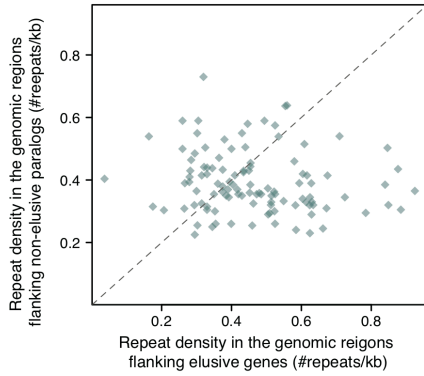
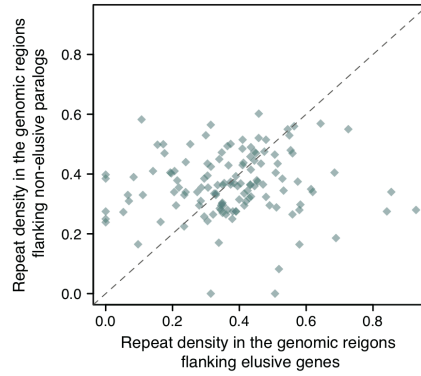


## Additional file 13

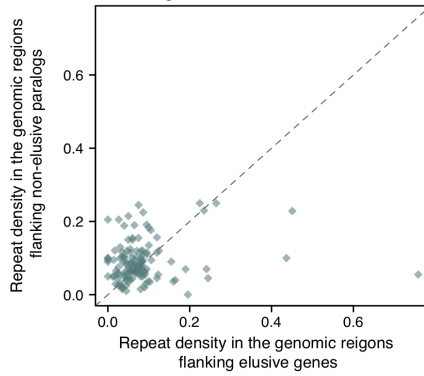
**a** Chinese softshell turtle



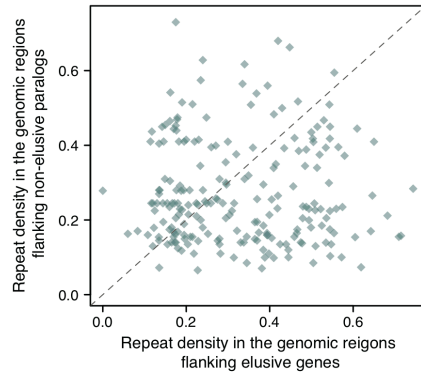
**b** American alligator



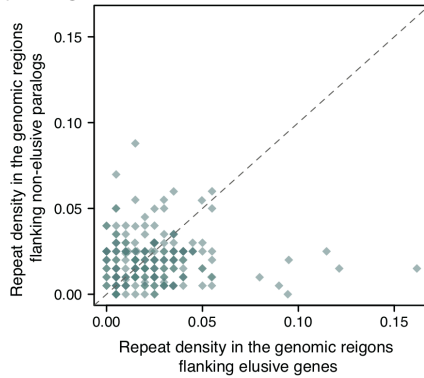
**c** western clawed frog



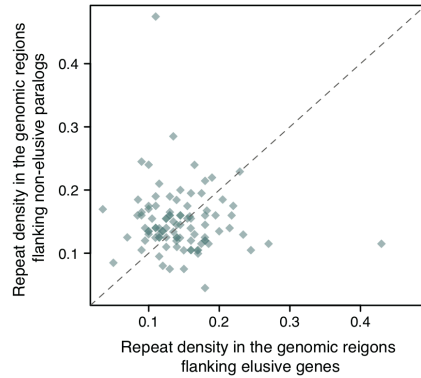
**d** coelacanth



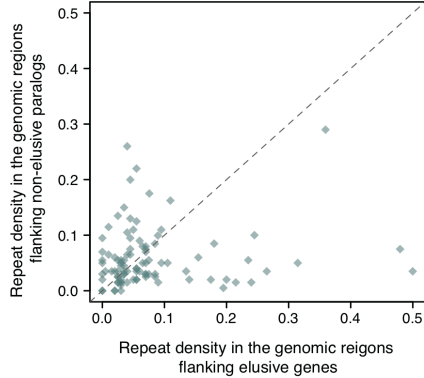
**e** spotted gar



**f** zebrafish



**g** stickleback



**Figure S10. Repeat densities in the genomic regions including the orthologs of the elusive reptile genes and their non-elusive gene**

Repeat densities of the genomic regions consisting of the elusive genes and their non-elusive paralogs with their flanking regions are shown for reptiles and outgroups. We selected the species that repeat elements were already annotated and released as RepeatMasker Genomic Datasets

(<http://www.repeatmasker.org/genomicDatasets/RMGenomicDatasets.html>).

Additionally, repeat elements of the Chinese softshell turtle were annotated with RepeatMasker. *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)**  $p = 9.94 \times 10^{-5}$ ,  $r = 0.332$ ; **(b)**  $p = 0.757$ ,  $r = 0.00106$ ; **(c)**  $p = 0.101$ ,  $r = -0.167$ ; **(d)**  $p = 2.25 \times 10^{-7}$ ,  $r = 0.351$ ; **(e)**  $p = 0.00571$ ,  $r = 0.0198$ ; **(f)**  $p = 0.0413$ ,  $r = -0.164$ ; **(g)**  $p = 0.215$ ,  $r = -0.155$ .