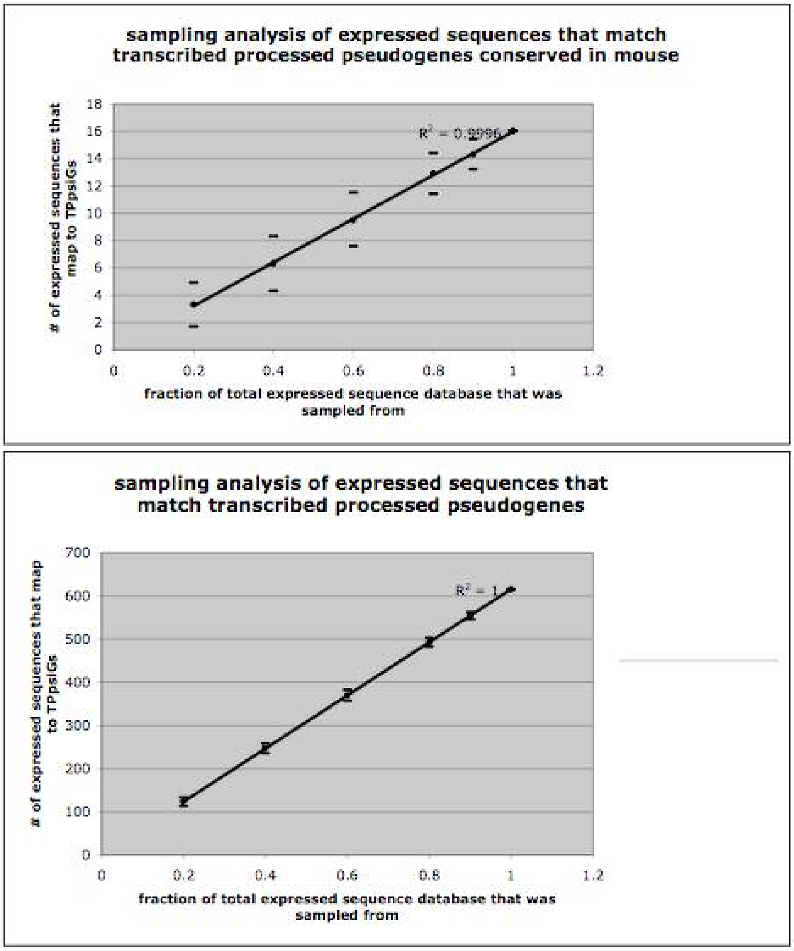
Supplementary Figure 1



Legend: The lower panel shows a plot of the number of expressed sequences that map to TPΨGs, for each sampling of the total expressed sequence database (ESTs, Unigene consensus sequences and Refseq mRNAs in combination). The total expressed sequence database was sampled 500 times at 0.2, 0.4, 0.6, 0.8 and 0.9 of its total size, and the number of TPΨG-matching expressed sequences were tallied in each case. Error bars (standard deviations) for the 500 samplings are indicated for each point. The upper panel shows the results of the same procedure for the small subset of expressed sequences that match TPΨGs with potential orthologs in mouse. In each case, the sampling shows no evidence of saturation of expressed sequence databases for detection of human TPΨGs.