

(1)

Gene name (gene ID is available) or YourID for fasta sequence

User's gene ID as input

(1) Check Gene ID

Click this button

Step 1

Pick Genome (Please select one!):

Chromosome (Please select one!):

CDS (Coding sequence); OR your fasta sequence:

As default for query gene

Upstream (kb), max input should <=100 (kb)

Downstream (kb), max input should <=100 (kb)

(0-100kb) as input

(0-100kb) as input

User can update two values later

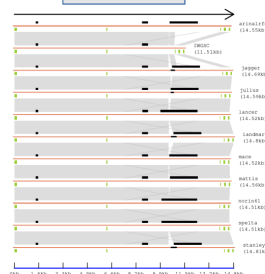
Distance filter between mapped clusters (1kb-50kb):

Expected CDS size compared to IWGSC (fold change:0.25-4):

Click this button

Step 2

Figure1



(2)

(2) Submit

(3) TREE

Step 3

Figure2

Clustering on all haplotypes

You can do tree cut on Height (y-axis) using single_click

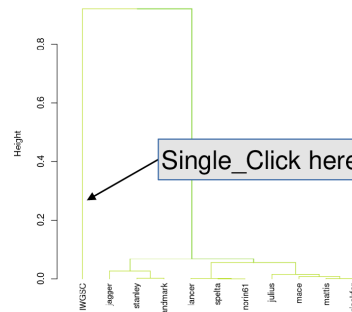
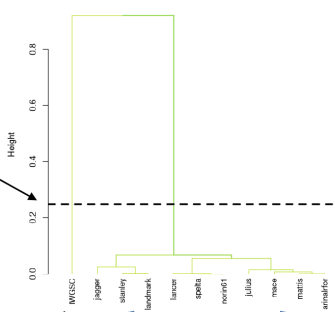


Figure2

Clustering on all haplotypes

You can do tree cut on Height (y-axis) using single_click



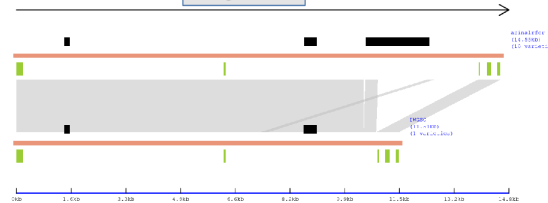
IWGSC

One of these

Next step

(3)

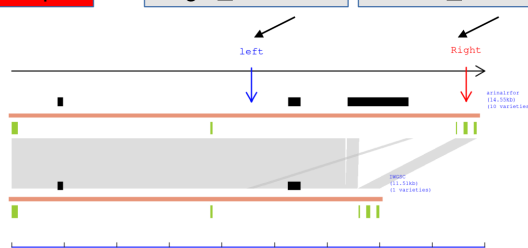
Figure3



Step 5

Single_Click here

Double_Click here



(4)

Figure4

(4) Plot selected haplotypes

Candidate haplotypes for plotting

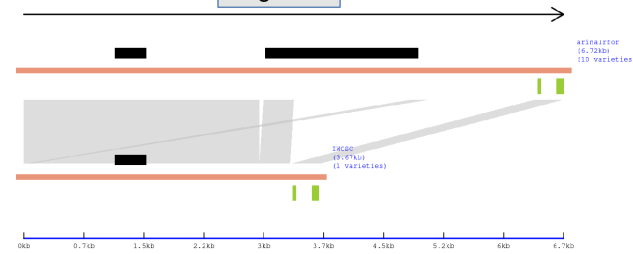
Order of plot

arinalfor

IWGSC

(5) Trim

Step 6



(5) Trim

Extract trimmed fasta

Prepare To Download

Save compressed results to ...

DONE

Optional buttons

Delete all User's files and refresh app's page

Step 4

Candidate haplotypes for plotting

Order of plot

arinalfor

IWGSC

From User's tree cut

User selected coordinates

Left coordinate - 7,51kb; right coordinate - 14,23kb

You can click on Trim Button ...