



Fr-Agencode: an update

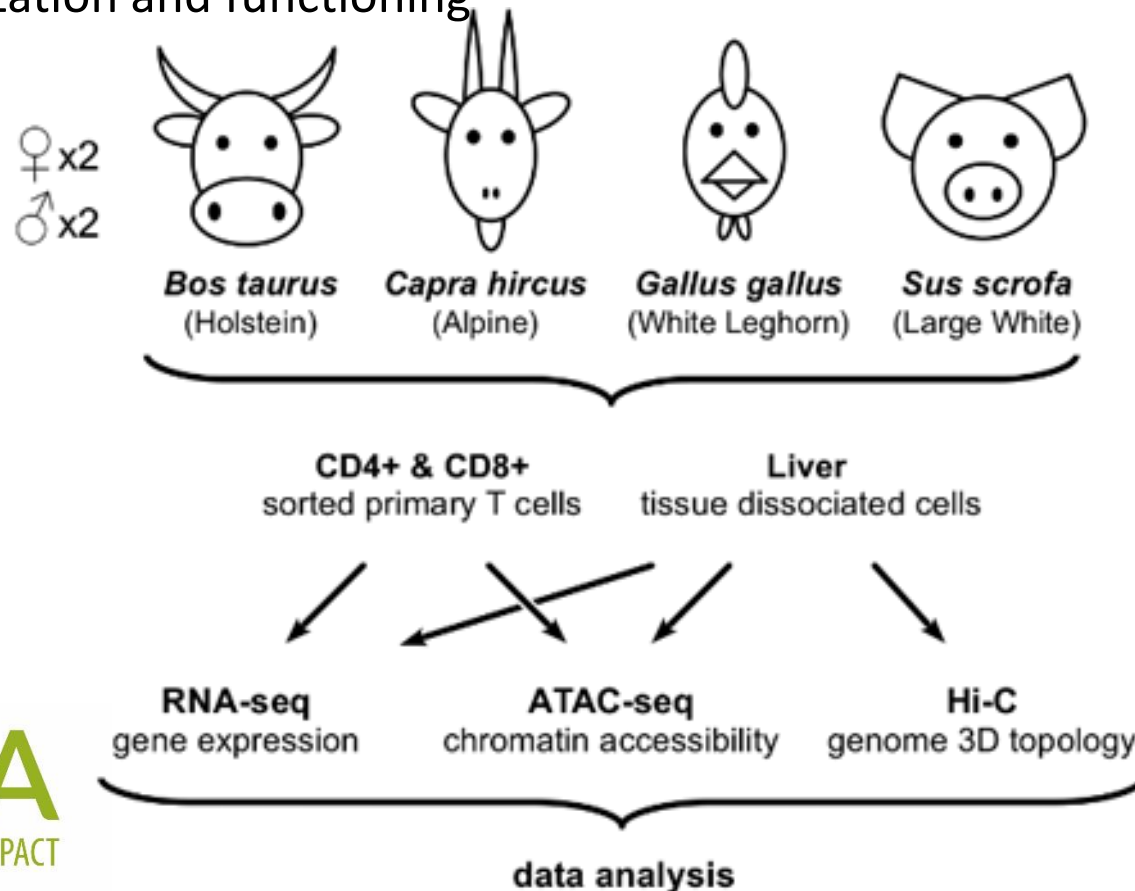
S. Foissac, S. Djebali, Andrea Rau, S. Lagarrigue,
H. Acloque, **E. Giuffra**, the FR-AgENCODE group

Plant and Animal Genome XXVII Conference – FAANG workshop – January 11th 2019 – San Diego (USA)



A multi-species pilot FAANG project:

- ❖ Realize an exhaustive FAANG sample collection from four main farm species
- ❖ Implement core FAANG assays on tissue dissociated cells (liver) and sorted primary cells (CD3+CD4+, CD3+CD8+ T cells)
- ❖ Compare whole transcriptome - chromatin accessibility - genome 3D topology for comparative analyses of genome organization and functioning



- Funded by INRA, SelGen metaprogramme (<http://www.selgen.inra.fr/>) between 2015-17
- Coordinated by Elisabetta Giuffra and Sylvain Foissac



Management



Elisabetta Giuffra (coordination)

Sylvain Foissac (coordination)

Sandrine Lagarrigue

Marie-Hélène Pinard-Van der Laan



**Federation of 14 research labs
& facilities**

Sampling and assays



Hervé Acloque

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Fany Blanc

Sophie Dhorne-Pollet

Françoise Drouet

Diane Esquerre

Stéphane Fabre

Joël Gautron

Adeline Goubil

Sonia Lacroix-Lamandé

Fabrice Laurent

Florence Mompert

Pascale Queré

Michèle Tixier-Boichard

Gwenola Tosser-Klopp

Silvia Vincent-Naulleau

Data analysis



Philippe Bardou

Cédric Cabau

Elisa Crisci

Thomas Derrien

Sarah Djebali-Quelen

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Ignacio Gonzalez

Christophe Klopp

Sandrine Lagarrigue

Sylvain Marthey

Maria Marti-Marimon

Raphaëlle Momal-Leisenring

Kylie Munyard

Kévin Muret

Andrea Rau

David Robelin

Magali San Cristobal

Nathalie Vialaneix

Matthias Zytnicki



Main results



1. 5,482 BioSamples entries available at the INRA biorepository
2. Improvement of the reference annotations with thousands of new genes and transcripts, including lncRNAs Analysis (analysis of small RNA-seq dataset still in progress).
3. Extensive chromatin accessibility profiling (ATAC-seq) pointing to potential regulatory sites.
4. 3D cartography data of the genome (Hi-C), including Topologically Associating Domains (TADs) and A/B compartments.

Foissac S, Djebali S, Munyard K, Villa-Vialaneix N, Rau A, et al. 2018. Livestock genome annotation: transcriptome and chromatin structure profiling in cattle, goat, chicken and pig. bioRxiv. <https://doi.org/10.1101/316091> (*submitted*)

Muret K, Klopp C, Wucher V, Esquerré D, Legeai F, et al. 2017. Long noncoding RNA repertoire in chicken liver and adipose tissue. *Genet. Sel. Evol.* 49:6

1) 5,482 Samples available at the INRA biorepository (as part of CRB-Anim collection)




Requests ▾ Administration ▾
My account
Tixier-Boichard Michèle ▾
My cryobasket 

Biological Resource Centre
for domestic animals



5482 Sample matching your criteria

| | Identifier ▾ | Breed ▾ | Sample type ▾ | Species ▾ | |
|-------------------------------------|--|--|--|--|---------------------------------------|
| <input type="checkbox"/> | <input type="text" value="Add a filter..."/> | <input type="text" value="Add a filter..."/> | <input type="text" value="Add a filter..."/> | <input type="text" value="Add a filter..."/> | |
| <input checked="" type="checkbox"/> | CRB165628 | Holstein | tissue | Bos taurus | <input type="button" value="Infos."/> |
| <input checked="" type="checkbox"/> | CRB165629 | Holstein | tissue | Bos taurus | <input type="button" value="Infos."/> |
| <input type="checkbox"/> | 1630 | Holstein | tissue | Bos taurus | <input type="button" value="Infos."/> |

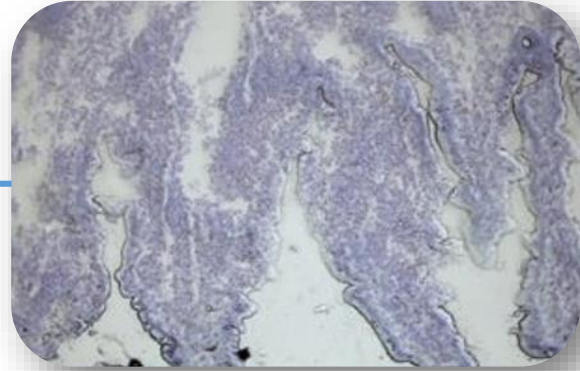


<https://crb-anim.fr/access-to-collection>

1) Subsets of cryoconserved tissue samples were embedded in OCT for laser microdissection

RNA isolation of chosen cell types

Chicken intestine



RIN: 8.50

Microdissected crypts

No RIN Value
(non detectable)



Microdissected enterocytes

No RIN Value
(non detectable)



CD30, Villin1, Vimentin) and 1 ref. gene (*HRP1*) well detectable by qPCR in all microdissected cells

Connecting FAANG protocols to the preparation of ISO technical standards

Draft on technical specifications in preparation (#20388) on:

- **The collection, processing, transportation and storage requirements for animal biological materials**

By: ISO (International Standard Organisation), Working group 2 of Technical Committee #276 in Biotechnology (led by China National Gene Bank)

Aims: Improving reliability and reproductibility of research, by providing a reference for the quality assesement of animal biological materials from time of sampling until storage in a biobank

2) “FR-AgENCODE transcripts” set: between 58,000 and 85,000 transcripts identified, depending on species

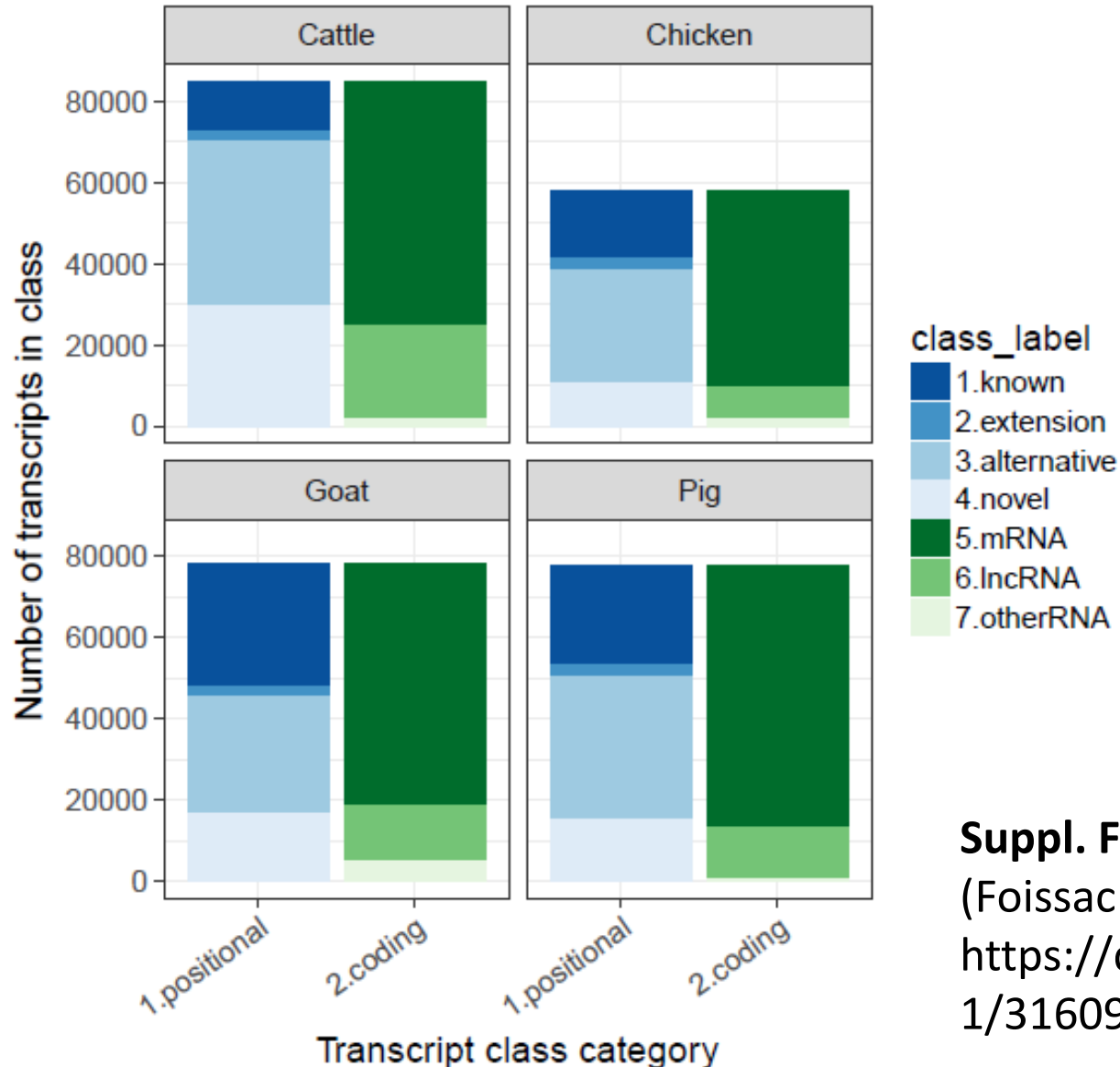


| Species | Reference transcripts | | FR-AgENCODE transcripts | | | |
|---------|-----------------------|-----------|-------------------------|--------|---------|--------|
| | All | Expressed | # | mRNAs | lncRNAs | |
| | | # | % of total | | | |
| Cattle | 26,740 | 16,100 | 60.2 | 84,971 | 59,801 | 22,724 |
| Goat | 53,266 | 34,442 | 64.7 | 78,091 | 64,962 | 13,864 |
| Chicken | 38,118 | 22,180 | 58.2 | 57,817 | 47,567 | 7,502 |
| Pig | 49,448 | 29,786 | 60.2 | 77,540 | 63,721 | 12,587 |

Table 1 (Foissac et al.; bioRxiv. <https://doi.org/10.1101/316091>)

- Differential analyses of gene expression in liver and T cells yielded results consistent with known metabolism and immunity functions.

2) Analysis of new transcripts improves and extends gene structure annotation of the four species



“FR-AgENCODE transcripts”:

- Distributed into four positional (known, extension, alternative, novel) and three coding (mRNA, lncRNA, otherRNA) classes.
- The « alternative » class (**new splice variants of known genes**) predominates in all species.

Suppl. Figure 10A

(Foissac et al.; bioRxiv.
<https://doi.org/10.1101/316091>)

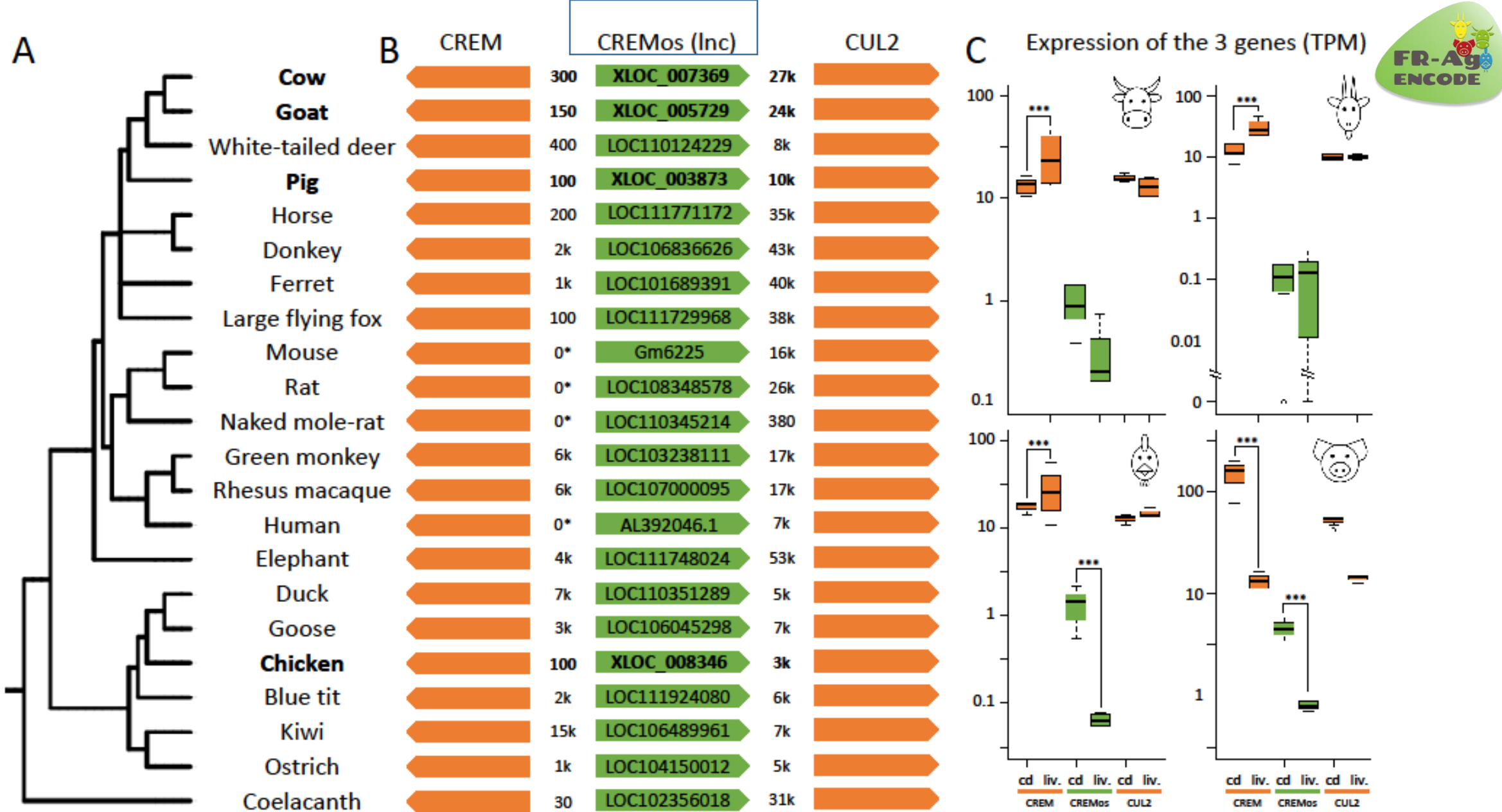


Figure 4 (Foissac et al.; bioRxiv. <https://doi.org/10.1101/316091>)

An atlas of chicken long non-coding RNAs gathering multiple sources: gene models and expression across more than twenty tissues

Frédéric Jehl*, Kévin Muret*, Maria Bernard*, Diane Esquerré, Hervé Acloque, Elisabetta Giuffra, Sarah Djebali, Sylvain Foissac, Thomas Derrien, Tatiana Zerjal, Christophe Klopp[§] and Sandrine Lagarrigue[§]

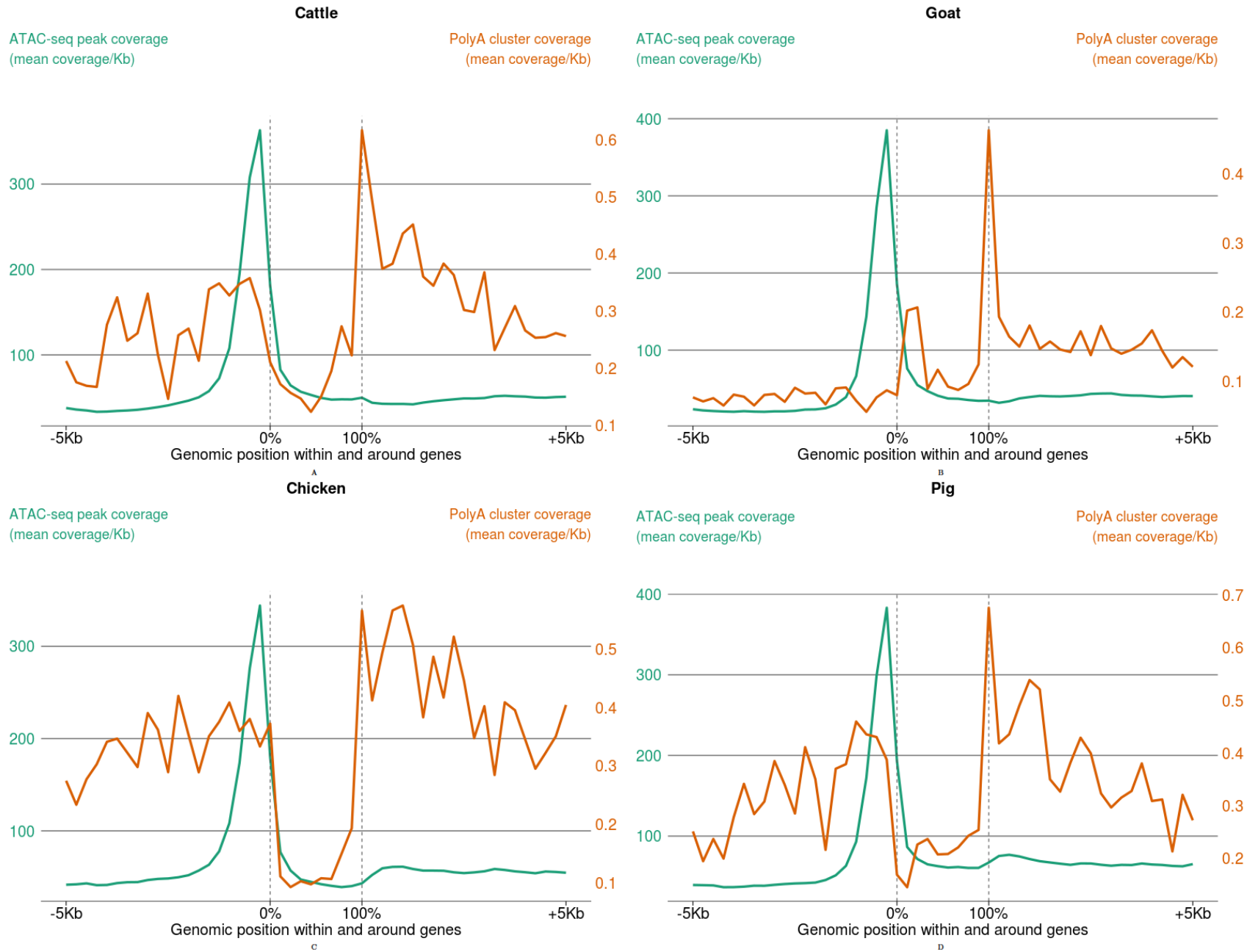
Sunday, January 13th talk: **Non-coding RNA workshop**
Poster board number: **PO0423**

- ✓ **A large catalogue of chicken lncRNAs at the gene level by gathering different sources**
4,640 from V94 ensembl => **30,084 lncRNAs**
- ✓ **A rough annotation of all these genes, based on their expression pattern across 21 chicken tissues and their position relative to the nearest coding gene**

Perspective:

Will use these data to study the genetic component of feed efficiency in layer chicken

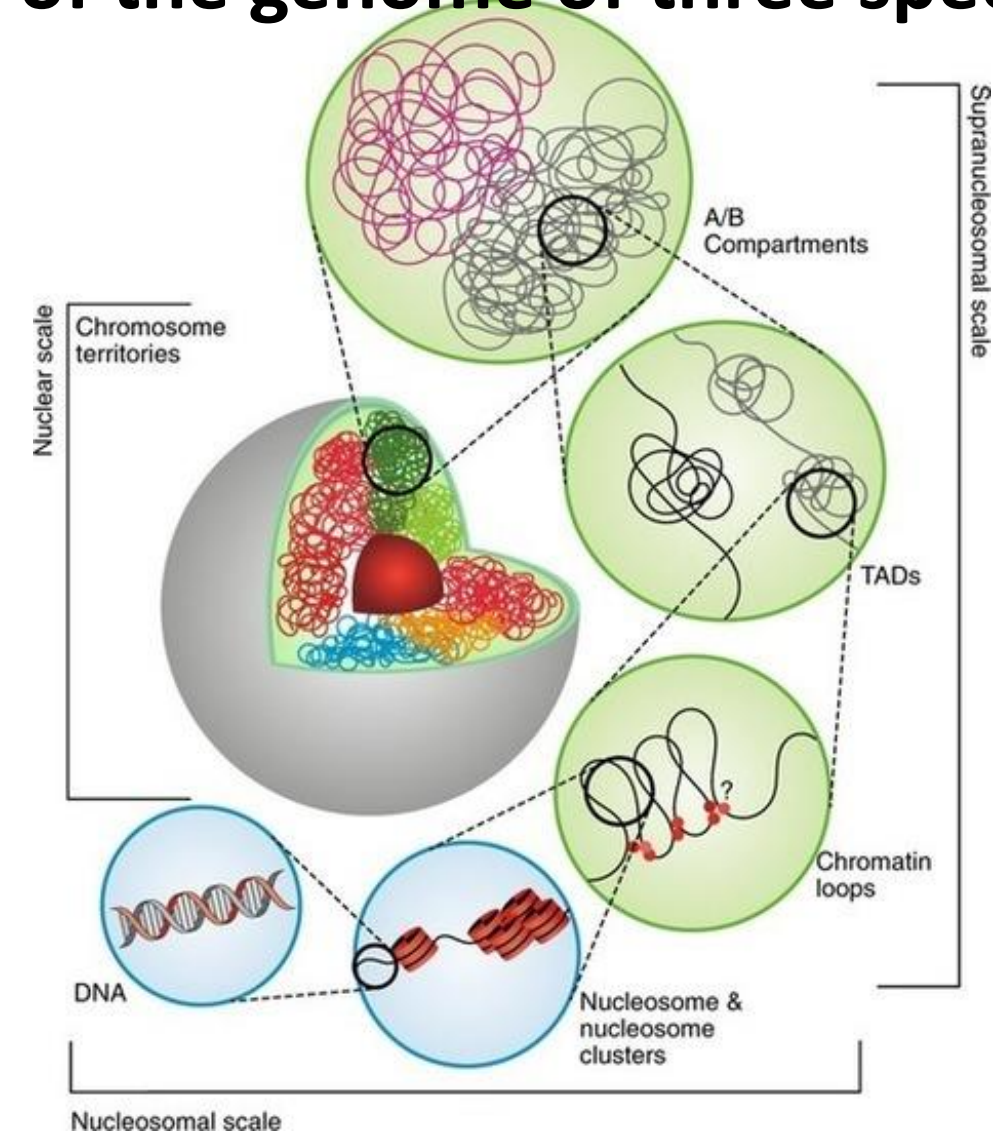
3) Chromatin accessibility profiling



- Between 26,000 (pig, liver) and 111,000 (pig, cd8) ATAC-seq peaks per tissue; **most either intronic or intergenic.**
- Average peak size 600 bp for all species, except for chicken (<500 bp).
- **ATAC-seq peak distribution within and around reference genes showed a clear signal at the TSS for all species**

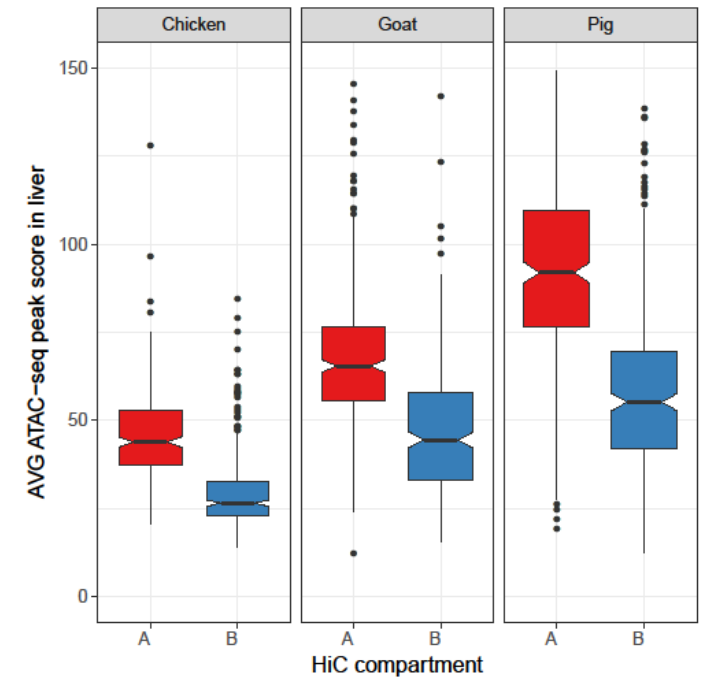
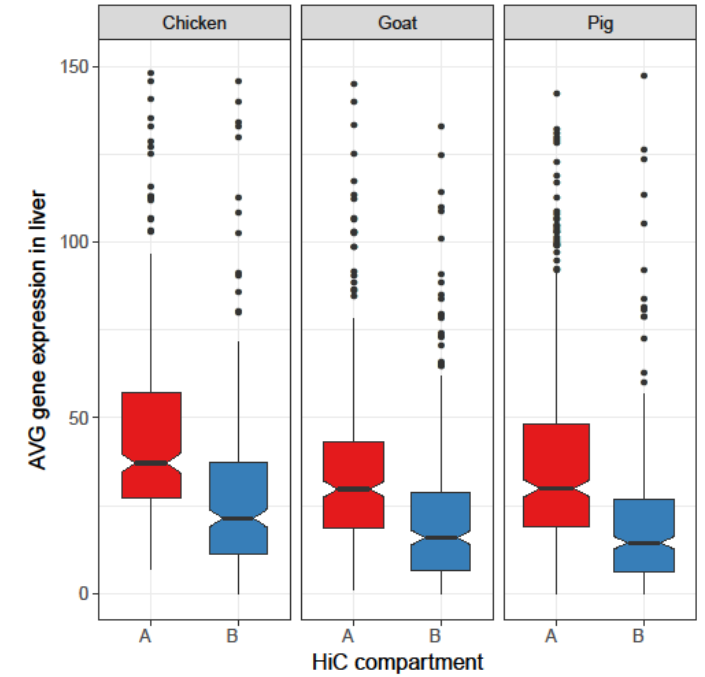
Figure 5 (Foissac et al.; bioRxiv. <https://doi.org/10.1101/316091>)

4) Genome-wide 3D interaction maps by Hi-C of the genome of three species (liver)



- High consistency with gene expression and chromatin accessibility data

Figure 8 (Foissac et al.; bioRxiv. <https://doi.org/10.1101/316091>)



All FR-AgENCODE datasets are shared in FAANG DCC (<http://data.faang.org>)



| Dataset ID | Title | Species | Archive |
|-------------------|--|--|---------|
| PRJEB27455 | Transcriptome profiling of liver and T cells in 4 livestock species by the FAANG pilot project FR-AgENCODE | <i>Bos taurus, Gallus gallus, Sus scrofa, Capra hircus</i> | ENA |
| PRJEB27111 | Chromatin accessibility profiling of liver and T cells in 4 livestock species by the FAANG pilot project FR-AgENCODE | <i>Bos taurus, Gallus gallus, Sus scrofa, Capra hircus</i> | ENA |
| PRJEB27364 | High-throughput chromosome conformation capture of liver cells in 4 livestock species by the FAANG pilot project FR-AgENCODE | <i>Sus scrofa, Gallus gallus, Capra hircus</i> | ENA |

Implement technology and analysis pipelines improvements within new FAANG-related research programs



✓ **GENE-SWitCH** (H2020, SFS30 Scope A) was selected and is now in negotiation with the EC

The three **selected SFS30 projects (GENE-SWitCH, BOVREG and Aqua-FAANG)** are committed to efficient clustering within FAANG.

In addition:

Collaboration to a project proposal “Hunting for determinants of immune capacity in pigs: a step forward in system immunology” (PI: O. Distl, Germany; co-PIs: C. Rogel-Gaillard, S. Hammer). Work will include functional genome annotations focused on SLA and immune-related traits.