Extended Data Figure 10 | Additional data on clonal origin of MkP. **a**, Three independent transposon tag libraries were prepared and sequenced for LT-HSC, MPP, and the five Lin^+ populations, from one mouse at four weeks. Each column represents the combined tags detected from three amplicon libraries prepared for each population, to facilitate visualization of the smallest clones. Tags are coloured by frequency in each lineage, and organized by rank. **b**, Origin of megakaryocytes. Alignment of all MkP clones that had detectable tags in HSC/MPPs from a mixed library combining three independent sequencing reactions. Tags are coloured by frequency in each lineage (except for MkP), and organized by rank. Arrows indicate tags verified by clone-specific PCR. **c**, Alignment of transposon tags from all Lin^+ populations, LT-HSCs, and MPPs collected from 30-week-chased mice. Tags are coloured by frequency in each lineage, and organized by rank. **d**, Experimental design for testing *in vitro* myeloid and lymphoid potential from sorted LT-HSCs. **e**, *In vitro* myeloid potential of LT-HSCs. Alignment of donor Lin^+ tags with transposon tags obtained from myeloid and lymphoid cells derived from donor LT-HSCs after two weeks in culture. **f**, Clonal output of $CD41^{hi}$ and $CD41^{lo}$ LT-HSCs at four weeks after labelling. **g**, Quantification of megakaryocyte lineage replacement by $CD41^{hi}$ versus $CD41^{lo}$ LT-HSCs (measured as the percentage of overlapping/total MkP reads) at four weeks after labelling. Values are mean ± s.e.m. of three independent mice.