SI Table 3. *In silico* search for potential hematopoietic enhancers

Conserved TFBS combination	Window, bp	No. of clusters
2 [Ets] + 1 [Gata]*	50	12,388
6 [Ets] + 2 [Gata] + 1 [E-Box][†]	220	335
4 [Ets] + 2 [Gata] + 1 [E-Box][†]	100	133
4 N[Ets]*N* + 2 N[Gata]*N* + 1 N[E-Box]N[†‡]	100	43

Combinations of Ets, GATA, and E-Box transcription factor binding sites (TFBS) conserved between human and mouse were selected on the basis of the Scl+19, Fli1+12, and Hhex+1 enhancers. Ets, GGAW; Gata, GATA; E-Box, CANNTG.

*Combination selected on the basis of the Scl+19 enhancer.

†Combination selected on the basis of the Fli1+12 and Hhex+1 enhancers.

‡The stringency of the filters was increased by varying the number of TFBS within a defined nucleotide window and requiring conservation of nucleotides flanking the core consensus sequence N[TFBS]N. The *Gata2*-3 hematopoietic enhancer passed each of these filters.