

Figure S1. PCR result of 22 radish breeding lines ('SJ-1~22') using class I, II kinase domain of SRK (SRK-KD) primer set. (A) PCR amplification of class I SRK-KD using UVSRK-F + UVSRK-R primer set; (B): PCR amplification of class II SRK-KD using KS2 + KA2 primer set; M: 100bp size marker.

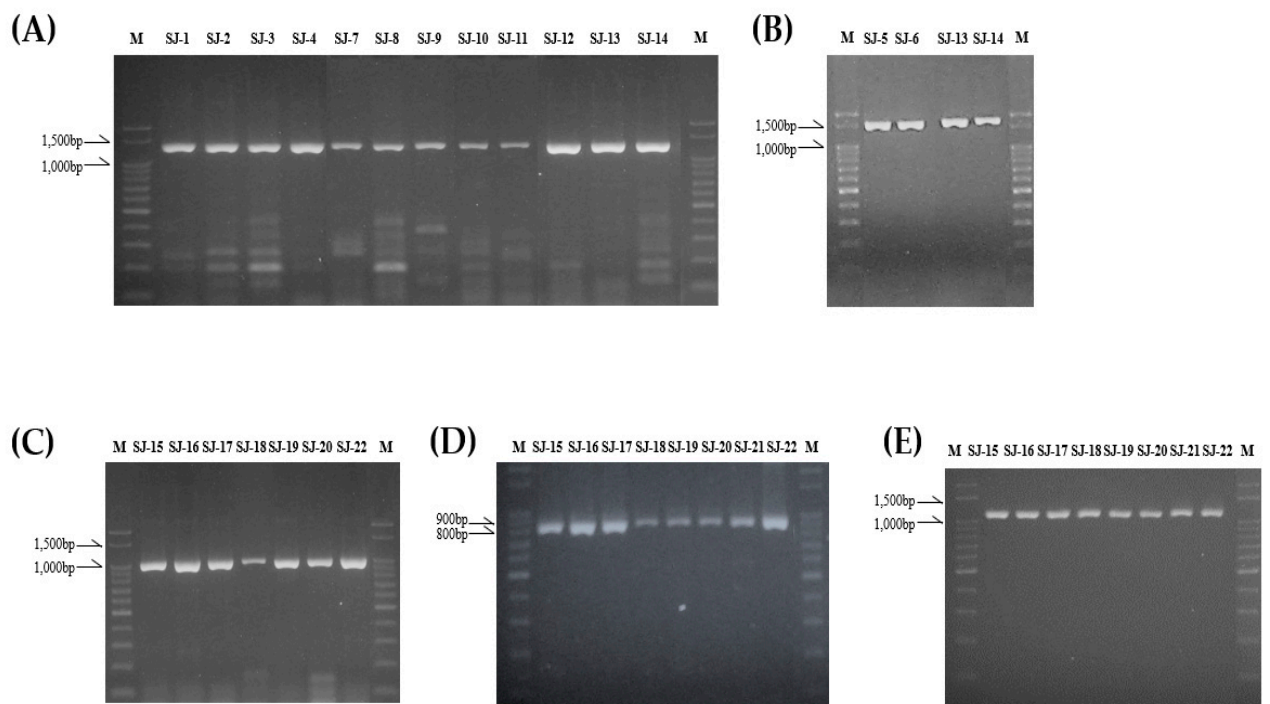


Figure S2. PCR result of 22 radish breeding lines ('SJ-1~22') using class I, II SLG primer set. (A) PCR amplification of class I SLG using SLG-I-F + SLG-I-R primer set; (B): PCR amplification of class I SLG using PS22 + SLG-I-R primer set; (C): PCR amplification of class II SLG using SLG-II-F + SLG-II-R primer set; (D): PCR amplification of class II SLG using Rs9 SLG-F + Rs9 SLG-R primer set; M: 100bp size marker; (E): PCR amplification of class II SLG using UVSLGII-F + UVSLGII-R primer set; M: 100bp size marker.

Figure S3. Continued.

Exon 7		
a	SRK1-KD(Haseyama)	GTGTTCAAGAACGTGCCGAGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGAGATTCTTAAGCCTAATCCGCCAGGTTATTACGTGCGAAGATGTCTT
	SRK2-KD(Haseyama)	GTGTTCAAGAACCTTGCAAGAGACAGACCAACATGTGCTCTGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCCAT
	SRK4-KD(Haseyama)	GTGTTCAAGATCTTGCAAGAGACAGACCAACCATGTCAATTTGTGGTTTGGATGCTTGGAAATGAAGCAACAGAGATTCTCAGCCTAAATGCGCAGGTTATTGCCTCGAAGAAAGTCCCT
	SRK5-KD(Haseyama)	GTGTTCAAGAACGTGCGGAGCAGACCAACATGTCGTGAGTGGTTCGGATGCTTGGAAAGTGAAGCAATAGAGATTCTCAGCCTAAACCCCGAGGTTATTGCCTCGTAAGAAAGTCATT
	SRK17-KD(Haseyama)	GTGTTCAAGAGCGTGCAGAGCACAGACCAACGATGTCGTGCGTAGTTTGGATGCTTGGAAAGTGAAGCAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCTTT
	SRK18-KD(Haseyama)	GCCTTCAAGAACGTGCAAGACAGACCAACGATGTCGTCTGTGGTTTGGATGCTTGGAAAGTGAAGTAAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCTTT
	SRK23-KD(Haseyama)	GTATTCAAGAACGTGCGGTGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK31-KD(Haseyama)	GTATTCAAGAACGTGCGGAGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK7-KD(Kim)	GTATTCAAGAACGTGCGG-----
	SRK10-KD(Kim)	GTATTCAAGAACGTGCGG-----
	SRK16-KD(Kim)	GTATTCAAGAACGTGCGG-----
	SRK17-KD(Kim)	GTATTCAAGAACGTGCGG-----
	SRK11-KD(Lim)	GTATTCAAGAACGTGCGGAGCACAGACCAACGATGTCGTGCGTGGTTTGGGTCCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK29-KD(Lim)	GTATTCAAGAACGTGCGGAGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK1-KD(Lim)	GTGTTCAAGAACCTTGCAAGAGACAGACCAACGATGTCGACTGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCTTT
	SRK8-KD(Lim)	GCCTTCAAGAACGTGCAAGACAGACCAACGATGTCGTCTGTGGTTTGGATGCTTGGAAAGTGAAGTAAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCTTT
	SRK10-KD(Lim)	GTATTCAAGAACGTGCGGTGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK16-KD(Lim)	GTATTCAAGAACGTGCGGAGCACAGACCAACGATGTCGTGCGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGCGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCATACCAAGTCTTT
	SRK18-KD(Lim)	GTGTTCAAGAACATGCAAGGACAGACCAACGATGCCACTGTGGTTTGGATGCTTGGAAAGTGAAGCAACAGAGATTCTCAGCCTAAACCCGCAATGTCATTGCCTCGAAGAAAGTCTCT
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b	SRK1-KD(Haseyama)	ATGAAATAATCCTTCATCAAGTAGGCTTTGCGATGACTATGAATCCT-----
	SRK2-KD(Haseyama)	ATGAACTTGATCCTTCATTAAAGTAGGCAGTGTACGACGATGAATCCTGG-----
	SRK4-KD(Haseyama)	ACGAACTTGATCCTTCATCAAGTAGGCAGTGTGCGAC-----
	SRK5-KD(Haseyama)	ATGAAATAAACCTTCCTCAAGTAGGCAGTGCAGCAGATGAATCCTGGAGC-----
	SRK17-KD(Haseyama)	ATGCAATAATCCTTCCTCAAGTAGGCATTGCGAAGACATGAATCCTGG-----
	SRK18-KD(Haseyama)	ATGAACTTGATCCTTCATCAAGTAGGCAGTGTGACGACGATCAATCC-----
	SRK23-KD(Haseyama)	ATGCAATAATCCTTCCTCAGTAGGCATCCAGCAGATGAATCCTGGAGCAGTGAACG
	SRK31-KD(Haseyama)	ATGCAATAATCCTTCCTCAGTAGGCATCCAGCAGATGAATCC-----
	SRK7-KD(Kim)	-----
	SRK10-KD(Kim)	-----
	SRK16-KD(Kim)	-----
	SRK17-KD(Kim)	-----
	SRK11-KD(Lim)	ATGCAATAATCCTTCCTCAGTAGGCATCCAGCAGATGAATCCTGGAGCAGTGAACG
	SRK29-KD(Lim)	ATGCAATAATCCTTCCTCAGTAGGCATCCAGCAGATGAATCCTGGAGCAGTGAACG
	SRK1-KD(Lim)	ATGAAACAG-----CAAGTAAAGCAGTTGGACGACGATGAATCCTGGACGGTGAAC
	SRK8-KD(Lim)	ATGAACTTGATCCTTCATCAAGTAGGCAGTGTGACGACGATCAATCCTGGAGCGTGAAC
	SRK10-KD(Lim)	ATGCAATAATCCTTCCTCAGTAGGCATCCAGCA-CGATGAATCCTGGAGCAGTGAACG
	SRK16-KD(Lim)	ATGCAATAATCCTTCCTCAGTAGGCCTCCAGCAGATGAATCCTGGAGCAGTGAACG
	SRK18-KD(Lim)	ATGAACTAGATCCTTCAGCAAGTAGGCAGTGTGATGACGATGAATCCTGGAGCGTGAACG
c	SRK1-KD(Haseyama)	993
	SRK2-KD(Haseyama)	984
	SRK4-KD(Haseyama)	1036
	SRK5-KD(Haseyama)	1344
	SRK17-KD(Haseyama)	979
	SRK18-KD(Haseyama)	1164
	SRK23-KD(Haseyama)	1020
	SRK31-KD(Haseyama)	963
	SRK7-KD(Kim)	823
	SRK10-KD(Kim)	824
	SRK16-KD(Kim)	824
	SRK17-KD(Kim)	824
	SRK11-KD(Lim)	1020
	SRK29-KD(Lim)	1021
	SRK1-KD(Lim)	1014
	SRK8-KD(Lim)	995
	SRK10-KD(Lim)	970
	SRK16-KD(Lim)	997
	SRK18-KD(Lim)	1027

Figure S3. Continued.

HV III-2		
a	SLG1 (Sakamoto)	TGAGCAGCGGGATCTAAGAGACCCGTCAGGTGGGTGTATAAGGAGGGCGCGCTTAGCTGCAGTGGTGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1085
	SLG2 (Sakamoto)	TGAGCAGTGGGATCTGAAAAGCTGGTCAGGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTAGAGAT-----GGTTTTACAGGATGAAGAACGTGAAGTTGCCAGAACTACGA1076
	SLG3 (Sakamoto)	TGAGCAGTGGGCTCTGAGAACTCTCAATAAGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGTGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTGCGA1079
	SLG4 (Sakamoto)	TGAGCAGTGGGCTCTGAGAACTCTCGATAAGTGGGTGTAAAAGGAGGACGCGCTTAGCTGCAGTGGTGATGGCTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1091
	SLG5 (Sakamoto)	TGAGCAGTGGGATCTGAGAGTCTGGGCAAGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1082
	SLG7 (Sakamoto)	TGATCAGTGGGATCTGGGAGACGGGTAGGTGGATGTATAAGGAGGACGCGCTTAGCTGCAGTGGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1105
	SLG8 (Sakamoto)	TGAGCAGTGGGATCTGAGAGACGGGTAGGTGGGTGTATCAGAGGACGCGCTTAGCTGCAGTGGTGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1085
	SLG18 (Haseyama)	TGAGCAGTGGGATCTGAAAAGCTGGTCAGGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA583
b	SLG25 (Haseyama)	AGAGCAGTGGGATCTGAGAGAACCGTCAAGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGTGAT-----AGCTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA588
	SLG31 (Haseyama)	AGAGCAGTGGTATCTGAGAGACTGGTCAAGTGGGTGTACAAAGGAGGACGCGCTTAGCTGCAGTGGGAT-----GTTTTTACTAGGATGAAGAAATGAAGTTGCCAGAACTACGA592
	SLG1 (Lim)	TGAAAAAGTGGAACTGAGATCCCACTCAGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1032
c	SLG8 (Lim)	TGAGCAGTGGGATCAGAGATCCTGGTCAGTGGGTGTATAAGGAGGACGCTGCTTAGCTGCAGTGGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA1104
	SLG10 (Lim)	AAAGCAGTGGGATATGCAAGATTGGTCAAGCGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTGGTGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAGACTACGA1039
	SLG16 (Lim)	TGATCAGTGGGATCTGGGAGACGGGTAGGTGGATGTATAAGGAGGACGCGCTTAGCTGCAGTGGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACGA995
	SLG18 (Lim)	TGAGCAGTGGGATCTGAGAGCCTGGTCAGGTGGGTGTATAAGGAGGACGCGCTTAGCTGCAGTAGAGAT-----GGTTTTACAGGATGAAGAAATGAAGTTGCCAGAACTACTA1062
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a	SLG1 (Sakamoto)	TGGCTATTGTGACAGGAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACGGCTGTGTGATTT1205
	SLG2 (Sakamoto)	TGGCTATTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACGGGTGTGTGATTT1196
	SLG3 (Sakamoto)	TGGCTATTGTGACCGGAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACAGGTGTGCTAAATTT1199
	SLG4 (Sakamoto)	TGGCTATTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCAGAAACCGTGGGACAGGCTGTGTGATTT1211
	SLG7 (Sakamoto)	TGGCAGCTGTGACCGGAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCTGATATCCGGAATGGTGGGACGGGTGTGTGATTT1202
	SLG8 (Sakamoto)	TGGCAGCTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACAGGTGTGTGATTT1225
	SLG18 (Haseyama)	TGGCAGCTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCTGATGTCCGGAATGGTGGGACGGGTGTGTGATTT1205
	SLG18 (Haseyama)	TGGCTATTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACGGGTGTGTGATTT703
b	SLG25 (Haseyama)	TGGCAGCTGTGACCGCAGTATTGATGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACGGGTGTGTGATTT688
	SLG31 (Haseyama)	TGGCAATTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCAGAAACCGTGGGACAGGCTGTGTGATTT712
	SLG1 (Lim)	TGGCAGCTGTGACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCTGATATCCGGAATGGTGGGACGGGATGTGTGATTT1152
c	SLG8 (Lim)	TGGCAGCTGTGACCCCAATATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCAGAAACCGTGGGACAGGCTGTGTGAG---1221
	SLG10 (Lim)	TGGCAGTGTGACCGGAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACGGGTGTGTGATTT1159
	SLG16 (Lim)	TGGCAGCTGTGACCCCAATATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGACTGTAAATTGTACCGGTTTGCAAAATGCGGATATCCGGAATGGTGGGACAGGTGTGTGATTT1115
	SLG18 (Lim)	TGGCAGCTGTCAACCGCAGTATTGGTGTGAAAAGATGTGAGAGAGGTGCCTTAGCGATTGTAAATTGTACCGGTTTGCAAAATGCTGATATCCGGAATGGTGGGACGGGTGTGTGATTT1182
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a	SLG1 (Sakamoto)	GGACAGGAGAGCTCGAGGATATCCGGACCTACCTTGCTGACGGTCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1289
	SLG2 (Sakamoto)	GGACCGGAGCGCTTGAGGATATCCGGACTTACTTTGCTGAAGGTCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1280
	SLG3 (Sakamoto)	GGACCGGAGCGCTTGACGATATCGGGAATTACGTTACTGACGGTCAAGATCTTTATGTCGATTGGCAGCTGCTGACCTTGTTT1283
	SLG4 (Sakamoto)	GGACCGGAGCAGCTTGACGATATCGGGAATTACGTTGCTGACGGTCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1295
	SLG5 (Sakamoto)	GGACCGGAGCGCTTGAGGATATCCGGACTTACTTTGCTGAAGGTCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1286
	SLG7 (Sakamoto)	GGACCGGAGCGCTTGACGATATCGGGAATTACGTTGCTGACGGTCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1309
	SLG8 (Sakamoto)	GGACCGGAAAGCTTGATGATATCAGGAATTATTTGAAAGACGGGCAAGATCTTTATGTCGATTGGCTGCTGCTGACCTTGTTT1289
	SLG18 (Haseyama)	GGACCGGAGCGCTTGAGGATATCCGGACTTACTTTGCTGAAGGTCAAGATCTTTATGTC-----762
b	SLG25 (Haseyama)	GGACCGGAGATCTCGAGGATATCCGGACATACCATGCCGAAGGTCAAGATCTTTATGTCAGTGGCTGCT-----759
	SLG31 (Haseyama)	GGACCGGAGACCTTGACGATATCGGGAATTACGTTGGTGAAGGTCAAGATCTTTATGTC-----771
	SLG8 (Lim)	GGACCGGAGAGCTCGAGGATATCCGGACTTACGTTGCTGACGGTCAAGATCTTTATGTCAGATTGG-----1220
c	SLG10 (Lim)	-----1221
	SLG16 (Lim)	GGACAGGAGAGCTCGAGGATATCCGGACCTACCTTGCTGACGCG-----1202
	SLG18 (Lim)	GGACCGGAGCGCTTGACGATATCGGGAATTACGTTGCTGACGGTCAAGATCTTT-----1168
	SLG18 (Lim)	GGACCGGAGCGCTTACGATATCGGGAATTACGTTGCTGACGGTCAAGATCTTT-----1235

Figure S4. Continued.

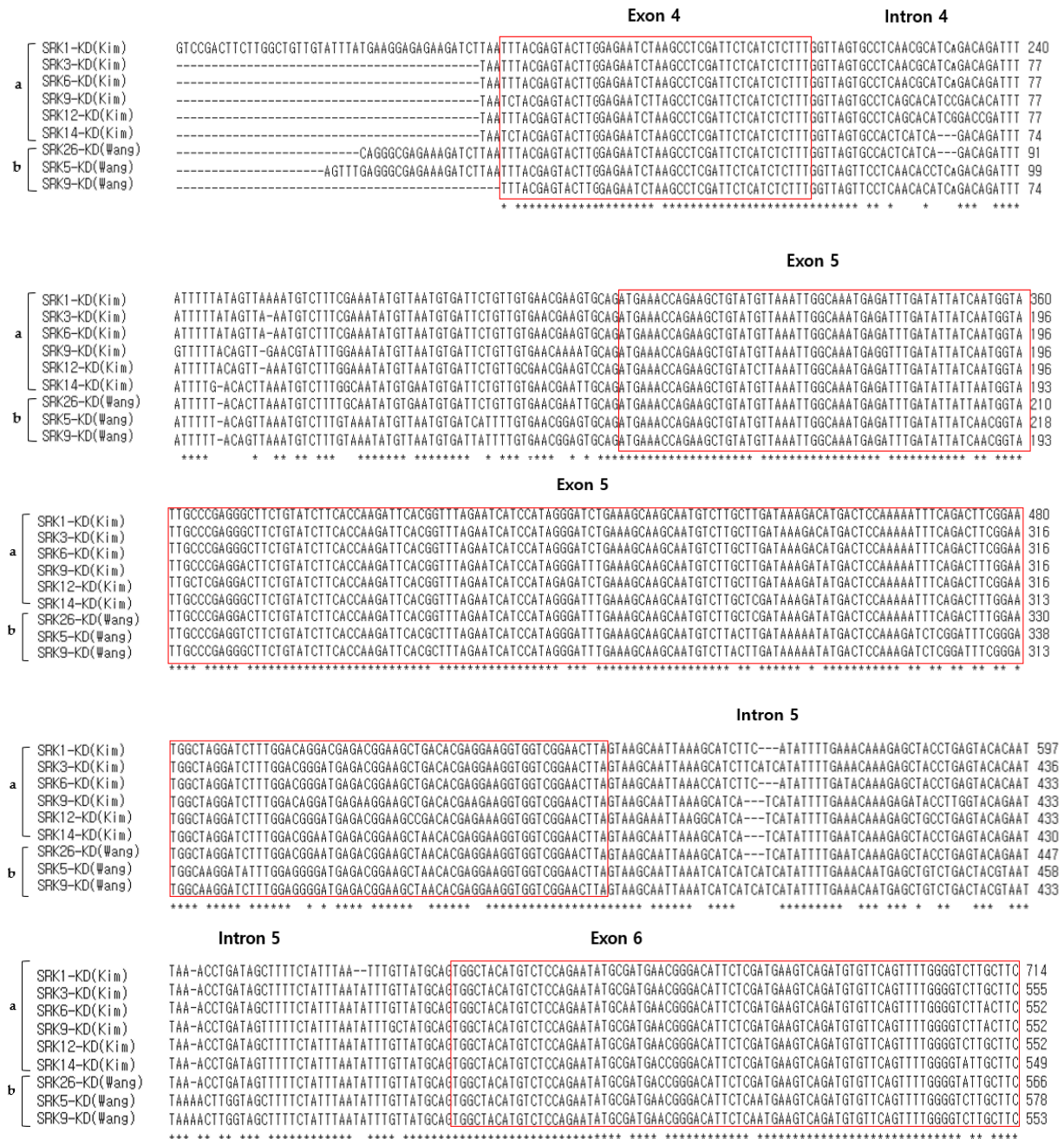


Figure S5. Multiple sequence alignment of the nucleotide sequences of the 9 class II S haplotype kinase domain of SRK alleles; a: S haplotype published by Kim (2016); b: S haplotype published by Haseyama (2018); c: S haplotype published by Lim (2002); Red box: 4th to 7th exons of the SRK; Asterisk: conserved nucleotide.

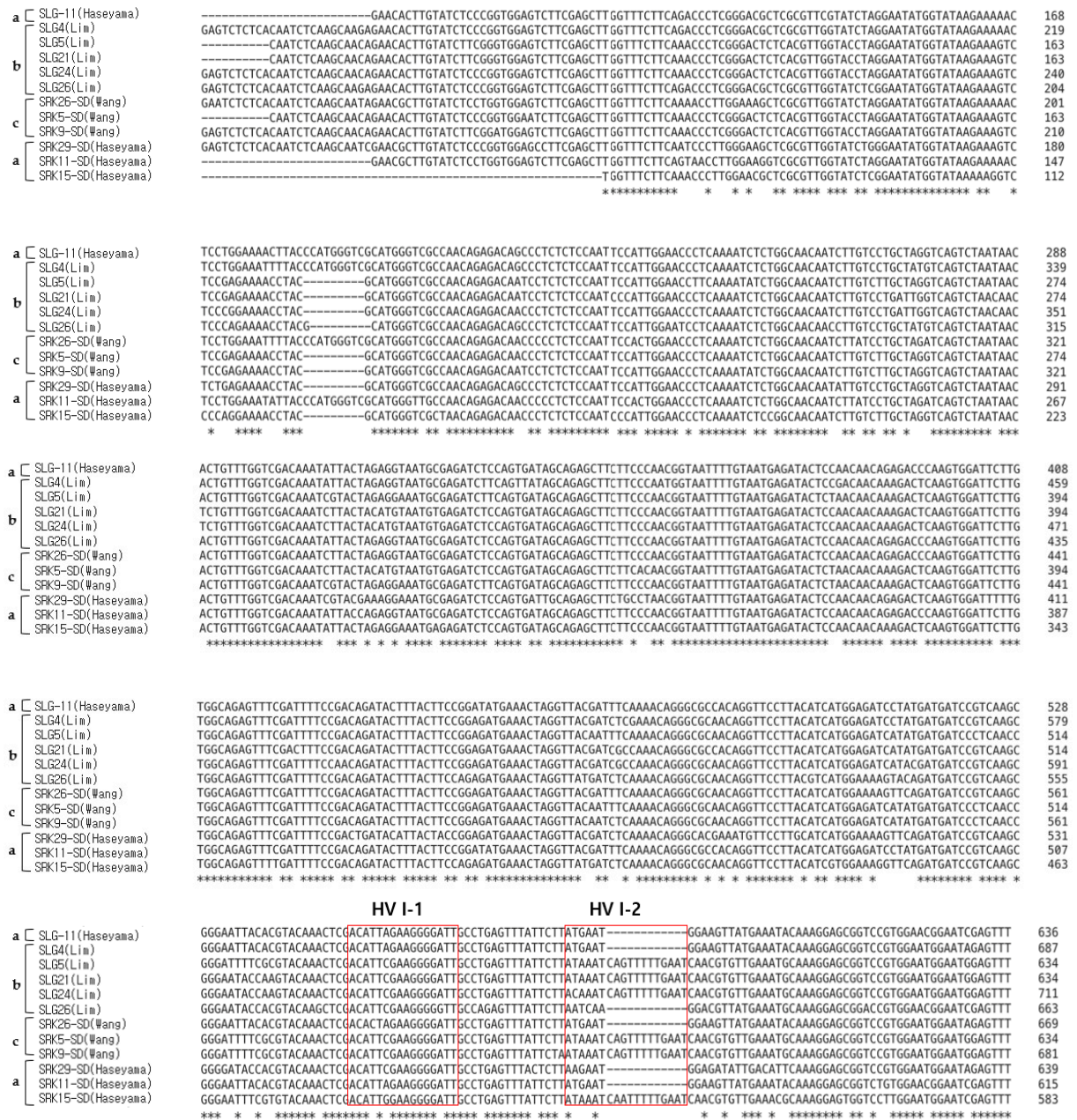


Figure S6. Multiple sequence alignment of the nucleotide sequences of the 12 class II S haplotype SLG and S domain of SRK alleles; a: S haplotype published by Haseyama (2018); b: S haplotype published by Lim (2002); c: S haplotype published by Wang (2018); Red box: hypervariable region I to III of SLG; Asterisk: conserved nucleotide.

Figure S6. Continued.

a	SRK10(Lim)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	180
	SRK11(Lim)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	177
	SRK16(Lim)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	177
	SRK20(Lim)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	177
	SRK29(Lim)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	177
b	SRK-22(Haseyama)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	128
	SRK-23(Haseyama)	AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	176
	SRK-31(Haseyama)	-AATTCTTGCGCTGTTGCATTGACGCGGACGAGAGATGCTGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	119
	SRK7(Kim)	-----TGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	82
c	SRK10(Kim)	-----TGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	82
	SRK16(Kim)	-----TGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	82
	SRK17(Kim)	-----TGATATATGAGTATTTGGAAAAATCAAGCCTGGATTATTTCTCTTCGCTTAGACTCTCATCTCTTCCAAAGCTCTATACAA	82

a	SRK10(Lim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	300
	SRK11(Lim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	296
	SRK16(Lim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	297
	SRK20(Lim)	CAATTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	297
	SRK29(Lim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	297
b	SRK-22(Haseyama)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	248
	SRK-23(Haseyama)	CAATTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	296
	SRK-31(Haseyama)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	239
	SRK7(Kim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	201
c	SRK10(Kim)	CAATTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	202
	SRK16(Kim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	202
	SRK17(Kim)	CAGTTGAATGTTGATAGAAATAAGCTAACTGATTGGCTGTGATAATTCTTAGGAAAAAGCGAAGCTCTAATTTAAATTTGGAAGGACAGGTTGCCATTACAAATGGTGTGCTCGAG	202
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a	SRK10(Lim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	420
	SRK11(Lim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	416
	SRK16(Lim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	417
	SRK20(Lim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	417
	SRK29(Lim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	417
b	SRK-22(Haseyama)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	368
	SRK-23(Haseyama)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	416
	SRK-31(Haseyama)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	359
	SRK7(Kim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	321
c	SRK10(Kim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	322
	SRK16(Kim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	322
	SRK17(Kim)	GGCTTTGATATCTTCATCAAGACTCCCGGTTTAGGATAATCCACAGGGATATGAAAGCAGGTAACATTTTGCTAGATAAAAAATGATCCCAAGATCTCGGATTTTGGGCTGGCCAGAA	322

a	SRK10(Lim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	540
	SRK11(Lim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	536
	SRK16(Lim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	537
	SRK20(Lim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	537
	SRK29(Lim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	537
b	SRK-22(Haseyama)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	488
	SRK-23(Haseyama)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	536
	SRK-31(Haseyama)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	479
	SRK7(Kim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	441
c	SRK10(Kim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	442
	SRK16(Kim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	442
	SRK17(Kim)	TCATTGCAAGGGACCAAACTGAAGCTAGCAGAGATAATCCGATCGGAACCTAGTAAGCAAACTCTTAAAGATATTTCTTACCCATAACTCTATAGAAGCTCATGACCTCTAAGTTCAAAT	442

a	SRK10(Lim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	660
	SRK11(Lim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	656
	SRK16(Lim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	657
	SRK20(Lim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	657
	SRK29(Lim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	657
b	SRK-22(Haseyama)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	608
	SRK-23(Haseyama)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	656
	SRK-31(Haseyama)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	599
	SRK7(Kim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	561
c	SRK10(Kim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	562
	SRK16(Kim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	562
	SRK17(Kim)	TTTTGCTACTCAGCGGCTACATGTCTCCGAGTAGCAATGTATGGGATCTCTCCGAAA AAACAGATGTTTTCAGTTTGGAGTCATAGTCTTGAAATTTGTTACTGGAAAAAGGAACA	562

Figure S7. Multiple sequence alignment of SRK10 (Lim, AY052579), SRK16 (Lim, AY052579) and other 10 S haplotypes; Asterisk: conserved nucleotide; a: S haplotype published by Lim (2002); b: S haplotype published by Haseyama (2018); c: S haplotype published by Kim (2016).

a	SRK10(Lin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	780
	SRK11(Lin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	776
	SRK16(Lin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	777
	SRK20(Lin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	777
	SRK29(Lin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	777
b	SRK-22(Haseyama)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	728
	SRK-23(Haseyama)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	776
	SRK-31(Haseyama)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	719
c	SRK7(Kin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	681
	SRK10(Kin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	682
	SRK16(Kin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	682
	SRK17(Kin)	GAGGATTCTACGAGTCAACCCGGAAGACAATCTTGATGCTATGTAAGTTTAAAGAACCAATAATTTCTATCTACTCTCGAGATTGCCAAAAACACTTTAAATGCTTTTATATTATAAA	682

a	SRK10(Lin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	900
	SRK11(Lin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	896
	SRK16(Lin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	897
	SRK20(Lin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	897
	SRK29(Lin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	897
b	SRK-22(Haseyama)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	848
	SRK-23(Haseyama)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	896
	SRK-31(Haseyama)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	839
c	SRK7(Kin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	801
	SRK10(Kin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	802
	SRK16(Kin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	802
	SRK17(Kin)	CAGGCATGGACTCATTGGGCGCAGGGAAGAGCGCTAGAAATCGTAGATCCCGTCATCGTAGATTCATTGTGCATCAACATTTCAACCAAAAAGAGTCTCTAAAATGCATACAAATTTGGTCTC	802

a	SRK10(Lin)	TTGTGTATTCAAGAACGTGCGGTGCACAGCAACGATGTGTCGCGTGGTTTGGATGCTT	960
	SRK11(Lin)	TTATGTATTCAAGAACGTGCGGAGCAGCAAGCAACGATGTGTCGCGTGGTTTGGGTGCTT	956
	SRK16(Lin)	TTGTGTATTCAAGAACGTGCGGAGCAGCAAGCAACGATGTGTCGCGTGGTTTGGATGCTT	957
	SRK20(Lin)	TTGTGTATTCAAGAACGTGCGGTGCACAGCAACGATGTGTCGCGTGGTTTGGATGCTT	957
	SRK29(Lin)	TTGTGTATTCAAGAACGTGCGGAGCAGCAAGCAACGATGTGTCGCGTGGTTTGGATGCTT	957
b	SRK-22(Haseyama)	TTGTGTATTCAAGAACGTGCGGAGCAGCAAGCAACGATGTGTCGCGTGGTTTGGATGCTT	908
	SRK-23(Haseyama)	TTGTGTATTCAAGAACGTGCGGTGCACAGCAACGATGTGTCGCGTGGTTTGGATGCTT	956
	SRK-31(Haseyama)	TTGTGTATTCAAGAACGTGCGGAGCAGCAAGCAACGATGTGTCGCGTGGTTTGGATGCTT	899
c	SRK7(Kin)	TTGTGTATTCAAGAACGTGCGG-----	823
	SRK10(Kin)	TTGTGTATTCAAGAACGTGCGG-----	824
	SRK16(Kin)	TTGTGTATTCAAGAACGTGCGG-----	824
	SRK17(Kin)	TTGTGTATTCAAGAACGTGCGG-----	824
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Figure S7. Continued.