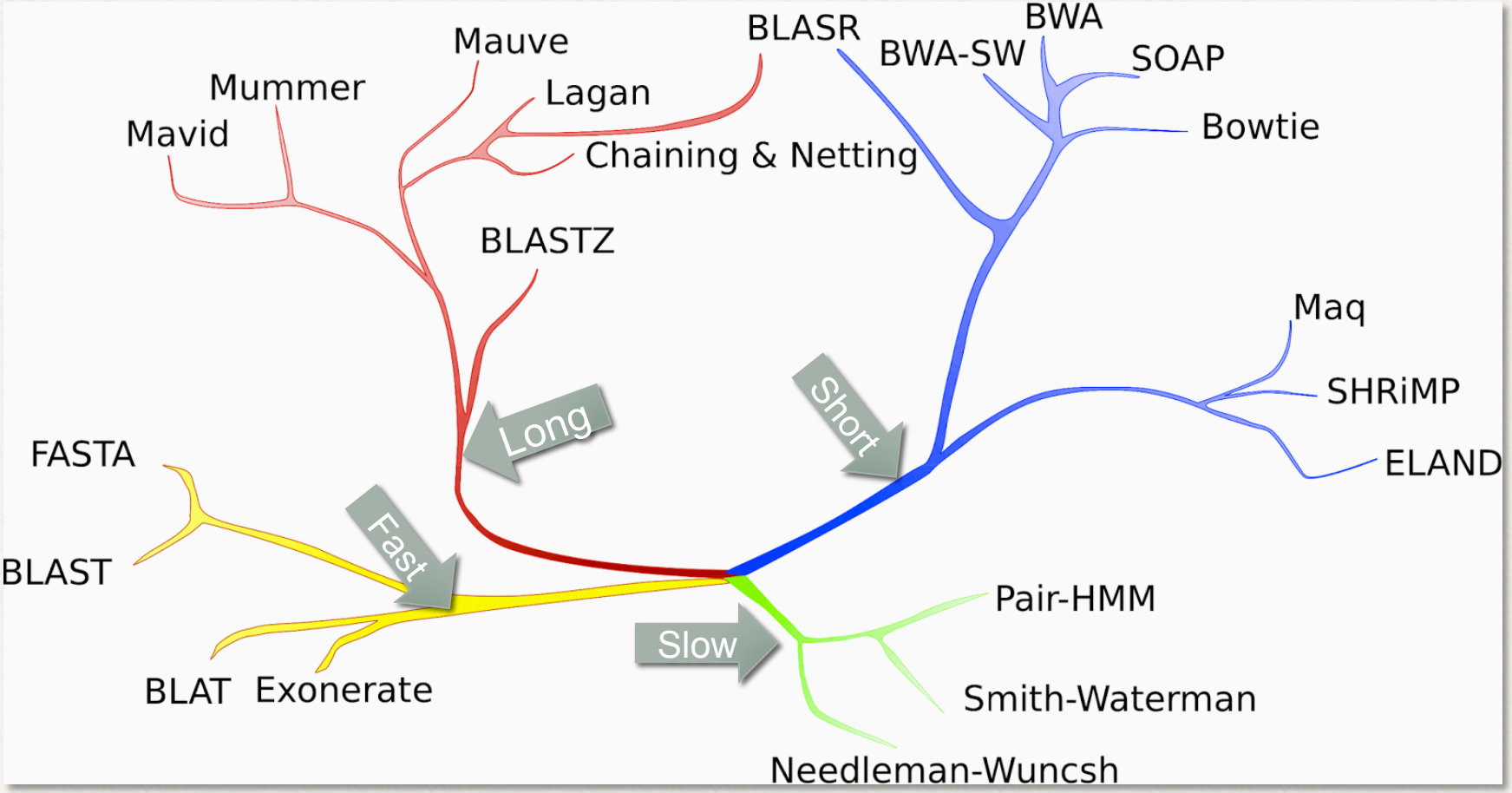
WHOLE GENOME ALIGNMENT

The phylogeny of pairwise alignment



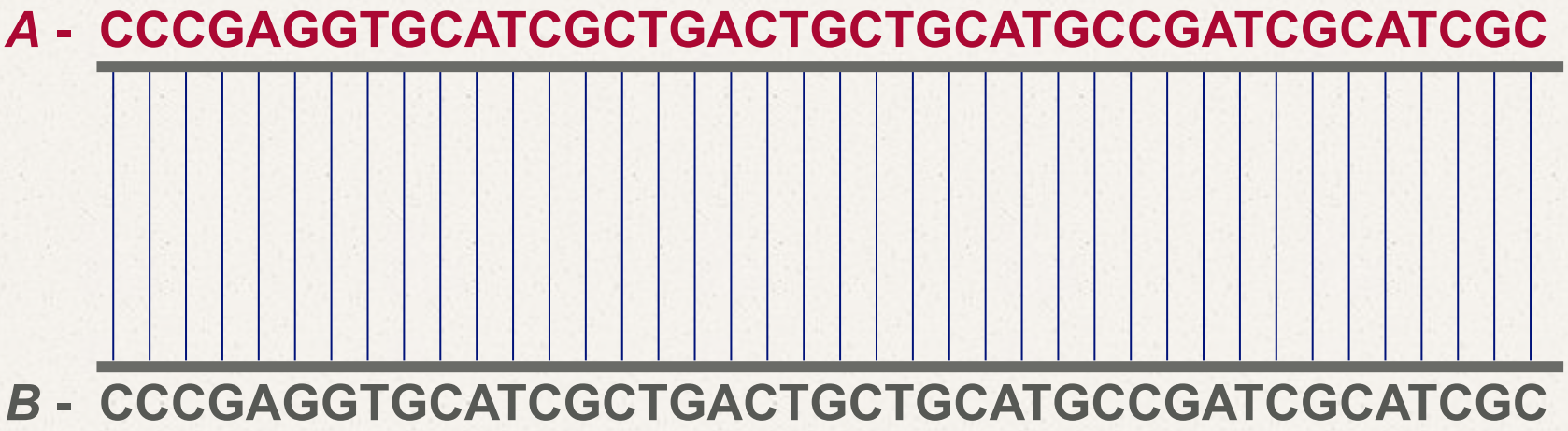
Chaisson & Tesler 2012, *BMC Bioinformatics*

Goals

- Why Align Genomes?
- Examples from the Literature
- Available Tools
- Afternoon: WGA Tutorial

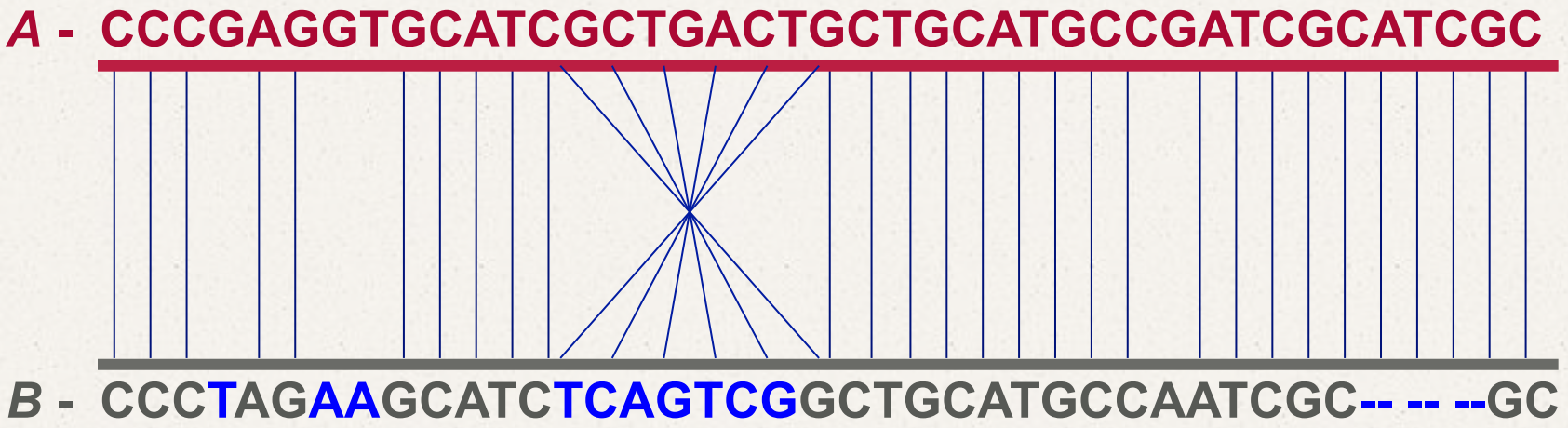
What is a WGA?

- For two genomes, identify the position in genome *A* that corresponds with the same position in genome *B*
  - Predict homologous pairs of positions between multiple genomes



What is a WGA?

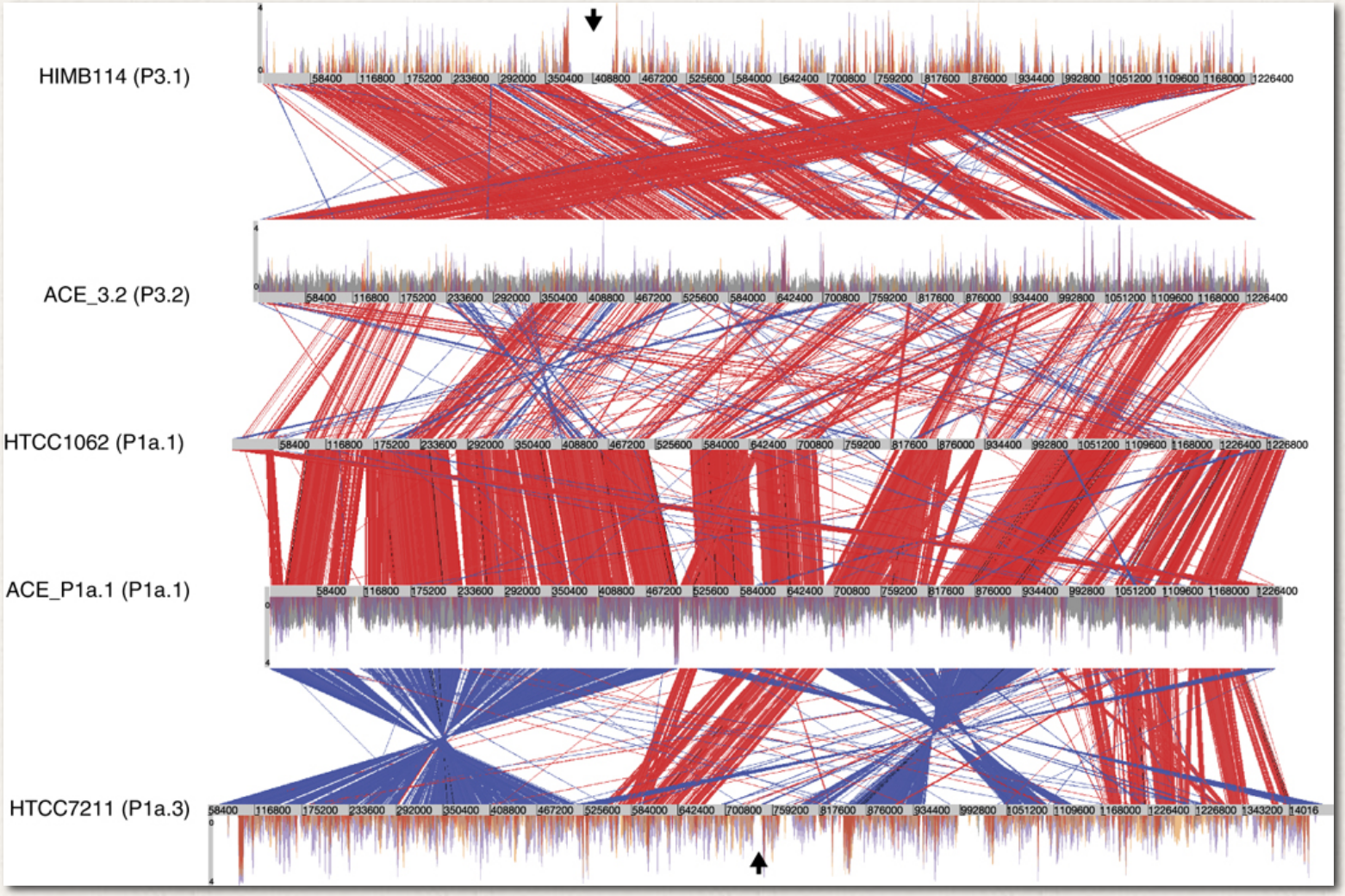
- But…
  - Indels
  - Repetitive elements
  - Variants (SNPs, errors)
  - Duplications
  - Inversion
  - Tanslocations
- All of the above



Why align genomes?

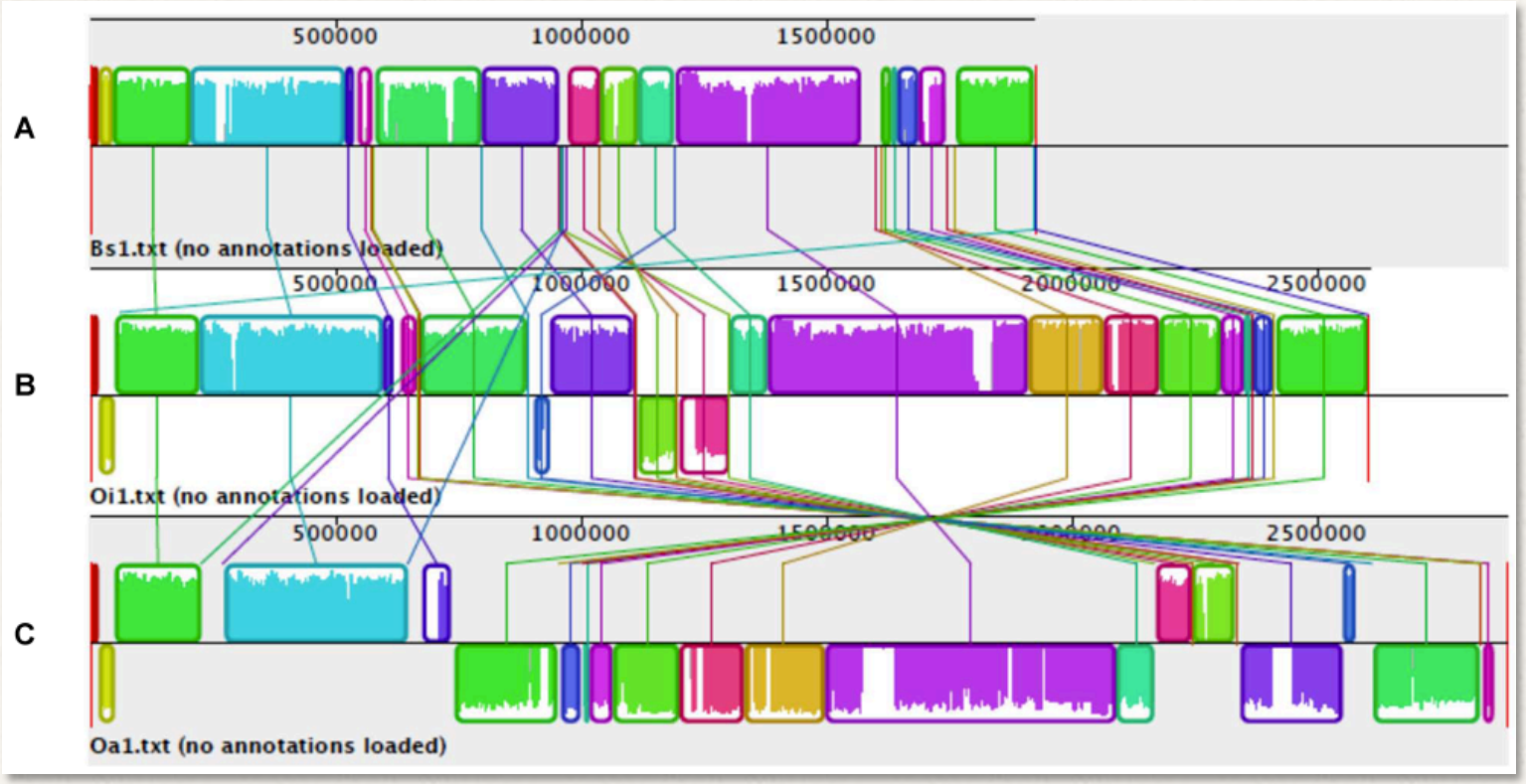
- Find syntenic regions (genomic structure)
  - Synteny: conservation of the order of regions

WGA: Genome synteny and recruitment plots of SAR11 genomes.



Brown et al. Mol Syst Biol 2012;8:595

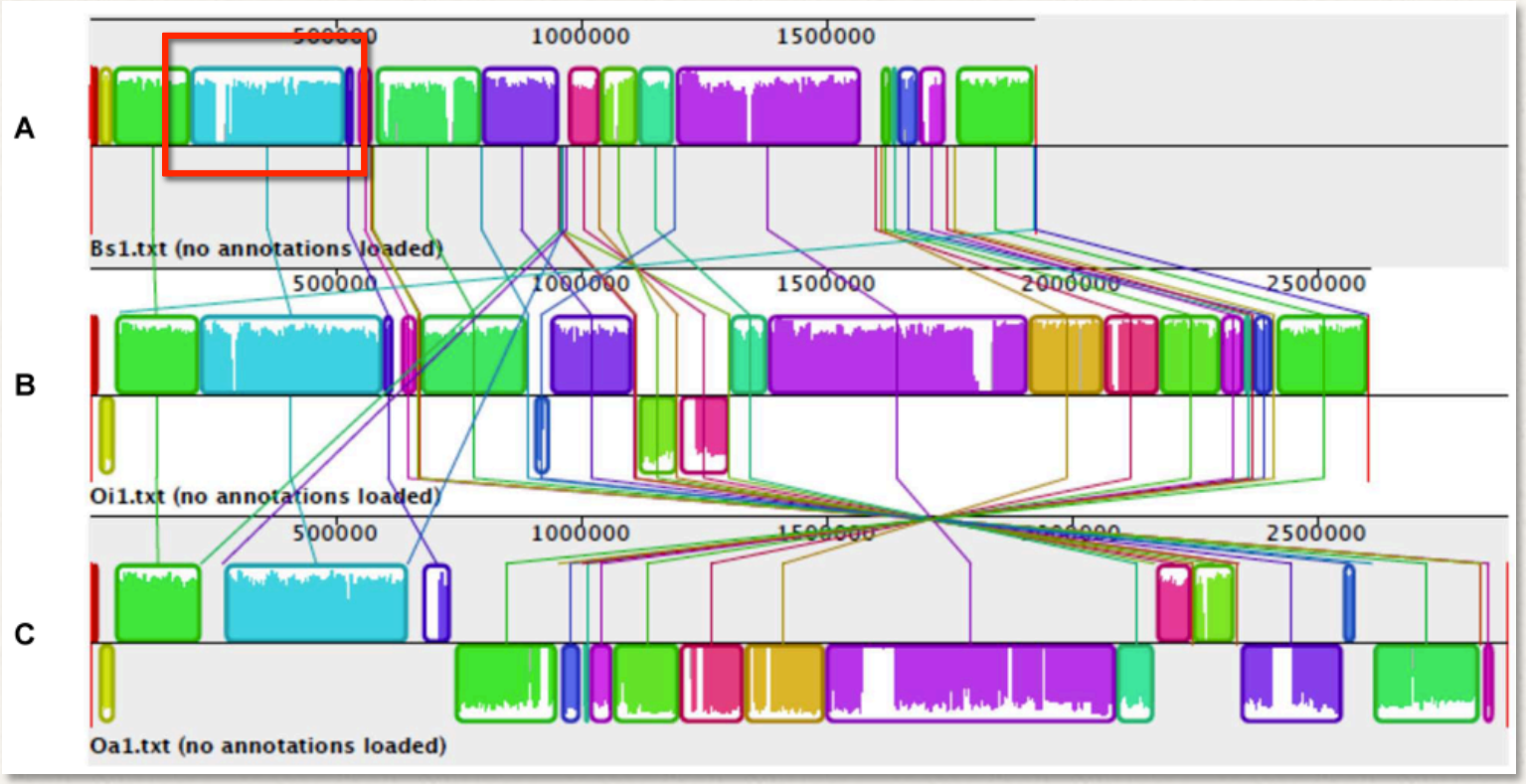
WGA: *Brucella suis, Ochtrobactrum intermedium & O. anthropi*



Aujoulat et al. 2012, Genes

WGA: *Brucella suis, Ochtrobactrum intermedium & O. anthropi*

Block: homologous and co-linear



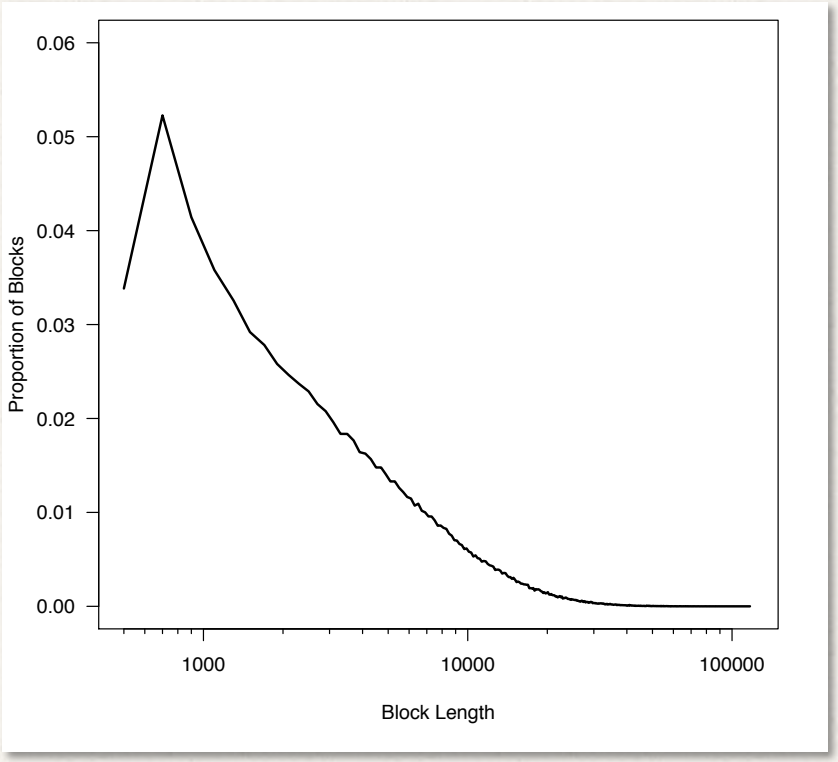
Aujoulat et al. 2012, Genes

Why align genomes?

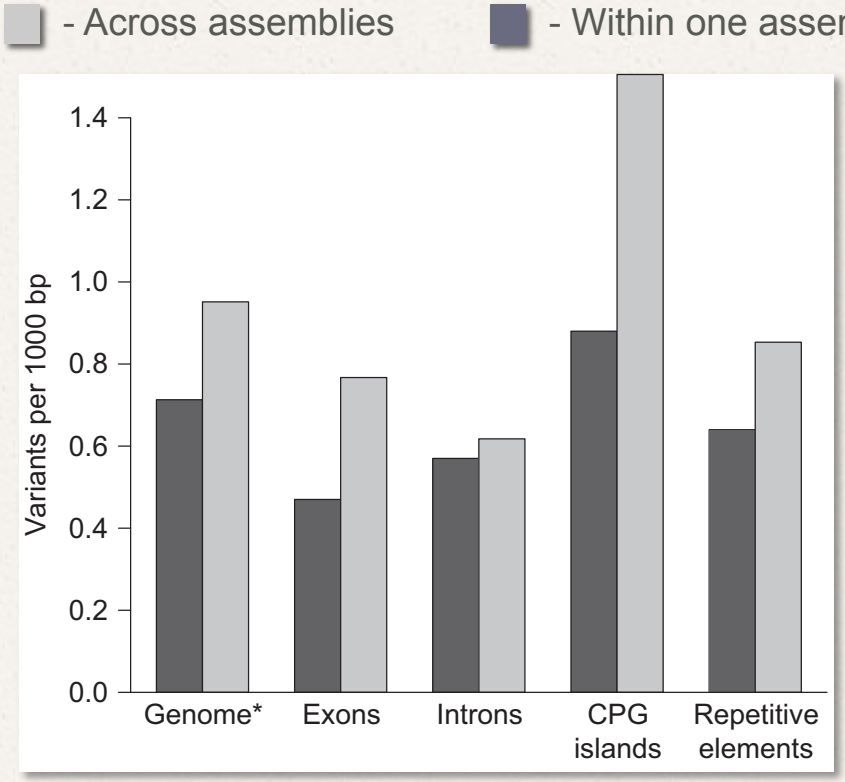
- Find syntenic regions (genomic structure)
  - Synteny: conservation of the order of regions
- Detect intergenomic variants (polymorphisms)

WGA: Two dromedary reference genomes

Block length histogram



Variants



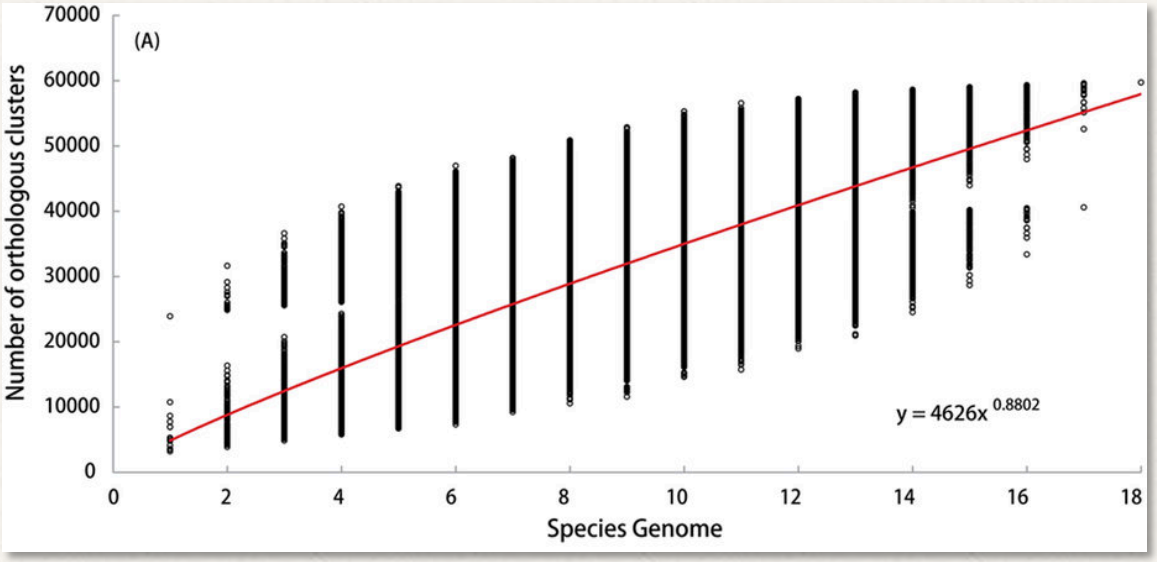
Fitak et al. 2016, Mol Ecol Res 16:314-324

Why align genomes?

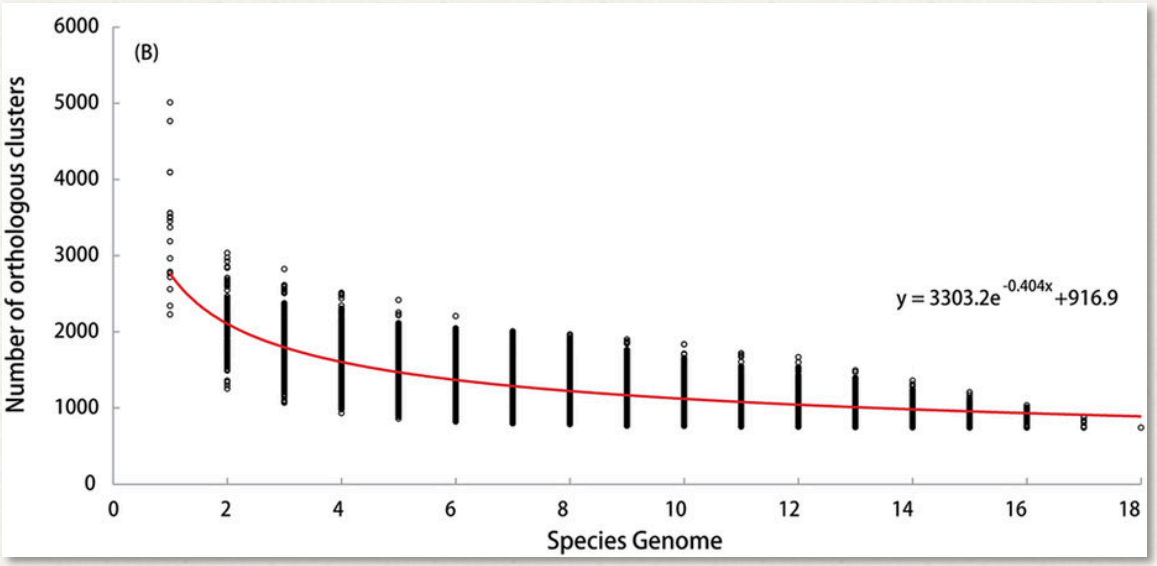
- Find syntenic regions (genomic structure)
  - Synteny: conservation of the order of regions
- Detect intergenomic variants (polymorphisms)
- Identify conserved regions
- Identify unique regions

WGA: 18 *Leptospira* species genomes

Pan-genome:



Core genome:

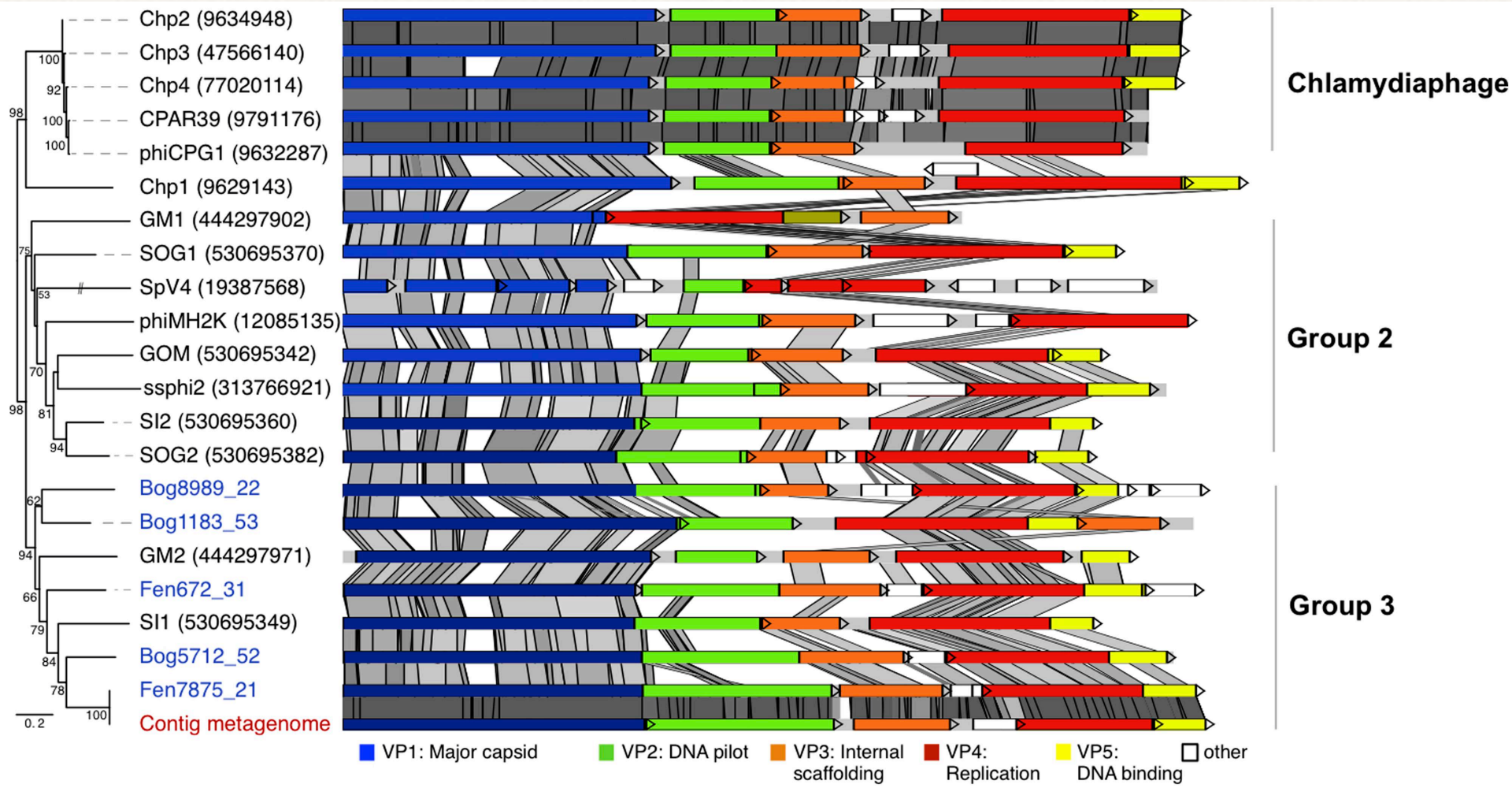


Xu et al. 2016, Sci Rep 6:20020

Why align genomes?

- Find syntenic regions (genomic structure)
  - Synteny: conservation of the order of regions
- Detect intergenomic variants (polymorphisms)
- Identify conserved regions
- Identify unique regions
- Phylogenomics

WGA: *Gokushovirinae* bacteriophages



Quaiser et al. 2015, Front Microbiol 6:375

WGA Tools

Software	Type	Pairwise vs Multiple
LastZ	Local	pairwise
MUMer	Local	pairwise
Mugsy	Hierarchical	multiple
Mauve	Hierarchical	multiple
MultiZ	Local	multiple
LAGAN	Global	both
Mavid	Global	multiple
progressiveCactus	Hierarchical/Cactus graphs	multiple

A Great Review:
Dewey 2012. Whole-Genome Alignment.
In *Evolutionary Genomics: Statistical and Computational Methods. p. 237-257*

WGA: File formats

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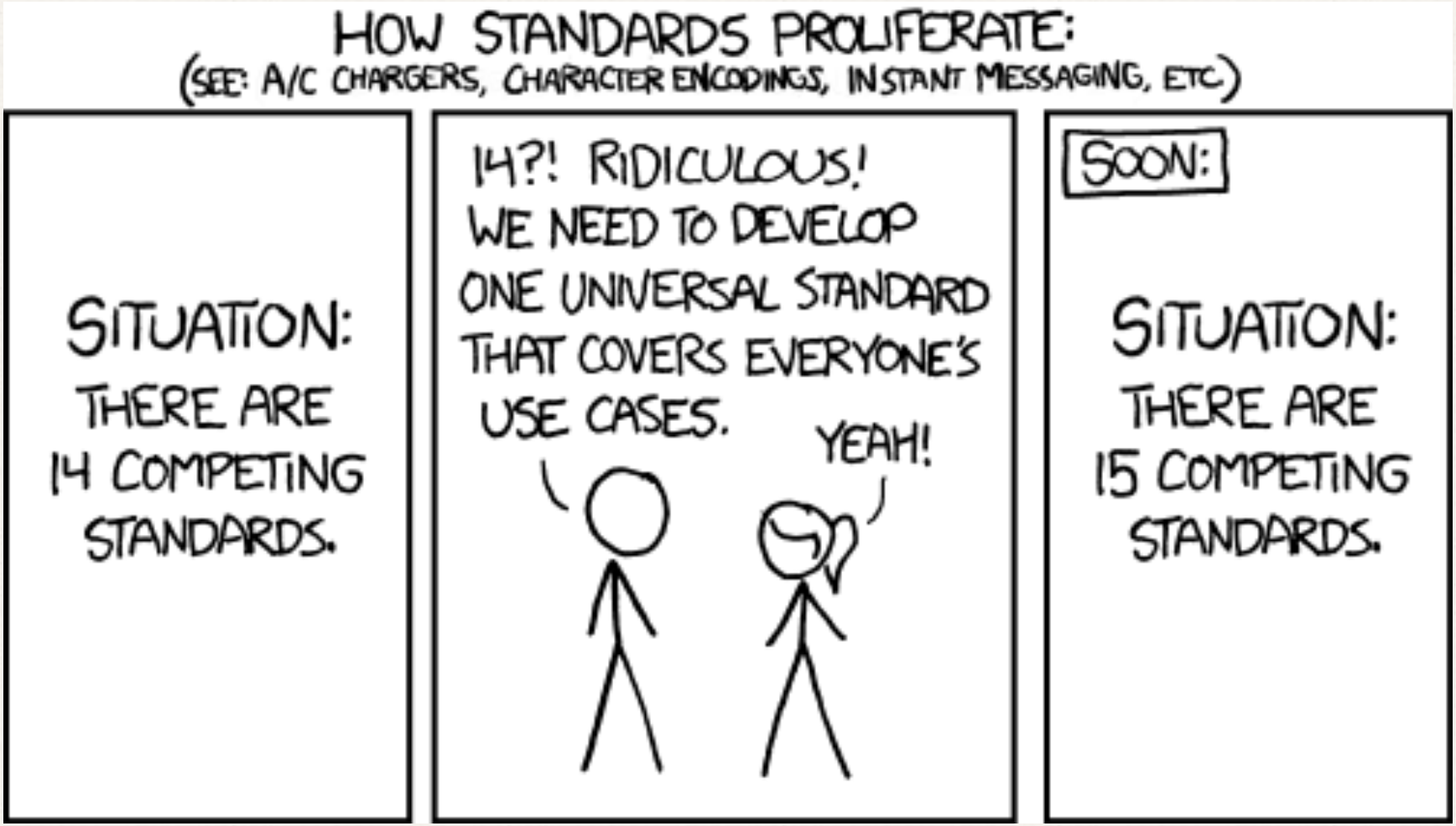

WGA: File formats

- MAF (multiple alignment format)

```
##maf version=1 scoring=tba.v8
# tba.v8 (((human chimp) baboon) (mouse rat))
# multiz.v7
# maf_project.v5 _tba_right.maf3 mouse _tba_C
# single_cov2.v4 single_cov2 /dev/stdin

a score=23262.0
s hg16.chr7     27578828 38 + 158545518 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s panTro1.chr6 28741140 38 + 161576975 AAA-GGGAATGTTAACCAAATGA---ATTGTCTCTTACGGTG
s baboon         116834 38 +   4622798 AAA-GGGAATGTTAACCAAATGA---GTTGTCTCTTATGGTG
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Header

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```

Block

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```

Score

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```

Sequence IDs

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Start

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```

Length Strand

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Source length

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```
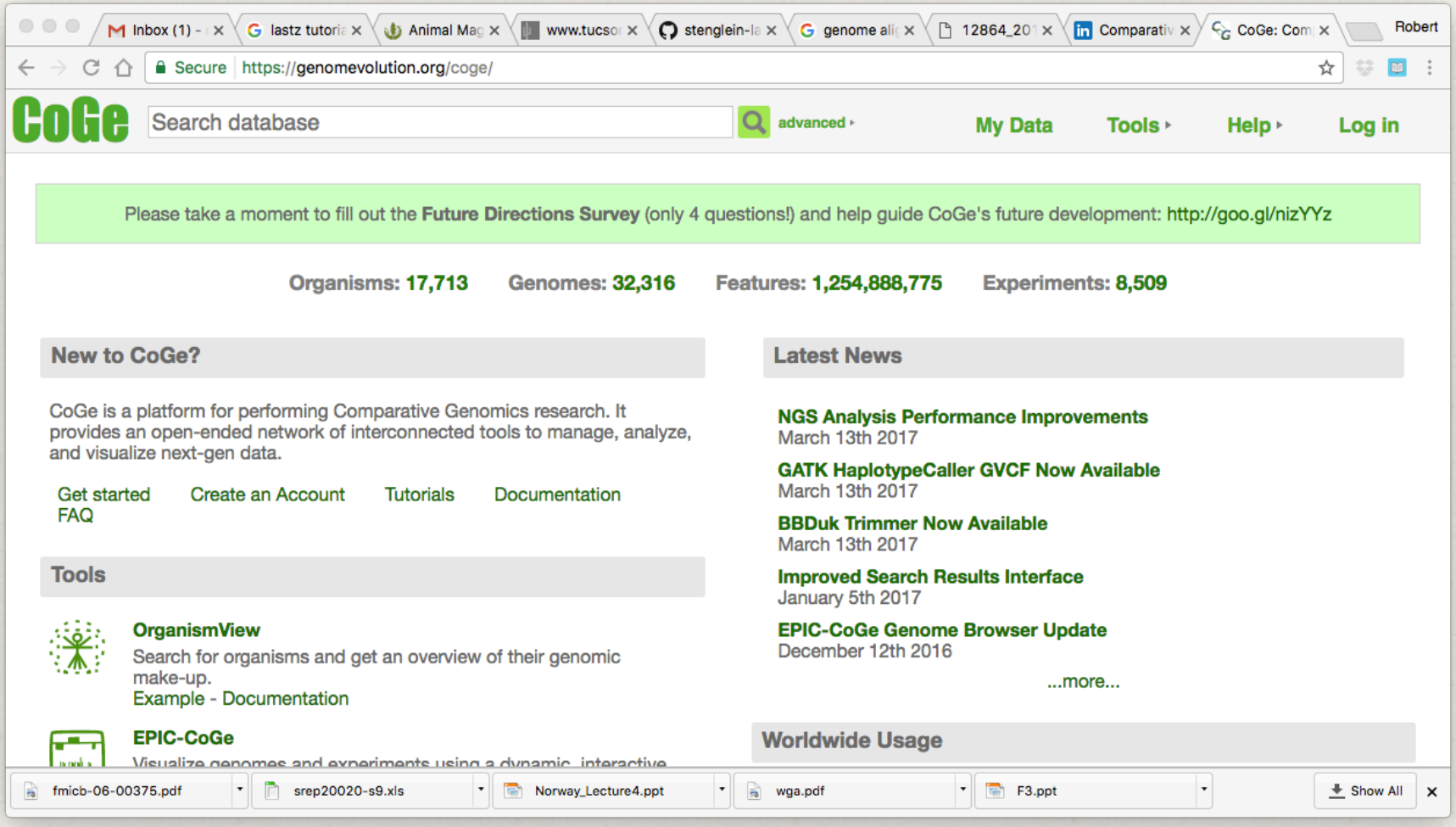

Aligned sequence block

CoGe: www.genomeevolution.org/coge



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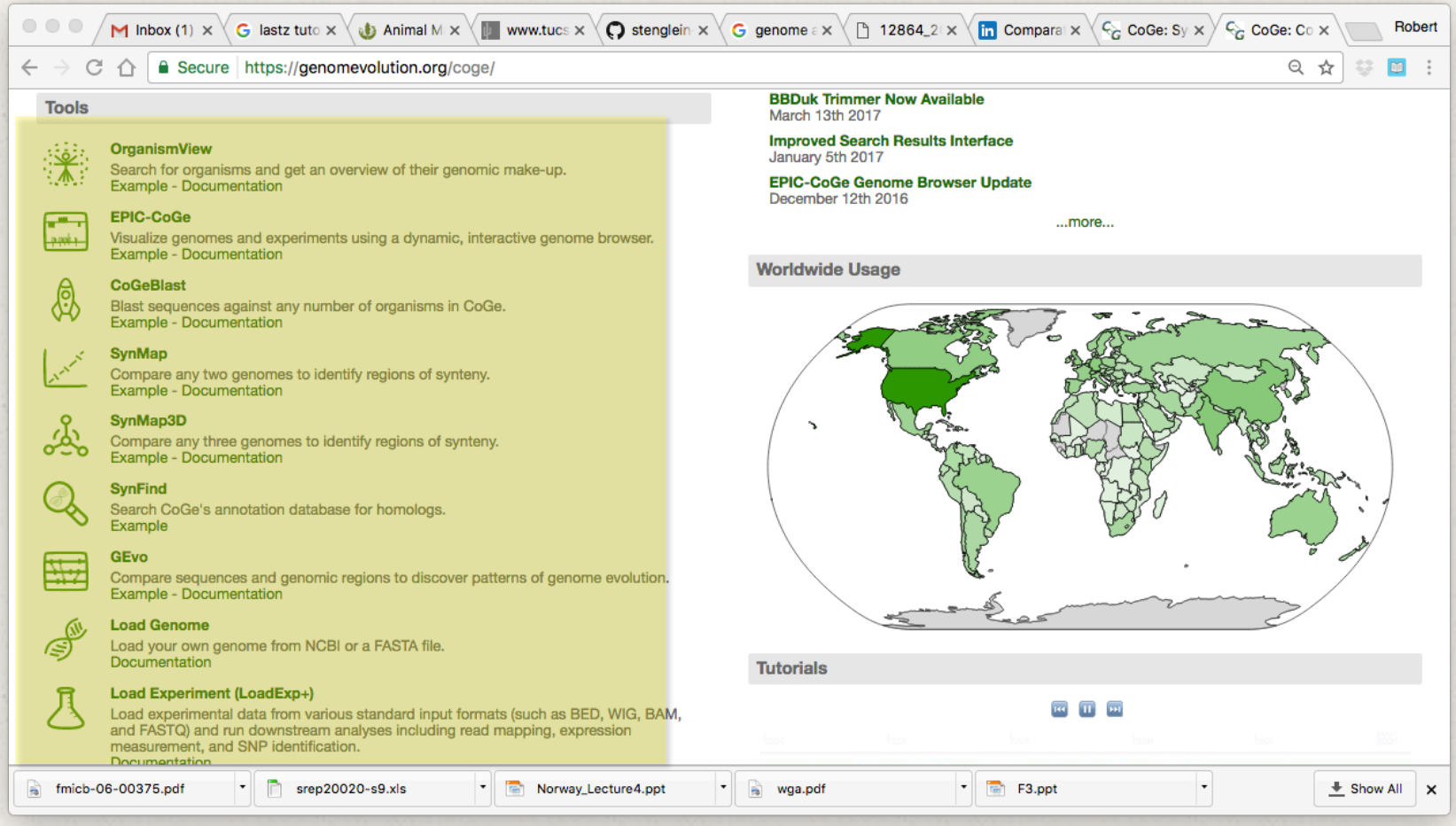

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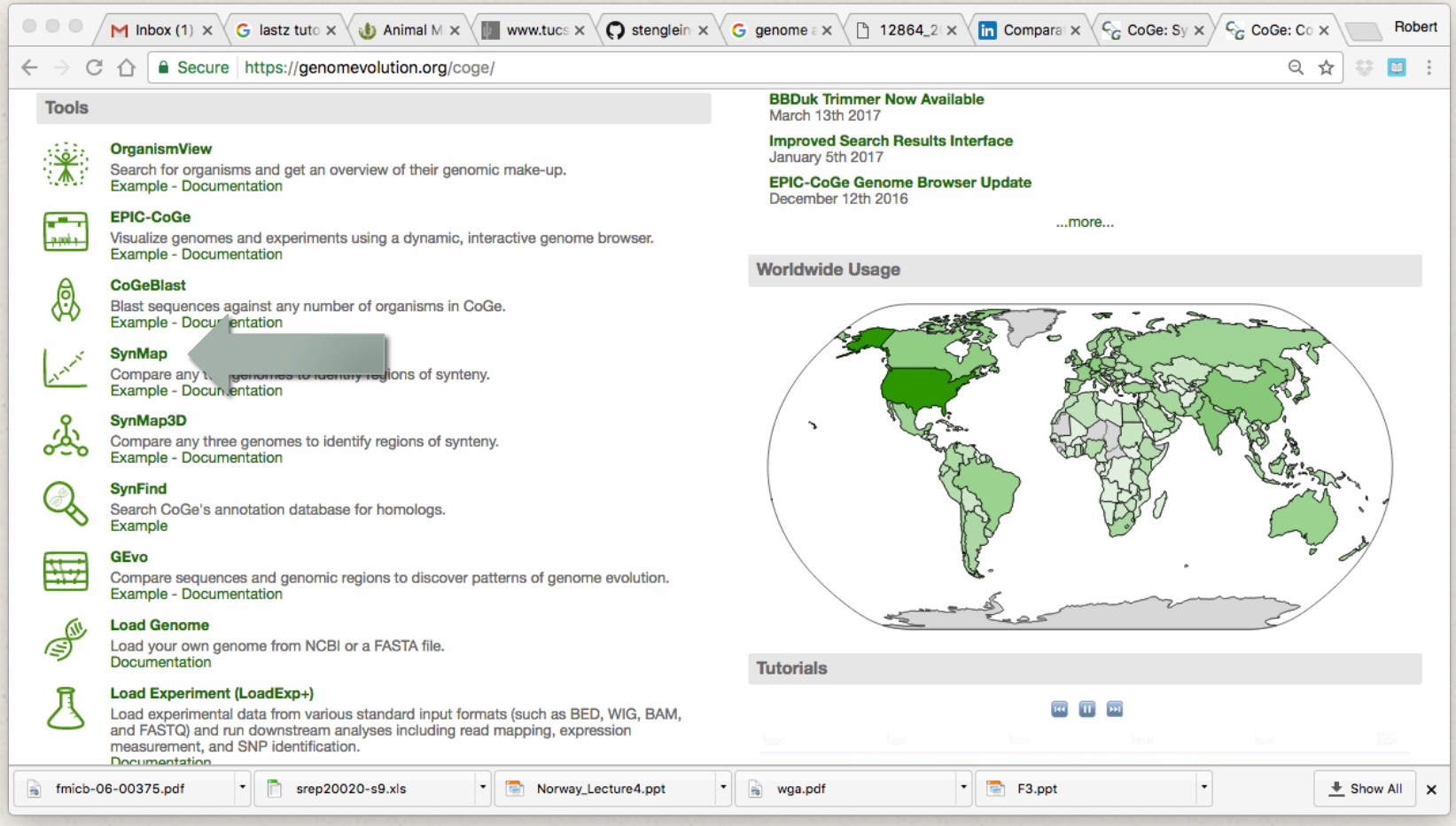

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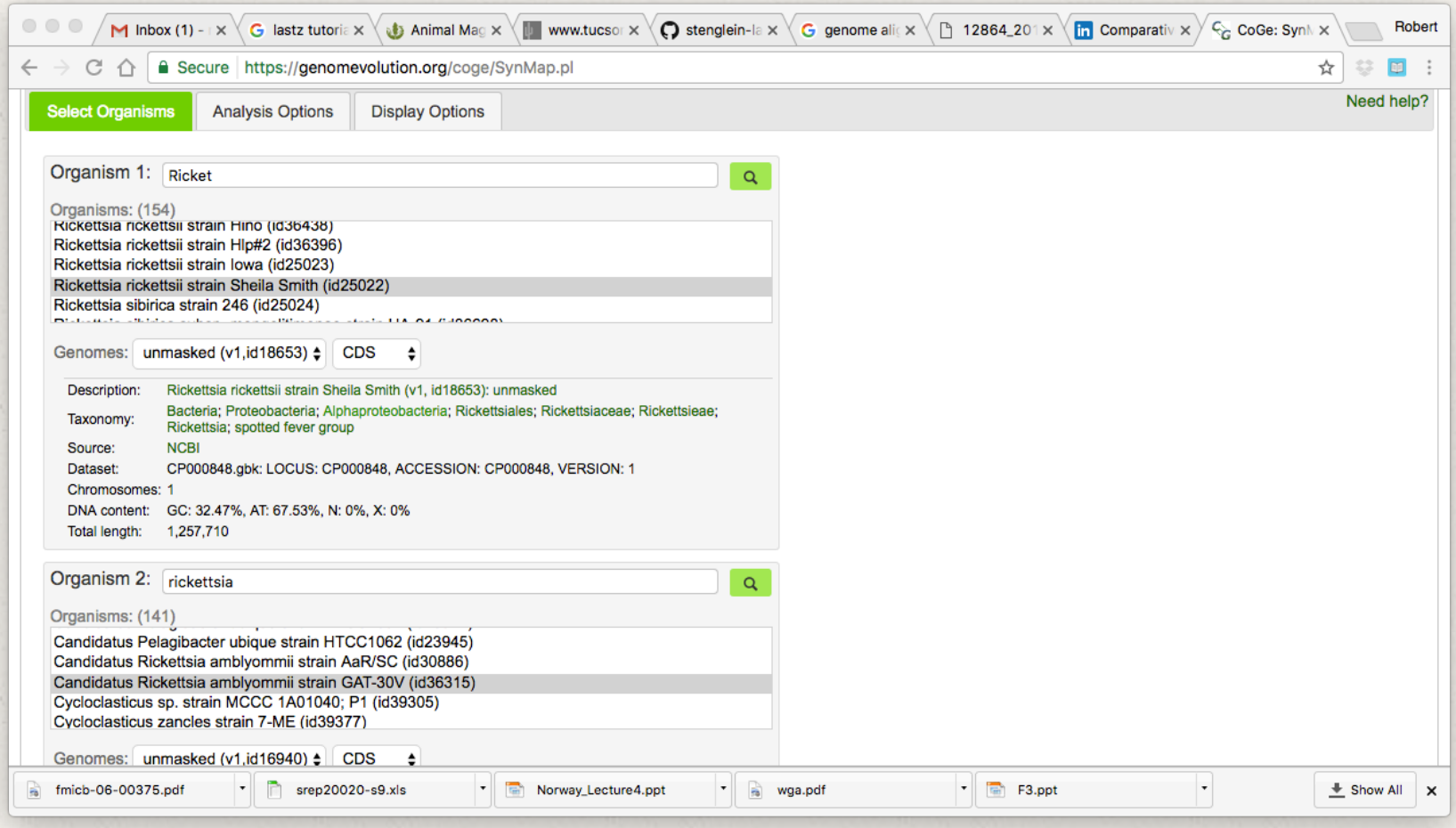

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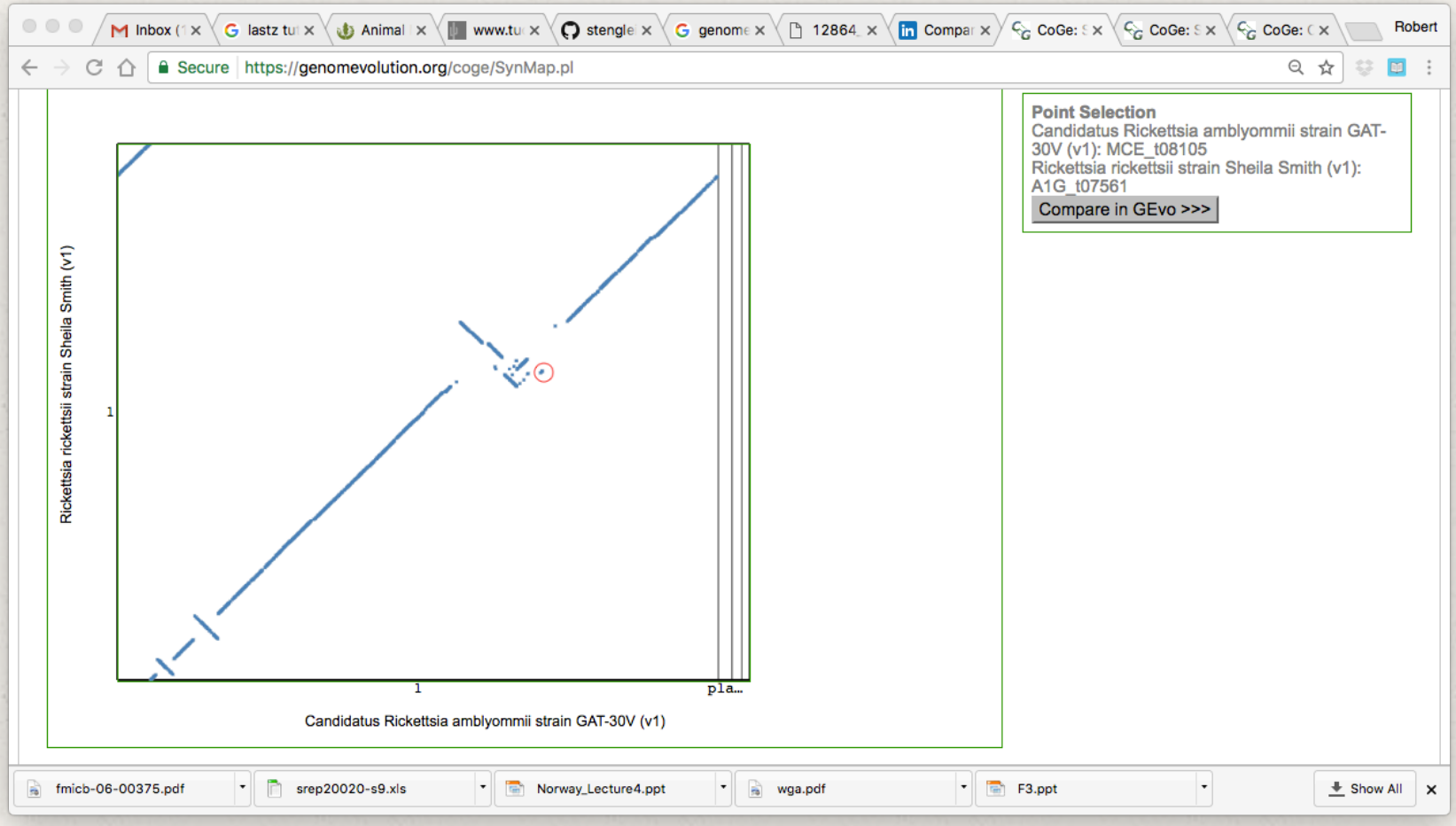

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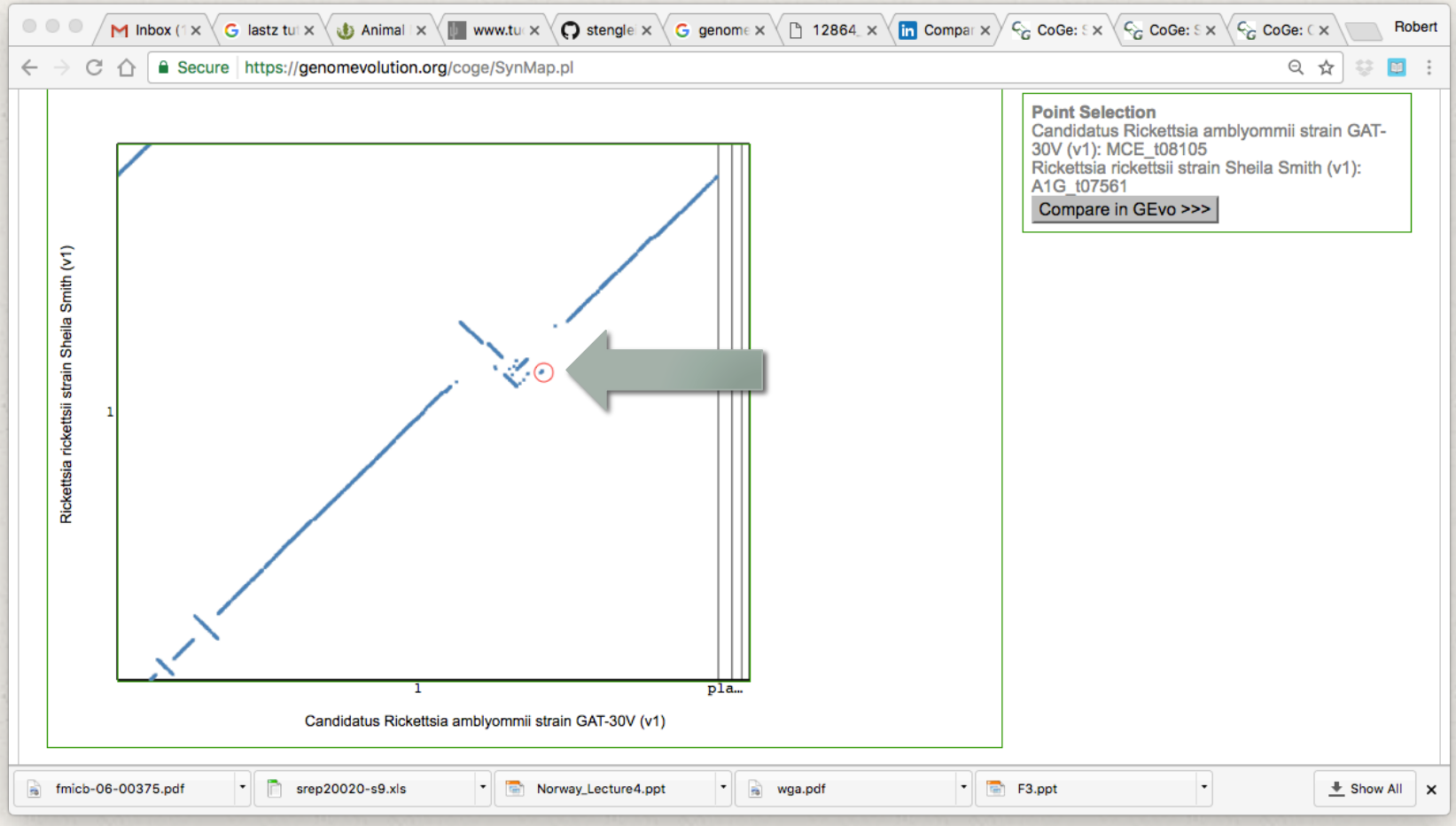

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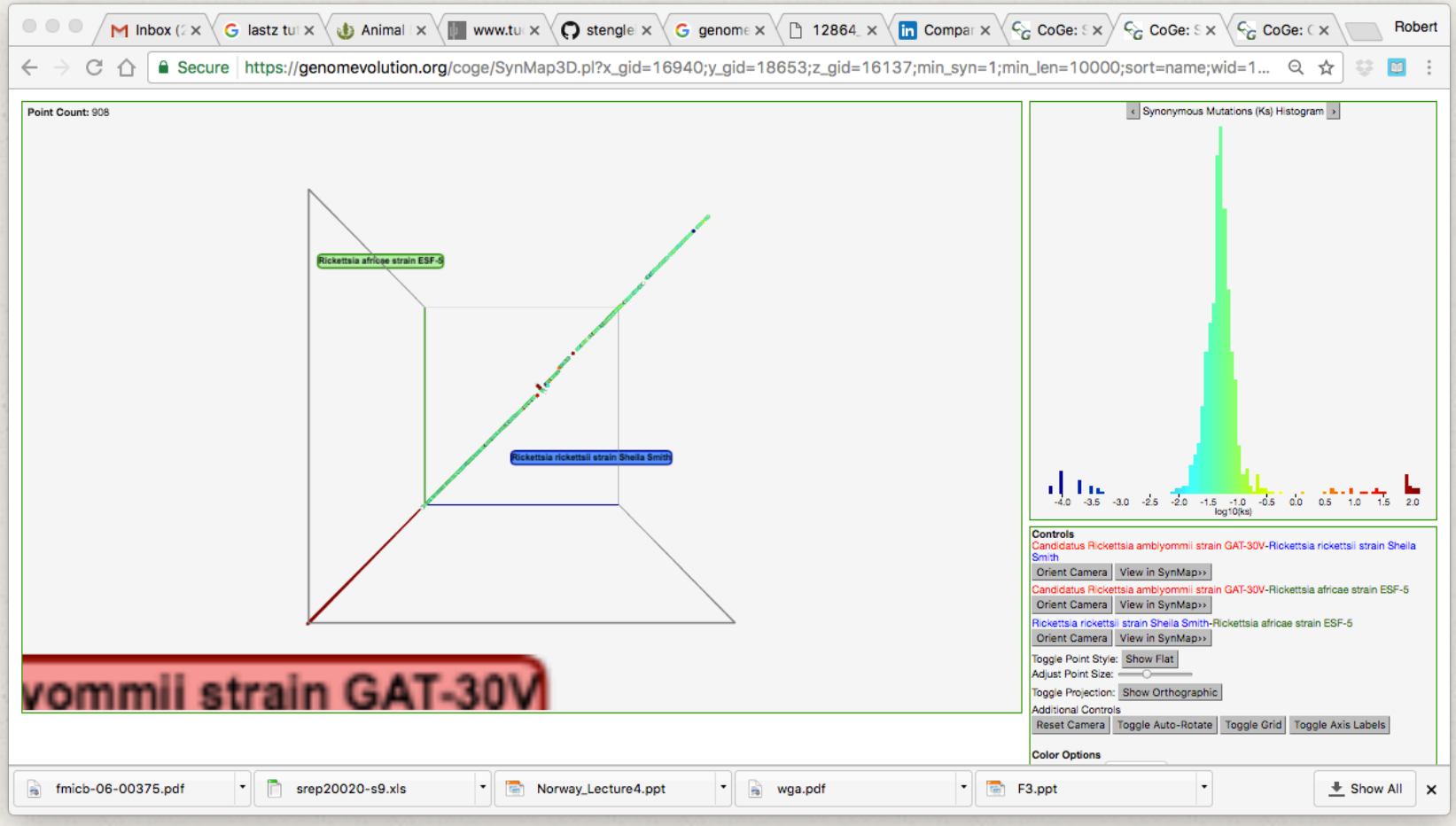

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