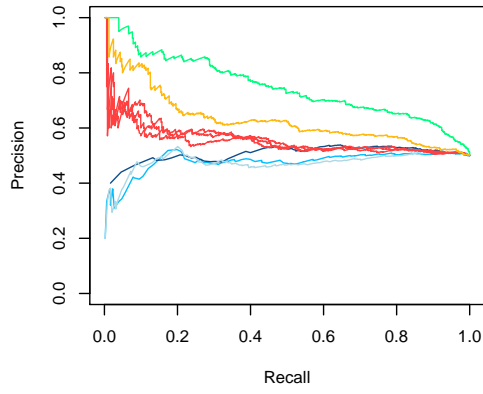


Additional File 4: Full classification performance comparison

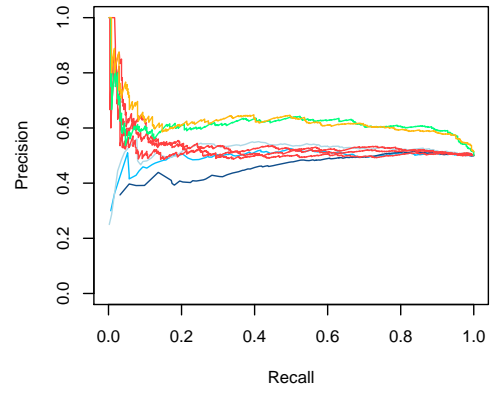
On the following pages, we show Precision-Recall curves of classification performance for all four tested tools on 25 CLIP-Seq datasets. For two datasets, SFRS1 and DICER, *MEMERIS* did not terminate within seven days which is why no curve is shown for this tool on these two proteins.

The plots contain curves for *MEMERIS* (blue), *GraphProt* (green), *RNAcontext* (yellow) and ssHMM (red). *MEMERIS* was executed in three different settings, with $pi=0$ (strong structural prior directs motif finding to single-stranded regions, dark blue), $pi=100$ (effectively sequence-only motif finding similar to *MEME*, light blue), and the in-between setting of $pi=1$ (sky blue). For ssHMM, three independent runs were performed because of the non-deterministic nature of the algorithm.

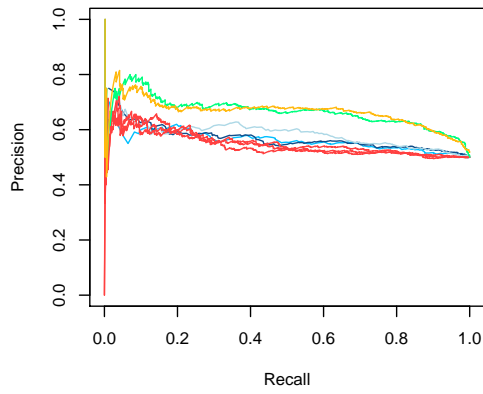
AGO1234



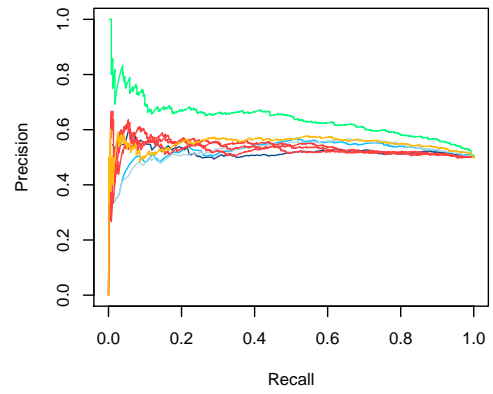
AGO2_HITSCLIP



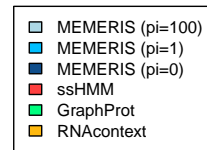
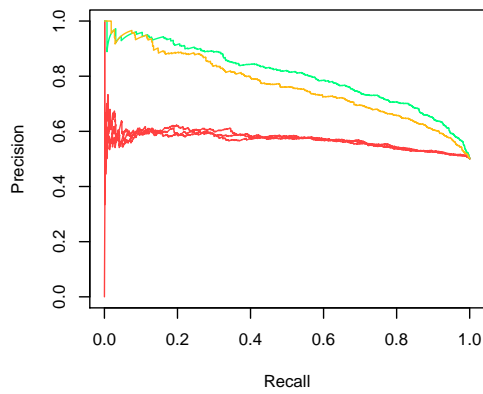
AGO2_PARCLIP

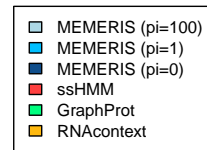
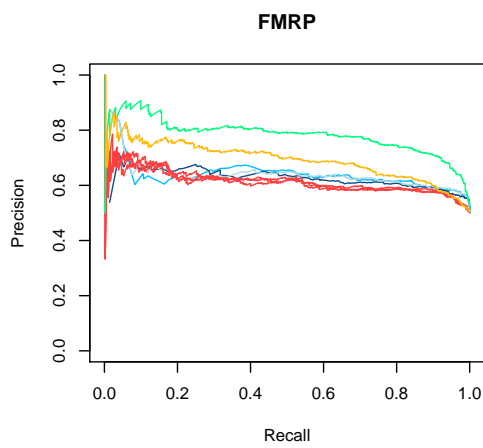
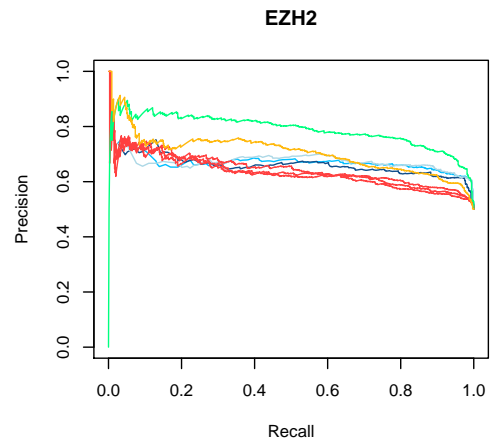
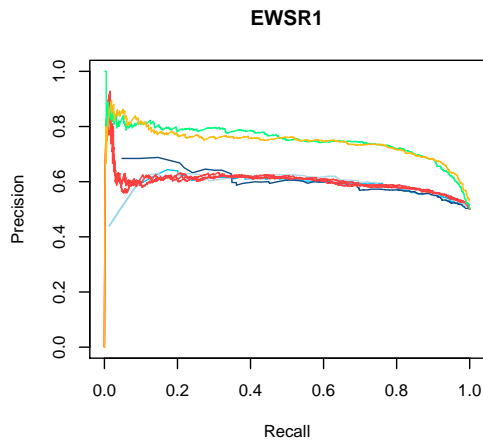
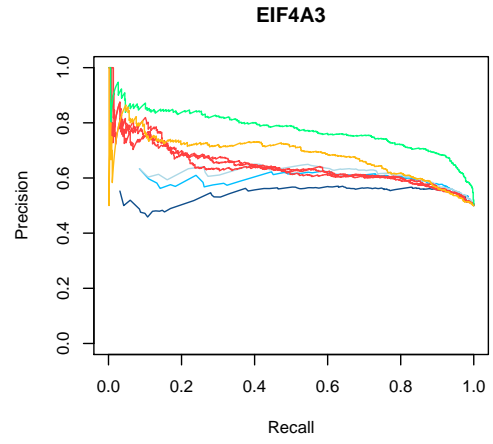
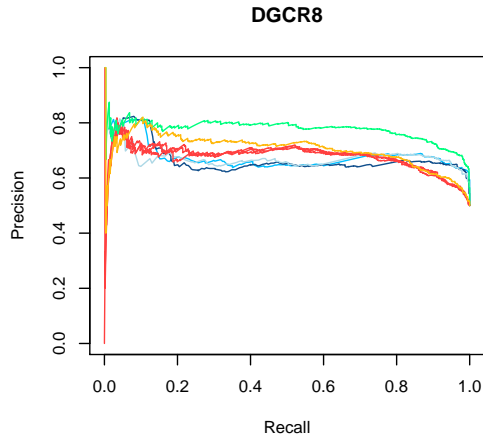


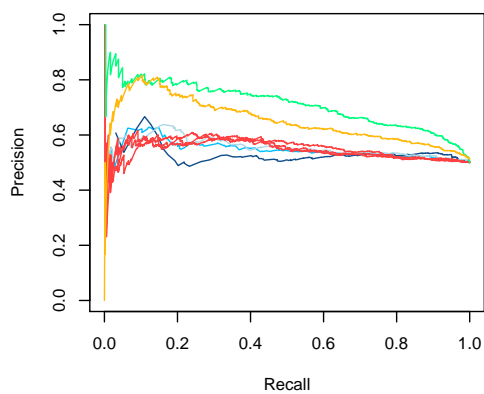
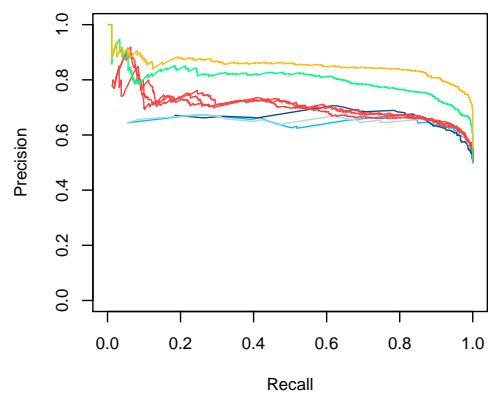
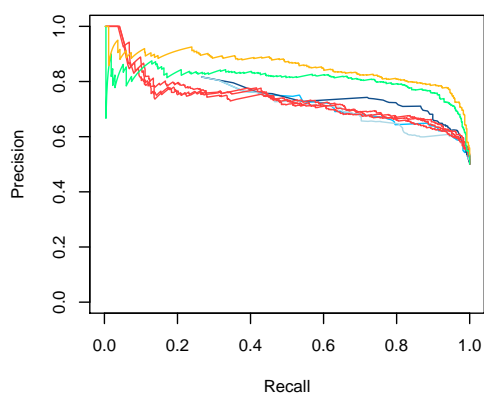
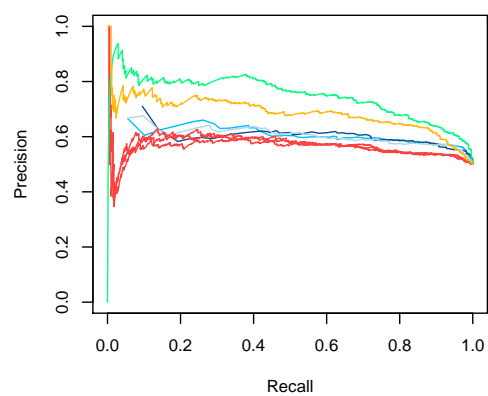
CAPRIN1



DICER





FXR2**HuR_HITSCLIP****HuR_PARCLIP****IGF2BP123****LIN28B**