SUPPLEMENTAL MATERIAL

Ungerbäck et al., **http://www.jem.org/cgi/content/full/jem.20132100/DC1**

Table S1. Analysis of Ebf1 ChIP-seq data in *Wt*, *TH (Ebf1$^{+/-}$ Pax5$^{+/-}$)*, *Ebf1*$^{+/-}$ and *Pax5*$^{+/-}$ pro–B cells

	Enriched motif	p-value	% targets/ background	Motif
Wt		1×10^{-4878}	65/5	EBF
		1×10^{-337}	31/14	Fli1(ETS)
		1×10^{-167}	13/5	RUNX1(Runt)
		1×10^{-118}	11/5	E2A(bHLH)
TH		1×10^{-5013}	73/5	EBF
		1×10^{-433}	33/13	ERG(ETS)
		1×10^{-248}	22/9	RUNX2
		1×10^{-72}	3/0.5	Oct4
Ebf$^{+/-}$		1×10^{-3407}	51/3	EBF
		1×10^{-315}	29/12	Ets1-distal(ETS)
		1×10^{-146}	24/13	RUNX1(Runt)
		1×10^{-77}	16/10	Ptf1a(bHLH)
Pax5$^{+/-}$		1×10^{-6178}	44/5	EBF
		1×10^{-940}	29/12	ETS1(ETS)
		1×10^{-443}	16/7	RUNX1(Runt)
		1×10^{-208}	20/12	E2A(bHLH)

Duplicate experiments in each genotype were combined into one sequence file. Motif analysis on peak files generated from Ebf1 ChIP-seq on indicated genotypes resulted in Ebf1 as top enriched motif in all 4 genotypes, top 4 motifs are illustrated.