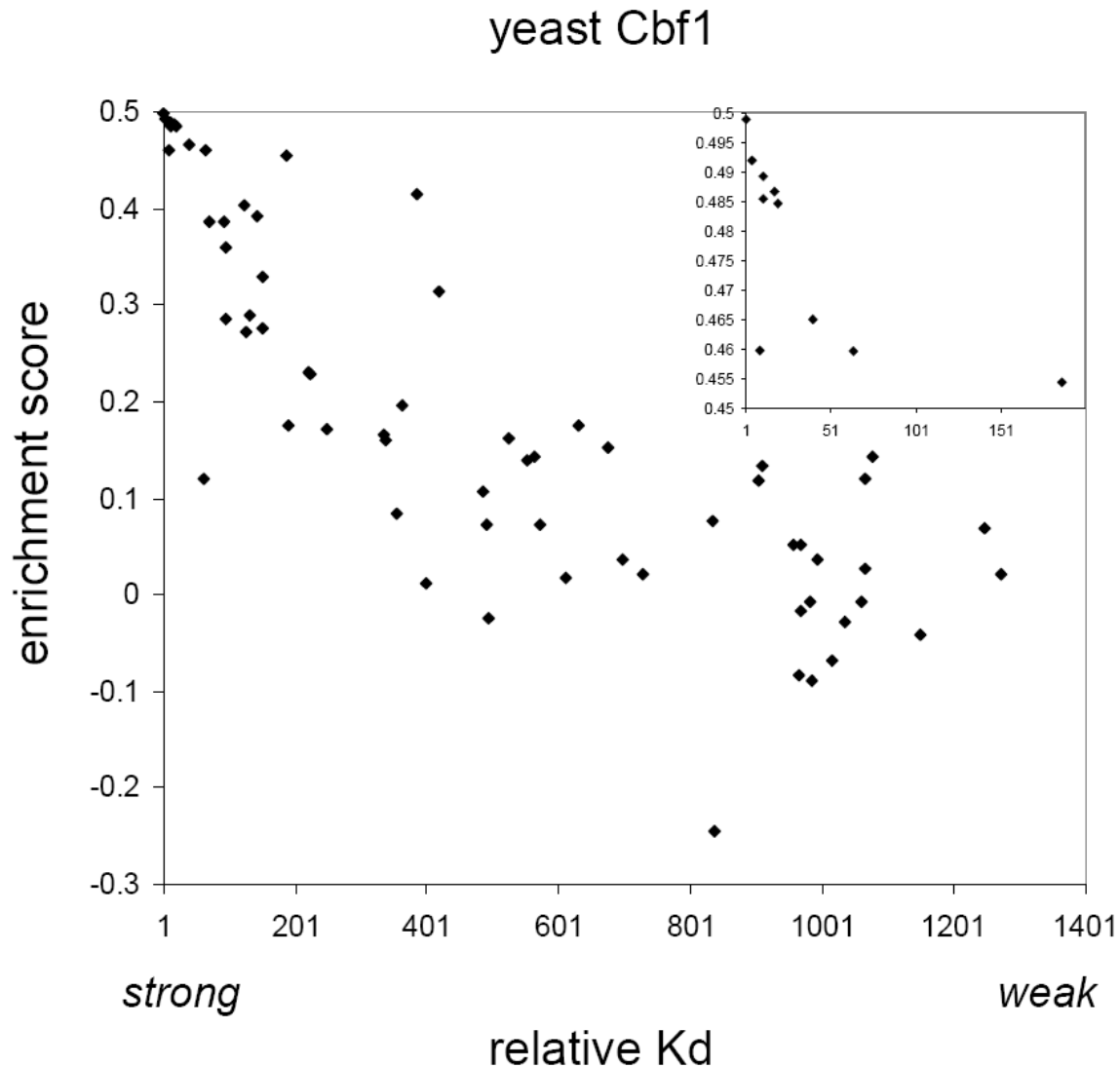


(A)



**Figure S6. Comparison of PBM data versus  $K_d$  data.**  $k$ -mers with higher median signal intensity are of higher DNA binding affinity, as shown in PBM enrichment score versus relative  $K_d$  plots for (A) yeast Cbf1 (data shown for 8-mers analyzed by Maerkl and Quake, *Science* (2007)) and (B) (next page) murine/human Max (data shown for median of all 8-mers that contain each 7-mer analyzed by Maerkl and Quake, *Science* (2007)). Yeast Cbf1 PBM data are from Berger *et al.*, *Nature Biotechnology* (2006). Max PBM data are for murine Max from this paper.  $K_d$  data were calculated from ddG data from Maerkl and Quake, *Science* (2007), and correspond to affinities for the highest affinity sequences, of 16.6 nM for Cbf1 and 67.0 nM for human MAX isoform A. The lower limit of detection of the MITOMI assays was ~18  $\mu$ M, as reported in that study. Note: Maerkl and Quake, *Science* (2007) examined human Max protein. Additional comparisons of PBM versus  $K_d$  data were shown previously in Berger *et al.*, *Nature Biotechnology* (2006) for Egr1 (Zif268).

(B)

mouse/human Max

