

Welcome to RAP2 Galaxy Explorer

This user manual guides you for basic and professional application step by step.

1) Register in RAP2 Galaxy Explorer

RAP2 Galaxy Explorer
Welcome to the RAP2 Galaxy Explorer -- a webserver to make gene prediction and GWAS biological interpretation.

Tools to make gene expression and GWAS biological interpretation

RAP2 Galaxy Explorer

Model Build

- Gene expression
- Gene annotation
- Sequence feature
- Network connection

Gene Prediction

- Gene Functions Prediction
- Gene predict functions
- New Candidates Prediction
- New candidates

GWAS Interpretation

- GO enrichment
- Prioritize genes outside
- Filter significant genes

Improve GWAS

Prioritized Performance

workflow Standard input and output

Get started with RAP2 Galaxy Explorer

If you are new to Galaxy, please [take a guide tour](#) for a comprehensive understanding of basic procedure (e.g., how to upload your files, how to display and download the data) through Galaxy user

After select **Register** button, you will go into the register form:

Create account

Email address:
Basic_Application@163.com

Password:

Confirm password:

Public name:
basic_application

Your public name is an identifier that will be used to generate addresses for information you share publicly. Public names must be at least three characters in length and contain only lower-case letters, numbers, dots, underscores, and dashes ('.', '_', '-').

Submit

Then click **Return to the home page**:

Now logged in as Basic_Application@163.com.
[Return to the home page.](#)

Select the User menu to **Logged in as Basic_Application@163.com**:

RAP2 Galaxy Explorer
Welcome to the RAP2 Galaxy Explorer -- a webserver to make gene prediction and GWAS biological interpretation.

Tools to make gene expression and GWAS biological interpretation

RAP2 Galaxy Explorer

Logged in as Basic_Application@163.com

- Preferences
- Custom Builds
- Logout
- Saved Histories
- Saved Datasets
- Saved Pages

After the registration, you can use the RAP2 Galaxy Explorer smoothly.

2) For basic application, we provide four tools: *Gene Expression QC*, *Gene Functions Prediction*, *New Candidates Prediction*, and *GWAS Interpretation*.

- Select *Gene Expression QC* to filter low quality samples (marginal from the population) and return the high quality samples (consistence population structure) for further analysis.

First, you should upload a gene expression profile into the Galaxy history:

Gene Expression QC gene expression quality control (Galaxy Version 1.0.0)

gene expression profile

What it does

gene expression quality control is used to filter low quality samples (marginal from the population) and return the high quality samples (consistence population structure) for further analysis.

Inputs

gene expression profile - the row represents the genes and the column represents the samples

	Samples1	Samples2	Samples3	Samples4
AT10010101	6.135	6.690	6.345	6.07
AT10010102	6.330	6.325	5.950	5.730
AT10010103	9.495	9.275	8.710	8.135
AT10010105	11.730	11.540	11.650	11.620

Outputs

PDF1 - PCA conducted on samples

PCA Conducted on Samples

Summary gene test patterns

	Samples1	Samples2	Samples3	Samples4
AT10010101	6.135	6.690	6.345	6.07
AT10010102	6.330	6.325	5.950	5.730
AT10010103	9.495	9.275	8.710	8.135
AT10010105	11.730	11.540	11.650	11.620

After click the **upload button** (red rectangle), you can Choose local file (e.g., AraGeneExp.txt can be download from <https://github.com/cma2015/RAP2/tree/master/exampleData>):

Download from web or upload from disk

Regular Composite Collection

You added 1 file(s) to the queue. Add more files or click 'Start' to proceed.

Name	Size	Type	Genome	Settings	Status
AraGeneExp.txt	178.7 MB	Auto-detect	Additional Species Are B...		

Type (set all): Auto-detect Genome (set all): Additional Species Are B...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

After select **Start** the file will be uploaded into the Galaxy history:

Download from web or upload from disk

Regular Composite Collection

Name	Size	Type	Genome	Settings	Status
AraGeneExp.txt	178.7 MB	Auto-detect	Additional Species Are B...		100%

Type (set all): Auto-detect Genome (set all): Additional Species Are B...

Choose local file Choose FTP file Paste/Fetch data Pause Reset Start Close

History

search datasets

Unnamed history

178.72 MB

1: AraGeneExp.txt

Then, select the file in the **gene expression profile** window from Galaxy history:

Gene Expression QC gene expression quality control (Galaxy Version 1.0.0)

gene expression profile

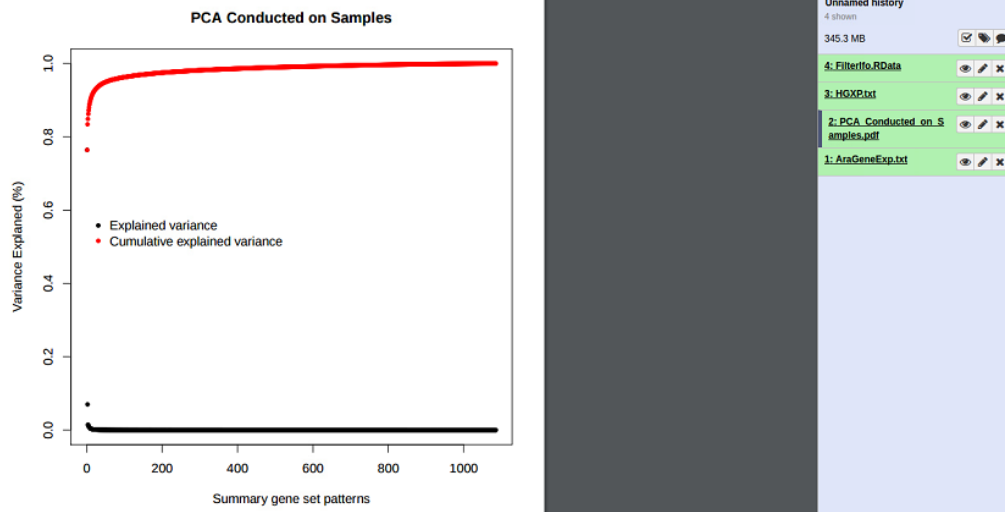
1: AraGeneExp.txt

Execute

After click **Execute**, the *Gene Expression QC* will be work:



These three files will be output. You can view the output files through the eye button:



And download through the **disk button** (red rectangle):



- b. Select **Gene Functions Prediction** to predict functions of an interested gene.
First, you should select the **species** (e.g., *Arabidopsis*),
Second, you should input a gene (e.g., AT1G01030),
For basic application, keep the **gene function prediction** by default (generated from our data):

Gene Functions Prediction predict functions of an interest gene (Galaxy Version 1.0.0)

Options

species

Arabidopsis

a gene looking for its functions

AT1G01030

gene functions prediction

default

Execute

What it does

- predict functions of an interest gene is used to predict the possible functions of the interest gene based on the pre-prepared GO annotations.
- The predict functions includes two parts: label and unlabel represent the gene was experimentally verified or not, respectively.

Inputs

species - Arabidopsis and Maize are supported currently

a gene looking for its functions - the interest gene

AT1G01030

gene functions prediction - the gene functions prediction file

geneName	score	GO	domain	annotate	GODescription
AT1G01030	1.000	GO:1901371	BP	label	regulation of leaf morphogenesis
AT1G01030	1.000	GO:1905421	BP	label	regulation of plant organ morphogenesis
AT1G01040	1.000	GO:0004521	MF	unlabel	endonuclease activity namespace: molecular_function name: endonuclease activity
AT1G01050	0.521	GO:0006796	BP	unlabel	phosphate-containing compound metabolic process

Outputs

geneFunctions - the gene's predict functions (label or unlabel represents the gene was experimentally verified or not)

geneName	description
AT1G01030	[NCBI Source:UniProtKB/TrEMBL:Acc:AA178W3T3]

geneName	score	GO	domain	annotate	GODescription
AT1G01030	1.000	GO:1901371	BP	label	regulation of leaf morphogenesis
AT1G01040	1.000	GO:1905421	BP	label	regulation of plant organ morphogenesis
AT1G01030	1.000	GO:0010476	BP	unlabel	gibberellin mediated signaling pathway

Note

- It should be note that for most common application, the users only select the species and input the interest gene, the result will be output based on default data.
- For advanced application, the professional users can select gene functions prediction by choosing the responsive data uploading from Galaxy calculated from their personal data through Build RAP2 Model tool.

The red rectangle is the main run window, the blue rectangle is the help window.

After click **Execute** button, the *Gene Functions Prediction* will be work:

1 job has been successfully added to the queue - resulting in the following datasets:

5: geneFunctions.txt

You can check the status of queued jobs and view the resulting data by refreshing the History pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

History

search datasets

Unnamed history

5 shown

345.3 MB

5: geneFunctions.txt

The geneFunctions.txt will be output:

geneName	description
AT1G01030	WGA3 [Source:UniProtKB/TrEMBL:Acc:AA178W3T3]

geneName	score	GO	domain	annotate	GODescription
AT1G01030	1	GO:1901371	BP	label	regulation of leaf morphogenesis
AT1G01030	1	GO:1905421	BP	label	regulation of plant organ morphogenesis
AT1G01030	0.937	GO:1906618	BP	label	regulation of shoot system morphogenesis
AT1G01030	0.81	GO:0048366	BP	label	leaf development namespace: biological_process name: leaf development
AT1G01030	0.784	GO:0048827	BP	label	phyllome development namespace: biological_process name: phyllome development
AT1G01030	0.755	GO:2000624	BP	label	regulation of leaf development
AT1G01030	0.435	GO:0009088	BP	label	flower development namespace: biological_process name: flower development
AT1G01030	0.414	GO:0095567	BP	label	reproductive shoot system development
AT1G01030	1	GO:0010476	BP	unlabel	gibberellin mediated signaling pathway

History

search datasets

Unnamed history

5 shown

345.44 MB

5: geneFunctions.txt

- c. Select *New Candidates Prediction* to predict new candidates of an interest gene set.

First, you should select the **species** (e.g., *Arabidopsis*),

Second, you should input a gene set (e.g., AT1G01120,AT1G06080,AT1G13580,AT1G19440,AT1G25450,AT1G67730,AT1G68530,AT1G71160,AT1G80950,AT2G15090,AT2G16280,AT2G26250,AT2G31360,AT2G34770,AT2G45670,AT3G23840,AT3G25540,AT3G28910,AT3G54010,AT4G13840,AT4G24510,AT4G34520,AT4G36830,AT5G10480,AT5G23190,AT5G47120,AT5G49070,AT4G34250,AT4G34510),

For basic application, keep the **gene set patterns** by default (generated from our data):

New Candidates Prediction predict new candidates of an interest gene set (Galaxy Version 1.0.0)

Options

species

Arabidopsis

interest gene set

AT1G01120,AT1G06080,AT1G13580,AT1G19440,AT1G25450,AT1G67730,AT1G68530,AT1G71160,AT1G80950,AT2G15090,AT2G16280,AT2G26250,AT2G31360,AT2G34770,AT2G45670,AT3G23840,AT3G25540,AT3G28910,AT3G54010,AT4G13840,AT4G24510,AT4G34520,AT4G36830,AT5G10480,AT5G23190,AT5G47120,AT5G49070,AT4G34250,AT4G34510

gene set patterns

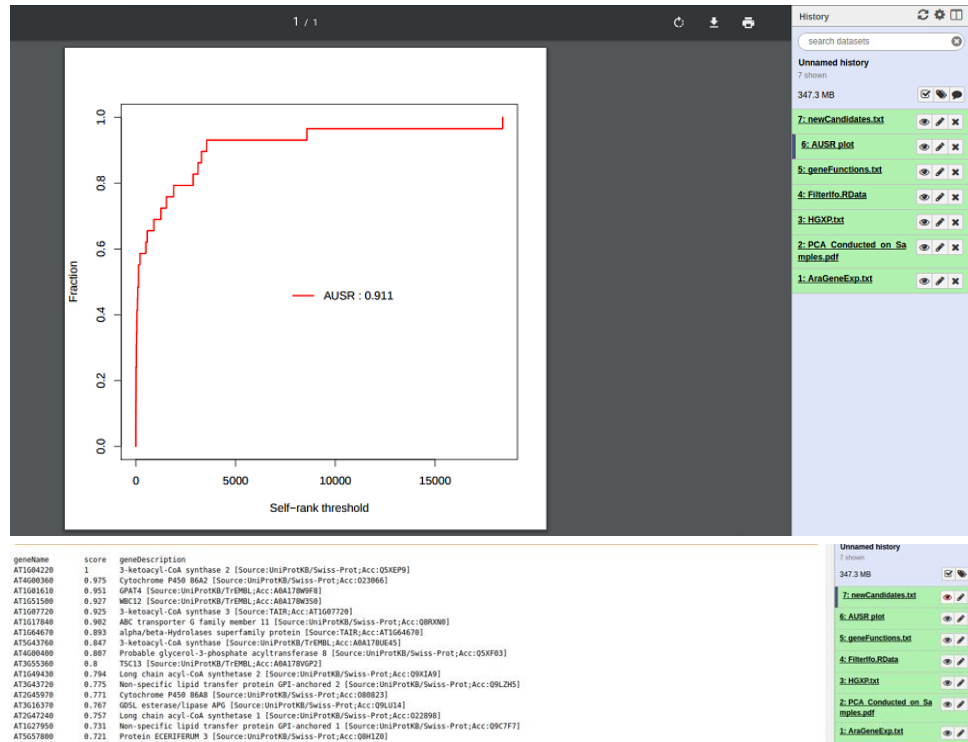
default

Execute

After click **Execute** button, the *New Candidates Prediction* will be work:

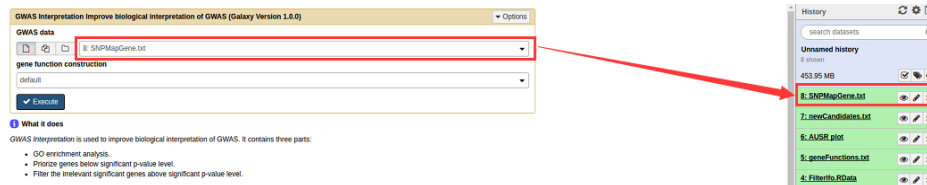


The **AUSR plot** and **newCandidates.txt** will be output:



- d. Select **GWAS Interpretation** to improve biological interpretation of GWAS.

First, you should upload a gene expression profile into the Galaxy history (e.g., SNPMapGene.txt can be download from <https://github.com/cma2015/RAP2/tree/master/exampleData>), Then, select the file in the **GWAS data** window from Galaxy history, For basic application, keep the **gene function construction** by default (generated from our data):



After click **Execute** button, the *GWAS Interpretation* will be work:



The **Geneplot.pdf**, **FilterSigGene.pdf**, **highQualityGene.txt**, **geneSetEnrichment.txt**,

Figure 1: Genomic tracks and gene expression analysis.

Top Panel: Manhattan Plot

The top panel displays a Manhattan plot showing the association of genomic regions with the phenotype. The x-axis represents chromosomes (1 to 5), and the y-axis represents the negative logarithm of the p-value ($-\log_{10}(p)$). A significant peak is observed on chromosome 4, reaching a $-\log_{10}(p)$ value of approximately 7.5.

Middle Panel: Heatmap

The middle panel is a heatmap showing the expression levels (log2(RPKM)) of 13 genes across 13 samples. The color scale ranges from -0.4 (blue) to 0.8 (red). The genes are listed on the y-axis, and the samples are listed on the x-axis. The heatmap shows a clear pattern of gene expression across the samples.

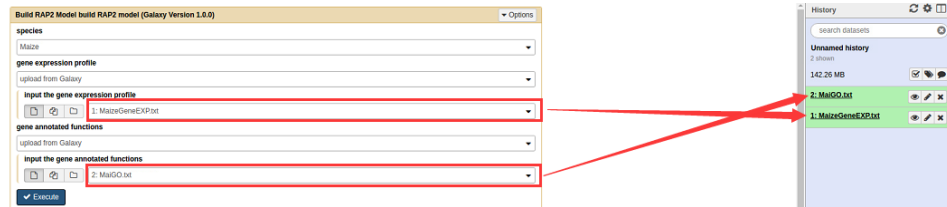
Bottom Panel: Gene Expression Data

gene name	description	GO	fdr	function	domain	PCC	description
AT4G00720	Shaggy related protein kinase theta [Source:UniProtKB/TrEMBL;Acc:Q0W04Y]						
AT5G10030	AT5G10030 [Source:UniProtKB/TrEMBL;Acc:Q24333]						
AT5G10140	AT5G10140 [Source:UniProtKB/TrEMBL;Acc:Q09931]						
AT4G00650	Inactive protein FRIGIDA [Source:UniProtKB/Swiss-Prot;Acc:Q07293]						
AT4G00730	Homeobox-leucine zipper protein ANTHOCYANINLESS 2 [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	B3 domain-containing transcription repressor VALL [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	delay of germination 1 [Source:TAIR;Acc:AT5G10140]						
AT5G10140	Mediator of RNA polymerase II transcription subunit 12 [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	Putative ubiquitin-like-specific protease 1B [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	Mediator of RNA polymerase II transcription subunit 12 [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	Protein of unknown function (DUF3741) [Source:TAIR;Acc:AT5G10140]						
AT5G10140	Gamma-tubulin complex component [Source:UniProtKB/TrEMBL;Acc:Q0W012]						
AT5G10140	AT5G10140 [Source:UniProtKB/TrEMBL;Acc:Q0W012]						
AT5G10140	Plant URB domain-containing protein 9 [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	COP1-interacting protein-like protein [Source:UniProtKB/TrEMBL;Acc:Q0W012]						
AT5G10140	FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: Fe superoxide dismutase 2 (TAD2;AT5G10140); has 34 Blast hits to 36 proteins in 11 spec. // rhca - 0; Bacteria - 0; Metazoa - 0; Fungi - 34; Viruses - 0; Other Eukaryotes - 0 [Source:NCBI;BLAST]; [Source:TAIR;Acc:AT5G10140]						
AT5G10140	Protein OUPREAR OF PL [Source:UniProtKB/Swiss-Prot;Acc:Q0W012]						
AT5G10140	Microfibrillar-associated protein-like protein [Source:UniProtKB/TrEMBL;Acc:Q22281]						

- 3) For **advanced application**, we provide four tools: ***Build RAP2 Model***, ***Gene Functions Prediction***, ***New Candidates Prediction***, and ***GWAS Interpretation***. It should be note that, after build RAP2 model based on your personal data to fit for your rigorous demand, the following application is the same with those in the **basic application** by just selecting the corresponding

parameters **upload from Galaxy** history instead of default.

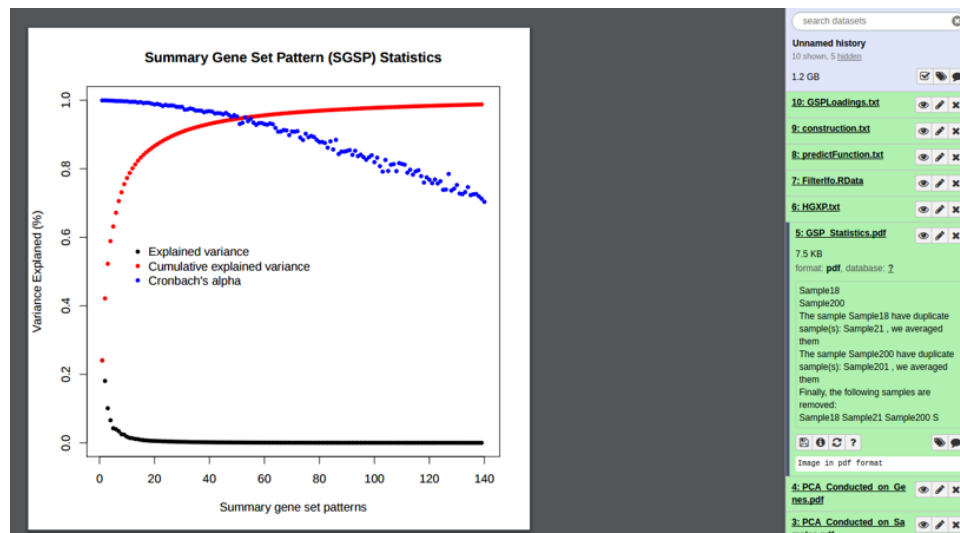
- a. Select **Build RAP2 Model** to build RAP2 model based on your personal data. We also provide default data to help you understand what we used to build our RAP2 model. First, upload the gene expression and GO data, then select them in the Galaxy history (we used the **Maize** as an example, the MaizeGeneEXP.txt and MaiGO.txt can be download from <https://github.com/cma2015/RAP2/tree/master/exampleData>):



After click **Execute**, the **Build RAP2 Model** will be work:



These eight files will be output. You can view the output files through the eye button:



- b. Select **Gene Functions Prediction** to predict functions of an interested gene. First, you should select the **species** (e.g., Maize), Second, you should input a gene (e.g., Zm00001d028815), For advanced application, select the **gene function prediction** from Galaxy history (generated from your personal data):

After click **Execute** button, the *Gene Functions Prediction* will be work:

The **geneFunctions.txt** will be output:

- c. Select *New Candidates Prediction* to predict new candidates of an interest gene set.

First, you should select the **species** (e.g., Maize),

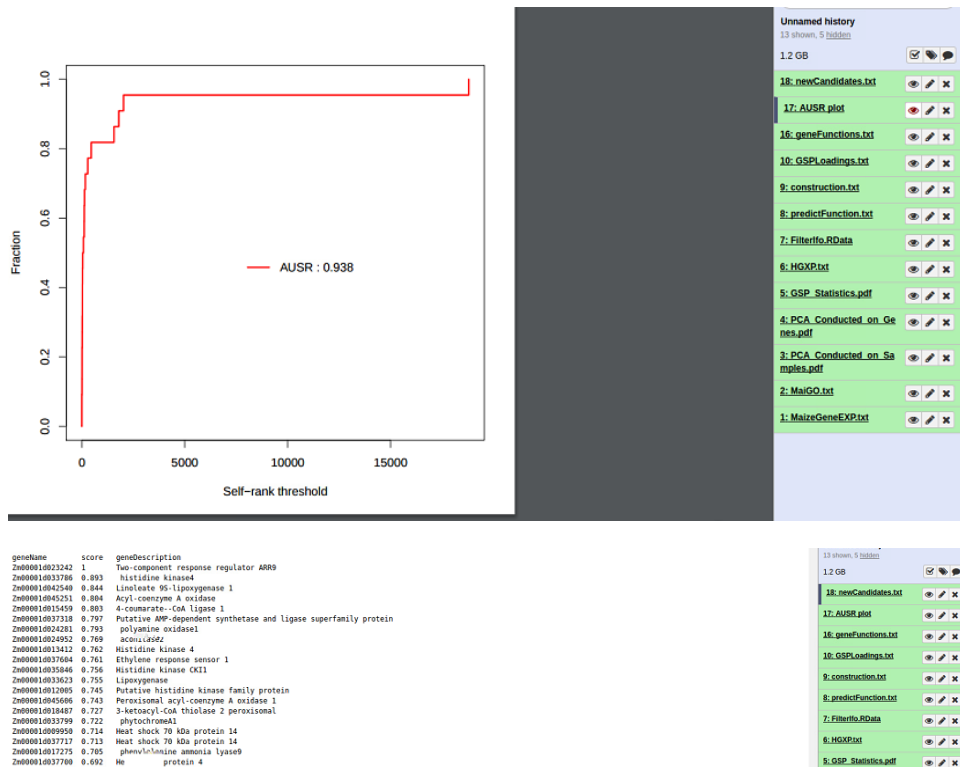
Second, you should input a gene set (e.g.,

Zm00001d028816,Zm00001d014848,Zm00001d042066,Zm00001d015521,Zm00001d054044,Zm00001d001865,Zm00001d026594,Zm00001d042312,Zm00001d046170,Zm00001d017274,Zm00001d002000,Zm00001d012675,Zm00001d011849,Zm00001d028815,Zm00001d027511,Zm00001d028814,Zm00001d053675,Zm00001d014297,Zm00001d048046,Zm00001d050768,Zm00001d009990,Zm00001d042541),

For advanced application, select the **gene set patterns** from Galaxy history (generated from your personal data):

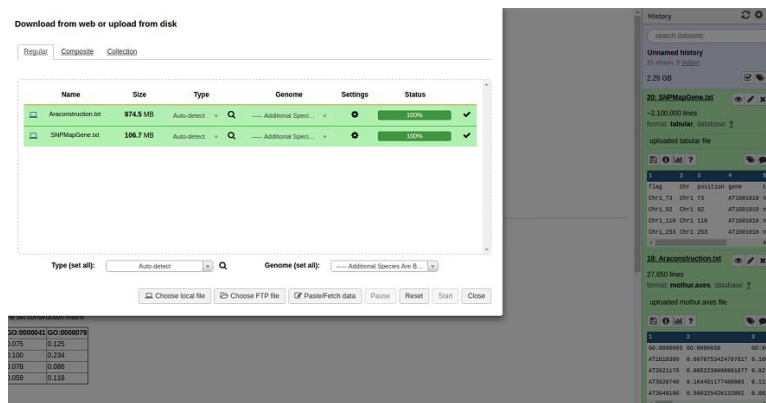
After click **Execute** button, the *New Candidates Prediction* will be work:

The **AUSR plot** and **newCandidates.txt** will be output:

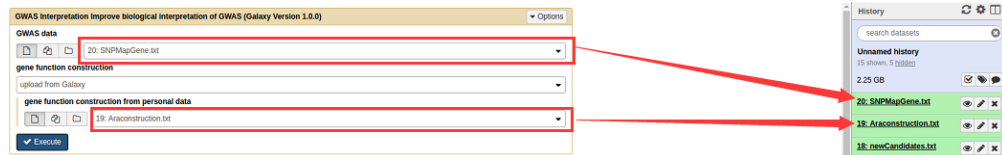


Note:

- (i) It should be note that the maize gene expression data contains 279 samples of 36,580 genes, the maize annotation data contains 97 GO terms of 168 genes (download from <https://github.com/cma2015/RAP2/tree/master/exampleData>). It takes about 3 hours to build the RAP2 model. While for *Arabidopsis*, gene expression data contains 1,096 samples of 20,356 genes, the annotation data contains 2623 GO terms of 9509 genes. It takes about 3 days to build the RAP2 model. For efficient guide, we only provide how to build RAP2 model on the maize data, it is the same process with *Arabidopsis*.
- (ii) Since the experimentally verified genes are not large enough for improving biological interpretation of GWAS. Currently, we only support Arabidopsis for this tool.
- (iii) For efficient guide, we upload the GWAS data (e.g., SNPMapGene.txt) and the gene function construction (e.g., Araconstruction.txt) generated from our default data (the SNPMapGene.txt and Araconstruction.txt can be download from <https://github.com/cma2015/RAP2/tree/master/exampleData>).



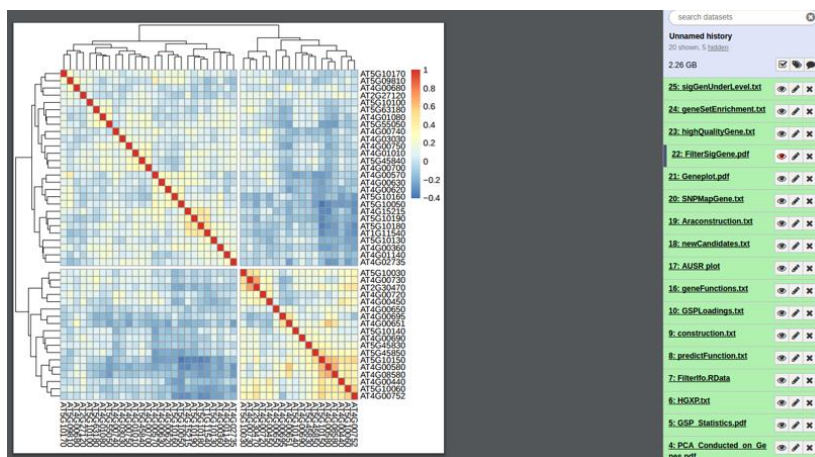
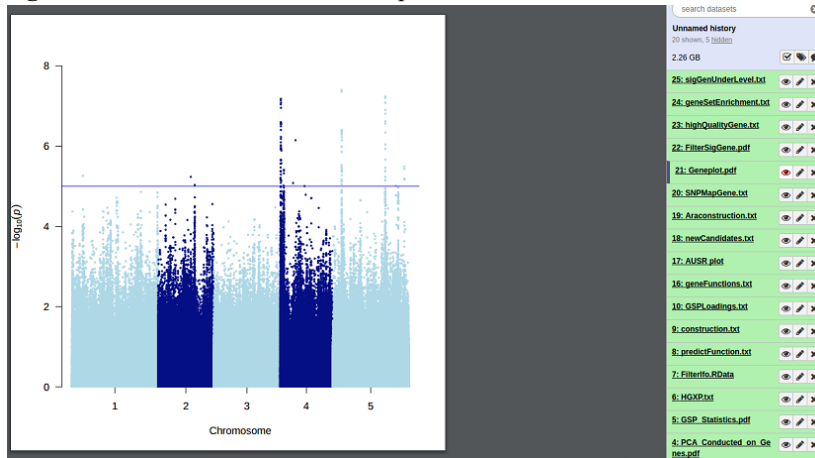
- d. Select **GWAS Interpretation** to improve biological interpretation of GWAS.
- First, you should upload a gene expression profile into the Galaxy history (e.g., SNPMapGene.txt can be download from <https://github.com/cma2015/RAP2/tree/master/exampleData>),
- Then, select the file in the **GWAS data** window from Galaxy history,
- For advanced application, select the **gene function construction** from Galaxy history (generated from your personal data):



After click **Execute** button, the **GWAS Interpretation** will be work:



The **Geneplot.pdf**, **FilterSigGene.pdf**, **highQualityGene.txt**, **geneSetEnrichment.txt**, **sigGenUnderLevel.txt** will be output:



geneName	description	
AT4G08728	Shaggy related protein kinase theta [Source:UniProtKB/TrEMBL;Acc:O0MW4]	
AT5G16130	AT5G16130 [Source:UniProtKB/TrEMBL;Acc:O24321]	
AT5G16140	AT5G16140 [Source:UniProtKB/TrEMBL;Acc:O20911]	
AT5G08739	Homeobox leucine zipper protein ANTHOCYANINLESS 2 [Source:UniProtKB/Swiss-Prot;Acc:O0WV12]	
AT5G34370	B3 domain-containing transcription repressor VAL2 [Source:UniProtKB/Swiss-Prot;Acc:O0W4L3]	
AT5G45839	delay of germination 1 [Source:TAIR;Acc:AT5G45839]	
AT5G06568	Mediator of RNA polymerase II transcription subunit 12 [Source:UniProtKB/Swiss-Prot;Acc:HKQYV6]	
AT4G06099	Putative ubiquitin-like-specific protease 18 [Source:UniProtKB/Swiss-Prot;Acc:O0S278]	
AT5G45850	Protein of unknown function (DUF488) [Source:TAIR;Acc:AT5G45850]	
AT4G06440	Protein of unknown function (DUF3741) [Source:TAIR;Acc:AT4G06440]	
AT5G06995	Gamma tubulin complex component [Source:UniProtKB/TrEMBL;Acc:FA2WF1]	
AT5G10868	AT5G10868 [Source:UniProtKB/TrEMBL;Acc:O0G0M8]	
AT5G08752	Plant ABC domain-containing protein 9 [Source:UniProtKB/Swiss-Prot;Acc:O4V2D3]	
AT4G06589	COP1-interacting protein-like protein [Source:UniProtKB/TrEMBL;Acc:O0S287]	
AT5G06051	FUNCTION IN: Molecular function unknown, ENVELOPE 2K: biological process unknown; LOCATED IN: endomembrane system, BEST Arabidopsis thaliana protein match is: Fe superoxide dismutase 2 (TAIR:AT5G051100.1); Has 34 Blast hits to 34 proteins in 11 spec ./../rcae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other eukaryotes - 9 [Source: NCBI BLAST] [Source:TAIR;Acc:AT5G06051]	
AT5G12159	Protein UPSTREAM OF FLC [Source:UniProtKB/Swiss-Prot;Acc:O9LX14]	
AT4G06589	Microfibrillar-associated protein-like protein [Source:UniProtKB/TrEMBL;Acc:O22281]	

GO	fr	function	domain
GO:000991	3.11e-04	trehalose metabolic process	biological process
GO:0006541	2.25e-04	glutamine metabolic process	biological process
GO:0006276	5.85e-04	lipid metabolic process	biological process
GO:0006631	4.35e-06	fatty acid metabolic process	biological process
GO:0006664	3.55e-04	glycolipid metabolic process	biological process
GO:0006899	3.89e-07	nitric oxide biosynthetic process	biological process
GO:0006272	6.18e-13	sulfate transport namespace: biological process	name: sulfate transport biological process
GO:0006010	4.72e-04	lipid biosynthetic process	biological process
GO:0009059	1.827e-05	macromolecule biosynthetic process	biological process
GO:0009074	2.705e-06	aromatic amino acid family catabolic process	biological process
GO:0009267	7.837e-05	cellular response to starvation	biological process
GO:0009414	2.281e-04	response to water deprivation	biological process
GO:0009415	2.43e-04	response to water	biological process
GO:0009555	2.018e-04	pollen development namespace: biological process	name: pollen development biological process
GO:0009511	5.902e-05	response to wounding	biological process
GO:0009617	4.255e-04	response to bacterium	biological process
GO:0009620	6.909e-05	response to fungus	biological process
GO:0009624	7.879e-04	response to nematode	biological process
GO:0009626	1.43e-06	plant-type hypersensitive response	biological process
GO:0009627	5.208e-05	systemic acquired resistance	biological process

geneName	-log10(pvalue)	fdr	PCC	description
AT1G39870	0.827	0	0.843	ABC transporter 0 family member 36 [Source:UniProtKB/Swiss-Prot;Acc:O9X1E2]
AT1G66570	2.424	0	0.873	ABC transporter 0 family member 39 [Source:UniProtKB/Swiss-Prot;Acc:O7PC84]
AT1G49240	0.939	0	0.875	Actin-8 [Source:UniProtKB/Swiss-Prot;Acc:O9Q293]
AT1G45370	1.501	0	0.817	Cytochrome P450 84B4 [Source:UniProtKB/Swiss-Prot;Acc:O08023]
AT3G34880	1.356	0	0.835	ABC transporter 0 family member 37 [Source:UniProtKB/Swiss-Prot;Acc:O9LPH0]
AT5G44520	1.556	0	0.928	Actin-12 [Source:UniProtKB/Swiss-Prot;Acc:PS3807]
AT3G12110	1.198	0	0.886	Actin-11 [Source:UniProtKB/Swiss-Prot;Acc:PS3496]
AT5G53370	1.495	0	0.928	Actin-4 [Source:UniProtKB/Swiss-Prot;Acc:PS3494]
AT1G01750	1.793	0	0.813	actin depolymerizing factor 11 [Source:TAIR;Acc:AT1G01750]
AT4G13230	0.895	0	0.895	ABC transporter 0 family member 38 [Source:UniProtKB/Swiss-Prot;Acc:O0G252]
AT4G32010	1.489	0	0.845	B3 domain-containing transcription repressor VAL2 [Source:UniProtKB/Swiss-Prot;Acc:O5CK44]
AT1G28420	0.712	0	0.813	Homeobox-DOT domain protein BLT1 [Source:UniProtKB/Swiss-Prot;Acc:FA0Y56]
AT3G16340	1.582	0	0.891	ABC transporter 0 family member 29 [Source:UniProtKB/Swiss-Prot;Acc:O94A18]
AT2G26310	0.482	0	0.835	PRC1 [Source:UniProtKB/TrEMBL;Acc:AAAT700A5]
AT2G29940	2.414	0	0.821	ABC transporter 0 family member 31 [Source:UniProtKB/Swiss-Prot;Acc:O7PC88]
AT3G33750	2.224	0	0.985	Actin-3 [Source:UniProtKB/Swiss-Prot;Acc:PGC347]
AT2G37620	1.348	0	0.985	Actin-3 [Source:UniProtKB/Swiss-Prot;Acc:PGC347]

History

Search datasets

Unnamed history

2.26 GB

25. sigGenEnrichment.txt

24. geneSetEnrichment.txt

23. HighQualityGene.pdf

22. FilterSigGene.pdf

21. Geneset.pdf

20. SNPMapGene.txt

History

Search datasets

Unnamed history

2.26 GB

25. sigGenEnrichment.txt

24. geneSetEnrichment.txt

23. HighQualityGene.txt

22. FilterSigGene.pdf

21. Geneset.pdf

History

Search datasets

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2.26 GB

25. sigGenEnrichment.txt

24. geneSetEnrichment.txt

23. HighQualityGene.txt

22. FilterSigGene.pdf

Thanks for reading this user manual for basic and advanced application!
Enjoy RAP2 Galaxy Explorer!