SUPPLEMENTARY INFORMATION

Supplementary Table 1. Sorted cells, clones identified and % DsRed in each population analysed. This table compiles the information of numbers of barcodes and % of DsRed from each mouse analysed, including the sorting logics for each population in each experiment.

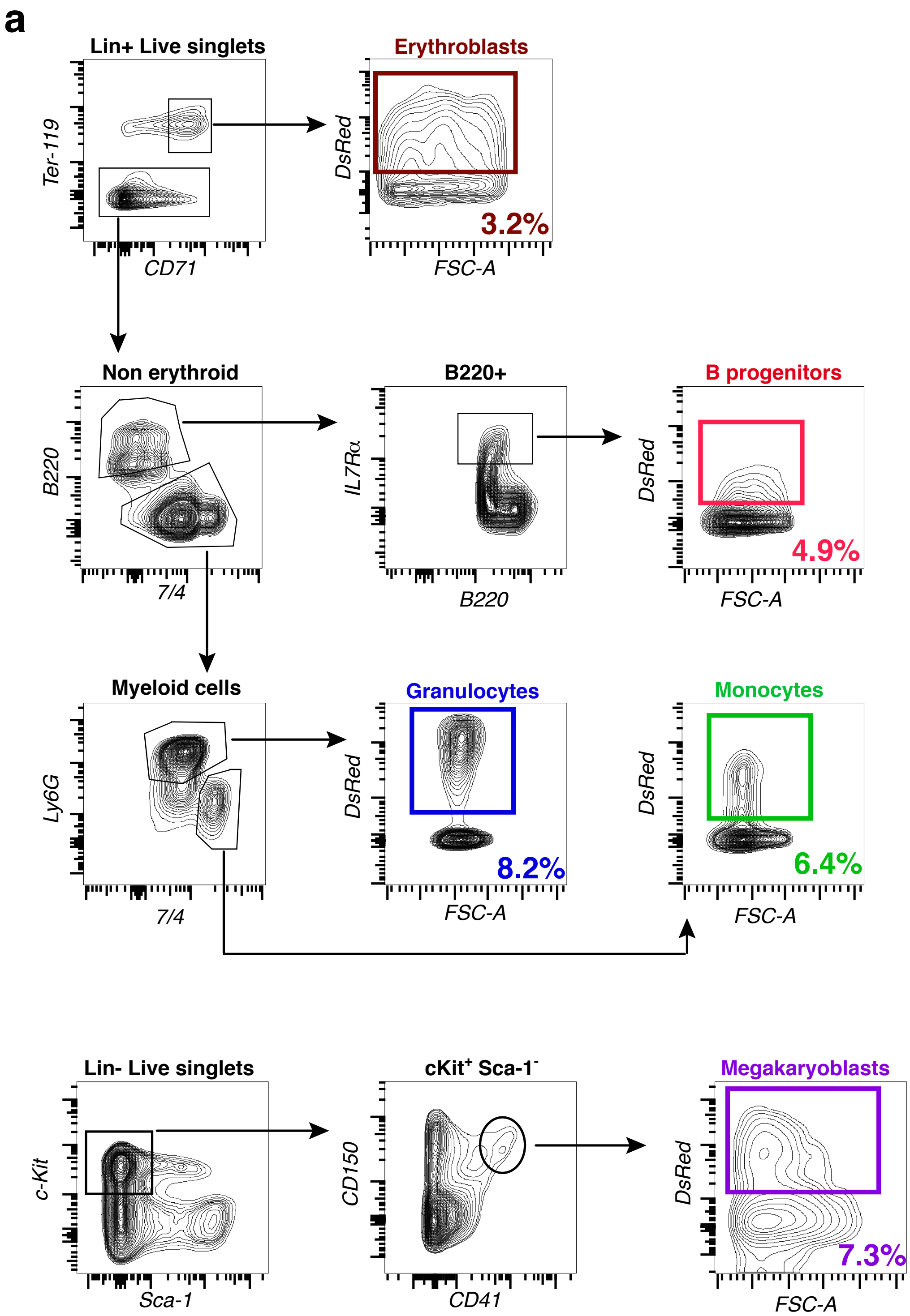
Supplementary Table 2. Cluster differential expression analysis results. This set of tables contains the raw results of cluster differential expression analysis for each cluster under different tabs.

Supplementary Figure 1. Sorting scheme for granulocytes, monocytes, erythroblasts, megakaryoblasts and B-cell precursors. a, Frequency of DsRed+ cells in granulocytes, monocytes, erythroblasts, megakaryoblasts and B-progenitors in the bone marrow of M2/HSB/Tn mice pulsed with Dox for 48h and chased for 1 week. Shown are representative FACS plots from three independent experiments.

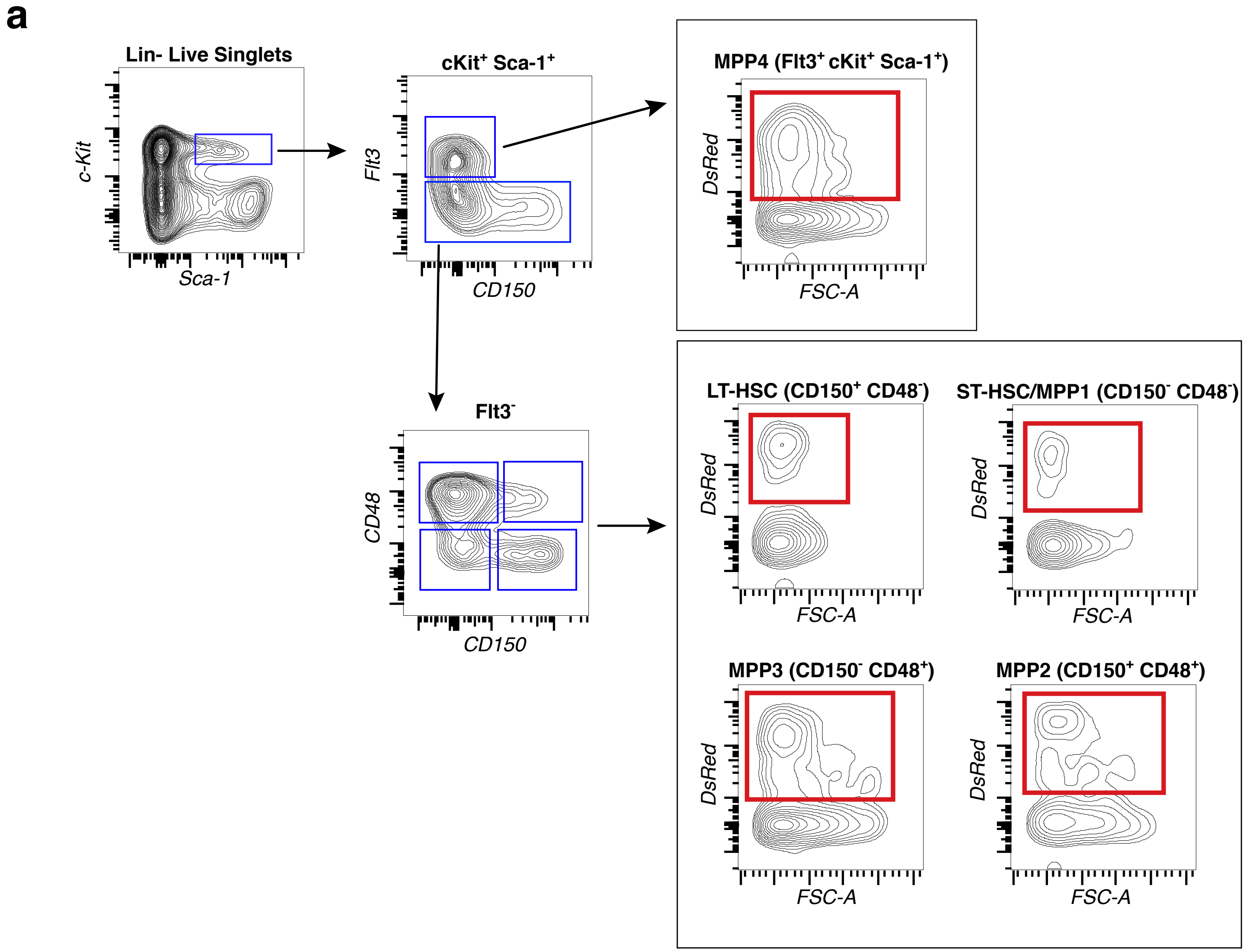
Supplementary Figure 2. Sorting scheme for HSC and MPP subpopulations. a, Frequency of DsRed+ cells in LT-HSC, MPP1, MPP2, MPP3 and MPP4 in the bone marrow of M2/HSB/Tn mice pulsed with Dox for 48h and chased for 1 week. Shown are representative FACS plots from three independent experiments.

Supplementary Figure 3. Additional sorting gating schemes. This image contains remaining sorting schemes not shown in Extended Data figures.

Supplementary fig. 1

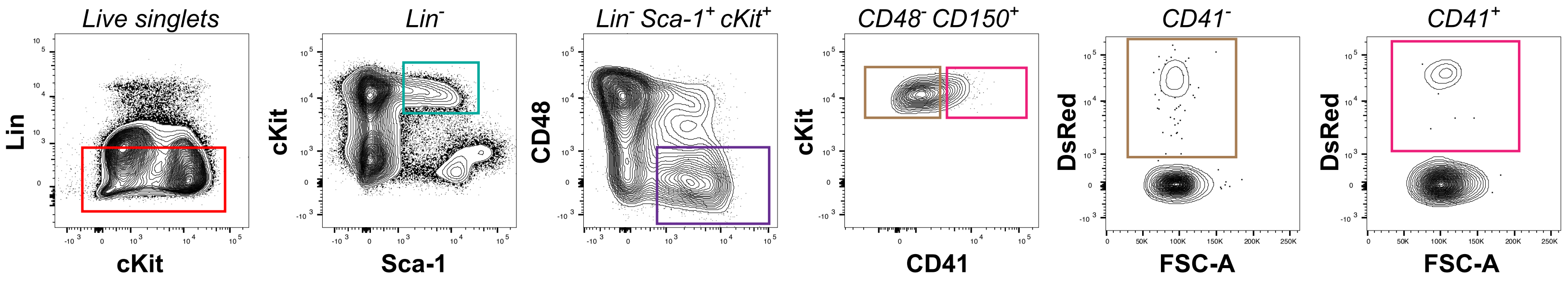


Supplementary fig. 2

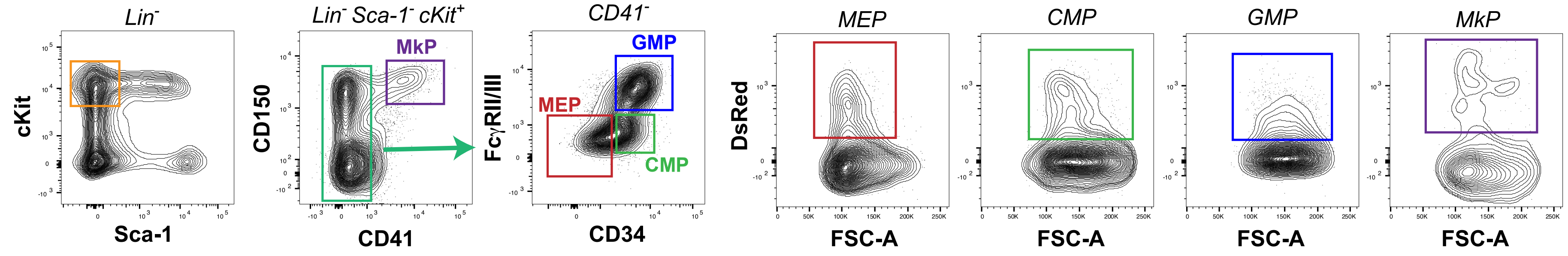


Supplementary fig. 3

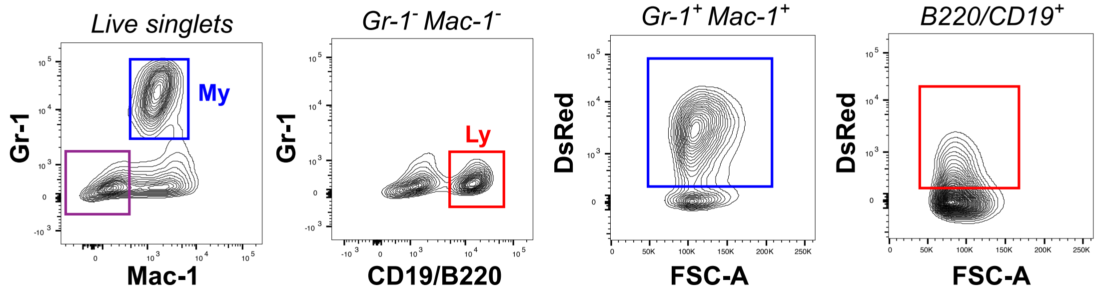
Strategy for sorting CD41+ and CD41- SLAM HSCs:



Strategy for sorting GMP/CMP/MEP/MkP:



Strategy for sorting Myeloid vs. Lymphoid cultures:



Strategy for sorting donor Lin+ in transplants: