



Additional data file 12. Saturation analyses in the concatenated datasets of total, intron, exon, and third codon positions, respectively. The x-axis represents corrected pairwise divergence estimated by maximum likelihood and the y-axis is the observed divergence (uncorrected *P*-distance). Transitions are shown as the blue diamonds and transversions are the red squares. A best-fit second degree polynomial is applied to describe the trend.