

Legend to Supplemental Figures

Supplemental Figure 1. Alignments of newly characterized DeuSINE families and subfamilies. (A) AmnSINE1 from human, (B) AmnSINE1 from chicken, (C) LmeSINE1a from coelacanth, (D) LmeSINE1b from coelacanth, (E) SINE3_IP from catfish, (F) OS-SINE1 from rainbow trout, (G) SacSINE1 from dogfish shark, (H) EbuSINE1 from hagfish, (I) EbuSINE2 from hagfish, and (J) BflSINE1 from amphioxus. The top sequence in each panel corresponds to the respective consensus sequence shown in Figures 1–4. Dots indicate nucleotides identical to those in the consensus sequence, and dashes indicate gaps inserted to improve the alignment. The color lines above the consensus sequences represent SINE regions which correspond to the color boxes in Fig. 1.

Supplemental Figure 2. Information on 105 AmnSINE1 loci in the human genome with corresponding conservation graphs. The position information in human was determined from genomic sequence data in UCSC Genome Bioinformatics (ver. hg17). “Chr” refers to chromosome number. PhastCons conservation scores of the 1.5 kbp region around and including each AmnSINE1 were obtained by comparing human, chimpanzee, mouse, rat and dog sequences, and the graphs are displayed for each locus. The black region in each graph denotes the AmnSINE1 sequence and the gray represents the flanking region corresponding to the given position.

Supplemental Figure 3. Information of detailed conservation for 10 AmnSINE1 loci shown in Fig. 6B. Each window is 5 kbp in which the SINE sequence is set in the middle. These conservation graphs are obtained from UCSC Genome Bioinformatics website.