

Figure S4. *In vitro* binding analysis to fragments representing ChIP-enriched genomic regions. In this figure, all EMSAs are shown that yield nonspecific, low-affinity or no binding at all for the fragments containing the best potential motif predicted with the energy based position weight matrix. Protein concentrations are identical for all EMSAs and are given in the upper left EMSA. Targets are named according to the gene closest to or overlapping the ChIP peak. Disappearance of DNA at the highest protein concentrations indicates that non-specific binding causes the material to remain in the wells.

