Table S1. Taxon and voucher information.

Species	Orders/Families	Museum[a]	Catalog/ collection#	Locality	Collector
Gallus gallus[b]	Galliformes				
Chauna torquata	Anseriformes	USNM	614546	Argentina	J.P. Angle
Bucorvus abyssinia	Bucerotiformes	FLMNH	45218	Captive	---
Upupa epops	Bucerotiformes	USNM	586147	Russia (USSR)	A. Vanushkin
Aegotheles insignis	Caprimulgiformes	KUMNH	95997	Papua New Guinea	---
Steatornis caripensis	Caprimulgiformes	LSUMNS	32579	Peru	C.C. Witt
Cariama cristata	Cariamidae	LSUMNS	8656	Captive	---
Colius colius	Coliiformes	USNM	622447	Captive	---
Urocolius indicus	Coliiformes	LSUMNS	34225	South Africa	R.G. Moyle
Coracias caudata	Coraciiformes	USNM	621662	Captive	---
Momotus momota	Coraciiformes	USNM	609134	Guyana	M.J. Braun
Coua cristata	Cuculiformes	FMNH	352800	Madagascar	S.M. Goodman
Crotophaga sulcirostris	Cuculiformes	USNM	607659	Panama	C. Smith
Falco mexicanus	Falconidae	MSB	103400	New Mexico, USA	---
Herpetotheres cachinnans	Falconidae	USNM	612262	Panama	---
Grus canadensis	Gruiformes	USNM	621384	Captive	---
Rallus limicola	Gruiformes	FLMNH	43762	Florida, USA	---
Acanthisitta chloris	Passeriformes	MVZ	No voucher	New Zealand	C. Sibley collection (#1023)
Menura novaehollandiae	Passeriformes	ANWC	42757	Australia	---
Regulus calendula	Passeriformes	USNM	601728	USA	P.R. Windler
Smithornis rufolateralis	Passeriformes	FMNH	429425	Central African Republic	D.E. Willard
Taeniopygia guttata[b]	Passeriformes				
Tyrannus tyrannus	Passeriformes	USNM	586080	USA	B.K. Schmidt
Bucco macrodactylus	Piciformes	FMNH	433243	Peru	T. Pequeno
Capito niger	Piciformes	KUMNH	88938	Guyana	M.B. Robbins
Cacatua sulphurea	Psittaciformes	USNM	542225	Captive	---
Nestor notabilis	Psittaciformes	USNM	615000	Captive	---
Trogon personatus	Trogoniformes	LSUMNS	7644	Peru	G.H. Rosenberg

NOTE.—[a] ANWC=Australian National Wildlife Collection, FLMNH=Florida Museum of Natural History, FMNH=Field Museum of

Natural History, KUMNH=University of Kansas Natural History Museum & Biodiversity Center, LSUMNS=Louisiana State University Museum of Natural Science, MSB=Museum of Southwestern Biology (University of New Mexico), MVZ=Museum of Vertebrate Zoology (University of California, Berkeley), USNM=National Museum of Natural History.

[b] Data taken from complete genomic sequences.

Table S2. Locus information.

HUGO name	Chr.[a]	Gene Description	Length[b]	Intron(s)[c]	AIC$_c$ model[d]	Alpha[e]
ADAM10	10	ADAM metallopeptidase domain 10	526	7	TVM+Γ	6.50
ARNTL5	5	Aryl hydrocarbon receptor nuclear translocator-like	433	12	GTR+Γ	3.06
CALB1	2	Calbindin 1, 28kDa	565	9, 10	GTR+Γ	1.49
CLTCL1	15	Clathrin, heavy chain-like 1	512	7	TIM+I+Γ	7.02
CSDE1	26	Cold shock domain containing E1, RNA-binding	372	5	TVM+I+Γ	2.67
CSNK1E	1	Casein kinase 1, epsilon	456	6	TVM+Γ	4.65
DDX5	18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	381	5	TVM+Γ	6.26
E1F5	5	Eukaryotic translation initiation factor 5	508	6	TVM+I+Γ	6.09
ENO1	21	Enolase 1, (alpha)	452	9	TVM+I+Γ	2.60
GRIA2	4	Glutamate receptor, ionotropic, AMPA2	493	10	TVM+Γ	1.95
GTF3C3	7	General transcription factor IIIC, polypeptide 3, 102kDa	474	4	GTR+Γ	3.93
HNRPA2B1	2	Heterogeneous nuclear ribonucleoprotein A2/B1	400	4	TVM+I+Γ	3.28
KCNQ5	3	Potassium voltage-gated channel, KQT-like subfamily, member 5	420	5	TVM+Γ	2.81
OPN1LW	19	Opsin 1 (cone pigments), long-wave-sensitive	517	1	K81uf+Γ	2.19
PARK7	21	Parkinson disease (autosomal recessive, early onset) 7	563	2	TVM+Γ	4.01
PDE6B	Z	Phosphodiesterase 6B, cGMP-specific, rod, beta	546	10	TIM+Γ	3.62
PER2	9	Period homolog 2	416	9	TVM+Γ	3.55
POLL	6	Polymerase (DNA directed), lambda	521	4	TVM+Γ	3.62
PPP2CB	4	Protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform	323	6	TVM+Γ	2.70
PRDX6	8	Peroxiredoxin 6	580	4	HKY+Γ	3.44
PSMA2	2	Proteasome (prosome, macropain) subunit, alpha type, 2	434	3	TVM+I+Γ	3.77
SBDS	19	Shwachman-Bodian-Diamond syndrome	559	4	GTR+Γ	3.30
SEPT2	15	Septin 2	465	5	GTR+Γ	2.26
SH3GLB2	17	SH3-domain GRB2-like endophilin B2	475	4	K81uf+Γ	2.55
SRSF3	26	Serine/arginine-rich splicing factor 3	453	3'UTR	TVM+Γ	1.09
SUCLG1	4	Succinate-CoA ligase, GDP-forming, alpha subunit	527	3	GTR+Γ	3.36
SURF1	7	Surfeit1	612	5	K80+I+Γ	2.33
TXNDC12	8	Thioredoxin domain containing 12 (endoplasmic reticulum)	416	6	TVM+Γ	4.04
VDAC2	6	Voltage-dependent anion channel 2	457	5	GTR+I+Γ	10.18

Table S2. Continued

HUGO name	Chr.[a]	Gene Description	Length[b]	Intron(s)[c]	AIC$_c$ model	Alpha
VIM	2	Vimentin	467	8	TVM+Γ	6.43

NOTE.—[a] Chr. refers to the chromosome in the chicken genome.

[b] Length of the *Gallus gallus* sequence.

[c] Intron number(s) were determined as described in Kimball et al. (2009). The amplified region of SRSF3 is 3' UTR.

[d] The best fitting model based on the second-order variant of the AIC criterion.

[e] Shape parameter of a gamma distribution.

Table S3. Amplification and sequencing primers plus PCR conditions.

Locus	Primer Name	Sequence (5' – 3')	Annealing T^o (Mg^{++} conc.)[a]
ADAM10	ADAM10.7F	CCAGCCATGTTAAAGCAATTGA	60°-50° (2.0mM)
	ADAM10.8R	GGTCCTTCTCATCTACAGTTGTG	
ARNTL[b]	ARNTL.12F	TGGTTCAGTTTCATGAACCCTTG	55° (2.0mM)
	ARNTL.13R	CCTGAAGCACRCTGTCCATGCT	
CALB1[c]	CAL.9F	AGGGTGTCAARATGTGTGSGAAAGA	58°-48° (1.5mM)
	CAL.11R	GTANAGCTTCCCTCCATCNGACAA	
CLTCL1[b]	CLTCL1.e7F	CACCAATGTTCTGCAGAATCCTGA	55° (2.5 mM)
	CLTCL1.e8Rnew	CCAGCTTATCTTCCTTNAGCCATTTCTC	
	CLTCL1.e8Ralt	GGCTGAGCTGGTACACTCTGGAACTTCC	58° (2.0mM)
CSDE1[b]	CSDE.5F	CTGGTGCTGTAAGTGCTCGTAAC	59° (2.5mM)
	CSDE.6R	CCAGGCTGTAAGGTTTCTAGGTCAC	
CSNK1E[d]	CSNK1E.6F	GACTACGTCTTTGACTGGAACATGCT	62°-55° (1.5mM)
	CSNK1E.7R	ATCCTCAGGGTTTCGGGCTG	
DDX5[d]	DDX.5F	CATATAAATCATCAGCCATTCCTGG	55° (1.5mM)
	DDX.6R	GTTGGTGCCAGCACAAGAC	
E1F5[d]	EIF.6F	GTCCAGCAATGAGACACCTCCAC	60° (1.5mM)
	EIF.7R	CCAGTCATCATCGTCCTCCTCC	
ENO1[d]	ENO.e9F	GGTGATGATCTGACTGTGACCAACC	60° (1.5mM)
	ENO.e10R	CATCACACCCCAGCCATTGGAC	
GRIA2[d]	GRIA.10F	GGTTGGAGAACTTGTTTATGG	52° (2.0mM)
	GRIA.11R	GGCTCATAAAGGGCTTTG	
GTF3C3	GTF3C3.4F	CTGATGTGCATGGAGATCATT	60°-50° (2.0mM)
	GTF3C3.5R	TCATAGATCATGGCAAGAGTG	
HNRPA2B1[d]	HNRP.e4F	CATTTGATGACCATGATCCTGTGG	58° (1.5mM)
	HNRP.e5R	GCATTCCTGTCTAGAGAGGGCTTTC	
KCNQ5[d]	KCNQ.5F	CATGGACCGAAGAGGAGGCACT	68° (2.0mM)
	KCNQ.6R	CCAGAGAGCATCTGCATATGTGGAG	
OPN1LW[d]	OPN1LW.1F	GTGAGCTGGAGGGCTTCATGGT	57°-47° (1.5mM)
	OPN1LW.2R	AAATCTCCCAGGGGTCTGCAGAC	
PARK7[b]	PARK.2F	GCAGGCCTRRCTGGAAAAGARCC	56° (1.5mM)
	PARK.3R	TTCTGAGCTCCWAGRTTACC	

Table S3. Continued

Locus	Primer Name	Sequence (5' – 3')	Annealing T^o (Mg^{++} conc.)[a]
PDE6B[d]	PDE6B.10F	CCACGTGAANTGTGACAAGGATGA	53° (2.0mM)
	PDE6B.11R	TCCTTCCCCAGCTTTTCTCGTGT	
PER2[b]	PER.9F	CATCTTCAYCCAAATGACAGACC	55° (2.0mM)
	PER.10R	CCTGATTGGTGAATAGTCAAAAGG	
POLL	POLL.4F	CACAAACCGGTCACCTCCTA	60°-50° (2.0mM)
	POLL.5R	TCCCAGGAATTTTACAGGCT	
PPP2CB[d]	PPP2.6F	GCTATCATGGAACTAGATGACACT	55° (1.5mM)
	PPP2.7R	CTCTCCACGACGAGGTGCT	
PRDX6	PRDX6.4F	TGCAGCTGACAGCATACAAG	60°-50° (2.0mM)
	PRDX6.5R	TAAGGTGGGCACAACCATGA	
PSMA2[d]	PSMA2.e3F	GTATAGTGGTATGGGTCCAGATTAC	58°-48° (1.5mM)
	PSMA2.e4R	GCTGTTGGAATGGGCTCATGATAAAC	
SBDS	SBDS.4F	GCTCAAGCCACTGATTAAAGT	55°-47° (2.0mM)
	SBDS.5R	CTCATCAATCTCTCTGAAGCAG	
SEPT2[d]	SEPT.e5F	CTTGGCGATCACAGGGACAATG	58° (1.5mM)
	SEPT.e6R	GAACAGGCGCCACATTATAGACAATAG	
SH3GLB2	SH3GLB2.4F	TGCCTCCATCAACTTCCTGAC	60°-50° (2.0mM)
	SH3GLB2.5R	TTGCAGGCATCCAGATCCAG	
SRSF3[d]	SRSF3.e6F	GCTGTGTATTTGGTCTATTCAGAG	58°-48° (1.5mM)
	SRSF3.e7R	CAGGTGGCAAATGTAAAGATGTG	
SUCLG1[d]	SUCLG.e6F	GGGTCTGCCTGTGTTTAATTCTGT	63° (1.5mM)
	SUCLG.e7R	GCAGCAGCAAANGGAGGAGGTAC	
SURF1	SURF1.5F	TTTGACCACTCCAAGGAGCTCTA	60°-50° (2.0mM)
	SURF1.6R	GGCACAAATCCTCGGTTGACT	
TXNDC12[b]	TXN.6F	GGAAACCCCAGCTACAAGTATTTC	57° (1.5mM)
	TXN.7R	GGCCTCCTTCATCCCTTGG	
VDAC2[d]	VDAC.e5F	GTCAACGTCACAACCTAGG	52° (1.5mM)
	VDAC.e6R	CAACTTTCTCACCAAATACAGG	
VIM[b]	VIM.8F	GACCGTGGAAACTAGAGATGGAC	57° (1.5mM)
	VIM.9R	GTCATCGTGATGCTGGGAAGTTTC	

NOTE.—[a] Tm range means a touchdown PCR was used for this locus, with an 0.5° drop with each cycle.

[b] Originally published in Kimball et al. 2009.
[c] Originally published in Cox et al. 2007.
[d] Designed by Jordan V. Smith (2009 and pers comm.).

Table S4. Alignment distance between the manual alignment and all others (all pair-wise comparisons were performed, but only these are shown as representatives).

Alignment	Distance	Num. Sites[a]	% variable[b]	% informative[c]
Manual	n/a	25700	54.7	33.5
Clustal	0.73	6467	44.6	26.7
Mafft	0.30	17954	47.5	28.8
Mafft_BR	0.36	16281	43.9	25.6
Mafft_HA	0.36	16251	43.6	25.5
Mafft_LZ	0.37	16097	43.4	25.4
Mafft_SA	0.36	16291	43.8	25.6
Mafft_ep0.01	0.35	16552	43.6	25.3
Mafft_op1	0.36	16301	43.6	25.5
Mafft_op3	0.39	15602	41.2	23.9
Muscle	0.37	16023	45.4	26.8
Prank_BR	0.80	5051	9.2	3.0
Prank_BR_12	0.55	11559	37.8	21.3
Prank_BR_55	0.49	13224	39.2	22.2
Prank_HA	0.80	5167	9.4	3.2
Prank_HA_12	0.54	11928	36.5	20.5
Prank_HA_55	0.47	13540	38.1	21.5
Prank_LZ	0.80	5224	9.1	3.0
Prank_LZ_12	0.55	11560	36.1	20.4
Prank_LZ_55	0.47	13702	38.1	21.7
Prank_SA	0.79	5300	9.5	3.5
Prank_SA_12	0.52	12220	37.2	21.0
Prank_SA_55	0.46	13886	38.7	22.3
SATe_mafft	0.39	15241	45.5	26.5
SATe_BR_mafft	0.91	2328	21.6	13.7
SATe_HA_mafft	0.96	1099	20.9	13.0
SATe_LZ_mafft	0.94	1556	11.5	6.7
SATe_SA_mafft	0.90	2466	39.6	24.3
SATe_prank	0.42	14785	39.1	22.2
SATe_BR_prank	0.94	1665	27.7	17.4
SATe_HA_prank	0.95	1338	14.3	8.3
SATe_LZ_prank	0.94	1441	30.3	19.3
SATe_SA_prank	0.96	1131	15.3	8.6
Tcoffee	0.87	3252	13.3	7.3

NOTE.—[a] number of identical columns between each alignment and the manual alignment.

[b] Percentage of variable sites of the identical columns.

[c] Percentage of informative sites of the identical columns. The alignment distance was negatively correlated with the percent of informative sites (spearman's $r = -0.82$, $n = 32$, $p < 0.001$).

Table S5. Unpartitioned ML Gene jackknifing analyses based on manual alignment.

Excluding gene	PP		PPFC		CPBT		Coliiformes-CPBT	
	Present[a]	BS%[b]	Present	BS%	Present	BS%	Present	BS%
ADAM10	Yes	15	Yes	38	Yes	90	Yes	---
ANRTL	Yes	30	Yes	42	Yes	89	Yes	---
CALB1	Yes	35	Yes	50	Yes	87	Yes	55
CLTCL1	Yes	50	Yes	49	Yes	90	Yes	54
CSDE1	Yes	41	Yes	50	Yes	85	Yes	54
CSNK1E	Yes	34	Yes	50	Yes	91	Yes	50
DDX5	Yes	37	Yes	43	Yes	88	Yes	---
E1F5	Yes	53	Yes	44	Yes	82	Yes	68
ENO1	Col	---	Col	---	Yes	96	No	---
GRIA2	Yes	31	Yes	46	Yes	89	Yes	48
GTF3C3	Yes	32	Yes	49	Yes	87	Yes	55
HNRPA2B1	Yes	37	Yes	54	Yes	88	Yes	56
KCNQ5	Yes	37	Yes	39	Yes	97	Yes	---
OPN1LW	Yes	---	Yes	---	Yes	92	Yes	---
PARK7	Yes	40	Yes	50	Yes	86	Yes	50
PDE6B	Col	28	Col	37	Yes	93	No	---
PER2	Yes	34	Yes	49	Yes	88	Yes	47
POLL	Yes	32	Yes	41	Yes	89	Yes	---
PPP2CB	Yes	40	Yes	50	Yes	89	Yes	55
PRDX6	Yes	36	Yes	42	Yes	90	Yes	46
PSMA2	Col	26	Col	33	Yes	98	No	---
SBDS	Yes	50	Yes	41	Yes	81	Yes	55
SEPT2	Yes	33	Yes	41	Yes	89	Yes	49
SH3GLB2	Yes	43	Yes	42	Yes	93	Yes	51
SRSF3	Yes	38	Yes	53	Yes	95	No	---
SUCLG1	Yes	33	Yes	51	Yes	85	Yes	52
SURF1	Yes	40	Yes	49	Yes	76	Yes	61
TXNDC12	Yes	30	Yes	41	Yes	93	No	---

Table S5. Continued

Excluding gene	PP		PPFC		CPBT		Coliiformes-CPBT	
	Present[a]	BS%[b]	Present	BS%	Present	BS%	Present	BS%
VDAC2	Col	26	Col	38	Yes	89	No	---
VIM	Col	---	Col	---	Yes	92	No	---
ENO1 + SRSF3[c]	Yes	37[f]	Yes	38[f]	Yes	96[f]	No	---
Upper quartile RCV[d]	Yes	51[f]	Col	---	Yes	80[f]	No	---
Saturated loci[e]	Yes	45[f]	Yes	28[f]	Yes	66[f]	Yes	57[f]

NOTE.—PP: Passeriformes-Psittaciformes, PPFC: Passeriformes-Psittaciformes-Falconidae-Cariamidae, CPBT: Coraciiformes-Piciformes-Bucerotiformes-Trogoniformes.

[a] Whether clades presented in the ML best trees. Col: Colliformes are included in specific clades.

[b] BS% is based on 100 bootstrap analyses, ---: Specific clades did not show in consensus trees.

[c] Two genes biased from compositional homogeneity in χ^2 test.

[d] Seven loci among the upper quartile RCV values are ENO1, KCNQ5, PPP2CB, PSMA2, SBDS, SRSF3, and SURF1.

[e] Eight loci that failed substitution saturation test are E1F5, ENO1, HNRPA2B1, PARK7, POLL, PPP2CB, PRDX6, and SBDS.

[f] Unpartitioned analyses are presented. Bootstrap supports under partitioned analyses are similar as that of unpartitoned analyses.

Table S6. Bootstrap supporting results by different methods

Methods	Parameter & Analyses[a]	PP (BS%)		PPFC (BS%)		CPBT		Coliiformes-sister	
		All taxa[b]	-Col[c]	All taxa	-Col	All taxa	-Col	Sister clade	BS%
Manual	MLp	**28**	50	**37**	86	92	100	PPFC	55
Noambiguous	ML	34	50	45	81	89	100	CPBT	54
	MLp	**24**	44	**30**	79	94	100	PPFC	54
Nogappy	ML	39	58	48	82	89	100	CPBT	50
Noambiguous + Nogappy	ML	30	53	43	79	90	100	CPBT	54
Prank	SA_MLp	33	46	45	82	100	100	CPBT	58
	SA_12_ML	No	No	35	71	100	100	CPBT	51
	SA_12_MLp	No	No	30(+Col)	73	100	100	Psittaciformes	52
	SA_55_ML	51	67	44	73	99	100	CPBT	69
	SA_55_MLp	47	60	41	79	100	100	CPBT	57
	LZ_MLp	66	78	41	54	78(+Col)	99	*Trogon*	76
	LZ_12_ML	89	84	No	No	86(+Col)	82	*Trogon*	100
	LZ_12_MLp	89	88	No	No	82(+Col)	85	*Trogon*	99
	LZ_55_ML	60	66	No	No	85(+Col)	99	*Trogon*	85
	LZ_55_MLp	54	64	47	57	83(+Col)	99	*Trogon*	84
	BR_MLp	67	82	69(+Col)	65	95	97	Falconidae	83
	BR_12_ML	60	70	61(+Col)	72	86	94	Falconidae	69
	BR_12_MLp	51	71	64(+Col)	67	85	93	Falconidae	70
	BR_55_ML	53	71	53(+Col)	51	93	99	Falconidae	79
	BR_55_MLp	49	67	58(+Col)	56	93	98	Falconidae	79
	HA_MLp	99	99	67(+Col)	86	89	100	PP	55
	HA_12_ML	98	100	78	96	95	100	CPBT	84
	HA_12_MLp	95	99	69	96	94	100	CPBT	74
	HA_55_ML	100	100	60(+Col)	80	93	100	PPF	42
	HA_55_MLp	99	100	67(+Col)	85	92	100	PPF	40
Mafft	MLp	23(+Col)	44	52(+Col)	71	95	99	Passeriformes	38
	op1_ML	32(+Col)	55	52(+Col)	75	93	99	Passeriformes	47
	op1_MLp	32(+Col)	54	64(+Col)	80	95	99	Passeriformes	44
	op3_ML	No	52	No	63	94	99	PPF	51
	op3_MLp	No	No	44(+Col)	66	96	100	Passeriformes	51

Table S6. Continued

Methods	Parameter & Analyses[a]	PP (BS%) All taxa[b]	-Col[c]	PPFC (BS%) All taxa	-Col	CPBT All taxa	-Col	Coliiformes-sister Sister clade	BS%
	ep0.01_ML	**34**	66	41(+Col)	69	93	100	PP	27
	ep0.01_MLp	25(+Col)	55	62(+Col)	75	95	99	Psittaciformes	34
	SA_MLp	26(+Col)	62	54(+Col)	80	94	99	Psittaciformes	42
	LZ_MLp	No	35	68(+Col)	84	90	99	Psittaciformes	43
	BR_MLp	33(+Col)	39	60(+Col)	74	92	99	Psittaciformes	46
	HA_MLp	43	58	40	74	90	100	CPBT	45
SATe_Prank	MLp	No	50	**34**	81	94	99	PPFC	53
	SA_MLp	80(+Col)	89	64(+Col)	92	99	100	Psittaciformes	68
	LZ_MLp	49	51	No	No	58	100	CPBT	85
	BR_MLp	45	58	54(+Col)	74	79	99	Falconidae	18
	HA_MLp	No	No	45	87	93	100	CPBT	61
SATe_Mafft	MLp	56(+Col)	63	58(+Col)	71	98	99	Passeriformes	37
	SA_MLp	52	86	72(+Col)	88	88	100	PP	51
	LZ_MLp	61	75	40	77	88	98	CPBT	59
	BR_MLp	70	83	39	66	89	99	CPBT	65
	HA_MLp	81	93	46	92	94	100	CPBT	48
Muscle	MLp	45(+Col)	58	71(+Col)	78	96	99	Psittaciformes	49
T-coffee	MLp	62	80	36	86	86	98	PPFC	63
ClustalW2	MLp	No	No	No	No	No	No	Psittaciformes	93
% Analyses with clade		65%	90%	41%	90%	88%	98%	31%[f]	
Concatenated 49 loci	28taxa_ML	78	92	83	100	79	100	CPBT	63
	28taxa_MLp	69	90	79	100	86	100	CPBT	56
Menura[d]	23taxa_ML	79	94	85	100	80	100	CPBT	62
Menura + Acanthisitta[e]	24taxa_ML	62	88	74	100	83	100	CPBT	59

NOTE.—PP: Passeriformes-Psittaciformes, PPFC: Passeriformes-Psittaciformes-Falconidae-Cariamidae, CPBT: Coraciiformes-Piciformes-Bucerotiformes-Trogoniformes, PPF: Passeriformes-Psittaciformes-Falconidae.
[a]12: gaprate=0.01, gapextension=0.2. 55: gaprate=0.05, gapextension=0.5. op1: gap open penalties = 1, op3: gap open penalties = 3, ep0.01: gap extension penalties=0.01. SA: guide tree based on Sibley and Ahlquist (1990) topology, LZ: guide tree based on Livezey and Zusi (2007) topology, BR: guide tree based on Brown et al. (2008) topology, HA: guide tree based on Hackett et al. (2008) topology. ML: unpartitioned ML analyses, MLp: partitioned ML analyses.

[b] Bold numbers represent that potential clades are supported by bootstrap analyses but not shown in the optimal ML trees. +Col: Coliiformes are included in the potential clades. The numbers outside the parenthesis represent the bootstrap support for the specific clades including Coliiformes.
[c] -Col: Analyses based on dataset that excluded Coliiformes.
[d] Dataset has only *Menura* representing Passeriformes.
[e] Dataset has *Menura + Acanthisitta* representing Passeriformes.
[f] Percentage of analyses where Coliiformes sister to CPBT.

Table S7. Substitution saturation and compositional heterogeneity test

	Substitution Saturation test[a]				Compositional Hetergeneity[c]	
	I_{ss}	$I_{ss.c}$	P	Category[b]	χ^2 (P)	RCV
ADAM10	0.32	0.62	0.00	A	0.925	0.046
ANRTL	0.32	0.54	0.00	A	1.000	0.041
CALB1	0.24	0.68	0.00	A	1.000	0.047
CLTCL1	0.27	0.65	0.00	A	0.999	0.054
CSDE1	0.26	0.58	0.00	A	1.000	0.042
CSNK1E	0.30	0.52	0.00	A	1.000	0.043
DDX5	0.39	0.49	0.01	A	0.999	0.053
E1F5	0.35	0.37	0.81	**B**	0.993	0.049
ENO1	0.28	0.13	0.14	**D**	**0.019**	**0.089**
GRIA2	0.29	0.63	0.00	A	0.396	0.051
GTF3C3	0.27	0.44	0.00	A	0.995	0.046
HNRPA2B1	0.38	0.42	0.46	**B**	1.000	0.056
KCNQ5	0.29	0.60	0.00	A	0.646	**0.062**
OPN1LW	0.28	0.59	0.00	A	0.972	0.053
PARK7	0.18	0.10	0.10	**D**	0.990	0.048
PDE6B	0.32	0.68	0.00	A	1.000	0.042
PER2	0.34	0.48	0.00	A	1.000	0.037
POLL	0.25	0.29	0.27	**B**	1.000	0.046
PPP2CB	0.31	0.38	0.19	**B**	0.674	**0.060**
PRDX6	0.39	0.22	0.00	**C**	0.739	0.048
PSMA2	0.28	0.55	0.00	A	0.522	**0.067**
SBDS	0.35	0.38	0.49	**B**	0.219	**0.062**
SEPT2	0.21	0.60	0.00	A	0.996	0.054
SH3GLB2	0.29	0.58	0.00	A	1.000	0.037
SRSF3[d]	0.24	0.53	0.00	A	**0.014**	**0.090**
SUCLG1	0.25	0.59	0.00	A	1.000	0.044
SURF1	0.30	0.50	0.00	A	0.653	**0.076**

Table S7. Continued

	Substitution Saturation test[a]				Compositional Hetergeneity[c]	
	I_{ss}	$I_{ss.c}$	P	Category[b]	χ^2 (P)	RCV
TXNDC12	0.27	0.51	0.00	A	0.998	0.058
VDAC2	0.30	0.63	0.00	A	0.999	0.047
VIM	0.29	0.61	0.00	A	0.941	0.053

NOTE.—[a] Parameters are based on Xia et al. (2003).
[b] A: Little saturation, B: Substantial saturation, C: Useless sequences, D: Very poor for phylogenetics.
[c] Bold numbers represent loci that either failed compositional homogeneity χ^2 test or were among the upper quartile of RCV values.
[d] NJ tree of SRSF3 based on base-compositional distances showed a clade with all members of passerines and parrots, and *Bucorvus*.

Table S8. Branch length estimates for members of Neoaves.

Taxon	Order/Family	Total Branch Length Estimate[a]				
		Mean	SA Tree	LZ Tree	HA Tree	BR Tree
Upupa epops	Bucerotiformes	**0.2526**	**0.2495**	**0.2549**	**0.2549**	**0.2526**
Regulus calendula	Passeriformes	**0.2137**	**0.2110**	**0.2163**	**0.2182**	**0.2137**
Taeniopygia guttata	Passeriformes	**0.2093**	**0.2069**	**0.2113**	**0.2139**	**0.2093**
Capito niger	Piciformes	**0.1965**	**0.1924**	**0.1974**	**0.2008**	**0.1965**
Smithornis rufolateralis	Passeriformes	**0.1805**	0.1752	**0.1930**	**0.1813**	**0.1805**
Colius colius	Coliiformes	**0.1805**	**0.1760**	**0.1833**	**0.1829**	**0.1805**
Urocolius indicus	Coliiformes	**0.1796**	**0.1753**	0.1824	**0.1818**	**0.1796**
Tyrannus tyrannus	Passeriformes	0.1790	0.1739	**0.1916**	0.1796	0.1790
Acanthisitta chloris	Passeriformes	0.1710	**0.1814**	0.1727	0.1695	0.1710
Rallus limicola	Gruiformes	0.1671	0.1678	0.1628	0.1659	0.1671
Bucco macrodactylus	Piciformes	0.1664	0.1627	0.1683	0.1697	0.1664
Coua cristata	Cuculiformes	0.1536	0.1530	0.1558	0.1499	0.1536
Menura novaehollandiae	Passeriformes	0.1483	0.1456	0.1512	0.1526	0.1483
Momotus momota	Coraciiformes	0.1430	0.1395	0.1454	0.1460	0.1430
Trogon personatus	Trogoniformes	0.1420	0.1408	0.1435	0.1438	0.1420
Crotophaga sulcirostris	Cuculiformes	0.1375	0.1369	0.1397	0.1339	0.1375
Nestor notabilis	Psittaciformes	0.1333	0.1302	0.1332	0.1358	0.1333
Cacatua sulphurea	Psittaciformes	0.1298	0.1266	0.1297	0.1323	0.1298
Bucorvus abyssinia	Bucerotiformes	0.1239	0.1211	0.1256	0.1268	0.1239
Coracias caudata	Coraciiformes	0.1232	0.1194	0.1254	0.1261	0.1232
Falco mexicanus	Falconidae	0.1142	0.1130	0.1126	0.1174	0.1142
Aegotheles insignis	Caprimulgiformes	0.1129	0.1131	0.1162	0.1073	0.1129
Steatornis caripensis	Caprimulgiformes	0.1018	0.1019	0.1052	0.0963	0.1018
Grus canadensis	Gruiformes	0.0874	0.0898	0.0843	0.0845	0.0874
Herpetotheres cachinnans	Falconidae	0.0827	0.0814	0.0811	0.0861	0.0827
Cariama cristata	Cariamidae	0.0782	0.0781	0.0735	0.0821	0.0782

NOTE.—[a] Total branch length estimates are the sum of all branch lengths from the base of Neoaves to the indicated tip. Branch lengths are ML estimates obtained using the GTR+Γ model in PAUP* and the indicated topologies (or the mean of the branch length estimates for each topology). Rate estimates in the upper quartile are emphasized in bold and passerines are presented in red.

Table S9. Analyses of the PPFC clade using divergent outgroups support the PP clade.

Outgroup	Passerine taxon sample	Wang et al. data matrix (30 loci)		Combined data matrix (49 loci)	
		Topology[a]	Bootstrap support for PP clade	Topology	Bootstrap support for PP clade
Upupa	All taxa	((PP)(FC))	51%	((PP)(FC))	84%
	Acanthisitta + Menura	((PP)(FC))	48%	((PP)(FC))	78%
	Menura	((PP)(FC))	66%	((PP)(FC))	84%
Gallus	All taxa	(((PP)C)F)	51%	(((PP)C)F)	92%
	Acanthisitta + Menura	((PP)(FC))	51%	((PP)(FC))	91%
	Menura	(((PP)C)F)	69%	(((PP)C)F)	93%

NOTE.— [a] PP: Passeriformes-Psittaciformes, F: Falconidae, C: Cariamidae

Table S10. Representatives of leaf stability test using 500 bootstrap results of different programs.

Taxon	Manual	Mafft	M^a BR	M^a SA	M^a LZ	M^a HA	P^b BR	P^b SA	P^b LZ	P^b HA	SATé M^a	SATé P^b	Tcoffee	Muscle
Gallus	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93
Chauna	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93	0.93
Bucorvus	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.90	0.88	0.92	0.90	0.89	0.88	0.90
Upupa	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.90	0.88	0.92	0.90	0.89	0.88	0.90
Aegotheles	0.84	0.78	0.85	0.83	0.81	0.83	0.80	0.77	0.78	0.86	0.81	0.80	0.84	0.80
Steatornis	0.84	0.78	0.85	0.83	0.81	0.83	0.80	0.77	0.78	0.86	0.81	0.80	0.84	0.80
Cariama	0.77	0.71	0.74	0.75	0.79	0.71	**0.72**	**0.75**	**0.74**	0.82	**0.73**	0.76	0.74	0.77
Colius	**0.68**	**0.70**	**0.74**	**0.71**	**0.74**	**0.71**	0.82	0.78	0.84	**0.74**	0.80	**0.67**	**0.68**	**0.76**
Urocolius	**0.68**	**0.70**	**0.74**	**0.71**	**0.74**	**0.71**	0.82	0.78	0.84	**0.74**	0.80	**0.67**	**0.68**	**0.76**
Coracias	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.90	0.88	0.92	0.90	0.89	0.88	0.90
Momotus	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.90	0.88	0.92	0.90	0.89	0.88	0.90
Coua	0.83	0.79	0.82	0.80	0.81	0.84	0.81	0.77	0.78	0.86	0.80	0.80	0.81	0.81
Crotophaga	0.83	0.79	0.82	0.80	0.81	0.84	0.81	0.77	0.78	0.86	0.80	0.80	0.81	0.81
Falco	0.82	0.79	0.83	0.84	0.83	0.79	0.82	0.81	0.76	0.87	0.84	0.83	0.80	0.84
Herpetotheres	0.82	0.79	0.83	0.84	0.83	0.79	0.82	0.81	0.76	0.87	0.84	0.83	0.80	0.84
Grus	0.79	0.77	0.82	0.81	0.78	0.82	0.79	0.78	0.79	0.85	0.81	0.81	0.81	0.82
Rallus	0.79	0.77	0.82	0.81	0.78	0.82	0.79	0.78	0.79	0.85	0.81	0.81	0.81	0.82
Acanthisitta	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Menura	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Regulus	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Smithornis	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Taeniopygia	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Tyrannus	0.88	0.87	0.89	0.89	0.89	0.88	0.89	0.88	0.87	0.92	0.90	0.88	0.88	0.90
Bucco	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.89	0.88	0.92	0.90	0.89	0.88	0.90
Capito	0.90	0.87	0.90	0.90	0.91	0.88	0.89	0.89	0.88	0.92	0.90	0.89	0.88	0.90
Cacatua	0.84	0.80	0.84	0.86	0.84	0.85	0.86	0.85	0.84	0.92	0.87	0.85	0.87	0.86
Nestor	0.84	0.80	0.84	0.86	0.84	0.85	0.86	0.85	0.84	0.92	0.87	0.85	0.87	0.86
Trogon	0.89	0.86	0.89	0.89	0.91	0.87	0.88	0.90	0.86	0.91	0.90	0.88	0.87	0.90

NOTE.—[a] M: Mafft, [b] P: Prank. Bold numbers represent the lowest scores of each leaf stability test.
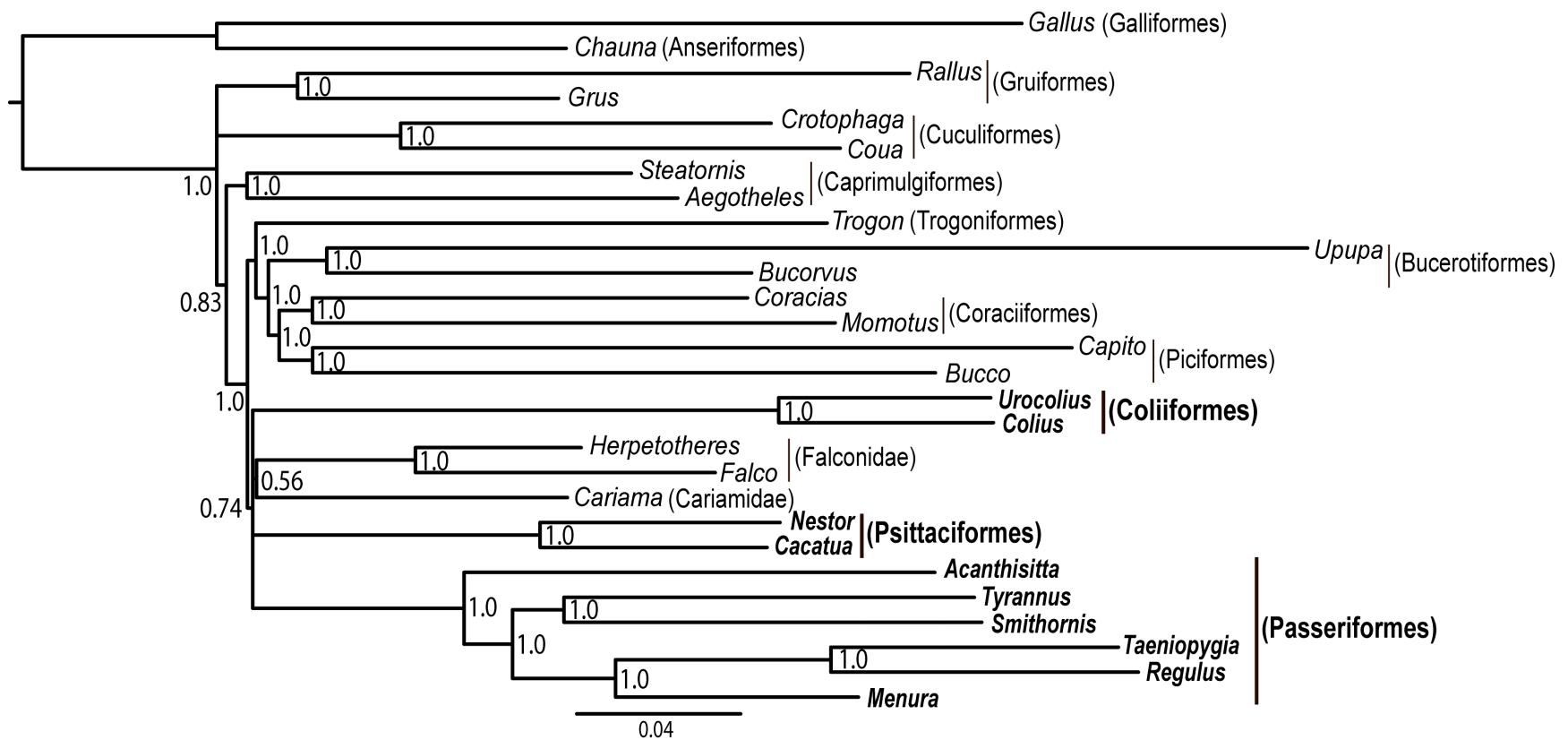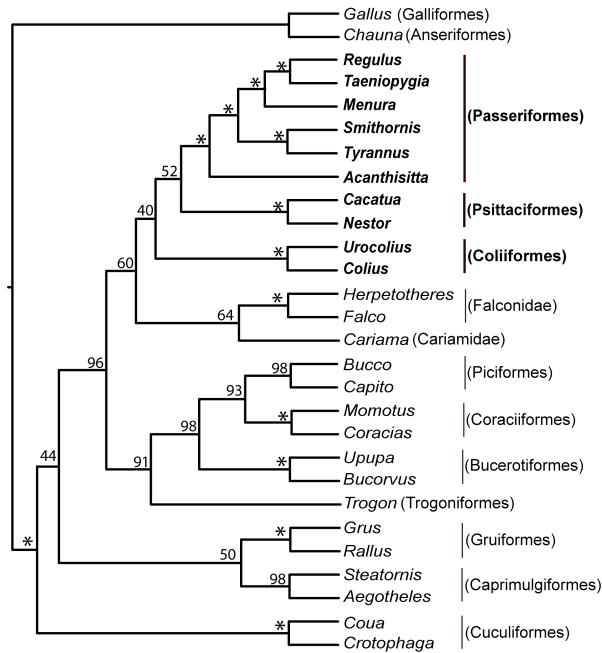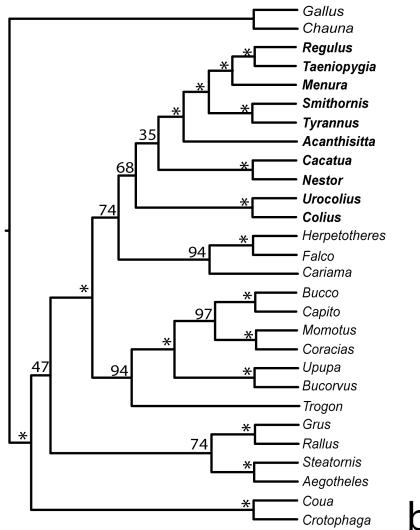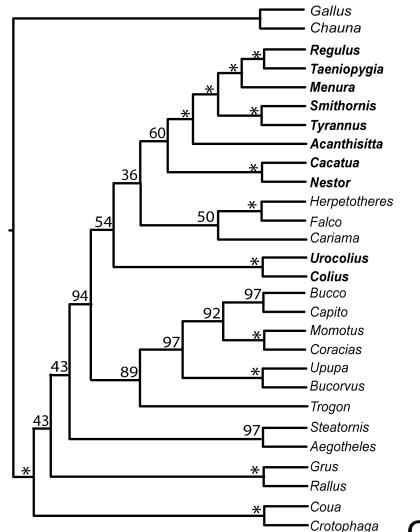
FIG. S1. Phylobayes analyses of the manual alignment using the QMM model. Values at the nodes represent the posterior probability (only values >0.5 are shown).

FIG. S2. Majority rule consensus trees based on the trees that generated in this study.
a: Consensus of all trees (n=106). b: Consensus of trees based upon alignments filtered using Gblocks (n=34). c: Consensus trees from analyses of complete data matrices (n=72). Numbers at nodes represent percentage of trees that support that clade.
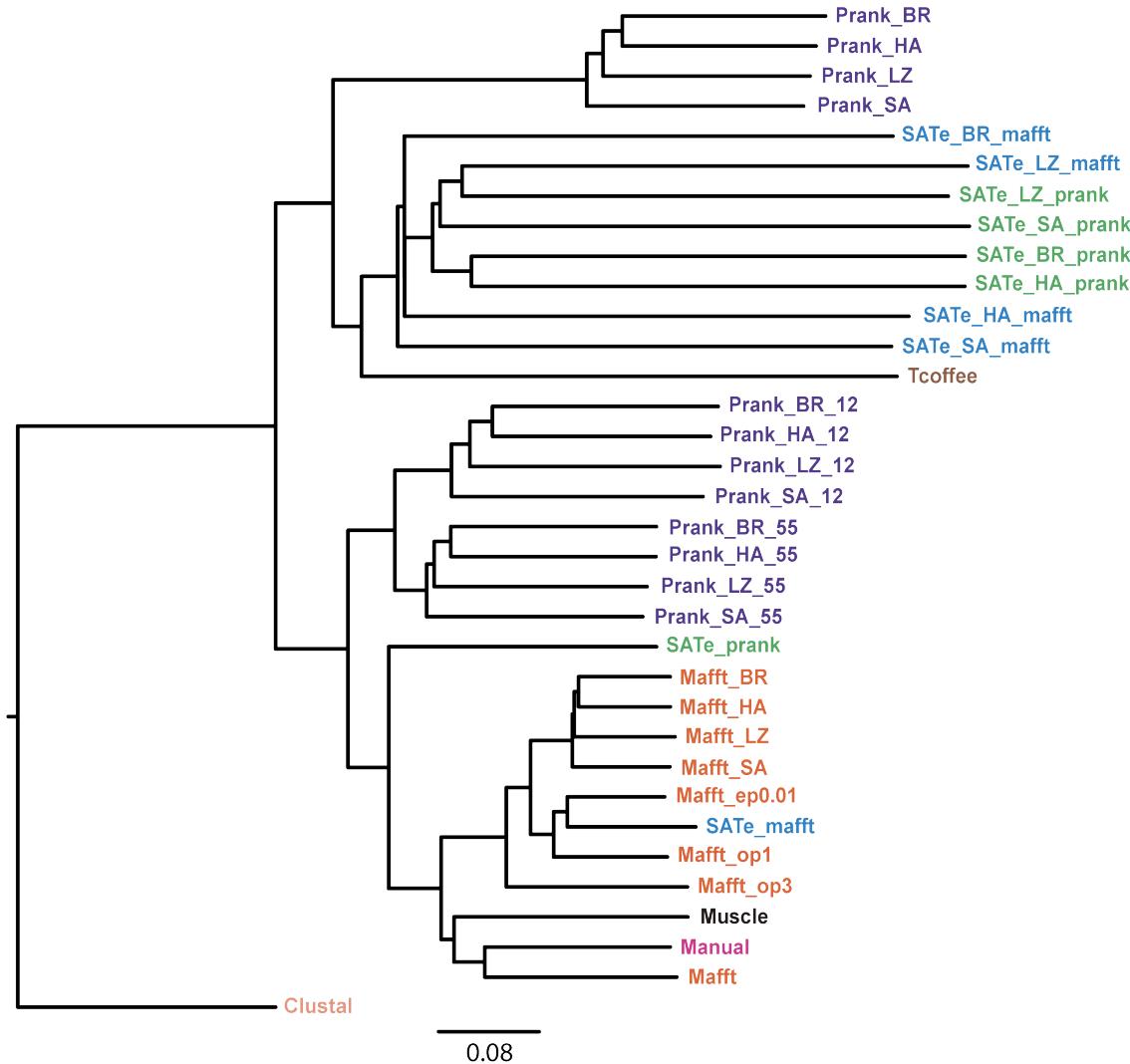
FIG. S3. Neighbor joining of alignment distances. Different colors represent the different alignment methods.
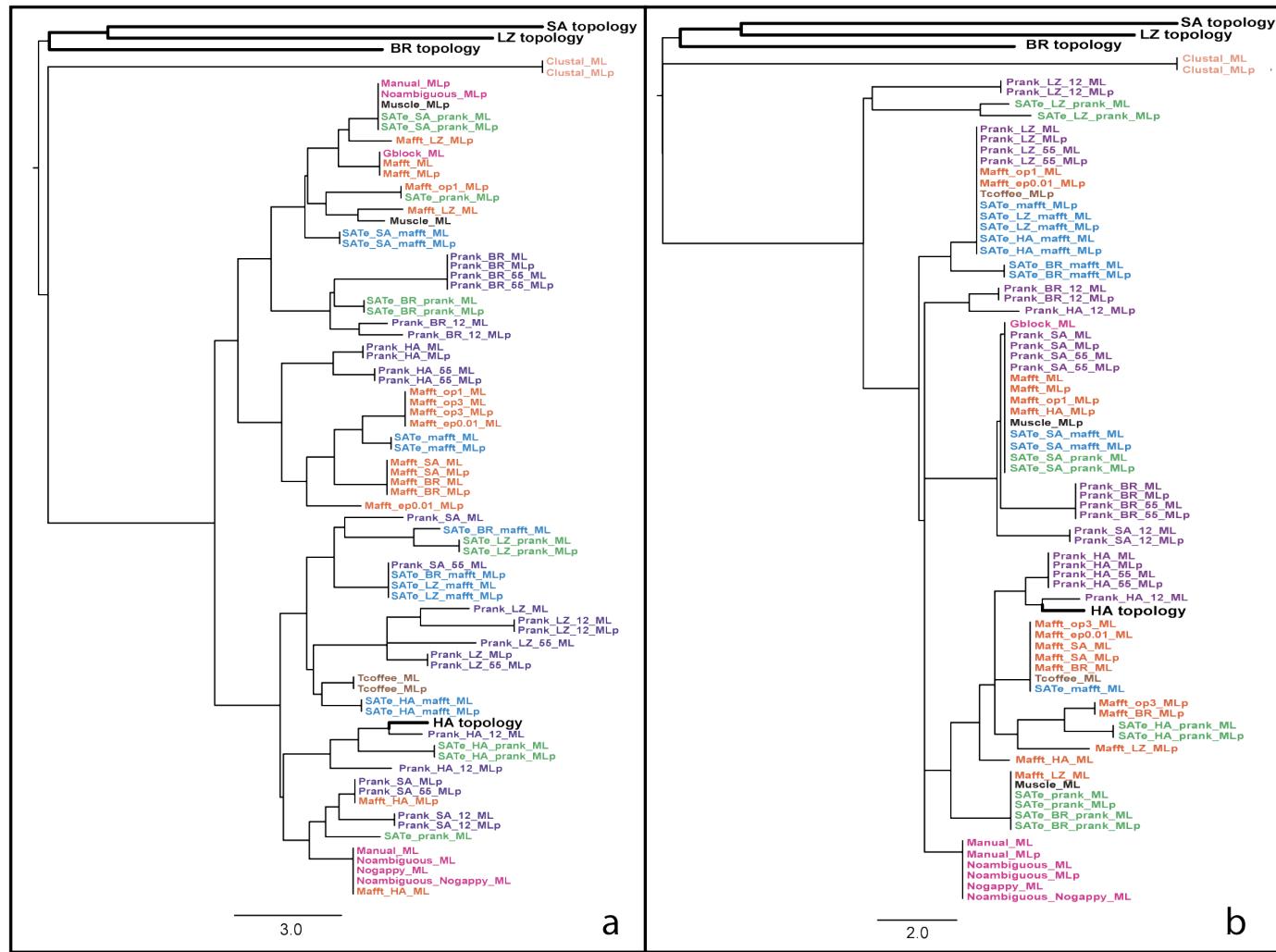
FIG. S4. Neighbor joining clustering of different analyses based on RF distances.
a: Datasets contain all 28 taxa. b: Datasets contain 26 taxa (excluding Coliiformes). Different colors represent different alignment methods.