Article

Independent duplications of the Golgi phosphoprotein 3 oncogene in birds

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Abstract

Golgi phosphoprotein 3 (GOLPH3) was the first reported oncoprotein of the Golgi apparatus. It was identified as an evolutionarily conserved protein upon its discovery about 20 years ago, but its function remains puzzling in normal and cancer cells. The GOLPH3 gene is part of a group of genes that also includes the GOLPH3L gene. Because cancer has deep roots in multicellular evolution, studying the evolution of the GOLPH3 gene family in non-model species represents an opportunity to identify new model systems that could help better understand the biology behind this group of genes. The main goal of this study is to explore the evolution of the GOLPH3 gene family in birds as a starting point to understand the evolutionary history of this oncoprotein. We identified a repertoire of three GOLPH3 genes in birds. We found duplicated copies of the GOLPH3 gene in all main groups of birds other than paleognaths, and a single copy of the GOLPH3L gene. We suggest there were at least three independent origins for GOLPH3 duplicates. Amino acid divergence estimates show that most of the variation is located in the N-terminal region of the protein. Our transcript abundance estimations show that one paralog is highly and ubiquitously expressed, and the others were variable. Our results are an example of the significance of understanding the evolution of the GOLPH3 gene family, especially for unraveling its structural and functional attributes.

Introduction

Golgi phosphoprotein 3 (GOLPH3) is a highly conserved protein of the Golgi apparatus [1,2] considered the first oncoprotein of this subcellular compartment [3]. The GOLPH3 gene family comprises the conserved GOLPH3 gene and the GOLPH3L gene found only in vertebrates [1,2]. Despite the vast amount of empirical evidence demonstrating the contribution of GOLPH3 to tumorigenesis and cancer, a full understanding of its molecular role has not yet emerged. This is mainly due to multiple functions attributed to GOLPH3 [3], including, the sorting of Golgi glycosyltransferases [4–6], the modulation of focal adhesion dynamics [7], induction of membrane curvature [8], and an intriguing function for a Golgi protein, regulating mitochondrial function [9]. Because cancer has deep evolutionary roots that arise as a consequence of the multicellularity [10], and is widespread across animals [11], studying the evolution of the GOLPH3 gene family in non-model species can provide significant information for a comparative oncology approach, which is emerging as an integrative field to tackle cancer [10].

The availability of whole-genome sequences opens an opportunity to understand the evolution of gene families. The annotation of gene repertoires in different species has revealed that copy number variation is an important source of variability that should be considered when making functional comparisons [12,13]. Phylogenetic reconstructions show that the evolution of gene families follows complex pathways, including gene gain and losses and independent origins, making it challenging to perform direct interspecies comparisons. Thus, understanding the variability of gene repertoires and their duplicative history represents an essential piece of information to understand the biological functions associated with a group of genes and make biologically meaningful comparisons. Today, the GOLPH3 gene family is viewed as a group of genes containing two paralogs (GOLPH3 and GOLPH3L) with 1:1 orthologs among most vertebrate species [1,2]. Among amniotes, it is suggested that, in contrast to mammals, birds are less susceptible to cancer[10,14–18]; however, this information should be taken with caution given sampling bias [19]. Thus, the study of genes associated with cancer in birds could provide clues about the genetic bases associated with this difference and suggest additional model systems that could help to understand the biology of the GOLPH3 gene family.

The main goal of this study was to analyze the evolutionary history of the GOLPH3 gene family in birds. We took advantage of whole genome sequences in representative species of all main lineages of birds to understand the evolutionary pathways that gave rise to GOLPH3 paralogs. According to our assessment, we identified a repertoire of three GOLPH3 genes in birds. We found duplicated copies of the GOLPH3 gene in all main groups of birds other than paleognaths, and a single copy of the GOLPH3L gene that would be derived from the common ancestor of all birds. In the case of the GOLPH3 gene, our gene tree suggests at least three independent origins for the duplicated copies, in the ancestor of Galliformes and Anseriformes, in the ancestor of Anseriformes, and the ancestor of Neoaves. Divergence estimates between duplicated genes showed that most of the variation is located in the N-terminal region of the protein. Our transcript abundance estimations showed that one paralog was highly and ubiquitously expressed, while the others were variable. Our evolutionary analyses suggest a more complex than anticipated evolutionary history of the GOLPH3 gene family, a scenario that could have implications for cancer.

Results and Discussion

Independent duplication events characterize the evolution of the GOLPH3 gene family member in birds

Comparing the sister group relationship among gene family members, i.e. gene tree, with the species tree represents a fundamental strategy to understand homologous relationships, duplicative history, and modes of evolution of any group of genes [20,21]. In our case, our gene tree did not significantly deviate from the most updated phylogenetic hypotheses for the main group of birds [22–25](Fig. 1), suggesting that GOLPH3 was present in the ancestor of the group as a single copy gene. We recovered a clade containing GOLPH3 sequences from paleognaths (ostriches, tinamous, and allies) sister to GOLPH3 sequences from all other birds (Fig. 1). Further, we recovered the sister group relationship of the GOLPH3 sequences from Galliformes (chickens, pheasants, and allies) and Anseriformes (ducks, swans, and allies), in turn, this clade was recovered sister to GOLPH3 sequences from Neoaves (Fig. 1).

We found a single copy gene, located on chromosome Z, in most paleognaths species, except in the white-throated tinamou (*Tinamus guttatus*), where two copies were identified (Fig. 1), suggesting that this species independently gave rise to a second GOLPH3 copy located on chromosome W. The location of these genes on sexual chromosomes, and given the sex-determination system of birds [26], indicates that only females (ZW) can express both paralogs. In the case of Neoaves, our tree topology is not well resolved, being difficult to anticipate details regarding the duplicative history of the GOLPH3 paralog in this group (Fig. 1). However, for a diversity of species (e.g., zebra finch, common canary, kakapo), we found duplicated copies on different chromosomes, suggesting that the duplication event that gave rise to them occurred in the ancestor of Neoaves. Similar to the case of the white-throated tinamou (*Tinamus guttatus*), we found duplicated copies in the killdeer (*Charadrius vociferus*) that were recovered sister to each other (Fig. 1), suggesting that they arose as a product of a species-specific gene duplication event.

The evolutionary history of the GOLPH3 gene in the clade that includes Galliformes and Anseriformes followed a more complicated evolutionary pathway (Fig. 1). According to our assessment, we found a repertoire of two copies in species belonging to both groups (Fig. 1); however, our gene tree suggests that the events that gave rise to them followed a pattern of gene birth-and-death [27](Fig. 2). The reconciliation of the gene tree with the species tree suggests that the last common ancestor of Anseriformes and Galliformes, which lived 80 million years ago approximately [28], had a single copy gene that underwent a duplication event (Fig. 2), giving rise to a repertoire of two GOLPH3 copies (Fig. 2). One of the copies was retained in Galliformes (Fig. 2; GOLPH3.1$_{GA}$; red lineage), but lost in Anseriformes (Fig. 2; red lineage). This GOLPH3 gene copy is located on chromosome W. The other copy, also originated in the ancestor of Galliformes and Anseriformes, was also retained in Galliformes (Fig. 3; GOLPH3.2$_{GA}$; pink lineage) and is located on chromosome Z. In the last common ancestor of Anseriformes, this copy underwent a duplication event giving rise to two copies (Fig. 3; GOLPH3.2.1$_{A}$, purple lineage and GOLPH3.2.2$_{A}$, light purple lineage). Like other cases, in Anseriformes, one of the copies is located on chromosome Z, while the other on chromosome W; the exception is the mallard (*Anas platyrhynchos*) in which is found on chromosome 22.

Thus, the main groups of birds possess gene repertoires with different evolutionary origins (Fig. 2). Most paleognaths retained the ancestral condition of a single gene copy, whereas Galliformes, Anseriformes, and Neoaves possess duplicated copies that originated independently (Fig. 2). Anseriformes and Neoaves gave rise to their repertoire in the ancestor of each group (Fig. 2), while Galliformes retained copies that originated in the ancestor of Galliformes and Anseriformes (Fig. 2). The independent origin of gene families in different groups is not an unusual

event during the evolutionary process [29–33]; however, it should be taken into account when making comparisons because non-orthologous genes - i.e., genes with different evolutionary origin - are being compared. Our results also highlight the importance of manual curation in defining the composition of gene families. The description of new genes is also not uncommon [34–36], and their discovery could be attributed to their presence in non-model species and/or the absence of appropriate evolutionary analyses. The presence of species with different gene repertoires represents an opportunity to understand the evolutionary fate of duplicated genes [37] and the biological functions associated with a group of genes. This phenomenon, variation in gene copy number, has been associated with differences in susceptibility to diseases in different taxonomic groups. For example, in the African elephant (*Loxodonta africana*), it has been claimed that an expansion in the number of TP53 "the guardian of the genome" gene copies could help to explain the lower risk of developing cancer in this large and long-lived animal [12,13]. Similarly, in whales there are also an expansion of gene families related to cancer, and an accelerated rate of evolution in genomic regions enriched with pathways involved in cancer [38,39]. Further evidence comes from bats, a group in which the lifespan exceeds the expectation based on their body size [40]. In this group, it has been documented the expansion of several genes, for example, FBXO31, which is related to cell cycle arrest and response to DNA damage diminishing the probability of developing cancer [41–43]. Thus, the expanded repertoire of GOLPH3 genes in birds could be part of a set of genomic traits that account for their lower susceptibility to cancer than mammals.

Molecular divergence between duplicated copies of GOLPH3 genes

According to our analyses, the divergence values between duplicated GOLPH3 copies are low. In Galliformes, the divergence values ranged from 1.79% to 4.76%. However, by checking the amino acid alignment, we realized that most of the observed differences are in the first ~50 amino acids of the N-terminal region of the protein (Fig. 3). By estimating amino acid sequence divergence for the N- and C- terminal regions separately, we observed that the divergence values for the C-terminal region ranged from 1.79% to 2.47%, while for the N-terminal region, which represents only ~1/6 of the amino acid sequence, ranged from 15.69% to 17.65%. In this group of birds we found eleven amino acid positions in the alignment that unequivocally distinguish between both paralogs (Fig. 3). Six of them are in the N-terminal region, while the others are in the C-terminal portion of the molecule (Fig. 3). In Anseriformes (Fig. 4), the divergence values range from 1.69% to 4.49%, similar to those estimated for Galliformes. Also, most of the observed differences are in the N-terminal region of the molecule with divergence values ranging from 5.66% to 9.62%. In the case of the C-terminal region, the values varied from 0.8% to 2.9%. In this group of birds there are three amino acid positions that unequivocally distinguish both paralogs (Fig. 4), one of them is located on the N-terminal region of the molecule, whereas the other two in the C-terminal region (Fig. 4). In Neoaves we found the same evolutionary pattern as described for Anseriformes and Galliformes, i.e. most of the amino acid replacements are found in the N-terminal portion of the protein. The divergence values for the whole protein ranged from 1.36% to 3.72%, for the N-terminal region varied from 3.92% to 15.38%, whereas for the C-terminal region went from 0.41% to 2.06%. Unlike the previous cases we did not identify amino acid sites in the alignment that distinguish both paralogs (Fig. 5).

These differences in amino acid sequence divergence for the N- and C- terminal regions of the GOLPH3 paralogs could have arisen as a consequence of different structural and functional constraints during its evolution. Secondary structure prediction indicates that the region comprising the first ~40-60 amino acids of GOLPH3 is disordered in a variety of organisms (e.g.,

yeast, fruit fly, spotted gar, human) that share a common ancestor more than a billion of years ago (Fig. 6A and Supplementary Figure 1). Accordingly, only the crystal structures of N-terminal truncation variants of GOLPH3 and Vps74 (GOLPH3 in yeasts) have been solved [44,45]. Both structures are remarkably similar (backbone atom root mean square deviation of ~1.0 Å), consisting of a single globular domain that is predominantly α-helical, with a central four-helix bundle surrounded by solvent-exposed loops, and eight amphipathic helices [44,45]. The overall structure of the N-terminal truncated GOLPH3 protein is unique, with no strong structural homology to known protein folds, resulting so far challenging to predict its function based on its structure. Protein structure homology modeling of GOLPH3.1$_{GA}$ and GOLPH3.2$_{GA}$ of chicken (Supplementary Figure 2) showed that of the divergent amino acids in the C-terminal region only L255 in GOLPH3.1$_{GA}$ and Q256 in GOLPH3.2$_{GA}$ are non-conservative (Fig. 3) [46]. The position of Q256 is predicted to be exposed at the surface of GOLPH3.2$_{GA}$, like it is for Q260 in human GOLPH3. However, the variant L255 in GOLPH3.1$_{GA}$ is intriguing because the preferred position of leucine residues is buried in regions of proteins facing hydrophobic cores and not exposed on protein surfaces/boundaries such as in this case.. None of the divergent amino acids of the C-terminal region in Anseriformes and Neoaves are structurally disfavored. The C-terminal region of GOLPH3 is sufficient for GOLPH3 physical interaction with the membrane of the Golgi apparatus [1]. This interaction is mediated by a series of highly conserved residues that are postulated to interact with phosphate groups and the inositol ring of phosphatidylinositol 4-phosphate located in the cytosolic leaflet of the Golgi membrane [44], set of residues that are also conserved in both copies of GOLPH3 in birds (Figs. 3-5 and Supplementary Figures 1 and 3). In contrast, the N-terminal disordered region has no known function. Intriguingly, some proteins containing disordered regions have the capacity to undergo liquid-liquid phase separation that could result in their partitioning in functional biomolecular condensates also known as membrane-less compartments [1,47]. However, it is unknown whether GOLPH3 has this capacity. In any case, the distinct amino acid sequence divergence values for the N-terminal disordered region of GOLPH3 suggest a more flexible functional role. Thus, it will be important to determine whether this domain contributes to the functions of GOLPH3 as oncoprotein.

Evolution of GOLPH3L paralog

In contrast to GOLPH3, GOLPH3L is largely uncharacterized. Although the amino acid sequences of human GOLPH3 and GOLPH3L are 78% similar (65% identical), it has been suggested that GOLPH3L antagonizes the functions of GOLPH3 [48]. Despite this, other reports suggest a similar function to GOLPH3 for GOLPH3L in some types of cancer [49–53]. The evolutionary history of GOLPH3L followed a different trajectory in comparison to the GOLPH3 gene (Fig. 7). In this case, our gene tree recovered the main groups of birds according to the most updated organismal phylogenies [22–25]; nevertheless, it was not possible to define the relationships among them (Fig. 7). We will assume that the lack of resolution is mainly caused by the limited amount of phylogenetic information contained in a single gene , instead of more complex evolutionary scenarios invoking gene duplications and reciprocal loss in the ancestor of the main groups of birds. Thus, according to our results the GOLPH3L gene was present in the ancestor of birds as a single copy gene (Fig. 2), and this gene was inherited by all descendant lineages (Fig. 2). Thus, GOLPH3L genes in different bird species are 1:1 orthologs. Amino acid divergence values show a similar trend as we described for GOLPH3, i.e., the N-terminal portion of the protein is more divergent than the C-terminal region (Fig. 8). In the case of Galliformes, the divergence values for the N-terminal part of the molecule ranged from 5.71% to 17.14%, while for the C-terminal region it varied from

3.28% to 6.97%. In Anseriformes, the values for the N-terminal region ranged from 7.89% to 26.32%, whereas for the C-terminal portion varied from 2.05% to 4.92%. In the case of Neoves, the evolutionary trend is the same, although the values for the N-terminal region are higher. Thus, the values for the N-terminal part of the molecule ranged from 20% to 43.34%, while for the C-terminal region varied from 4.10% to 17.55%. The secondary structure prediction indicates that this region in GOLPH3L, although shorter than in GOLPH3, is also disordered (Fig. 6B).

One thing that seems interesting is the number of changes accumulated in the branch leading to Galliformes and to manakins (Fig. 7). This phenomenon could be indicative of an acceleration of the rate of fixation of amino acid changing mutations in the ancestors of both groups. To test this hypothesis, we estimated the omega value (d_N/d_S), i.e., the ratio of non-synonymous (d_N) to synonymous substitutions (d_S), in the branches leading to both groups. In brief, if non-synonymous substitutions are neutral, then the rate of fixation of d_N and d_S will be very similar, and $d_N/d_S \approx 1$. Under negative selection, most non-synonymous substitutions are deleterious, and $d_N/d_S < 1$. Finally, under positive selection non-synonymous (d_N) replacements are advantageous and will be fixed at a greater rate than synonymous substitutions (d_S) and in consequence $d_N/d_S > 1$ [54]. According to our analyses, in the ancestor of Galliformes the model in which the omega value was estimated from the data was not significantly different from the model in which the omega value was fixed to 1 (neutral evolution)(LRT=0.142, $P > 0.05$). On the other hand, in the case of manakins the model in which the omega value was estimated from the data (d_N/d_S=6.2) was significantly different from the null hypothesis of neutral evolution (LRT=7.19, $P < 0.01$), indicating that the rate of fixation of non-synonymous substitutions (d_N) is higher in comparison to the neutral expectation (d_S) and suggesting an event of positive selection in the ancestor of manakins. According to the Bayes Empirical Bayes (BEB) approach five sites (152C/G, 191R, 230A, 233R and 263G) were inferred under positive selection with a posterior probability higher than 0.95. All of them are located in the C-terminal region of the protein. Given the limited understanding of the biological functions associated with the GOLPH3 gene family, in particular of the GOLPH3L gene [3], it is challenging to explain the consequences of positive selection in GOLPH3L in this group of birds. However, it could be interesting to carry out functional assays in which the performance of manakins GOLPH3L protein is compared to the one in other birds.

Expression pattern of GOLPH3 gene family members

Our next step was to investigate the expression pattern of the GOLPH3 gene family members, especially for the duplicated copies derived independently in different groups of birds. To do this, we mapped RNASeq reads to reference gene sequences in the chicken (*Gallus gallus*) and mallard (*Anas platyrhynchos*) and examined transcript abundance in a panel of nine tissues (Fig. 9). It is important to say that in chicken, the duplicated GOLPH3 copies are located on chromosome Z ($GOLPH3.2_{GA}$) and W ($GOLPH3.1_{GA}$), while GOLPH3L is on chromosome 25. Therefore, females (ZW) can express all gene family members, whereas males (ZZ) can only express $GOLPH3.2_{GA}$ and GOLPH3L. This situation is somewhat similar to the allelic trichromacy observed in New World monkeys, where some females (XX) possess trichromatic color vision due to a polymorphism of an opsin gene located on chromosome X, while males (XY) are all dichromatic [55]. The case is different in mallard, as one copy is located on chromosome Z ($GOLPH3.2.1_A$) but $GOLPH3.2.2_A$ and GOLPH3L are autosomal genes, so both sexes can potentially express all paralogs.

In both species, the paralog located on the Z chromosome (GOLPH3.2$_{GA}$ in chicken and GOLPH3.2.1$_{A}$ in mallard) was highly and ubiquitously expressed across all tissues (Fig. 9). We collected chicken libraries from both male and female tissues, and unfortunately the sex of the individuals for some tissues was not declared (Supplemental Table S2). As such GOLPH3.1$_{GA}$ exhibited variable expression from mixed sex sampling (Fig 9A). Thus, GOLPH3.1$_{GA}$ was highly expressed in the brain and ovary where all libraries were constructed from female individuals (Fig 9A). Although we do not know the sex of the individuals for the intestine libraries of the chicken, based on the consistent expression of the gene located on chromosome W, we can presume that they were all from female individuals (Fig. 9A). As a validation of what we mentioned above, GOLPH3.1$_{GA}$ was not expressed in all known male tissue libraries, which was most noticeable in the male specific testes (Fig. 9A). All autosomal paralogs in both species were variably expressed among and within tissues (Fig 9). In the case of the chicken GOLPH3L, we recovered expression in all tissues but at variable levels, from low values in the brain and heart to higher values in the intestine and kidney (Fig. 9A). By contrast GOLPH3L was universally expressed in all mallard tissues (Fig. 9B). GOLPH3.2.2$_{A}$ in mallard was not expressed in the brain, liver and testes, but highly expressed in the ovary, spleen and intestine. In both species, all GOLPH3 paralogs were consistently expressed in the intestine (Fig. 9).

In humans, both paralogs are ubiquitously expressed across all tissues [56], suggesting that they are required for the maintenance of basic cellular functions [57]; however, GOLPH3L seems to be expressed at lower levels. Similarly, the relative expression levels of GOLPH3 and GOLPH3L in several mammalian cell lines with epithelial, fibroblast, myeloid and neuronal characteristics, and in a variety of tissues from mice also indicates that GOLPH3 is also ubiquitously expressed at higher levels than GOLPH3L [48]. Further, GOLPH3L is expressed more in cells with secretory epithelial characteristics [48], suggesting a distinct function for this gene family member. The expression pattern observed in the mallard is similar to what is observed in model species (Fig. 9B). One of the GOLPH3 duplicates (GOLPH3.2.1$_{A}$) is expressed in all examined tissues at high levels, while GOLPH3L is also expressed in all tissues, but at lower levels. The expression of the other duplicate (GOLPH3.2.2$_{A}$) is variable, including tissues in which it is not detected (Fig. 9). The case of the chicken seems to be more dissimilar. In this species one of the GOLPH3 duplicates (GOLPH3.2$_{GA}$) possesses an expression pattern similar to the human GOLPH3 (Fig. 9A), however the other two copies seem to follow a specific expression pattern (Fig. 9A).

Conclusions

Our study shows that the evolution of the GOLPH3 gene family followed a more complicated evolutionary pathway than previously thought. Although the history of the GOLPH3L paralog is according to the current knowledge, the one of GOLPH3 is not. The most exciting thing about the evolution of GOLPH3 in birds is that they possess extra GOLPH3 gene copies never described before, and that all main groups independently originated their repertoire. In other words, they do not have the same evolutionary origin, and in consequence, they are not 1:1 orthologs and are not directly comparable. Most paleognaths retained the ancestral condition of a single gene copy, whereas Galliformes, Anseriformes, and Neoaves possess duplicated copies that were originated independently. Thus, birds represent a natural experiment of gene copy number variation [58], that in addition to the differences in expression of individuals of different sex, could help us improve our understanding of the biological functions associated with the GOLPH3 gene family. Our results also highlight the power of manually curating genetic data to define gene repertoires, and the reconciliation of gene trees with species trees [59] to understand the duplicative

history of gene families to perform biologically meaningful comparisons [21,60]. Finally, the conservation of the N-terminal portion of GOLPH3 paralogs as a disordered region for more than a billion of years of evolution and the fact that it displays a higher degree of divergence among species, compared to the C-terminal portion, strongly suggests that it performs an essential, specialized and adapted cellular function conserved in distantly related species like yeasts and humans that remains to be elucidated.

Material and Methods

DNA sequences and phylogenetic analyses

We performed searches for GOLPH3 sequences in avian genomes in the National Center for Biotechnology Information (NCBI) [61] and the Ensembl v.102 databases [62]. We retrieved orthologs and paralogs from the NCBI [61] using the chicken (*Gallus gallus*), zebra finch (*Taeniopygia guttata*), and mallard (*Anas platyrhynchos*) sequences using the program blast (blastn) [63] against the non-redundant database (nr) with default parameters. Additionally, we also retrieved sequences from the Ensembl v.102 database [62]. In cases where sequences are not complete we manually annotated them. To do so, we first identified the genomic fragment containing the GOLPH3 gene in Ensembl v.102 [62] or NCBI databases [64]. Once identified, genomic fragments were extracted, including flanking genes. After extraction, we manually annotated GOLPH3 genes by comparing known exon sequences from a species that share a common ancestor most recently in time to the species of which the genomic piece is being annotated using the program Blast2seq v2.5 [65] with default parameters. Accession numbers and details about the taxonomic sampling are available in Supplementary Table S1.

We performed separate phylogenetic analyses for GOLPH3 and GOLPH3L paralogs. Amino acid sequences were aligned using MAFFT v.7 [66], allowing the program to choose the alignment strategy (L-INS-i in both cases). Nucleotide alignments were generated using the amino acid alignments as templates using the software PAL2NAL [67]. We used the proposed model tool of IQ-Tree v.1.6.12 [68] to select the best-fitting model of codon substitution, which selected MGK+F1X4+R3 for GOLPH3 and MGK+F3X4+G4 for GOLPH3L. This approach uses a more realistic description of the evolutionary process at the protein-coding sequence level by incorporating the genetic code structure in the model. We used the maximum likelihood method to obtain the best trees using the program IQ-Tree v1.6.12 [69]. We assessed support for the nodes using three strategies: a Bayesian-like transformation of aLRT (aBayes test) [70], SH-like approximate likelihood ratio test (SH-aLRT) [71] and the ultrafast bootstrap approximation [72]. In each case (GOLPH3 and GOLPH3L), we carried out 25 independent runs to explore the tree space, and the tree with the highest likelihood score was chosen. In both cases, GOLPH3 and GOLPH3L sequences from crocodiles and turtles were used as outgroups (Supplementary Table S1).

Molecular Evolution analysis

To measure variation in functional constraint among the GOLPH3L genes and to test for evidence of positive selection, we estimated the omega parameter (d_N/d_S), using a maximum-likelihood approach [73] implemented in the CODEML module of the program PAML v.4.8a [74]. We implemented branch-site models, which explore changes in the omega parameter for a set of sites in a specific branch of the tree to assess changes in their selective regime [75]. In this case, we conducted two separate analyses. In the first, the ancestral branch of Galliformes was labeled as the foreground branch, while in the second, the branch leading to manakins was labeled as a foreground branch. We compared the modified model A [75–77], in which some sites are allowed to

change to an omega value > 1 in the foreground branch, with the corresponding null hypothesis of neutral evolution using a Likelihood Ratio Test (LRT). Three starting omega values (0.5, 1, and 2) were used to check the existence of multiple local optima. The Bayes Empirical Bayes (BEB) method was used to identify sites under positive selection [78,79].

Secondary structure and disordered region prediction and protein structure homology modeling

Secondary structure and disordered region prediction was performed using the PredictProtein server (https://predictprotein.org/)[80]. Multiple sequence alignment was performed using MAFFT v.7 server (https://mafft.cbrc.jp/alignment/server/) with default parameters [81]. Multiple sequence alignment editing was performed using Jalview software v.2.11.1.3 [82]. Protein structure homology modeling was performed using the SWISS-MODEL server (https://swissmodel.expasy.org/)[83]. Structural figures were prepared with PyMOL Molecular Graphics System, Version 2.0.6 Schrödinger, LLC.

Transcript abundance analyses

GOLPH3 transcript abundance was measured in chicken (*Gallus gallus*) and mallard (*Anas platyrhynchos*). We collected three RNASeq libraries from brain, heart, intestine, kidney, liver, lung, spleen, ovary, and testis from each species gathered from the NCBI Short Read Archive (SRA) [84]. Accession numbers can be found in Supplemental Table S2. Reference transcript sequences were collected from Ensembl v.102 [62], and we only included the longest transcript for each gene. For each library, adapters were removed using Trimmomatic 0.38 [85], and reads were filtered for quality using the parameters HEADCROP:5, SLIDINGWINDOW:5:30, and MINLEN:50. We mapped quality filtered paired-end RNAseq reads back to reference sequences using Bowtie 1.2.2 [86] and default parameters of RSEM [87]. Normalization of raw read counts for each species was performed using the estimateSizeFactors and estimateDispersions functions in DESeq2 v1.26 [88].

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Author contributions

JCO and GAM designed the study. MWV, JG, KZ, JCO, GAM collected and/or analyzed data. JCO and GAM wrote the manuscript. MWV, LV-C, FJM reviewed and edited the manuscript. All authors contributed to the article and approved the submitted version.

Competing Interests

The authors declare no competing of interest

419 **Figure legends**
420 **Figure 1.** Maximum likelihood tree showing sister group relationships among GOLPH3 genes of
421 birds. Numbers above the nodes correspond to support values from the ultrafast bootstrap routine.
422 GOLPH3 sequences from crocodiles and turtles were used as outgroups (not shown). The scale
423 denotes substitutions per site and colors represent gene lineages. In the case of the Northern fulmar
424 and Dalmatian pelican, there is no syntenic information to define to which gene lineage they
425 belong. In consequence, they were not included in any shading or do not have a gene name
426
427 **Figure 2.** An evolutionary hypothesis regarding the evolution of the Golgi phosphoprotein 3
428 (GOLPH3) gene family in birds. According to our results, the last common ancestor of birds had
429 a repertoire of two GOLPH3 genes (GOLPH3 and GOLPH3L). The GOLPH3L gene was inherited
430 by all species of birds and maintained as a single copy gene (brown lineage). The evolution of the
431 GOLPH3 gene is more complicated. The gene present in the bird ancestor was inherited by
432 paleognaths (ostriches, tinamous and allies) and maintained as a single copy gene in most species.
433 In the case of Neoaves (zebra finches, kakapos and allies), the ancestral GOLPH3 gene underwent
434 a duplication event in the ancestor of the group giving rise to a repertoire of two genes (blue and
435 light blue gene lineages). In the last common ancestor of Anseriformes (ducks, swans and allies)
436 and Galliformes (chickens, pheasants and allies) the ancestral GOLPH3 gene underwent a
437 duplication event giving rise to a repertoire of two genes, one of the copies was retained in
438 Galliformes (red lineage), but lost in Anseriformes (red lineage). The other copy originated in the
439 ancestor of Galliformes and Anseriformes, was also retained in Galliformes (pink lineage),
440 however, in the last common ancestor of Anseriformes underwent a duplication event giving rise
441 to the repertoire of two copies (purple and light purple lineages). We use the subscripts to indicate
442 the ancestor in which the gene repertoires were originated, N = the ancestor of Neoaves, A = the
443 ancestor of Anseriformes and GA = the galliform/anseriform ancestor. Silhouette images were
444 obtained from PhyloPic (http://phylopic.org/).
445
446 **Figure 3.** Alignment of Golgi phosphoprotein 3 (GOLPH3) amino acid sequences from chicken
447 (*Gallus gallus*), ring-necked pheasant (*Phasianus colchicus)*, turkey (*Meleagris gallopavo*) and
448 japanese quail (*Coturnix japonica*). Amino acids positions that differentiate between paralogs are
449 in pink and red. The N-terminal region of the protein is shaded.
450
451 **Figure 4.** Alignment of Golgi phosphoprotein 3 (GOLPH3) amino acid sequences from mallard
452 (*Anas platyrhynchos*), Tufted duck (*Aythya fuligula)*, swan goose (*Anser cygnoides*) and ruddy
453 duck (*Oxyura jamaicensis*). Amino acids positions that differentiate between paralogs are in purple
454 and light purple. The N-terminal region of the protein is shaded.
455
456 **Figure 5.** Alignment of Golgi phosphoprotein 3 (GOLPH3) amino acid sequences from lance
457 tailed manakin (*Chiroxiphia lanceolata*), kakapo (*Strigops habroptilus*), New caledonian crow
458 (*Corvus moneduloides*) and zebra finch (*Taeniopygia guttata*). The N-terminal region of the
459 protein is shaded.
460
461 **Figure 6.** Secondary structure and disordered region predictions of GOLPH3 (A) and GOLPH3L
462 (B) in human (*Homo sapiens*), mouse (*Mus musculus*), chicken (*Gallus gallus*), Western clawed
463 frog (*Xenopus tropicalis*), coelacanth (*Latimeria chalumnae*), spotted gar (*Lepisosteus oculatus*),

464 thorny skate (*Amblyraja radiata*), fruit fly (*Drosophila melanogaster*), roundworm
465 (*Caenorhabditis elegans*) and brewer yeast (*Saccharomyces cerevisiae*).
466
467 **Figure 7.** Maximum likelihood tree showing sister group relationships among GOLPH3L genes
468 of birds. Numbers above the nodes correspond to support values from the ultrafast bootstrap
469 routine. GOLPH3L sequences from crocodiles and turtles were used as outgroups (not shown).
470 The scale denotes substitutions per site.
471
472 **Figure 8.** Alignment of Golgi phosphoprotein 3L (GOLPH3L) amino acid sequences from mallard
473 (*Anas platyrhynchos*), Tufted duck (*Aythya fuligula)*, black swan (*Cygnus atratus*), ruddy duck
474 (*Oxyura jamaicensis*), chicken (*Gallus gallus*), ring-necked pheasant (*Phasianus colchicus)*,
475 turkey (*Meleagris gallopavo*), japanese quail (*Coturnix japonica*), lance tailed manakin
476 (*Chiroxiphia lanceolata*), kakapo (*Strigops habroptilus*), New caledonian crow (*Corvus*
477 *moneduloides*) and zebra finch (*Taeniopygia guttata*). The N-terminal region of the protein is
478 shaded.
479
480 **Figure 9**. Transcript abundance measurements of GOLPH3 paralogs across a panel of nine tissues
481 in A) chicken (*Gallus gallus*) and B) mallard (*Anas platyrhynchos*). The mean and standard
482 deviation are plotted for three replicates per tissue. In many cases the standard deviation was
483 smaller than the size of the circle representing the mean and appears hidden.
484
485
486

487 **References**

488 1. Wu, C. C. *et al.* GMx33: a novel family of trans-Golgi proteins identified by proteomics.
489 *Traffic* **1**, 963–975 (2000).
490 2. Bell, A. W. *et al.* Proteomics characterization of abundant Golgi membrane proteins. *J.*
491 *Biol. Chem.* **276**, 5152–5165 (2001).
492 3. Sechi, S., Frappaolo, A., Belloni, G., Colotti, G. & Giansanti, M. G. The multiple cellular
493 functions of the oncoprotein Golgi phosphoprotein 3. *Oncotarget* **6**, 3493–3506 (2015).
494 4. Ali, M. F., Chachadi, V. B., Petrosyan, A. & Cheng, P.-W. Golgi phosphoprotein 3
495 determines cell binding properties under dynamic flow by controlling Golgi localization of
496 core 2 N-acetylglucosaminyltransferase 1. *J. Biol. Chem.* **287**, 39564–39577 (2012).
497 5. Pereira, N. A., Pu, H. X., Goh, H. & Song, Z. Golgi phosphoprotein 3 mediates the Golgi
498 localization and function of protein O-linked mannose β-1,2-N-
499 acetylglucosaminyltransferase 1. *J. Biol. Chem.* **289**, 14762–14770 (2014).
500 6. Isaji, T. *et al.* An oncogenic protein Golgi phosphoprotein 3 up-regulates cell migration via
501 sialylation. *J. Biol. Chem.* **289**, 20694–20705 (2014).
502 7. Arriagada, C. *et al.* The knocking down of the oncoprotein Golgi phosphoprotein 3 in T98G
503 cells of glioblastoma multiforme disrupts cell migration by affecting focal adhesion
504 dynamics in a focal adhesion kinase-dependent manner. *PLoS One* **14**, e0212321 (2019).
505 8. Rahajeng, J. *et al.* Efficient Golgi Forward Trafficking Requires GOLPH3-Driven, PI4P-
506 Dependent Membrane Curvature. *Dev. Cell* **50**, 573–585.e5 (2019).
507 9. Nakashima-Kamimura, N. *et al.* MIDAS/GPP34, a nuclear gene product, regulates total
508 mitochondrial mass in response to mitochondrial dysfunction. *J. Cell Sci.* **118**, 5357–5367
509 (2005).
510 10. Boddy, A. M., Harrison, T. M. & Abegglen, L. M. Comparative Oncology: New Insights

511 into an Ancient Disease. *iScience* **23**, 101373 (2020).

512 11. Albuquerque, T. A. F., Drummond do Val, L., Doherty, A. & de Magalhães, J. P. From
513 humans to hydra: patterns of cancer across the tree of life. *Biol. Rev. Camb. Philos. Soc.* **93**,
514 1715–1734 (2018).

515 12. Abegglen, L. M. *et al.* Potential Mechanisms for Cancer Resistance in Elephants and
516 Comparative Cellular Response to DNA Damage in Humans. *JAMA* **314**, 1850–1860
517 (2015).

518 13. Sulak, M. *et al.* TP53 copy number expansion is associated with the evolution of increased
519 body size and an enhanced DNA damage response in elephants. (2016)
520 doi:10.7554/eLife.11994.

521 14. Pang, V. F. *et al.* Spontaneous neoplasms in zoo mammals, birds, and reptiles in Taiwan – a
522 10-year survey. *Anim. Biol. Leiden Neth.* **62**, 95–110 (2012).

523 15. Lombard, L. S. & Witte, E. J. Frequency and types of tumors in mammals and birds of the
524 Philadelphia Zoological Garden. *Cancer Res.* **19**, 127–141 (1959).

525 16. Ratcliffe, H. L. Incidence and Nature of Tumors in Captive Wild Mammals and Birds. *Am.*
526 *J. Cancer* **17**, 116–135 (1933).

527 17. Møller, A. P., Erritzøe, J. & Soler, J. J. Life history, immunity, Peto's paradox and tumours
528 in birds. *J. Evol. Biol.* **30**, 960–967 (2017).

529 18. Effron, M., Griner, L. & Benirschke, K. Nature and rate of neoplasia found in captive wild
530 mammals, birds, and reptiles at necropsy. *J. Natl. Cancer Inst.* **59**, 185–198 (1977).

531 19. Hochberg, M. E. & Noble, R. J. A framework for how environment contributes to cancer
532 risk. *Ecol. Lett.* **20**, 117–134 (2017).

533 20. Nei, M. & Rooney, A. P. Concerted and birth-and-death evolution of multigene families.

534 *Annu. Rev. Genet.* **39**, 121–152 (2005).

535 21. Glover, N. *et al.* Advances and Applications in the Quest for Orthologs. *Mol. Biol. Evol.* **36**,
536 2157–2164 (2019).

537 22. Kimball, R. T. *et al.* A Phylogenomic Supertree of Birds. *Diversity* **11**, 109 (2019).

538 23. Prum, R. O. *et al.* A comprehensive phylogeny of birds (Aves) using targeted next-
539 generation DNA sequencing. *Nature* **526**, 569–573 (2015).

540 24. Feng, S. *et al.* Dense sampling of bird diversity increases power of comparative genomics.
541 *Nature* **587**, 252–257 (2020).

542 25. Kuhl, H. *et al.* An Unbiased Molecular Approach Using 3'-UTRs Resolves the Avian
543 Family-Level Tree of Life. *Mol. Biol. Evol.* **38**, 108–127 (2021).

544 26. Chue, J. & Smith, C. A. Sex determination and sexual differentiation in the avian model.
545 *FEBS J.* **278**, 1027–1034 (2011).

546 27. Hughes, A. L. & Nei, M. Nucleotide substitution at major histocompatibility complex class
547 II loci: evidence for overdominant selection. *Proc. Natl. Acad. Sci. U. S. A.* **86**, 958–962
548 (1989).

549 28. Hedges, S. B., Marin, J., Suleski, M., Paymer, M. & Kumar, S. Tree of life reveals clock-
550 like speciation and diversification. *Mol. Biol. Evol.* **32**, 835–845 (2015).

551 29. Hoffmann, F. G., Storz, J. F., Gorr, T. A. & Opazo, J. C. Lineage-specific patterns of
552 functional diversification in the alpha- and beta-globin gene families of tetrapod vertebrates.
553 *Mol. Biol. Evol.* **27**, 1126–1138 (2010).

554 30. Gramzow, L., Lobbes, D., Innard, N. & Theißen, G. Independent origin of MIRNA genes
555 controlling homologous target genes by partial inverted duplication of antisense-transcribed
556 sequences. *Plant J.* **101**, 401–419 (2020).

557 31. Opazo, J. C. & Zavala, K. Phylogenetic evidence for independent origins of GDF1 and
558 GDF3 genes in anurans and mammals. *Sci. Rep.* **8**, 13595 (2018).
559 32. Goodman, M., Czelusniak, J., Koop, B. F., Tagle, D. A. & Slightom, J. L. Globins: a case
560 study in molecular phylogeny. *Cold Spring Harb. Symp. Quant. Biol.* **52**, 875–890 (1987).
561 33. Kriener, K., O'hUigin, C. & Klein, J. Independent origin of functional MHC class II genes
562 in humans and New World monkeys. *Hum. Immunol.* **62**, 1–14 (2001).
563 34. Wichmann, I. A. *et al.* Evolutionary history of the reprimo tumor suppressor gene family in
564 vertebrates with a description of a new reprimo gene lineage. *Gene* **591**, 245–254 (2016).
565 35. Opazo, J. C., Zavala, K., Vandewege, M. W. & Hoffmann, F. G. Phylogenetic
566 diversification of sirtuin genes with a description of a new family member. *bioRxiv* (2020)
567 doi:10.1101/2020.07.17.209510.
568 36. Himmel, N. J., Gray, T. R. & Cox, D. N. Phylogenetics Identifies Two Eumetazoan TRPM
569 Clades and an Eighth TRP Family, TRP Soromelastatin (TRPS). *Mol. Biol. Evol.* **37**, 2034–
570 2044 (2020).
571 37. Lynch, M. & Conery, J. S. The evolutionary fate and consequences of duplicate genes.
572 *Science* vol. 290 1151–1155 (2000).
573 38. Tollis, M. *et al.* Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean
574 Genomes Including an Assembly for the Humpback Whale (Megaptera novaeangliae). *Mol.*
575 *Biol. Evol.* **36**, 1746–1763 (2019).
576 39. Tejada-Martinez, D., de Magalhães, J. P. & Opazo, J. C. Positive selection and gene
577 duplications in tumour suppressor genes reveal clues about how cetaceans resist cancer.
578 *Cold Spring Harbor Laboratory* 2020.01.15.908244 (2021)
579 doi:10.1101/2020.01.15.908244.

580 40. de Magalhães, J. P. & Costa, J. A database of vertebrate longevity records and their relation
581 to other life-history traits. *J. Evol. Biol.* **22**, 1770–1774 (2009).
582 41. Seim, I. *et al.* Genome analysis reveals insights into physiology and longevity of the
583 Brandt's bat Myotis brandtii. *Nat. Commun.* **4**, 1–8 (2013).
584 42. Zhang, G. *et al.* Comparative analysis of bat genomes provides insight into the evolution of
585 flight and immunity. *Science* **339**, 456–460 (2013).
586 43. Santra, M. K., Wajapeyee, N. & Green, M. R. F-box protein FBXO31 mediates cyclin D1
587 degradation to induce G1 arrest after DNA damage. *Nature* **459**, 722–725 (2009).
588 44. Wood, C. S. *et al.* PtdIns4P recognition by Vps74/GOLPH3 links PtdIns 4-kinase signaling
589 to retrograde Golgi trafficking. *J. Cell Biol.* **187**, 967–975 (2009).
590 45. Schmitz, K. R. *et al.* Golgi localization of glycosyltransferases requires a Vps74p oligomer.
591 *Dev. Cell* **14**, 523–534 (2008).
592 46. Barnes, M. R. & Gray, I. C. *Bioinformatics for Geneticists*. (Wiley, 2003).
593 47. Borcherds, W., Bremer, A., Borgia, M. B. & Mittag, T. How do intrinsically disordered
594 protein regions encode a driving force for liquid-liquid phase separation? *Curr. Opin.*
595 *Struct. Biol.* **67**, 41–50 (2020).
596 48. Ng, M. M., Dippold, H. C., Buschman, M. D., Noakes, C. J. & Field, S. J. GOLPH3L
597 antagonizes GOLPH3 to determine Golgi morphology. *Mol. Biol. Cell* **24**, 796–808 (2013).
598 49. Sotgia, F. *et al.* Mitochondria 'fuel' breast cancer metabolism: fifteen markers of
599 mitochondrial biogenesis label epithelial cancer cells, but are excluded from adjacent
600 stromal cells. *Cell Cycle* **11**, 4390–4401 (2012).
601 50. Kunigou, O. *et al.* Role of GOLPH3 and GOLPH3L in the proliferation of human
602 rhabdomyosarcoma. *Oncol. Rep.* **26**, 1337–1342 (2011).

603 51. Feng, Y. *et al.* GOLPH3L is a Novel Prognostic Biomarker for Epithelial Ovarian Cancer.
604 *J. Cancer* **6**, 893–900 (2015).
605 52. Feng, Y. *et al.* The Role of GOLPH3L in the Prognosis and NACT response in Cervical
606 Cancer. *J. Cancer* **8**, 443–454 (2017).
607 53. He, S. *et al.* The oncogenic Golgi phosphoprotein 3 like overexpression is associated with
608 cisplatin resistance in ovarian carcinoma and activating the NF-κB signaling pathway. *J.*
609 *Exp. Clin. Cancer Res.* **36**, 137 (2017).
610 54. Yang, Z. & Bielawski, J. P. Statistical methods for detecting molecular adaptation. *Trends*
611 *Ecol. Evol.* **15**, 496–503 (2000).
612 55. Jacobs, G. H. Primate photopigments and primate color vision. *Proc. Natl. Acad. Sci. U. S.*
613 *A.* **93**, 577–581 (1996).
614 56. Uhlén, M. *et al.* Proteomics. Tissue-based map of the human proteome. *Science* **347**,
615 1260419 (2015).
616 57. Eisenberg, E. & Levanon, E. Y. Human housekeeping genes, revisited. *Trends Genet.* **29**,
617 569–574 (2013).
618 58. Albertson, R. C., Cresko, W., Detrich, H. W., 3rd & Postlethwait, J. H. Evolutionary mutant
619 models for human disease. *Trends Genet.* **25**, 74–81 (2009).
620 59. Goodman, M., Czelusniak, J., Moore, G. W., Romero-Herrera, A. E. & Matsuda, G. Fitting
621 the Gene Lineage into its Species Lineage, a Parsimony Strategy Illustrated by Cladograms
622 Constructed from Globin Sequences. *Systematic Biology* vol. 28 132–163 (1979).
623 60. Gabaldón, T. Large-scale assignment of orthology: back to phylogenetics? *Genome Biology*
624 vol. 9 235 (2008).
625 61. Sharma, S. *et al.* The NCBI BioCollections Database. *Database* **2018**, (2018).

626 62. Yates, A. D. *et al.* Ensembl 2020. *Nucleic Acids Res.* **48**, D682–D688 (2020).
627 63. Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J. Basic local alignment
628 search tool. *J. Mol. Biol.* **215**, 403–410 (1990).
629 64. Geer, L. Y. *et al.* The NCBI BioSystems database. *Nucleic Acids Res.* **38**, D492–6 (2010).
630 65. Tatusova, T. A. & Madden, T. L. BLAST 2 Sequences, a new tool for comparing protein
631 and nucleotide sequences. *FEMS Microbiol. Lett.* **174**, 247–250 (1999).
632 66. Katoh, K. & Standley, D. M. MAFFT multiple sequence alignment software version 7:
633 improvements in performance and usability. *Mol. Biol. Evol.* **30**, 772–780 (2013).
634 67. Suyama, M., Torrents, D. & Bork, P. PAL2NAL: robust conversion of protein sequence
635 alignments into the corresponding codon alignments. *Nucleic Acids Res.* **34**, W609–12
636 (2006).
637 68. Kalyaanamoorthy, S., Minh, B. Q., Wong, T. K. F., von Haeseler, A. & Jermiin, L. S.
638 ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat. Methods* **14**,
639 587–589 (2017).
640 69. Trifinopoulos, J., Nguyen, L.-T., von Haeseler, A. & Minh, B. Q. W-IQ-TREE: a fast online
641 phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Res.* **44**, W232–5 (2016).
642 70. Anisimova, M., Gil, M., Dufayard, J.-F., Dessimoz, C. & Gascuel, O. Survey of branch
643 support methods demonstrates accuracy, power, and robustness of fast likelihood-based
644 approximation schemes. *Syst. Biol.* **60**, 685–699 (2011).
645 71. Guindon, S. *et al.* New algorithms and methods to estimate maximum-likelihood
646 phylogenies: assessing the performance of PhyML 3.0. *Syst. Biol.* **59**, 307–321 (2010).
647 72. Hoang, D. T., Chernomor, O., von Haeseler, A., Minh, B. Q. & Vinh, L. S. UFBoot2:
648 Improving the Ultrafast Bootstrap Approximation. *Mol. Biol. Evol.* **35**, 518–522 (2018).

649 73. Goldman, N. & Yang, Z. A codon-based model of nucleotide substitution for protein-coding
650 DNA sequences. *Molecular Biology and Evolution* (1994)
651 doi:10.1093/oxfordjournals.molbev.a040153.
652 74. Yang, Z. PAML 4: phylogenetic analysis by maximum likelihood. *Mol. Biol. Evol.* **24**,
653 1586–1591 (2007).
654 75. Yang, Z. & dos Reis, M. Statistical properties of the branch-site test of positive selection.
655 *Mol. Biol. Evol.* **28**, 1217–1228 (2011).
656 76. Yang, Z., Wong, W. S. W. & Nielsen, R. Bayes empirical bayes inference of amino acid
657 sites under positive selection. *Mol. Biol. Evol.* **22**, 1107–1118 (2005).
658 77. Zhang, J., Nielsen, R. & Yang, Z. Evaluation of an improved branch-site likelihood method
659 for detecting positive selection at the molecular level. *Mol. Biol. Evol.* **22**, 2472–2479
660 (2005).
661 78. Nielsen, R. & Yang, Z. Likelihood models for detecting positively selected amino acid sites
662 and applications to the HIV-1 envelope gene. *Genetics* **148**, 929–936 (1998).
663 79. Yang, Z., Nielsen, R., Goldman, N. & Pedersen, A. M. Codon-substitution models for
664 heterogeneous selection pressure at amino acid sites. *Genetics* **155**, 431–449 (2000).
665 80. Yachdav, G. *et al.* PredictProtein--an open resource for online prediction of protein
666 structural and functional features. *Nucleic Acids Res.* **42**, W337–43 (2014).
667 81. Katoh, K., Rozewicki, J. & Yamada, K. D. MAFFT online service: multiple sequence
668 alignment, interactive sequence choice and visualization. *Brief. Bioinform.* **20**, 1160–1166
669 (2019).
670 82. Waterhouse, A. M., Procter, J. B., Martin, D. M. A., Clamp, M. & Barton, G. J. Jalview
671 Version 2--a multiple sequence alignment editor and analysis workbench. *Bioinformatics*

672 **25**, 1189–1191 (2009).

673 83. Waterhouse, A. *et al.* SWISS-MODEL: homology modelling of protein structures and
674 complexes. *Nucleic Acids Res.* **46**, W296–W303 (2018).

675 84. Leinonen, R., Sugawara, H., Shumway, M. & International Nucleotide Sequence Database
676 Collaboration. The sequence read archive. *Nucleic Acids Res.* **39**, D19–21 (2011).

677 85. Bolger, A. M., Lohse, M. & Usadel, B. Trimmomatic: a flexible trimmer for Illumina
678 sequence data. *Bioinformatics* **30**, 2114–2120 (2014).

679 86. Langmead, B., Trapnell, C., Pop, M. & Salzberg, S. L. Ultrafast and memory-efficient
680 alignment of short DNA sequences to the human genome. *Genome Biol.* **10**, R25 (2009).

681 87. Li, B. & Dewey, C. N. RSEM: accurate transcript quantification from RNA-Seq data with
682 or without a reference genome. *BMC Bioinformatics* vol. 12 (2011).

683 88. Love, M. I., Huber, W. & Anders, S. Moderated estimation of fold change and dispersion
684 for RNA-seq data with DESeq2. *Genome Biol.* **15**, 550 (2014).

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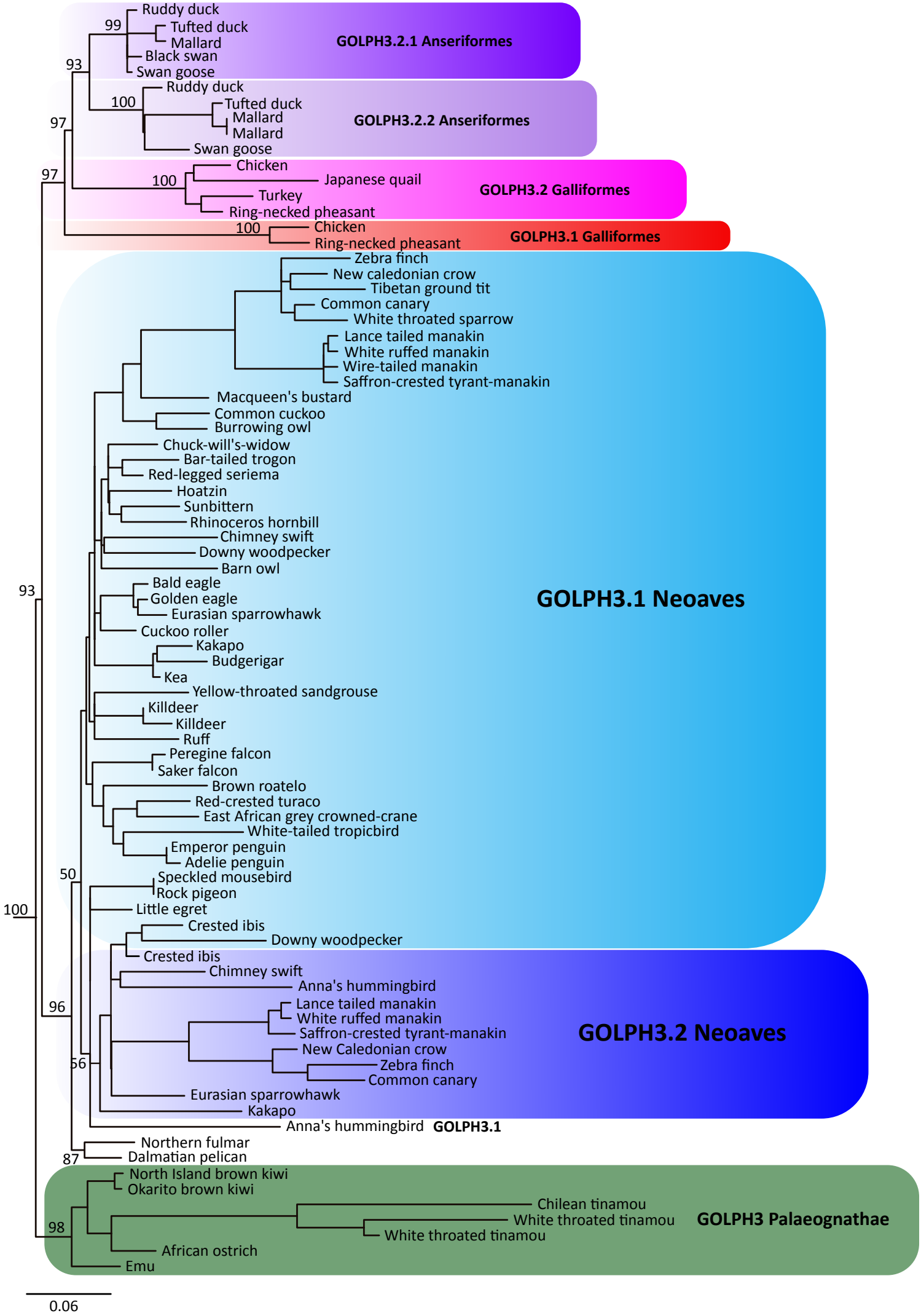
687


Ruddy duck
Tufted duck
Mallard
Black swan
Swan goose
GOLPH3.2.1 Anseriformes
Ruddy duck
Tufted duck
Mallard
Mallard
Swan goose
GOLPH3.2.2 Anseriformes
Chicken
Japanese quail
Turkey
Ring-necked pheasant
GOLPH3.2 Galliformes
Chicken
Ring-necked pheasant
GOLPH3.1 Galliformes
Zebra finch
New caledonian crow
Tibetan ground tit
Common canary
White throated sparrow
Lance tailed manakin
White ruffed manakin
Wire-tailed manakin
Saffron-crested tyrant-manakin
Macqueen's bustard
Common cuckoo
Burrowing owl
Chuck-will's-widow
Bar-tailed trogon
Red-legged seriema
Hoatzin
Sunbittern
Rhinoceros hornbill
Chimney swift
Downy woodpecker
Barn owl
Bald eagle
Golden eagle
Eurasian sparrowhawk
Cuckoo roller
Kakapo
Budgerigar
Kea
Yellow-throated sandgrouse
Killdeer
Killdeer
Ruff
Peregine falcon
Saker falcon
Brown roatelo
Red-crested turaco
East African grey crowned-crane
White-tailed tropicbird
Emperor penguin
Adelie penguin
Speckled mousebird
Rock pigeon
Little egret
GOLPH3.1 Neoaves
Crested ibis
Downy woodpecker
Crested ibis
Chimney swift
Anna's hummingbird
Lance tailed manakin
White ruffed manakin
Saffron-crested tyrant-manakin
New Caledonian crow
Zebra finch
Common canary
Eurasian sparrowhawk
Kakapo
GOLPH3.2 Neoaves
Anna's hummingbird
GOLPH3.1
Northern fulmar
Dalmatian pelican
North Island brown kiwi
Okarito brown kiwi
Chilean tinamou
White throated tinamou
White throated tinamou
African ostrich
Emu
GOLPH3 Palaeognathae
99
93
100
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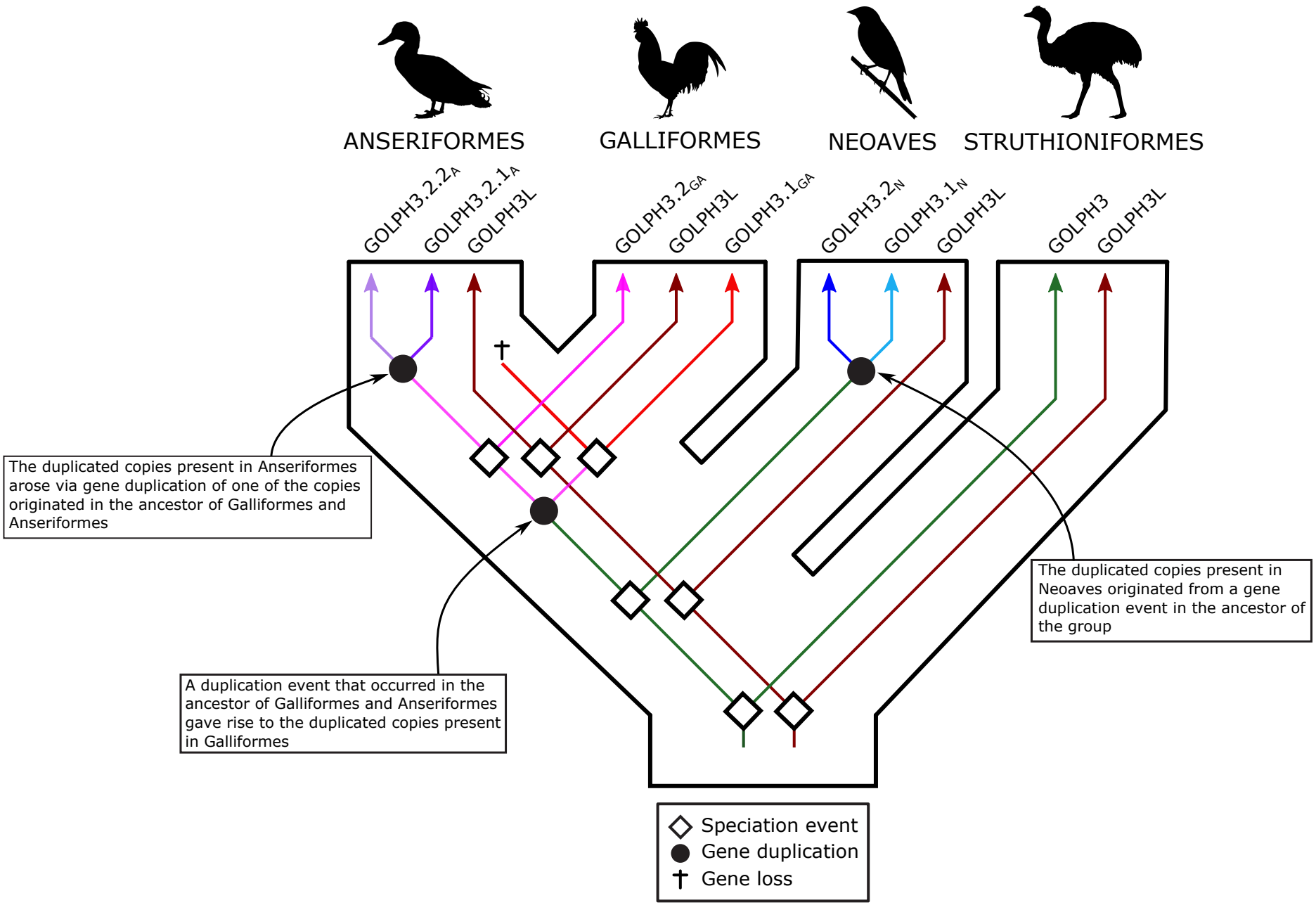
0.06


ANSERIFORMES
GALLIFORMES
NEOAVES
STRUTHIONIFORMES
GOLPH3.2.2A
GOLPH3.2.1A
GOLPH3L
GOLPH3.2GA
GOLPH3L
GOLPH3.1GA
GOLPH3.2N
GOLPH3.1N
GOLPH3L
GOLPH3
GOLPH3L
The duplicated copies present in Anseriformes arose via gene duplication of one of the copies originated in the ancestor of Galliformes and Anseriformes
A duplication event that occurred in the ancestor of Galliformes and Anseriformes gave rise to the duplicated copies present in Galliformes
The duplicated copies present in Neoaves originated from a gene duplication event in the ancestor of the group
Speciation event
Gene duplication
Gene loss

N-terminal

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                                  1         10        20        30        40        50        60        70
Chicken GOLPH3.2GA                MTSLTQRSSGLVQRRTEASRSAAADKERGAGGGSEDEGRREEPGDDEKGDSKETRLTLMEEVLLLGLKDREGYT
Ring-necked pheasant GOLPH3.2GA   MTSLTQRSSGLVQRRTEASRSAAADKERGAGGGPEDEGRREEPGDDEKGDSKETRLTLMEEVLLLGLKDREGYT
Turkey GOLPH3.2GA                 -------------------------------------------------------------------GYT
Japanese quail GOLPH3.2GA         MTSLTQRSSGLVQRRTEASRSAAADKERGAGGGPEDEGRREEPGDDEKGDSKETRLTLMEEVLLLGLKDREGYT

Chicken GOLPH3.1GA                MTSLTQRCSGLVQRRTEASRS-AADEERGARGGPEDEGCRDELGDDEKGDCKQTRLTLMEEVLLLGLKDREGYT
Ring-necked pheasant GOLPH3.1GA   MTSLTQRCSGLVQRRTEASRS-AADEERGARGGLENEGRRDELGDDEKGDSKQTRLTLMEEVLLLGLKDREGYT

                                  80        90        100       110       120       130       140
Chicken GOLPH3.2GA                SFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQNW
Ring-necked pheasant GOLPH3.2GA   SFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQNW
Turkey GOLPH3.2GA                 SFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQNW
Japanese quail GOLPH3.2GA         SFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQNW

Chicken GOLPH3.1GA                SFWNDCISSGLRGCMLIELSLRGRLQLEACGMRRKSLLTRKVICKSDVPTGDVLLDEALKHIKETQPPETVQNW
Ring-necked pheasant GOLPH3.1GA   SFWNDCISSGLRGCMLIELSLRGRLQLEACGMRRKSLLTRKVICKSDVPTGDVLLDEALKHIKETQPPETIQNW

                                  150       160       170       180       190       200       210       220
Chicken GOLPH3.2GA                IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV
Ring-necked pheasant GOLPH3.2GA   IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV
Turkey GOLPH3.2GA                 IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV
Japanese quail GOLPH3.2GA         IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV

Chicken GOLPH3.1GA                IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV
Ring-necked pheasant GOLPH3.1GA   IELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDKWV

                                  230       240       250       260       270       280       290   294
Chicken GOLPH3.2GA                NDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Ring-necked pheasant GOLPH3.2GA   NDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Turkey GOLPH3.2GA                 NDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Japanese quail GOLPH3.2GA         NDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK

Chicken GOLPH3.1GA                NDPHRMDKRLLALIYLAHASDVLENAFAPLLDELYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Ring-necked pheasant GOLPH3.1GA   NDPHRMDKRLLALIYLAHASDVLENAFAPLLDELYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
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                                 1         10        20        30        40        50        60        70
Mallard GOLPH3.2.1A              MTSLTQRSSGLVQRRTEASRS-AAAADKERGAGGGPEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Tufted duck GOLPH3.2.1A          MTSLTQRSSGLVQRRTEASRS-AAAADKERGAGGGPEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Swan goose GOLPH3.2.1A           MTSLTQRSSGLVQRRTEASRS-AAAADKERGAGGGPEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Ruddy duck GOLPH3.2.1A           MTSLTQRSSGLVQRRTEASRS-AAAADKERGAGGGPEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG

Mallard GOLPH3.2.2A              MTSLTQRSSGLVQRRTEASRS-AAAADKEWGAGGGLEDEGHRDELGDDEKGDSKETRLTLMEEVLLLGLKDREG
Tufted duck GOLPH3.2.2A          MTSLTQRSSGLVQRRTEASRS-AAAADKEWGAGGGLEDEGHRDELGDDVKGDSKETRLTLMEEVLLLGLKDREG
Swan goose GOLPH3.2.2A           MTSLTQRSSGLVQRRTEASRSAAAAAAKERGTGGGLEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDRXG
Ruddy duck GOLPH3.2.2A           MTSLTQRNSGLVQRRTEASRSAAAAADKERGAGGGLEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG

                                         80        90       100       110       120       130       140
Mallard GOLPH3.2.1A              YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Tufted duck GOLPH3.2.1A          YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Swan goose GOLPH3.2.1A           YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Ruddy duck GOLPH3.2.1A           YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ

Mallard GOLPH3.2.2A              YTSFWNDCISSGLRGCMLIELALRGRLQLEACGIRRKSLLTRKVICKSDTSTGDVLLDEALKHIKETQPPETVQ
Tufted duck GOLPH3.2.2A          YTSFWNDCISSGLRGCMLIELALRGRLQLEACGIRRKSLLTRKVICKSDTSTGDVLLDEALKHIKETQPPETVQ
Swan goose GOLPH3.2.2A           YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDTSTGDVLLDEALKHIKETQPPETVQ
Ruddy duck GOLPH3.2.2A           YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDTSTGDVLLDEALKHIKETQPPETVQ

                                        150       160       170       180       190       200       210       220
Mallard GOLPH3.2.1A              NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Tufted duck GOLPH3.2.1A          NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Swan goose GOLPH3.2.1A           NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Ruddy duck GOLPH3.2.1A           NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK

Mallard GOLPH3.2.2A              NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Tufted duck GOLPH3.2.2A          NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Swan goose GOLPH3.2.2A           NWIELLS-------------------------------------------------------------------
Ruddy duck GOLPH3.2.2A           NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK

                                            230       240       250       260       270       280       290   296
Mallard GOLPH3.2.1A              WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Tufted duck GOLPH3.2.1A          WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Swan goose GOLPH3.2.1A           WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Ruddy duck GOLPH3.2.1A           WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK

Mallard GOLPH3.2.2A              WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRMRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Tufted duck GOLPH3.2.2A          WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRMRQLLDLDPEVECMKANTNEVLWAVVAAFTK
Swan goose GOLPH3.2.2A           ------------------------------------------------------------------------------
Ruddy duck GOLPH3.2.2A           WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
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N-terminal

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                                                  1         10        20        30        40        50        60        70
Lance tailed manakin GOLPH3.1N   MTSLTQRSSGLVQRRTEASRS--AAADKERGAGGGSDDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Kakapo GOLPH3.1N                 MTSLTQRSSGLVQRRTEASRS--AAADKERGAGGGSEDEGRRDESGDDEKGDSKETRLTLMEEVLLLGLKDREG
New Caledonian crow GOLPH3.1N    MTSLTQRSSGLVQRRTEASRSAAAAADKERGAGGGPEDEGRRDESGDDEKGDSKETRLTLMEEVLLLGLKDREG
Zebra finch GOLPH3.1N            MTSLTQRSSGLVQRRTEASRS-AAAADKERGAGGGPEDEGRRDESGDDEKGDSKETRLTLMEEVLLLGLKDREG

Lance tailed manakin GOLPH3.2N   MTSLTQRSSGLVQRRTEASRS--AAADKDREAGGGSEDGGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Kakapo GOLPH3.2N                 MTSLTQRSSGLVQRRTEASRS--TAAGKERGAGGGPEDEGRRDDPGDDEKGDSKEIRLTLMEEVLLLGLKDREG
New Caledonian crow GOLPH3.2N    MTSLTQRSSGLVQRRTEASRS--AAADKEREAGGGSEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG
Zebra finch GOLPH3.2N            MTSLTQRSSGLVQRRTEAFRN--AAAAKEREAGGSSEDEGRRDEPGDDEKGDSKETRLTLMEEVLLLGLKDREG

                                                 80        90       100       110       120       130       140
Lance tailed manakin GOLPH3.1N   YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Kakapo GOLPH3.1N                 YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
New Caledonian crow GOLPH3.1N    YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Zebra finch GOLPH3.1N            YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ

Lance tailed manakin GOLPH3.2N   YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Kakapo GOLPH3.2N                 YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLSRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
New Caledonian crow GOLPH3.2N    YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ
Zebra finch GOLPH3.2N            YTSFWNDCISSGLRGCMLIELALRGRLQLEACGMRRKSLLTRKVICKSDAPTGDVLLDEALKHIKETQPPETVQ

                                 150       160       170       180       190       200       210       220
Lance tailed manakin GOLPH3.1N   NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Kakapo GOLPH3.1N                 NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
New Caledonian crow GOLPH3.1N    NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Zebra finch GOLPH3.1N            NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK

Lance tailed manakin GOLPH3.2N   NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Kakapo GOLPH3.2N                 NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVVDK
New Caledonian crow GOLPH3.2N    NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK
Zebra finch GOLPH3.2N            NWIELLSGETWNPLKLHYQLRNVRERLAKNLVEKGVLTTEKQNFLLFDMTTHPLTNNNIKQRLIKKVQEAVLDK

                                          230       240       250       260       270       280       290     296
Lance tailed manakin GOLPH3.1N   WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKTNTNEVLWAVVAAFTK
Kakapo GOLPH3.1N                 WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANTNEVLWAVVAAFTK
New Caledonian crow GOLPH3.1N    WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKTNTNEVLWAVVAAFTK
Zebra finch GOLPH3.1N            WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKTNTNEVLWAVVAAFTK

Lance tailed manakin GOLPH3.2N   WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANMNEVLWAVVAAFTK
Kakapo GOLPH3.2N                 WVNDPHRMDKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEAECMKANTNEVLWAVVAAFTK
New Caledonian crow GOLPH3.2N    WVNDPHRMEKRLLALVYLAHASDVLENAFAPLLDEQYDLATKRVRQLLDLDPEVECMKANMNEVLWAVVAAFTK
Zebra finch GOLPH3.2N            WVNDPHRMEKRLLALVYLAHASDVLENAFSPLLDEQYDLATKRVRQLLDLDPEVECMKANMNEVLWAVVAAFTK
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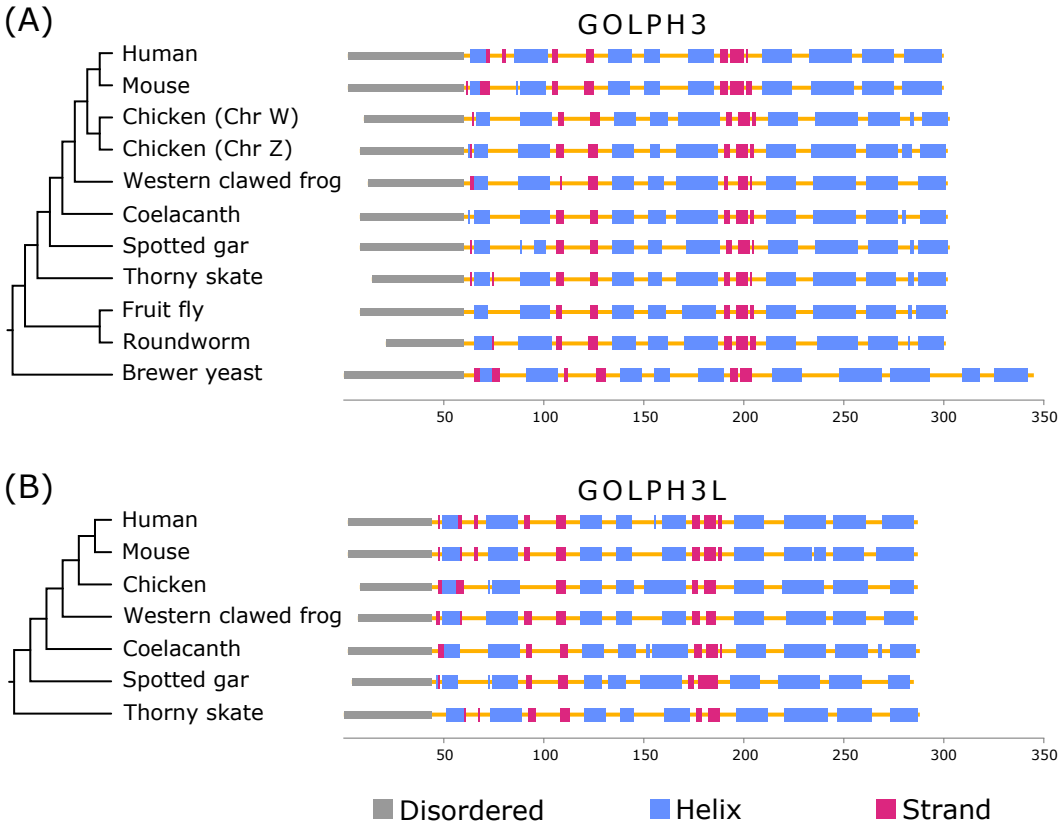
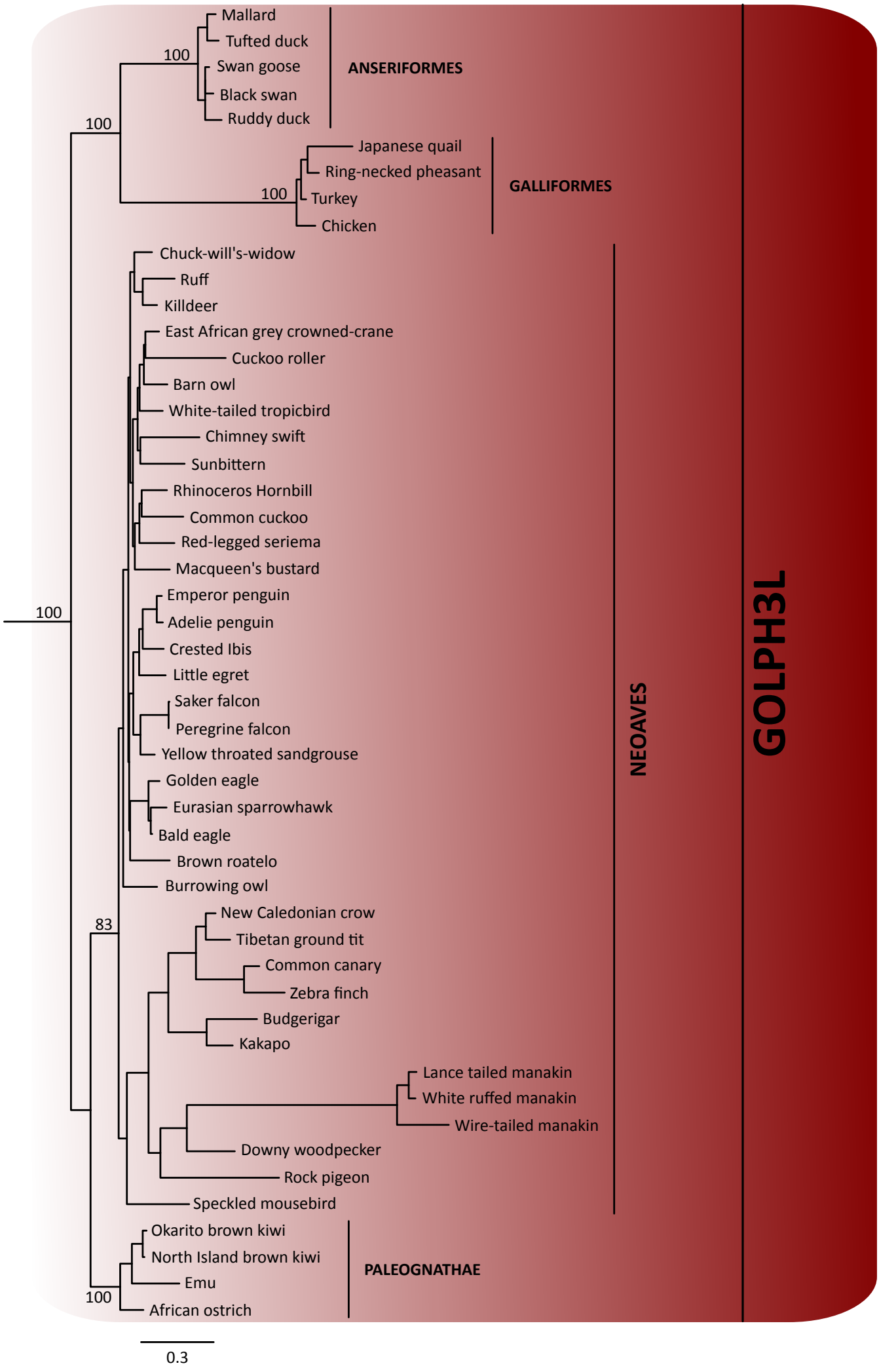

(A)
GOLPH3
Human
Mouse
Chicken (Chr W)
Chicken (Chr Z)
Western clawed frog
Coelacanth
Spotted gar
Thorny skate
Fruit fly
Roundworm
Brewer yeast
50
100
150
200
250
300
350
(B)
GOLPH3L
Human
Mouse
Chicken
Western clawed frog
Coelacanth
Spotted gar
Thorny skate
50
100
150
200
250
300
350
Disordered
Helix
Strand


Mallard
Tufted duck
Swan goose
Black swan
Ruddy duck
100
ANSERIFORMES
100
Japanese quail
Ring-necked pheasant
Turkey
Chicken
100
GALLIFORMES
Chuck-will's-widow
Ruff
Killdeer
East African grey crowned-crane
Cuckoo roller
Barn owl
White-tailed tropicbird
Chimney swift
Sunbittern
Rhinoceros Hornbill
Common cuckoo
Red-legged seriema
Macqueen's bustard
Emperor penguin
Adelie penguin
Crested Ibis
Little egret
Saker falcon
Peregrine falcon
Yellow throated sandgrouse
Golden eagle
Eurasian sparrowhawk
Bald eagle
Brown roatelo
Burrowing owl
New Caledonian crow
Tibetan ground tit
Common canary
Zebra finch
Budgerigar
Kakapo
Lance tailed manakin
White ruffed manakin
Wire-tailed manakin
Downy woodpecker
Rock pigeon
Speckled mousebird
NEOAVES
100
83
Okarito brown kiwi
North Island brown kiwi
Emu
African ostrich
100
PALEOGNATHAE
GOLPH3L
0.3

N-terminal

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                                  1         10        20        30        40        50        60        70        80        90
Mallard GOLPH3L                   MTTLTHRGRRSEAGGSVGKRLDGEEE---ERDP--EEDDDSKGTRLTLMEEVLLLGLKDK-GYTSFWNDCISSGLRGGILIELALRGRIQLEPLTA
Tufted duck GOLPH3L               MTTLTHRGRRTEAGGSVGKRVDGEE----ERDL---EDDDSKGTRLTLMEEVLLLGLKDKQGYTSFWNDCISSGLRGGILIELALRGRIQLEPLTA
Black swan GOLPH3L                MTTLTHRGRRTEAGGSTGKKLDDEEEAAAERDP---EDDDSKGTRLTLMEEVLLLGLKDKQGYTSFWNDCISPGLRGGILVELALRGRIQLEPLTT
Ruddy duck GOLPH3L                MTTLTHRGRRGDAGGSVGKKLDDEEEAAAERDP---EDDDSKGTRLTLMEEVLLLGLKDKQGYTSFWNDCISPGLRGGILVELALRGRIQLEPLTA

Chicken GOLPH3L                   MTTLTRRGWRGD------KRTEPEEDAAGDREQPDDDSDNSKATRLTLMEEVLLLGLQDKEGYPSFWNDCLSPGLRGGILIELALRGRIHLEPLTA
Ring-necked pheasant GOLPH3L      MTTLTRRGWRGD------KRTEPEEDVAADRELPDDDSDNSKAPRLTLMEEVLLLGLQDKEGYPSFWNDCLSPGLRGGILIELALRGRIHLEPLTA
Turkey GOLPH3L                    MTTLTRRGWRGD------KRTEPEEDAAADRELPDDDSDNSKAPRLTLMEEVLLLGLQDKEGYPSFWNDCLSPGLRGGILIELALRGRIHLEPLTA
Japanese quail GOLPH3L            MTTLTHRGWRGD------KRAEPEEDVAADKELPDDDSDNSKAPRLTLMEEVLLLGLQDKEGYPSFWNDCLSPGLRGGILIELALRGRIHLEPLTA

Lance tailed manakin GOLPH3L      MTTLTHRARRGDPGGGSAKRPDGEEDGAADREPGEEEPDDSKDIRLTLMEEVLLLGLKDKEGYTSFWNDCISSGLRGGILIELALRGRIRLEPLAL
Kakapo GOLPH3L                    MTTLTHRSRRAE-GRSTDRKPTGEEDAAADRDLNDEDPDDSKDIRLTLMEEVLLLGLKDKEGYTSFWNDCISSGLRGGILIELAFRGRIRLEPPSM
New Caledonian crow GOLPH3L       MTTLTHRGRRVE-GRNSDKKPDGEEDAAADRDLNEDDPDDSKDIRLTLMEEVLLLGLKDKEGYTSFWNDCISSGLRGGILIELALRGRIRLEPLSL
Zebra finch GOLPH3L               MTTLTHRGRRAE-GRSADRRTEGEEEAAADGELSQEHPEDSKDIRLTLMEEVLLLGLKDKEGYTSFWNDCISSGLRGGILIELALRGRIRLEPPAL

                                      100       110       120       130       140       150       160       170       180       190
Mallard GOLPH3L                   RKKRLLDRKVHLKSDAPTGDILLDETLRHIKATEPAETVQTWIELLTGETWNPFKLQYQLRNVRERIAKNLVEKGILTTEKQNFLLFDMTTHPVSN
Tufted duck GOLPH3L               RKKRLLDRKVHLKSDAPTGDILLDETLRHIKATEPAETVQTWIELLTGETWNPFKLQYQLRNVRERIAKSLVEKGILTTEKQNFLLFDMTTHPVSN
Black swan GOLPH3L                RKKRLLDRKVHLKSDTPTGDILLDETLRHIKATEPAETVQTWIELLTGETWNPFKLQYQLRNVRERIAKNLVEKGILTTEKQNFLLFDMTTHPVSN
Ruddy duck GOLPH3L                RKKRLLDRKVHLKSDTPTGDILLDETLRHIKATEPAETVQTWIELLTGETWNPFKLQYQLRNVRERIAKSLVEKGILTTEKQNFLLFDMTTHPVSN

Chicken GOLPH3L                   RKKRLLDRKVLLKSAAPTGDVLLDETLRHIKASESTETVQTWIELLTGETWNPFKLQYQLRNVRERVAKGLVEKGILTTGKQSFLLFDMTTHPICD
Ring-necked pheasant GOLPH3L      RKKRLLDRKVLLKSAAPTGDVLLDETLRHIKASESMETVQTWIELLTGETWNPFKLQYQLRNVRERVAKGLVEKGILTTGKQSFLLFDMTTHPICD
Turkey GOLPH3L                    RKKRLLDRKVLLKSAAPTGDVLLDETLRHIKASESTETVQTWIELLTGETWNPFKLQYQLRNVRERVAKGLVEKGILTTGKQSFLLFDMTTHPVCD
Japanese quail GOLPH3L            RKKRLLDRKVLLKSAAPTGDVLLDETLRHIKAAESIETVQTWIELLTGETWNPFKLQYQLRNVREHVAKGLVEKGILTTGKQSFLLFDMTTHPVCD

Lance tailed manakin GOLPH3L      RRKRLLDRKVLLKSDTPTGDVLLDETLRHIKGSECPETVPTWIELLTGETWNPFKLQFQLRNVRERLAKALVEKGILGTEKQNFLLFDMTTHPLSN
Kakapo GOLPH3L                    RKKRLLERKVLLKSDAPTGDVLLDETLRHIKATEAAESVQTWIELLTGETWNPFKLQYQLRNVRERVAKALVEKGILTTEKQNFLLFDMTTHPVSN
New Caledonian crow GOLPH3L       RKKRLLERKVLLKSDAPTGDVLLDETLRHIKATESAETVQTWIELLTGETWNPFKLQYQLRNVRERLAKALVEKGILTTEKQNFLLFDMTTHPVSN
Zebra finch GOLPH3L               RRKRLLERKVLLKSDAPTGDVLLDETLRHIKATEPAETVQSWIELLTGETWNPFKLQYQLRNVRERLAKALVEKGILTTEKQNFLLFDMTTHPVSN

                                          200       210       220       230       240       250       260       270       280     286
Mallard GOLPH3L                   AAEKQRLLKRLQEGVLERWAGDPHRMDRRTLALLVLAHSSDVLENAFSSLTDERYEAAMNRTKEVLDADPEVEAAKNR-GTEMIWAILAAFNKA
Tufted duck GOLPH3L               AAEKQRLLKRLQEGVLERWAGDPHRMDRRTLALLVLAHSSDVLENAFSSLTDDRYEVAMNRTKEVLDADPEVEAAKNR-DTEMIWAILAAFNKA
Black swan GOLPH3L                AAEKQRLLKRLQEGVLERWAGDPHRMDRRTLALLVLAHSSDVLENAFSSLADDRYEVAMNRTKEVLDADPEVEAAKGR-GTEMIWAILAAFNKA
Ruddy duck GOLPH3L                AAEKQRLLKRLQEGVLERWVGDPHRMDRRTLALLVLAHSSDVLENAFSSLEDDRYKVAMNRTKEVLDADPEVEAAKGR-GTEMIWAILAVFNKA

Chicken GOLPH3L                   TTEKQRLLKKLQGSVLERWTGDLRRMDHRLLALLVLAHASDVLEKALGSLEDTQYEMAMSRAKDVLEANAELEAAQGR-GTEVIWAVLAAFSRA
Ring-necked pheasant GOLPH3L      TTEKQRLLRKLQDSLLERWTGDPRRMDRRLLALLVLAHASDVLEKALGGLEDTQYEMAMSRVRDVLEADAELEAAQGK-GTEVIWAVLAAFNRA
Turkey GOLPH3L                    TTEKQRLLRKLQDSVLERWMGDPRRMDRRLLALLVLAHASDVLEKALGSLEDTQYEMAMSRAKDVLEADAELEAAQGR-GTEVIWAVLAAFSRA
Japanese quail GOLPH3L            TTEKQRLLRKLQSSLLERWTGDVRRMERRLLALLVLAHTSDVLEKALGGLEDTQYELAMSRAKDVLEADTELEAAQGR-GTEVIWAVLAALSRA

Lance tailed manakin GOLPH3L      GAEKLRLQRRLQESVLERWARDPRRLEPRTLALLVLAHSSDVLEGVFGALADDRYELALARARDLLDLDPELEAAKARGGCEMIWAVLAAFNKG
Kakapo GOLPH3L                    GTEKQRLVRRLQESVLERWVNDPHRMDRRTLALLVLAHSSDVLENVFASLADDKYDVAMNRTKDLLDMDPEVEAAKAK-GTEMVWAVLAAFNKS
New Caledonian crow GOLPH3L       ASEKQRLVKKLQESVLERWVNDPQRMERRTLALLVLAHASDVLENVFASLADDKYDVAMNRTKDLLDMDPEVEAAKAR-GTEMIWAVLAAFNKS
Zebra finch GOLPH3L               ASEKQRLLKKLQESVLERWVNEPQRMERRTLALLVLAHASDVLENVFGSLADDKYDVAMNRTKDLLDMDPEVEAAKGK-GTEMIWAVLAAFNKS
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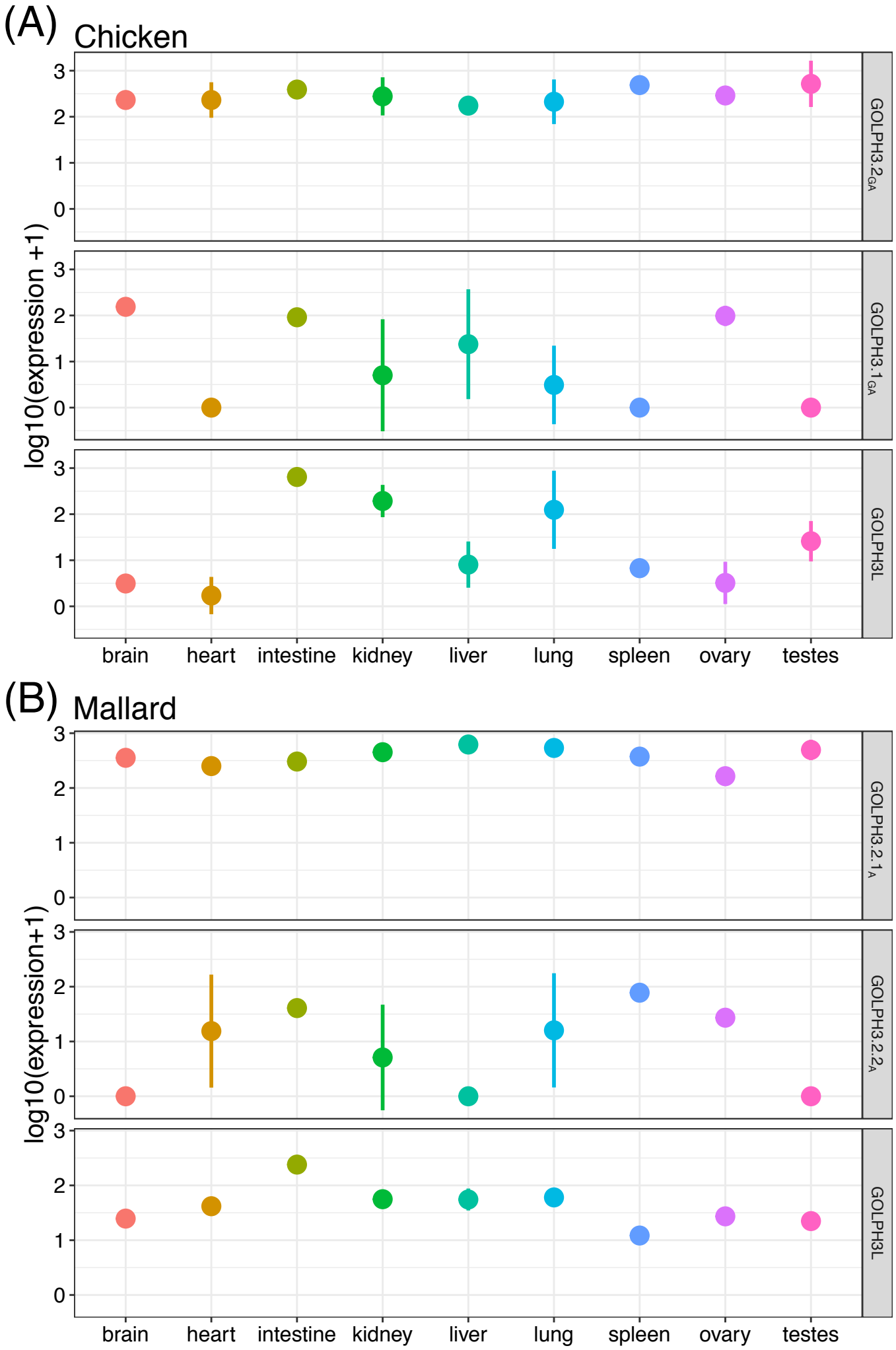
(A)
Chicken
log10(expression +1)
GOLPH3.2GA
GOLPH3.1GA
GOLPH3L
brain
heart
intestine
kidney
liver
lung
spleen
ovary
testes
(B)
Mallard
log10(expression+1)
GOLPH3.2.1A
GOLPH3.2.2A
GOLPH3L
brain
heart
intestine
kidney
liver
lung
spleen
ovary
testes