



Transcriptomics of Feed Efficiency in Nordic Dairy Cattle

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Feed Utilization Nordic Cattle (FUNC) - Experiment

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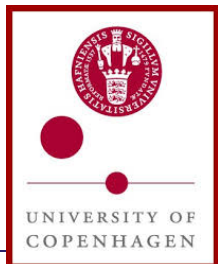
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Why transcriptomics and why on FE?

- Feed efficiency - important trait to be improved – for the sustainability
- Exploit the availability of sequence data-biological information (e.g. liver for FE)
- RNAseq experiments - high-throughput biological assays for measuring the abundance of mRNA
 - To identify candidate genes
 - Differentially expressed
 - Pathways
 - etc



Main Objectives

Bioinformatics research for Feed Efficiency – To identify

- Differentially expressed (DE) genes
- Biological function of the DE genes
- Potential interaction between FE and different diets
- Potential hub genes/biomarkers
- Molecular pathways involved

Experimental design

- **2 levels of FE** (High and Low) in 2 breeds

	HOLSTEINS	JERSEYS	Total
HIGH FE	5	5	10
LOW FE	5	5	10
Total	10	10	20

- **2 types of feed diet**
 - control (low concentrate) diet and High concentrate diet

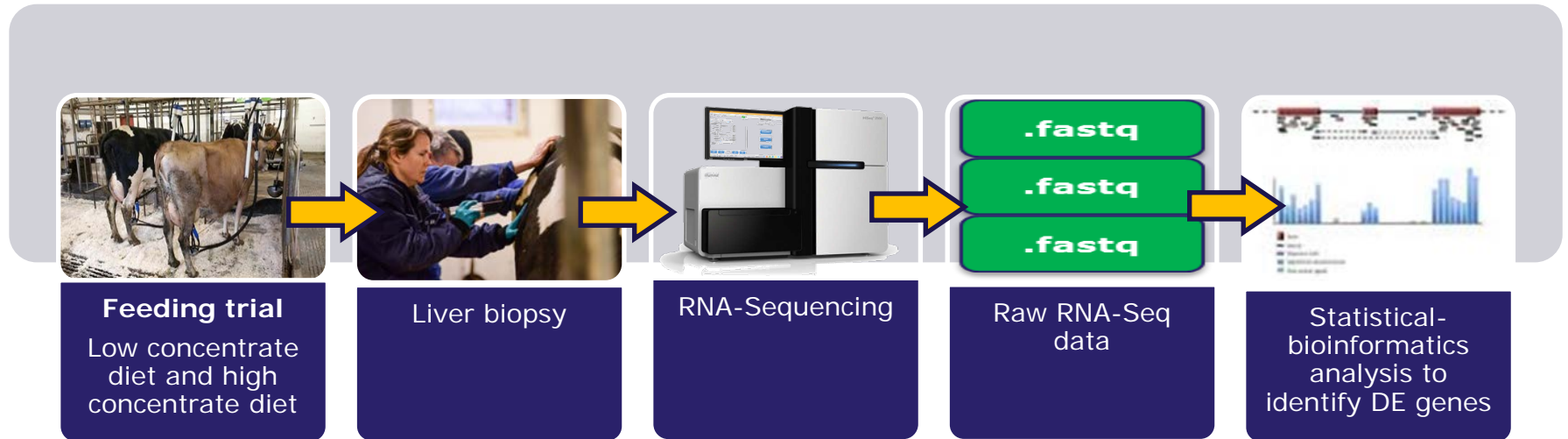
	Control	HC
Forage:concentrate	70:30	40:60

- **2 FE x 2 feed diet in each breed**

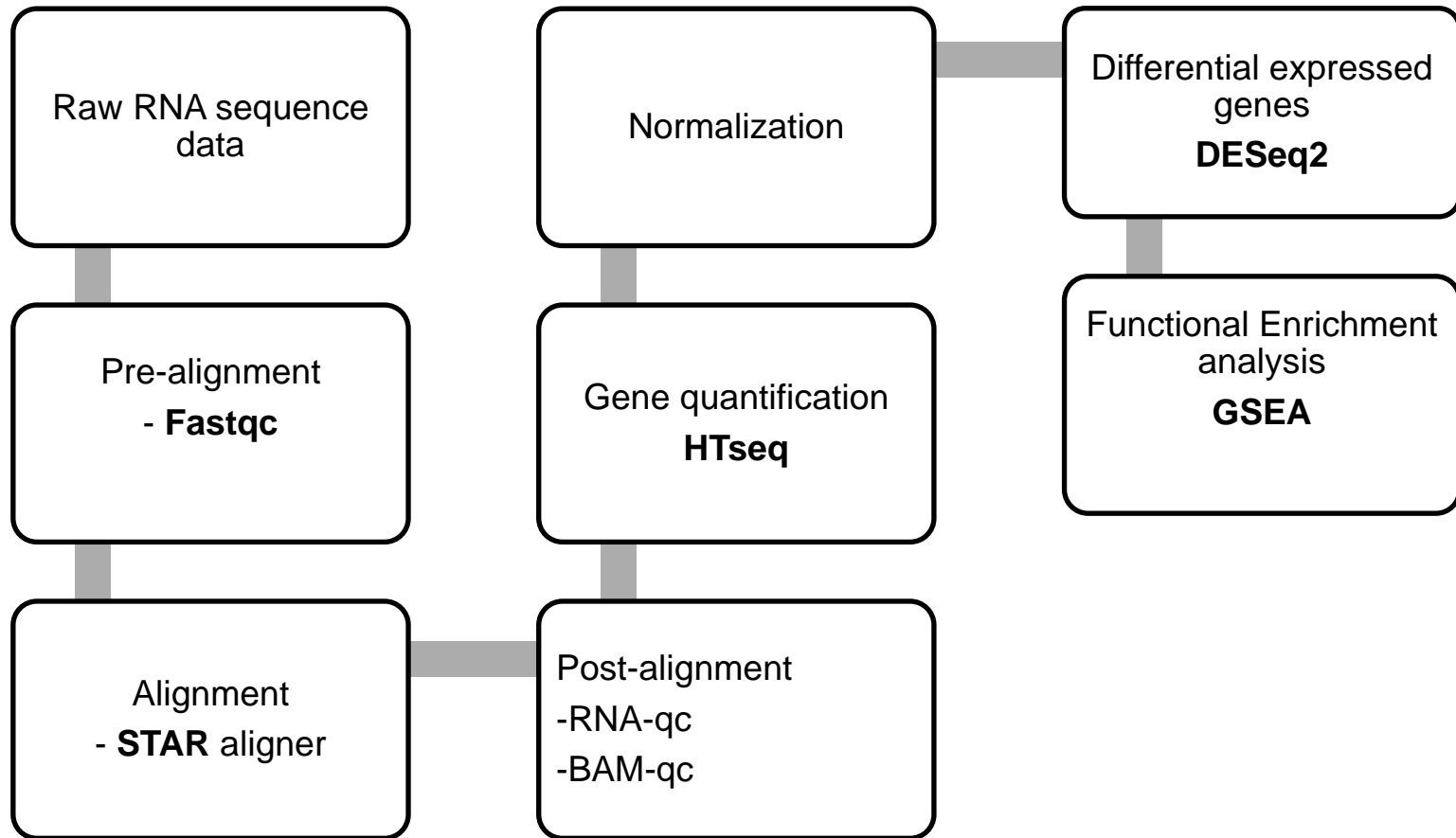
	High FE	Low FE	Total
Control	5	5	10
High Concentrate	5	5	10
Total	10	10	20



Experimental Workflow



RNA-Seq Analysis Pipeline





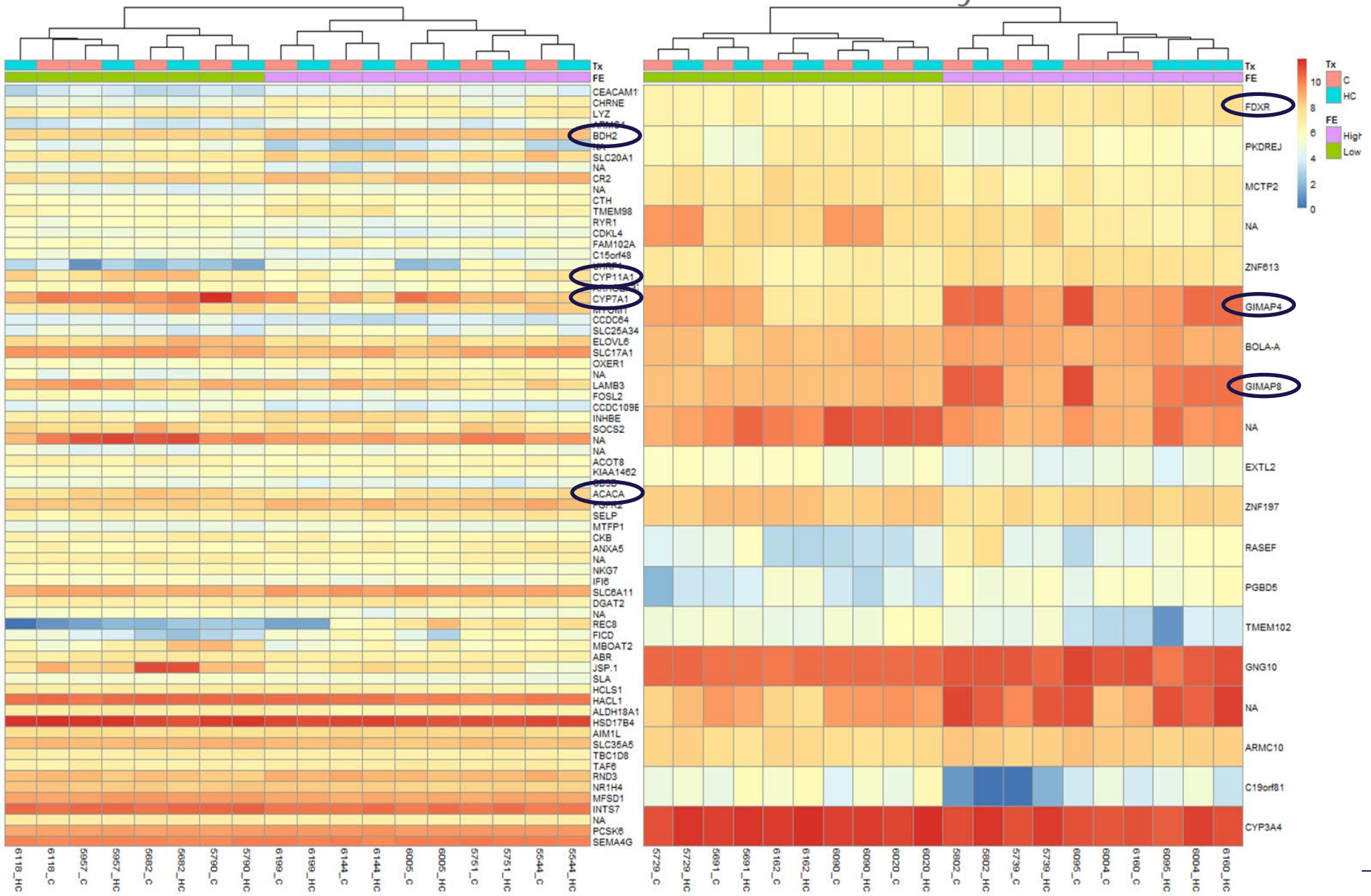
OUTPUT AND RESULTS



Differentially Expressed genes

Holstein

Jersey



DEG biological functions - Holstein

CYP11A1 and *CYP7A1*

- **Upregulated** in low FE
- Synthesis of cholesterol, steroids and other lipids

ACACA

- **Upregulated** in low FE
- Cause the deposition of fat in low FE

BDH2

- **Downregulated** in low FE
- Metabolism, synthesis and degradation of ketone bodies



DEG biological functions - Jersey

FDXR

- **Upregulated** in high FE
- cholesterol metabolism, which is also part of steroid metabolism

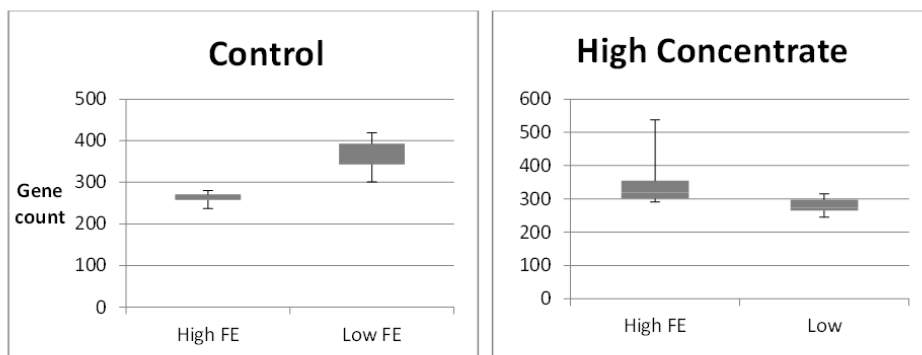
GIMAP4 and *GIMAP8*

- **Upregulated** in the high FE group
- controlling the immune system and involved in responses to infections

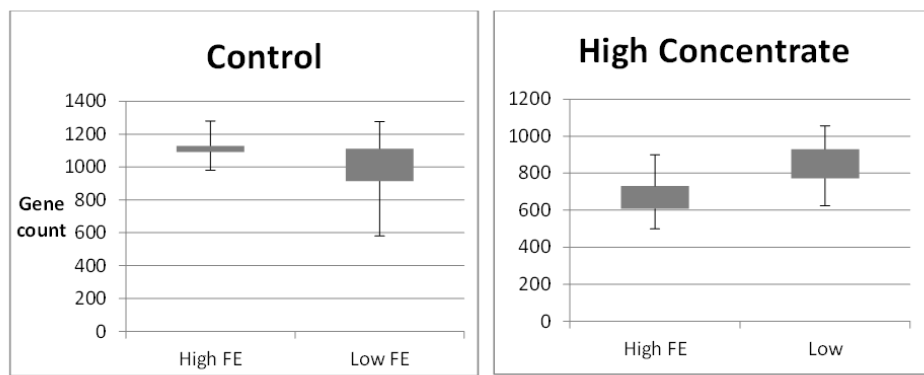


Genes in FE x diet interaction in Jersey

FIZ1



SEC24D



- Protein coding gene
- Related pathways
 - Metabolism and transport to the Golgi and subsequent modification
 - Transcriptional regulation



Functional enrichment

Gene Set Enrichment Analysis (GSEA) – Holstein

Downregulated KEGG pathways for FDR q-value <0.05 from the output of GSEA in Holstein

	Name	FDR q-value
1	Primary immunodeficiency	0.000
2	Natural killer cell mediated cytotoxicity	0.000
3	T cell receptor signaling pathway	0.000
4	Leukocyte transendothelial migration	0.002
5	Chemokine signaling pathway	0.002
6	FC gamma R mediated phagocytosis	0.008
7	Propanoate metabolism	0.009
8	Rig I like receptor signaling pathway	0.013
8	Cell adhesion molecules cams	0.012
9	Calcium signaling pathway	0.012
10	B cell receptor signaling pathway	0.021
11	Viral myocarditis	0.031
12	Nod like receptor signaling pathway	0.028
13	FC epsilon RI signaling pathway	0.038
14	Leishmania infection	0.043



GSEA - Jersey

Downregulated KEGG pathways for FDR q-value <0.05 from the output of GSEA in Jersey

	Pathways name	FDR q-value
1	Primary immunodeficiency	0.010
2	Leukocyte transendothelial migration	0.006
3	Leishmania infection	0.015
4	Cytosolic DNA sensing pathway	0.013
5	Hematopoietic cell lineage	0.044

Upregulated KEGG pathways for FDR q-value <0.05 from the output of GSEA in Jersey

	Pathways name	FDR q-value
1	Metabolism of xenobiotics by cytochrome P450	0.003
2	Retinol metabolism	0.002
3	Sphingolipid metabolism	0.015
4	Starch and sucrose metabolism	0.012
5	Ether lipid metabolism	0.009
6	Steroid hormone biosynthesis	0.013
7	Glycolysis gluconeogenesis	0.025
8	Arachidonic acid metabolism	0.023
9	Drug metabolism cytochrome P450	0.029
10	Pentose phosphate pathway	0.029

Santana et al 2015 and 2016

McCabe et al, 2012



Conclusions

This study provides information of liver transcriptome of **high** versus **low feed efficient** cows.

- The DE genes - Top genes
 - **CYP's** genes in Holstein
 - **GIMAP** genes in Jersey.
 - 2 genes FE x Diet interaction in Jersey
- Functional enrichment- the DE genes involved in pathways:
 - Primary immunodeficiency,
 - Retinol metabolism
 - Starch, sucrose , sphingolipid and lipid metabolisms
- The pathways are involved in controlling the FE– shows the complexity of the trait



Implications and future works

- Possible inclusion in genomic selection
 - sgBLUP (System genomic BLUP)
 - BLUP|GA (BLUP approach given the Genetic Architecture)
 - Bayes R
- Conduct an integrative analysis
 - Gene co-expression networks
 - eQTL analysis
 - Metabolomics analysis





THANK YOU

