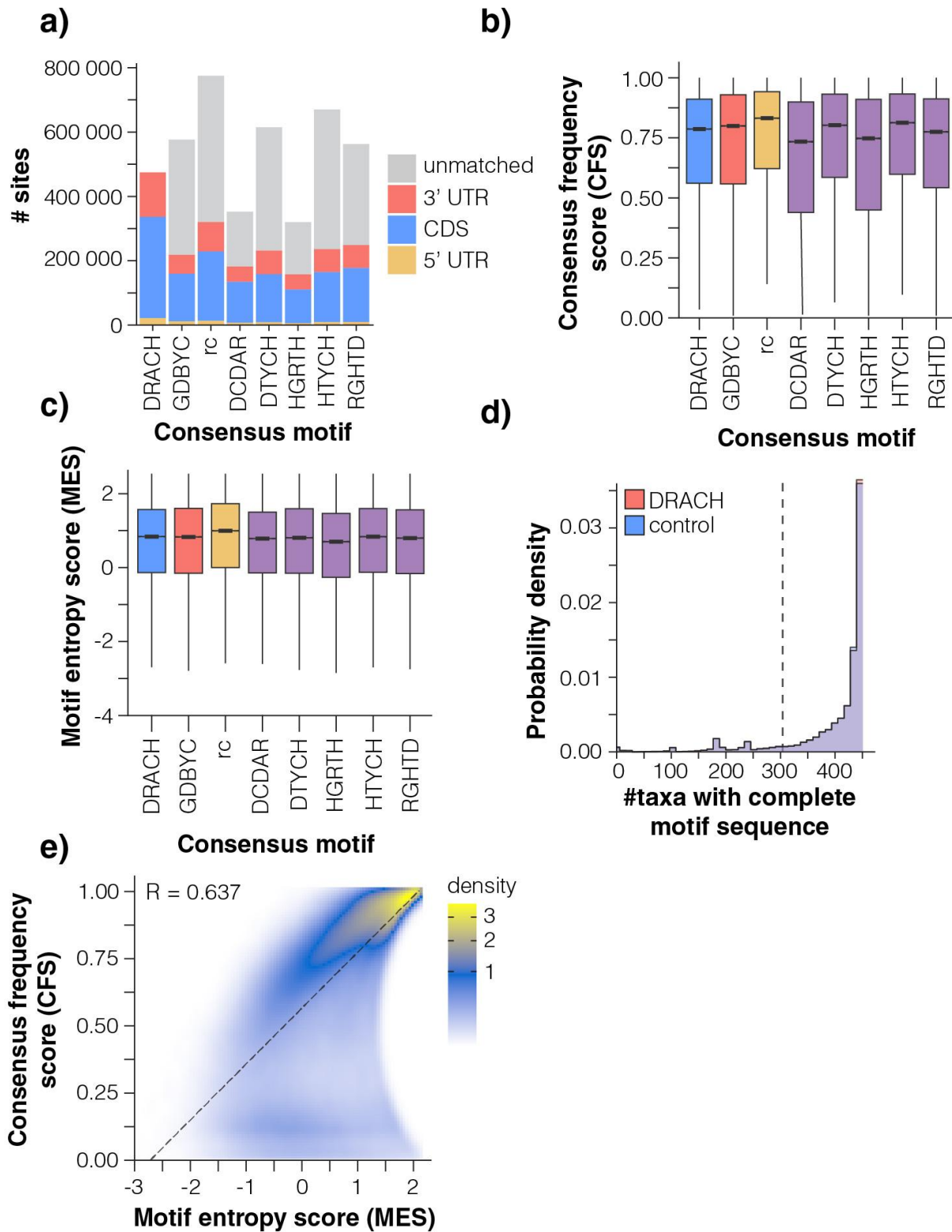
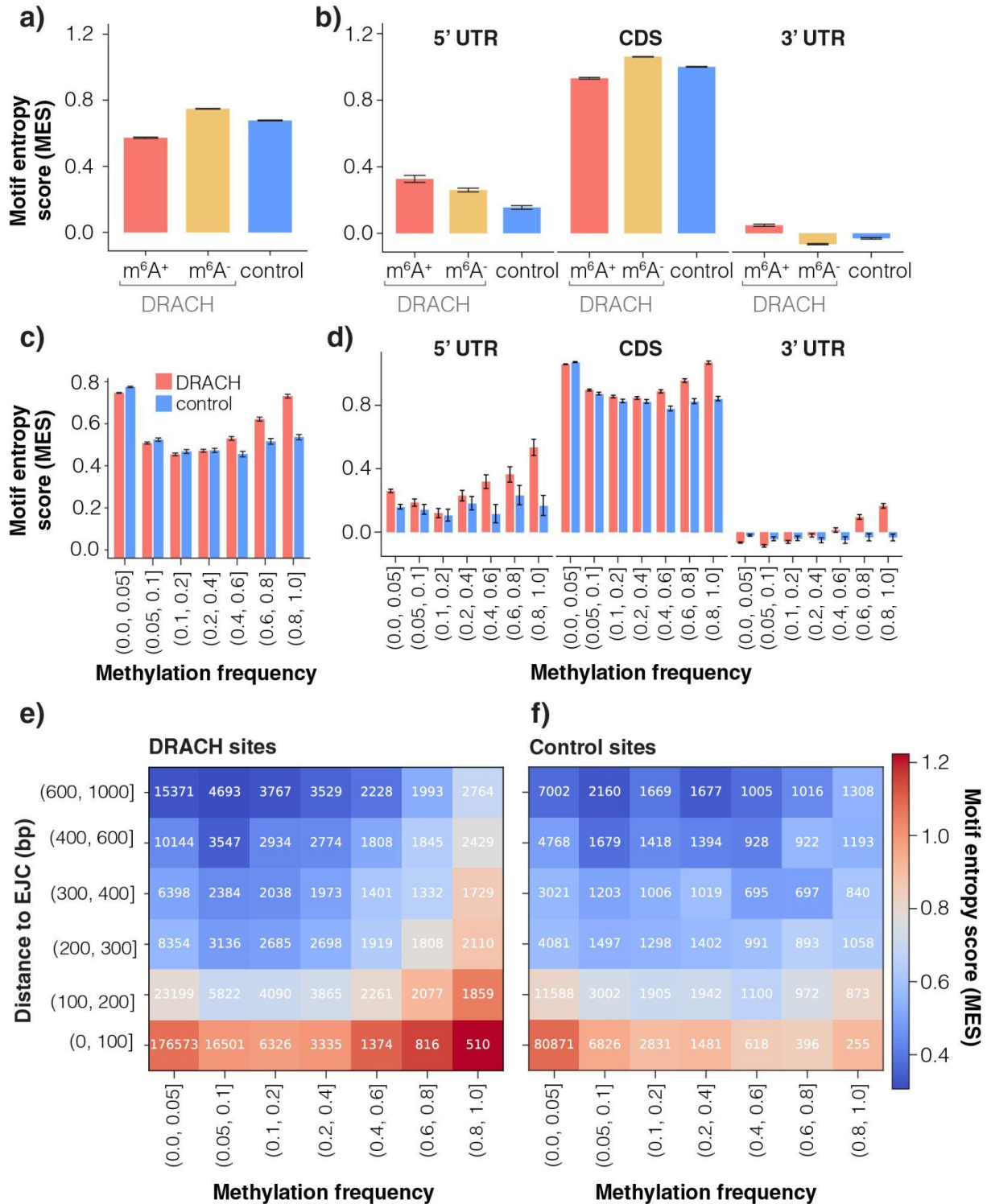




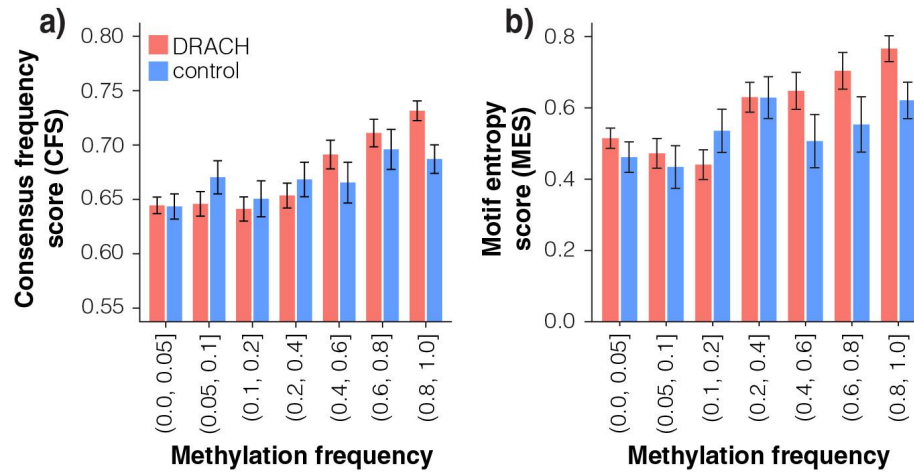
Supplementary Figure 1 - Dataset composition and conservation metrics for consensus motifs. (a) Number of sites included in analysis for each consensus motif used, grouped by

RNA region. This includes the methylatable DRACH motif and various candidate control motifs: the inverse DRACH motif (GDBYC), reverse complements of each motif within DRACH (rc), and five consensus motifs with comparable sequence properties to DRACH (DCDAR, DTYCH, HGRTH, HTYCH, and RGHTD). Control motif sites that did not match with a DRACH site (see Methods) are labeled as 'unmatched'. (b, c) Distribution of evolutionary conservation metrics for consensus frequency score (CFS) and motif entropy score (MES) for each of the previously mentioned consensus motifs used in the analysis. (d) Distribution of taxa counts with complete homologous motif sequences (no indels) for each site identified in *Homo sapiens*. The dashed grey line indicates the minimum threshold of 304 taxa required for inclusion in analysis, representing the top 75% of sites. (e) Correlation between both conservation metrics for all DRACH sites used in the analysis (n = 474,226).



Supplementary Figure 2 - Evolutionary conservation analysis using entropy based metric. (a) Comparison of evolutionary conservation between methylated (m^6A^+) and unmethylated (m^6A^-) DRACH sites to matched control (GDBYC) sites using motif entropy score (MES), and (b) separated by RNA region. (c) Comparison of MES of DRACH and control motifs grouped by methylation frequency, and (d) separated by RNA region. (c, d) Conservation

heatmaps showing MES for (e) DRACH sites and (f) matched control sites grouped by methylation frequency and EJC proximity. Color intensity represents conservation strength, with darker red indicating higher conservation. Numbers within cells show the count of sites per group.



Supplementary Figure 3 - Evolutionary conservation analysis of intron-less genes. Comparison of evolutionary conservation between DRACH sites and matched control (GDBYC) sites in intron-less/single-exon genes using (a) consensus frequency score (CFS) and (b) motif entropy score (MES).