

## **Supplementary materials: figures**

SF1. Genome assembly pipeline

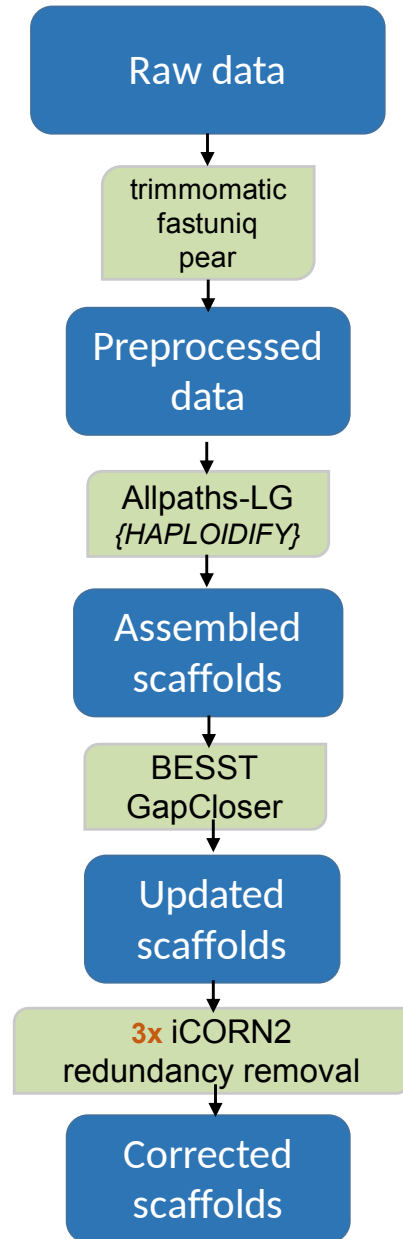
SF2. Gene annotation pipeline

SF3. Genome-wide synteny between *O. felineus*, *O. viverrini* and *C. sinensis*

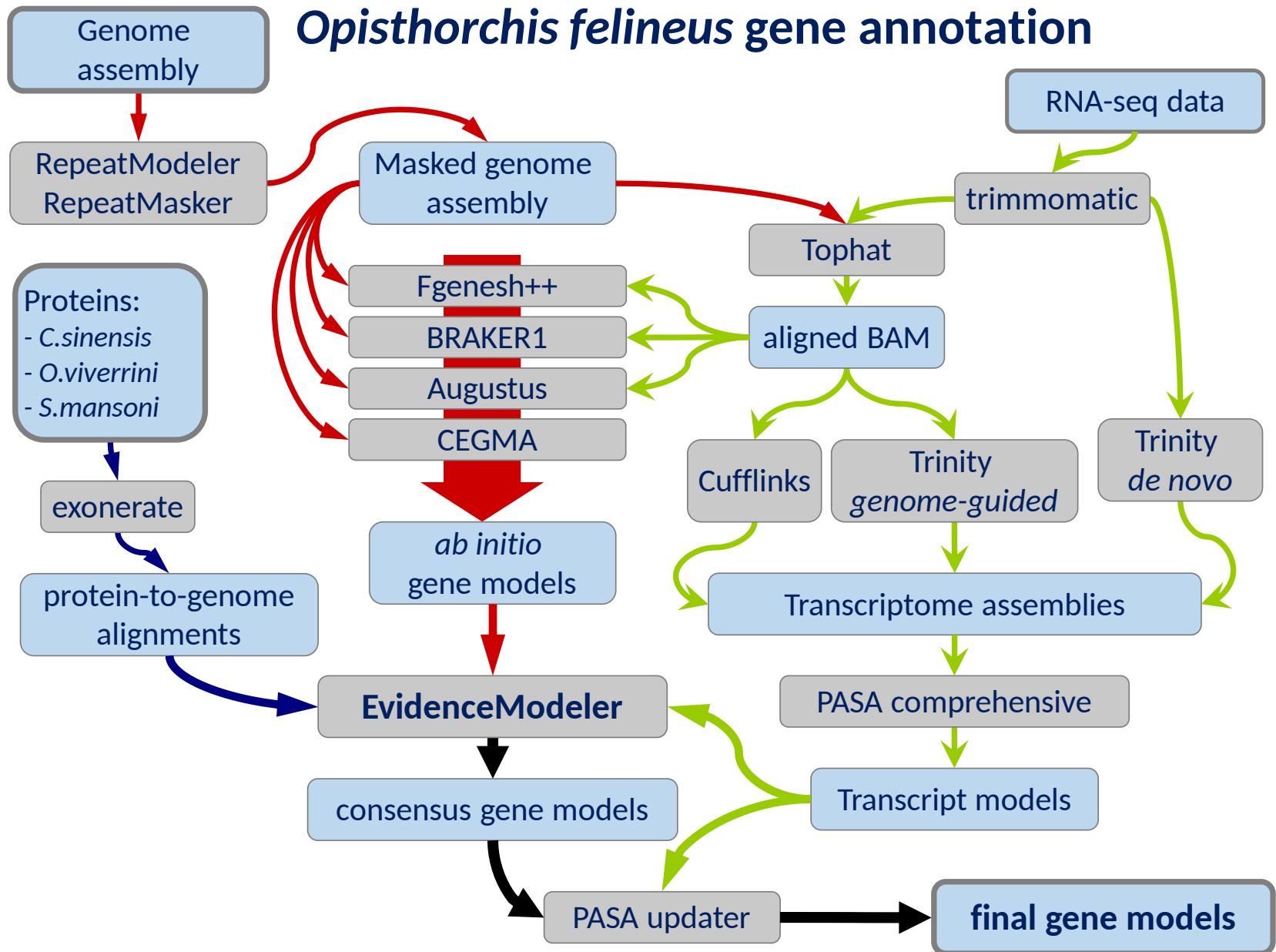
SF4. Repetitive elements in *O. felineus*, *C. sinensis*, *O. viverrini* and *F. hepatica* genomes

SF5. Stage-specific expression of detoxification genes estimated on *O. felineus* transcriptome data.

## SF1. Genome assembly pipeline



## SF2. Gene annotation pipeline

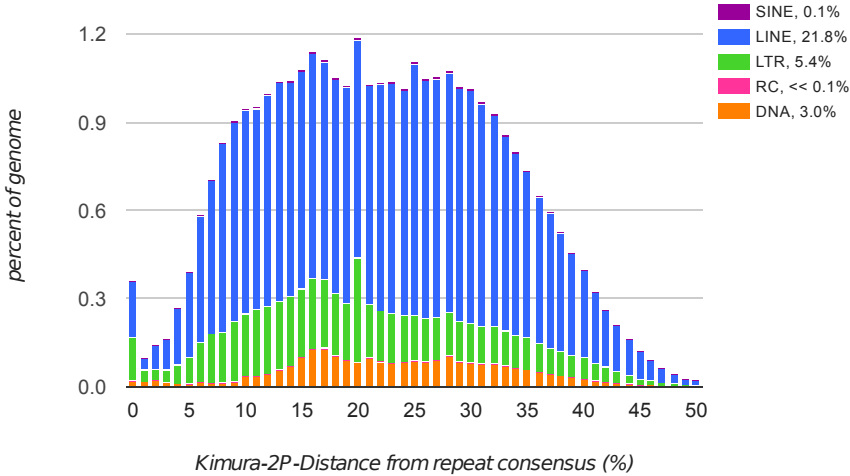




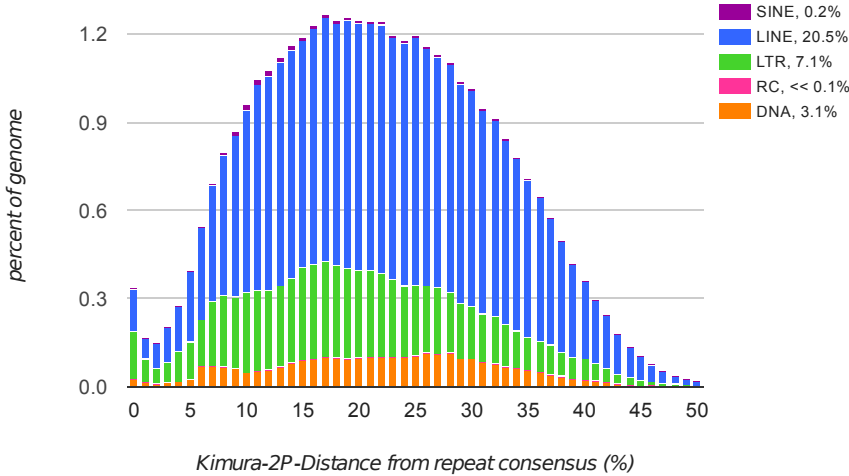
**SF3. Alignment of the top 10 *O. felinus* contigs with the highest coverage by *O. viverrini* and *C. sinensis* genomic sequences.** The *O. felinus* contig sequence is represented by middle grey bar. Alignment of the *C. sinensis* genomic sequences is shown by upper bar denoted by 'Cs' on the left. Alignment of the *O. viverrini* genomic sequences is shown by upper bar denoted by 'Ov' on the left. Aligned sequences from the same contig have the same color. Colors of *O. viverrini* and *C. sinensis* contigs are shown as color bars at the bottom of the figure. Colors reflect relative degree of contigs similarity from highest (red) to lowest (blue).

# SF4.Repetitive elements in *O. felinus*, *C. sinensis*, *O. viverrini*, and *F. hepatica* genomes

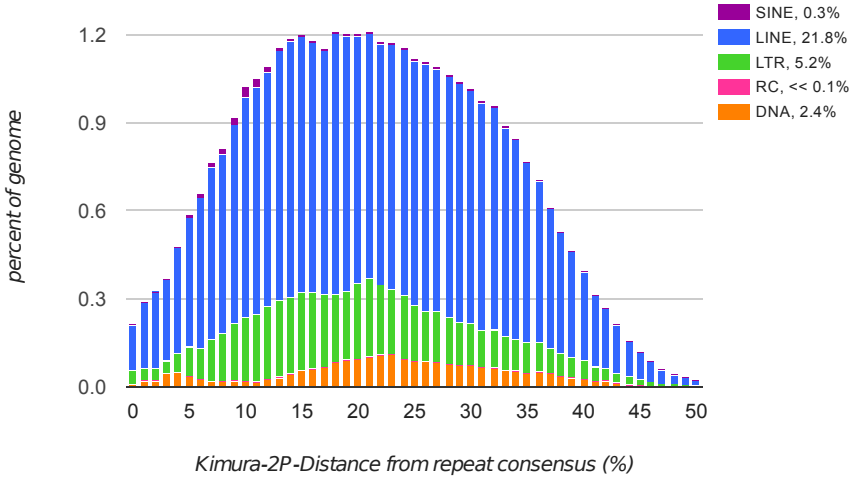
*Opisthorchis felinus* ( 30.3% total masked )



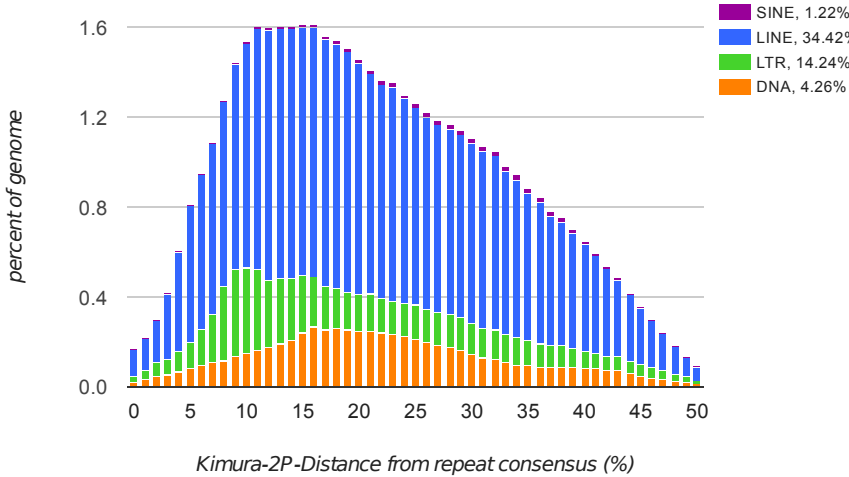
*Opisthorchis viverrini* ( 30.9% total masked )

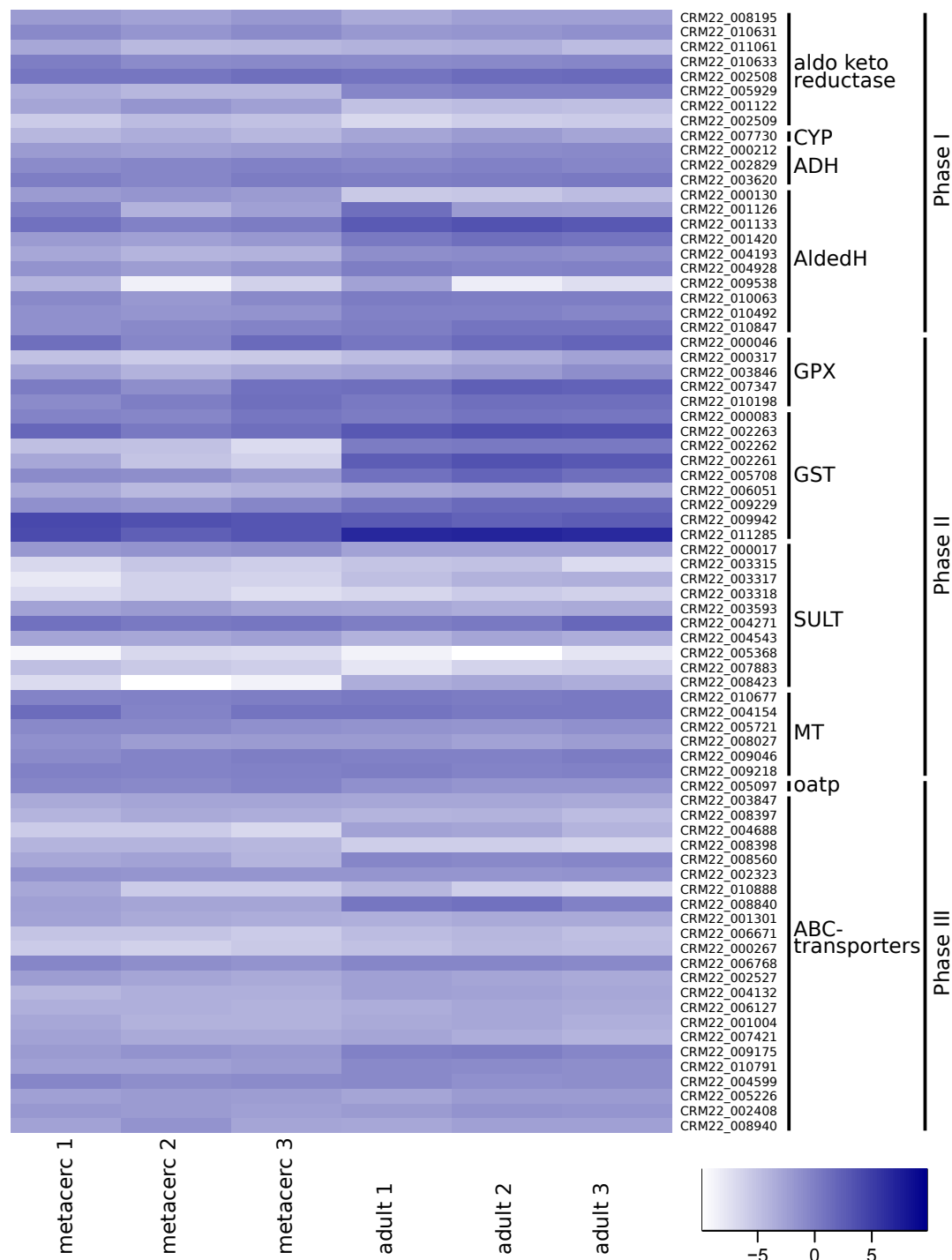


*Clonorchis sinensis* ( 29.6% total masked )



*Fasciola hepatica* ( 54.23% total masked )





## SF5. Stage-specific expression of detoxification genes estimated on *O. felineus* transcriptome data.

To analyze expression differences between genes, normalized read counts from RNA-seq data were transformed into log<sub>2</sub>(FPKM) values, i.e. transcript abundance.