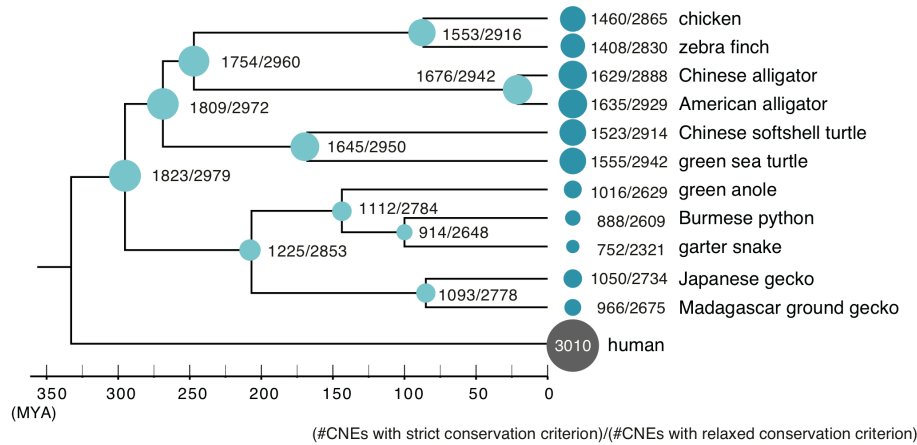


Additional file 18

a



b

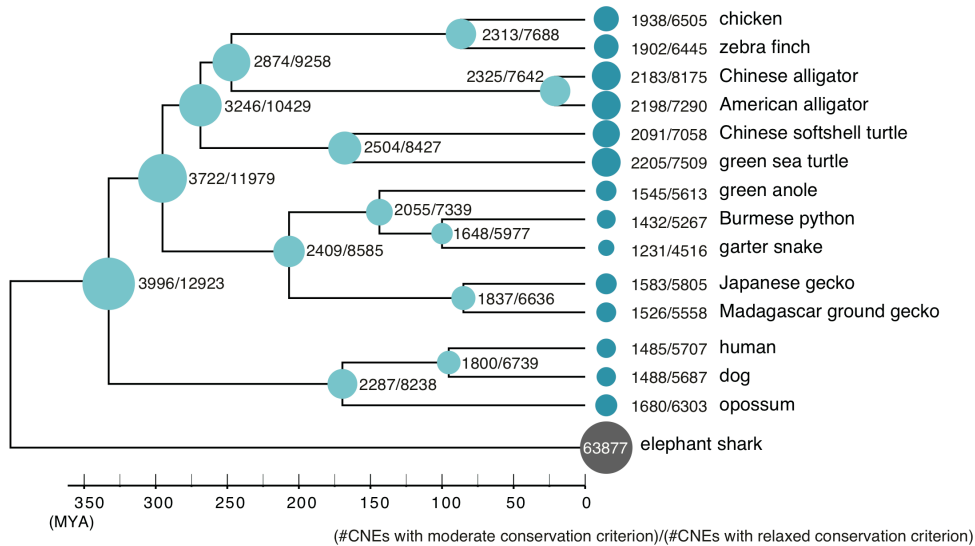


Figure S15. Conserved noncoding elements among amniotes

(a) Variation of retention of the human CNEs among sauropsid genomes. The human CNEs were obtained from the CONDOR database [93], in which conserved elements were identified based on the genome comparisons between the fugu and mammalian genomes. Values at the leaves of the species tree represent numbers of CNEs identified in the genome sequences based on the strict criterion (left, ≥ 100 bp match with $>95\%$ similarity) and the relaxed criterion (right, ≥ 60 bp match with $>80\%$ similarity). Values within light blue denote numbers of CNEs inferred in the ancestral genomes. The total number of the human CNEs is shown in a gray circle. (b) Variation of retention of the elephant shark CNEs among amniotes. The elephant shark CNEs were obtained from Venkatesh et al. (2014) [94]. Values at the leaves of the tree represent numbers of CNEs

identified in the genomes based on the moderate criterion (left, ≥ 80 bp match with $>85\%$ similarity) and the relaxed criterion (right). Values within light blue circles denote numbers of CNEs inferred in the ancestral genome genomes. The total number of the elephant shark CNEs is shown in a gray circle.