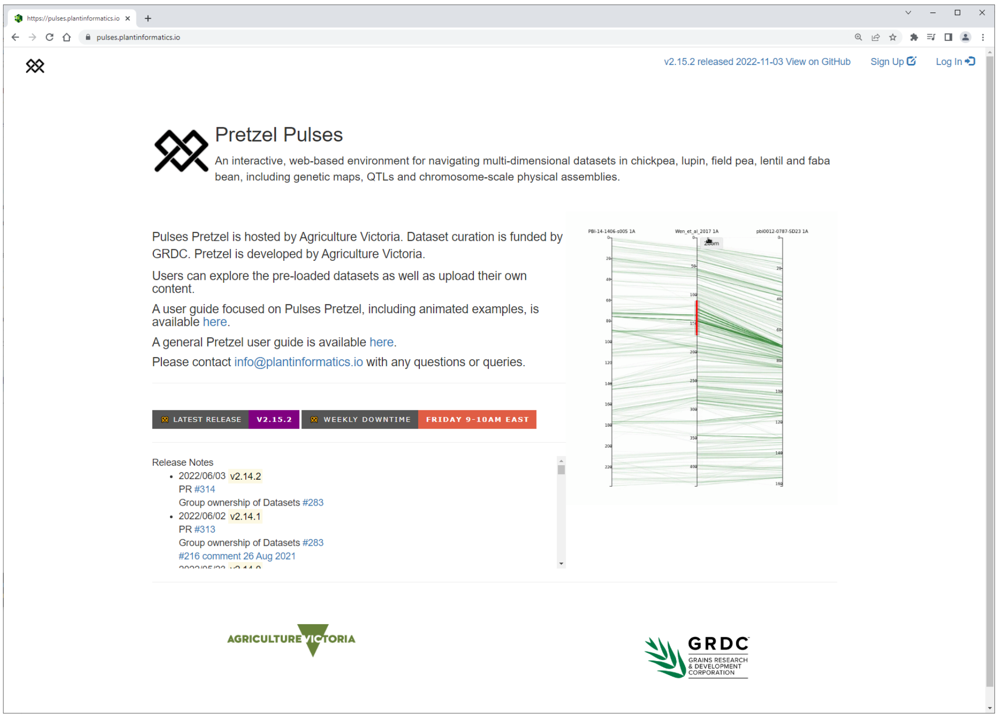
Pretzel instructions

1. Log in

Access Pretzel Pulses URL: https://pulses.plantinformatics.io/
Click Log In in top right



Pretzel Pulses

An interactive, web-based environment for navigating multi-dimensional datasets in chickpea, lupin, field pea, lentil and faba bean, including genetic maps, QTLs and chromosome-scale physical assemblies.

Pulses Pretzel is hosted by Agriculture Victoria. Dataset curation is funded by GRDC. Pretzel is developed by Agriculture Victoria.

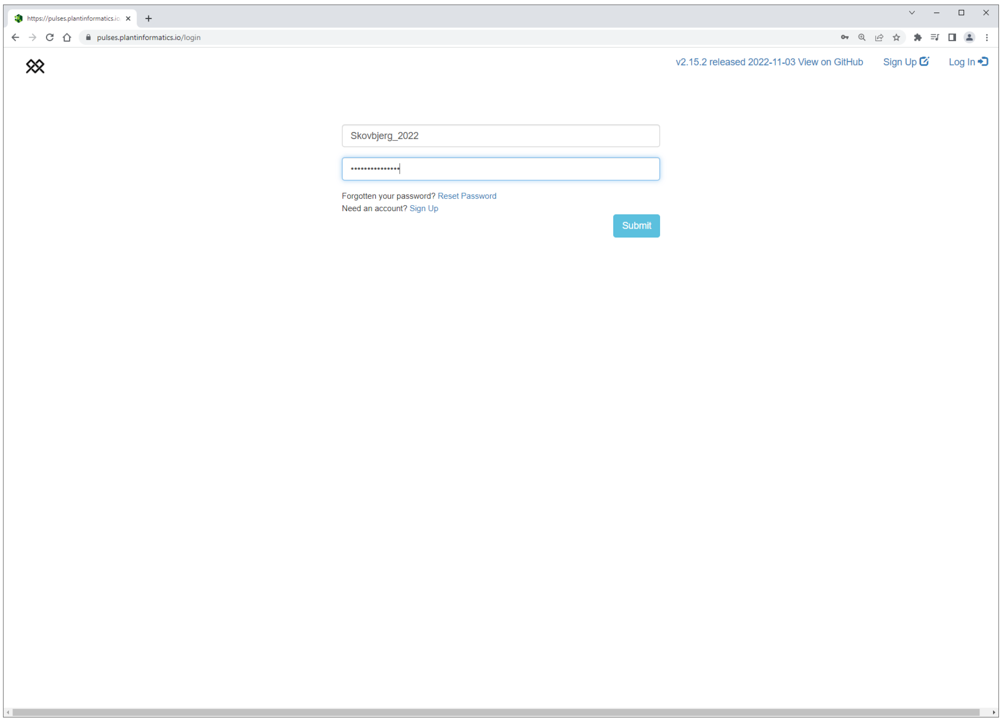
Users can explore the pre-loaded datasets as well as upload their own content.

A user guide focused on Pulses Pretzel, including animated examples, is available here.

A general Pretzel user guide is available here.

Please contact info@plantinformatics.io with any questions or queries.

Release Notes
- 2022/06/03 v2.14.2
  PR #314
  Group ownership of Datasets #283
- 2022/06/02 v2.14.1
  PR #313
  Group ownership of Datasets #283
  #216 comment 26 Aug 2021



Skovbjerg_2022

••••••••••••••

Forgotten your password? Reset Password
Need an account? Sign Up

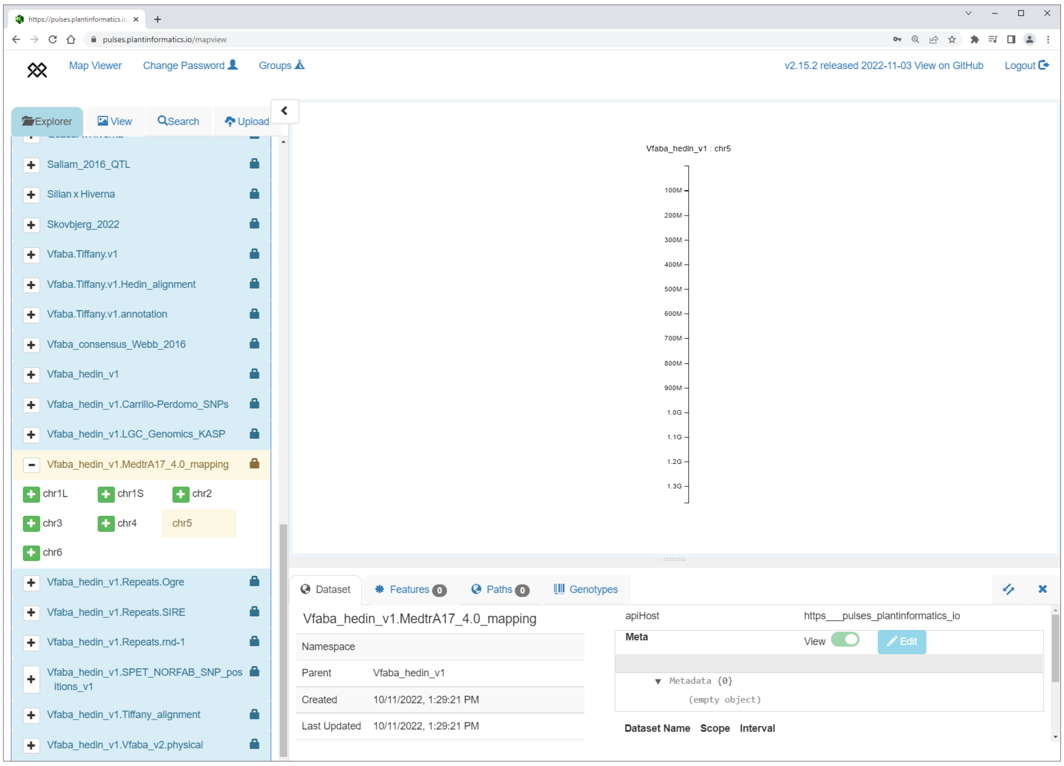
Log in with the following details:

Username: Skovbjerg_2022
Password: FabaBean&ABC123

2. Load datasets

Scroll down the dataset explorer on the left of the screen to select the following datasets:

- Vfaba_hedin_v1.MedtrA17_4.0_mapping – chr5



Vfaba_hedin_v1.MedtrA17_4.0_mapping

Namespace	
Parent	Vfaba_hedin_v1
Created	10/11/2022, 1:29:21 PM
Last Updated	10/11/2022, 1:29:21 PM

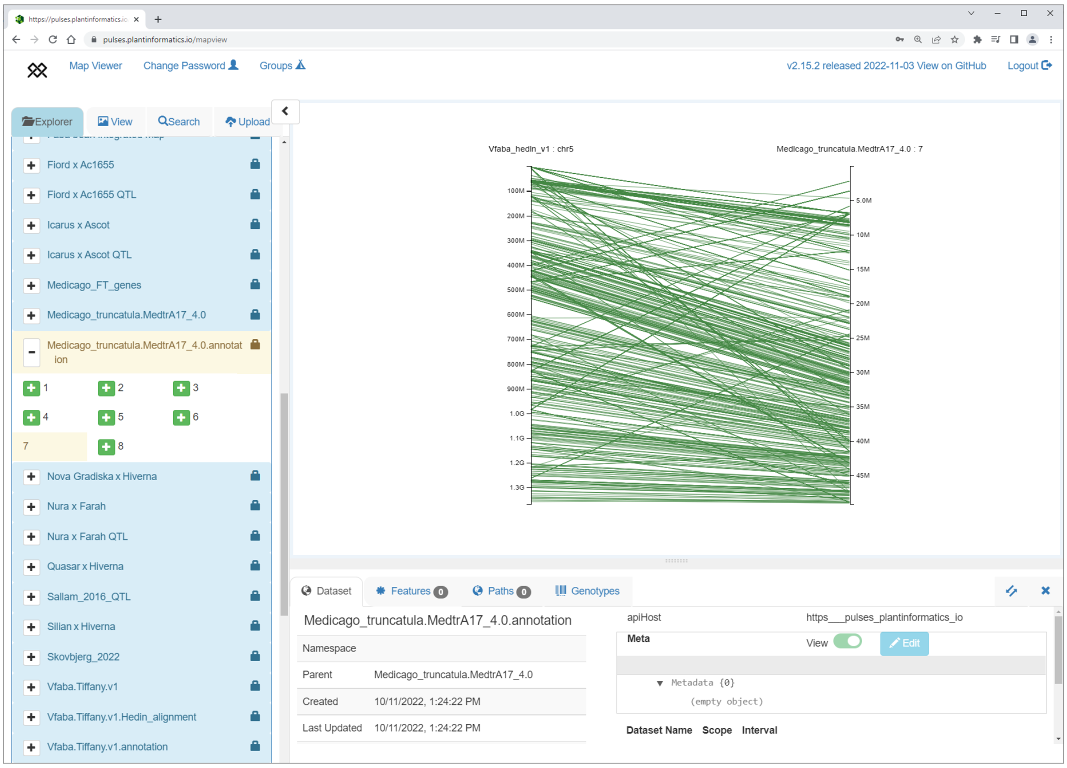
apiHost https___pulses_plantinformatics_io

Meta

```
▼ Metadata {0}
    (empty object)
```

Dataset Name Scope Interval

- Medicago_truncatula.MedtrA17_4.0.annotation – chr7



Medicago_truncatula.MedtrA17_4.0.annotation

Namespace	
Parent	Medicago_truncatula.MedtrA17_4.0
Created	10/11/2022, 1:24:22 PM
Last Updated	10/11/2022, 1:24:22 PM

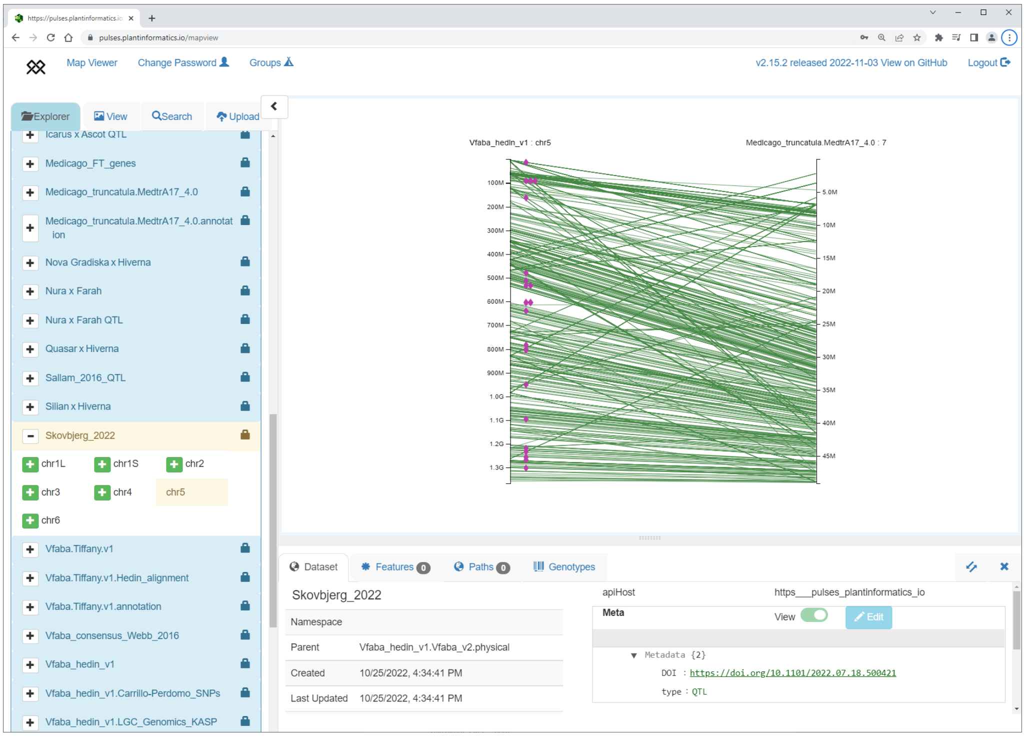
apiHost https___pulses_plantinformatics_io

Meta

```
▼ Metadata {0}
    (empty object)
```

Dataset Name Scope Interval

- Skovbjerg_2022 – chr5



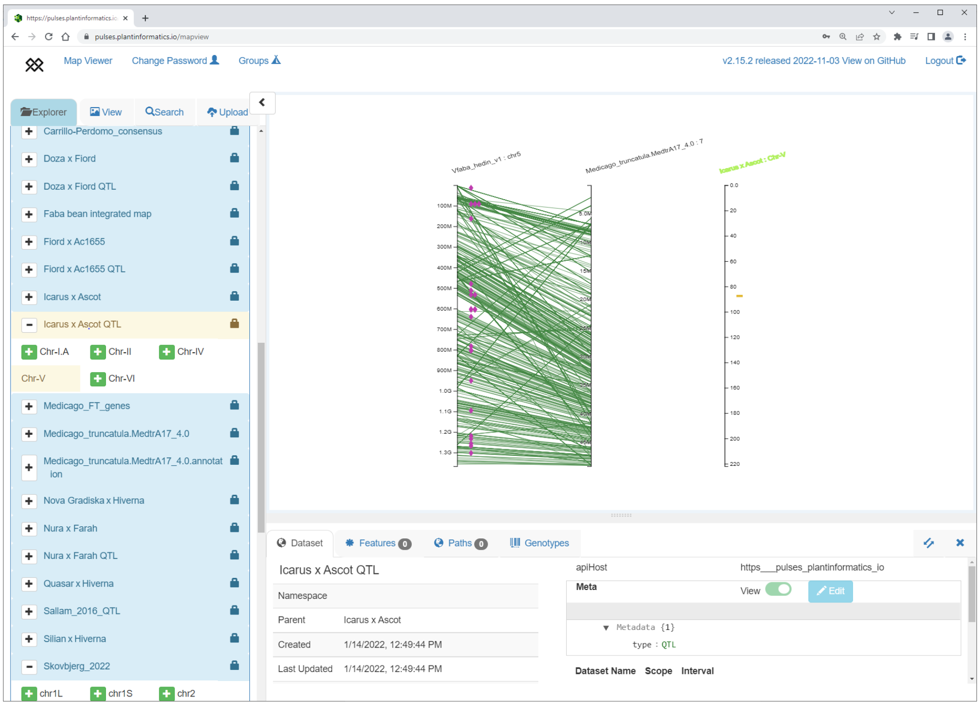
Skovbjerg_2022

Namespace	
Parent	Vfaba_hedin_v1.Vfaba_v2.physical
Created	10/25/2022, 4:34:41 PM
Last Updated	10/25/2022, 4:34:41 PM

apiHost https___pulses_plantinformatics_io

```
▼ Metadata {2}
    DOI : https://doi.org/10.1101/2022.07.18.500421
    type : QTL
```

- 20210909_Fababean_SNP_SSR_Seq_Info – chr5
- Icarus x Ascot QTL – Chr-V



Icarus x Ascot QTL

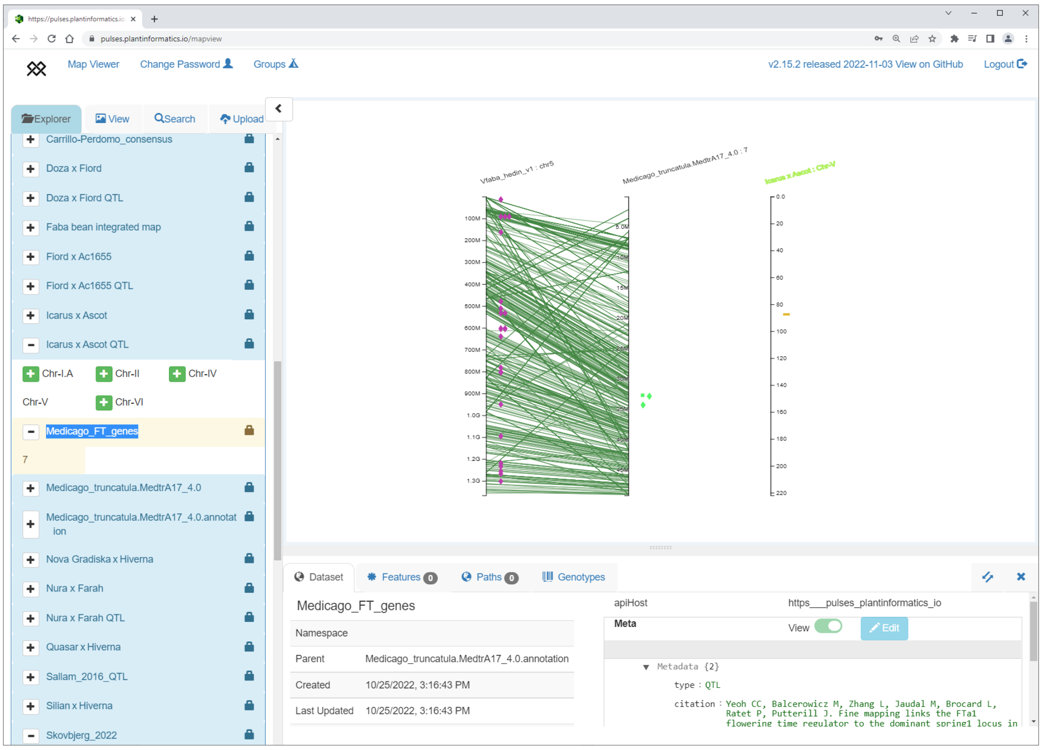
Namespace	
Parent	Icarus x Ascot
Created	1/14/2022, 12:49:44 PM
Last Updated	1/14/2022, 12:49:44 PM

apiHost https___pulses_plantinformatics_io

```
▼ Metadata {1}
    type : QTL
```

Dataset Name	Scope	Interval

- Medicago_FT_genes - 7



Medicago_FT_genes

Namespace

Parent Medicago_truncatula.MedtrA17_4.0.annotation

Created 10/25/2022, 3:16:43 PM

Last Updated 10/25/2022, 3:16:43 PM

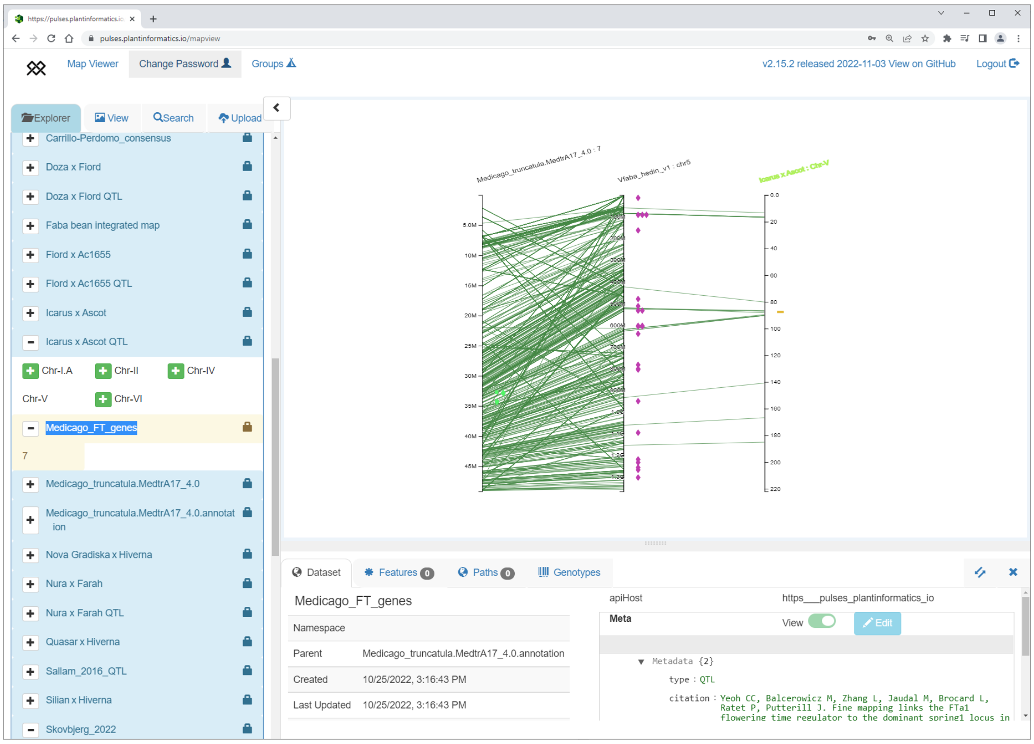
apiHost https___pulses_plantinformatics_io

Meta

Metadata {2}
type : QTL
citation : Yeoh CC, Balcerowicz M, Zhang L, Jaudal M, Brocard L, Ratet P, Putterill J. Fine mapping links the FTa1 flowering time regulator to the dominant spring1 locus in

3. Re-arrange axes

Hold the CTRL key, click and drag on the Medicago axis to move it to the left side.



Medicago_FT_genes

Namespace

Parent Medicago_truncatula.MedtrA17_4.0.annotation

Created 10/25/2022, 3:16:43 PM

Last Updated 10/25/2022, 3:16:43 PM

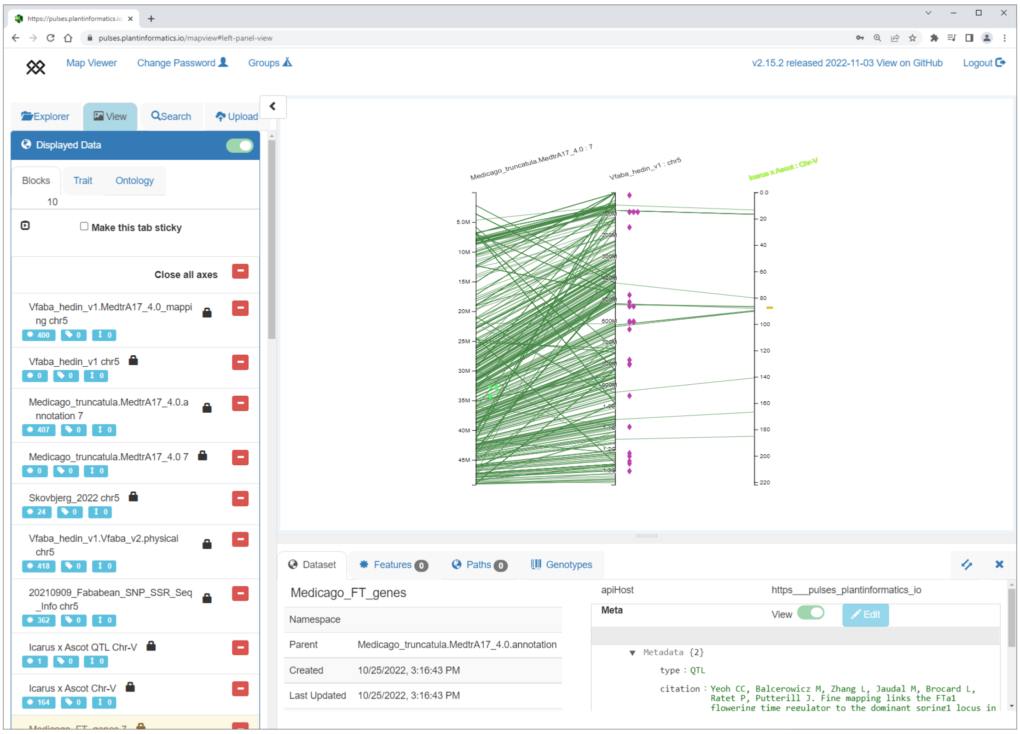
apiHost https___pulses_plantinformatics_io

Meta

Metadata {2}
type : QTL
citation : Yeoh CC, Balcerowicz M, Zhang L, Jaudal M, Brocard L, Ratet P, Putterill J. Fine mapping links the FTa1 flowering time regulator to the dominant spring1 locus in

4. Toggle displayed traits

Click on the View tab on the left side panel.



Block	Features	Tags	Paths
Vfaba_hedin_v1.MedtrA17_4.0_mapping chr5	400	0	0
Vfaba_hedin_v1 chr5	0	0	0
Medicago_truncatula.MedtrA17_4.0.annotation 7	407	0	0
Medicago_truncatula.MedtrA17_4.0 7	0	0	0
Skovbjerg_2022 chr5	24	0	0
Vfaba_hedin_v1.Vfaba_v2.physical chr5	418	0	0
20210909_Fababean_SNP_SSR_Seq_Info chr5	362	0	0
Icarus x Ascot QTL Chr-V	1	0	0
Icarus x Ascot Chr-V	164	0	0

Medicago_FT_genes

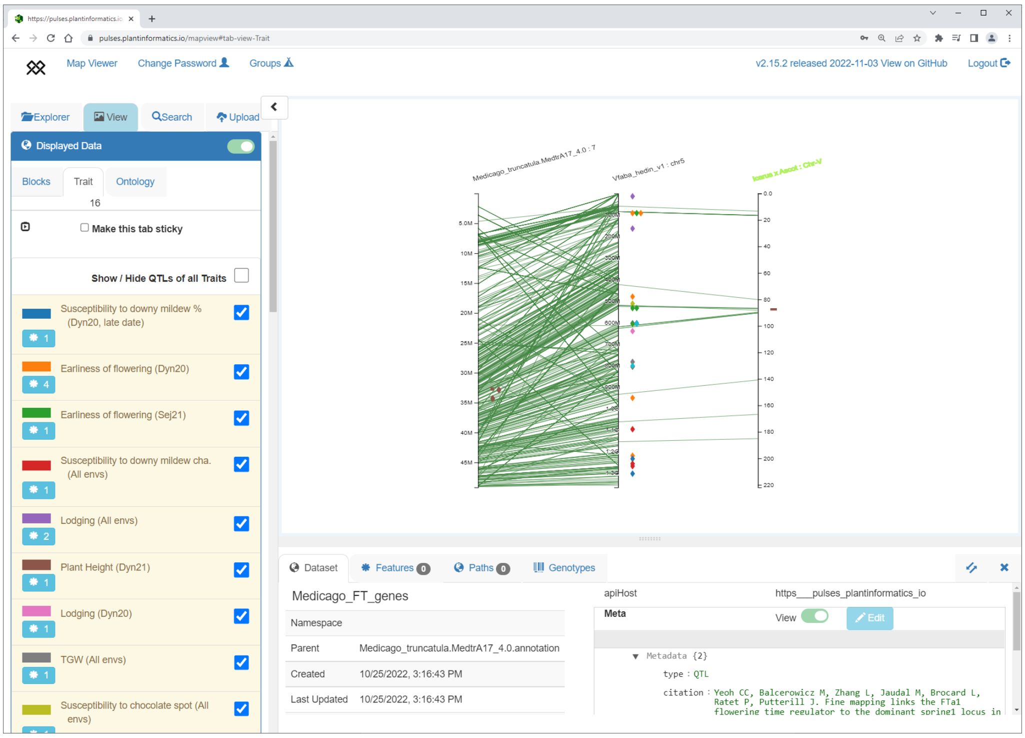
Namespace	
Parent	Medicago_truncatula.MedtrA17_4.0.annotation
Created	10/25/2022, 3:16:43 PM
Last Updated	10/25/2022, 3:16:43 PM

apiHost https___pulses_plantinformatics_io

Meta View

```
▼ Metadata {2}
    type : QTL
    citation : Yeoh CC, Balcerowicz M, Zhang L, Jaudal M, Brocard L,
               Ratet P, Putterill J. Fine mapping links the FTa1
               flowering time regulator to the dominant spring1 locus in
```

Within the Displayed Data sub-panel, select the Trait tab at the top.



Show / Hide QTLs of all Traits ☐

	Trait	QTLs	
🟦	Susceptibility to downy mildew % (Dyn20, late date)	1	☑
🟧	Earliness of flowering (Dyn20)	4	☑
🟩	Earliness of flowering (Sej21)	1	☑
🟥	Susceptibility to downy mildew cha. (All envs)	1	☑
🟪	Lodging (All envs)	2	☑
🟫	Plant Height (Dyn21)	1	☑
▬	Lodging (Dyn20)	1	☑
⬛	TGW (All envs)	1	☑
🟨	Susceptibility to chocolate spot (All envs)		☑

Medicago_FT_genes

Namespace	
Parent	Medicago_truncatula.MedtrA17_4.0.annotation
Created	10/25/2022, 3:16:43 PM
Last Updated	10/25/2022, 3:16:43 PM

apiHost https___pulses_plantinformatics_io

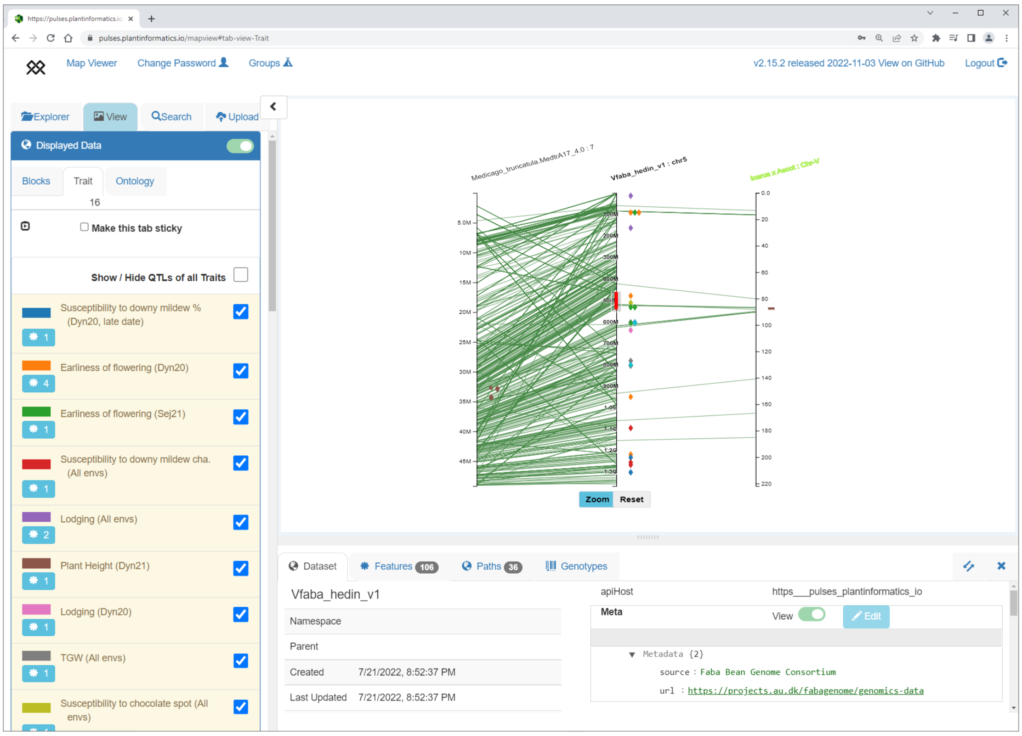
Meta View

```
▼ Metadata {2}
    type : QTL
    citation : Yeoh CC, Balcerowicz M, Zhang L, Jaudal M, Brocard L,
               Ratet P, Putterill J. Fine mapping links the FTa1
               flowering time regulator to the dominant spring1 locus in
```

This colours the QTL symbols according to trait. Mouse over any trait symbols for detail on that QTL.

5. Brush (select) a region of an axis

Move the mouse over the axis, click and drag up or down to “brush” (make a selection on) the axis.



16

☐ Make this tab sticky

Show / Hide QTLs of all Traits ☐

- Susceptibility to downy mildew % (Dyn20, late date) 1 ☑
- Earliness of flowering (Dyn20) 4 ☑
- Earliness of flowering (Sej21) 1 ☑
- Susceptibility to downy mildew cha. (All envs) 1 ☑
- Lodging (All envs) 2 ☑
- Plant Height (Dyn21) 1 ☑
- Lodging (Dyn20) 1 ☑
- TGW (All envs) 1 ☑
- Susceptibility to chocolate spot (All envs) ☑

Vfaba_hedin_v1

Namespace	
Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM

apiHost https___pulses_plantinformatics_io

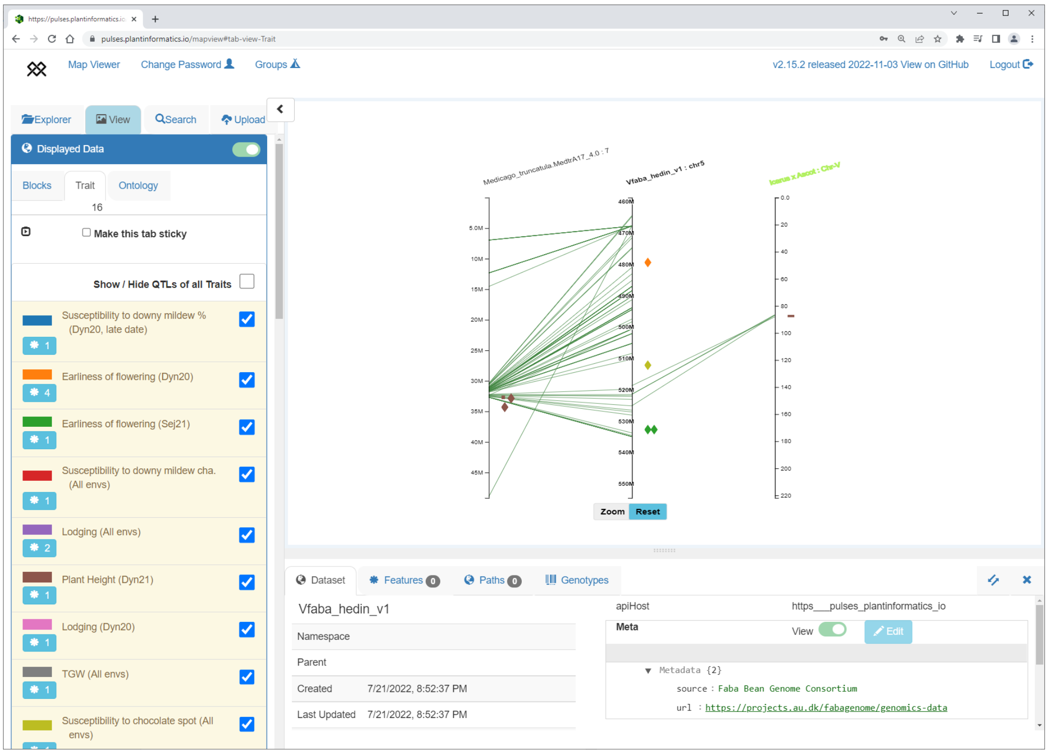
Meta View Edit

▾ Metadata {2}
source : Faba Bean Genome Consortium
url : https://projects.au.dk/fabagenome/genomics-data

The selected region will be indicated by a grey rectangle and underlying features shown in red.

6. Zoom on selected region

Click the Zoom button to zoom the axis to the selected region.



16

☐ Make this tab sticky

Show / Hide QTLs of all Traits ☐

- Susceptibility to downy mildew % (Dyn20, late date) 1 ☑
- Earliness of flowering (Dyn20) 4 ☑
- Earliness of flowering (Sej21) 1 ☑
- Susceptibility to downy mildew cha. (All envs) 1 ☑
- Lodging (All envs) 2 ☑
- Plant Height (Dyn21) 1 ☑
- Lodging (Dyn20) 1 ☑
- TGW (All envs) 1 ☑
- Susceptibility to chocolate spot (All envs) ☑

Vfaba_hedin_v1

Namespace	
Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM

apiHost https___pulses_plantinformatics_io

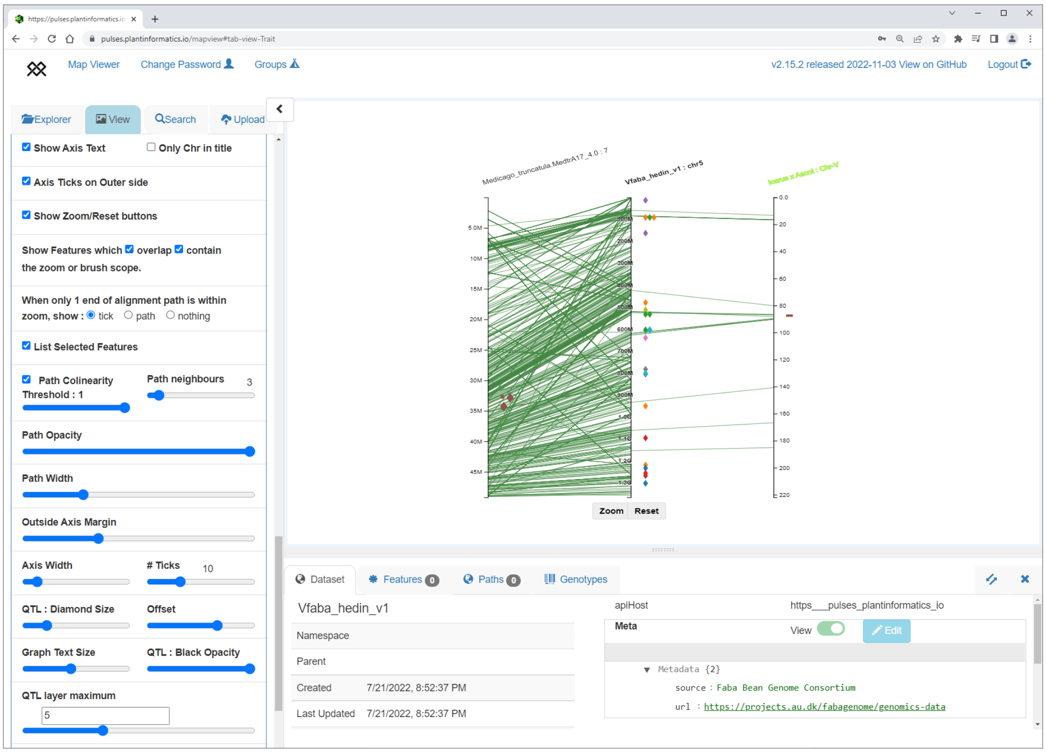
Meta View Edit

▾ Metadata {2}
source : Faba Bean Genome Consortium
url : https://projects.au.dk/fabagenome/genomics-data

Reset the zoom by clicking the Reset button.

7. Tweak visualisation options

In the View tab of the left panel, scroll down to access visualisation options.



☑ Show Axis Text ☐ Only Chr in title

☑ Axis Ticks on Outer side

☑ Show Zoom/Reset buttons

Show Features which ☑ overlap ☑ contain the zoom or brush scope.

When only 1 end of alignment path is within zoom, show : ● tick ○ path ○ nothing

☑ List Selected Features

☑ Path Colinearity Threshold : 1

Path neighbours 3

Path Opacity

Path Width

Outside Axis Margin

Axis Width

Ticks 10

QTL : Diamond Size

Offset

Graph Text Size

QTL : Black Opacity

QTL layer maximum 5

Dataset | Features 0 | Paths 0 | Genotypes

Vfaba_hedin_v1

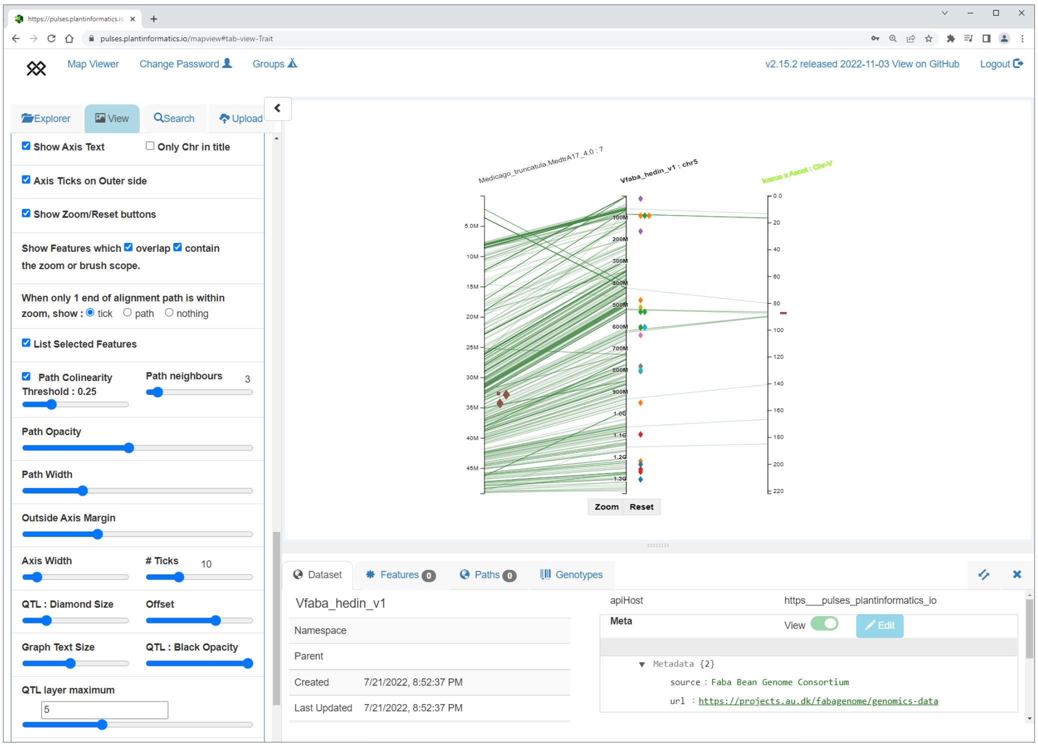
Namespace	
Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM

apiHost https___pulses_plantinformatics_io

Meta View Edit

```
▼ Metadata {2}
    source : Faba Bean Genome Consortium
    url : https://projects.au.dk/fabagenome/genomics-data
```

Reduce Path Opacity to reduce the opacity of the paths and the Path Collinearity Threshold to remove some of the cross-over paths.



☑ Show Axis Text ☐ Only Chr in title

☑ Axis Ticks on Outer side

☑ Show Zoom/Reset buttons

Show Features which ☑ overlap ☑ contain the zoom or brush scope.

When only 1 end of alignment path is within zoom, show : ● tick ○ path ○ nothing

☑ List Selected Features

☑ Path Colinearity Threshold : 0.25

Path neighbours 3

Path Opacity

Path Width

Outside Axis Margin

Axis Width

Ticks 10

QTL : Diamond Size

Offset

Graph Text Size

QTL : Black Opacity

QTL layer maximum 5

Dataset | Features 0 | Paths 0 | Genotypes

Vfaba_hedin_v1

Namespace	
Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM

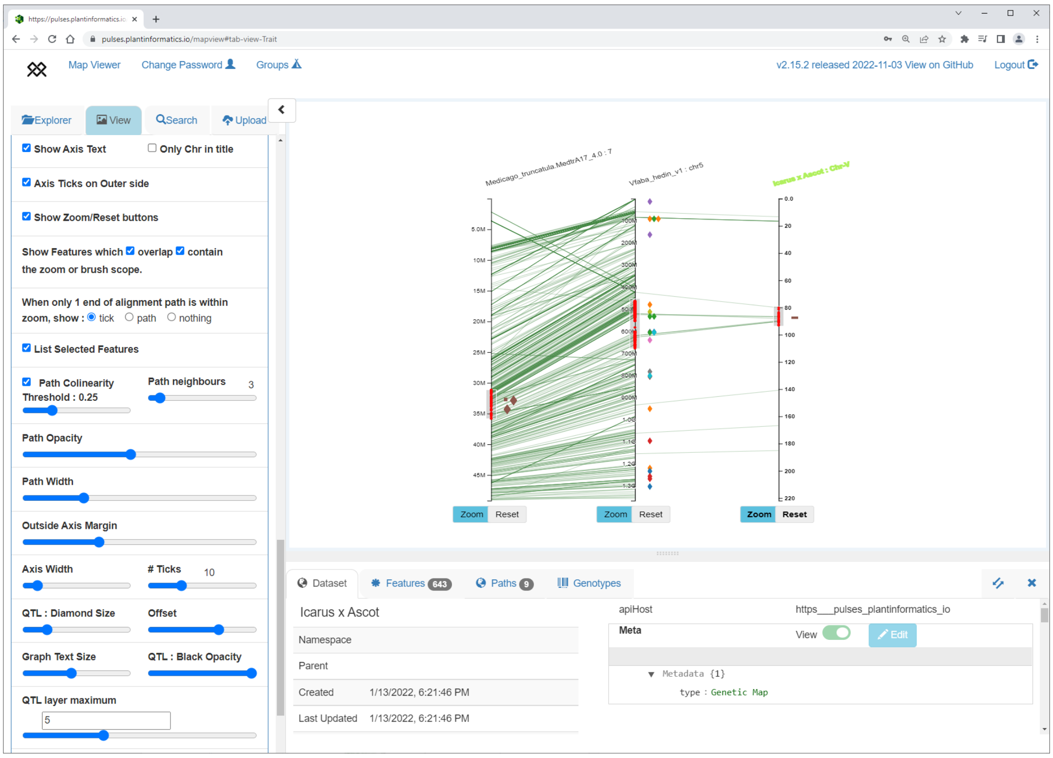
apiHost https___pulses_plantinformatics_io

Meta View Edit

```
▼ Metadata {2}
    source : Faba Bean Genome Consortium
    url : https://projects.au.dk/fabagenome/genomics-data
```

8. Zoom in to regions of interest

Using the brush operation described in step 5 above, select the regions of interest around the QTLs loaded.



☑ Show Axis Text ☐ Only Chr in title

☑ Axis Ticks on Outer side

☑ Show Zoom/Reset buttons

Show Features which ☑ overlap ☑ contain the zoom or brush scope.

When only 1 end of alignment path is within zoom, show : ● tick ○ path ○ nothing

☑ List Selected Features

☑ Path Colinearity Threshold : 0.25

Path neighbours 3

Path Opacity

Path Width

Outside Axis Margin

Axis Width

Ticks 10

QTL : Diamond Size

Offset

Graph Text Size

QTL : Black Opacity

QTL layer maximum 5

Icarus x Ascot

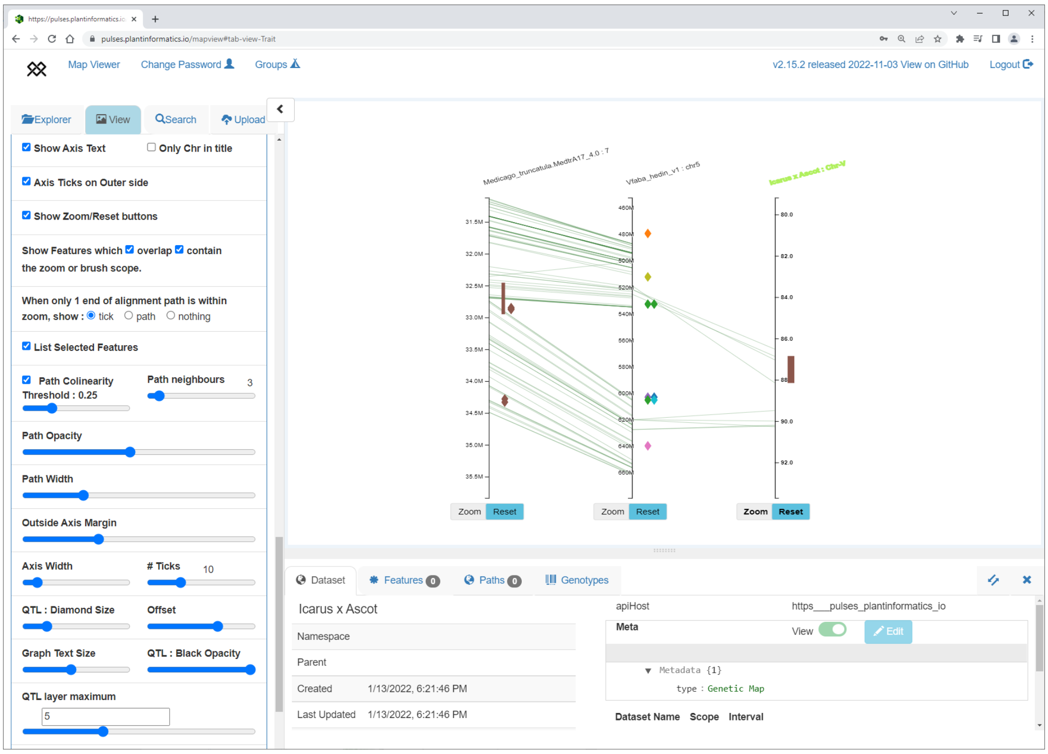
Namespace	
Parent	
Created	1/13/2022, 6:21:46 PM
Last Updated	1/13/2022, 6:21:46 PM

apiHost https___pulses_plantinformatics_io

Meta View Edit

▼ Metadata {1}
type : Genetic Map

Zoom in to the brushed regions.



☑ Show Axis Text ☐ Only Chr in title

☑ Axis Ticks on Outer side

☑ Show Zoom/Reset buttons

Show Features which ☑ overlap ☑ contain the zoom or brush scope.

When only 1 end of alignment path is within zoom, show : ● tick ○ path ○ nothing

☑ List Selected Features

☑ Path Colinearity Threshold : 0.25

Path neighbours 3

Path Opacity

Path Width

Outside Axis Margin

Axis Width

Ticks 10

QTL : Diamond Size

Offset

Graph Text Size

QTL : Black Opacity

QTL layer maximum 5

Icarus x Ascot

Namespace	
Parent	
Created	1/13/2022, 6:21:46 PM
Last Updated	1/13/2022, 6:21:46 PM

apiHost https___pulses_plantinformatics_io

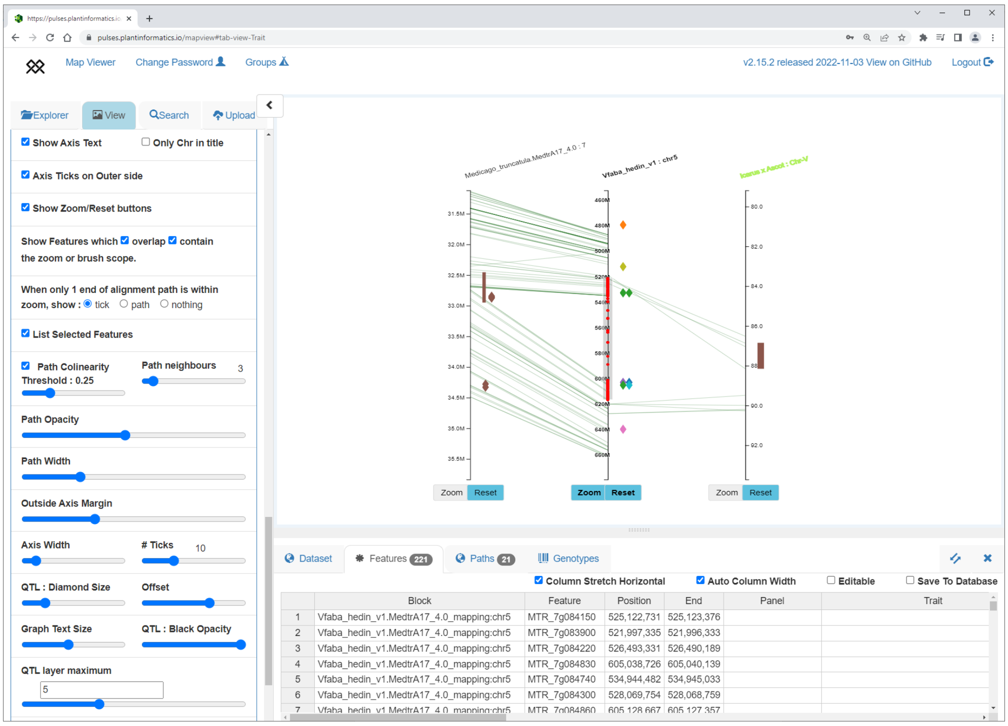
Meta View Edit

▼ Metadata {1}
type : Genetic Map

Dataset Name Scope Interval

9. Visualise features in a table

Once a region of interest has been brushed, click the Features tab in the bottom panel.



☑ Show Axis Text ☐ Only Chr in title

☑ Axis Ticks on Outer side

☑ Show Zoom/Reset buttons

Show Features which ☑ overlap ☑ contain the zoom or brush scope.

When only 1 end of alignment path is within zoom, show : ● tick ○ path ○ nothing

☑ List Selected Features

☑ Path Colinearity Threshold : 0.25

Path neighbours 3

Path Opacity

Path Width

Outside Axis Margin

Axis Width

Ticks 10

QTL : Diamond Size

Offset

Graph Text Size

QTL : Black Opacity

QTL layer maximum 5

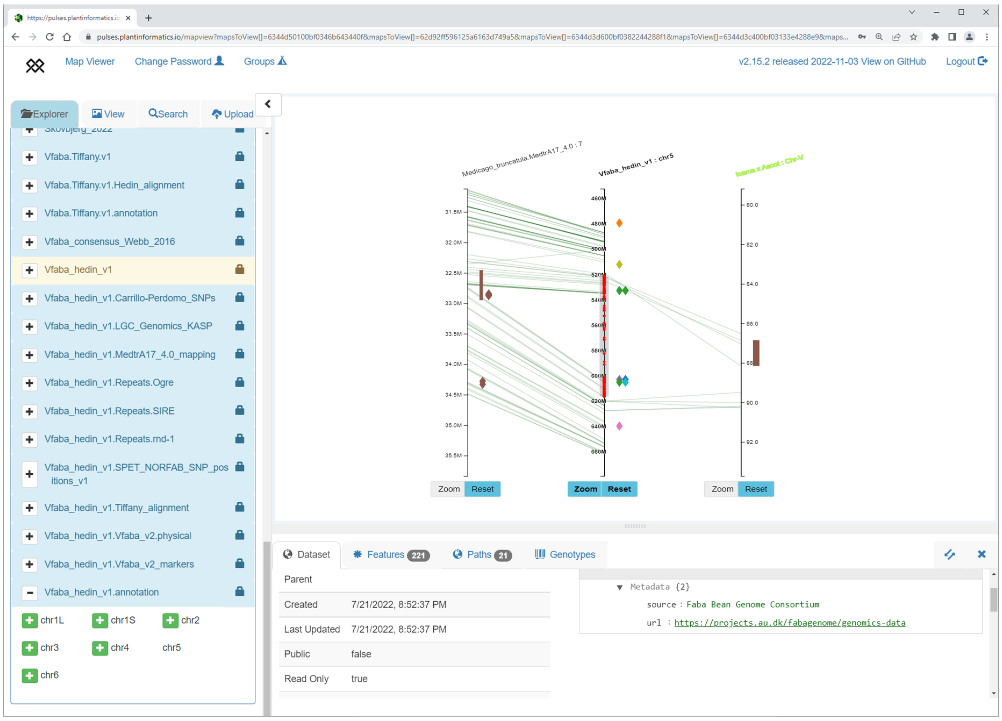
☑ Column Stretch Horizontal ☑ Auto Column Width ☐ Editable ☐ Save To Database

	Block	Feature	Position	End	Panel	Trait
1	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084150	525,122,731	525,123,376		
2	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g083900	521,997,335	521,996,333		
3	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084220	526,493,331	526,490,189		
4	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084830	605,038,726	605,040,139		
5	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084740	534,944,482	534,945,033		
6	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084300	528,069,754	528,068,759		
7	Vfaba_hedin_v1.MedtrA17_4.0_mapping:chr5	MTR_7g084860	605,128,667	605,127,357		

The displayed table shows all features in the brushed region (based on the datasets loaded in step 2 above).

10. Explore candidate genes in brushed region

Click the Explorer tab on the left panel and add the dataset Vfaba_hedin_v1.annotation – chr5.

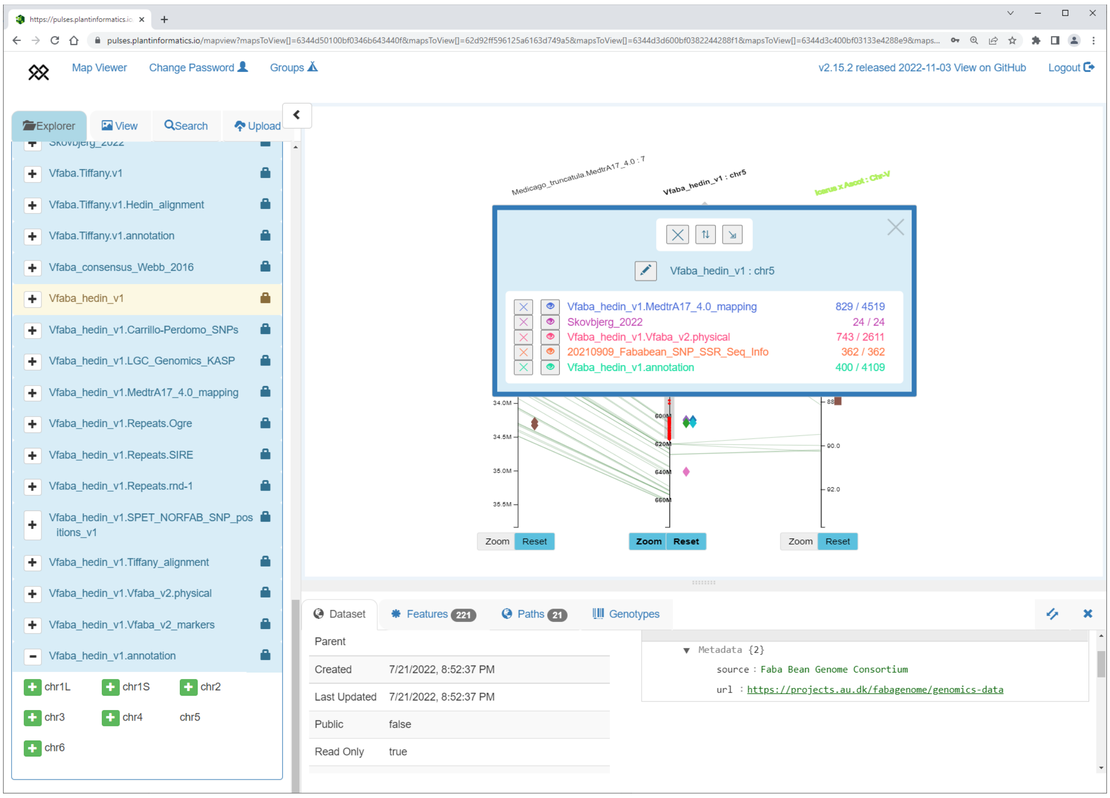


- Skovbjerg_2022
- Vfaba.Tiffany.v1
- Vfaba.Tiffany.v1.Hedin_alignment
- Vfaba.Tiffany.v1.annotation
- Vfaba_consensus_Webb_2016
- Vfaba_hedin_v1
- Vfaba_hedin_v1.Carrillo-Perdomo_SNPs
- Vfaba_hedin_v1.LGC_Genomics_KASP
- Vfaba_hedin_v1.MedtrA17_4.0_mapping
- Vfaba_hedin_v1.Repeats.Ogre
- Vfaba_hedin_v1.Repeats.SIRE
- Vfaba_hedin_v1.Repeats.md-1
- Vfaba_hedin_v1.SPET_NORFAB_SNP_positions_v1
- Vfaba_hedin_v1.Tiffany_alignment
- Vfaba_hedin_v1.Vfaba_v2.physical
- Vfaba_hedin_v1.Vfaba_v2_markers
- Vfaba_hedin_v1.annotation
  - chr1L
  - chr1S
  - chr2
  - chr3
  - chr4
  - chr5
  - chr6

Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM
Public	false
Read Only	true

```
▼ Metadata {2}
    source : Faba Bean Genome Consortium
    url : https://projects.au.dk/fabagenome/genomics-data
```

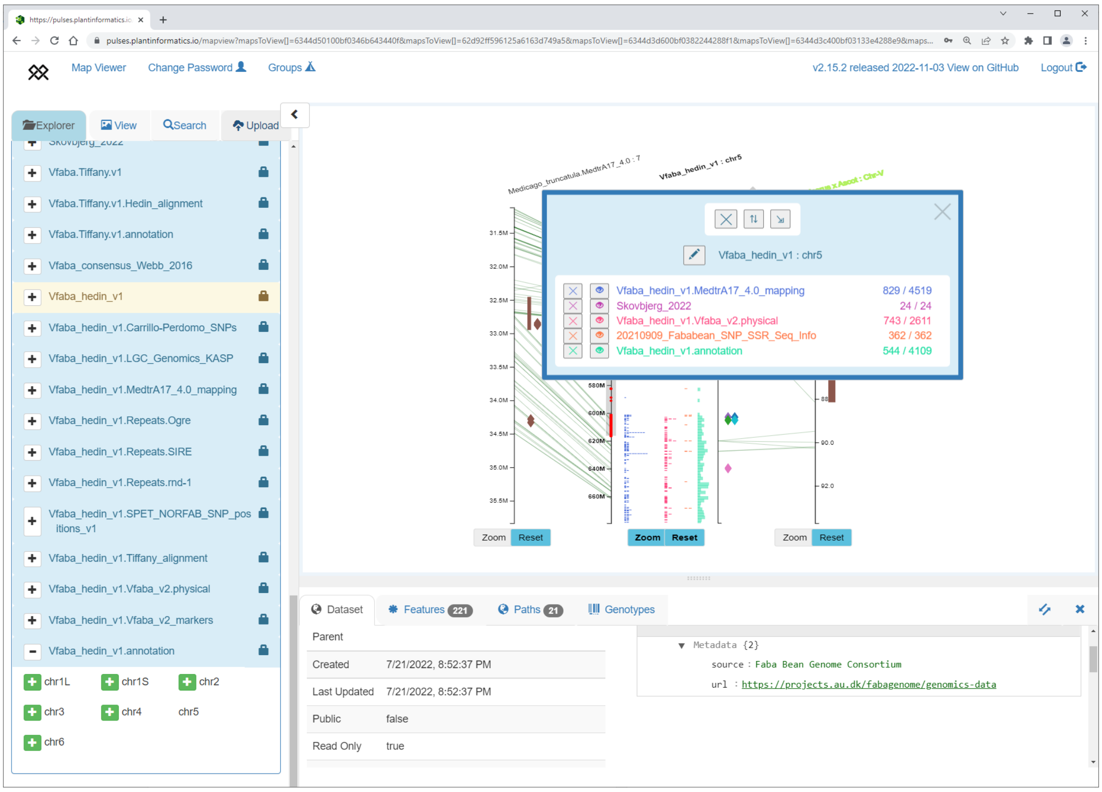
Click on the **Vfaba_hedin_v1 : chr5** text at the top of the axis to open the axis menu.



Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM
Public	false
Read Only	true

```
▼ Metadata {2}
    source : Faba Bean Genome Consortium
    url : https://projects.au.dk/fabagenome/genomics-data
```

Click the icon with arrow pointing to the bottom right to split the axis.

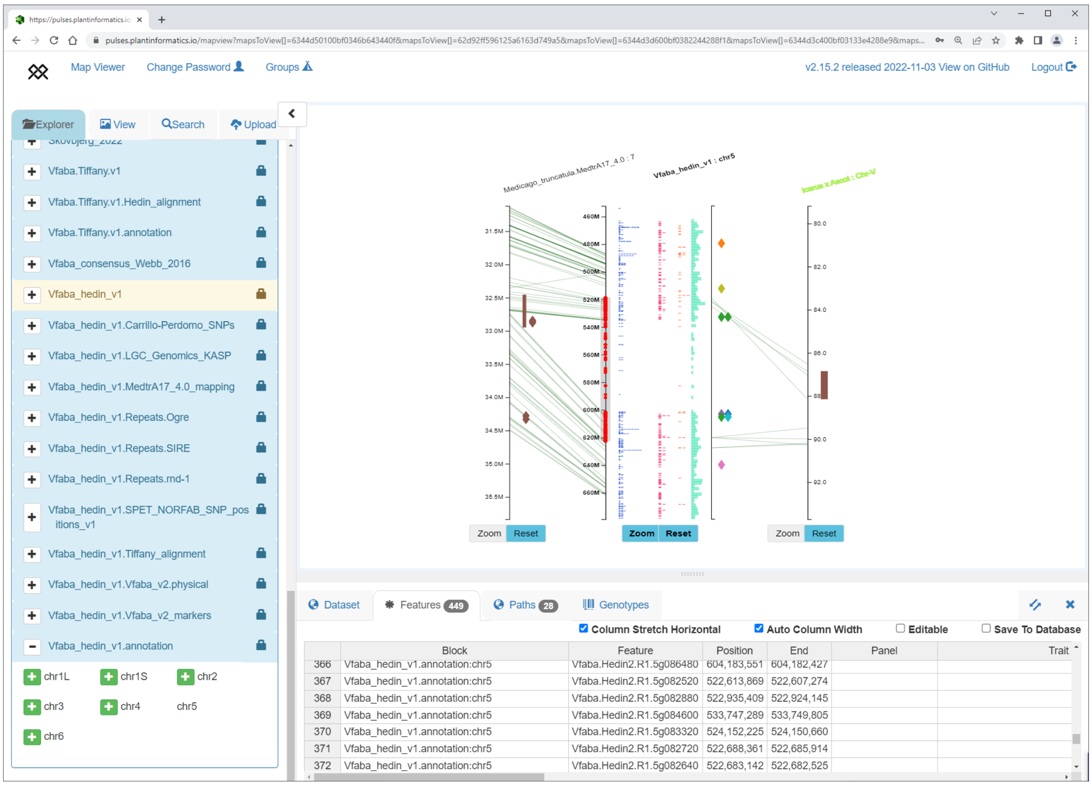


Parent	
Created	7/21/2022, 8:52:37 PM
Last Updated	7/21/2022, 8:52:37 PM
Public	false
Read Only	true

```
▼ Metadata {2}
    source : Faba Bean Genome Consortium
    url : https://projects.au.dk/fabagenome/genomics-data
```

The split axis now displays the loaded datasets as individual features, or histograms if too many to draw. Zooming in will progressively re-draw the features.

Click the cross in the top right of the axis menu to close it. Now brush a region of interest and explore the Features table by clicking the Features tab in the bottom panel.



☑ Column Stretch Horizontal ☑ Auto Column Width ☐ Editable ☐ Save To Database

	Block	Feature	Position	End	Panel	Trait
366	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g086480	604,183,551	604,182,427		
367	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g082520	522,613,869	522,607,274		
368	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g082880	522,935,409	522,924,145		
369	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g084600	533,747,289	533,749,805		
370	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g083320	524,152,225	524,150,660		
371	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g082720	522,688,361	522,685,914		
372	Vfaba_hedin_v1.annotation:chr5	Vfaba.Hedin2.R1.5g082640	522,683,142	522,682,525		