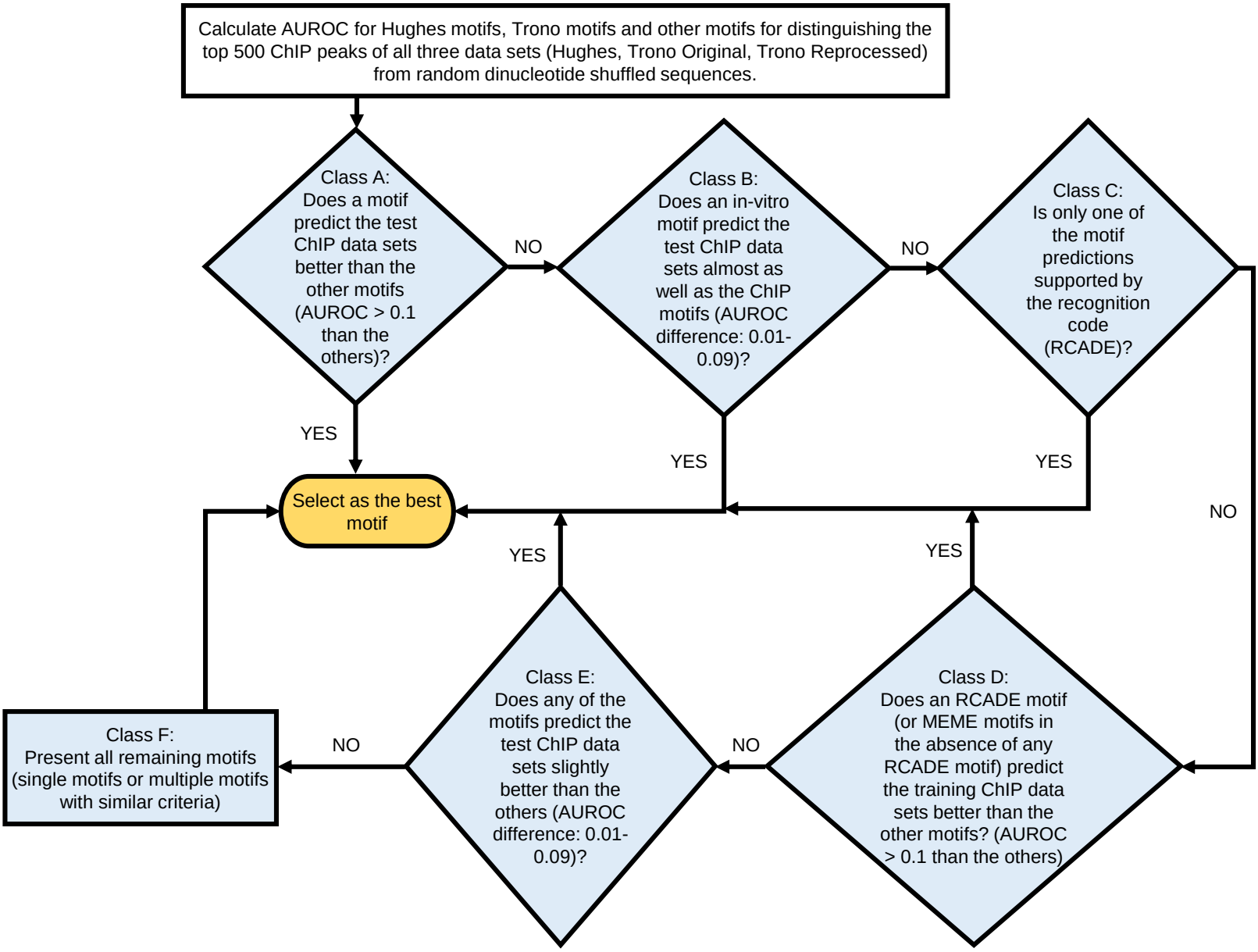
Figure S2


Calculate AUROC for Hughes motifs, Trono motifs and other motifs for distinguishing the top 500 ChIP peaks of all three data sets (Hughes, Trono Original, Trono Reprocessed) from random dinucleotide shuffled sequences.
Class A: Does a motif predict the test ChIP data sets better than the other motifs (AUROC > 0.1 than the others)?
NO
Class B: Does an in-vitro motif predict the test ChIP data sets almost as well as the ChIP motifs (AUROC difference: 0.01-0.09)?
NO
Class C: Is only one of the motif predictions supported by the recognition code (RCADE)?
YES
YES
YES
NO
Select as the best motif
YES
YES
Class E: Does any of the motifs predict the test ChIP data sets slightly better than the others (AUROC difference: 0.01-0.09)?
NO
NO
Class D: Does an RCADE motif (or MEME motifs in the absence of any RCADE motif) predict the training ChIP data sets better than the other motifs? (AUROC > 0.1 than the others)
Class F: Present all remaining motifs (single motifs or multiple motifs with similar criteria)