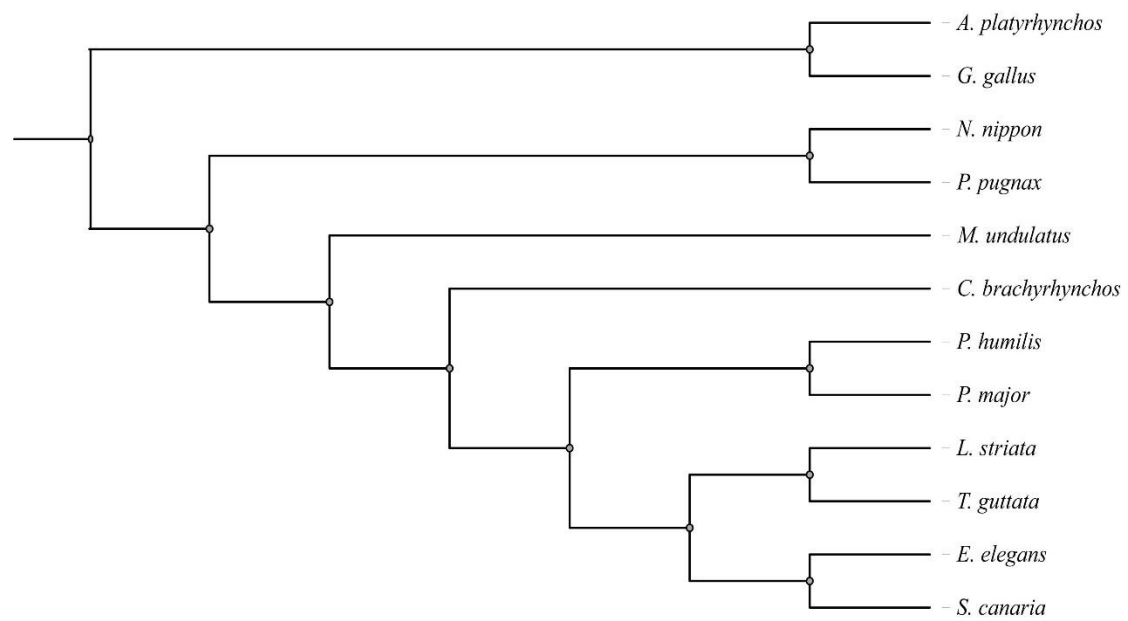
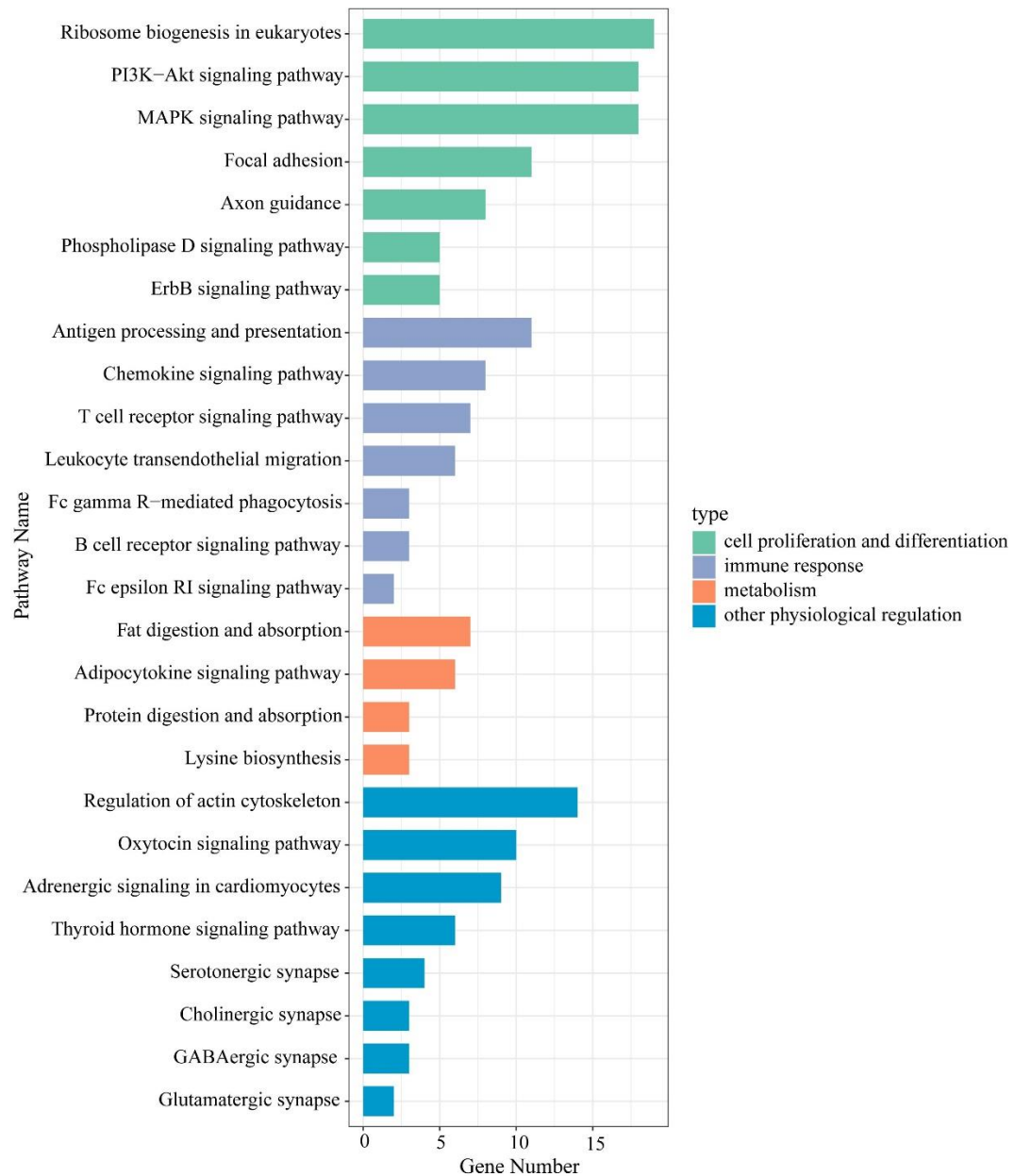


**Figure S1.** The number of different orthologous genes within the 12 avian species. X-axis denotes species, while the Y-axis indicates the number of genes. The single-copy orthologous, multiple-copy orthologous, species-specific orthologous, and other orthologous of each species are represented by red, orange, brown, and green, respectively.



**Figure S2.** Species trees of 12 birds were constructed using maximum-likelihood trees of each single-copy orthologous gene family using MP-EST.



**Figure S3.** Horizontal bar plots represent significantly enriched positively selected gene pathway types and gene numbers. The horizontal axis is the number of genes, and the vertical axis is the pathway's name.

**Table S1.** Genomic characteristics statistics of *E. elegans* obtained by using K-mer analysis.

K-mer	K-mer number	K-mer Depth	Genome Size (Mbp)	Revised Genome Size (Mbp)	Heterozygous Ratio (%)	Repeat (%)
17	62,559,975,660	42	1,489.52	1,486.61	0.66	47.81

**Table S2.** Repetitive element statistics.

Type	Length (bp)	Percentage (%)
DNAs	1,112,875	0.10
LINEs	40,322,527	3.52
SINEs	97,924	0.01
LTRs	151,768,505	13.26
Unclassified	9,606,478	0.84
Total	190,253,193	16.62

Note: Abbreviations indicate DNA transposons (DNAs), long interspersed nuclear elements (LINEs), short interspersed nuclear elements (SINEs), and long terminal repeats (LTRs).

**Table S3.** Statistical analysis of functional annotated protein-coding genes.

	Type	Number	Percent (%)
Annotation	KEGG	13,482	85.0
	GO	10,979	69.2
	KOG	14,696	92.6
	SwissProt	14,945	94.2
	InterPro	14,891	93.8
	NR	15,382	96.9
Total	Annotated genes	15,416	97.2
	Total Genes	15,868	-

Note: “Annotation” is the annotation results of each database and the proportion of annotation coverage. “Annotated genes” represent non-redundant results based on annotations. “Total Genes” is the total number of protein-coding genes (annotated genes + unannotated genes).

**Table S4.** Statistical results of non-coding RNAs.

Type	Copy (w*)	Average length (bp)	Total length (bp)	Percentage (%)
miRNA	308	89.27	27,495	0.002402
tRNA	329	75.18	24,735	0.002161
rRNA	151	269.78	40,737	0.003559
snRNA	284	129.94	36,904	0.003224

Note: Abbreviations indicate transfer RNA (tRNA), ribosomal RNA (rRNA), small nuclear RNA (snRNA), and microRNA (miRNA).

**Table S5.** Positively selected genes' significantly enriched pathways in KEGG enrichment analysis.

KO number	Pathway name	Gene number	P-value	Corrected P-value
KO04360	Axon guidance	8	2.00E-04	4.20E-02
KO04510	Focal adhesion	11	4.18E-04	4.28E-02
KO03008	Ribosome biogenesis in eukaryotes	19	5.09E-04	4.29E-02
KO04151	PI3K-Akt signaling pathway	18	8.59E-04	4.29E-02
KO04724	Glutamatergic synapse	2	9.68E-04	4.29E-02
KO00300	Lysine biosynthesis	3	9.91E-04	4.29E-02
KO04072	Phospholipase D signaling pathway	5	2.01E-03	7.64E-02
KO04810	Regulation of actin cytoskeleton	14	4.28E-03	0.1181
KO04725	Cholinergic synapse	3	5.16E-03	0.1302
KO04974	Protein digestion and absorption	3	9.80E-03	0.1820
KO04062	Chemokine signaling pathway	8	0.0114	0.1820
KO04612	Antigen processing and presentation	11	0.0166	0.2511
KO04921	Oxytocin signaling pathway	10	0.0186	0.2575
KO04012	ErbB signaling pathway	5	0.0187	0.2575
KO04726	Serotonergic synapse	4	0.0217	0.2738
KO04010	MAPK signaling pathway	18	0.0301	0.2868
KO04660	T cell receptor signaling pathway	7	0.0310	0.2868
KO04664	Fc epsilon RI signaling pathway	2	0.0312	0.2868
KO04727	GABAergic synapse	3	0.0312	0.2868
KO04666	Fc gamma R-mediated phagocytosis	3	0.0312	0.2868
KO04670	Leukocyte transendothelial migration	6	0.0390	0.3378
KO04662	B cell receptor signaling pathway	3	0.0417	0.3417
KO04662	Thyroid hormone signaling pathway	6	0.0433	0.3417
KO04662	Adrenergic signaling in cardiomyocytes	9	0.0488	0.3417
KO04975	Fat digestion and absorption	7	0.0462	0.3417
KO04920	Adipocytokine signaling pathway	6	0.0488	0.3417



**Table S6.** Positively selected genes associated with circadian rhythms and fat metabolism from KEGG enrichment analysis.

Function	Gene name	Pathway name (KO number)	Gene ID
Circadian rhythm	PER3	Circadian rhythm (KO04710)	evm.model.FRAGSCAFF_SCAFFOLD_66.166
	SKP1	Circadian rhythm (KO04710)	evm.model.ORIGINAL_SCAFFOLD_803.36.1
	PRKAG2	Circadian rhythm (KO04710)	evm.model.FRAGSCAFF_SCAFFOLD_205.172.1
Fat metabolism	MOGAT2	Fat digestion and absorption (KO04975)	evm.model.FRAGSCAFF_SCAFFOLD_195.124
	PLA2G10	Fat digestion and absorption (KO04975)	evm.model.FRAGSCAFF_SCAFFOLD_242.142
	ABCG8	Fat digestion and absorption (KO04975)	evm.model.ORIGINAL_SCAFFOLD_2636.347
	CEL	Fat digestion and absorption (KO04975)	evm.model.FRAGSCAFF_SCAFFOLD_183.2355
	PLA2G3	Fat digestion and absorption (KO04975)	evm.model.ORIGINAL_SCAFFOLD_3106.270.1
	PLA2G5	Fat digestion and absorption (KO04975)	evm.model.FRAGSCAFF_SCAFFOLD_66.297
	SCARB1	Fat digestion and absorption (KO04975)	evm.model.FRAGSCAFF_SCAFFOLD_183.1779
	G6PC2	Adipocytokine signaling pathway (KO04920)	evm.model.ORIGINAL_SCAFFOLD_3574.260
	RSPH10B	Adipocytokine signaling pathway (KO04920)	evm.model.FRAGSCAFF_SCAFFOLD_196.301
	CIDEA	Adipocytokine signaling pathway (KO04920)	evm.model.ORIGINAL_SCAFFOLD_1430.189
	POMC	Adipocytokine signaling pathway (KO04920)	evm.model.FRAGSCAFF_SCAFFOLD_101.79
	C1QTNF3	Adipocytokine signaling pathway (KO04920)	evm.model.ORIGINAL_SCAFFOLD_2528.122

PPARA

Adipocytokine signaling pathway (KO04920)

evm.model.FRAGSCAFF\_SCAFFOLD\_183.929

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