DETERMINING DIFFERENTIAL SPLICE JUNCTION USAGE IN THE SUCKLING LAMB ADIPOSE TISSUE TRANSCRIPTOME BY COMPARING PERIRENAL AND TAIL FAT

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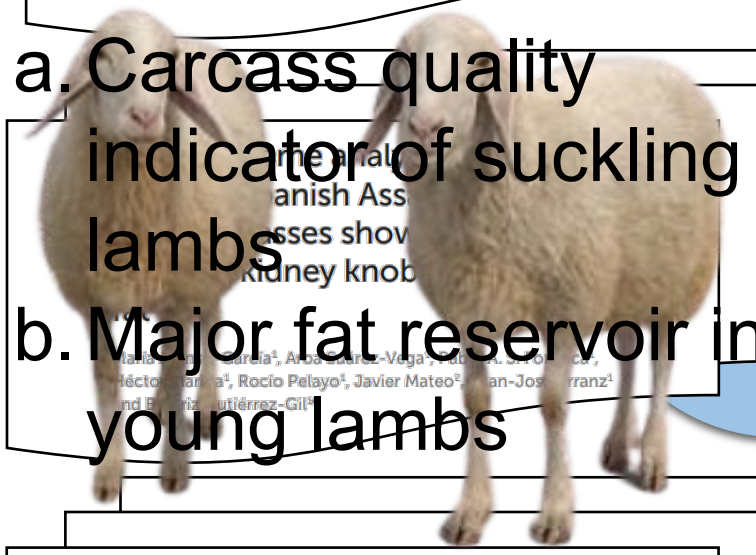
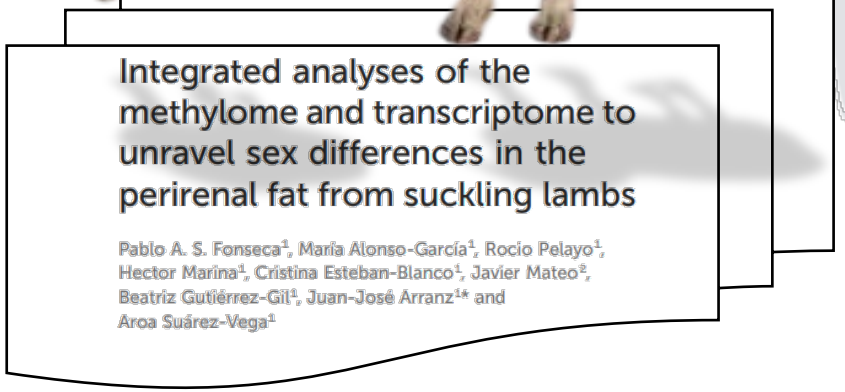
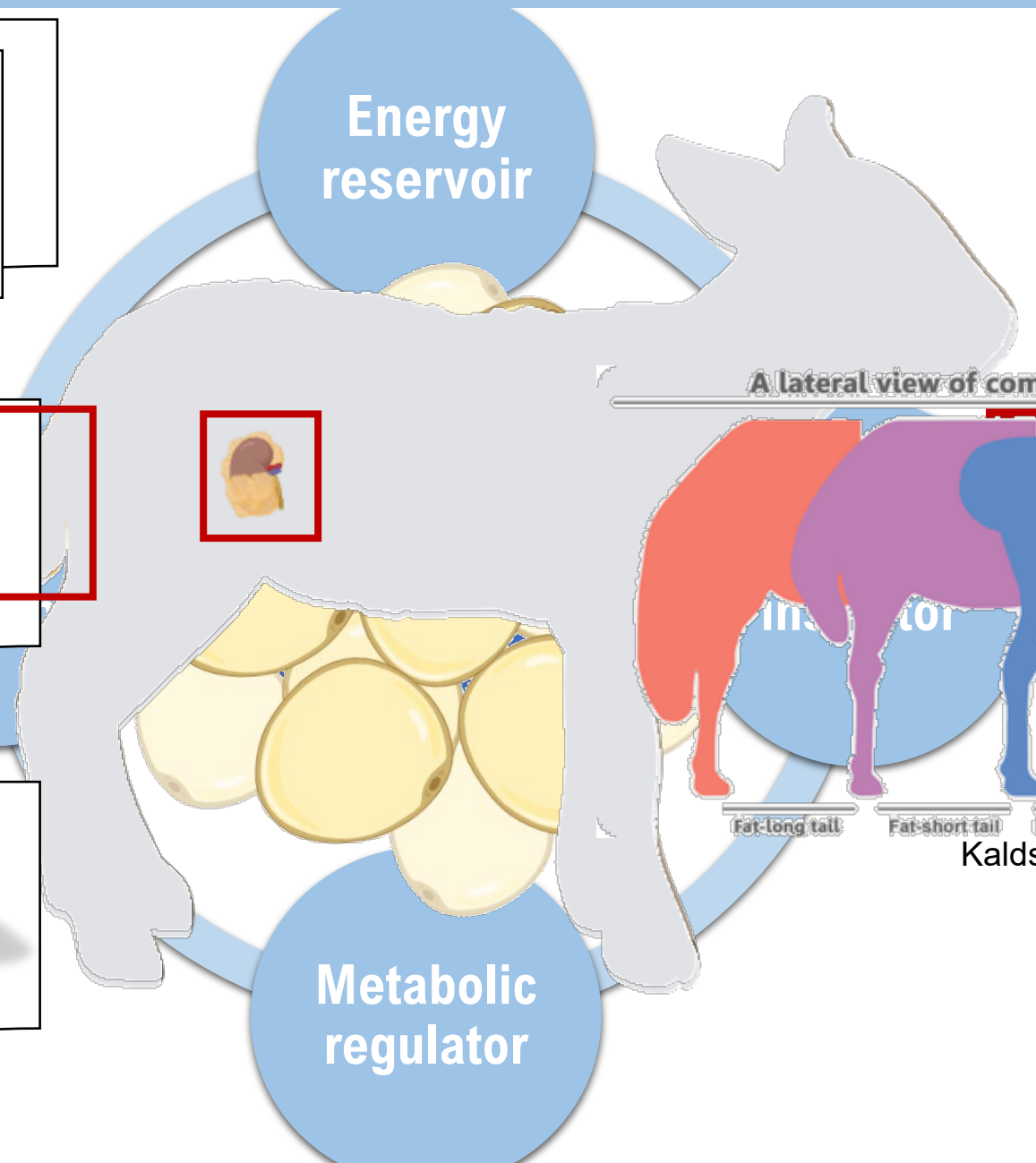
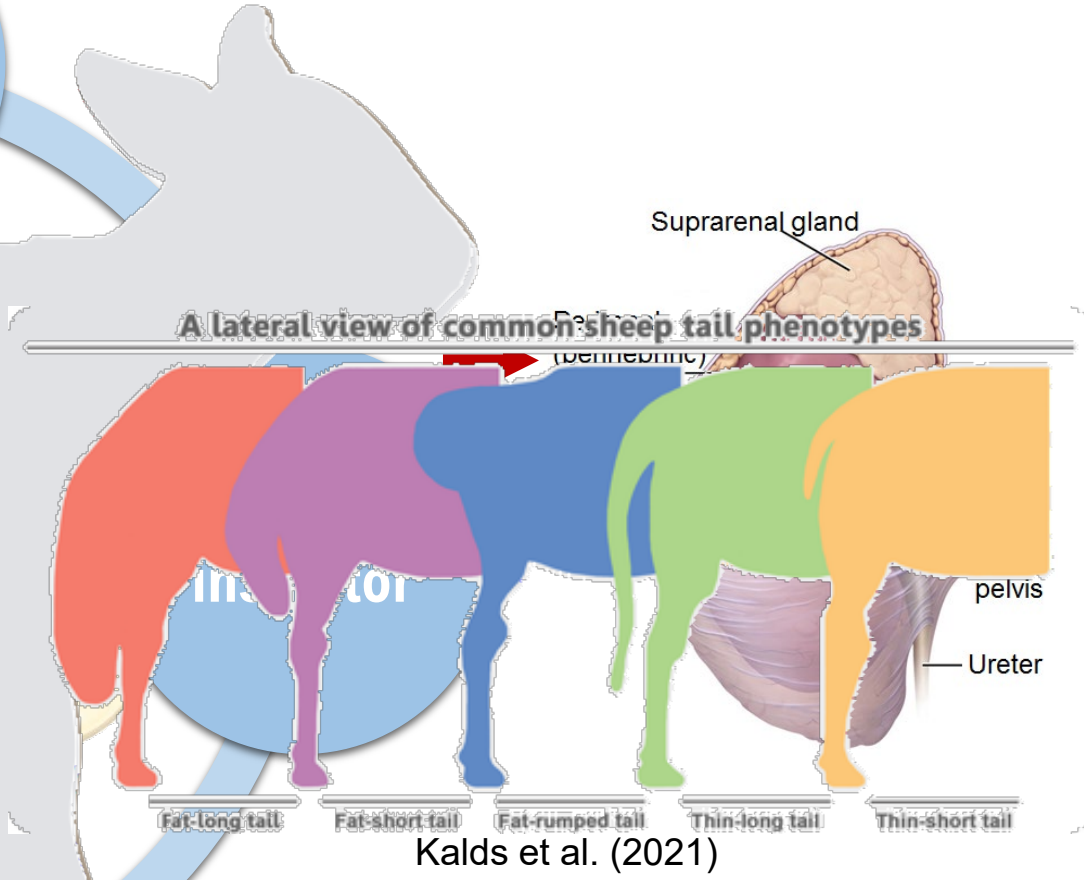
INTRODUCTION





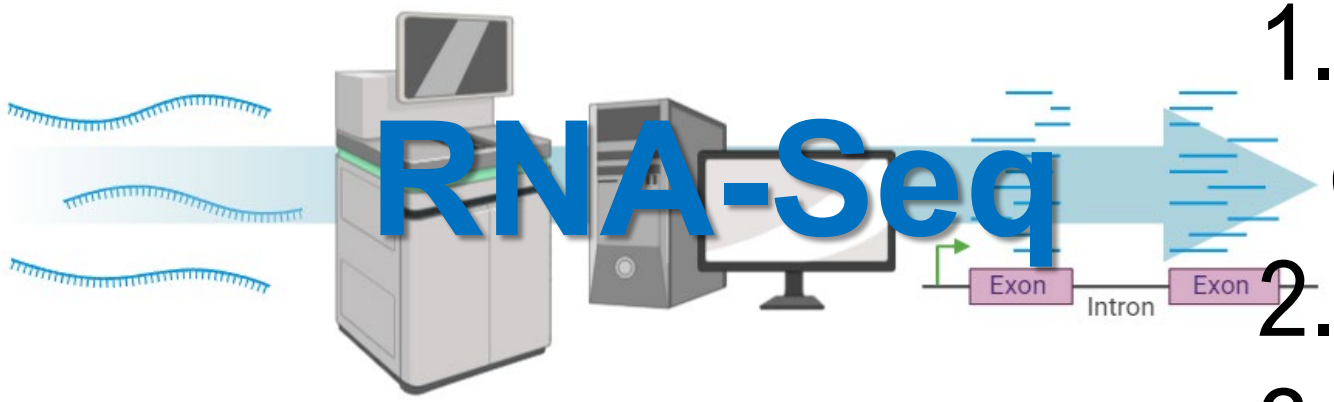
a. Carcass quality indicator of suckling lambs
b. Major fat reservoir in young lambs





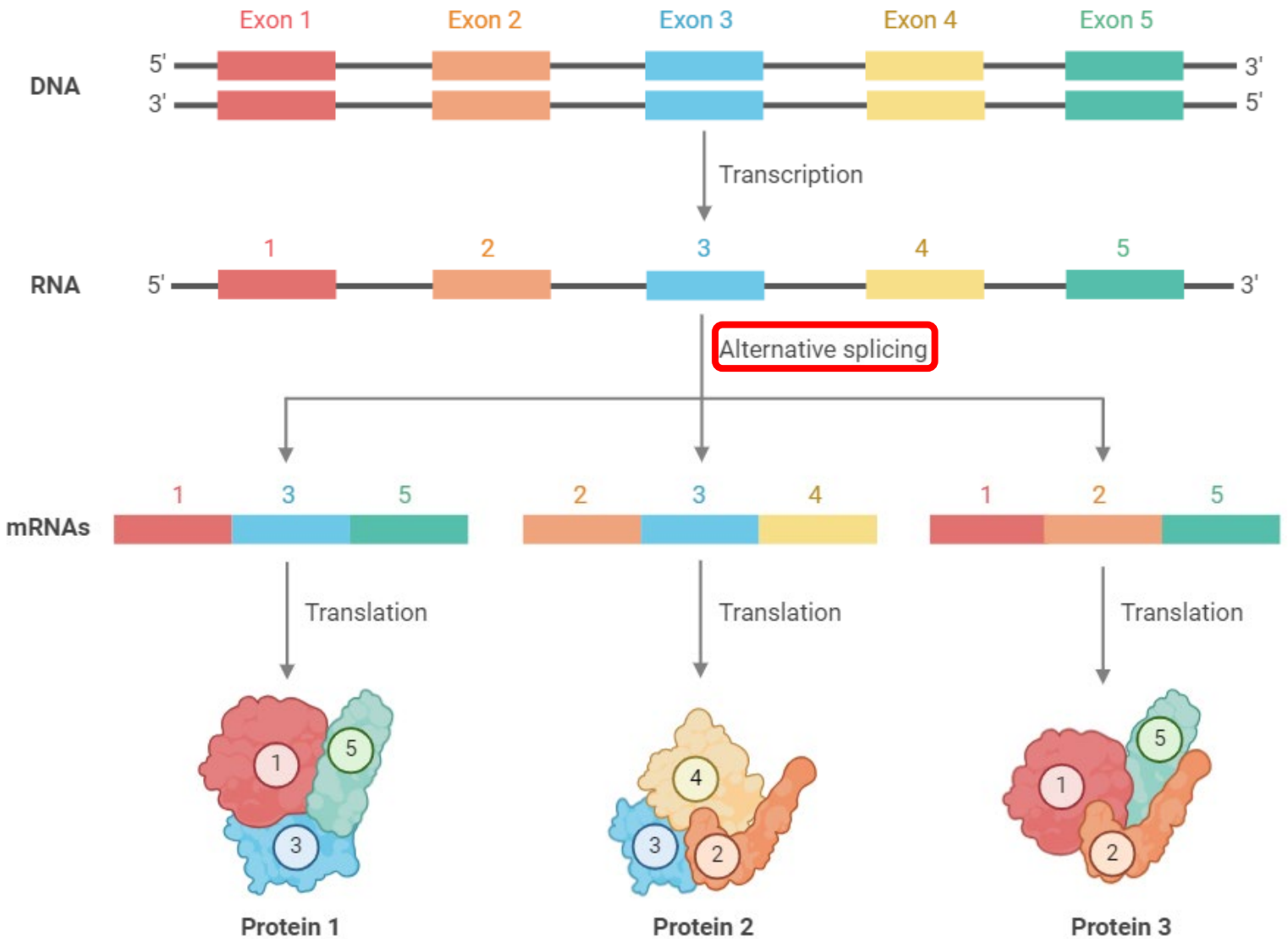
Kalds et al. (2021)

INTRODUCTION



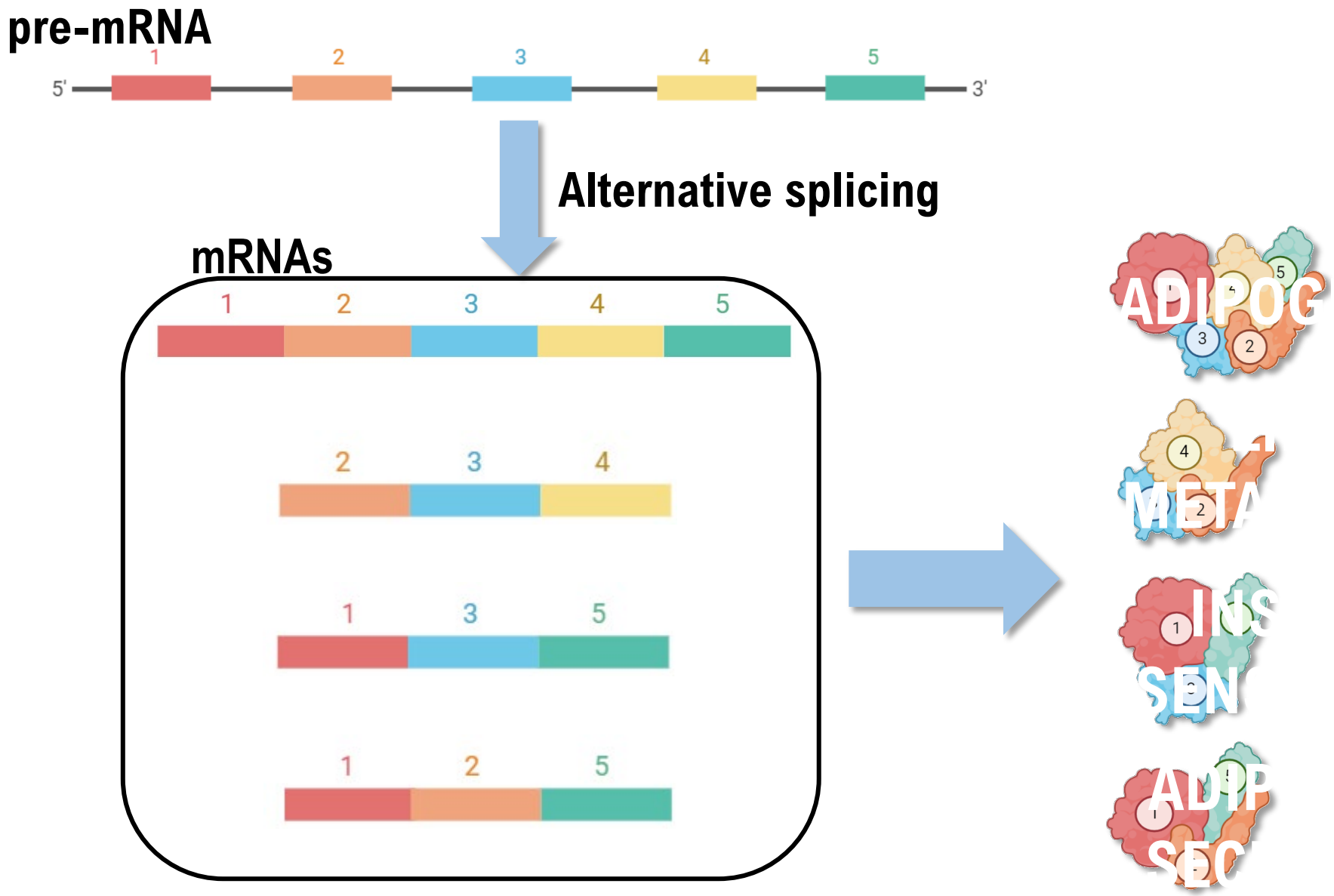
1. Quantitative measurements of **gene expression**
2. Detection of **lncRNAs**
3. Identification of **alternative splicing events**

INTRODUCTION



Alternative splicing (AS) is a **fundamental biological process** that regulates **gene expression** and increases **protein diversity** by producing **tissue-specific protein isoforms**.

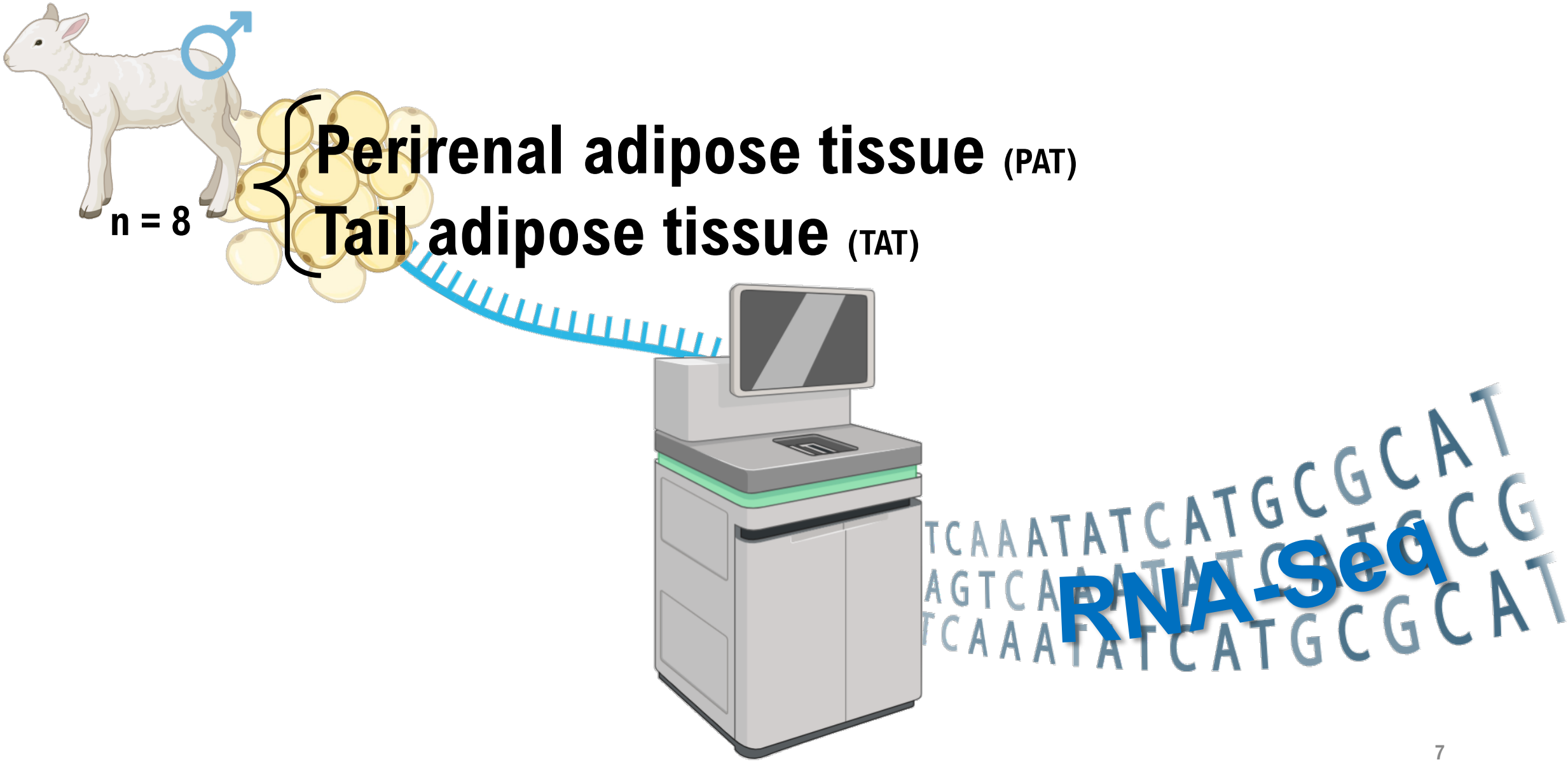
INTRODUCTION



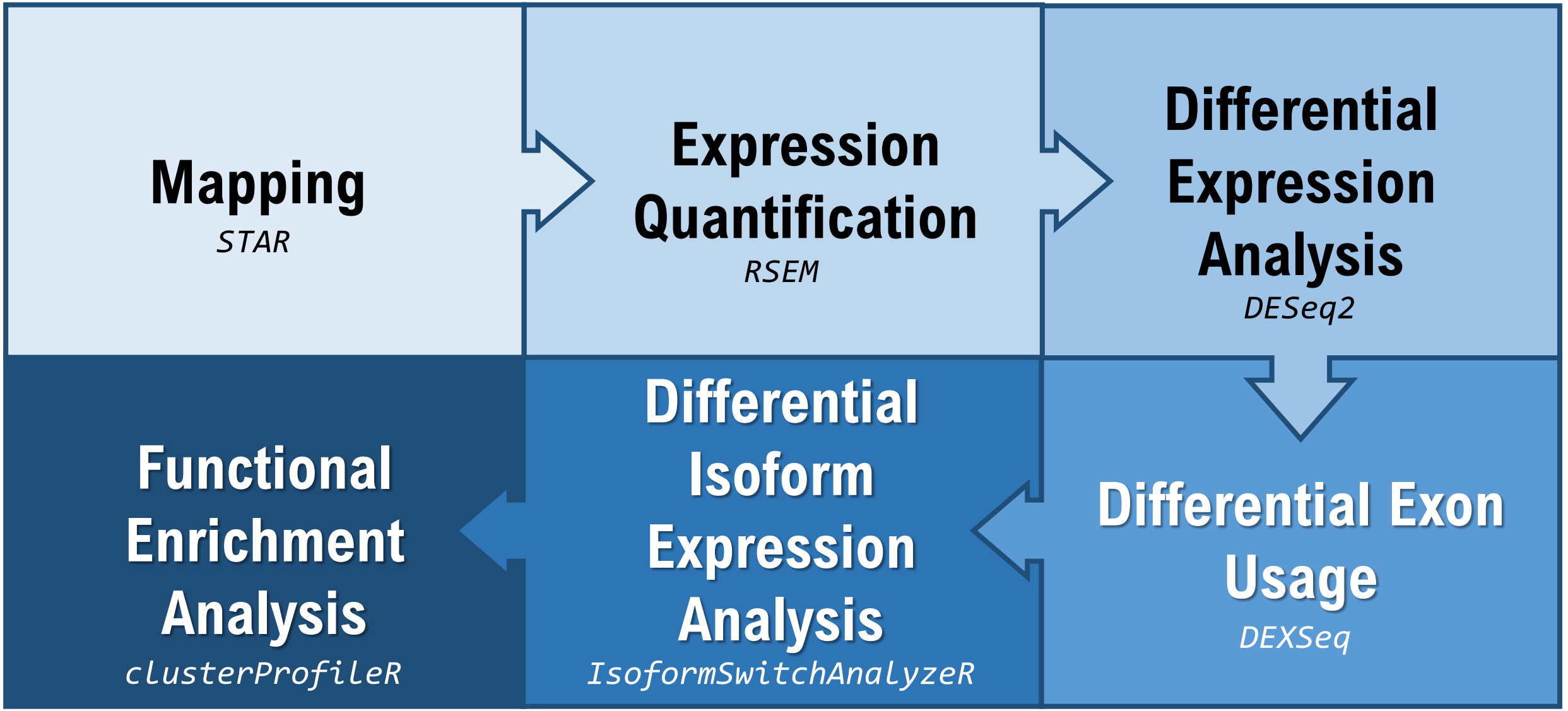
INTRODUCTION

The aim of this study is to characterize the AS events and isoform expression in the fat transcriptome, and to elucidate the potential pathways and biological functions specifically associated to two key adipose tissues in Assaf suckling lambs, tail and perirenal fat

MATERIAL AND METHODS

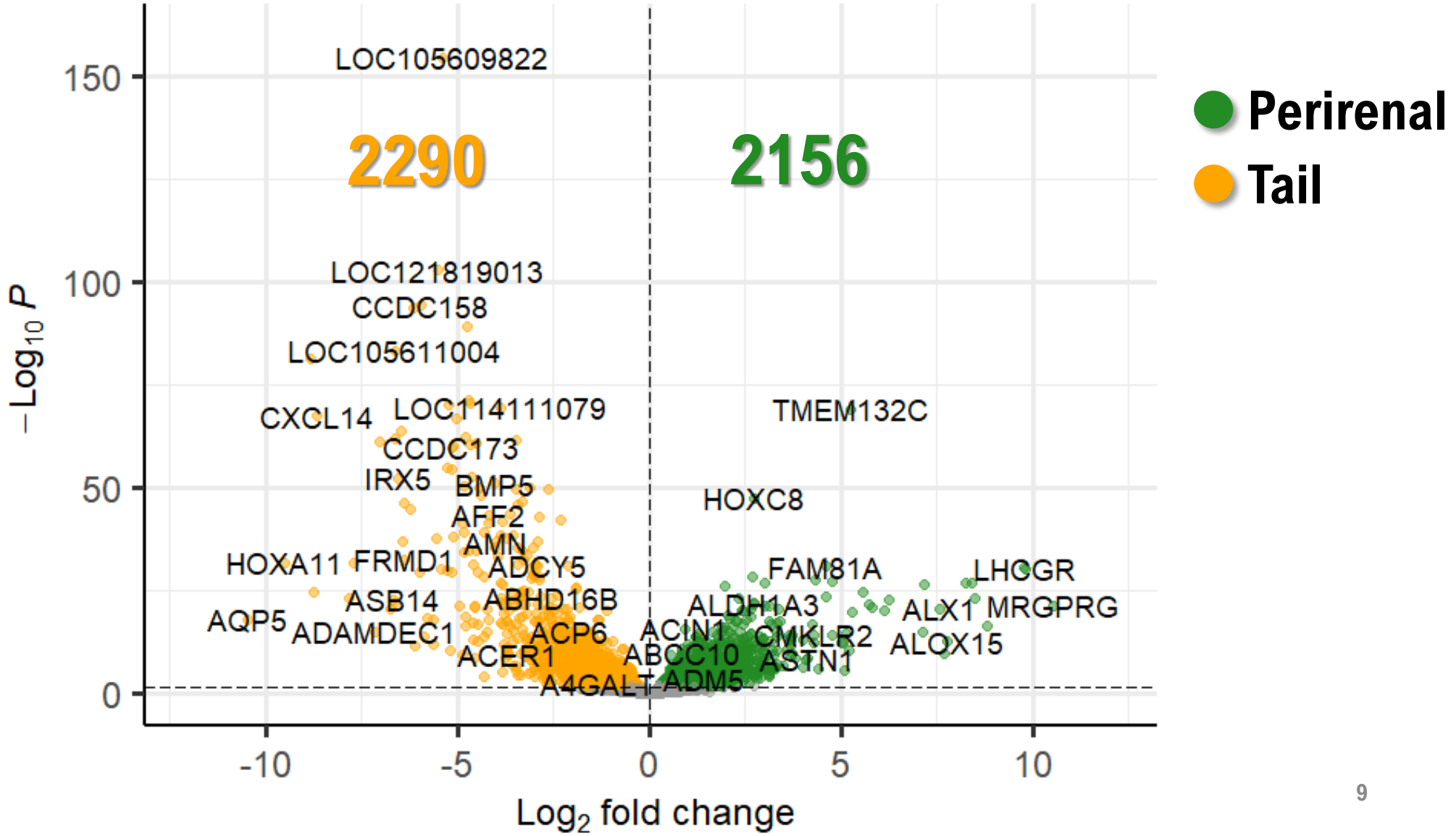


MATERIAL AND METHODS



RESULTS

Differential Expression Analysis



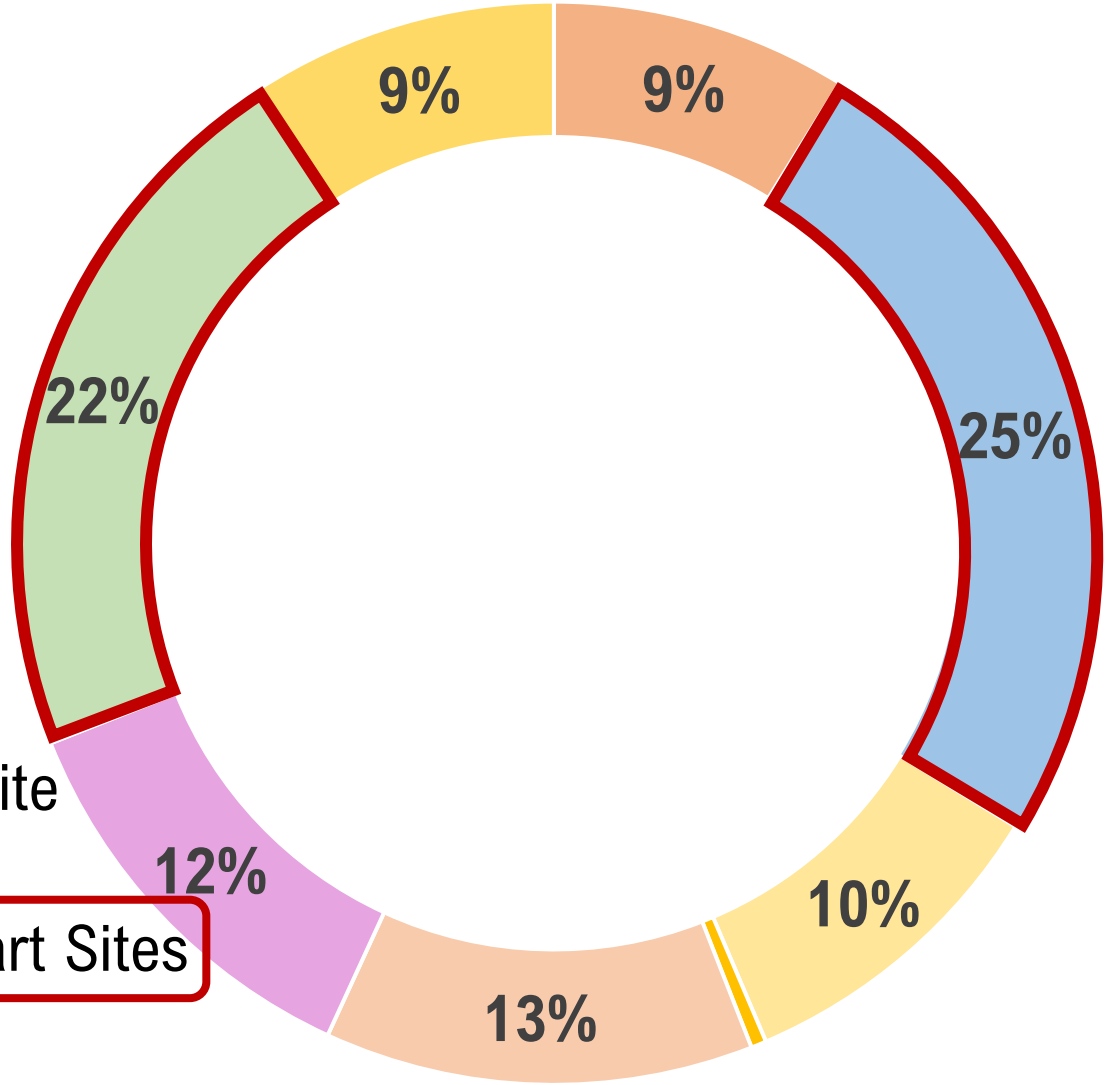
RESULTS

386 DEIs in annotated genes

Deciphering the role of alternative splicing as a potential regulator in fat-tail development of sheep: a comprehensive RNA-seq based study

Bakhtiarizadeh (2024)

- Intron Retention
- Exon Skipping
- Multiple Exon Skipping
- Mutually exclusive exon
- Alternative 5'end donor site
- Alternative 3'end acceptor site
- Alternative Transcription Start Sites
- Alternative Transcription Termination Sites

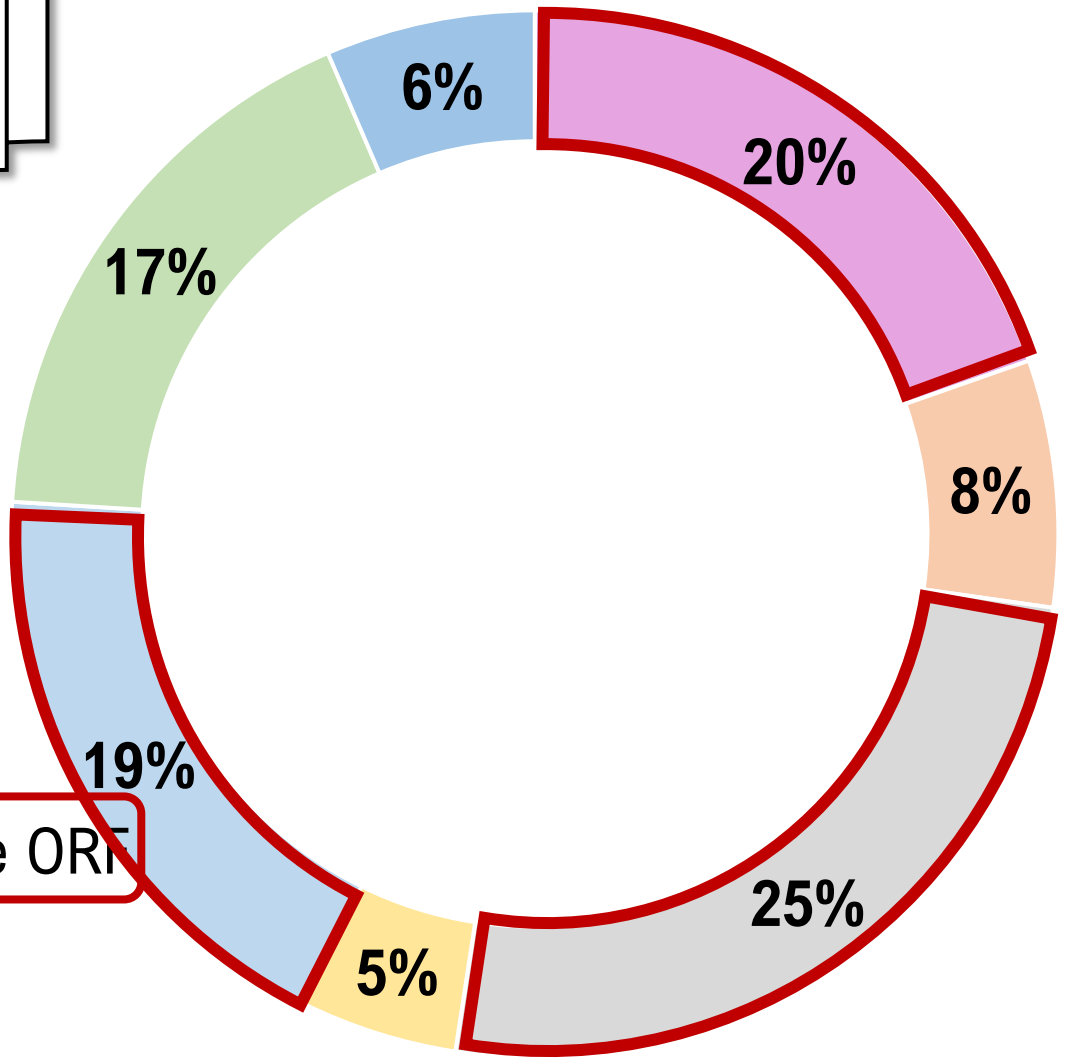


RESULTS

386 DEIs in annotated genes

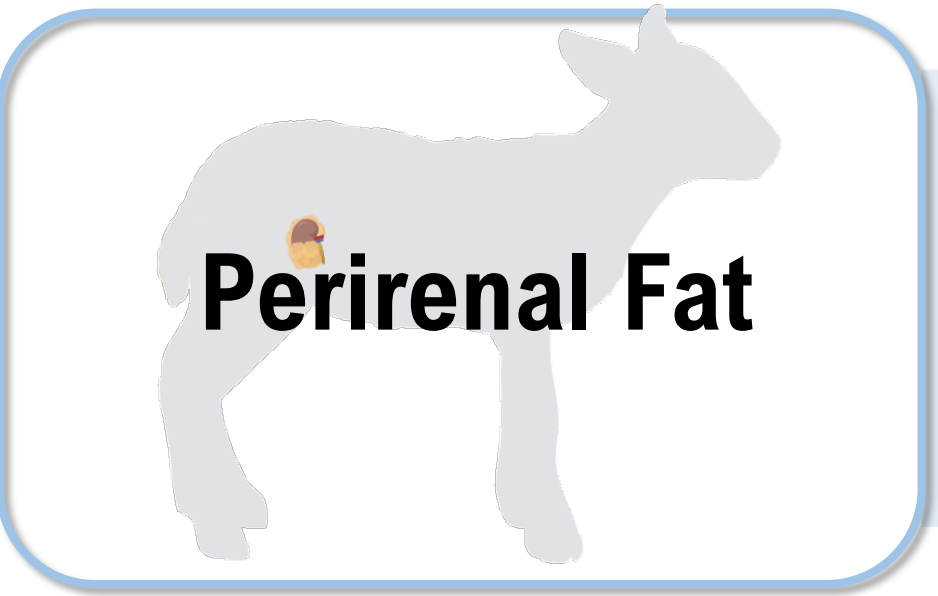
129 DEGs with DEIs

- Differences in Exon Number
- Intron Retention
- Differences in Intron Structure
- Different use of Last Exon
- Differences in genomic position of the ORF
- Different Transcription Start Site
- Different Transcription Termination Site

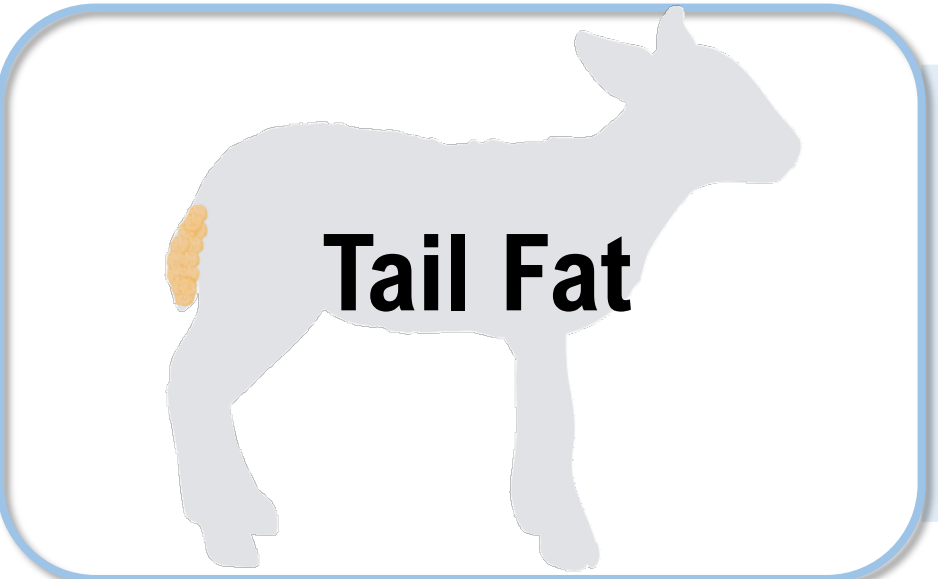


RESULTS

Functional Enrichment Analysis



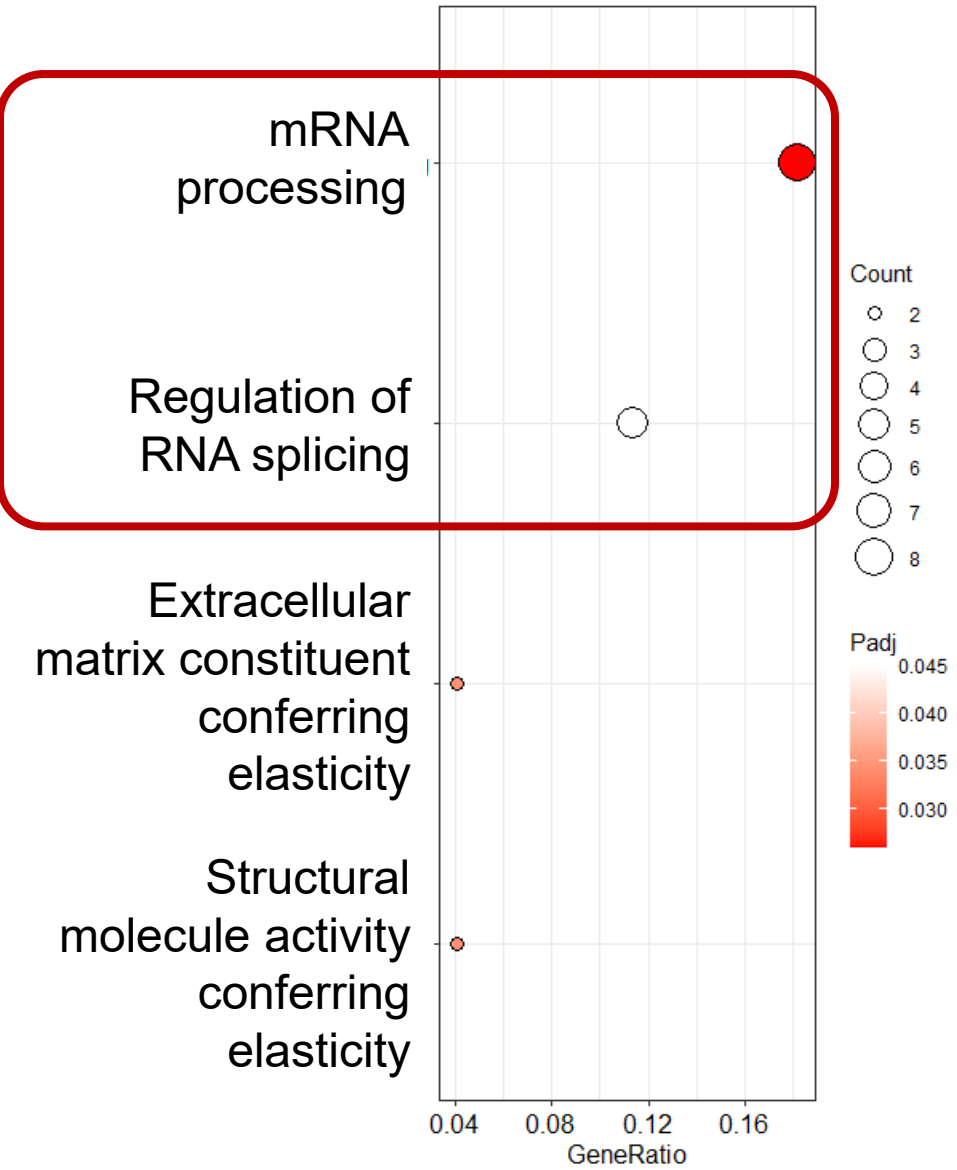
- **4** enriched terms from **Gene Ontology: Biological Process** category

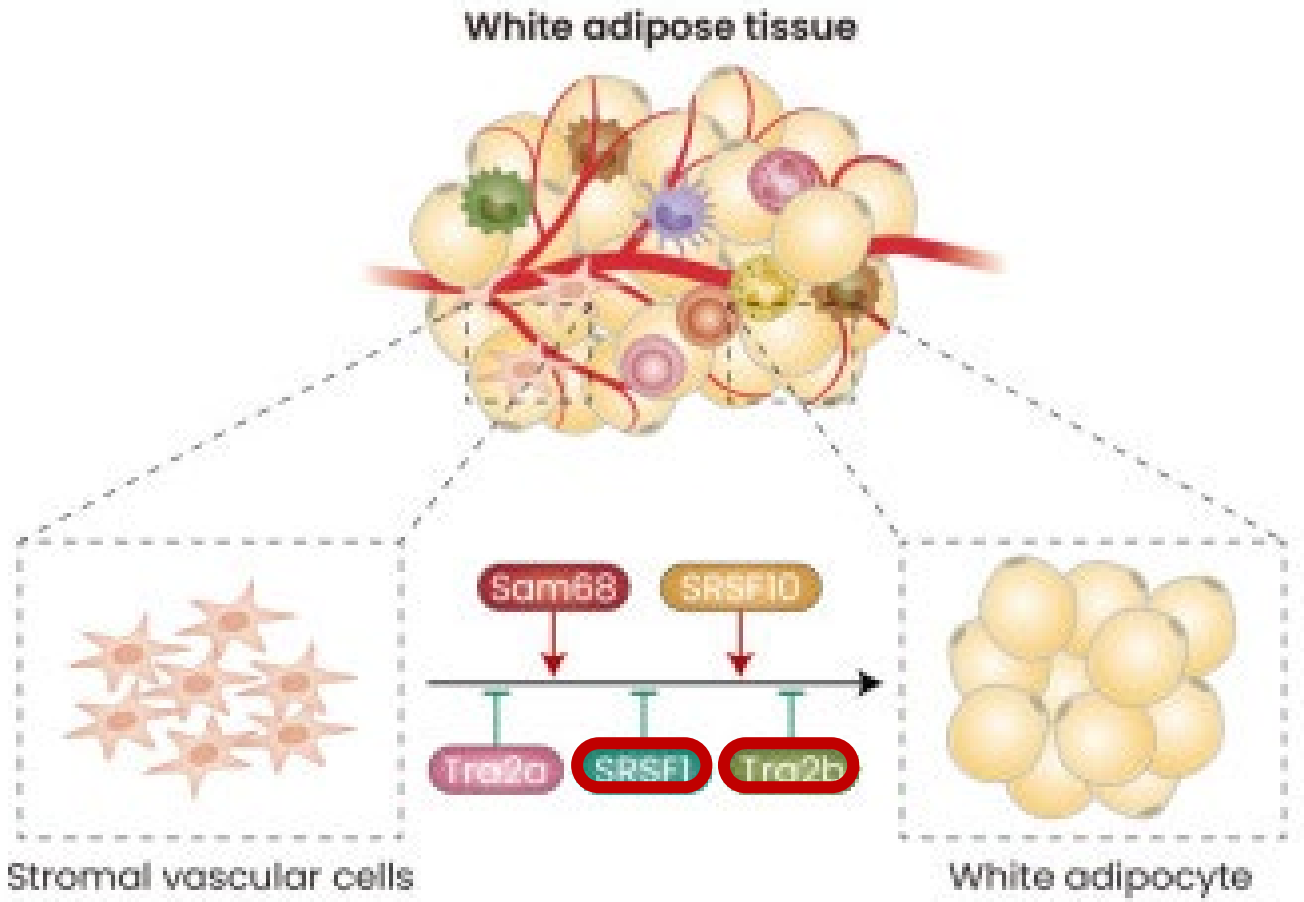


- **2** enriched terms from **Gene Ontology: Biological Process** category
- **2** enriched terms from **Gene Ontology: Cellular Component** category

RESULTS

Perirenal Fat Tissue

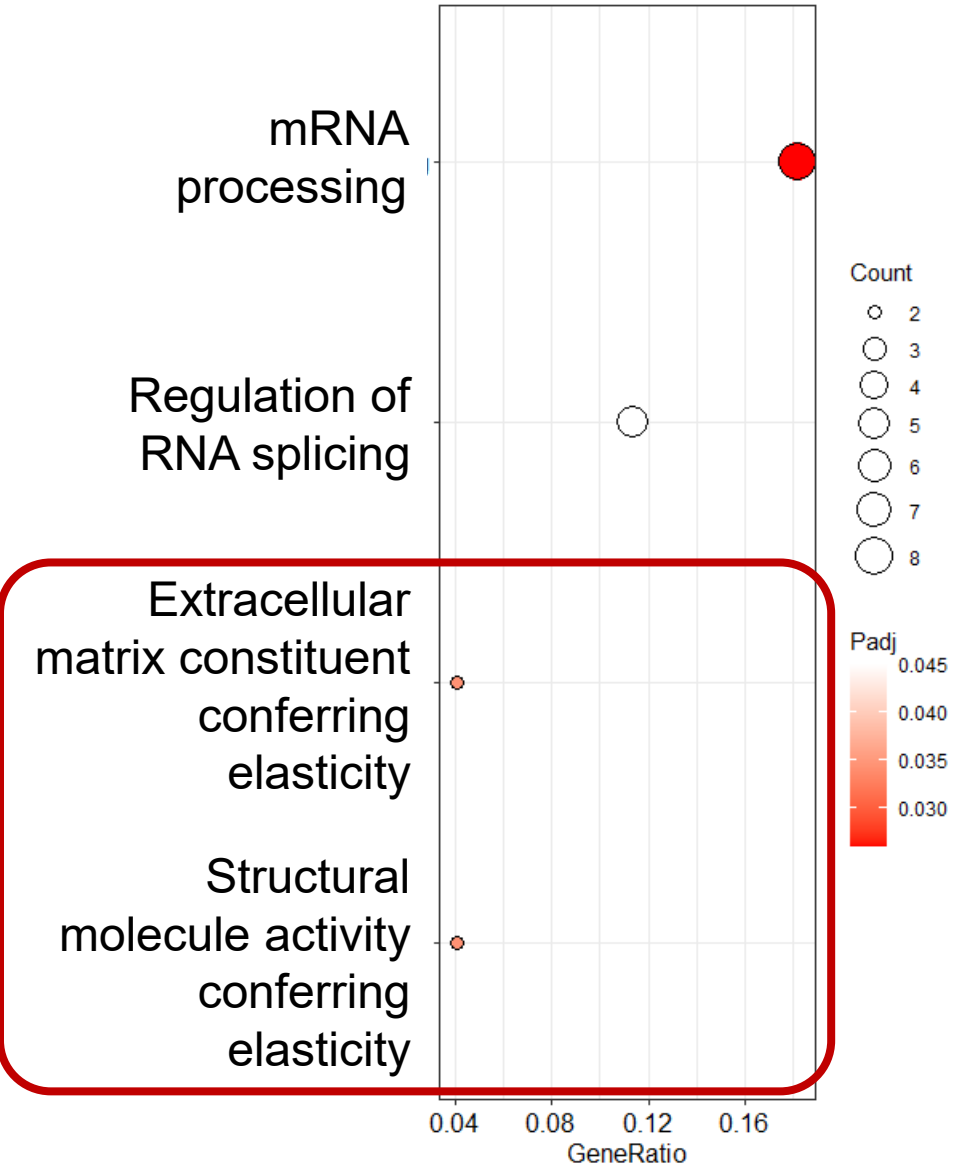


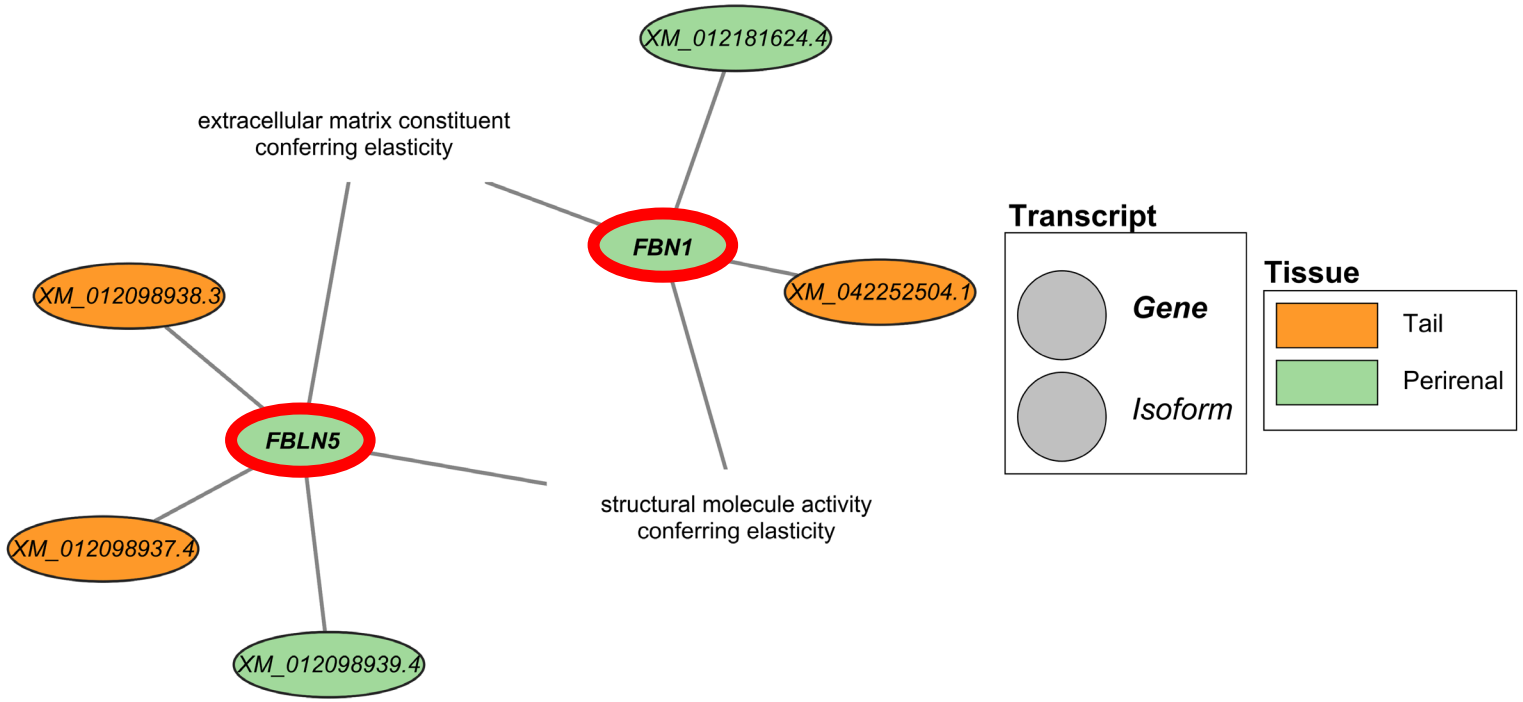


Review by T. Naing & Sun (2023)

RESULTS

Perirenal Fat Tissue



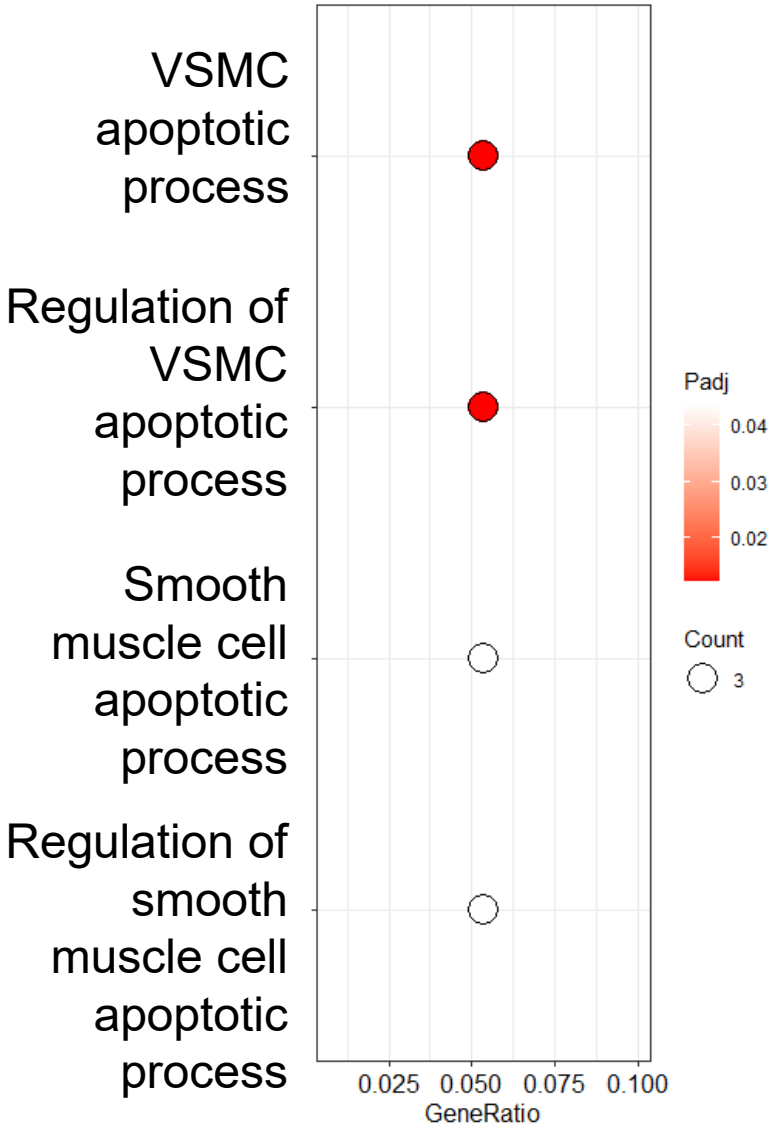


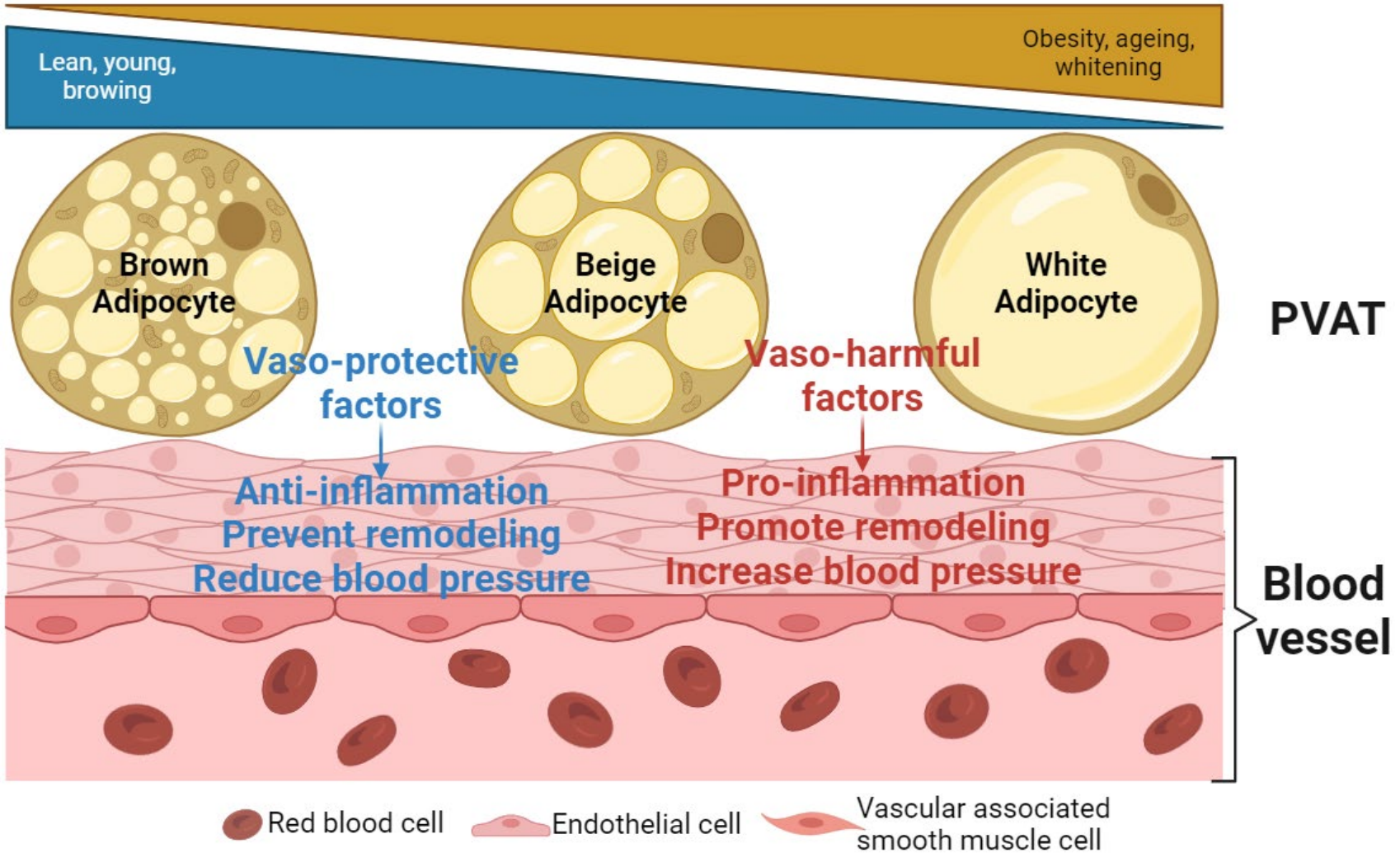
Defining the Regulated Secreted Proteome of Rodent Adipocytes upon the Induction of Insulin Resistance

Jae-Min Lim,[†,‡] Dan Sherling,[†] Chin Fen Teo,[†,§] Dorothy B. Hausman,[∥] Dawei Lin,[⊥] and Lance Wells*[,†,‡,§]

RESULTS

Tail Fat Tissue

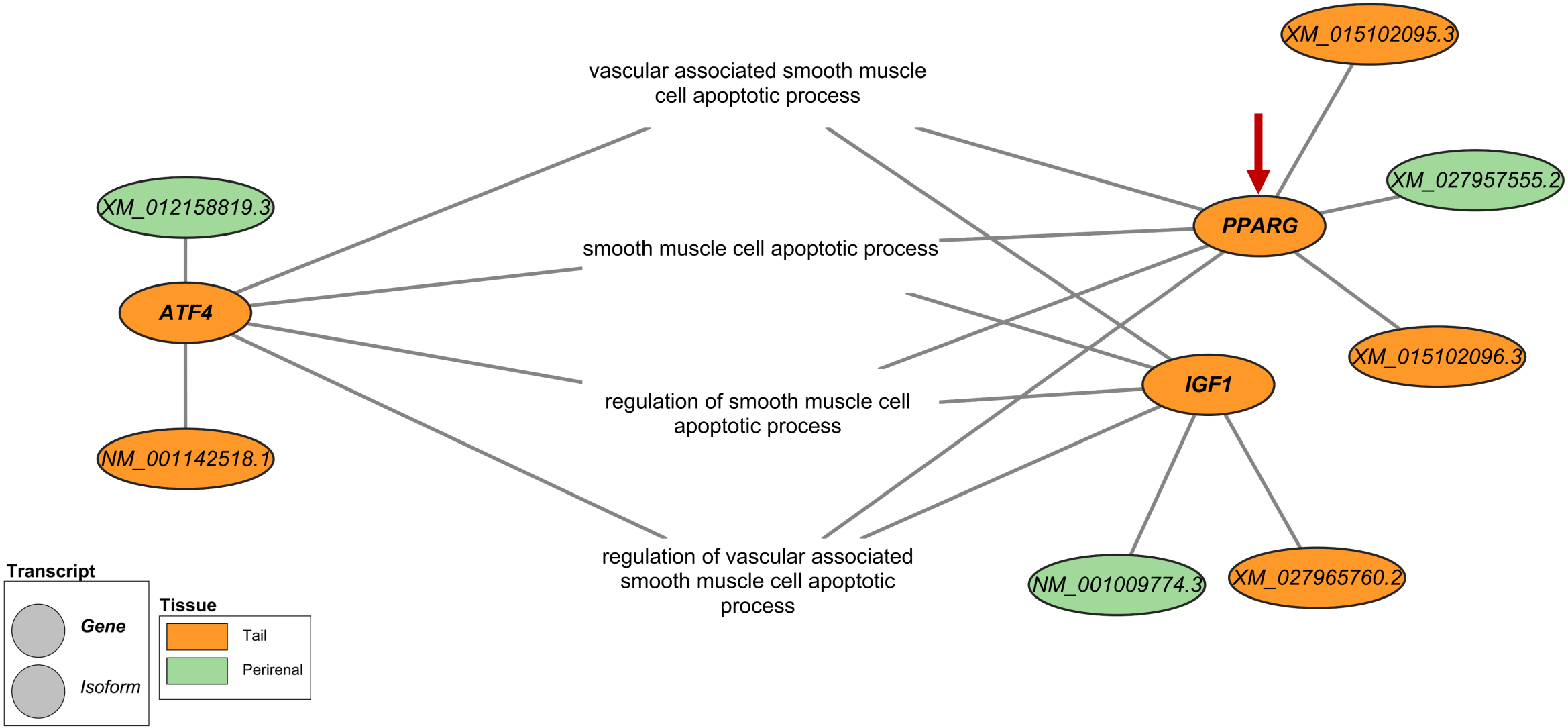




Modified from Chang, García-Barrio & Chen (2020)

RESULTS

Tail Fat Tissue



DISCUSSION

PPARG

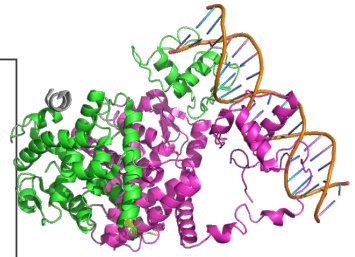
Adipocyte differentiation

Regulation of insulin sensitivity

Lipogenesis

Adipocyte survival

Adipocyte function



CONCLUSIONS

- We detected significant differences in AS events and isoform expression between the perirenal and tail fat depots in suckling lambs.
- These findings underscore the complexity of adipose tissue regulation and highlight the importance of specific genes and biological processes.
- Future analyses should focus on the detection of isoforms that are actively involved in the differential fat deposition between the two tissues.

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