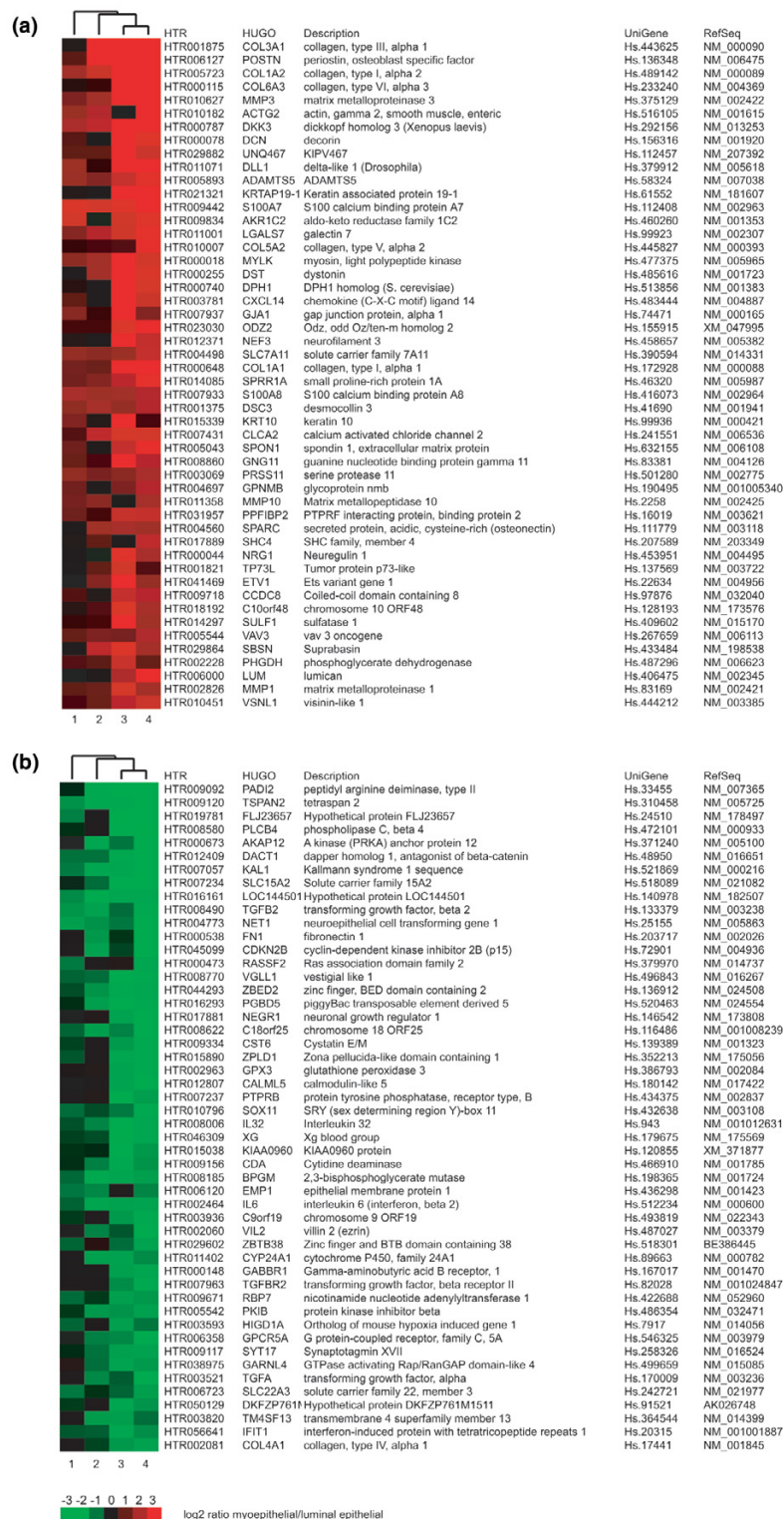


Figure 3

Heatmap of the top 50 genes from the luminal-specific and myoepithelial-specific transcriptomes. Genes were ranked in order of fold change (myoepithelial over luminal) for each platform separately after which a median rank over all four platforms was determined. Genes are listed with their human transcriptome database (HTR) cluster, HUGO Name, description and UniGene and RefSeq identifiers. Green corresponds to luminal-type; red to myoepithelial-type; black indicates no corresponding microarray feature. Expression measurements obtained by: 1, Agilent; 2, 20 k brk; 3, CodeLink; 4, Affymetrix platform.