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Fabien Degalez, Mathieu Charles, Sylvain Foissac, Haijuan Zhou, Dailu Guan, Coralie Alain, Lingzhao Fang, Christophe Klopp, Laetitia Lagoutte, Bénédicte Lebez, et al.

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A lncRNA GENE-ENRICHED ATLAS FOR THE GRCg7b CHICKEN GENOME AND ITS FUNCTIONAL ANNOTATION ACROSS 47 TISSUES

fabien.degalez@inrae.fr

F. Degalez¹ & S. Lagarrigue¹

sandrine.lagarrigue@institut-agro.fr

¹PEGASE, INRAE, Institut Agro, 35590 Saint Gilles, France

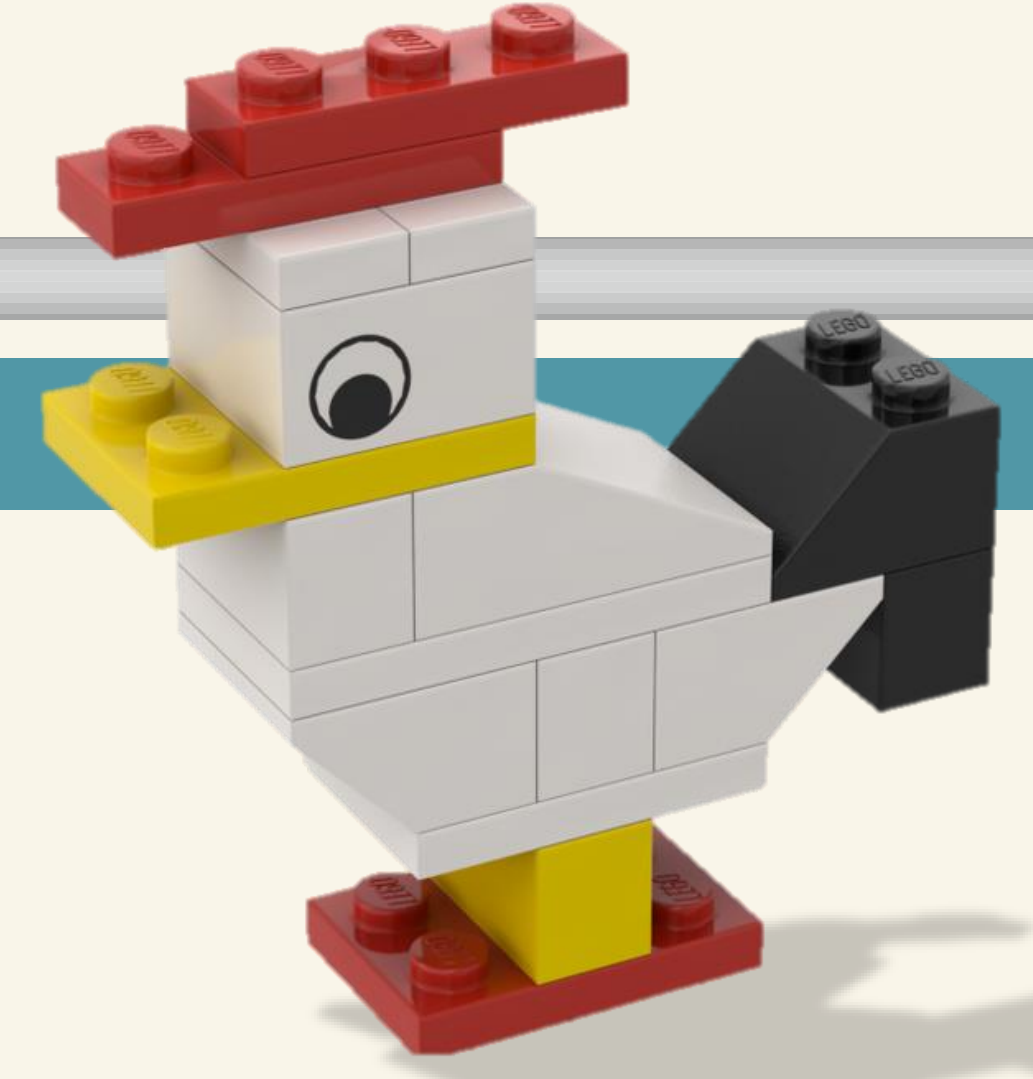
CONTEXT

While protein-coding genes (PCG) are relatively well known in livestock genomes, long non-coding RNA (lncRNA) 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 lncRNA identified using additional resources from multi-tissue projects or specialist databases.
- Provide a genomic and functional annotation for the community working on gene expression (lncRNAs and/or PCGs) to elucidate, for example, the molecular mechanisms linking non-coding variants and relevant phenotypes.



MATERIALS & METHODS

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

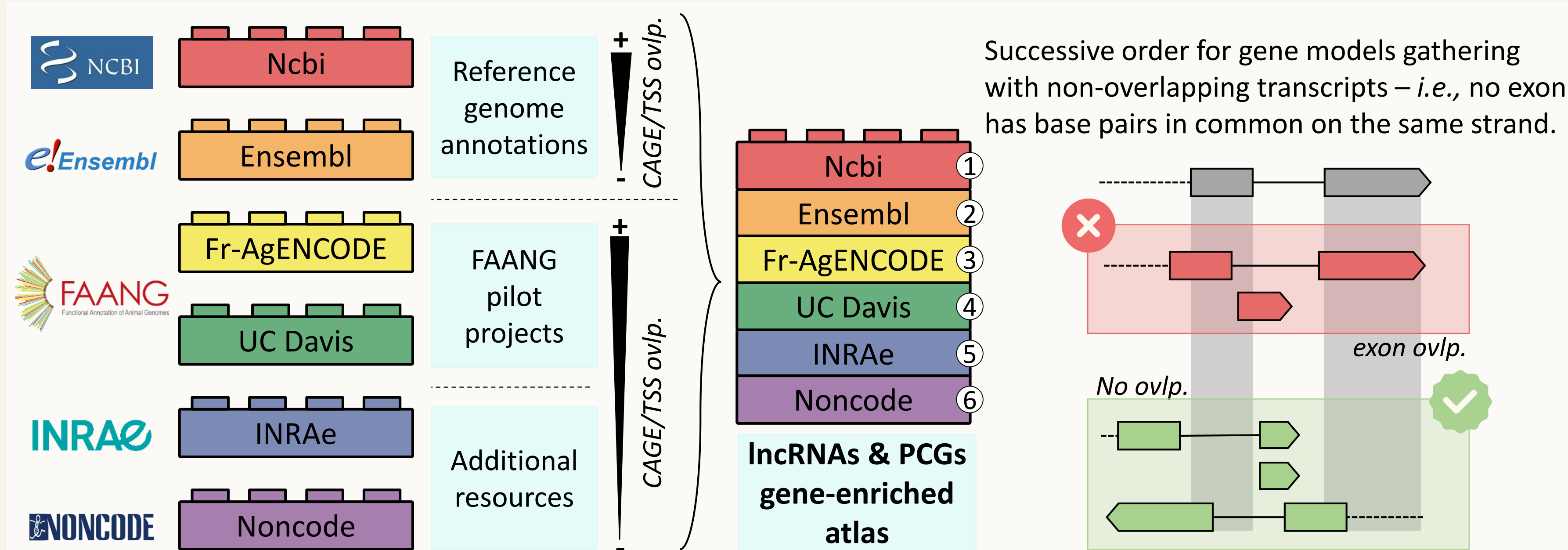
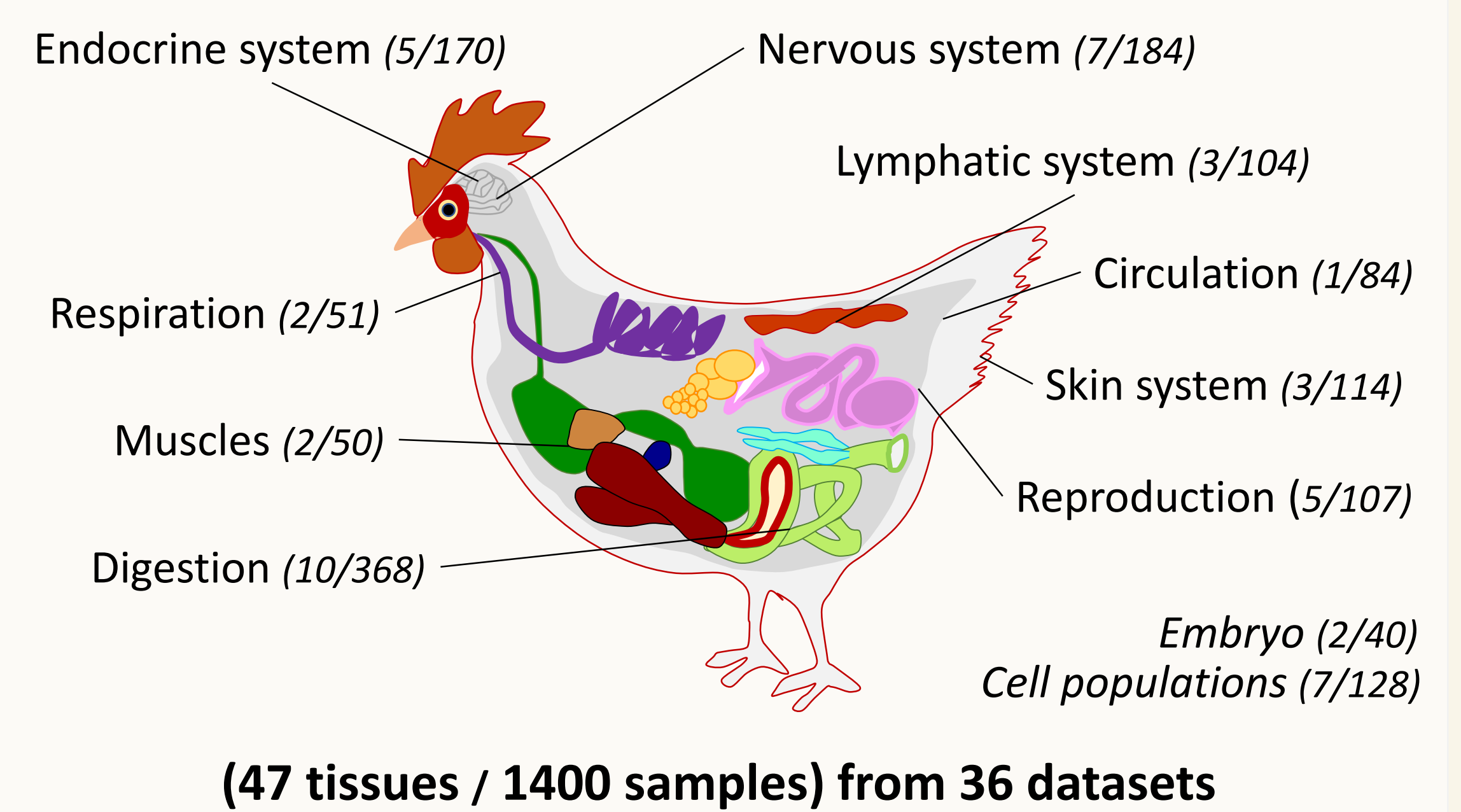


Fig. 2: A diversity of 47 tissues used for gene expression



RESULTS

Fig. 3: Number of genes in the enriched atlas

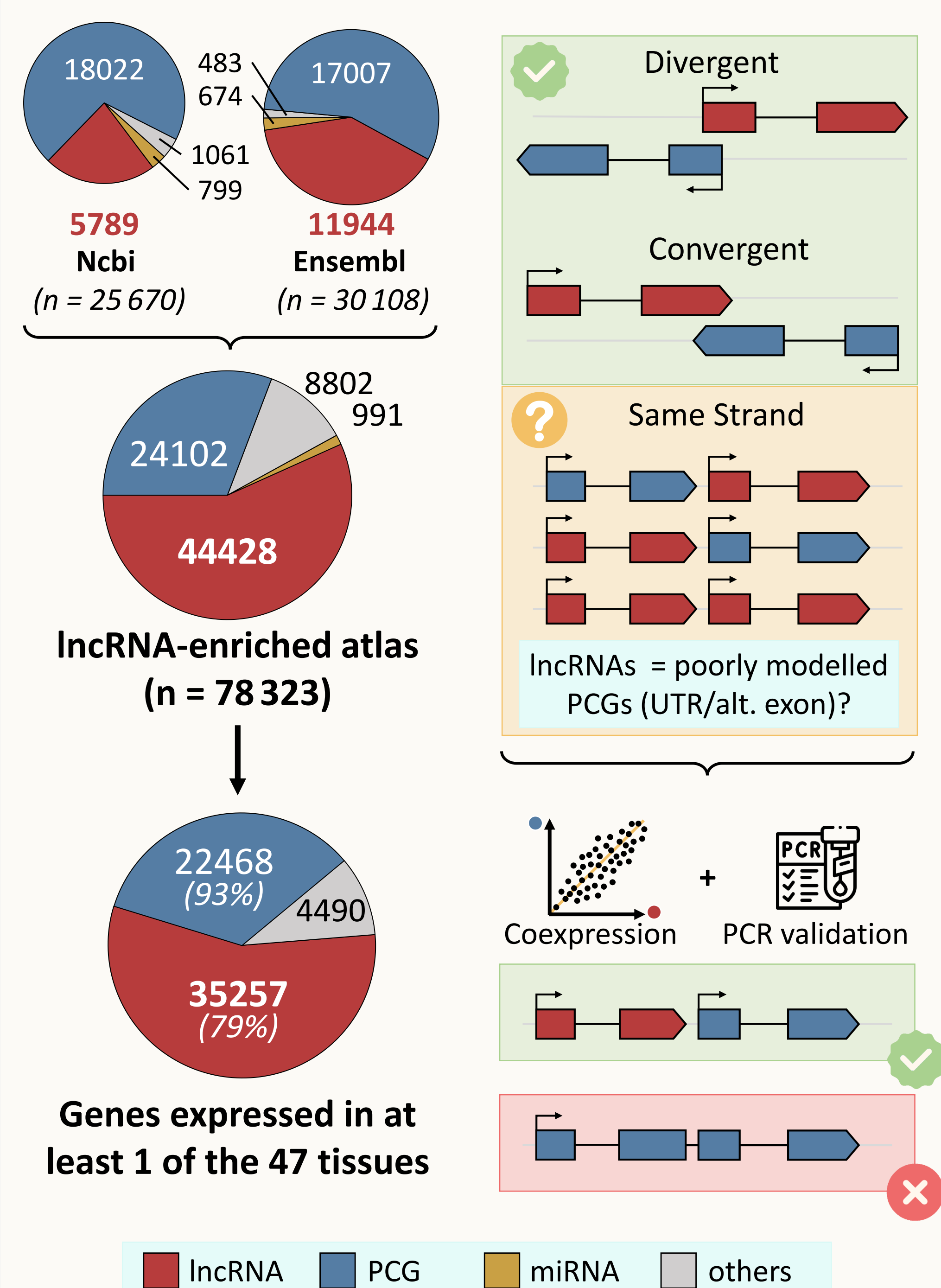
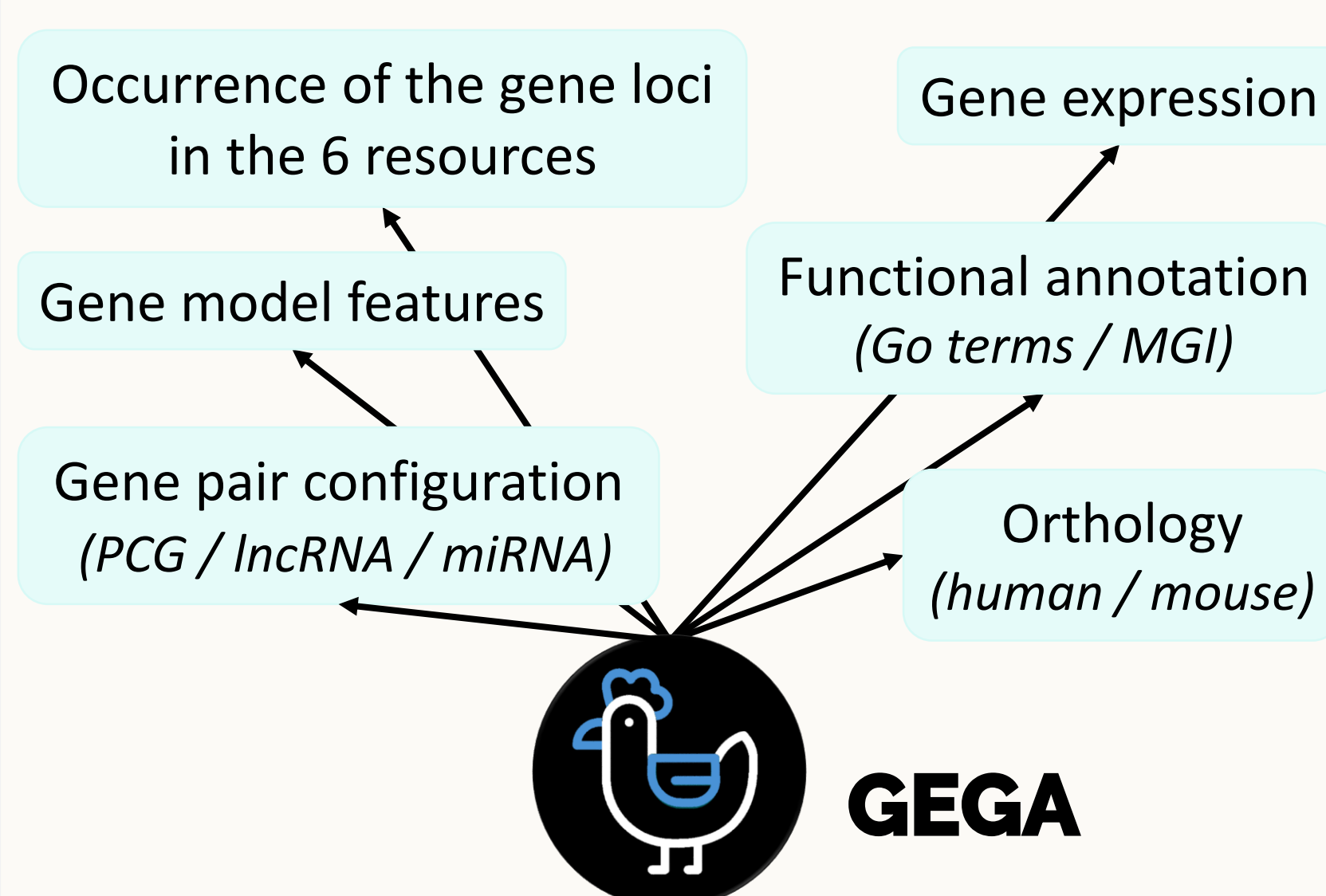
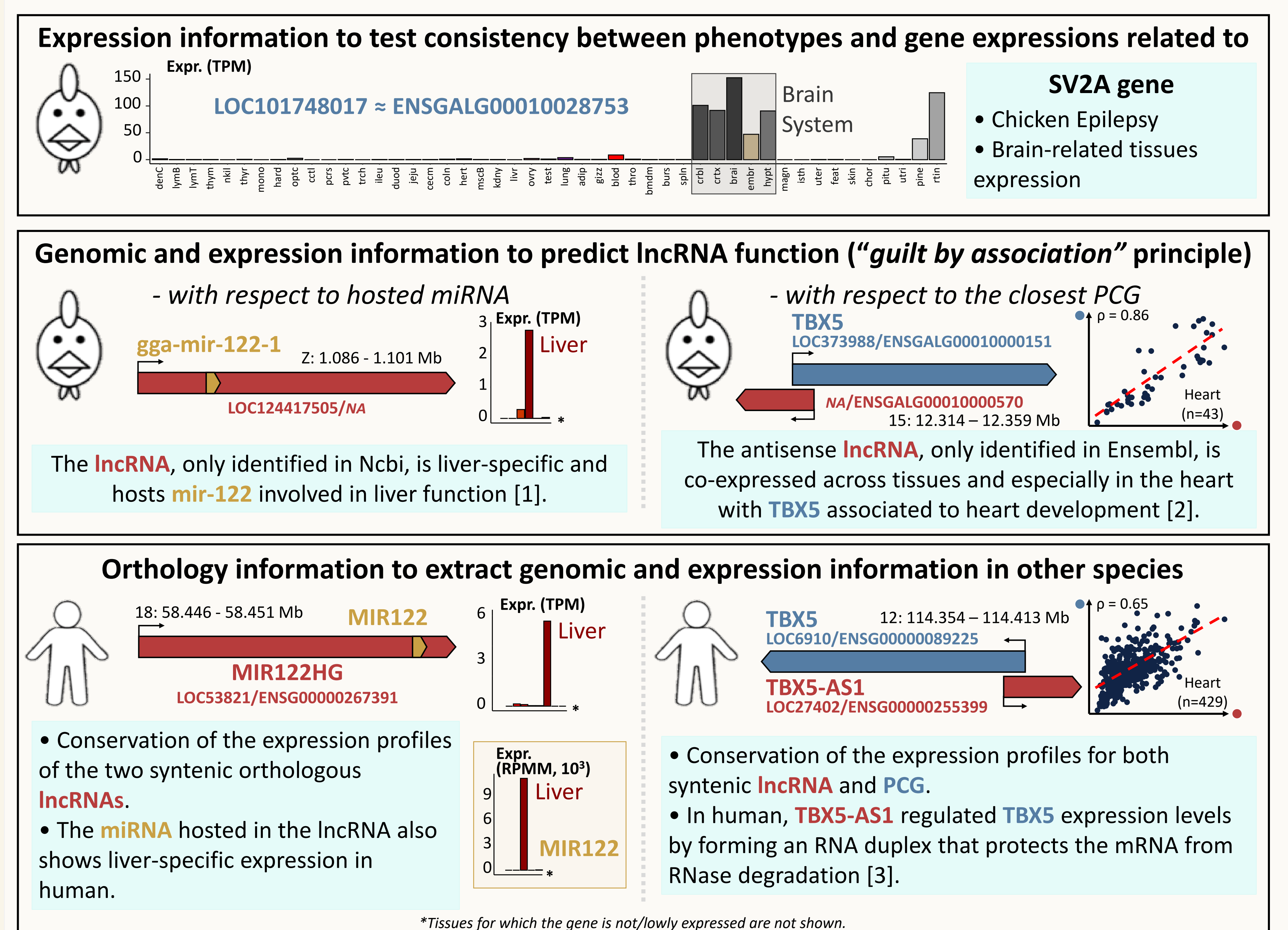


Fig. 4: Functional gene annotation, a resource for a variety of analyses



WEBSITE

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.sigene.org

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