





Additional data file 2: Analysis of percent sequence comprised by each class of repeat element separated by each region (In alphabetical order, and as shown in yellow highlight, Additional Data file 4). The black lines indicate the percent sequence for each repeat class, within each cluster. A) When all regions were combined for analysis (Figure 3) only LTRs and DNA elements showed a significant change in percent sequence coverage between platypus and therian mammals. However, when each region was examined individually for repeats, there were clear differences between the non-significant repeat classes within specific regions. Simple repeats were noticeably lower in the GNAS and IGF2R regions of the platypus when compared with all therians. Similarly, low complexity repeats were noticeably lower in the GRB10 and DLK1 regions of the platypus compared to therians. B) Other repeat classes did not show any noticeable trends. This analysis also showed an unexpected increase in small RNAs that is unique to the platypus GNAS locus, suggesting this region may be predisposed to the accumulation of repeat elements.