

Table S1. Transcriptional “LT-HSC-specific” signature in immunophenotypically sorted HSCs

	Fbw7 ^{+/+} LKS ⁺ > LKS ^{-a}	Jankovic et al. PNAS, 2007. (LKS > CMP) ^b	Terskikh et al. Blood, 2003. (LKS-enriched) ^b	Forsberg et al. Plos Genetics, 2005. (LT-HSC > ST-HSC/MPP) ^c	Mansson et al. Immunity, 2007. (LT-HSC > ST-HSC/MPP) ^c
Evi1	+	+	+	ND	+
Hlf	+	+	+	ND	ND
Agpt	+	+	ND	+	+
Eya1	+	+	+	ND	ND
Mpl	+	+	+	ND	+
Meis1	+	+	ND	ND	+
Ndn	+	+	ND	+	+
Thy1	+	+	ND	+	ND
Pbx3	+	+	ND	+	+
Eya2	+	+	+	+	ND
HoxB3	+	+	+	ND	ND
Egr1	+	+	+	ND	ND
HoxA5	+	+	+	+	ND
HoxA9	+	+	+	ND	ND
Mcl1	+	+	+	ND	ND
Mlt3	+	+	ND	+	+

Transcripts most prominently enriched in primitive progenitors (LKS⁺ cells) compared to the committed progenitors (LKS² cells) that were associated with the HSC phenotype in the previous independent microarray studies.+, detected; ND, not detected.

^aPresent study (LKS⁺, lineage⁻c-kit⁺Sca-1⁺ cells; LKS⁻, lineage⁻c-kit⁺Sca-1⁻ cells).

^bLineage⁻c-kit⁺Sca-1⁺ cells.

^cLT-HSC, LKS-CD34-Flt3⁻; ST-HSC, LKS-CD34+Flt3⁻; ST-HSC, LKS CD34+Flt3⁺.