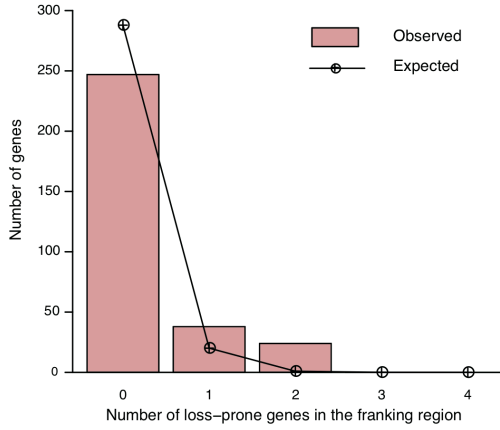
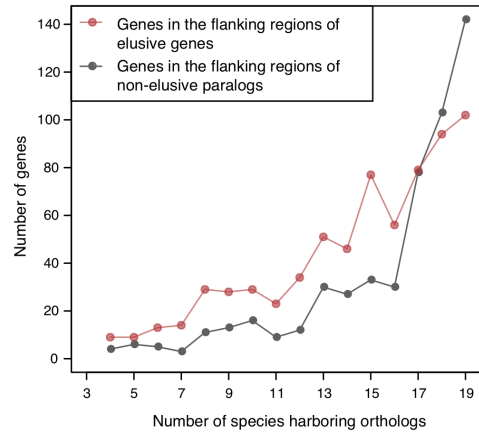


Additional file 10

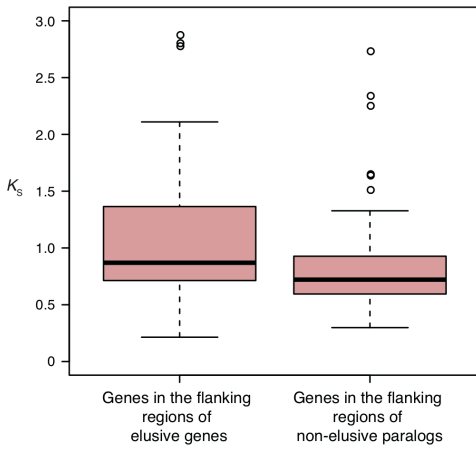
a Positional proximity between elusive genes



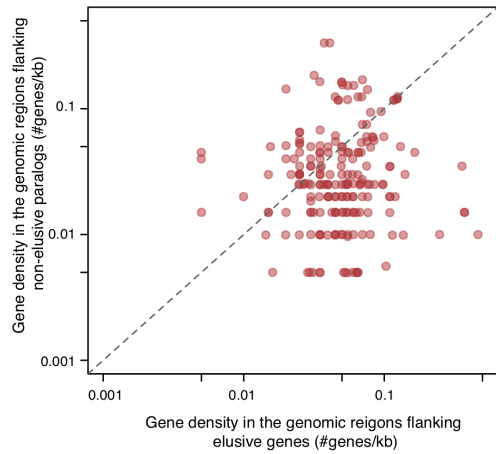
b Gene retention frequency among species



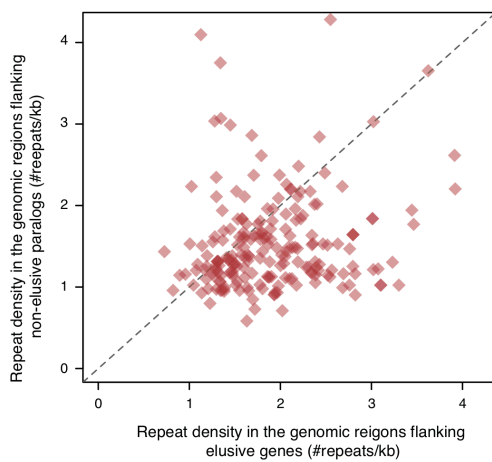
c Synonymous substitution rates (K_s) between *P. picta* and *G. japonicus* orthologs



d Gene density



e Repeat density



f GC-content

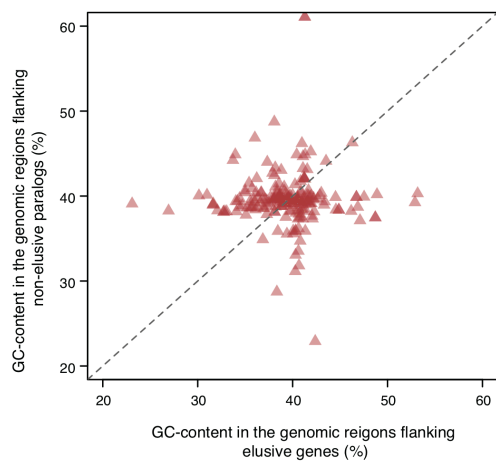


Figure S7. Genomic characters of the elusive and their non-elusive paralogs in the anole genome

(a) Fractions of the 298 elusive genes in the anole genome flanking other elusive genes. The observed and expected values are significantly different ($p = 1.53 \times 10^{-27}$, the exact test of goodness of fit). (b) Frequency distributions of the genes flanked by the 176 elusive genes and their non-elusive paralogs in accordance with the numbers of species retaining their orthologs. The two distributions exhibit a significant difference ($p = 3.37 \times 10^{-16}$, Mann–Whitney U test). (c) Comparison of synonymous substitution rates (K_s) comparison between the genes flanking the elusive and non-elusive genes. These K_s were significantly different ($p = 1.55 \times 10^{-5}$, Mann–Whitney U test). Each K_s was computed with an ortholog pair of Madagascar ground gecko and green anole. (d) Gene densities in the flanking regions of the elusive genes and their non-elusive paralogs, which are significantly different between these two regions ($p = 1.37 \times 10^{-8}$, Wilcoxon signed-rank test). (e) Repeat densities of the genomic regions containing the elusive genes or their non-elusive paralogs with their flanking regions, which are significantly different between the two regions ($p = 7.94 \times 10^{-15}$, Wilcoxon signed-rank test). (f) GC-contents consisting of the elusive genes or their non-elusive paralogs and their flanking regions, which are significantly different between the two regions ($p = 0.539$, Wilcoxon signed-rank test). See methodological details in Fig. 5.