

Table S1. Transcription factors and data included in the study.

Factor	DNA-binding domain [35]	Cell type	PMID of the original ChIP-seq study	Perturbation experiment	Gene Expression Omnibus (GSE) or Array Express accession	Reference for perturbation data
HemoChIP [15]						
CEBPA	bZIP	Mac	20513432	CEBPA+ and CEBPA- bone marrow LSK cells (*)	GSE23800	[36]
CEBPB	bZIP	Mac	20513432	bone marrow-derived macrophages isolated from <i>Cebpb</i> -WT and <i>Cebpb</i> -KO mice	GSE23821	[37]
CTCF	Zinc finger, C2H2	ES Pre-Adi Pro-B cell	20720539 20887899 20543837	-	-	-
E2A	bHLH	Pre-Pro-B cell Pro-B cell	20543837 20543837	bone marrow-derived LMPP progenitor cells isolated from <i>E2a</i> -WT and <i>E2a</i> -KO mice	GSE11982	[38]
EBF	bHLH	Pro-B cell	20451411	fetal liver-derived <i>Ebf</i> ^{+/fl} and <i>Ebf</i> ^{fl/fl} pro-B cells after induction Cre recombinase	E-GEOD-21454	[39]
ERG	ETS-type	HPC7	20887958	-	-	-
ETO2	-	Ery-MEL Ind-Ery-MEL	20123907 20123907	control-siRNA and <i>Eto2</i> -siRNA treated induced G1E-ER-GATA-1 cells	E-GEOD-24333	[40]
FLI1	ETS-type	HPC7	20887958	-	-	-

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FOXO1	Fork head	Pro-B cell	20543837	Treg cells isolated from <i>Foxo1/3</i> -WT and <i>Foxo1/3</i> -KO mice	GSE21678	[41]
GATA1	Zinc finger, GATA	Ery-G1ER Ery-MEL Ind-Ery-MEL	19887574 20123907 20123907	fetal liver-derived progenitors grown into megakaryocytes isolated from <i>Gata1</i> -WT and <i>Gata1</i> -KO mice	GSE2527	[42]
GATA2	Zinc finger, GATA	eHPC HPC7	21186366 20887958	-	-	-
GFI1B	Zinc finger, C2H2	HPC7	20887958	-	-	-
LDB1	-	Ery-MEL eHPC Ind-Ery-MEL	20123907 21186366 20123907	-	-	-
LMO2	-	HPC7	20887958	control-siRNA and <i>Lmo2</i> -siRNA treated induced G1E-ER-GATA-1 cells	E-GEOD- 24336	[40]
LYL1	bHLH	HPC7	20887958	-	-	-
MEIS1	TALE homeodomain	HPC7	20887958	-	-	-
MTGR1	-	Ery-MEL Ind-Ery-MEL	20123907 20123907	-	-	-
OCT2	POU homeodomain	B cell	20513432	-	-	-
P300	-	Mac	20206554	bone marrow-derived LSK cells isolated from <i>P300</i> -WT and <i>P300</i> -KO mice	E-TABM- 1050	[43]
P65	Rel homology region	Act.Mac	21106671	-	-	-
PPARG	Zinc finger, C4	Mac	20176806	-	-	-

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PU1	ETS-type	Act.Mac B cell Mac Mac HPC7	20206554 20513432 20206554 20513432 20887958	bone marrow-derived HSC cells isolated from <i>Pu1</i> -WT and <i>Pu1</i> -KD mice	GSE5654	[44]
RAG2	-	Thy	20398922	-	-	-
RUNX1	Runt domain	HPC7	20887958	-	-	-
SCL	bHLH	Ery-MEL eHPC Ind-Ery-MEL HPC7 Ery-FL (RER) Ery-FL (WT)	20123907 21186366 20123907 20887958 20887958 20887958	fetal liver-derived progenitors grown into megakaryocytes isolated from <i>Scl^{f1/fl}</i> mice, treated and untreated with Cre recombinase	GSE14478	[45]
STAT3	STAT domain	T cell	20493732	-	-	-
STAT4	STAT domain	T cell	20620946	T cells isolated from <i>Stat4</i> -WT and <i>Stat4</i> -KO mice	GSE22081	[46]
STAT5A	STAT domain	13h-T cell 2r-T cell 8h-T cell	18820682 18820682 18820682	-	-	-
STAT5B	STAT domain	13h-T cell 2r-T cell 8h-T cell	18820682 18820682 18820682	-	-	-
STAT6	STAT domain	T cell	20620946	T cells isolated from <i>Stat6</i> -WT and <i>Stat6</i> -KO mice	GSE22081	[46]
ESChIP [12]						
CMYC	bHLH-ZIP	ES	-	-	-	-
CTCF	Zinc finger, C2H2	ES	-	-	-	-
E2F1	Fork head / winged helix	ES	-	T cells isolated from <i>E2f1</i> -WT and <i>E2f1</i> -KO mice	E-MEXP- 1991	[47]
ESRRB	Zinc finger, C4	ES	-	control-shRNA and <i>Esrrb</i> -shRNA treated ES cells	E-GEOD- 13212	[48]

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KLF4	Zinc finger, C2H2	ES	-	-	-	-
NANOG	Homeodomain	ES	-	control-RNAi and <i>Nanog</i> -RNAi treated ES cells	GSE4189	[9]
NMYC	bHLH-ZIP	ES	-	-	-	-
OCT4	POU homeodomain	ES	-	control-RNAi and <i>Oct4</i> -RNAi treated ES cells	GSE4189	[9]
P300	-	ES	-	-	-	-
SMAD1	SMAD/NF-1 domain	ES	-	embryonic lung <i>Smad1</i> -WT and <i>Smad1</i> -CKO cells	GSE26502	[49]
SOX2	HMG	ES	-	control-shRNA and <i>Sox2</i> -shRNA neural stem cells	E-MEXP- 2743	[50]
STAT3	STAT domain	ES	-	-	-	-
SUZ12	-	ES	-	ES cells isolated from <i>Suz12</i> -WT and <i>Suz12</i> -KO mice	GSE31354	[51]
TCFCP2L1	Grainyhead	ES	-	-	-	-
ZFX	Zinc finger, C2H2	ES	-	<i>Zfx</i> -WT and <i>Zfx</i> -KO ES cells	GSE7069	[52]

The representative ChIP-seq studies used for target prediction in the majority of the analyses and evaluation tests are marked in bold.

(*) Wild-type LSK cells sorted into CEBPA⁺ and CEBPA⁻.

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