,00	0,00	1,18	0,00	
PFDN5	0,00	0,00	0,86	0,00	
EIF1AX;EIF1AY	0,00	0,00	0,82	0,00	
HSPE1;HSPE1-MOB4	0,00	0,00	0,81	0,00	
PACSIN3	0,00	0,00	0,76	0,00	
PLAT	0,00	0,00	0,75	0,00	
TUFM	0,00	0,00	0,74	0,00	
SHPRH	0,00	0,00	0,53	0,00	
TOM1	0,00	0,00	0,49	0,00	
SDC4	0,00	0,00	0,32	0,00	
ANLN	0,00	0,00	0,27	0,17	
GATAD2A	0,00	0,00	0,25	-0,03	
MAP1A	0,00	0,00	0,24	-0,32	
GTF3C2	0,00	0,00	0,15	-0,09	
WARS2	0,00	0,00	0,14	0,04	
KRT77	0,00	0,00	0,13	0,00	
EIF1;EIF1B	0,00	0,00	0,10	0,00	
BHLHE40	0,00	0,00	0,05	-0,48	
ERC1	0,00	0,00	0,04	0,00	
H3F3B;H3F3A;HIST3H3;H3F3C	0,00	0,00	0,00	8,94	Other
HSPA6;HSPA7	0,00	0,00	0,00	8,45	Other
GMIP	0,00	0,00	0,00	7,72	
HIST1H3A	0,00	0,00	0,00	7,69	Other

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
CT45A2;CT45A9;CT45A8	0,00	0,00	0,00	7,61	Other
CEP85	0,00	0,00	0,00	7,29	Other
FAM60A	0,00	0,00	0,00	7,26	Other
CCDC158	0,00	0,00	0,00	7,22	Other
CT45A10	0,00	0,00	0,00	7,20	Other
PRSS1;PRSS3P2;PRSS2	0,00	0,00	0,00	7,15	Other
DNAH3	0,00	0,00	0,00	6,86	Other
MRPL33	0,00	0,00	0,00	6,84	Other
NPM3	0,00	0,00	0,00	6,74	Other
RPL39P5;RPL39	0,00	0,00	0,00	6,51	Other
SFRP1	0,00	0,00	0,00	6,02	
PTPRJ	0,00	0,00	0,00	5,96	
CTBP1;CTBP2	0,00	0,00	0,00	5,91	
MRPL34	0,00	0,00	0,00	5,91	
UTS2	0,00	0,00	0,00	5,90	
AURKAIP1	0,00	0,00	0,00	5,82	
CD59	0,00	0,00	0,00	5,80	
COA5	0,00	0,00	0,00	5,76	
KRT35;KRT33B;KRT31	0,00	0,00	0,00	5,74	
STRBP	0,00	0,00	0,00	5,71	
PTN	0,00	0,00	0,00	5,65	
SAMM50	0,00	0,00	0,00	5,61	
GTF2IRD1	0,00	0,00	0,00	5,49	GTF
BPTF	0,00	0,00	0,00	5,47	
CDH8	0,00	0,00	0,00	5,44	
KDM2A	0,00	0,00	0,00	5,40	
BIRC5	0,00	0,00	0,00	5,40	
ZBTB7A	0,00	0,00	0,00	5,38	
S100A8	0,00	0,00	0,00	5,37	
OFD1	0,00	0,00	0,00	5,36	
TUBB8	0,00	0,00	0,00	5,35	
NFIA	0,00	0,00	0,00	5,33	
KRT4	0,00	0,00	0,00	5,30	
SHROOM2	0,00	0,00	0,00	5,27	
MRPS18C	0,00	0,00	0,00	5,20	
F2	0,00	0,00	0,00	5,19	
HDAC1	0,00	0,00	0,00	5,09	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
C18orf21	0,00	0,00	0,00	5,08	
EHMT1	0,00	0,00	0,00	5,07	
RAC1;RAC3;RAC2	0,00	0,00	0,00	5,07	
S100A13	0,00	0,00	0,00	5,04	
KRT73;KRT74;KRT71	0,00	0,00	0,00	4,99	
PCIF1	0,00	0,00	0,00	4,92	
FBXO32	0,00	0,00	0,00	4,91	
PDAP1	0,00	0,00	0,00	4,90	
MYH14	0,00	0,00	0,00	4,87	
ZNF687	0,00	0,00	0,00	4,85	
MTX2	0,00	0,00	0,00	4,83	
ATXN2L	0,00	0,00	0,00	4,82	
PFDN6	0,00	0,00	0,00	4,81	
CUX1	0,00	0,00	0,00	4,77	
SERF2	0,00	0,00	0,00	4,74	
MRPL4	0,00	0,00	0,00	4,71	
BAZ2B	0,00	0,00	0,00	4,68	
PDCD7	0,00	0,00	0,00	4,64	
POLR2J2	0,00	0,00	0,00	4,62	
TUBGCP5	0,00	0,00	0,00	4,62	
GNG12	0,00	0,00	0,00	4,58	
LSM3	0,00	0,00	0,00	4,58	
DARS	0,00	0,00	0,00	4,55	
PDIA6	0,00	0,00	0,00	4,54	
WDR74	0,00	0,00	0,00	4,51	
BRD2	0,00	0,00	0,00	4,50	
PPP2CA	0,00	0,00	0,00	4,48	
MTG1	0,00	0,00	0,00	4,45	
ZNF706	0,00	0,00	0,00	4,44	
PCM1	0,00	0,00	0,00	4,44	
CCDC43	0,00	0,00	0,00	4,39	
EXOSC9	0,00	0,00	0,00	4,37	Termination
CAPN11	0,00	0,00	0,00	4,36	
TOX4;TOX;TOX3	0,00	0,00	0,00	4,34	
GTF2H1	0,00	0,00	0,00	4,33	GTF
UBN1	0,00	0,00	0,00	4,32	
TSR2	0,00	0,00	0,00	4,32	
THAP4	0,00	0,00	0,00	4,31	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
KRT81;KRT86;KRT83;KRT85	0,00	0,00	0,00	4,31	
NLE1	0,00	0,00	0,00	4,30	
NUP88	0,00	0,00	0,00	4,27	
SPAG6	0,00	0,00	0,00	4,27	
SDC1	0,00	0,00	0,00	4,26	
TTF1	0,00	0,00	0,00	4,26	
YWHAE	0,00	0,00	0,00	4,24	
PHF13	0,00	0,00	0,00	4,23	
SNX9	0,00	0,00	0,00	4,23	
HBA2;HBA1	0,00	0,00	0,00	4,22	
CCL20	0,00	0,00	0,00	4,20	
NUFIP2	0,00	0,00	0,00	4,19	
LAMB3	0,00	0,00	0,00	4,18	
TNNI2	0,00	0,00	0,00	4,17	
TOP2B	0,00	0,00	0,00	4,17	
NRF1	0,00	0,00	0,00	4,16	
NUMBL	0,00	0,00	0,00	4,13	
MYBPC3	0,00	0,00	0,00	4,12	
MBD2	0,00	0,00	0,00	4,09	
KLF14	0,00	0,00	0,00	4,08	
FRMD5	0,00	0,00	0,00	4,08	
RASA1	0,00	0,00	0,00	4,07	
CDCA5	0,00	0,00	0,00	4,06	
SFN	0,00	0,00	0,00	4,05	
AP1B1	0,00	0,00	0,00	4,05	
GHITM	0,00	0,00	0,00	4,05	
GNB2L1	0,00	0,00	0,00	4,00	
FREM2	0,00	0,00	0,00	3,99	
HOXC4	0,00	0,00	0,00	3,97	
SEC13	0,00	0,00	0,00	3,97	
ZNHIT6	0,00	0,00	0,00	3,96	
IGF2BP3	0,00	0,00	0,00	3,96	
CTDSPL2	0,00	0,00	0,00	3,95	
CFL1	0,00	0,00	0,00	3,94	
CTNNA2	0,00	0,00	0,00	3,92	
TLK1	0,00	0,00	0,00	3,92	
EIF2B4	0,00	0,00	0,00	3,91	
C3	0,00	0,00	0,00	3,90	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZNF280C	0,00	0,00	0,00	3,89	
EIF4H	0,00	0,00	0,00	3,89	
EML4	0,00	0,00	0,00	3,89	
DNAJB6	0,00	0,00	0,00	3,88	
ZBTB20;ZBTB45	0,00	0,00	0,00	3,86	
MGST3	0,00	0,00	0,00	3,85	
GSG2	0,00	0,00	0,00	3,83	
FLYWCH1	0,00	0,00	0,00	3,83	
EIF3J	0,00	0,00	0,00	3,80	
MRPL54	0,00	0,00	0,00	3,76	
DEF6	0,00	0,00	0,00	3,74	
PPIL3	0,00	0,00	0,00	3,74	
NUP54	0,00	0,00	0,00	3,73	
DNAJC11	0,00	0,00	0,00	3,71	
GPRC5A	0,00	0,00	0,00	3,69	
ATAD3B	0,00	0,00	0,00	3,69	
DLG5	0,00	0,00	0,00	3,64	
TFPI	0,00	0,00	0,00	3,62	
CHCHD6	0,00	0,00	0,00	3,62	
HTATSF1	0,00	0,00	0,00	3,62	
CIT	0,00	0,00	0,00	3,62	
MT-CO2	0,00	0,00	0,00	3,59	
MYADM	0,00	0,00	0,00	3,57	
ZCCHC10	0,00	0,00	0,00	3,57	
EXOSC2	0,00	0,00	0,00	3,57	
ATP5O	0,00	0,00	0,00	3,56	
DEK	0,00	0,00	0,00	3,55	
FANCC	0,00	0,00	0,00	3,55	
XPO1	0,00	0,00	0,00	3,53	
HOXA9	0,00	0,00	0,00	3,49	
SORBS1	0,00	0,00	0,00	3,47	
STT3B	0,00	0,00	0,00	3,47	
UQCRH	0,00	0,00	0,00	3,46	
MACF1	0,00	0,00	0,00	3,46	
TRMT2B	0,00	0,00	0,00	3,45	
EXOC3	0,00	0,00	0,00	3,43	
WAPAL	0,00	0,00	0,00	3,43	
CAMK2G;CAMK2B	0,00	0,00	0,00	3,43	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZNF174	0,00	0,00	0,00	3,42	
DR1	0,00	0,00	0,00	3,41	
PKM	0,00	0,00	0,00	3,39	
DAPK3	0,00	0,00	0,00	3,37	
KPRP	0,00	0,00	0,00	3,36	
PAWR	0,00	0,00	0,00	3,36	
NFAT5	0,00	0,00	0,00	3,35	
GOLGA2	0,00	0,00	0,00	3,34	
TUBB3	0,00	0,00	0,00	3,34	
MICALL2	0,00	0,00	0,00	3,32	
BRI3BP	0,00	0,00	0,00	3,31	
UPF3A	0,00	0,00	0,00	3,30	
ZHX1	0,00	0,00	0,00	3,30	
TCEB2	0,00	0,00	0,00	3,30	
NOVA2	0,00	0,00	0,00	3,28	
TAF10	0,00	0,00	0,00	3,25	
FABP5	0,00	0,00	0,00	3,24	
ORC5	0,00	0,00	0,00	3,21	
LZTS2	0,00	0,00	0,00	3,21	
MRTO4	0,00	0,00	0,00	3,20	
POLR1D	0,00	0,00	0,00	3,20	
LEMD3	0,00	0,00	0,00	3,19	
FAM195B	0,00	0,00	0,00	3,17	
GSPT2	0,00	0,00	0,00	3,16	
NFIX	0,00	0,00	0,00	3,14	
CENPA	0,00	0,00	0,00	3,13	
MELK	0,00	0,00	0,00	3,09	
HOXB8;HOXC8	0,00	0,00	0,00	3,06	
CCT6B	0,00	0,00	0,00	3,05	
CLTB	0,00	0,00	0,00	3,03	
OSTC	0,00	0,00	0,00	3,01	
GLG1	0,00	0,00	0,00	3,00	
AHSA1	0,00	0,00	0,00	2,97	
FHL2	0,00	0,00	0,00	2,94	
CASP14	0,00	0,00	0,00	2,93	
PPIA	0,00	0,00	0,00	2,91	
EEFSEC	0,00	0,00	0,00	2,89	
MYO18A	0,00	0,00	0,00	2,89	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
THY1	0,00	0,00	0,00	2,88	
TMCO1	0,00	0,00	0,00	2,84	
GTPBP1	0,00	0,00	0,00	2,84	
NOM1	0,00	0,00	0,00	2,83	
C19orf47	0,00	0,00	0,00	2,83	
TGIF2LY;TGIF2LX	0,00	0,00	0,00	2,83	
TUBB4A	0,00	0,00	0,00	2,81	
HMGB3	0,00	0,00	0,00	2,81	
ECM1	0,00	0,00	0,00	2,78	
TFCP2	0,00	0,00	0,00	2,77	
RPA3	0,00	0,00	0,00	2,76	
IGF2R	0,00	0,00	0,00	2,76	
UBE2I	0,00	0,00	0,00	2,75	
MCF2L	0,00	0,00	0,00	2,74	
MPHOSPH6	0,00	0,00	0,00	2,74	
SPIN3;SPIN1	0,00	0,00	0,00	2,72	
ANXA11	0,00	0,00	0,00	2,72	
MRPL36	0,00	0,00	0,00	2,71	
AIMP2	0,00	0,00	0,00	2,71	
CENPW	0,00	0,00	0,00	2,68	
ELF2	0,00	0,00	0,00	2,64	
TTC14	0,00	0,00	0,00	2,62	
KIAA2026	0,00	0,00	0,00	2,62	
ZNF185	0,00	0,00	0,00	2,62	
RECQL4	0,00	0,00	0,00	2,61	
MRPL47	0,00	0,00	0,00	2,61	
C9orf85	0,00	0,00	0,00	2,61	
FTO	0,00	0,00	0,00	2,60	
MTCH2	0,00	0,00	0,00	2,59	
ARPC1B	0,00	0,00	0,00	2,58	
NDUFA13	0,00	0,00	0,00	2,54	
BRPF3	0,00	0,00	0,00	2,54	
DNAJC7	0,00	0,00	0,00	2,52	
FHOD1	0,00	0,00	0,00	2,50	
CPNE8;CPNE5;CPNE2;CPNE3;CPNE9;CPNE4;CPNE6;CPNE7	0,00	0,00	0,00	2,50	
TRPT1	0,00	0,00	0,00	2,50	
RIOK2	0,00	0,00	0,00	2,49	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
PAICS	0,00	0,00	0,00	2,46	
FSD1	0,00	0,00	0,00	2,45	
EXOSC1	0,00	0,00	0,00	2,45	
ZCCHC9	0,00	0,00	0,00	2,45	
DHX29	0,00	0,00	0,00	2,45	
NDUFA10	0,00	0,00	0,00	2,42	
RTF1	0,00	0,00	0,00	2,40	EF
CCDC101	0,00	0,00	0,00	2,40	
SNAPC1	0,00	0,00	0,00	2,39	
FKBP4	0,00	0,00	0,00	2,39	
PPP1R9A	0,00	0,00	0,00	2,38	
NFKBIL1	0,00	0,00	0,00	2,38	
NFKB1	0,00	0,00	0,00	2,38	
SLC38A10	0,00	0,00	0,00	2,37	
WDR55	0,00	0,00	0,00	2,35	
TAF7	0,00	0,00	0,00	2,35	
RPA1	0,00	0,00	0,00	2,34	
DNAJC2	0,00	0,00	0,00	2,33	
BRK1	0,00	0,00	0,00	2,32	
HEATR4	0,00	0,00	0,00	2,32	
RPP40	0,00	0,00	0,00	2,31	
NDUFA8	0,00	0,00	0,00	2,30	
CDYL	0,00	0,00	0,00	2,24	
OSBPL8	0,00	0,00	0,00	2,23	
GUF1	0,00	0,00	0,00	2,22	
GTPBP8	0,00	0,00	0,00	2,21	
IPO7	0,00	0,00	0,00	2,20	
DKFZp434B156;WDR92	0,00	0,00	0,00	2,18	
SEPT5	0,00	0,00	0,00	2,17	
DIEXF	0,00	0,00	0,00	2,13	
ARHGEF39	0,00	0,00	0,00	2,13	
LDHAL6B	0,00	0,00	0,00	2,11	
URB1	0,00	0,00	0,00	2,11	
CDK3;CDK2	0,00	0,00	0,00	2,06	
TOPORS	0,00	0,00	0,00	2,04	
KDM2B	0,00	0,00	0,00	2,02	
COPB2	0,00	0,00	0,00	2,00	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ACTR3C;ACTR3;ACTR3B	0,00	0,00	0,00	1,98	
POGLUT1	0,00	0,00	0,00	1,98	
ITIH3	0,00	0,00	0,00	1,97	
ITPR3	0,00	0,00	0,00	1,97	
ATP6AP1	0,00	0,00	0,00	1,92	
ATP6V0D2	0,00	0,00	0,00	1,91	
HSPH1	0,00	0,00	0,00	1,89	
MNAT1	0,00	0,00	0,00	1,89	
SLC39A7	0,00	0,00	0,00	1,88	
PAM16;CORO7-PAM16	0,00	0,00	0,00	1,82	
DNAJB1	0,00	0,00	0,00	1,82	
DHX40	0,00	0,00	0,00	1,81	
EMC1	0,00	0,00	0,00	1,79	
HSPA14	0,00	0,00	0,00	1,77	
NMT2	0,00	0,00	0,00	1,76	
PARN	0,00	0,00	0,00	1,75	
TK1	0,00	0,00	0,00	1,74	
XPC	0,00	0,00	0,00	1,69	
DCP1A	0,00	0,00	0,00	1,68	
DCAF4	0,00	0,00	0,00	1,66	
IFRD2	0,00	0,00	0,00	1,64	
MSN	0,00	0,00	0,00	1,64	
PARP9	0,00	0,00	0,00	1,60	
TAF5	0,00	0,00	0,00	1,59	
CLK2	0,00	0,00	0,00	1,59	
PSMA1	0,00	0,00	0,00	1,58	
EP400	0,00	0,00	0,00	1,55	
BCKDK	0,00	0,00	0,00	1,53	
NR1H3;NR1H2	0,00	0,00	0,00	1,53	
PAK4	0,00	0,00	0,00	1,53	
RBM45	0,00	0,00	0,00	1,51	
RBM26	0,00	0,00	0,00	1,50	
MPP5	0,00	0,00	0,00	1,49	
TIMM50	0,00	0,00	0,00	1,46	
CDC42EP4;CDC42EP1	0,00	0,00	0,00	1,44	
ZBTB48	0,00	0,00	0,00	1,43	
ZXDC;ZXDA;ZXDB	0,00	0,00	0,00	1,41	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
IQGAP3	0,00	0,00	0,00	1,32	
SIPA1	0,00	0,00	0,00	1,30	
ANAPC4	0,00	0,00	0,00	1,29	
LSM1	0,00	0,00	0,00	1,28	
ABI1	0,00	0,00	0,00	1,26	
TP53BP1	0,00	0,00	0,00	1,22	
CDK13	0,00	0,00	0,00	1,20	
RLF	0,00	0,00	0,00	1,18	
RTFDC1	0,00	0,00	0,00	1,17	
L1RE1	0,00	0,00	0,00	1,09	
ANAPC1	0,00	0,00	0,00	1,09	
CAMKV	0,00	0,00	0,00	1,08	
KIF1B;KIF1Bbeta;KIF1A;KIF1C	0,00	0,00	0,00	1,07	
PATL1	0,00	0,00	0,00	1,03	
HOXA11	0,00	0,00	0,00	1,03	
REPS1	0,00	0,00	0,00	0,88	
KAT7	0,00	0,00	0,00	0,85	
NCAPD2	0,00	0,00	0,00	0,83	
PRIM2	0,00	0,00	0,00	0,79	
NDUFV2	0,00	0,00	0,00	0,77	
DKFZp686P0738;GJC1	0,00	0,00	0,00	0,74	
SNRNP35	0,00	0,00	0,00	0,72	
SCARF2	0,00	0,00	0,00	0,72	
CUL3	0,00	0,00	0,00	0,65	
LAMB1	0,00	0,00	0,00	0,61	
MRPS11	0,00	0,00	0,00	0,58	
NEFL	0,00	0,00	0,00	0,54	
TOMM40	0,00	0,00	0,00	0,53	
CENPQ	0,00	0,00	0,00	0,52	
MTERF1	0,00	0,00	0,00	0,49	
ANAPC5	0,00	0,00	0,00	0,38	
PKP4;CTNND2	0,00	0,00	0,00	0,26	
WHSC1L1	0,00	0,00	0,00	0,11	
PHIP	0,00	0,00	0,00	-0,09	
NAF1	0,00	0,00	0,00	-0,11	
MYST3;KAT6A	0,00	0,00	0,00	-0,27	
THYN1	0,00	0,00	0,00	-0,30	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
HIRA	0,00	0,00	0,00	-0,49	
SLIT2	0,00	0,00	0,00	-0,90	
MTF2	0,00	0,00	0,00	-0,92	
ERICH3	0,00	0,00	0,00	-1,08	
BANP	0,00	0,00	0,00	-1,16	
MUS81	0,00	0,00	0,00	-1,55	
CHD3	0,00	0,00	0,00	-1,62	
SP2	0,00	0,00	0,00	-2,52	
DGKZ	0,00	0,00	-0,10	0,00	
CLASP1	0,00	0,00	-0,11	-0,24	
ZC3H15	0,00	0,00	-0,22	0,07	
C1QB	0,00	0,00	-0,24	-0,41	
EIF5A;EIF5A2;EIF5AL1	0,00	0,00	-0,29	-0,91	
CYFIP2	0,00	0,00	-0,29	0,00	
BLMH	0,00	0,00	-0,32	0,00	
MCTS1	0,00	0,00	-0,39	-0,22	
HMG20A	0,00	0,00	-0,40	0,00	
C1orf174	0,00	0,00	-0,42	-0,28	
ACOT9	0,00	0,00	-0,44	-0,10	
MRPL38	0,00	0,00	-0,51	0,00	
ARG1	0,00	0,00	-0,62	0,00	
KIAA0101	0,00	0,00	-0,88	-0,54	
HOXB9	0,00	0,00	-0,95	-0,79	
HEATR3	0,00	0,00	-0,99	0,00	
MRPL14	0,00	0,00	-1,04	0,00	
ZSCAN26;ZNF187	0,00	0,00	-1,05	-0,42	
KRT17	0,00	0,00	-1,10	-1,20	
SHMT2	0,00	0,00	-1,24	-1,59	
METTL8	0,00	0,00	-1,66	-1,63	
EBF3;EBF1;EBF2	0,00	-0,03	0,00	0,63	
PRDM15	0,00	-0,08	0,00	0,23	
UTP18	0,00	-0,23	-0,03	-0,21	
HMGN1	0,00	-0,24	-0,52	-0,36	
RRP8	0,00	-0,30	0,06	0,12	
ADNP2	0,00	-0,32	0,00	0,00	
PPP1CC	0,00	-0,44	-1,55	0,47	
MAP7D3	0,00	-0,46	-0,37	0,00	
ZNF24	0,00	-0,47	-0,27	-0,13	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
PRDX3	0,00	-0,49	0,21	0,20	
ZNF142	0,00	-0,56	0,00	-0,15	
ELMSAN1	0,00	-0,75	-0,64	-1,08	
ECT2	0,00	-0,79	-0,35	-0,63	
USF2	0,00	-0,90	0,00	-0,65	
RPP38	0,00	-0,98	-1,27	-0,88	
HELLS	0,00	-1,05	0,00	0,00	
ZNF292	0,00	-1,08	0,00	0,00	
BHLHA15	0,00	-1,11	0,00	-1,44	
IGKV4-1	0,00	-1,17	-0,54	-0,38	
WT1	0,00	-1,20	0,00	-0,42	
RXRB;RXRG;RXRA	0,00	-1,27	-0,89	-0,76	
KIF22	0,00	-1,32	0,00	-1,08	
CXXC1	0,00	-1,36	0,00	0,00	
ING5	0,00	-1,49	-1,88	-1,79	
CASZ1	0,00	-1,67	-1,15	-0,35	
CUL1	0,00	-1,76	-0,63	-0,94	
RNMTL1	0,00	-1,89	0,00	-2,01	
PRDM10	0,00	-1,94	-1,80	-1,02	
CBX4	0,00	-2,56	0,00	0,00	
KRT16	0,00	-3,19	-2,93	-1,45	
HSPB1	0,00	0,42	0,55	1,06	
AKAP17A	0,00	-0,43	-1,02	-0,62	
CKAP4	0,00	-0,53	0,64	0,14	
CTNNA1	0,00	-0,62	-0,22	0,05	
ANXA2;ANXA2P2	0,00	-0,46	0,12	-0,39	
HIST1H2BC;HIST1H2BK;HIST1H2BN;H2BFS;HIST1H2BM;HIST1H2BH;HIST2H2BF;HIST1H2BD;HIST1H2BL	0,00	0,11	0,27	0,15	
FCF1	0,00	0,15	-0,03	0,35	
SMARCA5	-0,01	0,04	0,13	0,21	
MICU2	-0,01	-0,50	0,47	-0,05	
RBBP4	-0,01	-0,03	0,18	0,01	
AP2B1	-0,01	-0,72	-0,10	-0,18	
EEF1A1;EEF1A1P5	-0,01	0,10	0,59	0,26	
PRPF31	-0,02	0,08	-0,52	-0,40	
PYCR1	-0,02	-0,39	0,17	0,29	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
EMD	-0,02	-0,29	0,00	0,51	
TJP2	-0,03	-0,13	-0,36	-0,11	
SMARCA1	-0,03	-0,33	-0,25	-0,15	
VIM	-0,03	-0,14	-0,13	0,20	
F13A1	-0,03	0,00	0,57	0,58	
RUVBL1	-0,04	-0,01	0,37	0,22	
EIF3D	-0,04	0,07	0,55	-0,25	
USP39	-0,04	-0,13	0,03	-0,25	
SVIL	-0,05	-0,36	-0,26	-0,16	
RPL18A	-0,05	0,06	0,55	0,71	
TMOD3	-0,05	-0,77	-0,19	-0,10	
SYNPO	-0,05	-0,24	-0,41	0,01	
TPM3;DKFZp686J1372	-0,05	0,00	0,02	-0,22	Other
RPL14	-0,06	-0,01	0,09	0,53	
RPL22L1	-0,06	-0,21	0,61	0,33	
CCT2	-0,06	0,03	0,92	0,24	
VASP	-0,06	-0,15	0,25	-0,45	
RAB1B;RAB1A;RAB1C;RAB8B;RAB13;RAB8A;RAB15	-0,06	0,02	0,33	0,57	
H2AFV;H2AFZ	-0,06	0,26	-0,02	0,20	
ACTB	-0,06	-0,21	-0,05	-0,08	
CDK12	-0,07	-0,35	-0,39	-0,96	
NOP9	-0,07	-0,27	-0,30	-0,01	
PRDX2	-0,07	-0,63	-0,41	0,08	
MLLT4	-0,07	0,28	0,49	0,12	
SPECC1	-0,07	-0,47	-0,84	-0,31	
CAAP1	-0,07	-0,37	-0,33	0,06	
CDC42	-0,08	0,26	0,84	0,85	
TPX2	-0,08	-0,33	-0,07	-0,18	
CEBPZ	-0,08	0,15	0,37	0,58	
SPATS2L	-0,08	-0,05	0,77	0,73	
PHLDB2	-0,08	-0,65	-0,05	-0,19	
VAPB	-0,09	0,00	0,49	0,39	
UBP1	-0,09	0,30	-0,01	-0,22	
RPL3	-0,09	-0,45	0,36	0,25	
TJP1	-0,09	-0,09	-0,40	-0,17	
SRRM1	-0,10	0,01	-0,22	-0,28	
TCEB1	-0,10	-0,26	0,16	-0,08	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
PPP1R9B	-0,10	-0,42	-0,51	-0,14	
POLR1B	-0,11	0,02	0,26	0,72	
RUNX1	-0,11	-0,21	-0,20	-0,16	
PARP1	-0,11	0,10	-0,04	0,05	
DUSP11	-0,12	0,13	-0,75	-0,51	
HSD17B4	-0,12	0,13	0,13	0,25	
ZFP64	-0,12	0,20	0,01	0,33	
BRD9	-0,12	0,00	-0,67	-0,03	
MPRIP	-0,13	-0,27	-0,14	-0,46	
CHD2	-0,13	0,00	0,00	0,00	
CCNB1	-0,13	0,68	0,02	-0,09	
NEXN	-0,13	-0,27	-0,36	-0,18	
CAPZA1	-0,14	-0,55	-0,27	-0,07	
RPL36	-0,14	-0,16	0,42	0,45	
MBD3	-0,14	-0,07	-0,20	0,08	
MTPAP	-0,15	-0,44	0,08	-0,15	
GTPBP4	-0,15	-0,06	1,29	1,31	
CALD1	-0,15	-0,40	0,49	0,24	
RNF2	-0,15	-0,27	-0,33	-0,20	
RPL35A	-0,15	-0,19	0,54	0,28	
APEX1	-0,15	-0,06	0,66	0,11	
RPSA	-0,17	-0,34	0,17	0,25	
PLAGL2	-0,17	-0,06	0,41	0,10	
TGM3	-0,17	0,00	0,29	0,00	
RPL6	-0,17	-0,03	0,16	0,02	
MYNN	-0,18	0,54	0,00	-0,24	
RPS28	-0,18	-0,52	-0,17	-0,35	
HBS1L	-0,18	-0,04	0,68	0,81	
HIST2H2BE;HIST1H2BJ;HIST1H2BB;HIST1H2BO;HIST3H2BB	-0,19	-0,14	-0,17	-0,06	
SMNDC1	-0,19	-0,18	-0,41	-0,77	
NPM1	-0,19	-0,20	0,13	0,17	
CACTIN	-0,20	0,39	-0,99	-0,33	
RPL22	-0,20	0,04	0,41	0,42	
HRNR	-0,20	-1,08	0,14	-0,94	
RPS15A	-0,20	-0,22	0,17	0,25	
MDC1	-0,21	0,14	0,05	-0,17	
NAA40	-0,21	-0,03	-0,25	-0,21	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SRPRB	-0,21	-0,27	0,00	0,02	
LRRC59	-0,21	-0,57	-0,04	0,14	
CCT7	-0,22	-0,29	0,55	-0,17	
FOXK1	-0,22	0,15	0,55	0,41	
SUB1	-0,22	-0,12	0,65	0,27	
NUP153	-0,22	0,03	0,00	-0,02	
NFIB	-0,22	-0,14	0,16	0,12	
XRCC6	-0,23	-0,25	0,13	-0,07	
HIST2H2AB	-0,23	-0,18	-2,18	-0,81	
SGPL1	-0,23	-0,10	0,81	0,55	
PRR3	-0,23	-0,19	-0,91	-0,27	
SPEN	-0,23	-0,41	-1,42	-0,90	
POLRMT	-0,24	-0,13	-0,49	0,07	
BRD4	-0,24	-0,45	-0,12	-0,59	
CDH2	-0,25	0,00	-0,17	0,01	
ACTN4	-0,26	-0,61	-0,53	-0,19	
SMARCC1	-0,26	-0,18	0,04	-0,03	
MAP4	-0,26	-0,29	0,44	0,13	
CHAMP1	-0,26	-0,65	-0,41	-0,57	
MED19	-0,26	-0,74	0,43	0,26	
TIMM13	-0,27	-0,61	-0,05	-0,56	
JUP	-0,28	-0,11	0,80	-0,28	
XRCC5	-0,28	-0,08	0,19	-0,18	
SPHK2	-0,28	-0,58	-0,55	0,09	
C19orf53	-0,28	-0,39	-0,17	-0,27	
CNOT2	-0,28	-0,32	-0,02	0,00	
PCBP1	-0,28	-0,30	-0,62	-0,39	
Cxorf56	-0,29	0,00	0,00	0,00	
CSRP1	-0,29	-0,38	0,60	-0,10	
RAB11FIP5	-0,30	-0,42	-0,50	-0,63	
RRP12	-0,30	-0,34	-0,41	-0,03	
RBM42	-0,31	0,00	-0,36	-0,73	
EIF2B1	-0,31	-0,43	0,44	0,14	
DDX49	-0,31	-0,11	-0,55	-0,20	
USP42	-0,31	-0,35	-0,56	-0,52	
CFAP20	-0,31	0,19	-0,33	-0,28	
ABCF1	-0,32	-0,07	0,27	0,14	
TMPO	-0,32	-0,63	0,12	0,15	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
RSRC1	-0,32	-0,27	-0,78	-0,41	
CBX6	-0,33	-0,44	0,12	-0,04	
POGZ	-0,33	0,27	0,11	0,01	
NES	-0,33	-0,48	-0,26	0,23	
SMARCE1	-0,34	0,00	-0,18	-0,23	
RCC2	-0,34	-0,02	0,55	0,48	
BYSL	-0,34	0,24	-0,13	0,09	
RPL24	-0,34	0,24	0,86	0,44	
MAGED2	-0,34	-0,80	0,08	-0,23	
DDB1	-0,34	-0,13	0,04	-0,17	
RPL26L1	-0,34	-0,44	-0,24	-0,38	
MRPS25	-0,35	-1,35	0,13	-0,54	
ESF1	-0,37	-0,30	-0,29	0,21	
RPS11	-0,37	-0,30	0,19	0,62	
NUMA1	-0,37	-0,33	-0,11	-0,29	
RFC3	-0,37	-0,54	-0,26	-0,49	
WDR5	-0,38	-0,45	-0,10	-0,54	
WDR12	-0,38	-0,05	-0,21	0,45	
RPS3	-0,38	-0,58	-0,03	-0,06	
RAB11FIP1	-0,38	-0,02	-0,28	0,27	
RPL10A	-0,38	-0,42	-0,16	-0,17	
SARNP	-0,39	-0,38	0,05	-0,23	
NXF1	-0,39	-0,35	-0,25	-0,30	
RPS19	-0,39	-0,55	0,32	-0,02	
RPL27A	-0,39	-0,55	0,33	0,79	
ZC3H3	-0,39	0,00	0,00	0,00	
ERCC3	-0,39	-0,29	-0,38	-0,45	
CORO1C	-0,39	-0,79	0,31	-0,48	
PPP1R18	-0,39	-0,67	-0,03	-0,40	
TCEANC2	-0,40	0,00	0,00	0,00	
RAD23B	-0,40	-0,51	0,51	-0,20	
RPL34	-0,40	-0,79	-0,15	-0,33	
PRRC2A	-0,40	0,00	-0,05	-0,43	
SAGE1	-0,41	0,00	0,00	-0,29	
NAT10	-0,41	-0,41	-0,11	0,09	
BAIAP2	-0,41	-0,20	-0,55	-0,21	
TLN1	-0,41	-0,27	0,04	-0,10	
BAZ2A	-0,41	-1,19	-0,68	-0,63	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZNF787	-0,42	-0,37	-0,02	0,19	
RPL7A	-0,42	-0,32	-0,03	0,11	
SFSWAP	-0,42	-0,45	-0,34	-0,69	
ZNF592	-0,42	0,08	-0,31	-0,29	
CCNT1	-0,43	-0,34	0,26	-0,32	
DDX24	-0,43	-0,18	-0,18	-0,25	
RPL10	-0,44	-0,60	-0,11	-0,11	
RAN	-0,44	-0,70	-0,59	-0,54	
RPL5	-0,45	-0,59	0,24	0,01	
RPL13A;RPL13a	-0,45	-0,37	0,32	0,05	
TCEB3	-0,45	-0,28	-0,39	-0,44	
CLK1	-0,45	-0,30	-0,63	-0,36	
TRIP12	-0,45	-0,56	-0,38	-0,19	
SMARCC2	-0,46	-0,34	-0,10	-0,42	
KLF16	-0,47	-0,41	0,13	0,11	
FLNB	-0,47	-0,36	-0,30	-0,10	
DCAF13	-0,47	-0,10	-0,13	0,03	
MISP	-0,48	-0,63	-1,12	-1,19	
NUMB	-0,49	-0,52	-0,10	-0,42	
RPL19	-0,50	-0,61	0,29	0,09	
RIF1	-0,50	-0,58	-0,07	-0,28	
TCF20	-0,50	-0,40	-0,30	-0,20	
RPS9	-0,50	-0,34	0,12	0,01	
DNAJA3	-0,50	-0,53	-0,44	-0,74	
BOP1	-0,50	-0,15	-0,05	0,24	
RPL18	-0,51	-0,28	-0,11	0,14	
FIZ1	-0,51	-0,26	-0,17	-0,07	
MKI67	-0,51	-0,82	-0,49	-0,64	
NR2F2;NR2F1	-0,52	-0,46	-0,44	-0,34	
EEF2	-0,52	0,30	0,52	1,06	
RPP30	-0,52	-0,51	-0,39	-0,26	
RSBN1L	-0,52	-0,46	-0,24	-0,19	
TAOK1	-0,52	-0,70	0,45	-0,14	
H2AFY	-0,53	-0,52	-0,52	-0,34	
HADHB	-0,53	-1,25	-0,66	-0,70	
EIF2S3;EIF2S3L	-0,53	-0,68	0,24	-0,03	
CENPC	-0,53	-0,48	-0,49	0,04	
NSUN2	-0,53	-0,46	0,67	-0,01	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SSBP1	-0,53	-0,16	-0,14	0,11	
HDGF	-0,53	0,00	0,63	-0,14	
NOP58	-0,54	-0,32	0,12	0,35	
HIST2H2AC;HIST2H2AA3;HIST1H2AJ;HIST1H2AH;H2AFJ;HIST1H2AC;HIST3H2A;HIST1H2AD;HIST1H2AG;HIST1H2AB;HIST1H2AA;H2AFX	-0,54	-0,57	-0,26	-0,30	
RPF1	-0,54	-0,24	0,06	0,45	
LRRC47	-0,55	0,00	1,30	0,41	
DTX3L	-0,56	-0,10	-0,10	0,00	
METAP1	-0,56	-0,41	-0,09	-0,09	
DNMT1	-0,57	-0,42	-0,13	-0,33	
NHP2L1	-0,58	-0,41	-0,28	0,60	
EXOSC6	-0,58	0,00	-0,50	-0,79	
RACGAP1	-0,58	-0,86	-0,22	-0,24	
KRR1	-0,58	-0,10	0,43	0,54	
RBM28	-0,58	-0,75	-0,02	-0,08	
PNO1	-0,58	-0,32	-0,41	-0,01	
NOB1	-0,59	-0,25	0,10	0,05	
ZNF836	-0,59	-0,90	-0,57	-0,48	
BAZ1B	-0,59	-0,40	-0,39	0,10	
DPF2	-0,59	-0,54	-0,24	-0,14	
RPS4X	-0,59	-0,57	-0,22	-0,14	
RPL32	-0,60	-0,54	-0,35	0,17	
KIF2A	-0,60	-0,20	0,30	0,11	
TIGD2	-0,60	-0,82	-0,58	-0,14	
ZBTB9	-0,60	0,37	0,53	-0,55	
DDX41	-0,60	-0,51	-0,51	-0,39	
H2AFY2	-0,61	-0,37	-0,71	-0,08	
TOP1	-0,61	-0,77	-0,60	-0,47	
RFC5	-0,61	-0,44	-0,42	-0,37	
PRRC2C	-0,61	-0,46	-0,46	-0,46	
LRWD1	-0,61	-0,57	-0,15	-0,23	
TWISTNB	-0,61	-0,67	0,33	-0,57	
LARP7	-0,62	-0,43	-0,20	-0,18	
HMGN4	-0,62	-0,35	-0,41	-0,45	
SIN3A	-0,63	-0,25	-0,22	-0,31	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
IFI16	-0,64	-0,49	-0,08	-0,16	
RPL30	-0,64	-0,60	0,44	1,02	
KIF4A	-0,64	-0,69	0,00	-0,50	
LIMA1	-0,65	-0,65	-0,75	-0,54	
DAXX	-0,65	0,00	-0,10	-0,93	
PXDN	-0,65	-1,04	-0,29	-0,28	
RPL27	-0,65	-0,86	0,18	0,08	
DAP3	-0,65	-1,26	-0,28	-1,07	
ZNF316	-0,65	-0,64	0,04	-0,15	
PRPF4B	-0,66	-0,28	-1,01	-0,75	
CHAF1B	-0,66	-0,64	-0,44	-0,27	
POLR1C	-0,66	-0,27	-0,30	-0,29	
ZSCAN25	-0,67	-0,05	1,12	1,07	
KTN1	-0,67	-0,95	-0,10	-0,40	
FOSL1	-0,68	-0,36	-0,44	0,65	
NACA	-0,68	-0,80	0,32	0,00	
PTRF	-0,68	-0,91	-0,76	-0,82	
RPL11	-0,68	-0,87	0,36	-0,04	
MRPL49	-0,69	-1,29	-0,82	-1,20	
BAIAP2L1	-0,69	-0,85	0,05	-0,20	
MRPS12	-0,69	0,00	-0,32	-0,79	
C12orf43	-0,69	-0,12	-0,20	0,14	
PLCB3	-0,69	-0,99	0,42	-0,35	
LTV1	-0,70	-0,60	-0,21	-0,13	
S100A9	-0,70	-0,08	0,96	0,74	
NMT1	-0,71	-0,64	0,10	-0,09	
NAP1L1	-0,71	-0,70	-0,30	-0,32	
PPIB	-0,71	-0,70	-0,12	-0,43	
ZFX;ZFY	-0,71	-0,76	-0,62	-0,42	
FXR2	-0,72	-0,64	-0,19	-0,42	
RSL1D1	-0,72	-0,39	-0,39	-0,06	
PDS5A	-0,72	-0,16	-0,30	-0,09	
CAPZB	-0,72	-0,87	-0,25	-0,86	
RFC4	-0,73	-0,72	-0,06	-0,55	
RPS5	-0,73	-0,48	0,07	0,00	
LBR	-0,73	-0,41	0,35	-0,05	
RPL13	-0,74	-0,95	0,11	-0,15	
MRPS18B	-0,74	-1,07	-0,18	-0,77	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ARRB2;DKFZp686L0365	-0,74	0,00	0,00	0,00	
CTCF	-0,74	-0,57	-0,43	-0,12	
ZNF653	-0,74	-0,73	-1,20	-0,66	
RPS14	-0,75	-0,90	0,17	0,00	
KRT9	-0,75	-1,36	-0,20	-0,93	
KLF2	-0,75	-0,60	-0,35	-0,51	
EIF2S1	-0,75	-0,92	0,02	-0,39	
RPL37A	-0,75	-0,91	-0,12	-0,52	
RFC1	-0,75	-0,82	-0,52	-0,97	
NOG	-0,76	0,00	-0,18	0,00	
ERI1	-0,76	-0,46	0,25	-0,13	
NHP2	-0,76	0,00	-0,47	-0,44	
DMAP1	-0,77	-1,22	-0,71	-1,06	
EIF6	-0,77	-0,43	0,08	0,05	
MAP7D1	-0,78	-0,97	-0,21	-0,31	
RPL36AL	-0,78	-0,53	-0,10	-0,35	
ISG20L2	-0,79	-0,33	-0,08	0,08	
TOMM20	-0,79	-0,54	-0,34	-0,57	
BMS1	-0,79	-0,54	-0,18	-0,03	
RFC2	-0,79	0,00	-0,20	-0,46	
TXN	-0,79	-0,64	0,24	-0,57	
MRPS5	-0,80	-0,95	0,01	-0,87	
MAP1B	-0,80	-0,83	0,23	0,22	
FLG2	-0,80	-1,09	0,10	-0,74	
RPS10;RPS10-NUDT3;RPS10P5	-0,80	-0,63	-0,13	-0,38	
SBSN	-0,80	-0,98	0,26	0,00	
PLAG1	-0,81	-0,98	-0,72	-0,96	
INCENP	-0,81	-0,64	-0,99	-0,53	
DDX10	-0,81	-0,34	-0,30	0,37	
HMGXB4	-0,81	-1,12	-0,60	-0,22	
GGH	-0,81	-0,85	0,09	-0,48	
LSG1	-0,81	0,00	-0,61	-0,20	
KRT1	-0,82	-1,36	0,03	-0,78	
SART1	-0,83	-0,68	-1,03	-0,97	
RRS1	-0,83	-0,24	-0,26	-0,04	
FAM32A	-0,83	-0,46	-0,68	-0,53	
NOA1	-0,83	-1,67	-0,45	-0,72	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
RSBN1	-0,83	-0,77	-0,62	-0,54	
DDX52	-0,83	-0,56	-0,76	-0,42	
CDCA8	-0,84	-0,73	-0,82	-0,66	
ZBTB24	-0,84	-0,51	-0,11	-0,14	
RPS26;RPS26P11	-0,86	-0,83	-0,15	-0,49	
CDC5L	-0,86	-0,89	-0,74	-0,83	
LGALS1	-0,86	-1,30	-0,38	-0,98	
DDX47	-0,87	-0,76	-0,56	-0,42	
TMA16	-0,87	-0,69	-0,41	-0,28	
RPL31	-0,88	-0,96	-0,50	-0,59	
KRI1	-0,88	0,00	-0,83	0,19	
TFAM	-0,88	-0,77	-0,47	-0,43	
HSPA9	-0,88	-1,25	-0,50	-0,93	
DNAJC9	-0,89	-0,88	-0,17	-0,02	
RPS18	-0,89	-1,26	-0,65	-0,81	
FBXL6	-0,89	-1,05	-0,26	-0,09	
RBM34	-0,90	-0,77	0,00	-0,75	
KMT2A	-0,90	-0,78	-0,46	-0,76	
RRP36	-0,90	-0,88	-0,58	-0,38	
CCDC55;NSRP1	-0,90	-0,23	-0,96	-0,79	
RAD51AP2	-0,91	-0,68	0,00	-0,56	
NFIC	-0,91	-0,88	-0,39	-0,22	
RPL23	-0,91	-0,36	-0,19	-0,07	
DDX55	-0,91	-0,85	-0,69	-0,86	
NFYA	-0,91	-0,78	-1,22	-0,99	
WBP11	-0,91	-1,14	-0,90	-0,88	
MAZ	-0,91	-0,76	-0,57	-0,56	
TSR1	-0,92	-1,01	0,04	-0,10	
BTF3	-0,92	-0,88	0,57	-0,02	
RPS8	-0,92	-0,95	-0,16	-0,42	
RPL26	-0,92	-1,07	-0,62	-0,62	
BLM	-0,92	-0,56	-1,00	-0,55	
SLIRP	-0,92	0,00	-0,73	-0,60	
RRP7A	-0,93	-0,93	-0,88	-0,61	
RPS25	-0,93	-0,86	-0,18	-0,29	
RPS3A	-0,93	-1,00	-0,08	-0,23	
AATF	-0,94	-0,89	-0,62	-0,39	
ATF2	-0,94	-0,59	0,20	-0,22	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZNF146	-0,94	-0,95	-1,07	-0,67	
PINX1	-0,94	-0,91	-0,54	-0,31	
DDX31	-0,94	-0,71	-0,20	-0,51	
PWP1	-0,94	-0,88	-0,60	-0,83	
SKP1	-0,95	-0,95	-0,40	-0,95	
HDGFRP3	-0,95	-1,14	-0,26	-0,56	
E4F1	-0,95	-0,58	-1,00	-0,29	
RPS17	-0,96	-1,16	-0,58	-0,48	
WDR46	-0,97	-0,90	-0,85	-0,67	
TFB2M	-0,97	-1,04	0,00	-0,34	
KIAA0020	-0,97	-0,58	-1,42	-0,95	
UPF3B	-0,97	-0,82	-0,46	-0,44	
EIF2S2	-0,97	-1,33	-0,40	-0,58	
PUF60	-0,97	-0,50	-0,62	-0,34	
C9orf114	-0,97	-1,09	-0,71	-0,64	
GRWD1	-0,98	-1,06	-0,42	-0,53	
MEAF6	-0,98	-1,38	-1,03	-0,92	
C4A;C4B	-0,98	-1,38	0,00	-0,58	
SRSF11	-0,98	-0,18	-0,88	-0,79	
RPL8	-0,98	-1,12	-0,65	-0,94	
RPS23	-0,98	-0,99	-0,39	-0,59	
MTDH	-0,98	-1,29	-0,44	-0,66	
MINA	-0,98	-0,75	-0,36	-0,50	
ESRRA	-0,98	-0,37	-0,11	0,41	
SP140L	-0,99	-0,89	-0,84	-0,84	
WBSCR22	-0,99	-0,91	-0,14	-0,21	
PHF6	-0,99	-0,81	-0,45	-0,47	
ARL6IP4	-0,99	-0,21	-0,51	-0,50	
FIP1L1	-1,00	-1,17	-1,18	-0,97	
RPS7	-1,00	-1,11	-0,31	-0,41	
FOSL2	-1,00	-1,66	-0,59	-0,90	
SNRPB2	-1,00	-0,70	-0,71	-1,03	
CENPV	-1,00	-0,74	-0,55	-0,36	
MAGEA4	-1,01	-1,01	-0,72	-0,47	
TSR3	-1,01	-0,79	-0,13	-0,54	
SREK1	-1,01	-0,60	-0,71	-0,45	
JUN	-1,01	-2,02	0,00	0,00	
ZNF646	-1,01	-0,52	-0,75	-0,45	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
S100A16	-1,02	-0,90	0,19	-0,13	
CT45A3;CT45A1;CT45A7;CT45A5;CT45A6	-1,02	-0,87	-0,55	-0,36	
LUC7L2	-1,02	-0,60	-0,63	-0,34	
H1F0	-1,02	-1,29	-0,45	-0,69	
KRT5	-1,02	-1,08	-0,01	-0,88	
YBX1	-1,03	-0,70	-0,28	-0,46	
AHCTF1	-1,03	-1,12	-0,90	-1,08	
MYO7B	-1,03	-1,02	-0,25	-0,73	
CD3EAP	-1,03	-1,03	-0,66	-0,52	
KLF10	-1,03	-0,68	-0,28	-0,42	
RCC1	-1,03	-1,24	-0,70	-0,69	
BCCIP	-1,04	-1,19	0,13	-0,84	
ZNF771	-1,04	-0,73	-0,48	-0,50	
JUNB	-1,04	-0,95	-0,57	-0,46	
YBX2	-1,04	-0,81	-0,23	-0,16	
ZNF512	-1,04	-1,29	-0,89	-0,51	
SP110	-1,05	-1,19	-0,70	-1,23	
CEBPB	-1,05	-1,05	-1,25	-1,34	
NSD1	-1,06	-1,23	-0,33	-0,38	
MRGBP	-1,06	-0,92	-0,67	-0,78	
RPUSD4	-1,06	-1,06	-1,21	-0,58	
NKAP;NKAPL	-1,06	-0,21	0,00	0,00	
NOP2	-1,07	-1,19	-0,46	-0,61	
CCDC124	-1,07	-1,37	-0,34	-0,74	
EPB41L3	-1,07	-1,61	-0,79	-0,76	
USF1	-1,07	-0,66	-1,52	-0,35	
CBFB	-1,08	0,00	0,00	0,00	
NOC3L	-1,08	-1,21	-1,25	-0,71	
FRG1	-1,08	-0,61	-0,62	-0,15	
MRPL50	-1,09	-1,41	-0,98	0,00	
SAMD1	-1,09	-1,53	-0,48	-0,72	
NO66	-1,09	-1,01	-0,97	-0,85	
ZNF579	-1,09	-0,72	-0,57	-0,29	
AURKB	-1,10	-0,80	-0,96	-0,74	
TEFM	-1,10	-0,73	-0,78	-0,44	
DDX18	-1,10	-1,13	-0,61	-0,40	
NR2C2	-1,10	-1,85	-1,16	-1,47	
U2AF1	-1,11	-0,76	-0,52	-0,17	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
CCDC59	-1,11	-0,76	-0,97	-0,66	
C19orf43	-1,11	-0,25	-1,12	0,00	
DNAJB11	-1,11	-1,17	-0,02	-0,53	
CHAF1A	-1,12	-1,37	-0,62	-0,50	
KRT2	-1,13	-1,38	-0,27	-1,03	
PRPF4	-1,13	-1,08	-1,06	-0,79	
KRT10	-1,13	-1,35	0,06	-0,88	
PHF20L1	-1,14	-0,94	-0,40	-0,68	
LSM14B	-1,14	-0,90	-0,90	-0,88	
POP4	-1,14	-0,90	-0,56	-0,70	
RPL7L1	-1,14	-0,64	-1,02	-0,68	
DDX27	-1,14	-1,27	-1,14	-0,73	
DIDO1	-1,14	-1,37	-2,05	-2,00	
WHSC1	-1,15	-1,80	-0,95	-1,07	
MPG	-1,16	-1,14	-0,94	-0,66	
HSPA5	-1,16	-1,12	-0,25	-0,51	
ZNF281	-1,16	-1,10	-1,10	-0,94	
RPS6	-1,16	-1,19	-0,34	-0,61	
ATF7	-1,17	-0,87	-0,99	-0,28	
EPB41L2	-1,17	-1,68	-0,53	-0,81	
TBP	-1,18	-0,59	0,00	-0,88	
MOGS	-1,18	-1,68	-0,96	-0,98	
CREB1	-1,18	-1,13	-1,14	-0,91	
POLR1E	-1,19	-1,04	-0,60	-0,64	
CBX8	-1,19	-1,25	-1,26	-0,88	
BRIX1	-1,20	-0,91	-0,82	-0,59	
ZNF740	-1,20	-1,18	-1,04	-0,92	
DSP	-1,20	-2,11	0,10	-1,13	
ANKZF1	-1,20	0,00	0,11	-0,42	
ZNF219	-1,21	-1,10	-0,72	-0,27	
BRD7	-1,21	-1,34	0,00	-1,19	
RPL9	-1,21	-1,24	-0,03	-0,30	
MRPL1	-1,21	-1,21	-0,42	-0,71	
RPL38	-1,21	-0,72	-0,54	-0,32	
RPS15	-1,21	-1,39	-0,42	-0,99	
JDP2	-1,22	-1,26	-1,15	-0,17	
BAZ1A	-1,22	-1,09	-0,74	-0,66	
ZNF691	-1,22	-0,87	-1,00	-0,52	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
PDIA5	-1,23	-1,40	-0,46	-0,57	
C7orf50	-1,23	-1,25	-0,56	-0,64	
MEN1	-1,23	-1,06	-1,03	-0,95	
MECP2	-1,23	-1,53	-1,05	-1,11	
HPSE	-1,24	-1,25	-1,22	-1,10	
RRP1B	-1,24	-1,16	-0,67	-0,64	
MAFF	-1,24	-1,06	-1,24	-0,67	
ZFP91;ZFP91-CNTF	-1,24	-1,13	-0,78	-0,82	
PPIH	-1,25	-1,07	-1,36	-1,14	
POP1	-1,25	-1,20	-0,70	-0,84	
ZNF532	-1,25	0,00	0,00	0,00	
UTP11L	-1,25	-0,99	-0,93	-0,61	
SIRT7	-1,25	-0,88	-0,56	-0,63	
ZNF275	-1,25	-0,82	0,00	-0,98	
RPS13	-1,25	-1,06	-0,77	-0,77	
NF2	-1,25	-1,83	-0,41	-0,72	
DNTTIP2	-1,26	-0,72	-0,37	0,03	
PRPF3	-1,26	-1,19	-1,21	-1,10	
PAK1IP1	-1,26	-1,07	-0,42	-0,55	
DOT1L	-1,26	-1,28	-0,91	-0,87	
PSIP1	-1,26	-1,23	-0,86	-0,87	
HIST1H1A	-1,28	-1,49	-0,68	-0,79	
ASF1A	-1,28	-1,19	-1,16	-0,73	
NFKB2	-1,28	0,00	-1,72	-1,84	
RBBP6	-1,28	-0,89	-1,05	-1,08	
SRP19	-1,28	-0,43	0,55	-0,36	
RPL23A	-1,28	-1,27	-0,60	-0,68	
CHD7	-1,28	-0,79	-0,96	-0,72	
SP3	-1,29	-1,31	-1,29	-0,90	
METTL17	-1,29	-1,79	-0,22	-0,66	
MRPS30	-1,29	-1,23	-1,00	-0,53	
TFB1M	-1,30	-1,57	-0,84	-1,01	
SRP14	-1,30	-1,10	-0,63	-0,90	
WDR89	-1,30	-1,25	-0,63	-1,12	
EPB41L4B	-1,31	-0,43	-0,65	-0,07	
NSUN4	-1,31	-0,88	-1,11	-0,95	
CREB5	-1,32	-0,52	-0,84	-0,21	
SRP68	-1,32	-1,36	-0,39	-0,81	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
RSL24D1	-1,32	-1,04	0,00	-0,63	
KNOP1	-1,32	-1,16	-0,78	-0,97	
LUC7L	-1,32	-0,89	-1,02	-0,76	
SNRPA1	-1,33	-1,08	-0,97	-1,16	
SDAD1	-1,33	-1,09	-0,66	-0,79	
MTHFD2	-1,33	-1,52	-1,03	-1,13	
TRMT112	-1,34	-1,07	-0,97	-1,31	
C11orf31;SELH	-1,34	-1,05	-0,37	-0,25	
NOP16	-1,34	-1,43	-0,93	-1,01	
AP4M1	-1,35	-1,39	-1,37	-1,36	
TSPYL5	-1,35	-1,26	-1,00	-0,68	
RPL17;RPL17-C18orf32	-1,35	-1,53	-0,82	-0,93	
ZNF652	-1,36	-0,33	-0,42	-0,27	
CALM2;CALM1;CALM3	-1,36	-1,83	-0,31	0,00	
FARP2	-1,36	0,00	0,00	0,00	
FTSJ2	-1,36	0,00	-0,90	-0,73	
HMGA2	-1,37	-2,11	-1,23	-1,67	
RPL37	-1,37	-0,61	-0,11	-0,89	
MRPS7	-1,38	-2,26	-0,82	-1,32	
YBX3	-1,38	-0,80	-0,61	-0,57	
NSUN5	-1,38	-1,28	-0,79	-0,60	
RPL35	-1,38	-1,57	-1,10	-1,18	
LYAR	-1,39	-1,32	-1,12	-0,79	
C1QA	-1,39	-1,36	-0,68	-0,77	
IMP3	-1,39	-1,09	-1,05	-1,05	
DDX54	-1,40	-1,62	-0,70	-0,95	
CMAS	-1,40	-1,37	-1,12	-0,91	
SRFBP1	-1,40	-1,15	-0,40	-0,68	
ZNF319	-1,41	-0,94	-1,71	-0,89	
UTP14A	-1,41	-1,30	-1,25	-0,83	
IMP4	-1,41	-1,22	-1,12	-0,83	
DNTTIP1	-1,42	-1,21	-1,05	-0,70	
MBD1	-1,42	-1,05	-1,03	-1,02	
RBM39	-1,42	-0,88	-1,56	-1,23	
SRP72	-1,42	-1,48	-0,45	-0,85	
RPL21	-1,43	-1,65	-0,41	-0,64	
MAFK	-1,43	-1,17	-1,25	-1,03	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
MRPS9	-1,43	-1,75	-1,20	-1,13	
TCOF1	-1,44	-0,95	-1,13	-0,91	
NOL12	-1,44	-1,34	-0,95	-1,17	
MRPL41	-1,45	-1,79	-0,85	-1,40	
MICU1	-1,46	-2,09	-0,92	-1,66	
GNL2	-1,46	-1,52	-0,92	-1,07	
NIFK	-1,46	-1,34	-0,97	-0,83	
RBM27	-1,47	-1,23	-1,02	-1,09	
RRP1	-1,48	-1,51	-0,43	-0,47	
NOP14	-1,48	-1,34	-0,85	-0,78	
FAU	-1,48	-1,07	-0,71	-0,70	
H1FX	-1,48	-1,72	-0,99	-1,14	
ARGLU1	-1,48	-0,81	-1,12	-0,75	
NOL10	-1,49	-2,24	-1,04	-1,66	
U2AF2	-1,49	-1,16	-0,90	-0,82	
VEZF1	-1,49	-1,44	-1,61	-1,22	
EGR1	-1,49	-1,49	-1,54	-1,02	
DHX37	-1,50	-1,33	-0,94	-0,85	
MRPL30	-1,50	-1,83	-1,40	-1,30	
MRPS2	-1,50	-1,82	-1,21	-1,24	
SNIP1	-1,50	-1,24	-1,52	-0,88	
DDX56	-1,51	-1,27	-1,50	-1,51	
GNL3	-1,51	-1,64	-0,48	-0,74	
SURF6	-1,52	-1,19	-0,83	-1,04	
TERF1	-1,52	-1,47	-1,21	-1,07	
KRT78	-1,52	0,00	-0,18	-2,07	
GTPBP10	-1,53	0,00	-0,85	-1,28	
UTP3	-1,53	-1,16	-1,36	-0,73	
MORF4L2	-1,53	-1,39	-0,73	-0,88	
NGDN	-1,53	-1,60	-1,22	-1,16	
INO80B;INO80B-WBP1	-1,55	-1,72	-1,11	-0,89	
MEPCE	-1,55	-1,50	-0,97	-1,22	
C11orf57	-1,55	-1,05	-1,60	-1,34	
C8orf33	-1,56	-0,75	-0,24	-0,44	
HMGA1	-1,56	-1,72	-0,97	-1,37	
PTRH1	-1,57	-1,04	-1,61	-0,79	
DDX28	-1,57	-1,69	-1,19	-1,17	
PLCD3	-1,57	-0,99	-0,63	-0,75	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
MARK2	-1,58	-1,11	-0,84	-0,59	
DIMT1	-1,58	-1,23	-0,89	-0,81	
MORF4L1	-1,58	-1,62	-1,13	-1,29	
NOL7	-1,58	-1,32	-1,37	-1,00	
MRPL15	-1,58	-2,08	-1,37	-1,59	
GPATCH4	-1,59	-1,55	-0,98	-1,17	
ZNF148	-1,59	-1,60	-1,55	-1,30	
CCDC86	-1,60	-1,29	-1,37	-0,84	
ZNF593	-1,60	-1,57	-0,90	-1,08	
RRP15	-1,61	-1,52	-0,45	-0,73	
CENPVL1	-1,61	-1,19	-1,11	-0,40	
GNL3L	-1,61	-1,13	-0,58	-0,28	
TAF3	-1,62	-1,53	-0,76	-0,84	
PES1	-1,62	-1,75	-1,65	-1,38	
REXO4	-1,63	-1,20	-0,84	-0,67	
RPS19BP1	-1,63	-1,56	-1,13	-0,81	
MRPL16	-1,63	-1,12	-0,47	-0,84	
RPUSD3	-1,64	-1,68	-1,10	-1,28	
C8orf59	-1,64	-1,82	-1,80	-1,59	
HP1BP3	-1,64	-1,80	-0,97	-1,12	
IGKV2D-29;IGKV2D-26;IGKV2-40;IGKV2D-30;IGKV2D-28;IGKV2-24;IGKV2D-24	-1,65	-1,55	-1,13	-0,80	
EMG1	-1,65	-1,44	-0,98	-0,98	
CTGF	-1,67	0,00	-2,12	0,00	
CYR61	-1,67	-2,64	-1,09	-1,21	
SP4	-1,67	0,00	-1,08	-0,93	
FTSJ3	-1,68	-1,64	-0,95	-0,96	
RPS24	-1,69	-1,51	-0,82	-1,20	
MRPL11	-1,70	-2,08	-1,08	-1,62	
UTP23	-1,70	-0,75	-0,53	0,27	
CMSS1	-1,71	-1,34	-1,31	-0,65	
FAM133B	-1,71	-0,87	-0,47	-0,88	
HMGN2	-1,73	-1,32	0,27	-1,18	
KRT14	-1,73	-1,93	-0,85	-1,18	
CGGBP1	-1,74	-1,14	-0,32	-1,16	
SNRNP27	-1,75	-1,37	-1,47	-1,22	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
ZCCHC17	-1,76	-1,37	-1,35	-1,53	
MRM1	-1,79	-2,31	-1,13	-1,55	
GTF2B	-1,79	-1,47	-0,87	-0,82	
EPB41L5	-1,79	-1,89	-0,96	-1,00	
MPHOSPH10	-1,79	-1,61	-1,75	-1,23	
KLF3	-1,80	-1,80	-1,45	-1,45	
MRPS23	-1,80	-2,36	-1,30	-1,40	
ZKSCAN1	-1,80	-1,42	-0,56	-0,72	
HIST1H1C;HIST1H1D	-1,83	-1,76	-0,95	-1,17	
MAGEB2	-1,83	-1,91	-0,82	-1,33	
GLYR1	-1,84	-1,79	-1,28	-1,22	
TRPS1	-1,85	-1,12	0,00	-0,77	
RPL29	-1,86	-1,97	-0,77	-1,32	
MRPL46	-1,86	-2,24	-0,97	-1,27	
JUND	-1,87	-2,06	-1,49	-1,02	
CCDC84	-1,87	0,00	0,00	-1,49	
MAFG	-1,88	-1,83	-1,80	-1,63	
PRR12	-1,88	0,00	-1,63	-1,75	
KIAA1522	-1,90	-1,89	-0,81	-1,40	
CCDC137	-1,90	-1,58	-2,05	-1,74	
MRPL48	-1,90	-2,33	-1,02	-1,48	
CIR1	-1,92	-0,87	-2,00	-1,80	
MRPL12	-1,94	-2,34	-1,25	-2,11	
NKX2-5	-1,94	-1,34	-1,56	-0,62	
LLPH	-1,95	-3,45	-0,95	-1,63	
SREK1IP1	-1,95	-0,96	-0,84	-1,32	
EBNA1BP2	-2,02	-1,70	-1,31	-1,26	
GPNMB	-2,03	0,00	0,00	-1,70	
MRPL9	-2,04	-2,36	-1,24	-1,59	
TAF2	-2,08	-1,72	-1,30	-0,86	
TRMT10C	-2,09	-2,50	-1,64	-1,87	
MRPS28	-2,11	-2,06	-1,55	-1,54	
MRPL22	-2,11	-2,18	-1,50	-1,61	
MMTAG2	-2,12	-1,24	-1,38	-1,91	
C11orf98	-2,20	-2,13	-1,70	-1,92	
GLTSCR2	-2,20	-2,14	-2,10	-1,67	
RPL28	-2,21	-1,48	-1,70	-1,13	
ZNF444	-2,22	-1,83	0,00	-1,87	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
RP9	-2,31	-1,26	-2,04	-1,60	
HSD17B10	-2,32	-3,13	-1,91	-2,30	
MRPL55	-2,41	0,00	-2,05	0,00	
NSA2	-2,71	-2,40	-2,46	-1,61	
KLF13	-2,78	-3,43	-2,04	-2,06	
FAM207A	-2,81	-2,04	-1,66	-1,65	
DHRS2	-2,86	-3,65	-2,72	-2,76	
EPB41	-2,87	-2,58	-1,21	-1,28	
MRPL40	-3,30	-4,31	-1,80	-2,55	
KRT6A	-3,89	-1,83	-2,88	-1,29	
BRD7	-1,21	-1,34	0,00	-1,19	
RPL9	-1,21	-1,24	-0,03	-0,30	
MRPL1	-1,21	-1,21	-0,42	-0,71	
RPL38	-1,21	-0,72	-0,54	-0,32	
RPS15	-1,21	-1,39	-0,42	-0,99	
JDP2	-1,22	-1,26	-1,15	-0,17	
BAZ1A	-1,22	-1,09	-0,74	-0,66	
ZNF691	-1,22	-0,87	-1,00	-0,52	
PDIA5	-1,23	-1,40	-0,46	-0,57	
C7orf50	-1,23	-1,25	-0,56	-0,64	
MEN1	-1,23	-1,06	-1,03	-0,95	
MECP2	-1,23	-1,53	-1,05	-1,11	
HPSE	-1,24	-1,25	-1,22	-1,10	
RRP1B	-1,24	-1,16	-0,67	-0,64	
MAFF	-1,24	-1,06	-1,24	-0,67	
ZFP91;ZFP91-CNTF	-1,24	-1,13	-0,78	-0,82	
PPIH	-1,25	-1,07	-1,36	-1,14	
POP1	-1,25	-1,20	-0,70	-0,84	
ZNF532	-1,25	0,00	0,00	0,00	
UTP11L	-1,25	-0,99	-0,93	-0,61	
SIRT7	-1,25	-0,88	-0,56	-0,63	
ZNF275	-1,25	-0,82	0,00	-0,98	
RPS13	-1,25	-1,06	-0,77	-0,77	
NF2	-1,25	-1,83	-0,41	-0,72	
DNTTIP2	-1,26	-0,72	-0,37	0,03	
PRPF3	-1,26	-1,19	-1,21	-1,10	
PAK1IP1	-1,26	-1,07	-0,42	-0,55	
DOT1L	-1,26	-1,28	-0,91	-0,87	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
PSIP1	-1,26	-1,23	-0,86	-0,87	
HIST1H1A	-1,28	-1,49	-0,68	-0,79	
ASF1A	-1,28	-1,19	-1,16	-0,73	
NFKB2	-1,28	0,00	-1,72	-1,84	
RBBP6	-1,28	-0,89	-1,05	-1,08	
SRP19	-1,28	-0,43	0,55	-0,36	
RPL23A	-1,28	-1,27	-0,60	-0,68	
CHD7	-1,28	-0,79	-0,96	-0,72	
SP3	-1,29	-1,31	-1,29	-0,90	
METTL17	-1,29	-1,79	-0,22	-0,66	
MRPS30	-1,29	-1,23	-1,00	-0,53	
TFB1M	-1,30	-1,57	-0,84	-1,01	
SRP14	-1,30	-1,10	-0,63	-0,90	
WDR89	-1,30	-1,25	-0,63	-1,12	
EPB41L4B	-1,31	-0,43	-0,65	-0,07	
NSUN4	-1,31	-0,88	-1,11	-0,95	
CREB5	-1,32	-0,52	-0,84	-0,21	
SRP68	-1,32	-1,36	-0,39	-0,81	
RSL24D1	-1,32	-1,04	0,00	-0,63	
KNOP1	-1,32	-1,16	-0,78	-0,97	
LUC7L	-1,32	-0,89	-1,02	-0,76	
SNRPA1	-1,33	-1,08	-0,97	-1,16	
SDAD1	-1,33	-1,09	-0,66	-0,79	
MTHFD2	-1,33	-1,52	-1,03	-1,13	
TRMT112	-1,34	-1,07	-0,97	-1,31	
C11orf31;SELH	-1,34	-1,05	-0,37	-0,25	
NOP16	-1,34	-1,43	-0,93	-1,01	
AP4M1	-1,35	-1,39	-1,37	-1,36	
TSPYL5	-1,35	-1,26	-1,00	-0,68	
RPL17;RPL17-C18orf32	-1,35	-1,53	-0,82	-0,93	
ZNF652	-1,36	-0,33	-0,42	-0,27	
CALM2;CALM1;CALM3	-1,36	-1,83	-0,31	0,00	
FARP2	-1,36	0,00	0,00	0,00	
FTSJ2	-1,36	0,00	-0,90	-0,73	
HMGA2	-1,37	-2,11	-1,23	-1,67	
RPL37	-1,37	-0,61	-0,11	-0,89	
MRPS7	-1,38	-2,26	-0,82	-1,32	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
YBX3	-1,38	-0,80	-0,61	-0,57	
NSUN5	-1,38	-1,28	-0,79	-0,60	
RPL35	-1,38	-1,57	-1,10	-1,18	
LYAR	-1,39	-1,32	-1,12	-0,79	
C1QA	-1,39	-1,36	-0,68	-0,77	
IMP3	-1,39	-1,09	-1,05	-1,05	
DDX54	-1,40	-1,62	-0,70	-0,95	
CMAS	-1,40	-1,37	-1,12	-0,91	
SRFBP1	-1,40	-1,15	-0,40	-0,68	
ZNF319	-1,41	-0,94	-1,71	-0,89	
UTP14A	-1,41	-1,30	-1,25	-0,83	
IMP4	-1,41	-1,22	-1,12	-0,83	
DNTTIP1	-1,42	-1,21	-1,05	-0,70	
MBD1	-1,42	-1,05	-1,03	-1,02	
RBM39	-1,42	-0,88	-1,56	-1,23	
SRP72	-1,42	-1,48	-0,45	-0,85	
RPL21	-1,43	-1,65	-0,41	-0,64	
MAFK	-1,43	-1,17	-1,25	-1,03	
MRPS9	-1,43	-1,75	-1,20	-1,13	
TCOF1	-1,44	-0,95	-1,13	-0,91	
NOL12	-1,44	-1,34	-0,95	-1,17	
MRPL41	-1,45	-1,79	-0,85	-1,40	
MICU1	-1,46	-2,09	-0,92	-1,66	
GNL2	-1,46	-1,52	-0,92	-1,07	
NIFK	-1,46	-1,34	-0,97	-0,83	
RBM27	-1,47	-1,23	-1,02	-1,09	
RRP1	-1,48	-1,51	-0,43	-0,47	
NOP14	-1,48	-1,34	-0,85	-0,78	
FAU	-1,48	-1,07	-0,71	-0,70	
H1FX	-1,48	-1,72	-0,99	-1,14	
ARGLU1	-1,48	-0,81	-1,12	-0,75	
NOL10	-1,49	-2,24	-1,04	-1,66	
U2AF2	-1,49	-1,16	-0,90	-0,82	
VEZF1	-1,49	-1,44	-1,61	-1,22	
EGR1	-1,49	-1,49	-1,54	-1,02	
DHX37	-1,50	-1,33	-0,94	-0,85	
MRPL30	-1,50	-1,83	-1,40	-1,30	
MRPS2	-1,50	-1,82	-1,21	-1,24	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
SNIP1	-1,50	-1,24	-1,52	-0,88	
DDX56	-1,51	-1,27	-1,50	-1,51	
GNL3	-1,51	-1,64	-0,48	-0,74	
SURF6	-1,52	-1,19	-0,83	-1,04	
TERF1	-1,52	-1,47	-1,21	-1,07	
KRT78	-1,52	0,00	-0,18	-2,07	
GTPBP10	-1,53	0,00	-0,85	-1,28	
UTP3	-1,53	-1,16	-1,36	-0,73	
MORF4L2	-1,53	-1,39	-0,73	-0,88	
NGDN	-1,53	-1,60	-1,22	-1,16	
INO80B;INO80B-WBP1	-1,55	-1,72	-1,11	-0,89	
MEPCE	-1,55	-1,50	-0,97	-1,22	
C11orf57	-1,55	-1,05	-1,60	-1,34	
C8orf33	-1,56	-0,75	-0,24	-0,44	
HMGA1	-1,56	-1,72	-0,97	-1,37	
PTRH1	-1,57	-1,04	-1,61	-0,79	
DDX28	-1,57	-1,69	-1,19	-1,17	
PLCD3	-1,57	-0,99	-0,63	-0,75	
MARK2	-1,58	-1,11	-0,84	-0,59	
DIMT1	-1,58	-1,23	-0,89	-0,81	
MORF4L1	-1,58	-1,62	-1,13	-1,29	
NOL7	-1,58	-1,32	-1,37	-1,00	
MRPL15	-1,58	-2,08	-1,37	-1,59	
GPATCH4	-1,59	-1,55	-0,98	-1,17	
ZNF148	-1,59	-1,60	-1,55	-1,30	
CCDC86	-1,60	-1,29	-1,37	-0,84	
ZNF593	-1,60	-1,57	-0,90	-1,08	
RRP15	-1,61	-1,52	-0,45	-0,73	
CENPVL1	-1,61	-1,19	-1,11	-0,40	
GNL3L	-1,61	-1,13	-0,58	-0,28	
TAF3	-1,62	-1,53	-0,76	-0,84	
PES1	-1,62	-1,75	-1,65	-1,38	
REXO4	-1,63	-1,20	-0,84	-0,67	
RPS19BP1	-1,63	-1,56	-1,13	-0,81	
MRPL16	-1,63	-1,12	-0,47	-0,84	
RPUSD3	-1,64	-1,68	-1,10	-1,28	
C8orf59	-1,64	-1,82	-1,80	-1,59	
HP1BP3	-1,64	-1,80	-0,97	-1,12	

Gene names	**log2FC MYC ON**	**log2FC MYC HIGH**	**log2FC MYC ON +Flavo**	**log2FC MYC HIGH +Flavo**	**Function**
IGKV2D-29;IGKV2D-26;IGKV2-40;IGKV2D-30;IGKV2D-28;IGKV2-24;IGKV2D-24	-1,65	-1,55	-1,13	-0,80	
EMG1	-1,65	-1,44	-0,98	-0,98	
CTGF	-1,67	0,00	-2,12	0,00	
CYR61	-1,67	-2,64	-1,09	-1,21	
SP4	-1,67	0,00	-1,08	-0,93	
FTSJ3	-1,68	-1,64	-0,95	-0,96	
RPS24	-1,69	-1,51	-0,82	-1,20	
MRPL11	-1,70	-2,08	-1,08	-1,62	
UTP23	-1,70	-0,75	-0,53	0,27	
CMSS1	-1,71	-1,34	-1,31	-0,65	
FAM133B	-1,71	-0,87	-0,47	-0,88	
HMGN2	-1,73	-1,32	0,27	-1,18	
KRT14	-1,73	-1,93	-0,85	-1,18	
CGGBP1	-1,74	-1,14	-0,32	-1,16	
SNRNP27	-1,75	-1,37	-1,47	-1,22	
ZCCHC17	-1,76	-1,37	-1,35	-1,53	
MRM1	-1,79	-2,31	-1,13	-1,55	
GTF2B	-1,79	-1,47	-0,87	-0,82	
EPB41L5	-1,79	-1,89	-0,96	-1,00	
MPHOSPH10	-1,79	-1,61	-1,75	-1,23	
KLF3	-1,80	-1,80	-1,45	-1,45	
MRPS23	-1,80	-2,36	-1,30	-1,40	
ZKSCAN1	-1,80	-1,42	-0,56	-0,72	
HIST1H1C;HIST1H1D	-1,83	-1,76	-0,95	-1,17	
MAGEB2	-1,83	-1,91	-0,82	-1,33	
GLYR1	-1,84	-1,79	-1,28	-1,22	
TRPS1	-1,85	-1,12	0,00	-0,77	
RPL29	-1,86	-1,97	-0,77	-1,32	
MRPL46	-1,86	-2,24	-0,97	-1,27	
JUND	-1,87	-2,06	-1,49	-1,02	
CCDC84	-1,87	0,00	0,00	-1,49	
MAFG	-1,88	-1,83	-1,80	-1,63	
PRR12	-1,88	0,00	-1,63	-1,75	
KIAA1522	-1,90	-1,89	-0,81	-1,40	
CCDC137	-1,90	-1,58	-2,05	-1,74	

Gene names	log2FC MYC ON	log2FC MYC HIGH	log2FC MYC ON +Flavo	log2FC MYC HIGH +Flavo	Function
MRPL48	-1,90	-2,33	-1,02	-1,48	
CIR1	-1,92	-0,87	-2,00	-1,80	
MRPL12	-1,94	-2,34	-1,25	-2,11	
NKX2-5	-1,94	-1,34	-1,56	-0,62	
LLPH	-1,95	-3,45	-0,95	-1,63	
SREK1IP1	-1,95	-0,96	-0,84	-1,32	
EBNA1BP2	-2,02	-1,70	-1,31	-1,26	
GPNMB	-2,03	0,00	0,00	-1,70	
MRPL9	-2,04	-2,36	-1,24	-1,59	
TAF2	-2,08	-1,72	-1,30	-0,86	
TRMT10C	-2,09	-2,50	-1,64	-1,87	
MRPS28	-2,11	-2,06	-1,55	-1,54	
MRPL22	-2,11	-2,18	-1,50	-1,61	
MMTAG2	-2,12	-1,24	-1,38	-1,91	
C11orf98	-2,20	-2,13	-1,70	-1,92	
GLTSCR2	-2,20	-2,14	-2,10	-1,67	
RPL28	-2,21	-1,48	-1,70	-1,13	
ZNF444	-2,22	-1,83	0,00	-1,87	
RP9	-2,31	-1,26	-2,04	-1,60	
HSD17B10	-2,32	-3,13	-1,91	-2,30	
MRPL55	-2,41	0,00	-2,05	0,00	
NSA2	-2,71	-2,40	-2,46	-1,61	
KLF13	-2,78	-3,43	-2,04	-2,06	
FAM207A	-2,81	-2,04	-1,66	-1,65	
DHRS2	-2,86	-3,65	-2,72	-2,76	
EPB41	-2,87	-2,58	-1,21	-1,28	
MRPL40	-3,30	-4,31	-1,80	-2,55	
KRT6A	-3,89	-1,83	-2,88	-1,29	

7.3.7 Table with values corresponding to Figure 4.12

Table 7.10: Values corresponding to Figure 4.12.

Gene name	log2FC MYC ON +Flavo	log2FC MYC OFF +Flavo	Function
POLR2I	8,96	7,30	RNAPII
POLR2C	8,66	7,53	RNAPII
POLR2J;POLR2J3	8,55	6,74	RNAPII

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
POLR2D	8,49	6,41	RNAPII
GTF2F1	8,06	6,02	GTF
GTF2F2	7,98	6,28	GTF
POLR2G	7,71	6,81	RNAPII
POLR2A	7,37	5,70	RNAPII
TCEA1	7,12	5,27	EF
MED17	6,84	5,71	Mediator
POLR2E	6,81	4,61	RNAPII
INTS6	6,73	5,32	Integrator
INTS9	6,14	5,20	Integrator
MED8	6,13	3,89	Mediator
POLR2H	6,10	4,49	RNAPII
MED21	6,02	4,71	Mediator
POLR2F	5,96	5,12	RNAPII
INTS4	5,96	5,37	Integrator
ASUN	5,81	4,64	Integrator
MED22	5,80	3,21	Mediator
RPRD2	5,71	3,93	Other
IXL;MED29	5,49	3,65	Mediator
CPSF3L	5,37	4,69	Integrator
POLR2B	5,36	4,03	RNAPII
MED14	5,09	4,23	Mediator
MED16	5,05	3,47	Mediator
RPRD1B	4,94	2,27	Other
PAF1	4,89	1,83	EF
MED1	4,88	4,67	Mediator
INTS5	4,76	5,27	Integrator
MED23	4,76	4,41	Mediator
MED4	4,71	3,06	Mediator
MED6	4,70	0,00	Mediator
MED20	4,69	3,17	Mediator
VWA9	4,53	3,48	Integrator
RECQL5	4,44	1,45	Other
INTS1	4,39	3,47	Integrator
MED15	4,37	2,80	Mediator
MED27	4,37	3,43	Mediator
MED10	4,11	3,14	Mediator
PPP2R1A	3,99	3,17	Other
CTR9	3,80	1,74	EF

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
INTS7	3,66	3,00	Integrator
MED26	3,59	1,65	Mediator
INTS2	3,39	2,95	Integrator
VIM	3,31	2,51	Other
MED19	3,31	2,16	Mediator
PPP2CB	3,15	2,61	Other
CDKN2AIP	3,13	1,43	Other
CDC73	3,13	1,27	EF
MED7	3,06	3,64	Mediator
BCLAF1	2,96	2,97	Other
INTS10	2,92	3,36	Integrator
INTS8	2,70	2,24	Integrator
PABPC1;PABPC3	2,51	3,50	Termination
SUPT6H	2,51	1,28	EF
RPRD1A	2,50	2,07	Other
TCEA3	2,47	0,86	EF
RPS21	2,45	0,41	Other
CHTOP	2,31	1,09	Other
DCD	2,18	0,07	Other
NMT1	2,04	1,61	Other
SRSF6	2,03	2,02	Splicing
SRSF11	2,03	1,57	Splicing
SERBP1	1,99	0,39	Other
EPB41L4B	1,92	0,81	
ARGLU1	1,91	0,03	
INTS3	1,90	0,89	Integrator
SCAF11	1,83	0,09	
SRP14	1,81	0,86	
DDX46	1,80	1,74	
RPL13	1,77	1,23	
SNRPC	1,76	1,18	
MAP7	1,74	-0,64	
FAM76B	1,74	0,71	
VEZF1	1,74	0,11	Other
PHF5A	1,73	0,04	
GRB10	1,72	2,55	Other
PABPN1	1,71	0,16	
GATA3	1,70	0,00	
RPS23	1,63	1,71	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
CAPRIN1	1,57	1,16	
RBM17	1,56	0,36	
U2SURP	1,55	1,35	
XRN2	1,55	0,56	Termination
ZRANB2	1,55	0,38	Splicing
ZCCHC17	1,52	0,00	
SNRNP27	1,49	-0,31	
BTF3	1,49	1,73	
DSC1	1,48	0,00	
PPIL1	1,47	0,29	
S100A9	1,43	0,00	
SREK1	1,43	0,57	
RPS2	1,43	1,91	
SSB	1,40	1,17	
THRAP3	1,40	1,44	
EIF3I	1,40	1,36	
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	1,37	1,15	
SCAF8	1,34	1,51	EF
SF3B4	1,33	-0,04	
RPS17	1,33	0,11	
MFAP1	1,28	-0,72	
CWC25	1,27	-0,14	
GATAD2B	1,27	0,02	
RPS27	1,26	1,26	
LUC7L3	1,25	0,91	
YTHDC1	1,25	-0,27	
IWS1	1,24	-0,02	
RPS12	1,22	1,88	
SAP30BP	1,22	0,85	
SUPT5H	1,21	1,27	EF
SNRNP70	1,21	0,97	
EIF3F	1,20	1,25	
RPL17;RPL17-C18orf32	1,19	0,62	
NCL	1,18	0,38	
LYAR	1,18	0,14	
CPSF7	1,18	0,23	
TCF7;TCF7L2	1,15	-0,17	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
RNPS1	1,12	1,16	
ZC3H18	1,12	-0,07	
LUC7L2	1,11	-0,05	
EIF3C;EIF3CL	1,11	0,89	
TCF7	1,07	-1,91	
CALML5	1,06	1,14	
SYNCRIP	1,05	3,44	Splicing
RBBP6	1,04	-1,30	
CCAR1	1,04	0,35	
DPF2	1,03	-0,12	
SNRPD3	1,03	0,81	
RPS28	1,03	0,46	
SREK1IP1	1,03	-1,79	
RPS8	1,03	1,07	
NOLC1	1,02	-2,02	
RAE1	1,02	1,76	
CBX5	1,02	2,09	Other
TCEB2	1,01	0,63	
IKZF5	1,00	0,28	
MTA2	0,99	0,14	
SAP18	0,98	0,17	
SAFB	0,98	0,40	
KHDRBS1	0,98	0,62	
PCF11	0,97	-0,99	Termination
RPS27L	0,94	0,98	
SRFBP1	0,93	-0,60	
LUC7L	0,91	-0,37	
CDC42	0,87	1,15	
HDGFRP2	0,87	-0,20	
KLF13	0,84	-0,72	
SNRPE	0,84	0,82	
DDX39A	0,83	2,32	
SCAF4	0,83	-0,18	
PYCR1	0,83	1,35	
SRRM1	0,83	0,13	
TARDBP	0,82	0,75	
RUNX2	0,80	-0,13	
BCAS2	0,79	1,46	Splicing
WWP2	0,77	-0,49	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
HSD17B10	0,77	0,34	
PRPF38A	0,75	1,08	
SNRPD2	0,73	-0,41	
NPM1	0,73	0,27	
RPS24	0,73	0,46	
XAB2	0,73	1,60	Splicing
HNRNPA3	0,73	-0,26	
CHMP4B	0,72	1,15	
DYNLL1	0,72	-0,41	
BUD31	0,71	0,69	
RPS26;RPS26P11	0,71	0,38	
SRSF3	0,69	0,45	
SNRPF	0,68	0,59	
ZSCAN25	0,68	-2,19	
SP3	0,68	-0,54	
UPF3B	0,66	-0,34	
RPL38	0,65	0,73	
RPS27A;UBB;UBC;UBA52	0,64	1,10	
SNW1	0,64	-0,42	
RPL36A;RPL36A-HNRNPH2	0,64	-0,62	
PKM	0,64	4,24	Other
CCT3	0,63	3,42	Other
MYH9	0,62	4,63	Other
ARL6IP4	0,62	-1,08	
RBM39	0,61	-0,41	
CSTF2	0,61	-0,08	
PRDX1	0,61	0,67	
CPSF6	0,60	0,83	
DENND2D	0,60	-0,43	
YBX3	0,58	-2,67	
SF3A2	0,58	-0,50	
SCAF1	0,57	0,15	
SF3B6	0,57	1,17	
TRA2B	0,56	1,90	
NACA	0,55	1,52	
UTP3	0,55	-1,37	
CCDC137	0,55	0,00	
CBX3	0,54	1,35	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
HCFC1	0,54	-0,40	
SART1	0,53	-0,34	
SMNDC1	0,53	-0,15	
DUT	0,52	-0,26	
SRRM2	0,51	0,34	
FIP1L1	0,51	-0,79	
SNRNP40	0,47	0,05	Splicing
RPL24	0,46	0,20	
SF3A1	0,46	-0,28	
ZNF148	0,45	-0,12	
ERH	0,42	1,28	
PNN	0,41	0,40	
RBM8A	0,40	0,54	
CHERP	0,40	-0,68	
RPL27A	0,39	0,48	
RPL14	0,38	2,84	Other
SUB1	0,38	-0,02	
CDC40	0,37	0,57	
SF1	0,37	-0,84	
PPP2R1B	0,37	0,28	
RPS16;ZNF90	0,36	1,11	
SRP72	0,36	0,06	
HAUS8	0,35	-1,99	
UBTF	0,35	-0,02	
PRDM10	0,35	-1,07	
CCT2	0,34	2,11	
ZNF865	0,34	-2,21	
NXF1	0,32	0,65	
TCEB1	0,32	-0,89	
SRSF2	0,31	-0,46	
RPL6	0,31	0,70	
TRA2A	0,31	1,16	
GTPBP4	0,30	0,40	
HNRNPAB	0,29	-0,60	
DDX39B	0,29	0,80	
NSD1	0,28	0,00	
DDX17	0,28	0,28	
SP2	0,28	-0,99	
LMNB1	0,28	0,70	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
DNAJA2	0,27	1,16	
CREB1	0,27	-1,98	
HNRNPA0	0,26	1,00	
CHAMP1	0,25	-0,53	
SRSF7	0,24	1,04	
RPS6	0,24	-0,91	
FAU	0,24	-0,64	
H1F0	0,24	-0,47	
RPS5	0,23	-0,15	
POLDIP3	0,23	-1,02	
RPLP2	0,22	1,84	
RPS25	0,21	-0,87	
U2AF1	0,20	-0,27	
RPL39P5;RPL39	0,20	0,00	
RPS11	0,20	0,39	
HNRNPH1	0,20	0,92	
NHP2L1	0,19	0,55	
PRPF40A	0,19	-0,54	
WBP11	0,18	-0,55	
RBMX	0,18	-0,52	
CCT8	0,17	2,73	
HIST1H2AC	0,17	-0,40	
RPL34	0,16	-0,10	
MYL6	0,16	1,68	
PRPF4B	0,16	-0,15	
FTSJ3	0,16	-2,59	
RPL28	0,16	0,91	
RBBP7	0,14	-0,07	
RPL35A	0,14	0,65	
RPS3A	0,14	-0,49	
MAZ	0,13	-1,73	
HNRNPM	0,13	0,75	
SNRPB;SNRPN	0,13	0,21	
U2AF2	0,12	-1,01	
ZSCAN26;ZNF187	0,12	-0,63	
LSM14B	0,12	-2,00	
HSPA8	0,11	0,13	
PQBP1	0,11	-1,70	
RPS7	0,10	-0,61	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
ELAVL1	0,10	0,46	
RBM27	0,10	-0,74	
RPL19	0,08	-0,37	
RPS19	0,08	-0,11	
EPB41	0,07	0,39	
RPS18	0,07	0,68	
RPS4X	0,06	-0,23	
KRT1	0,06	-1,51	
EEF1A1;EEF1A1P5	0,06	1,50	
TCERG1	0,06	-0,49	
PUF60	0,02	-0,05	
RPS20	0,02	1,03	
RBBP4	0,02	-0,42	
RPL37	0,02	-2,52	
DNAJA1	0,01	1,06	
EIF2S2	0,00	0,09	
CAD	0,00	7,12	Other
PSMD11	0,00	7,07	Other
AHCY	0,00	6,60	Other
POLR2L	0,00	6,44	RNAPII
DYNC1H1	0,00	6,30	Other
PSMC5	0,00	5,93	Other
UBA1	0,00	5,75	Other
TKT	0,00	5,67	Other
PSMD1	0,00	5,55	Other
PSMC6	0,00	5,51	Other
ACO2	0,00	5,50	Other
NEDD4	0,00	5,17	Other
PHB	0,00	5,07	Other
GARS	0,00	4,92	Other
PA2G4	0,00	4,75	Other
UPF1	0,00	4,69	Other
PSMC2	0,00	4,56	Other
PSMC3	0,00	4,54	Other
IMMT	0,00	4,50	Other
IDH3A	0,00	4,42	Other
EIF3A	0,00	4,33	Other
EPRS	0,00	4,26	Other
MTHFD1	0,00	4,06	

Gene name	log2FC MYC ON +Flavo	log2FC MYC OFF +Flavo	Function
CCT5	0,00	4,06	Other
GNB2L1	0,00	4,03	Other
PSMD12	0,00	4,00	Other
SAMM50	0,00	3,93	Other
CCT4	0,00	3,88	
POLR2K	0,00	3,73	RNAPII
PTGES3	0,00	3,70	Other
PSMC4	0,00	3,67	Other
TUFM	0,00	3,67	Other
PABPC4	0,00	3,64	Termination
STAT5A	0,00	3,53	Other
CLTC	0,00	3,53	
NSF	0,00	3,52	Other
PSMD6	0,00	3,51	Other
CFL1	0,00	3,46	Other
PHGDH	0,00	3,39	
PSMD7	0,00	3,38	
PSMD3	0,00	3,33	Other
TCP1	0,00	3,29	Other
SND1	0,00	3,23	
EEF1G	0,00	3,20	Other
PSMD14	0,00	3,18	
TPI1	0,00	3,18	Other
VDAC3	0,00	3,16	Other
YWHAE	0,00	3,14	Other
VDAC2	0,00	3,12	Other
ABCE1	0,00	3,09	Other
RAB1A	0,00	3,08	
SRSF10	0,00	3,08	Splicing
PSMC1	0,00	3,08	Other
YWHAZ	0,00	3,08	Other
GNAI3	0,00	3,06	Other
VDAC1	0,00	3,05	Other
VCP	0,00	3,05	Other
PSMD2	0,00	3,04	Other
PGK1	0,00	3,03	
EIF5A;EIF5AL1	0,00	3,02	Other
PRPS1	0,00	3,00	
CNOT1	0,00	2,96	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
COPA	0,00	2,92	
ALDH18A1	0,00	2,91	
RRM1	0,00	2,90	Other
GNAI2	0,00	2,84	Other
CCT7	0,00	2,83	Other
EIF3M	0,00	2,82	
LARS	0,00	2,81	Other
ATAD3A	0,00	2,81	Other
TMEM263	0,00	2,75	Other
DNAJC7	0,00	2,74	
GLUD1;GLUD2	0,00	2,74	
INTS12	0,00	2,72	Integrator
DARS	0,00	2,72	Other
PHB2	0,00	2,70	Other
HYOU1	0,00	2,68	Other
G3BP1	0,00	2,63	
TUBB2A	0,00	2,61	
MSH6	0,00	2,59	
CCT6A	0,00	2,56	
VARS	0,00	2,52	
ETFA	0,00	2,50	
UBA2	0,00	2,48	
NUP160	0,00	2,47	
EIF3B	0,00	2,41	Other
ADK	0,00	2,41	
KIAA0368;ECM29	0,00	2,38	
TXNL1	0,00	2,38	
PPIA	0,00	2,37	
SHMT2	0,00	2,37	
CLIC1	0,00	2,36	
RAP1B;RAP1A	0,00	2,31	
GART	0,00	2,30	
TNPO1	0,00	2,29	
CELF1	0,00	2,23	
TBL3	0,00	2,22	
RARS	0,00	2,21	
KIF23	0,00	2,19	
MTHFD1L	0,00	2,19	
SUCLG1	0,00	2,18	

Gene name	log2FC MYC ON +Flavo	log2FC MYC OFF +Flavo	Function
BANF1	0,00	2,18	
GMPS	0,00	2,17	
MSH2	0,00	2,17	
ZAP70	0,00	2,17	
RHOA	0,00	2,16	
EDC4	0,00	2,15	
CTPS1	0,00	2,14	
ARPC4;ARPC4-TTLL3	0,00	2,14	
GSPT1;GSPT2	0,00	2,14	
MED11	0,00	2,13	Mediator
CHCHD3	0,00	2,11	
MED24	0,00	2,09	Mediator
GNB2	0,00	2,09	
DKC1	0,00	2,08	
PFKL	0,00	2,07	
DNM2	0,00	2,05	
CS	0,00	2,03	
STRAP	0,00	2,02	
PDHA1	0,00	2,00	
ANP32E	0,00	1,99	
GLRX3	0,00	1,98	
ACTA1;ACTC1;ACTG2;ACTA2	0,00	1,98	
EIF4G2	0,00	1,95	
IPO7	0,00	1,94	
AARS	0,00	1,94	
FASN	0,00	1,94	
GCN1L1	0,00	1,93	
EIF4G1	0,00	1,93	
USP5	0,00	1,92	
CAT	0,00	1,91	
MDH2	0,00	1,90	
YWHAQ	0,00	1,89	
EEF1D	0,00	1,87	
BAZ1B	0,00	1,85	
NUP98	0,00	1,85	
MAT2A	0,00	1,85	
SLC25A5	0,00	1,84	
THOC2	0,00	1,84	Other
ATIC	0,00	1,83	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
SMC4	0,00	1,82	
DDX1	0,00	1,81	
CHDH	0,00	1,79	
FUBP3	0,00	1,79	
ATP2A2	0,00	1,78	
DDX19A;DDX19B	0,00	1,77	
COPB2	0,00	1,77	
ACLY	0,00	1,76	
STAT3	0,00	1,76	
RAD50	0,00	1,74	
ALDH2	0,00	1,73	
FARSB	0,00	1,71	
DDOST	0,00	1,67	
STK4	0,00	1,66	
DDB1	0,00	1,64	
C14orf166	0,00	1,63	
MGEA5	0,00	1,62	
GLS	0,00	1,57	
NASP	0,00	1,57	
PAICS	0,00	1,56	
NARS	0,00	1,55	
COPG1	0,00	1,54	
SPOCK2	0,00	1,52	
NVL	0,00	1,51	
ACSL3	0,00	1,51	
FARSA	0,00	1,50	
LONP1	0,00	1,50	
MED30	0,00	1,49	Mediator
CSE1L	0,00	1,48	
KIF4A;KIF4B	0,00	1,47	
XPO1	0,00	1,47	
KHSRP	0,00	1,44	
COPB1	0,00	1,44	
RPL13A;RPL13a	0,00	1,40	
STIP1	0,00	1,40	
HSPA4	0,00	1,40	
GRAP2	0,00	1,37	
RAN	0,00	1,35	
UCHL5	0,00	1,35	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
PYCR2	0,00	1,34	
ACTR3	0,00	1,32	
PCYT1A;PCYT1B	0,00	1,32	
NUP155	0,00	1,30	
OGDH	0,00	1,30	
ADH5	0,00	1,30	
G3BP2	0,00	1,30	
ACTR2	0,00	1,29	
HDLBP	0,00	1,29	
MAGOH;MAGOHB	0,00	1,28	
IGF2BP2	0,00	1,28	
SEC61B	0,00	1,28	
FEN1	0,00	1,26	
RBM10	0,00	1,26	Other
TUBA1A	0,00	1,26	
CYB5A	0,00	1,25	
NUDCD2	0,00	1,25	
NIPBL	0,00	1,24	
MYL12A;MYL12B	0,00	1,24	
SUCLG2	0,00	1,23	
EIF3K	0,00	1,22	
BDH1	0,00	1,22	
TRAP1	0,00	1,21	
TOMM70A	0,00	1,19	
TOP2B	0,00	1,18	
ATP5B	0,00	1,17	
ETF1	0,00	1,14	
MED25	0,00	1,14	Mediator
HABP2	0,00	1,13	
HNRNPH2	0,00	1,11	
UBXN1	0,00	1,11	
GNB1	0,00	1,09	
HMGCS1	0,00	1,08	
01. Sep	0,00	1,08	
CENPV	0,00	1,06	
HNRNPLL;HNRPLL	0,00	1,04	
ARL8B	0,00	1,03	
PAK2	0,00	1,02	
NAA15	0,00	1,02	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
XRCC6	0,00	1,02	
MAK16	0,00	1,00	
ACADS	0,00	0,99	
RPS6KB1	0,00	0,99	
CUL2	0,00	0,99	
CSK	0,00	0,99	
GEMIN5	0,00	0,98	
UBE2C	0,00	0,98	
SEC13	0,00	0,97	
MTCH2	0,00	0,96	
STOML2	0,00	0,95	
RANBP1	0,00	0,94	
PCNA	0,00	0,94	
WDR75	0,00	0,92	
PRMT1	0,00	0,92	
GTF2E1	0,00	0,91	GTF
EIF3E	0,00	0,91	
IDH3G	0,00	0,88	
HBS1L	0,00	0,88	
PSMD13	0,00	0,88	
TAGLN2	0,00	0,87	
SEC22B	0,00	0,87	
TPR	0,00	0,86	
HADHB	0,00	0,86	
ACACA	0,00	0,85	
CCAR2	0,00	0,85	
PSPC1	0,00	0,85	
MARS	0,00	0,84	
ME2	0,00	0,84	
IARS	0,00	0,83	
PTBP3	0,00	0,83	
GFM1	0,00	0,83	
ZAK;pk	0,00	0,81	
RAC1	0,00	0,80	
SEH1L	0,00	0,79	
RPAP3	0,00	0,79	
TUBB3	0,00	0,79	
RAB7A	0,00	0,77	
MYEF2	0,00	0,77	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
HNRNPD	0,00	0,76	
MBNL1	0,00	0,75	
TBC1D10B	0,00	0,74	
PHF2	0,00	0,74	
NCAPD2	0,00	0,73	
TAF15	0,00	0,73	GTF
EIF4H	0,00	0,73	
NOP10	0,00	0,68	
MTX2	0,00	0,68	
PSMD4	0,00	0,68	
PDS5B	0,00	0,67	
PPP1CB	0,00	0,67	
AK5	0,00	0,67	
PPP6C	0,00	0,66	
MPP1	0,00	0,65	
YWHAG	0,00	0,65	
RAB2A;DKFZp313C1541;RAB2B	0,00	0,65	
VAPA	0,00	0,64	
BAZ1A	0,00	0,64	
RASA1	0,00	0,63	
MYO1G	0,00	0,63	
MTAP	0,00	0,62	
HDAC2	0,00	0,59	
FXR1	0,00	0,59	
SNRPG;SNRPGP15	0,00	0,59	
SNX3	0,00	0,58	
UQCRC1	0,00	0,58	
NUP35	0,00	0,56	
PPA1	0,00	0,55	
SMARCB1	0,00	0,55	
UBAP2L	0,00	0,55	
SMARCD2	0,00	0,54	
ARF1;ARF3	0,00	0,54	
PSMA1	0,00	0,52	
MED12;TNRC11	0,00	0,51	
RFC5	0,00	0,50	
AIMP2	0,00	0,50	
SACM1L	0,00	0,50	
OGT	0,00	0,50	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
RANBP2	0,00	0,50	
PSMD8	0,00	0,50	
SEC23B	0,00	0,50	
TUBG1;TUBG2	0,00	0,48	
RAD21	0,00	0,48	
DHX38	0,00	0,47	
TPM3;DKFZp686J1372	0,00	0,44	
SARS	0,00	0,43	
PDCD4	0,00	0,43	
RAVER1	0,00	0,43	
SRP19	0,00	0,41	
ARCN1	0,00	0,40	
QRICH1	0,00	0,39	
CHD1	0,00	0,39	
RIF1	0,00	0,39	
CLPX	0,00	0,39	
EIF3L	0,00	0,37	
APEX1	0,00	0,37	
ATP5C1	0,00	0,36	
BAT3;BAG6	0,00	0,36	
CDK9	0,00	0,35	
SHMT1	0,00	0,34	
NIP7	0,00	0,32	
RANGAP1	0,00	0,32	
EIF3G	0,00	0,32	
PBDC1	0,00	0,32	
RAB10	0,00	0,31	
TLN1	0,00	0,31	
HSPA6;HSPA7	0,00	0,30	
IPO5	0,00	0,30	
RPL18	0,00	0,29	
THOC7;NIF3L1BP1	0,00	0,28	
GTF2H2C;GTF2H2	0,00	0,28	GTF
BZW1	0,00	0,28	
ASNA1	0,00	0,27	
ACSL4	0,00	0,26	
SUZ12	0,00	0,26	
MDN1	0,00	0,25	
SMCHD1	0,00	0,25	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
WDR12	0,00	0,25	
NUMA1	0,00	0,24	
SRP9	0,00	0,23	
NCBP1	0,00	0,19	Other
SF3B5	0,00	0,19	
ESYT1	0,00	0,19	
RFC4	0,00	0,14	
LARP1	0,00	0,13	
EED	0,00	0,13	
ACTL6A	0,00	0,13	
ARPC1B	0,00	0,12	
FMR1	0,00	0,11	
ATRX	0,00	0,11	
FAM98A	0,00	0,11	
MCM7	0,00	0,09	
GNL3L	0,00	0,08	
CYP51A1	0,00	0,05	
NXT1	0,00	0,05	
EIF5B	0,00	0,03	
NUP153	0,00	0,02	
ATP5O	0,00	0,02	
DLAT	0,00	0,01	
BMS1	0,00	0,01	
EIF6	0,00	0,01	
HSP90B1	0,00	-0,03	
WDR3	0,00	-0,03	
KIF15	0,00	-0,03	
NDUFS1	0,00	-0,03	
CBFB	0,00	-0,04	
WDR43	0,00	-0,04	
RPS29	0,00	-0,05	
CIRH1A	0,00	-0,06	
TRRAP	0,00	-0,06	Other
UBR5	0,00	-0,08	
RQCD1	0,00	-0,08	
KIF2C	0,00	-0,08	
EWSR1	0,00	-0,09	Other
TEX10	0,00	-0,09	
CDC2;CDK1	0,00	-0,10	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
RPS6KA5	0,00	-0,10	
NOP9	0,00	-0,10	
PREP	0,00	-0,12	
METTL13	0,00	-0,13	
AQR	0,00	-0,14	
ADNP	0,00	-0,14	
DNAJC9	0,00	-0,15	
PDS5A	0,00	-0,15	
SMARCE1	0,00	-0,15	
RFC3	0,00	-0,16	
SYMPK	0,00	-0,17	
SRPR	0,00	-0,18	
THOC5	0,00	-0,18	
DRG1	0,00	-0,19	
BUD13	0,00	-0,20	
HADHA	0,00	-0,21	
MRTO4	0,00	-0,21	
DMAP1	0,00	-0,22	
EXOSC10	0,00	-0,23	
ALDOA	0,00	-0,24	
QARS	0,00	-0,24	
USP7	0,00	-0,25	
NOP16	0,00	-0,25	
NOL10	0,00	-0,26	
EIF4B	0,00	-0,26	
PSMA2	0,00	-0,29	
FKBP8	0,00	-0,30	
RNGTT	0,00	-0,30	
CMAS	0,00	-0,30	
DDX42	0,00	-0,31	Other
GLG1	0,00	-0,31	
DDX6	0,00	-0,32	
ERCC3	0,00	-0,36	
IDH3B	0,00	-0,36	
CNBP	0,00	-0,38	
HNRNPDL	0,00	-0,42	
DDX50	0,00	-0,43	
RCL1	0,00	-0,44	
CTNNBL1	0,00	-0,45	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
IMP3	0,00	-0,45	
HIST1H2BL	0,00	-0,47	
PLRG1	0,00	-0,48	
DHX37	0,00	-0,48	
EPB41L5	0,00	-0,49	
NUP205	0,00	-0,50	
DNAJB11	0,00	-0,53	
WDR82	0,00	-0,54	
SLC25A12	0,00	-0,54	
GTF2H1	0,00	-0,54	
ILF2	0,00	-0,55	
WDR26	0,00	-0,57	
RAB11A;RAB11B	0,00	-0,58	
CRNKL1	0,00	-0,61	Splicing
BYSL	0,00	-0,61	
OLA1	0,00	-0,61	
RBM34	0,00	-0,62	
KIF2A	0,00	-0,63	
KIF11	0,00	-0,63	
ESF1	0,00	-0,64	
CAAP1	0,00	-0,65	
CMSS1	0,00	-0,67	
ARRB2	0,00	-0,70	
UTP18	0,00	-0,73	
USP39	0,00	-0,77	
PDK1	0,00	-0,78	
DCP1A	0,00	-0,82	
CWC22	0,00	-0,88	
FUS	0,00	-0,88	
ILF3	0,00	-0,88	
ADRBK1;ADRBK2	0,00	-0,89	
MRPL12	0,00	-0,91	
POLR1A	0,00	-0,94	
EXOSC2	0,00	-0,96	
GTF2E2	0,00	-0,98	
UTP15	0,00	-1,02	
ZBTB7A	0,00	-1,03	
UTP23	0,00	-1,04	
VRK1	0,00	-1,05	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
MRPL22	0,00	-1,15	
PPP1CC	0,00	-1,15	
YME1L1	0,00	-1,17	
RBM42	0,00	-1,18	
RRP12	0,00	-1,20	
RBX1	0,00	-1,20	
SRSF9	0,00	-1,22	
RRP15	0,00	-1,22	
HIST2H2AC;HIST2H2AA3	0,00	-1,26	
SMARCA4	0,00	-1,29	
TFB1M	0,00	-1,31	
MAP2K4	0,00	-1,33	
MRPL46	0,00	-1,39	
UHRF1	0,00	-1,40	
DDX31	0,00	-1,41	
LBR	0,00	-1,43	
DDX49	0,00	-1,47	
NEIL1	0,00	-1,49	
CCDC86	0,00	-1,53	
CWC15	0,00	-1,55	
USP3	0,00	-1,60	
HMGB1	0,00	-1,67	
RPP30	0,00	-1,68	
AURKB	0,00	-1,70	
C19orf53	0,00	-1,71	
RTF1	0,00	-1,79	
SRBD1	0,00	-1,82	
IMP4	0,00	-1,85	
NSA2	0,00	-1,89	
C9orf114	0,00	-1,90	
RNF2	0,00	-2,15	
SRPK1	0,00	-2,37	
VPS25	0,00	-2,47	
MARK2	0,00	-2,65	
CFAP20	0,00	-2,85	
LEO1	0,00	-3,00	
CSNK1A1	0,00	-3,16	
RRP7A;RRP7BP	0,00	-3,30	
RPF1	0,00	-3,78	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
CLK3	0,00	-4,82	
SSRP1	0,00	0,08	
HNRNPC	-0,03	-0,45	
SRRT	-0,03	-0,59	
KRT2	-0,03	-1,76	
PARP1	-0,06	0,27	
SRSF5	-0,06	0,53	
SLK	-0,06	0,60	
MATR3	-0,06	0,39	
GTF2I	-0,06	0,26	
RPL31	-0,07	-0,41	
HNRNPF	-0,07	1,04	
PCBP1	-0,07	-0,50	
SP1	-0,09	-1,17	
RUVBL2	-0,11	-0,23	
PCBP2;Isoform	-0,11	1,71	
MPHOSPH10	-0,11	-0,57	
RALY	-0,12	-1,09	
RBM25	-0,12	-0,44	
EIF3D	-0,13	0,75	
RPL3	-0,14	-0,55	
SNIP1	-0,14	-1,51	
MRPL9	-0,14	-1,42	
RFC2	-0,15	0,12	
ZNF740	-0,16	-2,21	
PPIG	-0,16	0,48	
DSP	-0,17	0,00	Other
ZNF207	-0,17	-0,52	
RPL12	-0,18	2,28	
PRPF6	-0,18	0,18	
NOP2	-0,19	-0,78	
SMAD3	-0,19	-0,42	
NOP14	-0,21	-1,85	
RPS19BP1	-0,23	-1,69	
RPS14	-0,24	-0,74	
GTF2B	-0,24	-1,23	
PWP1	-0,25	-1,98	
HDAC1	-0,27	0,57	
NGDN	-0,27	-1,89	

Gene name	log2FC MYC ON +Flavo	log2FC MYC OFF +Flavo	Function
RPL35	-0,28	-0,49	
BUB3	-0,28	-1,07	
DDX27	-0,30	-0,79	
RBM28	-0,30	-0,81	
HIST1H2BC	-0,30	-1,02	
ZNF593	-0,33	-2,10	
SF3A3	-0,33	0,00	
HSP90AA1	-0,34	4,59	Other
MCM4	-0,34	0,28	
RPL11	-0,35	-0,14	
TRMT10C	-0,35	0,13	
YBX1	-0,35	-3,19	
HIST1H1E;HIST1H1D	-0,35	-1,08	
GTPBP1	-0,36	0,56	
LRRC59	-0,36	0,95	
HSPD1	-0,36	2,69	Other
MEPCE	-0,36	-1,85	
ACIN1	-0,36	0,34	
PPP1CA	-0,37	0,34	
HMGA1	-0,37	-1,41	
HNRNPL	-0,38	-0,50	
RPL32	-0,39	0,07	
RUVBL1	-0,39	0,03	
HNRNPK	-0,39	0,11	
SNRPD1	-0,40	-0,39	
DDX23	-0,41	-0,73	
TUBB	-0,42	2,68	Other
SON	-0,42	-1,01	
CSTF1	-0,42	-2,03	
KPNB1	-0,43	1,52	
MRPL48	-0,43	-1,80	
ZNF524	-0,43	-2,76	
CTNNB1	-0,43	0,45	
SRSF1	-0,44	1,10	
PRDM15	-0,45	0,00	
UBA52	-0,45	-1,56	
PRPF8	-0,46	0,20	
C19orf43	-0,48	-1,80	
MAFG	-0,48	-3,25	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
RPL30	-0,50	-1,70	
DHX8	-0,52	-0,62	
KPNA2	-0,52	-2,22	
CPSF3	-0,53	-1,79	
DDX5	-0,53	-0,78	
EIF2S3;EIF2S3L	-0,53	-0,23	
RPL23	-0,53	-0,15	
ZNF48	-0,54	-3,53	
RTCB	-0,54	1,14	
RPL26	-0,54	-1,01	
FAM32A	-0,55	-2,59	
RBPJ	-0,55	0,00	
RPL23A	-0,55	-1,77	
SET;SETSIP	-0,56	-1,02	
RPS13	-0,57	-0,51	
HNRNPA2B1	-0,58	0,23	
HNRNPA1;HNRNPA1L2	-0,58	-0,13	
PTBP1	-0,58	0,70	
ZNF771	-0,59	-2,63	
DDX52	-0,59	-1,26	
SMC2	-0,59	-0,04	
PRPF19	-0,60	-0,13	
ENO1	-0,60	4,47	Other
HSPA9	-0,60	1,37	
ZNF787	-0,60	-1,60	
IK	-0,61	-0,20	
HELLS	-0,61	-1,88	
ACTB	-0,61	1,50	
H2AFV;H2AFZ	-0,62	0,15	
SNRNP200	-0,65	0,33	
TUBA1B	-0,65	2,65	
TCEB3	-0,65	-2,05	
RPS10;RPS10-NUDT3	-0,68	-1,11	
DEK	-0,68	0,00	
ATP5A1	-0,70	2,86	
DDX3X;DDX3Y	-0,70	-0,39	
PPIL4	-0,70	-0,08	
RRS1	-0,70	-1,62	
HIST1H3A;H3F3C	-0,70	0,02	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
HSP90AB1	-0,70	0,87	
GNL3	-0,71	-2,17	
EFTUD2	-0,72	0,62	
ZNF281	-0,73	-2,61	
RPLP0;RPLP0P6	-0,73	1,38	
PRPF31	-0,73	-1,11	
CTCF	-0,75	-2,39	
DSG1	-0,78	-1,08	
EIF2S1	-0,78	-0,43	
RBM14	-0,79	-0,42	
PPIH	-0,79	-1,87	
MCM2	-0,79	0,61	
RPL10	-0,80	2,10	
RBM15	-0,81	-0,26	
CSNK2A1;CSNK2A3	-0,81	0,26	
CDC5L	-0,81	-0,39	
PSIP1	-0,82	-1,42	
FAM120A	-0,83	0,28	
GRWD1	-0,83	-2,07	
HP1BP3	-0,83	-1,71	
FRG1	-0,83	-1,82	
SKP1	-0,85	-1,55	
NOP58	-0,87	2,29	
EBNA1BP2	-0,87	-1,53	
RPS3	-0,87	-0,55	
HNRNPR	-0,90	0,72	
TMPO	-0,91	0,49	
SRP68	-0,91	-1,48	
TUBB4B	-0,92	2,58	
SFPQ	-0,92	-1,18	
GLYR1	-0,92	-0,23	
CPSF4	-0,93	-1,87	
HIST1H4A	-0,94	-0,72	
MORF4L2	-0,94	0,00	
PES1	-0,95	-2,32	
MCM6	-0,95	0,72	
SNRPA1	-0,96	-1,34	
MCM3	-0,96	0,55	
HNRNPUL2;HNRNPUL2-BSCL2	-0,97	-1,27	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
DHX15	-0,97	-0,61	
RPL21	-0,98	-0,19	
WBSCR22	-0,99	-1,84	
SF3B2	-1,01	-0,91	
CSDE1	-1,01	2,83	
CDK13	-1,01	-1,69	
RPSA	-1,02	0,80	
RPL7A	-1,02	-1,10	
RPL27	-1,03	-1,88	
RPL36	-1,04	-0,08	
RPL22L1	-1,05	-1,61	
ZFP91;ZFP91-CNTF	-1,06	-3,22	
RPL8	-1,06	-1,21	
SMU1	-1,07	-0,93	
NONO	-1,08	-0,35	
PHF6	-1,10	-1,98	
RPL37A	-1,11	-0,72	
RBM26	-1,12	-1,54	
NUDT21	-1,13	-0,64	
RRP36	-1,18	0,00	
SLTM	-1,19	-2,89	
RSBN1	-1,19	-2,02	
RCC2	-1,19	-1,34	
CPSF2	-1,20	-1,49	
REXO4	-1,20	-1,30	
FCF1	-1,21	-1,97	
HIST2H3PS2	-1,21	0,56	
EEF2	-1,22	0,92	
RPL4	-1,22	0,65	
METAP1	-1,22	-1,82	
EMG1	-1,23	-1,19	
LARP7	-1,24	-0,84	
CHD4	-1,27	0,89	
ZFX;ZFY	-1,27	-2,08	
HNRNPU	-1,28	-0,88	
SMC1A	-1,28	-0,88	
SMARCC1	-1,29	-0,70	
RPL5	-1,30	-0,94	
EIF4A3	-1,30	0,55	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
H2AFY	-1,33	-1,09	
CXorf56	-1,33	0,00	
RPS15	-1,33	-1,90	
DCAF13	-1,34	-3,55	
RPS9	-1,35	-1,35	
YARS	-1,37	-0,79	
MECP2	-1,39	-1,93	
KPNA3	-1,40	-0,66	
CDC2L1;CDK11B;CDK11A	-1,41	-1,50	
WDR33	-1,43	-2,67	
EIF4A1	-1,44	2,10	
TOP1	-1,44	-2,22	
HMGN2	-1,44	-0,54	
GNL2	-1,44	-2,36	
WWP1	-1,46	-1,82	
MAFK	-1,46	-3,72	
HNRNPA3	-1,48	-0,59	
NUP93	-1,48	1,49	
ZNF319	-1,49	-3,31	
RPS15A	-1,51	-0,62	
RPL15	-1,52	-1,13	
ABCF1	-1,54	-1,35	
SMC3	-1,54	-1,06	
ZNF652	-1,55	-3,48	
SF3B3	-1,56	-1,67	
SUPT16H	-1,56	-1,05	
FIZ1	-1,58	-2,98	
FBL	-1,59	0,58	
TRIM28	-1,60	0,99	
DDX41	-1,61	-2,18	
FXR2	-1,61	-0,45	
GAPDH	-1,61	3,63	Other
PRPF3	-1,62	-2,37	
RPL7	-1,66	-0,64	
RPL10A	-1,68	-0,84	
DIMT1	-1,69	-2,51	
POP1	-1,69	-3,48	
DDX21	-1,70	-2,50	
NAP1L1	-1,73	-0,28	

Gene name	**log2FC MYC ON +Flavo**	**log2FC MYC OFF +Flavo**	**Function**
SIRT7	-1,75	-2,52	
DNMT1	-1,76	-1,31	
PRPF4	-1,78	-2,32	
SF3B1	-1,79	-1,81	
RPL22	-1,79	-1,31	
NOP56	-1,80	1,34	
RPL9	-1,84	-0,92	
PATZ1	-1,84	-3,66	
KRR1	-1,85	-2,79	
BRIX1	-1,89	-1,20	
MICU1	-1,90	-1,34	
DDX55	-1,92	-2,85	
ZNF444	-1,93	-4,77	
WDR46	-1,93	-2,91	
MYBBP1A	-1,94	-4,59	
ERI1	-1,94	-2,98	
HSPA5	-1,96	-0,25	
ABCF2	-1,97	1,08	
MCM5	-1,97	0,43	
IMPDH2	-1,97	3,85	Other
HSPH1	-2,00	4,47	Other
NAT10	-2,00	-0,58	
SNRPB2	-2,03	-2,70	
CSTF3	-2,04	-2,98	
KIAA0020	-2,07	-3,40	
TRIP12	-2,15	-0,21	
WDR5	-2,21	-1,76	
DHX9	-2,27	-0,99	
TOP2A	-2,27	-0,85	
TRMT112	-2,27	-2,44	
RPF2	-2,39	-1,98	
RSBN1L	-2,44	-1,20	
TP53BP1	-2,60	0,00	
ALYREF	-2,63	-3,03	
HIST1H1B	-2,64	-2,93	
TSR1	-2,64	-3,48	
SMARCA5	-2,67	-1,26	
RPL18A	-2,78	0,62	
DDX56	-2,84	-3,32	

Gene name	log2FC MYC ON +Flavo	log2FC MYC OFF +Flavo	Function
NSUN5	-2,89	-3,62	
BRD2	-2,90	-3,68	
MORF4L1	-3,01	-4,29	
IGKV2D-29;IGKV2D-26	-3,07	0,00	
RCC1	-3,11	-3,52	
DDX18	-3,27	-3,20	
CPSF1	-3,28	-4,32	
NSUN2	-3,40	-3,12	
NO66	-3,50	-2,91	
IQGAP1	-3,53	-0,56	
SKIV2L2	-3,62	-1,63	
DDX47	-3,84	-3,37	
CUL1	-4,01	-4,56	

7.3.8 Table with values corresponding to Figure 4.16

Table 7.11: Values corresponding to Figure 4.16.A. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
MYC	10,31	10,30	27	2
MAX	9,85	9,37	11	2
TRRAP	9,41	7,52	111	2
HUWE1	9,10	6,11	71	2
PSMA3	8,19	4,21	8	2
PSMA7	8,38	4,15	9	2
PSMD6	8,32	4,11	11	2
PSMD7	8,33	4,07	8	2
PSMD11	8,40	4,06	19	2
BAG2	8,22	4,00	4	2
ZNF281	8,20	3,93	5	2
CSNK2A1;CSNK2A3	8,10	3,80	8	2
EIF3A	8,11	3,54	11	2
MCM5	8,08	3,49	8	2
PSMB1	8,10	3,44	6	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PSMD1	8,25	3,39	16	2
CCT7	8,06	3,32	8	2
PSMD14	7,97	3,32	3	2
PSMD13	7,99	3,21	7	2
HNRNPA1;HNRNPA1L2	8,29	3,15	8	2
PSMC6	8,52	3,15	14	2
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B—991	8,08	3,11	5	2
PSMA1	8,26	3,10	8	2
PSMA6	8,41	3,01	6	2
HADHA	8,60	2,97	6	2
CSDE1	7,84	2,86	9	2
PSMB3	7,97	2,83	5	2
ANP32E	8,35	2,82	6	2
FBXW7	7,86	2,78	5	2
MCM7	7,88	2,77	8	2
PSMD2	8,63	2,75	25	2
HSPH1	8,39	2,74	11	2
PSMA4	7,98	2,73	5	2
ACO2	8,15	2,67	12	2
PSMC3	8,43	2,67	13	2
VIM	7,65	2,67	6	2
GCN1L1	7,87	2,67	13	2
PSMC2	8,56	2,67	18	2
PSMB5	7,95	2,61	5	2
MTHFD1	7,87	2,58	7	2
LARS	7,94	2,57	7	2
PSMD8	7,88	2,55	5	2
PSMD3	8,45	2,54	12	2
MDH2	7,91	2,49	6	2
EIF4A1	8,97	2,46	19	2
PAICS	7,91	2,44	3	2
UBR5	8,02	2,44	18	2
MTHFD1L	7,86	2,42	5	2
GART	7,84	2,40	7	2
DHX29	7,93	2,40	3	2
SHMT2	7,88	2,36	8	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CCT2	8,46	2,33	10	2
CBFB	7,79	2,33	5	2
VARS	7,80	2,31	6	2
UBA1	7,97	2,31	9	2
PSMC5	8,50	2,26	14	2
MCM2	8,29	2,25	15	2
DMAP1	7,83	2,24	7	2
HNRNPD	7,87	2,24	4	2
BDH1	7,88	2,23	3	2
CCT4	8,25	2,22	10	2
PSMC1	8,38	2,21	9	2
PSMB2	7,95	2,20	6	2
IMPDH2	8,14	2,19	10	2
PSMA2	8,21	2,18	6	2
PA2G4	8,20	2,16	8	2
PABPC4	7,94	2,14	5	2
HDAC1	8,28	2,14	8	2
KIAA0368;ECM29	7,93	2,13	11	2
PSMD12	7,96	2,12	7	2
DARS	8,26	2,12	9	2
PPP2CA	7,80	2,12	8	2
PSMC4	8,56	2,11	13	2
IMMT	7,72	2,10	4	2
PSMA5	8,32	2,10	7	2
EIF3M	7,86	2,09	6	2
CYB5A	8,30	2,09	3	2
EEF1D	7,86	2,06	5	2
MAT2A	7,90	2,05	5	2
DIAPH3	7,90	2,03	7	2
SMARCD2	7,79	2,00	9	2
GMPS	7,70	1,98	7	2
TRAP1	7,82	1,98	5	2
ATAD3A	8,74	1,93	11	1
MATR3	8,66	1,92	16	1
RBBP7	8,43	1,92	12	2
OGT	7,60	1,92	3	2
MTA2	7,95	1,91	5	2
RARS	7,94	1,91	6	2

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RUNX2	7,87	1,90	5	2
EIF3L	7,96	1,88	10	2
GLUD1;GLUD2	7,79	1,88	5	2
HNRNPR	7,64	1,86	4	2
PTGES3	8,35	1,86	5	2
FLNA	7,18	1,84	5	2
PGAM5	7,78	1,83	4	2
EP400	7,78	1,82	8	2
POLR2B	8,27	1,82	17	2
PTBP1	8,58	1,78	6	1
CTPS1	7,66	1,76	4	2
CCT3	8,61	1,74	14	1
RPS28	8,70	1,73	3	0
ACTL6A	8,11	1,72	5	2
EPRS	8,25	1,71	12	2
UMPS	7,74	1,70	5	2
PDS5A	7,63	1,70	4	2
WDR26	7,58	1,69	5	0
NAP1L1	8,72	1,69	4	0
USP5	7,50	1,69	4	0
LIG1	7,81	1,68	7	2
CCT8	8,52	1,68	14	1
MDN1	7,83	1,68	9	2
UTP20	7,72	1,66	5	2
HSPD1	9,07	1,65	18	0
WDR46	8,80	1,64	7	0
NSF	7,78	1,64	6	2
DDX19A;DDX19B	7,64	1,63	3	2
RALY	8,13	1,63	3	2
IDH3A	7,65	1,62	4	2
CCT5	8,00	1,62	6	2
MSH2	7,79	1,61	5	2
CHDH	7,84	1,60	4	2
STK4;STK3	7,52	1,60	4	2
GARS	7,66	1,59	3	2
EIF3H	7,86	1,58	2	2
TOP2A	8,58	1,58	18	0
SDAD1	7,58	1,58	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GAPDH	9,00	1,56	7	0
GTF2I	8,63	1,56	19	0
SMARCC1	8,07	1,56	9	1
BCAS2	7,63	1,53	4	0
SYNCRIP	8,31	1,53	9	1
PSMD4	8,06	1,50	4	1
STIP1	7,49	1,50	3	0
SUPT5H	7,97	1,50	10	1
PKM	8,77	1,50	14	0
ABCE1	7,91	1,49	7	1
DHX9	8,60	1,48	14	0
ENO1	8,65	1,47	8	0
RRM1	7,67	1,47	3	1
WDR5	8,57	1,47	10	0
EIF3E	8,38	1,47	14	1
MTSS1	7,90	1,46	7	1
ABCF2	8,19	1,46	9	1
RPL36	8,85	1,45	3	0
PDCD4	7,70	1,45	5	1
RUVBL1	9,13	1,44	18	0
PFKL	7,67	1,44	3	0
ATP1A1	7,77	1,42	5	0
IPO5	7,75	1,42	8	0
POLDIP2	7,57	1,41	3	0
TARDBP	8,34	1,40	5	0
ATIC	7,73	1,39	4	0
PNO1	7,81	1,39	4	0
RUVBL2	9,10	1,39	19	0
RPS21	7,85	1,38	3	0
PHGDH	8,26	1,38	7	0
PABPC1;PABPC3	8,48	1,37	7	0
RAC2;RAC3	7,67	1,37	3	0
ACACA	7,73	1,36	9	0
PRDX1	9,23	1,35	6	0
PBRM1	7,66	1,35	4	0
TKT	7,62	1,34	4	0
TUFM	8,81	1,34	10	0
SYMPK	7,51	1,34	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SMC4	7,66	1,34	5	0
SMARCA4	8,54	1,33	21	0
SET;SETSIP	8,07	1,32	7	0
PGK1	7,64	1,32	3	0
DPY30	7,83	1,30	2	0
DNMT1	7,92	1,30	6	0
PPFIBP1	7,54	1,30	3	0
SKIV2L	7,19	1,30	2	0
MSH6	8,08	1,29	6	0
MCM3	8,62	1,29	18	0
GATAD2B	7,86	1,28	5	0
PLK1	7,77	1,28	4	0
AHNAK	7,56	1,27	3	0
RPF1	9,00	1,27	11	0
EIF3F	7,98	1,27	7	0
SMC2	7,93	1,26	6	0
SUPT16H	8,31	1,26	12	0
HSP90AA1	8,90	1,26	17	0
PHB	7,77	1,26	6	0
NPM1	9,18	1,25	8	0
SMC1A	7,73	1,24	9	0
IPO7	7,73	1,23	8	0
KIF2C	7,64	1,23	5	0
NCL	8,84	1,22	8	0
CDK1;CDC2	8,18	1,22	6	0
DDX39A	8,59	1,22	10	0
AHCY	8,02	1,21	6	0
KPNB1	8,28	1,21	10	0
CCT6A	8,41	1,21	10	0
HADHB	8,52	1,20	5	0
MCM4	8,27	1,20	15	0
SPOCK2	8,18	1,20	3	0
CBX3	8,09	1,20	6	0
HEATR1	7,49	1,20	5	0
DDX1	7,91	1,19	6	0
SUPT6H	7,76	1,19	9	0
ATP5B	9,04	1,16	19	0
CAD	9,08	1,15	34	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ELAVL1	8,15	1,15	6	0
MCM6	8,20	1,14	12	0
STAT5B	8,21	1,14	9	0
HNRNPA2B1	8,85	1,13	11	0
HSP90AB1	9,72	1,13	31	0
EIF3B	8,60	1,13	17	0
BAT3;BAG6	7,64	1,12	6	0
GNL3	9,18	1,10	2	0
DHX33	7,52	1,10	3	0
NOP56	8,91	1,10	15	0
COPB2	8,05	1,09	12	0
ANKRD44	7,37	1,09	4	0
HNRNPU	9,33	1,08	15	0
HABP2	7,56	1,07	3	0
VCP	8,48	1,07	19	0
RPL15	9,16	1,06	12	0
GNB2L1	9,19	1,05	16	0
HNRNPM	9,25	1,05	22	0
CUL1	7,70	1,05	7	0
RBBP4	8,11	1,05	6	0
TNPO1	7,72	1,04	4	0
ILF2	7,80	1,04	4	0
EIF5A	8,85	1,04	5	0
PES1	8,55	1,03	6	0
P4HB	7,64	1,03	4	0
EIF5B	7,70	1,03	3	0
CSTF1	7,57	1,02	4	0
FXR1	7,93	1,02	3	0
RPS27A	9,79	1,02	6	0
BLM	7,62	1,02	3	0
KDM1A	7,54	1,01	5	0
UPF1	8,35	1,01	14	0
TPM3;DKFZp686J1372	7,79	1,01	3	0
ZRANB2	8,79	1,01	14	0
PPP2R1A	8,43	1,00	14	0
GTF3A	8,80	1,00	3	0
ACTB	9,97	1,00	22	0
RFC3	8,04	1,00	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
LMNB1	8,84	1,00	16	0
RFC5	7,85	0,99	3	0
HSPA4	7,58	0,99	6	0
HNRNPA3	8,82	0,99	13	0
RFC2	7,82	0,98	2	0
SMU1	8,14	0,98	10	0
RPL35A	8,70	0,98	6	0
SMC3	7,64	0,98	10	0
CALM2;CALM1;CALM3	8,16	0,97	3	0
HNRNPC	8,85	0,97	7	0
HNRNPA0	8,32	0,96	3	0
AIMP2	7,52	0,95	3	0
SIN3A	7,19	0,95	3	0
SERBP1	8,58	0,95	9	0
RPLP2	9,12	0,94	5	0
DNAJA2	8,82	0,93	11	0
HNRNPF	8,89	0,93	6	0
POLRMT	7,76	0,93	2	0
GOT2	7,56	0,91	3	0
PDS5B	8,11	0,91	11	0
MYBBP1A	8,22	0,91	3	0
SF3A2	7,41	0,91	4	0
RPL18	8,93	0,89	4	0
RPSA	9,48	0,89	14	0
CSE1L	7,71	0,89	7	0
EIF3C;EIF3CL	8,28	0,89	11	0
TCP1	8,87	0,88	19	0
NOP58	8,78	0,88	14	0
ARHGEF1	7,55	0,87	4	0
RPS12	9,13	0,87	9	0
RPL12	8,98	0,86	6	0
RPL13	9,64	0,86	9	0
RPL32	9,40	0,86	7	0
AIFM1	8,29	0,86	7	0
ATP5A1	9,28	0,86	20	0
MARS	7,70	0,85	3	0
NHP2L1	8,44	0,85	4	0
POLR2H	7,56	0,85	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
GPAM	7,44	0,84	5	0
RPL14	8,93	0,84	2	0
RPL7	9,14	0,84	10	0
TIMM50	7,83	0,84	2	0
HCFC1	8,36	0,84	13	0
TARS	7,57	0,83	4	0
VDAC3	7,53	0,83	2	0
HNRNPK	8,88	0,83	11	0
LDHA	8,12	0,82	2	0
MRTO4	7,76	0,82	6	0
GTF3C1	7,64	0,82	5	0
CFL1	8,52	0,81	6	0
CDK12	8,64	0,81	7	0
PSIP1	7,55	0,80	4	0
PDCD11	8,06	0,80	10	0
EIF3I	8,35	0,79	11	0
ALDOA	7,61	0,79	5	0
GSPT1;GSPT2	7,93	0,78	4	0
PPP2R2A;PPP2R2D	8,09	0,78	7	0
YTHDF2	7,66	0,78	3	0
RPS19	9,16	0,77	7	0
DNAJA1	9,11	0,77	17	0
XRN2	7,90	0,77	8	0
TPI1	8,34	0,77	6	0
CS	7,72	0,77	4	0
ATP2A2	7,75	0,77	8	0
NACC1	7,67	0,76	5	0
SMARCB1	7,63	0,76	5	0
RCC2	9,05	0,75	14	0
G3BP2	7,63	0,74	3	0
PRPS1	8,72	0,74	10	0
DNAJC7	7,51	0,74	3	0
GTPBP4	8,43	0,73	10	0
ADK	7,49	0,73	3	0
RRP12	8,75	0,72	14	0
SSRP1	8,18	0,72	12	0
NRF1	7,57	0,71	3	0
RPL7A	9,78	0,71	16	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RANGAP1	7,55	0,71	3	0
CDC73	7,50	0,70	5	0
DDX21	9,53	0,70	17	0
RPL4	9,49	0,70	18	0
RAD50	7,44	0,69	5	0
FBL	8,70	0,69	10	0
RPL5	9,28	0,69	11	0
CSTF2;CSTF2T	7,44	0,68	4	0
DDX49	7,51	0,68	5	0
RPL35	10,47	0,68	5	0
PPAN-P2RY11;PPAN	8,58	0,68	4	0
PCNA	7,99	0,68	3	0
NEDD4	8,63	0,67	13	0
MYO1D	7,67	0,67	2	0
RPS25	9,90	0,67	9	0
ZC3H18	8,23	0,67	6	0
CHD4	8,90	0,66	32	0
UBA52;UBB;RPS27A;UBC	8,49	0,66	1	0
EEF2	9,13	0,66	28	0
RPLP0;RPLP0P6	9,25	0,66	10	0
UBAP2L	7,55	0,65	4	0
CAT	7,66	0,65	4	0
PPIA	8,37	0,65	3	0
RFC4	8,06	0,64	5	0
TUBA4A	8,23	0,63	3	0
EBNA1BP2	9,16	0,63	8	0
COPG1	7,67	0,62	6	0
WDR74	7,40	0,62	4	0
TCF12	7,76	0,62	4	0
COPA	8,46	0,62	25	0
HSPA9	9,59	0,62	27	0
LYAR	8,11	0,62	2	0
PRPF8	9,28	0,62	74	0
RAD21	7,66	0,61	6	0
HNRNPH1	9,12	0,61	10	0
GNL2	9,25	0,60	17	0
CIRH1A	7,32	0,60	3	0
PRPF38B	8,20	0,60	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NMT1	7,91	0,60	7	0
RPL6	9,94	0,60	8	0
ADNP	7,55	0,60	3	0
EEF1G	8,44	0,59	9	0
SRSF2	8,93	0,58	9	0
RPS10;RPS10-NUDT3	9,17	0,58	8	0
DNAJA3	8,13	0,57	3	0
RPS8	10,45	0,57	19	0
NOP9	7,46	0,56	2	0
TUBB	9,65	0,56	6	0
PPIH	7,80	0,56	4	0
PRMT1	7,82	0,56	4	0
NOP16	8,23	0,55	3	0
EP300	7,33	0,55	5	0
DCAF8	7,43	0,55	4	0
POLR2A	8,28	0,54	21	0
RPS5	9,43	0,54	12	0
YWHAQ	8,04	0,54	3	0
SRPK1	8,22	0,54	5	0
DDX54	7,98	0,54	6	0
RPL21	9,22	0,54	4	0
YWHAB	7,73	0,53	3	0
RPS7	10,05	0,53	18	0
RPL34	9,33	0,53	6	0
RPL3	9,53	0,52	13	0
ESF1	7,44	0,52	3	0
SND1	8,64	0,51	18	0
EIF3D	8,57	0,51	10	0
NONO	7,96	0,51	5	0
HSPA8	10,14	0,49	28	0
RPL13A;RPL13a	9,17	0,49	4	0
RPL23A	10,34	0,49	17	0
POLR2C	7,82	0,49	7	0
MYL12A;MYL12B	8,20	0,49	5	0
IK	7,67	0,48	3	0
CLTC	8,99	0,48	44	0
EIF2S2	8,16	0,48	5	0
HELLS	7,54	0,47	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HSP90B1	8,10	0,47	5	0
APEX1	7,73	0,46	4	0
RPL28	9,52	0,46	7	0
RPS6	10,68	0,46	21	0
SRP68	8,64	0,45	13	0
G3BP1	7,85	0,44	3	0
PATZ1	8,95	0,44	17	0
UBE2C	7,53	0,44	3	0
RPL27A	9,98	0,44	5	0
SRM	7,42	0,44	3	0
ATP5C1	8,57	0,44	4	0
MYH9	9,18	0,44	44	0
CSNK2A2	7,51	0,44	5	0
RAB11B;RAB11A	7,59	0,44	3	0
RAN	8,64	0,43	7	0
POLE	7,36	0,43	3	0
BANF1	8,38	0,42	3	0
TECR	7,72	0,42	3	0
SRSF3	9,22	0,42	8	0
DDB1	8,76	0,42	18	0
HNRNPL	8,77	0,42	7	0
RPL19	9,76	0,42	12	0
CUL2	8,01	0,41	8	0
BOP1	8,04	0,41	4	0
DDX47	8,11	0,41	4	0
EIF3G	8,00	0,41	4	0
THOC2	7,54	0,41	5	0
MYO5A	7,47	0,41	6	0
PRPF40A	8,92	0,41	17	0
RPS18	9,77	0,40	12	0
NCAPD2	7,59	0,39	3	0
USP7	8,27	0,39	16	0
RPL11	9,65	0,39	7	0
CCDC86	8,81	0,39	2	0
RPP30	8,22	0,39	2	0
RPL26	10,04	0,39	12	0
TAF6L	7,45	0,38	3	0
WDR3	7,51	0,38	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TMPO	7,93	0,38	4	0
MORF4L1	8,20	0,38	8	0
RPL27	9,41	0,38	7	0
MRPL22	8,66	0,37	5	0
RBM10	7,71	0,37	4	0
BMS1	7,54	0,37	5	0
KIAA0020	8,79	0,36	8	0
ZNF444	8,39	0,36	4	0
MGEA5	7,51	0,36	6	0
CSTF3	7,61	0,36	3	0
UBTF	7,92	0,36	5	0
PRPF6	8,04	0,35	11	0
PPIL2	7,77	0,35	2	0
MYO1G	7,41	0,35	4	0
RPS27L	8,84	0,34	5	0
PRPF4	8,30	0,34	11	0
GTF2H4	7,48	0,34	3	0
ENY2	7,55	0,34	2	0
SF3A3	7,96	0,34	6	0
SF3B3	8,70	0,34	24	0
EFTUD2	9,10	0,34	36	0
RPL18A	9,51	0,33	12	0
ARF5;ARF3	7,30	0,33	2	0
NSUN2	8,81	0,33	12	0
PHB2	8,60	0,32	12	0
RBM25	9,10	0,32	23	0
RPS15	10,10	0,32	6	0
NOP2	8,63	0,32	6	0
CCNL1	7,39	0,31	4	0
STRAP	7,79	0,31	7	0
RANBP10	7,41	0,31	3	0
RBM26	9,04	0,29	10	0
LRRC59	8,15	0,29	3	0
RPS9	10,47	0,29	20	0
C5orf30	7,57	0,29	3	0
TUBA1B	10,23	0,29	24	0
HMGB1;HMGB1P1	7,85	0,29	3	0
PAXIP1	7,57	0,28	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNRNP200	9,18	0,28	60	0
ALDH18A1	7,82	0,28	6	0
RPL30	9,72	0,28	8	0
RPS16;ZNF90	9,53	0,28	11	0
SF3B6	8,04	0,27	6	0
CTNNB1	8,94	0,27	25	0
RPF2	8,48	0,27	5	0
UTP14A	8,46	0,27	3	0
ACTN1	7,59	0,27	5	0
RRS1	8,62	0,27	6	0
RPL9	8,98	0,27	7	0
RPS24	10,03	0,25	8	0
MRPL48	8,01	0,25	3	0
HIST1H4A	10,06	0,25	10	0
RBM28	8,60	0,25	5	0
RPS20	9,37	0,25	5	0
GNAI2;GNAI1	8,21	0,25	6	0
SMARCA5	8,68	0,25	25	0
RPA1	7,82	0,24	4	0
CWC22	7,43	0,24	6	0
SMCHD1	7,71	0,24	6	0
NUP93	8,11	0,24	9	0
RPL31	10,02	0,24	13	0
NAT10	8,87	0,23	23	0
SPATA5	7,40	0,23	3	0
AQR	8,36	0,23	14	0
DYNC1H1	8,10	0,23	28	0
RPS14	9,56	0,22	7	0
DNAJB6	7,90	0,22	3	0
RPL36A;RPL36A-HNRNPH2	9,75	0,22	4	0
RNPS1	8,53	0,22	4	0
NGDN	8,56	0,22	5	0
RPS26;RPS26P11	10,33	0,22	8	0
IKBKAP	7,60	0,22	4	0
RPS17	10,23	0,22	11	0
RPL10A	9,12	0,22	9	0
SNRPC	7,89	0,22	3	0
RPL17;RPL17-C18orf32	10,48	0,21	16	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MAFG	8,08	0,21	2	0
EIF6	8,59	0,21	3	0
ARPC4-TTLL3;ARPC4	7,59	0,21	4	0
PNN	8,43	0,21	11	0
SLC25A13	8,32	0,21	7	0
RPL8	10,55	0,21	25	0
HIRA	7,39	0,20	4	0
DNM2	7,46	0,20	3	0
CLPX	7,50	0,19	5	0
HNRNPAB	8,02	0,19	3	0
RTCB	7,94	0,18	3	0
PRPSAP1	6,89	0,17	2	0
GRWD1	8,68	0,17	5	0
GNB2	7,99	0,17	5	0
TRIM28	8,94	0,17	16	0
SF3B1	8,80	0,17	26	0
SLC25A4	7,82	0,17	2	0
HSPA14	7,46	0,17	3	0
PBDC1	8,20	0,16	4	0
H2AFV;H2AFZ	8,35	0,16	3	0
PPP1CB	8,68	0,16	13	0
MRPL46	8,05	0,16	2	0
TOP2B	7,49	0,15	5	0
BRIX1	9,40	0,15	10	0
RNF2	7,90	0,14	4	0
UPF3B	7,71	0,14	3	0
FAU	9,61	0,14	4	0
HDLBP	7,48	0,14	3	0
SLC25A1	8,36	0,14	6	0
CDK11B;CDC2L1;CDK11A	8,19	0,14	8	0
TP53BP1	8,48	0,14	8	0
DDX10	8,87	0,13	13	0
TCERG1	7,75	0,13	6	0
ZFP64	8,00	0,13	3	0
EIF2S1	8,38	0,12	9	0
RPL10	9,75	0,12	13	0
SNX1	8,10	0,12	8	0
PLRG1	8,29	0,12	9	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EIF2S3;EIF2S3L	8,70	0,12	14	0
DCAF13	9,00	0,12	9	0
TUBG1;TUBG2	7,49	0,11	4	0
SMAD3;SMAD2	7,90	0,11	5	0
RPS11	10,39	0,11	17	0
AATF	7,85	0,10	3	0
C14orf166	8,01	0,10	8	0
RBM22	7,90	0,10	7	0
AP1B1	7,59	0,10	3	0
SNRNP70	9,06	0,10	15	0
TFB1M	8,85	0,09	5	0
PPIG	8,65	0,09	11	0
EIF4A3	8,85	0,09	13	0
PWP1	8,38	0,09	6	0
RPS3	9,73	0,09	22	0
CTR9	7,60	0,09	3	0
HIST2H3A;HIST1H3A;HIST3H3	9,56	0,08	3	0
RIF1	7,37	0,08	3	0
RSRC1	8,04	0,08	3	0
ZNF800	8,97	0,07	11	0
RPS3A	10,45	0,07	23	0
CLASP2	7,64	0,06	5	0
ABCF1	8,42	0,06	6	0
BTF3	8,18	0,05	3	0
NASP	8,30	0,05	5	0
CRNKL1	8,11	0,05	10	0
TXNL1	7,63	0,04	3	0
SLC25A22;SLC25A18	7,81	0,04	4	0
UBA2	7,48	0,04	3	0
UTP18	8,02	0,04	3	0
SF3B5	7,84	0,04	3	0
CIR1	7,99	0,04	3	0
KRR1	8,90	0,03	8	0
PCBP2	8,91	0,03	7	0
RPS13	10,59	0,03	13	0
SSR1	7,59	0,03	2	0
SLC25A5	9,89	0,03	15	0
RBM39	10,68	0,03	30	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SNW1	8,30	0,03	8	0
XAB2	8,13	0,02	14	0
SF3B4	7,90	0,02	5	0
GPATCH8	7,94	0,02	5	0
BUB3	8,07	0,02	8	0
PPP1CC	7,84	0,02	2	0
YBX3	9,10	0,02	4	0
HSD17B10	8,38	0,02	2	0
BARX1	7,47	0,01	3	0
SNRPD3	8,78	0,01	4	0
SRSF5	8,41	0,01	6	0
VPRBP	7,36	0,00	5	0
MRPL15	8,89	0,00	6	0
YWHAZ	8,30	0,00	5	0
CHAMP1	8,28	0,00	5	0
NUP155	7,59	0,00	3	0
ARF4	7,59	0,00	2	0
IKZF4	8,33	-0,01	2	0
LCP1	8,14	-0,01	8	0
SKIV2L2	8,33	-0,01	9	0
YWHAE	8,42	-0,01	7	0
DDX17	8,98	-0,01	15	0
CDK9	7,71	-0,01	5	0
SNRNP27	8,70	-0,02	3	0
SNRNP40	8,37	-0,02	9	0
SNRPE	8,32	-0,02	3	0
INTS6	7,72	-0,02	6	0
SNX5	7,98	-0,02	9	0
CPSF3	8,70	-0,02	11	0
SSB	7,87	-0,02	3	0
VRK1	7,68	-0,02	3	0
NSUN5	8,31	-0,02	3	0
DHX16	7,35	-0,03	4	0
FTSJ3	9,57	-0,03	13	0
RPP14	7,67	-0,03	2	0
PARP1	8,13	-0,03	7	0
RPS15A	9,77	-0,03	8	0
TUBB4B	10,26	-0,04	22	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ATP5O	8,55	-0,04	2	0
ZNF593	9,19	-0,04	3	0
KHDRBS1	8,51	-0,04	5	0
SNRPD1	8,57	-0,04	3	0
RPL24	9,88	-0,04	14	0
RBM14	8,43	-0,04	9	0
HNRNPLL;HNRPLL	8,20	-0,05	8	0
SRSF6	8,85	-0,05	5	0
SFPQ	8,62	-0,05	10	0
TAOK1	8,06	-0,05	6	0
DHX15	9,01	-0,05	27	0
DDX6	7,86	-0,05	5	0
CDK2;CDK3	7,36	-0,06	2	0
DPF2	7,97	-0,06	4	0
CDC5L	9,24	-0,06	23	0
MINA	8,55	-0,06	3	0
FBXO33	7,78	-0,06	3	0
NME1-NME2;NME2;NME2P1	8,09	-0,06	4	0
RPS23	10,56	-0,06	13	0
LARP1	8,27	-0,07	10	0
WDR12	8,27	-0,07	8	0
COPB1	7,79	-0,08	9	0
DDX27	9,26	-0,08	15	0
RP9	9,22	-0,08	5	0
NO66	8,82	-0,09	5	0
SRRM1	9,81	-0,09	15	0
DEK	8,16	-0,10	4	0
HIST2H2AC;HIST2H2AA3;HIST1H2AJ;HIST1H2AH;H2AFJ;HIST1H2AD;HIST1H2AG	10,44	-0,10	5	0
SF3B2	8,24	-0,11	8	0
ARPC3	7,56	-0,11	3	0
TRIP12	7,92	-0,11	8	0
MAZ	8,68	-0,12	6	0
YWHAG	7,70	-0,12	3	0
MAPKAP1	7,52	-0,12	2	0
DDX23	7,90	-0,12	4	0
DNAJC9	7,91	-0,12	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DIMT1	9,87	-0,13	17	0
RNF138	7,83	-0,13	2	0
LRRC47	7,71	-0,13	6	0
CPSF1	9,28	-0,14	38	0
DDX18	8,81	-0,14	11	0
DENND2D	8,56	-0,14	8	0
SNRPD2	8,50	-0,14	7	0
RPL38	9,25	-0,14	5	0
DDX55	8,88	-0,14	8	0
DDX50	8,45	-0,15	8	0
PTPN14	7,68	-0,15	2	0
RRP36	8,47	-0,16	4	0
SRSF11	9,22	-0,16	6	0
PRPF31	8,55	-0,16	9	0
ZAP70	8,13	-0,16	7	0
RPL37A	9,54	-0,17	6	0
RPS4X	10,57	-0,17	22	0
DHX35	7,91	-0,17	8	0
MRPL9	8,64	-0,17	3	0
PSME3	7,49	-0,17	2	0
MYCBP2	7,32	-0,18	3	0
SLK	8,13	-0,18	5	0
CUL4A	7,46	-0,18	4	0
METTL13	7,52	-0,19	3	0
TRMT10C	8,61	-0,20	4	0
SDHA	7,85	-0,20	5	0
CWC15	7,81	-0,21	3	0
DDX31	9,22	-0,22	11	0
FASN	7,93	-0,22	4	0
PYCR1	8,62	-0,22	2	0
AP2A1	7,60	-0,22	6	0
SKP1	9,04	-0,22	10	0
HIST1H2BL	10,46	-0,22	10	0
ARGLU1	10,52	-0,23	17	0
DDX3X;DDX3Y	9,68	-0,23	26	0
SNRPN;SNRPB	8,22	-0,24	5	0
PCBP1	9,97	-0,24	16	0
PPIE	7,88	-0,24	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PRPF19	8,87	-0,24	7	0
PHF5A	7,78	-0,24	2	0
SF3A1	7,92	-0,25	3	0
SCAF4	8,84	-0,25	8	0
GNAI3	7,53	-0,25	3	0
NOM1	7,84	-0,25	3	0
SLTM	8,68	-0,26	7	0
LUC7L	10,01	-0,26	11	0
FAM133B	8,50	-0,26	3	0
EEF1A1;EEF1A1P5	10,42	-0,26	19	0
LUC7L3	9,64	-0,27	25	0
SAP18	8,71	-0,27	9	0
NACA	8,79	-0,27	4	0
PRPF38A	8,33	-0,27	7	0
NCBP1	8,01	-0,27	7	0
MSN	7,94	-0,27	4	0
RAB1B	8,17	-0,27	6	0
SLC25A12	8,48	-0,27	10	0
MPP1	7,52	-0,27	4	0
KPNA3	8,40	-0,27	9	0
PPP6R3	7,56	-0,28	4	0
RRP7A	8,04	-0,28	2	0
ARRB2	8,34	-0,28	10	0
DDX5	9,81	-0,28	24	0
FAM32A	8,84	-0,28	5	0
TFIP11	7,71	-0,29	3	0
BUD31	8,01	-0,29	4	0
IKZF1	8,61	-0,29	5	0
SLC25A6	7,92	-0,29	2	0
CDC42	8,28	-0,29	6	0
ESYT1	7,86	-0,30	4	0
TMEM263	7,79	-0,30	4	0
CTCF	9,70	-0,30	24	0
SNIP1	8,77	-0,30	7	0
CYC1	7,81	-0,30	3	0
MYL6	8,88	-0,31	6	0
HNRNPUL2;HNRNPUL2-BSCL2	9,04	-0,31	17	0
DHX8	8,72	-0,31	17	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CPSF2	9,06	-0,31	22	0
FCF1	9,23	-0,31	8	0
HIST1H1C	10,67	-0,32	13	0
PYCR2	8,29	-0,32	5	0
HSPA5	9,42	-0,34	22	0
SREK1IP1	9,75	-0,34	6	0
EMG1	8,46	-0,34	4	0
XPO1	7,39	-0,35	4	0
DHX37	8,27	-0,35	4	0
WDR33	9,08	-0,36	13	0
ZFX;ZFY	8,86	-0,36	14	0
CFAP20	8,28	-0,36	7	0
PABPN1	7,52	-0,36	3	0
CDK13	9,22	-0,36	22	0
POC1A	7,85	-0,36	5	0
TRA2A	8,38	-0,38	6	0
SP1	8,20	-0,38	3	0
DNAJC13	7,45	-0,38	5	0
H2AFY	9,10	-0,38	12	0
KPNA2	8,13	-0,38	6	0
MAGOHB	8,48	-0,38	4	0
RAB7A	8,01	-0,38	6	0
RBM27	9,59	-0,39	16	0
UTP3	8,43	-0,39	3	0
ZSCAN21	7,67	-0,40	3	0
CDC40	8,35	-0,41	12	0
SRP72	8,91	-0,41	11	0
TUBB3	8,16	-0,41	6	0
INTS3	7,36	-0,41	3	0
C9orf114	10,09	-0,42	10	0
SAFB	7,78	-0,42	3	0
CCDC12	7,77	-0,42	3	0
NSA2	9,49	-0,42	10	0
FAM120A	8,60	-0,42	16	0
SLC25A11	7,65	-0,42	6	0
GDI2	7,57	-0,42	4	0
ACTR1A	7,64	-0,43	1	0
ALYREF	8,45	-0,44	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PRPF4B	9,53	-0,44	23	0
UBR4	7,59	-0,44	7	0
MEPCE	9,55	-0,44	11	0
GRB7	8,44	-0,44	2	0
UFM1	7,60	-0,45	2	0
EPB41L2	8,54	-0,45	6	0
MAD2L1	8,19	-0,46	5	0
RPN1	7,98	-0,46	6	0
CHD1	8,21	-0,46	9	0
HIST1H1B	10,02	-0,46	3	0
EPB41	9,28	-0,46	16	0
TAF10	8,16	-0,47	3	0
RPL7L1	8,92	-0,47	4	0
SREK1	9,01	-0,47	9	0
TBC1D10B	8,51	-0,47	8	0
CHERP	8,69	-0,47	12	0
MAK16	7,59	-0,48	3	0
UTP23	9,16	-0,48	3	0
SRRM2	9,20	-0,48	15	0
PPIL1	7,70	-0,48	4	0
AP2B1	7,90	-0,48	7	0
DDX46	9,19	-0,49	31	0
EED	7,80	-0,49	5	0
DDX52	8,32	-0,50	6	0
IKZF5	8,07	-0,50	3	0
RBM8A	8,59	-0,50	7	0
UTP11L	9,12	-0,51	5	0
RPL22L1	9,09	-0,51	3	0
ABT1	8,38	-0,51	5	0
LARP7	8,06	-0,51	2	0
KPNA4	8,27	-0,51	6	0
AKAP17A	8,46	-0,51	2	0
REXO4	8,89	-0,52	5	0
MASP1	7,54	-0,52	2	0
ABCB7	7,49	-0,53	4	0
MFAP1	8,27	-0,54	5	0
SCAF1	8,20	-0,54	3	0
WDR83	7,88	-0,55	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TXN	8,42	-0,55	2	0
CSNK1A1;CSNK1A1L	7,48	-0,55	2	0
MYNN	8,06	-0,55	5	0
ZNF740	8,01	-0,55	3	0
YME1L1	7,67	-0,55	5	0
TOP1	8,80	-0,55	13	0
ZCCHC17	9,84	-0,56	8	0
OSBPL7	8,00	-0,56	3	0
PUF60	9,83	-0,56	23	0
ZNF148	8,10	-0,56	3	0
ZNF532	7,79	-0,57	4	0
TAF8	8,54	-0,57	7	0
CCDC137	8,24	-0,57	2	0
WRNIP1	7,75	-0,58	3	0
SRSF1	8,57	-0,58	8	0
ACIN1	8,74	-0,58	7	0
FIZ1	8,75	-0,58	5	0
DYNLL1;DYNLL2	8,92	-0,58	4	0
KNOP1	7,46	-0,58	2	0
TAF2	9,40	-0,59	31	0
ZFP91;ZFP91-CNTF	9,01	-0,59	13	0
SP3	8,18	-0,59	5	0
LUC7L2	10,70	-0,60	22	0
SRSF7	8,96	-0,60	8	0
U2SURP	9,99	-0,60	23	0
WDR6	7,67	-0,60	2	0
NXT1	8,41	-0,60	4	0
FEM1B	7,56	-0,61	4	0
GTF2B	8,69	-0,61	9	0
SCAF8	7,96	-0,61	4	0
U2AF1	10,58	-0,61	14	0
GTPBP1	8,24	-0,61	7	0
EME1	7,70	-0,62	3	0
SRRT	8,34	-0,62	12	0
HP1BP3	8,80	-0,62	5	0
PPIL4	8,21	-0,63	7	0
SRP19	7,95	-0,63	2	0
MMTAG2	9,74	-0,63	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CNOT1	7,37	-0,63	7	0
ARL8A	7,62	-0,63	3	0
MRPS25	8,08	-0,64	4	0
GRB10	9,30	-0,64	8	0
POLDIP3	7,94	-0,64	4	0
IMP3	8,58	-0,64	5	0
BUD13	8,49	-0,64	6	0
SON	9,25	-0,64	8	0
PCMT1	9,08	-0,65	7	0
WHSC1	8,70	-0,66	14	0
DDX56	8,70	-0,66	6	0
OGDH;OGDHL	7,48	-0,66	3	0
SNRPA1	8,94	-0,66	9	0
RSBN1L	8,83	-0,66	7	0
ZNF638	8,54	-0,66	4	0
METAP1	8,71	-0,66	11	0
SEC61A1	8,17	-0,67	4	0
MAP7	8,81	-0,68	6	0
EPB41L3	8,64	-0,68	3	0
MED19	8,66	-0,68	4	0
FRG1	9,41	-0,69	15	0
RPL22	9,18	-0,70	3	0
POP1	9,17	-0,70	8	0
U2AF2	10,55	-0,71	22	0
SRP14	9,35	-0,71	2	0
VEZF1	8,99	-0,71	11	0
SRSF10	8,65	-0,71	9	0
DDX51	8,57	-0,71	6	0
CPSF6	9,51	-0,72	9	0
NOL12	9,20	-0,72	3	0
ZNF319	8,27	-0,73	6	0
NKAP	8,85	-0,73	8	0
ZSCAN26;ZNF187	8,58	-0,73	3	0
MEAF6	7,54	-0,73	2	0
PAXBP1	7,64	-0,73	4	0
RBBP6	9,30	-0,73	19	0
RPUSD4	8,49	-0,73	5	0
IQGAP1	9,65	-0,74	42	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SART1	8,36	-0,74	5	0
CXXC1	8,50	-0,75	9	0
RPS2	9,86	-0,75	15	0
TRA2B	9,14	-0,76	9	0
RPL23	10,25	-0,76	12	0
IMP4	8,54	-0,77	7	0
MPHOSPH10	8,65	-0,77	5	0
TCEB1	8,51	-0,77	7	0
PHF6	9,27	-0,78	14	0
HEATR3	7,04	-0,78	2	0
CCDC84	8,05	-0,78	2	0
THRAP3	9,01	-0,78	13	0
DNAJB11	8,82	-0,79	9	0
NXF1	8,79	-0,80	7	0
CACTIN	8,35	-0,81	6	0
ASF1A	8,57	-0,82	6	0
THAP11	7,81	-0,82	3	0
RSBN1	8,84	-0,83	10	0
YBX1	10,43	-0,84	17	0
WBP11	9,12	-0,84	8	0
SF1	8,61	-0,87	9	0
GNL3L	8,79	-0,87	7	0
YARS	9,07	-0,88	19	0
BCLAF1	8,60	-0,89	8	0
FIP1L1	9,76	-0,91	14	0
NUDT21	9,30	-0,91	9	0
CWC25	8,96	-0,91	8	0
RAB11FIP5	9,12	-0,91	6	0
BRD7	8,87	-0,92	7	0
PHC2	7,41	-0,93	2	0
CPSF4	9,41	-0,93	14	0
TCEB2	8,31	-0,94	4	0
SNRPB2	8,61	-0,94	4	0
PRPF3	8,14	-0,94	3	0
ARHGEF39	8,08	-0,97	2	0
CLK3	9,49	-0,98	14	0
MARK3	7,68	-1,00	4	0
TCF7;TCF7L2;LEF1	9,16	-1,02	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CBX6	7,95	-1,04	4	0
WWP1	8,30	-1,04	5	0
C3	8,18	-1,05	3	0
ZNF771	9,09	-1,06	12	0
EIF1;EIF1B	7,81	-1,06	3	0
RPS19BP1	8,86	-1,08	3	0
DDX24	7,79	-1,10	3	0
SRP9	8,73	-1,13	2	0
SIRT7	9,96	-1,14	15	0
TUBB2B	9,15	-1,14	6	0
HMGXB4	7,64	-1,16	2	0
SFSWAP	8,65	-1,16	6	0
GTF2F1	7,53	-1,17	2	0
ERH	8,90	-1,19	3	0
BRD9	8,41	-1,24	3	0
YTHDC1	8,59	-1,24	7	0
DPYSL2	8,32	-1,24	6	0
RBMX	8,73	-1,25	6	0
GLYR1	9,97	-1,27	21	0
VANGL2	8,22	-1,27	8	0
GTPBP2	7,75	-1,27	4	0
WWC1	8,43	-1,27	8	0
TUBA1A	8,42	-1,28	3	0
WWP2	8,64	-1,28	13	0
GTF2F2	8,61	-1,30	10	0
Cxorf56	8,47	-1,35	6	0
DCD	8,71	-1,36	3	0
SUB1	8,62	-1,37	3	0
DUT	9,45	-1,39	4	0
SP2	8,57	-1,43	7	0
DDX28	7,84	-1,43	2	0
MAP7D1	7,98	-1,44	2	0
DYNC1I2	7,29	-1,45	3	0
ZNF653	8,08	-1,56	4	1
DDX41	9,91	-1,57	34	0
KLF13	9,10	-1,59	10	0
EPB41L5	9,74	-1,64	13	0
H1F0	9,66	-1,72	6	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
DSP	8,32	-1,73	7	1
EPB41L4B	9,66	-1,74	13	0
MICU1	9,15	-1,94	13	0
S100A9	8,55	-2,10	4	1
S100A8	8,32	-2,78	2	2
ANXA2;ANXA2P2	7,64	-3,74	2	2

Table 7.12: Values corresponding to Figure 4.16.B. Peptide counts indicate size of each circle representing one identified protein. Significance is indicated by different colouring with a value of 2 shown in red (highly significant), a value of 1 in green (significant), and a value of 0 in grey (not significant). Values are sorted according to log10 intensity and log2FC.

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
MYC	10,68	11,94	30	2
MAX	10,76	10,62	19	2
TRRAP	9,56	6,18	109	2
EP400	8,22	4,16	15	2
HUWE1	8,04	3,53	23	2
TCEB1	7,82	3,22	3	2
LYAR	9,15	2,97	15	1
CEBPB	7,74	2,89	3	2
GTF3C1	8,17	2,82	16	1
PSMC1	8,00	2,71	6	1
GAR1	7,74	2,33	3	1
NOP2	9,17	2,33	17	1
MRPS6	7,57	2,31	3	1
SPTLC1	7,70	2,21	5	1
PDS5B	7,61	2,11	6	0
GTF3C5	7,69	2,02	8	0
CTR9	7,66	1,96	7	0
RAD21	7,60	1,92	4	0
BAZ1A	7,70	1,86	5	0
ZBTB20	7,63	1,85	5	0
ZNF281	8,96	1,76	12	0
RBBP5	7,44	1,75	3	0
LAS1L	8,38	1,75	15	0
SQSTM1	8,10	1,74	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ATAD3A	8,56	1,72	17	0
POM121;POM121C;POMZP3	7,67	1,71	4	0
SETD1A	7,66	1,70	4	0
RFC1	7,73	1,68	6	0
PTCD3	7,54	1,66	4	0
TOP2A	8,60	1,65	23	0
DDX10	9,27	1,63	28	0
TOP2B	7,73	1,63	6	0
PLK1	7,72	1,60	7	0
RNH1	7,70	1,60	4	0
PSMD1	7,71	1,59	8	0
POLR2C	7,66	1,59	8	0
PSMD13	7,72	1,58	4	0
PDCD11	8,20	1,56	15	0
CXXC1	8,71	1,55	15	0
DYNC1H1	7,86	1,54	3	0
DDX31	9,89	1,54	44	0
MRPS31	7,39	1,53	3	0
SMARCA4	8,56	1,49	19	0
HADHA	8,88	1,49	23	0
USP7	7,95	1,48	10	0
WDR5	8,65	1,47	10	0
FASTKD2	7,36	1,47	8	0
DEK	9,14	1,46	9	0
METTL17	8,72	1,46	9	0
GPATCH4	9,40	1,44	27	0
PTPMT1	6,95	1,44	2	0
ADNP	7,58	1,43	4	0
NOL9	8,26	1,42	9	0
DNTTIP2	9,17	1,41	14	0
SLC25A13	8,27	1,41	17	0
ZNF638	9,27	1,40	25	0
CAD	8,72	1,39	42	0
POLR2A	7,99	1,37	9	0
AHCTF1	7,54	1,37	9	0
MRPS25	8,35	1,36	9	0
ACTL6A	8,25	1,36	7	0
RPF2	8,07	1,34	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DDX24	8,44	1,33	22	0
DHX33	7,88	1,33	5	0
RPUSD4	8,85	1,32	14	0
MDC1	7,54	1,31	4	0
USP36	7,62	1,31	6	0
PSMD6	7,93	1,26	9	0
DNAJA2	8,65	1,25	9	0
BAG2	8,51	1,24	9	0
DNAJA1	9,08	1,23	16	0
MRPS35	7,79	1,23	5	0
PNPLA6	7,33	1,22	4	0
TOR4A	7,52	1,22	3	0
BMS1	8,60	1,20	17	0
DDX51	7,91	1,16	8	0
ZNF114	8,26	1,16	4	0
NUP133	7,89	1,13	10	0
DMAP1	8,02	1,13	7	0
CMSS1	9,57	1,09	11	0
DHX37	8,56	1,08	9	0
NUP160	7,54	1,07	8	0
RANBP2	8,07	1,07	11	0
POLR2B	8,44	1,06	23	0
CAAP1	8,08	1,06	4	0
TIMM50	7,83	1,05	6	0
SLC25A19	7,07	1,05	2	0
RUNX1	7,51	1,05	4	0
TNFAIP8L1	7,35	1,05	3	0
SLC25A22;SLC25A18	8,10	1,05	7	0
SFXN3	7,51	1,04	4	0
KRR1	8,37	1,04	10	0
KIAA0020	9,06	1,03	21	0
CDK9	7,50	1,02	3	0
MRPL49	8,11	1,02	4	0
RFC3	8,01	0,99	8	0
PSMD3	8,16	0,99	12	0
RECQL	7,82	0,98	6	0
BRIX1	9,55	0,98	20	0
EME1	7,78	0,96	7	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
PSMC5	8,30	0,96	10	0
MRPS22	8,18	0,95	11	0
TUBA4A	7,90	0,95	3	0
CDC27	7,48	0,93	4	0
XAB2	8,01	0,92	4	0
RUVBL2	8,93	0,92	22	0
DCAF4	7,82	0,92	6	0
EPB41L3	9,37	0,91	29	0
TMX3	7,60	0,91	4	0
EBNA1BP2	9,58	0,91	18	0
BLM	8,30	0,90	15	0
MRPS18C	7,67	0,90	2	0
SSRP1	8,23	0,90	11	0
DNAJB6	7,73	0,89	4	0
IMP4	9,65	0,88	17	0
RUVBL1	8,94	0,86	16	0
EIF6	9,38	0,86	8	0
NOL6	7,69	0,84	9	0
COIL	7,70	0,84	5	0
TUBA3C;TUBA3E	8,19	0,84	2	0
MAP4K4;TNIK	7,94	0,83	3	0
CDCA8	8,64	0,83	9	0
AKAP8	7,86	0,82	5	0
PRDM10	7,49	0,82	3	0
ZNF800	8,84	0,82	20	0
MAP7D1	8,43	0,81	10	0
HADHB	8,75	0,81	15	0
BUD13	8,14	0,80	5	0
C12orf43	7,57	0,80	2	0
IMP3	9,73	0,80	15	0
NOP58	8,77	0,80	19	0
ZSCAN25	7,63	0,79	5	0
CSNK2A1;CSNK2A3	8,15	0,79	8	0
MRPS10	7,71	0,78	4	0
WDR75	7,97	0,78	9	0
MRPS16	7,99	0,78	4	0
MPHOSPH10	9,90	0,78	18	0
ABCE1	7,42	0,77	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NUP98	7,13	0,77	3	0
PTPN1	7,49	0,77	3	0
NGDN	9,27	0,77	14	0
MRPL57	8,38	0,74	2	0
HEATR1	7,89	0,74	13	0
CHD4	8,74	0,74	35	0
PSMC2	8,24	0,74	9	0
RALY	8,81	0,74	10	0
GRWD1	9,09	0,73	17	0
POLRMT	8,70	0,73	25	0
UTP3	9,06	0,73	13	0
ASH2L	7,54	0,73	4	0
PSMD8	7,70	0,73	4	0
NOC2L	7,68	0,73	7	0
ZNF592	7,81	0,73	7	0
PWP1	8,21	0,71	6	0
ZNF280C	7,40	0,71	3	0
ERBB2IP	7,67	0,71	7	0
WDR3	7,44	0,71	5	0
NOP56	8,69	0,71	19	0
TOPORS	7,46	0,70	4	0
PELP1	7,90	0,70	8	0
NTN1	8,04	0,70	10	0
SLC25A1	8,19	0,70	6	0
RFC4	8,09	0,68	9	0
ZNF275	7,42	0,67	4	0
NFIC	8,33	0,67	7	0
ZNHIT6	7,95	0,67	6	0
CDK11B;CDC2L1;CDK11A	8,22	0,67	5	0
POP1	10,05	0,66	51	0
FBL	8,81	0,66	11	0
HDAC1	8,26	0,66	4	0
RAD18	7,55	0,66	4	0
NKTR	8,74	0,66	7	0
KLF2	8,46	0,66	7	0
PSMC6	8,01	0,66	6	0
C9orf114	8,81	0,65	14	0
DAXX	8,62	0,65	13	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MRPS34	7,69	0,65	5	0
POLR1E	9,31	0,64	19	0
TUBA1A	8,22	0,64	1	0
PSMD2	8,33	0,64	11	0
ZNF668	7,95	0,63	5	0
MTG2	7,44	0,63	3	0
GTF3C3	7,58	0,62	10	0
UTP20	7,80	0,62	7	0
NOL11	7,76	0,62	7	0
KRI1	7,84	0,61	6	0
POLR1A	7,21	0,61	6	0
HCFC1	8,29	0,61	6	0
UBTF	8,17	0,60	7	0
MYO1B	8,39	0,60	21	0
SP3	8,77	0,59	8	0
PNO1	8,29	0,59	10	0
EPRS	8,09	0,59	5	0
BAZ2A	7,97	0,59	5	0
MRPS27	7,76	0,59	4	0
CHD7	7,40	0,59	4	0
MUS81	8,26	0,59	11	0
FAM210A	7,35	0,58	2	0
RCL1	7,70	0,58	5	0
AATF	7,86	0,58	11	0
COPB2	7,82	0,58	6	0
DDX49	7,57	0,58	5	0
CHAF1A	7,19	0,58	3	0
PDS5A	7,35	0,57	4	0
KDM2A	7,40	0,57	6	0
EXOSC9	7,44	0,57	2	0
SNRNP200	9,08	0,57	51	0
NSA2	9,31	0,56	9	0
TUBA1B	10,02	0,56	22	0
EPB41L4B	9,28	0,56	18	0
FTSJ3	10,28	0,55	40	0
MRPL19	7,36	0,55	3	0
BOP1	8,91	0,55	18	0
PSMD11	8,24	0,55	9	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
CDK5RAP1	7,40	0,55	5	0
LRPPRC	9,15	0,55	43	0
SUPT5H	8,06	0,55	9	0
SCRIB	8,10	0,54	9	0
FOSL1	7,91	0,54	2	0
SUPT16H	8,30	0,53	16	0
NCAPG	6,91	0,53	3	0
MRPL21	7,27	0,53	2	0
WDR43	8,05	0,53	11	0
ZNF316	8,52	0,53	11	0
TUBB	9,41	0,53	6	0
HIST2H2BE;HIST1H2BB;HIST1H2BO;HIST1H2BJ	9,50	0,53	2	0
UBR5	7,58	0,52	9	0
FARP2	8,07	0,52	7	0
POP4	8,33	0,52	5	0
	8,37	0,52	8	0
TUBB6	7,94	0,51	6	0
CD3EAP	8,62	0,51	5	0
MRPS30	7,57	0,51	2	0
FRMD6	8,47	0,50	13	0
AIMP2	7,56	0,50	2	0
DNAJC10	8,48	0,50	13	0
RACGAP1	7,38	0,50	2	0
PRDM15	7,81	0,50	7	0
PLEKHG3	8,21	0,50	10	0
ZBTB7A	8,00	0,49	6	0
DPM1	8,13	0,49	6	0
UTP15	8,44	0,49	13	0
RRS1	8,86	0,49	15	0
SMARCA5	8,57	0,49	19	0
OSBPL8	7,36	0,49	4	0
GNL3	10,50	0,48	40	0
FAR1	7,27	0,48	2	0
FMNL3	8,55	0,48	17	0
WDR55	8,18	0,47	9	0
C18orf21	9,12	0,47	8	0
SP140	7,96	0,47	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TPX2	7,68	0,47	5	0
POLR1B	7,19	0,47	5	0
DHX8	9,14	0,47	30	0
FAM111A	8,19	0,46	9	0
COPA	8,34	0,46	16	0
HNRNPU	9,44	0,46	19	0
C11orf98	9,39	0,46	4	0
BIRC5	7,59	0,46	2	0
FAM208A	7,18	0,46	4	0
USP42	9,00	0,45	16	0
NDUFA9	8,23	0,45	10	0
DDX50	9,26	0,45	25	0
MRPL2	7,75	0,45	4	0
CEBPZ	8,59	0,44	18	0
PSMC4	8,25	0,44	9	0
hCG_1984214;MRPS17	8,34	0,44	4	0
BBX	6,82	0,44	2	0
SRFBP1	9,00	0,44	11	0
ZNF326	7,31	0,44	3	0
TUBB4B	9,96	0,44	22	0
FCF1	9,76	0,44	10	0
UTP23	9,33	0,44	10	0
PRPF8	9,08	0,44	42	0
ZBTB24	8,20	0,43	7	0
ZNF512	9,27	0,43	19	0
ATF1	9,10	0,43	4	0
DDX47	8,51	0,43	13	0
ZNF646	8,44	0,43	16	0
PAK1IP1	9,54	0,43	21	0
RPL24	10,00	0,42	15	0
WHSC1	8,60	0,42	20	0
AURKB	8,11	0,42	8	0
ERCC3	7,15	0,42	3	0
RPL7	9,22	0,42	11	0
SMARCC1	7,74	0,42	5	0
PSMD4	7,84	0,42	3	0
MCAT	7,17	0,42	2	0
GTF3C2	7,79	0,41	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
DNAJA3	8,25	0,41	7	0
DNAJB12	7,66	0,41	4	0
RFC2	7,93	0,40	5	0
PSMD7	8,01	0,40	4	0
EMG1	8,36	0,40	8	0
RPS27L	8,80	0,40	4	0
RBM19	7,13	0,40	2	0
SON	10,50	0,40	41	0
MRPL27	8,23	0,40	4	0
DAP3	8,74	0,40	12	0
PSMB5	7,69	0,40	4	0
ZMYM3	7,42	0,39	3	0
NOA1	7,50	0,39	5	0
HSPA8	10,07	0,38	30	0
RPL4	9,29	0,38	17	0
DDX28	9,67	0,38	27	0
PSMC3	8,15	0,38	10	0
ZNF148	8,11	0,37	6	0
DDB1	8,80	0,37	29	0
MRPL38	8,03	0,37	5	0
USP46;USP12	7,13	0,36	3	0
PTRH1	8,60	0,36	9	0
MRPL48	7,78	0,36	3	0
NO66	9,42	0,36	23	0
DCAF13	8,79	0,36	15	0
FARP1	8,10	0,36	9	0
MRPL37	7,41	0,36	3	0
MATR3	9,25	0,36	26	0
DHX30	7,66	0,35	8	0
DDX21	9,72	0,35	46	0
WDR18	7,89	0,35	8	0
MRPL44	7,50	0,34	5	0
MBD1	8,01	0,34	6	0
FYTTD1	8,51	0,34	6	0
CDC5L	10,13	0,34	35	0
RBM28	8,11	0,33	6	0
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B--991	8,12	0,33	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PSMB2	7,72	0,33	2	0
NRDE2	7,99	0,33	7	0
DPF2	7,99	0,33	6	0
SCAF1	8,70	0,33	11	0
C2orf47	7,68	0,32	3	0
AIFM1	8,07	0,32	8	0
SLC25A5	9,58	0,32	13	0
CTCF	9,73	0,32	28	0
RFC5	7,94	0,32	9	0
RSL24D1	8,68	0,31	4	0
NSUN5	8,66	0,31	16	0
LPCAT1	7,48	0,31	4	0
KIF23	7,75	0,31	5	0
DDX52	8,34	0,31	16	0
REST	8,20	0,31	10	0
RPP38	7,63	0,31	4	0
HIRA	7,53	0,30	8	0
SLIRP	8,41	0,30	4	0
EIF2B4	7,64	0,30	4	0
POGZ	7,76	0,30	6	0
PINX1	8,26	0,30	8	0
IQGAP3	7,23	0,30	4	0
POLDIP2	7,59	0,30	7	0
MRPL15	9,61	0,29	23	0
EFTUD2	8,95	0,28	26	0
SGPL1	9,14	0,28	15	0
EMD	8,16	0,28	6	0
MRPL23	8,19	0,28	4	0
RPL14	8,78	0,28	4	0
MTPAP	8,58	0,27	10	0
HNRNPUL2;HNRNPUL2-BSCL2	8,98	0,27	23	0
TUBB2B	8,19	0,27	5	0
TRMT2A	7,83	0,27	8	0
ABT1	8,21	0,27	10	0
RPS28	8,49	0,27	3	0
SPHK2	7,66	0,27	6	0
ZNF697	7,78	0,26	4	0
MRPS7	8,77	0,26	10	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PPP2R2A;PPP2R2D	8,13	0,26	6	0
EXOSC3	7,58	0,26	4	0
NUP155	7,62	0,26	7	0
SMARCD2	7,36	0,26	3	0
MRPS5	7,97	0,26	7	0
HIST1H2BL	10,63	0,26	7	0
DDX54	10,15	0,25	48	0
NUP205	7,73	0,25	9	0
AGO2;AGO3	7,35	0,25	4	0
TUBB4A	7,44	0,25	1	0
MGEA5	7,41	0,25	3	0
DDX46	8,88	0,25	24	0
CLK1	8,58	0,25	12	0
PRPF4B	9,48	0,24	25	0
INTS3	6,93	0,24	2	0
SP110	8,74	0,24	14	0
GTPBP4	8,22	0,24	11	0
PDCD2L	7,93	0,24	2	0
MRM1	8,85	0,24	11	0
H2AFV;H2AFZ	9,21	0,24	3	0
GTPBP10	7,94	0,23	4	0
MRPL24	7,97	0,23	6	0
REXO4	8,43	0,23	10	0
LARP7	7,96	0,22	7	0
RBM27	9,19	0,22	11	0
PWP2	7,38	0,22	4	0
RPL18A	9,39	0,22	13	0
MINA	9,41	0,22	17	0
ASPH	7,85	0,21	8	0
GTF2B	8,40	0,21	7	0
PSMA2	7,93	0,21	4	0
CENPV	8,85	0,21	9	0
TBL2	7,55	0,21	3	0
PSMB3	7,79	0,21	3	0
TFB2M	7,69	0,21	4	0
ERAL1	8,50	0,21	8	0
DNTTIP1	7,62	0,20	6	0
SH3BP4	7,36	0,20	5	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HIST2H2AC;HIST2H2AA3;HIST1H2AJ;HIST1H2AH;H2AFJ;HIST1H2AD;HIST1H2AG	10,60	0,20	5	0
MRPL40	7,98	0,20	4	0
DUSP11	8,66	0,20	11	0
SURF6	9,79	0,19	18	0
PATZ1	8,04	0,19	2	0
FAM83H	8,23	0,19	14	0
ZFP64	8,32	0,19	8	0
RPL6	9,49	0,19	16	0
DIMT1	10,47	0,19	25	0
RRP1	9,08	0,18	11	0
DDX55	8,86	0,18	18	0
WDR12	8,32	0,18	7	0
COPG1	7,54	0,18	6	0
LSG1	7,95	0,18	9	0
GNL3L	8,48	0,18	12	0
SRP9	8,79	0,17	5	0
MRPS14	8,24	0,17	2	0
NOG	7,95	0,17	3	0
AP2M1	7,75	0,17	3	0
RNPS1	8,08	0,17	3	0
SNRPB2	8,78	0,17	5	0
PLCD3	9,64	0,16	33	0
TRIP12	7,98	0,16	19	0
HNRNPF	8,88	0,16	9	0
SLC25A11	7,63	0,16	7	0
RPUSD3	8,41	0,16	10	0
CDCA2	7,06	0,15	3	0
RPL8	10,38	0,15	25	0
NUP93	8,02	0,15	10	0
BYSL	7,47	0,15	2	0
ZNF512B	7,26	0,15	2	0
LUC7L3	9,41	0,15	20	0
RPL7A	9,58	0,15	14	0
MTA2	7,61	0,15	5	0
PSMA6	8,16	0,15	8	0
FNDC3B	8,15	0,15	11	0
RPL10A	8,96	0,15	8	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NPM1	9,73	0,15	11	0
DHRS2	9,46	0,15	12	0
TJP1	7,33	0,14	4	0
MRPS15	8,27	0,14	5	0
GTF2H4	7,16	0,14	3	0
SAGE1	7,46	0,14	2	0
MRPL47	8,22	0,14	6	0
RPL13A;RPL13a	9,32	0,14	8	0
ESYT1	7,92	0,14	10	0
FLII	7,18	0,13	5	0
TEFM	8,18	0,13	7	0
KPNA2	8,60	0,13	11	0
RPS21	8,02	0,13	2	0
PARS2	7,27	0,12	2	0
TFB1M	9,54	0,12	21	0
RPL7L1	9,38	0,12	13	0
PPP2CA	8,10	0,12	4	0
CLK3	8,79	0,12	10	0
NUP62	7,48	0,12	2	0
SMARCA1	7,61	0,12	4	0
RPL3	9,69	0,11	21	0
MRPS23	8,54	0,11	8	0
HP1BP3	9,58	0,11	20	0
MRPL17	7,81	0,11	5	0
C8orf33	7,77	0,11	2	0
RPL27	9,81	0,11	9	0
ARHGEF2	7,72	0,11	5	0
MRPS18B	8,25	0,11	6	0
C11orf31;SELH	7,97	0,10	3	0
GTF3C4	7,61	0,10	4	0
STK10	8,02	0,10	4	0
ZSCAN26;ZNF187	8,09	0,10	9	0
SKIV2L2	8,53	0,10	24	0
MCM5	8,29	0,10	10	0
CRNKL1	7,82	0,09	6	0
MRPS11	8,24	0,09	6	0
CENPVL3	9,14	0,09	15	0
MRPL41	8,36	0,09	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MSH6	7,83	0,09	8	0
VRK2	7,65	0,09	3	0
DDX41	9,72	0,08	37	0
PSMA3	7,76	0,08	2	0
PPP2R1A	8,55	0,08	14	0
MRPS9	8,57	0,08	10	0
FBXW7	7,39	0,08	3	0
LGALS3BP	7,58	0,08	2	0
SP140	9,05	0,08	30	0
MYO1C	8,40	0,07	17	0
SNRPF	7,79	0,07	2	0
MRPL4	8,47	0,07	9	0
ATP5C1	8,52	0,07	9	0
PAF1	7,70	0,06	5	0
DPY30	7,96	0,06	2	0
RBM42	8,31	0,06	5	0
KIF22	7,34	0,06	3	0
MRPL50	8,40	0,06	5	0
MTHFD1L	8,03	0,06	9	0
DKC1	7,92	0,05	5	0
NUP188	7,24	0,05	3	0
UBN1	7,37	0,05	3	0
PRKDC	8,82	0,05	51	0
ZCCHC17	10,07	0,05	14	0
SART1	8,61	0,05	14	0
HIST1H4A	10,31	0,05	13	0
NPM3	8,09	0,04	4	0
H2AFY	9,38	0,04	17	0
NSD1	8,26	0,04	8	0
RPL34	9,33	0,04	7	0
NKAP	8,57	0,04	7	0
PUS1	7,36	0,04	3	0
PRPF6	7,88	0,04	11	0
RPL12	8,64	0,03	4	0
ZFX;ZFY	8,70	0,03	9	0
UBR4	7,20	0,03	6	0
CBX3	8,42	0,03	6	0
UTP14A	8,67	0,03	20	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
IK	7,70	0,02	4	0
DYNLL1;DYNLL2	8,97	0,02	4	0
MRPL30	8,23	0,02	3	0
SNRNP40	8,15	0,02	4	0
RPLP0;RPLP0P6	8,86	0,02	10	0
UTP18	7,89	0,02	8	0
PHF20L1	9,15	0,02	16	0
HSPA1B;HSPA1A	9,28	0,02	23	0
DHX15	8,93	0,02	29	0
SPEN	7,29	0,02	2	0
RPS16;ZNF90	9,26	0,02	9	0
SRSF11	9,58	0,02	11	0
ZNF787	7,64	0,02	3	0
YME1L1	7,64	0,02	4	0
RECQL4	7,15	0,01	3	0
METTL8	7,95	0,01	3	0
MRPL39	7,49	0,01	3	0
NDUFAF7	7,30	0,01	3	0
ZBTB38	7,98	0,01	7	0
NAT10	8,84	0,01	34	0
FLYWCH1	8,19	0,01	8	0
DDX5	9,99	0,01	33	0
NOP9	7,27	0,01	4	0
MRPS2	8,51	0,01	8	0
AQR	7,87	0,00	5	0
SREK1	9,58	0,00	18	0
ZKSCAN1	7,81	0,00	4	0
EPB41L1	7,35	0,00	2	0
ZNF319	8,14	0,00	4	0
PRPF19	8,79	0,00	12	0
CCDC86	9,83	-0,01	19	0
RPL35A	8,78	-0,01	4	0
CYC1	7,72	-0,01	4	0
PAXBP1	7,31	-0,01	2	0
CCNB1	7,22	-0,01	2	0
HNRNPLL;HNRPLL	7,70	-0,01	3	0
THOC2	7,40	-0,01	3	0
FOXK1	7,25	-0,01	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PTRF	8,12	-0,01	5	0
HSD17B10	9,92	-0,01	14	0
HDAC2	7,55	-0,01	3	0
SP1	8,06	-0,01	3	0
RSL1D1	10,42	-0,02	37	0
RPL18	9,00	-0,02	6	0
MRPS12	8,05	-0,02	3	0
RPS5	9,09	-0,02	10	0
GTF2I	7,52	-0,02	2	0
SMC1A	7,29	-0,02	4	0
RPL15	8,77	-0,02	9	0
ZNF451	7,78	-0,03	4	0
KPNA3	7,85	-0,03	3	0
NOL10	7,79	-0,03	7	0
PSMA1	8,11	-0,03	5	0
ZNF444	8,64	-0,04	12	0
RPL9	9,03	-0,04	10	0
RPL32	9,58	-0,04	7	0
TCOF1	10,41	-0,04	25	0
TAF3	8,73	-0,04	6	0
MRPS28	8,35	-0,04	7	0
TRMT10C	9,99	-0,05	24	0
IFI16	7,94	-0,05	9	0
RPL17;RPL17-C18orf32	10,99	-0,05	18	0
TIMM44	7,79	-0,06	4	0
DDX27	9,24	-0,06	28	0
VEZF1	9,08	-0,06	13	0
UPF3A	7,43	-0,06	2	0
EIF3B	8,52	-0,06	11	0
APOBEC3B	8,26	-0,06	7	0
UTP11L	8,98	-0,06	9	0
MRPL11	7,65	-0,06	2	0
KLF5	7,76	-0,07	2	0
ADAR	8,24	-0,07	13	0
ACIN1	8,24	-0,07	6	0
LMNB1	9,13	-0,07	29	0
SFRP1	8,12	-0,07	6	0
CSNK2A2	7,58	-0,08	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
H2AFY2	7,91	-0,08	4	0
MRPL9	9,56	-0,08	12	0
U2AF1	10,68	-0,08	13	0
FDFT1	7,23	-0,08	3	0
DDX56	9,24	-0,08	26	0
ZFP64	7,38	-0,08	2	0
ZNF652	8,05	-0,09	4	0
RPS15	9,93	-0,09	7	0
IPO4	7,40	-0,09	6	0
ZBTB4	7,60	-0,09	3	0
CDK1;CDC2	8,17	-0,09	4	0
HNRNPM	9,22	-0,09	24	0
TAOK2	8,40	-0,09	9	0
C11orf57	8,56	-0,10	4	0
SNX18	8,15	-0,10	4	0
SNIP1	9,05	-0,10	15	0
PSMA7	8,36	-0,10	7	0
DDX23	7,83	-0,10	7	0
PLRG1	8,39	-0,10	10	0
RPL31	10,41	-0,10	14	0
RPF1	8,84	-0,10	13	0
HIST2H3A;HIST1H3A; HIST3H3	9,96	-0,10	4	0
NIFK	10,77	-0,11	27	0
RPL19	9,91	-0,11	13	0
NXF1	8,02	-0,11	8	0
MAFG	8,20	-0,11	3	0
RRP7A	8,98	-0,11	10	0
SNRPA1	9,22	-0,11	13	0
RBMX2	8,37	-0,11	8	0
RSBN1	8,69	-0,11	17	0
THOC6	7,40	-0,11	2	0
PUF60	10,18	-0,12	24	0
PSMA4	7,76	-0,12	3	0
EPB41	8,99	-0,12	16	0
LONP1	6,99	-0,13	3	0
CTSB	8,75	-0,13	5	0
METAP1	8,57	-0,13	11	0
RPL21	9,24	-0,13	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PRPF38A	8,24	-0,14	5	0
NHP2	7,91	-0,14	3	0
SLIT2	6,90	-0,14	2	0
DDX17	9,12	-0,14	17	0
SRCAP	7,30	-0,14	5	0
FXR2	7,60	-0,14	3	0
MRPL16	7,80	-0,14	4	0
TMA16	9,06	-0,14	9	0
NOL12	9,59	-0,15	12	0
SAP18	8,31	-0,15	6	0
TFAM	9,26	-0,15	9	0
MPG	7,10	-0,15	2	0
RBM12B	7,23	-0,15	3	0
FAM111B	8,71	-0,15	15	0
MRPL45	7,35	-0,15	2	0
ZNF524	7,57	-0,15	3	0
SRP68	9,98	-0,16	48	0
RPL13	9,71	-0,16	13	0
RPL5	9,41	-0,16	12	0
GPATCH1	7,73	-0,16	3	0
HSPA9	9,73	-0,16	31	0
SRPRB	7,99	-0,16	6	0
MAZ	8,66	-0,16	7	0
MEPCE	9,79	-0,16	31	0
MRPL22	9,31	-0,17	9	0
CPSF6	8,42	-0,17	5	0
SDF2	7,78	-0,17	3	0
PLEC	10,01	-0,17	182	0
SF3B2	8,28	-0,17	8	0
SRP19	8,67	-0,18	7	0
HNRNPH1	9,18	-0,18	12	0
NDUFA4	8,37	-0,18	4	0
C3	7,89	-0,18	2	0
NIFK	7,38	-0,19	2	0
SP140L	8,07	-0,19	5	0
CFAP20	8,03	-0,19	6	0
LRRC59	8,37	-0,19	7	0
RPS26;RPS26P11	10,71	-0,20	9	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
IARS	7,70	-0,20	4	0
CBX6	7,82	-0,20	2	0
SNRPD1	8,51	-0,20	4	0
RPS27A	9,67	-0,21	9	0
IQGAP1	8,98	-0,21	32	0
LARP4	8,10	-0,21	4	0
MRPL10	7,57	-0,21	3	0
SNRNP70	8,96	-0,21	14	0
SEC61A1	8,00	-0,22	3	0
PSMB1	7,99	-0,22	4	0
EPB41L5	9,94	-0,22	30	0
CPSF7	7,48	-0,22	5	0
PES1	9,20	-0,22	20	0
WDR46	8,91	-0,22	20	0
NOL7	9,19	-0,22	9	0
WDR48	7,29	-0,22	3	0
LANCL1	7,64	-0,23	2	0
MAFF	9,14	-0,23	6	0
EIF4A3	8,68	-0,23	9	0
RNMT	7,85	-0,23	6	0
BCCIP	7,50	-0,23	2	0
CT45A2;CT45A9;CT45A8	10,30	-0,23	11	0
PHGDH	8,23	-0,23	3	0
SNRPD2	8,57	-0,24	7	0
S100A13	9,18	-0,24	4	0
RPL30	9,49	-0,24	6	0
MRPL46	7,89	-0,24	5	0
XRCC5	8,74	-0,24	18	0
RPL11	9,72	-0,24	6	0
FGF5	7,76	-0,24	2	0
SAP30	7,44	-0,25	2	0
SMU1	8,18	-0,25	7	0
NUMA1	8,44	-0,25	26	0
CCDC47	7,73	-0,25	5	0
NUDT21	8,31	-0,26	5	0
RPL36	9,27	-0,26	5	0
DHX9	8,90	-0,26	26	0
CHD3	7,82	-0,26	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RBBP4	8,37	-0,26	5	0
TSR3	7,85	-0,27	4	0
ATP5O	8,86	-0,27	8	0
PSMA5	8,19	-0,27	5	0
INCENP	7,59	-0,27	5	0
ZNF335	7,45	-0,27	4	0
NRBP1	7,03	-0,27	2	0
TRMT112	8,70	-0,27	3	0
MTHFD2	8,71	-0,27	8	0
TOP1	8,98	-0,28	21	0
TAOK1	7,99	-0,28	5	0
PDIA5	7,98	-0,28	5	0
SMAD3;SMAD2	7,70	-0,28	3	0
MRE11A	7,29	-0,28	4	0
NOC3L	8,20	-0,29	6	0
RPS24	10,47	-0,29	11	0
DNAJB11	8,89	-0,29	10	0
RPS25	9,64	-0,29	4	0
RPS8	10,72	-0,29	20	0
RBM22	7,82	-0,29	4	0
NMT2	7,89	-0,29	4	0
SF3B6	8,14	-0,29	5	0
NMT1	8,62	-0,29	14	0
RPL23A	10,77	-0,30	21	0
TRA2B	8,51	-0,30	6	0
GLYR1	9,35	-0,30	20	0
MICU2	8,27	-0,30	5	0
CYR61	9,60	-0,30	22	0
HIST1H1C	11,08	-0,30	23	0
RBBP6	9,82	-0,30	15	0
PPP1CA	7,81	-0,30	3	0
NFKBIL1	7,13	-0,30	3	0
SRPK1	8,11	-0,31	7	0
CACTIN	8,17	-0,31	12	0
ZNF771	8,25	-0,31	6	0
PXDN	8,58	-0,31	24	0
LAMB3	7,81	-0,31	4	0
SREK1IP1	10,18	-0,31	7	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
U2AF2	10,86	-0,31	21	0
ZFR	7,98	-0,31	9	0
SFSWAP	8,38	-0,31	9	0
AURKC	7,12	-0,31	4	0
SF3B1	8,81	-0,32	19	0
NHP2L1	8,36	-0,32	4	0
SMOC1	8,19	-0,32	5	0
RPS13	10,61	-0,32	13	0
SEC24C	7,27	-0,32	3	0
FAM173A	7,09	-0,32	2	0
MRPL1	8,01	-0,33	6	0
RPL23	10,32	-0,33	13	0
TSR1	8,44	-0,33	13	0
RPS9	10,79	-0,33	23	0
TCERG1	7,74	-0,33	4	0
CPSF1	7,29	-0,33	5	0
DDX3X;DDX3Y	9,44	-0,33	31	0
SSBP1	7,89	-0,34	3	0
RRP36	8,11	-0,34	6	0
GCN1L1	7,68	-0,34	9	0
FHL2	8,51	-0,34	10	0
CTNND1	7,64	-0,34	5	0
CSTB	7,73	-0,35	2	0
UBA52;UBB;RPS27A;UBC	9,04	-0,35	2	0
MRPL36	7,52	-0,35	2	0
RBBP7	8,44	-0,35	7	0
KLF10	8,11	-0,36	4	0
MORF4L1	8,24	-0,36	6	0
PYCR1	8,18	-0,36	6	0
RRP1B	8,36	-0,36	10	0
RPL28	9,52	-0,37	12	0
SMCR7L	7,57	-0,37	2	0
RPS10;RPS10-NUDT3	9,00	-0,38	11	0
SRRM1	9,16	-0,38	12	0
MKI67	8,76	-0,38	22	0
RPS3A	10,95	-0,38	32	0
PPP1CC	7,85	-0,38	2	0
RPL10	10,06	-0,38	14	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
NKX2-5;NKX2-4;NKX2-1	7,55	-0,39	2	0
S100A16	9,26	-0,39	6	0
RPS6	10,88	-0,39	24	0
CCDC84	7,87	-0,39	3	0
SND1	8,30	-0,39	13	0
MTDH	7,88	-0,39	3	0
SNW1	8,14	-0,40	6	0
RBM8A	8,43	-0,40	7	0
EIF2B1	9,32	-0,40	14	0
COX7A2	7,86	-0,40	2	0
MFAP1	8,03	-0,40	5	0
MAFK	8,73	-0,41	7	0
RNMTL1	7,63	-0,41	4	0
SF3B3	8,74	-0,41	21	0
RPS11	10,80	-0,41	19	0
TAF8	8,55	-0,42	9	0
ZFP91;ZFP91-CNTF	9,12	-0,42	20	0
SRP14	9,33	-0,42	7	0
DDX6	7,84	-0,42	3	0
PTMS	8,45	-0,42	3	0
MEN1	7,45	-0,42	4	0
RSRC1	8,11	-0,42	4	0
RPS19	8,95	-0,43	8	0
CUL4A	7,36	-0,43	5	0
MRPL33	8,17	-0,43	2	0
ABCF1	8,03	-0,43	7	0
DDX42	7,52	-0,43	4	0
H1FX	10,09	-0,43	14	0
PPP1CB	8,70	-0,44	10	0
FOSL2	7,92	-0,44	3	0
RPS18	9,92	-0,44	14	0
SSSCA1	7,81	-0,44	4	0
HNRNPH2	7,82	-0,44	4	0
RPS12	8,96	-0,44	7	0
BAG3	7,81	-0,44	4	0
XRCC6	8,67	-0,44	19	0
MICU1	8,81	-0,45	11	0
SEH1L	7,58	-0,45	4	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RRP12	9,56	-0,45	28	0
PNN	8,53	-0,45	14	0
H1F0	10,60	-0,45	12	0
TAF10	8,08	-0,45	2	0
GZF1	7,33	-0,45	4	0
RPS15A	10,03	-0,45	10	0
FIZ1	7,92	-0,45	3	0
MAGOHB	8,26	-0,46	6	0
CTGF	7,86	-0,46	6	0
SLC25A3	8,17	-0,46	3	0
EIF3E	8,40	-0,47	13	0
RPS3	9,60	-0,47	19	0
PCMT1	9,18	-0,47	11	0
GNB2L1	8,93	-0,47	12	0
G3BP2	7,71	-0,47	3	0
BRD7	8,34	-0,47	10	0
NOP14	7,69	-0,47	6	0
WBSCR22	7,83	-0,47	2	0
FAM207A	8,89	-0,47	12	0
IMMT	7,94	-0,48	6	0
HPSE	7,76	-0,48	2	0
RPL29	10,14	-0,48	2	0
RPL22L1	8,74	-0,48	3	0
CLTC	9,14	-0,48	44	0
COA7	7,46	-0,48	2	0
SNRPE	8,20	-0,48	2	0
LUC7L2	10,33	-0,49	22	0
CGGBP1	7,45	-0,49	2	0
KPNA4	7,42	-0,49	3	0
PLAGL2	7,55	-0,49	4	0
SNRPN;SNRPB	8,18	-0,49	3	0
RPL22	9,02	-0,50	4	0
LMNA	9,29	-0,50	32	0
RPS14	10,16	-0,50	8	0
TECR	7,42	-0,50	2	0
SRP72	9,92	-0,50	30	0
SIRT7	8,73	-0,51	15	0
BUD31	7,58	-0,51	2	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
CCAR2	7,84	-0,51	6	0
ARGLU1	10,09	-0,51	11	0
KLF13	8,34	-0,51	5	0
TARDBP	8,05	-0,51	2	0
HNRNPL	8,99	-0,51	14	0
EIF3F	8,04	-0,51	4	0
MED19	8,15	-0,51	4	0
EIF3I	8,23	-0,52	5	0
CXorf56	8,01	-0,52	5	0
SF1	8,49	-0,53	7	0
XPO1	7,54	-0,53	6	0
SCAF8	7,99	-0,53	8	0
PRPF31	8,03	-0,53	5	0
FXR1	8,53	-0,54	7	0
C8orf82	7,55	-0,54	4	0
RPL27A	10,49	-0,54	10	0
SKP1	8,61	-0,54	8	0
PLBD2	7,56	-0,54	4	0
PRPF40A	8,71	-0,54	10	0
MCM3	8,37	-0,54	16	0
NCL	9,27	-0,54	20	0
NDUFS3	7,16	-0,55	5	0
RPS20	9,34	-0,55	4	0
TGM2	9,35	-0,55	20	0
INO80B;INO80B-WBP1	8,04	-0,55	1	0
SNRPD3	8,68	-0,55	4	0
IPO7	7,83	-0,55	8	0
STAU1	7,72	-0,55	5	0
PHF6	8,92	-0,55	12	0
09. Sep	7,67	-0,55	5	0
DDX18	9,61	-0,55	30	0
LAMTOR1	7,41	-0,55	2	0
RPSA	9,31	-0,55	12	0
VIM	10,21	-0,56	46	0
HSPA5	9,68	-0,56	26	0
NOMO1;NOMO3;NOMO2	7,38	-0,56	3	0
USP39	7,88	-0,56	6	0
TUFM	9,11	-0,56	17	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
TRA2A	7,89	-0,57	2	0
GTF3A	8,58	-0,57	11	0
RPL39P5;RPL39	10,73	-0,57	3	0
PPIH	8,08	-0,57	4	0
SNX8	7,28	-0,58	3	0
HBS1L	7,77	-0,58	4	0
QARS	7,49	-0,58	4	0
EPB41L2	9,12	-0,58	23	0
LUC7L	9,94	-0,59	10	0
MAGED2	8,55	-0,59	12	0
PRPF4	8,66	-0,59	14	0
SPCS2	7,53	-0,59	2	0
PIP	7,36	-0,59	3	0
ZNF593	9,40	-0,59	7	0
SRSF10	8,32	-0,60	5	0
CLPX	7,56	-0,60	4	0
HSDL2	7,08	-0,60	2	0
SNRPC	7,96	-0,60	3	0
GNL2	9,15	-0,60	19	0
ERH	8,70	-0,60	3	0
EIF3G	7,91	-0,61	3	0
MACF1	7,54	-0,61	4	0
FBXL6	8,41	-0,61	10	0
PDHB	7,45	-0,61	2	0
DDX54	8,65	-0,61	2	0
PRPF38B	7,71	-0,61	5	0
WBP11	9,33	-0,62	9	0
ACSL3	7,70	-0,62	6	0
U2SURP	9,99	-0,62	27	0
FHL3	7,64	-0,62	3	0
KDM4D	7,07	-0,62	3	0
WDR83	7,76	-0,63	4	0
ABCF2	7,69	-0,63	2	0
NSUN2	8,59	-0,63	14	0
RPL37	9,09	-0,63	6	0
NF2	8,75	-0,63	17	0
TRIM28	8,30	-0,63	11	0
CAPZB	8,14	-0,64	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
RBM14	8,54	-0,64	11	0
PTRH2	7,61	-0,64	3	0
MDK	9,17	-0,65	7	0
PELO	7,64	-0,65	3	0
PPIG	8,27	-0,65	7	0
FIP1L1	8,39	-0,65	5	0
RBM23	7,54	-0,65	2	0
RBM14	7,37	-0,65	2	0
PSPC1	7,43	-0,65	2	0
MRPL28	7,33	-0,65	3	0
HNRNPC	9,09	-0,66	16	0
CCDC137	8,97	-0,66	11	0
GLTSCR2	9,41	-0,66	14	0
RPS4X	10,76	-0,67	23	0
PLEKHO1	8,31	-0,67	10	0
MMTAG2	9,47	-0,68	19	0
NAP1L1	8,82	-0,68	5	0
PSIP1	7,72	-0,68	4	0
STRAP	7,92	-0,68	5	0
DNAJC9	8,79	-0,69	10	0
ACP1	7,78	-0,69	3	0
TMPO	7,90	-0,69	4	0
DLST	8,28	-0,69	7	0
DNAJC7	7,57	-0,69	3	0
TAF2	8,51	-0,69	3	0
SRRM2	9,34	-0,69	22	0
ING5	8,26	-0,69	3	0
RCC1	8,22	-0,69	5	0
FLNB	8,44	-0,69	22	0
NDUFB9	7,52	-0,69	2	0
RPS7	10,65	-0,70	22	0
AGPS	7,92	-0,70	7	0
DSC1	7,80	-0,70	2	0
FARSA	7,06	-0,70	2	0
RPL36AL	9,21	-0,70	2	0
MALSU1	7,70	-0,70	2	0
ADRM1	7,58	-0,70	3	0
SDAD1	8,88	-0,70	15	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
AP2A1	7,49	-0,70	4	0
TCP1	8,71	-0,71	12	0
LRRC47	7,55	-0,71	3	0
RPS2	9,65	-0,71	15	0
CHERP	8,69	-0,71	12	0
PHF5A	7,78	-0,71	2	0
BUB3	8,09	-0,71	7	0
TAF2	9,52	-0,72	39	0
ALDH18A1	7,87	-0,72	6	0
NSUN4	8,53	-0,72	8	0
EIF3C;EIF3CL	8,09	-0,73	5	0
SDF2L1	8,21	-0,73	6	0
SPTBN1	8,22	-0,73	11	0
SFXN1	7,84	-0,73	3	0
SAFB	7,90	-0,73	4	0
RARS	7,75	-0,74	5	0
KLF12	7,99	-0,74	3	0
RP9	9,60	-0,74	11	0
ATL3	7,57	-0,75	3	0
YLPM1	7,11	-0,75	3	0
KHDRBS1	8,13	-0,75	5	0
SEC22B	8,34	-0,75	5	0
PRDX4	8,25	-0,75	7	0
ASF1A	8,38	-0,76	6	0
RPS23	10,62	-0,76	9	0
LAMP2	7,35	-0,76	2	0
RBM25	8,92	-0,76	14	0
PRPF3	8,50	-0,77	8	0
NES	8,93	-0,78	23	0
GLUD1;GLUD2	7,88	-0,78	3	0
CSTF2;CSTF2T	7,57	-0,78	2	0
RPL38	8,72	-0,78	3	0
HIST1H1A	10,17	-0,78	11	0
CMAS	8,35	-0,78	6	0
RPLP2	8,79	-0,79	5	0
MAP1B	7,70	-0,79	3	0
NOP16	8,72	-0,79	8	0
HMGA1	7,93	-0,79	1	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
PFDN6	7,39	-0,79	2	0
MAPK1	7,76	-0,80	5	0
GLYR1	8,65	-0,80	2	0
FLNC	9,10	-0,80	40	0
SRSF3	8,67	-0,80	3	0
CPOX	7,80	-0,80	3	0
ATP5A1	8,98	-0,81	17	0
RSBN1L	9,18	-0,81	22	0
PCBP1	9,79	-0,81	16	0
RCC2	8,38	-0,81	9	0
EEF1A1;EEF1A1P5	10,06	-0,82	15	0
RPS17	10,48	-0,82	12	0
SCAF4	9,19	-0,82	13	0
CIR1	8,46	-0,83	8	0
SP2	8,26	-0,84	2	0
SMARCC2	7,27	-0,84	2	0
CXorf67	8,61	-0,84	10	0
MCM7	8,02	-0,84	5	0
GFPT1	8,03	-0,84	8	0
PHB2	8,77	-0,84	10	0
ARG1	7,64	-0,85	4	0
SFPQ	8,96	-0,85	13	0
SF3B5	7,86	-0,86	4	0
CCT2	8,55	-0,86	18	0
CTNNA1	7,80	-0,87	3	0
KIF2A	8,69	-0,87	15	0
PPM1G	7,58	-0,87	3	0
CCT6A	8,40	-0,87	10	0
SERBP1	8,58	-0,88	6	0
SRSF7	8,70	-0,88	5	0
NUDC	8,12	-0,88	5	0
SLC3A2	8,50	-0,89	10	0
C1QBP	8,49	-0,89	5	0
ILF2	8,54	-0,89	10	0
RPL36A;RPL36A-HNRNPH2	10,06	-0,89	6	0
RBM17	7,55	-0,90	2	0
PCBP2	8,73	-0,90	6	0
RPL35	10,94	-0,91	15	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
ACTR1A	7,35	-0,91	1	0
PRMT1	7,84	-0,91	3	0
MAT2A	7,86	-0,91	3	0
NUMB	7,71	-0,92	2	0
CHAF1B	7,35	-0,92	3	0
ALDH1B1	7,54	-0,92	2	0
GPR125	8,58	-0,92	5	0
CCT4	8,38	-0,92	8	0
CHP1	7,74	-0,92	3	0
TBC1D10B	7,48	-0,93	2	0
CCT8	8,64	-0,93	19	0
BRD9	8,45	-0,94	9	0
NACA	8,44	-0,94	4	0
MYH9	9,09	-0,95	41	0
TRIM21	11,08	-0,95	43	0
RCN2	8,52	-0,96	9	0
ZNF579	8,91	-0,96	11	0
PMPCB	7,45	-0,97	2	0
TXN	8,41	-0,97	5	0
UMPS	7,39	-0,98	3	0
RPL26	10,55	-0,98	16	0
RBM39	10,45	-0,98	31	0
RPL37A	9,86	-0,98	7	0
HNRNPDL	8,28	-0,99	4	0
THRAP3	8,56	-0,99	11	0
CTSD	7,39	-0,99	2	0
BCLAF1	8,44	-0,99	6	0
RBM3	7,85	-1,00	2	0
HNRNPA3	8,91	-1,01	11	0
VANGL1	7,39	-1,01	2	0
AHSA1	7,48	-1,01	2	0
STOML2	8,09	-1,01	5	0
AP2B1	7,74	-1,01	5	0
HDGF	7,97	-1,02	5	0
CWC25	9,12	-1,02	13	0
C5orf30	7,55	-1,03	2	0
ALYREF	8,74	-1,03	7	0
RRBP1	8,14	-1,03	6	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HK1	8,34	-1,04	13	0
EIF5B	7,74	-1,04	6	0
TNPO1	7,63	-1,05	3	0
EIF4E	7,89	-1,05	2	0
EIF2S2	8,20	-1,06	5	0
EIF3D	8,19	-1,06	3	0
PTBP1	8,39	-1,06	7	0
MAGEA4	8,90	-1,06	10	0
G3BP1	8,07	-1,06	4	0
XRN2	7,86	-1,06	7	0
TSPYL5	9,09	-1,07	14	0
MCM4	7,90	-1,07	6	0
CCT3	8,68	-1,07	12	0
KPNB1	8,40	-1,09	7	0
LLPH	8,71	-1,09	3	0
GRN	8,03	-1,09	3	0
EIF3A	8,03	-1,09	9	0
ELAVL1	8,36	-1,09	6	0
S100A7;S100A7A	8,07	-1,10	3	0
HIST1H1E;HIST1H1D	9,95	-1,11	3	0
SRSF6	8,39	-1,12	3	0
SF3A3	7,99	-1,12	4	0
EIF4G1	7,80	-1,12	4	0
DDX1	8,30	-1,13	11	0
NONO	8,31	-1,13	6	0
HNRNPK	9,11	-1,14	14	0
DBN1	8,27	-1,15	6	0
FAM133B	8,39	-1,15	3	0
LMNB2	7,99	-1,15	7	0
DCD	8,65	-1,16	5	0
ARF4	7,51	-1,16	1	0
HNRNPR	8,45	-1,16	11	0
RAC1	7,74	-1,17	2	0
CACYBP	7,67	-1,17	2	0
HSD17B4	7,85	-1,17	3	0
PAICS	8,29	-1,17	8	0
RTCB	8,24	-1,19	6	0
S100A9	8,33	-1,19	3	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
MYL12A;MYL12B	8,07	-1,20	3	0
SSR4	7,98	-1,21	2	0
FRG1	9,28	-1,21	14	0
DDX39A	8,60	-1,22	5	0
EIF2S1	8,19	-1,23	7	0
YTHDF2	7,77	-1,23	3	0
YBX3	9,80	-1,23	17	0
CDC42	8,30	-1,24	5	0
ACTB	10,31	-1,25	19	0
ATP5F1	7,78	-1,25	3	0
IPO5	7,57	-1,25	3	0
ERI1	8,18	-1,25	7	0
NOLC1	8,40	-1,26	5	0
HNRNPA0	8,26	-1,26	7	0
PRDX1	9,22	-1,27	13	0
FAU	10,48	-1,27	5	0
YBX1	10,52	-1,27	22	0
C14orf166	8,09	-1,27	8	0
AP1B1	7,10	-1,27	2	0
MYL6	8,50	-1,27	5	0
HACD3	7,73	-1,27	3	0
PRDX5	8,01	-1,27	3	0
SRRT	7,88	-1,27	4	0
CAPZA1	8,31	-1,28	6	0
ARL6IP4	8,42	-1,28	4	0
RBM5	7,28	-1,29	2	0
KIAA1522	8,40	-1,29	5	0
URB1	7,14	-1,30	3	0
COX4I1	7,94	-1,30	2	0
CTPS1	7,84	-1,31	5	0
PSME3	7,44	-1,32	1	0
CCT5	8,05	-1,33	7	0
EIF3L	8,08	-1,33	6	0
EEF1G	8,72	-1,33	9	0
CSE1L	7,99	-1,34	7	0
DSP	7,94	-1,34	6	0
SYNCRIP	8,41	-1,34	7	0
LBR	9,03	-1,35	7	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
SF3A1	8,09	-1,35	6	0
RBMX	8,69	-1,35	10	0
FLNA	9,57	-1,36	79	0
PRR11	8,62	-1,36	4	0
FASN	8,87	-1,37	36	0
EIF1;EIF1B	7,64	-1,39	4	0
BCAR3	8,36	-1,41	9	0
TWISTNB	7,12	-1,42	3	0
COX5A	8,02	-1,42	3	0
RAP1B;RAP1A	7,43	-1,43	3	0
LSM14B	8,48	-1,43	6	0
YWHAQ	8,09	-1,45	3	0
HSPD1	9,46	-1,45	27	0
RPS29	8,71	-1,45	2	0
SSR1	7,40	-1,46	1	0
EIF2S3;EIF2S3L	8,41	-1,47	8	0
EIF5A	8,59	-1,47	5	0
HSPH1	8,09	-1,48	9	0
CISD2	7,35	-1,49	2	0
MAPRE1	7,81	-1,49	2	0
ANXA2;ANXA2P2	9,57	-1,49	20	0
EIF3M	7,71	-1,50	2	0
SET;SETSIP	8,28	-1,51	4	0
IDH3A	7,78	-1,51	3	0
ALDH3A2	7,22	-1,52	3	0
GLS	7,76	-1,52	3	0
ATP1A1	8,23	-1,53	8	0
CALM2;CALM1;CALM3	8,46	-1,53	3	0
CSTA	7,92	-1,53	4	0
CCT7	8,29	-1,58	8	0
GNB2	8,12	-1,58	3	0
SRSF1	8,39	-1,59	6	0
ATP2A2	7,72	-1,60	4	0
ITGB1	8,26	-1,62	2	0
DDOST	7,76	-1,62	2	0
BCAR1	9,77	-1,64	30	0
EIF4A1	8,63	-1,65	8	0
KLF16	8,78	-1,65	10	0

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
HSP90AB1	9,66	-1,66	22	0
CORO1C	7,80	-1,67	3	0
HNRNPA1;HNRNPA1L2	9,27	-1,68	12	0
PRDX2	7,93	-1,68	3	0
ILF3	8,36	-1,69	8	0
EEF2	9,03	-1,69	18	0
FUS	8,54	-1,70	3	0
RTN4	8,24	-1,70	4	0
PRDX3	7,98	-1,71	3	0
ATP5H	7,99	-1,71	2	0
HNRNPAB	8,30	-1,72	4	0
TRAP1	7,93	-1,72	2	0
RPN1	8,52	-1,73	15	0
ACTA1;ACTC1;ACTG2;ACTA2	8,97	-1,73	1	0
FAM120A	8,27	-1,75	6	0
HNRNPD	8,64	-1,76	9	0
RAN	8,58	-1,77	6	0
RAB1B	8,27	-1,79	3	0
IMPDH2	8,35	-1,80	8	0
HNRNPH3	8,31	-1,83	5	0
RPL26L1	9,04	-1,84	2	0
TFRC	8,16	-1,87	6	0
MAGEB2	8,82	-1,89	6	0
PABPC1;PABPC3	8,48	-1,90	7	0
TLN1	9,02	-1,91	9	1
LAMP1	7,91	-1,93	3	0
LGALS1	9,38	-1,93	8	1
RPN2	8,00	-1,94	6	0
EEF1A2	8,13	-1,95	2	0
TXNDC5	8,31	-1,97	6	0
ATP5B	8,83	-1,97	12	1
RAB7A	8,00	-1,98	3	0
SUB1	8,54	-1,99	3	0
TARS	7,82	-2,07	3	0
ERP44	8,17	-2,09	5	0
YWHAB	7,98	-2,13	2	0
PGRMC1	7,75	-2,14	2	0

Gene name	log10 intensity	log2FC	peptide counts (circle size)	significance (colour)
NME1-NME2;NME2;NME2P1	8,62	-2,16	6	0
HNRNPA2B1	9,37	-2,16	14	1
HSPA4	7,97	-2,18	5	0
SHMT2	8,31	-2,21	4	0
CD59	8,05	-2,24	2	0
VDAC3	7,90	-2,25	2	0
AZGP1	7,34	-2,25	2	1
APEX1	7,99	-2,28	2	0
SERPINH1	8,57	-2,29	7	0
ACTN4	8,22	-2,30	6	0
APMAP	7,63	-2,34	2	1
HSP90AA1	8,47	-2,34	6	0
B2M	7,88	-2,35	2	1
PHB	8,49	-2,37	9	0
PPIB	8,81	-2,39	6	1
YWHAE	8,53	-2,42	6	0
AHCY	8,30	-2,43	2	0
HSPB1	9,04	-2,49	10	1
STIP1	8,14	-2,49	3	1
GAPDH	9,14	-2,52	12	1
EEF1B2	8,05	-2,53	2	1
VCP	8,86	-2,53	11	1
RAB11FIP5	8,95	-2,55	18	1
PPIA	8,71	-2,56	3	1
GANAB	8,38	-2,57	7	0
CFL1	8,73	-2,61	8	1
GNAI3	7,33	-2,61	1	1
TAGLN2	8,26	-2,75	5	0
MSN	8,44	-2,82	7	0
VDAC2	8,15	-2,88	4	1
ACTN1	8,89	-2,90	17	1
YWHAZ	8,59	-2,97	4	1
HSP90B1	8,82	-3,01	6	1
PDIA6	8,90	-3,04	14	1
CANX	8,75	-3,12	8	1
PSAP	8,21	-3,15	2	1
VDAC1	8,47	-3,21	4	1
AHNAK	8,65	-3,22	11	1

Gene name	**log10 intensity**	**log2FC**	**peptide counts (circle size)**	**significance (colour)**
EEF1D	8,53	-3,27	6	1
PKM	9,14	-3,36	10	2
P4HB	8,88	-3,37	12	2
CS	8,02	-3,40	2	1
MDH2	8,65	-3,51	5	1
UBA1	7,93	-3,62	2	1
LDHB	8,54	-3,65	3	1
ENO1	9,02	-3,71	6	2
GOT2	8,16	-3,79	3	1
TPM3;DKFZp686J1372	8,36	-3,80	3	1
PFN1	8,28	-3,90	2	1
LDHA	8,70	-3,99	6	2
ANXA1	8,28	-4,16	3	1
HYOU1	8,19	-4,32	3	2
HSPE1;HSPE1-MOB4	8,90	-4,45	5	2
PTMA	8,48	-4,69	2	1
PDIA3	8,88	-4,72	7	2
TPI1	8,74	-5,71	3	2

7.3.9 Table with values corresponding to Figure 4.17

Table 7.13: Values corresponding to Figure 4.17. Values are sorted according to mean log2FC and p-value. Genes marked in bold were determined as significant MYC interactors according 488ot he cutoffs: log2FC>1, q-value<0.1. This interactome was published in (Baluapuri et al. 2019).

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
MYC	10,70	2,05E-09	2,14E-06	
MAX	10,28	4,86E-09	2,54E-06	
TRRAP	7,54	1,05E-07	3,65E-05	Chromatin Remodelling
HUWE1	6,36	3,21E-05	8,39E-03	Degradation
BAG2	2,96	9,34E-05	1,95E-02	Other
PSMD1	2,51	1,40E-04	2,44E-02	Degradation
EP400	3,14	8,29E-04	3,21E-02	Chromatin Remodelling
HADHA	3,10	4,61E-04	3,21E-02	Other
PSMD13	2,69	4,59E-04	3,21E-02	Degradation
PSMD6	2,62	4,72E-04	3,21E-02	Degradation

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
MTHFD1	2,60	5,60E-04	3,21E-02	Other
PABPC4	2,54	6,32E-04	3,21E-02	Transcription
ZNF281	2,53	6,09E-04	3,21E-02	Transcription
KIAA0368;ECM29	2,50	7,65E-04	3,21E-02	Degradation
CSDE1	2,50	8,28E-04	3,21E-02	Other
CSNK2A1;CSNK2A3	2,47	5,61E-04	3,21E-02	Other
PSMC1	2,45	6,27E-04	3,21E-02	Degradation
ABCE1	2,27	2,71E-04	3,21E-02	Other
ATAD3A	2,17	4,09E-04	3,21E-02	Other
PSMC6	2,13	2,61E-04	3,21E-02	Degradation
SMARCA4	2,02	7,96E-04	3,21E-02	Chromatin Remodelling
PSMD3	2,02	2,79E-04	3,21E-02	Degradation
WDR5	1,94	7,17E-04	3,21E-02	Transcription
PSMD8	1,93	8,16E-04	3,21E-02	Degradation
HDAC1	1,84	7,86E-04	3,21E-02	Chromatin Remodelling
PSMC5	1,82	5,65E-04	3,21E-02	Degradation
DMAP1	2,32	9,13E-04	3,41E-02	Chromatin Remodelling
TOP2A	1,97	9,74E-04	3,44E-02	Transcription
PLK1	1,79	9,89E-04	3,44E-02	Other
MCM2	2,60	1,10E-03	3,46E-02	Replication
RUNX2	2,27	1,13E-03	3,46E-02	Transcription
ACTL6A	2,01	1,04E-03	3,46E-02	Chromatin Remodelling
PSMC2	1,73	1,17E-03	3,50E-02	Degradation
PNO1	1,72	1,23E-03	3,52E-02	Transcription
RUVBL1	1,64	1,25E-03	3,52E-02	Other
PSMD11	2,84	1,37E-03	3,75E-02	Degradation
ANP32E	2,23	1,48E-03	3,96E-02	Chromatin Remodelling
MATR3	1,67	1,67E-03	4,36E-02	Transcription
RUVBL2	1,53	1,72E-03	4,37E-02	Chromatin Remodelling
UTP20	1,58	1,77E-03	4,40E-02	Other
PSMB5	1,68	2,05E-03	4,87E-02	Degradation
EPRS	1,44	2,31E-03	5,36E-02	Other
HADHB	1,89	2,64E-03	6,00E-02	Other
MRPS22	1,95	2,82E-03	6,18E-02	Other
PSMD14	1,90	3,14E-03	6,18E-02	Degradation
MCM5	1,73	2,92E-03	6,18E-02	Replication

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
PSMD2	1,55	3,11E-03	6,18E-02	Degradation
BLM	1,44	2,91E-03	6,18E-02	Other
SUPT16H	1,43	3,10E-03	6,18E-02	Chromatin Remodelling
PSMC4	1,43	3,05E-03	6,18E-02	Degradation
UBR5	2,43	3,28E-03	6,34E-02	Degradation
PSMD7	2,25	3,83E-03	6,45E-02	Degradation
CBFB	1,84	3,55E-03	6,45E-02	Transcription
PA2G4	1,83	3,58E-03	6,45E-02	Transcription
CSNK2B;CSNK2B-LY6G5B-1181;CSNK2B-LY6G5B—991	1,59	3,79E-03	6,45E-02	Other
POLR2B	1,59	3,69E-03	6,45E-02	Transcription
CAD	1,55	3,54E-03	6,45E-02	Other
SUPT5H	1,52	3,99E-03	6,62E-02	Transcription
SMARCC1	2,05	4,67E-03	7,49E-02	Chromatin Remodelling
RPS28	1,32	4,83E-03	7,53E-02	Other
RAD21	1,62	4,92E-03	7,55E-02	Chromatin Remodelling
GART	1,76	5,13E-03	7,63E-02	Other
DARS	1,71	5,05E-03	7,63E-02	Other
PSMB2	1,54	5,19E-03	7,63E-02	Degradation
PSMA3	1,81	5,61E-03	7,87E-02	Degradation
NOP56	1,24	5,58E-03	7,87E-02	Other
MDN1	1,68	5,93E-03	8,04E-02	Other
DHX33	1,42	6,13E-03	8,07E-02	Other
RFC3	1,30	6,13E-03	8,07E-02	Replication
PFKL	1,69	6,30E-03	8,08E-02	Other
PSMD12	1,66	6,35E-03	8,08E-02	Degradation
SMARCD2	2,07	6,71E-03	8,44E-02	Chromatin Remodelling
MCM7	1,61	6,99E-03	8,62E-02	Replication
NOP58	1,23	7,02E-03	8,62E-02	Other
AIMP2	1,24	7,25E-03	8,80E-02	Other
PSMC3	1,81	7,43E-03	8,92E-02	Degradation
PSMA6	1,54	7,69E-03	9,02E-02	Degradation
SSRP1	1,28	7,65E-03	9,02E-02	Chromatin Remodelling
SUPT6H	1,73	9,39E-03	9,86E-02	Transcription
GATAD2B	1,59	9,20E-03	9,86E-02	Transcription

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
NASP	1,57	8,94E-03	9,86E-02	Other
NSF	1,53	8,82E-03	9,86E-02	Other
EIF3H	1,52	8,97E-03	9,86E-02	Other
MTHFD1L	1,29	9,48E-03	9,86E-02	Other
PSMA2	1,28	9,01E-03	9,86E-02	Degradation
PDS5B	1,19	8,65E-03	9,86E-02	Chromatin Remodelling
PSMB3	1,16	9,63E-03	9,86E-02	Degradation
RALY	1,13	9,48E-03	9,86E-02	Transcription
DNAJA1	1,30	9,91E-03	1,00E-01	
DNAJA2	1,31	1,02E-02	1,02E-01	
PSMA1	1,52	1,03E-02	1,02E-01	
ACACA	1,52	1,06E-02	1,04E-01	
GMPS	1,47	1,07E-02	1,04E-01	
DNMT1	1,63	1,09E-02	1,05E-01	
PDCD11	1,60	1,11E-02	1,05E-01	
DIAPH3	1,50	1,12E-02	1,05E-01	
CHD4	1,12	1,18E-02	1,10E-01	
CBX3	1,37	1,22E-02	1,12E-01	
RFC5	1,06	1,26E-02	1,13E-01	
GNL3	1,04	1,26E-02	1,13E-01	
CUL1	1,79	1,29E-02	1,14E-01	
MRPS16	1,41	1,30E-02	1,14E-01	
PTGES3	1,42	1,36E-02	1,16E-01	
WDR43	1,40	1,33E-02	1,16E-01	
RFC2	1,02	1,35E-02	1,16E-01	
POLRMT	1,08	1,38E-02	1,16E-01	
PPP2R2A	1,15	1,40E-02	1,17E-01	
HCFC1	1,07	1,41E-02	1,17E-01	
NACC1	1,52	1,46E-02	1,17E-01	
GCN1L1	1,50	1,46E-02	1,17E-01	
HEATR1	1,45	1,48E-02	1,17E-01	
TIMM50	1,16	1,48E-02	1,17E-01	
HNRNPU	1,01	1,46E-02	1,17E-01	
PDS5A	1,20	1,55E-02	1,21E-01	
PSMD4	1,04	1,54E-02	1,21E-01	
MTA2	2,07	1,57E-02	1,22E-01	
SMC4	1,41	1,62E-02	1,23E-01	
DYNC1H1	1,43	1,65E-02	1,25E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
LARS	1,47	1,78E-02	1,27E-01	
PDCD4	1,38	1,70E-02	1,27E-01	
GTF3C3	1,35	1,72E-02	1,27E-01	
WDR46	1,21	1,76E-02	1,27E-01	
GTF2I	1,06	1,74E-02	1,27E-01	
HNRNPF	1,01	1,77E-02	1,27E-01	
GAR1	1,66	1,82E-02	1,29E-01	
NOP2	1,61	1,88E-02	1,33E-01	
PSMA4	1,40	1,89E-02	1,33E-01	
PPP2CA	1,21	1,94E-02	1,33E-01	
PSMA5	1,18	1,94E-02	1,33E-01	
MYO5A	2,33	1,97E-02	1,33E-01	
SMC2	1,28	2,01E-02	1,33E-01	
CYB5A	1,36	2,17E-02	1,40E-01	
PSMA7	1,89	2,22E-02	1,42E-01	
GARS	1,21	2,43E-02	1,50E-01	
GTF3C1	1,73	2,46E-02	1,51E-01	
MYO1C	1,57	2,59E-02	1,56E-01	
SMC3	1,25	2,67E-02	1,58E-01	
VIM	1,37	2,85E-02	1,62E-01	
PSMB1	1,35	2,81E-02	1,62E-01	
CMSS1	1,24	2,82E-02	1,62E-01	
STK4;STK3	1,18	2,85E-02	1,62E-01	
LMNB1	1,05	2,82E-02	1,62E-01	
EIF3A	1,96	3,03E-02	1,68E-01	
VARS	1,38	3,01E-02	1,68E-01	
MSH2	1,20	3,03E-02	1,68E-01	
TOP2B	1,36	3,23E-02	1,76E-01	
MCM6	1,12	3,32E-02	1,79E-01	
TCF12	1,35	3,40E-02	1,81E-01	
ADNP	1,12	3,48E-02	1,83E-01	
RBBP4	1,35	3,64E-02	1,87E-01	
UPF1	1,09	3,87E-02	1,96E-01	
BDH1	1,22	4,04E-02	2,01E-01	
FBXW7	1,31	4,07E-02	2,01E-01	
PGAM5	1,06	4,17E-02	2,03E-01	
SKIV2L	1,06	4,17E-02	2,03E-01	
ACO2	1,39	4,30E-02	2,06E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
USP7	1,03	4,30E-02	2,06E-01	
DKC1	1,14	4,35E-02	2,07E-01	
WDR26	1,03	4,50E-02	2,07E-01	
EIF3E	1,12	4,80E-02	2,17E-01	
PBRM1	1,12	4,80E-02	2,17E-01	
DNTTIP2	1,36	4,93E-02	2,19E-01	
POLR2A	1,08	4,91E-02	2,19E-01	
DPM1	1,01	4,95E-02	2,19E-01	
DHX29	1,52	5,07E-02	2,21E-01	
UBAP2L	1,00	5,11E-02	2,21E-01	
LYAR	1,60	5,81E-02	2,37E-01	
RARS	1,07	6,10E-02	2,44E-01	
IKBKAP	1,01	6,30E-02	2,46E-01	
HDAC2	1,02	6,46E-02	2,51E-01	
SMC1A	1,02	9,05E-02	3,02E-01	
CTPS1	1,03	1,24E-01	3,51E-01	
METTL17	1,13	1,34E-01	3,66E-01	
SPTBN1	1,08	1,45E-01	3,83E-01	
RPL37	1,44	1,54E-01	3,93E-01	
MYO1G	1,09	1,59E-01	3,99E-01	
NAP1L1	0,99	6,39E-02	2,49E-01	
BAT3;BAG6	0,99	5,18E-02	2,22E-01	
POLR2H	0,99	7,05E-02	2,61E-01	
DDX10	0,99	1,10E-01	3,32E-01	
HSPH1	0,98	1,36E-01	3,66E-01	
STAT5B	0,98	5,33E-02	2,24E-01	
CCT2	0,98	7,99E-02	2,85E-01	
DDX49	0,97	1,99E-02	1,33E-01	
MAT2A	0,97	9,35E-02	3,07E-01	
FXR1	0,97	5,33E-02	2,24E-01	
COPA	0,96	2,10E-02	1,37E-01	
MSH6	0,96	1,94E-02	1,33E-01	
KIAA0020	0,96	4,52E-02	2,07E-01	
OGT	0,96	5,73E-02	2,35E-01	
PHGDH	0,96	3,05E-02	1,69E-01	
SF3B6	0,96	9,08E-02	3,02E-01	
SPOCK2	0,95	5,91E-02	2,40E-01	
TXNL1	0,95	8,77E-02	2,96E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
COPB2	0,95	2,38E-02	1,50E-01	
USP5	0,95	6,07E-02	2,44E-01	
ARHGEF1	0,94	6,27E-02	2,46E-01	
NPM1	0,93	2,13E-02	1,38E-01	
RECQL	0,93	1,17E-01	3,43E-01	
UBTF	0,93	7,72E-02	2,79E-01	
IPO7	0,93	6,23E-02	2,45E-01	
RFC4	0,92	2,77E-02	1,62E-01	
DDX21	0,92	2,34E-02	1,48E-01	
GTPBP4	0,91	2,41E-02	1,50E-01	
RAC2;RAC3	0,91	6,99E-02	2,61E-01	
CTNNB1	0,91	1,04E-01	3,22E-01	
TUBA4A	0,90	5,12E-02	2,21E-01	
CCT4	0,90	1,06E-01	3,25E-01	
KAT8	0,89	7,59E-02	2,77E-01	
PPP2R1A	0,89	2,59E-02	1,56E-01	
CCT7	0,89	1,38E-01	3,71E-01	
KIF23	0,89	7,36E-02	2,71E-01	
NCAPD2	0,89	7,63E-02	2,78E-01	
POLE	0,88	1,24E-01	3,51E-01	
FBL	0,88	3,34E-02	1,79E-01	
RPL7	0,88	2,69E-02	1,58E-01	
CCT5	0,88	1,31E-01	3,63E-01	
COPB1	0,87	5,54E-02	2,30E-01	
SLC25A13	0,87	9,77E-02	3,13E-01	
HNRNPM	0,87	3,48E-02	1,83E-01	
MRPL2	0,87	8,64E-02	2,93E-01	
KDM1A	0,86	8,35E-02	2,88E-01	
WDR3	0,86	4,16E-02	2,03E-01	
NUP93	0,86	5,28E-02	2,24E-01	
STIP1	0,86	9,17E-02	3,02E-01	
EIF3B	0,86	3,59E-02	1,87E-01	
NOL10	0,84	9,90E-02	3,13E-01	
PES1	0,84	4,27E-02	2,06E-01	
PAF1	0,84	9,10E-02	3,02E-01	
POLR2C	0,83	6,06E-02	2,44E-01	
NRF1	0,83	9,10E-02	3,02E-01	
RPL12	0,83	4,28E-02	2,06E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
CCT3	0,83	1,30E-01	3,63E-01	
DDX19A;DDX19B	0,83	1,15E-01	3,40E-01	
GSPT1;GSPT2	0,83	9,06E-02	3,02E-01	
WDR74	0,82	9,40E-02	3,07E-01	
DPY30	0,82	3,96E-02	1,99E-01	
EIF4A1;EIF4A2	0,82	1,85E-01	4,30E-01	
EIF3M	0,81	1,84E-01	4,30E-01	
MYH9	0,81	1,87E-01	4,33E-01	
ATIC	0,81	9,92E-02	3,13E-01	
RBBP7	0,81	7,80E-02	2,79E-01	
CCT8	0,79	1,31E-01	3,63E-01	
IPO5	0,79	1,63E-01	4,04E-01	
BARX1	0,79	1,49E-01	3,87E-01	
TUBB	0,78	5,15E-02	2,21E-01	
CDC73	0,78	1,06E-01	3,25E-01	
EBNA1BP2	0,78	1,30E-01	3,63E-01	
MRTO4	0,78	1,06E-01	3,25E-01	
G3BP2	0,78	9,15E-02	3,02E-01	
RPL35A	0,78	4,53E-02	2,07E-01	
DNAJA3	0,78	4,49E-02	2,07E-01	
ADK	0,77	1,12E-01	3,36E-01	
DDX47	0,77	5,07E-02	2,21E-01	
ASH2L	0,77	1,12E-01	3,36E-01	
MCM3	0,77	8,42E-02	2,88E-01	
DDX31	0,75	2,36E-01	4,87E-01	
CSTF1	0,75	1,17E-01	3,42E-01	
AIFM1	0,75	5,13E-02	2,21E-01	
RPL14	0,75	4,89E-02	2,19E-01	
HSPA8	0,75	5,37E-02	2,25E-01	
MRPL41	0,75	1,18E-01	3,43E-01	
SMARCB1	0,75	1,24E-01	3,51E-01	
RPF2	0,75	1,40E-01	3,73E-01	
DHX9	0,74	7,05E-02	2,61E-01	
PRPS1	0,74	1,23E-01	3,51E-01	
CSNK2A2	0,74	5,62E-02	2,32E-01	
ALDOA	0,73	1,34E-01	3,66E-01	
COPG1	0,72	5,49E-02	2,29E-01	
BOP1	0,72	6,99E-02	2,61E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	Function
POLDIP2	0,72	9,62E-02	3,11E-01	
CDK1;CDC2	0,72	6,69E-02	2,55E-01	
RPL4	0,72	6,53E-02	2,52E-01	
DDX24	0,72	2,89E-01	5,36E-01	
MARS	0,71	1,34E-01	3,66E-01	
MYL12A;MYL12B	0,71	2,40E-01	4,89E-01	
RPL36	0,71	8,40E-02	2,88E-01	
PRPF8	0,71	7,01E-02	2,61E-01	
TNPO1	0,70	1,80E-01	4,25E-01	
SMARCA5	0,70	8,27E-02	2,87E-01	
ANKRD44	0,70	1,48E-01	3,87E-01	
RPL15	0,70	6,92E-02	2,61E-01	
MRPS25	0,70	1,99E-01	4,40E-01	
LIG1	0,69	1,47E-01	3,85E-01	
RPF1	0,69	7,79E-02	2,79E-01	
GRWD1	0,69	9,79E-02	3,13E-01	
EIF3C;EIF3CL	0,68	1,46E-01	3,84E-01	
PPIL1	0,68	2,31E-01	4,80E-01	
KRR1	0,68	1,55E-01	3,94E-01	
HNRNPR	0,67	1,94E-01	4,39E-01	
IMMT	0,67	1,22E-01	3,51E-01	
DDB1	0,67	7,75E-02	2,79E-01	
PGK1	0,66	1,73E-01	4,16E-01	
DDX54	0,66	8,05E-02	2,85E-01	
YTHDF2	0,65	1,68E-01	4,09E-01	
SLC25A22;SLC25A18	0,65	1,91E-01	4,37E-01	
NOC2L	0,64	1,44E-01	3,83E-01	
SMCHD1	0,64	1,97E-01	4,40E-01	
RPA1	0,64	1,98E-01	4,40E-01	
PTBP1	0,64	2,06E-01	4,49E-01	
RPS27L	0,64	9,66E-02	3,11E-01	
RPLP0;RPLP0P6	0,63	8,43E-02	2,88E-01	
RPL3	0,63	8,49E-02	2,89E-01	
TRAP1	0,63	2,84E-01	5,31E-01	
RAD50	0,62	1,87E-01	4,32E-01	
EIF3F	0,62	1,33E-01	3,66E-01	
MYBBP1A	0,62	2,05E-01	4,48E-01	
UBE2C	0,61	1,96E-01	4,40E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
RPL32	0,61	9,44E-02	3,07E-01	
SYNCRIP	0,61	2,44E-01	4,90E-01	
BANF1	0,61	2,00E-01	4,42E-01	
RBM10	0,61	1,98E-01	4,40E-01	
BYSL	0,61	1,94E-01	4,39E-01	
CCAR2	0,61	2,66E-01	5,11E-01	
NUP155	0,60	1,08E-01	3,27E-01	
APEX1	0,60	2,48E-01	4,93E-01	
DPF2	0,60	1,51E-01	3,89E-01	
IK	0,60	1,00E-01	3,13E-01	
ZSCAN25	0,60	1,88E-01	4,33E-01	
RPL5	0,60	1,06E-01	3,25E-01	
SYMPK	0,60	2,00E-01	4,42E-01	
PPIH	0,60	2,39E-01	4,89E-01	
TCEB1	0,60	4,29E-01	6,61E-01	
XAB2	0,60	2,05E-01	4,48E-01	
RPL18	0,60	1,04E-01	3,23E-01	
MAFK	0,60	2,44E-01	4,90E-01	
ACTB	0,60	2,40E-01	4,89E-01	
RPUSD4	0,59	3,28E-01	5,72E-01	
CCT6A	0,59	2,08E-01	4,51E-01	
RRP12	0,59	1,77E-01	4,21E-01	
HNRNPH1	0,59	1,13E-01	3,37E-01	
MGEA5	0,58	2,26E-01	4,72E-01	
SNRNP200	0,58	1,52E-01	3,91E-01	
EIF6	0,58	3,02E-01	5,49E-01	
ESF1	0,58	2,18E-01	4,64E-01	
TAF6L	0,58	2,16E-01	4,61E-01	
RPL7A	0,58	1,16E-01	3,41E-01	
NCL	0,58	1,61E-01	4,02E-01	
CAT	0,58	2,53E-01	4,95E-01	
TPM3;DKFZp686J1372	0,57	5,24E-01	7,25E-01	
NMT1	0,57	1,34E-01	3,66E-01	
PWP1	0,57	2,52E-01	4,95E-01	
KIF2C	0,57	2,29E-01	4,78E-01	
BMS1	0,57	3,47E-01	5,89E-01	
TUBA1B	0,56	1,63E-01	4,04E-01	
PAXIP1	0,56	2,53E-01	4,95E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
KPNB1	0,56	2,42E-01	4,90E-01	
IMPDH2	0,55	3,47E-01	5,89E-01	
RPS16	0,55	1,35E-01	3,66E-01	
TUFM	0,55	2,05E-01	4,48E-01	
ERCC3	0,54	2,88E-01	5,36E-01	
TCP1	0,54	1,97E-01	4,40E-01	
DNAJC7	0,54	2,04E-01	4,48E-01	
VPRBP	0,54	3,25E-01	5,70E-01	
RPS27A	0,54	1,45E-01	3,83E-01	
TARDBP	0,54	1,94E-01	4,39E-01	
MTSS1	0,53	3,41E-01	5,83E-01	
TRIP12	0,53	1,81E-01	4,26E-01	
PSIP1	0,53	1,85E-01	4,30E-01	
KPNA2	0,53	2,70E-01	5,13E-01	
LCP1	0,53	3,31E-01	5,74E-01	
POLR1B	0,53	3,16E-01	5,65E-01	
STRAP	0,53	2,09E-01	4,51E-01	
NGDN	0,52	2,18E-01	4,64E-01	
EIF3L	0,52	3,18E-01	5,65E-01	
PCNA	0,52	2,56E-01	5,00E-01	
DCAF13	0,52	1,74E-01	4,16E-01	
ZBTB24	0,52	5,10E-01	7,16E-01	
ENY2	0,52	2,65E-01	5,10E-01	
GTF2H4	0,52	1,51E-01	3,90E-01	
NAT10	0,51	1,59E-01	3,99E-01	
IARS	0,51	2,73E-01	5,17E-01	
H2AFV;H2AFZ	0,51	1,71E-01	4,12E-01	
CUL2	0,51	2,68E-01	5,12E-01	
RPL9	0,51	1,65E-01	4,04E-01	
ATP5C1	0,50	1,57E-01	3,98E-01	
IMP3	0,50	4,27E-01	6,58E-01	
RPL27	0,50	1,59E-01	3,99E-01	
RRS1	0,50	2,45E-01	4,90E-01	
ATF1	0,50	3,38E-01	5,80E-01	
GAPDH	0,50	4,61E-01	6,82E-01	
BRIX1	0,50	3,23E-01	5,70E-01	
ILF2	0,50	2,41E-01	4,90E-01	
HSPA9	0,49	1,66E-01	4,06E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	Function
MCM4	0,49	2,84E-01	5,31E-01	
NSUN5	0,49	2,14E-01	4,58E-01	
ALDH18A1	0,49	2,51E-01	4,95E-01	
SRM	0,49	3,42E-01	5,83E-01	
CSTF3	0,48	2,89E-01	5,36E-01	
NOP16	0,48	2,69E-01	5,13E-01	
HNRNPA1;HNRNPA1L2	0,48	3,61E-01	6,02E-01	
HNRNPC	0,48	2,35E-01	4,87E-01	
EIF3I	0,48	2,09E-01	4,51E-01	
DDX39A	0,48	3,10E-01	5,59E-01	
RPS12	0,48	1,94E-01	4,39E-01	
MYO1D	0,47	3,00E-01	5,48E-01	
TFIP11	0,47	3,98E-01	6,36E-01	
RPL34	0,47	1,90E-01	4,35E-01	
HIRA	0,46	2,26E-01	4,72E-01	
FTSJ3	0,46	2,45E-01	4,91E-01	
UBA2	0,46	3,16E-01	5,65E-01	
SND1	0,46	2,18E-01	4,64E-01	
DDX51	0,46	4,19E-01	6,56E-01	
SRP68	0,45	1,95E-01	4,40E-01	
RPS19	0,45	2,20E-01	4,66E-01	
ATP1A1	0,45	4,48E-01	6,72E-01	
SNX18	0,44	3,26E-01	5,70E-01	
CCNL1	0,44	3,26E-01	5,70E-01	
POLR1A	0,44	4,16E-01	6,55E-01	
GNL2	0,44	2,44E-01	4,90E-01	
ZNF658;ZNF334;DKFZp572F2170;ZNF12;ZNF891;ZFP37;ZNF658B	0,44	4,26E-01	6,58E-01	
EFTUD2	0,44	2,37E-01	4,88E-01	
TKT	0,44	4,45E-01	6,70E-01	
PABPC1;PABPC3	0,44	4,35E-01	6,64E-01	
SMU1	0,43	2,36E-01	4,87E-01	
PPFIBP1	0,43	3,55E-01	5,97E-01	
PPAN-P2RY11;PPAN	0,43	3,47E-01	5,89E-01	
CLASP2	0,43	3,68E-01	6,08E-01	
SLC25A1	0,43	3,29E-01	5,72E-01	
TCERG1	0,43	2,62E-01	5,08E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
MRPL15	0,43	2,48E-01	4,93E-01	
TUBG1;TUBG2	0,42	3,47E-01	5,89E-01	
RPLP2	0,42	2,98E-01	5,47E-01	
FCF1	0,42	3,09E-01	5,58E-01	
RPL10A	0,42	2,40E-01	4,89E-01	
NEDD4	0,42	3,62E-01	6,02E-01	
RPL13A;RPL13a	0,41	2,48E-01	4,93E-01	
RPS5	0,40	2,51E-01	4,95E-01	
CXXC1	0,40	5,57E-01	7,50E-01	
HNRNPL	0,40	2,77E-01	5,21E-01	
CALM2;CALM1;CALM3	0,40	4,24E-01	6,58E-01	
MRPL22	0,40	2,53E-01	4,95E-01	
SNX1	0,40	4,00E-01	6,37E-01	
EIF3G	0,40	3,06E-01	5,54E-01	
HSPD1	0,39	4,41E-01	6,68E-01	
RNF138	0,39	4,36E-01	6,65E-01	
MORF4L1	0,39	2,76E-01	5,21E-01	
CCNT1	0,38	4,35E-01	6,64E-01	
HSPA14	0,38	4,42E-01	6,69E-01	
SKIV2L2	0,38	2,93E-01	5,40E-01	
RPSA	0,38	3,20E-01	5,67E-01	
UBA1	0,37	6,61E-01	8,21E-01	
CAPZB	0,37	4,62E-01	6,82E-01	
UTP14A	0,37	2,89E-01	5,36E-01	
TUBB4B	0,37	3,59E-01	6,01E-01	
SRPK1	0,36	3,01E-01	5,49E-01	
CHD8	0,36	4,43E-01	6,70E-01	
EIF3D	0,35	4,52E-01	6,77E-01	
NHP2L1	0,35	3,24E-01	5,70E-01	
FLNA	0,35	4,93E-01	7,06E-01	
HELLS	0,35	4,31E-01	6,61E-01	
ELAVL1	0,35	4,21E-01	6,58E-01	
PRDM15	0,35	5,38E-01	7,35E-01	
RPS10;RPS10-NUDT3	0,35	3,23E-01	5,70E-01	
ABCF2	0,35	4,08E-01	6,44E-01	
EIF5A	0,34	4,73E-01	6,92E-01	
RCC2	0,34	3,91E-01	6,32E-01	
CAPZA1	0,34	5,75E-01	7,60E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
ATP2A2	0,34	5,01E-01	7,13E-01	
PAICS	0,34	5,36E-01	7,33E-01	
GTF3A	0,34	3,84E-01	6,27E-01	
PARP1	0,33	4,79E-01	6,97E-01	
RPL18A	0,33	3,66E-01	6,07E-01	
NOP9	0,33	4,53E-01	6,77E-01	
ARPC4-TTLL3;ARPC4	0,33	4,70E-01	6,90E-01	
RPL11	0,33	3,36E-01	5,80E-01	
CRNKL1	0,33	3,52E-01	5,95E-01	
CDC5L	0,33	4,02E-01	6,40E-01	
ZNF444	0,33	3,97E-01	6,36E-01	
RPL24	0,32	4,40E-01	6,68E-01	
AATF	0,32	4,62E-01	6,82E-01	
RPL30	0,32	3,53E-01	5,95E-01	
HNRNPA0	0,31	4,85E-01	7,01E-01	
RPL10	0,31	3,87E-01	6,28E-01	
GNAI2;GNAI1	0,31	4,86E-01	7,01E-01	
AQR	0,31	3,76E-01	6,18E-01	
SEH1L	0,30	5,08E-01	7,16E-01	
KPNA3	0,30	4,25E-01	6,58E-01	
RPS18	0,30	3,86E-01	6,28E-01	
CSE1L	0,30	5,31E-01	7,31E-01	
RBM22	0,30	3,85E-01	6,28E-01	
DDX1	0,29	5,05E-01	7,14E-01	
XRN2	0,29	4,88E-01	7,02E-01	
HNRNPK	0,28	4,99E-01	7,12E-01	
EIF5B	0,28	5,00E-01	7,12E-01	
ATP5A1	0,28	4,69E-01	6,90E-01	
HNRNPA3	0,28	4,89E-01	7,03E-01	
RPS8	0,28	4,18E-01	6,56E-01	
HIST1H4A	0,28	4,25E-01	6,58E-01	
ZNF800	0,27	5,86E-01	7,64E-01	
SERBP1	0,27	4,96E-01	7,09E-01	
G3BP1	0,27	5,22E-01	7,23E-01	
PRDX1	0,27	5,55E-01	7,50E-01	
MAFG	0,27	4,31E-01	6,61E-01	
DHX37	0,26	4,84E-01	7,01E-01	
RPL6	0,26	5,15E-01	7,20E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
CWC22	0,26	5,55E-01	7,50E-01	
LARP1	0,26	5,79E-01	7,62E-01	
RPL13	0,26	4,57E-01	6,80E-01	
IDH3A	0,25	6,22E-01	7,94E-01	
UTP18	0,25	5,81E-01	7,62E-01	
UMPS	0,25	6,00E-01	7,78E-01	
TARS	0,25	6,33E-01	8,00E-01	
CDK11B;CDC2L1;CDK11A	0,24	5,73E-01	7,60E-01	
PLRG1	0,24	4,73E-01	6,92E-01	
SDAD1	0,23	6,53E-01	8,16E-01	
RPS26;RPS26P11	0,23	4,96E-01	7,09E-01	
DNM2	0,23	6,03E-01	7,79E-01	
RPS3	0,23	5,14E-01	7,19E-01	
SNRPC	0,23	5,26E-01	7,26E-01	
SLC25A5	0,23	5,53E-01	7,49E-01	
RPL28	0,22	5,13E-01	7,19E-01	
UBR4	0,22	5,10E-01	7,16E-01	
MRPL48	0,22	5,92E-01	7,69E-01	
AP2M1	0,22	6,51E-01	8,15E-01	
CLTC	0,22	5,21E-01	7,23E-01	
DDX17	0,21	5,31E-01	7,31E-01	
PRPF6	0,21	5,56E-01	7,50E-01	
UTP11L	0,21	6,01E-01	7,78E-01	
HSD17B10	0,21	5,42E-01	7,36E-01	
PABPN1	0,21	6,34E-01	8,02E-01	
DDX52	0,21	6,13E-01	7,87E-01	
HNRNPD	0,20	6,95E-01	8,46E-01	
TFB1M	0,20	5,73E-01	7,60E-01	
WDR12	0,20	5,83E-01	7,63E-01	
PPP1CB	0,20	5,58E-01	7,50E-01	
GLUD1;GLUD2	0,20	6,66E-01	8,23E-01	
NSUN2	0,20	5,78E-01	7,62E-01	
CCDC86	0,20	5,94E-01	7,71E-01	
SMAD3;SMAD2	0,20	5,59E-01	7,50E-01	
IMP4	0,19	7,13E-01	8,55E-01	
DHX15	0,19	5,81E-01	7,62E-01	
RPL19	0,19	5,81E-01	7,62E-01	
DDX50	0,19	6,55E-01	8,17E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
ZNF740	0,19	7,31E-01	8,63E-01	
HSP90AB1	0,19	6,91E-01	8,44E-01	
RPS25	0,19	6,06E-01	7,82E-01	
EMG1	0,18	6,44E-01	8,09E-01	
SET;SETSIP	0,18	7,02E-01	8,49E-01	
NSA2	0,18	6,87E-01	8,41E-01	
PBDC1	0,17	6,90E-01	8,44E-01	
RPS14	0,17	6,09E-01	7,84E-01	
POP1	0,17	7,23E-01	8,63E-01	
PPP6R3	0,17	6,99E-01	8,49E-01	
ZNF593	0,17	6,29E-01	7,99E-01	
GNB2L1	0,17	6,64E-01	8,23E-01	
ABCF1	0,16	6,31E-01	7,99E-01	
PRPF4	0,16	6,44E-01	8,09E-01	
SPATA5	0,16	7,16E-01	8,56E-01	
RPS20	0,16	6,44E-01	8,09E-01	
ZC3H18	0,16	7,40E-01	8,66E-01	
RRP7A	0,15	6,70E-01	8,26E-01	
ARF5;ARF3	0,15	7,41E-01	8,66E-01	
PPP1CA	0,14	7,40E-01	8,66E-01	
C9orf114	0,14	7,51E-01	8,74E-01	
PPP1CC	0,14	6,74E-01	8,29E-01	
NO66	0,14	7,31E-01	8,63E-01	
PTPN14	0,14	7,59E-01	8,78E-01	
CYC1	0,13	7,06E-01	8,49E-01	
HIST1H2BL	0,13	7,41E-01	8,66E-01	
SF3B2	0,13	7,04E-01	8,49E-01	
RPL31	0,13	7,13E-01	8,55E-01	
ATP5B	0,13	8,02E-01	9,08E-01	
HIST2H3A;HIST1H3A; HIST3H3	0,12	7,12E-01	8,55E-01	
TRMT112	0,12	7,27E-01	8,63E-01	
SF3B3	0,12	7,25E-01	8,63E-01	
RPS9	0,12	7,26E-01	8,63E-01	
ATP5O	0,12	7,28E-01	8,63E-01	
RPS15	0,12	7,33E-01	8,64E-01	
RTCB	0,11	7,86E-01	8,96E-01	
GPAM	0,11	7,96E-01	9,04E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
HIST2H2AC;HIST2H2AA3;HIST1H2AJ;HIST1H2AH;H2AFJ;HIST1H2AD;HIST1H2AG	0,11	7,72E-01	8,88E-01	
ZFP64	0,10	7,71E-01	8,88E-01	
ARPC3	0,10	8,16E-01	9,17E-01	
MRPL9	0,10	7,67E-01	8,85E-01	
CACYBP	0,10	8,02E-01	9,08E-01	
DDX27	0,09	7,85E-01	8,96E-01	
INTS6	0,09	8,32E-01	9,26E-01	
UTP23	0,09	8,26E-01	9,24E-01	
UTP3	0,09	8,56E-01	9,40E-01	
CDK9	0,09	8,39E-01	9,30E-01	
KHDRBS1	0,09	8,03E-01	9,08E-01	
KLF16	0,09	8,80E-01	9,52E-01	
SNIP1	0,09	8,02E-01	9,08E-01	
PRMT1	0,09	8,14E-01	9,17E-01	
IKZF4	0,08	8,57E-01	9,40E-01	
CSTF2;CSTF2T	0,08	8,29E-01	9,26E-01	
CNOT1	0,08	8,63E-01	9,45E-01	
PPIL2	0,08	8,60E-01	9,43E-01	
RPL21	0,08	8,34E-01	9,27E-01	
RPL8	0,07	8,53E-01	9,40E-01	
PRPF19	0,07	8,31E-01	9,26E-01	
DDX3X;DDX3Y	0,07	8,33E-01	9,26E-01	
PRDM10	0,07	9,13E-01	9,64E-01	
RNPS1	0,07	8,63E-01	9,45E-01	
EEF2	0,07	8,81E-01	9,52E-01	
RPS7	0,07	8,49E-01	9,37E-01	
DDX5	0,07	8,52E-01	9,40E-01	
WHSC1	0,07	8,82E-01	9,52E-01	
SF3B1	0,06	8,46E-01	9,35E-01	
AHCY	0,06	9,04E-01	9,59E-01	
UPF3B	0,06	8,86E-01	9,53E-01	
SP3	0,06	8,86E-01	9,53E-01	
RPL17;RPL17-C18orf32	0,06	8,70E-01	9,48E-01	
SLC25A3	0,06	8,94E-01	9,57E-01	
EME1	0,06	9,18E-01	9,67E-01	
RPS11	0,05	8,69E-01	9,47E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
RNF2	0,05	9,02E-01	9,59E-01	
DIMT1	0,05	8,92E-01	9,56E-01	
DNAJC13	0,05	9,26E-01	9,72E-01	
DDX23	0,05	8,84E-01	9,53E-01	
NONO	0,05	9,01E-01	9,59E-01	
SNRPD1	0,05	8,86E-01	9,53E-01	
SHMT2	0,05	9,30E-01	9,73E-01	
TECR	0,04	9,00E-01	9,59E-01	
ESYT1	0,04	9,09E-01	9,62E-01	
SNW1	0,04	9,01E-01	9,59E-01	
DENND2D	0,04	9,30E-01	9,73E-01	
HNRNPUL2;HNRNPUL2-BSCL2	0,04	9,28E-01	9,73E-01	
THOC2	0,03	9,23E-01	9,69E-01	
CCDC59	0,03	9,40E-01	9,74E-01	
NOM1	0,03	9,48E-01	9,77E-01	
BUB3	0,03	9,33E-01	9,74E-01	
TMPO	0,03	9,38E-01	9,74E-01	
RPS15A	0,03	9,38E-01	9,74E-01	
HNRNPLL;HNRPLL	0,03	9,44E-01	9,76E-01	
MYL6	0,02	9,57E-01	9,79E-01	
PRPSAP1	0,02	9,56E-01	9,79E-01	
RPP14	0,02	9,59E-01	9,79E-01	
EIF4A3	0,02	9,54E-01	9,79E-01	
DHX8	0,02	9,67E-01	9,82E-01	
HSP90AA1	0,02	9,73E-01	9,87E-01	
SFPQ	0,02	9,65E-01	9,81E-01	
DHX35	0,01	9,77E-01	9,90E-01	
SON	0,01	9,91E-01	9,98E-01	
RPS3A	0,01	9,88E-01	9,97E-01	
MAZ	0,00	9,91E-01	9,98E-01	
SNX5	0,00	9,94E-01	9,99E-01	
EEF1G	0,00	9,98E-01	9,99E-01	
U2AF1	0,00	1,00E+00	1,00E+00	
CLPX	0,00	9,98E-01	9,99E-01	
MPHOSPH10	0,00	9,99E-01	9,99E-01	
EIF2S2	0,00	9,96E-01	9,99E-01	
RPS17	0,00	9,95E-01	9,99E-01	
HNRNPA2B1	-0,01	9,90E-01	9,98E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	Function
PPIE	-0,01	9,81E-01	9,93E-01	
CIRH1A	-0,01	9,82E-01	9,93E-01	
SNRPD3	-0,01	9,67E-01	9,82E-01	
RPS6	-0,02	9,64E-01	9,81E-01	
PKM	-0,02	9,78E-01	9,91E-01	
SNRPD2	-0,02	9,57E-01	9,79E-01	
PRPF40A	-0,02	9,55E-01	9,79E-01	
METTL13	-0,02	9,64E-01	9,81E-01	
RRP36	-0,02	9,49E-01	9,77E-01	
RBM27	-0,02	9,56E-01	9,79E-01	
RIF1	-0,02	9,59E-01	9,79E-01	
SP1	-0,02	9,48E-01	9,77E-01	
TRIM28	-0,02	9,41E-01	9,75E-01	
PHB2	-0,03	9,36E-01	9,74E-01	
RPL23A	-0,03	9,39E-01	9,74E-01	
SNRNP40	-0,03	9,35E-01	9,74E-01	
RPP30	-0,03	9,48E-01	9,77E-01	
TP53BP1	-0,03	9,42E-01	9,75E-01	
PNN	-0,03	9,19E-01	9,67E-01	
EEF1D	-0,04	9,52E-01	9,79E-01	
SSB	-0,04	9,31E-01	9,73E-01	
C14orf166	-0,04	9,15E-01	9,65E-01	
ZAP70	-0,04	9,22E-01	9,69E-01	
MINA	-0,04	9,04E-01	9,59E-01	
PRPF38A	-0,05	8,95E-01	9,57E-01	
ZRANB2	-0,05	9,35E-01	9,74E-01	
NCBP1	-0,05	9,14E-01	9,64E-01	
LARP7	-0,05	9,04E-01	9,59E-01	
DNAJC9	-0,05	8,87E-01	9,53E-01	
UBA52;UBB;RPS27A;UBC	-0,05	8,79E-01	9,52E-01	
ACP1	-0,06	9,00E-01	9,59E-01	
CFAP20	-0,06	8,66E-01	9,45E-01	
KIF2A	-0,06	8,97E-01	9,59E-01	
RPS24	-0,06	8,56E-01	9,40E-01	
TUBB3	-0,06	8,89E-01	9,54E-01	
SNRPN;SNRPB	-0,07	8,45E-01	9,35E-01	
RAN	-0,07	8,79E-01	9,52E-01	
SAP18	-0,07	8,67E-01	9,46E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
SDF2L1	-0,07	8,79E-01	9,52E-01	
RBM14	-0,07	8,36E-01	9,28E-01	
MPP1	-0,07	8,72E-01	9,49E-01	
SNRPE	-0,08	8,20E-01	9,20E-01	
ZNF668	-0,08	9,10E-01	9,63E-01	
PCBP2	-0,08	8,16E-01	9,17E-01	
CDK12	-0,08	8,80E-01	9,52E-01	
DDX55	-0,08	8,45E-01	9,35E-01	
PRPF31	-0,09	7,88E-01	8,96E-01	
EIF1;EIF1B	-0,09	8,65E-01	9,45E-01	
PATZ1	-0,09	8,19E-01	9,20E-01	
GTF2B	-0,09	8,22E-01	9,20E-01	
SF3B4	-0,09	8,29E-01	9,26E-01	
ZCCHC17	-0,10	8,04E-01	9,08E-01	
TOP1	-0,10	7,82E-01	8,94E-01	
SEC61A1	-0,10	7,67E-01	8,85E-01	
PYCR2	-0,10	8,14E-01	9,17E-01	
NSD1	-0,10	7,75E-01	8,89E-01	
MFAP1	-0,11	7,52E-01	8,74E-01	
RPS13	-0,11	7,52E-01	8,74E-01	
SLC25A11	-0,11	7,88E-01	8,96E-01	
DDX18	-0,11	7,37E-01	8,66E-01	
SRSF2	-0,12	8,30E-01	9,26E-01	
RBM25	-0,12	7,31E-01	8,63E-01	
KPNA4	-0,12	7,29E-01	8,63E-01	
STAU1	-0,12	7,81E-01	8,94E-01	
XPO1	-0,12	7,14E-01	8,55E-01	
SNRNP70	-0,12	7,38E-01	8,66E-01	
ZSCAN26;ZNF187	-0,12	7,75E-01	8,89E-01	
CTCF	-0,12	7,82E-01	8,94E-01	
CPSF3	-0,13	7,77E-01	8,90E-01	
RPL26	-0,13	7,22E-01	8,63E-01	
ING5	-0,13	7,71E-01	8,88E-01	
CHAMP1	-0,13	7,66E-01	8,85E-01	
RPL27A	-0,13	7,25E-01	8,63E-01	
PPIG	-0,13	7,03E-01	8,49E-01	
MRPL46	-0,14	7,00E-01	8,49E-01	
CPSF1	-0,14	6,71E-01	8,26E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
YWHAG	-0,14	7,43E-01	8,66E-01	
YWHAB	-0,14	7,51E-01	8,74E-01	
IKZF1	-0,15	7,41E-01	8,66E-01	
ZFX;ZFY	-0,15	7,04E-01	8,49E-01	
GNL3L	-0,15	7,30E-01	8,63E-01	
RPL38	-0,15	6,56E-01	8,18E-01	
C5orf30	-0,16	7,34E-01	8,64E-01	
AP1B1	-0,16	6,60E-01	8,21E-01	
DDX28	-0,16	7,55E-01	8,75E-01	
FAM32A	-0,17	7,03E-01	8,49E-01	
RSRC1	-0,17	6,27E-01	7,97E-01	
RPL37A	-0,17	6,23E-01	7,94E-01	
YWHAQ	-0,17	6,65E-01	8,23E-01	
TMEM263	-0,17	6,95E-01	8,46E-01	
EEF1A1;EEF1A1P5	-0,17	6,12E-01	7,86E-01	
EED	-0,18	7,06E-01	8,49E-01	
SLK	-0,18	6,85E-01	8,40E-01	
REXO4	-0,18	6,66E-01	8,23E-01	
SLC25A6	-0,19	6,71E-01	8,26E-01	
U2AF1	-0,19	6,25E-01	7,96E-01	
FEM1B	-0,19	6,93E-01	8,45E-01	
EPB41L3	-0,19	6,63E-01	8,23E-01	
SLC25A12	-0,20	6,52E-01	8,15E-01	
SF3B5	-0,20	5,59E-01	7,50E-01	
SRSF11	-0,20	6,22E-01	7,94E-01	
RPL22L1	-0,20	5,69E-01	7,59E-01	
CWC15	-0,21	6,35E-01	8,02E-01	
TRMT10C	-0,21	5,92E-01	7,69E-01	
SNRPA1	-0,22	5,71E-01	7,59E-01	
CPSF7	-0,22	6,76E-01	8,30E-01	
ZNF148	-0,22	6,30E-01	7,99E-01	
CSNK1A1;CSNK1A1L	-0,22	6,43E-01	8,09E-01	
MRPS12	-0,22	5,71E-01	7,59E-01	
GNB2	-0,22	5,75E-01	7,60E-01	
AP2A1	-0,22	5,08E-01	7,16E-01	
HDLBP	-0,22	6,17E-01	7,90E-01	
TAOK1	-0,22	5,41E-01	7,36E-01	
CORO1C	-0,23	6,76E-01	8,30E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
DEK	-0,23	8,06E-01	9,09E-01	
ABT1	-0,23	6,08E-01	7,84E-01	
LUC7L3	-0,24	5,82E-01	7,62E-01	
SRP72	-0,24	4,86E-01	7,01E-01	
SF3A3	-0,24	5,17E-01	7,22E-01	
H2AFY	-0,24	5,39E-01	7,35E-01	
POC1A	-0,24	5,84E-01	7,63E-01	
ZBTB7A	-0,25	6,09E-01	7,84E-01	
TCOF1	-0,25	6,48E-01	8,13E-01	
PSME3	-0,25	5,10E-01	7,16E-01	
PHB	-0,25	6,47E-01	8,12E-01	
SCAF1	-0,25	5,79E-01	7,62E-01	
ZNF638	-0,25	7,56E-01	8,76E-01	
EPB41L2	-0,25	4,72E-01	6,92E-01	
BTF3	-0,25	5,67E-01	7,58E-01	
ENO1	-0,25	7,05E-01	8,49E-01	
VCP	-0,25	6,17E-01	7,90E-01	
ARF4	-0,26	4,67E-01	6,88E-01	
RBM39	-0,26	4,58E-01	6,81E-01	
ZNF652	-0,26	4,84E-01	7,01E-01	
MAK16	-0,26	5,71E-01	7,59E-01	
YME1L1	-0,26	5,19E-01	7,23E-01	
DDX6	-0,27	4,31E-01	6,61E-01	
HNRNPAB	-0,27	4,99E-01	7,12E-01	
DDX56	-0,27	4,62E-01	6,82E-01	
GFPT1	-0,27	5,41E-01	7,36E-01	
CUL4A	-0,27	4,27E-01	6,58E-01	
ARRB2	-0,27	4,86E-01	7,01E-01	
RPS4X	-0,27	4,16E-01	6,55E-01	
AKAP17A	-0,27	5,51E-01	7,47E-01	
CIR1	-0,28	4,23E-01	6,58E-01	
TAF10	-0,28	4,25E-01	6,58E-01	
CDC40	-0,28	5,34E-01	7,32E-01	
RP9	-0,28	4,07E-01	6,44E-01	
EIF2S3;EIF2S3L	-0,28	4,55E-01	6,79E-01	
ABCB7	-0,28	5,62E-01	7,52E-01	
HSPA5	-0,29	3,99E-01	6,37E-01	
TAF8	-0,29	4,41E-01	6,68E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
PRPF4B	-0,29	5,33E-01	7,32E-01	
ALYREF	-0,29	4,45E-01	6,70E-01	
MAGOHB	-0,29	4,08E-01	6,44E-01	
NOP14	-0,29	5,21E-01	7,23E-01	
POLDIP3	-0,29	5,22E-01	7,23E-01	
PCBP1	-0,30	3,90E-01	6,32E-01	
SRRM2	-0,30	4,08E-01	6,44E-01	
VRK1	-0,30	5,09E-01	7,16E-01	
DYNLL1;DYNLL2	-0,30	4,61E-01	6,82E-01	
KNOP1	-0,30	5,21E-01	7,23E-01	
EPB41	-0,30	4,23E-01	6,58E-01	
CHD1	-0,30	5,04E-01	7,13E-01	
RBM8A	-0,30	3,73E-01	6,16E-01	
RPL35	-0,31	4,50E-01	6,75E-01	
PAXBP1	-0,31	4,44E-01	6,70E-01	
MAD2L1	-0,31	4,88E-01	7,02E-01	
SART1	-0,31	4,55E-01	6,79E-01	
LUC7L	-0,31	3,62E-01	6,02E-01	
CANX	-0,32	5,89E-01	7,68E-01	
CFL1	-0,32	5,28E-01	7,28E-01	
EIF2S1	-0,32	3,78E-01	6,21E-01	
SKP1	-0,32	3,55E-01	5,97E-01	
HP1BP3	-0,32	4,57E-01	6,80E-01	
HMGB1;HMGB1P1	-0,32	5,34E-01	7,32E-01	
RPL23	-0,32	3,96E-01	6,35E-01	
SRSF5	-0,32	4,83E-01	7,01E-01	
VDAC3	-0,32	6,02E-01	7,78E-01	
SNRNP27	-0,33	5,02E-01	7,13E-01	
LRRC47	-0,33	3,38E-01	5,80E-01	
ZNF771	-0,33	5,51E-01	7,47E-01	
WDR83	-0,33	3,42E-01	5,83E-01	
PCMT1	-0,34	3,57E-01	5,98E-01	
IQGAP1	-0,34	3,76E-01	6,18E-01	
ZFP91;ZFP91-CNTF	-0,34	3,35E-01	5,78E-01	
CHERP	-0,34	3,18E-01	5,65E-01	
HIST1H1C	-0,35	3,61E-01	6,02E-01	
SRSF3	-0,35	3,93E-01	6,33E-01	
WDR33	-0,35	4,34E-01	6,64E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	Function
SREK1IP1	-0,35	3,42E-01	5,83E-01	
SREK1	-0,36	3,97E-01	6,36E-01	
UFM1	-0,36	4,23E-01	6,58E-01	
NXF1	-0,36	3,73E-01	6,16E-01	
RPL7L1	-0,36	3,02E-01	5,49E-01	
RPL22	-0,37	3,16E-01	5,65E-01	
PIP	-0,37	4,18E-01	6,56E-01	
DDX46	-0,37	4,40E-01	6,68E-01	
RPL36A;RPL36A-HNRNPH2	-0,37	3,29E-01	5,72E-01	
HSPA4	-0,37	3,86E-01	6,28E-01	
METAP1	-0,38	3,37E-01	5,80E-01	
CDC42	-0,38	2,83E-01	5,30E-01	
FAU	-0,38	2,98E-01	5,47E-01	
SSR1	-0,38	3,03E-01	5,49E-01	
FASN	-0,39	2,92E-01	5,38E-01	
NOL12	-0,39	3,26E-01	5,70E-01	
MAP1B	-0,39	3,82E-01	6,27E-01	
MYCBP2	-0,39	4,06E-01	6,44E-01	
ACTR1A	-0,39	2,60E-01	5,05E-01	
RPS23	-0,39	2,89E-01	5,36E-01	
ARGLU1	-0,40	2,62E-01	5,08E-01	
ZNF48	-0,40	3,84E-01	6,27E-01	
AHNAK	-0,40	5,68E-01	7,58E-01	
PUF60	-0,40	3,28E-01	5,72E-01	
SCAF4	-0,40	2,52E-01	4,95E-01	
P4HB	-0,40	4,74E-01	6,92E-01	
MAPK1	-0,41	3,67E-01	6,07E-01	
MMTAG2	-0,41	2,51E-01	4,95E-01	
NKAP	-0,42	3,11E-01	5,60E-01	
BRD7	-0,42	3,54E-01	5,95E-01	
MDH2	-0,42	5,58E-01	7,50E-01	
RAB7A	-0,42	3,22E-01	5,70E-01	
SLTM	-0,43	3,53E-01	5,95E-01	
FLII	-0,43	5,03E-01	7,13E-01	
RBBP6	-0,43	2,71E-01	5,14E-01	
RSBN1	-0,43	2,91E-01	5,37E-01	
RAB1B	-0,43	2,65E-01	5,10E-01	
ACIN1	-0,44	3,00E-01	5,48E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
PPIA	-0,44	3,92E-01	6,32E-01	
SCAF8	-0,44	2,25E-01	4,71E-01	
SAFB	-0,45	2,05E-01	4,48E-01	
CPSF2	-0,45	3,19E-01	5,66E-01	
RPS2	-0,45	2,19E-01	4,65E-01	
RBM28	-0,46	3,90E-01	6,32E-01	
DSC1	-0,46	3,13E-01	5,63E-01	
AP2B1	-0,47	1,85E-01	4,30E-01	
CBX4	-0,47	3,01E-01	5,49E-01	
TAF2	-0,48	1,78E-01	4,21E-01	
MEPCE	-0,48	2,43E-01	4,90E-01	
ZNF319	-0,48	2,59E-01	5,04E-01	
SRP14	-0,49	1,97E-01	4,40E-01	
SF3A1	-0,49	1,82E-01	4,28E-01	
CCDC84	-0,50	1,99E-01	4,40E-01	
NACA	-0,50	1,65E-01	4,04E-01	
CACTIN	-0,50	2,08E-01	4,51E-01	
CCDC137	-0,50	1,85E-01	4,30E-01	
INTS3	-0,50	4,78E-01	6,97E-01	
WDR6	-0,51	2,75E-01	5,21E-01	
MED19	-0,51	1,71E-01	4,12E-01	
SRSF6	-0,52	1,60E-01	4,01E-01	
GNAI3	-0,53	2,65E-01	5,10E-01	
TRA2A	-0,53	1,53E-01	3,91E-01	
SRRT	-0,53	1,65E-01	4,04E-01	
YBX1	-0,53	1,76E-01	4,20E-01	
THAP11	-0,55	2,70E-01	5,13E-01	
MAP7	-0,55	2,43E-01	4,90E-01	
NME1-NME2;NME2;NME1;NME2P1	-0,55	1,85E-01	4,30E-01	
MARK3	-0,56	3,18E-01	5,65E-01	
OGDH;OGDHL	-0,57	2,23E-01	4,70E-01	
SRRM1	-0,57	1,88E-01	4,33E-01	
U2AF2	-0,57	1,60E-01	4,01E-01	
NDUFS3	-0,57	2,49E-01	4,94E-01	
DNAJB11	-0,57	1,62E-01	4,04E-01	
HSP90B1	-0,57	2,67E-01	5,11E-01	
TUBB2B	-0,58	2,77E-01	5,22E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
PRPF3	-0,58	1,64E-01	4,04E-01	
SF3A2	-0,58	2,12E-01	4,55E-01	
U2SURP	-0,58	1,26E-01	3,55E-01	
GRB7	-0,58	2,11E-01	4,54E-01	
CLK3	-0,58	2,38E-01	4,89E-01	
ARL6IP4	-0,59	2,11E-01	4,54E-01	
TLN1	-0,59	2,84E-01	5,31E-01	
LUC7L2	-0,60	1,34E-01	3,66E-01	
LDHA	-0,60	3,32E-01	5,75E-01	
FRG1	-0,60	1,10E-01	3,32E-01	
C1QA	-0,60	1,39E-01	3,72E-01	
GTPBP1	-0,61	1,94E-01	4,39E-01	
TRA2B	-0,61	1,36E-01	3,67E-01	
HIST1H1B	-0,61	1,90E-01	4,35E-01	
PHF6	-0,61	1,09E-01	3,30E-01	
ERH	-0,62	1,14E-01	3,39E-01	
DDX41	-0,62	2,64E-01	5,10E-01	
SSR4	-0,63	1,79E-01	4,23E-01	
BUD13	-0,63	3,93E-01	6,33E-01	
SF1	-0,64	1,20E-01	3,46E-01	
SRSF7	-0,64	8,22E-02	2,87E-01	
WRNIP1	-0,65	1,69E-01	4,10E-01	
BRD9	-0,65	1,19E-01	3,44E-01	
GDI2	-0,65	1,72E-01	4,15E-01	
VEZF1	-0,65	1,75E-01	4,19E-01	
CDK13	-0,66	1,69E-01	4,10E-01	
WWP1	-0,66	2,30E-01	4,78E-01	
SUB1	-0,67	9,97E-02	3,13E-01	
GLYR1	-0,67	1,42E-01	3,79E-01	
ARL8A	-0,68	1,53E-01	3,91E-01	
PHF5A	-0,68	1,07E-01	3,27E-01	
GRB10	-0,68	1,49E-01	3,88E-01	
FIP1L1	-0,69	8,98E-02	3,02E-01	
FAM120A	-0,70	7,35E-02	2,71E-01	
FAM133B	-0,70	7,46E-02	2,73E-01	
EWSR1	-0,70	1,50E-01	3,88E-01	
SRSF10	-0,71	7,02E-02	2,61E-01	
FIZ1	-0,72	6,48E-02	2,51E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
ZSCAN21	-0,72	1,35E-01	3,66E-01	
WBP11	-0,72	6,79E-02	2,58E-01	
PHC2	-0,73	1,58E-01	3,99E-01	
RBMX2	-0,75	1,16E-01	3,41E-01	
S100A7;S100A7A	-0,75	1,18E-01	3,43E-01	
YWHAZ	-0,76	1,18E-01	3,43E-01	
CHTOP	-0,76	1,28E-01	3,62E-01	
YWHAE	-0,76	8,25E-02	2,87E-01	
ILF3	-0,76	1,24E-01	3,51E-01	
MYNN	-0,76	1,15E-01	3,40E-01	
FBXL6	-0,78	1,45E-01	3,83E-01	
CS	-0,79	1,74E-01	4,16E-01	
RBM26	-0,79	2,25E-01	4,71E-01	
RAP1B;RAP1A	-0,79	1,04E-01	3,22E-01	
ZNF532	-0,79	1,02E-01	3,20E-01	
GOT2	-0,81	2,37E-01	4,88E-01	
C3	-0,81	9,64E-02	3,11E-01	
RSBN1L	-0,81	4,96E-02	2,19E-01	
TUBA1A	-0,82	2,24E-01	4,71E-01	
ACTN4	-0,82	1,43E-01	3,81E-01	
YBX3	-0,83	6,11E-02	2,44E-01	
PRPF38B	-0,84	1,22E-01	3,50E-01	
BUD31	-0,85	8,05E-02	2,85E-01	
DHX16	-0,86	8,14E-02	2,86E-01	
EPB41L4B	-0,87	2,10E-01	4,53E-01	
Cxorf56	-0,88	6,20E-02	2,45E-01	
ARG1	-0,89	9,37E-02	3,07E-01	
THRAP3	-0,90	2,80E-02	1,62E-01	
RPS19BP1	-0,90	9,73E-02	3,13E-01	
ACTN1	-0,90	1,03E-01	3,20E-01	
CWC25	-0,91	2,59E-02	1,56E-01	
CPSF6	-0,92	9,86E-02	3,13E-01	
SFSWAP	-0,92	5,14E-02	2,21E-01	
CPSF4	-0,92	8,11E-02	2,86E-01	
GPATCH8	-0,94	1,35E-01	3,66E-01	
SRSF1	-0,94	2,07E-02	1,36E-01	
ARHGEF39	-0,95	6,68E-02	2,55E-01	
ASF1A	-0,96	3,07E-02	1,69E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
TCEB2	-0,96	6,23E-02	2,45E-01	
MAP7D1	-0,97	1,29E-01	3,62E-01	
RBMX	-0,97	2,65E-02	1,58E-01	
RPS29	-0,97	4,04E-02	2,01E-01	
TBC1D10B	-0,97	7,78E-02	2,79E-01	
CBX6	-0,98	6,61E-02	2,54E-01	
CSTA	-0,98	3,26E-02	1,76E-01	
EEF1B2	-0,98	8,36E-02	2,88E-01	
SIRT7	-0,99	3,81E-02	1,95E-01	
MASP1	-0,99	6,18E-02	2,45E-01	
SNRPB2	-1,00	8,26E-02	2,87E-01	
RPN1	-1,00	2,02E-02	1,33E-01	
HMGXB4	-1,03	1,46E-02	1,17E-01	
YARS	-1,03	4,46E-02	2,07E-01	
SRP9	-1,04	9,90E-02	3,13E-01	
IKZF5	-1,06	5,50E-02	2,29E-01	
PPIB	-1,07	5,33E-02	2,24E-01	
DCD	-1,07	2,67E-02	1,58E-01	
RAB11FIP5	-1,07	1,73E-02	1,27E-01	
TCF7;TCF7L2;LEF1	-1,09	4,44E-02	2,07E-01	
H1F0	-1,09	4,50E-02	2,07E-01	
NXT1	-1,09	4,45E-02	2,07E-01	
OSBPL7	-1,12	3,45E-02	1,83E-01	
BCLAF1	-1,12	1,61E-02	1,23E-01	
NUDT21	-1,13	5,69E-02	2,34E-01	
SIN3A	-1,14	3,64E-02	1,87E-01	
KLF13	-1,15	3,18E-02	1,74E-01	
MSN	-1,16	1,98E-02	1,33E-01	
PPIL4	-1,17	3,60E-02	1,87E-01	
LSM14B	-1,21	2,89E-02	1,63E-01	
PDIA6	-1,24	4,34E-02	2,07E-01	
EPB41L5	-1,25	3,83E-02	1,95E-01	
PLEC	-1,25	1,34E-01	3,66E-01	
TPI1	-1,27	1,54E-01	3,93E-01	
TXN	-1,28	2,30E-02	1,46E-01	
WWP2	-1,34	1,93E-02	1,33E-01	
CAAP1	-1,39	3,90E-02	1,97E-01	
SP2	-1,41	9,59E-03	9,86E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**Function**
YTHDC1	-1,42	1,25E-02	1,13E-01	
GLYR1	-1,46	9,21E-03	9,86E-02	
GTF2F2	-1,48	1,36E-02	1,16E-01	
DSP	-1,50	5,65E-03	7,87E-02	
AZGP1	-1,58	7,89E-03	9,16E-02	
S100A9	-1,58	1,06E-02	1,04E-01	
MICU1	-1,62	1,77E-02	1,27E-01	
GTF2F1	-1,66	6,19E-03	8,07E-02	
VANGL2	-1,66	5,92E-03	8,04E-02	
PDIA3	-1,71	4,67E-02	2,13E-01	
HSPE1;HSPE1-MOB4	-1,73	2,43E-02	1,50E-01	
WWC1	-1,78	4,20E-03	6,86E-02	
GTPBP2	-1,84	3,81E-03	6,45E-02	
DPYSL2	-1,87	3,79E-03	6,45E-02	
ANXA2;ANXA2P2	-2,15	5,16E-04	3,21E-02	
DUT	-2,19	1,82E-03	4,41E-02	
EPB41L5	-2,33	4,78E-03	7,53E-02	
IGKV4-1	-2,33	5,43E-03	7,87E-02	
ZNF653	-2,48	1,07E-03	3,46E-02	
S100A8	-2,50	1,21E-02	1,12E-01	

7.3.10 Table with values corresponding to Figure 4.18.A and Figure 4.19.A and Figure 4.20.A

Table 7.14: Values corresponding to Figure 4.18.A and Figure 4.19.A and Figure 4.20.A. Values are sorted according to mean log2FC and p-value. Genes marked in bold were determined as significant MYC interactors in T-lymphoma cells according to the cutoffs: log2FC>1, q-value<0.1.

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
MAX	9,99	6,81E-09	6,59E-06	10,06	2,50E-11	2,23E-08	
MYC	9,65	1,76E-08	8,53E-06	10,11	8,85E-11	3,94E-08	
TRRAP	7,99	7,41E-08	2,39E-05	1,34	2,11E-02	1,18E-01	Chromatin remodelling
EP400	2,85	1,41E-05	3,42E-03	0,00	1,00E+00	1,00E+00	Chromatin remodelling
HUWE1	5,68	1,05E-04	2,04E-02	0,62	3,13E-01	5,34E-01	Degradation
SUPT6H	3,70	1,71E-04	2,48E-02	4,28	1,92E-03	3,60E-02	Transcription

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
KIAA0368;ECM29	2,36	1,93E-04	2,48E-02	2,54	1,43E-05	2,67E-03	Degradation
PSMD11	2,31	2,05E-04	2,48E-02	2,26	7,27E-05	8,09E-03	Degradation
CSNK2A1;CSNK2A3	2,81	3,72E-04	2,57E-02	3,06	4,07E-04	1,64E-02	Other
HADHA	2,66	3,11E-04	2,57E-02	2,63	1,50E-05	2,67E-03	Other
FBXW7	2,65	3,54E-04	2,57E-02	0,00	1,00E+00	1,00E+00	Degradation
DMAP1	1,98	3,48E-04	2,57E-02	0,00	1,00E+00	1,00E+00	Chromatin remodelling
GATAD2B	1,75	3,61E-04	2,57E-02	0,94	3,17E-02	1,56E-01	Transcription
PSMC4	1,88	4,50E-04	2,75E-02	1,90	3,11E-04	1,63E-02	Degradation
RARS	1,71	4,55E-04	2,75E-02	1,77	3,80E-04	1,63E-02	Other
BAG2	2,25	6,97E-04	2,99E-02	3,50	6,10E-06	1,81E-03	Other
MCM5	2,24	7,76E-04	2,99E-02	1,58	4,12E-03	4,99E-02	Replication
WDR5	2,21	6,87E-04	2,99E-02	2,55	4,78E-04	1,70E-02	Transcription
PSMB5	2,18	7,23E-04	2,99E-02	0,00	1,00E+00	1,00E+00	Degradation
SMARCA4	1,89	7,27E-04	2,99E-02	1,28	2,46E-03	4,13E-02	Chromatin remodelling
CSNK2B;CSNK2B-LY6G5B-1181; CSNK2B-LY6G5B-991	1,88	5,80E-04	2,99E-02	1,47	1,77E-03	3,43E-02	Other
RUVBL1	1,87	8,35E-04	2,99E-02	1,27	3,15E-03	4,57E-02	Chromatin remodelling
PSMA2	1,65	6,00E-04	2,99E-02	1,27	1,48E-02	9,51E-02	Degradation
PSMA3	1,59	7,62E-04	2,99E-02	1,10	6,94E-03	6,79E-02	Degradation
PSMD3	1,55	7,57E-04	2,99E-02	1,63	4,41E-04	1,69E-02	Degradation
PSMC5	1,48	8,22E-04	2,99E-02	1,29	2,94E-03	4,51E-02	Degradation
RUNX2	1,69	9,10E-04	3,14E-02	1,72	5,35E-04	1,83E-02	Transcription
UBR5	3,27	9,70E-04	3,24E-02	1,92	2,24E-03	3,91E-02	Degradation
RUVBL2	1,62	1,02E-03	3,29E-02	1,07	8,45E-03	7,17E-02	Chromatin remodelling
POLR2B	1,77	1,16E-03	3,52E-02	0,77	7,21E-02	2,35E-01	Transcription
PSMD12	1,44	1,15E-03	3,52E-02	1,51	9,23E-04	2,49E-02	Degradation
CBFB	1,98	1,23E-03	3,62E-02	3,02	3,21E-04	1,63E-02	Transcription
WDR46	1,65	1,31E-03	3,73E-02	0,94	4,06E-02	1,70E-01	Other
PSMA6	1,87	1,58E-03	4,23E-02	1,58	1,70E-03	3,43E-02	Degradation
PSMC2	1,56	1,64E-03	4,23E-02	1,69	3,49E-04	1,63E-02	Degradation
NAP1L1	1,30	1,64E-03	4,23E-02	1,20	8,82E-03	7,24E-02	Chromatin remodelling
EIF3E	1,53	1,75E-03	4,34E-02	1,51	1,44E-03	3,40E-02	Other
RPS28	1,23	2,05E-03	4,72E-02	1,80	3,17E-04	1,63E-02	Other
DYNC1H1	1,34	2,12E-03	4,78E-02	2,14	6,41E-05	8,09E-03	Other

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
CAD	1,22	2,31E-03	5,07E-02	0,98	1,20E-02	8,49E-02	Other
PSMD8	1,52	2,37E-03	5,09E-02	1,32	1,01E-02	7,71E-02	Degradation
GART	1,33	2,44E-03	5,14E-02	1,48	1,58E-03	3,43E-02	Other
SMARCD2	2,47	2,62E-03	5,24E-02	0,00	1,00E+00	1,00E+00	Chromatin remodelling
ATAD3A;ATAD3B	2,39	2,65E-03	5,24E-02	1,42	2,55E-02	1,33E-01	Other
ACTL6A	1,97	2,64E-03	5,24E-02	1,18	2,36E-02	1,27E-01	Chromatin remodelling
CTPS1	1,66	2,82E-03	5,29E-02	1,46	6,14E-03	6,28E-02	Other
PDS5A	1,22	2,84E-03	5,29E-02	1,13	9,72E-03	7,52E-02	Chromatin remodelling
HADHB	2,00	2,91E-03	5,31E-02	2,28	7,26E-05	8,09E-03	Other
CSDE1	1,82	3,26E-03	5,36E-02	2,07	7,24E-04	2,18E-02	Other
HDAC1	1,46	3,40E-03	5,36E-02	1,37	2,19E-03	3,89E-02	Chromatin remodelling
LMNB1	1,34	3,29E-03	5,36E-02	0,86	2,74E-02	1,39E-01	Other
PSMA4	1,24	3,17E-03	5,36E-02	1,13	2,60E-02	1,34E-01	Degradation
CCT4	1,20	3,38E-03	5,36E-02	1,75	2,80E-04	1,63E-02	Other
CCT3	1,20	3,19E-03	5,36E-02	1,53	7,60E-04	2,18E-02	Other
PSMA7;PSMA8	2,15	4,04E-03	5,84E-02	2,00	8,24E-04	2,29E-02	Degradation
GCN1L1	1,55	4,13E-03	5,84E-02	1,94	1,85E-04	1,55E-02	Other
IPO5	1,24	3,99E-03	5,84E-02	1,22	4,79E-03	5,27E-02	Other
PES1	1,11	4,22E-03	5,84E-02	0,40	2,43E-01	4,50E-01	Other
MATR3	1,11	4,84E-03	6,33E-02	0,81	4,04E-02	1,70E-01	Transcription
MSH6	1,07	4,83E-03	6,33E-02	0,66	8,17E-02	2,49E-01	Replication
MDN1	1,48	4,92E-03	6,36E-02	0,00	1,00E+00	1,00E+00	Other
MTA2	1,96	5,08E-03	6,48E-02	1,72	1,28E-03	3,19E-02	Other
F13A1	1,67	5,67E-03	6,94E-02	1,85	1,49E-03	3,40E-02	Other
COPA	1,07	5,88E-03	7,03E-02	1,16	8,13E-03	7,17E-02	Other
SMARCC1	2,03	6,92E-03	7,12E-02	1,16	9,25E-03	7,35E-02	Chromatin remodelling
MYL12A;MYL12B	1,55	6,74E-03	7,12E-02	2,70	7,47E-04	2,18E-02	Other
CCT5	1,36	6,61E-03	7,12E-02	1,89	1,26E-03	3,19E-02	Other
IKBKAP	1,27	6,25E-03	7,12E-02	0,83	7,64E-02	2,42E-01	Other
PSMD2	1,26	6,82E-03	7,12E-02	1,43	1,72E-03	3,43E-02	Degradation
PFKL	1,21	6,15E-03	7,12E-02	1,53	7,97E-03	7,17E-02	Other
RBBP4	1,19	6,79E-03	7,12E-02	1,03	1,25E-02	8,61E-02	Other
CHD4	1,14	6,77E-03	7,12E-02	1,02	1,21E-02	8,49E-02	Other
ACACA	1,43	7,41E-03	7,17E-02	1,58	4,04E-03	4,99E-02	Other
PA2G4	1,16	7,39E-03	7,17E-02	1,54	1,29E-03	3,19E-02	Transcription
PSMC3	2,20	7,59E-03	7,28E-02	2,41	3,40E-04	1,63E-02	Degradation

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BDH1	1,97	7,77E-03	7,31E-02	1,36	5,04E-02	1,92E-01	Other
STRAP	1,32	7,86E-03	7,31E-02	1,54	4,53E-03	5,11E-02	Other
IPO7	1,30	7,97E-03	7,31E-02	1,38	1,04E-02	7,78E-02	Other
EIF3A	1,75	8,89E-03	7,63E-02	2,46	1,92E-04	1,55E-02	Other
SUPT5H	1,64	9,13E-03	7,63E-02	1,51	7,80E-03	7,17E-02	Transcription
PSMB2	1,56	8,77E-03	7,63E-02	1,23	1,90E-02	1,11E-01	Degradation
AIMP2	1,11	9,23E-03	7,63E-02	1,43	3,24E-03	4,57E-02	Other
PSMC1	1,05	8,81E-03	7,63E-02	0,91	3,31E-02	1,57E-01	Degradation
TRAP1	1,03	9,29E-03	7,63E-02	0,00	1,00E+00	1,00E+00	Other
PSMB3	1,63	9,69E-03	7,74E-02	1,38	1,17E-02	8,44E-02	Degradation
SMC1A	1,48	9,54E-03	7,74E-02	1,05	3,53E-02	1,61E-01	Chromatin remodelling
PSMC6	1,41	9,86E-03	7,74E-02	1,64	4,55E-04	1,69E-02	Degradation
DARS	1,18	9,75E-03	7,74E-02	1,32	3,11E-03	4,57E-02	Other
SMC4	1,27	1,03E-02	7,82E-02	1,16	2,03E-02	1,16E-01	Chromatin remodelling
WDR26	1,26	1,04E-02	7,82E-02	1,45	8,12E-03	7,17E-02	Other
SUPT16H	1,23	1,04E-02	7,82E-02	1,14	1,34E-02	8,97E-02	Chromatin remodelling
TSR1	1,18	1,27E-02	8,94E-02	1,22	1,77E-02	1,06E-01	Other
HSPH1	1,07	1,42E-02	9,67E-02	1,43	2,76E-03	4,39E-02	Other
PSMD6	1,73	1,45E-02	9,77E-02	2,27	1,65E-04	1,55E-02	Degradation
DKC1	1,14	1,46E-02	9,77E-02	0,79	9,93E-02	2,70E-01	Other
DNAJB6	1,10	1,54E-02	1,00E-01	0,81	8,39E-02	2,52E-01	
PLK1	1,32	1,61E-02	1,03E-01	0,00	1,00E+00	1,00E+00	
NACC1	1,17	1,65E-02	1,05E-01	1,63	7,04E-04	2,18E-02	
UTP20	1,77	1,69E-02	1,05E-01	0,00	1,00E+00	1,00E+00	
HNRNPR	1,14	1,72E-02	1,05E-01	0,54	2,97E-01	5,11E-01	
CUL1	1,35	1,78E-02	1,06E-01	0,00	1,00E+00	1,00E+00	
PDCD4	1,13	1,84E-02	1,07E-01	0,72	4,93E-02	1,90E-01	
MCM2	1,42	1,85E-02	1,07E-01	1,20	2,50E-02	1,32E-01	
HEATR1	1,37	2,02E-02	1,14E-01	0,88	7,02E-02	2,32E-01	
PSMB1	1,61	2,15E-02	1,18E-01	1,34	1,84E-02	1,09E-01	
PGAM5	1,09	2,19E-02	1,18E-01	0,98	5,67E-02	2,07E-01	
HCFC1	2,32	2,23E-02	1,20E-01	2,81	3,23E-03	4,57E-02	
PPP2CA;PPP2CB	1,22	2,25E-02	1,20E-01	1,46	8,44E-03	7,17E-02	
PSMA5	1,05	2,37E-02	1,21E-01	0,66	1,20E-01	2,96E-01	
SMC3	1,02	2,51E-02	1,24E-01	1,06	3,34E-02	1,57E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
PSMD7	1,63	2,76E-02	1,29E-01	2,09	2,16E-04	1,60E-02	
PPP2R2A;PPP2R2D	1,40	2,88E-02	1,30E-01	1,21	3,32E-02	1,57E-01	
GPC1	1,20	2,86E-02	1,30E-01	1,27	1,53E-02	9,73E-02	
ANP32E	1,33	3,35E-02	1,41E-01	0,95	1,01E-01	2,72E-01	
RPL18	1,14	3,88E-02	1,52E-01	1,37	2,42E-03	4,13E-02	
PSMD1	1,65	4,11E-02	1,56E-01	1,61	2,10E-02	1,18E-01	
PSMD14	1,31	4,18E-02	1,58E-01	0,76	1,88E-01	3,87E-01	
MYH9	1,12	4,63E-02	1,64E-01	2,40	7,97E-03	7,17E-02	
TCF12	1,08	4,62E-02	1,64E-01	1,32	4,34E-03	5,02E-02	
CCT7	1,04	4,73E-02	1,65E-01	1,58	3,94E-03	4,95E-02	
ABCE1	1,11	6,01E-02	1,90E-01	1,60	4,23E-03	4,99E-02	
HNRNPD	1,01	8,28E-02	2,23E-01	1,59	2,05E-02	1,16E-01	
MYO5A	1,90	9,11E-02	2,36E-01	0,00	1,00E+00	1,00E+00	
MYO1G	1,16	1,12E-01	2,67E-01	0,00	1,00E+00	1,00E+00	
NASP	1,01	1,35E-01	3,03E-01	1,88	7,15E-03	6,91E-02	
TOP2A	0,99	1,58E-02	1,02E-01	0,76	7,89E-02	2,45E-01	
ZNF281	0,99	3,93E-02	1,53E-01	0,00	1,00E+00	1,00E+00	
EIF3C;EIF3CL	0,99	6,63E-03	7,12E-02	1,28	3,63E-03	4,78E-02	
DIAPH3	0,98	4,34E-02	1,60E-01	0,00	1,00E+00	1,00E+00	
GNL3	0,97	2,06E-02	1,15E-01	0,96	8,26E-02	2,50E-01	
RPL35A	0,96	9,01E-03	7,63E-02	1,26	3,71E-03	4,78E-02	
HNRNPM	0,96	8,00E-03	7,31E-02	0,95	1,68E-02	1,03E-01	
EIF3D	0,95	2,19E-02	1,18E-01	1,12	1,34E-02	8,97E-02	
RAD21	0,95	8,38E-02	2,25E-01	0,00	1,00E+00	1,00E+00	
GTF2I	0,95	6,78E-03	7,12E-02	1,05	9,20E-03	7,35E-02	
RBBP7	0,94	8,10E-03	7,33E-02	1,33	1,98E-03	3,60E-02	
MAT2A	0,94	9,82E-02	2,46E-01	0,43	4,08E-01	6,11E-01	
BAT3;BAG6	0,93	2,94E-02	1,30E-01	1,04	3,24E-02	1,57E-01	
MTSS1	0,92	6,24E-02	1,94E-01	0,94	1,54E-01	3,47E-01	
SMC2	0,92	2,51E-02	1,24E-01	0,75	6,19E-02	2,18E-01	
GAPDH	0,92	4,69E-02	1,64E-01	0,93	1,67E-02	1,03E-01	
SKIV2L	0,91	3,35E-02	1,41E-01	1,42	7,79E-03	7,17E-02	
GNL2	0,91	3,81E-02	1,50E-01	0,61	1,04E-01	2,75E-01	
EIF3F	0,91	1,75E-02	1,06E-01	1,18	5,91E-03	6,12E-02	
RPL13	0,91	5,48E-02	1,79E-01	1,33	3,01E-03	4,53E-02	
EIF4A1;EIF4A2	0,91	1,01E-01	2,50E-01	1,16	2,04E-02	1,16E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
TCP1	0,91	8,33E-03	7,40E-02	1,18	4,18E-03	4,99E-02	
RFC5	0,90	1,50E-02	9,92E-02	0,76	4,61E-02	1,85E-01	
CCT8	0,90	2,99E-02	1,31E-01	1,47	1,46E-03	3,40E-02	
SMARCB1	0,89	3,74E-02	1,49E-01	0,00	1,00E+00	1,00E+00	
PSMA1	0,89	2,95E-01	4,68E-01	0,64	2,34E-01	4,40E-01	
SF3B6	0,89	1,02E-01	2,52E-01	0,00	1,00E+00	1,00E+00	
KDM1A	0,89	6,99E-02	2,10E-01	1,37	1,28E-02	8,73E-02	
PAXIP1	0,88	3,62E-02	1,47E-01	0,00	1,00E+00	1,00E+00	
ESF1	0,88	1,27E-01	2,91E-01	0,00	1,00E+00	1,00E+00	
KPNB1	0,88	1,09E-02	8,08E-02	0,54	1,66E-01	3,61E-01	
RFC2	0,88	3,84E-02	1,51E-01	0,73	1,17E-01	2,91E-01	
PBRM1	0,87	4,83E-02	1,67E-01	1,00	4,44E-02	1,83E-01	
CCT2	0,87	4,46E-02	1,62E-01	1,39	3,41E-03	4,66E-02	
CCT6A	0,86	2,00E-02	1,13E-01	1,27	2,71E-03	4,39E-02	
KPNA2	0,86	5,17E-02	1,72E-01	0,89	7,84E-02	2,45E-01	
DNAJA1	0,85	1,23E-02	8,75E-02	1,47	1,62E-03	3,43E-02	
DDX49	0,85	4,66E-02	1,64E-01	0,24	5,93E-01	7,56E-01	
EIF3B	0,85	1,39E-02	9,62E-02	0,94	2,02E-02	1,16E-01	
METTL17	0,85	1,83E-01	3,59E-01	0,00	1,00E+00	1,00E+00	
RRP12	0,84	2,88E-02	1,30E-01	0,82	5,70E-02	2,07E-01	
CYB5A	0,84	5,71E-02	1,84E-01	0,62	1,67E-01	3,62E-01	
RCC2	0,84	2,28E-02	1,20E-01	0,54	1,35E-01	3,21E-01	
ATIC	0,83	6,50E-02	2,01E-01	1,36	8,99E-03	7,27E-02	
MAFK	0,82	7,06E-02	2,11E-01	0,37	4,20E-01	6,20E-01	
AIFM1	0,81	2,16E-02	1,18E-01	0,76	5,34E-02	1,98E-01	
CTNNB1	0,81	3,27E-02	1,39E-01	1,11	2,15E-02	1,19E-01	
EIF3L	0,81	4,24E-02	1,58E-01	1,34	2,86E-03	4,47E-02	
HSPA9	0,81	3,93E-02	1,53E-01	0,43	2,26E-01	4,33E-01	
PSMD4	0,80	6,10E-02	1,91E-01	1,02	3,66E-02	1,61E-01	
UPF1	0,80	1,41E-02	9,67E-02	0,73	4,60E-02	1,85E-01	
POLDIP2	0,79	5,12E-02	1,72E-01	0,00	1,00E+00	1,00E+00	
DPY30	0,79	1,53E-02	1,00E-01	1,30	9,49E-03	7,46E-02	
SYNCRIP	0,78	7,58E-02	2,17E-01	0,82	1,07E-01	2,78E-01	
GTF3C1	0,78	8,20E-02	2,23E-01	0,00	1,00E+00	1,00E+00	
MSH2	0,78	4,59E-02	1,64E-01	1,11	8,14E-03	7,17E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
CAPZA1	0,77	5,58E-02	1,81E-01	0,00	1,00E+00	1,00E+00	
IMMT	0,76	3,44E-02	1,43E-01	0,79	3,56E-02	1,61E-01	
VARS	0,75	9,79E-02	2,46E-01	1,18	2,79E-02	1,40E-01	
PSIP1	0,75	6,01E-02	1,90E-01	0,00	1,00E+00	1,00E+00	
LARS	0,75	1,23E-01	2,84E-01	1,09	1,70E-02	1,03E-01	
EIF3M	0,75	1,47E-01	3,16E-01	0,75	1,95E-01	3,97E-01	
GTPBP4	0,75	2,34E-02	1,21E-01	0,74	4,64E-02	1,85E-01	
PHGDH	0,75	7,78E-02	2,19E-01	0,89	5,22E-02	1,96E-01	
DNAJC7	0,75	6,32E-02	1,96E-01	0,00	1,00E+00	1,00E+00	
RPL11	0,74	6,81E-02	2,06E-01	0,85	3,62E-02	1,61E-01	
DCAF13	0,74	5,99E-02	1,90E-01	-0,30	3,83E-01	5,90E-01	
MTHFD1L	0,73	1,00E-01	2,49E-01	0,00	1,00E+00	1,00E+00	
GRWD1	0,72	1,16E-01	2,75E-01	0,51	2,14E-01	4,19E-01	
CUL2	0,72	5,78E-02	1,85E-01	1,34	1,94E-03	3,60E-02	
EIF3H	0,72	1,04E-01	2,54E-01	0,97	4,57E-02	1,85E-01	
NOP56	0,72	4,09E-02	1,56E-01	0,68	8,25E-02	2,50E-01	
PNO1	0,72	7,24E-02	2,14E-01	0,00	1,00E+00	1,00E+00	
MCM7	0,71	1,52E-01	3,22E-01	1,15	1,09E-02	8,10E-02	
RPS21	0,71	1,44E-01	3,16E-01	1,62	8,87E-03	7,24E-02	
CDK1;CDC2	0,71	2,44E-02	1,23E-01	0,56	1,13E-01	2,86E-01	
EIF3I	0,71	2,42E-02	1,23E-01	0,64	9,42E-02	2,67E-01	
DDB1	0,70	5,08E-02	1,72E-01	0,99	2,46E-02	1,30E-01	
TUBB	0,70	4,12E-02	1,56E-01	0,51	1,45E-01	3,32E-01	
DNAJA2	0,70	2,54E-02	1,25E-01	1,19	4,65E-03	5,17E-02	
TIMM50	0,70	7,55E-02	2,17E-01	0,75	1,06E-01	2,78E-01	
NRF1	0,69	7,97E-02	2,20E-01	0,77	9,95E-02	2,70E-01	
DNMT1	0,69	7,28E-02	2,14E-01	0,40	3,23E-01	5,41E-01	
DDX21	0,69	2,89E-02	1,30E-01	0,34	3,30E-01	5,42E-01	
HSPA8	0,69	3,63E-02	1,47E-01	1,28	4,26E-03	4,99E-02	
STAT5B	0,69	3,10E-02	1,33E-01	0,92	2,97E-02	1,48E-01	
MCM3	0,69	7,44E-02	2,17E-01	0,73	5,99E-02	2,14E-01	
RPL7	0,68	2,77E-02	1,29E-01	1,10	8,34E-03	7,17E-02	
XRN2	0,68	3,75E-02	1,49E-01	0,78	4,71E-02	1,86E-01	
PPIL1	0,68	1,80E-01	3,56E-01	0,00	1,00E+00	1,00E+00	
NAT10	0,67	8,19E-02	2,23E-01	0,32	3,79E-01	5,90E-01	
MTHFD1	0,67	6,11E-02	1,91E-01	0,71	1,30E-01	3,14E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PDS5B	0,67	2,92E-02	1,30E-01	1,13	5,43E-03	5,82E-02	
ARHGEF1	0,67	1,03E-01	2,54E-01	0,00	1,00E+00	1,00E+00	
TUBA4A	0,66	9,06E-02	2,36E-01	1,00	1,80E-02	1,07E-01	
CANX	0,66	1,58E-01	3,29E-01	0,60	2,17E-01	4,23E-01	
ATP2A2	0,65	9,57E-02	2,44E-01	0,00	1,00E+00	1,00E+00	
RPL14	0,65	3,49E-02	1,43E-01	0,82	3,60E-02	1,61E-01	
RPL36	0,64	7,74E-02	2,19E-01	1,65	5,79E-04	1,91E-02	
RAD50	0,64	9,95E-02	2,48E-01	0,85	7,20E-02	2,35E-01	
TUFM	0,64	5,45E-02	1,79E-01	0,19	5,95E-01	7,56E-01	
PSMD13	0,63	2,67E-01	4,48E-01	0,82	9,91E-02	2,70E-01	
RPSA	0,63	4,06E-02	1,56E-01	1,10	7,71E-03	7,17E-02	
SND1	0,63	4,28E-02	1,58E-01	0,68	6,30E-02	2,21E-01	
CBX3	0,63	3,22E-01	4,95E-01	1,77	4,52E-03	5,11E-02	
COPB2	0,63	4,66E-02	1,64E-01	1,26	1,37E-02	9,03E-02	
SSRP1	0,63	8,18E-02	2,23E-01	0,62	1,18E-01	2,94E-01	
USP7	0,63	4,71E-02	1,64E-01	0,99	1,76E-02	1,06E-01	
EPRS	0,63	1,92E-01	3,70E-01	1,05	1,04E-02	7,78E-02	
NCBP1	0,62	2,69E-01	4,49E-01	0,00	9,92E-01	9,95E-01	
HNRNPF	0,62	8,53E-02	2,27E-01	0,70	6,69E-02	2,27E-01	
RFC3	0,62	5,82E-02	1,86E-01	0,60	1,85E-01	3,85E-01	
G3BP2	0,61	1,07E-01	2,61E-01	0,94	4,84E-02	1,90E-01	
SRM	0,61	1,35E-01	3,03E-01	0,94	1,59E-02	1,00E-01	
ACTB	0,61	1,91E-01	3,69E-01	1,38	4,51E-02	1,84E-01	
PPAN;PPAN-P2RY11	0,61	9,73E-02	2,46E-01	0,48	2,57E-01	4,63E-01	
POLR2H	0,61	8,57E-02	2,28E-01	1,09	2,72E-02	1,38E-01	
RPL32	0,61	4,25E-02	1,58E-01	0,38	2,92E-01	5,06E-01	
MGEA5	0,60	1,10E-01	2,66E-01	1,40	7,83E-03	7,17E-02	
RPS10;RPS10-NUDT3	0,60	6,19E-02	1,93E-01	1,20	5,89E-03	6,12E-02	
TNPO1	0,60	2,86E-01	4,59E-01	1,20	2,14E-02	1,19E-01	
RPL12	0,60	1,26E-01	2,90E-01	1,44	8,37E-03	7,17E-02	
BANF1	0,60	1,48E-01	3,17E-01	-0,31	5,90E-01	7,54E-01	
RPS15	0,60	1,61E-01	3,31E-01	0,85	1,10E-01	2,83E-01	
CFAP20	0,59	2,14E-01	3,95E-01	0,39	3,59E-01	5,72E-01	
IK	0,59	5,01E-02	1,71E-01	0,24	5,10E-01	6,90E-01	
PPP1CC	0,59	1,64E-01	3,34E-01	0,66	1,13E-01	2,86E-01	
NOP58	0,59	1,24E-01	2,85E-01	0,66	9,25E-02	2,64E-01	
DDX19A;DDX19B	0,59	1,39E-01	3,10E-01	0,06	8,81E-01	9,27E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
LRRC59	0,59	1,61E-01	3,31E-01	0,00	1,00E+00	1,00E+00	
HSPD1	0,58	1,21E-01	2,81E-01	0,50	2,48E-01	4,55E-01	
RNF138	0,58	2,67E-01	4,48E-01	0,00	1,00E+00	1,00E+00	
IMPDH2	0,58	2,17E-01	3,96E-01	0,63	1,97E-01	3,99E-01	
RPL27	0,58	8,83E-02	2,32E-01	0,82	4,88E-02	1,90E-01	
NPM1	0,58	1,08E-01	2,63E-01	0,71	1,39E-01	3,24E-01	
PRPS1	0,58	5,78E-02	1,85E-01	0,27	4,19E-01	6,20E-01	
BCAS2	0,58	1,27E-01	2,91E-01	0,36	4,10E-01	6,14E-01	
RPP30	0,57	2,46E-01	4,26E-01	0,87	7,02E-02	2,32E-01	
ZNF593	0,57	1,86E-01	3,61E-01	0,06	8,76E-01	9,27E-01	
DHX33	0,57	1,40E-01	3,11E-01	0,00	1,00E+00	1,00E+00	
PPP2R1A	0,57	1,53E-01	3,24E-01	0,59	1,39E-01	3,24E-01	
ILF2	0,57	1,30E-01	2,95E-01	0,37	3,51E-01	5,63E-01	
HNRNPH1	0,56	5,57E-02	1,81E-01	0,64	8,03E-02	2,47E-01	
PTBP1	0,56	1,97E-01	3,75E-01	0,81	7,66E-02	2,42E-01	
PDCD11	0,56	2,44E-01	4,25E-01	0,31	4,42E-01	6,34E-01	
UMPS	0,55	3,21E-01	4,93E-01	0,95	5,54E-02	2,03E-01	
GMPS	0,55	1,80E-01	3,56E-01	0,96	2,61E-02	1,34E-01	
RALY	0,55	1,38E-01	3,08E-01	0,81	3,46E-02	1,60E-01	
RPF1	0,55	9,52E-02	2,44E-01	0,75	6,87E-02	2,31E-01	
RPL15	0,55	7,56E-02	2,17E-01	1,01	1,41E-02	9,21E-02	
LIG1	0,55	2,01E-01	3,81E-01	0,36	4,32E-01	6,28E-01	
RPS18	0,55	7,49E-02	2,17E-01	0,63	8,55E-02	2,55E-01	
EEF1D	0,54	1,46E-01	3,16E-01	0,87	6,57E-02	2,24E-01	
PLRG1	0,54	1,88E-01	3,65E-01	0,08	8,03E-01	8,83E-01	
NSF	0,54	2,79E-01	4,55E-01	1,81	1,76E-03	3,43E-02	
SLC25A13	0,54	1,77E-01	3,53E-01	0,00	1,00E+00	1,00E+00	
ADK	0,53	1,50E-01	3,20E-01	0,83	7,55E-02	2,40E-01	
SMU1	0,53	1,31E-01	2,97E-01	0,18	6,43E-01	7,87E-01	
CAT	0,53	2,27E-01	4,09E-01	1,15	3,84E-02	1,64E-01	
HNRNPU	0,53	1,19E-01	2,77E-01	0,67	7,29E-02	2,37E-01	
ALDOA	0,53	1,54E-01	3,25E-01	1,04	7,33E-02	2,37E-01	
RPLP0;RPLP0P6	0,52	6,73E-02	2,04E-01	1,33	2,68E-03	4,39E-02	
PRPF4	0,52	9,53E-02	2,44E-01	-0,24	4,83E-01	6,67E-01	
RBM10	0,52	1,65E-01	3,36E-01	0,60	1,81E-01	3,80E-01	
RPL5	0,52	7,91E-02	2,20E-01	0,81	5,08E-02	1,93E-01	
VIM	0,52	3,39E-01	5,08E-01	2,43	3,70E-03	4,78E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
RPL28	0,52	1,10E-01	2,66E-01	0,80	4,77E-02	1,88E-01	
RPA1	0,52	2,05E-01	3,83E-01	0,00	1,00E+00	1,00E+00	
BLM	0,52	1,61E-01	3,31E-01	0,00	1,00E+00	1,00E+00	
ATP5A1	0,51	7,56E-02	2,17E-01	0,35	3,28E-01	5,42E-01	
DHX9	0,51	1,21E-01	2,81E-01	0,65	1,09E-01	2,81E-01	
UBA1	0,51	2,52E-01	4,31E-01	0,90	6,49E-02	2,24E-01	
SNX5	0,51	1,68E-01	3,41E-01	0,29	5,06E-01	6,88E-01	
PABPC1;PABPC3	0,51	2,73E-01	4,52E-01	0,84	1,03E-01	2,74E-01	
PAICS	0,51	8,27E-02	2,23E-01	0,00	1,00E+00	1,00E+00	
ABCF2	0,51	8,52E-02	2,27E-01	0,17	6,49E-01	7,87E-01	
MCM6	0,51	1,85E-01	3,61E-01	0,65	1,37E-01	3,24E-01	
GTF3A	0,51	1,78E-01	3,54E-01	0,20	6,47E-01	7,87E-01	
RPL18A	0,50	1,66E-01	3,37E-01	1,25	5,65E-03	5,99E-02	
RPS8	0,50	1,18E-01	2,77E-01	0,49	1,66E-01	3,61E-01	
MARS	0,50	7,96E-02	2,20E-01	0,80	4,94E-02	1,90E-01	
SPOCK2	0,50	1,60E-01	3,31E-01	0,86	2,26E-02	1,24E-01	
BAZ1B	0,50	1,73E-01	3,47E-01	0,00	1,00E+00	1,00E+00	
PRPF8	0,50	9,29E-02	2,41E-01	0,61	9,88E-02	2,70E-01	
EIF4G2	0,49	1,98E-01	3,77E-01	0,00	1,00E+00	1,00E+00	
TXNL1	0,49	8,62E-02	2,28E-01	0,00	1,00E+00	1,00E+00	
STK4;STK3	0,48	2,04E-01	3,83E-01	1,05	1,48E-02	9,51E-02	
DHX35	0,48	2,61E-01	4,41E-01	0,15	7,35E-01	8,46E-01	
TCERG1	0,47	2,50E-01	4,31E-01	0,71	1,40E-01	3,24E-01	
TARDBP	0,47	1,85E-01	3,61E-01	0,58	1,94E-01	3,96E-01	
RFC4	0,47	9,46E-02	2,44E-01	0,26	4,43E-01	6,35E-01	
RPS14	0,47	1,35E-01	3,03E-01	0,66	8,95E-02	2,59E-01	
SMCHD1	0,46	2,37E-01	4,19E-01	0,00	1,00E+00	1,00E+00	
CSE1L	0,46	2,04E-01	3,83E-01	1,32	1,12E-02	8,14E-02	
UBE2C	0,46	2,04E-01	3,83E-01	0,00	1,00E+00	1,00E+00	
UTP14A	0,46	2,32E-01	4,14E-01	0,00	1,00E+00	1,00E+00	
RRP15	0,46	2,47E-01	4,27E-01	0,56	2,29E-01	4,36E-01	
GARS	0,46	2,51E-01	4,31E-01	1,10	1,55E-02	9,78E-02	
KAT8	0,46	2,23E-01	4,06E-01	0,00	1,00E+00	1,00E+00	
PTGES3	0,45	3,66E-01	5,34E-01	0,85	1,02E-01	2,73E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
PKM	0,45	1,82E-01	3,58E-01	0,74	9,10E-02	2,62E-01	
SHMT2	0,45	4,12E-01	5,76E-01	1,40	2,33E-02	1,26E-01	
SERBP1	0,44	1,18E-01	2,77E-01	1,39	3,53E-03	4,77E-02	
RPL9	0,44	1,23E-01	2,84E-01	0,74	7,73E-02	2,43E-01	
DENND2D	0,44	2,60E-01	4,39E-01	1,01	3,49E-02	1,60E-01	
ATP1A1	0,43	2,80E-01	4,55E-01	0,86	8,83E-02	2,59E-01	
RPS16	0,43	1,29E-01	2,94E-01	0,92	2,01E-02	1,16E-01	
PRMT1	0,43	1,58E-01	3,29E-01	0,50	1,65E-01	3,61E-01	
MRTO4	0,43	1,41E-01	3,11E-01	0,81	3,89E-02	1,66E-01	
ACO2	0,43	5,31E-01	6,74E-01	0,65	2,92E-01	5,06E-01	
EIF1AX;EIF1AY	0,42	2,61E-01	4,41E-01	1,05	8,85E-03	7,24E-02	
HNRNPC	0,42	1,72E-01	3,46E-01	0,53	1,52E-01	3,45E-01	
MCM4	0,42	2,30E-01	4,12E-01	0,62	1,20E-01	2,96E-01	
RPS20	0,42	1,46E-01	3,16E-01	0,80	3,70E-02	1,61E-01	
PPP6R3	0,41	2,73E-01	4,52E-01	0,70	1,37E-01	3,24E-01	
PGK1	0,41	2,70E-01	4,49E-01	0,63	2,13E-01	4,19E-01	
PAF1	0,41	4,05E-01	5,70E-01	0,67	2,03E-01	4,06E-01	
CSNK2A2	0,41	2,91E-01	4,65E-01	0,47	1,96E-01	3,99E-01	
RPL4	0,41	1,47E-01	3,16E-01	0,72	8,28E-02	2,50E-01	
HSP90AB1	0,41	2,13E-01	3,93E-01	0,91	3,34E-02	1,57E-01	
RPL7A	0,40	1,48E-01	3,17E-01	0,41	2,46E-01	4,55E-01	
PPP1CB	0,40	1,48E-01	3,17E-01	0,99	2,64E-02	1,35E-01	
KIF2C	0,40	2,82E-01	4,56E-01	0,95	5,17E-02	1,95E-01	
GSPT1;GSPT2	0,40	2,63E-01	4,43E-01	0,78	9,14E-02	2,62E-01	
RPLP2	0,40	2,02E-01	3,81E-01	1,15	8,64E-03	7,24E-02	
DDX39A	0,40	3,46E-01	5,14E-01	0,65	1,12E-01	2,86E-01	
ENY2	0,40	2,74E-01	4,53E-01	0,00	1,00E+00	1,00E+00	
SKIV2L2	0,39	2,02E-01	3,81E-01	0,08	8,18E-01	8,94E-01	
RTCB	0,39	2,92E-01	4,66E-01	0,42	2,83E-01	4,95E-01	
DDX24	0,39	3,00E-01	4,71E-01	0,34	4,36E-01	6,28E-01	
CCDC59	0,38	2,95E-01	4,68E-01	0,00	1,00E+00	1,00E+00	
TAF6L	0,38	2,80E-01	4,55E-01	0,00	1,00E+00	1,00E+00	
RPL3	0,38	1,58E-01	3,29E-01	0,53	2,10E-01	4,18E-01	
DNTTIP2	0,38	4,05E-01	5,70E-01	0,00	1,00E+00	1,00E+00	
POLR2A	0,38	1,69E-01	3,42E-01	0,16	6,49E-01	7,87E-01	
USP5	0,38	3,32E-01	5,03E-01	0,84	6,98E-02	2,32E-01	
ZSCAN25	0,38	2,93E-01	4,66E-01	-0,05	9,11E-01	9,41E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
EIF5A	0,38	3,35E-01	5,05E-01	0,37	3,39E-01	5,50E-01	
NHP2L1	0,37	2,97E-01	4,69E-01	0,73	1,25E-01	3,05E-01	
UBA2	0,37	2,93E-01	4,66E-01	0,00	1,00E+00	1,00E+00	
RPS27A	0,37	2,57E-01	4,35E-01	0,49	2,03E-01	4,06E-01	
EFTUD2	0,36	2,08E-01	3,87E-01	0,40	2,53E-01	4,61E-01	
RPL37A	0,36	3,64E-01	5,34E-01	0,65	1,34E-01	3,21E-01	
RPS17	0,36	2,06E-01	3,83E-01	0,43	2,31E-01	4,36E-01	
POLRMT	0,36	3,21E-01	4,93E-01	0,05	9,00E-01	9,34E-01	
TUBA1A;TUBA3C;TUBA3E	0,36	2,55E-01	4,34E-01	0,68	6,92E-02	2,31E-01	
HELLS	0,36	3,15E-01	4,88E-01	0,00	1,00E+00	1,00E+00	
NOP2	0,36	2,08E-01	3,87E-01	0,00	9,94E-01	9,95E-01	
UBAP2L	0,35	2,98E-01	4,69E-01	0,60	2,31E-01	4,36E-01	
NCL	0,35	3,32E-01	5,03E-01	0,89	9,36E-02	2,66E-01	
MRPL22	0,35	3,26E-01	4,99E-01	-0,18	6,82E-01	8,08E-01	
ATP5C1	0,35	1,91E-01	3,69E-01	0,38	2,67E-01	4,72E-01	
EIF3G	0,35	2,30E-01	4,12E-01	0,43	2,42E-01	4,50E-01	
DNM2	0,35	3,31E-01	5,03E-01	0,93	5,09E-02	1,93E-01	
SRP68	0,35	2,30E-01	4,12E-01	0,09	8,05E-01	8,85E-01	
SPATA5	0,34	3,52E-01	5,22E-01	0,00	1,00E+00	1,00E+00	
HNRNPA0	0,34	3,10E-01	4,83E-01	0,48	2,57E-01	4,63E-01	
ZNF891;ZNF658;ZNF585B;ZNF175	0,34	4,87E-01	6,37E-01	0,29	5,15E-01	6,95E-01	
SNRNP200	0,34	2,47E-01	4,26E-01	0,43	2,19E-01	4,24E-01	
CHD8	0,34	3,54E-01	5,23E-01	0,00	1,00E+00	1,00E+00	
FBLL1	0,33	4,93E-01	6,42E-01	0,20	6,95E-01	8,18E-01	
EEF1G	0,33	2,42E-01	4,24E-01	1,39	3,95E-03	4,95E-02	
SET;SETSIP	0,33	3,61E-01	5,29E-01	0,47	3,28E-01	5,42E-01	
MRPL15	0,33	3,03E-01	4,75E-01	-0,09	7,93E-01	8,81E-01	
DNAJA3	0,33	2,24E-01	4,07E-01	-0,02	9,58E-01	9,69E-01	
LYAR	0,33	3,60E-01	5,29E-01	0,00	1,00E+00	1,00E+00	
BMS1	0,32	3,51E-01	5,21E-01	0,33	3,46E-01	5,58E-01	
CWC22	0,32	2,48E-01	4,28E-01	0,42	2,31E-01	4,36E-01	
TOP2B	0,32	3,12E-01	4,84E-01	0,77	9,80E-02	2,70E-01	
RPS27L	0,32	2,30E-01	4,12E-01	0,81	3,78E-02	1,63E-01	
CDC73	0,32	2,39E-01	4,21E-01	0,31	3,65E-01	5,77E-01	
KPNA3	0,31	3,44E-01	5,13E-01	-0,16	7,08E-01	8,29E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
MAZ	0,31	4,13E-01	5,76E-01	0,35	3,68E-01	5,82E-01	
KTN1	0,31	4,08E-01	5,73E-01	0,61	1,72E-01	3,65E-01	
GTF2H4	0,31	3,76E-01	5,42E-01	0,44	3,15E-01	5,36E-01	
MORF4L1	0,30	3,91E-01	5,59E-01	0,18	6,72E-01	8,02E-01	
NONO	0,30	3,88E-01	5,56E-01	0,56	1,24E-01	3,04E-01	
RPS3	0,30	2,86E-01	4,59E-01	0,74	7,39E-02	2,37E-01	
CREB1;CREM;ATF1	0,30	4,65E-01	6,19E-01	0,00	1,00E+00	1,00E+00	
EEF2	0,30	2,96E-01	4,68E-01	0,89	3,37E-02	1,58E-01	
TARS	0,30	4,02E-01	5,68E-01	0,96	4,68E-02	1,86E-01	
DDX10	0,29	2,65E-01	4,45E-01	-0,07	8,38E-01	9,02E-01	
ATP5B	0,29	4,01E-01	5,68E-01	0,33	4,26E-01	6,22E-01	
DDX17	0,29	3,36E-01	5,06E-01	0,51	1,84E-01	3,83E-01	
TP53BP1	0,28	4,23E-01	5,87E-01	0,26	4,97E-01	6,79E-01	
RPS19	0,28	3,31E-01	5,03E-01	0,98	3,10E-02	1,53E-01	
BRIX1	0,28	4,25E-01	5,88E-01	0,74	9,14E-02	2,62E-01	
SNX1	0,27	4,64E-01	6,18E-01	0,09	8,39E-01	9,02E-01	
TUBG1;TUBG2	0,27	4,37E-01	5,96E-01	0,00	1,00E+00	1,00E+00	
ENO1	0,27	4,90E-01	6,40E-01	0,82	1,07E-01	2,78E-01	
MRPL9	0,27	4,29E-01	5,91E-01	-0,34	3,83E-01	5,90E-01	
SRPK1	0,27	3,04E-01	4,76E-01	0,07	8,69E-01	9,20E-01	
CACYBP	0,27	4,36E-01	5,96E-01	0,38	3,84E-01	5,90E-01	
RBM22	0,27	4,34E-01	5,96E-01	0,39	3,76E-01	5,89E-01	
LARP1	0,27	3,38E-01	5,07E-01	1,35	6,35E-03	6,35E-02	
CYC1	0,27	4,47E-01	6,03E-01	0,72	9,89E-02	2,70E-01	
RPS7	0,26	3,53E-01	5,22E-01	0,52	1,63E-01	3,59E-01	
RPL10A	0,26	3,20E-01	4,93E-01	1,00	1,22E-02	8,51E-02	
MYL6	0,26	4,79E-01	6,31E-01	1,47	4,31E-02	1,78E-01	
CCDC86	0,25	4,24E-01	5,87E-01	0,55	1,87E-01	3,87E-01	
RPS9	0,25	3,99E-01	5,67E-01	0,37	3,24E-01	5,42E-01	
GNAI2;GNAI1	0,25	3,38E-01	5,07E-01	1,19	3,58E-02	1,61E-01	
CSTF2	0,25	5,09E-01	6,57E-01	0,19	6,19E-01	7,71E-01	
PRPF19	0,25	4,83E-01	6,36E-01	0,27	4,55E-01	6,46E-01	
FAM32A	0,25	5,34E-01	6,76E-01	0,10	8,19E-01	8,94E-01	
MFAP1	0,24	5,07E-01	6,57E-01	0,06	8,56E-01	9,11E-01	
CLTC	0,24	3,67E-01	5,35E-01	0,76	4,94E-02	1,90E-01	
PSME3	0,24	4,97E-01	6,46E-01	0,77	9,81E-02	2,70E-01	
PRPF40A	0,24	4,36E-01	5,96E-01	0,31	3,80E-01	5,90E-01	
SNRPD3	0,24	4,59E-01	6,14E-01	0,24	5,31E-01	7,08E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
EBNA1BP2	0,24	4,51E-01	6,06E-01	0,77	7,89E-02	2,45E-01	
RPL26;RPL26L1	0,24	4,50E-01	6,06E-01	0,55	1,40E-01	3,24E-01	
C14orf166	0,23	5,17E-01	6,64E-01	0,35	4,35E-01	6,28E-01	
RPL38	0,23	5,29E-01	6,73E-01	0,38	3,38E-01	5,49E-01	
RPS25	0,23	4,63E-01	6,18E-01	0,54	1,35E-01	3,21E-01	
ELAVL1	0,23	5,62E-01	7,06E-01	0,34	4,45E-01	6,37E-01	
SF3B3	0,22	4,23E-01	5,87E-01	0,33	3,35E-01	5,48E-01	
RPS15A	0,22	4,12E-01	5,76E-01	0,59	1,31E-01	3,15E-01	
AHCY	0,22	6,11E-01	7,42E-01	0,63	1,96E-01	3,99E-01	
HSP90AA1	0,22	5,22E-01	6,66E-01	0,85	4,46E-02	1,83E-01	
PCBP2	0,22	4,33E-01	5,96E-01	0,14	6,75E-01	8,02E-01	
APEX1	0,21	5,33E-01	6,76E-01	0,00	1,00E+00	1,00E+00	
HNRNPL	0,21	4,72E-01	6,23E-01	0,15	6,63E-01	7,96E-01	
DDX47	0,21	4,35E-01	5,96E-01	0,51	1,59E-01	3,55E-01	
NSUN5	0,21	5,92E-01	7,27E-01	-0,23	6,26E-01	7,73E-01	
FBL	0,21	5,19E-01	6,65E-01	0,44	2,20E-01	4,24E-01	
PYCR2	0,20	5,65E-01	7,09E-01	1,08	2,18E-02	1,20E-01	
GNB2L1	0,20	5,12E-01	6,59E-01	1,24	1,00E-02	7,68E-02	
DDX54	0,20	4,43E-01	6,02E-01	0,72	8,73E-02	2,56E-01	
ALDH18A1	0,19	5,87E-01	7,27E-01	0,00	1,00E+00	1,00E+00	
TRIM28	0,19	4,83E-01	6,36E-01	0,40	2,62E-01	4,66E-01	
RIF1	0,19	5,86E-01	7,27E-01	0,00	1,00E+00	1,00E+00	
KIAA0020	0,19	4,63E-01	6,18E-01	0,23	5,08E-01	6,90E-01	
NCAPD2	0,18	5,85E-01	7,27E-01	0,68	1,35E-01	3,21E-01	
AQR	0,18	4,93E-01	6,42E-01	0,50	1,77E-01	3,73E-01	
RPS26;RPS26P11	0,18	4,85E-01	6,36E-01	0,29	3,96E-01	5,99E-01	
NOP9	0,18	6,56E-01	7,74E-01	0,98	4,26E-02	1,77E-01	
RPL22L1	0,18	6,33E-01	7,52E-01	0,65	1,46E-01	3,33E-01	
NGDN	0,17	5,06E-01	6,57E-01	0,13	7,37E-01	8,46E-01	
SLC25A22;SLC25A18	0,17	6,28E-01	7,51E-01	0,00	1,00E+00	1,00E+00	
PROX1	0,17	7,15E-01	8,17E-01	1,34	3,29E-02	1,57E-01	
CRNKL1	0,17	5,20E-01	6,65E-01	0,16	6,43E-01	7,87E-01	
RRP36	0,17	5,73E-01	7,15E-01	0,18	6,59E-01	7,94E-01	
RPL13A;RPL13a	0,17	5,40E-01	6,82E-01	0,71	5,87E-02	2,11E-01	
GLUD1;GLUD2	0,16	6,81E-01	7,95E-01	0,28	4,85E-01	6,69E-01	
TFIP11	0,15	7,07E-01	8,13E-01	0,00	1,00E+00	1,00E+00	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
POLE	0,15	7,06E-01	8,13E-01	0,00	1,00E+00	1,00E+00	
CSTF3	0,15	6,57E-01	7,74E-01	0,00	1,00E+00	1,00E+00	
ZC3H18	0,15	6,19E-01	7,47E-01	0,16	6,74E-01	8,02E-01	
OGT	0,15	7,75E-01	8,66E-01	0,00	1,00E+00	1,00E+00	
RAB7A	0,15	6,22E-01	7,47E-01	0,78	1,07E-01	2,78E-01	
FTSJ3	0,15	5,72E-01	7,15E-01	-0,20	5,67E-01	7,32E-01	
RPS24	0,15	6,32E-01	7,52E-01	0,04	9,00E-01	9,34E-01	
RRS1	0,14	6,03E-01	7,38E-01	-0,03	9,21E-01	9,45E-01	
COPG1	0,14	7,37E-01	8,36E-01	1,46	6,33E-03	6,35E-02	
PPIL2	0,14	5,85E-01	7,27E-01	0,17	6,26E-01	7,73E-01	
TFB1M	0,14	6,44E-01	7,62E-01	-0,65	9,71E-02	2,70E-01	
MAP7	0,14	7,36E-01	8,36E-01	0,05	8,85E-01	9,27E-01	
TUBB4B;TUBB4A	0,14	6,25E-01	7,49E-01	0,40	2,39E-01	4,47E-01	
BARX1	0,13	7,18E-01	8,19E-01	0,00	1,00E+00	1,00E+00	
RPL10	0,13	6,67E-01	7,83E-01	0,63	9,97E-02	2,70E-01	
HNRNPA1;HNRNPA1L2	0,13	8,06E-01	8,84E-01	0,60	2,60E-01	4,64E-01	
PHB2	0,13	6,14E-01	7,44E-01	0,30	3,76E-01	5,89E-01	
POLR2C	0,12	7,11E-01	8,15E-01	-0,06	8,83E-01	9,27E-01	
WDR3	0,12	7,12E-01	8,16E-01	0,14	7,41E-01	8,48E-01	
RPS11	0,12	6,48E-01	7,66E-01	0,07	8,44E-01	9,03E-01	
NSUN2	0,12	6,58E-01	7,74E-01	0,01	9,67E-01	9,76E-01	
IDH3A	0,12	7,52E-01	8,47E-01	0,09	8,27E-01	8,96E-01	
HNRNPA3	0,11	7,39E-01	8,37E-01	0,34	4,13E-01	6,15E-01	
DDX52	0,11	7,17E-01	8,19E-01	0,24	5,54E-01	7,22E-01	
NEDD4	0,11	6,95E-01	8,04E-01	0,64	8,66E-02	2,55E-01	
RAN	0,10	7,26E-01	8,27E-01	0,47	2,16E-01	4,22E-01	
XAB2	0,10	6,93E-01	8,04E-01	0,02	9,55E-01	9,67E-01	
FAU	0,10	7,67E-01	8,60E-01	0,68	8,91E-02	2,59E-01	
DDX1	0,09	7,86E-01	8,71E-01	0,51	2,47E-01	4,55E-01	
YBX1	0,09	8,30E-01	8,99E-01	0,85	6,40E-02	2,23E-01	
SMARCA5	0,09	7,81E-01	8,69E-01	0,20	5,61E-01	7,27E-01	
DDX51	0,09	8,10E-01	8,87E-01	-0,17	6,50E-01	7,87E-01	
WDR12	0,09	7,42E-01	8,38E-01	0,36	3,01E-01	5,17E-01	
RPL23A	0,09	8,05E-01	8,84E-01	0,54	1,66E-01	3,61E-01	
RPL31	0,09	7,71E-01	8,62E-01	0,25	4,99E-01	6,81E-01	
PPIH	0,09	7,84E-01	8,71E-01	-0,17	6,22E-01	7,73E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PPFIBP1	0,08	8,12E-01	8,88E-01	0,00	1,00E+00	1,00E+00	
COPB1	0,08	8,06E-01	8,84E-01	0,60	1,79E-01	3,77E-01	
RPL6	0,08	7,98E-01	8,81E-01	0,43	2,11E-01	4,18E-01	
HNRNPK	0,08	8,16E-01	8,90E-01	0,40	3,19E-01	5,40E-01	
SMAD3;SMAD2	0,08	8,18E-01	8,90E-01	0,05	9,15E-01	9,43E-01	
DPF2	0,07	8,37E-01	9,01E-01	0,00	1,00E+00	1,00E+00	
RPS12	0,07	8,62E-01	9,19E-01	0,63	2,43E-01	4,50E-01	
SP3	0,07	8,50E-01	9,11E-01	0,00	1,00E+00	1,00E+00	
CDK12	0,07	8,44E-01	9,07E-01	0,11	8,00E-01	8,83E-01	
TMPO	0,07	8,33E-01	8,99E-01	0,18	6,72E-01	8,02E-01	
TUBA1B	0,07	8,18E-01	8,90E-01	0,44	2,03E-01	4,06E-01	
WDR33	0,06	8,65E-01	9,19E-01	0,14	7,44E-01	8,49E-01	
UTP18	0,06	8,64E-01	9,19E-01	-0,59	1,87E-01	3,87E-01	
RNF2	0,06	8,63E-01	9,19E-01	0,38	3,87E-01	5,93E-01	
GTPBP1	0,06	9,04E-01	9,49E-01	0,38	3,17E-01	5,38E-01	
KRR1	0,05	8,33E-01	8,99E-01	-0,13	6,92E-01	8,17E-01	
SCAF11	0,05	8,76E-01	9,28E-01	0,08	8,80E-01	9,27E-01	
CCNL1	0,05	8,82E-01	9,33E-01	0,00	1,00E+00	1,00E+00	
RPL8	0,05	8,85E-01	9,35E-01	0,77	7,47E-02	2,38E-01	
PRDX1	0,05	9,20E-01	9,55E-01	0,33	3,78E-01	5,90E-01	
RPS13	0,04	8,87E-01	9,37E-01	0,13	7,13E-01	8,29E-01	
SEC61A1	0,04	9,05E-01	9,49E-01	0,19	5,61E-01	7,27E-01	
PRPF3	0,04	9,12E-01	9,54E-01	0,00	1,00E+00	1,00E+00	
CDK9	0,04	9,01E-01	9,47E-01	0,57	2,31E-01	4,36E-01	
HSPA4	0,04	9,16E-01	9,55E-01	1,07	1,37E-02	9,03E-02	
PHB	0,03	9,43E-01	9,65E-01	0,78	2,01E-01	4,05E-01	
PRPF31	0,03	9,01E-01	9,47E-01	0,04	9,01E-01	9,34E-01	
TRIP12	0,03	9,06E-01	9,49E-01	0,33	4,50E-01	6,41E-01	
SFPQ	0,03	9,20E-01	9,55E-01	0,41	2,70E-01	4,76E-01	
KHDRBS1	0,03	9,17E-01	9,55E-01	0,43	2,17E-01	4,23E-01	
GNL3L	0,03	9,31E-01	9,59E-01	-0,11	7,42E-01	8,49E-01	
AP1B1	0,02	9,45E-01	9,66E-01	0,00	1,00E+00	1,00E+00	
SLC25A5	0,02	9,40E-01	9,64E-01	0,16	6,64E-01	7,96E-01	
CIR1	0,02	9,54E-01	9,70E-01	-0,06	8,85E-01	9,27E-01	
WDR74	0,02	9,53E-01	9,70E-01	0,00	1,00E+00	1,00E+00	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
DHX15	0,02	9,40E-01	9,64E-01	0,10	7,55E-01	8,54E-01	
SAP30BP	0,02	9,48E-01	9,68E-01	0,74	1,40E-01	3,24E-01	
INTS6	0,01	9,70E-01	9,79E-01	0,29	5,10E-01	6,90E-01	
PTPN14	0,01	9,70E-01	9,79E-01	0,38	3,90E-01	5,95E-01	
SF3B2	0,01	9,76E-01	9,83E-01	0,06	8,63E-01	9,16E-01	
EMG1	0,00	9,91E-01	9,95E-01	-0,59	1,99E-01	4,02E-01	
P4HB	0,00	1,00E+00	1,00E+00	0,00	1,00E+00	1,00E+00	
SLC25A1	0,00	1,00E+00	1,00E+00	0,48	2,43E-01	4,50E-01	
NIP7	0,00	9,98E-01	1,00E+00	0,15	7,49E-01	8,52E-01	
EIF6	0,00	9,95E-01	9,98E-01	0,73	6,21E-02	2,18E-01	
TRMT2A	-0,01	9,82E-01	9,87E-01	0,00	1,00E+00	1,00E+00	
CLPX	-0,01	9,80E-01	9,86E-01	0,34	4,34E-01	6,28E-01	
RPL17;RPL17-C18orf32	-0,01	9,73E-01	9,81E-01	0,20	5,80E-01	7,44E-01	
DDX3X;DDX3Y	-0,02	9,49E-01	9,68E-01	0,07	8,37E-01	9,02E-01	
EIF2S3;EIF2S3L	-0,02	9,43E-01	9,65E-01	0,61	1,15E-01	2,90E-01	
ZNF740	-0,02	9,66E-01	9,78E-01	0,00	1,00E+00	1,00E+00	
RPS23	-0,02	9,57E-01	9,70E-01	0,34	4,52E-01	6,43E-01	
RPP14	-0,02	9,53E-01	9,70E-01	-0,11	7,98E-01	8,83E-01	
ACTN4	-0,02	9,65E-01	9,77E-01	2,46	3,84E-04	1,63E-02	
VPRBP	-0,02	9,56E-01	9,70E-01	0,33	4,57E-01	6,48E-01	
ZRANB2	-0,02	9,56E-01	9,70E-01	0,30	4,66E-01	6,53E-01	
RBM25	-0,02	9,36E-01	9,63E-01	0,02	9,50E-01	9,64E-01	
RPL34	-0,02	9,27E-01	9,57E-01	0,28	4,27E-01	6,22E-01	
ABCB7	-0,03	9,40E-01	9,64E-01	0,00	1,00E+00	1,00E+00	
PBDC1	-0,03	9,15E-01	9,55E-01	0,17	6,12E-01	7,70E-01	
ARRB2	-0,03	9,22E-01	9,56E-01	0,52	1,39E-01	3,24E-01	
PWP1	-0,03	9,29E-01	9,58E-01	-0,16	7,13E-01	8,29E-01	
UPF3B	-0,03	9,27E-01	9,57E-01	-0,16	7,09E-01	8,29E-01	
FASN	-0,03	9,18E-01	9,55E-01	0,80	8,62E-02	2,55E-01	
FAM120A	-0,04	9,14E-01	9,55E-01	0,10	7,82E-01	8,71E-01	
RPL22	-0,04	9,24E-01	9,56E-01	0,22	5,40E-01	7,13E-01	
G3BP1	-0,04	9,18E-01	9,55E-01	0,40	3,28E-01	5,42E-01	
ATP5O	-0,04	8,66E-01	9,19E-01	-0,42	2,27E-01	4,34E-01	
NUP93	-0,04	8,65E-01	9,19E-01	0,27	4,24E-01	6,22E-01	
RPF2	-0,05	8,50E-01	9,11E-01	0,11	7,39E-01	8,48E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
DDX27	-0,05	8,50E-01	9,11E-01	0,30	4,12E-01	6,15E-01	
GNAI3	-0,05	8,91E-01	9,38E-01	1,46	1,31E-02	8,90E-02	
EIF2S2	-0,06	8,58E-01	9,17E-01	0,69	6,06E-02	2,15E-01	
SF3B1	-0,06	8,17E-01	8,90E-01	0,32	3,60E-01	5,72E-01	
ARL1	-0,06	8,70E-01	9,22E-01	0,00	1,00E+00	1,00E+00	
MRPS25	-0,06	8,89E-01	9,37E-01	0,00	1,00E+00	1,00E+00	
SNRPD1	-0,06	8,25E-01	8,96E-01	0,77	5,44E-02	2,01E-01	
HSD17B10	-0,06	8,05E-01	8,84E-01	-0,11	7,54E-01	8,54E-01	
CWC15	-0,06	8,30E-01	8,99E-01	0,02	9,47E-01	9,62E-01	
ALYREF	-0,06	8,35E-01	9,00E-01	-0,58	1,61E-01	3,57E-01	
EED	-0,06	8,23E-01	8,94E-01	0,24	4,92E-01	6,76E-01	
GNB2	-0,07	7,93E-01	8,77E-01	1,05	3,69E-02	1,61E-01	
FLNA	-0,07	8,33E-01	8,99E-01	0,77	9,92E-02	2,70E-01	
PRPF6	-0,07	8,18E-01	8,90E-01	0,07	8,29E-01	8,97E-01	
ARF5;ARF3;ARF4	-0,07	7,77E-01	8,67E-01	0,39	2,79E-01	4,91E-01	
RPL19	-0,07	8,02E-01	8,84E-01	0,59	9,76E-02	2,70E-01	
SKP1	-0,07	8,05E-01	8,84E-01	-0,05	8,80E-01	9,27E-01	
SNW1	-0,07	7,63E-01	8,57E-01	-0,10	7,59E-01	8,57E-01	
NSA2	-0,08	7,93E-01	8,77E-01	-0,09	7,93E-01	8,81E-01	
HNRNPA2B1	-0,08	8,56E-01	9,15E-01	0,28	5,44E-01	7,15E-01	
HSPA14	-0,08	8,41E-01	9,04E-01	0,00	1,00E+00	1,00E+00	
EIF4A3	-0,08	7,35E-01	8,36E-01	-0,01	9,87E-01	9,93E-01	
SRP72	-0,09	7,61E-01	8,56E-01	-0,18	5,93E-01	7,56E-01	
UTP11L	-0,09	7,79E-01	8,68E-01	-0,21	5,34E-01	7,08E-01	
HBS1L	-0,09	7,85E-01	8,71E-01	0,00	1,00E+00	1,00E+00	
RPS4X	-0,10	7,41E-01	8,38E-01	0,27	4,80E-01	6,65E-01	
PPIE	-0,10	7,14E-01	8,17E-01	-0,27	4,15E-01	6,16E-01	
LCP1	-0,10	7,87E-01	8,72E-01	1,33	1,18E-02	8,44E-02	
MPP1	-0,10	7,06E-01	8,13E-01	0,57	2,18E-01	4,23E-01	
EPB41L2	-0,10	7,40E-01	8,37E-01	-0,10	7,60E-01	8,57E-01	
MINA	-0,10	7,10E-01	8,15E-01	0,20	6,23E-01	7,73E-01	
HNRNPLL;HNRPLL	-0,10	7,58E-01	8,54E-01	0,04	9,16E-01	9,43E-01	
CDC5L	-0,10	6,86E-01	7,98E-01	-0,30	3,81E-01	5,90E-01	
TPM3;DKFZp686J1372	-0,11	9,25E-01	9,57E-01	4,01	5,34E-03	5,80E-02	
CPSF1	-0,11	6,87E-01	7,98E-01	-0,23	4,94E-01	6,77E-01	
SSB	-0,11	7,48E-01	8,44E-01	0,28	5,17E-01	6,95E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PARP1	-0,11	7,71E-01	8,62E-01	0,25	5,55E-01	7,22E-01	
PPIA	-0,12	7,00E-01	8,08E-01	0,26	5,72E-01	7,35E-01	
CPSF3	-0,12	6,39E-01	7,57E-01	-0,12	7,12E-01	8,29E-01	
RPS6	-0,12	6,85E-01	7,98E-01	0,06	8,60E-01	9,15E-01	
CIRH1A	-0,13	7,69E-01	8,62E-01	0,00	1,00E+00	1,00E+00	
SF3B4	-0,13	6,95E-01	8,04E-01	-0,11	8,00E-01	8,83E-01	
PRPF38A	-0,13	6,22E-01	7,47E-01	0,49	1,93E-01	3,96E-01	
DDX5	-0,13	6,18E-01	7,46E-01	-0,21	5,54E-01	7,22E-01	
EIF2S1	-0,13	6,32E-01	7,52E-01	0,59	1,09E-01	2,82E-01	
BOP1	-0,14	6,91E-01	8,02E-01	0,04	9,08E-01	9,39E-01	
MRPL48	-0,14	6,30E-01	7,51E-01	0,09	8,01E-01	8,83E-01	
RRP7A;RRP7BP	-0,14	6,05E-01	7,38E-01	0,00	9,96E-01	9,96E-01	
RBM14	-0,14	5,91E-01	7,27E-01	0,05	8,94E-01	9,32E-01	
SRSF2	-0,14	6,75E-01	7,91E-01	0,20	6,49E-01	7,87E-01	
EEF1A1;EEF1A1P5	-0,14	5,89E-01	7,27E-01	-0,05	8,78E-01	9,27E-01	
RPN1	-0,15	6,75E-01	7,91E-01	0,00	1,00E+00	1,00E+00	
ARPC4;ARPC4-TTLL3	-0,15	6,09E-01	7,41E-01	0,81	8,86E-02	2,59E-01	
SNIP1	-0,15	5,92E-01	7,27E-01	-0,49	1,56E-01	3,49E-01	
THOC2	-0,15	6,22E-01	7,47E-01	0,59	1,17E-01	2,91E-01	
CDC40	-0,15	6,09E-01	7,41E-01	-0,08	8,26E-01	8,96E-01	
IKZF1	-0,15	5,72E-01	7,15E-01	0,21	5,64E-01	7,29E-01	
SF3A1	-0,15	5,76E-01	7,19E-01	-0,01	9,84E-01	9,91E-01	
SYMPK	-0,15	6,57E-01	7,74E-01	0,25	4,71E-01	6,56E-01	
TECR	-0,15	5,91E-01	7,27E-01	0,52	2,50E-01	4,58E-01	
PCNA	-0,16	5,89E-01	7,27E-01	0,56	1,55E-01	3,48E-01	
SF3A3	-0,16	5,55E-01	7,00E-01	0,28	4,16E-01	6,17E-01	
WWP1	-0,16	6,82E-01	7,96E-01	0,93	6,91E-02	2,31E-01	
YWHAB	-0,16	6,80E-01	7,95E-01	0,61	1,88E-01	3,87E-01	
RPS5	-0,16	6,38E-01	7,57E-01	0,31	5,47E-01	7,18E-01	
SSR1	-0,17	6,28E-01	7,51E-01	-0,13	7,72E-01	8,65E-01	
DNAJC9	-0,17	6,34E-01	7,52E-01	-0,08	8,56E-01	9,11E-01	
NMT1	-0,17	6,14E-01	7,44E-01	0,59	1,09E-01	2,81E-01	
MMTAG2	-0,17	6,10E-01	7,42E-01	0,24	5,72E-01	7,35E-01	
GAR1	-0,18	7,07E-01	8,13E-01	0,00	1,00E+00	1,00E+00	
SNRPE	-0,18	6,01E-01	7,37E-01	0,05	9,03E-01	9,36E-01	
KPNA4	-0,18	5,59E-01	7,03E-01	0,43	2,62E-01	4,66E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BUB3	-0,18	5,51E-01	6,95E-01	0,19	6,01E-01	7,59E-01	
ARPC3	-0,18	5,89E-01	7,27E-01	0,00	1,00E+00	1,00E+00	
EPB41	-0,19	5,95E-01	7,31E-01	0,19	6,28E-01	7,73E-01	
SRRT	-0,19	5,30E-01	6,74E-01	-0,23	5,14E-01	6,95E-01	
SLC25A12	-0,19	4,67E-01	6,20E-01	0,45	2,10E-01	4,18E-01	
YBX3	-0,19	6,21E-01	7,47E-01	0,06	8,86E-01	9,27E-01	
IKZF5	-0,20	6,79E-01	7,95E-01	-0,15	7,14E-01	8,30E-01	
GPAM	-0,20	6,04E-01	7,38E-01	0,00	1,00E+00	1,00E+00	
DIMT1	-0,20	4,56E-01	6,11E-01	-0,20	5,96E-01	7,56E-01	
NO66	-0,21	4,45E-01	6,03E-01	-0,45	2,19E-01	4,24E-01	
RBM39	-0,21	4,16E-01	5,79E-01	-0,11	7,52E-01	8,54E-01	
PCMT1	-0,21	5,12E-01	6,59E-01	-0,55	1,73E-01	3,66E-01	
SNRNP40	-0,21	4,39E-01	5,98E-01	0,28	4,27E-01	6,22E-01	
RPL21	-0,21	4,84E-01	6,36E-01	0,16	6,50E-01	7,87E-01	
POP1	-0,21	5,03E-01	6,54E-01	-0,96	2,84E-02	1,42E-01	
RBM28	-0,22	5,81E-01	7,24E-01	0,31	4,49E-01	6,41E-01	
YWHAG	-0,22	5,14E-01	6,60E-01	0,60	1,00E-01	2,70E-01	
HSP90B1	-0,22	5,09E-01	6,57E-01	0,12	7,75E-01	8,65E-01	
CSK	-0,22	5,33E-01	6,76E-01	0,00	1,00E+00	1,00E+00	
GOT2	-0,22	6,15E-01	7,45E-01	0,00	1,00E+00	1,00E+00	
AP2A1	-0,22	5,08E-01	6,57E-01	0,38	3,88E-01	5,93E-01	
FCF1	-0,23	4,47E-01	6,03E-01	-0,20	5,59E-01	7,27E-01	
SON	-0,23	4,22E-01	5,87E-01	-0,25	5,17E-01	6,95E-01	
SNRPD2	-0,23	3,69E-01	5,37E-01	0,17	6,13E-01	7,71E-01	
RP9	-0,24	3,59E-01	5,28E-01	0,16	7,16E-01	8,31E-01	
RPL30	-0,24	5,29E-01	6,73E-01	0,35	3,27E-01	5,42E-01	
MRPL46	-0,24	4,36E-01	5,96E-01	-0,38	2,83E-01	4,95E-01	
ZFX;ZFY	-0,24	4,45E-01	6,03E-01	-0,11	7,61E-01	8,57E-01	
WHSC1	-0,24	4,46E-01	6,03E-01	-0,52	1,43E-01	3,27E-01	
TCEB1	-0,24	5,19E-01	6,65E-01	0,09	7,92E-01	8,81E-01	
ZFP64	-0,25	4,71E-01	6,23E-01	0,00	1,00E+00	1,00E+00	
TAF2	-0,25	4,52E-01	6,06E-01	-0,07	8,52E-01	9,10E-01	
NOM1	-0,25	5,58E-01	7,02E-01	0,00	1,00E+00	1,00E+00	
SLC25A6	-0,25	4,70E-01	6,22E-01	0,00	1,00E+00	1,00E+00	
DDX31	-0,25	3,32E-01	5,03E-01	-0,23	4,97E-01	6,79E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
HNRNPUL2; HNRNPUL2-BSCL2	-0,26	3,44E-01	5,13E-01	0,25	4,80E-01	6,65E-01	
DDX18	-0,26	3,74E-01	5,41E-01	-0,11	7,46E-01	8,50E-01	
TMEM263	-0,26	3,27E-01	5,00E-01	0,33	3,44E-01	5,56E-01	
DHX37	-0,26	4,69E-01	6,22E-01	-0,14	7,54E-01	8,54E-01	
ERI1	-0,26	4,61E-01	6,16E-01	0,00	1,00E+00	1,00E+00	
SLTM	-0,26	3,74E-01	5,41E-01	-0,34	3,35E-01	5,48E-01	
SF3B5	-0,27	3,11E-01	4,83E-01	-0,29	3,88E-01	5,93E-01	
TKT	-0,27	6,28E-01	7,51E-01	0,65	2,66E-01	4,72E-01	
CSNK1A1;CSNK1A1L	-0,27	4,90E-01	6,40E-01	0,00	1,00E+00	1,00E+00	
DDX23	-0,27	4,29E-01	5,91E-01	0,13	7,69E-01	8,63E-01	
DDX56	-0,27	3,58E-01	5,28E-01	0,03	9,28E-01	9,48E-01	
ARGLU1	-0,28	3,31E-01	5,03E-01	-0,14	7,10E-01	8,29E-01	
PCBP1	-0,28	2,89E-01	4,62E-01	-0,31	3,52E-01	5,63E-01	
PPIG	-0,29	4,05E-01	5,70E-01	-0,09	8,18E-01	8,94E-01	
MAD2L1	-0,29	4,08E-01	5,73E-01	0,48	1,66E-01	3,61E-01	
SRSF3	-0,29	3,99E-01	5,67E-01	-0,05	8,92E-01	9,31E-01	
CDK11B;CDC2L1; CDK11A	-0,30	2,74E-01	4,53E-01	0,26	4,63E-01	6,53E-01	
DHX8	-0,31	2,79E-01	4,55E-01	0,12	7,43E-01	8,49E-01	
SP1	-0,31	3,89E-01	5,56E-01	-0,28	5,50E-01	7,20E-01	
POC1A	-0,31	3,82E-01	5,49E-01	0,15	7,23E-01	8,37E-01	
NOL12	-0,31	3,65E-01	5,34E-01	0,11	8,35E-01	9,01E-01	
TPI1	-0,31	4,10E-01	5,75E-01	0,31	4,65E-01	6,53E-01	
RPL35	-0,32	3,75E-01	5,42E-01	-0,05	8,99E-01	9,34E-01	
VCP	-0,32	4,46E-01	6,03E-01	0,47	3,14E-01	5,35E-01	
RPS3A	-0,32	2,69E-01	4,49E-01	-0,10	7,64E-01	8,58E-01	
SF1	-0,33	4,00E-01	5,68E-01	0,34	3,54E-01	5,66E-01	
AATF	-0,33	3,82E-01	5,49E-01	0,38	3,92E-01	5,97E-01	
RBM27	-0,33	2,55E-01	4,34E-01	-0,25	4,72E-01	6,57E-01	
RPUSD4	-0,33	3,30E-01	5,03E-01	-0,76	1,01E-01	2,70E-01	
RSRC1	-0,33	3,74E-01	5,41E-01	0,00	1,00E+00	1,00E+00	
KNOP1	-0,33	3,84E-01	5,50E-01	0,00	1,00E+00	1,00E+00	
MEPCE	-0,34	3,41E-01	5,10E-01	0,34	4,27E-01	6,22E-01	
TAF8	-0,34	2,86E-01	4,59E-01	0,00	9,93E-01	9,95E-01	
SNRPC	-0,34	3,95E-01	5,64E-01	0,40	3,72E-01	5,85E-01	
SRP14	-0,34	2,42E-01	4,24E-01	-0,30	4,33E-01	6,28E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
DSC1	-0,35	3,53E-01	5,22E-01	-0,41	4,31E-01	6,27E-01	
ABT1	-0,35	2,80E-01	4,55E-01	-0,18	6,47E-01	7,87E-01	
NACA	-0,35	2,11E-01	3,91E-01	0,08	8,18E-01	8,94E-01	
ZFP91;ZFP91-CNTF	-0,35	2,56E-01	4,35E-01	-0,61	9,91E-02	2,70E-01	
MAK16	-0,35	3,34E-01	5,04E-01	0,04	9,30E-01	9,48E-01	
SLK	-0,36	1,83E-01	3,59E-01	0,28	4,27E-01	6,22E-01	
SRSF5	-0,36	2,45E-01	4,26E-01	0,04	9,08E-01	9,39E-01	
YWHAQ	-0,36	3,65E-01	5,34E-01	0,16	6,94E-01	8,18E-01	
DDX55	-0,36	2,34E-01	4,16E-01	-0,54	1,29E-01	3,13E-01	
BTF3	-0,36	3,07E-01	4,78E-01	0,07	8,27E-01	8,96E-01	
RNPS1	-0,36	2,12E-01	3,92E-01	-0,21	5,32E-01	7,08E-01	
SNRPA1	-0,36	2,45E-01	4,26E-01	-0,39	2,67E-01	4,72E-01	
VRK1	-0,36	3,18E-01	4,92E-01	0,00	1,00E+00	1,00E+00	
SRP9	-0,37	4,27E-01	5,90E-01	0,44	2,41E-01	4,50E-01	
C1QA	-0,37	3,72E-01	5,40E-01	-0,16	6,63E-01	7,96E-01	
CGGBP1	-0,37	2,92E-01	4,66E-01	0,00	1,00E+00	1,00E+00	
CPSF2	-0,37	2,32E-01	4,14E-01	-0,21	5,32E-01	7,08E-01	
DDX6	-0,38	2,86E-01	4,59E-01	0,15	6,54E-01	7,91E-01	
SNRNP70	-0,38	2,16E-01	3,96E-01	0,18	6,17E-01	7,71E-01	
REXO4	-0,38	2,25E-01	4,08E-01	-0,43	2,48E-01	4,55E-01	
HNRNPAB	-0,38	2,79E-01	4,55E-01	0,03	9,29E-01	9,48E-01	
HSPA5	-0,38	1,62E-01	3,33E-01	-0,01	9,66E-01	9,76E-01	
ABCF1	-0,38	3,42E-01	5,11E-01	0,25	4,69E-01	6,56E-01	
ZNF444	-0,38	3,05E-01	4,77E-01	-0,55	2,59E-01	4,64E-01	
CHD1	-0,38	2,98E-01	4,69E-01	-0,45	3,16E-01	5,37E-01	
AKAP17A	-0,39	1,85E-01	3,61E-01	0,68	1,70E-01	3,63E-01	
SNRPN;SNRPB	-0,40	2,13E-01	3,93E-01	0,30	3,70E-01	5,84E-01	
NXF1	-0,40	2,41E-01	4,24E-01	-0,17	6,26E-01	7,73E-01	
CHERP	-0,40	1,46E-01	3,16E-01	-0,35	3,22E-01	5,41E-01	
ZAP70	-0,40	2,37E-01	4,18E-01	-0,09	8,26E-01	8,96E-01	
PNN	-0,41	1,46E-01	3,16E-01	-0,25	4,65E-01	6,53E-01	
CHAMP1	-0,41	2,80E-01	4,55E-01	-0,07	8,56E-01	9,11E-01	
HIST1H1E; HIST1H1D	-0,41	1,63E-01	3,34E-01	-0,43	2,55E-01	4,62E-01	
SCAF4	-0,41	1,35E-01	3,03E-01	0,16	6,80E-01	8,07E-01	
RPL24	-0,41	1,61E-01	3,31E-01	-0,22	5,27E-01	7,04E-01	
TCEB2	-0,42	2,25E-01	4,08E-01	0,31	4,82E-01	6,66E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
ALDH2	-0,42	2,74E-01	4,53E-01	0,00	1,00E+00	1,00E+00	
ZSCAN26; ZNF187	-0,42	1,80E-01	3,56E-01	-0,53	2,12E-01	4,19E-01	
UFM1	-0,43	2,35E-01	4,17E-01	0,00	1,00E+00	1,00E+00	
MYCBP2	-0,43	2,44E-01	4,25E-01	0,00	1,00E+00	1,00E+00	
CDK13	-0,43	1,94E-01	3,72E-01	-0,09	7,98E-01	8,83E-01	
XPO1	-0,43	2,76E-01	4,54E-01	0,33	4,67E-01	6,53E-01	
POLDIP3	-0,43	1,42E-01	3,13E-01	0,00	1,00E+00	1,00E+00	
UBR4	-0,43	2,43E-01	4,25E-01	0,23	6,55E-01	7,91E-01	
CFL1	-0,43	4,02E-01	5,68E-01	0,24	6,19E-01	7,71E-01	
GTF2B	-0,44	1,14E-01	2,72E-01	-0,67	6,57E-02	2,24E-01	
TOP1	-0,44	1,58E-01	3,29E-01	-0,58	1,17E-01	2,91E-01	
CDC42	-0,44	2,19E-01	3,99E-01	0,09	8,43E-01	9,03E-01	
WDR83	-0,44	2,34E-01	4,16E-01	-0,27	5,27E-01	7,04E-01	
ZNF48	-0,44	2,30E-01	4,12E-01	-0,10	8,19E-01	8,94E-01	
DDX50	-0,45	1,24E-01	2,85E-01	-0,40	2,56E-01	4,63E-01	
RPS2	-0,46	1,17E-01	2,76E-01	0,19	6,14E-01	7,71E-01	
PUF60	-0,46	1,43E-01	3,14E-01	-0,20	5,55E-01	7,22E-01	
FRG1	-0,46	1,14E-01	2,72E-01	-0,31	3,94E-01	5,99E-01	
RPL36A;RPL36A-HNRNPH2;RPL36AL	-0,46	1,46E-01	3,16E-01	0,72	1,05E-01	2,78E-01	
ACTR1A	-0,48	1,97E-01	3,75E-01	0,16	7,12E-01	8,29E-01	
HIST1H4A	-0,48	2,69E-01	4,49E-01	-0,44	3,23E-01	5,41E-01	
IMP3	-0,48	9,76E-02	2,46E-01	0,00	1,00E+00	1,00E+00	
ZNF652;ZBTB47	-0,49	1,95E-01	3,73E-01	-0,42	3,80E-01	5,90E-01	
ESYT1	-0,49	9,67E-02	2,46E-01	0,67	7,35E-02	2,37E-01	
ZNF800	-0,49	1,11E-01	2,67E-01	-0,30	3,97E-01	5,99E-01	
HDLBP	-0,50	1,72E-01	3,46E-01	0,00	1,00E+00	1,00E+00	
TUBB3	-0,50	1,00E-01	2,49E-01	-0,02	9,47E-01	9,62E-01	
CLIC1	-0,50	3,21E-01	4,93E-01	1,21	1,68E-02	1,03E-01	
RAB1A	-0,50	8,38E-02	2,25E-01	-0,11	7,55E-01	8,54E-01	
ZNF148	-0,50	1,78E-01	3,54E-01	0,14	7,10E-01	8,29E-01	
IQGAP1	-0,51	8,93E-02	2,33E-01	-0,02	9,52E-01	9,65E-01	
SUB1	-0,51	2,16E-01	3,96E-01	0,00	1,00E+00	1,00E+00	
PATZ1	-0,51	1,16E-01	2,75E-01	-0,18	5,88E-01	7,53E-01	
SRSF6	-0,51	7,62E-02	2,17E-01	-0,16	6,25E-01	7,73E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BRD7	-0,51	1,41E-01	3,11E-01	-0,56	2,28E-01	4,34E-01	
TAF10	-0,52	7,50E-02	2,17E-01	-0,48	1,70E-01	3,63E-01	
LDHA	-0,52	3,05E-01	4,77E-01	-0,05	9,23E-01	9,46E-01	
SNRNP27	-0,52	1,21E-01	2,81E-01	-0,62	1,69E-01	3,63E-01	
LRRC47	-0,52	1,58E-01	3,29E-01	0,09	8,40E-01	9,02E-01	
PRPF38B	-0,52	2,81E-01	4,55E-01	-0,20	6,19E-01	7,71E-01	
SCAF8	-0,52	6,72E-02	2,04E-01	-0,10	7,68E-01	8,62E-01	
NUP155	-0,53	1,72E-01	3,46E-01	0,00	1,00E+00	1,00E+00	
NSD1	-0,53	1,78E-01	3,54E-01	0,00	1,00E+00	1,00E+00	
C9orf114	-0,53	6,95E-02	2,09E-01	-0,51	1,41E-01	3,25E-01	
ARL6IP4	-0,53	1,51E-01	3,21E-01	1,06	2,65E-01	4,71E-01	
CBX6	-0,53	1,55E-01	3,25E-01	-0,34	4,39E-01	6,31E-01	
TAOK1	-0,54	1,16E-01	2,75E-01	-0,46	2,27E-01	4,34E-01	
THAP11	-0,54	1,95E-01	3,73E-01	0,00	1,00E+00	1,00E+00	
OGDH	-0,54	1,46E-01	3,16E-01	0,00	1,00E+00	1,00E+00	
IMP4	-0,54	1,09E-01	2,65E-01	0,49	3,76E-01	5,89E-01	
H2AFV;H2AFZ	-0,54	2,85E-01	4,59E-01	-0,18	7,29E-01	8,42E-01	
RPL23	-0,54	8,66E-02	2,29E-01	-0,65	8,61E-02	2,55E-01	
UTP3	-0,55	6,53E-02	2,01E-01	-0,35	4,17E-01	6,18E-01	
HIST1H2BL; HIST3H2BB	-0,55	7,14E-02	2,13E-01	-0,43	2,48E-01	4,55E-01	
ASF1A	-0,55	2,80E-01	4,55E-01	-1,25	1,48E-02	9,51E-02	
CBX4	-0,55	1,37E-01	3,05E-01	-0,10	8,29E-01	8,97E-01	
MARK3	-0,56	2,53E-01	4,32E-01	-0,44	3,29E-01	5,42E-01	
TUBB2B	-0,57	1,53E-01	3,24E-01	0,33	3,49E-01	5,61E-01	
HMGB1;HMGB1P1	-0,57	1,60E-01	3,31E-01	0,46	3,38E-01	5,49E-01	
SYF2	-0,57	1,91E-01	3,69E-01	0,00	1,00E+00	1,00E+00	
CS	-0,58	2,18E-01	3,98E-01	-0,43	3,33E-01	5,46E-01	
U2AF2	-0,58	1,05E-01	2,56E-01	-0,14	6,91E-01	8,17E-01	
ZCCHC17	-0,58	6,08E-02	1,91E-01	-0,43	2,57E-01	4,63E-01	
DDX28	-0,59	2,05E-01	3,83E-01	-0,38	4,01E-01	6,04E-01	
SCAF1	-0,59	4,66E-02	1,64E-01	-0,36	2,95E-01	5,10E-01	
PHF6	-0,59	4,91E-02	1,69E-01	-0,18	6,62E-01	7,96E-01	
RPS19BP1	-0,59	9,72E-02	2,46E-01	-0,55	1,66E-01	3,61E-01	
RAB11FIP5	-0,61	7,66E-02	2,17E-01	-0,41	3,46E-01	5,58E-01	
RSBN1	-0,62	4,90E-02	1,69E-01	-0,47	1,77E-01	3,72E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
U2SURP	-0,62	5,26E-02	1,74E-01	-0,05	8,91E-01	9,31E-01	
SLC25A11	-0,62	1,04E-01	2,54E-01	-0,44	3,30E-01	5,42E-01	
TXN	-0,63	1,66E-01	3,37E-01	-1,02	3,74E-02	1,62E-01	
SRRM2	-0,63	4,56E-02	1,64E-01	-0,37	3,00E-01	5,15E-01	
HIST1H2AC;HIST3H2A; HIST1H2AB;HIST1H2AJ; HIST1H2AH;H2AFJ; HIST1H2AD;HIST1H2AG	-0,63	6,68E-02	2,04E-01	-0,44	2,56E-01	4,63E-01	
RSBN1L	-0,63	4,47E-02	1,62E-01	-0,66	9,48E-02	2,68E-01	
ZC3H13	-0,64	1,42E-01	3,13E-01	0,63	3,36E-01	5,48E-01	
LUC7L	-0,64	4,77E-02	1,65E-01	-0,54	1,42E-01	3,25E-01	
SAP18	-0,64	3,53E-02	1,44E-01	-0,29	3,98E-01	6,01E-01	
YWHAE	-0,64	6,69E-02	2,04E-01	0,20	5,96E-01	7,56E-01	
LUC7L3	-0,64	4,94E-02	1,69E-01	-0,24	5,02E-01	6,84E-01	
HIST2H3A;HIST1H3A; HIST3H3	-0,64	1,80E-01	3,56E-01	-0,29	5,48E-01	7,18E-01	
CHTOP	-0,65	4,48E-02	1,62E-01	0,39	3,20E-01	5,40E-01	
RBMX;RBMXL1	-0,65	8,58E-02	2,28E-01	-0,72	5,52E-02	2,03E-01	
HP1BP3	-0,65	4,01E-02	1,55E-01	-0,68	6,46E-02	2,24E-01	
WRNIP1	-0,66	8,88E-02	2,32E-01	0,00	1,00E+00	1,00E+00	
HIST1H1B	-0,66	3,11E-02	1,33E-01	-0,50	1,69E-01	3,63E-01	
TCF7;TCF7L2;LEF1	-0,66	7,44E-02	2,17E-01	-0,12	7,31E-01	8,43E-01	
EWSR1	-0,66	9,84E-02	2,46E-01	0,32	4,61E-01	6,53E-01	
SREK1	-0,66	4,42E-02	1,62E-01	-0,04	9,15E-01	9,43E-01	
GRB10	-0,66	2,96E-02	1,30E-01	-0,67	7,05E-02	2,32E-01	
ZSCAN21	-0,67	8,78E-02	2,31E-01	-0,64	1,59E-01	3,55E-01	
AP2B1	-0,68	3,66E-02	1,47E-01	0,03	9,29E-01	9,48E-01	
RPL7L1	-0,68	9,44E-02	2,44E-01	-0,85	6,91E-02	2,31E-01	
RBM26	-0,68	8,16E-02	2,23E-01	-0,20	6,31E-01	7,76E-01	
SART1	-0,68	3,46E-02	1,43E-01	-0,22	6,18E-01	7,71E-01	
FIZ1	-0,68	3,06E-02	1,32E-01	-0,28	4,36E-01	6,28E-01	
ARL8A	-0,69	7,95E-02	2,20E-01	0,44	3,20E-01	5,40E-01	
GLYR1	-0,69	7,24E-02	2,14E-01	-0,44	2,25E-01	4,33E-01	
YWHAZ	-0,69	7,26E-02	2,14E-01	0,31	4,47E-01	6,39E-01	
YME1L1	-0,69	7,77E-02	2,19E-01	-0,41	3,55E-01	5,67E-01	
RBMX2	-0,69	1,16E-01	2,75E-01	0,33	4,76E-01	6,61E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
CLK4	-0,70	7,66E-02	2,17E-01	-0,42	3,46E-01	5,58E-01	
NME1-NME2; NME2;NME2P1	-0,70	5,27E-02	1,74E-01	0,00	9,93E-01	9,95E-01	
RBM8A	-0,70	2,62E-02	1,26E-01	-0,44	2,13E-01	4,19E-01	
GRB7	-0,70	7,81E-02	2,19E-01	-0,85	7,20E-02	2,35E-01	
ACIN1	-0,71	2,78E-02	1,29E-01	-0,14	6,86E-01	8,11E-01	
PHC2	-0,71	9,83E-02	2,46E-01	0,00	1,00E+00	1,00E+00	
MDH2	-0,72	2,35E-01	4,17E-01	0,04	9,46E-01	9,62E-01	
SRRM1	-0,72	8,24E-02	2,23E-01	0,06	8,63E-01	9,16E-01	
RBBP6	-0,72	2,94E-02	1,30E-01	-0,57	1,17E-01	2,91E-01	
DNAJB11	-0,72	2,49E-02	1,24E-01	-0,15	6,75E-01	8,02E-01	
ZNF319	-0,72	4,06E-02	1,56E-01	-0,43	2,59E-01	4,64E-01	
CTCF	-0,72	2,29E-02	1,20E-01	-0,67	6,51E-02	2,24E-01	
ZNF532	-0,73	6,84E-02	2,06E-01	-0,39	3,71E-01	5,84E-01	
SRSF11	-0,73	3,42E-02	1,43E-01	-0,22	5,33E-01	7,08E-01	
RPL27A	-0,74	1,28E-01	2,93E-01	-0,29	5,19E-01	6,97E-01	
MED19	-0,75	1,82E-02	1,07E-01	-0,30	3,81E-01	5,90E-01	
WBP11	-0,75	2,79E-02	1,29E-01	-0,43	2,96E-01	5,11E-01	
BRD9	-0,76	3,41E-02	1,43E-01	0,07	8,83E-01	9,27E-01	
GDI2	-0,76	6,63E-02	2,04E-01	0,32	4,89E-01	6,72E-01	
YARS	-0,76	2,83E-02	1,30E-01	-0,27	4,70E-01	6,56E-01	
ZNF771	-0,76	2,41E-02	1,23E-01	-0,36	2,92E-01	5,06E-01	
FAM133B	-0,76	7,25E-02	2,14E-01	-0,95	5,87E-02	2,11E-01	
THRAP3	-0,77	1,90E-02	1,09E-01	-0,37	2,86E-01	5,00E-01	
TRA2A	-0,77	1,77E-02	1,06E-01	-0,54	1,31E-01	3,15E-01	
UBA52;UBB; RPS27A;UBC	-0,77	2,05E-01	3,83E-01	0,37	4,08E-01	6,11E-01	
TRMT10C	-0,77	2,92E-02	1,30E-01	-0,34	3,11E-01	5,32E-01	
MAGOH; MAGOHB	-0,78	3,01E-02	1,31E-01	-0,25	4,65E-01	6,53E-01	
SAFB2	-0,78	1,98E-02	1,13E-01	-0,12	7,75E-01	8,65E-01	
CCDC84	-0,78	5,71E-02	1,84E-01	-0,73	1,12E-01	2,86E-01	
NKAP	-0,78	1,69E-02	1,05E-01	-0,81	4,99E-02	1,91E-01	
RBM15	-0,79	2,74E-02	1,29E-01	-0,55	2,21E-01	4,25E-01	
ERH	-0,79	2,94E-02	1,30E-01	-0,65	8,13E-02	2,49E-01	
PRPF4B	-0,79	2,25E-02	1,20E-01	-0,58	1,06E-01	2,78E-01	
CXorf56	-0,79	1,02E-01	2,52E-01	-1,11	2,58E-02	1,34E-01	
MSN	-0,80	7,96E-02	2,20E-01	0,21	6,33E-01	7,77E-01	
FIP1L1	-0,80	1,54E-02	1,00E-01	-0,72	5,86E-02	2,11E-01	
BUD31	-0,80	5,16E-02	1,72E-01	0,08	8,10E-01	8,89E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PHF5A	-0,80	8,07E-02	2,22E-01	-0,04	9,21E-01	9,45E-01	
MYNN	-0,80	5,10E-02	1,72E-01	0,01	9,74E-01	9,82E-01	
GPATCH8	-0,81	7,95E-02	2,20E-01	-0,16	6,44E-01	7,87E-01	
CLK3	-0,81	2,51E-02	1,24E-01	-0,08	8,21E-01	8,94E-01	
RPS29	-0,81	5,12E-02	1,72E-01	0,36	4,02E-01	6,04E-01	
JUP	-0,82	2,52E-01	4,31E-01	0,00	1,00E+00	1,00E+00	
CSTA	-0,83	1,69E-02	1,05E-01	-0,73	5,32E-02	1,98E-01	
LUC7L2	-0,83	1,32E-02	9,18E-02	-0,55	1,22E-01	2,98E-01	
DHX16	-0,85	1,45E-02	9,77E-02	0,00	1,00E+00	1,00E+00	
HMGXB4	-0,85	4,27E-02	1,58E-01	-0,55	2,33E-01	4,39E-01	
CXXC1	-0,85	4,26E-02	1,58E-01	-0,98	4,59E-02	1,85E-01	
ARHGEF39	-0,85	4,46E-02	1,62E-01	0,24	5,73E-01	7,35E-01	
MPHOSPH10	-0,86	1,08E-02	8,02E-02	-0,37	2,89E-01	5,04E-01	
SRSF7	-0,87	1,14E-02	8,32E-02	-0,49	1,55E-01	3,48E-01	
METAP1	-0,87	1,04E-02	7,82E-02	-0,56	1,29E-01	3,13E-01	
U2AF1	-0,88	1,71E-02	1,05E-01	-0,58	1,06E-01	2,78E-01	
PAXBP1	-0,88	4,18E-02	1,58E-01	0,00	1,00E+00	1,00E+00	
BUD13	-0,89	1,79E-02	1,07E-01	-0,71	1,20E-01	2,96E-01	
PPIL4	-0,89	1,64E-02	1,05E-01	-0,20	5,98E-01	7,57E-01	
CNOT1	-0,90	3,62E-02	1,47E-01	-0,23	6,03E-01	7,60E-01	
EME1	-0,90	3,68E-02	1,47E-01	-0,38	3,96E-01	5,99E-01	
WWP2	-0,91	2,75E-02	1,29E-01	0,61	1,98E-01	4,01E-01	
CWC25	-0,91	9,13E-03	7,63E-02	-0,59	1,47E-01	3,34E-01	
DDX46	-0,92	1,27E-02	8,94E-02	-0,20	6,20E-01	7,71E-01	
TRA2B	-0,94	7,96E-03	7,31E-02	-0,59	9,61E-02	2,70E-01	
SRSF10	-0,94	7,12E-03	7,17E-02	-0,63	7,91E-02	2,45E-01	
ZBTB7A	-0,95	3,48E-02	1,43E-01	-0,25	5,69E-01	7,33E-01	
DDX41	-0,97	2,78E-02	1,29E-01	-0,66	1,17E-01	2,91E-01	
SNRPB2	-0,97	2,57E-02	1,25E-01	-0,73	1,22E-01	2,98E-01	
SRSF1	-0,98	6,97E-03	7,12E-02	-0,49	1,73E-01	3,66E-01	
DYNLL1;DYNLL2	-0,98	1,02E-02	7,82E-02	0,09	7,82E-01	8,71E-01	
H2AFY	-0,99	1,71E-02	1,05E-01	-0,94	1,88E-02	1,11E-01	
TBC1D10B	-0,99	5,16E-02	1,72E-01	-0,21	7,64E-01	8,58E-01	
DPYSL2	-0,99	5,32E-02	1,75E-01	0,04	9,00E-01	9,34E-01	
BCLAF1	-1,00	6,98E-03	7,12E-02	-0,50	1,60E-01	3,55E-01	
CACTIN	-1,01	5,28E-03	6,64E-02	-0,64	8,64E-02	2,55E-01	
SRP19	-1,02	2,32E-02	1,21E-01	-0,50	2,68E-01	4,72E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
YTHDC1	-1,03	6,78E-03	7,12E-02	-0,79	3,40E-02	1,58E-01	
OSBPL7	-1,03	2,10E-02	1,17E-01	0,00	1,00E+00	1,00E+00	
SP2	-1,05	2,17E-02	1,18E-01	-0,33	3,82E-01	5,90E-01	
SIN3A	-1,05	2,58E-02	1,25E-01	-0,35	4,22E-01	6,22E-01	
NXT1	-1,06	2,35E-02	1,21E-01	-1,01	5,24E-02	1,96E-01	
SFSWAP	-1,08	7,20E-03	7,17E-02	-0,73	7,37E-02	2,37E-01	
MAP7D1	-1,10	1,88E-02	1,08E-01	-0,28	5,40E-01	7,13E-01	
MASP1	-1,11	2,56E-02	1,25E-01	-0,08	8,51E-01	9,10E-01	
UTP23	-1,11	1,82E-02	1,07E-01	-0,30	5,07E-01	6,88E-01	
SIRT7	-1,12	4,50E-03	6,05E-02	-0,34	3,26E-01	5,42E-01	
EPB41L4B	-1,15	2,28E-02	1,20E-01	-0,52	1,83E-01	3,82E-01	
SREK1IP1	-1,15	2,68E-02	1,28E-01	-0,78	8,58E-02	2,55E-01	
KLF13	-1,15	5,77E-03	6,99E-02	-0,80	3,65E-02	1,61E-01	
DUT	-1,18	6,77E-03	7,12E-02	-0,29	4,13E-01	6,15E-01	
CPSF6	-1,19	8,28E-03	7,40E-02	-0,95	3,49E-02	1,60E-01	
C3	-1,23	9,91E-03	7,74E-02	-0,33	4,65E-01	6,53E-01	
ANXA2;ANXA2P2	-1,25	9,31E-03	7,63E-02	0,00	1,00E+00	1,00E+00	
CCNK	-1,27	3,02E-02	1,31E-01	-0,81	8,09E-02	2,48E-01	
GTF2F2	-1,35	1,13E-02	8,25E-02	-0,33	4,24E-01	6,22E-01	
NUDT21	-1,37	7,31E-03	7,17E-02	-0,63	1,39E-01	3,24E-01	
H1F0	-1,38	2,96E-03	5,31E-02	-0,90	3,67E-02	1,61E-01	
VEZF1	-1,39	1,97E-03	4,72E-02	-0,91	2,28E-02	1,24E-01	
DCD	-1,40	9,79E-03	7,74E-02	-0,57	2,02E-01	4,05E-01	
ZNF638	-1,42	2,02E-03	4,72E-02	-0,69	1,37E-01	3,24E-01	
EPB41L5	-1,46	2,73E-03	5,29E-02	-0,55	1,83E-01	3,82E-01	
GTF2F1	-1,56	4,20E-03	5,84E-02	-0,77	9,63E-02	2,70E-01	
VANGL2	-1,57	3,43E-03	5,36E-02	-1,85	1,53E-03	3,41E-02	
CAAP1	-1,60	3,76E-03	5,78E-02	0,00	1,00E+00	1,00E+00	
GTPBP2	-1,65	3,19E-03	5,36E-02	-0,13	7,33E-01	8,44E-01	
WWC1	-1,66	4,41E-03	6,01E-02	0,76	1,47E-01	3,34E-01	
ZNF653	-1,67	1,21E-02	8,68E-02	-0,97	6,01E-02	2,14E-01	
DSP	-1,72	3,88E-03	5,84E-02	-1,33	3,32E-02	1,57E-01	
S100A9	-1,79	1,16E-02	8,38E-02	-1,23	2,39E-02	1,28E-01	
IGKV4-1	-1,85	3,19E-02	1,36E-01	0,23	6,00E-01	7,58E-01	
CPSF4	-1,92	4,22E-03	5,84E-02	-1,41	9,56E-03	7,46E-02	
MICU1	-2,02	1,66E-03	4,23E-02	-0,82	3,98E-02	1,69E-01	
AP3D1	-2,52	3,67E-04	2,57E-02	-1,30	3,84E-02	1,64E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
S100A8	-2,52	5,52E-03	6,85E-02	0,00	1,00E+00	1,00E+00	
PDCD6				0,26	6,28E-01	7,73E-01	
HMGCS1				2,31	2,95E-04	1,63E-02	
CAPZB				1,75	1,21E-02	8,49E-02	
ACTA1;ACTC1; ACTG2;ACTA2				1,74	3,35E-03	4,66E-02	
TLN1				1,55	6,82E-03	6,75E-02	
CHMP4B				1,47	7,96E-02	2,46E-01	
RAC2;RAC3;RAC1				1,22	3,29E-02	1,57E-01	
VDAC2				1,01	4,05E-02	1,70E-01	
ACTR3				0,78	9,14E-02	2,62E-01	
CCNT1				0,75	1,03E-01	2,73E-01	
HIST1H2BN;HIST1H2BM;HIST1H2BH;HIST2H2BF;HIST1H2BC;HIST1H2BD;HIST1H2BK;H2BFS;HIST2H2BE;HIST1H2BB;HIST1H2BO;HIST1H2BJ				0,73	1,16E-01	2,91E-01	
UHRF1				0,70	2,11E-01	4,18E-01	
KARS				0,63	1,62E-01	3,57E-01	
STAT3				0,62	1,67E-01	3,62E-01	
RPL37				0,54	3,95E-01	5,99E-01	
YTHDF2				0,52	2,40E-01	4,48E-01	
U2AF2				0,49	3,25E-01	5,42E-01	
AARS				0,49	3,22E-01	5,41E-01	
CDK2				0,29	5,25E-01	7,04E-01	
PYCR1				0,27	5,41E-01	7,13E-01	
FBXO33				0,26	5,41E-01	7,13E-01	
TEX10				0,23	5,96E-01	7,56E-01	
SNRPG; SNRPGP15				0,17	7,10E-01	8,29E-01	
PDIA3				0,11	8,01E-01	8,83E-01	
MOGS				-0,04	9,24E-01	9,46E-01	
GATA3				-0,11	8,35E-01	9,01E-01	
MRPS12				-0,15	6,71E-01	8,02E-01	
PLAGL2				-0,15	7,32E-01	8,43E-01	
SMNDC1				-0,15	7,22E-01	8,37E-01	
AP1M1				-0,19	6,57E-01	7,93E-01	
ACP1				-0,26	5,42E-01	7,13E-01	
CCDC12				-0,40	3,64E-01	5,77E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
MAPK1				-0,52	2,52E-01	4,60E-01	
FBXL6				-0,62	1,69E-01	3,63E-01	
ZNF668				-0,63	1,60E-01	3,55E-01	
FUS				-0,64	1,70E-01	3,63E-01	
DSG1				-1,06	6,52E-02	2,24E-01	
AZGP1				-1,40	1,10E-02	8,11E-02	

7.3.11 Table with values corresponding to Figure 4.18.B and Figure 4.19.B and Figure 4.20.B

Table 7.15: Values corresponding to Figure 4.18.B and Figure 4.19.B and Figure 4.20.B. Values are sorted according to mean log2FC and p-value of MYC-WT. Genes marked in bold were determined as significant MYC interactors in U2OS cells according to the cutoffs: log2FC>1, q-value<0.1.

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
MAX	10,43	6,43E-08	6,00E-05	10,60	5,05E-07	5,01E-04	
MYC	9,99	1,22E-07	6,00E-05	9,87	3,13E-06	1,55E-03	
TRRAP	7,23	2,33E-07	7,68E-05	3,66	3,08E-03	7,12E-02	Chromatin remodelling
TOP2A	3,67	6,33E-05	1,42E-02	1,85	5,54E-04	5,00E-02	Chromatin remodelling
SLC25A13	2,76	1,03E-04	1,70E-02	2,13	1,99E-04	3,96E-02	Other
PDCD11	2,89	1,91E-04	2,10E-02	0,75	8,96E-02	2,99E-01	Other
PGAM5	2,13	2,08E-04	2,10E-02	1,43	1,05E-02	1,11E-01	Other
SMARCA4	2,28	3,01E-04	2,38E-02	1,60	1,49E-03	6,12E-02	Chromatin remodelling
POLR2B	2,00	3,58E-04	2,38E-02	1,99	3,44E-04	4,87E-02	Transcription
PSMD3	1,91	2,87E-04	2,38E-02	1,36	9,04E-03	1,08E-01	Degradation
CAD	3,63	5,23E-04	2,43E-02	3,58	1,62E-04	3,96E-02	Other
NOL9	2,40	4,71E-04	2,43E-02	1,64	1,24E-03	6,12E-02	Other
BAG2	2,01	5,50E-04	2,43E-02	1,65	4,48E-04	4,94E-02	Other
NOL6	1,92	5,23E-04	2,43E-02	0,56	1,17E-01	3,38E-01	Other
ACTL6A	1,86	5,92E-04	2,43E-02	1,14	2,32E-03	7,01E-02	Chromatin remodelling
PSMC6	1,76	5,84E-04	2,43E-02	0,00	1,00E+00	1,00E+00	Degradation
PSMC5	1,87	7,11E-04	2,81E-02	1,25	1,84E-03	6,47E-02	Degradation
HCFC1	1,53	9,03E-04	3,30E-02	1,42	3,28E-03	7,13E-02	Other
SQSTM1	1,93	9,42E-04	3,32E-02	1,71	1,32E-03	6,12E-02	Other

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
EP400	2,85	1,04E-03	3,41E-02	-1,41	6,28E-03	9,65E-02	Chromatin remodelling
MYO1B	1,96	1,10E-03	3,41E-02	0,72	2,22E-02	1,55E-01	Other
SNRNP200	1,54	1,21E-03	3,41E-02	1,39	1,91E-03	6,47E-02	Transcription
RAI14	2,15	1,26E-03	3,42E-02	0,00	1,00E+00	1,00E+00	Other
HADHA	1,89	1,34E-03	3,42E-02	1,78	1,53E-03	6,12E-02	Other
ATAD3A	1,66	1,30E-03	3,42E-02	0,78	2,01E-02	1,49E-01	Other
UTP15	1,66	1,37E-03	3,42E-02	0,79	1,01E-01	3,15E-01	Transcription
SSRP1	1,46	1,40E-03	3,42E-02	0,86	2,94E-02	1,80E-01	Chromatin remodelling
PSMD2	1,44	1,49E-03	3,49E-02	1,06	1,02E-02	1,09E-01	Degradation
RUVBL2	1,40	1,66E-03	3,80E-02	0,86	1,68E-02	1,37E-01	Chromatin remodelling
SUPT16H	2,22	1,82E-03	3,83E-02	1,50	3,30E-03	7,13E-02	Chromatin remodelling
HEATR1	1,75	1,76E-03	3,83E-02	1,01	5,05E-02	2,25E-01	Other
WDR43	1,58	1,78E-03	3,83E-02	0,50	1,40E-01	3,63E-01	Other
RANBP2	1,39	1,87E-03	3,84E-02	1,22	1,16E-02	1,15E-01	Other
PSMC2	1,54	2,03E-03	4,08E-02	1,11	1,31E-02	1,26E-01	Degradation
WDR5	1,60	2,13E-03	4,20E-02	1,65	8,28E-04	6,12E-02	Transcription
CHD4	1,39	2,26E-03	4,29E-02	1,33	1,56E-03	6,12E-02	Other
LRPPRC	2,09	2,77E-03	4,76E-02	0,78	2,42E-01	4,89E-01	Other
DNAJA1	1,51	2,74E-03	4,76E-02	1,68	2,90E-03	7,01E-02	Other
DNAJA2	1,50	2,68E-03	4,76E-02	1,51	2,36E-03	7,01E-02	Other
RUVBL1	1,25	2,92E-03	4,89E-02	0,70	3,67E-02	1,95E-01	Chromatin remodelling
HUWE1	3,16	3,39E-03	5,32E-02	2,27	1,15E-03	6,12E-02	Degradation
LAS1L	1,80	3,69E-03	5,61E-02	0,94	1,28E-02	1,24E-01	Other
HADHB	1,41	3,95E-03	5,91E-02	1,52	2,04E-03	6,55E-02	Other
NOP56	1,20	4,22E-03	6,04E-02	0,34	2,15E-01	4,61E-01	Other
RFC4	1,15	4,20E-03	6,04E-02	1,05	3,25E-03	7,13E-02	Replication
PSMC3	1,14	4,17E-03	6,04E-02	1,04	4,81E-03	8,30E-02	Degradation
UTP18	1,49	4,35E-03	6,13E-02	0,90	3,12E-02	1,84E-01	Transcription
COPA	1,41	4,61E-03	6,26E-02	2,08	5,05E-03	8,50E-02	Other
PSMD8	1,14	4,63E-03	6,26E-02	1,00	2,28E-02	1,57E-01	Degradation
ZNF114	1,38	5,15E-03	6,76E-02	0,23	5,40E-01	7,29E-01	Transcription
POLRMT	1,14	5,62E-03	7,11E-02	0,49	1,06E-01	3,21E-01	Other
PSMC1	1,45	6,15E-03	7,58E-02	0,92	8,07E-02	2,87E-01	Degradation
MYBBP1A	1,75	6,73E-03	7,72E-02	0,84	1,25E-01	3,45E-01	Other
HIST2H2BE; HIST1H2BB; HIST1H2BO;	1,22	6,65E-03	7,72E-02	1,07	8,98E-03	1,08E-01	Other

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
HIST1H2BJ; HIST3H2BB							
WDR75	1,18	6,62E-03	7,72E-02	0,35	3,08E-01	5,55E-01	Other
NOP58	1,06	6,52E-03	7,72E-02	0,31	2,14E-01	4,61E-01	Other
MRPS22	1,10	6,84E-03	7,76E-02	0,55	5,49E-02	2,37E-01	Other
WDR36	1,31	6,94E-03	7,78E-02	0,00	1,00E+00	1,00E+00	Other
KIAA0020	1,59	7,22E-03	7,92E-02	0,85	7,60E-02	2,78E-01	Other
CIRH1A	1,48	7,45E-03	7,97E-02	0,40	2,91E-01	5,45E-01	Other
DCAF4	1,09	7,59E-03	7,97E-02	0,83	8,75E-03	1,08E-01	Other
NOL11	1,23	7,78E-03	8,08E-02	0,50	1,39E-01	3,62E-01	Other
RFC3	1,37	8,15E-03	8,38E-02	1,59	4,13E-03	7,52E-02	Replication
MYO1C	1,16	8,61E-03	8,59E-02	1,16	7,43E-03	1,05E-01	Other
AIFM1	1,00	9,33E-03	8,94E-02	0,32	2,34E-01	4,82E-01	Other
NOC2L	1,44	1,01E-02	9,41E-02	0,25	5,49E-01	7,29E-01	Other
KRR1	1,27	1,02E-02	9,41E-02	1,39	7,27E-03	1,05E-01	Other
PSMD11	1,21	1,01E-02	9,41E-02	0,52	1,25E-01	3,45E-01	Degradation
PSMD1	1,12	1,07E-02	9,82E-02	0,63	9,17E-02	2,99E-01	Degradation
DHX33	1,35	1,13E-02	1,02E-01	0,00	1,00E+00	1,00E+00	
TTF1	1,72	1,20E-02	1,04E-01	0,22	4,66E-01	6,81E-01	
TUBA1B	1,28	1,24E-02	1,04E-01	2,72	1,23E-03	6,12E-02	
DDX10	1,10	1,17E-02	1,04E-01	0,45	8,72E-02	2,96E-01	
CSNK2A1;CSNK2A3	1,09	1,30E-02	1,06E-01	1,47	1,30E-03	6,12E-02	
WDR3	1,28	1,40E-02	1,13E-01	-0,01	9,83E-01	9,90E-01	
PSMD6	1,14	1,46E-02	1,15E-01	0,70	9,14E-02	2,99E-01	
PRKDC	2,13	1,60E-02	1,17E-01	2,18	7,80E-03	1,08E-01	
RPF2	1,41	1,64E-02	1,17E-01	0,00	1,00E+00	1,00E+00	
ATAD2	1,22	1,56E-02	1,17E-01	0,00	1,00E+00	1,00E+00	
WDR55	1,00	1,50E-02	1,17E-01	0,93	2,64E-02	1,70E-01	
ZNF316	1,23	1,88E-02	1,29E-01	1,22	1,95E-03	6,47E-02	
TIMM50	1,19	1,87E-02	1,29E-01	1,12	2,33E-02	1,57E-01	
PSMC4	1,00	1,92E-02	1,30E-01	1,05	2,23E-02	1,55E-01	
SLC25A6	1,27	1,97E-02	1,32E-01	0,00	1,00E+00	1,00E+00	
CEBPZ	1,02	2,05E-02	1,35E-01	-0,19	5,30E-01	7,26E-01	
TEX10	1,27	2,24E-02	1,43E-01	0,28	2,58E-01	5,05E-01	
TOP2B	1,14	2,35E-02	1,47E-01	0,00	1,00E+00	1,00E+00	
GTPBP4	1,11	2,47E-02	1,48E-01	0,71	2,34E-02	1,57E-01	
RPS5	1,35	2,54E-02	1,50E-01	1,12	5,04E-02	2,25E-01	
PLRG1	1,24	2,55E-02	1,50E-01	1,19	5,75E-02	2,43E-01	
PARP1	1,54	2,70E-02	1,52E-01	1,02	8,74E-02	2,96E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
DKC1	1,38	2,66E-02	1,52E-01	0,74	4,56E-02	2,13E-01	
EXOSC10	1,03	2,83E-02	1,52E-01	0,00	1,00E+00	1,00E+00	
FAM83H	1,70	2,87E-02	1,53E-01	2,46	5,30E-04	5,00E-02	
NUP133	1,39	3,14E-02	1,56E-01	0,92	4,64E-02	2,16E-01	
CBX3	1,25	4,01E-02	1,83E-01	0,61	2,23E-01	4,69E-01	
GTF3C1	1,52	4,72E-02	1,95E-01	1,21	4,80E-02	2,21E-01	
CDK11B;CDK11A; CDC2L1	1,18	4,60E-02	1,95E-01	0,00	1,00E+00	1,00E+00	
AHCTF1	1,14	4,55E-02	1,95E-01	0,00	1,00E+00	1,00E+00	
ZBTB7A	1,04	4,96E-02	1,98E-01	0,73	6,50E-02	2,57E-01	
RSL24D1	1,81	6,19E-02	2,30E-01	0,00	1,00E+00	1,00E+00	
CD3EAP	1,61	6,91E-02	2,42E-01	0,70	5,23E-01	7,23E-01	
COIL	1,05	7,75E-02	2,54E-01	0,00	1,00E+00	1,00E+00	
DAXX	1,18	1,90E-01	4,05E-01	1,44	1,09E-01	3,28E-01	
MDK	1,18	3,01E-01	5,08E-01	0,69	7,01E-01	8,33E-01	
SDC4	0,99	3,44E-02	1,64E-01	1,12	4,88E-02	2,21E-01	
MRPS35	0,98	9,67E-02	2,87E-01	0,00	1,00E+00	1,00E+00	
HMGA1	0,98	1,26E-01	3,21E-01	-0,01	9,80E-01	9,88E-01	
DDX51	0,98	4,56E-02	1,95E-01	0,04	8,75E-01	9,29E-01	
DDX24	0,98	5,38E-02	2,09E-01	-0,03	9,17E-01	9,52E-01	
PWP1	0,97	3,55E-02	1,69E-01	0,23	4,66E-01	6,81E-01	
ZNF800	0,97	3,90E-02	1,80E-01	0,62	4,81E-02	2,21E-01	
MRPS16	0,96	8,71E-03	8,59E-02	0,00	1,00E+00	1,00E+00	
SLC25A3	0,96	7,18E-02	2,48E-01	0,82	8,90E-02	2,98E-01	
SLC25A22	0,95	2,01E-02	1,33E-01	0,74	3,96E-02	2,00E-01	
RBM28	0,95	1,24E-02	1,04E-01	-0,04	8,98E-01	9,44E-01	
C18orf21	0,94	1,18E-02	1,04E-01	0,74	5,42E-02	2,37E-01	
ZSCAN26;ZNF187	0,94	9,97E-02	2,91E-01	1,23	2,92E-02	1,80E-01	
MRPS34	0,92	1,30E-02	1,06E-01	0,25	2,75E-01	5,27E-01	
SEC61A1	0,92	8,45E-02	2,67E-01	1,02	4,87E-02	2,21E-01	
DNAJC10	0,92	4,74E-02	1,95E-01	1,36	3,10E-02	1,84E-01	
PPAN-P2RY11; PPAN	0,91	1,62E-01	3,68E-01	0,18	5,22E-01	7,23E-01	
PRPF8	0,91	2,94E-02	1,53E-01	0,76	4,45E-02	2,11E-01	
USP7	0,90	2,05E-01	4,21E-01	0,70	2,40E-01	4,89E-01	
PSMA6	0,90	1,13E-01	3,06E-01	0,60	3,14E-01	5,57E-01	
PSMA1	0,90	7,40E-02	2,50E-01	0,54	2,02E-01	4,46E-01	
MDC1	0,90	1,31E-02	1,06E-01	0,28	4,18E-01	6,44E-01	
BMS1	0,89	1,44E-02	1,14E-01	0,40	1,02E-01	3,16E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
UTP20	0,88	4,74E-02	1,95E-01	0,09	7,68E-01	8,78E-01	
UBTF	0,88	1,61E-02	1,17E-01	0,00	1,00E+00	1,00E+00	
TBL3	0,88	4,74E-02	1,95E-01	0,00	1,00E+00	1,00E+00	
FAM111A	0,88	1,57E-02	1,17E-01	1,45	3,47E-03	7,27E-02	
CBX5	0,87	5,74E-02	2,17E-01	0,00	1,00E+00	1,00E+00	
NPM1	0,86	2,90E-02	1,53E-01	0,26	3,16E-01	5,59E-01	
EFTUD2	0,86	3,13E-02	1,56E-01	0,97	1,11E-02	1,15E-01	
TUBA3C;TUBA3E	0,86	8,18E-02	2,62E-01	1,63	8,87E-03	1,08E-01	
H2AFV;H2AFZ	0,85	3,21E-02	1,56E-01	0,29	2,90E-01	5,45E-01	
PPP2R2A	0,85	6,19E-02	2,30E-01	1,37	1,46E-02	1,29E-01	
EMD	0,83	2,42E-02	1,48E-01	0,36	1,37E-01	3,59E-01	
PSMB2	0,83	6,37E-02	2,30E-01	0,00	1,00E+00	1,00E+00	
RRP8	0,83	4,69E-02	1,95E-01	-0,11	7,48E-01	8,66E-01	
FBL	0,83	1,71E-02	1,21E-01	0,12	5,97E-01	7,60E-01	
DDX31	0,83	3,11E-02	1,56E-01	0,52	5,16E-02	2,29E-01	
NDUFA9	0,83	1,13E-01	3,06E-01	0,93	2,73E-02	1,74E-01	
PSMA5	0,82	1,81E-01	3,91E-01	0,52	2,35E-01	4,82E-01	
EBNA1BP2	0,82	6,23E-02	2,30E-01	0,12	6,06E-01	7,67E-01	
DMAP1	0,82	4,72E-02	1,95E-01	0,00	1,00E+00	1,00E+00	
ADAR	0,82	4,43E-02	1,93E-01	0,77	3,89E-02	2,00E-01	
ZBTB24	0,82	8,57E-02	2,68E-01	0,36	2,24E-01	4,69E-01	
MAP4K4	0,81	7,74E-02	2,54E-01	1,30	4,17E-03	7,52E-02	
RPUSD4	0,81	3,23E-02	1,56E-01	0,23	5,47E-01	7,29E-01	
RCL1	0,81	2,00E-02	1,33E-01	0,40	2,68E-01	5,17E-01	
GRWD1	0,80	3,21E-02	1,56E-01	0,43	1,29E-01	3,51E-01	
SLC25A11	0,80	1,89E-02	1,29E-01	0,43	2,94E-01	5,45E-01	
WHSC1	0,80	2,46E-02	1,48E-01	0,76	3,08E-02	1,84E-01	
RPL4	0,79	2,42E-02	1,48E-01	0,45	7,31E-02	2,73E-01	
CAAP1	0,79	1,16E-01	3,09E-01	0,22	6,14E-01	7,71E-01	
PLEKHG3	0,78	1,39E-01	3,31E-01	1,30	2,90E-03	7,01E-02	
IMP4	0,78	3,09E-02	1,56E-01	0,48	6,65E-02	2,59E-01	
SMARCA5	0,78	2,46E-02	1,48E-01	0,38	1,54E-01	3,82E-01	
PSMB1	0,78	8,83E-02	2,75E-01	0,31	3,60E-01	5,95E-01	
CSNK2B-LY6G5B-1181;CSNK2B;CSNK2B-LY6G5B--991; CSNK2B-LY6G5B-562	0,78	7,07E-02	2,46E-01	0,97	2,77E-02	1,75E-01	
ZNF22	0,78	1,20E-01	3,16E-01	0,00	1,00E+00	1,00E+00	
RFC2	0,77	2,91E-02	1,53E-01	1,02	3,59E-03	7,27E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BRIX1	0,76	3,77E-02	1,75E-01	0,37	1,22E-01	3,42E-01	
NOP2	0,75	5,71E-02	2,17E-01	-0,12	6,13E-01	7,71E-01	
FARP1	0,75	7,55E-02	2,54E-01	0,94	1,07E-02	1,12E-01	
IMP3	0,75	5,90E-02	2,22E-01	0,30	2,27E-01	4,73E-01	
DDX21	0,73	2,82E-02	1,52E-01	0,21	3,59E-01	5,95E-01	
PSMB3	0,73	8,42E-02	2,67E-01	0,00	1,00E+00	1,00E+00	
PLK1	0,73	5,17E-02	2,03E-01	0,49	1,47E-01	3,72E-01	
HNRNPU	0,73	2,71E-02	1,52E-01	0,55	4,02E-02	2,02E-01	
DPM1	0,72	2,75E-02	1,52E-01	0,49	7,59E-02	2,78E-01	
HDAC2	0,72	2,76E-02	1,52E-01	0,77	1,44E-02	1,29E-01	
TUBA1C;TUBA1B	0,72	1,11E-01	3,03E-01	1,86	2,64E-03	7,01E-02	
PSMA3	0,72	9,42E-02	2,83E-01	0,03	9,20E-01	9,52E-01	
TJP1	0,72	1,40E-01	3,33E-01	0,00	1,00E+00	1,00E+00	
MRPL16	0,71	1,04E-01	2,99E-01	0,48	1,95E-01	4,38E-01	
POLR1E	0,71	4,10E-02	1,85E-01	0,23	3,15E-01	5,58E-01	
UBA52;UBB; RPS27A;UBC	0,70	3,15E-01	5,24E-01	-0,78	5,81E-01	7,50E-01	
NCL	0,70	1,31E-01	3,23E-01	0,14	7,19E-01	8,45E-01	
PSMD13	0,70	2,11E-01	4,27E-01	0,00	1,00E+00	1,00E+00	
HSPA8	0,70	4,20E-02	1,86E-01	1,00	7,74E-03	1,08E-01	
AATF	0,70	4,02E-02	1,83E-01	0,08	7,27E-01	8,49E-01	
POLR2C	0,69	9,33E-02	2,82E-01	0,43	8,02E-02	2,87E-01	
RPL12	0,69	7,50E-02	2,53E-01	-0,20	7,63E-01	8,78E-01	
DHX8	0,69	5,15E-02	2,03E-01	1,13	6,28E-03	9,65E-02	
DDX47	0,68	3,59E-02	1,69E-01	0,50	6,74E-02	2,60E-01	
RIF1	0,68	4,83E-02	1,96E-01	0,79	2,43E-02	1,59E-01	
MRPL46	0,68	1,69E-01	3,80E-01	-0,20	5,66E-01	7,40E-01	
HIST1H4A	0,67	7,96E-02	2,57E-01	0,05	8,69E-01	9,27E-01	
ZBTB38	0,66	5,53E-02	2,12E-01	0,00	1,00E+00	1,00E+00	
TUBB	0,65	1,03E-01	2,98E-01	1,65	2,84E-03	7,01E-02	
SLC25A1	0,65	6,88E-02	2,42E-01	0,89	9,11E-03	1,08E-01	
STAU1	0,65	2,00E-01	4,18E-01	0,81	8,81E-02	2,97E-01	
MRPL49	0,64	1,19E-01	3,16E-01	-0,32	1,97E-01	4,39E-01	
MATR3	0,64	4,34E-02	1,90E-01	0,45	8,87E-02	2,97E-01	
DDB1	0,63	4,89E-02	1,97E-01	0,64	3,89E-02	2,00E-01	
SCRIB	0,63	9,03E-02	2,76E-01	0,99	1,47E-02	1,29E-01	
TOR4A	0,62	1,15E-01	3,08E-01	0,83	2,18E-02	1,55E-01	
GTF3A	0,62	1,95E-01	4,13E-01	1,69	1,48E-03	6,12E-02	
RPL7	0,62	5,25E-02	2,06E-01	-0,01	9,67E-01	9,81E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
CTCF	0,62	7,67E-02	2,54E-01	0,28	3,84E-01	6,15E-01	
EMG1	0,62	7,37E-02	2,50E-01	0,49	7,21E-02	2,71E-01	
SLIRP	0,61	1,09E-01	3,03E-01	-0,36	1,39E-01	3,62E-01	
C9orf114	0,61	1,41E-01	3,35E-01	-0,06	8,08E-01	8,97E-01	
EPB41L3	0,61	8,98E-02	2,75E-01	0,90	1,97E-02	1,48E-01	
HIST2H3PS2;H3F3B;H3F3C;HIST2H3A;HIST3H3;H3F3A;HIST1H3A	0,61	6,79E-02	2,42E-01	0,16	4,82E-01	6,96E-01	
CLK1	0,61	5,43E-02	2,10E-01	0,41	1,03E-01	3,17E-01	
NUP155	0,61	1,30E-01	3,23E-01	0,66	8,51E-02	2,93E-01	
RBM42	0,60	1,74E-01	3,83E-01	0,47	2,98E-01	5,49E-01	
DHX9	0,60	1,11E-01	3,03E-01	0,28	3,76E-01	6,10E-01	
SCAF11	0,60	1,56E-01	3,59E-01	1,02	1,57E-02	1,37E-01	
KLF2	0,60	9,77E-02	2,89E-01	0,52	1,13E-01	3,36E-01	
EPB41L4B	0,59	6,84E-02	2,42E-01	-0,15	5,17E-01	7,22E-01	
RPL15	0,59	1,20E-01	3,16E-01	0,47	1,50E-01	3,74E-01	
RPLP0;RPLP0P6	0,59	9,26E-02	2,81E-01	0,70	1,74E-02	1,39E-01	
RPL14	0,58	1,11E-01	3,03E-01	0,38	1,20E-01	3,39E-01	
TUBB4B	0,58	1,45E-01	3,41E-01	0,85	8,20E-02	2,89E-01	
REST	0,57	1,52E-01	3,56E-01	1,01	9,03E-03	1,08E-01	
AURKB	0,57	6,84E-02	2,42E-01	0,28	2,80E-01	5,31E-01	
RPL10A	0,57	6,17E-02	2,30E-01	0,31	2,04E-01	4,49E-01	
SLC25A5	0,57	8,86E-02	2,75E-01	0,41	2,79E-01	5,30E-01	
ABT1	0,57	2,22E-01	4,38E-01	0,36	3,11E-01	5,57E-01	
C2orf47	0,57	8,46E-02	2,67E-01	0,82	4,01E-02	2,02E-01	
ZNF771	0,57	1,08E-01	3,03E-01	0,66	7,90E-02	2,84E-01	
XRCC6	0,57	3,93E-01	5,99E-01	1,36	8,36E-02	2,91E-01	
SRSF9	0,57	1,69E-01	3,80E-01	0,00	1,00E+00	1,00E+00	
RRP15	0,56	1,69E-01	3,80E-01	0,28	3,99E-01	6,29E-01	
DDX49	0,56	2,26E-01	4,42E-01	0,18	5,45E-01	7,29E-01	
TMX3	0,56	2,06E-01	4,21E-01	0,00	1,00E+00	1,00E+00	
MPHOSPH10	0,56	1,28E-01	3,21E-01	0,17	4,33E-01	6,55E-01	
RFC5	0,56	7,66E-02	2,54E-01	1,23	8,67E-03	1,08E-01	
GNB2L1	0,55	2,09E-01	4,24E-01	0,89	3,14E-02	1,84E-01	
MRPL21	0,55	2,15E-01	4,29E-01	0,00	1,00E+00	1,00E+00	
MSH6	0,55	1,22E-01	3,16E-01	0,74	4,37E-02	2,10E-01	
RFC1	0,55	8,43E-02	2,67E-01	0,79	1,87E-02	1,44E-01	
PNO1	0,54	9,56E-02	2,85E-01	0,42	1,41E-01	3,63E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PRPF6	0,54	7,27E-02	2,49E-01	0,50	3,00E-01	5,51E-01	
BANF1	0,54	4,01E-01	6,09E-01	0,17	8,57E-01	9,24E-01	
DNTTIP2	0,54	1,28E-01	3,21E-01	0,27	2,33E-01	4,82E-01	
XRCC5	0,54	2,06E-01	4,21E-01	0,82	4,07E-02	2,03E-01	
ZNF512	0,54	1,03E-01	2,98E-01	0,55	6,10E-02	2,50E-01	
PSMA7;PSMA8	0,54	2,04E-01	4,21E-01	0,44	2,63E-01	5,12E-01	
CDCA8	0,54	1,81E-01	3,91E-01	0,26	2,97E-01	5,49E-01	
FLYWCH1	0,53	7,77E-02	2,54E-01	0,28	3,65E-01	6,01E-01	
UTP23	0,53	9,97E-02	2,91E-01	0,04	8,73E-01	9,29E-01	
POP1	0,53	1,11E-01	3,03E-01	-0,01	9,55E-01	9,74E-01	
RPL18	0,52	2,43E-01	4,57E-01	-0,22	4,17E-01	6,44E-01	
DNAJA3	0,52	8,72E-02	2,72E-01	0,37	1,70E-01	4,04E-01	
RPP38	0,52	2,03E-01	4,21E-01	0,00	1,00E+00	1,00E+00	
EME1	0,51	1,61E-01	3,68E-01	0,95	1,02E-02	1,09E-01	
GFPT1	0,51	2,73E-01	4,83E-01	1,35	8,16E-03	1,08E-01	
MRM1	0,50	1,28E-01	3,22E-01	0,08	7,13E-01	8,41E-01	
POLR2A	0,50	2,29E-01	4,44E-01	0,59	3,57E-01	5,95E-01	
MUS81	0,50	1,71E-01	3,81E-01	1,06	4,66E-03	8,25E-02	
NO66	0,50	9,94E-02	2,91E-01	-0,42	2,04E-01	4,49E-01	
GPATCH8	0,50	2,13E-01	4,28E-01	0,90	3,92E-02	2,00E-01	
RPS16	0,50	1,21E-01	3,16E-01	0,50	5,21E-02	2,30E-01	
MTHFD1L	0,50	2,35E-01	4,48E-01	-0,01	9,65E-01	9,81E-01	
RPLP1	0,50	3,81E-01	5,83E-01	1,59	1,02E-01	3,16E-01	
PWP2	0,50	2,07E-01	4,23E-01	-0,52	1,56E-01	3,84E-01	
LARP7	0,49	1,96E-01	4,13E-01	0,53	1,27E-01	3,49E-01	
NDUFA4	0,49	1,04E-01	2,99E-01	0,47	7,82E-02	2,84E-01	
KRI1	0,49	2,60E-01	4,74E-01	0,00	1,00E+00	1,00E+00	
MCM5	0,49	2,44E-01	4,57E-01	0,94	4,22E-02	2,06E-01	
RPL6	0,49	1,31E-01	3,23E-01	-0,04	8,64E-01	9,26E-01	
DUSP11	0,49	1,72E-01	3,82E-01	0,25	3,60E-01	5,95E-01	
SUPT5H	0,49	3,27E-01	5,34E-01	0,00	1,00E+00	1,00E+00	
RSL1D1	0,48	1,46E-01	3,44E-01	-0,20	4,28E-01	6,52E-01	
SLTM	0,48	1,09E-01	3,03E-01	0,13	5,77E-01	7,49E-01	
NSA2	0,48	1,55E-01	3,59E-01	0,23	3,06E-01	5,54E-01	
BAZ2A	0,48	3,75E-01	5,77E-01	0,00	1,00E+00	1,00E+00	
DAP3	0,47	1,17E-01	3,10E-01	0,30	1,96E-01	4,38E-01	
NOP14	0,47	2,51E-01	4,65E-01	0,30	2,12E-01	4,58E-01	
PPP2R1A	0,47	1,35E-01	3,26E-01	1,49	3,80E-03	7,41E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
ZNF148	0,47	1,57E-01	3,60E-01	0,69	1,86E-02	1,44E-01	
RPS27L	0,47	1,32E-01	3,24E-01	0,62	1,48E-01	3,72E-01	
MOGS	0,46	2,45E-01	4,57E-01	0,18	5,93E-01	7,57E-01	
SMARCC1	0,46	1,24E-01	3,18E-01	0,35	2,93E-01	5,45E-01	
SGPL1	0,46	1,27E-01	3,21E-01	1,06	1,45E-02	1,29E-01	
MBD1	0,46	1,74E-01	3,83E-01	0,51	1,03E-01	3,16E-01	
TEFM	0,46	2,28E-01	4,43E-01	0,08	7,23E-01	8,47E-01	
RALY	0,46	1,23E-01	3,18E-01	0,40	9,76E-02	3,10E-01	
APOBEC3B	0,46	2,29E-01	4,44E-01	1,00	5,64E-03	9,33E-02	
TRMT2A	0,46	2,92E-01	5,00E-01	0,27	2,57E-01	5,04E-01	
SNRNP40	0,45	1,85E-01	3,98E-01	0,80	2,14E-02	1,55E-01	
NKTR	0,44	2,94E-01	5,02E-01	0,50	9,81E-02	3,10E-01	
BAZ1B	0,44	2,47E-01	4,59E-01	0,00	1,00E+00	1,00E+00	
MRPS30	0,44	2,65E-01	4,79E-01	0,00	1,00E+00	1,00E+00	
FTSJ3	0,43	2,16E-01	4,29E-01	0,04	8,52E-01	9,22E-01	
BOP1	0,43	1,36E-01	3,26E-01	-0,12	6,72E-01	8,06E-01	
DNAJB12	0,43	2,75E-01	4,84E-01	0,22	5,40E-01	7,29E-01	
DDX52	0,42	2,54E-01	4,68E-01	0,51	6,72E-02	2,60E-01	
DDX28	0,41	1,55E-01	3,59E-01	-0,05	8,15E-01	9,00E-01	
RPLP2	0,41	3,02E-01	5,09E-01	0,16	5,33E-01	7,28E-01	
DDX54	0,41	1,61E-01	3,68E-01	0,11	6,03E-01	7,65E-01	
MRPL38	0,41	3,32E-01	5,38E-01	0,36	2,10E-01	4,57E-01	
RPF1	0,41	1,97E-01	4,15E-01	0,18	5,42E-01	7,29E-01	
MRPL33	0,41	2,55E-01	4,69E-01	-0,07	7,86E-01	8,92E-01	
RACGAP1	0,41	4,36E-01	6,41E-01	-0,06	8,61E-01	9,25E-01	
NOL10	0,41	1,87E-01	4,00E-01	-0,25	4,31E-01	6,54E-01	
GNL3	0,40	2,98E-01	5,06E-01	-0,30	2,01E-01	4,46E-01	
PAK1IP1	0,39	2,31E-01	4,44E-01	0,02	9,23E-01	9,53E-01	
RPL7L1	0,39	1,96E-01	4,13E-01	-0,22	3,20E-01	5,62E-01	
MRPL57	0,39	2,90E-01	4,98E-01	-0,15	5,01E-01	7,11E-01	
EIF3B	0,39	2,29E-01	4,44E-01	0,67	3,85E-02	2,00E-01	
LYAR	0,38	2,62E-01	4,77E-01	-0,77	1,94E-02	1,48E-01	
NFIC	0,38	3,66E-01	5,67E-01	0,26	5,47E-01	7,29E-01	
RPL18A	0,38	2,63E-01	4,77E-01	0,26	3,22E-01	5,63E-01	
FMNL3	0,38	2,25E-01	4,41E-01	0,63	5,56E-02	2,37E-01	
TAF1B	0,38	3,11E-01	5,20E-01	0,00	1,00E+00	1,00E+00	
CMSS1	0,37	3,26E-01	5,33E-01	0,55	1,27E-01	3,49E-01	
MRPL23	0,37	3,16E-01	5,25E-01	0,77	1,45E-01	3,68E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
hCG_1984214; MRPS17	0,37	2,27E-01	4,42E-01	-0,58	1,12E-01	3,33E-01	
ARHGEF39	0,37	2,95E-01	5,03E-01	0,80	1,41E-02	1,29E-01	
POP4	0,37	3,23E-01	5,31E-01	-0,04	9,09E-01	9,49E-01	
DIMT1	0,37	2,16E-01	4,29E-01	-0,18	4,49E-01	6,73E-01	
RPS12	0,37	3,33E-01	5,38E-01	0,19	6,51E-01	7,99E-01	
EIF3I	0,37	3,09E-01	5,18E-01	0,61	8,20E-02	2,89E-01	
NUMA1	0,37	2,36E-01	4,48E-01	0,52	7,00E-02	2,66E-01	
SPATS2L	0,36	4,08E-01	6,15E-01	0,67	5,57E-02	2,37E-01	
TCP1	0,36	5,11E-01	6,93E-01	0,39	3,81E-01	6,12E-01	
RPS19	0,36	3,20E-01	5,29E-01	0,53	6,85E-02	2,63E-01	
DHX15	0,36	2,43E-01	4,57E-01	0,27	3,18E-01	5,61E-01	
WDR18	0,35	3,47E-01	5,51E-01	-0,24	4,28E-01	6,52E-01	
MRPL48	0,35	3,41E-01	5,47E-01	-0,30	3,41E-01	5,80E-01	
RPL24	0,35	3,25E-01	5,32E-01	0,08	8,61E-01	9,25E-01	
EIF6	0,35	2,69E-01	4,82E-01	0,02	9,21E-01	9,52E-01	
RRS1	0,35	2,39E-01	4,52E-01	-0,06	7,98E-01	8,93E-01	
KPNA2	0,35	2,31E-01	4,44E-01	0,15	5,39E-01	7,29E-01	
MKI67	0,34	3,83E-01	5,86E-01	-0,10	8,10E-01	8,97E-01	
ESYT1	0,34	2,89E-01	4,98E-01	1,44	1,52E-03	6,12E-02	
NOC4L	0,34	2,75E-01	4,84E-01	0,20	6,61E-01	8,01E-01	
TSR1	0,33	2,36E-01	4,49E-01	0,11	7,11E-01	8,41E-01	
HSD17B10	0,33	3,36E-01	5,40E-01	-0,51	1,14E-01	3,37E-01	
MAZ	0,33	4,02E-01	6,09E-01	0,59	1,15E-01	3,38E-01	
SRPRB	0,33	2,98E-01	5,06E-01	0,06	8,35E-01	9,13E-01	
RPL35A	0,33	2,88E-01	4,98E-01	0,62	6,35E-02	2,56E-01	
RPL27	0,32	2,71E-01	4,82E-01	0,19	4,34E-01	6,56E-01	
RRP1	0,32	3,71E-01	5,72E-01	-0,26	2,74E-01	5,26E-01	
NSUN5	0,31	2,67E-01	4,79E-01	0,55	4,47E-02	2,11E-01	
PRPF38A	0,31	3,22E-01	5,31E-01	0,00	9,89E-01	9,93E-01	
LAMB3	0,31	4,55E-01	6,54E-01	0,52	1,31E-01	3,55E-01	
HIST1H2BN; HIST1H2BM; HIST1H2BH; HIST2H2BF; HIST1H2BC; HIST1H2BD; HIST1H2BK; H2BFS; HIST1H2BL	0,31	3,17E-01	5,26E-01	-0,26	3,74E-01	6,09E-01	
CHP1	0,30	5,80E-01	7,36E-01	0,00	1,00E+00	1,00E+00	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
NGDN	0,30	3,22E-01	5,31E-01	-0,11	6,48E-01	7,97E-01	
MRPL4	0,30	2,76E-01	4,85E-01	-0,15	5,92E-01	7,57E-01	
DCAF13	0,30	2,72E-01	4,82E-01	-0,12	5,85E-01	7,53E-01	
WDR46	0,30	2,90E-01	4,98E-01	0,15	5,24E-01	7,23E-01	
ZNF281	0,30	4,25E-01	6,28E-01	0,18	5,22E-01	7,23E-01	
UTP3	0,30	4,68E-01	6,64E-01	-0,11	6,52E-01	8,00E-01	
EXOSC9	0,30	4,15E-01	6,20E-01	0,00	1,00E+00	1,00E+00	
NHP2	0,29	3,30E-01	5,36E-01	-0,11	6,42E-01	7,96E-01	
RPL7A	0,29	2,86E-01	4,97E-01	-0,02	9,37E-01	9,60E-01	
BCAS2	0,29	4,66E-01	6,63E-01	0,00	1,00E+00	1,00E+00	
NOM1	0,29	4,16E-01	6,20E-01	-0,03	9,02E-01	9,45E-01	
CDC5L	0,29	3,57E-01	5,60E-01	0,24	3,90E-01	6,21E-01	
CENPVL3	0,28	2,97E-01	5,05E-01	-0,37	2,54E-01	5,00E-01	
ZNF638	0,28	3,14E-01	5,23E-01	0,38	1,20E-01	3,39E-01	
HNRNPM	0,28	3,45E-01	5,51E-01	0,17	4,39E-01	6,61E-01	
LMNB1	0,28	3,19E-01	5,29E-01	0,14	5,15E-01	7,21E-01	
RBBP4	0,28	3,54E-01	5,59E-01	0,52	8,42E-02	2,91E-01	
RPL5	0,28	3,43E-01	5,49E-01	0,13	5,77E-01	7,49E-01	
JUNB	0,28	4,22E-01	6,25E-01	0,08	8,41E-01	9,16E-01	
ADNP	0,27	5,07E-01	6,93E-01	0,39	3,05E-01	5,54E-01	
TCEB1	0,27	6,67E-01	8,04E-01	0,00	1,00E+00	1,00E+00	
FCF1	0,27	3,68E-01	5,69E-01	0,03	8,90E-01	9,37E-01	
MRPS25	0,27	4,54E-01	6,54E-01	-0,41	1,11E-01	3,32E-01	
PINX1	0,26	4,60E-01	6,59E-01	-0,37	1,32E-01	3,56E-01	
MRPS18B	0,26	3,61E-01	5,64E-01	0,18	4,54E-01	6,74E-01	
RPL3	0,26	3,59E-01	5,62E-01	0,76	1,16E-02	1,15E-01	
AKAP8	0,26	5,45E-01	7,16E-01	0,00	1,00E+00	1,00E+00	
SCAF1	0,26	4,47E-01	6,53E-01	0,03	8,77E-01	9,31E-01	
VRK2	0,26	4,76E-01	6,69E-01	0,54	1,15E-01	3,38E-01	
METAP1	0,26	5,17E-01	6,98E-01	0,00	1,00E+00	1,00E+00	
RPL13A;RPL13a	0,25	3,47E-01	5,51E-01	0,32	1,82E-01	4,25E-01	
ZNF319	0,25	5,57E-01	7,24E-01	-0,26	7,25E-01	8,48E-01	
WDR12	0,25	4,11E-01	6,18E-01	-0,26	3,95E-01	6,26E-01	
PDCD2L	0,25	4,18E-01	6,22E-01	-0,04	8,72E-01	9,28E-01	
RPL32	0,25	6,26E-01	7,75E-01	-0,10	7,96E-01	8,93E-01	
HSPA1B;HSPA1A	0,25	4,54E-01	6,54E-01	0,33	3,04E-01	5,54E-01	
ZSCAN25	0,23	5,36E-01	7,12E-01	0,61	2,15E-01	4,61E-01	
RPS11	0,23	4,73E-01	6,69E-01	0,25	4,75E-01	6,90E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
FRMD6	0,23	5,35E-01	7,12E-01	1,84	6,91E-04	5,72E-02	
RBM14	0,23	4,91E-01	6,82E-01	-0,29	2,94E-01	5,45E-01	
AKAP17A	0,23	4,58E-01	6,56E-01	0,15	5,23E-01	7,23E-01	
DHX30	0,23	5,39E-01	7,12E-01	-0,31	3,30E-01	5,71E-01	
HNRNPH1	0,23	4,78E-01	6,69E-01	0,33	2,53E-01	4,99E-01	
DDX5	0,23	4,02E-01	6,09E-01	0,26	2,65E-01	5,13E-01	
MRPS5	0,23	5,43E-01	7,15E-01	0,30	3,19E-01	5,61E-01	
MRPL1	0,22	5,58E-01	7,24E-01	0,16	7,79E-01	8,88E-01	
DPF2	0,22	5,41E-01	7,13E-01	0,33	2,75E-01	5,27E-01	
MRPS2	0,22	4,67E-01	6,63E-01	-0,49	6,49E-02	2,57E-01	
HNRNPF	0,22	4,17E-01	6,22E-01	0,09	6,93E-01	8,25E-01	
ATP5C1	0,22	4,43E-01	6,48E-01	0,05	8,23E-01	9,03E-01	
HNRNPC	0,22	4,95E-01	6,85E-01	-0,18	5,37E-01	7,29E-01	
GNL2	0,21	4,83E-01	6,73E-01	-0,22	3,33E-01	5,73E-01	
MRPS14	0,21	4,62E-01	6,59E-01	0,27	2,44E-01	4,91E-01	
TAOK2	0,21	5,59E-01	7,24E-01	0,00	1,00E+00	1,00E+00	
MRPS12	0,21	5,67E-01	7,25E-01	-0,61	8,69E-02	2,96E-01	
PLCD3	0,21	4,52E-01	6,54E-01	0,40	1,03E-01	3,16E-01	
MRPL30	0,21	4,76E-01	6,69E-01	-0,13	6,68E-01	8,05E-01	
FN1	0,20	6,34E-01	7,78E-01	0,73	1,19E-01	3,39E-01	
BLM	0,20	4,86E-01	6,75E-01	0,79	1,58E-02	1,37E-01	
SRSF10	0,20	6,98E-01	8,25E-01	0,00	1,00E+00	1,00E+00	
RPL30	0,20	4,98E-01	6,85E-01	-0,09	8,80E-01	9,31E-01	
SMARCA1	0,20	4,52E-01	6,54E-01	0,56	1,17E-01	3,38E-01	
FNDC3B	0,20	6,63E-01	8,02E-01	1,94	4,33E-04	4,94E-02	
RPL23	0,20	5,52E-01	7,22E-01	0,35	2,33E-01	4,82E-01	
ACIN1	0,19	5,92E-01	7,46E-01	0,24	4,32E-01	6,55E-01	
EIF2B4	0,19	5,31E-01	7,11E-01	0,63	1,02E-01	3,16E-01	
SF3B3	0,19	5,60E-01	7,24E-01	0,40	1,69E-01	4,04E-01	
MED19	0,19	6,20E-01	7,69E-01	0,18	6,27E-01	7,82E-01	
FBXW7	0,19	5,11E-01	6,93E-01	0,00	1,00E+00	1,00E+00	
UBR5	0,19	6,09E-01	7,59E-01	0,36	2,97E-01	5,49E-01	
HNRNPUL2; HNRNPUL2-BSCL2	0,19	5,08E-01	6,93E-01	0,41	1,66E-01	4,01E-01	
RBMX2	0,19	5,62E-01	7,24E-01	-0,15	5,53E-01	7,31E-01	
RBM12B	0,19	6,06E-01	7,58E-01	0,00	1,00E+00	1,00E+00	
DPY30	0,19	5,90E-01	7,46E-01	0,17	5,56E-01	7,32E-01	
NUP93	0,18	6,03E-01	7,57E-01	0,00	1,00E+00	1,00E+00	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
NAT10	0,18	5,10E-01	6,93E-01	-0,23	3,19E-01	5,61E-01	
SPHK2	0,18	6,16E-01	7,65E-01	0,01	9,69E-01	9,81E-01	
U2AF1	0,18	5,70E-01	7,26E-01	0,92	9,34E-03	1,08E-01	
DDX50	0,18	5,32E-01	7,11E-01	0,13	5,77E-01	7,49E-01	
LMNB2	0,18	7,74E-01	8,86E-01	-0,28	5,07E-01	7,18E-01	
NOL7	0,18	5,37E-01	7,12E-01	-0,03	8,83E-01	9,33E-01	
DDX23	0,17	6,32E-01	7,78E-01	0,48	9,78E-02	3,10E-01	
SP3	0,17	5,61E-01	7,24E-01	0,74	1,36E-02	1,27E-01	
H2AFY	0,17	5,27E-01	7,06E-01	-0,08	7,15E-01	8,43E-01	
HNRNPUL1	0,17	6,45E-01	7,87E-01	0,07	8,00E-01	8,93E-01	
COPG1	0,17	6,39E-01	7,82E-01	0,27	5,09E-01	7,19E-01	
CENPV	0,16	5,48E-01	7,18E-01	-0,53	1,08E-01	3,27E-01	
MTPAP	0,16	5,57E-01	7,24E-01	0,00	9,87E-01	9,92E-01	
RNMTL1	0,16	5,62E-01	7,24E-01	-0,11	7,32E-01	8,54E-01	
MRPS23	0,16	5,90E-01	7,46E-01	-0,71	3,16E-02	1,84E-01	
RPL11	0,16	5,64E-01	7,25E-01	0,37	1,33E-01	3,58E-01	
ZNF646	0,16	5,93E-01	7,47E-01	0,19	4,12E-01	6,38E-01	
H2AFY2	0,16	5,67E-01	7,25E-01	0,40	1,06E-01	3,21E-01	
PDIA5	0,15	6,78E-01	8,11E-01	0,14	7,12E-01	8,41E-01	
NIFK	0,15	5,86E-01	7,42E-01	-0,34	1,72E-01	4,07E-01	
UHRF1	0,15	5,85E-01	7,42E-01	-0,30	4,60E-01	6,78E-01	
ARHGEF2	0,15	6,71E-01	8,06E-01	0,50	1,86E-01	4,27E-01	
PELP1	0,14	7,82E-01	8,86E-01	0,19	6,15E-01	7,71E-01	
SRFBP1	0,14	7,82E-01	8,86E-01	-0,05	8,65E-01	9,26E-01	
IQGAP3	0,14	7,81E-01	8,86E-01	0,71	3,39E-01	5,77E-01	
PRPF19	0,14	6,07E-01	7,58E-01	0,05	8,05E-01	8,95E-01	
DHRS2	0,14	6,13E-01	7,63E-01	-0,55	3,95E-02	2,00E-01	
DHX37	0,13	6,37E-01	7,81E-01	-0,15	5,00E-01	7,11E-01	
MAGOHB; MAGOH	0,13	7,11E-01	8,36E-01	-0,39	2,25E-01	4,70E-01	
U2AF2	0,13	7,37E-01	8,57E-01	1,17	1,66E-02	1,37E-01	
REXO4	0,13	6,89E-01	8,17E-01	-0,06	7,92E-01	8,93E-01	
MRPS9	0,13	6,41E-01	7,83E-01	-0,34	1,80E-01	4,22E-01	
ILF3	0,12	8,10E-01	9,03E-01	-0,31	4,57E-01	6,75E-01	
TRA2B	0,12	6,50E-01	7,92E-01	0,20	3,52E-01	5,92E-01	
GNL3L	0,12	6,55E-01	7,97E-01	-0,12	5,98E-01	7,60E-01	
ATF1	0,12	7,80E-01	8,86E-01	-0,12	7,03E-01	8,33E-01	
ERAL1	0,12	6,83E-01	8,14E-01	0,06	8,18E-01	9,02E-01	
ZFX;ZFY	0,12	6,64E-01	8,02E-01	0,41	2,47E-01	4,94E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PLEC	0,12	6,79E-01	8,11E-01	0,34	1,66E-01	4,01E-01	
CYR61	0,11	7,55E-01	8,71E-01	0,18	6,46E-01	7,97E-01	
PES1	0,11	6,79E-01	8,11E-01	-0,07	7,60E-01	8,76E-01	
ATP5O	0,11	6,71E-01	8,06E-01	0,11	6,11E-01	7,70E-01	
IK	0,11	7,54E-01	8,70E-01	-0,21	3,86E-01	6,17E-01	
SF3B1	0,11	7,22E-01	8,47E-01	0,33	2,49E-01	4,95E-01	
MAP7D1	0,10	7,07E-01	8,34E-01	0,64	2,87E-02	1,79E-01	
SDF2L1	0,10	7,92E-01	8,93E-01	0,84	7,55E-02	2,78E-01	
TFB1M	0,10	7,11E-01	8,36E-01	-0,04	8,55E-01	9,22E-01	
GPATCH4	0,10	7,98E-01	8,94E-01	-0,27	3,72E-01	6,08E-01	
TOP1	0,10	7,23E-01	8,48E-01	-0,15	5,59E-01	7,35E-01	
TRMT10C	0,10	7,71E-01	8,84E-01	-0,73	5,96E-02	2,49E-01	
RPS3	0,10	7,34E-01	8,57E-01	0,06	7,65E-01	8,78E-01	
TUBA4A	0,09	9,16E-01	9,67E-01	0,47	6,45E-01	7,97E-01	
RPL34	0,09	7,27E-01	8,51E-01	0,02	9,32E-01	9,58E-01	
SRRT	0,09	7,97E-01	8,94E-01	-0,09	7,66E-01	8,78E-01	
SURF6	0,09	8,30E-01	9,16E-01	-0,48	8,52E-02	2,93E-01	
LRRC59	0,09	7,96E-01	8,94E-01	-0,02	9,49E-01	9,70E-01	
HIST1H2AJ; HIST1H2AH; H2AFJ; HIST2H2AC; HIST2H2AA3; HIST1H2AD; HIST1H2AG; HIST1H2AC; HIST3H2A; HIST1H2AB	0,08	8,21E-01	9,08E-01	-0,30	3,10E-01	5,56E-01	
TRIP12	0,08	7,71E-01	8,84E-01	0,23	4,10E-01	6,37E-01	
PPP1CB	0,08	7,83E-01	8,86E-01	0,16	5,13E-01	7,21E-01	
DDX55	0,08	7,86E-01	8,88E-01	-0,34	1,81E-01	4,22E-01	
C11orf31;SELH	0,08	8,13E-01	9,03E-01	-0,19	5,45E-01	7,29E-01	
NSUN2	0,08	8,36E-01	9,18E-01	0,42	2,01E-01	4,46E-01	
CPSF6	0,08	7,81E-01	8,86E-01	0,87	1,62E-02	1,37E-01	
MICU2	0,08	7,82E-01	8,86E-01	0,68	2,04E-02	1,49E-01	
SF1	0,07	8,76E-01	9,42E-01	0,79	2,65E-01	5,13E-01	
SLC3A2	0,07	8,32E-01	9,16E-01	-0,18	5,91E-01	7,57E-01	
GTF3C3	0,07	8,24E-01	9,11E-01	0,19	5,53E-01	7,31E-01	
MRPS11	0,06	8,13E-01	9,03E-01	0,07	7,83E-01	8,92E-01	
NKX2-5;NKX2-4; NKX2-1	0,06	8,63E-01	9,35E-01	0,00	1,00E+00	1,00E+00	
SNIP1	0,06	8,40E-01	9,21E-01	0,33	1,88E-01	4,28E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
TAOK1	0,05	8,79E-01	9,44E-01	0,31	3,67E-01	6,04E-01	
CCDC59	0,05	8,49E-01	9,23E-01	-0,27	2,41E-01	4,89E-01	
NOG	0,05	8,80E-01	9,44E-01	0,85	4,22E-02	2,06E-01	
PNN	0,05	8,42E-01	9,22E-01	-0,30	2,42E-01	4,89E-01	
VEZF1	0,05	8,47E-01	9,23E-01	0,45	8,04E-02	2,87E-01	
MINA	0,05	8,53E-01	9,25E-01	0,10	6,47E-01	7,97E-01	
USP42	0,04	8,97E-01	9,54E-01	-0,15	5,29E-01	7,26E-01	
MRPL9	0,04	8,70E-01	9,38E-01	0,09	6,71E-01	8,06E-01	
UBN1	0,04	8,82E-01	9,45E-01	0,00	1,00E+00	1,00E+00	
RBMX	0,04	9,31E-01	9,79E-01	-0,60	6,30E-02	2,56E-01	
CLTC	0,04	9,33E-01	9,79E-01	0,91	9,29E-02	3,01E-01	
DDX41	0,04	8,97E-01	9,54E-01	0,03	9,09E-01	9,49E-01	
MEPCE	0,04	8,91E-01	9,51E-01	0,20	3,56E-01	5,95E-01	
SNW1	0,03	9,33E-01	9,79E-01	0,17	5,48E-01	7,29E-01	
METTL17	0,03	9,22E-01	9,73E-01	-0,29	2,18E-01	4,64E-01	
RBM26	0,03	9,40E-01	9,84E-01	0,41	1,78E-01	4,17E-01	
PYCR1	0,02	9,57E-01	9,89E-01	0,00	1,00E+00	1,00E+00	
CYC1	0,02	9,50E-01	9,89E-01	-0,03	9,14E-01	9,51E-01	
RPSA	0,02	9,51E-01	9,89E-01	0,26	3,12E-01	5,57E-01	
MRPL15	0,02	9,52E-01	9,89E-01	-0,13	5,54E-01	7,31E-01	
PTRH2	0,02	9,63E-01	9,91E-01	0,00	1,00E+00	1,00E+00	
ZNF740	0,02	9,56E-01	9,89E-01	0,14	5,82E-01	7,50E-01	
RNPS1	0,02	9,53E-01	9,89E-01	-0,47	2,16E-01	4,61E-01	
FYTTD1	0,01	9,64E-01	9,91E-01	-0,09	7,85E-01	8,92E-01	
EPB41L2	0,01	9,57E-01	9,89E-01	0,95	1,34E-02	1,27E-01	
SRP68	0,01	9,64E-01	9,91E-01	0,06	8,21E-01	9,03E-01	
PRPF4B	0,01	9,74E-01	9,93E-01	0,06	8,18E-01	9,02E-01	
ZNF444	0,01	9,71E-01	9,92E-01	-0,75	2,37E-02	1,57E-01	
KLF5	0,01	9,77E-01	9,95E-01	0,00	1,00E+00	1,00E+00	
SRSF6	0,01	9,86E-01	9,95E-01	-0,83	8,55E-03	1,08E-01	
SND1	0,01	9,86E-01	9,95E-01	0,17	5,92E-01	7,57E-01	
MRPL47	0,01	9,85E-01	9,95E-01	0,06	8,04E-01	8,95E-01	
DDX17	0,01	9,84E-01	9,95E-01	0,10	6,54E-01	8,00E-01	
IFI16	0,00	9,95E-01	9,99E-01	0,00	1,00E+00	1,00E+00	
MRPS7	0,00	9,97E-01	9,99E-01	-0,05	8,50E-01	9,22E-01	
RSBN1	0,00	9,99E-01	9,99E-01	0,51	6,76E-02	2,60E-01	
RPS18	0,00	9,99E-01	9,99E-01	-0,12	5,81E-01	7,50E-01	
TSR3	0,00	9,97E-01	9,99E-01	-0,04	8,46E-01	9,19E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
RPL31	0,00	9,95E-01	9,99E-01	0,06	7,91E-01	8,93E-01	
RPS10;RPS10-NUDT3	0,00	9,93E-01	9,99E-01	0,16	4,79E-01	6,94E-01	
EIF4A3	0,00	9,94E-01	9,99E-01	-0,18	5,36E-01	7,29E-01	
SFSWAP	0,00	9,91E-01	9,99E-01	-0,15	6,61E-01	8,01E-01	
IQGAP1	-0,01	9,85E-01	9,95E-01	0,62	4,95E-02	2,23E-01	
RPL8	-0,01	9,82E-01	9,95E-01	0,14	5,28E-01	7,26E-01	
POGZ	-0,01	9,86E-01	9,95E-01	0,17	6,22E-01	7,79E-01	
RRP12	-0,01	9,83E-01	9,95E-01	-0,35	2,12E-01	4,58E-01	
ZNF524	-0,01	9,80E-01	9,95E-01	-0,56	1,17E-01	3,38E-01	
RPUSD3	-0,01	9,72E-01	9,92E-01	-0,03	9,20E-01	9,52E-01	
SMOC1	-0,01	9,68E-01	9,92E-01	0,16	6,82E-01	8,16E-01	
MRPL22	-0,01	9,56E-01	9,89E-01	-0,25	2,88E-01	5,45E-01	
KPNA3	-0,01	9,68E-01	9,92E-01	0,26	3,98E-01	6,29E-01	
ZNF593	-0,01	9,62E-01	9,91E-01	-0,16	4,65E-01	6,81E-01	
RBM8A	-0,02	9,60E-01	9,91E-01	-0,75	6,59E-02	2,58E-01	
ZNF532	-0,02	9,51E-01	9,89E-01	0,59	9,10E-02	2,99E-01	
TMEM33	-0,02	9,70E-01	9,92E-01	1,24	5,05E-02	2,25E-01	
EIF3G	-0,02	9,55E-01	9,89E-01	0,17	4,92E-01	7,04E-01	
FAR1	-0,02	9,70E-01	9,92E-01	0,00	1,00E+00	1,00E+00	
SNRNP70	-0,02	9,47E-01	9,89E-01	0,07	7,99E-01	8,93E-01	
RECQL4	-0,02	9,51E-01	9,89E-01	0,29	2,62E-01	5,10E-01	
ZFP64	-0,03	9,35E-01	9,80E-01	-0,03	9,02E-01	9,45E-01	
LSG1	-0,03	9,47E-01	9,89E-01	0,03	9,61E-01	9,79E-01	
SKIV2L2	-0,03	9,26E-01	9,76E-01	0,23	3,24E-01	5,66E-01	
RPL28	-0,03	8,96E-01	9,54E-01	0,19	4,00E-01	6,29E-01	
RPS27A	-0,03	9,02E-01	9,58E-01	-0,88	1,52E-01	3,78E-01	
CCAR2	-0,03	9,24E-01	9,74E-01	0,09	7,69E-01	8,78E-01	
MRPS31	-0,03	9,34E-01	9,79E-01	0,00	1,00E+00	1,00E+00	
SNRPD2	-0,04	9,14E-01	9,67E-01	-0,33	3,79E-01	6,10E-01	
TIMM44	-0,04	9,15E-01	9,67E-01	-0,46	1,63E-01	3,98E-01	
MRPL50	-0,04	8,85E-01	9,47E-01	-0,65	3,43E-02	1,91E-01	
EIF3C; EIF3CL	-0,04	8,89E-01	9,49E-01	0,04	8,40E-01	9,16E-01	
NUDC	-0,05	8,98E-01	9,54E-01	0,19	5,16E-01	7,21E-01	
PTRF	-0,05	8,66E-01	9,36E-01	0,71	2,03E-02	1,49E-01	
MRPL40	-0,05	8,87E-01	9,49E-01	-0,62	9,35E-02	3,02E-01	
MRPS28	-0,06	8,53E-01	9,25E-01	-0,71	2,43E-02	1,59E-01	
PRPF3	-0,06	8,31E-01	9,16E-01	-0,04	8,41E-01	9,16E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
ILF2	-0,06	8,48E-01	9,23E-01	-0,41	2,27E-01	4,73E-01	
LGALS3BP	-0,06	8,52E-01	9,25E-01	0,24	4,24E-01	6,51E-01	
GTF2B	-0,06	8,68E-01	9,37E-01	0,47	9,99E-02	3,14E-01	
IMMT	-0,06	8,72E-01	9,39E-01	0,00	1,00E+00	1,00E+00	
SF3B2	-0,06	8,40E-01	9,21E-01	-0,19	4,07E-01	6,35E-01	
RNMT	-0,07	8,07E-01	9,01E-01	-0,03	9,19E-01	9,52E-01	
SP110	-0,07	8,11E-01	9,03E-01	-0,15	4,94E-01	7,05E-01	
DDX46	-0,07	9,06E-01	9,61E-01	0,28	7,05E-01	8,35E-01	
DYNLL1;DYNLL2	-0,07	8,13E-01	9,03E-01	-0,53	4,13E-01	6,40E-01	
KDM2A	-0,08	8,70E-01	9,38E-01	-0,10	8,67E-01	9,26E-01	
KNOP1	-0,08	7,98E-01	8,94E-01	-0,15	5,23E-01	7,23E-01	
NOC3L	-0,08	7,95E-01	8,94E-01	-1,02	1,44E-02	1,29E-01	
SP140	-0,08	7,83E-01	8,86E-01	-0,72	1,61E-02	1,37E-01	
RPS6	-0,08	7,71E-01	8,84E-01	-0,15	5,99E-01	7,61E-01	
CBX6	-0,08	8,04E-01	8,98E-01	0,65	3,58E-02	1,92E-01	
PPP1CC	-0,08	8,16E-01	9,04E-01	-0,24	4,54E-01	6,74E-01	
C5orf30	-0,08	8,66E-01	9,36E-01	0,00	1,00E+00	1,00E+00	
SIRT7	-0,09	7,99E-01	8,94E-01	0,45	9,82E-02	3,10E-01	
FXR1	-0,09	7,32E-01	8,55E-01	0,10	6,39E-01	7,93E-01	
RPS28	-0,09	8,14E-01	9,03E-01	0,00	9,94E-01	9,95E-01	
UTP11L	-0,09	7,36E-01	8,57E-01	-0,18	4,11E-01	6,37E-01	
CDC42	-0,09	8,45E-01	9,23E-01	0,80	8,41E-02	2,91E-01	
RPS20	-0,09	7,85E-01	8,88E-01	0,15	5,47E-01	7,29E-01	
RPL10	-0,09	7,65E-01	8,81E-01	0,00	1,00E+00	1,00E+00	
CT45A3;CT45A1; CT45A7;CT45A5; CT45A6	-0,10	8,33E-01	9,16E-01	-0,36	4,51E-01	6,74E-01	
HNRNPL	-0,10	7,48E-01	8,64E-01	-0,02	9,59E-01	9,78E-01	
RPL22	-0,10	7,37E-01	8,57E-01	0,07	8,05E-01	8,95E-01	
EXOSC3	-0,10	7,81E-01	8,86E-01	0,00	1,00E+00	1,00E+00	
FHL2	-0,10	7,07E-01	8,34E-01	0,39	2,90E-01	5,45E-01	
PTRH1	-0,10	7,69E-01	8,84E-01	-0,03	9,02E-01	9,45E-01	
RPL21	-0,11	6,88E-01	8,17E-01	-0,03	9,10E-01	9,49E-01	
NOA1	-0,11	8,47E-01	9,23E-01	0,00	1,00E+00	1,00E+00	
CCT8	-0,11	8,31E-01	9,16E-01	0,67	2,78E-01	5,30E-01	
RPS21	-0,12	7,95E-01	8,94E-01	-0,73	1,47E-01	3,72E-01	
PLAGL2	-0,12	7,45E-01	8,64E-01	0,31	4,94E-01	7,05E-01	
TCEB2	-0,13	7,46E-01	8,64E-01	0,00	1,00E+00	1,00E+00	
DDX56	-0,13	6,28E-01	7,76E-01	-0,22	3,35E-01	5,74E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PHB2	-0,13	6,96E-01	8,24E-01	-0,10	7,54E-01	8,71E-01	
SKP1	-0,13	6,34E-01	7,78E-01	-0,12	6,06E-01	7,67E-01	
SF3B5	-0,13	7,21E-01	8,47E-01	0,40	3,58E-01	5,95E-01	
SNRPE	-0,13	6,29E-01	7,76E-01	-0,17	4,41E-01	6,62E-01	
PHF20L1	-0,13	6,52E-01	7,94E-01	0,08	7,40E-01	8,60E-01	
FBXL6	-0,13	7,26E-01	8,51E-01	0,36	3,06E-01	5,54E-01	
DNTTIP1	-0,13	6,84E-01	8,14E-01	0,13	7,23E-01	8,47E-01	
RPS8	-0,14	6,16E-01	7,65E-01	0,24	3,60E-01	5,95E-01	
SRSF7	-0,14	6,66E-01	8,04E-01	-0,29	2,20E-01	4,66E-01	
RBM27	-0,14	6,68E-01	8,04E-01	0,56	6,02E-02	2,50E-01	
HSPA9	-0,14	6,07E-01	7,58E-01	-0,33	1,83E-01	4,26E-01	
CUL2	-0,15	7,80E-01	8,86E-01	-0,11	8,03E-01	8,95E-01	
EIF2B1	-0,15	5,69E-01	7,26E-01	0,33	1,70E-01	4,04E-01	
SNRPA1	-0,15	6,26E-01	7,75E-01	0,02	9,32E-01	9,58E-01	
RSRC1	-0,16	6,59E-01	7,98E-01	-0,09	6,68E-01	8,05E-01	
G3BP2	-0,16	6,57E-01	7,97E-01	-0,29	3,51E-01	5,92E-01	
C8orf33	-0,16	5,40E-01	7,13E-01	-0,05	8,70E-01	9,27E-01	
MAFG	-0,16	6,85E-01	8,15E-01	-0,27	3,51E-01	5,92E-01	
NSUN4	-0,16	5,68E-01	7,25E-01	-0,15	5,80E-01	7,50E-01	
KPNB1	-0,17	7,47E-01	8,64E-01	0,19	6,43E-01	7,96E-01	
SP140L	-0,17	6,39E-01	7,82E-01	0,00	1,00E+00	1,00E+00	
INO80B; INO80B-WBP1	-0,17	5,38E-01	7,12E-01	0,05	8,34E-01	9,13E-01	
RSBN1L	-0,18	5,08E-01	6,93E-01	0,30	2,09E-01	4,56E-01	
RPL9	-0,18	6,05E-01	7,58E-01	0,26	2,78E-01	5,30E-01	
PRPF4	-0,18	5,15E-01	6,97E-01	-0,10	6,61E-01	8,01E-01	
RPL27A	-0,18	5,26E-01	7,06E-01	-0,24	3,56E-01	5,95E-01	
RRP1B	-0,18	5,35E-01	7,12E-01	-0,80	1,84E-02	1,44E-01	
MTHFD2	-0,19	4,98E-01	6,85E-01	-0,30	2,89E-01	5,45E-01	
DDX54	-0,19	5,03E-01	6,89E-01	0,46	8,77E-02	2,96E-01	
PHF6	-0,19	4,96E-01	6,85E-01	0,25	3,25E-01	5,66E-01	
PSMA2	-0,19	7,45E-01	8,64E-01	-0,02	9,63E-01	9,80E-01	
CXorf67	-0,19	4,92E-01	6,82E-01	0,13	5,50E-01	7,29E-01	
SCAF4	-0,19	5,04E-01	6,89E-01	0,98	5,98E-03	9,65E-02	
MRPS15	-0,20	5,39E-01	7,12E-01	-0,12	6,43E-01	7,96E-01	
RCC1	-0,20	4,57E-01	6,55E-01	-0,32	3,32E-01	5,73E-01	
ZNF652	-0,20	4,84E-01	6,74E-01	-0,03	9,42E-01	9,65E-01	
RPS4X	-0,20	4,81E-01	6,72E-01	0,05	7,97E-01	8,93E-01	
ATP1A1	-0,21	6,94E-01	8,22E-01	0,00	1,00E+00	1,00E+00	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BRD7	-0,21	5,16E-01	6,98E-01	-0,23	3,11E-01	5,57E-01	
MRPL14	-0,21	5,56E-01	7,24E-01	-0,38	2,33E-01	4,82E-01	
TAF3	-0,21	6,57E-01	7,97E-01	-0,09	7,90E-01	8,93E-01	
SRP72	-0,22	4,18E-01	6,22E-01	-0,04	8,67E-01	9,26E-01	
EIF3A	-0,22	5,48E-01	7,18E-01	0,44	2,16E-01	4,61E-01	
DDX3X;DDX3Y	-0,22	4,76E-01	6,69E-01	0,02	9,30E-01	9,58E-01	
FAM111B	-0,22	4,49E-01	6,54E-01	0,23	3,86E-01	6,17E-01	
RPS19BP1	-0,22	5,11E-01	6,93E-01	-0,15	5,43E-01	7,29E-01	
TMA16	-0,22	4,22E-01	6,25E-01	-0,23	5,10E-01	7,19E-01	
KIF2A	-0,22	4,37E-01	6,41E-01	0,72	1,68E-02	1,37E-01	
RPS3A	-0,22	4,52E-01	6,54E-01	-0,11	6,27E-01	7,82E-01	
RRP7A	-0,22	4,15E-01	6,20E-01	-0,22	3,36E-01	5,75E-01	
PUF60	-0,22	4,21E-01	6,25E-01	0,27	2,55E-01	5,00E-01	
CCT7	-0,22	6,74E-01	8,08E-01	0,10	7,41E-01	8,60E-01	
RPS15A	-0,22	5,59E-01	7,24E-01	-0,07	8,66E-01	9,26E-01	
EIF3E	-0,23	6,12E-01	7,63E-01	0,31	4,96E-01	7,07E-01	
GRN	-0,23	6,76E-01	8,10E-01	0,85	1,40E-01	3,63E-01	
DDX27	-0,23	5,45E-01	7,16E-01	-0,67	2,90E-02	1,80E-01	
PPP2CA	-0,23	5,75E-01	7,32E-01	0,71	7,67E-02	2,80E-01	
DDX18	-0,23	4,03E-01	6,09E-01	-0,23	3,17E-01	5,59E-01	
GLYR1	-0,23	4,03E-01	6,09E-01	-0,06	8,31E-01	9,11E-01	
SERBP1	-0,23	4,70E-01	6,65E-01	-0,04	8,79E-01	9,31E-01	
KLF10	-0,23	4,79E-01	6,69E-01	-0,16	5,91E-01	7,57E-01	
EPB41	-0,23	4,26E-01	6,28E-01	-0,18	4,53E-01	6,74E-01	
SNRPD1	-0,23	5,19E-01	7,00E-01	-0,48	1,50E-01	3,74E-01	
MRPL44	-0,23	5,55E-01	7,24E-01	0,00	1,00E+00	1,00E+00	
EIF3D	-0,24	5,65E-01	7,25E-01	0,07	8,38E-01	9,16E-01	
VIM	-0,24	3,69E-01	5,70E-01	-0,10	6,55E-01	8,00E-01	
DNAJB11	-0,24	4,28E-01	6,30E-01	0,03	8,88E-01	9,36E-01	
HSPH1	-0,24	5,27E-01	7,06E-01	-0,27	3,79E-01	6,10E-01	
SRSF11	-0,25	4,62E-01	6,59E-01	0,24	2,93E-01	5,45E-01	
HACD3	-0,25	5,38E-01	7,12E-01	-0,31	3,32E-01	5,73E-01	
SF3A3	-0,25	5,66E-01	7,25E-01	-0,06	8,83E-01	9,33E-01	
RPL19	-0,25	4,10E-01	6,17E-01	0,12	6,53E-01	8,00E-01	
TAF2	-0,25	3,87E-01	5,92E-01	-0,24	5,64E-01	7,38E-01	
FLNC	-0,26	4,55E-01	6,54E-01	0,38	1,56E-01	3,84E-01	
DNAJC9	-0,27	3,23E-01	5,31E-01	0,01	9,69E-01	9,81E-01	
RBM23	-0,27	4,65E-01	6,62E-01	0,35	1,93E-01	4,37E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
CCT4	-0,28	5,00E-01	6,87E-01	0,11	7,49E-01	8,66E-01	
CCT3	-0,28	5,98E-01	7,52E-01	0,30	3,76E-01	6,10E-01	
TCERG1	-0,28	4,43E-01	6,48E-01	0,00	1,00E+00	1,00E+00	
CACTIN	-0,28	4,05E-01	6,11E-01	-0,17	5,60E-01	7,35E-01	
UTP14A	-0,29	3,62E-01	5,64E-01	-0,53	9,12E-02	2,99E-01	
NMT1	-0,29	3,01E-01	5,08E-01	0,33	1,87E-01	4,28E-01	
NKAP	-0,30	4,55E-01	6,54E-01	-0,62	1,69E-01	4,04E-01	
RPL13	-0,30	2,86E-01	4,97E-01	-0,13	6,49E-01	7,97E-01	
HNRNPA3	-0,30	4,52E-01	6,54E-01	-0,57	6,37E-02	2,56E-01	
CCDC137	-0,30	4,48E-01	6,53E-01	-0,76	3,36E-02	1,89E-01	
SART1	-0,30	3,50E-01	5,56E-01	-0,14	5,13E-01	7,21E-01	
EPB41L5	-0,31	2,89E-01	4,98E-01	0,07	7,30E-01	8,52E-01	
ZCCHC17	-0,31	3,51E-01	5,56E-01	-0,20	3,79E-01	6,10E-01	
RPL23A	-0,31	2,73E-01	4,83E-01	-0,33	1,85E-01	4,27E-01	
BCAR3	-0,31	5,92E-01	7,46E-01	0,38	2,49E-01	4,95E-01	
C1QBP	-0,32	2,69E-01	4,82E-01	-1,31	6,38E-03	9,65E-02	
SREK1	-0,32	3,00E-01	5,07E-01	0,39	1,23E-01	3,43E-01	
CIR1	-0,32	2,87E-01	4,97E-01	-0,17	6,14E-01	7,71E-01	
HNRNPR	-0,33	4,75E-01	6,69E-01	-0,60	3,81E-02	1,99E-01	
TAF2	-0,33	2,65E-01	4,78E-01	0,00	9,93E-01	9,95E-01	
TGM2	-0,33	3,40E-01	5,46E-01	0,45	8,11E-02	2,88E-01	
LMNA	-0,33	3,24E-01	5,31E-01	-0,34	2,49E-01	4,95E-01	
NOLC1	-0,33	4,16E-01	6,20E-01	-0,84	3,57E-02	1,92E-01	
ERI1	-0,34	2,64E-01	4,78E-01	0,60	2,96E-02	1,80E-01	
SNRPG;SNRPGP15	-0,34	3,63E-01	5,64E-01	-0,43	1,93E-01	4,37E-01	
TUFM	-0,34	2,26E-01	4,42E-01	-0,19	4,42E-01	6,64E-01	
RPL37A	-0,34	2,67E-01	4,80E-01	-0,08	7,92E-01	8,93E-01	
PPIH	-0,34	3,56E-01	5,60E-01	-0,69	6,59E-02	2,58E-01	
XRN2	-0,34	4,33E-01	6,36E-01	-0,35	3,95E-01	6,26E-01	
ABCF1	-0,34	2,46E-01	4,58E-01	0,09	6,96E-01	8,28E-01	
RPL10	-0,34	3,76E-01	5,78E-01	0,11	6,85E-01	8,19E-01	
RPS24	-0,35	2,32E-01	4,44E-01	-0,26	3,93E-01	6,25E-01	
FIZ1	-0,35	2,41E-01	4,55E-01	0,25	2,95E-01	5,46E-01	
LARP4	-0,35	2,72E-01	4,82E-01	-0,17	4,92E-01	7,04E-01	
RPS2	-0,36	2,03E-01	4,21E-01	-0,18	4,30E-01	6,54E-01	
MYH9	-0,36	4,78E-01	6,69E-01	0,42	3,35E-01	5,74E-01	
LUC7L3	-0,36	3,47E-01	5,51E-01	0,22	4,71E-01	6,86E-01	
HP1BP3	-0,36	3,55E-01	5,60E-01	-0,04	8,54E-01	9,22E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
MAGED2	-0,36	2,13E-01	4,28E-01	0,83	1,01E-02	1,09E-01	
PCBP1	-0,36	2,66E-01	4,79E-01	-0,34	2,46E-01	4,93E-01	
PRPF40A	-0,37	2,54E-01	4,68E-01	-0,34	1,44E-01	3,67E-01	
WBSCR22	-0,37	3,62E-01	5,64E-01	-0,10	7,40E-01	8,60E-01	
FAM207A	-0,37	2,20E-01	4,36E-01	-0,15	5,35E-01	7,29E-01	
RRP36	-0,37	3,57E-01	5,60E-01	-0,27	3,28E-01	5,70E-01	
BYSL	-0,38	4,78E-01	6,69E-01	0,00	1,00E+00	1,00E+00	
MRPL41	-0,38	3,30E-01	5,36E-01	-0,32	2,43E-01	4,89E-01	
MORF4L1	-0,38	3,30E-01	5,36E-01	0,00	1,00E+00	1,00E+00	
CMAS	-0,38	2,14E-01	4,28E-01	0,38	1,33E-01	3,58E-01	
MMTAG2	-0,39	2,82E-01	4,94E-01	-0,35	3,47E-01	5,88E-01	
TFRC	-0,40	5,62E-01	7,24E-01	-1,56	1,10E-01	3,31E-01	
DGKZ	-0,40	2,83E-01	4,94E-01	-0,01	9,80E-01	9,88E-01	
ARG1	-0,40	3,98E-01	6,07E-01	-0,26	5,19E-01	7,23E-01	
RPL36	-0,40	2,93E-01	5,01E-01	-0,44	1,01E-01	3,15E-01	
LUC7L2	-0,40	1,55E-01	3,59E-01	0,26	3,73E-01	6,09E-01	
SRRM2	-0,41	1,54E-01	3,59E-01	-0,32	1,83E-01	4,25E-01	
G3BP1	-0,41	1,74E-01	3,83E-01	-0,15	5,48E-01	7,29E-01	
PCMT1	-0,41	1,72E-01	3,82E-01	-0,16	4,85E-01	6,98E-01	
CCT6A	-0,41	4,97E-01	6,85E-01	0,33	4,63E-01	6,81E-01	
EIF4G1	-0,41	2,70E-01	4,82E-01	-0,11	7,18E-01	8,44E-01	
METTL8	-0,41	2,09E-01	4,24E-01	-0,66	8,42E-02	2,91E-01	
THRAP3	-0,42	1,97E-01	4,15E-01	-0,19	3,74E-01	6,09E-01	
PPIG	-0,42	2,75E-01	4,84E-01	0,00	1,00E+00	1,00E+00	
RBBP6	-0,42	1,73E-01	3,83E-01	-0,39	1,35E-01	3,59E-01	
RPS9	-0,42	2,01E-01	4,18E-01	-0,19	4,80E-01	6,94E-01	
GTPBP10	-0,42	3,10E-01	5,20E-01	-0,45	1,85E-01	4,27E-01	
SSR4	-0,42	3,35E-01	5,40E-01	0,21	4,52E-01	6,74E-01	
MAFK	-0,42	2,31E-01	4,44E-01	-0,15	6,55E-01	8,00E-01	
S100A13	-0,43	1,81E-01	3,91E-01	0,47	1,14E-01	3,37E-01	
KHDRBS1	-0,43	1,36E-01	3,26E-01	-0,16	4,69E-01	6,85E-01	
NES	-0,43	1,90E-01	4,05E-01	-1,31	8,84E-03	1,08E-01	
RNF138	-0,43	2,58E-01	4,72E-01	0,82	1,84E-01	4,26E-01	
SRSF3	-0,43	1,85E-01	3,98E-01	-0,41	1,38E-01	3,60E-01	
CTSB	-0,43	1,75E-01	3,83E-01	0,54	1,17E-01	3,38E-01	
FASN	-0,43	5,35E-01	7,12E-01	-0,30	6,62E-01	8,01E-01	
RPS13	-0,43	1,33E-01	3,24E-01	-0,13	5,42E-01	7,29E-01	
NOL12	-0,43	2,48E-01	4,59E-01	-0,39	1,17E-01	3,38E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
C11orf98	-0,44	6,30E-01	7,76E-01	-0,27	6,09E-01	7,69E-01	
MAP1B	-0,44	2,59E-01	4,73E-01	0,36	2,38E-01	4,87E-01	
SRP14	-0,44	1,40E-01	3,33E-01	-0,09	7,67E-01	8,78E-01	
SREK1IP1	-0,44	4,94E-01	6,84E-01	-1,23	2,17E-01	4,63E-01	
MFAP1	-0,44	1,99E-01	4,16E-01	-0,33	2,81E-01	5,33E-01	
YTHDF2	-0,44	3,80E-01	5,83E-01	-0,25	4,59E-01	6,77E-01	
RPS14	-0,44	1,67E-01	3,77E-01	-0,25	3,09E-01	5,55E-01	
CCDC86	-0,45	2,58E-01	4,72E-01	-0,65	3,62E-02	1,93E-01	
GLTSCR2	-0,45	1,27E-01	3,21E-01	-0,65	3,29E-02	1,88E-01	
MRPL43	-0,45	2,84E-01	4,96E-01	-0,87	5,53E-02	2,37E-01	
NSD1	-0,45	3,05E-01	5,12E-01	0,55	3,72E-01	6,08E-01	
RPN1	-0,45	3,57E-01	5,60E-01	-0,30	4,71E-01	6,86E-01	
H1FX	-0,46	1,76E-01	3,85E-01	0,23	3,05E-01	5,54E-01	
PCBP2	-0,46	1,29E-01	3,23E-01	-0,05	8,21E-01	9,03E-01	
SRP9	-0,46	2,87E-01	4,97E-01	-0,23	6,71E-01	8,06E-01	
DEK	-0,46	3,60E-01	5,63E-01	0,13	6,92E-01	8,25E-01	
SDAD1	-0,46	1,81E-01	3,91E-01	-0,72	2,24E-02	1,55E-01	
RPS23	-0,47	1,24E-01	3,18E-01	0,00	9,98E-01	9,98E-01	
RPL26L1	-0,47	2,59E-01	4,73E-01	0,11	7,78E-01	8,87E-01	
RPS15	-0,47	1,14E-01	3,08E-01	-0,39	1,04E-01	3,18E-01	
SP2	-0,47	2,39E-01	4,52E-01	0,18	6,62E-01	8,01E-01	
NUMB	-0,47	2,43E-01	4,57E-01	0,12	6,91E-01	8,25E-01	
ATP5A1	-0,47	2,04E-01	4,21E-01	-0,50	1,37E-01	3,59E-01	
CTGF	-0,47	2,36E-01	4,48E-01	0,33	2,08E-01	4,56E-01	
S100A16	-0,47	1,07E-01	3,01E-01	0,41	1,18E-01	3,38E-01	
AP2B1	-0,47	1,43E-01	3,38E-01	-0,15	5,78E-01	7,49E-01	
LUC7L	-0,47	1,22E-01	3,16E-01	0,22	3,90E-01	6,21E-01	
RPS26; RPS26P11	-0,48	1,32E-01	3,24E-01	0,03	8,95E-01	9,42E-01	
EIF5B	-0,48	1,33E-01	3,24E-01	-0,46	1,00E-01	3,14E-01	
EEF1A1; EEF1A1P5	-0,48	1,37E-01	3,29E-01	0,28	2,35E-01	4,82E-01	
TFAM	-0,48	3,32E-01	5,38E-01	-0,99	6,04E-02	2,50E-01	
FRG1	-0,48	1,53E-01	3,58E-01	-0,16	5,43E-01	7,29E-01	
SRP19	-0,48	2,32E-01	4,44E-01	-0,33	3,59E-01	5,95E-01	
IGKV4-1	-0,48	2,79E-01	4,90E-01	0,22	5,29E-01	7,26E-01	
RPS17	-0,48	1,07E-01	3,01E-01	0,00	9,92E-01	9,95E-01	
C14orf166	-0,48	2,23E-01	4,38E-01	-0,01	9,68E-01	9,81E-01	
MICU1	-0,49	1,06E-01	3,00E-01	0,07	7,47E-01	8,66E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
PTMS	-0,49	1,99E-01	4,16E-01	-0,30	2,09E-01	4,56E-01	
SON	-0,50	1,33E-01	3,24E-01	-0,20	4,02E-01	6,31E-01	
MCM3	-0,50	2,09E-01	4,24E-01	0,39	2,21E-01	4,66E-01	
NF2	-0,51	8,93E-02	2,75E-01	0,55	5,89E-02	2,47E-01	
BCCIP	-0,52	2,05E-01	4,21E-01	0,00	1,00E+00	1,00E+00	
KLF16	-0,52	1,21E-01	3,16E-01	0,10	6,80E-01	8,14E-01	
RPL26	-0,53	9,44E-02	2,83E-01	-0,19	5,17E-01	7,22E-01	
HSPA5	-0,53	8,16E-02	2,62E-01	-0,22	3,41E-01	5,80E-01	
RPL17;RPL17-C18orf32	-0,53	1,64E-01	3,73E-01	-0,22	4,07E-01	6,35E-01	
RPS29	-0,54	1,29E-01	3,23E-01	0,39	3,99E-01	6,29E-01	
BCLAF1	-0,54	1,31E-01	3,23E-01	-0,19	4,39E-01	6,61E-01	
MAGEA4	-0,55	1,10E-01	3,03E-01	-0,15	5,38E-01	7,29E-01	
SRRM1	-0,55	7,73E-02	2,54E-01	-0,15	5,36E-01	7,29E-01	
ZNF451	-0,55	8,92E-02	2,75E-01	0,28	2,40E-01	4,89E-01	
CT45A10	-0,56	2,20E-01	4,36E-01	-1,29	1,50E-01	3,74E-01	
MEN1	-0,56	1,80E-01	3,91E-01	0,00	1,00E+00	1,00E+00	
RBM25	-0,56	7,91E-02	2,57E-01	-0,48	7,30E-02	2,73E-01	
PTBP1	-0,56	2,30E-01	4,44E-01	-0,19	6,61E-01	8,01E-01	
CDK5RAP1	-0,57	2,21E-01	4,37E-01	0,00	1,00E+00	1,00E+00	
ZFP91;ZFP91-CNTF	-0,57	7,97E-02	2,57E-01	-0,18	5,33E-01	7,28E-01	
GPR125	-0,57	6,52E-02	2,34E-01	-0,33	1,67E-01	4,02E-01	
SCAF8	-0,57	6,53E-02	2,34E-01	0,39	1,94E-01	4,38E-01	
MAFF	-0,57	3,12E-01	5,21E-01	-0,29	4,86E-01	6,98E-01	
RBM39	-0,58	7,11E-02	2,46E-01	-0,39	1,24E-01	3,44E-01	
ACTB	-0,58	1,34E-01	3,24E-01	-0,37	2,43E-01	4,89E-01	
RTCB	-0,58	1,53E-01	3,58E-01	0,08	8,57E-01	9,24E-01	
POLR1A	-0,58	3,65E-01	5,67E-01	0,00	1,00E+00	1,00E+00	
PXDN	-0,59	1,56E-01	3,59E-01	1,43	3,02E-02	1,82E-01	
TRMT112	-0,59	5,72E-02	2,17E-01	-0,30	1,89E-01	4,31E-01	
CWC25	-0,59	9,69E-02	2,87E-01	-0,44	9,55E-02	3,07E-01	
SRSF1	-0,59	2,15E-01	4,29E-01	-1,62	8,09E-03	1,08E-01	
WBP11	-0,59	1,31E-01	3,23E-01	-0,07	7,66E-01	8,78E-01	
SFPQ	-0,60	5,44E-02	2,10E-01	-0,47	7,59E-02	2,78E-01	
CXorf56	-0,61	7,00E-02	2,44E-01	-0,16	4,64E-01	6,81E-01	
C1QA	-0,61	7,22E-02	2,48E-01	-0,21	5,25E-01	7,23E-01	
CCT2	-0,61	2,16E-01	4,29E-01	0,12	6,38E-01	7,93E-01	
RPS7	-0,62	6,28E-02	2,30E-01	0,06	7,99E-01	8,93E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
TRIM21	-0,62	1,88E-01	4,01E-01	0,45	1,95E-01	4,38E-01	
TRIM28	-0,62	1,22E-01	3,16E-01	-0,05	8,66E-01	9,26E-01	
U2SURP	-0,63	4,70E-02	1,95E-01	-0,05	8,06E-01	8,95E-01	
RPS25	-0,64	1,67E-01	3,77E-01	-0,41	1,61E-01	3,95E-01	
NAP1L1	-0,64	1,02E-01	2,97E-01	0,07	8,10E-01	8,97E-01	
TAF8	-0,64	8,49E-02	2,67E-01	-0,41	1,42E-01	3,66E-01	
C11orf57	-0,64	1,94E-01	4,11E-01	-1,03	2,87E-02	1,79E-01	
PLEKHO1	-0,64	4,95E-02	1,98E-01	-0,29	2,15E-01	4,61E-01	
DDX39B	-0,65	2,12E-01	4,28E-01	-0,76	1,77E-01	4,15E-01	
CCDC84	-0,65	1,26E-01	3,21E-01	-0,26	3,08E-01	5,55E-01	
RAN	-0,65	3,34E-01	5,38E-01	-0,65	1,69E-01	4,04E-01	
RP9	-0,66	4,03E-02	1,83E-01	-0,64	3,23E-02	1,86E-01	
RPL35	-0,66	4,13E-02	1,85E-01	-0,55	4,79E-02	2,21E-01	
EEF2	-0,66	1,51E-01	3,56E-01	-0,47	2,21E-01	4,66E-01	
ZNF207	-0,67	1,10E-01	3,03E-01	-0,26	3,01E-01	5,51E-01	
ARGLU1	-0,67	5,66E-02	2,16E-01	-0,37	1,24E-01	3,44E-01	
ERH	-0,67	2,45E-01	4,57E-01	0,03	9,37E-01	9,60E-01	
ELAVL1	-0,67	4,41E-02	1,93E-01	-1,19	1,22E-02	1,20E-01	
PRDX5	-0,67	1,14E-01	3,08E-01	-0,08	8,11E-01	8,97E-01	
RCC2	-0,68	1,14E-01	3,08E-01	0,51	5,63E-02	2,39E-01	
YWHAQ	-0,68	1,07E-01	3,01E-01	-0,79	7,02E-02	2,66E-01	
HSPD1	-0,68	6,26E-02	2,30E-01	-0,81	5,56E-02	2,37E-01	
EIF2S2	-0,68	1,04E-01	2,99E-01	-0,45	1,91E-01	4,34E-01	
ZNF579	-0,68	3,60E-02	1,69E-01	0,02	9,16E-01	9,51E-01	
SMNDC1	-0,68	7,35E-02	2,50E-01	-0,17	5,69E-01	7,42E-01	
HNRNPA0	-0,69	1,25E-01	3,21E-01	-0,76	4,19E-02	2,06E-01	
DLST	-0,69	4,17E-02	1,85E-01	-0,54	8,61E-02	2,95E-01	
CHERP	-0,70	4,16E-02	1,85E-01	-0,87	5,79E-02	2,44E-01	
CAPZB	-0,70	9,44E-02	2,83E-01	-0,58	1,23E-01	3,43E-01	
FLNA	-0,70	4,82E-02	1,96E-01	0,31	2,51E-01	4,97E-01	
RPL38	-0,71	3,18E-02	1,56E-01	-0,51	6,11E-02	2,50E-01	
RPL29	-0,71	1,10E-01	3,03E-01	-0,70	2,35E-02	1,57E-01	
LSM14B	-0,72	3,33E-02	1,59E-01	0,30	2,19E-01	4,66E-01	
EEF1G	-0,72	1,57E-01	3,60E-01	-0,46	1,96E-01	4,39E-01	
RPL36AL	-0,72	2,99E-02	1,55E-01	-0,13	6,33E-01	7,87E-01	
TSPYL5	-0,73	2,84E-02	1,52E-01	-0,16	5,24E-01	7,23E-01	
RCN2	-0,74	2,71E-02	1,52E-01	-0,29	3,35E-01	5,74E-01	
ASF1A	-0,74	3,79E-02	1,76E-01	-0,09	7,21E-01	8,47E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
HNRNPK	-0,74	4,45E-02	1,93E-01	-0,42	2,10E-01	4,57E-01	
HSP90AB1	-0,75	7,31E-02	2,50E-01	-0,58	1,20E-01	3,39E-01	
FAU	-0,76	5,33E-02	2,08E-01	-0,55	4,48E-02	2,11E-01	
EIF3L	-0,77	1,05E-01	3,00E-01	-0,79	1,04E-01	3,17E-01	
HMGXB4	-0,78	2,50E-02	1,49E-01	-0,15	4,76E-01	6,92E-01	
NUDT21	-0,78	7,91E-02	2,57E-01	0,75	1,61E-02	1,37E-01	
POLDIP3	-0,78	3,04E-02	1,56E-01	-0,55	1,66E-01	4,01E-01	
PELO	-0,78	7,76E-02	2,54E-01	0,27	4,25E-01	6,51E-01	
ACTN1	-0,79	2,57E-01	4,72E-01	-0,12	8,53E-01	9,22E-01	
PQBP1	-0,79	6,91E-02	2,42E-01	-0,14	6,59E-01	8,01E-01	
ALYREF	-0,80	1,30E-01	3,23E-01	-0,79	1,43E-01	3,66E-01	
GNB1	-0,81	4,69E-02	1,95E-01	-0,51	1,43E-01	3,66E-01	
YBX3	-0,81	2,79E-02	1,52E-01	-0,13	5,69E-01	7,42E-01	
FIP1L1	-0,81	5,01E-02	1,99E-01	-0,06	7,84E-01	8,92E-01	
TAF10	-0,81	2,37E-02	1,47E-01	-0,60	5,44E-02	2,37E-01	
SNRPB2	-0,81	2,06E-01	4,21E-01	-0,47	3,13E-01	5,57E-01	
H1F0	-0,81	6,19E-02	2,30E-01	-0,30	2,42E-01	4,89E-01	
KLF12	-0,82	3,19E-02	1,56E-01	0,42	1,29E-01	3,51E-01	
SRSF2	-0,83	8,90E-02	2,75E-01	-0,93	3,53E-02	1,92E-01	
HNRNPA1; HNRNPA1L2	-0,84	4,86E-02	1,97E-01	-0,66	3,36E-02	1,89E-01	
DDX1	-0,85	1,10E-01	3,03E-01	-0,03	9,08E-01	9,49E-01	
CAPZA1	-0,86	2,18E-02	1,42E-01	-0,42	1,17E-01	3,38E-01	
SAP18	-0,86	1,33E-01	3,24E-01	-0,31	6,26E-01	7,82E-01	
LBR	-0,86	1,52E-02	1,17E-01	0,07	7,97E-01	8,93E-01	
MECP2	-0,87	1,15E-01	3,08E-01	-0,91	3,76E-02	1,99E-01	
HNRNPH3	-0,87	9,95E-02	2,91E-01	-1,26	9,70E-03	1,09E-01	
FAM133B	-0,88	2,61E-02	1,52E-01	-0,28	2,65E-01	5,13E-01	
CALM2;CALM1; CALM3	-0,88	2,46E-02	1,48E-01	-0,44	1,70E-01	4,04E-01	
PABPC1	-0,88	8,32E-02	2,66E-01	-0,55	1,16E-01	3,38E-01	
TCOF1	-0,88	1,70E-01	3,81E-01	-1,00	8,42E-02	2,91E-01	
SSSCA1	-0,89	1,17E-01	3,11E-01	0,46	3,45E-01	5,84E-01	
HK1	-0,90	6,32E-02	2,30E-01	0,09	7,35E-01	8,56E-01	
IKZF4	-0,90	1,80E-02	1,25E-01	-0,47	9,13E-02	2,99E-01	
ARL6IP4	-0,91	2,22E-02	1,43E-01	-0,90	1,68E-02	1,37E-01	
PSIP1	-0,91	7,62E-02	2,54E-01	-0,96	1,34E-01	3,58E-01	
MYL6	-0,92	3,05E-02	1,56E-01	-0,06	8,54E-01	9,22E-01	
NACA	-0,92	1,64E-02	1,17E-01	-0,60	6,35E-02	2,56E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
BRD9	-0,92	2,32E-02	1,46E-01	-0,33	1,64E-01	4,00E-01	
ATP5H	-0,92	4,69E-02	1,95E-01	0,00	1,00E+00	1,00E+00	
RPN2	-0,93	1,10E-01	3,03E-01	0,00	1,00E+00	1,00E+00	
HIST1H1C	-0,94	1,00E-01	2,92E-01	-0,76	9,75E-02	3,10E-01	
KTN1	-0,96	4,79E-02	1,96E-01	-0,77	1,74E-01	4,11E-01	
NOP16	-0,97	1,71E-01	3,81E-01	-1,63	1,15E-02	1,15E-01	
VDAC1	-0,98	1,21E-01	3,16E-01	-0,99	2,93E-01	5,45E-01	
AURKC	-1,00	3,63E-02	1,70E-01	0,00	1,00E+00	1,00E+00	
SYNCRIP	-1,01	3,12E-02	1,56E-01	-0,52	6,43E-02	2,56E-01	
ANXA2;ANXA2P2	-1,01	1,61E-02	1,17E-01	-0,19	5,47E-01	7,29E-01	
HNRNPAB	-1,02	1,25E-02	1,04E-01	-1,10	1,96E-02	1,48E-01	
FOSL2	-1,03	9,47E-02	2,83E-01	0,38	3,25E-01	5,66E-01	
VDAC2	-1,04	9,23E-02	2,81E-01	-1,67	2,52E-02	1,64E-01	
FAM32A	-1,05	1,22E-02	1,04E-01	0,11	6,07E-01	7,67E-01	
CCT5	-1,05	4,08E-02	1,85E-01	0,00	1,00E+00	1,00E+00	
PRDX1	-1,05	1,21E-02	1,04E-01	-0,20	5,12E-01	7,21E-01	
PRDX3	-1,06	1,22E-02	1,04E-01	-0,85	4,31E-02	2,09E-01	
MYL12A;MYL12B; MYL9	-1,07	2,77E-02	1,52E-01	-0,06	8,23E-01	9,03E-01	
SNRNP27	-1,10	2,88E-02	1,53E-01	-0,01	9,75E-01	9,85E-01	
IMPDH2	-1,11	6,31E-02	2,30E-01	-1,13	1,22E-01	3,42E-01	
PHB	-1,14	1,81E-01	3,91E-01	0,00	1,00E+00	1,00E+00	
HSP90AA1	-1,15	2,30E-02	1,45E-01	-1,08	9,96E-03	1,09E-01	
EIF2S1	-1,17	1,77E-02	1,24E-01	-0,40	3,00E-01	5,51E-01	
HNRNPD	-1,19	1,61E-02	1,17E-01	-1,22	4,85E-03	8,30E-02	
HNRNPA2B1	-1,22	1,59E-02	1,17E-01	-1,30	1,61E-03	6,12E-02	
SUB1	-1,22	2,83E-02	1,52E-01	-0,42	3,38E-01	5,77E-01	
NONO	-1,23	4,79E-03	6,39E-02	-0,85	1,55E-01	3,84E-01	
CORO1C	-1,23	1,49E-02	1,17E-01	-0,84	6,38E-02	2,56E-01	
RAB1A;RAB1B	-1,23	2,74E-02	1,52E-01	-0,78	1,18E-01	3,38E-01	
HIST1H1A	-1,24	2,70E-02	1,52E-01	-0,32	1,97E-01	4,39E-01	
YBX1	-1,24	5,76E-03	7,20E-02	-0,02	9,13E-01	9,51E-01	
MSN	-1,24	1,84E-01	3,96E-01	-0,66	3,01E-01	5,51E-01	
ATP5B	-1,25	3,12E-02	1,56E-01	-1,47	4,08E-03	7,52E-02	
LLPH	-1,26	1,21E-01	3,16E-01	-1,06	4,05E-03	7,52E-02	
RPL22L1	-1,26	2,27E-02	1,45E-01	-0,83	3,11E-02	1,84E-01	
BCAR1	-1,30	2,34E-03	4,35E-02	-0,29	2,24E-01	4,69E-01	
PPIB	-1,36	2,75E-03	4,76E-02	-1,13	3,56E-03	7,27E-02	
CANX	-1,39	3,26E-02	1,57E-01	-1,16	1,38E-02	1,28E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
YWHAE	-1,41	6,82E-02	2,42E-01	-1,20	2,97E-02	1,80E-01	
TXN	-1,42	5,49E-03	7,03E-02	-0,77	1,69E-01	4,04E-01	
PRDX2	-1,52	7,40E-03	7,97E-02	-0,76	1,36E-01	3,59E-01	
KIAA1522	-1,52	3,12E-03	5,01E-02	0,18	4,57E-01	6,75E-01	
HSPB1	-1,54	7,55E-03	7,97E-02	-0,90	7,89E-02	2,84E-01	
VCP	-1,60	5,02E-02	1,99E-01	-0,95	1,32E-01	3,56E-01	
RPL37	-1,60	9,20E-03	8,90E-02	-2,05	4,40E-02	2,10E-01	
PDIA6	-1,62	1,15E-03	3,41E-02	-0,74	7,58E-02	2,78E-01	
RAB5C	-1,63	5,21E-03	6,76E-02	0,00	1,00E+00	1,00E+00	
RAB11FIP5	-1,63	1,79E-03	3,83E-02	-0,94	6,42E-03	9,65E-02	
ING5	-1,66	2,10E-02	1,37E-01	-0,76	2,29E-02	1,57E-01	
EIF5A;EIF5A2; EIF5AL1	-1,67	1,42E-03	3,42E-02	-1,12	3,55E-02	1,92E-01	
DSC1	-1,69	1,54E-02	1,17E-01	-0,53	3,79E-01	6,10E-01	
EIF4A1;EIF4A2	-1,70	4,42E-03	6,15E-02	-1,20	1,01E-02	1,09E-01	
NUSAP1	-1,71	3,13E-02	1,56E-01	-0,10	7,93E-01	8,93E-01	
SERPINH1	-1,73	4,23E-02	1,86E-01	-0,64	4,22E-01	6,50E-01	
KRT2	-1,86	7,13E-03	7,91E-02	-0,63	4,10E-01	6,37E-01	
GAPDH	-1,90	7,79E-04	2,96E-02	-0,86	3,49E-02	1,92E-01	
RAB7A	-1,91	3,15E-03	5,01E-02	0,00	1,00E+00	1,00E+00	
LGALS1	-1,93	3,52E-03	5,43E-02	-0,59	1,51E-01	3,76E-01	
AHNAK	-1,95	9,14E-03	8,90E-02	-0,63	1,31E-01	3,55E-01	
CSTA	-1,96	2,24E-03	4,29E-02	-0,81	6,59E-02	2,58E-01	
PRR11	-1,97	2,62E-02	1,52E-01	-1,18	2,92E-03	7,01E-02	
S100A7	-1,97	1,63E-02	1,17E-01	-0,77	1,20E-01	3,39E-01	
RRBP1	-2,00	6,33E-02	2,30E-01	-1,81	2,73E-01	5,25E-01	
SFN	-2,00	6,70E-03	7,72E-02	-1,42	4,11E-02	2,03E-01	
TXNDC5	-2,01	1,24E-02	1,04E-01	-2,29	1,82E-02	1,44E-01	
DKFZp686J1372; TPM3	-2,03	3,09E-03	5,01E-02	-0,72	2,72E-01	5,25E-01	
PPIA	-2,04	4,33E-04	2,43E-02	-0,92	3,25E-02	1,87E-01	
HSP90B1	-2,10	8,61E-03	8,59E-02	-2,04	2,47E-04	4,09E-02	
NME1-NME2;NME2; NME1;NME2P1	-2,13	2,13E-04	2,10E-02	-1,17	9,17E-03	1,08E-01	
MAGEB2	-2,15	1,00E-03	3,41E-02	-1,20	2,82E-03	7,01E-02	
DCD	-2,16	8,28E-03	8,42E-02	-0,74	1,34E-01	3,58E-01	
P4HB	-2,18	1,20E-03	3,41E-02	-1,48	2,96E-03	7,01E-02	
YWHAZ	-2,28	3,62E-04	2,38E-02	-1,08	9,25E-03	1,08E-01	
CFL1	-2,30	1,15E-03	3,41E-02	-1,42	6,14E-03	9,65E-02	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
DSP	-2,56	9,51E-03	9,02E-02	-0,58	5,93E-01	7,57E-01	
PKM	-2,61	6,39E-03	7,72E-02	-1,12	5,39E-02	2,37E-01	
LDHA	-3,06	3,60E-04	2,38E-02	-1,33	4,09E-02	2,03E-01	
HSPE1;HSPE1-MOB4	-3,07	5,87E-04	2,43E-02	-3,06	1,60E-03	6,12E-02	
DSG1	-3,45	5,11E-04	2,43E-02	-0,60	4,09E-01	6,37E-01	
S100A9	-3,65	2,80E-03	4,76E-02	-3,08	2,04E-02	1,49E-01	
ENO1	-4,18	1,33E-04	1,87E-02	-1,59	2,35E-02	1,57E-01	
PDIA3	-4,35	7,20E-05	1,42E-02	-2,95	2,72E-05	9,02E-03	
CDC2;CDK1				0,21	4,89E-01	7,02E-01	
MDH2				-3,17	2,66E-03	7,01E-02	
CALML5				-2,69	1,71E-02	1,38E-01	
TPI1				-2,65	3,71E-03	7,38E-02	
LDHB				-2,08	1,66E-03	6,12E-02	
EEF1B2				-2,07	6,89E-03	1,01E-01	
STIP1				-1,82	2,64E-03	7,01E-02	
EEF1D				-1,79	6,86E-03	1,01E-01	
SBSN				-1,42	4,34E-02	2,09E-01	
YWHAG				-1,24	9,85E-03	1,09E-01	
SET;SETSIP				-1,15	2,17E-02	1,55E-01	
LAMP1				-0,97	2,69E-02	1,72E-01	
TAGLN2				-0,94	3,53E-02	1,92E-01	
SNRPD3				-0,64	1,64E-01	4,00E-01	
CKAP4				-0,64	9,01E-02	2,99E-01	
PDS5B				-0,61	9,46E-02	3,05E-01	
FUS				-0,60	1,36E-01	3,59E-01	
HPSE				-0,54	1,47E-01	3,72E-01	
MTDH				-0,51	1,36E-01	3,59E-01	
PLCB3				-0,51	2,55E-01	5,00E-01	
SNAP29				-0,46	2,33E-01	4,82E-01	
ALDH3A2				-0,44	5,07E-01	7,18E-01	
JUP				-0,43	7,60E-01	8,76E-01	
SF3A1				-0,43	3,98E-01	6,29E-01	
STOML2				-0,39	3,24E-01	5,66E-01	
CASP14				-0,38	3,05E-01	5,54E-01	
APEX1				-0,37	4,86E-01	6,98E-01	
B2M				-0,37	3,61E-01	5,95E-01	
BTF3				-0,35	3,35E-01	5,74E-01	
TLN1				-0,34	3,13E-01	5,57E-01	

Gene name	**mean log2FC MYC-WT**	**p-vlaue MYC-WT**	**q-value MYC-WT**	**mean log2FC MYC-dN1**	**p-vlaue MYC-dN1**	**q-value MYC-dN1**	**Function**
C8orf82				-0,25	5,04E-01	7,15E-01	
AP2A1;AP2A2				-0,25	4,53E-01	6,74E-01	
MAPRE1				-0,24	4,32E-01	6,55E-01	
SRPK1				-0,17	5,95E-01	7,58E-01	
MGEA5				-0,15	6,28E-01	7,82E-01	
TARDBP				-0,12	7,09E-01	8,40E-01	
DDX6				-0,06	8,43E-01	9,16E-01	
EIF2S3;EIF2S3L				-0,05	9,14E-01	9,51E-01	
WDR77				0,01	9,87E-01	9,92E-01	
ZNF668				0,01	9,70E-01	9,81E-01	
AGPS				0,02	9,48E-01	9,69E-01	
CPSF7				0,02	9,36E-01	9,60E-01	
PLBD2				0,03	9,26E-01	9,55E-01	
PPHLN1				0,06	8,85E-01	9,34E-01	
ZNF275				0,10	8,00E-01	8,93E-01	
INCENP				0,12	7,91E-01	8,93E-01	
MRPS27				0,13	6,68E-01	8,05E-01	
CRNKL1				0,13	6,71E-01	8,06E-01	
TNFAIP8L1				0,17	5,79E-01	7,49E-01	
SAP30				0,19	5,56E-01	7,32E-01	
ZNF768				0,20	5,57E-01	7,32E-01	
CDK9				0,24	4,82E-01	6,96E-01	
THBS1				0,24	5,16E-01	7,21E-01	
GPATCH1				0,26	3,55E-01	5,95E-01	
XPO1				0,27	3,82E-01	6,13E-01	
SH3BP4				0,27	4,25E-01	6,51E-01	
NIFK				0,28	3,68E-01	6,04E-01	
PRPF31				0,28	4,56E-01	6,75E-01	
SP1				0,29	3,54E-01	5,94E-01	
FABP5				0,31	5,63E-01	7,38E-01	
GNAI3;GNAI1				0,36	3,78E-01	6,10E-01	
NMT2				0,37	2,91E-01	5,45E-01	
KIF2C				0,39	2,53E-01	5,00E-01	
SMAD3				0,41	2,03E-01	4,48E-01	
PSMA4				0,41	2,47E-01	4,94E-01	
RPS27				0,43	4,28E-01	6,52E-01	
SPTBN1				0,44	1,86E-01	4,27E-01	
FAM64A				0,52	1,34E-01	3,58E-01	

Gene name	mean log2FC MYC-WT	p-vlaue MYC-WT	q-value MYC-WT	mean log2FC MYC-dN1	p-vlaue MYC-dN1	q-value MYC-dN1	Function
LRRC47				0,56	1,44E-01	3,68E-01	
RUNX1				0,59	3,42E-02	1,91E-01	
ASPH				0,63	7,02E-02	2,66E-01	
PSMD4				0,64	9,24E-02	3,01E-01	
DNAJB6				0,70	4,03E-01	6,31E-01	
FLNB				0,76	4,82E-02	2,21E-01	
CFAP20				0,79	7,76E-02	2,82E-01	
GTF3C2				0,91	3,48E-02	1,92E-01	
HBS1L				0,93	3,78E-02	1,99E-01	
BUB3				0,99	7,08E-02	2,67E-01	
CXXC1				1,19	1,16E-02	1,15E-01	
TUBB2B				1,38	1,32E-02	1,26E-01	
CLK3				1,49	1,80E-02	1,43E-01	
ERBB2IP				1,54	1,19E-03	6,12E-02	
TUBB6				1,81	2,22E-02	1,55E-01	
RECQL				1,87	6,06E-02	2,50E-01	

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7.5 Publication list

B. Adhikari, J. Bozilovic, M. Diebold, J.D. Schwarz, **J. Hofstetter**, M. Schröder, M. Wanior, A. Narain, M. Vogt, N. Dudvarski Stankovic, A. Baluapuri, L. Schönemann, L. Eing, P. Bhandare, B. Kuster, A. Schlosser, S. Heinzlmeir, C. Sotriffer, S. Knapp, E. Wolf (2020). PROTAC-mediated degradation reveals a non-catalytic function of AURORA-A kinase. *Nature Chemical Biology*; 2020 Sep 28

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* These authors contributed equally.

G. Büchel, A. Carstensen, K-Y. Mak, I. Roeschert, E. Leen, O. Sumara, **J. Hofstetter**, S. Herold, J. Kalb, A. Baluapuri, E. Poon, C. Kwok, L. Chesler, H.M. Maric, D.S. Rickman, E. Wolf, R. Bayliss, S. Walz, M. Eilers (2017). Association with Aurora-A Controls N-MYC-Dependent Promoter Escape and Pause Release of RNA Polymerase II during the Cell Cycle. *Cell Reports*; 2017 Dec 19;21(12):3483-3497.

7.6 Curriculum vitae

7.7 Affidavit

I hereby confirm that my thesis entitled „MYC shapes the composition of RNA polymerase II through direct recruitment of transcription elongation factors" is the result of my own work. I did not receive any help or support from commercial consultants. All sources and / or materials applied are listed and specified in the thesis.

Furthermore, I confirm that this thesis has not yet been submitted as part of another examination process neither in identical nor in similar form.

Place, Date

Signature

7.8 Eidesstattliche Erklärung

Hiermit erkläre ich an Eides statt, die Dissertation „MYC beeinflusst die Zusammensetzung der RNA-Polymerase II durch die direkte Rekrutierung von Transkriptions-Elongationsfaktoren" eigenständig, d.h. insbesondere selbständig und ohne Hilfe eines kommerziellen Promotionsberaters, angefertigt und keine anderen als die von mir angegebenen Quellen und Hilfsmittel verwendet zu haben.

Ich erkläre außerdem, dass die Dissertation weder in gleicher noch in ähnlicher Form bereits in einem anderen Prüfungsverfahren vorgelegen hat.

Ort, Datum

Unterschrift