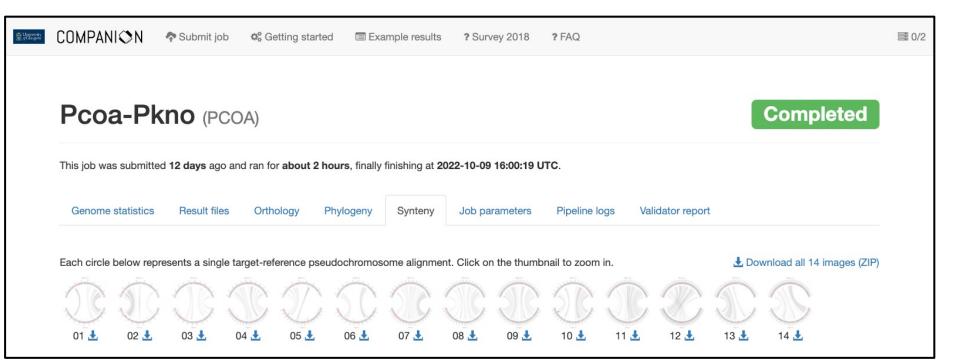
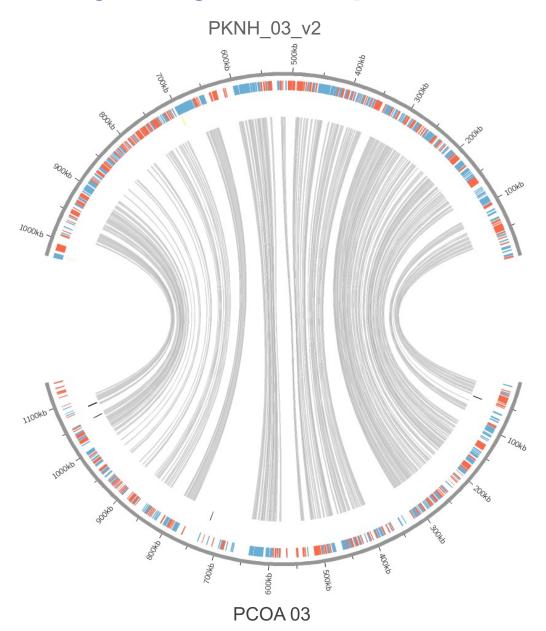
09:30-11:15 BST 10:30-12:15 CAT	8	Group exercise: Companion results analysis ACT.
15 minutes		Coffee Break
11:30-12:30 BST		
12:30-13:30 CAT	9	Introduction to Linux
1 hour		Lunch Break
13:30-16:15 BST		45-minute talk then
14:30-17:15 CAT	11	Group exercise: Introduction to HTS & mapping exercise (Linux)
15 minutes		Tea Break
16:30-17:30 BST		
17:30-18:30 CAT	12	Variation searches in VEuPathDB (SNPs and CNVs)

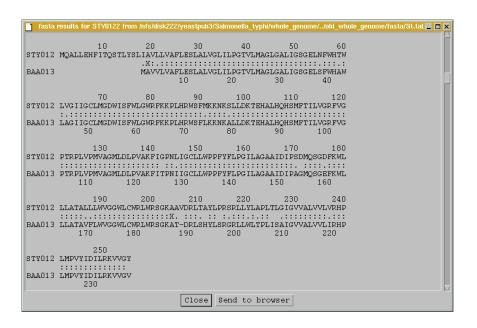
Synteny in Companion

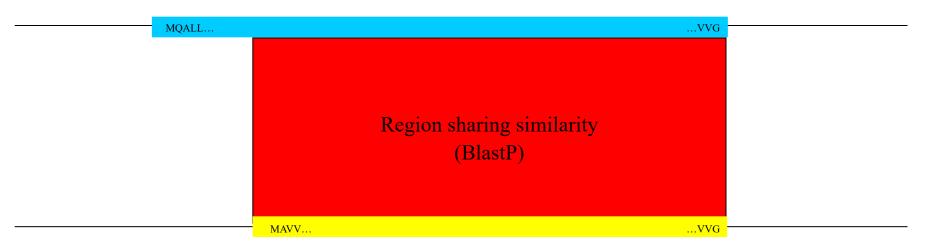


Synteny in Companion

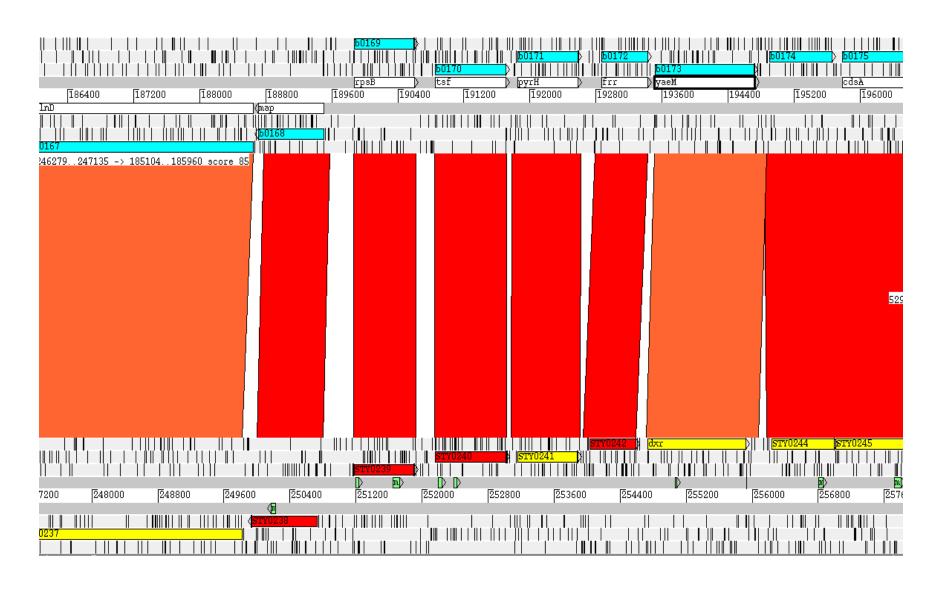


Representing sequence similarity/identity



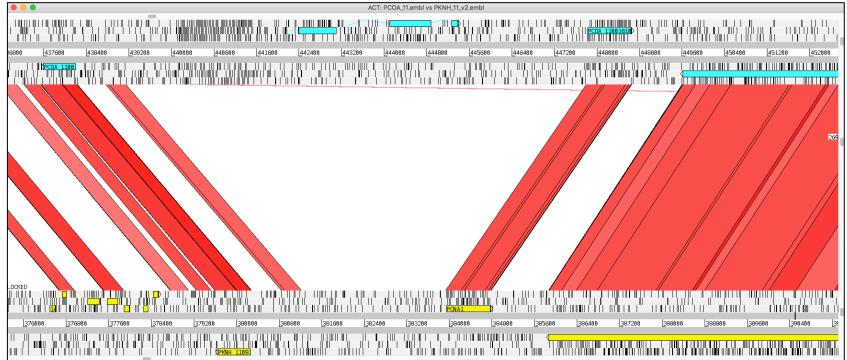


ACT - Artemis Comparison Tool



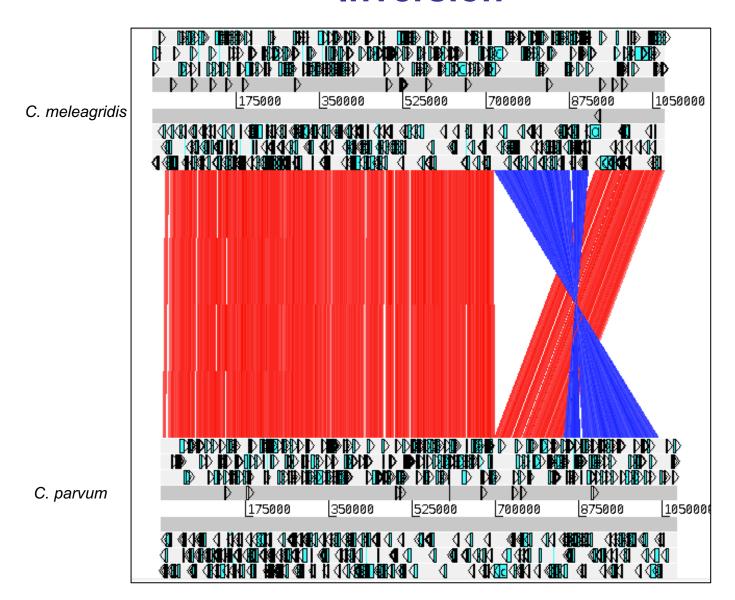
Synteny break

P. coatneyi



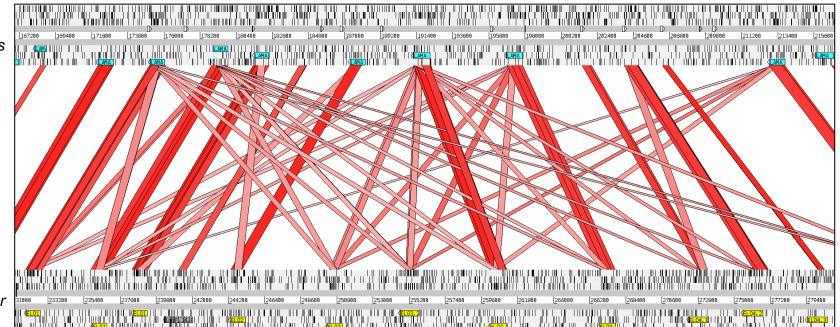
P. knowlesi

Inversion



Gene family

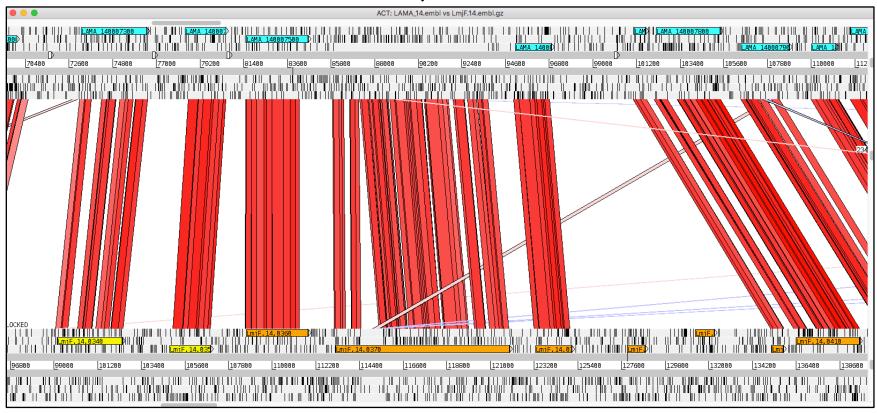
L. amazonensis



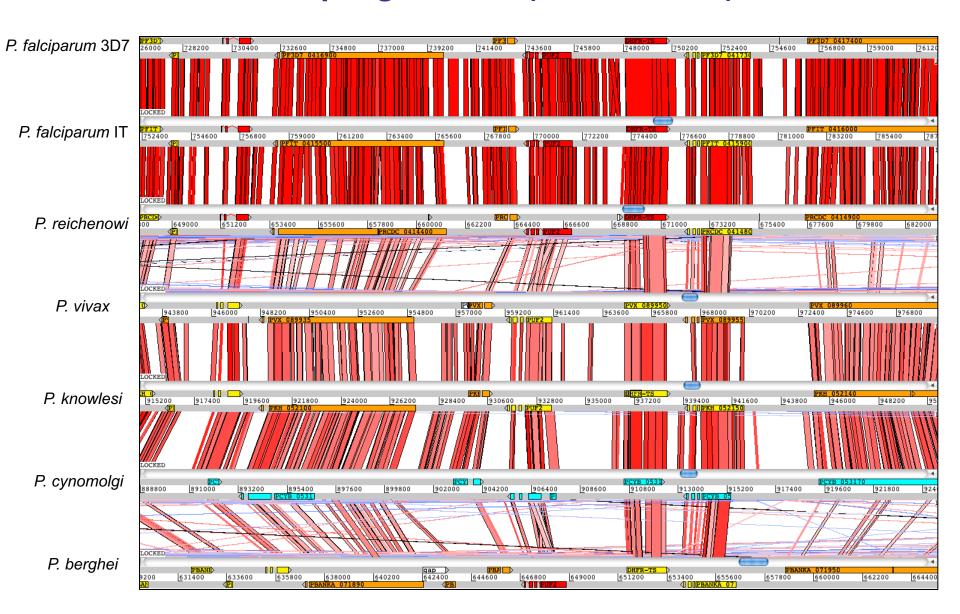
L. major

Missing gene





Multiple genomes (Plasmodium)



Additional information on ACT http://sanger-pathogens.github.io/Artemis/ACT/



Home | Artemis | ACT | BamView | DNAPlotter |

Artemis Comparison Tool (ACT)

ACT is a Java application for displaying pairwise comparisons between two or more DNA sequences. It can be used to identify and analyse regions of similarity and difference between genomes and to explore conservation of synteny, in the context of the entire sequences and their annotation. It can read complete EMBL, GENBANK and GFF entries or sequences in FASTA or raw format.

Comparison files can be generated in a number of ways, including via the NCBI Blast web site. This is detailed in the ACT manual.