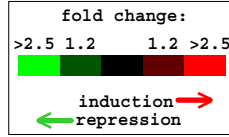


### Hierarchical clustergram of 2.0r outlier genes with full annotation.

An addendum to Figure 3, the log ratios of all 2.0r outlier genes are shown hierarchically clustered (Pearson correlation, average linkage). Gene annotations include IMAGE clone ID and UniGene cluster name (according to UniGene Build #129). Gene expression patterns are shown in rows; tissue profiles in columns. Degree of color saturation reflects the magnitude of the expression ratio. Note that for optimal clustering, the expression data for each individual dye-swap experiment was used (see key in figure for directionality of expression via color pairs). Gene names colored in green indicate the immune response/lymphocyte-related cluster. Red colored gene names denote the lipogenesis cluster. Gene names colored in blue indicate the cell cycle/growth inhibitor genes.



- = up in iT3, or up in RTH (PV)
- = down in iT3, or down in RTH (PV)