

Additional file 12

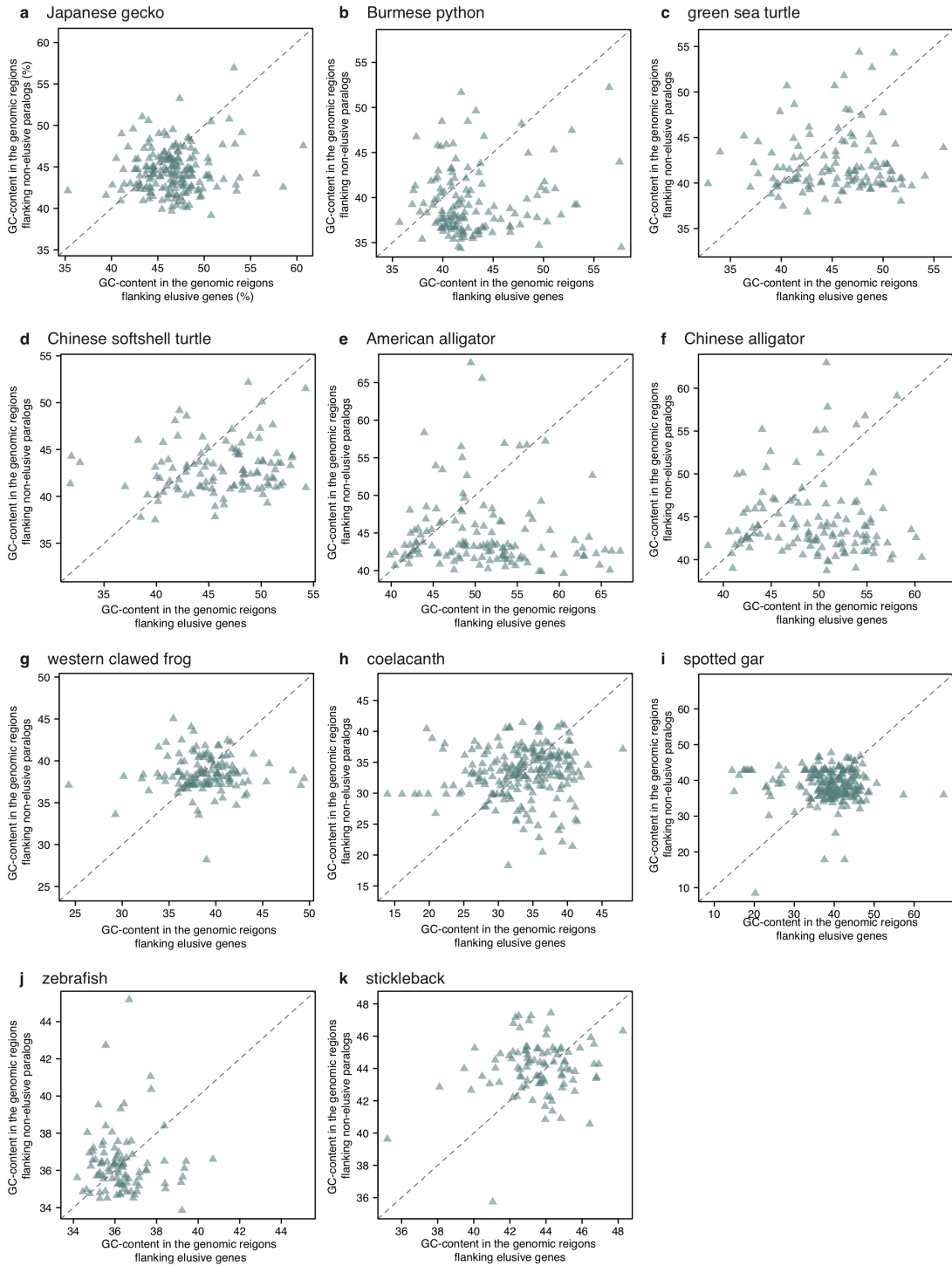


Figure S9. GC-content in the genomic regions including the orthologs of the elusive reptile genes and their non-elusive genes

GC-content of the genomic regions consisting of the elusive genes and their non-elusive paralogs with their flanking regions are shown for reptiles and outgroups. *P*-values and effect size below were computed based on the Wilcoxon signed-rank test and signed Pearson *r* between the two classes for each species, respectively: **(a)** $p = 4.85 \times 10^{-11}$, $r = 0.475$; **(b)** $p = 1.80 \times 10^{-13}$, $r = 0.591$; **(c)** $p = 2.51 \times 10^{-9}$, $r = 0.515$; **(d)** $p = 1.02 \times 10^{-10}$, $r = 0.552$; **(e)** $p = 1.65 \times 10^{-11}$, $r = 0.551$; **(f)** $p = 8.64 \times 10^{-13}$, $r = 0.509$; **(g)** $p = 0.776$, $r = -0.0250$; **(h)** $p = 0.188$, $r = 0.0922$; **(i)** $p = 0.0118$, $r = 0.170$; **(j)** $p = 0.0163$, $r = -0.143$; **(k)** $p = 0.0680$, $r = 0.159$.