

**A**

-171 ACCCAAGACT TTTTATTGCT TCTTCCTTTC TTATGACACA CCGTTTTCAA CCGAGAGTCG  
-111 TTTGGGATCA GAAAAGAAAT GGCTTTTGAC ACTTCAGAAG CTTTTAGGTA AGAAAGGTGT  
-51 CCTCTTTATT CATCTCGCCA ACAAAGGTT GATACTTTGG TAAAGGAACT AATGAAAGAAG  
RKS1 Start codon  
+10 CAGTATCTGA AATCTGGATC TGGGACAAGG AAGGAAAAGG ACAAGGCGAA GAGGTGGTTC  
+70 TTGGATAACG GAAGCATCTT CTTAAGAGAA CTTGTAGCTG ATTGTAACGG TAAATCCATT  
+130 CCTATTCGCA GTTTTTCTCC TGAGCAGATA TTGAAAGCCA CCAACAATTT CGATTCTAGC  
+190 TGTTTTGTCT CGCAAGATGT ATACTATAAA TGGTATAGAG GTGAAATTGA AGATAGATCT  
+250 TACATGATCA AGAGATTCTC AGAGGATGAG ATTACAGGAA AACGACATAG AGTTAAAGAG  
273F/298R  
+310 GTTTACAACG ACATTGTCTT GTCTGCTCGG ATGAGTAATC ACAGTAACTT TCTTCACTT  
+370 TAGGATGTT GTCTCGAGTT TCCTTTTCCG GTTCTTGTGT TTGAATTTGC AGAACATGGA  
+430 GCTATGAATC AGCGAGGAGG TGTTATAGTT AATGGTGAAG AATCTTTATT GCCGTGGAGT  
+490 GTACGGTTGA AGATTGGGAA AGAGATTGCT AATGCGGTGA CTTATCTTCA CACGGCATTC  
+550 CCTAAGATCA TCATACATAG AGATGTTAAA CCGATGCATG TTTTCTTGA CAAGAATTGG  
+610 ACCGCAAAGT TGTCTGATTT ATCTTCTCA ATATCTCTAC CTGAGGGAAA ATCGAGAATA  
+670 GAAGCTGAAT GGGTTCTAGG AACATTTGGG TACATCGATC CATTATATCA TAAGACGTGT  
+730 TTTGTGACTG AATATACAGA TGTCTACAGC TTTGGAATCT GTTTGCTGGT TATTATTACT  
+790 GGTAAACCGG CTATCATGAC TATTTCTGAT GGAGATCTCC AAGGTATTCT TAGCTTAGTG  
+850 AGAGAGTTAT GTGAGAATGG GAAGCTTGAT GAAGTGATAG ATCCGAGGTT GATGAAAGAT  
+910 ATCACAAGTG GTCAAAGGTT GCAAGTGGA GCATGTGTGG TGCTGGCTTT GAGATGCTGT  
+970 AAGGAGAGAG ATGAAGACAG ACCAAAGATG ATCCAAGTAG CTAAAGAACT CAAGCAGATT  
+1030 GAAGCATCAT TGAAAAATTC TAGCTAGAGA TCCGCAAGGA ACTTTTTGGA TATTGAGATA  
RKS1 Stop codon  
+1090 TCTTCGCGGA GTAGGCATCA CAAGAACATG ACTGAAGATA GGAGCATCTT TGGTGCCCAA  
+1150 AAGAAGAGGT ATCAGTTGCT TGGACTATAT AAATCTAAGT AAACAATTCT TGCATTGTGT  
+1210 AGCAAGGAAA CTCAGATTCT TACATACAAC ATATTTAATA AAAGCTCGAT CAAAAACAAG  
+1270 ATACAGTGAT TGCAATTTTC ACTCTAAGC CTGTATAATA GATAGACCTG TTTCAAGTCG  
+1330 CATTAGAAAA GGTTGCATGG TCATATATGT TTCTCTATCT TCTTAAGCTC TTTTGCAACG  
Stop codon At3g57700

## B

RACE 5'										
Accession	Number of colonies	Base position of 5'end of <i>RKS1</i> transcripts relative to the position of the "A" (+1) in the start codon ATG								
		-129	-113	-110	-108	-105	-102	-99	-10	-1
Col-0	11	1	1	4	1			2		2
Kas-1	10				1	1	1		3	

RACE 3'							
Accession	Number of colonies	Base position of 3'end of <i>RKS1</i> transcripts relative to the position of the "A" (+1) in the start codon ATG					
		+366	+370	+1268	+1293	+1330	+1334
Col-0	10			3	2	5	
Kas-1	12	5	4	1			2

**Figure S7. Schematic illustration of the 5'-end and 3'-end products of *RKS1* transcripts identified by respectively 5' and 3'RACE.** (A) Nucleotide sequence of *RKS1* from Col-0. The ATG and TAG codons are underlined and bold. The SNP present in the coding region of *RKS1* between the Col-0 and Kas-1 alleles is boxed. The primer specific of *RKS1* (reverse and forward) used to amplify 5' and 3' ends is underlined. In blue, the location of *RKS1* 5' ends of Col-0 leaves, in pink the location of *RKS1* 5' ends of Kas-1 leaves. In red, the location of *RKS1* 3' ends of Kas-1 leaves; in green of Col-0 leaves. (B) Location and frequency (number of clones) of *RKS1* 5' ends and *RKS1* 3' ends products.