

SUPPLEMENTARY INFORMATION

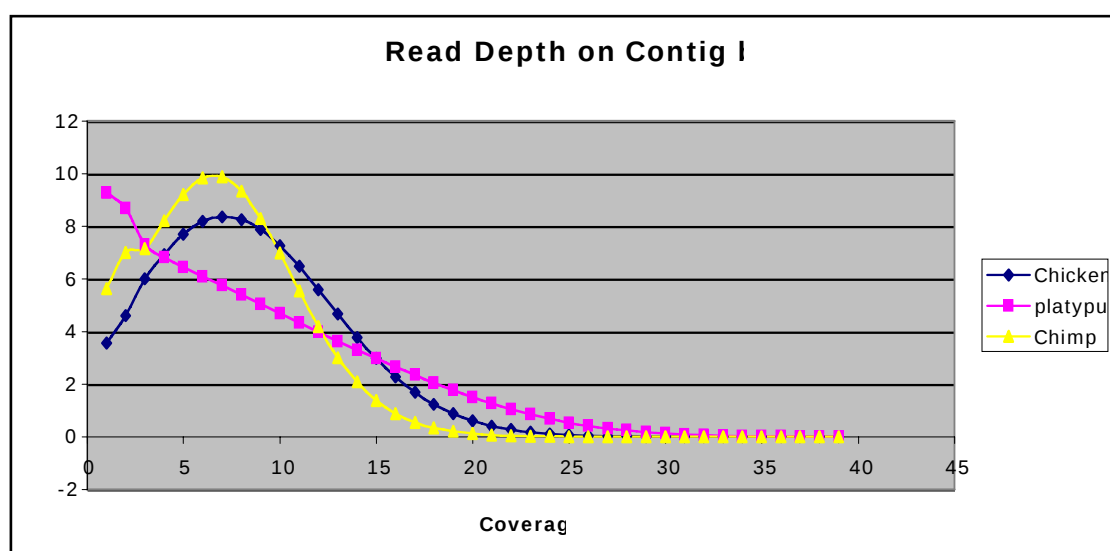
Figure A1. Describes format followed for read depth distribution.**Figure A2.** Read depth on contig base pairs.

Figure A3. Distribution of read depths.

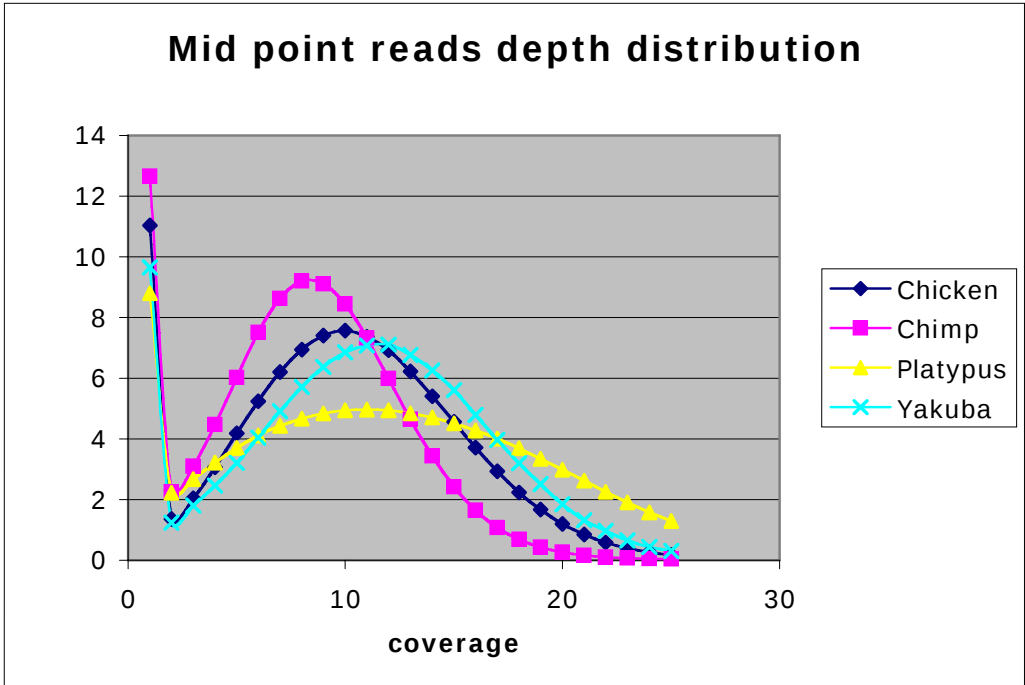


Figure A4. Platypus segmental duplication by alignment length for intrachromosomal and interchromosomal location.

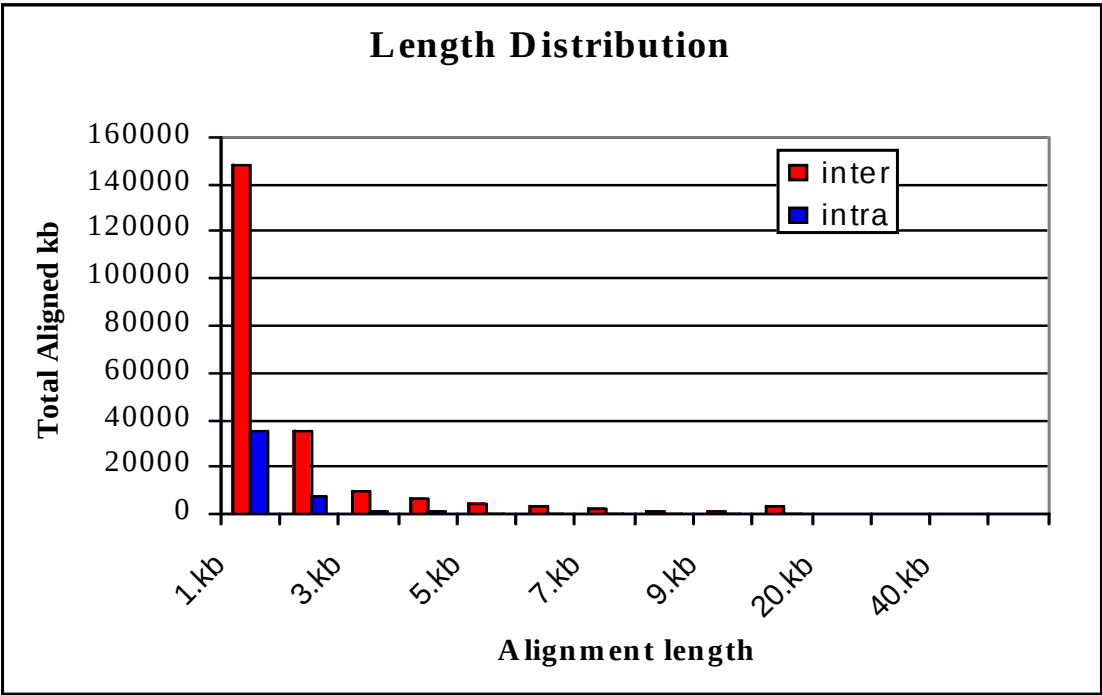


Figure A5. Platypus segmental duplication by alignment identity.

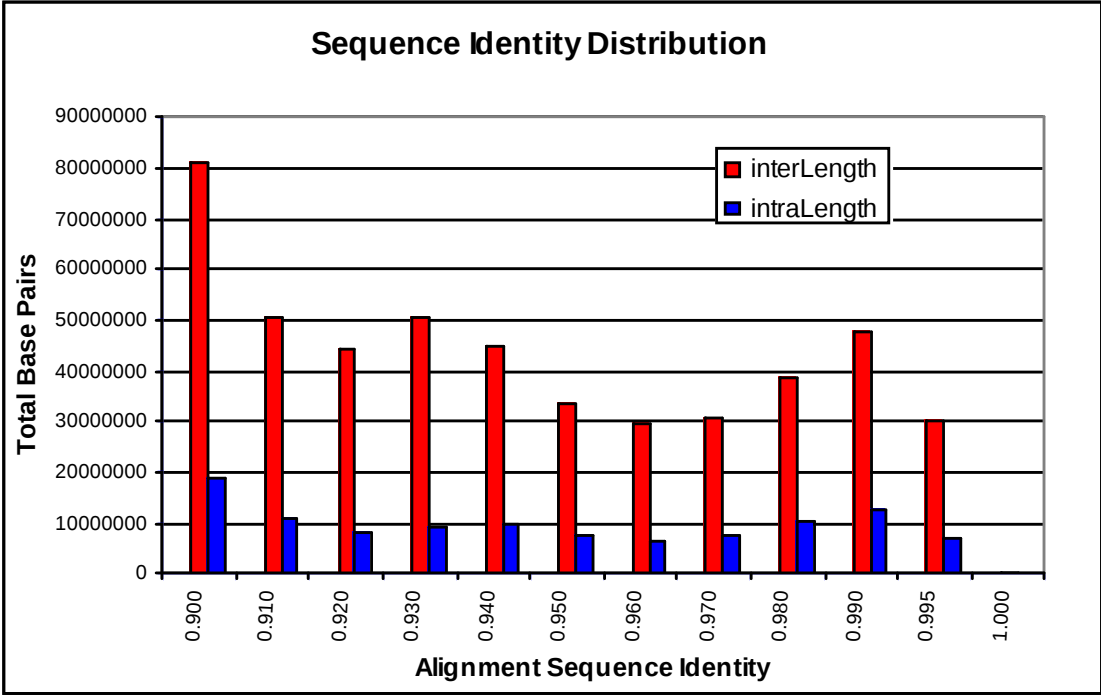


Figure A6. Segmental duplication sequences by chromosome (>5kb at 90% identity).

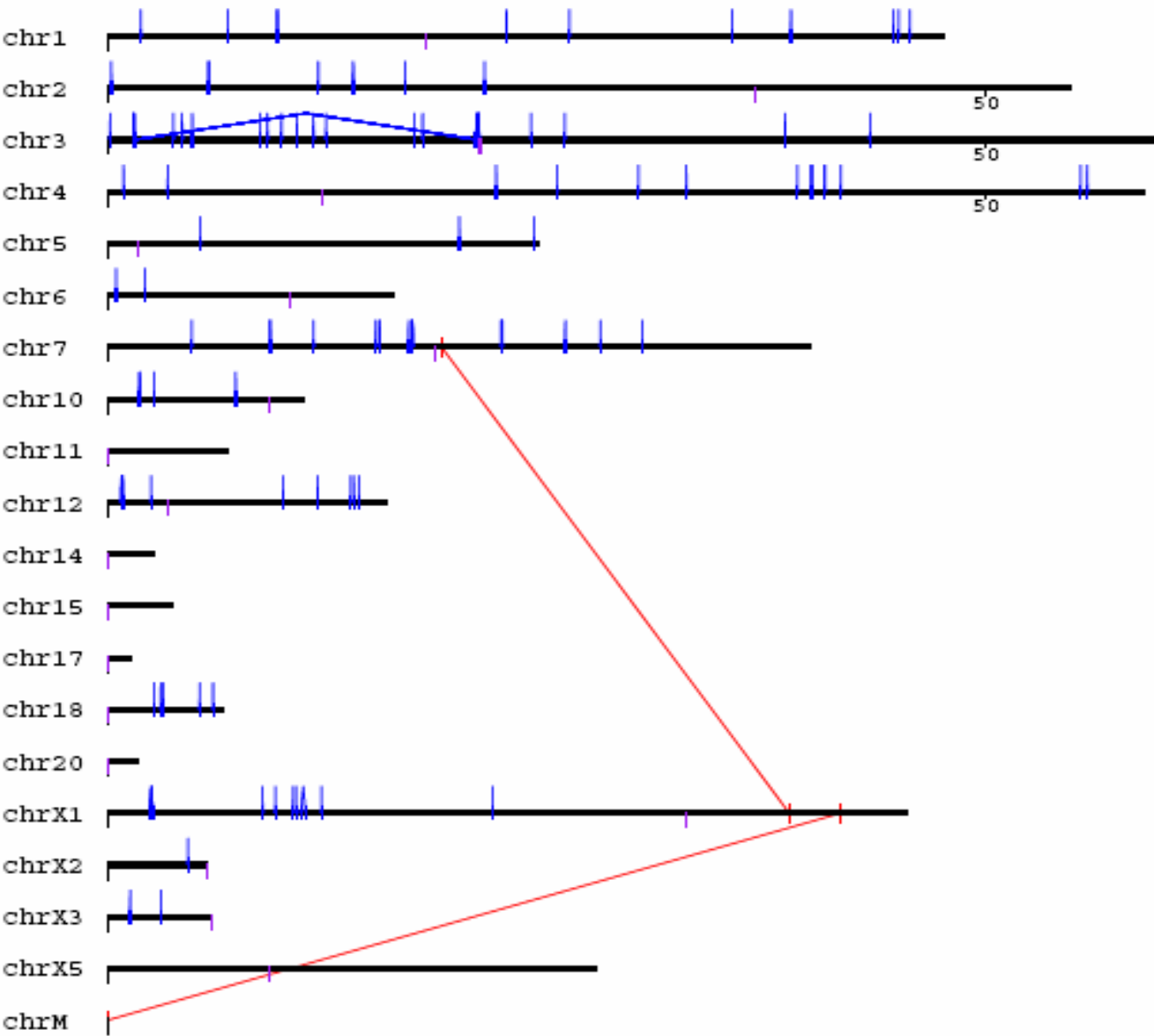


Figure A7. Chimeric read types.

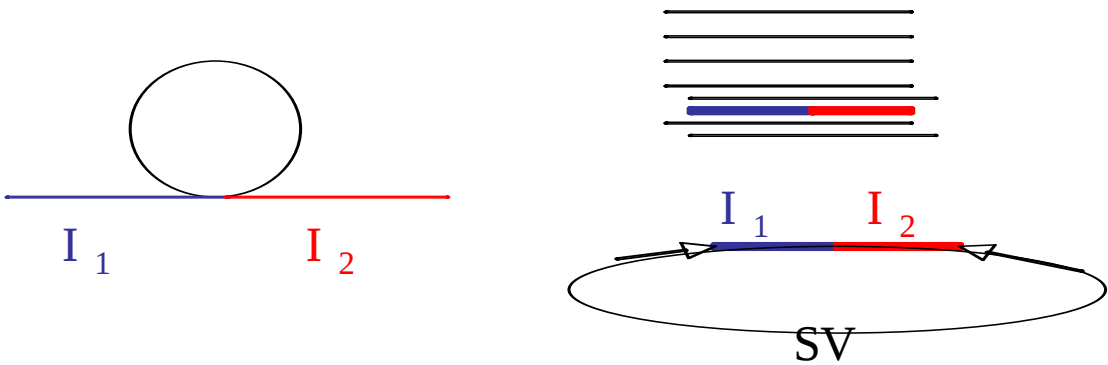


Figure A8. Combinations of reads at the end of contigs.

0_0_0	---->	<----	<----
0_0_1	<----	<----	<----
0_1_0	---->	<----	---->
0_1_1	<----	<----	---->
1_0_0	---->	---->	<----
1_0_1	<----	---->	<----
1_1_0	---->	---->	---->
1_1_1	<----	---->	---->

Figure A9. GC content for ABI3730 and 454 read types.

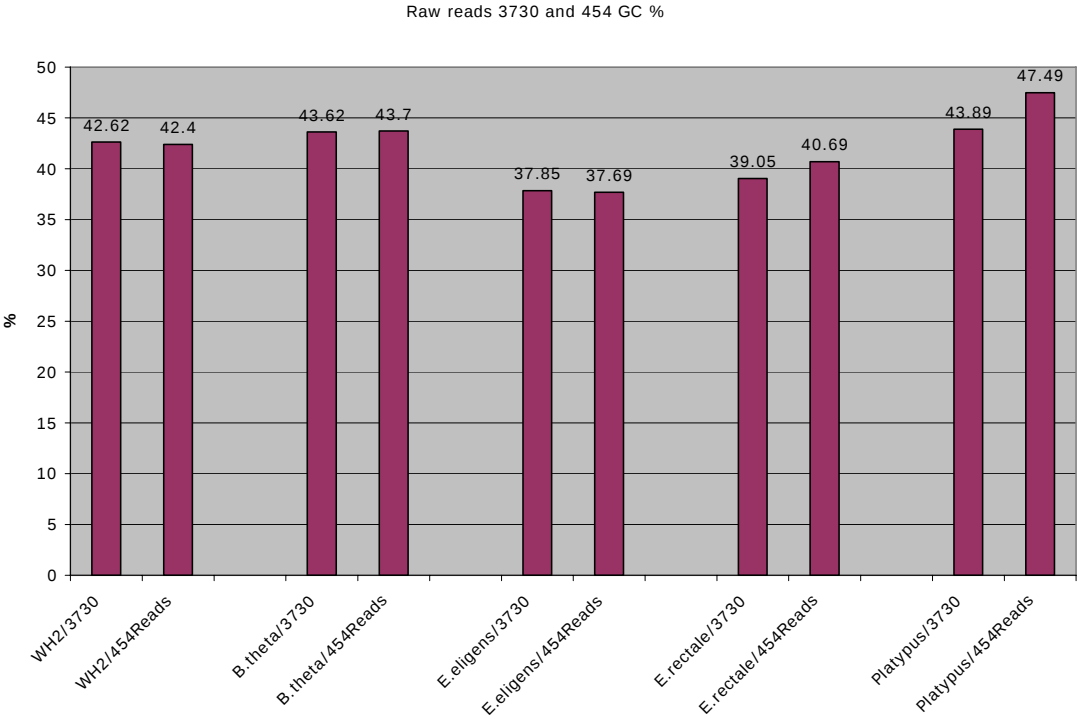


Figure A10. Multiple species GC content for reads and contigs.

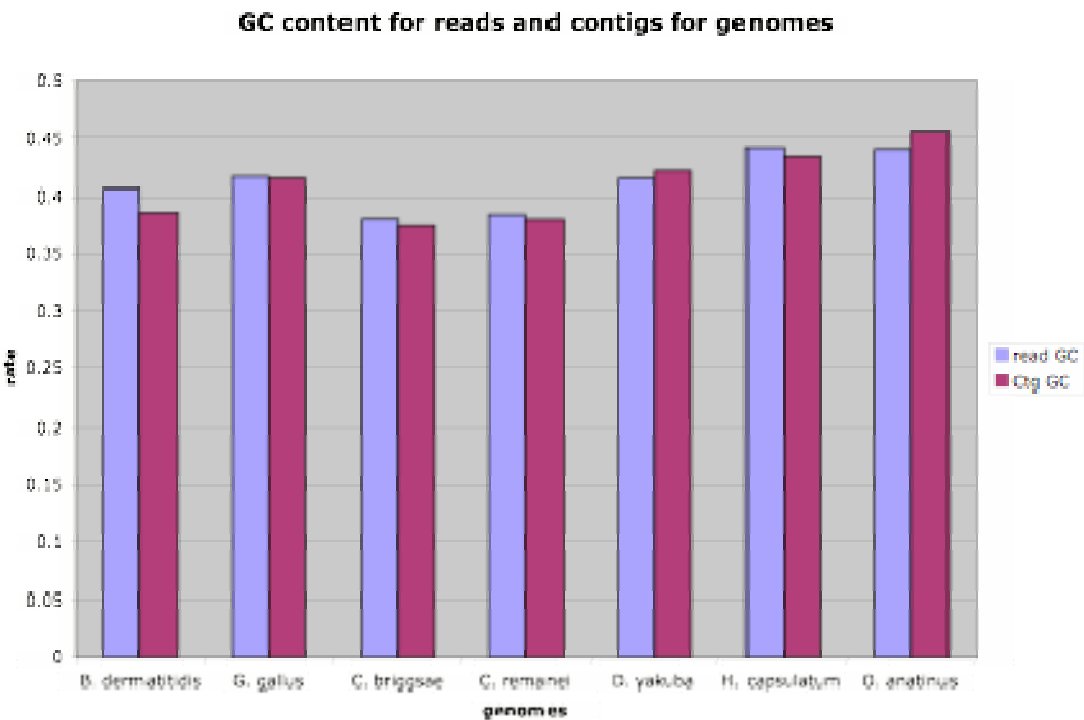
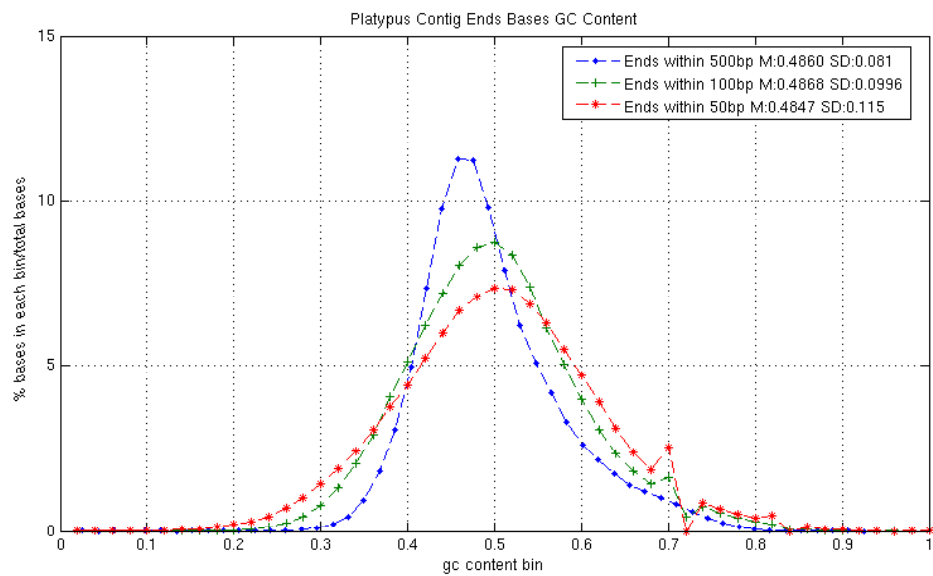


Figure A11. GC content by contig ends and read depth a) platypus contig end GC content b) platypus GC content in high and low read depth regions.

a



b

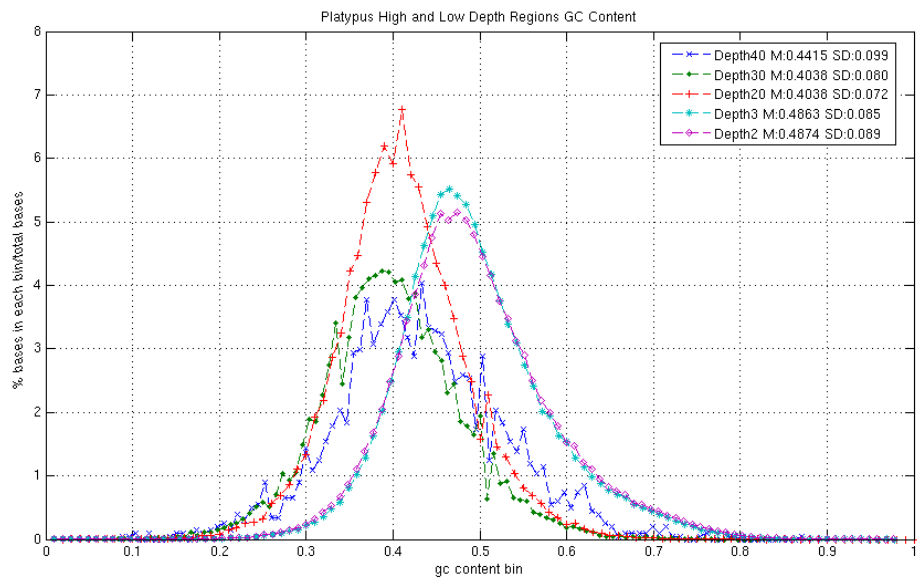


Figure A12. Lineages leading to chicken or mouse have a larger distance to root than other lineages. Shown are cumulative distributions of the distance to root for each species normalized by the median distance to root of each tree.

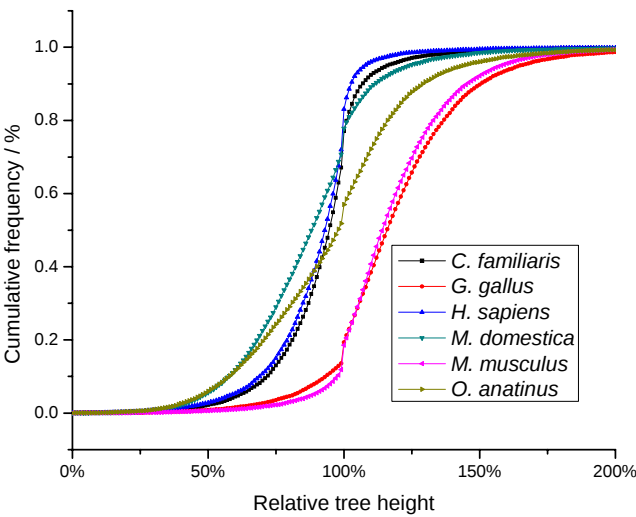


Figure A13. Genome-wide d_S (left) and d_N (right) values for pairs of species computed with different methods. Each spoke in the wheel corresponds to a species pair (see Accessory Table A13 for values). Method 1 (Pairwise) provides the median values from pairwise comparisons of all 1:1 orthologues. Method 2 (PairwiseStrict) provides the median values from pairwise comparisons of 1:1 orthologues drawn only from the simple $(1:1)^n$ orthologue set. Method 3 (TreeMedian) provides the median values from rate estimates inferred across the species phylogeny for each simple $(1:1)^n$ orthologue set. Method 4 (SampleAverage) provides values inferred from 20 samples of 200 concatenated multiple alignments from the simple $(1:1)^n$ orthologue set (See Accessory Table A12).

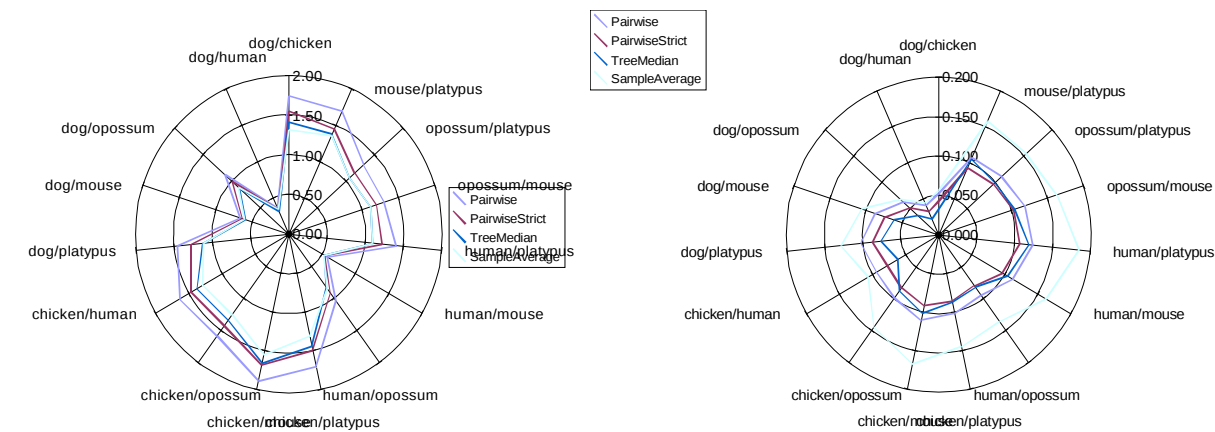


Figure A14. Overview of our approach for finding phylogenetically informative retroposed elements.

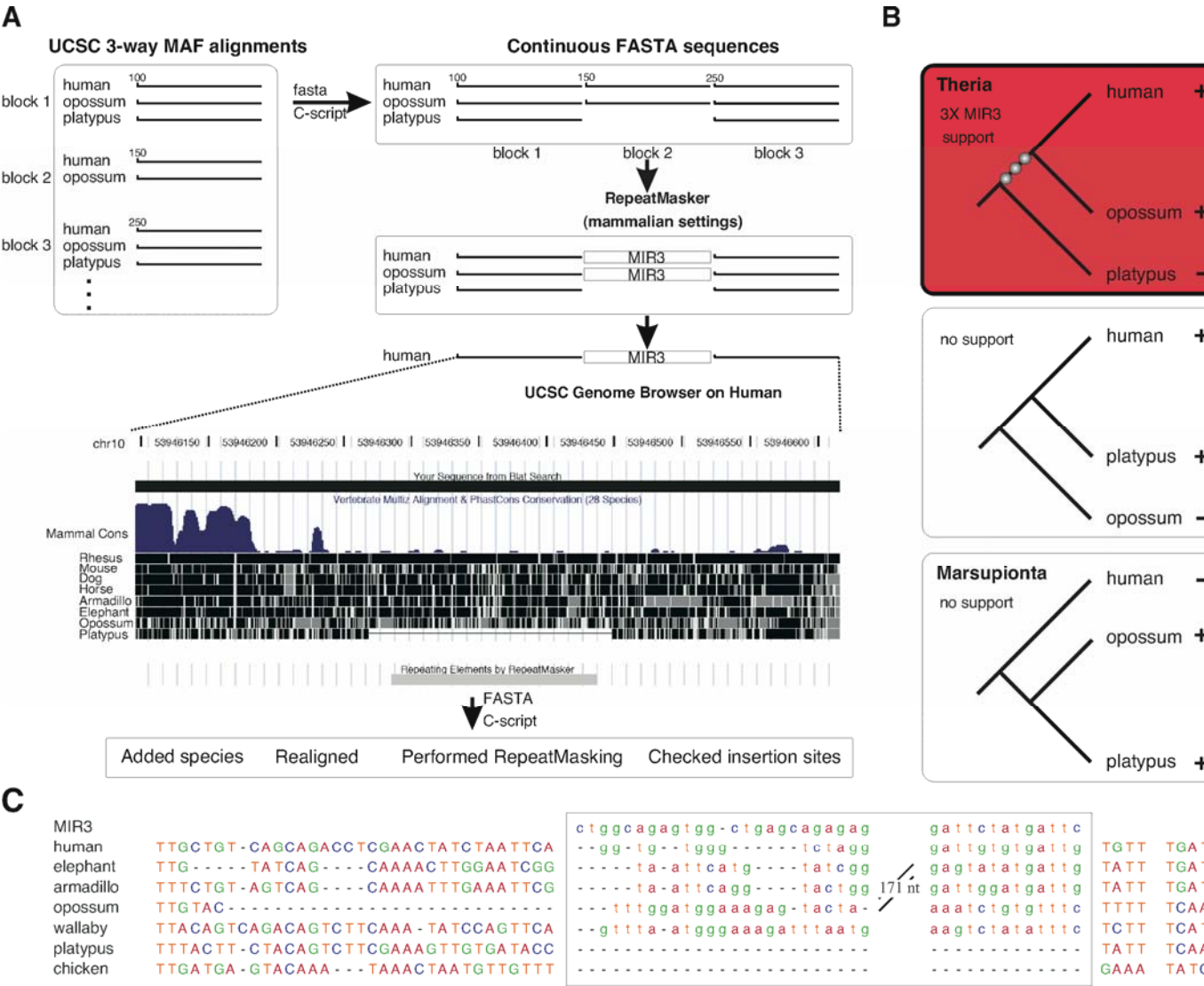


Figure A15. A platypus population structure plot for 90 individuals. Each platypus individual is represented by a vertical bar. The color composition of each vertical bar represents the probability of assignment for each individual to each of the four inferred population clusters as estimated using Structure 2.1.

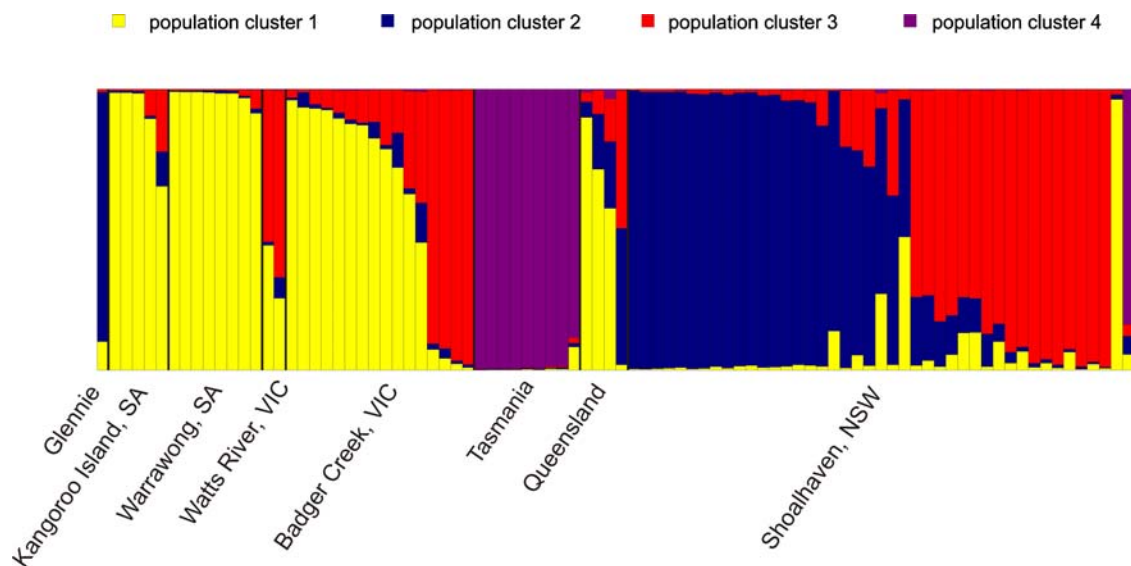


Figure A16. TinT distribution: Activity pattern of platypus specific non-LTR retroposed elements over evolutionary time.

