

# THE EFFECT OF PRODUCTION SYSTEMS ON ADIPOSE TISSUE GENE EXPRESSION IN KRŠKOPOLJE PIG

## OBJECTIVE

Transcriptomic characterization of adipose tissue of the local breed Krškopolje pig kept indoors (IND) and outdoors (OUT).

## CONCLUSION

Genes involved in the inflammatory response were downregulated, and genes involved in collagen synthesis were upregulated in the IND compared with the OUT system.

## MATERIALS AND METHODS

### ANIMALS

- 48 **Krškopolje pigs**; raised **indoor** (IND; n=24) or **outdoor** (i.e. fenced open area with trees and shelter; OUT; n=24).
- Equal dietary regime.
- Slaughtered at the age of  $330 \pm 2$  days (mean  $\pm$  SE).
- Live weight (IND=183 kg, OUT=167 kg).
- Average backfat thickness (IND=44 mm, OUT=52 mm).

### RNA-SEQ and BIOINFORMATIC ANALYSIS

- **RNA-seq library** preparation of 6 pooled samples per group and sequencing on Illumina NovaSeq 6000 (150 bp paired-end reads).
- **Data analysis:** FastQC software, mapping on *Sscrofa 11.1*, hit counts calculation, differential gene expression analysis using DESeq2, gene ontology analysis using clusterProfiler R package.

## RESULTS

### RNA-SEQ DATA

- Sequencing yielded on average 66.8 million paired-end reads.
- More than 92.2% of the reads were uniquely assigned to the reference *Sscrofa11.1* genome.

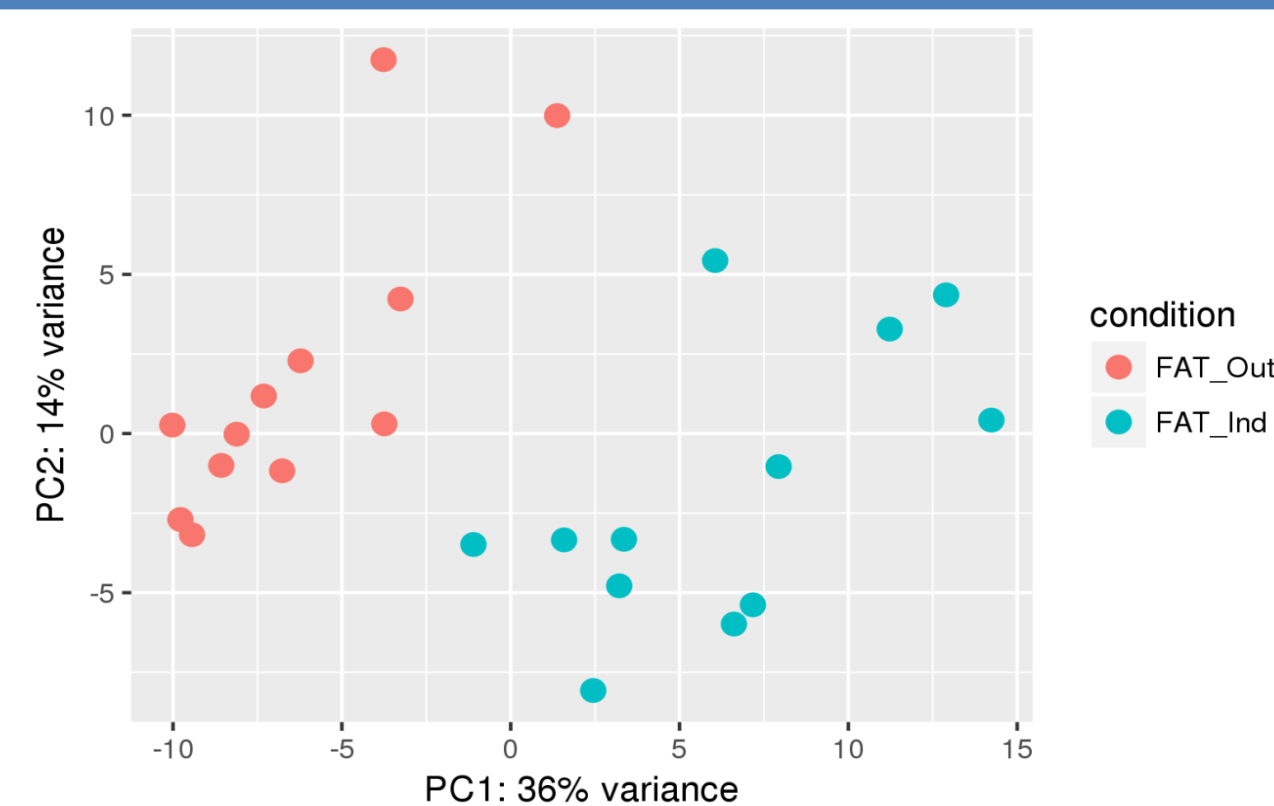


Figure 1: Sample similarity assessment.

### DIFFERENTIAL GENE EXPRESSION ANALYSIS

- **Upregulated genes in IND group:** collagen synthesis (e.g. *COL11A1*, *COL11A2*, *COL2A1*, *COL28A1*, *COL4A3*, *COL28A1*); energy homeostasis (i.e. *LEPR*).
- **Downregulated genes in IND group:** regulation of immune system and immune response (e.g. *CTLA4*, *CCL11*, *TLR8*, *CCR1*, *ICOS*); lipid metabolism (e.g. *FASN*, *ME1*, *SCD*).

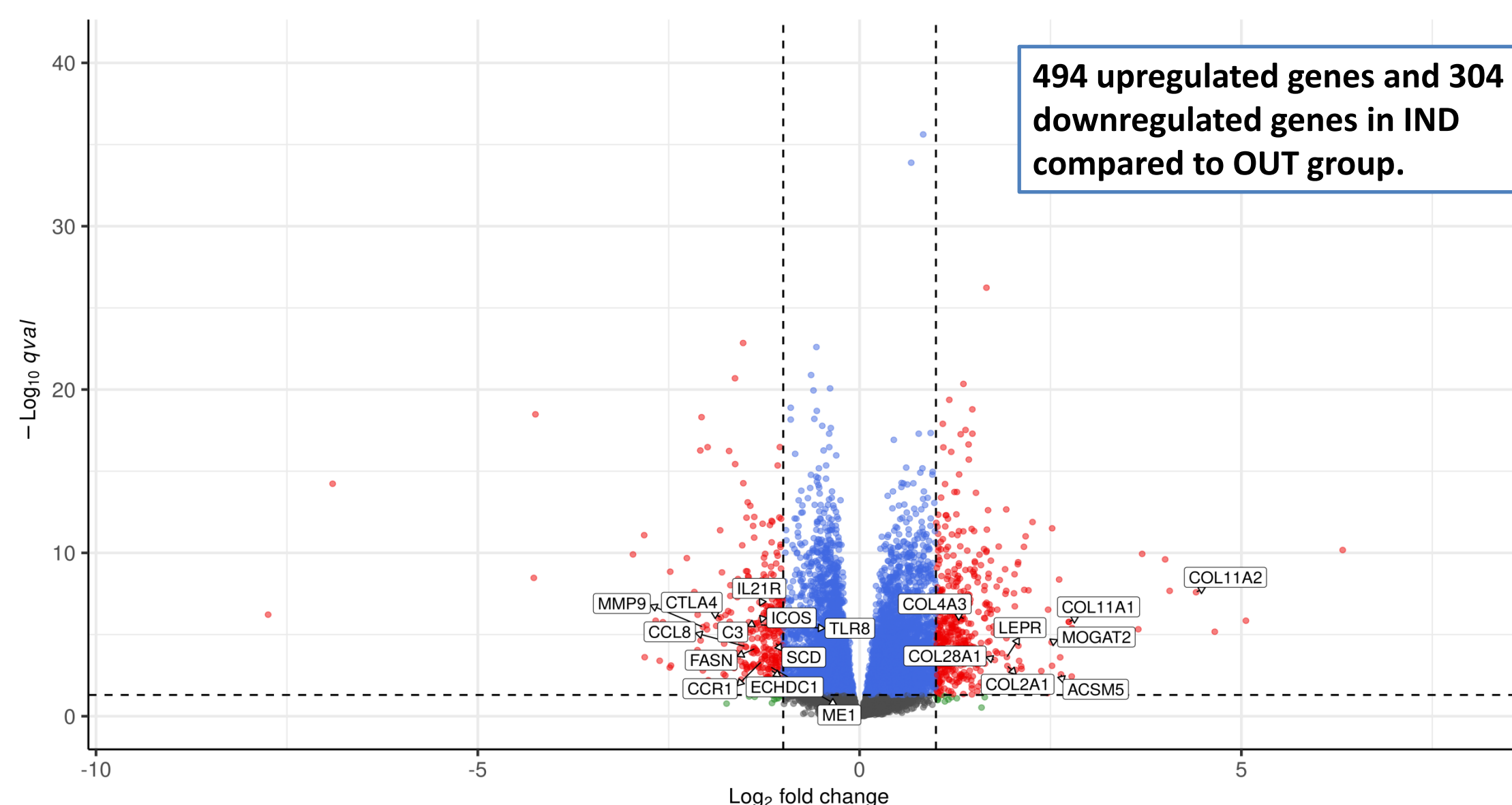


Figure 2: Volcano plot depicting genes expressed in the backfat tissue of Krškopolje pigs reared in indoor (IND) and outdoor (OUT) production systems. The horizontal lines indicate the significance threshold of differentially expressed genes at  $p$ -adjusted value of 0.05. The vertical lines represent the threshold of  $|\log_2(\text{Fold change})| > 1$ .

### GENE ONTOLOGY OVER-REPRESENTATION ANALYSIS

- No significantly enriched terms for the upregulated genes in IND compared with OUT group.
- Gene ontology terms for downregulated genes were mainly related to inflammatory response (Figure 3).

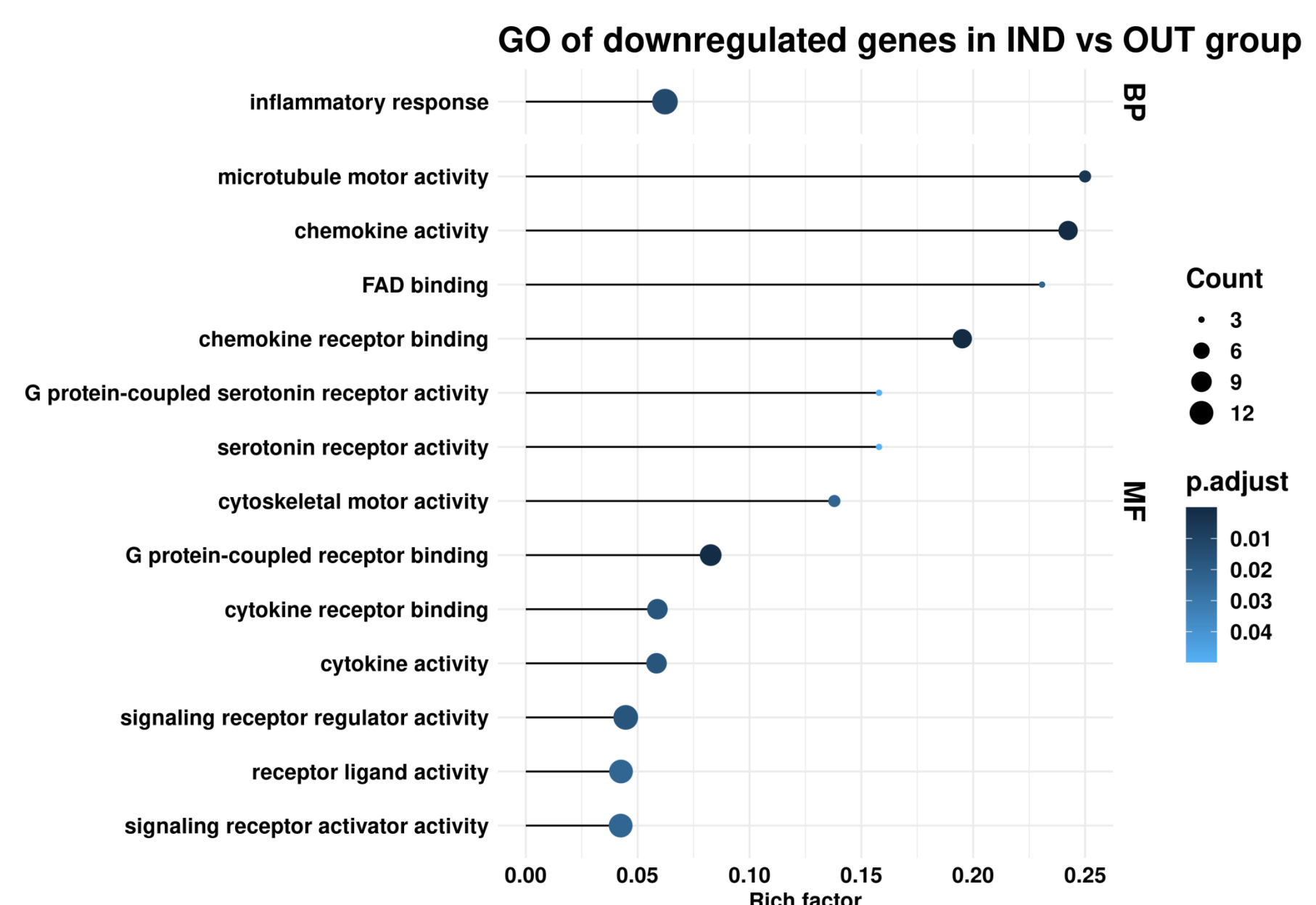


Figure 3: Gene-ontology over-representation analysis of downregulated genes in indoor (IND) compared with outdoor (OUT) group. BP = biological processes, MF = molecular functions.

### ACKNOWLEDGEMENT

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