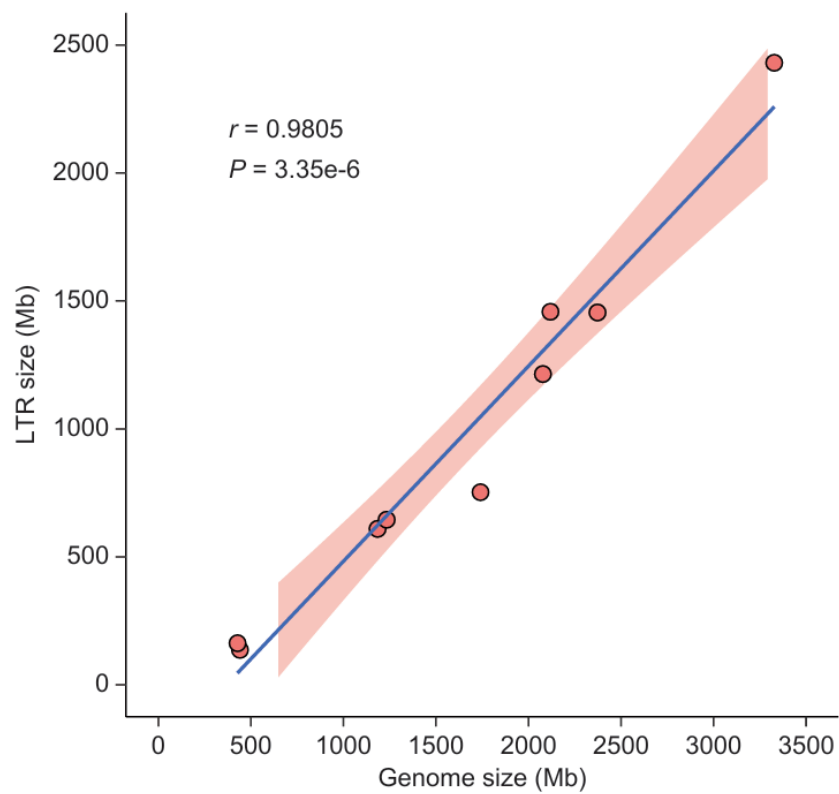




Supplementary Fig. 8 Correlation analysis of genome size with LTR retrotransposon content.

Pearson's correlation coefficient (r) and P value was calculated with R function `cor.test`. The points represent independent genomes. Blue lines indicate fitted curves for linear regression. The pink shaded areas represent 95% confidence interval.