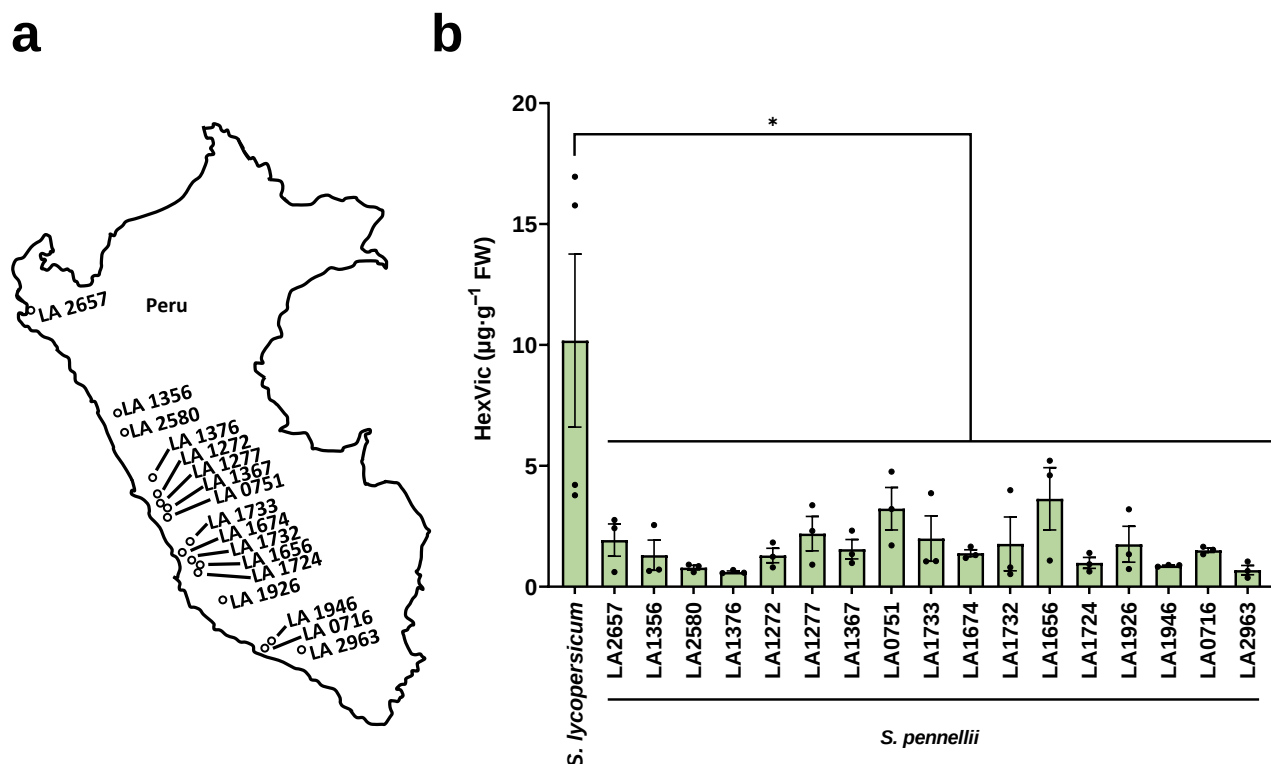
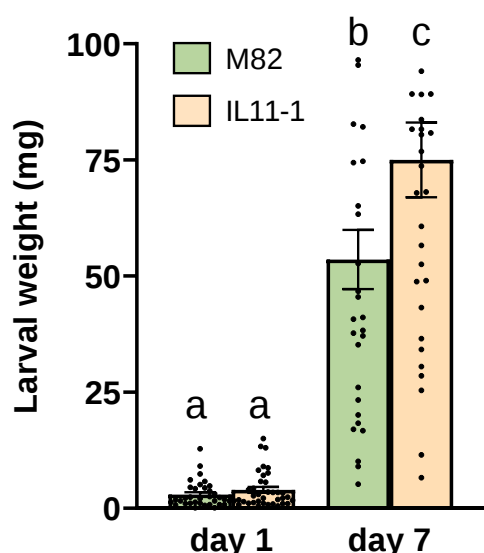
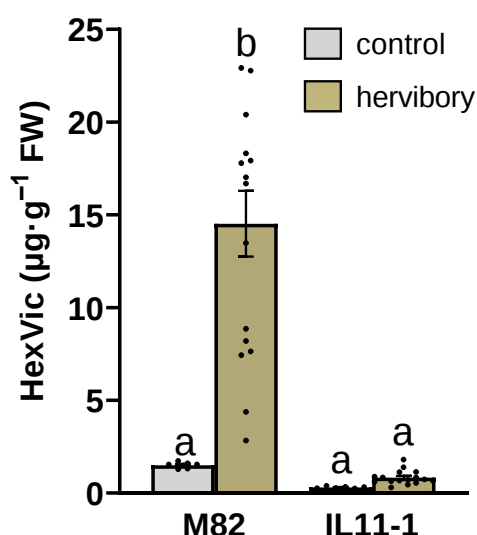




**Supplementary Figure 1: HexVic accumulation in various *S. pennellii* accessions.**

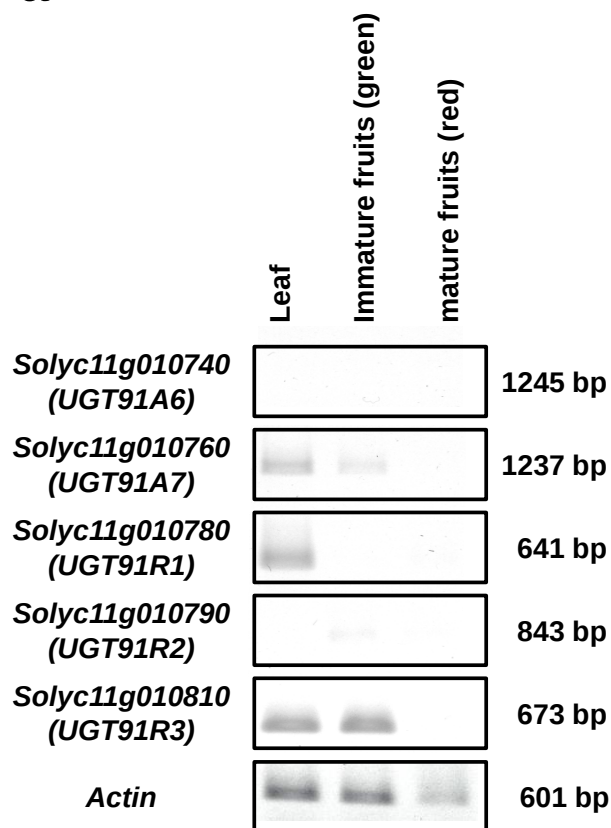
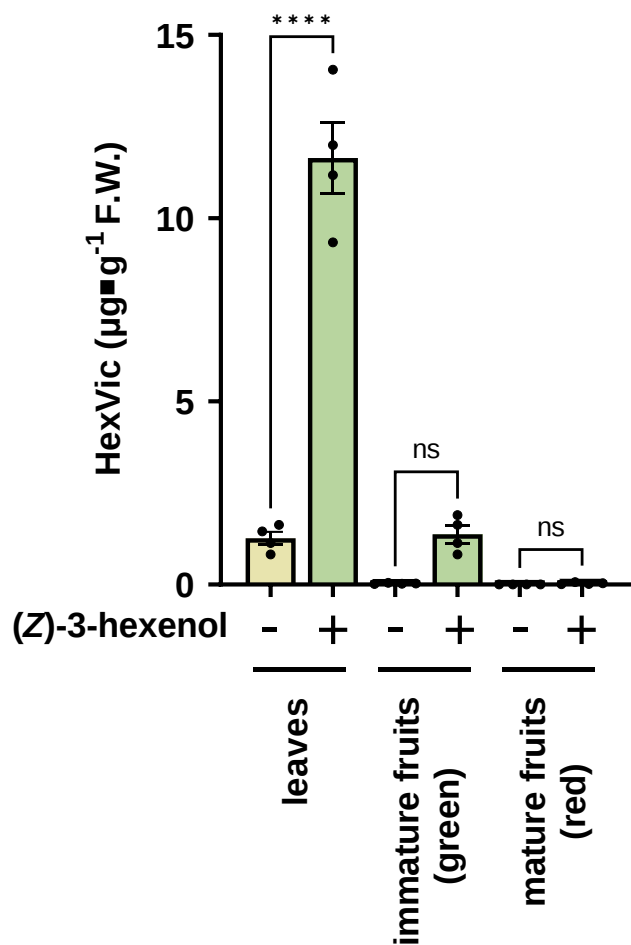
**a** Map showing geographical distribution of *S. pennellii* accession collection sites in Peru.

**b** HexVic contents in leaves of (Z)-3-hexenol-exposed plants of different *S. pennellii* accessions. Error bars indicate standard error of the mean from independent experiments (four plants for *S. lycopersicum* cv. M82 and three plants for each *S. pennellii* genotypes). Statistical significances were determined by Dunnett's multiple comparisons test. Statistically significant differences are indicated as  $*p < 0.05$

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

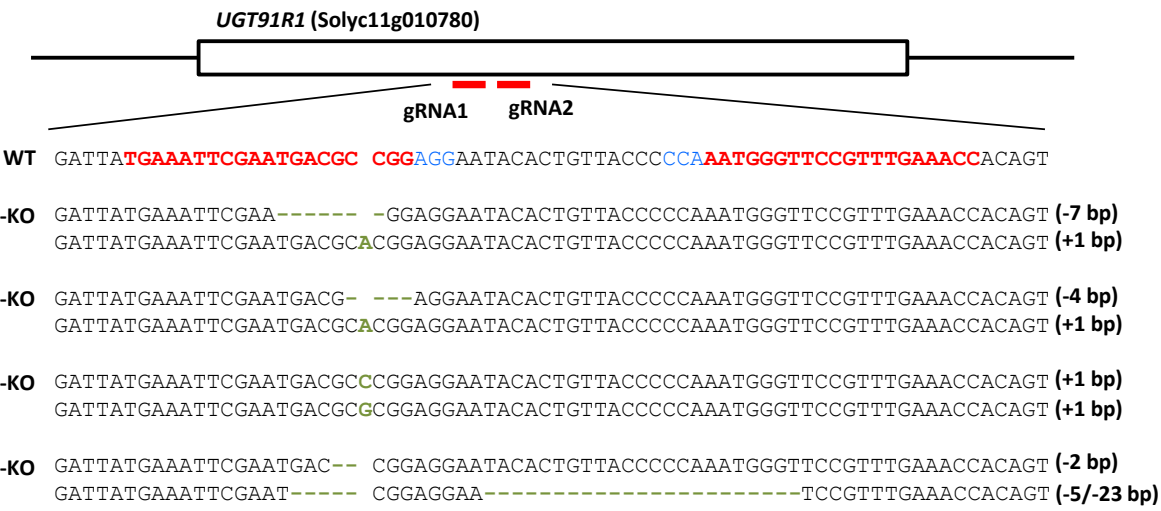
**Supplementary Figure 2: Plant and insect phenotypes of HexVic-deficient tomato.**

**a** Appearance of introgression lines (ILs). Five-week-old IL11-2 had a different shape and soft, light greenish leaves compared to wild-type M82 and IL11-1. **b** Weights of common cutworms before and after growth for seven days on M82 (green box) or IL11-1 (orange box). Each plant was challenged with a single third instar, and insects were weighed on days 1 and 7 after infestation. Data are means  $\pm$  SE from 8 independent experiments (thirty-four plants for M82 and thirty-seven plants for IL11-1 on day 1, and thirty plants for M82 and thirty-two plants for IL11-1 on day 7). Differences among lines and time points were analyzed using the Tukey's multiple comparison test, and significant differences are indicated with different characters ( $p < 0.05$ ). **c** HexVic content in leaves of M82 and IL11-1 plants challenged or not with common cutworms for two days. Data are means  $\pm$  SE from 3 independent experiments (six plants for M82 and IL11-1 as control, and sixteen plants for M82 and IL11-1 for herbivory treatment). Differences among species and treatments were analyzed using the Tukey's multiple comparison test, and statistical differences are indicated with different characters ( $p < 0.05$ ).

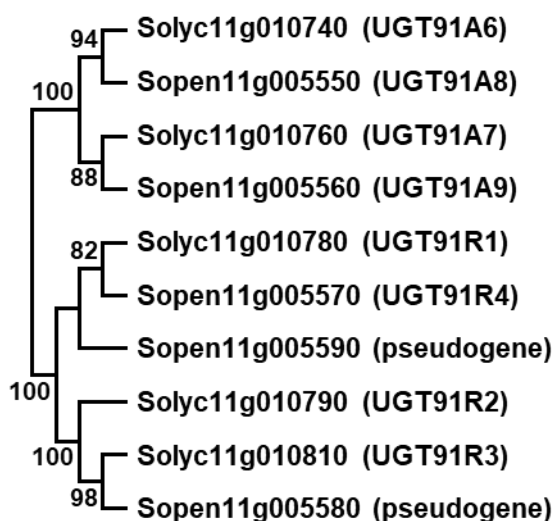
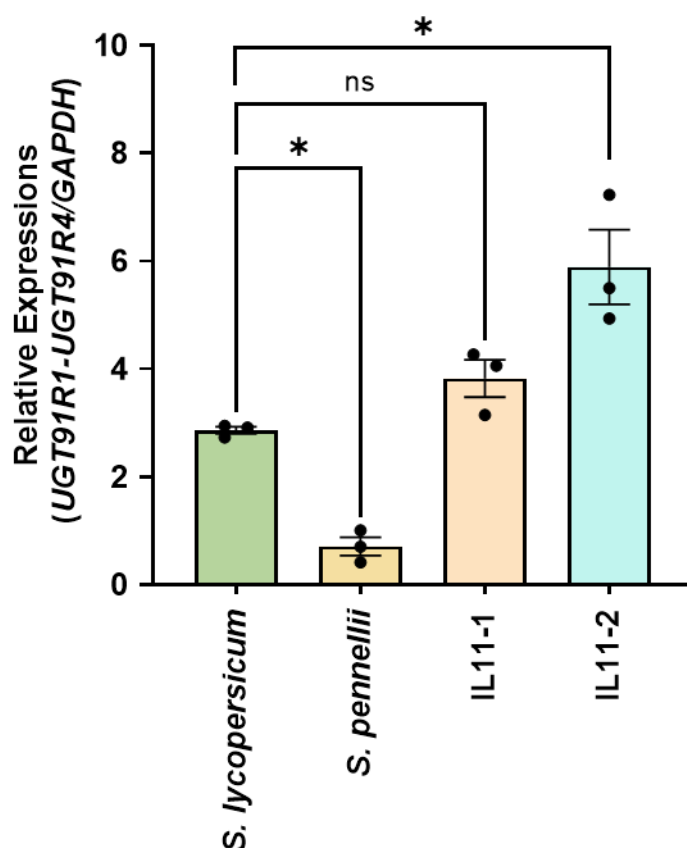
**a****b**

**Supplementary Figure 3: Tissue-specific biosynthesis of HexVic in *S. lycopersicum* cv. M82.**

**a** Gene expression of *UGT91* in different tissues of *S. lycopersicum* as analyzed using semiquantitative RT-PCR. **b** HexVic contents in leaves of *S. lycopersicum* exposed (+) or not (-) to (Z)-3-hexenol. Data are means  $\pm$  SE from 4 independent experiments. *P* values were analyzed using One-way ANOVA test with the Tukey's multiple comparison. Statistical significant differences are indicated as \*\*\*\**p* < 0.0001. ns indicates no statistical difference.



**Supplementary Figure 4: Mutation alleles of tomato UGT91R1.** Gene model of *UGT91R1* (*Solyc11g010780*) was depicted with a solid line (intergenic region) and open box (exon). Two gRNA regions for CRISPR-Cas9-based genome editing are indicated by red lines. Nucleotide sequence of target region contained gRNA and PAM sequences as red and blue characters, respectively. Nucleotide sequences of four knockout mutants harboring biallelic mutation are shown below sequence of WT. Insertion and deletion by genome editing are indicated as green characters.

**a****b**

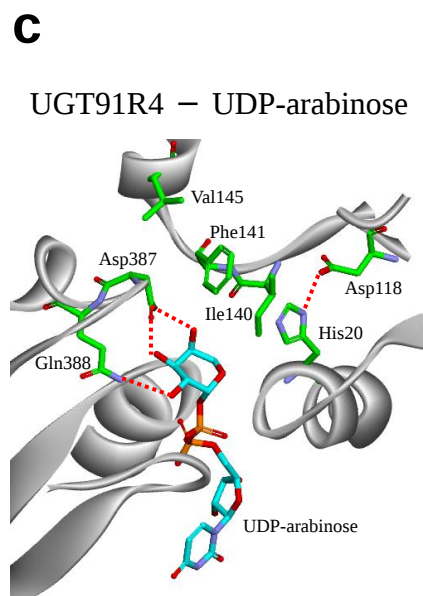
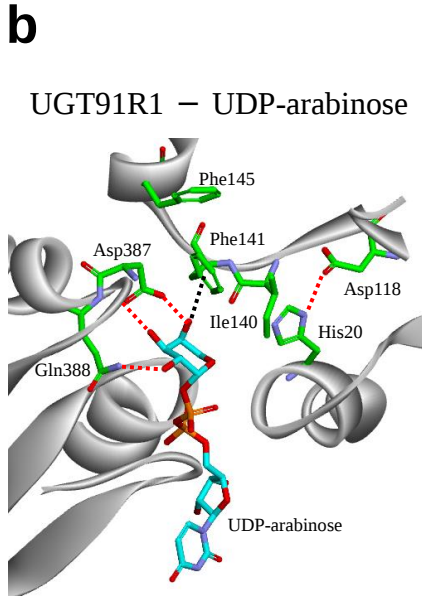
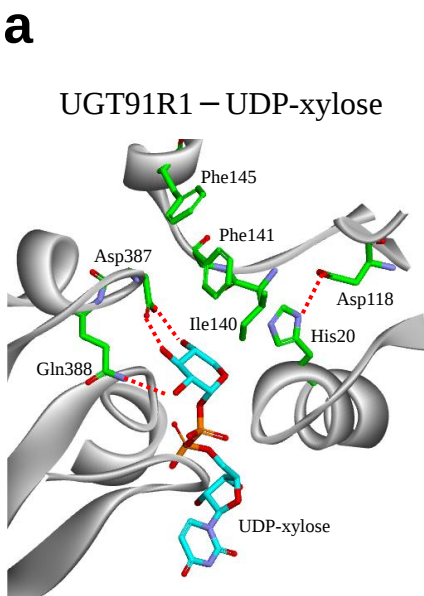
**Supplementary Figure 5: Phylogenetic relationships of tomato *UGT91*s in tomato and *UGT91T1/UGT91R4* expression.** **a** Nucleotide sequences of *UGT91* coding region were extracted from genome sequences of *S. lycopersicum* and *S. pennellii*. Phylogenetic tree was constructed using the maximum-likelihood method with 1000 bootstrap replications. **b** qRT-PCR analysis of *UGT91R1* and *UGT91R4* of leaves in *S. lycopersicum*, *S. pennellii* and two introgression lines (IL11-1 and IL11-2). Data are means  $\pm$  SE from 3 independent experiments. *p* values were analyzed using One-way ANOVA test followed by the Tukey's multiple comparison. Statistical significant differences are indicated as \**p* < 0.05. ns indicates no statistical difference.

|         |                                                              |     |
|---------|--------------------------------------------------------------|-----|
| UGT91R1 | ATGGCGGAAAACGGAAAAAATTGCATATTGCAGTATTTCCATGGCTAGCTTTTGGTCAT  | 60  |
| UGT91R1 | M A E N G K K L H I A V F P W L A F G H                      |     |
| UGT91R4 | M A E N G K K L H I A V F P W L A F G H                      |     |
| UGT91R4 | ATGGCGGAAAACGGCAAAAAATTGCATATTGCAGTATTTCCATGGCTAGCTTTTGGTCAT | 60  |
|         | *****                                                        |     |
| UGT91R1 | ATGATTCCGTATTTAGAGCTATCAAAGCTTATAGCTCAAAGGGTCATAAATTTCATTC   | 120 |
| UGT91R1 | M I P Y L E L S K L I A Q K G H K I S F                      |     |
| UGT91R4 | M I P Y L E L S K L I A Q K G H I I S F                      |     |
| UGT91R4 | ATGATTCCGTATTTAGAGCTATCAAAGCTCATAGCTCAAAGGGTCATATAATTTCATTC  | 120 |
|         | *****                                                        |     |
| UGT91R1 | ATTTGCACTCCTAGAAAATTGATCGTCTCCAAAACCTCCACCAAATCTCACCCCTTTT   | 180 |
| UGT91R1 | I S T P R N I D R L P K L P P N L T P F                      |     |
| UGT91R4 | I S T P R N I D R L P K L P P N L T P F                      |     |
| UGT91R4 | ATTTGCACTCCTAGAAATATTGATCGTCTCCAAAACCTCCACCAAATCTTACTCCCTTT  | 180 |
|         | ***** ** **                                                  |     |
| UGT91R1 | TTAATTTTGTCAAACTTCCGATGCCCCACGTGAAAAGTTGCCGAAAATGCTGAAGCC    | 240 |
| UGT91R1 | L N F V K L P M P H V E K L P E N A E A                      |     |
| UGT91R4 | F N F V K L P M P H V E K L P E N A E A                      |     |
| UGT91R4 | TTCAATTTCGTCAAACTTCCGATGCCCCACGTGAAAAGTTGCCGAAAATGCAAGAAGCC  | 240 |
|         | ** *****                                                     |     |
| UGT91R1 | ACCATTGATTTACCTTACGAGCAAGTCAAGTACCTCAAACCTGCTCAAGATGCACTACAA | 300 |
| UGT91R1 | T I D L P Y E Q V K Y L K L A Q D A L Q                      |     |
| UGT91R4 | T I D L P Y E Q V K Y L K L A H D A L Q                      |     |
| UGT91R4 | ACCATTGATTTACCTTATGAGCAAGTCAAGTATCTCAAACCTGCTCATGATGCACTACAA | 300 |
|         | *****                                                        |     |
| UGT91R1 | GAATCGATGTCTAAGTTTATCGAAGATTGAGATATTGATTTTATACTATTGATTTTACT  | 360 |
| UGT91R1 | E S M S K F I E D S D I D F I L F D F T                      |     |
| UGT91R4 | E S M A K F L E D S D I D F I L F D F A                      |     |
| UGT91R4 | GAATCAATGGCTAAGTTTCTCGAAGATTGAGATATTGATTTTATACTATTGATTTTGCC  | 360 |
|         | ***** ** ***** *                                             |     |
| UGT91R1 | TCTTATTGGTTTCCTTCAATTGCTTCAAATTCAACATTCGTCGGGATATTTTCAGCATA  | 420 |
| UGT91R1 | S Y W V P S I A S K F N I P S G Y F S I                      |     |
| UGT91R4 | S Y W I P S I A S K F N I P T G Y F S I                      |     |
| UGT91R4 | TCTTATTGGATTTCCTTCAATTGCTTCAAATTCAACATTCGACGGGTACTTCAGCATA   | 420 |
|         | ***** *****                                                  |     |
| UGT91R1 | TTCATCGCTGCGTTTCTGGGTTTCACCGACCTGTGCCGGGATTGAACAATGATTATGAA  | 480 |
| UGT91R1 | F I A A F L G F T G P V P G L N N D Y E                      |     |
| UGT91R4 | F I A A V L G F I G S E P G L N N D Y Q                      |     |
| UGT91R4 | TTCATAGCTGCGGTTCTGGGTTTCATCGGATCTGAGCCAGGATTGAACAATGATTATCAA | 480 |
|         | ***** *****                                                  |     |
| UGT91R1 | ATTCGAATGACGCCGAGGAATACACTGTTACCCCAAATGGGTTCGGTTTGAAACCACA   | 540 |
| UGT91R1 | I R M T P E E Y T V T P K W V P F E T T                      |     |
| UGT91R4 | I R K T P E E Y T V S P N W V P F E T T                      |     |
| UGT91R4 | ATTCGGAAGACGCCAGAGGAATACACTGTTTCCCAAATGGGTGCCGTTTGAAACCACA   | 540 |
|         | ***** * *****                                                |     |

|         |                                                               |      |
|---------|---------------------------------------------------------------|------|
| UGT91R1 | GTTGCTTTCAAGCTTTTTCGAAGTCTCGAGAATCTTGAAGCTTCCATGAAAGGAGAGGAA  | 600  |
| UGT91R1 | V A F K L F E V S R I F E A S M K G E E                       |      |
| UGT91R4 | V A F K L F E V S R I F E A S M K G E E                       |      |
| UGT91R4 | GTTGCTTTCAAGCTTTTTCGAAGTTTCGAGAATCTTGAAGCTTCCATGAAGGGAGAAGAA  | 600  |
|         | *****                                                         |      |
| UGT91R1 | GAGAACATTGCTGATATTGTTGCTACTATAGATCTGTTGAAAACTGTGATTTTTTGCTT   | 660  |
| UGT91R1 | E N I A D I V R Y Y R S V E N C D F L L                       |      |
| UGT91R4 | D N V S D I I R M Y K G L R Y S D F L L                       |      |
| UGT91R4 | GACAAATGTTTCTGATATTATTCGTATGTATAAAGGCTTAGATACTCTGATTTTTTGCTT  | 660  |
|         | ** ** * ***** ***** **** * * ** * ** *****                    |      |
| UGT91R1 | GTGAGGAGCTGTTCAGAAATTTGAACCAAGATGGTTGAAAGTTGTCGGAGATATTACACGG | 720  |
| UGT91R1 | V R S C S E F E P E W L K V V G D I H R                       |      |
| UGT91R4 | V R S C S E F E P E W L K V V G D I H R                       |      |
| UGT91R4 | GTGAGGAGCTGTTCGGAATTTGAACCGAATGGTTGAAAGTTGTCGGAGATATCCACCGG   | 720  |
|         | *****                                                         |      |
|         | Primer F for qRT-PCR --                                       |      |
| UGT91R1 | AAACCGGTTTTTCCGGTGGGTCAACTTCCGACTACACCGTATGAAGATGACAGCACGAAG  | 780  |
| UGT91R1 | K P V F P V G Q L P T T P Y E D D S T K                       |      |
| UGT91R4 | K P V F P V G Q L P T T P Y E D D S T K                       |      |
| UGT91R4 | AAGCCGGTTTTTCCGGTGGGTCAACTTCCGACTACGCCGTATGAAGATGACAGCACGAAG  | 780  |
|         | ** *****                                                      |      |
|         | ----->                                                        |      |
| UGT91R1 | ATCGATGCATGGAGAGAGATAAAGCTATGGCTTGATAAGCAAGAAAAGGGGAAAGTTATT  | 840  |
| UGT91R1 | I D A W R E I K L W L D K Q E K G K V I                       |      |
| UGT91R4 | I D A W R E I K L W L D K Q E K G K V I                       |      |
| UGT91R4 | ATCGATGCATGGAGAGAGATAAACTATGGCTTGATAAGCAAGAAAAGGGGAAAGTTATT   | 840  |
|         | *****                                                         |      |
| UGT91R1 | TACGTTGCATTTGGGAGCGAGGCCAAAACCGAGTCAAAATGAACTTACTGAGTTATCTCTT | 900  |
| UGT91R1 | Y V A F G S E A K P S Q N E L T E L S L                       |      |
| UGT91R4 | Y V A F G S E A K P S Q N E L T E L S L                       |      |
| UGT91R4 | TACGTTGCATTTGGGAGCGAGGCCAAAACCGAGTCAAAATGAACTTACTGAGTTATCACTC | 900  |
|         | ***** *                                                       |      |
| UGT91R1 | GGGTTAGAGCTTTCTGGGTTGCCATTCTTTGGGTTTTAAGAATTAAGAGGGGAGTCC     | 960  |
| UGT91R1 | G L E L S G L P F F W V L R I K R G E S                       |      |
| UGT91R4 | G L E L S G L P F F W V L R I K R G E S                       |      |
| UGT91R4 | GGACTAGAGCTTTCTGGGTTGCCATTCTTTGGGTTTTAAGAATTAAGAGGGGAGTCC     | 960  |
|         | ** *****                                                      |      |
|         | -----< Primer R for qRT-PCR                                   |      |
| UGT91R1 | GATGATGAATTGATTCAATTACCAGAAGGTTTCGAAGAACGAACAAAGGGAAGAGGAATA  | 1020 |
| UGT91R1 | D D E L I Q L P E G F E E R T K G R G I                       |      |
| UGT91R4 | D D E L I Q L P E G F E E R T K G R G I                       |      |
| UGT91R4 | GATGATGAATTGATTCAATTACCAGAAGGTTTCGAAGAACGAACAAAGGGAAGAGGAATA  | 1020 |
|         | *****                                                         |      |
| UGT91R1 | GTGTGCACGAGTTGGGCACCACAACCTCAAGATACTGAGTCATGACTCAGTGGGTGGATT  | 1080 |
| UGT91R1 | V C T S W A P Q L K I L S H D S V G G F                       |      |
| UGT91R4 | V Y T S W A P Q L K I L S H D S V G G F                       |      |
| UGT91R4 | GTGTACACAAGTTGGGCCCCACAACCTCAAGATACTGAGTCATGATTCAGTAGGTGGTTT  | 1080 |
|         | **** ** ***** *****                                           |      |

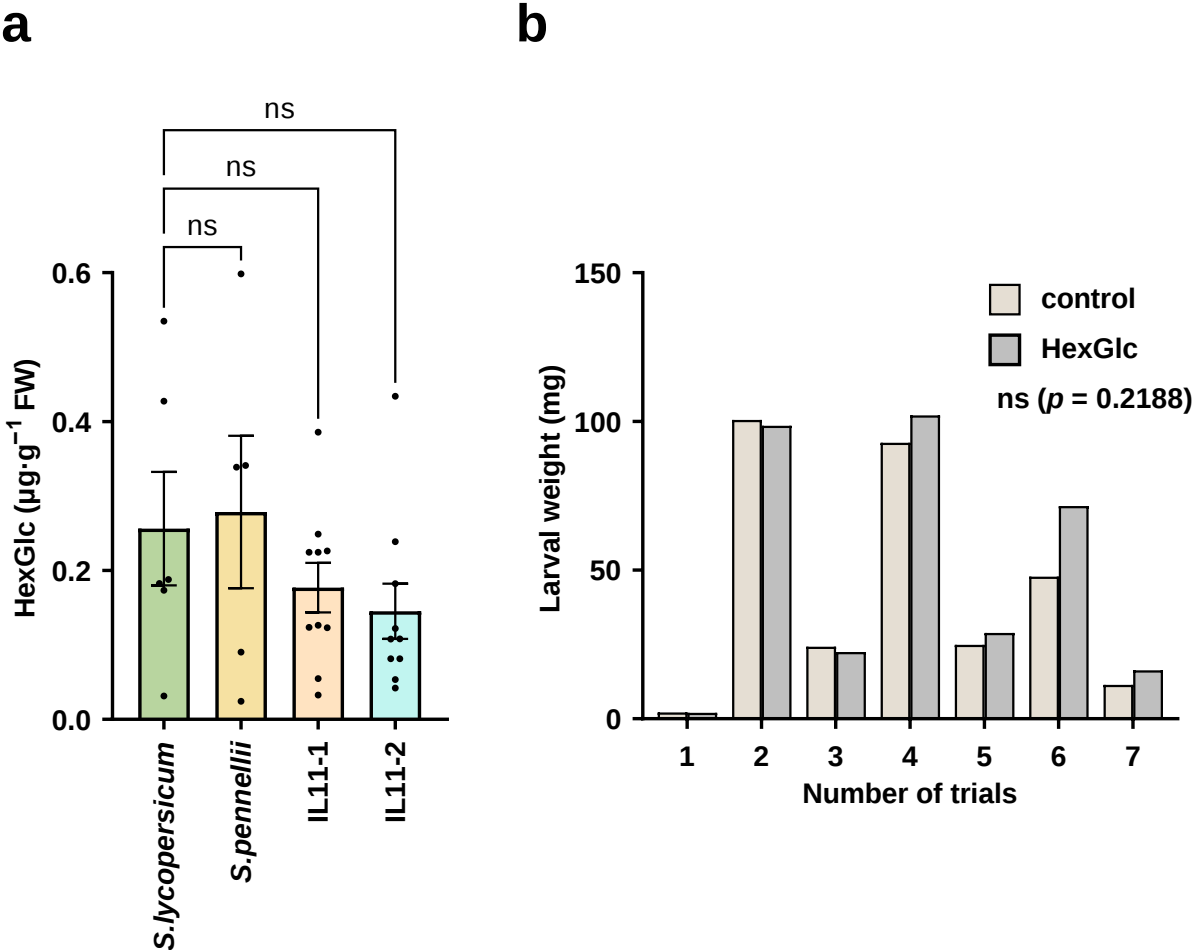
|           |                                                 |                              |                         |            |                            |                                      |                                      |      |
|-----------|-------------------------------------------------|------------------------------|-------------------------|------------|----------------------------|--------------------------------------|--------------------------------------|------|
| UGT91R1   | TTGACTCATT CAGGATGGAGTTCAGTAGTCGAGGCAATACAATTGA | AAGTCATTGGTT                 | 1140                    |            |                            |                                      |                                      |      |
| UGT91R1   | L T H S G W S S V V E A I Q F E K S L V         |                              |                         |            |                            |                                      |                                      |      |
| UGT91R4   | L T H S G W S S V V E A I Q F E K S L V         |                              |                         |            |                            |                                      |                                      |      |
| UGT91R4   | TTGACTCATT CAGGATGGAGTTCAGTAGTCGAGGCAATACAATTGA | AAGTCATTGGTT                 | 1140                    |            |                            |                                      |                                      |      |
| *****     |                                                 |                              |                         |            |                            |                                      |                                      |      |
| UGT91R1   | CTCTTAACATTTTTGGCTGATCAAGGGATAAATGCTAGGCT       | TTTGGAGGAGAAGAA              | AATG                    | 1200       |                            |                                      |                                      |      |
| UGT91R1   | L L T F L A D Q G I N A R L L E E K K M         |                              |                         |            |                            |                                      |                                      |      |
| UGT91R4   | L L T F L A D Q G I N A R L L E E K K M         |                              |                         |            |                            |                                      |                                      |      |
| UGT91R4   | CTCTTAACATTTTTGGCTGATCAAGGGATAAATGCTAGGCT       | CTTGGAGGAGAAGAA              | GATG                    | 1200       |                            |                                      |                                      |      |
| *****     |                                                 |                              |                         |            |                            |                                      |                                      |      |
| UGT91R1   | GC                                              | GATTCGATACCGAGAAATGATCAAGACG | GATC                    | ATTCACTCGT | GACTCAGTGGCCGAG            | 1260                                 |                                      |      |
| UGT91R1   | A Y S I P R N D Q D G S F T R                   | D                            | S V A E                 |            |                            |                                      |                                      |      |
| UGT91R4   | A Y S I P R N D Q D G S F T R                   | H                            | S V A E                 |            |                            |                                      |                                      |      |
| UGT91R4   | GC                                              | AATTCGATACCGAGAAATGATCAAGACG | GTC                     | GTTCACTCGT | C                          | ACTCAGTGGCCGAG                       | 1260                                 |      |
| ** *****  |                                                 |                              |                         |            |                            |                                      |                                      |      |
| UGT91R1   | TC                                              | ACTGA                        | ATTGGTACT               | CGT        | TAA                        | GAAGAGGGTTTTATTTATCGAGAAAAGATTAAAGAG | 1320                                 |      |
| UGT91R1   | S L                                             | N                            | L V L                   | V          | K E                        | E G F I Y R E K I K E                |                                      |      |
| UGT91R4   | S L                                             | K                            | L V L                   | T          | K K                        | E G F I Y R E K I K E                |                                      |      |
| UGT91R4   | TC                                              | ATTGA                        | AACTGGTACT              | C          | ACT                        | TAA                                  | GAAGAGGGTTTTATTTATCGAGAAAAGATTAAAGAG | 1320 |
| *** ***** |                                                 |                              |                         |            |                            |                                      |                                      |      |
| UGT91R1   | ATGAAA                                          | GATCTTTTCTGTGACAAG           | AAA                     | AGG        | CAAAATAATTATGTGGAGAATTTGTT | AAGT                                 | 1380                                 |      |
| UGT91R1   | M K                                             | D                            | L F C D K               | K          | R Q N N Y V E N L L S      |                                      |                                      |      |
| UGT91R4   | M K                                             | N                            | L F C D K               | E          | R Q N N Y V E N L L S      |                                      |                                      |      |
| UGT91R4   | ATGAAA                                          | AATCTTTTCTGTGACAAG           | GA                      | CGA        | CAAAATAATTATGTGGAGAATTTGTT | GAGT                                 | 1380                                 |      |
| *****     |                                                 |                              |                         |            |                            |                                      |                                      |      |
| UGT91R1   | TTTCTTCA                                        | AG                           | ACTATGAAAAGATTAAAGCATGA |            |                            |                                      | 1413                                 |      |
| UGT91R1   | F L Q                                           | D                            | Y E K I K A *           |            |                            |                                      |                                      |      |
| UGT91R4   | F L Q                                           | N                            | Y E K I K A *           |            |                            |                                      |                                      |      |
| UGT91R4   | TTTCTTCA                                        | AA                           | ATTATGAAAAGATTAAAGCATGA |            |                            |                                      | 1413                                 |      |
| *****     |                                                 |                              |                         |            |                            |                                      |                                      |      |

**Supplementary Figure 6: Comparison of putative amino acid sequence and ORF sequence of UGT91R1 and UGT91R4.** Different bases in nucleotide sequence are indicated in red letters. Different bases in nucleotide sequence are indicated in red letters. Different residues in amino acid sequence are shown in red and yellow highlights. Blue arrows indicate annealing regions of specific primers for qRT-PCR.

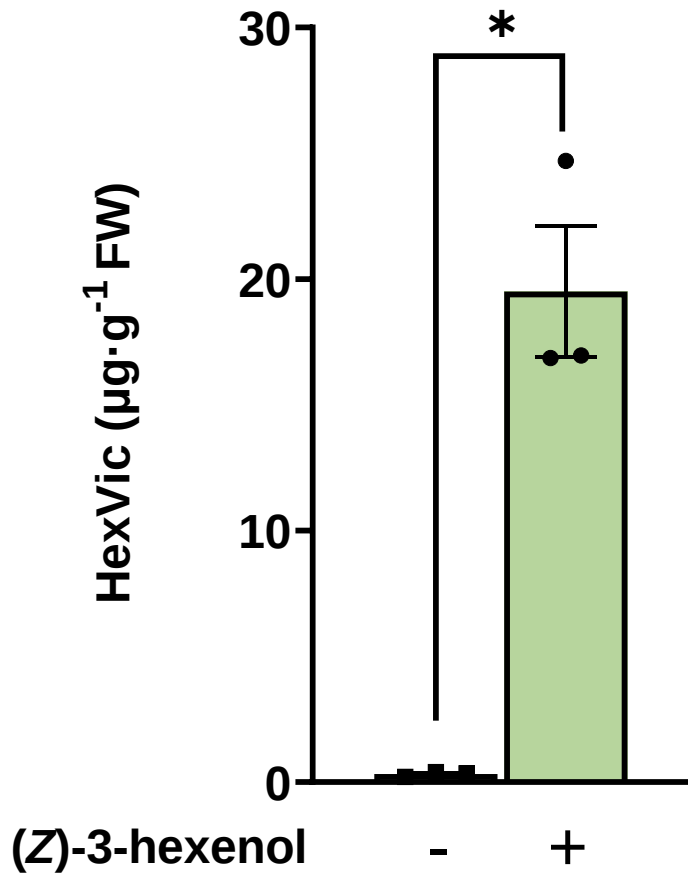


..... Hydrogen bonds  
 ..... OH- $\pi$  interaction

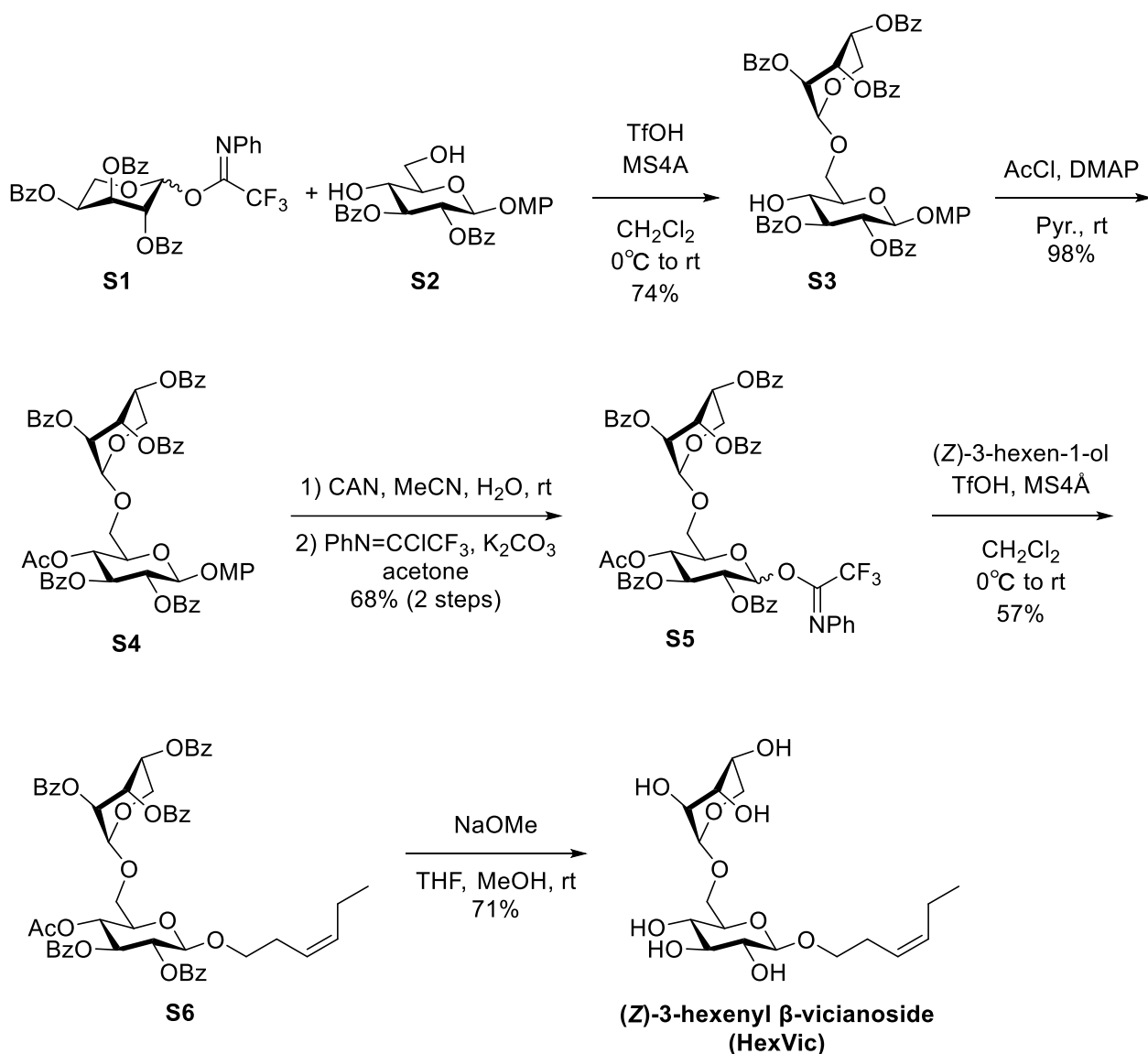
**Supplementary Figure 7: Homology models of UGT91R1 and UGT91R4 with UDP-sugar (UDP-xylose/UDP-arabinose).** **a** Homology model of UGT91R1 docking with UDP-xylose. **b** Homology model of UGT91R1 docking with UDP-arabinose. **c** Homology model of UGT91R4 docking with UDP-arabinose. Gene 3D models for UGT91R1 and UGT91R4 were constructed using the crystal structure of At\_UGT72B1 (PDB code 2vce) as a template. For homology models, crucial amino acid residues in the active site and UDP sugars are drawn as sticks. Carbon atoms are colored green for UGT amino acid residues and cyan for UDP sugars. Oxygen atoms are red, nitrogen atoms are blue, and phosphorus atoms are orange. Red dotted lines indicate plausible hydrogen bonds, and a black dotted line indicates OH- $\pi$  interaction. The sugar acceptor's structure is removed to simplify the models' visibility.



**Supplementary Figure 8: Biosynthesis and function of (Z)-3-hexenyl  $\beta$ -D-glucopyranoside.** **a** HexGlc content in leaves of *S. lycopersicum*, *S. pennellii*, and two introgression lines (IL11-1 and IL11-2). Plants were exposed to (Z)-3-hexenol for 6 h. Data are means  $\pm$  SE from six plants for *S. lycopersicum*, five plants for *S. pennellii* and ten plants for two introgression lines (IL11-1 and IL11-2). Statistical significance tests were analyzed using one-way ANOVA test with Tukey's multiple comparison. ns indicates no statistical difference. **b** Common cutworms were weighed before and after a 7-day experimental period on a control or HexGlc-containing artificial diet. Data are from 7 independent experiments and were analyzed using the Wilcoxon signed-rank tests.



**Supplementary Figure 9: HexVic contents in roots of *S. lycopersicum* cv. M82 exposed to (Z)-3-hexenol.** A plus symbol indicates (Z)-3-hexenol exposure and a minus symbol indicates control. Data are presented as the means  $\pm$  SE from three independent experiments. Statistical significance test was analyzed using two-tailed unpaired *t*-test. Statistical significant difference is indicated as  $*p < 0.05$ .



**Supplementary Figure 10: Synthesis of (Z)-3-hexenyl  $\beta$ -vicianoside (HexVic).** **S1**; 2,3,4-tri-O-Benzoyl-L-arabinopyranosyl (N-phenyl)trifluoroacetimidate, **S2**; *p*-methoxyphenyl 2,3-di-O-benzyl- $\beta$ -D-glucopyranoside, **S3**; *p*-methoxyphenyl (2,3,4-tri-O-Benzoyl- $\alpha$ -L-arabinopyranosyl) - (1 $\rightarrow$ 6)-2,3-di-O-benzyl- $\beta$ -D-glucopyranoside, **S4**; *p*-methoxyphenyl (2,3,4-tri-O-Benzoyl- $\alpha$ -L-arabinopyranosyl)-(1 $\rightarrow$ 6)-2,3-di-O-benzyl-4-O-acetyl- $\beta$ -D-glucopyranoside, **S5**; (2,3,4-tri-O-Benzoyl- $\alpha$ -L-arabinopyranosyl)-(1 $\rightarrow$ 6)-2,3-di-O-benzyl-4-O-acetyl-D-glucopyranosyl 2,2,2-trifluoro-N-phenyl-acetimidate, **S6**; 3-*cis*-hexenyl (2,3,4-tri-O-Benzoyl- $\alpha$ -L-arabinopyranosyl)-(1 $\rightarrow$ 6)-2,3-di-O-benzyl-4-O-acetyl- $\beta$ -D-glucopyranoside.

**Supplementary Table 1. List of genes located at the loci where IL11-1 and IL11-2 overlap.**

Red characters indicate UGT91 genes.

| Gene ID |                  | description                                                          |                                                          |
|---------|------------------|----------------------------------------------------------------------|----------------------------------------------------------|
| 30165   | Solyc11g008070.1 | Protein FAM126B                                                      | IPR018619 Hyccin                                         |
| 30166   | Solyc11g008080.1 | Unknown Protein                                                      | IPR012862 Protein of unknown function DUF1635            |
| 30167   | Solyc11g008090.1 | Shugoshin-1                                                          |                                                          |
| 30168   | Solyc11g008100.1 | Unknown Protein                                                      |                                                          |
| 30169   | Solyc11g008110.1 | Genomic DNA chromosome 5 P1 clone                                    | MJJ3                                                     |
| 30170   | Solyc11g008120.1 | Genomic DNA chromosome 5 P1 clone                                    | MJJ3                                                     |
| 30171   | Solyc11g008130.1 | Nuclear pore complex protein-related protein (Fragment)              |                                                          |
| 30172   | Solyc11g008140.1 | Pectate lyase family protein                                         | IPR002022 Pectate lyase_Amb allergen                     |
| 30173   | Solyc11g008150.1 | Transcription elongation factorspt5                                  | IPR005100 Supt5 repeat                                   |
| 30174   | Solyc11g008160.1 | Ulp1 protease family C -terminal catalytic domain containing protein | IPR003653 Peptidase C48, SUMO_Sentrin_Ubl1               |
| 30175   | Solyc11g008180.1 | Nodulin family protein                                               | IPR010658 Nodulin -like                                  |
| 30176   | Solyc11g008190.1 | Nodulin family protein                                               | IPR010658 Nodulin -like                                  |
| 30177   | Solyc11g008200.1 | Nodulin-like protein (Fragment)                                      | IPR010658 Nodulin -like                                  |
| 30178   | Solyc11g008210.1 | Glycine-rich RNA-binding protein-like                                | IPR015465 RNA recognition motif, glycine rich protein    |
| 30179   | Solyc11g008220.1 | Unknown Protein                                                      |                                                          |
| 30180   | Solyc11g008230.1 | SKP1-like 1                                                          | IPR016897 E3 ubiquitin ligase, SCF complex, Skp subunit  |
| 30181   | Solyc11g008240.1 | SKP1-like protein                                                    | IPR016897 E3 ubiquitin ligase, SCF complex, Skp subunit  |
| 30182   | Solyc11g008250.1 | Single-stranded nucleic acid binding R3H domain protein              | IPR003959                                                |
| 30183   | Solyc11g008260.1 | Cysteine proteinase cathepsin F                                      | IPR013128 Peptidase C1A, papain                          |
| 30184   | Solyc11g008270.1 | Genomic DNA chromosome 3 P1 clone                                    | MSJ11                                                    |
| 30185   | Solyc11g008280.1 | Serine carboxypeptidase                                              | IPR001563 Peptidase S10, serine carboxypeptidase         |
| 30186   | Solyc11g008290.1 | RNA binding protein                                                  | IPR012677 Nucleotide -binding, alpha-beta plait          |
| 30187   | Solyc11g008300.1 | F-box family protein                                                 | IPR001810 Cyclin -like F-box                             |
| 30188   | Solyc11g008310.1 | Unknown Protein                                                      | IPR019320 Protein of unknown function NEP                |
| 30189   | Solyc11g008320.1 | Lysine-specific histone demethylase 1                                | IPR002937 Amine oxidase                                  |
| 30190   | Solyc11g008330.1 | Zeta2-COP                                                            | IPR011012 Longin -like                                   |
| 30191   | Solyc11g008340.1 | Exocyst complex component 4                                          | IPR007191 Sec8 exocyst complex component specific domain |
| 30192   | Solyc11g008350.1 | Kinesin-like protein                                                 | IPR001752 Kinesin, motor region                          |
| 30193   | Solyc11g008360.1 | Pseudouridine synthase family protein                                | IPR 006145 Pseudouridine synthase, RsuA and RluB_C_D_E_F |
| 30194   | Solyc11g008370.1 | Mitochondrial glycerol-3-phosphate dehydrogenase                     |                                                          |

|       |                  |                                                                      |           |                                                                                   |                                                |
|-------|------------------|----------------------------------------------------------------------|-----------|-----------------------------------------------------------------------------------|------------------------------------------------|
| 30195 | Solyc11g008380.1 | Glycerol-3-phosphate dehydrogenase                                   | IPR000447 | FAD                                                                               | -dependent glycerol -3-phosphate dehydrogenase |
| 30196 | Solyc11g008390.1 | U-box domain-containing protein 14                                   | IPR011989 | Armadillo                                                                         | -like helical                                  |
| 30197 | Solyc11g008400.1 | SKP1-like protein                                                    | IPR016897 | E3 ubiquitin ligase, SCF complex, Skp subunit                                     |                                                |
| 30198 | Solyc11g008410.1 | Unknown Protein                                                      |           |                                                                                   |                                                |
| 30199 | Solyc11g008420.1 | SKP1-like protein                                                    | IPR016897 | E3 ubiquitin ligase, SCF complex, Skp subunit                                     |                                                |
| 30200 | Solyc11g008430.1 | Ras-related protein Rab-5C                                           | IPR015599 | Rab5                                                                              | -related                                       |
| 30201 | Solyc11g008440.1 | Amino acid transporter                                               | IPR013057 | Amino acid transporter, transmembrane                                             |                                                |
| 30202 | Solyc11g008450.1 | Thioredoxin family protein                                           | IPR013766 | Thioredoxin domain                                                                |                                                |
| 30203 | Solyc11g008460.1 | U4_U6.U5 tri-snRNP-associated protein 1                              | IPR005011 | SART                                                                              | -1 protein                                     |
| 30204 | Solyc11g008470.1 | U4_U6.U5 tri-snRNP-associated protein 1                              | IPR005011 | SART                                                                              | -1 protein                                     |
| 30205 | Solyc11g008480.1 | Photosystem II oxygen evolving complex protein PsbP                  | IPR016123 | Mog1_PsbP,                                                                        | alpha_beta_alpha sandwich                      |
| 30206 | Solyc11g008490.1 | Pumilio-like                                                         | IPR011989 | Armadillo                                                                         | -like helical                                  |
| 30207 | Solyc11g008500.1 | Actin                                                                | IPR004000 | Actin_actin                                                                       | -like                                          |
| 30208 | Solyc11g008510.1 | 60S ribosomal protein L38                                            | IPR002675 | Ribosomal protein L38e                                                            |                                                |
| 30209 | Solyc11g008520.1 | Ribonuclease 3-like protein 3                                        | IPR000999 | Ribonuclease III                                                                  |                                                |
| 30210 | Solyc11g008530.1 | Ribonuclease 3-like protein 3                                        | IPR000999 | Ribonuclease III                                                                  |                                                |
| 30211 | Solyc11g008540.1 | Ribonuclease 3-like protein 3                                        | IPR000999 | Ribonuclease III                                                                  |                                                |
| 30212 | Solyc11g008550.1 | Lecithin cholesterol acyltransferase family protein                  | IPR003386 | Lecithin:cholesterol                                                              | acyltransferase                                |
| 30213 | Solyc11g008560.1 | AP2-like ethylene                                                    |           | -responsive transcription factor At1g16060                                        | IPR001471                                      |
|       |                  | Pathogenesis-related transcriptional factor and ERF, DNA-binding     |           |                                                                                   |                                                |
| 30214 | Solyc11g008570.1 | Calcineurin-related phosphoesterase-like                             | IPR004843 | Metallophosphoesterase                                                            |                                                |
| 30215 | Solyc11g008580.1 | Ariadne-like ubiquitin ligase                                        | IPR002867 | Zinc finger, C6HC                                                                 | -type                                          |
| 30216 | Solyc11g008590.1 | UDP-galactose transporter-like protein                               | IPR0072   | 71                                                                                | Nucleotide -sugar transporter                  |
| 30217 | Solyc11g008600.1 | Genomic DNA chromosome 5 P1 clone MUA2                               |           |                                                                                   |                                                |
| 30218 | Solyc11g008610.1 | Nucleotide-sugar transporter UDP N                                   |           | -acetylglucosamine-like signal peptide 9 or more transmembrane domains (Fragment) | IPR007271                                      |
|       |                  | Nucleotide-sugar transporter                                         |           |                                                                                   |                                                |
| 30219 | Solyc11g008620.1 | Phosphoglycolate phosphatase                                         | IPR006349 | 2                                                                                 | -phosphoglycolate phosphatase, eukaryotic      |
| 30220 | Solyc11g008630.1 | Hydroxycinnamoyl CoA shikimate_quininate hydroxycinnamoyltransferase |           | -like protein (Fragment)                                                          | IPR003480                                      |
|       |                  | Transferase                                                          |           |                                                                                   |                                                |
| 30221 | Solyc11g008640.1 | Flowering locus T                                                    | IPR008914 | Phosphatidylethanolamine                                                          | -binding protein PEBP                          |
| 30222 | Solyc11g008650.1 | Flowering locus T1                                                   | IPR008914 | Phosphatidylethanolamine                                                          | -binding protein PEBP                          |
| 30223 | Solyc11g008660.1 | Flowering locus T                                                    | IPR008914 | Phosphatidylethanolamine                                                          | -binding protein PEBP                          |
| 30224 | Solyc11g008670.1 | At1g65470_F5I14_33 (Fragment)                                        |           |                                                                                   |                                                |

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|-------|------------------|-------------------------------------------------------------------------------------------------------------------|
| 30225 | Solyc11g008680.1 | Acyl- IPR005067 Fatty acid desaturase, type 2                                                                     |
| 30226 | Solyc11g008690.1 | TO23-3 (Fragment)                                                                                                 |
| 30227 | Solyc11g008700.1 | Splicing factor U2AF-associated protein IPR012677 Nucleotide -binding, alpha-beta<br>plait                        |
| 30228 | Solyc11g008710.1 | 30S ribosomal protein S5 IPR 000851 Ribosomal protein S5                                                          |
| 30229 | Solyc11g008720.1 | Beta-glucosidase G4 IPR001360 Glycoside hydrolase, family 1                                                       |
| 30230 | Solyc11g008730.1 | U11_U12 small nuclear ribonucleoprotein protein IPR019955 Ubiquitin supergroup                                    |
| 30231 | Solyc11g008740.1 | Double-strand-break repair protein rad21 IPR006910 Rad21_Rec8 like protein, N -<br>terminal                       |
| 30232 | Solyc11g008750.1 | Unknown Protein                                                                                                   |
| 30233 | Solyc11g008760.1 | Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat                                    |
| 30234 | Solyc11g008770.1 | LETM1 and EF -hand domain -containing protein 1, mitochondrial IPR011685<br>LETM1-like                            |
| 30235 | Solyc11g008780.1 | Acetolactate synthase small subunit IPR004789 Acetolactate synthase, small subunit                                |
| 30236 | Solyc11g008790.1 | ARV1 IPR007290 Arv1 -like protein                                                                                 |
| 30237 | Solyc11g008800.1 | Inositol 1 4 5 -trisphosphate 5 -phosphatase-like protein IPR000300 Inositol<br>polyphosphate related phosphatase |
| 30238 | Solyc11g008810.1 | Beta-hexosaminidase b IPR001540 Glycoside hydrolase, family 20                                                    |
| 30239 | Solyc11g008820.1 | Endoglucanase IPR001701 Glycoside hydrolase, family 9                                                             |
| 30240 | Solyc11g008830.1 | LOB domain protein IPR004883 Lateral organ boundaries, LOB                                                        |
| 30241 | Solyc11g008840.1 | En_Spm-like transposon protein                                                                                    |
| 30242 | Solyc11g008850.1 | Serine protease IPR015724 Serine endopeptidase DegP2                                                              |
| 30243 | Solyc11g008860.1 | Laccase-2 IPR001117 Multicopper oxidase, type 1                                                                   |
| 30244 | Solyc11g008870.1 | Methylenetetrahydrofolate reductase IPR004621 Eukaryotic -type<br>methylenetetrahydrofolate reductase             |
| 30245 | Solyc11g008880.1 | Wiscott-Aldrich syndrome C-terminal IPR000095 PAK -box_P21-Rho-binding                                            |
| 30246 | Solyc11g008890.1 | Predicted membrane protein (Fragment) IPR001727 Uncharacterised protein family<br>UPF0016                         |
| 30247 | Solyc11g008900.1 | Zinc finger CCCH domain -containing protein 66 IPR0005 71 Zinc finger, CCCH -<br>type                             |
| 30248 | Solyc11g008910.1 | Cysteine-rich peptide                                                                                             |
| 30249 | Solyc11g008920.1 | Unknown Protein                                                                                                   |
| 30250 | Solyc11g008930.1 | Lysine ketoglutarate reductase trans -splicing related 1 -like IPR007877 Protein of<br>unknown function DUF707    |
| 30251 | Solyc11g008940.1 | Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat                                    |
| 30252 | Solyc11g008950.1 | Unknown Protein                                                                                                   |
| 30253 | Solyc11g008960.1 | Receptor like kinase, RLK                                                                                         |

|       |                  |                                                                                 |            |                                             |
|-------|------------------|---------------------------------------------------------------------------------|------------|---------------------------------------------|
| 30254 | Solyc11g008970.1 | Pentatricopeptide repeat-containing protein                                     | IPR002885  | Pentatricopeptide repeat                    |
| 30255 | Solyc11g008980.1 | Os02g0726600 protein (Fragment)                                                 |            |                                             |
| 30256 | Solyc11g008990.1 | Phage shock protein A PspA                                                      | IPR007157  | PspA_IM30                                   |
| 30257 | Solyc11g009000.1 | Carboxylesterase bioH                                                           | IPR000073  | Alpha_beta hydrolase fold -1                |
| 30258 | Solyc11g009010.1 | Hydrolase alpha_beta fold family protein                                        | IPR000073  | Alpha_beta hydrolase fold -1                |
| 30259 | Solyc11g009020.1 | HAD-superfamily hydrolase subfamily IA variant 3 containing protein expressed   | IPR005834  | Haloacid dehalogenase -like hydrolase       |
| 30260 | Solyc11g009030.1 | Ribosomal protein L37                                                           |            |                                             |
| 30261 | Solyc11g009040.1 | EPIDERMAL PATTERNING FACTORlike protein 1                                       |            |                                             |
| 30262 | Solyc11g009050.1 | F-box protein-like                                                              | IPR001810  | Cyclin -like F-box                          |
| 30263 | Solyc11g009060.1 | Unknown Protein                                                                 |            |                                             |
| 30264 | Solyc11g009070.1 | Genomic DNA chromosome 5 P1 clone MQN23                                         |            |                                             |
| 30265 | Solyc11g009080.1 | Phospho-2-dehydro-3-deoxyheptonate aldolase 1                                   | IPR002480  | DAHP synthetase, class II                   |
| 30266 | Solyc11g009090.1 | Polyadenylate-binding protein family protein                                    | IPR012677  | Nucleotide -binding, alpha-beta plait       |
| 30267 | Solyc11g009100.1 | ABC transporter G family member 11                                              | IPR013525  | ABC -2 type transporter                     |
| 30268 | Solyc11g010100.1 | Ras-related protein Rab-25                                                      | IPR015595  | Rab11 -related                              |
| 30269 | Solyc11g010110.1 | Ribosomal RNA small subunit methyltransferase F_eukaryotic nucleolar NOL1_Nop2p |            |                                             |
| 30270 | Solyc11g010120.1 | Peroxidase 17                                                                   | IPR002016  | Haem peroxidase, plant_fungal_bacterial     |
| 30271 | Solyc11g010130.1 | Serine-threonine protein kinase                                                 | IPR015740  | Plant protein serine_threonine kinase -like |
| 30272 | Solyc11g010140.1 | Unknown Protein                                                                 |            |                                             |
| 30273 | Solyc11g010150.1 | Serine-threonine protein kinase                                                 | IPR017442  | Serine_threonine protein kinase -related    |
| 30274 | Solyc11g010160.1 | Cc-nbs-lrr, resistance protein                                                  |            |                                             |
| 30275 | Solyc11g010170.1 | LanC-like protein 2                                                             | IPR020464  | LanC -like protein, eukaryotic              |
| 30276 | Solyc11g010180.1 | Mitochondrial_chloroplast ribosomal protein L54_L37 (ISS)                       | IPR013870  | Ribosomal protein L37, mitochondrial        |
| 30277 | Solyc11g010190.1 | Prohibitin                                                                      | IPR000163  | Prohibitin                                  |
| 30278 | Solyc11g010200.1 | 14-3-3 protein beta_alpha-1                                                     | IPR 000308 | 14 -3-3 protein                             |
| 30279 | Solyc11g010210.1 | SKIP interacting protein 3 (Fragment)                                           |            |                                             |
| 30280 | Solyc11g010220.1 | Pentatricopeptide repeat-containing protein                                     | IPR002885  | Pentatricopeptide repeat                    |
| 30281 | Solyc11g010230.1 | Histone H3                                                                      | IPR000164  | Histone H3                                  |
| 30282 | Solyc11g010240.1 | Protein SCAI                                                                    |            |                                             |
| 30283 | Solyc11g010250.1 | Avr9_Cf-9 rapidly elicited protein 75                                           |            |                                             |
| 30284 | Solyc11g010260.1 | Pentatricopeptide repeat-containing protein                                     | IPR002885  | Pentatricopeptide repeat                    |
| 30285 | Solyc11g010270.1 | Homeobox-leucine zipper protein                                                 | IP R001356 | Homeobox                                    |

|       |                  |                                                  |           |                                                      |
|-------|------------------|--------------------------------------------------|-----------|------------------------------------------------------|
| 30286 | Solyc11g010280.1 | Unknown Protein                                  |           |                                                      |
| 30287 | Solyc11g010290.1 | 2-oxoglutarate_malate translocator               | IPR001898 | Sodium_sulphate symporter                            |
| 30288 | Solyc11g010300.1 | 3 4-dihydroxy-2-butanone 4-phosphate synthase    | IPR000422 | DHBP synthase RibB                                   |
| 30289 | Solyc11g010310.1 | ATP dependent RNA helicase                       | IPR014001 | DEAD -like helicase, N-terminal                      |
| 30290 | Solyc11g010320.1 | AT2G46550 protein (Fragment)                     |           |                                                      |
| 30291 | Solyc11g010330.1 | RING finger protein                              | IPR018957 | Zinc finger, C3HC4 RING -type                        |
| 30292 | Solyc11g010340.1 | BHLH transcription factor                        | IPR001092 | Basic helix -loop-helix dimerisation region bHLH     |
| 30293 | Solyc11g010350.1 | Glucan 1 3-beta-glucosidase                      | IPR001547 | Glycoside hydrolase, family 5                        |
| 30294 | Solyc11g010360.1 | Plant-specific domain TIGR01570 family protein   | IPR006460 | Protein of unknown function DUF617, plant            |
| 30295 | Solyc11g010370.1 | At4g40080-like protein (Fragment)                | IPR013809 | Epsin -like, N-terminal                              |
| 30296 | Solyc11g010380.1 | Mate efflux family protein                       | IPR002528 | Multi antimicrobial extrusion protein MatE           |
| 30297 | Solyc11g010390.1 | Unknown Protein                                  |           |                                                      |
| 30298 | Solyc11g010400.1 | 1-aminocyclopropane-1-carboxylate oxidase        | IPR005123 | Oxoglutarate and iron dependent oxygenase -          |
| 30299 | Solyc11g010410.1 | 1-aminocyclopropane-1-carboxylate oxidase        | IPR005123 | Oxoglutarate and iron dependent oxygenase -          |
| 30300 | Solyc11g010420.1 | Ovarian cancer-associated gene 2 protein homolog | IPR005645 | Protein of unknown function DUF341                   |
| 30301 | Solyc11g010430.1 | Ovarian cancer-associated gene 2 protein homolog | IPR005645 | Protein of unknown function DUF341                   |
| 30302 | Solyc11g010440.1 | FIP1                                             | IPR004182 | GRAM                                                 |
| 30303 | Solyc11g010450.1 | Phosphofructokinase family protein               | IPR012004 | Pyrophosphate -dependent phosphofructokinase TP0108  |
| 30304 | Solyc11g010460.1 | Cyclin D2                                        | IPR015451 | Cyclin D                                             |
| 30305 | Solyc11g010470.1 | 14-3-3 protein beta_alpha                        | IPR000308 | 14 -3-3 protein                                      |
| 30306 | Solyc11g010480.1 | Threonine endopeptidase                          |           |                                                      |
| 30307 | Solyc11g010490.1 | Genomic DNA chromosome 5 P1 clone MNA5           |           |                                                      |
| 30308 | Solyc11g010500.1 | Mitochondrial carrier family                     | IPR001993 | Mitochondrial substrate carrier                      |
| 30309 | Solyc11g010510.1 | Thymidylate synthase (Fragment)                  | IPR001498 | Uncharacterised protein family UPF0029, N-terminal   |
| 30310 | Solyc11g010520.1 | Unknown Protein                                  | IPR010800 | Glycine rich                                         |
| 30311 | Solyc11g010530.1 | Unknown Protein                                  | IPR010800 | Glycine rich                                         |
| 30312 | Solyc11g010540.1 | DnaJ domain containing protein expressed         | IPR015609 | Molecular chaperone, heat shock protein, Hsp40, DnaJ |
| 30313 | Solyc11g010550.1 | GPI ethanolamine phosphate transferase           | IPR017850 | Alkaline -phosphatase-like, core                     |

|              |                         |                                                                  |                         |                                    |                                              |
|--------------|-------------------------|------------------------------------------------------------------|-------------------------|------------------------------------|----------------------------------------------|
| 30314        | Solyc11g010560.1        | Kinesin-like protein                                             | IPR0 01752              | Kinesin, motor region              |                                              |
| 30315        | Solyc11g010570.1        | MADS box transcription factor                                    | IPR002100               | Transcription factor, MADS         | -box                                         |
|              |                         | IPR002487                                                        | Transcription factor, K | -box                               |                                              |
| 30316        | Solyc11g010580.2        | Unknown Protein                                                  |                         |                                    |                                              |
| 30317        | Solyc11g010590.1        | Protein-tyrosine phosphatase-like member A                       | IPR007482               | Protein                            | -tyrosine                                    |
|              |                         | phosphatase-like, PTPLA                                          |                         |                                    |                                              |
| 30318        | Solyc11g010600.1        | Os01g0841200 protein (Fragment)                                  | IPR004348               | Protein of unknown function        |                                              |
|              |                         | DUF246, plant                                                    |                         |                                    |                                              |
| 30319        | Solyc11g010610.1        | Small conductance mechanosensitive (MscS                         | -family)                | ion channel                        | IPR006685                                    |
|              |                         | Mechanosensitive ion channel MscS                                |                         |                                    |                                              |
| 30320        | Solyc11g010620.1        | Unknown Protein                                                  |                         |                                    |                                              |
| 30321        | Solyc11g010630.2        | Unknown Protein                                                  |                         |                                    |                                              |
| 30322        | Solyc11g010650.2        | Unknown Protein                                                  | IPR000868               | Isochorismatase                    | -like                                        |
| 30323        | Solyc11g010660.1        | SGT1 protein                                                     | IPR010770               | SGT1                               |                                              |
| 30324        | Solyc11g010670.1        | Unknown Protein                                                  |                         |                                    |                                              |
| 30325        | Solyc11g010680.2        | Unknown Protein                                                  |                         |                                    |                                              |
| 30326        | Solyc11g010690.1        | Nucleobase ascorbate transporter                                 | IPR006043               | Xanthine_uracil_vitamin C permease |                                              |
| 30327        | Solyc11g010700.1        | Receptor-like protein kinase                                     | IPR001245               | Tyrosine protein kinase            |                                              |
| 30328        | Solyc11g010710.1        | AP2-like ethylene-responsive transcription factor                | At1g16060               | IPR001471                          |                                              |
|              |                         | Pathogenesis-related transcriptional factor and ERF, DNA-binding |                         |                                    |                                              |
| 30329        | Solyc11g010720.1        | Genomic DNA chromosome 5 TAC clone K21L13                        | IPR01 1990              | Tetratricopeptide                  | -like                                        |
|              |                         | helical                                                          |                         |                                    |                                              |
| 30330        | Solyc11g010730.1        | Receptor-like kinase                                             | IPR002290               | Serine_threonine protein kinase    |                                              |
| <b>30331</b> | <b>Solyc11g010740.1</b> | <b>UDP-glucosyltransferase</b>                                   | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| <b>30332</b> | <b>Solyc11g010750.1</b> | <b>UDP-glucosyltransferase</b>                                   | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| <b>30333</b> | <b>Solyc11g010760.1</b> | <b>UDP-glucosyltransferase</b>                                   | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| 30334        | Solyc11g010770.1        | Unknown Protein                                                  |                         |                                    |                                              |
| <b>30335</b> | <b>Solyc11g010780.1</b> | <b>Glucosyltransferase</b>                                       | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| <b>30336</b> | <b>Solyc11g010790.1</b> | <b>Glucosyltransferase</b>                                       | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| <b>30337</b> | <b>Solyc11g010800.1</b> | <b>Anthocyanidin 3-O-glucosyltransferase</b>                     | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| <b>30338</b> | <b>Solyc11g010810.1</b> | <b>Glucosyltransferase</b>                                       | <b>IPR002213</b>        | <b>UDP</b>                         | <b>-glucuronosyl_UDP-glucosyltransferase</b> |
| 30339        | Solyc11g010830.1        | Unknown Protein                                                  |                         |                                    |                                              |
| 30340        | Solyc11g010840.1        | Poly(RC) binding protein 3                                       | IPR018111               | K Homology, type 1, subgroup       |                                              |

|       |                  |                                                 |           |                                                    |   |
|-------|------------------|-------------------------------------------------|-----------|----------------------------------------------------|---|
| 30341 | Solyc11g010850.1 | 1-deoxy-D-xylulose 5-phosphate synthase 2       | IPR005477 | Deoxyxylulose -5-phosphate synthase                |   |
| 30342 | Solyc11g010860.1 | RING-finger protein like                        | IPR018957 | Zinc finger, C3HC4 RING -type                      |   |
| 30343 | Solyc11g010870.1 | Unknown Protein                                 |           |                                                    |   |
| 30344 | Solyc11g010880.1 | Unknown Protein                                 |           |                                                    |   |
| 30345 | Solyc11g010890.1 | Exostosin family protein                        | IPR004263 | Exostosin -like                                    |   |
| 30346 | Solyc11g010900.1 | RRNA methyltransferase                          | IPR001537 | tRNA_rRNA methyltransferase, SpoU                  |   |
| 30347 | Solyc11g010910.1 | WD repeat protein                               | IPR020472 | G -protein beta WD-40 repeat, region               |   |
| 30348 | Solyc11g010920.1 | Kinesin                                         | IPR001752 | Kinesin, motor region                              |   |
| 30349 | Solyc11g010930.1 | HVA22-like protein e                            | IPR004345 | TB2_DP1 and HVA22 related protein                  |   |
| 30350 | Solyc11g010940.1 | Dof zinc finger protein 6                       | IPR003851 | Zinc finger, Dof -type                             |   |
| 30351 | Solyc11g010950.1 | Elongator complex protein 4                     | IPR008728 | Elongator complex protein 4                        |   |
| 30352 | Solyc11g010960.1 | Alcohol dehydrogenase                           | IPR002085 | Alcohol dehydrogenase superfamily, zinc containing | - |
| 30353 | Solyc11g010980.1 | Alcohol dehydrogenase                           | IPR002085 | Alcohol dehydrogenase superfamily, zinc containing | - |
| 30354 | Solyc11g010990.1 | Alcohol dehydrogenase                           | IPR002085 | Alcohol dehydrogenase superfamily, zinc containing | - |
| 30355 | Solyc11g011000.1 | Cysteine-rich repeat secretory protein 60 DUF26 | IPR002902 | Protein of unknown function                        |   |
| 30356 | Solyc11g011010.1 | Erwinia induced protein 2                       |           |                                                    |   |
| 30357 | Solyc11g011020.1 | Receptor like kinase, RLK                       |           |                                                    |   |
| 30358 | Solyc11g011030.1 | Pto-responsive gene 1 protein                   | IPR010399 | Tify                                               |   |
| 30359 | Solyc11g011040.1 | ADP-ribosylation factor-like protein            | IPR006688 | ADP -ribosylation factor                           |   |
| 30360 | Solyc11g011050.1 | MYB transcription factor                        | IPR015495 | Myb transcription factor                           |   |
| 30361 | Solyc11g011060.1 | AT5g16610_MTG13_5 (Fragment)                    |           |                                                    |   |
| 30362 | Solyc11g011070.1 | Genomic DNA chromosome 5 P1 clone MTG13         |           |                                                    |   |
| 30363 | Solyc11g011080.1 | Tir-nbs-lrr, resistance protein                 |           |                                                    |   |
| 30364 | Solyc11g011090.1 | Tir-nbs-lrr, resistance protein                 |           |                                                    |   |
| 30365 | Solyc11g011100.1 | Unknown Protein                                 |           |                                                    |   |
| 30366 | Solyc11g011110.1 | GDSL esterase_lipase At5g37690                  | IPR001087 | Lipase, GDSL                                       |   |
| 30367 | Solyc11g011120.1 | Calmodulin-binding heat-shock protein           | IPR002921 | Lipase, class 3                                    |   |
| 30368 | Solyc11g011130.1 | THO complex subunit 4                           | IPR012677 | Nucleotide -binding, alpha-beta plait              |   |
| 30369 | Solyc11g011140.1 | 50S ribosomal protein L23                       | IPR013025 | Ribosomal protein L25_L23                          |   |
| 30370 | Solyc11g011150.1 | DNA repair protein Rad4 family                  | IPR004583 | DNA repair protein Rad4                            |   |
| 30371 | Solyc11g011160.1 | High mobility group protein                     | IPR005818 | Histone H1_H5                                      |   |
| 30372 | Solyc11g011170.1 | ATA15 protein                                   |           |                                                    |   |

|       |                  |                                                                                                                 |
|-------|------------------|-----------------------------------------------------------------------------------------------------------------|
| 30373 | Solyc11g011180.1 | LRR receptor-like serine_threonine-protein kinase, RLP                                                          |
| 30374 | Solyc11g011190.1 | Exostosin family protein IPR004263 Exostosin -like                                                              |
| 30375 | Solyc11g011200.1 | Post-GPI attachment to proteins factor 3 IPR007217 Per1 -like                                                   |
| 30376 | Solyc11g011210.1 | Gibberellin regulated protein IPR003854 Gibberellin regulated protein                                           |
| 30377 | Solyc11g011220.1 | Unknown Protein                                                                                                 |
| 30378 | Solyc11g011230.1 | F-box family protein IPR001810 Cyclin -like F-box                                                               |
| 30379 | Solyc11g011240.1 | Geranylgeranyl pyrophosphate synthase 1 IPR000092 Polyprenyl synthetase                                         |
| 30380 | Solyc11g011250.1 | Chloride intracellular channel 6 IPR017933 Glutathione S-transferase_chloride channel, C-terminal               |
| 30381 | Solyc11g011260.1 | GAI-like protein 1 (Fragment) IPR005202 GRAS transcription factor                                               |
| 30382 | Solyc11g011270.1 | Rhamnogalacturonate lyase IPR010325 Rhamnogalacturonate lyase                                                   |
| 30383 | Solyc11g011280.1 | LG127_30 like gene IPR008979 Galactose -binding like                                                            |
| 30384 | Solyc11g011290.1 | Rhamnogalacturonate lyase IPR010325 Rhamnogalacturonate lyase                                                   |
| 30385 | Solyc11g011300.1 | Rhamnogalacturonate lyase IPR010325 Rhamnogalacturonate lyase                                                   |
| 30386 | Solyc11g011310.1 | Rhamnogalacturonate lyase IPR010325 Rhamnogalacturonate lyase                                                   |
| 30387 | Solyc11g011320.1 | Rhamnogalacturonate lyase IPR010325 Rhamnogalacturonate lyase                                                   |
| 30388 | Solyc11g011330.1 | Cinnamyl alcohol dehydrogenase IPR002085 Alcohol dehydrogenase superfamily, zinc-containing                     |
| 30389 | Solyc11g011340.1 | Alcohol dehydrogenase IPR002085 Alcohol dehydrogenase superfamily, zinc-containing                              |
| 30390 | Solyc11g011350.1 | Tir-nbs-lrr, resistance protein                                                                                 |
| 30391 | Solyc11g011360.1 | Nudix hydrolase 4 IPR000086 NUDIX hydrolase domain                                                              |
| 30392 | Solyc11g011370.1 | Condensin complex subunit 3 IPR016024 Armadillo -type fold                                                      |
| 30393 | Solyc11g011380.1 | Glutamine synthetase IPR008146 Glutamine synthetase, catalytic region                                           |
| 30394 | Solyc11g011390.1 | TPR repeat Kinesin light chain Kinesin light chain IPR011990 Tetratricopeptide -like helical                    |
| 30395 | Solyc11g011400.1 | Unknown Protein                                                                                                 |
| 30396 | Solyc11g011410.1 | Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat                                  |
| 30397 | Solyc11g011420.1 | Peptidyl-prolyl cis-trans isomerase IPR001179 Peptidyl -prolyl cis-trans isomerase, FKBP-type                   |
| 30398 | Solyc11g011430.1 | Ycf2 IPR008543 Chloroplast Ycf2                                                                                 |
| 30399 | Solyc11g011440.1 | Aspartic proteinase nepenthesin-1 IPR001461 Peptidase A1                                                        |
| 30400 | Solyc11g011450.1 | Glutathione-dependent formaldehyde -activating GFA IPR006913 Glutathione-dependent formaldehyde-activating, GFA |
| 30401 | Solyc11g011460.1 | ATP-dependent RNA helicase IPR001650 DNA_RNA helicase, C-terminal                                               |
| 30402 | Solyc11g011470.1 | NADH-ubiquinone oxidoreductase subunit IPR010228 NADH:ubiquinone oxidoreductase, subunit G                      |

|       |                  |                                                                                                                        |
|-------|------------------|------------------------------------------------------------------------------------------------------------------------|
| 30403 | Solyc11g011480.1 | Nicastrin IPR008710 Nicastrin                                                                                          |
| 30404 | Solyc11g011490.1 | CTV.12                                                                                                                 |
| 30405 | Solyc11g011500.1 | Potassium channel IPR002110 Ankyrin                                                                                    |
| 30406 | Solyc11g011510.1 | Unknown Protein                                                                                                        |
| 30407 | Solyc11g011520.1 | Unknown Protein                                                                                                        |
| 30408 | Solyc11g011530.1 | Unknown Protein                                                                                                        |
| 30409 | Solyc11g011540.1 | F-box family protein IPR001810 Cyclin -like F-box                                                                      |
| 30410 | Solyc11g011550.1 | Unknown Protein                                                                                                        |
| 30411 | Solyc11g011560.1 | PHD finger family protein IPR011011 Zinc finger, FYVE_PHD-type                                                         |
| 30412 | Solyc11g011570.1 | RING finger protein 44 IPR011016 Zinc finger, RING -CH-type                                                            |
| 30413 | Solyc11g011580.1 | FIP1 IPR004182 GRAM                                                                                                    |
| 30414 | Solyc11g011590.1 | FIP1 IPR004182 GRAM                                                                                                    |
| 30415 | Solyc11g011600.1 | GRAM-containing_ABA-responsive protein (Fragment)                                                                      |
| 30416 | Solyc11g011610.1 | Fatty acid -binding protein -like protein IPR014878 Region of unknown function DUF1794                                 |
| 30417 | Solyc11g011620.1 | Fatty acid -binding protein -like protein IPR014878 Region of unknown function DUF1794                                 |
| 30418 | Solyc11g011630.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein                                                |
| 30419 | Solyc11g011640.1 | Auxin-responsive protein IPR003676 Auxin responsive SAUR protein                                                       |
| 30420 | Solyc11g011650.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR p rotein                                               |
| 30421 | Solyc11g011660.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein                                                |
| 30422 | Solyc11g011670.1 | Auxin-responsive protein IPR003676 Auxin responsive SAUR protein                                                       |
| 30423 | Solyc11g011680.1 | Auxin-induced SAUR-like protein IPR 003676 Auxin responsive SAUR protein                                               |
| 30424 | Solyc11g011690.1 | Auxin-responsive protein IPR003676 Auxin responsive SAUR protein                                                       |
| 30425 | Solyc11g011700.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein                                                |
| 30426 | Solyc11g011710.1 | Auxin-responsive protein IPR003676 Auxin responsive SAUR protein                                                       |
| 30427 | Solyc11g011720.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protein                                                |
| 30428 | Solyc11g011730.1 | Auxin-induced SAUR-like protein IPR003676 Auxin responsive SAUR protei n                                               |
| 30429 | Solyc11g011740.1 | Ethylene-responsive transcription factor 2 IPR001471 Pathogenesis -related transcriptional factor and ERF, DNA-binding |
| 30430 | Solyc11g011750.1 | Ethylene-responsive transcription factor 2 IPR001471 Pathogenesis -related transcriptional factor and ERF, DNA-binding |
| 30431 | Solyc11g011760.1 | Genomic DNA chromosome 5 P1 clone MQK4                                                                                 |
| 30432 | Solyc11g011770.1 | Myb family transcription factor -like IPR006447 Myb -like DNA -binding region, SHAQKYF class                           |
| 30433 | Solyc11g011780.1 | Nonsense-mediated mRNA decay NMD3 family protein IPR007064 NMD3                                                        |
| 30434 | Solyc11g011790.1 | Importin beta-3 IPR011989 Armadillo -like helical                                                                      |

|       |                  |                                                                                                                       |    |
|-------|------------------|-----------------------------------------------------------------------------------------------------------------------|----|
| 30435 | Solyc11g011800.1 | Importin beta IPR011989 Armadillo -like helical                                                                       |    |
| 30436 | Solyc11g011810.1 | Oxidoreductase family protein-binding domain                                                                          |    |
| 30437 | Solyc11g011820.1 | Oxidoreductase                                                                                                        |    |
| 30438 | Solyc11g011830.1 | Unknown Protein                                                                                                       |    |
| 30439 | Solyc11g011840.1 | Oxidoreductase family protein-binding domain                                                                          |    |
| 30440 | Solyc11g011850.1 | Galactosylgalactosylxylosylprotein 3 -beta-glucuronosyltransferase 1 IPR0050 Glycosyl transferase, family 43          | 27 |
| 30441 | Solyc11g011860.1 | Pentatricopeptide repeat-containing protein IPR002885 Pentatricopeptide repeat                                        |    |
| 30442 | Solyc11g011870.1 | RLK, Receptor like protein, putative resistance protein with an antifungal domain                                     |    |
| 30443 | Solyc11g011880.1 | RLK, Receptor like protein, putative resistance protein with an antifungal domain                                     |    |
| 30444 | Solyc11g011890.1 | Zinc finger protein 7 IPR007087 Zinc finger, C2H2 -type                                                               |    |
| 30445 | Solyc11g011900.1 | Ubiquitin family protein IPR019956 Ubiquitin subgrou p                                                                |    |
| 30446 | Solyc11g011910.1 | Transmembrane 9 superfamily protein member 1                                                                          |    |
| 30447 | Solyc11g011920.1 | Glutamate decarboxylase IPR010107 Glutamate decarboxylase                                                             |    |
| 30448 | Solyc11g011930.1 | Isocitrate dehydrogenase IPR004790 Isocitrate dehydrogenase NADP -dependent, eukaryotic                               |    |
| 30449 | Solyc11g011940.1 | Homeobox-leucine zipper protein PROTODERMAL FACTOR 2 IPR002913 Lipid - binding START                                  |    |
| 30450 | Solyc11g011950.1 | Unknown Protein                                                                                                       |    |
| 30451 | Solyc11g011960.1 | UTP-glucose 1 phosphate uridylyltransferase IPR016267 UTP --glucose-1-phosphate uridylyltransferase, subgroup         |    |
| 30452 | Solyc11g011970.1 | Tyrosine phosphatase family protein IPR020428 Protein -tyrosine phosphatase, dual specificity phosphatase, eukaryotic |    |
| 30453 | Solyc11g011980.1 | WD-40 repeat protein IPR020472 G -protein beta WD-40 repeat, region                                                   |    |
| 30454 | Solyc11g011990.1 | Plastid terminal oxydase                                                                                              |    |

**Supplementary Table 2: UGT91 family genes in *S. lycopersicum* and *S. pennellii*.**

| <i>S. lycopersicum</i>      |                | <i>S. pennellii</i>         |                |
|-----------------------------|----------------|-----------------------------|----------------|
| Gene ID in SGN <sup>1</sup> | UGT ID         | Gene ID in SGN <sup>1</sup> | UGT ID         |
| <i>Solyc11g010740</i>       | <i>UGT91A6</i> | <i>Sopen11g005550</i>       | <i>UGT91A8</i> |
| <i>Solyc11g010750</i>       | pseudogene     | -                           | -              |
| <i>Solyc11g010760</i>       | <i>UGT91A7</i> | <i>Sopen11g005560</i>       | <i>UGT91A9</i> |
| <i>Solyc11g010780</i>       | <i>UGT91R1</i> | <i>Sopen11g005570</i>       | <i>UGT91R4</i> |
| <i>Solyc11g010790</i>       | <i>UGT91R2</i> | <i>Sopen11g005590</i>       | pseudogene     |
| <i>Solyc11g010800</i>       | pseudogene     | -                           | -              |
| <i>Solyc11g010810</i>       | <i>UGT91R3</i> | <i>Sopen11g005580</i>       | pseudogene     |

<sup>1</sup> Sol Genomics Network (<https://solgenomics.net/>)

Supplementary Table 3: Primers using in this study.

| Target gene ID                                          | Forward (5'-3')                     | Reverse (5'-3')                             | Objectives             |
|---------------------------------------------------------|-------------------------------------|---------------------------------------------|------------------------|
| <i>Solyc11g010780 &amp; Sopen11g005570 (UGT91R1/R4)</i> | AGATCGATGCATGGA<br>GAGAGA           | GGTAATTGAATCAATT<br>CATCATC                 | Quantitative<br>RT-PCR |
| <i>GAPDH</i>                                            | CAAGGATTGGAGAGG<br>TGGAA            | CCTGACTGTGAGGTC<br>AACCA                    | Quantitative<br>RT-PCR |
| <i>Solyc11g010740</i>                                   | ATGGAAACTCAACTT<br>GTCAAATCC        | ACCAACCCCTTTGTCC<br>TGTAG                   | RT-PCR                 |
| <i>Solyc11g010760</i>                                   | GCCACAAAATTTTCGTT<br>TATCTCAAC      | CTAAATATCGAACTCA<br>ATTCCTTTGC              | RT-PCR                 |
| <i>Solyc11g010780</i>                                   | CTTCGAAGCTTCCATG<br>AAAGGA          | GTATCGAATACGCCAT<br>TTTCTTC                 | RT-PCR                 |
| <i>Solyc11g010790</i>                                   | CTTCCACCAAGTCTTA<br>TTCCC           | TTCTCCGAAACCTTCT<br>GGTAG                   | RT-PCR                 |
| <i>Solyc11g010810</i>                                   | TCAGCTCCTGATTTC<br>TACTC            | GTTCTTCGAAACCTTC<br>TGGTAC                  | RT-PCR                 |
| <i>ACTIN</i>                                            | ATGACTCAAATCATGT<br>TTGAGAC         | CAGTGAATTCCTTGCT<br>CATAC                   | RT-PCR                 |
| <i>UGT91R1-Target-1</i>                                 | ATTGGGTTTCAAACG<br>GAACCCATT        | AAACAATGGGTTCGG<br>TTTGAAACC                | gRNA cloning           |
| <i>UGT91R1-Target-2</i>                                 | ATTGTGAAATTCGAAT<br>GACGCCGG        | AAACCCGGCGTCATT<br>CGAATTTC                 | gRNA cloning           |
| <i>UGT91R1-Seq</i>                                      | CGATTCCACAAGACA<br>ATTGG            | AGCAGAAAAGTGTA<br>A<br>CCCAC                | Sequencing             |
| <i>UGT91R1-OX</i>                                       | ACTGTTGATAGTCGAA<br>TGGCGGAAAACGGAA | TGTAGTCCATGTCGAC<br>TGCTTTAATCTTTTCA<br>TAG | UGT91R1-OX<br>cloning  |