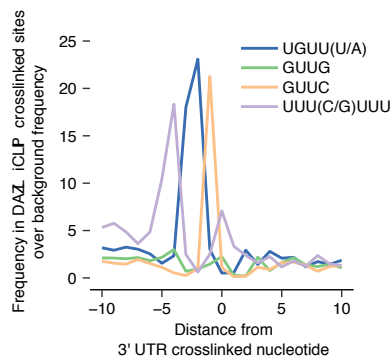


Frequency in DAZL 3' UTR crosslinked sites over background frequency






Distance from 3' UTR crosslinked nucleotide

Legend: UGUU(U/A) (blue), UGUU (green), GUU(U/A) (orange)

Distance from 3' UTR crosslinked nucleotide	UGUU(U/A)	UGUU	GUU(U/A)
-10	3.0	2.5	2.5
-9	3.5	3.0	2.5
-8	3.0	3.0	2.5
-7	2.5	2.5	2.5
-6	2.0	2.0	2.0
-5	1.5	1.5	1.5
-4	18.0	10.0	2.0
-3	23.0	18.0	5.0
-2	18.0	10.0	10.0
-1	23.0	18.0	17.0
0	2.0	1.0	2.0
1	1.0	1.0	1.0
2	2.0	4.0	1.0
3	3.0	2.0	2.0
4	3.0	3.0	2.0
5	2.0	1.0	2.0
6	2.0	2.0	2.0
7	2.0	1.0	2.0
8	2.0	2.0	2.0
9	2.0	2.0	2.0
10	2.0	2.0	2.0



Motif	Percentage of binding sites with motif
GUU	~78
UGUU(U/A)	~40
UUU	~79
UGUU	~50
GUU(U/A)	~65
GUUG	~11
GUUC	~16
UUU(C/G)UUU	~10

DAZL iCLIP from P6 testes (Zagore et al., 2018)					
Region					
	Adjusted <i>P</i> value	Adjusted <i>P</i> value	Adjusted <i>P</i> value	Adjusted <i>P</i> value	Adjusted <i>P</i> value
3' UTR	2.33e-49	1.01e-31	1.03e-9	5.50e-14	2.80e-2

DAZL iCLIP from testes enriched for undifferentiated spermatogonia

Region	Adjusted <i>P</i> value	Adjusted <i>P</i> value
3' UTR	0.00e+0	0.00e+0
5' UTR	3.38e-8	4.40e-7
CDS	1.16e-8	4.00e-10
ncRNA	4.40e-8	5.56e-7
Retrogene	9.76e-12	3.88e-8

3' UTR of *Lin28a*

Mouse chr4: 134003641 134003631 134003621

Species	Sequence
Mouse	GUA U - CUCC - AUGUUUACUGCUA
Rat	GUA U - CUCC - AUGUUUACUGCUA
Squirrel	GUA A - CUCC - AUGUUUACUGCUA
Rabbit	GUA A - CUCC - AUGUUUA UGC UA
Human	GUA A - CUCC - AUGUUUA UGC UA
Chimp	GUA A - CUCC - AUGUUUA UGC UA
Rhesus	GUA A - CUCC - AUGUUUA UGC UA
Pig	GUA A - CUCC - AUGUUUA UGC UA
Cow	GUA A - CUCC - AUGUUUA UGC UA
Cat	GUA A - CUCC - AUGUUUA UGC UA
Dog	GUA A - CUCC AUGUUUA UGC UA
Elephant	GUA A - CCC - AUGUUUA UGC UA
Chicken	GUA A - CUCC - AUGUUUA UGC UA
Lizard	GUA A CUUCC - GUGUUUA UGC UA
Coelacanth	GUA A GCCAC - AUGUUUACUGCUA
Consensus	GUA A - CUCC - AUGUUUACUGCUA

[illegible]