BV-BRC Test Report

A11. Service – Genome Alignment - Bacteria

Item to test	Genome Alignment Service using bacterial genomes
URL	https://www.bv-brc.org/app/GenomeAlignment
Prerequisites	Bacterial genome group in the workspace
References	https://www.bv-brc.org/docs/quick_references/services/genome_alignment_service.html
Tester(s)	Rebecca Wattam, Maulik Shukla
Test date	08-May-2022 (follow-up from original test)
Test result	**Passed**

Overview

- Test the Genome Alignment Service using exemplar bacterial genomes.
- Test input options, i.e., adding one genome at a time and using genome group.
- For each job submitted, verify successful completion of the job and presence of output files.
- Review the interactive genome alignment viewer and ensure the quality of the results.
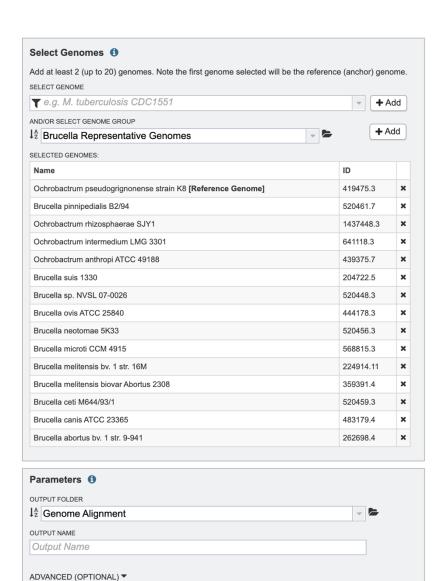
Test Data

Dataset	Rational	Input Format	Input
Brucella Representative Genomes	Workshop example	Genome Group	

- All test datasets and corresponding job results are available in the following public workspace:
  https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/Genome%20Alignment

Test Results

- All jobs completed successfully, without any errors.
- All jobs resulted in expected output files in corresponding job output directory.
- The interactive genome alignment viewer loaded and worked as expected. All the functions, zoom in, zoom out, rearranging genomes, and showing and hiding connecting lines worked as expected.
- All test datasets and corresponding job results are available in the following public workspace:
  https://www.bv-brc.org/workspace/BVBRC@patricbrc.org/BVBRC%20Tests/Genome%20Alignment
- Below are a series of screenshots showing successful completion of the jobs, availability of the result files in the workspace, and the interactive genome alignment viewer.
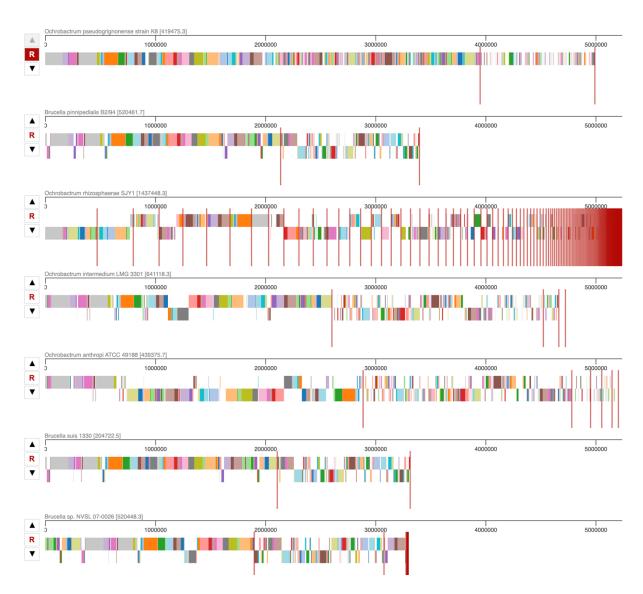
Select Genomes ⓘ

Add at least 2 (up to 20) genomes. Note the first genome selected will be the reference (anchor) genome.

SELECT GENOME

🔻 *e.g. M. tuberculosis CDC1551* ▾   **+ Add**

AND/OR SELECT GENOME GROUP

⬇A̲z Brucella Representative Genomes ▾ 📂   **+ Add**

SELECTED GENOMES:

Name	ID	
Ochrobactrum pseudogrignonense strain K8 **[Reference Genome]**	419475.3	✖
Brucella pinnipedialis B2/94	520461.7	✖
Ochrobactrum rhizosphaerae SJY1	1437448.3	✖
Ochrobactrum intermedium LMG 3301	641118.3	✖
Ochrobactrum anthropi ATCC 49188	439375.7	✖
Brucella suis 1330	204722.5	✖
Brucella sp. NVSL 07-0026	520448.3	✖
Brucella ovis ATCC 25840	444178.3	✖
Brucella neotomae 5K33	520456.3	✖
Brucella microti CCM 4915	568815.3	✖
Brucella melitensis bv. 1 str. 16M	224914.11	✖
Brucella melitensis biovar Abortus 2308	359391.4	✖
Brucella ceti M644/93/1	520459.3	✖
Brucella canis ATCC 23365	483179.4	✖
Brucella abortus bv. 1 str. 9-941	262698.4	✖

Parameters ⓘ

OUTPUT FOLDER

⬇A̲z Genome Alignment ▾ 📂

OUTPUT NAME

Output Name

ADVANCED (OPTIONAL) ▾

Your job has been submitted successfully. Please visit your Jobs List to check the status of your job and access the results.

Reset   Submit
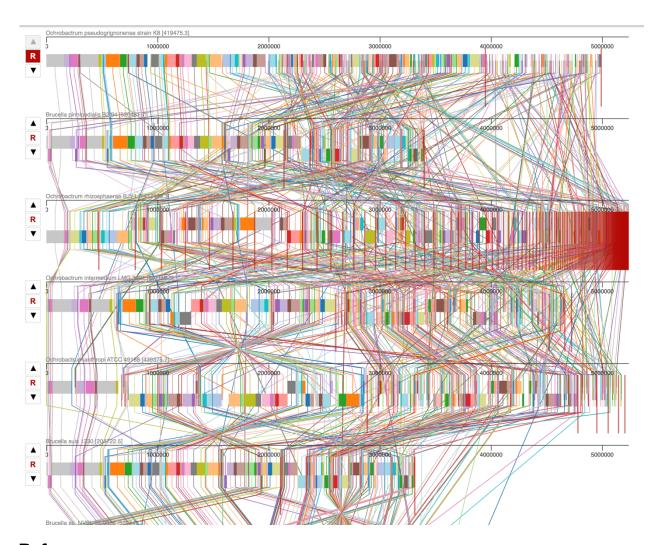
Status	ID	Service	Output Name	Submit ▾	Start	Completed	⊙
completed	7747177	GenomeAlignment	Brucella Representative Genome Alignment	5/7/22, 6:42 PM	5/7/22, 6:42 PM	5/7/22, 8:38 PM	

BVBRC / BVBRC Tests / Genome Alignment (2 items)   UPLOAD   ADD FOLDER   SHOW HIDDEN

	Name	Size	Owner	Members	Created	
⤒	Parent folder		-			
♥	Brucella Representative Genomes	15 genomes	me	Public	5/7/22, 6:40 PM	
⚑	Brucella Representative Genome Alignment	5.2 kB	me	Public	5/7/22, 8:38 PM	

Name	Size	Owner	Members	Created	●
⤴ Parent folder			-		
📄 alignment.json	1.1 MB	me	Public	5/7/22, 8:38 PM	
📄 alignment.xmfa	91.3 MB	me	Public	5/7/22, 8:38 PM	
📄 alignment.xmfa.backbone	3.2 MB	me	Public	5/7/22, 8:38 PM	
📄 alignment.xmfa.bbcols	712.6 kB	me	Public	5/7/22, 8:38 PM	

Ochrobactrum pseudogrignonense strain K8 [419475.3]

Brucella pinnipedialis B2/94 [520461.7]

Ochrobactrum rhizosphaerae SJY1 [1437448.3]

Ochrobactrum intermedium LMG 3301 [641118.3]

Ochrobactrum anthropi ATCC 49188 [439375.7]

Brucella suis 1330 [204722.5]

Brucella sp. NVSL 07-0026 [520448.3]

References

- [Genome Alignment Service Quick Reference Guide](#)