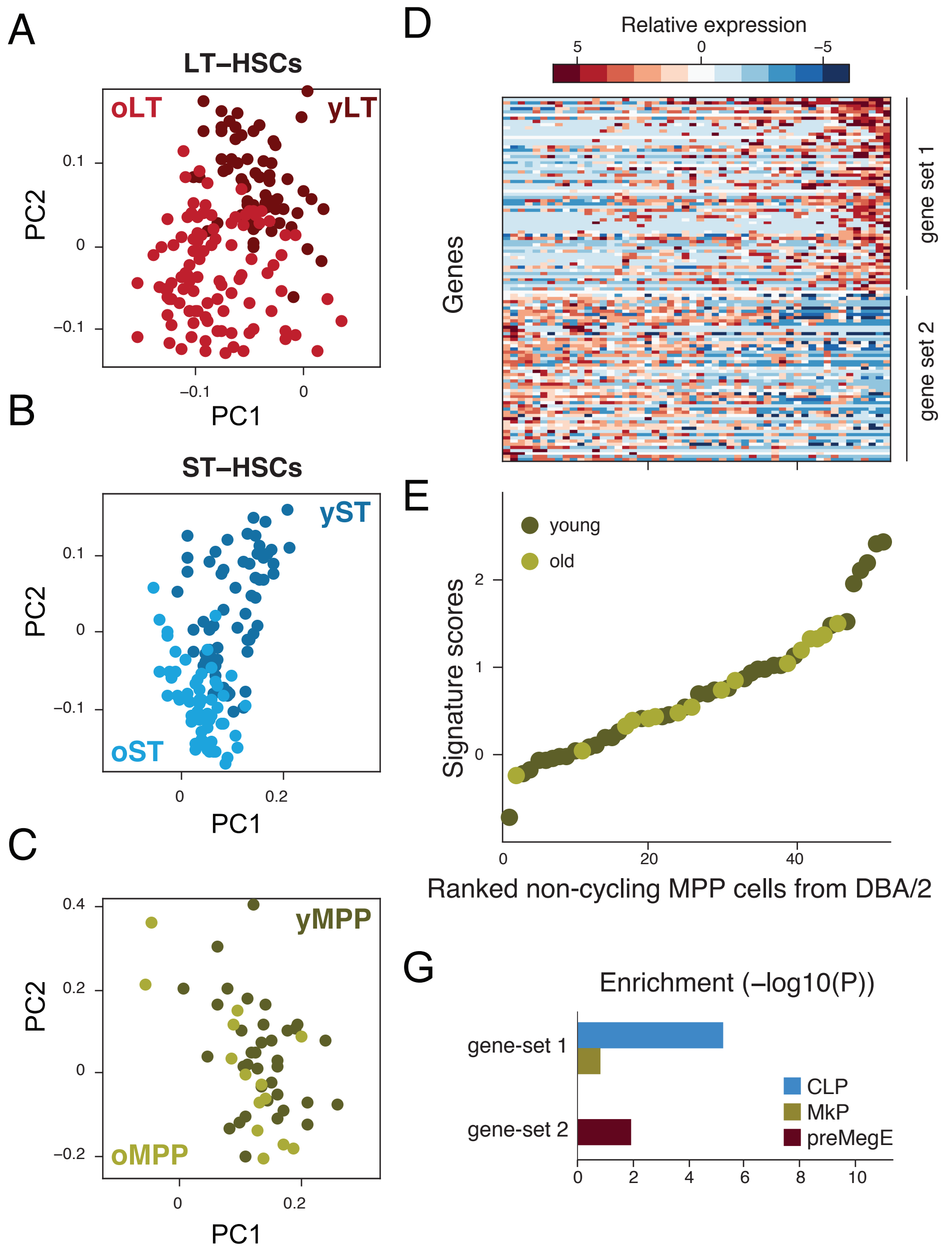

Figure S7. Subset of cells within immunophenotypically defined MPPs in DBA/2
(A-C) MPPs profiles are not distinguishable by age. PCA was performed independently for non-cycling LT-HSCs (A), ST-HSCs (B) and MPPs (C). Each plot shows the loadings of PC1 and PC2, colored based on their cell type and age. Higher scores for young HSCs and lower scores for old cells are characteristic for LT-HSCs (A) and ST-HSCs (B), but not for MPPs (C). Two distinct modules in MPPs. Heat map shows the expression of genes from two distinct gene sets (rows; gene set 1 – lymphoid-biased; and gene set 2 – myeloid-biased) across all non-cycling MPPs (columns). (E) Non-cycling MPPs from both young and old DBA/2 mice form a continuous spectrum along the two states. Shown are the signature scores (average normalized expression of gene set1 minus that of gene-set2) for each non-cycling MPP from young (dark green) or old (light green) mouse. MPPs are ranked by increasing scores (x-axis). (G) Gene set enrichment analysis based on defined progenitor sets (CLP, MkP and preMegE) within gene sets (gene set 1 and gene set 2) defining two subsets of MPPs in DBA/2.