

Supplemental Figure 3

Unsupervised average-linkage hierarchical clustering of 18 renal allograft biopsies obtained at implantation, after exclusion of probe sets associated with donor gender.

Unsupervised average-linkage hierarchical clustering of 18 renal allograft biopsies obtained at implantation, after filtering with a threshold of at least a 3-fold difference from the median expression in at least 5 different samples and exclusion of probe sets associated with donor gender. The degree of relatedness of the expression patterns in biopsy samples is represented by the dendrogram at the top of the panel, the degree of relatedness of gene expression in the dendrogram on the left. The color in each cell reflects the level of expression of the corresponding gene in the corresponding sample, relative to its mean level of expression in the entire set of biopsy samples. The clustering was performed using Cluster and Treeview software(8). Two clusters of expression patterns in the biopsy samples could be identified, either higher (Cluster A) or lower (Cluster B) expressed in the kidneys from deceased donors. The colored bars on the right of the diagram indicate these clusters with high discrimination scores.

