

# 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, BnaA02G01560002S, FLOWERING LOCUS T

Gene region:  ?  
e.g. A01:159000\_230000

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

**2. Basic information of gene(s)**

Search:

Selector	ZS11 Gene ID	Darmor Gene ID	ATGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA02G01560002S	BnaA02G01560002S	AT1G65480	FT	A02:9104462-9107270	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering
<input type="checkbox"/>	BnaA07G02627002S	BnaA07G02627002S	AT1G65480	FT	A07:26253195-26255555	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering
<input type="checkbox"/>	BnaA07G030851002S	BnaA07G0312200	AT1G65480	FT	A07:30865418-30865169	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering
<input type="checkbox"/>	BnaC02G02090002S	BnaC02G45250	AT1G65480	FT	C02:16837203-16839559	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering
<input type="checkbox"/>	BnaC04G01814002S	BnaC04G14850	AT1G65480	FT	C04:17073818-17073769	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering
<input type="checkbox"/>	BnaC06G03238002S	BnaC06G27000	AT1G65480	FT	C06:42937446-42939716	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flowering

Showing 1 to 6 of 6 entries. 1 row selected

**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	BnaA02G01560002S; BnaA07G02627002S; BnaA07G030851002S; BnaC02G02090002S; BnaC04G01814002S; BnaC06G03238002S

Showing 1 to 1 of 1 entries

**4. Phylogenetic tree**

Chr. Start End Length Gene structure

Phylogenetic tree showing relationships between BnaA02G01560002S, BnaA07G02627002S, BnaA07G030851002S, BnaC02G02090002S, BnaC04G01814002S, BnaC06G03238002S, and AT1G65480.

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BnIR is developed by the Yanghui 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

**BnRBR Brassica rapa** *snapus* information resource  
A Pan-Genome-Based Multiomics Database for Brassica napus biological study  
e.g. FLC or ATG102279

Home Genomics Population Variation Transcription Phenotype Epigenetics Miscellaneous Multiscale Network Tools Downloads Help

### 1 Gene cluster

Gene ID: **AT106548D**

e.g. FT, ATR, OSMY-BL, BnaAC25C15S00023, FLOWERING LOCUS T, Branking02500

Submit View

### 2 ▼ Gene cluster table

Search:

ZS11 Gene ID	Darmorc Gene ID
BnaAC2G121300Z, BnaACTG2282T782U, BnaADTG23551BCLJ, BnaCGTG23503BUJS, BnaCSGT218140DUJ, BnaCWBCO3238CUJ, BnaAGTG12138U, BnaACTG2301UD, BnaADTG13191UC, BnaCCG24623UC, BnaCDG1483UC, BnaCOG2710U	

Showing 1 to 1 of 1 entries Previous Next

▼ Basic gene distribution in genome groups

You can click on the genome bar to see how each gene in the genome is distributed on the chromosomes.

### 3 The distribution of gene sets on chromosomes

You can click on the genome bar to see distribution of individual genomes on a single chromosome.

### 4 ▼ Basic information of ZS11 gene(s)

Search:

ZS11 Gene ID	Darmorc Gene ID	ABGI	Symbol	Full name	Description
BnaAC2G121300Z	BnaAGTG12130U	AT106548D	FT	A22 9154482, 9154270	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti
BnaACTG2282T782U	BnaAGTG2282U	AT106548E	FT	A22 26253195, 26255595	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti
BnaACTG2301U	BnaAGTG2310U	AT106548F	FT	A22 30986418, 30988169	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti
BnaCCG24623UC	BnaCCG24623U	AT106548G	FT	C02 18637303, 18639599	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti
BnaCDG1483UC	BnaCDG1483U	AT106548H	FT	G04 17075818, 17073789	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti
BnaCOG2710U	BnaCOG2710U	AT106548I	FT	C06 4203744E, 42039740	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GA+HT PEH1 SV#2 FT, together with LFY, promotes flowering and is anti

Showing 1 to 6 of 6 entries Previous Next

### 5 ▼ The physical location of the genes

Search:

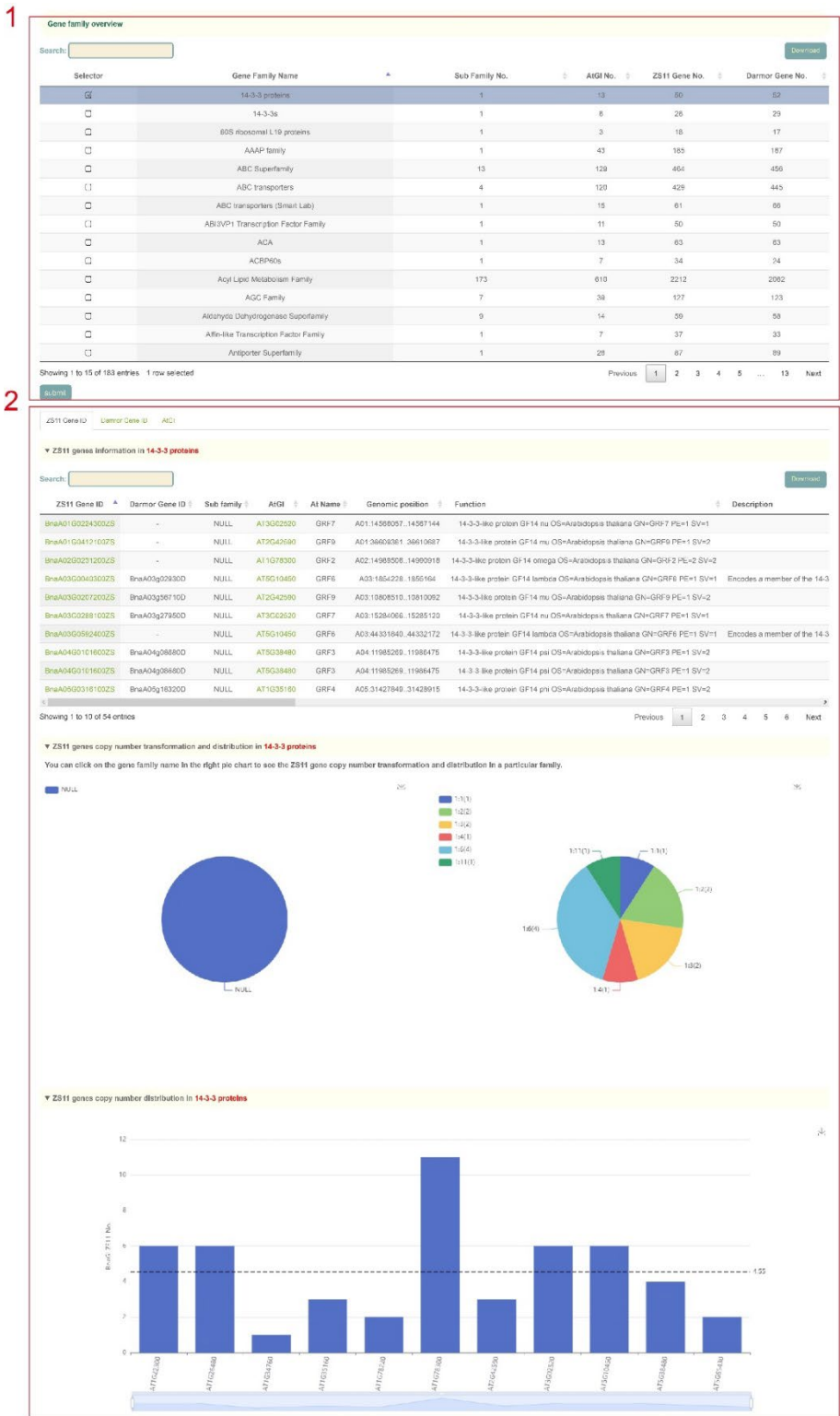
Genome	Gene	Chr.	Start	End
Darmorc	BnaAC2G121300Z	chrAC2	6379036	6379058
Darmorc	BnaACTG2282T782U	chrAC7	18655196	18657652
Darmorc	BnaACTG2301U	chrAC7	37787807	37788354
Darmorc	BnaCCG24623UC	chrCO2_random	906055	906785
Darmorc	BnaCDG1483UC	chrCO4	12135271	12137614
Darmorc	BnaCOG2710U	chrCO6	78655368	78655318
Darmorc_sub	A202g12340_1_BnaDAR	AD2	9117702	9120548
Darmorc_sub	A07g13569_1_BnaDAR	AD7	23554996	2357253
Darmorc_sub	A07g14258_1_BnaDAR	AD7	28826790	28828297
Darmorc_sub	O02g21430_1_BnaDAR	OD2	15201528	1520314

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# 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).



## 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

Gene ID  ?  
e.g. FT, AT1G65480, BnaA02G0156900ZS, FLOWERING LOCUS T

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

Gene Index  ?  
 e.g. example\_1 or example\_2

2

▼ Basic information of gene(s)

Search:

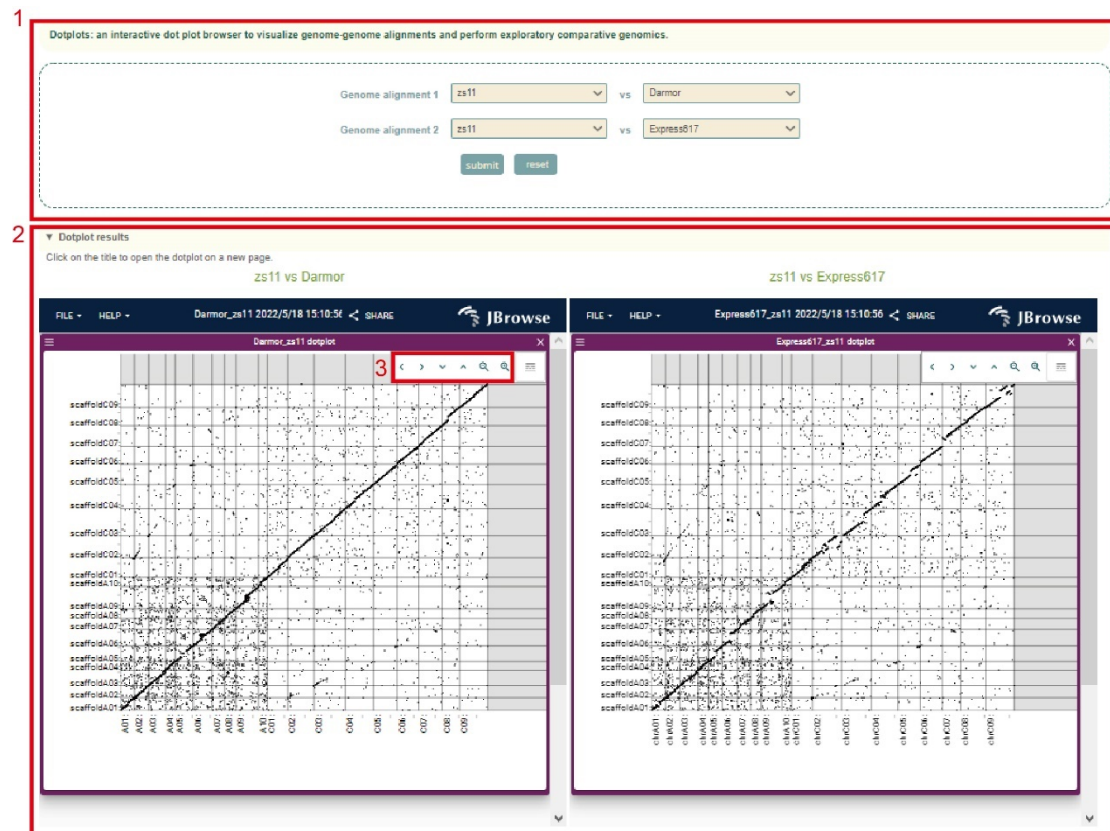
ZS11 Gene ID	Darmor Gene ID	Darmor-bzh Gene ID	ExpressS17 Gene ID	GanganF73 Gene ID	No2127 Gene ID	NY7 Gene ID	quinta Gene ID	Shangli3 Gene ID
BnaA02G0156900ZS	BnaA02g12130D	A02p13240_1_BnaDAR	A02p017120_1_BnaEXP	BnaA02G0152300GG	BnaA02G0156600NO	-	BnaA02G0156700QU	BnaA02G0159500SL
BnaA07G0282700ZS	BnaA07g25310D	A07p32850_1_BnaDAR	A07p033170_1_BnaEXP	BnaA07G0278500GG	BnaA07G0275700NO	-	BnaA07G0239900QU	BnaA07G0266400SL
BnaA07G0385100ZS	BnaA07g33120D	A07p42500_1_BnaDAR	A08p003900_1_BnaEXP	BnaA07G0378900GG	-	-	BnaA07G0320800QU	BnaA07G0346400SL
BnaC02G020600ZS	BnaC02g45290D	C02p21420_1_BnaDAR	C02p045130_1_BnaEXP	BnaC02G0184100GG	BnaC02G0153000NO	-	BnaC02G0154400QU	BnaC02G0115900SL
BnaC04G0181400ZS	BnaC04g14850D	C04p21000_1_BnaDAR	C04p028460_1_BnaEXP	BnaA03G0499400GG	BnaC04G0172900NO	chrC04g001840	BnaC04G0173400QU	BnaC04G0170300SL
BnaC06G0323800ZS	BnaC06g27090D	C06p39080_1_BnaDAR	C06p028960_1_BnaEXP	BnaC06G0311400GG	BnaC06G0313200NO	chrA07g002859,chrC06g003298	BnaC06G0319300QU	BnaC06G0308400SL

## Genome synteny

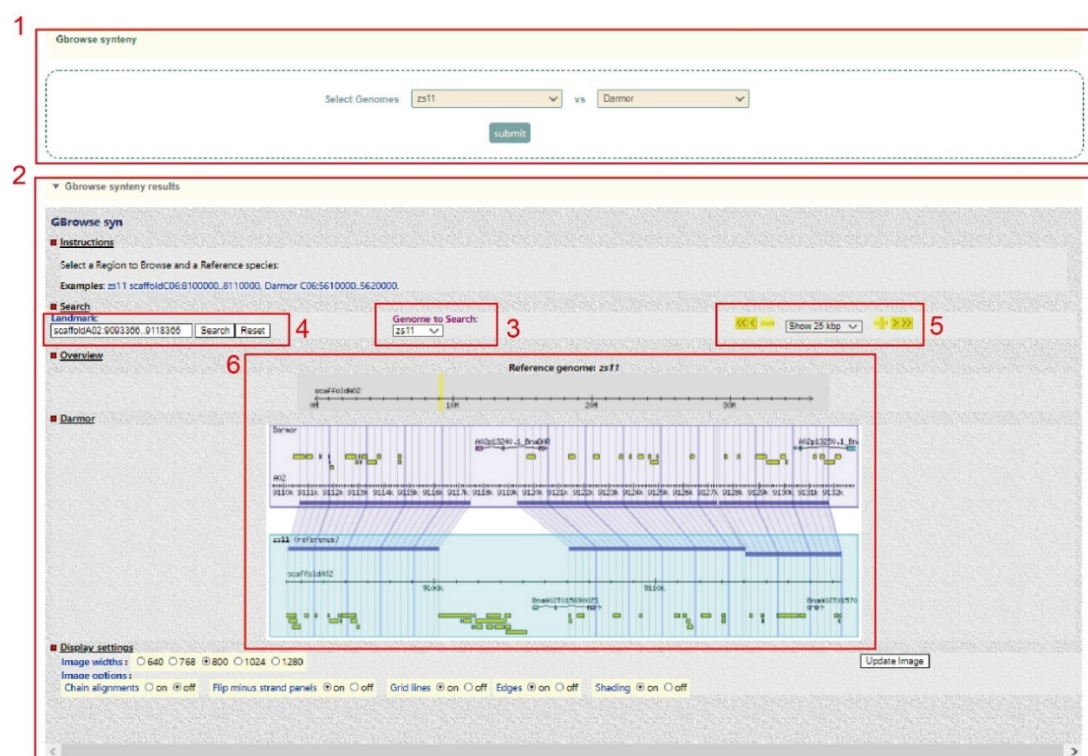
We collected 14 genome assemblies including the diploids *Brassica rapa* accessions Chinese cabbage Chiifu-401-41, sarson Z1, *Brassica oleracea* accessions HDEM, To1000, and 11 *Brassica napus* accessions. By genome alignment, genomic synteny was constructed. We integrated Gbrowser\_syn and Dotplot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





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).

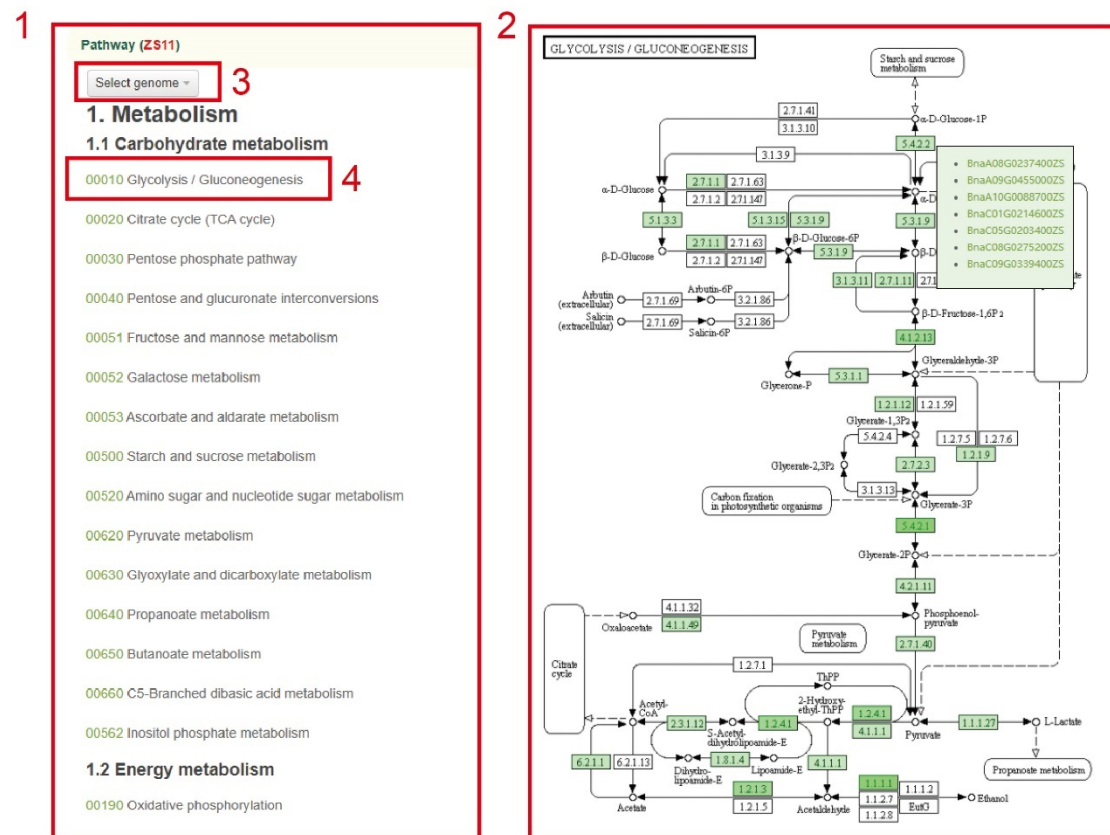


## Pan-browser

Pan-browser is a Jbrowser of *Brassica napus* pangenome[1].

## Pathway

In the Pathway module, we integrated the pathway information of seven *B. napus* genomes(box1). The user can switch the genome by "Select genome" (box3). By selecting the number of the pathway and clicking, you can get the result(box4). The boxes with different colors indicate the number of genes corresponding to different metabolites in this genome(box2). By hovering the mouse over the box, you can view the list of genes related to the metabolite.



## Transcription factor(TF)

In Transcription factor module, we annotated a total of 5,956 genes encoding transcription factors in 58 families based on the TF information in the Arabidopsis genome and the homologous gene relationship between ZS11 and Arabidopsis genomes. Users can browse the number of genes in all gene families using "Browse by Family" (box 1), and view the number of genes in that family by clicking on the gene family name. For example, when you click on AP2 (box 2), you will get a list of genes belonging to this family (box 3). In addition, users can also enter the gene ID in "Search by Gene ID" to check whether the gene is a transcriptome factor and its gene family information.

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)	ARR-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)
NF-YA (8)	NF-YA (36)	NF-YB (50)	NF-YC (25)	NZZ/SPL (4)
Nin-like (47)	RAV (27)	STFa-like (7)	SAP (2)	SBP (62)
SRS (40)	STAT (2)	TALE (59)	TCP (81)	Trithelix (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

ZS11 Gene ID	TF Type	AtGI	At Name	Genomic Position
BnaA05G0174006ZS	AP2	AT1G51190	PLT2	A05:11630717..11633517
BnaA05G0349600ZS	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
BnaC03G0068200ZS	AP2	AT4G37750	ANT	C03:66180962..66183331
BnaC03G0521400ZS	AP2	AT5G65510	AIL7	C03:38755316..38758409
BnaC03G00246700ZS	AP2	AT2G41710	--	C03:14607205..14609753
BnaC07G00207000ZS	AP2	AT5G67180	TOE3	C07:34317906..34319983

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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.

# Population

## Population information

In the Population information module, users can query the related information of the collected 2311 *Brassica napus* accessions. Users can filter accessions according to their Origin, Subpopulation, Resource, and sequencing depth (box1). Then, the user will get information such as germplasm name, geographic origin, subgroup, sequencing depth, and data source of these accessions (box 2), as well as the proportion of accessions from different subpopulations on each continent (box 3).

1

Origin:  
Asia  
Europe  
North America  
South America  
Africa  
Oceania  
Unknown

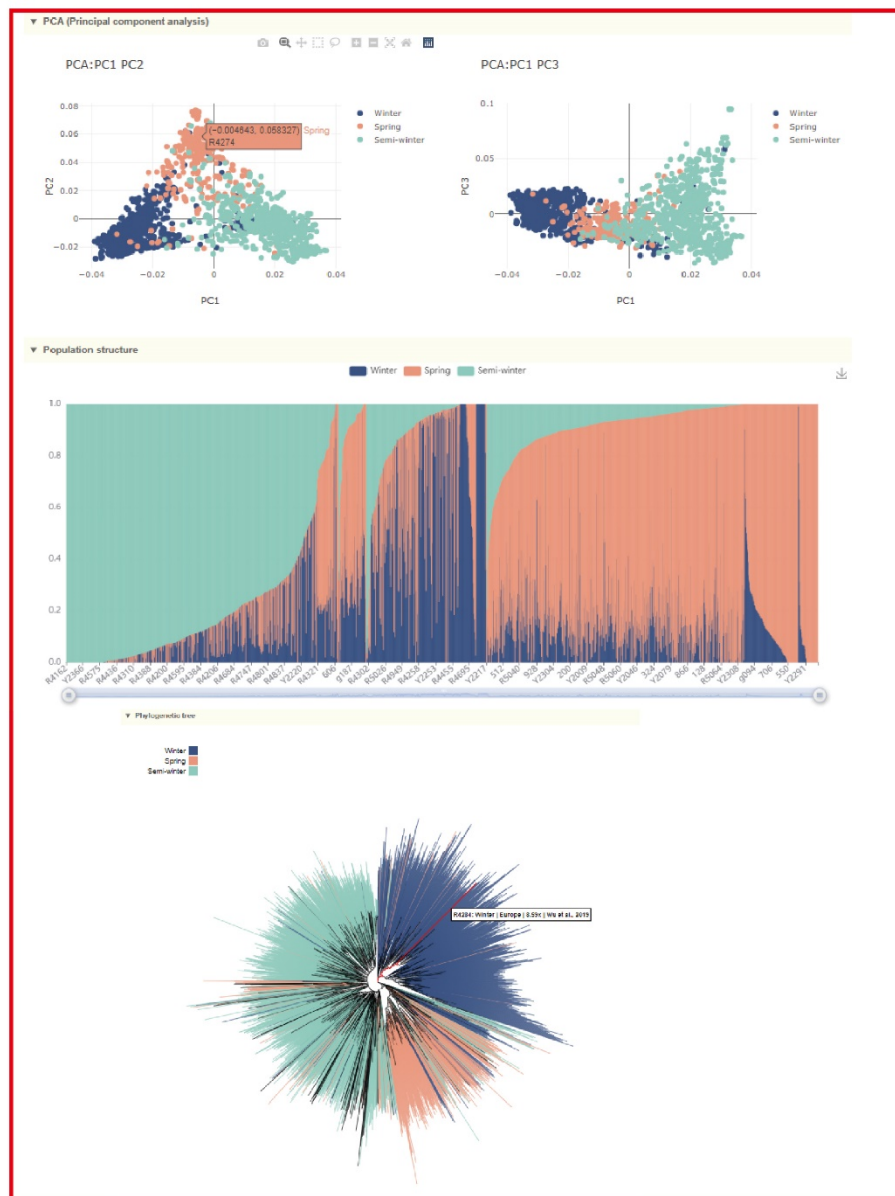
Subpopulation:  
Winter  
Spring  
Semi-winter  
Unknown

Resource:  
(Song et al., 2020)  
(Tang et al., 2021)  
(Wu et al., 2019)  
(Lu et al., 2019)

Depth of sequencing data:  
0

submit

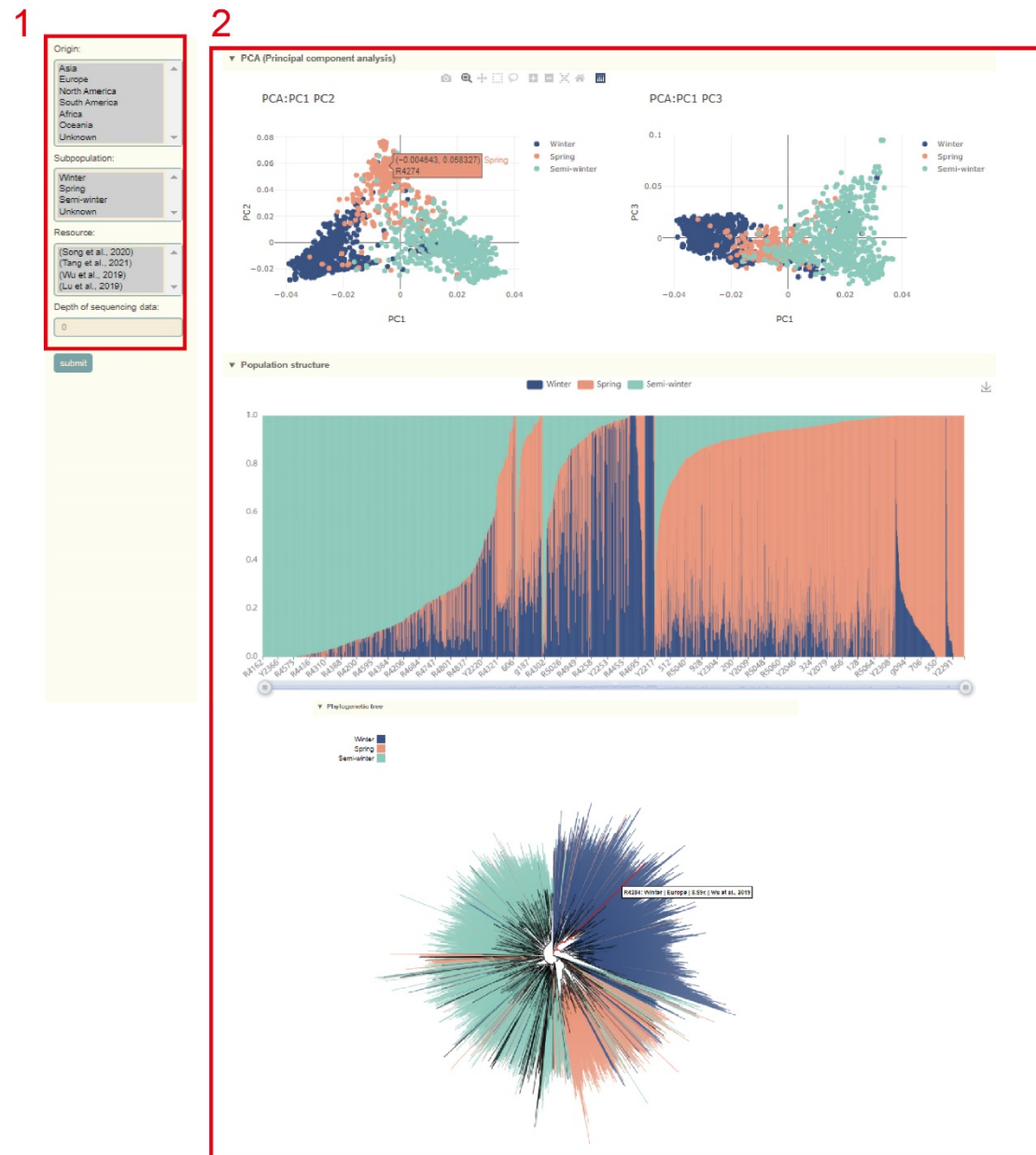
2



## Population structure

In the Population information module, users can query the population structure information of the 2311 *Brassica napus* accessions. Users can filter accessions according to their Origin,

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)**

A01:0.38150000

选择文件 | 未选择任何文件

e.g. BnaA07G0282706ZS, A01:0.38150000, BnaA0905250D

submit reset

2 **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	50001	550000	300000	0.099	0.113	0.123
<input type="checkbox"/>	A01	100001	600000	350000	0.086	0.114	0.130
<input type="checkbox"/>	A01	150001	650000	400000	0.077	0.117	0.137
<input type="checkbox"/>	A01	200001	700000	450000	0.069	0.113	0.133
<input type="checkbox"/>	A01	250001	750000	500000	0.065	0.111	0.133
<input type="checkbox"/>	A01	300001	800000	550000	0.053	0.107	0.136
<input type="checkbox"/>	A01	350001	850000	600000	0.039	0.100	0.139
<input type="checkbox"/>	A01	400001	900000	650000	0.025	0.099	0.130
<input type="checkbox"/>	A01	450001	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

4 **A01:1..1000000**

Legend: Semi-winter/Winter (blue line), Semi-winter/Spring (orange line), Spring/Winter (green line)

0.15  
0.12  
0.09  
0.06  
0.03  
0

250,000 500,000 750,000 1,000,000

Zoom in to see sequence

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

π (Z511)

A01:1..1807270

选择文件 未选择任何文件

e.g. BnaA07G02827002S, A01:1..1807270, BnaA07G0250D

2

submit reset

▼ Nucleotide diversity (π)

Search:

Download

Selector	Chr.	Start	End	Position	PI_W	PI_S	PI_SW
<input type="checkbox"/>	A01	1	800000	250000	0.000477	0.000839	0.000834
<input type="checkbox"/>	A01	50001	550000	300000	0.000511	0.000938	0.001091
<input type="checkbox"/>	A01	100001	800000	350000	0.000556	0.001056	0.001338
<input type="checkbox"/>	A01	150001	850000	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	0.000726	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	0.001816

Showing 1 to 10 of 33 entries

Previous 1 2 3 4 Next

3

▼ Plot of nucleotide diversity (π)

Chr:

Start:

End:

submit

4

A01:1..2100000

Winter Spring Semi-winter

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

[submit](#) [reset](#)

▼ Basic information of gene(s)

Search:  [Download](#)

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	BnaC03g46148D	AT4G34520(FAE1)	C03:35858639..35860030	Seq Exp JBR	1	0/1/0/0	0	0/0	<input type="checkbox"/>

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4

▼ Phylogenetic tree, gene structure and variation distribution

5

▼ Gene structure and SNP distribution

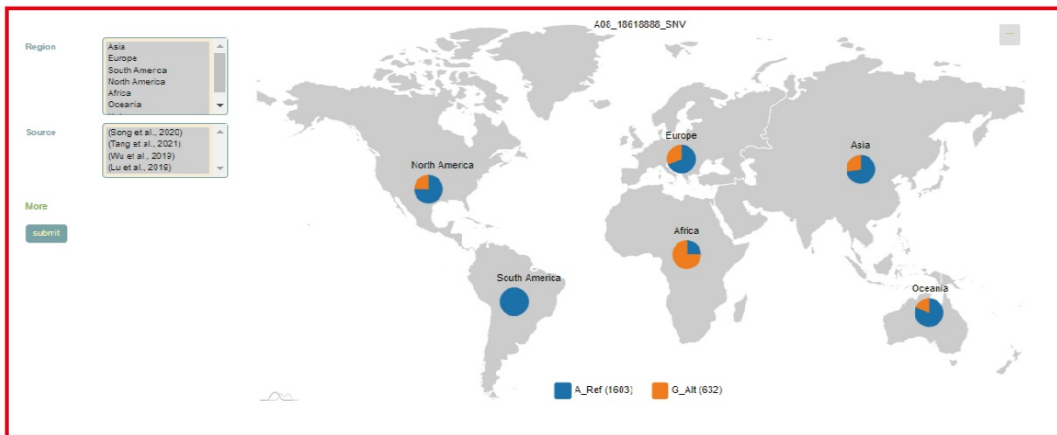
The inverted triangle symbols indicate variations, click it to see detailed information in table.

[Download](#)

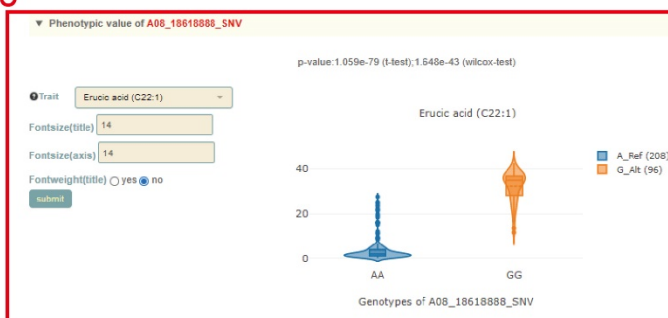
Chr	Position	Alt (allele)	Ref (allele)	JBrowse	Alt (frequency)	Ref (frequency)	PIC	Alt (num)	Ref (num)	Function_type	Variation_type
A08	18618888	G	A	JBR	0.29	0.71	0.33	640	1614	MODERATE	misense_variant

Showing 1 to 1 of 1 entries [Previous](#) 1 [Next](#)

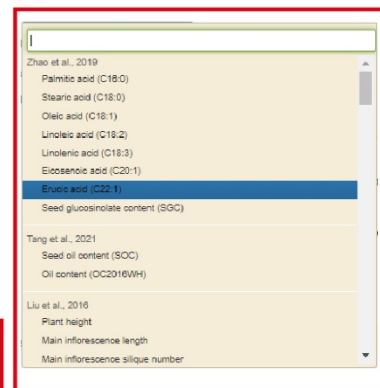
9



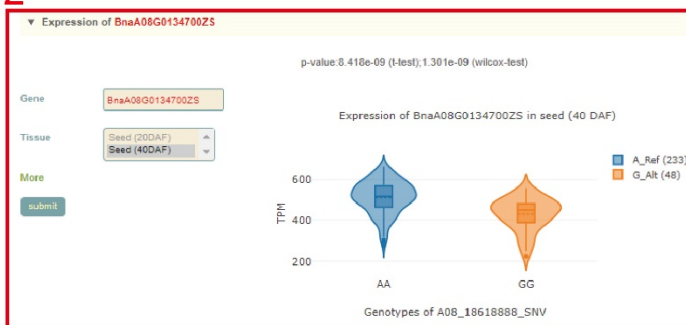
10

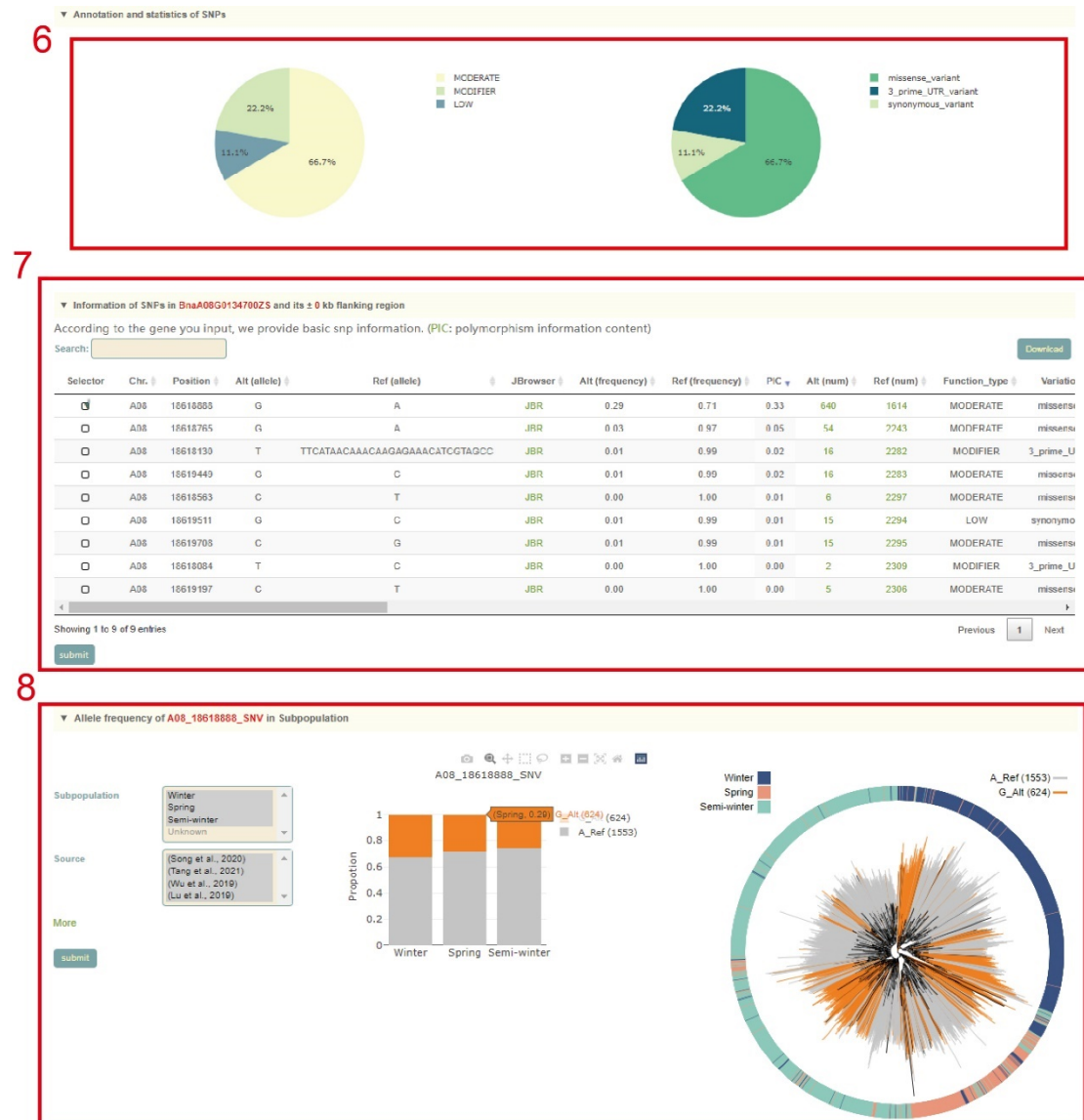


11



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 (Z591)

Region/Name:

SNP basic information

Search:

<input type="checkbox"/>	GeneRegion	Chr.	Position	Alt (allele)	Ref (allele)	JBrowse	Alt (frequency)	Ref (frequency)	PIC	Alt (num)	Ref (num)	Function_Type	Variation_Type
<input checked="" type="checkbox"/>	BnaC03G0745900Z	C03	72305785	GTT	G	JBR	0.48	0.52	0.37	1096	1137	HIGH	frameshift_variant
<input type="checkbox"/>	BnaC03G0745900Z	C03	72305841	G	CCTCA	JBR	0.21	0.79	0.27	427	1768	HIGH	frameshift_variant
<input type="checkbox"/>	BnaC03G0745900Z	C03	72310132	G	A	JBR	0.00	1.00	0.01	8	2382	MODERATE	missense_variant
<input type="checkbox"/>	BnaC03G0745900Z	C03	72310665	G	T	JBR	0.00	1.00	0.01	9	2382	MODERATE	missense_variant
<input type="checkbox"/>	BnaC03G0745900Z	C03	72310722	C	T	JBR	0.00	1.00	0.01	9	2382	LOW	synonymous_variant

Showing 1 to 5 of 5 entries 1 row selected

Results of the locus combinations

Search:

<input type="checkbox"/>	ID	locus combination	Frequency	Sample
<input checked="" type="checkbox"/>	hap_0	G_A_C	0.307	517
<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

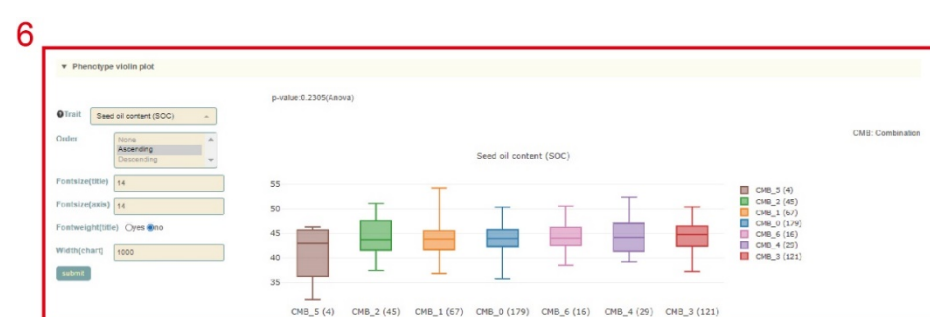
Showing 1 to 8 of 8 entries 7 rows selected

Brief table of the locus combinations

Search:

ID	Freq	No.	C03 72305785	A08 10018090	A05 40593972
combination_0	0.307	617	G	A	C
combination_1	0.178	357	GTT	G	C
combination_2	0.176	354	G	A	T
combination_3	0.169	339	GTT	A	C
combination_4	0.069	139	GTT	A	T
combination_5	0.064	128	GTT	G	T
combination_6	0.027	54	G	G	C
combination_7	0.009	19	G	G	T

Showing 1 to 8 of 8 entries



## Customized phenotype association

In the Customized phenotype association module, users can directly paste the phenotype data (box1) 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	30.20800007
100	27.39233333
106	28.97800007
126	10.993
128	27.42300007
138	27.41533333
144	29.83833333
150	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

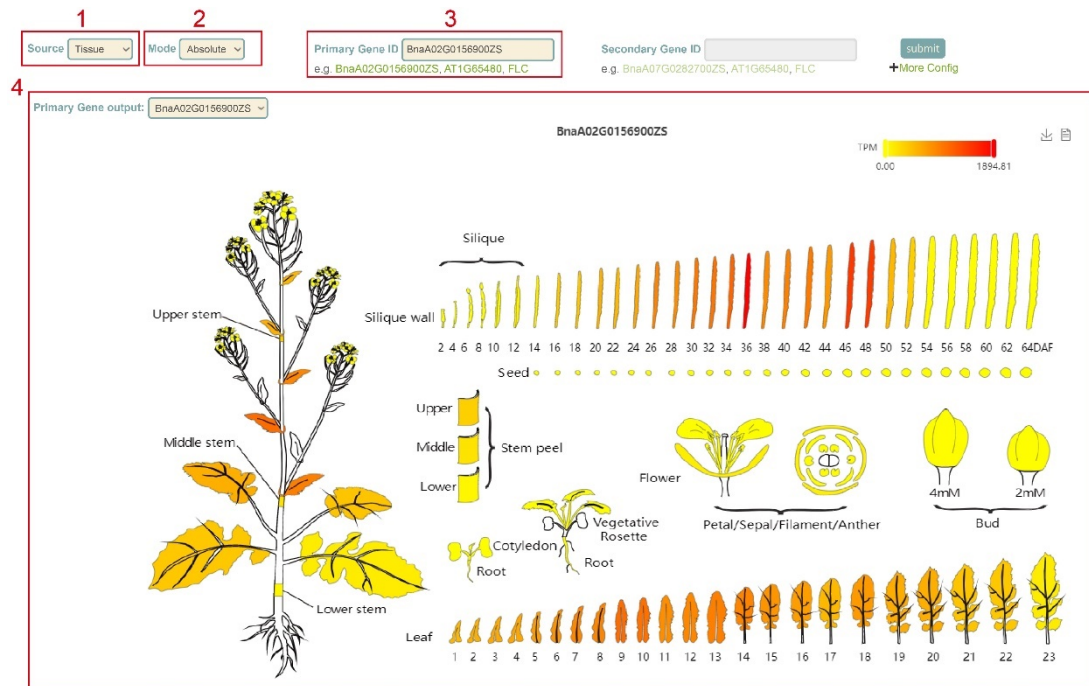
We integrated the gene expression data of 700 samples of seeds and leaves at 20 days after flowering, 40 days after flowering. The user can enter the Arabidopsis gene ID, *B. napus* gene list or genomic region, and then select the tissue to query the expression level of the gene of interest. For example, 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' (box1), one mode from 'Absolute', 'Relative' and 'Compare' (box2) and Gene ID (box3). 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.

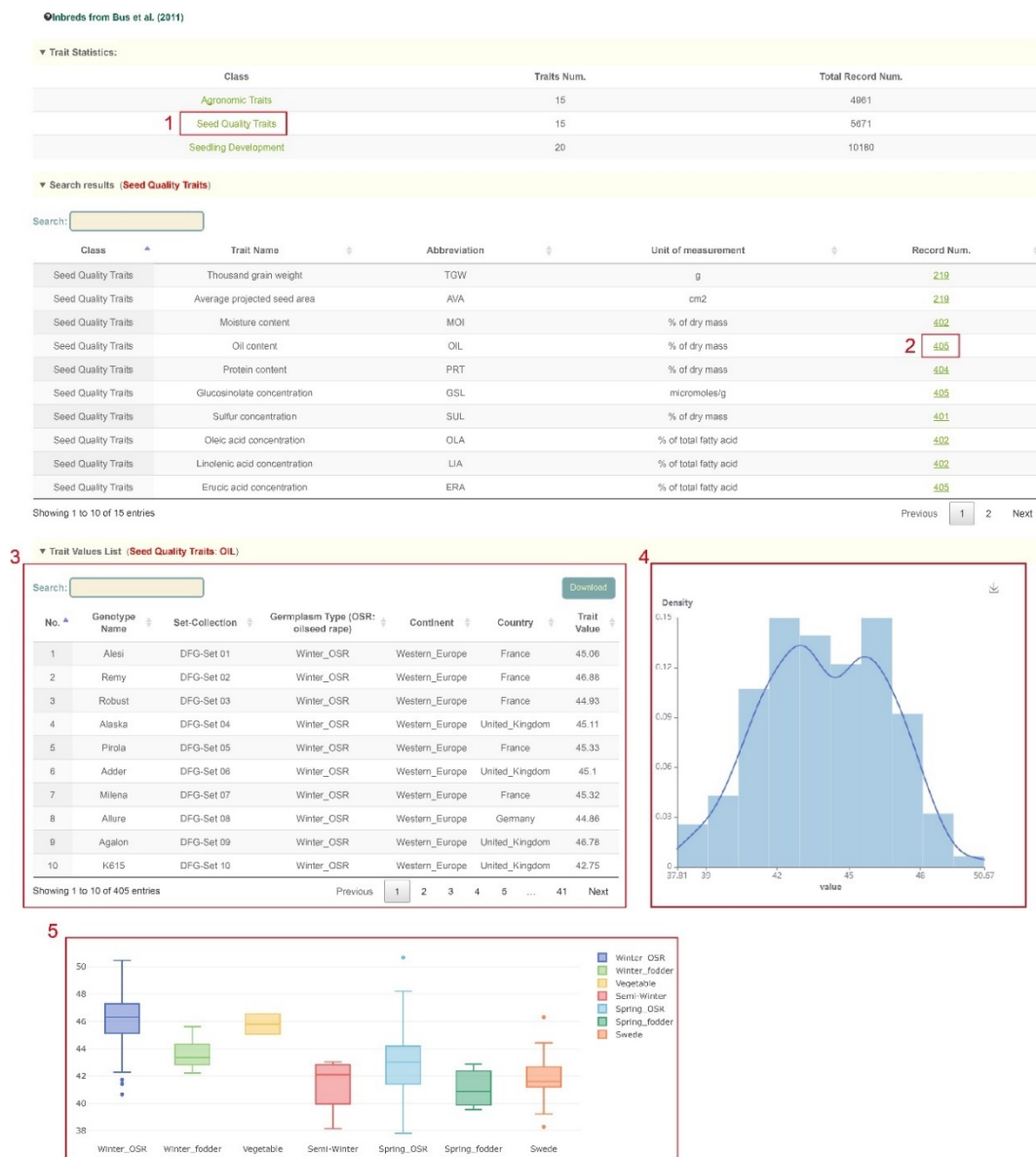


## eFP(multiple gene module)

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).



# 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 BnaA02G016890ZS or FLOWERING LOCUS T

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

Gene Index:  ?  
选择文件 e.g. example\_1 or example\_2

2 Flanking region (s): ☐ 0.5kb ☐ 1kb ☐ 1.5kb ☐ 2kb ☒ 3kb

3

Datasets

root seed leaf flowerbud silique

H3K27ac H3K27me3 H3K4me1 H3K4me3 H3K9me2 RNAPII

2063A B409 Z311 wester BraunerSchönle Damor Mendel Laurentian

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 checked="" type="checkbox"/>	BnaA02G016890ZS	BnaA02g12130D	AT1G65480	FT	A02:9104462..9107270	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flower
<input type="checkbox"/>	BnaA07G0282700ZS	BnaA07g25310D	AT1G65480	FT	A07:26253195..26259555	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flower
<input type="checkbox"/>	BnaA07G0305100ZS	BnaA07g33120D	AT1G65480	FT	A07:30986418..30988169	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flower
<input type="checkbox"/>	BnaC02G0200600ZS	BnaC02g45250D	AT1G65480	FT	C02:16937203..16938959	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flower
<input type="checkbox"/>	BnaC04G0181400ZS	BnaC04g14650D	AT1G65480	FT	C04:17070618..17073789	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with LFY, promotes flower
<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 flower

Showing 1 to 6 of 6 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
A02:9104394..9104750	357	9104594	14.36	5.13515	3.29269	3.84781	leaf_H3K27me3_B409_rep2_peak_2966	leaf	H3K27me3	B409
A02:9105115..9106434	1320	9105726	34.16	20.6283	7.03209	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 1 Next

6

▼ JBrowse

9,102,500 9,103,750 9,105,000 9,106,250 9,107,500 9,108,750 9,110,000

z311.v0.gff3

BnaA02G016890ZS

leaf\_H3K27me3\_B409\_rep2.bw

leaf\_H3K27me3\_B409\_rep1.bw

## 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 BnaA02G0156900ZS 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 *FAE1* as an example, first enter *FAE1* 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 *FAE1* 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 BnaA08G030500ZS

Gene region:  ?  
e.g. A08:150000\_230000

Gene Index:  ?

2

3

Flanking region (±): ☐ 0.5kb ☐ 1kb ☐ 1.5kb ☐ 2.5kb ☒ 3kb

Datasets:

submit reset

4

▼ Basic information of gene(s)

Search:

Download

Selector	ZS11 Gene ID	Dammar Gene ID	AtGI	At Name	Genomic position	Function	Description
<input type="checkbox"/>	BnaA03G0397300ZS	BnaA03G390100	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"/>	BnaA08G01134700ZS	BnaA08G111300	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	BnaC03G461400	AT4G34520	FAE1	C03:25858639_25860030	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	BnaC03G659800	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

submit Previous 1 Next

5

▼ Basic information of peak(s)

Search:

Download

Genomic position	Length	Abs_submits	Pileup	-Log10(pvalue)	Fold_enrichment	-Log10(qvalue)	Name	Tissue	Signal	Variety
A08:18617117_18617325	209	19617216	23.00	6.91599	3.17824	4.68773	seed_ATACseq_NY10_rep1_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 BnaA02G01569002S or FLOWERING LOCUS T

Gene region  ?  
 e.g. A01 150000 400000

Gene Index  ?  
 e.g. example\_1 or example\_2 Upload the gene index file

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"/>	BnaA02G01569002S	BnaA02g121300	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"/>	BnaA07G02827002S	BnaA07g253100	AT1G65480	FT	A07:26253195..26255955	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with Lf-Y, promotes flow
<input type="checkbox"/>	BnaA07G03651002S	BnaA07g331200	AT1G65480	FT	A07:30585418..30588159	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with Lf-Y, promotes flow
<input type="checkbox"/>	BnaC02G02009002S	BnaC02g452500	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"/>	BnaC04G01814002S	BnaC04g148500	AT1G65480	FT	C04:117070818..117073769	Protein FLOWERING LOCUS T OS=Arabidopsis thaliana GN=FT PE=1 SV=2	FT, together with Lf-Y, promotes flow
<input type="checkbox"/>	BnaC06G03238002S	BnaC06g270500	AT1G65480	FT	C06:425937446..42593745	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
Z127	A02	9100001	9200000	0.0456005	A	0.2108	128
NY7	A02	9100001	9200000	0.0331374	A	0.2108	128
ZS11	A02	9100001	9200000	0.0504709	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
Z127	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

Search:   e.g. A001500000, 19030000 or A001500000 or A001500000 or A001500000

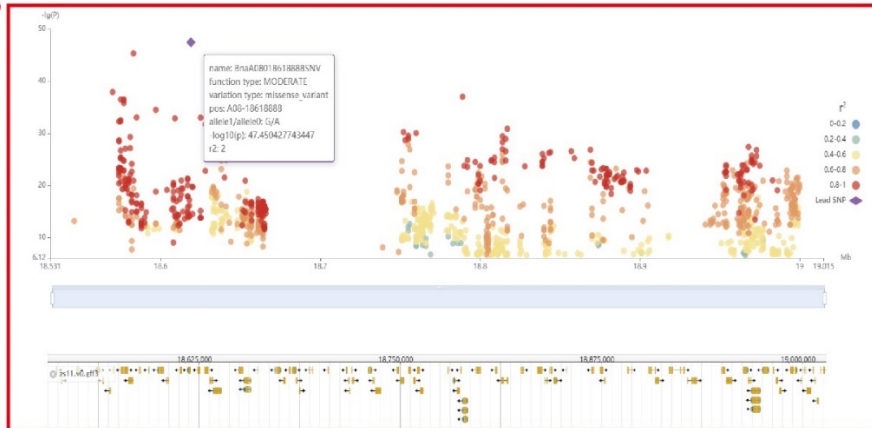
Download

SNP	-log10(P)	r <sup>2</sup>	Chr	Pos	allele1/allele2	Variation type	Function type
BnaA00010616686SNV	71.82	2	A08	18518566	G/A	missense_variant	MODERATE
BnaA00010616686SNV	67.72	0.876681	A08	18559719	A/G	upstream_gene_variant	MODIFIER
BnaA00010624567SNV	59.69	0.847259	A08	18624567	C/T	missense_variant	MODERATE
BnaA00010625071SNV	59.40	0.812665	A08	18555071	G/GTA	upstream_gene_variant	MODIFIER
BnaA00010625800SNV	57.21	0.8327	A08	18598600	T/C	upstream_gene_variant	MODIFIER
BnaA00010626066SNV	57.03	0.79577	A08	18526066	G/A	upstream_gene_variant	MODIFIER
BnaA00010626379SNV	56.19	0.836768	A08	18563379	C/A	downstream_gene_variant	MODIFIER
BnaA00010626329SNV	54.55	0.691485	A08	18789329	A/C	synonymous_variant	LOW
BnaA00010627774SNV	53.63	0.7484	A08	18577774	G/A/C	splice_region_variant, splice_variant	LOW
BnaA00010635071SNV	51.94	0.750421	A08	18535071	T/G	upstream_gene_variant	MODIFIER

Showing 1 to 10 of 1,548 entries

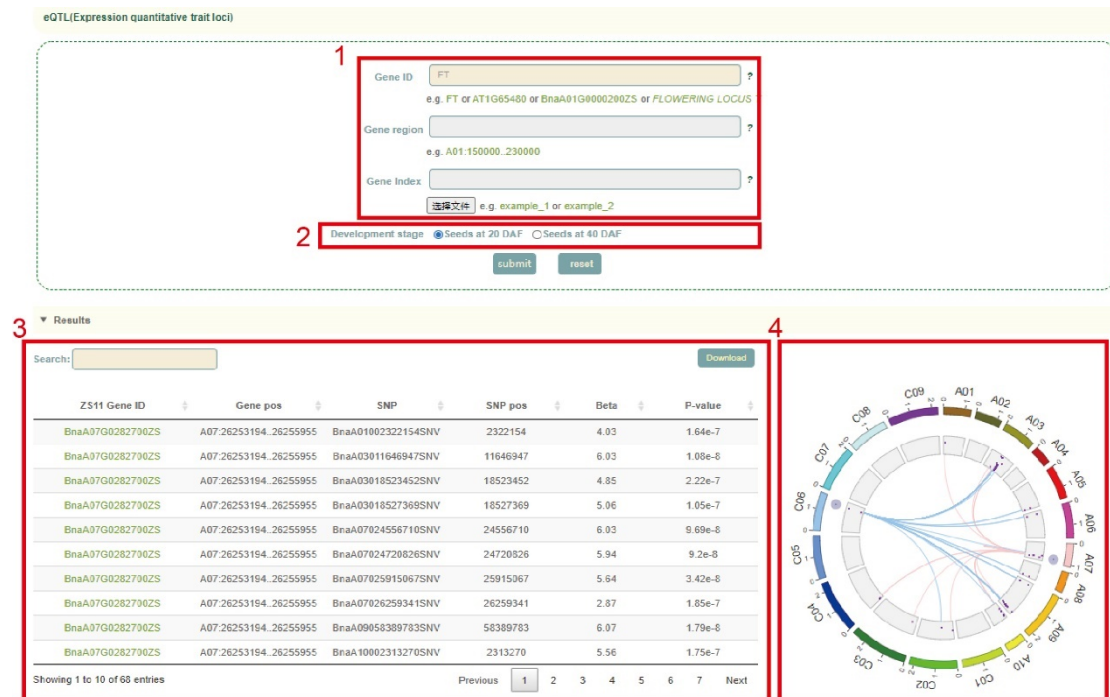
Previous 1 2 3 4 5 ... 155 Next

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).



## 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: **Palmitic acid (C16:0)**

2 Development stage: ☒ Seeds at 20 DAF ☐ Seeds at 40 DAF

submit

3

4

Gene: BnaA08G014020025  
P(SMR): 13.6871  
P(HEIDI): 3.616098e-07  
AIC(symbols): AT4G33870(GALDH)  
topSNP: BnaA08G18358751SNV  
topSNP\_chr/topSNP\_bp: A08(18858753)  
Allele1/Allele2: G/A  
Freq: 0.222112  
Beta(GWAS): -0.269441  
SE(GWAS): 0.0283777  
P(GWAS): 19.0043  
Beta(eQTL): -0.661312  
SE(eQTL): 0.051255  
P(eQTL): 37.3546  
Beta(SMR): 0.407434  
SE(SMR): 0.0532795  
Function: L-galactose dehydrogenase OS=Arabidopsis thaliana  
GN=LGALDH PE=1 SV=1

5

List of significant SMR loc (p\_HEIDI>1.87e-3) (Trait: Palmitic acid (C16:0))

Search:

Selector	ZS11 Gene ID	P(SMR)	P(HEIDI)	Darmor Gene ID	AGI	At Name	Genomic position	Function
<input type="checkbox"/>	BnaA08G013340025	5.0635	3.529766e-01	-	AT4G33820	VHA-C3	A08:18549157..18550150	V-type proton ATPase subunit c5 OS=Arabidopsis thaliana GN=VHA-c5 PE=2
<input type="checkbox"/>	BnaA08G014490025	5.57664	2.230419e-01	BnaA08g12070D	AT4G332700	TEB	A08:19285889..19306644	Helicase and polymerase containing protein TEB1 OS=Arabidopsis thaliana GN=TEB1 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014310025	6.75455	1.441400e-01	BnaA08g11510D	AT4G33090	APM1	A08:19125052..19129209	Aminopeptidase M1 OS=Arabidopsis thaliana GN=APM1 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014300075	5.40554	1.135017e-01	BnaA08g11900D	AT4G33100	-	A08:19123722..19124334	Uncharacterized protein At4g33100 OS=Arabidopsis thaliana GN=At4g33100 PE=1 SV=1
<input type="checkbox"/>	BnaA08G013750025	7.04458	8.311524e-02	BnaA08g11350D	AT4G34131	UGT73B3	A08:18760639..18762173	UDP-glucosyltransferase 73B3 OS=Arabidopsis thaliana GN=UGT73B3 PE=2
<input type="checkbox"/>	BnaA08G014530025	4.91433	6.830058e-02	BnaA08g12190D	AT4G33470	CQR7-1	A08:19360001..19360512	Cytochrome b-c1 complex subunit 7-1 OS=Arabidopsis thaliana GN=CQR7-1 PE=1 SV=1
<input type="checkbox"/>	BnaA08G014900025	4.8567	6.653656e-02	-	AT5G10360	RPS6B	A08:19627361..19628729	40S ribosomal protein S6.2 OS=Arabidopsis thaliana GN=RPS6B PE=1 SV=1
<input type="checkbox"/>	BnaA08G013530025	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"/>	BnaA08G010190075	4.9917	5.507700e-02	BnaA08g08120D	AT4G16800	-	A08:16195038..16199778	Methylglutaryl-CoA hydratase, mitochondrial OS=Dictyostelium discoideum GN=mtHSDH PE=1 SV=1
<input type="checkbox"/>	BnaA08G014530025	8.23659	4.937500e-02	BnaA08g12110D	AT4G32680	-	A08:19319437..19320633	-

Showing 1 to 10 of 16 entries

6

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

Gene ID:

Gene region:

Gene Index:

submit reset

7

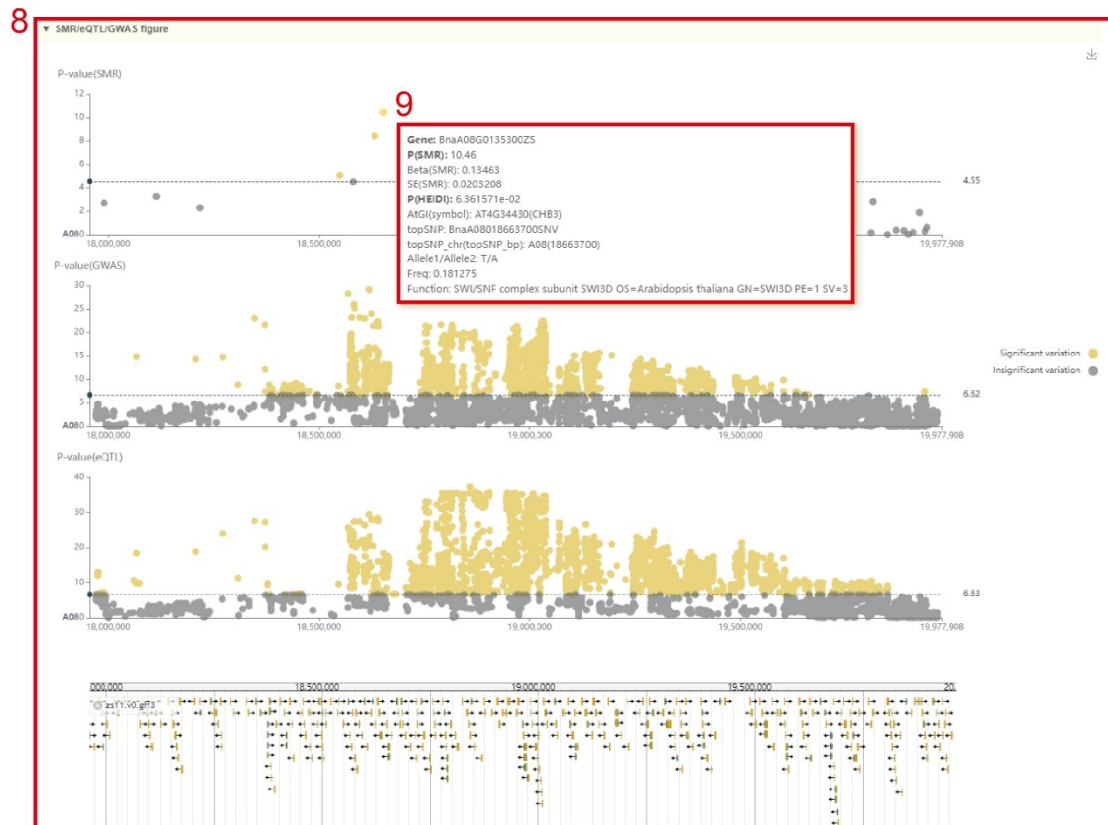
Basic information of gene(s) for custom search

Search:

Selector	ZS11 Gene ID	Darmor Gene ID	AGI	At Name	Genomic position	Function	Description
<input checked="" type="checkbox"/>	BnaA08G014020025	BnaA08g11488D	AT4G33670	LGALDH	A08:18866145..18867908	L-galactose dehydrogenase OS=Arabidopsis thaliana GN=LGALDH 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 PPH<sub>0</sub>, PPH<sub>1</sub>, PPH<sub>2</sub>, PPH<sub>3</sub>, PPH<sub>4</sub>. 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 PPH<sub>4</sub> value is the largest among all PPH values, the text of the PPH<sub>4</sub> hypothesis is marked in red, indicating to accept H<sub>4</sub>, which is "both traits are associated and share a single causal variant". On the premise of accepting H<sub>4</sub>, the P-values of GWAS and eQTL and PPH<sub>4</sub> 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: All Trait: All

Search:

[Download](#)

eQTL	Phenotype	Phenotype source	QTL	Lead SNP	Gene	COLOC <sup>A</sup>	COLOC_pph0	COLOC_pph
<input checked="" type="checkbox"/> seed_40DAF	Branch angle	Sun, C. et al. (2016)	qBA.A07.1	BnaA070015012/0SNV	BnaA0700018100ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Oil content	Tang, S., et al. (2021)	qOC.A05.1	BnaA05041113970SNV	BnaA05G0437200ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Oil content	Tang, S., et al. (2021)	qOC.A05.2	BnaA05041245313SNV	BnaA05G0440100ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Oil content	Tang, S., et al. (2021)	qOC.C05.1	BnaC05G03831616SNV	BnaC05G0499000ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Oil content	Tang, S., et al. (2021)	qOC.C05.1	BnaC05G03831616SNV	BnaC05G0499200ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Oil content	Tang, S., et al. (2021)	qOC.C05.1	BnaC05G03831616SNV	BnaC05G0499400ZS	TRUE	0	0
<input type="checkbox"/> seed_40DAF	Tolerance coefficients of ground dry weight at the mature stage	Zhang, G., et al. (2022)	qM_GDW_R2.A03.1	BnaA03010015040SNV	BnaA03G0192800ZS	TRUE	0.000002	0.000002
<input type="checkbox"/> seed_40DAF	Plant height of high salt-alkali condition at the mature stage	Zhang, G., et al. (2022)	qM_PH_HA10.4	BnaA10G24374757SNV	BnaA10G0251700ZS	TRUE	0	0.00023
<input type="checkbox"/> seed_40DAF	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 1,849 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)

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

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

3

**COLOC results**

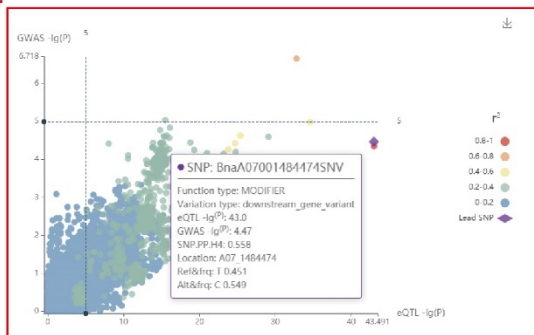
Search:

[Download](#)

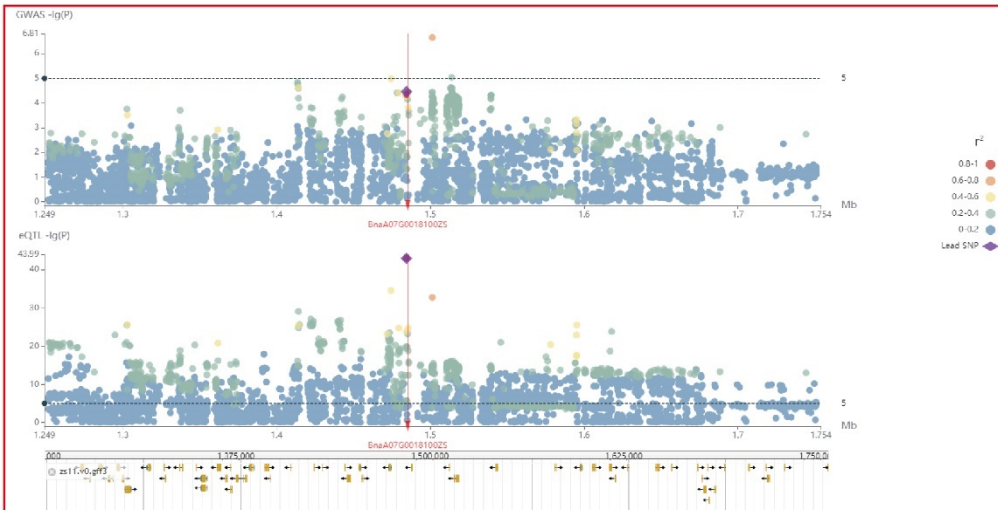
SNP	P(GWAS)	P(eQTL)	SNP_PP.H4
BnaA07001484474SNV	0.0000340	1.01e-43	0.558
BnaA07001484465SNV	0.0000450	1.01e-43	0.442
BnaA07001474334SNV	0.0000103	2.77e-35	6.09e-15
BnaA070015012705SNV	2.18e-7	1.42e-33	7.47e-16
BnaA07001414204SNV	0.0000253	7.55e-30	2.10e-23
BnaA070014221788SNV	0.000151	7.78e-28	6.92e-27
BnaA07001411381SNV	0.000260	1.51e-27	2.50e-27
BnaA07001439980SNV	0.000253	3.29e-27	9.45e-28
BnaA07001439985SNV	0.000253	3.29e-27	9.45e-28
BnaA070014239285SNV	0.000517	2.07e-27	4.77e-20

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

4



5



## 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 CO<sub>2</sub>" 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 CO<sub>2</sub>" 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

Search:

[Download](#)

Selector	Class	Compounds
<input checked="" type="checkbox"/>	5 min significantly increased metabolites	56
<input type="checkbox"/>	5 min significantly decreased metabolites	9
<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 8 of 8 entries 1 row selected

Previous **1** Next

2

Search:

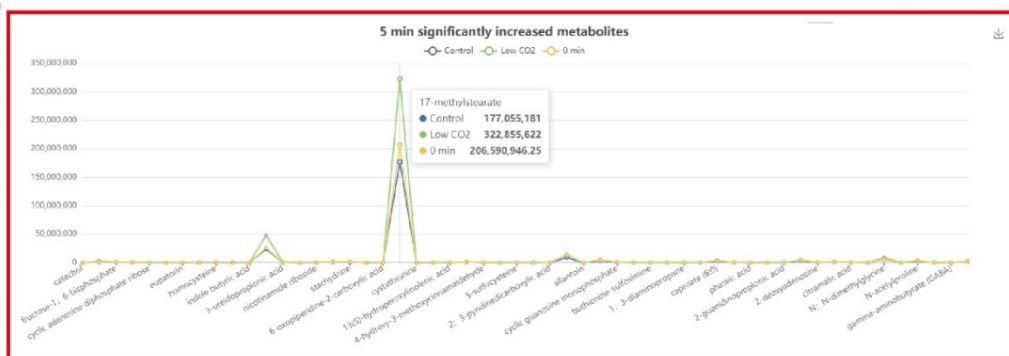
[Download](#)

Metabolome Name	Information
1-palmitoylglycerophosphoglycerol	<a href="#">View</a>
13(5)-hydroperoxylinoleic acid	<a href="#">View</a>
17-methylstearate	<a href="#">View</a>
1; 3-diaminopropane	<a href="#">View</a>
2-deoxyadenosine	<a href="#">View</a>
2-deoxyinosine	<a href="#">View</a>
2-guadinopropionic acid	<a href="#">View</a>
2-isopropylmalic acid	<a href="#">View</a>
2-palmitoylglycerol (2-monopalmitin)	<a href="#">View</a>
2; 3-pyridinedicarboxylic acid	<a href="#">View</a>

Showing 1 to 10 of 56 entries

Previous **1** 2 3 4 5 6 Next

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

**3** Co-expression information

Search:

Source Gene ID	Target Gene ID	PCC-value	Source Gene description
BnaA03G0318200ZS	BnaA03G0323400ZS	0.98	--
BnaA03G0318200ZS	BnaA04G0134400ZS	0.90	--
BnaA03G0318200ZS	BnaA04G0178100ZS	0.93	Putative F-box protein At1g237
BnaA03G0318200ZS	BnaA05G0358000ZS	0.92	--
BnaA03G0318200ZS	BnaA09G0119800ZS	0.90	Spermidine hydroxyinnamoyl tr
BnaA03G0318200ZS	BnaA10G0105500ZS	0.93	--
BnaA03G0318200ZS	BnaC04G0262200ZS	0.92	--
BnaA03G0318200ZS	BnaC08G0458200ZS	0.91	MATH domain and coiled-coil domain-containing
BnaA03G0323400ZS	BnaA09G0119800ZS	0.93	--
BnaA05G0358000ZS	BnaA10G0105500ZS	0.92	--
BnaA05G0358000ZS	BnaC04G0262200ZS	0.93	--
BnaA10G0105500ZS	BnaC04G0262200ZS	0.98	MATH domain and coiled-coil domain-containing
BnaA10G0105500ZS	BnaC08G0458200ZS	0.91	--
BnaC04G0262200ZS	BnaC08G0458200ZS	0.94	MATH domain and coiled-coil domain-containing protein At3g58360 OS=Arabidopsis thaliana (GN=At3g58360) PE=3 SV=1

Showing 11 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 regulators 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

BnaC03G051500ZS

submit reset

TF regulation network

274 regulations are found.

TF Target

Download

TF regulation basic information

Search:

Download

TF Gene ID	Genomic position(TF Gene)	AtGI/At Name(TF Gene)	Target Gene ID	Genomic position(Target Gene)	AtGI/At Name(Target Gene)
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G001440ZS	A01:688366..887739	AT4G03740/-
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G002980ZS	A01:1654444..1058287	AT3G028410/-
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G003000ZS	A01:1601702..1662810	AT4G35390/AHL25
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G006860ZS	A01:3699425..3700818	AT1G177340/-
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G008370ZS	A01:4718445..4720350	AT4G28680/TYRDC
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G013490ZS	A01:8085665..8087084	AT4G23900/NDK4
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaC07G019600ZS	C07:33216675..33218908	AT2G38650/-
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G021790ZS	A01:1393721..13939049	AT3G17700/CNGC20
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA01G040500ZS	A01:36111823..36115115	AT3G03800/CCT8
BnaC03G051500ZS	C03:38172484..38173884	AT5G67580/TRB2	BnaA02G003500ZS	A02:2053141..2053737	AT5G10280/MYB2

Showing 1 to 10 of 274 entries

Previous

1

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...

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Next

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## Jbrowser

Usage: The user clicks the circle in front of the genome assembly to select the genome, and then in the Jbrowser, the local track file can be uploaded in Track module.



Usage:

1. Click the circle in front of the genome assembly and sequence to select the genome and sequence type;
2. Paste the sequence to be queried in the sequence box below;
3. Select the database type and click 'Submit' to submit.

The first is a graphical representation of the genomic positions to which the sequences are aligned. Then there is a list of all the positions aligned, and the user can click them to query the detailed sequence alignment.





## Seq fetch

Usage: Paste the gene list to be aligned in the sequence box or upload the gene list file to be extracted and click “Submit” to submit.

Results: You can directly copy the sequences extracted from the dialog box or click on "CDS", "gDNA" and "Protein" in "Download Sequences of all Input Genes" to download these sequences.

[illegible]

## Variation annotation

Usage: Paste the variant data to be aligned in the sequence box or upload the variation file with VCF format to be extracted and click “Submit” to submit.

Results: Click "Variation annotation.vcf" to download.



Variation annotation using SnpEff

Genome: ☒ ZS11 ☐ Damrui

#CHROM	POS	ID	REF	ALT	QUAL	FILTER	INFO	FORMAT	sample1	sample2
A01	124600	A01_124600_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.

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

Brassica napus  
**ZS11**  
 Damrcr.v10  
 Damrcr.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](#)

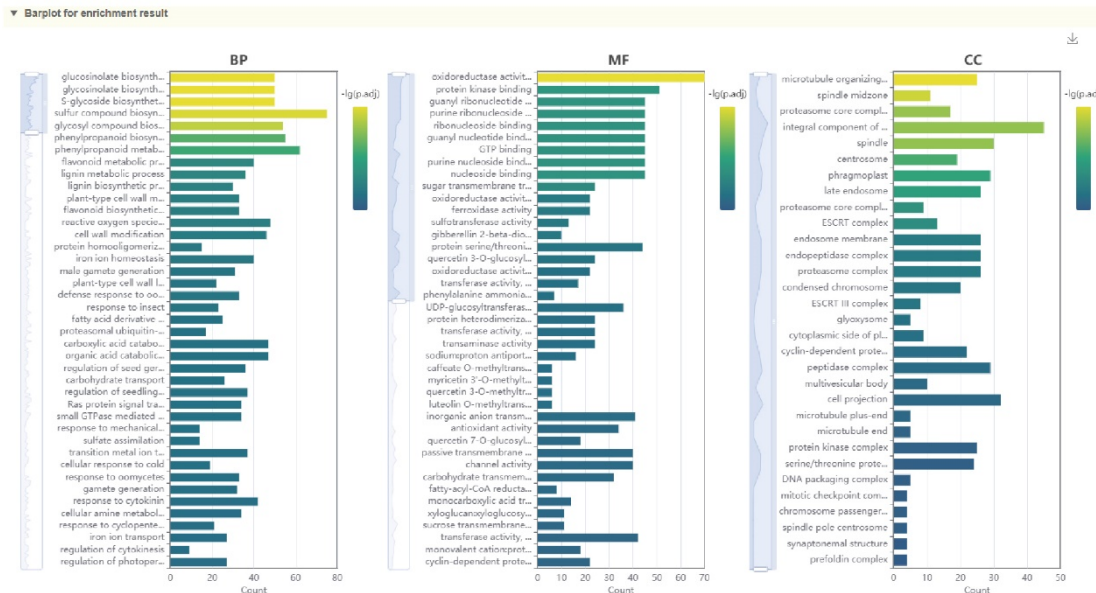
Search:

[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	1.8202535549522e-17	BnaC09G028800ZS/Bna...	50
BP	GO:0019758	glycosinolate biosynthetic process	50/2895	228/62797	2.43103073555425e-20	2.28898675766619e-17	1.8202535549522e-17	BnaC09G028800ZS/Bna...	50
BP	GO:0019761	glucosinolate biosynthetic process	50/2895	228/62797	2.43103073555425e-20	2.20596675766619e-17	1.8202535549522e-17	BnaC09G028800ZS/Bna...	50
BP	GO:0044272	sulfur compound biosynthetic process	75/2895	452/62797	1.15778277102578e-19	8.23564694265915e-17	6.55790987728675e-17	BnaC09G0409100ZS/Bna...	75
BP	GO:1901659	glycosyl compound biosynthetic process	54/2895	289/62797	1.65875264491000e-18	9.4151024225827e-16	7.49709062997499e-16	BnaC09G028800ZS/Bna...	54
BP	GO:0009699	phenylpropanoid biosynthetic process	55/2895	374/62797	3.8180083557788e-14	1.7950957261942e-11	1.42940592688372e-11	BnaC09G0462800ZS/Bna...	55
BP	GO:0009698	phenylpropanoid metabolic process	62/2895	481/62797	4.10582943096827e-13	1.65509256068827e-10	1.31792291615473e-10	BnaC09G0462800ZS/Bna...	62
BP	GO:0009812	flavonoid metabolic process	40/2895	305/62797	3.33423416415085e-09	1.17575547963350e-05	9.35234703463251e-07	BnaC09G0689500ZS/Bna...	40
BP	GO:0009808	lignin metabolic process	36/2895	262/62797	5.75391614600693e-09	1.80353304876506e-06	1.43612363223144e-06	BnaC09G0462800ZS/Bna...	36
BP	GO:0009809	lignin biosynthetic process	30/2895	204/62797	2.18027986343853e-08	6.15059595118009e-06	4.89750712763981e-06	BnaC09G0462800ZS/Bna...	30

Showing 1 to 10 of 331 entries

Previous 1 2 3 4 5 ... 34 Next



## KEGG enrichment

Usage:

1. Select the genome in "Dataset";



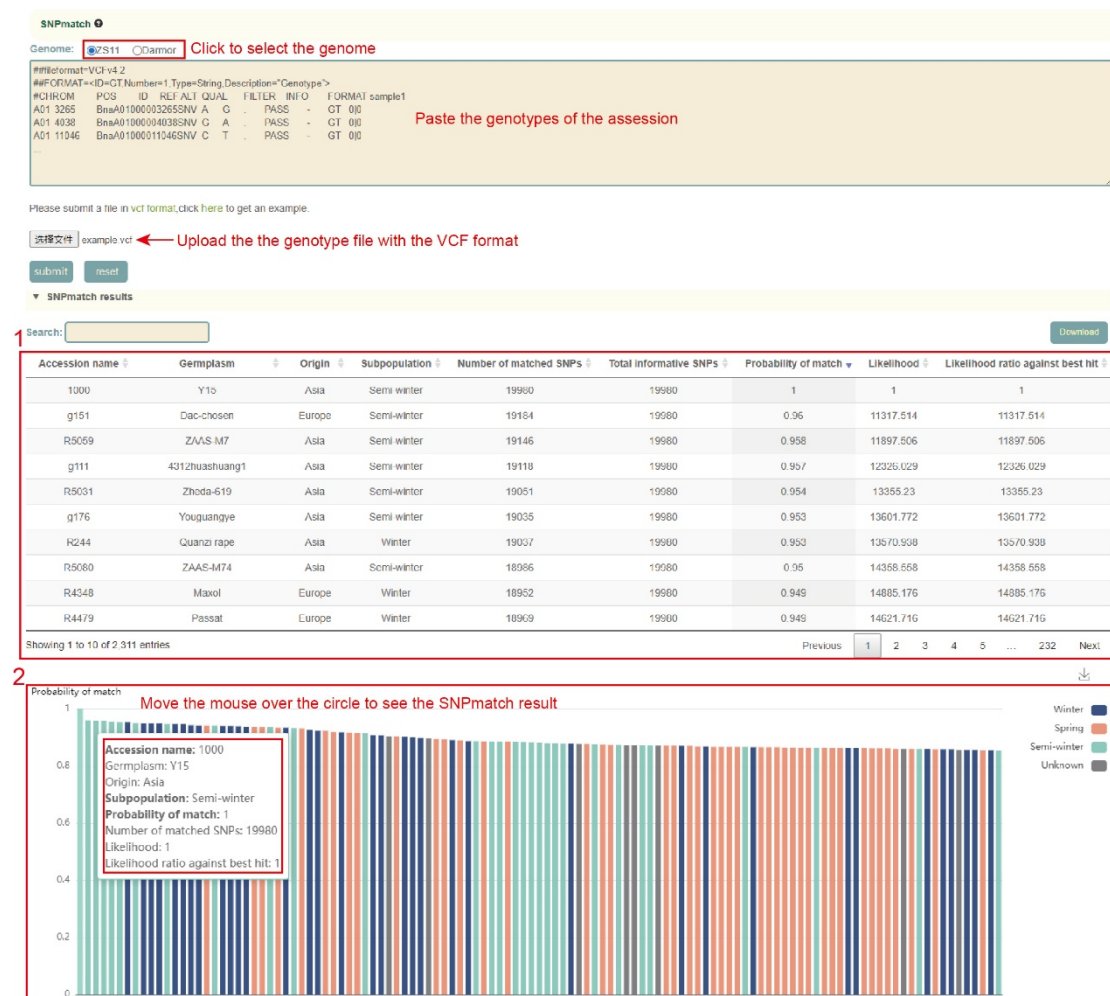
## SNP match

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.



## 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.

NCBI e-PCR

Dataset: **ZS11** Click to switch the genome →

Mode: ☒ STS ☐ Primers

Primers:

STS-1: CTGGTADGGCAACAGTGTATGA CCGTTCAATGCTCGTATCGTAA  
 STS-2: CCGAGCTAATTCANCTCCCAAGA TTGTCACTCTCTTTGGCCATAA

Paste the primer sequences

选择文件 click here to get example Upload the primer sequence file

Mism:  Set max allowed mismatches per primer for lookup.

Gaps:  Set max allowed indels per primer for lookup.

lo-hi:  Set default STS size range - values used for STSs that have no size associated in file.

Click to submit

Brassica napus

ZS11

Darmor.v10

Darmor.v4.1

Gangsen.v0

Ningyou7.v2

No2127.v0

Quinta.v0

Shengli.v0

Express617.v1

Tapidor.v0

Westar.v0

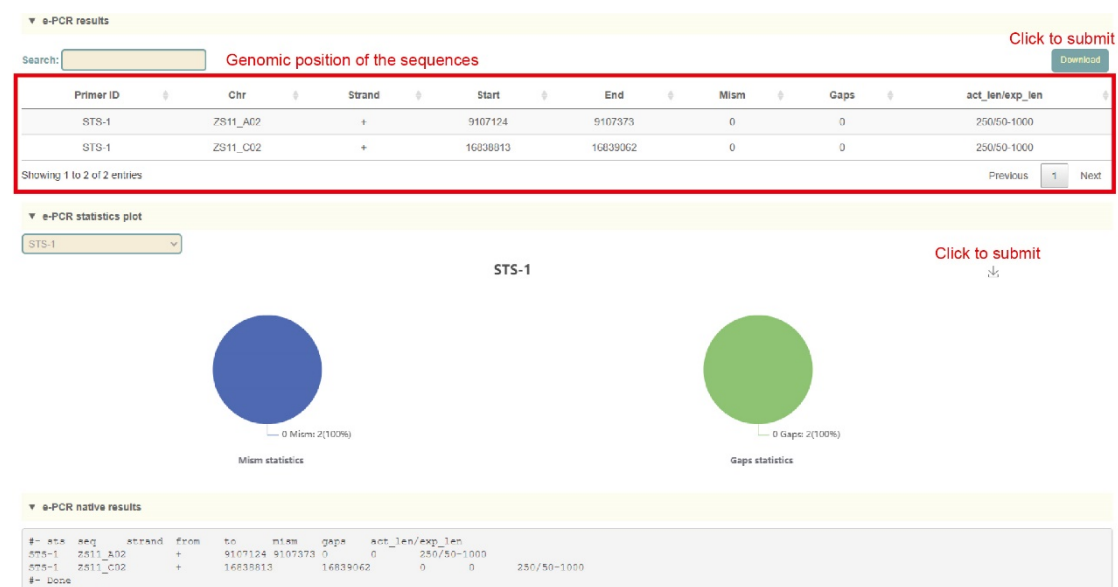
Zhnyou.v0

Arabidopsis thaliana

TAIR10

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.



## 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.

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:

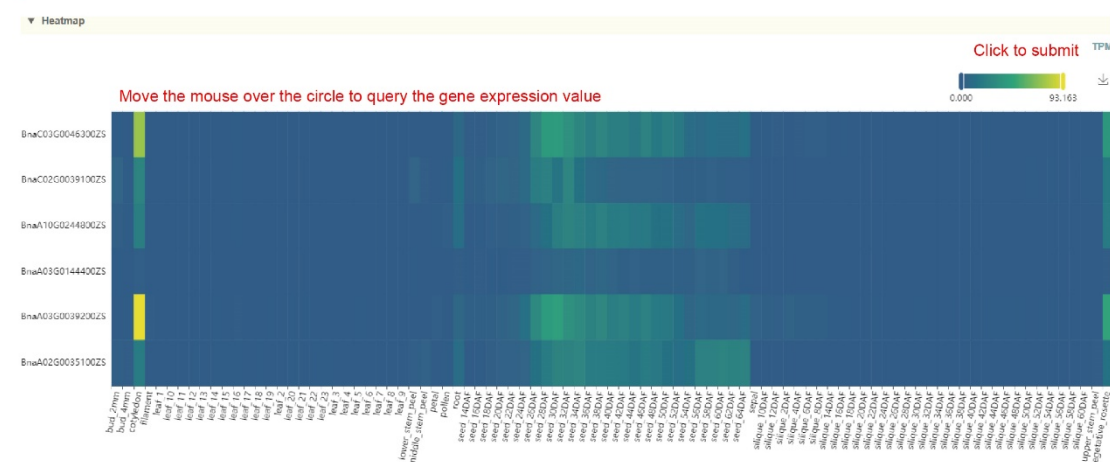
Click to submit [Download](#)

**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	leaf_20
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	0.355	0.312	0
BnaA03G0039200ZS	0.239	0.416	93.163	1.058	0.054	0.020	0.113	0.187	0.190	0.450	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	0.136	0.0	0.059	0.028	0.028	0
BnaA10G0244800ZS	2.087	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	0.051	0.085	0.236	0.714	0.100	0.195	0.049	0

Showing 1 to 6 of 6 entries

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## LDheatmap

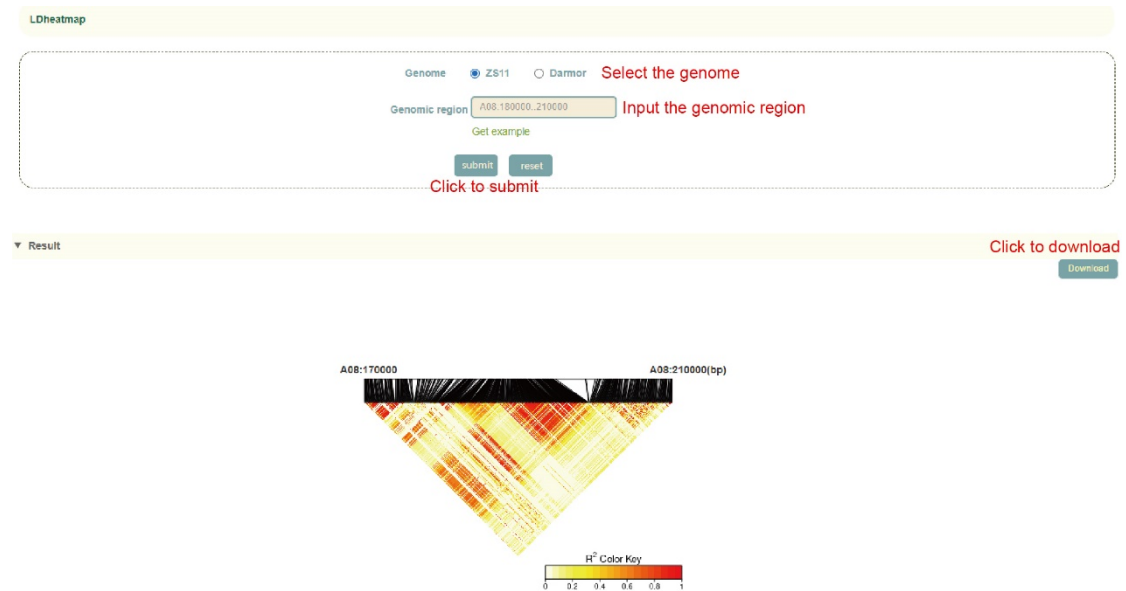
Usage:



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**

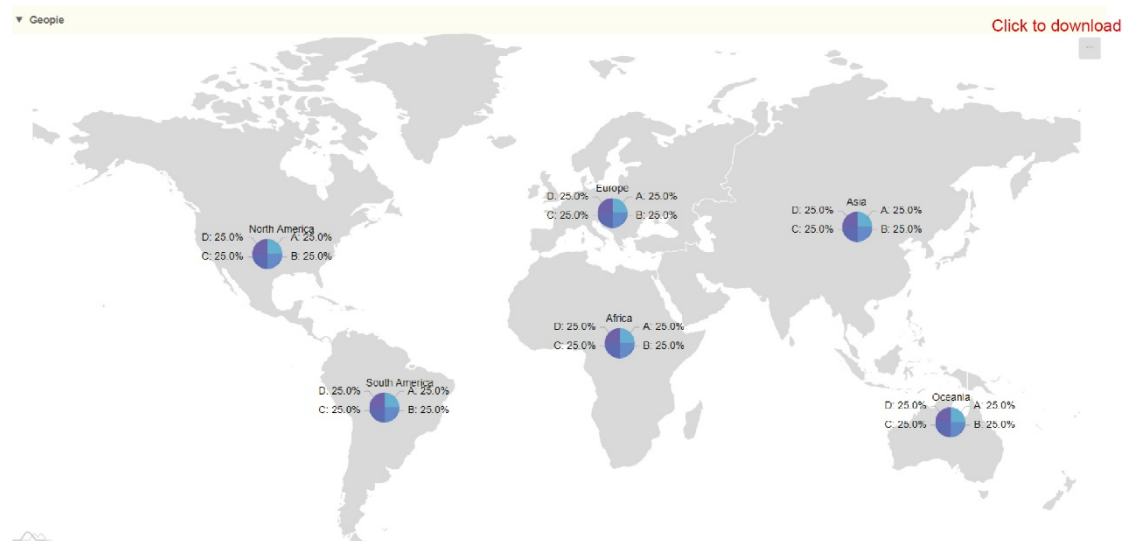
Data

**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.

**Data2heatmap**

Gene ID

```
gene A B C D E F G H
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 "\n")

Upload the data file

Value

☒ value  $C \log_2(\text{value}+1)$   $C \log_{10}(\text{value}+1)$ 

Select the normalization method

Height(heatmap)

10

Width(heatmap)

60

Color

☒ ☐

Fontsize

12

Fontcolor

#1F1D1D

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.

