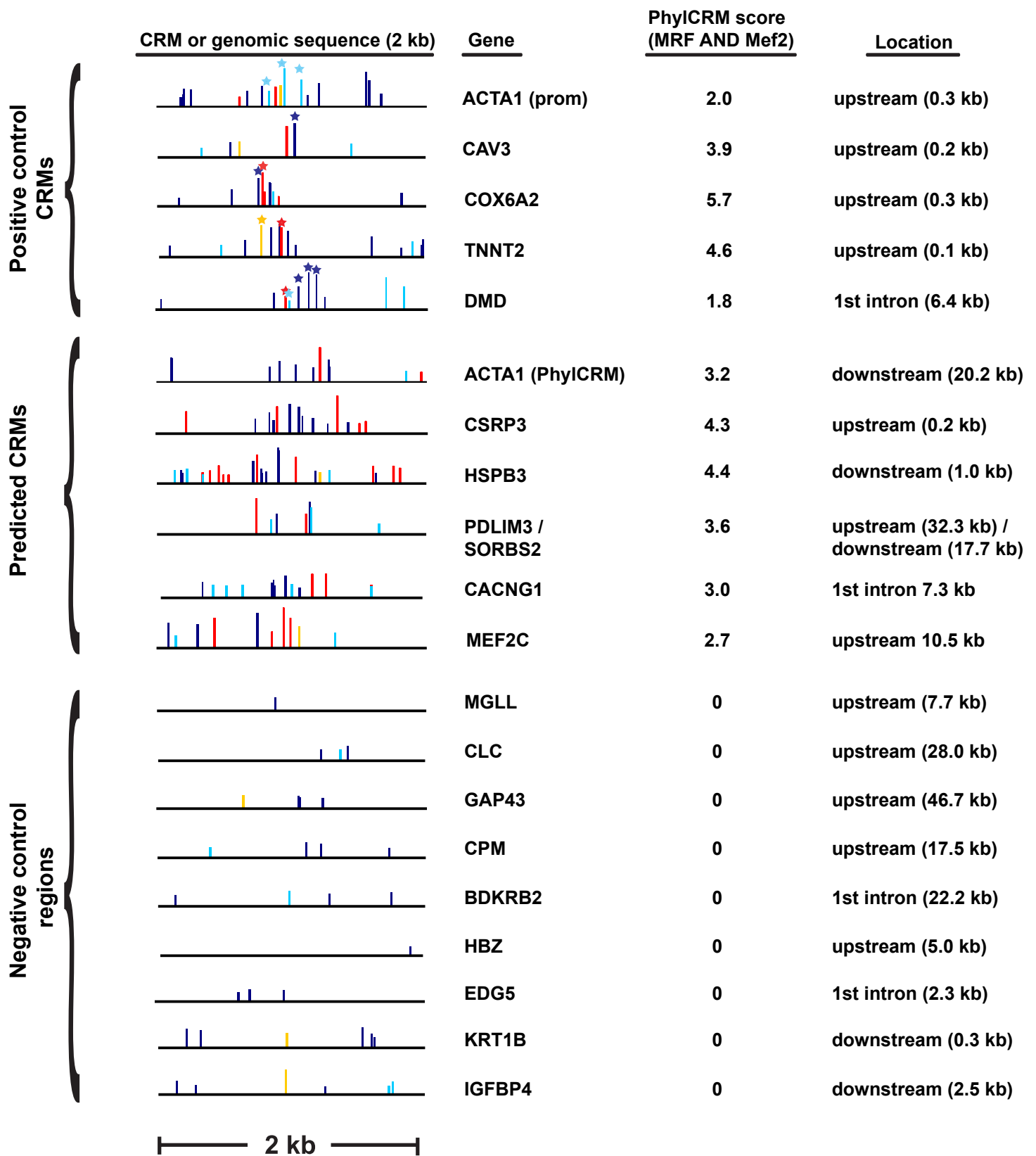


TF binding sites: MRF Mef2 SRF Tead } Known binding sites



**Supplementary Figure 6. Schematic display of computationally predicted human CRMs and control sequences.**

Previously described CRMs were used as positive controls in ChIP assays; see Supplementary Methods for full descriptions of the known and candidate CRMs. Negative control regions used in ChIP assays were chosen to not contain matches to the MRF AND Mef2 motif combinations, and to also not be enriched for the other binding sites under consideration (MRF = blue, Mef2 = red, SRF = cyan, Tead = gold), where stars indicate known binding sites. The PhylCRM score of the degree of enrichment for MRF AND Mef2 is shown (see Supplementary Methods for a description of the PhylCRM scoring scheme). Locations of sequence windows in relation to transcriptional start (if upstream or intronic) or stop (if downstream) are shown. We note that the region labeled “PDLIM3/SORBS2” was located between the PDLIM and SORBS2 genes. Also, we note that “ACTA 1 (prom)” refers to a previously known CRM located at transcriptional start, while “ACTA 1 (PhylCRM)” refers to a novel PhylCRM prediction.