Supplementary Table S1 siRNA sequences.

siRNA	Passenger strand (5’→3’)	Guide strand (5’→3’)
siLuc-36	CAUUCUAUCCGCUGGAAGAUG	UCUUCCAGCGGAUAGAAUGGC
siLuc-309	CCGCGAACGACAUUUAUAAUG	UUAUAAAUGUCGUUCGCGGGC
siLuc-774	GAUUUCGAGUCGUCUUAAUGU	AUUAAGACGACUCGAAAUCCA
siLuc2-153	CGUACGCGGAAUACUUCGAUU	UCGAAGUAUUCCGCGUACGUG
siVIM-269	GCCAUCAACACCGAGUUCAAG	UGAACUCGGUGUUGAUGGCGU
siVIM-270	CCAUCAACACCGAGUUCAAGA	UUGAACUCGGUGUUGAUGGCG
siVIM-596	GAAAACACCCUGCAAUCUUUC	GGCUUUUGUGGGACGUUAGAA
siVIM-805	GCGUGACGUACGUCAGCAAUA	UUGCUGACGUACGUCACGCAG
siVIM-812	GUACGUCAGCAAUAUGAAAGU	UUUCAUAUUGCUGACGUACGU
siVIM-1128	CUCGUCACCUUCGUGAAUACC	UAUUCACGAAGGUGACGAGCC
siVIM-1261	GAACCUGAGGGAAACUAAUCU	AUUAGUUUCCCUCAGGUUCAG
siOct-670	GAGAAAGCGAACUAGCAUUGA	AAUGCUAGUUCGCUUUCUCUU
siOct-797	GUUCGAGUAUGGUUCUGUAAC	UACAGAACCAUACUCGAACCA
siOct-821	CGCCAGAAGGGCAAAAGAUCA	AUCUUUUGCCCUUCUGGCGCC
siGRK4-934	CUUGAAGCCUGAGAAUAUUCU	AAUAUUCUCAGGCUUCAAGUC
siCLTC-2416	GGUGAAUCCAAGUCGACUUCC	AAGUCGACUUGGAUUCACCUU
siCLTC-3114	GUGUUAUGGAGUAUAUUAACC	UUAAUAUACUCCAUAACACGU
siCLTC-4819	GACAAAGGUGGAUAAAUUAGA	UAAUUUAUCCACCUUUGUCAA
siPLS3-1310	GUUCCUGUUGACUGGAGUAAG	UACUCCAGUCAACAGGAACUU
siPLS3-1528	GGAAGAUCUUGGAGAUGGUCA	ACCAUCUCCAAGAUCUUCCAG
siPLS3-1657	GGCAGUUGUGGAUUUAAUUGA	AAUUAAAUCCACAACUGCCAA
siCCNC-571	GUAUCCUCCUUUCAUGAUAGC	UAUCAUGAAAGGAGGAUACAG
siKIF23-430	GUCAUUUCAAGCUAAACGAUA	UCGUUUAGCUUGAAAUGACCC
siTUBA2-714	CGGCCUCCCUGCGAUUUGACG	UCAAAUCGCAGGGAGGCCGUG
siITGA10-2803	CCUCAGCCUACAUCCAAUAUG	UAUUGGAUGUAGGCUGAGGUC
siMC4R-490	GCGGGUUGGGAUCAUCAUAAG	UAUGAUGAUCCCAACCCGCUU
siVIM-270/812	CCAUCAACACCAUAUGAAAGU	UUUCAUAUGGUGUUGAUGGCG
siVIM-812/270	GUACGUCAGCAGAGUUCAAGA	UUGAACUCUGCUGACGUACGU
siVIM-270m2	CCAUCAACACCGAGUUCGAGA	UCGAACUCGGUGUUGAUGGCG
siVIM-270m3	CCAUCAACACCGAGUUUAAGA	UUAAACUCGGUGUUGAUGGCG
siVIM-270m5	CCAUCAACACCGAGCUCAAGA	UUGAGCUCGGUGUUGAUGGCG
siVIM-270m6	CCAUCAACACCGAAUUCAAGA	UUGAAUUCGGUGUUGAUGGCG
siVIM-270m7	CCAUCAACACCGGGUUCAAGA	UUGAACCCGGUGUUGAUGGCG
siGY-441	CAGCCACAACGUCUAUAUCAU	CCAUGAUAUAGACGUUGUGGC

Supplementary Table S2 Target sequences in psiCHECK-cm and psiCHECK-sm.

Target sequences in psiCHECK-cm.

Target	Target sequence (5’→3’)
Luc-36-cm	GCCAUUCUAUCCGCUGGAAGAUG
Luc-309-cm	GCCCGCGAACGACAUUUAUAAUG
Luc-774-cm	UGGAUUUCGAGUCGUCUUAAUGU
Luc2-153-cm	CACGUACGCGGAAUACUUCGAAA
VIM-269-cm	ACGCCAUCAACACCGAGUUCAAG
VIM-270-cm	CGCCAUCAACACCGAGUUCAAGA

VIM-596-cm	CCGAAAACACCCUGCAAUCUUUC
VIM-805-cm	CUGCGUGACGUACGUCAGCAAUA
VIM-812-cm	ACGUACGUCAGCAAUAUGAAAGU
VIM-1128-cm	GGCUCGUCACCUUCGUGAAUACC
VIM-1261-cm	CUGAACCUGAGGGAAACUAAUCU
Oct-670-cm	AAGAGAAAGCGAACUAGCAUUGA
Oct-797-cm	UGGUUCGAGUAUGGUUCUGUAAC
Oct-821-cm	GGCGCCAGAAGGGCAAAAGAUCA
GRK4-934-cm	GACUUGAAGCCUGAGAAUAUUCU
CLTC-2416-cm	AAGGUGAAUCCAAGUCGACUUCC
CLTC-3114-cm	ACGUGUUAUGGAGUAUAUUAACC
CLTC-4819-cm	UUGACAAAGGUGGAUAAAUUAGA
PLS3-1310-cm	AAGUUCCUGUUGACUGGAGUAAG
PLS3-1528-cm	CUGGAAGAUCUUGGAGAUGGUCA
PLS3-1657-cm	UUGGCAGUUGUGGAUUUAAUUGA
CCNC-571-cm	CUGUAUCCUCCUUUCAUGAUAGC
KIF23-430-cm	GGGUCAUUUCAAGCUAAACGAUA
TUBA2-714-cm	CACGGCCUCCCUGCGAUUUGACG
ITGA10-2803-cm	GACCUCAGCCUACAUCCAAUAUG
MC4R-490-cm	AAGCGGGUUGGGAUCAUCAUAAG
VIM-270/812-cm	CGCCAUCAACACCAUAUGAAAGU
VIM-812/270-cm	ACGUACGUCAGCAGAGUUCAAGA
VIM-270m2-cm	CGCCAUCAACACCGAGUUCGAGA
VIM-270m3-cm	CGCCAUCAACACCGAGUUUAAGA
VIM-270m5-cm	CGCCAUCAACACCGAGCUCAAGA
VIM-270m6-cm	CGCCAUCAACACCGAAUUCAAGA
VIM-270m7-cm	CGCCAUCAACACCGGGUUCAAGA

Target sequences in psiCHECK-sm.

Target	**Target sequence (5’→3’)**
Luc-36-sm	CUUUGGAUGAAACCUGGAAGAUG
Luc-309-sm	ACUAACCCCUAAUAUUUAUAAUG
Luc-774-sm	UAGGAUGCCAUCGGUCUUAAUGU
Luc2-153-sm	AAGCGGUGCCAAGUACUUCGAAA
VIM-269-sm	CAAUGAUGCACCAGGAGUUCAAG
VIM-270-sm	AAGGAAGGGAGAGGAGUUCAAGA
VIM-270-sm2	AAUGAUGCACCAGGAGAGUUCAA
VIM-596-sm	CGUUACUCUCGGAGCAAUCUUUC
VIM-805-sm	GGUGCCCAAGGAAGUCAGCAAUA
VIM-812-sm	CUAGGUGAAACUUAUAUGAAAGU
VIM-1128-sm	GAGGCAAAUGACGCGUGAAUACC
VIM-1261-sm	CAUGUCAUUACACAAACUAAUCU
Oct-670-sm	UACCUACACUAAUCUAGCAUUGA
Oct-797-sm	GCUGAAGCUAGUAGUUCUGUAAC
Oct-821-sm	CACUGAGCGGUUUCAAAAGAUCA
GRK4-934-sm	AGGCAAGCGGCGAAGAAUAUUCU
CLTC-2416-sm	CCGAGCAAGUGGUGUCGACUUCC
CLTC-3114-sm	CACUUGCCACUCAUAUAUUAACC

CLTC-4819-sm	ACUUGCUCGAGUCAUAAAUUAGA
PLS3-1310-sm	GCCAAUAUCGAUCCUGGAGUAAG
PLS3-1528-sm	GGUUAUCUCUUCCGAGAUGGUCA
PLS3-1657-sm	UCGUGCUGAAAGUAUUUAAUUGA
CCNC-571-sm	GGUCUUCUCUCGAUCAUGAUAGC
KIF23-430-sm	GAAUGCGCAACACCUAAACGAUA
TUBA2-714-sm	CUAUGACCGGCACCGAUUUGACG
ITGA10-2803-sm	ACGUAUGAACUGGAUCCAAUAUG
MC4R-490-sm	CAUCCUCUGGUUUUCAUCAUAAG
VIM-270m2-sm2	AAUGAUGCACCAGGAGUUCGAGA
VIM-270m3-sm2	AAUGAUGCACCAGGAGUUUAAGA
VIM-270m5-sm2	AAUGAUGCACCAGGAGCUCAAGA
VIM-270m6-sm2	AAUGAUGCACCAGGAAUUCAAGA
VIM-270m7-sm2	AAUGAUGCACCAGGGGUUCAAGA
WDR82	CUGUAGUUUCCAAGAGUUCAGCU
CEP350	GACUACCAGUAUGGAGUUCAUAG
WBP4	UUCUGUUCUUCAGGAGUUCACAU
COPB1	UUAUAUAGAAUCUGAGUUCAUGC
TMEM41A	UUCACAAGGUCAGGAGUUCAAGA
HSC20	AUGACAAGGUCAGGAGUUCAAGA
VAPA1	GUGGUUUUAAUAAGAGUUCAAGA

Supplementary Table S3 Primer sequences used for qRT-PCR.

Gene	**Forward primer (5’→3’)**	**Reverse primer (5’→3’)**
β-actin	CACACTGTGCCCATCTACGA	GCCATCTCTTGCTCGAAGTC
vimentin	CAGGACTCGGTGGACTTCTC	GTCGATGTAGTTGGCGAAGC
VAPA	TTCAGGAAATGCCAAGAGGT	TCAACAACTGCCTCACAAGG
MTPN	TAGGTGCAGTGTGTGGAAGC	TGCATGGAAGAAAACAGCAG
PTPRF	CTGGTTTGCAGCTGTTTTCA	CCTCAGCAAGCTGGGATAAT
MRPS16	TTGCCCTCAACCTAGACAGG	CGTTTCCTTCGCAGTCTCTC
COPS8	TGGGCAAAGAAGCTATGAAGA	CAGAGGGCTGTCACACAGAG
COPB1	TGAAATGCCTGACTCCAGAA	ATCTGGTCCCTGGTGAATTG
RAB31	CACGCTTCCACTTCACTCAA	AAATGCCGCTTGCTAACAGT
ARPC2	CTTGAAAATCTTCCGGCATC	CTCCTTCCTTGCCCTCTTCT
PLEKHC1	CATGATTTGCCACAATGTCC	CACCCTTTTGGGCTATGTGA
DR1	TGGATGTCATACCCATGAAGTG	CAAATTAGAAAAGCCAACACG
WDR82	GCCAAAGCCACTGATGTTTA	TTTGGGTGGCAAACTTGATT
SURF4	GTCAAGGTTGGTTGGCTGAT	GCCAGGAGAAACAGGAACAC
CALM2	TGCAAACGGGTGTATTATCC	AGGCAAATTGTGCCATAAGC
HINT1	GCTGATCTGGGCCTGAATAA	ATCCCCAAAACGTGCTTAAC
TRUB1	TGTGTGCAGATGCAGAATGA	CCAACTGCAAGGCCATTTAT
BTF3L4	ACTGGCCCTAGGAGGATTTC	GTGCTCCCCTCAAAGCATTA
BECN1	AGGTTGAGAAAGGCGAGACA	GCTTTTGTCCACTGCTCCTC
SSR1	ATTGATGGCACAAATCAGCA	CGCATTAAACAGCAGCAAAA
TFP1	GTGGTGCAATCACAGGACAC	AGCCCAGGTGTTCAAGACAA

TMEM30A	TTGCTTACATCGCTGTTGGA	CTTGATGCACATGCAGATGA
POGK	ACAAGGCCCATTGACTCATC	CAGGGCAGGAGATCAGAAGT
HDAC2	AGGAGGTCGAAGAAATGTGG	TTCACCACTGTTGTCCTTGG
PSAP	GGCCATCTGCCTGAATGTAA	AACAGCCAGGGACATGTAGG
CAPRIN1	TGCATGGGTCCTAATCACAC	TTTTGCATCTTGGCTTTGTC

Supplementary Table S4 Effects of G:U pairing and its reversion on standard free energy change.

Position	Parental		G:U pairing		Revertant	
	Base pair	ΔG (kcal/mol)	Base pair	ΔG (kcal/mol)	Base pair	ΔG (kcal/mol)
P2	A:U	-13.9	G:U	-13.7	G:C	-15.2
P3	C:G	-13.9	U:G	-11.5	U:A	-11.9
P5	U:A	-13.9	U:G	-13.2	C:G	-15.5
P6	G:C	-13.9	G:U	-11.0	A:U	-11.8
P7	A:U	-13.9	G:U	-13.1	G:C	-15.7