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

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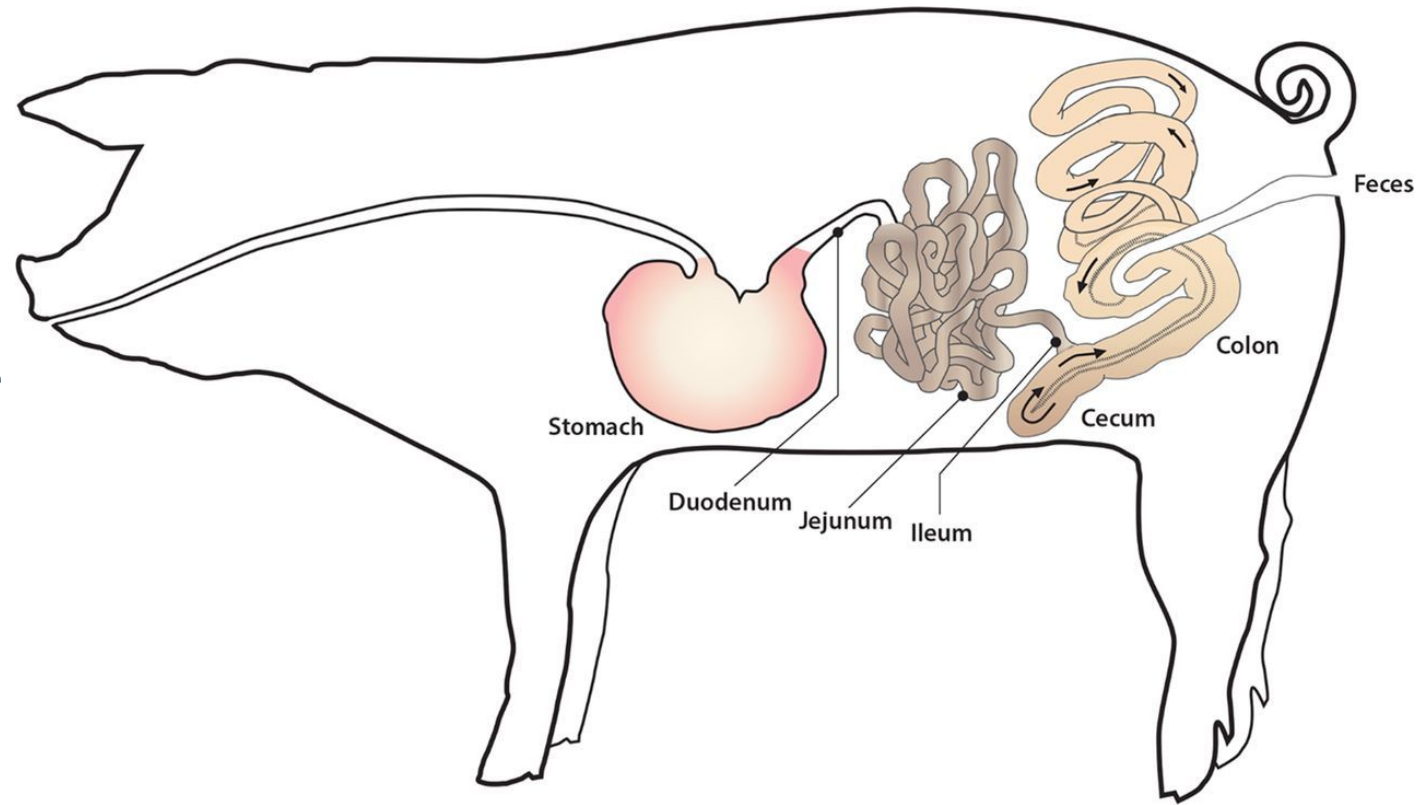
@G\_Devailly(@mamot.fr)

# The duodenum: a key organ for efficient pig farming

Pig gastrointestinal tract is involved in:

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

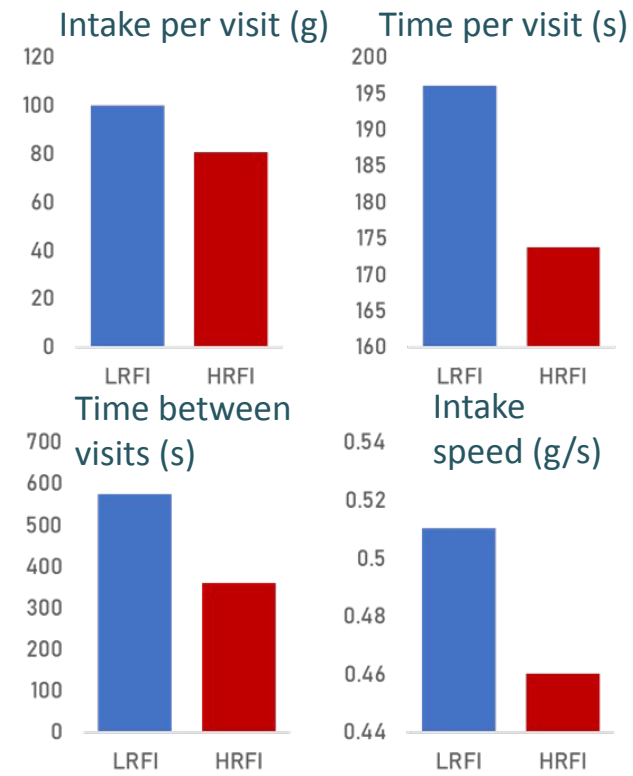
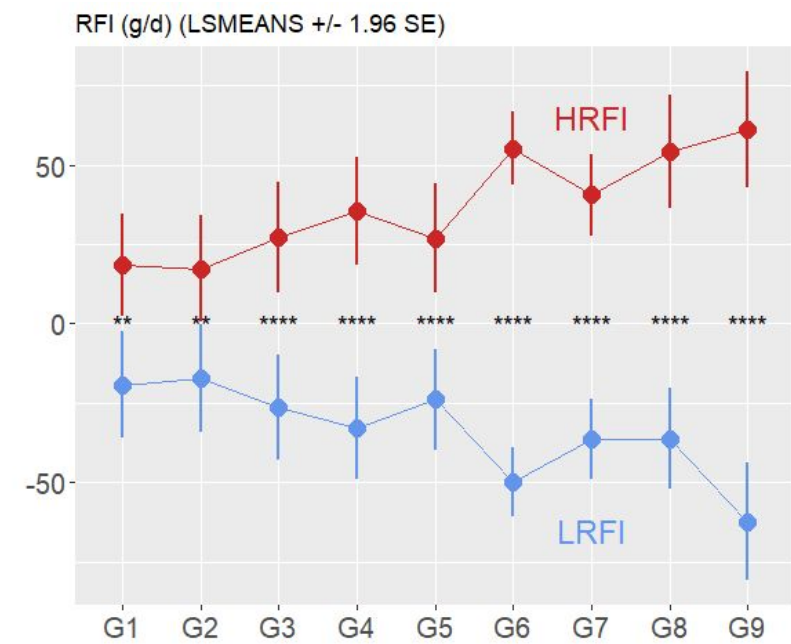
The duodenum is a key organ contributing to the hunger/satiety loop.



<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

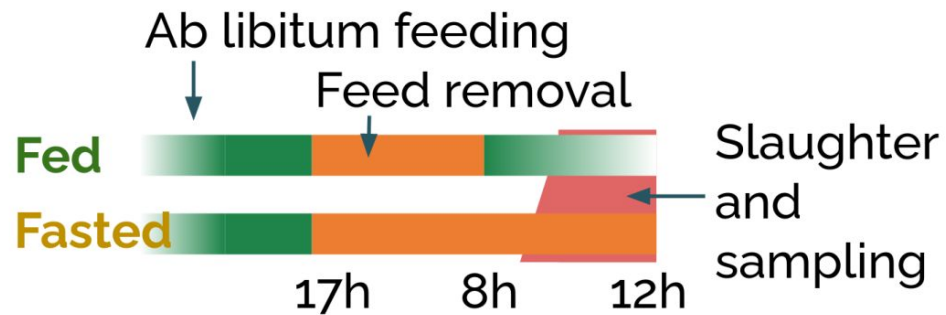
■ A ■ B ■ C ■ D ■ E ■ F

### Sex

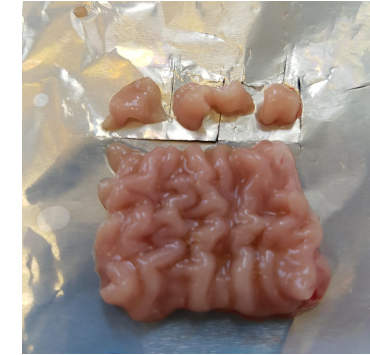
■ F ■ M

### Condition

■ fasted ■ fed



## Duodenum mucosa dissection



## PolyA RNA-seq

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

**nf-core**   
nf-core/rnaseq

## MeDP-seq

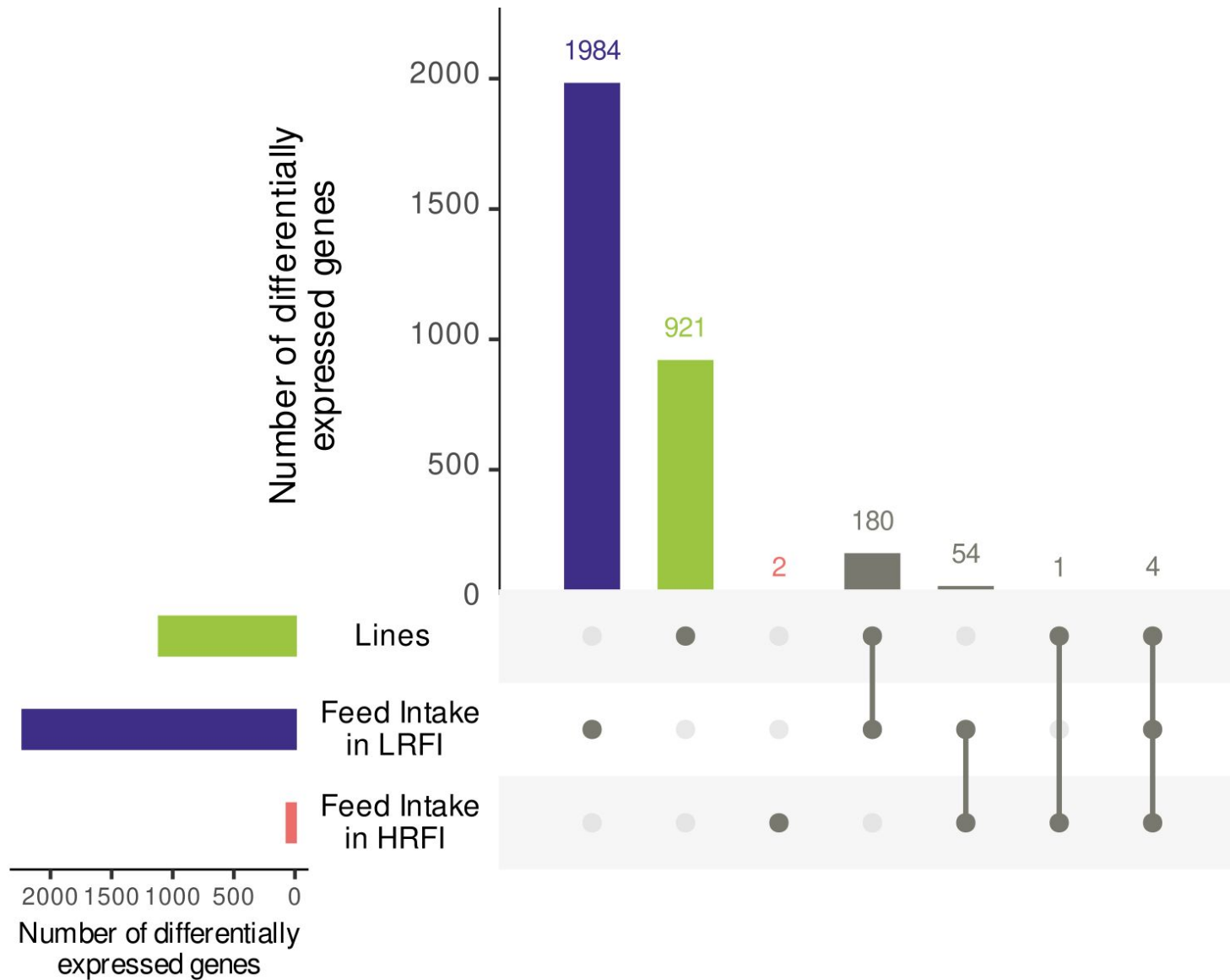
Illumina, 2x100, 70M reads  
BWA alignment

**nf-core**   
nf-core/chipseq

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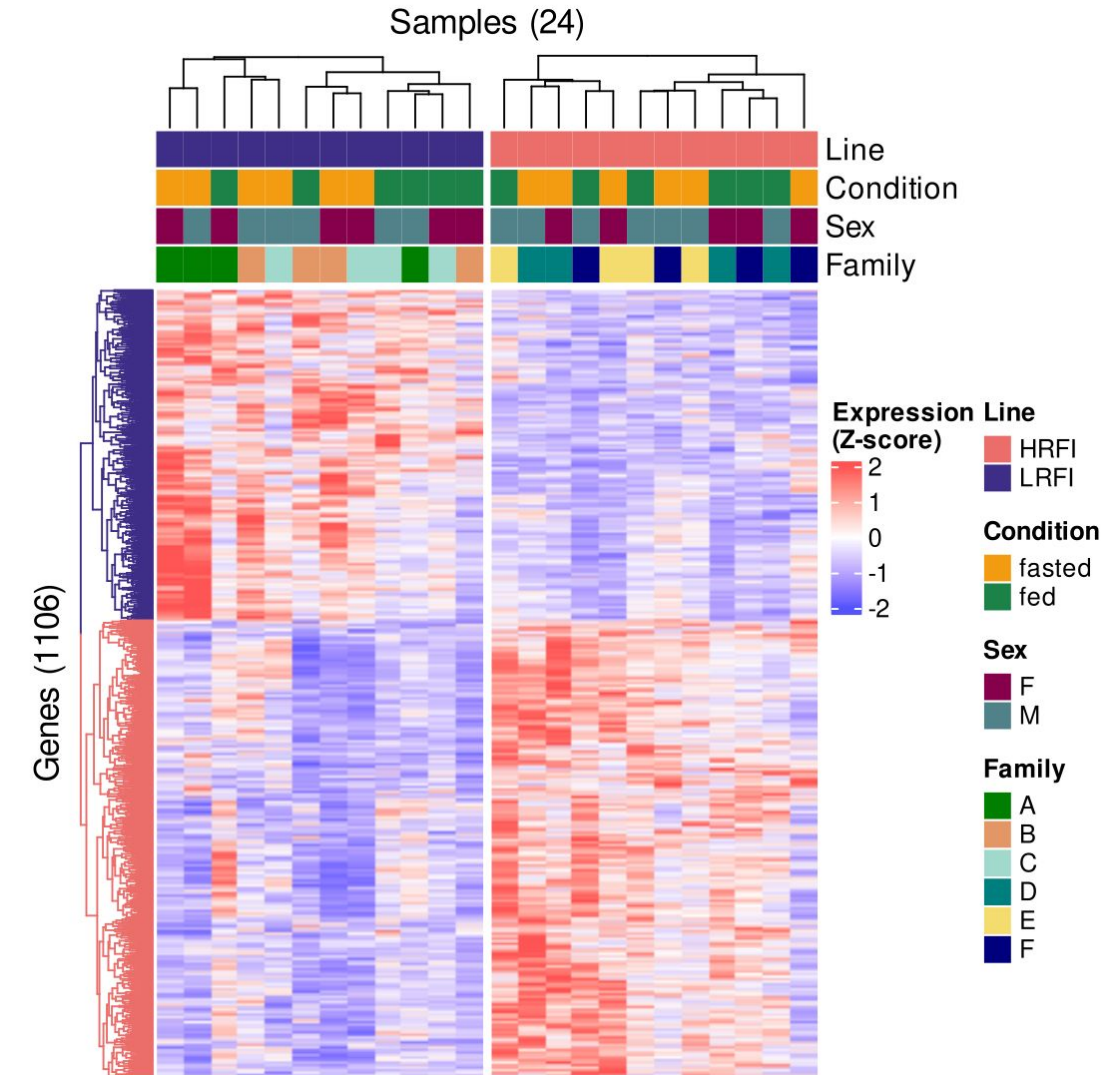
# Investigating the duodenum transcriptomic response to feed intake



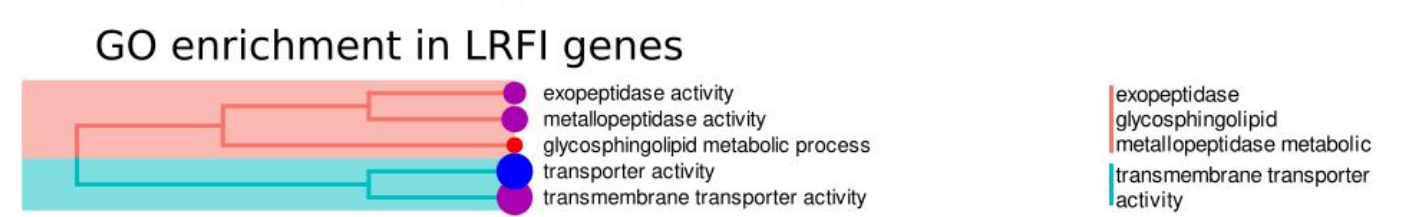
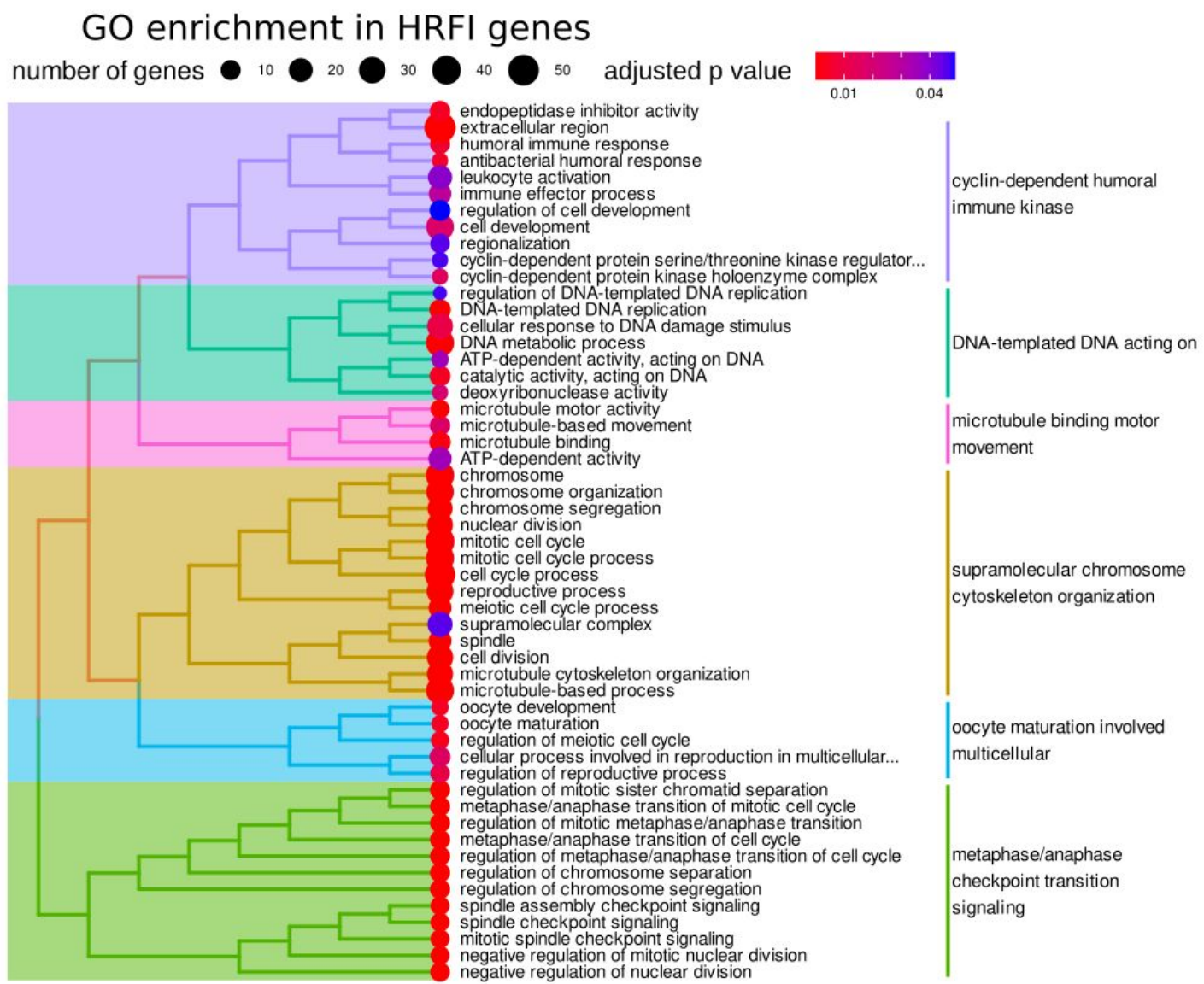
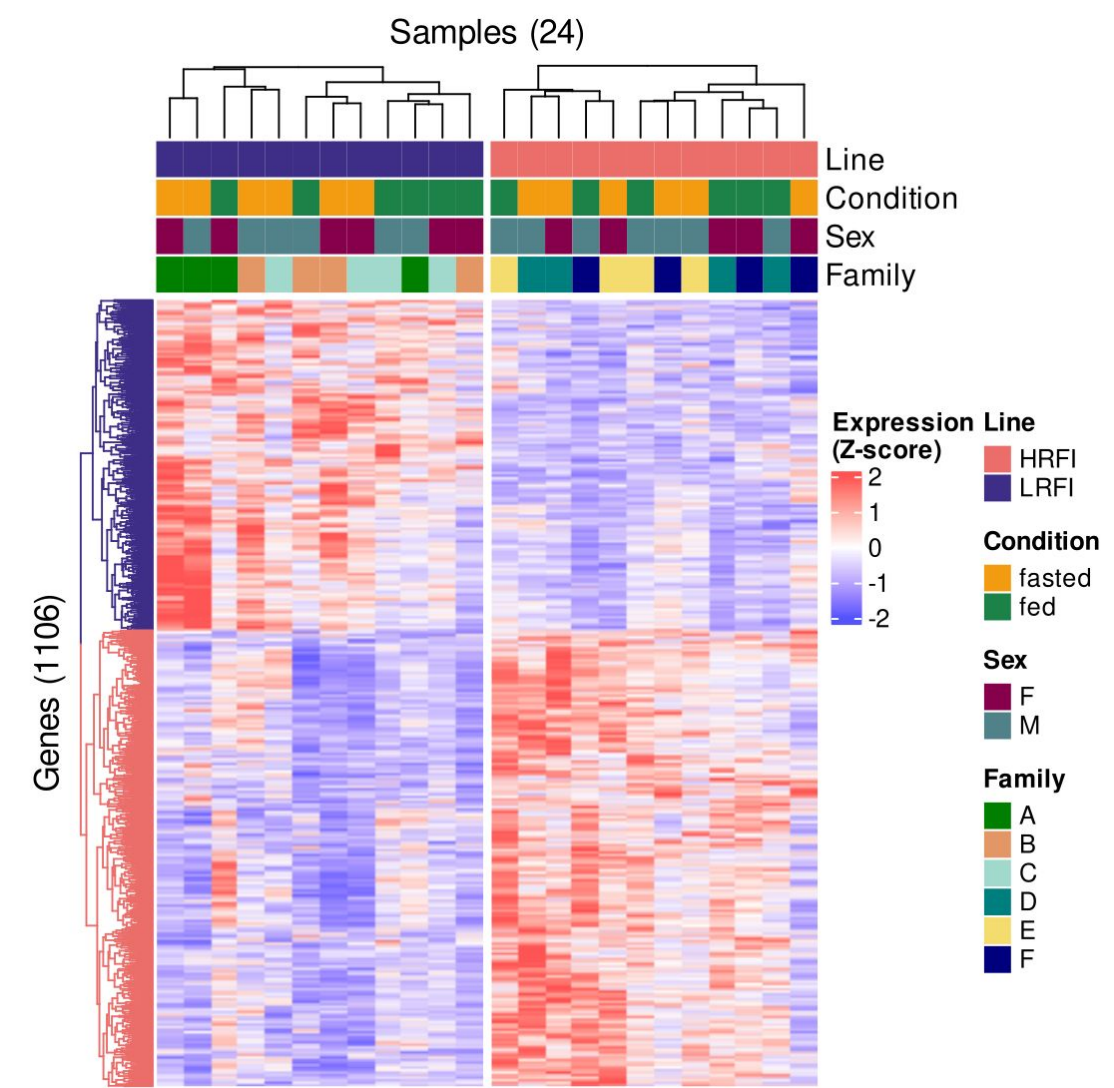
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# The duodenum transcriptome is distinct between LRFI and HRFI

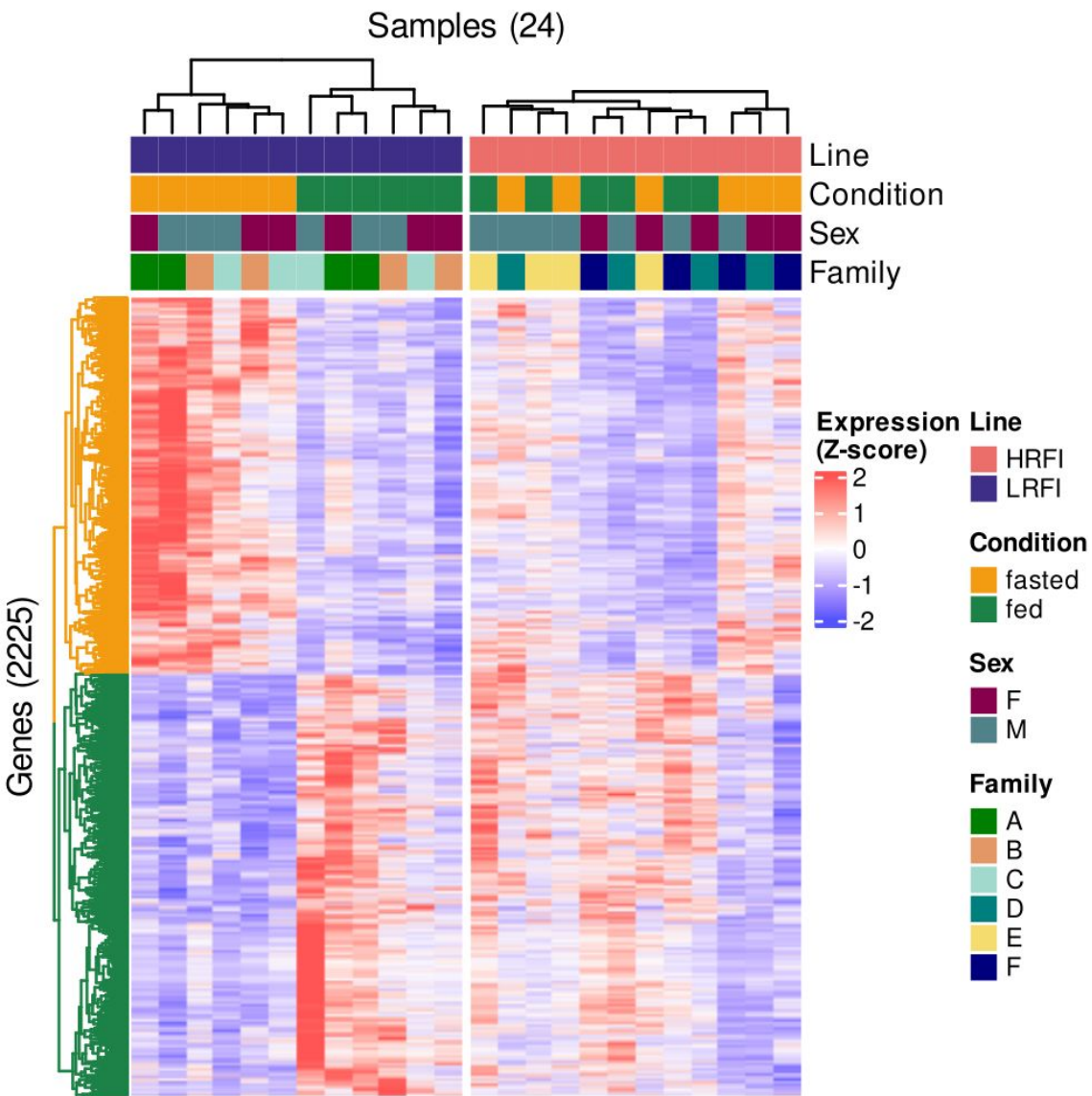


# The duodenum transcriptome is distinct between LRFI and HRFI

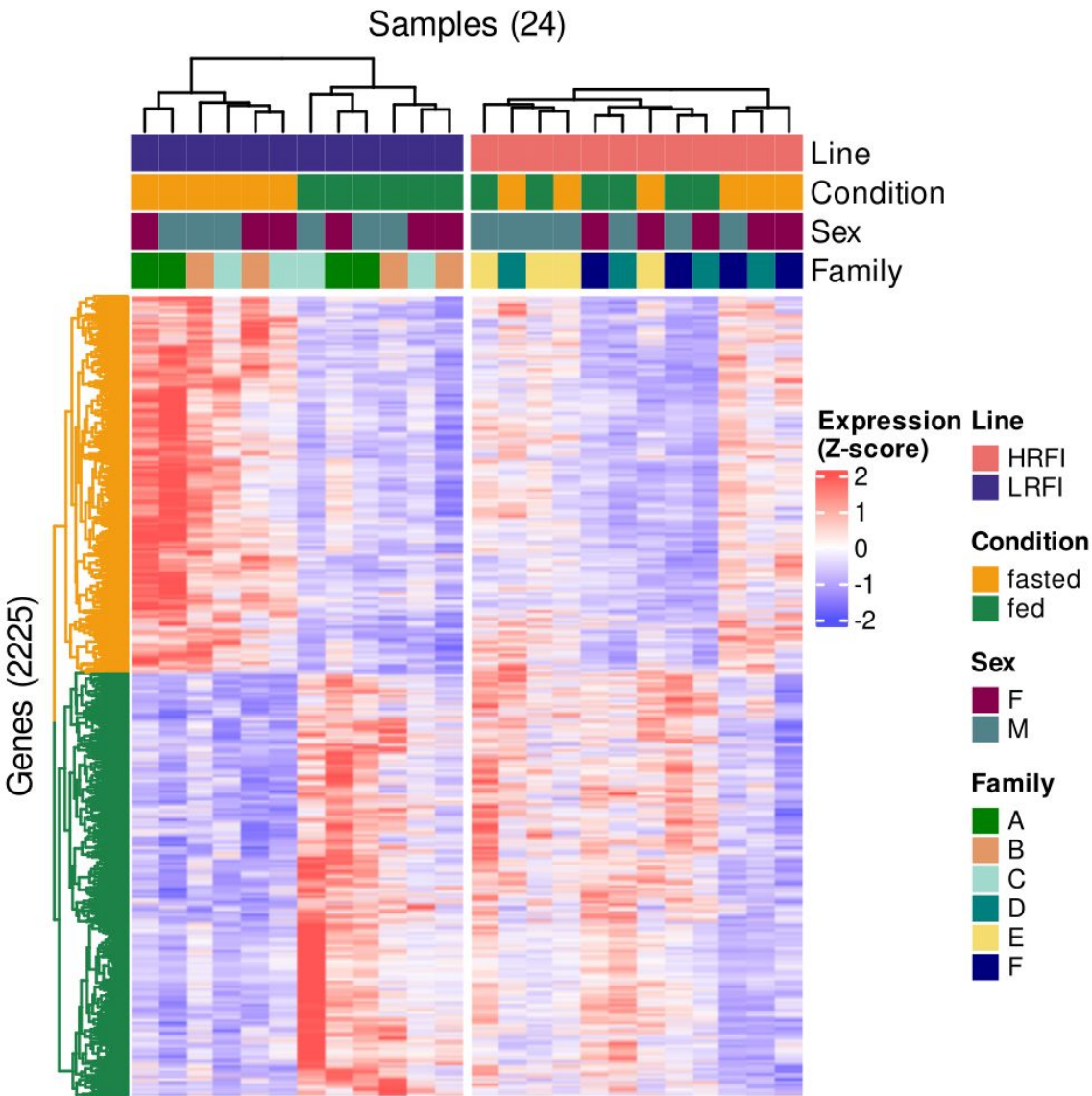




# Higher transcriptomic response to feed intake in the LRFI line



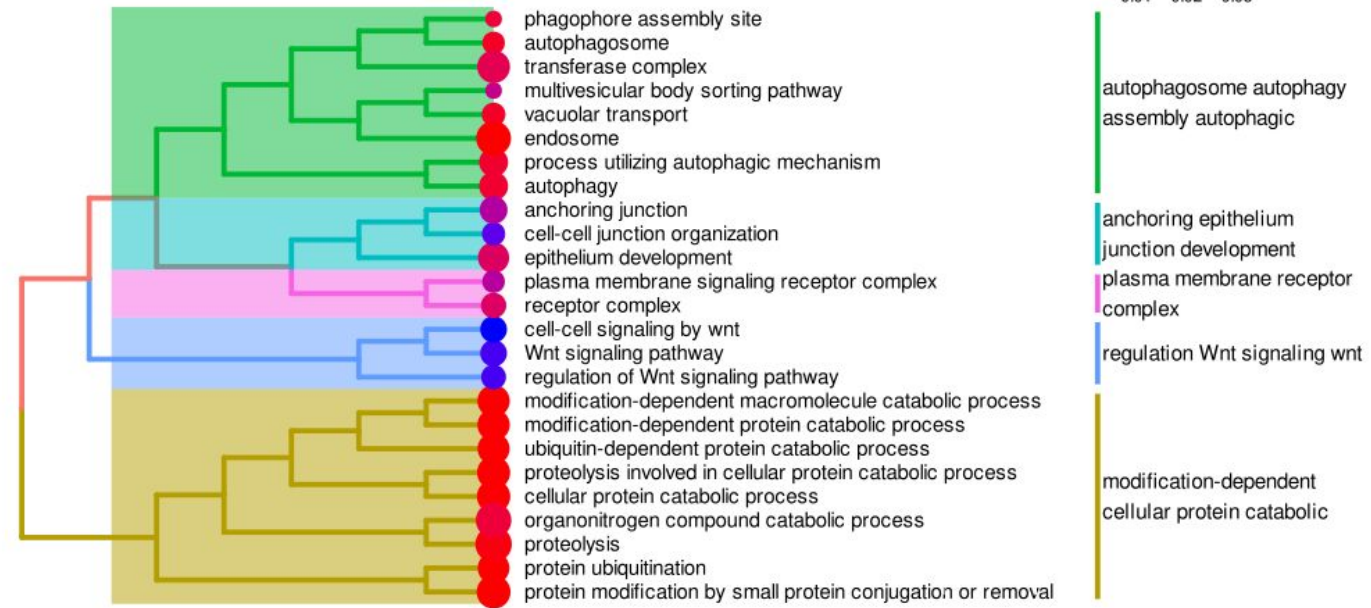
# Higher transcriptomic response to feed intake in the LRFI line



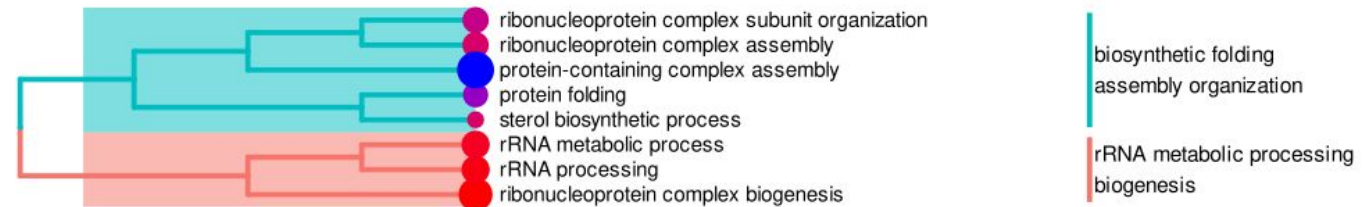
## GO enrichment in fasted genes (LRFI)

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

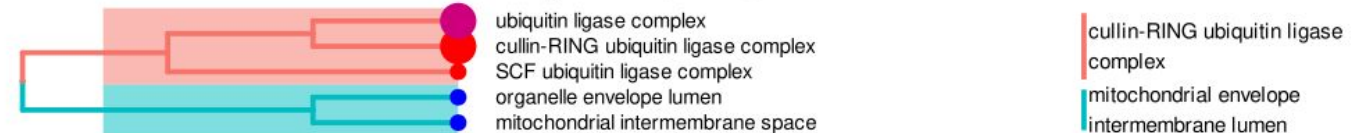
adjusted p value  
0.01 0.02 0.03



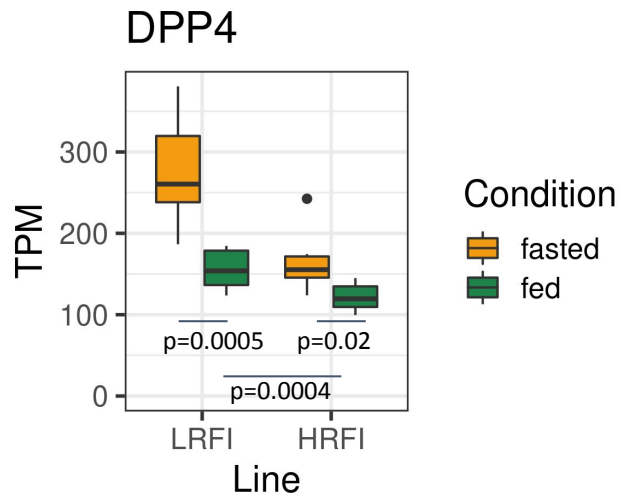
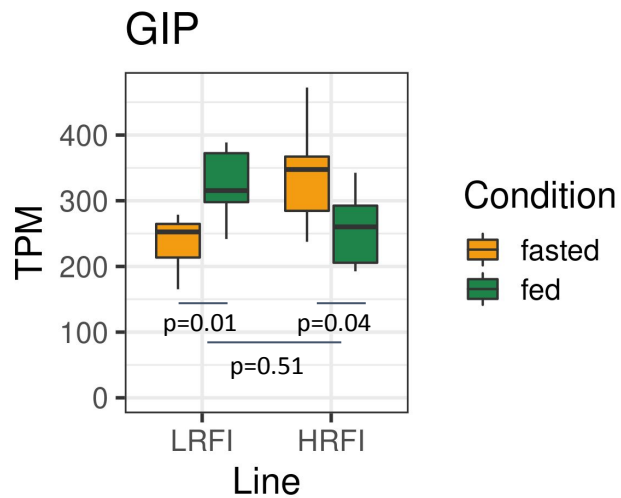
## GO enrichment in fed genes (LRFI)



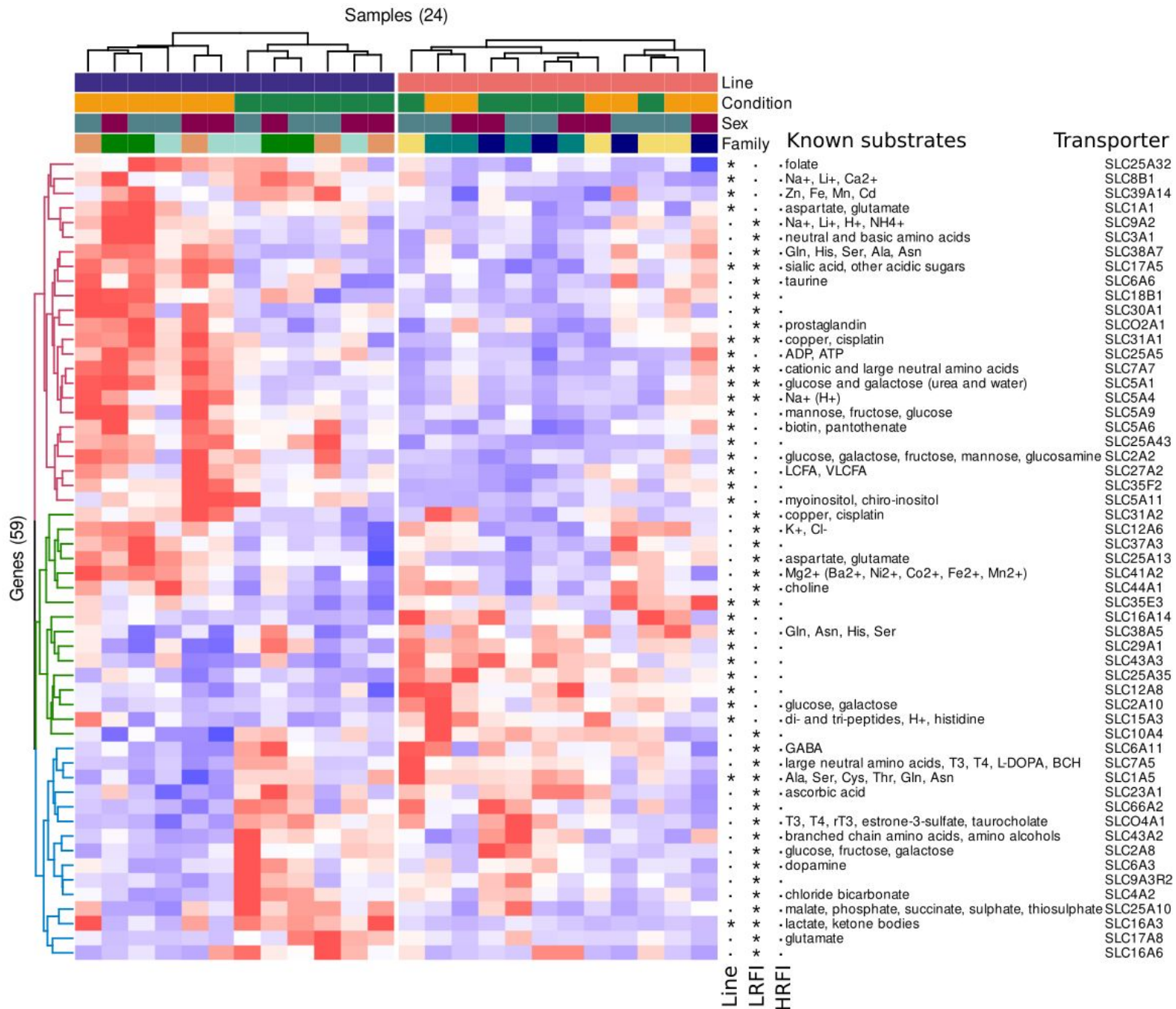
## GO enrichment in fasted genes (HRFI)



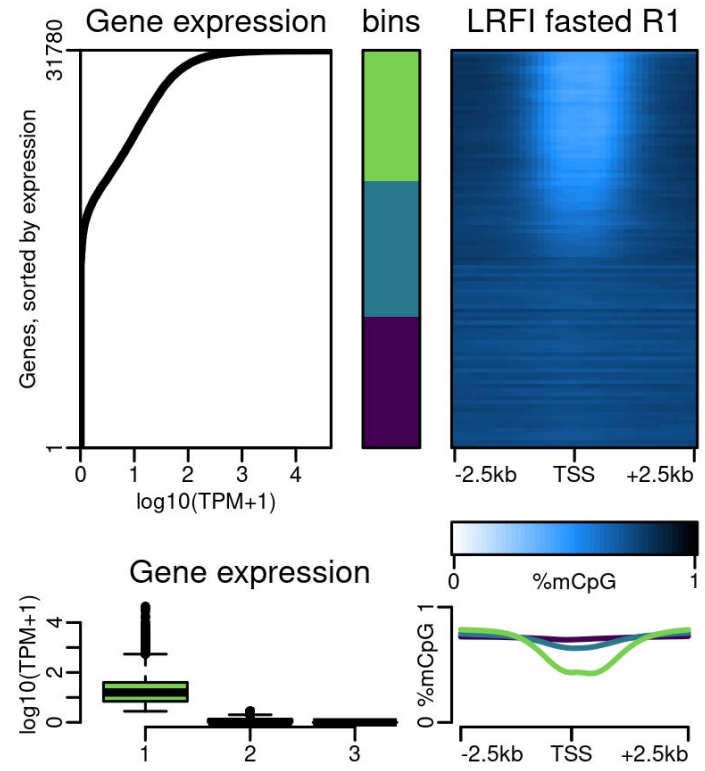
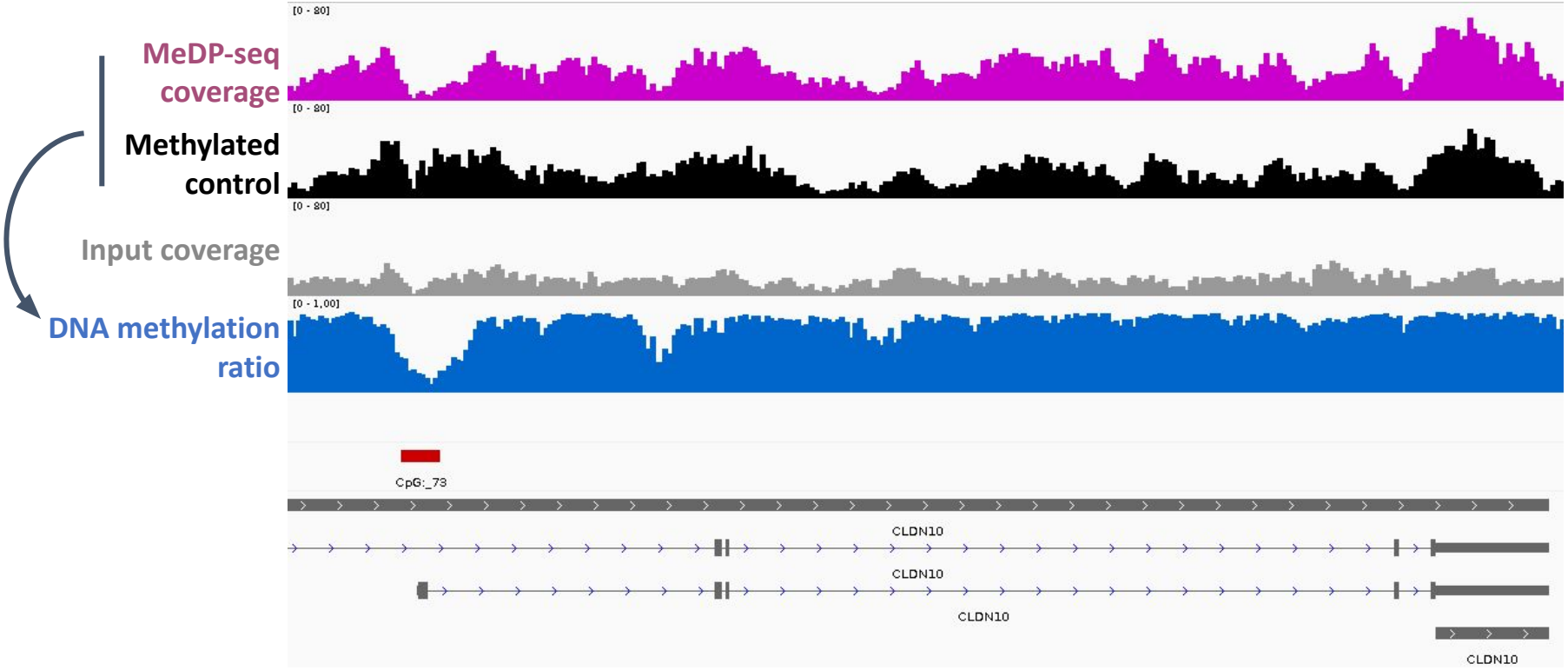
# Satiety regulation, nutrient transporter



## Transmembrane transporter family SLC



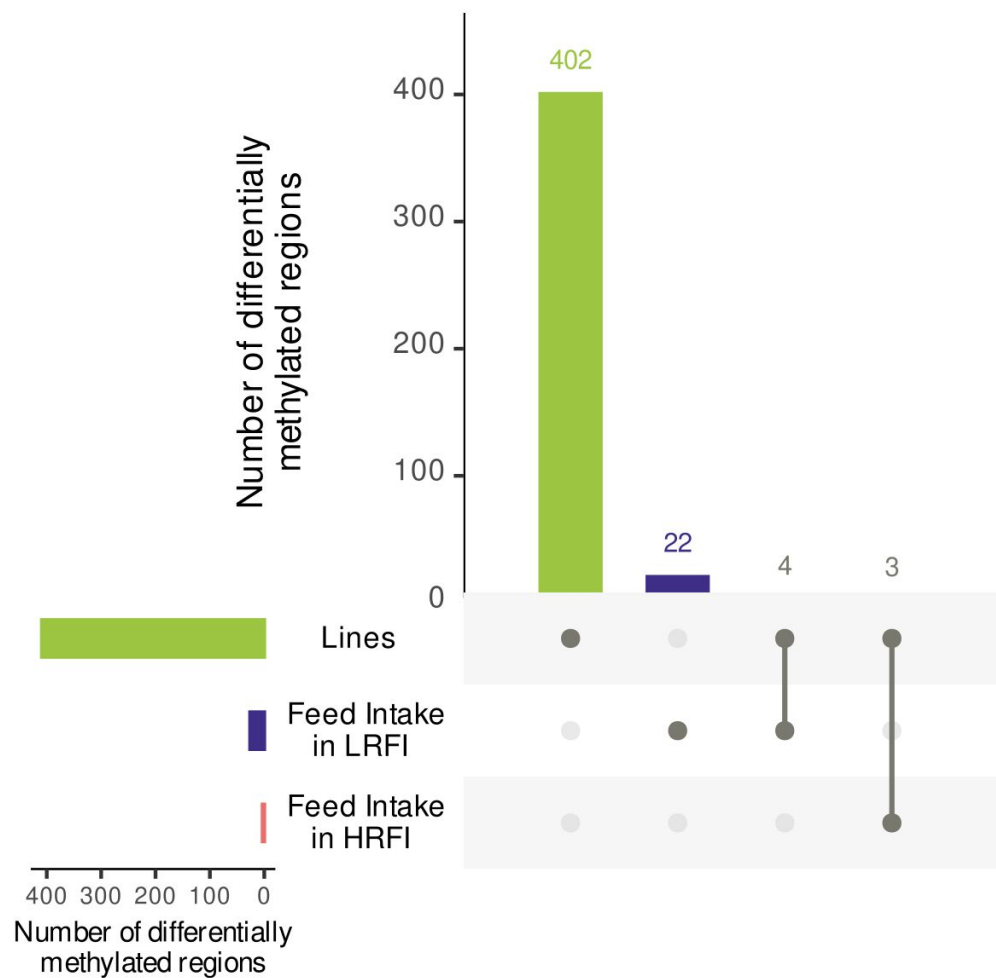
# Measuring DNA methylation by MeDP-seq



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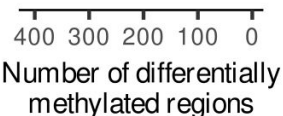
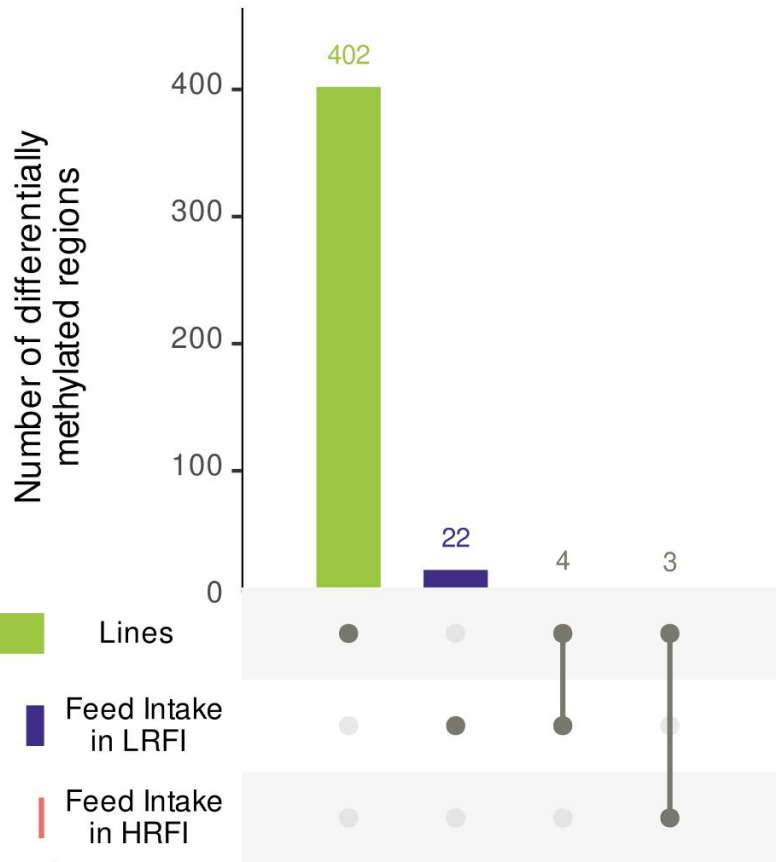
# Differential DNA methylation analysis



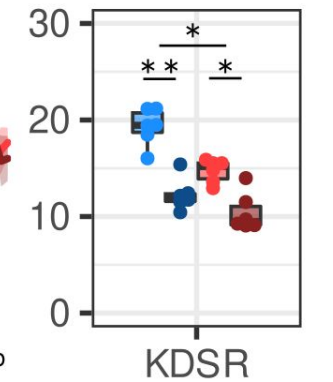
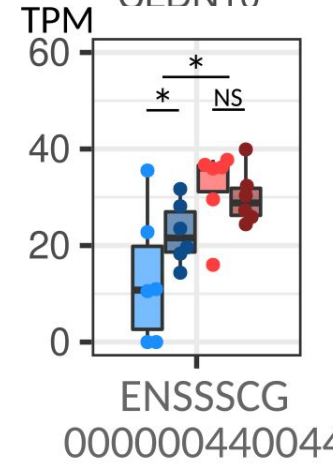
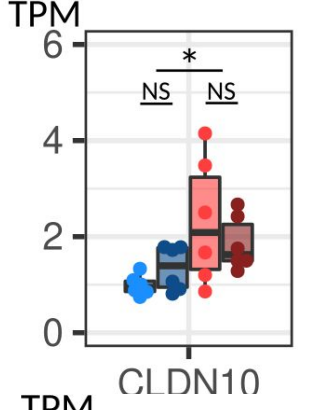
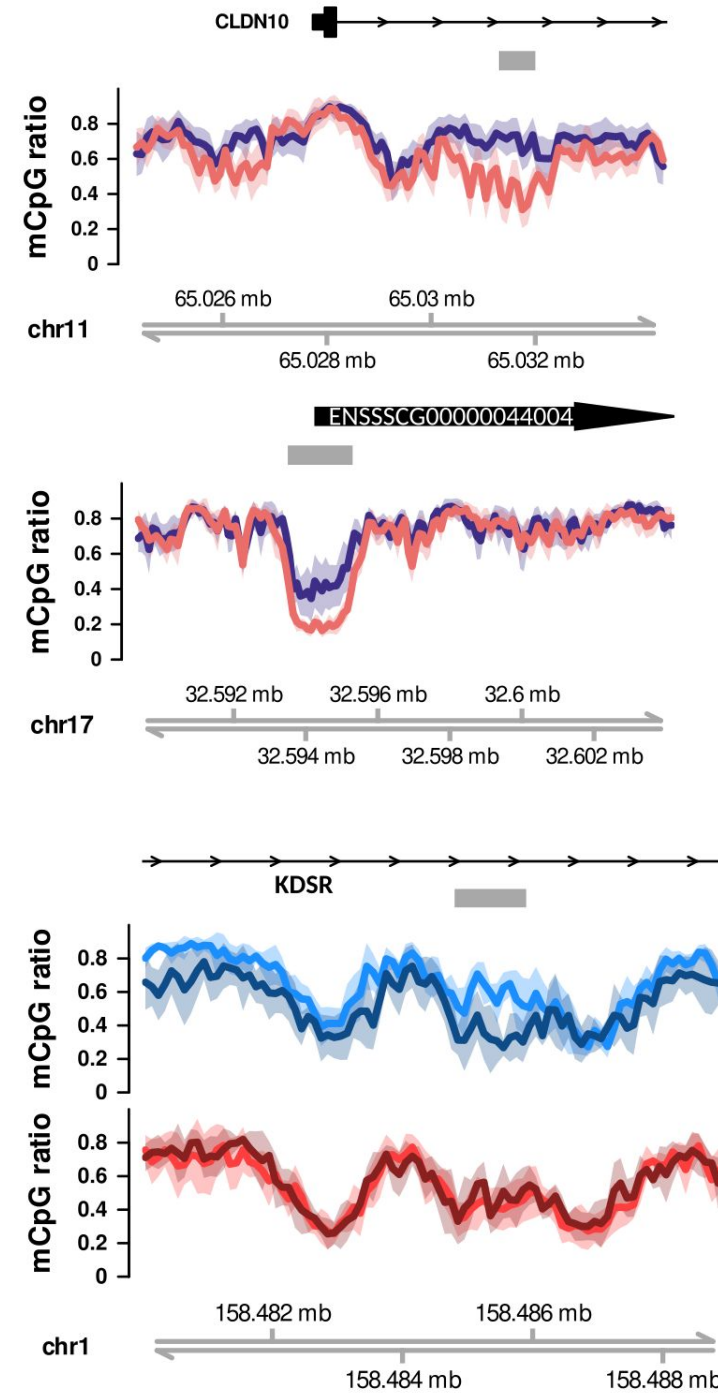
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# Differential DNA methylation analysis



- 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**

**SeqOclin**



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



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# Acknowledgments

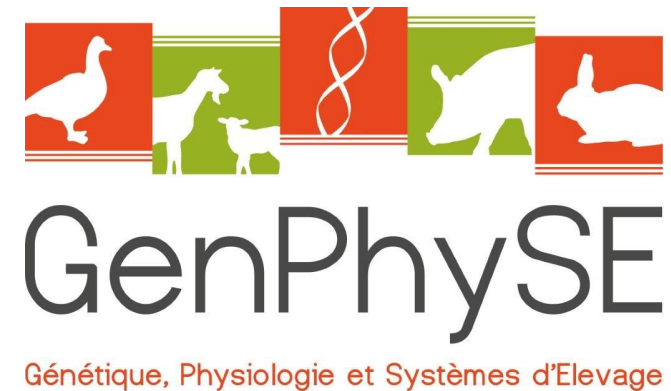
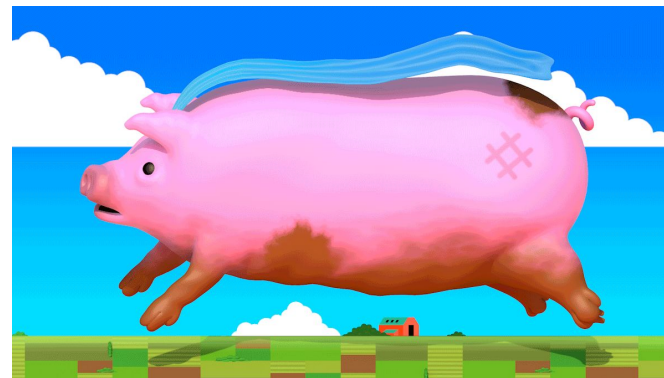
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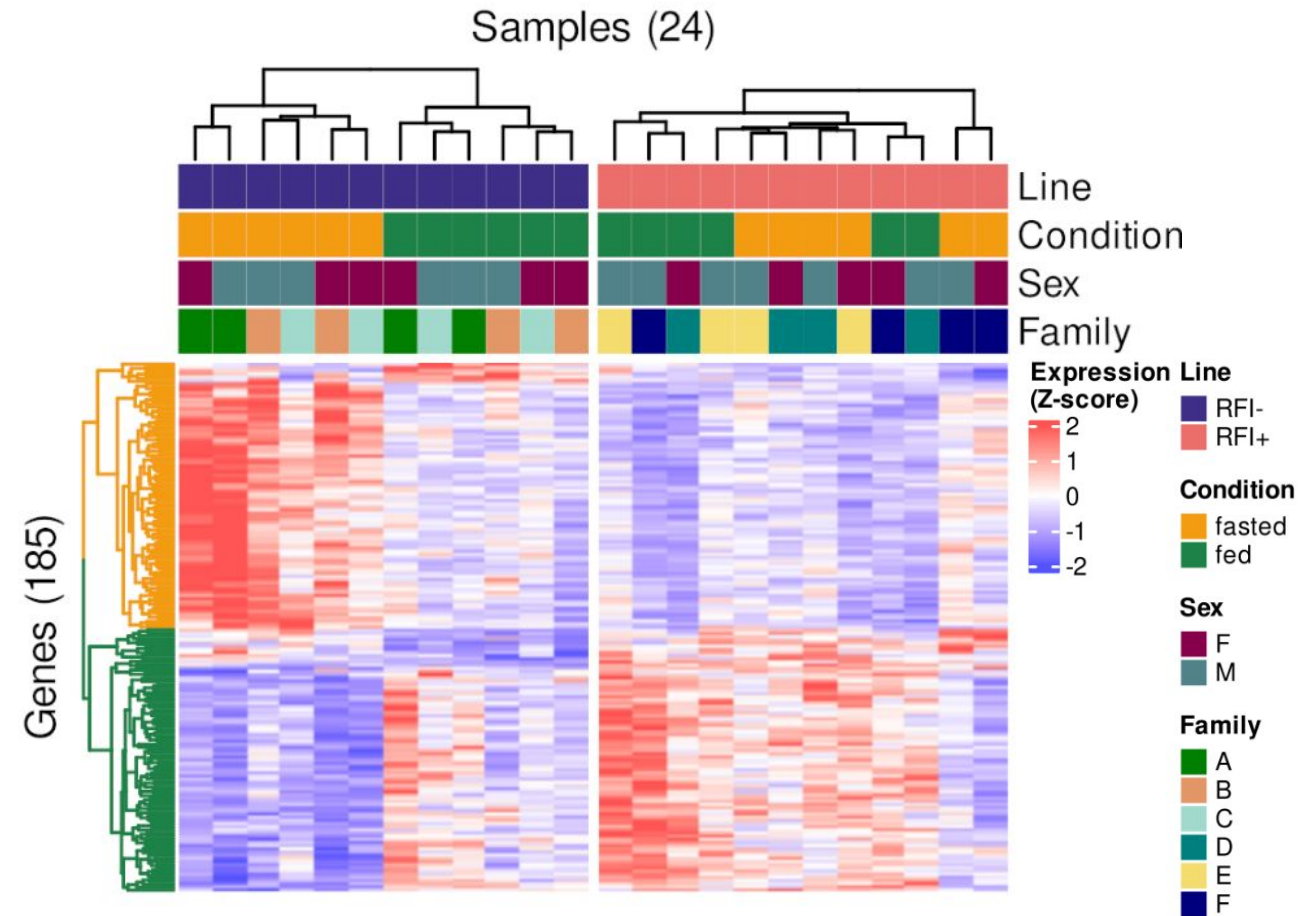
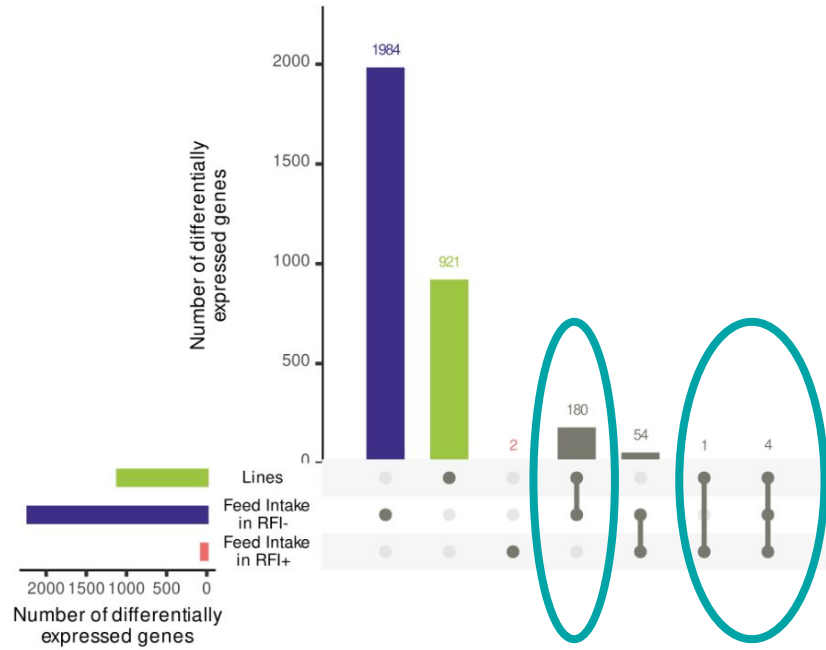


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# Line x feed intake interactions?



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