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Stronger transcriptomic response to feed intake in the duodenum of pig with high feed efficiency from a divergent selection experiment

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Guillaume Devailly, Katia Feve, Safia Saci, Julien Sarry, Sophie Valière, et al.. Stronger transcriptomic response to feed intake in the duodenum of pig with high feed efficiency from a divergent selection experiment. International Congress on Animal Science EAAP 2023, Aug 2023, Lyon, France. 10.15454/1.5572415481185847E12 . hal-04195417

HAL Id: hal-04195417

<https://hal.inrae.fr/hal-04195417>

Submitted on 4 Sep 2023

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➤ Stronger transcriptomic response to feed intake in the duodenum of pig with high feed efficiency from a divergent selection experiment

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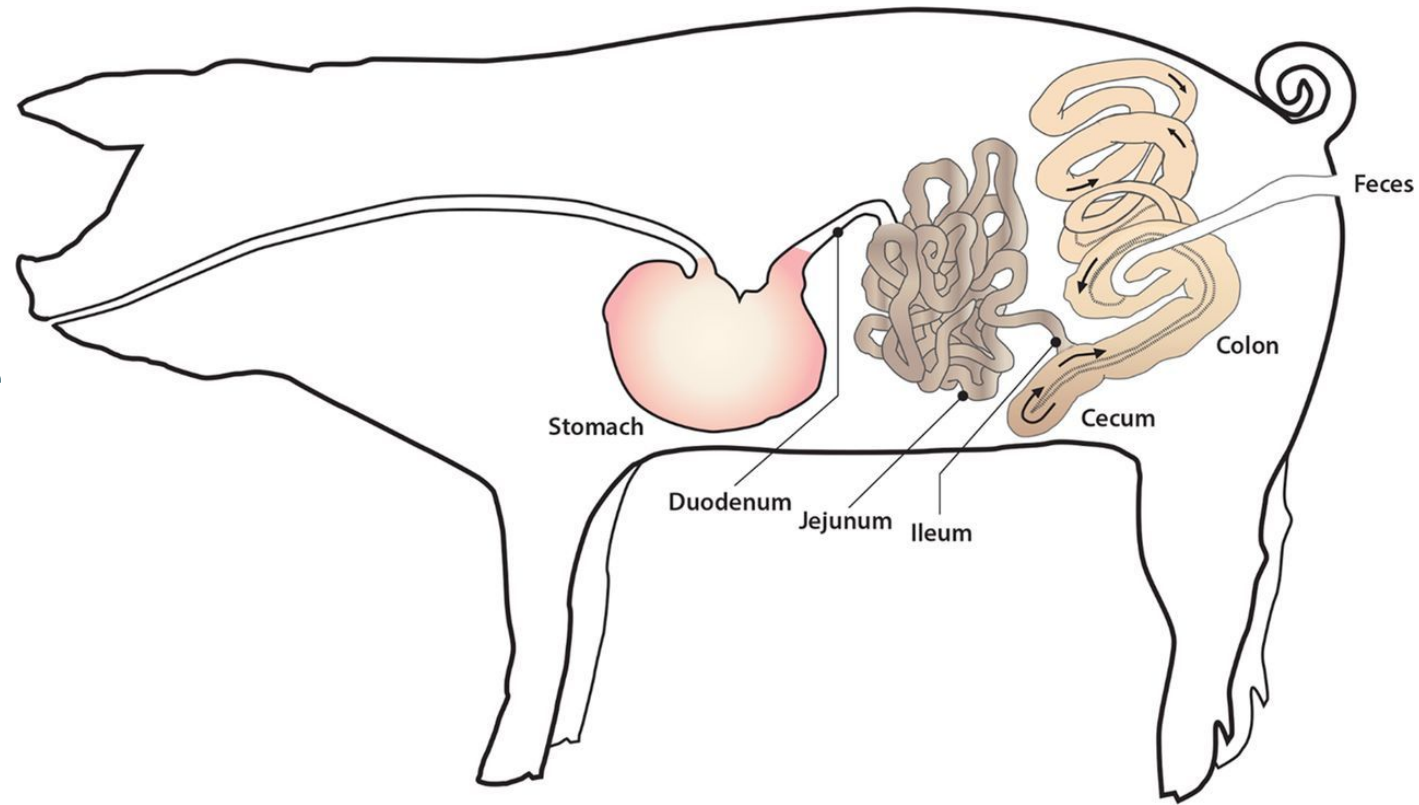
@G_Devailly(@mamot.fr)

The duodenum: a key organ for efficient pig farming

Pig gastrointestinal tract is involved in:

- feed efficiency
- by products, alternative feed
- post-weaning diarrhea

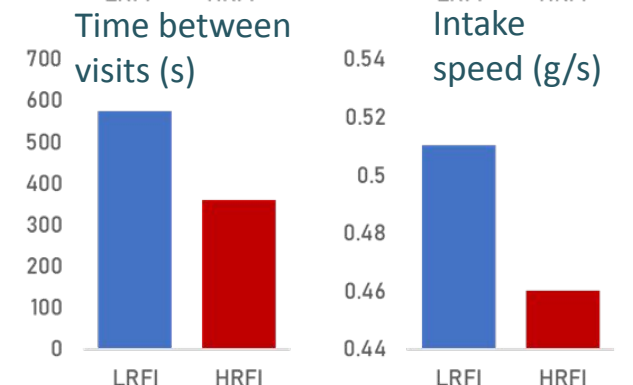
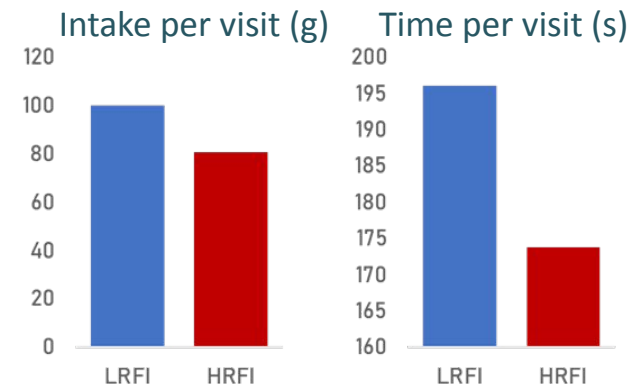
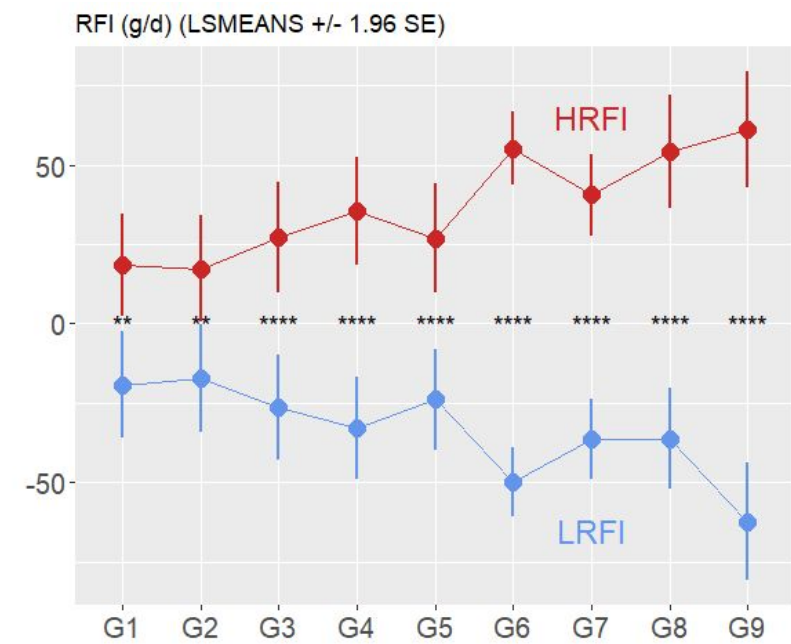
The duodenum is a key organ contributing to the hunger/satiety loop.



<https://doi.org/10.1128/mSystems.00004-17>

Selecting for feed efficiency in pigs

- **Divergent selection for residual feed intake in the growing pig** (Review: Gilbert et al. 2017, doi: 10.1017/S175173111600286X)
- **Lower environmental impact of the LRFI line** (Soleimani et al. 2021, doi: 10.1093/jas/skab051)
- **Transcriptomic comparison of muscle, liver and adipose tissues (G8), with differences affecting immune response, response to oxidative stress and protein metabolism** (Gondret et al. 2017, doi: 10.1186/s12864-017-3639-0)
- **Genetic architecture of the response to selection** (Delpuech et al. 2021, doi: 10.1186/s12711-021-00642-1)
- **Differences in faecal microbiota composition** (Aliakbari et al. 2021, doi: 10.1111/jbg.12539)
- **Distinct feeding behaviour between the HRFI and LRFI lines**



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Investigating the duodenum DNA methylation & transcriptomic response to feed intake

Experimental setup



Line

■ LRFI ■ HRFI

Family

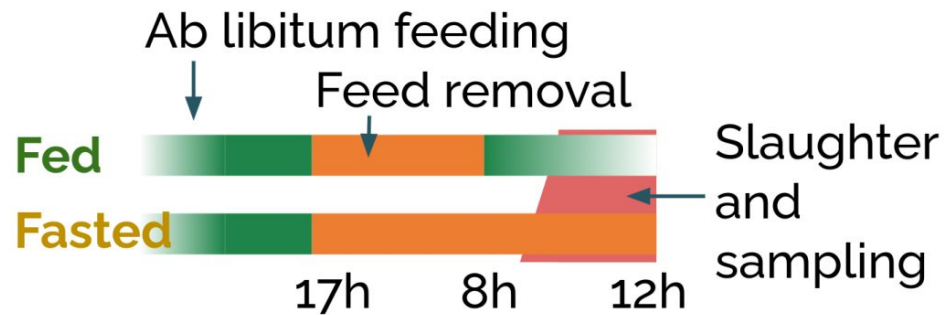
■ A ■ B ■ C ■ D ■ E ■ F

Sex

■ F ■ M

Condition

■ fasted ■ fed



Duodenum mucosa dissection



PolyA RNA-seq

Illumina, 2x150, 40M reads
Salmon pseudo-alignment

nf-core 
nf-core/rnaseq

MeDP-seq

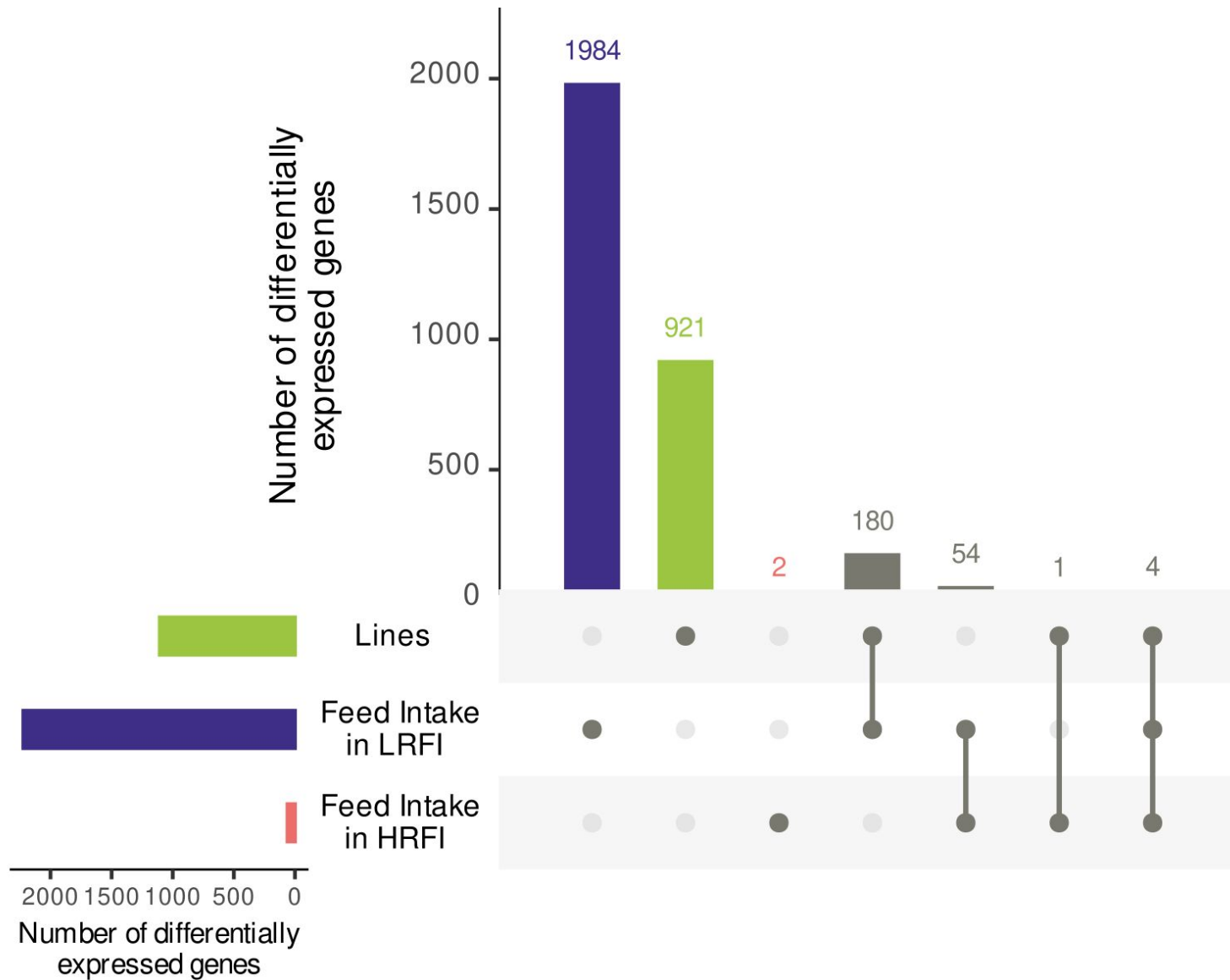
Illumina, 2x100, 70M reads
BWA alignment

nf-core 
nf-core/chipseq

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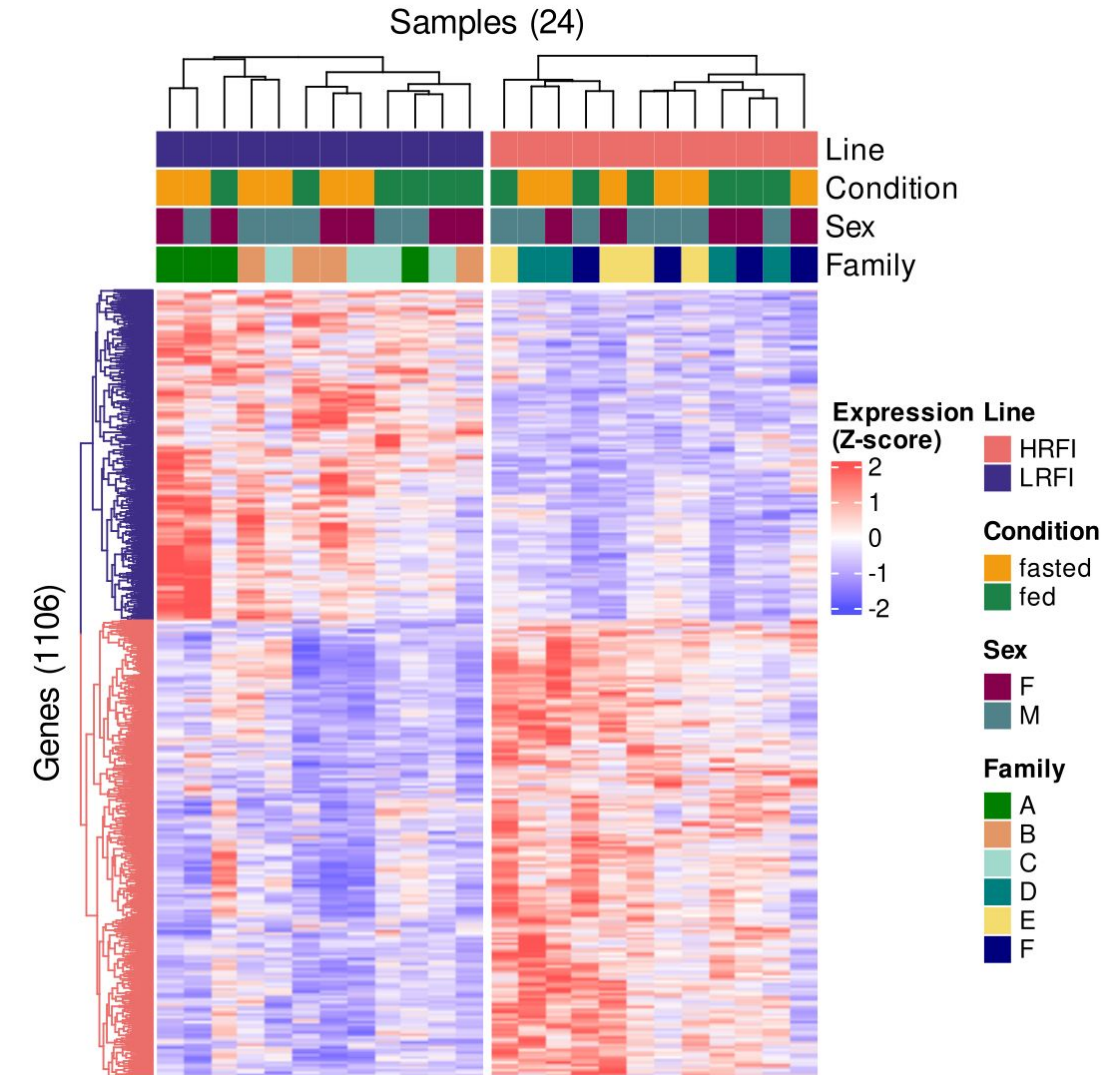
Investigating the duodenum transcriptomic response to feed intake



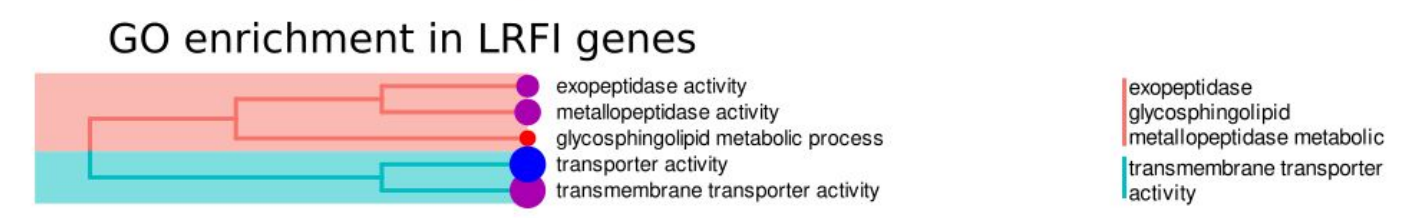
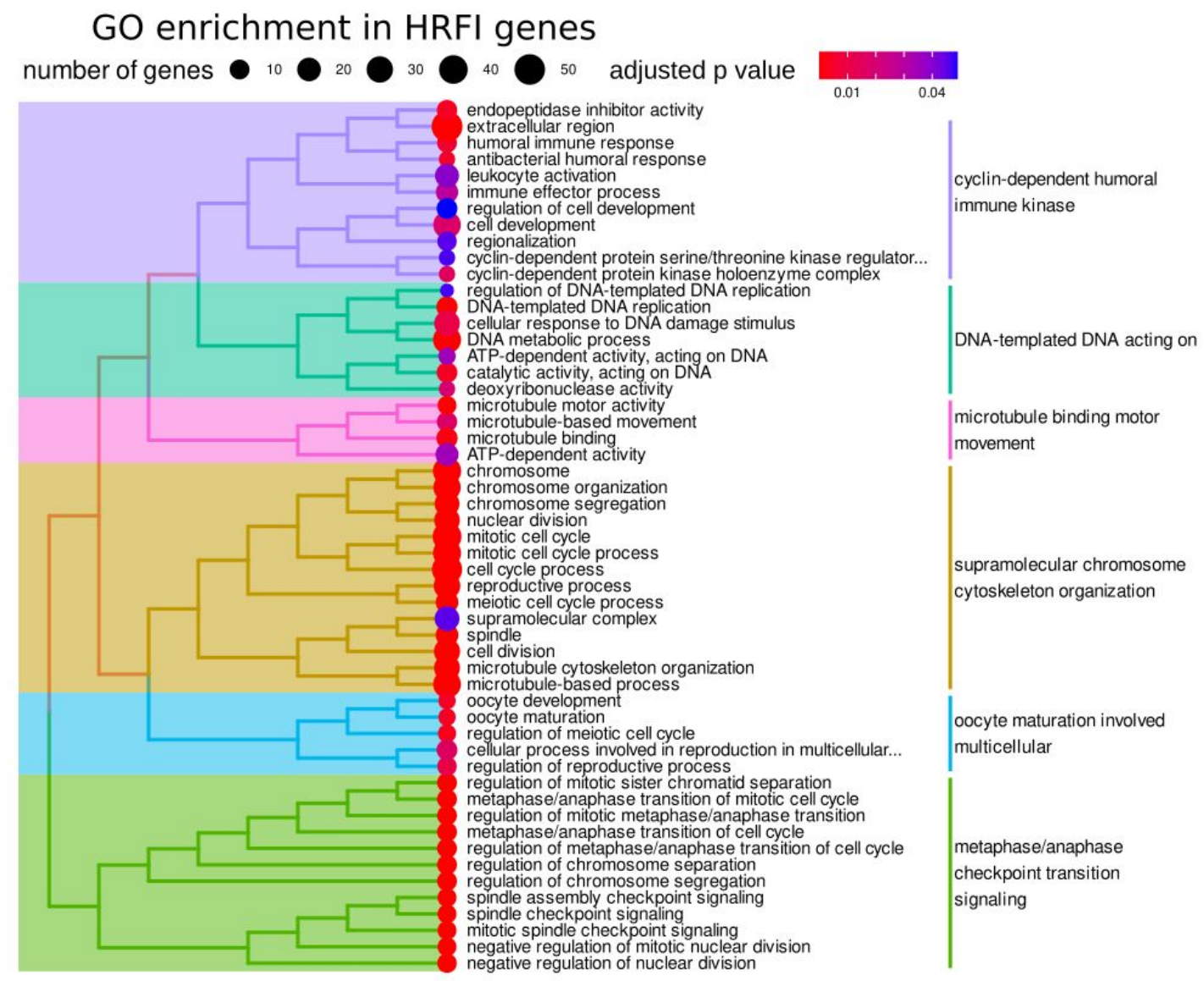
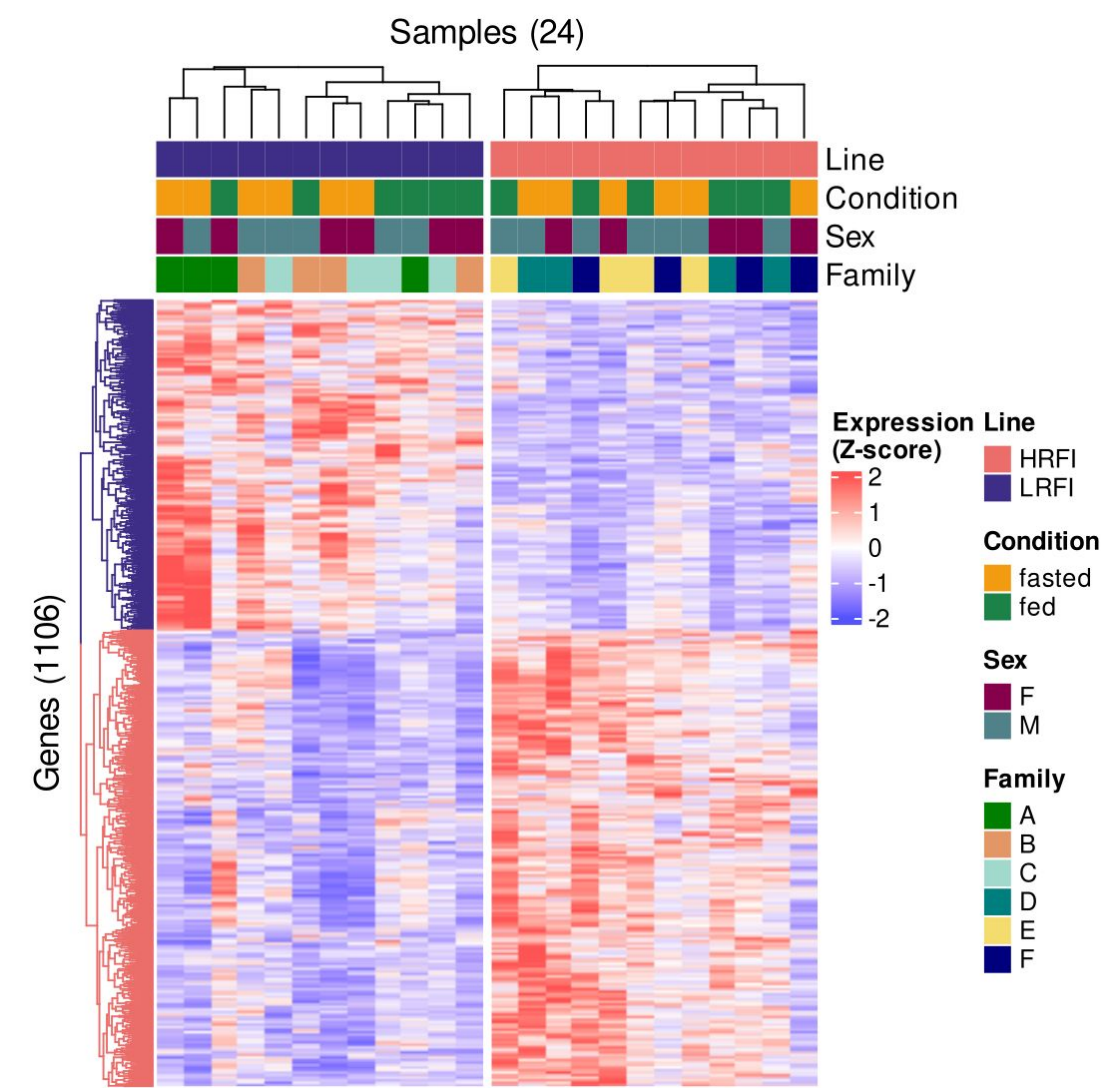
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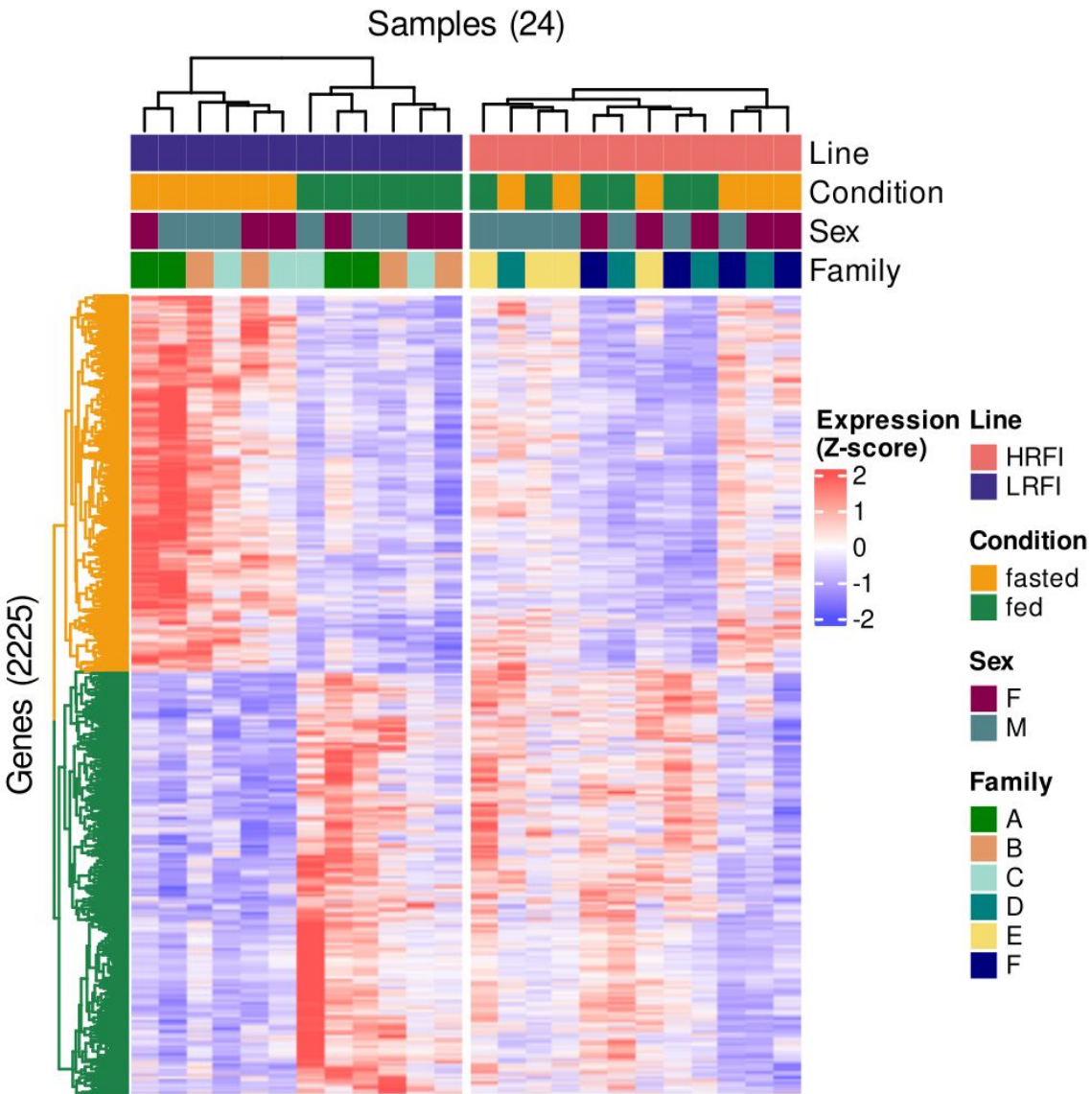
The duodenum transcriptome is distinct between LRFI and HRFI



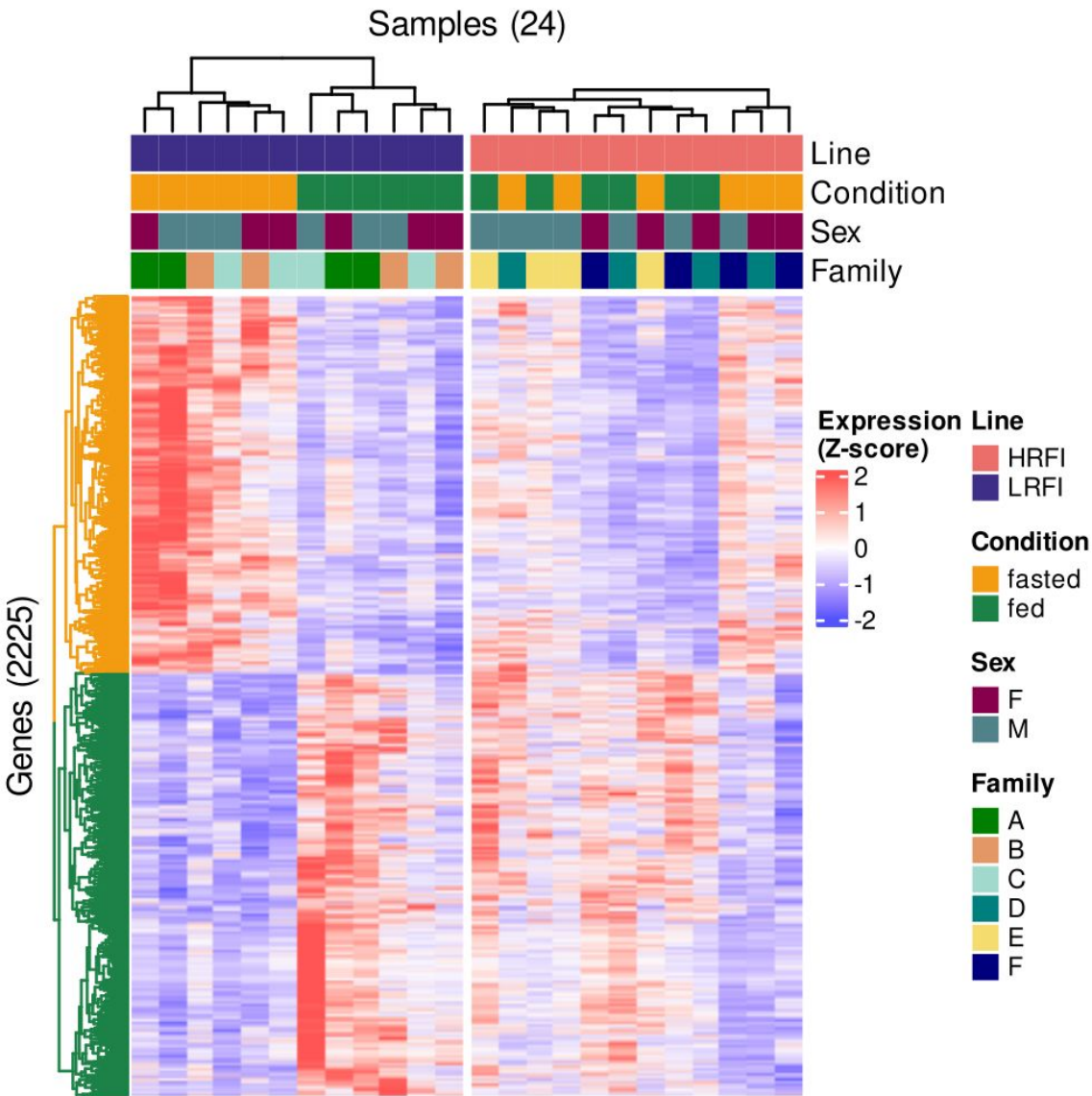
The duodenum transcriptome is distinct between LRFI and HRFI



Higher transcriptomic response to feed intake in the LRFI line



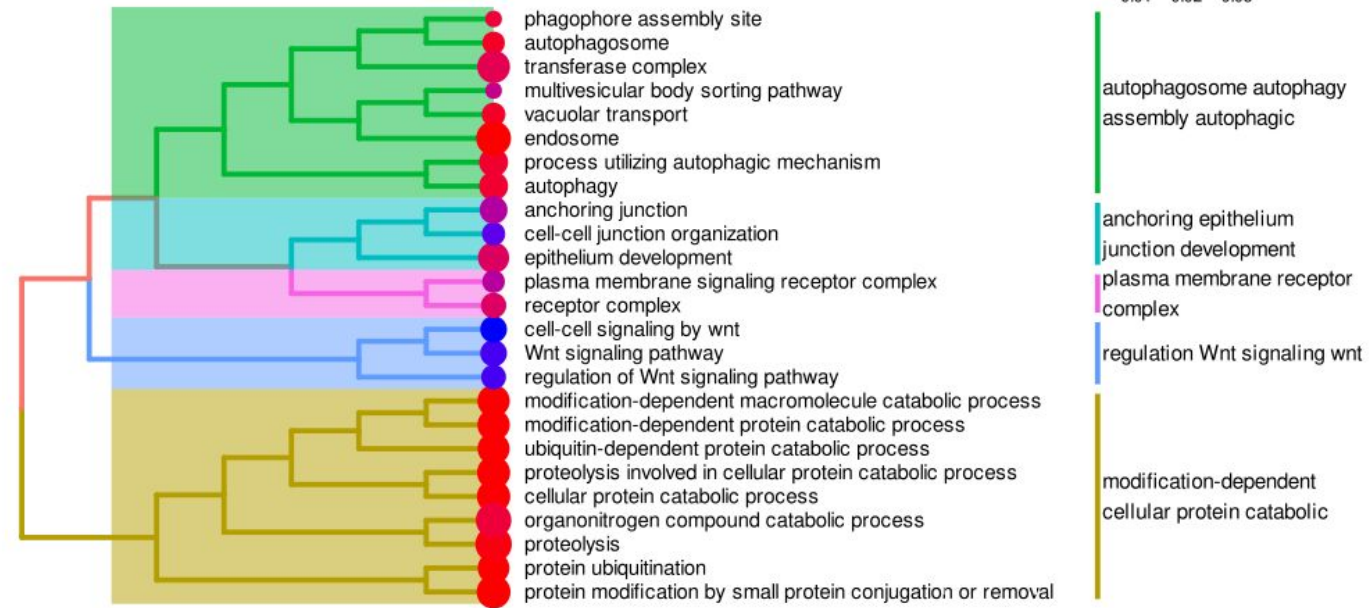
Higher transcriptomic response to feed intake in the LRFI line



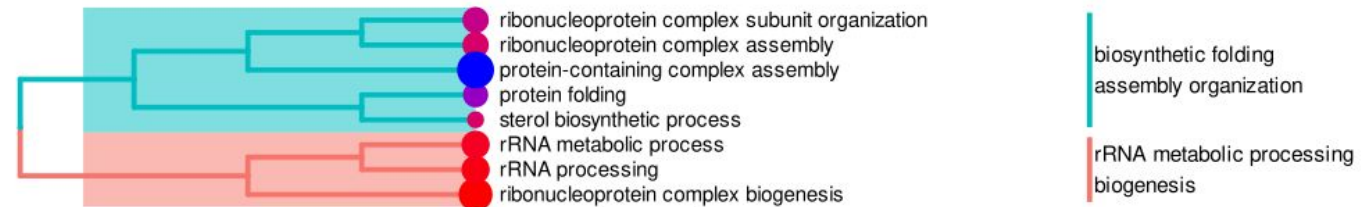
GO enrichment in fasted genes (LRFI)

number of genes ● 10 ● 20 ● 30 ● 40 ● 50

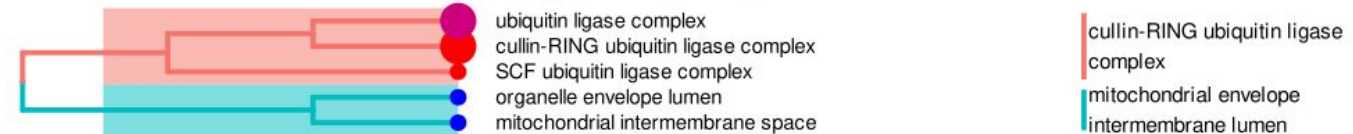
adjusted p value
0.01 0.02 0.03



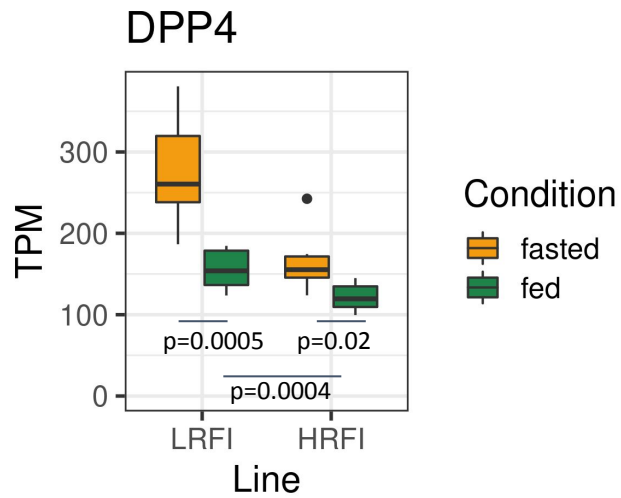
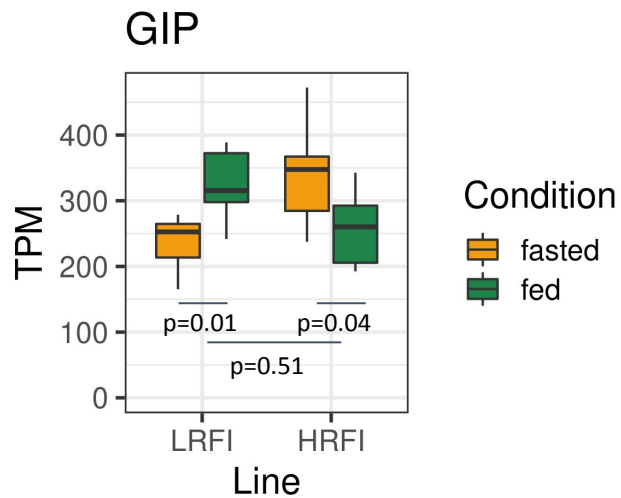
GO enrichment in fed genes (LRFI)



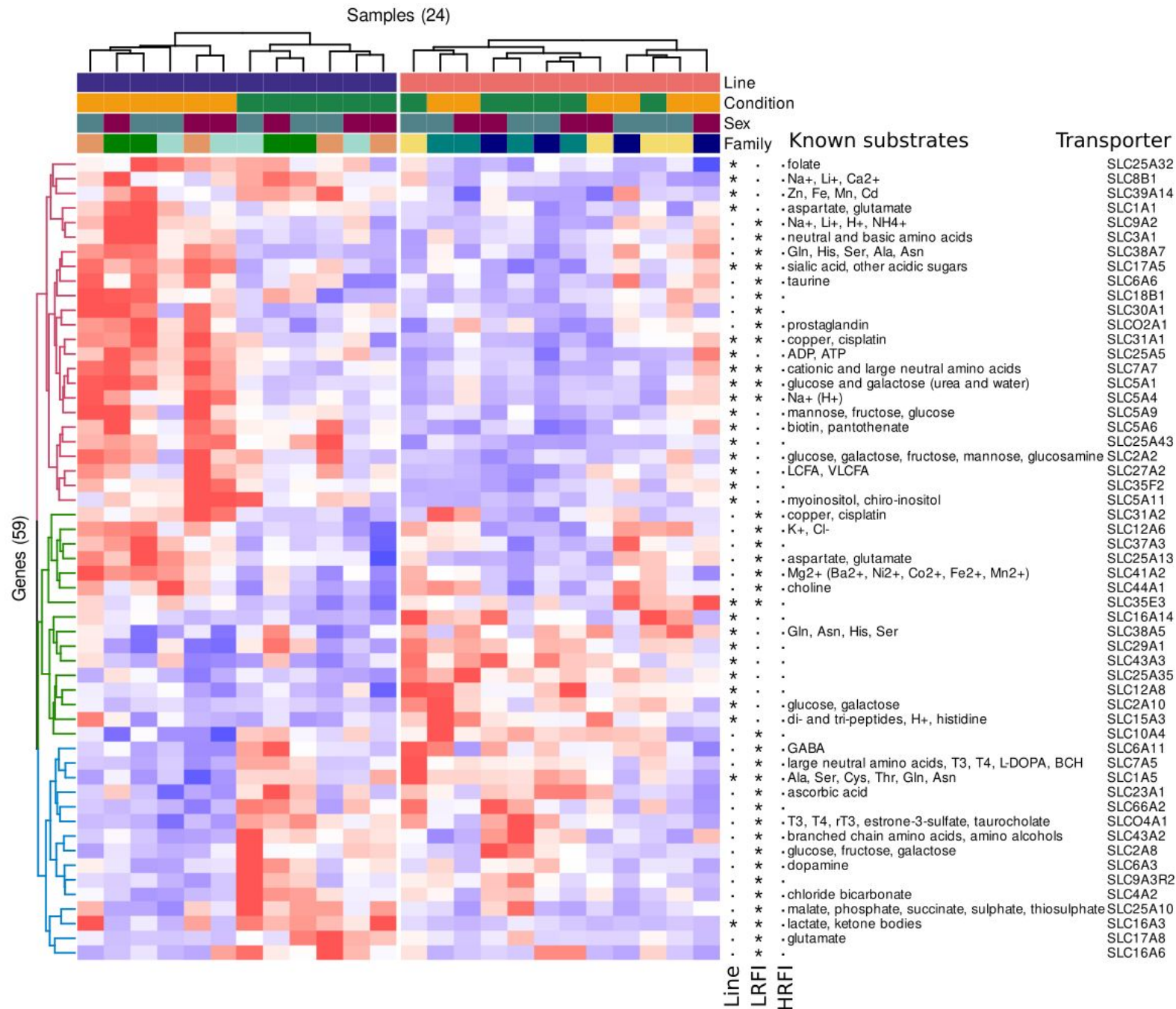
GO enrichment in fasted genes (HRFI)



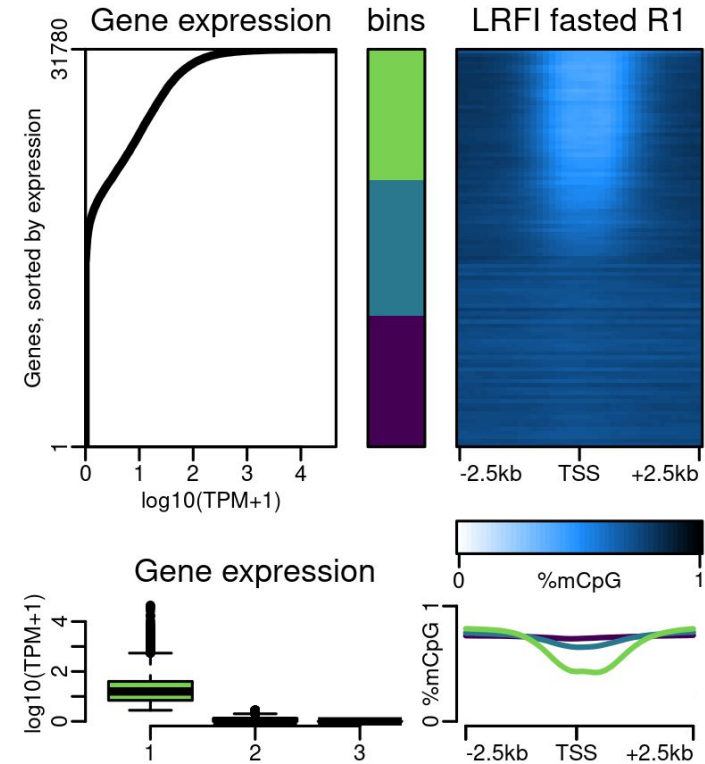
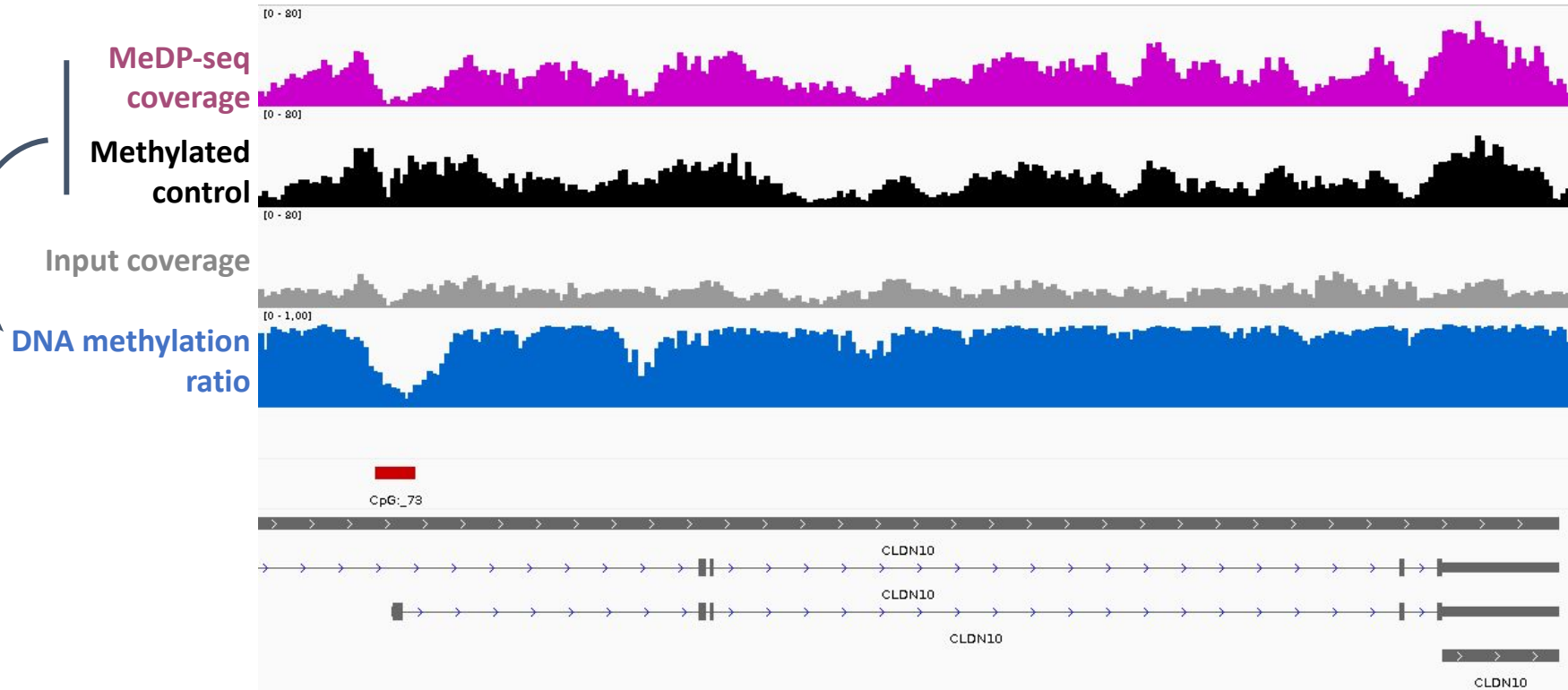
Satiety regulation, nutrient transporter



Transmembrane transporter family SLC



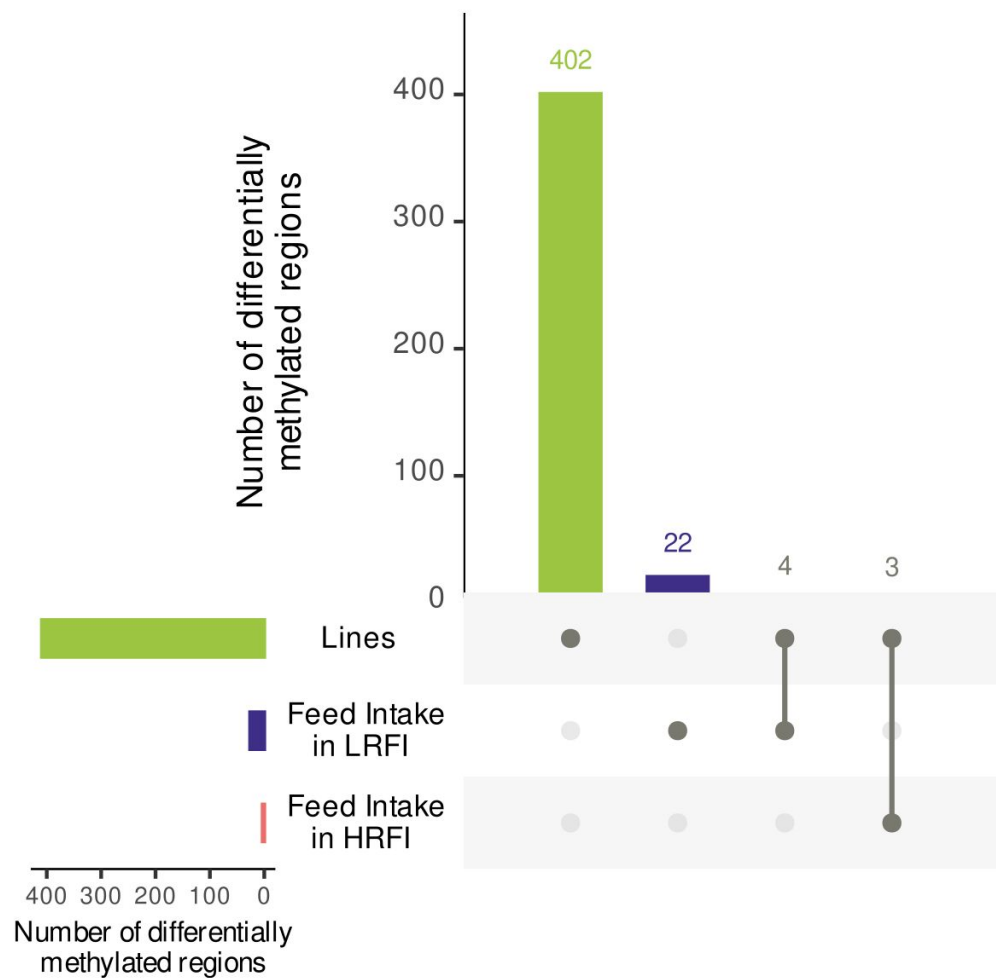
Measuring DNA methylation by MeDP-seq



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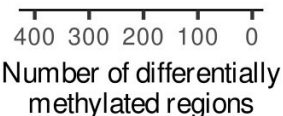
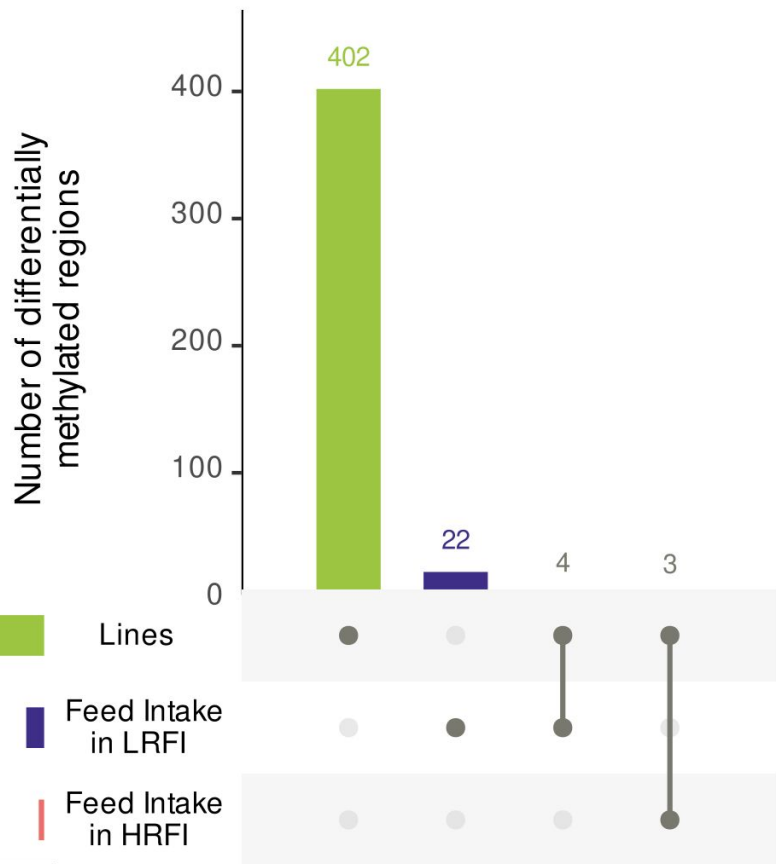
Differential DNA methylation analysis



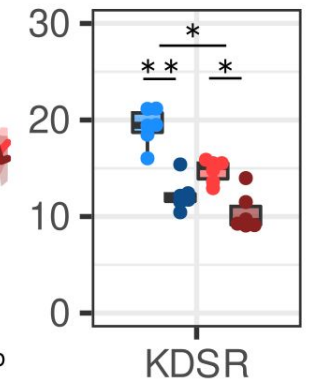
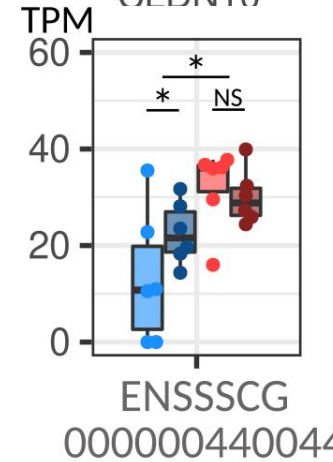
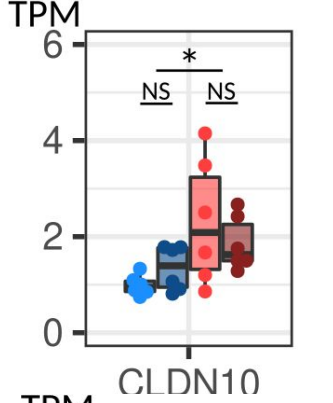
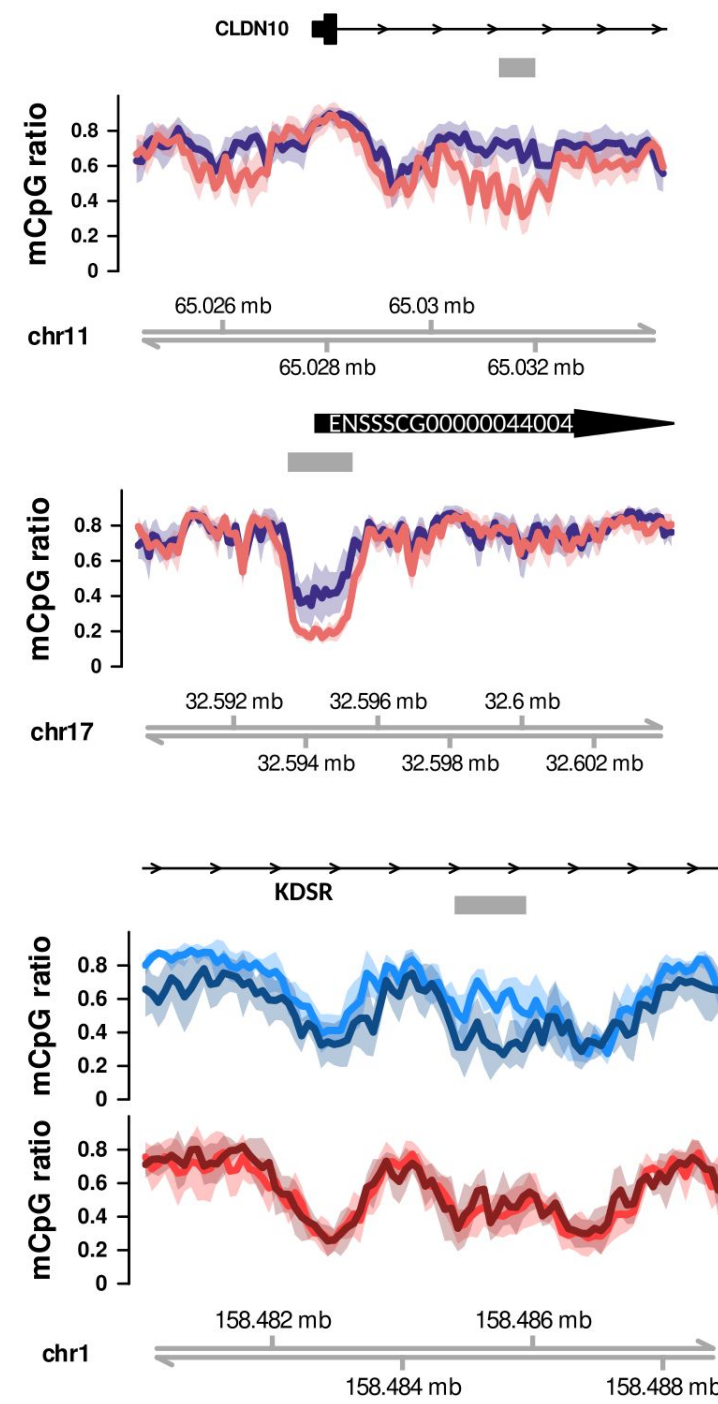
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Differential DNA methylation analysis



- LRFI
- HRFI
- LRFI fasted
- HRFI fasted
- LRFI fed
- HRFI fed



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Conclusion

- Distinct duodenum transcriptomes & DNA methylation profiles between LRFI and HRFI
- Duodenum transcriptomic response to feed intake is **lower in HRFI than in LRFI**
- **> 2000 genes** differentially expressed after feed intake in LRFI (but not much DNA methylation changes by feed intake)

Perspectives

- Circulating hormone levels: GLP-1, GIP, Ghrelin, Insulin, Glucagon, Leptin
- Transcriptomic and DNA methylation profiles of the **stomach mucosa**

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doi: <https://doi.org/10.1101/2022.11.03.515018>



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Acknowledgments

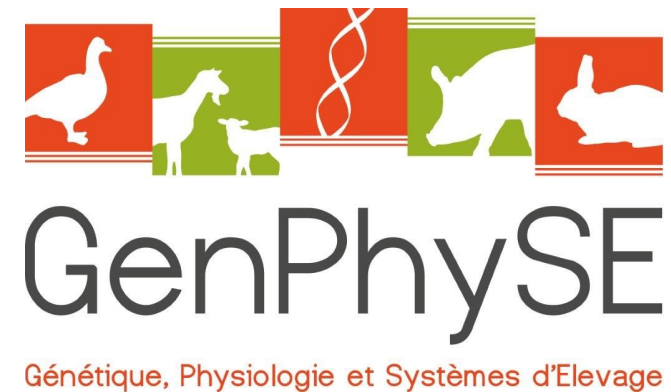
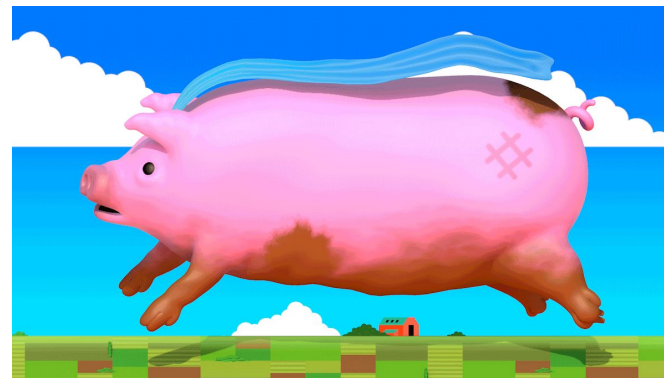
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The GenEpi team
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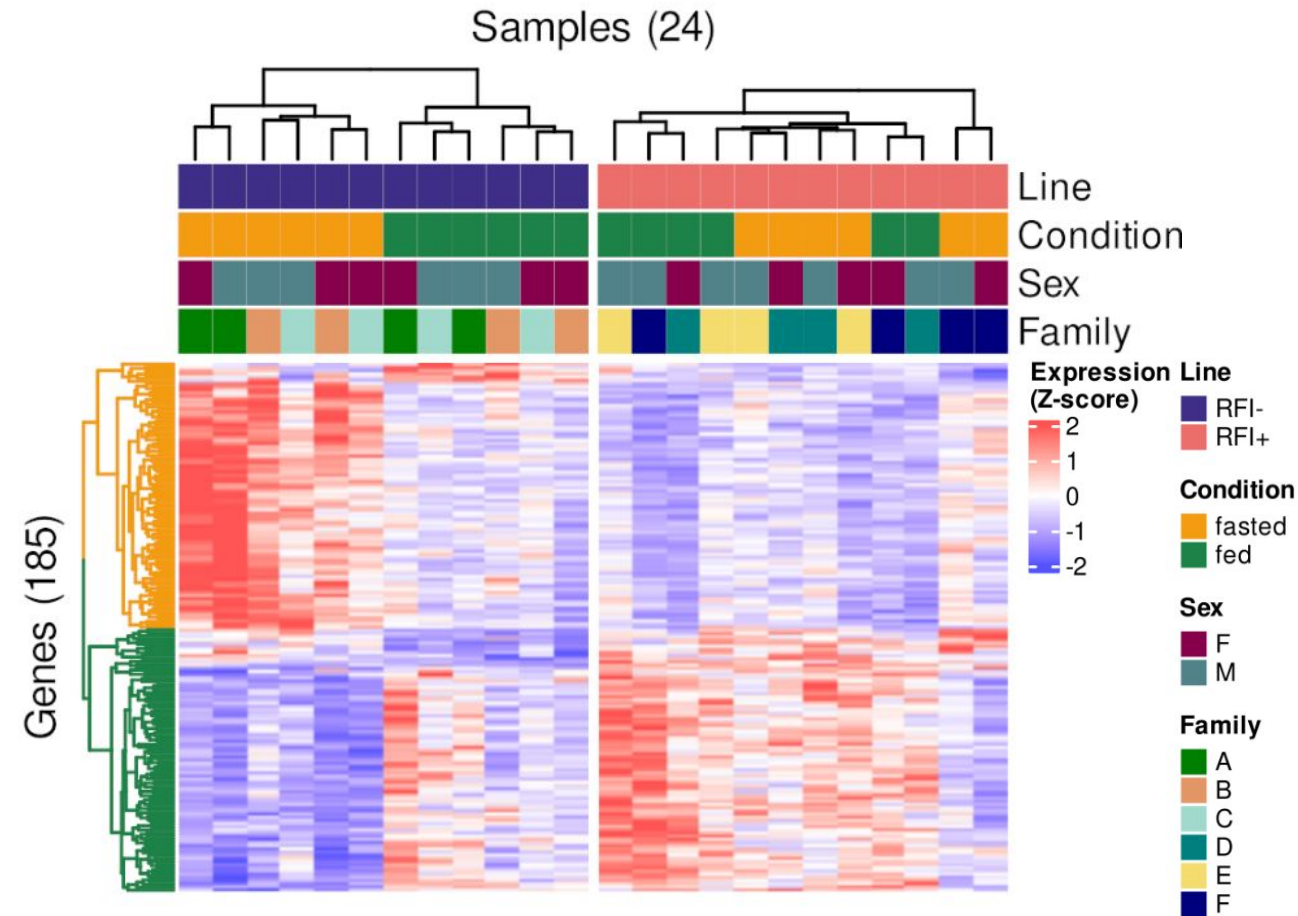
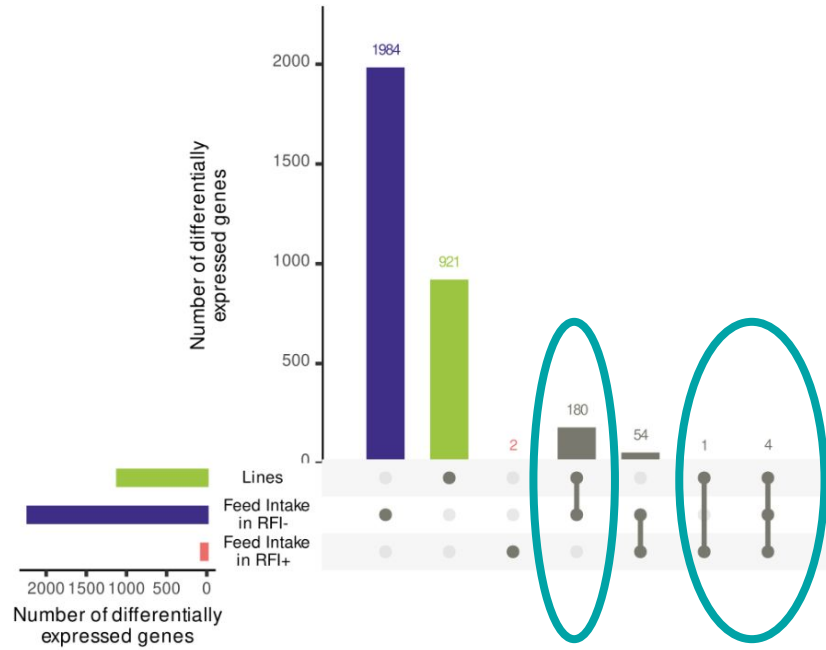
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Line x feed intake interactions?



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