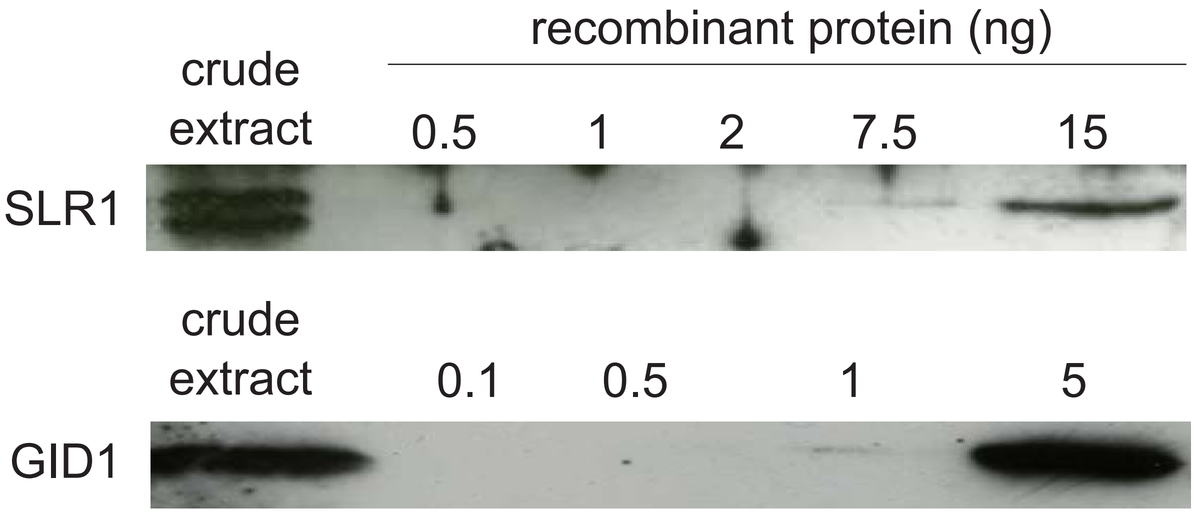
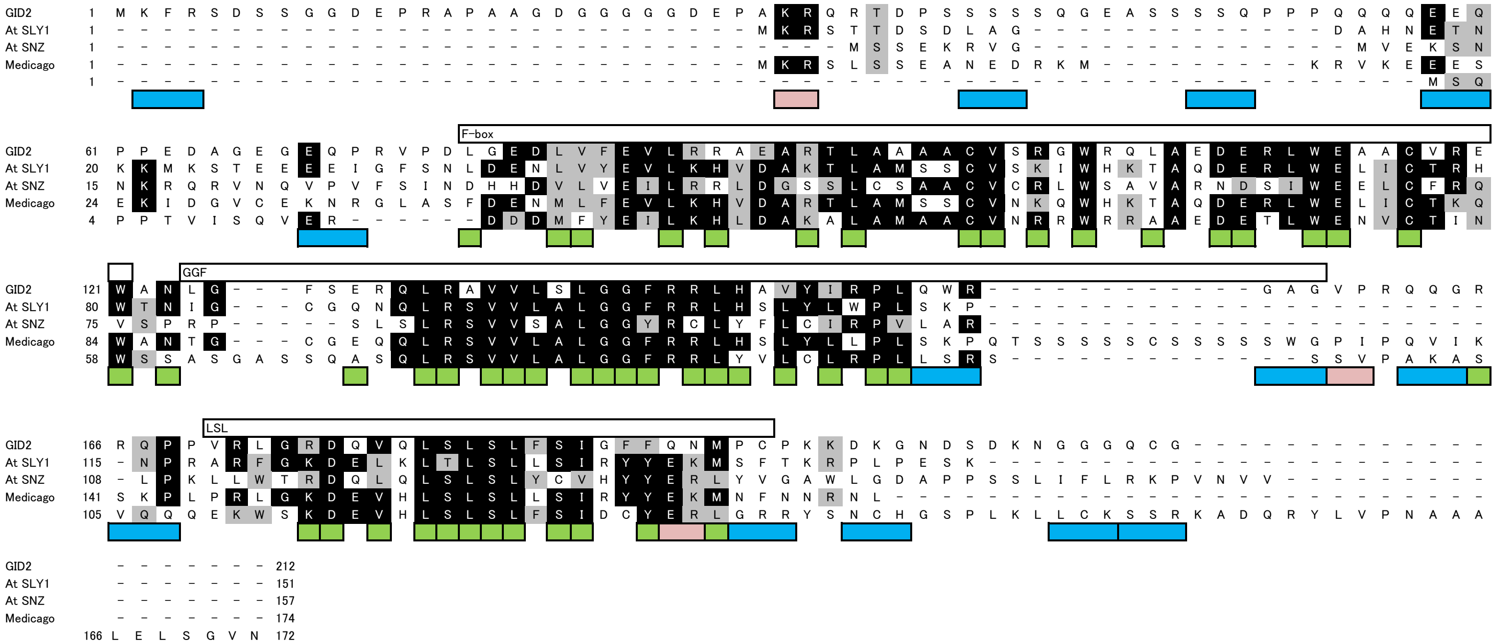
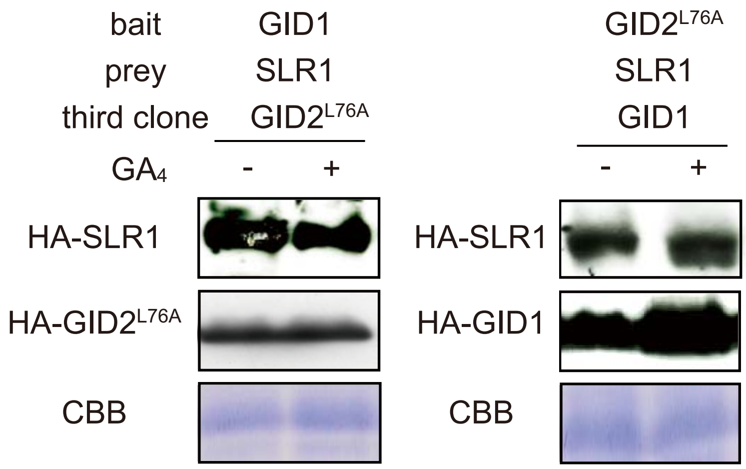


Supplemental Figure 1. Amount of SLR1 and GID1 protein in rice cells. Identical amount of crude protein extract from Taichung 65 rice was subject to immunoblot analyses using an anti-SLR1 antibody (top panel, leftmost lane) or anti-GID1 antibody (bottom panel, leftmost lane), respectively. Immunoblot analyses of recombinant SLR1 or GID1 proteins expressed in *E. coli* were used to estimate the amount of endogenous SLR1 and GID1 protein level. Note that amount of SLR1 protein is more abundant (> 15 ng) than GID1 (< 5 ng) in rice cells.

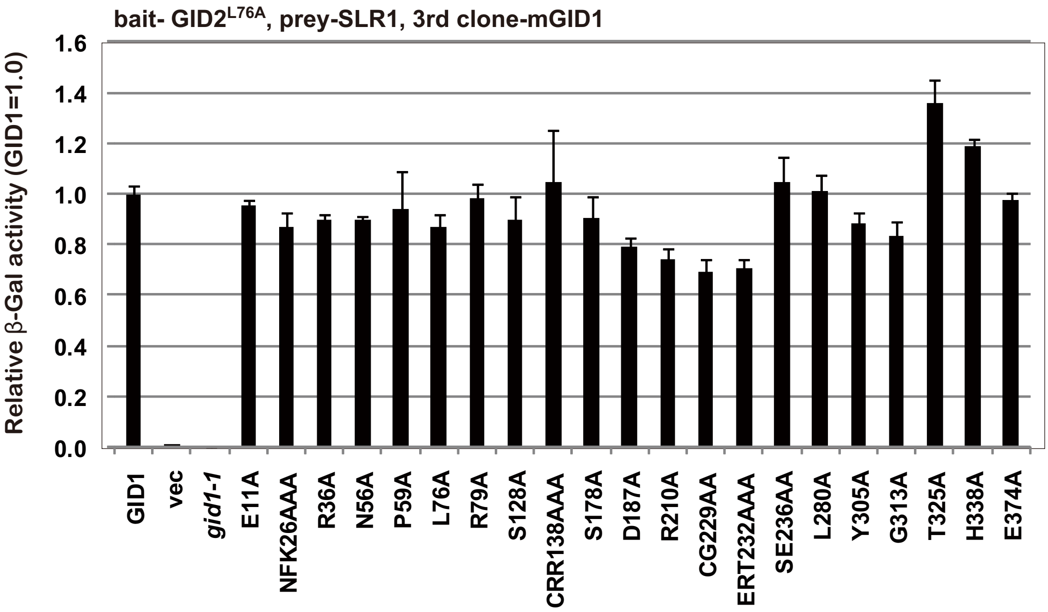


Supplemental Figure 2. Comparison of Amino Acid Sequences of Vascular Plant GID2 Proteins.
Amino acids that were included in alanine scanning are shown in colored boxes at the bottom of the alignment. Box colors indicate the number of amino acids replaced within each mutant protein. Green, 1 amino acid change; pink, 2 changes; blue, 3 changes. Black and grey indicate identical and similar amino acids, respectively. At, *Arabidopsis thaliana*; Sm, *Selaginella moellendorffii*.



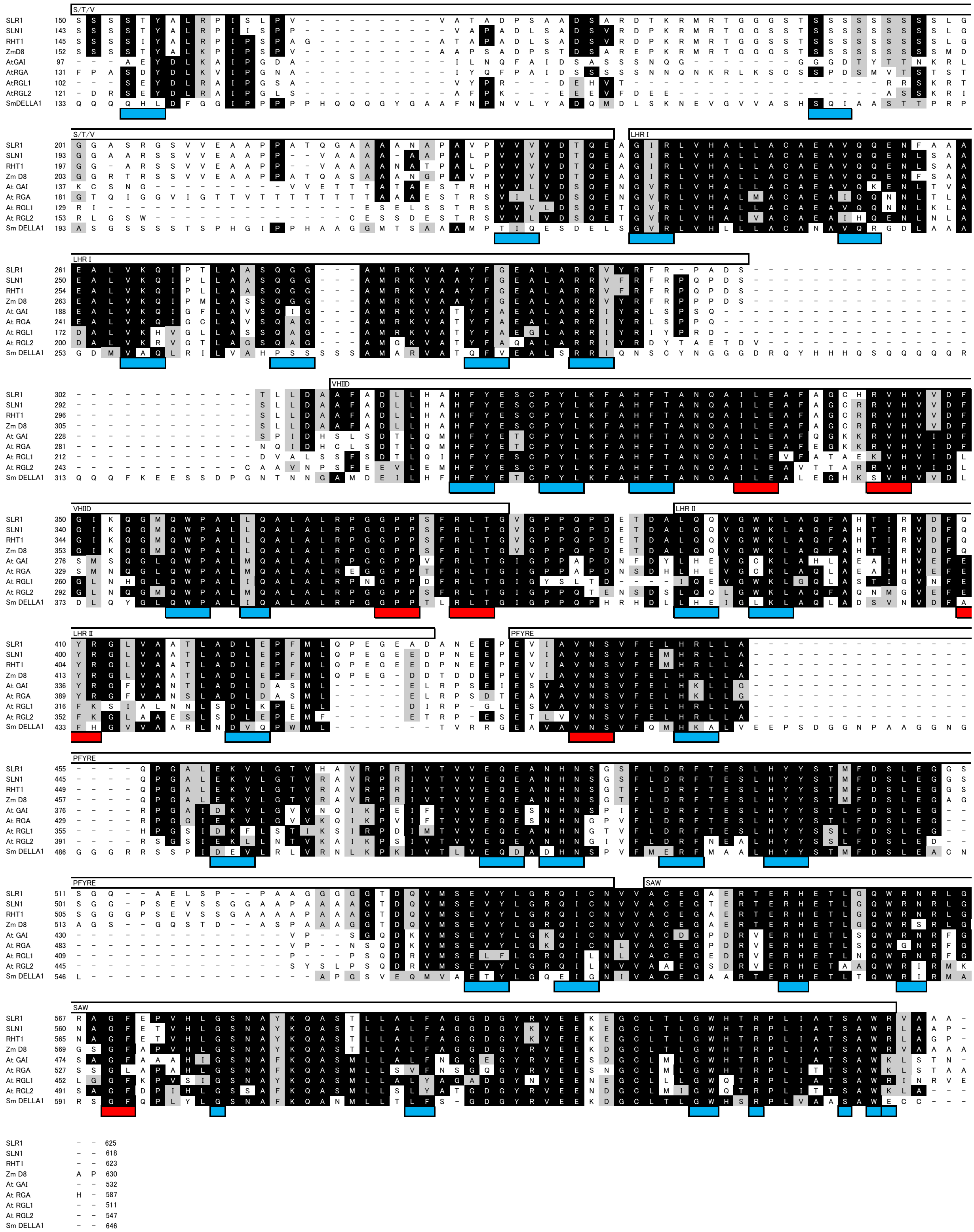
Supplemental Figure 3. Mutation in the F-box Domain of GID2 Abolishes the GA-, GID1-, and GID2-dependent Degradation of SLR1.

Accumulation of AD-HA-SLR1, HA-GID2^{L76A}, and HA-GID1 protein in yeast cells. Crude protein extracts from yeast grown in the absence or presence of 10^{-4} M GA_4 were subject to immunoblot analysis and detected using HA antibody for HA-SLR1 and HA-GID2^{L76A}, and anti-GID1 antibody for HA-GID1. The loading control of Coomassie Brilliant Blue (CBB) staining is shown in the bottom panels.

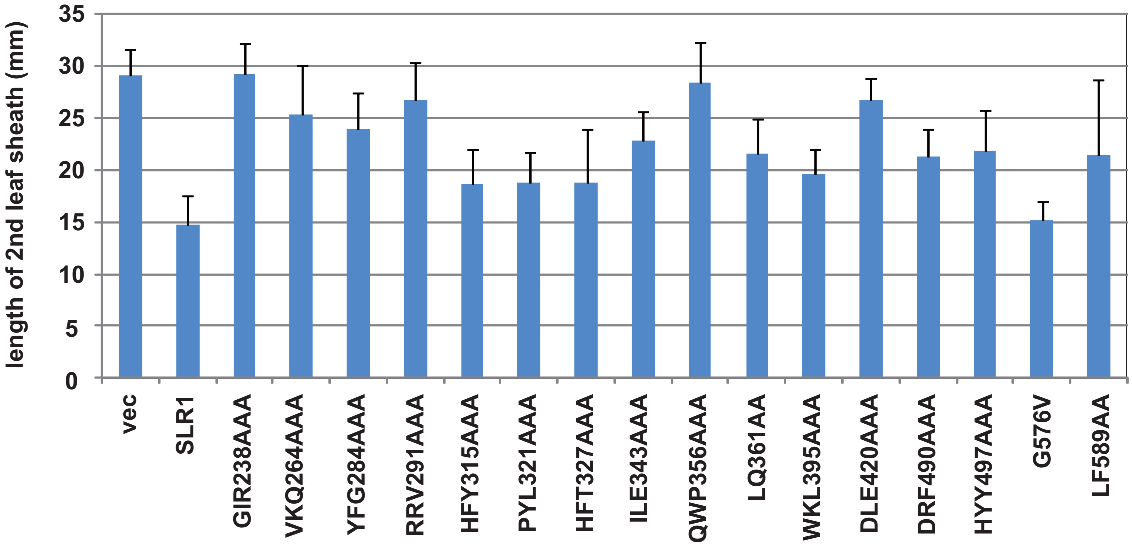


Supplemental Figure 4. Effect of GID1 Amino Acid Substitutions on SLR1-GID2 Interaction in Yeast.

Y3H assay using $GID2^{L76A}$ as bait, SLR1 as prey, and alanine-mutated GID1 proteins (mGID1s) as third clones with 10^{-4} M GA_4. mGID1s previously shown to interact with SLR1 in the Y2H liquid assay (Ueguchi-Tanaka et al., 2007) were used as third clones (means ± SD; n = 3). GID1 and *gid1-1* mutant protein used as a positive and negative control, respectively. Interacting activities are shown as relative rates, with activity of SLR1-GID2 in the presence of wild-type GID1 set 1.



Supplemental Figure 5. Comparison of amino acid sequences of vascular plant DELLA proteins. Sequences have been aligned from the poly S/T/V domain to the end of each protein. Amino acids that were subject to alanine scanning are shown in blue boxes at the bottom of the alignment. Red boxes indicate sites that could not be expressed in yeast when mutated and were not studied further. Black and grey indicate identical and similar amino acids, respectively. Zm, *Zea mays*; At, *Arabidopsis thaliana*; Sm, *Selaginella moellendorffii*.



Supplemental Figure 6. Comparison of second leaf sheath length of transgenic seedlings grown under GA-deficient conditions. Seedlings were grown in the presence of 10^{-6} M uniconazole. Wild-type and mSLR1s fused with FLAG tag were overproduced in wild-type T65 rice. vec, T65 transformed with *proAct*-FLAG/pCAMBIA control vector. The measurements are the means ± SE (n = 10 to 17).

Supplemental Table 1. Primers used in this study

Primer	Sequence (5' to 3')	Note
Y2H & Y3H experiment/ amplifying DNA fragments for cloning into pGADT7 vector		
pGADT7.slr1-d4.F	GGAATTCCATATGAAGCGCGAGTACCAAGA	5' primer amplifying *slr1-d4* with *Nde*I site
pGADT7.slr1-d4.R	GCAAGCTTGAATTCCTAGTAGTAGAGGTTAG	3' primer amplifying *slr1-d4* with *Eco*RI site
pGADT7. SLR1 (E4-R125).F	GGAATTCGAGTACCAAGAAGCCGGCGG	5' primer amplifying *SLR1 (E4-R125)* with *Eco*RI site
pGADT7. SLR1 (E4-R125).R	TCCCCCGGGGCGGGCAGCCGGCGGCGCTG	3' primer amplifying *SLR1 (E4-R125)* with *Sma*I site
pGADT7.GID1.F	GGAATTCATGGCCGGCAGCGACGAGGT	5' primer amplifying *GID1* with *Eco*RI site
pGADT7.GID1.R	GGAATTCCTAGTAGTAGAGGTTAGCGT	3' primer amplifying *GID1* with *Eco*RI site
Y2H & Y3H experiments/ amplifying DNA fragments for cloning into pBRIDGE vector		
pBr BD-GID2.F	GGAATTCATGAAGTTCCGCTCTGATTC	5' primer amplifying *GID2* with *Eco*RI site
pBr BD-GID2.R	CGGGATCCCTACCCGCATTGGCCCCCTC	3' primer amplifying *GID2* with *Bam*HI site
pBr BD-GID2 3rd-GID1.F	GGAATTCATGGCCGGCAGCGACGAGGT	5' primer amplifying *GID1* with *Bgl*II site
pBr BD-GID2 3rd-GID1.R	CGGGATCCCTAGTAGTAGAGGTTAGCGT	3' primer amplifying *GID1* with *Bgl*II site
pBr BD-GID1.F	GGAATTCATGGCCGGCAGCGACGAG	5' primer amplifying *GID1* with *Eco*RI site
pBr BD-GID1.R	CGGGATCCCTAGTAGTAGAGGTTAGC	3' primer amplifying *GID1* with *Bam*HI site
pBr BD-GID1 3rd-GID2.F	GAAGATCTATGAAGTTCCGCTCTGAT	5' primer amplifying *GID2* or *GID2*^{L76A} with *Bgl*II site
pBr BD-GID1 3rd-GID2.R	GAAGATCTCTACCCGCATTGGCCCCC	3' primer amplifying *GID2* or *GID2*^{L76A} with *Bgl*II site
pBr BD-GID2^{L76A}.F	GGAATTCATGAAGTTCCGCTCTGATTC	3' primer amplifying *GID2*^{L76A} with *Eco*RI site
pBr BD-GID2^{L76A}.R	TCCCCCGGGCTACCCGCATTGGCCCCCTC	3' primer amplifying *GID2*^{L76A} with *Sma*I site
pBr BD-GID2 (E114-P193) 3rd-GID1.F	GGAATTCGAGGCCGCGTGCGTGCGGGA	3' primer amplifying *GID2 (E114-P193)* with *Eco*RI site
pBr BD-GID2 (E123-P193) 3rd-GID1.F	GGAATTCAACCTCGGCTTCTCCGAGCG	3' primer amplifying PpGID1L2 with *Eco*RI site
pBr BD-GID2 (E114-P193) 3rd-GID1.R	TCCCCCGGGAGGCATATTCTGAAAGAACC	3' primer amplifying *GID2 (E114-P193)* or *GID2 (E123-P193)* with *Sma*I site
pBr BD- GID2^{L76A} 3rd-mGID1s.F	TCCCCCGGGAATGGCCGGCAGCGACGAGGT	3' primer amplifying *mGID1s* with *Sma*I site
pBr BD- GID2^{L76A} 3rd-mGID1s.R	TCCCCCGGGCTAGTAGTAGAGGTTAGCGT	3' primer amplifying *mGID1s* with *Sma*I site
Production of GST-SLR1, its mutant proteins (GST-mSLR1s), and GST-SLR1 (E4-R125)/amplifying various forms of *SLR1* for cloning into pGEX-6P-1 vector, and amplifying various forms of *GST-SLR1s* for cloning into pEU101 vector		
pGEX6P. SLR1.F	GGAATTCATGAAGCGCGAGTACCAAGA	5' primer amplifying *SLR1* or *mSLR1s* with *Eco*RI site
pGEX6P. SLR1.R	TCCCCCGGGTCACGCCGCGGCGACGCGCC	3' primer amplifying *SLR1* or *mSLR1s* with *Sma*I site
pGEX6P. SLR1 (E4-R125).F	GGAATTCGAGTACCAAGAAGCCGGCGG	5' primer amplifying *SLR1 (E4-R125)* with *Eco*RI site
pGEX6P. SLR1 (E4-R125).R	TCCCCCGGGGCGGGCAGCCGGCGGCGCTG	3' primer amplifying *SLR1 (E4-R125)* with *Sma*I site
pEU101.GST-SLR1.F	GCCGATATCATGTCCCCTATACTAGGTT	5' primer amplifying *GST-SLR1 or GST-mSLR1s, and GST-SLR1 (E4-R125)* with
pEU101.GST-SLR1.R	TCCCCCGGGTCACGCCGCGGCGACGCGCC	3' primer amplifying *GST-SLR1* or *GST-HYY497AAA SLR1* with *Sma*I site
pEU101.GST-mSLR1.R	GGGGTACCTCACGCCGCGGCGACGCGCC	3' primer amplifying *GST-mSLR1s* (except for *GST-HYY497AAA SLR1)* with *Kpn*I site
pEU101.GST-SLR1 (4E-R125).R	TCCCCCGGGTCACGCCGCGGCGACGCGCC	3' primer amplifying SLR1 (4E-R125) with *Sma*I site
Transgenic experiment/ amplifying *SLR1* and *mSLR1*s for cloning into pAct3XFLAG/pCAMBIA vector		
pCAMBI.pAct-3XFLAG-SLR1.F	TCCCCCGGGATGAAGCGCGAGTACCAAGA	5' primer amplifying *SLR1 or mSLR1s* with *Sma*I site
pCAMBI.pAct-3XFLAG-SLR1.R	GACTAGTTCACGCCGCGGCGACGCGCC	3' primer amplifying *SLR1* or *mSLR1s* with *Spe*I site
Production of recombinant SLR1, GID1, GID2, and OsSkp15 protein for in vitro pull down experiments		
pGEX4T.SLR1.F	GGAATTCATGAAGCGCGAGTACCAAGA	5' primer amplifying *SLR1* with *Eco*RI site
pGEX4T.SLR1.R	GGAATTCTCACGCCGCGGCGACGCGCC	3' primer amplifying *SLR1* with *Eco*RI site
pET52b.cMyc-GID1.F	GGGGTACCAAATGGAGGAGCAGAAGCTG	5' primer amplifying *cMyc-GID1* with *Kpn*I site
pET52b.cMyc-GID1.R	CGGGATCCTTGTAGTAGAGGTTAGCGTT	3' primer amplifying *cMyc-GID1* with *Bam*HI site
pGEX SLR1- rbs+cMyc-GID1.F	GCCGATATCCCCCTCTAGAAATAATTTT	5' primer amplifying *rbs+cMyc-GID1* with *EcoR*V site
pGEX SLR1- rbs+cMyc-GID1.R	GGCGATATCTTAGTGGTGGTGATGGTGA	3' primer amplifying *rbs+cMyc-GID1* with *EcoR*V site
pET3d-OsSkp15.F	CGGGATCCATGGCGGCTGAGGGAGAGAA	5' primer amplifying *OsSkp15* with *Bam*HI site
pET3d-OsSkp15.R	CGGGATCCCTACTCAAAAGCCCACTGGT	3' primer amplifying *OsSkp15* with *Bam*HI site
pGEX rbs-OsSkp15.F	CCGCTCGAGCGGTTTCCCTCTAGAAATAA	5' primer amplifying *rbs+OsSkp15* with *Xho*I site
pGEX rbs-OsSkp15.R	CCGCTCGAGCTACTCAAAAGCCCACTGGT	3' primer amplifying *rbs+OsSkp15* with *Xho*I site
pGEX 3HA-GID2+rbs-OsSkp15.F	GGAATTCATGAAGTTCCGCTCTGATTC	5' primer amplifying *3HA-GID2* with *Eco*RI site
pGEX 3HA-GID2+rbs-OsSkp15.R	TCCCCCGGGCTACCCGCATTGGCCCCCTC	3' primer amplifying *3HA-GID2* with *Sma*I site
pET15b 3HA-GID2+rbs-OsSkp15.F	GCCGATATCGAATTCATGGAGTACCCAT	3' primer amplifying *3HA-GID2+rbs-OsSkp15* with *EcoR*V site
pET15b 3HA-GID2+rbs-OsSkp15.R	GGCGATATCCTCGAGGGATCCCTACTCAA	3' primer amplifying *3HA-GID2+rbs-OsSkp15* with *EcoR*V site
Construction for BiFc		
pBI101.GID1.F	TCCCCCGGGATGGCCGGCAGCGACGAGGT	5' primer amplifying *GID1* with *Sma*I site
pBI101.GID1.R	CGAGCTCCTAGTAGTAGAGGTTAGCGT	3' primer amplifying*GID1* with *Sac*I site
Constructions for GID2 alanine scanning		
KFR2AAA..GID2.F	CCGAATTCATGGCAGCAGCATCTGATTCGT	
KFR2AAA..GID2.R	ACGAATCAGATGCTGCTGCCATGAATTCGG	
KR30AA.GID2.F	GACGAGCCGGCCGCCGCCCAGCGGACCGAT	
KR30AA.GID2.R	ATCGGTCCGCTGGGCGGCGGCCGGCTCGTC	
SSS39AAA.GID2.F	ATCCGTCCTCCGCCGCCGCCCAGGGCGAGG	
SSS39AAA.GID2.R	CCTCGCCCTGGGCGGCGGCGGAGGACGGAT	
SSQ48AAA.GID2.F	AGGCCTCCTCTGCCGCAGCCCCGCCACCGC	
SSQ48AAA.GID2.R	GCGGTGGCGGGGCTGCGGCAGAGGAGGCCT	
EEQ58AAA.GID2.F	AGCAGCAGCAGGCCGCAGCCCCTCCGGAGG	
EEQ58AAA.GID2.R	CCTCCGGAGGGGCTGCGGCCTGCTGCTGCT	
EQP69AAA.GID2.F	CGGGAGAGGGCGCCGCAGCCAGGGTTCCGG	
EQP69AAA.GID2.R	CCGGAACCCTGGCTGCGGCGCCCTCTCCCG	
L76A.GID2.F	CGAGGGTTCCGGATGCCGGGGAGGACCTGG	
L76A.GID2.R	CCAGGTCCTCCCCGGCATCCGGAACCCTCG	
L80A.GID2.F	ATCTCGGGGAGGACGCCGTGTTCGAGGTGC	
L80A.GID2.R	GCACCTCGAACACGGCGTCCTCCCCGAGAT	
V81A.GID2.F	TCGGGGAGGACCTGGCCTTCGAGGTGCTGC	
V81A.GID2.R	GCAGCACCTCGAAGGCCAGGTCCTCCCCGA	
L85A.GID2.F	TGGTGTTCGAGGTGGCCCGGCGAGCGGAGG	

L85A.GID2.R	CCTCCGCTCGCCGGGCCACCTCGAACACCA
R87A.GID2.F	TCGAGGTGCTGCGGGCAGCGGAGGCGCGGA
R87A.GID2.R	TCCGCGCCTCCGCTGCCCGCAGCACCTCGA
R91A.GID2.F	GGCGAGCGGAGGCGGCCACGCTGGCGGCCG
R91A.GID2.R	CGGCCGCCAGCGTGGCCGCCTCCGCTCGCC
L93A.GID2.F	CGGAGGCGCGGACGGCCGCGGCCGCGGCGT
L93A.GID2.R	ACGCCGCGGCCGCGGCCGTCCGCGCCTCCG
C98A.GID2.F	TGGCGGCCGCGGCGGCCGTGAGCAGGGGGT
C98A.GID2.R	ACCCCCTGCTCACGGCCGCCGCGGCCGCCA
V99A.GID2.F	CGGCCGCGGCGTGCGCCAGCAGGGGGTGGC
V99A.GID2.R	GCCACCCCCTGCTGGCGCACGCCGCGGCCG
R101A.GID2.F	CGGCGTGCGTGAGCGCCGGGTGGCGGCAGC
R101A.GID2.R	GCTGCCGCCACCCGGCGCTCACGCACGCCG
W103A.GID2.F	GCGTGAGCAGGGGGGCCCGGCAGCTCGCGG
W103A.GID2.R	CCGCGAGCTGCCGGGCCCCCCTGCTCACGC
L106A.GID2.F	GGGGGTGGCGGCAGGCCGCGGAGGACGAGC
L106A.GID2.R	GCTCGTCCTCCGCGGCCTGCCGCCACCCCC
D109A.GID2.F	GGCAGCTCGCGGAGGCCGAGCGGCTCTGGG
D109A.GID2.R	CCCAGAGCCGCTCGGCCTCCGCGAGCTGCC
E110A.GID2.F	AGCTCGCGGAGGACGCCCGGCTCTGGGAGG
E110A.GID2.R	CCTCCCAGAGCCGGGCGTCCTCCGCGAGCT
W113A.GID2.F	AGGACGAGCGGCTCGCCGAGGCCGCGTGCG
W113A.GID2.R	CGCACGCGGCCTCGGCGAGCCGCTCGTCCT
E114A.GID2.F	ACGAGCGGCTCTGGGCCGCCGCGTGCGTGC
E114A.GID2.R	GCACGCACGCGGCGGCCCAGAGCCGCTCGT
C117A.GID2.F	TCTGGGAGGCCGCGGCCGTGCGGGAGTGGG
C117A.GID2.R	CCCACTCCCGCACGGCCGCGGCCTCCCAGA
W121A.GID2.F	CGTGCGTGCGGGAGGCCGCGAACCTCGGCT
W121A.GID2.R	AGCCGAGGTTCGCGGCCTCCCGCACGCACG
N123A.GID2.F	TGCGGGAGTGGGCGGCCCTCGGCTTCTCCG
N123A.GID2.R	CGGAGAAGCCGAGGGCCGCCCACTCCCGCA
E128A.GID2.F	ACCTCGGCTTCTCCGCCCGGCAGCTCCGGG
E128A.GID2.R	CCCGGAGCTGCCGGGCGGAGAAGCCGAGGT
L131A.GID2.F	TCTCCGAGCGGCAGGCCCGGGCCGTGGTGC
L131A.GID2.R	GCACCACGGCCCGGGCCTGCCGCTCGGAGA
R132A.GID2.F	CCGAGCGGCAGCTCGCCGCCGTGGTGCTCT
R132A.GID2.R	AGAGCACCACGGCGGCGAGCTGCCGCTCGG
V134A.GID2.F	GGCAGCTCCGGGCCGCCGTGCTCTCCCTCG
V134A.GID2.R	CGAGGGAGAGCACGGCGGCCCGGAGCTGCC
V135A.GID2.F	AGCTCCGGGCCGTGGCCCTCTCCCTCGGTG
V135A.GID2.R	CACCGAGGGAGAGGGCCACGGCCCGGAGCT
L136A.GID2.F	TCCGGGCCGTGGTGGCCTCCCTCGGTGGAT
L136A.GID2.R	ATCCACCGAGGGAGGCCACCACGGCCCGGA
L138A.GID2.F	CCGTGGTGCTCTCCGCCGGTGGATTCCGCC
L138A.GID2.R	GGCGGAATCCACCGGCGGAGAGCACCACGG
G139A.GID2.F	TGGTGCTCTCCCTCGCCGGATTCCGCCGGC
G139A.GID2.R	GCCGGCGGAATCCGGCGAGGGAGAGCACCA
G140A.GID2.F	TGCTCTCCCTCGGTGCCTTCCGCCGGCTCC
G140A.GID2.R	GGAGCCGGCGGAAGGCACCGAGGGAGAGCA
F141A.GID2.F	TCTCCCTCGGTGGAGCCCGCCGGCTCCACG
F141A.GID2.R	CGTGGAGCCGGCGGGCTCCACCGAGGGAGA
R143A.GID2.F	TCGGTGGATTCCGCGCCCTCCACGCTGTCT
R143A.GID2.R	AGACAGCGTGGAGGGCGCGGAATCCACCGA
L144A.GID2.F	GTGGATTCCGCCGGGCCCACGCTGTCTACA
L144A.GID2.R	TGTAGACAGCGTGGGCCCGGCGGAATCCAC
H145A.GID2.F	GATTCCGCCGGCTCGCCGCTGTCTACATCC
H145A.GID2.R	GGATGTAGACAGCGGCGAGCCGGCGGAATC
V147A.GID2.F	GCCGGCTCCACGCTGCCTACATCCGCCCCC
V147A.GID2.R	GGGGGCGGATGTAGGCAGCGTGGAGCCGGC
I149A.GID2.F	TCCACGCTGTCTACGCCCGCCCCCTGCAGT
I149A.GID2.R	ACTGCAGGGGGCGGGCGTAGACAGCGTGGA
P151A.GID2.F	CTGTCTACATCCGCGCCCTGCAGTGGCGTG
P151A.GID2.R	CACGCCACTGCAGGGCGCGGATGTAGACAG
L152A.GID2.F	TCTACATCCGCCCCGCCCAGTGGCGTGGCG
L152A.GID2.R	CGCCACGCCACTGGGCGGGGCGGATGTAGA
QWR153AAA.GID2.F	ATCCGCCCCCTGGCCGCCGCCGGCGCCGGCG
QWR153AAA.GID2.R	CGCCGGCGCCGGCGGCGGCCAGGGGGCGGAT
GAG156AAA.GID2.F	TGCAGTGGCGTGCCGCAGCCGTGCCCAGGC
GAG156AAA.GID2.R	GCCTGGGCACGGCTGCGGCACGCCACTGCA
VPR159AAA.GID2.F	GTGGCGCCGGCGCCGCCGCCCAACAGGGGA
VPR159AAA.GID2.R	TCCCCTGTTGGGCGGCGGCGCCGGCGCCAC
QQG162AAA.GID2.F	GCGTGCCCAGGGCAGCCGCCAGGCGGCAGC
QQG162AAA.GID2.R	GCTGCCGCCTGGCGGCTGCCCTGGGCACGC
R165A.GID2.F	CCAGGCAACAGGGGGCCCGGCAGCCGCCGG
R165A.GID2.R	CCGGCGGCTGCCGGGCCCCCTGTTGCCTGG
RQP166AAA.GID2.F	AACAGGGGAGGGCCGCAGCCCCGGTGAGGT
RQP166AAA.GID2.R	ACCTCACCGGGGCTGCGGCCCTCCCCTGTT
R174A.GID2.F	CGGTGAGGTTGGGCGCCGACCAGGTTCAGC
R174A.GID2.R	GCTGAACCTGGTCGGCGCCCAACCTCACCG
D175A.GID2.F	TGAGGTTGGGCCGGGCCCAGGTTCAGCTCT
D175A.GID2.R	AGAGCTGAACCTGGGCCCGGCCCAACCTCA
V177A.GID2.F	TGGGCCGGGACCAGGCCCAGCTCTCGCTGT
V177A.GID2.R	ACAGCGAGAGCTGGGCCTGGTCCCGGCCCA

L179A.GID2.F	GGGACCAGGTTCAGGCCTCGCTGTCACTGT
L179A.GID2.R	ACAGTGACAGCGAGGCCTGAACCTGGTCCC
S180A.GID2.F	ACCAGGTTCAGCTCGCCCTGTCACTGTTCT
S180A.GID2.R	AGAACAGTGACAGGGCGAGCTGAACCTGGT
L181A.GID2.F	AGGTTCAGCTCTCGGCCTCACTGTTCTCCA
L181A.GID2.R	TGGAGAACAGTGAGGCCGAGAGCTGAACCT
S182A.GID2.F	TTCAGCTCTCGCTGGCACTGTTCTCCATTG
S182A.GID2.R	CAATGGAGAACAGTGCCAGCGAGAGCTGAA
L183A.GID2.F	AGCTCTCGCTGTCAGCCTTCTCCATTGGGT
L183A.GID2.R	ACCCAATGGAGAAGGCTGACAGCGAGAGCT
S185A.GID2.F	CGCTGTCACTGTTCGCCATTGGGTTCTTTC
S185A.GID2.R	GAAAGAACCCAATGGCGAACAGTGACAGCG
I186A.GID2.F	TGTCACTGTTCTCCGCCGGGTTCTTTCAGA
I186A.GID2.R	TCTGAAAGAACCCGGCGGAGAACAGTGACA
F189A.GID2.F	TCTCCATTGGGTTCGCCCAGAATATGCCTT
F189A.GID2.R	AAGGCATATTCTGGGCGAACCCAATGGAGA
QN190AA.GID2.F	ATTGGGTTCTTTGCCGCCATGCCTTGTCCT
QN190AA.GID2.R	AGGACAAGGCATGGCGGCAAAGAACCCAAT
192MA.GID2.F	GGTTCTTTCAGAATGCCCCTTGTCCTAAGA
192MA.GID2.R	TCTTAGGACAAGGGGCATTCTGAAAGAACC
PCP193AAA.GID2.F	TTCAGAATATGGCCGCAGCCAAGAAAGACA
PCP193AAA.GID2.R	TGTCTTTCTTGGCTGCGGCCATATTCTGAA
DKG198AAA.GID2.F	GTCCTAAGAAAGCCGCCGCAAATGACAGTG
DKG198AAA.GID2.R	CACTGTCATTTGCGGCGGCTTTCTTAGGAC
SDK203AAA.GID2.F	AGGGAAATGACGCCGCAGCCAATGGAGGGG
SDK203AAA.GID2.R	CCCCTCCATTGGCTGCGGCGTCATTTCCCT
GGG207AAA.GID2.F	GTGATAAGAATGCAGCCGCCCAATGCGGGT
GGG207AAA.GID2.R	ACCCGCATTGGGCGGCTGCATTCTTATCAC
QCG210AAA.GID2.F	ATGGAGGGGGCGCAGCCGCCTAGCCCGGGA
QCG210AAA.GID2.R	TCCCGGGCTAGGCGGCTGCGCCCCCTCCAT

Constructions for SLR1 alanine scanning

STY153AAA.SLR1.F	ACTCGTCGAGTGCCGCAGCCGCCCTCAGGC
STY153AAA.SLR1.R	GCCTGAGGGCGGCTGCGGCACTCGACGAGT
SSS190AAA.SLR1.F	GCGGCAGCACGGCCGCAGCCTCATCGTCGT
SSS190AAA.SLR1.R	ACGACGATGAGGCTGCGGCCGTGCTGCCGC
VVV229AAA.SLR1.F	CCGCCGTGCCGGCCGCAGCCGTTGACACGC
VVV229AAA.SLR1.R	GCGTGTCAACGGCTGCGGCCGGCACGGCGG
GIR238AAA.SLR1.F	CGCAGGAGGCTGCCGCAGCCCTGGTGCACG
GIR238AAA.SLR1.R	CGTGCACCAGGGCTGCGGCAGCCTCCTGCG
VQQ252AAA.SLR1.F	GCGCGGAGGCCGCCGCAGCCGAGAACTTCG
VQQ252AAA.SLR1.R	CGAAGTTCTCGGCTGCGGCGGCCTCCGCGC
VKQ264AAA.SLR1.F	CGGAGGCGCTGGCCGCAGCCATCCCCACGC
VKQ264AAA.SLR1.R	GCGTGGGGATGGCTGCGGCCAGCGCCTCCG
QGG274AAA.SLR1.F	TGGCCGCGTCCGCCGCAGCCGCCATGCGCA
QGG274AAA.SLR1.R	TGCGCATGGCGGCTGCGGCGGACGCGGCCA
YFG284AAA.SLR1.F	AGGTCGCTGCCGCCGCAGCCGAGGCCCTCG
YFG284AAA.SLR1.R	CGAGGGCCTCGGCTGCGGCGGCAGCGACCT
RRV291AAA.SLR1.F	AGGCCCTCGCCGCCGCAGCCTACCGCTTCC
RRV291AAA.SLR1.R	GGAAGCGGTAGGCTGCGGCGGCGAGGGCCT
HFY315AAA.SLR1.F	TTCTGCACGCCGCCGCAGCCGAGTCCTGCC
HFY315AAA.SLR1.R	GGCAGGACTCGGCTGCGGCGGCGTGCAGAA
PYL321AAA.SLR1.F	ACGAGTCCTGCGCCGCAGCCAAGTTCGCCC
PYL321AAA.SLR1.R	GGGCGAACTTGGCTGCGGCGCAGGACTCGT
HFT327AAA.SLR1.F	TCAAGTTCGCCGCCGCCGCCGCAAATCAAG
HFT327AAA.SLR1.R	CTTGATTTGCGGCGGCGGCGGCGAACTTGA
ILE334AAA.SLR1.F	CAAATCAAGCCGCCGCAGCCGCTTTCGCCG
ILE334AAA.SLR1.R	CGGCGAAAGCGGCTGCGGCGGCTTGATTTG
RVH343AAA.SLR1.F	CCGGCTGCCACGCCGCAGCCGTCGTCGACT
RVH343AAA.SLR1.R	AGTCGACGACGGCTGCGGCGTGGCAGCCGG
QWP356AAA.SLR1.F	AGCAGGGGATGGCCGCCGCCGCTCTCCTCC
QWP356AAA.SLR1.R	GGAGGAGAGCGGCGGCGGCCATCCCCTGCT
LQ361AAA.SLR1.F	GGCCAGCTCTCGCCGCAGCCCTCGCCCTTC
LQ361AAA.SLR1.R	GAAGGGCGAGGGCTGCGGCGAGAGCTGGCC
GPP370AAA.SLR1.F	TTCGTCCCGGCGCCGCAGCCTCGTTCCGCC
GPP370AAA.SLR1.R	GGCGGAACGAGGCTGCGGCGCCGGGACGAA
RLT375AAA.F	CCCCATCGTTCGCCGCCGCCGGCGTCGGCC
RLT375AAA.R	GGCCGACGCCGGCGGCGGCGAACGATGGGG
LQQ390AAA.SLR1.F	AGACCGACGCCGCCGCAGCCGTGGGTTGGA
LQQ390AAA.SLR1.R	TCCAACCCACGGCTGCGGCGGCGTCGGTCT
WKL395AAA.SLR1.F	AGCAGGTGGGTGCCGCAGCCGCCCAGTTCG
WKL395AAA.SLR1.R	CGAACTGGGCGGCTGCGGCACCCACCTGCT
QYR409AAA.SLR1.F	GCGTCGACTTCGCCGCAGCCGGACTCGTCG
QYR409AAA.SLR1.R	CGACGAGTCCGGCTGCGGCGAAGTCGACGC
DLE420AAA.SLR1.F	CCACTCTCGCGGCCGCAGCCCCGTTCATGC
DLE420AAA.SLR1.R	GCATGAACGGGGCTGCGGCCGCGAGAGTGG
VNS443AAA.SLR1.F	GGTGATCGCCGCCGCAGCCGTGTTCGAGCT
VNS443AAA.SLR1.R	AGCTCGAACACGGCTGCGGCGGCGATCACC
HRL450AAA.SLR1.F	GTTCGAGCTGGCCGCAGCCCTCGCGCAGCC
HRL450AAA.SLR1.R	GGCTGCGCGAGGGCTGCGGCCAGCTCGAAC
EKV460AAA.SLR1.F	CCGGCGCGCTGGCCGCAGCCCTGGGCACGG
EKV460AAA.SLR1.R	CCGTGCCCAGGGCTGCGGCCAGCGCGCCGG
EQE478AAA.SLR1.F	TCACCGTGGTAGCCGCAGCCGCCAACCACA

EQE478AAA.SLR1.R	TGTGGTTGGCGGCTGCGGCTACCACGGTGA
NHN482AAA.SLR1.F	AGCAGGAGGCCGCCGCAGCCTCCGGCTCAT
NHN482AAA.SLR1.R	ATGAGCCGGAGGCTGCGGCGGCCTCCTGCT
DRF490AAA.SLR1.F	GCTCATTCCTCGCCGCAGCCACCGAGTCGC
DRF490AAA.SLR1.R	GCGACTCGGTGGCTGCGGCGAGGAATGAGC
HYY497AAA.SLR1.F	CCGAGTCGCTGGCCGCAGCCTCCACCATGT
HYY497AAA.SLR1.R	ACATGGTGGAGGCTGCGGCCAGCGACTCGG
EVY533AAA.SLR1.F	AGGTCATGTCCGCCGCAGCCCTCGGCCGGC
EVY533AAA.SLR1.R	GCCGGCCGAGGGCTGCGGCGGACATGACCT
QIC539AAA.SLR1.F	CCTCGGCCGGGCCGCAGCCAACGTCGTGGC
QIC539AAA.SLR1.R	GCCACGACGTTGGCTGCGGCCCGGCCGAGG
RH554AA.SLR1.F	GAGCGCACGGAGGCCGCCGAGACGCTGGGG
RH554AA.SLR1.R	CCCCAGCGTCTCGGCGGCCTCCGTGCGCTC
RN562AA.SLR1.F	CTGGGGCAGTGGGCCGCCCGCCTCGGCCGC
RN562AA.SLR1.R	GCGGCCGAGGCGGGCGGCCCACTGCCCCAG
GF569AA.SLR1.F	CTCGGCCGCGCCGCCGCCGAGCCCGTGCAC
GF569AA.SLR1.R	GTGCACGGGCTCGGCGGCGGCGCGGCCGAG
LF589AA.SLR1.F	ACGCTCCTCGCGGCCGCCGCCGGCGGCGAC
LF589AA.SLR1.R	GTCGCCGCCGGCGGCGGCCGCGAGGAGCGT
GW608AA.SLR1.F	TGCCTCACGCTGGCCGCCCACACGCGCCCG
GW608AA.SLR1.R	CGGGCGCGTGTGGGCGGCCAGCGTGAGGCA
RP612AA.SLR1.F	GGCTGGCACACGGCCGCCCTCATCGCCACC
RP612AA.SLR1.R	GGTGGCGATGAGGGCGGCCGTGTGCCAGCC
S618A.SLR1.F	CGCTCATCGCCACCGCCGCATGGCGCGTCG
S618A.SLR1.R	CGACGCGCCATGCGGCGGTGGCGATGAGCG
W620A.SLR1.F	TCGCCACCTCGGCAGCCCGCGTCGCCGCGG
W620A.SLR1.R	CCGCGGCGACGCGGGCTGCCGAGGTGGCGA
R621A.SLR1.F	CCACCTCGGCATGGGCCGTCGCCGCGGCGT
R621A.SLR1.R	ACGCCGCGGCGACGGCCCATGCCGAGGTGG