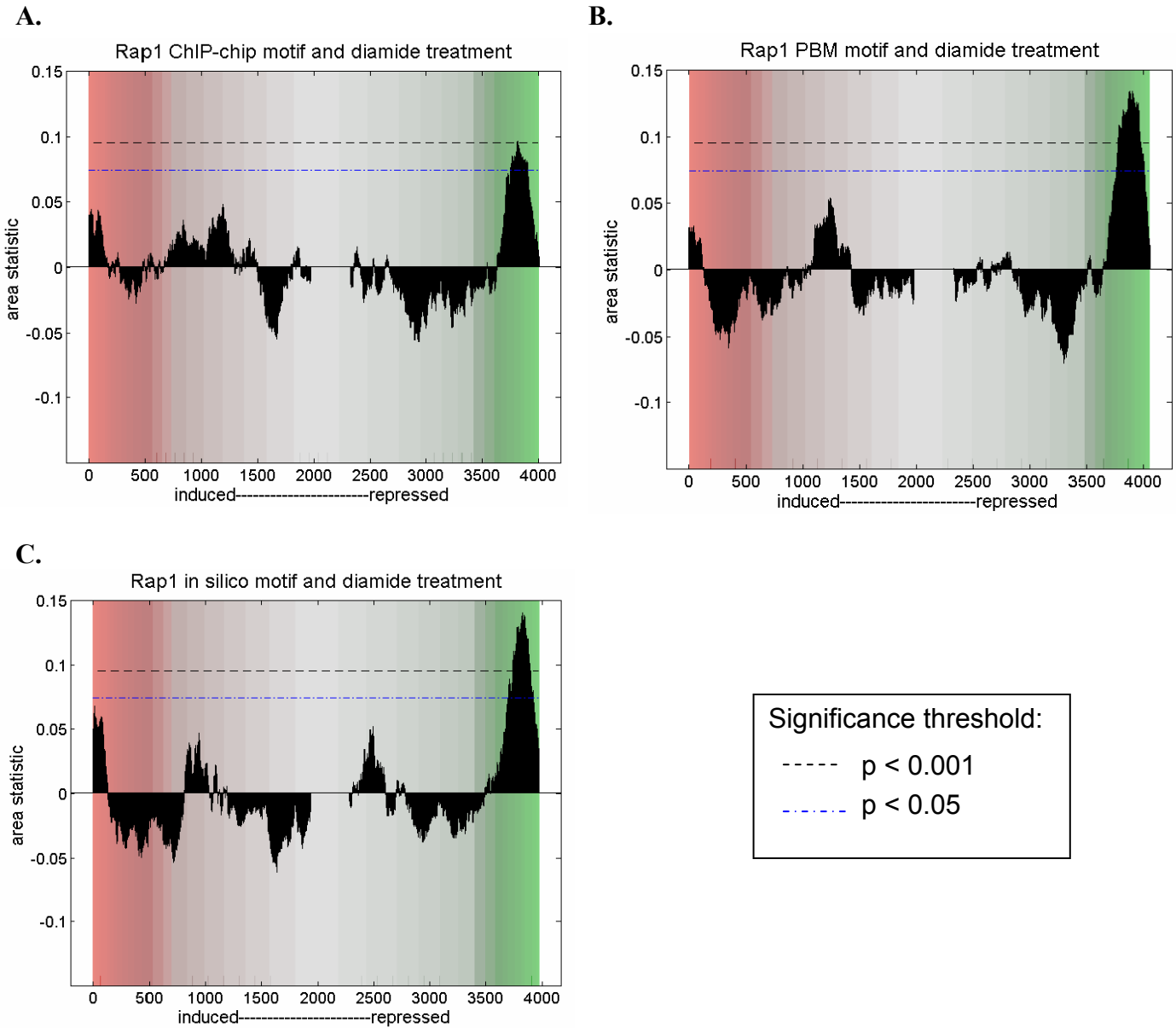


Supplementary Figure 3.



Supplementary Figure 3. CRACR analysis may be applied to various TF binding site data types. The 1.5 mM diamide treatment expression condition gives similar patterns of enrichment when combined with intergenic region ranks based on matches to motifs derived from: **(A)** ChIP-chip data for Rap1 (Harbison et al., 2004), **(B)** PBM data for Rap1 (Mukherjee et al., 2004), and **(C)** AlignACE motif searching of IGRs upstream of annotated ribosomal protein genes (Hughes et al., 2000a). Expression color scale is as indicated in Figure 1.