

VIEWpoly

A Visualization Tool to Integrate and Explore Results of Polyploid Genetic Analysis

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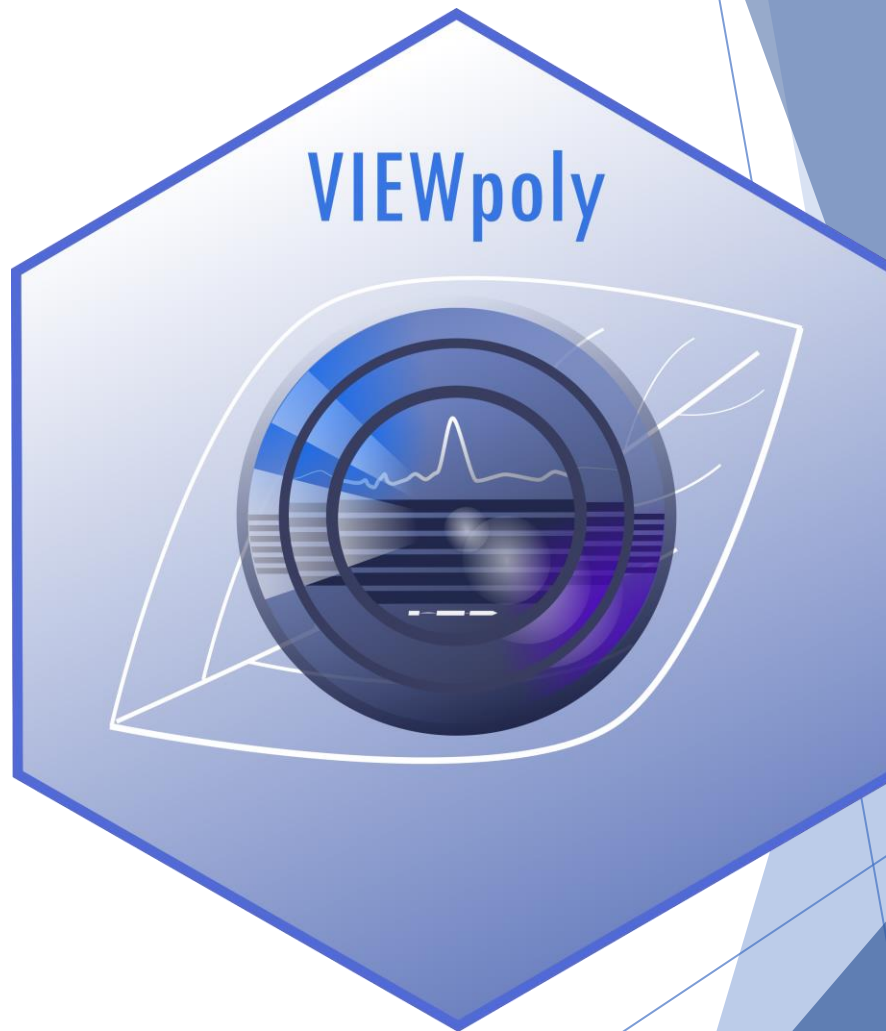
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Oscar Riera-Lizarazu

Marcelo Mollinari



Tools for Polyploids Project

- ▶ Tools for Genomics-Assisted Breeding in Polyploids: Development of a Community Resource
- ▶ <https://www.polypldids.org/>
- ▶ Twitter:
 - ▶ @polypldtools
- ▶ Computational support:
 - ▶ Slack channel
- ▶ Workshops - this year:
 - ▶ January 13th and 14th

The screenshot shows the homepage of the Tools for Polyploids website. The header includes a navigation menu with links for Home, About, Team, Tools, News, Workshops, Outreach, Mailing Lists, Contact Us, and Log in. A prominent announcement banner states: "ANNOUNCEMENT - The 2022 Tools for Polyploids Training Workshop has been moved to a fully virtual format. We will no longer be meeting in person. You can still register to attend virtually using the link below. Any questions can be sent to toolstorpolypldids@tamu.edu." Below this, a section titled "Tools for Polyploids Workshop" features four buttons: "2022 Workshop Agenda", "2022 Workshop Forms", "Registration for 2022 Virtual Training Workshop", and "2022 Digital Poster Session". A "News" section on the right lists three project spotlights: Dr. Chris Maliepaard, Dr. Oscar Riera-Lizarazu, and Dr. Jeffrey Endelman. On the far right, there is a "User login" form with fields for Username and Password, a "Log in" button, and links for "Create new account" and "Reset your password". Below the login form, a "Tweets" section displays a tweet from @polypldtools announcing the move to a virtual format, dated Jan 5, 2022. The footer contains support information: "Supported by a partnership of NIFA USDA SCRI Award # 2020-51181-32156 to PD Byrne (Texas A&M), USDA-ARS, Industry and US Land Grant Universities. Copyright © 2021 This site is designed to work with IE, Chrome, Firefox, Safari and Opera. Hosted at Washington State University by Mainlab Bioinformatics."

Project Members



Tools for Polyploids Project














































- ▶ Autopolyploids
- ▶ Dosage calling
- ▶ Linkage mapping
- ▶ QTL analysis
- ▶ GWAS

<https://polyploids.r-universe.dev/>

The 'polyploids' universe

```
# Enable universe(s) by polyploids
options(repos = c(
  polyploids = 'https://polyploids.r-universe.dev',
  CRAN = 'https://cloud.r-project.org'))

# Install some packages
install.packages('mappoly')
```

Commit	Package	Version	Maintainer	Src	Build	R-4.1	R-4.0	System Dependencies
2022-01-07	mmollina/mappoly 	0.3.0	Marcelo Mollinari		2022-01-07			libstdc++6 (10.3.0)
2022-01-06	jendelman/diaQTL	1.01	Jeffrey Endelman		2022-01-06			
2022-01-03	mmollina/viewpoly 	0.1.1	Cristiane Taniguti		2022-01-03			
2021-12-29	lvclark/polyRAD 	1.6	Lindsay V. Clark		2021-12-29			libstdc++6 (10.3.0)
2021-12-16	gabrielgesteira/qtIpoly 	0.2.2	Gabriel de Siqueira Gesteira		2021-12-16			liblapack3 (3.9.0) libblas3 (3.9.0) libstdc++6 (10.3.0) libgomp1 (10.3.0)
2021-12-09	cran/polyqtlR 	0.0.7	Peter Bourke		2022-01-07			libstdc++6 (10.3.0)
2021-10-25	dcgerard/updog 	2.1.1	David Gerard		2021-12-23			liblapack3 (3.9.0) libblas3 (3.9.0) libstdc++6 (10.3.0) libgomp1 (10.3.0)
2021-09-17	jendelman/GWASpoly	2.09	Jeffrey Endelman		2021-12-15			
2021-07-30	jendelman/polyBreedR	0.25	Jeffrey Endelman		2021-12-26			
2021-06-17	cran/PolyHaplotyper 	1.0.1	Roeland E. Voorrips		2021-12-13			
2021-03-09	cran/polymapR 	1.1.2	Peter Bourke		2022-01-02			
2018-03-16	cran/fitPoly 	3.0.0	Roeland E. Voorrips		2021-12-24			

Users' challenges

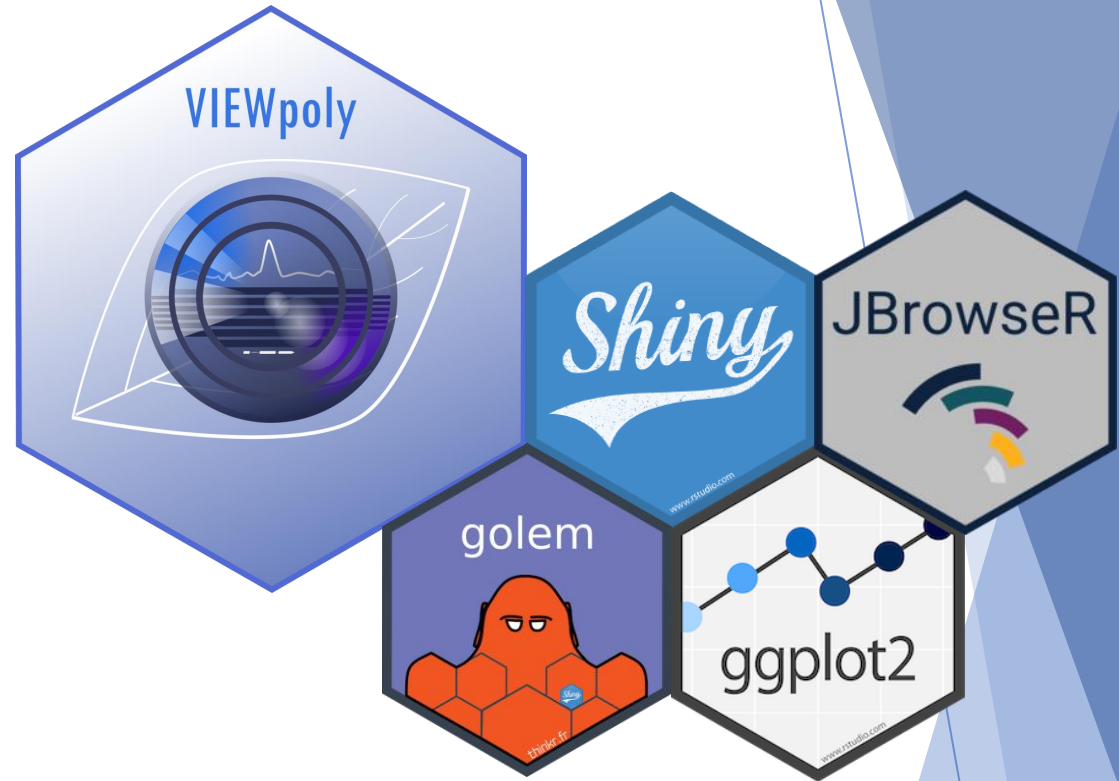
- ▶ Many combinations:

Linkage Map Software x QTL Software x Traits x
Linkage Groups x QTL x Genomic Information

- ▶ Different file formats
- ▶ Programming language
- ▶ Unclear differences and similarities between software

VIEWpoly

- ▶ Interactive exploration
- ▶ Easy access to all combinations
- ▶ Standardized formats
- ▶ Collaborative results interpretation
- ▶ Free access data publications
- ▶ Highlight upstream software features



Implementation

- ▶ R package:

<https://cran.r-project.org/package=viewpoly>

- ▶ Development:

<https://github.com/mmollina/viewpoly>

- ▶ Deploy locally or through server

```
> install.packages("viewpoly")  
> viewpoly::run_app()
```

development active License GPL v3 CRAN 0.1.1 r-universe 0.1.1 downloads 265/month

VIEWpoly

VIEWpoly is a shiny app and R package for visualizing and exploring results from [polyploid computational tools](#) using an interactive graphical user interface. The package allows users to directly upload output files from [polymapR](#), [MAPpoly](#), [polyqtlR](#), [QTLpoly](#), [diaQTL](#) and genomic assembly, variants, annotation and alignment files. VIEWpoly uses [shiny](#), [golem](#), [ggplot2](#), [plotly](#), and [JBrowseR](#) libraries to graphically display the QTL profiles, positions, alleles estimated effects, progeny individuals containing specific haplotypes and their breeding values. It is also possible to access marker dosage and parental phase from the linkage map. If genomic information is available, the corresponding QTL positions are interactively explored using [JBrowseR](#) interface, allowing the search for candidate genes. It also provides features to download specific information into comprehensive tables and images for further analysis and presentation.



Quick Start

You can run VIEWpoly locally installing the package and accessing the graphical interface through a web browser. To use the stable version, please install the package from CRAN:

```
install.packages("viewpoly")  
viewpoly::run_app()
```

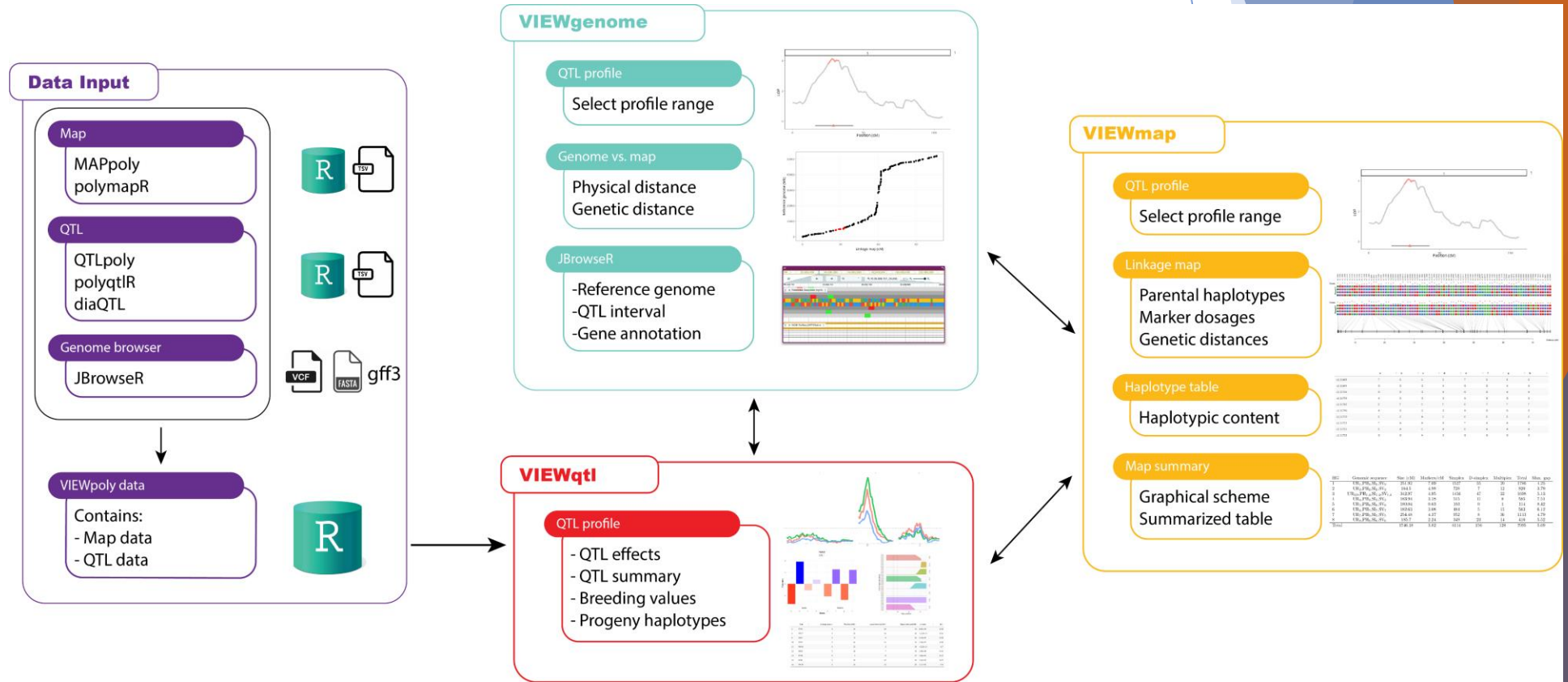
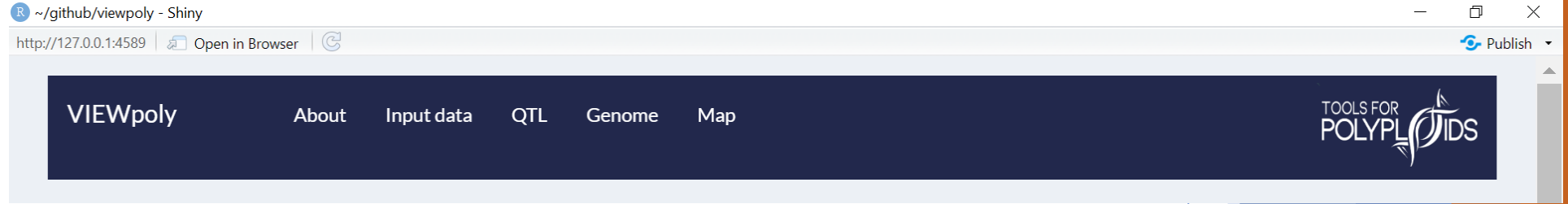
If you want to use the latest development version, go ahead and install VIEWpoly from our Github repository:

```
# install.packages("devtools")  
devtools::install_github("mmollina/viewpoly")  
viewpoly::run_app()
```

Languages

● R 100.0%

Modules



Input data



The screenshot shows the 'Input data' page of the VIEWpoly web application. The navigation bar at the top includes 'VIEWpoly', 'About', 'Input data' (highlighted with a red box), 'QTL', 'Genome', and 'Map'. The 'TOOLS FOR POLYPLAIDS' logo is in the top right corner. The main heading is 'Input data', with 'Exit' and 'Next' buttons to its right. Below the heading is the instruction: 'Use this module to select an example dataset or to upload yours.' A list of six options is provided, each with a plus sign icon on the right:

- Available example datasets
- Upload linkage map files
- Upload QTL analysis files
- Upload Genome Browser files
- Download VIEWpoly dataset
- Upload VIEWpoly dataset

Input data

- ▶ Example subset:
 - ▶ Tetraploid potato

VIEWpoly About Input data QTL Genome Map TOOLS FOR POLYPLAIDS

Input data

Use this module to select an example dataset or to upload yours.

Exit Next

Available example datasets

They contain the entire linkage map and QTL analysis but just a subset of individuals.

- ▶ Potato - Atlantic x B1829-5

Access complete example datasets [here](#)

- ▶ Complete datasets evaluated with all software:
 - ▶ Tetraploid potato
 - ▶ Hexaploid sweetpotato

<u>Name</u>	<u>Last modified</u>	<u>Size</u>	<u>Description</u>
Parent Directory		-	
MAPpoly/	2021-12-15 01:37	-	
QTLpoly/	2021-12-15 01:37	-	
diaQTL/	2021-12-15 01:37	-	
genome-browser/	2021-12-15 01:37	-	
polyqtlR/	2021-12-15 01:37	-	

Apache/2.4.41 (Ubuntu) Server at wenjuanwei_pc-zbz.statgen.ncsu.edu Port 80

Input data

- ▶ Choose software or standard format

The screenshot shows a web interface with two main sections. The top section, titled "Available example datasets", has a blue header and contains the text "They contain the entire linkage map and QTL analysis but just a subset of individuals." Below this, there is a radio button selected next to "Potato - Atlantic x B1829-5". At the bottom of this section is a link: "Access complete example datasets [here](#)". The bottom section, titled "Upload linkage map files", also has a blue header and a "reset" button in the top right corner. It contains three upload options, each with a blue arrow pointing right and a plus sign: "Upload MAPpoly output", "Upload polymapR output", and "Upload linkage map files with standard format (.csv, .tsv or .tsv.gz)".

Available example datasets


They contain the entire linkage map and QTL analysis but just a subset of individuals.


Potato - Atlantic x B1829-5


Access complete example datasets [here](#)

Upload linkage map files

[reset](#)

Upload MAPpoly output  +

Upload polymapR output  +

Upload linkage map files with standard format (.csv, .tsv or .tsv.gz)  +

Input data

1. Check instructions
2. Upload file
3. Submit

Upload linkage map files

[here](#)

[here](#)

Object of class `mappoly.map`.
File: my_mappoly_list.RData

No file selected

Upload polymapR output +

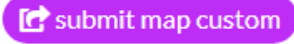
Upload linkage map files with standard format (.csv, .tsv or .tsv.gz) +

Input data

1. Download example file
2. Upload file
3. Submit



Upload linkage map files with standard format (.csv, .tsv or .tsv.gz)

3 

File: dosages.tsv

Browse... No file selected

File: genetic_map.tsv

Browse... No file selected

File: phases.tsv

Browse... No file selected

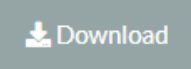
Upload here an RDS file with table with three columns: 1) marker ID; 2) genome position; 3) chromosome

File: marker information

Browse... No file selected

Check the input file formats with the example files:

dosages.tsv genetic_map.tsv phases.tsv



Input data

Upload QTL analysis files

[reset](#)

Upload QTLpoly output

Upload diaQTL output

Upload polyqtIR output

Upload QTL analysis results with standard format (.csv, .tsv or .tsv.gz)

Upload QTLpoly output

[submit QTLpoly](#)

[Access further information about how to perform QTL analysis with QTLpoly here](#)

[Access a example code of how to obtain these inputs using QTLpoly functions here](#)

File: QTLpoly_data.RData
Object of class: qtlpoly.data
 No file selected

File: QTLpoly_remim.mod.RData
Object of class: qtlpoly.remim
 No file selected

File: QTLpoly_est.effects.RData
Object of class: qtlpoly.effects
 No file selected

File: QTLpoly_fitted.mod.RData
Object of class: qtlpoly.fitted
 No file selected

Input data

▶ JBrowseR inputs:

- ▶ FASTA
- ▶ GFF
- ▶ VCF
- ▶ BAM/CRAM
- ▶ bigWig

▶ Indexes

Upload Genome Browser files

JBrowseR tutorial

Access further information about the files expected in this section [here](#)

Upload genome information reset

Warning! The uploaded .fasta, .gff3, .vcf, .bam, .cram, .wig genome version must be the same one used to build the genetic map submit

Upload .fasta/.fasta.gz and .fasta.fai/.fasta.gz.fai,.fasta.gz.gzi file with assembly information. Using this option, a local HTTP server will be generated.

Files: genome_v2.fasta.gz, genome_v2.fasta.gz.fai, genome_v2.fasta.gz.gzi

Browse... No file selected

or

Add the URL of the hosted FASTA file location. The loading procedure is more efficient using this option.

<https://jbrowse.org/genomes/sars-cov2/fasta/sars-cov2.fa.gz>

Upload .gff3/.gff3.gz and .gff3.tbi/.gff3.gz.tbi file with annotation information

Files: genome_v2.gff3.gz, genome_v2.gff3.gz.tbi

Browse... No file selected

Input data

- ▶ VIEWpoly dataset:
 - ▶ Linkage map
 - ▶ QTL analysis
- ▶ Easy storage
- ▶ Easy access

Download VIEWpoly dataset

The uploaded data are converted to the viewpoly format. It keeps the map and the QTL information. Genome information is not stored.

Define the dataset name. Do not use spaces between words.

[Download](#)

Upload VIEWpoly dataset

Check one of the available datasets:

There is no viewpoly object in your R environment. Load viewpoly object or convert formats below

[reset](#)

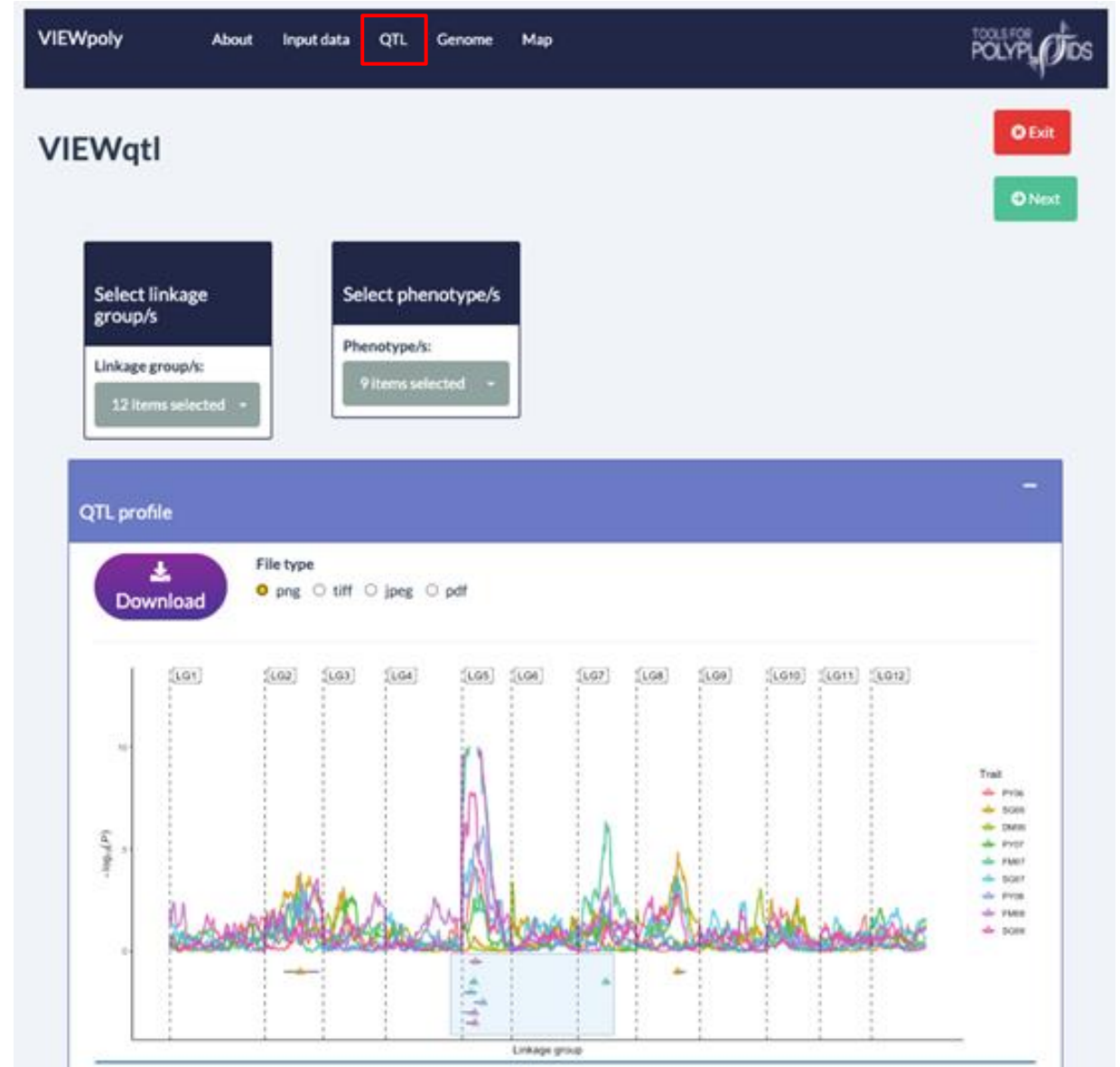
[submit VIEWpoly file](#)

Upload VIEWpoly RData file here:

File: dataset_name.RData

VIEWqtl

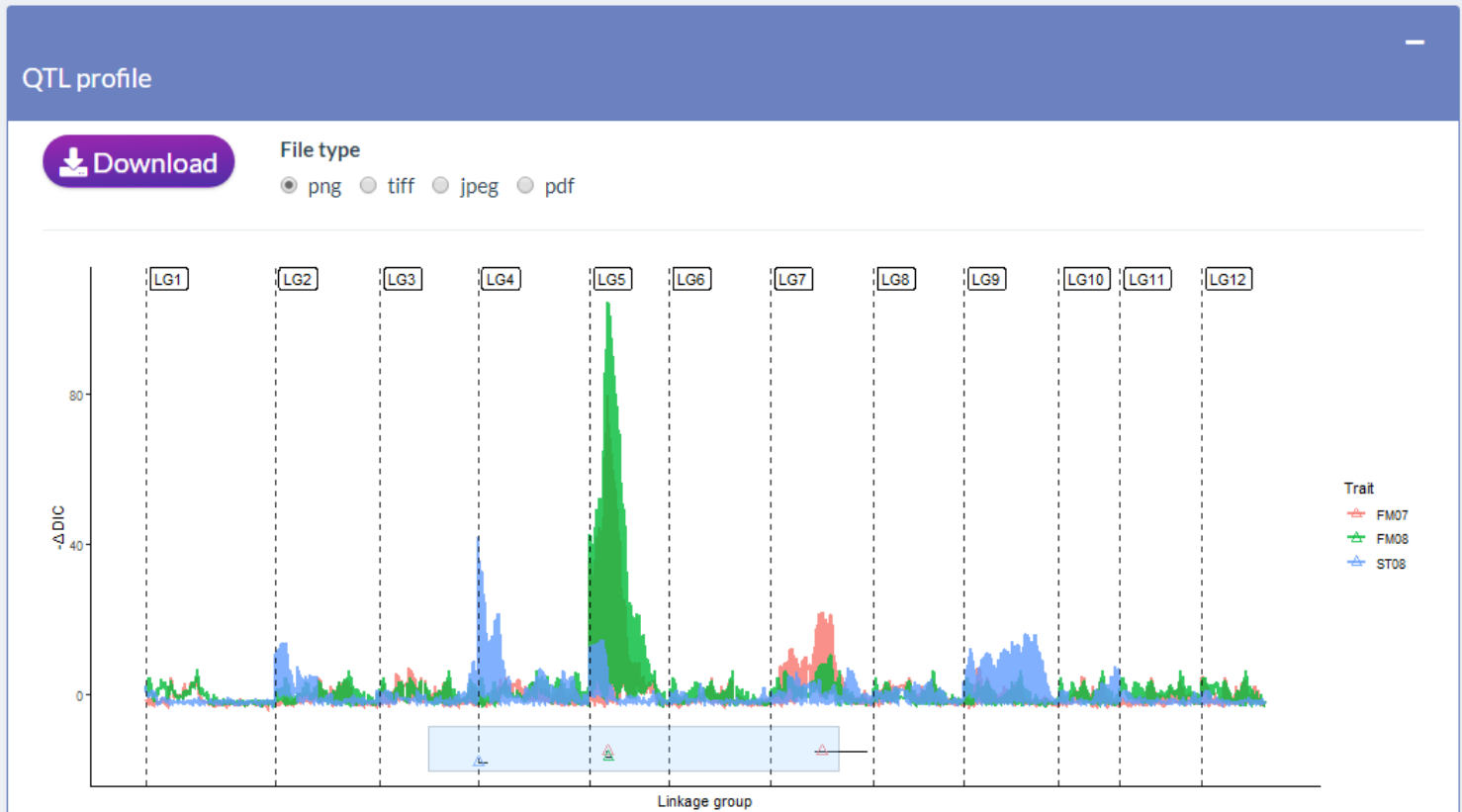
- ▶ Select linkage groups
- ▶ Select phenotypes
- ▶ Profile curve
- ▶ Select QTL



VIEWqtl

diaQTL

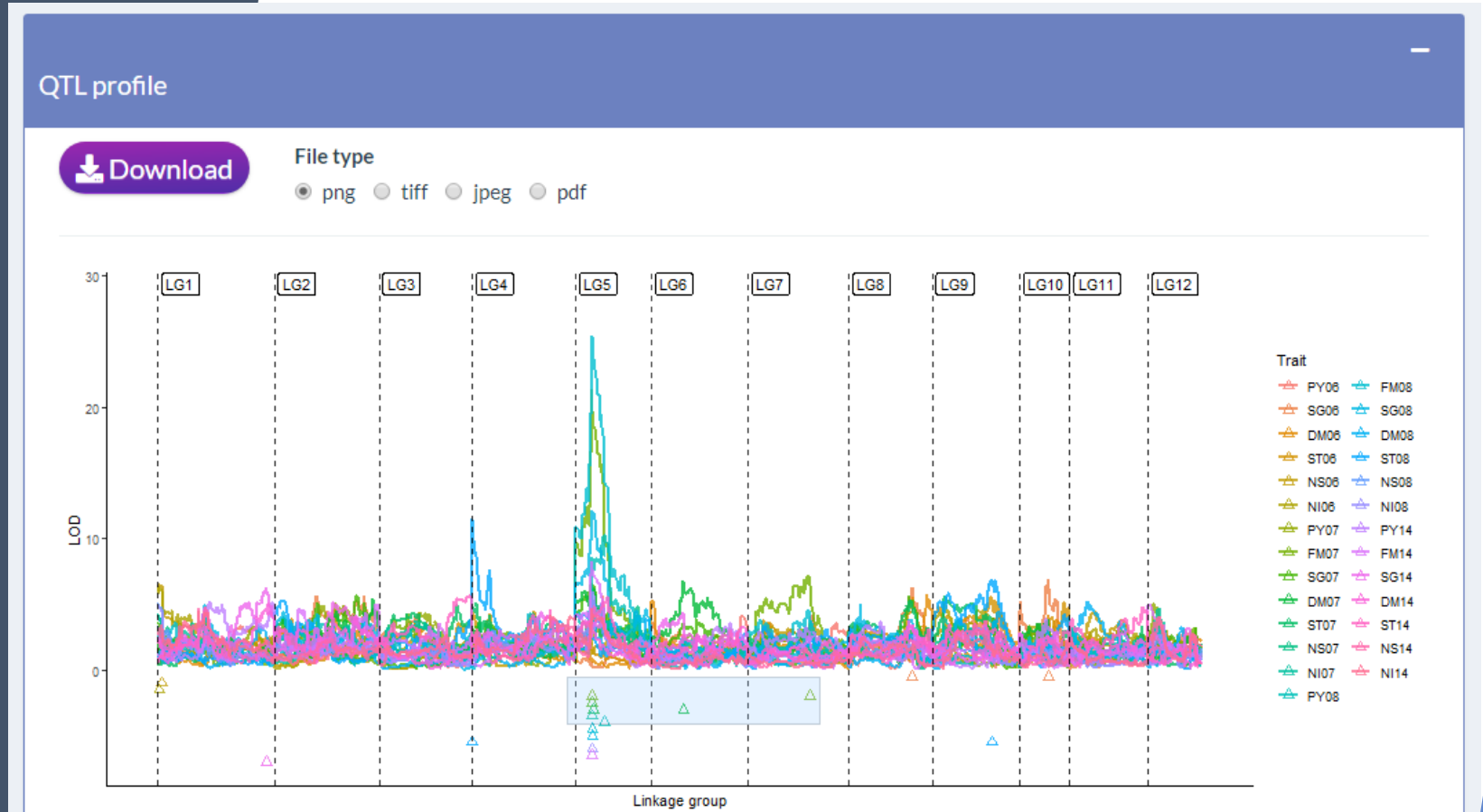
- ▶ Select linkage groups
- ▶ Select phenotypes
- ▶ Profile curve
- ▶ Select QTL



VIEWqtl

polyqtlR

- ▶ Select linkage groups
- ▶ Select phenotypes
- ▶ Profile curve
- ▶ Select QTL



VIEWqtl

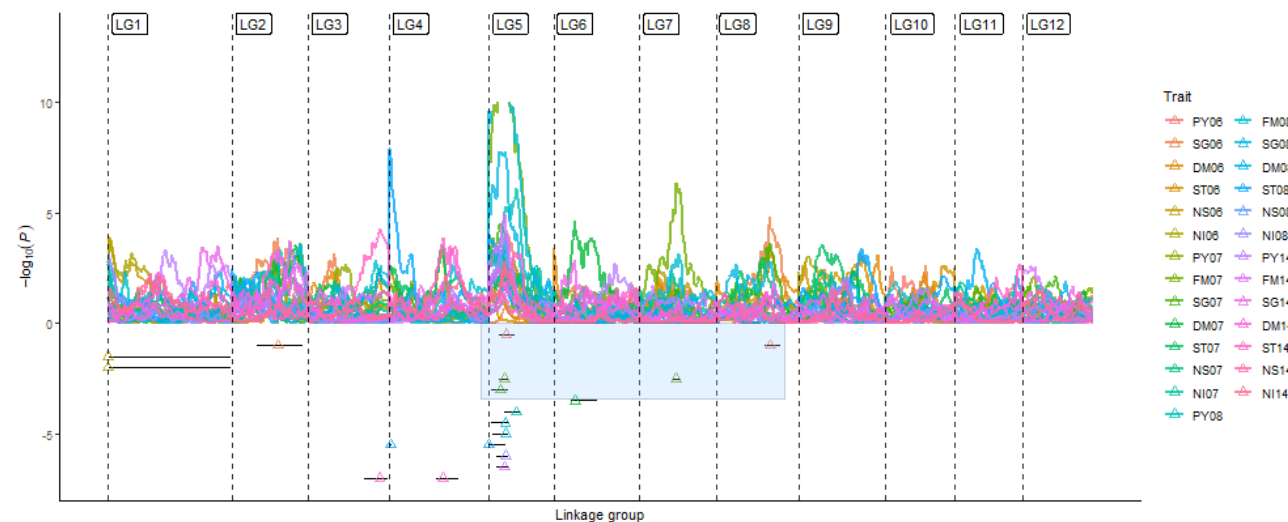
► Open other boxes

QTL profile

Download

File type

png tiff jpeg pdf



Effects



Progeny haplotypes



Breeding values



QTL summary



VIEWqtl

Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations



VIEWqtl

diaQTL

Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Effects

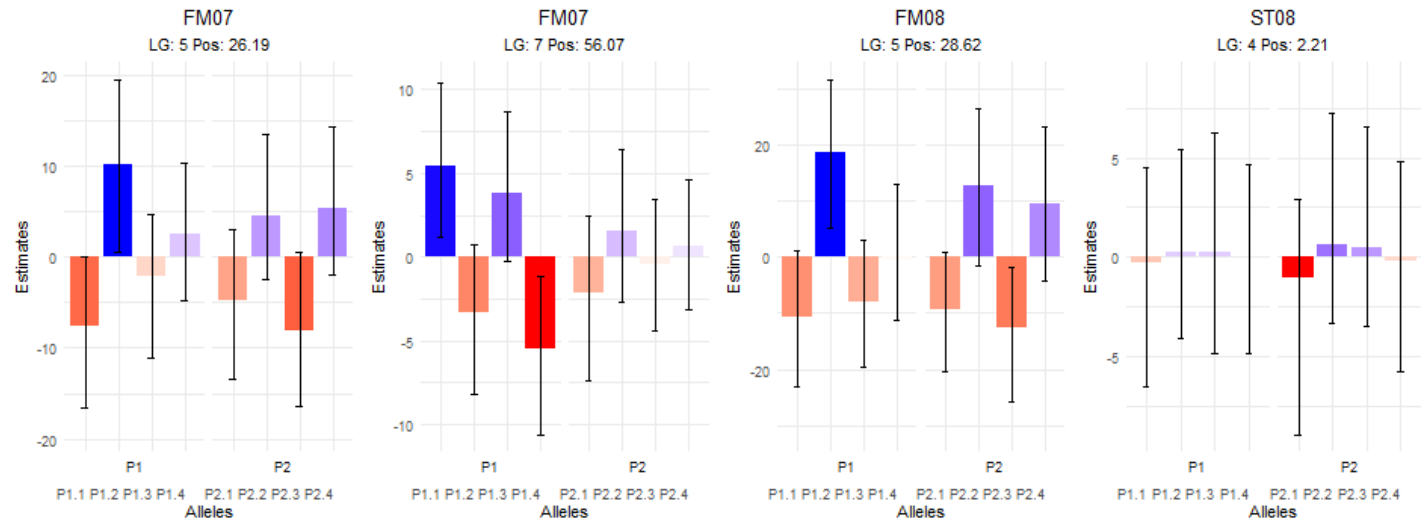


File type

png tiff jpeg pdf

Design

Additive (bar) Additive (circle) Alleles combination



VIEWqtl

Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Effects

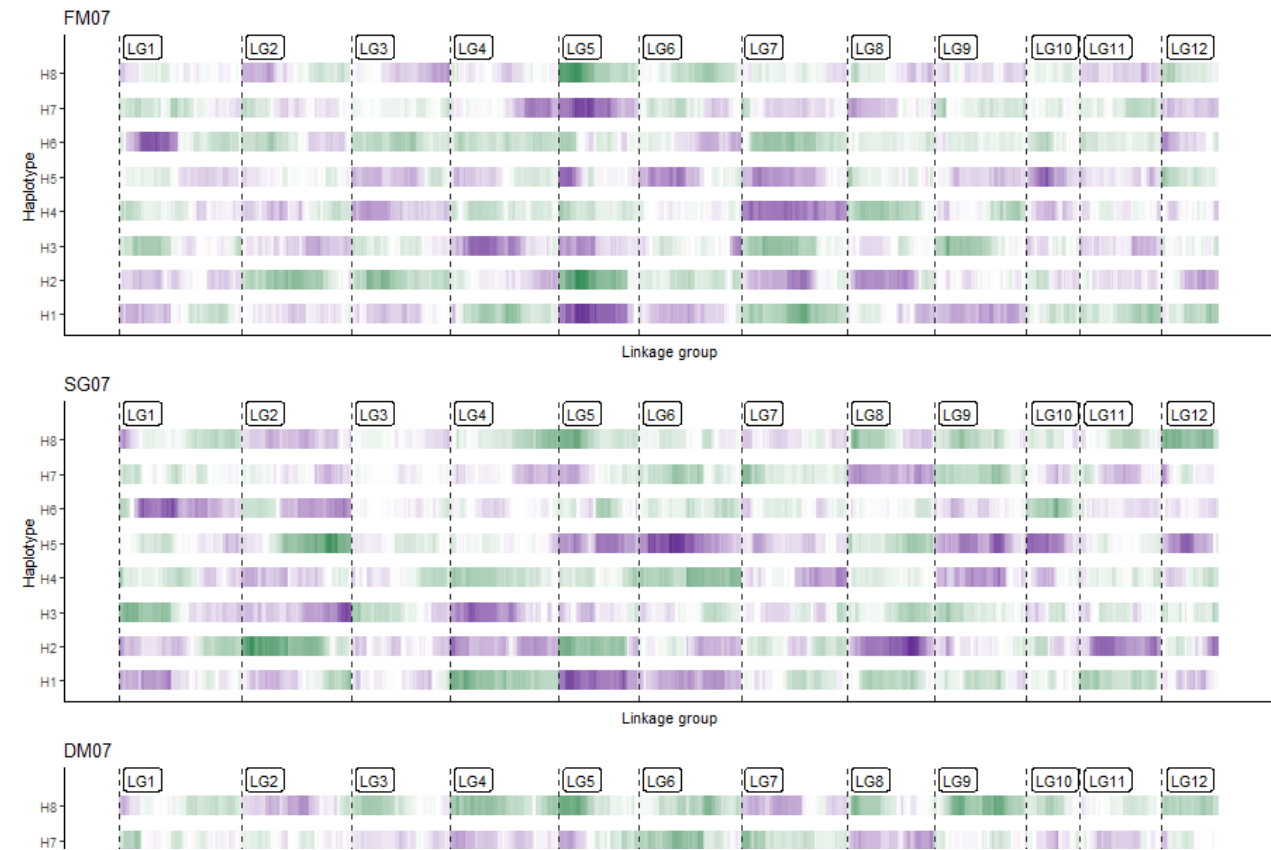


File type

png tiff jpeg pdf

Design

Additive (bar) Additive (circle) Alleles combination



VIEWqtl

Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Effects



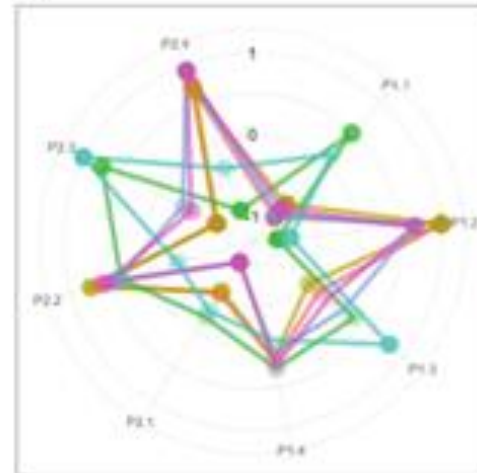
File type

png
 tiff
 jpeg
 pdf

Design

Additive (bar)
 Additive (circle)
 Alleles combination

LG5



● FMS1 LG 5/ P1x26
 ● FMS2 LG 5/ P1x27
 ● FMS3 LG 5/ P1x28
 ● FMS4 LG 5/ P1x46
 ● SGM1 LG 5/ P1x19
 ● SGM2 LG 5/ P1x28

LG7



● FMS1 LG 7/ P1x41

VIEWqtl

diaQTL

▶ Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Effects



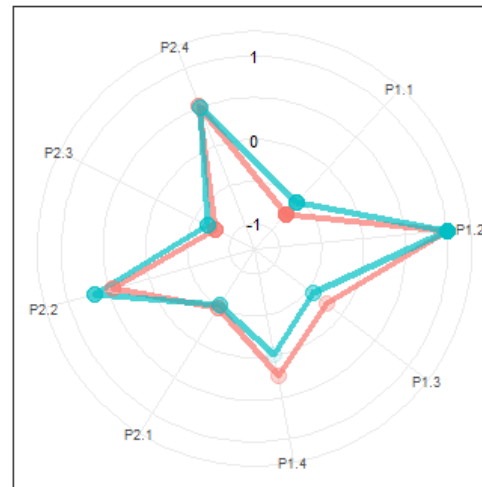
File type

- png
- tiff
- jpeg
- pdf

Design

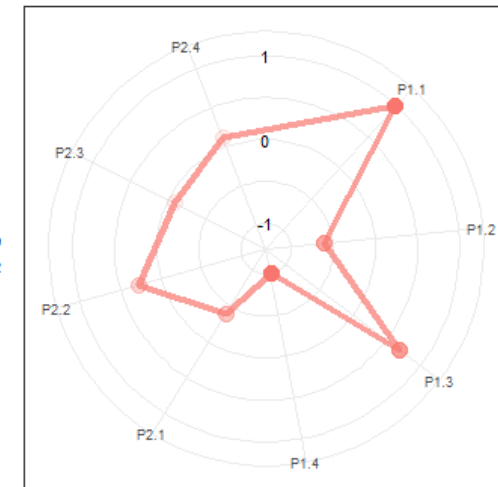
- Additive (bar)
- Additive (circle)
- Alleles combination

LG5



● FM07/ LG:5/ Pos:28.19
● FM08/ LG:5/ Pos:28.62

LG7



● FM07/ LG:7/ Pos:58.07

VIEWqtl

Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Download

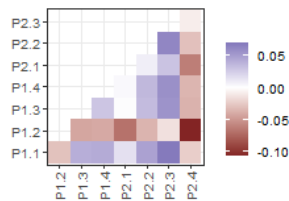
File type

- png
- tiff
- jpeg
- pdf

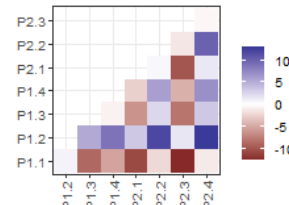
Design

- Additive (bar)
- Additive (circle)
- Alleles combination

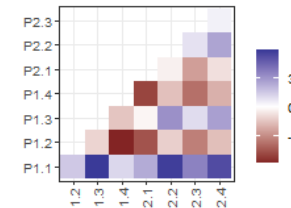
Trait: PY06
LG: 5 Pos: 29



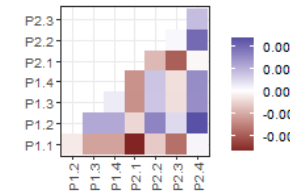
Trait: FM07
LG: 5 Pos: 26



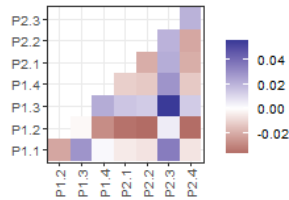
Trait: FM07
LG: 7 Pos: 61



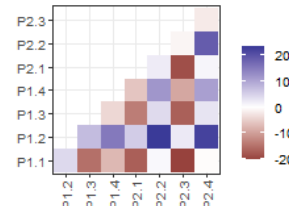
Trait: SG07
LG: 5 Pos: 19



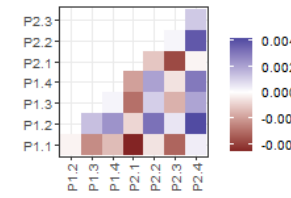
Trait: PY08
LG: 5 Pos: 46



Trait: FM08
LG: 5 Pos: 27



Trait: SG08
LG: 5 Pos: 28



VIEWqtl

diaQTL

▶ Effects

- ▶ Additive (bar)
- ▶ Additive (circle)
- ▶ Alleles combinations

Effects



File type

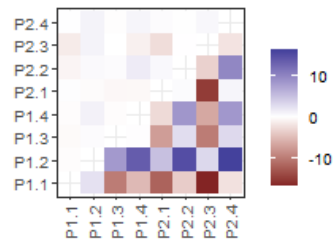
png tiff jpeg pdf

Design

Additive (bar) Additive (circle) Alleles combination

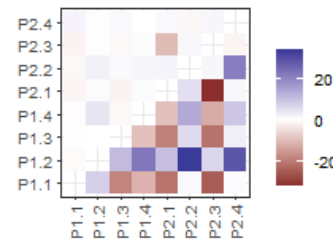
Trait: FM07

LG: 5 Pos: 26.19



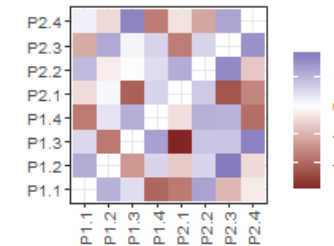
Trait: FM08

LG: 5 Pos: 28.62



Trait: ST08

LG: 4 Pos: 2.21



VIEWqtl

► Progeny haplotypes

1. Update
2. Select haplotypes
3. Submit

QTLpoly

Linkage group

Legend:

- SG07
- DM07
- ST07
- NS07
- NI07
- PY08
- SG14
- DM14
- ST14
- NS14
- NI14

Effects

Progeny haplotypes

1 update available haplotypes

Select haplotypes

Click on "update available haplotype" to update

3 submit selected haplotypes

Download

File type: png tiff jpeg pdf

Progeny haplotypes

update available haplotypes

Select haplotypes

Trait:FM07_LG:5_Pos:26_homolog:P1.1,Trait:FM07_LG:5_Pos:26_homolog:P1.2,Trait:FM0

Select All Deselect All

Trait:FM07_LG:5_Pos:26_homolog:P1.1	2 ✓
Trait:FM07_LG:5_Pos:26_homolog:P1.2	✓
Trait:FM07_LG:5_Pos:26_homolog:P1.3	
Trait:FM07_LG:5_Pos:26_homolog:P1.4	
Trait:FM07_LG:5_Pos:26_homolog:P2.1	
Trait:FM07_LG:5_Pos:26_homolog:P2.2	
Trait:FM07_LG:5_Pos:26_homolog:P2.3	
Trait:FM07_LG:5_Pos:26_homolog:P2.4	
Trait:FM07_LG:7_Pos:61_homolog:P1.1	
Trait:FM07_LG:7_Pos:61_homolog:P1.2	
Trait:FM07_LG:7_Pos:61_homolog:P1.3	
Trait:FM07_LG:7_Pos:61_homolog:P1.4	
Trait:FM07_LG:7_Pos:61_homolog:P2.1	
Trait:FM07_LG:7_Pos:61_homolog:P2.2	
Trait:FM07_LG:7_Pos:61_homolog:P2.3	

VIEWqtl

- ▶ Check linkage map quality

Progeny haplotypes

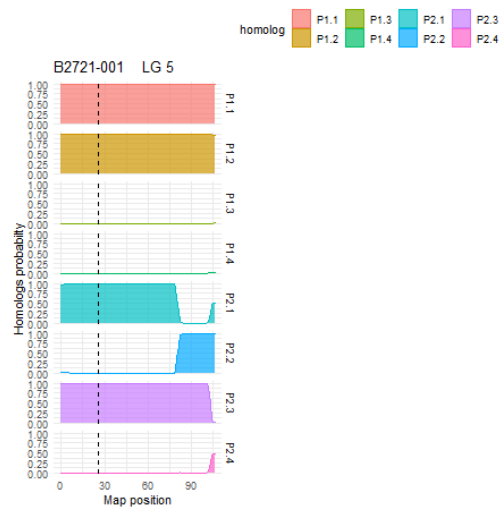
[update available haplotypes](#)

Select haplotypes

Trait:FM07_LG:5_Pos:26_homolog:P1.1, Trait:FM07_LG:5_Pos:26_homolog:P1.2, Trait:FM0

[submit selected haplotypes](#)

Download png tiff jpeg pdf



Progeny haplotypes

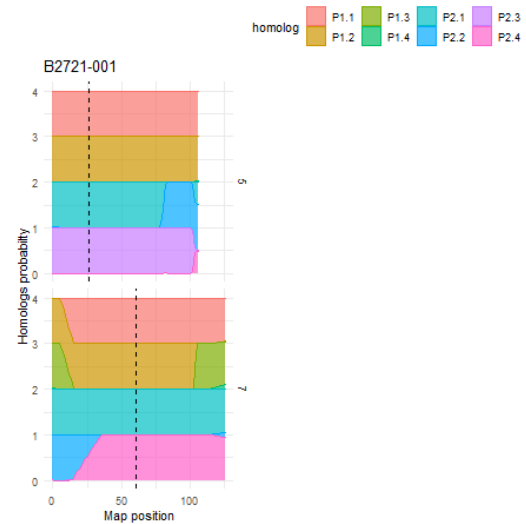
[update available haplotypes](#)

Select haplotypes

Trait:FM07_LG:5_Pos:26_homolog:P1.1, Trait:FM07_LG:5_Pos:26_homolog:P1.2, Trait:FM0

[submit selected haplotypes](#)

Download png tiff jpeg pdf



VIEWqtl

- ▶ Breeding values
- ▶ QTL summary

Breeding values

Copy CSV Excel PDF Search:

	gen	PY06	FM07	SG07	PY08	FM08	SG08
1	B2721-001	1.01	57.97	1.07	0.28	57.65	1.06
2	B2721-002	1.14	63.56	1.08	0.2	67.92	1.07
3	B2721-003	1.06	70.33	1.07	0.28	76.69	1.07
4	B2721-004	0.99	62.96	1.07	0.31	66.73	1.07
5	B2721-005	1.06	67.1	1.07	0.31	65.28	1.07

Show 10 entries Previous 1 Next

QTL summary

Copy CSV Excel PDF Search:

	Trait	Linkage group	Position (cM)	Lower interval (cM)	Upper interval (cM)	p-value	h ²
1	PY06	5	29	16	43	8.35e-05	0.18
4	FM07	5	26	16	33	<2.22e-16	0.56
5	FM07	7	61	56	70	4.52e-07	0.13
6	SG07	5	19	4	32	3.10e-05	0.28
7	PY08	5	46	25	52	7.60e-07	0.38
8	FM08	5	27	5	34	<2.22e-16	0.7
9	SG08	5	28	7	32	1.98e-08	0.46

Show 10 entries Previous 1 Next

VIEWgenome

- ▶ Select phenotypes
- ▶ Select linkage group
- ▶ Map range
- ▶ QTL profile

VIEWpoly About Input data QTL **Genome** Map TOOLS FOR POLYPLOTS

VIEWgenome

[Exit](#)
[Next](#)

Select phenotypes

Select phenotypes
27 items selected

Select linkage group

Linkage group
5

Map range (cM)
0 11 21 32 42 53 64 74 85 96 106.2

QTL

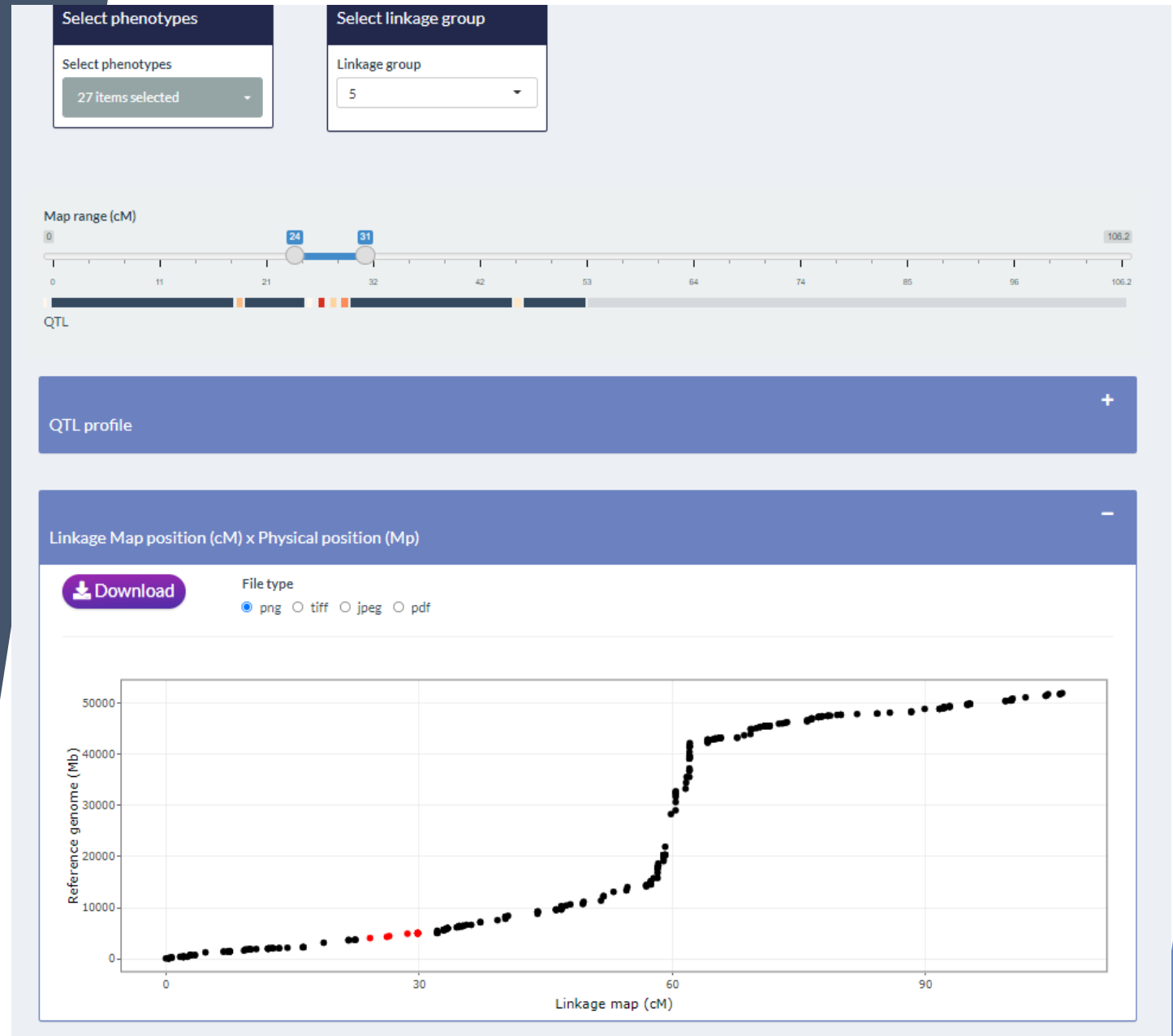
QTL profile

[Download](#) File type: png tiff jpeg pdf

Trait (PY06,1) (SG06,1) (DM06,1) (ST06,1) (NS06,1) (NI06,1) (PY07,1) (FM07,1) (SG07,1)
(DM07,1) (ST07,1) (NS07,1) (NI07,1) (PY08,1) (FM08,1) (SG08,1) (DM08,1) (ST08,1)
(NS08,1) (NI08,1) (PY14,1) (FM14,1) (SG14,1) (DM14,1) (ST14,1) (NS14,1) (NI14,1)

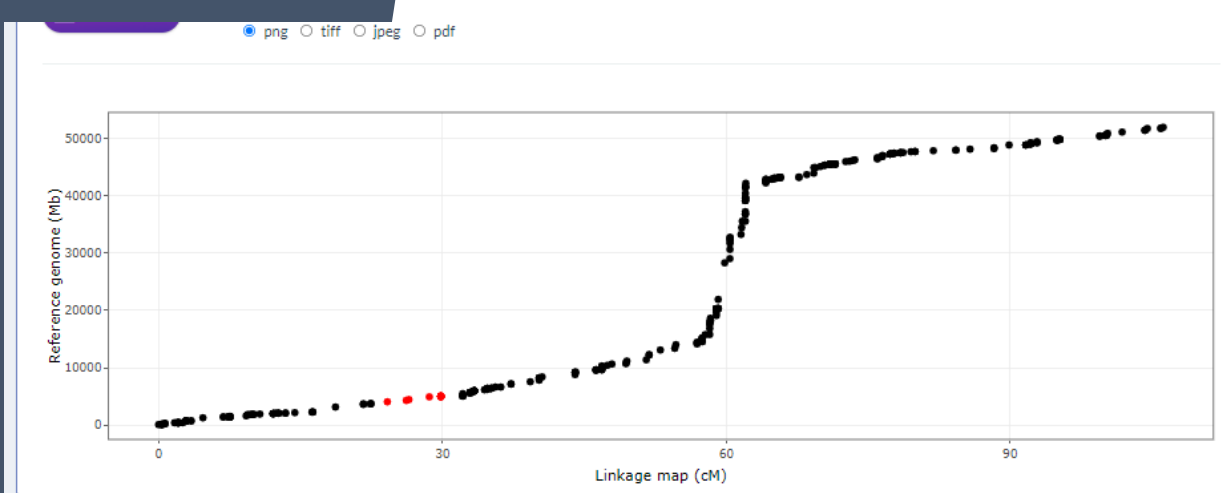
VIEWgenome

- ▶ Genetic x Physical position



VIEWgenome

- ▶ JBrowseR features
- ▶ Local server or URL



JBrowseR

Open JBrowseR

Local server: ON

ST4.03ch05

Reference Sequence (Substratum, 448 v4)

Zoom in to see sequence

Substratum, 448 v4

PGSC0003DMG400030538

PGSC0003DMG400030551

PGSC0003DMG400030550

PGSC0003DMG400030542

PGSC0003DMG400030492

PGSC0003DMG400030537

PGSC0003DMG400018405

VIEWgenome

- ▶ If GFF file available
- ▶ Annotation inside range

Annotation table

Copy CSV Excel PDF Search:

	seqid	source	type	start	end	score	strand	phase	attributes
1	ST4.03ch05	phytozomev12	gene	4046728	4053695	.	+	.	ID=PGSC0003DMG400030548.v4.03;Name=PG
2	ST4.03ch05	phytozomev12	mRNA	4046728	4048209	.	+	.	ID=PGSC0003DMT400078477.v4.03;Name=PG
3	ST4.03ch05	phytozomev12	CDS	4046728	4046860	.	+	0	ID=PGSC0003DMT400078477.v4.03.CDS.1;Pan
4	ST4.03ch05	phytozomev12	exon	4046728	4046860	.	+	.	ID=PGSC0003DMT400078477.v4.03.exon.1;Par
5	ST4.03ch05	phytozomev12	mRNA	4046761	4053695	.	+	.	ID=PGSC0003DMT400078474.v4.03;Name=PG
6	ST4.03ch05	phytozomev12	CDS	4046761	4046860	.	+	0	ID=PGSC0003DMT400078474.v4.03.CDS.1;Pan
7	ST4.03ch05	phytozomev12	exon	4046761	4046860	.	+	.	ID=PGSC0003DMT400078474.v4.03.exon.1;Par
8	ST4.03ch05	phytozomev12	exon	4047232	4047361	.	+	.	ID=PGSC0003DMT400078477.v4.03.exon.2;Par
9	ST4.03ch05	phytozomev12	CDS	4047232	4047361	.	+	2	ID=PGSC0003DMT400078474.v4.03.CDS.2;Pan
10	ST4.03ch05	phytozomev12	CDS	4047232	4047361	.	+	2	ID=PGSC0003DMT400078477.v4.03.CDS.2;Pan

Show 10 entries

Previous 1 2 3 4 5 ... 121 Next

VIEWmap

VIEWpoly About Input data QTL Genome **Map** TOOLS FOR POLYPLAIDS

VIEWmap [Exit](#)

Select phenotypes

Select phenotypes

27 items selected

Select linkage group

Linkage group

5

Show SNP names

Map range (cM)

QTL

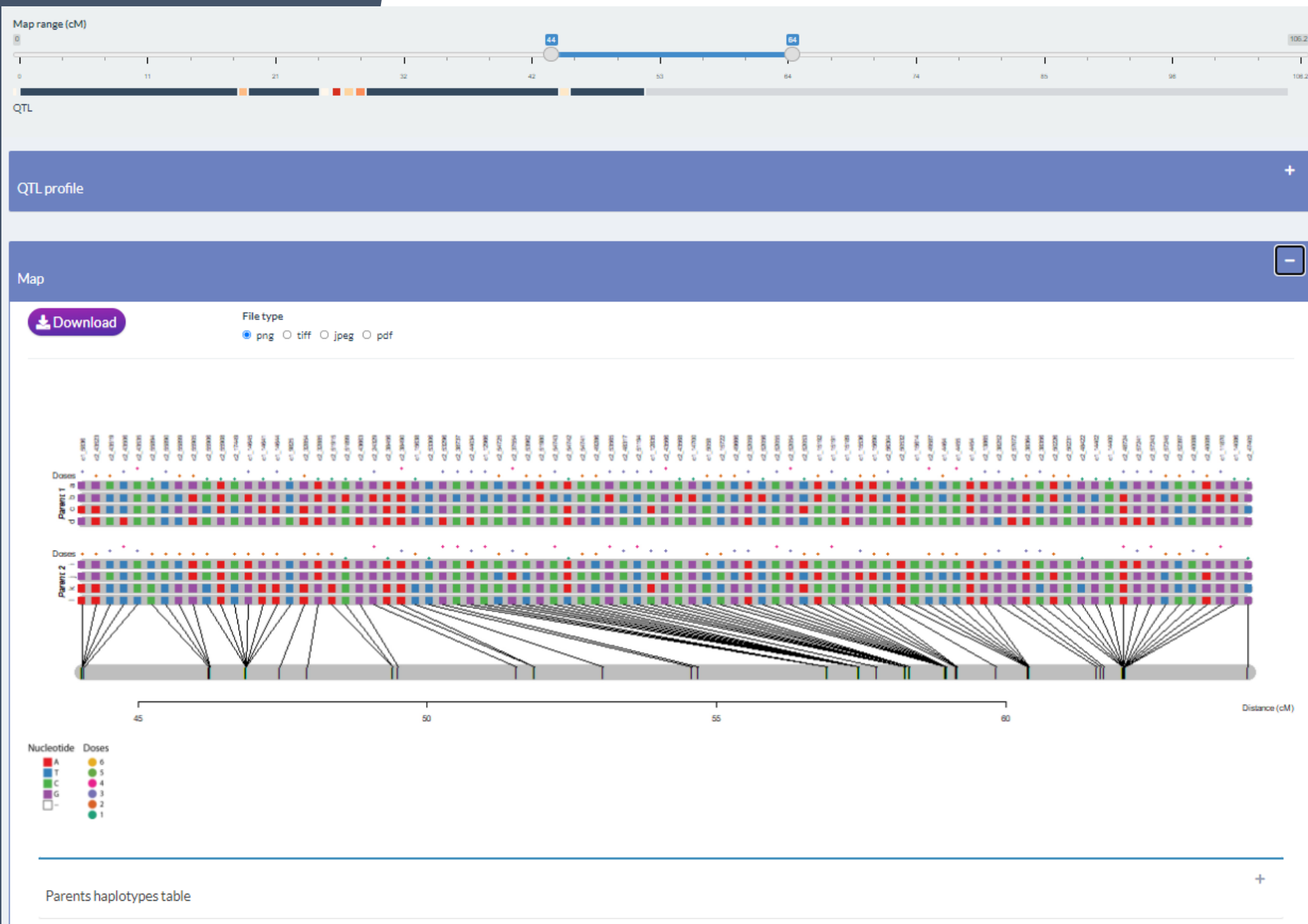
QTL profile +

Map +

Map summary +

VIEWmap

- ▶ Parents haplotypes
- ▶ Marker doses
- ▶ Linkage map



VIEWmap

- ▶ Parents haplotypes table

Parents haplotypes table

Copy CSV Excel PDF Search:

	a	b	c	d	e	f	g	h
c2_11829	C	T	T	T	T	T	T	C
c2_22986	T	C	C	C	C	C	T	C
c2_22959	G	G	T	T	G	G	G	G
c2_23052	G	T	G	G	T	T	T	G
c2_23055	C	C	C	C	C	C	C	T
c2_23056	G	G	G	G	G	G	G	A
c2_50296	T	T	A	A	T	T	A	T
c2_50312	G	G	G	G	G	G	G	A
c2_50314	A	G	G	G	G	G	G	G
c2_50281	C	C	C	C	C	C	C	T

Show 10 entries Previous 1 2 Next

Map summary +

VIEWmap

- ▶ Linkage map summary table
- ▶ Linkage map figure

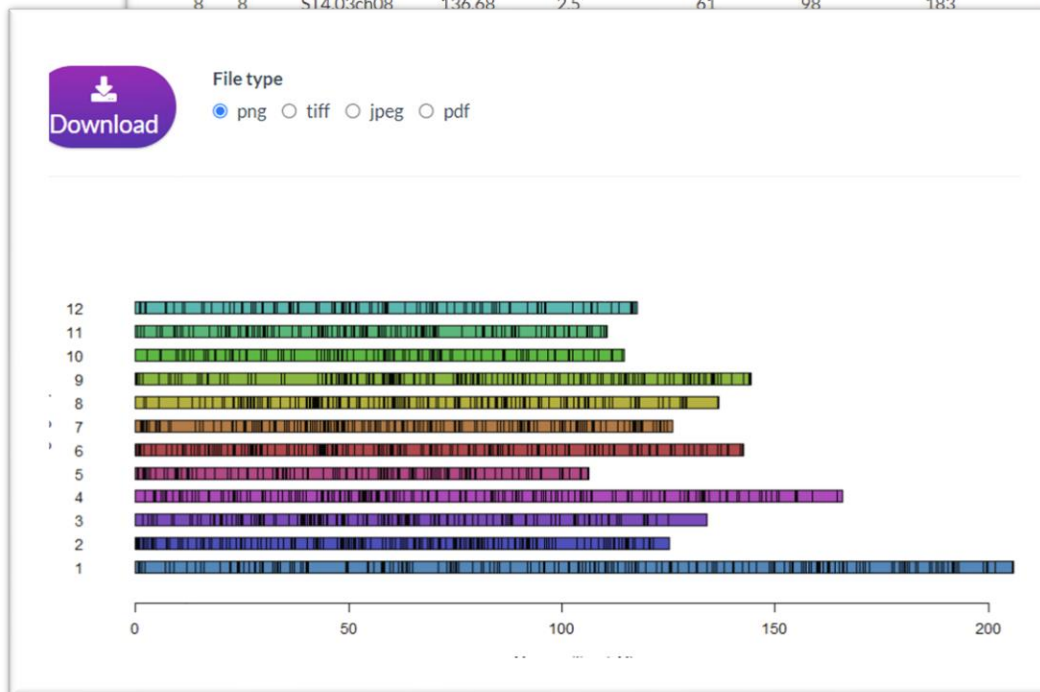
Map summary

Copy CSV Excel PDF Search:

	LG	Genomic sequence	Map length (cM)	Markers/cM	Simplex	Double-simplex	Multiplex	Total	Max gap
1	1	ST4.03ch01	205.88	2.31	102	122	252	476	9.01
2	2	ST4.03ch02	125.11	3.44	131	139	160	430	4.9
3	3	ST4.03ch03	134.07	2.85	151	21	210	382	9.09
4	4	ST4.03ch04	165.9	2.56	114	87	224	425	5.74
5	5	ST4.03ch05	106.2	2.93	124	53	134	311	4.22
6	6	ST4.03ch06	142.7	2.78	73	75	249	397	3.83
7	7	ST4.03ch07	126.09	3.28	136	94	184	414	5.65
8	8	ST4.03ch08	136.68	2.5	61	98	183	342	7.32
									6 7.79
									7 5.27

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2 Next



Tutorials

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 - Select linkage groups and phenotypes
 - QTL profile
- VIEWgenome: the Genome Browser
 - Select phenotypes and linkage group
 - QTL profile
 - Linkage Map x Physical
 - JBrowseR

VIEWpoly: a visualization tool to integrate and explore results of polyploid genetic analysis

Cristiane Taniguti, Gabriel de Siqueira Gesteira, Jeekin Lau, Guilherme da Silva Pereira, David Byrne, Zhao-Bang Zeng, Oscar Riera-Lizarazu and Marcelo Mollinari

2021-12-17

Introduction

VIEWpoly is a shiny app and R package for visualizing and exploring results from [polyploid computational tools](#) using an interactive graphical user interface. The package allows users to directly upload output files from [polymapR](#) (Bourke et al. (2018)), [MAPpoly](#) (Mollinari et al. (2019)), [polyqtR](#) (Bourke et al. (2021)), [QTLpoly](#) (Pereira et al. (2019)), [diaQTL](#) (Amadeu et al. (2021)) and genomic assembly, variants, annotation and alignment files. VIEWpoly uses [shiny](#), [golem](#), [ggplot2](#), [plotly](#), and [JBrowseR](#) libraries to integrate and graphically display the QTL profiles, positions, estimated allele effects, progeny individuals containing specific haplotypes, and their breeding values. When genomic information is available, QTL positions can be interactively explored using JBrowseR interface, allowing the search for candidate genes. The software allows for visualization of parental haplotypes and marker dosages, and provides features to download specific information into comprehensive tables and images for further analysis and presentation.

The app is organized in the `Input data` section and three main modules: `VIEWqtl`, `VIEWgenome`, and `VIEWmap`. Please check our [tutorial video](#) for a step-by-step guide through all VIEWpoly's features and functionalities.

Install and run the app

VIEWpoly is available in both stable and development versions. To install and load its stable version from the CRAN repository, please run:

```
install.packages("viewpoly")
```



Perspectives

- ▶ Modules structure make it easy to expand
- ▶ Need for help with datasets and feedbacks
- ▶ Future versions:
 - ▶ PolyOrigin
 - ▶ Preferential paring
 - ▶ Double-reduction
 - ▶ GWAS
- ▶ Issues or suggestions: GitHub or chtaniguti@tamu.edu

Acknowledgment



Other Collaborators



Neuhouse
Farms



Wolf Roses
L.L.C.

