

Supplemental

Table. S1. Primers used for plasmid construction

(Restriction sites are underlined and mismatched bases are shown in bold type)

Plasmid	Primer sequence(5'-3')
CUL4B Forward	<u>CGCGGATCC</u> ATGTTTCCAACAGGTTT
CUL4B Reverse	<u>CCGCTCGAGT</u> GCAATATAGTTGTACTG

	Plasmid	Primer sequence(5'-3')
Reverse Primers	CUL4B 1-36	<u>CGGGATCCC</u> GGGCAGAGGTGGGCGG
	CUL4B 1-40	<u>CGGGATCCC</u> GCTTTCTCTTCTTGGCAG
	CUL4B 1-50	<u>CGGGATCCC</u> GGTTACTGCTGCTACT
	CUL4B 1-115	<u>CGGGATCCC</u> GCTTCGCATCAAACCC
Forward primer		<u>CCGCTCGAGT</u> CATGTTTCCAACAGG

	Plasmid	Primer sequence(5'-3')
Forward primer	CUL4B 37-895	<u>CGGGGTACCA</u> AGAAGAGAAAGTTAAAC
	CUL4B 41-895	<u>CGGGGTACCTT</u> AAACAGCAGCAGCAGT GCAGCAGTAA
	CUL4B 150-895	<u>CGGGGTACCG</u> CTTCGGTGCATCATGCA
Reverse Primers		CAGCCTGGTAGAGTTCTTCTAAAT

Plasmid	Primer sequence(5'-3')	
CUL4B 1-729 Forward	TATGGCAAGGATGTTTTTGAGGC	
CUL4B- 1-729 Reverse	<u>AGGGGGCCCA</u> AGAGAGACCTGGAGT	
RNAi-resistant Plasmid	Primer sequence(5'-3')	
Outer primers	Forward	TATGGCAAGGATGTTTTTGAGGC
	Reverse	<u>CCGCTCGAGT</u> GCAATATAGTTGTACTG
Internal primers	Forward	TCAGAACGTACCCGGAAATATTG
	Reverse	CAATATTTCCGGGTACGTTCTGA

Mutant plasmid		Primer sequence(5'-3')
Outer primers	Mu Forward	<u>GGGGTACCATGTTTCCAACAGGTTT</u>
	Mu Reverse	TCTAGACGTTTGTTAACATG
Internal primers	Mu-1 Forward	CCGCCACCTCTGCCGCGAAGAGA
	Mu-1 Reverse	TCTCTTCGCGGCAGAGGTGGGCGG
	Mu-2 Forward	TCTGCCAAGAAGAGAGCGTTAAAC
	Mu-2 Reverse	GTTTAAACGCTCTCTTCTTGGCAGA
	Mu-3 Forward	CCCACCTCTGCCAAGGCGAGAAAG
	Mu-3 Reverse	CTTTCTCGCCTTGGCAGAGGTGGG
	Mu-4 Forward	TCTGCCAAGAAGGCAAAGTTAAAC
	Mu-4 Reverse	GTTTAACTTTGCCTTCTTGGCAGA
	Mu-5 Forward	TCTGCCAAGGCGGCAAAGTTAAAC
	Mu-5 Reverse	GTTTAACTTTGCCGCCTTGGCAGA
	Δ37-40 Forward	CCGCCACCTCTGCCTTAAACAGCAGCA GCAGTAGCAGCAGTAAC
	Mu-Δ37-40 Reverse	GCTGCTGCTGTTTAAGGCAGAGGTGGGC GGAGTGGTGCTGGT

Table. S2. Primers used for Real-time PCR

Name	Primer sequence(5'-3')
CUL4A Forward	CATCAACAAGAGACCCAACAAGC
CUL4A Reverse	CCGTGGATAAACCTGAACAGGAT
CUL4A Probe	FAM-TCCAACGTCCGCTCCAGCTCCTCG -ECLIPSE
CUL4B Forward	TGGAAGTTCATTTACCACCAGAGATG
CUL4B Reverse	TTCTGCTTTTAAACACACAGTGTCCTA
CUL4B Probe	FAM-TGACTGCCACTGAAGTTTCCTGCCAC-TAMRA
GAPDH Forward	CCAGGTGGTCTCCTCTGACTT
GAPDH Reverse	GTTGCTGTAGCCAAATTCGTTGT
GAPDH Probe	FAM-AACAGCGACACCCACTCCTCCACC-TAMRA
Cyclin E Forward	GAGCCAGCCTTGGGACAATAA
Cyclin E Reverse	GCACGTTGAGTTTGGGTAAACC

FIGURE. S1. CUL4B has a unique N-terminus. A sequence alignment of the human CUL4A with CUL4B was carried out using ClustalW alignment program. Missing amino acids are denoted by hyphens. Identical residues are highlighted in gray.

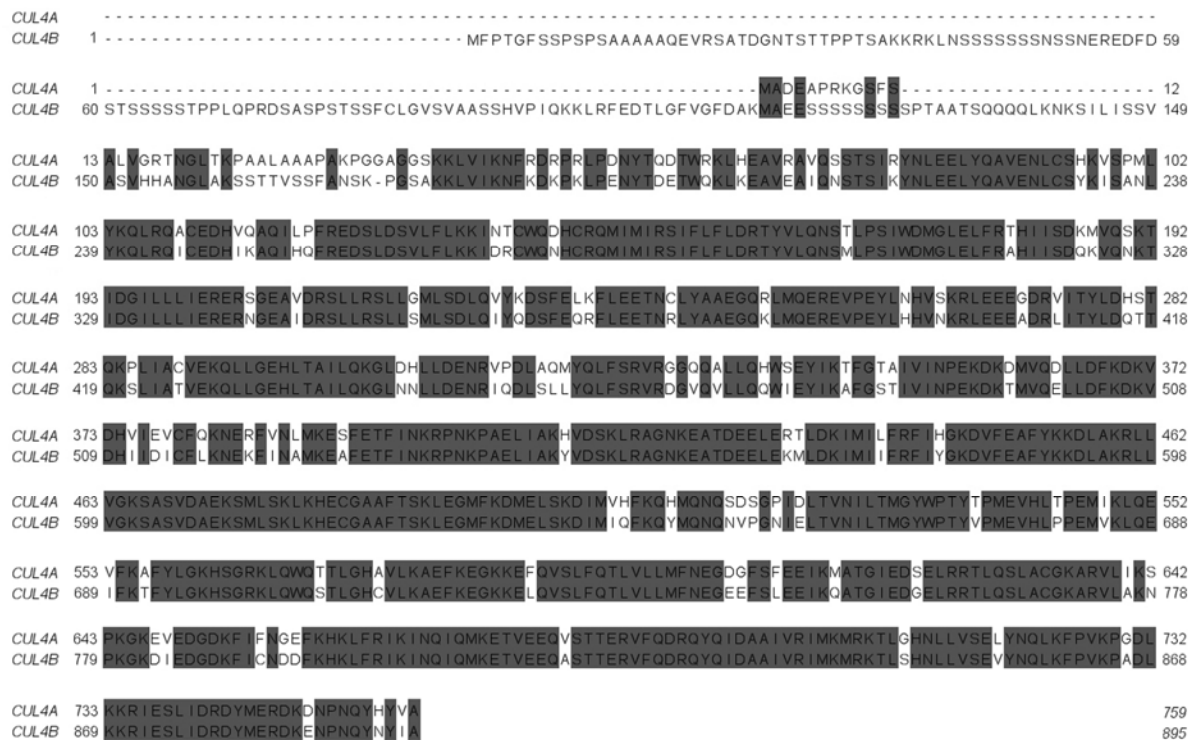


FIGURE. S2. Effects of CUL4B RNAi on several cell cycle regulators. Equal amounts (60µg) of total cell lysates of indicated asynchronous cells were subjected to SDS-PAGE and detected with indicated antibodies.

