

The Rat Genome Database resources for de novo rat strain assemblies

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Complex Trait Community and Rat Genomics meeting

September 29, 2022

RGD is a cross-species knowledgebase providing data linking disease to the genome

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RGD virtual office hours are now by appointment.
When: At your convenience! [Contact us](#) to schedule a time.
Who: Anyone is welcome!

Other Species Portals

Search

Genes Strains Ontology & Annotation Ontomate (Literature) QTL Orthologs Genomic Region All...

Analysis and Visualization

JBrowse
Genome Browser

Variant Visualizer

	C	A	T	
ACI/N (KNAW)	A	C	A	T
BBDP/WorN (ICL)	G	C	G	T
ACI/EurMcwi (ICL)	A	C	A	T
BN-Lx/Cub (ICL)	G	A	G	C

Genome Information

base pairs	3,044,300,753
Total Sequence Length (bp)	2,870,184,193
Total Assembly Gap Length (bp)	140,198,789
Gaps Between	440

Tweets from @ratgenome

Rat Genome ... @ratg... · Sep 27

@ratgenome PhenoMiner is a tool for ontology-based storage and mining of quantitative phenotype data for rat. Check out the video tutorial on PhenoMiner to query and visualize this data between studies and across rat strains - tinyurl.com/yep48hkj

OLGA **Disease Portals** **Phenotypes and Models**

RGD is committed to the integration of the full spectrum of genomic data to support research into the underlying causes of human disease.




WGS and de novo assembly resulted in reference-quality assemblies for strains SHR/Utx, SHRSP/BbbUtx and WKY/Bbb

- The SHR and SHRSP strains are models of hypertension and stroke; WKY is a commonly used control strain for hypertension
- The sequencing, performed by Dr. Peter Doris and colleagues, employed long-read technologies (PacBio, HiC and BioNano)
- Long reads facilitated the assembly of highly repetitive regions, e.g., the Y chromosome
 - mRatBN7.2 Y has an assembled length of 18,315,841
 - UTH_Rnor_SHR_Utx Y has an assembled length of 32,175,099
 - UTH_Rnor_SHRSP_BbbUtx_1.0 Y has an assembled length of 38,271,881
 - UTH_Rnor_WKY_Bbb_1.0 Y has an assembled length of 31,627,559
- NCBI RefSeq did genome annotation to map genes and transcripts onto the new assemblies but have not performed manual curation

Data for the SHR, SHRSP and WKY strains are available on RGD

- For genes that have been mapped to any or all of these assemblies, positions are available on the gene report pages.


RGD maintains positions for all assemblies and maps on gene pages, including the SHR, SHRSP and WKY assemblies



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Enter Search Term... Advanced Search (OLGA)



molecular Pathway

References

- References - curated
- PubMed References

Genomics

- Comparative Map Data
- Position Markers
- QTLs in Region (mRatBN7.2)
- miRNA Target Status

Expression

- RNA-SEQ Expression

Sequence


- Nucleotide Sequences
- Protein Sequences
- Protein Domains
- Protein Structures
- Transcriptome
- Promoters

Gene: Atp1a3 (ATPase Na⁺/K⁺ transporting subunit alpha 3) Rattus norvegicus


General | Array IDs

Symbol: Atp1a3
Name: ATPase Na⁺/K⁺ transporting subunit alpha 3
RGD ID: 2169
Description: Enables D1 dopamine receptor binding activity and amyloid-beta binding activity. Involved in several processes, including cellular reion transport. Located in several cellular components, including axon; dendritic spine; and myelin sheath. Part of sodium:potassium postsynapse. Is integral component of presynaptic membrane. Human ortholog(s) of this gene implicated in alternating hemiplegia encephalopathy; dystonia 12; and epilepsy. Orthologous to human ATP1A3 (ATPase Na⁺/K⁺ transporting subunit alpha 3); PARTIC receptor agonist and beta-blocker pharmacodynamics pathway; alfentanil pharmacodynamics pathway; INTERACTS WITH 2,3,7,8 acetamide.
Type: protein-coding
RefSeq Status: PROVISIONAL
Previously known as: Atpa1a3; ATPase Na⁺/K⁺ transporting alpha 3 subunit; ATPase, Na⁺/K⁺ transporting, alpha 3 polypeptide; ATPase, Na⁺/K⁺ transport na(+)/K(+)-ATPase alpha-3 subunit; Na⁺/K⁺ -ATPase alpha 3 subunit; NA,K-ATPase alpha subunit 3; sodium pump subunit alpha-3

RGD Orthologs



Alliance Genes



More Info [more info ...](#)

Latest Assembly: mRatBN7.2 - mRatBN7.2 Assembly

Position:

Rat Assembly	Chr	Position (strand)	Source	Genome Browsers		
				JBrowse	NCBI	UCSC Ensembl
mRatBN7.2	1	80,572,790 - 80,601,936 (-)	NCBI	mRatBN7.2	mRatBN7.2	



Data for the SHR, SHRSP and WKY strains are available on RGD

- For genes that have been mapped to any or all of these assemblies, positions are available on the gene report pages.
- The SHR, SHRSP and WKY assemblies are included in RGD's Search by Position tool

Search by position is available for the new assemblies


Search for genes, SSLPs and QTLs by position

Species: Assembly: Chromosome: Start(bp): Stop(bp):

UTH_Rnor_SHR_Utx
UTH_Rnor_SHRSP_BbbUtx_1.0
UTH_Rnor_WKY_Bbb_1.0
Rnor_6.0
Rnor_5.0
RGSC_v3.4
RGSC_v3.1
Celera

Search by position is available for the new assemblies

Search for genes, SSLPs and QTLs by position

Species:	Assembly:	Chromosome:	Start(bp):	Stop(bp):	
Rat	UTH_Rnor_5	1	85900000	90000000	
	<ul style="list-style-type: none">mRatBN7.2UTH_Rnor_SHR_UtxUTH_Rnor_SHRSP_BbbUtx_1.0UTH_Rnor_WKY_Bbb_1.0Rnor_6.0Rnor_5.0RGSC_v3.4RGSC_v3.1Celera				

Search by position is available for the new assemblies

Search for genes


Species:

Rat

Assembly:

- UTH_Rnor_S
- mRatBN7.2
- UTH_Rnor_S
- UTH_Rnor_S
- UTH_Rnor_V
- Rnor_6.0
- Rnor_5.0
- RGSC_v3.4
- RGSC_v3.1
- Celera

Total Objects in the selected region:

Download All Objects Here: 

Genes - 109



QTLs - 0



SSLPs - 0



Genes 



RGD ID	Type	Symbol	Name	Chr	Start	Stop
620951	protein-coding	Arhgef1	Rho guanine nucleotide exchange factor 1	1	85891659	85913491
621002	protein-coding	Rabac1	Rab acceptor 1	1	85956606	85959730
2169	protein-coding	Atp1a3	ATPase Na ⁺ /K ⁺ transporting subunit alpha 3	1	85965362	85994505
2735	protein-coding	Grik5	glutamate ionotropic receptor kainate type subunit 5	1	85998459	86059573
1311420	protein-coding	Zfp574	zinc finger protein 574	1	86064885	86070148
621690	protein-coding	Pou2f2	POU class 2 homeobox 2	1	86079615	86116737
620351	protein-coding	Gsk3a	glycogen synthase kinase 3 alpha	1	86208062	86217908
1311991	protein-coding	Erf	Ets2 repressor factor	1	86222152	86230605
1310706	protein-coding	Cic	capicua transcriptional repressor	1	86246136	86272754

Data for the SHR, SHRSP and WKY strains are available on RGD

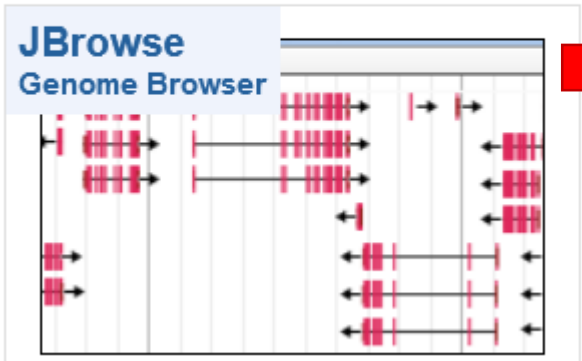
- For genes that have been mapped to any or all of these assemblies, positions are available on the gene report pages.
- The SHR, SHRSP and WKY assemblies are included in RGD's Search by Position tool
- RGD has created JBrowse genome browsers for the SHR, SHRSP and WKY assemblies

RGD has created JBrowse genome browsers for the SHR, SHRSP and WKY assemblies

Position:	Rat Assembly	Chr Position (strand)		Source	Genome Browser
					JBrowse
	mRatBN7.2	1	80,572,790 - 80,601,936 (-)	NCBI	mRatBN7.2
	mRatBN7.2 Ensembl	1	80,572,796 - 80,601,918 (-)	Ensembl	
	UTH_Rnor_SHR_Utx	1	85,965,362 - 85,994,505 (-)	NCBI	Rnor_SHR
	UTH_Rnor_SHRSP_BbbUtx_1.0	1	94,516,223 - 94,545,362 (-)	NCBI	Rnor_SHRSP
	UTH_Rnor_WKY_Bbb_1.0	1	87,721,120 - 87,750,267 (-)	NCBI	Rnor_WKY

Access JBrowse from the position section of the gene page, or use the link in the Analysis and Visualization section of the RGD home page.

Analysis and Visualization



The screenshot shows the JBrowse Genome Browser interface with a title bar that reads "JBrowse Genome Browser". The main area displays a genomic track with several gene models represented by red boxes and arrows indicating the direction of transcription. A red arrow points from this section towards the "Available Datasets" section.

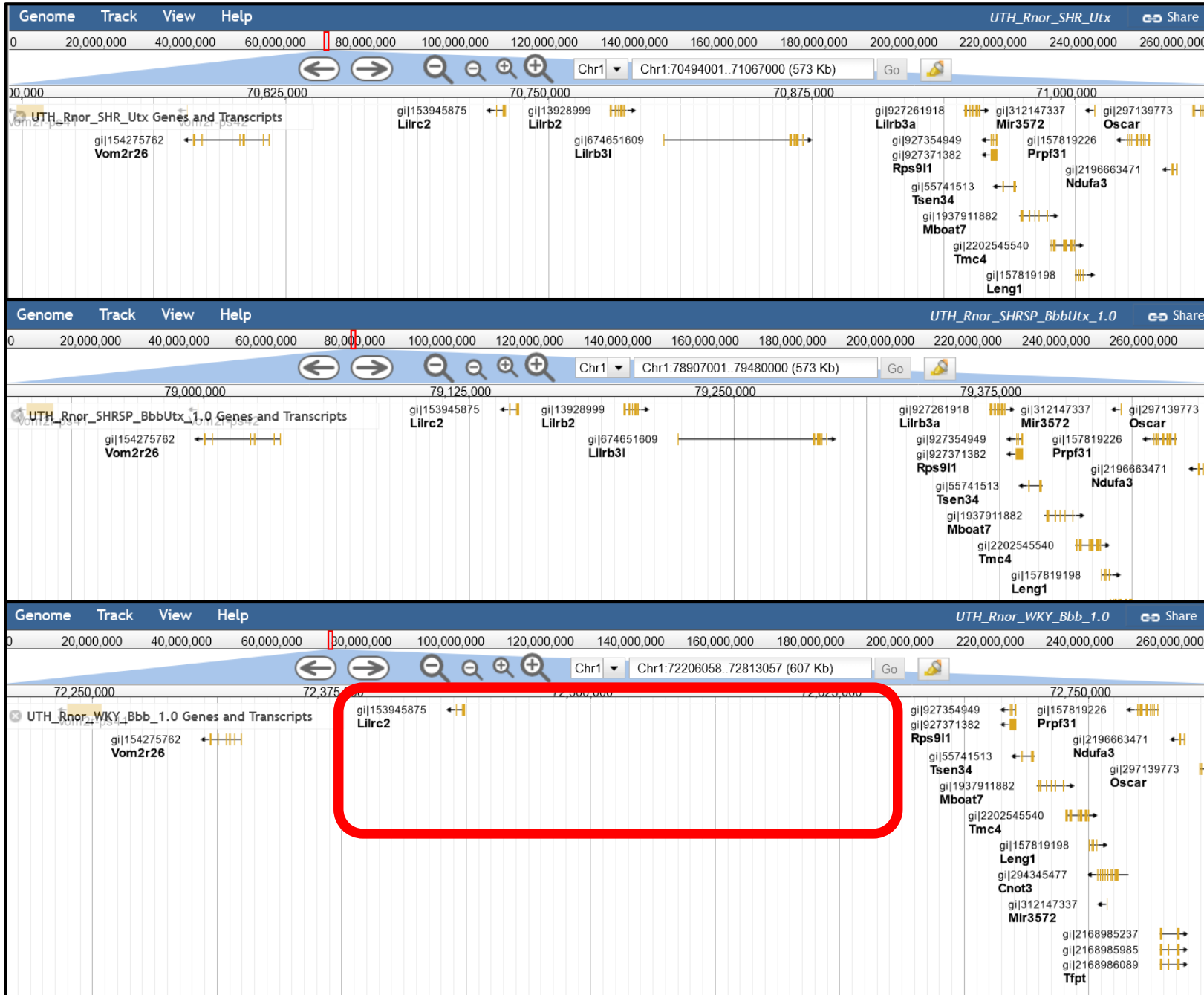
Available Datasets

- [RGD mRatBN7.2](#)
- [UTH_Rnor_SHR_Utx](#)
- [UTH_Rnor_SHRSP_BbbUtx_1.0](#)
- [UTH_Rnor_WKY_Bbb_1.0](#)
- [Rat Genome Database v6](#)
- [Rat Genome Database v5](#)
- [Rat Genome Database v3.4](#)

SHR

SHRSP

WKY



Looking at the region around the gene Lilrc2 you can see that SHR and SHRSP have two genes, Lilrb2 and Lilrb3l, that are missing from the WKY assembly

Data for the SHR, SHRSP and WKY strains are available on RGD

- For genes that have been mapped to any or all of these assemblies, positions are available on the gene report pages.
- The SHR, SHRSP and WKY assemblies are included in RGD's Search by Position tool
- RGD has created JBrowse genome browsers for the SHR, SHRSP and WKY assemblies
- RGD has produced pairwise gene comparison files for all combinations of mRatBN7.2, SHR, SHRSP and WKY



RGD has produced pairwise gene position comparison files

Index of /data_release

<u>Name</u>	<u>Last modified</u>	<u>Size</u>
GENES_BONOBO.txt	2022-09-23 23:41	17M
GENES_CHINCHILLA.txt	2022-09-23 23:41	14M
GENES_DOG.txt	2022-09-23 23:42	35M
GENES_HUMAN.txt		
GENES_MOUSE.txt		
GENES_OBSOLETE_IDS.txt		
GENES_PIG.txt		
GENES_RAT.txt		
GENES_RAT_assembly_comparison/		
GENES_README		

Each folder contains files for genes that map to different chromosomes in the two assemblies and the genes that are only found on one or the other assembly.

Name	Date modified	Type
rn7 vs 3.4	9/27/2022 11:41 AM	File folder
rn7 vs rn5	9/27/2022 11:41 AM	File folder
rn7 vs rn6	9/27/2022 11:41 AM	File folder
UTH_Shr vs rn7	9/27/2022 11:41 AM	File folder
UTH_Shr vs UTH_Shrsp	9/27/2022 11:41 AM	File folder
UTH_Shr vs UTH_WKY	9/27/2022 11:41 AM	File folder
UTH_Shrsp vs rn7	9/27/2022 11:41 AM	File folder
UTH_Shrsp vs UTH_WKY	9/27/2022 11:41 AM	File folder
UTH_WKY vs rn7	9/27/2022 11:41 AM	File folder

As a member of the Genome Reference Consortium, RGD is working to improve the reference assembly

- NCBI's RefSeq curators reported 214 genomic regions with suspected assembly problems.
- Dr. Peter Doris also created a list of 287 problematic genes from analysis of the mRatBN7.2 assembly compared to the SHR, SHRSP and WKY assemblies.
- Of those 287 genes, 179 were also in the group reported by RefSeq curators.
- RGD curator Wendy Demos has closed 25 tickets, 24 of which are from the overlap group

As a member of the Genome Reference Consortium, RGD is working to improve the reference assembly

Rat Genome Issues

Show issue locations on

mRatBN7.2

Search

Examples
 Gene: [Tnf](#)
 Location: [chr20:3,621,000-3,626,000](#)
 Clone accession: [JACYVU010000001.1](#)
 Clone name: N/A
 Issue ID: [RG-4](#)

Filter

Type

- Gap (3)
- Clone Problem (194)
- Path Problem (2)
- Variation (0)
- Localization Problem (0)
- [More...](#)

Status

- Resolved (25)
- Unresolved (189)
- Open (183)
- Under Review (5)
- Awaiting Elec Data (0)
- Awaiting Exptl Data (0)

Issue ID	Type	Location	Total placements	Status	Fix version	View in browsers	Summary
RG-237	Clone Problem	chr3:16,048,566-16,053,198	1	Open		NCBI	GenelD: 362112 (Tor2a), poor quality (includes component misassembly)
RG-236	Clone Problem	chr3:108,914,650-108,970,620	1	Open		NCBI	GenelD: 311368 (Ctdspl2), poor quality (includes component misassembly)
RG-235	Clone Problem	chr15:31,665,795-31,688,840	1	Open		NCBI	GenelD: 691799 (Il17d), poor quality (includes component misassembly)
RG-234	Clone Problem	chr3:106,734,675-106,741,552	1	Open		NCBI	GenelD: 311337 (Ltk), poor quality (includes component misassembly)
RG-233	Missing sequence		0	Open			GenelD: 266768 (Ly49s3), missing in assembly
RG-232	Clone Problem	chr5:67,337,151-67,340,909	1	Open		NCBI	GenelD: 298046 (Olr845), poor quality (includes component misassembly)

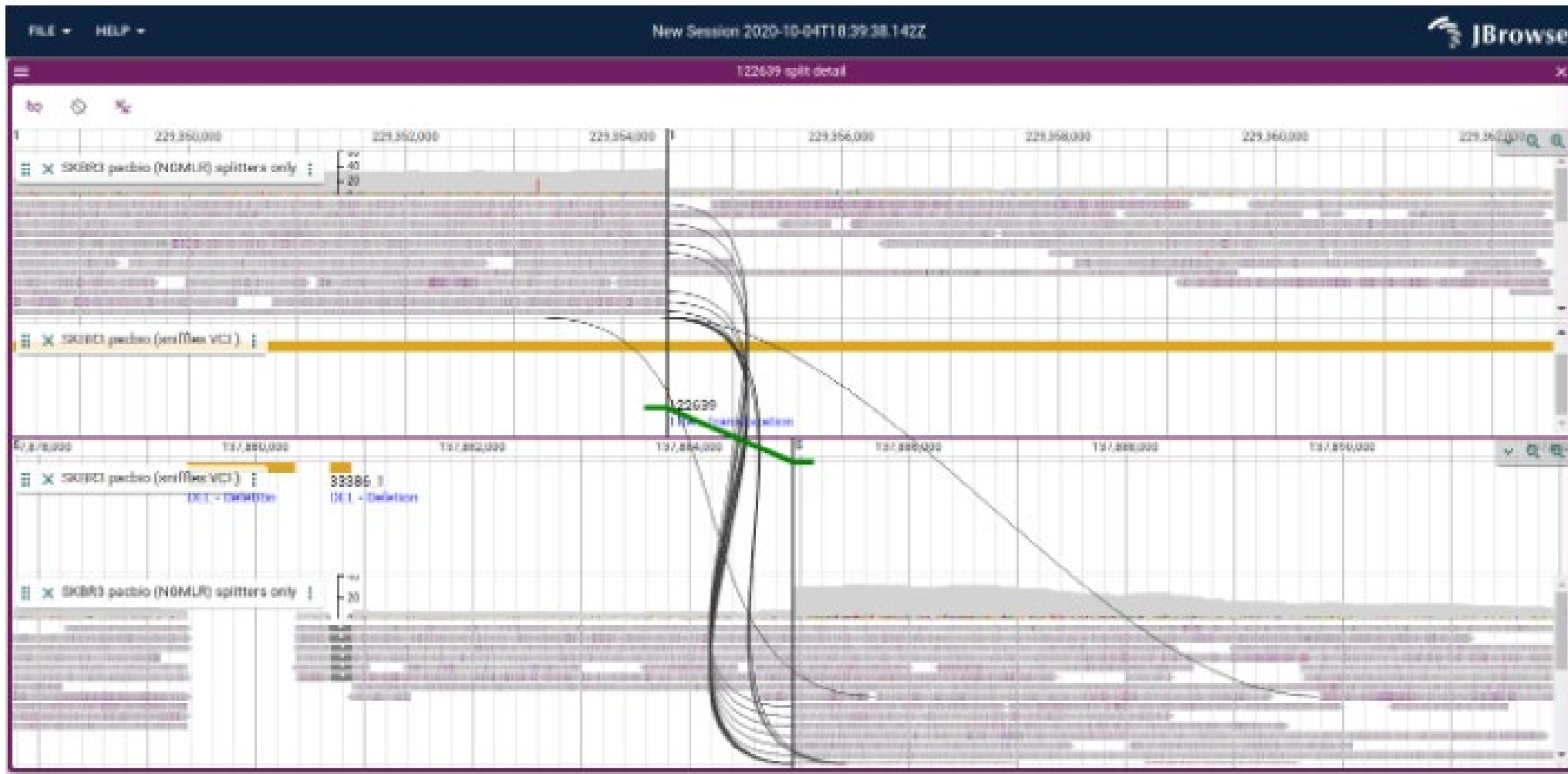
Items 1 - 30 of 214 << First < Prev Page 1 of 8 Next > Last >>



RGD is upgrading our genome browsers to JBrowse 2.0

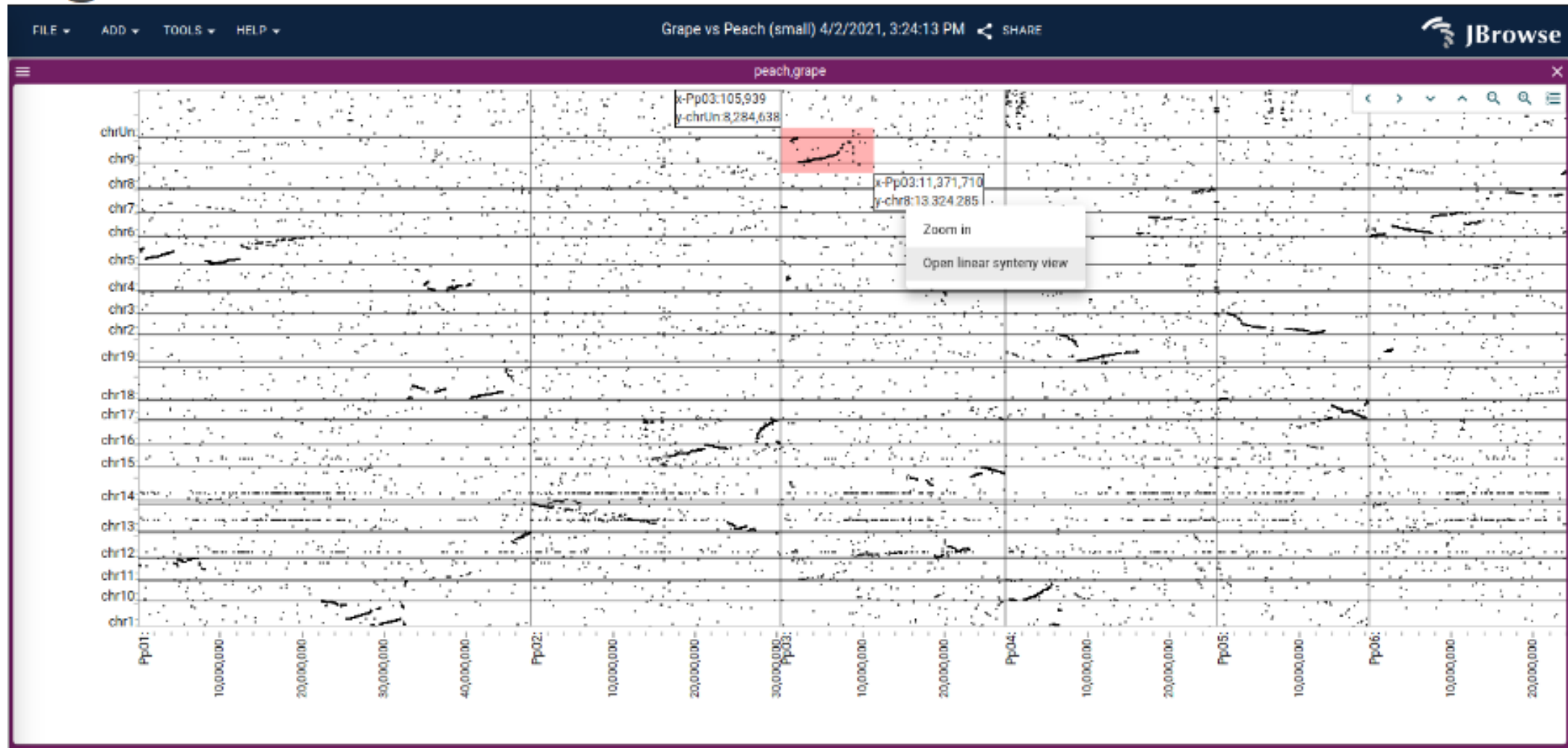
- JBrowse 2 is more feature-rich and has functionality that is designed to facilitate comparisons, including...
 - Breakpoint Split Viewer
 - Whole Genome Alignment Dotplot Viewer
 - Linear Synteny Viewer

Breakpoint Split Viewer

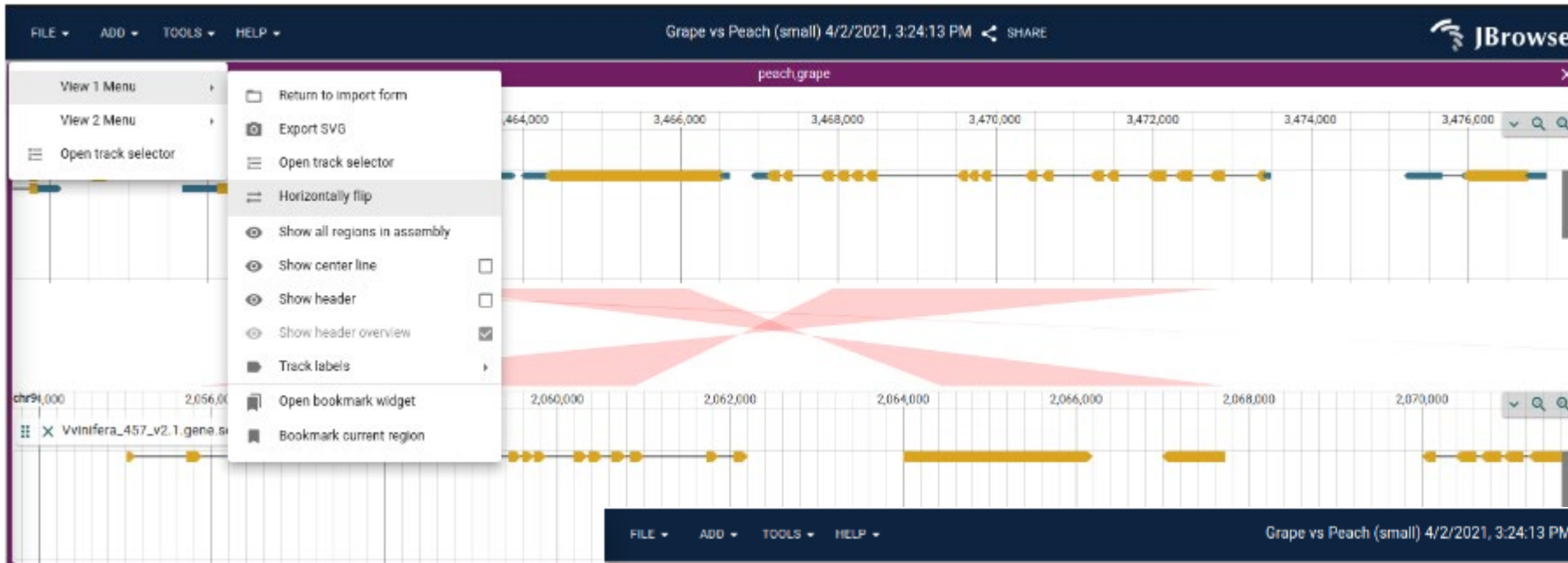


From <https://jbrowse.org/demos/pag2022/>

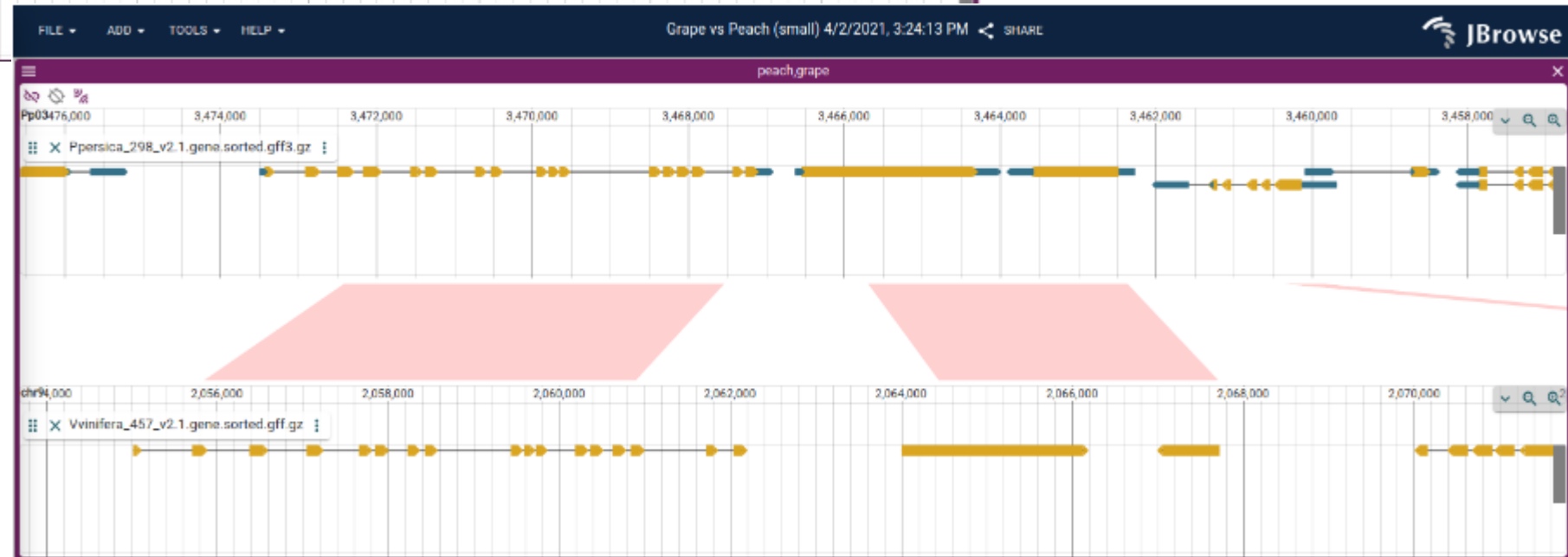
Whole Genome Alignment Dotplot Viewer



Linear Synteny Viewer



“The [top] picture shows an inverted region being aligned, and the [bottom] applies the ‘horizontally flip’ action to the top panel, allowing the synteny to be viewed in a co-linear way”



From <https://jbrowse.org/demos/pag2022/>

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Thank you!



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