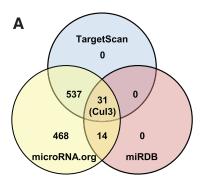
Supplementary Data



В

Target	Canonical seed sequence	Seed match	TargetScan	microRNA.org	miRDB
	5'- ₂₄₉ GCGUUUUGUUUUCUU <mark>UACUGUA</mark> ₂₇₀ -3'	7mer-1A	•		
Human Cul3	5'- ₁₃₆₆ UUCGUUGACUAUCA <mark>GUACUGUU</mark> ₁₃₈₇ -3'	7mer-m8		•	•
Human Cuis	5'- ₁₅₅₇ UUUUGUCUCCAUCU <mark>GUACUGUA</mark> ₁₅₇₈ -3'	8mer		•	•
	5'- ₂₉₃₇ UUAUCUUUGCCUGUC <mark>UACUGUA</mark> ₂₉₅₈ -3'	7mer-1A	•		
	5'- ₃₉₆ CAUGCAAACUUUAUU <mark>UACUGUA</mark> ₄₁₇ -3'	7mer-1A	•	•	
Human Cul4B	5'- ₁₂₄₈ ACAAAAUGGCAAAA <mark>GUACUGUU</mark> ₁₂₆₉ -3'	7mer-m8	•	•	
Human Cul5			•		
Human miR-101					

Human miR-101	3'-AAGUCAAUAGUGUCAUGACAU-5'

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	Mouse Cul3	5'- ₁₆₁₆ AAUUUGCUUUUAUAU <mark>GUACUGU</mark>	U ₁₆₂₂ -3'	7mer-m8	•	
ì				1		
	Mouse miR-101	3'-AAGUCGAUAGUGUCAUGACA	U-5'			

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Human Cul3	Wild type	5'- ₁₃₆₆ UUCGUUGACUAUCAGUACUGUU ₁₃₈₇ -3'	5'- ₁₅₅₇ UUUUGUCUCCAUCUGUACUGUA ₁₅₇₈ -3'
Tiuman Cuis	Mutant	5'- ₁₃₆₆ UUCGUUGACUAUCACAUGACAA ₁₃₈₇ -3'	5'- ₁₅₅₇ UUUUGUCUCCAUCUCATGACAU ₁₅₇₈ -3'

SUPPLEMENTARY FIG. S1. Computational prediction of miR-101 targets. (A) Venn diagram displaying mRNAs computationally predicted to targets Cul3 by TargetScan, microRNA.org, and miRDB. Highly reliable targets were selected using cutoff scores of ≤ 0.1 for TargetScan and miRDB and ≥ 60 for microRNA.org. (B) Alignment of potential binding sites of human in the 3'UTRs of human cullin gene family. (C) Alignment of potential binding site of mouse miR-101 in the 3'UTR of mouse Cul3. (D) The sequence of Cul3 3'UTR mutants used for the reporter assay. 3'UTR, 3'untranslated region; Cul, cullin; miRNA, miR, microRNA.