# Supplementary Figure S1
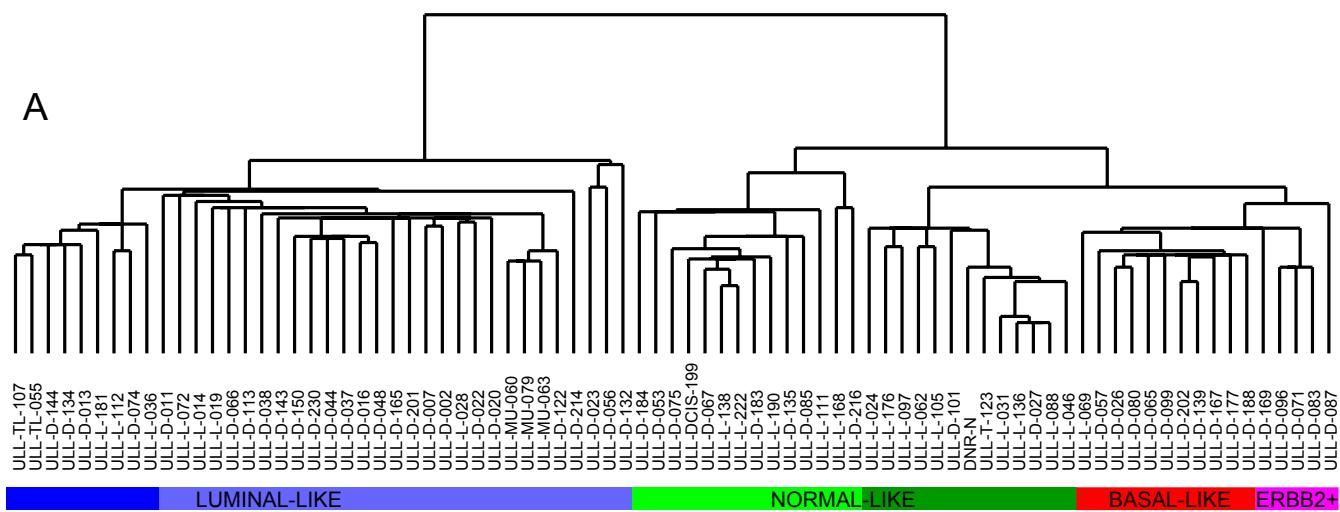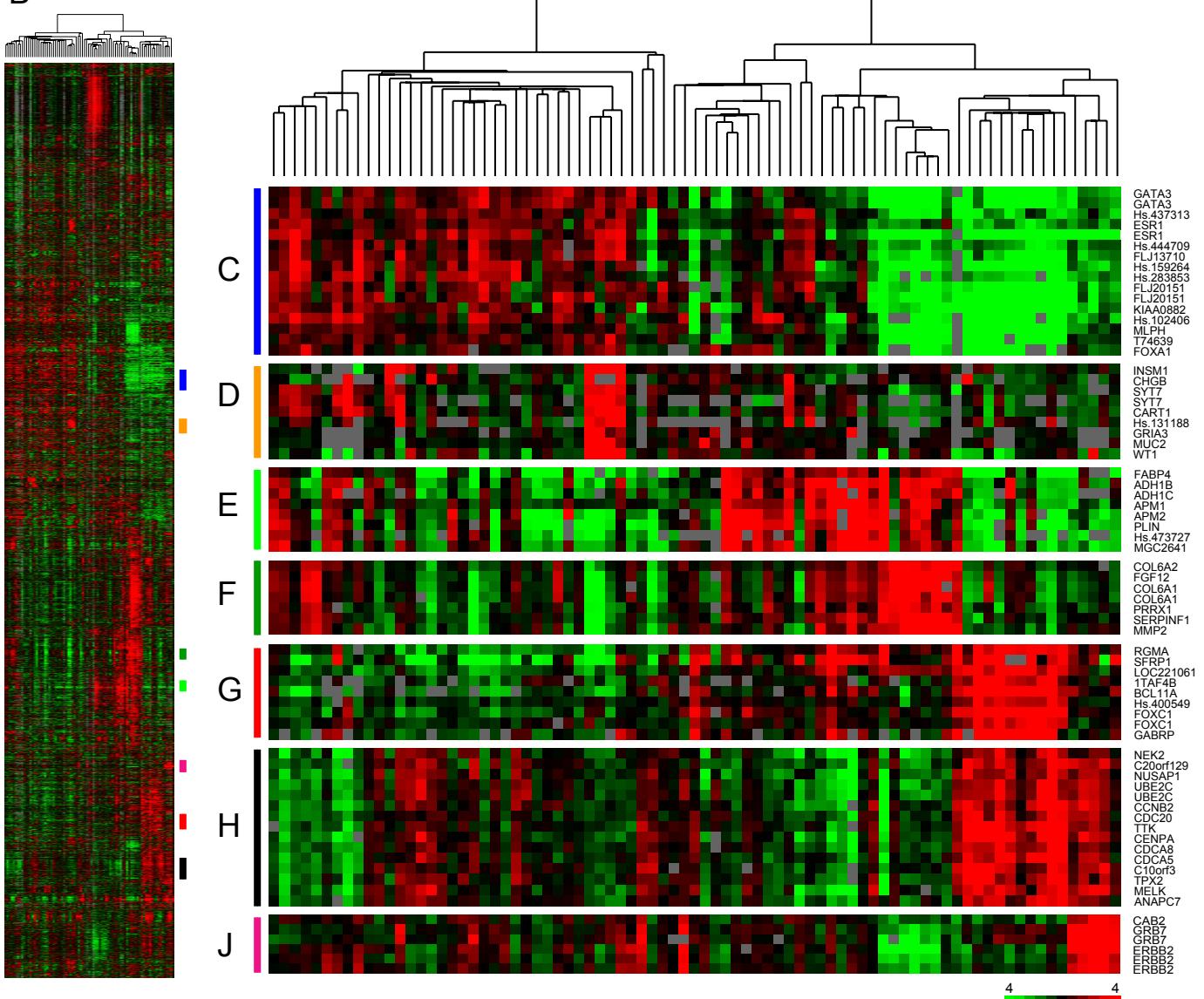
Hierarchical clustering using the "total list" of genes. Hierarchical clustering of 80 samples using the total set of 7,214 clones (representing 6,323 genes corresponding to a single unique UniGene cluster in SOURCE; http://source.stanford.edu) whose expression varied at least 3-fold from the mean abundance across all samples in at least 3 samples and was measurable in at least 70% of the samples included in the analysis. Gene clusters characterizing the subgroups distinguished in the dendrogram (A) are genes related to the cells' ER status (C), mucinous carcinomas cells (D), adipose cells (E), stromal cells (F), basal epithelial cells (G), dividing and proliferating cells (H), and ERBB2+ cells (J).