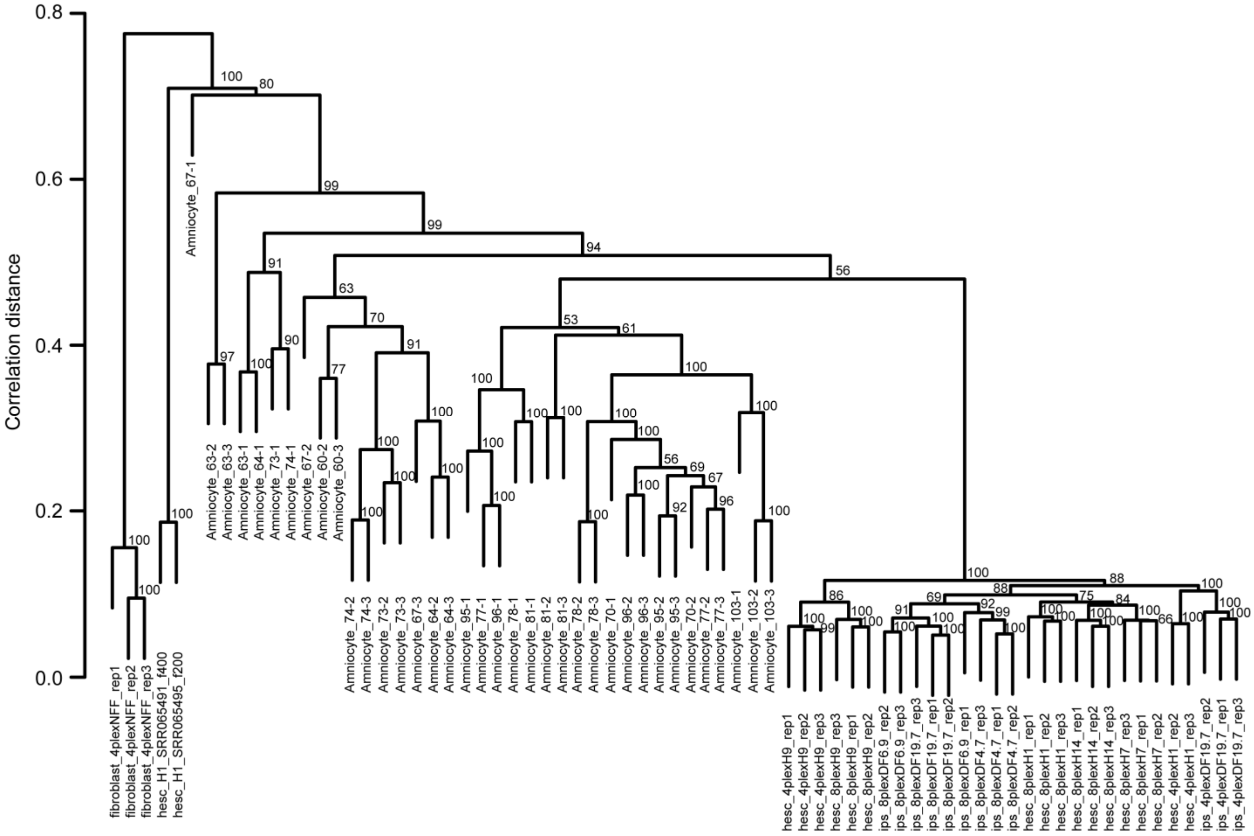

Figure S1. Hierarchical clustering analysis of all samples. RNA-seq datasets were generated from 1) amniocytes, 2) ESC (H1, H7, H9, and H14 cell lines); 2) iPSC; and 3) iPSC parental newborn foreskin fibroblasts (NFF). 71 samples clustered by variance-stabilized mRNA−seq read counts of 24,612 genes (mean read count > 4). Bootstrapping values are based on 100 randomized replicates. Correlation distance is 1 - | Pearson’s r |.