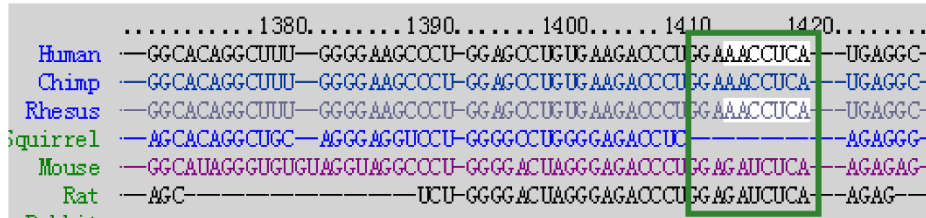**Figure S1. The binding site with the highest score between miR-377-5p and Arc 3'UTR predicted by the website.**


```
..........1380.......1390......1400......1410......1420........
Human    —GGCACAGGCUUU—GGGGAAGCCCU-GGAGCCUGUGAAGAGCCCU GGAAACCUCA —UGAGGC-
Chimp    —GGCACAGGCUUU—GGGGAAGCCCU-GGAGCCUGUGAAGAGCCCU GGAAACCUCA —UGAGGC-
Rhesus   —GGCACAGGCUUU—GGGGAAGCCCU-GGAGCCUGUGAAGAGCCCU GGAAACCUCA —UGAGGC-
Squirrel —AGCACAGGCUGC—AGGGAGGUCCU-GGGGCCUGGGGGAGACCUC ————————— —AGAGGG-
Mouse    —GGCAUAGGGUGUGUAGGUAGGCCCU-GGGGACUAGGGAGACCCU GGAGAUCUCA —AGAGAG-
Rat      —AGC————————————————UCU-GGGGACUAGGGAGACCCU GGAGAUCUCA —AGAG—
```

Arc 3'UTR   5'-GCTGCCGCCC**AGGGCAACC**GGCC-3'

                              | | | | | | | | |

Mmu-mir-377-5p 3'-CTTAAGTGGT**TCCCGTTGG**AGA-5'

	Predicted consequential pairing of target region (top) and miRNA (bottom)		Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_CT
Position 436-442 of ARC 3' UTR	5' ...CAGAGAUGCUGAGGGAACCUCAA...	‖‖‖‖	7mer-A1	-0.03	34	-0.03	0	N/A
mmu-miR-377-5p	3' CUUAAGUGGUUCCCGUUGGAGA							
Position 436-442 of ARC 3' UTR	5' ...CAGAGAUGCUGAGGGAACCUCAA...	‖‖‖‖	7mer-A1	-0.03	20	-0.01	0	N/A
mmu-miR-672-5p	3' AGUGUGUGUCAUGUGGUUGGAGU							
Position 1273-1279 of ARC 3' UTR	5' ...UGAUUGCCCAGCUGAAACCUCAG... ‖‖ ‖‖‖‖		7mer-A1	-0.08	57	-0.08	0.113	N/A
mmu-miR-377-5p	3' CUUAAGUGGUUCCCGUUGGAGA							

Poorly conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)		Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_CT
Position 1235-1241 of ARC 3' UTR	5' ...UGAUUGCCCAGCUGGAACCUCAU... ‖‖ ‖‖‖‖		7mer-A1	-0.07	54	-0.07	0.113	N/A
rno-miR-377-5p	3' CUUAAGUGGUUCCCGUUGGAGA							
Position 1235-1241 of ARC 3' UTR	5' ...UGAUUGCCCAGCUGG—AACCUCAU... ‖‖ ‖‖‖‖		7mer-A1	-0.04	44	-0.04	0.113	N/A
rno-miR-672-5p	3' AGUGUGUGUCAUGUGGUUGGAGU							

Poorly conserved

	Predicted consequential pairing of target region (top) and miRNA (bottom)		Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	P_CT
Position 137-143 of DLG4 3' UTR	5' ...UCUAACUGGAUCGAGCCCACUGG... ‖‖‖‖‖‖		7mer-m8	-0.11	71	-0.11	0	N/A
rno-miR-194-3p	3' UCUAUUGUCGUGGGGUGACC							
Position 295-301 of DLG4 3' UTR	5' ...CCAUGCACACAUAGACCCACUGG... ‖‖ ‖‖‖‖		7mer-m8	-0.12	73	-0.12	0.091	N/A
rno-miR-194-3p	3' UCUAUUGUCGUCG—GGGUGACC							