Table S3. Comparison of the individual branches model performance measured in AUC scores on RBP-31 dataset.

	RBP-31		
Protein	**Seq**	**Cons**	**SecStruct**
Ago/EIF	0.717	**0.857**	0.574
Ago2-MNase	0.594	**0.695**	0.515
Ago2-1	0.836	**0.913**	0.534
Ago2-2	0.852	**0.900**	0.535
Ago2	0.621	**0.638**	0.476
eIF4AIII-1	0.932	**0.962**	0.606
eIF4AIII-2	**0.938**	0.935	0.553
ELAVL1-1	**0.920**	0.777	0.637
ELAVL1-MNase	0.584	**0.714**	0.535
ELAVL1A	0.854	**0.861**	0.678
ELAVL1-2	**0.933**	0.887	0.698
EWSR1	**0.899**	0.792	0.689
FUS	**0.946**	0.709	0.660
Mut FUS	**0.939**	0.829	0.656
IGFBP1-3	0.681	**0.829**	0.565
hnRNPC-1	**0.953**	0.672	0.622
hnRNPC-2	**0.978**	0.552	0.599
hnRNPL-1	**0.699**	0.661	0.514
hnRNPL-2	**0.652**	0.564	0.530
hnRNPL-like	0.643	**0.676**	0.519
MOV10	0.814	**0.827**	0.473
Nsun2	0.751	**0.767**	0.634
PUM2	**0.959**	0.878	0.599
QKI	**0.958**	0.703	0.721
SRSF1	**0.883**	0.873	0.625
TAF15	**0.767**	0.554	0.591
TDP-43	**0.909**	0.645	0.535
TIA1	0.867	**0.875**	0.608
TIAL1	**0.890**	0.774	0.602
U2AF2	**0.969**	0.830	0.585
U2AF2(KD)	**0.923**	0.805	0.550