New Phytologist

***New Phytologist* Supporting Information**

Article title:
Tomato geranylgeranyl diphosphate synthase isoform 1 is involved in the stress-triggered production of diterpenes in leaves and strigolactones in roots

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The following Supporting Information is available for this article:

**Methods S1.** Metabolite analyses.

**Methods S2.** Gene expression analyses.

**Methods S3.** Co-immunoprecipitation assays.

**Fig. S1.** DNA sequence alignment of *SlG1* CRISPR mutants.

**Fig. S2.** Protein alignments of SlG1 wild-type sequences with the selected CRISPR mutants.

**Fig. S3.** *SlG1*, *SlG2* and *SlG3* transcript levels in different tissues and developmental stages.

**Fig. S4.** Expression levels of genes encoding GLS and GGPPS isoforms in leaves after *Pseudomonas syringae* infection.

**Fig. S5.** SlG1-Myc is able to specifically bind to protein partners.

**Fig. S6.** Root parameters in SL-defective mutants.

**Table S1.** List of primers used in this work.

**Table S2.** Constructs and cloning details.

**Table S3.** Co-expression of tomato GGPPS paralogs (guide genes) with isoprenoid-related genes (query genes) in root tissue.

**SUPPORTING METHODS**

**Methods S1. Metabolite analyses.**

Isoprenoid extraction and quantification. Carotenoids, chlorophylls and tocopherols were extracted as described (Barja et al., 2021; Ezquerro et al., 2022) with some modifications. Freeze-dried tissue powder from roots (25 mg) or leaves (8 mg) was mixed in 2 ml Eppendorf tubes with 375 µl of methanol as extraction solvent, 25 µl of a 10 % (w/v) solution of canthaxanthin (Sigma) in chloroform as internal control, and three 2 mm glass beads. In the case of pericarp tissue, freeze-dried powder (20 mg) was 1 ml of 2:1:1 hexane:acetone:methanol was used instead of methanol. Following extraction as described (Barja et al., 2021; Ezquerro et al., 2022), dry residues were resuspended in 200 µl of acetone by using an ultrasound bath and filtered with 0.2 µm filters into amber-colored 2 ml glass vials. Separation and quantification of individual carotenoids, chlorophylls and tocopherols was performed as described (Barja et al., 2021).

ABA extraction and quantification. For ABA quantification, 20 mg of freeze-dried root powder was mixed using 1 ml of 10% methanol in water (containing internal ABA standard) by shaking in a TissueLyser II (Quiagen) at 27 Hz for 3 min. Next, samples were placed in a rotator for 1 hour at 4°C. Extracts were then centrifuged at 14000 x*g* at 4°C for 15 min. Around 800 µl of the liquid phase was recovered in 1.5 ml Eppendorf for further steps. Eluted liquid was run through an Oasis HLB (reverse phase) column as described (Flokova et al., 2014). The dry residues were dissolved in 1 ml of pure methanol and after, dried under a nitrogen flow in a fume hood for 40 min. The eluate was dissolved in 5% acetonitrile and ABA was detected using a reverse phase UHPLC chromatography. The gradient used contains 5 to 50% acetronitrile with 0.05% acetic acid, at a flow speed of 400 µL/min over 21 min. Quantification of ABA was perform with a Q-Exactive mass spectrometer (Orbitrap detector; ThermoFisher Scientific) in conjunction with internal standards (deuterium-labelled hormone at 1pmol/µl), calibration curves and the TraceFinder 4.1 SP1 software.

SL extraction and quantification. Tomato seedlings growing in a mixture of river sand and a clay granulate (1:1) were supplied with half-strength Hoagland solution twice a week for 28 days. After 28 days, plants were divided into two groups of which one continued to get the half-strength Hoagland solution for 7 days, while the other was exposed to phosphorus deficiency (by using half-strength Hoagland solutions without phosphate) to induce SL biosynthesis and exudation. Pots were washed with 100 ml of sterile milli-Q water to collect the SLs, which were then concentrated using C18 SPE columns (SUPELCO, Discovery® DSC-18 SPE, 500 mg/3 mL) and analyzed by LC-MS/MS as described (Zhang et al., 2014; 2018). Identification of individual SLs was based on earlier publications on tomato SLs, using authentic standards of solanacol, orobanchol, oxo-orobanchol and tentatively identified hydroxyl-orobanchol, kindly provided by Koichi Yoneyama (Xie et al., 2009; Kohlen et al., 2012; Wang et al., 2022).

Analysis of volatile organic compounds. For the analysis of VOCs, frozen tomato leaf powder (150 mg) was mixed in a 15 ml glass vial with 1 mL of a saturated $CaCl_2$ solution and 100 µL of 750 mM EDTA (pH 7.5). The vial was sealed and sonicated for 5 min and volatile compounds extraction was performed by Head Space Solid-Phase Microextraction (HS-SPME) as previously reported (López-Gresa et al., 2017). VOCs were analyzed in an Agilent 6890N (Santa Clara, CA, USA) gas chromatograph coupled to an Agilent 5975B Inert XL electronic impact (EI) mass detector with an ionization energy of 70 eV and a source temperature of 300°C. Chromatograms were processed using the Enhanced ChemStation software (Agilent). Final identification of and quantification of GL was performed using a commercial standard (Sigma).

**Methods S2. Gene expression analyses.**

Gene co-expression network (GCN) analyses. The data set used for Gene co-expression network construction was previously described (Wang et al., 2021) and it is publicly available in https://dataview.ncbi.nlm.nih.gov/ object/ PRJNA 679261? reviewer=vs5lk 0a94j04c2rgieta1lrlro. It is composed by tomato root samples grown in +P and -P conditions. Tomato isoprenoid biosynthetic genes were retrieved from Plaza 4.0 using Arabidopsis homologs as queries (https://bioinformatics.psb.ugent.be/plaza/) as previously described (Wang et al., 2022). Pairwise Pearson correlation coefficients (PCC) were calculated between every two genes using *SlG1*, *SlG2* and *SlG3* as baits and tomato isoprenoid biosynthetic genes as preys. Figures were constructed using R software (https://www.r-project.org/).

RNA extraction and RT-qPCR analyses. Total RNA from freeze-dried leaves and roots was extracted using TriPure isolation reagent (Sigma) combined with a Qiagen RNeasy mini spin column kit following manufacturer's instructions. RNA was quantified using a NanoDropTM 8000 spectrophotometer (ThermoFisher Scientific). ThermoFisher First Strand cDNA synthesis kit using oligo(dT) primer was used to reverse transcribe 1000 ng of RNA into 20 µL of cDNA, which was subsequently diluted 10-fold with mili-Q water and stored at -20 °C for further analysis. Relative mRNA abundance was evaluated via Real-Time Quantitative Polymerase Chain Reaction (RT-qPCR) in a reaction volume of 10 µL containing 5 µL of SYBR Green Master Mix (Thermo Fisher Scientific), 0.3 µM of each specific forward and reverse primer (Table S1) and 2 µL of cDNA. Transcript abundance was evaluated via real-time quantitative PCR (RT-qPCR) in a reaction volume of 10 µl containing 2 µl of the cDNA dilution, 5 µl of SYBR Green Master Mix (Thermo Fisher Scientific), and 0.3 µM of each specific forward and reverse primer (Table S1). The RT-qPCR was carried out on a QuantStudio 3 Real-Time PCR System (Thermo Fisher Scientific) using three independent biological samples and three technical replicates of each sample. Normalized transcript abundance was calculated as previously described (Simon, 2003) using tomato *ACT4* (Solyc04g011500) as endogenous reference gene.

**Methods S3. Co-immunoprecipitation assays.**

Co-immunoprecipitation experiments were carried out as described (Barja & Rodríguez-Concepción, 2020; Barja et al., 2021) (Methods S3). Constructs encoding Myc- and HA-tagged tomato GGPPS and PSY proteins (Table S2) (Barja et al., 2021) were transformed into *A. tumefaciens* GV3101 strains. A plasmid containing the Arabidopsis phosphoribulokinase protein with a Myc tag (pGWB417_PRK-Myc) was used as negative control. Agroinfiltration of *N. benthamiana* leaves, sample collection, protein extraction and immunoprecipitation of proteins was performed as described (Barja et al., 2021). Myc- and HA-tagged proteins in input and Co-IP samples were detected by immunoblot analyses using 1:2000 αMyc (Sigma) and 1:1000 αHA (Roche) dilutions. Horseradish peroxidase (HRP)-conjugated secondary antibodies against mouse and rat IgGs, respectively were used in a 1:10000 dilution. Amersham ECL Prime Western Blotting Detection Kit (GE Healthcare) was used for detection and the signal was visualized using the Amersham ImageQuant 800 Western blot imaging system.

**SUPPORTING FIGURES**

**Figure S1. DNA sequence alignment of *SlG1* CRISPR mutants.** Alignment was performed using Clustal Omega (https://www.ebi.ac.uk/Tools/msa/clustalo/) with default settings. The sequence encoding the predicted plastid-targeting peptide is marked in green. Designed single-guide RNAs (sgRNA) are highlighted in blue and genotyping oligonucleotides are highlighted in fuchsia. Protospacer adjacent motifs (PAM) are highlighted in red. Translation stop codons are underlined and marked in bold. Numbers at the end of each sequence indicate DNA sequence length.

```
SLG1      ATGGCATTTTTAGCTACCATTTCTGGCCTTGACAATCTGTTCCTTTCTAATACCCCAAAC 60
slg1-1    ATGGCATTTTTAGCTACCATTTCTGGCCTTGACAATCTGTTCCTTTCTAATACCCCAAAC 60
slg1-2    ATGGCATTTTTAGCTACCATTTCTGGCCTTGACAATCTGTTCCTTTCTAATACCCCAAAC 60
          ************************************************************

SLG1      AATAACTTTGCTTTCAGTAGAAAACTCCCACCAAGCCAATCTTACAGTTTCCTTCACAAG 120
slg1-1    AATAACTTTGCTTTCAGTAGAAAACTCCCACCAAGCCAATCTTACAGTTTCCTTCACAAG 120
slg1-2    AATAACTTTGCTTTCAGTAGAAAACTCCCACCAAGCCAATCTTACAGTTTCCTTCACAAG 120
          ************************************************************

SLG1      AAAATACACGCTAGCGATGTTGCGAACTCGTTCCAAACTTTTCAAGTCAAGGAACGAGAT  180
slg1-1    AAAATACACGCTAGCGATGTTGCGAACTCGTTCCAAACTTTTCAAGTCAAGGAACGAGAT  180
slg1-2    AAAATACACGCTAGCGATGTTGCGAACTCGTTCCAAACTTTTCAAGTCAAGGAACGAGAT  180
          ************************************************************

SLG1      GTTTCATCCAAGGCAGAGAAATTCATCTTGCCTGAGTTTGAGTTTCAAGAATACATGGTA 240
slg1-1    GTTTCATCCAAGGCAGAGAAATTCATCTTGCCTGAGTTTGAGTTTCAAGAATACATGGTA 240
slg1-2    GTTTCATCCAAGGCAGAGAAATTCATCTTGCCTGAGTTTGAGTTTCAAGAATACATGGTA 240
          ************************************************************

SLG1      ACGAAGGCAATCAAGGTAAACAAAGCACTAGATGAAGCAATACCAATGCAAGAGCCTATA 300
slg1-1    ACGAAGGCAATCAAGGTAAACAAAGCACTAGATGAAGCAATACCAATGCAAGAGCCTATA 300
slg1-2    ACGAAGGCAATCAAGGTAAACAAAGCACTAGATGAAGCAATACCAATGCAAGAGCCTATA 300
          ************************************************************

SLG1      AAAGTTCATGAAGCCATGAGGTACTCACTTCTAGCTGGAGGAAAACGTGTCCGGCCGATC 360
slg1-1    AAAGTTCATGAAGCCATGAGGTACTCACTTCTAGCTGGAGGAAAACGTGTCCGGCCGATC 360
slg1-2    AAAGTTCATGAAGCCATGAGGTACTCACTTCTAGCTGGAGGAAAACGTGTCCGGCCGATC 360
          ************************************************************

SLG1      CTCTGCATGGCTTCTTGTGAAGTTGTAGGAGGGGATGAATCCTTAGCTATACCTGCAGCT 420
slg1-1    CTCTGCATGGCTTCTTGTGAAGTTGTAGGAGGGGATGAATCCTTAGCTATACCTGCAGCT 420
slg1-2    CTCTGCATGGCTTCTTGTGAAGTTGTAGGAGGGGATGAATCCTTAGCTATACCTGCAGCT 420
          ************************************************************
          G1 CRISPR Geno F
SLG1      TGCGCAGTTGAGATGATCCATACCATGTCACTCGTCCATGATGATCTTCCCTGCATGGAC 480
slg1-1    TGCGCAGTTGAGATGATCCATACCATGTCACTCGTCCATGATGATCTTCCCTGCATGGAC 480
slg1-2    TGCGCAGTTGAGATGATCCATACCATGTCACTCGTCCATGATGATCTTCCCTGCATGGAC 480
          ************************************************************

SLG1      AACGATGATCTACGTCGTGGCAAGCCCACGAACCATAAGGTTTTTGGAGAAAACACTGCA 540
slg1-1    AACGATGATCTACGTCGTGGCAAGCCCACGAACCATAAGGTTTTTGGAGAAAACACTGCA 540
slg1-2    AACGATGATCTACGTCGTGGCAAGCCCACGAACCATAAGGTTTTTGGAGAAAACACTGCA 540
          ************************************************************

SLG1      GTTCTTGCAGGGGATGCACTTTTATCTTTGGCCTTTGAACATGTGGCTACCAAGACTCAG 600
slg1-1    GTTCTTGCAGGGGATGCACTTTTATCTTTGGCCTTTGAACATGTGGCTACCAAGACTCAG 600
slg1-2    G-------------------------------------------------------------  541
          *
```

sgRNA-1

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SLG1      AATGTGCCACCCCAAAGAGTGGTCCAAGCCATTGGGGAATTGGGTTCAGCTGTTGGCTCA 660
slg1-1    AATGTGCCACCCCAAAGAGTGGTCCAAGCCATTGGGGAATTGGGTTCAGCTGTTGGCTCA 660
slg1-2    ------------------------------------------------------------541
```

PAM

```
SLG1      GAAGGGCTCGTGGCAGGGCAAATTGTGGACTTGGCGAGTGAAGGAAAACAAGTTAGCCTA 720
slg1-1    GAAGGGCTCGTGGCAGG---------------------------------------------- 677
slg1-2    ------------------------------------------------------------ 541
```

sgRNA-2 PAM

```
SLG1      ACTGAACTGGAGTACATTCACCACCATAAGACGGCGAAGCTTTTGGAGGCTGCTGTGGTT 780
slg1-1    ------------------------------------------------------------ 677
slg1-2    ------------------------------------------------------------ 541

SLG1      TGTGGGGCAATAATGGGGGGAGGAAATGAGGTTGATGTGGAGCGAATGAGGAGCTATGCT 840
slg1-1    ------------------------------------------------------------ 677
slg1-2    ------------------------------------------------------------ 541

SLG1      AGGTGCATTGGACTGTTATTTCAAGTGGTAGATGATATTCTTGATGTTACCAAGTCATCA 900
slg1-1    ------------------------------------------------------------ 677
slg1-2    -----------------------------------TTCTTGATGTTACCAAGTCATCA 569

SLG1      GATGAGCTGGGAAAGACAGCGGGTAAGGACCTAATAACAGATAAGGCTACATATCCTAAG 960
slg1-1    ----------------------GTAAGGACCTAATAACAGATAAGGCTACATATCCTAAG 715
slg1-2    GATGAGCTGGGAAAGACAGCGGGTAAGGACCTAATAACAGATAAGGCTACATATCCTAAG 644
                                ************************************
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G1 CRISPR Geno R

```
SLG1      TTGATGGGGCTAGAAAAGGCTCGACAATATGCCGGTGAGCTGATGGCTAAGGCCATGAAT 1020
slg1-1    TTGATGGGGCTAGAAAAGGCTCGACAATATGCCGGTGAGCTGATGGCTAAGGCCATGAAT 775
slg1-2    TTGATGGGGCTAGAAAAGGCTCGACAATATGCCGGTGAGCTGATGGCTAAGGCCATGAAT 684
          ************************************************************

SLG1      GAGCTAAGCTACTTCGACTATGCAAAGGCAGCACCTCTTTATCATATTGCTAGTTATATT 1080
slg1-1    GAGCTAAGCTACTTCGACTATGCAAAGGCAGCACCTCTTTATCATATTGCTAGTTATATT 835
slg1-2    GAGCTAAGCTACTTCGACTATGCAAAGGCAGCACCTCTTTATCATATTGCTAGTTATATT 744
          ************************************************************

SLG1      GCAAATCGACAGAATTGA 1098
slg1-1    GCAAATCGACAGAATTGA 853
slg1-2    GCAAATCGACAGAATTGA 762
          ******************
```

**Figure S2. Protein alignments of SlG1 wild-type sequences with the selected CRISPR mutants.** Multiple sequence alignment was performed using *Clustal Omega* (https://www.ebi.ac.uk/Tools/msa/clustalo/) with default settings**.** The predicted targeting peptides, the region of the designed sgRNAs and the catalytic motifs FARM (first aspartate-rich motif) and SARM (second-aspartate rich motif) are boxed in green, blue and black, respectively. The protein-protein interaction CxxxC (x = any hydrophobic residue) motifs are highlighted in pink. Numbers at the end of each sequence indicate protein length.

**Figure S3. *SlG1, SlG2 and SlG3* transcript levels in different tissues and developmental stages.** **(a)** RNAseq data retrieved from the *Tomato eFP Browser* database (http://bar.utoronto.ca/efp_tomato/cgi-bin/efpWeb.cgi). Levels are represented as RPKM (Reads per Kilobase of transcript per Million mapped reads). **(b)** RNAseq data obtained from Genevestigator (https://genevestigator.com). Levels are represented as log2 TPM (Transcripts Per Million mapped reads). Abbreviations: DPA, days post-anthesis; IG, immature green; MG, mature green; B, breaker; O, orange, R, red. YL, young leaves; ML, mature leaves.

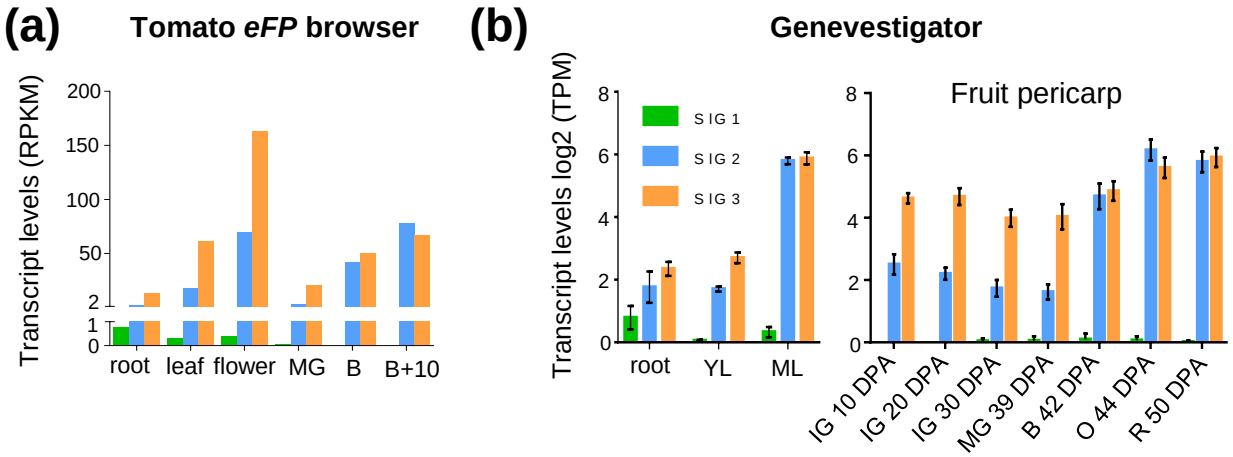


**Figure S4. Expression levels of genes encoding GLS and GGPPS isoforms in leaves after *Pseudomonas syringae* infection.** RNAseq data obtained from Genevestigator (https://genevestigator.com) of three different tomato infection experiments with *P. syringae pv. tomato* DC3000, using samples collected at 9 (Ailsa Craig) or 6 (Rio Grande) hours post infection. Plots show the transcript levels of the indicated genes in leaves of both cultivars during *P. syringae pv. tomato* DC3000 infection and are shown as log2 TPM (Transcripts per Million mapped reads).

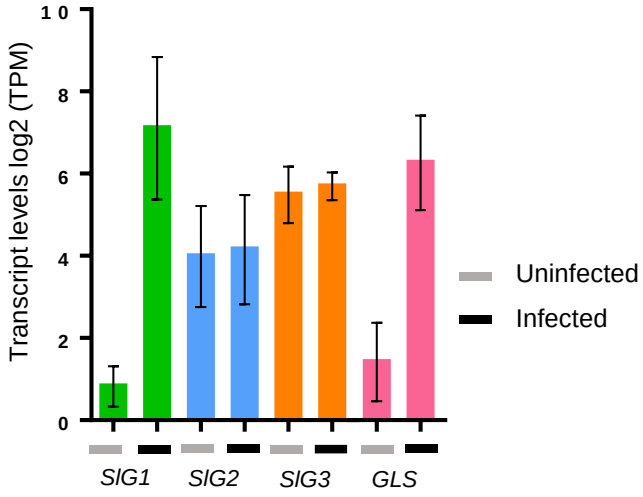


**Figure S5. SlG1-Myc is able to specifically bind to protein partners.** *N. benthamiana* leaves were co-agroinfiltrated with constructs encoding the indicated proteins tagged with C-terminal Myc or HA epitopes. Immunoblot analysis of crude extracts (INPUT) with anti-Myc (dark blue) and anti-HA (purple) antibodies was carried out to confirm successful protein production. The same samples were used for immunoprecipitation (IP) with anti-Myc followed by immunodetection with anti-Myc (to confirm successful IP) or anti-HA (to identify co-immunoprecipitated partners). Predicted protein molecular weights (KDa): PRK-Myc, 52.1; SlG1-Myc, 56.9; SlG1-HA 47.8.

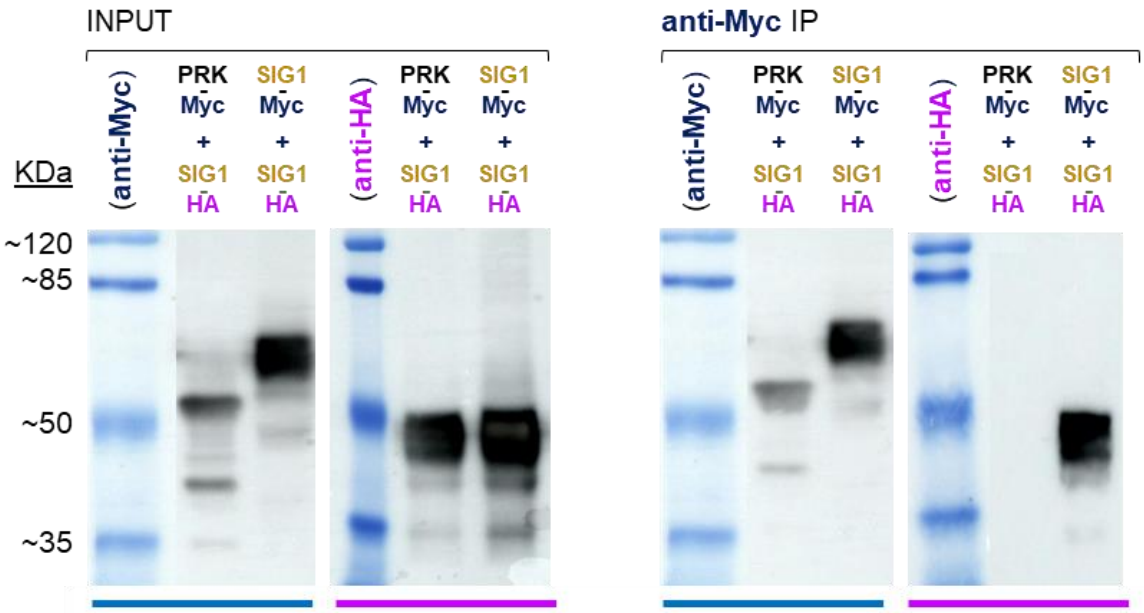
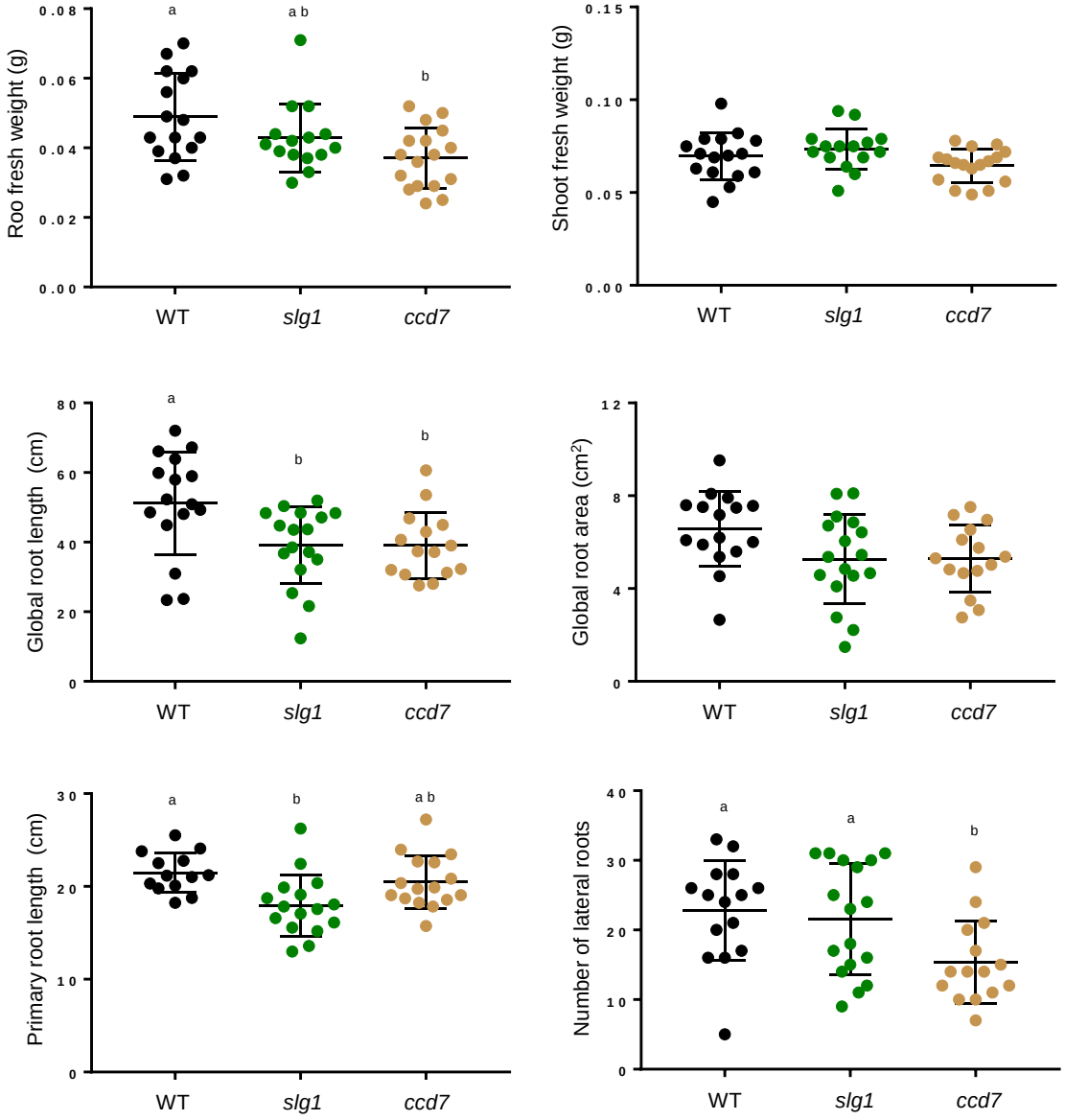


**Figure S6. Root parameters in SL-defective mutants.** WT, *slg1-1* and *ccd7* lines were germinated and grown for two weeks on vertical plates with solid medium lacking P. The lower section of the dishes was covered with aluminum foil so only the shoots were directly exposed to light. Individual measurements (colored dots) and well as mean and SD of the indicated parameters are shown. In all plots, letters represent statistically significant differences ($P < 0.05$) among means according to post hoc Tukey's tests run when one way ANOVA detected different means.



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## SUPPORTING TABLES

**Table S1.** List of primers used in this work.

| Use | Name | Sequence (5'-3')[1] |
|---|---|---|
| Cloning | SlG1-attB1-F | **GGGGACAAGTTTGTACAAAAAAGCAGGCTGG**ATGGCATTTTTAGCTACCATTTCTG |
| | SlG1-attB2-R | **GGGGACCACTTTGTACAAGAAAGCTGGGTG**ATTCTGTCGATTTGCAATATAACTAGC |
| | SlPSY3-attB1-F | **GGGGACAAGTTTGTACAAAAAAGCAGGCTGG**ATGTGTCCAGCAACACTTTCTTATT |
| | SlPSY3-attB2-R | **GGGGACCACTTTGTACAAGAAAGCTGGGTG**TTGAATGGCTAAACTAGGCAAAGATAAAG |
| | AtPRK-attB1-F | **GGGGACAAGTTTGTACAAAAAAGCAGGCT**ATGGCTGTCTCAACTATCTAC |
| | AtPRK-attB2-R | **GGGGACCACTTTGTACAAGAAAGCTGGGT**CGGCTTTAGCTTCTGCACGAGC |
| RT-qPCR | SlPSY1-qPCR-F | ACAGGCAGGTCTATCCGATG |
| | SlPSY1-qPCR-R | ACGCCTTTCTCTGCCTCATC |
| | SlPSY2-qPCR-F | CAGGGCTCTCCGATGAAGAC |
| | SlPSY2-qPCR-R | CACCGGCCATCTACTAGCAG |
| | SlPSY3-qPCR-F | TTGGATGCAATAGAGGAGAATG |
| | SlPSY3-qPCR-R | ATTGAATGGCTAAACTAGGCAAAG |
| | SlG1-qPCR-F | GGCCTTTGAACATGTGGCTACC |
| | SlG1-qPCR-R | ACTCGCCAAGTCCACAATTTGC |
| | SlG2-qPCR-F | AAAGTCATCGTCGGAGCTCG |
| | SlG2-qPCR-R | GTTTAGCTTCGCCGTTGAGC |
| | SlG3-qPCR-F | AGGAGGTGCACCAGATGAAG |
| | SlG3-qPCR-R | TCAGCAACCAAGTCCTTCCC |
| | SlGLS-qPCR F | TTGCTCATGACCACAACTCG |
| | SlGLS-qPCR R | GGAGCTTCATTGTTCTTGGCA |
| | SlACT4-qPCR-F | CCTTCCACATGCCATTCTCC |
| | SlACT4-qPCR-R | CCACGCTCGGTCAGGATCT |
| sgRNAs for CRISPR-Cas9 gene impairment | SlG1-sgRNA-1 F | ATTGGTTCAGCTGTTGGCTCAGAA |
| | SlG1-sgRNA-1 R | AAACTTCTGAGCCAACAGCTGAAC |
| | SlG1-sgRNA-2 F | ATTGGTACATTCACCACCATAAGA |
| | SlG1-sgRNA-2 R | AAACTCTTATGGTGGTGAATGTAC |
| CRISPR plants genotyping | SlG1 Geno F | GCTTGCGCAGTTGAGATGATCC |
| | SlG1 Geno R | GGTCCTTACCCGCTGTCTTTCC |
| | Cas9 F | TCCCTCATCAGATCCACCTC |
| | Cas9 R | CTGAAACGTGAGCCTTCTGG |
| | NTP II F | GAAGGGGATAGAAGGCGA |
| | NTP II R | AGATGGATTGCACGCAGG |

[1]Gateway recombination sites in bold

**Table S2.** Constructs and cloning details.

| Use | Construct | Template | Primers[1] | Sequence cloned[2] | Cloning method | Entry plasmid | Destiny plasmid |
|---|---|---|---|---|---|---|---|
| Co-immunoprecipitation assays | *SlG1-HA* | Tomato root cDNA | 1+2 | $SlG1_{1-1098}$ | Gateway | pDONR207 | pGWB414 |
| | *SlPSY1-HA* | Tomato fruit cDNA | | $SlPSY1_{1-1236}$ | Gateway | pDONR207 | pGWB414 |
| | *SlPSY2-HA* | Tomato leaf cDNA | | $SlPSY2_{1-1314}$ | Gateway | pDONR207 | pGWB414 |
| | *SlPSY3-HA* | Tomato root cDNA | 3+4 | $SlPSY3_{1-1186}$ | Gateway | pDONR207 | pGWB414 |
| | *SlG1-Myc* | Tomato root cDNA | 1+2 | $SlG1_{1-1098}$ | Gateway | pDONR207 | pGWB420 |
| | *SlG2-Myc* | Tomato flower cDNA | | $SlG2_{1-1089}$ | Gateway | pDONR207 | pGWB420 |
| | *SlG3-Myc* | Tomato flower cDNA | | $SlG3_{1-1080}$ | Gateway | pDONR207 | pGWB420 |
| | *AtPRK-Myc* | Arabidopsis seedling cDNA | 5+6 | $AtPRK_{1-1556}$ | Gateway | pDONR207 | pGWB417 |
| CRISPR-Cas9 gene impairment | *pEN-SlG1(sg1)* | - | 23+24 | $SlG1_{644-664}$ | *BbsI* / T4 ligase | pENC1.1 | - |
| | *pEN-SlG1(sg2)* | - | 25+26 | $SlG1_{732-752}$ | *BbsI* / T4 ligase | pENC1.1 | - |
| | *pDE-SlG1(1+2)* | *pEN-SlG1(sg1) + (sg2)* | - | $SlG2_{644-664}$ + $SlG2_{732-752}$ | (*sg1*)*MluI* + *Bsu36I* / T4 ligase (sg2)Gateway | *pEN-SlG1(sg1) + (sg2)* | pDE-Cas9 |

[1]Constructs without primers reported in Barja et al.(2021)

[2]Numbers indicate the first and last nucleotide positions cloned from the coding sequence of the indicated gene.

New Phytologist

**Table S3. Co-expression of tomato GGPPS paralogs (guide genes) with isoprenoid-related genes (query genes) in root tissue.** Significant pairwise Pearson correlations between guide and query genes (≥0.55) are highlighted in red (when positive) or green (when negative). Arabidopsis genes were used as queries in PLAZA 4 to search for tomato homologs (https://bioinformatics.psb.ugent.be/plaza/versions/plaza_v4_dicots/). Genes are organized by pathways.

| | | | SlG1 | SlG2 | SlG3 |
|---|---|---|---|---|---|
| Pathway/Family | Name | SOL Tomato gene | Solyc11g011240 | Solyc04g079960 | Solyc02g085700 |
| MEP pathway | DXS1 | Solyc01g067890 | 0.227817285 | -0.432217062 | 0.28528147 |
| MEP pathway | DXS2 | Solyc11g010850 | 0.997036917 | -0.103686573 | 0.326655343 |
| MEP pathway | DXS3a | Solyc01g028900 | 0.055742093 | -0.087928801 | 0.718940454 |
| MEP pathway | DXS3b | Solyc08g066950 | 0.639972045 | -0.070017463 | 0.741305712 |
| MEP pathway | DXR1 | Solyc03g114340 | 0.983938259 | -0.082546381 | 0.410076944 |
| MEP pathway | DXR2 | Solyc06g060860 | 0.199524053 | 0.166352456 | -0.292225453 |
| MEP pathway | CMK | Solyc01g009010 | 0.884968181 | 0.014512289 | 0.480860925 |
| MEP pathway | MCT | Solyc01g102820 | 0.488415714 | 0.40006911 | 0.364206591 |
| MEP pathway | MDS | Solyc08g081570 | 0.213003447 | 0.122519655 | 0.623933883 |
| MEP pathway | HDS | Solyc11g069380 | 0.882686457 | 0.057137735 | 0.423279789 |
| MEP pathway | HDR | Solyc01g109300 | -0.092325695 | -0.444207896 | -0.15767962 |
| IPP isomerases | IDI1 | Solyc08g075390 | -0.053766114 | -0.27002078 | 0.408431113 |
| IPP isomerases | IDI2 | Solyc05g055760 | -0.01368272 | 0.152778807 | 0.657783139 |
| IPP isomerases | IDI3 | Solyc04g056390 | 0.29426506 | -0.292380737 | 0.371964203 |
| GGDR | GGDR1 | Solyc01g088310 | -0.130952114 | 0.708765564 | -0.384847304 |
| GGDR | GGDR2 | Solyc03g115980 | -0.396270784 | 0.152964101 | -0.09490842 |
| Tocopherol biosynthesis | HPPD1/PDS1a | Solyc05g041200 | -0.003258982 | -0.363823003 | 0.48259298 |
| Tocopherol biosynthesis | HPPD2/PDS1b | Solyc07g045050 | 0.002860197 | -0.071459139 | -0.200460026 |
| Tocopherol biosynthesis | VTE2 | Solyc07g017770 | 0.553561893 | 0.064150277 | 0.381503736 |
| Tocopherol biosynthesis | VTE3a | Solyc03g005230 | 0.424721351 | 0.110779221 | 0.105863188 |
| Tocopherol biosynthesis | VTE3b | Solyc09g065730 | 0.228218686 | 0.081748204 | 0.610840864 |
| Tocopherol biosynthesis | VTE1 | Solyc08g068570 | 0.616813434 | 0.325744429 | 0.431115249 |
| Tocopherol biosynthesis | VTE4a | Solyc08g076360 | -0.151515162 | 0.236492581 | 0.506975932 |
| Tocopherol biosynthesis | VTE4b | Solyc04g063230 | -0.110780823 | 0.36361524 | -0.302450315 |
| Tocopherol biosynthesis | VTE4c | Solyc08g077240 | -0.303071631 | -0.145364926 | -0.583830612 |
| Tocopherol biosynthesis | VTE4d | Solyc03g116150 | -0.290047454 | -0.003146301 | 0.334972422 |
| Chlorophyll biosynthesis | HEMA1 | Solyc04g076870 | -0.105259917 | -0.274261136 | 0.419202338 |
| Chlorophyll biosynthesis | HEMA2 | Solyc01g106390 | 0.040718913 | -0.159382416 | 0.72009636 |
| Chlorophyll biosynthesis | HEMA3 | Solyc01g089840 | #N/A | #N/A | #N/A |
| Chlorophyll biosynthesis | GSA | Solyc04g009200 | -0.082894254 | -0.089319358 | 0.612747431 |
| Chlorophyll biosynthesis | HEMB | Solyc08g069030 | -0.151430238 | -0.405537832 | 0.478103613 |
| Chlorophyll biosynthesis | HEMC | Solyc07g066470 | -0.071151521 | 0.459018759 | 0.129818671 |
| Chlorophyll biosynthesis | HEMD | Solyc04g079320 | 0.469479524 | -0.246514255 | 0.214036299 |
| Chlorophyll biosynthesis | HEME1 | Solyc10g007320 | 0.465700714 | 0.057792204 | 0.15566927 |
| Chlorophyll biosynthesis | HEME2 | Solyc06g048730 | 0.211799103 | -0.094178477 | 0.065673668 |
| Chlorophyll biosynthesis | HEMF | Solyc10g005110 | 0.665308945 | 0.044622375 | 0.339341703 |
| Chlorophyll biosynthesis | HEMG1 | Solyc01g079090 | 0.117133036 | -0.407554853 | 0.350194089 |
| Chlorophyll biosynthesis | HEMG2 | Solyc03g005080 | 0.467537798 | -0.369333515 | 0.659054874 |
| Chlorophyll biosynthesis | CHLH | Solyc04g015750 | -0.26701238 | -0.110482093 | -0.566896786 |
| Chlorophyll biosynthesis | CHLI | Solyc10g008740 | 0.594459595 | -0.038296053 | -0.114544313 |
| Chlorophyll biosynthesis | CHLD | Solyc04g015490 | 0.556081009 | -0.167039536 | 0.183230703 |
| Chlorophyll biosynthesis | CHLM | Solyc03g118240 | 0.458485616 | 0.400565799 | 0.182033019 |
| Chlorophyll biosynthesis | CHL27-CRD | Solyc10g077040 | -0.223630138 | -0.00816874 | -0.307798293 |
| Chlorophyll biosynthesis | DVR | Solyc01g067290 | -0.010768598 | 0.348905198 | 0.097673629 |
| Chlorophyll biosynthesis | PORA | Solyc12g013710 | -0.134290208 | -0.112528933 | 0.241062199 |
| Chlorophyll biosynthesis | PORB | Solyc07g054210 | -0.196642498 | -0.364421753 | -0.136536604 |
| Chlorophyll biosynthesis | PORC | Solyc10g006900 | 0.099037913 | 0.045790641 | -0.121562843 |
| Chlorophyll biosynthesis | CHLG1 | Solyc05g024190 | -0.162371852 | 0.001311095 | 0.31995561 |
| Chlorophyll biosynthesis | CHLG2 | Solyc09g014760 | 0.467429605 | 0.065746944 | -0.1716427 |
| Chlorophyll biosynthesis | CAOa | Solyc06g060310 | -0.140415216 | -0.307867459 | -0.346880611 |
| Chlorophyll biosynthesis | CAOb | Solyc11g012850 | -0.134284865 | -0.135540982 | 0.160700206 |
| Chlorophyll degradation | CHL1 | Solyc09g065620 | #N/A | #N/A | #N/A |
| Chlorophyll degradation | CHL2a | Solyc06g053980 | 0.135263552 | 0.414254359 | -0.090432445 |
| Chlorophyll degradation | CHL2b | Solyc09g082600 | -0.189527461 | -0.431145721 | -0.485581871 |
| Chlorophyll degradation | CHL2c | Solyc12g005300 | 0.063207593 | 0.494543447 | -0.189462652 |

| | | | SlG1 | SlG2 | SlG3 |
|---|---|---|---|---|---|
| Pathway/Family | Name | SOL Tomato gene | Solyc11g011240 | Solyc04g079960 | Solyc02g085700 |
| Chlorophyll degradation | CLD1 | Solyc02g070490 | 0.097418732 | -0.019030447 | -0.121496138 |
| Chlorophyll degradation | SGR1 | Solyc08g080090 | 0.334525535 | 0.351924964 | 0.239984752 |
| Chlorophyll degradation | SGR2 | Solyc12g056480 | #N/A | #N/A | #N/A |
| Chlorophyll degradation | SGR3 | Solyc04g063240 | #N/A | #N/A | #N/A |
| Chlorophyll degradation | PPH | Solyc01g088090 | -0.02570926 | 0.102250436 | 0.624178482 |
| Chlorophyll degradation | PAO1 | Solyc11g066440 | 0.075470096 | -0.407248086 | 0.574465029 |
| Chlorophyll degradation | PAO2 | Solyc04g040160 | #N/A | #N/A | #N/A |
| Chlorophyll degradation | PAO3 | Solyc12g096550 | -0.441818414 | -0.426715473 | -0.264975363 |
| Chlorophyll degradation | RCCR | Solyc03g044470 | 0.252496332 | -0.050336257 | 0.221137805 |
| Chlorophyll degradation | PK1 | Solyc03g071720 | 0.306310405 | -0.274536284 | 0.638200534 |
| Chlorophyll degradation | PK2 | Solyc09g018510 | -0.002769879 | -0.124326081 | -0.192384004 |
| Chlorophyll degradation | NYC1 | Solyc07g024000 | 0.079814353 | -0.037916608 | 0.65448831 |
| Chlorophyll degradation | CBR/NOL | Solyc05g032660 | 0.747124715 | 0.111886245 | 0.146036329 |
| Chlorophyll degradation | HCAR | Solyc09g091100 | -0.0128925 | -0.289975445 | -0.294073066 |
| Phylloquinone biosynthesis | ICS1/MENF | Solyc06g071030 | #N/A | #N/A | #N/A |
| Phylloquinone biosynthesis | PHYLLO/MEND1 | Solyc04g005190 | 0.610474528 | -0.184506979 | 0.118924512 |
| Phylloquinone biosynthesis | PHYLLO/MEND2 | Solyc04g005200 | 0.622287417 | 0.021210242 | -0.02088809 |
| Phylloquinone biosynthesis | PHYLLO/MEND3 | Solyc04g005180 | 0.475484562 | -0.108459214 | 0.163378551 |
| Phylloquinone biosynthesis | AAE14 | Solyc02g069920 | 0.06366328 | 0.073537116 | -0.109614114 |
| Phylloquinone biosynthesis | DHNS/MENB | Solyc05g005180 | 0.811508543 | -0.001651354 | 0.216802597 |
| Phylloquinone biosynthesis | DHNAT1 | Solyc02g078410 | -0.143053242 | -0.125034472 | 0.501479632 |
| Phylloquinone biosynthesis | DHNAT2 | Solyc03g006440 | #N/A | #N/A | #N/A |
| Phylloquinone biosynthesis | DHNAT3 | Solyc03g006450 | #N/A | #N/A | #N/A |
| Phylloquinone biosynthesis | ABC4 | Solyc01g105460 | 0.45668733 | 0.076177322 | 0.606850632 |
| Phylloquinone biosynthesis | MENG | Solyc12g019010 | 0.355667655 | -0.429933867 | -0.182348 |
| Plastoquinone biosynthesis | TAT7/HPPS1 | Solyc10g007110 | -0.211383766 | 0.21345445 | -0.302773187 |
| Plastoquinone biosynthesis | TAT7/HPPS2 | Solyc12g088000 | -0.23856167 | 0.12907316 | -0.477127228 |
| Plastoquinone biosynthesis | TAT7/HPPS3 | Solyc12g096240 | -0.183757802 | 0.101931181 | 0.050024062 |
| Plastoquinone biosynthesis | PDS2/HST | Solyc03g051810 | 0.449387501 | -0.187413559 | 0.21955408 |
| Plastoquinone biosynthesis | AAAT1 | Solyc07g053720 | -0.015951791 | -0.366235433 | 0.43220791 |
| Plastoquinone biosynthesis | AAAT2 | Solyc10g008200 | 0.217492085 | 0.566893925 | 0.166994149 |
| Plastoquinone biosynthesis | AAAT3 | Solyc07g053710 | 0.17507915 | 0.196294288 | 0.588052247 |
| Plastoquinone biosynthesis | ACS12 | Solyc03g007070 | -0.050853036 | -0.291718623 | -0.376091867 |
| Plastoquinone biosynthesis | TAA1 | Solyc05g031600 | -0.259243414 | -0.139275642 | -0.375694205 |
| Carotenoid biosynthesis | PSY1 | Solyc03g031860 | 0.48436295 | -0.068458482 | 0.183689089 |
| Carotenoid biosynthesis | PSY2 | Solyc02g081330 | -0.372992877 | 0.255376259 | -0.563151392 |
| Carotenoid biosynthesis | PSY3 | Solyc01g005940 | 0.9887403 | -0.031173898 | 0.291125507 |
| Carotenoid biosynthesis | PDS | Solyc03g123760 | 0.993379539 | -0.045712605 | 0.322656275 |
| Carotenoid biosynthesis | ZDS | Solyc01g097810 | 0.960459119 | -0.021713467 | 0.302818591 |
| Carotenoid biosynthesis | Z-ISO | Solyc12g098710 | 0.738619978 | -0.091519099 | 0.551931703 |
| Carotenoid biosynthesis | CRTISO1 | Solyc10g081650 | 0.943765101 | -0.100731764 | 0.464601885 |
| Carotenoid biosynthesis | CRTISO2 | Solyc05g010180 | #N/A | #N/A | #N/A |
| Carotenoid biosynthesis | LCY-B1 | Solyc04g040190 | -0.060826955 | 0.034921071 | 0.126715816 |
| Carotenoid biosynthesis | LCY-B2/CYC-B | Solyc10g079480 | 0.47083548 | 0.004718384 | 0.258287127 |
| Carotenoid biosynthesis | LCY-E | Solyc12g008980 | #N/A | #N/A | #N/A |
| Carotenoid biosynthesis | BCH1 | Solyc06g036260 | -0.494401783 | -0.110140751 | -0.278124838 |
| Carotenoid biosynthesis | BCH2 | Solyc03g007960 | 0.022206108 | 0.123623457 | -0.182607406 |
| Carotenoid biosynthesis | CYP97B3 | Solyc05g016330 | 0.247342197 | -0.15114203 | -0.143317243 |
| Carotenoid biosynthesis | CYP97A3 | Solyc04g051190 | 0.934087572 | 0.079186798 | 0.433488572 |
| Carotenoid biosynthesis | CYP97C1 | Solyc10g083790 | 0.656435414 | 0.092000116 | 0.720760803 |
| Carotenoid biosynthesis | ZEP1 | Solyc06g060880 | 0.092497037 | 0.119284103 | -0.356821625 |
| Carotenoid biosynthesis | NSY1 | Solyc02g089050 | -0.141068334 | 0.150647962 | -0.429764058 |
| Carotenoid biosynthesis | VDE | Solyc04g050930 | 0.710345593 | 0.09745212 | 0.163692149 |
| Carotenoid degradation | CCD1A | Solyc01g087250 | 0.897385096 | -0.097410517 | 0.413828304 |
| Carotenoid degradation | CCD1B | Solyc01g087260 | -0.486507306 | -0.319343808 | 0.12600825 |
| Carotenoid degradation | CCDX | Solyc08g066720 | 0.962831828 | 0.005214157 | 0.244918912 |
| Carotenoid degradation | CCD4A | Solyc08g075480 | #N/A | #N/A | #N/A |
| Carotenoid degradation | CCD4B | Solyc08g075490 | #N/A | #N/A | #N/A |
| Orange proteins | Or1 | Solyc03g093830 | 0.956695311 | -0.047672533 | 0.407062323 |
| Orange proteins | Or2 | Solyc09g010110 | 0.429020461 | -0.375775452 | 0.375550783 |
| ABA metabolism | NCED2 | Solyc08g016720 | 0.877409595 | 0.007780788 | 0.427354139 |
| ABA metabolism | NCED3 | Solyc07g056570 | 0.471895819 | 0.112222671 | 0.570947911 |
| ABA metabolism | NCED6 | Solyc05g053530 | #N/A | #N/A | #N/A |

| | | | SlG1 | SlG2 | SlG3 |
|---|---|---|---|---|---|
| Pathway/Family | Name | SOL Tomato gene | Solyc11g011240 | Solyc04g079960 | Solyc02g085700 |
| ABA metabolism | ABA2a | Solyc04g071940 | 0.028984238 | 0.338164225 | -0.549218342 |
| ABA metabolism | ABA2b | Solyc04g071960 | #N/A | #N/A | #N/A |
| ABA metabolism | ABA2c | Solyc10g085380 | -0.288588412 | 0.346337388 | -0.511417212 |
| ABA metabolism | ABA2d | Solyc11g018600 | #N/A | #N/A | #N/A |
| ABA metabolism | AAO3a | Solyc11g065920 | 0.053296522 | -0.464463544 | 0.571416643 |
| ABA metabolism | AAO3b | Solyc11g065930 | -0.22308611 | 0.03808593 | 0.499516268 |
| ABA metabolism | ABA3 | Solyc07g066480 | 0.498915173 | 0.063687929 | 0.200693733 |
| ABA metabolism | ABA4 | Solyc02g063170 | -0.388641886 | -0.152190581 | -0.427829713 |
| ABA metabolism | CYP707A1 | Solyc04g078900 | #N/A | #N/A | #N/A |
| ABA metabolism | CYP707A2 | Solyc08g075320 | 0.121000641 | -0.263589633 | -0.418754624 |
| ABA metabolism | CYP707A3a | Solyc01g108210 | 0.191959425 | -0.166036381 | 0.502077133 |
| ABA metabolism | CYP707A3b | Solyc08g005610 | 0.005129081 | -0.321170606 | -0.244657287 |
| ABA metabolism | CYP707A3c | Solyc04g071150 | 0.911640177 | -0.093816362 | 0.087467239 |
| ABA metabolism | CYP707A3d | Solyc04g080650 | -0.279642404 | 0.32164075 | 0.116087837 |
| ABA metabolism | ABA1/ZEP | Solyc02g090890 | -0.51934943 | -0.030013217 | -0.538058819 |
| ABA metabolism | NSY3 | Solyc02g086050 | 0.185788857 | 0.303292174 | 0.269656709 |
| ABA metabolism | NSY5 | Solyc06g074240 | 0.992272356 | -0.075441014 | 0.340861095 |
| SL biosynthesis | MAX3 (CCD7) | Solyc01g090660 | 0.992904154 | -0.106902828 | 0.300371981 |
| SL biosynthesis | MAX1 | Solyc08g062950 | 0.986086882 | -0.065425469 | 0.276445814 |
| SL biosynthesis | MAX4 (CCD8) | Solyc08g066650 | 0.996596827 | -0.059714661 | 0.297058985 |
| Gibberellin metabolism | CPS1 | Solyc06g084240 | 0.997400089 | -0.102023381 | 0.306665528 |
| Gibberellin metabolism | CPS2 | Solyc08g005710 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | CPS3 | Solyc09g065230 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | KS1a | Solyc07g066670 | 0.797763542 | 0.116676707 | 0.341005665 |
| Gibberellin metabolism | KS1b | Solyc08g005720 | 0.45802595 | 0.427222273 | -0.164064737 |
| Gibberellin metabolism | KO | Solyc04g083160 | 0.99177426 | -0.02644603 | 0.273361971 |
| Gibberellin metabolism | KAO1 | Solyc01g080900 | 0.925218611 | 0.063463248 | 0.195364444 |
| Gibberellin metabolism | KAO2 | Solyc08g007050 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | KAO3 | Solyc12g006460 | -0.043884958 | 0.538148128 | 0.135522157 |
| Gibberellin metabolism | KAO4 | Solyc10g007860 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA20ox1 | Solyc03g006880 | 0.990700671 | -0.061266037 | 0.279604246 |
| Gibberellin metabolism | GA20ox2 | Solyc09g009110 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA20ox3 | Solyc11g072310 | 0.764067607 | 0.079907645 | 0.030099693 |
| Gibberellin metabolism | GA20ox4 | Solyc06g035530 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA20ox5 | Solyc01g093980 | 0.979136723 | -0.070374827 | 0.274557014 |
| Gibberellin metabolism | GA20ox6 | Solyc06g050110 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA20ox7 | Solyc11g013360 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA3ox1 | Solyc06g066820 | 0.97438317 | -0.042467304 | 0.262767095 |
| Gibberellin metabolism | GA3ox2 | Solyc03g119910 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA3ox3 | Solyc00g007180 | #N/A | #N/A | #N/A |
| Gibberellin metabolism | GA3ox4 | Solyc01g058250 | -0.158328167 | -0.133515069 | 0.596201491 |
| Gibberellin metabolism | GA3ox5 | Solyc05g052740 | #N/A | #N/A | #N/A |
| MVA pathway | HMGS1 | Solyc08g080160 | #N/A | #N/A | #N/A |
| MVA pathway | HMGS2 | Solyc08g007790 | -0.082203011 | -0.171648603 | 0.636394447 |
| MVA pathway | HMGS3 | Solyc12g056450 | 0.108375307 | -0.083799696 | -0.282527204 |
| MVA pathway | HMGS4 | Solyc08g080170 | -0.119184485 | 0.064018582 | 0.67219755 |
| MVA pathway | HMGR1 | Solyc03g032020 | 0.233838251 | -0.269895899 | 0.493862077 |
| MVA pathway | HMGR2 | Solyc02g082260 | -0.243850449 | -0.482597207 | -0.321043725 |
| MVA pathway | HMGR3 | Solyc02g038740 | -0.08065974 | -0.159039759 | 0.64130647 |
| MVA pathway | HMGR4 | Solyc03g032010 | 0.448026273 | 0.140362687 | 0.252487654 |
| MVA pathway | MVK | Solyc01g098840 | -0.101188848 | -0.192849616 | 0.63006538 |
| MVA pathway | PMK1 | Solyc08g076140 | 0.118637298 | -0.392787149 | 0.587969204 |
| MVA pathway | PMK2 | Solyc06g066310 | 0.063436412 | -0.060619985 | 0.729922806 |
| MVA pathway | MVD1 | Solyc04g009650 | 0.028841528 | 0.197760815 | 0.612150651 |
| MVA pathway | MVD2 | Solyc11g007020 | -0.120558081 | -0.097527905 | 0.629381981 |
| MVA pathway | AACT1 | Solyc05g017760 | 0.185899173 | 0.615360485 | 0.347271304 |
| MVA pathway | AACT2 | Solyc07g045350 | -0.108831687 | -0.122710038 | 0.650776949 |
| MVA pathway | AACT3 | Solyc04g015100 | 0.088470241 | 0.04828122 | 0.728496447 |
| FDS | FDS1 | Solyc10g005840 | 0.523849783 | -0.102281461 | 0.102421253 |
| FDS | FDS2 | Solyc12g015860 | -0.079504135 | -0.031898035 | 0.637541783 |
| FDS | FDS3 | Solyc10g005810 | 0.4018755 | 0.248462877 | 0.32880738 |
| FDS | FDS4 | Solyc10g005820 | 0.375810018 | 0.419812374 | 0.253962811 |
| Ubiquinone biosynthesis | PPT1 | Solyc03g114300 | 0.388805365 | -0.095730347 | 0.673083897 |
| Ubiquinone biosynthesis | CoQ3 | Solyc07g055850 | 0.43200067 | 0.35963032 | 0.07331323 |
| Ubiquinone biosynthesis | CoQ5a | Solyc01g081470 | 0.074871819 | 0.06013107 | 0.559041736 |
| Ubiquinone biosynthesis | CoQ6 | Solyc09g091570 | 0.68029036 | -0.227989585 | 0.196851133 |

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