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VizFaDa: Visualisations of FAANG data

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Abstract

- Functional Annotation of Animal Genomes (FAANG) is an open consortia gathering genome regulation data in farmed animals: 
- Raw genomic data and rich sample metadata are freely available through a data portal hosted at EMBL-EBI: data.faang.org
- We aim to provide data visualisations of FAANG datasets (RNA-seq, ChIP-seq, ATAC-seq, DNA methylation), embedded to the FAANG data portal.
- Visualisations will provide an overview of the available data to foster data re-use.

➤ Data processing &

Nextflow pipelines based on nf-core:

- A Nextflow module to get metadata & download data
- Fast RNA-seq quantification using Salmon pseudo-aligner
 - Pearson correlation on log₁₀(TPM + 1)
- ChIP-seq processing using bwa and macs2
 - Jaccard index from bedtools

➤ Notable by-products

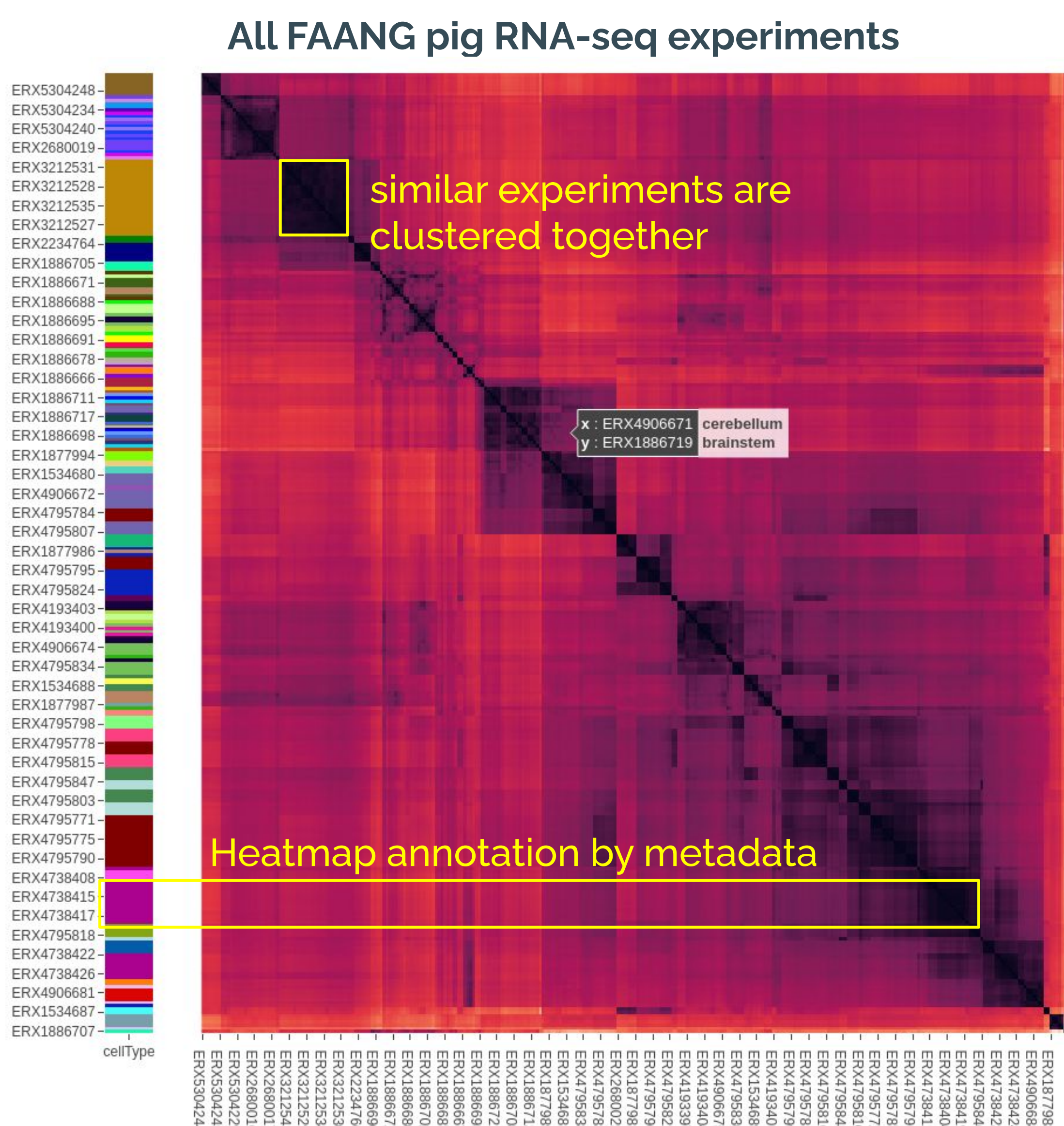
Uniformly processed outputs on FAANG data:

- FastQC reports
- Gene and transcript expression matrices (count & TPM)
- ChIP-seq peaks and bigwig tracks

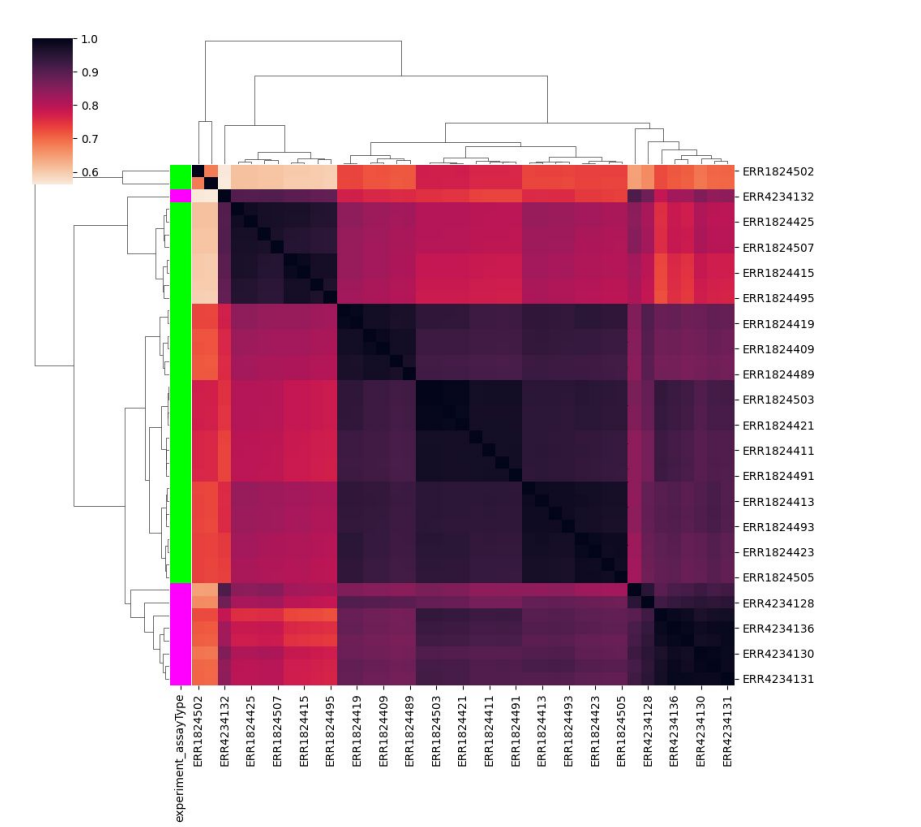
➤ Sample-to-sample correlation heatmaps

By species and by experiment types (RNA-seq, ChIP-seq, DNA methylation)

- overview of available data
- visualising the relationships between samples
- outlier identification



Heatmaps are subsettable by metadata fields



- Soon: upload your own data
- RNA-seq: gene expression table (count, TPM)
 - ChIP-seq: peak bed file

➤ Epigenetic profiles at TSS

Generated using the R package Epistack:

- github.com/GenEpi-GenPhySE/epistack

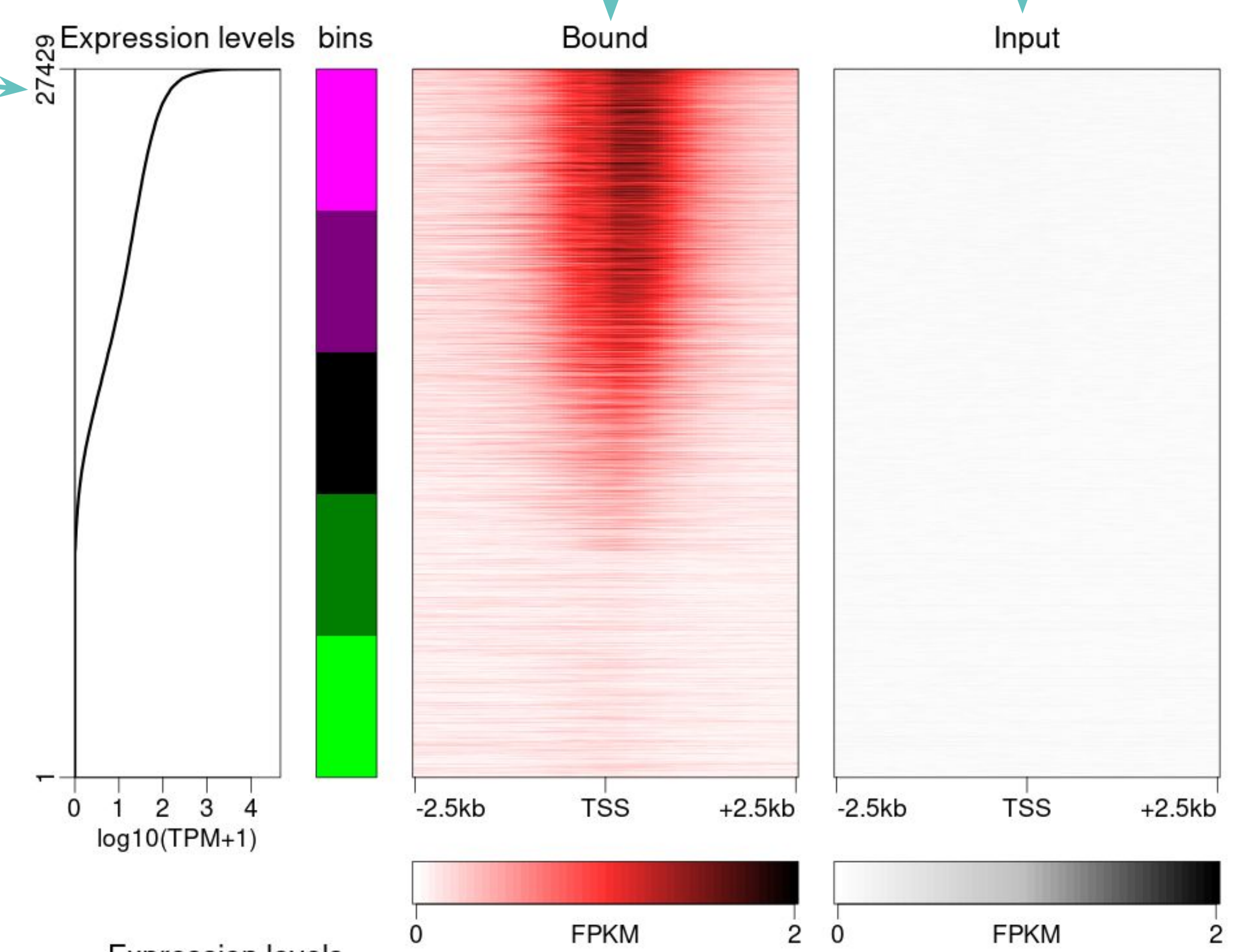
Integrative analysis of RNA-seq and ChIP-seq / DNA methylation data:

- data quality
- exploratory analysis

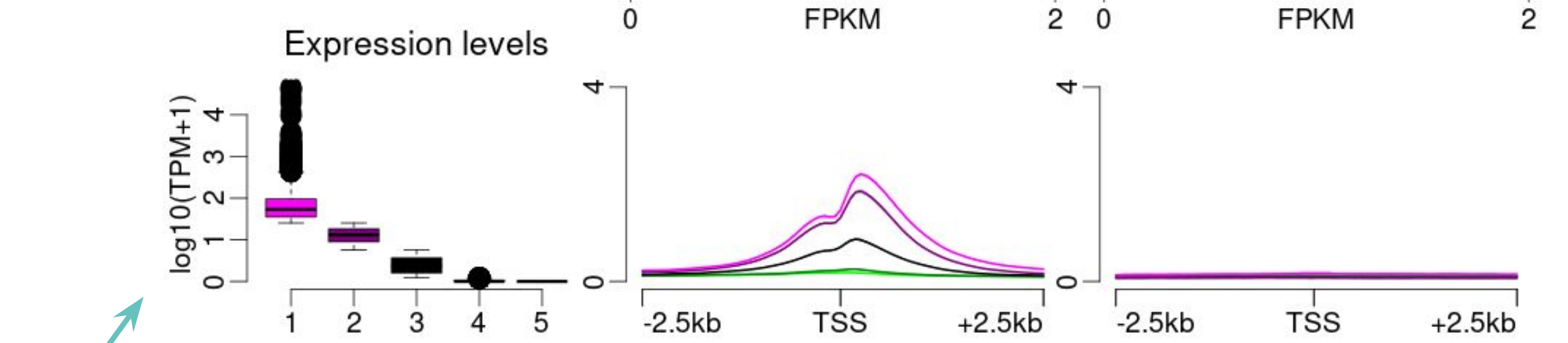
H3K4me3 ChIP-seq from a cow cerebellum

2- ChIP-seq profiles around Transcription Start Sites

3- ChIP-seq control profiles



1- The 27,429 annotated *Bos taurus* genes are sorted according to their expression level from a matching FAANG RNA-seq experiment



4- Genes are grouped in 5 bins from their expression levels

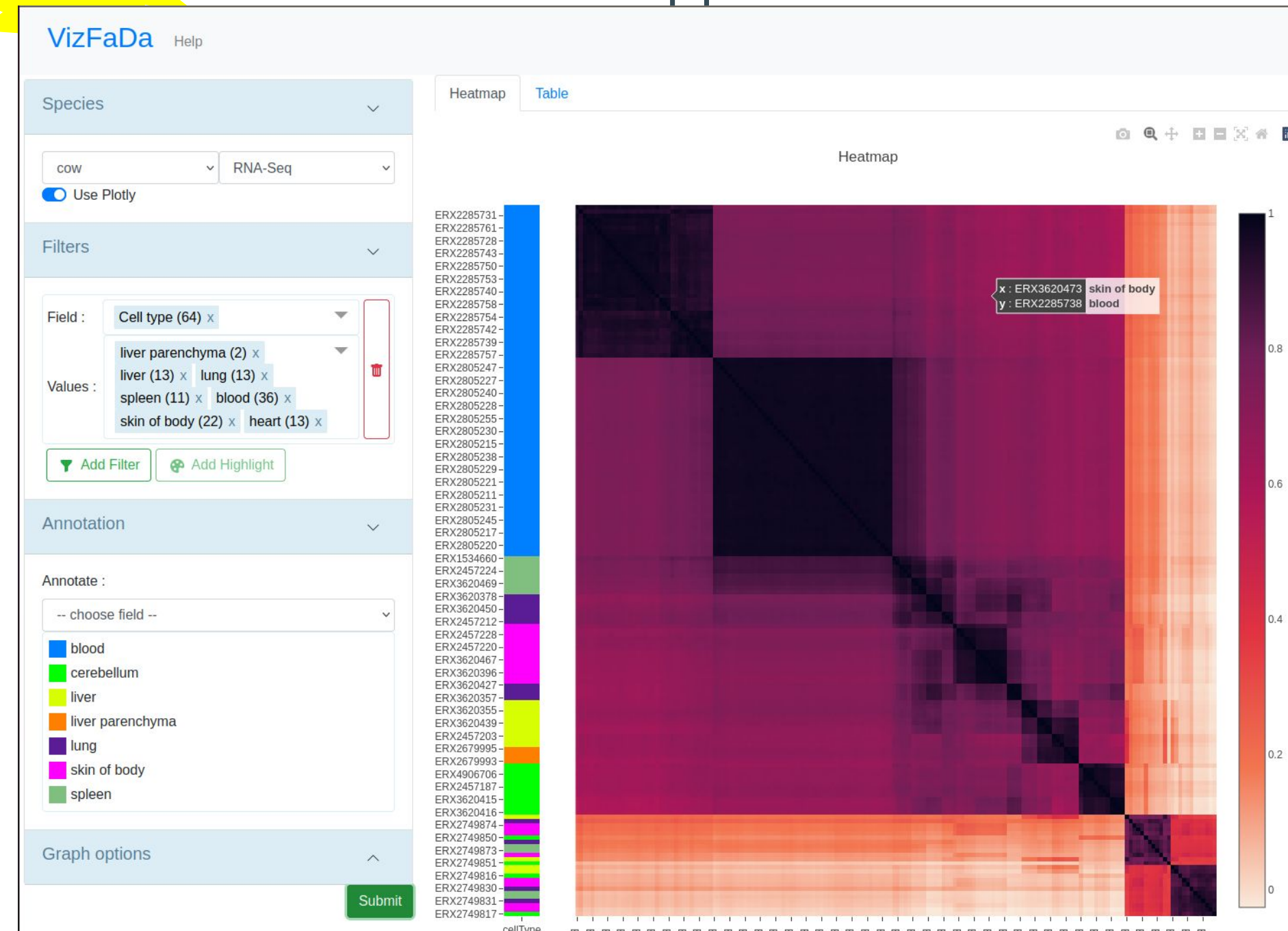
5- ChIP-seq average profiles per bin around TSS

➤ VizFaDa timeline

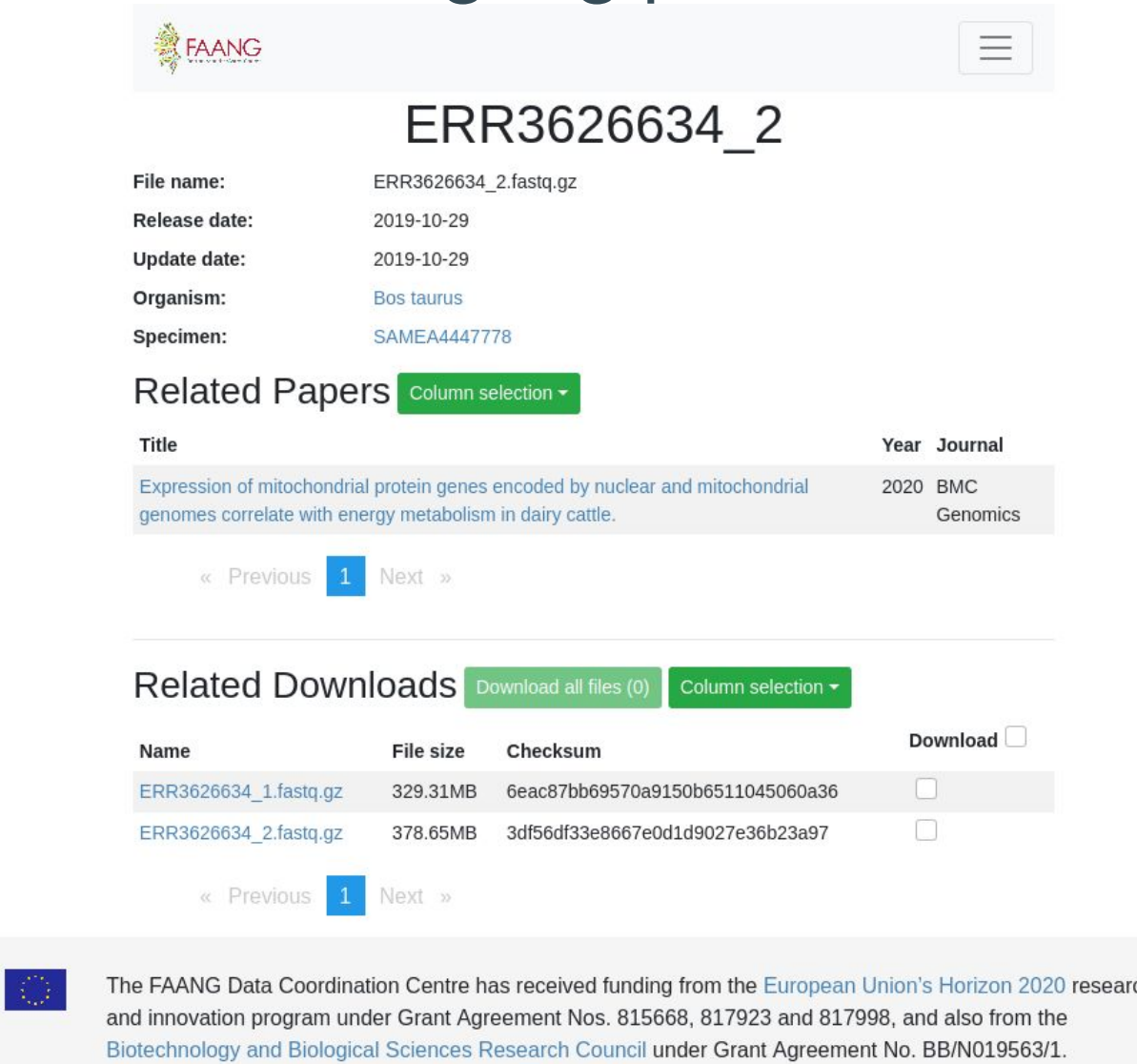
| 2020-07 | 2021-01 | 2021-07 | 2022-01 | 2022-07 |
|----------------|-----------------------|-----------------|-------------------------------|---|
| VizFaDa starts | All RNA-seq processed | Web-app (alpha) | All ChIP-seq processed | Web app (beta) |
| | | | All DNA methylation processed | Maintenance: |
| | | | | <ul style="list-style-type: none"> ➤ new FAANG data ➤ using new reference genomes and annotations |

➤ Web applications

Soon: a dedicated web-app for visualisations



Soon: integrations to the data.faang.org portal



➤ Fundings

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