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EumicrobeDB

JBrowse2 INPUT Box

(Enter correct organism ID into this box and click on Jbrowse in Navbar above)

Phyag_NZFS3770

Organism ID Search Box

In the search box below, type in the organism prefix (for eg: for Phytophthora agathicida type Phyag) to know the list of organism IDs of all isolates of that species available in our database

Type and search

Organism List

+Phytophthora agathicida

+Phytophthora aleatoria

+Phytophthora boehmeriae

+Phytophthora cactorum

+Phytophthora capsici

.

A

A large, light gray arrow pointing downwards, indicating a flow or continuation from the text 'A' above it.

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☰

Assembly
Phyag_NZFS3770
Select assembly to view

LGTS01000001.1
Enter a sequence or location

OPEN

SHOW ALL
REGIONS IN
ASSEMBLY

EumicrobeDB

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Phyag_NZFS3770

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- + Phytophthora agathicida
- + Phytophthora aleatoria
- + Phytophthora boehmeriae
- + Phytophthora cactorum
- + Phytophthora capsici

B



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LGTS01000001.10,000 20,000 30,000 40,000 50,000 60,000 70,000 80,000 90,000 100,000 110,000 120,000

LGTS01000001.1 20,000

Reference Sequence (Phyag_NZFS3770) Zoom

Phyag_NZFS3770 (GFF3Tabix)

GTP_EFTU,IF-2 Thioredoxin_8 DUF3638,DUF3645 PHD Ank_2 DUF3638,DUF3645 Hypothet

RXLR

SSR

Available tracks

Filter tracks

Tracks

- ☒ Reference sequence (Phyag_NZFS3770) ...
- ☒ SSR ...
- ☒ RXLR ...

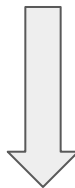
Genes

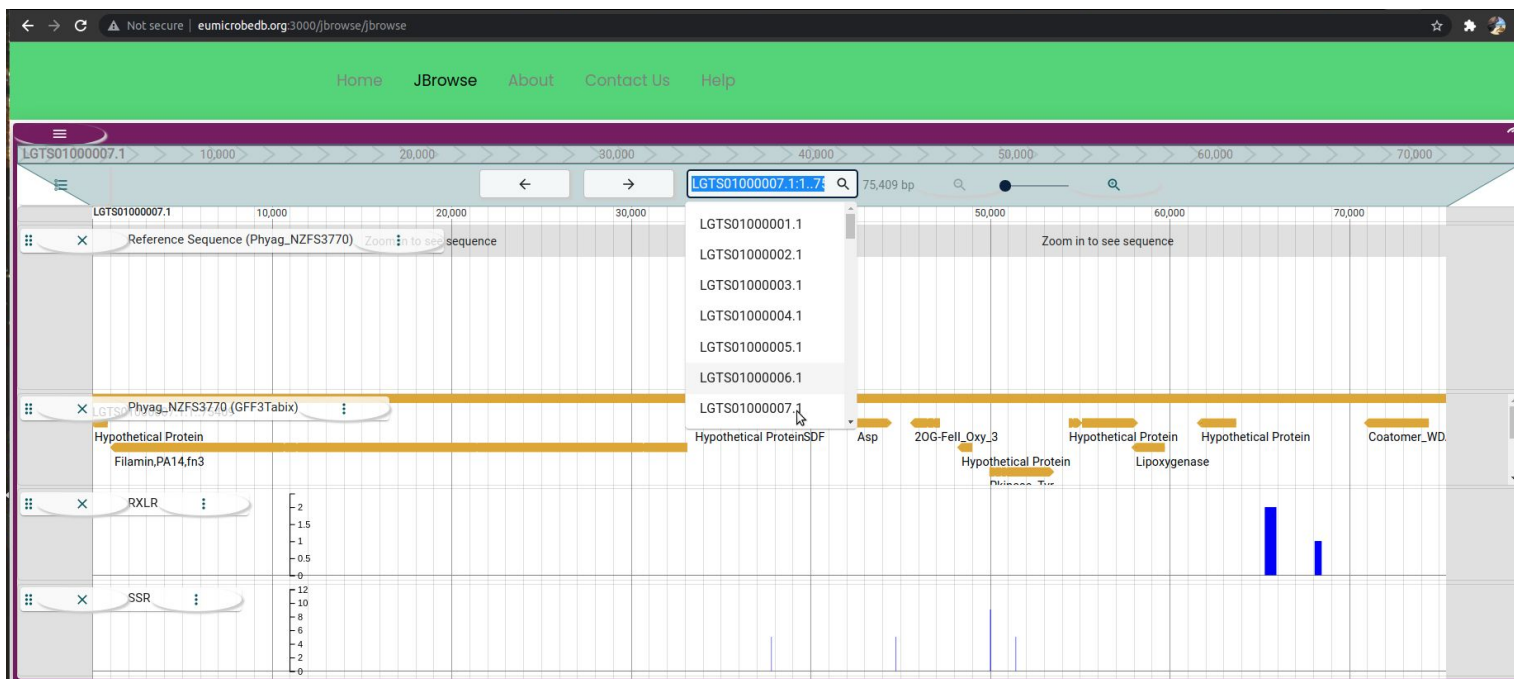
- ☒ Phyag_NZFS3770 (GFF3Tabix) ...

ATPase,HMA,Hydrolase Aa_trans ABC2_m

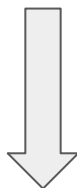
Myb_DNA-binding Pkinase ABC2_membrane,AB

C





D



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Feature details

HYPOTHETICAL PROTEIN - GENE

Core details	
Position	LGTS01000007.1:33,584..34,468 (-)
Name	Hypothetical Protein
Length	885
Type	gene
Attributes	
source	funannotate
phase	0
id	FUN_000562
product	Hypothetical Protein

SUBFEATURES

FUN_000562-T1 - MRNA

Core details	
Position	LGTS01000007.1:33,584..34,468 (-)
Length	885
Type	mRNA
Attributes	
source	funannotate
phase	0
id	FUN_000562-T1
parent	FUN_000562
product	Hypothetical Protein

CDS

Protein

Gene w/ introns

Gene w/ 10bp of intron

Gene w/ 500bp up+down stream

Gene w/ 500bp up+down stream w/ 10bp intron

cDNA

TTGGAAGGCTCCAGCTGCGCCGAGAGACGGCCAAGAGCTCCAGgagatcgacaagctgcttcgagatGACCTGGACGCAATTCACAACTGGTATCCATGGCACTTCATCGGCGCCAAACgtgttgaagaacgacggcagcagAGGTTGCAGCTTTGGGTGCGGTGCA

ctttctgctccttgccCGGCGCGGTACGTGTGTGTCGACCGCTGACAGACTCGTCAAGCagatgctgaggaaggtggagctctTGGAATTCGTAGTGGCGTCTGCTGCGATTCCAGCCGTGCGaagtgcagaagaagccgcgagACGACCAAGTGGAGATGCTCC

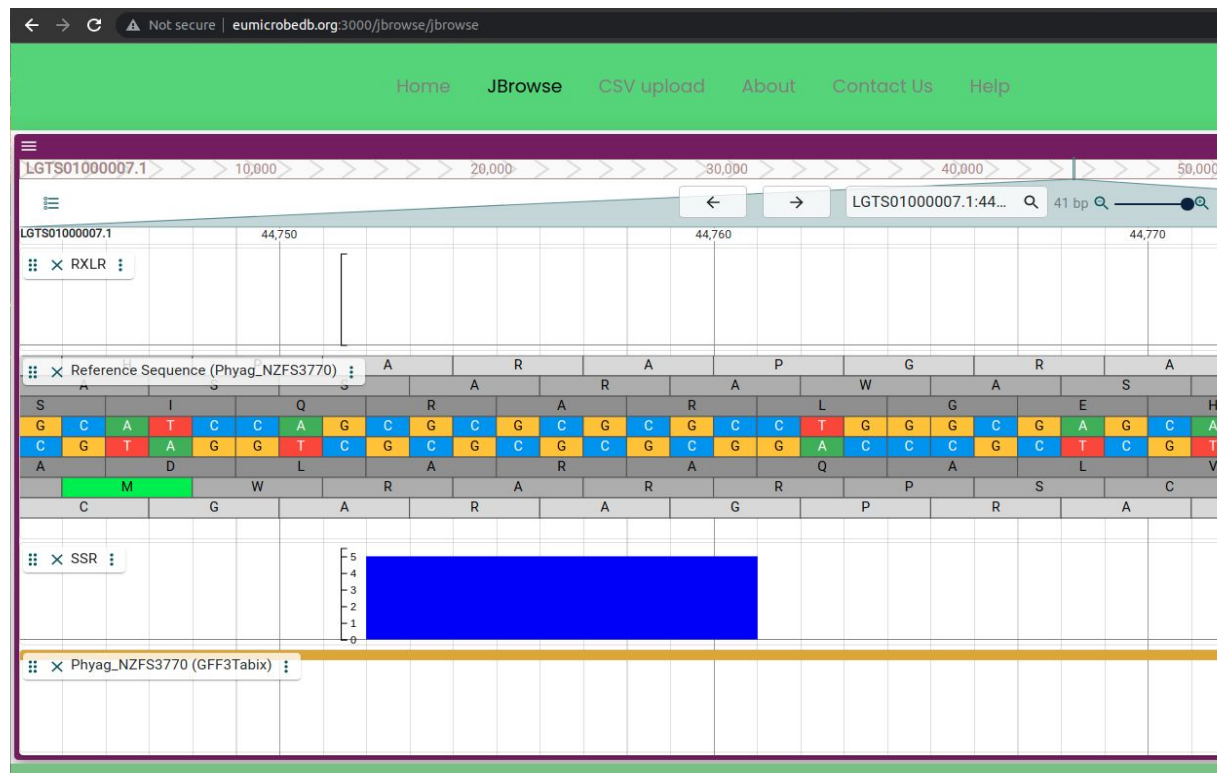
CTCGCGGCTCCAGTCCGCGGTTGGTGGCGTATCGACGATCTTCAGCGCACGAAGCGACAGCTTCAGactcgagagcagcagcgctgtgGCTGCGATTCAAGCCGCGAAGCAGCGATGGAAGCGGTGCGGCTTGAACACGACGCCAATTATCGCTGGACGGAG

IGTACCGCTCgtgatggagcaggagcttcaACGGCCAAGCGaagttgaagaagctgctgattgcAGATTGGAAAGACTCGGAAGTgtgacgtcgaagttgcctagAGACGCGcaagttggcagcagcgacgatgaatCCGAACGCTCCTGCGGTGGACATGGGGAGG

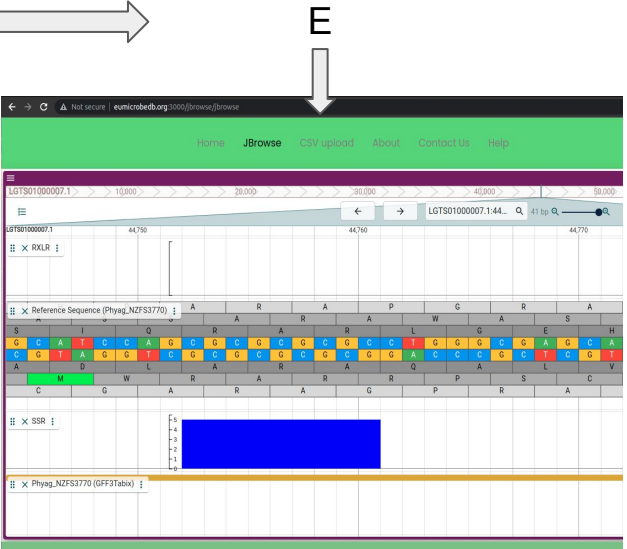
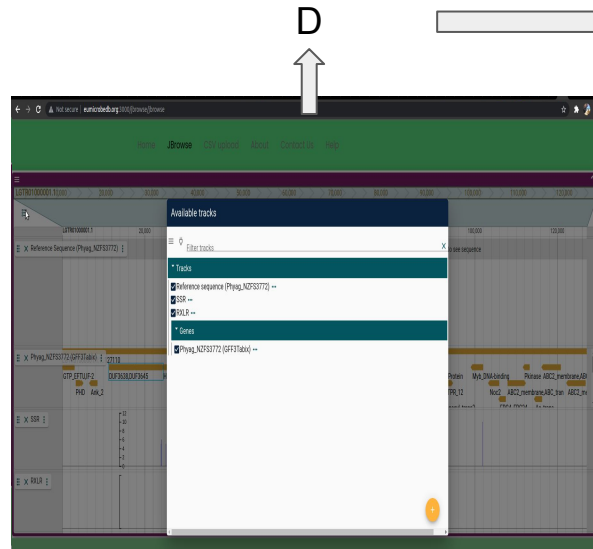
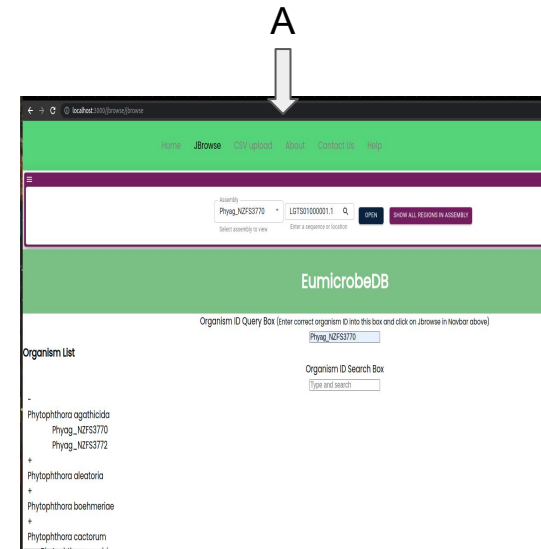
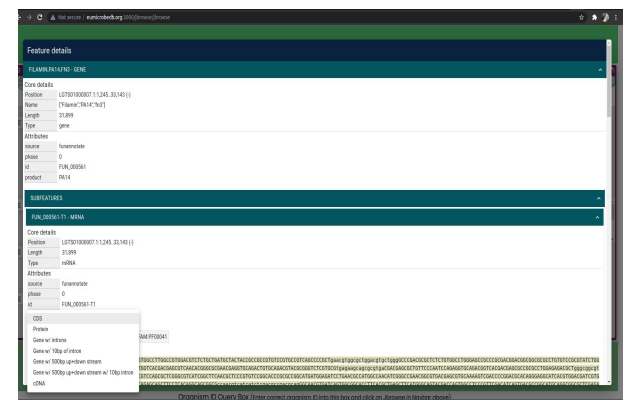
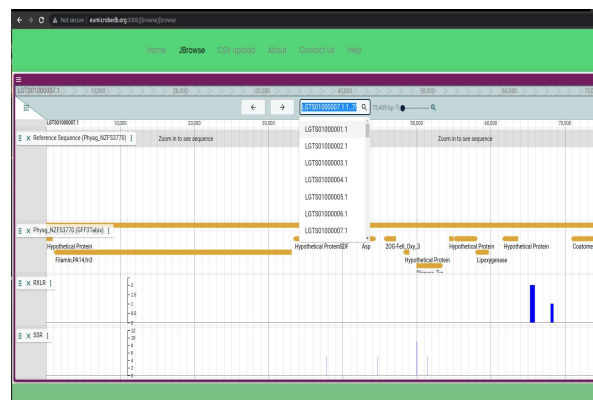
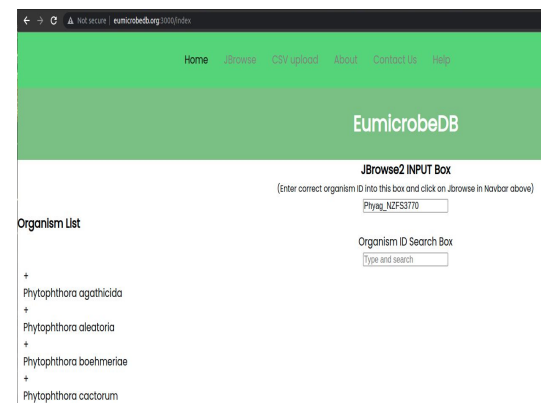
AGCGGATTGTCAATTGCATTCGGTAAATAG

E





F



Functionality of JBrowse2 as shown in the beta Eumicrobedb app : A) Shows the homepage of the Eumicrobedb app. From the tree view of *Phytophthora* isolates the organism ID is copied for a certain isolate and pasted in the “JBrowse2 INPUT BOX”. Following this JBrowse2 tab in the Nav Bar above is clicked. On opening the Homepage; the organism ID Phyag_NZFS3770 which represents *Phytophthora agathicida* is already provided in the box as a default value; and this is the one used in our example.

B) The assembly (sequence) and associated feature and variant tracks of the particular isolate is loaded by JBrowse2 and opened.

C) The variant tracks that user wants to display is selected by clicking on the .

D) A particular scaffold is chosen, in which Simple Sequence Repeat (SSR) regions are present.

E) On the feature (gfftabix) track; if a particular gene is clicked on; information about the gene or genomic feature as well as that of subfeatures is displayed on the webpage. The user also has the option of copying the sequence of the subfeature of interest.

F) An SSR region is zoomed in on; the 5' and 3' genomic sequences of the SSR as well as 6 possible translations of this sequence (due to 3 reading frames of each strand) can be determined by comparing the SSR region with the assembly or reference sequence. A scale bar beside the SSR region (blue rectangle) shows the height of the SSR box is 5. This corresponds to 5 repeats of the SSR motif. In our example the motif being repeated is a dinucleotide GC.