

Fly away Peter, come back Paul: the conservation and losses of avian non-coding RNAs

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Abstract

Here we present the results of a large-scale bioinformatic annotation of non-coding RNAs in 48 avian genomes. Our approach uses probabilistic models of hand-curated families from the Rfam database to infer conserved RNA families within each avian genome. We supplement these annotations with predictions from the tRNA annotation tool, tRNAscan-SE and microRNAs from miRBase. Although we show a significant number of lncRNAs are surprisingly well conserved between birds and mammals including several intriguing cases where the reported mammalian lncRNA function is not conserved in birds. In contrast, we show extensive conservation of classical ncRNAs (e.g., tRNAs) and more recently discovered ncRNAs (e.g., snoRNAs and miRNAs) in birds, we also demonstrate apparent “losses” in several RNA families. These include the divergence of some classical ncRNAs and the loss of several snoRNAs and microRNAs. These combined results illustrate the utility of applying homology based methods for annotating vertebrate genomes and illustrate many complex evolutionary patterns within the avian ncRNA cohort.

Introduction

Non-coding RNAs (ncRNAs) are an important class of genes, responsible for the regulation of many key cellular functions. The major RNA families include the classical, highly conserved RNAs, sometimes called “molecular fossils”, such as the transfer RNAs, ribosomal RNAs, RNA components of RNase P and the signal recognition particle [1]. Other classes appear to have evolved more recently, e.g. the small nucleolar RNAs (snoRNAs), microRNAs (miRNAs) and the long non-coding RNAs (lncRNAs) [2].

The ncRNAs pose serious research challenges, particularly for the field of genomics. For example, they lack the strong statistical signals associated with protein coding genes, e.g. open reading frames, G+C content and codon-usage biases [3]. Despite promising techniques such as RNA-seq [4], homology based methods, namely covariance models (CMs) remain state of the art for ncRNA analyses [5–7]. The CM based approach for annotating ncRNAs in genomes requires reliable alignments and consensus secondary structures of representative sequences of RNA families. These are used to train probabilistic models for each family. These models can be used to generate sequences with similar properties, score the likelihood that a sequence is generated by the same evolutionary processes as the training sequences and to build alignments based upon sequence and structural information [5–7]. The tRNAscan-SE software package uses CMs to accurately predict transfer RNAs [8,9]. The Rfam database contains thousands of curated alignments and consensus structures for diverse classes of ncRNAs [10–14]. Independent benchmarks of bioinformatic annotation tools have shown that the CM approaches dramatically out-perform alternative methods [15], although its sensitivity is limited for the most rapidly evolving families such as vault RNAs or telomerase RNA [16].

The CM based approach works well for almost all classes of ncRNA, but the long non-coding RNAs (lncRNAs) are a particular challenge [17]. Recent technological advances have led to dramatic speed and memory-usage enhancements for CM analyses [7,18–20]. However, CMs cannot model the exon-intron structures of spliced lncRNAs, nor can they deal simply with the repeats that many lncRNAs host. Consequently in the latest release of Rfam the lncRNA families that were added were composed of local conserved and structured elements within lncRNAs, analogous to the “domains” housed within protein sequences [14]. The functions determined to date for lncRNAs range from regulating chromatin status to chromosomal inactivation [21,22]. Yet functional characterisation of these genes is a lengthy and expensive process [17].

The publication of 48 avian genomes, including the previously published chicken [23], zebra finch [24] and turkey [25] with the newly published 45 avian genomes [26,27], provides exciting opportunities to to

explore ncRNA conservation in unprecedented detail.

In the following we explore the conservation patterns of the major classes of avian ncRNA in further detail. The collection of ncRNA sequences is generally biased towards model organisms [2, 28]. We focus our report on the unusual results within the avian lineages. These are either unexpectedly well-conserved RNAs or unexpectedly poorly-conserved RNAs. The former are RNAs we would not have expected to be conserved between the birds and the organisms these genes were initially identified in; Usually, this hypothesis is based upon the function of the RNA which is not conserved in avian species. The latter are apparent losses of RNA genes that were expected to be conserved; Usually, this hypothesis is based upon the conservation of these RNAs in other vertebrate species. We use three models of “loss” that explain the data: Firstly, these could be genuine cases of an ancestral gene-loss along the avian lineage. Secondly, this could be a case of “divergence” where a RNA gene has undergone significant sequence and structural alterations, so much so, that our homology search tools can no longer detect a relationship between vertebrate exemplars and the avian varieties. Thirdly, we consider the possibility that the available genome assemblies have independently failed to capture these genes.

Results

Unusually well conserved RNAs

The bulk of the “unusually well conserved RNAs” belong to the long non-coding RNA (lncRNA) group. The lncRNAs are a diverse group of RNAs that have been implicated in a multitude of functional processes [17, 21, 22]. These RNAs have largely been characterised in mammalian species, particularly human and mouse. Consequently, we generally do not expect these to be conserved outside of mammalia. Notable examples include Xist [29] and H19 [30]. There is emerging evidence for the conservation of “mammalian” lncRNAs in other vertebrates [31, 32]), however, like most lncRNAs, the function of these lncRNAs remains largely unknown. Here, we show the conservation of several well-characterised lncRNAs of known function in humans.

In general, Rfam cannot include the entire length of any large, spliced RNAs. This is a limitation of the covariance-models used for the homology-searches Rfam runs [7]. Consequently, only short, well-conserved regions with evolutionarily conserved secondary structures are included in Rfam. By analogy to protein-domains, we refer to these as RNA-domains [14].

When analysing the RNA-domain annotations it is striking that many of the lncRNAs with multiple RNA-domains are consistently preserved in the birds. The annotations of these domains lie in the same

genomic region, in the same order as in the mammalian homologs. Thus they support a high degree of evolutionary conservation for the entire lncRNA. In particular the HOXA11-AS1, PART1, PCA3, RMST, Six3os1, SOX2OT and ST7-OT3 lncRNAs have multiple, well conserved RNA-domains (See Figure 1). The conservation of these “human” lncRNAs among birds suggests they may also be functional in birds but what these functions is not immediately obvious. For example, PART1 and PCA3 are both described as prostate-specific lncRNAs that play a role in the human androgen-receptor pathway [33–35]. Birds lack a prostate but both males and females express the androgen receptor (AR or NR3C4) in gonadal and non-gonadal tissue [36–39]. Thus, we postulate that PART1 and PCA3 also play a role in the androgen-receptor pathway in birds but whether the expression of these lncRNAs are tissue specific is unknown at present. The HOX cluster lncRNAs HOTAIRM1 (5 RNA-domains), HOXA11-AS1 (6 RNA-domains), and HOTTIP (4 RNA domains) are remarkably well conserved. In the human genome they are located in the HOXA cluster (hg coordinates chr7:27135743-27245922), one of the most highly conserved regions in vertebrate genomes [40], in antisense orientation between HoxA1 and HoxA2, between HoxA11 and HoxA13, and upstream of HoxA13, respectively. Conservation and expression of HOTAIRM1 and HOXA11-AS1 within the HOXA cluster has been studied in some detail in marsupials [41]. Of the 15 RNA-domains five and six representing all three lncRNAs were recovered in the alligator and turtle genomes. All of them appear in the correct order at the expected, syntenically conserved positions within the HOXA cluster. In the birds, where two or more of the HOX cluster lncRNA RNA-domains were predicted on the same scaffold, this gene order and location within HOX was also preserved.

Many of the lncRNAs have been associated with cancer, sparking a minor review industry [42,43]. Three examples of these that are also conserved in the birds are described below.

The RMST (Rhabdomyosarcoma 2 associated transcript) RNA-domains 6, 7, 8, and 9 are conserved across the birds. In each bird the gene order was also consistent with the human ordering. In the alligator and turtle an additional RNA-domain was predicted in each, these were RNA-domains 2 and 4 respectively, again the ordering of the domains was consistent with human. This suggests that the RMST lncRNA is highly conserved. However, little is known about the function of this RNA. It was originally identified in a screen for differentially expressed genes in two Rhabdomyosarcoma tumor types [44].

In addition, the lncRNA DLEU2, is well conserved across the vertebrates, it is a host gene for two miRNA genes, miR-15 and miR-16, both of which are also well conserved across the vertebrates (See Supplemental Figure 2). DLEU2 is thought to be a tumor-suppressor gene as it is frequently deleted in malignant tumours [45,46].

The NBR2 lncRNA and BRCA1 gene share a bidirectional promotor [47]. Both are expressed in a broad range of tissues. Extensive research on BRCA1 has shown that it is involved in DNA repair [48]. The function of NBR2 remains unknown, yet its conservation across the vertebrates certainly implies a function (See Figure 1).

Of the other classes of RNAs, none showed an unexpected degree of conservation or expansion within the avian lineage. The only exception being the snoRNA SNORD93 which we show has 92 copies in the tinamou genome, whereas it only has 1-2 copies in all the other vertebrate genomes.

RNA Losses, divergence or missing data?

Much of the number of apparent losses and reduction in genomic sequence has been extensively discussed elsewhere [49]. Unsurprisingly, this reduction is reflected in the copy-number of RNA genes. Some of the most dramatic examples are the transfer RNAs and pseudogenes which average ≈ 900 and ≈ 580 copies in the human, turtle and alligator genomes, the average copies numbers of these drop to ≈ 280 and ≈ 100 copies in the avian genomes.

The absence of several well-conserved ncRNA families from many or even most bird genomes is unlikely to represent true gene losses. This concerns in particular the telomerase RNA, the RNA components of RNase P and MRP, the minor spliceosomal snRNAs U4atac and U11, the selenocystein tRNA (tRNA-Sec) as well as the vault RNAs. In order to get an idea to what extent the absence of these RNAs from the **infernai**-based annotation is caused by sequence divergence beyond the thresholds of the Rfam CMs and/or missing or incomplete data, we complemented our analysis by dedicated searches for a few of these RNA groups.

The simplest case are the selenocystein tRNAs. Here, tRNAscan is tuned for specificity and thus misses several occurrences that are easily found by **blastn** with $E \leq 10^{-30}$. In some cases the sequences appear degraded at the ends, which may be explained e.g. by low sequence quality at the very ends of contigs or scaffolds. A **blastn** search also readily retrieves additional RNase P and RNase MRP RNAs, capturing only the best conserved regions. In many cases these additional candidates are incomplete or contain undetermined sequence, explaining why they are missed by the CMs. Overall, we identify tRNA-Sec in most and RNase P and MRP RNAs in the majority of the genomes. An additional candidate could also be retrieved for telomerase RNA. Telomerase is well known to exhibit very poor sequence conservation and rapid variations in size that make it notoriously hard to identify by homology search [50]. The poor return thus does not come as a surprise. Since **blastn** searches remained unsuccessful we constructed a

sauropsid-specific CM for the vault RNA. In addition to the hits identified by the Rfam model we obtained three additional homologs. Vault RNAs, with a size of about 100 nt, exhibit conserved sequence patterns only at their ends, with essentially unconstrained sequence in the central part. Their identification is one of the well-know difficult problems for homology search [51].

Our ability to find additional homologs for several RNA families that fill gaps in the abundance matrices (Figure 2) strongly suggests that conspicuous absences, in particular of LUCA and LECA RNAs, are caused by incomplete data in the current assemblies and sequence divergence rather than true losses.

Vertebrate Y RNAs typically form a cluster comprising four well-defined paralog groups Y1, Y3, Y4, and Y5. In line with [52] we find that the Y5 paralog family is absent from all bird genomes, while it is still present in both alligator and turtle, see Supplemental Figure 4. Within bird, we find an the conserved Y4-Y3-Y1 cluster. Apparently, broken-up clusters are in most cases consistent with breaks in the available sequence assemblies. In several genomes we observe one or a few additional Y RNA homologs unlinked to the canonical Y RNA cluster. These sequences can be identified unambiguously as derived members of one of the three ancestral paralog groups, they almost always fit less well to the consensus (as measured by the CM bit score of paralog group specific covariance models) than the paralog linked to cluster, and there is no indication that any of these additional copies is evolutionarily conserved over longer time scales. We therefore suggest that most or all of these interspersed copies are in fact pseudogenes.

Nearly all microRNAs that are broadly conserved in fish, amphibians and mammals are also conserved in the birds. Nevertheless, there are obvious instances of microRNAs lost in all birds. For example, mammalian and ambhibian genomes contain three loci of clustered microRNAs from the mir-17 and mir-92 families [53]. One of these clusters (cluster II, with families mir-106b, mir-93 and mir-25) was not found in turtles, crocodiles and birds, see Supplemental Figure 6.

The microRNA family let-7 is the most diverse microRNA family with 14 paralogs in human. These genes also localize in 7 genomic clusters, together with mir-100 and mir-125 miRNA families (see previous study on the evolution of the let-7 miRNA cluster in [54]). In Sauropsids we observed that cluster A - which is strongly conserved in vertebrates has been completely lost in the avian lineage. Another obvious loss in birds is cluster F, containing two let-7 microRNA paralogs. Cluster H, on the other hand has been retained in all oviparous animals and completely lost later, after the split of Theria. See Supplemental Figure 7 for details.

Conclusions

In this work we have provided a comprehensive annotation of non-coding RNAs in genome sequences using homology-based methods. The homology-based tools have distinct advantages over experimental-based approaches as not all RNAs are expressed in any particular tissue-type or developmental-stage, in fact some RNAs have extremely specific expression profiles [55]. We have identified previously unrecognised conservation of ncRNAs in avian genomes as well as some surprising “losses” of otherwise well conserved ncRNAs. We suspect many of these losses are due to a combination of limitations in the homology search tools that we use for annotation and the ability of ncRNAs to tolerate large amounts of sequence variation while remaining functional, rather than *bona fide* gene loss. In some cases these losses could be due to missing data from the genome assemblies, but this unlikely to be the case for multiple independent assemblies.

These results indicate we are still in the very early phases of determining the functions of many RNA families. This is illustrated by the fact that the reported functions of some ncRNAs are mammal-specific, yet some are also found in bird genomes. CITE DAVE BURT ET AL AND THE COMPARATIVE ARTICLE?

Methods

Bird genomes were searched using the cmsearch program from INFERNAL 1.1 and the covariance models from the Rfam database v11.0 [13,14]. All matches above the curated GA threshold were included. Subsequently, all hits with an E-value greater than 0.0005 were discarded, so only matches which passed the model-specific GA threshold and had an E-value smaller than 0.0005 were retained. The Rfam database classifies non-coding RNAs into hierarchical groupings. The basic units are “families” which are groups of homologous, alignable sequences; “clans” which are groups of un-alignable (or functionally distinct), homologous families; and “classes” which are groups of clans and families with related biological functions e.g. spliceosomal RNAs, miRNAs and snoRNAs [10–14]; these categories have been used to classify our results.

In order to obtain good annotations of tRNA genes we also ran the specialist tRNA-scan version 1.3.1 annotation tool. This method also uses covariance models to identify tRNAs. However it also uses some heuristics to increase the search-speed, annotates the Isoacceptor Type of each prediction and uses sequence analysis to infer if predictions are likely to be functional or tRNA-derived pseudogenes [8,9]. Rfam matches and the tRNA-scan results for families belonging to the same clan were then “competed” so

that only the best match was retained for any genomic region [13]. To further increase the specificity of our annotations we filtered out families that were identified in four or fewer of the 51 vertebrate species we have analysed in this work. These filtered families largely corresponded to bacterial contamination within the genomic sequences.

999 microRNA sequence families, previously annotated in at least one vertebrate, were retrieved from miRBase (v19). Individual sequences or multiple sequence alignments were used to build covariance models with INFERNA1 (v1.1rc3), and these models were searched against the 48 bird genomes, and the genomes of the american alligator and the green turtle as outgroups. Hits with e-value $\leq 10^{-10}$ realigned with the query sequences and the resultant multiple sequence alignments manually inspected and edited using RALEE.

An additional snoRNA homology search was performed with snoStrip [56]. As initial queries we used deuterostomian snoRNA families from human [57], platypus [58], and chicken [59].

Chicken snoRNA and miRNA annotations were validated using small RNA-seq data comprising 27 samples from 14 different tissues. Since not all RNAs are expressed at any given time we expect to verify only a fraction of annotated RNAs using the expression data. Nevertheless 242 of 691 (35%) miRNAs as well as 328 of 376 (87%) snoRNAs of our homology-based annotations were found to be supported by the RNA-seq data.

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References

1. Jeffares DC, Poole AM, Penny D: **Relics from the RNA world.** *J Mol Evol* 1998, **46**:18–36.
2. Hoepfner MP, Gardner PP, Poole AM: **Comparative analysis of RNA families reveals distinct repertoires for each domain of life.** *PLoS Comput Biol* 2012, **8**(11):e1002752.
3. Rivas E, Eddy SR: **Secondary structure alone is generally not statistically significant for the detection of noncoding RNAs.** *Bioinformatics* 2000, **16**(7):583–605.
4. Croucher NJ, Thomson NR: **Studying bacterial transcriptomes using RNA-seq.** *Curr Opin Microbiol* 2010, **13**(5):619–24.
5. Sakakibara Y, Brown M, Hughey R, Mian IS, Sjölander K, Underwood RC, Haussler D: **Stochastic context-free grammars for tRNA modeling.** *Nucleic Acids Res* 1994, **22**(23):5112–20.

6. Eddy SR, Durbin R: **RNA sequence analysis using covariance models.** *Nucleic Acids Res* 1994, **22**(11):2079–88.
7. Nawrocki EP, Kolbe DL, Eddy SR: **Infernal 1.0: inference of RNA alignments.** *Bioinformatics* 2009, **25**(10):1335–7.
8. Lowe TM, Eddy SR: **tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence.** *Nucleic Acids Res* 1997, **25**(5):955–64.
9. Chan PP, Lowe TM: **GtRNAdb: a database of transfer RNA genes detected in genomic sequence.** *Nucleic Acids Res* 2009, **37**(Database issue):D93–7.
10. Griffiths-Jones S, Bateman A, Marshall M, Khanna A, Eddy SR: **Rfam: an RNA family database.** *Nucleic Acids Res* 2003, **31**:439–41.
11. Griffiths-Jones S, Moxon S, Marshall M, Khanna A, Eddy SR, Bateman A: **Rfam: annotating non-coding RNAs in complete genomes.** *Nucleic Acids Res* 2005, **33**(Database issue):D121–4.
12. Gardner PP, Daub J, Tate JG, Nawrocki EP, Kolbe DL, Lindgreen S, Wilkinson AC, Finn RD, Griffiths-Jones S, Eddy SR, Bateman A: **Rfam: updates to the RNA families database.** *Nucleic Acids Res* 2009, **37**(Database issue):D136–40.
13. Gardner PP, Daub J, Tate J, Moore BL, Osuch IH, Griffiths-Jones S, Finn RD, Nawrocki EP, Kolbe DL, Eddy SR, Bateman A: **Rfam: Wikipedia, clans and the "decimal" release.** *Nucleic Acids Res* 2011, **39**(Database issue):D141–5.
14. Burge SW, Daub J, Eberhardt R, Tate J, Barquist L, Nawrocki EP, Eddy SR, Gardner PP, Bateman A: **Rfam 11.0: 10 years of RNA families.** *Nucleic Acids Res* 2013, **41**(Database issue):D226–32.
15. Freyhult EK, Bollback JP, Gardner PP: **Exploring genomic dark matter: a critical assessment of the performance of homology search methods on noncoding RNA.** *Genome Res* 2007, **17**:117–125.
16. Menzel P, Gorodkin J, Stadler PF: **The Tedious Task of Finding Homologous Non-coding RNA Genes.** *RNA* 2009, **15**:2075–2082.
17. Guttman M, Amit I, Garber M, French C, Lin MF, Feldser D, Huarte M, Zuk O, Carey BW, Cassady JP, Cabili MN, Jaenisch R, Mikkelsen TS, Jacks T, Hacohen N, Bernstein BE, Kellis M, Regev A, Rinn JL, Lander ES: **Chromatin signature reveals over a thousand highly conserved large non-coding RNAs in mammals.** *Nature* 2009, **458**(7235):223–7.
18. Eddy SR: **A memory-efficient dynamic programming algorithm for optimal alignment of a sequence to an RNA secondary structure.** *BMC Bioinformatics* 2002, **3**:18.
19. Nawrocki EP, Eddy SR: **Query-dependent banding (QDB) for faster RNA similarity searches.** *PLoS Comput Biol* 2007, **3**(3):e56.
20. Eddy SR: **Accelerated Profile HMM Searches.** *PLoS Comput Biol* 2011, **7**(10):e1002195.
21. Rinn JL, Kertesz M, Wang JK, Squazzo SL, Xu X, Bruggmann SA, Goodnough LH, Helms JA, Farnham PJ, Segal E, Chang HY: **Functional demarcation of active and silent chromatin domains in human HOX loci by noncoding RNAs.** *Cell* 2007, **129**(7):1311–23.
22. Chow JC, Yen Z, Ziesche SM, Brown CJ: **Silencing of the mammalian X chromosome.** *Annu Rev Genomics Hum Genet* 2005, **6**:69–92.
23. International Chicken Genome Sequencing Consortium C: **Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution.** *Nature* 2004, **432**(7018):695–716.
24. Warren WC, Clayton DF, Ellegren H, Arnold AP, Hillier LW, Küstner A, Searle S, White S, Vilella AJ, Fairley S, Heger A, Kong L, Ponting CP, Jarvis ED, Mello CV, Minx P, Lovell P, Velho TA, Ferris M, Balakrishnan CN, Sinha S, Blatti C, London SE, Li Y, Lin YC, George J, Sweedler J, Southey B, Gunaratne P, Watson M, Nam K, Backström N, Smeds L, Nabholz B, Itoh Y, Whitney O, Pfenning AR, Howard J, Völker M, Skinner BM, Griffin DK, Ye L, McLaren WM, Flicek P, Quesada V, Velasco G, Lopez-Otin C, Puente XS, Olender T, Lancet D, Smit AF, Hubley R, Konkel MK, Walker JA, Batzer MA, Gu W, Pollock DD, Chen L, Cheng Z, Eichler EE, Stapley J, Slate J, Ekblom R, Birkhead T, Burke T, Burt D, Scharff C, Adam I, Richard H, Sultan M, Soldatov A, Lehrach H, Edwards SV, Yang SP, Li X, Graves T, Fulton L, Nelson J, Chinwalla A, Hou S, Mardis ER, Wilson RK: **The genome of a songbird.** *Nature* 2010, **464**(7289):757–62.

25. Dalloul RA, Long JA, Zimin AV, Aslam L, Beal K, Blomberg LA, Bouffard P, Burt DW, Crasta O, Crooijmans RP, Cooper K, Coulombe RA, De S, Delany ME, Dodgson JB, Dong JJ, Evans C, Frederickson KM, Flicek P, Florea L, Folkerts O, Groenen MA, Harkins TT, Herrero J, Hoffmann S, Megens HJ, Jiang A, de Jong P, Kaiser P, Kim H, Kim KW, Kim S, Langenberger D, Lee MK, Lee T, Mane S, Marcais G, Marz M, McElroy AP, Modise T, Nefedov M, Notredame C, Paton IR, Payne WS, Pertea G, Prickett D, Puiu D, Qiao D, Raineri E, Ruffier M, Salzberg SL, Schatz MC, Scheuring C, Schmidt CJ, Schroeder S, Searle SM, Smith EJ, Smith J, Sonstegard TS, Stadler PF, Tafer H, Tu ZJ, Van Tassell CP, Vilella AJ, Williams KP, Yorke JA, Zhang L, Zhang HB, Zhang X, Zhang Y, Reed KM: **Multi-platform next-generation sequencing of the domestic turkey (*Meleagris gallopavo*): genome assembly and analysis.** *PLoS Biol* 2010, **8**(9).
26. Consortium AGP: **Genome evolution and biodiversity of the avian class.** *In preparation* 2014.
27. Consortium AGP: **Genome evolution and biodiversity of the avian class.** *In preparation* 2014.
28. Gardner PP, Bateman A, Poole AM: **SnoPatrol: how many snoRNA genes are there?** *J Biol* 2010, **9**:4.
29. Duret L, Chureau C, Samain S, Weissenbach J, Avner P: **The Xist RNA gene evolved in eutherians by pseudogenization of a protein-coding gene.** *Science* 2006, **312**(5780):1653–5.
30. Smits G, Mungall AJ, Griffiths-Jones S, Smith P, Beury D, Matthews L, Rogers J, Pask AJ, Shaw G, VandeBerg JL, McCarrey JR, SAVOIR Consortium C, Renfree MB, Reik W, Dunham I: **Conservation of the H19 noncoding RNA and H19-IGF2 imprinting mechanism in therians.** *Nat Genet* 2008, **40**(8):971–6.
31. Chodroff RA, Goodstadt L, Sirey TM, Oliver PL, Davies KE, Green ED, Molnár Z, Ponting CP: **Long noncoding RNA genes: conservation of sequence and brain expression among diverse amniotes.** *Genome Biol* 2010, **11**(7):R72.
32. Ulitsky I, Shkumatava A, Jan CH, Sive H, Bartel DP: **Conserved function of lincRNAs in vertebrate embryonic development despite rapid sequence evolution.** *Cell* 2011, **147**(7):1537–50.
33. Bussemakers MJ, van Bokhoven A, Verhaegh GW, Smit FP, Karthaus HF, Schalken JA, Debruyne FM, Ru N, Isaacs WB: **DD3: a new prostate-specific gene, highly overexpressed in prostate cancer.** *Cancer Res* 1999, **59**(23):5975–9.
34. Lin B, White JT, Ferguson C, Bumgarner R, Friedman C, Trask B, Ellis W, Lange P, Hood L, Nelson PS: **PART-1: a novel human prostate-specific, androgen-regulated gene that maps to chromosome 5q12.** *Cancer Res* 2000, **60**(4):858–63.
35. Ferreira LB, Palumbo A, de Mello KD, Sternberg C, Caetano MS, de Oliveira FL, Neves AF, Nasciutti LE, Goulart LR, Gimba ER: **PCA3 noncoding RNA is involved in the control of prostate-cancer cell survival and modulates androgen receptor signaling.** *BMC Cancer* 2012, **12**:507.
36. Yoshimura Y, Chang C, Okamoto T, Tamura T: **Immunolocalization of androgen receptor in the small, preovulatory, and postovulatory follicles of laying hens.** *Gen Comp Endocrinol* 1993, **91**:81–9.
37. Veney SL, Wade J: **Steroid receptors in the adult zebra finch syrinx: a sex difference in androgen receptor mRNA, minimal expression of estrogen receptor alpha and aromatase.** *Gen Comp Endocrinol* 2004, **136**(2):192–9.
38. Fuxjager MJ, Schultz JD, Barske J, Feng NY, Fusani L, Mirzamani A, Day LB, Hau M, Schlinger BA: **Spinal motor and sensory neurons are androgen targets in an acrobatic bird.** *Endocrinology* 2012, **153**(8):3780–91.
39. Leska A, Kiezun J, Kaminska B, Duszka L: **Seasonal changes in the expression of the androgen receptor in the testes of the domestic goose (*Anser anser f. domestica*).** *Gen Comp Endocrinol* 2012, **179**:63–70.
40. Pascual-Anaya J, D’Aniello S, Kuratani S, Garcia-Fernández J: **Evolution of *Hox* gene clusters in deuterostomes.** *BMC Developmental Biology* 2013, **13**:26.
41. Yu H, Lindsay J, Feng ZP, Frankenberg S, Hu Y, Carone D, Shaw G, Pask AJ, O’Neill R, Papenfuss AT, Renfree MB: **Evolution of coding and non-coding genes in HOX clusters of a marsupial.** *BMC Genomics* 2012, **13**:251.
42. Prensner JR, Chinnaiyan AM: **The emergence of lncRNAs in cancer biology.** *Cancer Discov* 2011, **1**(5):391–407.
43. Spizzo R, Almeida MI, Colombatti A, Calin GA: **Long non-coding RNAs and cancer: a new frontier of translational research?** *Oncogene* 2012, **31**(43):4577–87.

44. Chan AS, Thorner PS, Squire JA, Zielenska M: **Identification of a novel gene NCRMS on chromosome 12q21 with differential expression between rhabdomyosarcoma subtypes.** *Oncogene* 2002, **21**(19):3029–37.
45. Lerner M, Harada M, Lovén J, Castro J, Davis Z, Oscier D, Henriksson M, Sangfelt O, Grandér D, Corcoran MM: **DLEU2, frequently deleted in malignancy, functions as a critical host gene of the cell cycle inhibitory microRNAs miR-15a and miR-16-1.** *Exp Cell Res* 2009, **315**(17):2941–52.
46. Klein U, Lia M, Crespo M, Siegel R, Shen Q, Mo T, Ambesi-Impiombato A, Califano A, Migliazza A, Bhagat G, Dalla-Favera R: **The DLEU2/miR-15a/16-1 cluster controls B cell proliferation and its deletion leads to chronic lymphocytic leukemia.** *Cancer Cell* 2010, **17**:28–40.
47. Xu CF, Brown MA, Nicolai H, Chambers JA, Griffiths BL, Solomon E: **Isolation and characterisation of the NBR2 gene which lies head to head with the human BRCA1 gene.** *Hum Mol Genet* 1997, **6**(7):1057–62.
48. Moynahan ME, Chiu JW, Koller BH, Jasin M: **Brca1 controls homology-directed DNA repair.** *Mol Cell* 1999, **4**(4):511–8.
49. Organ CL, Shedlock AM, Meade A, Pagel M, Edwards SV: **Origin of avian genome size and structure in non-avian dinosaurs.** *Nature* 2007, **446**(7132):180–4.
50. Xie M, Mosig A, Qi X, Li Y, Stadler PF, Chen JJJ: **Size Variation and Structural Conservation of Vertebrate Telomerase RNA.** *J. Biol. Chem.* 2008, **283**:2049–2059.
51. Stadler PF, Chen JJJ, Hackermüller J, Hoffmann S, Horn F, Khaitovich P, Kretzschmar AK, Mosig A, Prohaska SJ, Qi X, Schutt K, Ullmann K: **Evolution of Vault RNAs.** *Mol. Biol. Evol.* 2009, **26**:1975–1991.
52. Mosig A, Guofeng M, Stadler B, Stadler P: **Evolution of the vertebrate Y RNA cluster.** *Theory in Biosciences* 2007, **126**:9–14.
53. Tanzer A, Stadler P: **Molecular evolution of a microRNA cluster.** *J Mol Biol.* 2004, **339**(2):327–35.
54. Hertel J, Bartschat S, Wintsche A, C O, The Students of the Bioinformatics Computer Lab 2011, Stadler PF: **Evolution of the let-7 microRNA Family.** *"RNA Biol"* 2012. in press.
55. Johnston RJ, Hobert O: **A microRNA controlling left/right neuronal asymmetry in *Caenorhabditis elegans*.** *Nature* 2003, **426**(6968):845–9.
56. Bartschat S, Kehr S, Tafer H, Stadler PF, Hertel J: **snoStrip: A snoRNA annotation pipeline** preprint.
57. Lestrade L, Weber MJ: **snoRNA-LBME-db, a comprehensive database of human H/ACA and C/D box snoRNAs.** *Nucleic Acids Res* 2006, **34**(Database issue):D158–62.
58. Schmitz J, Zemann A, Churakov G, Kuhl H, Grützner F, Reinhardt R, Brosius J: **Retroposed SNOfall—a mammalian-wide comparison of platypus snoRNAs.** *Genome Res* 2008, **18**(6):1005–10.
59. Shao P, Yang JH, Zhou H, Guan DG, Qu LH: **Genome-wide analysis of chicken snoRNAs provides unique implications for the evolution of vertebrate snoRNAs.** *BMC Genomics* 2009, **10**:86.

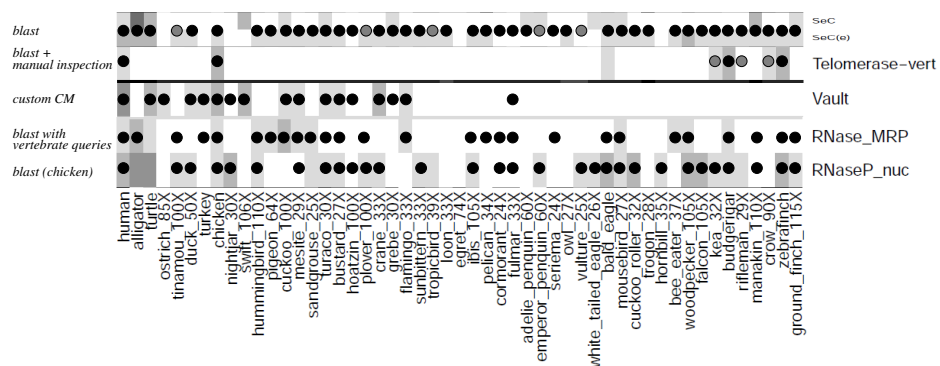


Figure 2: Additional homologs of some sparsely represented RNA families were discovered using dedicated search strategies combined with highly sensitive settings, synteny information, lineage-specific CMs and subsequent manual inspection.