

BnIR tutorial

Genomics

Gene search

The Gene search page provides gene structure and function information of ZS11 and Darmor genomes. In this module, the user can enter the gene ID of ZS11 or Darmor to query the related information of the interest gene. If users entered the gene ID or gene name of *Arabidopsis thaliana*, the structure and function information of all homologous genes and their phylogenetic relationship can be obtained. For example, if users entered 'AT1G65480'(box1), users can obtain the physical location and functional description information of all homologous genes corresponding to this gene (box2 and box3), the phylogenetic relationship of homologous genes (box4).

1 Gene search (ZS11)

Gene ID: ?
e.g. FT, AT1G65480, BnaA02G01568002S, FLOWERING LOCUS T

Gene region: ?
e.g. A01:159000..230000

Gene index: ?
BnIR: e.g. example 1 or example 2

2 Basic information of genes

Search:

Selector	ZS11 Gene ID	Darmor Gene ID	ATGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA02G01568002S	BnaA02g151100	AT1G65480	FT	A02:910482..910720	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow
<input type="checkbox"/>	BnaA07G02627002S	BnaA07g253700	AT1G65480	FT	A07:26253..95,2625595	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow
<input type="checkbox"/>	BnaA07G03651002S	BnaA07g312200	AT1G65480	FT	A07:3096418..3096518	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow
<input type="checkbox"/>	BnaC02G02090002S	BnaC02g452600	AT1G65480	FT	C02:16837203..16838959	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow
<input type="checkbox"/>	BnaC04G01814002S	BnaC04g148500	AT1G65480	FT	C04:17070918..17073769	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow
<input type="checkbox"/>	BnaC06G03238002S	BnaC06g270000	AT1G65480	FT	C06:4293746..4293876	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flow

Showing 1 to 6 of 6 entries 1 row selected Previous 1 Next

3 Function of related gene clusters

Search:

ATGI	Symbol	Full name	ZS11 Gene ID
AT1G65480	FT	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	BnaA02G01568002S;BnaA07G02627002S;BnaA07G03651002S;BnaC02G02090002S;BnaC04G01814002S;BnaC06G03238002S

Showing 1 to 1 of 1 entries Previous 1 Next

4 Phylogenetic tree

Chr.	Start	End	Length	Gene structure
A02	910482	910720	2809	
C02	16837203	16838959	1757	
A07	26253185	26255955	2761	
C06	42937440	42938746	2307	
A07	3096418	3096518	1100	
C04	17070918	17073769	2852	
Chr1	24331373	24339999	8227	

Showing 1 to 7 of 7 entries

BnIR is developed by the Yimlab at Huazhong Agricultural University.
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Gene cluster

Gene cluster provides a query of gene cluster results for 11 rapeseed genomes. The user can query

Gene family

Gene family integrates information from 183 gene families. The gene number of each gene family is listed in Gene family overview(box1). Check the box in the first column to submit to view the gene list of the corresponding gene family and the statistics of the copy number of *B. napus* genome corresponding to the Arabidopsis genes in this family(box2).

1

Gene family overview

Search: Download

Selector	Gene Family Name	Sub Family No.	AtGI No.	ZS11 Gene No.	Darmor Gene No.
<input checked="" type="checkbox"/>	14-3-3 proteins	1	13	80	52
<input type="checkbox"/>	14-3-3s	1	8	26	29
<input type="checkbox"/>	BSD Ribosomal L16 proteins	1	3	18	17
<input type="checkbox"/>	AAAP family	1	43	185	187
<input type="checkbox"/>	ABC Superfamily	13	129	464	456
<input type="checkbox"/>	ABC transporters	4	130	429	445
<input type="checkbox"/>	ABC transporters (Small Lab)	1	15	61	66
<input type="checkbox"/>	ABI3VP1 Transcription Factor Family	1	11	50	50
<input type="checkbox"/>	ACA	1	13	63	63
<input type="checkbox"/>	ACRP60s	1	7	34	34
<input type="checkbox"/>	Acyl Lipid Metabolism Family	173	810	2212	2062
<input type="checkbox"/>	AGG Family	7	38	127	123
<input type="checkbox"/>	Alcorycyl Dihydrogenase Supportfamily	9	14	56	56
<input type="checkbox"/>	Alike-like Transcription Factor Family	1	7	37	33
<input type="checkbox"/>	Antiporter Superfamily	1	28	87	89

Showing 1 to 10 of 183 entries. 1 row selected

Previous 1 2 3 4 5 ... 13 Next

2

ZS11 genes information in 14-3-3 proteins

Search: Download

ZS11 Gene ID	Darmor Gene ID	Sub family	AtGI	At Name	Genomic position	Function	Description
BnaA01G0224300Z5	-	NULL	AT3G02250	GRF7	A01:1458057..1458714	14-3-3-like protein GF14 nu OS=Arabidopsis thaliana GN=GRF7 PE=1 SV=1	
BnaA01G0419100Z5	-	NULL	AT3G04090	GRF9	A01:3660361..3661087	14-3-3-like protein GF14 mu OS=Arabidopsis thaliana GN=GRF9 PE=1 SV=2	
BnaA02G0232100Z5	-	NULL	AT1G07830	GRF2	A02:1498508..1499018	14-3-3-like protein GF14 omega OS=Arabidopsis thaliana GN=GRF2 PE=2 SV=2	
BnaA03G0040300Z5	BnaA03G029300	NULL	AT5G10450	GRF8	A03:1654228..1655164	14-3-3-like protein GF14 lambda OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=1	Encodes a member of the 14-3
BnaA03G0207200Z5	BnaA03G267100	NULL	AT2G04290	GRF9	A03:1080510..1081092	14-3-3-like protein GF14 mu OS=Arabidopsis thaliana GN=GRF9 PE=1 SV=2	
BnaA03G0288100Z5	BnaA03G279500	NULL	AT3G03630	GRF7	A03:1528406..1528510	14-3-3-like protein GF14 nu OS=Arabidopsis thaliana GN=GRF7 PE=1 SV=1	
BnaA03G0582400Z5	-	NULL	AT5G10450	GRF8	A03:44331940..44332172	14-3-3-like protein GF14 lambda OS=Arabidopsis thaliana GN=GRF8 PE=1 SV=1	Encodes a member of the 14-3
BnaA04G0101600Z5	BnaA04G268800	NULL	AT5G38480	GRF3	A04:11985269..11986475	14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	
BnaA04G0101600Z5	BnaA04G268800	NULL	AT5G38480	GRF3	A04:11985269..11986475	14-3-3-like protein GF14 psi OS=Arabidopsis thaliana GN=GRF3 PE=1 SV=2	
BnaA05G0318100Z5	BnaA05G183200	NULL	AT1G03510	GRF4	A05:31427840..31428915	14-3-3-like protein GF14 phi OS=Arabidopsis thaliana GN=GRF4 PE=1 SV=2	

Showing 1 to 10 of 54 entries

Previous 1 2 3 4 5 6 Next

ZS11 genes copy number transformation and distribution in 14-3-3 proteins

You can click on the gene family name in the right pie chart to see the ZS11 genes copy number transformation and distribution in a particular family.

■ NULL

ZS11 genes copy number distribution in 14-3-3 proteins

Gene index

Gene index constructed a total of 88,423 gene indexes by integrating the gene collinearity of 11 *B. napus* genomes. By entering the Arabidopsis gene ID, gene name or the gene ID of the *B. napus* genome(box1), users can view the gene index of related genes (box2).

1



2



ZS11 Gene ID	Darmor Gene ID	Darmor-bzh Gene ID	Express517 Gene ID	GanganF73 Gene ID	No2127 Gene ID	NY7 Gene ID	quinta Gene ID	Shangli3 Gene ID
BnaA02G0156900ZS	BnaA02g12130D	A02p13240_1_BnaDAR	A02p017120_1_BnaEXP	BnaA02G0152300GG	BnaA02G0156600NO	.	BnaA02G0156700QU	BnaA02G0159500SL
BnaA07G0282700ZS	BnaA07g25310D	A07p32850_1_BnaDAR	A07p033170_1_BnaEXP	BnaA07G0279500GG	BnaA07G0275700NO	.	BnaA07G0239900QU	BnaA07G02266400SL
BnaA07G0385100ZS	BnaA07g33120D	A07p42500_1_BnaDAR	A06p003900_1_BnaEXP	BnaA07G0378900GG	.	.	BnaA07G0320800QU	BnaA07G03346400SL
BnaC02G0206600ZS	BnaC02g45290D	C02p21420_1_BnaDAR	C02p045130_1_BnaEXP	BnaC02G0184100GG	BnaC02G0153000NO	.	BnaC02G0154400QU	BnaC02G0115900SL
BnaC04G0181400ZS	BnaC04g14850D	C04p21000_1_BnaDAR	C04p028460_1_BnaEXP	BnaA03G0498400GG	BnaC04G0172900NO	chrC04g001840	BnaC04G0173400QU	BnaC04G0170300SL
BnaC06G0323800ZS	BnaC06g27090D	C06p39080_1_BnaDAR	C06p028960_1_BnaEXP	BnaC06G0311400GG	BnaC06G0313200NO	chrA07g002859,chrC06g003298	BnaC06G0319300QU	BnaC06G0308400SL

Genome synteny

We collected 14 genome assemblies including the diploids *Brassica rapa* accessions Chinese cabbage Chiifu-401-41, sarson Z1, *Brassica oleracea* accessions HDEM, To1000, and 11 *Brassica napus* accessions. By genome alignment, genomic synteny was constructed. We integrated Gbrowser_syn and Dotplot browsers to browse the genome alignments.

The Dotplots browser can help users browse the global and local genome collinearity between genome assemblies. In Dotplots, users are allowed to browse the collinearity between two genome alignments simultaneously. The user selects the object of the gene alignment to be viewed in box1, and then gets the genome collinearity result in box2, and can browse by switching the position and resolution of the genome in box3.

1 Dotplots: an interactive dot plot browser to visualize genome-genome alignments and perform exploratory comparative genomics.

Genome alignment 1 vs
 Genome alignment 2 vs

2 Dotplot results
 Click on the title to open the dotplot on a new page.

zs11 vs Darmor zs11 vs Express617

Users can browse the alignment results of all regions between genomes using Gbrowse_syn. In Gbrowse, the user selects the object of the gene alignment to view(box1), and then gets the result(box2). The genomic collinearity (box6) is finally obtained by selecting the reference genome (box3), the genomic region to be viewed(box4), and the resolution (box5).

1 Gbrowse synteny
 Select Genomes vs

2 Gbrowse synteny results

GBrowse syn

Instructions
 Select a Region to Browse and a Reference species:
 Examples: zs11 scaffoldC06:8100000..8110000, Darmor C06:5610000..5620000.

Search
 Landmark: 4
 Genome to Search: 3
 5

Overview 6

Display settings
 Image width: 640 768 800 1024 1280
 Image options:
 Chain alignments on off
 Flip minus strand panels on off
 Grid lines on off
 Edges on off
 Shading on off

1

Browse by Family Search by Gene ID

Browse by Family (Total TF Number 5956)

The following is a collection of transcription factors in the family. Click to view all the rape genes contained in the family. Or you can enter interested genes and then get relevant genetic family information.

2 AP2 (57)	ARF (64)	JARR-B (45)	B3 (222)	BBR-BPC (24)
BES1 (23)	C2H2 (373)	C3H (155)	CAMTA (22)	CO-like (46)
CPP (34)	DBB (33)	Dof (149)	E2F/DP (31)	EIL (25)
ERF (464)	FAR1 (29)	G2-like (174)	GATA (114)	GRAS (105)
GRF (33)	GeBP (39)	HB-PHD (8)	HB-other (20)	HD-ZIP (191)
HRT-like (7)	HSF (63)	LBD (146)	LFY (4)	LSD (12)
M-type_MADS (142)	MYC_MADS (149)	MYB (462)	MYB_related (263)	NAC (393)
NFX1 (8)	NFYA (36)	NFYB (50)	NFYC (25)	NZZ/SPL (4)
Nin-like (47)	RAV (27)	S1Fa-like (7)	SAP (2)	SBP (62)
SRS (40)	STAT (2)	TALE (59)	TCP (81)	Trihelix (109)
VOZ (8)	WOX (57)	WRKY (278)	Whirly (6)	YABBY (22)
ZF-HD (65)	bHLH (566)	bZIP (271)		

3

▼ Results of AP2 Family

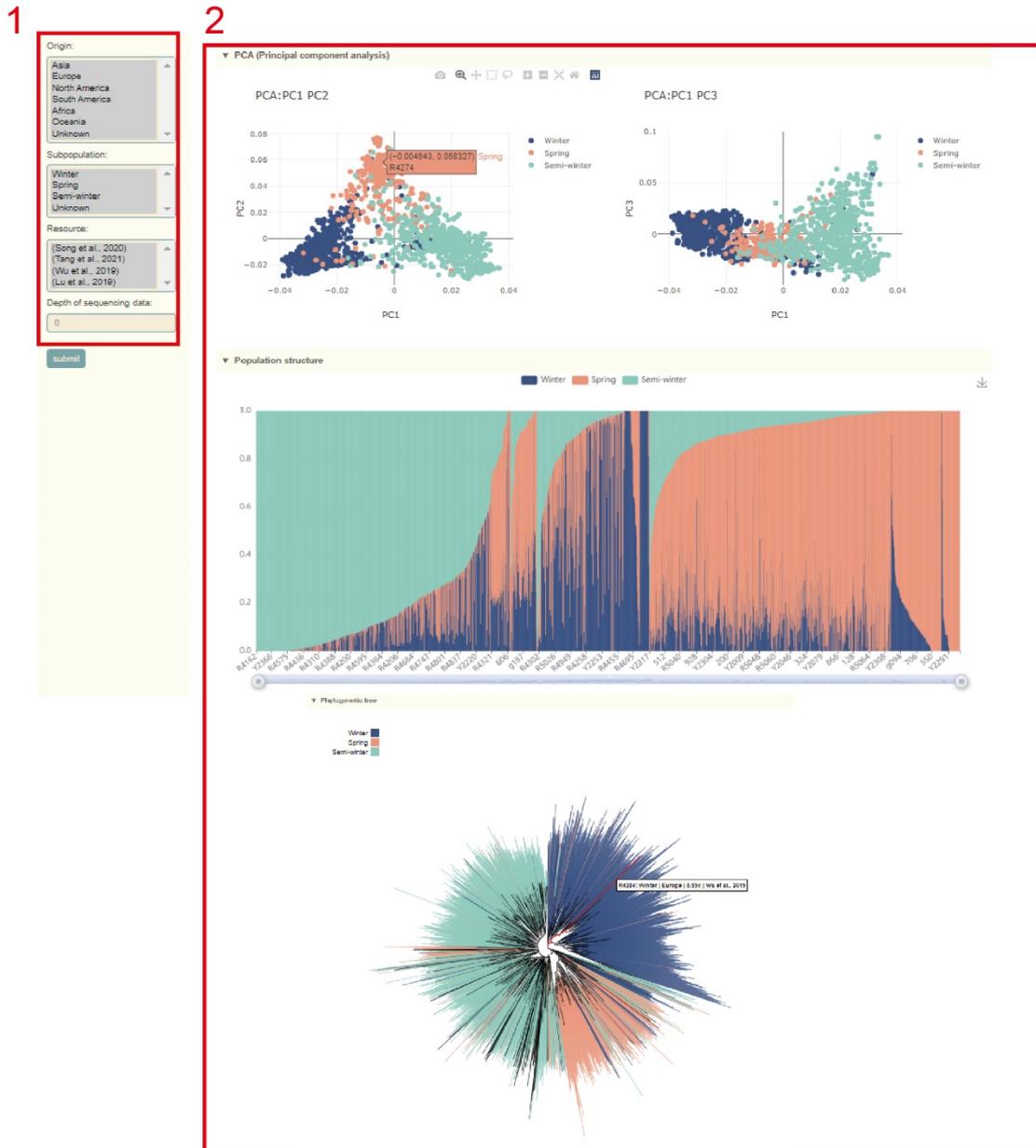
Search: Download

Zm1 Gene ID	TF Type	AtGI	At Name	Genomic Position
BnaA05G0174006ZS	AP2	AT1G51190	PLT2	A05:11630717..11633517
BnaA05G0348609ZS	AP2	AT3G20840	PLT1	A05:35123940..35126560
BnaA05G0026200ZS	AP2	AT2G41710	--	A05:1533138..1535395
BnaC04G0195600ZS	AP2	AT2G28550	RAP2-7	C04:18816935..18819650
BnaC04G0027800ZS	AP2	AT2G41710	--	C04:2608579..2610897
BnaC03G0048000ZS	AP2	AT5G10510	AIL6	C03:2451024..2454811
BnaC03G00686200ZS	AP2	AT4G37750	ANT	C03:66180962..66183331
BnaC03G0521400ZS	AP2	AT5G65510	AIL7	C03:38755316..38758409
BnaC03G00246700ZS	AP2	AT2G41710	--	C03:14687205..14689753
BnaC07G0207000ZS	AP2	AT5G67180	TOE3	C07:34317906..34319983

Showing 1 to 10 of 57 entries Previous 1 2 3 4 5 6 Next

1. Song JM, Guan Z, Hu J, Guo C, Yang Z, Wang S, et al. Eight high-quality genomes reveal pan-genome architecture and ecotype differentiation of *Brassica napus*. *Nat Plants*. 2020; 6:34-45.
2. Bus A, Korber N, Snowdon RJ, Stich B. Patterns of molecular variation in a species-wide germplasm set of *Brassica napus*. *Theor Appl Genet*. 2011; 123:1413-1423.

Subpopulation, Resource, and sequencing depth (box1). Then, users can obtain the results of PCA, population structure analysis, and phylogenetic analysis of these accessions (box 2). The user can move the mouse over these points or columns to query the population structure information of this accession.



selective signals

In the F_{ST} module, the user can submit the gene ID or genomic region in the search box(box1), and then clicks “submit” to submit. Then, the F_{ST} values (box2) and visualization results (box3, box4) of all windows (50 kb) in the area will be showed. The lines with different colors in the figure represent the F_{ST} values of the pairwise comparison between the three ecotypes. Users can also change this region on the left side of the page (box3).

1 **F_{ST} (Z511)**

选择文件 | 未选择任何文件
 e.g. BnaA07G028270ZS, A01.0..38150000, BnaAnng09259D

2

submit reset

▼ Fixation index (F_{ST})

Search: Download

Selector	Chr.	Start	End	Position	F _{ST} (Spring/Winter)	F _{ST} (Semi-winter/Spring)	F _{ST} (Semi-winter/Winter)
<input type="checkbox"/>	A01	1	500000	250000	0.114	0.113	0.118
<input type="checkbox"/>	A01	500001	550000	300000	0.099	0.113	0.123
<input type="checkbox"/>	A01	1000001	600000	350000	0.086	0.114	0.130
<input type="checkbox"/>	A01	1500001	650000	400000	0.077	0.117	0.137
<input type="checkbox"/>	A01	2000001	700000	450000	0.069	0.113	0.133
<input type="checkbox"/>	A01	2500001	750000	500000	0.065	0.111	0.133
<input type="checkbox"/>	A01	3000001	800000	550000	0.053	0.107	0.136
<input type="checkbox"/>	A01	3500001	850000	600000	0.039	0.100	0.139
<input type="checkbox"/>	A01	4000001	900000	650000	0.025	0.099	0.130
<input type="checkbox"/>	A01	4500001	950000	700000	0.025	0.100	0.126

Showing 1 to 10 of 750 entries Previous 1 2 3 4 5 ... 76 Next

submit

3

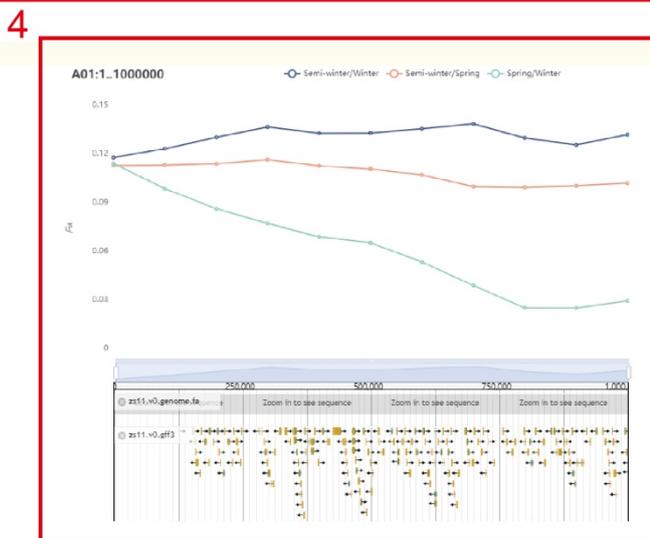
▼ Plot of Fixation index (F_{ST})

Chr:

Start:

End:

submit



The usage of the Pi module is similar to that of F_{ST} . The user first submits the gene ID or genomic region (box1) to query in the search box, and clicks “submit” to submit. Then, the Pi values (box2) and visualization results (box3, box4) of all windows (50 kb) will be obtained. Users can also change this region on the left side of the page (box3).

1

A01:1..1807270

e.g. BnaA07G02827002S, A01:1..1807270, BnaAnng00250D

2

3

▼ Nucleotide diversity (π)

Search:

Selector	Chr.	Start	End	Position	PI_W	PI_S	PI_SW
<input type="checkbox"/>	A01	1	500000	250000	0.000477	0.000839	0.000934
<input type="checkbox"/>	A01	50001	550000	300000	0.000511	0.000938	0.001091
<input type="checkbox"/>	A01	100001	600000	350000	0.000556	0.001056	0.001338
<input type="checkbox"/>	A01	150001	650000	400000	0.000627	0.001173	0.00159
<input type="checkbox"/>	A01	200001	700000	450000	0.000687	0.001248	0.001778
<input type="checkbox"/>	A01	250001	750000	500000	0.000729	0.001305	0.001851
<input type="checkbox"/>	A01	300001	800000	550000	0.000671	0.001203	0.001796
<input type="checkbox"/>	A01	350001	850000	600000	0.000731	0.001208	0.001909
<input type="checkbox"/>	A01	400001	900000	650000	0.000766	0.001162	0.001904
<input type="checkbox"/>	A01	450001	950000	700000	0.000815	0.001128	0.001819

Showing 1 to 10 of 33 entries

Previous 1 2 3 4 Next



In the KaKs module, the user first submits the gene ID or genomic region to query in the search box(box1), and clicks "submit" to submit. The Ka, Ks, and Ka/Ks values (box2) and visualization results (box3, box4) of the genes in this region are then obtained. Users can also search in the resubmission area on the left side of the page (box3).

Variation

Single-locus module

In the Single-locus module, users can search for genetic variation information in genes or genomic regions according to the gene ID, genomic region and gene index (box 1). The database integrated SNPs, InDels and SVs, and users can query by SNP or SV mode (box 2). In addition, users can also analyze the haplotypes composed of multiple SNPs in a gene through Haplotype mode, or perform combined analysis of SNPs and SVs using the merge mode (box2). Take the search for the *BnaA08.FAE1* (BnaA08G0134700ZS) gene as an example, the user enters “FAE1” in the Gene ID, then selects the SNP (box2), and then clicks 'submit' to query to obtain the related information. The first page of the results is the statistics of the variation data of all homologous genes of the FAE1 gene in the ZS11 genome, such as the number of SNPs and SVs in the gene region (box3). This is followed by a visualization of the distribution of variants in homologous genes, where different colored triangles represent variants with different variation effects. The user can move the mouse to the position of the corresponding mutation to view the specific information of the mutation (box4). Then there is the *BnaA08.FAE1* gene structure diagram, the user can move the mouse to the position of the corresponding variant and click to select the specific information to view the variant (box5). Next, the user will get the statistics of the variants contained in the gene (box6) and a list of all variants (box7). The user can check the variant he wants to find in the first column. Then, based on the variant selected by the user, the page will give the frequency distribution of the variant in different subgroups (box8) and the frequency distribution in the population in different geographic regions (box9). Then, users can submit the phenotype to browse in the phenotype search bar to view the difference in phenotype values of accessions with different genotypes (box10, box11). Users can also submit the gene of interest in the gene search bar to view the difference in gene expression levels of accessions with different genotypes (box 12).

Brassica napus Variation Search (ZS11)

1

Gene ID: ? [选择文件](#) 未选择任何文件
 e.g. FAE1, AT4G34520, BnaA08G0134700ZS, FLOWERING LOCUS C

Gene region: ?
 e.g. A01:450000..460000

Gene Index: ? [选择文件](#) 未选择任何文件
 e.g. BnaA08G0310400ZY, BnaA08g27310D, A01p00080_1_BnaDAR

2

Mode: SNP Haplotype SV Merged

Basic information of gene(s)

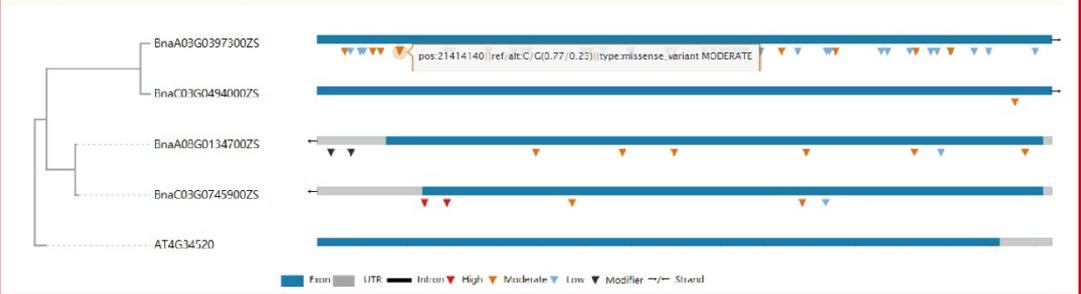
Search:

3

ZS11 ID	Darmor ID	ATGI/Name	Position	Seq/Exp/JBR	SNPs No.	SNP No. (High/Moderate/Low/Modifier)	SV No.	SV No. (INS/DEL)	Multi-locus selector
<input type="checkbox"/> BnaA03G0397300ZS	BnaA03g39010D	AT4G34520(FAE1)	A03:21413975..21415438	Seq Exp JBR	46	0/13/33/0	0	0/0	<input type="checkbox"/>
<input checked="" type="checkbox"/> BnaA08G0134700ZS	BnaA08g11130D	AT4G34520(FAE1)	A08:18618857..18619753	Seq Exp JBR	9	0/6/1/2	0	0/0	<input type="checkbox"/>
<input type="checkbox"/> BnaC03G0745900ZS	BnaC03g65980D	AT4G34520(FAE1)	C03:72309540..72311231	Seq Exp JBR	5	2/2/1/0	0	0/0	<input type="checkbox"/>
<input type="checkbox"/> BnaC03G0494000ZS	BnaC03g46140D	AT4G34520(FAE1)	C03:35858639..35860030	Seq Exp JBR	1	0/1/0/0	0	0/0	<input type="checkbox"/>

Showing 1 to 4 of 4 entries Previous Next

Phylogenetic tree, gene structure and variation distribution



Gene structure and SNP distribution

5

The inverted triangle symbols indicate variations, click it to see detailed information in table.

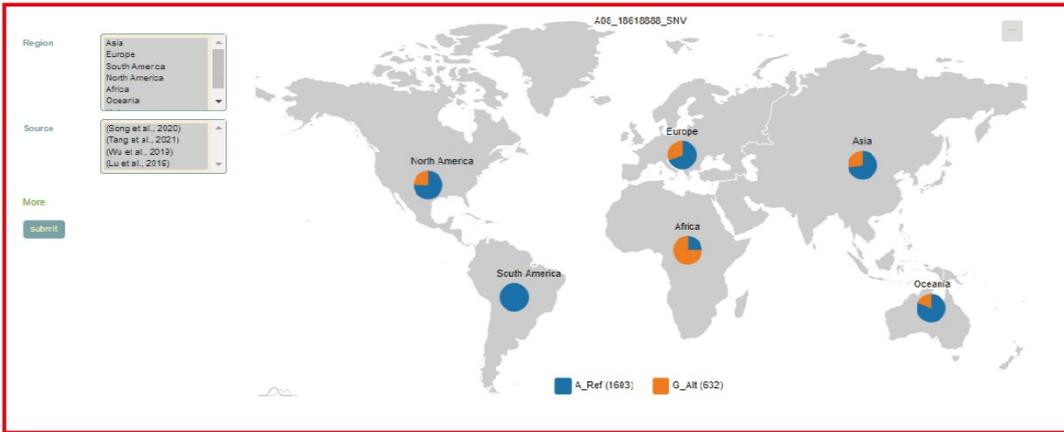
Legend: Exon (blue), UTR (grey), Intron (black), High (red), Moderate (orange), Low (blue), Modifier (grey), Strand (arrow)

pos:18618888 ||ref:alt:A/G(0.71/0.29)||type:misense_variant MODERATE
 BnaA08G0134700ZS/BnaA08g11130D chr. region A08:18618052...18619753 ±0 kb

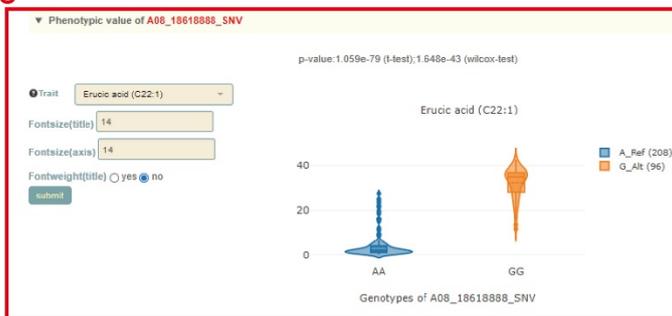
Chr.	Position	Alt (allele)	Ref (allele)	JBrowser	Alt (frequency)	Ref (frequency)	PIC	Alt (num)	Ref (num)	Function_type	Variation_type
A08	18618888	G	A	JBR	0.29	0.71	0.33	640	1614	MODERATE	misense_variant ANN-G[misense_varia

Showing 1 to 1 of 1 entries Previous Next

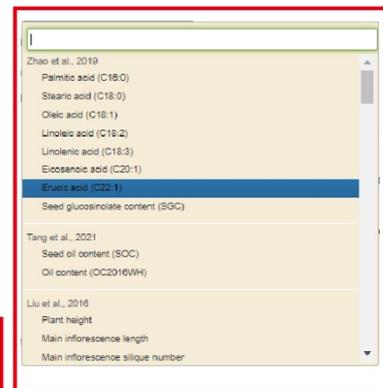
9



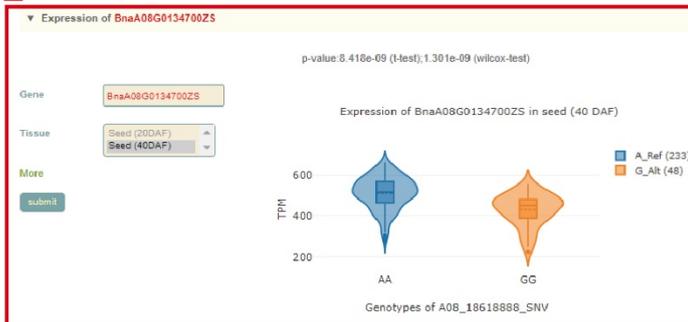
10

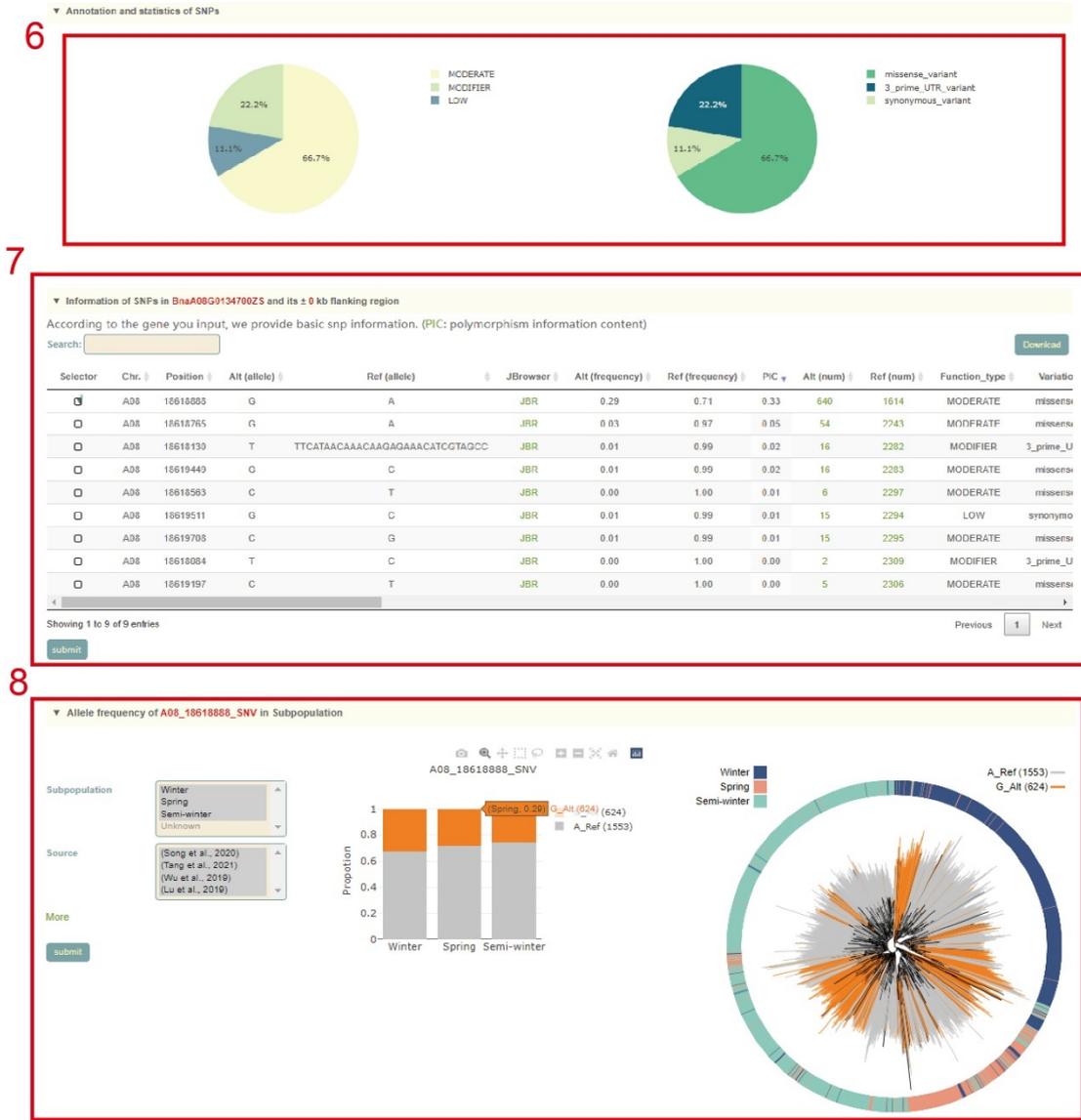


11



12





Multi-locus module

In the Multi-locus module, the user first entered the multiple gene IDs to query in the search box, and clicks 'submit' to submit (box1). Next, as for the queried genes (box2), the user selects the SNP ID to query and clicks 'submit' to submit (box3). Then, the page will list the different haplotypes composed of these SNPs and haplotype frequencies (box4). After users checked the haplotype they want to query in the first column, the page will list the sequence composition of the haplotype (box 5) based on the variants selected by the user. Then, the page will list the difference in phenotype values corresponding to accessions with different haplotypes(box 6). Users can also submit genes of interest in the gene search bar to view the differences in gene expression levels of accessions with the different haplotypes (box7).

Brassica napus multi-locus model variation search (ZSN1)

Region/Gene

BnaA08G0134700Z, BnaC03G0745960Z, BnaA05G0427800Z or AT4G34520, AT3G12120 or FAE1, FAD2 or BnaA66g111300, BnaC03g558600, BnaA05g269000 or A06:18618652..18619753, C03:72310540..72311231, A05:40553352..40558043

e.g. BnaA08G0134700Z, BnaC03G0745960Z, BnaA05G0427800Z or AT4G34520, AT3G12120 or FAE1, FAD2 or BnaA66g111300, BnaC03g558600, BnaA05g269000 or A06:18618652..18619753, C03:72310540..72311231, A05:40553352..40558043

提交文件 (txt.csv)

submit reset

SNP basic information

BnaC03G0745960Z BnaA08G0134700Z BnaA05G0427800Z

Search:

Download

<input type="checkbox"/>	Gene/Region	Chr.	Position	All (allele)	Ref (allele)	JBrowse	All (Frequency)	Ref (Frequency)	PIC	All (num)	Ref (num)	Function_Type	Variation_Type
<input checked="" type="checkbox"/>	BnaC03G0745960Z	C03	72309785	GTT	G	JBR	0.45	0.52	0.37	1066	1137	HIGH	frameshift_variant
<input type="checkbox"/>	BnaC03G0745960Z	C03	72309841	G	CCTGA	JBR	0.21	0.79	0.27	427	1768	HIGH	frameshift_variant
<input type="checkbox"/>	BnaC03G0745960Z	C03	72310132	C	A	JBR	0.00	1.00	0.01	8	2302	MODERATE	missense_variant
<input type="checkbox"/>	BnaC03G0745960Z	C03	72310665	G	T	JBR	0.00	1.00	0.01	9	2302	MODERATE	missense_variant
<input type="checkbox"/>	BnaC03G0745960Z	C03	72310722	C	T	JBR	0.00	1.00	0.01	9	2302	LOW	synonymous_variant

Showing 1 to 5 of 5 entries 1 row selected

Previous 1 Next

submit

4

Results of the locus combinations

Search:

Download

<input type="checkbox"/>	ID	locus combination	Frequency	Sample
<input checked="" type="checkbox"/>	hap_0	G_A_C	0.307	617
<input checked="" type="checkbox"/>	hap_1	GTT_G_C	0.178	357
<input checked="" type="checkbox"/>	hap_2	G_A_T	0.176	354
<input checked="" type="checkbox"/>	hap_3	GTT_A_C	0.169	339
<input checked="" type="checkbox"/>	hap_4	GTT_A_T	0.069	139
<input checked="" type="checkbox"/>	hap_5	GTT_G_T	0.064	128
<input checked="" type="checkbox"/>	hap_6	G_G_C	0.027	54
<input type="checkbox"/>	hap_7	G_G_T	0.009	19

Showing 1 to 8 of 8 entries 7 rows selected

submit

5

Brief table of the locus combinations

Search:

Download

ID	Freq	No.	C03 72309788	A06 10018098	A05 40553972
combinator_0	0.307	617	G	A	C
combinator_1	0.178	357	GTT	G	C
combinator_2	0.176	354	G	A	T
combinator_3	0.169	339	GTT	A	C
combinator_4	0.069	139	GTT	A	T
combinator_5	0.064	128	GTT	G	T
combinator_6	0.027	54	G	G	C
combinator_7	0.009	19	G	G	T

Showing 1 to 8 of 8 entries

6

Phenotype violin plot

Frailt: Seed oil content (SOC)

p-value: 0.2305 (Anova)

Order: None

Ascending

Descending

FontSize(title): 14

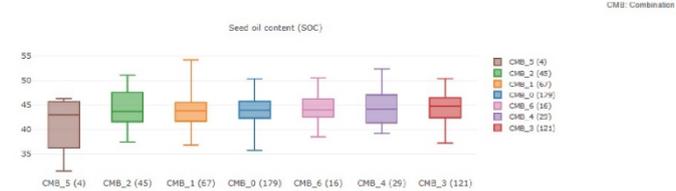
FontSize(axis): 14

FontWeight(title): Cyes

FontWeight(axis): no

Width(chart): 1000

submit



7

Expression violin plot

Gene: BnaA08G0134700Z

p-value: 0.4071 (Anova)

Tissue: Seed (20DAF)

Seed (20DAF)

Order: None

Ascending

Descending

FontSize(title): 14

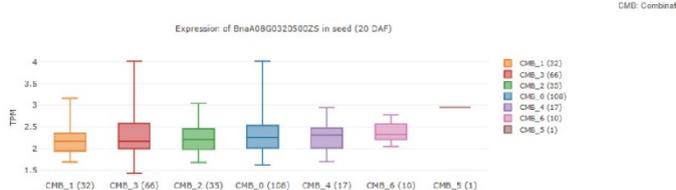
FontSize(axis): 14

FontWeight(title): Cyes

FontWeight(axis): no

Width(chart): 1000

submit



Customized phenotype association

In the Customized phenotype association module, users can directly paste the phenotype data (box 1) in Customize phenotype, or upload a local phenotypic data file, and then use it according to the operation mode of the Single-locus module.

Gene ID ? 未选择任何文件

e.g. *FAE1*, AT4G34520, BnaA08G0134700ZS, *FLOWERING LOCUS C*

Gene region ?

e.g. A01:450000..460000

Gene Index ? 未选择任何文件

e.g. BnaA08G0310400ZY, BnaA08g27310D, A01p00080.1_BnaDAR

Mode SNP Haplotype SV

Customize phenotype **1**

Accession_ID	Yield
26	27.19100007
34	27.61233333
44	27.547
46	28.199
50	27.49500007
60	27.24833333
66	27.53500007
72	27.32733333
80	27.114
88	30.26800007
100	27.39233333
106	28.97000007
126	10.993
128	27.42300007
138	27.41533333
144	29.83833333
158	27.507

example file or fpls_phe_1.txt or fpls_phe_2.txt

Transcriptomics

Expression profile (ZS11 library)

Expression profile (ZS11 library) module can facilitate the identification of gene functions, which is greatly needed in rapeseed. Expression profile (ZS11 library) module contains gene expression levels from 91 libraries of ZS11 (Zhongshuang11), including covering eight different tissues covering 3 distinct developmental stages during its life cycle, including cotyledon, root, stem peel, leaf, bud, flower, silique, silique wall and seed. Especially, there exist 26 and 23 time points in seed and silique wall respectively and 24 leaf developmental time points, with 2 day intervals. In this module, Users can search the expression level information of the gene of interest through three gene modes including gene ID, genome interval and gene index. For example, when the user enters FT, the information of the six homologous genes on the ZS11 genome will be obtained first in the "Basic information of genes", including the gene id of the corresponding Darmor genome, the corresponding *Arabidopsis thaliana* homologous gene ID and gene name, Physical location and functional descriptive information of genes. Then, in the "Summary of gene expression", the statistical information of gene expression level is obtained, including how many libraries it is expressed in, the mean, median, maximum, minimum, standard deviation and coefficient of variation of the expression. Then, the page will give data and visual displays of the expression levels of these genes in all libraries, such as heatmaps, line graphs, and boxplots.

Expression profile (meta library)

We collected gene expression profiles of 2,791 published RNA-seq libraries. Similar to Expression profile (ZS11 library), this module also supports three search modes: gene ID, genome interval and gene index. For example, when the user enters FT, the information on the 6 homologous genes on the ZS11 genome will be obtained first in the "Basic information of genes", including the gene id of the corresponding Darmor genome, the corresponding *Arabidopsis* homologous gene ID and gene name, the physical location and functional description of the gene. Then, in the "Summary of gene expression", the statistical information of the expression level of the gene is obtained, including how many of the 2,791 libraries are expressed, the mean, median, maximum, minimum, standard deviation and coefficient of variation. Then, the page will give the data and visualization of the expression levels of these genes in all libraries. Then, the user will get the expression of these genes in different ecotypes of rapeseed during the vernalization process and double-low and double-high rapeseed, and the user can know whether these genes are related to the breeding improvement process according to the difference in gene expression between accessions. In addition, we also provide a comparison of gene expression levels among heterosis accessions in groups, so that users can understand whether these genes are related to heterosis.

Population expression

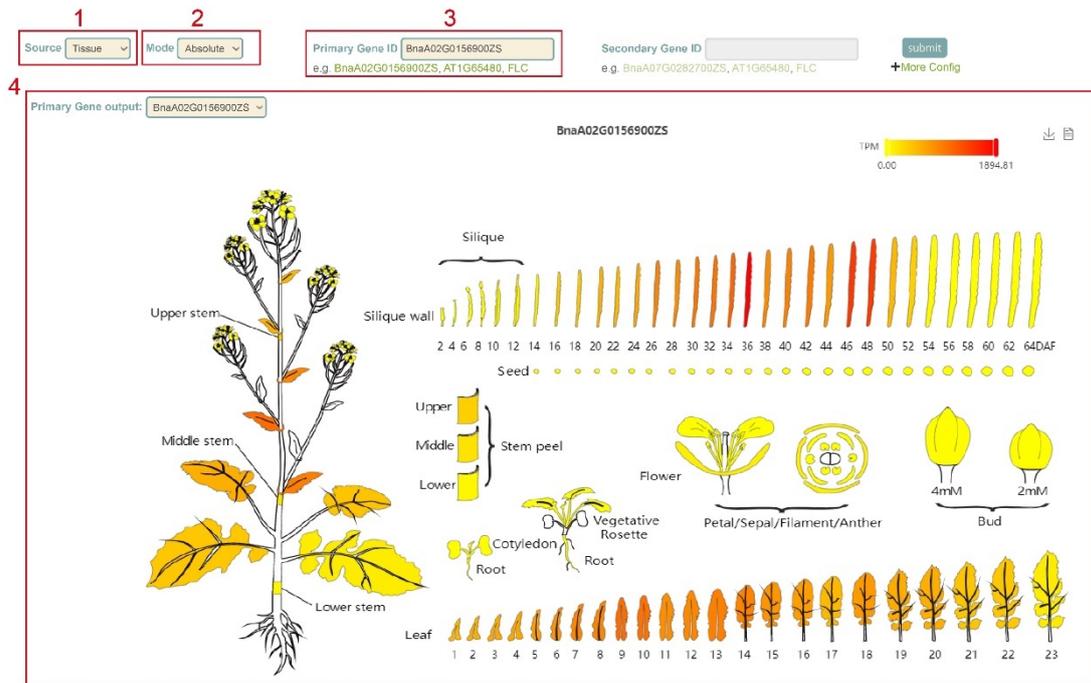
We integrated the gene expression data of 700 samples of seeds and leaves at 20 days after flowering, 40 days after flowering. The user can enter the Arabidopsis gene ID, *B. napus* gene list or genomic region, and then select the tissue to query the expression level of the gene of interest. For example, when the user enters FLC and selects "Leaves", the following result can be obtained. "Basic information of genes" (box 1) is the 10 homologous gene information on the ZS11 genome, including the gene id of the corresponding Darmor genome, the corresponding Arabidopsis homologous gene ID and gene name, and the physical location of the gene and functional description information. Then there are the clustering results of the expression levels of these genes in the population, and the texts in different colors on the horizontal axis represent rapeseed of different ecotypes (box 2). Finally, boxplots of gene expression levels of different ecotypes of *B. napus* can be viewed.

Transcriptomics-phenotype association

In the Transcriptomics-phenotype association module, we integrated data from seeds at 20 days after flowering, 40 days after flowering, and 20 phenotypes. Users can enter Arabidopsis gene ID, *B. napus* gene list or genomic region, and then select tissue to query the correlation between the expression level of the gene of interest and these phenotypes. When the user enters a gene ID and selects a tissue and clicks 'submit' to submit, "Basic information of genes" will give information on the homologous genes on the ZS11 genome. Then, by selecting the phenotype and clicking 'submit', users can obtain the correlation information of these genes and phenotypes and the scatter plot of genes and phenotypes in the "Expression-phenotype basic information" category.

eFP(single gene module)

eFP provides eFP browser, allowing users to comprehensively view gene expression levels among 8 tissues at different stages of development. By entering "Data Source", "Mode", "Primary Gene ID", "Secondary Gene ID", "Signal Threshold" and clicking "Go", you will see the specific expression of genes in various tissues under controlled conditions. User can select one data source from 'Tissue', 'Hormone' and 'Adversity' (box 1), one mode from 'Absolute', 'Relative' and 'Compare' (box 2) and Gene ID (box 3). Then, the eFP figure of gene expression will be obtained (box 4). Users can move the mouse over the tissue in the figure to query the gene expression value.



eFP(multiple gene module)

Similar to eFP(Single gene Module), eFP(Multiple gene Module) provides an eFP browser with multiple gene expressions. In this module, the user can view the sum of the expression levels of these homologous genes by entering the Arabidopsis gene ID to obtain the gene name in the eFP browser.

Phenotype

In Phenotype portal, we collected 118 traits of 2,512 accessions, including 50 traits of 525 inbred lines, 36 glucosinolate related traits of 288 accessions, five traits of 991 accessions, three flowering time traits of 210 accessions and 27 traits of 505 accessions. These phenotypic data are grouped into five modules based on their data sources, and users can browse these phenotypic datasets in the corresponding modules. Taking 522 Inbred Lines (Bus et al. 2011) as an example[2], clicking on 522 Inbred Lines (Bus et al. 2011) takes you to the phenotypic page of that population. The first is categorical statistics of all types of phenotypes. For example, if users want to search the oil content, users can click "Seed Quality Traits" (box1) to obtain 15 seed quality-related phenotypes, including oil content phenotype data of 405 accessions. Then click '405' (box2) to obtain the specific phenotypic value information of 405 samples (Box3), the histogram of phenotypic value distribution (box4) and the boxplot of phenotypic value of different rape types (box5).

● Inbreds from Bus et al. (2011)

▼ Trait Statistics:

Class	Traits Num.	Total Record Num.
Agronomic Traits	15	4961
1 Seed Quality Traits	15	5671
Seeding Development	20	10180

▼ Search results (Seed Quality Traits)

Search:

Class	Trait Name	Abbreviation	Unit of measurement	Record Num.
Seed Quality Traits	Thousand grain weight	TGW	g	219
Seed Quality Traits	Average projected seed area	A/A	cm2	219
Seed Quality Traits	Moisture content	MOI	% of dry mass	402
Seed Quality Traits	Oil content	OIL	% of dry mass	2 405
Seed Quality Traits	Protein content	PRT	% of dry mass	404
Seed Quality Traits	Glucosinolate concentration	GSL	micromoles/g	405
Seed Quality Traits	Sulfur concentration	SUL	% of dry mass	401
Seed Quality Traits	Oleic acid concentration	OLA	% of total fatty acid	402
Seed Quality Traits	Linolenic acid concentration	LIA	% of total fatty acid	402
Seed Quality Traits	Erucic acid concentration	ERA	% of total fatty acid	405

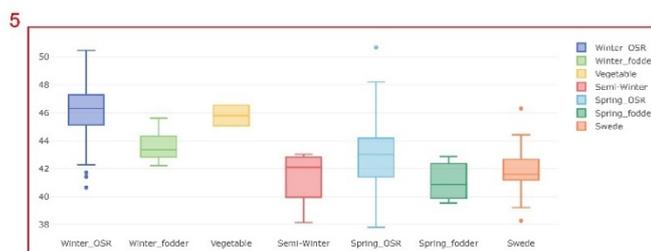
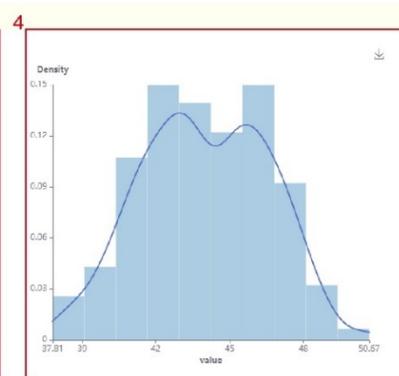
Showing 1 to 10 of 15 entries Previous **1** 2 Next

3 ▼ Trait Values List (Seed Quality Traits: OIL)

Search: Download

No.	Genotype Name	Set-Collection	Genoplasm Type (OSR: oilseed rape)	Continent	Country	Trait Value
1	Alesi	DFG-Set 01	Winter_OSR	Western_Europe	France	45.06
2	Remy	DFG-Set 02	Winter_OSR	Western_Europe	France	46.88
3	Robust	DFG-Set 03	Winter_OSR	Western_Europe	France	44.93
4	Alaska	DFG-Set 04	Winter_OSR	Western_Europe	United_Kingdom	45.11
5	Pirola	DFG-Set 05	Winter_OSR	Western_Europe	France	45.33
6	Adder	DFG-Set 06	Winter_OSR	Western_Europe	United_Kingdom	45.1
7	Milena	DFG-Set 07	Winter_OSR	Western_Europe	France	45.32
8	Allure	DFG-Set 08	Winter_OSR	Western_Europe	Germany	44.86
9	Agalon	DFG-Set 09	Winter_OSR	Western_Europe	United_Kingdom	46.78
10	K615	DFG-Set 10	Winter_OSR	Western_Europe	United_Kingdom	42.75

Showing 1 to 10 of 405 entries Previous **1** 2 3 4 5 ... 41 Next



Epigenetics

Histone modification

The user first enters the gene ID to query (box 1), the genomic region, histone modification type, accession and tissue. Take AT1G65480 as an example, first enter AT1G65480 in Gene ID, and choose the 3kb in Flanking region (box 2), then select tissue, histone modification type and accession in Datasets (box 3), and then click 'submit' to submit. In the Results section, the physical location and functional annotation information of the homologous genes of AT1G65480 in the ZS11 genome are listed first (box 4). Then there is the peak information in this region (box 5). The last is the coverage of reads in this region in the Jbrowser browser (box 6).

1

Histone modification

Gene ID: ?
 e.g. FT or AT1G65480 or BnaA02G019890ZS or FLOWERING LOCUS T

Gene region: ?
 e.g. A01:160000..230000

Gene Index: ?

e.g. example_1 or example_2

2 Flanking region (s) 0.5kb 1kb 1.5kb 2kb 2.5kb 3kb

3

Datasets

4

▼ Basic information of gene(s)

Search:

Selector	ZS11 Gene ID	Darmor Gene ID	ATGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA02G019890ZS	BnaA02g12130D	AT1G65480	FT	A02:9104462..9107270	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe
<input type="checkbox"/>	BnaA07G0282700ZS	BnaA07g25310D	AT1G65480	FT	A07:26253195..26259595	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe
<input type="checkbox"/>	BnaA07G0366100ZS	BnaA07g33120D	AT1G65480	FT	A07:30986418..30988169	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe
<input type="checkbox"/>	BnaC02G0200600ZS	BnaC02g45200D	AT1G65480	FT	C02:16937203..16938659	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe
<input type="checkbox"/>	BnaC04G0181400ZS	BnaC04g14850D	AT1G65480	FT	C04:17076818..17075789	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe
<input type="checkbox"/>	BnaC06G0323800ZS	BnaC06g27090D	AT1G65480	FT	C06:42937446..42939746	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowe

Showing 1 to 6 of 6 entries 1 row selected Previous Next

5

▼ Basic information of peak(s)

Search:

Genomic position	Length	Abs_submit	Pileup	-Log10(pvalue)	Fold_enrichment	-Log10(qvalue)	Name	Tissue	Signal	Variety
A02:9104394..9104750	357	9104694	14.36	5.13515	3.29269	3.84781	leaf_H3K27me3_B409_rep2_peak_2966	leaf	H3K27me3	B409
A02:9105115..9106434	1320	9105728	34.16	20.6283	7.03206	18.9595	leaf_H3K27me3_B409_rep2_peak_2967	leaf	H3K27me3	B409
A02:9105182..9106370	1189	9105611	18	14.0863	7.43882	12.3083	leaf_H3K27me3_B409_rep1_peak_3157	leaf	H3K27me3	B409
A02:9106790..9108448	1659	9107059	57.45	45.1584	11.6903	43.0236	leaf_H3K27me3_B409_rep2_peak_2968	leaf	H3K27me3	B409
A02:9106842..9107618	777	9107151	37	38.9337	15.3567	36.5377	leaf_H3K27me3_B409_rep1_peak_3158	leaf	H3K27me3	B409

Showing 1 to 5 of 5 entries Previous Next

6

▼ JBrowse

DNA methylation

In the DNA methylation module, we integrated data from 54 WGBS-seq libraries and calculated the methylation ratio of each gene region in each library. Users can enter the gene id or genomic region, then set the region size (box1) in Flanking region, select Tissue (box2), and click 'submit' to query.

DNA methylation

Gene ID ?
e.g. FT or AT1G65480 or BnaA02G015690ZS or FLOWERING LOCUS T

Gene region ?
e.g. A01:150000..230000

Gene Index ?
 e.g. example_1 or example_2

1 Flanking region (±) 0kb 1kb 1.5kb 2kb 2.5kb 3kb

2 Tissue Seed Leaf Root Silique Flowerbud

Chromatin accessibility

The user first enters the gene to query (box 1), the genomic region, histone modification type, the sample and the tissue. Take *FAEI* as an example, first enter *FAEI* in Gene ID, set a 3kb surrounding area in Flanking region (box 2), then select tissue and sample in Datasets (box 3), click 'submit', or chromatin accessibility values for the 3kb region surrounding this gene. In the Results section, the physical location and functional annotation information of *FAEI* homologous genes in the ZS11 genome are first listed (box 4). Then the peak information is listed (box 5). The last is the coverage of reads in this region in the Jbrowser browser (box 6).

1

Chromatin accessibility

Gene ID ?
 e.g. FLC or AT1G02970 or BnaA08G0320500ZS

Gene region ?
 e.g. A08:150000..230000

Gene Index ?

2
3

Flanking region (±) 0kb 1kb 1.5kb 2kb 2.5kb 3kb

Datasets

submit reset

4

▼ Basic information of gene(s)

Search: Download

Selector	ZS11 Gene ID	Darmor Gene ID	ATGI	At Name	Genomic position	Function	Description
<input type="checkbox"/>	BnaA03G0397300ZS	BnaA03g39010D	AT4G34520	FAE1	A03:21413975..21415438	3-ketoacyl-CoA synthase 18 OS=Arabidopsis thaliana GN=FAE1 PE=1 SV=1	Encodes KCS18, a member of the 3-k
<input checked="" type="checkbox"/>	BnaA08G0134700ZS	BnaA08g11130D	AT4G34520	FAE1	A08:19618052..19619753	3-ketoacyl-CoA synthase 18 OS=Arabidopsis thaliana GN=FAE1 PE=1 SV=1	Encodes KCS18, a member of the 3-k
<input type="checkbox"/>	BnaC03G0494000ZS	BnaC03g46140D	AT4G34520	FAE1	C03:35858639..35860030	3-ketoacyl-CoA synthase 18 OS=Arabidopsis thaliana GN=FAE1 PE=1 SV=1	Encodes KCS18, a member of the 3-k
<input type="checkbox"/>	BnaC03G0745900ZS	BnaC03g65980D	AT4G34520	FAE1	C03:72309540..72311231	3-ketoacyl-CoA synthase 18 OS=Arabidopsis thaliana GN=FAE1 PE=1 SV=1	Encodes KCS18, a member of the 3-k

Showing 1 to 4 of 4 entries 1 row selected Previous 1 Next

submit

5

▼ Basic information of peak(s)

Search: Download

Genomic position	Length	Abs_submit	Pileup	-Log10(pvalue)	Fold_enrichment	-Log10(qvalue)	Name	Tissue	Signal	Variety
A08:18617117..18617325	209	18617216	23.00	6.91599	3.17824	4.68773	seed_ATACseq_NY10_rep1_peak_11451	seed	ATACseq	NY10

Showing 1 to 1 of 1 entries Previous 1 Next

6

▼ JBrowse

Chromatin interaction

In Chromatin interaction module, we collected and analyzed the Hi-C data of the three published accessions and obtained their chromatin interaction features.

Firstly, the user enters the gene, genomic region or gene index to query, or uploads the gene index file. Then clicks "submit" to submit. Next, the user will get the information list of the queried genes.

The user can select the gene to be query by checking the first column (box1) and click "submit" to submit.

The user will then get the results of three parts including the A/B compartment(box2), the TAD(box3), and the chromatin interaction frequency for each 100kb region(box4). Users can click

"Download" in the upper right to download.

Gene ID: **Input gene ID** ?
 e.g. FT or AT1G65480 or BnaA02G015690G2S or FLOWERING LOCUS T

Gene region: **Input the genomic region** ?
 e.g. A01 150000 400000

Gene Index: **Input the gene index** ?
 e.g. example_1 or example_2 **Upload the gene index file**

Click to submit

1

▼ Basic information of gene(s)

Search:

Selector	ZS11 Gene ID	Darmor Gene ID	AtGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA02G015690G2S	BnaA02g12130D	AT1G65480	FT	A02:9104462..9107270	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow
<input type="checkbox"/>	BnaA07G028270D2S	BnaA07g25310D	AT1G65480	FT	A07:26283195..26255955	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow
<input type="checkbox"/>	BnaA07G036510D2S	BnaA07g33120D	AT1G65480	FT	A07:30595418..30598159	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow
<input type="checkbox"/>	BnaC02G020090G2S	BnaC02g45250D	AT1G65480	FT	C02:16837203..16838959	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow
<input type="checkbox"/>	BnaC04G0181400G2S	BnaC04g14850D	AT1G65480	FT	C04:17070818..17073769	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow
<input type="checkbox"/>	BnaC06G032390G2S	BnaC06g27050D	AT1G65480	FT	C06:42937446..42939746	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LF-Y, promotes flow

Showing 1 to 6 of 6 entries 1 row selected

2

▼ A/B compartment

Search:

Dataset	Chr	Start	End	Eigv_compartment_val	Compartment	Gene density	TE num
2127	A02	9100001	9200000	0.0456005	A	0.2108	128
NY7	A02	9100001	9200000	0.0331374	A	0.2108	128
ZS11	A02	9100001	9200000	0.0554709	A	0.2108	128

Showing 1 to 3 of 3 entries

3

▼ TAD

Search:

Dataset	Chr	Start	End
NY7	A02	7400000	12000000

Showing 1 to 1 of 1 entries

4

▼ Contact frequency

Search:

Dataset	Chr	Start	End	Gene density	TE num	Intrachr contact frequency	Interchr contact frequency	Sum contact frequency
2127	A02	9100001	9200000	0.2108	128	9859	9500	19359
NY7	A02	9100001	9200000	0.2108	128	3957	4977	8934
ZS11	A02	9100001	9200000	0.2108	128	17005	12550	29555

Showing 1 to 3 of 3 entries

Multi-omics

GWAS

In GWAS module, the user firstly clicked the phenotype name(box1), and then a dialog box for the phenotype list will pop up. The user selects the phenotype by checking the first column, then clicks 'OK', and then clicks 'submit', that is GWAS results for this phenotype can be viewed. The first is a manhattan plot (box3) of a 500kb window, in which we denote the p-value of each window by the p-value of the most significant SNP in it. Here, the user can zoom in or out by sliding the mouse wheel, and then move the mouse to the corresponding window to browse the lead SNP and the corresponding p-value (box4) in the window. The user can then click on the bars of this window to view all the significant SNPs within this region along with the corresponding GWAS statistics (box 5) and Manhattan plots (box 6).



5

Dena/Region: A08:19500000:19930000 e.g. A08:15000000:18600000 or A08:rs104802013590029

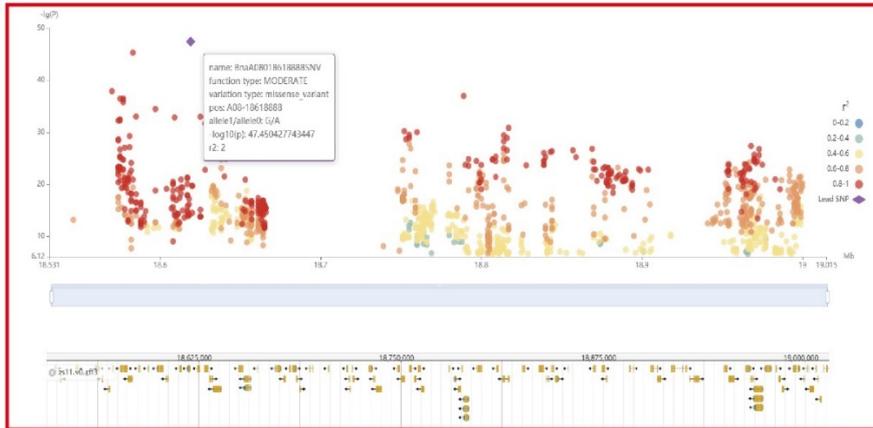
Search:

SNP	-log10(P)	r ²	Chr	Pos	allele1/allele2	Variation type	Function type
BnaA08010616886SNV	71.82	2	A08	18618566	G/A	missense_variant	MODERATE
BnaA08018569719SNV	67.72	0.876681	A08	18569719	A/G	upstream_gene_variant	MODIFIER
BnaA08018624567SNV	59.69	0.847259	A08	18624567	C/T	missense_variant	MODERATE
BnaA08018555071SNV	59.40	0.812665	A08	18555071	G/GTA	upstream_gene_variant	MODIFIER
BnaA08018598600SNV	57.21	0.8327	A08	18598600	T/C	upstream_gene_variant	MODIFIER
BnaA08010606686SNV	57.03	0.79577	A08	18606686	G/A	upstream_gene_variant	MODIFIER
BnaA08018530378SNV	56.19	0.836768	A08	18530378	C/A	downstream_gene_variant	MODIFIER
BnaA08018789329SNV	54.55	0.691485	A08	18789329	A/C	synonymous_variant	LOW
BnaA08018577748SNV	53.83	0.7484	A08	18577748	CA/VC	splice_region_variant&intron_variant	LOW
BnaA080106130071SNV	51.94	0.756421	A08	18633071	T/G	upstream_gene_variant	MODIFIER

Showing 1 to 10 of 1,548 entries

Previous 1 2 3 4 5 ... 156 Next

6



eQTL

In eQTL module, the user first searches for genes by gene ID(box1), genomic region or gene index, then selects the tissue in the "Development stage", and clicks "submit" to submit. In the results, the first is a list of all SNPs significantly associated with the expression of this gene and the corresponding statistics, including beta and P-value (box3). Finally, a circos diagram of the relationship between SNP and gene regulation was shown. Users can move the mouse to the corresponding point in the diagram to view the value of the statistic corresponding to 'eSNP-eGene' (box4).

eQTL(Expression quantitative trait loci)

1

Gene ID ?
 e.g. FT or AT1G65480 or BnaA01G000200ZS or FLOWERING LOCUS

Gene region ?
 e.g. A01:150000..230000

Gene Index ?
 e.g. example_1 or example_2

2

Development stage Seeds at 20 DAF Seeds at 40 DAF

3

Results

Search:

ZS11 Gene ID	Gene pos	SNP	SNP_pos	Beta	P-value
BnaA07G0282700ZS	A07:26253164..26255955	BnaA01002322154SNV	2322154	4.03	1.64e-7
BnaA07G0282700ZS	A07:26253164..26255955	BnaA03011646947SNV	11646947	6.03	1.08e-8
BnaA07G0282700ZS	A07:26253164..26255955	BnaA03018523452SNV	18523452	4.85	2.22e-7
BnaA07G0282700ZS	A07:26253164..26255955	BnaA03018527368SNV	18527369	5.06	1.05e-7
BnaA07G0282700ZS	A07:26253164..26255955	BnaA07024556710SNV	24556710	6.03	9.69e-8
BnaA07G0282700ZS	A07:26253164..26255955	BnaA07024720826SNV	24720826	5.94	9.2e-8
BnaA07G0282700ZS	A07:26253164..26255955	BnaA07025915067SNV	25915067	5.64	3.42e-8
BnaA07G0282700ZS	A07:26253164..26255955	BnaA07026259341SNV	26259341	2.87	1.85e-7
BnaA07G0282700ZS	A07:26253164..26255955	BnaA09058389783SNV	58389783	6.07	1.79e-8
BnaA07G0282700ZS	A07:26253164..26255955	BnaA10002313270SNV	2313270	5.56	1.75e-7

Showing 1 to 10 of 68 entries

Previous Next

4

TWAS

In the TWAS module, the user firstly clicked the phenotype name (box1), and a dialog box for the phenotype list will pop up. The user selects the phenotype by checking the first column, then clicks 'OK', and then selects the corresponding organization (box2), click 'submit' to view the TWAS results of the phenotype of the tissue. The first is a genome-wide Manhattan plot of all gene TWAS (box 3). Users can zoom in or out by sliding the mouse wheel, and then move the mouse to the corresponding point to browse the TWAS statistics of the gene (box4). The user can then click on the corresponding point to view the TWAS statistics for this gene (box 6). Users can also search for genes by Gene ID, genome interval or Gene index (box 5) to view the TWAS results of these genes and browse the structure of these genes and the distribution of genetic variation near them in the Jbrowser browser (box 7).

column, then clicks 'OK', and then selects the corresponding tissue (box3), click 'submit' to view the TWAS results of the phenotype of that tissue. The first is a Manhattan plot of the SMR of all genes in the whole genome (box4) and the information list of all significant genes (box5). The SMR significance threshold is: $P(\text{SMR}) < 1/n$ (20DAF: $n=35,633$, 40DAF: $n=38,747$), $P(\text{HEIDI test}) > 1.57 \times 10^{-3}$. Users can zoom in or out by sliding the mouse wheel, and then move the mouse to the corresponding point to browse the GWAS, eQTL and SMR statistics of the gene (box4). The user can then click on the corresponding point to view detailed statistics of the SMR for this gene (box 7). Users can also search for genes (box6) by Gene ID, genomic region, or gene index to view SMR results of these genes. Next, the page gives the local Manhattan map of SMR, GWAS, and eQTL in the 1Mb region near the gene (box8). Users can move the mouse to these points to view the corresponding SNP/Gene statistics (box9). Finally, users can browse the structure of these genes and the distribution of genetic variation in their vicinity in the Jbrowser browser.

SMR (Summary data-based Mendelian randomization analysis)

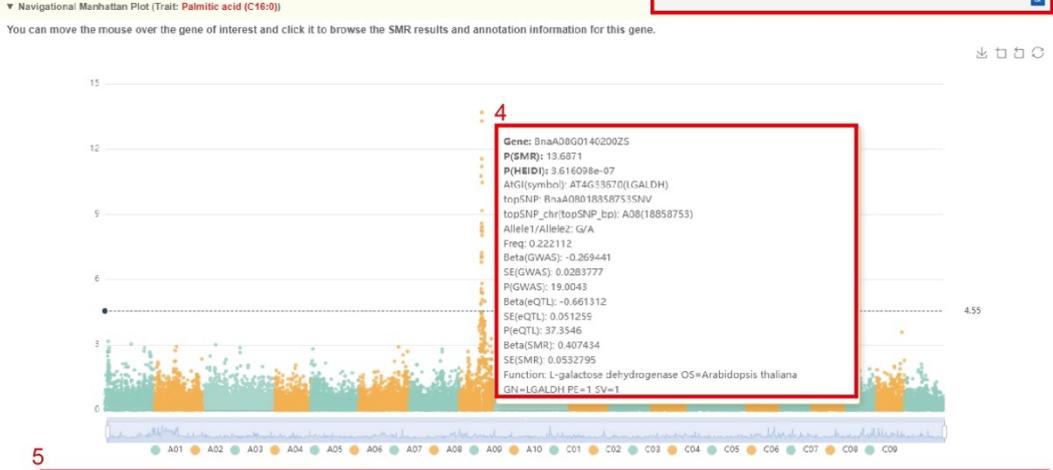
1 Trait:

3 Development stage: Seeds at 20 DAF Seeds at 40 DAF

submit

2

Study	Year	Case	Trait	Trait type	Ref name
1	2019	-	-	-	Palmitic acid (C16:0)
2	2019	-	-	-	Stearic acid (C18:0)
3	2019	-	-	-	Stearic acid (C18:0)
4	2019	-	-	-	Linoleic acid (C18:2)
5	2019	-	-	-	Arachidonic acid (C20:4)
6	2019	-	-	-	Docosahexaenoic acid (C22:6)
7	2019	-	-	-	Palmitoleic acid (C16:1)
8	2019	-	-	-	Phosphatidylcholine (PC)
9	2019	-	-	-	Phosphatidylethanolamine (PE)
10	2019	-	-	-	Phosphatidylserine (PS)
11	2019	-	-	-	Phosphatidylinositol (PI)
12	2019	-	-	-	Phosphatidylglycerol (PG)
13	2019	-	-	-	Phosphatidylcholine (PC)
14	2019	-	-	-	Phosphatidylethanolamine (PE)
15	2019	-	-	-	Phosphatidylserine (PS)
16	2019	-	-	-	Phosphatidylinositol (PI)
17	2019	-	-	-	Phosphatidylglycerol (PG)
18	2019	-	-	-	Phosphatidylcholine (PC)
19	2019	-	-	-	Phosphatidylethanolamine (PE)
20	2019	-	-	-	Phosphatidylserine (PS)
21	2019	-	-	-	Phosphatidylinositol (PI)
22	2019	-	-	-	Phosphatidylglycerol (PG)
23	2019	-	-	-	Phosphatidylcholine (PC)
24	2019	-	-	-	Phosphatidylethanolamine (PE)
25	2019	-	-	-	Phosphatidylserine (PS)
26	2019	-	-	-	Phosphatidylinositol (PI)
27	2019	-	-	-	Phosphatidylglycerol (PG)
28	2019	-	-	-	Phosphatidylcholine (PC)
29	2019	-	-	-	Phosphatidylethanolamine (PE)
30	2019	-	-	-	Phosphatidylserine (PS)
31	2019	-	-	-	Phosphatidylinositol (PI)
32	2019	-	-	-	Phosphatidylglycerol (PG)
33	2019	-	-	-	Phosphatidylcholine (PC)
34	2019	-	-	-	Phosphatidylethanolamine (PE)
35	2019	-	-	-	Phosphatidylserine (PS)
36	2019	-	-	-	Phosphatidylinositol (PI)
37	2019	-	-	-	Phosphatidylglycerol (PG)
38	2019	-	-	-	Phosphatidylcholine (PC)
39	2019	-	-	-	Phosphatidylethanolamine (PE)
40	2019	-	-	-	Phosphatidylserine (PS)
41	2019	-	-	-	Phosphatidylinositol (PI)
42	2019	-	-	-	Phosphatidylglycerol (PG)
43	2019	-	-	-	Phosphatidylcholine (PC)
44	2019	-	-	-	Phosphatidylethanolamine (PE)
45	2019	-	-	-	Phosphatidylserine (PS)
46	2019	-	-	-	Phosphatidylinositol (PI)
47	2019	-	-	-	Phosphatidylglycerol (PG)
48	2019	-	-	-	Phosphatidylcholine (PC)
49	2019	-	-	-	Phosphatidylethanolamine (PE)
50	2019	-	-	-	Phosphatidylserine (PS)



5

▼ List of significant SMR loc (p_HEIDI>1.57e-3) (Trait: Palmitic acid (C16:0))

Search:

Download

Selector	ZS11 Gene ID	P(SMR)	P(HEIDI)	Darmer Gene ID	AGI	At Name	Genomic position	Function
<input type="checkbox"/>	BnaA08G013340Z5	5.0635	3.529766e-01	-	AT4G38920	VHA-C3	A08:18549157..18550150	V-type proton ATPase subunit c5 OS=Arabidopsis thaliana GN=VHA-c5 PE=2
<input type="checkbox"/>	BnaA08G014490Z5	5.57664	2.230419e-01	BnaA08g12070D	AT4G32700	TEB	A08:19295869..19306644	Helicase and polymerase-containing protein TEB/CHI OS=Arabidopsis thaliana GN=TEB/CHI PE=1 SV=1
<input type="checkbox"/>	BnaA08G014310Z5	6.75455	1.441400e-01	BnaA08g11910D	AT4G33090	APM1	A08:19125052..19129209	Aminopeptidase M1 OS=Arabidopsis thaliana GN=APM1 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014300Z5	5.40554	1.135017e-01	BnaA08g11900D	AT4G33100	-	A08:19123722..19124334	Uncharacterized protein Atg33100 OS=Arabidopsis thaliana GN=Atg33100 PE=1 SV=1
<input type="checkbox"/>	BnaA08G013760Z5	7.04458	8.311524e-02	BnaA08g11350D	AT4G34131	UGT73B3	A08:18760639..18762173	UDP-glycosyltransferase 73B3 OS=Arabidopsis thaliana GN=UGT73B3 PE=2
<input type="checkbox"/>	BnaA08G014630Z5	4.91423	6.830958e-02	BnaA08g12190D	AT4G33470	CQR7-1	A08:19380001..19380512	Cytochrome b-c1 complex subunit 7-1 OS=Arabidopsis thaliana GN=CQR7-1 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014900Z5	4.8567	6.653956e-02	-	AT5G10360	RPS6B	A08:19627361..19628729	40S ribosomal protein S6.2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=1
<input type="checkbox"/>	BnaA08G013530Z5	10.46	6.361571e-02	BnaA08g11190D	AT4G34430	SWI3D	A08:18652678..18657296	SWI/SNF complex subunit SWI3D OS=Arabidopsis thaliana GN=SWI3D PE=1 SV=1
<input type="checkbox"/>	BnaA08G010190Z5	4.9917	5.507709e-02	BnaA08g08120D	AT4G16800	-	A08:16195238..16199778	Methylglucosyl-CoA hydratase, mitochondrial OS=Dictyostelium discoideum GN=HSD17B10 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014530Z5	8.23659	4.937500e-02	BnaA08g12110D	AT4G32680	-	A08:19319437..19320633	-

Showing 1 to 10 of 18 entries

▼ Search by gene ID/region (Trait: Palmitic acid (C16:0))

6

Gene ID:

e.g. FT or AT1G65400 or BnaA02G015696Z5 or FLOWERING LOCUS T

Gene region:

e.g. A01:450000..460000

Gene Index:

选择文件: e.g. example_1 or example_2

submit reset

7

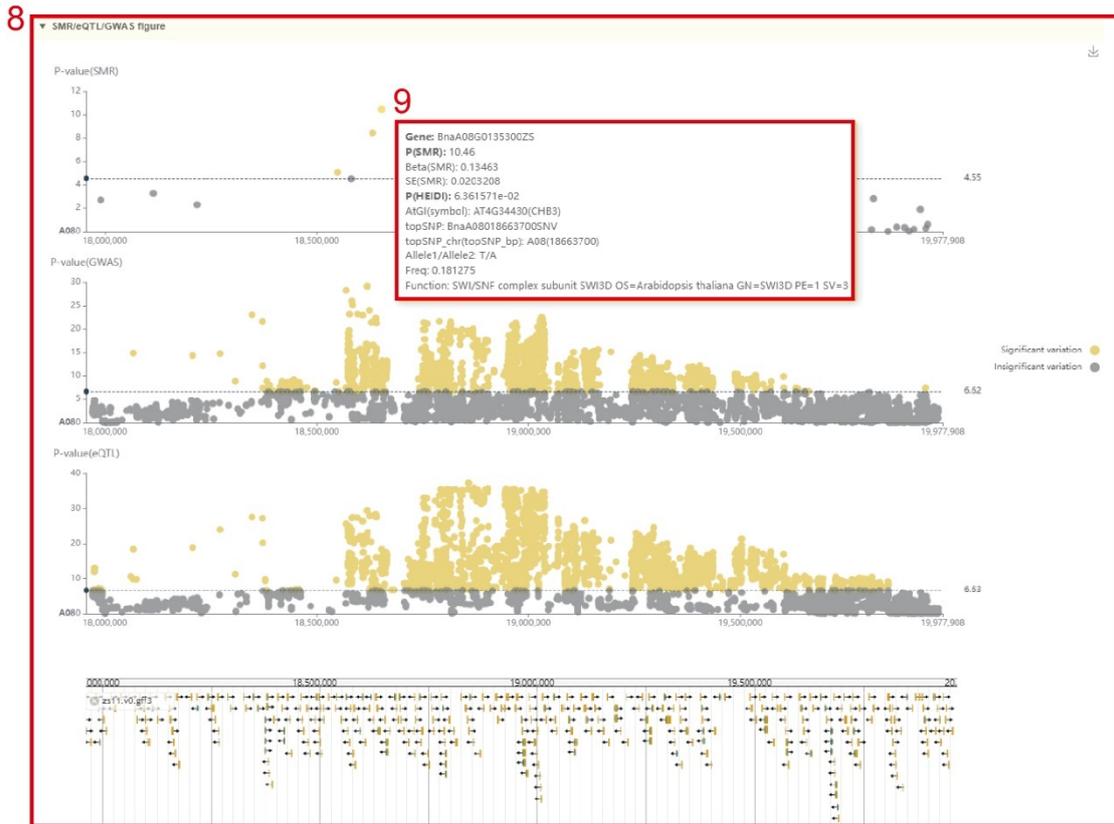
▼ Basic information of gene(s) for custom search

Search:

Download

Selector	ZS11 Gene ID	Darmer Gene ID	AGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA08G014020Z5	BnaA08g11480D	AT4G33670	L GALDH	A08:18566145..18567998	L-galactose dehydrogenase OS=Arabidopsis thaliana GN=L GALDH PE=1 SV=1	Encodes a L-galactose dehydrogenase

Showing 1 to 1 of 1 entries 1 row selected



Colocalization analysis

Based on the GWAS and eQTL results, we identified 1,849 associations between expressed genes with eQTL and GWAS loci by co-localization analysis. A total of 217 associations were identified by co-localization analysis, which were integrated into Colocalization analysis module.

In this module, the first part is a list of colocalization analysis results of eQTL and GWAS loci of 1,849 pairs of expressed genes (box1), including all statistics of colocalization analysis, such as PPH₀, PPH₁, PPH₂, PPH₃, PPH₄. Users can filter these results by selecting the tissue and phenotype by pulling down the Development stage and Trait menus. Then, the user can select the colocalization analysis results of the QTL and eQTL to be viewed next by checking the first column, and click 'submit' to submit. The results start with the main statistics of the results of the colocalization analysis of QTL and eQTL. The red text on the left represents the accepted hypothesis. If the PPH₄ value is the largest among all PPH values, the text of the PPH₄ hypothesis is marked in red, indicating to accept H₄, which is "both traits are associated and share a single causal variant". On the premise of accepting H₄, the P-values of GWAS and eQTL and PPH₄ values of all variants in this region are listed(box3), which can be used to locate the causal variation. And users can move the mouse to the figure to browse the detailed statistics of these variants(box4). Then comes the visualization of the local Manhattan plot of the GWAS and eQTL in the region, and the user can also move the mouse over the points in the plot to see detailed statistics of these variants (box5). Finally, users can browse the distribution of genetic variation near the gene in the Jbrowser browser.

1 COLOC (Colocalization analysis)

Development stage: Trait:

Search: Download

eQTL	Phenotype	Phenotype source	QTL	Lead SNP	Gene	COLOC ^A	COLOC_pph0	COLOC_pph
<input checked="" type="checkbox"/> seed_4DDAF	Branch angle	Sun, C. et al. (2016)	qBA.A07.1	BnaA070015012/DSNV	BnaA0700018100ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Oil content	Tang, S., et al. (2021)	qCC.A05.1	BnaA0504111397DSNV	BnaA05G0437200ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Oil content	Tang, S., et al. (2021)	qCC.A05.2	BnaA05041245313SNV	BnaA05G0440100ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Oil content	Tang, S., et al. (2021)	qCC.C05.1	BnaC05053831616SNV	BnaC05G0499000ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Oil content	Tang, S., et al. (2021)	qCC.C05.7	BnaC05053831616SNV	BnaC05G0499200ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Oil content	Tang, S., et al. (2021)	qCC.C05.1	BnaC05053831616SNV	BnaC05G0499400ZS	TRUE	0	0
<input type="checkbox"/> seed_4DDAF	Tolerance coefficients of ground dry weight at the mature stage	Zhang, G., et al. (2022)	qM_G/DW_R2.A03.1	BnaA03010015040SNV	BnaA03G0192800ZS	TRUE	0.000002	0.000032
<input type="checkbox"/> seed_4DDAF	Plant height of high salt-alkali condition at the mature stage	Zhang, G., et al. (2022)	qM_P/H_HA10.4	BnaA10024374757SNV	BnaA10G0251700ZS	TRUE	0	0.00023
<input type="checkbox"/> seed_4DDAF	Tolerance coefficients of yield at the mature stage	Zhang, G., et al. (2022)	qM_Y_R2.A03.1	BnaA03010015040SNV	BnaA03G0192800ZS	TRUE	0.000002	0.000032

Showing 1,841 to 1,845 of 1,849 entries 1 row selected

submit Previous 1 181 182 183 184 185 Next

2 Summary of colocalisation analysis (the number of SNPs analysed and the posterior probabilities of H0, H1, H2, H3 and H4)

H0: neither trait has a genetic association in the region
H1: only trait 1 has a genetic association in the region
H2: only trait 2 has a genetic association in the region
H3: both traits are associated, but with different causal variants
H4: both traits are associated and share a single causal variant

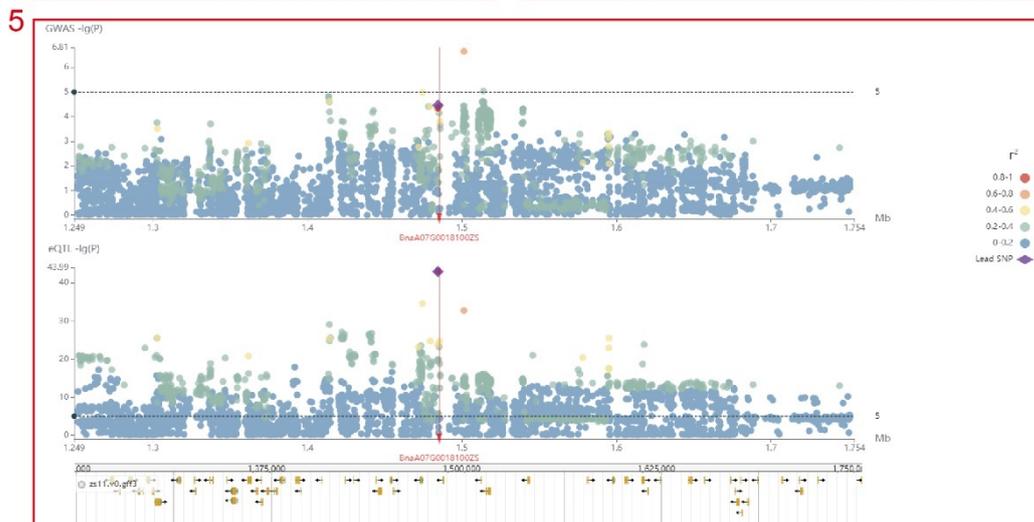
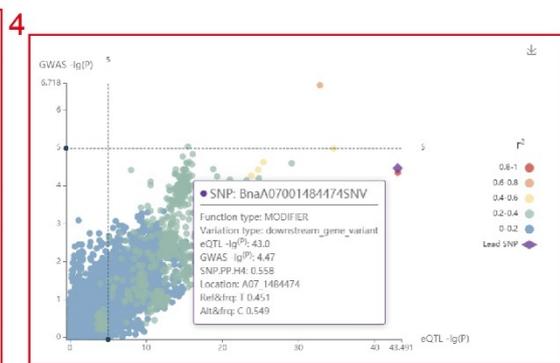
SNPs number	PP.H0.abf	PP.H1.abf	PP.H2.abf	PP.H3.abf	PP.H4.abf
5,015	3.79e-50	4.83e-49	0.0133	0.168	0.818

3 COLOC results

Search: Download

SNP	P(GWAS)	P(eQTL)	SNP_PP.H4
BnaA07001484474SNV	0.0000340	1.01e-43	0.558
BnaA07001484465SNV	0.0000450	1.01e-43	0.442
BnaA07001474334SNV	0.0000103	2.77e-35	6.09e-15
BnaA07001501270SNV	2.18e-7	1.42e-33	7.47e-16
BnaA07001414204SNV	0.0000253	7.95e-30	2.10e-23
BnaA07001422178SNV	0.000151	7.78e-28	6.90e-27
BnaA07001411381SNV	0.000268	1.54e-27	2.50e-27
BnaA07001439980SNV	0.000263	3.29e-27	9.45e-28
BnaA07001439985SNV	0.000253	3.23e-27	9.45e-28
BnaA07001423928SNV	0.000517	2.07e-27	4.77e-20

Showing 1 to 10 of 5,015 entries Previous 1 2 3 4 5 ... 502 Next



Metabolome

In the metabolome module, we collected data on 544 metabolites from 33 accessions from two studies. According to these two studies, it is divided into two modules, "Guard Cells in Response to Low CO₂" and "Laminae and midvein during leaf senescence", where users can search for corresponding sample and metabolite content information respectively. Take the "Guard Cells in Response to Low CO₂" module as an example. First, the eight accessions are listed and the user selects the accession to be query at the first column, and then clicks "submit" to submit (box1). Next, the information of all metabolites of this accession was listed, the user can click the link in the second column to query the relevant information of these metabolites (box2). Finally, the visualization of the content of different metabolites in the accession, the user can move the mouse to the corresponding point to view the specific value (box3).

1

Selector	Class	Compounds
<input checked="" type="checkbox"/>	5 min significantly increased metabolites	56
<input type="checkbox"/>	5 min significantly decreased metabolites	5
<input type="checkbox"/>	10 min significantly increased metabolites	43
<input type="checkbox"/>	10 min significantly decreased metabolites	40
<input type="checkbox"/>	30 min significantly increased metabolites	13
<input type="checkbox"/>	30 min significantly decreased metabolites	11
<input type="checkbox"/>	60 min significantly increased metabolites	17
<input type="checkbox"/>	60 min significantly decreased metabolites	31

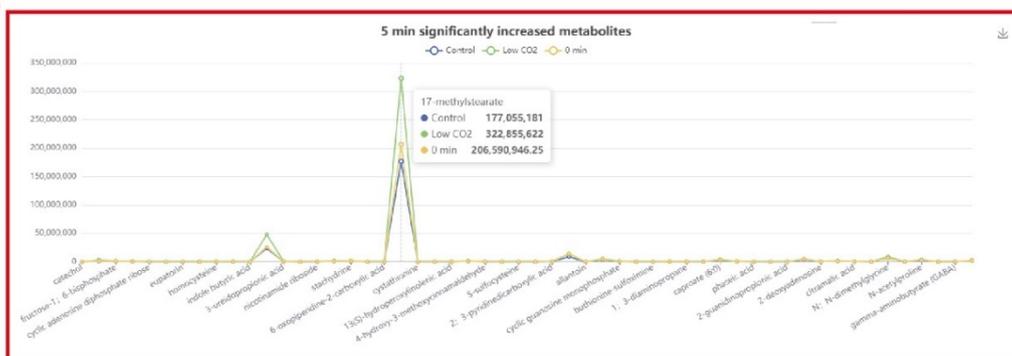
Showing 1 to 0 of 0 entries 1 row selected

2

Metabolome Name	Information
1-palmitoylglycerophosphoglycerol*	View
13(S)-hydroperoxylinolenic acid	View
17-methylstearate	View
1; 3-diaminopropane	View
2-deoxyadenosine	View
2-deoxyinosine	View
2-guanidinopropionic acid	View
2-isopropylmalic acid	View
2-palmitoylglycerol (2-monopalmitin)	View
2; 3-pyridinedicarboxylic acid	View

Showing 1 to 10 of 56 entries

3



Network

Co-expression

In the Co-expression module, the user first submits one or more gene IDs in the search box, and sets the depth of the network connection (1 or 2) (box1), and then clicks “submit” to submit. Next, the user will obtain the co-expression network figure of the gene or genes (box2) and the pearson correlation coefficients and functional information of the gene or genes (box3).

1 Co-expression

Gene ID: ?
 e.g. BnaA03G0318200ZS or BnaA03G0318200ZS BnaA03G0512200ZS

Search depth: 1 2

Threshold (pearson correlation coefficient):

2 Co-expression network

Source Target

3 Co-expression information

Search:

Source Gene ID	Target Gene ID	PCC-value	Source Gene description
BnaA03G0318200ZS	BnaA03G0323400ZS	0.90	--
BnaA03G0318200ZS	BnaA04G0134400ZS	0.90	--
BnaA03G0318200ZS	BnaA04G0178100ZS	0.93	Putative F-box protein At1g237
BnaA03G0318200ZS	BnaA05G0358000ZS	0.92	--
BnaA03G0318200ZS	BnaA09G0119800ZS	0.90	Spermidine hydroxycinnamoyl tr
BnaA03G0318200ZS	BnaA10G0108500ZS	0.93	--
BnaA03G0318200ZS	BnaC04G0282200ZS	0.92	MATH domain and coiled-coil domain-containing
BnaA03G0318200ZS	BnaC08G0448200ZS	0.91	--
BnaA03G0323400ZS	BnaA09G0119800ZS	0.93	Spermidine hydroxycinnamoyl tr
BnaA05G0358000ZS	BnaA10G0108500ZS	0.92	--
BnaA05G0358000ZS	BnaC04G0282200ZS	0.93	MATH domain and coiled-coil domain-containing
BnaA10G0108500ZS	BnaC04G0282200ZS	0.96	MATH domain and coiled-coil domain-containing
BnaA10G0108500ZS	BnaC08G0448200ZS	0.91	--
BnaC04G0282200ZS	BnaC08G0448200ZS	0.94	MATH domain and coiled-coil domain-containing protein At3g58360 OS=Arabidopsis thaliana (GN=At3g58360) PE=3 SV=1

Showing 1 in 14 of 14 entries Previous Next

TF regulation network

In the TF regulation network module, the user first submits one or more gene IDs (box1) in the search box, and sets the search modes including TF (to retrieve downstream regulated genes), Target (to retrieve the TF genes) or Genes (to retrieve the TF genes and regulated downstream genes) (box2), and then clicks “submit” to submit. Next, the user will get the network figure of TFs and the target genes (box3), the pearson correlation coefficients between them and the function information of the genes (box4).

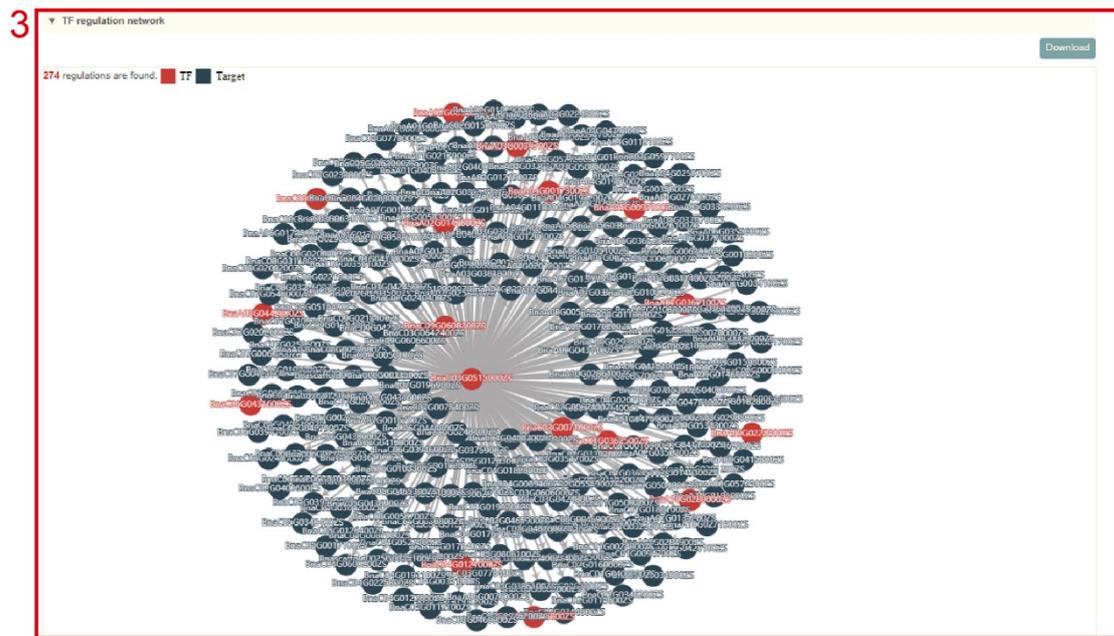
TF regulation network

Users can select one of the three modes to retrieve regulations according to your requirement:

- "TF(retrieve targets)" to retrieve the downstream targets of input TFs.
- "Target(retrieve TFs)" to retrieve the upstream regulators of input genes.
- "Gene (retrieve regulations among them)" to retrieve the input regulations among input genes in the regulation network, red nodes represented TF genes and the arrow points to the target genes.

Mode: TF(retrieve targets) Target(retrieve TFs) Genes(retrieve regulations among them)

Gene ID:



TF regulation basic information

Search:

TF Gene ID	Genomic position(TF Gene)	AtGI/At Name(TF Gene)	Target Gene ID	Genomic position(Target Gene)	AtGI/At Name(Target Gene)
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0014400ZS	A01:6883369..687739	AT4G37440/---
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0029800ZS	A01:1654444..1658287	AT3G28410/---
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0030000ZS	A01:1601702..1602610	AT4G35390/AHL25
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0088600ZS	A01:3699425..3700818	AT1G77340/---
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0083700ZS	A01:4718445..4720350	AT4G28880/TYRDC
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0134900ZS	A01:8085665..8087084	AT4G23900/NDK4
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaC07G0199000ZS	C07:33216675..33218908	AT2G38650/---
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0217900ZS	A01:1393721..13939049	AT3G17700/CNGC20
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G0405500ZS	A01:36111923..36115115	AT3G03800/CCT8
BnaC03G0515000ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA02G0035000ZS	A02:2053141..2053737	AT5G10280/MYR2

Showing 1 to 10 of 274 entries

Previous ... Next

Variation annotation using SnpEff

Genome: ZS11 Damror

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	sample1	sample2
A01	124800	A01_124800_SNV	C	T	.	PASS	.	GT	0/0	1/1
A01	124713	A01_124713_SNV	T	G	.	PASS	.	GT	0/0	0/0
A01	124751	A01_124751_SNV	A	G	.	PASS	.	GT	0/0	1/1
A01	124761	A01_124761_SNV	A	G	.	PASS	.	GT	0/0	0/0
A01	124767	A01_124767_SNV	C	T	.	PASS	.	GT	0/0	1/1
A01	125023	A01_125023_SNV	G	A	.	PASS	.	GT	0/0	1/1
A01	125046	A01_125046_SNV	A	G	.	PASS	.	GT	0/0	1/1

Paste the variations to be annotated

Please submit a file in vcf format, click here to get an example.

未选择任何文件 **Upload the variation file with the VCF format**

Click to submit

▼ Variation annotation result

Variation_annotation.vcf

▼ SnpEff: Variant analysis

You can click here to get statistical results.

GO enrichment

Usage:

1. Select the genome in "Dataset";
2. Paste the gene list in the sequence box or upload the gene list file, and click Submit;

Click to select the genome →

Dataset:

Gene List:

Paste the gene list

[click here to get example](#)

Click to submit

ZS11
 Damror.v10
 Damror.v4.1
 Gangen.v0
 Ningyou7.v2
 No2127.v0
 Quinta.v0
 Shengli.v0
 Express617.v1
 Tapidor.v0
 Westar.v0
 Zheyu.v0
 Brassica carinata
 z6-1.v0

Results:

1. List of results of GO enrichment analysis. You can switch the category of GO by clicking BP, MF and CC above, and click "Download" in the upper right to download;
2. The dot plot and bar plot of GO enrichment analysis results. Move the mouse over the figure to query the statistics of the corresponding GO enrichment analysis results. Click the arrow at the top right to download the image.

▼ GO enrichment result

BP MF CC [Click to switch the GO catalog](#)

Search:

[Click to download](#) [Download](#)

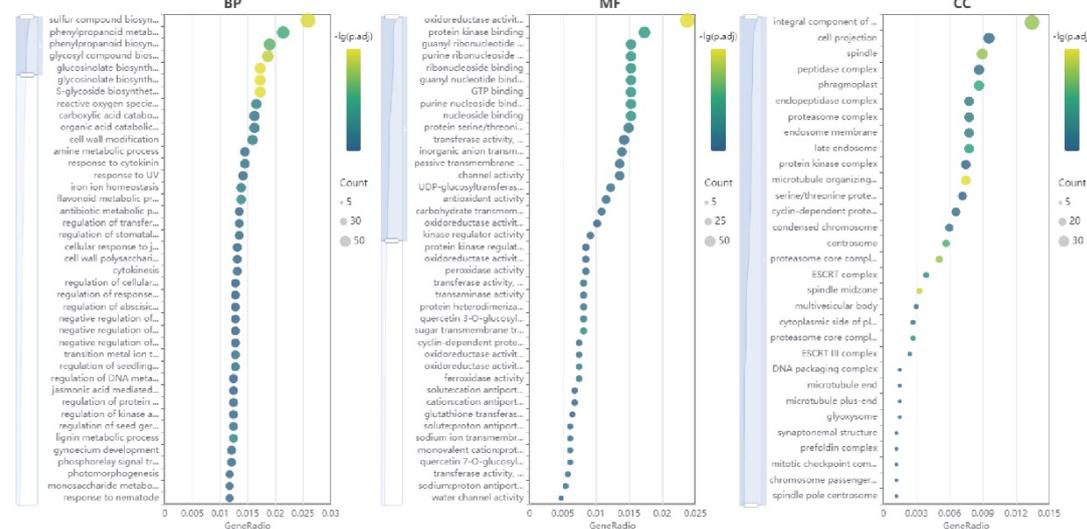
ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0016144	S-glycoside biosynthetic process	50/2895	228/62797	2.43103073555425e-20	2.20596675766619e-17	1.8202535549922e-17	BnaC09G0288000ZS/Bna...	50
BP	GO:0019758	glycosinolate biosynthetic process	50/2895	228/62797	2.43103873555428e-20	2.28938675766619e-17	1.8202535549922e-17	BnaC09G0288000ZS/Bna...	50
BP	GO:0019761	glucosinolate biosynthetic process	50/2895	228/62797	2.43103073555425e-20	2.20596675766619e-17	1.8202535549922e-17	BnaC09G0288000ZS/Bna...	50
BP	GO:0044272	sulfur compound biosynthetic process	75/2895	452/62797	1.1577727102579e-19	8.23654694265915e-17	6.55790987728675e-17	BnaC09G0409100Z3/Bna...	75
BP	GO:1901659	glycosyl compound biosynthetic process	54/2895	289/62797	1.66875264491000e-18	9.4151024225827e-16	7.49709082997499e-16	BnaC09G0288000ZS/Bna...	54
BP	GO:0009699	phenylpropanoid biosynthetic process	56/2895	374/62797	3.81800083557788e-14	1.7950987261942e-11	1.42940592688372e-11	BnaC09G0462800ZS/Bna...	56
BP	GO:0009699	phenylpropanoid metabolic process	62/2895	481/62797	4.10682943096827e-13	1.65509256068827e-10	1.31782291615473e-10	BnaC09G0462800ZS/Bna...	62
BP	GO:0009812	flavonoid metabolic process	40/2895	305/62797	3.33423416415085e-09	1.17575547363359e-05	9.36234703463251e-07	BnaC09G0689500ZS/Bna...	40
BP	GO:0009808	lignin metabolic process	36/2895	262/62797	5.75391614600639e-08	1.8035304976506e-06	1.43612363223144e-06	BnaC09G0462800ZS/Bna...	36
BP	GO:0009809	lignin biosynthetic process	30/2895	204/62797	2.18027988343853e-08	6.1505955118009e-06	4.89750712763981e-06	BnaC09G0462800ZS/Bna...	30

Showing 1 to 10 of 331 entries

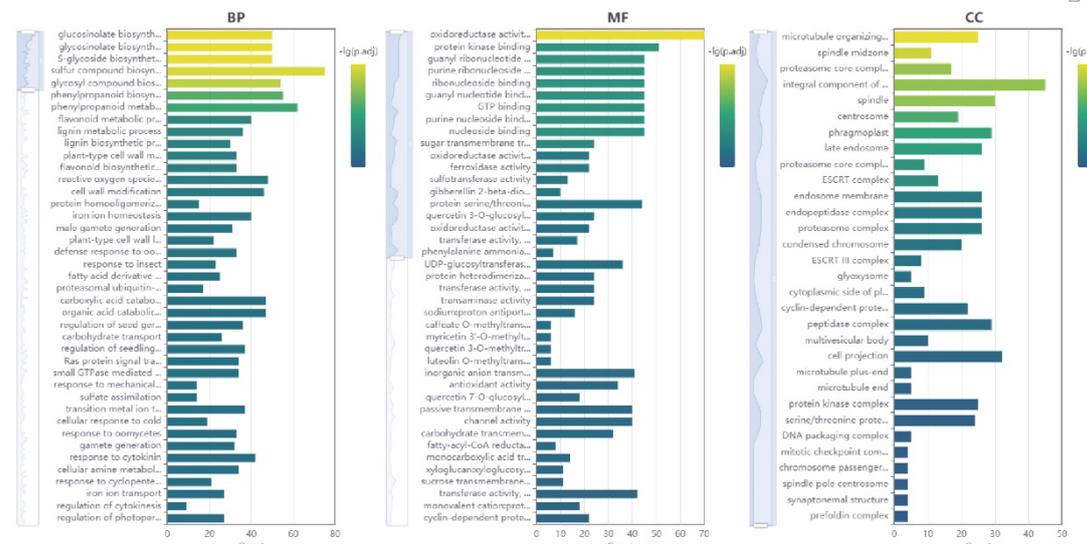
Previous 1 2 3 4 5 ... 34 Next

▼ Dotplot for enrichment result

Move the mouse over the circle to see the result of GO enrichment



▼ Barplot for enrichment result



KEGG enrichment

Usage:

1. Select the genome in "Dataset";

2. Paste the gene list in the sequence box or upload the gene list file, and click “Submit” to submit;

Click to select the genome

Dataset: ZS11

Gene List: BnaA01G0000700ZS
BnaA01G0001800ZS
BnaA01G0002600ZS
BnaA01G0003300ZS
BnaA01G0004000ZS

Paste the gene list

选择文件 click here to get example

submit reset

Click to submit

Results:

1. The result list of KEGG enrichment analysis. Click “Download” in the upper right to download;
2. Dot plot, bar plot and network plot of KEGG enrichment analysis results. Move the mouse over the figure to query the statistics of the corresponding KEGG enrichment analysis results. Click the arrow at the top right to download the image.

KEGG enrichment result

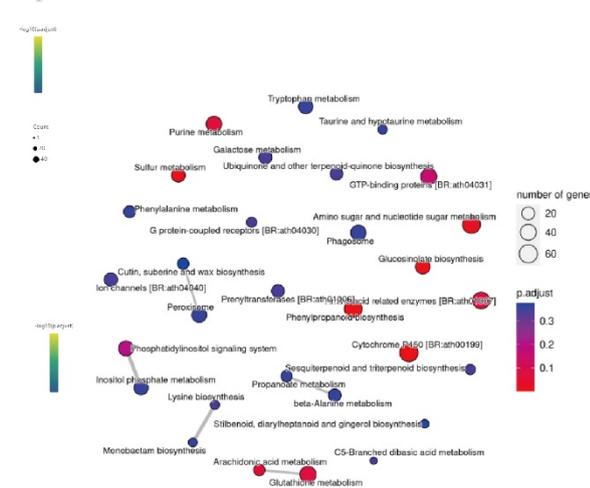
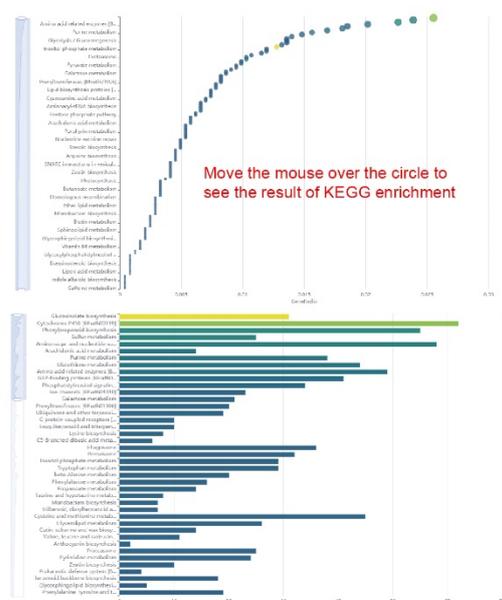
Search:

Click to download Download

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
ath00966	Glucosinolate biosynthesis	31/2430	119/32033	7.80149395687474e-10	1.02979716270747e-07	9.27967140238789e-06	BnaC08G00/4300ZS/Bna...	31
ath00199	Cytochrome P450 [BR:ath00199]	62/2430	402/32033	7.450550450/4089e-08	4.91742929/48899e-06	4.4311/6320/703/79e-06	BnaC09G0221300ZS/Bna...	62
ath00940	Phenylpropanoid biosynthesis	55/2430	431/32033	0.000108156057657487	0.00475886653692941	0.00428829281238456	BnaC09G0365300ZS/Bna...	55
ath00920	Sulfur metabolism	25/2430	156/32033	0.000297635562954643	0.0090219735/775032	0.00065074174049532	BnaC09G0091200ZS/Bna...	25
ath00520	Amino sugar and nucleotide sugar metabolism	58/2430	497/32033	0.00073279004317208	0.0193456571397429	0.0174326834480937	BnaC09G0298700ZS/Bna...	58
ath00590	Arachidonic acid metabolism	14/2430	80/32033	0.00261326092460539	0.0574917403413186	0.0518057516632297	BnaC07G0488200ZS/Bna...	14
ath00230	Purine metabolism	38/2430	316/32033	0.00331940688403267	0.062945260417389	0.0564049536630627	BnaC09G0437300ZS/Bna...	38
ath00480	Glutathione metabolism	44/2430	384/32033	0.00417061045369066	0.0680150724858959	0.06201039227179795	BnaC09G0314300ZS/Bna...	44
ath01007	Amino acid related enzymes [BR:ath01007]	49/2430	441/32033	0.0047528492149319	0.0700375121819001	0.063119527633942	BnaC09G058300ZS/Bna...	49
ath04031	GTP-binding proteins [BR:ath04031]	41/2430	375/32033	0.0110891377700982	0.156306516565297	0.141410165054053	BnaC09G0117200ZS/Bna...	41

Showing 1 to 10 of 132 entries

Previous 1 2 3 4 5 ... 14 Next



SNP match

Usage:

1. Select the genome, ZS11 or Darmor;
2. Paste the genotype data (VCF format) of the sample to be identified in the sequence box or upload the genotype file (VCF format) of the sample and click Submit. SNPmatch will then predict the similarity between the accession to be queried and the 2311 accessions based on the genotype information and output the accessions with a similarity of larger than 0.5.

Results:

1. The result list of SNPmatch: Click “Download” at the top right to download;
2. The bar plot of SNPmatch results, the x axis is the accession name in the population similar to the input accession, and the y axis is the similarity with the sample. Move the mouse to the figure to query the corresponding data. Click the arrow at the top right to download the image.

SNPmatch

Genome: ZS11 Darmor [Click to select the genome](#)

```
##format=VCF-v4.2
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
#CHROM POS ID REF ALT QUAL FILTER INFO FORMAT sample1
A01 3265 BnaA010000103265SNV A G . PASS . GT 00
A01 4030 BnaA010000104030SNV G A . PASS . GT 00
A01 11046 BnaA01000011046SNV C T . PASS . GT 00
...
```

Paste the genotypes of the accession

Please submit a file in vcf format,click here to get an example.

选择文件 example.vcf ← Upload the the genotype file with the VCF format

▼ SNPmatch results

Search:

Accession name	Gemtoplasm	Origin	Subpopulation	Number of matched SNPs	Total informative SNPs	Probability of match	Likelihood	Likelihood ratio against best hit
1000	Y10	Asia	Semi-winter	19980	19980	1	1	1
g151	Dac-chosen	Europe	Semi-winter	19184	19980	0.96	11317.514	11317.514
R5059	ZAAS-M7	Asia	Semi-winter	19146	19980	0.958	11897.506	11897.506
g111	4312huashuang1	Asia	Semi-winter	19118	19980	0.957	12326.029	12326.029
R5051	Zhoda-619	Asia	Semi-winter	19051	19980	0.954	13355.23	13355.23
q176	Youguangye	Asia	Semi-winter	19035	19980	0.953	13601.772	13601.772
R244	Quanzi rape	Asia	Winter	19037	19980	0.953	13570.938	13570.938
R5060	ZAAS-M74	Asia	Semi-winter	18986	19980	0.95	14358.558	14358.558
R4548	Maxol	Europe	Winter	18952	19980	0.949	14885.176	14885.176
R4479	Passat	Europe	Winter	18959	19980	0.949	14621.716	14621.716

Showing 1 to 10 of 2,311 entries Previous 1 2 3 4 5 ... 232 Next

2

Probability of match ↓

Move the mouse over the circle to see the SNPmatch result

Accession name: 1000
 Gemtoplasm: Y15
 Origin: Asia
 Subpopulation: Semi-winter
 Probability of match: 1
 Number of matched SNPs: 19980
 Likelihood: 1
 Likelihood ratio against best hit: 1

■ Winter
■ Spring
■ Semi-winter
■ Unknown

Primer3

Usage:

1. Enter gene ID, genomic region, gene index, or upload gene list or sequence file;

e-PCR

Usage:

1. Click on Dataset to select the genome;
2. Select the file format (STS or Primers) in Mode;
3. Paste the sequence into the dialog or upload the sequence file;
4. Adjust alignment parameters, including mismatch value(mism), gap size(gap) and sequence length range(lo-hi”);
5. Click Submit.

Results:

1. The list of e-PCR results, each row is the position of the sequence amplified by the primers;
2. Statistical chart of e-PCR comparison results, including the ratio of mismatches and gaps;
3. The raw output result of e-PCR.

e-PCR results

Search: Genomic position of the sequences Click to submit

Primer ID	Chr	Strand	Start	End	Mism	Gaps	act_len/exp_len
STS-1	ZS11_A02	+	9107124	9107373	0	0	250/50-1000
STS-1	ZS11_C02	+	16838813	16839062	0	0	250/50-1000

Showing 1 to 2 of 2 entries Previous 1 Next

e-PCR statistics plot

STS-1 Click to submit

Mism statistics

Gaps statistics

e-PCR native results

```

#- sts seq strand from to mism gaps act_len/exp_len
sts-1 2511_A02 + 9107124 9107373 0 0 250/50-1000
sts-1 2511_C02 + 16838813 16839062 0 0 250/50-1000
#- done
    
```

Heatmap

Usage:

1. Paste the gene list to be extracted into the dialog box;
2. Select the RNA-seq dataset, including Tissue, Hormone or Adversity;
3. Select RNA-seq samples and the normalization method for expression levels;
4. Set the parameters of the expression heatmap, such as max, min and colorbar, and click “Submit” to submit.

The screenshot shows the LDheatmap web interface. At the top, there is a text input field for "Gene ID" containing a list of gene IDs: BnaA02G0035100ZS, BnaA03G0039200ZS, BnaA03G0144400ZS, BnaA10G0244800ZS, BnaC02G0039100ZS, BnaC03G0046300ZS. Below this is a dropdown menu for "Library" set to "Tissue". A "Sample" field shows "91 samples selected". The "Value" field has radio buttons for "TPM", "log2(TPM+1)", and "log10(TPM+1)". There are input fields for "Height(heatmap)" set to 30 and "Width(heatmap)" set to 70. A color scale legend is shown with a gradient from blue to red. At the bottom are "submit" and "reset" buttons.

Results:

1. The gene expression matrix extracted from the list entered by the user and the selected data set can be downloaded by clicking "Download" in the upper right corner;
2. Gene expression quantification heat map drawn. Move the mouse over the graph to view the corresponding values. Click the arrow in the upper right corner to download.

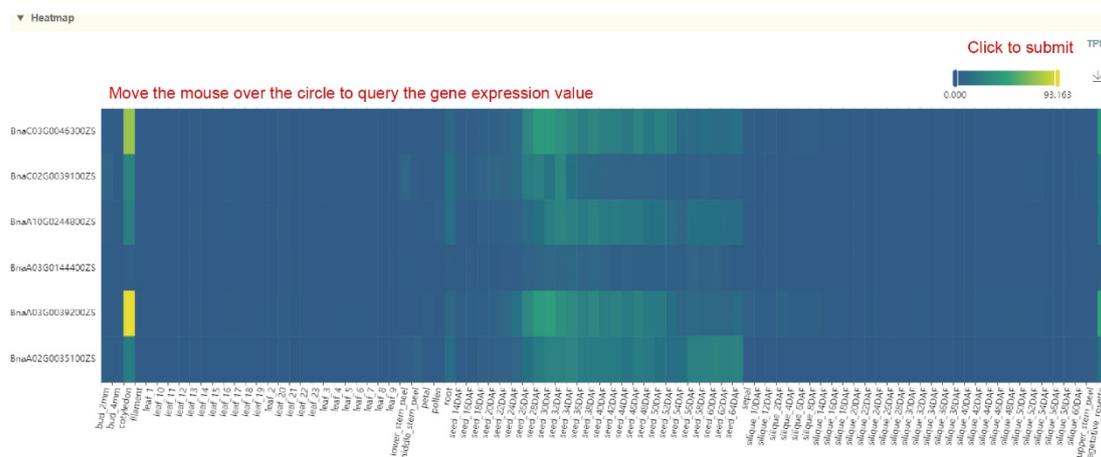
▼ Results

Search: [Click to submit](#) [Download](#)

Gene expression matrix

ZS11 Gene ID	bud_2mm	bud_4mm	cotyledon	filament	leaf_1	leaf_10	leaf_11	leaf_12	leaf_13	leaf_14	leaf_15	leaf_16	leaf_17	leaf_18	leaf_19	le
BnaA02G0035100ZS	2.097	1.049	20.703	0.136	0.094	0.059	0.216	0.429	0.0	0.429	0.912	0.689	0.266	0.395	0.312	0.
BnaA03G0039200ZS	0.239	0.416	93.163	1.058	0.054	0.020	0.113	0.187	0.190	0.430	0.157	1.039	0.238	0.285	0.323	0.
BnaA03G0144400ZS	0.442	0.024	1.691	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.136	0.0	0.059	0.028	0.
BnaA10G0244800ZS	2.067	0.452	22.501	0.089	0.0	0.0	0.087	0.0	0.064	0.141	0.0	0.341	0.0	0.0	0.0	0.
BnaC02G0039100ZS	0.627	0.829	26.378	0.151	0.099	0.097	0.0	0.170	0.093	0.159	0.037	0.412	0.021	0.053	0.022	0.
BnaC03G0046300ZS	0.410	0.156	74.243	0.0	0.0	0.0	0.129	0.026	0.031	0.085	0.236	0.714	0.100	0.195	0.049	0.

Showing 1 to 6 of 6 entries Previous 1 Next



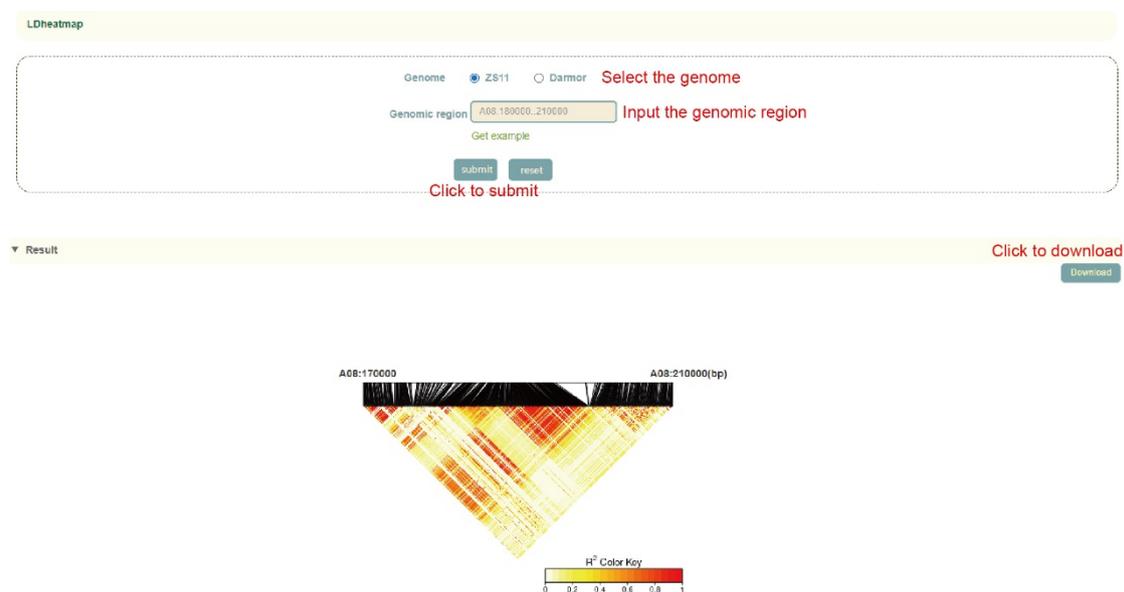
LDheatmap

Usage:

1. Select the genome, ZS11 or Darmor;
2. Enter the genomic region and click 'Submit' to submit.

Results:

Based on user-selected genomes and genomic region, genetic variants are extracted and LD heatmaps are generated. Click "Download" at the top right to download.



Data2geomap

Usage:

1. Select the image type(Geopie or Geoheatmap);
2. Select the region of the map (World, China or the United States);
3. Enter the drawing data and click "Submit" to submit.

Data2geomap

Mode Geopie Geoheatmap **Select the figure type**

Region **Select the region**

Data **Paste the dataset**

Click to submit

Results:

Generate geographic distribution maps based on user-selected image types, regions, and input data. Click the upper right icon to download.



Data2heatmap

Usage:

1. Paste the drawing data into the dialog box or upload the data file;
2. Select the normalization method and drawing parameters and click “Submit” to submit.

[Click to download](#)

```

gene ABCDEFGH
gene_1 1 2 3 4 1 2 3 4
gene_2 4 5 6 7 4 5 6 7
gene_3 8 9 10 11 7 4 5 6 7
gene_4 1 2 3 4 7 4 5 6 7
gene_5 4 5 6 7 7 4 5 6 7
gene_6 8 9 10 11 7 4 5 6 7

```

Paste the data

e.g. example data (Each line of input data can be split by ";" or "," or "." or "\r")

Upload the data file

Select the normalization method

Value: value C_{log2}(value+1) C_{log10}(value+1)

Height(heatmap):

Width(heatmap):

Color:

Fontsize:

Fontcolor:

Fontweight: yes no

Visualmap: yes no

Show_log: yes no

Click to submit

Adjust the parameters of the figure

Results:

Generate heatmaps based on user input data and drawing parameters. Click the upper right icon to download.

