

Changes in meta-transcriptome of rumen epimural microbial community and liver transcriptome in young calves with feed induced acidosis

Wenli Li¹, Sonia Gelsinger², Andrea Edwards¹ Christina Riehle³ and Daniel Koch⁴

¹The Cell Wall Utilization and Biology Laboratory, US Dairy Forage Research Center, USDA ARS, Madison, WI, 53706, USA

²Department of Dairy Science, University of Wisconsin-Madison, Madison, WI, 53706, USA

³Department of Genetics, University of Wisconsin-Madison, Madison, WI, 53706, USA

⁴Department of Computer Engineering, University of Wisconsin-Madison, Madison, WI, 53706, USA

Correspondence author: wenli.li@ars.usda.gov

Supplemental Dataset 1. The distribution of FPKM values.

Supplemental Dataset 2. Differentially expressed genes in the liver.

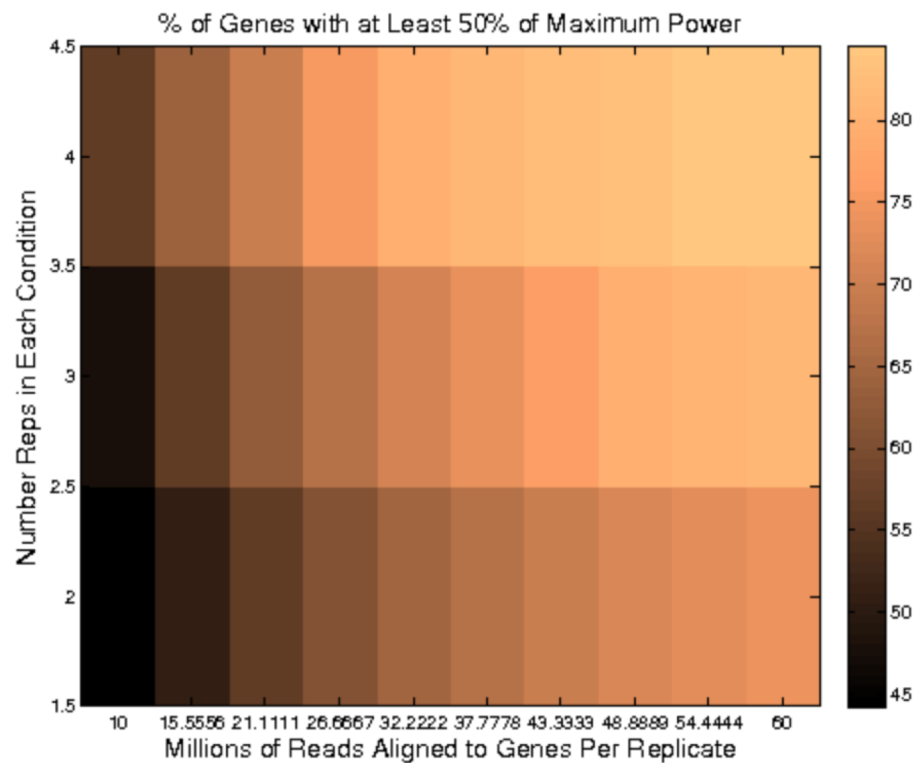
Supplemental Dataset 3. log2FC_all_GO_genes.

Supplemental Dataset 4. a.) Liver genes with positive correlation with the rumen epithelial microbial genus. **b.)** Genes involved in transferase activity and their positively correlated genera.

Supplemental Dataset 5. Liver genes with negative correlation with the rumen epithelial microbial genus.

Supplemental Figure 1. RNA-seq power analysis. Power analysis using Scotty indicated that: **A.** with an average of 60M reads and four replicates per treatment condition, one can achieve the power of identify 85% of the genes with at least 50% maximum power. And **B.** with this experiment design, one can identify 65% of the genes with at least 1.5X fold-change, 85% of the genes with at least 2X fold-change and 95% of the genes with at least 3X fold-change.

A.



B.

