

Supplementary Table 1: Description of the main features of the samples analyzed in this study.

	Clade	Number of RNA-seq samples	Sequencing depth ( <i>per</i> -base read) <sup>a</sup>	Fraction of analyzable introns <sup>b</sup>	Average number of introns <i>per</i> BUSCO gene	Fraction of major introns alternatively spliced <sup>c</sup>	Average AS rate among BUSCO introns	Fraction of rare SVs <sup>d</sup>
<b>Vertebrates</b>								
Callorhinchus milii	Chondrichthyes	11	1069	0.970	8.0	0.491	1.47 %	0.831
Gallus gallus	Aves	217	9591	0.986	8.4	0.854	1.59 %	0.958
Crocodylus porosus	Crocodylia	12	1819	0.975	8.5	0.817	3.02 %	0.908
Monodelphis domestica	Mammalia	269	11320	0.985	8.5	0.915	1.91 %	0.957
Heterocephalus glaber	Mammalia	54	2000	0.991	8.6	0.803	2.69 %	0.914
Macaca mulatta	Mammalia	177	5810	0.993	8.6	0.908	2.84 %	0.948
Oryctolagus cuniculus	Mammalia	338	15837	0.981	8.4	0.950	1.97 %	0.969
Rattus norvegicus	Mammalia	362	16643	0.968	8.5	0.953	1.89 %	0.965
Mus musculus	Mammalia	317	12261	0.974	8.4	0.937	1.87 %	0.958
Bos taurus	Mammalia	26	691	0.987	8.5	0.511	1.63 %	0.856
Loxodonta africana	Mammalia	23	3616	0.961	8.3	0.896	3.55 %	0.938
Sus scrofa	Mammalia	55	896	0.980	8.5	0.644	1.95 %	0.886
Canis lupus	Mammalia	5	350	0.930	8.2	0.436	2.18 %	0.764
Homo sapiens	Mammalia	313	10269	0.987	8.4	0.957	3.38 %	0.949
Equus caballus	Mammalia	19	995	0.987	8.5	0.658	2.16 %	0.884
<b>Insects</b>								
Bombyx mori	Lepidoptera	14	459	0.936	5.3	0.393	1.12 %	0.835
Athalia rosae	Hymenoptera	6	359	0.985	4.8	0.348	1.6 %	0.782
Cephus cinctus	Hymenoptera	17	2566	0.996	4.7	0.744	2.4 %	0.907
Orussus abietinus	Hymenoptera	2	198	0.971	4.7	0.370	2.03 %	0.763
Nasonia vitripennis	Hymenoptera	114	4827	0.973	4.5	0.648	1.21 %	0.913
Trichogramma pretiosum	Hymenoptera	4	361	0.984	4.4	0.268	0.98 %	0.782
Harpegnathos saltator	Hymenoptera	166	1923	0.993	4.7	0.565	2.02 %	0.886
Linepithema humile	Hymenoptera	23	1478	0.977	4.8	0.570	1.45 %	0.882
Camponotus floridanus	Hymenoptera	37	446	0.989	4.7	0.358	1.52 %	0.761
Pogonomyrmex barbatus	Hymenoptera	39	1386	0.949	4.5	0.579	1.91 %	0.866
Polistes canadensis	Hymenoptera	14	444	0.978	4.8	0.424	1.88 %	0.834
Polistes dominula	Hymenoptera	12	221	0.886	4.3	0.180	1.63 %	0.624
Solenopsis invicta	Hymenoptera	23	431	0.973	4.6	0.430	1.71 %	0.807
Acromyrmex echinator	Hymenoptera	42	1470	0.983	4.7	0.529	2.15 %	0.835
Megachile rotundata	Hymenoptera	108	3400	0.993	4.8	0.898	3.81 %	0.927
Apis mellifera	Hymenoptera	40	1777	0.991	4.9	0.673	2.3 %	0.892
Apis florea	Hymenoptera	4	503	0.888	4.4	0.318	1.85 %	0.711
Apis cerana	Hymenoptera	12	1401	0.985	4.6	0.578	2.36 %	0.839
Bombus terrestris	Hymenoptera	33	2648	0.964	4.7	0.763	2.33 %	0.922
Acyrtosiphon pisum	Hemiptera	35	3036	0.985	6.0	0.709	1.09 %	0.933
Cimex lectularius	Hemiptera	10	469	0.991	6.3	0.431	1.61 %	0.838
Halyomorpha halys	Hemiptera	6	1458	0.993	6.5	0.591	1.73 %	0.885
Aedes aegypti	Diptera	27	2418	0.967	2.6	0.514	1.35 %	0.870
Drosophila grimshawi	Diptera	30	253	0.928	2.7	0.168	0.8 %	0.726
Drosophila pseudoobscura	Diptera	32	3584	0.971	2.6	0.433	1.32 %	0.871
Drosophila melanogaster	Diptera	129	4530	0.990	2.7	0.551	1.22 %	0.909
Drosophila suzukii	Diptera	23	1913	0.938	2.6	0.287	1.17 %	0.810
Ceratitis capitata	Diptera	29	1171	0.983	3.3	0.418	1.45 %	0.860
Lucilia cuprina	Diptera	23	2446	0.937	2.8	0.268	0.85 %	0.823
Musca domestica	Diptera	12	1052	0.943	2.9	0.254	0.98 %	0.795
Onthophagus taurus	Coleoptera	53	647	0.971	3.2	0.377	1.34 %	0.810
Tribolium castaneum	Coleoptera	14	2620	0.968	3.6	0.556	1.15 %	0.881
Dendroctonus ponderosae	Coleoptera	30	2280	0.977	4.9	0.505	1.26 %	0.882
Anoplophora glabripennis	Coleoptera	20	320	0.948	4.1	0.299	1.13 %	0.781
Leptinotarsa decemlineata	Coleoptera	21	2050	0.929	3.8	0.512	1.21 %	0.883
Blattella germanica	Blattodea	30	939	0.907	5.4	0.423	1.26 %	0.827
Cryptotermes secundus	Blattodea	11	482	0.988	6.4	0.573	2.32 %	0.832
Zootermopsis nevadensis	Blattodea	53	3985	0.983	6.4	0.802	2.36 %	0.927

<sup>a</sup> Median *per*-base read coverage computed on BUSCO gene exons  
<sup>b</sup> Fraction of analyzable introns (*i.e.* with N ≥ 10) among BUSCO genes  
<sup>c</sup> Proportion of major introns for which alternative splicing has been detected (*i.e.* with N2 > 0) among BUSCO genes  
<sup>d</sup> Fraction of rare spliced variants introns (*i.e.* with MIRA ≤ 5%) among all protein-coding genes