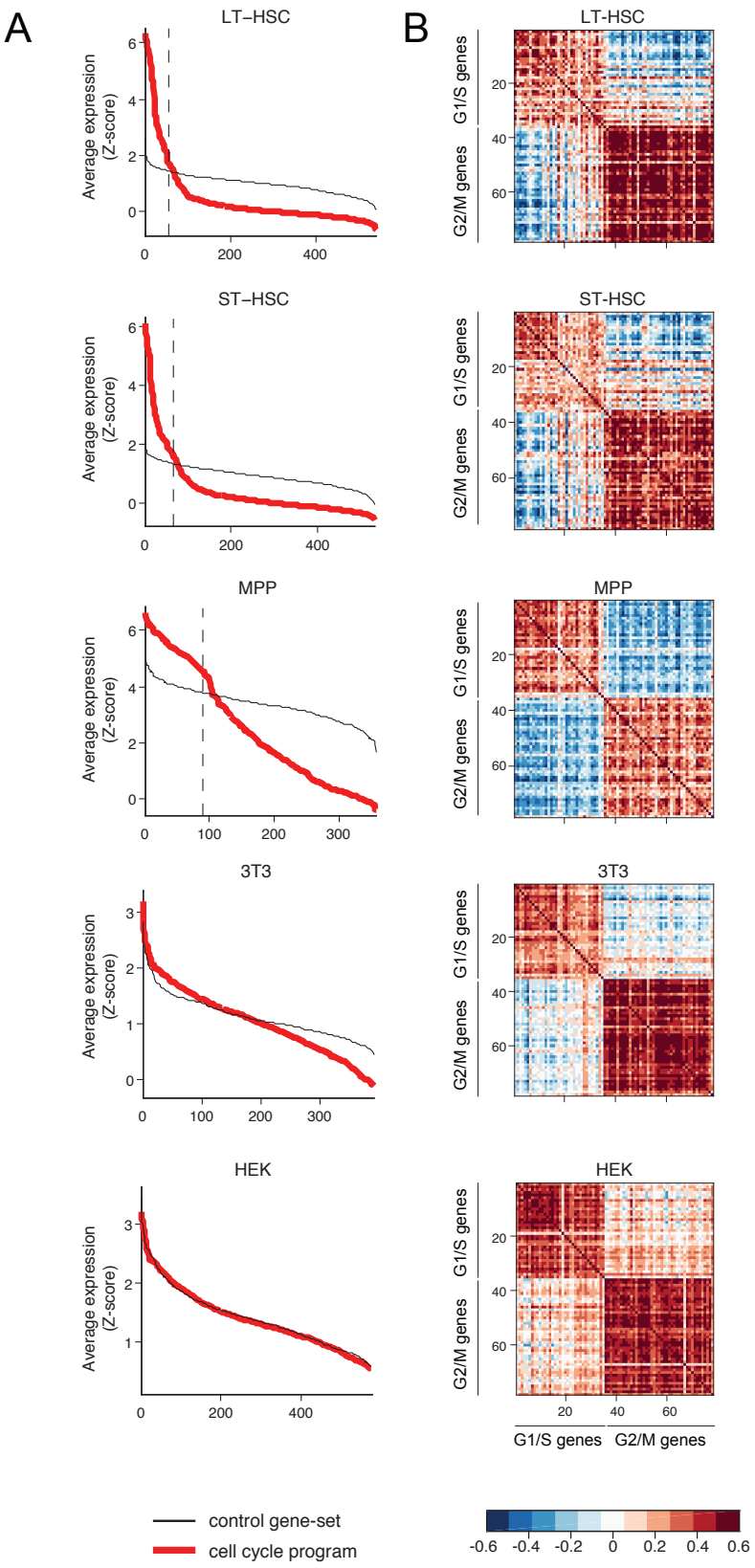

Figure S2. Meta analysis of cell cycle across 5 cell types

(A) Score of the cell cycle program (in red) defined as an average expression of G1/S and G2/M gene-sets (Z-score, *y*-axis), compared to the levels of randomly selected control gene-sets (in black) (with matched average expression level). Dashed line separates cycling (to the left of the line) and non-cycling (to the right) cells. (B) Co-expression of genes in the G1/S and in the G2/M programs among the subset of cells that were identified as cycling in (A).