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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.
Figure S3

Monodelphis domestica

Figure S4

Monodelphis domestica (close-up)
Macropus eugenii

Figure S5

Sarcophilus harrisii

Figure S6
Afrotheria

**Figure S7**

**Elephantulus edwardii**

![Graph showing coverage of Kimura substitution level (CpG adjusted) for Elephantulus edwardii. The graph plots coverage against Kimura substitution level, with different colors representing different categories (L1, Tx1, BovB).

**Figure S8**

**Echinops telfairi**

![Graph showing coverage of Kimura substitution level (CpG adjusted) for Echinops telfairi. The graph plots coverage against Kimura substitution level, with different colors representing different categories (L1, Tx1, BovB).
**Chrysochloris asiatica**

![Graph showing coverage of Kimura substitution level (CpG adjusted) for Chrysochloris asiatica](image1)

**Figure S9**

**Orycteropus afer**

![Graph showing coverage of Kimura substitution level (CpG adjusted) for Orycteropus afer](image2)

**Figure S10**
Trichechus manatus

![Graph showing coverage for Trichechus manatus with Kimura substitution level (CpG adjusted).](image)

Figure S11

Procavia capensis

![Graph showing coverage for Procavia capensis with Kimura substitution level (CpG adjusted).](image)

Figure S12
Chiroptera
Figure S15

Figure S16
**Figure S17**

Megaderma lyra

**Figure S18**

Rhinolophus ferrumequinum
Myotis brandtii

Figure S21

Myotis davidii

Figure S22
Myotis lucifugus

Figure S23

Myotis lucifugus (close-up)

Figure S24
Figure S25

Figure S26
**Equus caballus Mongolian**

![Graph of Equus caballus Mongolian](image)

Figure S27

**Equus caballus Thoroughbred**

![Graph of Equus caballus Thoroughbred](image)

Figure S28
Bovidae

Figure S29

Figure S30
Figure S31

Figure S32
Figure S33

Figure S34
Figure S35

Figure S36
Squamata

Figure S37

Bos mutus

Figure S38

Pogona vitticeps
**Figure S39**

Anolis carolinensis

**Figure S40**

Vipera berus
Figure S41

Vipera berus (close-up)

Figure S42

Crotalus mitchellii
Ophiophagus hannah

Figure S43

Python bivittatus

Figure S44
Amphibia

Xenopus tropicalis

Figure S45

Xenopus tropicalis (close-up)

Figure S46
Neopterygii

Figure S47

Figure S48
Figure S49

Figure S50
Centruroides exilicauda

![Graph showing coverage vs. Kimura substitution level for Centruroides exilicauda](image)

Figure S51

Helobdella robusta

![Graph showing coverage vs. Kimura substitution level for Helobdella robusta](image)

Figure S52
Figure S53

Strongylocentrotus purpuratus

Figure S54

Ciona savignyi
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.