

## Additional file 1: Figure S1:

*Gene ontology (GO) and enzyme classifications (EC) for S. lycopersicum stem trichome transcriptome at level 2. (a) Cellular component GO terms, (b) biological process GO terms, (c) molecular function GO terms and (d) general EC terms. Figure S2. Transactivation of terpene synthase promoters by 35S:RFP in N. benthamiana leaves. Letters indicate significant differences (n = 4, ANOVA,  $P < 0.05$  according to Tuckey's B posthoc test). The normalized GUS activity of the SITPS3, 7, 8 and 9 reporter constructs with the RFP effector construct is not significantly higher from the SITPS5 reporter construct with the RFP effector construct, indicating that any relevant activation of an effector construct (in Figures 3, 4, and Additional file 1: Figure S3) must be significantly higher than that of the SITPS5p:GUS reporter- 35S:RFP effector combination. Figure S3. Transactivation of terpene synthase promoters by SIWRKY78 and SIWRKY28 in N. benthamiana leaves. Letters indicate significant differences (n = 3, ANOVA,  $P < 0.05$  according to Tuckey's B posthoc test). Representative results from two experiments are shown. The normalized GUS activity of the 35S:WRKY28 effector-SITPS5p:GUS reporter construct combination was only marginally higher than that of the negative control (35S:RFP effector- SITPS5p:GUS reporter constructs) and was not further investigated. Figure S4. Nucleotide sequence of transcription factors SIWRKY78 (*Solyc07g055280.2.1*), SIWRKY28 (*Solyc12g011200.1.1*), SIWRKY73 (*Solyc03g113120.2.1*) and SIMYC1 (*KF430611*). The predicted coding sequences are in capital letters, 5' and 3' UTRs are in small letter type. Start and stop codons are in bold. Table S1. KEGG pathways found in the *S. lycopersicum* stem trichome transcriptome. Table S2. Selected regulatory motifs in the sequence of SITPS5, 3 and 7 promoters analyzed by PLACE [65]. Table S3. List of primers used.*