Additional data file 6. Gene ontology analyses with the most highly expressed protein-coding transcripts in three different human tissues. Expression data from prostate, liver and kidney were used to select the top 40% most highly expressed protein-coding genes. The BiNGO program was used to identify significantly ($p \leq 0.05$) enriched GO terms within these sets of selected protein-coding genes. (A) GO enriched categories for kidney are shown in colors, which are related to the degree of confidence (p-value) as indicated by the color bar-code; (B) GO enriched categories for prostate are shown; (C) GO enriched categories for liver are shown.
