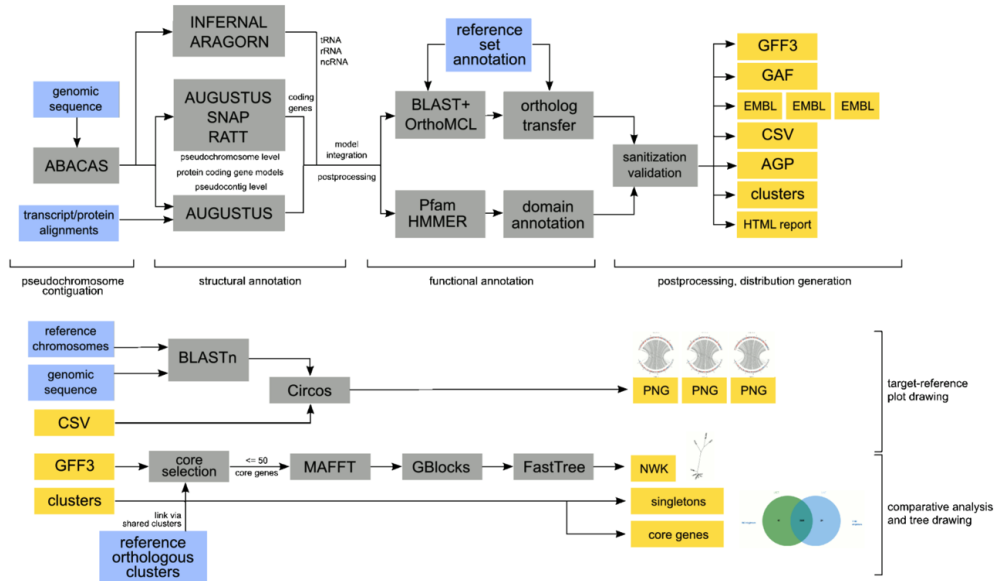# Genome Annotation with Companion (Part 2)

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?)

swfeltz_Cmel-Cpar (Cmel)   **Completed**

This job was submitted **7 days** ago and ran for **about 1 hour**, finally finishing at **2019-05-29 21:05:14 UTC**.

Genome statistics   Result files   Orthology   Phylogeny   Synteny   Job parameters

Pipeline logs   Validator report

	Value
Number of annotated regions/sequences	9
Number of genes	3241
Gene density (genes/megabase)	354.5
Number of coding genes	3181
Number of pseudogenes	618
Number of genes with function	2155
Number of pseudogenes with function	536
Number of non-coding genes	60
Number of genes with multiple CDSs	285
Overall GC%	30.97
Coding GC%	32.34

o What does the "Result files" tab contain? What is an AGP file? What is a GFF3 file?

o Upload the GFF3 file to GBrowse and compare your annotation with the genome in EuPathDB. You can download the GFF3 to the computer and upload to GBRrowse or you can copy the link from the Companion results and 'Upload via URL' into GBRowse. Which GFF3 file should you use?

swfeltz_Cmel-Cpar (Cmel)   **Completed**

This job was submitted **7 days** ago and ran for **about 1 hour**, finally finishing at **2019-05-29 21:05:14 UTC**.
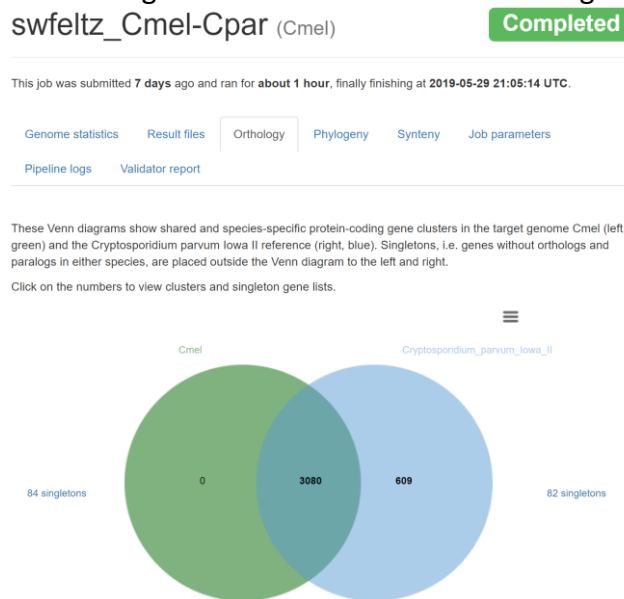
Genome statistics   Result files   Orthology   Phylogeny   Synteny   Job parameters

Pipeline logs   Validator report

|	Format	MD5	Size
⬇ Pseudochromosome level genomic sequence	FASTA	▥	2.5 MB
⬇ Pseudochromosome level gene annotations	GFF3	▥	2.74 MB
⬇ Pseudochromosome layout	AGP	▥	5.12 KB
⬇ Scaffold level genomic sequence	FASTA	▥	2.5 MB
⬇ Scaffold level gene annotations	GFF3	▥	2.83 MB
⬇ Scaffold layout	AGP	▥	2.84 KB
⬇ Pseudochromosome level sequence and annotation	EMBL	▥	4.95 MB
⬇ Gene Ontology function assignments	GAF1	▥	1.44 MB
⬇ Protein sequences	FASTA	▥	2.44 MB

Download the file or copy the link to GBRowse Custom Tracks tab.

o 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?

swfeltz_Cmel-Cpar (Cmel)   **Completed**

This job was submitted **7 days** ago and ran for **about 1 hour**, finally finishing at **2019-05-29 21:05:14 UTC**.

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These Venn diagrams show shared and species-specific protein-coding gene clusters in the target genome Cmel (left, green) and the Cryptosporidium parvum Iowa II reference (right, blue). Singletons, i.e. genes without orthologs and paralogs in either species, are placed outside the Venn diagram to the left and right.

Click on the numbers to view clusters and singleton gene lists.

≡

Cmel   Cryptosporidium_parvum_Iowa_II

84 singletons   0   3080   609   82 singletons

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

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: Cmel.

| Rectangular | Circular | Radial | Diagonal |
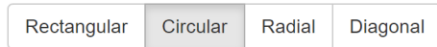
- ○ Examine the Synteny tab – are these genomes syntenic? Do you notice any differences between the two genomes?

swfeltz_Cmel-Cpar (Cmel)

Completed

This job was submitted **7 days** ago and ran for **about 1 hour**, finally finishing at **2019-05-29 21:05:14 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 9 images (ZIP)

1 ⬇   2 ⬇   3 ⬇   4 ⬇   5 ⬇   6 ⬇   7 ⬇   8 ⬇   Cmel_00 ⬇