**Supplementary Notes**

**Supplementary Note 1. Conversion of C-value to gigabases.** Genome size were converted from picogram to base pairs by the formula provided by Dolezel *et al*1.

**Supplementary Note 2. Rationale for excluding the *Rana catesbeiana* genome.** Annotated peptides in *Rana (Lithobates) catesbeiana* are slightly more than half the size of genes in the other species (Supplementary Table 4), suggesting a highly fragmented assembly. We posit that this is a technical artifact as this genome reported 40.7% of genes in the Core Eukaryotic Genes Mapping Approach (CEGMA) as complete2.