

**Table S2.** Results of ancestral state reconstructions for major avian clades, represented by at least three species in our dataset. The values reported in brackets in maximum likelihood analyses are proportional likelihoods. Abbreviations: CL – cervical locus, TL – thoracic locus.

Clade	Maximum parsimony	Maximum likelihood (equal length branches)	Maximum likelihood (time- calibrated branch lengths)
Neornithes	CL: present TL: present	CL: present (1) TL: likely present (0.906)	CL: present (1) TL: likely present (0.788)
Palaeognathae	CL: present TL: present	CL: present (1) TL: likely present (0.981)	CL: present (1) TL: likely present (0.950)
Neognathae	CL: present TL: present	CL: present (1) TL: likely present (0.872)	CL: present (1) TL: likely present (0.760)
Galloanserae	CL: present TL: ambiguous	CL: present (1) TL: ambiguous but likely present (0.558)	CL: present (1) TL: likely present (0.666)
Galliformes	CL: present TL: ambiguous	CL: present (1) TL: ambiguous but likely present (0.523)	CL: present (1) TL: likely present (0.732)
<i>Gallus + Coturnix</i>	CL: present TL: present	CL: present (1) TL: likely present (0.924)	CL: present (1) TL: likely present (0.983)
Anseriformes	CL: present TL: absent	CL: present (1) TL: likely absent (0.710)	CL: present (1) TL: likely absent (0.732)
Neoaves	CL: present TL: present	CL: present (1) TL: likely present (0.979)	CL: present (1) TL: likely present (0.759)
Charadriiformes + Psittacopasserae	CL: present TL: present	CL: present (1) TL: likely present (0.849)	CL: present (1) TL: likely present (0.748)
Charadriiformes	CL: present TL: present	CL: present (1) TL: likely present (0.972)	CL: present (1) TL: likely present (0.989)
Psittacopasserae	CL: present TL: absent	CL: present (1) TL: likely absent (0.869)	CL: present (1) TL: ambiguous but likely present (0.560)