**Figure 7—figure supplement 1. Motif preferences around m⁶A sites according to ECT2 binding.** From top to bottom: (1) motif logos for derived position weight matrices (PWMs); (2) distance-based enrichment of motifs at and around m⁶A-Nanopore* sites, plotted as motif counts per 1000 m⁶A sites (purple lines). Grey lines indicate the enrichment in a location-matched background set as in Figure 5D; (3) same as in 2 with sites split according to whether they sit on ECT2 targets; (4) same as in 2 with sites split according to the distance from the nearest ECT2 crosslink site (for ECT2-iCLIP targets only); (5) motif counts per 1000 iCLIP binding sites, as a function of distance from the iCLIP position, showing all sites against matched background sites (grey lines). Motifs are ordered according to the different relative enrichment upstream or downstream m⁶A sites according to ECT2 binding (see text below panels 3 and 4). * Parker et al. (2020).