EFFICIENT & ECOLOGICALLY-FRIENDLY PIG AND POULTRY PRODUCTION.

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

ECOFCE

BASIC DATA

Funding:
EU-FP7
(€ 6 million)

Start date:
1 February 2013

Duration:
48 months
(2013 to 2017)

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

Molecular alterations of broilers differing in feed conversion efficiency

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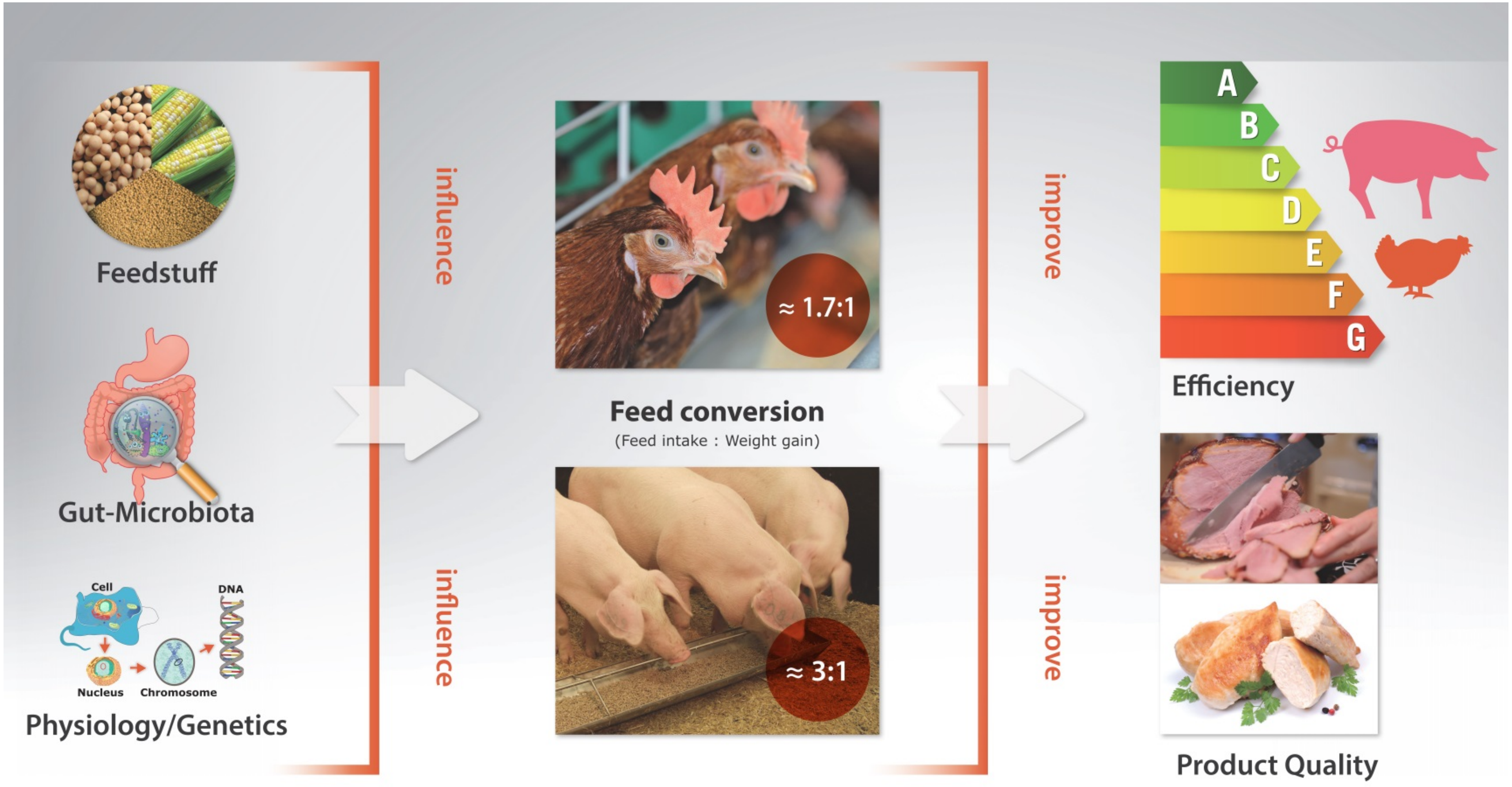
How to improve feed efficiency



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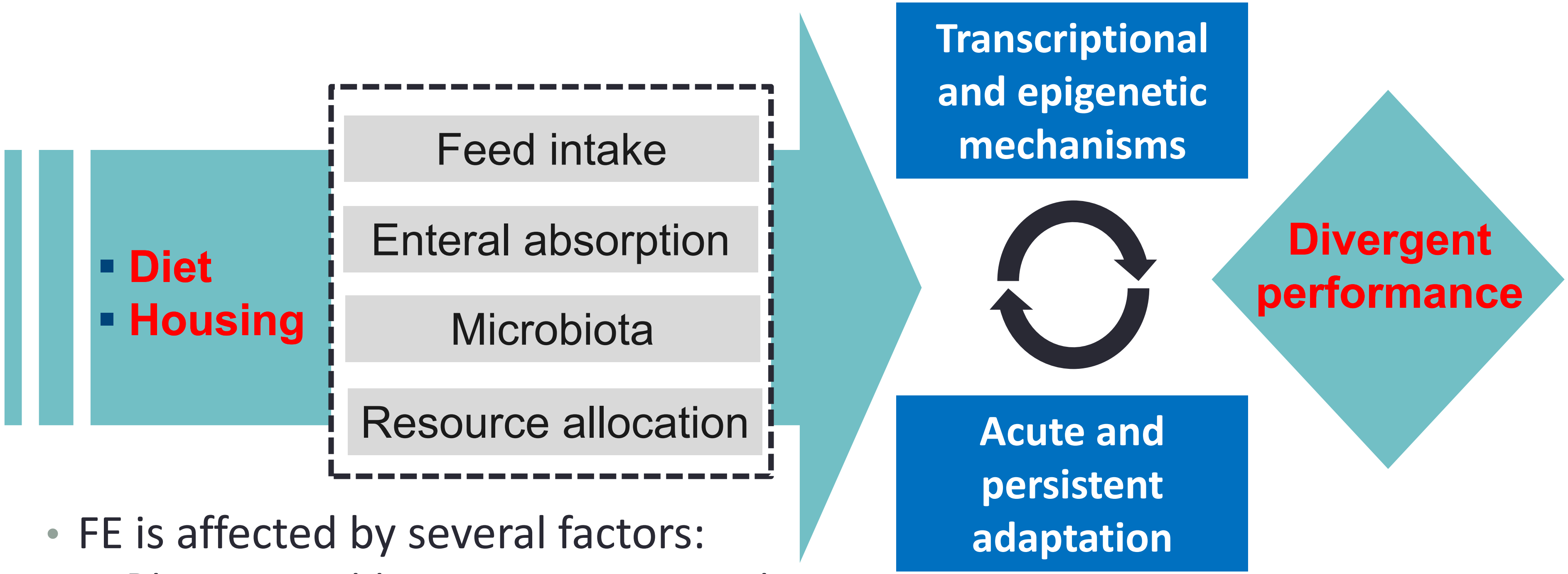
Factors driving feed efficiency (FE)



- FE is affected by several factors:
  - Diet: composition, energy concentration
  - Housing: temperature, humidity, space...
  - Animal: age, sex, health status...
- High animal-individual variation of FE under controlled conditions
  - cellular energy expenditure: ion pump, mitochondrial coupling/thermogenesis

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Organs/tissues driving feed efficiency (FE)

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- digestion and absorption of nutrients: **gut**
- partitioning and primary metabolism: **liver**
- growth, physical activity, and thermoregulation and major side of energy expenditure: **muscle**
- superior mechanisms to orchestrate resource allocation like feed intake, feeding behaviour, endocrine parameters: HPA axis; sympathetic activity (SAM system)…

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Known molecular routes affecting FE in chicken

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- Mitochondrial function [1]
  - Generate 90% of cellular ATP, uncoupling of electron transport chain (e.g. COXII, UCP, PPAR-γ)
- Energy expenditure [3]
  - maintaining energy homeostasis (AMPK)
  - sensors of energy status (mTOR)
  - energy allocation (PI3K/Akt pathway)
- Regulations via central nervous system (POMC, CRH, melanocortin receptors) [2]
- Recycling pathways (e.g. nitrogen recycling, transporters)

[1] Bottje and Carstens JAS (2009); [2] Ka et al. Neurogenetics (2011); [3]Song et al. Gen Comp Endocrinol (2013)

Objectives

Transcriptome-analysis:
To gain a new insight into the molecular mechanisms relevant for FCE by analysing the acquisition of genomic information

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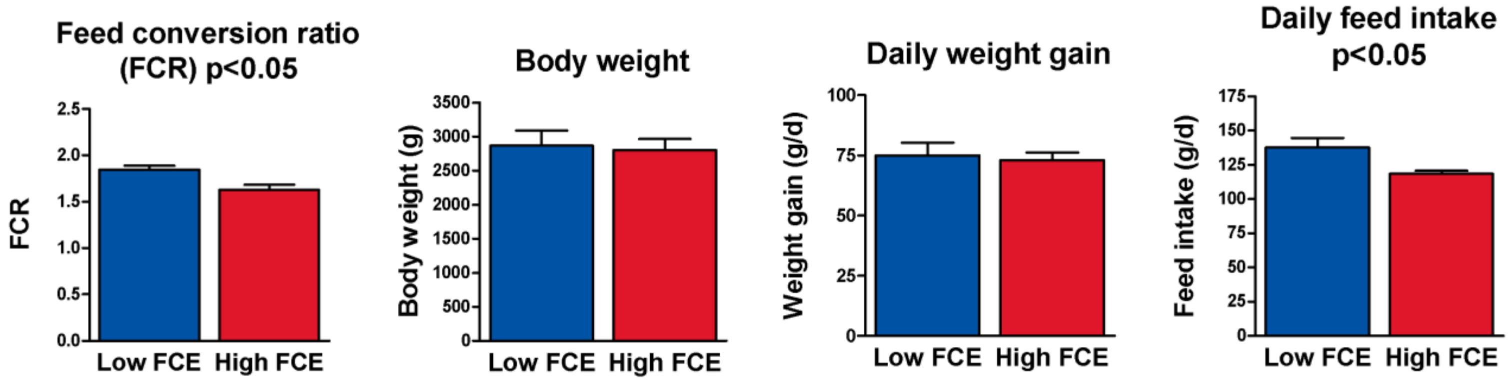
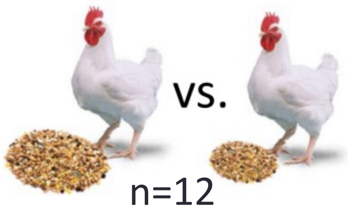
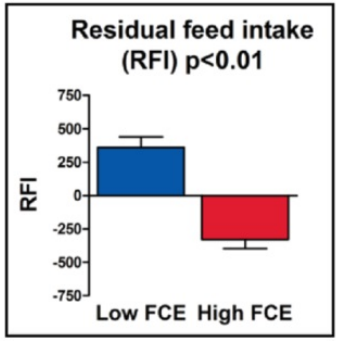
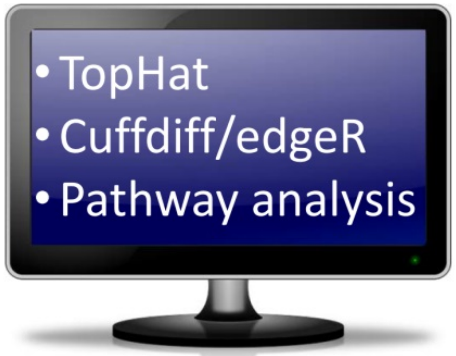
Chicken – Transcriptome analysis

Animals selected from FE-tested broilers from Vetmeduni and AFBI trials









Broiler feeding trail and sample collection → Sequencing HiSeq2500 → Data Analysis

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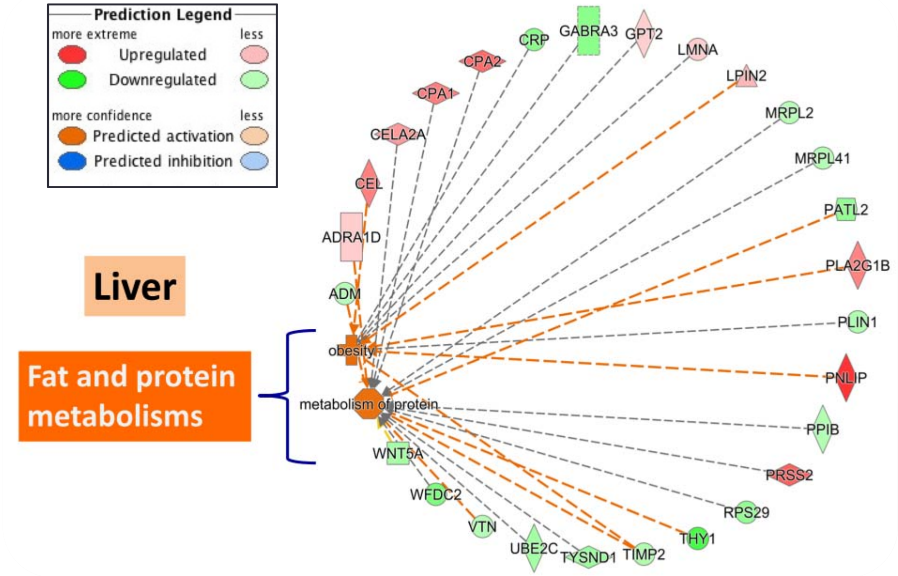
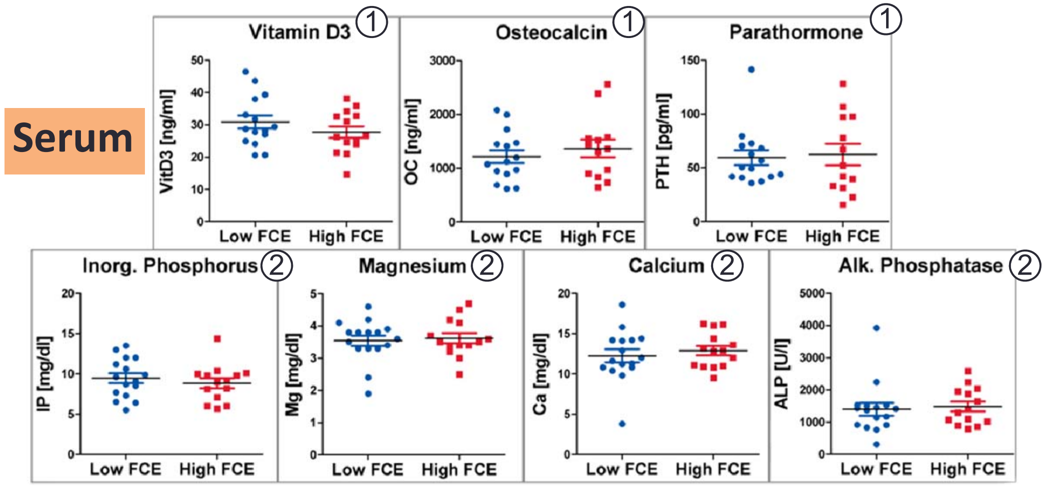
Phenotypic effects of improved FE in chicken



Altered molecular themes of lipid metabolism in liver and muscle reflect the influence on muscle-fat ratio



Liver and bone metabolism were unaffected between efficiency divergent chickens

① ELISA
② Blood chemistry

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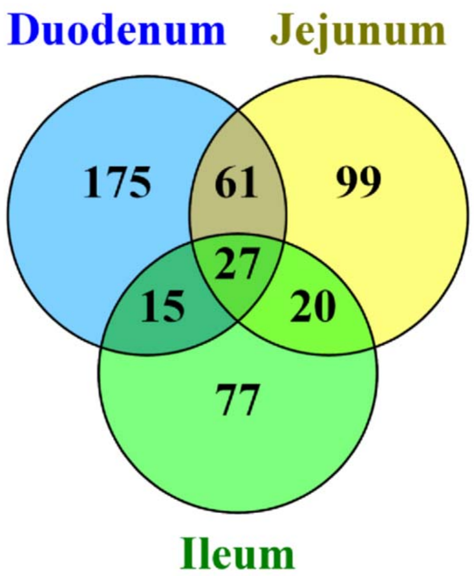
Tissue specific transcript abundance ($p<0.05$, $q<0.25$)

Tissue	high FCE > low FCE	low FCE > high FCE
Duodenum	150	154
Jejunum	118	108
Ileum	86	65
Liver	166	37
Breast muscle	159	135
Leg muscle	40	37



Expression profiles of the gut indicate for independent tissues with distinct functions for nutrient absorption and immune competence

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Regulated canonical pathways in small intestine

Tissue	Canonical pathway		p-value
Duodenum	• MIF Regulation of Innate Immunity	innate immunity	1.74E-03
	• Cdc42 Signaling	cell-cell adhaeson, cell polarity	2.00E-03
	• Superpathway of Cholesterol Biosynthesis	membran components	1.00E-16
	• Cholesterol Biosynthesis I	membran components	1.26E-13
Jejunum	• Granulocyte Adhesion and Diapedesis	inflammation, immunity	3.24E-03
	• LPS/IL-1 Mediated Inhibition of RXR Function	innate immunity	6.17E-03
	• Superpathway of Cholesterol Biosynthesis	membran components	3.31E-05
	• Mevalonate Pathway I	membran components	3.80E-04
Ileum	• Clathrin-mediated Endocytosis Signaling	endocytosis	1.29E-02
	• GPCR-Mediated Integration of Enteroendocrine Signaling Exemplified by an L Cell	intestinal chemosensation	1.51E-02
	• Phagosome Maturation	internalisation of particles	1.82E-03
	• Methylglyoxal Degradation III	detoxification	8.51E-03

Pathways with putative impact on:

➢ nutrient absorption especially in posterior parts of the small intestine (solute carriers and aquaporins are regulated in ileum)

➢ membrane functions (membrane lipids - cholesterol biosynthesis)

➢ altered host-microbe interaction

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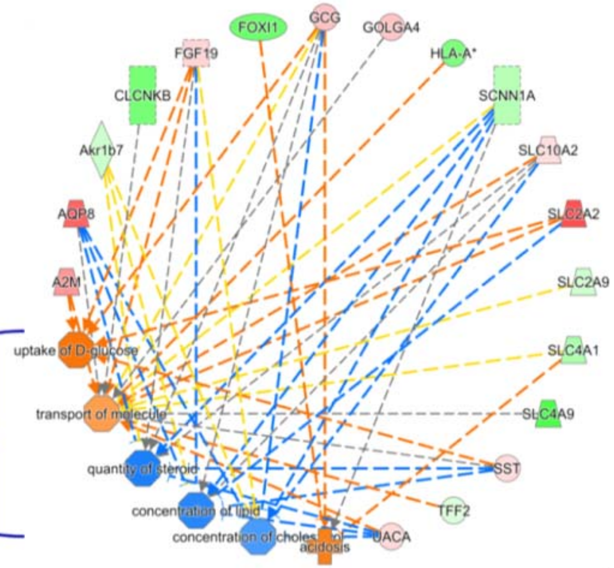
Regulated biofunctions in small intestine

Ileum

Glucose-uptake, Transporters

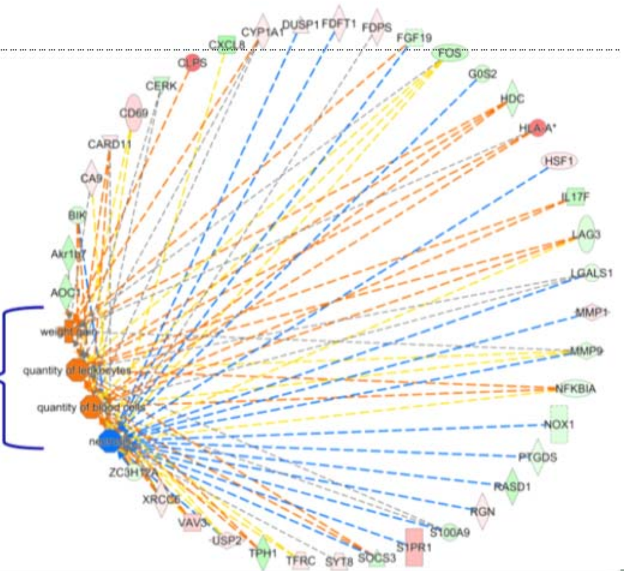
Lipid metabolism



Duodenum

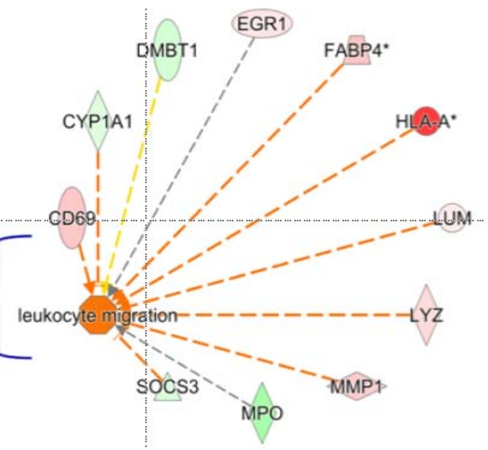
Weight gain
Immune

Cell death



Jejunum

Immune cells



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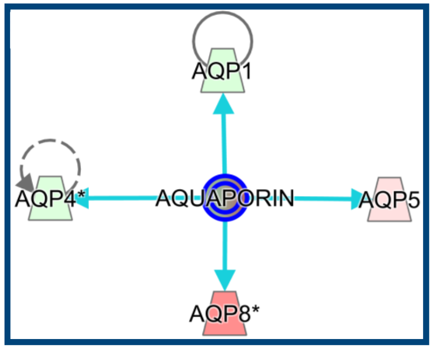
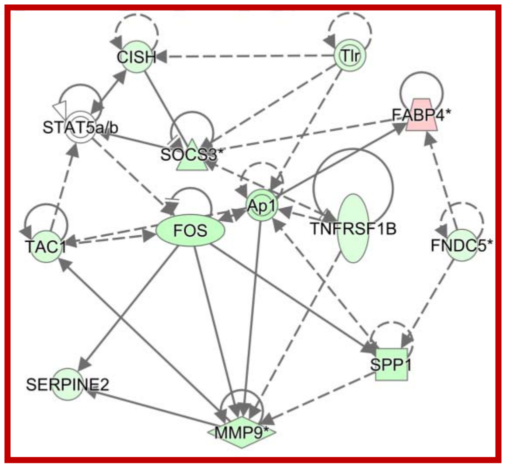
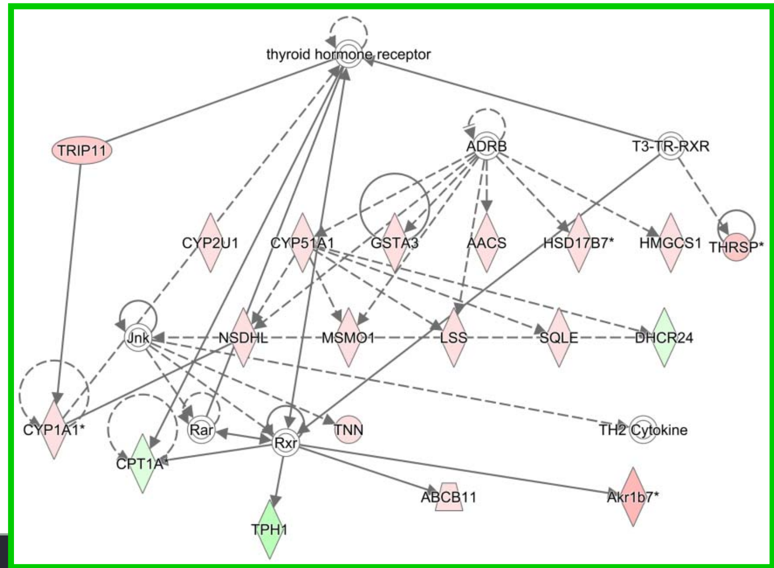
Hub molecules regulated in muscle and jejunum

Gene	P-value (NGS)	P-value (qPCR)	Expression	Biofunction
AQP4 (muscle)	0.04	<0.01	H>L	molecular transport
FNDC5 (muscle)	0.01	<0.01	H>L	cell-to-cell signaling and interaction
FABP4 (jejunum)	0.01	<0.01	H<L	
THRSP (jejunum)	0.04	<0.01	H<L	lipid metabolism and small molecule biochemistry







Conclusion

- No differences of major bio-functions known to be related with divergent FE e.g. AMPK, mTOR, UCP
  - →Improved genetics of commercial broilers regarding efficient energy utilisation
- Unaffected parameters representing liver and bone metabolism e.g. Vitamin D3, osteocalcin, parathyroid hormone
- BUT optimization potential towards improved FE:
  - →Molecular transport processes (role of aquaporins and solute carriers)
  - →Lipid metabolism (affected muscle-fat ratio related to FE; e.g. FABP4)
  - →Host-microbiota interaction
  - →Immune features with implications to health and welfare aspects (innate immunity)

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Outlook

- Importance of host-microbe interactions
  - → Integration of gut microbiota profiles and holistic expression patterns of high and low efficient animals
  - → Elucidation of gut barrier functions (induction of non-coding RNAs and antimicrobial peptides in gut and GALT-gut associated lymphoid tissue)
- Focus on the conversion of specific micro-and macronutrients
  - → Micronutrients: phosphorus, nitrate
  - → Macronutrients: alternative protein sources, regional fodder plants
- Superior endocrine regulations
  - → Thyroid hormones T3, T4

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Thank you for your attention!

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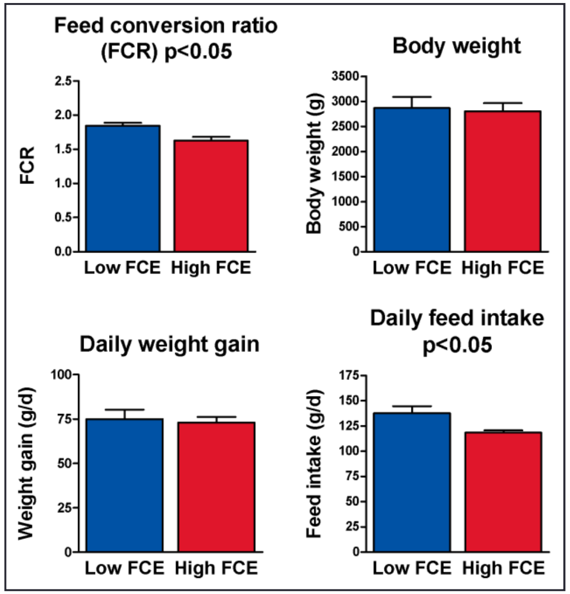
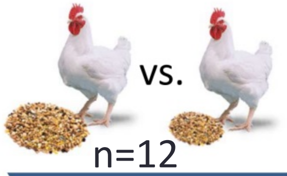
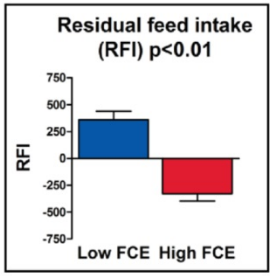
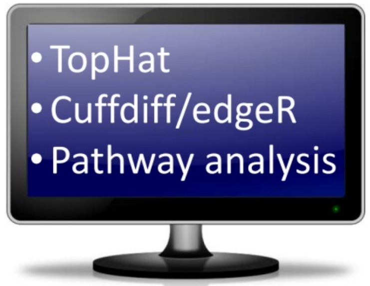
Chicken – Transcriptome analysis

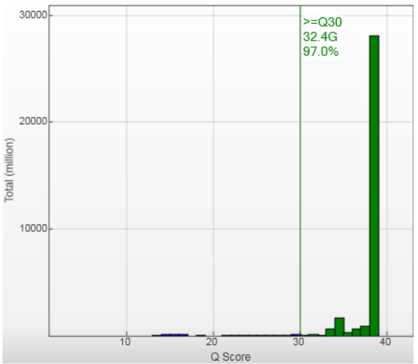








RNA-Seq statistics



Q-Score