



EVIDENCE OF miRNA REGULATION OF INTRAMUSCULAR FAT DEPOSITION IN BEEF CATTLE

Oliveira, GB^{1*}; Cesar, ASM¹; Felício, AM¹; Kappeler, BG¹; Poleti, MD¹; Regitano, LCA²; Coutinho, LL¹

¹ ESALQ/USP, Piracicaba, Brazil; ² Embrapa Southeast Livestock – São Carlos, Brazil

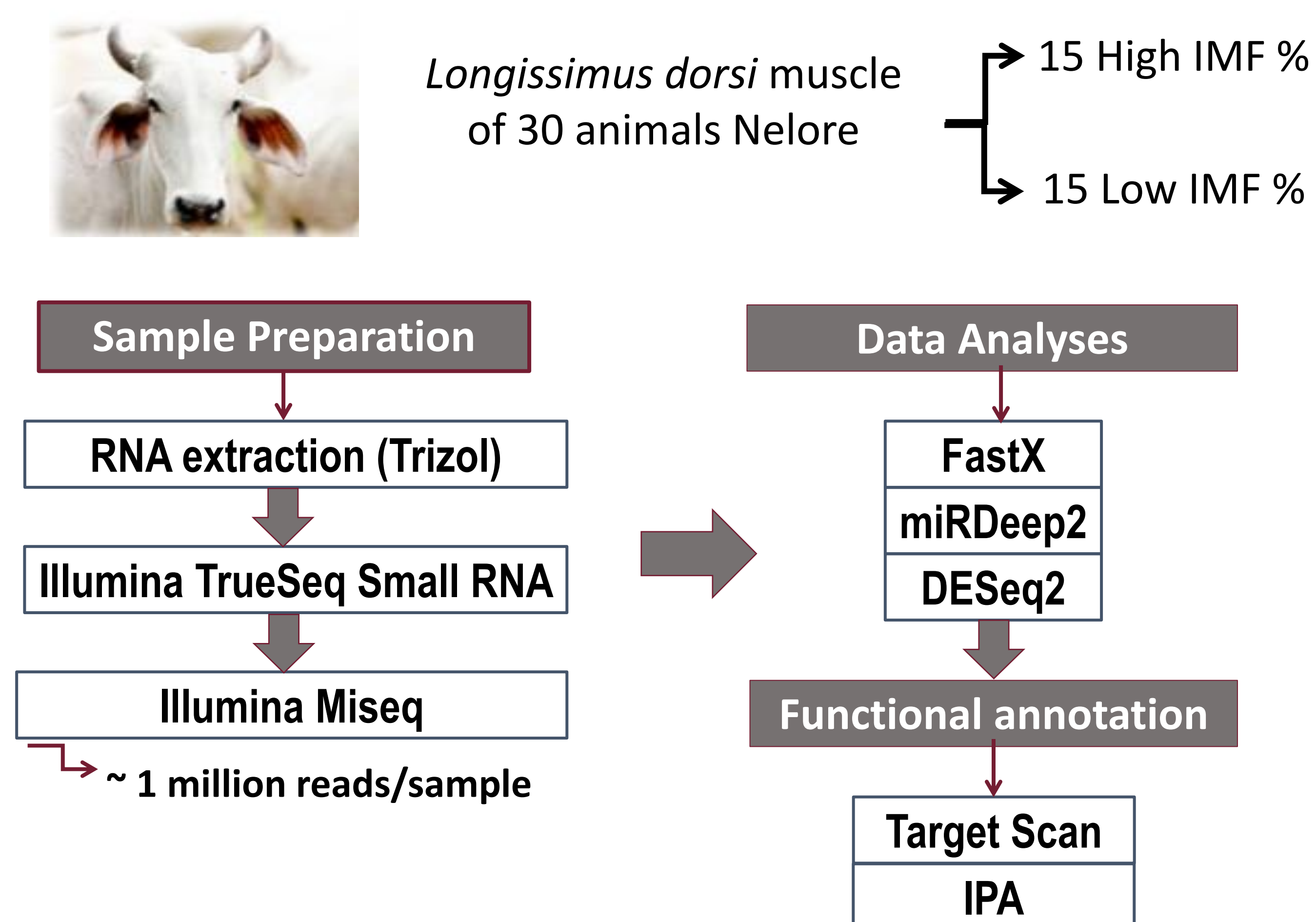
Introduction

MicroRNAs (miRNAs) were described to play an important role in the regulation of genes expression associated with the control of several important biological processes and there was a rapidly growing number of miRNAs involved in regulation of genes and signaling molecules involved in the control and maintenance of lipid homeostasis in different regulatory pathways.

Objective

The aim of this study was to identify known and novel miRNAs expressed in *Bos indicus* muscle, as well as changes in the expression level, in order to investigate the influence on regulatory pathways for intramuscular fat (IMF) deposition in Nelore cattle.

Material and Methods



Results and Discussion

| miRDeep2 | | | Target Scan | |
|----------------|-------|-----------------|--------------|------------|
| Mapped miRNAs | known | novel | Data set | # of genes |
| | 463 | 26 | Muscle genes | 15994 |
| DESeq2 | | | Target genes | |
| miRNA | FDR | Fold Change LxH | miRNA | # of genes |
| bta-let-7f | 0.04 | -1.671 | let-7 | 1218 |
| bta-let-7a-5p | 0.08 | -1.456 | miR-423 | 288 |
| bta-miR-146b | 0.08 | 1.557 | miR-100 | 173 |
| bta-miR-100 | 0.09 | 1.715 | miR-143 | 626 |
| bta-miR-143 | 0.09 | 1.309 | miR-146b | 530 |
| bta-miR-423-5p | 0.09 | -1.600 | | |

Results and Discussion

The list of differentially expressed (DE) miRNAs target genes was used in pathways enrichment analysis by the Ingenuity Pathway Analysis (IPA) software. Three regulatory pathways involved in lipid control were identified (Table 1).

Table 1 – Canonical pathways identified by IPA using the list of DE miRNAs target genes.

| Canonical Pathways | Target genes | P-Value |
|--------------------|--------------|----------|
| PPAR-RXR | 44 | 3.00E-06 |
| Adipogenesis | 27 | 0.003 |
| Insulin Receptor | 25 | 0.01 |

The miRNAs herein identified are involved in lipid metabolism regulation through PPAR-RXR signaling pathway according to IPA analysis. This pathway is up-regulated for fatty acid oxidation and down-regulated for adipogenesis and lipogenesis, by regulating the expression of PPAR α , PKA, ADIPOR, STAT5 and GHR genes (Figure 1). Also, these miRNAs are involved in inflammation and glucose pathways regulating the expression of genes such as IL-1R, NIK and GPDH.

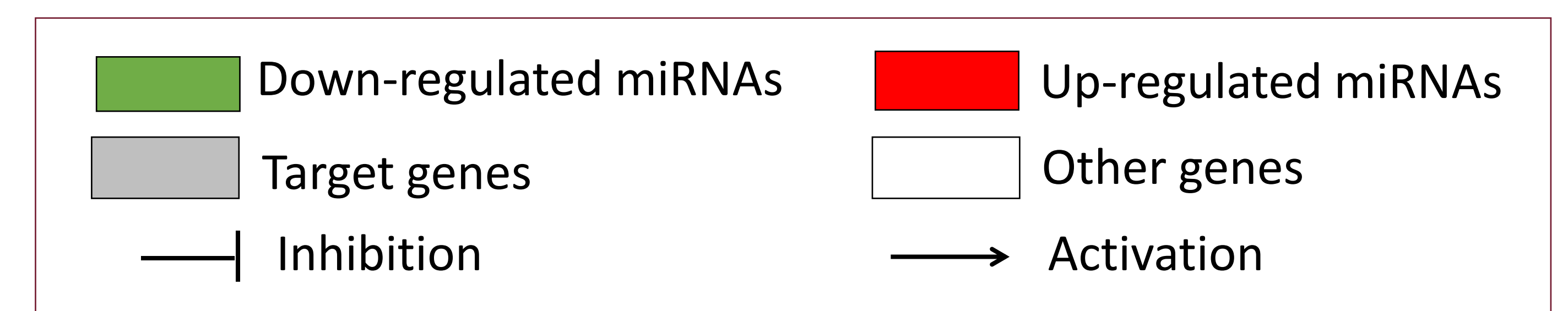
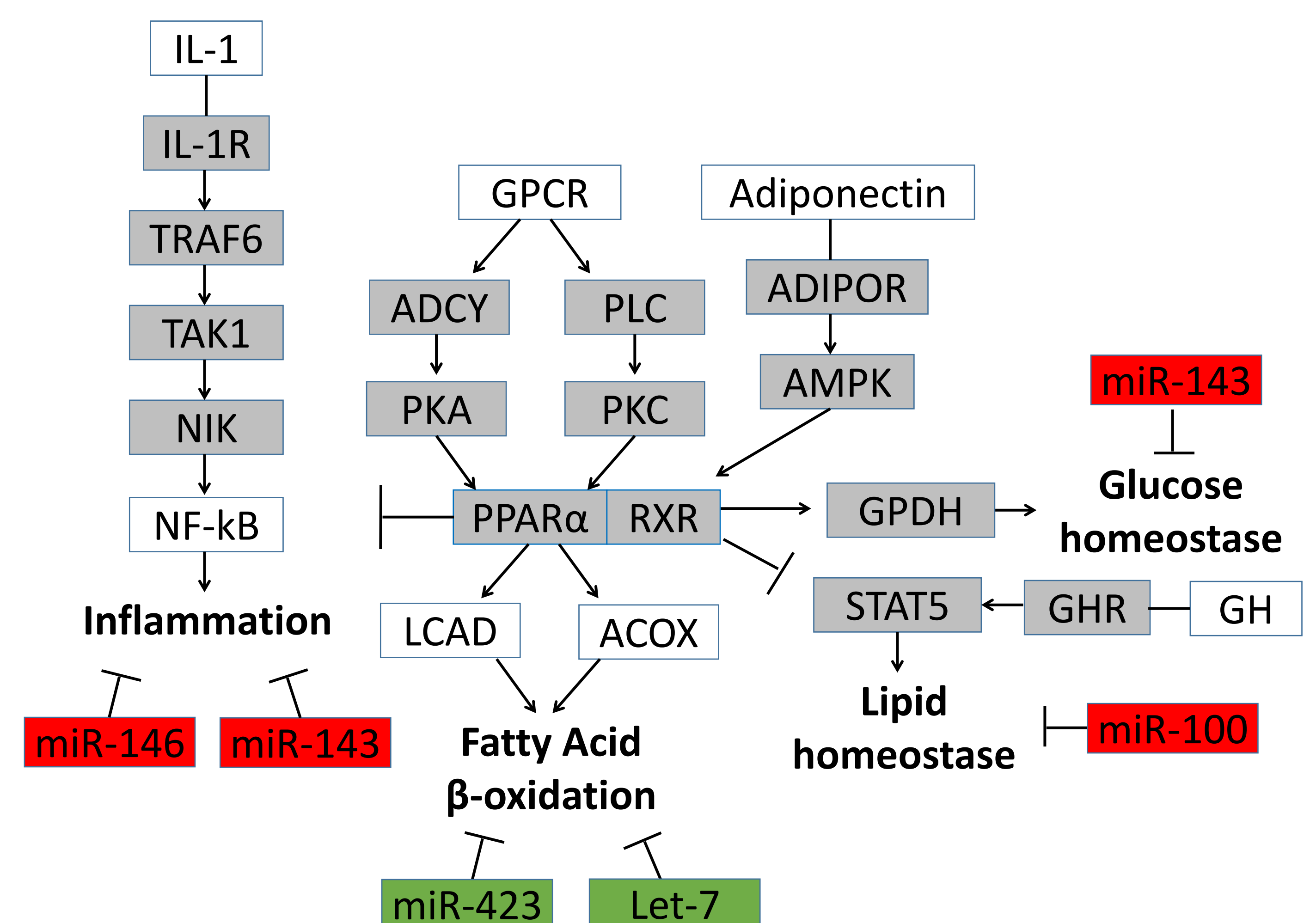


Figure 1 – PPAR-RXR signaling pathway regulation by miRNAs in the Low IMF content group.

Conclusions

These results agree with our hypothesis that microRNAs expression can modulate lipid metabolism and fat deposition.