Figure S5. Transcription of the lineage-affiliated genes is regulated by PIAS1. Quantitative real time polymerase chain reaction (Q-PCR) analyses were performed with total RNA from WT or \textit{Pias1}\textsuperscript{−/−} bone marrow (BM), or FACS-sorted HSC-enriched Lin\textsuperscript{−}Sca\textsuperscript{1}c-Kit\textsuperscript{+} (LSK), common lymphoid progenitors (CLP) and common myeloid progenitors (CMP) as defined in Supplementary Materials and Methods, using gene-specific primers. Each gene is indicated at the top left of each panel, and the results were adjusted by \textit{Hprt1}. Shown is the average of 2 independent experiments (n=5 for each experiment). Error bars represent SD. \textit{P} values were determined by non-paired \textit{t}-test.