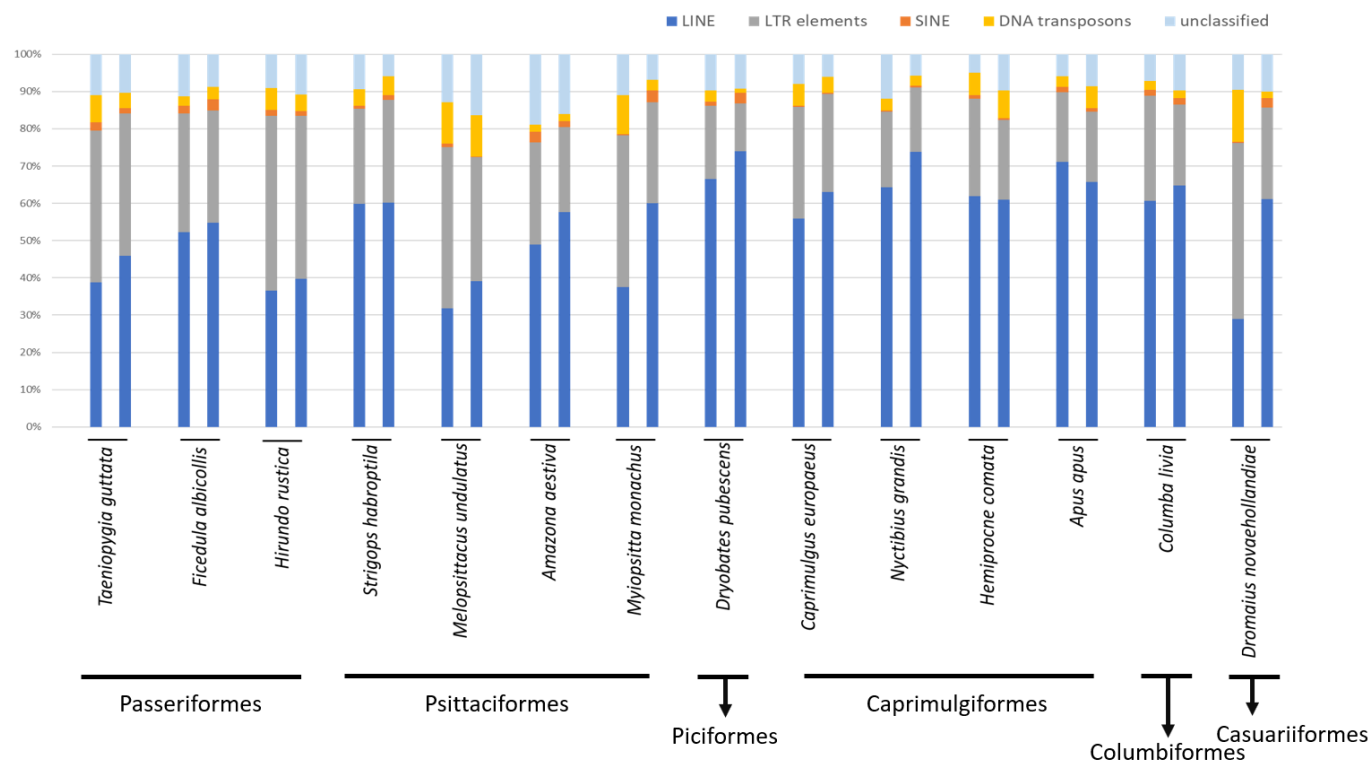


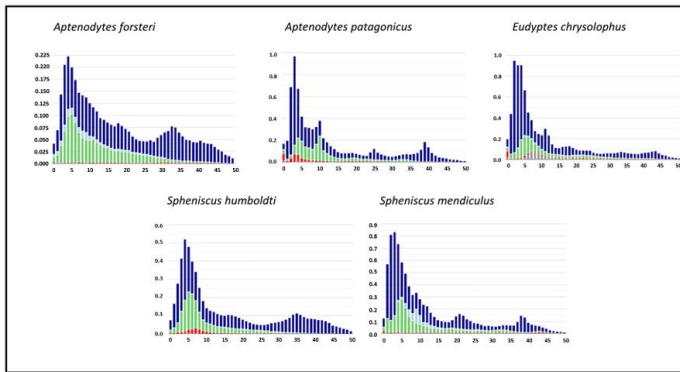
LTR retroelements and bird adaptation to arid environments.

Elisa Carotti^{1†}, Edith Tittarelli^{1†}, Adriana Canapa¹, Maria Assunta Biscotti¹, Federica Carducci^{1*} and Marco Barucca¹.

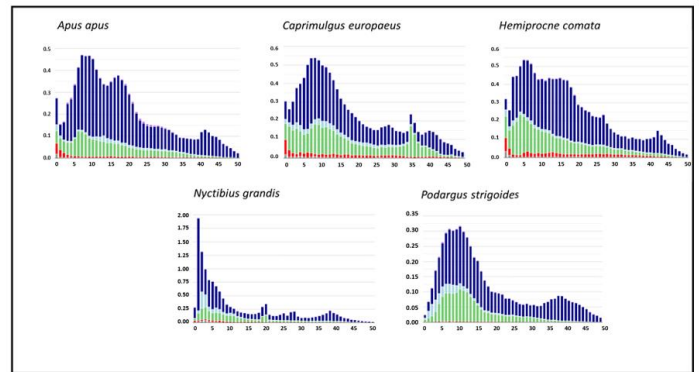


Supplementary Figure S1. TE relative abundance obtained analyzing 14 bird species. For each species the column on the left represents the values obtained considering chromosome level assembly while the column on the right represents the values obtained considering scaffold level assembly.

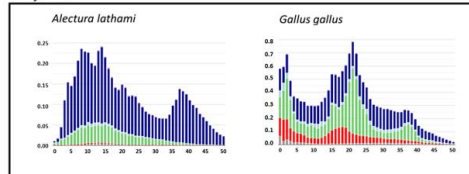
Sphenisciformes



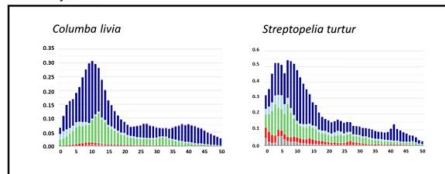
Caprimulgiformes



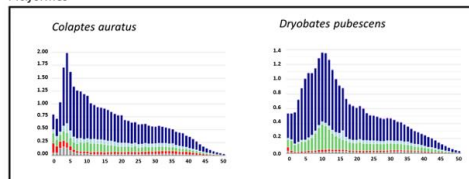
Galliformes



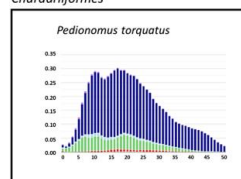
Columbiformes



Piciformes



Charadriiformes



Supplementary Figure S2. TE landscape plots obtained by Kimura distance-based copy divergence analyses of some species belonging to Sphenisciformes, Caprimulgiformes, Galliformes, Columbiformes, Piciformes, and Charadriiformes. X axis: Kimura substitution level (CpG adjusted); Y axis: percent of genome.

Supplementary Table S1. Accession numbers and information regarding the assembly level of genomes belonging to bird species used in this study are reported. For each species the common name is listed in the right column.

Assembly accession	Assembly level	Species	Common Name
GCA_013399715.1	Scaffold	<i>Alectura lathamii</i>	Australian brush-turkey
GCA_017639355.1	Chromosome	<i>Amazona aestiva</i>	Blue-fronted amazon
GCA_001420675.1	Scaffold		
GCF_000699145.1	Scaffold	<i>Aptenodytes forsteri</i>	Emperor penguin
GCA_010087175.1	Scaffold	<i>Aptenodytes patagonicus</i>	King penguin
GCA_020740795.1	Chromosome	<i>Apus apus</i>	Common swift
GCA_020740585.1	Scaffold		
GCA_907165065.1	Chromosome	<i>Caprimulgus europaeus</i>	Eurasian nightjar
GCA_907165095	Scaffold		
GCA_013396415.1	Scaffold	<i>Casuarus casuarus</i>	Southern cassowary
GCA_015227895.2	Chromosome	<i>Colaptes auratus</i>	Northern flicker
GCA_001887795.1	Chromosome	<i>Columba livia</i>	rock pigeon
GCF_000337935.1	Scaffold		
GCA_016128335.1	Chromosome	<i>Dromaius novaehollandiae</i>	Emu
GCA_013396795.1	Scaffold		
GCA_014839835.1	Chromosome	<i>Dryobates pubescens</i>	Downy woodpecker
GCF_000699005.1	Scaffold		
GCA_010084205.1	Scaffold	<i>Eudyptes chrysolophus</i>	Macaroni penguin
GCF_000247815.1	Chromosome	<i>Ficedula albicollis</i>	Collared flycatcher
GCF_000247815.1	Scaffold		
GCA_000002315.5	Chromosome	<i>Gallus gallus</i>	Chicken
GCA_020745705.1	Chromosome	<i>Hemiprocne comata</i>	Whiskered treeswift
GCA_020745695.1	Scaffold		
GCA_015227805.3	Chromosome	<i>Hirundo rustica</i>	Barn swallow
GCA_015227815.3	Scaffold		
GCF_012275295.1	Chromosome	<i>Melopsittacus undulatus</i>	Budgerigar
GCA_012275275.1	Scaffold		
GCA_017639245.1	Chromosome	<i>Myiopsitta monachus</i>	Monk parakeet

GCA_013036005.1	Scaffold		
GCA_013368605.1	Chromosome	<i>Nyctibius grandis</i>	Great potoo
GCA_013368595.1	Scaffold		
GCA_001700915.1	Chromosome	<i>Passer domesticus</i>	House sparrow
GCA_013398155.1	Scaffold	<i>Pedionomus torquatus</i>	Plains-wanderer
GCA_013399755.1	Scaffold	<i>Podargus strigoides</i>	Tawny frogmouth
GCA_003343005.1	Scaffold	<i>Rhea americana</i>	Greater rhea
GCA_010076325.1	Scaffold	<i>Spheniscus humboldti</i>	Humboldt's penguin
GCA_010077915.1	Scaffold	<i>Spheniscus mendiculus</i>	Galapagos penguin
GCA_901699155.2	Chromosome	<i>Streptopelia turtur</i>	European turtle-dove
GCF_004027225.2	Chromosome	<i>Strigops habroptila</i>	Kākāpō
GCA_004011185.1	Scaffold (partial)		
GCF_000698965.1	Scaffold	<i>Struthio camelus australis</i>	Common ostrich
GCF_003957565.2	Chromosome	<i>Taeniopygia guttata</i>	Zebra finch
GCA_003957525.2	Scaffold		

Supplementary Table S2. Accession numbers of scaffold-level assemblies.

Species	Assembly accession	Assembly Level
<i>H. rustica</i>	GCA_015227815.3	scaffold
<i>T. guttata</i>	GCA_003957525.2	scaffold
<i>F. albicollis</i>	GCA_000247815.1	scaffold
<i>M. undulatus</i>	GCA_012275275.1	scaffold
<i>S. habroptila</i>	GCA_004011185.1	scaffold
<i>A. aestiva</i>	GCA_001420675.1	scaffold
<i>M. monachus</i>	GCA_013036005.1	scaffold
<i>D. pubescens</i>	GCF_000699005.1	scaffold
<i>C. livia</i>	GCF_000337935.1	scaffold
<i>N. grandis</i>	GCA_013368595.1	scaffold
<i>C. europaeus</i>	GCA_907165095	scaffold

<i>H. comata</i>	GCA_020745695.1	scaffold
<i>A. apus</i>	GCA_020740585.1	scaffold
<i>D. novaehollandiae</i>	GCA_013396795.1	scaffold

Supplementary Table S3. Accession numbers of complete mitochondrial genome and positions related to 16S rDNA sequence. These sequences were used in vegan analyses. Species considered were listed and their abbreviations were reported in brackets.

Species	Accession number – mitochondrial DNA 16s
<i>A. aestiva</i> (Aae)	NC_033336.1:1106-2673
<i>A. apus</i> (Aap)	NC_008540.1:1115-2716
<i>A. forsteri</i> (Afo)	NC_027938.1:1119-2704
<i>A. lathamii</i> (Ala)	MW574353.1:2248-3860
<i>A. patagonicus</i> (Apa)	NC_045377.1:1140-2692
<i>C. casuarius</i> (Cca)	MN356153.1:1107-2701
<i>C. auratus</i> (Cau)	JAAWVA010000182.1:20328-21925
<i>C. livia</i> (Cli)	GU908131.1:1115-2700
<i>D. novaehollandiae</i> (Dno)	NC_002784.1:1108-2703
<i>D. pubescens</i> (Dpu)	MN356145.1:1114-2707
<i>E. crhyolophus</i> (Ecr)	MW074963.1:1117-2707
<i>F. albicollis</i> (Fal)	NC_021621.1:1120-2715
<i>G. gallus</i> (Gga)	KX987152.1:2351-3972
<i>H. comata</i> (Hco)	MN356189.1:1116-2705
<i>H. rustica</i> (Hru)	MN356225.1:1112-2719
<i>M. monachus</i> (Mmo)	NC_027844.1:2364-3942
<i>M. undulatus</i> (Mun)	EF450826.1:1117-2688
<i>N. grandis</i> (Ngr)	MN356216.1:1121-2718
<i>P. domesticus</i> (Pdo)	MN356394.1:1116-2715
<i>P. strigoides</i> (Pst)	MW883530.1:1100-2713
<i>P. torquatus</i> (Pto)	MN356368.1:1113-2696
<i>R. americana</i> (Ram)	Y16884.3:1103-2685
<i>S. camelus australis</i> (Sca)	NC_002785.1:1104-2683
<i>S. habroptila</i> (Sha)	MZ128785.1:1085-2674
<i>S. humboldti</i> (Shu)	MK760995.1:1145-2705
<i>S. mendiculus</i> (Sme)	MK760994.1:1145-2704
<i>S. turtur</i> (Stu)	CABFKC020000024.1:41166-42762
<i>T. guttata</i> (Tgu)	DQ453515.1:1120-2713

Supplementary Table S4. P-distance matrix performed on 16S rDNA sequences of species considered in the present study, exception made for *Caprimulgus europaeus* (please see material and methods for further details). Abbreviations used for species names were explained in Supplementary Table S3.

	Hru	Pdo	Tgu	Fal	Sha	Aae	Mmo	Mun	Dpu	Cau	Afo	Apa	Shu	Sme	Ech	Hco	Aap	Pto	Ngr	Cli	Stu	Dno	Cca	Sca	Ram	Pst	Ala	Gga
Hru																												
Pdo	0.10																											
Tgu	0.10	0.06																										
Fal	0.10	0.08	0.08																									
Sha	0.20	0.20	0.19	0.20																								
Aae	0.22	0.22	0.21	0.21	0.15																							
Mmo	0.21	0.20	0.20	0.19	0.13	0.12																						
Mun	0.21	0.21	0.20	0.20	0.15	0.14	0.13																					
Dpu	0.21	0.20	0.21	0.20	0.20	0.20	0.20	0.19																				
Cau	0.21	0.20	0.20	0.21	0.20	0.21	0.21	0.21	0.13																			
Afo	0.18	0.17	0.18	0.18	0.18	0.20	0.18	0.18	0.18	0.18																		
Apa	0.18	0.17	0.18	0.18	0.18	0.20	0.18	0.17	0.18	0.17	0.02																	
Shu	0.18	0.17	0.18	0.17	0.17	0.20	0.17	0.17	0.17	0.18	0.08	0.08																
Sme	0.18	0.17	0.18	0.18	0.17	0.20	0.17	0.17	0.17	0.18	0.08	0.08	0.00															
Ech	0.18	0.17	0.17	0.17	0.18	0.20	0.18	0.17	0.17	0.17	0.08	0.08	0.06	0.06														
Hco	0.17	0.17	0.17	0.17	0.17	0.20	0.18	0.18	0.18	0.18	0.15	0.16	0.15	0.15	0.15													
Aap	0.18	0.19	0.18	0.18	0.17	0.19	0.17	0.18	0.17	0.18	0.14	0.15	0.13	0.13	0.15	0.12												
Pto	0.19	0.19	0.19	0.19	0.19	0.20	0.19	0.18	0.19	0.19	0.16	0.15	0.16	0.16	0.15	0.16	0.17											
Ngr	0.21	0.20	0.20	0.19	0.18	0.21	0.19	0.19	0.19	0.20	0.17	0.17	0.16	0.16	0.16	0.16	0.17	0.18										
Cli	0.19	0.19	0.18	0.19	0.19	0.19	0.19	0.19	0.19	0.20	0.16	0.16	0.16	0.16	0.16	0.16	0.17	0.17	0.17	0.18								
Stu	0.19	0.18	0.18	0.18	0.19	0.20	0.20	0.19	0.18	0.20	0.17	0.16	0.16	0.16	0.16	0.16	0.17	0.17	0.17	0.18	0.08							
Dno	0.20	0.19	0.18	0.19	0.20	0.20	0.20	0.20	0.20	0.20	0.18	0.17	0.17	0.17	0.16	0.19	0.19	0.18	0.20	0.18	0.19							
Cca	0.20	0.20	0.19	0.19	0.20	0.21	0.20	0.20	0.20	0.21	0.16	0.15	0.16	0.16	0.15	0.19	0.19	0.17	0.19	0.18	0.19	0.09						
Sca	0.20	0.20	0.19	0.20	0.19	0.21	0.20	0.19	0.20	0.20	0.16	0.15	0.14	0.15	0.15	0.19	0.18	0.17	0.18	0.19	0.19	0.13	0.13					
Ram	0.18	0.19	0.18	0.18	0.20	0.21	0.20	0.19	0.19	0.20	0.17	0.17	0.17	0.17	0.17	0.18	0.17	0.18	0.19	0.20	0.19	0.14	0.14	0.14				
Pst	0.22	0.21	0.22	0.22	0.21	0.21	0.21	0.21	0.18	0.20	0.18	0.18	0.19	0.19	0.19	0.19	0.18	0.19	0.20	0.19	0.20	0.20	0.21	0.21				
Ala	0.21	0.21	0.21	0.20	0.20	0.20	0.20	0.19	0.20	0.20	0.18	0.18	0.18	0.18	0.17	0.19	0.18	0.19	0.20	0.21	0.20	0.19	0.19	0.18	0.19	0.22		
Gga	0.21	0.20	0.21	0.20	0.22	0.22	0.22	0.21	0.22	0.21	0.19	0.18	0.19	0.19	0.18	0.20	0.19	0.19	0.21	0.20	0.20	0.20	0.19	0.21	0.22	0.18		