Supplementary Figures

Figures S1-2: L1 discordant phylogenies

Potential L1 HT clusters were checked using both neighbour-joining and maximum likelihood methods to confirm that the tree topology differed from expected species relationships. The best supported cross-Phylum L1 phylogenies are shown in the main text; the remaining cross-Phylum clusters are shown here. Clusters are described in detail in Table S6.

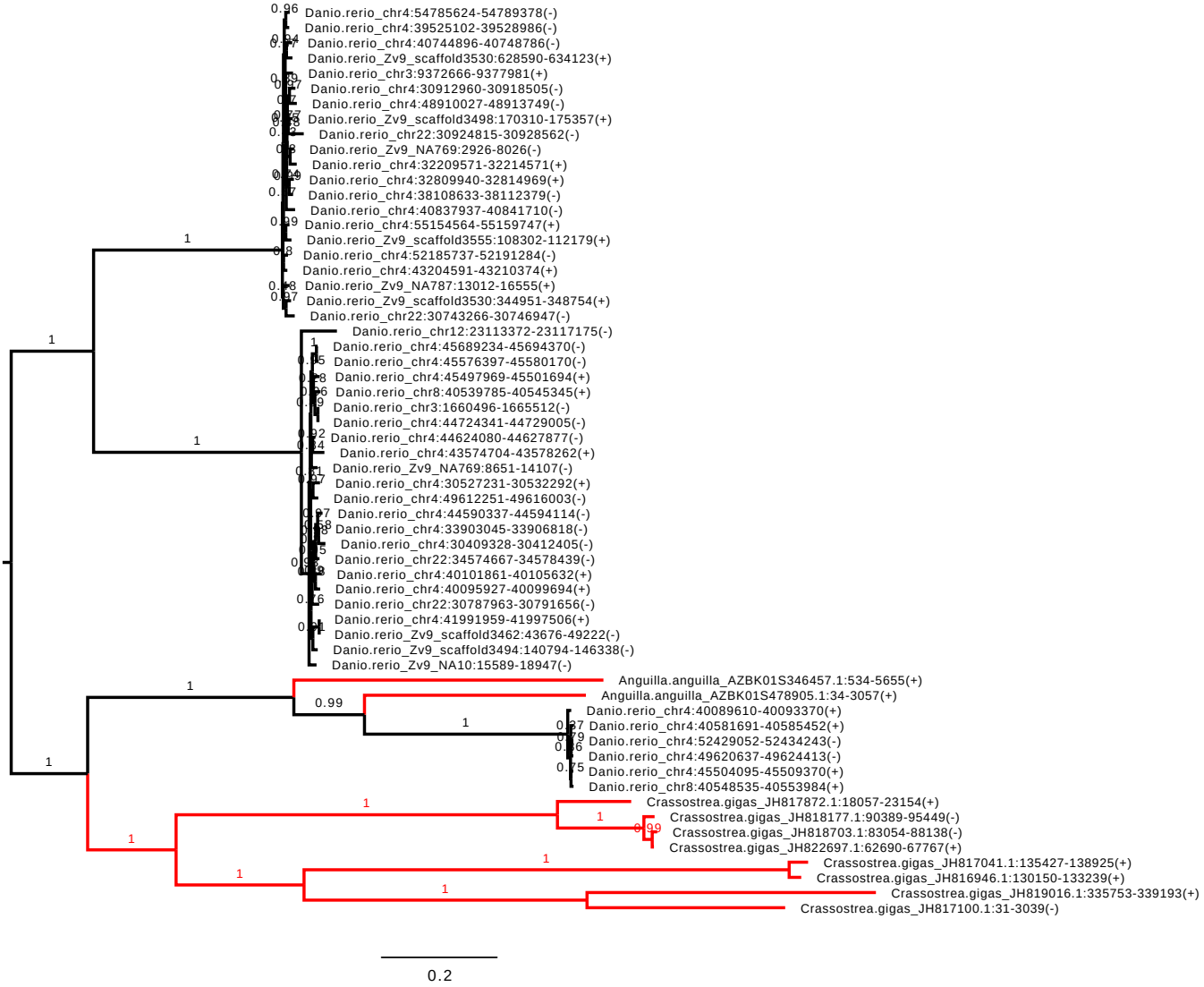


Figure S1: **L1 cluster c_25**

L1 nucleotide ORFs

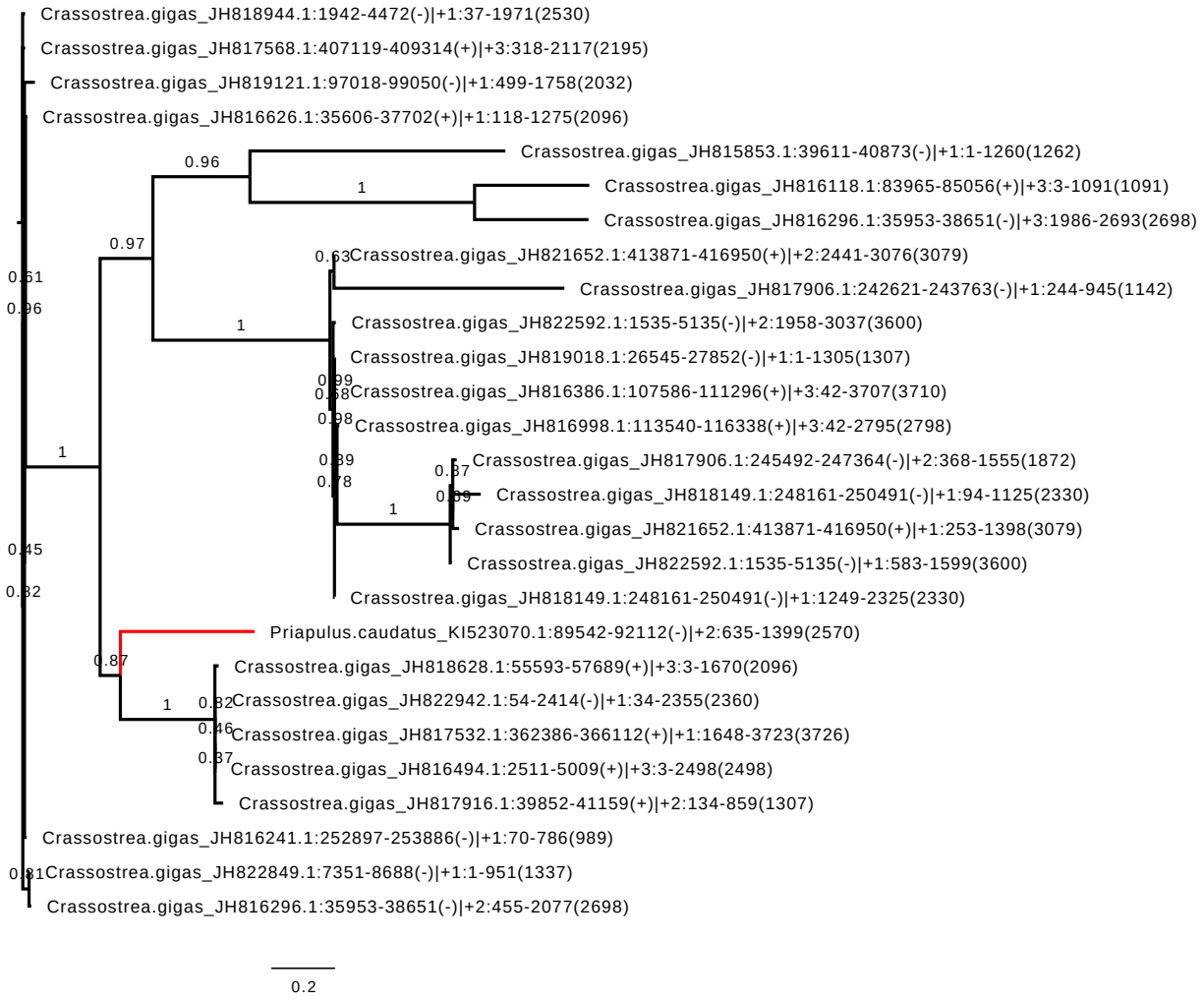


Figure S2: **L1 cluster o_666**

Figures S3-54: Kimura divergence plots for BovB and L1

RepeatMasker divergence plots represent Kimura substitution levels of TEs against the RepBase super consensus library. For example, Figure 5b in the main text shows the RepeatMasker divergence plot for the cow (*Bos taurus*), illustrating recent bursts of BovB and L1 activity in the genome with many copies sharing high identity to young, currently active elements.

The L1 superfamily includes both mammalian L1 elements (dark blue) and more diverse, frog-like Tx elements (light blue). Tx are typically found in fish, frogs and primitive eukaryotes (e.g. sea urchin *Strongylocentrotus purpuratus*). BovB elements are coloured in orange.

Typically, species within a clade show consistent divergence patterns of both TEs (particularly if there has been little recent activity - see Chiroptera). Recently TE-active species, on the other hand, are likely to show bursts of seemingly random activity. Consider the plots for the two lizard species, *Pogona vitticeps* and *Anolis carolinensis*. *Pogona* is implicated in many of the BovB HT events listed in Table S5, and this is supported by the huge burst of recent BovB activity shown in Figure S38. This is also seen in all four snake species. In contrast, the *Anolis* plot (Figure S39) indicates that L1s have become the dominant TE lineage in the genome.

By estimating TE divergence from super consensus sequences, we can visualise the contrasting (and sometimes competing) dynamics of BovB and L1 elements over time. This is particularly important for species where BovB or L1 (or both) have taken off and accumulated quickly within the genome.

Marsupialia

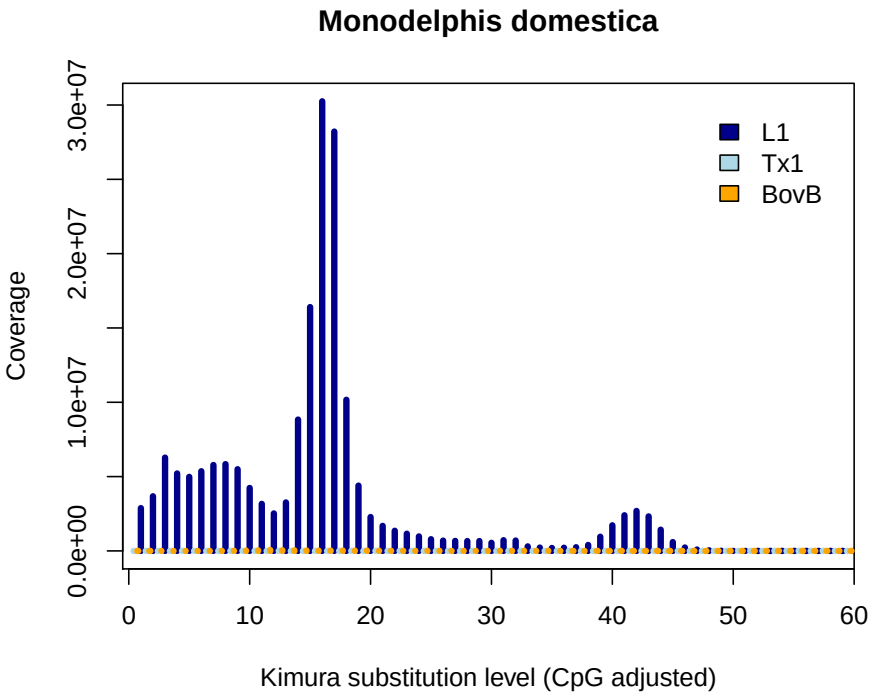


Figure S3

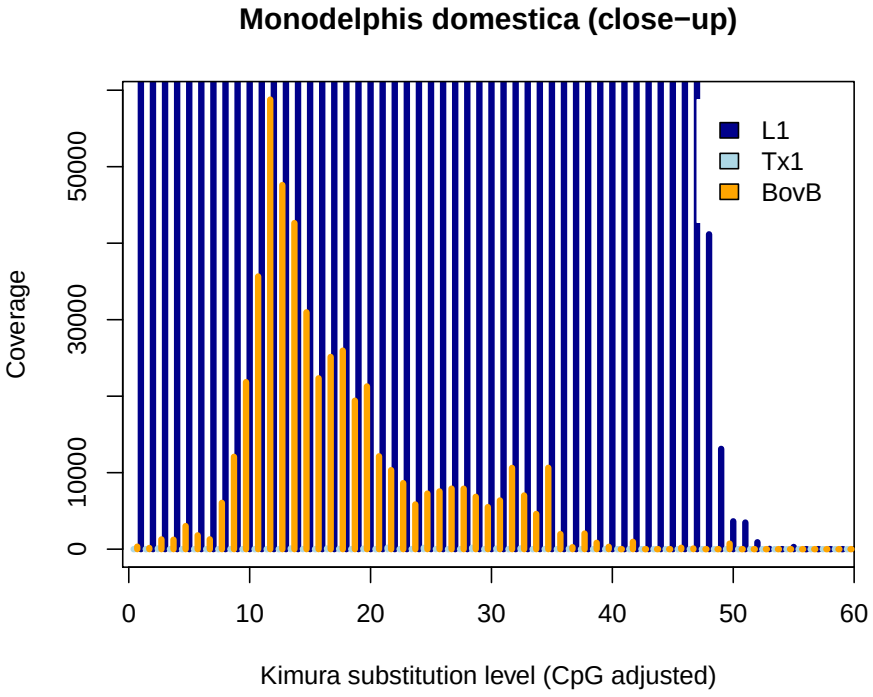


Figure S4

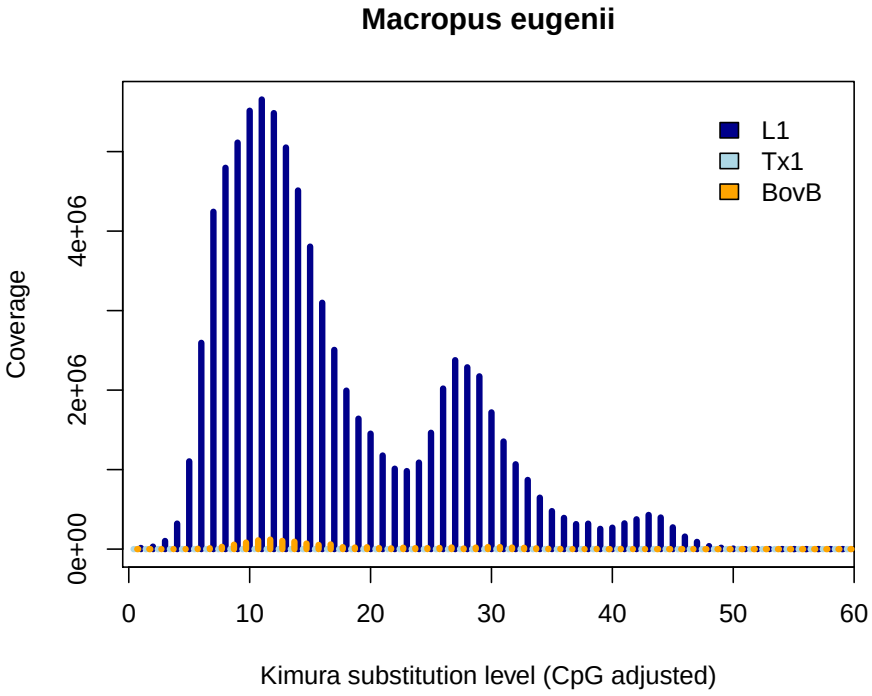


Figure S5

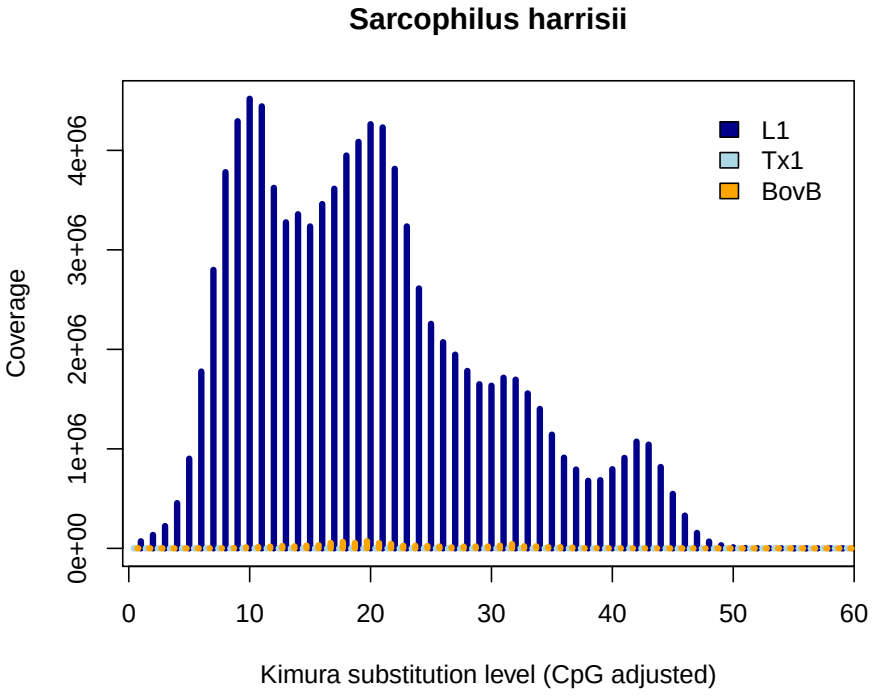
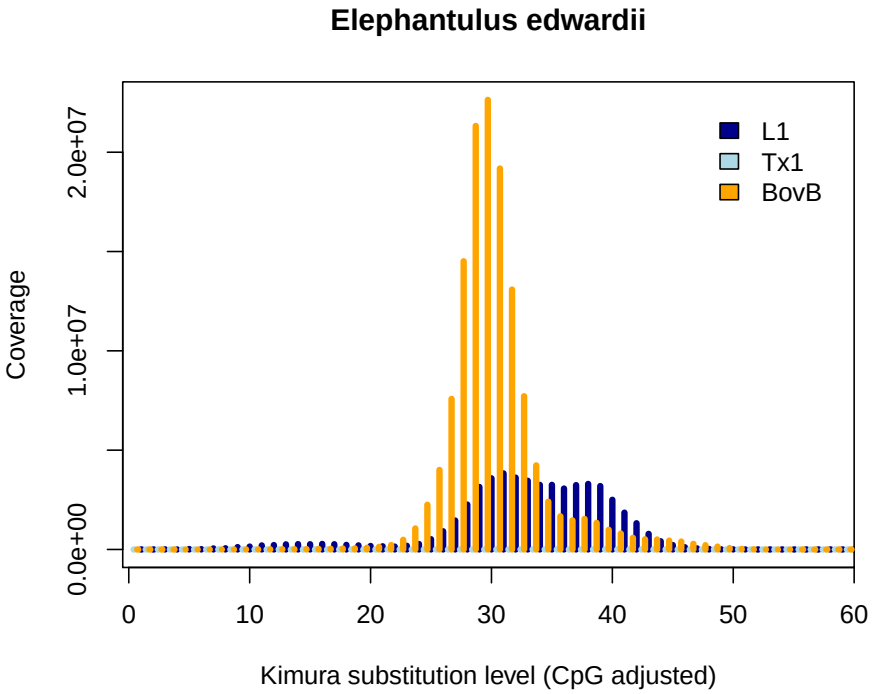


Figure S6

Afrotheria



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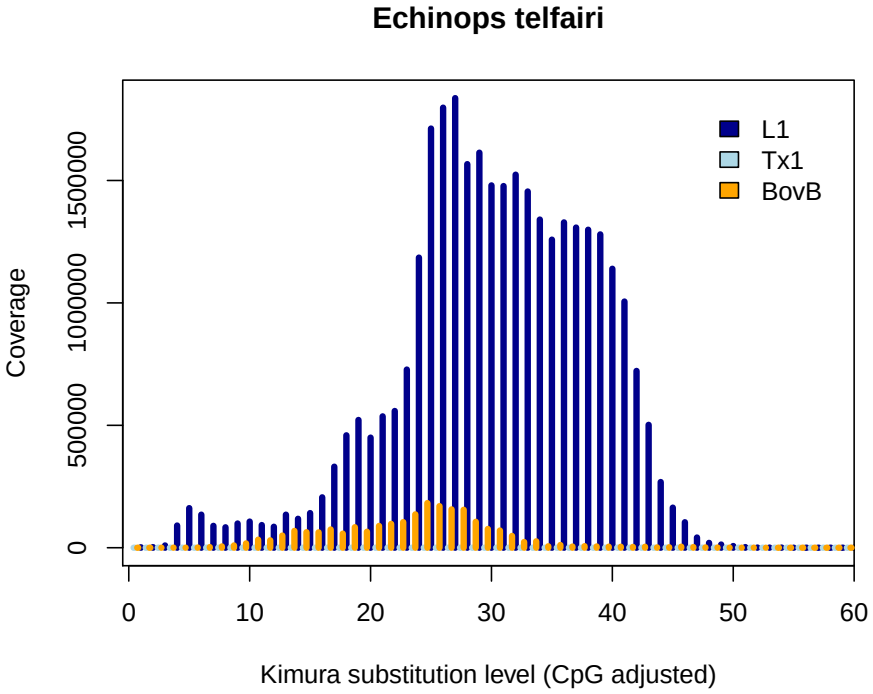
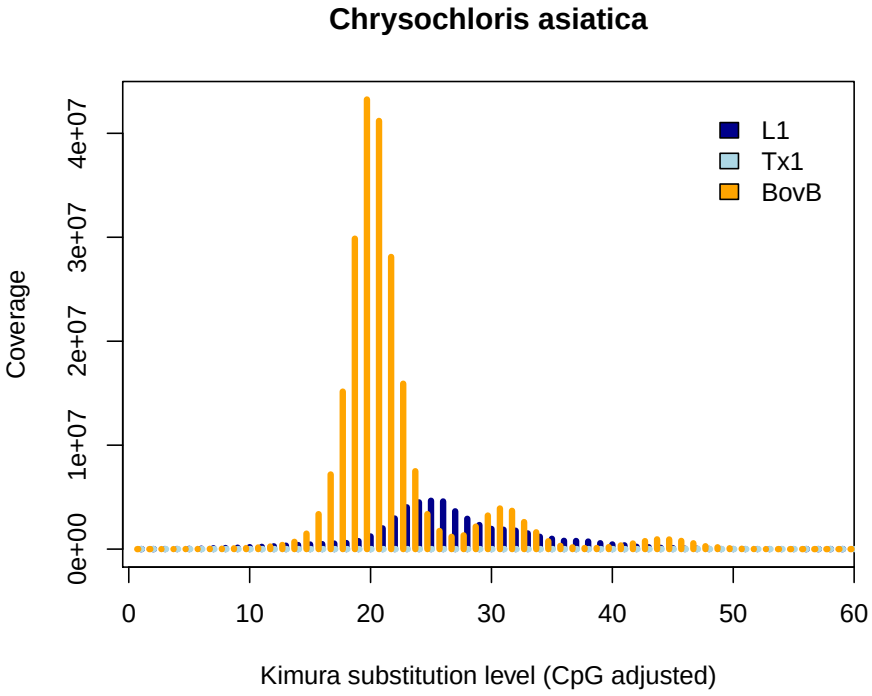


Figure S8



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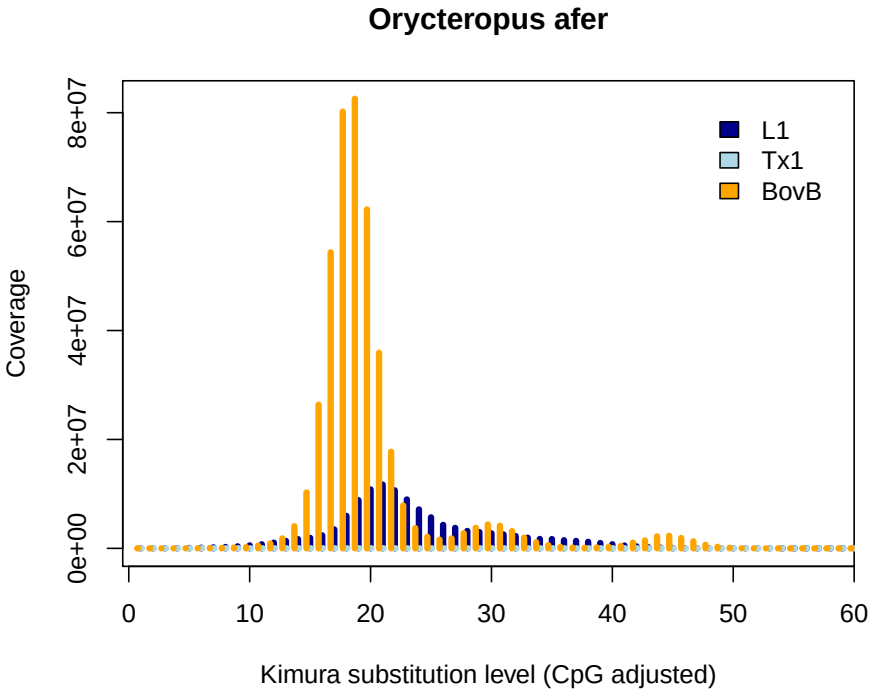

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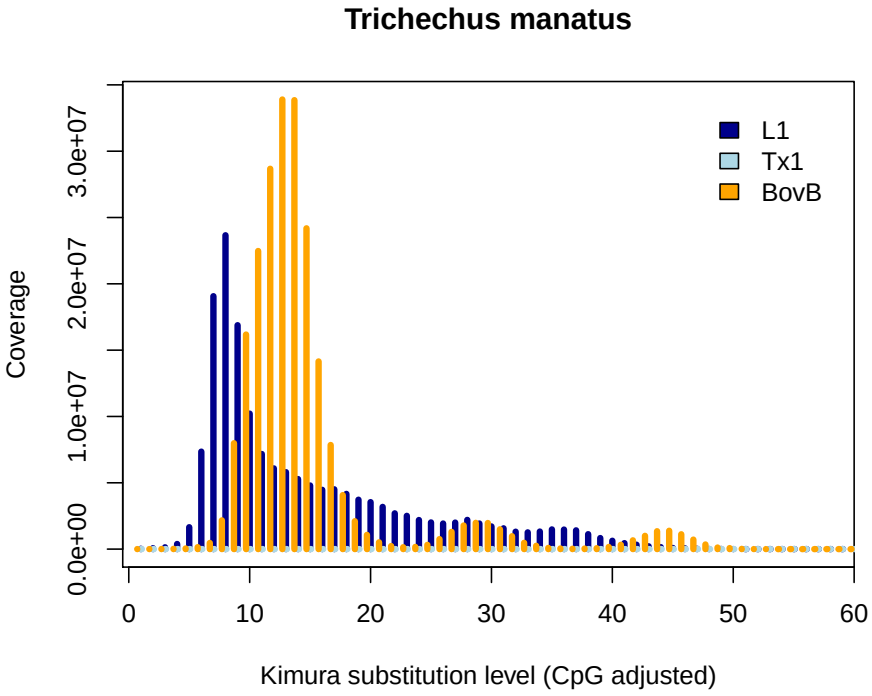

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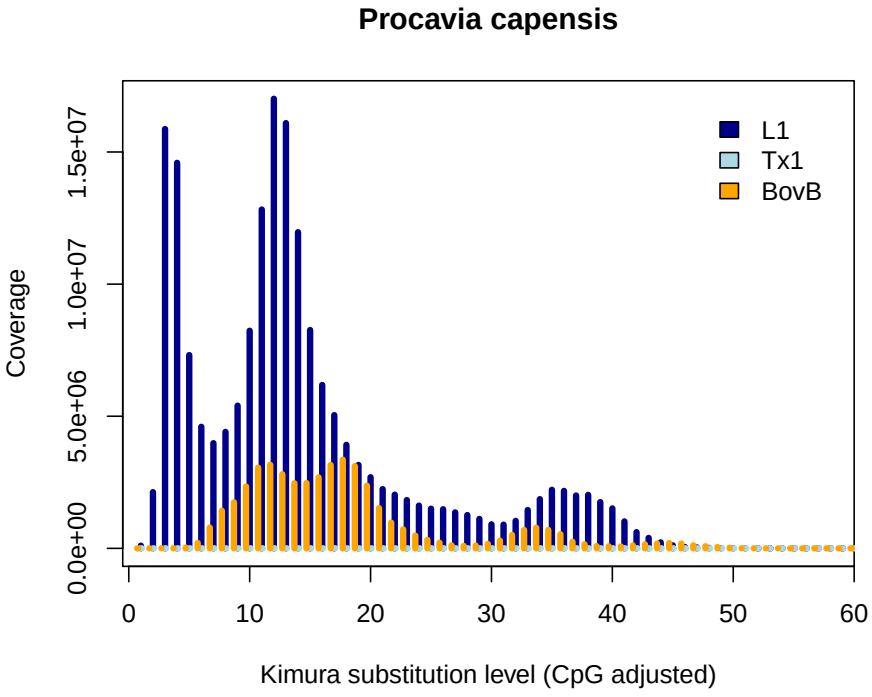

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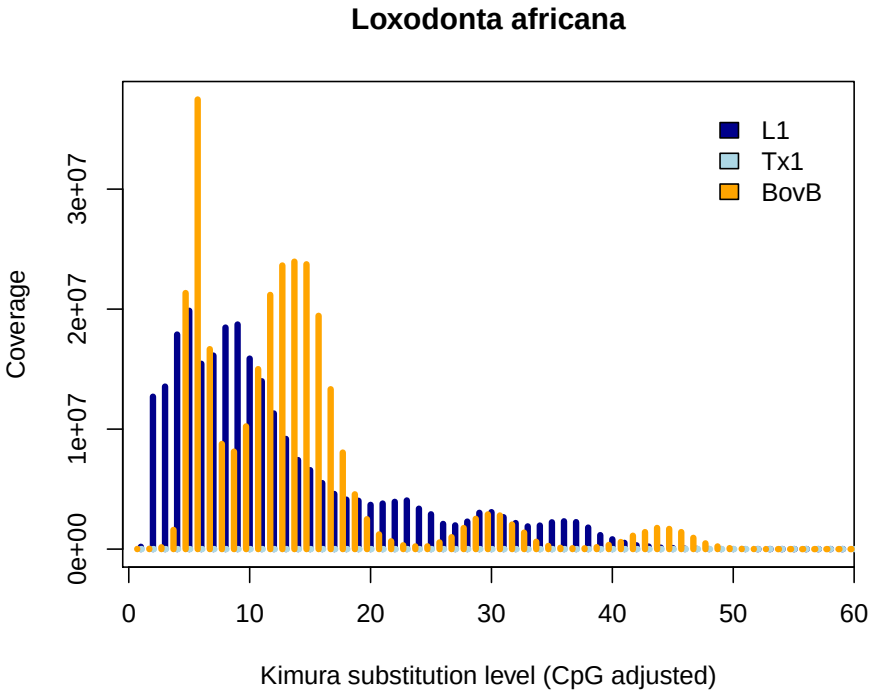
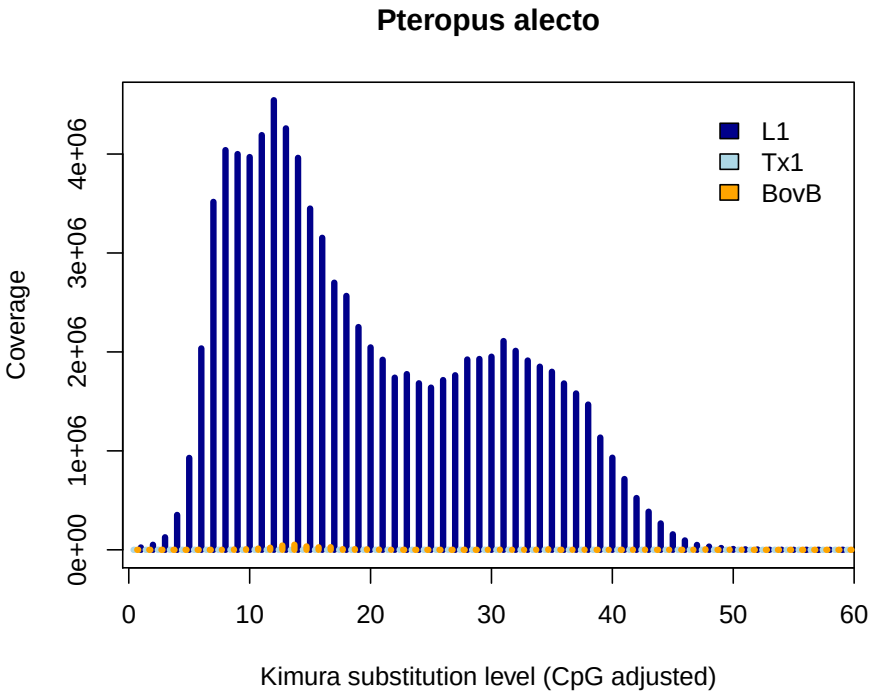


Figure S13

Chiroptera



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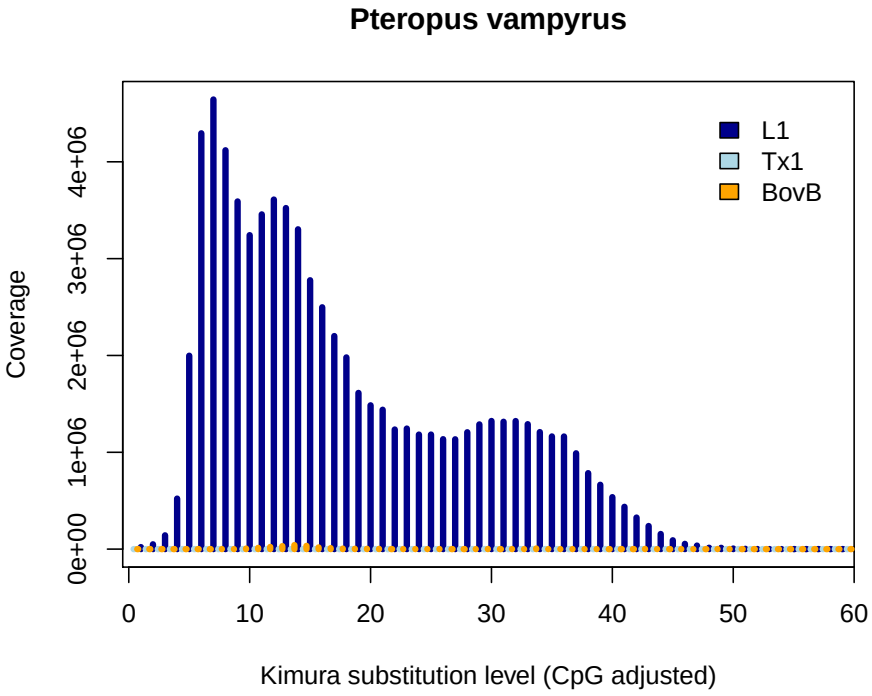

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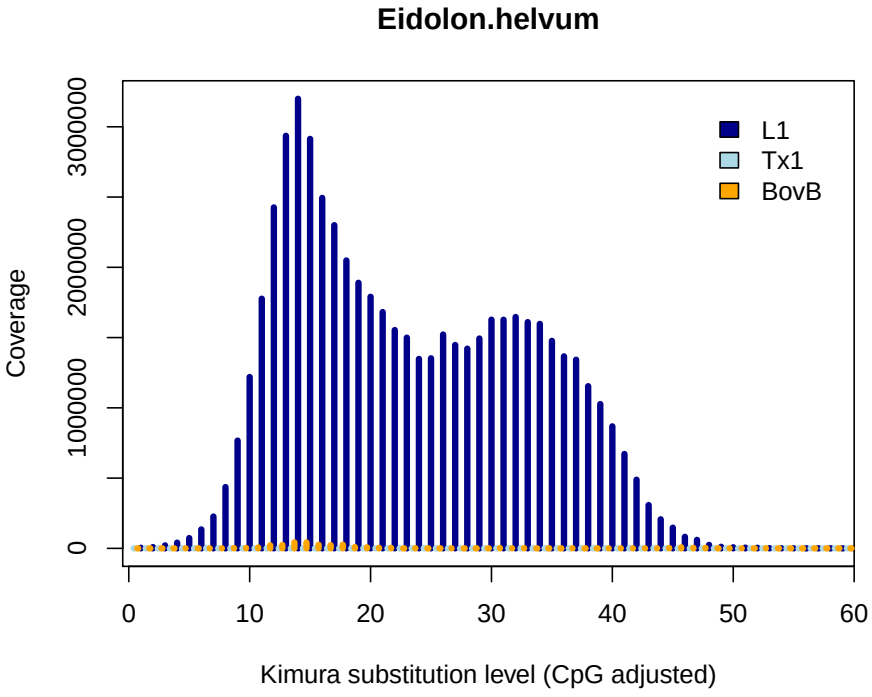

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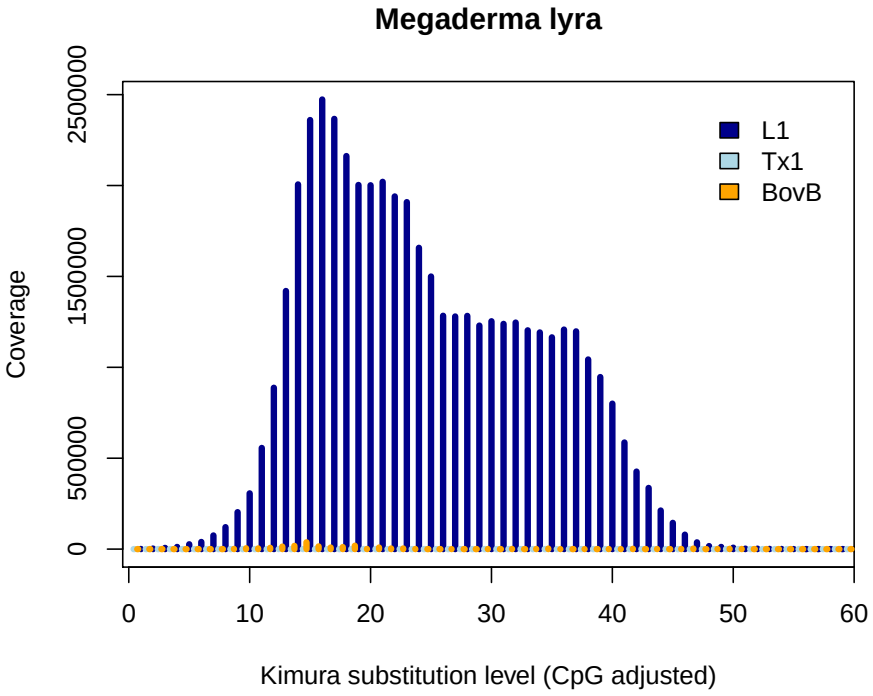

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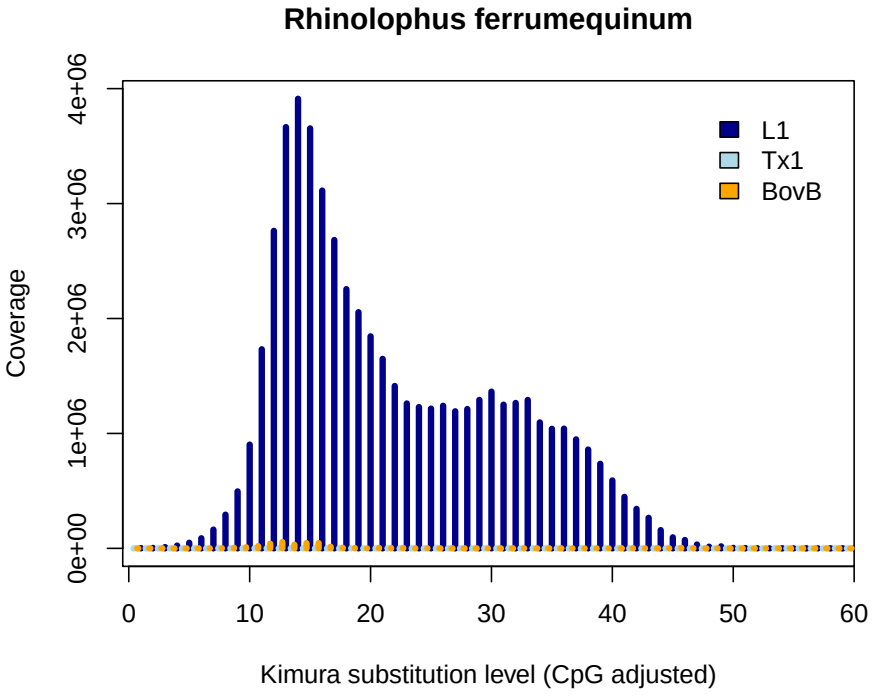

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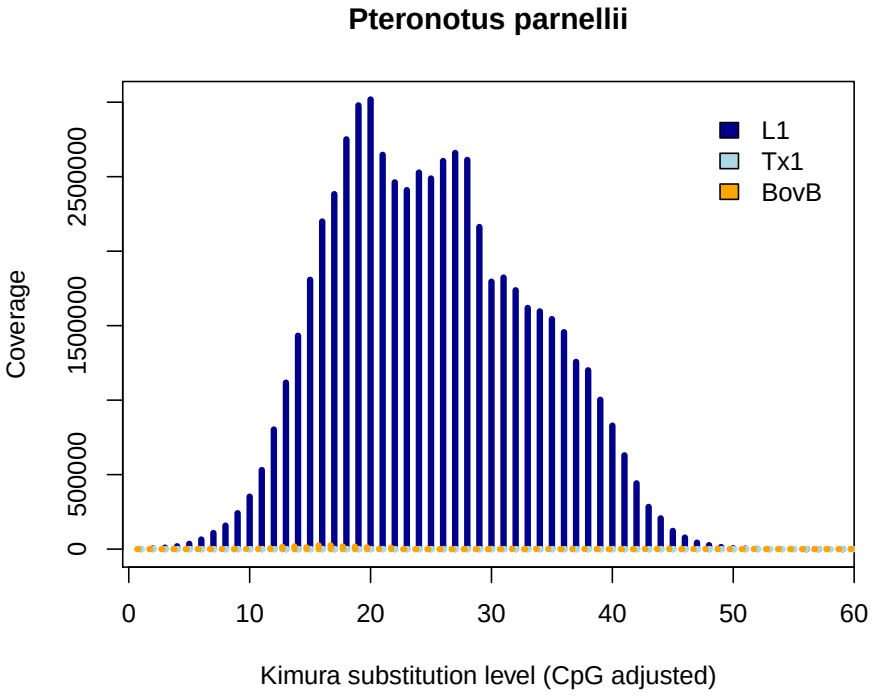

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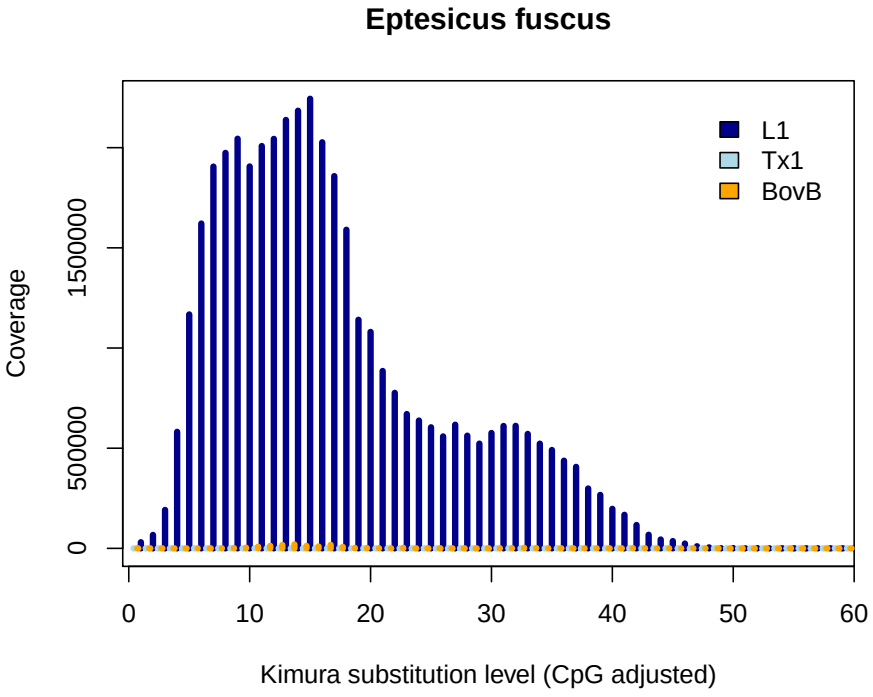

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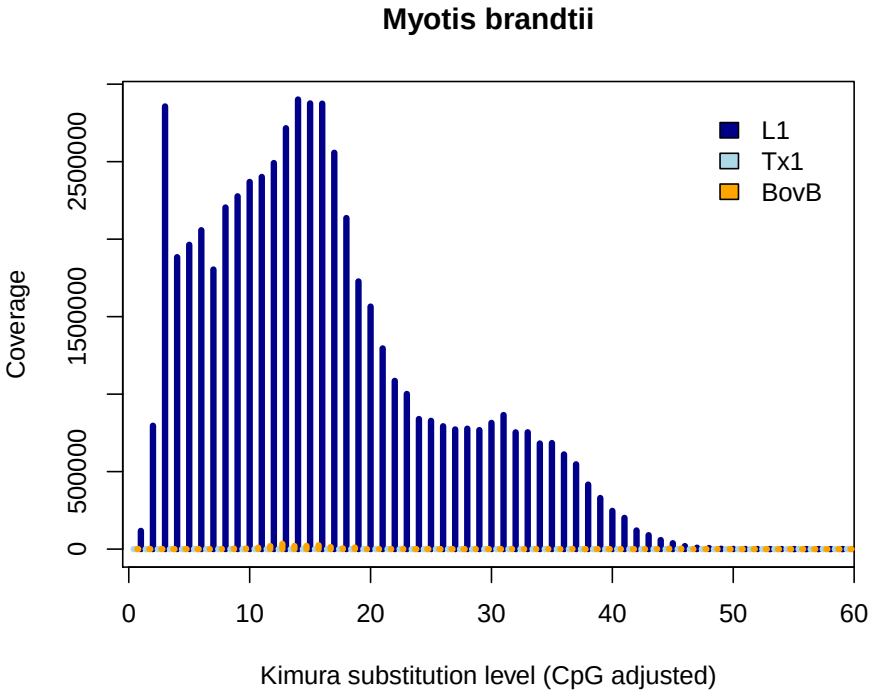

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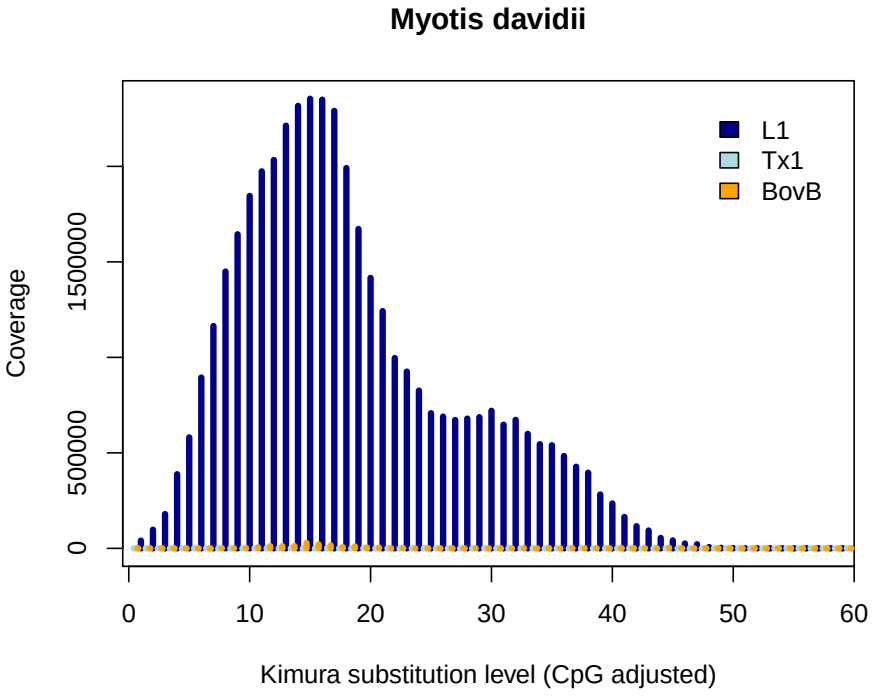

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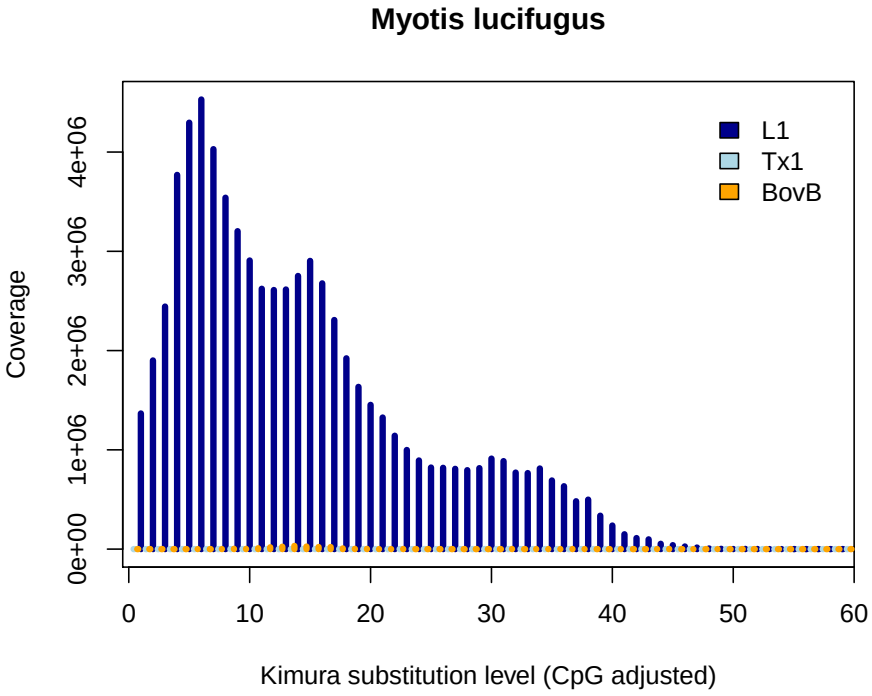

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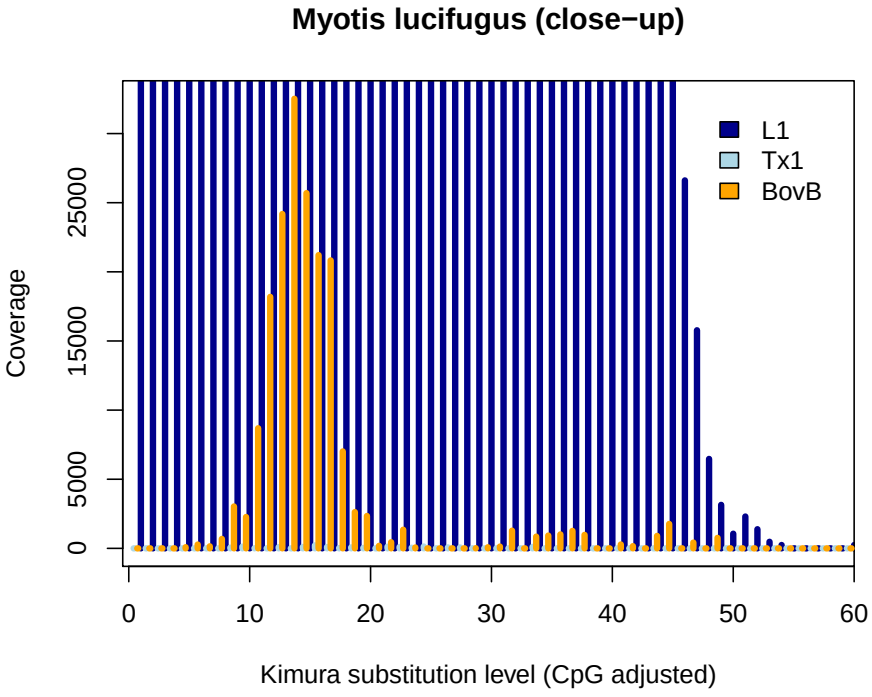
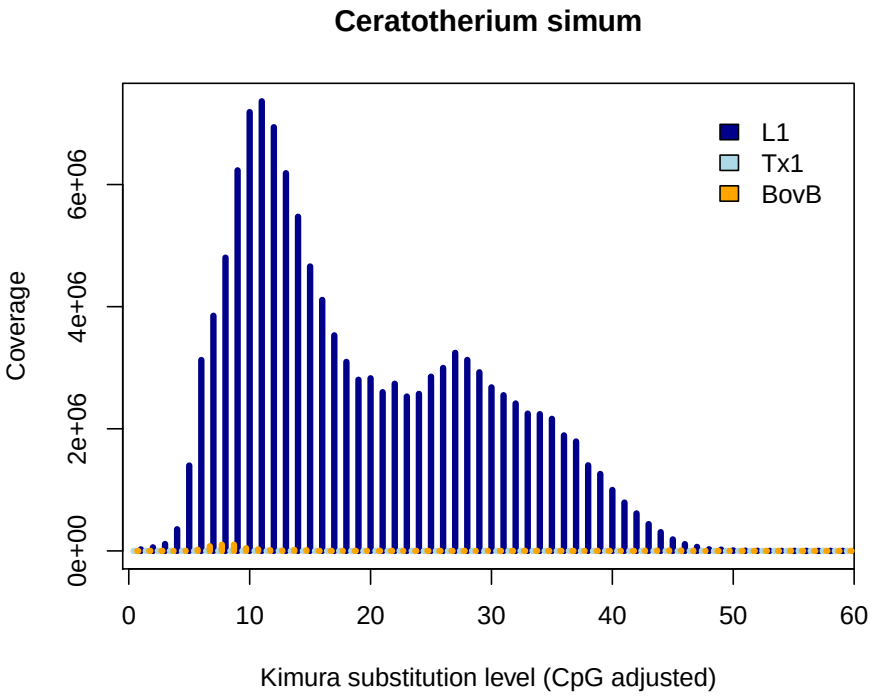


Figure S24

Perissodactyla



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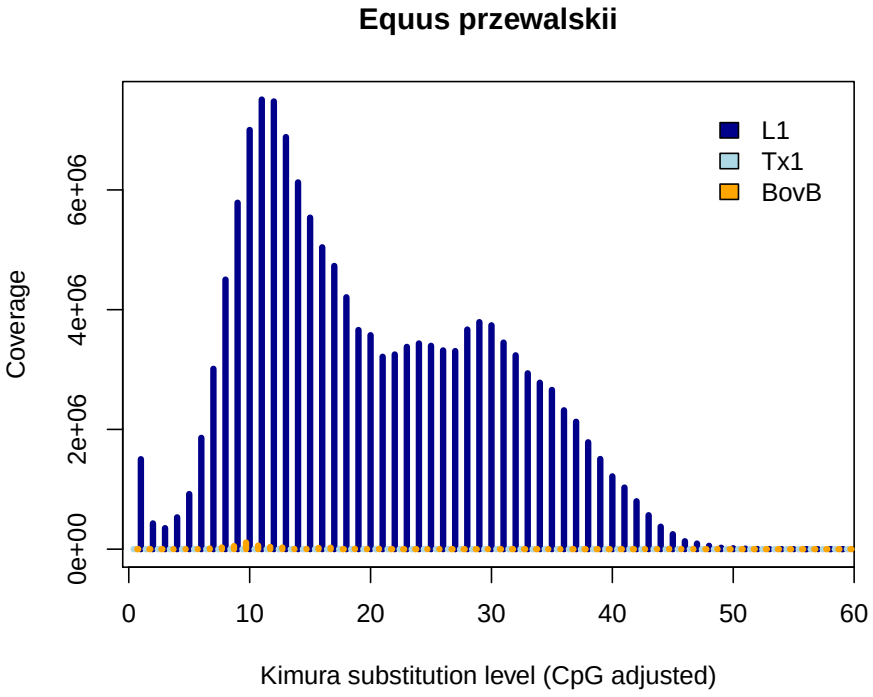

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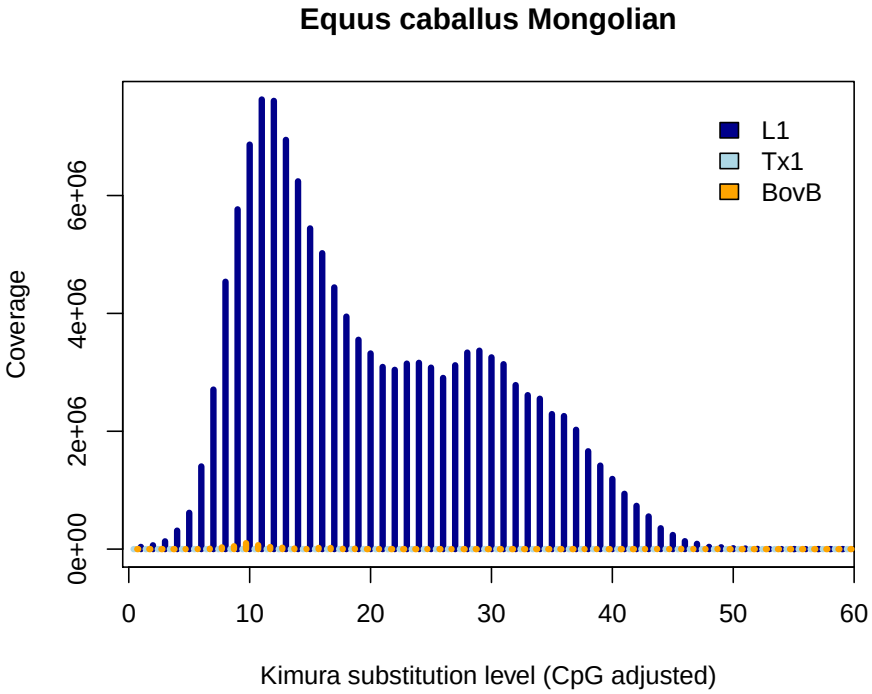

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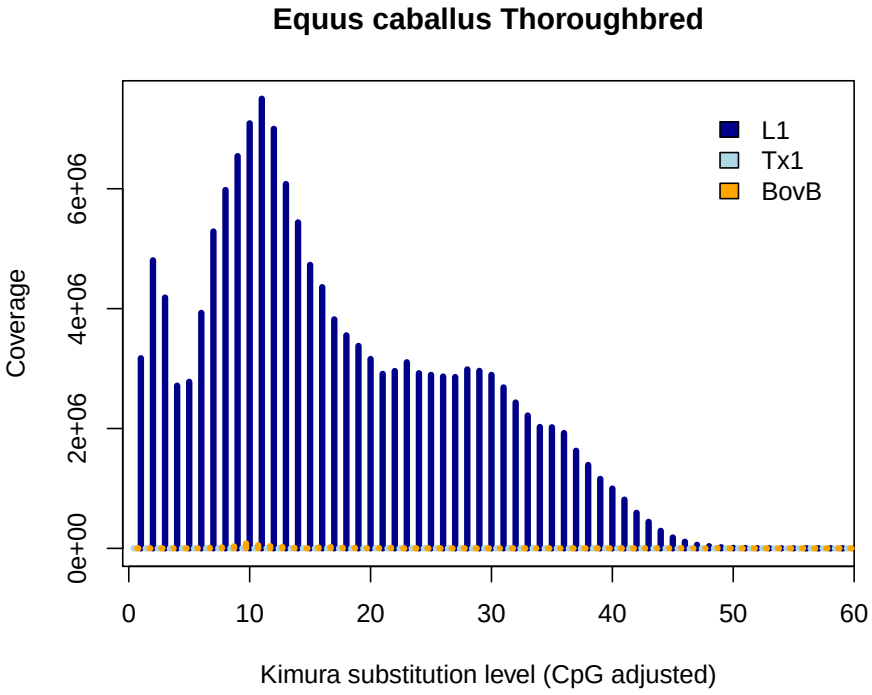

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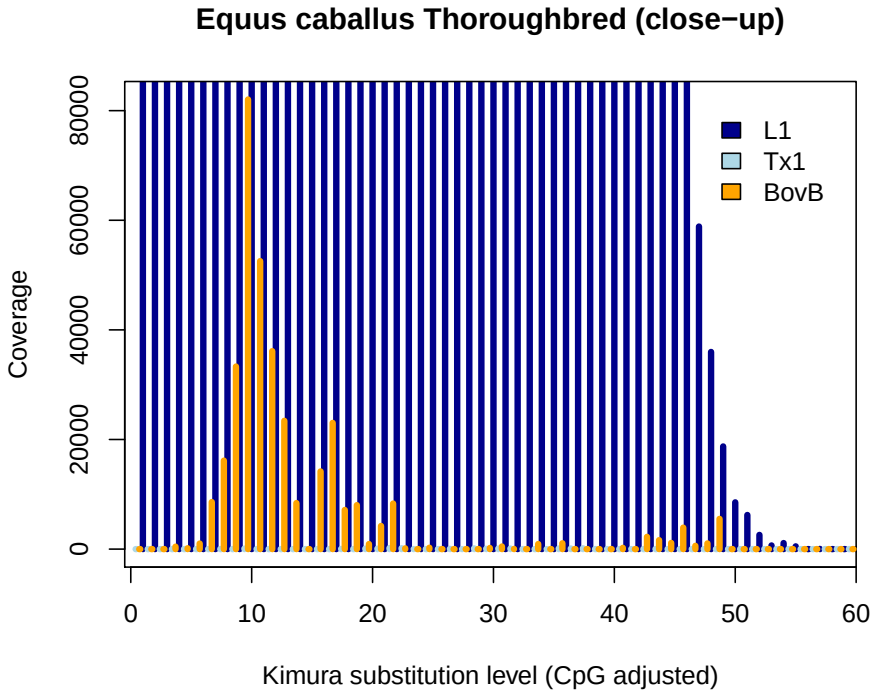
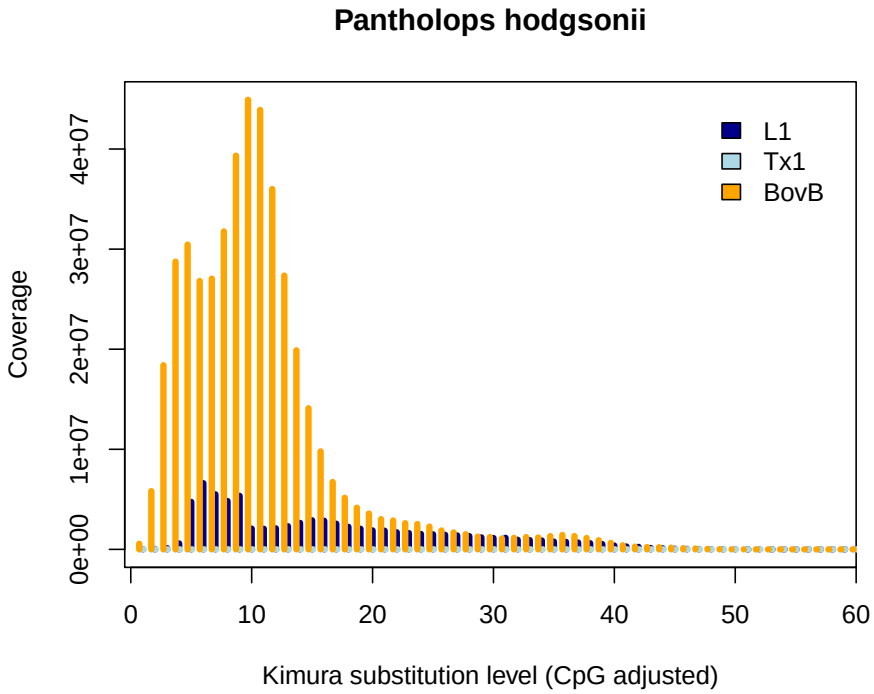


Figure S29

Bovidae



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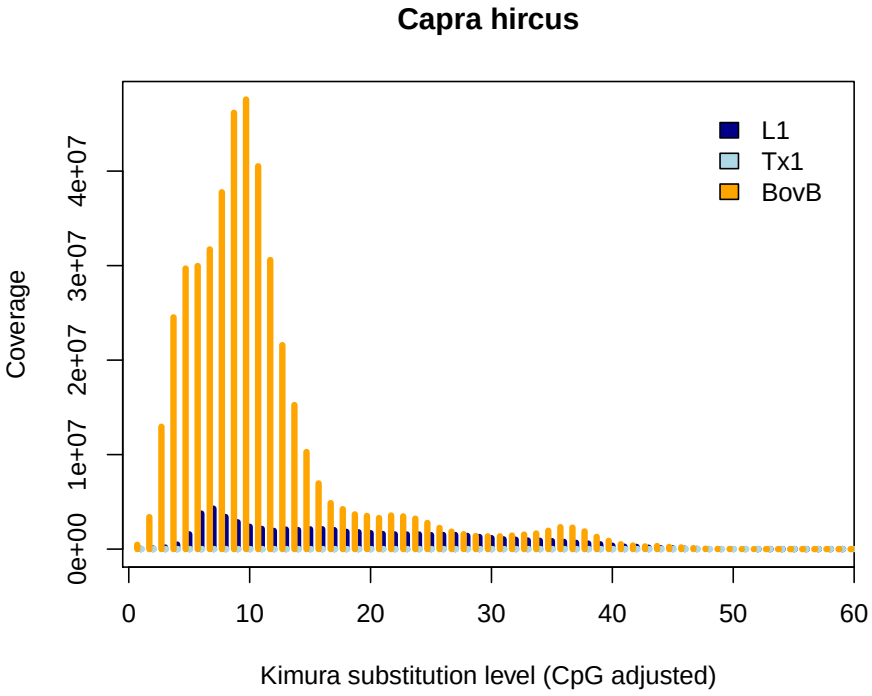

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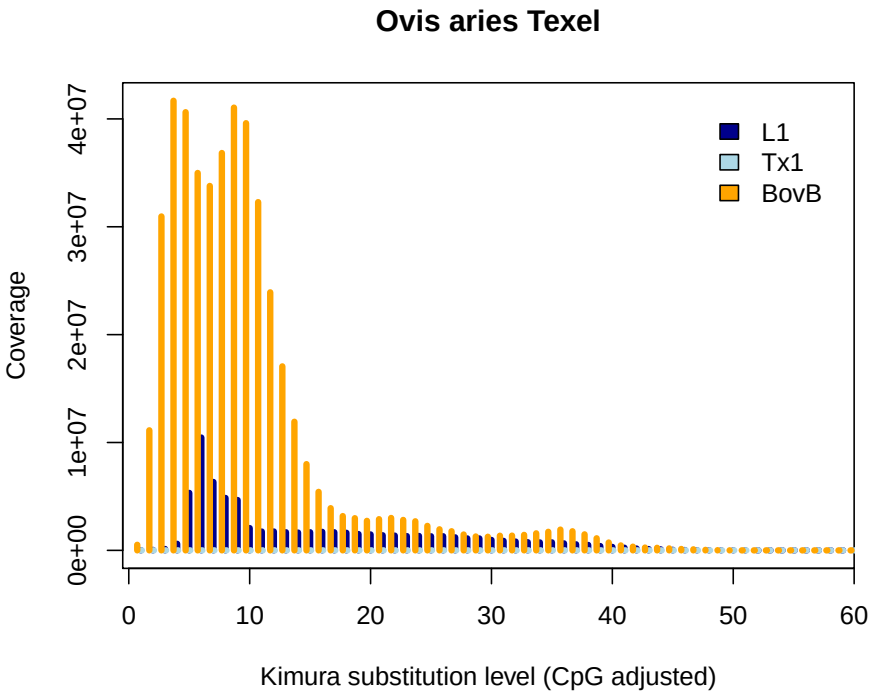

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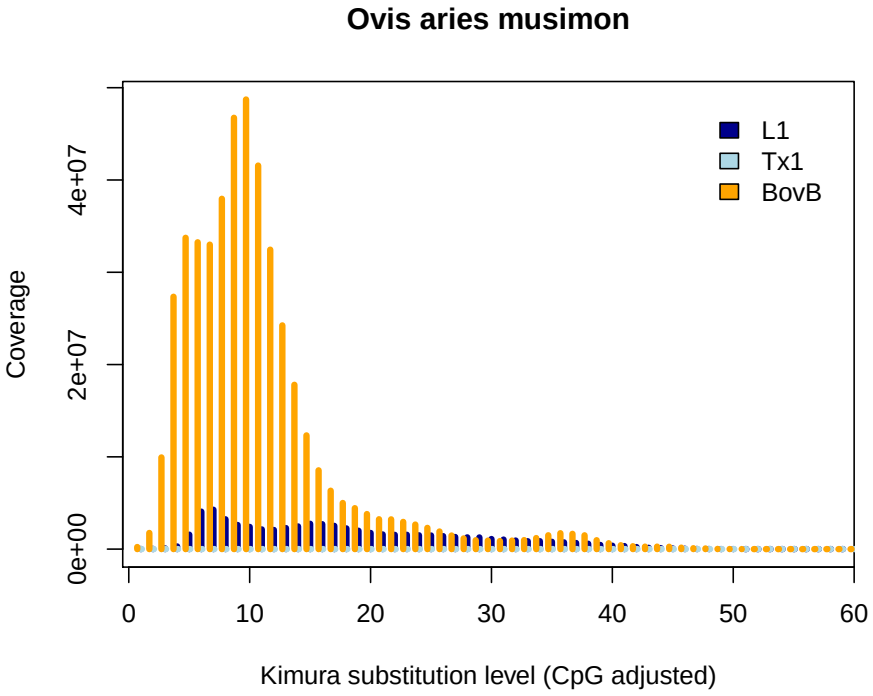

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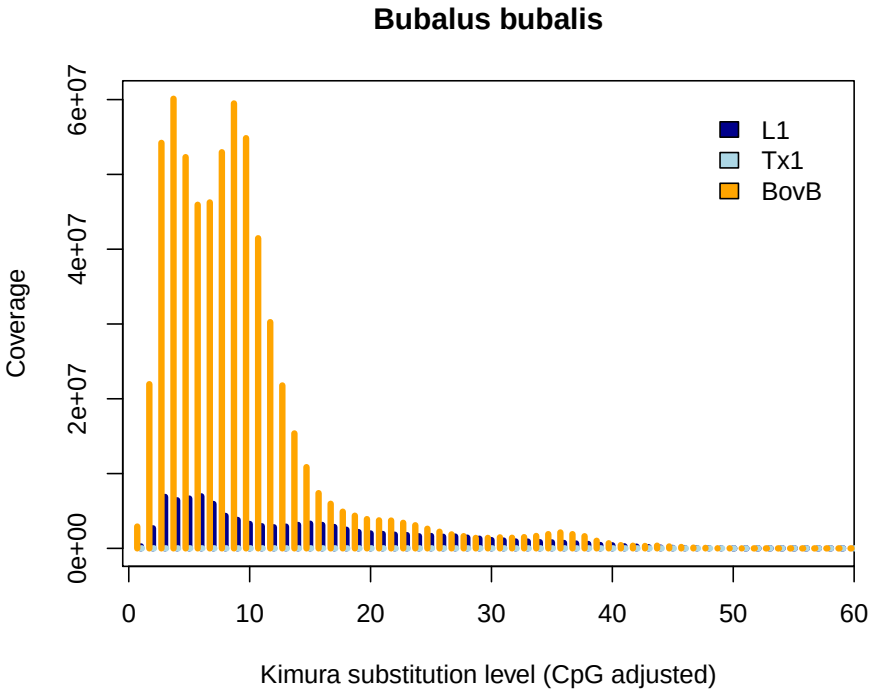

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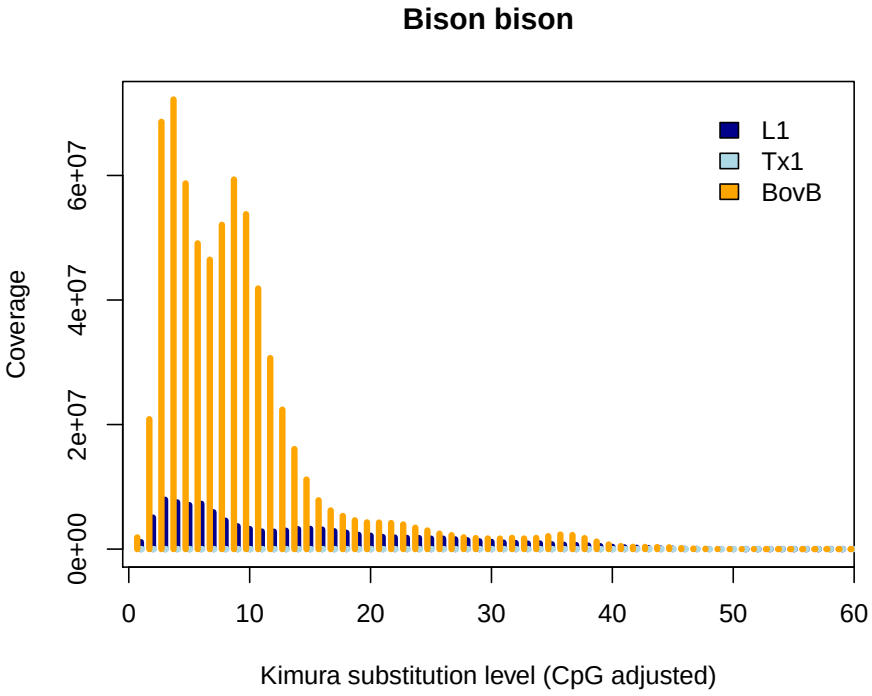

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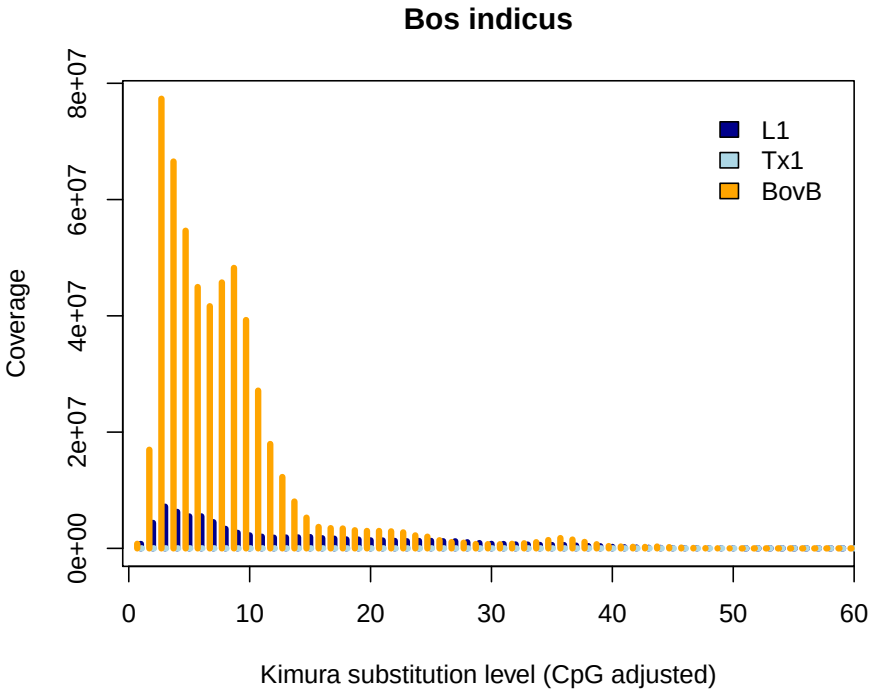

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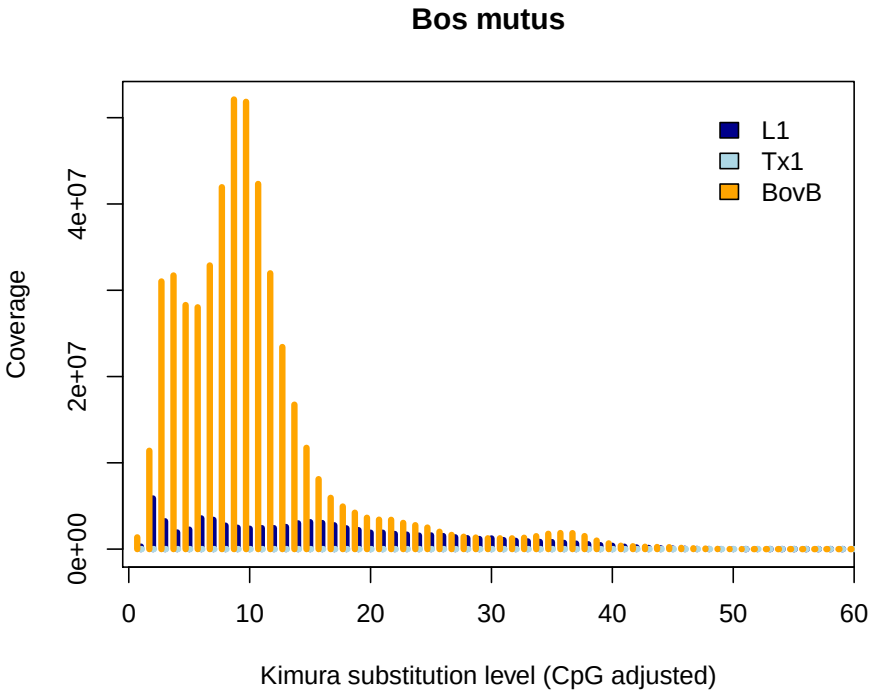


Figure S37

Squamata

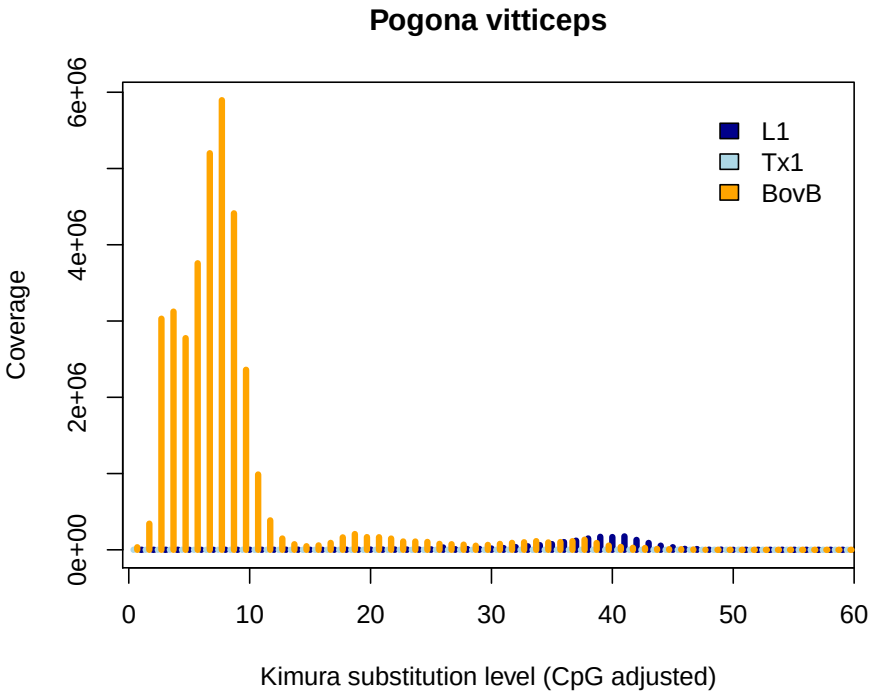
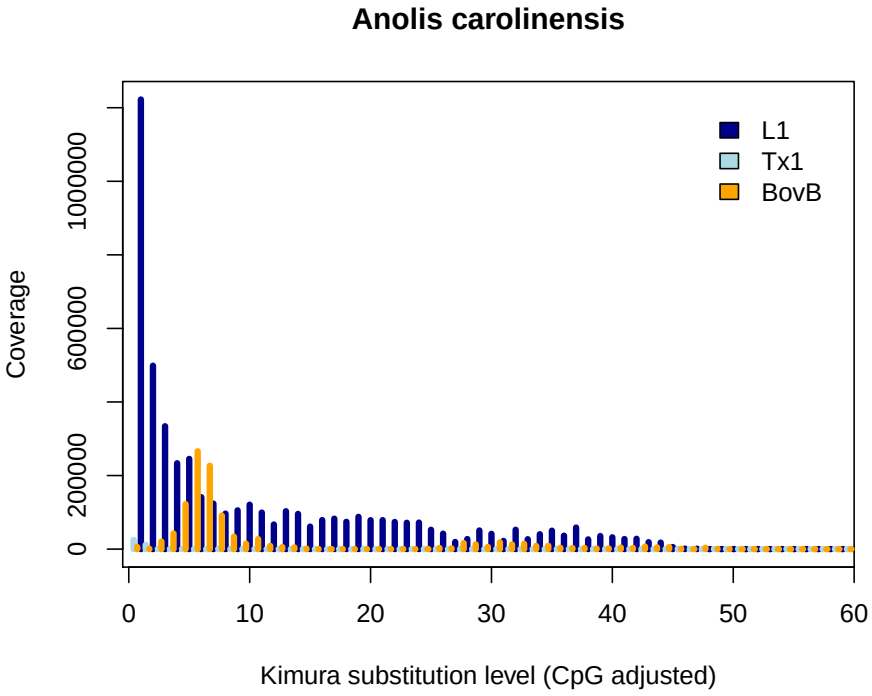


Figure S38



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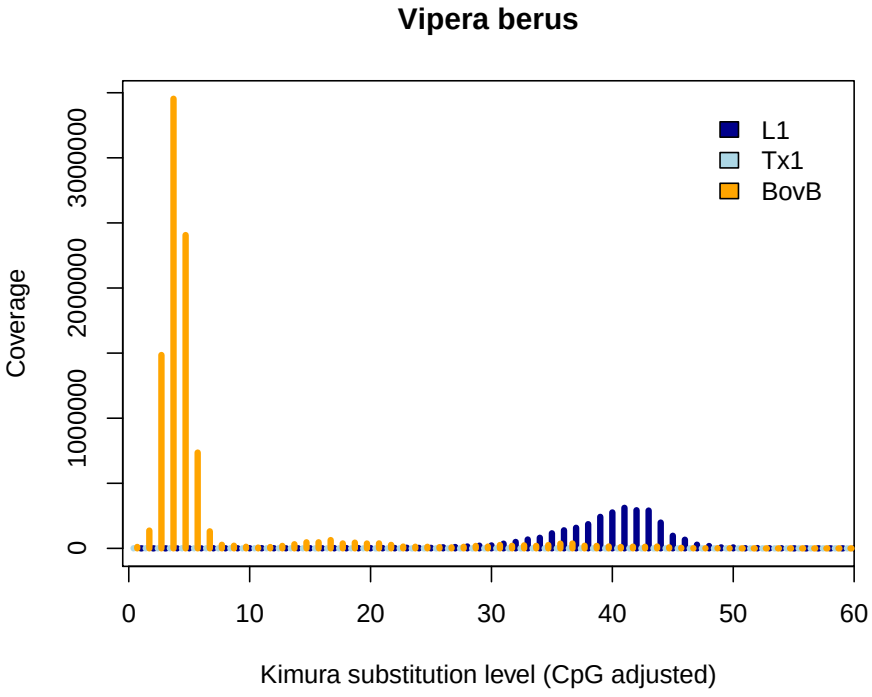

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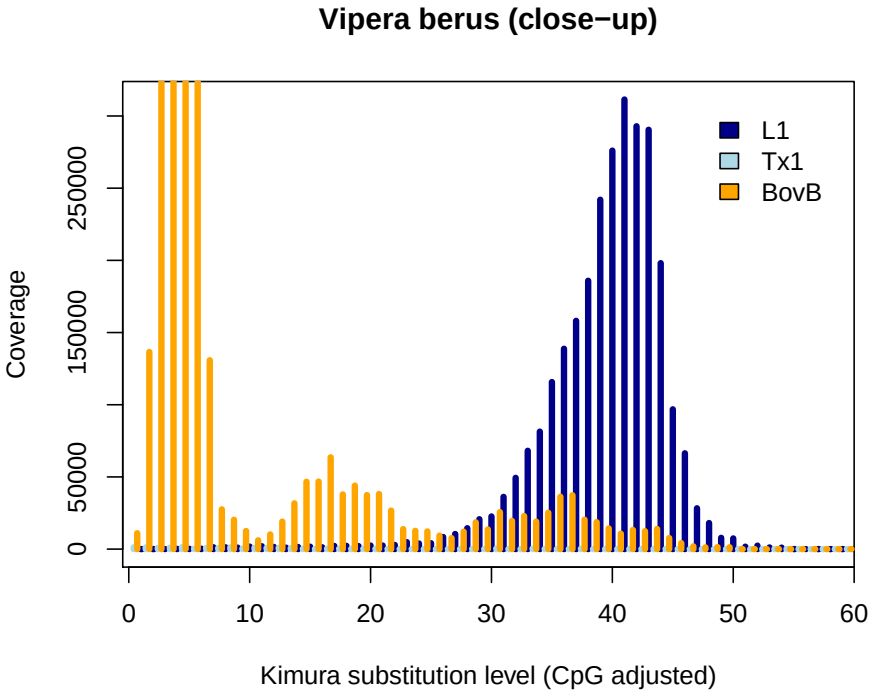

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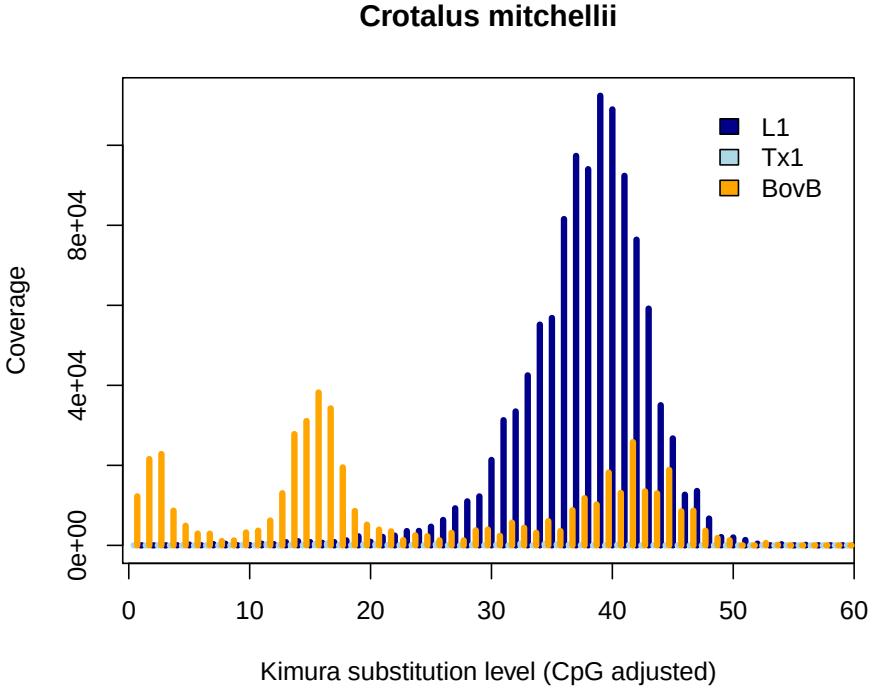

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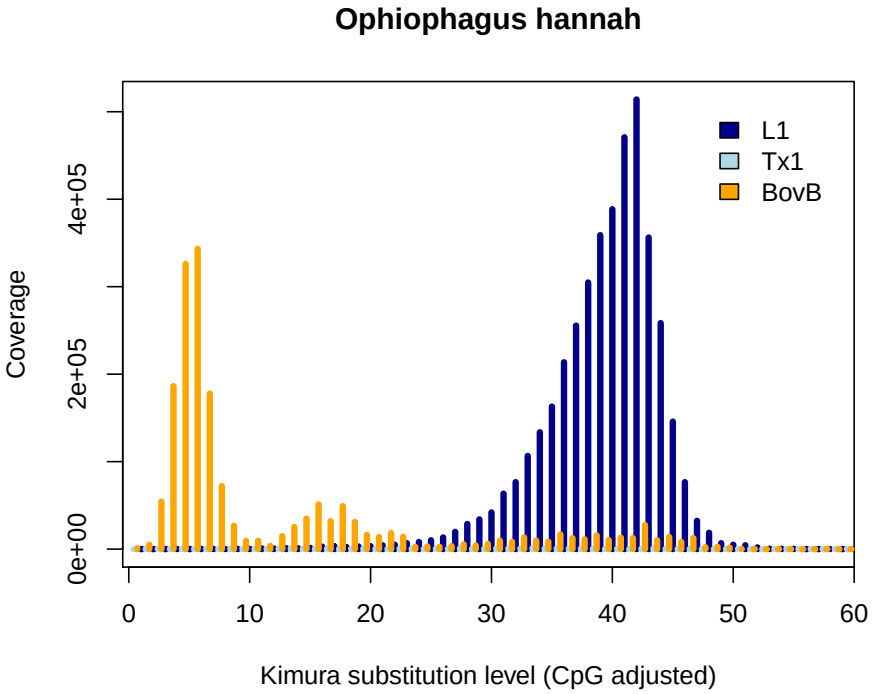

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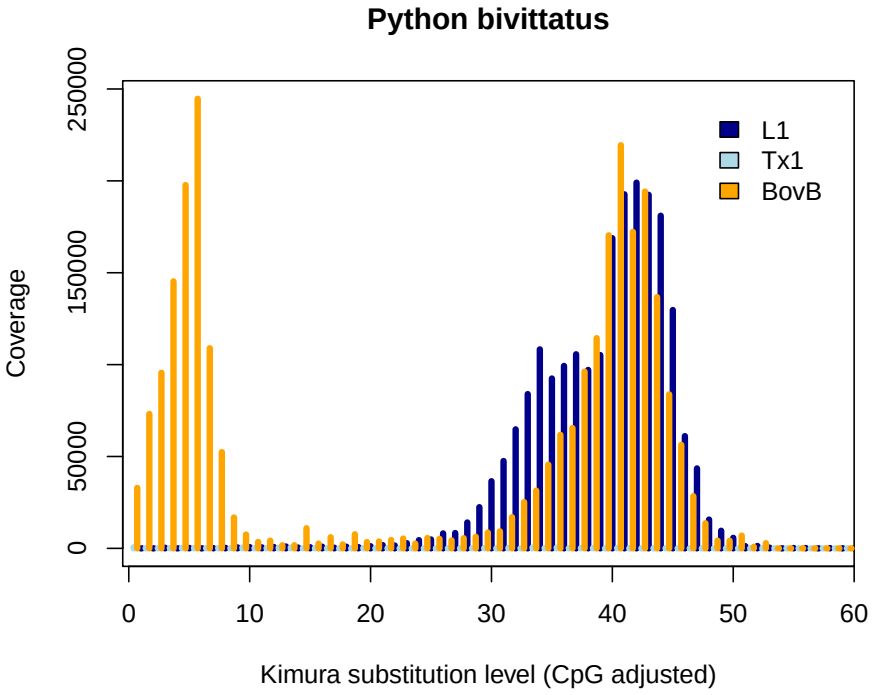
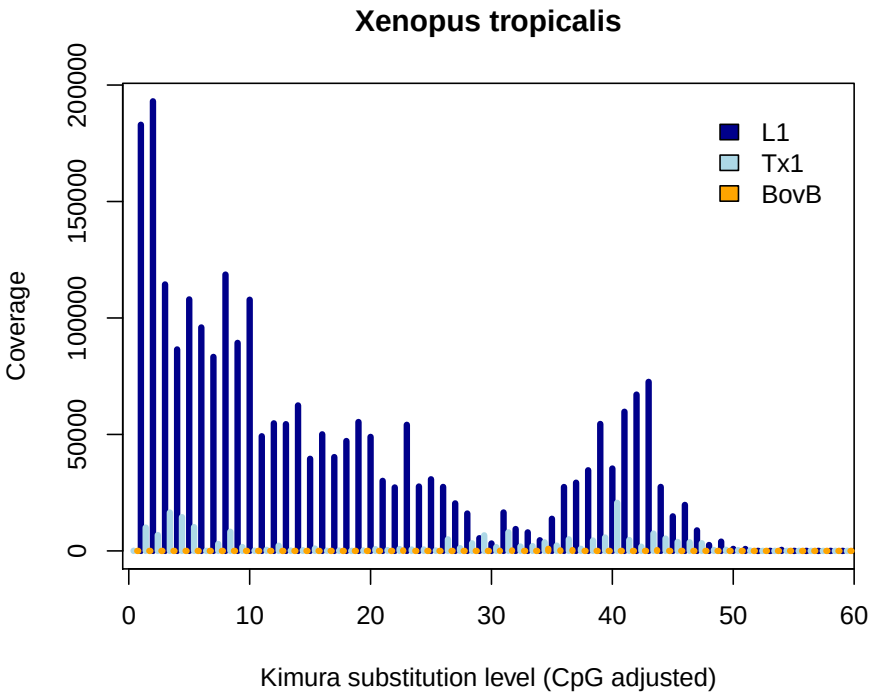


Figure S44

Amphibia



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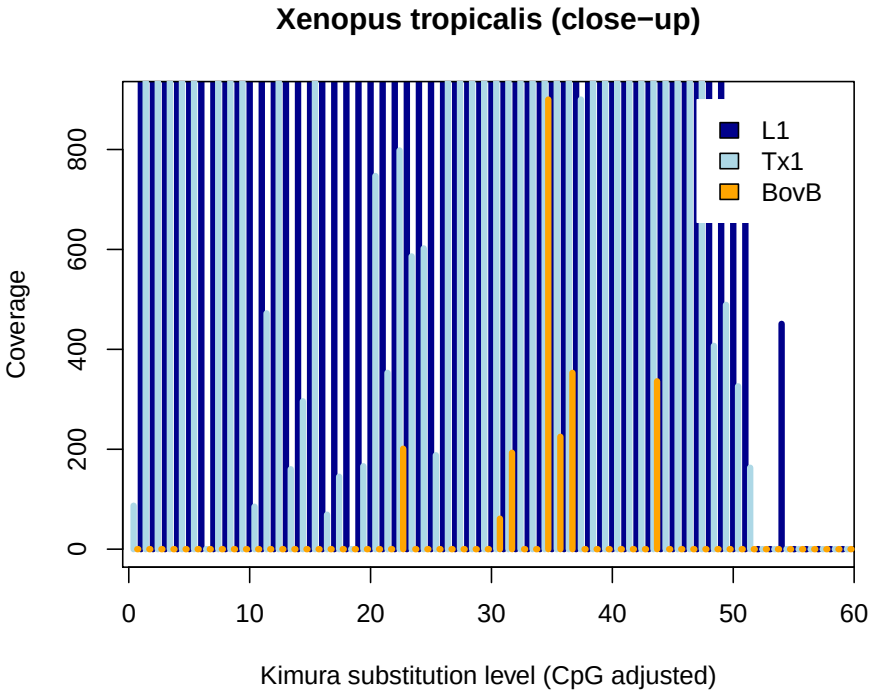

Figure S46

Neopterygii

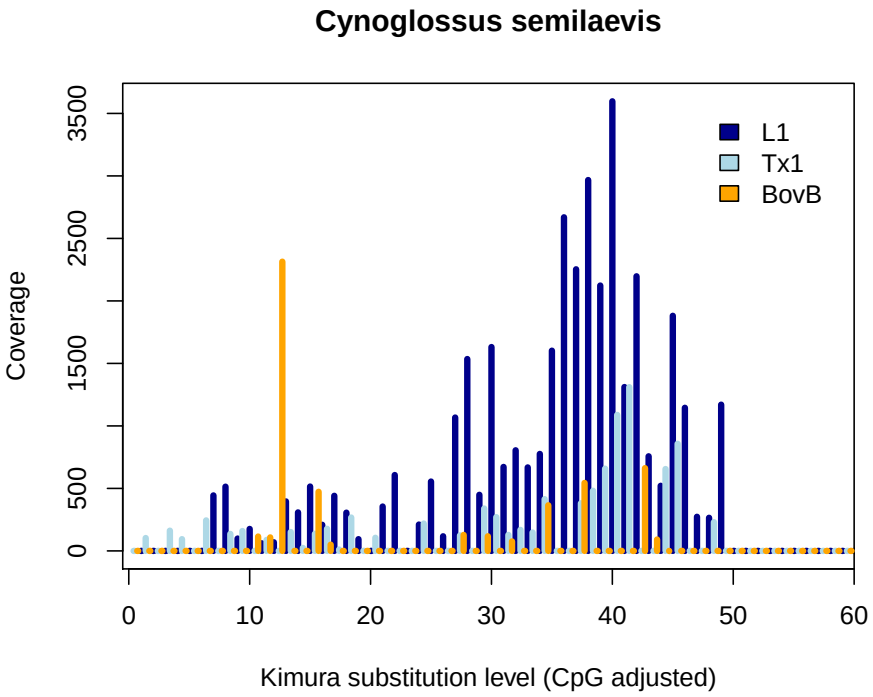

Figure S47

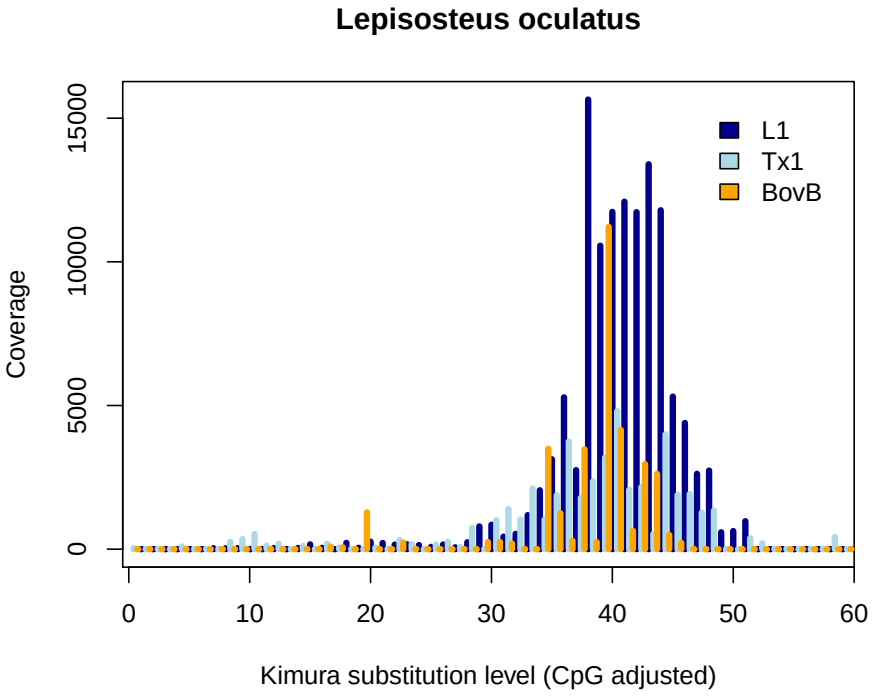

Figure S48

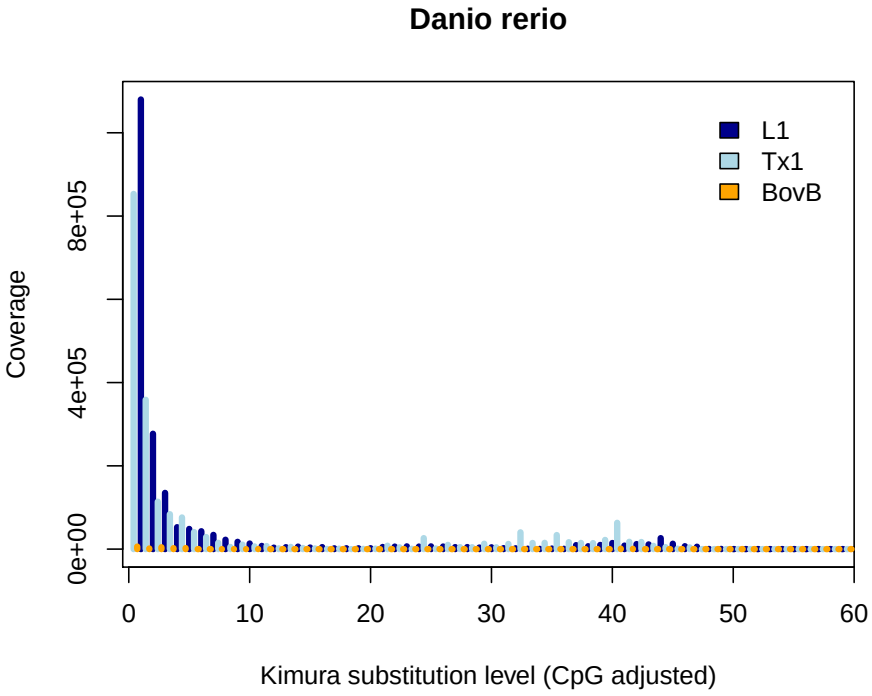

Figure S49

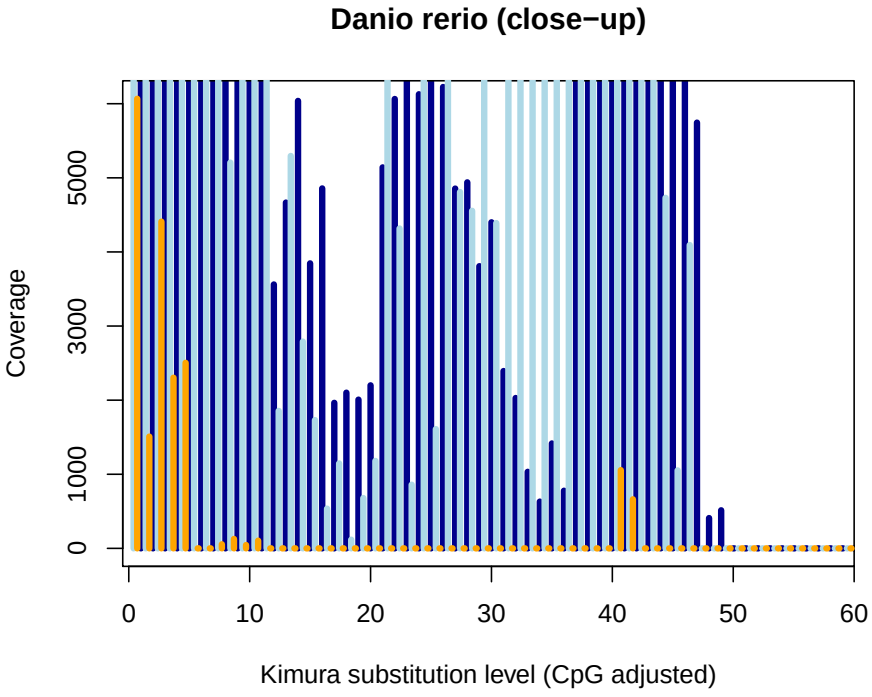

Figure S50

Other

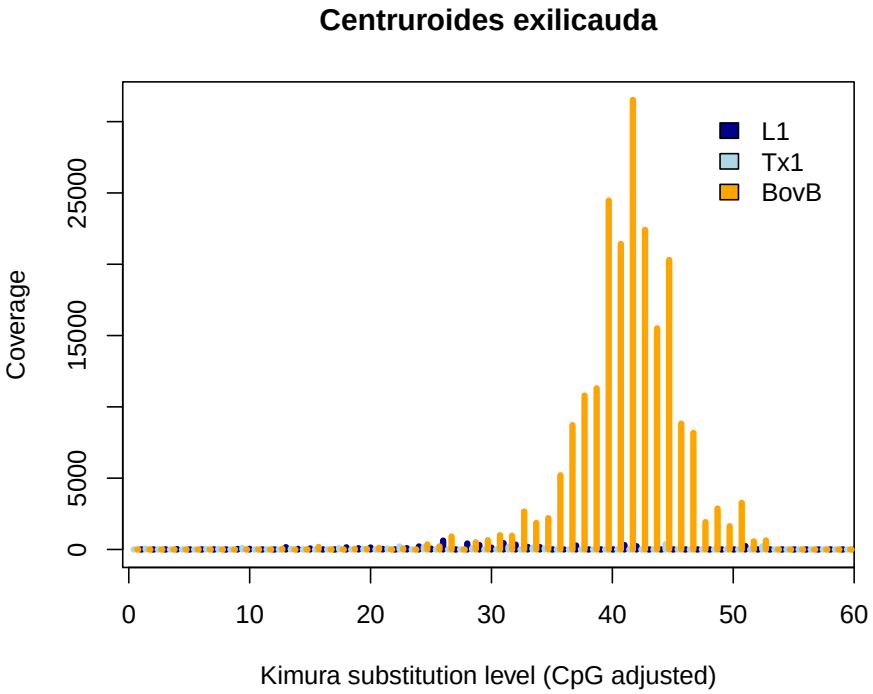

Figure S51

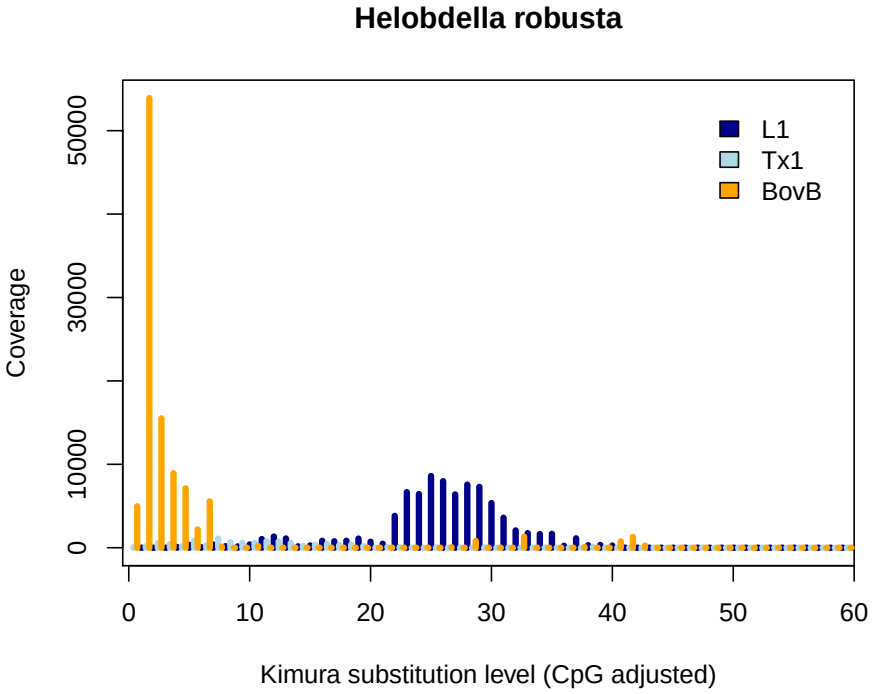

Figure S52

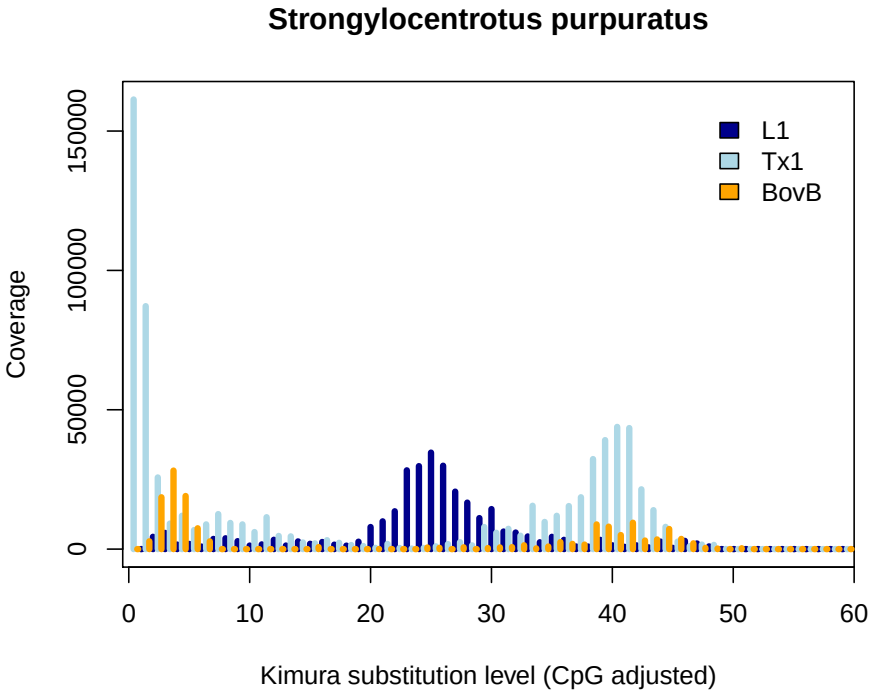

Figure S53

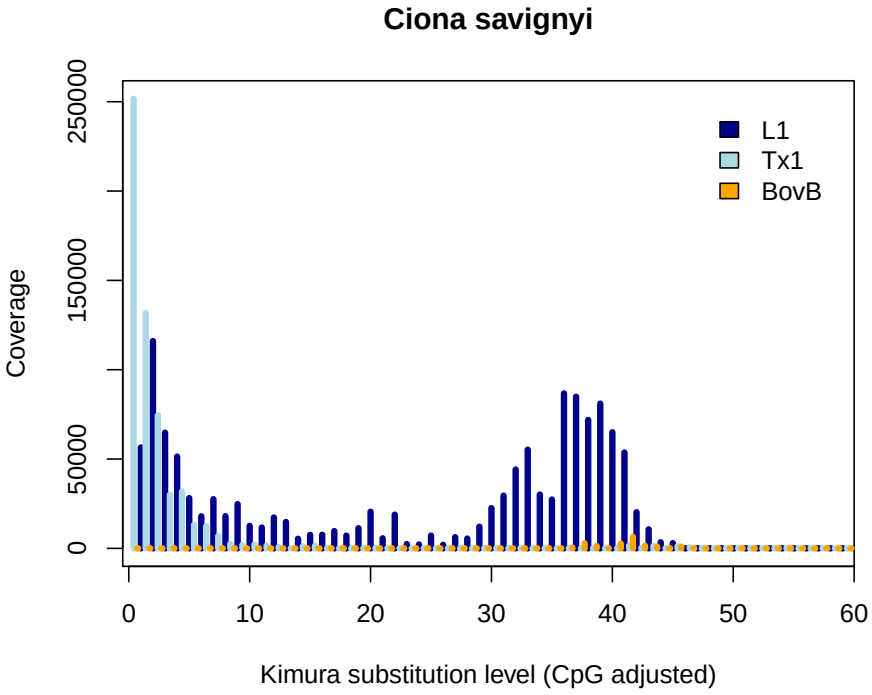

Figure S54

Figure S55: Chimeric L1-BovB

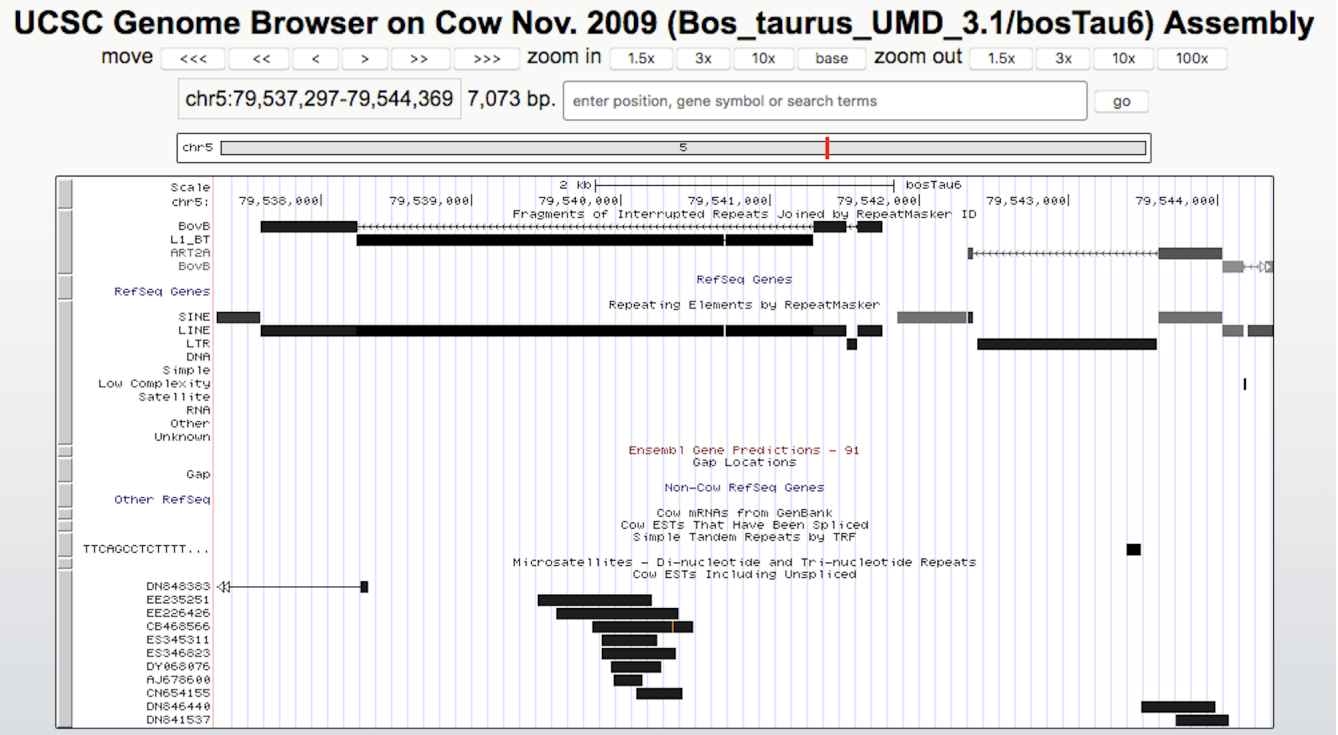

Figure S55: **Chimeric L1-BovB in cattle genomes.** Several cow ESTs overlap the L1 reverse transcriptase domain, but these may be artifacts/mismapped. No strong evidence to suggest transcription.