Extended Data Figure 2 | Evaluation of the TARIS method. a, Design for the detection limit experiment. Spike-ins of a known number of HEK293 cells carrying unique transposon integration tags were used in a mix of 10,000 $DsRed^+$ peripheral blood cells from a freshly induced HSB mouse. **b**, Detection limit chart. Values represent the read number for each clone and for each number of input cells. Both axes are in $\log_{10}$ scale. Values represent the sum of two independent experiments. **c**, Comparison of the average read number value between TARIS and the LM-PCR method. Values represent mean ± s.d. of five different transposon tag clones. **d**, Reproducibility analysis in a non-whole-genome amplified sample with high complexity (2×10^5 bone marrow granulocytes 4 weeks after pulse). **e**, Reproducibility in a whole-genome amplified sample with low complexity (863 LT-HSCs 4 weeks after pulse). **f**, Venn diagram showing overlapping transposon tag reads between two TARIS replicates from the same sample high-complexity sample (2×10^5 bone marrow monocytes at 4 weeks after induction). **g**, Venn diagram showing overlapping transposon tag reads between two TARIS replicates from the same low-complexity sample (863 LT-HSCs at 4 weeks after induction). **h**, Contamination analysis between samples from two different mice. The plot represents the read numbers of tags from Lin^+ populations from mouse 1, and their read number values in Lin^+ populations in mouse 2. High-confidence tags are selected as those tags with more than 25 reads, and at least 10 times higher read count compared with any of the samples from a separate mouse.