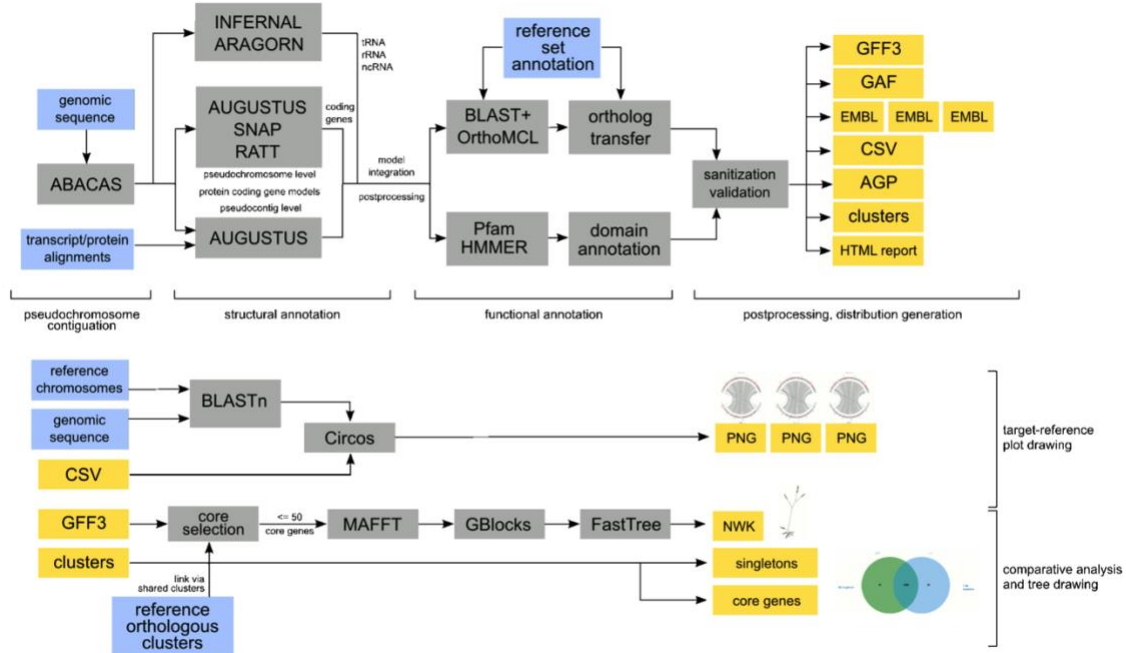


Genome Annotation with Companion (Part 2)

You should have gotten an email indicating the status of your annotation (ie. job started and job complete). The email contains a link to the annotation output.



- Explore your results with your group and discuss the annotation findings:
 - What does the genome statics tab tell you about your annotation? Are the results surprising? You can explore the reference genome you used in EuPathDB to help you assess the results. (For example, are you getting a reasonable number of genes? What about the GC content? Number of non-coding genes?)

This job was submitted **about 5 hours** ago and ran for **about 1 hour**, finally finishing at **2019-05-09 14:04:09 UTC**.

	Value
Number of annotated regions/sequences	78
Number of genes	3831
Gene density (genes/megabase)	416.98
Number of coding genes	3774
Number of pseudogenes	48
Number of genes with function	2326
Number of pseudogenes with function	24
Number of non-coding genes	57
Number of genes with multiple CDSs	17
Overall GC%	30.14
Coding GC%	31.76

- What does the “Result files” tab contain? What is an AGP file? What is a GFF3 file?

	Format	MD5	Size
Pseudochromosome level genomic sequence	FASTA		2.52 MB
Pseudochromosome level gene annotations	GFF3		2.78 MB
Pseudochromosome layout	AGP		3.92 KB
Scaffold level genomic sequence	FASTA		2.52 MB
Scaffold level gene annotations	GFF3		2.78 MB
Scaffold layout	AGP		16.2 KB
Pseudochromosome level sequence and annotation	EMBL		5.16 MB
Gene Ontology function assignments	GAF1		1.28 MB
Protein sequences	FASTA		2.33 MB

- What does the “orthology” tab display? How many predicted proteins from your new genome are in common with ones from the reference genome? How many are unique to yours? What do singletons represent (click on the singleton number to see what these genes are)?

- What does the phylogeny tab represent? Does it make sense?

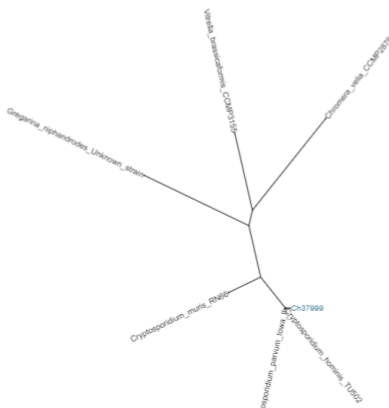
swfeltz_Chom37999 (Ch37999) Completed

This job was submitted **about 5 hours** ago and ran for **about 1 hour**, finally finishing at **2019-05-09 14:04:09 UTC**.

[Genome statistics](#) [Result files](#) [Orthology](#) **Phylogeny** [Synteny](#) [Job parameters](#) [Pipeline logs](#) [Validator report](#)

Click and drag in the diagram below to pan around. Use the mouse wheel to zoom in and out. The newly annotated genome in this job is highlighted: Ch37999.

Rectangular Circular Radial
Diagonal



- Examine the Synteny tab – are these genomes syntenic?

P_coatneyi_Hackeri (pcoa) Completed

This job was submitted **4 days** ago and ran for **about 4 hours**, finally finishing at **2016-02-13 08:49:01 UTC**.

[Genome statistics](#) [Result files](#) [Orthology](#) [Phylogeny](#) **Synteny** [Job parameters](#) [Pipeline logs](#) [Validator report](#)

Each circle below represents a single target-reference pseudochromosome alignment. Click on the thumbnail to zoom in. [Download all 15 images \(ZIP\)](#)

