



# **Session 3: Beginning manual curation**

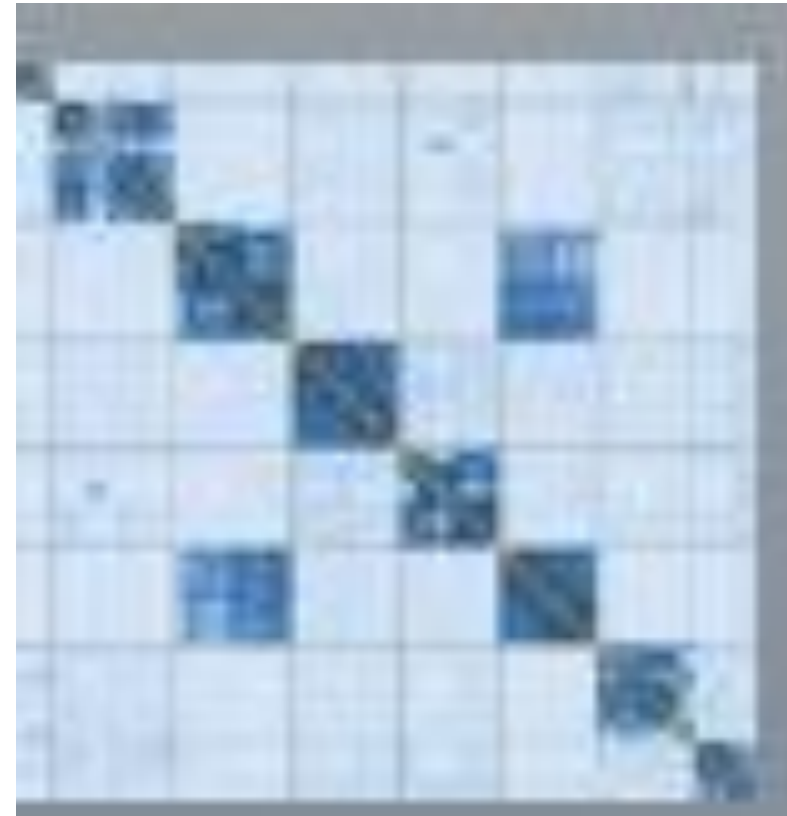
## **Day 2**

Genome Reference Informatics Team (GRIT)  
Wellcome Sanger Institute - Tree of Life

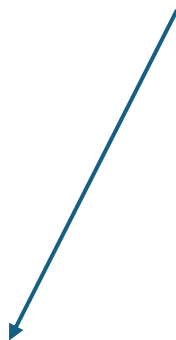


# Overview

- **Analysis pipelines**
  - Treeval
  - Curation pretext pipeline
- **Curation tools**
  - Jbrowse
  - Rapid curation workflow (tomorrow)
  - How to produce a curated fasta file
- **How to use PretextView**



# TreeVal as an aid for curation



**Jbrowse**

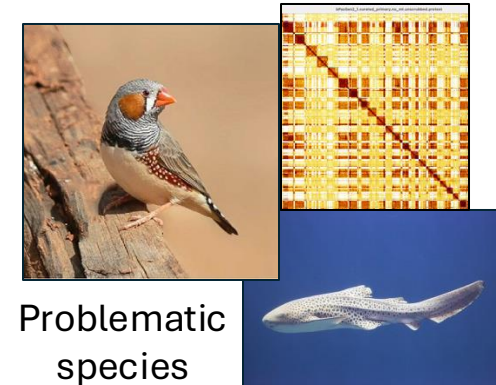
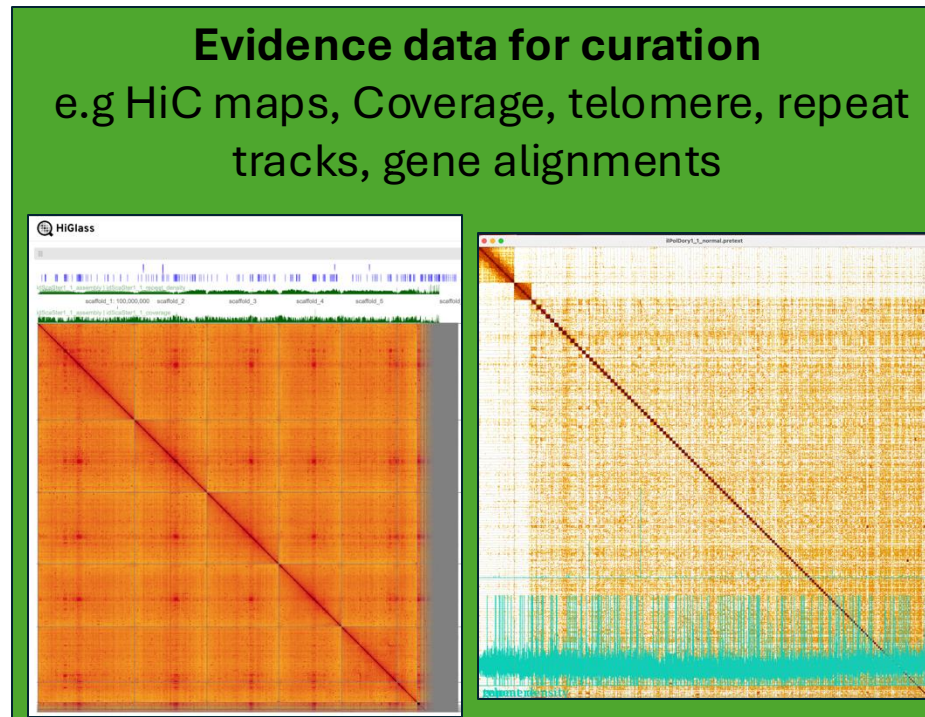
# TreeVal Browser

- All projects coming into the curation team now go through the TreeVal Pipeline ([github.com/sanger-tol/treeval](https://github.com/sanger-tol/treeval))

All draft assemblies



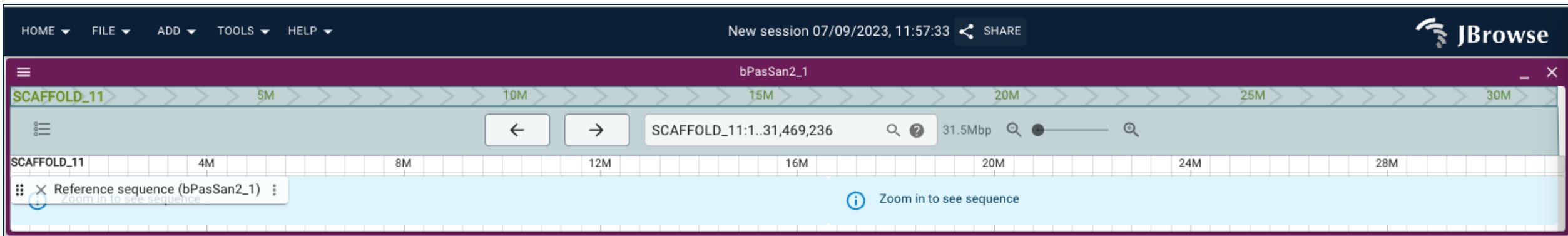
Might not be enough for curation



**TreeVal  
Browser**

In depth  
information is  
provided

# TreeVal Browser



## Why Jbrowse?

- Jbrowse provides the perfect platform for visualisation of assemblies:
- Simple to use, web-based, lightweight, interactive and scalable
- It's an extensible platform that utilizes multiple data types in a variety of genomic data formats such as FASTA, VCF, BAM, BED/BIGBED, HIC, CRAM, PAF and GFF3
- Highly customisable

# How to start using TreeVal (Jbrowse)?

<http://jbrowse.tol.sanger.ac.uk>



Type your TOLID here

TreeVal

ToLID	jBrowse	
rLacAgi1_1	Available	<a href="#">View</a>
ilColFlav1_1	Available	<a href="#">View</a>
ilLepSina1_1	Available	<a href="#">View</a>
rLacAgi1_2	Available	<a href="#">View</a>
rThaEle1_1	Available	<a href="#">View</a>
sScyCan1_1	Available	<a href="#">View</a>
icDorPara1_1	Available	<a href="#">View</a>
ilArgGoed1_1	Available	<a href="#">View</a>
nxOscSpes1_2	Available	<a href="#">View</a>
nxAuaSpee2_1	Available	<a href="#">View</a>

Showing 1 to 10 of 396 rows 10 rows per page

< 1 2 3 4 5 ... 40 >

TreeVal is developed within the [Tree of Life Programme](#) at the [Wellcome Sanger Institute](#)

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# How to start using TreeVal?



## TreeVal

ToLID	jBrowse	
<div>bmerAlb1_1</div>		
bMerAlb1_1	Available	<a href="#">View</a>

Showing 1 to 1 of 1 rows



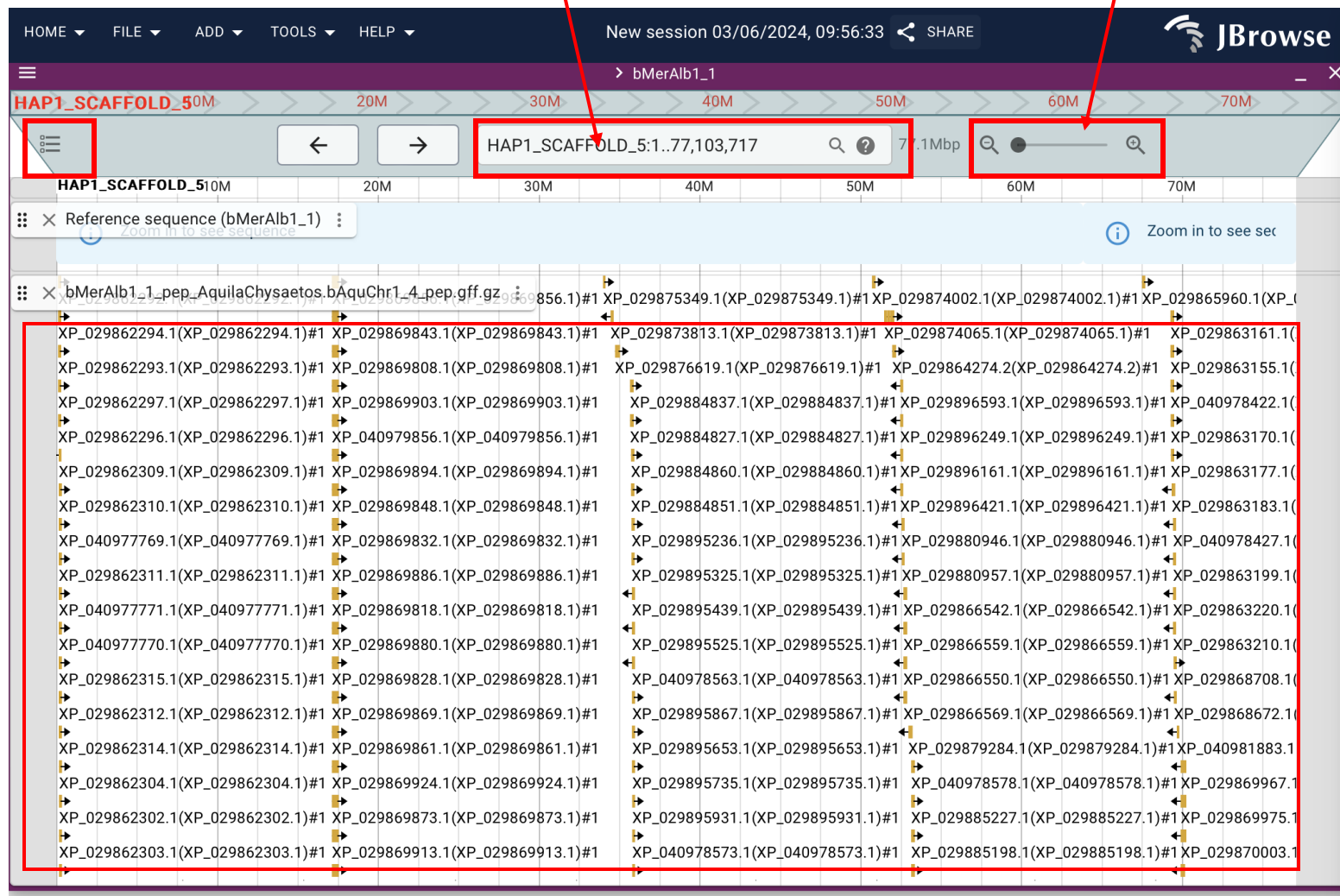
# How to start using TreeVal?



Click to see available tracks

Click or type to select scaffold

Click to zoom in/out



Available tracks

Filter tracks

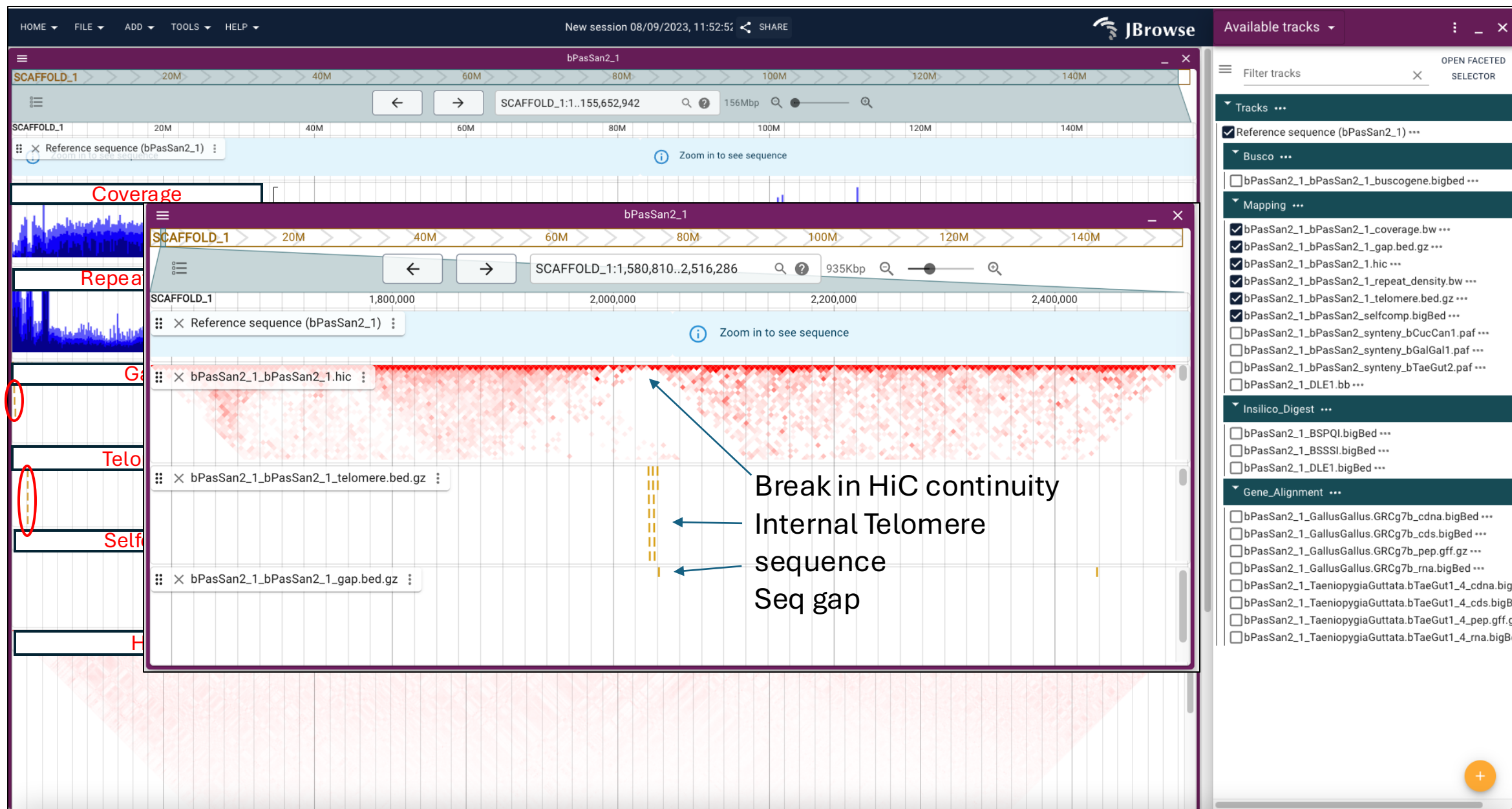
Tracks

- ☒ Reference sequence (bMerAlb1\_1) ...
- ☐ Gene\_Alignment ...
- ☐ bMerAlb1\_1\_AquilaChysaetos.bAquChr1\_4\_cds.bigBed ...
- ☐ bMerAlb1\_1\_AquilaChysaetos.bAquChr1\_4\_rna.bigBed ...
- ☒ bMerAlb1\_1\_pep\_AquilaChysaetos.bAquChr1\_4\_pep.gff.gz ...
- ☐ bMerAlb1\_1-TaeniopygiaGuttata.TaeGut3\_2\_4\_cdna.bigBed ...
- ☐ Busco ...
- ☐ bMerAlb1\_1\_bMerAlb1\_1\_buscogene.bigBed ...
- ☐ Mapping ...
- ☐ bMerAlb1\_1\_bMerAlb1\_1\_coverage\_kmer.bigWig ...
- ☐ bMerAlb1\_1\_bMerAlb1\_1\_coverage\_normal.bigWig ...
- ☐ bMerAlb1\_1\_bMerAlb1\_1\_selfcomp.bigBed ...
- ☐ bMerAlb1\_1\_gap\_bMerAlb1\_1.bed.gz ...
- ☐ bMerAlb1\_1\_repden\_bMerAlb1\_1.bed.gz ...
- ☐ bMerAlb1\_1\_telo\_bMerAlb1\_1.bed.gz ...
- ☐ Insilico\_Digest ...
- ☐ bMerAlb1\_1\_BSPQI.bigBed ...
- ☐ bMerAlb1\_1\_BSSI.bigBed ...
- ☐ bMerAlb1\_1\_DLE1.bigBed ...

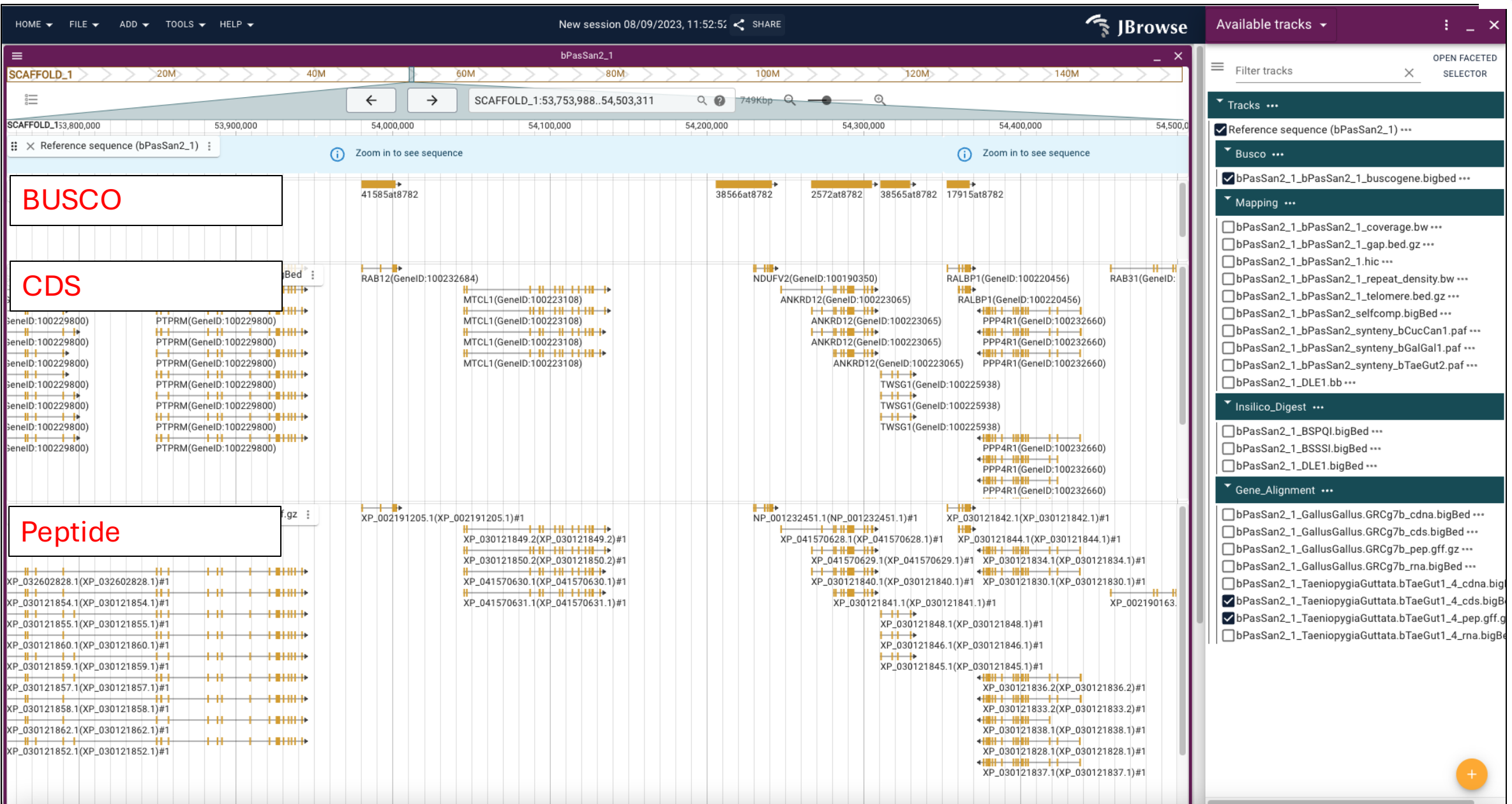
Proteins in  
the  
alignment



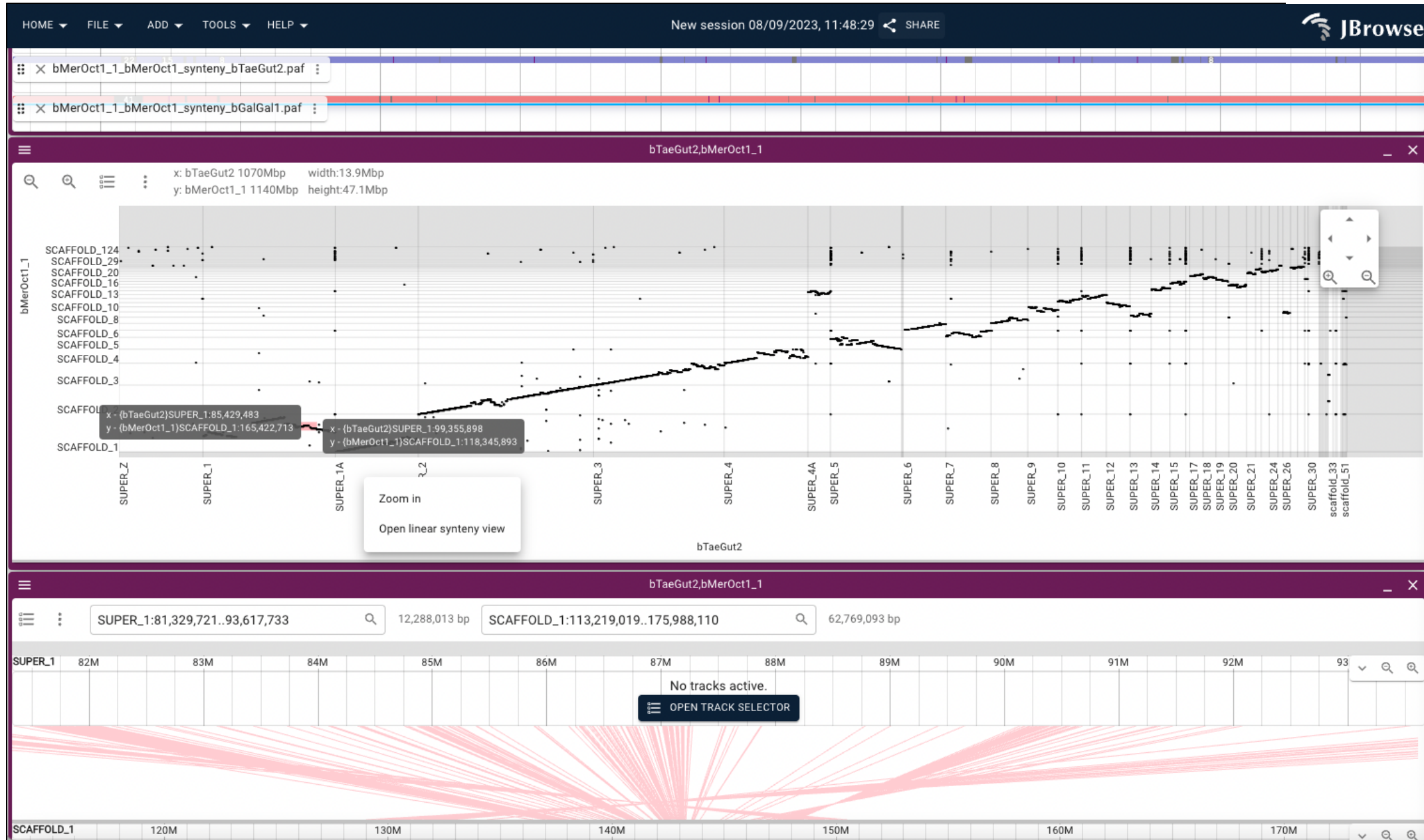
# Which data types do we align to our assemblies?



# Gene alignment data



# Synteny data



# How to use PretextView



Download PretextView from: <https://github.com/sanger-tol/PretextView>

**PretextView** Public

Watch 5 Fork 7 Star 28

master 1 Branch 21 Tags

Go to file Add file Code

**additive3** Update AGPCorrect 0cc4ed3 · last month 100 Commits

include	0.2.1-dev	3 years ago
libdeflate @ 448e3f3	Switching to meson...	3 years ago
subprojects	Switching to meson...	3 years ago
.gitmodules	Switching to meson...	3 years ago
AGPCorrect	Update AGPCorrect	last month
ColorMapData.cpp	0.2.3-dev	3 years ago
LICENCE.txt	0.2.3-dev	3 years ago
PretextView.cpp	Edit Mode -> pick up whole sequence option	2 years ago
PretextView.rc	add windows icon	4 years ago
README.md	Update README.md	3 years ago
Resources.cpp	0.2.3-dev	3 years ago
TextureLoadQueue.cpp	0.2.3-dev	3 years ago
glad.c	init	5 years ago
icon.icns	switching to meson...	3 years ago
install	MACOSX_DEPLOYMENT_TARGET	2 years ago
install.bat	Github actions	3 years ago
make_macos_app_plist.sh	switching to meson...	3 years ago
meson.build	0.2.5	2 years ago
pretextView_icon.ico	add windows icon	4 years ago

**About**

OpenGL Powered PretextView Contact Map Viewer

Readme View license Code of conduct Activity Custom properties 28 stars 5 watching 7 forks Report repository

**Releases** 21

**PretextView 0.2.5** Latest on Feb 3, 2022 + 20 releases

**Packages**

No packages published

**Contributors** 2

EdHarry Ed Harry additive3

**Languages**

C 51.7% C++ 48.2% Other 0.1%



**Assets** 5

- PretextView\_Linux-x86-64.zip
- PretextView\_MacOS-x86-64.zip
- PretextView\_Windows-x86-64.zip
- Source code (zip)
- Source code (tar.gz)

# How to use PretextView



- Click 'Load Map' and open a map
- Keyboard Shortcuts
- **Press 'U' to open menu**
- **Press 'E' to enter the Edit mode and make edits**
  - Press 'Q' to undo an edit
  - Press 'W' to redo an edit
  - Click middle button to flip (invert) a scaffold
- **Press 'S' to enter the Scaffold mode: Paint scaffolds blocks as chroms**
  - Click middle button to delete painting
  - Press 'A' to paint a block of scaffolds at once
  - Press Shift + 'D' to delete all the painting in the map



# How to use PretextView



- **Press ‘M’ to enter Metadata Tag mode:** add tags such as haplotigs, unloc, HAP1, HAP2, X, Z, Contaminant...
  - Use arrow keys in your keyboard to select the active tag
  - Press Shift + ‘D’ to delete all tags in your map
- Press ‘I’ to show ID bars: delimit and show orientation of the scaffolds
- Press ‘G’ to switch the grids on and off
- Press ‘B’ to show scale bars at the top
- Press ‘T’ to switch the tool tip on and off: show coordinates in the map and info about active tracks
  - Arrow keys left/right: adjust contrast
  - Arrow keys up/down: change color scheme in the map
- **Press ‘W’ to enter Waypoint edit mode: mark specific regions**