

Figure S9: Protein disorder analysis

Distributions of disorder scores for all 3-mers, 4-mers, and FIRE-pro motifs. Disordered regions of the *S. cerevisiae* proteome were determined by DisEMBL, putative instances of motifs or k-mers were identified, and the disorder score was defined as the percentage of motif instances across the entire proteome that lie in disordered regions. FIRE-pro motifs are found more frequently in regions of protein disorder than all 3-mers or 4-mers (Kolmogorov-Smirnov test: p<1e-175; FIRE-pro motifs: N=6,862; 3-mers: N=8,000; 4-mers: N=118,908).