

Transcriptomic analysis of key metabolic tissues to identify molecular regulatory patterns of feed efficiency

H.Z. Sun, K. Zhao, M. Zhou, Y. Chen, and L. L. Guan

*Department of Agricultural, Food and Nutritional Science
University of Alberta, Canada*

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Beef industry is one of the major Agriculture

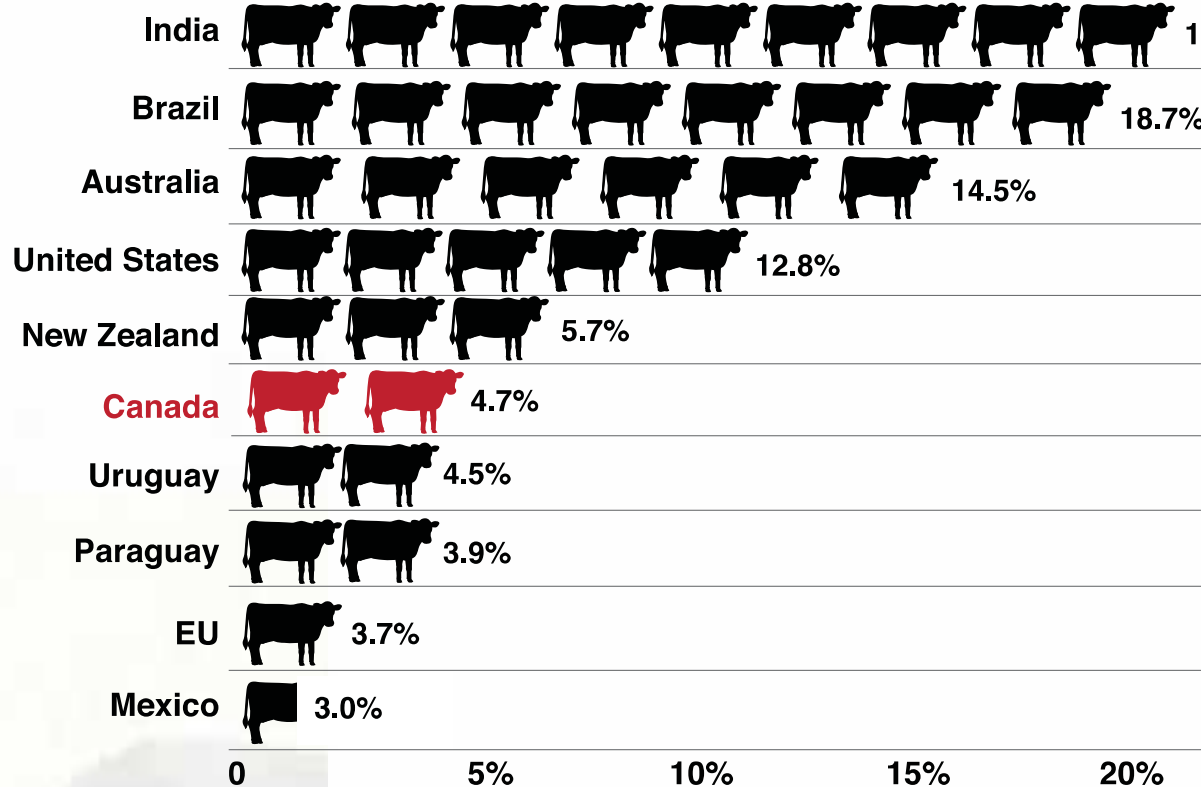
WORLD MAP AND ADES

W

Top 10 Beef Exporting Nations 2017p

(excludes live slaughter exports)

Top 12 Beef



Economy: the beef industry generated \$8.9 billion CAD in farm cash receipts (2013-2017 average).

Canada produce

Production is estimated at 62 million metric tonnes in 2017. USDA

Total Cattle and Calves Up 0.2% from 2016

Statistics Canada



Why feed efficiency?

Challenges in beef production

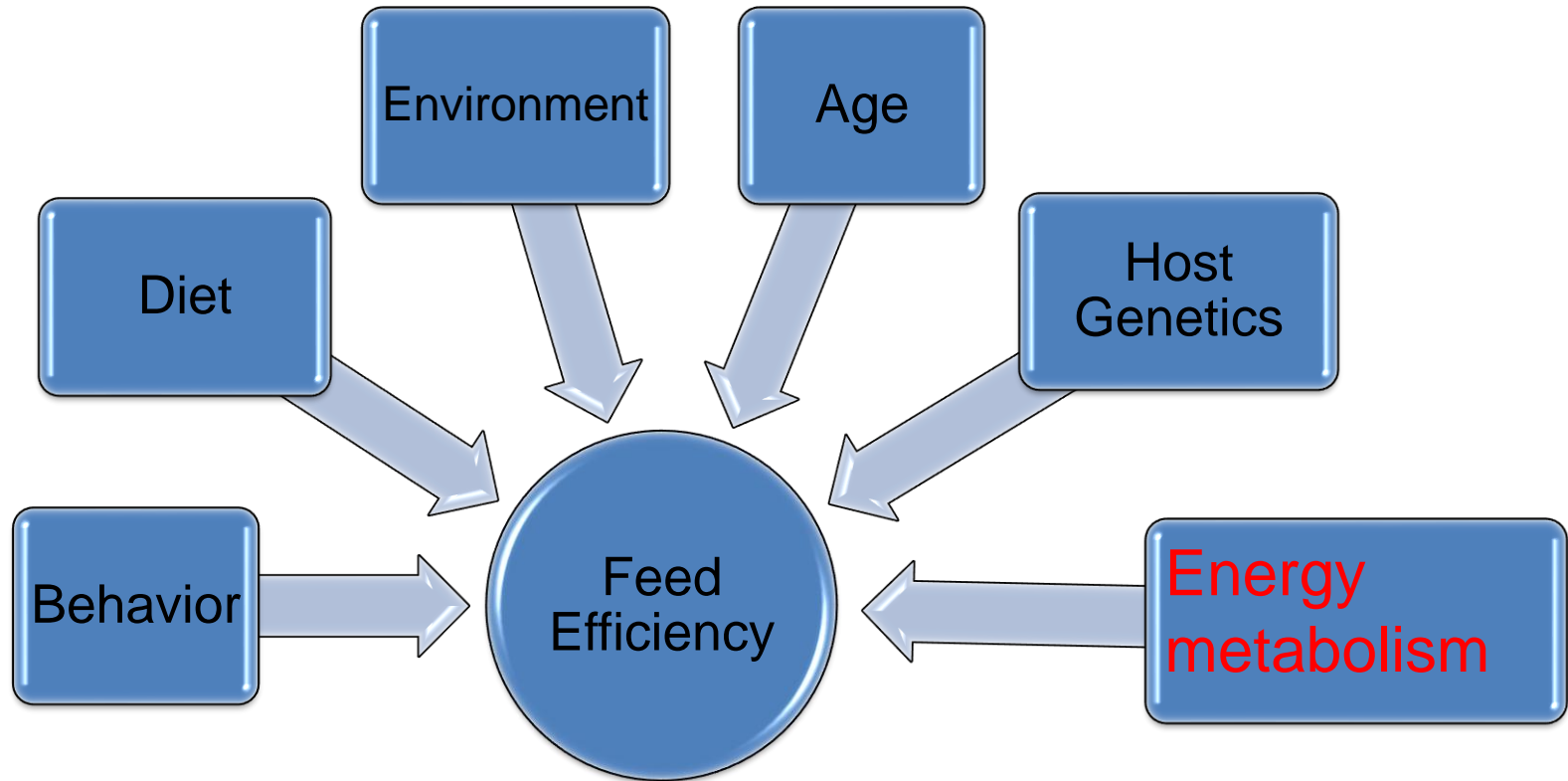
- Resource competitions
- Negative environmental effects

Feed efficiency

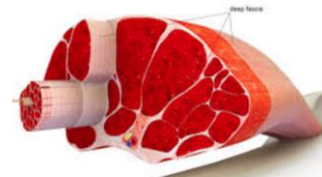
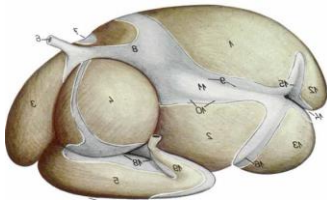
- Less feed (up to 3.77 kg/d)
- Less CH₄ (up to 25%)
- Increased profits for beef producers

(Basarab et al., 2003; Nkrumah et al., 2006; Statistics Canada, 2017)

Factors affecting feed efficiency



Key metabolic tissues related to energy metabolism



Questions?

- What is the global gene expression patterns across the four tissues?
- Can the gene expression landscape assist in revealing underlying mechanism of the improved feed efficiency?

Objectives

- To analyze the global gene expression landscape of rumen, liver, muscle and backfat tissues using the RNA-Seq based transcriptomics
- To investigate the weighted correlations of co-expression genes and feed efficiency related traits

◆ Animal and sampling:

- 48 beef steers with 3 breeds (Angus, Charolais, Kinsella composite)
16 for each breed (n=8 high RFI, n=9 low RFI)
- Age~400d, bodyweight~615kg
- Rumen epithelium, liver, muscle and backfat tissues at slaughter

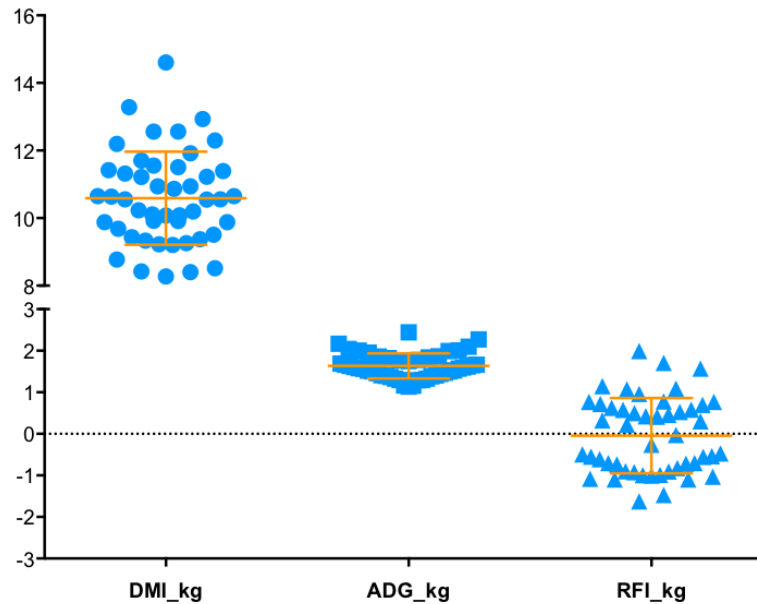
◆ RNA-Seq based transcriptomics

- Illumina HiSeq 4000 platform (PE100)
- The pipeline based on (Wang, et al., 2017)

◆ Data analysis

- **R packages:** WGCNA-co-expression & weighted correlation; Hmisc-correlation; mfuzz-soft clustering; devtools & ggfortify-PCA
- **Function and pathway analysis:** DAVID; KEGG; IPA
- **Network:** Cytoscape

Feed efficiency related traits

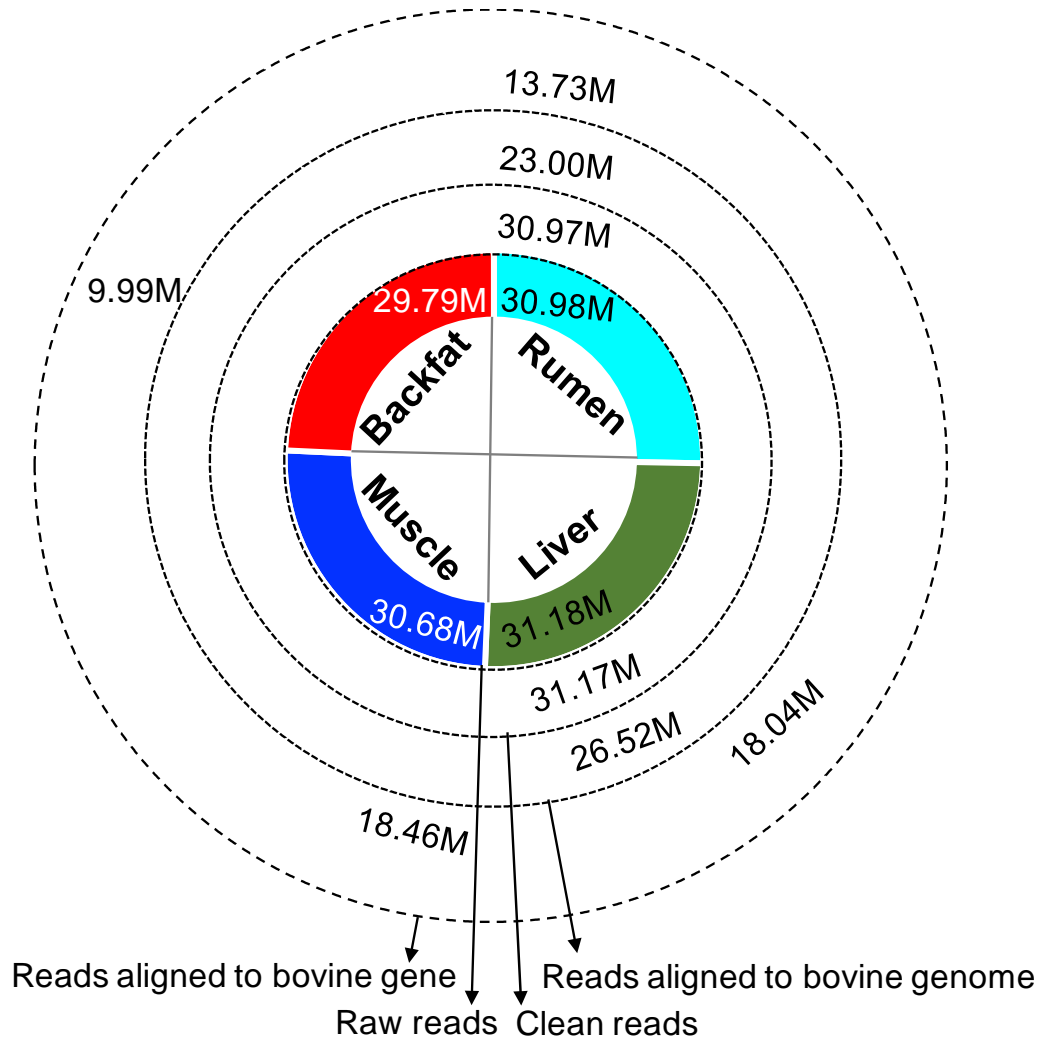


DMI: 8.27 to 14.61 kg/d

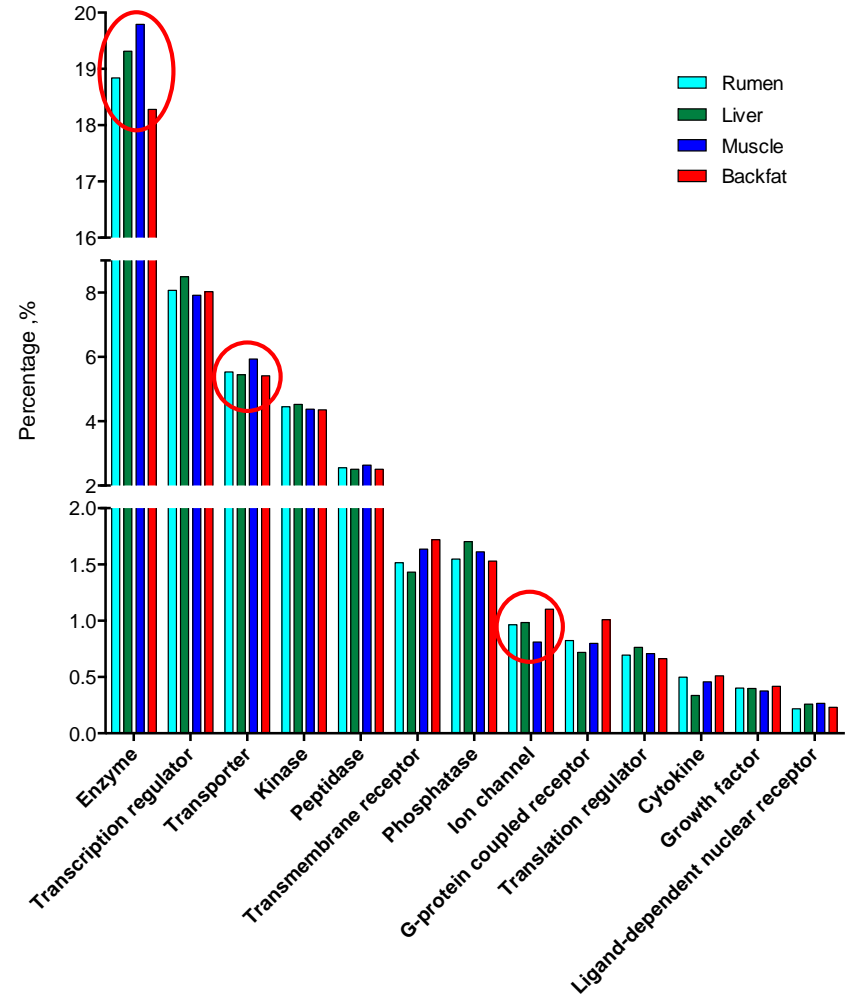
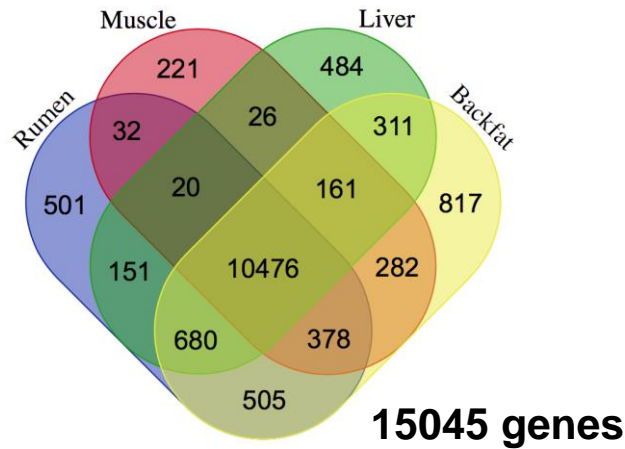
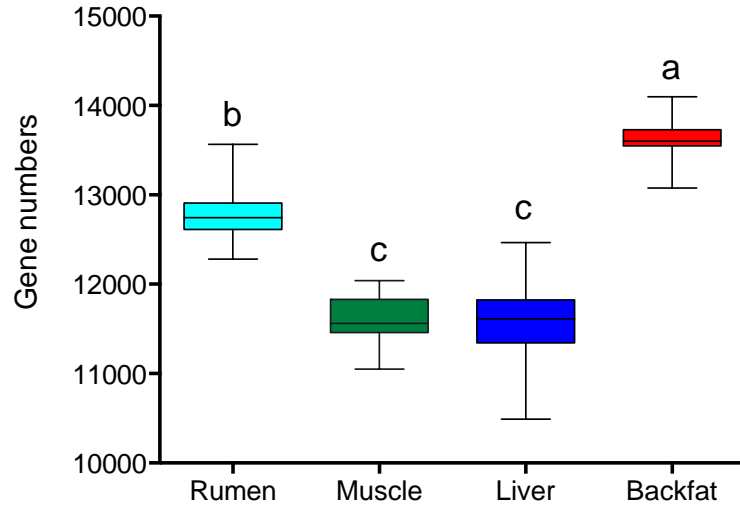
ADG: 1.14 to 2.44 kg/d

RFI: -1.63 to 1.99

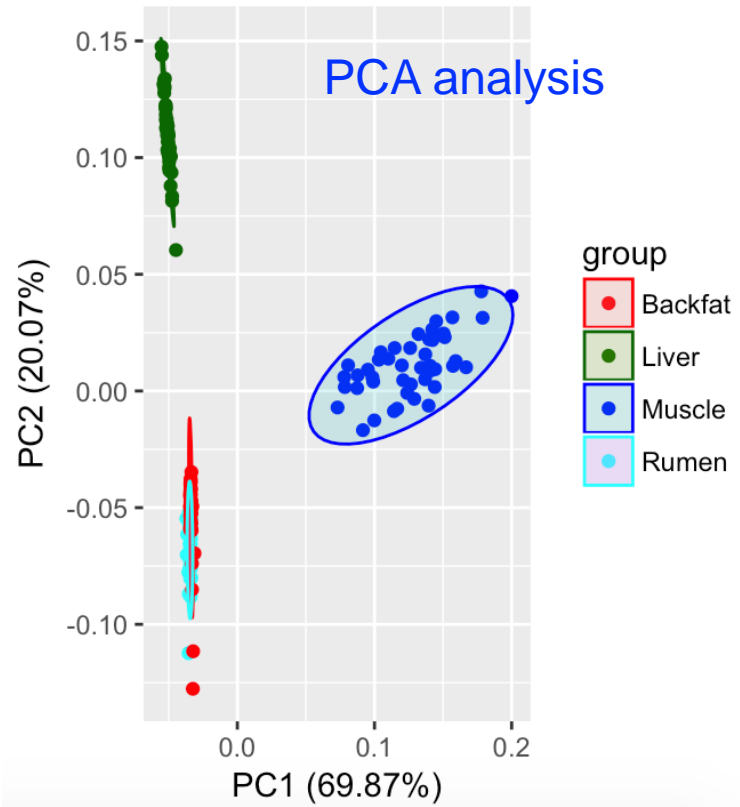
Transcriptome data



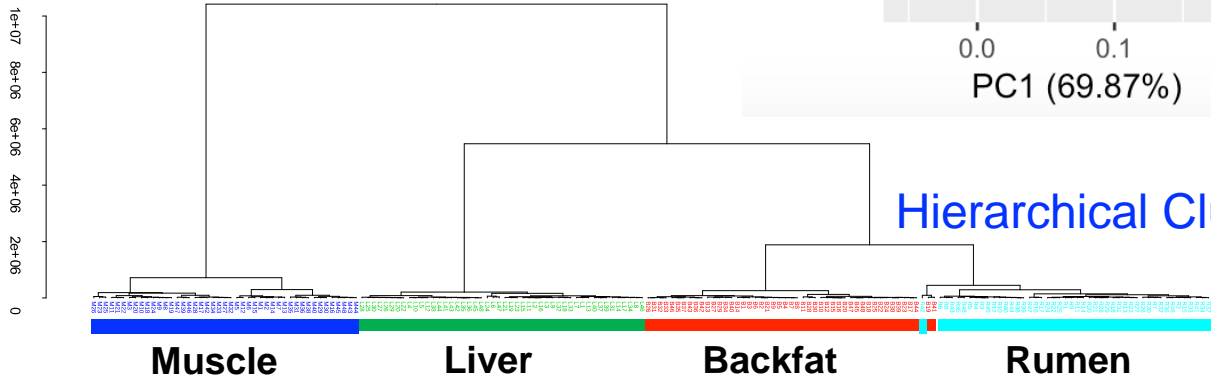
Expressed genes and functions



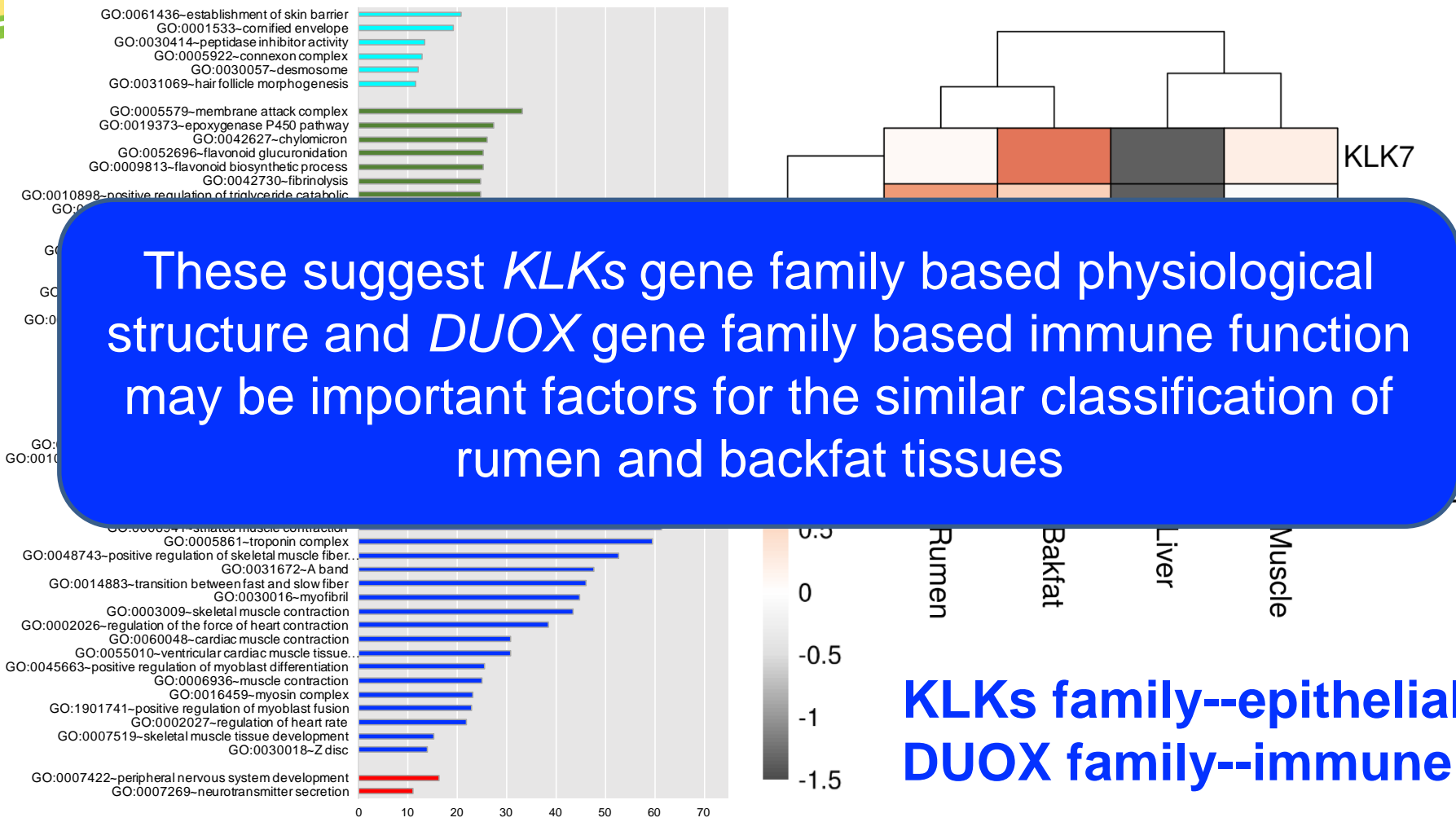
Comparison of Transcriptome profiles of four tissues



Soft clustering

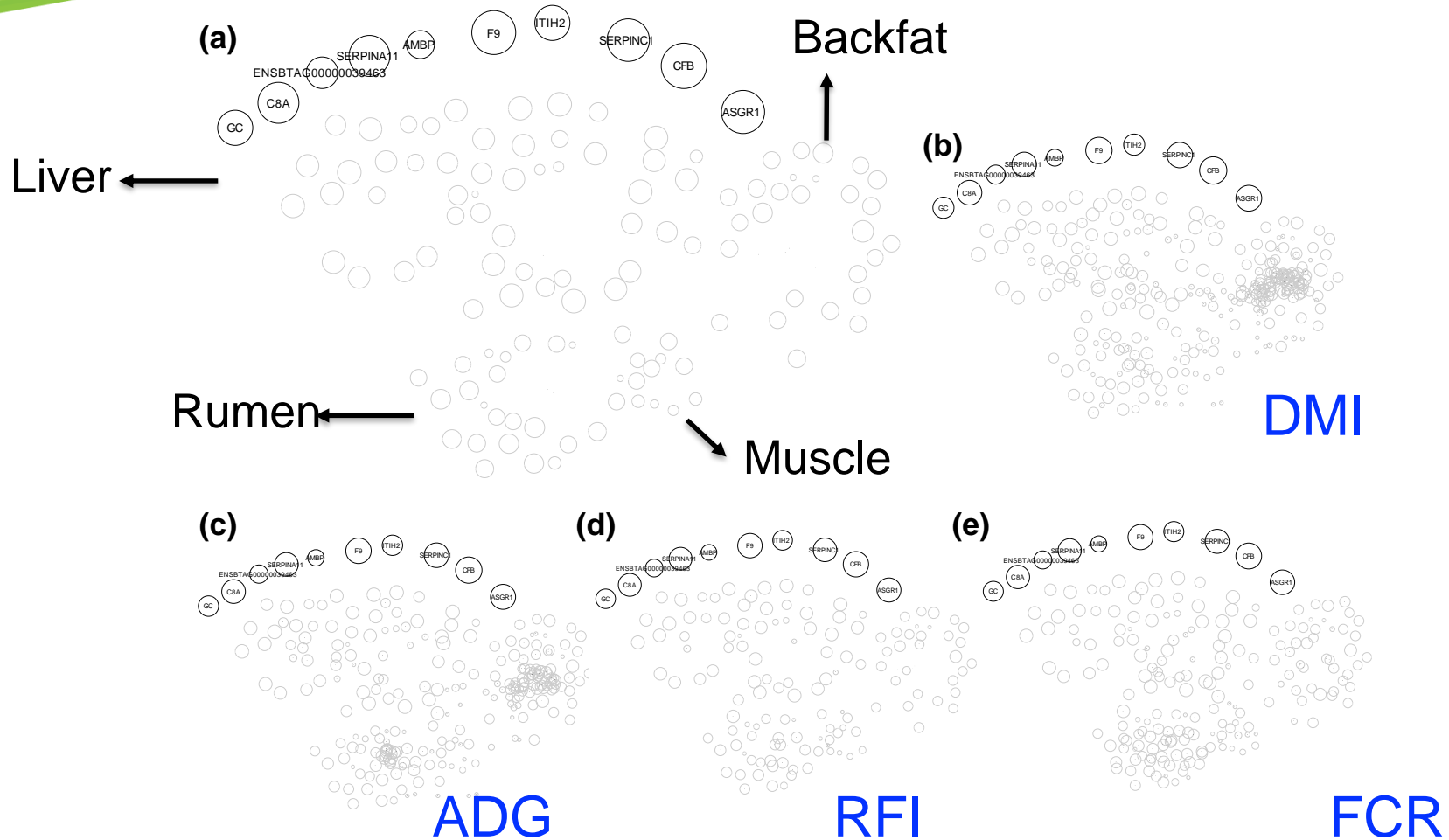


Rumen functions

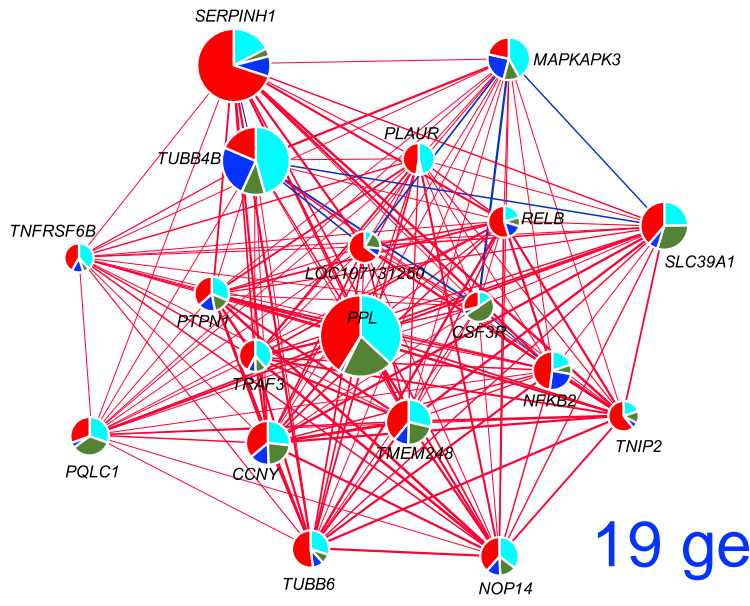
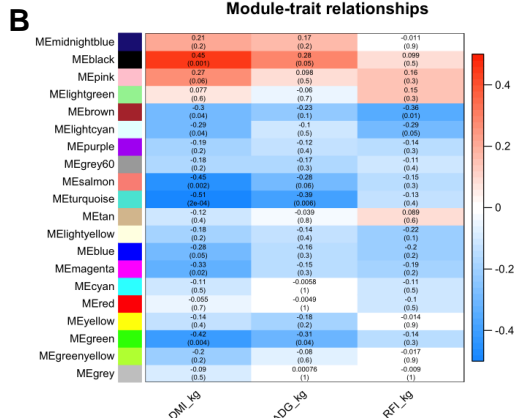
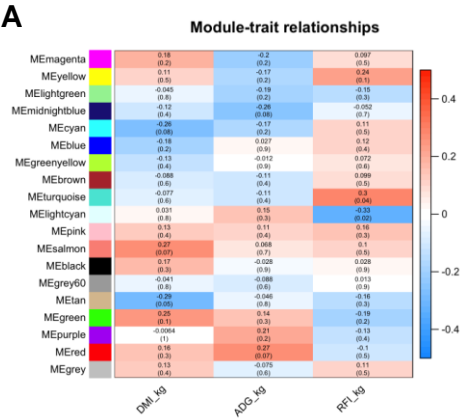


KLKs family--epithelial
DUOX family--immune

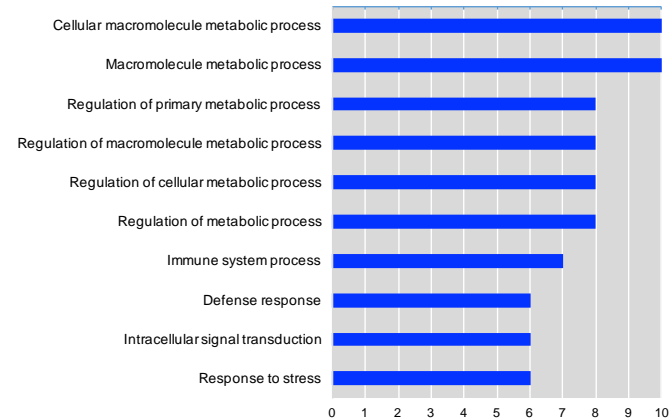
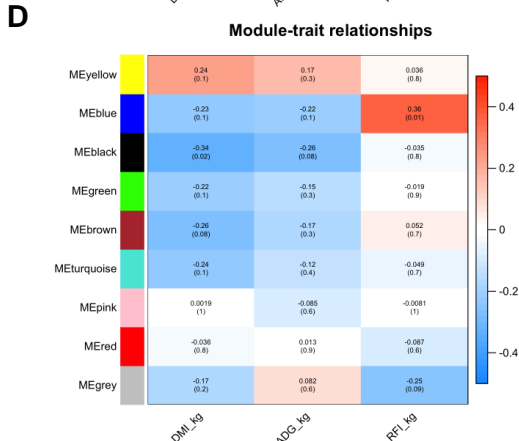
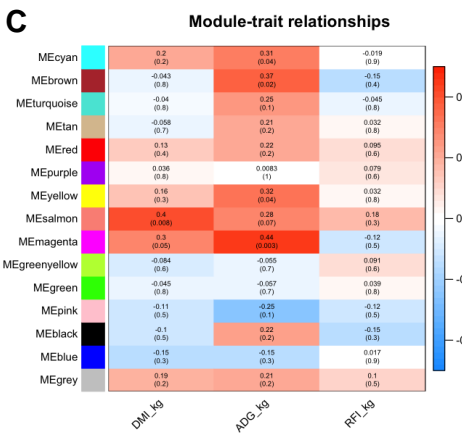
Gene networks of commonly expressed genes shared among four tissues



Gene marker discovery using co-expression analysis



19 genes



Summary

- This study exhibited the global gene expression landscapes of rumen, liver, muscle, and backfat tissues in beef cattle:
 - tissue unique functions
 - reference resources for cattle functional genomics, breeding, and biology mechanism for other production traits
- New insights and perspectives on the genetic basis of feed efficiency in beef cattle
 - 19 generic gene markers across different tissues correlated for molecular selection panel (validation in progress)

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Original Paper

OXFORD

Gene expression

Landscape of multi-tissue global gene expression reveals the regulatory signatures of feed efficiency in beef cattle

5  Hui-Zeng Sun¹, Ke Zhao^{1,2}, Mi Zhou¹, Yanhong Chen¹ and Le Luo Guan^{1,*}

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<https://www.cattleomics.com/>

Functions of potential gene marker for feed efficiency

<i>SERPINH1</i>	Collagen metabolism
<i>NOP14</i>	Pre-18S rRNA processing and small ribosomal subunit assembly
<i>PPL</i>	A link between the cornified envelope and desmosomes
<i>TMEM248</i>	Membrane proteins
<i>CCNY</i>	Control cell division cycles and regulate cyclin-dependent kinases
<i>NFKB2</i>	Transcription factor and involved in inflammation and immune function
<i>PTPN1</i>	Insulin receptor signaling pathway
<i>SLC39A1</i>	A major endogenous zinc uptake transporter
<i>PLAUR</i>	Plays a role in localizing and promoting plasmin formation
<i>CSF3R</i>	Cytokine receptor activity
<i>TRAF3</i>	Negative regulation of NF-kappaB transcription factor activity
<i>TNIP2</i>	Positive regulation of I-kappaB kinase/NF-kappaB signaling
<i>MAPKAPK3</i>	Stress-activated serine/threonine-protein kinase
<i>PQLC1</i>	
<i>TUBB4B</i>	GTPase activity and structural constituent of cytoskeleton
<i>TNFRSF6B</i>	
<i>RELB</i>	NIK/NF-kappaB signaling
<i>TUBB6</i>	GTPase activity and structural constituent of cytoskeleton
<i>LOC107131250</i>	Transcription factor and involved in inflammation and immune function