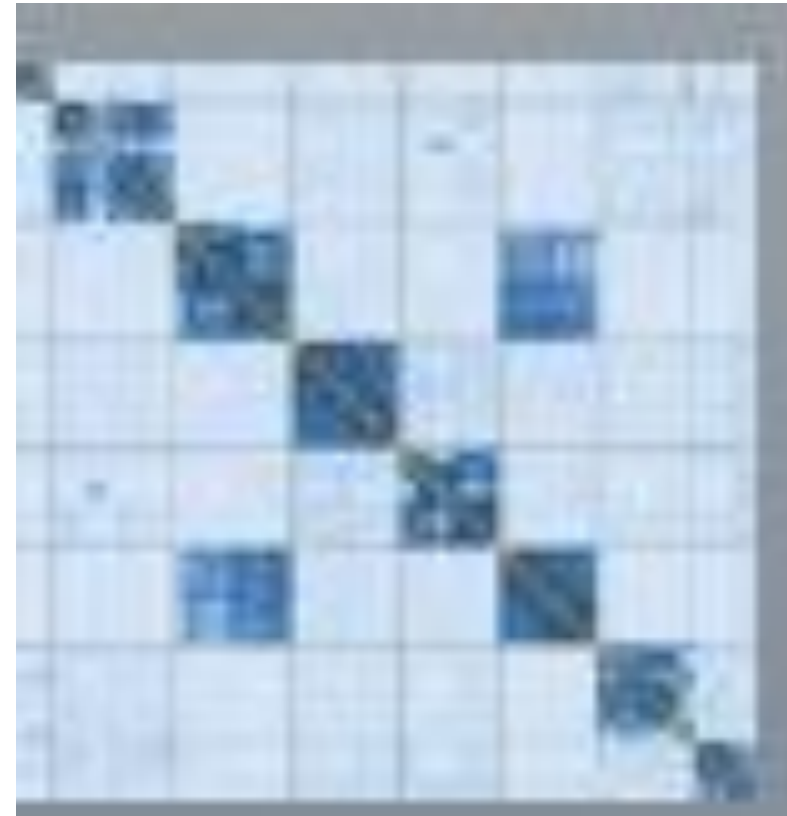# Session 3: Beginning manual curation
Day 2

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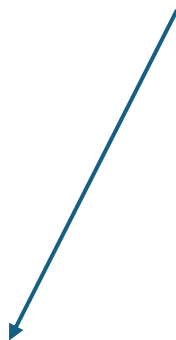Wellcome Sanger Institute - Tree of Life

Overview

- **Analysis pipelines**
- Treeval
- Curation pretext pipeline

- **Curation tools**
  - Jbrowse
  - Rapid curation workflow (tomorrow)
  - How to produce a curated fasta file

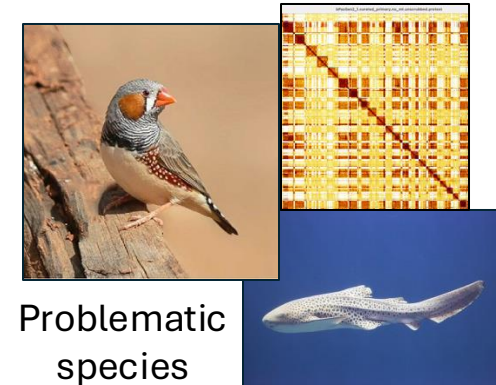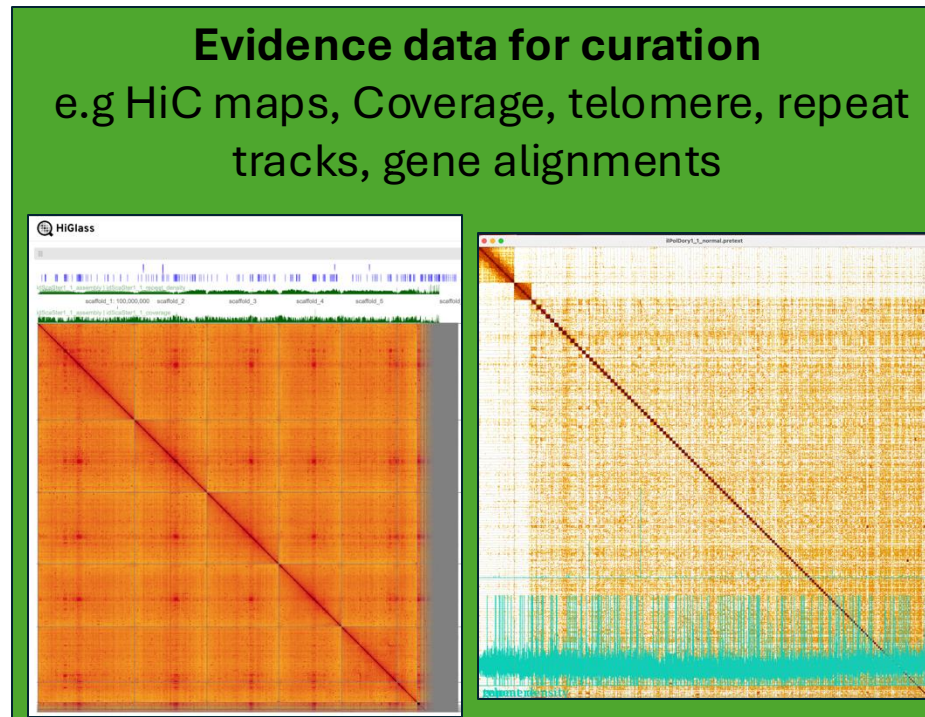- **How to use PretextView**

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)**

All draft assemblies

Might not be enough for curation

Evidence data for curation
e.g HiC maps, Coverage, telomere, repeat tracks, gene alignments

Problematic species

TreeVal Browser

In depth information is provided

By Jo Collins

TreeVal Browser
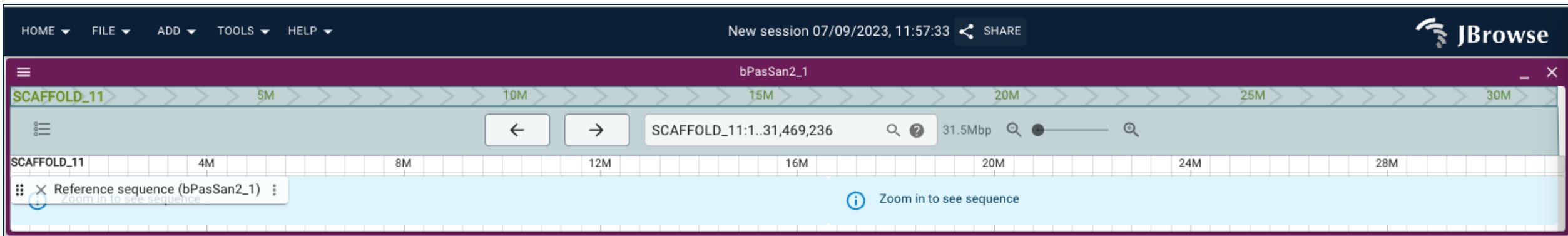
Why Jbrowse?

- 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

https://jbrowse.org/jb2/

How to start using TreeVal (Jbrowse)?

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

Type your TOLID here

TreeVal

ToLID	jBrowse	
rLacAgi1_1	Available	View
ilColFlav1_1	Available	View
ilLepSina1_1	Available	View
rLacAgi1_2	Available	View
rThaEle1_1	Available	View
sScyCan1_1	Available	View
icDorPara1_1	Available	View
ilArgGoed1_1	Available	View
nxOscSpes1_2	Available	View
nxAuaSpee2_1	Available	View

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
Copyright © 2020-2022 Genome Research Limited (reg no. 2742969) is a charity registered in England with number 1021457.
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How to start using TreeVal?

TreeVal

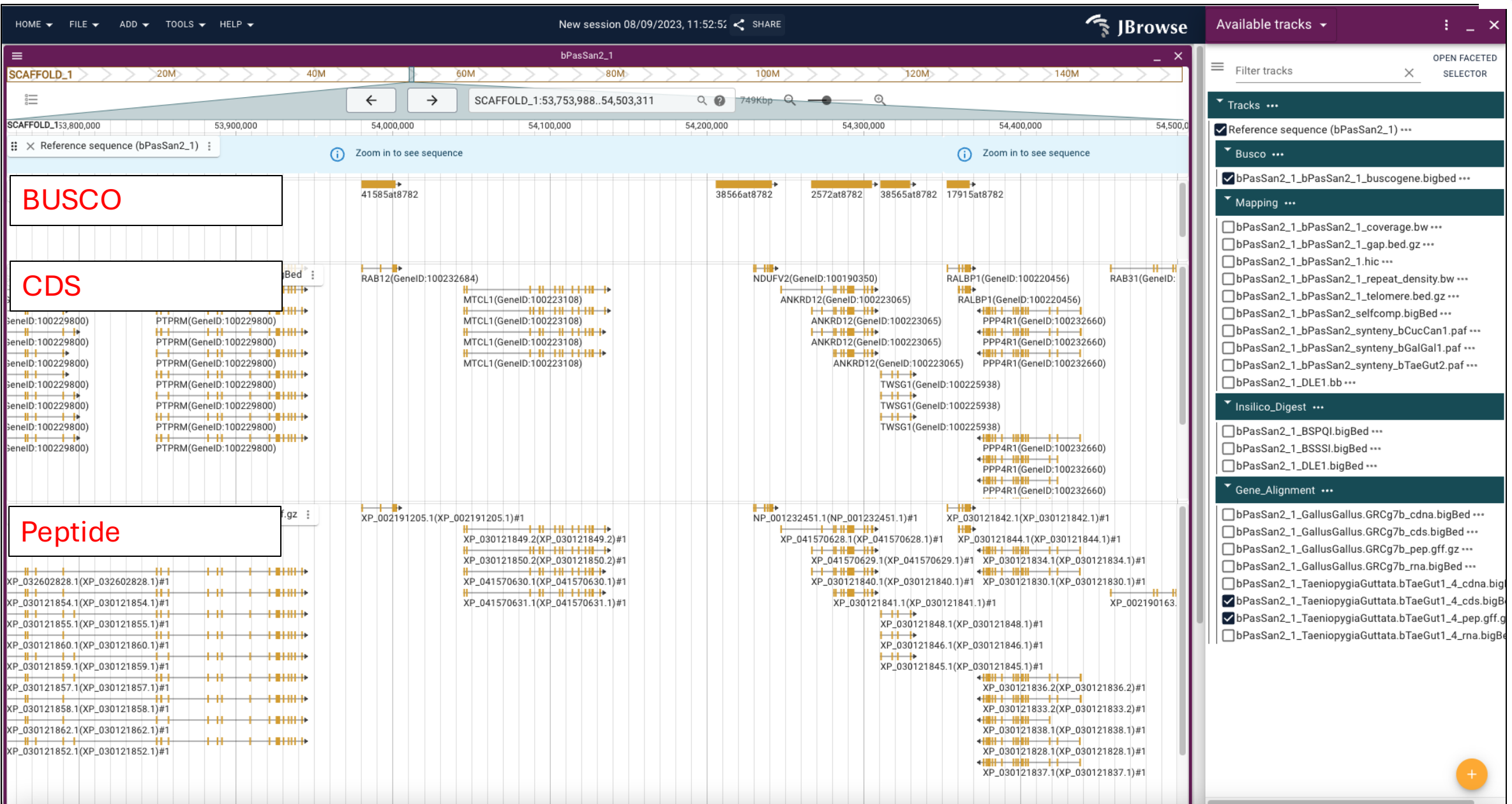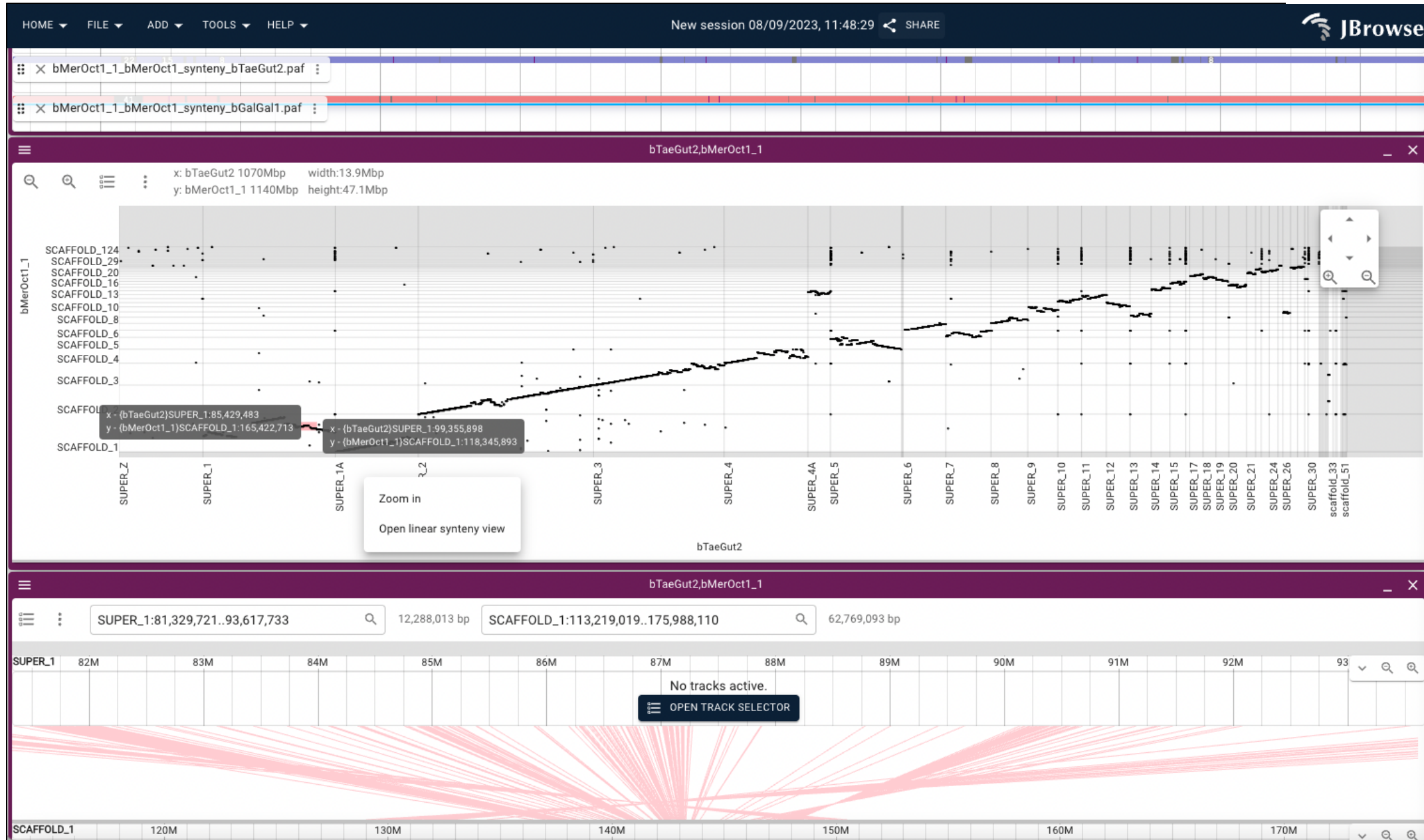| ToLID	jBrowse	
bmerAlb1_1 ⊗	⌄	
bMerAlb1_1	Available	View

Showing 1 to 1 of 1 rows

How to start using TreeVal?

Which data types do we align to our assemblies?
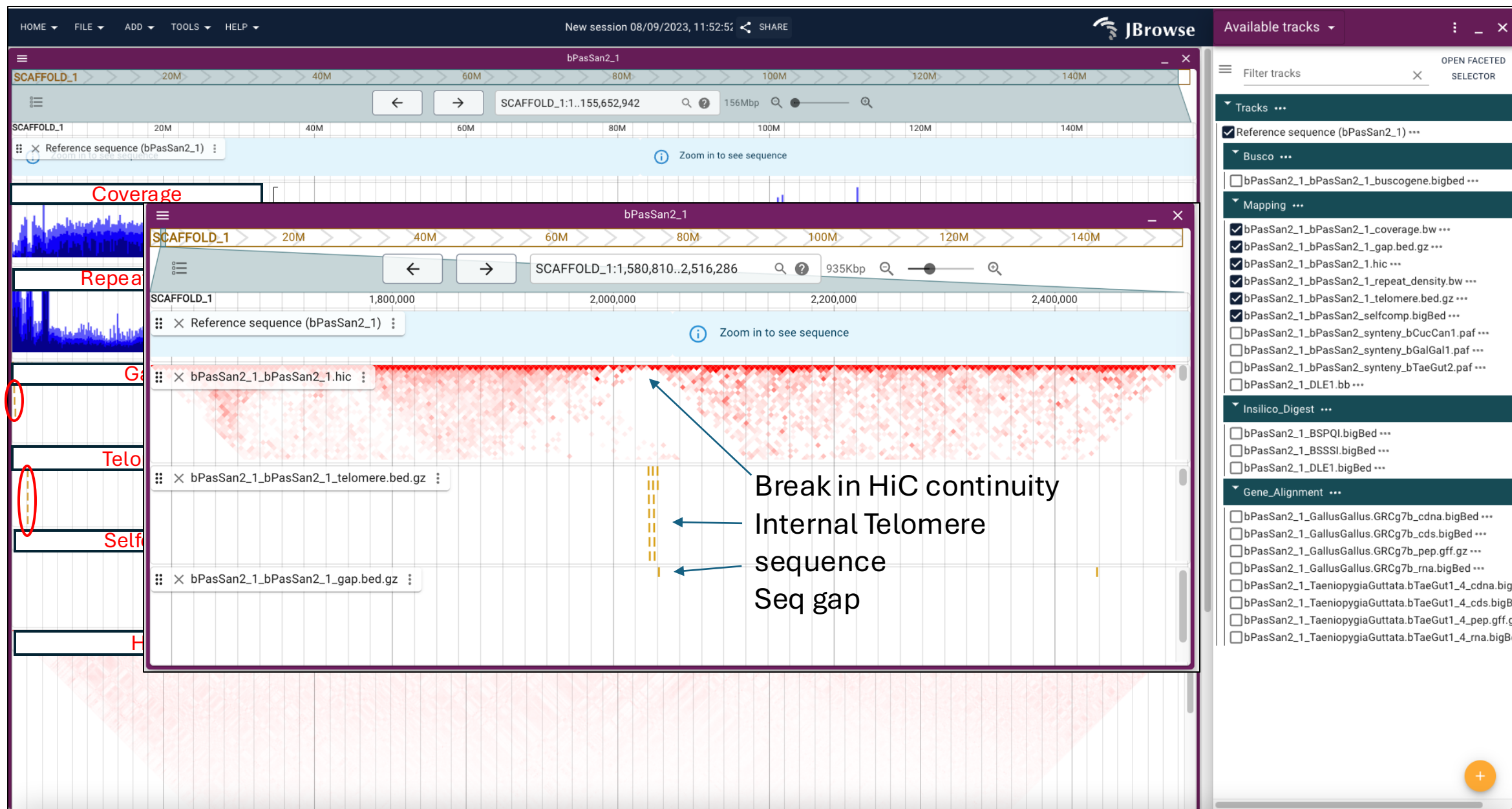
Gene alignment data

Synteny data

How to use PretextView

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

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**