Localizing cannabinoid-free k-mers to EH23a

Below, *CF k-mers* refers to the set of k-mers present in all 9 cannabinoid-free (CF) genomes (BH4, I3, I52, I53, I59, I61, I68, I75, I78), but absent from all other cannabis genomes in the current pangenome

Below are details of identifying cannabinoid-free contigs with dense clusters of CF k-mers, then localizing contigs to chromosomes of EH23a. The results are not yet comprehensive (only top 9 contigs from each CF genome are shown), provide useful context and illustrate the most obvious characteristics of CF k-mers.

The results of this dataset are broad/approximate mappgings of CF contigs to EH23a chromosomes. For more fine localization of k-mers at specific loci, refer to the browser tracks found at:

```
s3://salk-tm-shared/csat/cannabinoid-free/CF_kmers_bdg.tar.gz
s3://salk-tm-shared/csat/cannabinoid-free/CF_kmers_bw.tar.gz
```

Alignments

The alignment files mapping cannabinoid-free (CF) contigs to EH23a aren't included here but are found on AWS at:

```
s3://salk-tm-shared/csat/cannabinoid-free/EH23axCF.tar.gz
```

Data

```
cannabinoid-free/
  chromsizes/
    *.chromsizes
  kmers/
    *.kmers
  EH23a_mapping/
    *.tsv
    *_top9.tsv
    *_top9.bed
    *.pdf
    *.svg
  sort_contigs.py
  approx_position.py
  README.md
```

chromsizes

For each CF genome, the `.chromsizes` file contains the size of each contig in BP

kmers

For each CF genome, the `.kmers` file contains the area in bp occupied by CF k-mers

EH23a_mapping

The `.tsv` files are, for each CF genome, a table with a row for each contig and columns:

- **contig**: the contig ID
- **kmers_bp**: bp occupied by CF k-mers
- **total_bp**: total size of contig
- **chrom**: EH23a chromosome matching this contig

The `_top9.tsv` files are the top 9 contigs of each `*.tsv` file, with 3 additional columns:

- **approx_start**: approximate start position of the contig's mapping to EH23a
- **approx_center**: approximate center position
- **approx_end**: approximate end position

The `.bed`, `.pdf`, and `.svg` files are used to visualize the data in the `*_top9.tsv` files, see below.

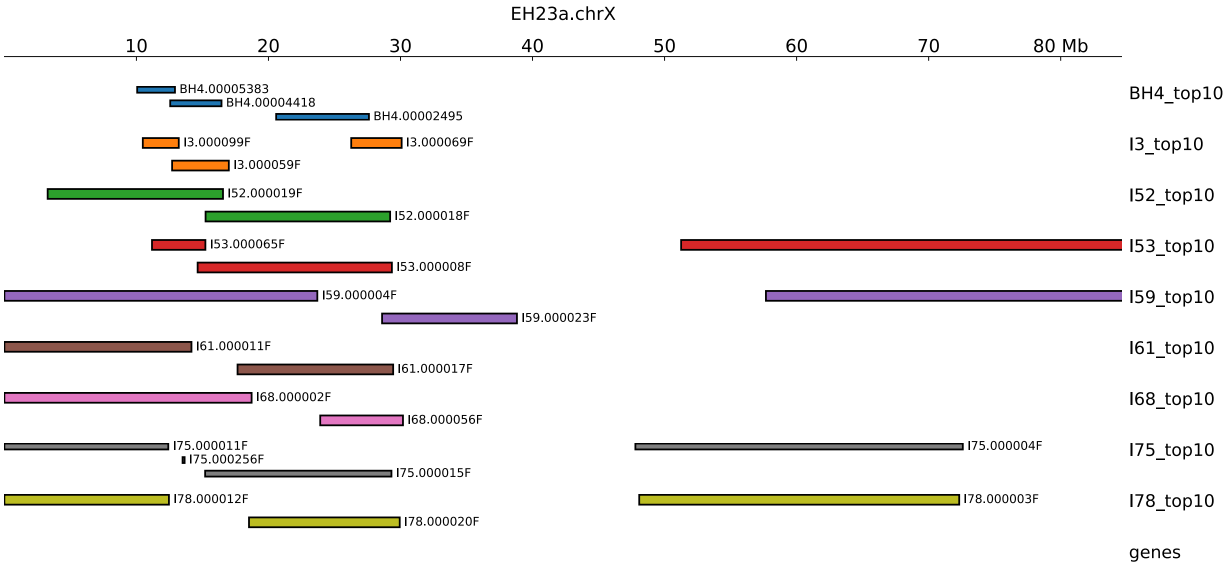
scripts

`sort_contigs.py` contains logic used to order contigs and generate the `*.tsv` files
`approx_position.py` contains logic used to generate approx coordinates for contigs in `*_top9.tsv` files

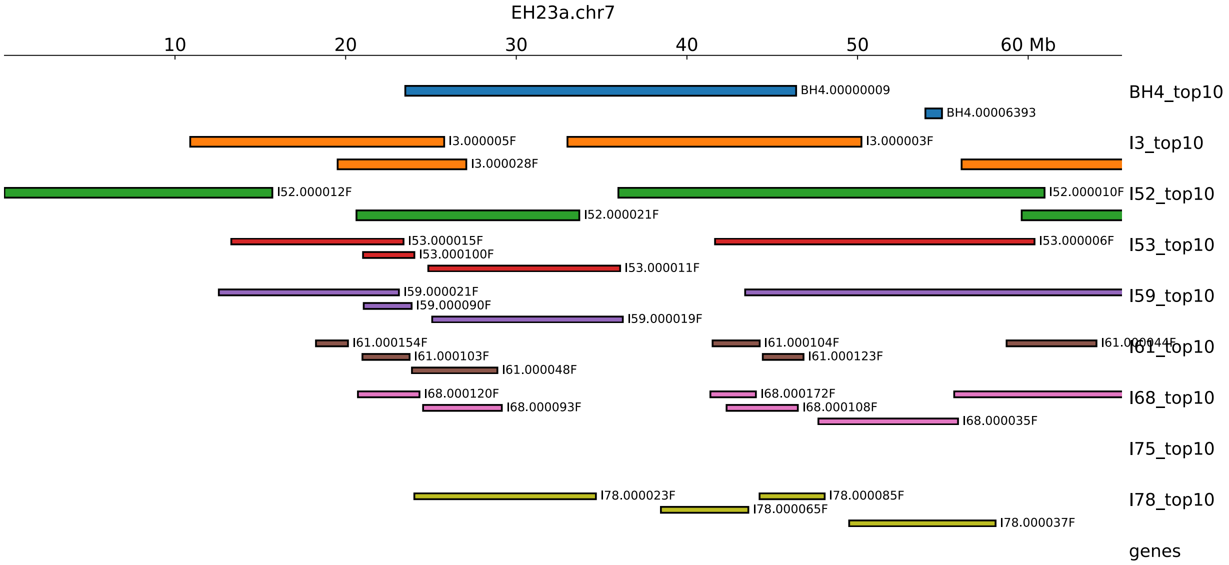
Results

Primary hits

Across all CF genomes there are signals mapping to EH23a.chrX, especially in the region from 10 Mb to 30 Mb. This seems to be strong support for the importance of the PT4 locus.

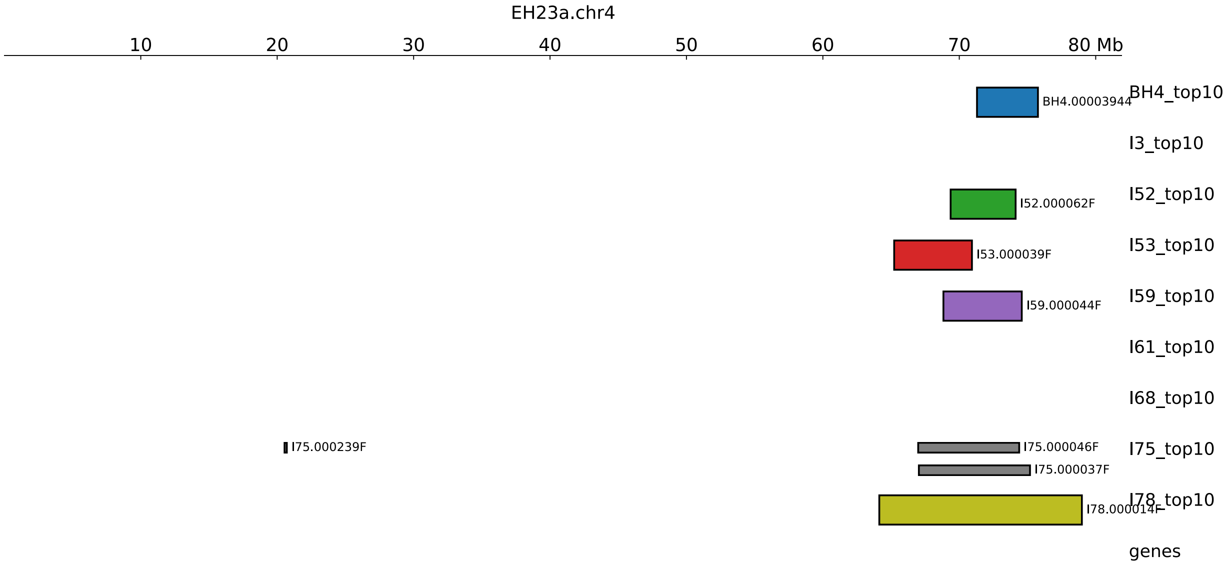


All CF genomes except I75 have signals mapping to EH23a.chr7.

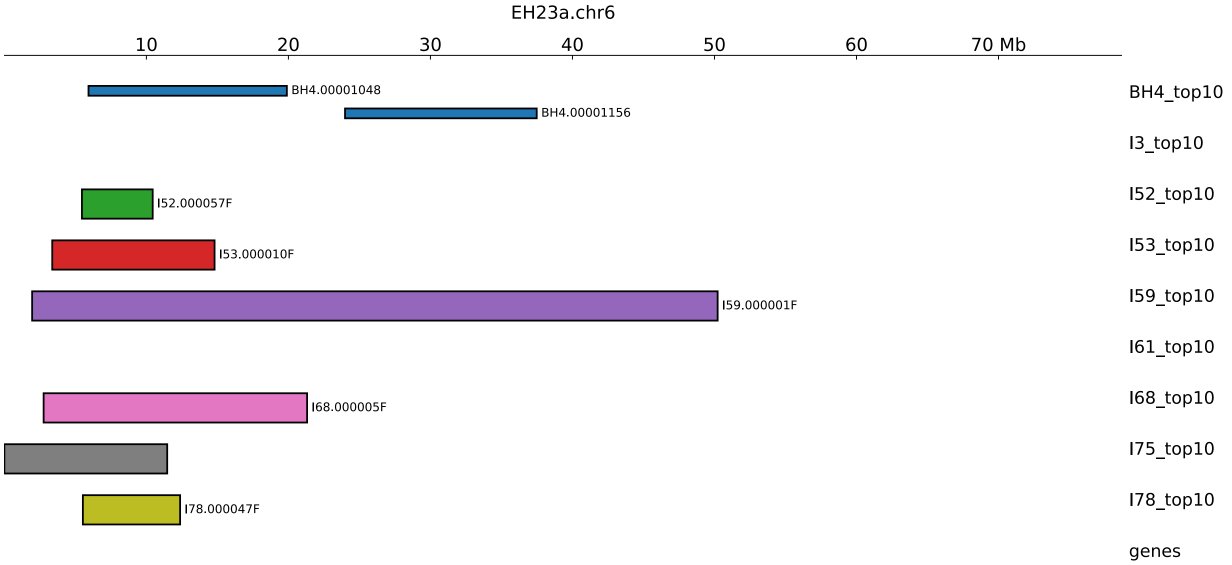


Secondary hits

There seem to be consistent signals in several CF genomes on EH12a.chr4 around 70 Mb:



And on chr6 around 10 Mb:


EH23a.chr6
70 Mb
BH4.00001048
BH4.00001156
I52.000057F
I53.000010F
I59.000001F
I68.000005F
I78.000047F
BH4_top10
I3_top10
I52_top10
I53_top10
I59_top10
I61_top10
I68_top10
I75_top10
I78_top10
genes