### Liang et al.: Supplemental Information

#### Supplemental Figures.

$\begin{split} S_{T}RNase: &RicaAcattaCitititititiCititititiCiticGetTiticTiticGetTiticCiticGetGetAcaAacaattetettititicCiticGetGetAcaAacaattetettititititicGetGetTiticGetTiticGetAcattetettititititititicGetGetAcattaCititititicGetAcattettitititicGetAcattettititititicGetAcattettititititititititititititititititit$
C2 S,-RNase: CACAGORGECC GCCTETIATECCAACAAATCAATECCAGAAGAAGGCCATCAGATTTCTTCTTCACAGECCIGTGGCCAGTAAACTCACCGCCACAGATTGGAAL 207 S,-RNase: CACGTGGCCCCCTTGGCTATTGCTGGAGTCAATGCGCCGTAATGGCCGTAACAGGGTCGCCGGGCAAAAACATTGGAL 200 S,-RNase: CACAGCTGGCCCCTTGGCTATTGCTGGAGTCAATGCGCCGTAAGGAAAGAAA
$ \begin{array}{c} S_{1}\text{-}RNase: \text{AATTCAG}CAAGGACATCCC}TEA TTCTCTCTCTCTCTCTCTAGGAATCATCTTTGGATAGAAATGATCGACGACTGGCAAGTCTGGGACATCC} : 303 \\ S_{2}\text{-}RNase: \text{GCTGACAAATAAATAAAAACAACCCACAATAAGTTCTAAAATCGCTCAAGGACATAATCTTTGGATAGAAATGGATCGCAAGTCTCAGGACGATCC} : 318 \\ S_{3}\text{-}RNase: GCTGACAAATAAATAAAACAACCA-CCTCCGGGGATTCTTGGATCGTCGAACATGATGAACCCTTTGGGATCATTTGATGAAATGGATCAGAACATCTTCCACATGGATCACAACCAAC$
$\begin{array}{llllllllllllllllllllllllllllllllllll$
S, RNase: AT ACACTG GGALA GTGTGAR CHACTGAGGAT TE GGALATCAL A THATC LA TCALGGAL TA GGALTA TC GALACTG GGALA ATTC TGC A CACTG CAL 513 S, RNase: GLGAACTAGCALA A TTACGACGALTAGGAACA TE GTGGAGAGG TGTATTC TA TCALGCALTA CCT A TT A TTALATGAGGCA TE TGC 522 S, RNase: GLGGAACTA CALGTTCACGALTTACTALATAC TE AACAGAGCT TE TAATGGALA ATTC TA ACCT A TT A TTALATGAGGCA TE TGC 522 S, RNase: AT AAACTA GGALA GTTCACGALTTACTALATAC TE AACAGAGCT TE TAATGGALA ATTC TA ACCT A TT A TTALATGAGGCA TE ACC S, RNase: AT AAACTA GGALA GTTCACGALTTACTALATAC TE AACAGAGCT TE TAATGGALA ATTC TA ACCT ACT ACTALAGT GGALA ATTC TA CC 533 S, RNase: AT AAACTA GGALA ATTGTCACGALTTACTALATAC TE AAACGGAL GTTALTTC C TA ACGALTA TC A ACCT AGTTC ACT A GGALA ATTGTCA CC 533 S, RNase: AT AAACTA GGALA ATTGTCACGALTAC TGAAGGCGALTTA A TAGTCC GGT A CCALTATCC TA CTALAGT AGC CC 7 A GC 7 1 466 S, RNase: AT AAACTA GGALA ATTGTCACGALTAC TGAAGAATATA A TAGTCC GGT A CCALTATCC TACCATA ATT A AGC CC 7 A GC 7 1 466 S, RNase: AT AAACTA GGALA ATGTCACGALTAA ATTGCCACTAAATA A TAGTCC AGT A CCALTATCC TACCATAGGA CTTGC A TTALAGACGC TTGC 7 A GC 7 1 466 S, RNase: AT AAACTA GGALA ATGTCACGALTAA AT TGCCACTAAATA A TAGTCC AGT ACCALTATCC TACCATAGGA TA AGC CC 7 A GC 7 1 466 S, RNase: AT AAACTA GGALA ATGTCCACTACTACTACGATAAA TE GCACTAAATA A TAGTCC AGT ACCALTACCATAGATTA AGC CC 7 A GC 7 1 474 S, RNase: AT AAACTA CGALA GTGTCACTACTACAGGAATAAA TE GCACTAAAAT TAGTCC A TTALCCATAGGATTA CC 7 A GC 7 TTATATAGAGCGC TTGC 7 1 504 S, RNase: AT AAACTA CGALA GTGTCACTATAAAGGAATATA A TAGTCC A TTALACGA CTACCAL GTT GATTAGAACGC TTGC 7 1 486 S, RNase: AT AAACTA CAACTA CGALA ATTACCACTATAAA TE CAACTAACTACAATA A TATTCC A TTALACGA CTACCAL GTT GATTAGAACGC TTGC 7 1 504 S, RNase: AT AAACTA CAACTA CGALA ATTACCACTATAAAA TE AAAGGAAA A TATTCC A TTALACGA CTACCAL GTT GAACGCC TTACCCACTACCACCACTACCACCACTATACACCACTAAACGC 7 1 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
$ \begin{array}{l} S_r, RNase: \mbox{Gamma} {\rm Gamma} {\rm $
S, $RNase:$ TGCAATCACGAAGAACGAACTAATTGCCTAAGAACATCATCATGACGACGACCTAA S, $RNase:$ TGCAATTACCGACGGGATCACCGCGCTTAAGGCAGCCAATAACACTCCCCGACCGA

#### Supplementary Figure 1. Nucleotide sequence alignments for the pummelo *S*<sub>1</sub>-RNase – *S*<sub>9</sub>-RNases.

The nucleotide sequence identities above 80% among *S-RNases* are indicated by shaded boxes: *black indicates* 100% conservation; *grey* indicates  $\geq$  80% conservation; *dashes* represent gaps. The citrus *S-RNases* contain five conserved domains (C1-C5) and five hypervariable regions (HV1-HV5).

		C1	_	C2	
S-PNaco	MNITFFLYMVLFISCIS				KNSSKDI 76
	MKATNLFRFALLAINVI				
	MKTKATYFLFFALLVSNIT				
SRNase:	MSATLFIFIVMFVSCIS	SGAAQNSSG-FDHFWLVQSW	PPVYCQQINCKRK	ASDFVLHGLWPV <mark>NSTGHS-</mark> L	KNSSKAT 76
	MKVASINICILLVYCIV				
	MGTNFLIIFVQFVSCIA				
	MKAAYLLSFVLLVLYII				
S-RNase:	MGIGFLIFFVLFVSSIA MKTRATYLFFYALLVSSIT	SVVTQNTSG-FHHFWLVQSW	IPPVFCQKYPCKNP	PLDFVLHGLWPVNSSGHT-I VCDFVIHCIWDVMFKEDM-I	KNSSRGK 76 PGTNRSO 78
$S_{g}$ Mase.	MAIRAIILFFIALLV3511		C1	C2	PGINKSQ /8
An_S,-RNase:	MANARKRDFFSLILLIVLL	SDSYTTTAVEFELLKLVLQW	VPNSYCSLSKRPCRRKPL	PSDFTIHGLWPDNRSWPI	LYNC-QFD 81
An $S_5$ -RNase:	MVAKKSHDHGQFSFLVLFVILLS	SYCFTANAKYFEILKLVLQW	VPNSYCSLKTSTCRRNPL	PLKFTIHGLWPDNYSWPI	LSDC-GYD 85
$An_{S_2}-RNase:$	MATVQKSQHSHFFLLVGCIVHLS	NFCSTTTAQ-FDYFKLVLQN C1	VPNSYCSLKTTHCPRTRL	PSQFTIHGLWPDNKSWPI C2	LSNCRDTS 85
Ni S-RNase:	MFRSQLVSIFFIL		PPTYCHEKSCARI	PTNFRIHGLWPDNQHELI	LNNCKKSF 72
Pe SRNase:	MFRSQLMSAFFIL	FLAQAPVYGVFDQIQLVLTW	PPSFCHTKPCKRT	PRNFTIHGLWPDDQHVLI	LNDCDKTY 72
$Pe S_2 - RNase:$	MFRLQLLSALFIL		VPASFCYP-KNFCKRK		LEFCTGDK 73
Ma C-BNaca	MGITGMIYIVTMVFSLI				PANCTNAT 80
Ma_SRNase: Pv S-RNase:	MGITGMIIIVTMVFSLI	VLILSSSTVGIDIEQETQQI	OLAVCISNETPCKDPT-	DKLETVHGLWPSNENGPH-	PANCPIRN 80
Pr S-RNase:	MAMLKSSLSFLVLGFAFFL	CFIISAGDGSYVYFOFVOOW	PPTTCRV-OKKCSKPRP	LONFTINGLWPSNYSNPTM	PSNCNGSR 83
			2		
	HV1	HV2 C	C3 HV3		C4
			<b>A</b>		
	PNFYSLL-RNHSFGMEMDEHWPSLG	TTDGHDPFKHIGFWTHEWEE	▲ LHGSGQPYADTYYLQ		QGIYPNGRSYW 162
$S_2 - RNase:$	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK	A HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ	RAVELAKTTDLRNTLAEF	QGIYPNGRSYW 162 KGVLPNGASYP 165
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV	HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR	RAVELAKTTDLRNTLAEF RAVELTKFTDLLNTLNRF	QGIYPNGRSYW 162 KGVLPNGASYP 165 AGIMENGNIYR 163
$S_2^{\dagger}$ -RNase: $S_3^{-}$ RNase: $S_4^{-}$ RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ	HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR 2HGSGQPYEGLYYVQ	RAVELAKTTDLRNTLAEF RAVELTKFTDLLNTLNRF AAIRLRKSVNLLRILGNQ	QGIYPNGRSYW 162 XGVLPNGASYP 165 AGIMENGNIYR 163 QGIFPDGRNYW 162
$S_2^-$ -RNase: $S_3^-$ RNase: $S_4^-$ RNase: $S_5^-$ RNase: $S_5^-$ RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWKHEWDE	HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR HGSGQPYEGLYYVQ HGSAFPHEPLDYFR HGSGQPSEPPDYFL	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNÇ RTVKL MKRMNLLSTLKAC AAITL RKNVDLLSTLRRY	QGIYPNGRSYW 162 KGVLPNGASYP 165 AGIMENGNIYR 163 QGIFPDGRNYW 162 GGVEPRTTSYP 153 KRIVPGGTSYP 156
$S_2^2$ -RNase: $S_3^2$ -RNase: $S_4^2$ -RNase: $S_5^2$ -RNase: $S_6^2$ -RNase: $S_7^2$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IRMIDILNRDTSLKSDMGKYWPSLA	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWKHEWDE SKISHKFWSRQWQK	HGSQPYADTYYLQ HGSSRKGMDPLDYFQ YHGSAQRRVKPPDYFR 2HGSQCPYEGLYYVQ HGSAFPHEPLDYFR HGSAQLLTSPPDYFL	RAVEL – AKTTDLRNTLAEF RAVEL – TKFTDLLNTLNRF AAIRL – RKSVNLLRILGNÇ RTVKL – MKRMNLLSTLKAC AAITL – RKNVDLLSTLRRY TAIRL – MKITNLQNKLAAF	2GIYPNGRSYW 162 CGVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 3GVEPRTTSYP 153 CRIVPGGTSYP 156 CGIVPNGTSYP 159
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase: $S_4^{-}$ -RNase: $S_5^{-}$ -RNase: $S_7^{-}$ -RNase: $S_7^{-}$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IFMIDILNRDTSLKSDMGKYWPSLV	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWVHEWDE SKISHKFWSRQWQK YSDSANFWEHEWEE	HGSQ2PYADTYYLQ (HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR 2HGSQCPYEGLYYVQ (HGSAGPHEPLDYFR HGSQ2PSEPPDYFL (HGSAQ-KLITSPEDYFR HGSQ2-PLMEPTEYFQ	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNÇ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRRY TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF	2GIYPNGRSYW 162 CGVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 GGVEPRTTSYP 153 CRIVPGGTSYP 156 CGIVPNGTSYP 159 2GILPNGTSYP 157
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase: $S_4^{-}$ -RNase: $S_5^{-}$ -RNase: $S_7^{-}$ -RNase: $S_7^{-}$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKWPSLA IRMIDILNRDTSLKSDMGKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWKHEWDE SKISHKFWSRQWQK YSDSANFWEHEWEE TWDKDKLQNFWIYQWKI	HGSQ2PYADTYYLQ HGSSQKGMDPLDYFQ HGSAQRVKPPDYFR 2HGSQCPYEGLYYVQ HGSAFPHEPLDYFR HGSQ2PSEPPDYFL HGSAQ-KLITSPEDYFR HGSQ2PLMEPTEYFQ HGSAQQQVVPPHYFR	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNÇ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRRY TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF	2GIYPNGRSYW 162 CGVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 GGVEPRTTSYP 153 CRIVPGGTSYP 156 CGIVPNGTSYP 159 2GILPNGTSYP 157
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase: $S_4^{-}$ -RNase: $S_5^{-}$ -RNase: $S_6^{-}$ -RNase: $S_8^{-}$ -RNase: $S_8^{-}$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IRMIDILNRDTSLKSDMGKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWVHEWDE SKISHKFWSRQWQK YSDSANFWEHEWEE TWDKDKLQNFWIYQWKI HVb	HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR HGSGQPYEGLYYVQ HGSAFPHEPLDYFR HGSGQPSEPPDYFL HGSAQ-KLITSPEDYFR HGSAQPLMEPTEYFQ HGSAQQQVVPPHYFR C3	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRLRKSVNLLRILGNQ RTVKLMKRMNLLSTLRAQ AAITLRKNVDLLSTLRRY TAIRLMKITNLQNKLAAF AAIRLRKSVDLMSTLKRF RAVQLTRYTDLLNTLNGF	QGIYPNGRSYW 162 XGVLPNGASYP 165 AGIMENGNIYR 163 QGIFPDGRNYW 162 GGVEPRTTSYP 153 XRIVPGGTSYP 156 XGIVPNGTSYP 159 EGILPNGTSYP 157 ADIHANGSSYP 163
$S_2^2$ -RNase: $S_3$ -RNase: $S_4$ -RNase: $S_5$ -RNase: $S_7$ -RNase: $S_7$ -RNase: $S_8$ -RNase: $S_9$ -RNase: An $S_7$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IRMIDILNRDTSLKSDMGKYWPSLA FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa FDIPEVGDQKFRQKLDVIWPDLR	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEC RRNTELFWVHEWKK SSDPTNFWKHEWDE SKISHKFWSRQWQK YSDSANFWEHEWEE TWDKDKLQNFWIYQWKI HVD	HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSSQRRVKPPDYFR HGSGQPYEGLYYVQ HGSAFPHEPLDYFR HGSGQPSEPPDYFL HGSAQ-KLITSPEDYFR HGSGQPLMEPTEYFQ G3 HGSCA-LPDISFIDYFT	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNQ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRAF TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRDILGRG	2GIYPNGRSYW 162 GVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 3GVEPRTTSYP 153 GRIVPNGTSYP 156 GGIVPNGTSYP 159 3GILPNGTSYP 157 ADIHANGSSYP 163 3KLYP-GDSYD 165
$S_2^2$ -RNase: $S_3$ -RNase: $S_4$ -RNase: $S_5$ -RNase: $S_7$ -RNase: $S_7$ -RNase: $S_8$ -RNase: $S_9$ -RNase: An_ $S_1$ -RNase: An_ $S_5$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IRMIDILNRDTSLKSDMGKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLKYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWVHEWDE SKISHKFWSRQWQK YSDSANFWEHEWEE TWDKDKLQNFWIYQWKI HVD LKRKRDPEQGFWITEWKF KRKNIR-KPDKTFWLTQWEK	A HGSGQPYADTYYLQ HGSSRKGMDPLDYFQ HGSAQRRVKPPDYFR HGSGQPYEGLYYVQ (HGSAFPHEPLDYFR HGSGQPSEPPDYFL HGSAQ-KLITSPEDYFR HGSQQPLMEPTEYFQ G3 HGSCA-LPDISFIDYFT HGTCA-LSVYTEDDYFR	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNQ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRAF TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRDILGRG ETLNM KRRFNILDMLQRF	2GIYPNGRSYW 162 XGVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 3GVEPRTTSYP 153 XRIVPGGTSYP 156 XGIVPNGTSYP 159 2GILPNGTSYP 157 ADIHANGSSYP 163 3GKLYP-GDSYD 165 XSMRPGDRVDP 171
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase: $S_4^{-}$ -RNase: $S_6^{-}$ -RNase: $S_7^{-}$ -RNase: $S_8^{-}$ -RNase: $S_9^{-}$ -RNase: An_ $S_1^{-}$ -RNase: An_ $S_2^{-}$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa FDIPEVGDQKFRQKLDVIWPDLR FTLPDITDKSLLKRLDRNWPDLT ADVLKITDKGLIQDLAVHWPDLT HVa	TTDGHDPFKHIGFWTHEWEE TVNKNY IAGFWIHEWEK TRDGDRLXYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTEL FWVHEWKK SSDPTN FWVHEWKK SSDPTN FWEHEWEE SKISHKFWEHEWEE TWDKDKLQNFWIYQWKI HVb LKRKRDPEQGFWITEWKF KRKNIR-KPDKTFWLTQWEK RRQRKVPGQKFWVTQWKK	HGSQQ PYADTYYLQ HGSSR - KGMD PLDYFQ HGSSQ RVKPPDYFR 2HGSQQ PYEGLYYQQ HGSAF PHEPLDYFR HGSQQ PSEPPDYFL HGSAQ - KLITSPEDYFR HGSQQ - PLMEPTEYFQ HGSAQ - QQVVPPHYFR C3 HGSCA - LPDISFIDYFT HGCA - LPMYSFNDYFV C3	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNQ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRRY TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRD ILGRG ETLNM KRRFNILDMLQRF KALEL KKRNNLDMLSRF 	2GIYPNGRSYW 162 CGVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 3GGVEPRTTSYP 153 CRIVPGGTSYP 155 CGIVPNGTSYP 155 2GILPNGTSYP 157 ADIHANGSSYP 163 3GKLYP-GDSYD 165 CSMRPGDRVDP 171 CSLTPGDQRVD 170
$S_2^{-}$ -RNase: $S_3^{-}$ -RNase: $S_4^{-}$ -RNase: $S_6^{-}$ -RNase: $S_7^{-}$ -RNase: $S_9^{-}$ -RNase: $S_9^{-}$ -RNase: An_ $S_1^{-}$ -RNase: An_ $S_2^{-}$ -RNase: Ni S-RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa FDIPEV-GDQKFRQKLDVIWPDLR FTLPDI-TDKSLLKRLDRNWPDLT ADVLKI-TDKGLIQDLAVHWPDLT HVa	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLXYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWVHEWKK SSDPTNFWEHEWEE TWDKDKLQNFWIYQWKI HVb LKRKRDPEQGFWITEWKF KRKNIR-KPDKTFWLTQWEK RRQRKVFGQKFWVTQWKF HVb	HGSQPYADTYYLQ HGSSRKGMDFLDYFQ HGSSQPYEGLYYQ HGSAQPYEGLYYQ HGSAQPYEGLYYQ HGSAQPFEPLDYFR HGSQQPSEPPDYFL HGSAQ-KLITSPEDYFR HGSQQQQVVPPHYFR C3 HGSCA-LPDISFIDYFT HGCA-LSYJFDDYFR C3 HGCC-TELYSQEAYFD	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNQ RTVKL MKRMNLLSTLKAG AAITL RKNVDLLSTLRRY TAIRL MKITNLQNKLAAF AAIRL RKSVDLMSTLKRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRD ILGRG ETLNM KRRFNILDMLQRF KALEL KKRNNUDMLSRF 	2GIYPNGRSYW 162 (GVLPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 3GVEPRTTSYP 153 (RIVPGGTSYP 155 GGILPNGTSYP 156 4DIHANGSSYP 163 3KLYP-GDSYD 165 KSMRPGDRVDP 171 KSLTFGDQRVD 170 2GVIP-GKTYT 154
$S_2^-$ -RNase: $S_3^-$ -RNase: $S_4^-$ -RNase: $S_5^-$ -RNase: $S_7^-$ -RNase: $S_7^-$ -RNase: $S_9^-$ -RNase: An_ $S_1^-$ -RNase: An_ $S_2^-$ -RNase: $n_S_2^-$ -RNase: Ni_ $S^-$ -RNase: Pe $S_7^-$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLA IRMIDILNRDTSLKSDMGKYWPSLA FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa FDIPEV-GDQKFRQKLDVIWPDLR FTLPDI-TDKSLLKRLDRNWPDLT HVa TTITNSSKSNALDDRWPDLK TTISDAREKKELDARWPDLK	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLXYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKK SSDPTNFWXHEWEE SKISHKFWSHQWE YSDSANFWSHQWQKI HVb LKRKRDPEQGFWITEWKF KRKNIR-KPDKTFWLTQWEK RRQRKVPGQKFWVTQWKK HVb SKMKT-IQTQDFWKYQVNK YTEKDA-IQLQSFWRYEYNK	A HGSQ2PYADTYYLQ HGSSQRWKPPDYFR 2HGSQ2PYEGLYYVQ HGSAQPYEFPDYFR HGSQ2PSEPPDYFL HGSQ2PLMEPTEYFQ HGSAQ-KLITSPEDYFR C3 HGSCA-LPDISFIDYFT HGTCA-LSVTFDDYFR C3 HGCCC-TELYSQEAYFD HGTCC-SERXDQEAYFN	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNC RTVKL MKRMNLLSTLRAC AAITL RKNVDLLSTLRRY TAIRL NKITNLQNKLAAF AAIRL RKSVDLMSTLRRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRDILGRC ETLNM KRRFNILDMLQRF C4 LAMKL KDKFDLLQMLKSC LAKNL KDKFDLLQMLKSC	2GIYPNGRSYW 162 CGUPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 2GVEPRTSYP 153 (RIVPGGTSYP 155 CGUPNGTSYP 157 ADIHANGSSYP 163 3GKLYP-GDSYD 165 SSMRPGDRVDP 171 KSLTPGDQRVD 170 2GVIP-GKTYT 154 2GIIP-GKTYP 154
$S_2^-$ -RNase: $S_3^-$ -RNase: $S_4^-$ -RNase: $S_5^-$ -RNase: $S_7^-$ -RNase: $S_7^-$ -RNase: $S_9^-$ -RNase: An_ $S_1^-$ -RNase: An_ $S_2^-$ -RNase: $n_S_2^-$ -RNase: Ni_ $S^-$ -RNase: Pe $S_7^-$ -RNase:	PNFYSLL-RNHSFGMEMDEHWPSLG NKILKSLKRDKSLEADLMKYWLSLS PGILASLEHDESLWDDLKKYWLSLS PNFYAMI-RNHSFAIEMDEYWPSLG DDIIDKINNDSSLVADMNRYWKSLL KNFQKKI-EHLPFRGELKKYWPSLI FDFVGTI-GNSSLRGELEKNWPSLV PEILESLKKDKSLWNNLMYYWLSLS HVa FDIPEV-GDQKFRQKLDVIWPDLR FTLPDI-TDKSLLKRLDRNWPDLT ADVLKI-TDKGLIQDLAVHWPDLT HVa	TTDGHDPFKHIGFWTHEWEE TVNKNYIAGFWIHEWEK TRDGDRLXYFWPYQWRV STEGHDPLKHIGFWEHEWEQ RRNTELFWVHEWKE SSDPTNFWVHEWKE SSDPTNFWEHEWEE TYDKDKLQNFWIYQWKI HVb LKRKRDPEQGFWITEWKF KRKNIR-KPDKTFWLTQWEK RRQRKVPGQKFWVTQWK HVb YSKMKT-IQTQDFWKYQYNK YTERDA-IQLQSFWRYEYNK FDEKYA-STKQPLWEHEYNF	A HGSQ2PYADTYYLQ HGSSQRWKPPDYFR 2HGSQ2PYEGLYYVQ HGSAQPYEFPDYFR HGSQ2PSEPPDYFL HGSQ2PLMEPTEYFQ HGSAQ-KLITSPEDYFR C3 HGSCA-LPDISFIDYFT HGTCA-LSVTFDDYFR C3 HGCCC-TELYSQEAYFD HGTCC-SERXDQEAYFN	RAVEL AKTTDLRNTLAEF RAVEL TKFTDLLNTLNRF AAIRL RKSVNLLRILGNQ RTVKL MKRNNLLSTLRAQ AAITL RKNVDLLSTLRRY TAIRL NKITNLQNKLAAF AAIRL RKSVDLMSTLRRF RAVQL TRYTDLLNTLNGF TATRL NKKFNIRDILGRQ ETLNM KRRFNILDMLQRF C4 LAMKL KDKFDLLQMLKSQ LAKNL KDKFDLLQMLKSQ LAIRL KDKFDLLQILRIQ	2GIYPNGRSYW 162 CGUPNGASYP 165 AGIMENGNIYR 163 2GIFPDGRNYW 162 2GVEPRTSYP 153 (RIVPGGTSYP 155 CGUPNGTSYP 157 ADIHANGSSYP 163 3GKLYP-GDSYD 165 SSMRPGDRVDP 171 KSLTPGDQRVD 170 2GVIP-GKTYT 154 2GIIP-GKTYP 154

$Ma\_S_2$ -RNase: vnshrikniqaqlkiiwpnvldrtnhlGfwnkqwikhgsCgnppimndthyfqtvinmyitqkqnvseilsrakieplgiqrp 163	
$Py_{S_5}$ -RNase: irkrekllepolatiwpnvfdrtknklfwdkewmkhgtcgyptidnenhyfetvikmyiskkonvsrilskakiepdgkkra 162	
$\Pr_{S_3}$ -RNase: fkkellsprmqsklkiswpnvvssndtkfwesewnkhgtqs-eqtlnqvqyfeishemwnsfnitdilknasivphptqtw 163	

HV4 C5 HV5	
S <sub>1</sub> -RNase: E-TGYIDATKHVYGYPILKCYKGYL-LKEVTICVD-GQARNLISCNHEERRSTNCRNIITFPPP*224	
$S_2^-$ RNase: K-fnymkaimaktchl-pmlrcvk-KDgynhlkeviicvg-vqannfrscnygvgsprckgdnikfpeptde*234	
$S_{3}$ -RNase: K-vefrkaikaktgyd-pilscvfsdgryq-lkevticvd-adatnfipcnpnkisrescrnnikfpapsptk*233	
$S_4$ -RNase: K-TAYVDAIKAIYGYPILKCYNGHL-LKELIICVD-GQARNFISCSKKEQGSSNCHKNIINFPPPK*226	
$S_5^{*}$ -RNase: K-SKYKDAIKAVTGSDSVILKCAYNETGYL-LQEVMLCTD-YEAETFIECNSYEMFEENCGPDIIFPPRW*221	
$S_{g}$ -RNase: I-TDYVKATKDIYGYPRITCYNRYL-LKEVNLCVD-RQARNFISCNHRERGSTTCGKNIKLPRYVKI*221	
$S_{\gamma}^{'}$ -RNase: K-DYYKSALEVIHGGESVMLACFSVNGIQL-LRDVYICLD-GQLRYFISCNKN-EFNKTENCGDDIMFPSKVQISSS*233	
$S_g$ -RNase: I-TDFVDATKDIYCHPRITCSYGYL-LNEVNLCVD-SQARNFISCNHRERKSTTCRKRITFPRHVKIENGYIWHEE* 231	
S <sub>g</sub> -RNase: K-VEFRKAIKTKTGHD-PSLSCVF-EGGHFQLKEVIICVD-AEATNFIPCQRNKINGESCRDTIMFPTRTK*231	
<u></u>	
An_S <sub>1</sub> -RNase: L-QQVESTLTKFIKKV-TVVKCPNGFLTEVIVCFD-PSGTSIIDCPGPYPCTYVTVNFPKAVKR* 227	
nse: revaraiskytnhe-pevkcregflteiticfdtgrdasytdcpgplctdpmydfprsyvrtir* 235	
$\operatorname{An}_{S_2}$ -RNase: V-SDVNGAITKVTGGI-AILKCPEGYLTEVIICFD-PSGFPVIDCPGPFPCKDDPLEFQVLSRRKFQDL* 237	
<u>C5</u>	
Ni_S-RNase: v-nkieeairevtqvy-pnlnCignplktmelkeigiCfn-reatevvaChrrktCnplnkneisfpl* 220	
$Pe_S_7$ -RNase: v-dkieeavkavthey-pniecvgdpyktlelkeigicln-peatkvtpchrrktckplnkkeisfpq* 220	
$Pe S_2 = RNase: F-GEIQKAIKTVTNNKDPDLKCVENIKGVKELNEIGICFN-PAADSFHDCRHSKTCDETDSTQTLFRR* 223$	
Ma_S <sub>2</sub> -RNase: L-VDIEKAIRNSINKKKPRFKCQN-NGGVTELVEISLCSD-RSLTQFRDCPHPFPPGSPYLCPADIQY*- 229	
$Py_{S_s}$ -RNase: L-LDIENAIRNGADNKKPKLKCQK-KGTTTELVEITLCSD-KSGEHFIDCPHPFEPISPHYCPTNNIKY*- 229	
$\Pr_{S_3}$ -RNase: kysdivsaiqsktqrt-pllrcktdpahpnantqllhevvfcyg-ynaikqidcnrtagcknqvnilfp* 231	

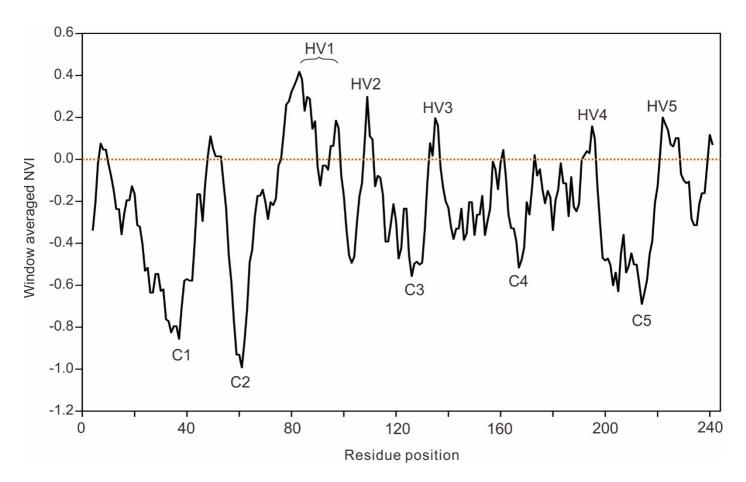
# Supplementary Figure 2. Amino acid sequence alignments of *S*-RNases from pummelo and Plantaginaceae (prefix An for *Antirrhinum*) and Solanaceae (prefixes Ni and Pe for *Nicotiana* and *Petunia*) and Rosaceae (prefixes Ma, Py and Pr for *Malus*, *Pyrus* and *Prunus*).

The pummelo *S*-RNase sequences used are *S*<sub>1</sub>-RNase to *S*<sub>9</sub>-RNase; Plantaginaceae *S*-RNase sequences (An\_S1-RNase: HE805271, An\_S5-RNase: X96464, An\_S2-RNase: X96465), Solanaceae *S*-RNase

sequences (Ni\_S-RNase: CAA05306, Pe\_S7-RNase: BAJ24847 and Pe\_S2-RNase: AAG21384) and Rosaceae *S*-RNase sequences (Ma\_S2-RNase: ADB85476, Py\_S5-RNase: BAA13577 and Pr\_S3-RNase: CAC27786) were downloaded from the NCBI protein database.

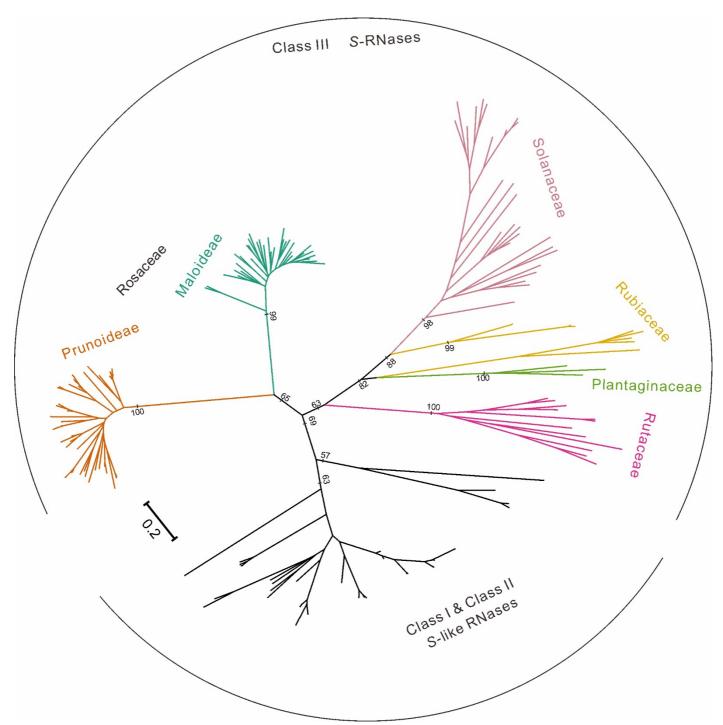
The conserved amino acids of *S*-RNases from pummelo, Plantaginaceae, Solanaseae and Rosaceae, respectively, are indicated by shaded boxes (grey indicates 100% identity; light grey  $\geq$  70% identity). The *S*-RNases from pummelo contain five conserved domains (C1-C5) and five hypervariable regions (HV1- HV5, indicated in red). HV1 and HV2 have the highest diversity and correspond to HVa and HVb of the *S*-RNases from Plantaginaceae and Solanaceae.

The three conserved histidine residues (triangles), six conserved cysteine residues (solid circles), and an amino-terminal signal peptide (underlined) present in the pummelo sequences are indicated. The asparagine amino acid residues (N), predicted to be potentially N-glycosylated, are indicated in blue font. The  $S_2$ -RNase has 1 such potentially N-glycosylated amino acids;  $S_3$ -,  $S_4$ -,  $S_5$ - and  $S_6$ -RNase have 3;  $S_1$ -,  $S_7$ -,  $S_8$ - and  $S_9$ -RNase have 4 potentially N-glycosylated asparagine amino acids.



### Supplementary Figure 3. Normed Variability Index (NVI) figure calculating the conserved and hypervariable sequences present in the nine pummelo *S*-RNases.

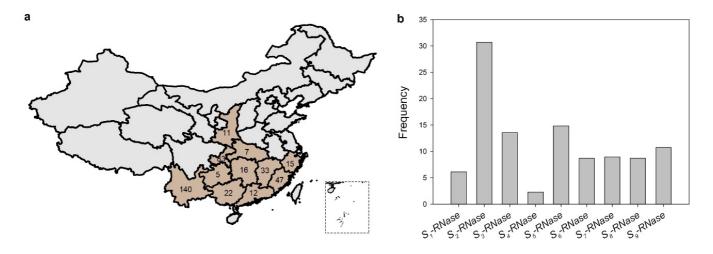
The averaged NVI value of each residue is calculated using a window of seven residues as described by Kheyr-Pour et al<sup>1</sup>. Analysis of the nine pummelo putative *S*-RNase sequences revealed five conserved regions (the valleys, C1- C5) and five hypervariable regions (the peaks, HV1- HV5). HV1 and HV2 have the highest sequence diversity so are the most polymorphic between the citrus sequences.



Supplementary Figure 4. Phylogeny of the S-RNases identified in pummelo (Rutaceae) and known S-RNases from Rosaceae, Solanaceae, Plantaginaceae and Rubiaceae.

The phylogenetic tree was constructed with deduced amino acid sequences using the maximum likelihood method with 1000 rapid bootstraps. The *S*-like RNase sequence from *Bryopsis maxima* (AB164318) was used as an outgroup. Genome-wide identification of T2/*S*-type ribonucleases in 'Wanbai' pummelo was carried out with HMMER<sup>2</sup> based on Liang's method<sup>3</sup> and the identified *S*-RNases were also submitted to the phylogenetic analysis. The putative Rubiaceae (*Coffea*) sequences<sup>4,5</sup> are also indicated here for completeness and for comparison.

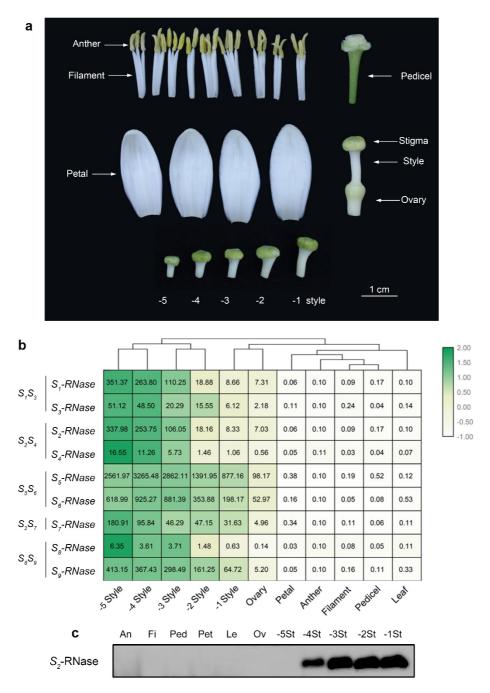
The T2/S-type ribonucleases grouped into Class I, II and III, as reported by Ramanauskas and Igić<sup>6</sup>. All functional S-RNases fall into the Class III clade). The class III T2/S-type RNases from the Roseaceae (Prunoideae and Maloideae) are well separated from the other class III T2/S-type RNases from the Solanaceae, Plantaginaceae and putative S-type RNases from the Rubiaceae. The S-type RNases from pummelo (Rutaceae) clustered together on an independent branch.



Supplementary Figure 5. Analysis of the S-haplotype of 391 Chinese pummelo accessions.

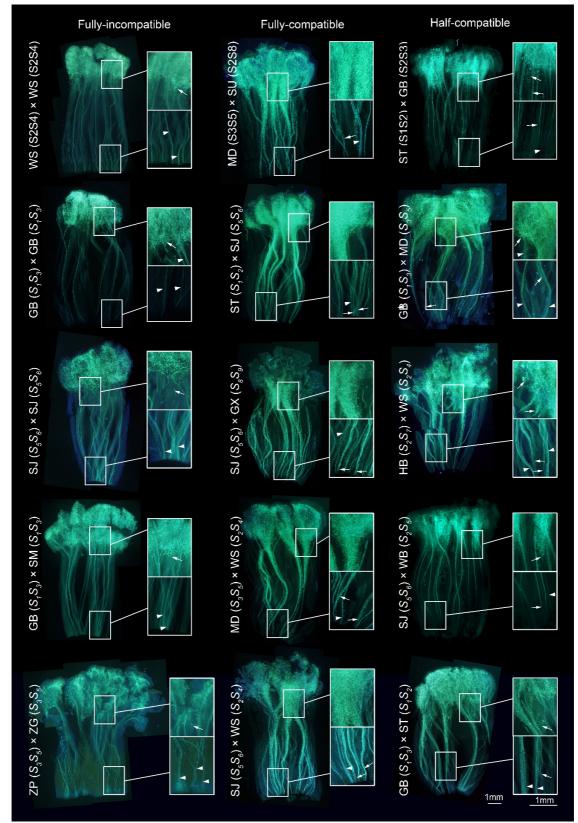
- (a) The distribution of 391 Chinese pummelo accessions. 391 pummelo accessions were collected from 11 provinces (brown) in China. The number of accessions from each province is indicated on the map.
- (b) The frequency of S<sub>1</sub>-RNase to S<sub>9</sub>-RNase in 391 pummelo accessions. The nine S-RNases identified, S<sub>1</sub>-RNase to S<sub>9</sub>-RNase were found in 76.2% of these accessions. Most occur at a low frequency, as expected for negative frequency dependent selection. The S<sub>2</sub>-RNase is present at the highest frequency with 30.2%. S<sub>4</sub>-RNase is present at the lowest frequency with 2.3%.

The S-haplotype of these pummelo accessions were assigned using PCR of leaf DNA with S-RNase ( $S_1$ -RNase to  $S_9$ -RNase) specific primers.



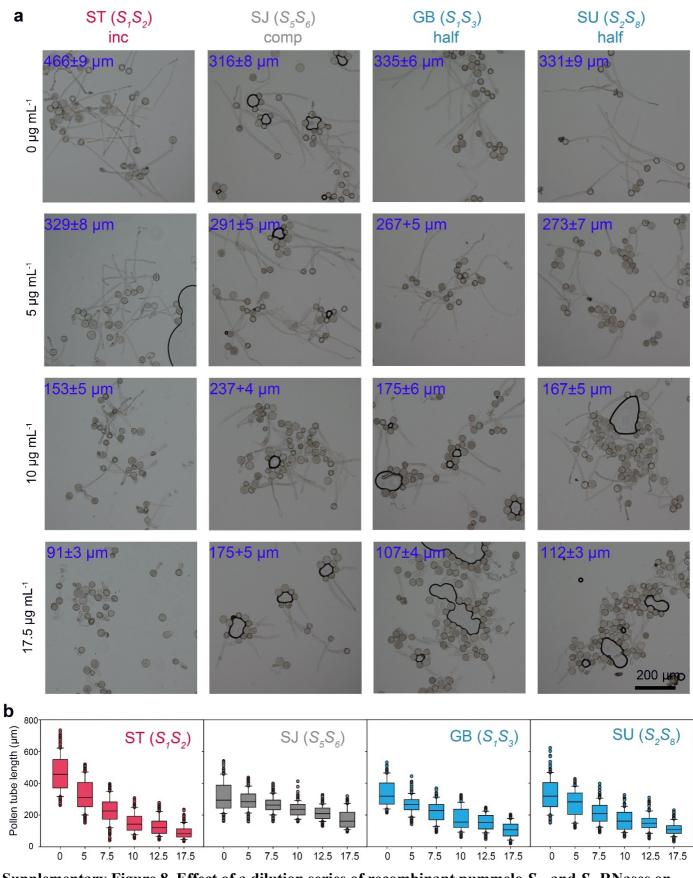
### Supplementary Figure 6. Morphology of pummelo floral organs and pistils at different developmental stages and expression of the *S*-RNases.

- (a) Images of pummelo floral organs. Top row: anthers, filaments and pedicel (stage 0 = open flower); middle row: petal and pistil (stage 0 = open flower); bottom row: pistils (stigma and style) at five stages during development: -5, -4, -3, -2, and -1 indicate days relative to anthesis; the mature style is ~1 cm in length.
- (b) qPCR showing temporal and tissue-specific expression of *S*<sub>1</sub>- to *S*<sub>9</sub>-*RNase* transcripts. The heat map shows the relative expression of nine *S*-*RNase* genes quantified using qRT-PCR in styles at different developmental stages: -5, -4, -3, -2, and -1 days before anthesis. An: anther; Fi: filament; Ped: pedicel; Pet: petal; Le: leaf; Ov: ovary; St: style. The scale bar (right) indicates expression levels (log<sub>2</sub>-transformed values). The mean transcript level (based on three biological replicates), is shown in each box.
- (c) Western blot showing expression of the  $S_2$ -RNase protein in various tissues and in pistils at different developmental stages ( $S_1S_2$  genotype). There was no expression in tissues except in style (St). In contrast to the transcript (see b), which peaked at -5 days and subsequently declined, protein levels were not detected at this early stage, and increased over time as the pistil matured. Experiments were repeated independently twice three times with similar results obtained for each.



**Supplementary Figure 7. Representative pollinated pummelo pistils stained with aniline blue**. Representative images (5 of each type of pollination, 15 in total) of aniline blue staining of pollinated pummelo pistils (5 days after pollination) classified in Supplementary Table 3. The accession names and their respective *S*-genotypes are indicated to the left of each block.

In fully-incompatible crosses, pollen tubes were inhibited near the top of the style (upper inset panel) and no significant long pollen tubes were observed in the style (lower inset panel); In fully-compatible crosses, bunches of pollen tubes extended through the pistil. In the half-compatible crosses; some pollen tubes extended to the base of the pistil, while others were inhibited near the top of the style. Pollen tubes (pt) are indicated with arrows. Vascular bundles (vb) are indicated with arrowheads. At least two pistils of each pollination combinations were observed (see **Supplementary Table 5**).



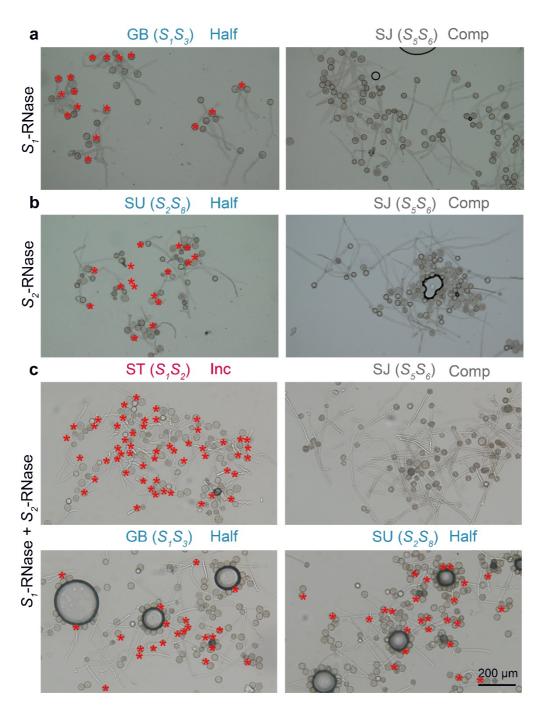
Supplementary Figure 8. Effect of a dilution series of recombinant pummelo  $S_1$ - and  $S_2$ -RNases on pollen tubes growing *in vitro*, showing increasing inhibitory activity (and some non-specific inhibitory activity).

(a) Representative images of the effect of a dilution series of *S*-RNase treatments on pummelo pollen tube growth using the *in vitro* bioassay. The concentrations of combined *S*<sub>1</sub>-RNase and *S*<sub>2</sub>-RNase are indicated at the left hand side of the panel (e.g. 5 μg mL<sup>-1</sup> indicates 5 μg mL<sup>-1</sup> *S*<sub>1</sub>-RNase + 5 μg mL<sup>-1</sup> *S*<sub>2</sub>-

RNase as a combined treatment). The mean pollen tube length  $\pm$  SEM for each treatment is shown in the upper left hand side of the corresponding representative image; > fifty pollen tubes were measured in three independent experiments (> 150 in total).

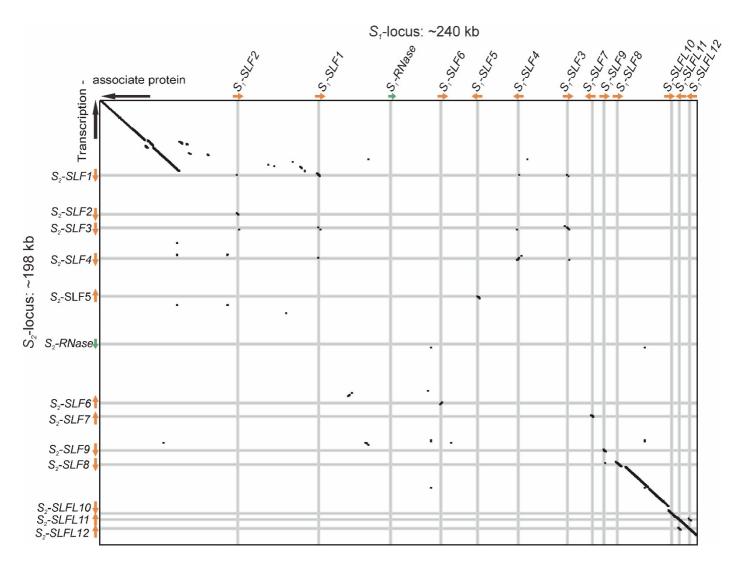
#### (b) Box plot showing quantitation of pollen tube length measured for the ST $(S_1S_2)$ , SJ $(S_5S_6)$ , GB

( $S_1S_3$ ) and SU ( $S_2S_8$ ) pummelo accessions. When treated with 10 µg mL<sup>-1</sup>  $S_1$ -RNase and 10 µg mL<sup>-1</sup>  $S_2$ -RNase combined, pollen from plants with genotype  $S_1S_2$  (an incompatible combination, red) showed a ~67% decrease in length compared to the untreated controls.  $S_5S_6$  pollen (a compatible combination, grey) showed some non-specific activity at higher concentrations. Pollen from plants of genotype  $S_1S_3$  or  $S_2S_8$  pollen (a half-compatible combination, blue) showed an overall ~50% decrease in pollen tube length. These dilution series were used to ascertain the optimal concentrations of  $S_1$ - and  $S_2$ -RNases for the in vitro SI bioassay. On the basis of these tests, a concentration of 10 µg mL<sup>-1</sup> was chosen for all the key test assays in this study, to obtain maximal inhibition with minimal non-specific activity. The length of >50 pollen tubes was measured for each replicate (n = 3 biologically independent replicates, >150 in total). Box and whisker plots show the distribution of individual pollen tube lengths in *in vitro* bioassays of recombinant  $S_1$ - and  $S_2$ -RNases with pollen from plants of different genotypes (box indicates the upper & lower quartile, with median; lines above and below indicate the range; dots indicate the outliers).



Supplementary Figure 9. Representative images of pummelo pollen tubes treated with recombinant *S*<sub>1</sub>-RNase and *S*<sub>2</sub>-RNase showing *S*-specific inhibitory activity.

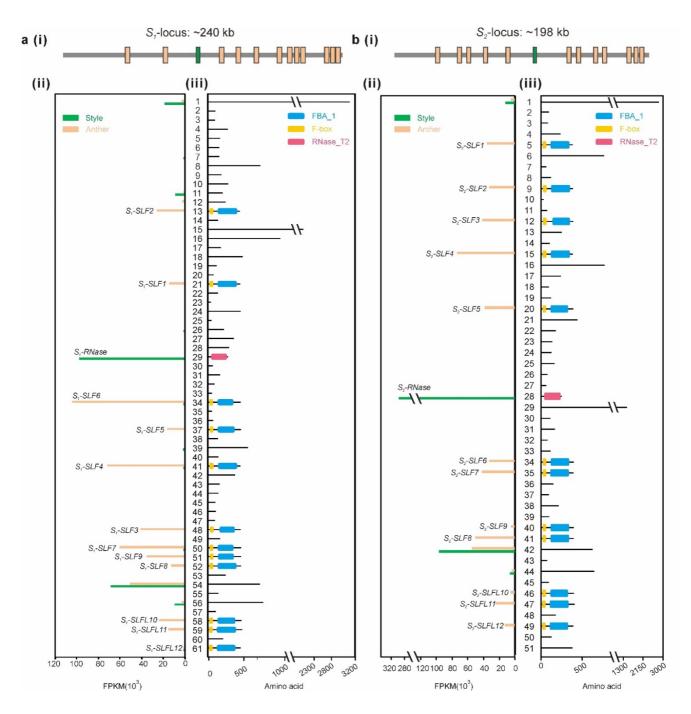
a - c, Representative images of the effect of recombinant  $S_I$ -RNase (a),  $S_2$ -RNase (b) and  $S_I$ - +  $S_2$ -RNase (c) treatments (10 µg mL<sup>-1</sup> per treatment) on pummelo pollen tube growth. For treatment of pollen with the  $S_I$ - or  $S_2$ -RNase separately, the outcomes are expected to be either half-compatible (half) where one S-allele is shared (e.g. for  $S_IS_2$ ) or fully compatible (comp); where no S-alleles are shared (e.g. for pollen from plants carrying  $S_5S_6$ ). Pollen tubes that were much shorter were judged to be inhibited (indicated by red asterisks). The accession name and S-genotype are indicated above each panel (e.g. accession ST has S-genotype  $S_IS_2$ ). Each treatments was repeated independently three times with similar results.



#### Supplementary Figure 10. Harr plot analysis between the pummelo S<sub>1</sub>-locus and the S<sub>2</sub>-locus.

Pattern matching analysis of homologies between DNA sequences (Harr plot analysis) between two pummelo *S*-loci ( $S_1$  and  $S_2$ ). Each citrus *S*-locus contains a *S*-*RNase* and 12 candidate *SLFs/SLFLs*. The arrows indicate the direction of transcription for each gene.

The Harr plot was carried out by GENETYX Ver. 14 (GENETYX Corp., Tokyo, Japan) using the following settings: Unit size to compare: 8 bases; Cut off number: 22 bases; Minimum length: 25 bases.



### Supplementary Figure 11. The FPKM and conserved domains of *SLF/SLFL* genes located at the pummelo $S_{1-}$ (a) and $S_{2-}$ locus (b).

(i) Cartoon showing the overall structure of the *S*-loci. The relative positions of the *S*-*RNase* (green box) and the *F*-box (cream boxes) genes on the pummelo *S*-locus are shown, with the length of the *S*-locus indicated above.

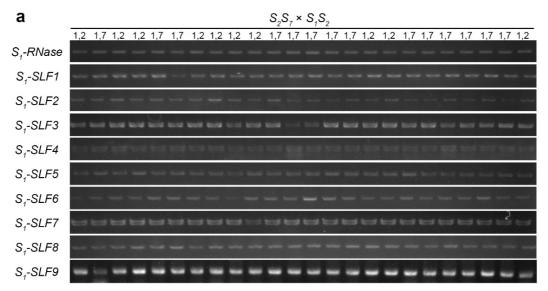
(ii) FPKM values for the 61 genes on the pummelo  $S_1$ -locus (a) and 51 genes on the  $S_2$ -locus (b). FPKM was calculated with pair-end reads from anthers and styles 5 days before anthesis from  $S_1S_3$  and  $S_2S_5$  pummelo respectively. The pummelo *S*-*RNase* gene was specifically expressed in the style (green bar) and *SLF/SLFL* genes were specifically expressed in anthers (cream bars).

(iii) Schematic diagram of the relative positions of the conserved F-box, FBA\_1 and RNase\_T2 domains in predicted proteins present at the pummelo  $S_I$ -locus (a) and  $S_2$ -locus (b). These domains were predicted by the conserved domains database (CDD) at NCBI. Each S-locus has one S-RNase (with RNase \_T2 domain, red block) and 12 SLFs/SLFLs, with F-box (yellow block) and FBA\_1 domain (blue block).

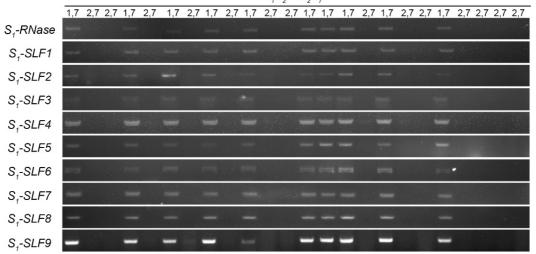
								<u> </u>		4.00
									1	2.83
1.00	1.72	1.39	0.97	0.80	0.59	21.60	14.75	10.21	S₁-SLF1	2.00 1.41
1.01	2.27	1.53	2.13	0.97	1.08	175.90	369.85	347.99	S₁-SLF2	1.00
1.00	0.17	0.93	0.58	0.02	0.09	166.52	443.93	483.01	S₁-SLF3	0.71 0.50
0.94	0.12	0.58	0.43	0.15	0.34	79.47	372.63	173.21	S₁-SLF4	
1.00	0.04	0.44	0.37	0.03	0.03	147.66	337.18	252.45	S₁-SLF5	
1.05	1.09	0.18	0.66	0.12	0.21	6.90	11.26	14.02	S₁-SLF6	
1.05	0.10	0.11	0.15	0.03	0.01	54.59	103.25	112.27	S₁-SLF7	
1.07	0.18	0.04	0.12	0.03	0.02	10.33	37.06	31.87	S₁-SLF8	
1.00	2.99	18.64	12.24	16.19	6.50	142.37	1690.87	1240.51	S₁-SLF9	
1.06	0.12	1.03	0.39	0.10	0.11	283.77	669.74	524.77	S <sub>2</sub> -SLF1	
1.00	0.00	0.17	0.26	0.00	0.00	110.50	137.52	701.37	S₂-SLF2	
1.01	4.23	1.03	1.16	0.22	0.14	41.78	73.06	71.08	S₂-SLF3	
1.04	0.59	1.34	0.58	0.40	0.67	70.73	456.49	388.17	S₂-SLF4	
1.00	0.13	0.12	0.14	0.00	0.05	48.39	143.79	166.56	S₂-SLF5	
1.00	1.42	0.47	1.00	1.77	2.01	111.30	113.09	201.04	S₂-SLF6	
1.01	0.05	0.13	0.16	0.02	0.03	68.77	96.81	104.07	S₂-SLF7	
1.07	0.59	0.25	0.35	0.18	0.46	6.43	86.59	65.48	S₂-SLF8	
1.00	2.39	18.64	2.00	2.55	1.22	42.91	696.33	212.81	S₂-SLF9	
style	veat <	Petal P	adicel Filf	iment C	wary Poller	tube p	ither F	ollen		

Supplementary Figure 12. Tissue-specific expression of pummelo SLF genes at the S<sub>1</sub>- and S<sub>2</sub>-loci.

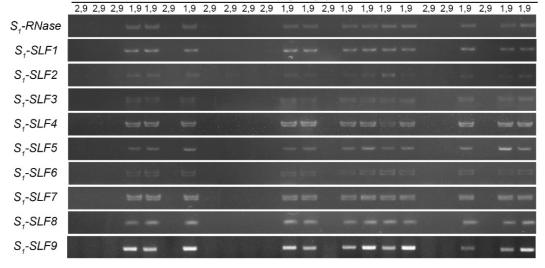
Heat map showing the relative expression of SLF genes in different tissues from pummelo. All the tissues were obtained from a plant with a  $S_1S_2$  genotype. The expression of each gene was quantified using qRT-PCR. The mean transcript levels (based on three biological replicates), is presented in each box. The scale bar on the right indicates the range of expression levels in log<sub>2</sub>-transformed values.

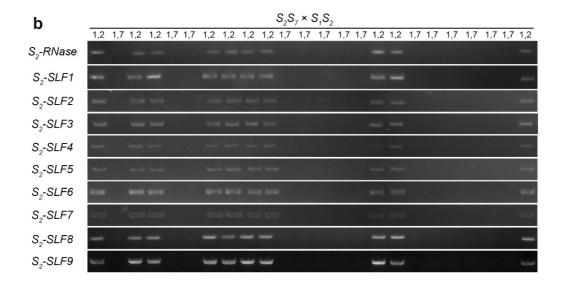


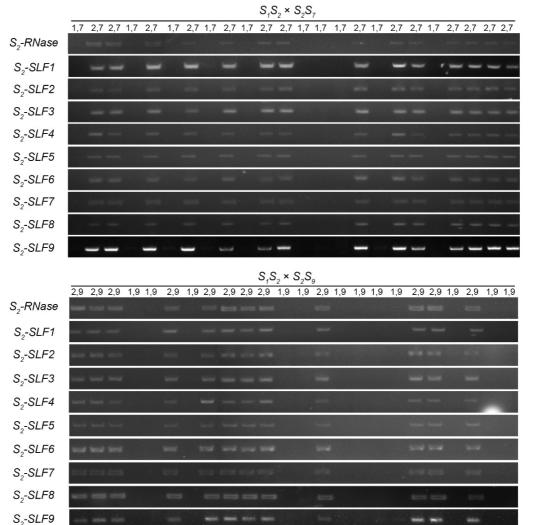
 $S_1S_2 \times S_2S_7$ 



 $S_1S_2 \times S_2S_9$ 







### Supplementary Figure 13. Genetic linkage between pummelo *S-RNase* and *SLF*s in the $S_{1-}$ (a) and $S_{2-}$ loci (b).

Tissue from full-sibling pummelo families segregating for haplotypes (1)  $S_2S_7 \times S_1S_2$ , (2)  $S_1S_2 \times S_2S_7$  and (3)  $S_1S_2 \times S_2S_3$  was used for PCR, with each family containing 24 individuals.

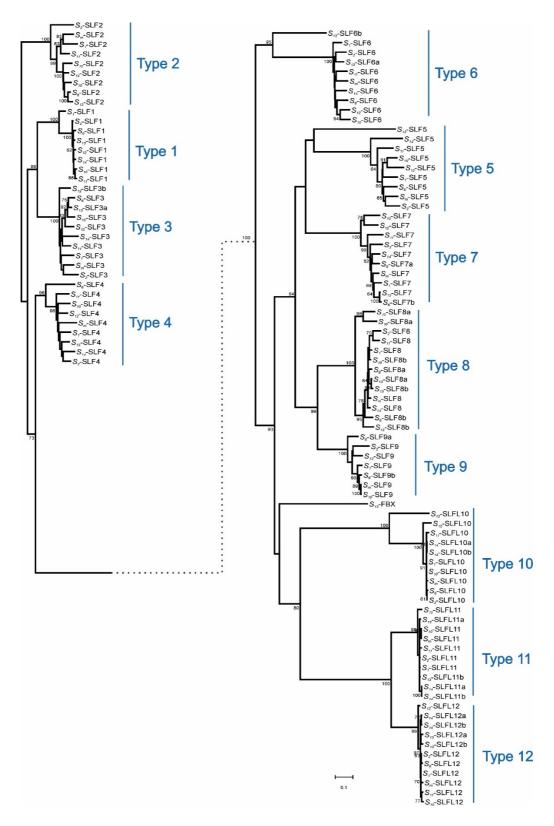
(a)  $SLF_{1-1}$  to  $SLF_{1-9}$  were only amplified from plants carrying the  $S_1$ -allele and not those carrying  $S_2$ ,  $S_7$ ,  $S_9$  alleles. (b)  $SLF_{2-1}$  to  $SLF_{2-9}$  were only amplified from plants carrying the  $S_2$ -allele and not those carrying  $S_1$ ,  $S_7$ ,  $S_9$  alleles. These data show that all the pummelo  $SLF_3$  are genetically linked to their cognate *S*-*RNase*. All of the genotypes were repeated independently two times with the same results.

S <sub>1</sub> (12)	T2 318 T1 279 R 181 T6 139 T5 150 T4 190 T3 85 T7 39 T9 38 T8 214 T10 1.5 T11 30 T12	BAC	C. maxima	
S <sub>2</sub> (12)	T1 16 1 T2 53 T3 124 T4 159 T5 20.8 R 24.8 T6 44 T7 144 T9 42 T8 21.8 T10 1.3 T11 3.0 T12	BAC	C. maxima	
S <sub>6</sub> (14)	T1 1.9 T2 5.2 T3 61.7 T4 11.3 R 186 T5 4.1 T6 41.2 T7 9.4 T9 2.9 T8 1.3 T7 4.6 T9 2.8 T8 26.2 T10	5.5 T12	chr1:1048218-1302327 C	C. maxima
S <sub>10</sub> (13)	T1 33 T2 59 T3 45 T4 23 R 338 T5 127 T8 243 T7 56 T8 263 T9 29 T8 204 T10 13 T1 26 T1	2	scaffold85925_cov91:1946194-	-2147329 C. reticulata
S <sub>11</sub> (11)	T1 20 T2 170 T3 244 T4 11.6 R 27.4 T5 17.0 T6 13.5 T7 36.5 T8 19.3 T10 1.3 T11 3.0 T12 scaffol	d_7: 977	7168-1204057 C. clementina	
S <sub>12</sub> (13)	T1 2.0 T2 14.9 T3 5.6 T4 0.7 R 36.7 T5 49.6 T7 56.4 T6 50.9 T8 6.0 T9 29.4 T8 24.8 T10 4.6 111 2.9 T1	2 sca	iffold_20559: 1812108-2222788	
S <sub>13</sub> (17)	71 20 72 74 73 160 73 4.1 74 34.9 76 36.5 7.4 R 7.6 710 R -67.7 76 39.1 77 6.6 78 14.9 78	18.9 T11	3.0 T12 11.2 T5 27.8 T11 3.0 T12	scaffold_470: 183317-210783 scaffold_539 <i>C. ichangensis</i> scaffold_315: 1-219005
S <sub>14</sub> (14)	11 21 12 113 13 219 14 294 (R 40.9 15) 2 - 37.6 16 35.0 17 53.5 18 2 - 21.6 110 1.3 111 3.1 112 2.2 110 1.	3 11 3.0	scaffold_12: 1-161191 <u>5 112</u> scaffold_698 <i>C. medic</i> scaffold_764: 99650-120	
S <sub>m</sub> (11)	12 29.9 13 28.0 14 49.0 R 18.8 15 51.0 16 8.5 17 21.7 19 2.9 18 20.6 110 1.3 111 3.0 112 chr1: 27,44	40,275-2	27,791,238 C. sinensis	

### Supplementary Figure 14. Schematic diagram of the *S-RNase* and *SLF/SLFL* genes at the citrus *S*-loci.

Each citrus *S*-locus contains one *S*-*RNase* and multiple *SLF/SLFL* genes; the number of *SLF/SLFL* genes is indicated at the left of each *S*-locus in brackets. Genes are indicated with block arrows. The point of each block arrow indicates the direction of transcription. *S*-*RNase* genes are indicated with black arrows labeled with "R". *SLF/SLFL* genes are indicated with arrows labeled with "Tx". The "x" indicates the type of *SLF/SLFL* genes. The 12 types of *SLF/SLFL* genes are indicated with different colors. *SLF/SLFL* gene that belonged to none of the 12 types is indicated with white arrows without any labeling. The *S*-haplotype identified from the *C. maxima* genome was named  $S_6$ , because the *S*-*RNase* on the *S*-locus is identical to  $S_6$ -*RNase*. The *S*-haplotype identified from the *C. sinensis* genome was named  $S_m$ , because the *S*-*RNase* (red star) on the *S*-locus is mutated and encodes a truncated protein (see **Supplementary Fig. 11**). Note that the *S*-locus of *C. clementina* (*S*<sub>11</sub>-locus) is located on scaffold 7, rather than scaffold 5 as previously reported<sup>7</sup>.

 $S_{1}$ - and  $S_{2}$ -loci were screened from a BAC library. The other S-loci were obtained from available genome databases and their locations are indicated at the right of each S-locus. Because the assembly of the genome sequences of these species is incomplete and still at the scaffold stage, for the  $S_{13}$ - and  $S_{14}$ -loci. we obtained two and three fragments respectively, based on BLAST results (each conserved end has a homologous fragment, but the fragments have not been assembled together).



#### Supplementary Figure 15. Phylogeny of 117 *F-box* genes from nine *S*-loci from citrus.

Sequences of F-box proteins from different citrus species (*C. maxima*, *C. reticulata*, *C. clementina*, *C. sinensis*, *C. medica*, *C. ichangensis* and *A. buxifolia*) were analysed and grouped into 12 types based on their deduced amino acid sequences. They were named  $S_n$ -SLFx/ $S_n$ -SLFLx, according to the nomenclature used by Kubo et al.<sup>8,9</sup>, with n and x indicating the S-haplotype and the type respectively. If two copies were present in one SLF type, they are indicated by a and b; e.g.  $S_{13}$ -SLF3a and  $S_{13}$ -SLF3b. The F-box that could not be grouped to the 12 types was named  $S_n$ -FBX, e.g.  $S_{13}$ -FBX. The allelic *SLFL*s within the type 10, 11 and 12 cluster grouped together on a very short branch.

SRNase : MKINFC	IFIVLFVYCIS	20 SGAAQNNSGFD SVENNSGFD SVENNSGFD	HFWLVLSWPP	VYCLQIRCER	<b>KPTDFVLHGL</b>	WPVNSTGHSL	KNSTNGT :	75 73 73
SRNase : PNFYSM	LRNHSFGIEMD	100 EHWPSLG <mark>TTD</mark> G EHWPSLGSKEG EHWPSLGSKEG	RDPYKHIRFW	EHEWEEHGSG	QPYGDTYYLQ	SAIRLRKSVN	LLRILRI :	: 150 : 148 : 148
SRNase : KEYFQM	EGVTGKL <mark>G</mark> TWM	A <mark>t</mark> khvygyp <b>i</b> l		VTICVDGQAR		RSTNCRNIIT	: 1	166

### Supplementary Figure 16. Deduced amino acid sequence alignments for the pummelo $S_1$ -, $S_m$ - and $S_m^R$ -RNases.

The sequence of the pummelo  $S_I$ -RNase, (which has the highest homology to the  $S_m$ -RNase, 77% deduced amino acid identity, encodes 222 amino acid residues.

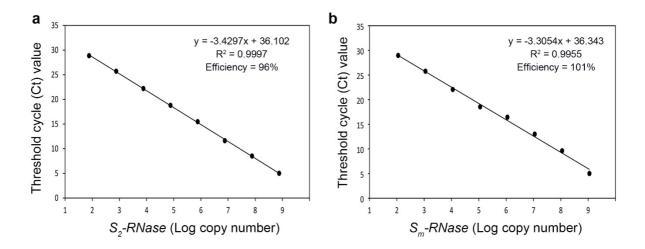
The natural mutant  $S_m$ -RNase gene has a stop codon at nucleotide position 498, resulting in a truncated coding sequence. The deduced amino acid sequence (166 residues) of  $S_m$ -RNase was, as expected, shorter than the unmutated  $S_l$ -RNases.

We engineered a "recovered" version ( $S_m^R$ -RNase) by inserting an adenine nucleotide at position 443 (red star, see **Supplementary Fig. 17**) in the truncated  $S_m$ -RNase. This resulted in the "recovered"  $S_m^R$ -RNase being extended to full length, equivalent to the normal S-RNase size, with a predicted transcript of 221 amino acids. The  $S_m$ -RNase has lost the hypervariable domains HV4 and HV5 and the conserved C4 and C5 domains.



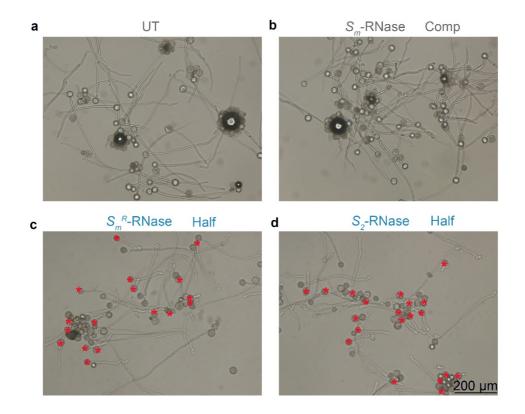
#### Supplementary Figure 17. Nucleotide sequence alignments of pummelo $S_1$ -, $S_m$ - and $S_m^R$ -RNase.

To recover the function of the pummelo  $S_m$ -RNase, an adenine ("A", red star) nucleotide was introduced in  $S_m^R$ -RNase using the sequence of the  $S_I$ -RNase, which has the nearest sequence identity (~85% nucleotide identity) to the  $S_m/S_m^R$ -RNase, as a template.



Supplementary Figure 18. Standard curves of the pummelo  $S_{2-}$  (a) and  $S_m$ -RNases (b) generated by real-time PCR.

Because we used different primers to amplify the pummelo  $S_2$ - and  $S_m$ -RNases, in order to be able to compare how their levels of expression compared, we needed to check that they had similar efficiencies. The Ct value over log copy number was plotted for the serial dilutions of input DNA templates. The efficiencies of the  $S_2$ - and  $S_m$ -RNase primers were calculated as described by Workenhe et al<sup>10</sup>, showing that the  $S_m$ - and  $S_2$ -RNase primers have comparable amplification efficiencies. The equation of each regression line is shown; this was used to calculate the absolute copy number of  $S_2$ - and  $S_m$ -RNase in Figure 4c.

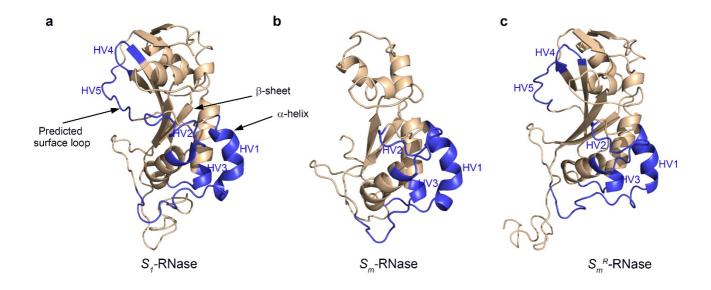


# Supplementary Figure 19. Representative images of pummelo pollen tubes from a plant with the $S_2S_m$ genotype growing in vitro after treatment with recombinant pummelo $S_m$ -RNase, $S_m^R$ -RNase or $S_2$ -RNase.

- (a) Untreated pollen (UT) had long pollen tubes.
- (b) Pollen from a plant with the  $S_2S_m$  genotype was not inhibited by the mutant  $S_m$ -RNase protein.
- (c) Pollen from a plant with the  $S_2S_m$  genotype had ~50% pollen tubes inhibited by the recombinant "recovered"  $S_m^R$ -RNase. This shows this recovered form has biological activity.
- (d) Pollen from a plant with the  $S_2S_m$  genotype had ~50% pollen tubes inhibited by the recombinant  $S_2$ -RNase. This shows that the  $S_2$  pollen is capable of being inhibited by cognate  $S_2$ -RNase.

This demonstrates the lack of pollen tube inhibitory activity of the mutant  $S_m$ -RNase protein and the S-specific inhibitory activity of the recovered  $S_m^R$ -RNase. Quantitation of these data are shown in Figure 4h.

Variant recombinant pummelo S-RNases (10  $\mu$ g mL<sup>-1</sup> per treatment) were added to pollen in the *in vitro* SI bioassay for 7 hours. All pollen was from a pummelo plant with the  $S_2S_m$  genotype (containing 50%  $S_m$  pollen and 50%  $S_2$  pollen). For the sake of clarity, inhibited pollen tubes are indicated with red asterisks. Each treatments was repeated independently three times with similar results.

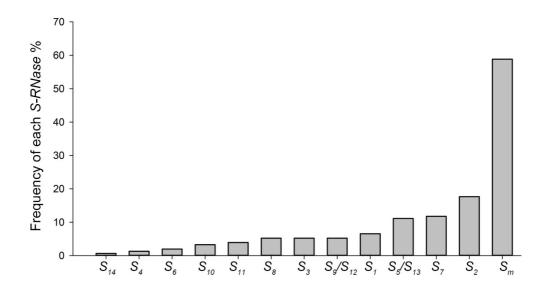


### Supplementary Figure 20. Three-dimensional structural predictions of $S_{1-}$ (a), $S_{m-}$ (b) and $S_{m}^{R}$ -RNase (c).

- (a) The predicted 3D structure of the S-RNase ( $S_1$ -RNase) proteins has five hypervariable regions (in blue) and all of them are predicted to reside at the surface of the protein.
- (b) The predicted 3D structure of the mutant  $S_m$ -RNase. The HV4 and HV5 domains are missing.
- (c) The predicted 3D structure of the "recovered"  $S_m^R$ -RNase is (as expected) similar to that of  $S_l$ -RNase with five hypervariable regions.

The predicted 3D structure of the *S*-RNases ( $S_1$ -RNase and  $S_m^R$ -RNase) comprises six  $\alpha$ -helices and six  $\beta$ -sheets. The hypervariable regions (HV1-HV5) are labelled in blue. Comparisons of these structural predictions (and with published *S*-RNase structural predictions from *Nicotiana*, which implicate HVa and HVb in recognition as they are within surface loops)<sup>11</sup>, suggest that the pummelo hypervariable domains HV4 and HV5, which are also predicted to reside at the surface of the protein may be involved in *S*-specific recognition, as the mutant  $S_m$ -RNase is defective: retaining RNase activity, but lacking pollen inhibitory activity).

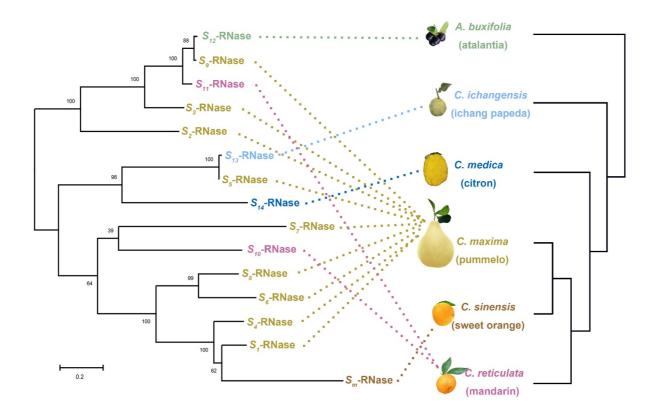
The structural predictions were carried out using I-TASSER server; see Methods for details.



#### Supplementary Figure 21. Frequency of S-RNase genes in 153 citrus accessions.

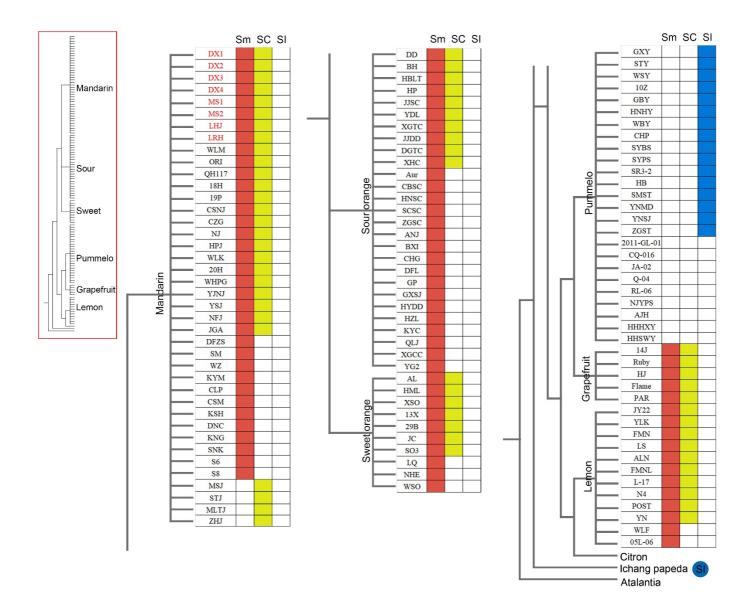
All of the *S-RNases* showed evidence of negative frequency dependent selection, with a low occurrence in the 153 citrus accessions examined. This pattern of distribution was also observed in 391 pummelo accessions (see **Supplementary Fig. 5b**). In contrast, the mutant  $S_m$ -RNase has a high occurrence (58.8% frequency) in the citrus accessions, which conflicts with it being controlled by negative frequency dependence.

Short read mapping failed to distinguish the  $S_9$ -RNase and  $S_{12}$ -RNase pairs of genes and those of the  $S_5$ -RNase and  $S_{13}$ -RNase because their sequences were similar. Thus, the bars of  $S_9/S_{12}$  and  $S_5/S_{13}$  represent the frequencies of both  $S_9$ -RNase and  $S_{12}$ -RNase and both  $S_5$ -RNase and  $S_{13}$ -RNase, respectively.



Supplementary Figure 22. Phylogeny of 15 S-RNases from citrus varieties.

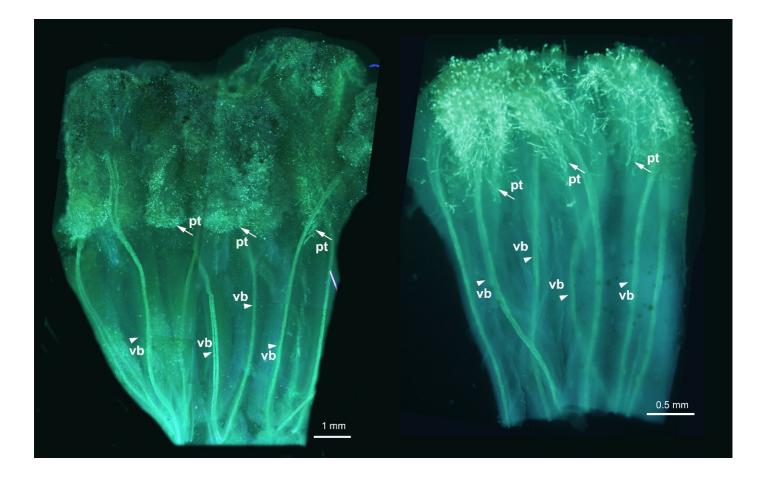
We put the phylogenetic tree for the citrus *S-RNases* together with the phylogenic tree of the citrus species, as described by Wang et al<sup>12</sup>. The different coloured text indicates the *S*-RNase from different citrus species. The phylogeny of the *S-RNases* was inconsistent with the phylogeny of citrus species. This suggests that the *S*-RNases are either older than the formation of these accessions or that the divergence of these *S*-RNases is earlier than citrus divergence.



#### Supplementary Figure 23. A tree illustration of the conservation of the *S*<sub>m</sub>-*RNase* in citrus accessions.

The phylogenic tree was drawn as described by Wang et al<sup>12</sup>. The main figure shows an expansion of the tree shown on the far left.

Ninety out of the 153 citrus accessions possess the  $S_m$ -RNase (red block), of which the self-compatibility of 56 accessions (>60%, yellow block) was demonstrated using aniline blue staining. Several accessions (MSJ, STJ, MLTJ and ZHJ) were self-compatible, but they did not have the  $S_m$ -RNase, suggesting that the disruptive  $S_m$ -RNase is the primary mutation responsible for the SC phenotype in citrus, but that it is not the only mutation. The  $S_m$ -RNase was not present in the self-incompatible accessions (blue blocks). *Ichang papeda*, which is self-incompatible (blue circle; see **Supplementary Fig. 23**), is an ancestral species, as shown in the tree. The wild mandarin accessions are indicated in red font.



#### Supplementary Figure 24. Evidence that *Ichang papeda* is self-incompatible.

Representative aniline blue staining of self-pollinated styles from two *Ichang papeda* accessions collected from different provinces. Five pollinations from each accession were examined. The pollen tubes of both of them were inhibited near the top of the style, which is a SI phenotype. Pollen tubes (pt) are indicated with arrows; vascular bundles (vb) are indicated with arrowheads. At least five self-pollinated pistils of the two accessions were observed.

#### Liang et. al., Supplemental Tables

No.	Accession name	Common name	Species	Scientific name <sup>a</sup>	Harvest place of the samples
1	ST	Shatian pummelo	Pummelo	C. maxima	Guilin City, Guangxi, China
2	SU	Sour pummelo	Pummelo	C. maxima	Guilin City, Guangxi, China
3	SJ	Shuijing pummelo	Pummelo	C. maxima	Dehong City, Yunnan, China
4	GX	Guanximiyou pummelo	Pummelo	C. maxima	Dehong City, Yunnan, China
5	MD	Burma pummelo	Pummelo	C. maxima	Dehong City, Yunnan, China
6	WS	Acidless pummelo	Pummelo	C. maxima	Dehong City, Yunnan, China
7	WB	Wanbai pummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
8	GB	Gaoban pummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
9	НВ	HB pummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
10	HN	Huanong red pummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
11	ZP	Purple pummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
12	TG	Thailand acidless ummelo	Pummelo	C. maxima	Wuhan City, Hubei, China
13	SM	Shimengshatian pummelo	Pummelo	C. maxima	Changde City, Hubei, China
14	ZG	Ziguishatian pummelo	Pummelo	C. maxima	Yichang City, Hubei, China
15	CL	Cilitian pummelo	Pummelo	C. maxima	Changsha City, Hunan, China

## Supplementary Table 1. Overview of the pummelo accessions used in the pollinations in this study

<sup>a</sup>: The names *C. maxima* and *C. grandis* are both currently used for pummelo. As *C. maxima* is adopted under the International Code of Botanical Nomenclature, we use *C. maxima* throughout.

	\$/ð	<b>GB</b> <i>S</i> <sub>1</sub> <i>S</i> <sub>3</sub>	HB S <sub>2</sub> S <sub>7</sub>	WB <i>S</i> <sub>2</sub> <i>S</i> <sub>5</sub>	SJ S5S6	GX <i>S</i> 8 <i>S</i> 9	MD <i>S</i> 3 <i>S</i> 5	<b>ST</b> <i>S</i> 1 <i>S</i> 2	SU S2S8	WS <i>S</i> 2 <i>S</i> 4	Unpollin ated
GB	Fruit set ratio (%)ª	0.00	22.45	23.26	39.39	21.88	30.95	21.62	27.27	33.33	0.00
<b>S</b> <sub>1</sub> <b>S</b> <sub>3</sub>	Seeds per fruit <sup>b</sup>	0	183±12	165±12	152±17	132±14	172±8	145±25	149±11	158±10	0
HB	Fruit set ratio (%)		3.03	23.33	34.00	47.06	40.35	77.36	60.53	43.18	5.26°
<b>S</b> <sub>2</sub> <b>S</b> <sub>7</sub>	Seeds per fruit		0	87±12	94±5	97±15	101±5	93±11	88±9	66±7	0
WB	Fruit set ratio (%)			12.12	54.55	8.70	41.18	42.86	18.60	17.95	6.06°
S <sub>2</sub> S <sub>5</sub>	Seeds per fruit			0	77±4	68±15	92±6	61±3	83±8	90±5	0
SJ	Fruit set ratio (%)				30.77	67.92	81.36	36.07	57.35	43.06	12.90°
S <sub>5</sub> S <sub>6</sub>	Seeds per fruit				0	179±11	197±3	142±32	183±22	221±21	0
GX	Fruit set ratio (%)					60.00	53.85	82.35	75.00	33.33	21.21°
S8S9	Seeds per fruit					0	120±11	110±9	108±9	111±6	0
MD	Fruit set ratio (%)						0.00	20.97	25.40	5.66	0.00
S <sub>3</sub> S <sub>5</sub>	Seeds per fruit						0	127±14	128±10	101±29	0
ST	Fruit set ratio (%)							0.00	9.26	6.00	0.00
<i>S</i> <sub>1</sub> <i>S</i> <sub>2</sub>	Seeds per fruit							0	67±10	104±17	0
SU	Fruit set ratio (%)								0.00	16.67	0.00
S <sub>2</sub> S <sub>8</sub>	Seeds per fruit								0	96±6	0
WS	Fruit set ratio (%)									0.00	0.00
S <sub>2</sub> S <sub>4</sub>	Seeds per fruit									0	0

### Supplementary Table 2. Fruit set and seed number of self- and cross-pollinations between different pummelos (*C. maxima*)

Self- and cross-pollinations between different pummelos (*C. maxima*) were performed. Fruit set and seed number established that these accessions were self-incompatible. Unpollinated flowers were also assessed and established several parthenocarpic accessions.

Fruit set ratios varied due to different climate and cultivation techniques in sampled provinces.

<sup>a</sup>: Fruit set ratio = Number of fruit/pollinated flowers\*100.

<sup>b</sup>: The seeds per fruit value is shown in mean  $\pm$  SEM (n > 5).

<sup>c</sup>: The non-zero fruit set ratio for non-pollination indicates that this accession is characterized by parthenocarpy.

Species (S- genotype)	Sample name <sup>a</sup>	Tissue <sup>b</sup>	Number of read pairs	Clean bases (G)	Read length (bp)	GC (%)	SRR id in GenBank
	SU_A1_1	Anther from -1	34986795	10.50	150	44.63	SRR8862738
	SU_A1_2	DBA	47440832	14.23	150	44.73	SRR8862737
	SU_S1_1	Style from -1	49400601	14.82	150	43.29	SRR8862740
Sour	SU_S1_2	DBA	46643336	13.99	150	43.34	SRR8862739
pummelo $(S_2S_8)$	SU_S3_1	Style from -3	46429691	13.93	150	43.86	SRR8862742
	SU_S3_2	DBA	49569693	14.87	150	44.37	SRR8862741
	SU_S5_1	Style from -5	34592510	10.38	150	44.54	SRR8862744
	SU_S5_2	DBA	38624135	11.59	150	44.26	SRR8862743
	SJ_A_1	Anther from -1	35650637	10.70	150	44.68	SRR8862889
	SJ_A_2	DBA	49096449	14.73	150	45.24	SRR8862888
c1	SJ_S1_1	Style from -1	48395409	14.52	150	44.20	SRR8862891
Shuijing pummelo	SJ_S1_2	DBA	57505312	17.25	150	44.18	SRR8862890
(S5S6)	SJ_S3_1	Style from -3	60446005	18.13	150	44.43	SRR8862893
	SJ_S3_2	DBA	48320149	14.50	150	44.83	SRR8862892
	SJ_S5_1	Style from -5	35372692	10.61	150	44.88	SRR8862895
	SJ_S5_2	DBA	56603062	16.98	150	44.17	SRR8862894
	GX_A_1	Anther from -1	35249007	10.57	150	44.18	SRR8863082
	GX_A_2	DBA	47088015	14.13	150	44.56	SRR8863081
	GX_S1_1	Style from -1	54147780	16.24	150	43.87	SRR8863080
Guanximiyou	GX_S1_2	DBA	51849281	15.55	150	44.53	SRR8863079
pummelo $(S_8S_9)$	GX_S3_1	Style from -3	42133229	12.64	150	44.42	SRR8863078
	GX_S3_2	DBA	49961516	14.99	150	44.52	SRR8863077
	GX_S5_1	Style from -5	34985907	10.50	150	44.38	SRR8863076
	GX_S5_2	DBA	47723135	14.32	150	44.96	SRR8863075
	MD_A1_1	Anther from -1	35202890	10.56	150	44.52	SRR8863197
	MD_A1_2	DBA	40000748	12.00	150	44.89	SRR8863198
	MD_S1_1	Style from -1	46929628	14.08	150	43.17	SRR8863195
Burma	MD_S1_2	DBA	50304716	15.09	150	43.39	SRR8863196
pummelo $(S_3S_5)$	MD_S3_1	Style from -3	48058900	14.42	150	44.20	SRR8863201
	MD_S3_2	DBA	42769012	12.83	150	44.26	SRR8863202
	MD_S5_1	Style from -5	35605996	10.68	150	44.36	SRR8863199
	MD_S5_2	DBA	38898539	11.67	150	44.49	SRR8863200
A ' 11	WS_A_1	Anther from -1	35131284	10.54	150	44.45	SRR9124567
Acidless pummelo	WS_A_2	DBA	48123801	14.44	150	45.32	SRR9124568
$(S_2S_4)$	WS_S1_1	Style from -1	42166068	12.65	150	44.40	SRR9124569
	WS_S1_2	DBA	50294489	15.09	150	44.15	SRR9124570

## Supplementary Table 3. Detailed information relating to data from citrus style and anther RNA-seq libraries.

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·	r	T	Т	1		1	
Acidless	WS_S3_1	Style from -3	51303398	15.39	150	44.36	SRR9124563
pummelo	WS_S3_2	DBA	53274604	15.98	150	44.31	SRR9124564
$(S_2S_4)$	WS_S5_1	Style from -5	35225241	10.57	150	44.51	SRR9124565
	WS_S5_2	DBA	54403425	16.32	150	44.45	SRR9124566
	WB_A_1	Anther from -1	34958874	10.49	150	44.59	SRR8868189
	WB_A_2	DBA	45894467	13.77	150	45.41	SRR8868188
	WB_S1_1	Style from -1	46744496	14.02	150	43.73	SRR8868191
Wanbai	WB_S1_2	DBA	43126224	12.94	150	44.27	SRR8868190
pummelo (S2S5)	WB_S3_1	Style from -3	57056644	17.12	150	43.49	SRR8868193
	WB_S3_2	DBA	44779195	13.43	150	44.30	SRR8868192
	WB_S5_1	Style from -5	34476290	10.34	150	44.47	SRR8868195
	WB_S5_2	DBA	49019973	14.71	150	45.10	SRR8868194
	GB_A_1	Anther from -1	35134343	10.54	150	44.35	SRR8872464
	GB_A_2	DBA	48866759	14.66	150	44.65	SRR8872465
G 1	GB_S1_1	Style from -1	47323297	14.20	150	44.05	SRR8872462
Gaoban pummelo	GB_S1_2	DBA	54437906	16.33	150	43.91	SRR8872463
$(S_1S_3)$	GB_S3_1	Style from -3	47402934	14.22	150	44.15	SRR8872468
	GB_S3_2	DBA	43047147	12.91	150	44.07	SRR8872469
	GB_S5_1	Style from -5	35295439	10.59	150	44.41	SRR8872466
	GB_S5_2	DBA	52479355	15.74	150	44.25	SRR8872467
	HB_A_1	Anther from -1	34354387	10.31	150	44.73	SRR8873603
	HB_A_2	DBA	37430244	11.23	150	45.16	SRR8873602
	HB_S1_1	Style from -1	48755530	14.63	150	44.65	SRR8873601
HB pummelo	HB_S1_2	DBA	45563444	13.67	150	44.63	SRR8873600
$(S_2S_7)$	HB_S3_1	Style from -3	48163285	14.45	150	44.90	SRR8873607
	HB_S3_2	DBA	52484687	15.75	150	44.80	SRR8873606
	HB_S5_1	Style from -5	34936798	10.48	150	44.45	SRR8873605
	HB_S5_2	DBA	53906104	16.17	150	44.29	SRR8873604
	JW_A_1	Anthor	39652164	11.90	150	44.18	SRR10168371
Cocktail grapefruit	JW_A_2	Anther	39805971	11.94	150	44.48	SRR10168370
$(S_2S_m)$	JW_S_1	Stula	40976310	12.29	150	44.49	SRR10168370
	JW_S_2	Style	44653340	13.40	150	44.50	SRR10168368

Data from 68 RNA-seq libraries of style and anther from eight pummelos and one grapefruit. Nine candidate S-RNase genes with complete open reading frames (ORFs) were identified. <sup>a</sup>: Sample name is designate as A-B-C, with A indicating the accession code (Supplementary Table 1), B indicates the tissue, C indicates the repetition.

<sup>b</sup>: -1, -2, -3, -4 and -5 DBA represents 1, 2, 3, 4, and 5 days before anthesis.

Supplementary Table 4. Predicted Mrs and IEFs for S-RNases from the Rutaceae with reference to
those in the Plantaginaceae, Solanaceae, and Rosaceae.

Gene	Organism	Full length	Amino acid	Molecular mass (kDa) <sup>a</sup>	Isoelectric point <sup>a</sup>	Source	Accession number
S <sub>1</sub> -RNase	C. maxima	669	222	23.38	8.23	In this study	MN652897
S <sub>2</sub> -RNase	C. maxima	699	232	24.17	9.22	In this study	MN652898
S <sub>3</sub> -RNase	C. maxima	696	231	24.06	9.11	In this study	MN652899
S4-RNase	C. maxima	675	224	23.16	8.84	In this study	MN652900
S5-RNase	C. maxima	660	219	23.16	7.71	In this study	MN652901
S <sub>6</sub> -RNase	C. maxima	660	219	22.96	9.39	In this study	MN652902
S <sub>7</sub> -RNase	C. maxima	696	231	24.02	8.93	In this study	MN652903
S <sub>8</sub> -RNase	C. maxima	690	229	24.47	7.67	In this study	MN652904
S9-RNase	C. maxima	690	229	24.10	9.33	In this study	MN652905
S10-RNase	C. reticulata	690	229	24.02	9.12	In this study	MN652906
S <sub>11</sub> -RNase	C. reticulata	690	229	24.08	9.47	In this study	MN652907
S <sub>12</sub> -RNase	A. buxifolia	690	229	24.25	9.30	In this study	MN652908
S13-RNase	C. ichangensis	660	219	23.22	7.71	In this study	MN652909
S14-RNase	C. medica	678	225	22.91	8.27	In this study	MN652910
Sm-RNase	C. sinensis	501	166	17.47	7.24	In this study	MN652911
Sm <sup>R</sup> -RNase	C. sinensis	666	221	23.59	8.23	In this study	MN652912
S <sub>5</sub> -RNase	Antirrhinum hispanicum	702	233	23.83	9.01	Xue et al, 1996 <sup>13</sup>	X96464
S7-RNase	Petunia x hybrida	657	218	23.08	8.32	Kubo et al, 2010 <sup>8</sup>	AB568388
Sc-RNase	Malus spectabilis	672	223	22.97	9.13	Ushijima et al, 1998 <sup>14,15</sup>	FJ943264

<sup>a</sup>: The molecular mass and the isoelectric point of the *S*-RNases were predicted using the mature protein sequence without the signal peptide.

All of the S-RNases from the Rutaceae have a similar full length (~ 660 bp) coding region, amino acid number (~ 220), molecular weight (~ 24 kDa) and basic isoelectric point. They are similar to the characteristics of sample S-RNases from the Plantaginaceae, Solanaceae, and Rosaceae (indicated in blue). S-RNases differ from other RNases in having unusually high isoelectric points, which is a key characteristic of these proteins.

₽/♂	ST <i>S</i> 1 <i>S</i> 2	GB <i>S</i> <sub>1</sub> <i>S</i> <sub>3</sub>	SM <i>S</i> 1 <i>S</i> 3	WS <i>S</i> <sub>2</sub> <i>S</i> <sub>4</sub>	TG <i>S</i> 2 <i>S</i> 4	WB <i>S</i> <sub>2</sub> <i>S</i> <sub>5</sub>	MD <i>S</i> <sub>3</sub> <i>S</i> <sub>5</sub>	ZP <i>S</i> 3 <i>S</i> 5	ZG <i>S</i> 3 <i>S</i> 5	SJ <i>S</i> 5 <i>S</i> 6	HB <i>S</i> <sub>2</sub> <i>S</i> <sub>7</sub>	CL <i>S</i> 1 <i>S</i> 7	HN <i>S</i> 1 <i>S</i> 8	SU S <sub>2</sub> S <sub>8</sub>	GX S8S9
ST <i>S</i> 1 <i>S</i> 2	(5/5)			+(2/3) ++(1/3)		+(2/4) ++(2/4)	++(3/3)			++(5/5)	+(2/2)			+(4/4)	++(4/4)
GB <i>S</i> 1 <i>S</i> 3	+(3/4) ++(1/4)	(10/10)	(12/12)	++(7/7)		++(3/3)	+(5/6) ++(1/6)			++(4/4)	++(5/5)		+(3/5) ++(2/5)	++(8/8)	++(9/9)
SM S1S3			(3/3)												
WS <i>S</i> <sub>2</sub> <i>S</i> <sub>4</sub>	+(4/5) ++(1/5)	++(6/6)		(3/3)	(6/6)	+(3/4) ++(1/4)	++(3/3)	++(7/7)		++(6/6)	+(3/3)		++(6/6)	+(5/6) ++(1/6)	++(4/4)
TG <i>S</i> 2 <i>S</i> 4					(4/4)										
WB <i>S</i> <sub>2</sub> <i>S</i> <sub>5</sub>	+(3/3)	++(5/5)		+(3/3)		(4/4)	+(1/3) ++(2/3)	+(10/15) ++(5/15)		+(4/5) ++(1/5)	+(3/3)		++(2/2)	+(1/2) ++(1/2)	++(5/5)
MD <i>S</i> 3 <i>S</i> 5	++(2/2)			++(10/10)		+(2/5) ++(3/5)	 (11/11)			+(2/4) ++(2/4)	++(2/2)			++(6/6)	++(9/9)
ZP <i>S</i> 3 <i>S</i> 5	++(5/5)	+(3/5) ++(2/5)		++(5/5)		+(5/6) ++(1/6)	 (17/17)	(14/14)	(4/4)	+(4/6) ++(2/6)			++(5/5)	++(7/7)	++(6/6)
ZG <i>S</i> 3 <i>S</i> 5									(2/2)						
SJ <i>S</i> 5 <i>S</i> 6	++(8/8)			++(7/7)		+(2/4) ++(2/4)	+(3/5) ++(2/5)			(5/5)				++(6/6)	++(7/7)
HB <i>S</i> <sub>2</sub> <i>S</i> <sub>7</sub>	+(3/3)	++(8/8)		+(5/5)		+(4/4)	++(5/5)	++(1/1)		++(5/5)	(8/8)		++(5/5)	+(3/4) ++(1/4)	++(4/4)
CL <i>S</i> 1 <i>S</i> 7												(5/5)			
HN <i>S</i> 1 <i>S</i> 8	+(4/6) ++(2/6)	+(4/7) ++(3/7)		++(7/7)		++(3/3)	++(5/5)	++(6/6)		++(6/6)			(13/13)	+(5/8) ++(3/8)	+(5/7) ++(2/7)
SU S <sub>2</sub> S <sub>8</sub>	+(2/2)					+(2/2)	++(4/4)			++(3/3)	+(4/4)			(2/2)	+(3/3)
GX <i>S</i> 8 <i>S</i> 9	++(4/4)			++(9/9)		++(8/8)	++(7/7)			++(8/8)				+(2/4) ++(2/4)	(6/6)

Supplementary Table 5. Compatibility relationships between different pummelo accessions, as assigned by aniline blue staining.

### Supplementary Table 5. Compatibility relationships between different pummelo accessions, as assigned by aniline blue staining.

The classification of pollinations to incompatible ("--"), half-compatible ("+") and fully compatible ("++") was performed by assessing aniline blue staining of pistils after pollination using multiple pollinations (see **Supplementary Fig. 7**). This method was used to assign the *S*-genotype of the pummelo accessions. For clarity and to show confidence in the assignment of these classifications, we have indicated the raw data here, showing the number of aniline blue pistils assigned to a particular compatibility class out of the number of pollinations made (indicated in the brackets; e.g. 5/5 indicates 5 classifications assigned this class out of 5 pollinations). We have also indicated the misclassifications here (indicated by red font), to show how we built confidence for the half-compatible assignments (e.g. 1/5 indicates 1 classifications in a block like this allows us to cross-check predicted outcomes and helps lend confidence to the classifications assigned. Here we show the result of 583 pollinations, of which 44 (< 8%) were misclassified; in all cases, it was clear what the correct classification should be, because of the pattern in which the pollinations were made.

The assignment of these classification classes (see **Supplementary Fig. 7** for examples of the pollinations) was as follows: When almost all pollen tubes were inhibited near the top of the style, the cross was assigned as fully-incompatible ("--", indicated by yellow boxes), with the same two *S*-alleles shared between the parents. When many pollen tube bunches extended to the base of the pistil, the cross was assigned as fully-compatible ("++", indicated by blue boxes), confirming that the parents did not share either *S*-alleles. When pollinations showed some pollen tubes inhibited in the upper style but some extended through the pistil, the cross was assigned as half-compatible ("+", indicated by green boxes), indicating that the parents have one common *S*-allele between them.

The numbering of *S*-alleles was started at  $S_1S_2$  for the first plant genotype. Compatibility with subsequent plants determined the assigned numbers: completely new numbers if assigned as fully compatible (as they cannot share any *S*-alleles), one new number if assigned as half-compatible (as they must share one *S*-allele), and the same number if assigned as incompatible (as they must share both *S*-alleles). In this way the accessions previously assigned the two-letter code (e.g. ST) were assigned an *S*-genotype.

### Supplementary Table 6. List of primer sequences

Name	Primer	Target / Purpose			
F-R1-F	ATGAACATTACTTTCTTCCTCTA	Full-length amplification of S <sub>1</sub> -			
F-R1-R	TTAAGGCGGGGGAAAGGTA	RNase			
F-R2-F	ATGATATCGACAAAGACGAAAA	Full-length amplification of S <sub>2</sub> -			
F-R2-R	CTACTCATCGGTCGGCTCG	RNase			
F-R3-F	ATGAAGACGAAGGCAACTTAC	Full-length amplification of $S_3$ -			
F-R3-R	CTACTTAGTCGGACTCGGAGCAG	RNase			
F-R4-F	ATGAGTGCTACTCTCTTCATTTTC	Full-length amplification of $S_4$ -			
F-R4-R	TTATTTAGGCGGGGGAAAG	RNase			
F-R5-F	ATGAAGGTGGCATCCATCAAC	Full-length amplification of S <sub>5</sub> -			
F-R5-R	CTACCACCGTGGTGGGAAAATAATATCC	RNase			
F-R6-F	ATGGGGACTAATTTCCTCATTATC	Full-length amplification of <i>S</i> <sub>6</sub> -			
F-R6-R	CTATATTTTAACGTATCGCGGC	RNase			
F-R7-F	ATGAAGGCAGCTTATCTTCTTC	Full-length amplification of S7-			
F-R7-R	TCAGGAGCTGCTAATTTGAACCTTGG	RNase			
F-R8-F	ATGGGGATTGGTTTCCTCATTTTC	Full-length amplification of S <sub>8</sub> -			
F-R8-R	TTATTCTTCATGCCAAATATATCCATTCTC	<i>RNase</i>			
F-R9-F	ATGAAGACAAGGGCAACTTAC	Full-length amplification of S <sub>9</sub> -			
F-R9-R	CTACTTAGTCCGAGTAGGGAAC	RNase			
F-Rm-F	ATGAAGATTAATTTCTGCATTTTC	Full-length amplification of <i>S</i> <sub>m</sub> -			
F-Rm-R	TTATTTATGCCGGGGGAAGCTGATAAC	<i>RNase</i>			
S-R1-F	ATGAACATTACTTTCTTCCTCTACA	Specific amplification of $S_{l}$ -			
S-R1-R	GTTGATCTCCGTTCTTCGTG	RNase			
S-R2-F	GACTAACCTCTTTCGCTTTGC	Specific amplification of <i>S</i> <sub>2</sub> -			
S-R2-R	CGGATCCATGCCTTTTCTAG	<i>RNase</i>			
S-R3-F	TCCAACATCACCTATTGTACAGC	Specific amplification of <i>S</i> <sub>3</sub> -			
S-R3-R	GATAACGACCATCACTAAAAACG	<i>RNase</i>			
S-R4-F	GTTTGTTTCCTGCATTTCCTC	Specific amplification of <i>S</i> <sub>4</sub> -			
S-R4-R	GACCCCTGTTCTTTTTACTGC	RNase			
S-R5-F	ATGAAGGTGGCATCCATCA	Specific amplification of <i>S</i> <sub>5</sub> -			
S-R5-R	AATAATATCCGGCCCACAG	RNase			
S-R6-F	ATGGGGACTAATTTCCTCATTATCTTT	Specific amplification of <i>S</i> <sub>6</sub> -			
S-R6-R	CTATATTTTAACGTATCGCGGCAA	RNase			
S-R7-F	TCTTTCTTTTGTTTTGCTTGTTC	Specific amplification of <i>S</i> <sub>7</sub> -			
S-R7-R	ATTTGAACCTTGGAAGGGAAC	RNase			
S-R8-F	GTTGTAACGCAAAACACTTCTG	Specific amplification of <i>S</i> <sub>8</sub> -			
S-R8-R	CGTATGAGCATGTTAGTCTTGG	RNase			
S-R9-F	CATTACCTATTCTGCTGCTCA	Specific amplification of S <sub>9</sub> -			
S-R9-R	CCGAGTAGGGAACATGATTG	RNase			
q-R1-F	AAGGCCATCAGATTTCGTTC	aRT-PCR of St-PMasa			
q-R1-R	CAGTGCTCATCCATTTCCATAC	qRT-PCR of <i>S</i> <sub>1</sub> - <i>RNase</i>			
q-R2-F	TTCATCCTACATGGGCTCTG	qRT-PCR of S2-RNase			
q-R2-R	TATCTCGCTTCAGCGATTTTAG	qui i cicoi b2-nivase			
q-R3-F	CCAACATCACCTATTGTACAGC	qRT-PCR of S <sub>3</sub> -RNase			
q-R3-R	ACGAACCATGTTACATTACGG	que i en or by tuvase			

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q-R4-F	GTGCTACTCTCTTCATTTCATTG	qRT-PCR of <i>S</i> <sub>4</sub> - <i>RNase</i>				
q-R4-R	CTGATGCTTTTCTTTTACAGTTG	qitt-i Cit of 54-Mivase				
q-R5-F	GCATCCATCAACATCTGTATTC	qRT-PCR of S5-RNase				
q-R5-R	TGAAGAACGAAGACTCCTGG	qitti i Cit of 53-hivuse				
q-R6-F	GCAAAATCCCTGCAATAACC	qRT-PCR of <i>S</i> <sub>6</sub> - <i>RNase</i>				
q-R6-R	CTGGAAATTCTTGAATGTGTGG	qrt1-1 Crt 01 56-rivuse				
q-R7-F	CCGCAATGGAACAAGTCTAC	qRT-PCR of <i>S</i> <sub>7</sub> - <i>RNase</i>				
q-R7-R	GCCAGTATTTTCCCATATCACTC	qK1-1 CK 01 5/-Kivase				
q-R8-F	GGTTGTAACGCAAAACACTTC	qRT-PCR of <i>S</i> <sub>8</sub> - <i>RNase</i>				
q-R8-R	AGGGGTATTTCTGGCAGAAG	qrt1-1 Crt 01 58-rtivase				
q-R9-F	GCATTACCTATTCTGCTGCTC	qRT-PCR of S9-RNase				
q-R9-R	TGACGAACCTTGATACATTTCG	qx1-1 CX 01 39-NIVase				
q-Actin-F	ATCTGCTGGAAGGTGCTGAG	apt DCD of Actin				
q-Actin-R	CCAAGCAGCATGAAGATCAA	qRT-PCR of <i>Actin</i>				
A-R2-F	TTCATCCTACATGGGCTCTG	Absolute quantification of S <sub>2</sub> -				
A-R2-R	TATCTCGCTTCAGCGATTTTAG	RNase				
A-Rm-F	AGGACGAGATCCGTACAAACATA	Absolute quantification of Sm-				
A-Rm-R	GTTTCCCAGTAACTCCTTCCATC	RNase				
RT-R2-F	GACTAACCTCTTTCGCTTTGC	RT-PCR of <i>S</i> <sub>2</sub> - <i>RNase</i>				
RT-R2-R	CGGATCCATGCCTTTTCTAG	RI-PCK of S2-RNase				
RT-Rm-F	AACAGATTTCGTCCTACACGG					
RT-Rm-R	CCAAAAGAATGATTGCGTAGC	RT-PCR of <i>S</i> <sub>m</sub> - <i>RNase</i>				
F-F1-1-F	ATGGTGATGACAAGCTATGGAG	Full-length amplification of S <sub>1</sub> -				
F-F1-1-R	CTATATATCCTCTTCTCTTACTATAATTAGAC	SLF1				
F-F1-2-F	ATGACGGTGATGACAGGC	Full-length amplification of <i>S</i> <sub>1</sub> -				
F-F1-2-R	TCAGAGTGTAATCAGACTCTCT	SLF2				
F-F1-3-F	ATGGGGAGAGAGACGACG	Full-length amplification of <i>S</i> <sub><i>l</i></sub> -				
F-F1-3-R	TTATGTATCCTCTTCTCTAACTATAATTAG	SLF3				
F-F1-4-F	ATGGCGAGAGAGGCTAGGGT	Full-length amplification of S				
F-F1-4-R	CTACATATCCTCTTCCTTCACTCTAAT	SLF4				
F-F1-5-F	ATGATGGTGACCTGTACTGG	Full-length amplification of S				
F-F1-5-R	TTATAAATACACACCCAATGTATG	SLF5				
F-F1-6-F	ATGGTAGAAAGCAATGGAGA	Full-length amplification of $S_{l}$ -				
F-F1-6-R	TTATTCCACTCCTAAGATATGCCATGG	SLF6				
F-F1-7-F	ATGGTGTTATTTGGCAAAGACG	Full-length amplification of $S_{l}$ -				
F-F1-7-R	TCAAACTCCTTCTGTTTGATACACAC	SLF7				
F-F1-8-F	ATGGCGAAATGTAACGGA	Full-length amplification of <i>S</i> <sub>1</sub> -				
F-F1-8-R	TTAACAGGAATTAGTTTGATAAACC	SLF8				
F-F1-9-F	ATGATGACAAGTGATGAACAG	Full-length amplification of S <sub>1</sub> -				
F-F1-9-R	CTATGGGAGTGATGCATCGATTAG	<i>SLF9</i>				
F-F2-1-F	ATGGTGATGACAAGCTATGGAG	Full-length amplification of S <sub>2</sub> -				
F-F2-1-R	CTAAATATCTTCTTTCTGACAATAATTAG	SLF1				
F-F2-2-F	ATGGAGAGAGAGATATGTCGGTGAT	Full-length amplification of S <sub>2</sub> -				
F-F2-2-R	CTATTCTTGGATTTTAATTAGACTTTCC	SLF2				
F-F2-3-F	ATGGAGAGGGAGATGATGG	Full-length amplification of S				
F-F2-3-R	CTATATATCCTCTACTCTAACTGAAATTAGAC	SLF3				
F-F2-4-F	ATGGCCAGAGAGACAAGG	Full-length amplification of <i>S</i> <sub>2</sub> -				
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F-F2-4-R	TTACTTCATTCTAATTAAACTCTCTTTTAAAATATG	SLF4		
F-F2-5-F	ATGGTGATAAATACTGGAGACTT	Full-length amplification of S <sub>2</sub> -		
F-F2-5-R	TTAATACACCCCAATGTATGC	SLF5		
F-F2-6-F	ATGGCGATAATGGTGGAAAGC	Full-length amplification of S <sub>2</sub> -		
F-F2-6-R	TCATTCATGTTCCACACCTAAGATATG	SLF6		
F-F2-7-F	ATGGTGTTATTAGACAACGAAGATTCAT	Full-length amplification of S <sub>2</sub> -		
F-F2-7-R	TCATTCTGTTTGATTTACATCCAAAAC	SLF7		
F-F2-8-F	ATGGCGAAAAGCAACAGCAAGT	Full-length amplification of S <sub>2</sub> -		
F-F2-8-R	TTAACAGGAATTAGTTTGATAAACTCCCA	SLF8		
F-F2-9-F	ATGATGATGACAAGTAATGAAG	Full-length amplification of S <sub>2</sub> -		
F-F2-9-R	CTAGGGGAGAGATCCATCATCG	SLF9		
S-F1-1-F	GGTTGAGACACTATCGAGGTTG	Specific amplification of S <sub>1</sub> -		
S-F1-1-R	CTTTCCTCATCGACTAAGGTG	SLF1		
S-F1-2-F	TTATTGGGTGGCATCGGG	Specific amplification of S <sub>1</sub> -		
S-F1-2-R	CATAAACCGGTAATTCCAAGATCC	SLF2		
S-F1-3-F	TGAATACAGAGTTGTTCCAGG	Specific amplification of $S_{I}$ -		
S-F1-3-R	ATGTGCCATCTCTTCTGAATATAG	SLF3		
S-F1-4-F	CTTCTCTATATTCCCCGATAAGAC	Specific amplification of S <sub>1</sub> -		
S-F1-4-R	AGAATGTGCGAACTTATCCG	SLF4		
S-F1-5-F	TGCAACTAAGGAGTCTAGGGC	Specific amplification of <i>S</i> <sub>1</sub> -		
S-F1-5-R	TTAAAGTCTCCGTATAGTTGCG	SLF5		
S-F1-6-F	TGAATACAGAGTTGTTCCAGG	Specific amplification of <i>S</i> <sub>1</sub> -		
S-F1-6-R	ATGTGCCATCTCTTCTGAATATAG	SLF6		
S-F1-7-F	AATACACGAGGGTTTTTGGTAC	Specific amplification of <i>S</i> <sub>1</sub> -		
S-F1-7-R	CCCGGTATCAGGCTCATAC	SLF7		
S-F1-8-F	TGGCGAAATGTAACGGAAAT	Specific amplification of <i>S</i> <sub>1</sub> -		
S-F1-8-R	CAAATCCCATAATAGTATCA	SLF8		
S-F1-9-F	GATGGAGCGTTTGATAGCG	Specific amplification of <i>S</i> <sub>1</sub> -		
S-F1-9-R	CCTCTTTCTTCACTCCAATAAGAC	SLF9		
S-F2-1-F	CCACGTAATACGACGGCTAAC	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-1-R	GAAAGGTCCGAAGGTCAAG	SLF1		
S-F2-2-F	GGTGATGACACGCTGTGAAG	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-2-R	AAGTATTGCTGGGAAGACGAG	SLF2		
S-F2-3-F	CAATGAGGGGAACTACAACTGG	Specific amplification of S <sub>2</sub> -		
S-F2-3-R	GTATCCAAGGACTCATCGCTG	SLF3		
S-F2-4-F	TATTCCCTGATAGGACACTAACAG	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-4-R	CCCAGTAACAATATCCATTCAAG	SLF4		
S-F2-5-F	AACTAAAGAGTATAGACCTGTCCC	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-5-R	CAAGTGGCTTAGACACTCCTA	SLF5		
S-F2-6-F	CTCACCTTGTTGGATACGAAAATAG	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-6-R	ACATAAAACCACAAACCTCGTAGC	SLF6		
S-F2-7-F	TGGTTGAAATTCTATCCAGGCTAC	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-7-R	ATATTTCGGGAGAGTAATGGACTC	SLF7		
S-F2-8-F	TGCCGGAGGATGTTATTATTG	Specific amplification of S <sub>2</sub> -		
S-F2-8-R	GAAGAGTTCTTGACTCCTTGGTTG	SLF8		
S-F2-9-F	GGAGAAGCACGACGGACCTGA	Specific amplification of <i>S</i> <sub>2</sub> -		
S-F2-9-R	CGTTACCTAGATGAAACGAAAGAAT	SLF9		

q-F1-1-F	ACTTTACTCAGAAGACGTCGC	
q-F1-1-R	CAGTCGTTTGTCATTTGATTCT	qRT-PCR of S <sub>1</sub> -SLF1
q-F1-2-F	GTCATTCAGCATGAGTGACGAG	
-		qRT-PCR of S1-SLF2
q-F1-2-R	CAACCATCGTATATGCCTATCG	
q-F1-3-F	GTACGCCGTCCTGATTATTAC	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF</i> 3
q-F1-3-R	CATCCAAGGTCTCATCGC	
q-F1-4-F	CAGTCAGTGAAGACACCTTGG	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF</i> 4
q-F1-4-R	AGAATGTGCGAACTTATCCG	
q-F1-5-F	GAGACTCACTCCGATCAGATG	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF</i> 5
q-F1-5-R	TTAAAGTCTCCGTATAGTTGCG	
q-F1-6-F	GAAATGTTGTTACGATTGCCG	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF6</i>
q-F1-6-R	ACAGTATACCAAGAGACGGGTGT	
q-F1-7-F	CCAACCACTCCTGTTTTGG	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF</i> 7
q-F1-7-R	CCCGGTATCAGGCTCATAC	
q-F1-8-F	GGATTTGGATTGGATATTATGAG	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF8</i>
q-F1-8-R	GGATTTGGATTGGATATTATGAG	
q-F1-9-F	GGGGTTTGTTATTGGTTATCT	qRT-PCR of <i>S</i> <sub>1</sub> - <i>SLF</i> 9
q-F1-9-R	TATGGCTCCTGTATTTCTTCG	
q-F2-1-F	TGCCTTTCTTTGCTATACTCAG	qRT-PCR of S2-SLF1
q-F2-1-R	GAAAGGTCCGAAGGTCAAG	
q-F2-2-F	ACTTGGTCCTTGTGATGGTAT	qRT-PCR of S2-SLF2
q-F2-2-R	AAGTATTGCTGGGAAGACGAG	
q-F2-3-F	CAATGAGGGGAACTACAACTG	qRT-PCR of <i>S</i> <sub>2</sub> - <i>SLF</i> <sub>3</sub>
q-F2-3-R	GAAGGCGAACTTCATAGCC	
q-F2-4-F	GTTGCATTGGGTTTAGATCTC	qRT-PCR of S2-SLF4
q-F2-4-R	CATGAAACGAATCTCTTTGATC	
q-F2-5-F	AGTAAATGCGGTGATGGG	qRT-PCR of S2-SLF5
q-F2-5-R	GTCTTTAATCGTCCATATTTCC	
q-F2-6-F	GGATTATTCGATGACTTACTGTCTC	qRT-PCR of S2-SLF6
q-F2-6-R	GTGTCAGGATCGTATAAGAGTAGTTG	
q-F2-7-F	TGAATCTAACTCTTCACAGTTGCTC	qRT-PCR of S2-SLF7
q-F2-7-R	AAACCAACAGCATTCGAGTTC	
q-F2-8-F	TGCCGGAGGATGTTATTATTG	qRT-PCR of S2-SLF8
q-F2-8-R	CTCTGCATACACACCTGAATCTTAG	
q-F2-9-F	CGCTACGTGCTAACTCTTGGA	qRT-PCR of S2-SLF9
q-F2-9-R	CAGATAACCAGTAACAAACCC	
BAC-R1-F	TTTATTTCCTGCATTTCCTCGG	
BAC-R1-R	ACTCCTTCCATTTGGATATATTCC GGAACCAAGACCAAGTACCATTATG	
BAC-R1-5'-F		Probe used to screen the $S_{I}$ -
BAC-R1-5'-R	AGTAAGAACTGACCAAAATTCACAG GAATCATCGTTTTGTGAAGAAGAG	locus from BAC library
BAC-R1-3'-F		
BAC-R1-3'-R	TCAATGCGGAGTTTAGGAAGA	
BAC-R2-F	CTCTTGAGGCTGATTTGATG	
BAC-R2-R	CGGGGAACTTGATATTGTCT	Probe used to screen the $S_2$ -
BAC-R2-5'-F	ACAAAACGCCATATAGAAAGAGTC	locus from BAC library
BAC-R2-5'-R	CATCCAAAGGAGTAATTCATCAC	
6P-R1-F	CGGAATTCAACAATTCTGGTTTTGACCACTT	<i>S</i> <sub>1</sub> - <i>RNase</i> cloned to pGEX-6P-1
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6P-R1-R	CCCTCGAGTTAAGGCGGGGGGAAAGGTA	
6P-R2-F	CGGAATTCTCCTCGCAATTGTTCGACC	S <sub>2</sub> -RNase cloned to pGEX-6P-1
6P-R2-R	CCCTCGAGCTACTCATCGGTCGGCTCG	S2-Rivase cloned to pGEX-0P-1
6P-Rm-F	GGATCCCCGGAATTCAATTCTGGTTTTGACCACTTTTGGC	C DNasa alamada a CEV (D 1
6P-Rm-R	ATGCGGCCGCTCGAGTTATTTATGCCGGGGGAAGCTGATAAC	<i>S</i> <sub><i>m</i></sub> -RNase cloned to pGEX-6P-1
6P-Rm <sup>R</sup> -F	GGATCCCCGGAATTCAATTCTGGTTTTGACCACTTTTGGC	
6P-Rm <sup>R</sup> -overlap-R	GATTTCTTAGTATTCTCAGCAGGTTCACAC	$S_m^R$ -RNase cloned to pGEX-6P-
6P-Rm <sup>R</sup> -overlap-F	GAATACTAAGAAATCAAGGAATATTTCCAGATGG	1
6P-Rm <sup>R</sup> -R	ATGCGGCCGCTCGAGTTATTTATGCCGGGGGAAGCTGATAAC	

Allele-specific primers were used to amplify full-length S-RNases; forward (F) and reverse (R).

Locus	Clone	Number of read pairs	Clean bases (G)	Read length (bp)	GC (%)	SRR id in GenBank
	84-N-5	4720	1.42	150	35.8	SRR10168706
S <sub>1</sub> -locus	10-J-4	4450	1.34	150	39.07	SRR10168705
	51-0-18	4597	1.38	150	39.96	SRR10168704
C le ave	72-E-8	3803	1.14	150	35.04	SRR10168708
$S_2$ -locus	57-F-22	4607	1.38	150	43.34	SRR10168709

Supplementary Table 7. Information regarding the BAC clones for the pummelo S<sub>1</sub>- and S<sub>2</sub>-loci

A BAC library constructed from a pummelo of genotype  $S_1S_2$  was arrayed in 108 different 384-well microtiter plates. Clones (three for the  $S_1$ -locus and two for the  $S_2$ -locus) were screened by using the probes (**Supplementary Table 6**) of  $S_1$ -*RNase* and  $S_2$ -*RNase* respectively. Clones were identified as containing the *S*-locus by sequencing, using the Illumina platform.

### Supplementary Table 8. Other genes identified at the *S*<sub>1</sub>-locus with functions predicted by the Swissprot database.

Gene	Annotation	E value	Description
S1.gene1	Transformation/transcription domain-associated protein	0	
S1.gene2	Unknown		
S1.gene3	Unknown		
S1.gene4	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	4.77E-101	
S1.gene5	Unknown		
S1.gene6	Unknown		
S1.gene7	Unknown		
S1.gene8	Putative AC transposase	1.44E-91	
S1.gene9	Unknown		
S1.gene10	Retrovirus-related Pol polyprotein from transposon	6.33E-14	
S1.gene11	Unknown		
S1.gene12	Putative ribonuclease H protein	9.48E-21	
S1.gene13	F-box/kelch-repeat protein	1.58E-19	S <sub>1</sub> -SLF2
S1.gene14	Unknown		
S1.gene15	Retrovirus-related Pol polyprotein from transposon	2.02E-55	
S1.gene16	Unknown		
S1.gene17	Unknown		
S1.gene18	CENP-B homolog protein 2	7.35E-55	
S1.gene19	Unknown		
S1.gene20	Unknown		
S1.gene21	Putative F-box protein	2.22E-18	S <sub>1</sub> -SLF1
S1.gene22	Unknown		
S1.gene23	Unknown		
S1.gene24	Unknown		
S1.gene25	Unknown		
S1.gene26	Unknown		
S1.gene27	Retrovirus-related Pol polyprotein from transposon	8.88E-05	
S1.gene28	Retrovirus-related Pol polyprotein from transposon	1.97E-07	
S1.gene29	Nicotiana alata Ribonuclease S7	5.99E-28	S <sub>1</sub> -RNase
S1.gene30	Probable cytokinin riboside 5'-monophosphate phosphoribohydrolase	1.77E-10	
S1.gene31	Copia protein	3.85E-10	
S1.gene32	Unknown		
S1.gene33	Unknown		
S1.gene34	F-box/kelch-repeat protein	5.07E-23	S <sub>1</sub> -SLF6
S1.gene35	Unknown		
S1.gene36	Unknown		

S1.gene37	Putative F-box protein	5.32E-15	S <sub>1</sub> -SLF5
S1.gene38	Unknown		
S1.gene39	Cytochrome P450	2.52E-132	
S1.gene40	Unknown		
S1.gene41	F-box protein	4.58E-17	S <sub>1</sub> -SLF4
S1.gene42	Retrovirus-related Pol polyprotein from transposon opus	8.99E-06	
S1.gene43	Pol polyprotein (Fragment)	5.89E-12	
S1.gene44	Probable cytokinin riboside 5'-monophosphate phosphoribohydrolase	1.49E-12	
S1.gene45	Unknown		
S1.gene46	Unknown		
S1.gene47	Unknown		
S1.gene48	Putative F-box protein	1.13E-17	S <sub>1</sub> -SLF3
S1.gene49	Unknown		
S1.gene50	F-box protein CPR1	1.32E-17	S <sub>1</sub> -SLF7
S1.gene51	F-box/kelch-repeat protein	7.49E-21	S <sub>1</sub> -SLF9
S1.gene52	F-box/kelch-repeat protein	3.00E-18	S <sub>1</sub> -SLF8
S1.gene53	Protein indeterminate-domain 7	1.95E-49	
S1.gene54	Calcium-dependent protein kinase 16	0	
S1.gene55	Unknown		
S1.gene56	DNA-(apurinic or apyrimidinic site) lyase 2	0	
S1.gene57	Unknown		
S1.gene58	Putative F-box/kelch-repeat protein	9.04E-14	S1-SLFL10
S1.gene59	Putative F-box/kelch-repeat protein	1.32E-15	S1-SLFL11
S1.gene60	Unknown		
S1.gene61	F-box protein	1.18E-18	S <sub>1</sub> -SLFL12

Gene	Annotation	E value	Description
S2.gene1	Transcription-associated protein	0	
S2.gene2	Unknown		
S2.gene3	Unknown		
S2.gene4	Cytokinin riboside 5'-monophosphate phosphoribohydrolase	1.37E-101	
S2.gene5	Putative F-box protein	2.72E-22	S <sub>2</sub> -SLF1
S2.gene6	Unknown		
S2.gene7	Unknown		
S2.gene8	Unknown		
S2.gene9	F-box/kelch-repeat protein	4.21E-18	S <sub>2</sub> -SLF2
S2.gene10	Unknown		
S2.gene11	Unknown		
S2.gene12	F-box protein	2.46E-16	S <sub>2</sub> -SLF3
S2.gene13	Unknown		
S2.gene14	Retrovirus-related Pol polyprotein from transposon	1.43E-37	
S2.gene15	Putative F-box protein	1.63E-15	S <sub>2</sub> -SLF4
S2.gene16	Unknown		
S2.gene17	L10-interacting MYB domain-containing protein	1.18E-06	
S2.gene18	Unknown		
S2.gene19	Unknown		
S2.gene20	F-box protein	7.54E-16	S <sub>2</sub> -SLF5
S2.gene21	Retrovirus-related Pol polyprotein from transposon	2.62E-13	
S2.gene22	Retrovirus-related Pol polyprotein from transposon	1.46E-45	
S2.gene23	Retrovirus-related Pol polyprotein from transposon	1.20E-31	
S2.gene24	Retrovirus-related Pol polyprotein from transposon	2.25E-24	
S2.gene25	Unknown		
S2.gene26	Unknown		
S2.gene27	Unknown		
S2.gene28	Petunia hybrida Ribonuclease S3	8.86E-17	S <sub>2</sub> -RNase
S2.gene29	Retrovirus-related Pol polyprotein from transposon	5.06E-169	
S2.gene30	Spermidine synthase 2	1.21E-06	
S2.gene31	Unknown		
S2.gene32	Unknown		
S2.gene33	Unknown		
S2.gene34	F-box/kelch-repeat protein	9.07E-22	S <sub>2</sub> -SLF6
S2.gene35	F-box/kelch-repeat protein	1.55E-16	<b>S</b> <sub>2</sub> - <b>S</b> <i>L</i> <b>F</b> 7
S2.gene36	Unknown		

# Supplementary Table 9. Other genes identified at the S<sub>2</sub>-locus with functions predicted by the Swissprot database.

S2.gene37	Unknown		
S2.gene38	Unknown		
S2.gene39	Unknown		
S2.gene40	F-box/kelch-repeat protein	9.15E-17	S <sub>2</sub> -SLF9
S2.gene41	F-box/kelch-repeat protein	1.16E-20	S <sub>2</sub> -SLF8
S2.gene42	Calcium-dependent protein kinase 16	0	
S2.gene43	Unknown		
S2.gene44	DNA-(apurinic or apyrimidinic site) lyase 2	0	
S2.gene45	Unknown		
S2.gene46	Putative F-box protein	2.33E-14	S <sub>2</sub> -SLFL10
S2.gene47	Putative F-box/kelch-repeat protein	2.51E-16	S <sub>2</sub> -SLFL11
S2.gene48	Unknown		
S2.gene49	F-box protein	2.97E-19	S <sub>2</sub> -SLFL12
S2.gene50	ABC transporter G family member 36	1.66E-27	
S2.gene51	ABC transporter G family member 40	4.34E-120	

# Supplementary Table 10. Pairwise sequence identities of the deduced amino acid sequence between the citrus Type 1 to Type 12 SLFs/SLFLs

Туре 1	Predicted interaction: $S_I$ -RNase + $S_2/S_6/S_{10}/S_{11}/S_{12}/S_{13}/S_{14}$ -SLF1								
	$S_2$ -SLF1	$S_6$ -SLF1	S10-SLF1	$S_{II}$ -SLF1	<i>S</i> <sub>12</sub> -SLF1	S13-SLF1	S14-SLF1		
$S_I$ -SLF1	89.646	88.011	87.466	88.011	88.767	88.556	88.011		
$S_2$ -SLF1		97.82	97.548	97.275	98.356	98.365	97.82		
$S_6$ -SLF1			97.275	97.275	97.275	97.82	97.275		
$S_{10}$ -SLF1				98.365	97.275	97.275	97.275		
$S_{11}$ -SLF1					97.275	97.275	97.275		
$S_{12}$ -SLF1						97.82	97.82		
<i>S</i> <sub>13</sub> -SLF1							97.82		

90% <identity< th=""></identity<>
80%≤Identity≤90%
70%≤Identity≤80%
Identity≤70%

Trme 1		Predicted interaction: $S_2$ -RNase + $S_1/S_{11}/S_m/S_{13}/S_{10}/S_6/S_{12}/S_{14}$ -SLF2									
Type 2	$S_I$ -SLF2	$S_{II}$ -SLF2	Sm-SLF2	S13-SLF2	S10-SLF2	$S_6$ -SLF2	S12-SLF2	S14-SLF2			
S <sub>2</sub> -SLF2	78.082	79.784	80.165	75.202	79.515	80.863	80.054	80.495			
$S_I$ -SLF2		87.123	87.637	78.356	82.74	84.384	83.836	84.254			
$S_{11}$ -SLF2			89.286	82.933	86.933	88.533	87.733	86.685			
$S_m$ -SLF2				80.939	86.188	86.813	85.635	86.188			
S13-SLF2					86.667	90.667	85.867	85.87			
$S_{10}$ -SLF2						93.867	92	91.848			
$S_6$ -SLF2							92	92.663			
<i>S</i> <sub>12</sub> -SLF2								90.761			

Туре3	S <sub>2</sub> -SLF3	Sm-SLF3	<i>S</i> <sub>14</sub> -SLF3	<i>S</i> <sub>13</sub> -SLF3b	S <sub>6</sub> -SLF3	S10-SLF3	<i>S</i> <sub>12</sub> -SLF3	S13-SLF3a	<i>S</i> <sub>11</sub> -SLF3
S <sub>1</sub> -SLF3	85.561	87.838	86.957	88.525	87.601	87.062	87.433	87.968	88.41
S <sub>2</sub> -SLF3		88.076	86.413	86.649	85.714	86.096	85.829	86.631	88.076
Sm-SLF3			85.87	88.556	87.297	88.076	87.568	88.108	88.618
S14-SLF3				88.011	86.957	87.772	88.043	88.587	90.217
S13-SLF3b					89.101	89.373	89.101	90.191	89.918
S6-SLF3						92.992	90.836	94.879	90.323
S10-SLF3							90.909	94.609	90.786
S12-SLF3								93.048	90.296
S13-SLF3a									91.87

Trme 4		Predicte	ed interaction	S6-RNase	$-S_m/S_{10}/S_{11}/S_$	$S_1/S_2/S_{12}/S_{14}/S_{14}$	513-SLF4	
Type 4	Sm-SLF4	S10-SLF4	$S_{II}$ -SLF4	$S_I$ -SLF4	$S_2$ -SLF4	$S_{12}$ -SLF4	$S_{14}$ -SLF4	S13-SLF4
S <sub>6</sub> -SLF4	75.946	77.717	76.902	77.151	78.202	77.957	76.075	77.628
Sm-SLF4		86.141	84.511	87.568	86.649	87.297	86.757	88.076
S10-SLF4			88.889	87.772	87.738	89.946	88.859	89.946
S11-SLF4				88.043	87.193	89.13	88.043	89.402
S <sub>1</sub> -SLF4					89.373	88.71	88.172	90.786
$S_2$ -SLF4						89.101	90.463	92.371
S12-SLF4							88.71	90.217
$S_{14}$ -SLF4								91.328

True 5		Predicte	ed interaction	S13-RNase	$+ S_{14}/S_{12}/S_{1}/S_{1}$	S <sub>2</sub> /S <sub>6</sub> /S <sub>10</sub> /S <sub>11</sub> /S	m-SLF5	
Type 5	<i>S</i> <sub>14</sub> -SLF5	<i>S</i> <sub>12</sub> -SLF5	S <sub>1</sub> -SLF5	S <sub>2</sub> -SLF5	S <sub>6</sub> -SLF5	S10-SLF5	S <sub>11</sub> -SLF5	Sm-SLF5
S13-SLF5	46.518	46.089	47.765	45.81	48.324	47.887	47.632	49.162
$S_{14}$ -SLF5		73.925	77.688	75.806	75.806	76.216	76.882	77.419
$S_{12}$ -SLF5			82.62	81.867	82.842	86.933	80	82.667
$S_I$ -SLF5				84.225	85.791	85.294	82.62	85.294
S <sub>2</sub> -SLF5					86.327	85.6	83.2	86.4
$S_6$ -SLF5						86.863	83.646	87.131
$S_{10}$ -SLF5							82.4	86.4
S11-SLF5								83.2

Type 6	Sm-SLF6	S12-SLF6	S10-SLF6	S <sub>6</sub> -SLF6	S <sub>11</sub> -SLF6	S <sub>1</sub> -SLF6	S <sub>2</sub> -SLF6	S13-SLF6a	S14-SLF6
S13-SLF6b	57.796	56.72	56.989	56.452	57.796	58.333	58.333	58.491	58.602
Sm-SLF6		87.366	87.903	88.889	88.71	89.008	88.472	88.978	88.889
S12-SLF6			90.667	89.067	89.572	89.247	87.733	87.968	88
S10-SLF6				89.6	87.433	89.247	87.733	88.235	87.733
S6-SLF6					87.701	90.323	88.564	89.572	88.451
S11-SLF6						90.054	89.037	89.182	88.503
S <sub>1</sub> -SLF6							89.247	90.323	89.516
S <sub>2</sub> -SLF6								90.909	90.133
S13-SLF6a									90.909

Trino 7		]	Predicted int	eraction: $S_I$	$_0/S_{12}$ -RNase +	$S_{11}/S_2/S_1/S_{13}/S_1$	S14/Sm-SLF7 a	nd S6-SLF7a/	b
Type 7	S12-SLF7	$S_{11}$ -SLF7	$S_2$ -SLF7	$S_I$ -SLF7	S6-SLF7a	S6-SLF7b	S13-SLF7	$S_{14}$ -SLF7	Sm-SLF7
S10-SLF7	84.777	80.366	80.628	81.365	82.275	83.508	83.508	81.675	82.723
<i>S</i> <sub>12</sub> -SLF7		80.628	81.414	81.89	82.54	83.246	83.77	82.461	82.723
S11-SLF7			85.676	86.702	86.863	85.942	86.207	86.737	85.942
$S_2$ -SLF7				88.298	90.323	88.859	89.39	89.125	89.655
$S_I$ -SLF7					91.421	92.021	92.287	90.691	92.287
S6-SLF7a						91.153	91.421	92.493	91.957
S6-SLF7b							98.939	90.981	92.838
S13-SLF7								91.247	93.103
$S_{14}$ -SLF7									92.042

Type 8	<i>S</i> <sub>12</sub> - SLF8a	<i>S</i> <sub>2</sub> - SLF8	<i>S</i> <sub>6</sub> - SLF8b	<i>S</i> <sub>12</sub> - SLF8b	<i>S</i> <sub>11</sub> - SLF8	<i>S</i> <sub>1</sub> - SLF8	<i>S</i> <sub>6</sub> - SLF8a	<i>S</i> <sub>10</sub> - SLF8b	<i>S</i> 13- SLF8a	<i>S</i> <sub>13</sub> - SLF8b	<i>S</i> <sub>14</sub> - SLF8	Sm- SLF8
S10-SLF8a	87.566	83.158	80.576	80.789	82.895	82.632	83.158	82.895	79.211	81.053	83.158	83.158
S12-SLF8a		83.069	80.216	82.275	83.069	83.069	84.392	83.333	79.894	80.952	83.598	83.598
S <sub>2</sub> -SLF8			89.928	88.158	92.895	93.684	92.105	93.947	88.421	89.211	92.895	92.368
S <sub>6</sub> -SLF8b				89.209	90.288	92.806	93.165	94.245	88.489	89.568	94.245	93.165
S12-SLF8b					88.684	90.526	90.789	90.789	86.579	88.158	91.053	90.789
S11-SLF8						93.947	92.632	94.211	88.158	88.947	92.895	92.632
$S_I$ -SLF8							96.579	98.158	92.105	92.895	96.579	96.842
S6-SLF8a								96.842	92.895	93.421	96.579	96.579
S10-SLF8b									92.895	93.684	97.105	97.632
S13-SLF8a										92.105	92.632	92.632
S13-SLF8b											93.421	93.421
S14-SLF8												97.105

Туре 9	Predicted int	teraction: $S_{11}$	$S_{13}/S_{14}$ -RNase	$+ S_2/S_{12}/S_1/S_{10}/S_{10}$	S <sub>m</sub> -SLF9 and S	6-SLF9a/b
Type 9	S <sub>2</sub> -SLF9	S12-SLF9	S <sub>1</sub> -SLF9	S <sub>6</sub> -SLF9a	S10-SLF9	Sm-SLF9
$S_{11}/S_{13}/S_{14}$ -SLF9 are absent						
S <sub>6</sub> -SLF9b	86.942	86.598	88.66	87.973	88.66	88.66
$S_2$ -SLF9		87.139	86.877	86.387	87.5	87.5
S <sub>12</sub> -SLF9			90.263	90	90	90
S <sub>1</sub> -SLF9				95.263	95.526	95.526
S <sub>6</sub> -SLF9a					97.638	97.638
<i>S</i> <sub>10</sub> -SLF9						100

	Pr	Predicted interaction: $S_{13}$ -RNase + $S_{12}/S_1/S_2/S_6/S_{10}/S_{11}/S_m$ -SLFL10 and $S_{14}$ -SLFL10a/									
Type 10	<i>S</i> <sub>12</sub> - SLFL10	$S_{I}$ -SLFL10	S2- SLFL10	<i>S</i> <sub>6</sub> - SLFL10	<i>S</i> <sub>10</sub> - SLFL10	$S_{II}$ -SLFL10	<i>S</i> <sub>14</sub> - SLFL10a	<i>S</i> <sub>14</sub> - SLFL10b	Sm- SLFL10		
<i>S</i> <sub>13</sub> -SLFL10	62.368	68.158	67.895	67.895	68.158	67.368	67.895	67.895	67.632		
S12-SLFL10		86.614	86.352	86.614	86.614	85.564	86.352	86.352	86.089		
S <sub>1</sub> -SLFL10			99.738	99.476	100	98.953	99.738	99.738	99.476		
$S_2$ -SLFL10				99.738	99.738	98.691	99.476	99.476	99.215		
S <sub>6</sub> -SLFL10					99.476	98.429	99.215	99.215	98.953		
S10-SLFL10						98.953	99.738	99.738	99.476		
S <sub>11</sub> -SLFL10							98.691	98.691	98.429		
S14-SLFL10a								100	99.215		
S14-SLFL10b									99.215		

Type 11	<i>S</i> <sub>13</sub> - SLFL11b	<i>S</i> <sub><i>I</i></sub> - SLFL11	<i>S</i> <sub>2</sub> - SLFL11	<i>S</i> <sub>10</sub> - SLFL11	<i>S</i> <sub>11</sub> - SLFL11	<i>S</i> <sub>12</sub> - SLFL11	<i>S</i> <sub>14</sub> - SLFL11a	<i>S</i> <sub>14</sub> - SLFL11b	$S_m$ -SLFL11
<i>S</i> <sub>13</sub> -SLFL11a	89.691	94.33	94.33	93.557	93.668	91.451	93.299	93.299	93.557
<i>S</i> <sub>13</sub> -SLFL11b		94.898	94.898	94.133	93.963	91.582	93.878	93.878	94.133
$S_I$ -SLFL11			99.49	98.724	98.688	96.173	98.469	98.469	98.724
$S_2$ -SLFL11				98.724	98.688	96.173	98.469	98.469	98.724
S10-SLFL11					98.163	95.408	97.704	97.704	100
$S_{II}$ -SLFL11						95.801	97.638	97.638	98.163
<i>S</i> <sub>12</sub> -SLFL11							95.153	95.153	95.408
S14-SLFL11a								100	97.704
<i>S</i> <sub>14</sub> -SLFL11b									97.704

Type 12	<i>S</i> <sub>2</sub> - SLFL12	<i>S</i> <sub>6</sub> - SLFL12	<i>S</i> <sub>10</sub> - SLFL12	<i>S</i> <sub>11</sub> - SLFL12	<i>S</i> <sub>12</sub> - SLFL12	<i>S</i> <sub>13</sub> - SLFL12a	<i>S</i> <sub>13</sub> - SLFL12b	<i>S</i> <sub>14</sub> - SLFL12a	<i>S</i> <sub>14</sub> - SLFL12b	Sm- SLFL12
S <sub>1</sub> -SLFL12	99.733	99.194	98.663	98.93	97.594	98.396	95.722	98.93	98.93	98.925
$S_2$ -SLFL12		99.462	98.396	98.663	97.326	98.128	95.455	98.663	98.663	98.656
$S_6$ -SLFL12			97.849	98.387	96.774	97.581	94.892	98.118	98.118	98.118
S10-SLFL12				98.663	96.257	97.059	94.652	97.594	97.594	98.118
<i>S</i> <sub>11</sub> -SLFL12					96.524	97.326	94.652	97.861	97.861	97.849
S12-SLFL12						96.524	94.652	97.059	97.594	96.505
<i>S</i> <sub>13</sub> -SLFL12a							95.187	97.861	97.861	97.312
S13-SLFL12b								95.455	95.722	94.624
<i>S</i> <sub>14</sub> -SLFL12a									99.465	97.849
S14-SLFL12b										97.849

These twelve tables show the pairwise % identities (using deduced amino acid sequences) for each of the twelve Types of citrus SLFs (indicated in red font, one for each table) based on pairwise sequence identities

of their deduced amino acid sequences. Different degrees of identity are indicated by grey shading (see key at top). Duplicate SLF copies within each type are indicated by a and b. The predicted interactions between SLF and *S*-RNase (based on the non-self model<sup>8,9,16</sup>) are shown on the top part of each table. The SLFs in each type indicated in orange are either diverged or deleted and their cognate *S*-RNases (also indicated in orange) are predicted to interact with the conserved SLFs under the non-self recognition model.

For type 1 SLFs, the  $S_1$ -SLF1 (indicated in orange) sequence is diverged, with 87.5 ~ 89.6% identity with other SLF1s ( $S_2$ -,  $S_6$ -,  $S_{10}$ -,  $S_{11}$ -,  $S_{12}$ -,  $S_{13}$ - and  $S_{14}$ -SLF1), while the pairwise identities of the other SLF1s range from 97.3 to 98.4%. The cognate S-RNase of  $S_1$ -SLF1,  $S_1$ -RNase (in orange), is predicted to interact with the  $S_2$ -,  $S_6$ -,  $S_{10}$ -,  $S_{11}$ -,  $S_{12}$ -,  $S_{13}$ - and  $S_{14}$ -SLF1 based on the non-self model. Similarly, the  $S_2$ -RNase is predicted to interact with the  $S_1$ -,  $S_{11}$ -,  $S_{12}$ -,  $S_{13}$ -,  $S_{10}$ -,  $S_{10}$ -,  $S_{12}$ -, and  $S_{14}$ -SLF2 (see type 2 table); the  $S_6$ -RNase is predicted to interact with the  $S_m$ -,  $S_{10}$ -,  $S_{11}$ -,  $S_2$ -,  $S_{12}$ -,  $S_{14}$ - and  $S_{13}$ -SLF4 (see type 4 table); the  $S_{13}$ -RNase is predicted to interact with the  $S_{14}$ -,  $S_{12}$ -,  $S_{1-}$ ,  $S_{1$ 

For the type 3, 11 and 12 SLFs, there are no diverged or deleted SLFs and the pairwise SLFs in each type show comparable identities, respectively ranging from  $85.6 \sim 94.9\%$ ,  $89.7 \sim 100\%$ ,  $94.6 \sim 99.7\%$ . For the type 6, the  $S_{I3}$ -haplotype has a diverged  $S_{I3}$ -SLF6b, but it also has a conserved  $S_{I3}$ -SLF6a. Similarly, the  $S_{I0}$ -haplotype has a diverged allele ( $S_{I0}$ -SLF8a) and a conserved allele ( $S_{I0}$ -SLF8b) in type 8. These suggest that the SLFs in type 3, 6, 8, 11, and 12 do not interact with the S-RNases identified in the study.

No.	Accession name	Марре	d <i>S</i> -RNase <sup>a</sup>	Catalog	Scientific name	Source	SRR id
1	DX1	Sm	$S_x$	Wild mandarin	C. reticulata	Wang et al, 2018 <sup>17</sup>	SRR5796819
2	DX2	Sm	$S_x$	Wild mandarin	C. reticulata	Wang et al, 2018	SRR5796821
3	DX3	Sm	$S_x$	Wild mandarin	C. reticulata	Wang et al, 2018	SRR5796820
4	DX4	Sm	$S_x$	Wild mandarin	C. reticulata	Wang et al, 2018	SRR5796645
5	MS1	Sm	S10	Wild mandarin	C. reticulata	Wang et al, 2018	SRR5796818
6	MS2	Sm	S10	Wild mandarin	C. reticulata	Wang et al, 2018	SRR5796635
7	LHJ	Sm	$S_x$	Wild mandarin	C. reticulata	In this study	SRR10163368
8	LRH	Sm	$S_x$	Wild mandarin	C. reticulata	In this study	SRR10163367
9	WLM	Sm	$S_{11}$	Cultivated mandarin	C. reticulata	Wu et al, 2018 <sup>18</sup>	SRR1023625
10	ORI	Sm	$S_{11}$	Cultivated mandarin	C. reticulata	Wang et al, 2017 <sup>12</sup>	SRR3820595
11	QH117	Sm	$S_7$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3822244
12	18H	Sm	$S_7$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3749605
13	19P	Sm	$S_2$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3747617
14	CSNJ	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3747609
15	CZG	Sm	<i>S</i> 11	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3747583
16	NJ	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3750668
17	HPJ	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3750611
18	WLK	Sm	S11	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3820551
19	20H	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3747635
20	WHPG	Sm	$S_2$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5796644
21	YJNJ	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5796865
22	YSJ	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3750648
23	NFJ	Sm	$S_7$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR5796630
24	JGA	Sm	$S_2$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5796822
25	DFZS	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5807899
26	SM	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5807909
27	WZ	Sm	$S_8$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5807910
28	KYM	Sm	$S_7$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3820643
29	CLP	$S_m$	$S_x$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188441
30	CSM	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188440
31	KSH	$S_m$	$S_7$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188456
32	DNC	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188439
33	KNG	$S_m$	$S_8$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188438
34	SNK	Sm	$S_x$	Cultivated mandarin	C. reticulata	Wu et al, 2018	SRR6188455
35	S6	$S_m$	$S_2$	Cultivated mandarin	C. reticulata	In this study	SRR10163366
36	<b>S</b> 8	Sm	$S_2$	Cultivated mandarin	C. reticulata	In this study	SRR10163366
37	MSJ	$S_x$	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3751832
38	STJ	$S_x$	$S_2$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3756933
39	MLTJ	$S_x$	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2017	SRR3750679
40	ZHJ	$S_x$	$S_x$	Cultivated mandarin	C. reticulata	Wang et al, 2018	SRR5796927
41	DD	$S_m$	$S_x$	Sour orange	C. aurantium	Wang et al, 2017	SRR3885049
42	BH	$S_m$	S5/S13	Sour orange	C. aurantium	In this study	SRR9127844
43	HBLT	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127845

# Supplementary Table 11. Detailed information relating to checking the S-haplotypes for 153 Citrus accessions

			r	r		7	
44	HP	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127842
45	JJSC	$S_m$	$S_8$	Sour orange	C. aurantium	In this study	SRR9127843
46	YDL	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127840
47	XGTC	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127841
48	JJDD	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127838
49	DGTC	Sm	$S_x$	Sour orange	C. aurantium	In this study	SRR9127839
50	XHC	$S_m$	$S_x$	Sour orange	C. aurantium	In this study	SRR9127848
51	Aur	$S_m$	$S_x$	Sour orange	C. aurantium	Wang et al, 2017	SRR3885125
52	CBSC	$S_m$	S5/S13	Sour orange	C. aurantium	Wang et al, 2017	SRR3915646
53	HNSC	$S_m$	S5/S13	Sour orange	C. aurantium	Wang et al, 2017	SRR3926631
54	SCSC	$S_m$	<i>S</i> <sub>7</sub>	Sour orange	C. aurantium	Wang et al, 2017	SRR3926581
55	ZGSC	$S_m$	$S_2$	Sour orange	C. aurantium	Wang et al, 2017	SRR3916939
56	ANJ	$S_m$	S5/S13	Sour orange	C. aurantium	In this study	SRR9127847
57	BXI	$S_m$	<i>S</i> <sub>7</sub>	Sour orange	C. aurantium	In this study	SRR9127857
58	CHG	Sm	Sx	Sour orange	C. aurantium	In this study	SRR9127858
59	DFL	Sm	S7	Sour orange	C. aurantium	In this study	SRR9127855
60	GP	Sm	Sx	Sour orange	C. aurantium	In this study	SRR9127856
61	GXSJ	Sm	$S_x$	Sour orange	C. aurantium	In this study	SRR9127853
62	HYDD	Sm	$S_{7}$	Sour orange	C. aurantium	In this study	SRR9127854
63	HZL	Sm Sm	S <sub>x</sub>	Sour orange	C. aurantium	In this study	SRR9127851
64	KYC	Sm Sm	S5/S13	Sour orange	C. aurantium	In this study	SRR9127852
65	QLJ	Sm Sm	S3/5/3 Sx	Sour orange	C. aurantium	In this study	SRR9127849
66	XGCC	Sm Sm	$S_x$	Sour orange	C. aurantium	In this study	SRR9127850
67	YG2	Sm Sm	$S_x$	Sour orange	C. aurantium	In this study	SRR9127846
68	AL	Sm Sm	$S_x$ $S_7$	Sweet orange	C. uaramaan C. sinensis	Wang et al, 2017	SRR3127646 SRR3883626
69	HML	Sm Sm	S7 S7	Sweet orange	C. sinensis	Wang et al, 2017 Wang et al, 2017	SRR3883647
70	XSO	Sm Sm	S7 S7	Sweet orange	C. sinensis	Wang et al, 2017 Wang et al, 2017	SRR4237671
70	13X	Sm Sm	S7 S7	Sweet orange	C. sinensis	Wang et al, 2017 Wang et al, 2017	SRR4237071 SRR3884813
71	29B	Sm Sm	S7 S7	Sweet orange	C. sinensis	Wang et al, 2017 Wang et al, 2017	SRR3804813 SRR3926732
	JC			Sweet orange	C. sinensis	<u> </u>	
73 74	SO3	Sm Sm	$S_7$ $S_x$	e	C. sinensis	Wang et al, 2017 Wang et al, 2017	SRR3884491 SRR5799051
				Sweet orange			
75	LQ	S <sub>m</sub>	S7	Sweet orange	C. sinensis	Wang et al, 2017	SRR3884773
76	NHE	Sm	Sx	Sweet orange	C. sinensis	Wang et al, 2017	SRR3927459
77	WSO	$S_m$	S7	Sweet orange	C. sinensis	Wang et al, 2017	SRR4240447
78	GXY	S9/S12	S8	Pummelo	C. maxima	Wang et al, 2017	SRR5802549
79	STY	$S_l$	$S_2$	Pummelo	C. maxima	Wang et al, 2017	SRR5796631
80	WSY	S4	S <sub>2</sub>	Pummelo	C. maxima	Wang et al, 2017	SRR5796633
81	10Z	S <sub>3</sub>	S <sub>5</sub> /S <sub>13</sub>	Pummelo	C. maxima	Wang et al, 2017	SRR3823645
82	GBY	S3	S <sub>1</sub>	Pummelo	C. maxima	Wang et al, 2017	SRR3823447
83	HNHY	$S_l$	S8	Pummelo	C. maxima	Wang et al, 2017	SRR3823230
84	WBY	$S_2$	S5/S13	Pummelo	C. maxima	Wang et al, 2017	SRR3823251
85	CHP	S <sub>4</sub>	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR1023627
86	SYBS	$S_8$	$S_2$	Pummelo	C. maxima	Wang et al, 2017	SRR3844987
87	SYPS	$S_{I}$	$S_2$	Pummelo	C. maxima	Wang et al, 2017	SRR3824065
88	MaJia	$S_x$	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3822290
89	HB	$S_7$	$S_2$	Pummelo	C. maxima	In this study	SRR9127779
90	SMST	$S_{I}$	$S_3$	Pummelo	C. maxima	In this study	SRR9127778

91         YNMD         S/S <sub>11</sub> S.         Pummelo         C. maxima         In this study         SRR012776           93         ZGST         S/S <sub>12</sub> S.         S/S <sub>12</sub> S/S         Pummelo         C. maxima         In this study         SRR0127780           94         2011-GL-1         S/a         S/a         Pummelo         C. maxima         Wang et al. 2017         SRR383213           95         CQ-016         S/a         S/a         Pummelo         C. maxima         Wang et al. 2017         SRR3823148           97         Q-04         S/S/12         S/a         Pummelo         C. maxima         Wang et al. 2017         SRR3823149           98         RL-06         S/S/13         S/a         Pummelo         C. maxima         Wang et al. 2017         SRR3823409           99         NJYPS         S/a         S/a         Pummelo         C. maxima         Wang et al. 2017         SRR3823409           100         HHILY         S/a         S/a         Pummelo         C. maxima         Wang et al. 2018         SRR4802755           101         HIILY         S/a         S/a         Grapefruit         C. paradist         Wang et al. 2017         SRR3802585           10					ſ			
93         Z438T         Sylip         Sylip         Sylip         Purmuelo         C. maxima         In this study         SRR358312           94         2011-GL-1         Sin         Sin         Furmuelo         C. maxima         Wang et al. 2017         SRR35832303           95         CQ-016         Sylip         Sin         Purmuelo         C. maxima         Wang et al. 2017         SRR3823148           97         Q-04         SinSylip         Sin         Purmuelo         C. maxima         Wang et al. 2017         SRR3823409           98         RL-06         SinSylip         Sin         Purmuelo         C. maxima         Wang et al. 2017         SRR3823409           99         NJYPS         Sin         Sin         Purmuelo         C. maxima         Wang et al. 2018         SRR5803252           101         HHHXY         Sin         Sin         Grapefruit         C. paradist         Wang et al. 2017         SRR392747           104         Ruby         Sa         Sin         Grapefruit         C. paradist         In this study         SRR392747           105         HJ         Sa         Sin         Grapefruit         C. paradist         In this study         SRR4128407           106	91	YNMD	S5/S13	$S_x$	Pummelo	C. maxima	In this study	SRR9127777
94         2011-GL-1 $S_{ii}$ <th< td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></th<>								
95         CQ-016 $S_{11}$ $S_{r}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR382303           96         JA-02 $S_{S}/S_{12}$ $S_{r}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR3823455           98         RL-06 $S_{S}/S_{12}$ $S_{r}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR3823459           99         NIYPS $S_{10}$ $S_{r}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR3823450           100 $AJH$ $S_{8}$ $S_{r}$ Purnnelo $C.maxima$ Wang et al, 2018         SRR5802552           101         HHRXY $S_{8}$ $S_{r}$ Grapefruit $C.paradisi$ Wang et al, 2017         SRR3927437           104         Ruby $S_{m}$ $S_{2}$ Grapefruit $C.paradisi$ Wang et al, 2017         SRR3927445           105         HJ $S_{m}$ $S_{2}$ Grapefruit $C.paradisi$ Wang et al, 2017         SRR3927445           106         Flame $S_{m}$ $S_{2}$ Lemon $C.limon$ Wang et al, 2017	93	ZGST	S5/S13		Pummelo	C. maxima	In this study	
96         JA-02         Sr. St.         Purnmelo         C. maxima         Wang et al. 2017         SRR3823148           97         Q-04         SySt:         Sr.         Purnmelo         C. maxima         Wang et al. 2017         SRR3823409           98         RL-06         SySt:         Sr.         Purnmelo         C. maxima         Wang et al. 2017         SRR3832409           90         NJYPS         Sr.         Sr.         Purnmelo         C. maxima         Wang et al. 2018         SRR5802352           101         HHHXY         Sr.         Sr.         Purnmelo         C. maxima         Wang et al. 2018         SRR5802582           103         141         Sm.         Sr.         Grapefruit         C. paradisi         Wang et al. 2017         SRR3927475           104         Ruby         Sm.         Sr         Grapefruit         C. paradisi         Wang et al. 2017         SRR39212405           105         HJ         Sm.         Sr         Grapefruit         C. paradisi         Wu et al. 2017         SRR39212405           106         Flame         Sm.         Sr         Grapefruit         C. paradisi         Wu et al. 2017         SRR392134           108         JY2         Sm.	94	2011-GL-1	S10	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3858312
97         Q-04 $S_{s}(2)_{1}$ $S_{s}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR3823455           98         RI-06 $S_{s}(2)_{12}$ $S_{s}$ Purnnelo $C.maxima$ Wang et al, 2017         SRR3823455           99         NJYPS $S_{10}$ $S_{s}$ Purnnelo $C.maxima$ Wang et al, 2018         SRR5802532           101         HHHXY $S_{s}$ $S_{s}$ Purnnelo $C.maxima$ Wang et al, 2018         SRR5802582           103         141 $S_{m}$ $S_{s}$ Grapefruit $C.paradisi$ Wang et al, 2017         SRR3927405           104         Ruby $S_{m}$ $S_{s}$ Grapefruit $C.paradisi$ Wang et al, 2017         SRR3927405           106         Flame $S_{m}$ $S_{s}$ Grapefruit $C.paradisi$ Wu et al, 2018         SRR4982134           108         JY22 $S_{m}$ Lemon $C.limon$ Wang et al, 2017         SRR3948107           109         YLK $S_{m}$ $S_{s}$ Lemon $C.limon$ Wang et al, 2017         SRR3948171	95	CQ-016	$S_{11}$	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3822303
98         RL-06 $S_yS_{12}$ $S_x$ Pummelo $C. maxima$ Wang et al, 2017         SRR3823409           99         NYPS $S_x$ $S_x$ Pummelo $C. maxima$ Wang et al, 2018         SRR3848607           100         AJH $S_x$ $S_x$ Pummelo $C. maxima$ Wang et al, 2018         SRR5802552           101         HHHXY $S_x$ $S_x$ Pummelo $C. maxima$ Wang et al, 2018         SRR5802552           103         141 $S_m$ $S_x$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3926757           104 $Ruby$ $S_m$ $S_x$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927405           105         HJ $S_m$ $S_x$ Lemon $C. limon$ Wang et al, 2017         SRR39218405           106         FV22 $S_m$ $S_x$ Lemon $C. limon$ Wang et al, 2017         SRR3951937           110         FMN $S_m$ $S_x$ Lemon $C. limon$ Wang et al, 2017         SRR3951931937 <t< td=""><td>96</td><td>JA-02</td><td>S5/S13</td><td><math>S_x</math></td><td>Pummelo</td><td>C. maxima</td><td>Wang et al, 2017</td><td>SRR3823148</td></t<>	96	JA-02	S5/S13	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3823148
99         NJYPS $S_{10}$ $S_{c}$ Pummelo $C. maxima$ Wang et al, 2017         SRR3848607           100 $AJH$ $S_{s}$ $S_{c}$ Pummelo $C. maxima$ Wang et al, 2018         SRR5802532           101         HHHXY $S_{s}$ $S_{c}$ Pummelo $C. maxima$ Wang et al, 2018         SRR5802556           103         14J $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3924747           105         HJ $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3921747           106         Flame $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3981870           107         PAR $S_{m}$ $S_{2}$ Lemon $C. limon$ Wang et al, 2017         SRR39818910           109         YLK $S_{m}$ $S_{2}$ Lemon $C. limon$ Wang et al, 2017         SRR3981891           109         YLK $S_{m}$ $S_{2}$ Lemon $C. limon$ In this stady         SRR19129115 <td>97</td> <td>Q-04</td> <td>S9/S12</td> <td><math>S_x</math></td> <td>Pummelo</td> <td>C. maxima</td> <td>Wang et al, 2017</td> <td>SRR3823455</td>	97	Q-04	S9/S12	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3823455
100         AJII $S_t$ Purmelo $C. maxima$ Wang et al, 2018         SRR5802532           101         HIIHXY $S_t$ $S_r$ Purmelo $C. maxima$ Wang et al, 2018         SRR5802582           103         I41 $S_n$ $S_r$ Grapefruit $C. paradisi$ Wang et al, 2018         SRR3926757           104         Ruby $S_n$ $S_r$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927675           105         HJ $S_m$ $S_r$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927447           106         Flame $S_m$ $S_r$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR39248190           107         PAR $S_m$ $S_r$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_r$ Lemon $C. limon$ Wang et al, 2017         SRR3948277           111         LS $S_m$ $S_r$ Lemon $C. limon$ In this study         SRR9129151           113         FMM	98	RL-06	S5/S13	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3823409
101         IHIHXY $S_8$ $S_7$ Pummelo $C. maxima$ Wang et al. 2018         SRR5802582           103         14J $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al. 2017         SRR3926757           104         Ruby $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al. 2017         SRR392747           105         HJ $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al. 2017         SRR3927407           106         Flame $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al. 2017         SRR3927407           108 $JY22$ $S_m$ $S_2$ Lemon $C. limon$ Wang et al. 2017         SRR394810           109         YLK $S_m$ $S_2$ Lemon $C. limon$ Wang et al. 2017         SRR394817           111         LS $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129150           113         FMNL $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129154           114	99	NJYPS	S10	$S_x$	Pummelo	C. maxima	Wang et al, 2017	SRR3848607
102         HHSWY $S_{r}$ $S_{r}$ Pummelo $C. maxima$ Wang et al, 2018         SRR802582           103         14J $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927477           104         Ruby $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927405           105         HJ $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wu et al, 2017         SRR3927405           107         PAR $S_{m}$ $S_{2}$ Grapefruit $C. paradisi$ Wu et al, 2017         SRR3981910           109         YLK $S_{m}$ $S_{2}$ Lemon $C. limon$ Wang et al, 2017         SRR3951937           110         FMN $S_{m}$ $S_{2}$ Lemon $C. limon$ In this study         SRR9129151           113         FMNL $S_{m}$ $S_{2}$ Lemon $C. limon$ In this study         SRR9129149           115         N4 $S_{m}$ $S_{2}$ Lemon $C. limon$ In this study         SRR9129153	100	AJH	$S_8$	$S_x$	Pummelo	C. maxima	Wang et al, 2018	SRR5802532
103         14J $S_m$ $S_2$ Grapefruit $C. paradist$ Wang et al, 2017         SRR3926757           104         Ruby $S_m$ $S_2$ Grapefruit $C. paradist$ Wang et al, 2017         SRR3927447           105         HIm $S_m$ $S_2$ Grapefruit $C. paradist$ Wang et al, 2017         SRR3927405           106         Flame $S_m$ $S_2$ Grapefruit $C. paradist$ Wu et al, 2018         SRR3927405           107         PAR $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3951937           111         L.S $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129151           113         FMNL $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129149           114         L-17 $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR91291414           115	101	HHHXY	$S_8$	$S_x$	Pummelo	C. maxima	Wang et al, 2018	SRR5802565
103         14J $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3926757           104         Ruby $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927447           105         HIm $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927405           106         Flame $S_m$ $S_2$ Grapefruit $C. paradisi$ Wu et al, 2018         SRR3927405           107         PAR $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3951937           111         LS $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129151           113         FMNL $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129149           114         L-17 $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR91291414           114	102	HHSWY	Sx	$S_x$	Pummelo	C. maxima	Wang et al, 2018	SRR5802582
104         Ruby $S_m$ $S_j$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927447           105         HJ $S_m$ $S_j$ Grapefruit $C. paradisi$ In this study         SRR9128709           106         Flame $S_m$ $S_j$ Grapefruit $C. paradisi$ Wu et al, 2017         SRR3927405           107         PAR $S_m$ $S_j$ Grapefruit $C. paradisi$ Wu et al, 2017         SRR3948190           109         YLK $S_m$ $S_j$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_j$ Lemon $C. limon$ Wang et al, 2017         SRR3948277           111         LS $S_m$ $S_j$ Lemon $C. limon$ In this study         SRR9129150           113         FMNL $S_m$ $S_j$ Lemon $C. limon$ In this study         SRR9129159           114         L-17 $S_m$ $S_j$ Lemon $C. limon$ In this study         SRR9129153           115         N4	103	14J	Sm	$S_2$	Grapefruit	C. paradisi		SRR3926757
105         HJ $S_m$ $S_r$ Grapefruit $C. paradisi$ In this study         SRR9128709           106         Flame $S_m$ $S_s$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927405           107         PAR $S_m$ $S_s$ Grapefruit $C. paradisi$ Wu et al, 2018         SRR6188447           108         JY22 $S_m$ $S_s$ Lemon $C. limon$ Wang et al, 2017         SRR3952134           109         YLK $S_m$ $S_s$ Lemon $C. limon$ Wang et al, 2017         SRR3952134           110         FMN $S_m$ $S_s$ Lemon $C. limon$ In this study         SRR9129151           111         LS $S_m$ $S_s$ Lemon $C. limon$ In this study         SRR9129151           114         L-17 $S_m$ $S_s$ Lemon $C. limon$ In this study         SRR9129148           115         N4 $S_m$ $S_s$ Lemon $C. limon$ In this study         SRR9129152           117         YN	104	Ruby	Sm	$S_3$		-		
106         Flame $S_m$ $S_2$ Grapefruit $C. paradisi$ Wang et al, 2017         SRR3927405           107         PAR $S_m$ $S_2$ Grapefruit $C. paradisi$ Wu et al, 2018         SRR6188447           108         JY22 $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3948170           110         FMN $S_m$ $S_2$ Lemon $C. limon$ Wang et al, 2017         SRR3948277           112         ALN $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129151           113         FMNL $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129149           115         N4 $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129153           118         WLF $S_m$ $S_2$ Lemon $C. limon$ In this study         SRR9129152           120         JY						-		
107         PAR $S_m$ $S_i$ Grapefruit $C. paradisi$ Wu et al, 2018         SRR6188447           108         JY22 $S_m$ $S_i$ Lemon $C. limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_i$ Lemon $C. limon$ Wang et al, 2017         SRR3952134           110         FMN $S_m$ $S_i$ Lemon $C. limon$ Wang et al, 2017         SRR3951937           111         LS $S_m$ $S_i$ Lemon $C. limon$ In this study         SRR3948277           112         ALN $S_m$ $S_i$ Lemon $C. limon$ In this study         SRR9129150           113         FMNL $S_m$ $S_i$ Lemon $C. limon$ In this study         SRR9129154           116         POST $S_m$ $S_i$ Lemon $C. limon$ In this study         SRR9129153           118         WLF $S_m$ $S_i$ Lemon $C. limon$ In this study         SRR3948174           120         JY $S_n'S_i$							•	
108         JY22 $S_m$ $S_2$ Lemon $C.\ limon$ Wang et al, 2017         SRR3948190           109         YLK $S_m$ $S_2$ Lemon $C.\ limon$ Wang et al, 2017         SRR3952134           110         FMN $S_m$ $S_2$ Lemon $C.\ limon$ Wang et al, 2017         SRR3952137           111         LS $S_m$ $S_2$ Lemon $C.\ limon$ Wang et al, 2017         SRR3948277           112         ALN $S_m$ $S_2$ Lemon $C.\ limon$ In this study         SRR9129150           114         L-17 $S_m$ $S_2$ Lemon $C.\ limon$ In this study         SRR9129149           115         N4 $S_m$ $S_2$ Lemon $C.\ limon$ In this study         SRR9129154           116         POST $S_m$ $S_2$ Lemon $C.\ limon$ In this study         SRR9129154           117         YN $S_m$ $S_2$ Lemon $C.\ limon$ In this study         SRR9129152           118         WLF $S_m$ <						-		
109         YLK $S_m$ $S_2$ Lemon $C.\ linon$ Wang et al, 2017         SRR3952134           110         FMN $S_m$ $S_2$ Lemon $C.\ linon$ Wang et al, 2017         SRR3951337           111         LS $S_m$ $S_2$ Lemon $C.\ linon$ Wang et al, 2017         SRR3948277           112         ALN $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR9129150           113         FMNL $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR9129149           114         L-17 $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR9129148           116         POST $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR9129153           117         YN $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR9129154           117         YN $S_m$ $S_2$ Lemon $C.\ linon$ In this study         SRR948129153           120         DYL $S_m^{\prime}$ <					-	1		
110         FMN $S_m$ $S_2$ Lemon $C.$ limon         Wang et al, 2017         SRR3951937           111         LS $S_m$ $S_2$ Lemon $C.$ limon         Wang et al, 2017         SRR3948277           112         ALN $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129151           113         FMNL $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129149           114         L-17 $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129148           116         POST $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129153           118         WLF $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129152           119         05L-06 $S_m$ $S_2$ Lemon $C.$ limon         In this study         SR8952242           119         05L-06 $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR938734           121         XZI $S_x$								
111         LS $S_m$ $S_2$ Lemon $C.$ limon         Wang et al, 2017         SRR3948277           112         ALN $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129151           113         FMNL $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129150           114         L-17 $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129148           115         N4 $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129148           116         POST $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129153           118         WLF $S_m$ $S_2$ Lemon $C.$ limon         In this study         SRR9129152           120         JY $Sy/S_{12}$ $S_x$ Citron $C.$ medica         Wang et al, 2017         SRR3938253           121         XZ1 $S_x$ $S_x$ Citron $C.$ medica         Wang et al, 2017         SRR3948093           124         JY4 $S_3$ <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>								
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	135	YCLS	$S_x$	$S_x$		C. ichangensis		SRR3929790
137YLS5/S13S10Ichang papedaC. ichangensisWang et al, 2017SRR3930078	136	YCYJ	$S_x$	$S_x$	Ichang papeda	C. ichangensis	Wang et al, 2017	SRR3929943
	137	YL	S5/S13	$S_{10}$	Ichang papeda	C. ichangensis	Wang et al, 2017	SRR3930078

138	ZY	$S_x$	$S_x$	Ichang papeda	C. ichangensis	Wang et al, 2017	SRR3931949
139	Ace	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3988226
140	Amo	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3989253
141	ARO	S9/S12	$S_{I}$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3989264
142	CDSJ	$S_x$	$S_{I}$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3989910
143	GDMM	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990142
144	HDGKZ	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990145
145	HKC	S9/S12	$S_2$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3988729
146	JBL	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3988460
147	JMPG1	$S_{I}$	$S_6$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990571
148	JMPG2	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990663
149	Sdi	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3989214
150	SND	$S_I$	S5/S13	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990714
151	WNNL	$S_x$	S5/S13	Atalantia	A. buxifolia	Wang et al, 2017	SRR3990759
152	WNSMW	$S_6$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3992564
153	WSD	$S_x$	$S_x$	Atalantia	A. buxifolia	Wang et al, 2017	SRR3992888

Genome sequences of 153 citrus accessions containing published and unpublished sources were mapped to 15 *S-RNase* sequences. As a result, 132/153 accessions were found to contain these *S-RNase* genes and 90/153 accessions harbor the  $S_m$ -RNase gene.

<sup>a</sup>: We assumed all accessions were heterozygous with two *S*-haplotypes segregating.  $S_x$ -*RNase* indicates the unmapped *S*-haplotypes.

Note that the sequences between  $S_9$ -RNase and  $S_{12}$ -RNase and between  $S_5$ -RNase and  $S_{13}$ -RNase are so highly similar that these pairs of genes cannot be distinguished from each other through reads mapping.

#### **References for Supplemental Information**

- 1 Kheyr-Pour, A. *et al.* Sexual plant reproduction sequence diversity of pistil S-proteins associated with gametophytic selfincompatibility in *Nicotiana alata. Sex. Plant Reprod.* **3**, 88-97 (1990).
- 2 Eddy, S. R. A new generation of homology search tools based on probabilistic inference. *Genome Inform.* 23, 205-211 (2009).
- 3 Liang, M. *et al.* Genome-wide identification and functional analysis of S-RNase involved in the self-incompatibility of citrus. *Mol. Genet. Genomics* **292**, 325-341 (2017).
- 4 Nowak, M. D., Davis, A. P., Anthony, F. & Yoder, A. D. Expression and trans-specific polymorphism of self-incompatibility RNases in *coffea* (Rubiaceae). *PloS One* **6**, e21019 (2011).
- 5 Asquini, E. *et al.* S-RNase-like sequences in styles of *Coffea* (Rubiaceae). Evidence for S-RNase based gametophytic self-Incompatibility? *Trop. Plant Biol.* **4**, 237-249 (2011).
- 6 Ramanauskas, K. & Igić, B. The evolutionary history of plant T2/S-type ribonucleases. *PeerJ* 5, e3790 (2017).
- 7 Tsuchimatsu, T. *et al.* Patterns of polymorphism at the self-incompatibility locus in 1,083 *Arabidopsis thaliana* genomes. *Mol. Biol. Evol.* **34**, 1878-1889 (2017).
- 8 Kubo, K. *et al.* Collaborative non-self recognition system in S-RNase–based self-incompatibility. *Science* **330**, 796-799 (2010).
- 9 Kubo, K. *et al.* Gene duplication and genetic exchange drive the evolution of S-RNase-based self-incompatibility in *Petunia*. *Nat. Plants* **1**, 14005 (2015).
- 10 Workenhe, S. T., Kibenge, M. J. T., Iwamoto, T. & Kibenge, F. S. B. Absolute quantitation of infectious salmon anaemia virus using different realtime reverse transcription PCR chemistries. *J. Virol. Methods* **154**, 128-134 (2008).
- 11 Ida, K. *et al.* The 1.55 Å resolution structure of *Nicotiana alata* S<sub>F11</sub>-RNase associated with gametophytic self-incompatibility. *J. Mol. Biol.* **314**, 103-112 (2001).
- 12 Wang, X. *et al.* Genomic analyses of primitive, wild and cultivated citrus provide insights into asexual reproduction. *Nat. Genet.* **49**, 765-772 (2017).
- 13 Xue, Y., Carpenter, R., Dickinson, H. G. & Coen, E. S. Origin of allelic diversity in antirrhinum *S* locus RNases. *Plant Cell* **8**, 805-814 (1996).
- 14 Ushijima, K. *et al.* Cloning and characterization of cDNAs encoding S-RNases from almond (*Prunus dulcis*): primary structural features and sequence diversity of the S-RNases in Rosaceae. *Mol. Gen. Genet.* **260**, 261-268 (1998).
- 15 Mir, J. *et al.* Molecular identification of S-alleles associated with self-incompatibility in apple (Malus spp.) genotypes. *Indian J. Agr. Sci.* **86**, 78-81 (2016).
- 16 Fujii, S., Kubo, K.-i. & Takayama, S. Non-self- and self-recognition models in plant self-incompatibility. *Nat. Plants* **2**, 16130 (2016).
- 17 Wang, L. *et al.* Genome of wild mandarin and domestication history of mandarin. *Mol. Plant* **11**, 1024-1037 (2018).
- 18 Wu, G. A. *et al.* Genomics of the origin and evolution of *Citrus. Nature* **554**, 311-316 (2018).