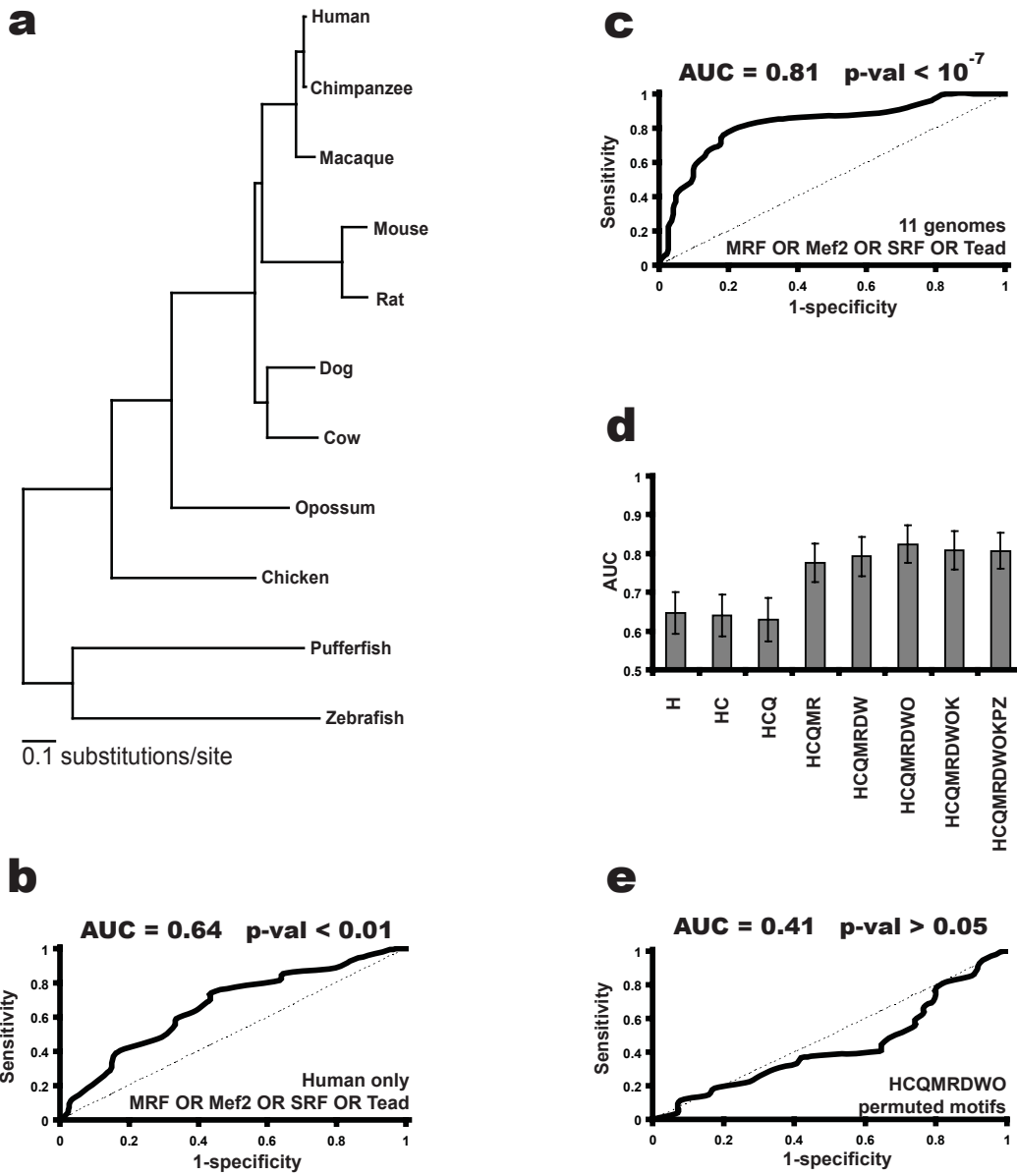


Supplementary Figure 4



Supplementary Figure 4: Evaluation of PhyICRM and the effect of phylogeny

(a) Phylogenetic tree of 11 vertebrates utilized in this study. (b) Sensitivity and specificity of PhyICRM on a collection of 27 sequences of length 75 kb containing a CRM, as compared to a collection of length-matched sequences. Sequences were scanned with the OR combination of MRF, Mef2, SRF and Tead, and using only human sequence. (c) Similar to (b) but using all 11 vertebrate genomes. (d) AUC values when using progressively larger phylogenies. H=Human, C=Chimpanzee, Q=Macaque, M=Mouse, R=Rat, D=Dog, W=Cow, O=Opossum, K=Chicken, P=Pufferfish, Z=Zebrafish. (e) Sensitivity and specificity when using the phylogeny HCQMRDWO and a permuted form of these motifs.