Table S2. List of primers.

Description	Name	Sequence
Genotyping *rupo+/-*	12426F1	AGGTCCTTGCCGTAGATGTG
	12426R1	AGGTGGTGTACCGGATCAAC
	Ngus-RB	AACGCTGATCAATTCCACAG
Genomic cloning	NF4	TCACTATGTATAACTTAATGTTGCACCAACAGTCAAC
	NR4	CCCAACCCCTCCTCTCACAACCCAA
Promoter	LF1	TAGTTGGAATGGGTTCGAATCACTATGTATAACTTAATGTTGCACCAACA
	LR2	TTATGGAGTTGGGTTCGAAGGTGGTGGGGTGGCCTACG
RT-PCR	RLIP1-LP2	GAGCCCGAGCTTCAACATG
	RLIP1-RP	TCTCGGTGTTGAACTCGTTG
qPCR	RLIP1-q1F	TCGCCATCGCCAATCCAAGACA
	RLIP1-q1R	TCGATCGTCGCGGTGGAACG
	18SF	CGGCTACCACATCCAAGGAA
	18SR	TGTCACTACCTCCCCGTGTCA
CRISPR lines	127CF2	CACTTCGTCCGCCTCTACCTCTTC
	127CR2	GTTGATCCGGTACACCACCT
Complementation	F(HindIII)	AAGCTTGCACCAACAGTCAACCGAAACAT
	R（EcoRI）	GAATTCATCCCTGGTTACTTGATTAGTCTGTG
	127RP	TCTCGGTGTTGAACTCGTTG
	RB	AACGCTGATCAATTCCACAG
	d127LP	CGGCGTACTACAAGGACATCGTCGT
	d127RP-1	TAGCGTTGTGATGGAGTGCATTCCAG
	d127RP-2	AGGTTAACCGCGTTGCTAAACCAGC
pET-RUPO-N	127NF1	TTAGAATTCCAGGGGCGGCCGGTCACC
	127NR1	ACACTCGAGGCGGCTGCCGCTGCCGTC
Y2H related		
Library construction	CDSIII	ATTCTAGAGGCCGAGGCGGCCGACATG-d(T)30VN
	SMARTIII	AAGCAGTGGTATCAACGCAGAGTGGCCATTATGGCCGGG
BD 515-845	127YF2	ACTGAATTCTTCGAGGAGAGCGCCATC
	127YR2	CACGGATCCTCACCTCCCCTTCATGTC
BD453-845	127YF3	ACTGAATTCTGGTACAAGCGGCCCCAG
	127YR2	CACGGATCCTCACCTCCCCTTCATGTC
BD515-820	127YF2	ACTGAATTCTTCGAGGAGAGCGCCATC
	127YR3	CACGGATCCTCAGCCGGAGCCGGAG
BD453-820	127YF3	ACTGAATTCTGGTACAAGCGGCCCCAG
	127YR3	CACGGATCCTCAGCCGGAGCCGGAG
BD453-708	127YF3	ACTGAATTCTGGTACAAGCGGCCCCAG
	127YR4	ATAGGATCCTCACTCGAGGAGCACGACG
BD515-708	127YF2	ACTGAATTCTTCGAGGAGAGCGCCATC

	127YR4	ATAGGATCCTCACTCGAGGAGCACGACG
BD453-788	127YF3	ACTGAATTCTGGTACAAGCGGCCCCAG
	127YR5	ATAGGATCCTCACGCGTACTCGAGGTTC
BD515-788	127YF2	ACTGAATTCTTCGAGGAGAGCGCCATC
	127YR5	ATAGGATCCTCACGCGTACTCGAGGTTC
AD-OsHAK1-C	PotassYF2	ATAGAATTCACGAGCTCGGCCGTGC
	PotassYR1	CGCGGATCCCTAGATTTCATACGTGA
AD-OsHAK19-C	PTF4	ATAGAATTCGCCGCGTTCCTCCTCGA
	PTR2	CGCGGATCCCTAAATCTCATAGGTGATC
AD-OsHAK20-C	PTF5	ATAGAATTCCTCAAGGTGTTCGTCTAC
	PTR3	CGCGGATCCCTAAATCTCATAAGTGATC
Kinase activity related		
MBP-RUPO515	GSTKinaseF	TCTGGATCCTTCGAGGAGAGCGCCATC
	GSTKinaseR	TCTGAATTCCCTCCCCTTCATGTCGGC
MBP-RUPO	MBPF1	TCTGGATCCCAG GGG CGG CCG GTC ACC
	HiskinaseR	TCTAAGCTTCCTCCCCTTCATGTCGGC
Point mutation	K543R For	CCAAGGTCGCCGTGAGGCGCGGGAAC
	K543R Rev	CTCACGGCGACCTTGGTGCCGTCGTCG
Localization		
35S::RUPOΔC-GFP	127DWF1	ATACTCGAGATGCGCCGCCGCGGGAG
	127DWR1	CCGACTAGTCCGAGGCCGAGGGTGGAG
Ubi::RUPO-GFP	127DWF2	ATAGGATCCATGCGCCGCCGCGGGAG
	127DWR2	ATAACTAGTGGCTGCAGCGGCCCTCCCCTTCATGTCG
Pull down related		
GST-RUPO-C	GSTKinaseF	TCTGGATCCTTCGAGGAGAGCGCCATC
	HiskinaseR	TCTAAGCTTCCTCCCCTTCATGTCGGC
MBP-OsHAK1-C	MBPHAKF1	TATGGATCCACGAGCTCGGCCGTGC
	MBPHAKR1	GAGAAGCTTCTAGATTTCATACGTGA
MBP-OsHAK19-C	MBPHAKF2	TATGGATCCGCCGCGTTCCTCCTCGA
	MBPHAKR2	CGCAAGCTTCTAAATCTCATAGGTGATC
MBP-OsHAK20-C	MBPHAKF3	TATGGATCCCTCAAGGTGTTCGTCTAC
	MBPHAKR3	GGCAAGCTTCTAAATCTCATAAGTGATC
Co-IP related		
FLAG-RUPO-C	IPF2	ATAACTAGTAGATTACAAGGATGACGACGATAAGTCGAGGAGAGCGCCATC
	IPR1	ATCGGATCCTCACCTCCCCTTCATGTC
GFP-OsHAK1-C	IPKTF1	GACTCTAGACACGAGCTCGGCCGTGC
	IPKTR1	CGCGGATCCCTAGATTTCATACGTGA
GFP-OsHAK19-C	IPKTF2	GACTCTAGACGCCGCGTTCCTCCTCGA
	IPKTR2	CGCGGATCCCTAAATCTCATAGGTGA
GFP-OsHAK20-C	IPKTF3	GACTCTAGACCTCAAGGTGTTCGTCTAC
	IPKTR3	CGCGGATCCCTAAATCTCATAAGTGA