TomAP manual

TomAP — Tomato multi-omics data Analysis Platform

Solyc03g111280.1

Quick search

Solanum lycopersicum

Solanum lycopersicum, the second most important vegetable crop in the world, is also an important model plant for the study of fruit ripening and disease resistance. Abundant germplasm resources and ease of transformation facilitate the first functional characterization of key genes which are involved in ethylene biosynthesis and fruit ripening. However, the function of tomato genes remains largely unknown. Its fruit is an important source of antioxidant compounds, such as lycopene, β-carotene, anthocyanin and ascorbic acid. Among these secondary metabolites (SMs), lycopene and anthocyanin can prevent some diseases and delay aging which benefit to human health. Therefore, it will be of great significance to study the pathways related to SMs biosynthesis in tomato.

About the database

We integrated 343 transcriptome and 136 epigenome data sets to construct co-expression network and define chromatin state, respectively. We identified 4,387 functional modules from global network and two conditional networks with expression view at multi-dimensional levels (development and stress), respectively, which covers diverse functions like secondary metabolite (SM) biosynthesis, pathogen resistance, fruit development and ripening. We added predicted protein-protein interaction (PPI) pairs and miRNA targets into the network. The visualization of chromatin states and association with protein-coding genes and epigenetic marks in genome were shown in UCSC genome browser. Some support analysis tools, such as gene set enrichment analysis (GSEA), module enrichment analysis, cis-element enrichment analysis and ID conversion, were also provided. We hope TomAP platform can help clarify the regulatory mechanism and identify functional genes or modules associated with important agronomic traits.

Contact us

If you have any questions or suggestions, please contact us: jjshe@cau.edu.cn, and zhensu@cau.edu.cn. If you want to know more about our work, please click here.

News

annotated.

2018.1.20: Several analysis tools, such as GSEA, module enrichment analysis, is supported in TomAP!

2017.5.02: The miRNA detail information pages is available.

update news

Links

Sol Genomics Network

Tomato Genetics Resource Center

TFGD

TomatoNET

TOMATOMICS

TomExpress

CoxPathDB

MethBank

Visitor Tracking
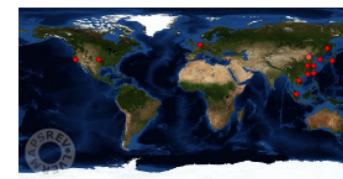
visitor tracking

Co-expression Network analysis

1. Global network search by typing your interested gene list

Gene list:
```
Solyc07g043490.1
```
Example

☑ Positive ☑ Negative ☑ Protein-Protein interaction ☑ miRNA-target

GO   RESET

2. Tissue preferential network search by typing your interested gene list

Gene list:
```
Solyc10g078220.1
Solyc10g078230.1
Solyc10g078240.1
```
Example

☑ Positive ☑ Negative ☑ Protein-Protein interaction ☑ miRNA-target
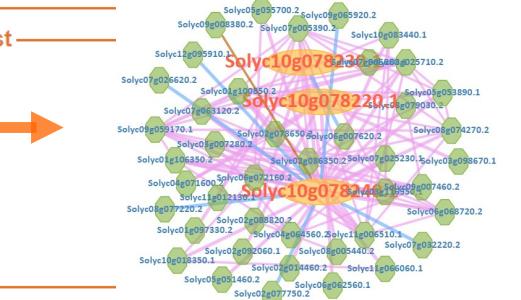
GO   RESET

3. Stress differential network search by typing your interested gene list

Gene list:
```
Solyc03g111280.1
Solyc03g111290.1
```
Example

☑ Positive ☑ Negative ☑ Protein-Protein interaction ☑ miRNA-target

GO   RESET
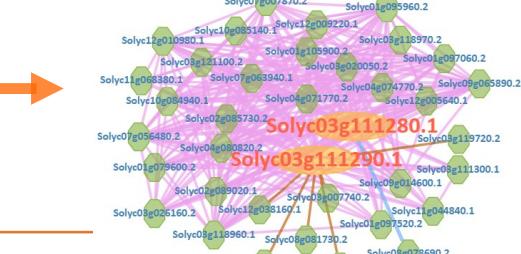
Motif analysis

GSEA analysis

Module enrichment analysis

Expression profiling analysis

Network compare
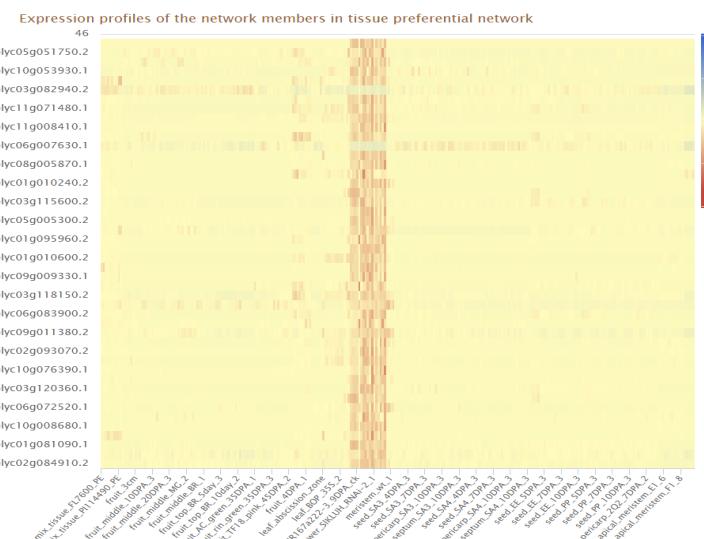
Module search

By gene search

Functional Module Search Results

This page displays **4** functional modules with the "steroidal glycoalkaloid biosynthesis" annotation.

module search

Input one interested gene or genelist to see detailed functional modules.

view all functional modules

Solyc07g043490.1
Solyc12g006460.1
Solyc08g077080.1
Solyc07g043410.1
Solyc12g088700.1
Solyc06g051800.2

Example

GO RESET

Module ID	Function Annotation
CFinderADM000244	metabolic process linalool biosynthesis II superpathway of linalool biosynthesis steroidal glycoalkaloid biosynthesis Monoterpenoid_biosynthesis Peroxisome Carotenoid_biosynthesis formation of glycosidic bonds, GlycosylTransferases: GTnc
CFinderADM000498	Transcription factor: TCP Transcription factor: RWP-RK fatty-acyl_CoA_reductase_(alcohol-forming)_activity steroidal glycoalkaloid biosynthesis Quorum_sensing

CFinderADM000244 module

Module search results

This page displays **12** functional modules basing on your interested gene or gene list.

| Module Member	Module ID	Function Annotation	Category
Solyc07g043490.1	TreatCFM000826	phosphatidylinositol phosphate kinase activity phosphatidylinositol metabolic process serine-type endopeptidase activity formation of glycosidic bonds, GlycosylTransferases: GTnc steroidal glycoalkaloid biosynthesis D-*myo*-inositol (1,4,5)-trisphosphate biosynthesis 3-phosphoinositide biosynthesis Choline metabolism in cancer	Stress differential network
Solyc08g077080.1	CFinderADM000244	metabolic process linalool biosynthesis II superpathway of linalool biosynthesis steroidal glycoalkaloid biosynthesis Monoterpenoid_biosynthesis Peroxisome Carotenoid_biosynthesis formation of glycosidic bonds, GlycosylTransferases: GTnc	global network

Chromatin state analysis

Four key genes involved in fruit ripening
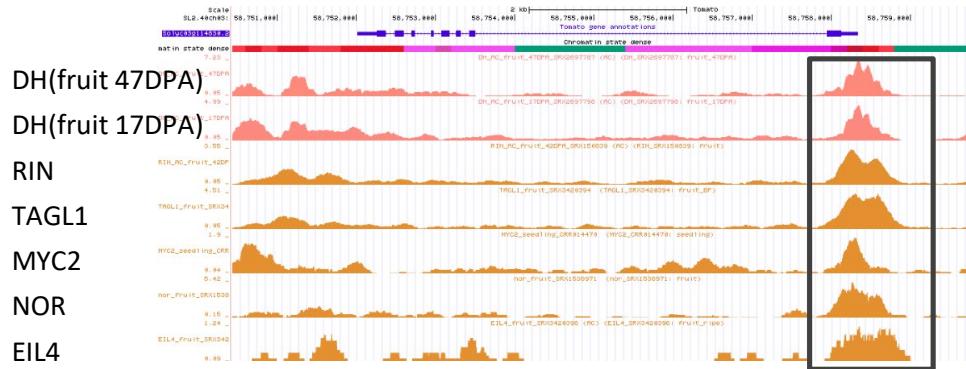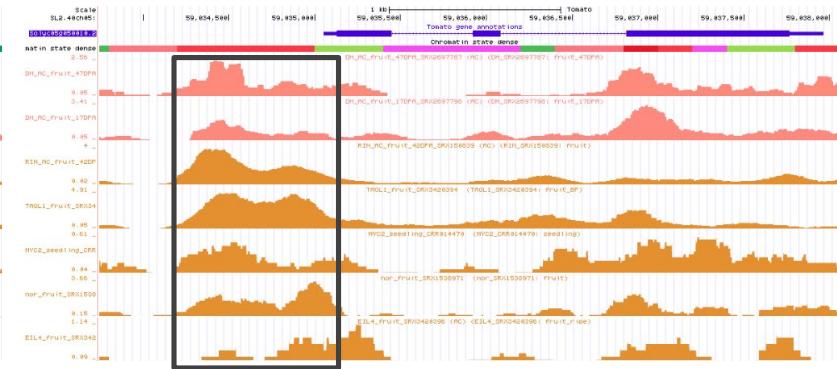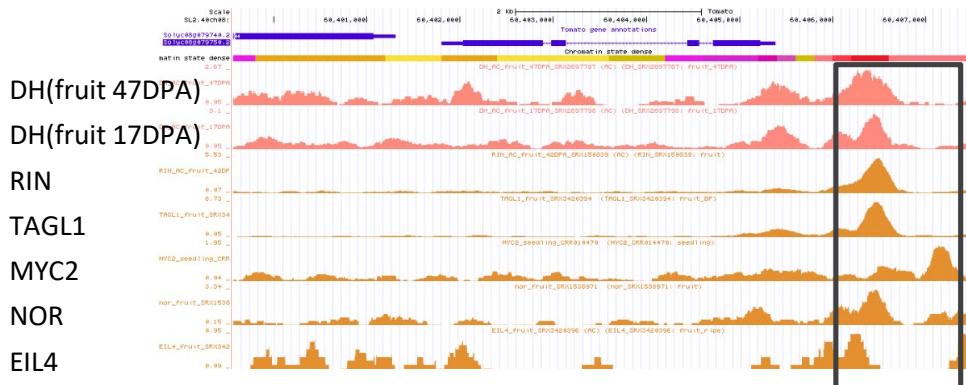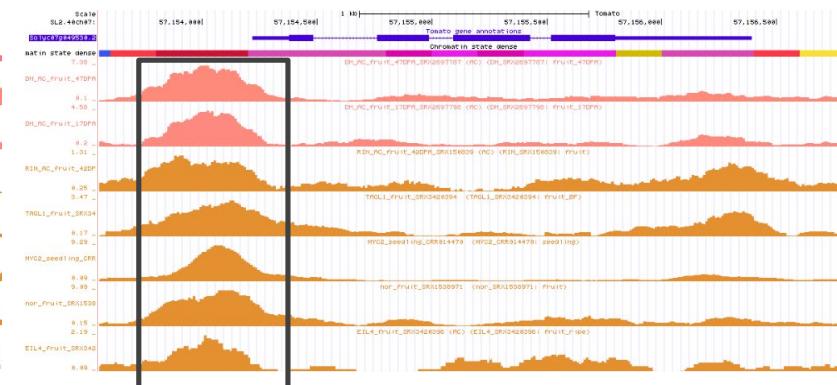
Network and chromatin state analysis

Eight glycoalkaloid metabolism (GAME) genes

Gene	Alias	Functional annotation
Solyc07g043490.1	GAME1	UDP-glucose glucosyltransferase
Solyc07g043410.1	GAME2	UDP-xylose xylosyltransferase
Solyc07g043460.2	GAME6	Cytochrome P450, subfamily 72
Solyc07g043420.2	GAME11	2-oxoglutarate-dependent dioxygenase
Solyc07g043480.1	GAME17	UDP-glucose glucosyltransferase
Solyc07g043500.1	GAME18	UDP-glucosyltransferase
Solyc12g006460.1	GAME4	Cytochrome P450, subfamily 88
Solyc12g006470.1	GAME12	Amine oxidase family protein

Chromatin state analysis
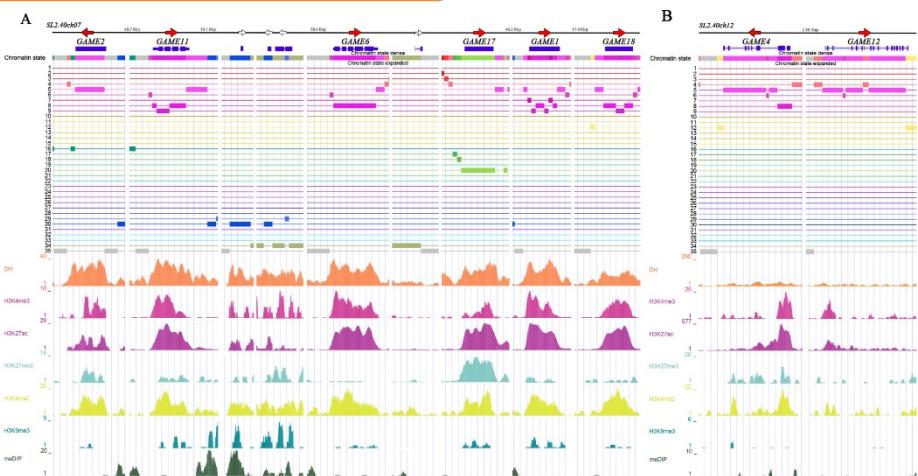
Note: *GAME* gene is essential for the synthesis of steroidal glycoalkaloid.

Gene set enrichment analysis (GSEA)

Gene set enrichment analysis (PlantGSEA)

The GO terms, gene families, pathway information from our functional annotations were used a[s] could submit gene list to obtain significantly gene sets.

Choose Gene Sets

- ☑ G1: Gene ontology gene sets
  - ☑ BP: GO biological process　　☑ CC: GO cellular component　　☑ MF: GO molecular function
- ☑ G2: Gene Family Based gene sets
- ☑ G3: Curated gene sets
  - ☑ PlantCyc: PlantCyc gene sets　　☑ KEGG: KEGG gene sets　　☑ LIT: References colleted gene sets
- ☑ G4: MicroRNA Targets
- ☐ G5: CFinder predicted modules based on co-expression network
  - ☐ Global network module
  - ☐ Tissue preferential network module
  - ☐ Stress differential network module

Choose Background

- ● Suggested background (Whole genome level)
- ○ Customized background

Submit Your Query

```
Solyc06g074710.1
Solyc07g042490.1
Solyc08g077490.1
Solyc12g088170.1
Solyc05g021580.2
Solyc07g008600.1
Solyc04g040130.1
Solyc03g007230.2
Solyc11g011240.1
Solyc08g078190.1
Solyc01g094130.2
Solyc04g074770.2
Solyc03g078330.1
Solyc04g021550.2
```
Example

Or you can upload file (size <= 5MB)

选择文件 | 未选择任何文件

GO **RESET**

GO term
plantCyc
KEGG pathway
Literature
Gene family
miRNA target
Functional module

GSEA results

Description	Category	NO. Genes in Overlap (k)	p value	FDR
Comparative Transcriptome Profiling between low-K+ tolerant JZ34 and low-K+ sensitive JZ18 of Tomato Genotypes in Response to Potassium-Deficiency Stress.	LIT	37	1.37e-26	1.14e-25
Comparative Transcriptome Profiling between low-K+ tolerant JZ34 and low-K+ sensitive JZ18 of Tomato Genotypes in Response to Potassium-Deficiency Stress.	LIT	14	8.78e-10	3.66e-09
Comparative Transcriptome Profiling between low-K+ tolerant JZ34 and low-K+ sensitive JZ18 of Tomato Genotypes in Response to Potassium-Deficiency Stress.	LIT	17	6.05e-09	1.68e-08
GO:0004144 diacylglycerol_O-acyltransferase_activity GOslim:molecular_function	GO_MF	4	2.16e-06	6.55e-4
Comparative Transcriptome Profiling between low-K+ tolerant JZ34 and low-K+ sensitive JZ18 of Tomato Genotypes in Response to Potassium-Deficiency Stress.	LIT	7	4.47e-4	9.31e-4
GO:0048046 apoplast, GOslim:cellular_component	GO_CC	4	1.4e-4	3.58e-3
GO:0045017 glycerolipid_biosynthetic_process GOslim:biological_process	GO_BP	3	4.18e-05	7.38e-3
wax esters biosynthesis I	PlantCyc	4	4.59e-05	0.0116
GO:0006073 cellular glucan metabolic process, GOslim:biological_process	GO_BP	4	1.4e-4	0.0124
hydrolysis and/or rearrangement of glycosidic bonds◆◆ Glycoside Hydrolases◆◆ GH89	GFam	1	1.54e-4	0.0133
GO:0016762 xyloglucan:xyloglucosyl transferase activity, GOslim:molecular_function	GO_MF	4	1.4e-4	0.0213
GO:0004866 endopeptidase inhibitor activity, GOslim:molecular_function	GO_MF	3	2.36e-4	0.0239
Plant_hormone_signal_transduction	KEGG	4	1.54e-4	0.0264
GO:0016747 transferase activity, transferring acyl groups other than amino-acyl groups, GOslim:molecular_function	GO_MF	6	4.56e-4	0.0346

ID conversion

ID conversion

Gene list:
```
Solyc10g081650.1
Solyc05g012020.2
Solyc02g077920.2
Solyc07g055920.2
Solyc02g071730.2
Solyc01g095080.2
Solyc07g049530.2
```

Example (SL2.40)

SL2.40->SL3.0 ▼

GO   RESET

Note: ID conversion data is obtained by the combination of blast alignment and Inparanoid algorithm.

ID conversion result

SL2.40	SL3.0	Method
Solyc10g081650.1	Solyc10g081650.2	Inparanoid algorithm
Solyc01g095080.2	Solyc01g095080.3	Inparanoid algorithm
Solyc07g049530.2	Solyc07g049530.3	Inparanoid algorithm
Solyc07g055920.2	Solyc07g055920.3	Inparanoid algorithm
Solyc02g071730.2	Solyc02g071730.3	Inparanoid algorithm
Solyc05g012020.2	Solyc05g012020.3	Inparanoid algorithm
Solyc02g077920.2	Solyc02g077920.3	Inparanoid algorithm