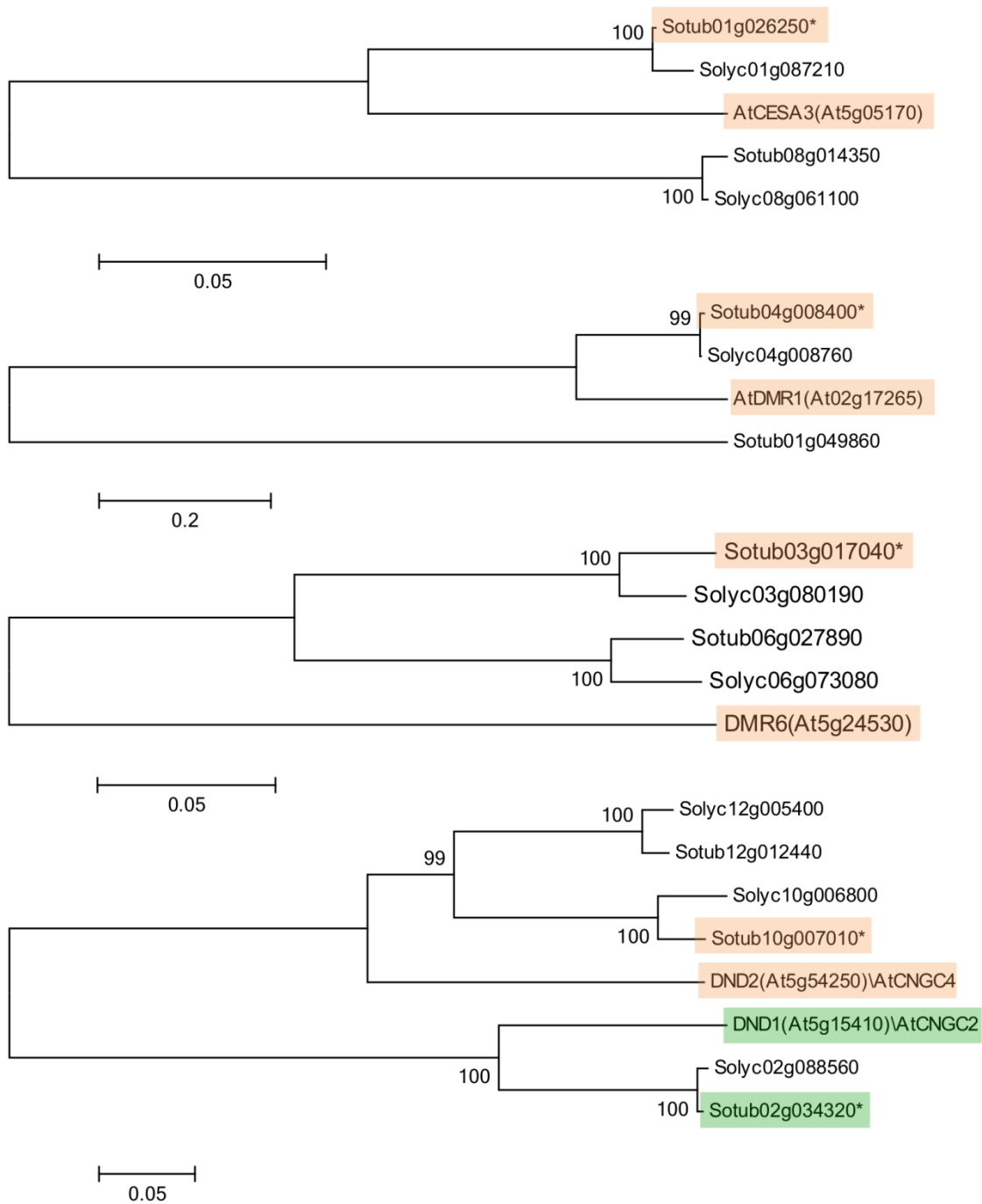
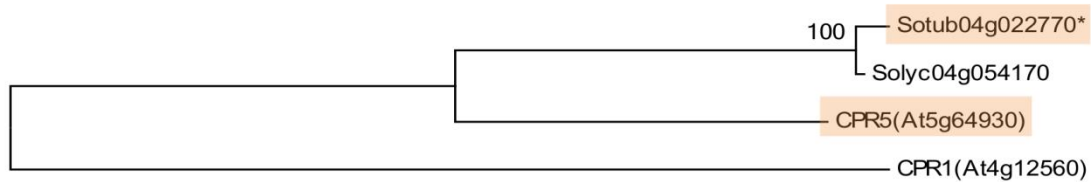
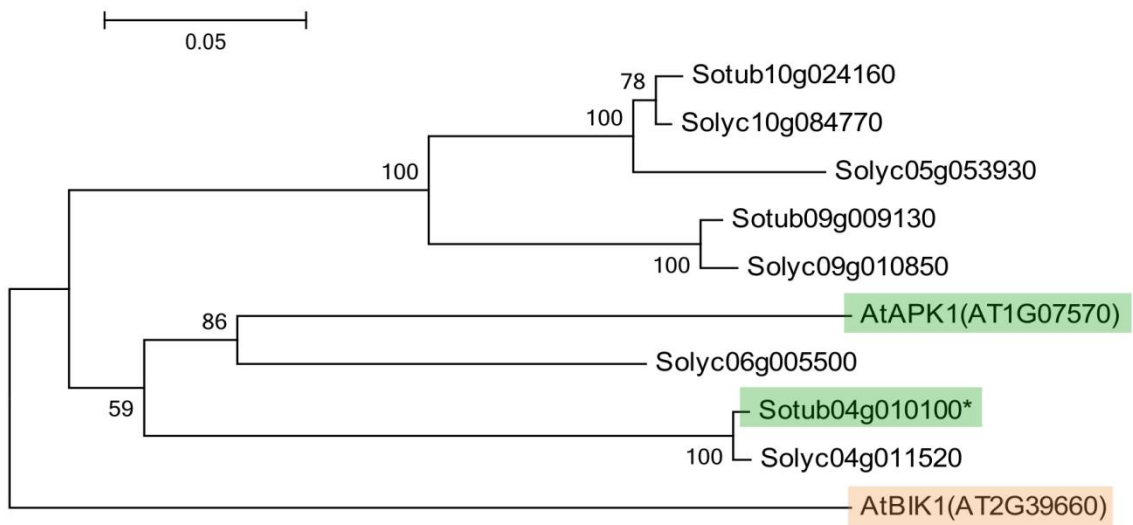
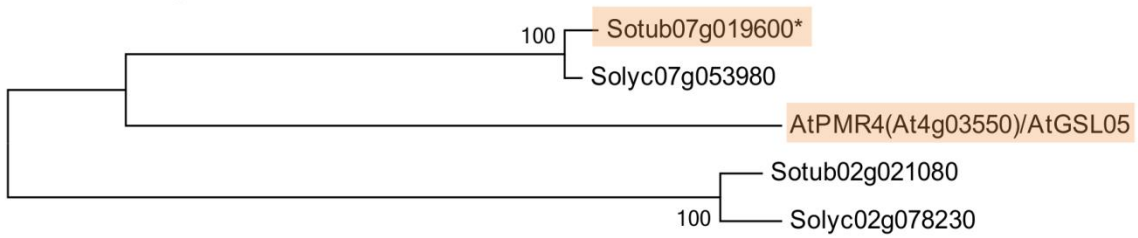
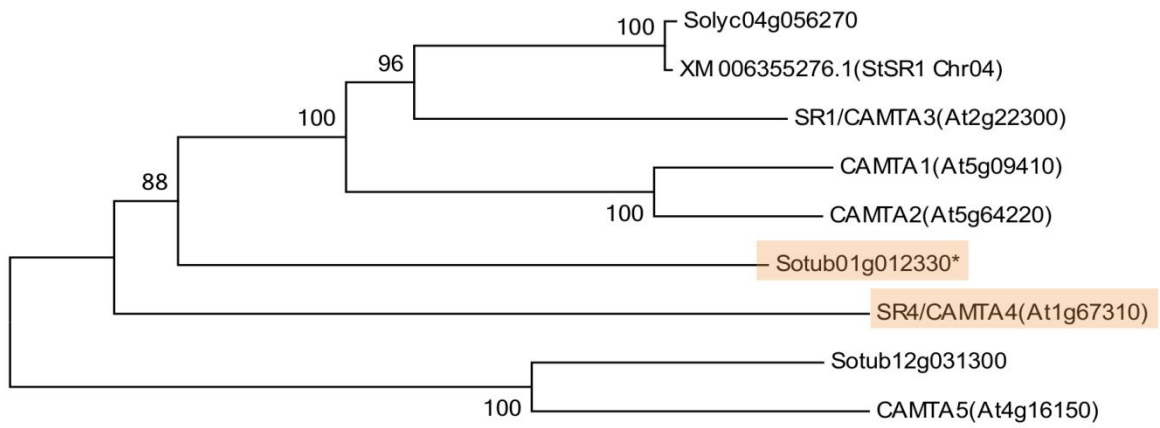
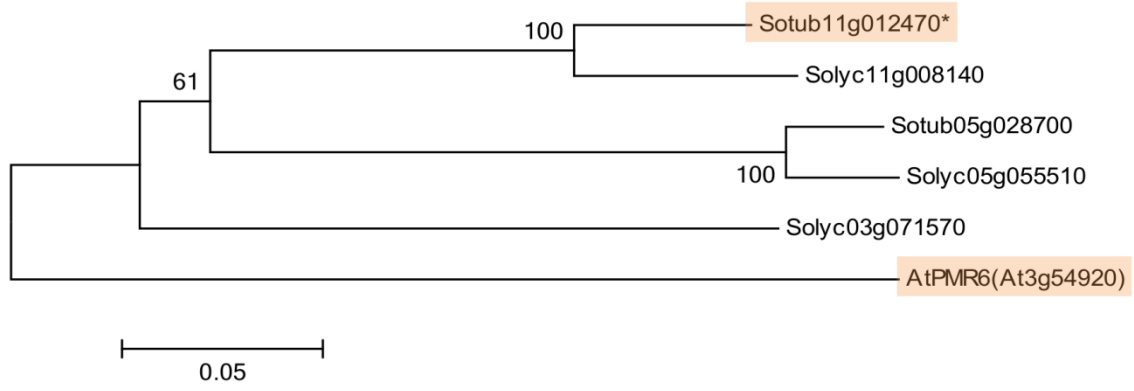
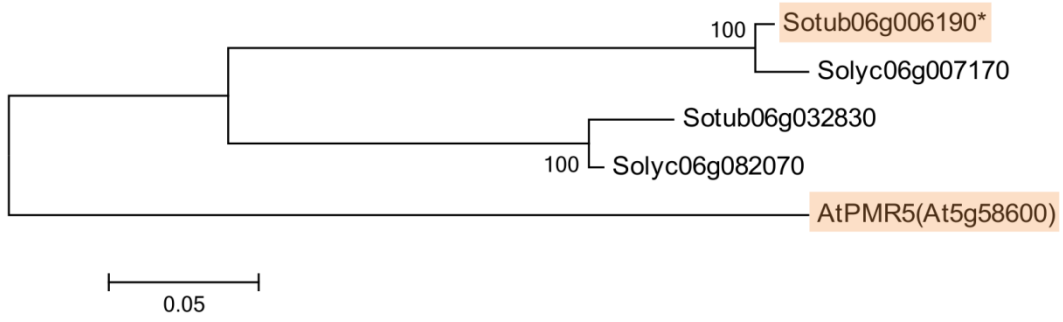


Supplementary Fig. 1. Individual phylogenetic trees of all 11 candidate susceptibility genes (*S*-genes) including homologs from tomato and potato. Sequences with an asterisk (*) which showed the highest degree of homology with the Arabidopsis *S*-gene were considered as the orthologs in potato. These are highlighted in orange, or in green in the case of multiple Arabidopsis *S*-genes in the same tree. The scale bar indicates amino acid substitutions per position. In the trees, the numbers above nodes indicate bootstrap support values based on 10,000 replicates.

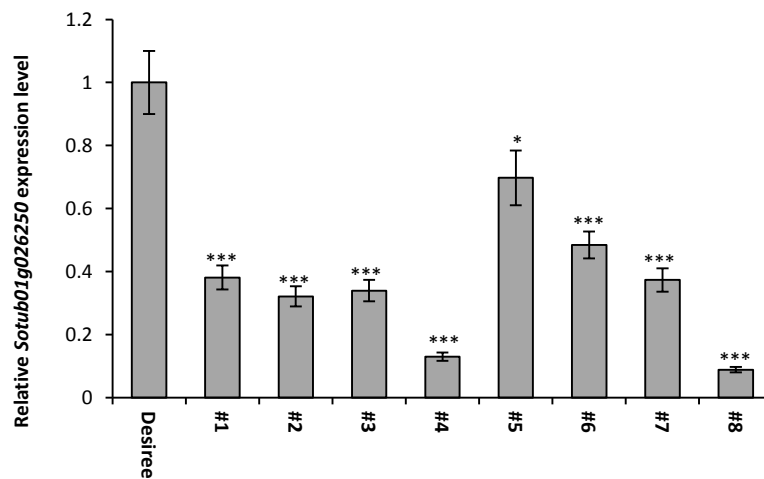
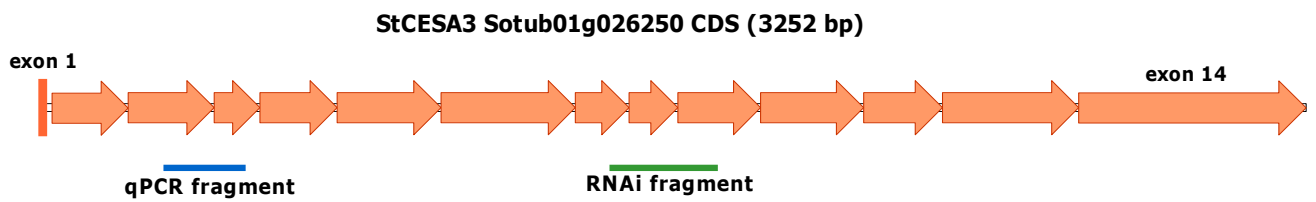




0.2

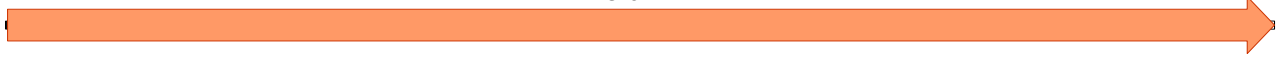


Supplementary Fig. 2. Information of RNAi silencing constructs and silencing effects in RNAi potato transformants. Location of the targeted regions of the RNAi constructs and qPCR fragments in 11 susceptibility genes (*S*-genes). Relative expression level of 11 potential *S*-genes in leaves of Desiree and independent potato RNAi transformants. Asterisks indicate degree of significant difference compared to Desiree plants (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$)

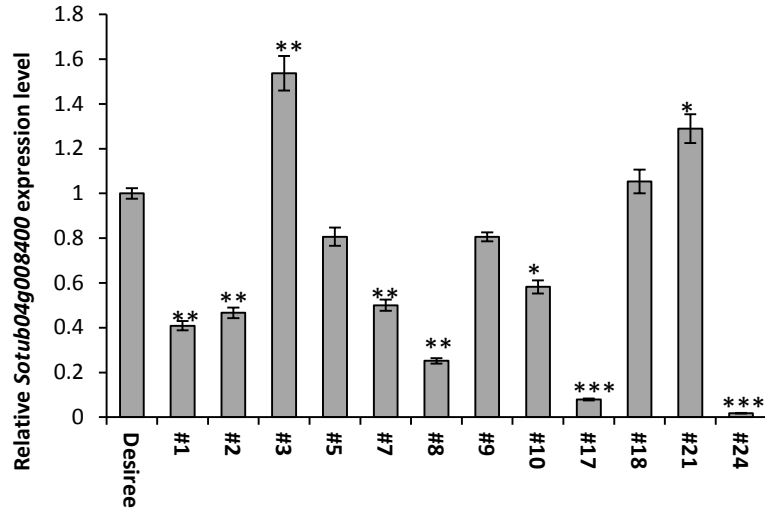


StDMR1 Sotub04g008400 CDS (1131 bp)

exon 1



RNAi fragment qPCR fragment



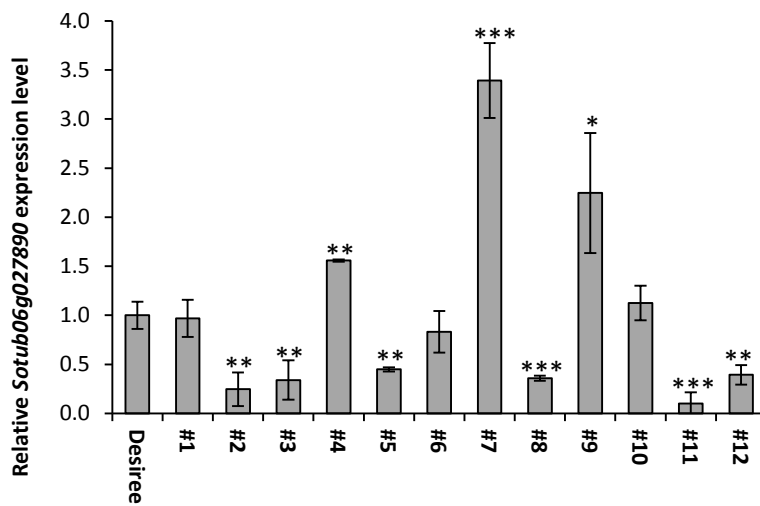
StDMR6 Sotub03g017040 CDS (1014 bp)

exon 1



qPCR fragment

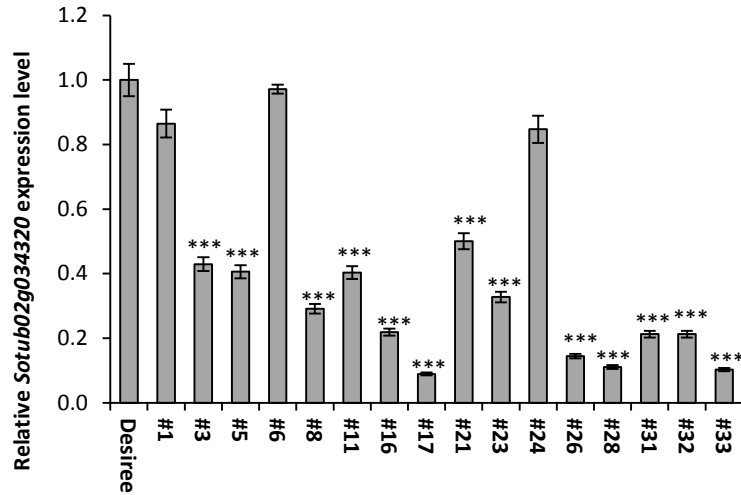
RNAi fragment



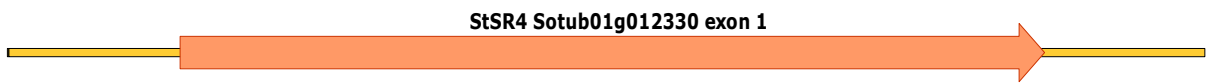
StDND1 Sotub02g034320 CDS (2127 bp)



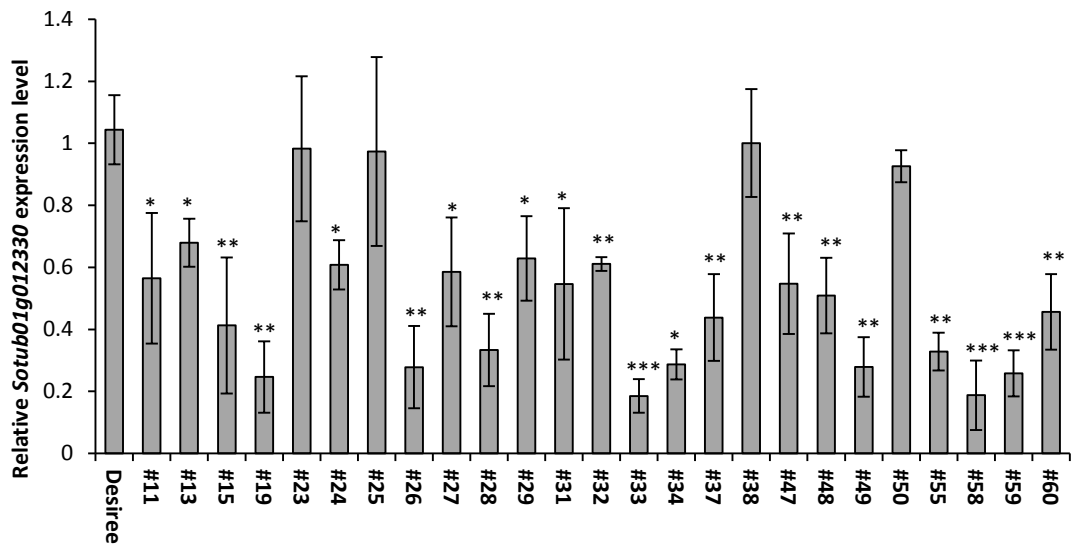
RNAi fragment (green bar)
qPCR fragment (blue bar)



PGSC0003DMT400038758 (2903 bp)



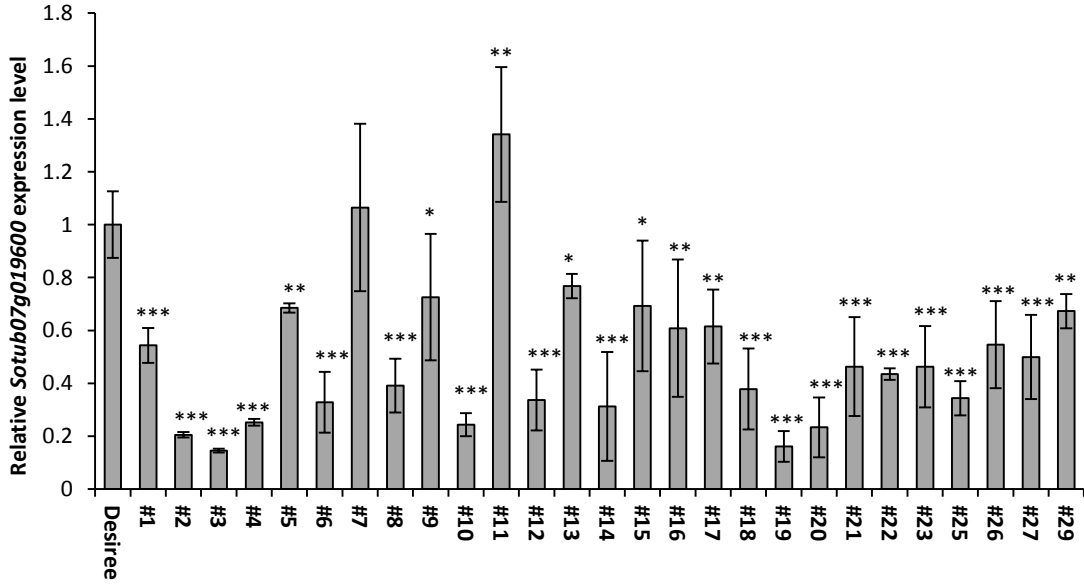
RNAi fragment (green bar)
qPCR fragment (blue bar)



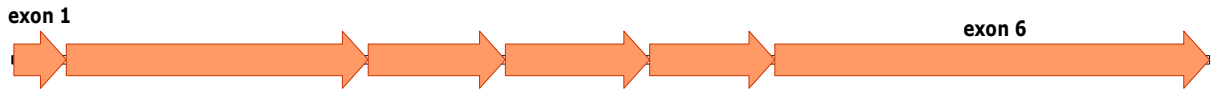
StPMR4 Sotub07g019600 CDS (5214 bp)



RNAi fragment qPCR fragment

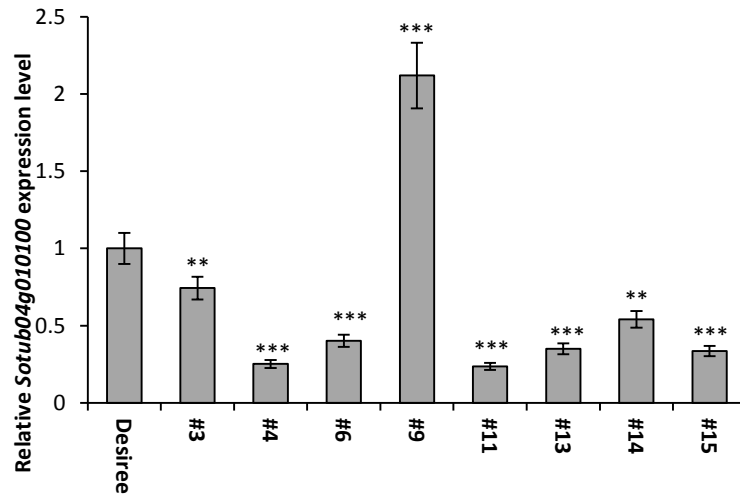


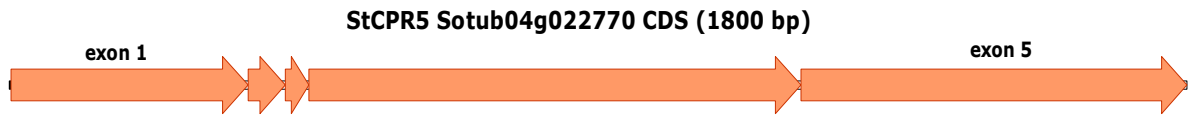
StBIK1/StAPK1 Sotub04g010100 CDS (1185 bp)



RNAi fragment

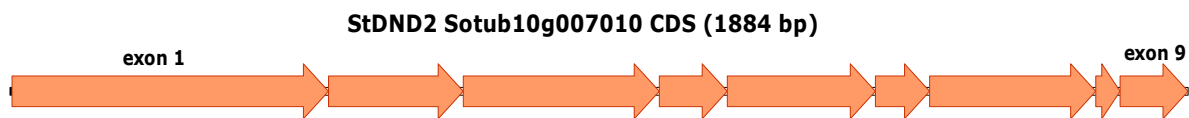
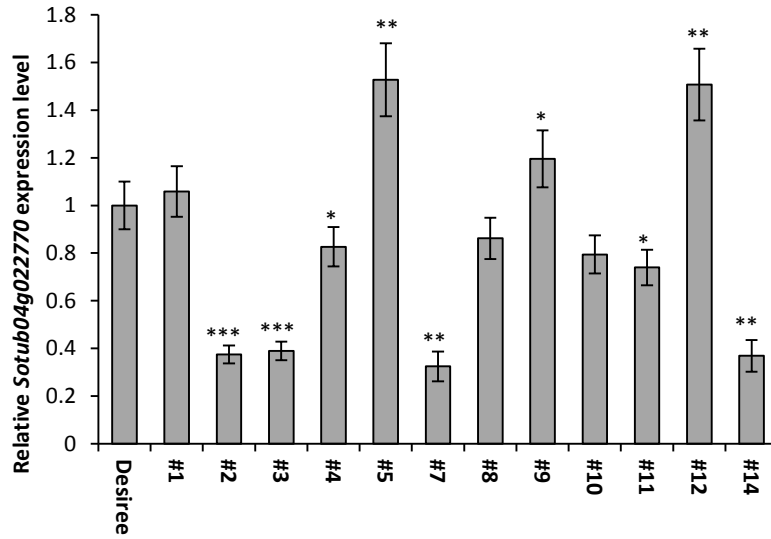
qPCR fragment





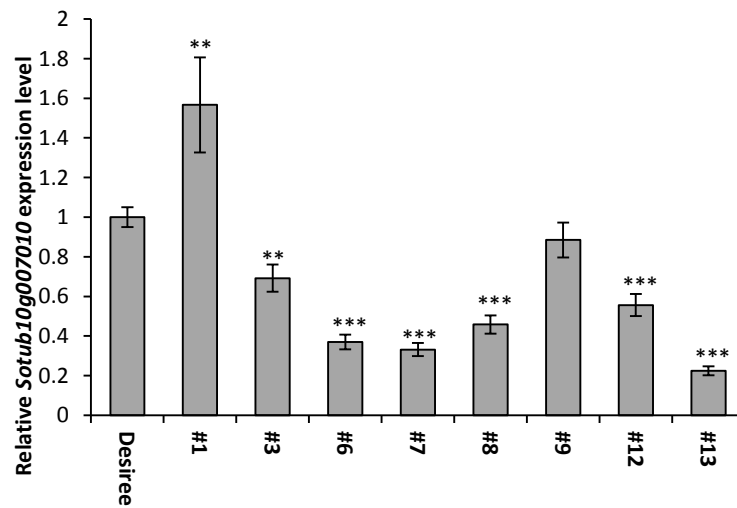
RNAi fragment

qPCR fragment

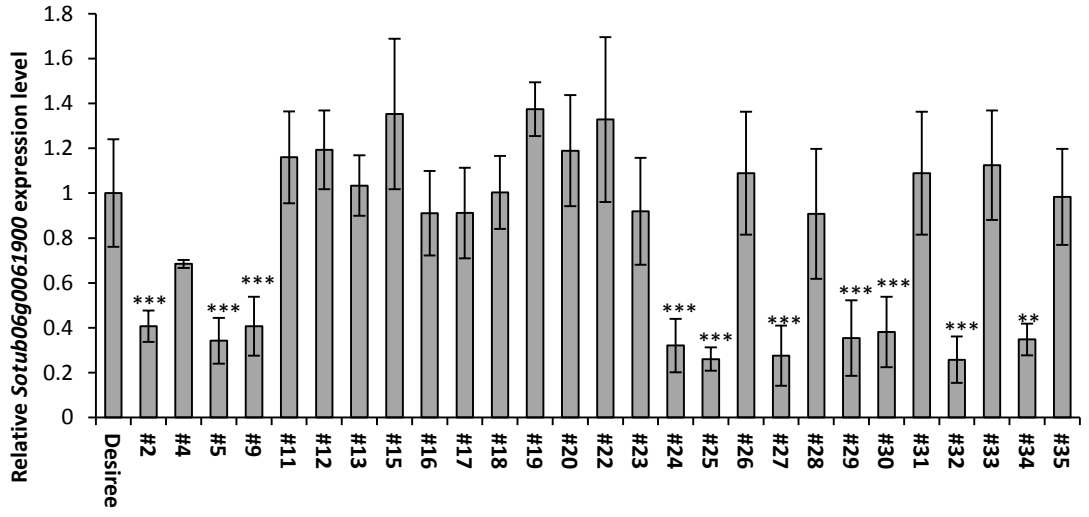
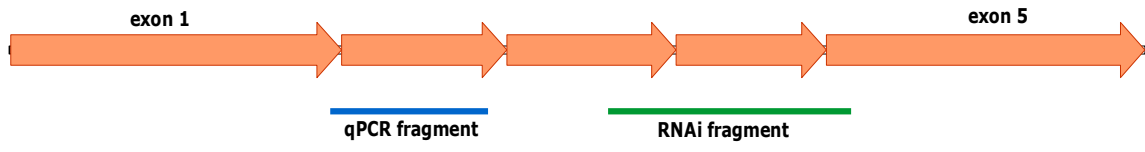


RNAi fragment

qPCR fragment



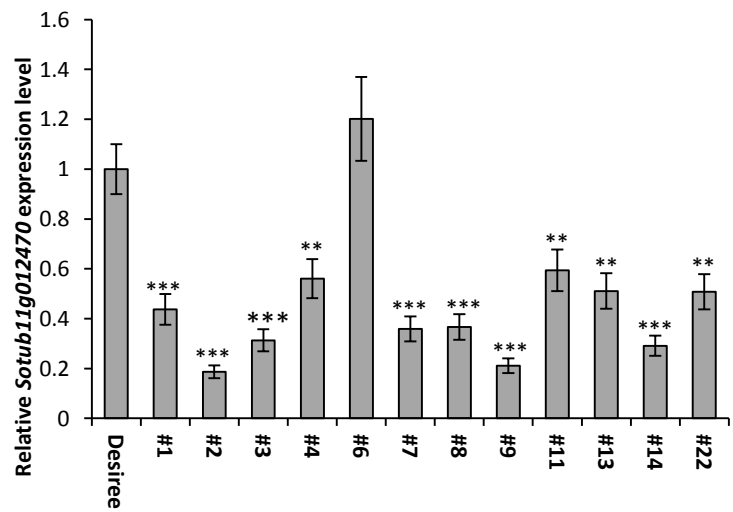
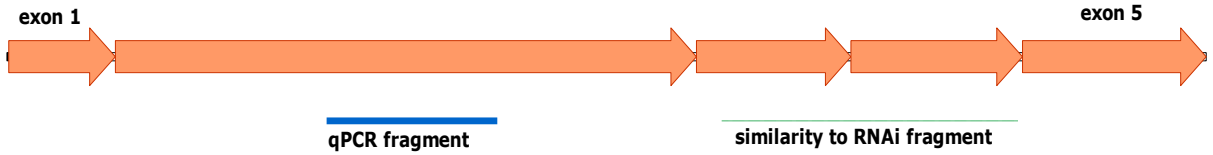
StPMR5 Sotub06g006190 CDS (1200 bp)



StPMR6 Sotub05g015080 CDS (1206 bp)



StPMR6 Sotub11g012470 CDS (1473 bp)



Supplementary Table 1. Primers used in this study

Primer name	Sequence (5' to 3')	Used for	Gene
Fw-SICESA3	caccGCACACCATGGCCTGGAAATAACACC	RNAi:: SICESA3 cloning	Solyc01g087210
Rv-SICESA3	AAAAGCACATTGCTTCTCTCAAAGCC		
Fw-StCESA3-qPCR	GAAGCAAAAAGTGGCTGACC	Determining relative transcript levels	Sotub01g026250
Rv-StCESA3-qPCR	GATGTGTTTTGCACCACCAG		
Fw-SIDMR1	caccAGTCGTTTGCTCCGGCCACTG	RNAi:: SIDMR1 cloning	Solyc04g008760
Rv-SIDMR1	CGCCGCAGCACTAGCAGCAC		
Fw-StDMR1-qPCR	TGGACGGAAGTTGAGTGTTG	Determining relative transcript levels	Sotub01g026250
Rv-StDMR1-qPCR	CCCTCATCTTCTTGTTGGA		
Fw-SIDND1	caccTGTCTTCTACCAAGACGTCCGC	RNAi:: SIDND1 cloning	Solyc02g088560
Rv-SIDND1	CGATGTGTGCCGGCTGCGAC		
Fw-StDND1-qPCR	GTTCCGGCGTGTATTAGACC	Determining relative transcript levels	Sotub02g034320
Rv-StDND1-qPCR	GAATCACCGTGACGATAGCC		
Fw-SIDMR6	caccTCATCTTTCAGGGAATCGTGAGCAG	RNAi:: SIDMR6 cloning	Solyc03g080190
Rv-SIDMR6	TGACAAAGGCGTCAGGTTGAGG		
Fw-StDMR6-qPCR	AGTTACATCCGACCCGAATC	Determining relative transcript levels	Sotub06g027890
Rv-StDMR6-qPCR	GACGGATTATTTGAGCTTGGTC		
Fw-StSR4	caccAGAATAGGTGCCTCCCGTCT	RNAi:: StSR4 cloning	PGSC0003DMT4 00038758/ Sotub01g012330
Rv-StSR4	GCGACCTCGAGAACTCCATA		
Fw-StSR4-qPCR	CTGGTAAAGCTCTGGCGAAC	Determining relative transcript levels	Sotub01g012330
Rv-StSR4-qPCR	GCAGTCTCCACCGATCTCTC		
	ATGAGCCTCCGGCAACGTTCAACGCCGGC GGCGAGACAAGTTTCTATAGATGAAGAAC CATATAACATCATTCCGATTCATAATCTTC TAGCTGACC*	RNAi:: SIPMR4 cloning	Solyc07g053980
Fw-StPMR4-qPCR	GGGGTGAGTCAGCGAATCTA	Determining relative transcript levels	Sotub07g019600
Rv-StPMR4-qPCR	GGGCAGTACCATTCCGACTA		
Fw-SIBIK1	caccAGCTGCAAGGCCAGGGACTG	RNAi:: SIBIK1 cloning	Solyc04g011520
Rv-SIBIK1	AGCTGCCTCGAGAGCAACCTTC		
Fw-StBIK1-qPCR	TCGTTCGAGTGATGGACAAAA	Determining relative transcript levels	Sotub04g010100
Rv-StBIK1-qPCR	CAGGCATTTGACAGCAAGAA		
Fw-SICPR5	caccTCTCAACCCGTCGATCCGCC	RNAi:: SICPR5 cloning	Solyc04g054170
Rv-SICPR5	TGCCGAGAGGAAGTGCAAGTG		
Fw-StCPR5-qPCR	GCAATTGGCTTCTGCTTCTT	Determining relative transcript levels	Sotub04g022770
Rv-StCPR5-qPCR	CTCTCCAAAAGGTTTCGCATC		
Fw-StDND2	caccTGACGATGAAGATGAAGATGATG	RNAi:: StDND2 cloning	Sotub10g007010
Rv-StDND2	CCCATTGTGCTTTAGGGTCT		
Fw-StDND2-qPCR	TTTGCCTCTTGAGAAGAATGC	Determining relative transcript levels	Sotub10g007010
Rv-StDND2-qPCR	ATTTGGCTGCCCTTTGAATA		
Fw-SIPMR5	caccTGCTTGGAGAGGTGTTGATGTCTTG	RNAi:: SIPMR5 cloning	Solyc06g007170
Rv-SIPMR5	ACGTGCCGGTGGTCCAATCG		
Fw-StPMR5-qPCR	TGAAATTCCAAGGTTCAATGG	Determining relative transcript levels	Sotub06g006190
Rv-StPMR5-qPCR	GAGGGTCACCCGTGATGTAT		

*Artificial sequence

Supplementary Table 1 (continued)

Primer name	Sequence (5' to 3')	Used for	Gene
Fw-SIPMR6	caccGGCTTGTGCAAAGGATGCCAAGATG	RNAi:: SIPMR6 cloning	Solyc05g014000
Rv-SIPMR6	TGCAACCAAGTGCACCAGCATTC		
Fw-StPMR6-qPCR	CCGTAATCCAGGAAGAACCA	Determining relative transcript levels	Sotub11g012470
Rv-StPMR6-qPCR	TATCCCCGACGGTAAACAG		
Fw-NPT II	ACTGGGCACAACAGACAATC	Verification of transgenic plants	
Rv-NPT II	TCGTCCTGCAGTTCATTCAG		
Fw-StEF1a	ATTGGAAATGGATATGCTCCA	Normalisation in qRT-PCR assays	Sotub06g010680
Rv-StEF1a	TCCTTACCTGAACGCCTGTCA		

Supplementary Table 2. Details of susceptibility genes identified in Arabidopsis

Gene name	Subcellular location	Function	Susceptibility mechanism	References
<i>CESA3</i>	Golgi apparatus, endosome, integral component of membrane, plasma membrane, plasmodesma, trans-Golgi network	Cellulose synthase	Probably DAMP induced defense suppression (JA, ET)	Ellis et al. (2002); Ellis and Turner (2001)
<i>DMR1</i>	Chloroplast, chloroplast stroma	Homoserine kinase	Amino acid metabolism	Huibers et al. (2013); Van Damme et al. (2005); van Damme et al. (2009)
<i>DMR6</i>	Cytoplasm	2-oxoglutarate-Fe oxygenase	Defense suppression (SA?)	Van Damme et al. (2005); Van Damme et al. (2008)
<i>DND1</i>	Plasma membrane	Cyclic nucleotide-gated ion channel	Defense suppression (SA, JA), regulator NO synthesis	Ahn (2007); Clough et al. (2000); Genger et al. (2008); Govrin and Levine (2000); Jurkowski et al. (2004); Su'udi et al. (2011)
<i>SRI</i>	Nucleus	Ca ²⁺ /calmoduline-binding transcription factor	Defense suppression (SA, ET)	Doherty et al. (2009); Du et al. (2009); Galon et al. (2008); Kim et al. (2013); Laluk et al. (2012); Nie et al. (2012); Qiu et al. (2012)
<i>PMR4</i>	1,3-beta-D-glucan synthase complex, Golgi apparatus, integral component of membrane, plasma membrane, plasmodesma	Callose synthase	Probably DAMP induced defense suppression (SA, JA)	Nishimura et al. (2003)
<i>BIK1</i>	Chloroplast, cytoplasm, nucleolus, nucleus, plasma membrane	Membrane-anchored protein kinase	Defense suppression PTI (SA?, ET)	Veronese et al. (2006)
<i>CPR5</i>	Chloroplast, integral component of membrane, membrane, nucleus	Transmembrane protein	Defense suppression (SA, JA, ET)	Bowling et al. (1997); Jing et al. (2007); Jing and Dijkwel (2008); Love et al. (2007)
<i>DND2</i>	Integral component of plasma membrane, membrane, plasma membrane	Cyclic nucleotide-gated ion channel	Defense suppression (SA, JA), regulator NO synthesis	Ahn (2007); Clough et al. (2000); Genger et al. (2008); Govrin and Levine (2000); Jurkowski et al. (2004); Su'udi et al. (2011)
<i>PMR5</i>	Endoplasmic reticulum, integral component of membrane	Unknown	Altered pectin composition of cell wall affecting either nutrition or endoreduplication	Chandran et al. (2013); Vogel et al. (2004)
<i>PMR6</i>	Anchored component of membrane, anchored component of plasma membrane, plasma membrane	Pectate lyase-like protein	Pectin accumulation in the extrahaustorial matrix possibly resulting in decreased nutrient availability to the pathogen	Chandran et al. (2013); Vogel et al. (2002)