

Supplementary Materials

Table S1. The primers of DACH1 sequence deletion and mutation vector construction.

Vector	Sense primer (5'-3')	Antisense primer (5'-3')
pGL3-DACH1-dS1	TAGGGTACCAAGGACTTCCAAAATACAGC	
pGL3-DACH1-dS2	TAGGGTACCCATCCACATCAAGGAAGC	GCGAAGATCTCACAAAGTGTCCCGAAG
pGL3-DACH1-dS3	TAGGGTACCCACTGAAAATGTCTG	
pGL3-DACH1-dS4		GCGAAGATCTGGACGAGTTGTTGTTG
pGL3-DACH1-dS5		GCGAAGATCTAGAGGGAGCGTGCGAGG
pGL3-DACH1-dS6	TAGGGTACCAAGGACTTCCAAAATACAGC	GCGAAGATCTCTCTCTACTACTACCGTTA
pGL3-DACH1-dS7		GCGAAGATCTAAACAATGCCCGCC
pGL3-DACH1-dS8		GCGAAGATCTGAAGCAAAGCGTAATGTT
pGL3-DACH1-mS1	CGAGTTCatcgtaGATAATTGGITAATACTAGTGAGT	AATTATCtagtaGAATCGGAGCAGAGACTCCG
pGL3-DACH1-mS2	CGGAGTCggatcgAGTTCTGGTTGATAATT	GAATCTGttactGACTCCGAGAGCGCGAGA
pGL3-DACH1-mS3	TCTCTGCTCatcgtaCTGGTTGATAATTGG	TCCAACCAGtcaggatGAGCAGAGACTCCGAGAGC
pGL3-DACH1-mS4	TTCCTGGTTGtcggcTGGTTAAATACTAGTGAGTGAGGT	TTAACCCAccggcaAACCAAGGAACTCGGAGC
pGL3-DACH1-mS5	GATAATTgttgcATACTAGTGAGTGAGGTTTGC	ACTAGTATGCCAACAAATTATCCAACCAGGAACTCGG

Note: Lowercases in primer sequence represent mutation sites.

Table S2. The primers for DACH1 shRNA lentivirus vectors

Vector	Sense primer (5'-3')	Antisense primer (5'-3')
DACH1-shRNA01	GATCCGCCTCTAACAGAGGACTCAACTTCTGTAGATTG	AATTCAAAAGCCTCTAACAGAGGACTCAATCTGACAGGAAGTTG
DACH1-shRNA02	GATCCGCACTGAGTTGAGACGACTCCCTGTAGA	AATTCAAAAGCACTGAGTTGAGACGATCTGACAGGAAGTCGT
DACH1-shRNA03	GATCCCTGAAAGTTGCCATAGCTTCTGTAGACTA	AATTCAAAACTGTGAAAGTTGCCATAGCTGACAGGAAGCTAT

Table S3. The primers for DACH1 SUMOylation site-directed mutation

Primer	Sequence (5'-3')
DACH1-mSF1	AAGGTGAAAAAAATCagaTTAGAAGCCAT
DACH1-mSR3	AGTTGCTCATGGCTTCTAAtctGATT
DACH1-mSF1	CTGGAAAAAAACTGAGCTGaggATGGATT
DACH1-mSR1	TCTTCCCTTAAAAATCCATcctCAGCTC
DACH1-mSF1	TAGTTCAAAAGAGGCTAaggAAGGAG
DACH1-mSR2	TGCCTTCTCTCCTTcctTAGCCT

Note: Lowercases in the sequence represent the lysine to be mutated.

-2000 CATAITTCATTTCCGTAGACAGTCTGCCACTATTGAACTGGGATTCACAGAGTCAAGGGTAAAGATATAAGAGAAATGT
 -1910 ATCATTTCAACACCAAGATGCCAAAATTTTATATAAAATTCGAACCTGTACTAACAGTTATTAAAATCTGTC
 -1820 AAATGCTAAAGCATTGCTTCATATCTTGAACCTACTGAACATGTGGACCGTCAAAGGCTAACAATTGAAGATACTTGAGAC
 -1731 ATGAGCACCAAATAGATTGACCCATATTCAAAATGATATGTAGTCAAAAATCCTGATAAAATACCTGACAAGTTAGAAAA
 AP-1 binding site
 -1648 GAAAAGAAAAGGAAGAGGAAGGAGAAGGGAGAATAGACTCAGTCTAAACTCAGCCTCATGTTGTTTAAGCACAGCTACCCAAGT
 AP-1 binding site
 -1558 CTTACAAAGTCAACTAGTGAGCTTGTGTTCTCCCATTATTACAAACATATACTGACAATTGAAAAGGACTTCCAAA
 AP-1 binding site
 -1468 ACTACAGCAGCACTTTCAACATGAAAAAAGAAAAAAACTATTGTGTGTCAAAAAACACATAGCAATTGGCTTGGTC
 -1381 TTAAGGAGCATGAGGATAGTGGTACTGTAGACAGGTAAATTAGATAGTTGGTAAGAAAACCCTTTCCACTTCTA
 -1648 AATCTCAAGGATACCTTATCTCTTGATAGCTTAGGTTAACAGTATTCTGACTGGCTTTGGGGAGACAGTGAAGTTATTCTAA
 CAAT box
 -1292 ATCATCCACATCAAGGCAAGCATTCTTCCAAACCTATTAGGAATATGGAATTGAAACAGACTTCCATTATTCTAACGCAATT
 -1113 CGGACTGACTTTCTCTCACCACCTGAAACCTCCTGGATTTCACATCTTATATAAAATAATTAGTAGAGAAATAACAA
 AP-1 binding site
 -1024 TCAGATGCAAAGAACATTACGCTTGCTTACATGTGAAATTCTCAAAATAATTCTGAAATAATCGTAAGTGGGGCTGTGTTTCG
 -934 TTCTAGCTATTGCAAACCCGTGGAGATGGATCTAAATCTGGAGAGAGCTCCGGCTAGGCTCTTTAAAGTTGG
 similar with Kip2-TRE
 -846 CGGGCGATTGTTAGAAGCTTGGAAAAAATTACAGTCCCCCGGGACGAAATTTGAATGTGAGACATGCAATCTAACGGTAGTAGTA
 similar with IP-TRE
 -759 GAAGAGAAAGTAGATGATTCTCCCTCTCCTTCCGATCGCCACTCTGTCCTCCGGCTTCTCTCCGTCCCTCCACAGTTCTTC
 NF- κ B binding site similar with Kip2-TRE
 -670 CGTATCCTCCCCCTCCCTCTCGCACGCTCCCTCCAGTGTCTCGCGCTCTGGAGTCTCTGCTCCGAGTTCCTGGTTGG
 similar with IP-TRE
 -580 ATAATTTGGGTTAATACTAGTGAAGGGTTTGCCTCAAGGGTATTCAAGGTTCTCCGGAGCTCTCCCTCTGACCCCTGTGAC
 -490 AACACAAACTCTGTCAGCCGCGAGCCCTGCACTTTCACTGCTATTCTCTGTCATTCCCTCTCAATCTTGTCAATGTACTTGCA
 -400 GGGAGAGGCCAACGTCCTAAACCTCTCTTCACCTTCATCTTAACTCTGTCAGAGCGAGACCCACACAAACACGGGACCC
 -312 CTCCCCGCCCACCCCCAACCCCAAAACAGGCTCGATCCCGAGGGAGACTCGCATTTGACTTGGACCTTGTG
 GC box
 -225 CGTCTCTCTCCAGGGCCCTCTCGTGTCTGCCCTCTTGCCTCGCTCTTATACCTTCACCTCTTCTCCCTCTCCCTTCTC
 -133 CTCTCGTTCTCCGGAGTTGTTGCCCCCTCGCTCTCTCCCTCTCCCTCCGGGGGTGTGGAACATT
 -42 TCCCTCGCTCTCTCCGTCTTCCCTTATATGTAGGCAGTGCGGCGCTTIGATCCCTCGACCCAGCTGGCCCCCT
 translation initiation site
 +49 CAACCCCAATCTCACGCTGCTTCTCTCTGGACCAACACCTCCACCTTCCGGGACTTCGTCCTGGCTCTCCATGGACC
 +138 CCCGGCTCCTGGCCAACCTGTTCCGGCCGGAGCCATCGTCTGGCCGGAGGGACCTGGGCGGGCGGCGGCGGCG

Figure S1. Promoter sequences of *DACH1*. The underlines in sequences are regulatory elements or compared with Kip2-TRE or IP-TRE.

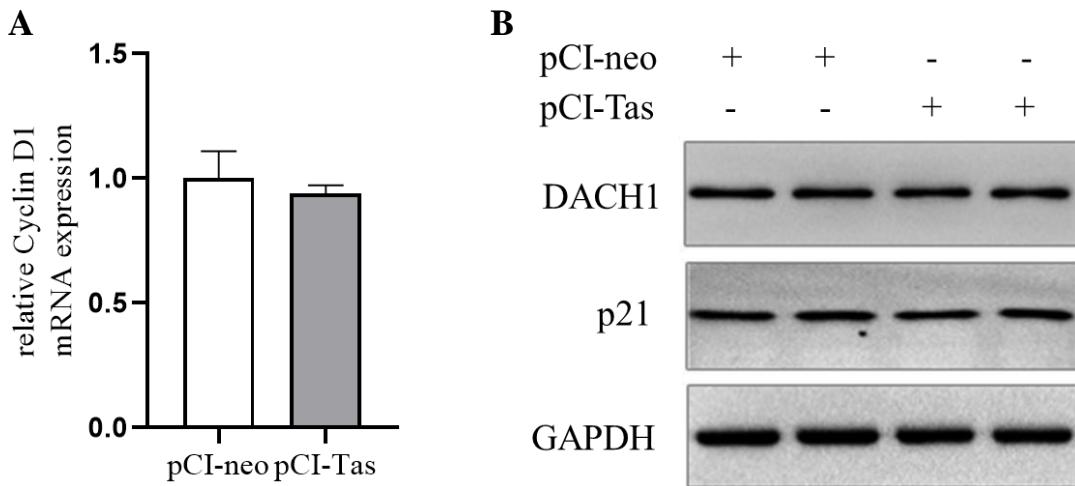


Figure S2. The mRNA expression of Cyclin D1 and protein expression of p21 after pCI-Tas transfection. (A)The mRNA expression of Cyclin D1 was unchanged after Tas transfection. HeLa cells were plated in a 12-well plate at 2×10^5 , pCI-neo (1 μ g) or pCI-Tas (1 μ g) was transfected into the cells, and RT-qPCR was utilized to detect the mRNA expression of Cyclin D1. (B) Tas transfection had no influence on the protein expression of p21. HeLa cells were plated in a 6-well plate at 5×10^5 , and transfected with pCI-neo (3 μ g) or pCI-Tas (3 μ g). After 48 h of transfection, the protein of cells was extracted and western blot was performed to assess the protein expression of p21, DACH1, and GAPDH.