

BnVIR Database Tutorial

Overview

BnVIR (*Brassica napus* variation information resource, <http://yanglab.hzau.edu.cn/BnVIR>) is a comprehensive *Brassica napus* (*B. napus*) variation database, integrating omics data of population of 2,311 *B. napus* accessions for genetic variations query and discovery for candidate variations of traits in *B. napus*. BnVIR includes:

- Basic information of 2,311 *B. napus* germplasms and their re-sequencing data;
- The population structure, pedigrees and the selective signals;
- Genetic variations including single-nucleotide polymorphisms (SNPs), small insertions and deletions (InDels) and large structure variations (SVs) identified from the population;
- The phenotypic and transcriptional effect of the genetic variations and gene-gene interaction;
- GWAS associating genetic variations with phenotype;

BnVIR comprises large genetic variations of *B. napus*, which are mapped to phenotype and gene expression, providing a powerful and convenient platform for users to carry out variation analysis, mine candidate variations/genes of traits and developing valuable markers for molecular breeding in *B. napus*.

1 Homepage

1.1 The Top Menu

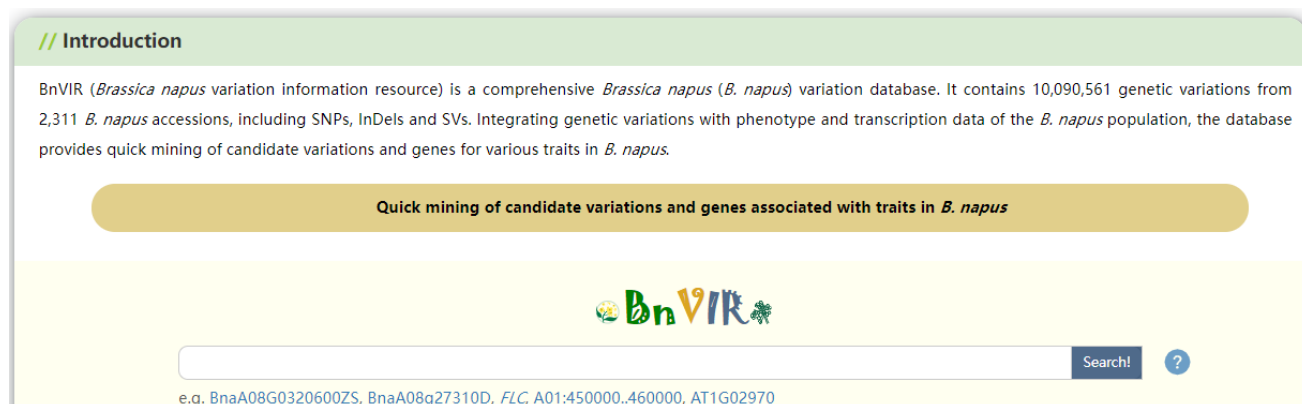
The top navigation menu gathers general functions of the database, including links to different modules and tools, and quick search of genetic variations.



The screenshot shows the top navigation menu of the BnVIR database. On the left, there is a logo for *Brassica napus* variation information resource. Below the logo, the text reads "BnVIR — Bridging the genotype-phenotype gap to accelerate mining candidate variation of traits in *Brassica napus*". To the right of the logo, there is a search bar with the text "eg: AT5G10140 or FLC" and a "search" button. Below the search bar, there is a horizontal navigation menu with the following items: Home, Sample, Variation, Evolution, JBrowser, Tools, Download, and Help.

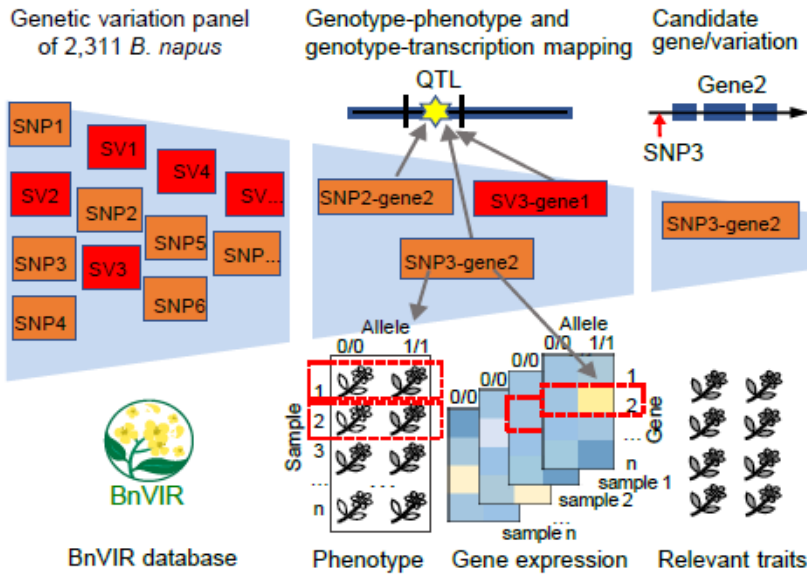
1.2 Brief introduction of BnVIR and quick start to perform candidate variations/genes mining.

For quick search of genetic variations, input of gene ID of *B. napus*, gene ID and name of Arabidopsis and genomic region are supported.



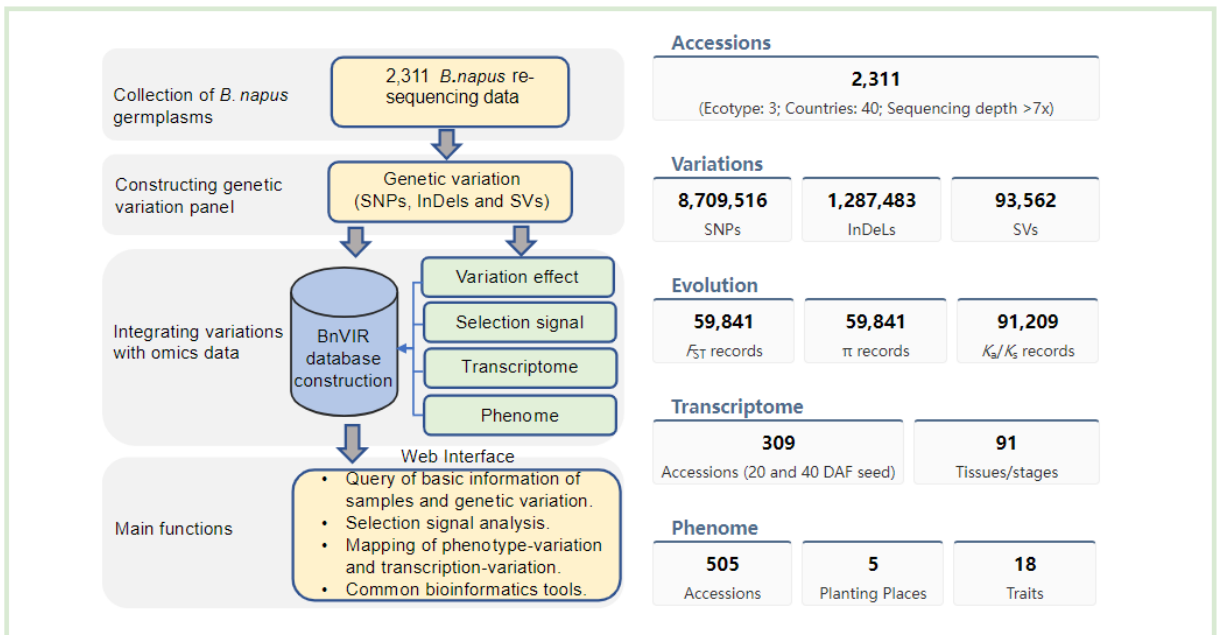
The screenshot shows the introduction page of the BnVIR database. At the top, there is a green header with the text "// Introduction". Below the header, there is a paragraph of text: "BnVIR (*Brassica napus* variation information resource) is a comprehensive *Brassica napus* (*B. napus*) variation database. It contains 10,090,561 genetic variations from 2,311 *B. napus* accessions, including SNPs, InDels and SVs. Integrating genetic variations with phenotype and transcription data of the *B. napus* population, the database provides quick mining of candidate variations and genes for various traits in *B. napus*." Below the paragraph, there is a yellow button with the text "Quick mining of candidate variations and genes associated with traits in *B. napus*". At the bottom of the page, there is a logo for BnVIR and a search bar with the text "Search!" and a question mark icon. Below the search bar, there is a list of example gene IDs: "e.g. BnaA08G0320600ZS, BnaA08g27310D, FLC, A01:450000..460000, AT1G02970".

1.3 Schematic diagram of core function of BnVIR.



1.4 Dataflow of BnVIR

// Schematic representation

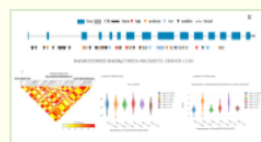


1.5 Quick entry of function module

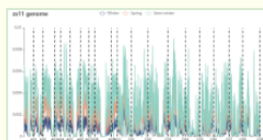
// Quick entry of function modules



Sample
Basic information of 2,311 *Brassica napus* accessions resequencing data and population structures analysis.



Variation
Collection of genetic variations including SNPs, InDels and SVs, and linkage between variation and gene expression, variation and trait.



Evolution
Calculation of selection signal, including F_{ST} , π and K_A/K_S ratio.



JBrowser
Visualization of genetic variations, gene expression and genomic feature in genome.

2 Sample module

2.1 Accession

Accession page presents basic information of *B. napus* accessions, comprising three parts. All the figures and tables can be download by clicking the button locate in the upper right corner.

Part1: Table of basic information *B. napus* accessions, including. Fuzzy search is supported for users (users can search samples by entering any characters relevant to accessions).

Part2: Geographic distribution of *B. napus* accessions.

Part3: Parameters that can be set to choose the subset of the samples, according origin, ecotype, source and depth of the sequencing data.

Parameters:

Origin:

- Asia
- Europe
- North America
- South America
- Africa
- Oceania
- Unknown

Subpopulation:

- Winter
- Spring
- Semi-winter
- Unknown

Source:

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

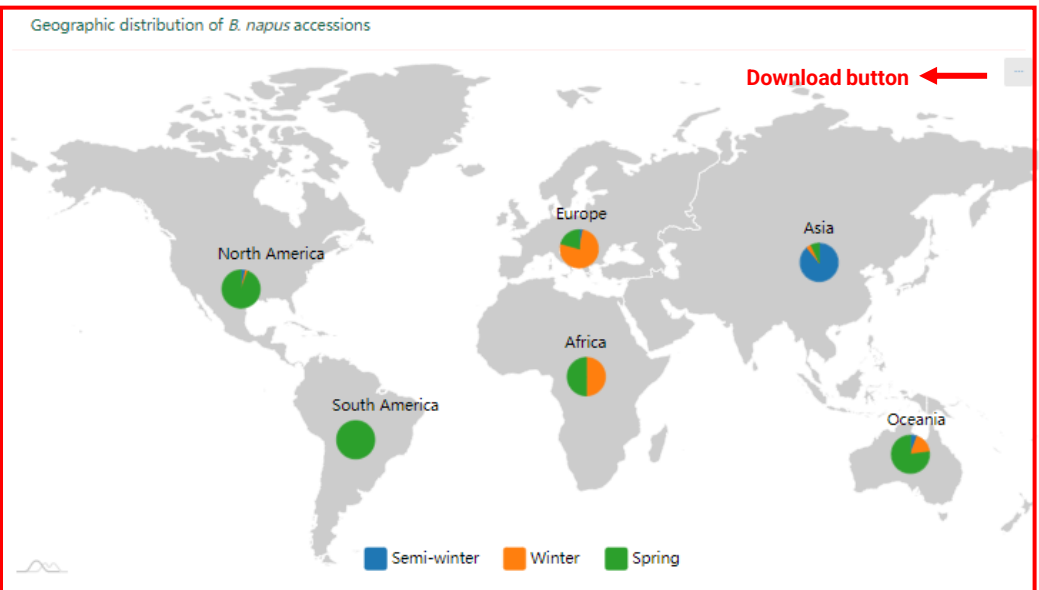
Depth of sequencing data:

The *B. napus* population in database comprises 2,311 *B. napus* accessions, including 1,259 from Asia, 928 from Europe, 60 from North America, two from South America, 38 from Oceania and four from Africa. Three ecotypes, including spring (354 accessions), winter (756 accessions) and semi-winter (1,122 accessions), were included in the population. "Unknown" indicates that region or ecotype of accession is unknown in the previous reports.

Search:

Accession name	Germplasm	Origin	Subpopulation	Depth	Source
1-C2	Canard	Europe	Unknown	7.00	(Song et al., 2020)
1-C3	Brutor	Europe	Spring	5.00	(Song et al., 2020)
10	Yan81-2	Asia	Semi-winter	10.00	(Tang et al., 2021)
100	Cy18Pwx-62	Asia	Semi-winter	8.00	(Tang et al., 2021)
1000	Y15	Asia	Semi-winter	8.00	(Tang et al., 2021)
1002	Y16	Asia	Semi-winter	8.00	(Tang et al., 2021)
1004	Y17	Asia	Semi-winter	9.00	(Tang et al., 2021)
1006	L508	Asia	Semi-winter	8.00	(Tang et al., 2021)
1010	Ningyou8	Asia	Semi-winter	8.00	(Tang et al., 2021)
1012	Ningyou6	Asia	Semi-winter	9.00	(Tang et al., 2021)

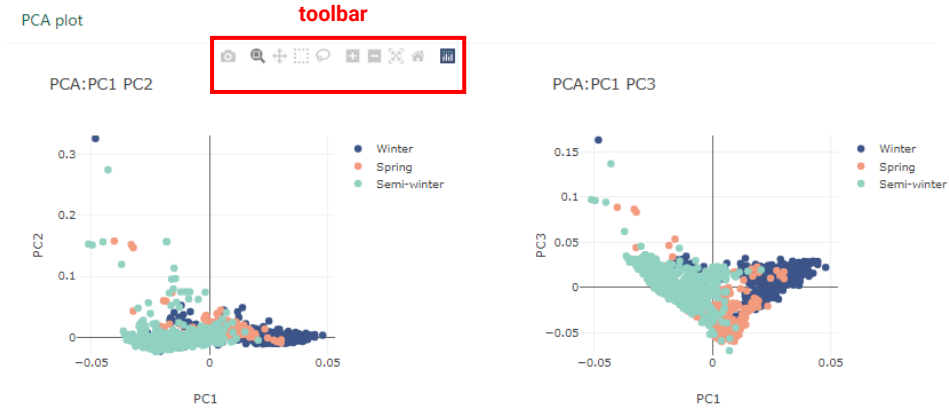
Showing 1 to 10 of 2,311 entries 1 ...



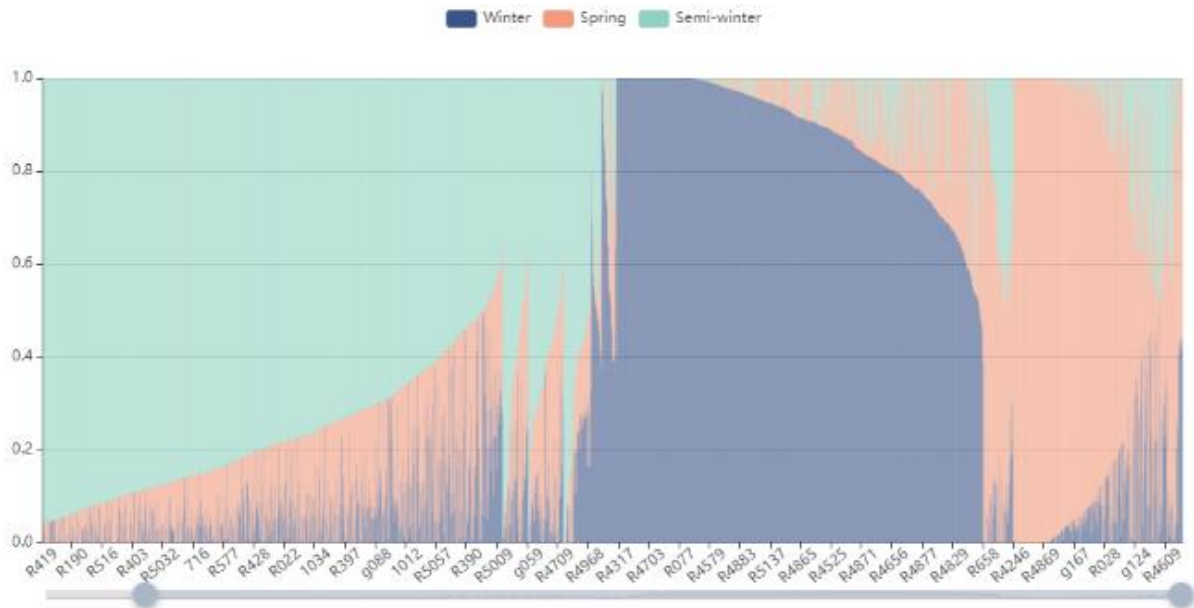
2.2 Population

This page shows the population analysis of the *B. napus* analysis, including PAC, Population structure and phylogenetics.

Part1: PCA analysis for *B. napus* population. More interactive features can be used via toolbar in the upper right hand corner.



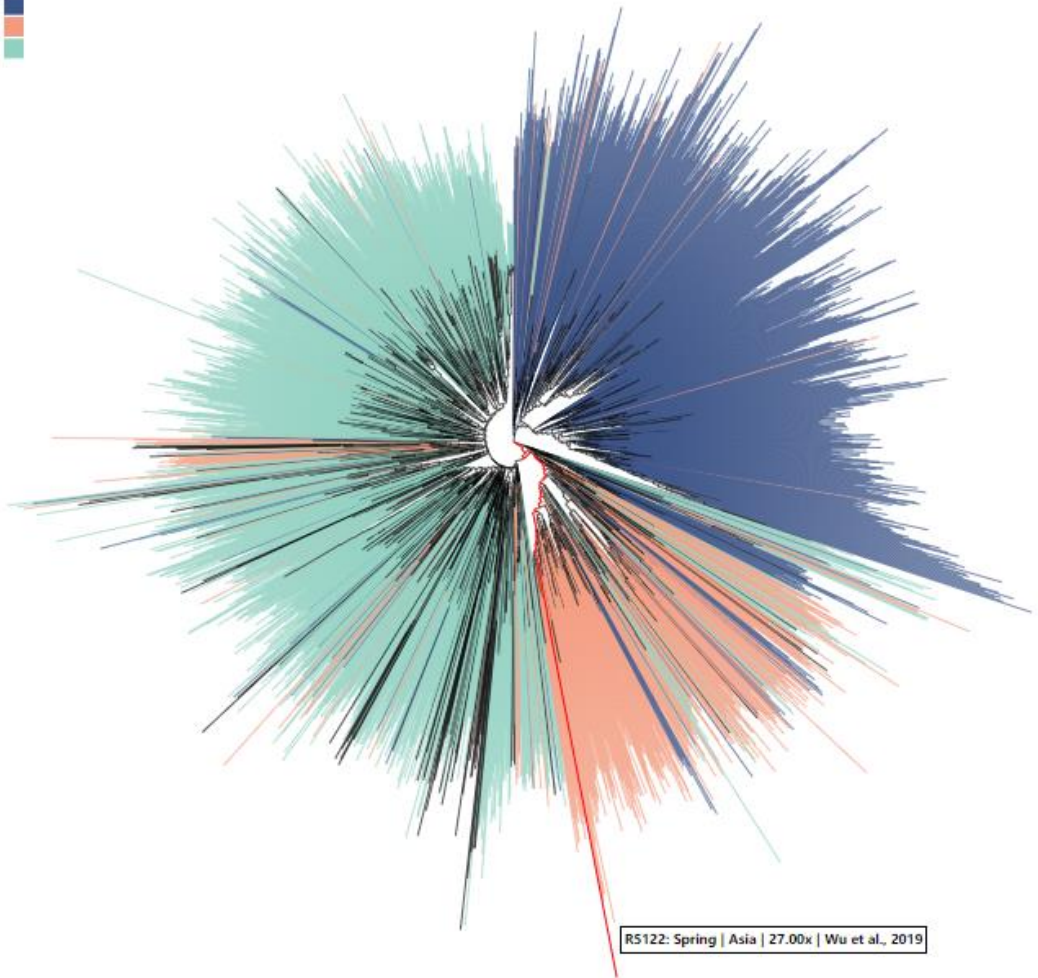
Part 2: Population structure of the *B. napus* population. Ecotypes of spring, winter and semi-winter were marked in red, blue and green color. When mouse over the bar, information of the accessions are shown.



Part 3: Phylogenetic tree of *B. napus* accessions. Ecotypes of spring, winter and semi-winter were marked in red, blue and green color. When mouse over the branches, information of the accessions are shown.

Part 4: Parameters that can be set to choose the subset of the samples, according origin, ecotype, source and depth of the sequencing data.

Winter ■
Spring ■
Semi-winter ■



2.3 About

More information about Sample module.

3 Variation

Variation module integrates genetic variations, phenotype and transcription data of the *B. napus* population, providing variation query and association between genotype and phenotype in mining candidate variations/genes of traits. There are four functional interfaces in Variation module, including Single-locus model, Multiple-locus model, GWAS and Customized phenotype. Information about variations, including annotation, allele frequency, distribution, description of gene expression and phenotypic values, are provide in Single-locus model, enabling user to screen candidate variations/genes of traits. Multi-locus model enables users to combine the multiple loci cross genes to check gene-gene interactions and their contribution to phenotype. GWAS interface provides browse of GWAS result for the *B. napus* population. In Customized phenotype, users can upload their own phenotype data to inspect the candidate variations/genes of traits. Users can choose ZS11 and Darmor-*bzh* genome as reference in each function page (except for Multiple-locus model) in secondary Menu.

The screenshot shows the website header with the logo and title "Brassica napus variation information resource". Below the header is a navigation bar with tabs: Home, Sample, Variation, Evolution, JBrowser, Tools, Download, and Help. The Variation tab is active, and a dropdown menu is open, showing options: Single-locus model (highlighted with a red box), Multi-locus model, Variation-phenotype association (GWAS), Customized phenotype, and About. The Single-locus model option has a sub-menu with "ZS11" (highlighted with a red box) and "Darmor" (highlighted with a red box). Below the menu is a search bar with a "search" button and a text input field containing "eg: AT5G10140 or FLC".

3.1 Single-locus model

3.1.1 Input

We will demonstrate the uses of Variation module based of ZS11 reference.
Gene ID: gene ID of ZS11 reference, gene ID and gene name of Arabidopsis.
Genomic region: genomic region of ZS11 genome in a format of "chr:start..end".
Gene index: gene ID of any published *B. napus* genomes.
Users can choose SNP, Haplotype, SV or all the three types of variations.

The screenshot shows the "Brassica napus Variation Search (ZS11)" form. It has three input fields: "Gene ID" with the value "FAE1", "Gene region" which is empty, and "Gene Index" which is empty. Each field has a "选择文件" (Choose file) button and a "未选择任何文件" (No file selected) message. Below the fields are radio buttons for "Mode": "SNP" (selected), "Haplotype", "SV", and "Merged". At the bottom are "submit" and "reset" buttons. Examples are provided for each field: "e.g. FAE1, AT1G02970, BnaA08G0320500ZS, FLOWERING LOCUS C" for Gene ID, "e.g. A01:450000..460000" for Gene region, and "e.g. BnaA08G0310400ZY, BnaA08g27310D, A01p00080_1_BnaDAR" for Gene Index.

3.1.2 Result page of SNP mode

We demonstrate the search results with the *FAEI* gene. After entering “*FAEI*” and choose “SNP” in search bar, the result page will be shown in minute. The result page comprises 11 parts. Figures and tables in the result page are interactive and downloadable by clicking the button located in the upper right-hand corner.

Part 1: Table of target genes and their basic information. Orthologs of *FAEI* in ZS11 are shown in the table. Users can click the blue column to get more information about the genes. Users can choose one gene for further analysis. BnaA08G0134700ZS is selected here.

Basic information of gene

Search: Download button

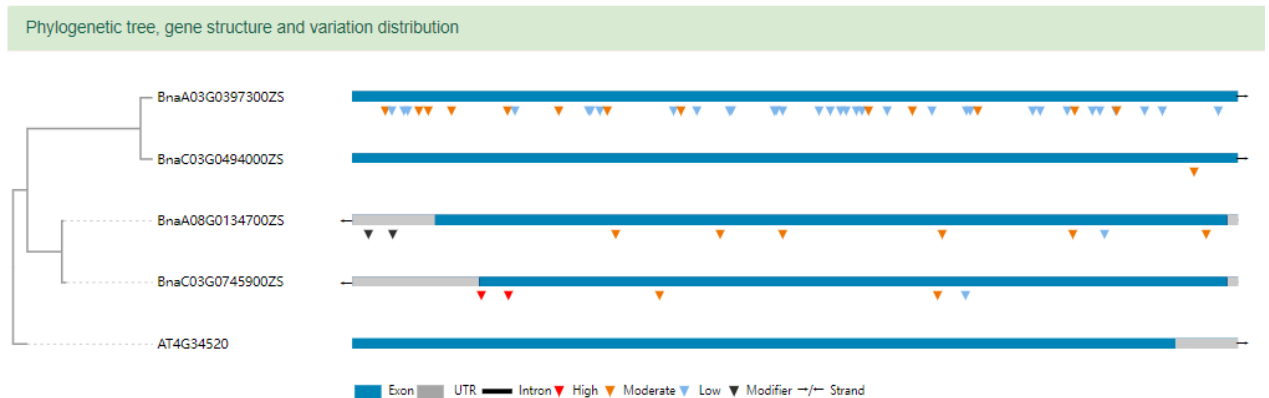
Select	ZS11 Gene ID	Darmor Gene ID	AtGI/Name	Position	Seq/Exp/JBR	SNPs No.	SNP No.(High/Moderate/Low/Modifier)	SV No.
<input checked="" type="checkbox"/>	BnaA03G0397300ZS	BnaA03g39010D	AT4G34520 (FAE1)	A03:21413975..21415438	.fa Exp JBR	46	0/13/33/0	0
<input type="checkbox"/>	BnaA08G0134700ZS	BnaA08g11130D	AT4G34520 (FAE1)	A08:18618052..18619753	.fa Exp JBR	9	0/6/1/2	0
<input type="checkbox"/>	BnaC03G0745900ZS	BnaC03g65980D	AT4G34520 (FAE1)	C03:72309540..72311231	.fa Exp JBR	5	2/2/1/0	0
<input type="checkbox"/>	BnaC03G0494000ZS	BnaC03g46140D	AT4G34520 (FAE1)	C03:35858639..35860030	.fa Exp JBR	1	0/1/0/0	0

Showing 1 to 4 of 4 entries

[Link to BnPIR to view more information of ZS11 gene](#)
 [Link to TAIR to view more information of At gene](#)
 [Link to BnTIR and JBrowse to view gene expression, sequence and genes in JBrowse](#)

submit Previous Next

Part 2: Phylogenetic tree of orthologous genes of *B. napus* and *Arabidopsis*. For each gene in the tree, the gene structure is shown with SNPs or short InDels at the bottom indicated by colored triangles. Mouse over to see brief information of the variation.



Part 3: Define the upstream and downstream of the target gene. “2 kb” is selected here.

Define the upstream and downstream of gene

Choose flanking regions of gene to show

- 0 kb
 1.5 kb
 2 kb
 3 kb
 5 kb
 10 kb

Part 4: Gene structure and distribution of the variations. Variations are represented by triangles with different colors. Mouse over to see brief information of the variation. Click the triangle to see annotation of variation in the table at bottom.

Gene structure and SNP distribution

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

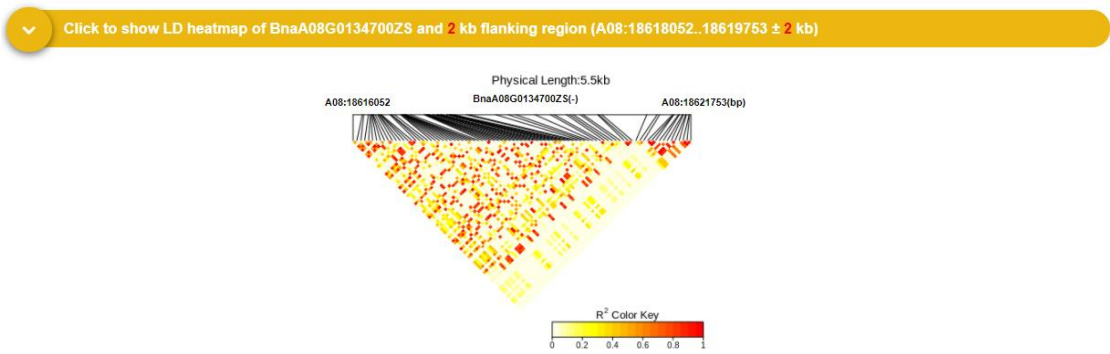
■ Exon
 ■ UTR
 — Intron
 ▼ High
 ▼ Moderate
 ▼ Low
 ▼ Modifier
 ↔ Strand

Download button ←

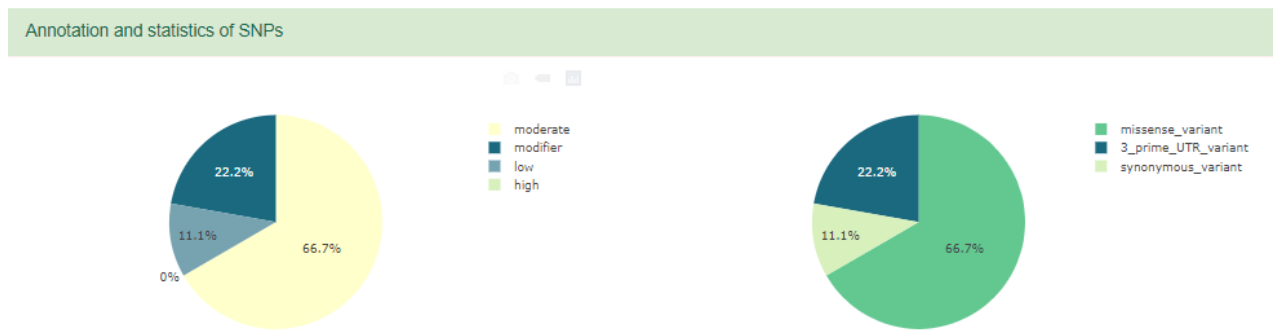
Chromosome	Position	Alt (allele)	Ref (allele)	JBrowse	Alt (frequency)	Ref (frequency)	PIC	Alt (num)	Ref (num)	Function_
A08	18618888	G	A	JBR	0.29	0.71	0.33	640	1614	MODERATE

Showing 1 to 1 of 1 entries

Part 5: LD heatmap of the gene and its up- and downstream.



Part 6: Statistics of the annotation result of variations.



Part 7: Table showing the detail information of the variations. Users can search variations by entering any characters relevant to variation. Click the “JBR” column will bring users to JBRrowse module for visualization of the variation. Click number of “Alt” and “Ref” column will bring users another view presenting a table of sample information.

Information of SNPs in BnaA08G0134700ZS and its ± 0 kb flanking region

According to the gene you input, we provide basic snp information. (PIC: polymorphism information content)

Search:

Download button → [Download](#)

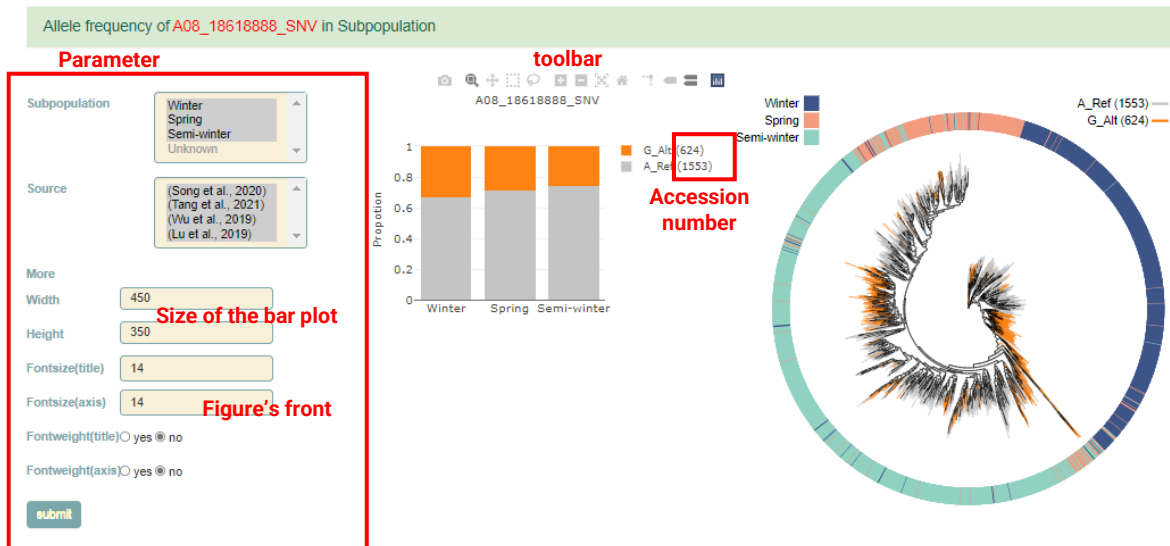
link to JBrowse

Select	Chromosome	Position	Alt (allele)	Ref (allele)	JBrowse	Alt (frequency)	Ref (frequency)	PIC	Alt (num)	Ref (num)
<input checked="" type="checkbox"/>	A08	18618888	G	A	JBR	0.29	0.71	0.33	640	1614
<input type="checkbox"/>	A08	18618765	G	A	JBR	0.03	0.97	0.05	54	2243
<input type="checkbox"/>	A08	18619449	G	C	JBR	0.01	0.99	0.02	16	2283
<input type="checkbox"/>	A08	18618130	T	TTCATAACAAACAAGAGAAACATCGTAGCC	JBR	0.01	0.99	0.02	16	2282
<input type="checkbox"/>	A08	18618563	C	T	JBR	0.00	1.00	0.01	6	2297
<input type="checkbox"/>	A08	18619708	C	G	JBR	0.01	0.99	0.01	15	2295
<input type="checkbox"/>	A08	18619511	G	C	JBR	0.01	0.99	0.01	15	2294
<input type="checkbox"/>	A08	18619197	C	T	JBR	0.00	1.00	0.00	5	2306
<input type="checkbox"/>	A08	18618084	T	C	JBR	0.00	1.00	0.00	2	2309

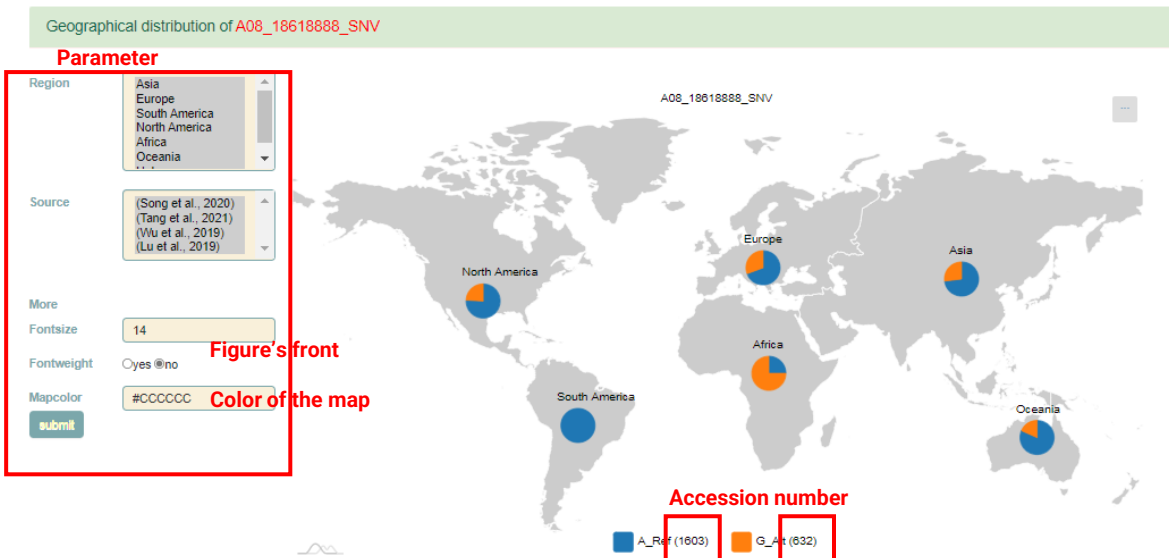
Showing 1 to 9 of 9 entries Previous Next

link to accession information

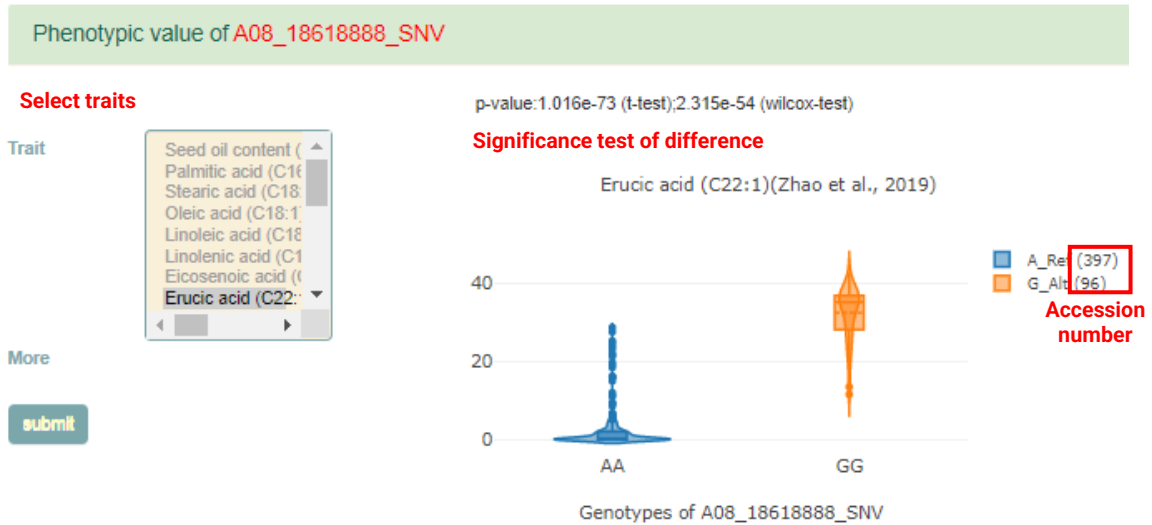
Part 8: Allele frequency of the selected variation. Bar plot and phylogenetic tree shows the allele frequency for each subpopulation. Mouse over the bar plot to get statistics result, and more interactive features are shown in toolbar at the top. Mouse over the branch in tree to see accessions information. Users can choose subpopulation and change style of the figure by setting the parameter in the left.



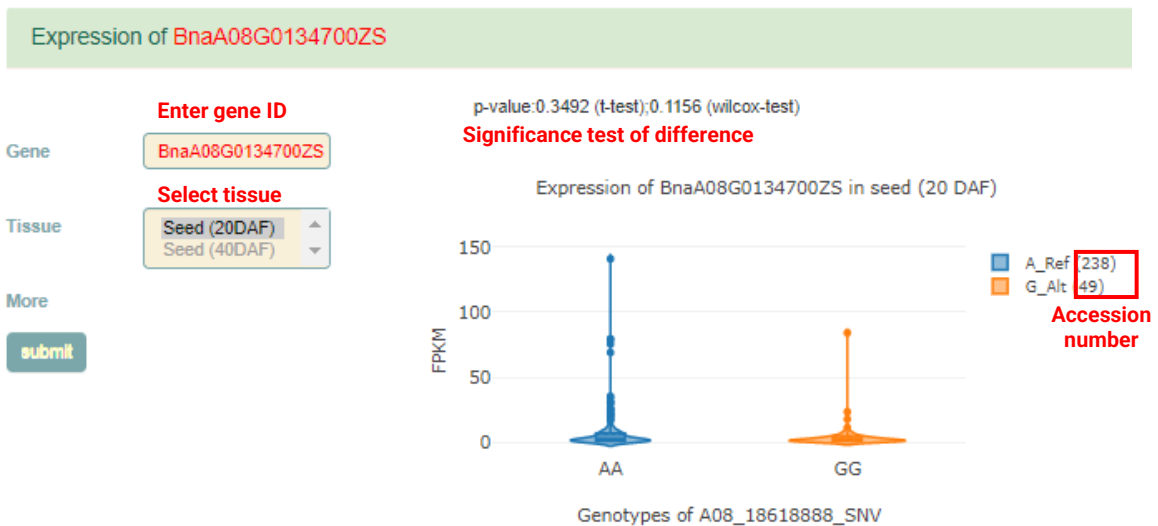
Part 9: Geographic distribution of the accessions with different alleles. Users can choose subpopulation and change style of the figure by setting the parameter in the left.



Part 10: Phenotypic effect of the selected variation. Violin plot shows the distribution of phenotype value of the *B. napus* accessions with different alleles. Number of accessions of “Alt” and “Ref” are shown in legend. Differenced determined by Student’s t-test and Wilcoxon test are shown at the top. 18 traits are provided to be choose in left hand.



Part 11: Gene expression of *B. napus* accessions with different alleles. Violin plot shows the distribution of gene expression level of the *B. napus* accessions with different alleles. Number of accessions of “Alt” and “Ref” are shown in legend. Differenced determined by Student’s t-test and Wilcoxon test are shown at the top. Users can enter gene ID and choose tissues in left hand.



3.1.3 result page of the Haplotype and SV mode

The result of Haplotype and SV mode are similar to that of SNP mode. Identification of haplotypes and SVs was description in Methods.

3.1.3 Result page of the merge mode

All the figures and table are arranged compactly. All the parameters are in the left hand. Users can quickly switch the result page of SNP, haplotype and SV by click them at the top.

Parameters:

Upstream/downstream:
 10 kb 1.5 kb 2 kb
 3 kb 5 kb 10 kb
 50 kb

Sub-populations:
 Winter
 Spring
 Semi-winter
 Unknown

Regions:
 Asia
 Europe
 South America
 North America
 Africa
 Oceania

Source:
 Gong et al., 2020
 Tang et al., 2021
 Wu et al., 2018
 Lu et al., 2018

Trait:
 Linoleic acid (C18:2)
 Linoleic acid (C18:2)
 Eicosanoic acid (C20)
 Oleic acid (C18:1n-7)
 Seed glucanin/oleic
 Plant height (Lu et al.)
 Main inflorescence 9

Expression:
 Seed (20 DAF)
 Seed (10 DAF)

Gene:
 BnaA03G039730025

[submit](#)

SNP

Haplotype

SV

Select variations

Search:

Select	Chromosome	Position	Alt(allele)	Ref(allele)	J-Diver	Alt(frequency)	Ref(frequency)	PIC	Alt(sum)	Ref(sum)
<input checked="" type="checkbox"/>	A03	21414086	G	T	JGR	0.30	0.70	0.33	606	153
<input type="checkbox"/>	A03	21414102	G	T	JGR	0.29	0.71	0.33	596	154
<input type="checkbox"/>	A03	21414319	G	T	JGR	0.29	0.71	0.33	604	155
<input type="checkbox"/>	A03	21414401	A	T	JGR	0.30	0.70	0.33	613	155
<input type="checkbox"/>	A03	21414609	A	G	JGR	0.29	0.71	0.33	603	159
<input type="checkbox"/>	A03	21415019	A	G	JGR	0.29	0.71	0.33	591	152
<input type="checkbox"/>	A03	21415373	A	G	JGR	0.30	0.70	0.33	611	159
<input type="checkbox"/>	A03	21416079	T	C	JGR	0.29	0.71	0.33	589	152
<input type="checkbox"/>	A03	21416662	C	T	JGR	0.29	0.71	0.33	590	152
<input type="checkbox"/>	A03	21416991	C	T	JGR	0.29	0.71	0.33	588	152

Showing 1 to 10 of 46 entries

Previous 1 2 3 4 5 Next

[submit](#)

Gene structure and variation distribution

Exon Intron High Moderate Low Mutation Strand

BnaA03G039730025 BnaA03G039730025 in unrefined:21414075..21415495 0 kb

LD heatmap

r^2 Color key

Variant classification and pie charts

A03_21414086_SNV

Legend: T_Ref (1588), G_Alt (800)

p-value: 0.0103 (Heat); 0.0336 (Wilco-test)

Seed oil content (SOC) (Tang et al., 2021)

Genotypes of A03_21414086_SNV

A03_21414086_SNV

p-value: 1.207e-21 (Heat); 5.919e-10 (Wilco-test)

Expression of BnaA03G039730025 in seed (20 DAF)

Genotypes of A03_21414086_SNV

3.2 Multi-locus model

This page enables users to combine the multiple loci cross genes to check gene-gene interactions and their phenotypic effect.

3.2.1 Input

Users can enter gene list (separated by comma), or genomic regions. Gene number should be not more than 10.

Brassica napus multi-locus model variation search (ZS11)

Region/Gene

BnaA08G0134700ZS,BnaC03G0745900ZS,BnaA05G0427800ZS

e.g. BnaA08G0134700ZS, BnaC03G0745900ZS, BnaA05G0427800ZS or AT4G34520, AT3G12120 or FAE1, FAD2 or BnaA08g11130D, BnaC03g65980D, BnaA05g26900D or A08:18618052..18619753, C03:72309540..72311231, A05:40593352..40596043

(txt,csv)

3.2.1 Result page

The result page including four parts. We show the result of the input of “BnaA08G0134700ZS,BnaC03G0745900ZS,BnaA05G0427800ZS” here.

Part 1: Variation information of each gene. Information of the variation table is described above. Click gene ID at the top of the result page and select interested variations for each genes and then submit. Four variations are selected here.

BnaA08G0134700ZS
BnaC03G0745900ZS
BnaA05G0427800ZS
Select variation table of gens to show

SNP basic information

Search:

<input checked="" type="checkbox"/>	Gene/Region	Chromosome	Position	Alt (allele)	Ref (allele)	JBrowser	Alt (frequency)	Ref (frequency)
<input checked="" type="checkbox"/>	BnaA08G0134700ZS (AT4G34520 FAE1)	A08	18618888	G	A	JBR	0.29	0.71
<input type="checkbox"/>	BnaA08G0134700ZS (AT4G34520 FAE1)	A08	18618765	G	A	JBR	0.03	0.97
<input type="checkbox"/>	BnaA08G0134700ZS (AT4G34520 FAE1)	A08	18618130	T	TTCATAACAAACAAGAGAAACATCGTAGCC	JBR	0.01	0.99
<input type="checkbox"/>	BnaA08G0134700ZS (AT4G34520 FAE1)	A08	18619449	G	C	JBR	0.01	0.99
<input type="checkbox"/>	BnaA08G0134700ZS (AT4G34520 FAE1)	A08	18618563	C	T	JBR	0.00	1.00

BnaA08 BnaC03G0745900ZS BnaA05G0427800ZS

BnaA08 SNP basic information

BnaA08 SNP basic information

BnaA08 SNP basic information

BnaA08 SNP basic information

Showing 1 to 9 of 9 entries

<input checked="" type="checkbox"/>	Gene/Region	Chromosome	Position	Alt (allele)	Ref (allele)	JBrowser	Alt (frequency)	Ref (frequency)	PIC	Alt (num)
<input checked="" type="checkbox"/>	BnaC03G0745900ZS (AT4G34520 FAE1)	C03	72309789	GTT	G	JBR	0.48	0.52	0.37	1066
<input checked="" type="checkbox"/>	BnaC03G0745900ZS (AT4G34520 FAE1)	C03	72309841	C	CCTGA	JBR	0.21	0.79	0.27	427
<input type="checkbox"/>	BnaC03G0745900ZS (AT4G34520 FAE1)	C03	72310132	G	A	JBR	0.00	1.00	0.01	8
<input type="checkbox"/>	BnaC03G0745900ZS (AT4G34520 FAE1)	C03	72310669	G	T	JBR	0.00	1.00	0.01	9
<input type="checkbox"/>	BnaC03G0745900ZS (AT4G34520 FAE1)	C03	72310722	C	T	JBR	0.00	1.00	0.01	9

BnaA08G0134700ZS BnaC03G0745900ZS BnaA05G0427800ZS

BnaA08 SNP basic information

Showing 21 to 30 of 49 entries 1 row selected

<input checked="" type="checkbox"/>	Gene/Region	Chromosome	Position	Alt (allele)	Ref (allele)	JBrowser	Alt (frequency)	Ref (frequency)	PIC	Alt (num)
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40594227	A	G	JBR	0.08	0.92	0.14	170
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40593478	C	CAG	JBR	0.07	0.93	0.13	152
<input checked="" type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40593933	A	ATCCT	JBR	0.06	0.94	0.11	113
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40593954	T	A	JBR	0.05	0.95	0.10	98
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40595001	T	G	JBR	0.06	0.94	0.10	118
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40594686	G	C	JBR	0.05	0.95	0.08	95
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40594689	G	A	JBR	0.05	0.95	0.08	97
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40595016	T	C	JBR	0.04	0.96	0.08	88
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40595400	T	G	JBR	0.03	0.97	0.05	48
<input type="checkbox"/>	BnaA05G0427800ZS (AT3G12120 FAD2)	A05	40593499	T	A	JBR	0.02	0.98	0.04	45

Previous 1 2 3 4 5 Next

Part 2: Detail information of the different four-alleles combinations, including allelic combination and their accession number, frequency. Click the number of the accession will bring users to the table with accession information.

locus combinations

Search:

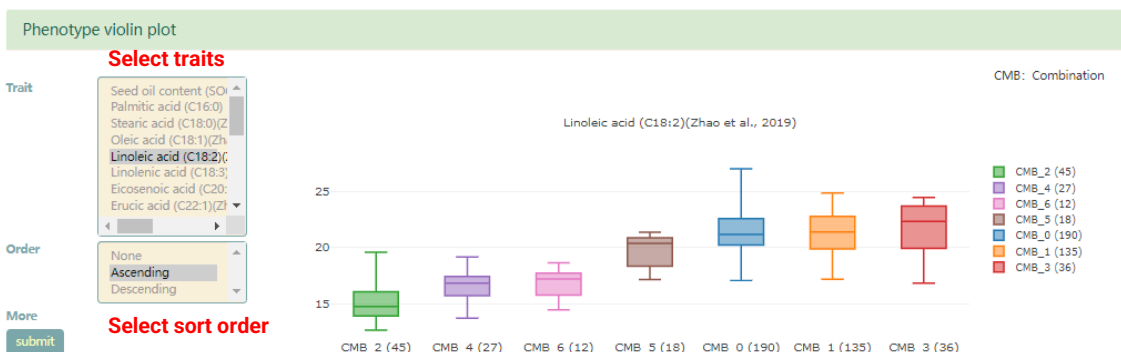
Select all Select none Download

<input checked="" type="checkbox"/>	ID	locus combination	Frequency	Sample
<input checked="" type="checkbox"/>	combination_0	A_G_C	0.307	617
<input checked="" type="checkbox"/>	combination_1	G_GTT_C	0.178	357
<input checked="" type="checkbox"/>	combination_2	A_G_T	0.176	354
<input checked="" type="checkbox"/>	combination_3	A_GTT_C	0.169	339
<input checked="" type="checkbox"/>	combination_4	A_GTT_T	0.069	139
<input checked="" type="checkbox"/>	combination_5	G_GTT_T	0.064	128
<input checked="" type="checkbox"/>	combination_6	G_G_C	0.027	54
<input type="checkbox"/>	combination_7	G_G_T	0.009	19

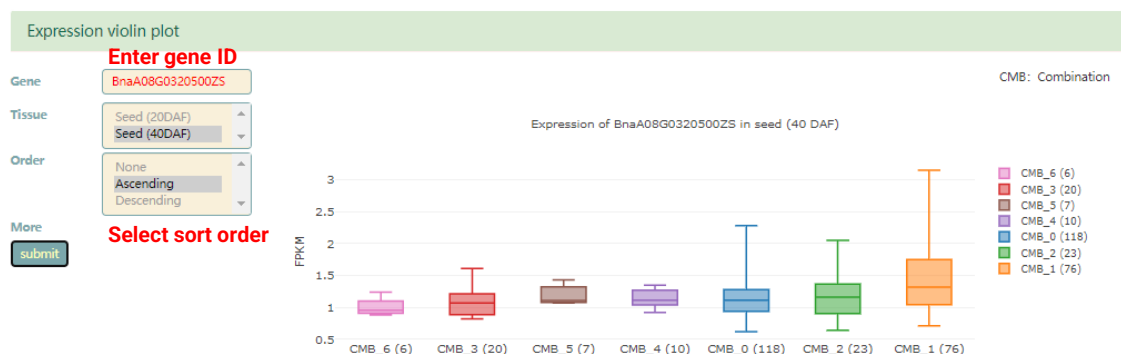
Showing 1 to 8 of 8 entries 7 rows selected

[Link to accession information](#)

Part 3: Phenotypic effect of the locus combinations. Violin plot shows the distribution of phenotype value of the *B. napus* accessions with different combinations. Number of accessions of each combination is shown in legend. 18 traits are provided to choose in left hand.



Part 4: Gene expression of *B. napus* accessions with different combinations. Violin plot shows the distribution of gene expression level of the *B. napus* accessions with different combinations. Number of each combination is shown in legend. Users can enter gene ID and choose tissues in left hand.



3.3 GWAS

GWAS interface provides browse of GWAS result for 18 traits in the *B. napus* population.

3.3.1 Setting

Firstly, users should set the threshold of the significant associations, and select the trait.

ZS11 Variation-phenotype association (GWAS)

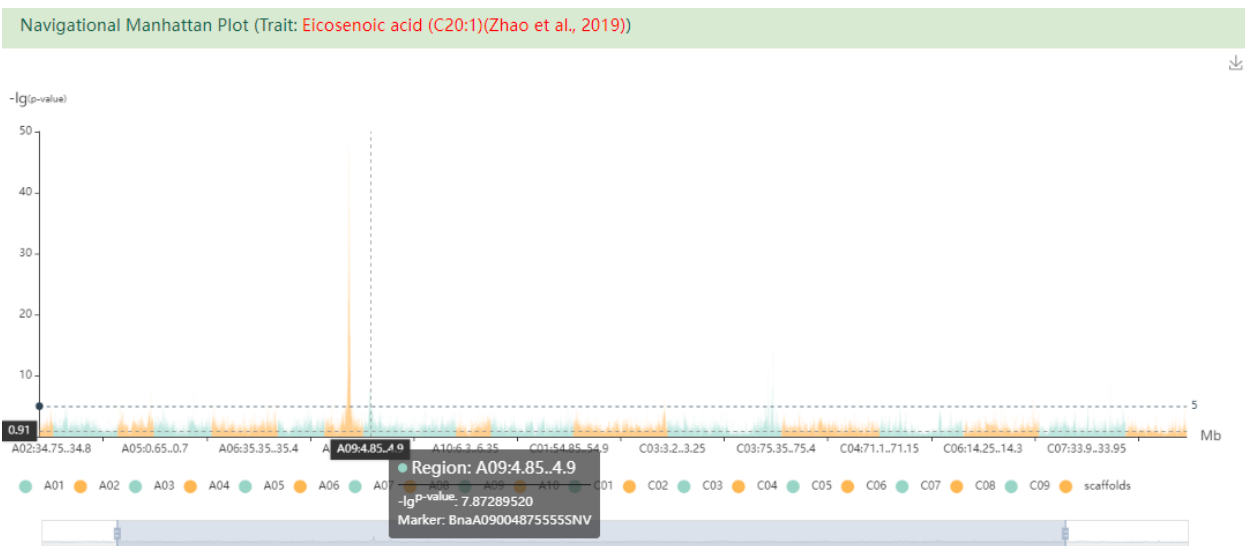
Threshold(" -log10(p)") ?

Trait ?

3.3.2 Result page

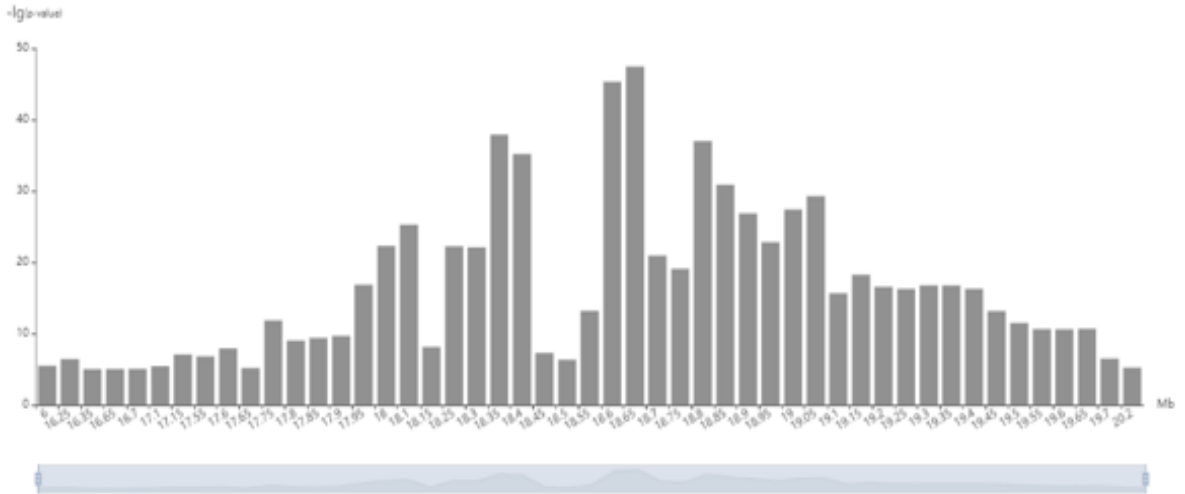
The result page provides global Manhattan plot and query of significance of the local region or gene.

Part 1: Manhattan plot of the genome. Users can zoom in and out the plot by scrolling the mouse. Users can also mouse over the bar to get the information of the region, including genome location, -lg(p value), variation ID.

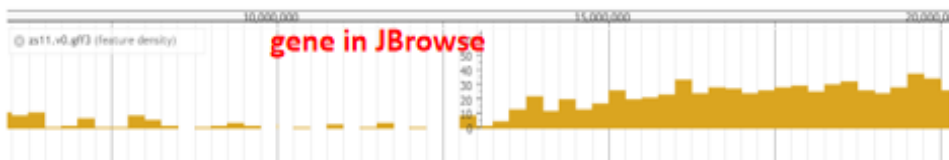
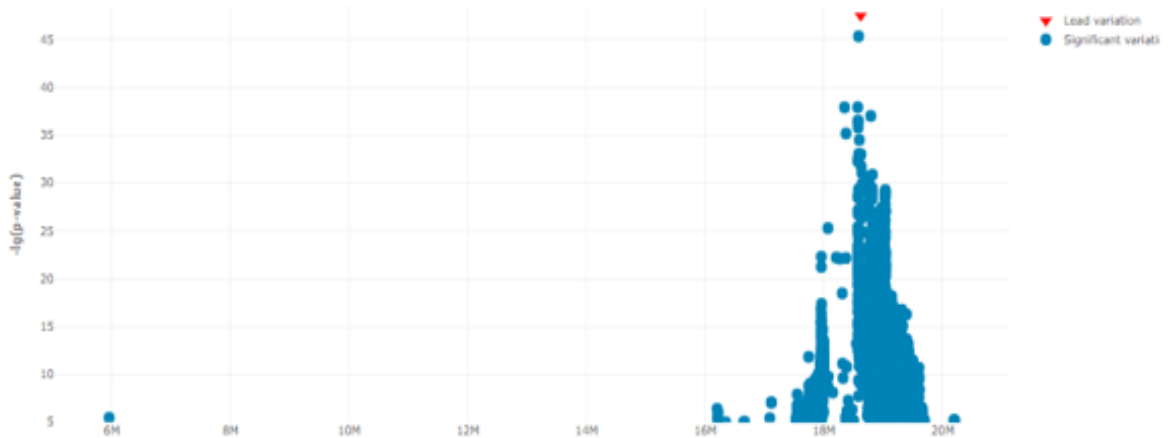


Part 2: Local Manhattan plot. Users can check specific genomic region by entering genomic region or gene ID in the search bar at the top. Top: Bar plot of the 50-kb. Middle: scatter plot the significant variations. Lead variations are indicated by red triangle. Bottom: JBrowse of the genome and genes. Users can mouse over these interactive plots to get the corresponding information.

gene/region e.g. A08:18000000..18500000 or A08 or BnaA08G0133900Z5



Lead variation



3.4 Customized phenotype

User can upload their own phenotype data to screen candidate variations/genes of the traits in the page.

3.4.1 Input

User can upload or copy the phenotype file in which rows represent the accession ID and columns represent the traits. Other input is same as the in Single-locus model. Note that although accession names overlap with those in the database, the seed stocks might be sourced from different origins with potentially different degrees of purity, or maintained in different collections with the possibility of outcrossing, which lead to an unreliable result.

Gene ID ? 未选择文件
example_file

e.g. *FAE1*, AT1G02970, BnaA08G0320500ZS, *FLOWERING LOCUS C*

Gene region ?

e.g. A01:450000..460000

Gene Index ? 未选择文件
example_file

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

Mode SNP Haplotype SV

Customize phenotype

Accession_ID	Yield
26	27.19166667
34	27.61233333
44	27.547
46	28.199
50	27.49566667
60	27.24833333
66	27.53566667
72	27.32733333
80	27.114
88	30.26866667
100	27.39233333

example file or fpls_phe_1.txt or fpls_phe_2.txt

3.4.2 Result page

The result page is similar to that of Single-locus model.

3.5 About

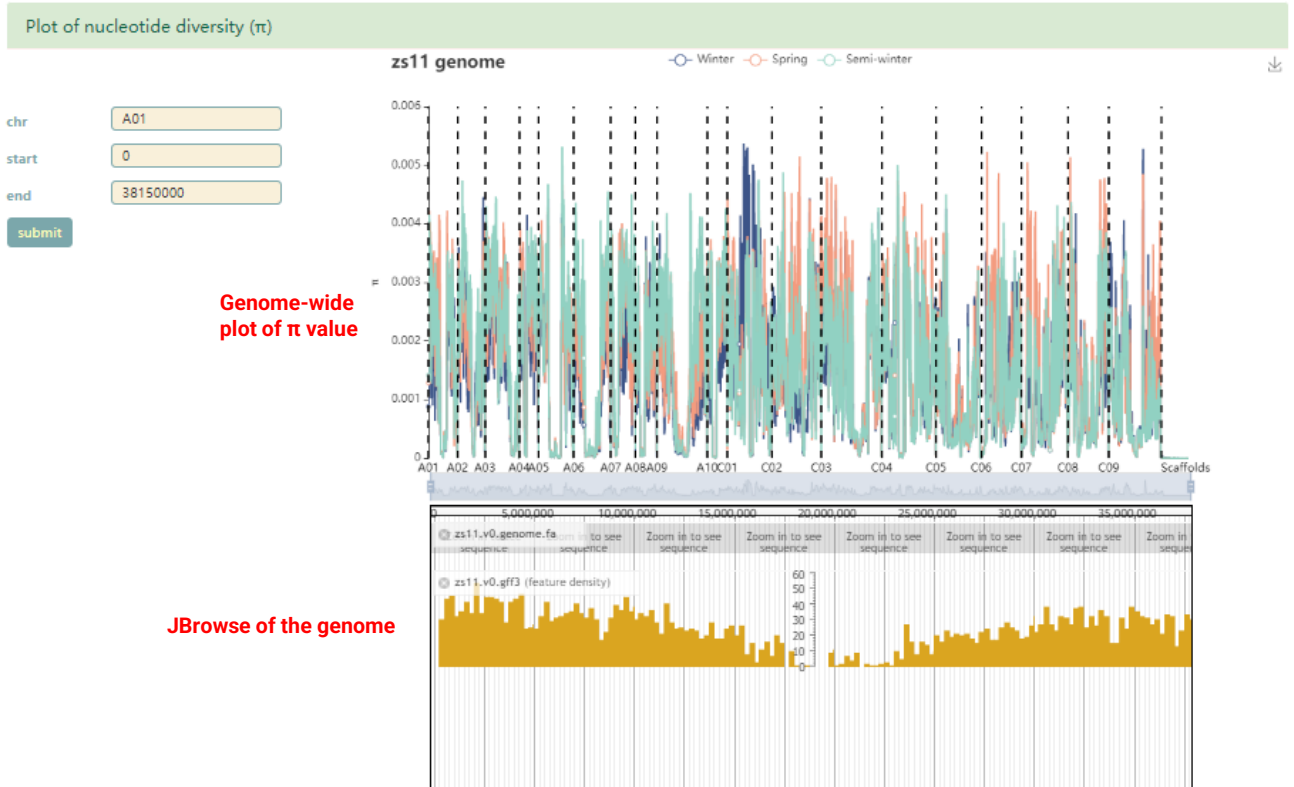
More information about Variation module.

4 Evolution

The Evolution module provides selection signals, including nucleotide diversity (π), fixation index (F_{ST}) and K_a/K_s ratio, for the detection of genomic regions or genes under selection.

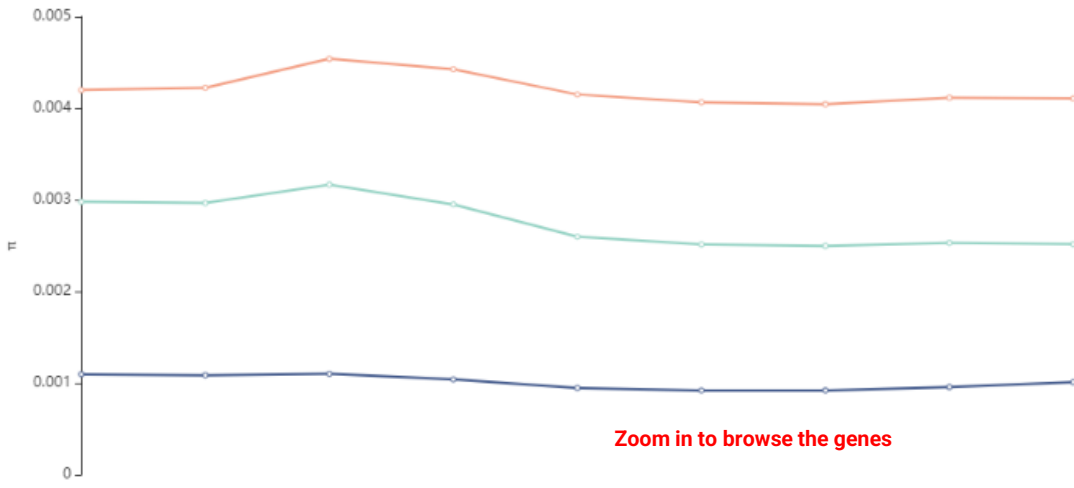
4.1 π

Users can zoom in and out the genome-wide plot to screen the π value of the specific region by scrolling the mouse. In line plot of π value at the top, three ecotypes are shown, respectively. Gene density, genes module and genome sequence will be shown in JBrowse at the bottom when gradually zoom out the line plot. Mouse over the line plot to view the π value and genome position.

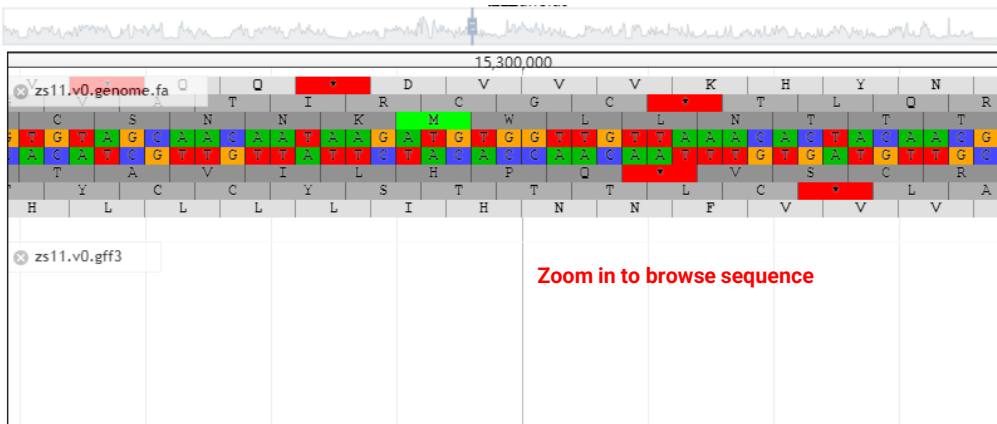
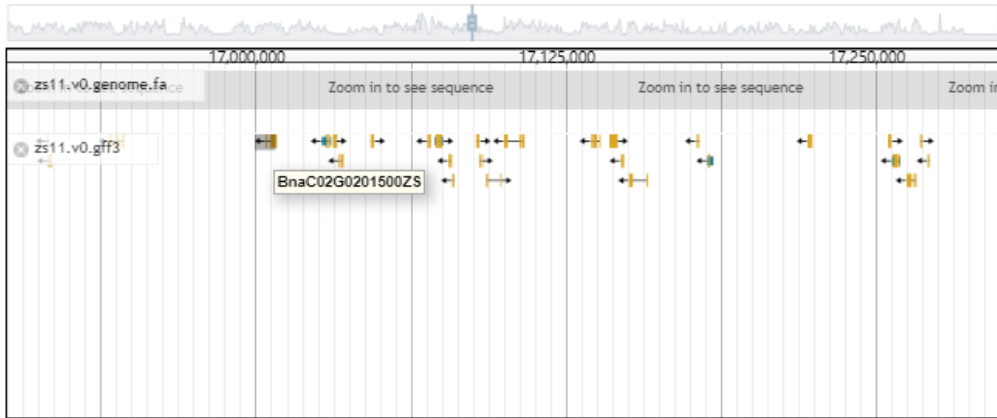


zs11 genome

Winter Spring Semi-winter



Zoom in to browse the genes



Zoom in to browse sequence

Users can also screen the π value of the specific region by entering genomic region or gene ID of *B. napus*. “BnaA07G0282700ZS” is entered here. In the result page, table with π value, line plot and JBrowse of target region are available for download or browse.

Selection signal search (ZS11)

BnaA07G0282700ZS

选择文件 未选择文件

e.g. BnaA07G0282700ZS, A01:1..1607270, BnaAnng09250D

submit reset

Nucleotide diversity (π)

Search:

Download button

Download

Select	Chromosome	Start	End	Position	PI_W	PI_S	PI_SW
<input type="checkbox"/>	A07	25800001	26300000	26050000	0.00290244	0.00257149	0.00286583
<input type="checkbox"/>	A07	25850001	26350000	26100000	0.00297163	0.00266476	0.00295574
<input type="checkbox"/>	A07	25900001	26400000	26150000	0.00283194	0.00271123	0.00301219
<input type="checkbox"/>	A07	25950001	26450000	26200000	0.00290673	0.00279882	0.00311513
<input type="checkbox"/>	A07	26000001	26500000	26250000	0.00268702	0.00264063	0.00282618
<input type="checkbox"/>	A07	26050001	26550000	26300000	0.00258051	0.00257858	0.00267581
<input type="checkbox"/>	A07	26100001	26600000	26350000	0.0024773	0.00252245	0.002726
<input type="checkbox"/>	A07	26150001	26650000	26400000	0.00230689	0.00213509	0.0024927
<input type="checkbox"/>	A07	26200001	26700000	26450000	0.00209713	0.00207168	0.00234642
<input type="checkbox"/>	A07	26250001	26750000	26500000	0.00198112	0.00210467	0.00228836

Showing 1 to 10 of 10 entries

Previous 1 Next

Plot of nucleotide diversity (π)

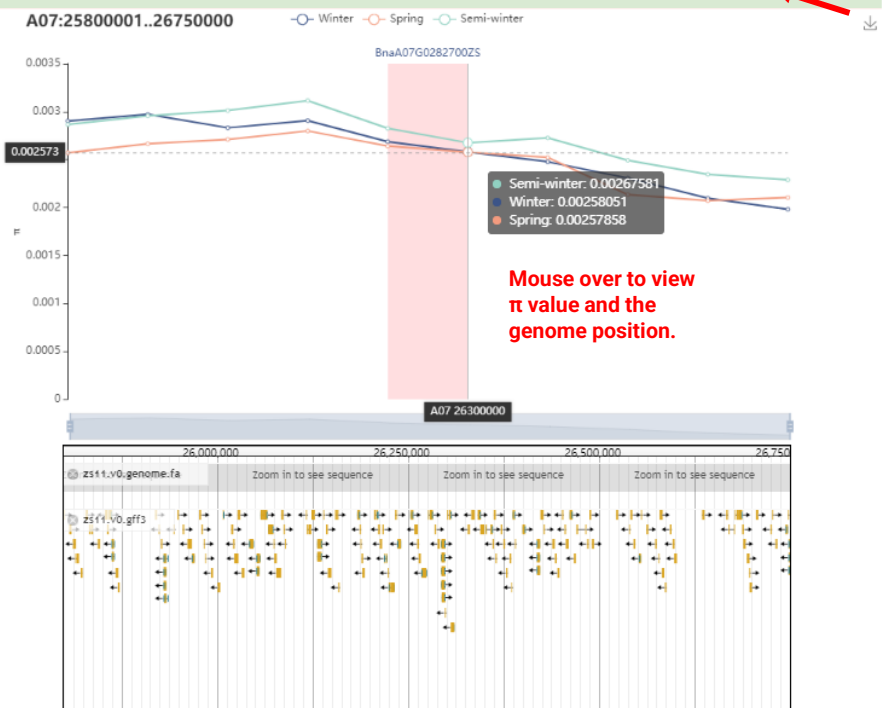
Download button

chr:

start:

end:

submit



4.2-4.3 F_{ST} and K_a/K_s

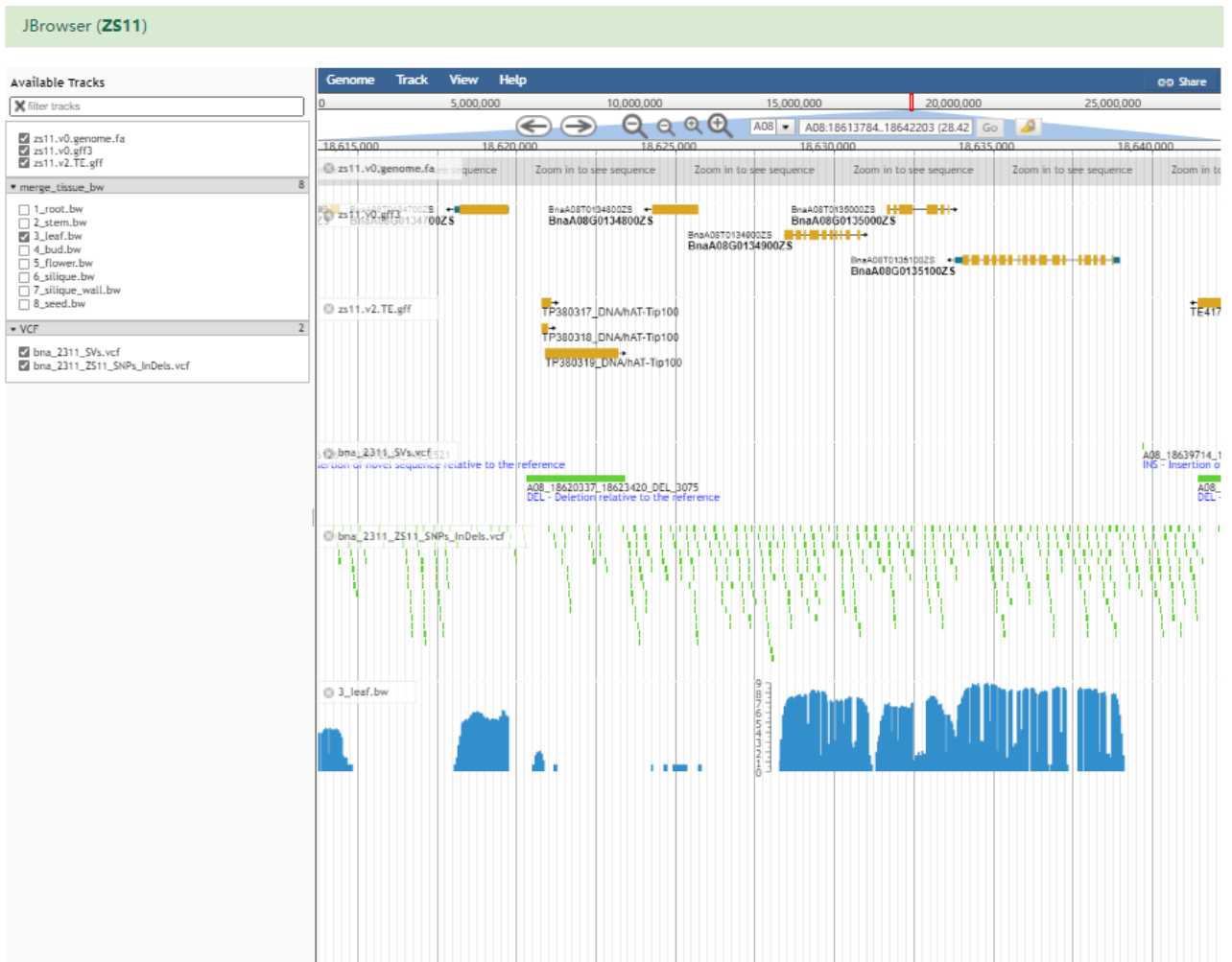
Input and the result pages of F_{ST} and K_a/K_s is similar to that of π .

4.4 About

More information about Evolution module.

5 JBrowse

This module enable users visualize genetic variations, gene features and transcription data in ZS11 and Darmor-*bzh* genome, respectively. There are 13 tracks can be selected to display, including nucleotide sequence, genes, transposable elements (TEs), expression profile data of different tissues and variation (SNPs, InDels and SVs). Description of the files in JBrowse are shown in the following table.



Description of the files in JBrowse are shown in the following table. And the generation of the file are description in About and Methods of website.

Reference	File	Description
ZS11	zs11.v0.genome.fa	DNA sequence of ZS11 genome (Song et al., 2020)
	zs11.v0.gff3	Gene annotation of ZS11 genome (Song et al., 2020)
	zs11.v2.TE.gff	TE annotation of ZS11 genome (Song et al., 2020)
	1_root.bw	mRNA read coverage of root by mapping to ZS11
	2_stem.bw	mRNA read coverage of stem by mapping to ZS11
	3_leaf.bw	mRNA read coverage of leaf by mapping to ZS11
	4_bud.bw	mRNA read coverage of bud by mapping to ZS11
	5_flower.bw	mRNA read coverage of flower by mapping to ZS11
	6_silique.bw	mRNA read coverage of silique by mapping to ZS11
	7_silique_wall.bw	mRNA read coverage of silique wall by mapping to ZS11
	8_seed.bw	mRNA read coverage of seed by mapping to ZS11
		bna_2311_SVs.vcf
	bna_2311_SNPs_InDels.vcf	Information of SNPs and InDels identified in population of 2,311 <i>B. napus</i> accessions ZS11 genome
Darmor- <i>bzh</i> v4	Darmor-bzh.v4.genome.fa	DNA sequence of Darmor- <i>bzh</i> genome (Chalhoub et al., 2014)
	Darmor.v5.gff3	Gene annotation of Darmor- <i>bzh</i> genome (Chalhoub et al., 2014)
	Darmor.TE.gff	TE annotation of Darmor- <i>bzh</i> genome (Chalhoub et al., 2014)
	1_root.bw	mRNA read coverage of root by mapping to Darmor- <i>bzh</i>
	2_stem.bw	mRNA read coverage of stem by mapping to Darmor- <i>bzh</i>
	3_leaf.bw	mRNA read coverage of leaf by mapping to Darmor- <i>bzh</i>
	4_bud.bw	mRNA read coverage of bud by mapping to Darmor- <i>bzh</i>
	5_flower.bw	mRNA read coverage of flower by mapping to Darmor- <i>bzh</i>
	6_silique.bw	mRNA read coverage of silique by mapping to Darmor- <i>bzh</i>
	7_silique_wall.bw	mRNA read coverage of silique wall by mapping to Darmor- <i>bzh</i>
	8_seed.bw	mRNA read coverage of seed by mapping to Darmor- <i>bzh</i>
		bna_2311_SVs.vcf
	bna_2311_SNPs_InDels.vcf	Information of SNPs and InDels identified in population of 2,311 <i>B. napus</i> accessions Darmor- <i>bzh</i> genome

6 Tools

Some useful bioinformatic tools are provided in this module.

6.1 Variation annotation

This page provides a handy way for users to annotate the variation of their own with SnpEff based on ZS11 and Darmor-*bzh* genome.

6.1.1 Input

Users can upload a vcf file of their own. Users can click “vcf Format” to know about the detail of vcf file. An example file is provided for test.

Variation annotation using SnpEff

Genome: ZS11 Darmor

Please submit a file in vcf format, [click here](#) to get an example.

未选择任何文件

6.1.2 Output

The output of vcf file and html file are available for download.

VCF output

[vcf_annotation.vcf](#)

HTML summary

You can [click here](#) to get statistical results.

6.2 Data2geomap

This function allows users to draw a geomap for data of their own.

6.2.1 Input

Users can upload sample data of their own. Example data are provided for test. Map of the world, China and US and two types of geomap, geopic and geoheatmap, can be chosen.

mode Geopic Geoheatmap

map

data

```
id A B C D
Asia 10 10 10 10
Europe 10 10 10 10
Africa 10 10 10 10
North_America 10 10 10 10
South_America 10 10 10 10
Oceania 10 10 10 10
```

example data

6.2.2 Output

Users can download the figure by click the button in the upper right corner.



6.3 LD heatmap

Users can obtain a LD heatmap estimated from variation panel of based on ZS11 and Darmor-*bzh* genome in database for a specific genomic region.

6.3.1 Input

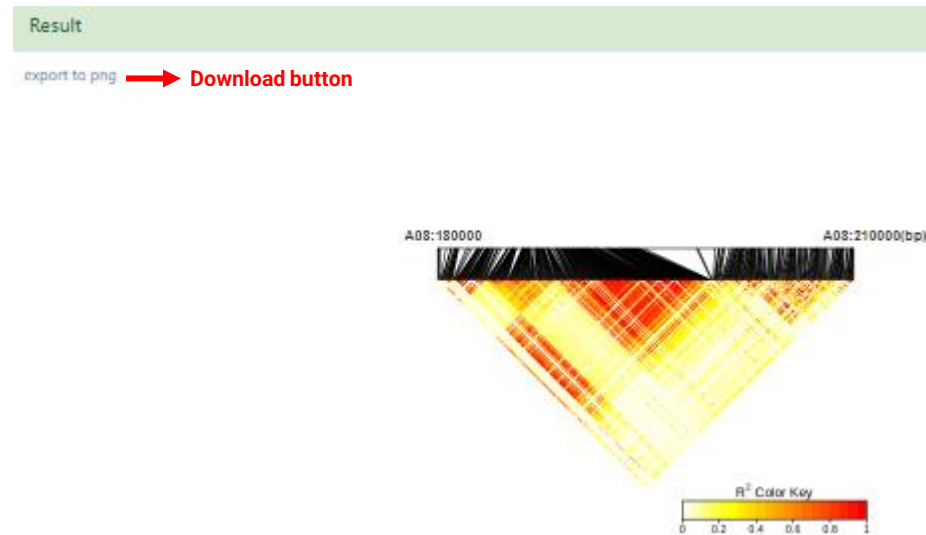
Reference genome should be chosen, and genomic region should be entered.

Genome ZS11 Darmor

Region

6.3.2 Output

Users can download the table by clicking the button in the upper right corner in the result page.



7 Download

Accession information, variation file of ZS11 and Darmor-*bzh*, phenotype data and database tutorial are available for download.

+ Accession information
<ul style="list-style-type: none">• Accession information.xlsx
+ Variation information(Genome: ZS11)
<ul style="list-style-type: none">• bna2311_ZS11_SNP.A01.vcf.gz• bna2311_ZS11_SNP.A02.vcf.gz• bna2311_ZS11_SNP.A03.vcf.gz• bna2311_ZS11_SNP.A04.vcf.gz• bna2311_ZS11_SNP.A05.vcf.gz• bna2311_ZS11_SNP.A06.vcf.gz• bna2311_ZS11_SNP.A07.vcf.gz• bna2311_ZS11_SNP.A08.vcf.gz• bna2311_ZS11_SNP.A09.vcf.gz• bna2311_ZS11_SNP.A10.vcf.gz• bna2311_ZS11_SNP.C01.vcf.gz• bna2311_ZS11_SNP.C02.vcf.gz• bna2311_ZS11_SNP.C03.vcf.gz• bna2311_ZS11_SNP.C04.vcf.gz• bna2311_ZS11_SNP.C05.vcf.gz• bna2311_ZS11_SNP.C06.vcf.gz• bna2311_ZS11_SNP.C07.vcf.gz• bna2311_ZS11_SNP.C08.vcf.gz• bna2311_ZS11_SNP.C09.vcf.gz• bna2311_ZS11_SNP.scaffold.vcf.gz
+ Variation information(Genome: Darmor)
+ Phenotype information
<ul style="list-style-type: none">• Flowering_time_data_from_Wu_2019.xlsx• Flowering_time_data_from_Song_2020.xlsx
+ Transcription information
<ul style="list-style-type: none">• Gene.expression.From.Tang_2021
+ Tutorial
<ul style="list-style-type: none">• Tutorial.pdf

7 Help

Database tutorial, methods of data analysis, pipeline of variation identification and contact are available in Help.