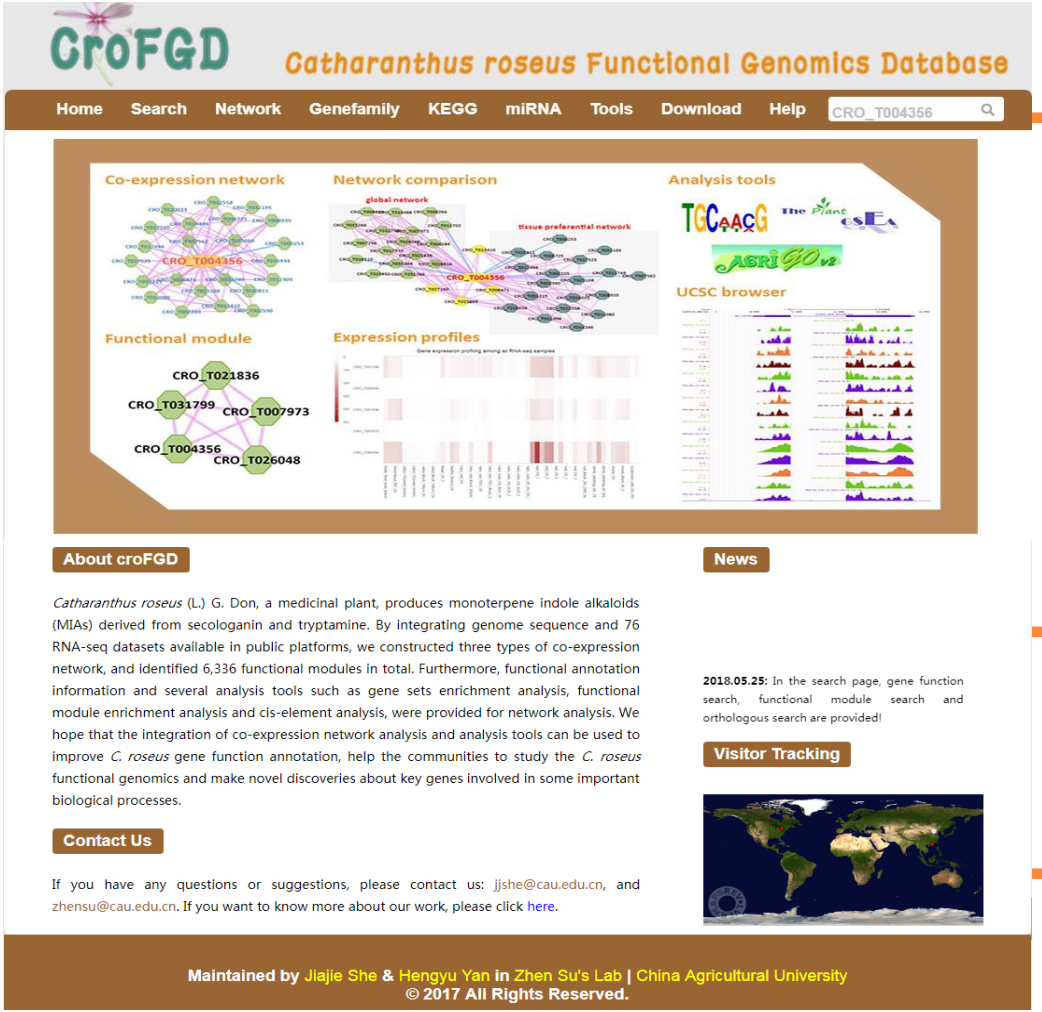
croFGD manual for users

Homepage



Search one gene for detailed information

update news

visitor tracking

Gene detail information

CRO_T004356's detailed information

functional annotation and data source

location information

top three hits in *Arabidopsis*

Gbrowser and UCSC visulization

top300 PCC genelist, PPI, miRNA-target and link to correspoding network

DNA, cds, transcript and protein sequence

functional module including the query gene

gene ontology

gene family and subfamily

Annotation (DRYAD)

Gene ID	Functional Annotation
CRO_T004356	O-methyltransferase family protein

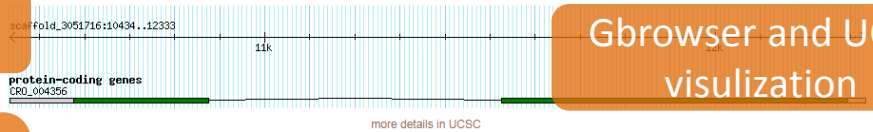
Location

Gene	Assembly	Scaffold	Start	End	Strand
CRO_T004356	scaffolds.min_1000bp	scaffold_3051716	10434	12333	-

Blast top3 hits

Species	Gene ID	E-value	Annotation
Arabidopsis thaliana	AT5G54160	8.00E-41	ATOMT1|O-methyltransferase 1;COMT1|caffeate O-methyltransferase 1
Arabidopsis thaliana	AT1G51990	9.00E-37	O-methyltransferase family protein
Arabidopsis thaliana	AT1G77520	4.00E-34	O-methyltransferase family protein

Gene detail image



Network

Network Category	Global Network	Tissue Preferential Network
Coexpression Positive	Top300 PCC Genelist	Top300 PCC Genelist
Coexpression Negative	Top300 PCC Genelist	Top300 PCC Genelist
PPI Relationship	Null	
miRNA-Target Relationship	Null	

Sequences

Gene:
CDS:
Transcript:
Protein:

Functional module

Module ID	Function Annotation	Category
CFinderADM000741	protein homodimerization activity endocytic vesicle cell surface root cap development regulation of asymmetric cell division Protein_kinases_phosphatases, PPC:1.4.1: Crinkly 4 Like Kinase Stilbenoid, diarylheptanoid and gingerol biosynthesis cytokinins 7-*N*-glucoside biosynthesis cytokinins 9-*N*-glucoside biosynthesis lateral root formation myricetin 3'-O-methyltransferase activity protein-cysteine S-palmitoyltransferase activity 11-O-demethyl-17-O-deacetylvindoline O-methyltransferase activity alkaloid biosynthetic process aromatic compound biosynthetic process vindoline and vinblastine biosynthesis quercetin 3-O-glucosyltransferase activity quercetin 7-O-glucosyltransferase activity flavonoid biosynthetic process embryo development ending in seed dormancy flavonoid glucuronidation methylation adhesion to carbohydrates, Carbohydrate-Binding Modules: CBM57 formation of glycosidic bonds, GlycosylTransferases: GTnc intracellular membrane-bounded organelle protein serine/threonine kinase activity protein phosphorylation	global network

Gene Ontology

GO term	Description	Category
GO:0005737	cytoplasm	cellular_component
GO:0009821	alkaloid biosynthetic process	biological_process
GO:0019438	aromatic compound biosynthetic process	biological_process
GO:0030766	11-O-demethyl-17-O-deacetylvindoline O-methyltransferase activity	molecular_function
GO:0032259	methylation	biological_process
GO:0033799	myricetin 3'-O-methyltransferase activity	molecular_function
GO:0042803	protein homodimerization activity	molecular_function

Gene family

Gene family	subfamily
--	--

Gene detail information

KEGG pathway

KO	Enzyme	Enzyme ID	Pathway	Pathway ID
K16040	ROMT	EC:2.1.1.240	Stilbenoid, diarylheptanoid and gingerol biosynthesis	ko00945

KEGG pathway predicted by GhostKOALA

PlantCyC

Gene	Enzyme ID	Description	Pathway	Pathway id
CRO_T004356	EC-2.1.1.94	16-hydroxytabersonine-O-methyltransferase	vindoline and vinblastine biosynthesis	PWY-5292

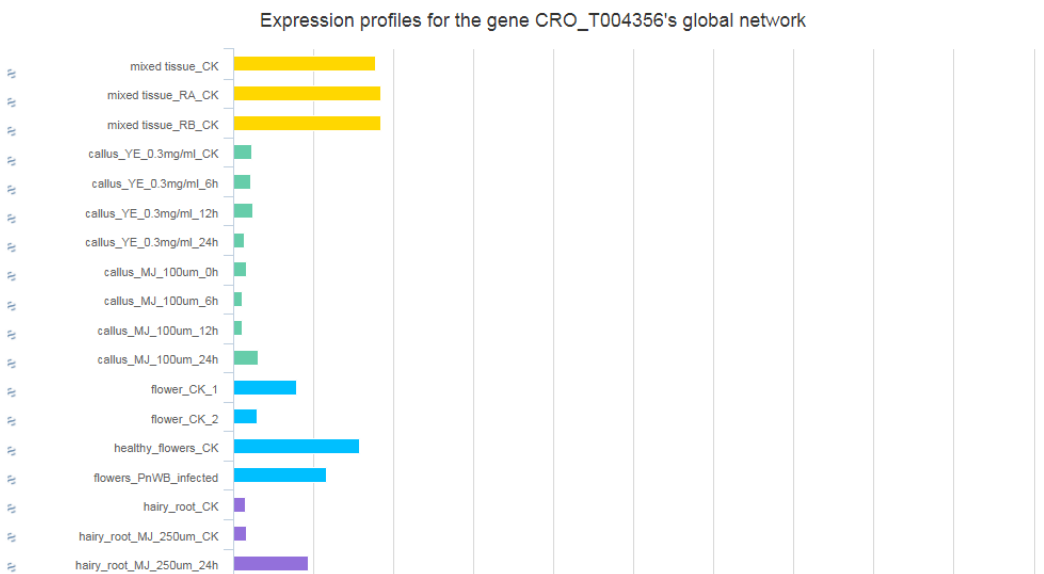
plantCyc pathway

Pfam domain

Pfam accession	Pfam name	Alignment start	Alignment end	E-value
PF08100.8	Dimerisation	27	76	2.2e-17
PF00891.15	Methyltransf_2	116	340	3.8e-65

Pfam domain

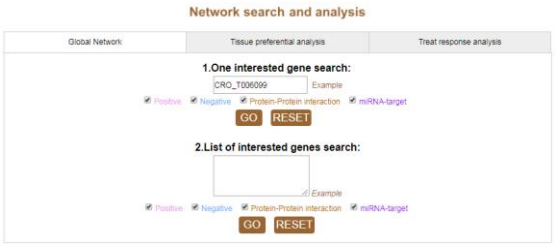
Expression pattern



bar chart according to FPKM in all samples

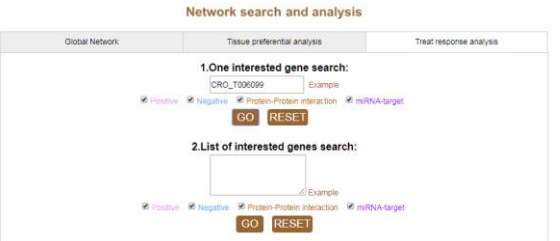
Network

input one gene or genelist

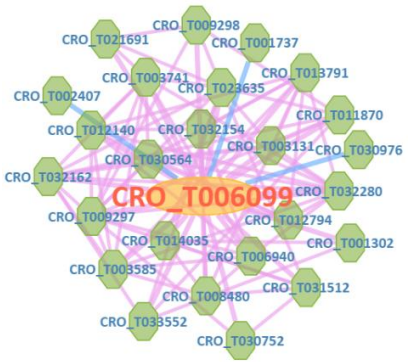


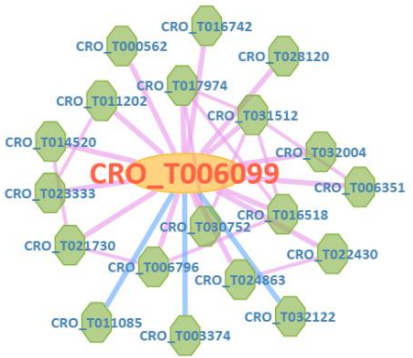
global network

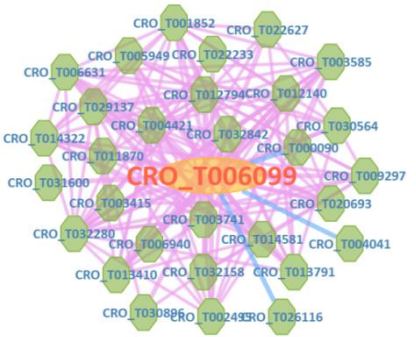
tissue-preferential analysis



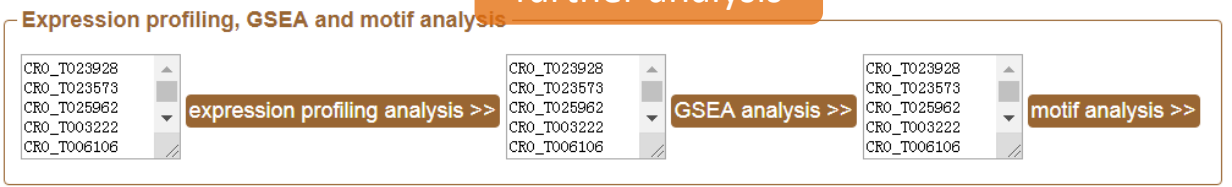
treat-response analysis







further analysis



Network compare

Network Compare Page

In this page,you can type a gene or gene list that you are interested in to see the differences between global network and conditional network.

Compare interested genes between global network and conditional network

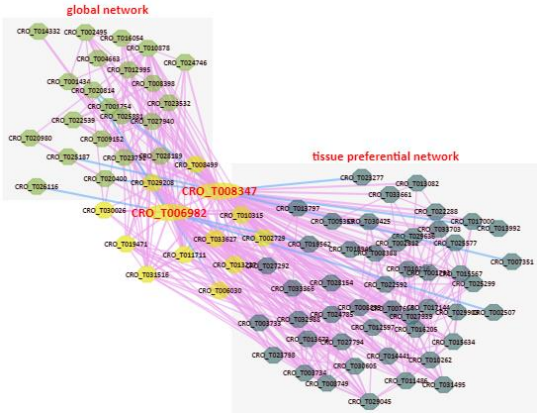
CRO_T017448
CRO_T006098

Example: (limit:4)

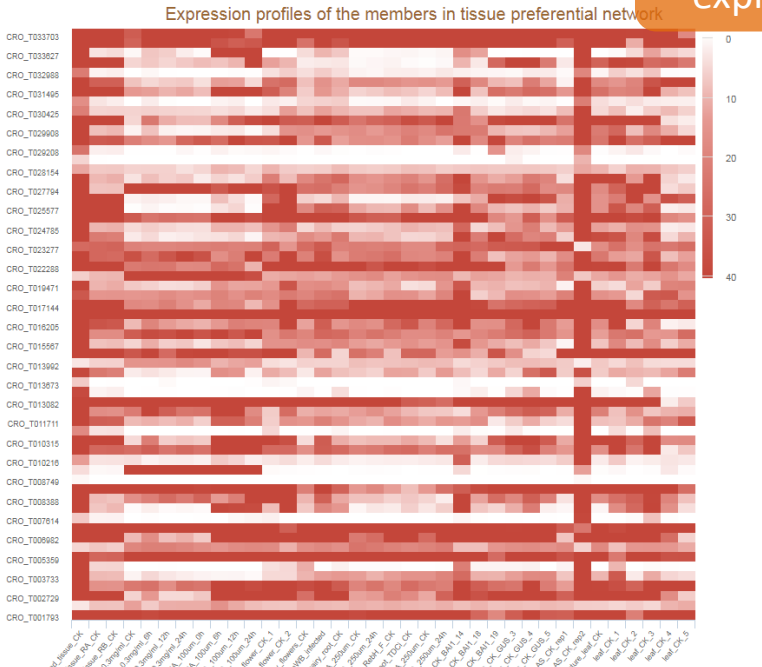
global vs tissue-preferential | global vs treat-response | tissue-preferential vs treat-response

GO RESET

Network comparsion results



two network member expression profiles



Module search

Module Search Page

We finally found 2,310 functional modules in the global network by CFinder algorithm. In this page, you can see the detailed information for these modules.

module search

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

view all functional modules

CRO_T004356
CRO_T006099
CRO_T015796
CRO_T017448

Example

GO RESET

all functional module detailed information

All functional module detail information

This page displays all 2310 functional modules.

Module ID	Function Annotation	gene count
CFinderADM000001	protein serine/threonine kinase activity monovalent cation:proton antiporter activity ATP binding intracellular cation transport regulation of pH endomembrane system membrane kinase activity phosphorylation peptidyl-serine phosphorylation intracellular signal transduction proteasome-mediated ubiquitin-dependent protein catabolic process metal ion binding transmembrane transport ubiquitin protein ligase activity hydrogen ion transmembrane transport PPC:1.14.2: Receptor Like Cytoplasmic Kinase IX PPC:4.2.6: IRE/NPH/PI dependent/S6 Kinase	5
CFinderADM000002	DNA-directed RNA polymerase activity GTPase activity binding transcription, DNA-templated nitrogen compound metabolic process multicellular organism development phosphatidylethanolamine binding regulation of flower development nickel cation binding transferase activity, transferring hexosyl groups transferase activity, transferring alkyl or aryl (other than methyl) groups photoperiodism, flowering Circadian rhythm - plant Terpenoid backbone biosynthesis Purine metabolism L-alanine biosynthesis III molybdenum cofactor biosynthesis Transcription factor: M-type Transcription factor: G2-like Transcription factor: MYB-related Transcription factor: B3 Transcription factor: NAC Transcription factor: FAR1	73
CFinderADM000003	PPC:2.1.4: GmPK6/AtMRK1 Family	5
CFinderADM000004		101
CFinderADM000005	hydrolysis and/or rearrangement of glycosidic bonds, Glycoside Hydrolases: GHnc tricarboxylic acid cycle S-methyltransferase activity monolayer-surrounded lipid storage body hydrolase activity, acting on ester bonds mannan endo-1,4-beta-mannosidase activity lipid storage mannan catabolic process proteolysis involved in cellular protein catabolic process Fructose and mannose metabolism Phenylpropanoid biosynthesis Transcription factor: AP2	348
CFinderADM000006	NADH dehydrogenase activity shikimate O-hydroxycinnamoyltransferase activity Oxidative phosphorylation	31

Functional module search results

Functional module search results

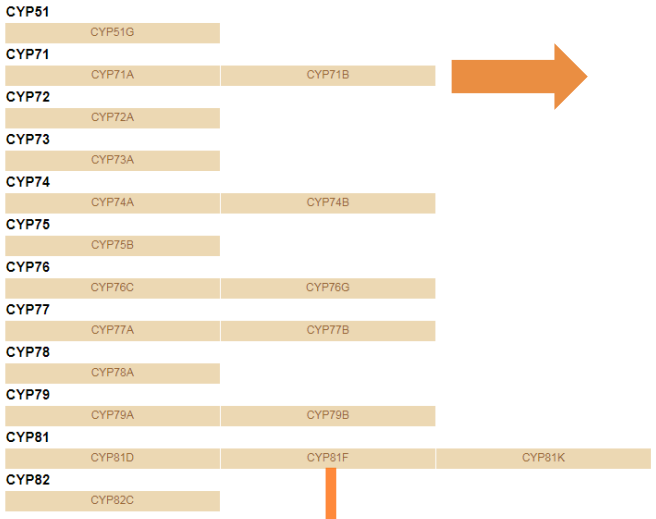
This page displays **5** functional modules based on your interested gene or genelist.

member	Module ID	Function Annotation
CRO_T020280	CFinderADM001015	pollen development auxin-activated signaling pathway auxin polar transport auxin homeostasis auxin efflux auxin efflux transmembrane transporter activity oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor 17-O-deacetylvindoline O-acetyltransferase activity flavin adenine dinucleotide binding intracellular auxin transport Antigen processing and presentation pyruvate decarboxylation to acetyl CoA glycine cleavage 2-oxoglutarate decarboxylation to succinyl-CoA 2-oxoisovalerate decarboxylation to isobutanoyl-CoA vindoline and vinblastine biosynthesis Transcription factor: OFP Transcription factor: NF-YA
CRO_T004356	CFinderADM000741	regulation of asymmetric cell division embryo development ending in seed dormancy flavonoid biosynthetic process alkaloid biosynthetic process cell surface lateral root formation aromatic compound biosynthetic process protein-cysteine S-palmitoyltransferase activity endocytic vesicle 11-O-demethyl-17-O-deacetylvindoline O-methyltransferase activity myricetin 3'-O-methyltransferase activity protein homodimerization activity root cap development quercetin 3-O-glucosyltransferase activity quercetin 7-O-glucosyltransferase activity Stilbenoid, diarylheptanoid and gingerol biosynthesis PPC:1.4.1: Crinkly 4 Like Kinase cytokinins 7-N-glucoside biosynthesis cytokinins 9-N-glucoside biosynthesis vindoline and vinblastine biosynthesis

Gene family

Cytochrome P450 Family

Cytochrome P450 of *Catharanthus roseus* is predicted by nucleotide and protein blast to David Nelson data downloaded from http://drnelson.uthsc.edu/CytochromeP450.html and filtered based on domain predicted by interproscan. There are 98 subfamilies and 191 members in our database.



family

family members

link to global network page

CYP71B's genelist

>>Gene Family>>P450 family>>CYP71B

Gene ID	Subfamily	E-value	Annotation	Network
CRO_T000344	CYP71B35	2.00E-111	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T000497	CYP71B34	1.00E-104	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T001995	CYP71B37	2.00E-97	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T004355	CYP71B34	6.00E-110	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T006603	CYP71B4	9.00E-99	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T009194	CYP71B34	3.00E-95	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T012698	CYP71B11	2.00E-98	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T013814	CYP71B34	1.00E-98	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T014272	CYP71B7	9.00E-102	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T015656	CYP71B4	6.00E-106	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T022496	CYP71B7	9.00E-103	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T022497	CYP71B35	4.00E-102	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T024635	CYP71B12	7.00E-104	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T024642	CYP71B13	1.00E-108	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T024642	CYP71B35	7.00E-107	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T026877	CYP71B2	5.00E-101	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T027852	CYP71B35	8.00E-96	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T029838	CYP71B34	8.00E-98	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T030268	CYP71B14	3.00E-107	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T031709	CYP71B14	5.00E-108	cytochrome P450, family 71, subfamily B, polypeptide	Network
CRO_T033545	CYP71B34	1.00E-98	cytochrome P450, family 71, subfamily B, polypeptide	Network

KEGG pathway

KEGG pathway

KEGG annotation was predicted by GhostKOALA tools. And 5,571 entries were annotated.

Expand All | Collapse All

- **Metabolism**
- **Genetic Information Processing**
- **Environmental Information Processing**
- **Cellular Processes**
- **Organismal Systems**

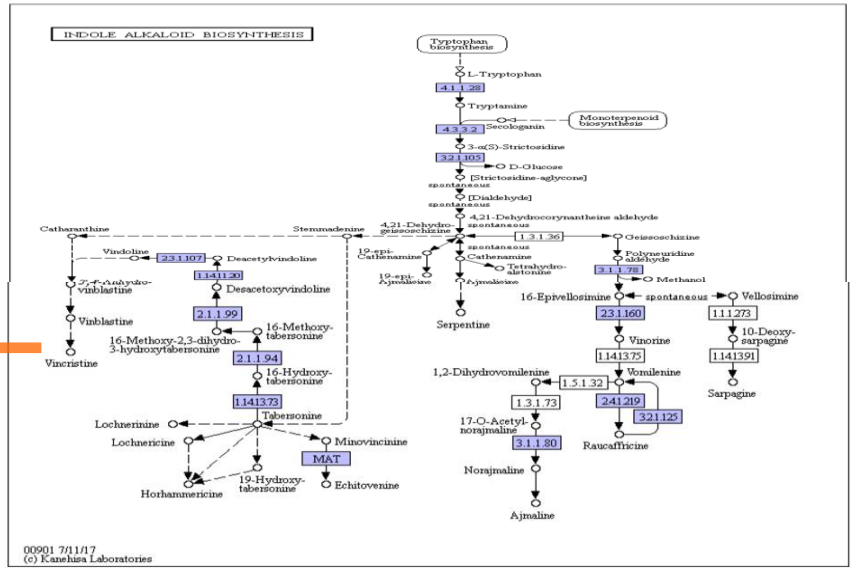
KEGG pathway detailed information

Indole alkaloid biosynthesis

pathway member information

Gene ID	Method: GhostKOALA					Annotation	Network
	KO	Enzyme	Enzyme ID	Pathway ID	Score		
CRO_T004579	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	281	polyneuridine-aldehyde esterase	Network
CRO_T005633	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	91	polyneuridine-aldehyde esterase	Network
CRO_T009857	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	302	polyneuridine-aldehyde esterase	Network
CRO_T017086	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	247	polyneuridine-aldehyde esterase	Network
CRO_T017087	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	310	polyneuridine-aldehyde esterase	Network
CRO_T017225	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	311	polyneuridine-aldehyde esterase	Network
CRO_T017226	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	345	polyneuridine-aldehyde esterase	Network
CRO_T025205	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	219	polyneuridine-aldehyde esterase	Network
CRO_T025252	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	327	polyneuridine-aldehyde esterase	Network
CRO_T029242	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	69	polyneuridine-aldehyde esterase	Network
CRO_T030883	K08233	E3.1.1.78	EC:3.1.1.78	ko00901	121	polyneuridine-aldehyde esterase	Network

indole alkaloid biosynthesis



miRNA infor

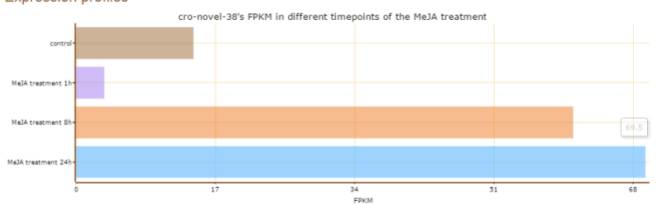
miRNA list

The microRNA sequences of *Catharanthus roseus* are integrated from the paper(PMCID:PMC5320439) and located by GMAP tools. In total,223 miRNA sequences are located and 4 miRNA sequences are not located.

miRNA	Scaffold	Start	End	Strand	Method
cro-miR1511	scaffold_3053372	4617	4637	+	computational prediction
cro-miR156-1	scaffold_3019819	8196	8216	+	computational prediction
cro-miR156-2	scaffold_3068177	7988	7967	-	computational prediction
cro-miR157	scaffold_3068332	5886	5907	+	computational prediction
cro-miR159a	scaffold_3041204	39922	39902	-	computational prediction
cro-miR160-1	scaffold_3016285	2736	2714	-	computational prediction
cro-miR160g	scaffold_3051564	5313	5333	+	computational prediction
cro-miR162-1	scaffold_3001524	26411	26432	+	computational prediction
cro-miR162a-5p	scaffold_3001524	26432	26411	-	computational prediction
cro-miR164e-5p	scaffold_3054985	13770	13750	-	computational prediction
cro-miR164-2	scaffold_3049961	14406	14426	+	computational prediction
cro-miR166-1	scaffold_3038334	13004	12984	-	computational prediction
cro-miR166	scaffold_3051709	45296	45317	+	computational prediction
cro-miR166-3	scaffold_2997365	8484	8464	-	computational prediction
cro-miR167-1	scaffold_2914716	8839	8816	-	computational prediction
cro-miR167-2	scaffold_3038662	3931	3953	+	computational prediction
cro-miR168	scaffold_3011104	8153	8176	+	computational prediction

miRNA expression profile

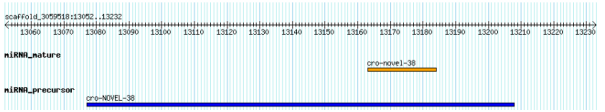
Expression profiles



Tissue	Treat	Normalization read count
seedling	control	14.31994855
seedling	MeJA treatment 1h	3.495968587
seedling	MeJA treatment 8h	60.73358467
seedling	MeJA treatment 24h	69.50450262

miRNA detail information

miRNA detail image



more details in UCSC

Gbrowser and UCSC visualization

Location informaition

Type	ID	Chr	Start	End	Strand
mature	cro-novel-38	scaffold_3059518	13163	13183	+
precursor	cro-NOVEL-38	scaffold_3059518	13077	13207	+

miRNA location info

Sequence and structure Info

Mature sequence[cro-novel-38]

UGAGCACGUGACUUGGGCAUG

Stem-loop sequence[cro-NOVEL-38]

AUGGCAUAAUCCGGAAAAAAUAAUCACGCUCAAGUUAUGUGGUCACCAUAACAAAAUCAAGCCAAAGACAAUUGCCAUUGUUCCGGUGAGCACGUGACUUGGGCAUGGUUAUUUUAGCUGGAUUCCGCCAC

Secondary structure of stem-loop sequence

To make high resolution picture for your own, please download the .ps file Download

miRNA seq and struture info

miRNA Targets Information

target name	Alignment				annotation	Expection	Method
CRO_T017355	ncRNA:	21	GUACGGGUUCAGUGCACGAGU	1	conserved hypothetical protein	3	psRNATarget[Detail]
	targets:	1289	UAUGAUCAAGUCACGUGCUCU	1309			
CRO_T021686	ncRNA:	21	GUACGGGUUCAGUGCACGAGU	1	NHL domain-containing protein	1	psRNATarget[Detail]
	targets:	3161	UAUGCCUAAGUCACGUGCUCA	3181			

miRNA target info

Tools: blast

Blast search

Program: Blastn ▾ Database: cro_cds ▾

Enter sequence below in **FASTA** format

```
>CRO_T031702
AAGCTTCTCTGTAGCATTTTCTTGCCGGCGACGGAGTTGGGATTTT
ATAATCTTTCTTGAGTTAATATAGTTAACGGGAGATGGATTCTAGC
TCGGAGAAGTTGTCGCCGTTCGAATTGATGAGCGCGATCTTGAAGG
GAGCTAAATTAGATGGGTCTAACTCTTCAGATTCTGGCGTAGCTGT
GTCGCCGGCAGTTATGGCTATGTTGTTGGAGAATAAGGAGTTAGTG
ATGATTTTGACTACTTCAGTGGCGGTTTTGATCGGTTGTGTCGTAG
TTTTGATATGGCGGCGATCTTCCGGATCGGGTAAAAAAGTCGTGGA
GCCTCCGAAGCTCATAGTGCCTAAATCTGTTGTAGAACCGGAGGAA
ATTGATGAAGGGAAGAAGAAATTTACCATATTTTTTGGAACACAAA
CTGGAACAGCTGAAGGCTTCGCTAAGGTGCGTTCTTTGGGTTTCCA
```

Example

Or upload file (max filesize 5MB) 选择文件 未选择任何文件

GO RESET

Parameter Options

Expect 10 ▾ Matrix BLOSUM62 ▾

☐ Perform ungapped alignment

☐ Graphical Overview

Descriptions 100 ▾

Alignments 50 ▾

program select

submit sequence in fasta

parameter select

Blast results

Blast result

Query ID	Subject ID	Alignment Length	Mismatches	Query Start	Query End	Subject Start	Subject End	Identity%	E-value	Blast Score
CRO_T031702	CRO_T031702	361	0	81	441	1	361	100.00	0.0	716
CRO_T031702	CRO_T031702	226	0	2565	2790	1041	1266	100.00	2e-124	448
CRO_T031702	CRO_T031702	202	0	1996	2197	746	947	100.00	4e-110	400
CRO_T031702	CRO_T031702	155	0	3051	3205	1349	1503	100.00	4e-82	307
CRO_T031702	CRO_T031702	153	0	3844	3996	1598	1750	100.00	7e-81	303
CRO_T031702	CRO_T031702	125	0	4269	4393	1827	1951	100.00	3e-64	248
CRO_T031702	CRO_T031702	117	0	4509	4625	1949	2065	100.00	2e-59	232
CRO_T031702	CRO_T031702	99	0	3467	3565	1501	1599	100.00	1e-48	196
CRO_T031702	CRO_T031702	100	1	2357	2456	941	1040	99.00	7e-47	190
CRO_T031702	CRO_T031702	87	0	2882	2968	1265	1351	100.00	2e-41	172
CRO_T031702	CRO_T031702	86	0	1282	1367	554	639	100.00	6e-41	170
CRO_T031702	CRO_T031702	84	0	4087	4170	1745	1828	100.00	1e-39	167
CRO_T031702	CRO_T031702	84	0	5072	5155	2062	2145	100.00	1e-39	167
CRO_T031702	CRO_T031702	80	0	901	980	421	500	100.00	2e-37	159
CRO_T031702	CRO_T031702	72	0	1838	1909	676	747	100.00	1e-32	143
CRO_T031702	CRO_T031702	65	0	698	762	357	421	100.00	2e-28	129
CRO_T031702	CRO_T031702	59	0	1108	1166	498	556	100.00	8e-25	117

Tools: motif analysis

Motif analysis of *Catharanthus roseus*

Combining text-mining technology with data sources from plantCARE, PLACE, AthMap etc. We collected 1035 motifs with published annotations. With these identified motifs and published annotations, we predicted TF/TR-binding regions. In addition to scanning for motif sequences, we offer a Z-score method that calculates the significance enrichment of motifs.

1.Sequence Scan

Please input a fasta sequence, we'll find out all the possible motifs.

Example

GO RESET

sequence scan

2.Name Scan

Please input a list of *Catharanthus roseus* gene names, and we'll compute the significant motifs located at 3000bp upstream of the gene, then show each motif and its frequency, users can also significantly analyze these motifs, and a job ID will generate.

Example

GO RESET

Or submit your previous job ID

GO RESET

motif analysis

3.Custom motif Scan

Please input a list of *Catharanthus roseus* gene names and the motif sequences you interested, we'll extract all these genes promoter sequence (3000bp upstream), then show each motif's frequency and significant analysis result.

Example

Please input motifs splited by ":"

GO RESET

Or submit your previous job ID

GO RESET

input your interested motif

Motif analysis of *Catharanthus roseus*

Motif scan of sequences

Factor	Motif	Count	Bg 1K	Bg 2K	Bg 3K
S000020	TAACARA	1	0.565520707085637	1.06349581719826	1.52803807384197
S000024	TGACG	1	0.48080049661533	0.907771438706435	1.3010139229655
S000028	CAAT	19	10.3122173283278	19.8951491324012	28.8786248485028
S000030	CCAAT	6	1.98770285849419	3.80466463685004	5.5440598303231
S000039	GATA	20	7.46732093765704	14.3896952319016	20.951018357031
S000067	TTWTWTTWTT	1	1.35425226876349	2.4480770936179	3.34479292914363
S000080	AATAAA	3	3.71663365751278	6.97537615655207	9.76635431138964
S000086	TGCAGG	1	0.179786573649827	0.361524136096249	0.547429720062668

Motif analysis of *Catharanthus roseus*

Motif scan of gene promoter

Your job ID: **job2017Dec18174010**
The following table deposited significant motifs (p-value <= 0.05) in promoters of these genes: CRO_T011620 CRO_T012804

Motifname	Count	Z-score	P-value
ABREOSRAB21	1	2.25	0.012243
ABREBZMRAB28	1	100.00	0.000000
REBETALGLHCB21	2	1.69	0.045513
E2FANTRNR	1	4.90	0.000000
E2F1OSPCNA	1	4.90	0.000000
LECPLEACS2	7	1.93	0.026916
HSRENTHSR203J	1	31.59	0.000000
CGCGBOXAT	6	2.72	0.003227
CAAT_box	1	2.62	0.004384
CCAAT_box	3	3.14	0.000857
DOCT	1	22.33	0.000000
HSFB2a-2	2	2.12	0.017111
HSFBC1-1	2	2.12	0.017111

Motif analysis of *Catharanthus roseus*

Custom motif analysis

Your job ID: **job2017Dec18174016**
Gene list for search: CRO_T011620 CRO_T012804

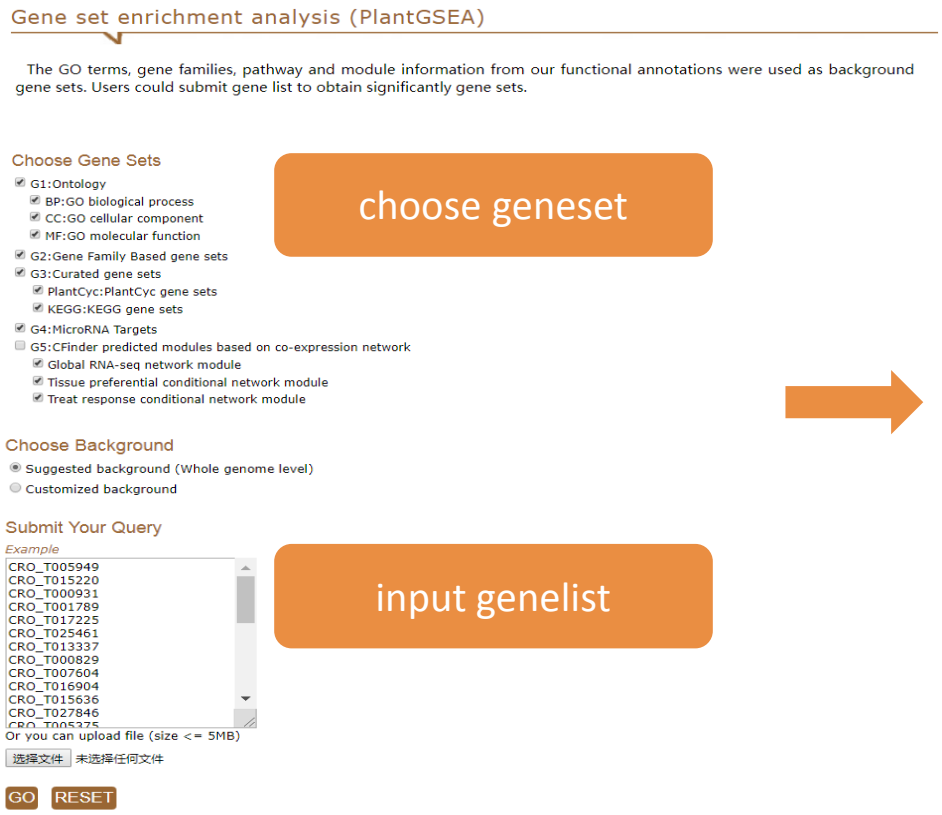
Table1: all of the deposited motifs in promoters of the searched genes:

Motif	Count	Detail
CGGTCA	1	details
CC[AT]ACC	0	details

Table2: deposited significant motifs (p-value <= 0.1) in promoters of the searched genes:

There are no significant motif(s), good luck next time!

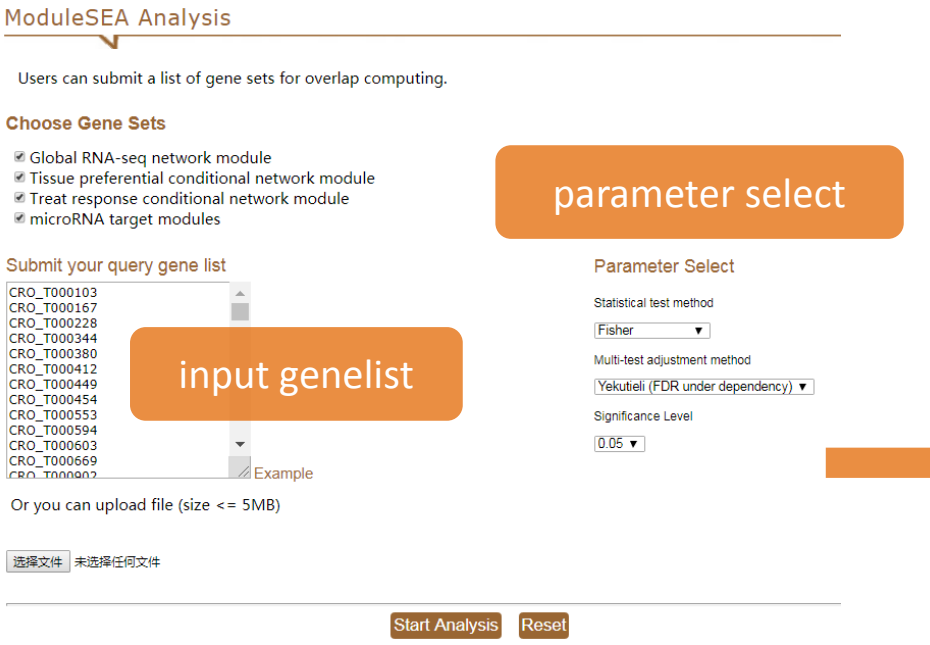
Tools: gene set enrichment analysis



GSEA analysis result:

Gene Set Name(NO. Genes)	Description	Category	NO. Genes in Overlap (k)	p value	FDR
TISSUECFM000075(57)	TissueCFM000075		15	2.61e-33	1.64e-31
OXIDATION-REDUCTION_PROCESS(1261)	GO:0055114 oxidation-reduction process, GOslim:biological_process	GO_BP	12	3.5e-10	3.51e-08
ISOPENTENYL_DIPHOSPHATE_BIOSYNTHETIC_PROCESS, METHYLERYTHRITOL_4-PHOSPHATE_PATHWAY(4)	GO:0019288 isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway, GOslim:biological_process	GO_BP	3	2.19e-08	1.1e-06
CFINDERADM001002(5)	CFinderADM001002		3	3.5e-08	1.16e-06
SECOLOGANIN_AND_STRICTOSIDINE_BIOSYNTHESIS(52)	secologanin and strictosidine biosynthesis		4	1.78e-07	9.63e-06
METHYLERYTHRITOL_PHOSPHATE_PATHWAY_II(15)	methylerythritol phosphate pathway II		3	5.08e-07	1.37e-05
MONOTERPENOID_BIOSYNTHETIC_PROCESS(2)	GO:0016099 monoterpenoid biosynthetic process, GOslim:biological_process	GO_BP	2	4.55e-06	1.52e-4
CFINDERADM000995(5)	CFinderADM000995		2	1.59e-05	1.76e-4
CFINDERADM002204(5)	CFinderADM002204		2	1.59e-05	1.76e-4
CFINDERADM002286(6)	CFinderADM002286		2	2.12e-05	1.76e-4
CFINDERADM001286(7)	CFinderADM001286		2	2.72e-05	1.81e-4
TERPENOID_BACKBONE_BIOSYNTHESIS(51)	Terpenoid backbone biosynthesis	KEGG	3	1.51e-05	2.74e-4
CARBON_METABOLISM(270)	Carbon metabolism	KEGG	4	9.74e-05	8.84e-4
TERPENOID_BIOSYNTHETIC_PROCESS(11)	GO:0016114 terpenoid biosynthetic process, GOslim:biological_process	GO_BP	2	5.88e-05	1.47e-3
METHYLERYTHRITOL_PHOSPHATE_PATHWAY_I(14)	methylerythritol phosphate pathway I		2	9.04e-05	1.63e-3
GERANIOL_AND_GERANIAL_BIOSYNTHESIS(17)	geraniol and geranial biosynthesis		2	1.29e-4	1.74e-3
ACETALDEHYDE_BIOSYNTHESIS_I(23)	acetaldehyde biosynthesis I		2	2.25e-4	2.43e-3
PYRUVATE_FERMENTATION_TO_ETHANOL_II(26)	pyruvate fermentation to ethanol II		2	2.83e-4	2.55e-3
CFINDERADM000985(6)	CFinderADM000985		1	6.19e-3	0.0187
CFINDERADM002224(5)	CFinderADM002224		1	5.3e-3	0.0187
CFINDERADM001380(5)	CFinderADM001380		1	5.3e-3	0.0187
CFINDERADM001467(6)	CFinderADM001467		1	6.19e-3	0.0187
CFINDERADM001746(5)	CFinderADM001746		1	5.3e-3	0.0187
CFINDERADM002213(5)	CFinderADM002213		1	5.3e-3	0.0187
IRON_ION_BINDING(271)	GO:0005506 iron ion binding, GOslim:molecular_function	GO_MF	4	9.88e-05	0.0195
TREATCFM001869(6)	TreatCFM001869		1	6.19e-3	0.0225

Tools: functional module enrichment analysis



module enrichment analysis result:

Information of module enrichment analysis results

Basic computing summary

ID number of the Job: 205210141(Available in 3 months for retrieving).
Categories selected: Mod TissueMod TreatMod MIR
NO. query list after removing redundancy: 519
NO. redundant list in original query: 0

we show gene sets which has more significant FDR(<**0.05**) for page display.You can download related analysis result below.

Geneset Name(NO Genes)	Description	Category	Overlap Genes	p value	FDR
TissueCFM000156(7)	Transcription_related, Transcription factor: M-type photosynthetic membrane ATP synthesis coupled electron transport photosynthesis, light reaction cellular metabolic process Photosynthesis iron-sulfur cluster binding quinone binding NADH dehydrogenase (ubiquinone) activity photosystem I membrane part Oxidative phosphorylation transport chloroplast thylakoid membrane metal ion binding mitochondrion chloroplast integral component of membrane plasma membrane nucleus ATP binding	coexpression module	5	5.6e-7	6.48e-4
TreatCFM000217(7)	tubulin binding polysome prefoldin complex Transcription_related, Transcription factor: bZIP tubulin complex assembly microtubule-based process Plant hormone signal transduction Spliceosome protein folding sequence-specific DNA binding transcription factor activity, sequence-specific DNA binding regulation of transcription, DNA-templated cytosol	coexpression module	4	1.6e-5	3.74e-3

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Sequence

cro_std_maker_anno.final.dna.fasta

cro_std_maker_anno.final.cds.fasta

cro_std_maker_anno.final.pep.fasta

cro_std_maker_anno.final.transcripts.fasta

Annotation

cro_std_maker_anno.final.gff3

cro_functional_annotation.final.txt

Top hits annotation

Gene ontology

Pathway

KEGG pathway

PlantCyC

Gene Family

Cytochrome P450

Transcription Factors

Protein Kinases

Ubiquitin

Carbohydrate-Active Enzymes

Functional modules

Global co-expression functional modules

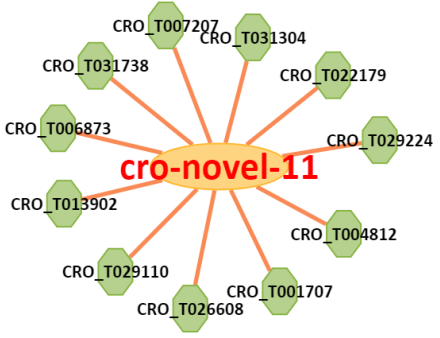
Tissue preferential co-expression functional modules

Treat response co-expression functional modules

MiRNA target functional modules

miRNA target functional modules

MiRNA target functional modules

cro-miR1511	cro-miR160-1	cro-miR160g	cro-miR166	cro-miR166-1
cro-miR166-3	cro-miR168	cro-miR172-1	cro-novel-107	cro-novel-11
cro-novel-128	cro-novel-13	cro-novel-136	cro-novel-139	cro-novel-157
cro-novel-158	cro-novel-16	cro-novel-160	cro-novel-166	cro-novel-2
cro-novel-26	cro-novel-27	cro-novel-34	cro-novel-49	cro-novel-6
cro-novel-60	cro-novel-63	cro-novel-7	cro-novel-75	cro-novel-87
cro-novel-95	cro-miR159a	cro-miR164-2	cro-miR164e-5p	cro-miR393a-5p
cro-miR394	cro-miR397	cro-miR398a-3p	cro-novel-1	cro-novel-102
cro-novel-125	cro-novel-142	cro-novel-149	cro-novel-169	cro-novel-170

miRNA target network and the expression profiles of target genes