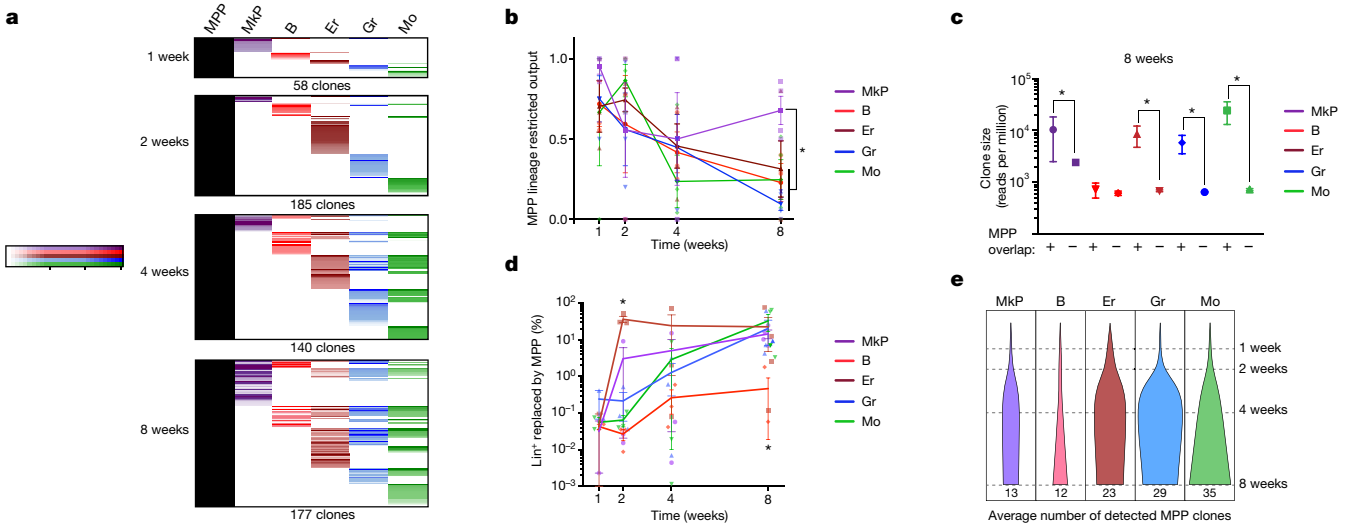

Figure 2 | Functional heterogeneity of MPP lineage fates in steady-state haematopoiesis. a, The alignment of all active MPP tags together with the five analysed blood lineages at each time point (all tags collected from three mice per time point). LT-HSC tags were analysed in parallel and excluded from the analysis to represent only MPP behaviour. **b**, Fraction of active MPP tags that overlap with a single lineage (calculated independently for each lineage). Values are mean ± s.e.m. from three mice. *$P_{MkP-Er} = 0.13$, $P_{MkP-Gr} = 0.03$, $P_{MkP-Mo} = 0.03$, $P_{MkP-B} = 0.001$ (8 weeks). Abbreviations as Fig. 1. **c**, Distribution of Lin$^+$ clone sizes comparing tags overlapping with MPP versus non-overlapping at eight weeks. Values are median and interquartile ranges of all detected clones from three mice. *Kolmogorov–Smirnov $P_{MkP} = 0.03$, $P_B = 0.25$, $P_{Er} = 0.03$, $P_{Gr} = 0.001$, $P_{Mo} = 0.003$. **d**, Fraction of each lineage replaced by MPPs calculated as the percentage of total MPP-overlapping lineage reads over time. Values are mean ± s.e.m. from three independent mice. *$P_{Er-Gr/Mo/B} = 0.04$, $P_{Er-MkP} = 0.03$ (2 weeks) and $P_{B-Er/MkP} = 0.03$, $P_{B-My} = 0.04$ (8 weeks). **e**, Average number of detected active MPP clones per lineage per mouse at different time points (normalized for percentage DsRed labelling efficiency).

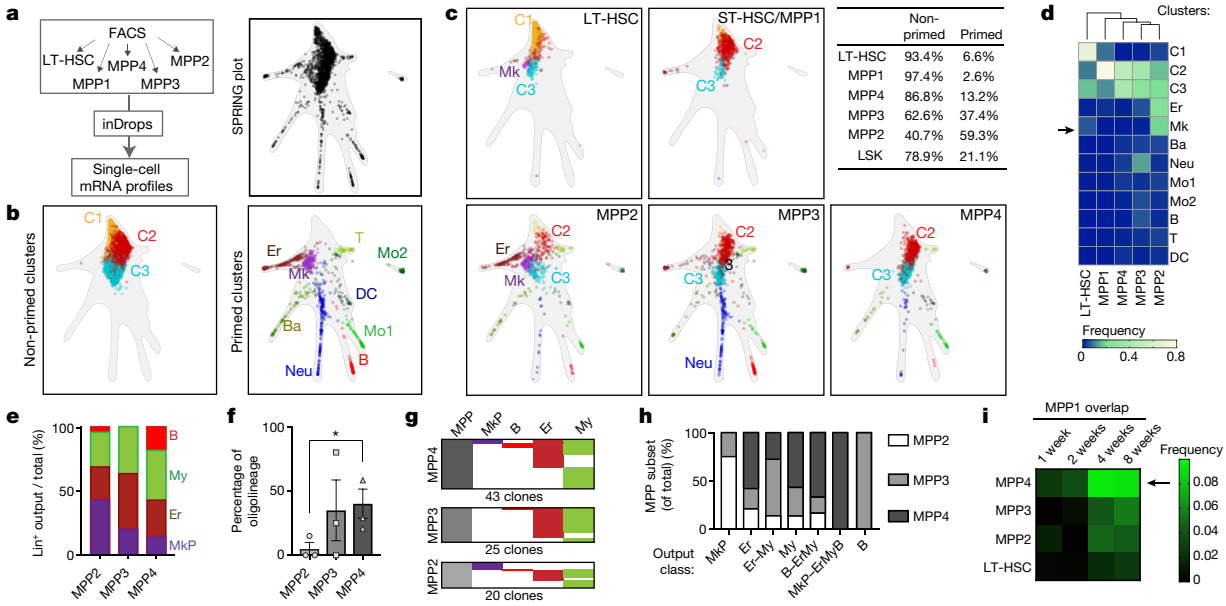

Figure 3 | Transcriptional and functional hierarchy of HSC and MPP subsets. a, Experimental design for inDrops experiment (left). Transcriptional fate map of combined fluorescence-activated cell sorting (FACS) subsets using the SPRING representation (subsampled *in silico* to represent proportions of the Lin$^-$Sca1$^+$Kit$^+$ (LSK) gate). Points represent a single HSC/MPP distributed according to their similarity using gene expression variation. **b**, *In silico* identification of different cell populations within all combined HSC and MPP subsets. Non-primed clusters 1–3 (C1–C3, left) and lineage-primed clusters (right) are presented separated and labelled according to their primed lineage signatures: Neu, neutrophil; DC, dendritic cell; T, T-cell progenitor; B, B-cell progenitor; Er, erythroid; Mk, megakaryocyte; Mo1 and Mo2 represent two monocyte-like signatures. **c**, Plots showing localization of each sorted HSC/MPP subset within the combined SPRING plot. Top right, fraction of cells from each sorted HSC/MPP subtype (and LSK cells) that group within primed or non-primed clusters. **d**, Hierarchical clustering (Ward) of sorted HSC/MPP subsets. For each FACS-sorted population, the fraction of cells corresponding to each cluster was used to analyse the similarity between subsets. The arrow points out the megakaryocyte-primed cluster within the LT-HSC gate. **e**, Fraction of lineage-restricted MPP-overlapping clones corresponding to each lineage, for each MPP subset at one week. Values are mean of three independent mice. NS, not significant. **f**, Fraction of oligolineage output of each MPP subset after 1 week. Values are mean ± s.e.m. of three independent mice. *Paired two-tailed *t*-test (MPP2 versus MPP4), $P = 0.033$ **g**, Alignment of Lin$^+$ progeny tags of different MPP subsets (excluding tags present in HSCs/MPP1s) at four weeks. **h**, Fraction corresponding to each MPP subset for each representative lineage fate (including restricted, oligolineage, and multilineage output) at four weeks (all tags detected from four mice). **i**, Frequency of MPP2/3/4 tags (and LT-HSC tags) overlapping with MPP1 at 1–8 weeks (average of three mice per time point).