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ERRATUM

Inferring condition-specific transcription factor function from DNA binding and gene expression data

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Correction to: *Molecular Systems Biology* **3**: 100. doi:10.1038/msb4100140; published online 17 April 2007

Since the publication of the above paper, the authors have noticed an error in Figure 1. During typesetting, Figure 1F was mistakenly replaced by Figure 1G. Thus, the two panels were shown as identical when they should have been different.

Please see the corrected figure on the next page.

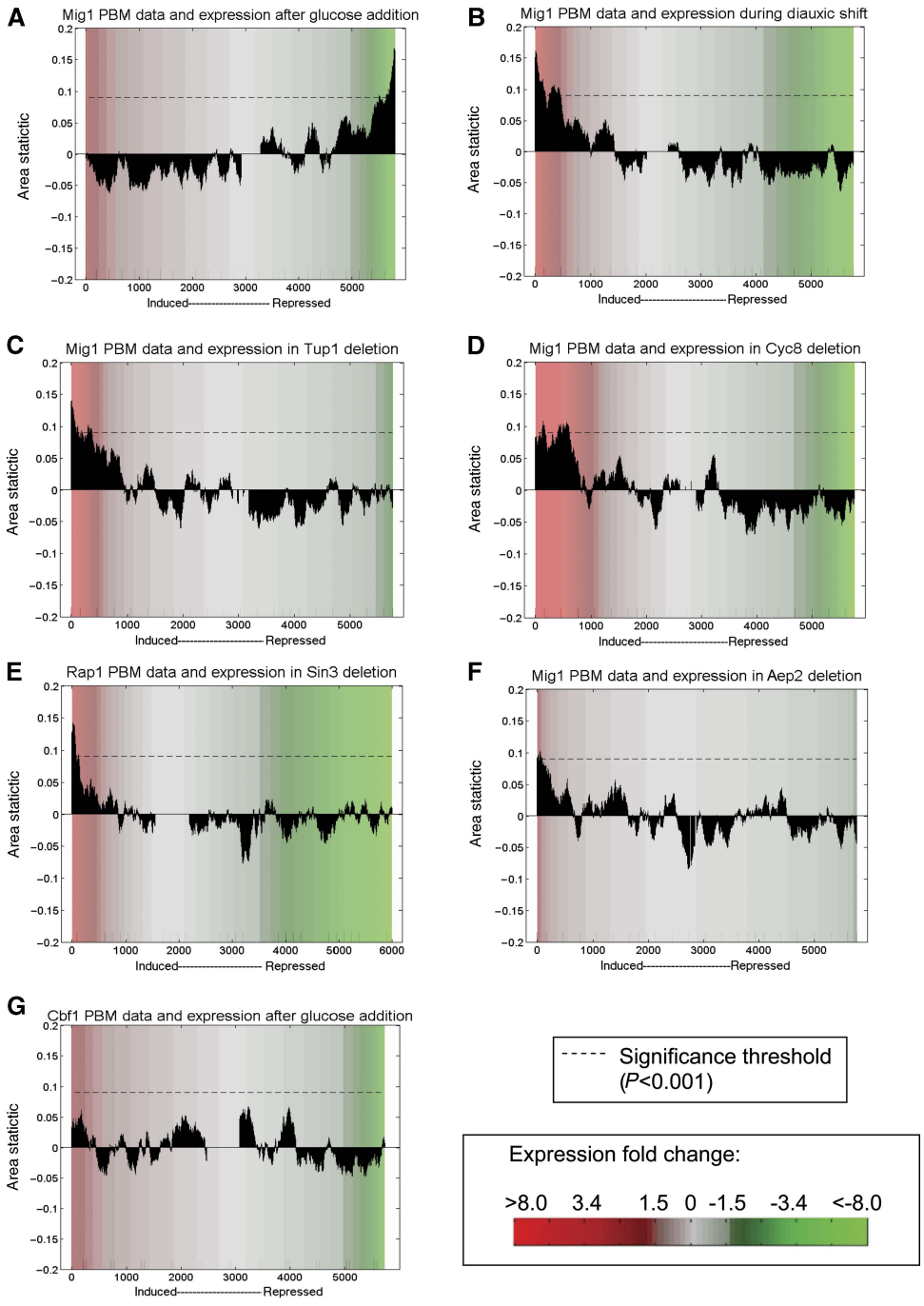

Figure 1 Results of CRACR analysis for various expression conditions. The area statistic for PBM target gene enrichment (see the Materials and methods section) is plotted (*y* axis) for each window of expression-ordered genes (*x* axis), using a window size of 200 genes. Mig1 target genes are significantly enriched (**A**) among repressed genes in glucose addition and (**B**) among derepressed genes in diauxic shift (the 21-h time point is shown). Deletion of either (**C**) Tup1 or (**D**) Cyc8 results in derepression of Mig1 targets. (**E**) Induction of Rap1 target genes in genetic interactor Sin3 deletion. (**F**) Induction of Mig1 targets in the Aep2 deletion. (**G**) Negative control: no enrichment for Cbf1 targets among differentially expressed genes in glucose addition. The dotted line in each panel indicates the $P<0.001$ significance threshold. The background color indicates gene expression fold change as depicted in the color bar.