

A lncRNA gene-enriched atlas for GRCg7b chicken genome and its functional annotation across 47 tissues

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A IncRNA GENE-ENRICHED ATLAS FOR THE GRCg7b CHICKEN GENOME AND ITS FUNCTIONAL ANNOTATION ACROSS 47 TISSUES F. Degalez¹ & S. Lagarrigue¹

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CONTEXT

While protein-coding genes (PCG) are relatively well known in livestock genomes, long non-coding RNA (IncRNA) gene loci, known to be regulatory genes, are more poorly described and differ greatly between reference genome annotations. Even if new expression data contribute to improve their identification, their low expression and high context-specificity remain a challenge.

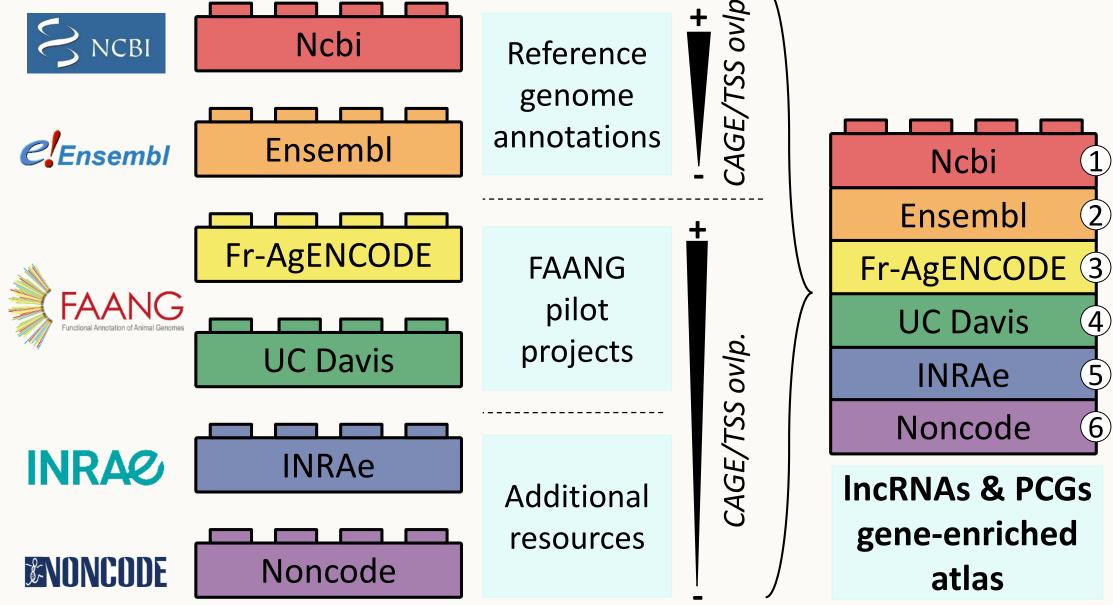
For the chicken, in 2022, the new GRCg7b chicken genome assembly with its associated genome annotations have been released.

OBJECTIVES

- Provide an annotation of the chicken genome according to the GRCg7b assembly.
- Integrate the two reference annotations including "NCBI-RefSeq" (Ncbi) and "EMBL-EBI Ensembl/GENCODE" (Ensembl).
- Ease the joint use of gene models from Ncbi & Ensembl and the switch between the galgal5, GRCg6a and GRCg7b chicken assemblies.
- Increase the number of IncRNA identified using additional resources from multi-tissue projects or specialist databases.
- Provide a genomic and functional annotation for the community working on gene expression (IncRNAs and/or PCGs) to elucidate,

MATERIALS & METHODS

Fig. 1: Origin and aggregation rules used to build the gene-enriched annotation



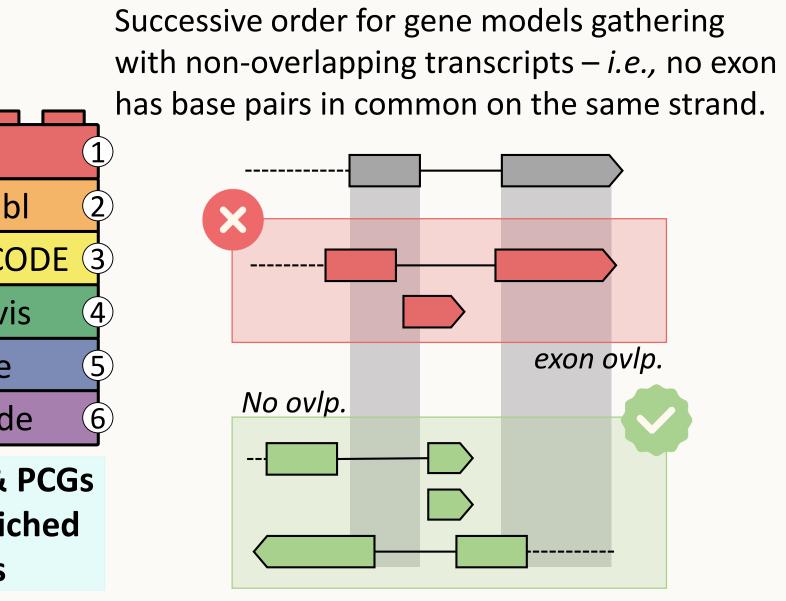
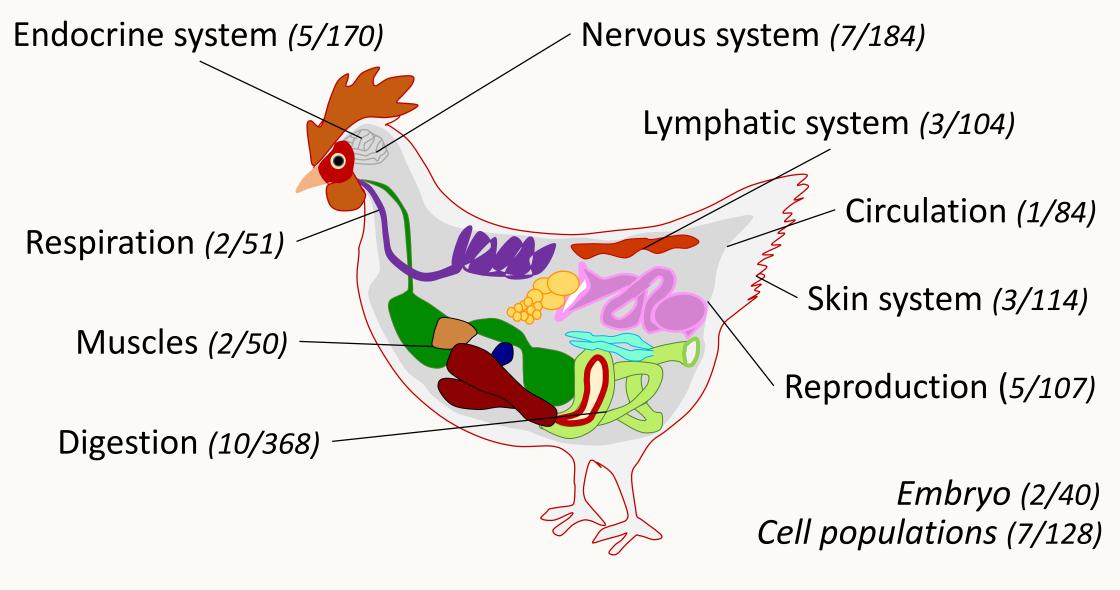


Fig. 2: A diversity of 47 tissues used for gene expression

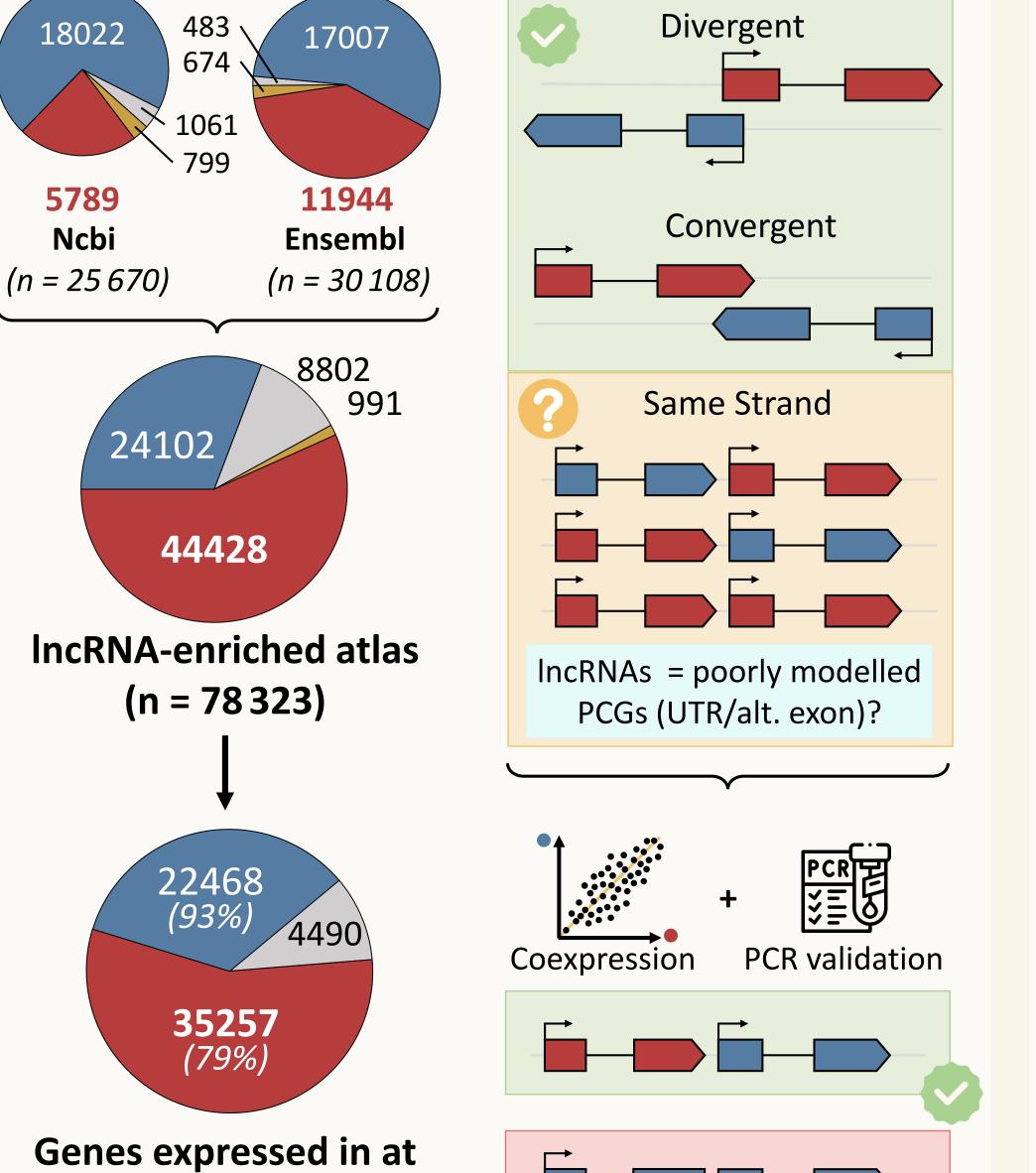


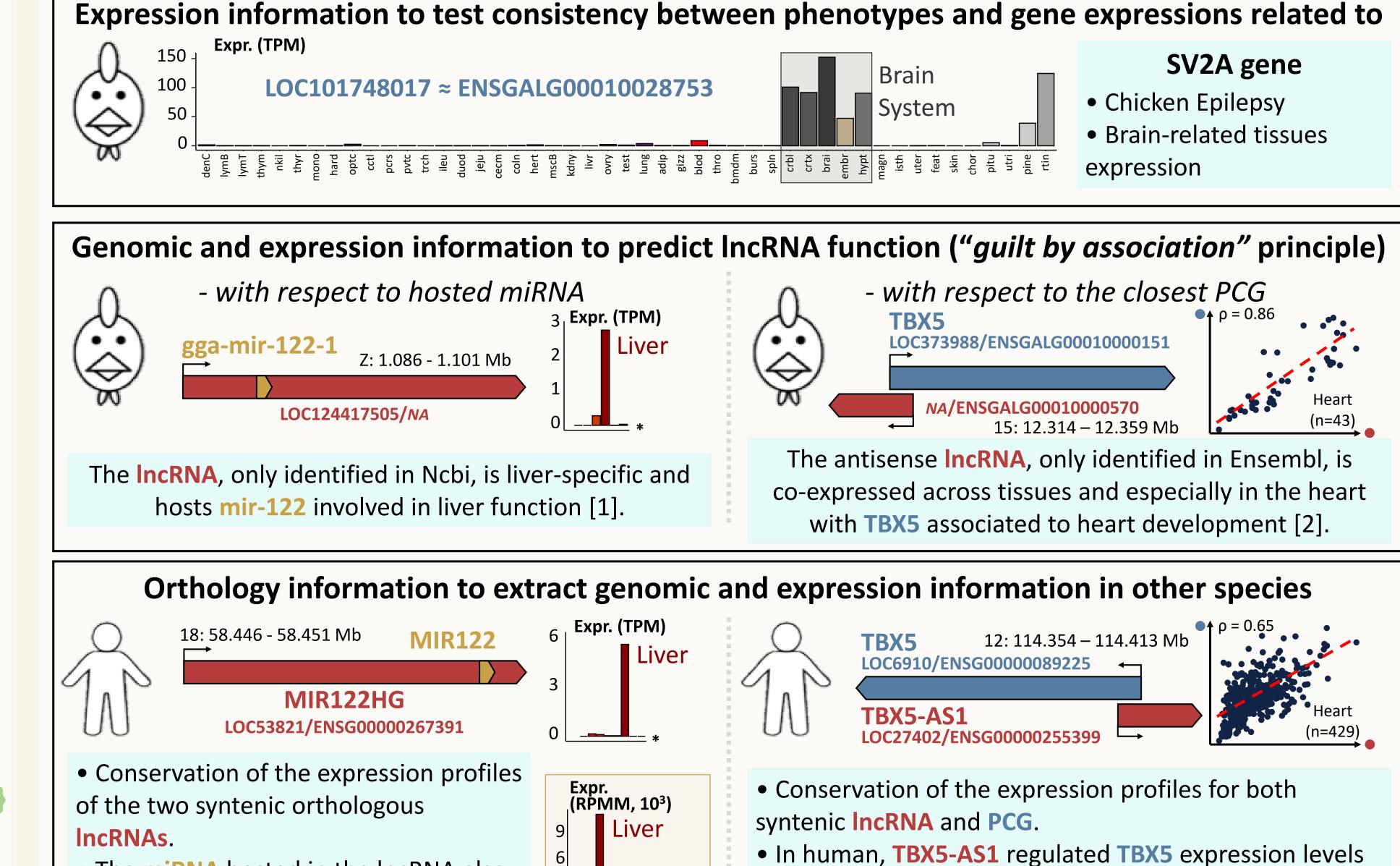
(47 tissues / 1400 samples) from 36 datasets

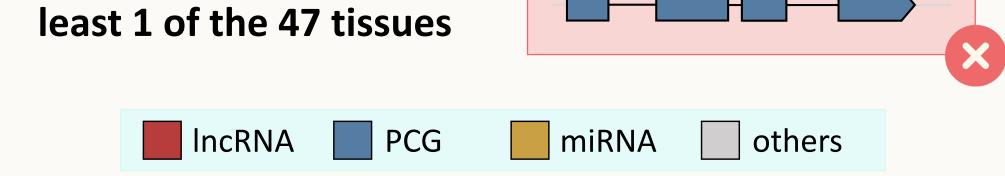
RESULTS

Fig. 3: Number of genes in the enriched atlas

Fig. 4: Functional gene annotation, a resource for a variety of analyses







Gene expression

Orthology

(human / mouse)

GEGA

• The miRNA hosted in the lncRNA also shows liver-specific expression in

3	MIR122
0	

by forming an RNA duplex that protects the mRNA from RNase degradation [3].

*Tissues for which the gene is not/lowly expressed are not shown.

Occurrence of the gene loci in the 6 resources **Functional annotation** Gene model features (Go terms / MGI) Gene pair configuration (PCG / IncRNA / miRNA)

WEBSITE

human.

To help in performing studies such as QTL, eQTL or differentially expressed genes analyses, all these data are easily accessible via a user-friendly online tool called GEGA (Gallus Enriched Gene Annotation) enabling efficient data analysis thanks to a multitude of modules and an ergonomic design. All results and a multitude of graphical representation can be simply produced and downloaded, ranging from basic gene information to detailed visualization of expression and co-expression. gega.sigenae.org

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References: [1] Bandiera S, et al. miR-122--a key factor and therapeutic target in liver disease. J Hepatol. 2015;62:448–57; [2] Steimle JD, Moskowitz IP. TBX5: A Key Regulator of Heart Development. Current Topics in Developmental Biology. Academic Press; 2017. p. 195–221. [3] Ma J, et al. Hypermethylationmediated down-regulation of IncRNA TBX5-AS1:2 in Tetralogy of Fallot inhibits cell proliferation by reducing TBX5 expression. Journal of Cellular and Molecular Medicine. 2020;24:6472–84.

