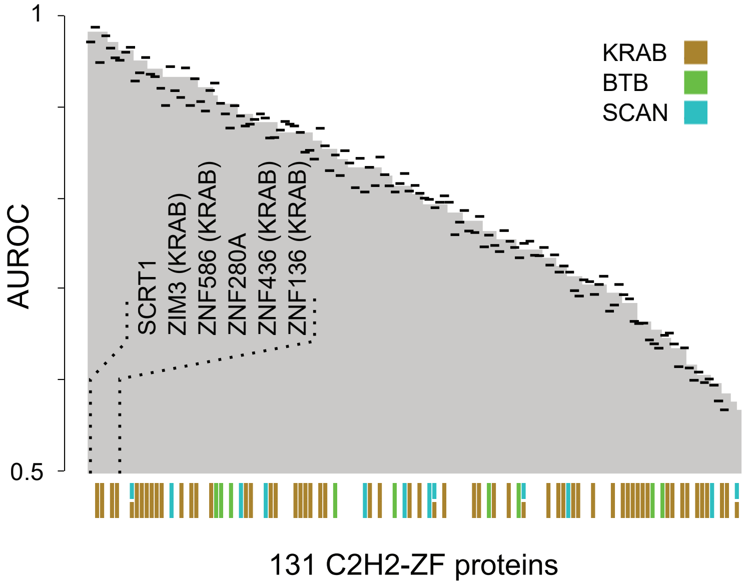

Supplemental Figure S2 (related to Figure 2). Distribution of AUROC values for 131 C2H2-ZF protein DNA-binding motifs, tested on ChIP-seq peaks. The AUROCs are calculated as described (Najafabadi et al., 2015b), comparing the top 500 peaks of each protein to dinucleotide-shuffled sequences (grey) or 500 randomly-selected genomic regions filtered to contain a matching distribution of length and dinucleotides, and to be composed of non-peak, non-ERE regions of the genome (black dashes). Effector domains are shown below; proteins with AUROC>0.98 are indicated with names.