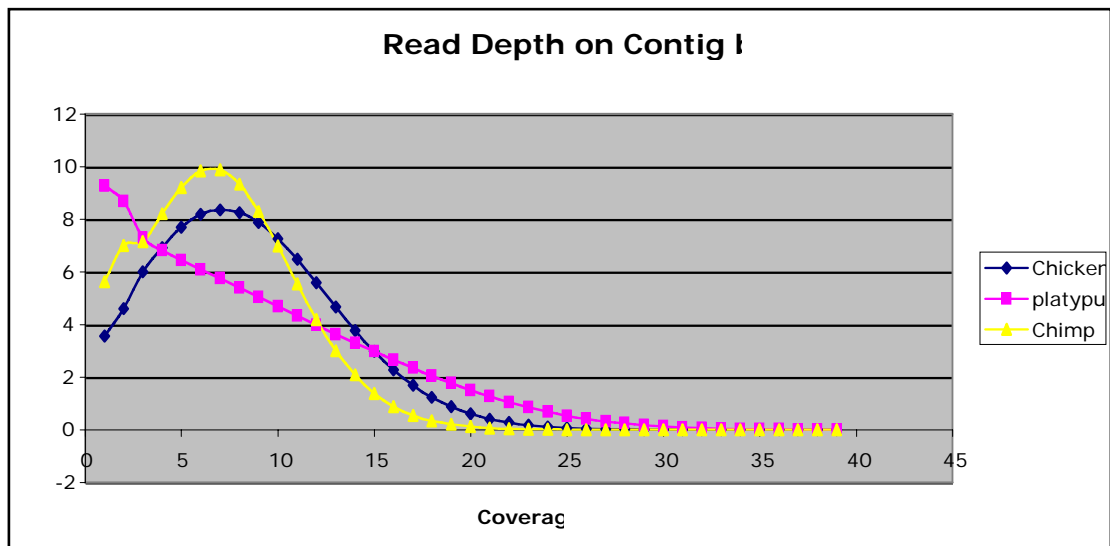
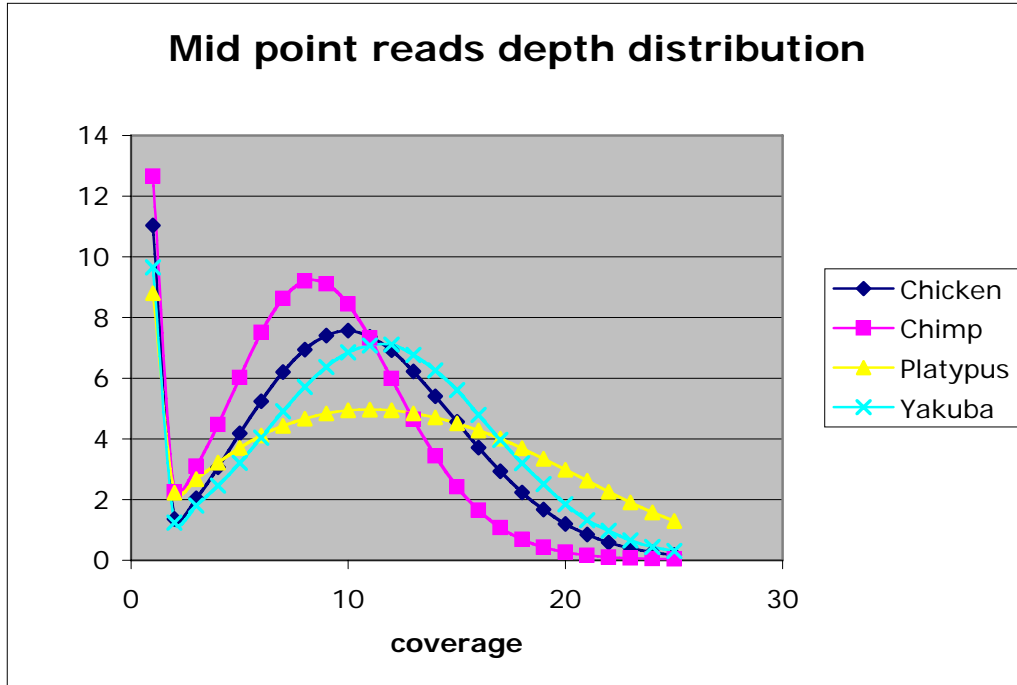
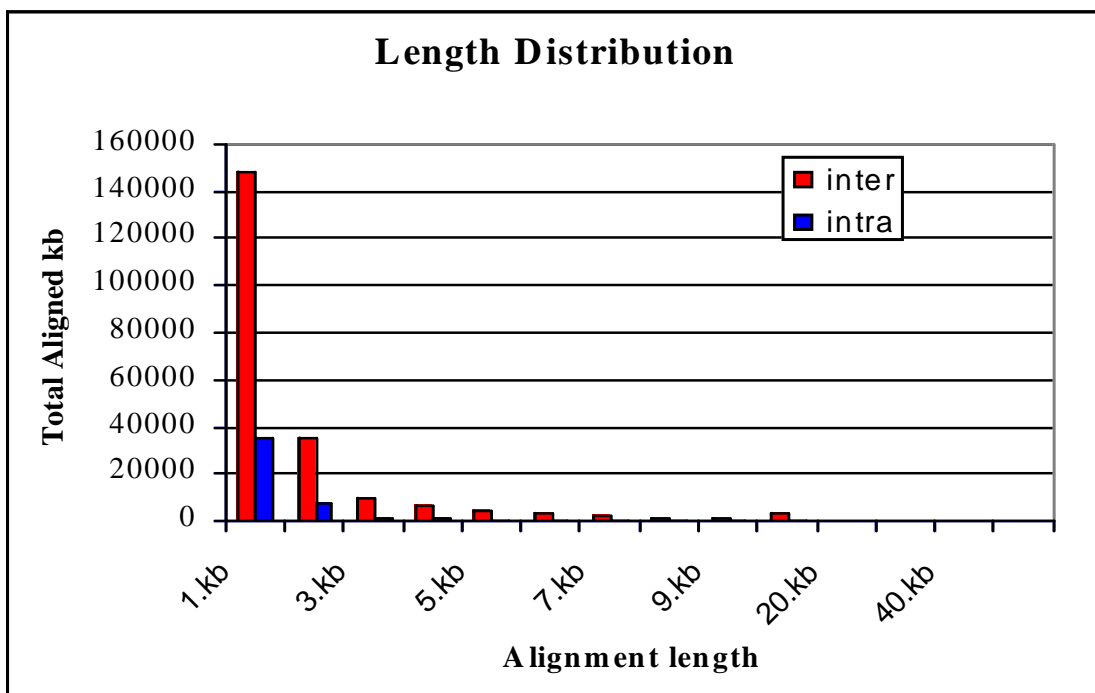


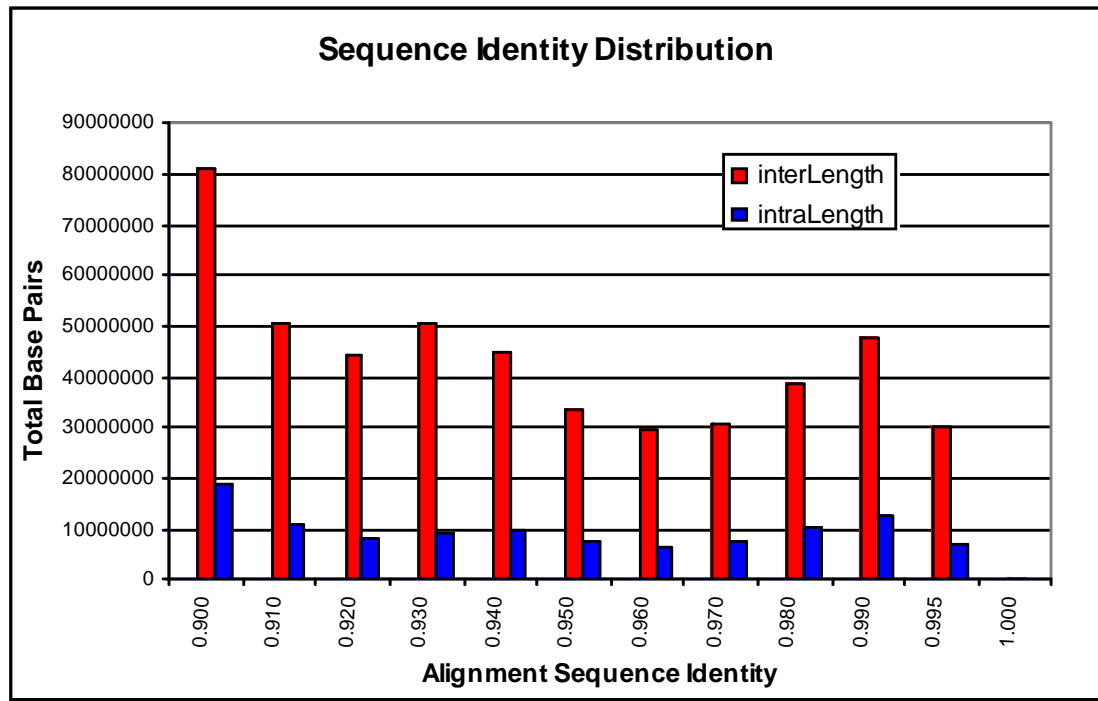
**Figure A1.** Describes format followed for read depth distribution.

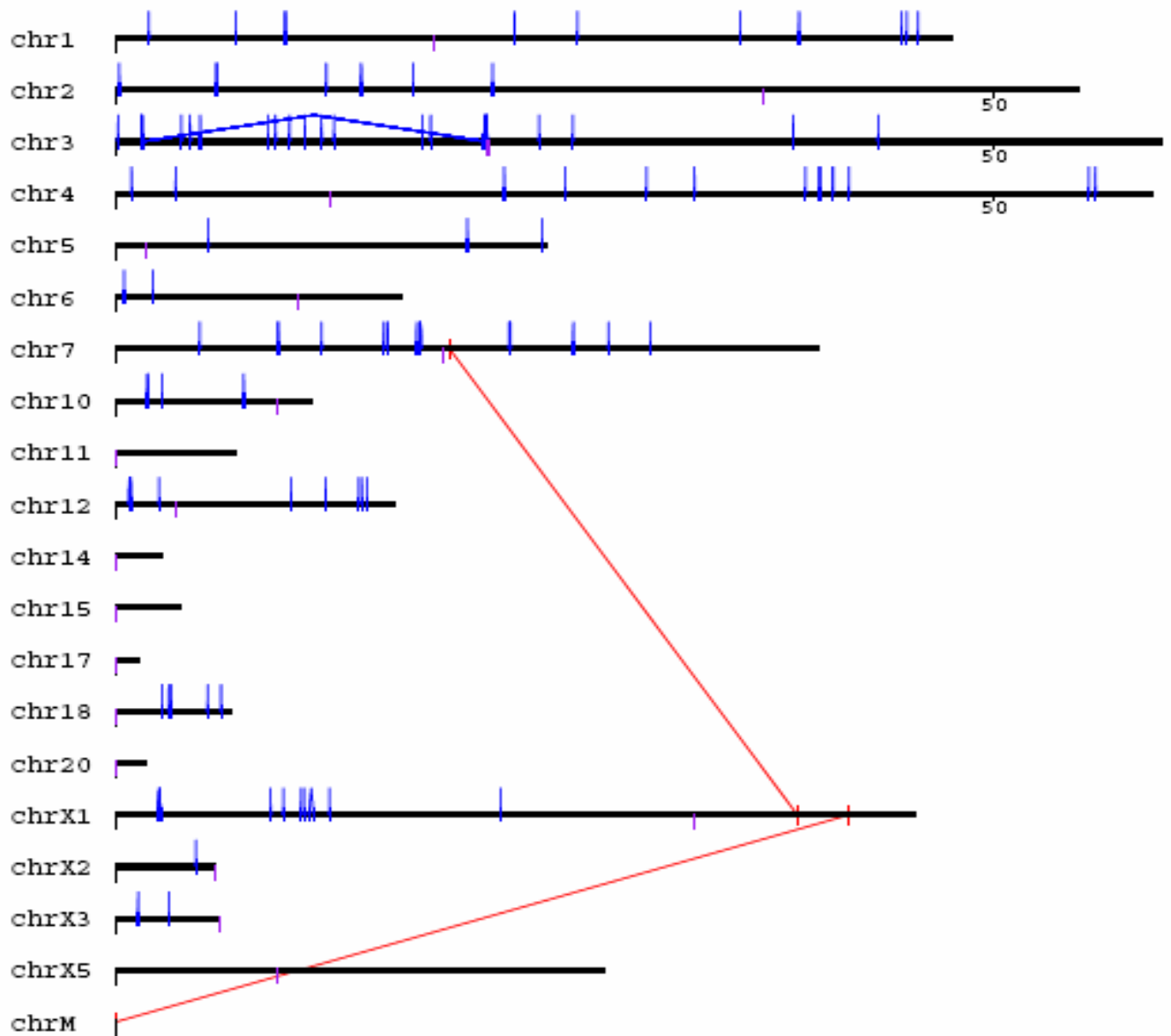


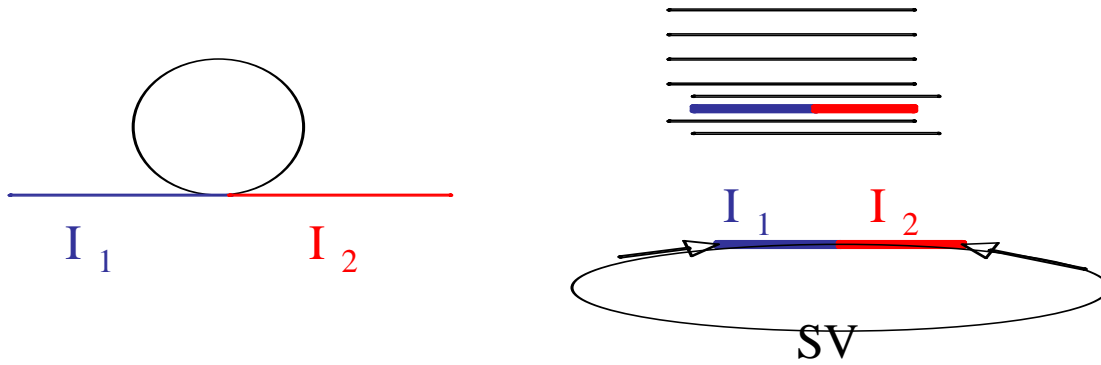
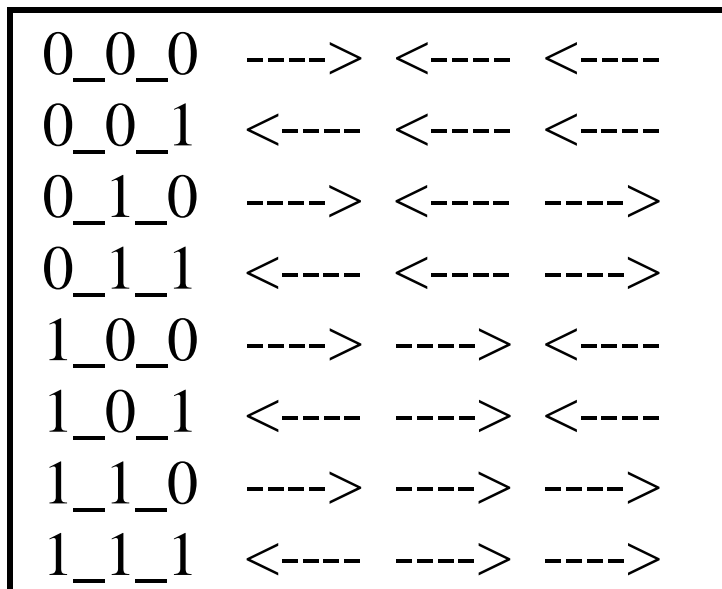
**Figure A2.** Read depth on contig base pairs.

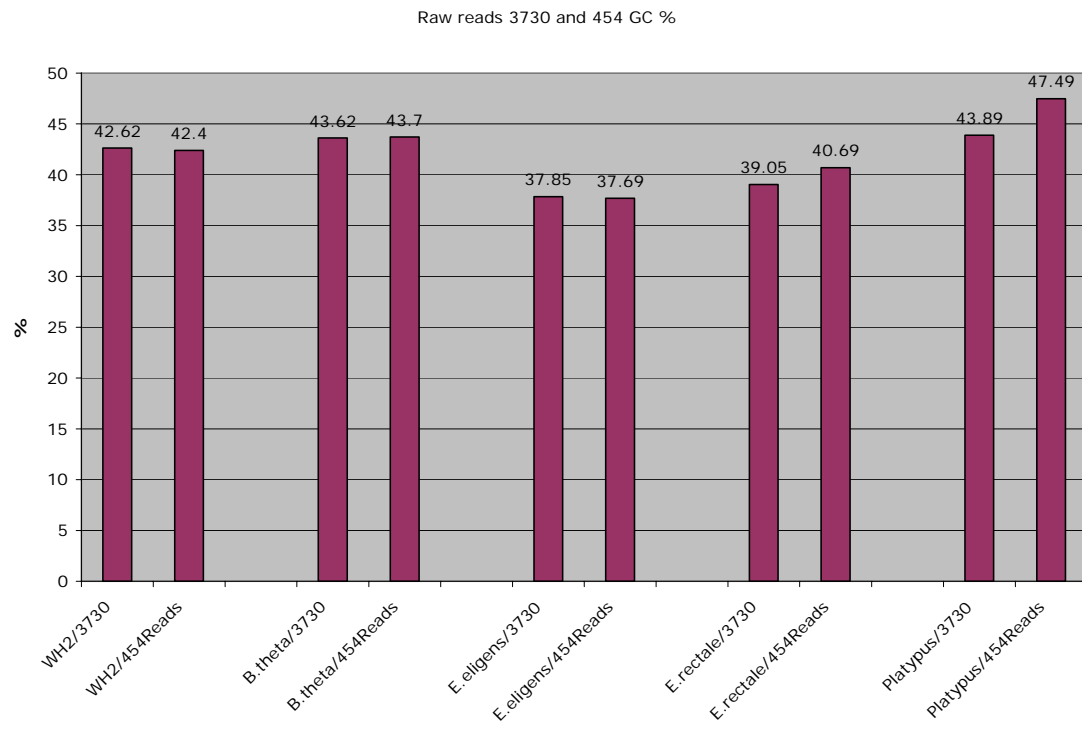


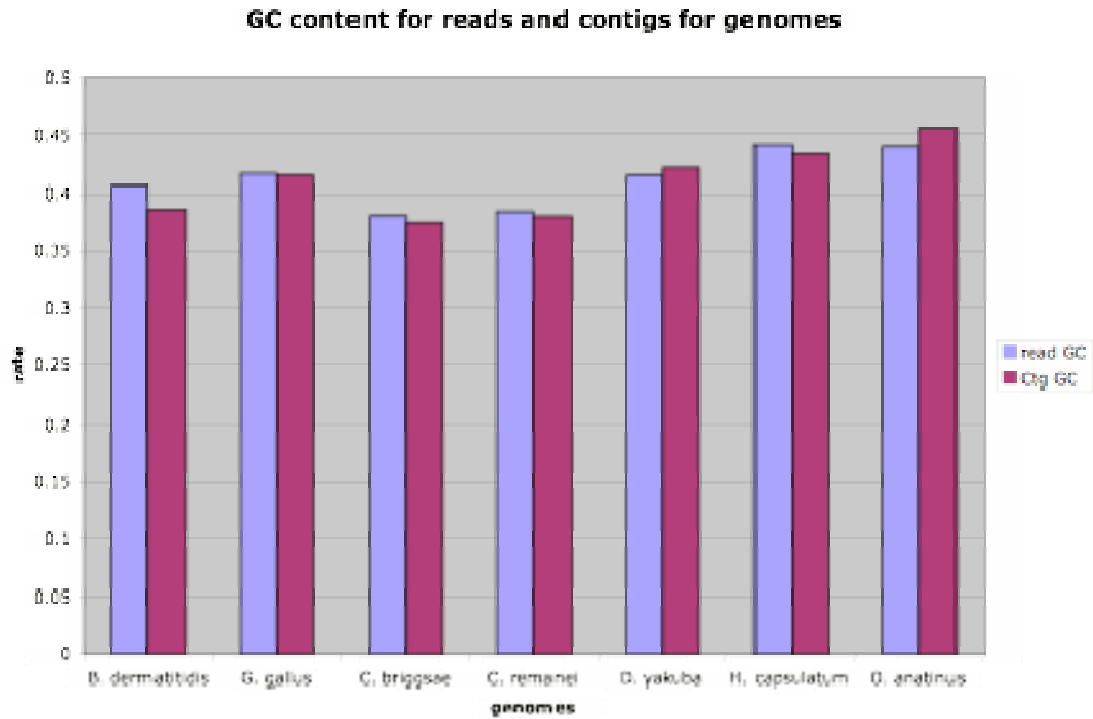
**Figure A3.** Distribution of read depths.**Figure A4.** Platypus segmental duplication by alignment length for intrachromosomal and interchromosomal location.

**Figure A5.** Platypus segmental duplication by alignment identity.

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

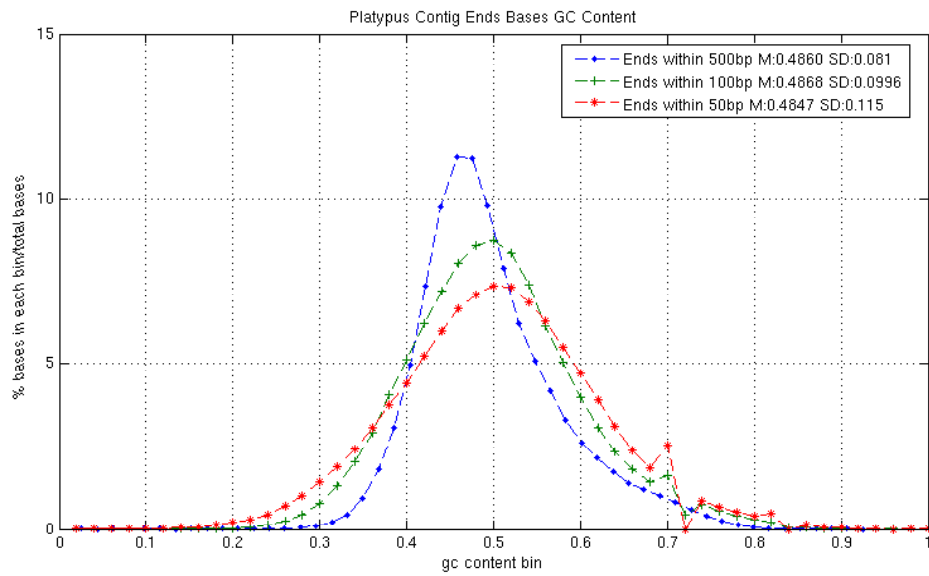
**Figure A7.** Chimeric read types.**Figure A8.** Combinations of reads at the end of contigs.

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

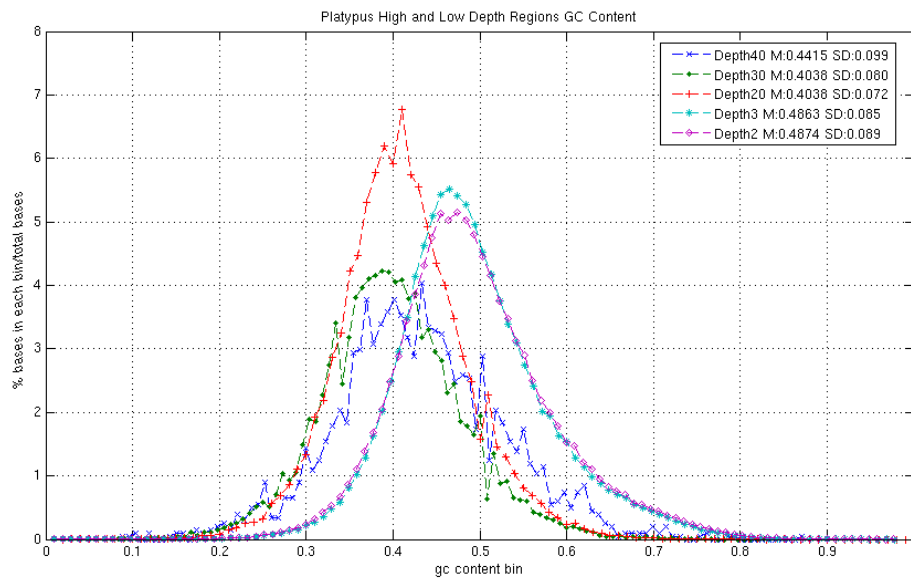
**Figure A10.** Multiple species GC content for reads and contigs.

**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**

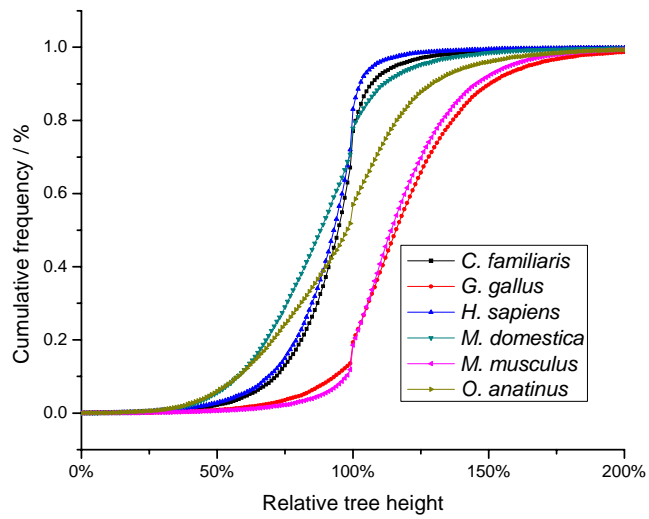


**b**

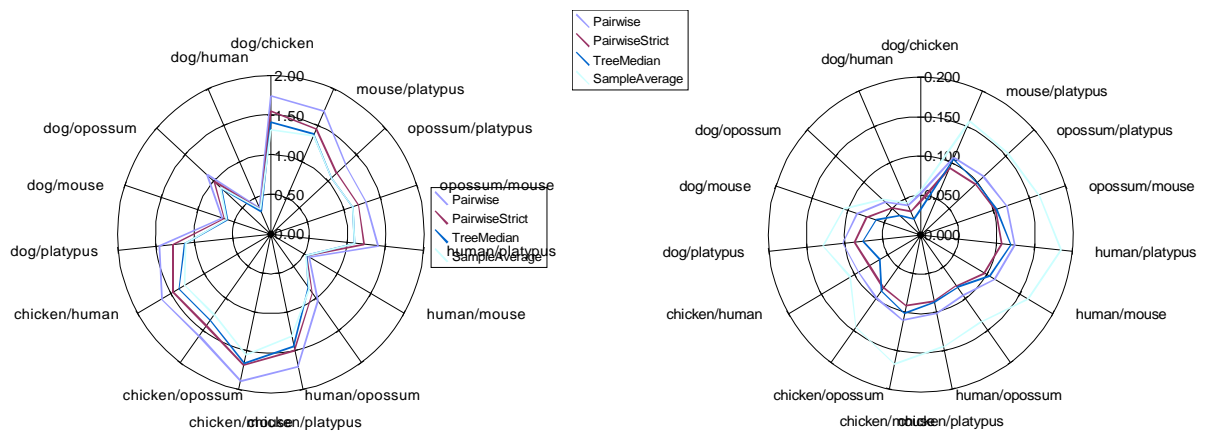




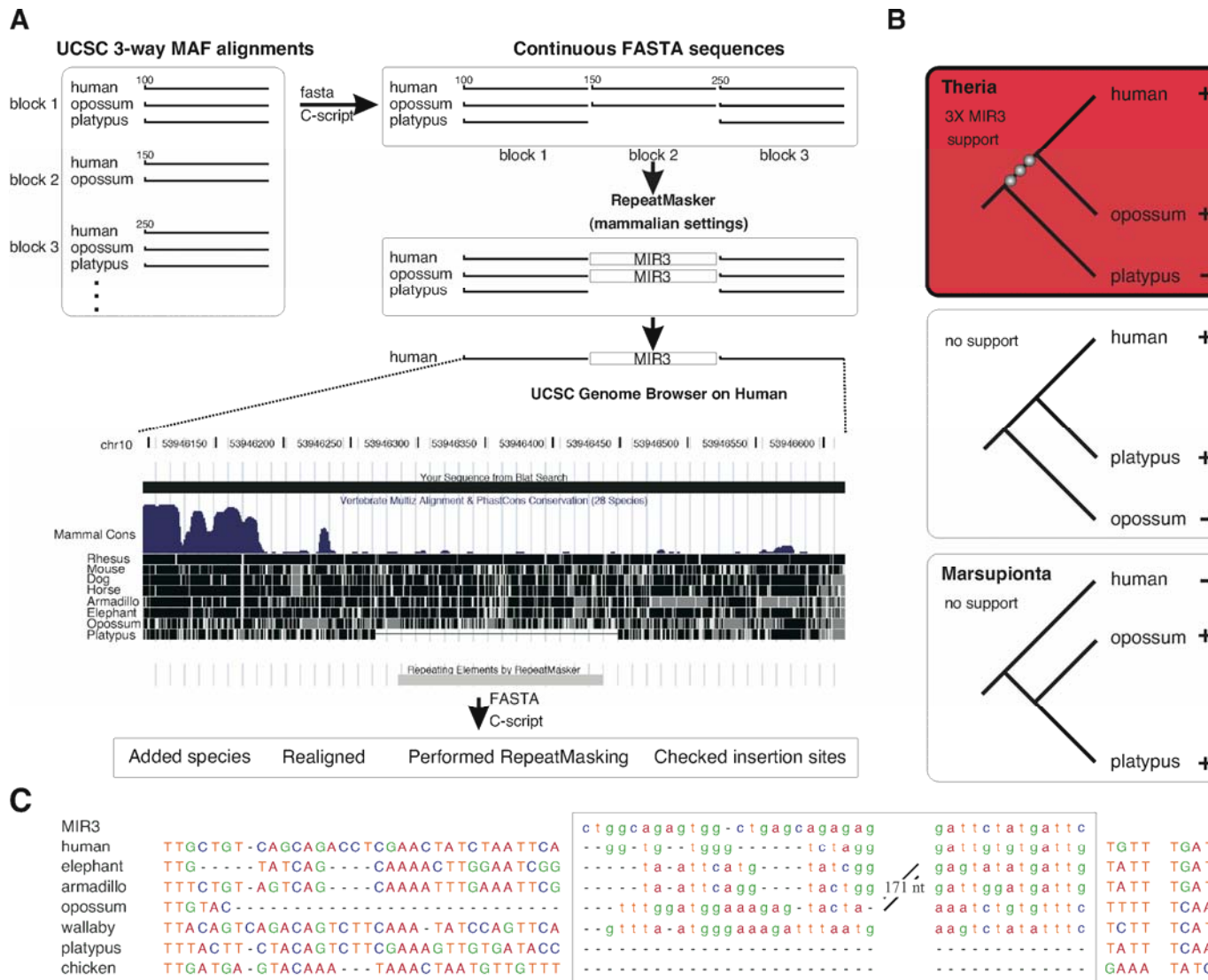
**Figure A12.** Lineages leading to chicken or mouse have a larger distance to root than other lineages. Shown are cumulative distributions of the distance to root for each species normalized by the median distance to root of each tree.



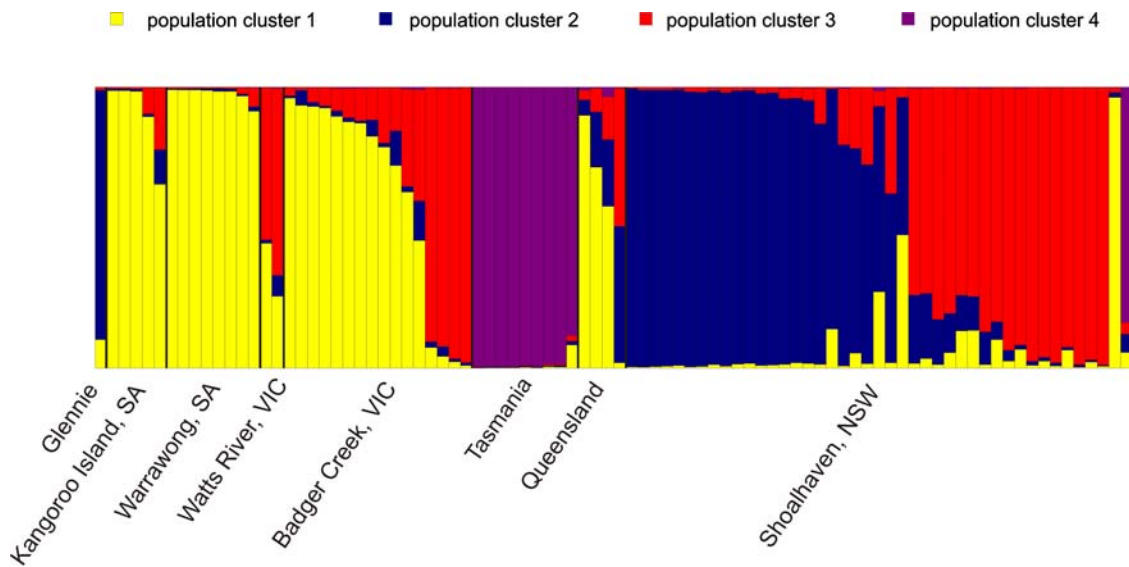
**Figure A13.** Genome-wide  $d_S$  (left) and  $d_N$  (right) values for pairs of species computed with different methods. Each spoke in the wheel corresponds to a species pair (see Accessory Table A13 for values). Method 1 (Pairwise) provides the median values from pairwise comparisons of all 1:1 orthologues.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

