

Figure S1: Southern blot analysis of the integration of pUE10::swo1 of strain *Taswo1-28*. Total DNA extracted from the wild type (WT) and from *Taswo1-28* strains and digested with *Bam*HI. **a)** Scheme of the recombination of pUE10-*TaSWO1* vector into the *BLU17* locus of *T. atroviride* genome. The restriction fragment pattern is explained for two integrations of vector in this region. **b)** Hybridization was performed with a ^{32}P labeled 420 bp fragment corresponding to partial *blu17* terminator. To the left, the DNA gel stained with ethidium bromide; to the right the autoradiography after hybridization. Arrows indicate the molecular weight of the fragments.

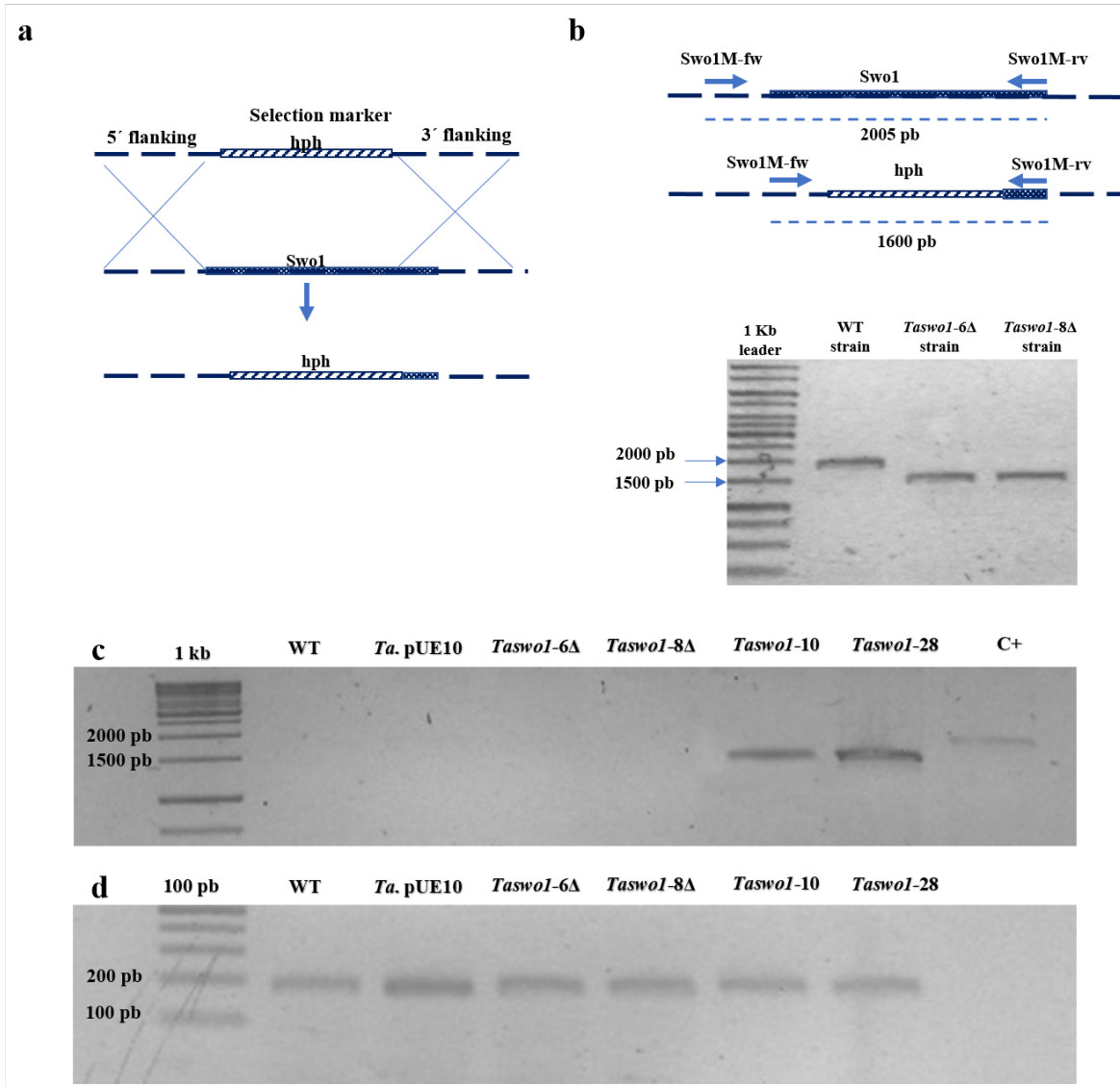


Figure S2: Construction and verification of *Taswo1* deletion mutants. **a)** Scheme of *SWO1* gene replacement by the hygromycin cassette, dotted lines represent genomic DNA. **b)** Upper part, scheme of the PCR band pattern expected for the wild type strain and the deletion mutants using primers Swo1-Mfwd and Swo-1M rev. Dotted lines represent genomic DNA, while small light blue lines represent the expected PCR product. Lower part, gel with the actual PCR products obtained using genomic DNA from each strain as template **c)** Transcriptional analysis of the RT-PCR products of WT and *TaSwo1* construct strains. RT-PCR was performed using RNA extracted from the different strains grown in PDA with hygromycin. C+ genomic DNA from the wild type was used as a positive control **d)** RT-PCR using *SWO1* primers Swo-F-n and Swo-R-n. **c)** Control using *GPD* Primers gpd-F and gpd-R

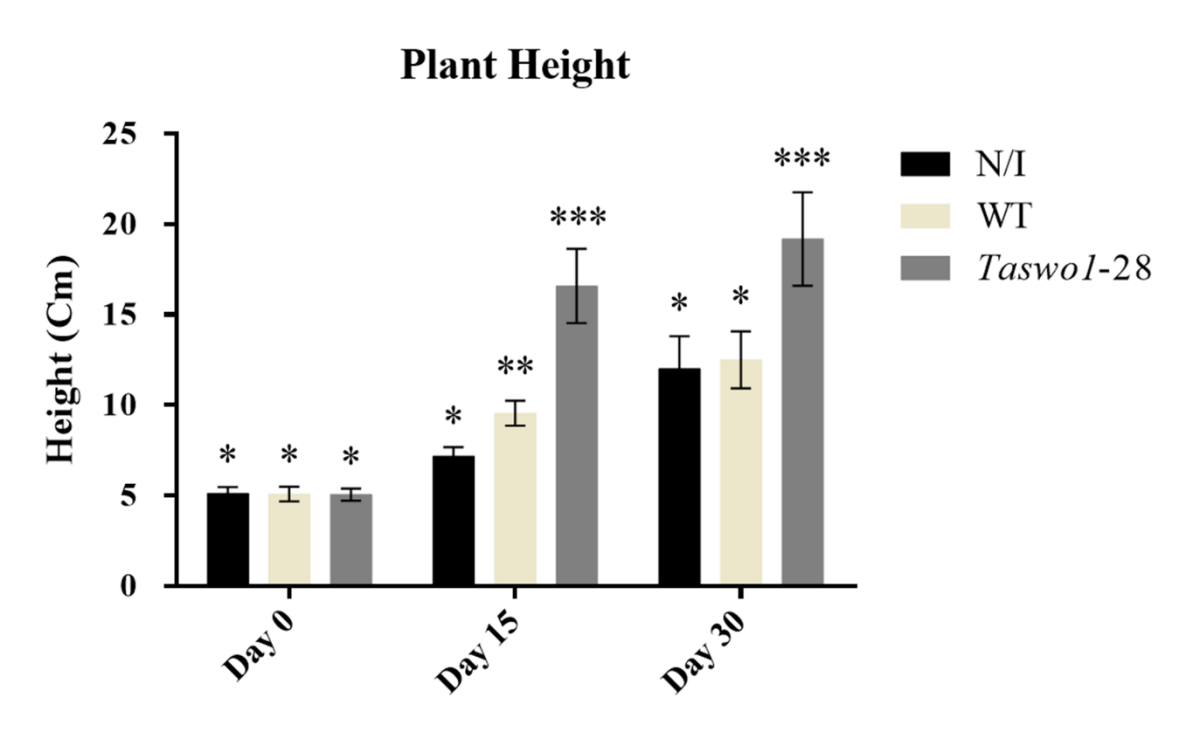


Figure S3: Height of *Solanum lycopersicum* plants inoculated with the Wild type *T. atroviride* (WT) strain or the *Taswo1-28* overexpressing. Means of three replicas are depicted in the graph. Bars indicate standard deviation. Different number of asterisks within the panels indicate that the average of each treatment is significantly different ($p < 0.05$).

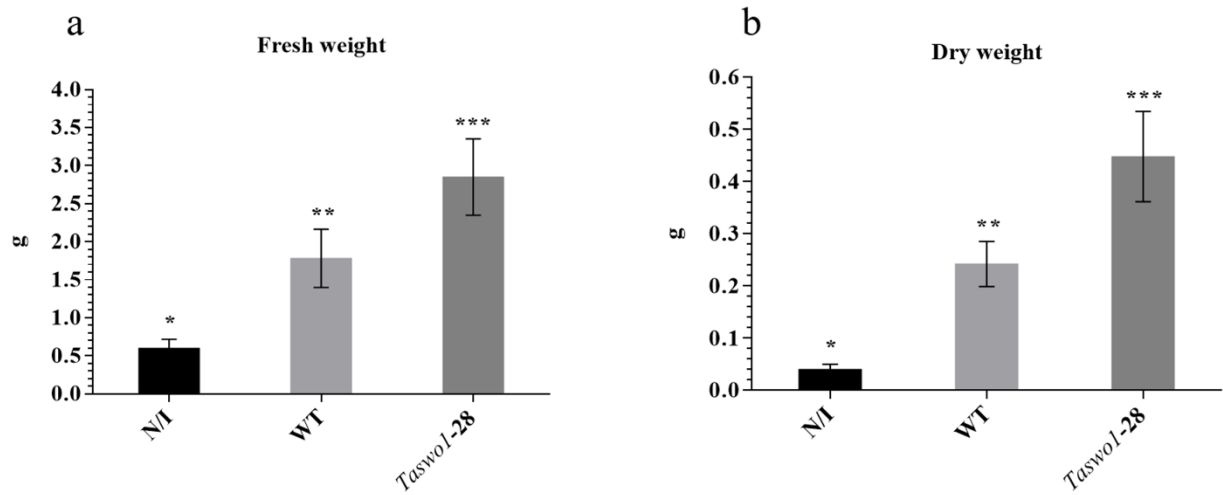
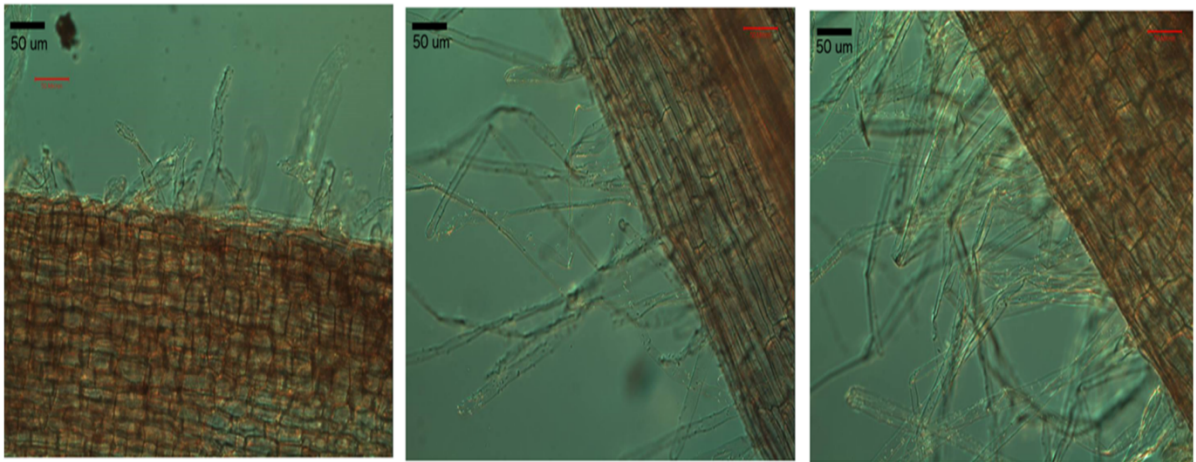


Figure S4. Biomass production of *S. lycopersicum* plants as determined by plant fresh weight (a) and dry weights (b). Means of three replicates are depicted in the graph. Bars indicate standard deviation. Different number of asterisks within the panels indicate that the average of each treatment is significantly different ($p < 0.05$). Note that scales are different for panels a) and b) so statistics are only comparable within each panel.

a



b

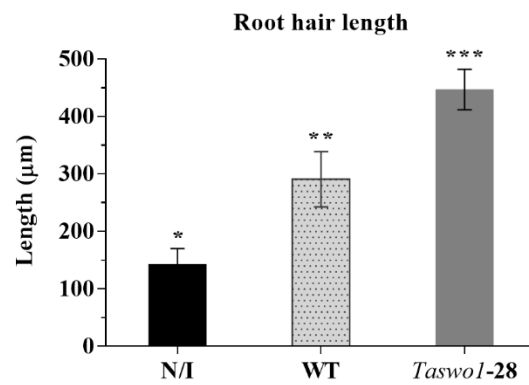


Figure S5: a) Root hair length in chili plants inoculated with the WT strain or *Taswo1-28*; as a control non-inoculated plant. b) Statistical analysis of treatments, different number of asterisks within the panels indicate that the average of each treatment is significantly different ($p < 0.05$)