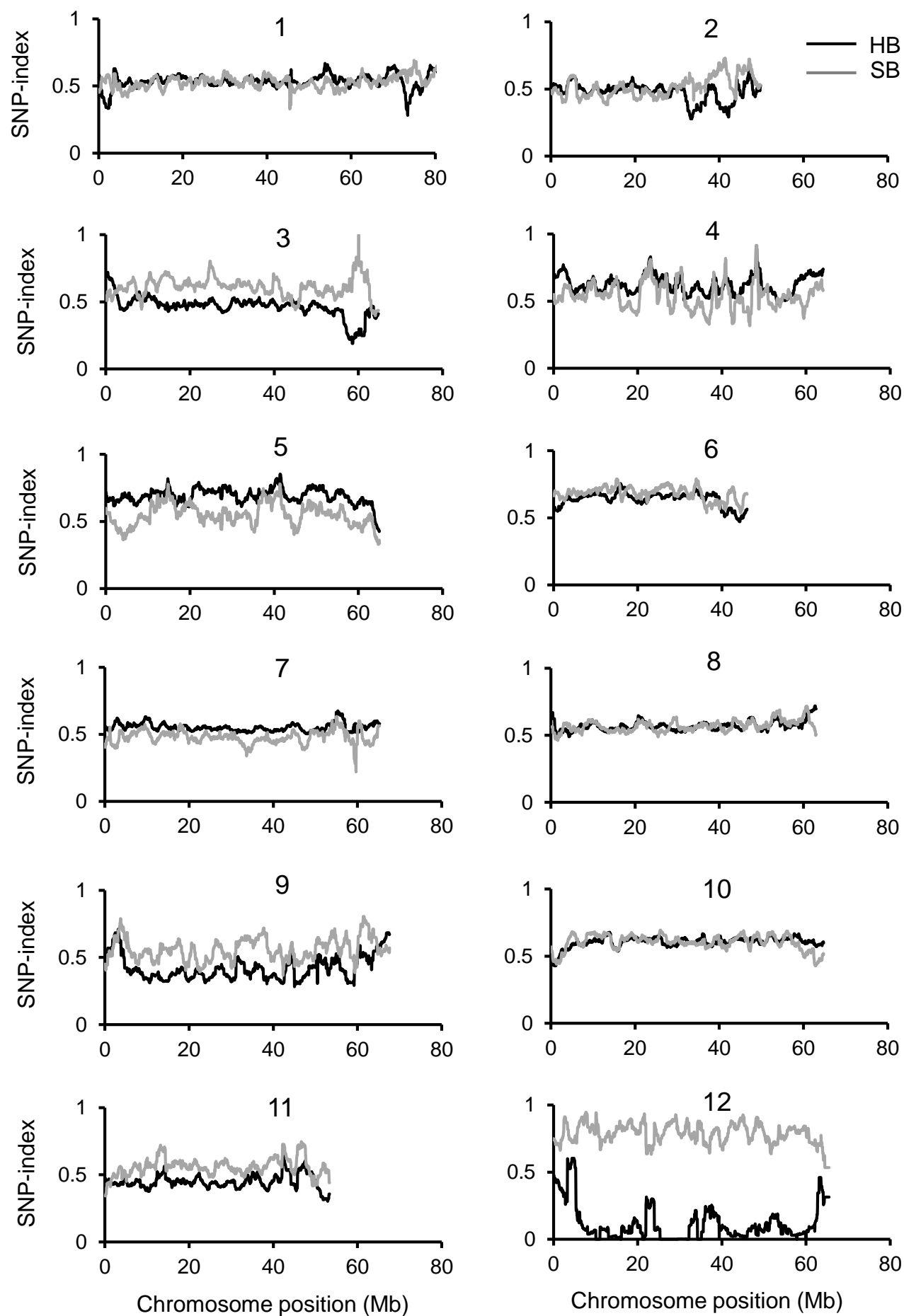
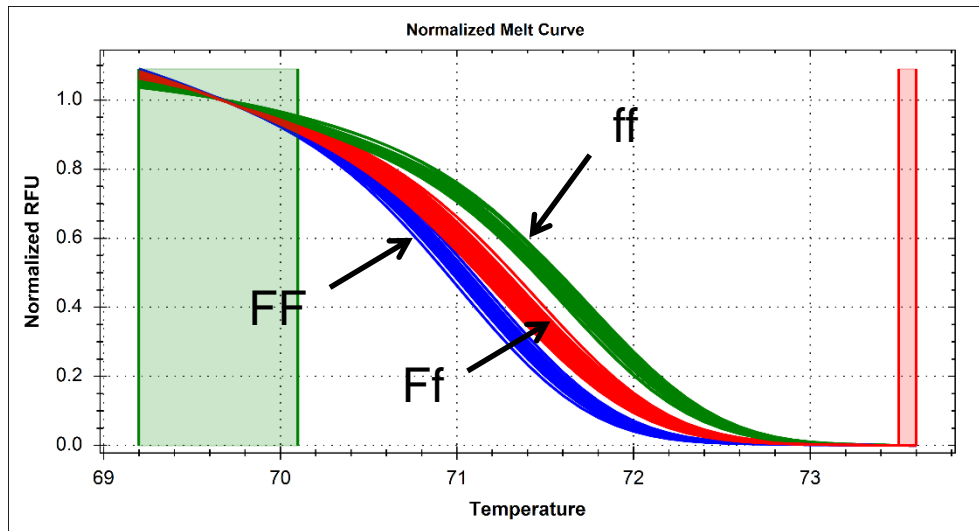


**Figure S1.** SNPs depth of whole genome. Dark line, depth of highly branched bulk (HB). Grey line, depth of single branch bulk (SB).

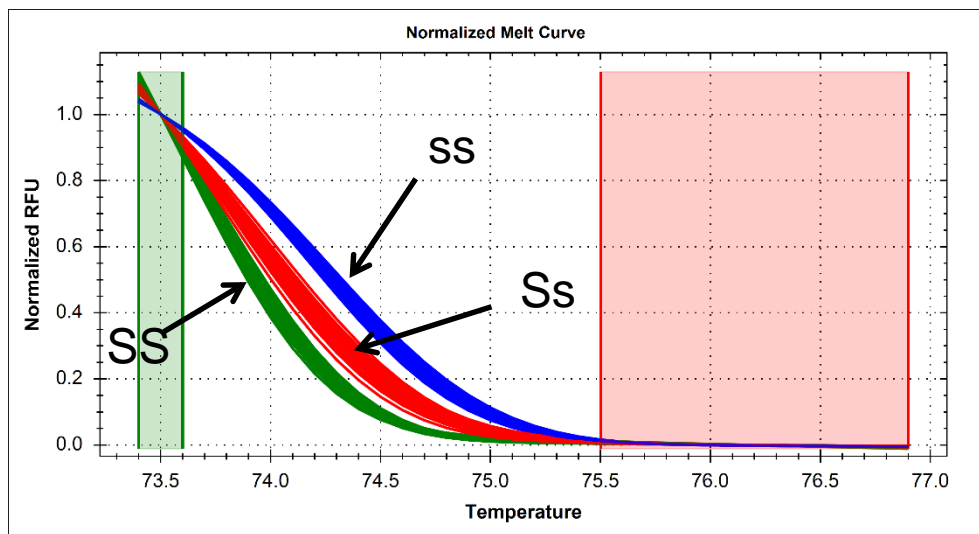


**Figure S2.** SNP-index graphs depict the single branch bulk (SB) and highly branched bulk (HB) generated from QTL-seq study. The X-axis denotes the physical positions (Mb) on tomato chromosomes. The Y-axis represents the SNP-index, which has been estimated for 2 Mb physical intervals with a 50 kb sliding window.

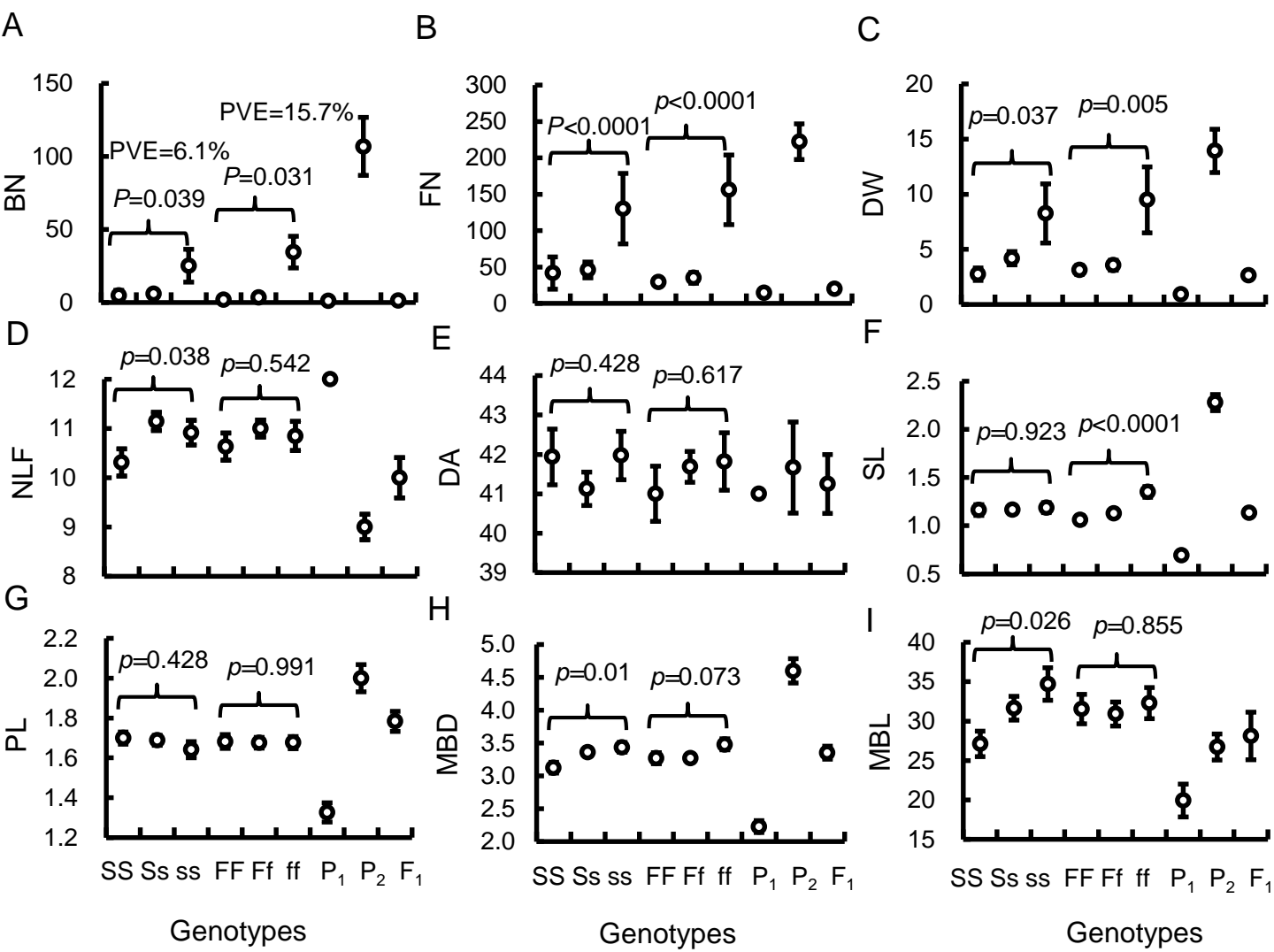
### FA gene's marker



### S gene's marker



**Figure S3.** Genotyping of *FA* and *S* in  $F_2$  individuals by HRM analysis. *S/s* represents *S* gene marker; *F/f* represents *FA* gene marker. Three genotypic classes of *S* and *FA* genes: *SS/FF* alleles, homozygous, from PI124039; *ss/ff* alleles, homozygous, from 10AS111A; *Ss/Ff* alleles, heterozygous, from  $F_1$ .



**Figure S4.** Quantitative effects associated with the *FA* and *S* genotypes. (A) The branch number per inflorescence (BN). (B) Flower number per inflorescence (FN). (C) Inflorescence dry weight (DW). (D) The number of leaves under the first inflorescence (NLF). (E) The days from sowing to the first flower anthesis (DA). (F) Floral trait, sepal length (SL). (G) Floral trait, petal length (PL). (H) The diameter of main inflorescence branch at the basal position (MBD). (I) The length of the main inflorescence branch (MBL). Trait values (mean ± SE) are plotted on the Y-axis of each graph, and genotypes with reference to *S* and *FA* in the parental lines and F<sub>1</sub> are plotted on the X-axis. The significance of variation in genotypes leading to variation in BN, FN, and DW was determined by Jonckheere-Terpstra test. Others traits and the  $p$  values for the associated ANOVA are also indicated. S/s represents *S* gene marker; F/f represents *FA* gene marker. Three genotypic classes of *S* and *FA* genes: SS/FF alleles, homozygous, from PI124039; ss/ff alleles, homozygous, from 10AS111A; Ss/Ff alleles, heterozygous, from F<sub>1</sub>. P<sub>1</sub>: *S. pimpinellifolium* PI124039; P<sub>2</sub>: *S. lycopersicum* 10AS111A; F<sub>1</sub>: the F<sub>1</sub> derived from P<sub>1</sub> and P<sub>2</sub>.

FA_wild type	MDPDAFSASLFKWDPRGAMPPSRLLLEPVAPPQPPPSLPPPPPPQPLPTSSYSI RSTREL	60
FA_strong mutation	MDPDAFSASLFKWDPRGAMPPSRLLLEPVAPPQPPPSLPPPPPPQPLPTSSYSI RSTREL	60
FA_weak mutation	MDPDAFSASLFKWDPRGAMPPSRLLLEPVAPPQPPPSLPPPPPPQPLPTSSYSI RSTREL	60
FA_PI124039	MDPDAFSASLFKWDPRGAMPPSRLLLEPVAPPQPPPSLPPPPPPQPLPTSSYSI RSTREL	60
FA_10AS111A	MDPDAFSASLFKWDPRGAMPPSRLLLEPVAPPQPPPSLPPPPPPQPLPTSSYSI RSTREL	60
FA_wild type	GGLEELFQAYGI RYYTAAKI AELGFTVNTLLDMKDEELDDMNSLSQI FRWDL LVGERYG	120
FA_strong mutation	GGLEELFQAYGI RYYTAAKI AELGFTVNTLLDMKDEELDDMNSLSQI FRWDL LVGERYG	120
FA_weak mutation	GGLEELFQAYGI RYYTAAKI AELGFTVNTLLDMKDEELDDMNSLSQI FRWDL LVGERYG	120
FA_PI124039	GGLEELFQAYGI RYYTAAKI AELGFTVNTLLDMKDEELDDMNSLSQI FRWDL LVGERYG	120
FA_10AS111A	GGLEELFQAYGI RYYTAAKI AELGFTVNTLLDMKDEELDDMNSLSQI FRWDL LVGERYG	120
FA_wild type	I KAAI RAEWRRLEEEEEARRRGHI LSDGGTNVLDALS QE. GLSEEPVQQQHEREAAGSGGG	179
FA_strong mutation	I KAAI RAEWRRLEEEEEARRRGHI LSDGGTNVLDALS QE. GLSEEPVQQQHER. . . . GGG	174
FA_weak mutation	I KAAI RAEWRRLEEEEEARRRGHI LSDGGTNVLDALS QEVGLSEEPVQQQHEREAAGSGGG	180
FA_PI124039	I KAAI RAEWRRLEEEEEARRRGHI LSDGGTNVLDALS QE. GLSEEPVQQQHEREAAGSGGG	179
FA_10AS111A	I KAAI RAEWRRLEEEEEARRRGHI LSDGGTNVLDALS QE. GLSEEPVQQQQEREAAGSGGG	179
N-terminal domain		
FA_wild type	GTWEVAAGGGGRMKQRRRKKAGRERRGEEDEETEELGEEDEENMNQGGGGGGI SERQREH	239
FA_strong mutation	GTWEVAAGGGGRMKQRRRKKAGRERRGEEDEETEELGEEDEENMNQGGGGGGI SERQREH	234
FA_weak mutation	GTWEVAAGGGGRMKQRRRKKAGRERRGEEDEETEELGEEDEENMNQGGGGGGI SERQREH	240
FA_PI124039	GTWEVAAGGGGRMKQRRRKKAGRERRGEEDEETEELGEEDEENMNQGGGGGGI SERQREH	239
FA_10AS111A	GTWEVAAGGGGRMKQRRRKKAGRERRGEEDEETEELGEEDEENMNQGGGGGGI SERQREH	239
FA_wild type	PFI VTEPGEVARGKKNGLDYLFHL YEQCRDFLI QVQTI AKERGEKCPTKVTNQVFRYAKK	299
FA_strong mutation	PFI VTEPGEVARGKKNGLDYLFHL YEQCRDFLI QVQTI AKERGEKCPTKVTNQVFRYAKK	294
FA_weak mutation	PFI VTEPGEVARGKKNGLDYLFHL YEQCRDFLI QVQTI AKERGEKCPTKVTNQVFRYAKK	300
FA_PI124039	PFI VTEPGEVARGKKNGLDYLFHL YEQCRDFLI QVQTI AKERGEKCPTKVTNQVFRYAKK	299
FA_10AS111A	PFI VTEPGEVARGKKNGLDYLFHL YEQCRDFLI QVQTI AKERGEKCPTKVTNQVFRYAKK	299
FA_wild type	AGAS YI NPKMRHYVHCYALHCLDEDAS NALRRAF KERGENVGAWRQACYKPLVAI AARQ	359
FA_strong mutation	AGAS YI NPKMRHYVHCYALHCLDEDAS NALRRAF KERGENVGAWRQACYKPLVAI AARQ	354
FA_weak mutation	AGAS YI NPKMRHYVHCYALHCLDEDAS NALRRAF KERGENVGAWRQACYKPLVAI AARQ	360
FA_PI124039	AGAS YI NPKMRHYVHCYALHCLDEDAS NALRRAF KERGENVGAWRQACYKPLVAI AARQ	359
FA_10AS111A	AGAS YI NPKMRHYVHCYALHCLDEDAS NALRRAF KERGENVGAWRQACYKPLVAI AARQ	359
FA_wild type	GWDI DAI FNAHPRLAI WYVPTKLRLCHSERS NAAAAASSS VS GGVADHLP H	411
FA_strong mutation	GWDI DAI FNAHPRLAI WYVPTKLRLCHSERS NAAAAASSS VS GGVADHLP H	406
FA_weak mutation	GWDI DAI FNAHPRLAI WYVPTKLRLCHSERS NAAAAASSS VS GGVADHLP H	412
FA_PI124039	GWDI DAI FNAHPRLAI WYVPTKLRLCHSERS NAAAAASSS VS GGVADHLP H	411
FA_10AS111A	GWDI DAI FNAHPRLAI WYVPTKLRLCHSERS NAAAAASSS VS GGVADHLP H	411
DNA binding domain		

**Figure S5.** Comparison of the FA alleles. Different amino acids are shaded in black and indicated by red arrows. The domains are indicated below the alignment by red line. FA\_wild type= *Solanum lycopersicum* Mill. FALSIFLORA (GenBank accession number AF197936).

S	MASSNRHWPSMFKSKPCNSHHHQWQHDI NSSI I QQRPPCNPEERSPEPKPRWNP RP EQI R	60
S_CLASSIC	MASSNRHWPSMFKSKPCNSHHHQWQHDI NSSI I QQRPPCNPEERSPEPKPRWNP RP EQI R	60
S_MULT	MASSNRHWPSMFKSKPCNSHHHQWQHDI NSSI I QQRPPCNPEERSPEPKPRWNP RP EQI R	60
S_PI124039	MASSNRHWPSMFKSKPCNSHHHQWQHDI NSSI I QQRPPCNPEERSPEPKPRWNP RP EQI R	60
S_10AS111A	MASSNRHWPSMFKSKPCNSHHHQWQHDI NSSI I QQRPPCNPEERSPEPKPRWNP RP EQI R	60
S	I LEAI FNS <b>G</b> MVNPPRDEI RK <b>I</b> RAKLQEYGVGDANVF YWFQNRKSRSKHKQRHLQAKAQQ	120
S_CLASSIC	I LEAI FNS <b>D</b> MVNPPRDEI RK <b>I</b> RAKLQEYGVGDANVF YWFQNRKSRSKHKQRHLQAKAQQ	120
S_MULT	I LEAI FNS <b>G</b> MVNPPRDEI RK <b>F</b> RAKLQEYGVGDANVF YWFQNRKSRSKHKQRHLQAKAQQ	120
S_PI124039	I LEAI FNS <b>G</b> MVNPPRDEI RK <b>I</b> RAKLQEYGVGDANVF YWFQNRKSRSKHKQRHLQAKAQQ	120
S_10AS111A	I LEAI FNS <b>G</b> MVNPPRDEI RK <b>I</b> RAKLQEYGVGDANVF YWFQNRKSRSKHKQRHLQAKAQQ	120
Homeodomain		
S	QHHNNNNNS SHQPI I TSSSSSSDKSSPNSLTFSI GTSNVMDLLNSPTSSVNQQNYNEFLS	180
S_CLASSIC	QHHNNNNNS SHQPI I TSSSSSSDKSSPNSLTFSI GTSNVMDLLNSPTSSVNQQNYNEFLS	180
S_MULT	QHHNNNNNS SHQPI I TSSSSSSDKSSPNSLTFSI GTSNVMDLLNSPTSSVNQQNYNEFLS	180
S_PI124039	QHHNNNNNS SHQPI I TSSSSSSDKSSPNSLTFSI GTSNVMDLLNSPTSSVNQQNYNEFLS	180
S_10AS111A	QHHNNNNNS SHQPI I TSSSSSSDKSSPNSLTFSI GTSNVMDLLNSPTSSVNQQNYNEFLS	180
S	NEQPFFFTVQPPP <b>V</b> MPTHDHS AGFCFQDSSFTTPHSSSSGLLLNEWMGGI STQAPNNSKK	240
S_CLASSIC	NEQPFFFTVQPPP <b>V</b> MPTHDHS AGFCFQDSSFTTPHSSSSGLLLNEWMGGI STQAPNNSKK	240
S_MULT	NEQPFFFTVQPPP <b>V</b> MPTHDHS AGFCFQDSSFTTPHSSSSGLLLNEWMGGI STQAPNNSKK	240
S_PI124039	NEQPFFFTVQPPP <b>V</b> MPTHDHS AGFCFQDSSFTTPHSSSSGLLLNEWMGGI STQAPNNSKK	240
S_10AS111A	NEQPFFFTVQPPP <b>V</b> EPTHDHS AGFCFQDSSFTTPHSSSSGLLLNEWMGGI STQAPNNSKK	240
S	DENDKI NLQS QLMS YTVTSTVSPLATTTI PTI SHI QGVTVDPNDAGPTRSTVFI NDVAFE	300
S_CLASSIC	DENDKI NLQS QLMS YTVTSTVSPLATTTI PTI SHI QGVTVDPNDAGPTRSTVFI NDVAFE	300
S_MULT	DENDKI NLQS QLMS YTVTSTVSPLATTTI PTI SHI QGVTVDPNDAGPTRSTVFI NDVAFE	300
S_PI124039	DENDKI NLQS QLMS YTVTSTVSPLATTTI PTI SHI QGVTVDPNDAGPTRSTVFI NDVAFE	300
S_10AS111A	DENDKI NLQS QLMS YTVTSTVSPLATTTI PTI SHI QGVTVDPNDAGPTRSTVFI NDVAFE	300
S	VGI GPFNVREVFGEDAVLI HSSGEPLI TNEWGI TI QPLQHGAFFYLLRTSSI ASTHH	357
S_CLASSIC	VGI GPFNVREVFGEDAVLI HSSGEPLI TNEWGI TI QPLQHGAFFYLLRTSSI ASTHH	357
S_MULT	VGI GPFNVREVFGEDAVLI HSSGEPLI TNEWGI TI QPLQHGAFFYLLRTSSI ASTHH	357
S_PI124039	VGI GPFNVREVFGEDAVLI HSSGEPLI TNEWGI TI QPLQHGAFFYLLRTSSI ASTHH	357
S_10AS111A	VGI GPFNVREVFGEDAVLI HSSGEPLI TNEWGI TI QPLQHGAFFYLLRTSSI ASTHH	357
C-terminal domain		

**Figure S6.** Comparison of the S alleles. Different amino acids are shaded in black and indicated by red arrows. The domains are indicated below the alignment by red line. S= *Solanum lycopersicum* COMPOUND INFLORESCENCE (GenBank accession number NP\_001234072).