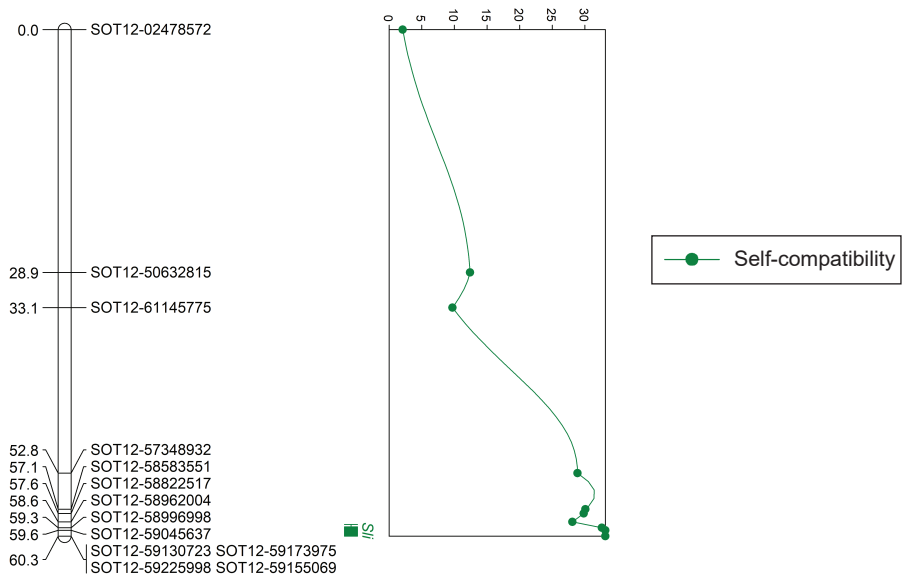


- = WGS used for marker development
- = Population used for mapping

**Supplementary Figure 1. Pedigree of mapping populations.** Genotypes highlighted in green were sequenced to enable marker development. Populations highlighted in yellow were used for QTL analysis.

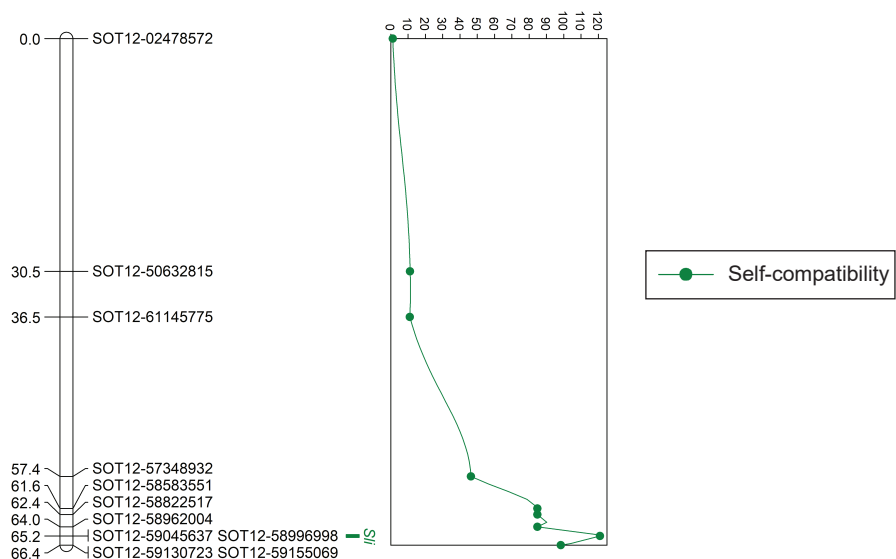
a

### Chr12



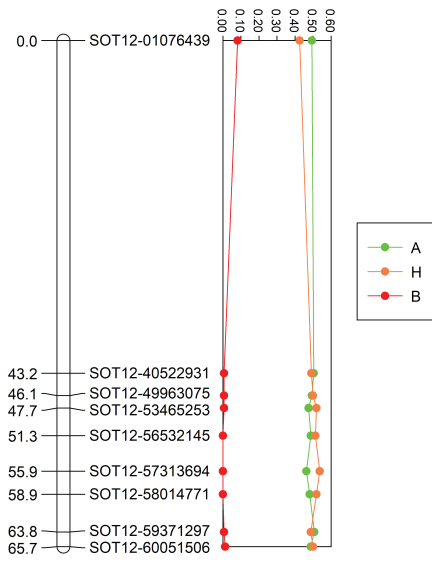
b

### Chr12

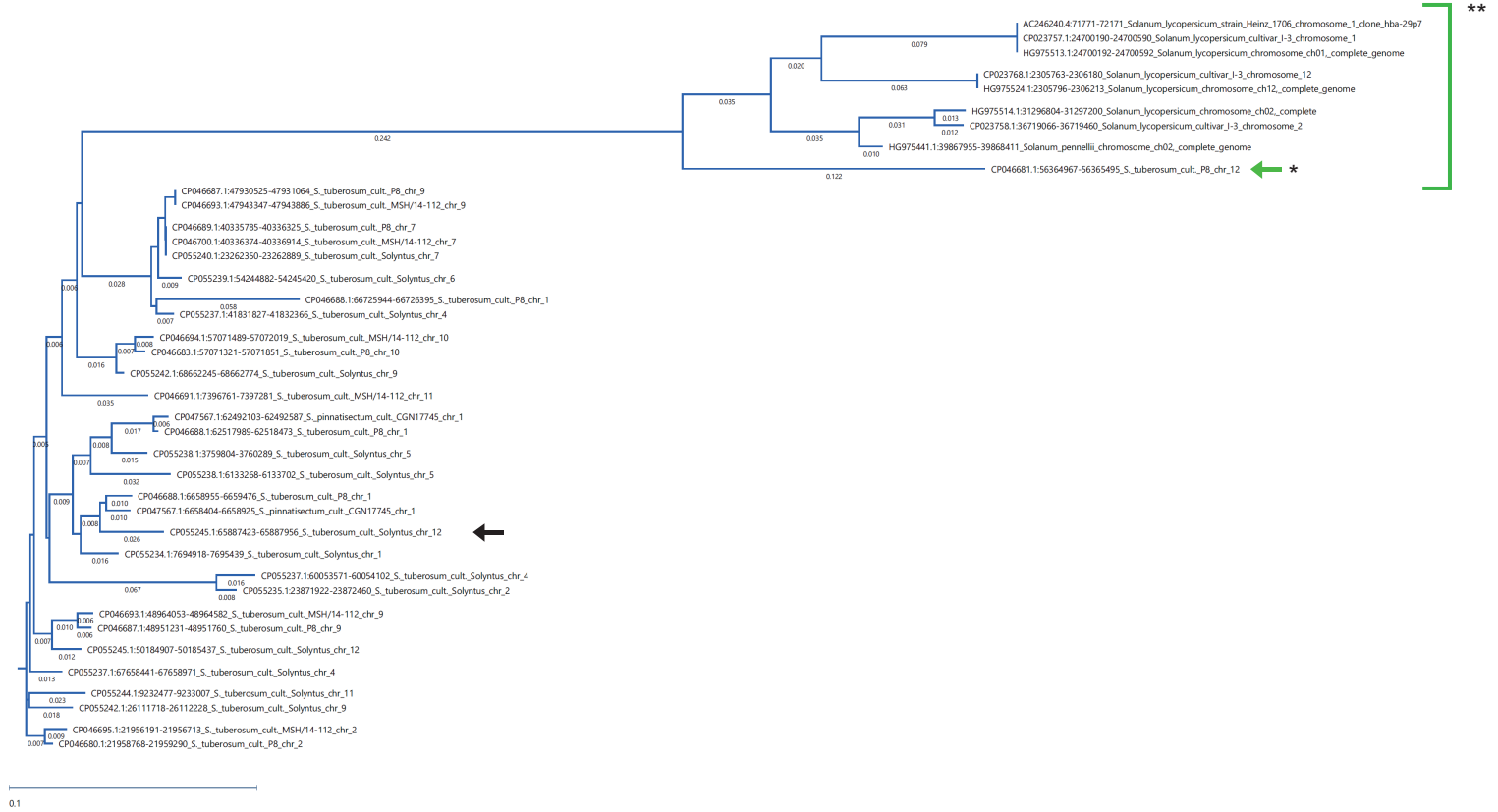
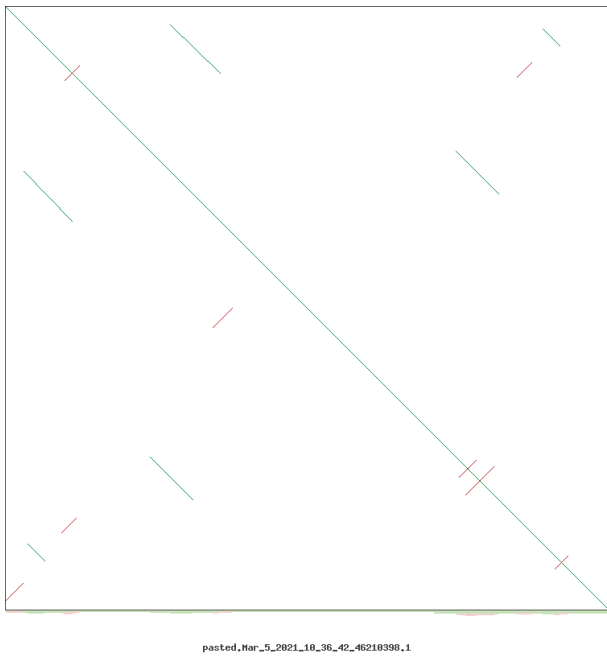


**Supplementary Figure 2. QTL analysis in populations 18SC11 and 18SC12. a.** LOD profile of QTL analysis for self-compatibility in population 18SC11. Green line shows LOD score. The 1-LOD and 2-LOD intervals are highlighted between the genetic map and the LOD profile. **b.** LOD profile of QTL analysis for self-compatibility in population 18SC12. Green line shows LOD score. The 1-LOD and 2-LOD intervals are highlighted between the genetic map and the LOD profile.

Chr12



**Supplementary Figure 3. Frequency of genotypes observed in the F2 population 19SC1 (n=160).** The proportion of plants homozygous for the HP66 haplotype are shown in green. The proportion of plants heterozygous for the HP66 and D16 haplotypes are shown in orange. The proportion of plants homozygous for the D16 haplotype are shown in red.

**a****b****c**

```
>SQ383018181 Solanum tuberosum, chromosome:chr01, from MITE family DTA_Sot42,
SuperFamily hAT, partial sequence
Length = 525

Score = 795 bits (401), Expect = 0.0
Identities = 497/525 (94%), Gaps = 3/525 (0%)
Strand = Plus / Plus

Query: 1   cagggcgctcaactgtatttggaggcctaaaacaaatttaataaaggcctaaaatc 60
Sbjct: 1   cagggcgctcaactgtatttggaggcctgaagcaaaatttaataaaggcctaaaatc 60

Query: 61   ttttagctgaggcaattataataaattgttaacattattctataagtaataagttgac 120
Sbjct: 61   ttttagctgaggcaattataataaattgttaacattattctataagtaataagttgac 120

Query: 121  aaaactgcttataaactcttttttatttaaaagcacataacataagtcacttaaca 180
Sbjct: 121  aaaactgcttataaactctttttt-atttaaaacacataaaaataatcaacttaata 179

Query: 181  ggcttgtaattcgtttatccaacacattagttttactattgattcatattttgataga 240
Sbjct: 180  agcttgtaattcgtttatccaacacattagttttactattgattcatattttgataga 238

Query: 241  gctctaacttacatagagtataaaagggtatagaaaattacaacgcgagagtaagttaa 300
Sbjct: 239  gctctaacttacatagagtataaaagggtctagaaaattacaacgcgagagtagtgtaa 298

Query: 301  gagagtgtaagaagacaaaacacgtttttcttgatttctctattgattgaggttaag 360
Sbjct: 299  gagagtgtaagaagacaaaacacattttcttgatttctctattgattgaggttaag 358

Query: 361  gagaataaaataatataatataatgaaagtacatttatcttaataatattttttctat 420
Sbjct: 359  gagaataaaatattatataatataatgaaatacatttatcttaataatattttttctat 418

Query: 421  aaaaaaattaacacataatttattgttgtaaaaattgaggccccctaaaattgggg 480
Sbjct: 419  aaaaaaattaacacataatttattgttgtaaaaattgagg-ccccctaaaattgggg 477

Query: 481  gcctaaggcatatgcctaatttttataagcattgagccggcactg 525
Sbjct: 478  gcctaaggcatatgcctaatttttataagcattgagccggctactg 522
```

**Supplementary Figure 4.** Analysis of the 533 bp insertion in the *Sli* promoter. **a.** Phylogenetic tree of sequences similar to the 533 bp insertion including similar sequences in *Solanum lycopersicum*. Interestingly, one *S. tuberosum* sequence (\*) is grouped together with the *S. pennellii* and *S. lycopersicum* sequences (\*\*). **b.** Dot-plot analysis of the 533 bp insertion showing the presence of miniature inverted repeats. **c.** Alignment of the 533 bp insertion with the highest score BLAST hit on the pMITE database showing high identity between the insertion and a MITE family DTA\_Sot42 TE from *S. tuberosum*.