

## **Additional Files**

### **Additional File 1 — Supplementary information**

This file contains supplementary information about ssHMM, in particular about the Gibbs sampling procedure, model parameters and motif output. Furthermore, it contains details about the datasets and program parameters used for evaluation and shows the full results for structure recovery, impact of sequence length on structure prediction, classification analysis, Fisher’s exact test and the runtime comparison.

### **Additional File 2 — Full CLIP-Seq results**

This file contains a table with the recovered motifs for all 25 CLIP-Seq datasets, including results by ssHMM, *MEMERIS*, *RNAcontext*, and *GraphProt* (with motif information contents).

### **Additional File 3 — ssHMM motifs for RNAshapes and RNAstructure**

This file contains a table with the ssHMM motifs for all 25 CLIP-Seq datasets based on structures predicted by RNAshapes or RNAstructure.

### **Additional File 4 — Full classification performance comparison**

This file contains Precision-Recall curves for all four tools on 25 CLIP-Seq datasets.