ECOFCE

EFFICIENT & ECOLOGICALLY-FRIENDLY PIG AND POULTRY PRODUCTION.

A WHOLE-SYSTEMS APPROACH TO OPTIMISING FEED EFFICIENCY AND REDUCING THE ECOLOGICAL FOOTPRINT OF MONOGASTRICS.

BASIC DATA

Funding:
EU-FP7
(€ 6 million)

Start date:
1 February 2013

Duration:
48 months
(2013 to 2016)

This project has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement No. 311794

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Holistic transcriptome-profiling of feed efficiency-divergent pigs

teagasc
Agriculture and Food Development Authority

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Agri-Food and Biosciences Institute

FBN
LEIBNIZ INSTITUTE
FOR FARM ANIMAL BIOLOGY

IRTA
RESEARCH & TECHNOLOGY
FOOD & AGRICULTURE

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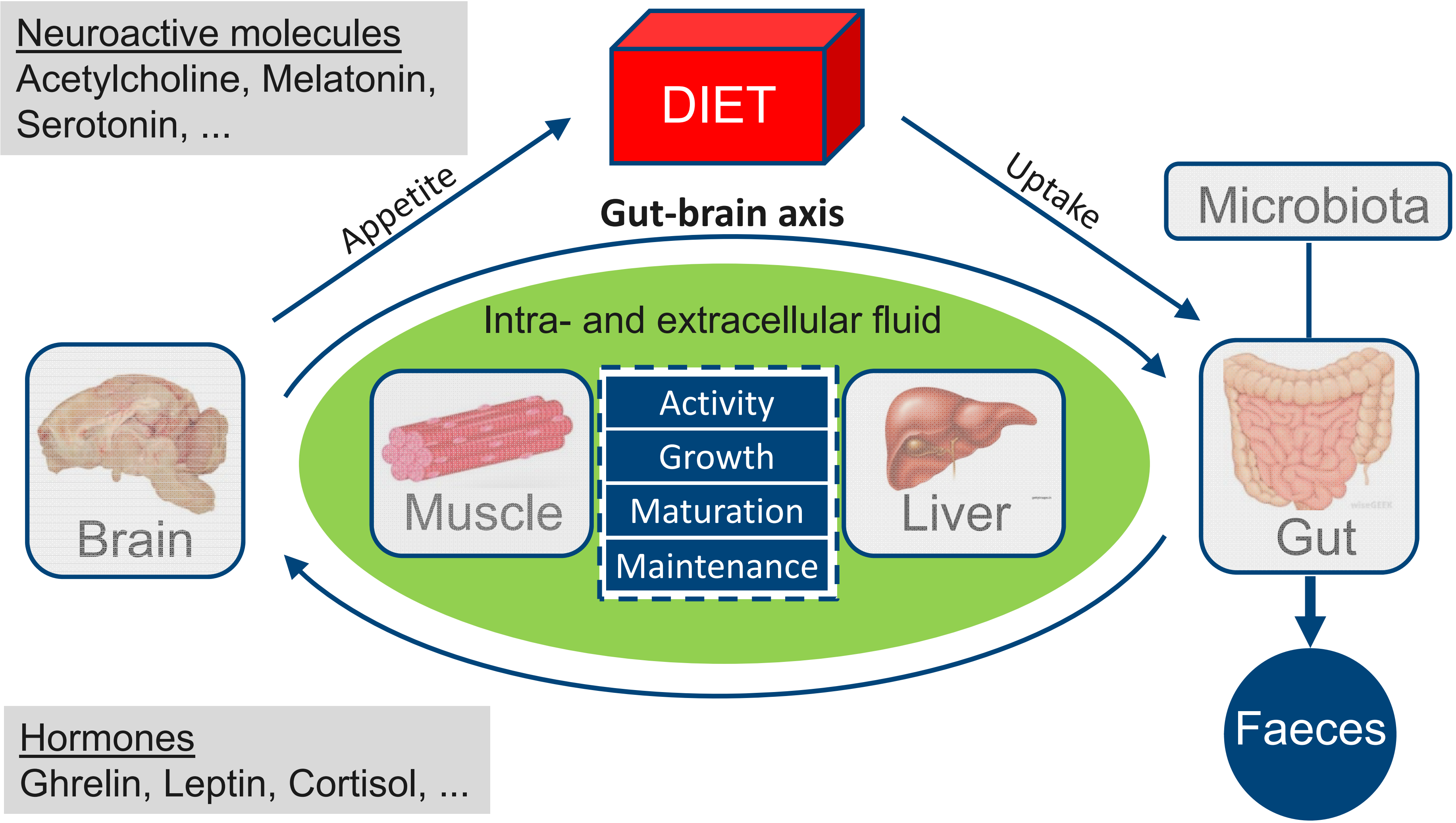
Systemic processes of energy usage



Neuroactive molecules
Acetylcholine, Melatonin, Serotonin, ...

Hormones
Ghrelin, Leptin, Cortisol, ...

Effects of FE on carcass composition and meat quality

- Population of 100 FE-tested German Landrace pigs

Trait	Low FE	Medium FE	High FE	p-value
loin eye area	41.3 ± 1.2	44.1 ± 1.2	46.6 ± 1.2	0.0012
fat area	15.2 ± 1.0	11.5 ± 1.0	11.6 ± 1.0	0.0038
lean %	52.6 ± 0.8	56.8 ± 0.8	57.7 ± 0.8	<.0001
back fat (total)	2.34 ± 0.07	2.07 ± 0.07	1.94 ± 0.07	<.0001
back fat (1)	3.49 ± 0.1	3.22 ± 0.09	3.04 ± 0.1	0.0003
back fat (2)	1.77 ± 0.07	1.54 ± 0.07	1.48 ± 0.07	0.0007
back fat (3)	1.74 ± 0.11	1.49 ± 0.1	1.36 ± 0.1	0.0009
pH_{45min}	6.39 ± 0.04	6.44 ± 0.04	6.36 ± 0.04	0.1257
pH_{24h}	5.46 ± 0.07	5.55 ± 0.07	5.44 ± 0.07	0.5262
L*	48.3 ± 0.6	49.1 ± 0.6	49.1 ± 0.6	0.1726
a*	7.53 ± 0.22	7.21 ± 0.21	7.43 ± 0.22	0.2807
b*	1.16 ± 0.18	1.2 ± 0.17	1.08 ± 0.17	0.7423

FE class associated with alterations of muscle/fat traits

No significant associations of FE groups with meat quality parameters

Objectives

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Dependence and interaction of different tissues in relation to feed efficiency

→ nutritional highly relevant tissues

- small intestine (duodenum, jejunum, ileum)
- liver (metabolism, protein synthesis, bile production)

→ regulatory tissues

- hypothalamus (central control of feed intake)

→ responsive tissues

- skeletal muscle (major consumer of energy)
- adipose tissue (major storage of energy)

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Overview of transcriptomic analysis

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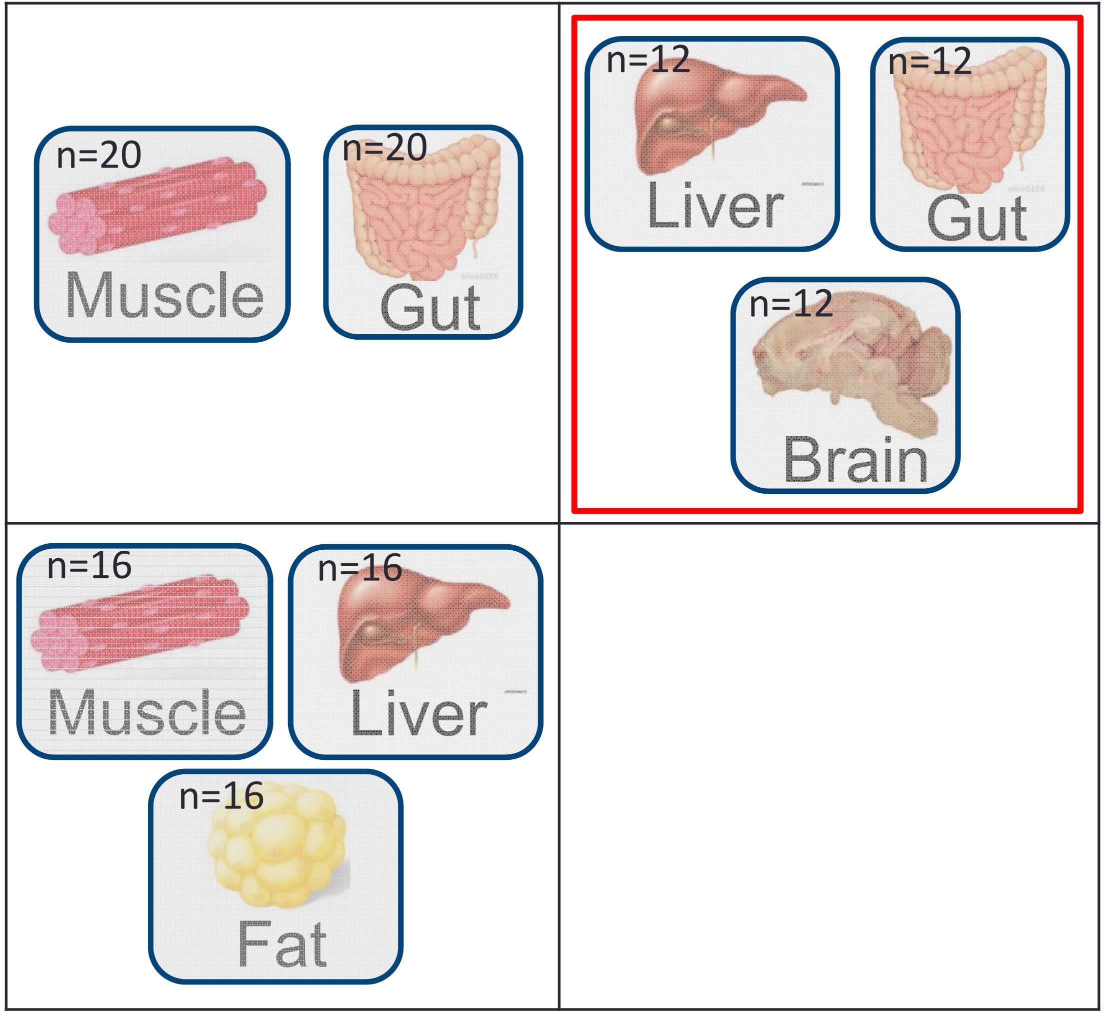
SNOWBALL
porcine microarray

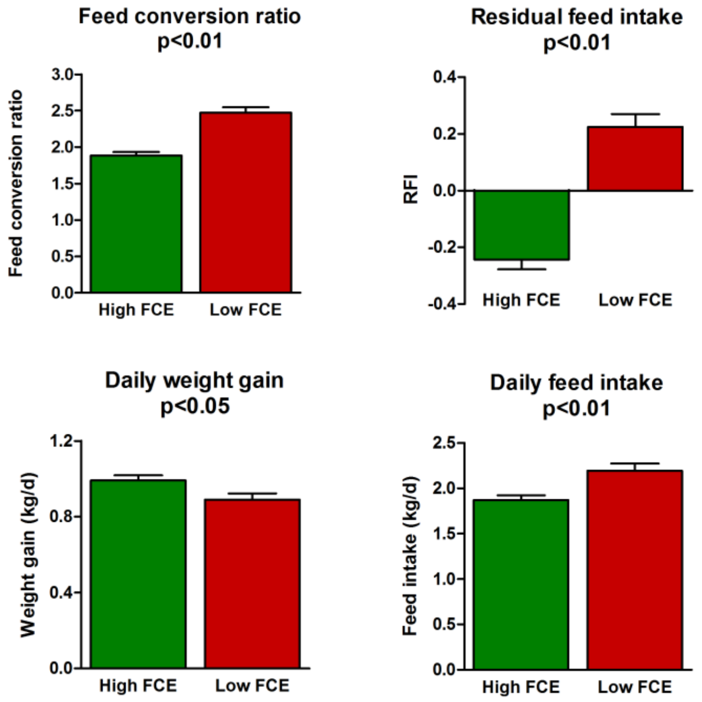
RNA-Seq on
HiSeq2500



Pig - Transcriptome analysis

Experiment AFBI – focus on tissues of the **gut-brain axis**

- Based on a population of 96 pigs, a subset of 12 pigs (~105kg) with **high** and **low** FE was selected (balanced for sex and pedigree)



Differentially abundant probe-sets ($p<0.05$, $q<0.3$):

	high FE >	low FE >
Tissue	low FE	high FE
Hypothalamus	46	32
Duodenum	25	37
Jejunum	56	30
Ileum	-	-
Liver	292	511

- ➢ hierarchical make-up of FE at the transcriptional level

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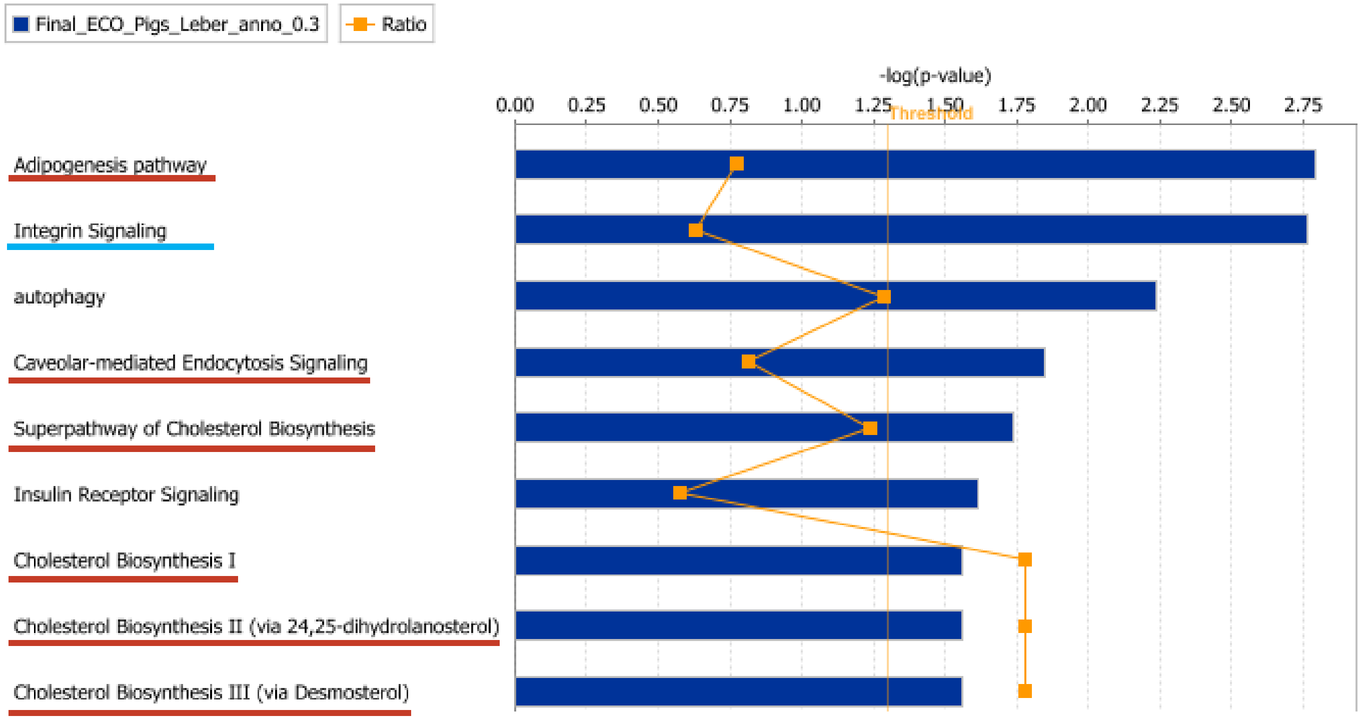
Transcriptome analysis of liver

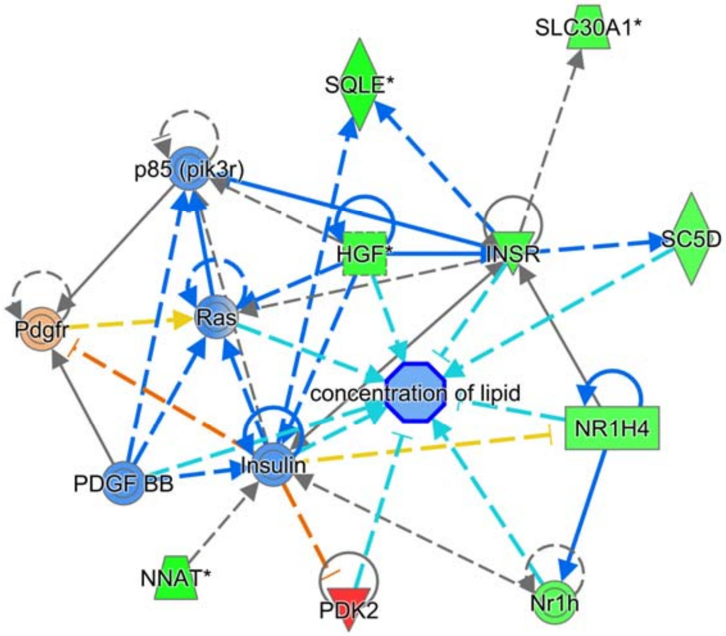
Regulated pathways in liver tissue of high vs. low FE pigs:

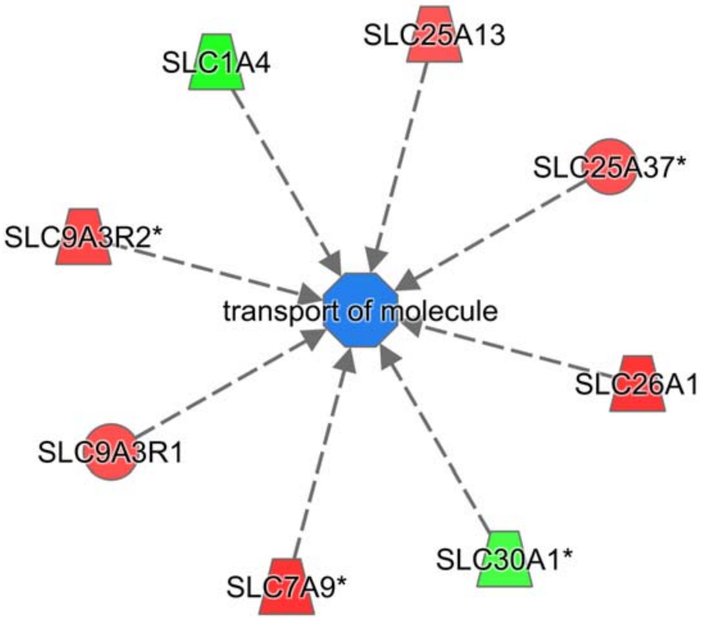


- enrichment of differentially expressed genes in pathways related to:
  - lipid metabolism → potential implications on muscle/fat ratio
  - cell communication and interaction → efficient usage of cellular infrastructure

Bio-functions affected in liver

Gene	P-value (array)	P-value (qPCR)	Correlation (p-value)	Expression (FE)	Bio-function
NR1H4	<0.01	0.06	0.75 (<0.01)	H<L	Lipid concentration
SQLE	<0.01	<0.01	0.82 (<0.01)	H<L	
SLC1A4	<0.01	<0.01	0.85 (<0.01)	H<L	Transport of molecules
SLC7A9	<0.01	0.02	0.87 (<0.01)	H>L	

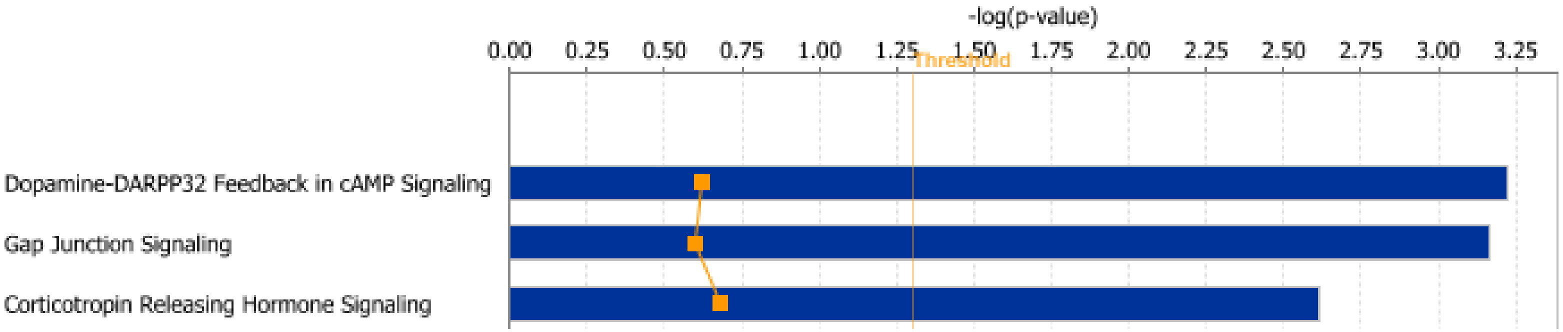




Hub molecules in hypothalamus and small intestine

- Hypothalamus:
  - TEAD3 ($p<0.01$) – transcription factor involved in T3-mediated regulations[1]
  - EHHADH ($p<0.01$) – involved in peroxisomal oxidation of fatty acids

- Small intestine
  - altered signalling within the gut-brain axis (CRH, dopamine)



  - potential hub molecules:

    GUCY1A3, GUCY1B3 (both $p<0.01$) – nitric oxide receptors

    DIO1 ($p<0.01$) – deiodination of T4 to T3

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[1] *Iwaki et al. PLOS ONE (2016)*

Conclusion

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- Transcriptional effects are cascaded and amplified throughout the organism from gut-brain axis to responsive tissues
- No consistent molecular alterations in all analysed tissues, but:
  - lipid metabolism pathways and bio-functions affected in liver
  - genes encoding for transporters are differentially abundant in liver
  - cell-to-cell signalling and interaction pathways enriched in liver and intestine
  - cross-talk between gut and brain influenced (NO, CRH, thyroid signalling)

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Outlook - molecular mechanisms of FE

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- Validation of the involvement of solute carriers and thyroid hormone signalling pathways in FE
- Regulated pathways of lipid metabolism
  - → Complement findings with fatty acid profiles
  - → Focus on muscle-fat ratio using RNA-Seq data of FE-divergent animals
- FE-related differences in energy metabolism
  - → Samples of pigs from respiratory chambers with measurements of heat production and gas emission
- Importance of host-microbe interactions
  - → Metagenomics combined with transcriptomics of ileum and caecum

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Thank you for your attention!

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