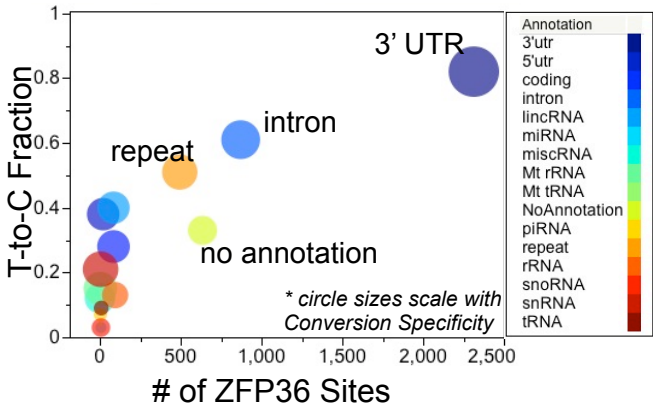
Supplemental Figure 1

A)

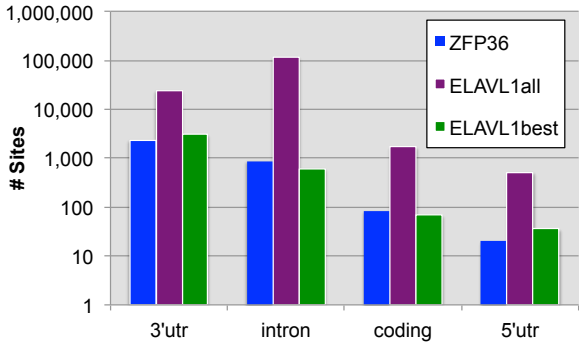
Summary Stats	ZFP36	Percent
Reads	6361864	100
Filtered Total	3405506	53.53
Quality	19208	0.3
Length <20 nts	3386298	53.23
3' Adapter	5890211	92.59
5' Adapter	71622	1.13
19 nt Marker	17690	0.28
24 nt Marker	20682	0.33
Post-Processing	2956358	46.47
Uniquely Aligned Reconciled Reads	328433	11.11
Site	4626	

Annotation	Reads	T2C Fraction	Conv Spec	Sites
3'utr	35011	0.82	1.34	2314
5'utr	1056	0.38	0.01	20
coding	7041	0.28	0.02	84
NoAnnotation	63021	0.33	-0.18	635
intron	38745	0.61	0.41	871
lincRNA	3387	0.4	0	84
miRNA	1936	0.03	-0.83	6
miscRNA	57	0.12	-0.11	0
Mt rRNA	605	0.15	0.07	2
Mt tRNA	130	0.04	-0.94	1
piRNA	14	0.07	-0.78	3
repeat	29970	0.51	0.18	494
rRNA	143782	0.13	-0.32	94
snoRNA	2502	0.03	-0.63	6
snRNA	270	0.21	0.2	4
tRNA	906	0.09	-0.74	8

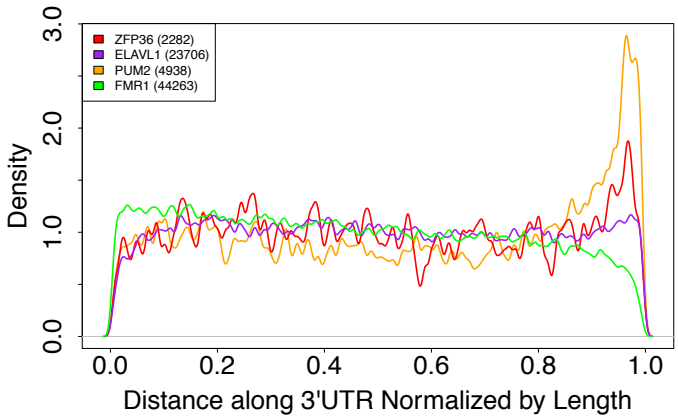
B)



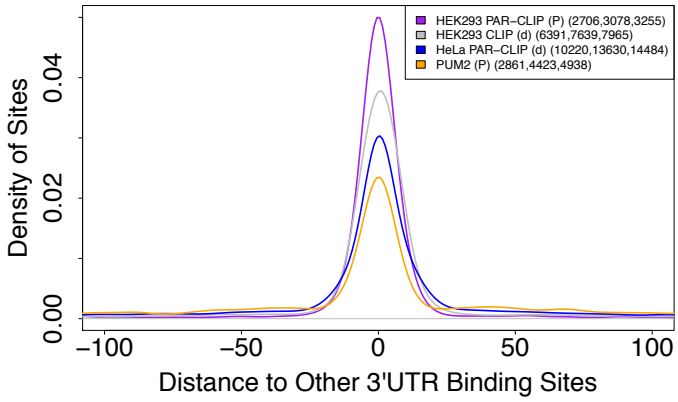
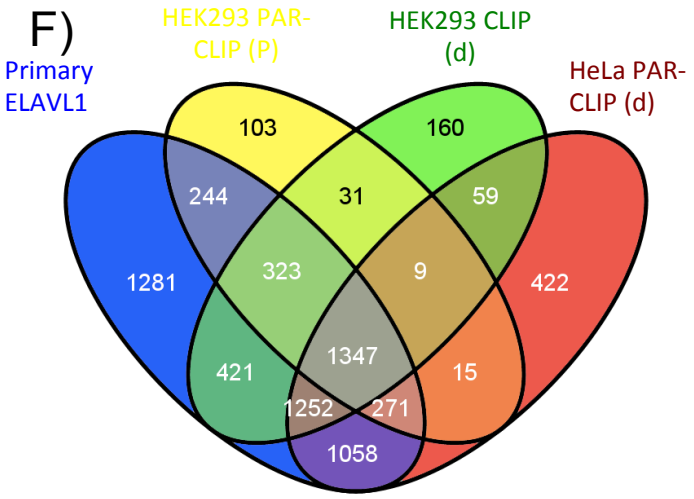
C)



D) **Normalized Distribution of 3'UTR sites across RBP's**



E)



F)