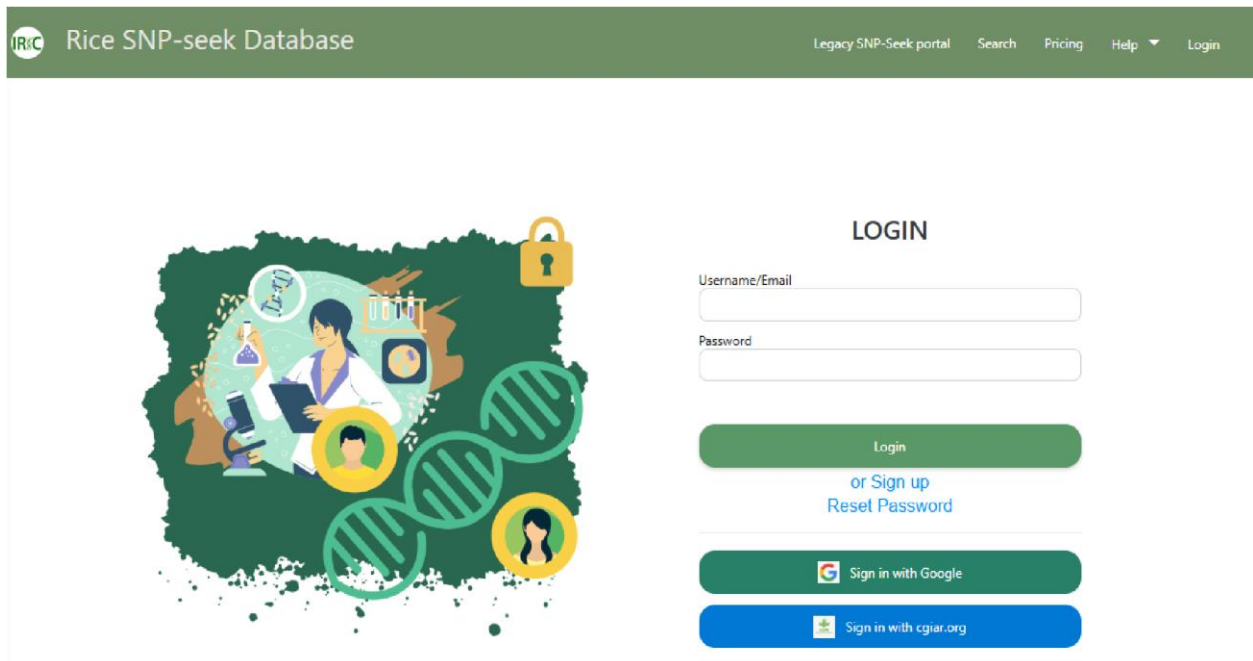


Local Genome Region Analysis using RiceSNPSeek (using v3)

QTL of Interest: [PHS](#)

Publication: Lee JS, Chebotarov D, McNally KL, Pede V, Setiyono TD, Raquid R, Hyun WJ, Jeung JU, Kohli A, Mo Y. *Novel Sources of Pre-Harvest Sprouting Resistance for Japonica Rice Improvement. Plants (Basel).* 2021 Aug 19;10(8):1709. doi: 10.3390/plants10081709. PMID: 34451754; PMCID: PMC8401653.

1.) Go to: <https://snp-seek.irri.org/>



- a. Login using your SNP-seek credentials. There are three ways to do this:
 - i. Username/email and Password
 - ii. Sign in using your Google account
 - iii. Sign in using [cgiar.org](#) (if you are part of this domain)
- b. Sign up if you do not have an account in SNPSeek yet.

2.) Search Genotypes:

Note that our QTL/trait of interest is in this region: **Chr4:4662701-4670717**
You can begin by searching for SNPS that lie within this region using the 3k rice dataset. There are 4 SNP Sets available:

- **3K All**: 32 million full 3K RG SNPs Dataset

This SNP Set contains the full set of 32 million biallelic & multiallelic SNP.

Total SNPs: 32,064,217

Samples : 3024

- **3kbase**: 18 million base SNP

The Base SNP set of ~18 million SNPs was created from the ~29 million biallelic SNPs subset from the 32M full SNP set by removing SNPs with excess of heterozygous calls.

- **3K core**: 404k CoreSNP dataset

The Core SNP set was obtained from the filtered SNP set by applying two-step LD pruning procedure as follows:

- 1.) LD pruning with window size 10kb, step 1 SNP, R2 threshold 0.8
- 2.) LD pruning with window size 50 SNPs, step 1 SNP, R2 threshold 0.8

- **3k filtered**: 4.8million filtered SNP dataset

The filtered SNP set was obtained from the Base SNP set by applying the following filtering criteria:

- 1.) alternative allele frequency at least 0.01
- 2.) proportion of missing calls per SNP at most 0.2

You may use different SNP sets but for this hands-on, we will use the **“3Kbase” SNP set**.

In the Chromosome, put **“Chr4”**, in Start use **“4662701”** and end **“4670717”**.

Click **“Search”** to retrieve the positions within this region within the 3KRG accessions.

Rice SNP-seek Database

Search By Genotype ☐ Include Advance Options

Dataset

Reference

Variety Set

Snip Set

Subpopulation

Variety List

Region

Chromosome

(ac. chr4)

Start End

Gene Locus

SNP List

Locus List

Options

Search Reset

3.) Query result

After querying the genotypes, you will have a table which displays the alleles for each 3KRG variety in a row, for all SNP positions within the specified region or gene. By default, the varieties are sorted by decreasing number of allele mismatches. The resulting table can be filtered using any of the column values, and sorted based on any column value by clicking the column header.

Result Allele Frequency Browse Snip Effect Haplotype

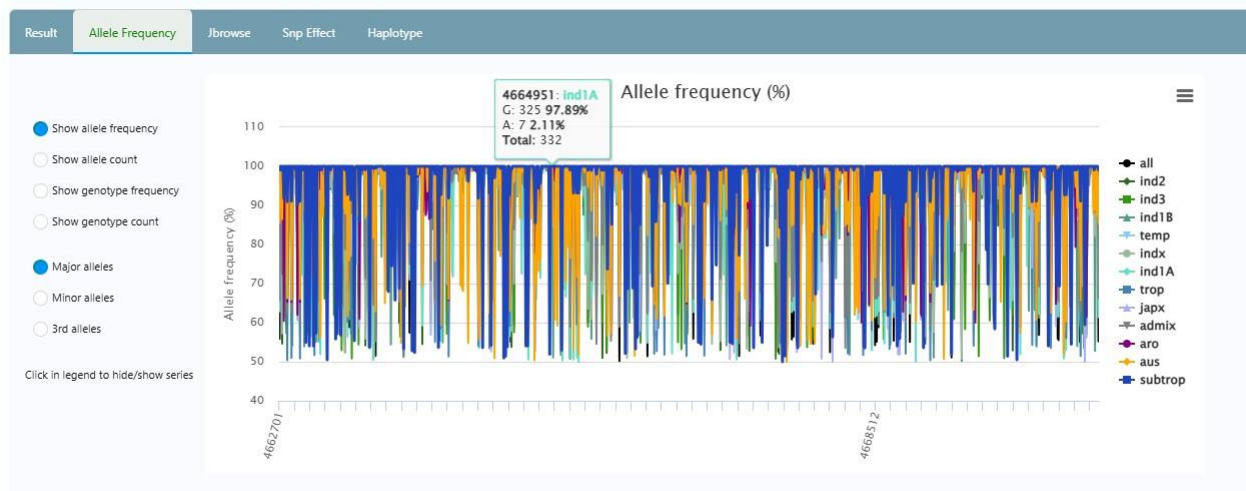
Download Listname Create List Filters Column: Value: Apply Filter Clear

Allele color code: mismatch miss synonymous splice donor SNP splice acceptor SNP gap

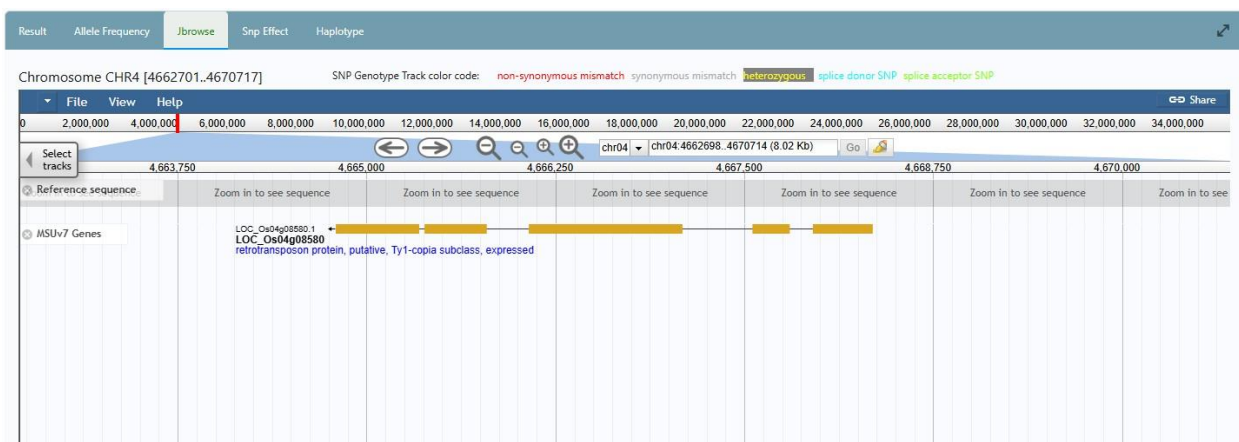
Japonica nipponbare positions	Assay	Accession	Variety 22	Assay	Accession	Subpopulation	Dataset	Mismatch	4662701	4662710	4662712	4662715	4662743	4662767	4662795	4662822	4662864	4662867	4662873	4662892	4662906	4662910	4662917
Japonica nipponbare									G	T	T	C	T	A	G	C	A	T	C	T	G	T	G
NCS 766-IRGC 62478-1	IRIS 313-11645	IRGC 127664	NCS 7 IRIS 3 IRGC	IRIS 313-11645	IRGC 127664	IRIS 313-11645	IRIS 313-11645	120.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
MELABOH-IRGC 66597-1	IRIS 313-8493	IRGC 128537	MELA IRIS 3 IRGC	IRIS 313-8493	IRGC 128537	IRIS 313-8493	IRIS 313-8493	119.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
AUS 177-IRGC 29009-1	IRIS 313-9066	IRGC 125659	AUS 1 IRIS 3 IRGC	IRIS 313-9066	IRGC 125659	IRIS 313-9066	IRIS 313-9066	118.5	A	T	T	G	T	T	G	C	A	T	C	T	G	T	G
ZINVA KOLAMBA-IRGC 52402-1	IRIS 313-11453	IRGC 127916	ZINVA IRIS 3 IRGC	IRIS 313-11453	IRGC 127916	IRIS 313-11453	IRIS 313-11453	118.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
KOLUBA-IRGC 30463-1	IRIS 313-11098	IRGC 134993	KOLU IRIS 3 IRGC	IRIS 313-11098	IRGC 134993	IRIS 313-11098	IRIS 313-11098	118.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
LINANGAN-IRGC 47255-2	IRIS 313-11381	IRGC 132351	LINAN IRIS 3 IRGC	IRIS 313-11381	IRGC 132351	IRIS 313-11381	IRIS 313-11381	118.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
MR19	CG317	IRGC 133992	MR19 CH311 IRGC	CG317	IRGC 133992	MR19 CH311 IRGC	MR19 CH311 IRGC	118.5	A	T	T	G	T	T	G	C	A	T	C	T	G	T	G
DA 7	IRIS 313-8703	IRGC 124432	DA 7 IRIS 3 IRGC	IRIS 313-8703	IRGC 124432	IRIS 313-8703	IRIS 313-8703	117.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
FACAGRO 64-IRGC 82059-1	IRIS 313-10114	IRGC 125739	FACAI IRIS 3 IRGC	IRIS 313-10114	IRGC 125739	IRIS 313-10114	IRIS 313-10114	117.0	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
NACHIN ER 12-IRGC 14146-1	IRIS 313-8407	IRGC 127306	NACH IRIS 3 IRGC	IRIS 313-8407	IRGC 127306	IRIS 313-8407	IRIS 313-8407	117.0	A	T	T	G	T	T	G	C	A	T	C	T	G	T	G
DAW NOK KAEN-IRGC 65548-1	IRIS 313-11700	IRGC 127306	DAW IRIS 3 IRGC	IRIS 313-11700	IRGC 127306	IRIS 313-11700	IRIS 313-11700	117.0	A	T	T	G	T	T	G	C	A	T	C	T	G	T	G
NS 199-IRGC 68864-1	IRIS 313-11761	IRGC 127683	NS 19 IRIS 3 IRGC	IRIS 313-11761	IRGC 127683	IRIS 313-11761	IRIS 313-11761	117.0	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
KHAO HAE-IRGC 29773-3	IRIS 313-11085	IRGC 132273	KR 60 IRIS 3 IRGC	IRIS 313-11085	IRGC 132273	IRIS 313-11085	IRIS 313-11085	116.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
CR 60-10-IRGC 15777-1	IRIS 313-9023	IRGC 125715	DAW IRIS 3 IRGC	IRIS 313-9023	IRGC 125715	IRIS 313-9023	IRIS 313-9023	116.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G
DAW NOK KAEN-IRGC 65548-1	IRIS 313-11700	IRGC 127306	ARC 1 IRIS 3 IRGC	IRIS 313-11700	IRGC 127306	IRIS 313-11700	IRIS 313-11700	116.5	A	T	T	G	T	T	G	C	G	T	C	T	G	T	G

2014 International Rice Research Institute, Los Banos, Laguna, Philippines. This site is under development. We schedule maintenance every Monday, 8:00 GMT (4:00 PM Manila) VERSION: 8.13.4

It will also report a graph of the allele frequencies where you can inspect the major and minor alleles per subpopulation for all SNP positions from the query.



In another panel, you can also view the region in a genome browser.



4.) SNP Effects

<https://pcingola.github.io/SnpEff/snpEff/inputoutput/#eff-field-vcf-output-files>

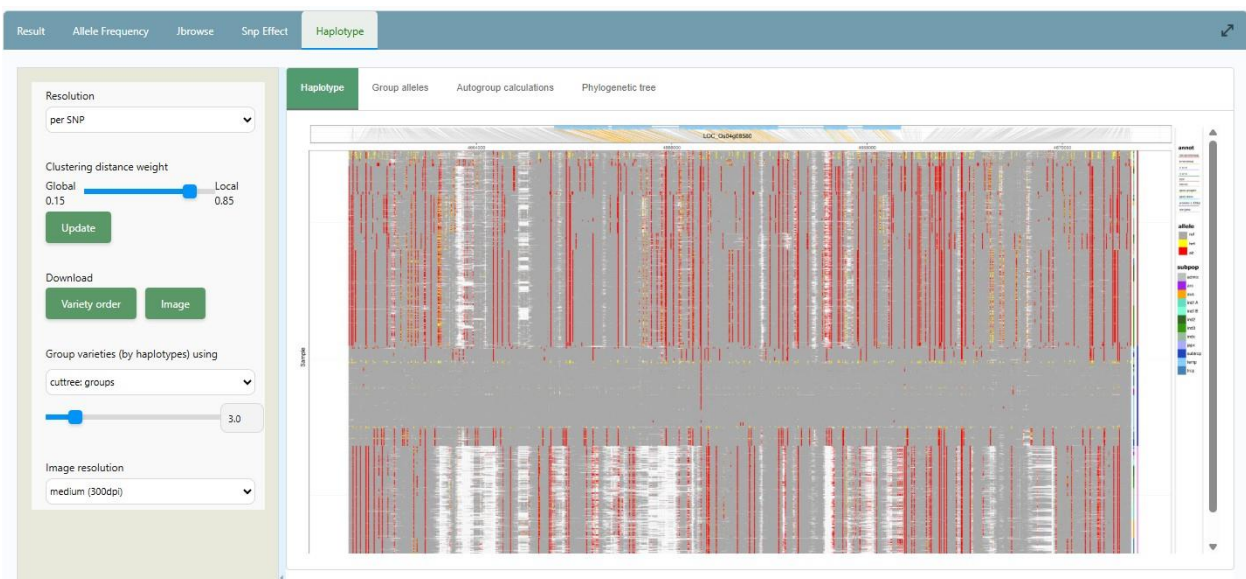
The Genotype query also returns a table containing the SNP effects detected on MSU gene models. This is calculated using the SnpEff program.

Result	Allele Frequency	Jbrowse	Snp Effect	Haplotype					
					Snp Effect				
Download									
POSITION	"DELETERIOUSNESS"	Alt (ANN)	Effect (ANN)	Putative_impact (ANN)	Gene Name (ANN)	Gene ID (ANN)	Feature type (ANN)	Feature ID (ANN)	Transcript B
chr04-4662701 30		A A	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662730 30		A A	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662732 30		G G	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662735 30		G G	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662743 30		G G	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662767 30		T T	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662795 30		C C	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662822 30		G G	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
chr04-4662864 30		G G	downstream_gene MODIFIER intergenic_region MODIFIER		LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	LOC_Os04g08580 LOC_Os04g08570- LOC_Os04g08580	transcript intergenic_region	LOC_Os04g08580.1 LOC_Os04g08570- LOC_Os04g08580	Coding -
2014 International Rice Research Institute, Los Banos, Laguna, Philippines. This site is under development. We schedule maintenance every Monday, 8-900 GMT (4-5PM Manila) VERSION: 8.13.4									

2014 International Rice Research Institute, Los Banos, Laguna, Philippines. This site is under development. We schedule maintenance every Monday, 8-900 GMT (4-5PM Manila) VERSION: 8.13.4

5.) Haplotype View

Another view for the result of the genotype query is the Haplotype View. This allows us to know whether our haplotypes make sense.



You should also see major grouping of alleles which contributes to the haplotype.

In this hands-on, you should see **3 major haplotype groups**.

Group major alleles

Download group alleles

[illegible]

6.) Downloading the results table

FILE FORMATS:

- **MAP** <https://zzz.bwh.harvard.edu/plink/data.shtml#map>
- **PED** <https://zzz.bwh.harvard.edu/plink/data.shtml#ped>

- Download the table in “Plink” format by clicking on the “Plink” button.
- This will give you two files in a zipped folder: a ped and map file that by now you should be familiar with.
- The first few lines of your downloaded .map file should look like this:

chr04	10404662701	0	4662701
chr04	10404662730	0	4662730
chr04	10404662732	0	4662732
chr04	10404662735	0	4662735
chr04	10404662743	0	4662743
chr04	10404662767	0	4662767
chr04	10404662795	0	4662795
chr04	10404662822	0	4662822
chr04	10404662864	0	4662864
chr04	10404662867	0	4662867
chr04	10404662873	0	4662873
chr04	10404662892	0	4662892
chr04	10404662906	0	4662906
chr04	10404662920	0	4662920
chr04	10404662927	0	4662927
chr04	10404662930	0	4662930

Likewise, the first few lines of your .ped file should be like this:

IRIS_313-11645	IRIS_313-11645	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-8493	IRIS_313-8493	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-9066	IRIS_313-9066	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11453	IRIS_313-11453	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11098	IRIS_313-11098	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11381	IRIS_313-11381	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
CX317	CX317	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-8703	IRIS_313-8703	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-10114	IRIS_313-10114	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-8407	IRIS_313-8407	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11700	IRIS_313-11700	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11761	IRIS_313-11761	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11085	IRIS_313-11085	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-9023	IRIS_313-9023	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11705	IRIS_313-11705	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-10863	IRIS_313-10863	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
B264	B264	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-10177	IRIS_313-10177	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11677	IRIS_313-11677	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11683	IRIS_313-11683	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11709	IRIS_313-11709	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11762	IRIS_313-11762	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11789	IRIS_313-11789	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-12259	IRIS_313-12259	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-11273	IRIS_313-11273	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
CX306	CX306	0	0	0	-9	A	A	T	T	T	T	C	C	T	T	T	T	G	G	C
IRIS_313-8356	IRIS_313-8356	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-10337	IRIS_313-10337	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-9160	IRIS_313-9160	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C
IRIS_313-10332	IRIS_313-10332	0	0	0	-9	A	A	T	T	T	T	G	G	T	T	T	T	G	G	C

7.) Creating a SNP list

From the map file, remove the middle columns such that only the 1st column and the last columns remain (chr, position).

Go to “My lists”. Select “SNP” in List Type. Click on “Create” to make a new list.

Paste the chr-position table from the map file.

You may tick the box on “Verify if SNP is in Variant set”. However, in this hands-on, we will not do that since we know that these SNPs already came as a result of the genotype query.

Add SNP List

List name:
PHS-CHR4

Set chromosome and SNP positions here

☐ Verify if SNP is inVariant set
☐ 3k-MH63v15
☐ 3kall
☐ 3kbase
☐ 3kcore

☒ Autoconfirm (forced for >50 positions)

☐ SNPs have allele column (for allele filtering)

☐ SNPs have -log(p) column (from GWAS analysis)

Format: chromosome position

chr04 4670576
chr04 4670599
chr04 4670605
chr04 4670609
chr04 4670611
chr04 4670612
chr04 4670614
chr04 4670617
chr04 4670618
chr04 4670622
chr04 4670623
chr04 4670630
chr04 4670641
chr04 4670653
chr04 4670655
chr04 4670656
chr04 4670662
chr04 4670663
chr04 4670668
chr04 4670672
chr04 4670673
chr04 4670684
chr04 4670685
chr04 4670698
chr04 4670717

Save Cancel

You will be able to see this new list on the left side of the panel.

My List

NOTE: Lists are not saved in the server and available only for this session. Click Download button to save your created lists for future reference. Click Upload button to recreate your list from previously downloaded MyList file.

List Type

List Type:
☐ Variety
☒ SNP
☐ Locus

SNP List

Select List

ANY:IKRICA3

ANY:AG2-SNPList

ANY:PHS-CHR4

Set Operations: (enabled on multiple list selection, press Ctrl+click to select multiple items)

Create

Delete

Download / Upload

Download

Upload

Open Query

965 items in list

(GENOME, CONTIG, POSITION)
(chr04,4662701)
(chr04,4662730)
(chr04,4662732)
(chr04,4662735)
(chr04,4662743)
(chr04,4662767)
(chr04,4662795)
(chr04,4662822)
(chr04,4662864)
(chr04,4662867)
(chr04,4662873)
(chr04,4662892)
(chr04,4662906)

<<

<

1

/ 20

>

>>

8.) Annotate SNP List

Next thing we want to do is to look for candidate genes within the QTL region in Nipponbare, go to “Search”-> “Gene Loci”.

Set “Japonica nipponbare” as reference genome.

Set “SNP Annotator (My SNP List)” in Search.

Set “All” to search all Gene models available.

Tick the box to “Include gene interactions (RiceNetv2, PRIN)” and “Gene Ontology” annotations. You may choose to add more to gather more annotations for this region.

Rice SNP-seek Database

Search By Gene Loci

Search

Reference Genome
Japonica nipponbare

Search By
SNP Annotator (My SNP List)

Gene Model
Maximum interacting loci

My SNP List

My SNP List ANY:PHS-CHR4

+/- 0 basepairs

☒ Include gene interactions (RiceNetv2, PRIN) (slow)

☐ FGenesh++, PlantPromDB

☒ Gene Ontology

☐ PO, TO, Q-TARO

☐ Q-TARO QTLs

The result should be a table which contains the annotations that can be grouped by marker position, gene locus, or by QTL.

Search by SNP List positions: Contig ANY, SNP List ANY:PHS-CHR4 RESULT:964 markers

Search By Gene Name/Symbol/Function Result

Download: CSV Tab Create Gene List: List Name

Group by: Marker/Position ☐ Gene locus ☐ QTL ☒ Include: ☒ gene model ☒ in promoter ☒ ricenet interaction ☒ prin interaction

CONTIG.POS.-LOGP	-LOGP	GENE MODELS	GO BIOLOGICAL PROCESS	GO CELLULAR COMPONENT	GO MOLECULAR FUNCTION
(chr04.4662730)		LOC_Os04g08580 chr04 [4664791	LOC_Os04g08580 chr04[4664796-	LOC_Os04g08580 chr04[4664796-4668349]	LOC_Os04g08580 chr04[4664796-4668349] -
(chr04.4662732)		4668349] -	4668349] -		GO:0003676 nucleic acid binding ()
(chr04.4662735)		retrotransposon protein, putative	GO:0015074 DNA integration ()		LOC_Os04g08580 chr04[4664796-4668349] - GO:0003677 D
(chr04.4662743)		copla subclass, expressed			
(chr04.4662767)					
(chr04.4662795)					
(chr04.4662822)					
(chr04.4662864)					
(chr04.4662867)					
(chr04.4662873)					

9.) Saving the Gene List

Set the List name as “PHS-genelist” and “click Create Gene List”.

Search by SNP List positions: Contig ANY, SNP List ANY:PHS-CHR4 RESULT:964 markers

Search By Gene Name/Symbol/Function Result

Download: List Name:

Group by: ☐ Marker/Position ☐ Gene locus ☐ QTL ☒ Include: ☒ gene model ☒ in promoter ☒ ricenet interaction ☒ prin interaction

CONTIG_POS_LOGP	-LOGP	GENE MODELS	GO BIOLOGICAL PROCESS	GO CELLULAR COMPONENT	GO MOLECULAR FUNCTION
{chr04.4662730} {chr04.4662732} {chr04.4662735} {chr04.4662743} {chr04.4662767} {chr04.4662795} {chr04.4662822}		LOC_Os04g08580 chr04 [4664791-4668349] - retrotransposon protein, putative copia subclass, expressed	LOC_Os04g08580 chr04[4664796-4668349] - GO:0015074 DNA integration ()		LOC_Os04g08580 chr04[4664796-4668349] - GO:0003676 nucleic acid binding () LOC_Os04g08580 chr04[4664796-4668349] - GO:0003677 D

Go to “My Lists” and you should see the gene locus/loci when you search under “Locus”.

Rice SNP-seek Database

My List

NOTE: Lists are not saved in the server and available only for this session.
Click Download button to save your created lists for future reference.
Click Upload button to recreate your list from previously downloaded MyList file.

List Type ▼

List Type: ☐ Variety ☐ SNP ☒ Locus

Locus List ▼

Select List

- bacterial-blight-genes
- BLB-related
- BLB-related-region
- PHS-gene
- PHS-genelist**
- PHS-genes

Set Operations: (enabled on multiple list selection, press Ctrl+click to select multiple items)

Download / Upload ▼

Open Query

1 items in list

NAME	CONTIG	START	STOP	STRAND	DESCRIPTION
LOC_OS04G08580	chr04	4664797	4668349	-1	

10.) Get Gene set/network

Using the gene list we generated, we will now do a gene enrichment analysis to know if there are other genes previously reported that are associated with our QTL of interest.

To do this, go to “Search”-> “Gene Loci.

Set as Reference genome: “Japonica Nipponbare”.

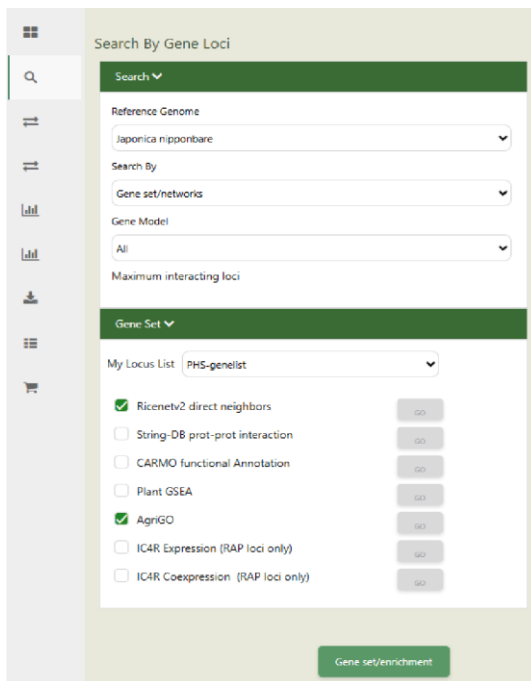
Set Search to: “Gene set/networks”.

Set Gene Models to: “All”.

Set the My Locus List to: “PHS-genegenes”.

Tick “Ricenetv2 direct neighbors” and “AgriGO”.

Click on “Gene set/enrichment”.



Unfortunately, this query will not return any result. Click the “Go” button beside the Ricenet option and it will give us this message:

“No ROC analysis, because the valid query set size < 4.”

In this case, our query size is very small. You can explore nearby regions and see if there are existing gene networks reported by increasing the upper and lower bound positions.

To know more about SNPSeek, visit the site: <https://snpseek.irri.org/>.