



Fold Change (x)

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Supplemental Figure 5. Distributions of expression changes in the V71-370 upper court among six functional categories. Six functional categories relevant to infection are shown. Distributions are shown for genes showing significant infection responses (Upper vs. Mock) in V71-370 as revealed by LMMA analysis of GC-RMA preprocessed microarray data with TST-FDR adjusted p value ≤ 0.01 . Histograms show the number of genes in each fold change range. The line graph connects dots showing the numbers of genes in all categories in each fold change range. A negative fold change indicates a reduction in expression by that factor. p-values in each panel indicate the result of a Kolmogorov-Smirnov test comparing the distribution of expression changes within the category to the distribution for all genes. The mean and median of each distribution were calculated using the log-fold changes.