

## Supplemental Methods

### Cell Culture

We isolated CD34<sup>+</sup> cells from human cord blood using EasySep™ Human CD34<sup>+</sup> Selection Kit II and tested for purity over 95% using flow cytometry. For erythroid differentiation, CD34<sup>+</sup> cells were cultured at 10<sup>5</sup> cells/ml for seven days in SFEM II medium, supplemented with 1% penicillin/streptomycin, 10 ng/ml stem cell factor, 10 ng/ml IL-3, and 3 IU/ml erythropoietin (EPO). Then, the cells were cultured at 4 × 10<sup>5</sup> cells/ml for four more days in SFEM II supplemented with stem cell factor and EPO, and cultured at 7.5 × 10<sup>5</sup> cells/ml for 3 more days in SFEM II supplemented with EPO. Human CB samples from full-term newborns were obtained from Beijing Obstetrics and Gynecology Hospital, Capital Medical University (Beijing, China) with parental consents. The subject has signed an informed consent form, and the research was approved by the ethical committee of Beijing Institute of Genomics (BIG), Chinese Academy of Sciences. To validate the functions of lncRNAs in erythropoiesis, a lentiviral overexpression system was used to overexpress *DANCR* and *PCED1B-AS1* in CD34<sup>+</sup> cells<sup>35</sup>. Cells were cultured in an incubator at 37°C with 5% CO<sub>2</sub>.

### Overexpression and knockdown of *DANCR* and *PCED1B-AS1*

The mRNA sequences of *DANCR* and *PCED1B-AS1* were obtained from NCBI and cloned into the lentiviral plasmid pHAGE-fEF-1a-IRES-ZsGreen-2. The overexpression plasmid or the empty plasmid, the packaging plasmids psPAX2 and pMD2.G were co-transfected into 293T cells at a ratio of 1:1:1. The *DANCR* and *PCED1B-AS1* shRNA were cloned into the lentiviral plasmid pSIH1-H1-puro-coGFP, The control and knockdown plasmids were co-transfected into 293T cells with the packaging plasmids pMDLg, VSVG, and pRSV-Rev at the ratio of 10:5:3:2. The cell culture medium was collected at the timepoint of 48h and 72h, and concentrated 50 times with PEG 8000 (Solarbio). The differentiated CD34<sup>+</sup> cells were infected on day 2 according to the MOI value of the virus, and the proportion of GFP-positive cells was analyzed by flow cytometry. Primer sequences used for overexpression or knockdown are shown in Supplementary Table 1 A-B.

### Dual-luciferase reporter assay

The promoter sequence of *PCED1B-AS1* (-984~+1) was amplified and cloned into PGL4.10 plasmid. JASPAR (<http://jaspar.genereg.net/>) was used to predict the GATA1 binding site (-

421~432) on the promoter. QuikChange Primer Design is used (<https://www.genomics.agilent.com/primerDesignProgram.jsp>) to design the primers for mutation and deletion. Using QuikChange Lightning (Agilent), normal plasmid is used as template to construct mutant and delete plasmids according to the method provided by the manufacturer. PGL4.10 empty plasmid and recombinant plasmid (100 ng) and internal reference plasmid PRL-TK (5 ng) were co-transfected into 293T cells ( $0.5 \times 10^5$ /well) using Lipofectamine 2000. After 48h, each well was lysed with 80  $\mu$ L 1 $\times$ Passive Lysis Buffer, 10  $\mu$ L of which was taken, and tested by a dual luciferase assay. Primer sequences used for dual luciferase assay are shown in Supplementary Table 1C.

### **Colony-forming unit assay**

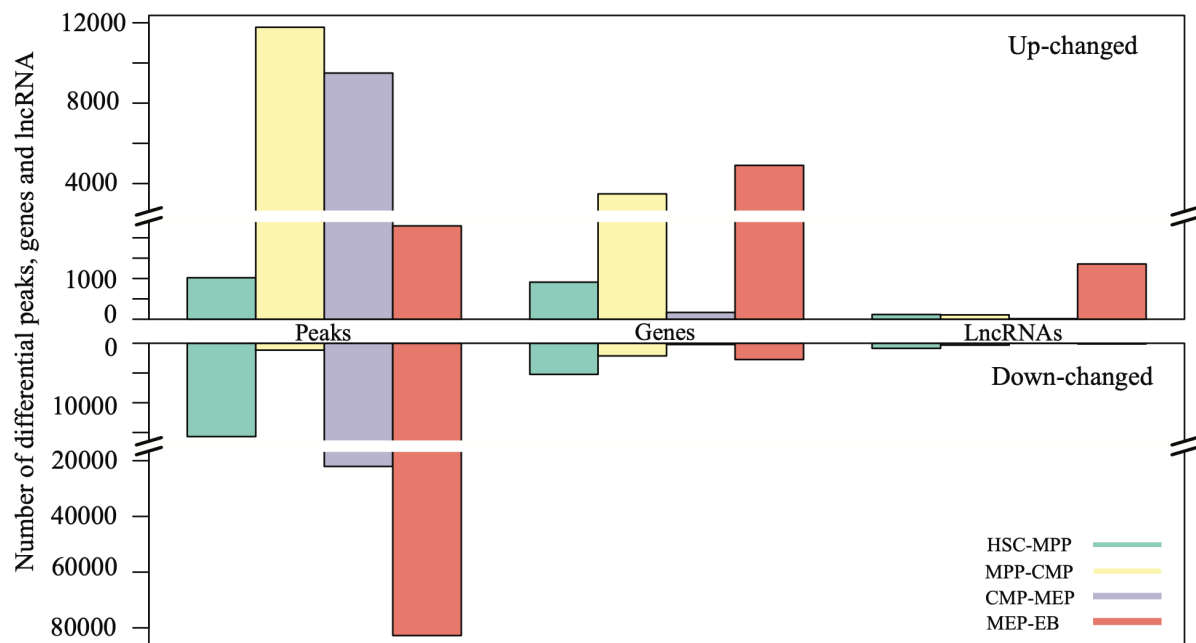
Colony-forming units (CFU) were generated in a cytokine-containing methylcellulose medium (MethoCult Media H4434, StemCell Technologies) by seeding 500 cells per well with 0.6 ml medium in a 12-well plate. After 12–14 days of culturing, multi-lineage colonies were counted under an inverted microscope.

### **In vitro RNA pull-down assay**

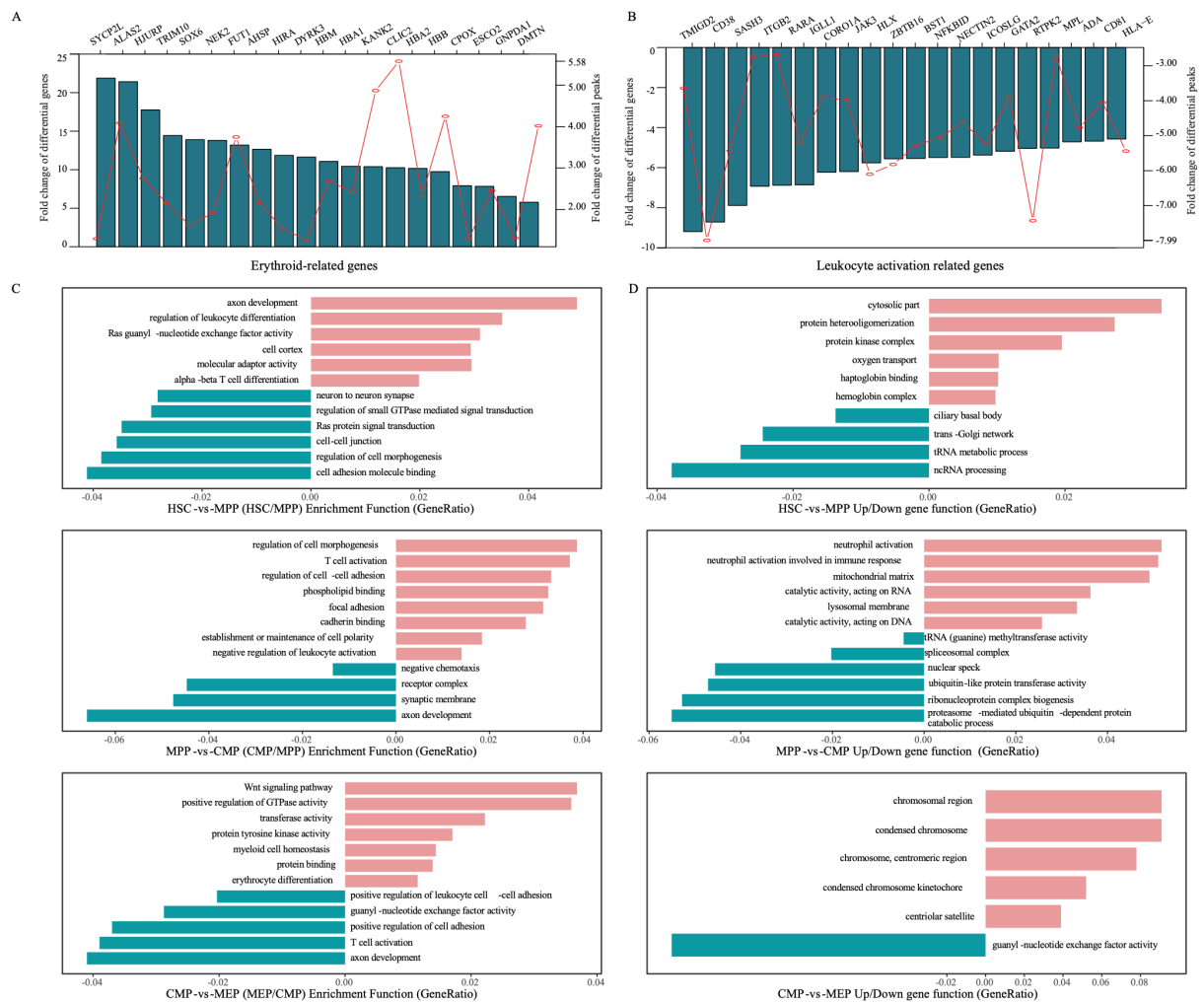
Substrate RNA for bead immobilization was in vitro transcribed in a 20  $\mu$ L reaction mix containing 1  $\mu$ g of template DNA of *PCED1B-AS1*, 4  $\mu$ L 5x T7 transcription buffer, and 1  $\mu$ L T7 RNA polymerase mix at 37 °C for 12 h. After purification with Trizol Reagent, the transcribed RNA was labelled with Biotinylated cytidine biphosphatem to form Biotin-RNA at 16 °C overnight. Then 150  $\mu$ L Pierce Nucleic-Acid Compatible Streptavidin Magnetic Beads (Thermo fisher, Cat# 20164) was mixed with Biotin-RNA and incubated in RNA Capture buffer for 15-30 minutes. After washing the RNA-bead complex twice with Wash Buffer, we resuspend the Beads with 1 x Protein-RNA Binding Buffer. Then the RNA-bead complex was incubated by rotating with the cell extracts of differentiated CD34<sup>+</sup> cells on day 11 at 4 °C for 1h. After washing the beads 5 times, 50  $\mu$ L Biotin Elution buffer was added to elute the proteins bound to the immobilized RNAs. The recovered proteins were resolved by gradient gel electrophoresis for identification by mass spectrometry. Primer sequences used for amplification of the template DNA are shown in Supplementary Table 1D.

## Additional Figure

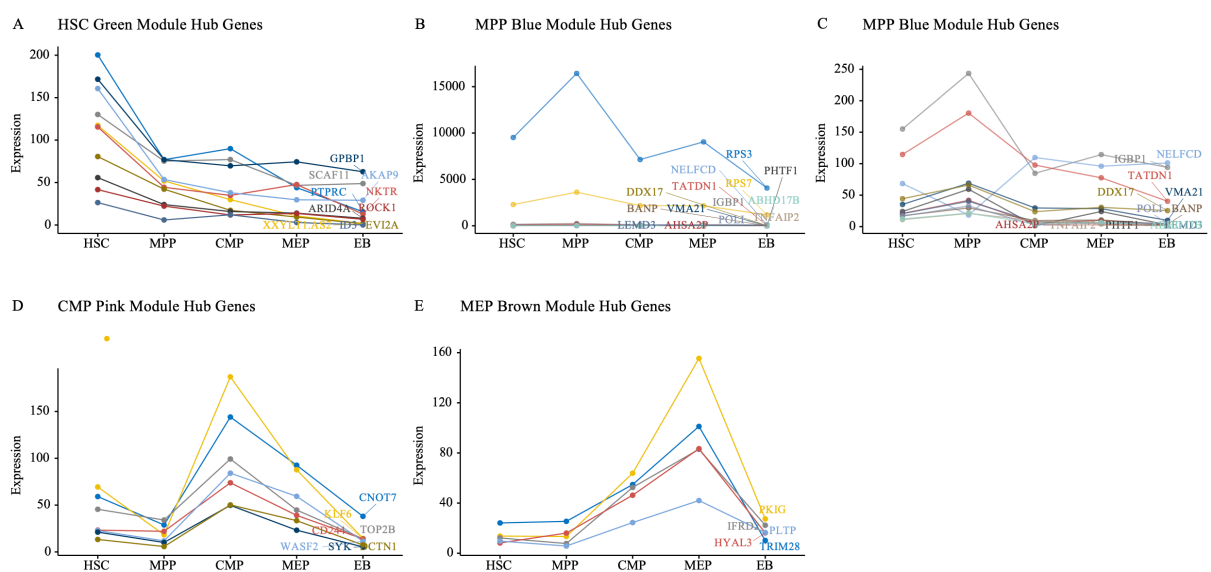
**Supplemental Figure 1. Number of differentially accessible peaks, genes, and lncRNAs at adjacent stages during erythroid differentiation.** The upper panel shows changes in the enhanced accessible chromatin, up-regulated genes, and lncRNAs of adjacent stages during erythroid differentiation, and the bottom panel displays the results of opposite changes.



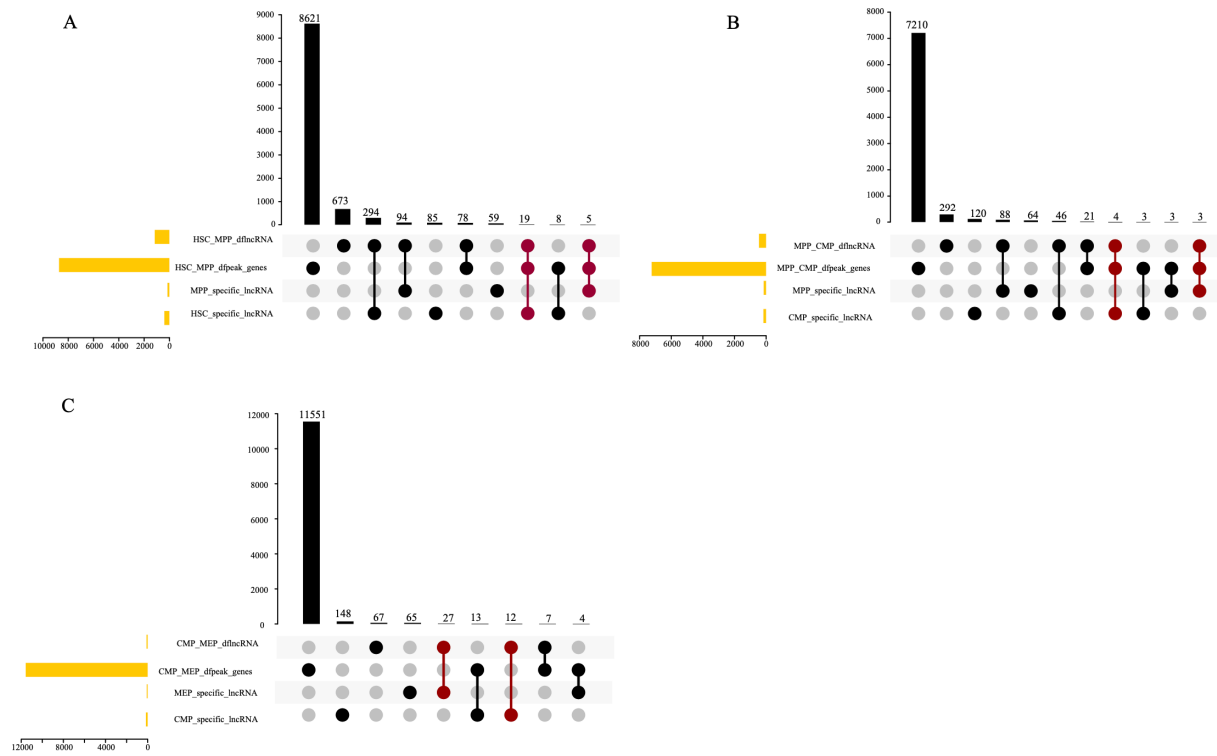
**Supplemental Figure 2. Relationship between mRNA-seq differential expression genes and chromatin accessibility change associated genes during MEP to EB.** (A). The changes of top 20 erythroid-related genes and associated chromatin accessibility during MEP to EB. (B). The changes of top 20 leukocyte activation related genes and associated chromatin accessibility of during MEP and EB. The blue bar plot represents the fold change of mRNA-seq differential genes, and the red line represents the fold change of differential peaks. Enriched function of differentially accessible chromatin (C) and expressed genes (D) during HSC differentiated into CMP.



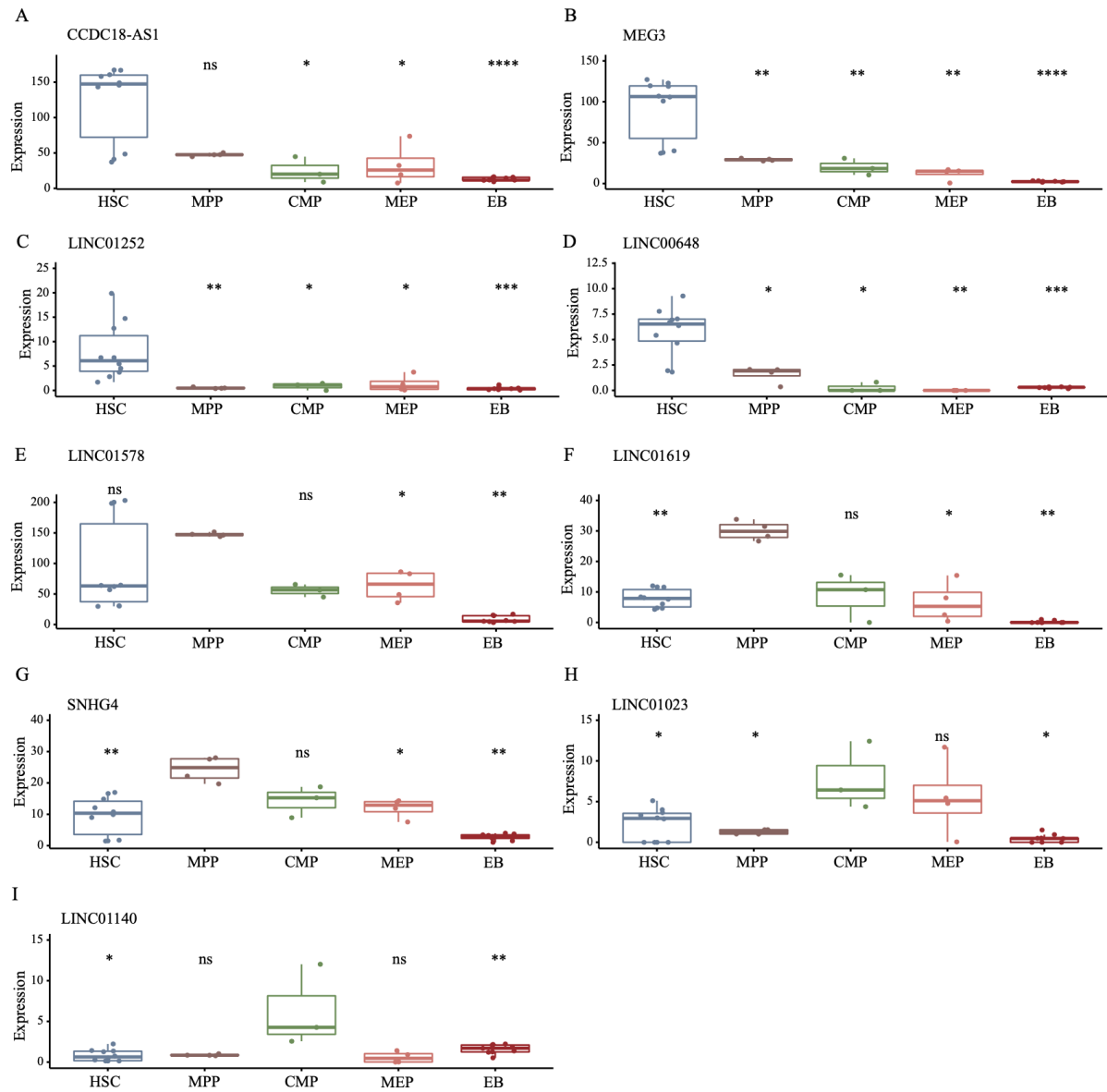
**Supplemental Figure 3. Expression of hub genes in significant modules of each stage during HSC differentiated into MEP.**



**Supplemental Figure 4. Integrative screening of lncRNAs.** The upset plot shows the number of intersecting lncRNAs among specific lncRNAs, differential lncRNAs, and genes annotated in differential accessible chromatin from HSC differentiated into MEP during erythroid differentiation.

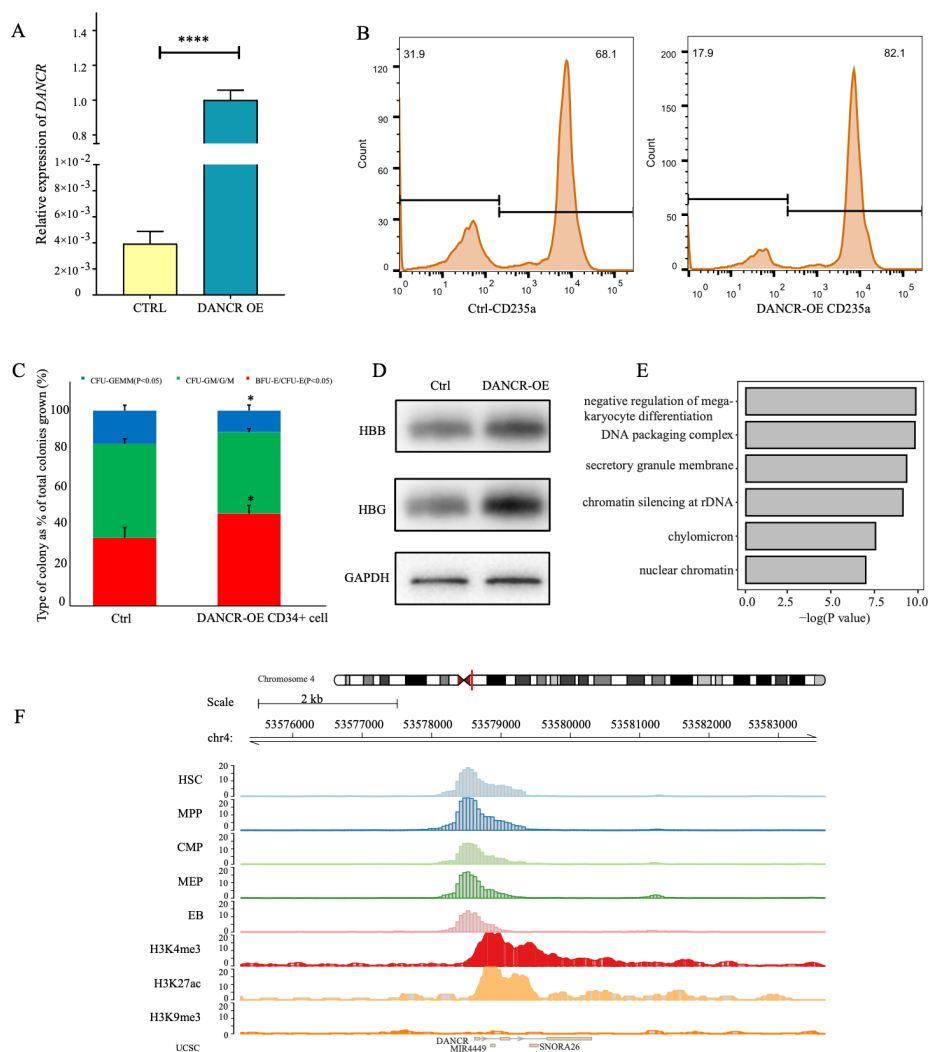


**Supplemental Figure 5. The expression of lncRNAs with potential regulatory functions at HSC (A, B, C, D, E), MPP (F, G) and CMP (H, I) stages.**

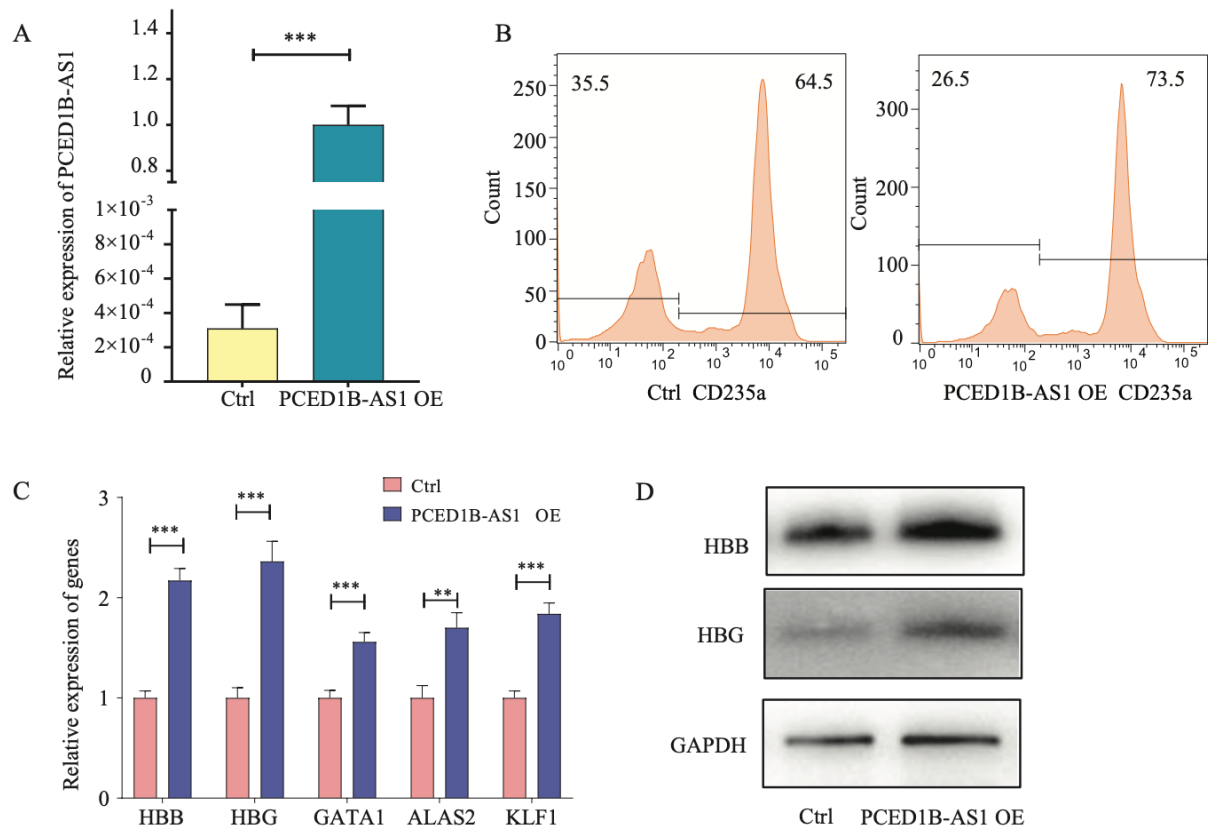


**Supplemental Figure 6. Overexpression of DANCER promotes erythroid differentiation by compromising megakaryocyte differentiation.**

(A) The detection of DANCER overexpression in differentiated CD34<sup>+</sup> cells (Day 11) by qPCR assay. (B) The expression of CD235a were detected by flow cytometry in the differentiated DANCER-OE CD34<sup>+</sup> cells (Day 13). (C) Colony-forming capacity analysis of DANCER overexpression in CD34<sup>+</sup> cells. The percentage of erythroid progenitor colonies (BFU-E/CFU-E, red) in DANCER-OE CD34<sup>+</sup> cells was higher than that of the control, while the percentage of colonies (CFU-GEMM, blue) containing megakaryocyte progenitors in DANCER-OE CD34<sup>+</sup> cells was lower than that of the control. (D) Overexpression of DANCER in CD34<sup>+</sup> cells promote the accumulation of  $\beta$ -hemoglobin (HBB) and  $\gamma$ -hemoglobin (HBG) proteins on Day 13. (E) Function enrichment of differently expressed genes caused by DANCER overexpression in K562 cells. The X axis is the negative logarithm of P value, the Y axis is the function items. Statistical results were analyzed by student's t-test and Kruskal-Wallis test, \**p* < 0.05, \*\**p* < 0.01, \*\*\**p* < 0.001.



**Supplemental Figure 7. Overexpression of PCED1B-AS1 promotes erythroid differentiation.** (A) The detection of PCED1B-AS1 overexpression in differentiated CD34+ cells (Day 11) by qPCR assay. (B) The detection of CD235a+ cells by flow cytometry in the PCED1B-AS1-OE differentiated CD34+ cells (Day 13). The percentage on right in each figure represents the proportion of CD235a+ cells. (C) Relative expression of erythroid related genes in differentiated PCED1B-AS1-OE CD34+ cells (Day 11) detected by qPCR assay. (D) The expression of  $\beta$ -hemoglobin (HBB) and  $\gamma$ -hemoglobin (HBG) proteins detected by western blot in differentiated PCED1B-AS1-OE CD34+ cells (Day 13). Statistical results were analyzed by student's t-test and Kruskal-Wallis test, \* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ . Ctrl: control group, OE: overexpression.





## Supplemental Table 1 Primer Sequences

### A: Primer sequences used for knockdown

Gene target	shRNA ID	mRNA target site	97mer oligo
<i>DANCR</i>	<i>DANCR</i> -sh1	GCTGGTAAAGAAATGG ATTAG	GATCCGCTGGTAAAGAAATGGATTAGC TTCCTGTCAGACTAATCCATTTCTTTAC CAGCTTTTTG
<i>DANCR</i>	<i>DANCR</i> -sh2	GATATGTCATCACCGGA AACT	GATCCGATATGTCATCACCGGAAACTCT TCCTGTCAGAAGTTTCCGGTGATGACA TATCTTTTTG
<i>PCED1B-ASI</i>	<i>PCED1B-ASI</i> -sh1	GCCAGTGTCAAGTCTTTG TTCC	GATCCGCCAGTGTCAAGTCTTTGTTCCC TTCCTGTCAGAGGAACAAAGACTGAC ACTGGCTTTTTG
<i>PCED1B-ASI</i>	<i>PCED1B-ASI</i> -sh2	GGAGAATCAGACATTA CTTTC	GATCCGGAGAATCAGACATTACTTTCC TTCCTGTCAGAGAAAGTAATGTCTGAT TCTCCTTTTTG

### B: Primer sequences used for overexpression

Primer name	Primer sequences (5'-3')
<i>DANCR</i> -F-NotI	GGGGCGGCCGCCCGCCCGCGCCGCCTCTC
<i>DANCR</i> -R-XbaI	GGGTCTAGAGTCAGGCCAAGTAAGTTTATT
<i>PCED1B-ASI</i> -F-NotI	GGGGCGGCCGCAGGAAGCGGAAGACTAATG
<i>PCED1B-ASI</i> -R-XbaI	GGGTCTAGAAGGAGACCAGGGTTTTAT

### C: Primer sequences used for dual-luciferase reporter assay

Primer name	Primer sequences (5'-3')
<i>PCED1B-ASI</i> -Promoter-F-KpnI	CCCGGTACCTCTTTCTGTCTCTCTCTCTCTCT
<i>PCED1B-ASI</i> -Promoter-R-SacI	CCCAGCTCTAAAGCAAGAACTAAATGCTGAC
<i>PCED1B-ASI</i> -Promoter-Del-421	TGTCCATTTTAATAAATTTACAAGTTTATCAATTTGTTATTGC CAAGCACCAGTTGTC
<i>PCED1B-ASI</i> -Promoter-Del-421-anti	GACAACTGGTGCTTGGCAATAACAAATTGATAAACTTGTA ATTTATTAATGGACA
<i>PCED1B-ASI</i> -Promoter-Mut-423	CTAAAGAGACAACCTGGTGCTTGGCAATAACAAATTTTTTT TGATTGATAAACTTGAAATTTATTAATGGACAGT
<i>PCED1B-ASI</i> -Promoter-Mut-423-anti	ACTGTCCATTTTAATAAATTTACAAGTTTATCAATCAAAAA AATTTGTTATTGCCAAGCACCAGTTGTCTCTTTAG

### D: Primer sequences used for RNA pull-down

Primer name	Primer sequences (5'-3')
<i>PCED1B-ASI</i> -sense-F	TAATACGACTCACTATAGGGAGGAAGCGGAAGACTAATGACCG
<i>PCED1B-ASI</i> -sense-R	AGGAGACCAGGGTTTTATTATTA
<i>PCED1B-ASI</i> -antisense-F	AGGAAGCGGAAGACTAATGACCG
<i>PCED1B-ASI</i> -antisense-R	TAATACGACTCACTATAGGGAGGAAGCGGAAGACTAATGACCG

**Supplemental Table 2: Motif enrichment results of specific peaks at each stage during erythroid differentiation.**

TFs	Expression					TF_motif	Enrichment score				
	EB	MEP	CMP	MPP	HSC		EB	MEP	CMP	MPP	HSC
ATF1	38.79	0.000706	4.714	0.144	4.041	Atf1(bZIP)/K562-ATF1-ChIP-Seq(GSE31477)/Homer-GATGACGTCA	20.1211	10.89	6.55	19.3675	8.888
ATF2	95.03	31.08	45.9	27.15	66.78	Atf2(bZIP)/3T3L1-Atf2-ChIP-Seq(GSE56872)/Homer-NRRTGACGTCAT	14.5667	26.765	14.49	16.1825	24.368
ATF3	131.7	1815	2183	3034	3111	Atf3(bZIP)/GBM-ATF3-ChIP-Seq(GSE33912)/Homer-DATGASTCATHN	7	8.6475	11.8467	3.93	6.691
ATF4	7.565	36.02	153.7	99.95	62.42	Atf4(bZIP)/MEF-Atf4-ChIP-Seq(GSE35681)/Homer-MTGATGCAAT	311.21	264.923	207.543	177.4	154.085
ATF7	50.19	0.04989	1.053	0.000166	1.478	Atf7(bZIP)/3T3L1-Atf7-ChIP-Seq(GSE56872)/Homer-NRGTGACGTCA	23.1022	24.51	18.56	23.6475	29.818
BACH1	298.6	1396	1594	1989	2042	Bach1(bZIP)/K562-Bach1-ChIP-Seq(GSE31477)/Homer-AWWNTGCTGAGTCAT	19.06	14.5925	25.79	15.705	16.738
BATF	143.1	1791	2087	3018	3001	BATF(bZIP)/Th17-BATF-ChIP-Seq(GSE39756)/Homer-DATGASTCAT	1.22556	11.6125	4.76333	0.1775	4.928
BCL6	0.001195	0.9147	0.3067	18.2	30.25	Bcl6(bZIP)/Liver-Bcl6-ChIP-Seq(GSE31578)/Homer-NNNCTTCCAGGAAA	0.747778	3.395	9.45667	8.4325	5.154
BHLHE40	19.97	0.001522	10.25	4.836	24.98	bHLHE40(bHLH)/HepG2-BHLHE40-ChIP-Seq(GSE31477)/Homer-KCAGTGMCMN	3.21778	7.09	10.94	13.08	2.051
CLOCK	39.13	10.06	48.4	85.51	121.8	CLOCK(bHLH)/Liver-Clock-ChIP-Seq(GSE39860)/Homer-GHCACGTG	1.5	1.315	5.19	3.585	4.905
CTCF	833.7	19320	13500	15930	13320	CTCF(Zf)/CD4+CTCF-ChIP-Seq(Barski_et_al)/Homer-AYAGTGCCMYCTRTGGCCA	11.8122	10.7525	5.42333	7.0525	4.798
E2F3	26.09	18	11.21	11.12	10.43	E2F3(E2F)/MEF-E2F3-ChIP-Seq(GSE1376)/Homer-BTKGGCGGAAA	6.17556	10.1525	7.81	4.5975	4.924
E2F4	71.67	31.57	30.28	14.6	40.03	E2F4(E2F)/K562-E2F4-ChIP-Seq(GSE31477)/Homer-GGCGGGAHAH	89.2576	12.7125	19.03	10.885	8.571
EGR1	6.566	27.36	22.96	45.23	50.68	Egr1(Zf)/K562-Egr1-ChIP-Seq(GSE3465)/Homer-TGCGTGGY	7.52778	3.925	6.19	2.155	2.586
ELF1	542.7	1748	2503	2701	2326	ELF1(ETS)/Jurkat-ELF1-ChIP-Seq(SRA014231)/Homer-AVCCGGAAGT	46.0789	259.183	273.437	300.023	303.693
ELK4	578.5	1349	1766	1865	2034	Elk4(ETS)/Hela-Elk4-ChIP-Seq(GSE31477)/Homer-NRYTCCGGY	5.04333	2.7825	3.28333	6.6275	5.921
ERG	190.5	4425	8251	10150	9051	ERG(ETS)/VCaP-ERG-ChIP-Seq(GSE14097)/Homer-ACAGGAAGTG	0.522222	37.605	56.6367	85.7	82.572
ETS1	221.6	4331	8000	9004	8043	ETS1(ETS)/Jurkat-ETS1-ChIP-Seq(GSE17954)/Homer-ACAGGAAGTG	0.571111	0.28	5.48	3.67	4.22
FOSL2	161.8	1843	2137	3107	2946	Fosl2(bZIP)/3T3L1-Fosl2-ChIP-Seq(GSE56872)/Homer-NATGASTCABNN	0.263333	4.765	5.43333	7.7475	7.154
FOXP2	21.4	65.9	33.19	61.74	20.21	FOXP2(Forkhead)/U2OS-FOXP2-ChIP-Seq(E-MTAB-2204)/Homer-SCHTGTTCACAT	2.66667	9.83	4.2	4.4625	3.37
FOXO1	69.87	354.3	493.3	644.3	605.3	Foxo1(Forkhead)/RAW-Foxo1-ChIP-Seq(Fan_et_al)/Homer-CTGTTTAC	1.23667	8.3625	4.93	4.5375	26.041
FOXO3	43.37	87.13	31.67	54.95	10.72	Foxo3(Forkhead)/U2OS-Foxo3-ChIP-Seq(E-MTAB-2701)/Homer-DGTAAACA	25.4811	14.8175	10.24	14.3275	17.493
FOXP1	35.03	73.46	11.35	54.48	8.823	FOXP1(Forkhead)/H9-FOXP1-ChIP-Seq(GSE31006)/Homer-NYTTTACHN	30.5578	85.5075	79.88	82.7825	77.698
GABPA	413.6	3405	6230	7025	6119	GABPA(ETS)/Jurkat-GABPA-ChIP-Seq(GSE17954)/Homer-RACCGGAAGT	4.79444	6.0775	8.17667	14.2325	14.749
GATA1	3044	8712	3805	1364	975.9	Gata1(Zf)/K562-GATA1-ChIP-Seq(GSE18829)/Homer-SAGATAAGRV	314.4	260.638	63.9467	8.4925	3.985
GATA2	3032	8923	3867	1384	901.4	Gata2(Zf)/K562-GATA2-ChIP-Seq(GSE18829)/Homer-BBCTTACTS	0.576667	35.645	46.01	2.715	4.739
GATA3	2826	8191	3222	941.4	615.1	GATA3(Zf)/Treg-Gata3-ChIP-Seq(GSE20898)/Homer-AGATAASR	0.054444	0.74	0.716667	6.105	2.896
HOX9A	1.20E-05	47.98	157.5	450.3	534.6	Hox9a(Hox)/HSC-Hox9a-ChIP-Seq(GSE33509)/Homer-GGCCATAAATCA	0.743333	31.5075	24.99	23.6025	29.943
IRF1	66.93	439.7	438.1	889.2	868	IRF1(IRF)/PBMC-IRF1-ChIP-Seq(GSE43036)/Homer-GAAAGTGAAGT	16.22	54.2775	55.9733	28.1125	42.147
IRF2	76.33	548.1	598.5	1140	1148	IRF2(IRF)/Erythroblasts-IRF2-ChIP-Seq(GSE36985)/Homer-GAAAYGAAASY	46.7078	4.6325	21.7033	5.5825	12.793
IRF3	43.01	406.3	543.3	908.4	916.7	IRF3(IRF)/BMDM-IRF3-ChIP-Seq(GSE67343)/Homer-AGTTCAKTTTC	4.75889	12.835	12.04	4.3675	6.186
IRF8	108.9	611.9	746.7	1332	1198	IRF8(IRF)/BMDM-IRF8-ChIP-Seq(GSE77884)/Homer-GRAASTGAAAST	0.044444	0.425	7.30667	0.9175	3.271
JUNB	145.8	1841	2191	3159	3144	JunB(bZIP)/DendriticCells-JunB-ChIP-Seq(GSE36099)/Homer-RATGASTCAT	0.157778	4.0875	7	0.735	0.739
JUND	111.2	110.7	111.4	93.45	128.6	JunD(bZIP)/K562-JunD-ChIP-Seq(Homer-ATGACGTATCN	2.46444	32.86	41.9	20.4975	8.562
KLF1	0.01698	0.01987	1.934	194.5	398.5	EKLf1(Zf)/Erythrocyte-Klf1-ChIP-Seq(GSE20478)/Homer-NWGGGTGTGGY	0.137	0.02	1.46	2.655	11.6
KLF3	1015	365.4	84.96	32.31	88.29	KLF3(Zf)/MEF-Klf3-ChIP-Seq(GSE44748)/Homer-NRGCCCRCCCHBN	16.7367	18.9325	16.03	32.795	32.351
KLF6	955	479.4	107.1	56.24	129.9	KLF6(Zf)/PDAC-KLF6-ChIP-Seq(GSE64557)/Homer-MKGGYGTGGCC	14.4256	87.72	186.987	18.29	69.397
MAFF	4.186	18.24	32.11	42.04	56.67	MafF(bZIP)/HepG2-MafF-ChIP-Seq(GSE31477)/Homer-HWWGTGAGCAWWTTT	0.744444	13.8	10.96	11.1725	10.232
MAX	27.52	76.46	99.98	88.6	137.6	Max(bHLH)/K562-Max-ChIP-Seq(GSE31477)/Homer-RCCAGTGGYNN	59.8767	104.433	79.33	166.47	123.601
MAZ	203.2	188.8	159.9	156.5	181	Maz(Zf)/HepG2-Maz-ChIP-Seq(GSE31477)/Homer-GGGGGGGG	16.83	40.295	29.27	4.0825	3.499
MEIS1	64.6	161.5	127.8	120.1	96	Meis1(Homeobox)/MastCells-Meis1-ChIP-Seq(GSE48085)/Homer-VGCTGWCAVB	33.2811	118.088	177.743	110.96	175.447
MITF	117.4	263.6	426.5	506.4	426.2	MITF(bHLH)/MastCells-MITF-ChIP-Seq(GSE48085)/Homer-RTCATGTGAC	9.81667	4.6325	1.94	1.7975	3.958
MYB	177.6	812	647.2	438.7	434.2	MYB(HTH)/ERMVb-Myb-ChIPSeq(GSE22095)/Homer-GGCVGTR	14.3344	53.705	61.6267	50.3425	37.316
NF1	116	413.6	288.9	477.4	485.6	NF1(CTF)/LNCAP-NF1-ChIP-Seq(Unpublished)/Homer-CYTGGCABNSTGCCAR	3.32	5.275	9.33667	21.52	17.839
NRF1	118.1	4.111	5.842	6.873	15.32	NRF1(NRF)/MCF7-NRF1-ChIP-Seq(Unpublished)/Homer-CTGCGCATGCGC	7.73333	5.81	1.53	2.3125	5.167
RFX2	134.5	354.8	360.8	409.8	467.6	Rfx2(HTH)/LoVo-RFX2-ChIP-Seq(GSE49402)/Homer-GTTGCCATGGCAACM	4.29889	12.12	10.8233	2.755	3.784
RFX5	87.43	222	220.2	241.3	302.7	Rfx5(HTH)/GM12878-Rfx5-ChIP-Seq(GSE31477)/Homer-SCCTAGCAACAG	20.92	27.6025	24.8967	12.115	18.325
RUNX1	27.84	4490	5929	5136	4254	RUNX1(Runt)/Jurkat-RUNX1-ChIP-Seq(GSE29180)/Homer-AAACCACARM	2.76222	24.7675	28.1933	41.325	42.406
RUNX2	25.18	4358	5207	4518	3670	RUNX2(Runt)/Pca-RUNX2-ChIP-Seq(GSE33889)/Homer-NWAACCACADNN	0.33	4.48	10.11	17.2075	14.75
SMAD2	7.397	105	71.16	69.02	59.72	Smad2(MAD)/ES-SMAD2-ChIP-Seq(GSE29422)/Homer-CTGTCTGG	34.4256	25.1875	39.5567	18.965	24.869
SMAD3	61.67	167.5	90.78	60.05	102.9	Smad3(MAD)/NPC-Smad3-ChIP-Seq(GSE36673)/Homer-TWGTCTGG	0.522222	9.685	3.51667	4.68	7.69
SMAD4	7.156	78.62	54.59	46.63	38.81	Smad4(MAD)/ESC-SMAD4-ChIP-Seq(GSE29422)/Homer-VBSYGTCTGG	5.49667	3.6525	6.58667	15.565	15.624
SOX6	0	42.12	35.3	26.6	13.28	Sox6(HMG)/Myotubes-Sox6-ChIP-Seq(GSE32627)/Homer-CCATTGTTNY	7.33	0.06	0.02	0	0.914
STAT1	23.36	19.86	10.06	42.68	49.59	STAT1(Stat)/HelaS3-STAT1-ChIP-Seq(GSE12782)/Homer-NATTTCCNGGAAAT	4.88889	11.6425	8.52	7.32	13.385
STAT3	47.91	24.02	19.01	45.8	79	Stat3(Stat)/mES-Stat3-ChIP-Seq(GSE11431)/Homer-CTCCGGGAA	20.2678	70.01	94.1267	19.525	49.657
STAT4	46.45	86.95	59.8	74.19	124.7	STAT4(Stat)/CD4-Stat4-ChIP-Seq(GSE22104)/Homer-NYTTCCWGGAAAR	0.535556	3.04	6.63333	3.4875	10.381
STAT6	0.3882	6.2	10.71	39.18	68.07	STAT6(Stat)/CD4-Stat6-ChIP-Seq(GSE22104)/Homer-ABTTCYRRGAA	8.55	22.88	26.07	5.95	13.152
TCF12	35.18	337.3	334.8	479.2	320.7	Tcf12(bHLH)/GM12878-Tcf12-ChIP-Seq(GSE32465)/Homer-VACGCTGYTG	7.05444	64.8475	43.1767	16.5425	34.177
TFE3	111.7	29.28	66.68	94.99	119.7	TFE3(bHLH)/MEF-TFE3-ChIP-Seq(GSE75757)/Homer-GTCACGTGACYV	1.63222	3.6775	6.15333	4.6275	2.704
TGIF1	56.92	295.4	318.8	333.5	254.7	Tgif1(Homeobox)/mES-Tgif1-ChIP-Seq(GSE5404)/Homer-YTGWCADY	47.1911	15.995	6.26	23.0375	23.894
TGIF2	80.01	622.5	595.7	768.2	540.5	Tgif2(Homeobox)/mES-Tgif2-ChIP-Seq(GSE5404)/Homer-TGTCANVT	3.78444	21.6875	18.3867	24.93	20.902
USF1	42.32	37.41	105	133.9	202.1	USF1(bHLH)/GM12878-Usf1-ChIP-Seq(GSE32465)/Homer-SGTCACTGGR	35.5989	36.96	21.6467	16.2625	10.359
USF2	40.7	18.71	80.15	88.57	121.7	Usf2(bHLH)/C2C12-Usf2-ChIP-Seq(GSE36030)/Homer-GTCACGTGTT	0.243333	2.5	6.26	0.66	0.484
ZBTB33	23.59	0.3781	14.89	5.273	8.827	ZBTB33(Zf)/GM12878-ZBTB33-ChIP-Seq(GSE32465)/Homer-GVYTCTCGGAGAAC	4.88444	6.4475	7.77	6.2575	8.823
ZFX	57.96	36.13	27.29	37.25	35.99	ZFX(Zf)/mES-Zfx-ChIP-Seq(GSE11431)/Homer-AGGCGCTRG	7.39222	6.4075	9.22333	11.1525	15.673

**Supplemental Table 3: Motif enrichment results of differential peaks during erythroid differentiation.**

TFs	Differential Gene Expression						TF_motif	Enrichment_score			
	MEP_EB	CMP_MEP	MPP_CMP	HSC_MPP	MEP_EB_up			MEP_EB_log2	CMP_MEP_log2	MPP_CMP_log2	HSC_MPP_log2
ATF3	1632	1113	328	1131	19.75	Atf3(bZIP)	GBM-ATF3-ChIP-Seq(GSE33912)/Homer-DATGASTCATHN	0.40406233	-1.154018551	1.830124542	-0.602455048
BACH1	1246	701.9	224.4	656	61.12	Bach1(bZIP)	K562-Bach1-ChIP-Seq(GSE31477)/Homer-AWWNTGCTGAGTCAT	1.214044256	-0.02220727	-1.398016948	0.968486622
BATF	1645	1113	308.8	1117	20.14	BATF(bZIP)	Th17-BATF-ChIP-Seq(GSE39756)/Homer-DATGASTCAT	-3.510111596	0.321597151	5.948022757	-4.932371478
BHLHE40	0.003359	11.89	0.1191	26.12	0.5315	bHLHE40(bHLH)	HepG2-BHLHE40-ChIP-Seq(GSE31477)/Homer-KCACGTGMCN	-0.417833685	-0.966038745	-0.991980092	2.907077368
CEBPB	88.06	132.2	76.95	21.14	2.076	CEBP-AP1(bZIP)	ThioMac-CEBPb-ChIP-Seq(GSE21512)/Homer-DRTGTTGCAA	2.673155224	-2.415889548	-0.412883341	1.757603462
DMC1	126.5	27.91	9.372	5.833	11.28	PRDM9(Zf)	Testis-DMC1-ChIP-Seq(GSE35498)/Homer-ADGGYAGYAGCATCT	2.678905626	-1.92930882	7.603877037	-5.862619311
EGR1	25.36	21.87	5.444	18.59	3.043	Egr1(Zf)	K562-Egr1-ChIP-Seq(GSE32465)/Homer-TGCGTGGG	4.17146296	-0.497319956	1.001243852	-0.164483344
ELF3	3534	3200	931.5	1300	0.02344	ELF3(ETS)	PDAC-ELF3-ChIP-Seq(GSE64557)/Homer-ANCAGGAAGT	12.25658002	-24.12229561	1.277571161	-1.320021294
ELK1	1220	941.4	314.6	580.2	0.005206	Elk1(ETS)	Hela-Elk1-ChIP-Seq(GSE31477)/Homer-HACTTCCGGY	0.285662813	0.290102514	8.255092584	-7.133552614
ELK4	1169	856.3	290.6	605.2	0.01124	Elk4(ETS)	Hela-Elk4-ChIP-Seq(GSE31477)/Homer-NRYTTCGGY	1.873447067	-0.278698808	-0.394945893	-0.144811729
FOXP1	50.81	24.56	7.875	3.619	20.97	FOXP1(Forkhead)	HEK293-FOXP1-ChIP-Seq(GSE15673)/Homer-NVWVGTITAC	-2.060786804	-0.342525173	1.540099562	0.53281205
FOXP2	40.63	29.41	3.316	4.339	12.89	FOXP2(Forkhead)	U2OS-FOXP2-ChIP-Seq(E-MTAB-2204)/Homer-SCHTGTITACAT	-1.429395934	0.870291915	0.011085584	1.249537677
FOXP3	86.79	33.01	13.11	5.285	20.14	Foxo3(Forkhead)	U2OS-Foxo3-ChIP-Seq(E-MTAB-2701)/Homer-DGTAACA	1.011747628	0.155354127	-0.07150852	-0.071754217
GATA1	7612	3060	3686	194.1	669.2	Gata1(Zf)	K562-GATA1-ChIP-Seq(GSE18829)/Homer-SAGATAAGRV	0.796145609	1.797369203	2.881538653	1.447295816
GATA2	7897	3124	3724	199.5	686.2	Gata2(Zf)	K562-GATA2-ChIP-Seq(GSE18829)/Homer-AGTATATCT	-5.181096582	0.077050094	3.95767625	-0.830261304
GATA3	7715	2908	3676	117.9	834.5	GATA3(Zf)	Treg-Gata3-ChIP-Seq(GSE20898)/Homer-AGATAAASR	-0.11543167	-0.743569553	-2.801225525	1.59003941
HOXA2	18.48	21.24	0.5467	32.58	0.1567	HOXA2(Homeobox)	mES-Hoxa2-ChIP-Seq(Donaldson_et_al)/Homer-GYCATCMATCAT	-6.593113145	8.606594931	-9.639042736	-0.558733244
HOXB4	68.26	70.37	13.64	78.99	3.494	Hoxb4(Homeobox)	ES-Hoxb4-ChIP-Seq(GSE34014)/Homer-GATTRATGGCY	0.544907056	1.777546017	-0.846120619	-0.90770406
IRF2	417.4	169.9	31.45	264.4	0.2881	IRF2(IRF)	Erythroblasts-IRF2-ChIP-Seq(GSE36985)/Homer-GAAASYGAAASY	4.309921734	-1.712115795	1.084665313	-1.090012984
IRF3	403.9	181.5	29.5	236.7	0.9241	IRF3(IRF)	BMDM-Irf3-ChIP-Seq(GSE67343)/Homer-AGTTTCAKTTTC	-2.122642978	-0.1420439	2.01968259	-0.326823598
IRF8	540.4	282.4	41.68	277.2	0.6695	IRF8(IRF)	BMDM-Irf8-ChIP-Seq(GSE78874)/Homer-GRAASTGAAAST	4.951639911	-3.383410913	1.511018482	-1.109489459
JUNB	1675	1097	341.9	1101	23.19	JunB(bZIP)	Dendritic-Cells-JunB-ChIP-Seq(GSE36099)/Homer-RATGASTCAT	-4.986800624	-0.508178629	2.68759904	0.350038838
JUND	67.87	53.18	34.72	48.62	17.45	JunD(bZIP)	K562-JunD-ChIP-Seq(Homer-ATGACGTATCATN	-2.593151599	0.104533466	0.320802421	1.36892091
KLF1	204.8	76.53	7.888	0.3107	182.5	EKLf(Zf)	Erythrocyte-Klf1-ChIP-Seq(GSE20478)/Homer-NWGGGTGTGGCY	3.039269689	1.146899922	5.274833963	-2.295958137
KLF4	170.6	45.13	2.025	1.252	196.4	Klf4(Zf)	mES-Klf4-ChIP-Seq(GSE11431)/Homer-GCCACACCCA	7.036871801	-4.72888546	-1.006160883	2.831289127
KLF5	258.4	76.85	17.93	17.25	247.4	KLF5(Zf)	LoVo-KLF5-ChIP-Seq(GSE49402)/Homer-DGGYKGGG	-0.874143412	-2.934001806	20.6898691	-7.24729325
KLF6	362.6	132.3	23.07	31.79	243	KLF6(Zf)	PDAC-KLF6-ChIP-Seq(GSE64557)/Homer-MKGGYGTGGCC	-1.424064166	-0.71235839	1.688512448	-0.55343079
KLF9	99.8	30.05	4.519	24.27	86.33	Klf9(Zf)	GBM-Klf9-ChIP-Seq(GSE62211)/Homer-GCCACRCCAGY	2.232536777	-0.925232556	0.54997491	-0.511967289
MAFK	397.7	179.9	82.92	277.8	19.8	MaFK(bZIP)	C2C12-MaFK-ChIP-Seq(GSE36030)/Homer-GRAASTGACGA	3.245741631	-4.401875621	4.701875457	-3.261649491
MAZ	120.3	135.5	25.6	38.23	33.4	Maz(Zf)	HepG2-Maz-ChIP-Seq(GSE31477)/Homer-GGGGGGGG	-0.575128031	0.877235109	2.404129919	0.206716986
MEF2D	16.98	43.67	3.657	26.67	0.2907	MeF2d(MADS)	Retina-MeF2d-ChIP-Seq(GSE61391)/Homer-GCTATTTTTAGC	-4.498953451	-0.588636443	0.229369549	1.533184237
MITF	179.1	180.5	103	228.2	5.467	MITF(bHLH)	MastCells-MITF-ChIP-Seq(GSE48085)/Homer-RTCATGTGAC	1.39426696	1.009016427	0.24900594	-1.176726165
NFATC1	63.46	1.369	1.65	18.61	0.1929	NFAT(RHD)	Jurkat-NFATc1-ChIP-Seq(jolna_et_al)/Homer-ATTTCCATT	-1.513793796	1.617841939	-2.714548342	-1.517291403
NFE2	1248	539.2	265.7	711.2	57.49	NF-E2(bZIP)	K562-NFE2-ChIP-Seq(GSE31477)/Homer-GATGACTCAGCA	1.544477022	0.427323482	3.988962084	-2.483002888
PRDM1	107.9	42.93	3.007	65.48	1.97	PRDM1(Zf)	Hela-PRDM1-ChIP-Seq(GSE31477)/Homer-ACTTTCACTTTC	2.106212308	-3.777671866	4.405158917	-1.726749133
RF2	321.5	199.5	54.75	146.9	2.369	Rf2(HTH)	LoVo-RF2-ChIP-Seq(GSE49402)/Homer-GTTCAGTGGCAACM	-0.49879608	-0.038744047	1.65255326	-0.153336768
SRF	40.36	3.676	7.25	4.055	9.26	CaRg(MADS)	PURF-Srf-ChIP-Seq(Sullivan_et_al)/Homer-CCATATATGGNM	-1.665610439	-0.035545137	1.818990922	-0.40842777
STAT3	12.34	1.193	0.01234	46.1	0.02915	Stat3(Stat)	mES-Stat3-ChIP-Seq(GSE11431)/Homer-CTTCCGGGAA	-0.957445361	-0.460606485	1.98414647	-1.219020204
TFAP4	310.4	390.5	172.4	108.3	62.33	Ap4(bHLH)	AML-Tfap4-ChIP-Seq(GSE45738)/Homer-NANCACTGD	0.776809942	1.283316966	3.248868211	-5.217638628
TFE3	17.81	18.12	9.998	53.29	3.632	TFE3(bHLH)	MEF-TFE3-ChIP-Seq(GSE75757)/Homer-GTCACTGACYV	-0.432356348	-0.932236915	0.31564466	1.007204764
TGIF1	350.4	132.9	39.16	34.97	21.2	Tgif1(Homeobox)	mES-Tgif1-ChIP-Seq(GSE55404)/Homer-YTGWCADY	1.572805597	-0.018418658	-0.927265033	0.129009178
THAP11	18.05	0.5761	5.731	38.37	2.48	Rothin(THAP)	ES-Thap11-ChIP-Seq(GSE51522)/Homer-RACTACAACCTCCAGVAKGC	-1.74464697	0.730305116	0.38132055	1.25249739
USF1	44.7	80.92	8.983	109.8	2.457	USF1(bHLH)	GMI12878-USf1-ChIP-Seq(GSE32465)/Homer-SGTCACGTGR	1.416803814	0.521962305	0.3203321	0.902122885
USF2	10.57	45.4	36.59	102.4	2.23	Usf2(bHLH)	C2C12-Usf2-ChIP-Seq(GSE36030)/Homer-GTCACTGGT	-3.239684838	-0.582231405	2.217556034	0.769604529

**Supplemental Table 4: The representative co-precipitated proteins with LncRNA PCED1B-AS1 in erythroblasts identified by mass spectrometry.**

Rank	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	Avg. Mass	Description
1	3890	Q15149	312.33	19	78	531796	Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3
2	176	Q08043	210.91	13	13	103241	Alpha-actinin-3 OS=Homo sapiens OX=9606 GN=ACTN3 PE=1 SV=2
3	559	Q81UE6	206.81	48	11	13995	Histone H2A type 2-B OS=Homo sapiens OX=9606 GN=HIST2H2AB PE=1 SV=3
4	89	A5A3E0	204.85	11	13	121444	POTE ankyrin domain family member F OS=Homo sapiens OX=9606 GN=POTEF PE=1 SV=2
5	28	Q13885	197.97	31	13	49907	Tubulin beta-2A chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1
6	111	Q9BYX7	189.8	19	9	42016	Putative beta-actin-like protein 3 OS=Homo sapiens OX=9606 GN=POTEKP PE=5 SV=1
7	86	P54652	188.84	14	11	70021	Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1
8	3904	P16401	186.45	31	11	22580	Histone H1.5 OS=Homo sapiens OX=9606 GN=HIST1H1B PE=1 SV=3
9	3892	O43390	180.97	21	10	70943	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens OX=9606 GN=HNRNPR PE=1 SV=1
10	345	P17844	177.22	17	9	69148	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=1
50	3971	P15976	112.01	8	2	42751	Erythroid transcription factor OS=Homo sapiens OX=9606 GN=GATA1 PE=1 SV=1
259	4182	Q93009	28.4	1	1	128302	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2

**Supplemental Table 5:** TFs related to *DANCR* presented in promoter region of *DANCR*.

Factor	Biosource	All_peak_number	Overlap_peak_number	Overlap_ratio
<b>CHD1</b>	K562;Erythroblast;Bone Marrow	2476	2	0.0008077544426494346
<b>SRSF3</b>	K562;Erythroblast;Bone Marrow	1786	1	0.0005599104143337066
<b>RUNX1</b>	TF-1;Erythroblast;Bone Marrow	1861	1	0.0005373455131649651
<b>PCGF1</b>	K562;Erythroblast;Bone Marrow	3135	1	0.0003189792663476874
<b>GTF2B</b>	K562;Haematopoietic and lymphoid	3257	1	0.00030703101013202335
<b>DPF1</b>	K562;Erythroblast;Bone Marrow	3262	1	0.00030656039239730225
<b>SAP30</b>	K562;Erythroblast;Bone Marrow	3283	1	0.0003045994517209869
<b>POLR2A</b>	K562;Erythroblast;Bone Marrow	4063	1	0.0002461235540241201
<b>ATF1</b>	K562;Erythroblast;Bone Marrow	4226	1	0.000236630383341221
<b>GTF2E2</b>	K562;Erythroblast;Bone Marrow	4462	1	0.00022411474675033618
<b>ATF1</b>	K562;Erythroblast;Bone Marrow	4684	1	0.0002134927412467976
<b>NRF1</b>	K562;Erythroblast;Bone Marrow	4702	1	0.0002126754572522331
<b>SIN3A</b>	K562;Erythroblast;Bone Marrow	4945	1	0.00020222446916076846
<b>BRD4</b>	K562;Erythroblast;Bone Marrow	5055	1	0.00019782393669634025
<b>GTF2B</b>	K562;Erythroblast;Bone Marrow	5161	1	0.00019376089905057158