# Companion
## Reference Based Genome Annotation and analysis of parasite genomes

https://companion.sanger.ac.uk/
https://doi.org/10.1093/nar/gkw292

- Web service pre-loaded with EuPathDB and GeneDB genomes
- Produces an annotation of your assembled genome
  - Gene models  (protein coding, ncRNA)
- Performs some analyses between your genome and reference
  - Visualization
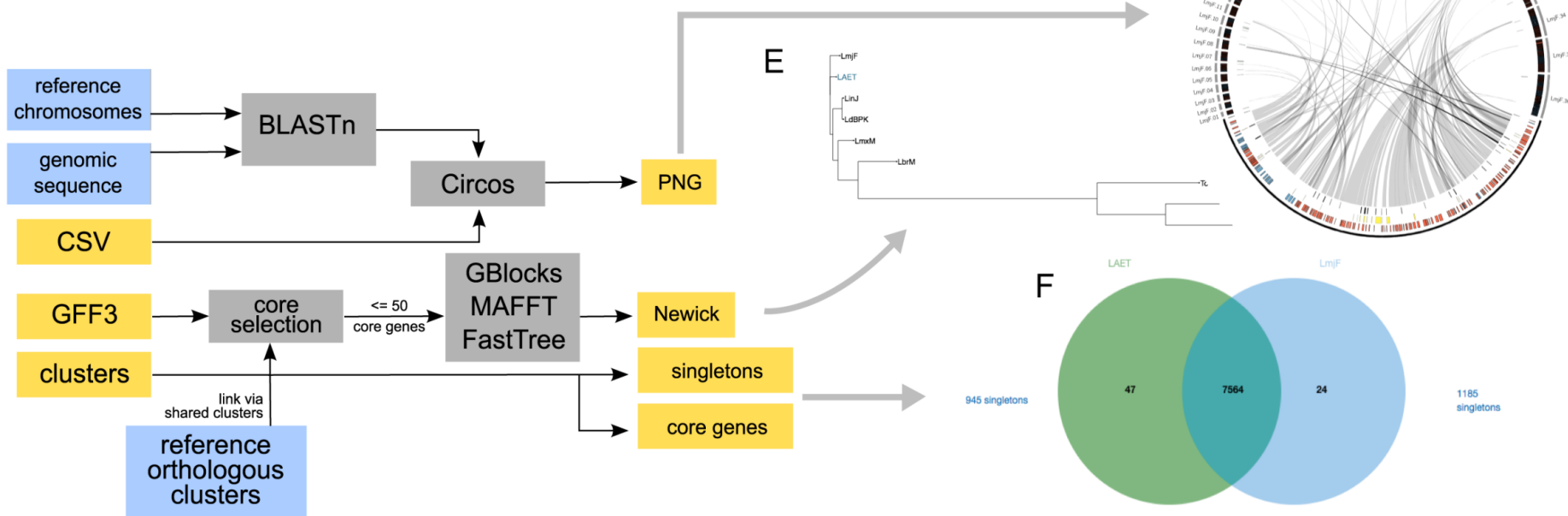  - Species tree
  - synteny

# ANNOTATION WORKFLOW
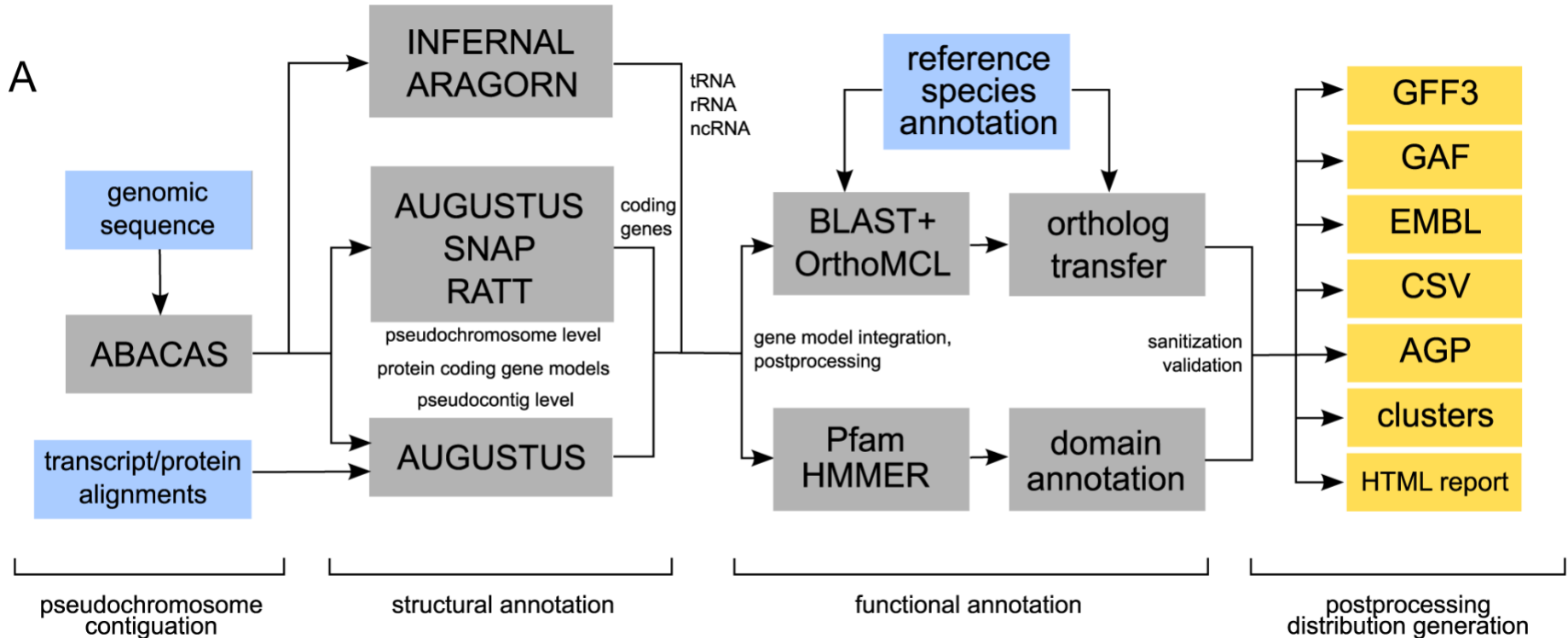


- INPUT – assembled genome (contigs, scaffolds or chromosomes)
- Pseudochromosome contiguation – Orient genomic sequences to match chromosome structure of the reference
- Structural annotation – produced gene models (homology and ab initio)
- Functional annotation – info about the activity/purpose/activity of the gene product (OrthoMCL and PfamHMMER)
- OUTPUT – files in yellow

# Analysis and Visualization



- VISUALIZATION and ANALYSES
  - Circos Synteny plots between your genome and reference
  - Species tree
  - Venn diagram of shared and species specific genes.

Upload genomic sequences in Fasta format
Choose params for the annotation run
Start the run
Look at results tomorrow