

**Suppl. Table S1:** Taxonomic information and genome versions used in the current study

Code	Common name	Scientific name	Ref.	Genome version
ALLIG	American alligator	<i>Alligator mississippiensis</i>	1	<a href="http://dx.doi.org/10.5524/101126">http://dx.doi.org/10.5524/101126</a>
ANAPL	Duck	<i>Anas platyrhynchos</i>	2	<a href="http://dx.doi.org/10.5524/101001">http://dx.doi.org/10.5524/101001</a>
DRONO	Emu	<i>Dromaius novaehollandiae</i>	n/a	Allan Baker (unpubl. data)
FALPE	Peregrine falcon	<i>Falco peregrinus</i>	2	<a href="http://dx.doi.org/10.5524/101006">http://dx.doi.org/10.5524/101006</a>
GALGA	Chicken	<i>Gallus gallus</i>	3	galGal3
GAVST	Red-throated loon	<i>Gavia stellata</i>	2	<a href="http://dx.doi.org/10.5524/101026">http://dx.doi.org/10.5524/101026</a>
HALLE	Bald eagle	<i>Haliaeetus leucocephalus</i>	2	<a href="http://dx.doi.org/10.5524/101040">http://dx.doi.org/10.5524/101040</a>
MANVI	Golden-collared manakin	<i>Manacus vitellinus</i>	2	<a href="http://dx.doi.org/10.5524/101010">http://dx.doi.org/10.5524/101010</a>
MELGA	Turkey	<i>Meleagris gallopavo</i>	4	WASHUC2
NOTPE	Chilean tinamou	<i>Nothoprocta perdicaria</i>	n/a	Allan Baker (unpubl. data)
PHORU	American flamingo	<i>Phoenicopterus ruber</i>	2	<a href="http://dx.doi.org/10.5524/101035">http://dx.doi.org/10.5524/101035</a>
PICPU	Downy woodpecker	<i>Picoides pubescens</i>	2	<a href="http://dx.doi.org/10.5524/101012">http://dx.doi.org/10.5524/101012</a>
PODCR	Great crested grebe	<i>Podiceps cristatus</i>	2	<a href="http://dx.doi.org/10.5524/101036">http://dx.doi.org/10.5524/101036</a>
PYGAD	Adelie penguin	<i>Pygoscelis adeliae</i>	2	<a href="http://dx.doi.org/10.5524/100006">http://dx.doi.org/10.5524/100006</a>
STRCA	Ostrich	<i>Struthio camelus</i>	2	<a href="http://dx.doi.org/10.5524/101013">http://dx.doi.org/10.5524/101013</a>
TAEGU	Zebra finch	<i>Taeniopygia guttata</i>	5	WUGSC 3.2.4/taeGut1
TINGU	White-throated tinamou	<i>Tinamus guttatus</i>	2	<a href="http://dx.doi.org/10.5524/101014">http://dx.doi.org/10.5524/101014</a>

**References:**

- 1 Green R.E., Braun E.L., Armstrong J., et al. 2014. Three crocodylian genomes reveal ancestral patterns of evolution among archosaurs. *Science* 346(6215):1254449.
- 2 Jarvis E.D., Mirarab S., Aberer A.J., et al. 2015. Phylogenomic analyses data of the avian phylogenomics project. *GigaScience* 4:4.
- 3 Hillier L.W., Miller W., Birney E., et al. 2004. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432(7018):695–716.
- 4 Dalloul R.A., Long J.A., Zimin A.V., et al. 2010. Multi-platform next-generation sequencing of the domestic turkey (*Meleagris gallopavo*): genome assembly and analysis. *PLoS Biology* 8(9):e1000475.
- 5 Warren W.C., Clayton D.F., Ellegren H., et al. 2010. The genome of a songbird. *Nature* 464(7289):757–762.

For Supplementary FileS2 please see separate file "Supplementary\_FileS2.xlsx"

**Suppl. Table S3:** Comparison of summary measures for SATé-MAFFT alignments with emu and Chilean tinamou profile aligned, and for *de novo* alignment of all sequences with MAFFT. Comparisons are given for both the full set of 3679 UCE loci, as well as the subset of 2232 UCEs that do not overlap introns or CNEEs.

	<b>All UCEs</b>						<b>Nonoverlapping UCEs</b>					
	SATé-MAFFT alignments			<i>De novo</i> MAFFT alignments			SATé-MAFFT alignments			<i>De novo</i> MAFFT alignments		
	Min.	Max.	Mean $\pm$ SD	Min.	Max.	Mean $\pm$ SD	Min.	Max.	Mean $\pm$ SD	Min.	Max.	Mean $\pm$ SD
Alignment length (bp)	2126	4279	2685.06 $\pm$ 239.03	2126	4368	2679.90 $\pm$ 256.06	2126	4279	2715.88 $\pm$ 252.76	2126	4368	2711.64 $\pm$ 272.44
Variable sites (%)	3.0	74.7	49.93 $\pm$ 9.94	2.9	71.6	49.73 $\pm$ 9.65	3.0	74.7	50.97 $\pm$ 10.45	2.9	71.6	50.73 $\pm$ 10.11
Informative sites (%)	0.3	51.9	26.08 $\pm$ 7.37	0.3	47.1	25.53 $\pm$ 6.82	0.3	51.9	26.73 $\pm$ 7.74	0.3	47.1	26.10 $\pm$ 7.12
Undetermined chars. (%)	0.3	56.5	23.79 $\pm$ 7.91	0.3	60.7	23.54 $\pm$ 8.42	0.3	56.5	25.14 $\pm$ 8.11	0.3	60.7	24.90 $\pm$ 8.66
Gaps/bp aligned	0	0.86	0.20 $\pm$ 0.09	0	0.81	0.20 $\pm$ 0.09	0	0.86	0.22 $\pm$ 0.09	0	0.81	0.21 $\pm$ 0.10
trimAl trimmed (%)	0.4	78.5	24.01 $\pm$ 8.89	0.4	81.2	24.15 $\pm$ 9.67	0.4	73.9	25.34 $\pm$ 9.31	0.4	81.2	25.54 $\pm$ 10.21

**Suppl. Table S4:** Comparison of summary measures for *de novo* alignment with MAFFT (CNEEs) and SATé-MAFFT alignment with emu and Chilean tinamou profile aligned (introns and UCEs) as used throughout the manuscript, versus alignment following the pipeline described in Jarvis et al. (2014; e.g. SATé-MAFFT alignment followed by filtering to mask unique and poorly aligning sequence, removal of gap-only columns after filtering, and final SATé-MAFFT alignment of the filtered sequences). Summary values are calculated from 3822 CNEEs, 3733 introns, and 3679 UCEs in each case.

	CNEEs						Introns						UCEs					
	MAFFT			SATé-MAFFT + filtering			SATé-MAFFT + profile alignment			SATé-MAFFT + filtering			SATé-MAFFT + profile alignment			SATé-MAFFT + filtering		
	Min.	Max.	Mean ± SD	Min.	Max.	Mean ± SD	Min.	Max.	Mean ± SD	Min.	Max.	Mean ± SD	Min.	Max.	Mean ± SD	Min.	Max.	Mean ± SD
Alignment length (bp)	390	1829	548.8 ± 151.6	386	1805	545.3 ± 149.4	401	22138	1957.1 ± 2102.8	286	20458	1776.0 ± 1895.3	2126	4279	2685.1 ± 239.0	1602	4237	2440.4 ± 233.5
Variable sites (%)	1.3	51.5	17.0 ± 8.2	1.3	51.1	16.9 ± 8.2	4.1	85.2	65.4 ± 7.2	4.1	83.2	68.3 ± 6.3	3	74.7	49.9 ± 9.9	2.9	72.5	48.6 ± 9.4
Informative sites (%)	0	22.7	5.8 ± 3.4	0	22.6	5.8 ± 3.4	1.3	56.7	35.8 ± 6.0	1.2	58.6	37.4 ± 6.0	0.3	51.9	26.1 ± 7.4	0.3	50.2	25.0 ± 6.7
Undetermined chars. (%)	0	32.4	2.3 ± 2.5	0	16.5	1.8 ± 1.6	2.2	61.0	24.1 ± 8.3	0.4	62.4	18.9 ± 6.9	0.3	56.5	23.8 ± 7.9	0.3	66.0	19.4 ± 9.6
Gaps/bp aligned	0	0.5	0.02 ± 0.02	0	0.1	0.01 ± 0.01	0.02	1.4	0.3 ± 0.2	0	1.5	0.2 ± 0.1	0	0.9	0.2 ± 0.1	0	1.0	0.1 ± 0.1
trimAl trimmed (%)	0	34.4	2.6 ± 2.8	0	22.3	2.0 ± 1.9	2.1	69.3	20.4 ± 9.7	0.5	72.7	13.3 ± 8.0	0.4	78.5	24.0 ± 8.9	0.4	76.4	16.3 ± 8.9
Jarvis filtering masked (%)	n/a			0	1.9	0.04 ± 0.1	n/a			0	8.4	1.5 ± 0.9	n/a			0	17.0	3.0 ± 2.2
Jarvis filtering trimmed (%)	n/a			0	32.88	0.6 ± 1.8	n/a			0	54.0	5.2 ± 6.0	n/a			0	37.7	9.9 ± 4.8

**Suppl. Table S5** Pairwise correlations in per-taxon GC content between marker types.  $P_{\text{adjusted}}$  gives Bonferroni adjusted P-values corrected for multiple comparisons.

	<b>Woodpecker included</b>		<b>Woodpecker excluded</b>	
	<b>Intron</b>	<b>UCE</b>	<b>Intron</b>	<b>UCE</b>
<b>CNEE</b>	$r = 0.5997$ $P = 0.0109$ $P_{\text{adjusted}} = 0.0328$	$r = 0.8479$ $P < 0.00001$ $P_{\text{adjusted}} = 0.0001$	$r = 0.2844$ $P = 0.2857$ $P_{\text{adjusted}} = 0.8572$	$r = 0.7731$ $P = 0.0004$ $P_{\text{adjusted}} = 0.0013$
<b>Intron</b>		$r = 0.7010$ $P = 0.0017$ $P_{\text{adjusted}} = 0.0052$		$r = 0.4599$ $P = 0.0731$ $P_{\text{adjusted}} = 0.2193$

**Suppl. Table S6:** Summary measures of locus characteristics for full and non-overlapping CNEE and UCE data sets

	<b>CNEEs</b>						<b>UCEs</b>					
	<b>All loci (n = 3822)</b>			<b>Nonoverlapping loci (n = 2318)</b>			<b>All loci (n = 3679)</b>			<b>Nonoverlapping loci (n = 2232)</b>		
	<b>Min.</b>	<b>Max.</b>	<b>Mean ± SD</b>	<b>Min.</b>	<b>Max.</b>	<b>Mean ± SD</b>	<b>Min.</b>	<b>Max.</b>	<b>Mean ± SD</b>	<b>Min.</b>	<b>Max.</b>	<b>Mean ± SD</b>
Alignment length (bp)	390	1829	548.77 ± 151.64	390	1770	516.54 ± 115.87	2126	4279	2685.06 ± 239.03	2126	4279	2715.88 ± 252.76
Variable sites (%)	1.3	51.5	16.95 ± 8.20	1.5	51.5	19.57 ± 8.38	3.0	74.7	49.93 ± 9.94	3	74.7	50.97 ± 10.45
Informative sites (%)	0	22.7	5.82 ± 3.37	0	22.7	6.70 ± 3.53	0.3	51.9	26.08 ± 7.37	0.3	51.9	26.73 ± 7.74
Global GC (%)	25.1	55.0	36.94 ± 4.12	25.1	55.0	37.00 ± 4.18	29.5	57.3	39.13 ± 4.15	29.5	57.3	39.59 ± 4.40
GC variance	0.01	22.15	0.82 ± 1.36	0.02	15.88	0.97 ± 1.46	0.06	42.71	3.91 ± 4.19	0.06	42.71	4.47 ± 4.67
Undetermined chars. (%)	0	32.4	2.31 ± 2.48	0	32.4	2.42 ± 2.42	0.3	56.5	23.79 ± 7.91	0.3	56.5	25.14 ± 8.11
Gaps/bp aligned	0	0.45	0.02 ± 0.02	0	0.45	0.02 ± 0.02	0	0.86	0.20 ± 0.09	0	0.86	0.22 ± 0.09
trimAl trimmed (%)	0	34.4	2.59 ± 2.75	0	34.4	2.71 ± 2.68	0.4	78.5	24.01 ± 8.89	0.4	73.9	25.34 ± 9.31
TiTv	0.60	9.95	2.44 ± 0.79	0.68	7.76	2.41 ± 0.72	0.93	4.52	1.79 ± 0.25	0.93	4.52	1.78 ± 0.26
Gamma	0.02	471.14	1.46 ± 16.72	0.02	471.14	1.36 ± 15.59	0.02	4.0	0.92 ± 0.44	0.02	4.0	0.99 ± 0.49
Avg. genetree bootstrap (%)	11.6	80.0	44.87 ± 10.70	14.2	75.9	46.27 ± 10.70	25.4	97.9	76.15 ± 7.97	25.4	97.9	75.85 ± 8.37
Consistency index	0.81	1	0.92 ± 0.03	0.81	1	0.92 ± 0.03	0	0.99	0.82 ± 0.03	0.71	0.99	0.82 ± 0.03

For Supplementary FileS7 please see separate file "Supplementary\_FileS7.xlsx"