

## Appendix 1A

Sequences of primer pairs used in qPCR to analyse expression of the SCL complex during siRNA knockdown assays

Gene	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
GATA1	CAAGCTACACCAGGTGAACCG	AGCTGGTCCTTCGGCTGC
SCL	TTTTGTGAAGACGGCACGG	TGAGAGCTGACAACCCCAGG
E12	CAACTGCACCTCAACAGCGAG	GCCGTTTCAAACAGGCTGC
E47	AGGTGCTGTCCCTGGAGGAG	CCGACTTGAGGTGCATCTGG
LDB1	CCAGCTAGCACCTTCGCC	GTCGTCAATGCCGTTGGC
LMO2	CGGCGCCTCTACTACAAACTG	CATTCATAGGCACGAATCCG

## Appendix 1B

Sequences of primer pairs used in qPCR to analyse expression of housekeeping genes during siRNA knockdown assays

Gene	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
β-actin	AGAAGGAGATCACTGCCCTGG	CACATCTGCTGGAAGGTGGAC
GAPDH	AGGTCCACCACTGACACGTTG	AGCTGAACGGGAAGCTCACT
RPL16	GGCTTGCCCTCTAGTGTCTC	CTGATCTGCTGACGGGAGTT
β-tubulin	GCAGATGCTTAACGTGCAGA	CAATGAAGGTGACTGCCATC

## Appendix 1C

Sequences of primer pairs used in qPCR to analyse expression of ChIP-on-chip target genes during time-course siRNA knockdown assays

Gene	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
BRD2	TAGGCCCTTCTGGCTTTGGA	CATGGGCCTGCTCTCTTCCT
CTCFL	AAGCTGCGAAGGGATGGAAG	TCTCTGCAGGCGACAGGAAA
EKLF	CACCAAGAGCTCCCACCTGA	CCCCGTGTGTTTCCGGTAGT
EPOR	CGAGCCCAGAGAGCGAGTTT	AGGACTTCCAGGGAAGCAGGT
ETO2	CGGTCATCAACCAGCAGGAG	CTTCTCCCAGTCCCGATGCT
EZH2	TGGGAAAGTACACGGGGATA	CAGGATCGTCTCCATCATCA
FBXL10	AGCAGACAGAAGCCACGAAC	TGTGGAAGTCGGTGAAACAA
JMJD2C	TGACTGGCCTTATGTGGTGA	GTTTGACCCACGGAAATGAC

LMO2	CGGCGCCTCTACTACAACTG	CATCTCATAGGCACGAATCCG
LYL1	CATCTTCCCTAGCAGCCGTTG	GTTGGTGAACACGCGCCG
PCQAP	AAGCCCCTGTGGATAGACC	GTGTTGAGCAAGGCGGTGAC
RSF1	AAGGCGAGTACACAAGCGAAGA	GCTTTCGAACTGACCGCTTTG
SCL	TTTTGTGAAGACGGCACGG	TGAGAGCTGACAACCCAGG
SMARCA5	AAGGCAGAGAAAAAGAAACGAGGA	TTTCTCCTCGACCATCAGGTG

## Appendix 1D

Sequences of primer pairs used in ChIP-qPCR to analyse enrichments of ChIP-on-chip target genes

Region name	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
BRD2	GGTTCACGGCACGGAGAGAT	AGGGAGTTTCTCGCCCTCGT
CTCFL	GGGTTGAAGTGGATGAGGAA	CCAGTATCTCAGTGCCTCCTG
EKLF (1)	TGCAACCCCTTCTCCCTGT	GCGGCAAGAGCTACACCAAG
EKLF (2)	GGCTGCCTCGTGAAGTCTGA	GGCCAACGTGAAGTTTGTGC
EPOR	GGGACGCGATCAGGAGTCTT	GCCATGCCTGTTTCTGGACTT
ETO2	CAGGCTGGGGAAGGTCTCC	GGCCCCAGATGGTTCTGT
EZH2 (1)	GGGGAAGTGGTTCCAGGACA	TCTTATATCCCAGGAAGCCAGGTA
EZH2 (2)	GAGAGGAAAGGAGAAATTGTTCAATGTT	GTGTTTTTGTATTATTTGAATGTGGGAAAC
EZH2 (3)	GAGTCCTGAGGCCAATGGGTA	TTCGCCCTTTGTTACAGCTC
FBXL10	GCGCTGGGTCACACAGTACA	CGCCCTCTGGAAACTGACCT
JMJD2C (1)	CTTCCGGGCAAGGTTCTGTG	CGCGCTGTGGTTAACTTAGGC
JMJD2C (2)	CCCGTTAGCCTTAGCTCAATTAATCA	TTGGGCTAATATGCTGAATTTTCTGTT
JMJD2C (3)	CTCGACGGGAGGGTGAGG	TTGGGAGACTTGTTCGCACT
LMO2 (1)	TGGGCTAATTGCTGCTTTG	CCTGCCCTCAGCCGTTAAGT
LMO2 (2)	CACTGGAGCCAATGAGGGAAG	GCAGACTTCCGACTGGCAGA
LYL1 (1)	CCCGGTTTCTCCCTCTCAC	TGGTTTCTCCGGGGTCAG
LYL1 (2)	GGGCCTCAGGGCAGGAAG	GTAGCCCCACGIGTCTTCG
LYL1 +33 region	GGGCCTGCGAACAGGAGATA	CCTCGTGGCTGCTCTGCTTT
PCQAP (1)	GGGGTCTGGATCTCAGGGACTA	ACACACGCCCTCTTCCAGT
PCQAP (2)	AAAATTAGCTGGGCTTCGTAGCAG	TGTTGCCAGACTGGAGTGC
PCQAP (3)	CTCCTGAGGCCCATGTTGGT	AGTTCTGCCTCCTTGGAAGTATGG
PCQAP (4)	CCTCACCACCGACTGCTTGT	TTTTCGGACTCAGCCCACCT
RSF1	CAGCGGCACCAGAGAGAGAA	GTCGTCTCCCTCCCATTTGC
SCL (Promoter 1a)	CGCCGCAGAGATAAGGCACT	CCCACTCCCTCCGGTGAAT

SCL +51 enhancer	TGACCTTACAGCCCTTCACCC	AGCTCCCTGCTCCCAGCAC
SMARCA5 (1)	TTCTTCTTCCCGGTCCTTGC	GGGCCTTCTCTCCCTTCACA
SMARCA5 (2)	TCAACTCTCGAAAAATGTGTCTCCTT	TGTAGTCTGTTTGATAACGAATCTGCAT
SMARCA5 (3)	AAGTCGGTGGCGTAGGTCGT	GTTGGGGGAAGGGAAAAGGA

## Appendix 1E

### Sequences of primer pairs for the negative control regions used in ChIP-qPCR

Region name	Amplicon name	Forward primer sequences (5'→3')	Reverse primer sequences (5'→3')
NC i	HSSIL/M10Aq	TCTCTTTGAACACAGGGCAATG	TATTAGTCTAGGTGTACTGGCAGTTG
NC ii	HSSIL/M51Bq	TGAATGCTTCCCTTGTGATG	GTAATGTTTCCTTACTGGTTAGCAAC
NC iii	HSSCL/M15Bq	GTGCCCTTGAGAGCCTAGGG	CCTCAACAGCCTGTCTTATAATTG
NC iv	HSTAL.138q	CATCACCTGCAAAAATGGAGG	TAAGCTGAGGCAGGCATTGTC
NC v	HSTAL.108q	GGATTGAGGAGAGGGCATGTG	GCACGGCTGTGGAGCTATG
NC vi	HSTAL.106q	CAGCAGAGGTCCCAAAGCC	CAGTACTCCCAGCTTGCTTCC
NC vii	HSTAL.77q	TTCTGTACCTGCCAGCCAAG	CCCGACGAGCGTTATGTAAG
NC viii	HSSIL/M55Aq	TCATGATGATATTTAGCATACTCAGCAAAG	GGAGAATGATAACTTGTGTCAGGC
NC ix	HSSCL/M137Aq	TCTCTGGAAGTCATAAATAACA	AATCTGCTCATCAAGTAATACG
NC x	HSSCL/M182Aq	TTTGCAGTGCCCTGTTCTTAG	TGTTGGCTACCTTGATCATGTG
NC xi	HSTAL.7q	TCATGCCATTTCGGTTGTAC	TTGAACACTTGAGATGATGATG
NC i	HSSIL/M10Aq	TCTCTTTGAACACAGGGCAATG	TATTAGTCTAGGTGTACTGGCAGTTG
NC ii	HSSIL/M51Bq	TGAATGCTTCCCTTGTGATG	GTAATGTTTCCTTACTGGTTAGCAAC
NC iii	HSSCL/M15Bq	GTGCCCTTGAGAGCCTAGGG	CCTCAACAGCCTGTCTTATAATTG
NC iv	HSTAL.138q	CATCACCTGCAAAAATGGAGG	TAAGCTGAGGCAGGCATTGTC
NC v	HSTAL.108q	GGATTGAGGAGAGGGCATGTG	GCACGGCTGTGGAGCTATG
NC vi	HSTAL.106q	CAGCAGAGGTCCCAAAGCC	CAGTACTCCCAGCTTGCTTCC
NC vii	HSTAL.77q	TTCTGTACCTGCCAGCCAAG	CCCGACGAGCGTTATGTAAG
NC viii	HSSIL/M55Aq	TCATGATGATATTTAGCATACTCAGCAAAG	GGAGAATGATAACTTGTGTCAGGC
NC ix	HSSCL/M137Aq	TCTCTGGAAGTCATAAATAACA	AATCTGCTCATCAAGTAATACG
NC x	HSSCL/M182Aq	TTTGCAGTGCCCTGTTCTTAG	TGTTGGCTACCTTGATCATGTG

## Appendix 2

### Gene Ontology classification of differentially expressed genes in Affymetric GeneChip analysis of siRNA knockdown study

#### Down-regulated genes in GATA1 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0006783	heme biosynthetic process	0.001	1.526718	16
GO:0042168	heme metabolic process	0.003211	1.526718	21
GO:0006366	transcription from RNA polymerase II promoter	0.00412	5.725191	637
GO:0046688	response to copper ion	0.005321	1.145038	8
GO:0030005	cellular di-, tri-valent inorganic cation homeostasis	0.007385	3.053435	182
GO:0006779	porphyrin biosynthetic process	0.007833	1.526718	26
GO:0055066	di-, tri-valent inorganic cation homeostasis	0.008977	3.053435	187
GO:0016568	chromatin modification	0.009466	3.435115	246
GO:0006357	regulation of transcription from RNA polymerase II promoter	0.00988	4.580153	450
GO:0016070	RNA metabolic process	0.009884	18.32061	4323
<b>Molecular function</b>				
GO:0005515	protein binding	9.86E-05	34.35115	9352
GO:0030528	transcription regulator activity	0.000571	12.21374	2181
GO:0008134	transcription factor binding	0.002783	4.580153	436
GO:0004998	transferrin receptor activity	0.006204	0.763359	2
GO:0003723	RNA binding	0.008275	6.870229	1008
<b>Cellular component</b>				
GO:0044424	intracellular part	7.08E-05	45.41985	13765
GO:0043231	intracellular membrane-bounded organelle	7.27E-05	34.35115	9375
GO:0043227	membrane-bounded organelle	7.34E-05	34.35115	9377
GO:0043229	intracellular organelle	0.000935	38.16794	11422
GO:0043226	organelle	0.000951	38.16794	11426
GO:0031974	membrane-enclosed lumen	0.001469	7.251908	1002
GO:0043233	organelle lumen	0.001469	7.251908	1002
GO:0031410	cytoplasmic vesicle	0.002717	4.580153	454
GO:0031982	vesicle	0.003221	4.580153	462
GO:0005737	cytoplasm	0.00622	28.24427	8035

GO:0016023	cytoplasmic membrane-bounded vesicle	0.009675	3.816794	365
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### Up-regulated genes in GATA1 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0048519	negative regulation of biological process	3.36E-13	9.04685	3.532632
GO:0048523	negative regulation of cellular process	7.32E-12	8.400646	3.327346
GO:0032502	developmental process	1.20E-10	15.34733	9.56006
GO:0008219	cell death	8.00E-10	6.946688	2.685827
GO:0016265	death	8.00E-10	6.946688	2.685827
GO:0050793	regulation of developmental process	2.50E-09	6.300485	2.329427
GO:0050793	regulation of developmental process	2.90E-09	6.300485	2.340832
GO:0048522	positive regulation of cellular process	4.93E-09	7.26979	3.076441
GO:0006915	apoptosis	6.31E-09	6.462036	2.514755
GO:0012501	programmed cell death	8.31E-09	6.462036	2.537565
GO:0042981	regulation of apoptosis	8.87E-09	5.169628	1.679354
GO:0043067	regulation of programmed cell death	1.20E-08	5.169628	1.699313
GO:0043067	regulation of programmed cell death	1.20E-08	5.169628	1.699313
GO:0048518	positive regulation of biological process	1.29E-08	7.592892	3.412882
GO:0007243	protein kinase cascade	2.31E-06	3.71567	1.134776
GO:0048856	anatomical structure development	3.30E-06	9.208401	5.465743
GO:0007154	cell communication	2.65E-05	19.063	16.10926
GO:0043066	negative regulation of apoptosis	5.13E-05	2.584814	0.658626
GO:0043069	negative regulation of programmed cell death	6.13E-05	2.584814	0.66718
GO:0007275	multicellular organismal development	6.53E-05	10.01616	6.737376
GO:0051093	negative regulation of developmental process	8.12E-05	3.069467	0.960853
GO:0007165	signal transduction	0.000114	17.60905	14.89465
GO:0006917	induction of apoptosis	0.00012	2.423263	0.613007
GO:0048731	system development	0.000127	7.754443	4.715878
GO:0012502	induction of programmed cell death	0.000128	2.423263	0.615858
GO:0050789	regulation of biological process	0.000194	28.43296	27.95028
GO:0006916	anti-apoptosis	0.000201	2.100162	0.470447
GO:0042127	regulation of cell proliferation	0.000486	3.392569	1.297294
GO:0051094	positive regulation of developmental process	0.000489	3.069467	1.080603
GO:0050794	regulation of cellular process	0.00049	27.6252	27.30876
GO:0042127	regulation of cell proliferation	0.000495	3.55412	1.411342
GO:0065007	biological regulation	0.000523	29.07916	29.15633

GO:0048513	organ development	0.000732	5.977383	3.392923
GO:0010627	regulation of protein kinase cascade	0.000859	1.938611	0.450489
GO:0010627	regulation of protein kinase cascade	0.000859	1.938611	0.450489
GO:0009966	regulation of signal transduction	0.001032	3.71567	1.593819
GO:0008283	cell proliferation	0.001048	4.523425	2.218231
GO:0007167	enzyme linked receptor protein signaling pathway	0.001211	2.746365	0.935192
GO:0009966	regulation of signal transduction	0.001429	3.55412	1.505432
GO:0045321	leukocyte activation	0.001507	2.100162	0.561686
GO:0032501	multicellular organismal process	0.001972	12.92407	10.52947
GO:0043065	positive regulation of apoptosis	0.002138	2.423263	0.769823
GO:0043068	positive regulation of programmed cell death	0.002447	2.423263	0.778377
GO:0006928	cell motion	0.002569	2.907916	1.09771
GO:0051674	localization of cell	0.002569	2.907916	1.09771
GO:0007242	intracellular signaling cascade	0.002836	8.239095	5.742309
GO:0008285	negative regulation of cell proliferation	0.003013	2.261712	0.692841
<b>Molecular pathway</b>				
GO:0005515	protein binding	7.13E-09	29.88691	13.54603
GO:0019899	enzyme binding	2.99E-07	3.392569	26.66439
GO:0019210	kinase inhibitor activity	1.91E-05	1.292407	0.895276
GO:0019207	kinase regulator activity	2.80E-05	1.938611	0.122601
GO:0005159	insulin-like growth factor receptor binding	0.000112	0.807754	0.362102
GO:0004860	protein kinase inhibitor activity	0.000237	1.130856	0.037066
GO:0019900	kinase binding	0.000835	1.453958	0.116899
GO:0019887	protein kinase regulator activity	0.003639	1.453958	0.26231
GO:0030234	enzyme regulator activity	0.006298	5.977383	0.313632
<b>Cellular component</b>				
GO:0031226	intrinsic to plasma membrane	5.36E-05	6.462036	3.666638
GO:0005737	cytoplasm	5.51E-05	24.23263	22.90936
GO:0005887	integral to plasma membrane	0.000104	6.300485	3.621019
GO:0005886	plasma membrane	0.000178	13.89338	11.35346
GO:0044459	plasma membrane part	0.000493	9.208401	6.671799

### Down-regulated genes in SCL knockdown

GO ID	GO term	p-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0048519	negative regulation of biological process	2.02E-10	8.352941	3.532632

GO:0048523	negative regulation of cellular process	3.13E-10	8	3.327346
GO:0033036	macromolecule localization	5.39E-08	7.294118	3.236108
GO:0016043	cellular component organization and biogenesis	1.37E-07	11.76471	6.706013
GO:0008104	protein localization	1.50E-07	6.941176	3.073589
GO:0050793	regulation of developmental process	2.86E-07	5.764706	2.329427
GO:0050793	regulation of developmental process	3.37E-07	5.764706	2.340832
GO:0015031	protein transport	1.51E-06	6.352941	2.851196
GO:0045184	establishment of protein localization	1.56E-06	6.352941	2.854047
GO:0016071	mRNA metabolic process	2.40E-06	3.176471	0.900978
GO:0032502	developmental process	4.05E-06	14.58824	9.56006
GO:0031324	negative regulation of cellular metabolic process	6.61E-06	3.882353	1.345765
GO:0048522	positive regulation of cellular process	7.93E-06	6.470588	3.076441
GO:0009892	negative regulation of metabolic process	9.00E-06	3.882353	1.362872
GO:0008380	RNA splicing	1.21E-05	2.588235	0.664329
GO:0007049	cell cycle	1.33E-05	5.764706	2.620249
GO:0010629	negative regulation of gene expression	1.63E-05	3.058824	0.920936
GO:0048518	positive regulation of biological process	1.84E-05	6.823529	3.412882
GO:0007243	protein kinase cascade	2.24E-05	3.411765	1.134776
GO:0006915	apoptosis	2.70E-05	5.529412	2.514755
GO:0016070	RNA metabolic process	2.77E-05	17.29412	12.32572
GO:0010605	negative regulation of macromolecule metabolic process	2.90E-05	3.529412	1.217461
GO:0012501	programmed cell death	3.55E-05	5.529412	2.537565
GO:0008219	cell death	7.45E-05	5.647059	2.685827
GO:0016265	death	7.45E-05	5.647059	2.685827
GO:0006469	negative regulation of protein kinase activity	0.000102	1.294118	0.176774
GO:0033673	negative regulation of kinase activity	0.000102	1.294118	0.176774
GO:0065009	regulation of molecular function	0.000114	4.705882	2.061415
GO:0042981	regulation of apoptosis	0.000133	4.117647	1.679354
GO:0051348	negative regulation of transferase activity	0.000144	1.294118	0.182477
GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.000167	2.941176	0.966555
GO:0043067	regulation of programmed cell death	0.000177	4.117647	1.699313
GO:0043067	regulation of programmed cell death	0.000177	4.117647	1.699313
GO:0051128	regulation of cellular component organization and biogenesis	0.000204	2.588235	0.778377
GO:0016044	membrane organization and biogenesis	0.000248	2.705882	0.852508
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic	0.000288	21.05882	16.37727

	process			
GO:0016481	negative regulation of transcription	0.000374	2.705882	0.872466
GO:0019222	regulation of metabolic process	0.000414	16.70588	12.33427
GO:0060255	regulation of macromolecule metabolic process	0.000499	16.35294	12.0463
GO:0060255	regulation of macromolecule metabolic process	0.000499	16.35294	12.0463
GO:0008285	negative regulation of cell proliferation	0.000522	2.352941	0.692841
GO:0051641	cellular localization	0.000574	6.470588	3.506971
GO:0009890	negative regulation of biosynthetic process	0.000603	2.941176	1.034984
GO:0016192	vesicle-mediated transport	0.000625	4.117647	1.793402
GO:0065008	regulation of biological quality	0.000634	6.352941	3.427138
GO:0043170	macromolecule metabolic process	0.000683	33.88235	29.49847
GO:0006397	mRNA processing	0.00072	2.352941	0.707097
GO:0008283	cell proliferation	0.000747	4.705882	2.218231
GO:0006886	intracellular protein transport	0.000868	3.882353	1.659396
GO:0010558	negative regulation of macromolecule biosynthetic process	0.001039	2.823529	0.995067
GO:0010558	negative regulation of macromolecule biosynthetic process	0.001039	2.823529	0.995067
GO:0042127	regulation of cell proliferation	0.001227	3.294118	1.297294
GO:0006996	organelle organization and biogenesis	0.001376	7.882353	4.74439
GO:0050790	regulation of catalytic activity	0.001629	4.117647	1.870385
GO:0043283	biopolymer metabolic process	0.001638	29.05882	24.80255
GO:0051246	regulation of protein metabolic process	0.001858	3.058824	1.174693
GO:0043086	negative regulation of catalytic activity	0.001969	1.529412	0.33359
GO:0051649	establishment of localization in cell	0.002042	6.117647	3.378667
GO:0042127	regulation of cell proliferation	0.002116	3.411765	1.411342
GO:0007249	I-kappaB kinase/NF-kappaB cascade	0.002187	1.647059	0.390614
GO:0006366	transcription from RNA polymerase II promoter	0.002275	4	1.816212
GO:0031323	regulation of cellular metabolic process	0.002485	15.88235	11.96077
GO:0016568	chromatin modification	0.002594	2.235294	0.701394
GO:0048869	cellular developmental process	0.003053	6.352941	3.612465
GO:0006897	endocytosis	0.003148	2	0.581644
GO:0010324	membrane invagination	0.003148	2	0.581644
GO:0043066	negative regulation of apoptosis	0.0042	2.117647	0.658626
GO:0010467	gene expression	0.004986	19.64706	15.7329
GO:0043069	negative regulation of programmed cell death	0.005032	2.117647	0.66718
GO:0046907	intracellular transport	0.00511	5.294118	2.845494
GO:0007242	intracellular signaling cascade	0.005441	8.823529	5.742309



GO:0022402	cell cycle process	0.005698	3.294118	1.40564
GO:0051093	negative regulation of developmental process	0.006743	2.588235	0.960853
GO:0006325	establishment and/or maintenance of chromatin architecture	0.007632	3.176471	1.348616
GO:0051726	regulation of cell cycle	0.007893	2.352941	0.826847
GO:0009966	regulation of signal transduction	0.008083	3.529412	1.593819
GO:0065007	biological regulation	0.009721	32.70588	29.15633
GO:0044238	primary metabolic process	0.009831	37.64706	34.37402
GO:0051276	chromosome organization and biogenesis	0.009934	3.529412	1.610926
<b>Molecular function</b>				
GO:0005515	protein binding	1.49E-20	38.70588	26.66439
GO:0003723	RNA binding	1.50E-06	6.235294	2.874006
GO:0019899	enzyme binding	4.32E-05	2.823529	0.895276
GO:0042802	identical protein binding	0.000306	3.176471	1.21461
GO:0019900	kinase binding	0.001686	1.294118	0.26231
GO:0016563	transcription activator activity	0.007084	2.352941	0.895276
GO:0004842	ubiquitin-protein ligase activity	0.009739	1.647059	0.496108
<b>Cellular component</b>				
GO:0043231	intracellular membrane-bounded organelle	2.34E-29	41.64706	26.72996
GO:0043227	membrane-bounded organelle	2.45E-29	41.64706	26.73567
GO:0044424	intracellular part	9.88E-26	52.82353	39.24671
GO:0043229	intracellular organelle	8.29E-24	45.76471	32.56636
GO:0043226	organelle	8.94E-24	45.76471	32.57777
GO:0005634	nucleus	9.26E-20	29.41176	18.29898
GO:0005737	cytoplasm	3.59E-19	34.23529	22.90936
GO:0005622	intracellular	3.80E-17	54.58824	44.60696
GO:0044446	intracellular organelle part	5.81E-15	21.29412	12.65931
GO:0044422	organelle part	7.28E-15	21.29412	12.68782
GO:0044428	nuclear part	8.03E-10	7.764706	3.350155
GO:0012505	endomembrane system	1.29E-07	7.411765	3.521227
GO:0031410	cytoplasmic vesicle	5.56E-07	3.882353	1.294443
GO:0031982	vesicle	8.57E-07	3.882353	1.317253
GO:0031974	membrane-enclosed lumen	9.56E-07	6.235294	2.856898
GO:0043233	organelle lumen	9.56E-07	6.235294	2.856898
GO:0044444	cytoplasmic part	1.36E-06	19.29412	13.87392
GO:0031090	organelle membrane	4.54E-06	8.705882	4.869843
GO:0016023	cytoplasmic membrane-bounded vesicle	1.11E-05	3.176471	1.040687

GO:0031988	membrane-bounded vesicle	1.46E-05	3.176471	1.054943
GO:0031981	nuclear lumen	1.60E-05	4.705882	2.0272
GO:0005794	Golgi apparatus	0.000159	4.705882	2.215379
GO:0005654	nucleoplasm	0.000342	3.647059	1.545348
GO:0030530	heterogeneous nuclear ribonucleoprotein complex	0.000384	0.705882	0.051322
GO:0005694	chromosome	0.001655	3.529412	1.588116
GO:0044451	nucleoplasm part	0.001808	3.176471	1.354318
GO:0000776	kinetochore	0.002892	0.941176	0.14256
GO:0042470	melanosome	0.003264	1.176471	0.236649
GO:0048770	pigment granule	0.003264	1.176471	0.236649
GO:0005783	endoplasmic reticulum	0.003991	4.941176	2.71719
GO:0044431	Golgi apparatus part	0.004245	3.058824	1.340062
GO:0044432	endoplasmic reticulum part	0.004425	3.647059	1.756337
GO:0005815	microtubule organizing center	0.005121	1.647059	0.479001
GO:0005813	centrosome	0.005351	1.529412	0.419126
GO:0005829	cytosol	0.006926	3.411765	1.628033
GO:0005635	nuclear envelope	0.007784	1.882353	0.630114
GO:0031252	leading edge	0.008146	1.058824	0.210989

### Up-regulated genes in SCL knockdown

GO ID	GO term	P-value	% in gene list	% in genome
<b>Biological process</b>				
GO:0032501	multicellular organismal process	1.22E-10	15.65558	10.52947
GO:0048856	anatomical structure development	1.98E-09	9.328115	5.465743
GO:0007275	multicellular organismal development	3.80E-09	10.82844	6.737376
GO:0032502	developmental process	1.95E-08	13.95956	9.56006
GO:0048731	system development	1.00E-07	8.023483	4.715878
GO:0048519	negative regulation of biological process	3.84E-07	6.392694	3.532632
GO:0048518	positive regulation of biological process	6.09E-07	6.196999	3.412882
GO:0048522	positive regulation of cellular process	1.58E-06	5.675147	3.076441
GO:0048523	negative regulation of cellular process	1.62E-06	6.001305	3.327346
GO:0048513	organ development	2.03E-06	6.066536	3.392923
GO:0048869	cellular developmental process	4.23E-05	6.066536	3.612465
GO:0006928	cell motion	9.01E-05	2.609263	1.09771
GO:0051674	localization of cell	9.01E-05	2.609263	1.09771
GO:0030154	cell differentiation	0.000163	5.479452	3.247512

GO:0009653	anatomical structure morphogenesis	0.000219	4.631442	2.603142
GO:0040011	locomotion	0.000319	2.08741	0.812591
GO:0048870	cell motility	0.00072	2.022179	0.801186
GO:0016477	cell migration	0.000739	1.956947	0.761269
GO:0050793	regulation of developmental process	0.001436	4.109589	2.329427
GO:0050793	regulation of developmental process	0.001689	4.109589	2.340832
GO:0048741	skeletal muscle fiber development	0.00203	0.652316	0.105494
GO:0048747	muscle fiber development	0.002655	0.652316	0.108345
GO:0014706	striated muscle development	0.002777	1.043705	0.279417
GO:0048468	cell development	0.00429	2.4788	1.183246
GO:0045445	myoblast differentiation	0.005172	0.456621	0.051322
GO:0051094	positive regulation of developmental process	0.008574	2.283105	1.080603
<b>Cellular component</b>				
GO:0031226	intrinsic to plasma membrane	1.74E-05	6.066536	3.666638
GO:0005887	integral to plasma membrane	3.66E-05	5.936073	3.621019
GO:0044459	plasma membrane part	0.000294	9.262883	6.671799

### Down-regulated genes in E2A knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0015031	protein transport	1.47E-06	8.78187	2.851196
GO:0045184	establishment of protein localization	1.51E-06	8.78187	2.854047
GO:0033036	macromolecule localization	2.11E-06	9.348442	3.236108
GO:0008104	protein localization	2.27E-06	9.065156	3.073589
GO:0008283	cell proliferation	6.94E-06	7.365439	2.218231
GO:0016070	RNA metabolic process	2.79E-05	20.67989	12.32572
GO:0007049	cell cycle	5.03E-05	7.648725	2.620249
GO:0006366	transcription from RNA polymerase II promoter	5.58E-05	6.232295	1.816212
GO:0044249	cellular biosynthetic process	6.35E-05	24.07932	15.58749
GO:0048522	positive regulation of cellular process	0.000106	8.215297	3.076441
GO:0016043	cellular component organization and biogenesis	0.000117	13.31445	6.706013
GO:0051726	regulation of cell cycle	0.000276	3.966006	0.826847
GO:0048518	positive regulation of biological process	0.000282	8.498584	3.412882
GO:0060255	regulation of macromolecule metabolic process	0.000551	19.26346	12.0463
GO:0060255	regulation of macromolecule metabolic process	0.000551	19.26346	12.0463
GO:0048519	negative regulation of biological process	0.000575	8.498584	3.532632

GO:0009058	biosynthetic process	0.000735	26.34561	18.62116
GO:0010604	positive regulation of macromolecule metabolic process	0.00123	4.532578	1.220312
GO:0019222	regulation of metabolic process	0.001276	19.26346	12.33427
GO:0010467	gene expression	0.001516	22.94618	15.7329
GO:0048523	negative regulation of cellular process	0.001618	7.932011	3.327346
GO:0031323	regulation of cellular metabolic process	0.001832	18.69688	11.96077
GO:0006357	regulation of transcription from RNA polymerase II promoter	0.002334	4.532578	1.283038
GO:0045893	positive regulation of transcription, DNA-dependent	0.002432	3.399433	0.727055
GO:0051254	positive regulation of RNA metabolic process	0.002635	3.399433	0.732757
GO:0044237	cellular metabolic process	0.002762	41.92635	35.0355
GO:0010468	regulation of gene expression	0.0029	17.84703	11.37342
GO:0031325	positive regulation of cellular metabolic process	0.002999	4.532578	1.308699
GO:0016192	vesicle-mediated transport	0.003074	5.382436	1.793402
GO:0009893	positive regulation of metabolic process	0.003829	4.532578	1.33436
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.003832	23.22946	16.37727
GO:0045941	positive regulation of transcription	0.005429	3.68272	0.923788
GO:0010468	regulation of gene expression	0.005664	17.56374	11.36202
GO:0010628	positive regulation of gene expression	0.006818	3.68272	0.943746
GO:0006351	transcription, DNA-dependent	0.007216	16.14731	10.20443
GO:0032774	RNA biosynthetic process	0.00758	16.14731	10.22154
GO:0042127	regulation of cell proliferation	0.007689	4.532578	1.411342
GO:0006355	regulation of transcription, DNA-dependent	0.007733	15.86402	9.982037
GO:0051252	regulation of RNA metabolic process	0.008538	15.86402	10.01625
GO:0010556	regulation of macromolecule biosynthetic process	0.009549	17.28045	11.30214
GO:0010556	regulation of macromolecule biosynthetic process	0.009549	17.28045	11.30214
<b>Molecular function</b>				
GO:0005515	protein binding	1.76E-15	43.62606	26.66439
GO:0003723	RNA binding	2.11E-06	8.498584	2.874006
GO:0008134	transcription factor binding	0.000101	4.815864	1.243121
GO:0003700	transcription factor activity	0.000224	9.631728	4.365181
GO:0030528	transcription regulator activity	0.001101	11.61473	6.218459
GO:0016563	transcription activator activity	0.001199	3.68272	0.895276
GO:0017111	nucleoside-triphosphatase activity	0.001385	7.082153	2.928178
GO:0016462	pyrophosphatase activity	0.002483	7.082153	3.030821
GO:0016818	hydrolase activity, acting on acid anhydrides, in phosphorus-	0.00295	7.082153	3.062185

	containing anhydrides			
GO:0016817	hydrolase activity, acting on acid anhydrides	0.003139	7.082153	3.073589
GO:0003712	transcription cofactor activity	0.003381	3.399433	0.843954
GO:0019899	enzyme binding	0.006038	3.399433	0.895276
GO:0003713	transcription coactivator activity	0.008901	2.549575	0.521769
<b>Cellular component</b>				
GO:0043231	intracellular membrane-bounded organelle	3.18E-24	48.72521	26.72996
GO:0043227	membrane-bounded organelle	3.27E-24	48.72521	26.73567
GO:0043229	intracellular organelle	3.57E-21	52.9745	32.56636
GO:0043226	organelle	3.73E-21	52.9745	32.57777
GO:0044424	intracellular part	1.23E-19	58.35694	39.24671
GO:0005622	intracellular	1.27E-15	60.62323	44.60696
GO:0044446	intracellular organelle part	1.30E-13	26.34561	12.65931
GO:0044422	organelle part	1.50E-13	26.34561	12.68782
GO:0005634	nucleus	3.85E-13	32.86119	18.29898
GO:0005737	cytoplasm	1.11E-12	37.67705	22.90936
GO:0031090	organelle membrane	3.61E-09	13.03116	4.869843
GO:0012505	endomembrane system	5.59E-09	10.76487	3.521227
GO:0044428	nuclear part	8.35E-08	9.915014	3.350155
GO:0016023	cytoplasmic membrane-bounded vesicle	1.55E-07	5.382436	1.040687
GO:0031410	cytoplasmic vesicle	1.69E-07	5.949008	1.294443
GO:0031988	membrane-bounded vesicle	1.94E-07	5.382436	1.054943
GO:0031982	vesicle	2.30E-07	5.949008	1.317253
GO:0044444	cytoplasmic part	3.28E-07	23.51275	13.87392
GO:0031974	membrane-enclosed lumen	1.39E-06	8.498584	2.856898
GO:0043233	organelle lumen	1.39E-06	8.498584	2.856898
GO:0030530	heterogeneous nuclear ribonucleoprotein complex	6.73E-05	1.416431	0.051322
GO:0031981	nuclear lumen	8.36E-05	6.232295	2.0272
GO:0031965	nuclear membrane	0.000109	3.116147	0.510364
GO:0042470	melanosome	0.000127	2.266289	0.236649
GO:0048770	pigment granule	0.000127	2.266289	0.236649
GO:0005792	microsome	0.000444	2.832861	0.47615
GO:0044432	endoplasmic reticulum part	0.000529	5.382436	1.756337
GO:0042598	vesicular fraction	0.000641	2.832861	0.496108
GO:0005635	nuclear envelope	0.000847	3.116147	0.630114
GO:0044431	Golgi apparatus part	0.000938	4.532578	1.340062

GO:0005624	membrane fraction	0.000971	5.09915	1.665099
GO:0005626	insoluble fraction	0.001338	5.09915	1.705015
GO:0005654	nucleoplasm	0.001405	4.815864	1.545348
GO:0005783	endoplasmic reticulum	0.002811	6.515581	2.71719
GO:0000267	cell fraction	0.003407	5.665722	2.186867
GO:0005794	Golgi apparatus	0.00409	5.665722	2.215379
GO:0044451	nucleoplasm part	0.004387	4.249292	1.354318
GO:0005789	endoplasmic reticulum membrane	0.006661	4.532578	1.57386
GO:0005813	centrosome	0.00877	2.266289	0.419126
GO:0042175	nuclear envelope-endoplasmic reticulum network	0.008948	4.532578	1.613777

### Up-regulated genes in E2A knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Molecular function</b>				
GO:0005515	protein binding	0.00035	33.41523	26.66439
<b>Cellular component</b>				
GO:0005634	nucleus	0.003608	23.83292	18.29898

### Down-regulated genes in LDB1 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0006396	RNA processing	1.96E-09	4.86618	1.551051
GO:0007049	cell cycle	2.13E-09	6.569343	2.620249
GO:0022403	cell cycle phase	5.05E-09	4.014599	1.12052
GO:0043933	macromolecular complex subunit organization	7.71E-09	6.326034	2.546118
GO:0016071	mRNA metabolic process	1.15E-08	3.527981	0.900978
GO:0008380	RNA splicing	6.23E-08	2.919708	0.664329
GO:0051301	cell division	1.02E-07	3.041363	0.73846
GO:0022402	cell cycle process	1.23E-07	4.257908	1.40564
GO:0065003	macromolecular complex assembly	1.59E-07	5.717762	2.349386
GO:0006397	mRNA processing	2.27E-07	2.919708	0.707097
GO:0044237	cellular metabolic process	4.28E-07	39.41606	35.0355
GO:0000279	M phase	5.83E-07	3.284672	0.92949
GO:0000278	mitotic cell cycle	6.59E-07	3.406326	1.00077
GO:0043283	biopolymer metabolic process	7.91E-07	29.80535	24.80255
GO:0044238	primary metabolic process	1.88E-06	38.44282	34.37402

GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	2.60E-06	21.28954	16.37727
GO:0007067	mitosis	2.76E-06	2.676399	0.675733
GO:0033036	macromolecule localization	4.60E-06	6.569343	3.236108
GO:0000087	M phase of mitotic cell cycle	5.92E-06	2.676399	0.704245
GO:0006974	response to DNA damage stimulus	1.07E-05	3.77129	1.357169
GO:0048519	negative regulation of biological process	1.41E-05	6.812652	3.532632
GO:0008104	protein localization	1.49E-05	6.20438	3.073589
GO:0048523	negative regulation of cellular process	2.96E-05	6.447689	3.327346
GO:0043170	macromolecule metabolic process	3.64E-05	33.21168	29.49847
GO:0034621	cellular macromolecular complex subunit organization	0.000136	4.501217	2.021498
GO:0006461	protein complex assembly	0.000168	3.284672	1.217461
GO:0015031	protein transport	0.000171	5.596107	2.851196
GO:0045184	establishment of protein localization	0.000176	5.596107	2.854047
GO:0016043	cellular component organization and biogenesis	0.000323	10.09732	6.706013
GO:0008152	metabolic process	0.000325	41.36253	39.29233
GO:0016070	RNA metabolic process	0.000616	15.93674	12.32572
GO:0006259	DNA metabolic process	0.000831	4.622871	2.269552
GO:0006281	DNA repair	0.001054	3.041363	1.177544
GO:0051726	regulation of cell cycle	0.001733	2.43309	0.826847
GO:0034622	cellular macromolecular complex assembly	0.002029	3.892944	1.813361
GO:0022613	ribonucleoprotein complex biogenesis and assembly	0.002078	2.311436	0.764121
GO:0006986	response to unfolded protein	0.002976	1.094891	0.173923
GO:0051789	response to protein stimulus	0.002976	1.094891	0.173923
GO:0006950	response to stress	0.004932	7.055961	4.459271
GO:0046500	S-adenosylmethionine metabolic process	0.007132	0.364964	0.008554
GO:0010467	gene expression	0.009963	18.61314	15.7329
<b>Molecular function</b>				
GO:0005515	protein binding	1.39E-21	37.7129	26.66439
GO:0003723	RNA binding	2.58E-08	6.569343	2.874006
GO:0000287	magnesium ion binding	7.02E-06	3.649635	1.314401
GO:0003729	mRNA binding	0.00044	0.973236	0.116899
GO:0003712	transcription cofactor activity	0.003273	2.311436	0.843954
GO:0003724	RNA helicase activity	0.005444	0.729927	0.079833
<b>Cellular component</b>				
GO:0043231	intracellular membrane-bounded organelle	5.39E-38	42.70073	26.72996

GO:0043227	membrane-bounded organelle	5.66E-38	42.70073	26.73567
GO:0044424	intracellular part	4.21E-35	53.64964	39.24671
GO:0043226	organelle	1.29E-26	45.01217	32.57777
GO:0043229	intracellular organelle	2.83E-26	44.89051	32.56636
GO:0005737	cytoplasm	7.01E-26	35.27981	22.90936
GO:0044428	nuclear part	2.59E-24	10.7056	3.350155
GO:0044422	organelle part	1.05E-23	23.35766	12.68782
GO:0044446	intracellular organelle part	2.14E-23	23.23601	12.65931
GO:0005622	intracellular	2.24E-23	54.62287	44.60696
GO:0005634	nucleus	1.75E-19	28.3455	18.29898
GO:0031974	membrane-enclosed lumen	1.53E-15	8.150852	2.856898
GO:0043233	organelle lumen	1.53E-15	8.150852	2.856898
GO:0031981	nuclear lumen	4.04E-12	6.082725	2.0272
GO:0005654	nucleoplasm	2.13E-11	5.109489	1.545348
GO:0044444	cytoplasmic part	7.15E-11	20.43796	13.87392
GO:0044451	nucleoplasm part	5.47E-10	4.501217	1.354318
GO:0042470	melanosome	2.12E-07	1.703163	0.236649
GO:0048770	pigment granule	2.12E-07	1.703163	0.236649
GO:0031090	organelle membrane	2.53E-06	8.515815	4.869843
GO:0005739	mitochondrion	4.78E-06	6.082725	3.016565
GO:0016604	nuclear body	2.20E-05	1.703163	0.336441
GO:0043234	protein complex	3.43E-05	12.0438	8.3426
GO:0012505	endomembrane system	0.000211	6.20438	3.521227
GO:0032991	macromolecular complex	0.000295	15.32847	11.90659
GO:0044464	cell part	0.000637	62.40876	65.22681
GO:0005623	cell	0.000642	62.40876	65.22966
GO:0031967	organelle envelope	0.00087	4.014599	1.961623
GO:0031975	envelope	0.000924	4.014599	1.967325
GO:0005681	spliceosome	0.001196	1.581509	0.40487
GO:0016607	nuclear speck	0.001393	1.216545	0.2395
GO:0031982	vesicle	0.001686	3.041363	1.317253
GO:0044429	mitochondrial part	0.002319	3.649635	1.781998
GO:0005819	spindle	0.002593	1.216545	0.256608
GO:0016023	cytoplasmic membrane-bounded vesicle	0.003552	2.554745	1.040687
GO:0031410	cytoplasmic vesicle	0.003716	2.919708	1.294443
GO:0031988	membrane-bounded vesicle	0.004344	2.554745	1.054943



GO:0005876	spindle microtubule	0.005795	0.608273	0.054173
GO:0000793	condensed chromosome	0.007003	1.094891	0.230947
GO:0005815	microtubule organizing center	0.007258	1.581509	0.479001
GO:0005813	centrosome	0.008522	1.459854	0.419126

### Up-regulated genes in LDB1 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0032502	developmental process	5.35E-07	16.56051	9.56006
GO:0048856	anatomical structure development	8.34E-07	11.1465	5.465743
GO:0007275	multicellular organismal development	3.46E-06	12.57962	6.737376
GO:0048731	system development	1.82E-05	9.55414	4.715878
GO:0007243	protein kinase cascade	7.36E-05	3.821656	1.134776
GO:0032501	multicellular organismal process	8.16E-05	16.56051	10.52947
GO:0007242	intracellular signaling cascade	0.000153	10.50955	5.742309
<b>Molecular function</b>				
GO:0005515	protein binding	1.08E-05	34.55414	26.66439
GO:0004674	protein serine/threonine kinase activity	0.003902	4.617834	2.024349
GO:0005201	extracellular matrix structural constituent	0.007076	1.592357	0.325036
<b>Cellular component</b>				
GO:0005737	cytoplasm	0.000852	28.98089	22.90936

### Down-regulated genes in LMO2 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Molecular function</b>				
GO:0043566	structure-specific DNA binding	0.004711	8.163265	0.47615
<b>Cellular component</b>				
GO:0044428	nuclear part	0.002122	18.36735	3.350155
GO:0031974	membrane-enclosed lumen	0.004614	16.32653	2.856898
GO:0043233	organelle lumen	0.004614	16.32653	2.856898
GO:0031253	cell projection membrane	0.00838	4.081633	0.034214

### Up-regulated genes in LMO2 knockdown

GO ID	GO term	P-value	% in gene list	% in human genome
<b>Biological process</b>				
GO:0048856	anatomical structure development	3.55E-05	9.529148	5.465743

GO:0032502	developmental process	4.35E-05	14.46188	9.56006
GO:0007610	behavior	0.000154	2.802691	0.886722
GO:0048519	negative regulation of biological process	0.000231	6.726457	3.532632
GO:0048523	negative regulation of cellular process	0.000353	6.390135	3.327346
GO:0048731	system development	0.00041	8.183857	4.715878
GO:0007275	multicellular organismal development	0.001617	10.42601	6.737376
GO:0048869	cellular developmental process	0.00216	6.502242	3.612465
GO:0030154	cell differentiation	0.007777	5.829596	3.247512

## Appendix 3A

### Characterisation of antibodies for the SCL erythroid complex for western blot

TF	Western blot (Fig. 3.3)	Name of antibody	Origin	Source	Poly- or mono-clonal	Target epitope	Catalog no.	Specificity and signal detection	Titrated dilution
SCL	A	Anti-TAL1	Rabbit	Abcam	Polyclonal	Amino acid 7-21 of human SCL protein	ab12115	No predicted protein bands identified	1:200
SCL	B	TAL1	Rabbit	Active Motif	Polyclonal	Amino acid 7-21 of human SCL protein	39066	Predicted protein bands identified	1:1000
SCL	C	Anti-TAL1 3BTL73	Mouse	Collaborator	Monoclonal	Full length human SCL protein	---	No predicted protein bands identified	1:100
E2A	D	Anti-TCF3	Rabbit	Abcam	Polyclonal	Amino acid 517-531 of human E2A protein	ab54462	No predicted protein bands identified	1:200
E2A	E	TCF3 M20	Goat	Santa Cruz	Polyclonal	C-terminus of mouse origin	sc-8635	No predicted protein bands identified	1:200
E2A	F	Anti-E2A	Mouse	BD Biosciences	Monoclonal	Amino acid 463-483 of human E2A protein	554102	No predicted protein bands identified	1:250
E47	G	E47 N649	Rabbit	Santa Cruz	Polyclonal	Full-length human E47 protein	sc-763	Predicted protein bands identified	1:5000
E12	H	E12 H208	Rabbit	Santa Cruz	Polyclonal	bHLH domain of human E12 protein	sc-762	Predicted protein bands identified	1:2000
E47	I	E47	Rabbit	Active Motif	Polyclonal	Amino acid 517-531 of human E47 protein	39314	No predicted protein bands identified	1:100
E47	J	E47 (Ab-1)	Rabbit	Merck	Polyclonal	Amino acid 517-531 of human E47 protein	PC695	No predicted protein bands identified	1:500
GATA1	K	GATA1 M20	Goat	Santa Cruz	Polyclonal	C-terminus of mouse origin	sc-1234	Predicted protein bands identified	1:1000
LDB1	L	CLIM-2 N18	Goat	Santa Cruz	Polyclonal	N-terminus of human origin	sc-11198	Predicted protein bands identified	1:1000
LMO2	M	LMO2 N16	Goat	Santa Cruz	Polyclonal	N-terminus of human origin	sc-10497	No predicted protein bands identified	1:100
LMO2	N	LMO2 G16	Goat	Santa Cruz	Polyclonal	C-terminus of human origin	sc-10499	No predicted protein bands identified	1:100
LMO2	O	LMO2	Sheep	Abcam	Polyclonal	Full-length human LMO2 protein	ab16132	No predicted protein bands identified	1:100

### Secondary antibodies used in western blotting

Name of antibody	Origin	Source	Poly- or mono-clonal	Catalog no.	Titrated dilution
Anti-goat IgG	Donkey	Santa Cruz	Polyclonal	sc-2020	1:20000
Anti-rabbit IgG	Goat	Santa Cruz	Polyclonal	sc-2004	1:20000
Anti-mouse IgG	Goat	Santa Cruz	Polyclonal	sc-2005	1:20000
Anti-sheep IgG	Rabbit	Abcam	Polyclonal	ab6747	1:20000

### Appendix 3B

#### Characterisation of antibodies for the SCL erythroid complex for ChIP-on-chip

TF	Name of antibody	Origin	Source	Poly- or mono-clonal	Target epitope	Catalogue no.	ChIP-on-chip results
SCL	TAL1	Rabbit	Active Motif	Polyclonal	Amino acid 7-21 of human SCL protein	39066	Substantial enrichments at +51 enhancer. Selected for subsequent analyses.
SCL	Anti-TAL1 3BTL73	Mouse	D. Mathieu	Monoclonal	Full length human SCL protein	---	Substantial enrichments at +51 enhancer.
E2A	Anti-TCF3	Rabbit	Abcam	Polyclonal	Amino acid 517-531 of human E2A protein	ab54462	No substantial enrichments at any enhancers or promoters.
E2A	Anti-E2A	Mouse	BD Biosciences	Monoclonal	Amino acid 463-483 of human E2A protein	554102	Substantial enrichments at +51 enhancer.
E47	E47 N649	Rabbit	Santa Cruz	Polyclonal	Full-length human E47 protein	sc-763	Substantial enrichments at +51, +3, -9/-10 enhancers and promoter 1a. Selected for subsequent analyses.
E12	E12 H208	Rabbit	Santa Cruz	Polyclonal	bHLH domain of human E12 protein	sc-762	Substantial enrichments at +51, +3, -9/-10 enhancers and promoter 1a. Selected for subsequent analyses.
GATA1	GATA1 M20	Goat	Santa Cruz	Polyclonal	C-terminus of mouse origin	sc-1234	Substantial enrichments at +51, +3, -9/-10 enhancers and promoter 1a. Selected for subsequent analyses.
LDB1	CLIM-2 N18	Goat	Santa Cruz	Polyclonal	N-terminus of human origin	sc-11198	Substantial enrichments at +51, +3, -9/-10 enhancers and promoter 1a. Selected for subsequent analyses.
LMO2	LMO2 N16	Goat	Santa Cruz	Polyclonal	N-terminus of human origin	sc-10497	Enrichments at +51 enhancer. Selected for subsequent analyses.
LMO2	LMO2 G16	Goat	Santa Cruz	Polyclonal	C-terminus of human origin	sc-10499	Enrichments at +51 enhancer.



## Appendix 4

### Multiple sequence alignments of transcription factor binding sites at promoter regions of selected putative target genes

E-box (E12, E47 and TAL1) and GATA motifs were identified by TESS and TFSEARCH in a 4 kb window spanning the transcription start sites of the 14 promoter regions of selected putative target genes. Multiple species sequence alignments showed one or more relatively conserved E-box or GATA motifs identified (named from 1 to 4 in brackets). Shaded in yellow are the conserved nucleotides for motifs found across a number of species. The motifs labelled with an asterisk (\*) were shown to have significant enrichments in the ChIP-qPCR studies (section 5.4.4 3). Panels A to N show the alignments for the 14 selected target genes. For SCL, shown in panel K, the sequence of the composite E-box/GATA motif in the +51 enhancer is shown.

A) BRD2		Human	aagtcacacatctgcggtcgcaccttatctctccc
	Mouse	acgt-----caaatc-----	
	Rat	acgt-----caaacc-----	
	Rabbit	acgcccacgtctacagcgcgcacctctcgcccc	
	Dog	acgccccatctaccggttctcagctcatttcccg	
	Armadillo	atttccacatctaccggttgcacagcccaaatcc	
	Elephant	aagtcacttctcccggttctctatctcccc	
		E12 E47	GATA

B) CTCFL		Human	tgagggggaatggataagg-----aggggag-----gagggccc-----acaggaggcactga
	Mouse	-----gctggagtcctgcg-----gagaagat-----gacggac-----agagggggc gctgg	
	Rat	caacaaggcaagagtgcgtg-----ggagag-----gaaggtcct-----gcaagagtc gagga	
	Dog	-----	
	Armadillo	-----	
	Elephant	-----	
	Opossum	cgaggggcccgggga aaa-----agggggccc--gaggtgcg-----tcgggggaa aagga	
	Chicken	tgacgycacgaggtgtggtagggcacaagggagggcatggggagggca-----caaggatgtgctga	
	X. tropicalis	tgggatagcaggtatagta-----gggagag-----atggtgcctatagtagcagtgggggataa	
	Tetraodon	ctgggtggagtgatccaa-----cggtgga-----ggtgtgcag-----ccagaccacacca	
		GATA	

C) EKLF		Human	cgccccctcacctgtgtgctgc-----gcagatgcgcc-----ttcaggtgggagctcttgg
	Rhesus	caccccctcacctgtgtgctgc-----gcagatgcgcc-----ttcaggtgggagctcttgg	
	Mouse	cccgcccttacccgtgtgctgc-----gcaggtgcgcc-----ttgaggtgcgagctcttgg	
	Dog	cgcgccctcacctgtgtgctgc-----gcagatgcgcc-----ttcaggtgtgagctcttgg	
(1)	Horse	-----	
	Armadillo	-----	
	Opossum	taggctctcacctgtgtgggttc-----ttagatgggccc-----ttgaggtgggaactcttgg	
	Platypus	ctcctctcacccgtgtgctgc-----tcagatgcgcc-----ttgagatcgaactcttgg	
	Lizard	-----c tttacctgtgtgggtgc-----gcagatgggccc-----ttagatgggagctcttgg	
	Chicken	-----ccttacccgtgtgctgc-----gcatgtgcgcc-----ttgaggtgggagctcttgg	
	X. tropicalis	cgctctgtttatgtgtattccccctcc tacaatacagatgccccccctgtaattccattcgcgtgattctg	
	Stickleback	-----aggtgggagctcttgg	
		E12 E47 TAL1	E12 E47
(2*)	Human	ctgtgatagc-----ttcgagggctc---ctctctgctctagctga--ttggtgcagcct-ctgata	
	Rhesus	ctgtgatagc-----ttcgagggctc---ctctctgctctagctga--ttggtgcagcct-ctgata	
	Mouse	ctaggaagttt---ttggagggctc---ctgtctgcccacatctga--ttggtgtcttcc-ctgata	
	Dog	caccaatggcccc---tcagagggctc---ctctctgctctagctga--ttggtgcagcct-ctgata	
	Horse	ctccagtggcccc---ttggagggctc---ctctctgctctagctga--ttggtgcgggccc-ctgata	
		GATA	GATA

**D) EPOR**

Human	cagtcacagctgg---gtcagcagctgcctc--cgccggagcagctgac---
Mouse	tagtccacagctgg---gtcagcagcagc-----tgccggacacagctgac---
Rat	tagtccacagctgg---gtcagcagcagc-----tgccggacacagctgac---
Rabbit	gggtcccagctgg---gccagcagctgcgtccgccccggacacagctggc---
Dog	cagtcacagctgg---gtcggcagctggctc--ctccagactcagctgac---
Armadillo	ctgtctgtggcgg---cgcagcaggtggttc--tgctgggcacagcgggc---
Elephant	NN
Opossum	gaggctacagctggagcaggcagcagctgcagt--atccggacacagctggcagc

E12 E47 TAL1      E12 E47 TAL1      E12 E47 TAL1

**E) ETO2**

Human	ycagccagctgtgtccccgtgataatgc
Mouse	ycagccagctgtgtcacagtgataatgc
Rat	ycagccagctgtgtcggcgtgataatgc
Dog	ycagccagctgtgtcacctgtatagtac
Opossum	ycagccagctgtggctcgggtgataatgc

E12 E47 TAL1      GATA

**F) EZH2**

(1)

Human	ctcggataccaaaatccacagatgctcaaaagtccctg
Rhesus	ctcggaaaccaaaatccacagatgctcaaaagtccctg
Mouse	=====
Dog	=====
Horse	=====
Armadillo	-----
Opossum	=====
Platypus	=====
Lizard	tgaagtatccatatacatggatgtcc--aggcccctt
Chicken	=====

GATA      E12 E47

(2)

Human	----tataacacctgtaaagcaggtt----aaaaatctagtg--tatcc tcaa--
Rhesus	----tgtaacacctttaaagcaggtt----aaaaatctagtg--tattc tcaa--
Mouse	----tgtagcatctttaaagcaggtt----aaaaatctagtg--ctcaccag--
Dog	----tgtagtatctttaaagcaggtt----aaacatctagtg--atttc tcaa--
Horse	----tgtaatatctttaaagcaggtt----aaaaatctagtg--atttc tcaa--
Armadillo	NNNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN
Opossum	----agcaatattcc taa----gtt----gtcaatgaaatt--aatctt--aa--
Platypus	-----catct-----t----tcaa tcaagtggc agctcccta--
Lizard	----atccacacacttttatcaagtc-----atctagcg--a--tcatacaa--
Chicken	----actcacatgct-----
X. tropicalis	gacaac ttgagaccacccaac ccagc tcatgaaatgtatagtg--ttatacaaaac
Stickleback	=====

E12 E47 TAL1      GATA

(3)

Human	aaccaccaacagatgacagag-
Rhesus	aatcaccaacaggtgacagag-
Mouse	=====
Dog	agcctcccaccagagacaagg-
Horse	aaccaccaacaatgataaag-
Armadillo	tgcaaccaa----aggtgag-
Opossum	=====
Platypus	=====
Chicken	=====

E12 E47

**G) FBXL10**

Human	gctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtaacggaaattgggctgcacctgaaagcaaag
Rhesus	gctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtaacggaaattgggctgcacctgaaaccaaag
Mouse	gctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtaacggaaattgggctgaaacctgaaagcagag
Dog	gctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtaacggaaattgggctgcacctgaaagcaaag
Horse	gctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtaacggaaattgggctgcacctgaaagcaaag
Armadillo	tctgggtcacacagtagcgtatctctccaggacataccagcacatctcatagtagaaggggtagcggaaattgggctgcacctgcaaccaaag
Opossum	gctgggtcacagtagcgtatctctccaaaacataccaacacatctcatagtagaaggggtaccggaaattgggctgtacctaaagagca-ac
Platypus	ggtgggtcagcagtagcgtacctctccaggacataccagcacatctcatagtagaaggggtaacggaaattggcctgcacctgaaagca-ag
Lizard	gctgggtcacagtagcgtacctctcttaggacataccaacacatctcatagtagaacgggtagcggaaattggcctgcacctgcgagcaaa-
Chicken	gctgggtcacacagtagcgtatctctccagaacataccagcacatttcatagtagaaggggtaacggaaattggcctgcacctgaaagcaag-
X. tropicalis	gtctgggtcaaaagacagacataacctctcttaggacataccaacacatctcataataaaaaggtagcggaaattggcctgcacctgaaagcaag-
Stickleback	gcttggtaggtagcgtatctctccaggacataccagcacatctcaagtagaaggggtaacggaaattgggctgcacctgaaagcaaaag

GATA      E12 E47 TAL1

**H) JMJD2C**

(1\*)

Human	ggttctgt---g <b>ca</b> ctgtt-----ttc---tccttctacgcgag <b>ta</b> -tctttccc	
Mouse	agatctgttg <b>gc</b> ca <b>ct</b> gct-----cc---ttctgcttcg <b>tc</b> ag <b>tg</b> tctttcctc	
Rat	agatctgt---g <b>ca</b> ctgtt-----cg---ttctgctttg <b>tc</b> ag <b>tg</b> -tctttcctc	
Rabbit	gattctgt---g <b>ca</b> ctgtc-----ct---cccttctg <b>tc</b> caag <b>ta</b> -tctttatc	
Dog	gcttctgt---g <b>ca</b> ctgtt-----cct---tcctgctg <b>tc</b> gaag <b>tg</b> -tctgcccc	
Armadillo	ggttctgt---g <b>ca</b> ctgtt-----tct---tcctgagggcccaag <b>ta</b> -tcttcctc	
Elephant	ggttctgt---g <b>ca</b> ctgtt-----ctttctgctcctccag <b>tc</b> caag <b>tg</b> -tcttt-tc	

E12 E47 TAL1 GATA

(2)

Human	t <b>cc</b> atctgtcctcacaatg <b>tt</b> ca <b>ccc</b> ag <b>tg</b> ag-aa <b>cg</b> ag <b>tt</b> caag-----cg <b>cg</b> gtg <b>g</b> taag <b>cg</b> g ---t <b>gt</b> cgat <b>at</b> -at <b>tt</b> tt	
Mouse	cc <b>ca</b> tctgtctttacag <b>tg</b> ctcc <b>ccc</b> ta <b>aaaa</b> -aa <b>=====</b>	
Rat	t <b>cc</b> atctgtttttacag <b>tg</b> atcctt <b>ta</b> aaa-aa <b>aa</b> ---ag <b>aaaa</b> acatt <b>ta</b> gggag <b>ct</b> tt <b>ta</b> aat <b>gg</b> ---t <b>gt</b> tg <b>aa</b> at-t <b>tt</b> ttt	
Rabbit	t <b>ca</b> atcag <b>tc</b> cttacaag <b>tc</b> tct <b>tg</b> cagagag-aa <b>aa</b> acag <b>tt</b> caagag <b>tg</b> ta--aacatg <b>g</b> taag <b>tg</b> a ---t <b>gt</b> tgagat <b>at</b> tt <b>tt</b>	
Dog	t <b>tc</b> atctgac <b>tc</b> cgatata <b>ct</b> ctt <b>ccc</b> agagat-aa <b>aa</b> agact <b>tc</b> aa <b>g</b> -----g <b>g</b> atg <b>g</b> caag <b>tg</b> g ---c <b>gt</b> tgagat-g <b>tt</b> ttt	
Armadillo	t <b>cc</b> atctgtcctcacaag <b>tg</b> cc <b>ccc</b> atcag <b>g</b> ag-aa <b>aa</b> agact <b>tc</b> aa <b>g</b> -----g <b>g</b> catg <b>g</b> taag <b>tg</b> g ---g <b>gt</b> tgag <b>g</b> t-a-t <b>tc</b> g	
Elephant	t <b>ct</b> atctgtcctcacaag <b>tg</b> t-g <b>tc</b> caacagag-gaa agatt <b>tc</b> aa <b>g</b> -----g <b>g</b> catg <b>g</b> taaaag <b>g</b> actt <b>g</b> ct <b>ta</b> g <b>g</b> t-a-t <b>ta</b> a	

E12 E47 GATA

(3)

Human	aacag <b>ct</b> gtc <b>ac</b> ctag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Mouse	aacag <b>ct</b> gtc <b>ac</b> ccag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Rat	aacag <b>ct</b> gtc <b>ac</b> ctag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Rabbit	aacag <b>ct</b> gtc <b>ac</b> ccag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Dog	aacag <b>ct</b> gtc <b>ac</b> ccag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Armadillo	ag <b>ca</b> g <b>ct</b> gtc <b>ac</b> ccag <b>tc</b> g <b>cg</b> ga <b>aca</b> a <b>g</b>	
Elephant	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	

E12 E47 TAL1

**I) LMO2**

(1\*)

Human	-ctgctt <b>tg</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>gg</b> gag <b>gc</b> ct <b>g</b> g c <b>ac</b> ctag <b>ca</b> ct <b>g</b> gtg <b>cc</b> ct <b>g</b> g	
Mouse	-ctgctt <b>ca</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>ag</b> gag <b>ac</b> ct <b>g</b> g t <b>ac</b> tct <b>aa</b> cc <b>ct</b> g <b>gt</b> g <b>cc</b> ct <b>g</b>	
Rat	-ctgctt <b>ca</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>ag</b> gag <b>gc</b> ct <b>g</b> g t <b>ac</b> ct <b>aa</b> ca <b>ct</b> g <b>gt</b> g <b>cc</b> ct <b>g</b>	
Rabbit	-ctg <b>cg</b> tc <b>gc</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>ag</b> gag <b>gc</b> cc <b>g</b> g c <b>ac</b> cccc <b>ca</b> ca <b>ct</b> g <b>gt</b> g <b>ct</b> tt <b>g</b>	
Dog	-ctgctt <b>ca</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>ag</b> gag <b>gc</b> ct <b>g</b> g c <b>tc</b> ctc <b>ag</b> tc <b>ca</b> atg <b>cc</b> ct <b>g</b> g	
Armadillo	-ctgctt <b>tg</b> ca <b>ct</b> gtt <b>ct</b> cttctc <b>ag</b> gag <b>gc</b> cc <b>ta</b> c <b>ac</b> ccaag <b>cc</b> ca <b>g</b> tc <b>gc</b> at <b>g</b>	
Elephant	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNN	
Opossum	:ag <b>gg</b> ca <b>ca</b> g <b>ca</b> ct <b>g</b> tt <b>ct</b> ctc <b>ag</b> gag <b>gc</b> ----- -cag <b>g</b> ag <b>tc</b> ag <b>ca</b> tc <b>gc</b> ag	
Chicken	=====	
X. tropicalis	=====	

E12 TAL1 E12 TAL1

(2)

Human	caatcgaacat <b>ttt</b> ct <b>tt</b> at <b>ct</b> tg <b>gc</b> ag <b>tg</b> tg <b>gt</b> ctg <b>tg</b> tg <b>gt</b> tag <b>ca</b> ta <b>ca</b> g <b>gg</b> tc <b>tc</b> tg <b>cc</b> ag <b>tc</b> g <b>g</b> aa <b>g</b> tc	
Mouse	caatc <b>ta</b> acat <b>ttt</b> ct <b>tt</b> at <b>ct</b> tg <b>gc</b> ag <b>tg</b> tg <b>gt</b> ctag <b>tg</b> tg <b>gt</b> tt <b>gc</b> acag <b>gg</b> tc <b>tc</b> tg <b>ca</b> ag <b>tc</b> g <b>g</b> aa <b>g</b> tc	
Rat	caatc <b>ta</b> acat <b>ttt</b> ct <b>tt</b> at <b>ct</b> tg <b>gc</b> ag <b>tg</b> tg <b>gt</b> ctag <b>tg</b> tg <b>gt</b> tt <b>gc</b> ac <b>gg</b> gag <b>tc</b> tg <b>ca</b> at <b>ca</b> g <b>g</b> aa <b>g</b> tc	
Rabbit	caatcgaacat <b>ttt</b> ct <b>tt</b> at <b>ct</b> tg <b>gc</b> ag <b>tg</b> tg <b>gt</b> ctg <b>tg</b> tg <b>gt</b> tt <b>gc</b> gcag <b>gg</b> tc <b>tc</b> tg <b>cc</b> ag <b>tc</b> g <b>g</b> aa <b>g</b> tc	
Dog	caatc <b>ta</b> acat <b>ttt</b> ct <b>tt</b> at <b>ct</b> tg <b>gc</b> ag <b>tg</b> tg <b>gt</b> ctg <b>tg</b> tg <b>gt</b> tt <b>gc</b> gt <b>gg</b> gc <b>tc</b> tg <b>ca</b> ag <b>tc</b> g <b>g</b> aa <b>g</b> tc	
Armadillo	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNN	
Elephant	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNNNNNNNNNN	
Opossum	=====	
Chicken	=====	
X. tropicalis	=====	

GATA

**J) LYL1**

(1\*)

Human	ag <b>tg</b> ca <b>g</b> ata <b>agg</b> g <b>cc</b> ag <b>g</b> ct <b>gc</b> ct gg <b>cc</b> g <b>cg</b> ct <b>g</b> ata <b>agg</b> ag <b>cc</b> tc	
Mouse	:gt <b>gc</b> ca <b>g</b> ata <b>agg</b> g <b>tc</b> g <b>g</b> ct <b>gc</b> ct gg <b>cc</b> g <b>cg</b> ct <b>g</b> ata <b>agg</b> ag <b>ca</b> at	
Rat	:gt <b>gc</b> ca <b>g</b> ata <b>agg</b> g <b>tc</b> g <b>g</b> ct <b>gc</b> ct gg <b>cc</b> g <b>cg</b> ct <b>g</b> ata <b>agg</b> ag <b>cg</b> gt	
Dog	g <b>gc</b> ca <b>g</b> ata <b>agg</b> g <b>tc</b> g <b>g</b> cc <b>g</b> act gg <b>cc</b> g <b>cg</b> ct <b>g</b> ata <b>agg</b> ag <b>cc</b> g	
Elephant	g <b>gc</b> ca <b>g</b> ata <b>agg</b> ag <b>cc</b> tc <b>g</b> g <b>cc</b> g <b>ct</b> gg <b>cc</b> g <b>cg</b> ct <b>g</b> ata <b>agg</b> ag <b>cc</b> g	
Opossum	=====	

GATA GATA

(2)

Human	:cag <b>gg</b> ca <b>g</b> g <b>aa</b> g <b>ca</b> ct <b>g</b> gt <b>ct</b> g <b>g</b> ag <b>cg</b> g <b>at</b> g <b>ca</b> ca <b>g</b> g <b>gc</b>	
Mouse	-cag <b>g</b> ca <b>g</b> g <b>aa</b> g <b>ca</b> ct <b>g</b> gt <b>ct</b> g <b>g</b> ag <b>cg</b> g <b>at</b> g <b>ca</b> ca <b>g</b> aa <b>t</b>	
Rat	-cag <b>g</b> ca <b>g</b> g <b>aa</b> g <b>ca</b> ct <b>g</b> gt <b>ct</b> g <b>g</b> ag <b>cg</b> g <b>at</b> g <b>ca</b> ca <b>g</b> aa <b>t</b>	
Dog	g <b>cg</b> g <b>ag</b> ca <b>g</b> g <b>aa</b> g <b>ca</b> ct <b>g</b> gt <b>ct</b> g <b>g</b> ag <b>cg</b> g <b>at</b> g <b>ca</b> ca <b>g</b> g <b>gc</b>	
Elephant	act <b>g</b> g <b>g</b> ca <b>g</b> g <b>aa</b> g <b>ca</b> ct <b>g</b> gt <b>ct</b> g <b>g</b> aa <b>cg</b> g <b>at</b> g <b>ca</b> ca <b>g</b> g <b>gc</b>	
Opossum	:c <b>g</b> g <b>g</b> g <b>cc</b> g <b>ag</b> g <b>gc</b> g <b>tc</b> act <b>aa</b> ag <b>tg</b> g <b>g</b> ct <b>cc</b> aa <b>acc</b>	

E12 E47 TAL1



**K) SCL**

```

Human   gcaggtggaatgagcgcgataaggattgggggt
Chimp   gcaggtggaatgagcgcgataaggattgggggt
Mouse   gcaggtggagctggcgataagga-agaggggt
Rat     gcaggtggaactggtgataagga-cgaggggt
Dog     gcaggtggaagaggcgataaggg-----
        'E-box'      'GATA'
    
```

**L) SMARCA5**

(1)

```

Human   ggatggccgagtgccgagtgaggataagcggg-gcgcagctgc
Mouse   ggagggccgagtgccgagtgaggataagcggg-gcgcagctgc
Rat     ggagggccgaatgccgagtgaggataagcggg-gcgcagctgc
Rabbit  ggatggccgagtgccgagtgaggatgagctggcgcgagctgc
Dog     ggaaggccgagtgccgagtgaggataagcggg-gcgcagctgc
Armadillo -ggggccgagtgccgagtgaggataaacggg-gcgcagctgc
Elephant ggatggc--gatgccgagtgaggatag--cgg-gcgcagctgc
Opossum =====
Chicken =====
X. tropicalis =====
                        GATA      E12 E47 TAL1
    
```

(2)

```

Human   ttcgttatcaaacagactaca ctttactc-----aacaacatttaga----gaatactgaatatgaggaataaaaaagataaaaa
Mouse   t-----gaatggaaca-- .ttttattc-----aacataggt-----ggggactaaata-atgggattaattaagat---aaa
Rat     -----tatttattc-----aatataggt-----ggggacgaaata-acgagcgggattaagatgacaaa
Rabbit  JNNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN NNNNN
Dog     =====
Armadillo tatgtctcaactggaataca ctttat-----aacactgatt-----gaataccggacatgggggtt--acaaagattaacaa
Opossum =====
Chicken =====
X. tropicalis =====
                GATA                                                    GATA
    
```

(3\*)

```

Human   :-gctggcgagatagatgttatcttcc-
Mouse   :ggctggaga---agagaatccactcc-
Rat     :ggttggaga---agataatctactcc-
Rabbit  :-gctggcgagctagatgatattctgcc-
Dog     :-gctggtgagatagatgatatttttcc-
Armadillo :-gctggcgagataggtattatattcc-
Elephant :-gctggcgacatagatgatattctgac-
Opossum :-ggtggcgaggaggggtgagaagcggc-
Chicken :-----
X. tropicalis :-----
                GATA      GATA
    
```

**M) PCQAP**

(1) Human --ggag**cacctg**ccgtg  
 Mouse =====  
 Rat =====  
 Rabbit --accg**cccttg**cc-tg  
 Dog ctggaatt**cccg**tcccg  
 Armadillo =====  
 Opossum =====  
 Chicken =====  
 X. tropicalis =====  
 E12 E47 TAL1

(2) Human **cacctg**taatccagctacttgggag  
 Mouse =====  
 Rat =====  
 Dog -----  
 Opossum =====  
 Chicken =====  
 X. tropicalis =====  
 E12 E47 TAL1

(3) Human **ccacc**-----**tg**gtgcttattgaccacttgggctccagattt tctcactgacacctcct-----c---- cccagggtagcagataaaggc  
 Mouse =====  
 Rat =====  
 Dog **tcact**-----**tg**gcacttgggaaccatctaggtttaggattt ttgccacctacccccacccc aaaac---- ccttgaggcacagacaagggc  
 Armadillo **ccacc**-----ttcttgtgaaccactggggttcagggttt ttgtcacctgcccggcctt-----tcttc cccagggacacaggaaacggt  
 Opossum =====  
 Chicken =====  
 X. tropicalis =====  
 E12 TAL1 GATA

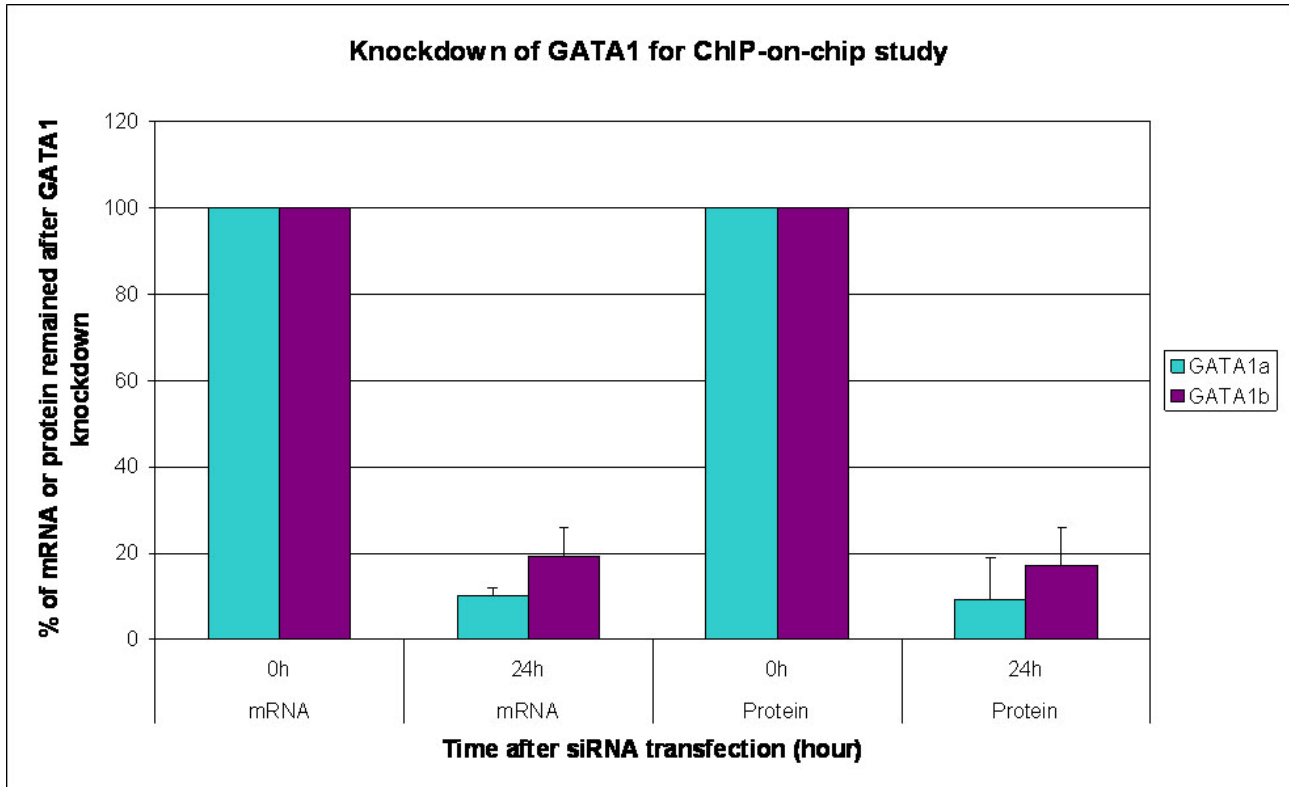
(4\*) Human ggggtg**cagg**tgggctgagtcggaaagagagtcagcgaagg**gagata**gggggtggggtcgttttataggat  
 Mouse -----  
 Rat -----  
 Rabbit -----  
 Dog -----  
 Armadillo -----  
 Opossum -----  
 Chicken -----  
 X. tropicalis -----  
 E12 E47 TAL1 GATA

**N) RSF1**

Human agcaccttcttca-----actggt  
 Mouse agcaccttcttca-----actggt  
 Rat agcaccttcttca-----actggt  
 Rabbit VNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN  
 Dog agcaccttcttca-----actggt  
 Armadillo agcaccttcttca-----actggt  
 Elephant agcacttcttca-----acaggt  
 Opossum agcaccttcttct-----gctggt  
 E12 E47

## Appendix 5

### Confirmation of GATA1 knockdown by qPCR and western blotting in GATA1 ChIP-on-chip study



Two siRNAs directed against GATA1 were used: GATA1a and GATA1b. Knockdown of GATA1 at the mRNA level was quantified by quantitative PCR as described in Chapter 3. Knockdown of GATA1 at the protein level was quantified by densitometry of bands as determined by immuno-detection of the western blotting. Bar chart showed the mRNA or protein level of GATA1 remaining (y-axis) after siRNA transfection relative to luciferase siRNA transfection across the time points (x-axis) Blue bars indicate mRNA levels in the GATA1a condition while the purple bars indicate mRNA levels in the GATA1b condition. Error bars show the standard deviation across three independent biological replicates.