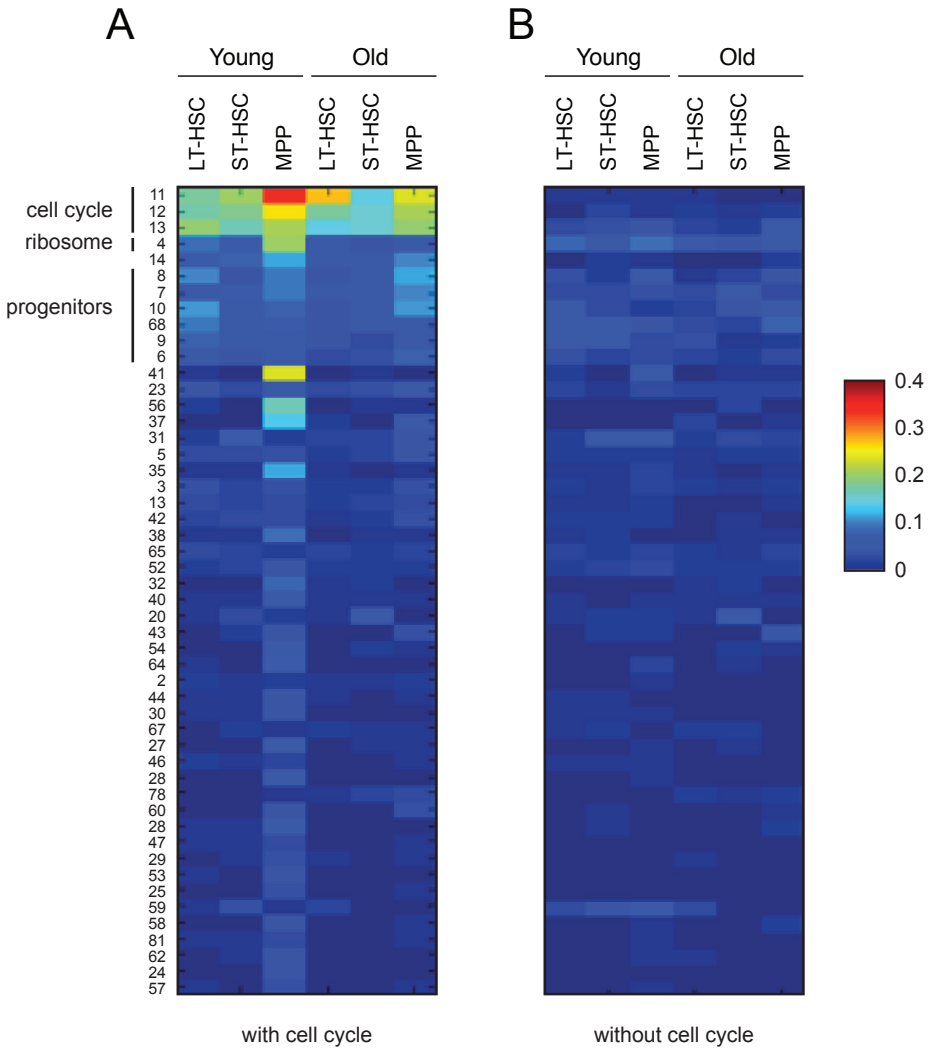

Figure S1. Coexpression of hematopoeitic transcriptional modules across single cells

(A-B) In each of the six cell populations (columns) shown is the average Pearson correlation coefficient (color bar, top) among genes from each Coarse Transcriptional Module defined by the Immunological Genome (ImmGen) Project (rows), sorted by their average coexpression, analyzed either on all cells (A) or after excluding all cycling cells (B). Module annotations are shown for some of the top modules in which annotations were defined by the ImmGen Consortium. Almost all of the highest correlations were cell cycle dependent and the strongest remaining coexpression was among ribosomal genes (module #4).