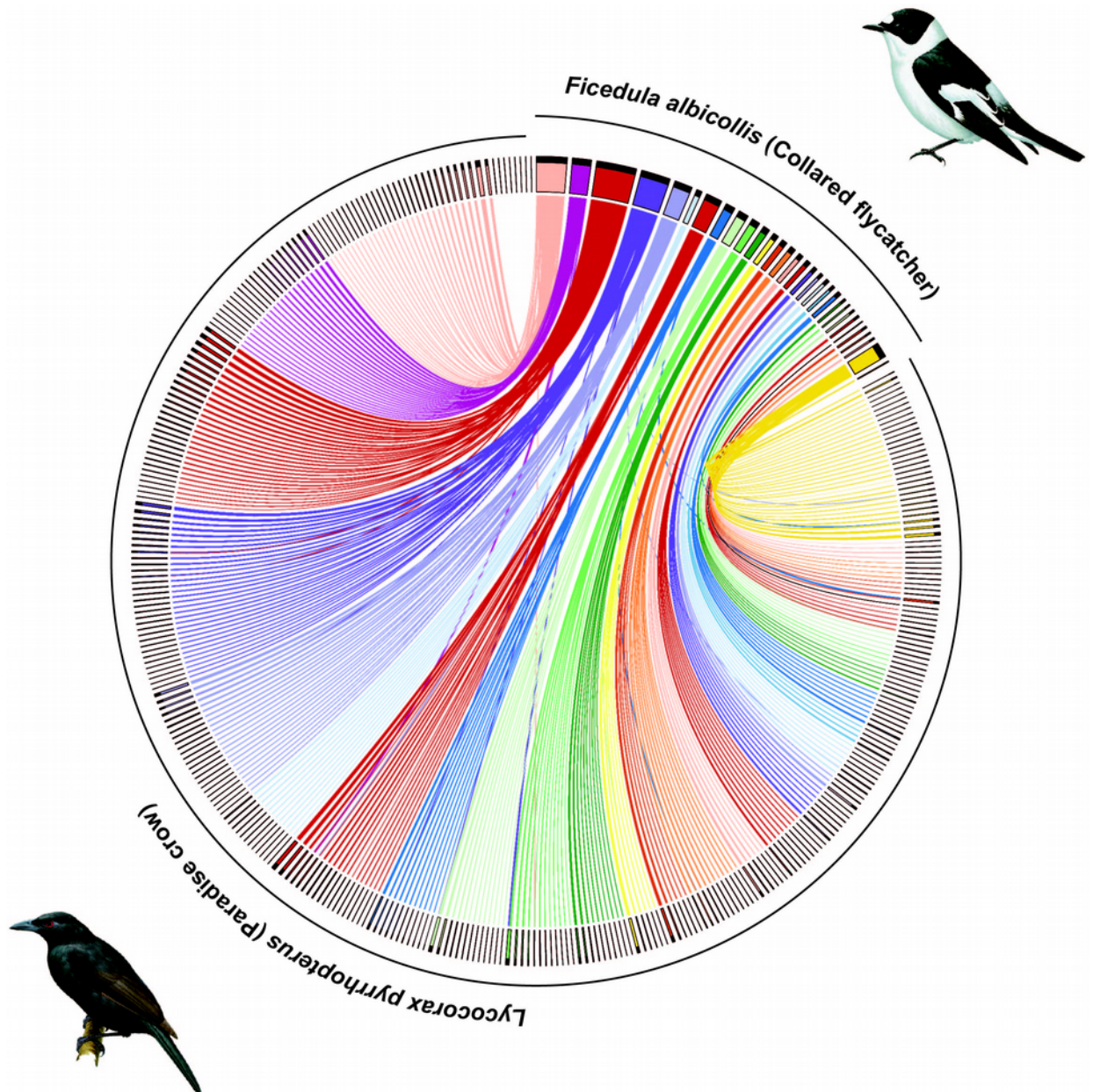
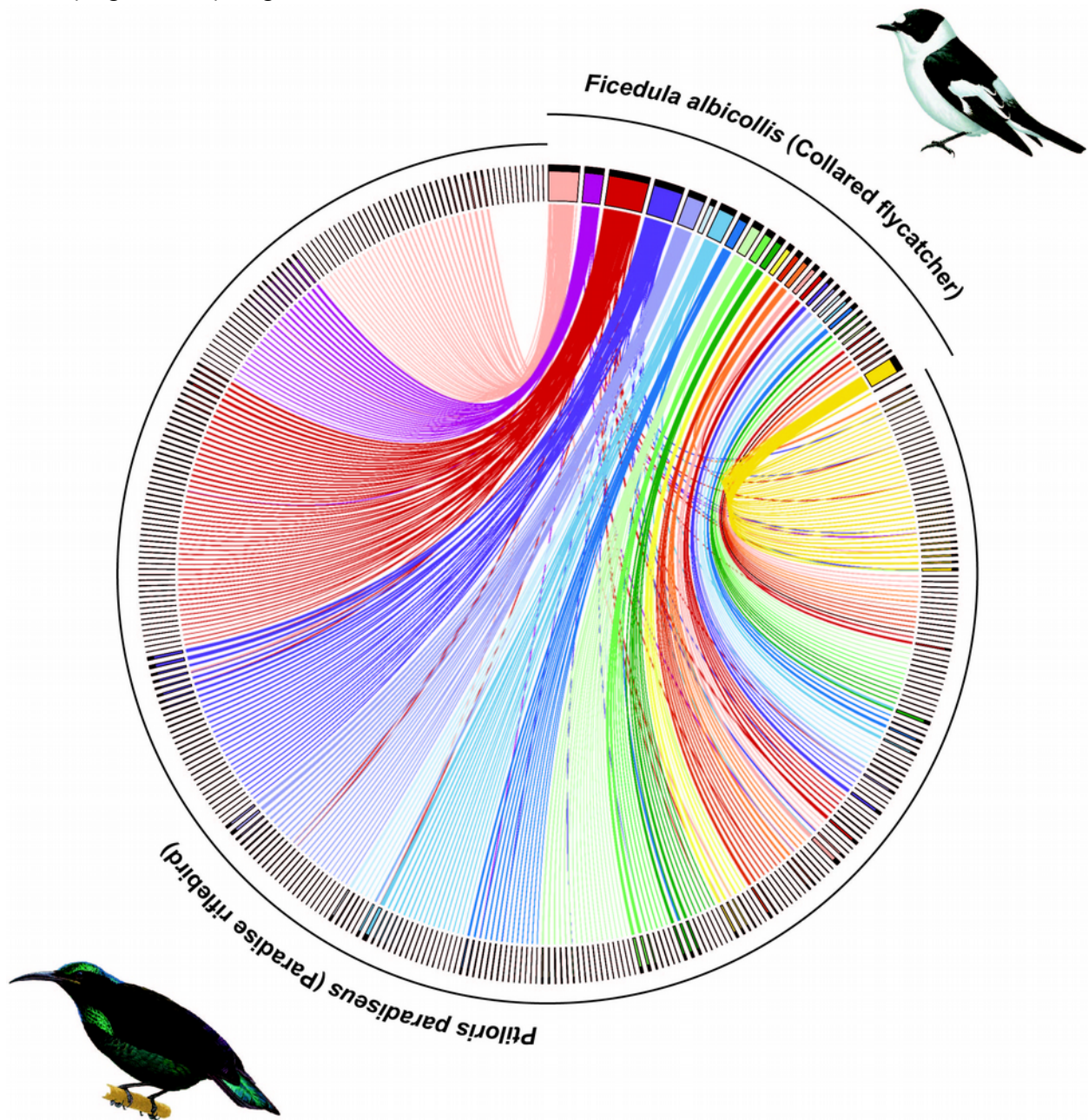


Supplementary

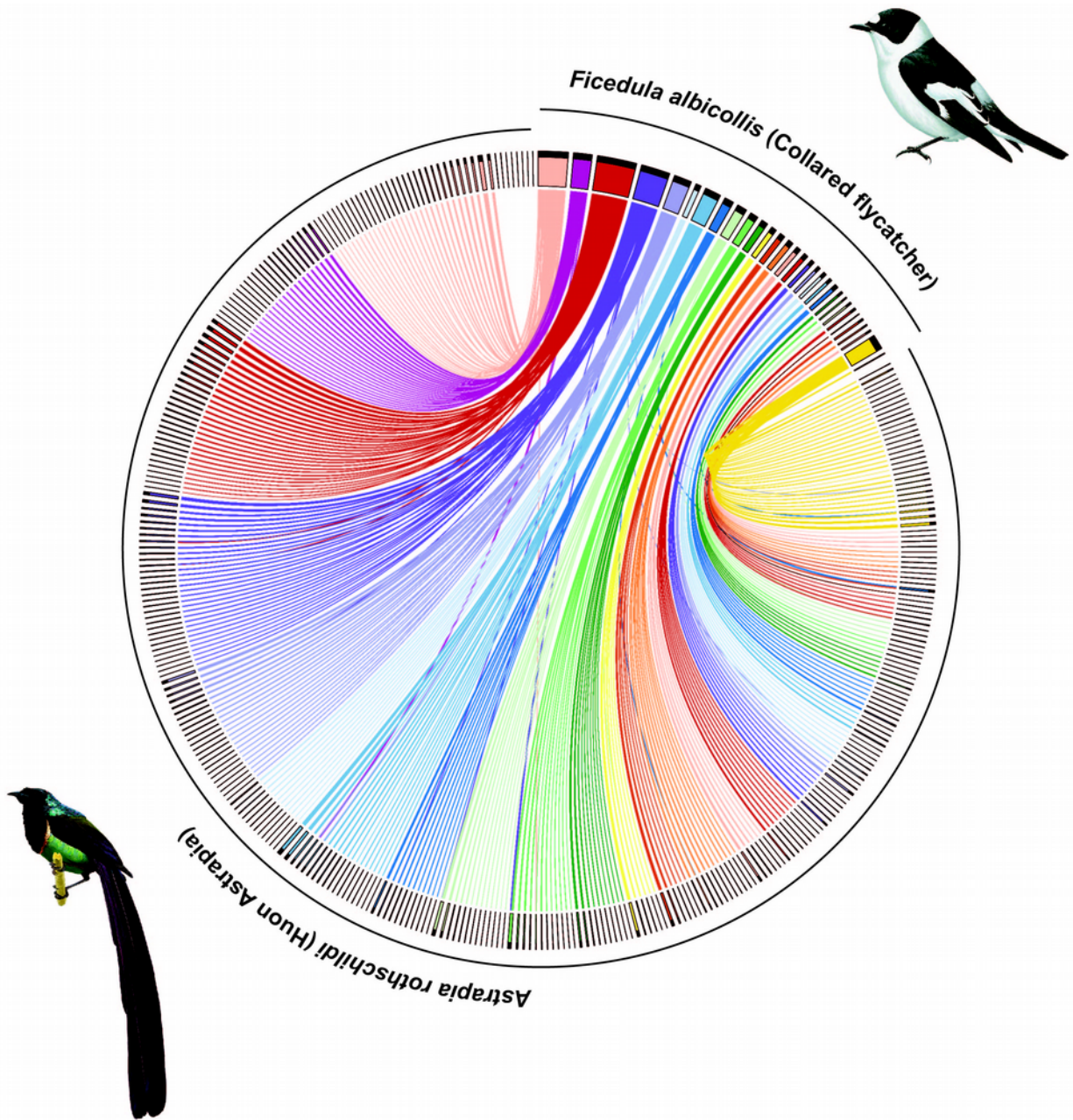
Supplementary Figures



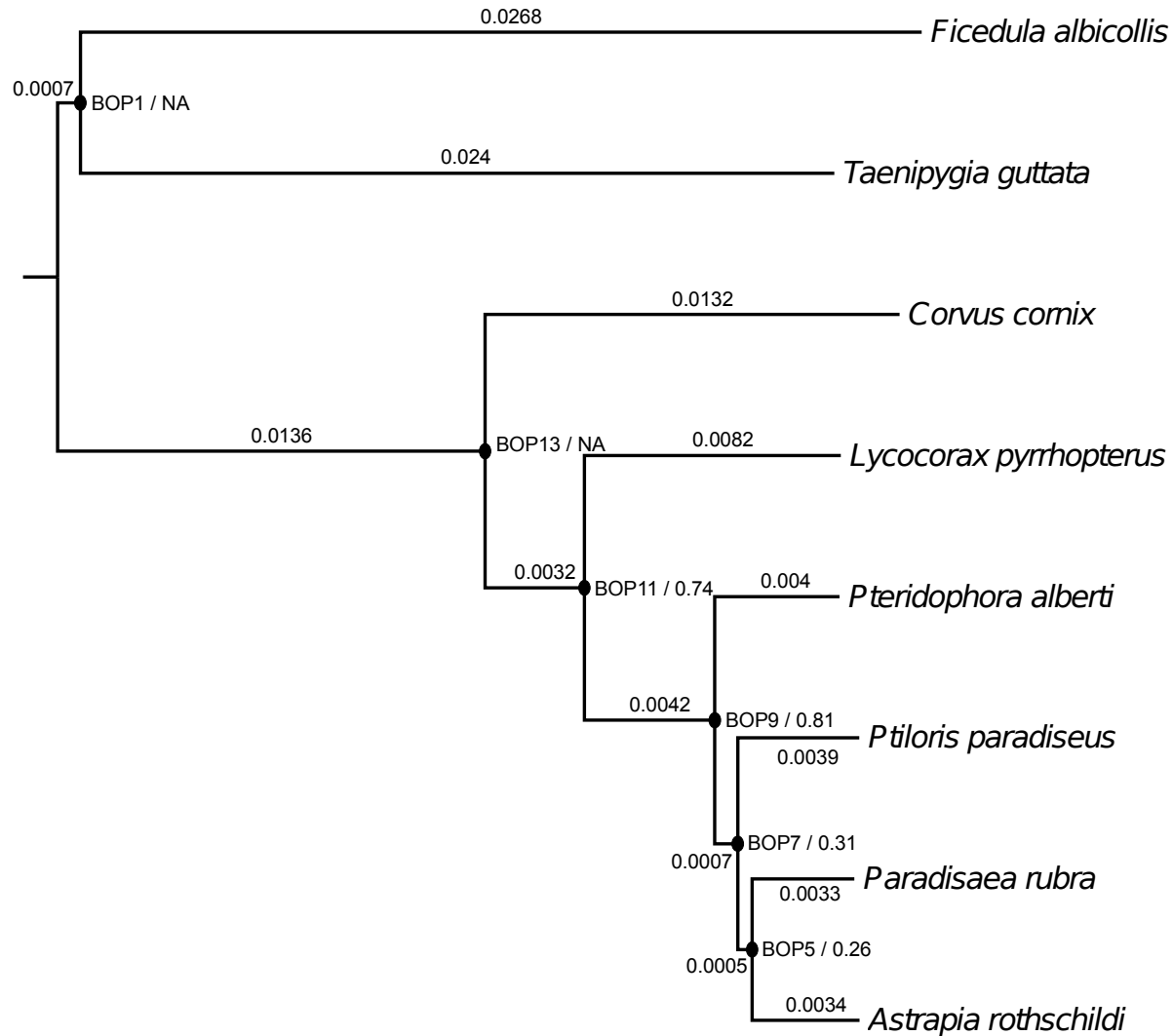
Supplementary Figure S1: Chromosomal synteny plot between the collared flycatcher and the paradise crow. The plot shows scaffolds larger than 50 kb and links (alignments) larger than 2 kb.



Supplementary Figure S2: Chromosomal synteny plot between the collared flycatcher and the paradise riflebird. The plot shows scaffolds larger than 50 kb and links (alignments) larger than 2 kb.



Supplementary Figure S3: Chromosomal synteny plot between the collared flycatcher and the Huon Astrapia. The plot shows scaffolds larger than 50 kb and links (alignments) larger than 2 kb.



Supplementary Figure S4: Phylogenetic species tree. The species tree was reconstructed from individual maximum likelihood-based gene trees using 4,656 exons and coalescent-based statistical binning (Astral). Branch lengths are depicted on the branches (calculated via a ML tree constructed using ExaML and 200 randomly selected genes). Nodes are labeled and concordance factor is shown next to the node labels (i.e. [node label] / [concordance factor]). All nodes have 100 bootstrap support.

Supplementary Tables

Supplementary Table S1: BUSCO scores. Scores were calculated using Busco2 and the aves_odb9 data set (4,915 genes total).

	Complete	Duplicated	Fragmented	Missing
<i>Astrapia rothschildi</i>	4,669 (95.0%)	48 (1.0%)	139 (2.8%)	107 (2.2%)
<i>Lycocorax pyrrhopterus</i>	4,659 (93.8%)	51 (1.0%)	161 (3.3%)	95 (1.9%)
<i>Ptiloris paradiseus</i>	4,675 (95.1%)	44 (0.9%)	135 (2.7%)	105 (2.2%)
<i>Paradisaea rubra</i>	4,662 (94.9%)	47 (1.0%)	150 (3.1%)	103 (2.0%)
<i>Pteridophora alberti</i>	4,661 (94.8%)	39 (0.8%)	155 (3.2%)	99 (2.0%)

Supplementary Table S2: Gene annotation.

	# of Transcripts	Average transcript size (bp)	Average introns size (kb, rounded)	Average # of introns per gene
<i>Astrapia rothschildi</i>	16,260	1,603	2.2	9
<i>Lycocorax pyrrhopterus</i>	17,023	1,572	2.2	9
<i>Ptiloris paradiseus</i>	17,269	1,584	2.2	9
<i>Paradisaea rubra</i>	16,822	1,561	2.2	9
<i>Pteridophora alberti</i>	16,721	1,562	2.2	9

Supplementary Table S3: RepeatMasker annotation of the three birds-of-paradise genome assemblies using a library of our *de novo* repeat annotations of birds-of-paradise merged with existing avian repeat libraries.

	<i>Astrapia rothschildi</i>			<i>Lycocorax pyrrhopterus</i>			<i>Ptiloris paradisaeus</i>		
Repeat type	Copies	Total bp	Total %	Copies	Total bp	Total %	Copies	Total bp	Total %
SINE	8,019	966,992	0.09	7,974	955,190	0.09	7,977	961,945	0.09
LINE	128,473	38,885,201	3.67	130,706	40,271,136	3.76	129,094	38,994,767	3.68
LTR	38,693	20,692,445	1.95	48,395	27,819,221	2.60	39,123	21,311,765	2.01
DNA	4,582	790,017	0.07	4,734	845,120	0.08	4,617	790,421	0.07
Unclassified	34,049	9,005,494	0.85	37,519	9,167,482	0.86	30,814	8,931,323	0.84
Total interspersed repeats	213,816	70,340,149	6.63	229,328	79,058,149	7.39	211,625	70,990,221	6.69
Small RNA	538	46,523	0.00	577	50,738	0.00	546	47,744	0.00
Satellites	2,884	623,756	0.06	2,706	572,161	0.05	2,855	646,354	0.06
Simple repeats	195,600	9,348,199	0.88	193,765	9,101,884	0.85	197,648	9,318,098	0.88
Low complexity	43,076	2,388,544	0.23	42,067	2,292,784	0.21	42,546	2,360,570	0.22
Total tandem repeats	242,098	12,407,022	1.17	239,115	12,017,567	1.11	243,595	12,372,766	1.16
Total repeats	455,914	82,747,171	7.80	468,443	91,075,716	8.50	455,220	83,362,987	7.85
Assembly		1.06Gb			1.07Gb			1.06Gb	
Gap ('N') bp		13,196,877			10,466,138			10,993,394	

Supplementary Table S4: Characteristics of the manually curated TE consensus sequences from *Lycocorax pyrrhopterus*, including lineage-specific LTR families termed as 'lycPyrLTR*'.

Class	Sub-class	Superfamil	Family	Subfamily	Similarity to known repeats	Consensus status	Consensus length	TS
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Retrotransposo	LTR	ERV1	lycPyrLTR1	lycPyrLTR1	None	Complete	463	4
Retrotransposo	LTR	ERV1	lycPyrLTR2	lycPyrLTR2	None	Complete	535	4
Retrotransposo	LTR	ERV1	lycPyrLTR3	lycPyrLTR3	None	Complete	623	4
Retrotransposo	LTR	ERV1	TguERV3	TguERV3_LTR2b-L_lycPyr	Partially TguERV3_LTR2b (68% similarity)	Complete	601	4
Retrotransposo	LTR	ERV1	TguERV1	TguERV1_LTR1a-L_lycPyr	Partially TguERV1_LTR1a (72% similarity)	Complete	600	4
Retrotransposo	LTR	ERV1	TguLTR11	TguLTR11L-L_lycPyr.inc	Partially TguLTR11L + TguERV2_I + TguERV1_I + TguERV3_I (79% + 65% + 63% + 66% similarity)	Incomplete 3' end	4535	?
Retrotransposo	LTR	ERV1	TguLTR12	TguLTR12-L_lycPyr.inc	Partially TguLTR12 (84% similarity)	Incomplete	625	?
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK1a	None	Complete	366	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK1b	None	Complete	366	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK2	None	Complete	647	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK3a	None	Complete	689	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK3b	None	Complete	744	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK4	None	Complete	605	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK5	None	Complete	397	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK6	None	Complete	666	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK7	None	Complete	334	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK8	None	Complete	408	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK9_LT	None	Complete	380	6
Retrotransposo	LTR	ERV2	lycPyrLTRK	lycPyrLTRK9_I.inc	None	Incomplete 3' end	537	6

Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL1	None	Complete	1171	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL2	None	Complete	1105	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL3	None	Complete	460	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL4	None	Complete	807	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL5	None	Complete	1281	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL6	None	Complete	670	5
Retrotransposo	LTR	ERV3	lycPyrLTRL	lycPyrLTRL7.inc	Partially Tgu_rep3 (80% similarity)	Incomplete 3' end	177	?
Retrotransposo	LTR	ERV3	TguERVL2	TguERVL2b-LTR- L_lycPyr	Partially TguERVL2b3_LTR + TguERVL2b1_LTR (85% + 79% similarity)	Complete	579	5
Retrotransposo	LTR	ERV3	TguERVL2	TguERVL2a2- LTR-L_lycPyr	Partially TguERVL2a2- LTR (93% similarity)	Complete	941	5
Retrotransposo	LTR	ERV3	TguLTRL1	TguLTRL1- La_lycPyr	Partially TguLTRL1a7 (75% similarity)	Complete	647	5
Retrotransposo	LTR	ERV3	TguLTRL1	TguLTRL1- Lb_lycPyr.inc	Partially TguERVL1_I5' end TguLTRL1a6 + TguLTRL1a7 (88% + 77% + 74% similarity)	Incomplete	2729	?
Retrotransposo	LTR	ERV3	TguLTRL1	TguLTRL1- Lc_lycPyr.inc	Partially TguERVL1_I5' and TguERVL2_I + TguLTRL6b (80% + 78% + 97% similarity)	Incomplete 3' ends	1754	?
Retrotransposo	LTR	ERV3	TguLTRL1	TguLTRL1- Ld_lycPyr.inc	Partially TguLTRL1a63' end TguLTRL1a7 + TguLTRL1_I (77% + 75% + 75% similarity)	Incomplete	2655	?

Retrotransposo	LTR	ERV3	TguLTRL1	TguLTRL1-Le_lycPyr.inc	Partially TguLTRL1a75+ and TguERVL1_I (75% + 77% similarity)	Incomplete 3' ends	3079	?
Unknown	Unknow	Unknown	Unknown	lycPyr5-275.3inc	None 3' end	Incomplete	177	?
Unknown	Unknow	Unknown	Unknown	lycPyr5-1942.inc	None 5' and 3' ends	Incomplete	620	?
Unknown	Unknow	Unknown	Unknown 947.inc_sat	lycPyr6-	None 5' and 3' ends	Incomplete	3602	?

Supplementary Table S5: Top 10 gene tree topology counts (423 total topologies in 4,450 rooted gene trees). Average Robinson-Foulds distance for all 4,656 gene trees is 3.92. Z: zebra finch; F: collared flycatcher; C: hooded crow; L: *Lycocorax*; Pte: *Pteridophora*; Pti: *Ptiloris*; Par: *Paradisaea*; A: *Astrapia*.

Topology	Count
((Z,F),(C,(L,(Pte,(Pti,(Par,A))))))	430
((Z,F),(C,(L,(Pte,((Pti,Par),A))))	357
((Z,F),(C,(L,(Pte,(Par,(Pti,A))))))	279
((Z,F),(C,(L,(Pti,(Pte,(Par,A))))))	224
((Z,F),(C,(L,((Pti,Par),(Pte,A))))	167
((Z,F),(C,(L,(Pti,((Pte,Par),A))))	166
((Z,F),(C,(L,(((Pti,Par),Pte),A))))	162
((Z,F),(C,(L,((Pte,Pti),(Par,A))))	161
((Z,F),(C,(L,((Pti,(Pte,Par)),A))))	159
((Z,F),(C,(L,(Pti,(Par,(Pte,A))))))	156

Supplementary Table S6: Saturation Analysis. Pairwise dN/dS ratio.

Astrapia							
Corvus	0.036						
Ficedula	0.046	0.063					
Taeniopygia	0.044	0.059	0.046				
Lycocorax	0.014	0.037	0.046	0.044			
Paradisaea	0.006	0.034	0.046	0.043	0.014		
Pteridophora	0.007	0.036	0.046	0.044	0.014	0.007	
Ptiloris	0.006	0.036	0.046	0.044	0.014	0.006	0.007

Supplementary Table S7. Genes under positive selection. Gene symbols in bold mark genes significant after multiple-testing correction using FDR (<0.05 cut-off).

GenBank Accession	Gene Symbol
XM_016302299.1	RSPH14
XM_005060676.1	SNX18
XM_005061576.2	RSG1
XM_016299097.1	COL4A1
XM_016304880.1	MCTP1
XM_016303427.1	FGD6
XM_005042552.1	NDRG1
XM_005062657.1	MRPL34
XM_005057187.1	BPIFB2
XM_010403165.3	C8orf48
XM_016298377.1	LOC101809528
XM_005057074.2	LOC101821424
XM_010401845.3	camC
XM_016301269.1	LOC101807976
XM_016302077.1	TRAFD1
XM_005048141.1	SH2D4B
XM_005044853.1	MGARP
XM_005039384.1	ADAMTS20
XM_005037072.1	TAF10
XM_005054309.2	C14H16orf71
XM_005056583.1	EVI2A
-	guaA
XM_005038551.2	CCDC181
XM_016298245.1	COL4A5
XM_005059334.2	LAD1
XM_016301828.1	LOC101813372
XM_019280702.1	act-2b
XM_016296212.1	AGAP3
XM_005051230.1	FETUB
XM_005043410.1	POLH
XM_004175487.1	CORIN
XM_019282258.2	Slc30a10
XM_005054364.2	DRC3

-	PRP5
XM_016300815.1	ZWILCH
XM_005043438.1	WDR27
XM_005058894.2	S100A11
XM_005046922.2	C5H11orf74
XM_016306090.1	SLC9A2
XM_005050076.2	LOC101808676
XM_016300582.1	ATP7B
XM_005051988.2	TCF12
XM_016303963.1	LOC107604184
XM_005061593.1	LOC101821569
XM_016298934.1	ITPK1
XM_016302041.1	CARHSP1
XM_005049042.2	LOC101807582
XM_016303572.1	IDO2
XM_005052727.1	LOC101813437
XM_005047366.2	GPATCH2L
XM_005057073.2	WISP2
XM_016303591.1	ADD2
XM_005055863.2	PMP22
XM_005062304.2	IGSF21
XM_016305344.1	LOC101812147
XM_005050061.1	CABP4
XM_016298968.1	LOC101816855
XM_005056673.2	LOC101817428
XM_005056783.1	CBX2
XM_005056335.1	PTDSS1
XM_005042325.2	BARHL1
XM_005055795.1	HABP2
XM_005048773.2	SYTL1
XM_016303687.1	PAQR7
XM_016303706.1	CCDC89
XM_016301660.1	KIF3C
XM_016305278.1	PHLDA3
XM_005059500.2	PHLDA1
XM_016303529.1	LOC101807907
XM_016299105.1	GPX2
XM_005044014.1	TPBG
XM_005049721.1	LOC101813208
XM_005039251.1	RNASEL
XM_005049817.2	GPR88
XM_005050542.1	NEXMIF
XM_005045976.1	LOC101813871
XM_005061804.2	MOB3C
XM_005050079.2	ITPKB
XM_005043012.2	LOC101811548
XM_005061100.2	SLC12A3
XM_005052526.1	LOC101822159
XM_005060823.1	DOCK8
XM_005060810.2	SLC7A2
XM_016298010.1	G6PC2
XM_016299897.1	ZEB1
XM_005040638.2	CCDC149
XM_005045593.1	ALAD
XM_005055395.2	SPAG16
XM_005048989.2	HAUS1
XM_016299631.1	NCKAP1
XM_005060340.1	SLC25A27
XM_005037255.2	Atp6ap2
XM_005044316.2	PTPN11
XM_005055265.2	SLC25A10
XM_005056255.2	LOC101816285
XM_016298524.1	TSPAN9
XM_005061480.2	TCAF2
XM_005061498.2	ANXA11
XM_016299390.1	TAF11

XM_005059540.1	NCLN
XM_016304488.1	NR2E3
XM_010400678.3	MAML2
XM_005051635.1	P3H4
XM_005059699.2	GAB2
XM_005044075.1	Lyrm2
XM_005038313.1	AGL
XM_016300131.1	TERT
XM_005058028.2	PPP2R2A
XM_016296086.1	FGFR1
XM_016303624.1	GCN1
XM_005040177.1	PARVB
XM_005055228.2	LIMS1
XM_005037507.2	PAFAH1B2
XM_005058597.2	LOC101821368
XM_005060625.1	UBE2Q1
XM_005059102.1	MZT1
XM_016297193.1	B3GLCT
XM_005038138.1	PDS5B
XM_005038022.1	LMO4
XM_005049530.2	asic4
XM_016300038.1	RBP2
XM_005050724.1	CYFIP2
XM_010399761.3	Pdgfrb
XM_005053530.2	STRA8
XM_005039572.1	TAF4B
XM_016300054.1	SERBP1
XM_005041939.2	COLEC12
XM_005042040.1	TUBB6
XM_005042005.2	SH3PXD2A
XM_005048677.1	IDE
XM_005048419.2	DNAJB12
XM_005047986.2	GSTK1
XM_005042269.2	WWP1
XM_016301762.1	NAGPA
XM_005044724.2	PPM1K
XM_005038401.1	DNAL1
XM_005038091.1	ZDHHC20
XM_005062085.1	ASIC1
XM_005046991.1	MYOC
XM_005049866.1	PLPP6
XM_005050007.1	NHP2
XM_005053617.2	LOC101815973
XM_005042611.1	OSTN
XM_005051099.1	MECOM
XM_005051315.2	CDADC1
XM_016296125.1	SUGT1
XM_005037953.1	RPS25
XM_016303810.1	TCIRG1
XM_016299107.1	ACSS3
XM_005039906.1	MYF5
XM_016304331.1	ARAP2
XM_005045389.2	SPECC1L
XM_005045346.2	MAPK1
XM_005054795.1	LOC101809314
XM_005054910.2	IMPG1
XM_005043131.2	TSR3
XM_005049273.2	Osgepl1
XM_016297079.1	LOC101822112
XM_005054684.2	SLC22A2
XM_005043198.2	RAB26
XM_005043614.2	SH3BGR
XM_005054428.1	SDK1
XM_005054008.1	RUNX1
XM_005037142.2	RIPK4
XM_016298043.1	LOC101812359

XM_005037183.2	NACA
XM_005045614.1	CTSD
XM_005061387.2	ERH
XM_005046816.1	LOC101810161
XM_005047384.1	PAPSS2
XM_005040064.1	ATP10B
XM_005048086.1	SPATA5L1
XM_016301575.1	AKAP13
XM_016300850.1	CBLL1
XM_005051920.2	FGF7
XM_016300780.1	RELN
XM_005039138.2	GNG10
XM_016303057.1	GNB1
XM_016304620.1	LOC101817904
XM_005057597.2	TRH
XM_005038109.2	LOC101809883
XM_005048122.2	BMPRI1A_1
XM_005053334.1	ATIC
XM_005037520.1	KCND3
XM_005048986.2	LOC101810386
XM_005059186.1	LOC107603674
XM_005059571.1	LOC101813292
XM_016298945.1	TAF4
XM_005037873.2	HTR2A
XM_002194111.2	PRUNE1
XM_016298921.1	PKP3
XM_005057359.1	ALDH3A2
XM_016300832.1	TRPM7
XM_005046501.2	BAIAP2L2
XM_002190982.3	SEN1
XM_005056669.2	WDR12
XM_005046073.2	GJB1
XM_005039746.2	RFC1
XM_005049157.1	MTBP
XM_016298059.1	SPCS3
XM_016296127.1	RPRML
XM_005045169.1	RASGEF1A
XM_005059547.1	NTRK2
XM_005048151.2	APOBEC2
XM_016305207.1	ZCCHC7
XM_005059489.1	CENPK
XM_016304871.1	DNAH9
XM_016304884.1	DCST2
XM_010405265.2	Cox7a2
XM_016302782.1	DNAH9
XM_005059010.2	DCST2
XM_002192079.3	PI4KB

Supplementary Table S8: Summary of gene gain and loss events inferred after correcting for annotation and assembly error across all 13 species.

The number of rapidly evolving families is shown in parentheses for each type of change.

	Expansions			Contractions			No Change	Avg. Expansion
	Families	Genes gained	Genes/ expansion	Families	Genes lost	Genes/ contraction		
Paradisaea	248 (40)	297	1.2	209 (3)	215	1.03	8555	0.009323
Astrapia	314 (40)	398	1.27	455 (31)	543	1.19	8243	-0.016537
Ficedula	329 (23)	480	1.46	560 (7)	671	1.2	8123	-0.020977
Lycocorax	513 (16)	612	1.19	338 (2)	358	1.06	8161	0.027747
Taeniopygia	1463 (17)	2009	1.37	977 (7)	1040	1.06	6572	0.091565
Ptiloris	334 (49)	401	1.2	203 (5)	219	1.08	8475	0.020200
Pteridophora	241 (13)	274	1.14	297 (6)	309	1.04	8474	-0.002997
Corvus	362 (6)	480	1.33	1708 (45)	2050	1.2	6942	-0.172475

Supplementary Table S9: Assembly/Annotation error estimation and gene gain/loss rates in a single λ model in the 13 mammals included in this study compared to previous studies using fewer species.

	λ (No Error Model)	ε (Estimated error)	λ (Error Model = ε)
8 bird species in this study	0.00221	0.01025	0.00205
12 Drosophila species*	0.00121	0.04102	0.00059
10 mammal species*	0.00238	0.07324	0.00186
16 fungi species*	0.0008	0.02771	0.00061

* Dataset from Han et al. 2013 [1].

Supplementary Table S10: Enriched GO terms in rapidly evolving birds-of-paradise families. The number in parentheses for rapidly evolving lineages indicates the extent of change along that lineage (e.g. *Astrapia* (+6) means that the *Astrapia* lineage gained 6 genes). Lineages within the BOP clade are indicated by bold text. See Figure S1 for internal node labels.

Family ID	GO accession: GO name	Rapidly evolving lineages	Enriched after FDR correction?
1	GO:0001077: transcriptional activator activity, RNA polymerase II core promoter proximal region sequence-specific binding	Astrapia (+6) BOP13 (-17) BOP1 (+9) Taeniopygia (+36) Pteridophora (-4) Crow (-12)	*
1	GO:0001078: transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding	Astrapia (+6) BOP13 (-17) BOP1 (+9) Taeniopygia (+36) Pteridophora (-4) Crow (-12)	
1	GO:0000978: RNA polymerase II core promoter proximal region sequence-specific DNA binding	Astrapia (+6) BOP13 (-17) BOP1 (+9) Taeniopygia (+36) Pteridophora (-4) Crow (-12)	*
1	GO:0000977: RNA polymerase II regulatory region sequence-specific DNA binding	Astrapia (+6) BOP13 (-17) BOP1 (+9) Taeniopygia (+36) Pteridophora (-4) Crow (-12)	*
1	GO:0001223: transcription coactivator binding	Astrapia (+6) BOP13 (-17) BOP1 (+9) Taeniopygia (+36) Pteridophora (-4) Crow (-12)	
13	GO:0004984: olfactory receptor activity	Astrapia (+6) Lycocorax (-6) Taeniopygia (+17) BOP9 (+5) Crow (-9)	*
26	GO:0005200: structural constituent of cytoskeleton	BOP11 (-26) Ficedula (+16) BOP13 (-21) BOP1 (+12) Taeniopygia (+20) BOP9 (-3)	*
30	GO:0001948: glycoprotein binding	Paradisaea (+6) Astrapia (-3)	

30	GO:0005041: low-density lipoprotein receptor activity	Paradisaea (+6) Astrapia (-3)	
31	GO:0001964: startle response	Paradisaea (+3) BOP9 (+5)	
31	GO:0008344: adult locomotory behavior	Paradisaea (+3) BOP9 (+5)	*
36	GO:0005112: Notch binding	Ptiloris (+3)	*
39	GO:0005198: structural molecule activity	BOP9 (-3)	*
49	GO:0003777: microtubule motor activity	Astrapia (+3) Crow (+15)	*
65	GO:0004222: metalloendopeptidase activity	Astrapia (+4) Ptiloris (-3)	*
67	GO:0005216: ion channel activity	BOP11 (+4) Crow (-4)	*
76	GO:0001657: ureteric bud development	BOP11 (+3) Crow (-4)	*
97	GO:0003958: NADPH-hemoprotein reductase activity	Astrapia (+3)	*
97	GO:0004517: nitric-oxide synthase activity	Astrapia (+3)	*
97	GO:0005272: sodium channel activity	Astrapia (+3)	*
102	GO:0007155: cell adhesion	Ptiloris (-2) Crow (+6)	*
121	GO:0060348: bone development	Astrapia (-4)	
121	GO:0002091: negative regulation of receptor internalization	Astrapia (-4)	*
130	GO:0005201: extracellular matrix structural constituent	Paradisaea (+3)	
138	GO:0014719: skeletal muscle satellite cell activation	BOP5 (+1)	*
170	GO:0006955: immune response	Astrapia (-2) Taeniopygia (+8) Ptiloris (+2) BOP5 (-3) Crow (-4)	*
252	GO:0019992: diacylglycerol binding	BOP11 (+2) Pteridophora (+2)	*
290	GO:0030234: enzyme regulator activity	Paradisaea (-3)	
312	GO:0003956: NAD(P)+-protein-arginine ADP-ribosyltransferase activity	Paradisaea (+2) Ficedula (+5) Taeniopygia (-3) Ptiloris (+2) BOP7 (+1) Crow (-3)	
321	GO:0017112: Rab guanyl-nucleotide exchange factor	Ptiloris (-2)	*

	activity	Pteridophora (+2)	
477	GO:0050699: WW domain binding	BOP11 (+2)	
584	GO:0004415: hyaluronoglucosaminidase activity	Lycocorax (+4)	*
637	GO:0005149: interleukin-1 receptor binding	Astrapia (+2) BOP9 (-2)	*
836	GO:0017080: sodium channel regulator activity	Paradisaea (+3) BOP9 (-2)	
867	GO:0002060: purine nucleobase binding	Paradisaea (+2) Ptiloris (+2)	*
867	GO:0004645: phosphorylase activity	Paradisaea (+2) Ptiloris (+2)	*

References

1. Han, M.V., Thomas, G.W., Lugo-Martinez, J., and Hahn, M.W. (2013). Estimating gene gain and loss rates in the presence of error in genome assembly and annotation using CAFE 3. *Molecular Biology and Evolution* 30, 1987-1997.