Summary Of Buttons

Button

Button (optional)

Button function

(1) Check Gene ID → Fill in matched reference genome and chromosome automatically

(2) Submit → Run BRIDGEcereal to get Figure1

(3) Tree → Clustering haplotypes (Figure2)

User defined Tree cut (Single_Click tree's Y axis) to obtain representative haplotypes

(4) Plot selected haplotypes → Reveal Figure3 based on User's tree cut

User defined region to trim (Single_Click at top of figure3 as left coordinate; Double_Click at top of figure3 as right coordinate)

(5) Trim → Reveal Figure4 based on User selected trimming region

Extract trimmed fasta → Extract *fasta* file based on User's trimmed coordinates

Prepare To Download → To compress User's BRIDGEcereal output as one .zip file

Save compressed results to ... → Ready to save .zip file to User defined folder ...

DONE → Delete all processed files of this User and refresh BRIDGEcereal page

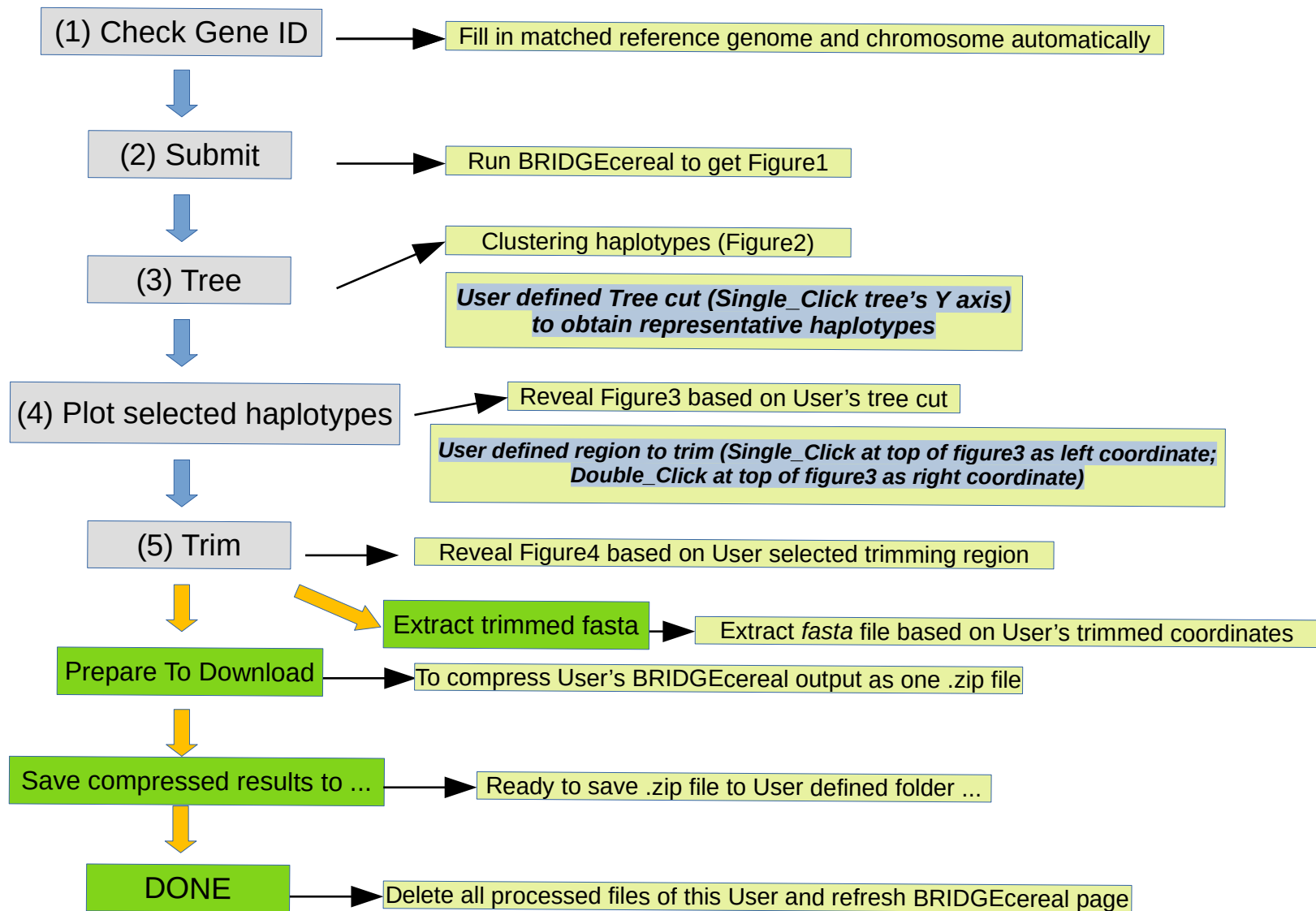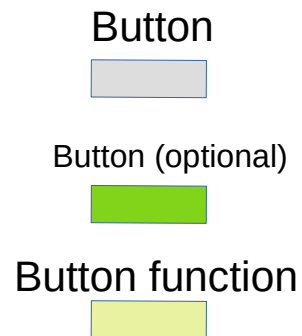**Gene ID is available**

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

TraesCS4A02G058900

User's gene ID as input

(1) Check Gene ID

Click this button   Step 1

Pick Genome (Please select one!) :

IWGSC

Fill in automatically

Chromosome (Please select one!)

chr4A

CDS (Coding sequence); OR your fasta sequence :

CDS

As default for query gene

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

0

(0-100kb) as input

Figure1

User can update two values later

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

0

(0-100kb) as input

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

1,000   20,000   50,000

1,000   5,900   10,800   15,700   20,600   25,500   30,400   35,300   40,200   45,100   50,000

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

0.25   0.75   1.25   4

0.25   0.65   1.05   1.45   1.85   2.25   2.65   3.05   3.45   3.85 4
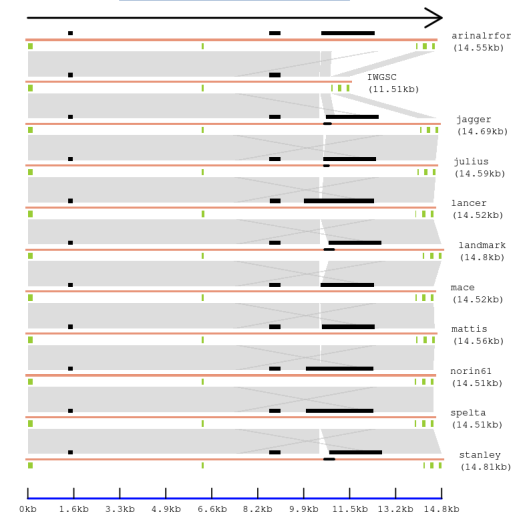
(2) Submit

Click this button

Step 2

Figure2

Clustering on all haplotypes
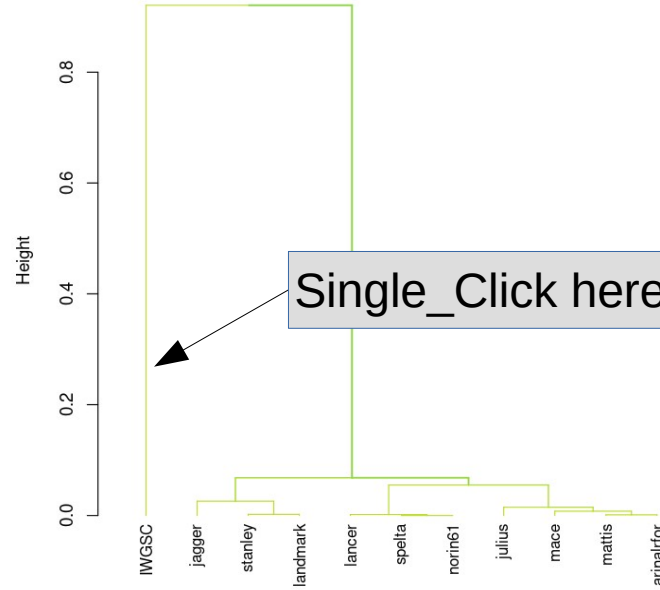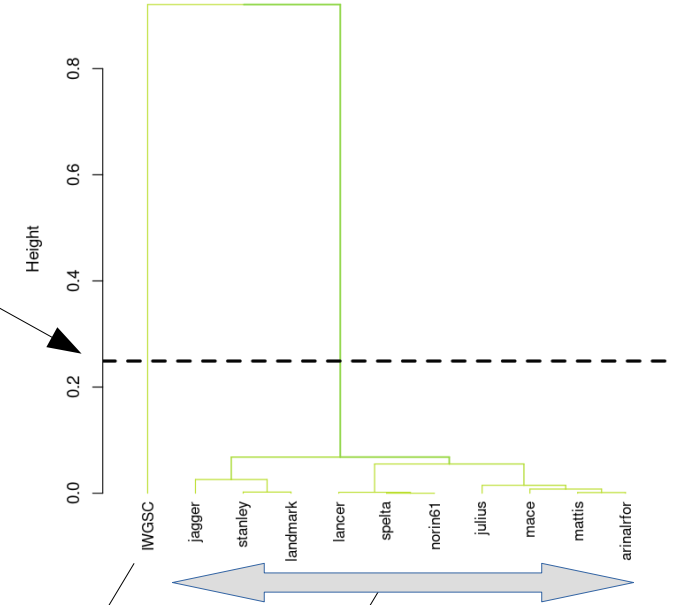**You can do tree cut on Height (y-axis) using single_click**

Figure2

Clustering on all haplotypes
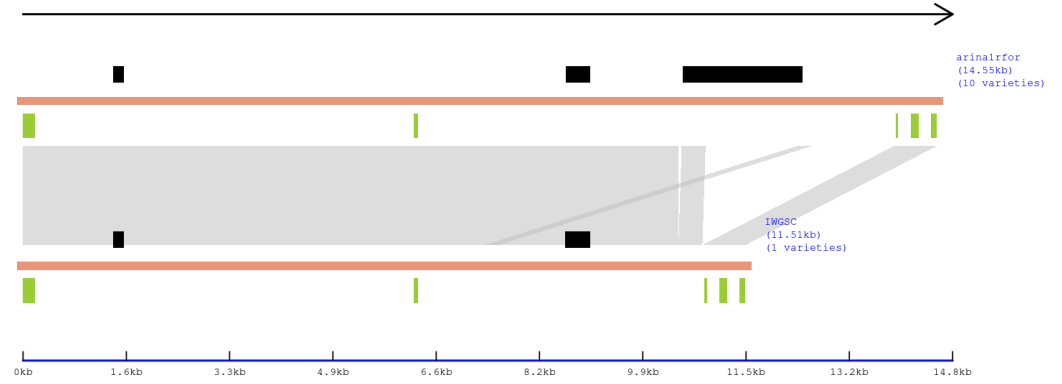**You can do tree cut on Height (y-axis) using single_click**

(2) Submit

(3) TREE

Step 3

Single_Click here

IWGSC

One of these

Next step

Figure3

arinalrfor
(14.55kb)
(10 varieties)

IWGSC
(11.51kb)
(1 varieties)

0kb   1.6kb   3.3kb   4.9kb   6.6kb   8.2kb   9.9kb   11.5kb   13.2kb   14.8kb

(2) Submit

(3) TREE

(4) Plot selected haplotypes

Step 4

Candidate haplotypes for plotting
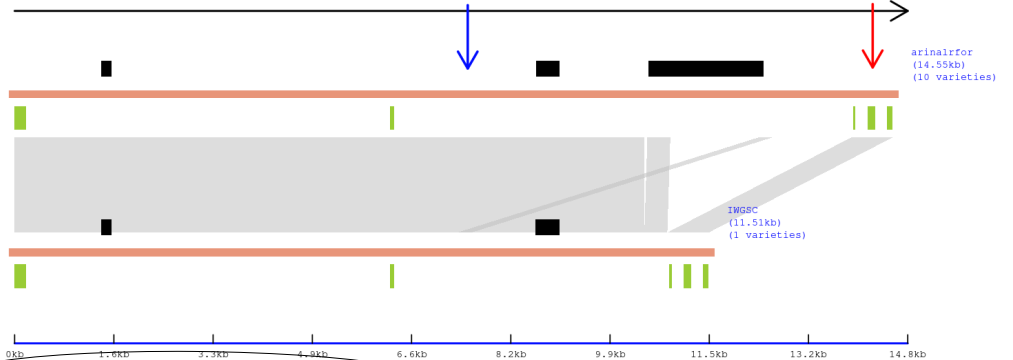
Order of plot

arinalrfor

IWGSC

From User's tree cut

Step 5

Single_Click here

Double_Click here

left

Right

arinalrfor
(14.55kb)
(10 varieties)

IWGSC
(11.51kb)
(1 varieties)

0kb   1.6kb   3.3kb   4.9kb   6.6kb   8.2kb   9.9kb   11.5kb   13.2kb   14.8kb
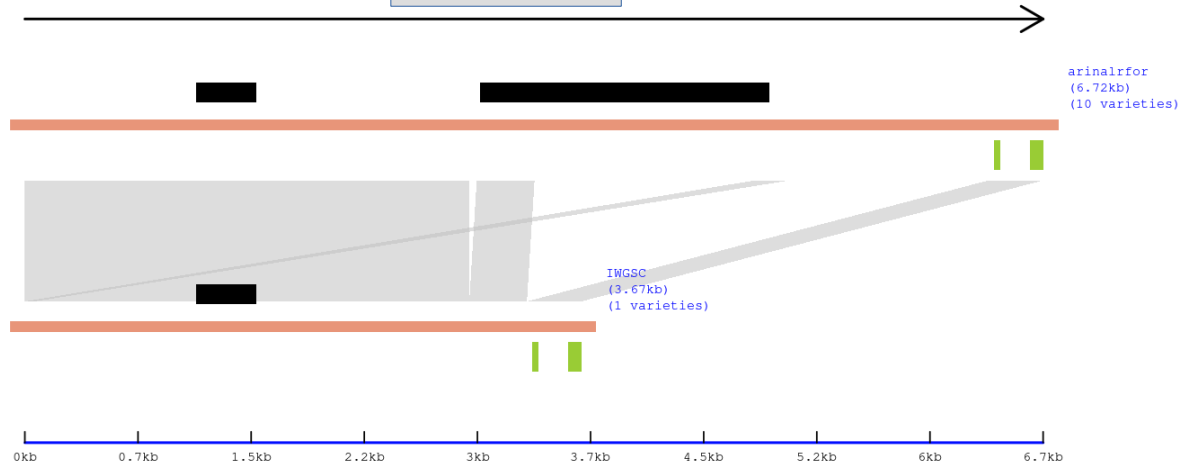
User selected coordinates

left coordinate ~ 7.51kb; right coordinate ~ 14.23kb. You can click on Trim Button ...

Figure4

Two default parameters explained

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

1,000   20,000   50,000

1,000 5,900 10,800 15,700 20,600 25,500 30,400 35,300 40,200 45,100 50,000

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

0.25   0.75   1.25   **Or Reference**   4
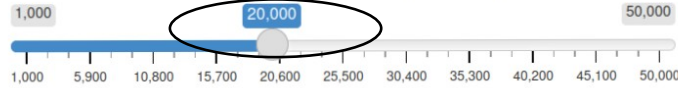
0.25 0.65 1.05 1.45 1.85 2.25 2.65 3.05 3.45 3.85 4
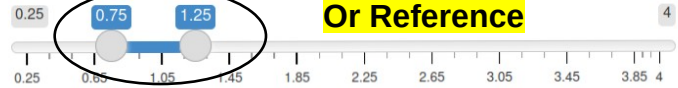
Example: Query gene includes 4 CDS

Size (length) of query gene's all CDS
will be calculated (CDS1+CDS2+CDS3+CDS4=**Ref_Size**)

Run blast may capture multiple hits on chrXX

| Cluster1 | Cluster2 | Cluster3 | Cluster4 |
| 20 kb (default) | 20 kb (default) | 20 kb (default) | 20 kb (default) |

chrXX

a1 a2 a3 a4   b1   c1 c2 c3   c4   d1 d2 d3

$0.75 <= (a1+a2+a3+a4)/$**Ref_Size**$ <= 1.25$ $(b1)/$**Ref_Size**< 0.75 $0.75 <= (c1+c2+c3+c4)/$**Ref_Size**$ <= 1.25$ $(d1+d2+d3)/$**Ref_Size**> 1.25
(default)   (default)
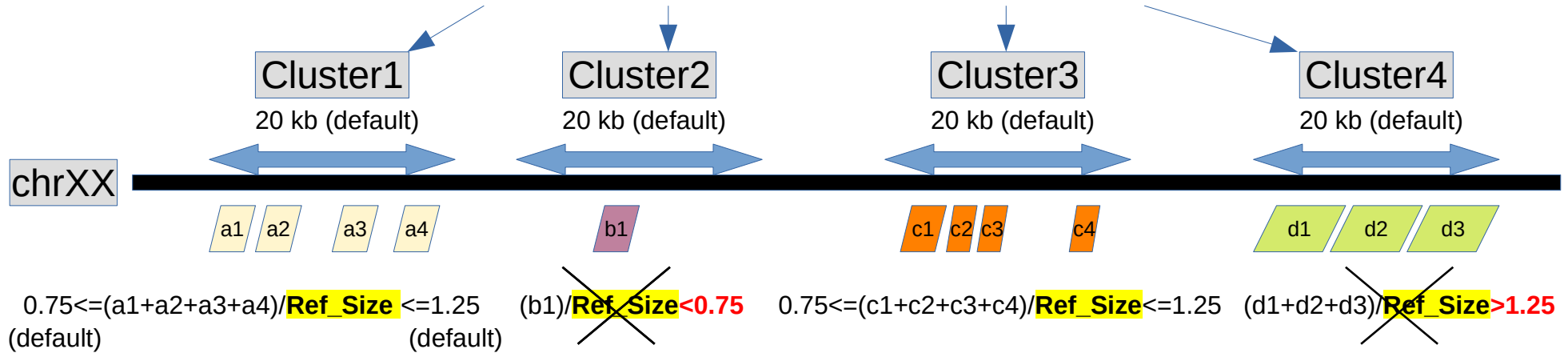
Blast similarity of [(a1+a2+a3+a4)/4] **>** Blast similarity of [(c1+c2+c3+c4)/4]

Cluster1 as BRIDGEcereal candidate

User wants to compare sequenced chromosome (or large DNA fragment) with pan-genomes for specific gene

Example: TraesCS4A02G058900

Prepare your .fa and .fa.gz files like this

Query chromosome

```
>chr4A
AACCCTAAACCCTAAACCCTAAACCCTAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACCCTAAACC
CTAAACCCAAAACAGTGTGTTATACCTTACGAAAACGGTCAGAAACGCTCGAAACGACGAGTTTTTACGACTTCAAAATA
GCCGTCTACCGGGGGTCACGAGCCATCGAAATCGTCCCCTGACCCCAAAAAAGTGTGTTATAGTCCACGAAAACGGCCAG
AAATGCTCGAAACGACGAATTTTGATGATGTCCAAATAGTTGTGTACTGGTGGTCACGGGCCATCGAAATCATCCCTGGA
CCACAAAACTGGGTGTTATAGCCCACGAAAACGGCAAAAAATGCTCGAAACGACGAGTTTTGATGACATCCAAATAGCCA
TGTACCGGGGGTGAAGGGACATGAAAACTGACCCCCGACCCCAAAACAGTGTTTATAGCCTACAAAAAAACCAGAAATGC
TCGAAACTACGAATTTTCACGACATCAAAATAGCCGTCTACCAAGGATCACTGCCATCGAAATCGTCCCCGGACCACAAA
ACAAGGTGTTATAGTCCACGAGAACGGCCAAAAATGCTCGAAATGACGAGTATTGACAACGTCAAAATAGCCGTCTACTG
GGGCCACGGGCCATTGAAATCGTCCCCGGACCCCAAAACAGTGTGTTATAGCCCACGAAAACGGCCAGAAATGGCCAAAA
CGACGAGTTTAGACCACGTCCAAATAGTCGTGTACCGGTGGTTATGGGCCATCAAAATCCTCCCCGACCGTCAAAATTG
TGTGCTATAGCCACTAAACGGCTAGAAATGCTCGAAACGATGACTTTTGACGATGTCCAAATAGCCGTGTACTGGTGGTC
ATAGGCCATCGAAATCGTCCCCGGACCCCAAAACAGTGTGTAGCCCATGAAAACAGCTAGAAATGCTCGAAACGACGAGT
TTTGACGACGTCCAAATAGCCGTATACCGCGGATCAAGGGACATGAAAACCGTCCTCAGACCCCAAAAAATGCGTTATAG
CCTACGAAAATGGCCAGAAATGCTCGAAACGACGAGTTTTGACGGCGTCAAAATAGTCGTCTACTGGGGGTCACGGGCCA
TCGAAATCGTCCCAGACCCCAAAAAAGTGCGAAAACGGCGAGAAATGCTCGAAACGACGAGTTTTGACGACGTCCAAATA
GTCGTGTACCGGGGGTCACGGGCCATCAAAATCGTCCCCGCACCCTAAAAACAATGTGCCAGAAATGCTTGAAACTATGA
ATTTTCACGGCGTCAAAATAGCCGTCAAGCAAGGATCACTGCACATCGAAATCGTCCCCGGACCACAAAACAAGGTGTTA
TAGCCCACGCAAATGGCCAAAAATGTTTGAAACGACAAGTTTTGATGACGTCCAAATAGCCGTGTACTGGGGGGTCAAGG
GACATGAAAATCGTCCCCGGATCCCAAAACAGTGTGTTATTTCCTATGAAAATGACCAGAAATGCTCGAAACGACGAGTT
```

⬇ bgzip

📦 Parent1_chr4A.fa.gz

Upload (max=300MB)

Gene name (gene ID is available) or YourID for fas...

TraesCS4A02G058900

Gene ID as input

(1) Check Gene ID

Click this button

Pick Genome (Please select one!) :

IWGSC

Fill in automatically

Chromosome (Please select one!)

chr4A ▾

CDS (Coding sequence); OR your fasta sequence :

CDS ▾

Your fasta sequence (Please add first line: >YourID Before pasting your DNA sequence!)

Upload Parent1 (Format: Parent1_chr**.fa.gz)

Browse... No file selected

Chromosome (Please select one!)

chr4A

CDS (Coding sequence); OR your fasta sequence :

CDS

Your fasta sequence (Please add first line: >YourID Before pasting your DNA sequence!)

Processing your compressed file Parent1 ... Almost there...

Upload Parent1 (Format: Parent1_chr.fa.gz)**

Browse... | Parent1_chr4A.fa.gz

Upload complete

Upload Parent2 (Format: Parent2_chr.fa.gz)**

Browse... | No file selected

Upload is done, and then processing User's file...

Figure1

(2) Submit

(2) Submit (large file)

Click this button
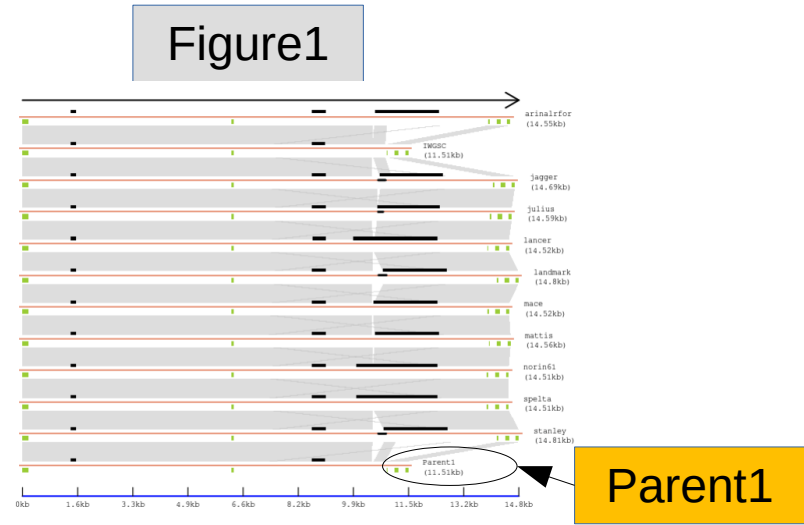
Parent1

Figure2

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

(2) Submit

(3) TREE

Height

Parent1

Parent1 IWGSC lancer spelta norin61 jagger stanley landmark julius mace mattis arinalrfor
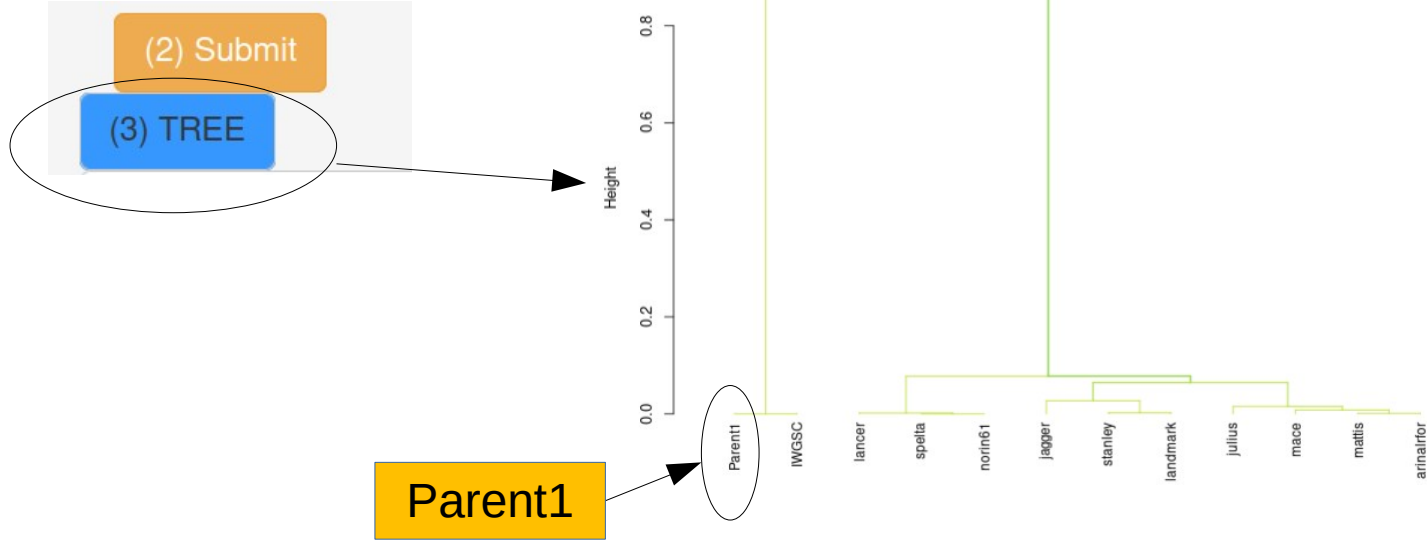
User needs to compare a fasta sequence with pan-genomes

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

YourID

YourID name as input

(1) Check Gene ID

Skip this button

Pick Genome (Please select one!) :

IWGSC

Select reference

Chromosome (Please select one!)

chr4A

Select target chromosome

CDS (Coding sequence); OR your fasta sequence :

fasta_seq

Select fasta_seq

Your fasta sequence (Please add first line: >YourID Before pasting your DNA sequence!)

>YourID
ATGGGTCGGGGGAAGGTGGAGATGAGGCGGATCGAGAACAAGATAAGC
CGGCAGGTGACG
TTCGCCAAGCGCCGGAATGGGCTGCTCAAGAAGGCCTACGAGCTCTCG
CTGCTCTGCGAC

Identical name !

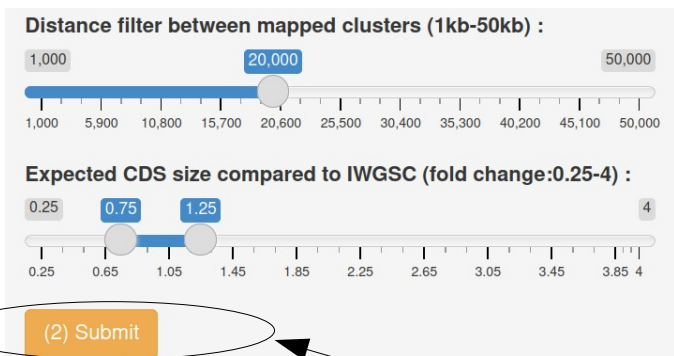**Distance filter between mapped clusters (1kb-50kb) :**

1,000   20,000   50,000

1,000 5,900 10,800 15,700 20,600 25,500 30,400 35,300 40,200 45,100 50,000

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

0.25   0.75   1.25   4

0.25 0.65 1.05 1.45 1.85 2.25 2.65 3.05 3.45 3.85 4

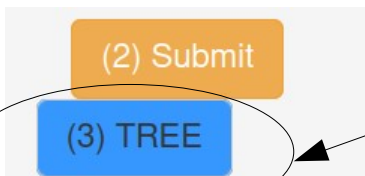(2) Submit
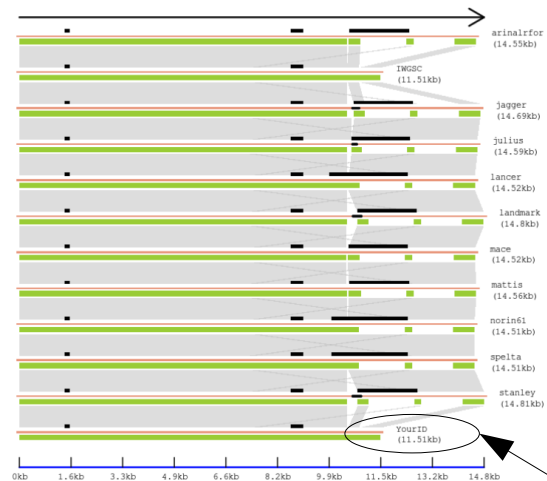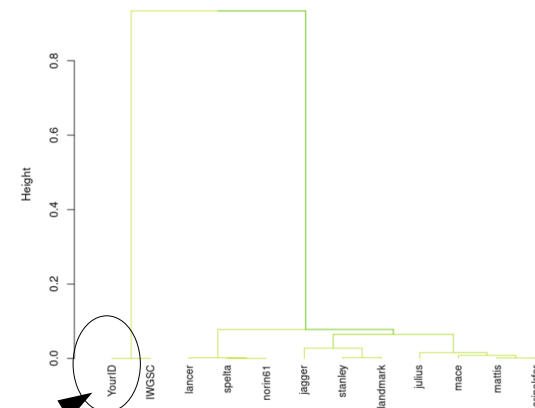
(2) Submit

(3) TREE

Click (2) and (3) buttons

Figure1

Figure2

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

arinalrfor (14.55kb)
IWGSC (11.51kb)
jagger (14.69kb)
julius (14.59kb)
lancer (14.52kb)
landmark (14.8kb)
mace (14.52kb)
mattis (14.56kb)
norin61 (14.51kb)
spelta (14.51kb)
stanley (14.81kb)
YourID (11.51kb)

0kb 1.6kb 3.3kb 4.9kb 6.6kb 8.2kb 9.9kb 11.5kb 13.2kb 14.8kb

Height

0.0 0.2 0.4 0.6 0.8

YourID IWGSC lancer spelta norin61 jagger stanley landmark julius mace mattis arinalrfor

YourID