Supplementary Figure 1

| False discovery rate for cell-type specific differential expression between monocytes of acute-rejection and stable patients are lowest when data is log transformed. |
Supplementary Figure 1: False discovery rates (FDR) for cell-type specific differential expression between monocytes of acute-rejection and stable patients are lowest when data is log transformed. csSAM was applied to the kidney transplant dataset described in Shen-Orr et al.\textsuperscript{1} with either log-transformed or anti-log transformed gene expression measurements used for the deconvolution of cell-type specific gene expression and for differential expression between acute rejection and stable groups. For the 5000 genes that vary most across all arrays, the number of genes which would be called differentially expressed in monocytes as a function of FDR is shown. (A) As in the original publication, both deconvolution and differential expression steps are performed on log-transformed RMA values. Shown in parentheses is the number of genes identified as differentially expressed below an FDR of 0.15. (B) Both deconvolution and differential expression are performed on anti-log expression values and (C) deconvolution is performed on anti-log values which are then log-transformed again to identify differentially expressed genes.