

Supplementary Information

Hox genes are involved in the differentiation of vascular wall-resident multipotent stem cells into smooth muscle cells

Diana Klein¹, Mohamed Benchellal¹, Veronika Kleff², Heinz Günther Jakob³ and Süleyman Ergün⁴

¹Institute of Cell Biology (Cancer Research), University of Duisburg-Essen, University Hospital, 45122 Essen, North Rhine-Westphalia, Germany.

²Institute of Anatomy, University of Duisburg-Essen, University Hospital, 45122 Essen, North Rhine-Westphalia, Germany.

³Department of Thoracic and Cardiovascular Surgery, University Duisburg-Essen, University Hospital, 45122 Essen, North Rhine-Westphalia Essen, Germany

⁴Institute of Anatomy and Cell Biology, University of Würzburg, 97070 Würzburg, Bayern, Germany.

Correspondence should be addressed to

Dr. rer. nat. Diana Klein

Institute of Cell Biology (Cancer Research)

University Hospital Essen

Hufelandstr.55

Ger-45147 Essen

Tel: +49-201-723 83342

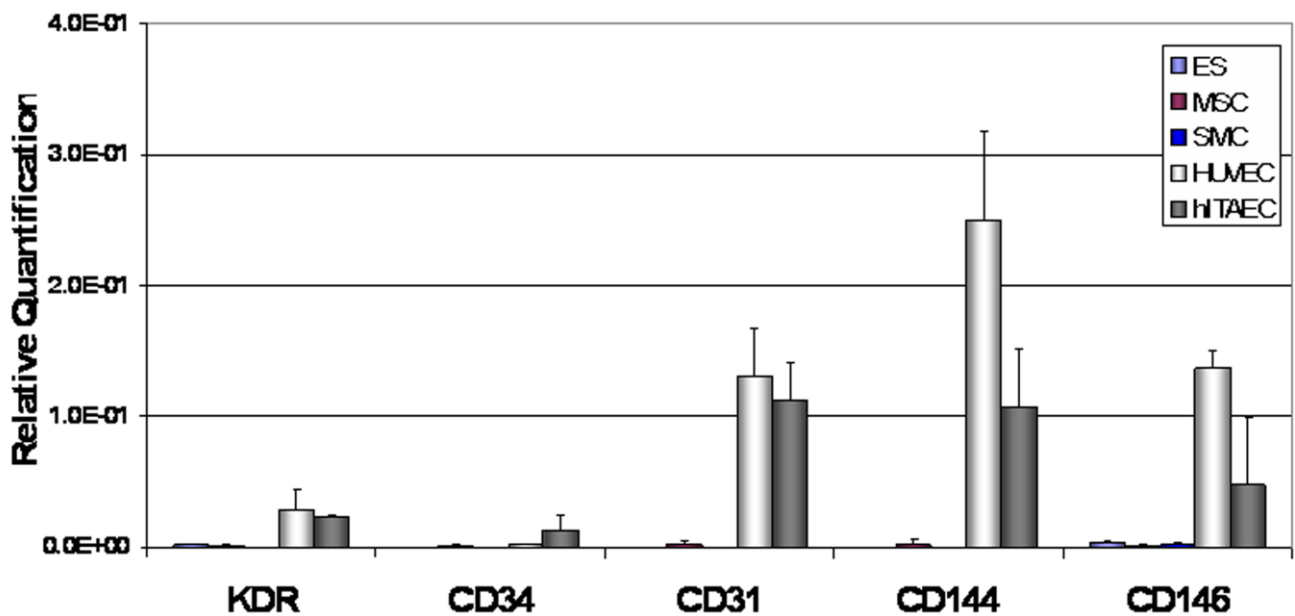
Fax: +49-201-723 5904

E-mail: Diana.Klein@uk-essen.de

Short title

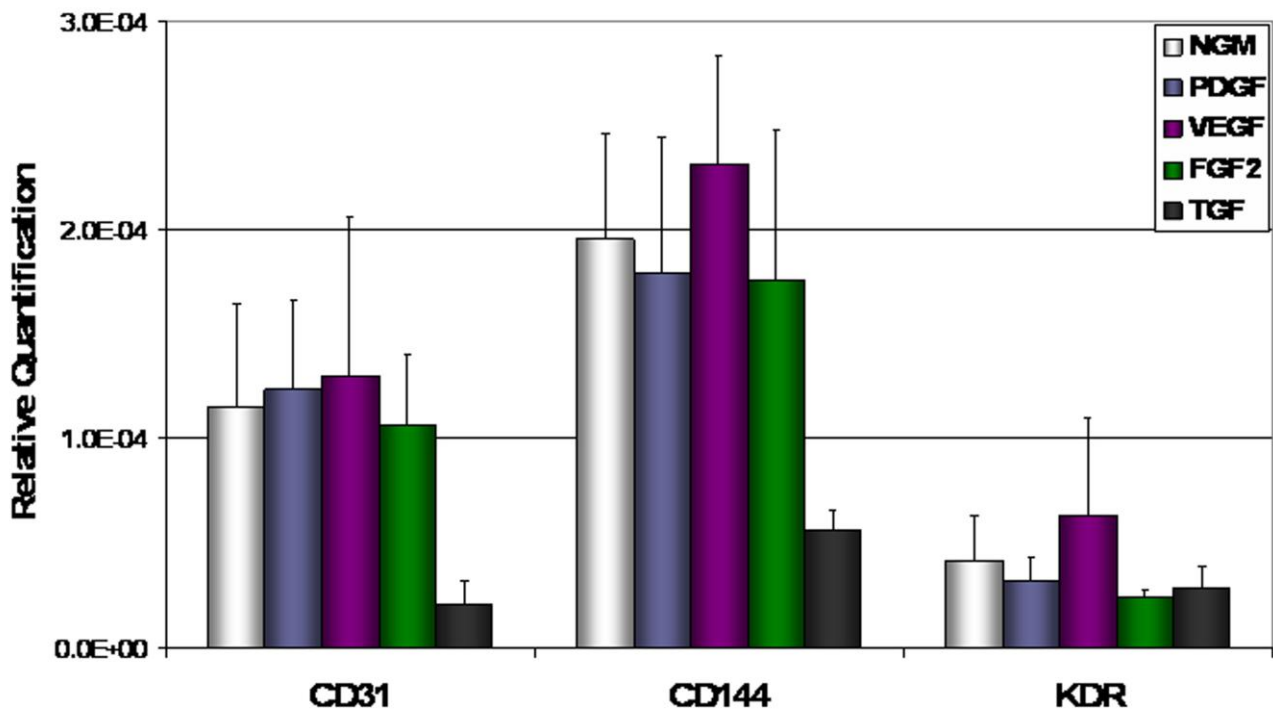
HOX code in vascular wall-resident CD44+ multipotent stem cells

Supplementary Figure S1



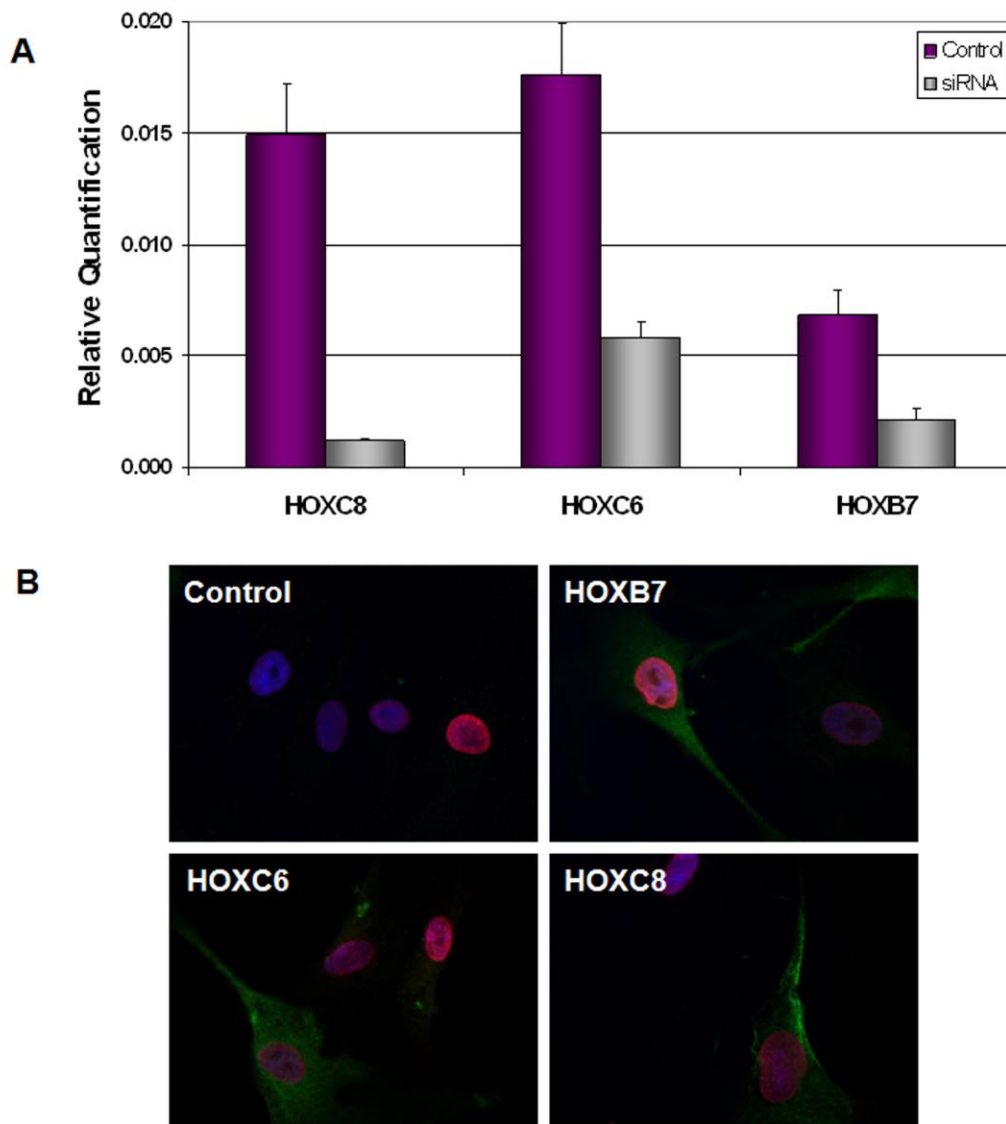
Supplementary Figure S1 | Analysis of endothelial marker gene expression in human vascular wall-resident multipotent stem cells. Real-Time RT-PCR quantification of well known endothelial gene mRNA expression in VW-MSCs (MSC, purple bars) as compared to human embryonic stem cells (ES, blue bars), aortic smooth muscle cells (SMC, dark blue bars), human umbilical cord endothelial cells (HUVEC, white bars) and freshly isolated endothelial cells from hITA fragments (hTAEC, grey bars) using specific primers for KDR/VEGFR2, CD34, CD31/PECAM1, CD144/VE-Cadherin and CD146/MCAM. Resulting expression levels of were normalized by division through the mean expression value of the reference gene (beta actin) and are shown as relative quantification units (RQ). Data are presented as mean \pm SD from three independent experiments measured two times each.

Supplementary Figure S2



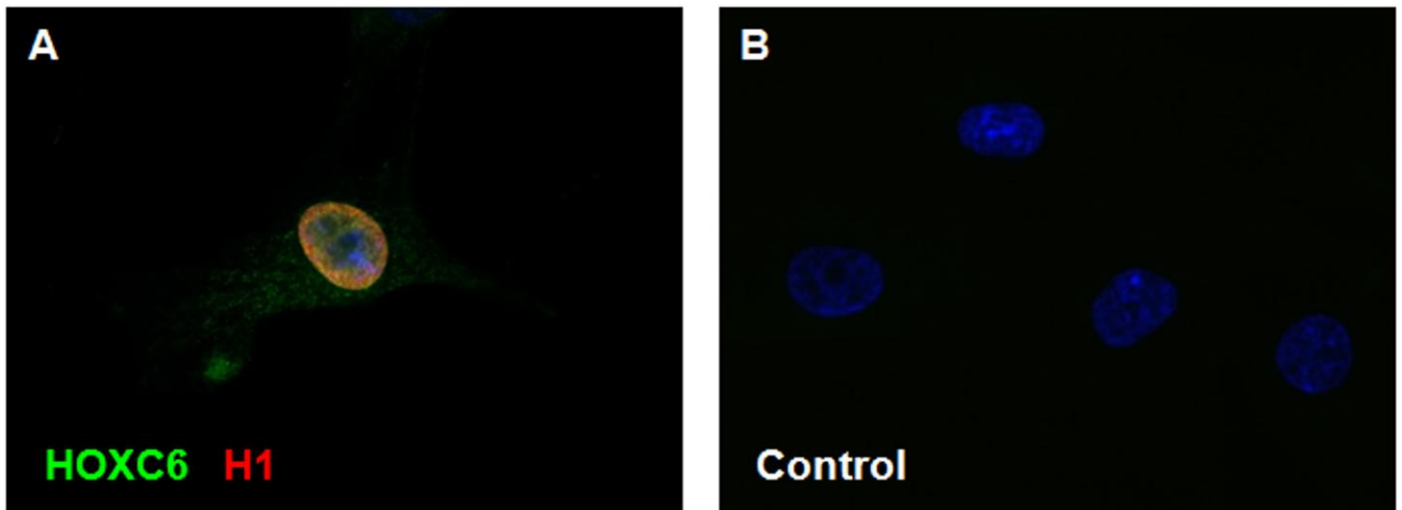
Supplementary Figure S2 | Exogenous growth factor treatment induces no endothelial cell differentiation of cultured vascular wall-derived MPSCs. VW-MPSCs cultured in normal growth media (NGM) supplemented with VEGF165, PDGF-BB, FGF2 (10ng/ml) and TGF β 1 (5ng/ml) for 14 days show no increase in the endothelial marker gene expression (CD31/PECAM1, CD144/VE-Cadherin, KDR/VEGFR2) indicating that the cells were not able to differentiate into the endothelial lineage. Data are presented as mean \pm SEM from 3 independent experiments performed in duplicates each

Supplementary Figure S3



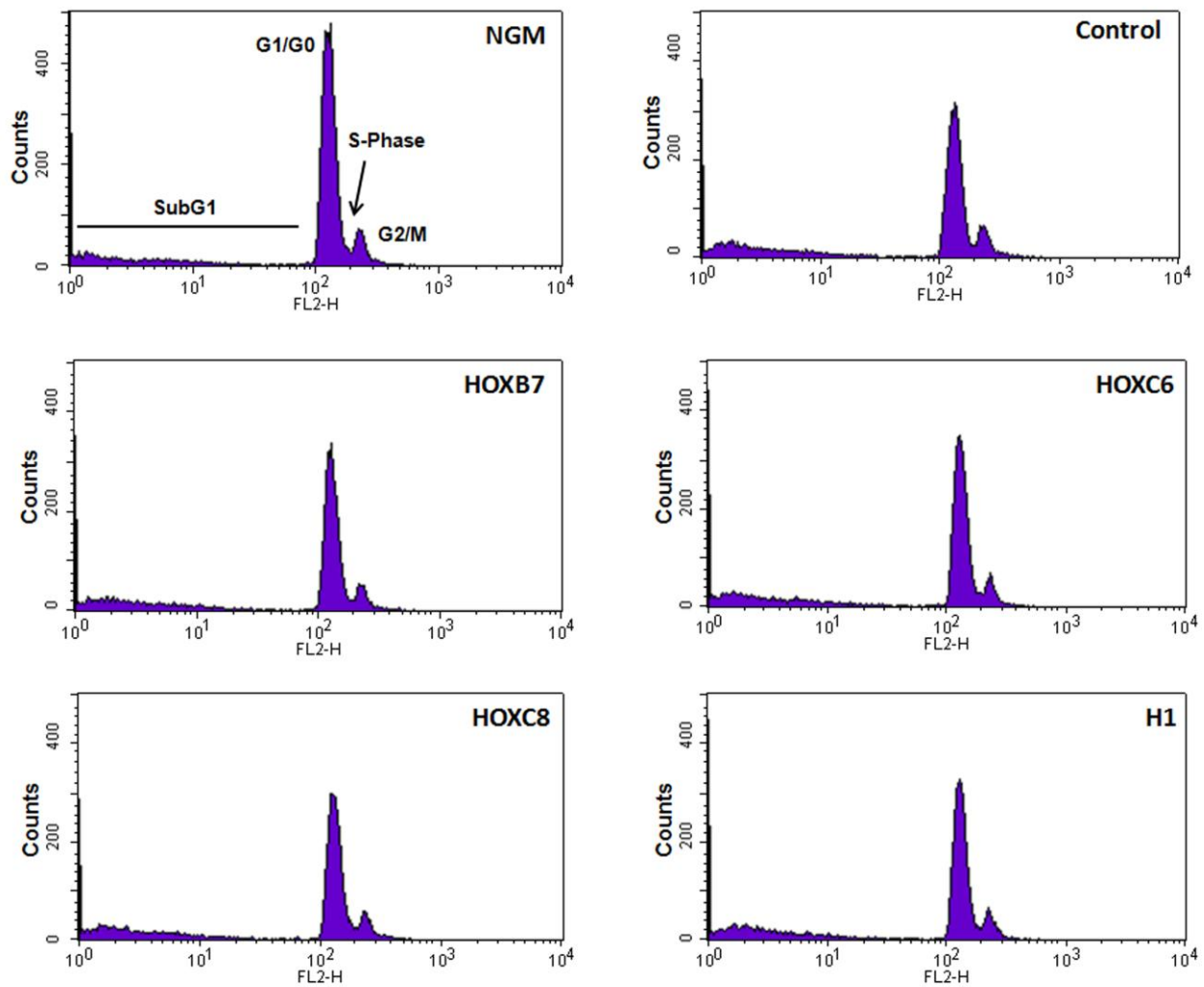
Supplementary Figure S3 | Silencing over-expressed HOX genes in cultured vascular wall-derived. VW-derived MPSCs were transfected with Control (non-silencing) or HOXC8, HOXC6, HOXB7 siRNA alone or in indicated combinations. After 4 days cells were harvested and subjected for mRNA isolation and Real-Time RT-PCR quantification of HOX gene silencing (A). Resulting expression levels of were normalized by division through the mean expression value of the reference gene (Actin) and are shown as relative quantification units (RQ). Data are presented as mean \pm SEM from 4 independent experiments performed in duplicates each. ** $p \leq 0.005$. Immunofluorescence analysis of H1 (red) and TAGLN (green) demonstrated an up regulation of TAGLN expression and partially of H1 upon HOX silencing (B).

Supplementary Figure S4



Supplementary Figure S4 | Silencing over-expressed HOX genes in cultured vascular wall-derived. Immunofluorescence analysis of H1 (red) and HOXC6 (green) demonstrated co-localization of both proteins in the nucleus. For control staining isotype controls were used.

Supplementary Figure S5

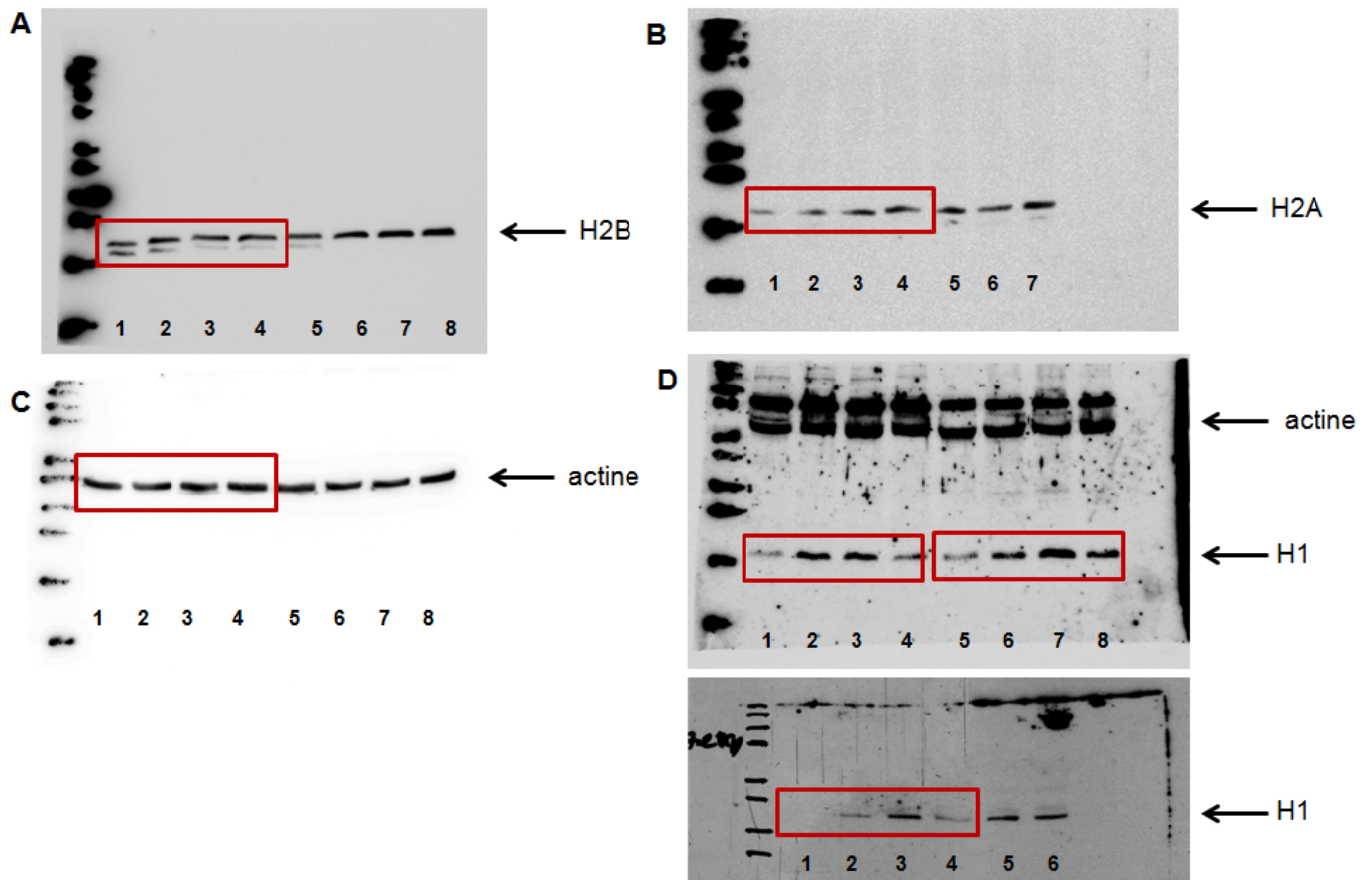


Supplementary Figure S5 | Cell cycle analysis after silencing over-expressed HOX genes in cultured vascular wall-derived. VW-derived MPSCs were transfected with Control (non-silencing) or HOXC8, HOXC6, HOXB7 siRNA alone or in indicated combinations and subjected for Nicoletti staining. Two-color flow cytometric analysis was used to determine cells actively synthesizing DNA and their position in G0/1, S, G2/M phase of the cell cycle. Representative graph for three independent experiments are shown.

Supplementary Information

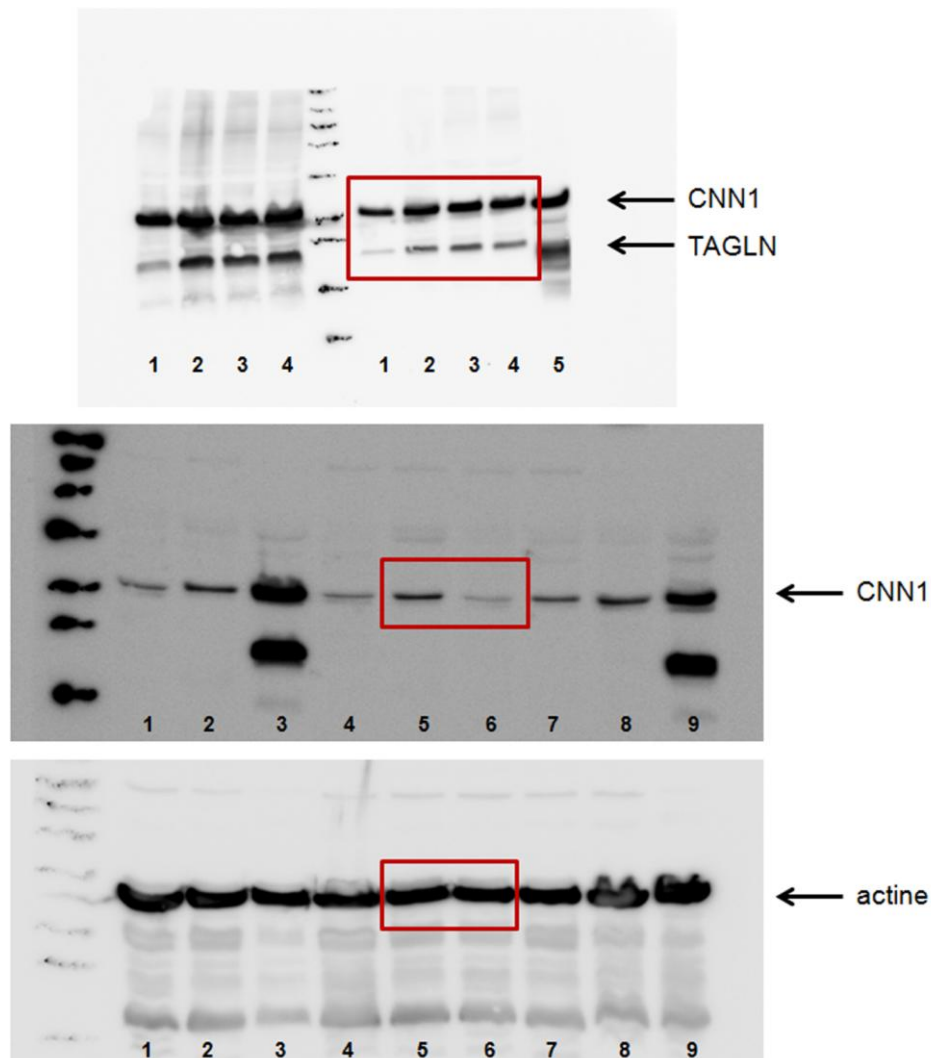
Full Gels

Supplementary Figure S7



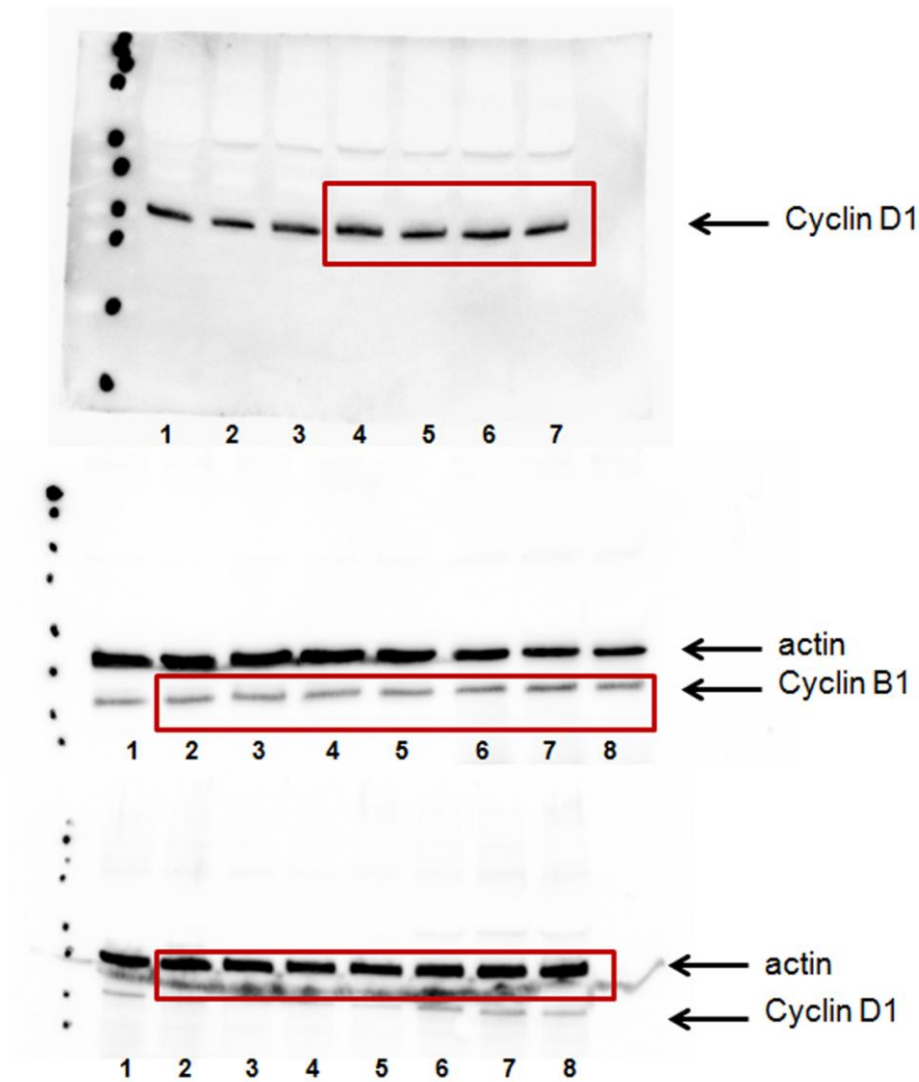
Supplementary Figure S7 | Full gels of cropped gels (emphasized by a red rectangle) as shown in Figure 4B. Histone H1, H2B, H2A protein levels were detected by Western blot. Equal protein amounts (50 μ g, whole cell lysate) were loaded. Beta-actin was included as a loading control. (A-C) Lanes: 1 Control, 2 HOXC8, 3 HOXC6, 4 HOXB7, 5 Control, 6 HOXC8, 7 HOXC6, 8 HOXB7 of a different experiment; (D) Lanes: upper panel 1 Control, 2 HOXC8, 3 HOXC6, 4 HOXB7, 5 Control, 6 HOXC6/B7, 7HOXC8/B7, 8 HOXC8/C6/B7; lower panel 1 Control, 2 HOXC8, 3 HOXC6, 4 HOXB7, 5 HOXC6/B7, 6 HOXC8/B7.

Supplementary Figure S8



Supplementary Figure S8 | Full gels of cropped gels (emphasized by a red rectangle) as shown in Figure 5B, D. TAGLN, CNN1 and H1 protein levels were detected by Western blot. Equal protein amounts (50 μ g, whole cell lysate) were loaded. (upper panel) Lanes: 1 Control, 2 HOXC8, 3 HOXC6, 4 HOXB7 of two independent experiments, 5 control lysate (human aortic smooth muscle cells, hAoSMC); (lower panels) Control, 6 HOXC8, 7 HOXC6, 8 HOXB7 of a different experiment; (D) Lanes: 1 H1, 2 Control, 3 hAoSMC, 4 H1, 5 Control, 6 H1, 7 H1, 8 NGM, 9 hAoSMC. Beta-actin was included as a loading control using the same membranes.

Supplementary Figure S9



Supplementary Figure S9 | Full gels of cropped gels (emphasized by a red rectangle) as shown in Figure 6B. Cyclin D1 and B1 protein levels were detected by Western blot. Equal protein amounts (50 μ g, whole cell lysate) were loaded. (upper panel) Lanes: 1 NGM, 2 Control, 3 NGM, 4 Control 5 HOXB7, 6 HOXC6, 7 HOXC8; (lower panels) Lanes: 1 NGM, 2 Control, 3 HOXB7, 4 HOXC6, 5 HOXC8, 6 HOXB7/HOXC6, 7 HOXB7/HOXC6/HOXC8, 8 NGM. Beta-actin was included as a loading control using the same membranes.

Supplementary Table S1
Oligonucleotides used for QRT-PCR

Gene	Primer Sequence	Gene	Primer Sequence
CD90 fw	ggactgagatcccagaacca	HIST1-H2B-E fw	gtgtacaaggctgaaacagg
CD90 bw	acgaaggctctgtccacta	HIST1-H2B-E bw	acttgagctggtgtacttggt
CD73 fw	taaaagggtccaccctgaagaa	HIST1-H2B-H fw	gggatcatgaattcctttgt
CD73 bw	cttctgtggaaaactgatcc	HIST1-H2B-H bw	atttgagctggtgtacttggt
CD105 fw	actctcccaaggacactgtga	HIST1-H2B-I fw	acagaagaaggatggcaagaag
CD105 bw	tgatgagctcgacaggatattg	HIST1-H2B-I bw	acttgagctggtgtacttggt
ACTA2 fw	tggctattcctctgtacta	HIST1-H2B-K fw	catgggaatcatgaactcctc
ACTA2 bw	cgatccagacagagtatttgc	HIST1-H2B-K bw	acttagcgctggtgtacttggt
TAGLN fw	tccagactgtgacctcttga	HIST1-H2B-F fw	cgcagaagaaggatggtaagaa
TAGLN bw	cctctccgctctaactgatgat	HIST1-H2B-F bw	gggattgggtatgaagacgta
CNN1 fw	gacgaaaggaaacaagggtgaac	HIST1-H2B-D fw	cctgaacctaccaagtctgctc
CNN1 bw	tcagacagtagctgggctgta	HIST1-H2B-D bw	aagatgctgtgacgaaggaat
KDR fw	aaaacctttgtgtctttgga	HIST1-H2B-A fw	aagggtctaccattccaagaa
KDR bw	gaaatgggattggaaggatga	HIST1-H2B-A bw	ctcagacacagcatgttagcc
CD144 fw	tggagactcctccagcttca	HIST1-H2B-B fw	atgcctgaacctctaagtctg
CD144 bw	gctccaccacgatctatac	HIST1-H2B-B bw	atggctgagcgcttatttagt
CD31 fw	gaagtacggatctatgactcag	HIST1-H2B-C fw	tgtgtacgtgtacaaggctg
CD31 bw	gtgagtcactggaatggtgca	HIST1-H2B-C bw	acttgagctggtgtacttggt
H2A FV w	gcatccacagacactgaagac	HIST1-H2B-G fw	ccgtgtatgtgtacaaggctg
H2A FV bw	cagttttctgtgtccctctt	HIST1-H2B-G bw	tggagctgtatactgtgtgaca
H2A FZ fw	aatctaggacgaccagctatgg	HIST1-H2A-A fw	gaaactatgcagagcggatag
H2A FZ bw	ctgtgtctctttctccaatc	HIST1-H2A-A bw	tactgtcttgggctttatggt
HIST1-H1-A fw	gagaaacctttagctggcaaga	HIST1-H2A-C fw	cgtaaaggcaactacgcagag
HIST1-H1-A bw	cccgtgccttagttttgtag	HIST1-H2A-C bw	gtgactctcggtctcttaggc
HIST1-H1-D fw	agactgtcctactgtctctac	HIST1-H2A-B fw	gctaagactcggtctctctg
HIST1-H1-D bw	gtacctttgtccaccaagctct	HIST1-H2A-B bw	cacgccccaaagagttattaag
HIST1-H1-C fw	ggagaaaaacaacagccgtatc	HIST1-H2A-D fw	cccagagtaaggctaagacc
HIST1-H1-C bw	gtttcttagcgctcttctcg	HIST1-H2A-D bw	caattgtgactttaccagcaa
HIST2-H4-A/B fw	ggaaaaggcttaggcaagg	HIST3-H2A fw	gagtacttgactgccgagatcc
HIST2-H4-A/B bw	gtgctcggtgtaggtgactg	HIST3-H2A bw	gggtgctctccgtctctt
HIST1-H4-A fw	gcggtactctggtctgatctac	HIST3-H2B-B fw	cccaagaagggttctaaaaagg
HIST1-H4-A bw	gaaatgcaagctgtggagaaat	HIST3-H2B-B bw	acttgagctggtgtacttggt
HIST1-H4-C fw	aacatccagggcattacaaaac	HIST2-H2A-A fw	gcggtcctcgagtatctgac
HIST1-H4-C bw	ccctgacgttttagggcata	HIST2-H2A-A bw	tccgtctcttagggagcagta
H1F0 fw	caccccaagtattcagacatga	HIST2-H2A-B fw	gagtacctgaccgcggaat
H1F0 bw	gtcttctgaaggccactgact	HIST2-H2A-B bw	gcttgactctccgttttctt
HIST2-H2B-E fw	cctaaaaagggtccaagaaag	HIST2-H2A-C fw	agtacctgaccgccgagat
HIST2-H2B-E bw	acttgagctggtgtacttggt	HIST2-H2A-C bw	gcatttattgtctttggctt
HOXA1 fw	gcctcaatacattcaccactca	HOXA6 fw	gttgaagtggaactcctctcc
HOXA1 bw	ggttctggaaccagatcttcac	HOXA6 bw	ggcctcggtttctattctgat
HOXA2 fw	acactcgacactgattcctct	HOXC5 fw	ctaagagcagtgaggagatcaa
HOXA2 bw	gaagctgtgtgtgtgtaagc	HOXC5 bw	agcctcttcttttcatctttg
HOXA3 fw	gtctcgacaaaaacaaagcag	HOXC6 fw	agatctactcgcggtaccagac
HOXA3 bw	cagcgaatgcatagagttcaga	HOXC6 bw	cctggctactcttctgcttct
HOXA9 fw	acgcttgacactcacactttgt	HOXC8 fw	aaggacaaggccacttaaatca
HOXA9 bw	ggttctggaaccagatcttgac	HOXC8 bw	atttcttctctccaccttc
HOXA10 fw	gctactccgccttctcag	HOXC9 fw	cagcaagcacaagaggagaag

HOXA10 bw	gcttctccgaccactctttg	HOXC9 bw	tttgtggggtttttgttttc
HOXA11 fw	ctttcgaccagttttcgagac	HOXC10 fw	caaagtgagttccctgagacc
HOXA11 bw	aggcgcttctctttgtaatgt	HOXC10 bw	attccagcgctctggtgttagt
HOXA13 fw	gaatttattcgtggcgattcc	HOXC11 fw	ctgaggaggagaacacaaatcc
HOXA13 bw	ctaaggagttcgccttctacca	HOXC11 bw	cggctctctctcagtttctttt
HOXB1 fw	accttcgactggatgaaggta	HOXC12 fw	gctcggctcaagtagcactac
HOXB1 bw	gtggctaggttcagttcaggag	HOXC12 bw	gtgatgaactcgttgaccagaa
HOXB2 fw	taattcctcctcctcctcttt	HOXC13 fw	cagtcaggtgtactgctccaag
HOXB2 bw	aagtggaattccttctccagttc	HOXC13 bw	ggttatggtaaaagcggagac
HOXB3 fw	ctaccagtgccactagcaacag	HOXD1 fw	ggatgaaagtgaagaggaatgc
HOXB3 bw	acaggtagcgggtaaaatggaa	HOXD1 bw	cttctcgttcccttttctctg
HOXB4 fw	agaggcgagagagcagctt	HOXD3 fw	tggatgaaagagtctcgacaga
HOXB4 bw	gtaattggggtttaccgtgct	HOXD3 bw	tggctcctctgtacttcatgc
HOXB5 fw	aatattcccctggatgaggaag	HOXD4 fw	gttaccctggatgaagaagg
HOXB5 bw	gctgtagccaggctcatacttt	HOXD4 bw	acgatgacctgccttagtggt
HOXB6 fw	gctttgccacttctcctatta	HOXD8 fw	gattttacgaccagcaagag
HOXB6 bw	gcgtctggaacgtgtgatgt	HOXD8 bw	tctgttctggaaccagatttt
HOXB7 fw	ccgagagtaactccggatcta	HOXD9 fw	ccacttcttatcctcctcctc
HOXB7 bw	atccctcacttctcttctct	HOXD9 bw	gaggaattcttctccagctca
HOXB8 fw	gcaaatccaggagtctaccac	HOXD10 fw	tgcatatggaaaagaagatgaa
HOXB8 bw	aataggaactccttctccagctc	HOXD10 bw	tttctaattccagcgtttggt
HOXB9 fw	gtccgtctaccacccttacatc	HOXD11 fw	acagggcttcgaccagttcta
HOXB9 bw	ctctagctccagcgtctggtat	HOXD11 bw	gagcatccgagagagttgaagt
HOXB13 fw	tgtggacagtaccagctctgg	HOXD12 fw	cgctcaactgaacatgacagt
HOXB13 bw	gcgagaaccttcttctttga	HOXD12 bw	gcttcttctatcacgctgtt
HOXC4 fw	gccagtatagctgcaccagtct	HOXD13 fw	tccttctaccaggctatacga
HOXC4 bw	ctccgttataattggggttca	HOXD13 bw	atggcatactcgttctccagtt
HOXA4 fw	tgtaccctggatgaagaagat	beta Actin fw	ggcaccacacttctacaatga
HOXA4 bw	gttgggcagtttgggtctt	beta Actin bw	tctctttaatgtcacgcacgat

Specific primers were synthesized based on available sequences for each listened gene. Primer design was done with the program Primer 3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Cross-reaction of primers with the genes was excluded by comparison of the sequence of interest with a database (Blast 2.2, U.S. National Centre for Biotechnology Information, Bethesda, MD, USA) and all primers used in our study were intron-spanning. PCR products are 300-400 bp in size.

Supplementary Table S2
QRT-PCR analysis of HOX gene expression levels

Real-Time RT-PCR quantification of HOX gene expression levels in VW-MPSCs as compared to human embryonic stem cells (hES), human aortic smooth muscle cells (hAoSMC) and human umbilical cord endothelial cells (HUVEC). was done using specific primers synthesized based on available sequences for HOX family members. Obtained expression levels were normalized by division through the mean expression value of the reference gene (Actin) and are shown as relative quantification units (RQ). Data are presented as mean \pm SD from four (MSC), three (human ES), four (SMC), three (HUVEC) and two (EC) independent experiments measured two times each.

	hES		VW-MSC		hAoSMC		HUVEC	
	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
HOXA1	1,34E-05	5,69E-06	1,74E-04	3,84E-05	3,12E-05	1,48E-05	1,56E-04	2,70E-05
HOXA2	4,78E-07	2,03E-07	4,79E-04	1,22E-04	1,21E-04	4,93E-05	1,00E-04	3,02E-05
HOXA3	1,22E-08	3,36E-09	2,31E-03	6,51E-04	8,35E-04	1,62E-04	1,06E-03	1,79E-04
HOXA4	1,70E-06	3,46E-07	9,04E-04	2,84E-04	1,98E-04	3,90E-05	8,95E-04	3,30E-04
HOXA5	2,61E-07	2,04E-07	2,49E-03	8,57E-04	3,98E-08	2,99E-08	2,05E-03	4,29E-04
HOXA6	3,30E-08	1,54E-08	4,72E-03	1,11E-03	2,21E-08	1,36E-08	1,82E-03	3,36E-04
HOXA7	1,09E-06	7,76E-07	7,01E-03	7,51E-04	5,89E-07	4,99E-07	3,43E-03	6,65E-04
HOXA9	5,56E-06	2,00E-06	4,91E-04	1,15E-04	3,18E-07	6,26E-08	2,21E-03	4,18E-04
HOXA10	1,05E-07	4,40E-08	5,66E-04	6,62E-05	7,13E-07	3,64E-07	7,26E-04	2,73E-04
HOXA11	3,74E-06	1,80E-06	4,56E-04	8,87E-05	5,46E-06	3,26E-06	2,96E-03	3,06E-04
HOXA13	4,16E-07	1,73E-07	4,34E-07	1,07E-07	6,69E-08	1,57E-08	1,62E-06	3,68E-07
HOXB1	9,71E-06	1,86E-06	2,77E-08	1,59E-08	2,42E-08	1,44E-08	3,20E-07	2,77E-07
HOXB2	9,42E-07	3,11E-07	6,43E-05	2,95E-05	4,56E-05	2,71E-05	1,65E-04	7,60E-05
HOXB3	1,05E-06	8,35E-07	3,47E-03	8,53E-04	8,83E-05	3,09E-05	2,32E-03	3,10E-04
HOXB4	8,02E-06	2,96E-06	2,36E-03	4,16E-04	3,09E-05	3,53E-06	2,79E-03	6,05E-05
HOXB5	1,94E-05	4,29E-06	4,44E-03	1,23E-03	9,94E-08	3,35E-08	1,36E-03	1,56E-04
HOXB6	3,86E-07	3,28E-07	8,76E-04	2,51E-04	3,59E-08	2,49E-08	1,54E-04	8,92E-06
HOXB7	8,83E-05	2,63E-05	2,16E-02	1,10E-03	1,87E-04	1,84E-04	3,06E-02	5,88E-03
HOXB8	2,28E-05	9,75E-06	1,06E-03	2,97E-04	1,19E-06	1,55E-07	4,03E-04	9,49E-05
HOXB9	4,22E-06	3,64E-06	4,36E-07	2,14E-07	4,78E-10	1,73E-10	1,10E-05	1,86E-06
HOXB13	7,58E-07	6,20E-07	2,38E-07	1,76E-07	1,59E-09	6,07E-10	9,29E-07	4,78E-07
HOXC4	2,14E-05	4,95E-06	4,66E-03	1,30E-03	3,05E-06	1,40E-06	2,83E-04	2,95E-05
HOXC5	9,01E-07	7,35E-07	4,57E-03	7,07E-04	2,35E-06	7,70E-07	5,74E-05	1,17E-06
HOXC6	2,25E-04	4,51E-05	2,84E-02	1,50E-03	1,78E-04	1,68E-04	1,63E-03	1,91E-04
HOXC8	5,30E-06	1,38E-06	1,83E-02	3,01E-03	2,09E-06	1,99E-06	3,55E-04	5,77E-05
HOXC9	4,05E-07	2,77E-07	2,88E-03	2,52E-04	2,73E-06	2,64E-06	1,37E-03	2,75E-04
HOXC10	2,22E-05	7,38E-06	7,93E-04	1,79E-04	1,42E-06	9,13E-07	2,74E-04	4,39E-05
HOXC11	6,13E-07	4,05E-07	3,60E-04	3,19E-04	1,59E-08	1,18E-08	2,23E-09	1,51E-09
HOXC12	2,46E-06	7,14E-07	5,73E-08	2,88E-08	1,11E-07	5,44E-08	3,04E-08	1,04E-08
HOXC13	1,13E-05	2,18E-06	5,55E-06	1,47E-06	2,38E-06	6,26E-08	1,79E-06	4,58E-07
HOXD1	1,36E-05	1,82E-06	4,09E-05	2,66E-05	2,09E-06	1,23E-06	2,95E-03	3,01E-04
HOXD3	3,79E-06	3,27E-06	9,05E-05	2,77E-05	1,28E-05	3,19E-06	8,01E-05	1,54E-05
HOXD4	6,29E-07	3,91E-07	9,06E-04	3,62E-04	3,87E-05	2,28E-05	8,45E-04	3,08E-04
HOXD8	5,27E-05	1,89E-05	2,40E-03	6,12E-04	8,07E-06	4,20E-06	3,00E-03	6,47E-04
HOXD9	1,23E-05	3,95E-06	2,99E-05	3,90E-06	1,02E-05	1,60E-06	4,22E-05	2,25E-05
HOXD10	2,77E-07	6,74E-08	4,13E-04	4,13E-04	1,42E-05	1,42E-05	8,42E-08	7,23E-08
HOXD11	1,31E-08	9,23E-09	1,41E-08	6,14E-09	3,60E-09	1,57E-09	2,15E-08	1,11E-08
HOXD12	8,68E-07	4,12E-07	4,13E-08	2,39E-08	1,43E-08	8,51E-09	3,41E-07	2,76E-07
HOXD13	8,98E-06	3,32E-06	6,82E-08	3,59E-08	1,86E-08	1,50E-08	1,11E-06	1,29E-07

Supplementary Table S3 HOX target genes

For each probe set three (control, HOXC6, HOXB7) and two (HOXC8) Affymetrix® DNA chips were used. Upon siRNA treatment expression of 1666 genes were significantly affected by HOXC8 gene silencing, 1609 genes by HOXC6 and 2075 genes by silencing HOXB7. Comparing all three target genes, gene expression of 373 genes was significantly altered: 172 genes were up-regulated and 201 genes were down-regulated as compared to control VW-MPSCs.

Gene Title	Gene Symbol	Public ID	Fold Change		
			(C6/Con)	(B7/Con)	(C8/Con)
pregnancy specific beta-1-glycoprotein 5	PSG5	NM_002781	9.12	5.47	4.20
pregnancy specific beta-1-glycoprotein 6	PSG6	M31125	7.70	6.70	3.50
activating transcription factor 3	ATF3	NM_001674	6.74	11.34	2.91
myxovirus (influenza virus) resistance 1	MX1	NM_002462	6.30	7.29	4.29
hypothetical protein LOC387763	LOC387763	AW276078	5.39	10.19	4.11
histone cluster 1, H2bd	HIST1H2BD	AL353759	4.68	5.31	4.83
interferon, alpha-inducible protein 27	IFI27	NM_005532	4.58	4.78	3.50
histone cluster 2, H4a	HIST2H4A	NM_003548	4.56	8.26	4.68
histone cluster 2, H4a	HIST2H4A	AI828075	4.40	5.07	4.79
histone cluster 1, H2ac	HIST1H2AC	AL353759	4.10	4.60	4.76
epithelial stromal interaction 1 (breast)	EPSTI1	AA633203	3.98	4.18	2.29
growth differentiation factor 15	GDF15	AF003934	3.77	3.29	2.83
interferon, alpha-inducible protein 6	IFI6	NM_022873	3.63	3.62	3.21
R-spondin 3 homolog (Xenopus laevis)	RSPO3	BF589322	3.49	5.98	4.99
ISG15 ubiquitin-like modifier	ISG15	NM_005101	3.44	3.32	2.74
DNA-damage-inducible transcript 3	DDIT3	BC003637	3.38	5.66	2.45
histone cluster 1, H2bd	HIST1H2BD	BC002842	3.35	3.95	3.72
musculin (activated B-cell factor-1)	MSC	AF060154	3.31	5.98	2.55
zinc finger, DHHC-type containing 11	ZDHHC11	AF267859	3.27	2.15	2.63
interferon induced transmembrane protein 1 (9-27)	IFITM1	AA749101	3.27	3.38	2.22
histone cluster 1, H2bc	HIST1H2BC	AA037483	3.19	4.08	4.09
transmembrane emp24 protein transport domain	---	BF002074	3.12	4.24	3.80
interferon induced transmembrane protein pseudogen	---	AL121994	3.09	4.24	2.00
histone cluster 3, H2a	HIST3H2A	BC001193	3.06	3.67	3.00
solute carrier family 15, member 3	SLC15A3	NM_016582	3.03	7.32	2.47
EF-hand calcium binding domain 7	EFCAB7	AL109925	3.01	3.66	1.44
histone cluster 1, H2bc	HIST1H2BC	NM_003526	2.93	2.94	4.13
histone cluster 2, H2be	HIST2H2BE	NM_003528	2.93	3.41	3.60
DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	DDX60	NM_017631	2.86	3.38	1.86
histone cluster 1, H2bh	HIST1H2BH	NM_003524	2.73	3.29	2.66
histone cluster 2, H2aa3 /// histone cluster 2, H2aa4	HIST2H2AA3	NM_003516	2.73	3.44	3.54
thioredoxin interacting protein	TXNIP	NM_006472	2.68	4.75	3.06
interferon induced transmembrane protein 1 (9-27)	IFITM1	NM_003641	2.68	2.77	2.08
GPS, PLAT and transmembrane domain-containing protein	LOC399491	AA308853	2.65	2.35	2.61
activating transcription factor 5	ATF5	NM_012068	2.64	4.53	1.79
Epithelial stromal interaction 1 (breast)	EPSTI1	AA781795	2.60	3.51	1.66
ectonucleotide pyrophosphatase/phosphodiesterase 2	ENPP2	D45421	2.55	2.37	2.16
pleckstrin homology-like domain, family A, member 3	---	AI624156	2.54	2.72	2.26
dapper, antagonist of beta-catenin, homolog 1 (X. laevis)	DACT1	NM_016651	2.51	2.59	3.38
nuclear factor, interleukin 3 regulated	NFIL3	NM_005384	2.50	3.74	2.06
signal transducer and activator of transcription 1, 91kDa	STAT1	HUMISGF3A	2.47	2.79	1.88
delta/notch-like EGF repeat containing	DNER	BF059512	2.43	3.38	1.91
transcription factor EB	TFEB	AI524138	2.38	3.08	2.05
Kruppel-like factor 7 (ubiquitous)	KLF7	BC012919	2.35	2.23	1.96
hypothetical LOC220930	LOC220930	AK026657	2.35	2.31	2.67

tuftelin 1	TUFT1	NM_020127	2.31	2.55	2.93
polo-like kinase 2 (Drosophila)	PLK2	NM_006622	2.31	2.86	2.49
solute carrier family 3	SLC3A2	NM_002394	2.30	3.11	1.72
follistatin	FST	NM_013409	2.27	2.83	1.59
ectonucleotide pyrophosphatase/phosphodiesterase 2	ENPP2	L35594	2.27	2.12	2.05
WNT1 inducible signaling pathway protein 1 isoform 2		AA147884	2.27	1.72	1.70
pre		AA994712	2.26	2.88	2.40
coiled-coil domain containing 80	CCDC80	AA994712	2.26	2.88	2.40
potassium voltage-gated channel, Isk-related family	KCNE4	AI002715	2.26	3.66	2.11
histone cluster 1, H2bi	HIST1H2BI	NM_003525	2.25	2.41	2.61
histone cluster 1, H2be	HIST1H2BE	NM_003523	2.20	2.18	2.43
chromosome 6 open reading frame 145	C6orf145	AK024828	2.20	2.61	2.25
BTG family, member 2	BTG2	NM_006763	2.19	1.90	1.36
interferon-related developmental regulator 1	IFRD1	NM_001550	2.15	2.63	2.08
Cbp/p300-interacting transactivator	CITED2	NM_006079	2.13	2.34	1.67
OTU domain containing 1	OTUD1	AI934347	2.12	3.08	2.23
nuclear pore complex interacting protein	NPIP	NM_006985	2.10	1.83	2.16
limb bud and heart development homolog (mouse)	LBH	NM_030915	2.10	2.77	2.72
interferon-related developmental regulator 1	IFRD1	AA747426	2.09	2.70	2.18
transporter 2, ATP-binding cassette, sub-family B	TAP2	AA573502	2.09	2.84	1.85
regulator of calcineurin 1	RCAN1	NM_004414	2.08	3.29	3.44
potassium voltage-gated channel, Isk-related family	KCNE4	NM_080671	2.08	2.99	2.01
histone cluster 1, H2bk	HIST1H2BK	NM_017445	2.05	2.13	2.55
Cbp/p300-interacting transactivator	CITED2	AF109161	2.05	2.28	1.57
histone cluster 1, H1c	HIST1H1C	BC002649	2.05	3.26	3.32
vestigial like 3 (Drosophila)	VGLL3	AI754423	2.02	2.28	1.90
immediate early response 3	IER3	NM_003897	2.01	2.94	2.36
transmembrane protein 200B	TMEM200B	N63821	2.01	2.84	1.80
insulin receptor substrate 2	IRS2	AF073310	2.01	2.82	1.74
sarcoglycan, gamma	SGCG	NM_000231	2.00	2.25	2.72
mitogen-activated protein kinase kinase kinase 8	MAP3K8	NM_005204	1.97	2.91	2.53
lectin, galactoside-binding, soluble, 3 binding protein	LGALS3BP	NM_005567	1.97	2.60	1.73
transgelin	TAGLN	NM_003186	1.95	1.49	2.00
fibroblast growth factor 7 (keratinocyte growth factor)	FGF7	AF523265	1.95	2.20	1.65
hypothetical protein LOC100288911	LOC100288911	AW014647	1.95	1.62	2.01
chromosome 9 open reading frame 150	C9orf150	AI972386	1.93	2.08	1.59
follistatin	FST	NM_006350	1.92	2.27	1.42
EPH receptor A4	EPHA4	AI799018	1.92	1.68	1.75
esterase D/formylglutathione hydrolase		AI379882	1.92	1.83	1.89
histone cluster 1, H2bk	HIST1H2BK	BC000893	1.90	2.04	2.21
MAP kinase interacting serine/threonine kinase 2	MKNK2	NM_017572	1.89	1.61	1.35
solute carrier family 6 (neurotransmitter transporter)	SLC6A8	NM_005629	1.89	1.85	2.36
lysophospholipase-like 1	LYPLAL1	AI953360	1.89	1.90	1.68
hypothetical LOC100288442	LOC100288442	AC002045	1.88	1.66	1.94
follistatin	FST	BF438173	1.87	2.41	1.46
inhibitor of DNA binding 4, dominant negative hIh protein	ID4	AW157094	1.86	3.59	1.64
WNT1 inducible signaling pathway protein 2	WISP2	NM_003881	1.84	2.91	1.45
dolichyl-phosphate mannosyltransferase polypeptide 1	Align!	AI733139	1.84	1.82	1.88
v-ets erythroblastosis virus E26 oncogene homolog (avian)	ERG	AI351043	1.81	1.71	1.52
SH3 domain binding glutamic acid-rich protein	SH3BGR	NM_007341	1.81	2.26	1.95
A kinase (PRKA) anchor protein 8-like	AKAP8L	NM_014371	1.80	1.97	1.53
follistatin-like 3 (secreted glycoprotein)	FSTL3	NM_005860	1.79	2.69	2.40
hypothetical protein LOC339047	LOC339047	AF229069	1.79	1.51	1.85
histone cluster 1, H2bf	HIST1H2BF	NM_003522	1.78	2.24	2.28
SCO cytochrome oxidase deficient homolog 2 (yeast)	SCO2	NM_005138	1.77	2.98	1.62
filamin A interacting protein 1-like	FILIP1L	AF329092	1.76	2.97	2.08
solute carrier family 16, member 3	SLC16A3	NM_004207	1.74	2.05	2.22
SH3-containing protein SH3GLB1		AA804585	1.73	1.74	1.97
ankyrin repeat and SOCS box-containing 5	ASB5	BF589787	1.72	1.91	2.00

fin bud initiation factor homolog (zebrafish)	FIBIN	AI802391	1.72	2.49	2.45
ring finger protein 19B	RNF19B	AL031602	1.72	2.76	1.83
Kruppel-like factor 7 (ubiquitous)	KLF7	AA488672	1.71	1.87	1.55
nuclear factor of activated T-cells, cytoplasmic	NFATC4	AI806528	1.71	2.30	1.74
signal-regulatory protein alpha	SIRPA	AB023430	1.70	2.46	1.72
CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3	AL136842	1.70	1.57	2.03
sorbin and SH3 domain containing 2	SORBS2	AI659533	1.69	2.25	2.17
vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR	AA772285	1.66	1.69	1.91
TSC22 domain family, member 3	TSC22D3	AL110191	1.64	1.48	1.75
hypothetical protein XP_002343017	---	AI916303	1.64	2.58	1.29
filamin A interacting protein 1-like	FILIP1L	NM_014890	1.64	2.46	1.83
EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	NM_004105	1.63	2.31	2.05
regulator of chromosome condensation (RCC1)	RCBTB2	NM_001268	1.61	1.57	1.53
inhibitor of DNA binding 3, dominant negative hlh protein	ID3	NM_002167	1.61	1.64	1.42
steroid-sensitive protein 1	---	AI088063	1.61	2.81	2.07
solute carrier family 19 (thiamine transporter), member 2	SLC19A2	AF153330	1.59	1.47	1.41
EGF-containing fibulin-like extracellular matrix protein 1	EFEMP1	AI826799	1.59	1.88	1.54
cysteine-rich, angiogenic inducer, 61	CYR61	AF003114	1.58	1.54	1.66
ring finger protein 19B	RNF19B	W27419	1.57	2.30	1.78
acid phosphatase-like 2	ACPL2	AW069729	1.57	1.88	1.36
fibronectin leucine rich transmembrane protein 2	FLRT2	NM_013231	1.57	1.39	1.42
tigger transposable element derived 7	TIGD7	AF251050	1.56	2.20	1.91
zinc finger protein 697	ZNF697	AW003092	1.55	1.45	1.41
hypothetical protein XP_002344302	---	BF691045	1.55	1.89	1.59
hypothetical gene supported by AK095117	FLJ37798	AI806330	1.54	1.75	1.67
cryptochrome 1 (photolyase-like)	CRY1	D83702	1.53	1.86	1.49
polycystic kidney disease 2 (autosomal dominant)	PKD2	NM_000297	1.53	1.58	1.52
v-abl Abelson murine leukemia viral oncogene homolog 2	ABL2	AW173164	1.53	1.99	1.05
RAB23, member RAS oncogene family	RAB23	NM_016277	1.52	1.52	1.82
vacuolar protein sorting 37 homolog A (S. cerevisiae)	VPS37A	AI866426	1.52	1.47	1.48
syntaxin 12	STX12	AI816243	1.50	1.63	1.48
protein phosphatase 1, regulatory (inhibitor) subunit 13 like	PPP1R13L	NM_006663	1.50	1.36	1.42
solute carrier family 7 (cationic amino acid transporter)	SLC7A5	AB018009	1.50	2.03	1.56
chromosome 21 open reading frame 91	C21orf91	AK023825	1.47	1.47	1.43
LIM domain only 4	LMO4	BC003600	1.47	1.35	1.55
RING1 and YY1 binding protein	RYBP	NM_012234	1.47	1.53	1.82
LATS, large tumor suppressor, homolog 2 (Drosophila)	LATS2	AI535735	1.47	1.51	1.39
serpin peptidase inhibitor, clade I (neuroserpin), member 1	SERPINI1	NM_005025	1.46	2.10	1.57
solute carrier family 16, member 3	SLC16A3	AL513917	1.46	1.73	2.04
protein phosphatase 1, regulatory (inhibitor) subunit 2	PPP1R2	NM_006241	1.46	1.42	1.38
chromosome 7 open reading frame 70	C7orf70	BC006110	1.45	1.48	1.50
regulator of chromosome condensation 2	RCC2	AB040903	1.44	1.53	1.28
jub, ajuba homolog (Xenopus laevis)	JUB	AK025567	1.43	1.49	1.79
spire homolog 1 (Drosophila)	SPIRE1	AJ277587	1.43	1.21	1.27
nuclear receptor subfamily 3, group C, member 1	NR3C1	X03348	1.43	1.47	1.27
spermatogenesis associated 18 homolog (rat)	SPATA18	AI559300	1.42	1.51	1.40
RING1 and YY1 binding protein	RYBP	AB029551	1.42	1.83	1.74
hypothetical protein MGC9913	MGC9913	BE855713	1.40	1.37	1.39
UBA domain containing 2	UBAC2	BC004528	1.39	1.52	1.31
choline phosphotransferase 1	CHPT1	AF195624	1.39	1.46	1.42
chromosome 4 open reading frame 18	C4orf18	NM_016613	1.37	2.02	1.89
MAX interactor 1	MXI1	NM_005962	1.37	1.34	1.35
CDC42 effector protein (Rho GTPase binding) 3	CDC42EP3	AI754416	1.36	1.38	1.81
lysophospholipase-like 1	LYPLAL1	AW612657	1.36	1.72	1.36
TP53 regulated inhibitor of apoptosis 1	TRIAP1	NM_016399	1.34	1.47	0.72
PHD finger protein 17	PHF17	AV646599	1.34	1.45	1.44
chromosome 4 open reading frame 18	C4orf18	AF260333	1.33	1.58	1.40

La ribonucleoprotein domain family, member 6	LARP6	NM_018357	1.33	1.57	1.42
hypothetical protein MGC9913	MGC9913	BE855713	1.32	1.40	1.40
ring finger protein 135	RNF135	BC005084	1.32	1.49	1.37
xenotropic and polytropic retrovirus receptor	XPR1	AF089744	1.31	1.39	1.44
FOS-like antigen 2	FOSL2	AI670862	1.30	1.55	1.57
vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR	NM_000376	1.30	1.47	1.33
taurine upregulated 1 (non-protein coding)	TUG1	AI687738	1.29	1.31	1.29
taurine upregulated 1 (non-protein coding)	TUG1	N37081	1.27	1.38	1.24
DPH3, KTI11 homolog (S. cerevisiae)	DPH3	AU151106	1.26	1.40	1.31
zinc finger protein 532	ZNF532	NM_018181	1.25	1.33	1.36
GLI pathogenesis-related 2	GLIPR2	H92988	1.25	1.38	1.90
adenylate cyclase 9	ADCY9	AB011092	1.13	1.08	1.27
protein tyrosine phosphatase, non-receptor type 14	---	AW129783	0.81	0.71	0.78
UDP-N-acetyl-alpha-D-galactosamine:polypeptide GalNAc	GALNT1	BC038440	0.80	0.60	0.70
ADP-ribosylation-like factor 6 interacting protein 5	ARL6IP5	N92494	0.79	0.73	0.72
recombination signal binding protein for ig kappa J region	RBPJ	NM_015874	0.79	0.65	0.71
diazepam binding inhibitor	DBI	NM_020548	0.77	0.69	0.58
proteolipid protein 2 (colonic epithelium-enriched)	PLP2	NM_002668	0.77	0.64	0.73
acyl-CoA synthetase short-chain family member 3	ACSS3	NM_024560	0.77	0.54	0.58
splicing factor, arginine/serine-rich 2	SFRS2	NM_003016	0.76	0.66	0.80
mesencephalic astrocyte-derived neurotrophic factor	MANF	NM_006010	0.76	0.73	0.74
zinc finger protein 207	ZNF207	BE871379	0.76	0.69	0.78
diazepam binding inhibitor	DBI	BC006466	0.75	0.62	0.52
diazepam binding inhibitor	DBI	M15887	0.75	0.62	0.50
KDEL (Lys-Asp-Glu-Leu) ER protein retention receptor 3	KDELR3	NM_006855	0.74	0.64	0.60
splicing factor proline/glutamine-rich	SFPQ	BG035151	0.74	0.54	0.72
myeloid/lymphoid or mixed-lineage leukemia 5	MLL5	AW082219	0.73	0.68	0.73
KH domain containing, RNA binding	KHDRBS1	BC000717	0.73	0.59	0.72
mitogen-activated protein kinase kinase kinase 4	MAP4K4	NM_017792	0.73	0.57	0.65
small nuclear ribonucleoprotein polypeptide A'	SNRPA1	NM_003090	0.73	0.76	0.71
discoidin, CUB and LCCL domain containing 2	DCBLD2	AI378788	0.73	0.31	0.30
retinol dehydrogenase 11 (all-trans/9-cis/11-cis)	RDH11	AF167438	0.73	0.67	0.83
synaptophysin-like 1	SYPL1	AI768845	0.72	0.63	0.68
protein tyrosine phosphatase-like A domain containing 1	PTPLAD1	NM_016395	0.72	0.59	0.73
sperm associated antigen 9	SPAG9	AK023512	0.71	0.60	0.68
heterogeneous nuclear ribonucleoprotein A	HNRNPA3	BG505670	0.71	0.63	0.82
thyroid hormone receptor associated protein 3	THRAP3	BE967048	0.71	0.52	0.54
discoidin, CUB and LCCL domain containing 2	DCBLD2	AA722799	0.71	0.55	0.48
deoxyribonuclease I-like 1	DNASE1L1	NM_006730	0.70	0.58	0.74
splicing factor, arginine/serine-rich 2	SFRS2	BG254869	0.69	0.63	0.77
mitogen-activated protein kinase kinase kinase 4	MAP4K4	NM_004834	0.69	0.55	0.64
sec1 family domain containing 2	SCFD2	AW205790	0.69	0.50	0.62
emopamil binding protein (sterol isomerase)	EBP	AV702405	0.68	0.51	0.65
Zwilch, kinetochore associated, homolog (Drosophila)	ZWILCH	AA824298	0.68	0.58	0.77
5'-nucleotidase domain containing 1	NT5DC1	AL515061	0.68	0.55	0.72
Rab interacting lysosomal protein-like 2	RILPL2	AI810244	0.67	0.51	0.51
neurotensin receptor 1 (high affinity)	NTSR1	NM_002531	0.67	0.38	0.50
synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP	AI472757	0.67	0.53	0.65
splicing factor, arginine/serine-rich 2	SFRS2	BE866585	0.67	0.59	0.71
hydroxyacyl-Co A dehydrogenase/3-ketoacyl-Co A thiolase	HADHA	BG472176	0.66	0.59	0.65
centrosomal protein 170kDa	CEP170	NM_014812	0.66	0.60	0.72
RAN binding protein 1	RANBP1	NM_002882	0.66	0.62	0.76
MOB1, Mps One Binder kinase activator-like 1B (yeast)	MOBK1B	NM_018221	0.66	0.61	0.44
Ankyrin repeat domain 12	ANKRD12	X80821	0.66	0.40	0.55
tissue factor pathway inhibitor	TFPI	BF511231	0.66	0.56	0.55
low density lipoprotein receptor-related protein 8	LRP8	NM_004631	0.66	0.46	0.50
signal peptide, CUB domain, EGF-like 3	SCUBE3	AI733234	0.65	0.22	0.27

mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	AL561281	0.65	0.47	0.49
peptidylprolyl isomerase (cyclophilin)-like 5	PPIL5	AA742244	0.65	0.67	0.61
lysophospholipase I	LYPLA1	AF077198	0.65	0.64	0.70
maternally expressed 3 (non-protein coding)	MEG3	AI291123	0.65	0.47	0.61
deoxyuridine triphosphatase	DUT	U62891	0.64	0.68	0.61
protocadherin 7	PCDH7	NM_002589	0.64	0.40	0.30
5'-nucleotidase domain containing 1	NT5DC1	AF245044	0.64	0.50	0.52
CHK1 checkpoint homolog (S. pombe)	CHEK1	AA224205	0.64	0.53	0.60
forkhead box C2/forkhead box L1	---	BF446723	0.64	0.35	0.38
methyltransferase like 9	METTL9	BC000195	0.64	0.70	0.61
ER degradation enhancer, mannosidase alpha-like 3	EDEM3	BF439488	0.63	0.46	0.58
cell division cycle 42 (GTP binding protein, 25kDa)	CDC42	BC002711	0.63	0.49	0.54
mitogen-activated protein kinase kinase kinase kinase 4	MAP4K4	AL561281	0.62	0.43	0.51
ST3 beta-galactoside alpha-2,3-sialyltransferase 5	ST3GAL5	NM_003896	0.62	0.28	0.59
DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9	AW241779	0.62	0.59	0.70
replication protein A3, 14kDa	RPA3	BC005264	0.62	0.65	0.68
heat shock protein 90kDa beta (Grp94), member 1	HSP90B1	AI582238	0.61	0.47	0.45
cAMP-regulated phosphoprotein, 19kDa	ARPP19	AF084555	0.61	0.72	0.79
endothelin receptor type B	EDNRB	M74921	0.61	0.36	0.31
G protein-coupled receptor 56	GPR56	AL554008	0.61	0.37	0.43
topoisomerase (DNA) I	TOP1	AW025108	0.61	0.45	0.46
CHK1 checkpoint homolog (S. pombe)	CHEK1	NM_001274	0.61	0.56	0.60
PHD finger protein 19	PHF19	BE544837	0.61	0.52	0.54
pleckstrin homology-like domain, family A, member 1	PHLDA1	AK026181	0.61	0.59	0.65
protocadherin 7	PCDH7	NM_002589	0.61	0.45	0.39
PTPRF interacting protein, binding protein 1 (liprin beta 1)	PPFIBP1	AI962377	0.60	0.65	0.53
HECT domain containing 1	HECTD1	BE243270	0.60	0.43	0.43
acidic (leucine-rich) nuclear phosphoprotein 32 family phosphatidic acid phosphatase type 2 domain containing 1B	ANP32E	AW612574	0.60	0.59	0.61
thymidylate synthetase	PPAPDC1B	BF111651	0.60	0.52	0.64
NudE nuclear distribution gene E homolog 1 (A. nidulans)	TYMS	NM_001071	0.60	0.61	0.53
KDEL (Lys-Asp-Glu-Leu) ER protein retention receptor 3	NDE1	AI857685	0.60	0.53	0.57
centrosomal protein 170kDa	KDELR3	NM_016657	0.60	0.52	0.56
heat shock 60kDa protein 1 (chaperonin)	CEP170	AA126789	0.60	0.46	0.67
interleukin enhancer binding factor 3, 90kDa	HSPD1	BE256479	0.60	0.58	0.81
sialic acid binding Ig-like lectin 15	ILF3	AF147209	0.60	0.67	0.69
PSMC3 interacting protein	SIGLEC15	AK025833	0.59	0.40	0.51
high mobility group AT-hook 2	PSMC3IP	BE964655	0.59	0.71	0.66
N-methylpurine-DNA glycosylase	HMGA2	NM_003483	0.59	0.29	0.50
SH2B adaptor protein 3	MPG	NM_002434	0.59	0.56	0.63
cell division cycle 27 homolog (S. cerevisiae)	SH2B3	NM_005475	0.58	0.40	0.47
major facilitator superfamily domain containing 6	CDC27	AI203880	0.58	0.67	0.71
cyclin-dependent kinase 2	MFSD6	AA133311	0.58	0.56	0.37
low density lipoprotein receptor-related protein 8 isoform	CDK2	M68520	0.58	0.53	0.71
small nuclear ribonucleoprotein polypeptide F		AL041761	0.58	0.40	0.62
BCL2-associated transcription factor 1	SNRPF	NM_003095	0.57	0.51	0.67
ribonucleotide reductase M1	BCLAF1	BE963370	0.57	0.48	0.70
deoxyuridine triphosphatase	RRM1	NM_001033	0.57	0.56	0.55
high-mobility group box 1	DUT	U90223	0.57	0.63	0.54
structural maintenance of chromosomes 3	HMGB1	BE311760	0.57	0.48	0.62
ankylosis, progressive homolog (mouse)	SMC3	AI373676	0.57	0.52	0.61
minichromosome maintenance complex component 4	ANKH	AA854943	0.57	0.46	0.62
family with sequence similarity 114, member A1	MCM4	AI859865	0.56	0.52	0.62
integrin beta 3 binding protein (beta3-endonexin)	FAM114A1	AI742174	0.56	0.44	0.60
collagen, type XXVIII precursor	ITGB3BP	NM_014288	0.56	0.61	0.53
deoxyuridine triphosphatase	Align!	AU156755	0.55	0.39	0.37
minichromosome maintenance complex component 5	DUT	AB049113	0.55	0.47	0.46
	MCM5	AA807529	0.55	0.43	0.56

phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	NM_012417	0.55	0.64	0.52
small VCP/p97-interacting protein	SVIP	AI150224	0.54	0.44	0.42
alpha thalassemia/mental retardation syndrome X-linked	ATRX	AI650257	0.54	0.42	0.59
TPX2, microtubule-associated, homolog (Xenopus laevis)	TPX2	AF098158	0.53	0.33	0.48
sparc/osteonectin, cwcv and kazal-like domains proteoglycan	SPOCK3	AI808090	0.53	0.35	0.54
prostaglandin F receptor (FP)	PTGFR	BC035694	0.53	0.52	0.32
thymidylate synthetase	TYMS	AB077208	0.53	0.49	0.57
WW domain containing transcription regulator 1	WWTR1	AA081084	0.53	0.41	0.59
DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9	BE551340	0.52	0.54	0.72
ankylosis, progressive homolog (mouse)	ANKH	T99215	0.52	0.40	0.52
kinesin family member 20A	KIF20A	NM_005733	0.52	0.36	0.53
leukemia inhibitory factor receptor alpha	LIFR	AI680541	0.52	0.43	0.44
cell division cycle 6 homolog (S. cerevisiae)	CDC6	NM_001254	0.52	0.45	0.45
CCCTC-binding factor (zinc finger protein)-like	CTCF	AC007277	0.52	0.44	0.61
ribonucleotide reductase M1	RRM1	AI692974	0.51	0.42	0.53
Norrie disease (pseudoglioma)	NDP	NM_000266	0.51	0.40	0.58
embigin homolog (mouse)	EMB	W84421	0.51	0.24	0.41
polymerase (DNA directed), epsilon 2 (p59 subunit)	POLE2	NM_002692	0.51	0.40	0.50
pituitary tumor-transforming 1	PTTG1	NM_004219	0.51	0.40	0.53
low density lipoprotein receptor-related protein 8	LRP8	NM_017522	0.51	0.42	0.43
thymidine kinase 1, soluble	TK1	BC007986	0.51	0.29	0.43
ventricular zone expressed PH domain homolog 1 (zebrafish)	VEPH1	AK022666	0.51	0.50	0.39
protein tyrosine phosphatase-like A domain containing 2	PTPLAD2	AI804932	0.50	0.51	0.49
cell division cycle associated 7-like	CDCA7L	AK022955	0.50	0.42	0.65
CHK1 checkpoint homolog (S. pombe)	CHEK1	NM_001274	0.50	0.47	0.43
Rac GTPase activating protein 1	RACGAP1	AU153848	0.50	0.39	0.49
structural maintenance of chromosomes 3	SMC3	BF795297	0.50	0.39	0.54
secreted frizzled-related protein 1	SFRP1	NM_003012	0.49	0.53	0.35
tetratricopeptide repeat domain 3	TTC3	AI652848	0.49	0.40	0.59
maternal embryonic leucine zipper kinase	MELK	NM_014791	0.49	0.50	0.53
transcription factor 19	TCF19	BC002493	0.48	0.42	0.52
ephrin-A5	EFNA5	BE464799	0.47	0.36	0.43
forkhead box M1	FOXM1	NM_021953	0.47	0.36	0.47
prostaglandin F receptor (FP)	PTGFR	NM_000959	0.47	0.56	0.28
centromere protein H	CENPH	AL572471	0.46	0.45	0.56
Fanconi anemia, complementation group I	FANCI	W74442	0.45	0.37	0.48
family with sequence similarity 64, member A	FAM64A	BC005004	0.45	0.34	0.37
protein regulator of cytokinesis 1	PRC1	NM_003981	0.45	0.30	0.40
cyclin-dependent kinase inhibitor 3	CDKN3	AF213033	0.45	0.24	0.41
sushi, nidogen and EGF-like domains 1	SNED1	BF509657	0.45	0.33	0.53
BRCA1 interacting protein C-terminal helicase 1	---	BF056791	0.45	0.47	0.43
ATPase family, AAA domain containing 2	ATAD2	NM_014109	0.45	0.34	0.56
gamma-glutamyl carboxylase	GGCX	BE326952	0.44	0.57	0.58
spindlin family, member 4	SPIN4	AU145277	0.44	0.45	0.53
hedgehog interacting protein	HHIP	AK098525	0.44	0.12	0.29
family with sequence similarity 54, member A	FAM54A	AL138828	0.44	0.32	0.48
leukemia inhibitory factor receptor alpha	LIFR	AA701657	0.43	0.33	0.46
ankylosis, progressive homolog (mouse)	ANKH	NM_019847	0.43	0.34	0.50
potassium channel tetramerisation domain containing 12	KCTD12	AA551075	0.43	0.20	0.54
DEP domain containing 1	DEPDC1	AI810054	0.43	0.26	0.41
minichromosome maintenance complex component 6	MCM6	NM_005915	0.43	0.44	0.44
transcription factor Dp-1	TFDP1	AI950069	0.42	0.57	0.61
secreted frizzled-related protein 1	SFRP1	AF017987	0.42	0.35	0.22
centromere protein N	CENPN	NM_018455	0.42	0.35	0.41
cell division cycle 6 homolog (S. cerevisiae)	CDC6	U77949	0.42	0.36	0.43
kinesin family member 4A	KIF4A	NM_012310	0.41	0.26	0.35
Transmembrane protein 49	TMEM49	AV660825	0.40	0.35	0.50

solute carrier family 14 (urea transporter), member 1	SLC14A1	BE673587	0.40	0.25	0.52
RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51	NM_002875	0.40	0.41	0.61
cyclin-dependent kinase inhibitor 3	CDKN3	AF213040	0.40	0.25	0.39
proline rich 11	---	BG165011	0.39	0.29	0.34
Opa interacting protein 5	OIP5	BE045993	0.39	0.24	0.37
anillin, actin binding protein	ANLN	NM_018685	0.39	0.27	0.46
baculoviral IAP repeat-containing 5	BIRC5	AB028869	0.39	0.30	0.43
anillin, actin binding protein	ANLN	AK023208	0.39	0.26	0.40
WD repeat domain 76	WDR76	NM_024908	0.39	0.39	0.39
EPH receptor A7	EPHA7	AA651750	0.38	0.27	0.42
apolipoprotein B mRNA editing enzyme	APOBEC3B	NM_004900	0.38	0.27	0.34
ribosomal protein L22-like 1	RPL22L1	BE274422	0.37	0.50	0.50
ATPase family, AAA domain containing 2	ATAD2	AI656807	0.37	0.31	0.52
pleckstrin homology domain containing, family O member 1		AI697657	0.37	0.31	0.48
zinc finger protein 367	ZNF367	N62196	0.37	0.24	0.37
SHC SH2-domain binding protein 1	SHCBP1	NM_024745	0.37	0.26	0.39
centrosomal protein 55kDa	CEP55	NM_018131	0.37	0.25	0.44
centromere protein K	CENPK	BC005400	0.36	0.35	0.35
denticleless homolog (Drosophila)	DTL	AK001261	0.36	0.23	0.43
ATPase family, AAA domain containing 2	ATAD2	AI925583	0.35	0.34	0.45
baculoviral IAP repeat-containing 5	BIRC5	NM_001168	0.34	0.24	0.38
discs, large (Drosophila) homolog-associated protein 5	DLGAP5	NM_014750	0.34	0.24	0.33
neuronal pentraxin I	NPTX1	NM_002522	0.33	0.50	0.39
minichromosome maintenance complex component 10	MCM10	NM_018518	0.33	0.34	0.52
solute carrier family 14 (urea transporter), member 1	SLC14A1	NM_015865	0.33	0.24	0.50
ubiquitin-like with PHD and ring finger domains 1	UHRF1	AK025578	0.33	0.30	0.47
secreted frizzled-related protein 1	SFRP1	AI332407	0.32	0.26	0.23
KIAA0101	KIAA0101	NM_014736	0.32	0.28	0.41
non-SMC condensin I complex, subunit G	NCAPG	NM_022346	0.32	0.27	0.38
GIN5 complex subunit 2 (Psf2 homolog)	GIN52	BC003186	0.30	0.31	0.37
non-SMC condensin I complex, subunit G	NCAPG	NM_022346	0.30	0.29	0.37
hypothetical protein	Align!	AI825833	0.29	0.42	0.56
hyaluronan-mediated motility receptor (RHAMM)	HMMR	NM_012485	0.29	0.22	0.30
nucleolar and spindle associated protein 1	NUSAP1	NM_018454	0.29	0.15	0.27
denticleless homolog (Drosophila)	DTL	NM_016448	0.28	0.22	0.36
topoisomerase (DNA) II alpha 170kDa	TOP2A	AU159942	0.28	0.18	0.33
PDZ binding kinase	PBK	NM_018492	0.28	0.26	0.42
thymosin beta 15a	TMSB15A	NM_021992	0.26	0.15	0.32
ribonucleotide reductase M2	RRM2	BE966236	0.25	0.30	0.45
ribonucleotide reductase M2	RRM2	BC001886	0.25	0.21	0.38
hepatocyte growth factor (hepapoietin A; scatter factor)	HGF	X16323	0.20	0.32	0.31
6720455I24Rik homolog	---	AA808178	0.14	0.03	0.20