

Supplementary Figures

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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.

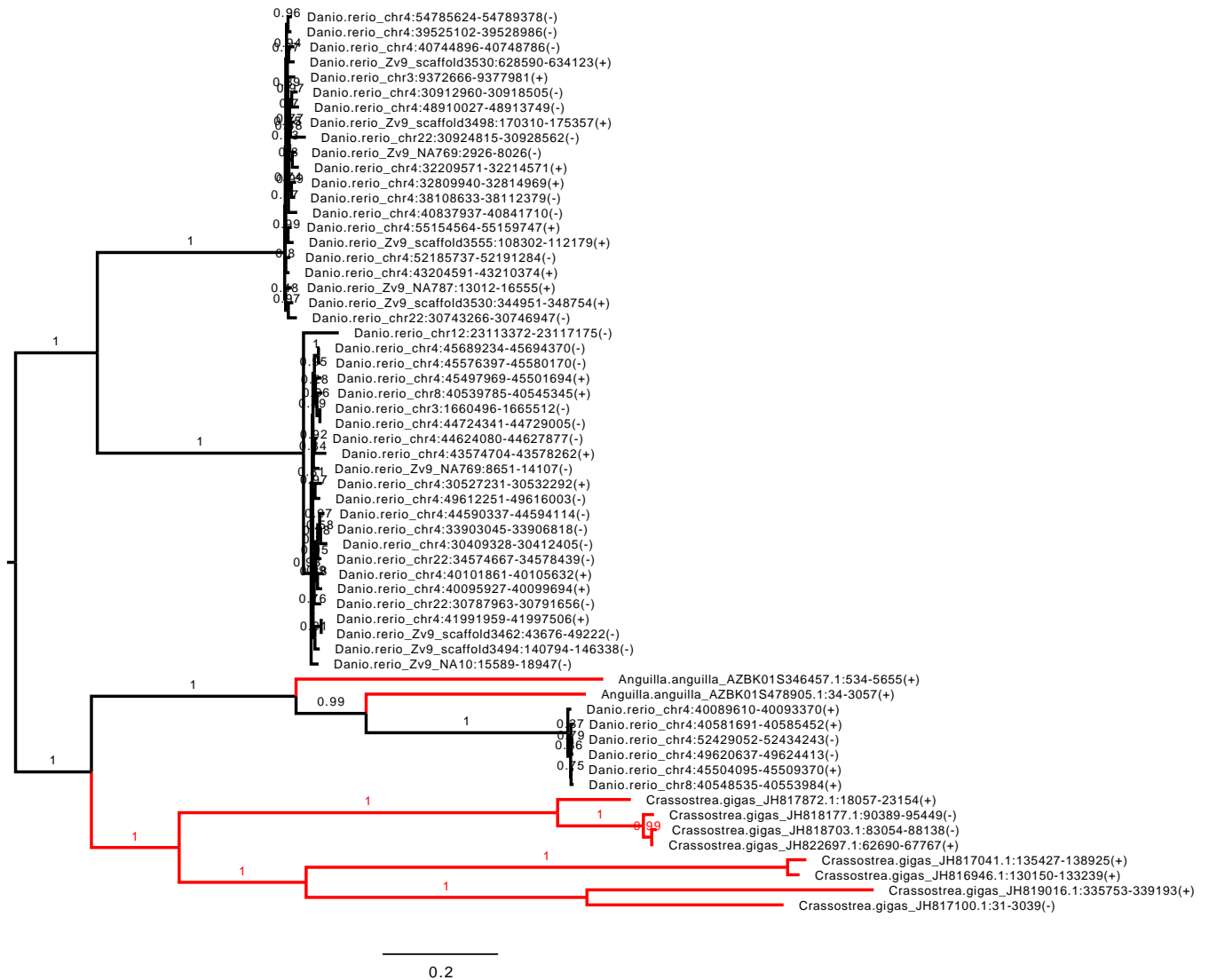


Figure S1: L1 cluster c_25

L1 nucleotide ORFs

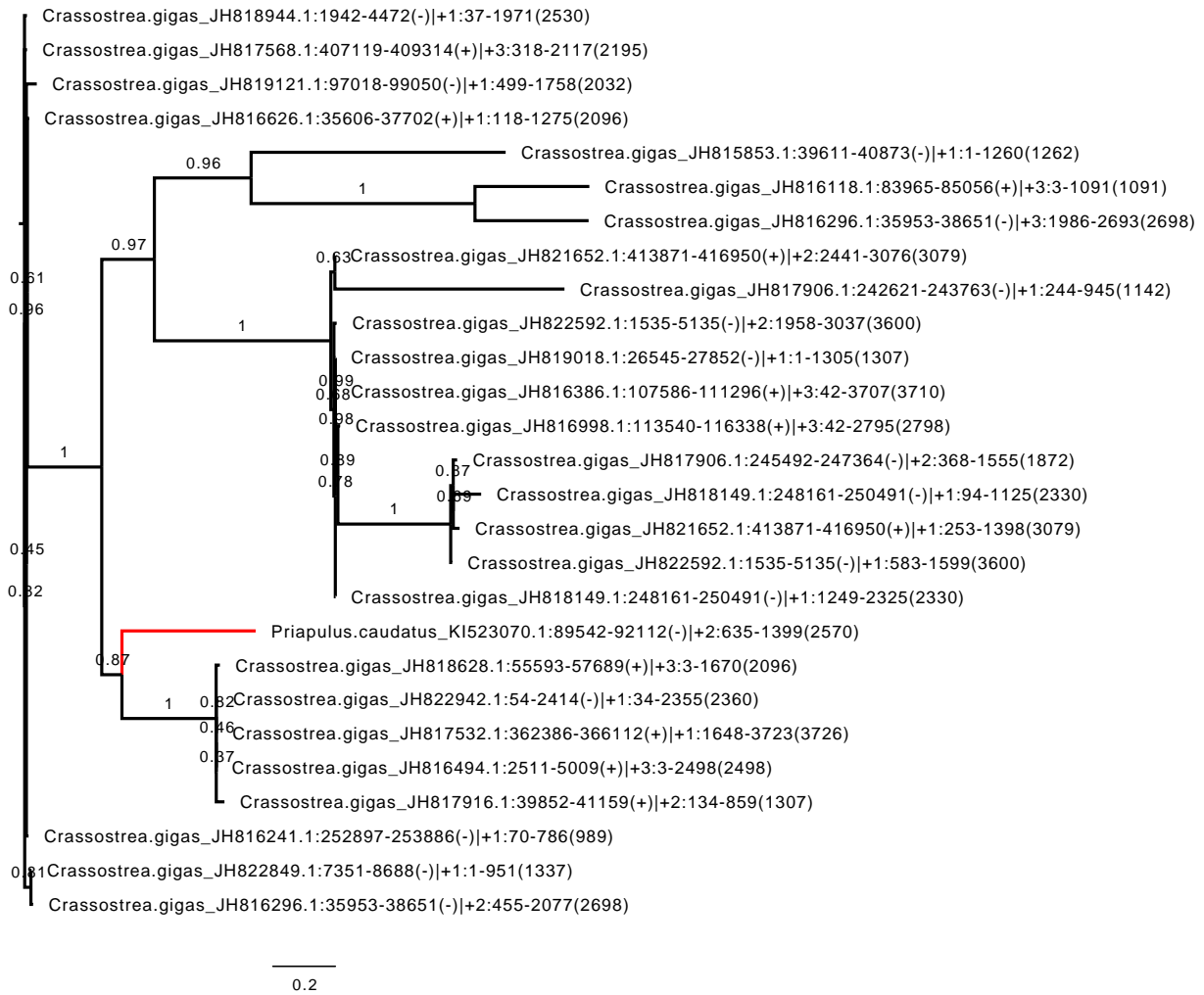


Figure S2: L1 cluster o_666

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

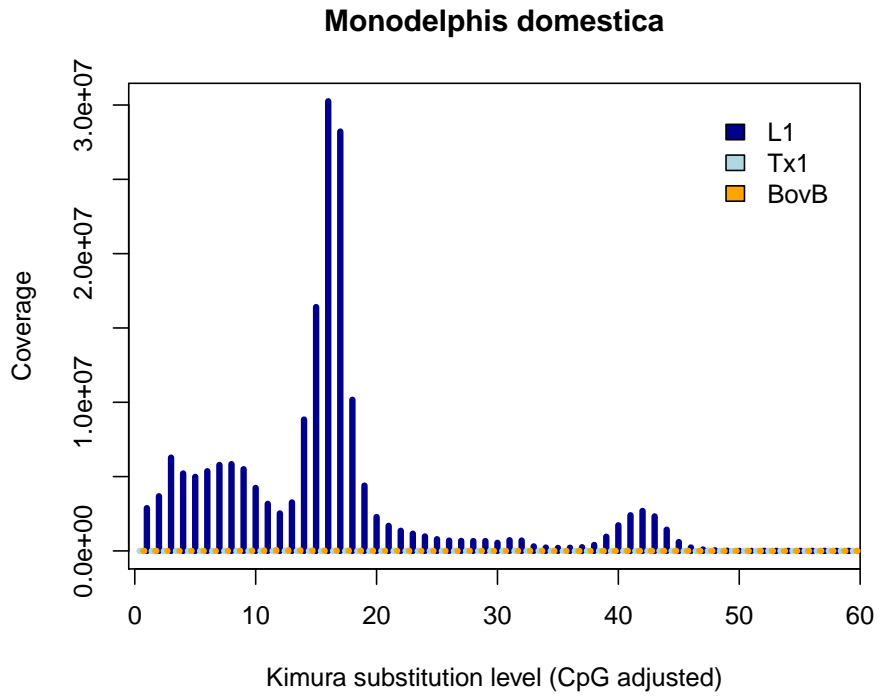


Figure S3

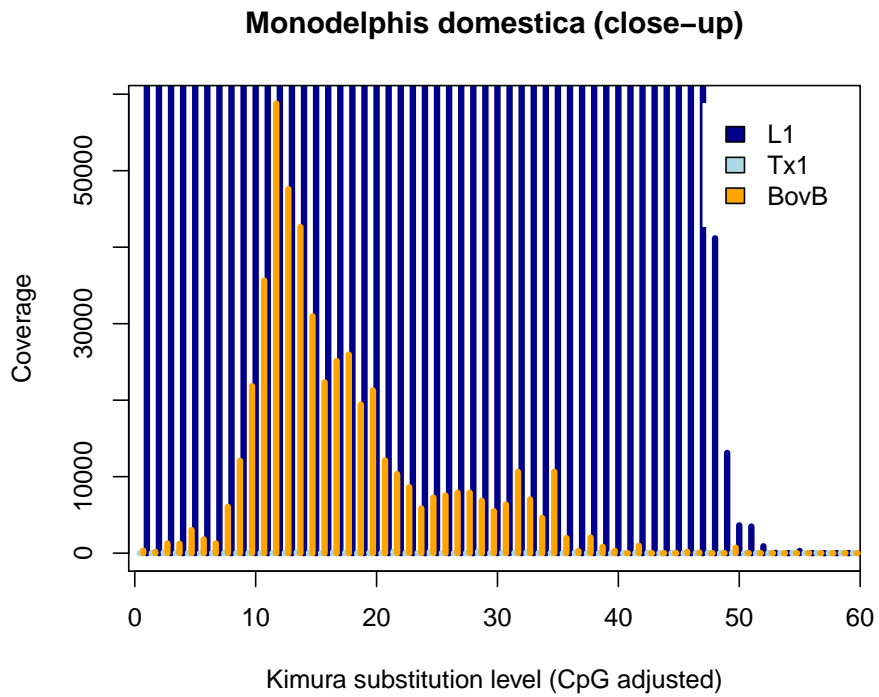


Figure S4

Macropus eugenii

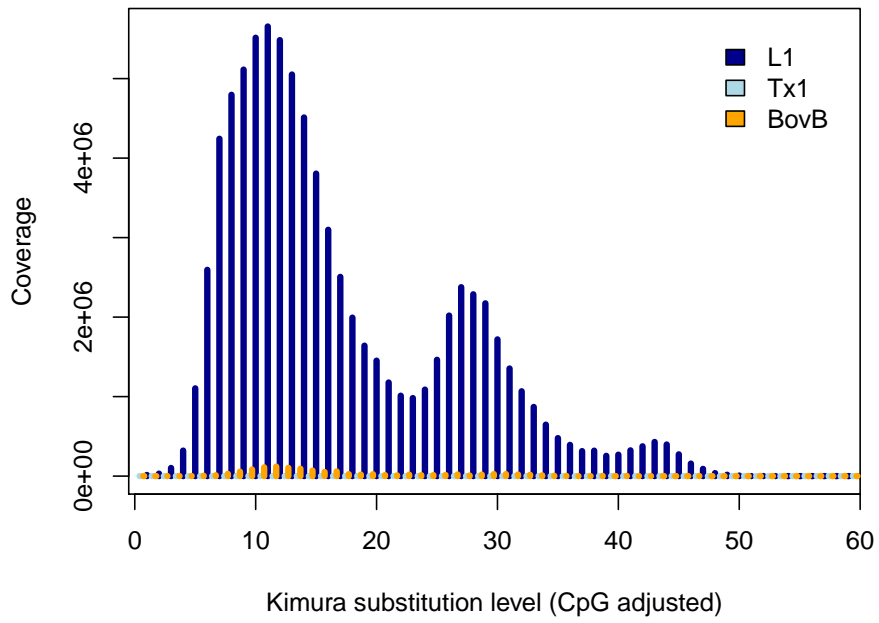


Figure S5

Sarcophilus harrisii

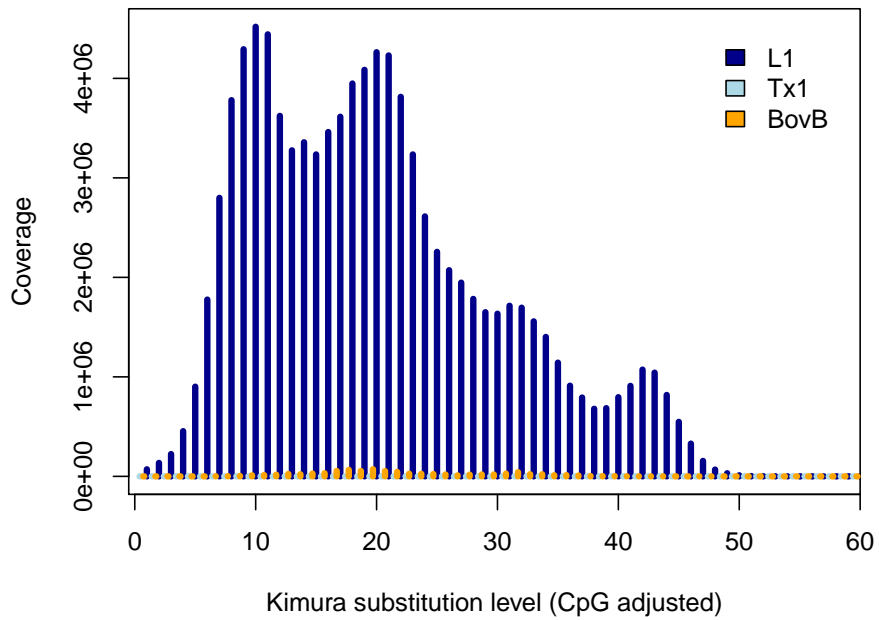


Figure S6

Afrotheria

Elephantulus edwardii

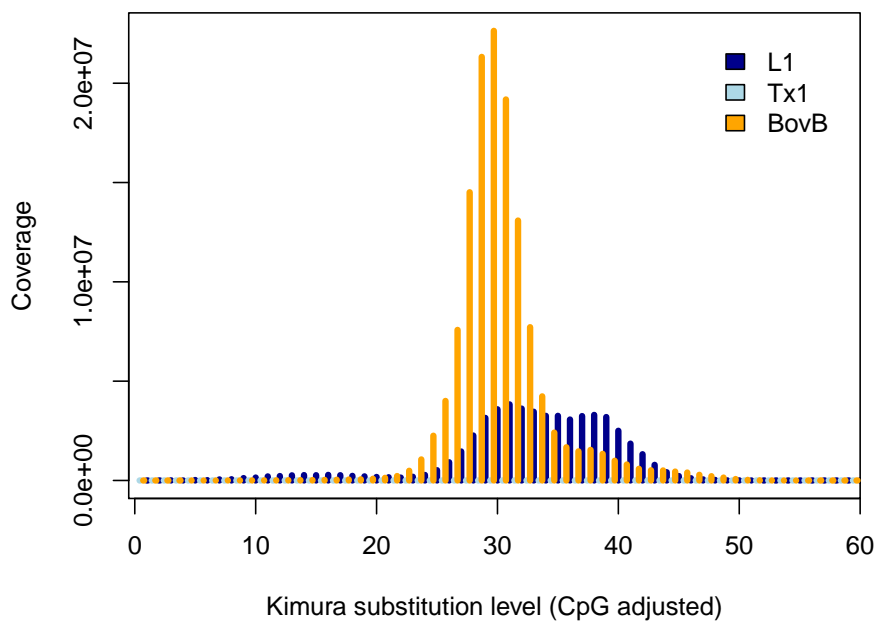


Figure S7

Echinops telfairi

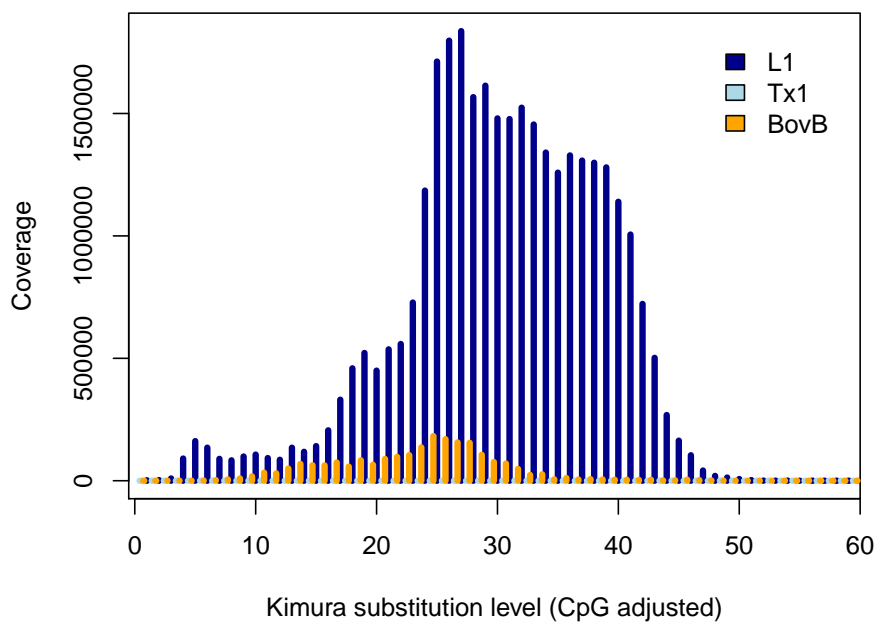


Figure S8

Chrysochloris asiatica

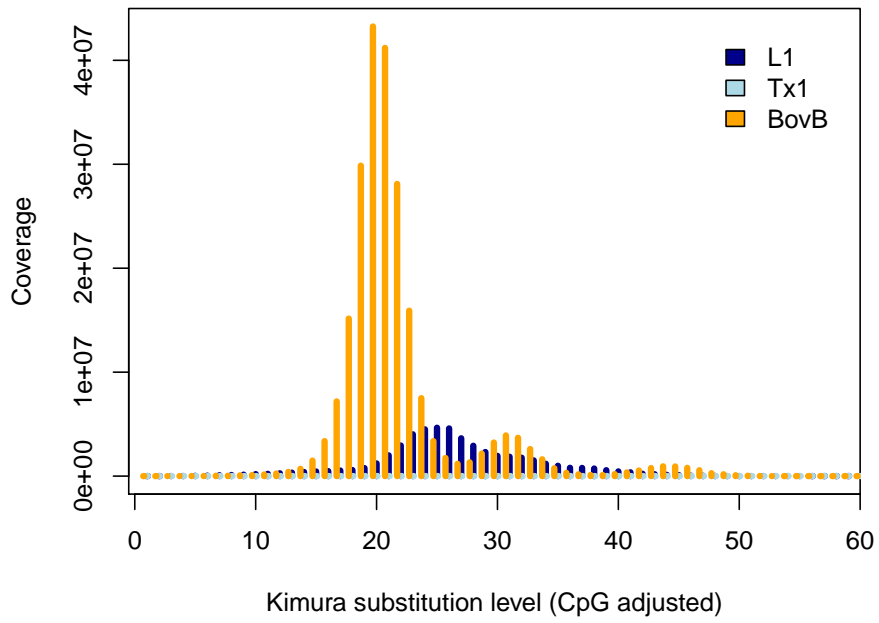


Figure S9

Orycteropus afer

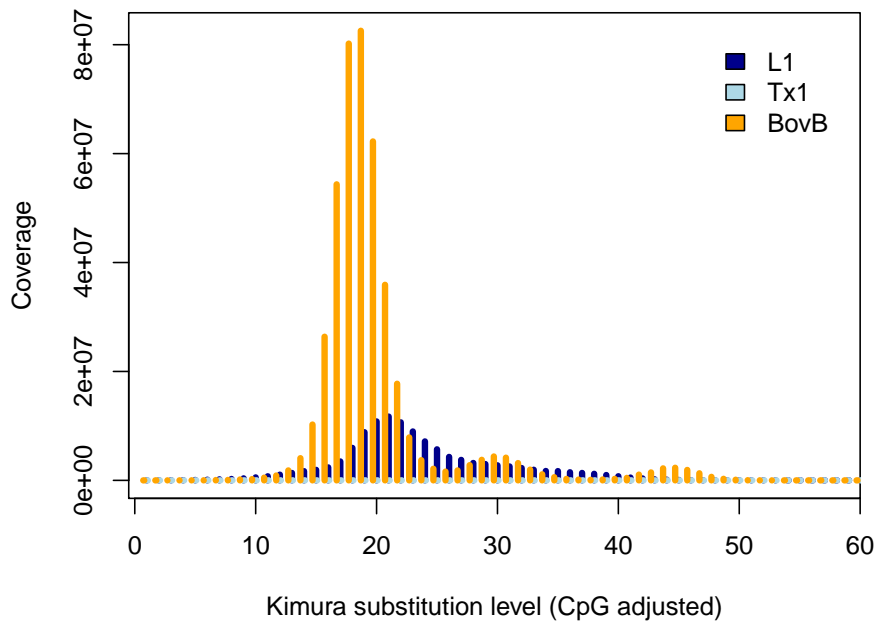


Figure S10

Trichechus manatus

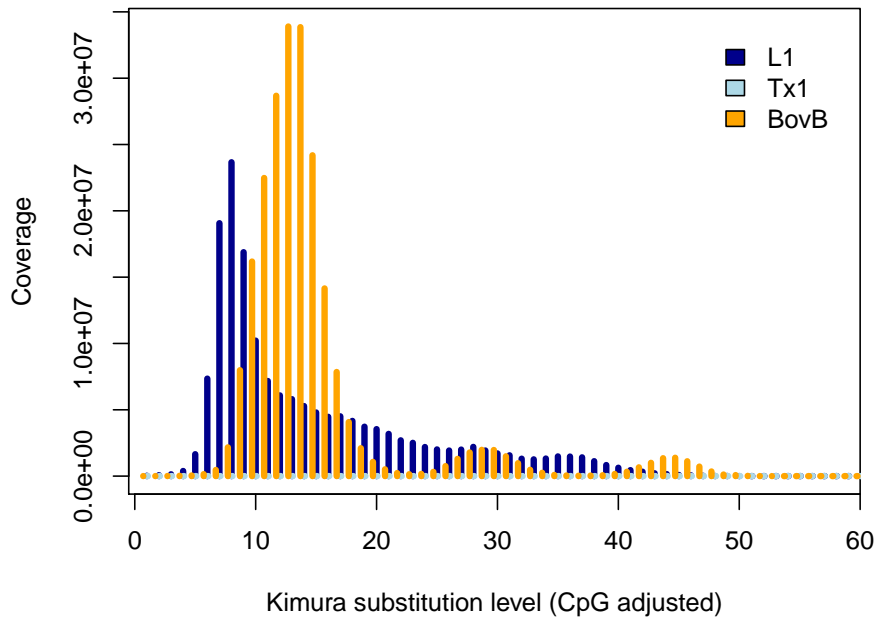


Figure S11

Procavia capensis

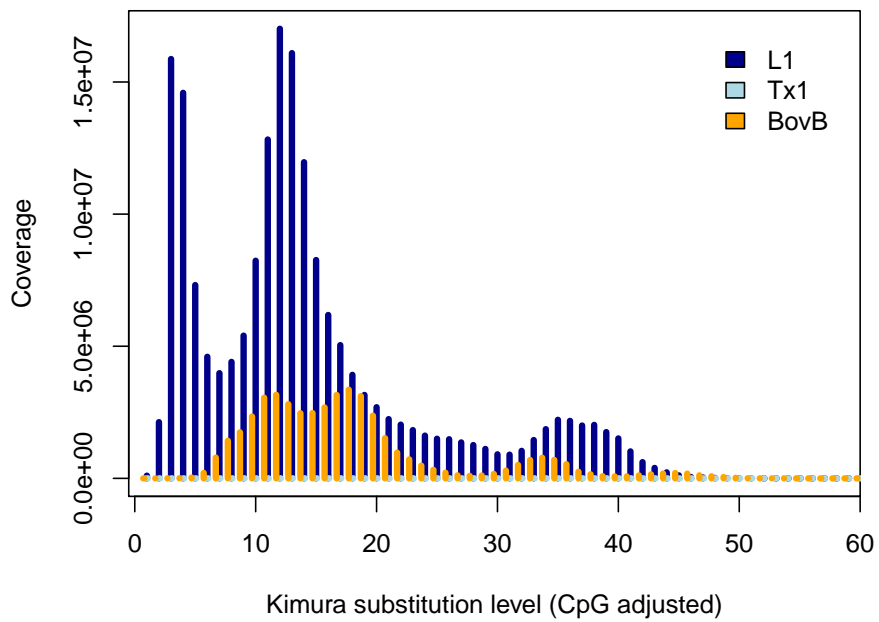


Figure S12

Loxodonta africana

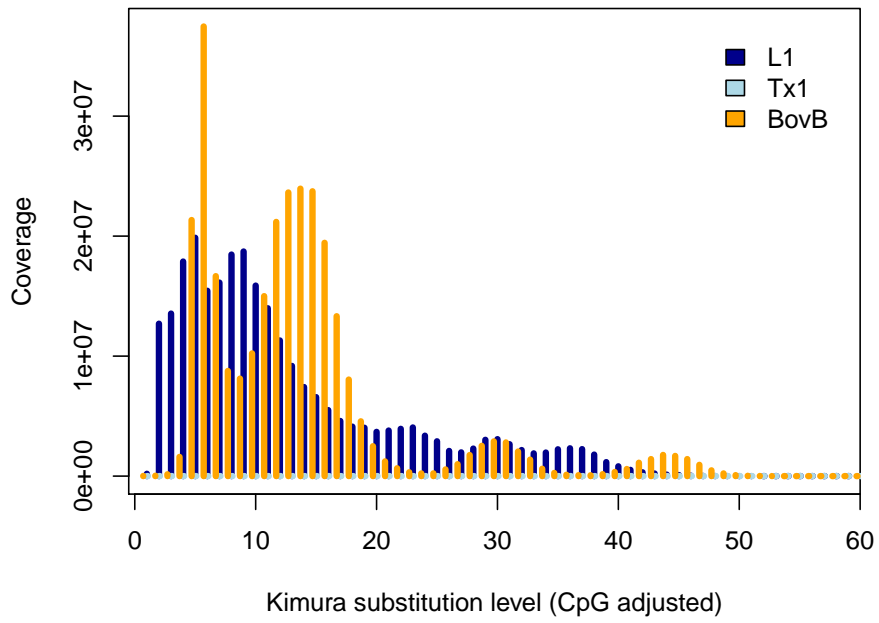


Figure S13

Chiroptera

Pteropus alecto

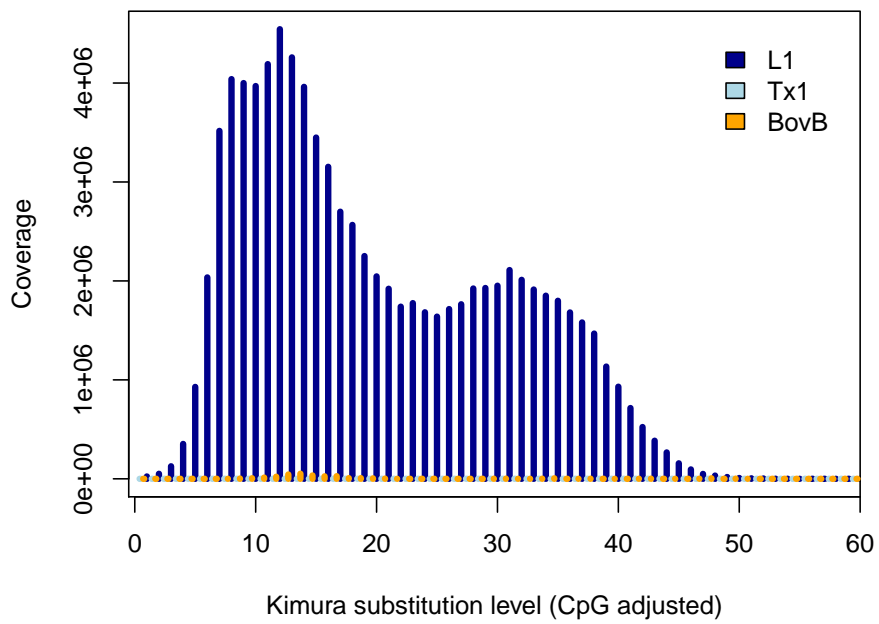


Figure S14

Pteropus vampyrus

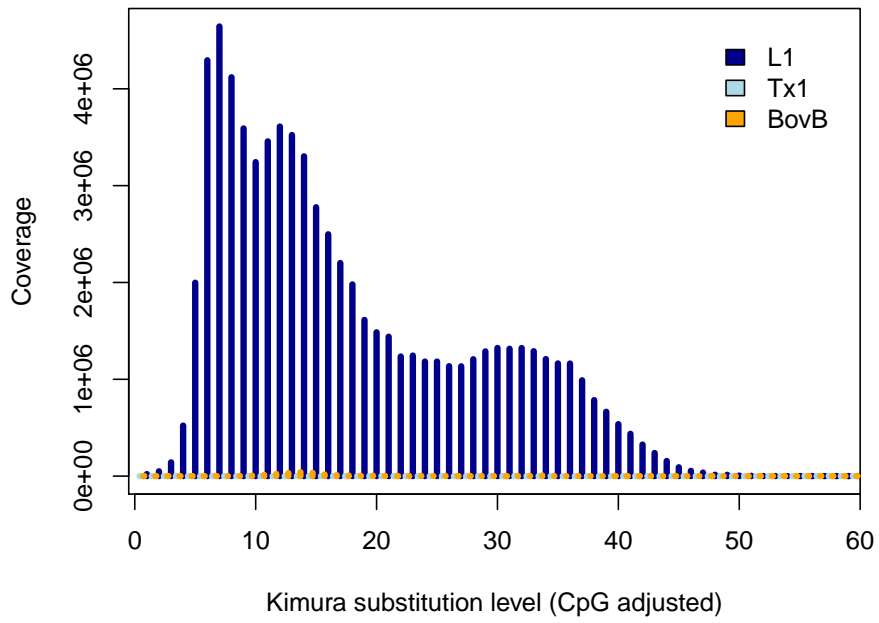


Figure S15

Eidolon.helvum

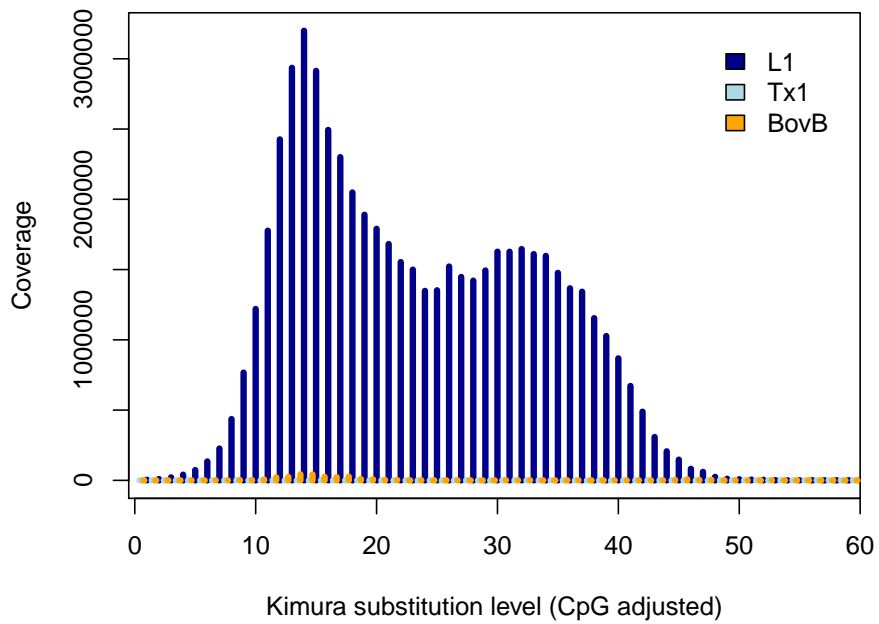


Figure S16

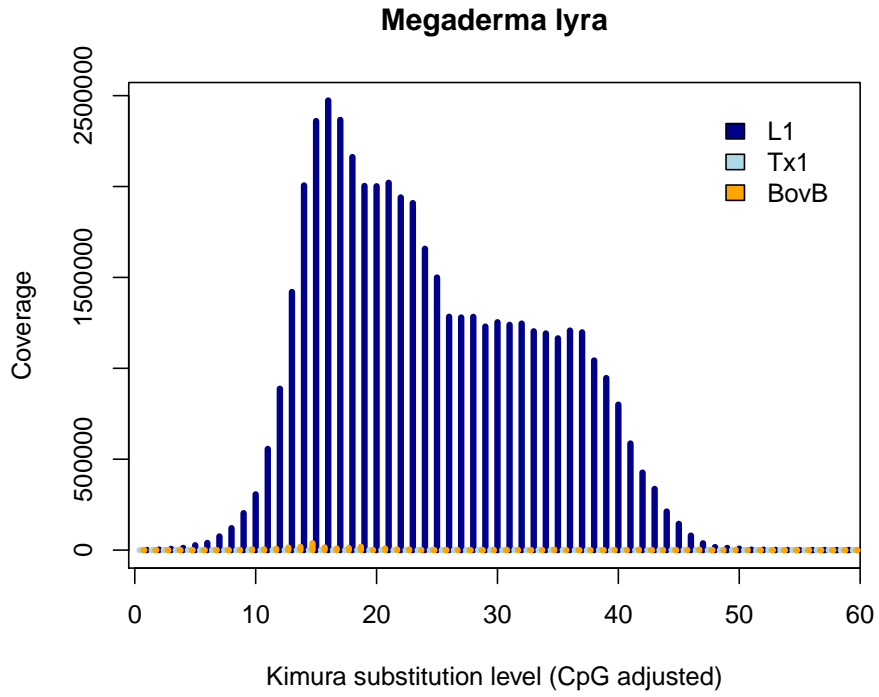


Figure S17

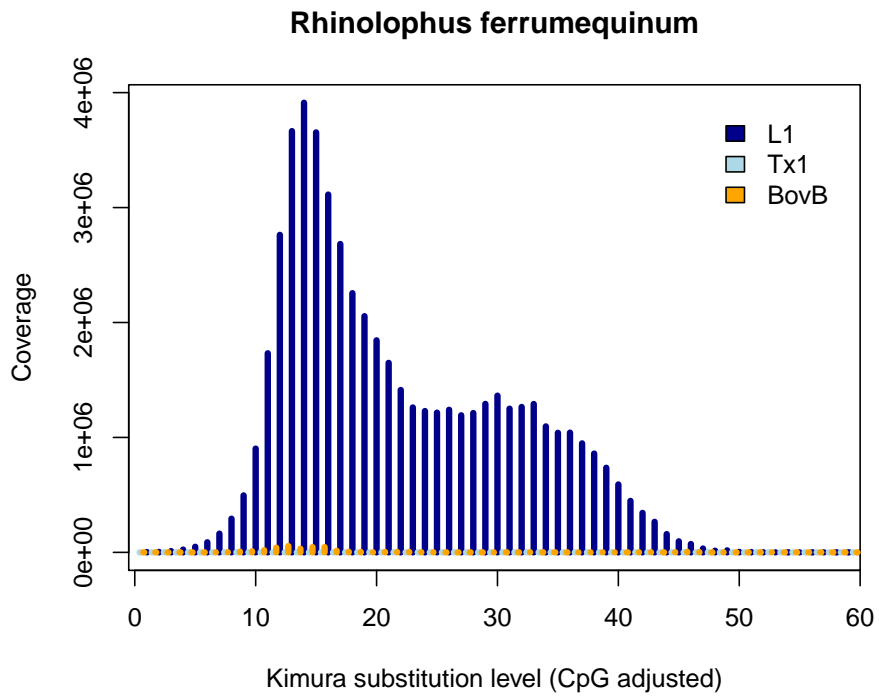


Figure S18

Pteronotus parnellii

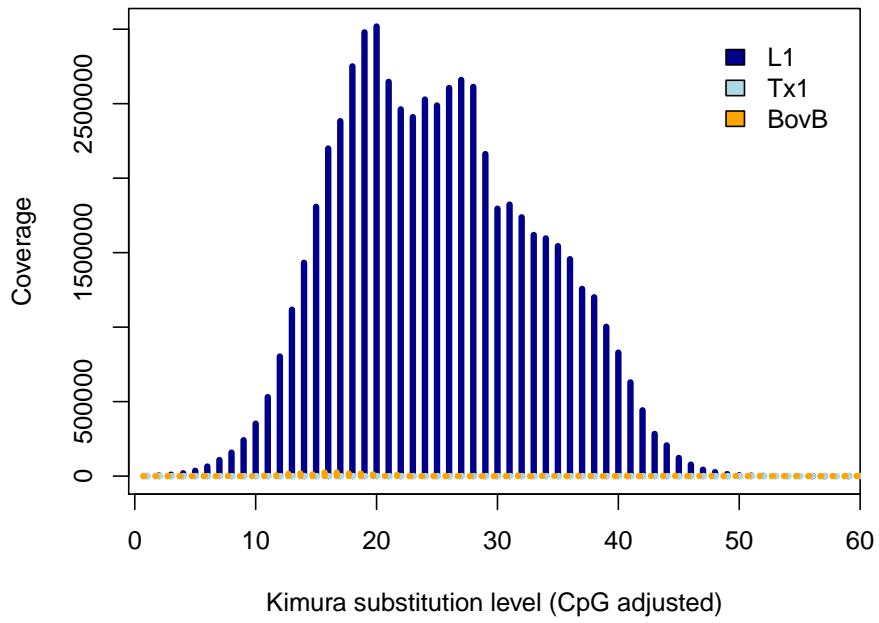


Figure S19

Eptesicus fuscus

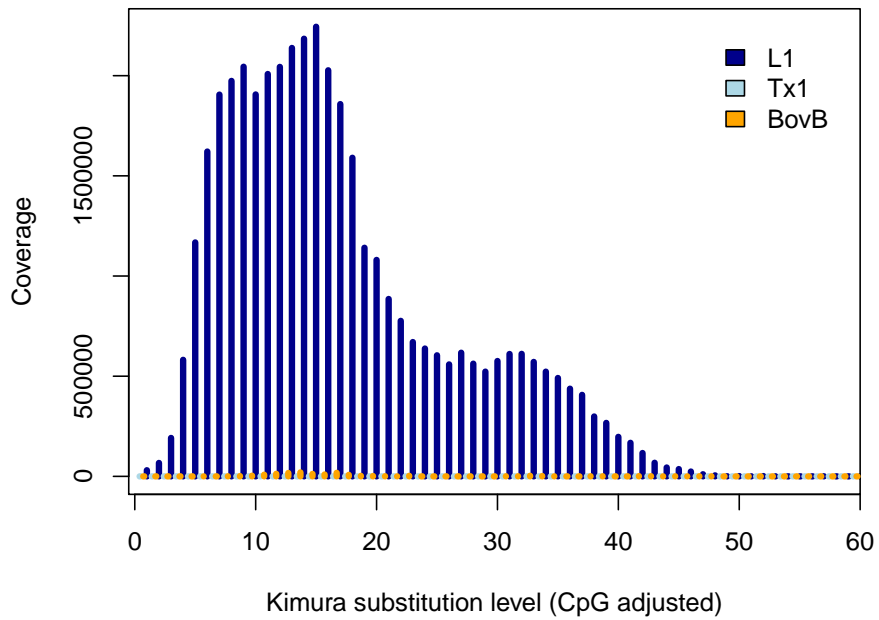


Figure S20

Myotis brandtii

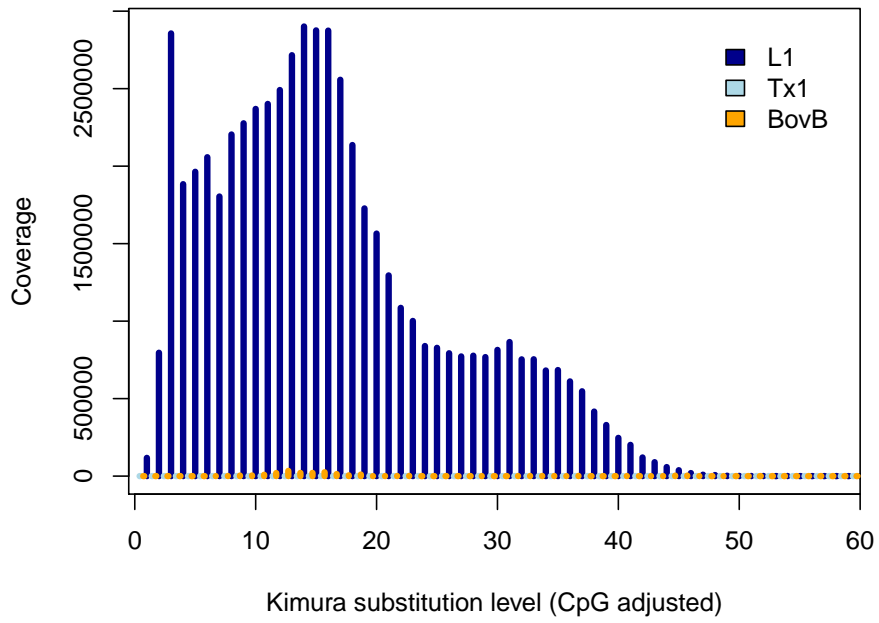


Figure S21

Myotis davidii

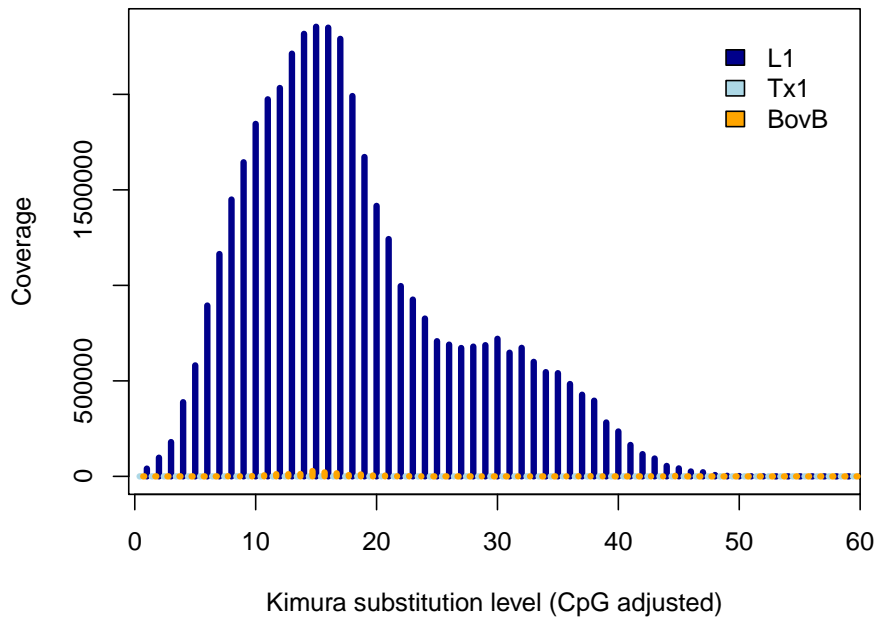


Figure S22

Myotis lucifugus

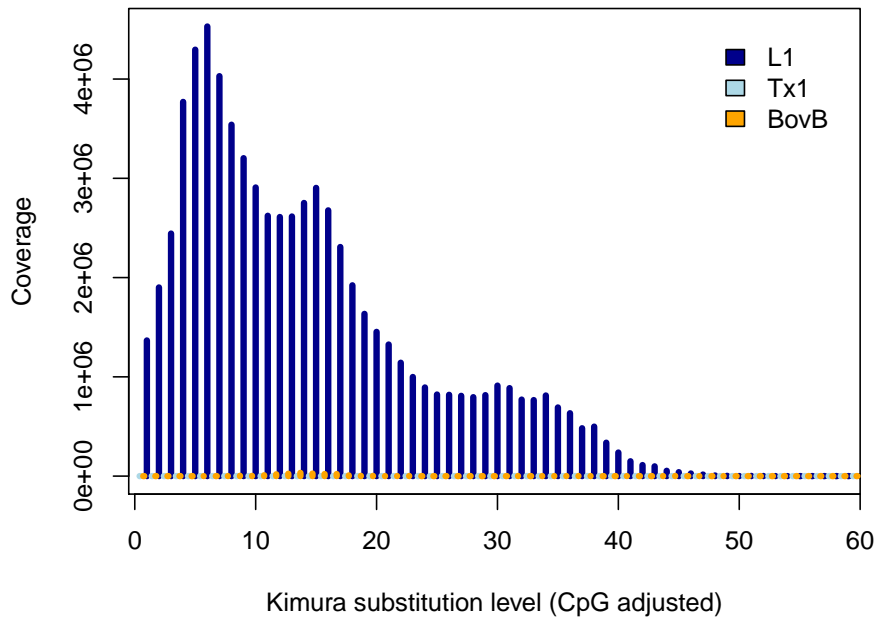


Figure S23

Myotis lucifugus (close-up)

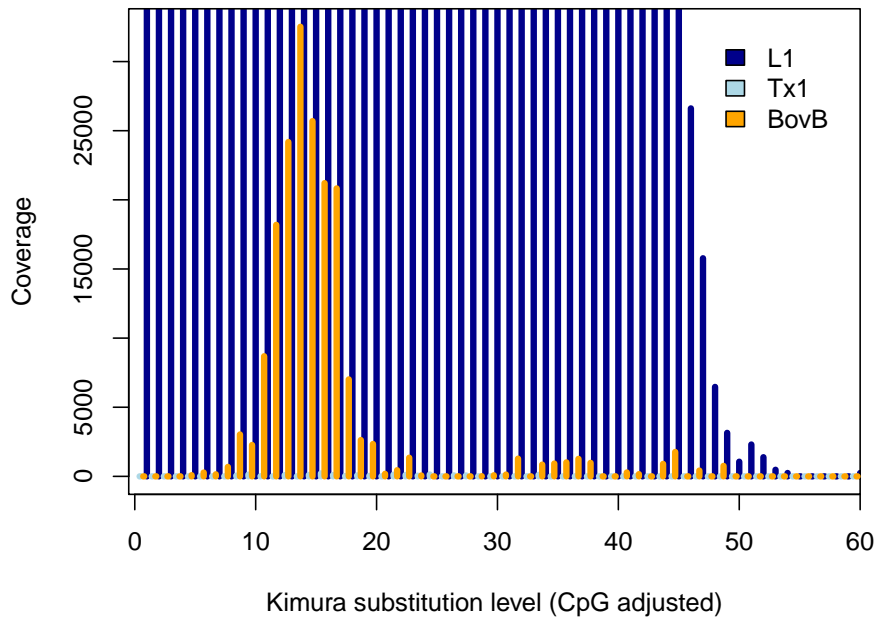


Figure S24

Perissodactyla

Ceratotherium simum

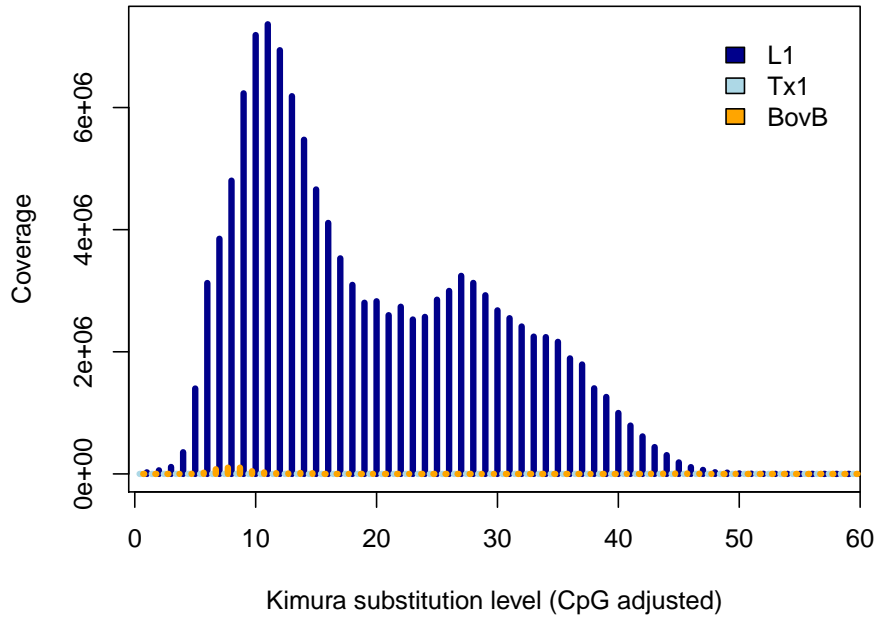


Figure S25

Equus przewalskii

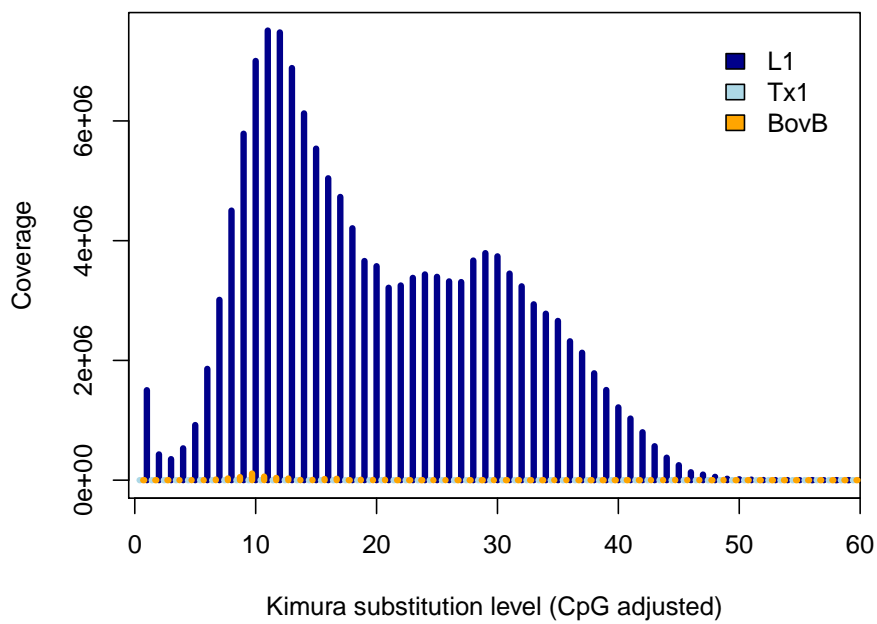


Figure S26

Equus caballus Mongolian

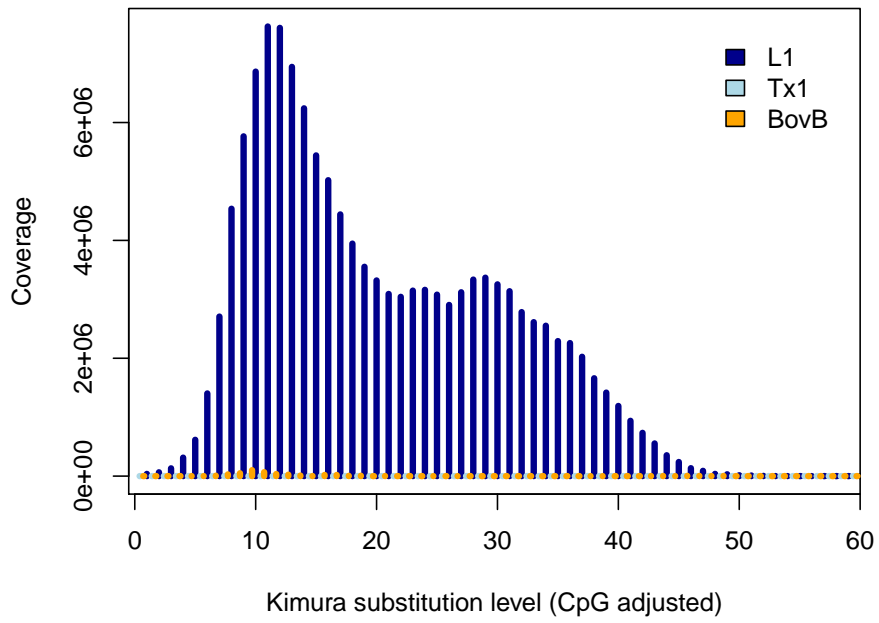


Figure S27

Equus caballus Thoroughbred

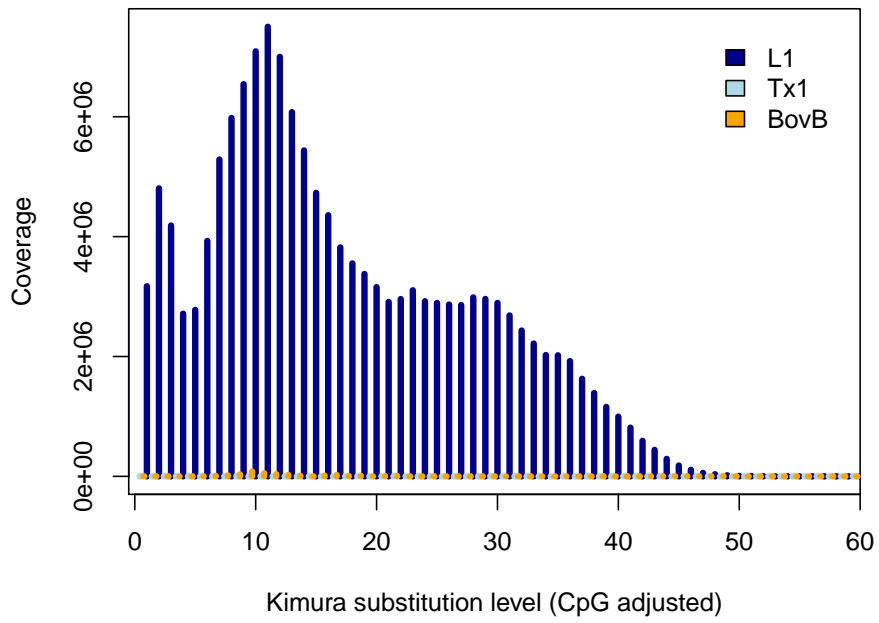


Figure S28

Equus caballus Thoroughbred (close-up)

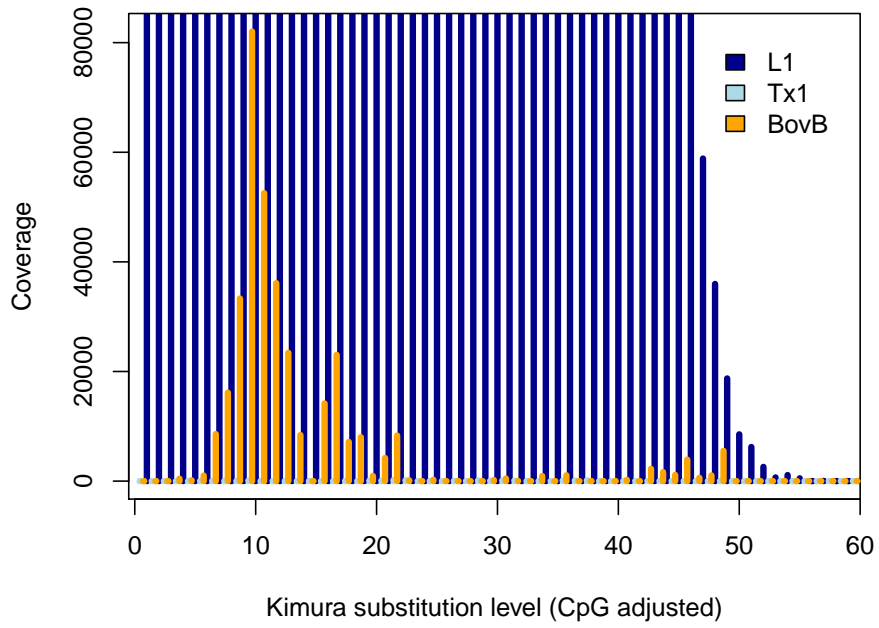


Figure S29

Bovidae

Pantholops hodgsonii

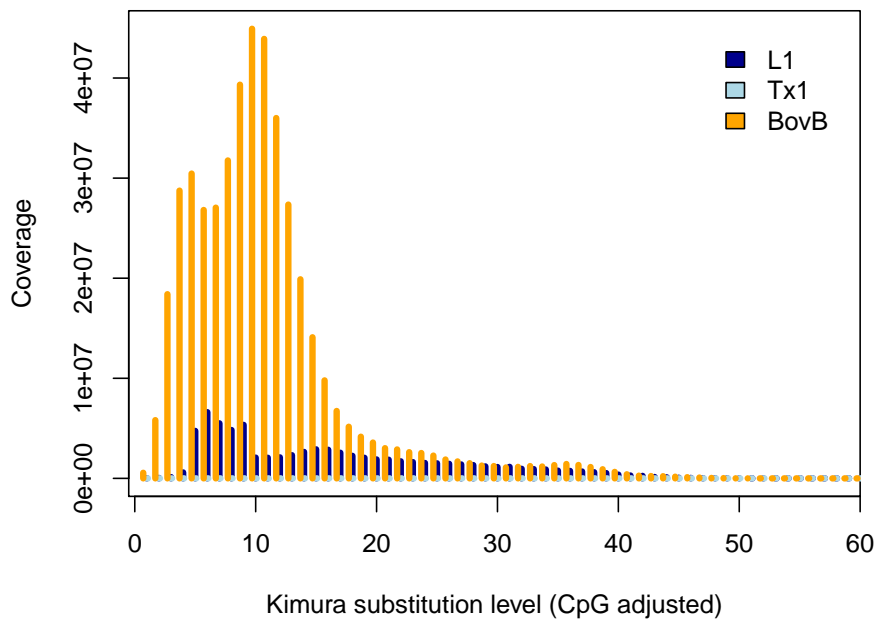


Figure S30

Capra hircus

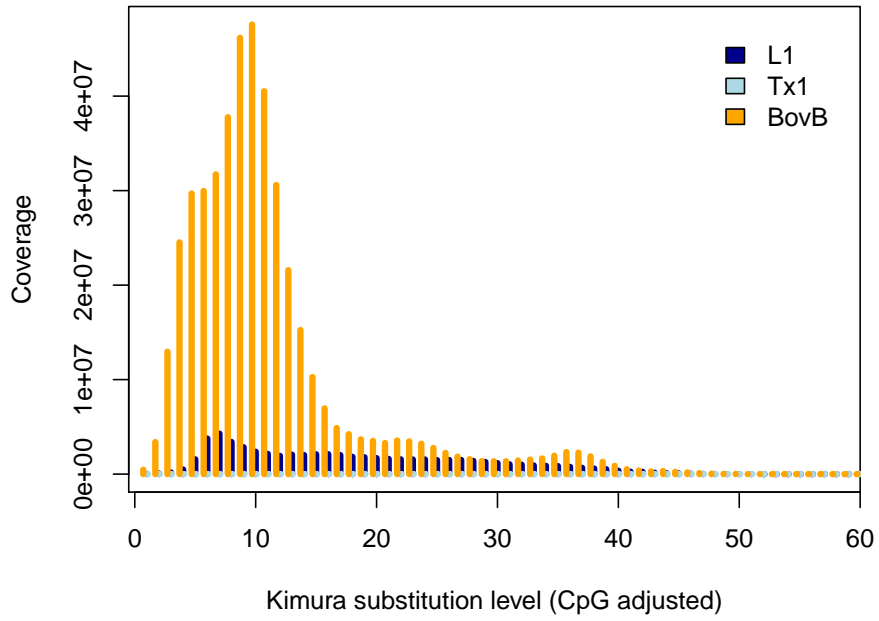


Figure S31

Ovis aries Texel

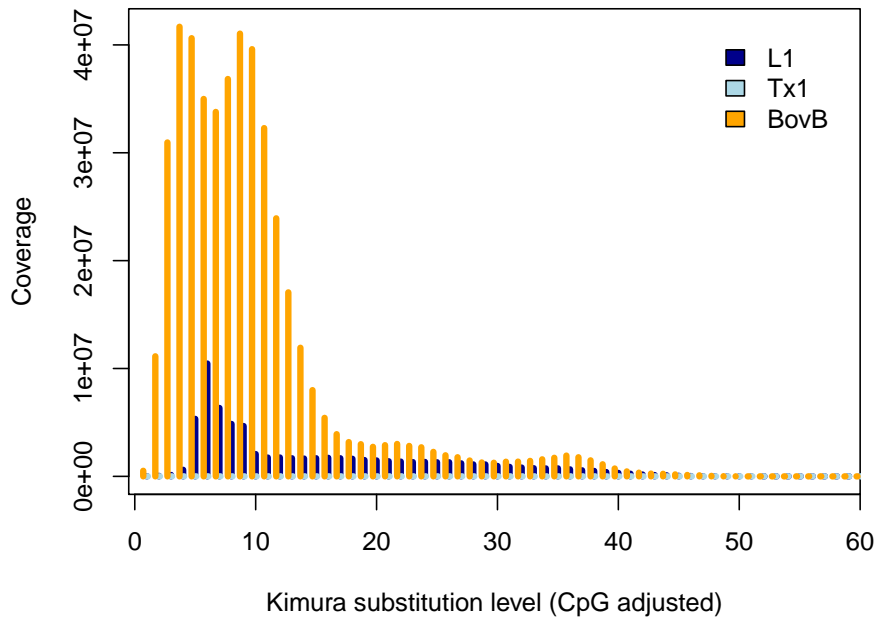


Figure S32

Ovis aries musimon

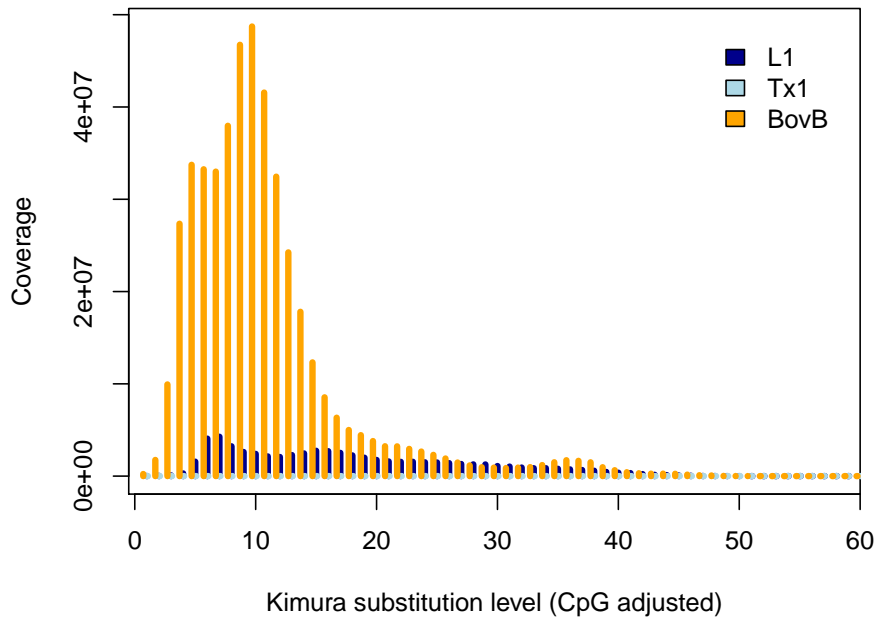


Figure S33

Bubalus bubalis

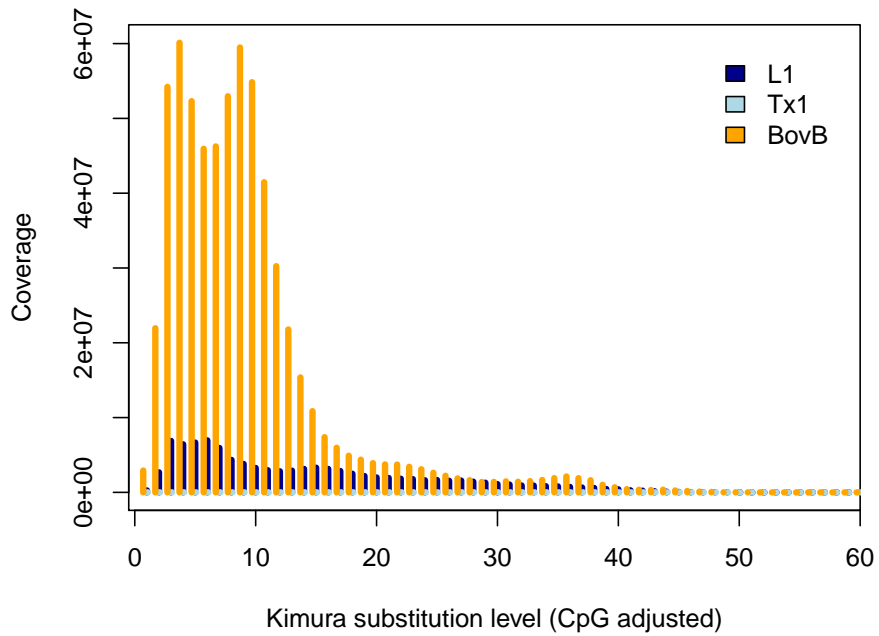


Figure S34

Bison bison

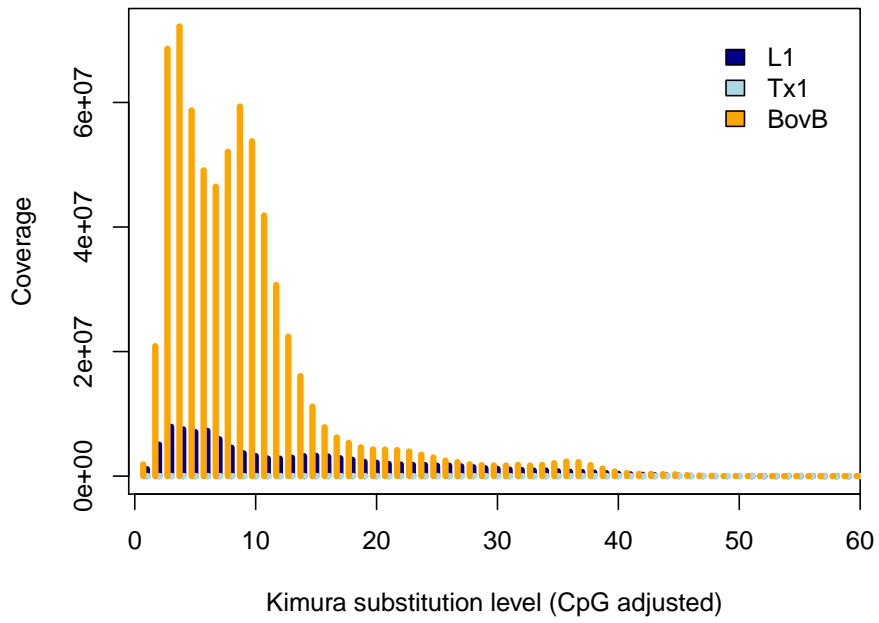


Figure S35

Bos indicus

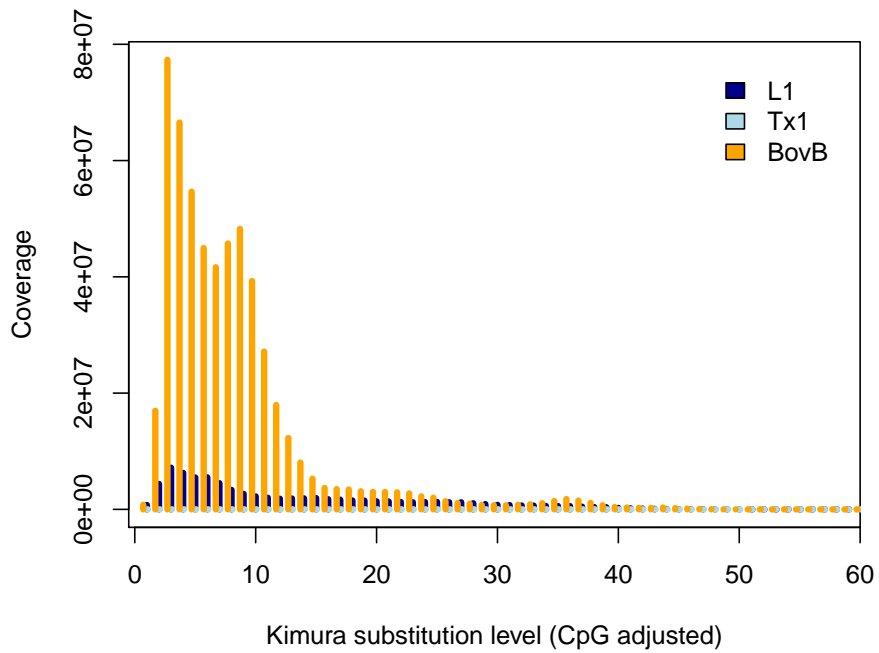


Figure S36

Bos mutus

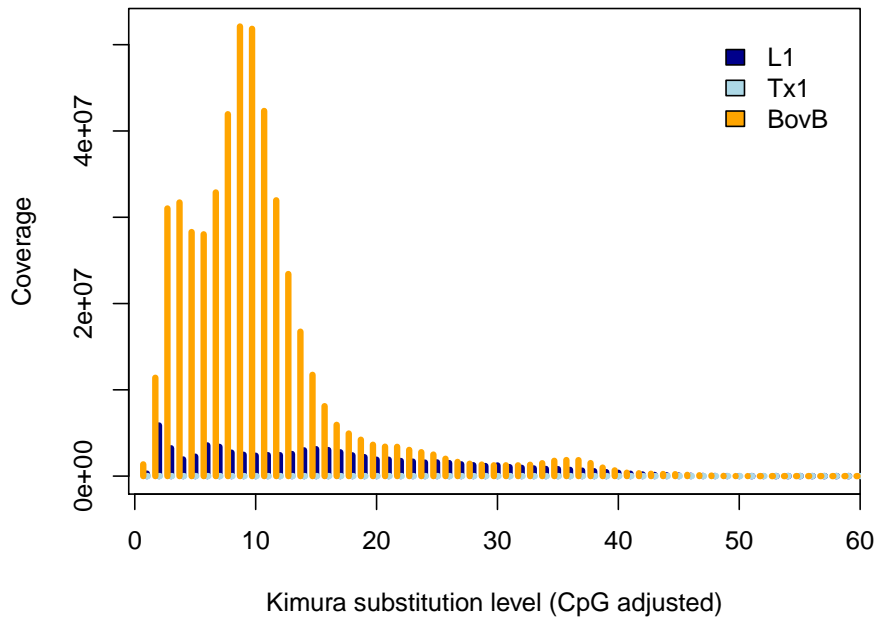


Figure S37

Squamata

Pogona vitticeps

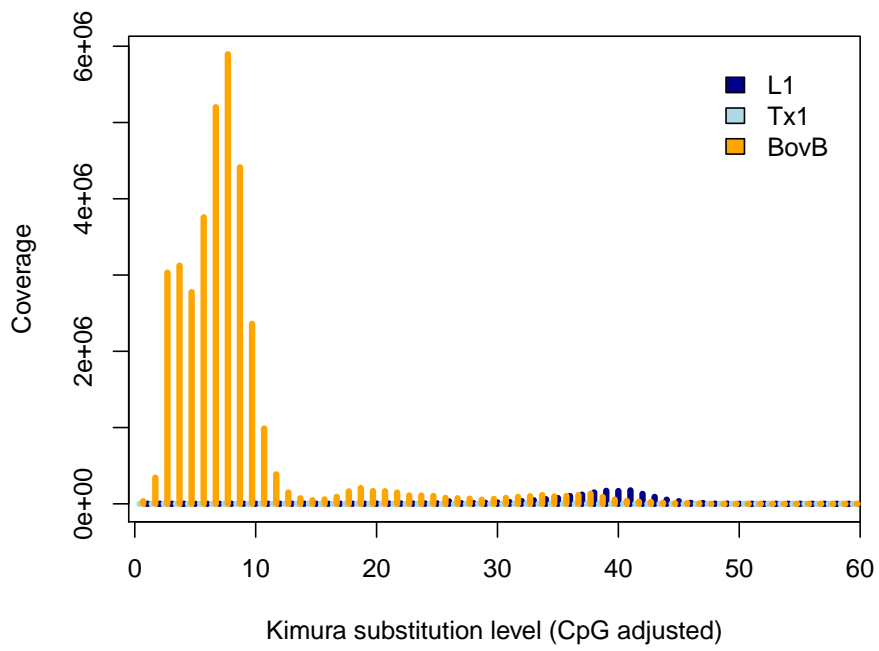


Figure S38

Anolis carolinensis

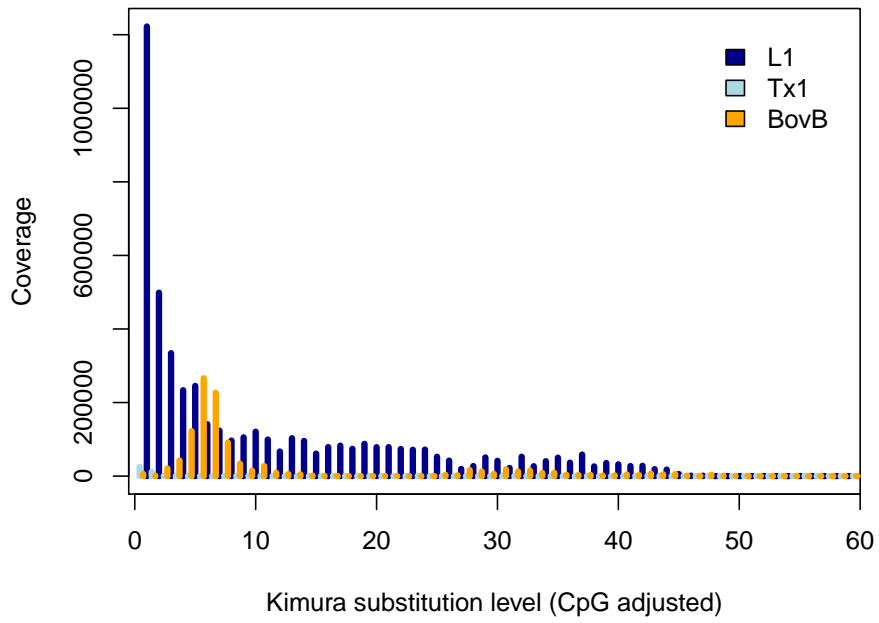


Figure S39

Vipera berus

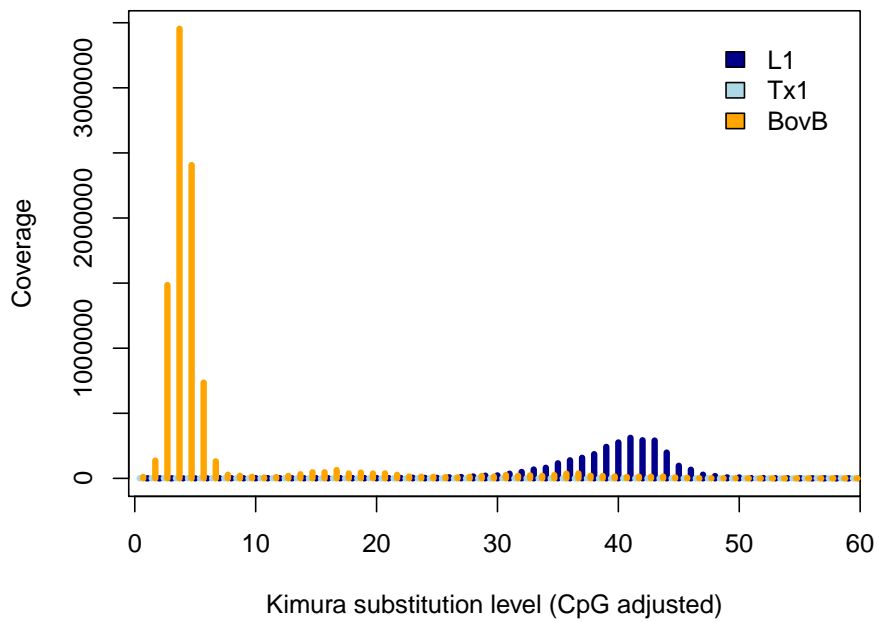


Figure S40

Vipera berus (close-up)

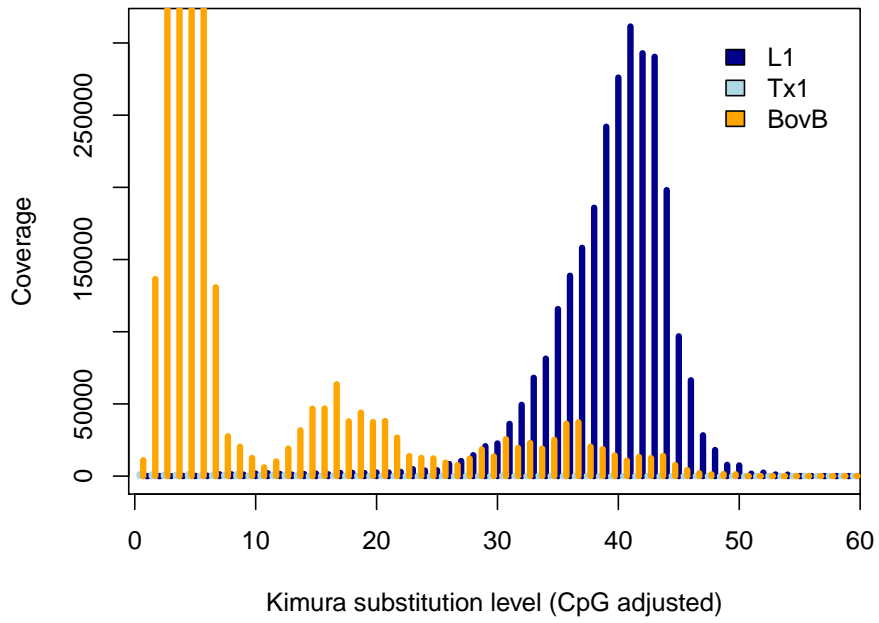


Figure S41

Crotalus mitchellii

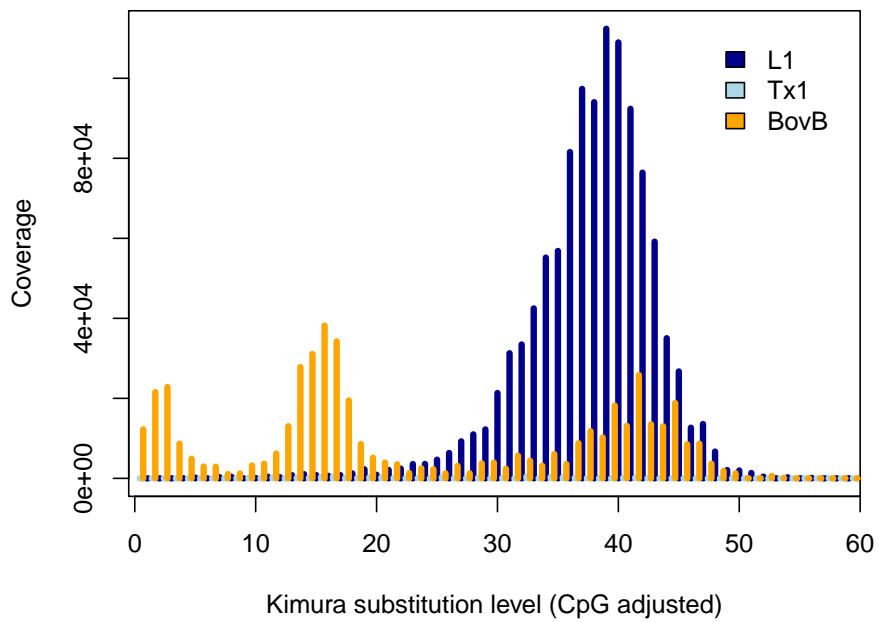


Figure S42

Ophiophagus hannah

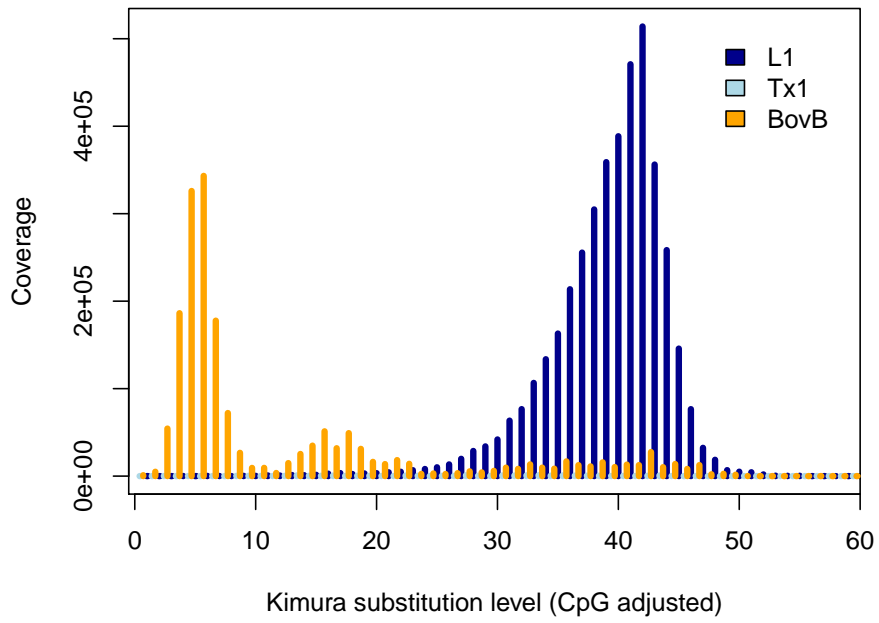


Figure S43

Python bivittatus

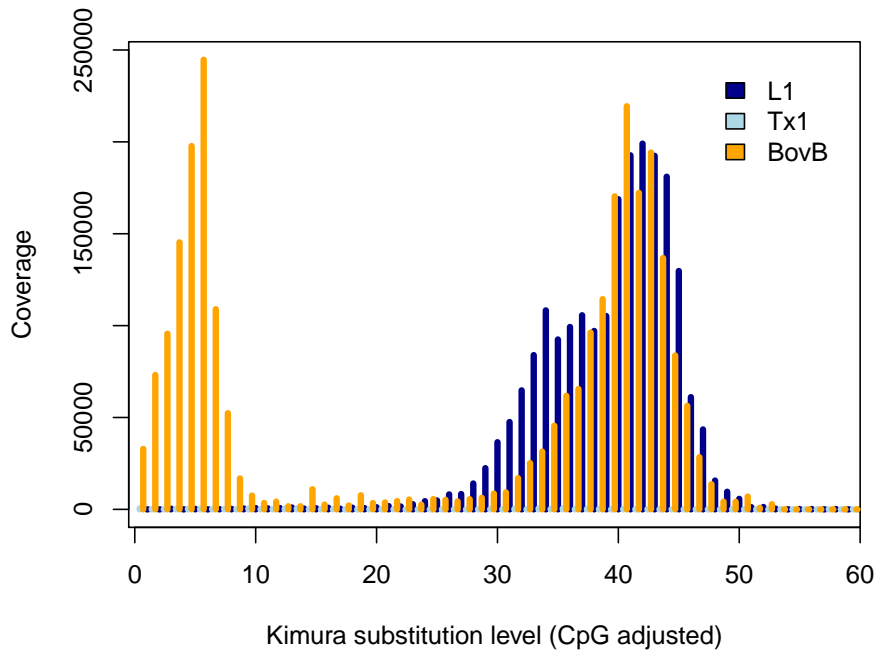


Figure S44

Amphibia

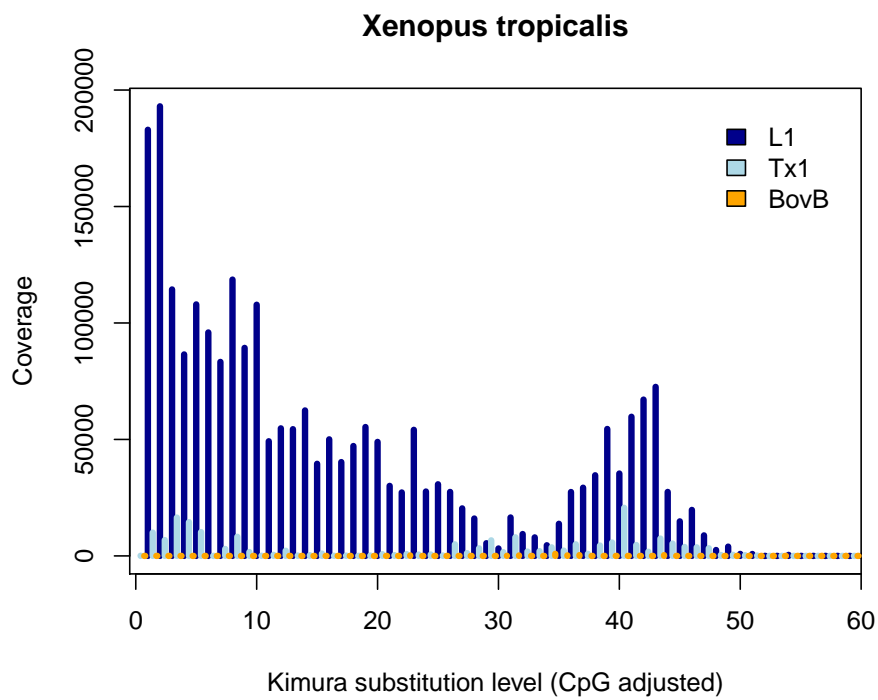


Figure S45

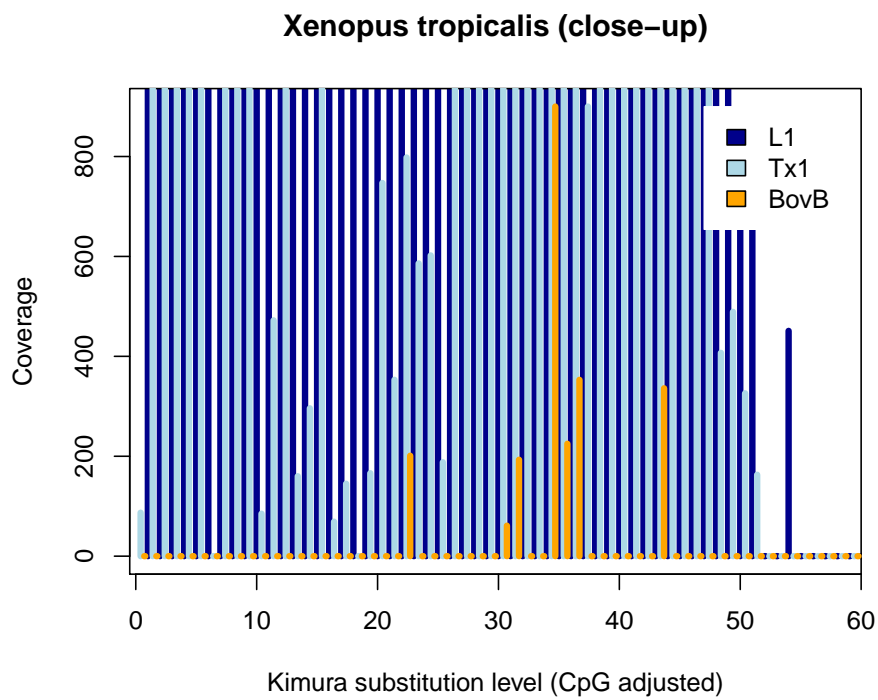


Figure S46

Neopterygii

Cynoglossus semilaevis

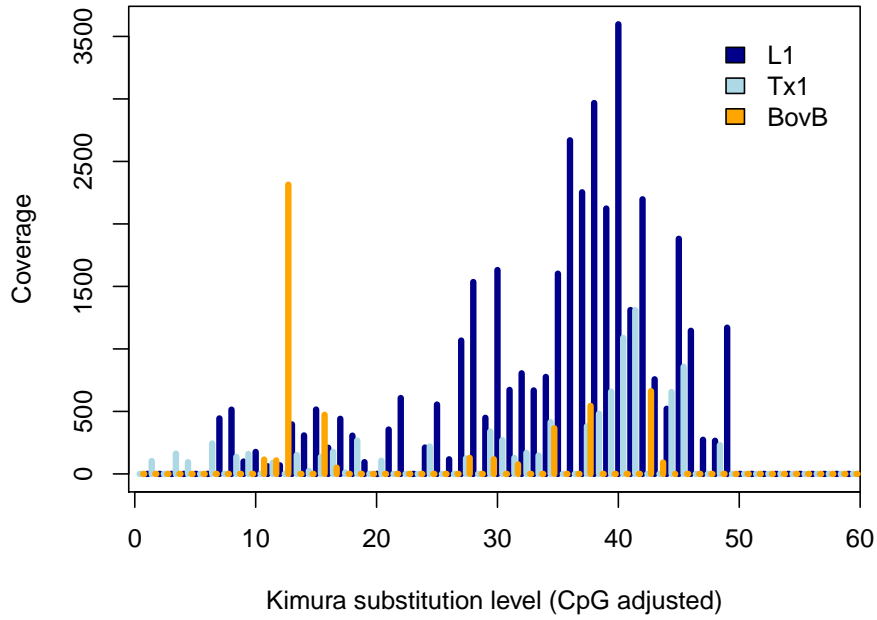


Figure S47

Lepisosteus oculatus

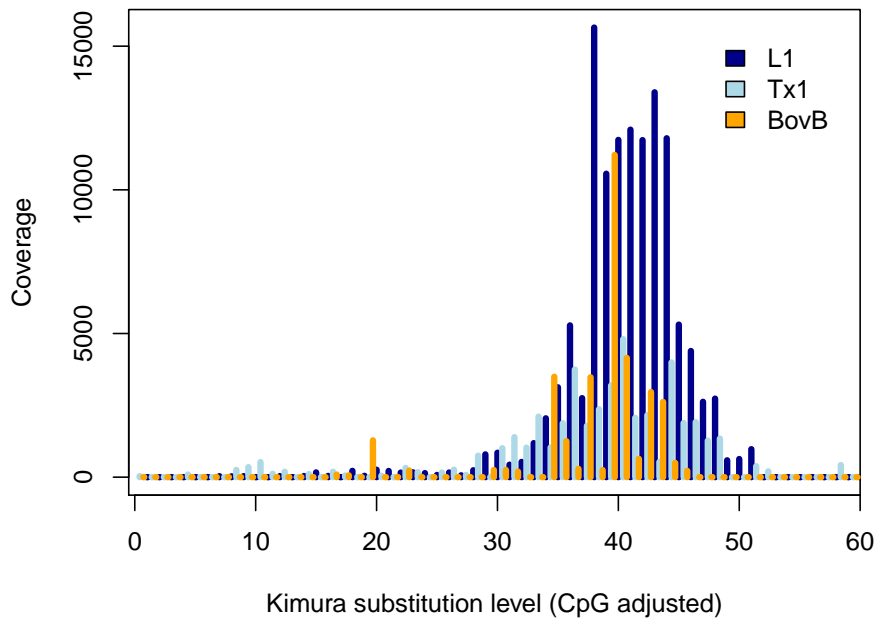


Figure S48

Danio rerio

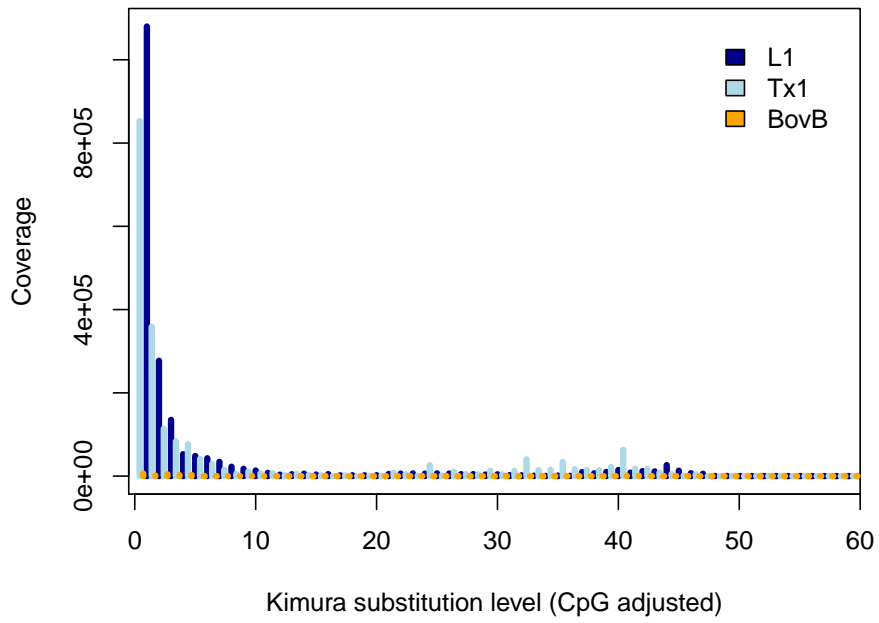


Figure S49

Danio rerio (close-up)

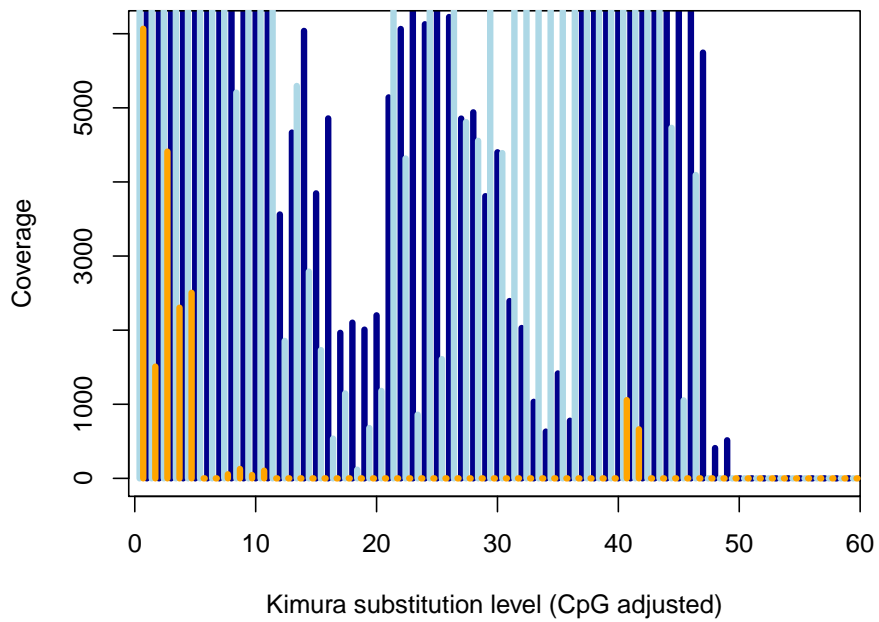


Figure S50

Other

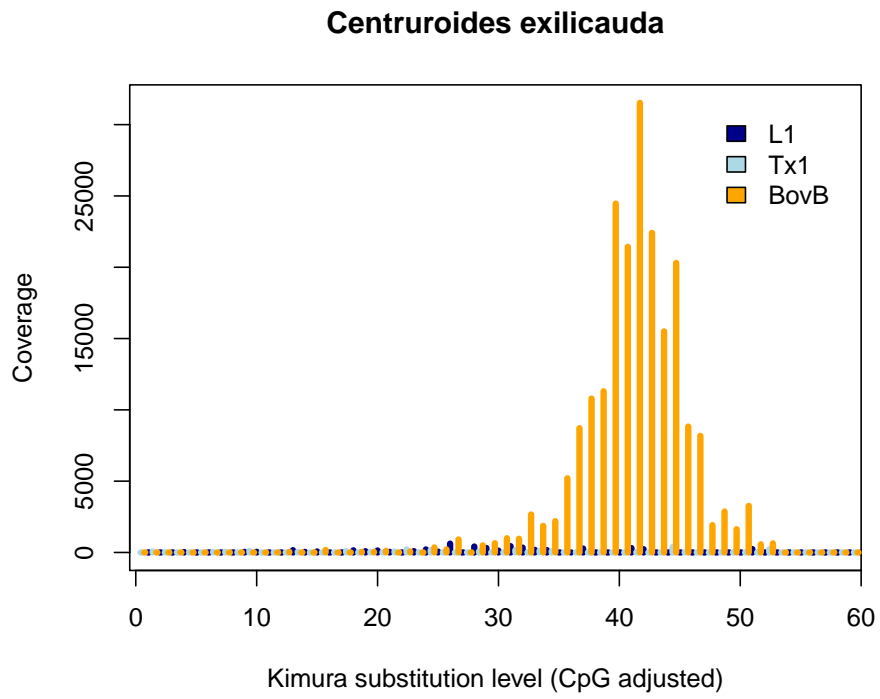


Figure S51

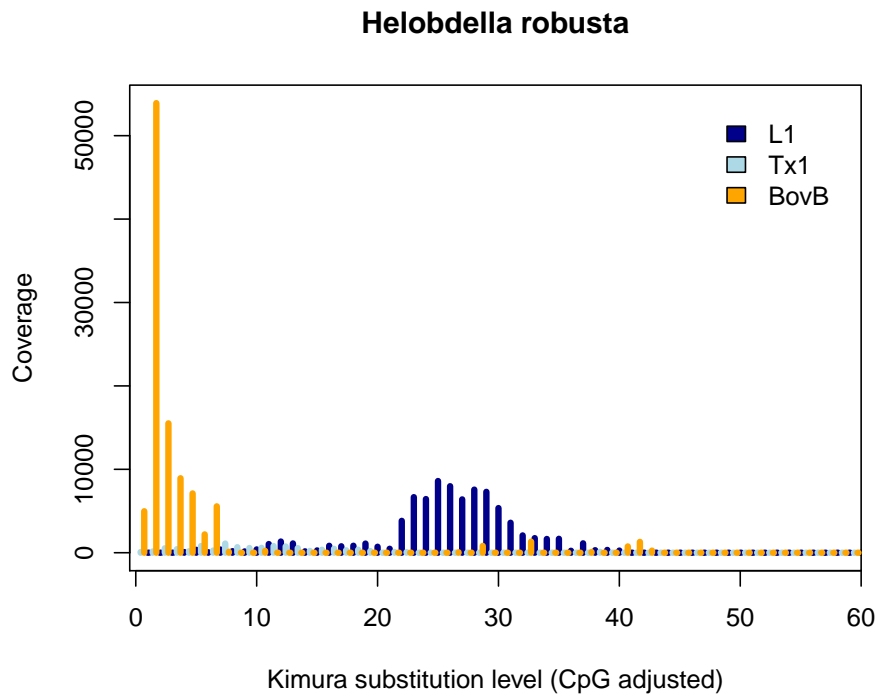


Figure S52

Strongylocentrotus purpuratus

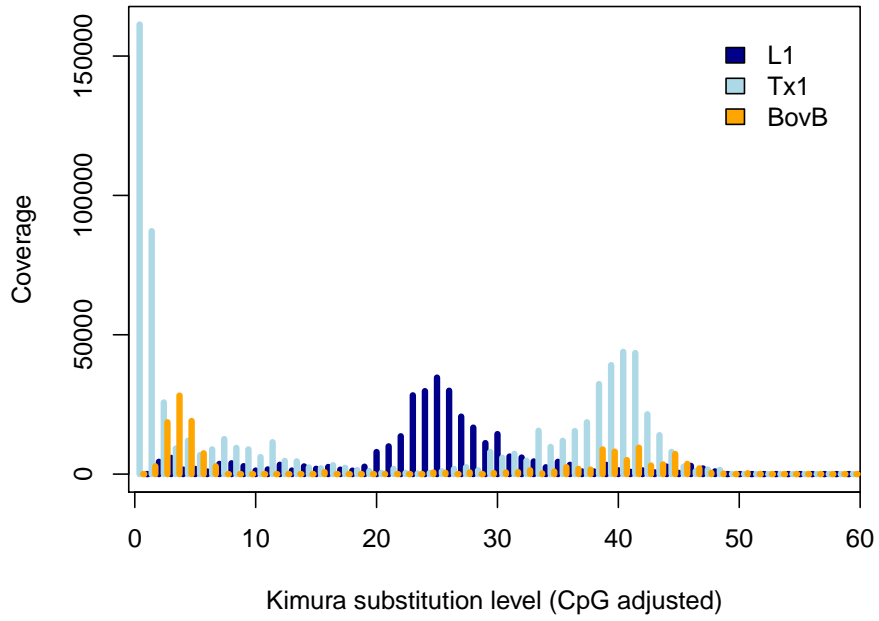


Figure S53

Ciona savignyi

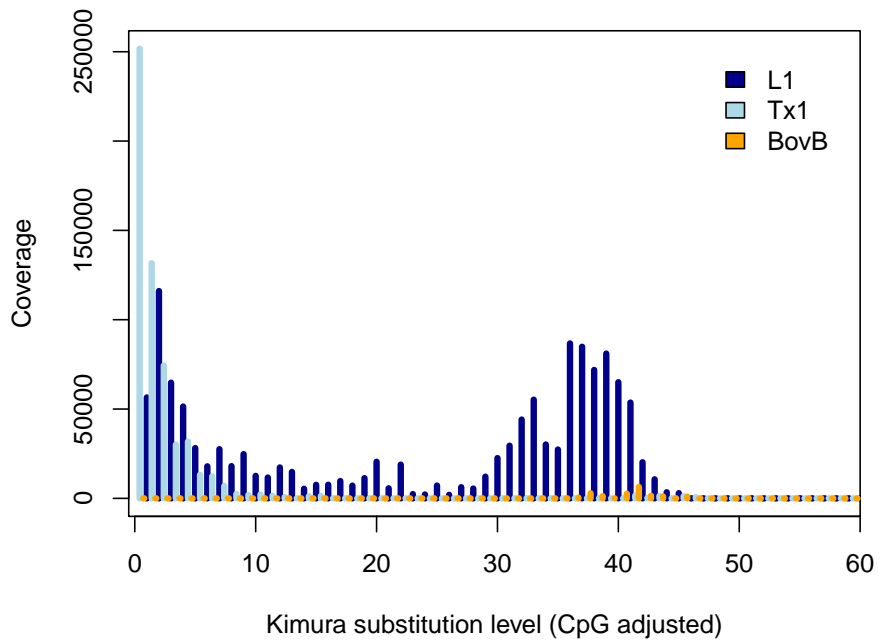


Figure S54

Figure S55: Chimeric L1-BovB

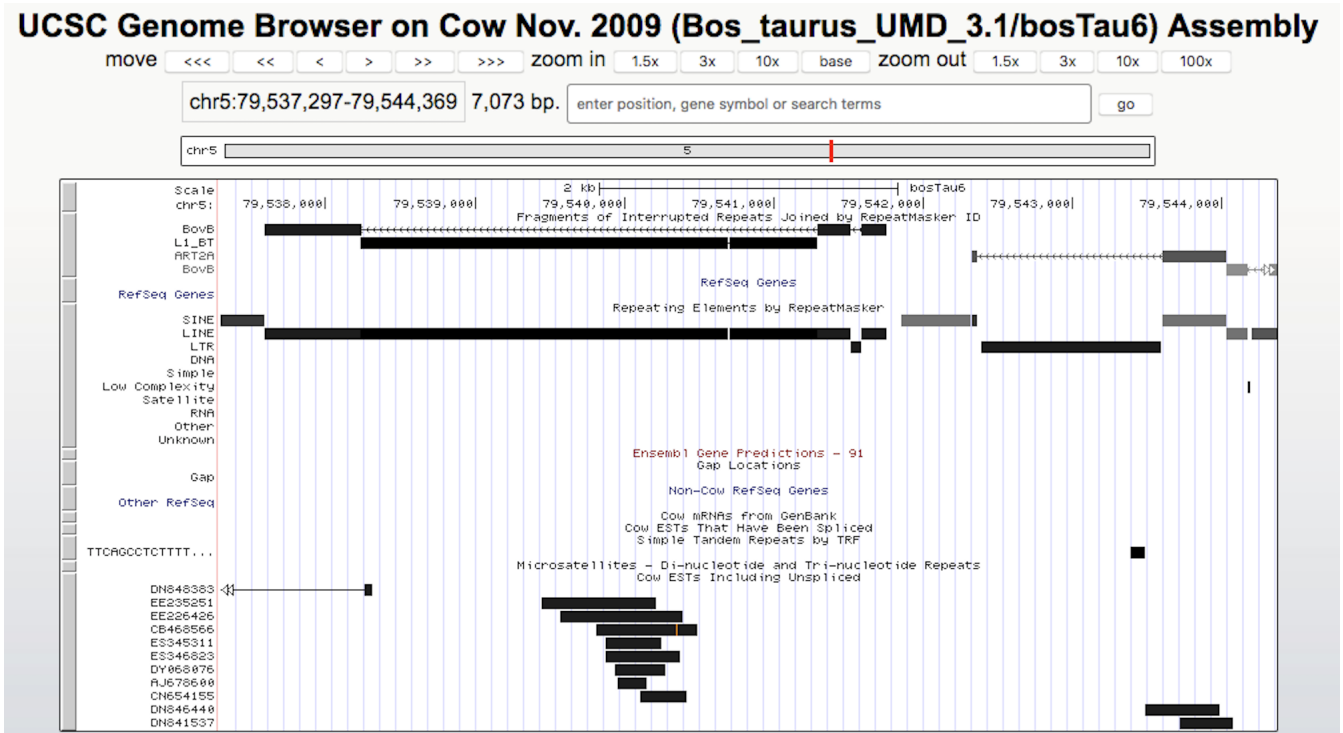


Figure S55: Chimeric L1-BovB in cattle genomes. Several cow ESTs overlap the L1 reverse transcriptase domain, but these may be artifacts/mismapped. No strong evidence to suggest transcription.