Table S1. Validation of EKLF occupancy

Site	Chromosomal location	Forward primer	Reverse primer	Genomic location	Fold increase mean	SD	P
Neg site 1	chr4:135660984-135661108	GGAAGCCTGGACTCTGGAA	CTGGGGAATCCAAACCAAC	intragenic	1.36	0.25	0.37
Peak 2	chr4:135696994-135697142	CATTTCAGCCTGGGAGCA	TCGGGGTTGGATAGGAGATT	5' distal *Id3*	**1.86**	**0.01**	**0.0002**
Peak 3	chr4:135700678-135700768	CGGAGTTATCAGCTGGAGGTAG	CGAGGGAGCCGTCAGTTT	intragenic *Id3*	**5.65**	**2.13**	**4.6E-05**
Peak 4	chr4:135742664-135742767	TGCCTCATTGTTCCTCTTCC	GCAGGACTGTCTGGCTCCT	5' proximal *E2f2*	**3.14**	**0.19**	**2.9E-06**
Neg site 5	chr4:135750036-135750121	CAGCTCATGACGGGATAGG	GACCACAGGAACCCTGGA	intragenic *E2f2*	1.37	0.24	0.34
Neg site 6	chr4:135771402-135771508	AGGGGTCAGAATCACACCAA	AACTGGCACCAAGACTGCTC	5' proximal *Ddef1*	1.31	0.10	0.007
Peak 7	chr4:135794364-135794519	TCGCTGAGGTGAAGAGCAG	AGCCTCCATCCCAGAGTCC	intragenic *Ddef1*	**1.97**	**0.27**	**0.0005**
Peak 8	chr2:154377695-154377917	CCAGTTATCCGCCCTGAA	AATGAAGGCAGCCTGTGG	intragenic *Apba2bp*	**7.41**	**0.38**	**0.0001**
Neg site 9	chr8:24135379-24135625	TCCCTGCAGTCTAGGTGGTT	GCCACTCTTCTGGTTCAAGG	5' proximal *Ank1*	1.19	0.11	0.41
Peak 10	chr8:24144641-24145055	ACACCCAGGTTCCAAAGACA	GACTAGACAGCAGGTAAAGG	5' proximal *Ank1*	**5.90**	**2.41**	**5.36E-05**
Neg site 11	chr8:24160706-24160833	ACTCGGTCACTTTGGTCATC	TCATTGCAGGGTAATCCCTAA	5' proximal *Ank1*	1.00	0.28	0.67
Neg site 12	chr8:24220968-24221063	AGGGCCCAGAGCTGACTAA	ATGCAGGATGAGCACAAACA	intragenic *Ank1*	1.19	0.01	0.54
Peak 13	chr8:24246144-24246247	GTGCGCTTCAGGAATACGAG	TAGGTTCCTTGCCAGCTTTG	intragenic *Ank1*	**2.70**	**0.06**	**1.11E-06**
Neg site 14	chr8:24268170-24268278	GGAGAACGAGGACGATGAGT	AGGCTGAGCACGGAGAAG	intragenic *Nkx6-3*	1.10	0.42	0.93
Neg site 15	chr8:24302930-24303058	CACTTCACTACACTGGCTGCTC	TTCAGGAACTTGCATTGGTAA	intragenic *Agpat6*	0.91	0.42	0.77

Peak 16	chr8:24318333-24318468	GATCTAACGCCGGGTTCTC	GACCGGTTTCTCTCCTCCTC	intragenic *Agpat6*	**3.539**	**0.48**	**2.32E-05**
Neg site 17	chr12:77636701-77636792	GACTGGAGGGTGCCACAA	AGACAACACCTCCCATCACC	5' proximal *Plekhg3*	1.19	0.03	0.82
Peak 18	chr12:77661130-77661200	GCTTGACCCTCCATCTGTCT	CTCCTGGCTGCCATCTTG	5' proximal *Plekhg3*	**4.21**	**2.08**	**0.0189**
Peak 19	chr12:77699511-77699629	GGACATGAGAACCAGTACCACA	CCTGGAGAAGCCCACCAC	intragenic *Spnb1*	**3.00**	**0.18**	**2.94E-06**
Peak 20	chr12:77704548-77704692	AATAGCGGTGCAGGTCGTAG	CACCATCGCTGAGTGGAAG	intragenic *Spnb1*	**3.67**	**0.55**	**4.12E-06**
Peak 21	chr12:77710011-77710085	CCCCCAGATCCCTTCTACAC	GGGCAAGGATCTCACCACT	intragenic *Spnb1*	**2.49**	**0.04**	**4.49E-06**
Peak 22	chr12:77723872-77723955	CTACAGAACGGGGTGTGAGG	ACCCTGGCACTGCAGAAA	intragenic Spnb1	**1.97**	**0.27**	**0.0005**
Peak 23	chr12:77841810-77841863	GCGATCAAGAGATCATCCAC	AAAAATTCCCCCACCCTGTT	5' distal *Spnb1*	**3.07**	**0.56**	**1.86E-06**
Peak 24	chr12:77852146-77852238	CAGGTCCACCCAGTGCTTAC	TCCATCGTCTCAAGGAAAGTG	intergenic	**2.23**	**0.07**	**0.0004**
Peak 25	chr11:102155504-102155607	AAGCGGGAAGCAGCAATAC	TGGGTTGGACATCTTTGGAC	intragenic *Atxn713*	**1.83**	**0.30**	**0.0004**
Peak 26	chr7:111009508-111009585	GGGTGTGTGGCCAGATGTTT	CACCTTCCCTGTGGACTTCCT	beta-globin HS2	**1.76**	**0.20**	**2.62E-05**
Peak 27	chr7:110962210-110962378	GTTAGTGCCTGCTGGAAAGC	GCACCTGACTGATGCTGAGA	5' proximal *Hbb-b1*	**10.89**	**0.05**	**5.79E-08**
Peak 28	chr7:110961078-110961319	ATGCCCAAAGGTCTTCATCA	GGTTCTTCCATCTTCCCACA	intragenic *Hbb-b1*	**1.44**	**0.01**	**0.0007**
Peak 29	chr2:102741149-102741324	CGGGCATCCAAGAGTACAGT	GGGATTTGGGGCTATGCTAT	5’ proximal *Cd44*	**10.5 (P)** 1.03 (E)	**2.53** 0.65	**0.001** 0.47

Table S2. EKLF motif analysis

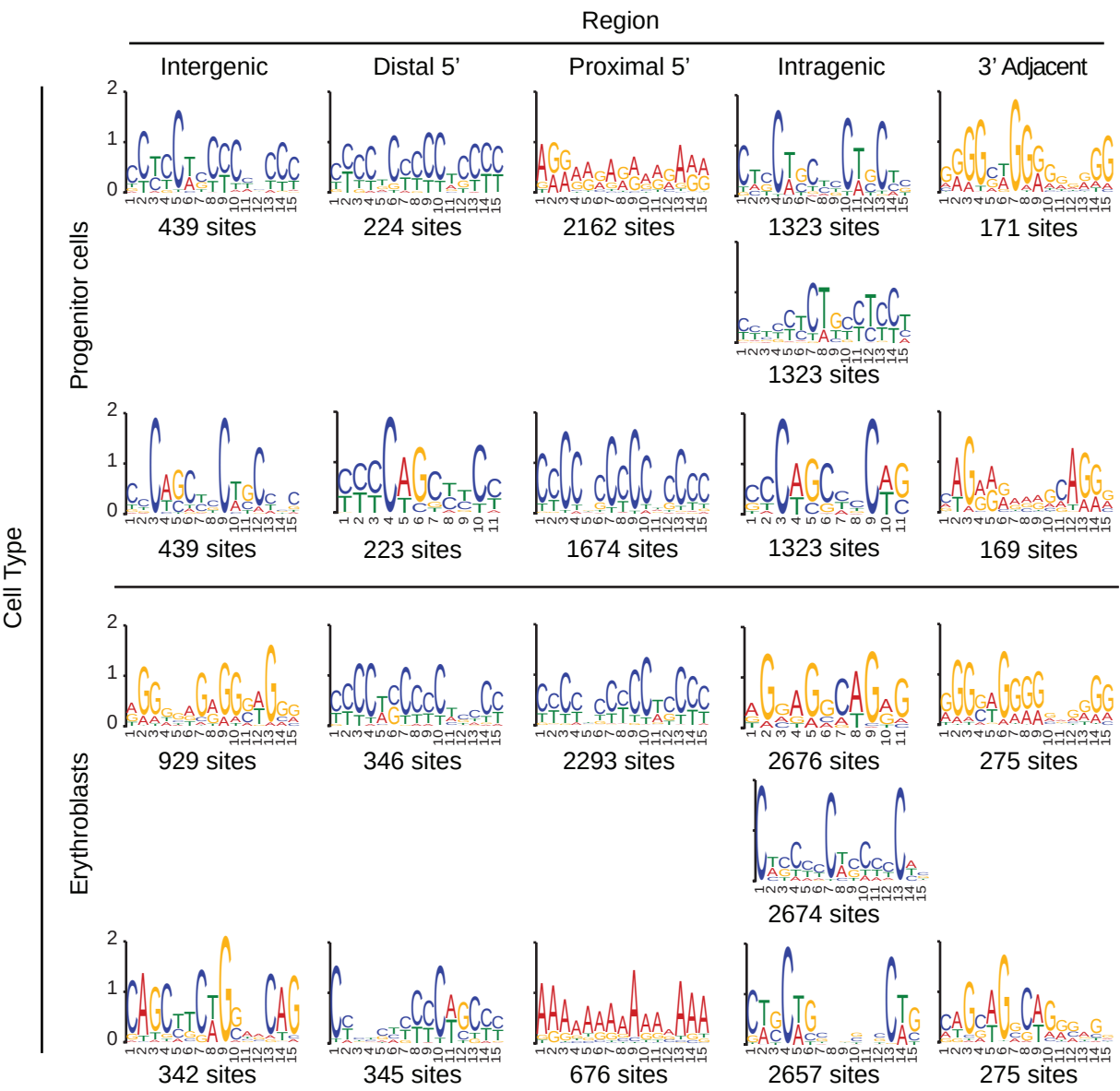

Table S3. Differentially expressed EKLF Target genes

Those genes that are occupied by EKLF only in progenitor cells or erythroblasts are referred to as Pro only and Ery only respectively. Genes that are occupied by EKLF in both progenitor cells and erythroblasts are referred to as Common. mRNA levels can change from high levels in Pro to lower levels in ERY (Hi>Lo) or vice versa. The number of genes with that particular expression pattern is indicated.

PRO only Hi -> Lo (190)	PRO only Lo -> Hi (26)	ERY only Hi -> Lo (692)	ERY only Lo -> Hi (246)	Common Lo -> Hi (27)	Common Hi -> Lo (70)
0910001L09Rik	Abhd4	0610009D07Rik	1300017J02Rik	Abca7	0610007L01Rik
1110038B12Rik	Acbd5	1110004E09Rik	1810058I24Rik	Acbd4	1300001I01Rik
1110058L19Rik	Apoa1	1110004F10Rik	2010011I20Rik	Ank1	2310011J03Rik
1810022K09Rik	Arfgap3	1110020P15Rik	2310035K24Rik	Arrdc2	2410001C21Rik
2510012J08Rik	Btrc	1500001M20Rik	2810453I06Rik	Brpf3	3110082I17Rik
2810002N01Rik	Cdkn2c	1500011K16Rik	4833442J19Rik	Ehbp1l1	Adrbk1
Abce1	Chd2	1700034H14Rik	4930523C07Rik	Epb42	Aes
Acat1	Cldn13	1810006K21Rik	5730469M10Rik	Fbxl15	Akt1
Acly	Creg1	1810009A15Rik	5830415F09Rik	Galnt10	Ankrd27
Adi1	Depdc1b	1810035L17Rik	AA986860	Gmpr	Ankrd52
Adprh	Dlk1	1810046J19Rik	AI317395	Gpr146	Ap2a1
Akr1b3	Dnajb6	2010107E04Rik	Abcb10	Hipk1	Arrb2
Aldh2	Dnase1l1	2310008H09Rik	Abtb1	Hmox1	Asrgl1
Aldoa	Eral1	2310016M24Rik	Ache	Itsn1	Bop1
Arf3	Gabbr2	2410016O06Rik	Acot11	Mgll	Cad
Asna1	Ift140	2500003M10Rik	Acp5	Mical3	Calm3
Atp5g2	Klhl25	2610002D18Rik	Adipor1	Mpp2	Capzb
Atxn10	Lgmn	2610027L16Rik	Adra2b	Mxi1	Ccnd2
Bat2	Ppox	2610301G19Rik	Adrb2	Pcx	Cdk2ap1
Bst2	Sept1	2610528E23Rik	Aff1	Rfx2	Chd4
Ccdc72	Sh3tc2	2700060E02Rik	Akap13	Sema4b	Coq7
Cct3	Snx15	2700094K13Rik	Akap7	Sertad3	Coro1c
Cct5	St3gal1	2810432D09Rik	Alas2	Slc2a4	Ctnnbl1
Cd44	Tnfrsf14	2900010J23Rik	Amigo3	Slc9a8	Dazap1
Cdc37	Trak2	2900010M23Rik	Ankrd43	Ston2	Dcakd
Cdc42se1	Zfp217	2900097C17Rik	Ankrd9	Tcf7l2	Dgkz
Cdca7		5730437N04Rik	Arhgef12	Tmod1	Drap1
Cdca7l		9530068E07Rik	Arid3b		E130309D02Rik
Cebpz		AU022870	Asb1		Ehmt2
Cherp		Aaas	Atg4d		Eif4ebp1
Clic1		Aarsd1	Atg9a		Galnt2
Clint1		Abcf1	Atp2b4		Gnai2
Copg		Abhd11	B230312A22Rik		H13
Cops8		Acads	Bbs7		H2afy
Cox7a2l		Acbd6	Bcl2l1		Lman2
Crip1		Acp5	Blvrb		Ly6e
Csk		Acsl5	Btg2		Mrpl38
Cstf2		Acss1	C330018D20Rik		Mrps2
Cuedc2		Actg1	Cadm3		Myh9
Cul4b		Actl6a	Car2		Phpt1
Cyba		Add3	Cat		Pkn1
D10Jhu81e		Adk	Cchcr1		Pola2

D19Bwg1357e
Dbnl
Dctn2
Dctn6
Ddx23
Ddx49
Dera
Dpm3
Ebna1bp2
Ech1
Eef1a1
Eef2
Efha1
Egfl7
Ei24
Eif4b
Eif4g1
Elp3
Eno1
Etfb
Exosc2
Fbl
Fbxl6
Fpgs
Gfm1
Grb10
Gsto1
Gtf2f2
Gtf3a
H1f0
H2-K1
H2-Ke2
Hars
Hira
Hk1
Hmgcl
Iars
Idh2
Ifngr1
Ilf3
Ipo11
Isg20l2
Isoc2a
Jagn1
Klhdc3
Krtcap2
Ldha
Lmo4
Lonp1
Lrrc59
Lypla2
Magoh
Mcm2
Mdh1
Adpgk
Adprhl2
Aggf1
Agpat5
Aifm1
Ak3
Aldh18a1
Aldh9a1
Alg8
Ampd2
Ankrd13a
Anp32a
Ap1b1
Ap1s1
Ap3s1
Apbb1ip
Apoa1bp
Aqp1
Arf6
Arhgef1
Arid1a
Arl5a
Arpc1b
Arpp19
Ash2l
Asns
Asnsd1
Atad1
Atad3a
Atic
Atp1b2
Atp5j
Atp5o
Atp6v0e
Atp6v1h
Aven
B230208H17Rik
BC005624
BC048355
Bak1
Bat2d
Baz1a
Bcap31
Bcat2
Blmh
Brd2
Brms1
Brp16
Bscl2
Bysl
Bzw1
C030046I01Rik
C80913
Calr
Ccndbp1
Ccrl2
Cd24a
Cd59a
Cd82
Cdc25b
Cdkl1
Cenpf
Cep76
Chac2
Clk3
Cln8
Cpeb4
Crat
Ctsf
D14Ertd436e
D18Ertd653e
D930015E06Rik
Dapk2
Ddhd1
Ddx26b
Dennd1a
Dnajb13
Dnajb3
Dnajb4
Dnajc4
Dtnb
Dusp8
Dyrk3
E130309D14Rik
E2f2
Eif2ak1
Eif5a2
Epb41
Epb49
Evi5
Ezh1
Fbxl3
Fbxo34
Fcho2
Fech
Fn3k
Frmd4a
Fryl
Ftl1
Fzd5
Fzr1
Gabarapl2
Gadd45a
Gclm
Gcnt1
Gfap
Ghitm
Gpr150
Polr3e
Ppih
Ppp1r9b
Ppp2r5d
Psma3
Ranbp3
Rbm19
Rcc2
Rpl3
Rpl6
Rpn1
Rpp21
Sept9
Sfrs3
Sh3bp1
Slc19a1
Slc38a1
Smyd2
Snrpa
Ssbp4
Ssr2
Tgfb1
Timm44
Trim27
Txlna
Wdr46
Wdr6
Ywhag

Mknk2
Mns1
Mpp6
Mrpl15
Mrpl27
Mrpl3
Mrpl54
Mrps14
Mta1
Nat10
Ncl
Ncoa5
Ndufb10
Ngp
Nolc1
Npepl1
Nudt16l1
Nudt21
Nudt3
Nvl
Otud4
Pbx2
Pebp1
Pelp1
Pfdn5
Pfkl
Pkm2
Pold1
Pold2
Pole2
Ppil3
Ppp1cc
Ppp2ca
Pprc1
Prkcsh
Prmt3
Prpsap1
Psmb5
Psmc2
Psmc4
Ptbp1
Ptma
Ptpn6
Pwp1
Rbm28
Riok2
Rnf187
Rnpep
Rpl37a
Rpp14
Rps25
Rps27a
Rps8
Scarb1
Cand1
Capza1
Ccdc101
Ccdc106
Ccdc115
Ccdc56
Ccdc86
Ccne1
Ccng1
Ccnh
Cct4
Cd3eap
Cd63
Cdc20
Cdc26
Cdk9
Cdt1
Cetn3
Cfdp1
Cfl1
Chaf1a
Chchd1
Chchd2
Chchd4
Churc1
Cirh1a
Clns1a
Clpp
Cmtm7
Cnbp
Cnih
Cnn2
Cnot10
Copa
Copb1
Cops4
Cops6
Coro1a
Cox8a
Cs
Cst3
Cstb
Cstf1
Ctsz
Cul1
Cuta
Cxxc1
Cyb5b
Cyc1
D10Wsu52e
D17Wsu104e
Dalrd3
Daxx
Dbi
Grap2
Grina
Gtpbp2
Gypa
H2-T23
H3f3a
Hace1
Hagh
Hba1
Hbb
Hdac11
Hemgn
Herc1
Hist1h2ab
Hist1h2ac
Hist1h2af
Hist1h2bf
Hist1h2bj
Hist1h4m
Hmbs
Hspbap1
Ibtk
Icam4
Igf2
Ikbkg
Josd2
Kctd9
Klf3
Klhl7
Loxl2
Lpin2
Mafg
Mafk
Map3k7ip3
Map4k5
Mapk8ip3
Mar2
Mare
Med12
Mgst3
Mki67
Mmel1
Mpp1
Mppe1
Mpst
Mst1
Mt1
Mxd1
Mxd3
Myo1d
Naprt1
Nbr1
Ncoa7
Nfe2

Sfrs4
Sfrs9
Shmt2
Slc25a5
Slc29a1
Smarca4
Smarcd2
Smchd1
Smu1
Snrpa1
Snrpb2
Snrpf
Srp9
Tagln2
Tbcb
Tbl1x
Thbs1
Timm8a1
Tk1
Tmem147
Tmem70
Tomm7
Tpm4
Tpr
Tpst2
Trappc4
Trappc6a
Trim28
Tspan3
Tsta3
Txn2
Txndc5
Ube2d2
Ube2n
Vars
Vasp
Vim
Ybx1
Zfp330
Zyx

Dcps
Dctn5
Ddx1
Ddx24
Ddx27
Ddx39
Ddx46
Ddx54
Deb1
Dhcr24
Dis3
Dlst
Dnaja2
Dnajc15
Dph5
Dtd1
Dtymk
Dynll2
E2f6
Ecd
Ecsit
Eef1g
Efhd2
Eif1b
Eif2b4
Eif2b5
Eif2s1
Eif2s3x
Eif4e
Eif4ebp2
Eif4h
Eif5a
Elac2
Elavl1
Elof1
Emd
Emp3
Eprs
Ergic1
Erh
Ero1l
Esf1
Exoc6
Exosc3
Exosc5
Exosc6
Exosc7
Ext2
Ezh2
Fbxl14
Fcf1
Fem1b
Fen1
Fkbp1a

Nqo1
Nt5c3
Nusap1
Otub2
Paqr3
Parp16
Pcmtd2
Pdzk1ip1
Pepd
Phospho1
Pigq
Pim1
Pip5k1a
Pir
Pkhd1l1
Pld3
Plek2
Pnpla8
Pnpo
Popdc2
Prdx2
Prnp
Prokr1
Rab3il1
Rad23a
Ranbp10
Rbm38
Rhd
Rnf123
Runx1t1
Sec23a
Senp7
Sertad2
Sh3yl1
Shb
Slc16a10
Slc1a5
Slc22a4
Slc25a37
Slc25a39
Slc2a1
Slc43a1
Slc4a1
Slc6a9
Smox
Snca
Snx22
Sorbs1
Sox6
Spata13
Sptb
Spsb3
Srxn1
Ssh1

Fkbp4
Fnta
Ftl1
Fto
Ftsj3
Galk1
Gart
Gcsh
Gemin5
Gga1
Glt25d1
Gltscr2
Gmps
Gna12
Gng10
Golt1b
Got1
Got2
Gpaa1
Gpr56
Gpr89
Gtf2i
Gusb
Gyg
Hadh
Hax1
Hba1
Hbb
Hdac1
Hdac2
Hdac3
Hdgfrp2
Heatr3
Hells
Hiatl1
Hibadh
Hint1
Hmga1
Hmga1-rs1
Hmgb3
Hmha1
Hnrpll
Hsbp1
Hsd17b4
Hsf1
Hspa14
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Hspa9
Htatsf1
Huwe1
Ide
Idh3b
Igfbp4
Ikzf1
St3gal5
Stk3
Synj1
Syt14
Tac2
Tax1bp1
Tbcel
Tcf19
Tcp11l2
Tfdp2
Timd2
Tmcc2
Tmco6
Trim10
Trim56
Trim58
Trp53bp1
Tspan33
Txnrd2
Ubap1
Ube2c
Ube2e3
Ube2h
Ube2l6
Ube2o
Ucp2
Ulk1
Unc5cl
Unkl
Urod
Vangl1
Wbp1
Wbp2
Wdr26
Xpa
Xpo7
Yipf4
Yod1
Ypel3
Ypel4
Zdhhc14
Zfp341

Ilf2
Ilkap
Imp4
Inpp5d
Ints10
Ipo7
Isyna1
Itm2b
Kars
Kctd10
Kdelr2
Khdrbs1
Khsrp
Klhl23
Kpna2
Lars
Lcp1
Ldb1
Leo1
Lgals1
Lig1
Lman1
Lmnb1
Lrp10
Lrpprc
Lsg1
Lsm12
Lsm2
Lsm5
Lsm6
Ltv1
Lyar
Mapre2
Mars
Mbd3
Mcm10
Mcm3
Mcm4
Mcm5
Mcm7
Mdh2
Med4
Med8
Metap1
Mettl2
Mif
Minpp1
Mki67ip
Morf4l2
Mphosph10
Mrpl11
Mrpl13
Mrpl14
Mrpl28

Mrpl33
Mrpl34
Mrpl37
Mrpl49
Mrps10
Mrps17
Mrps24
Mrps27
Mrps28
Mrps30
Mrps9
Msh2
Msn
Mtap
Mthfd1l
Mtx1
Myb
Myc
Myeov2
Myl6
Nans
Nap1l1
Nap1l4
Narg1
Nasp
Ncln
Ndufa10
Ndufa12
Ndufa4
Ndufa5
Ndufab1
Ndufb3
Ndufs2
Ndufs8
Nedd8
Nfu1
Ngdn
Nhp2l1
Nmd3
Nme2
Nme4
Nme6
Nmt1
Noc3l
Nol10
Nol6
Nol9
Nrgn
Nsd1
Nsmce4a
Nt5c
Nt5c2
Nt5dc2
Nubp2

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Nudcd2
Nudt1
Nup160
Nup188
Nup205
Nup37
Nup85
Nup93
Nxt1
Oat
Obfc2b
Orc3l
Orc5l
Oxa1l
Oxct1
Pa2g4
Pabpn1
Paf1
Park7
Parn
Parp1
Parp2
Pdcd11
Pdcd2
Pdia4
Pdk1
Pfas
Pfdn1
Pfkm
Pfn1
Pgd
Pgk1
Phb
Phf10
Pitpna
Pitpnb
Pmpcb
Pno1
Podxl
Poldip3
Polr2e
Polr2f
Polr2h
Pom121
Por
Ppan
Ppat
Ppia
Ppie
Ppil1
Ppp1ca
Ppp1r7
Ppp2r2a

Ppp3r1
Ppp5c
Prcc
Prdx6
Preb
Prep
Prim2
Prkar1a
Prkrir
Prmt1
Prpf38a
Prpf6
Prps2
Prtn3
Psap
Psat1
Psd4
Psen2
Psma1
Psma2
Psma4
Psma5
Psmb3
Psmb4
Psmb7
Psmc5
Psmd12
Psmd13
Psme1
Psme2
Ptcd3
Ptges3
Ptov1
Ptplad1
Ptpn11
Ptpn7
Pus1
Pycr2
Pycrl
Qars
Qdpr
Rab7
Rac2
Rad23b
Rad51
Rae1
Rap1gds1
Rapgef1
Raver1
Rbck1
Rcc1
Rcl1
Rexo2
Rfc2

Rfc5
Rgs10
Rnasen
Rnf126
Rnf130
Rpia
Rpl10a
Rpl13a
Rpl15
Rpl19
Rpl24
Rpl27
Rpl29
Rpl32
Rpl35
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Rpl7
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Rps4x
Rps9
Rqcd1
Rrm1
Rrn3
Rrp15
Rrp9
Rrs1
Rsl1d1
Rtcd1
Ruvbl1
Ruvbl2
Sae1
Samm50
Sap18
Sar1a
Sar1b
Sars
Sat1
Scamp3
Scap
Scd2
Sdha
Sdhb

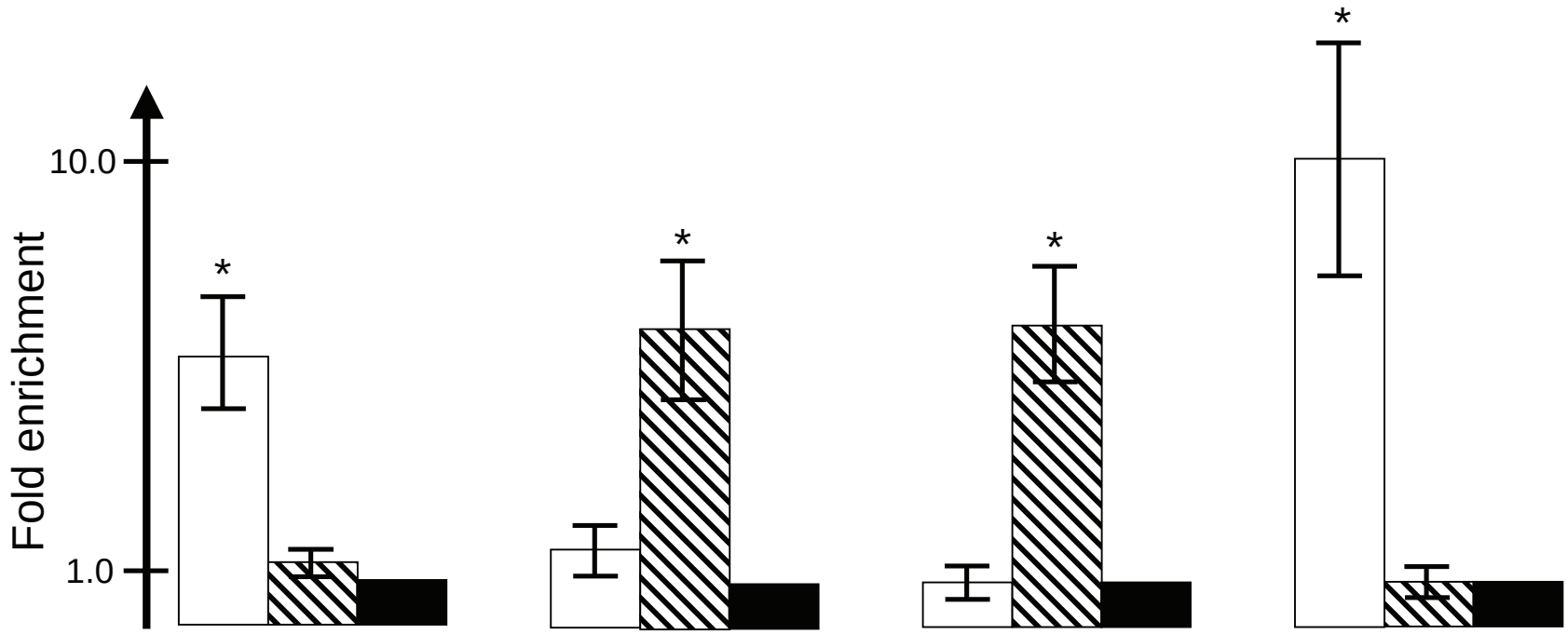
Sdhc
Sec11a
Sec11c
Sec13
Sec24c
Sec61a1
Serbp1
Set
Setdb1
Sf1
Sf3a1
Sf3b2
Sf3b3
Sfpi1
Sfxn1
Sgta
Sh3bgrl3
Siva1
Slc16a3
Slc25a11
Slc25a13
Slc25a17
Slc25a3
Slc35c2
Slc39a8
Slc4a1
Slc7a1
Smad2
Smarca5
Snap23
Snrpb
Snrpc
Snrpd1
Snrpd2
Snrpe
Snrpg
Snw1
Snx17
Snx6
Sord
Spag7
Spcs2
Sra1
Srm
Srp72
Srpk1
Ssb
Ssr1
St3gal6
Stmn1
Stra13
Stt3a
Stxbp2
Sucla2

Suclg1
Sumo1
Surf1
Surf2
Surf6
Syce2
Sympk
Syncrip
Taf10
Taf12
Tars
Tars2
Tarsl2
Tbca
Tbl3
Tbrg4
Tcerg1
Tcf25
Tcof1
Tex10
Tfdp1
Thg1l
Thoc3
Thoc4
Thoc5
Thoc7
Thop1
Thra
Tigd3
Timm23
Timm50
Timm9
Tipin
Tmbim4
Tmed10
Tmed2
Tmed9
Tnpo1
Tnpo3
Tomm40
Tomm70a
Top2b
Tpi1
Tra2a
Trappc3
Trmt1
Trp53
Tspan31
Tsr1
Ttc27
Ttll12
Tuba1a
Tubb5
Tut1

Txnrd1
Tysnd1
Ubap2
Ubap2l
Ube2e1
Ube2g2
Ube2i
Ube2m
Ube2q2
Ubqln4
Ubtf
Uchl3
Uchl5
Ufc1
Ugcg
Umps
Unc119
Ung
Uqcr
Uqcrb
Uqcrc1
Usmg5
Usp1
Usp10
Usp39
Usp5
Utp14a
Vac14
Vamp5
Vdac1
Vps25
Vps4b
Vps72
Wdr1
Wdr12
Wdr18
Wdr4
Wdr5
Wdr61
Wdr74
Wdr75
Wibg
Xpo1
Yars2
Yeats4
Yif1b
Ythdf1
Ythdf2
Zc3h14
Zfp36l2
Zmiz2
Zmpste24
Zmynd19
Znrd1

l7Rn6
rp9

Figure S1

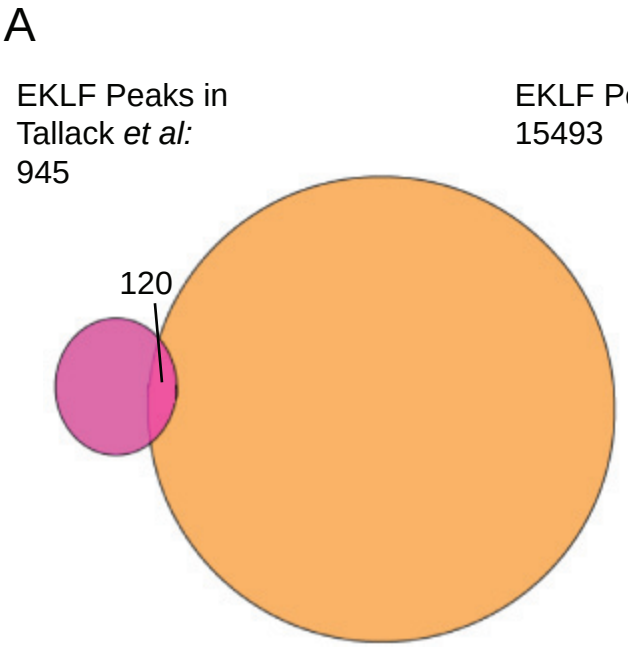


Locus:	*Ank1*	*Spnb*	*Spnb*	*Cd44*
Location:	1E promoter Fig. 1 peak 10	Intragenic Fig. 2 peak 19	Intragenic Fig. 1 peak 21	Promoter Fig. 5
Specificity: (ChIPSeq)	Progenitor	Erythroblast	Erythroblast	Progenitor

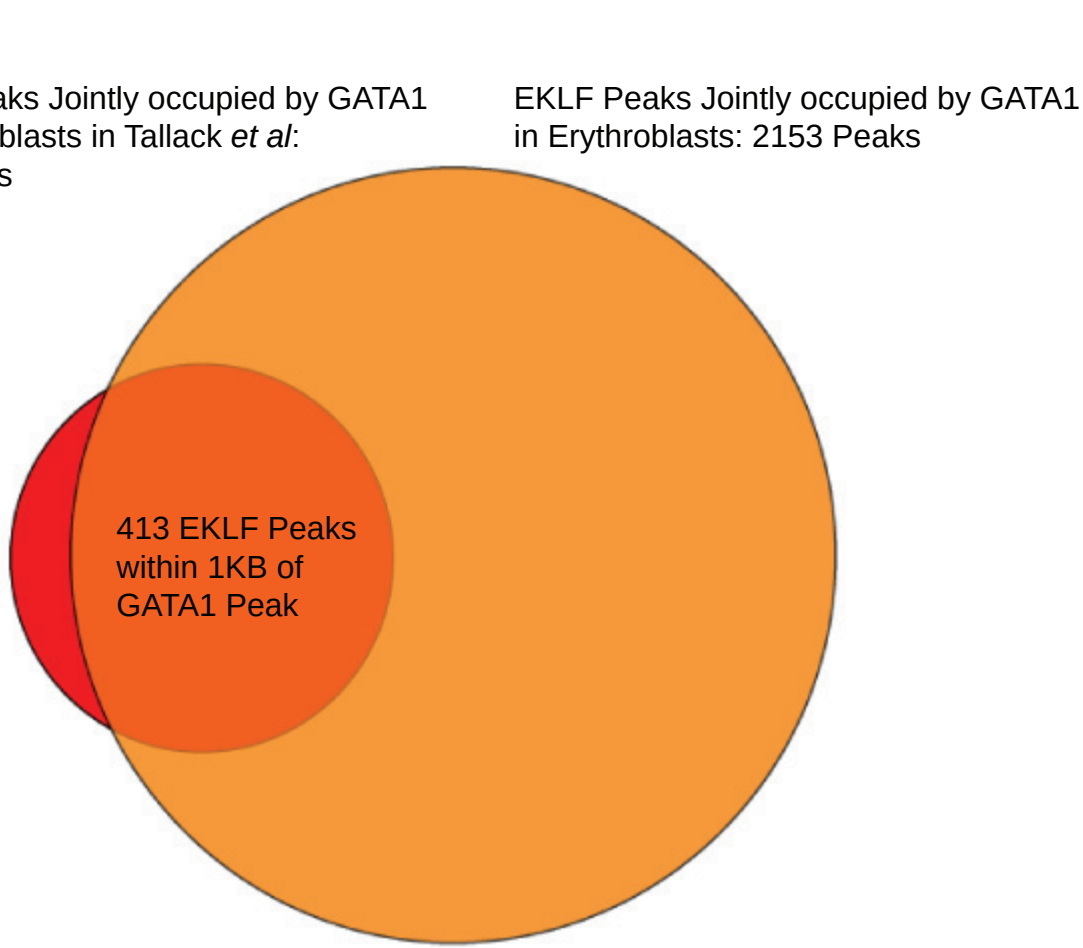
Figure S1. ChIP analysis of cell type specific EKLF occupancy. Chromatin was isolated from sorted day 13.5 HA-*Klf1* fetal liver progenitor cells (white bars) and Erythroblasts (hatched bars), and enriched with an anti-HA antibody. The enriched chromatin from each cell type was amplified along with unfractionated input chromatin (black bars) using the primers listed in Table S1. Significant enrichment in either progenitor cell or erythroblast chromatin was observed at all 4 locations (* $p<0.01$).

Figure S2

A



B



C

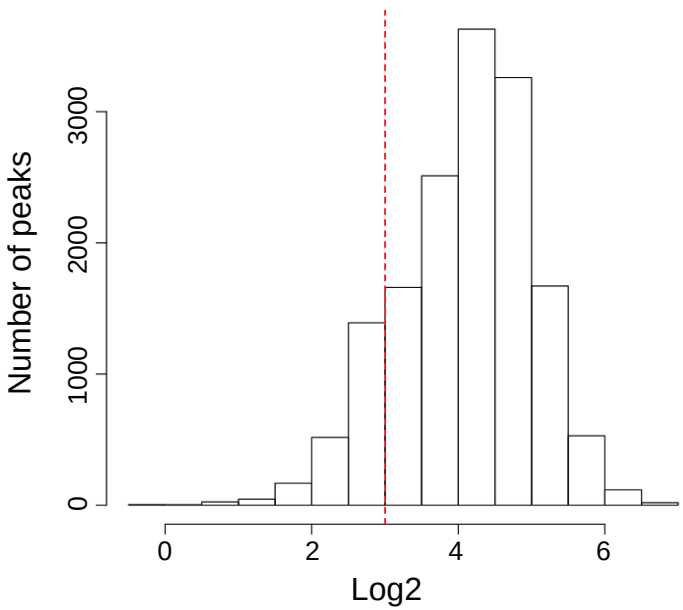


Figure S2. Comparison of EKLF occupancy. (A) Tallack et al. identified 945 EKLF peaks (pink) while this study identified over 15,000 EKLF peaks (orange), of which 120 were identical in both data sets. (B) Tallack et al. identified 454 EKLF peaks within 1 kb of a GATA1 occupied site. A similar analysis of our data identified over 2000 such peaks, of which 415 overlapped with the peaks identified by Tallack et al. (C) While the number of EKLF peaks in associated with GATA1 peaks was 48% of the peaks identified by Tallack et al., EKLF peaks within 1 kb of a GATA1 occupied site (left of the red vertical line) were only 14% of the peaks identified in our study.