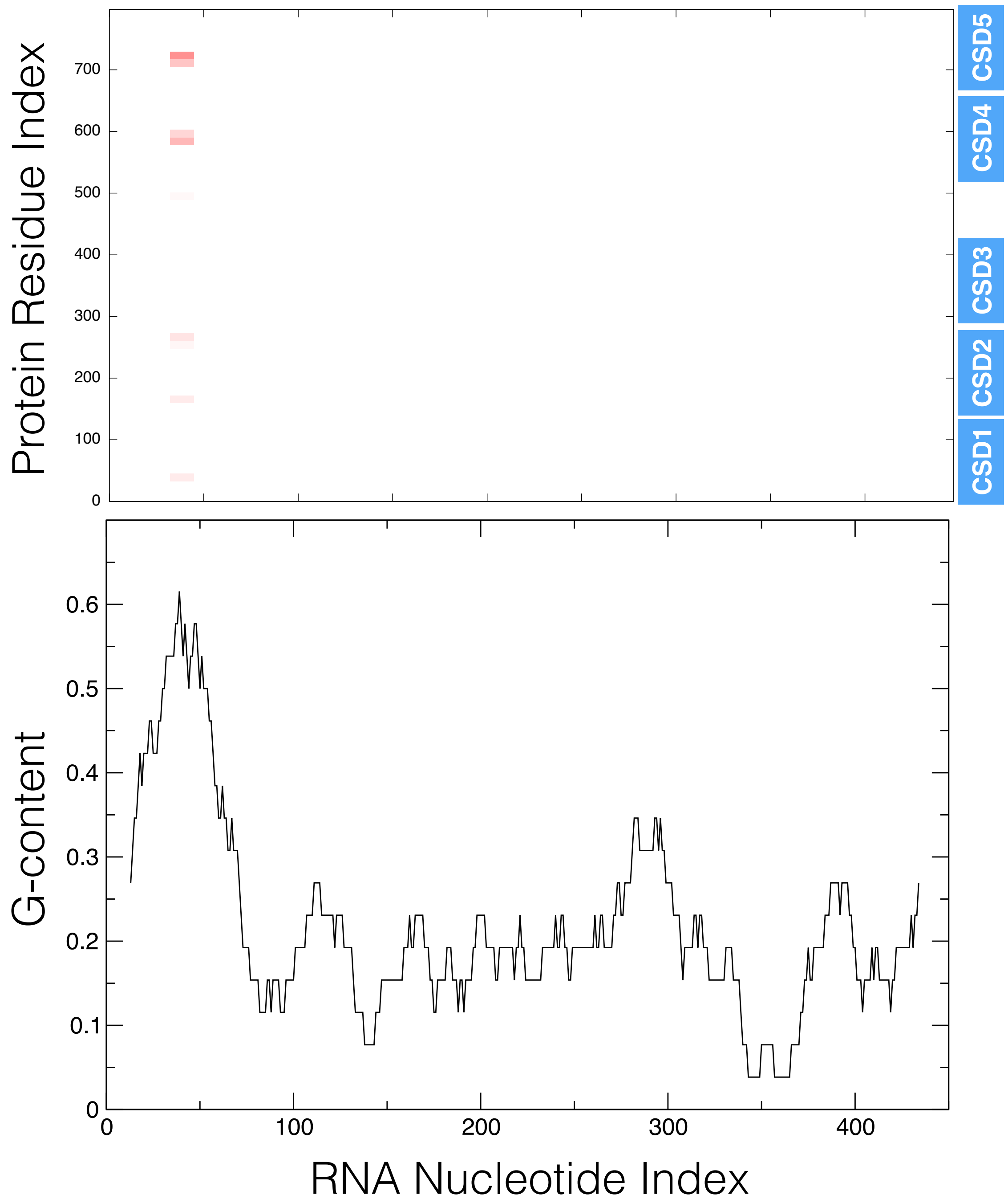
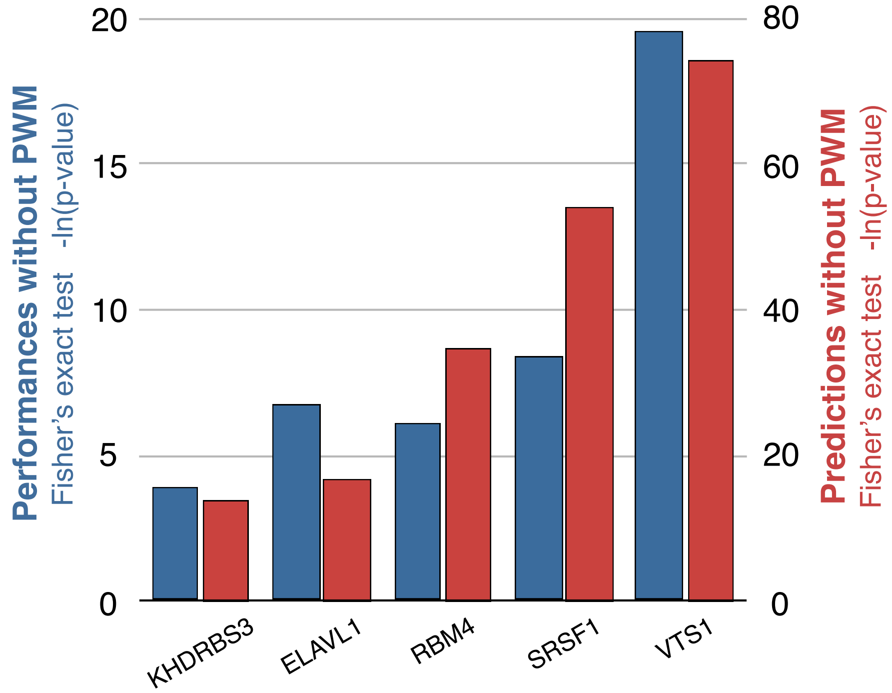
UNR Autogenous Interaction

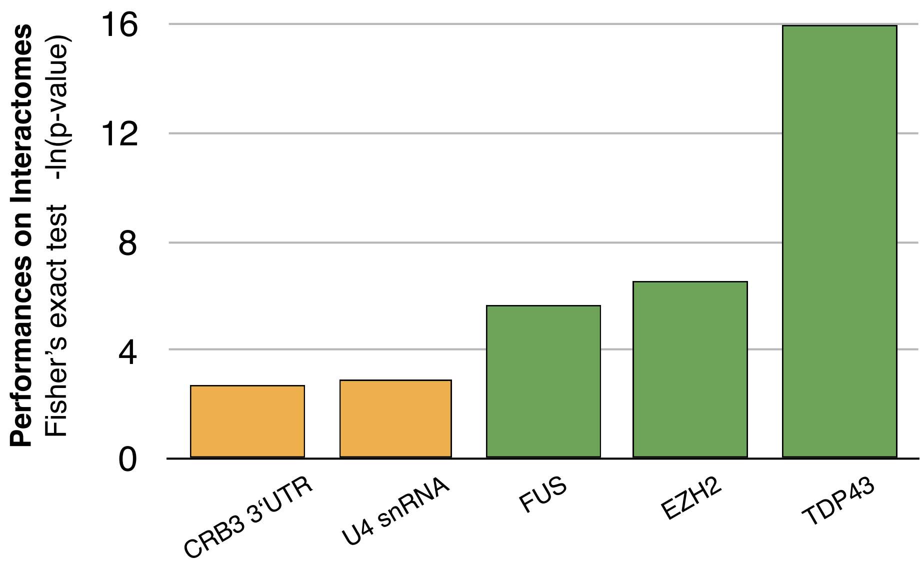


Organisms	Proteome (UniProt_2012_11)				Transcriptome (ENSEMBL68)	
	Full Proteins		Domains		coding RNAs	noncoding RNAs
	RNA	DNA	RNA	DNA		
Caenorhabditis elegans	79	304	255	339	16613	8385
Danio rerio	82	323	311	391	21752	4589
Drosophila melanogaster	71	283	318	447	6307	1109
Homo sapiens	472	2152	1907	7432	105586	18553
Mus musculus	379	1518	1573	3073	42951	7243
Rattus norvegicus	168	592	689	902	13593	4823
Saccharomyces cerevisiae	261	389	508	431	3711	396
Xenopus tropicalis	70	184	279	253	2260	1278
Total	**1582**	**5745**	**5840**	**13268**	**98548**	**46376**

Type of Analysis	Algorithm	Result	Examples
The protein-RNA pair of interest are < 750 aa and 1200 nt in length	*cat*RAPID *graphic* and *strength* modules	The score will provide the *propensity* to interact as well as an estimate of the *strength* of interaction	CSR regulatory system / FMRP (Modesto / Noble)
Protein (or RNA) is larger than 750 aa (1200 nt)	*cat*RAPID *fragments* (*protein and RNA* option)	The *binding sites* of both molecules are visualized	SNCA / UNR (Zanzoni / Cirillo)
RNA is > 10000 nt and protein < 750 aa	*cat*RAPID *fragments* (*long RNA* option)	The *binding sites* of the protein on the RNA sequence are identified	hnRNP-L / Xist (Mol Biosys / NAR)
Protein (transcript) partners of an RNA (protein) of interest	*cat*RAPID *omics*	*Propensity, strengths, binding motifs* are ranked in a table	HuR / LIN28B Genome Biology
Interacting protein (transcript) partners co-expressed in human tissues	*cat*RAPID *omics express*	*Propensity, strengths, binding motifs* and *expression patterns* are characterized	TIA1, MSI (Mol Biosys)



Performances without PWM
Fisher's exact test -ln(p-value)
Predictions without PWM
Fisher's exact test -ln(p-value)
20
15
10
5
0
80
60
40
20
0
KHDRBS3
ELAVL1
RBM4
SRSF1
VTS1


Performances on Interactomes
Fisher's exact test -ln(p-value)
16
12
8
4
0
CRB3 3'UTR
U4 snRNA
FUS
EZH2
TDP43