Supplement tables 1and 2 contain lists of statistically significant differentially expressed transcripts with an unadjusted p-value cut off equal to 0.001. Transcripts are sorted based on the p-value in ascending order. Each tables name includes information on two cell types compared.

Columns throughout all three spreadsheets contain the following information:
Column A - Affymetrix probe ID number;
Columns B-C - unadjusted p-value and p-values FDR adjusted according to Benjamini and Ho
Columns D-E - log 2signal intensity values averaged across all five technical replications;
Column F – fold change calculated based on the average signal intensity values;
Columns G and above contain all biological annotation available though NetAffx web analysis

ochberg procedure;

s tool version of April 2004.