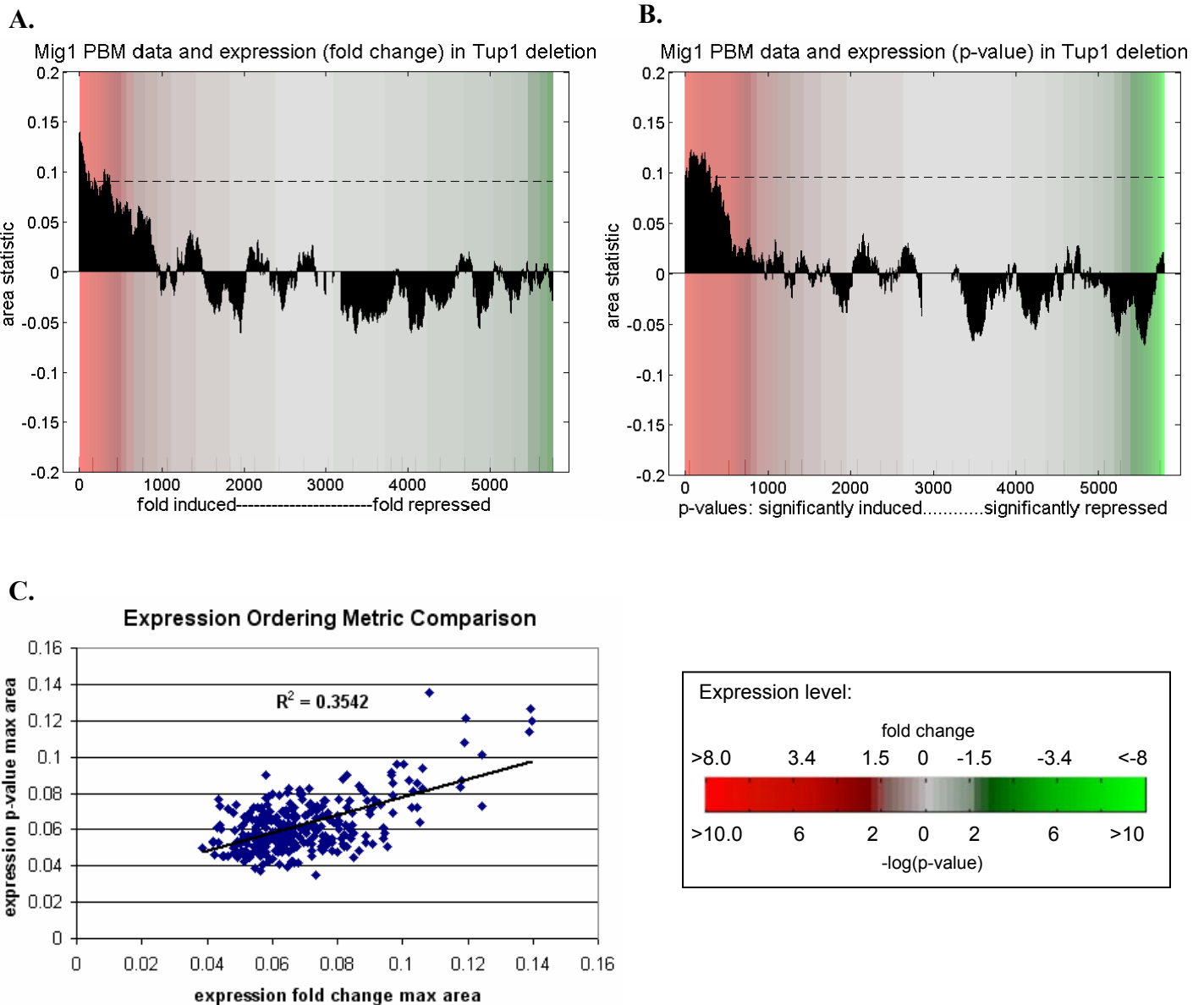


Supplementary Figure 4



Supplementary Figure 4: The example of Mig1 PBM data and expression in the Tup1 deletion strain shows that conditions that show highly significant enrichment statistics in CRACR when the genes are ordered by **(A)** expression fold-change also show significant enrichment when the genes are ordered by **(B)** an expression p-value that accounts for intrinsic biases in gene expression data (Hughes et al., 2000b). **(C)** The maximum area statistic for each condition calculated when expression is ordered by p-value is plotted vs. the maximum area when genes are ordered by their fold change. There is a clear positive correlation, but results for less significant conditions are variable.