

Discover potential regulatory mechanisms involved in rumen functional changes under high grain diet

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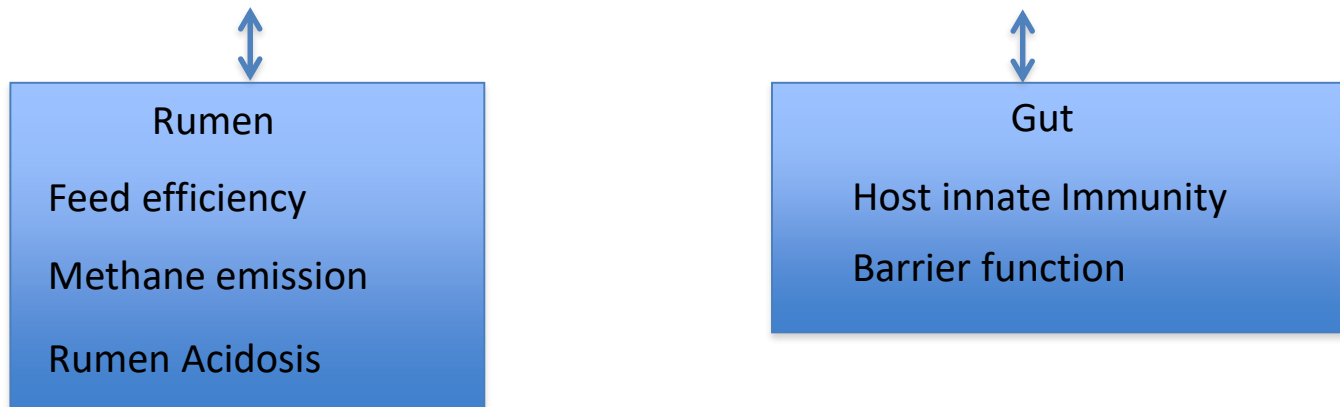
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EAAP 69th Annual Meeting, Dubrovnik, Croatia

Functional Genomics and Microbiology at University of Alberta

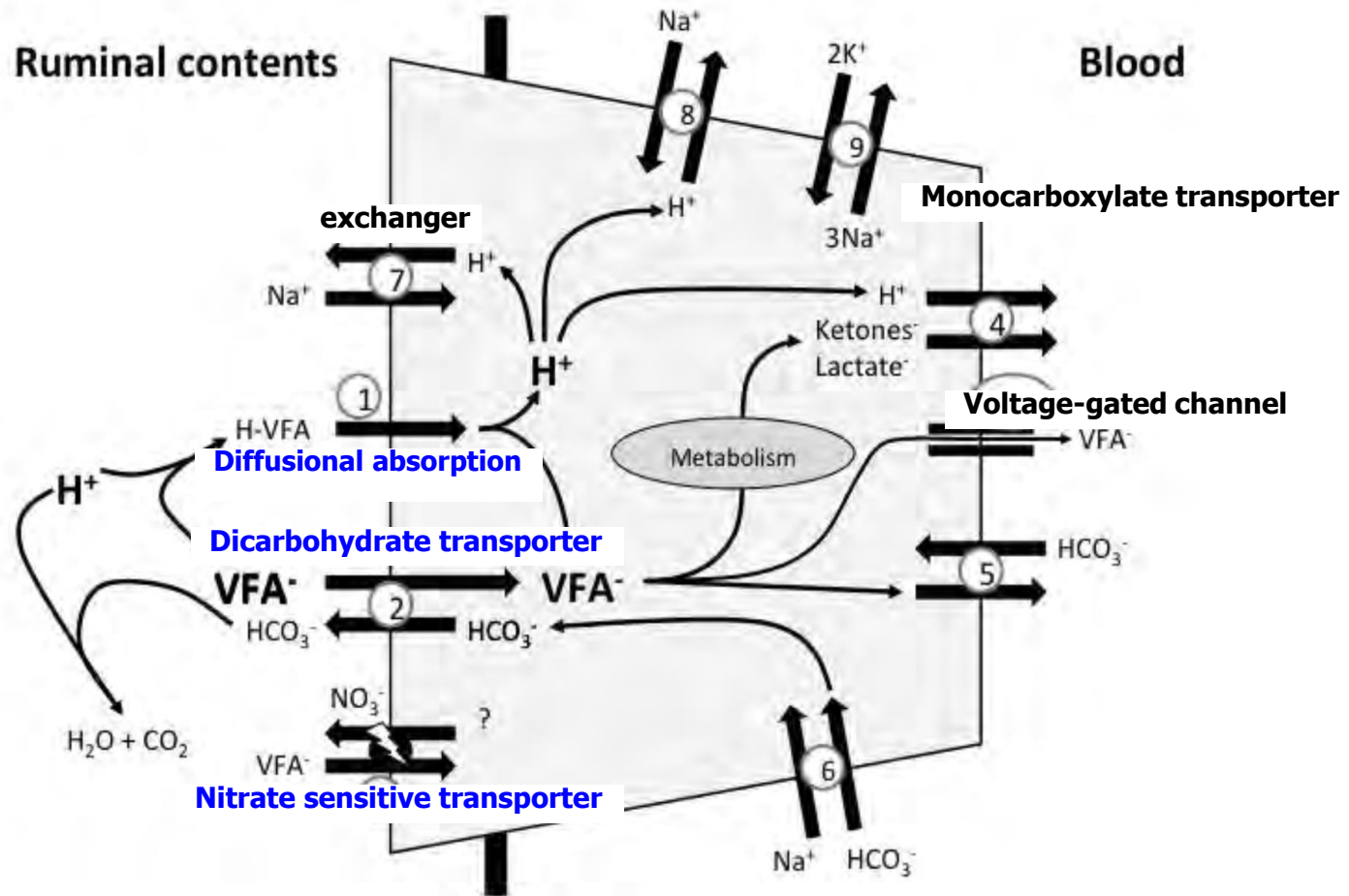
Molecular profiling of microbial community
Metagenomics, metatranscriptomics of gut microbiome
Host transcriptome and microRNA profiling
Metabolomics



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

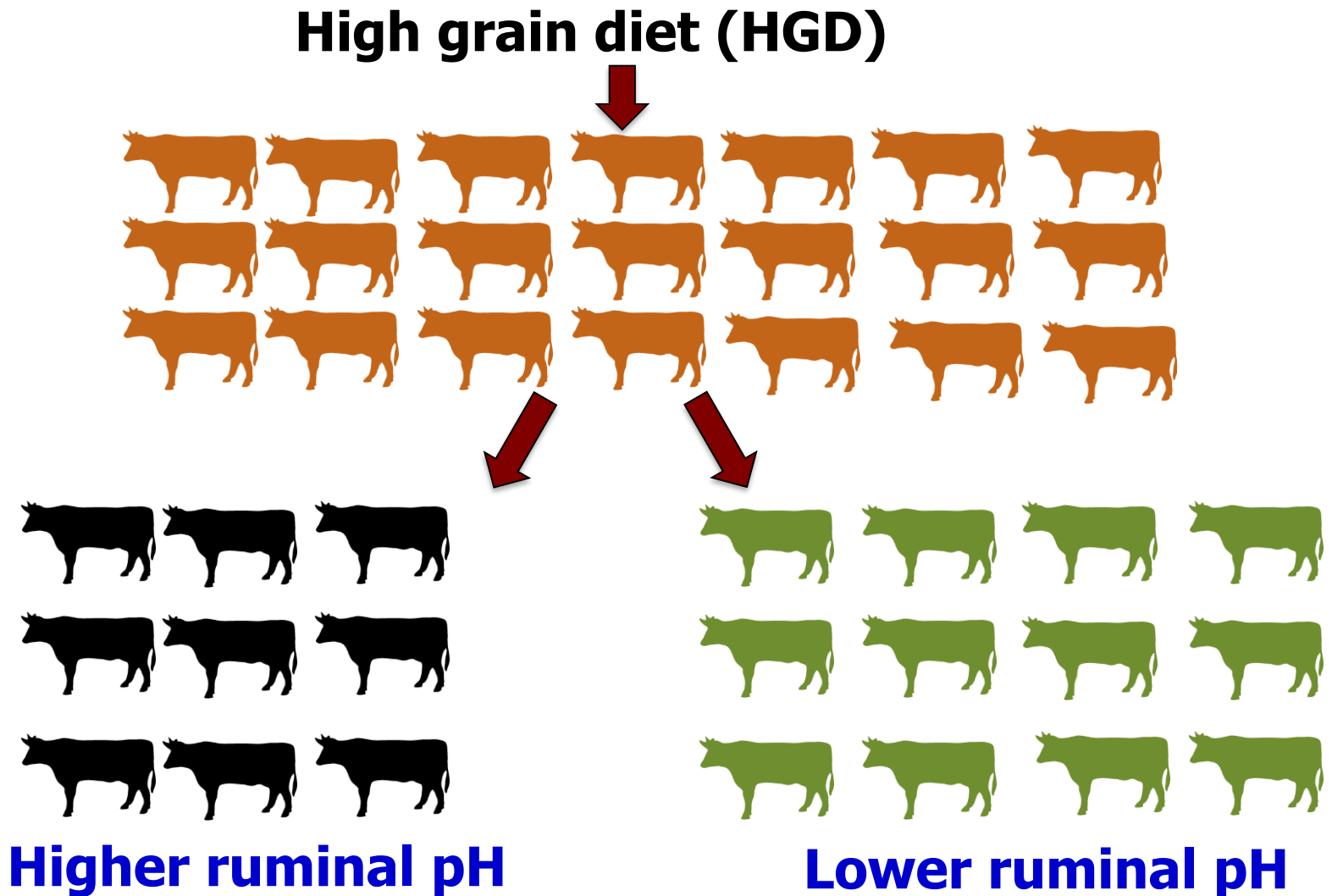
Ruminal epithelium – SCFA absorption and metabolism

- SCFA absorption accounted for up to 53% of the ruminal buffering capacity



(Gäbel *et al.*, 1991; Penner *et al.*, 2009; Aschenbach *et al.*, 2011; Schlau *et al.*, 2012; Steele *et al.*, 2012)

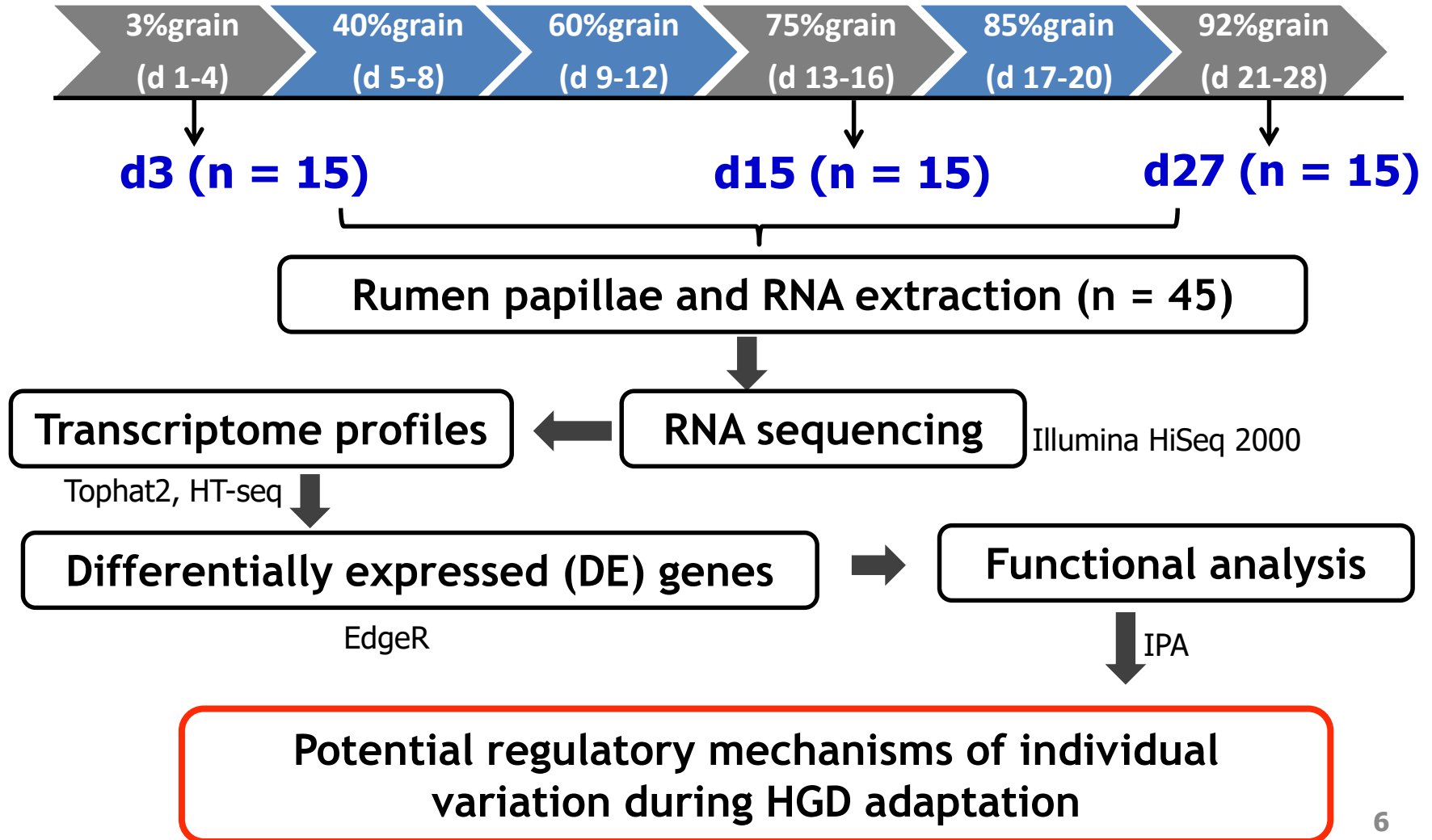
Distinct individual variation – adapt to HGD



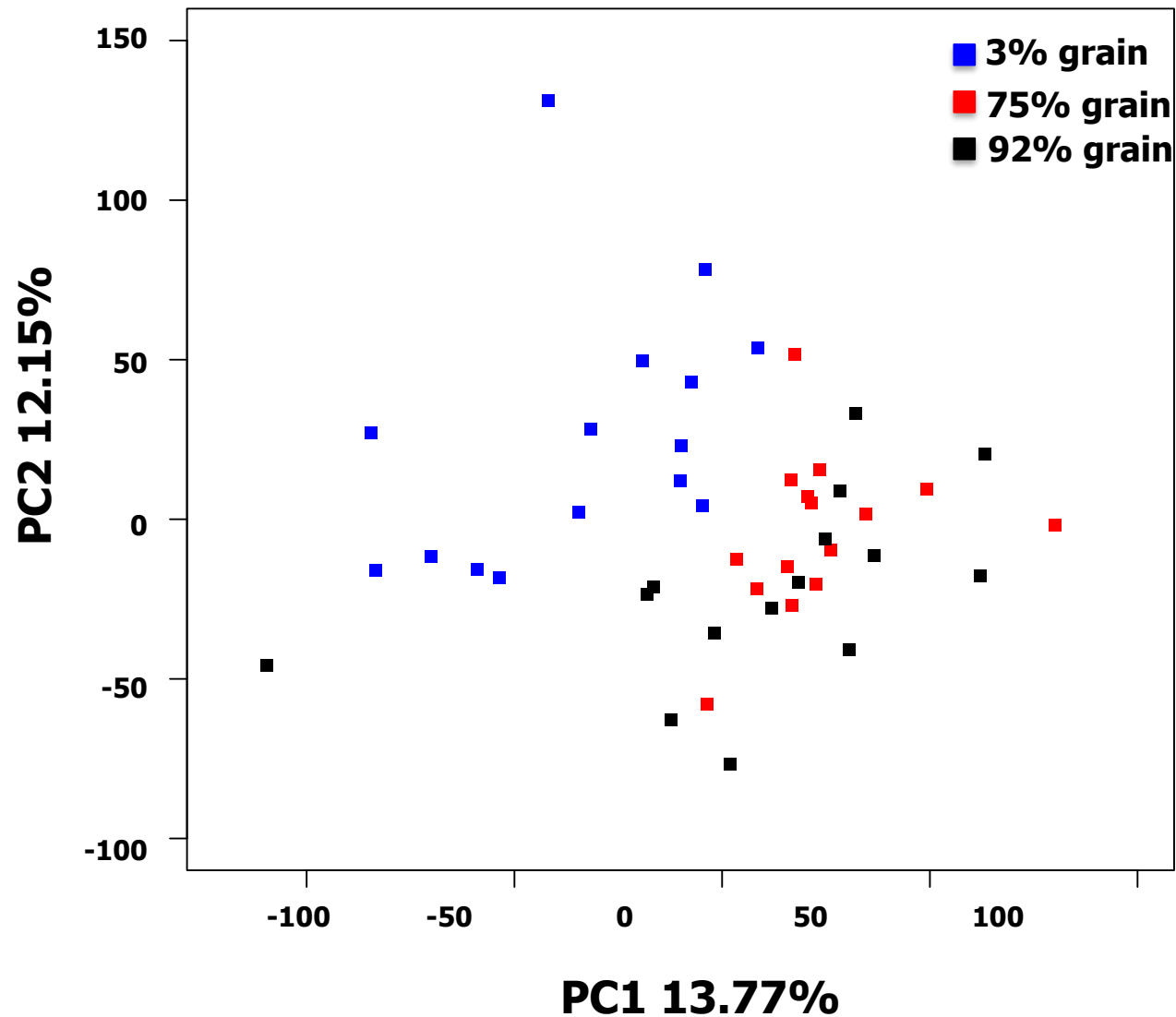
Hypothesis and objectives

- Hypothesis
 - The HGD change gene expression at whole transcriptome level
 - Individual variation during HGD adaptation can be explained by transcriptome variation of ruminal epithelium
- Objectives
 - To characterize transcriptome of ruminal epithelia during HGD transition using RNA-seq
 - To compare ruminal epithelia transcriptomes focusing on the difference of individual adaptation

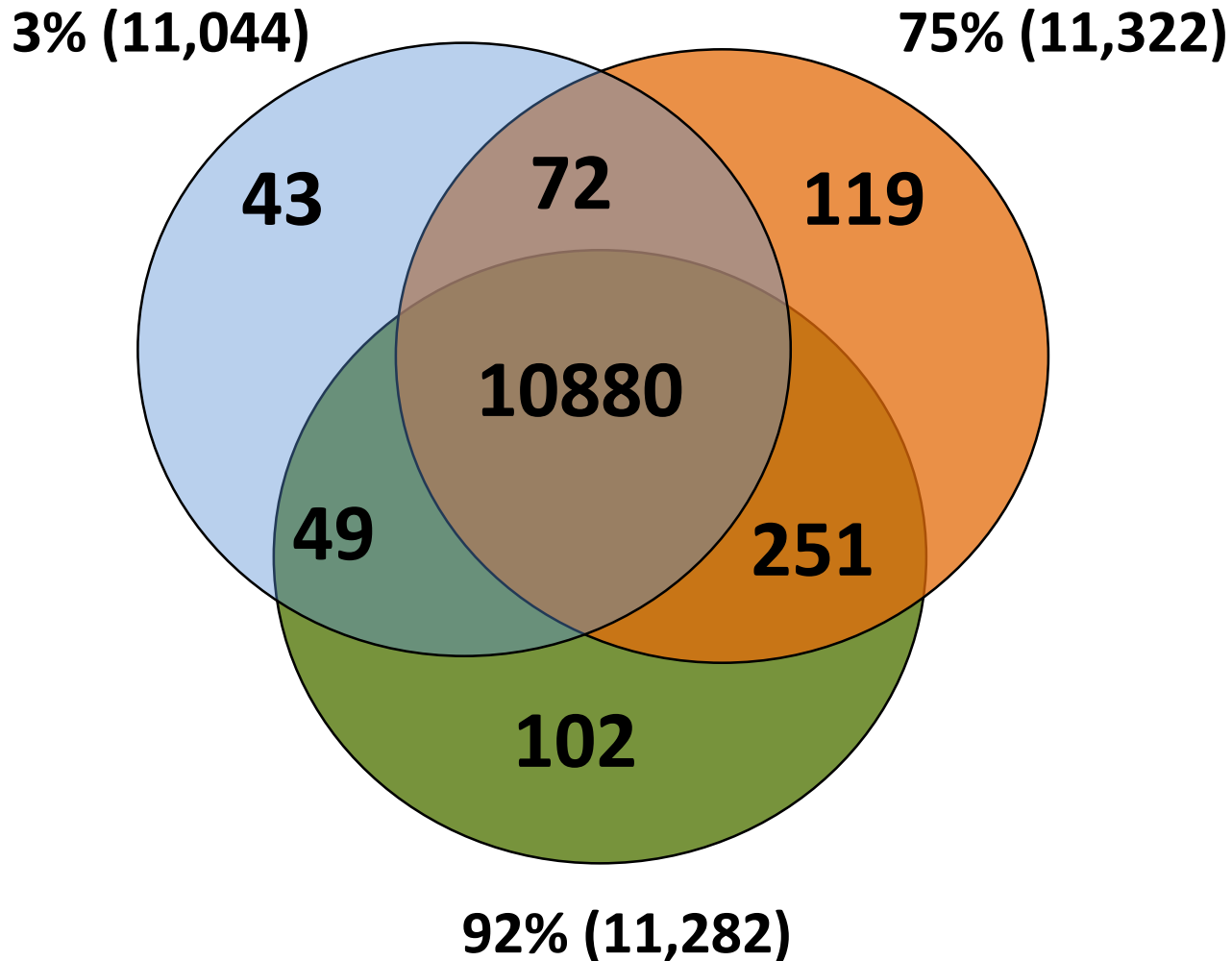
Experimental design



Transcriptome profiling under different grain diets

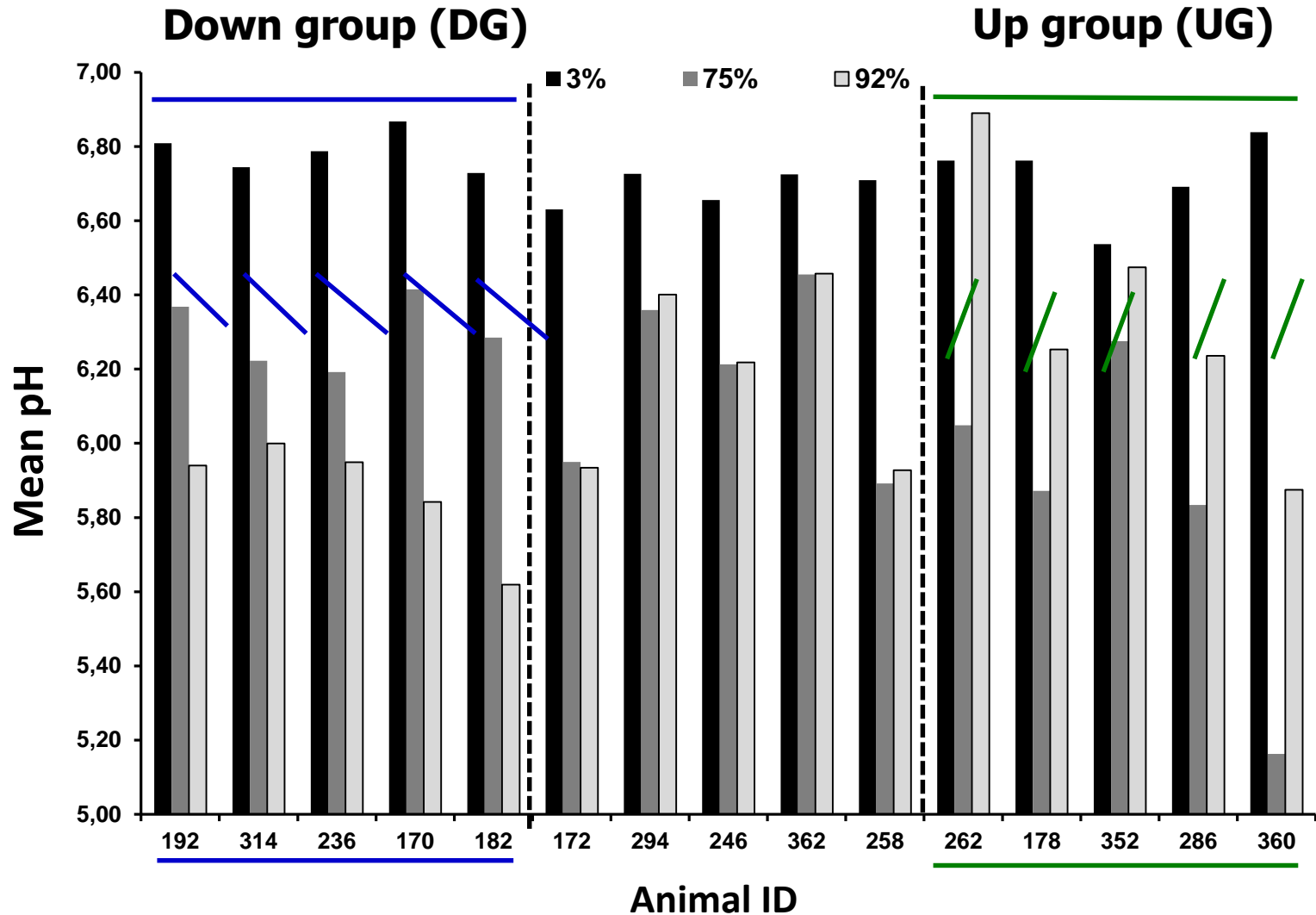


Dietary grain concentration affected transcriptome profile

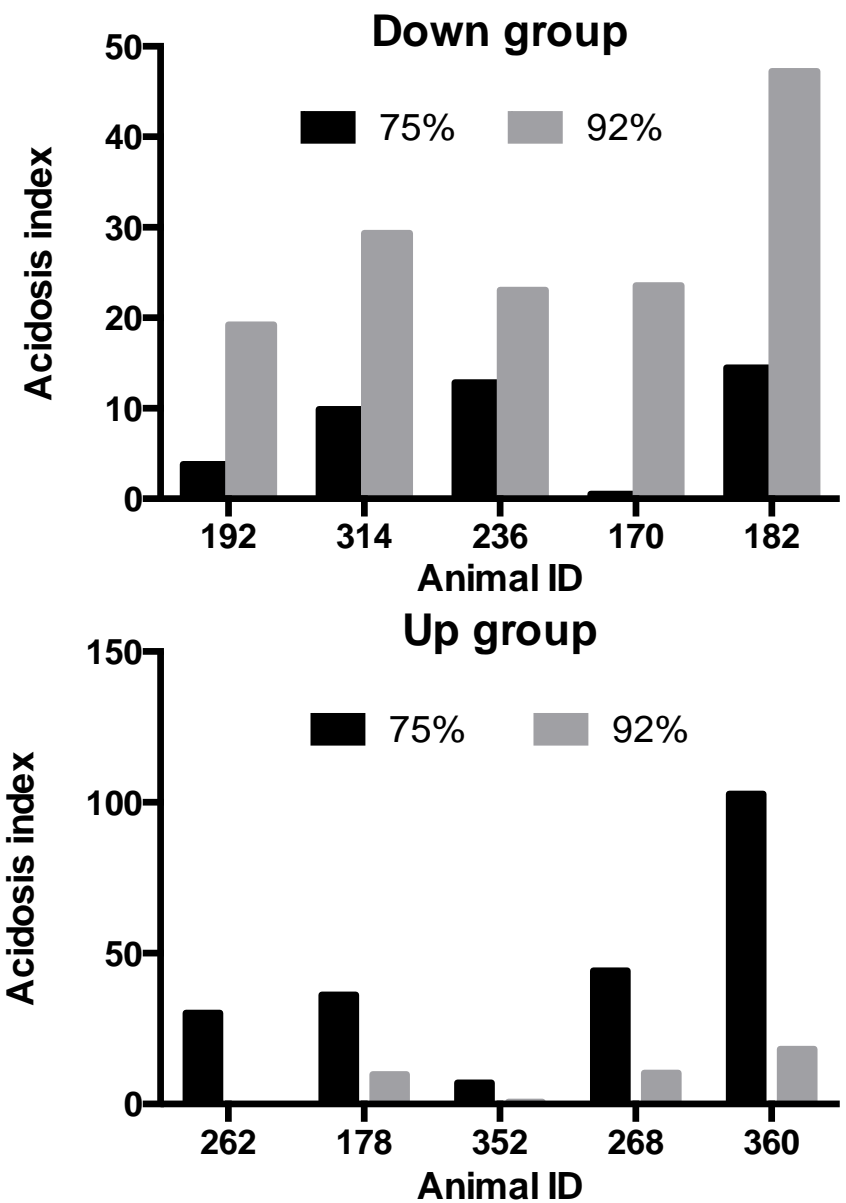


- The genes with reads per million (RPM) > 1 in 15 out of 15 cattle in at least 1 diet

Different pH trend during dietary adaptation

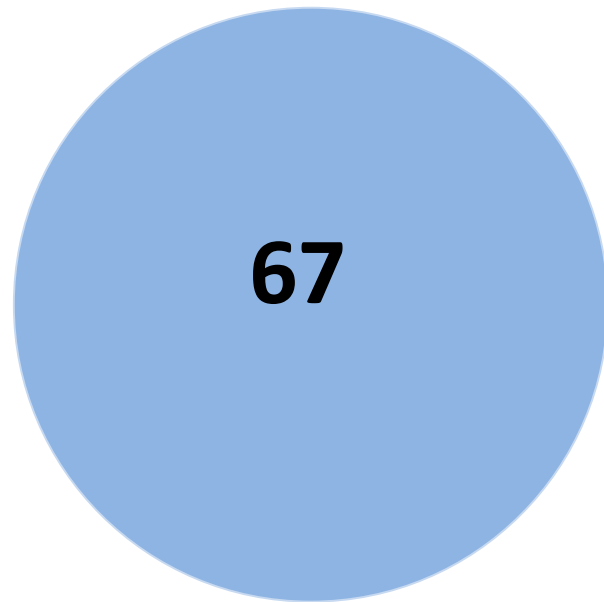


Acidosis index showed similar result with ruminal pH



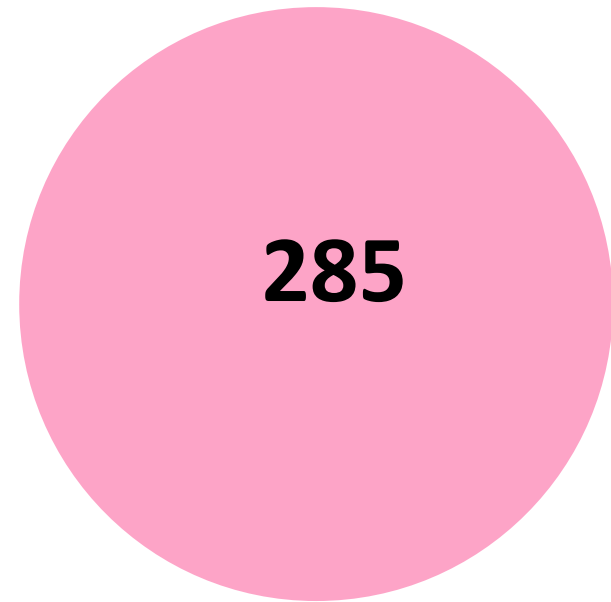
More DE genes were found in UG heifers

DG (92% vs.75%)



**22-up regulated
45-down regulated**

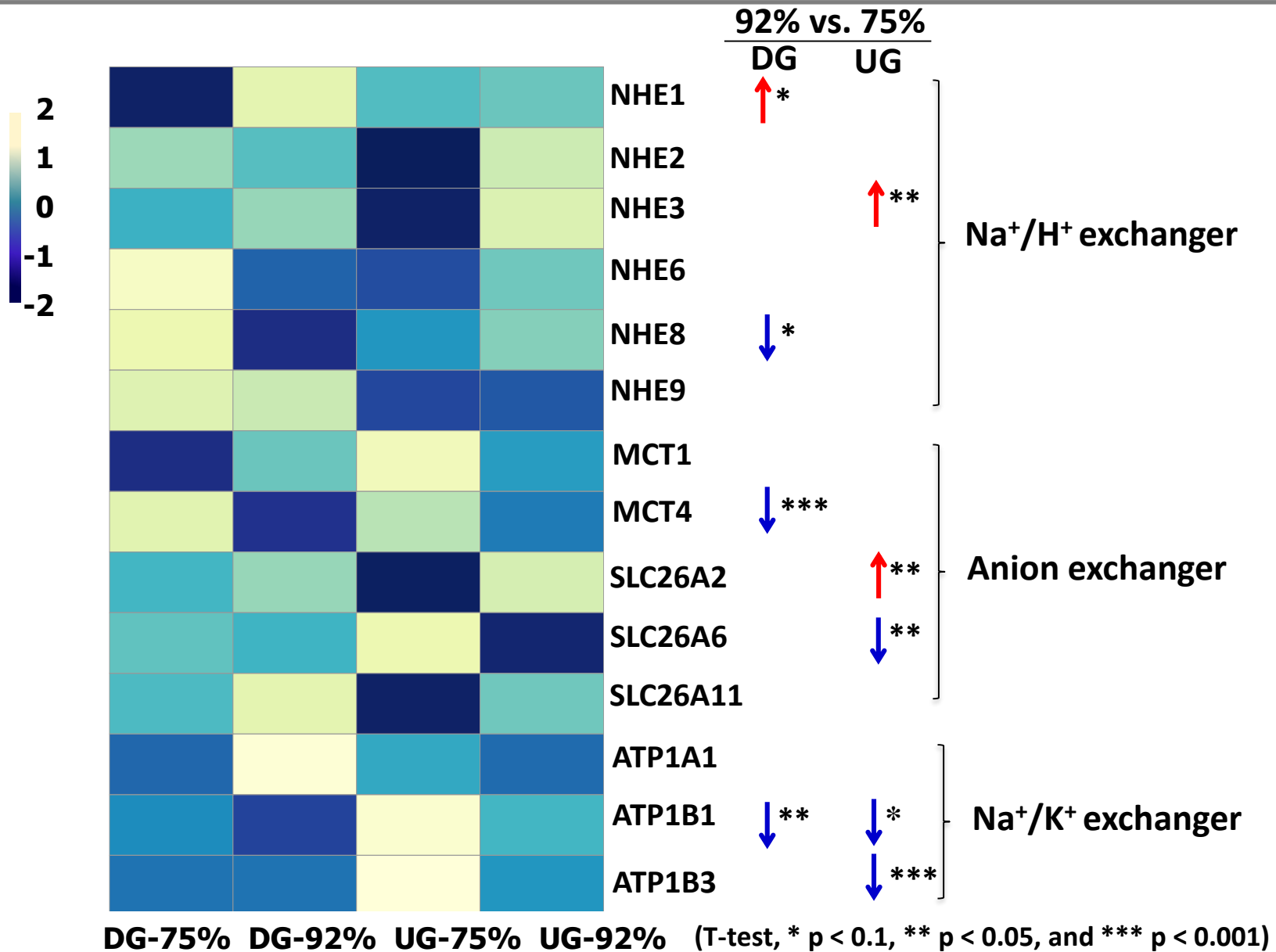
UG (92% vs. 75%)



**122-up regulated
163-down regulated**

- (RPM >1 in 5 out of 5 cattle in at least 1 diet, FC >1.5 or < -1.5 and FDR <0.05)

Intracellular pH was differentially regulated in DG and UG



Lipid metabolism was differently regulated in DG and UG

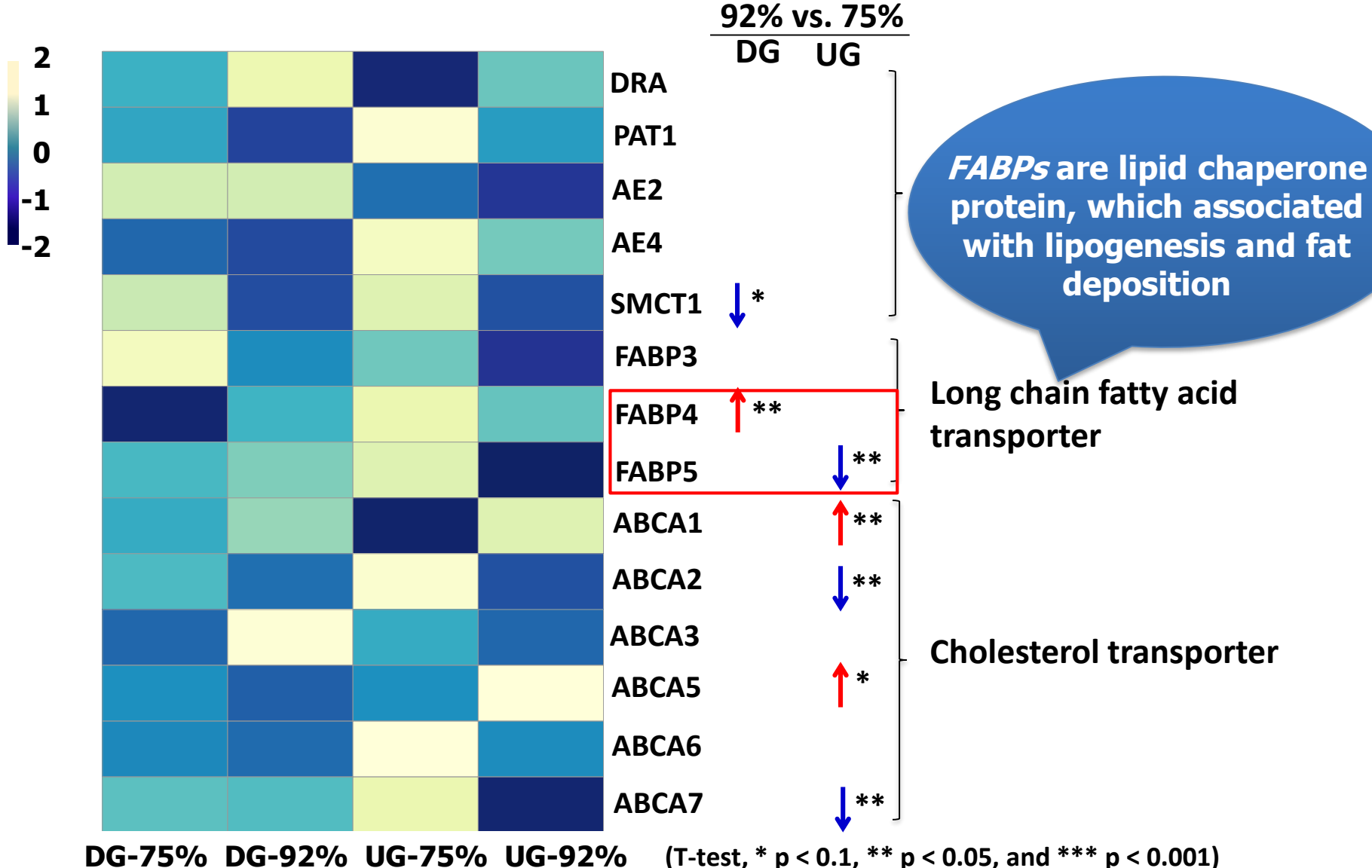
Top two functions of Up-regulated genes in DG

Diseases or Functions Annotation	P-Value	Z-score	Molecules
Up-regulated genes (n = 22)			
Concentration of lipid	9.29E-03	1.94↑	6
Concentration of triacylglycerol	9.29E-03	1.70↑	4

Top two functions of Up-regulated genes in UG

Diseases or Functions Annotation	P-Value	Z-score	Molecules
Up-regulated genes (n = 122)			
Storage of lipid	3.85E-03	-2.00↓	5
Oxidation of lipid	1.09E-02	2.00↑	7

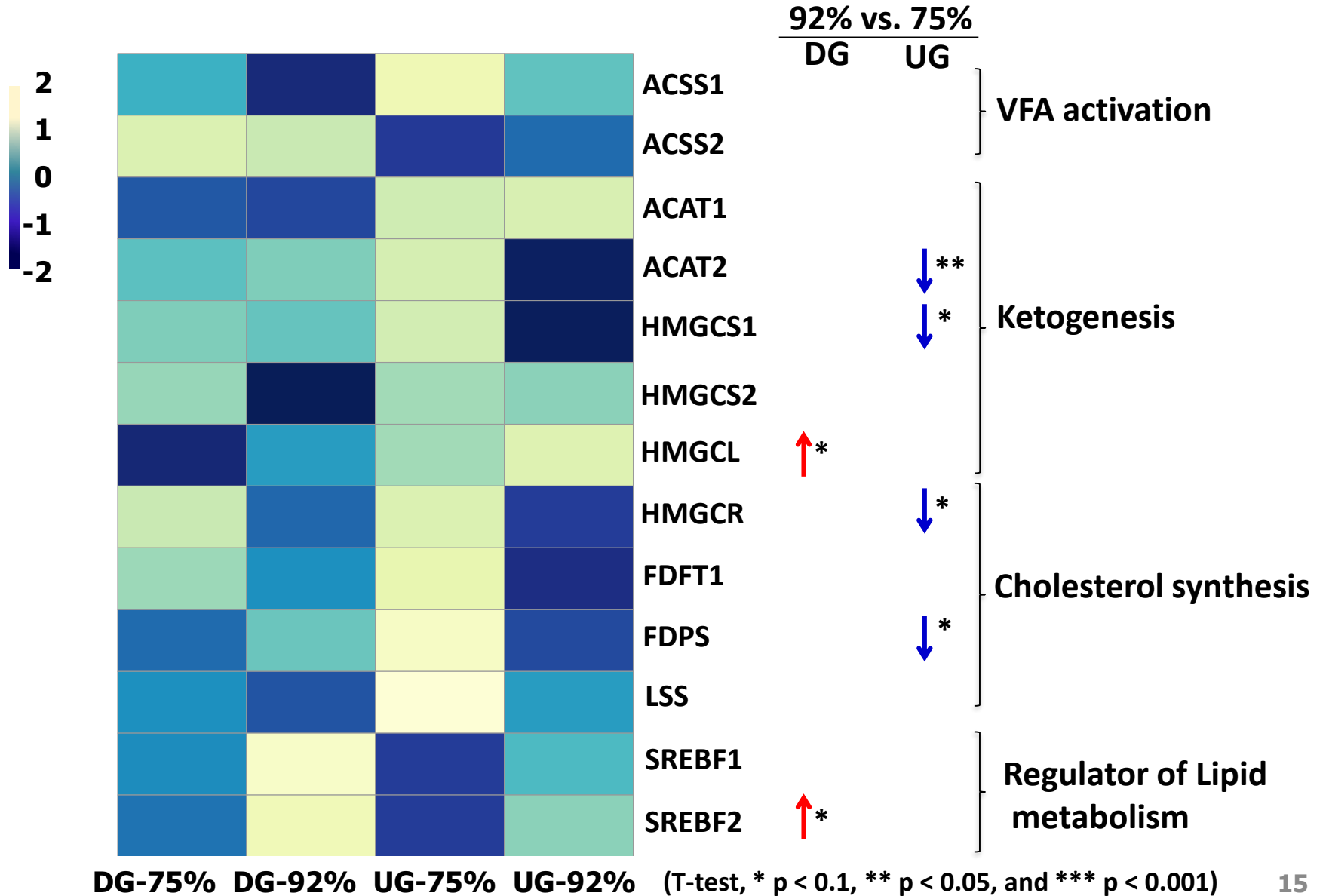
Expression of FABP4 increased in DG, FABP5 decreased in UG



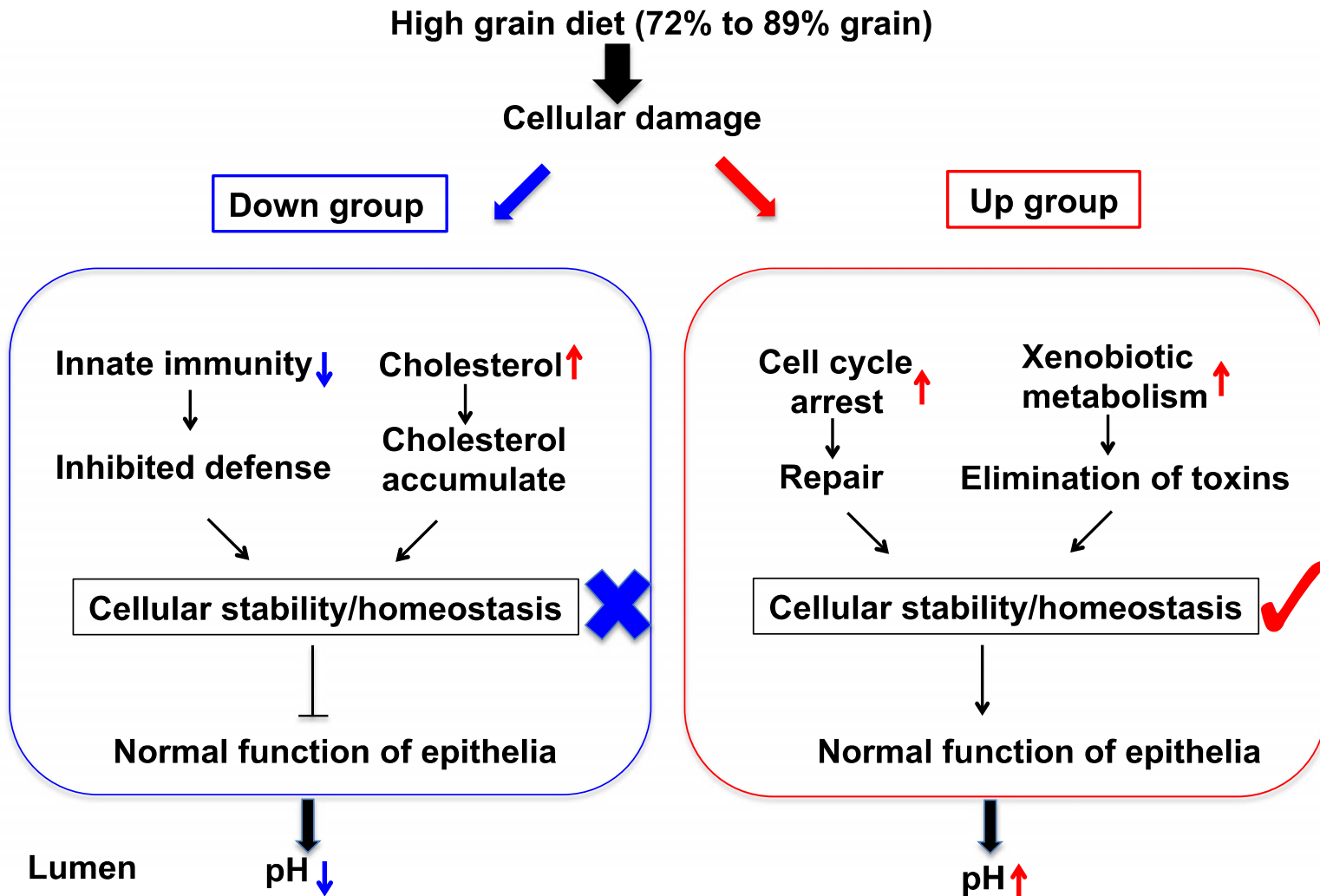
(T-test, * p < 0.1, ** p < 0.05, and *** p < 0.001)

(Specht et al., 1996; Hertzell et al., 2006; Michal et al., 2006)

Expression of ketogenesis and cholesterol synthesis related genes was increased in DG but decreased in UG



Summary



Summary

- **Dietary grain concentration affected gene expression of ruminal epithelium at whole transcriptome level**
- **Transcriptional regulation of lipid transport, fatty acid metabolism, and intracellular homeostasis might be the molecular mechanism accounting for individual variation during the diet transition to a high grain diet**
- **The identified genes could be potential gene markers for selecting cattle with maintained ruminal pH through a diet transition to a high grain diet**

RESEARCH ARTICLE

Open Access

Transcriptome analysis of ruminal epithelia revealed potential regulatory mechanisms involved in host adaptation to gradual high fermentable dietary transition in beef cattle



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Acknowledgement

All the co-authors

Dr. K. Zhao (Shanxi Normal University)

Dr. M. Oba (University of Alberta)

Dr. G. Penner (University of Saskatchewan)

All the members in my lab



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Alberta Livestock
and Meat Agency Ltd.



**NSERC
CRSNG**