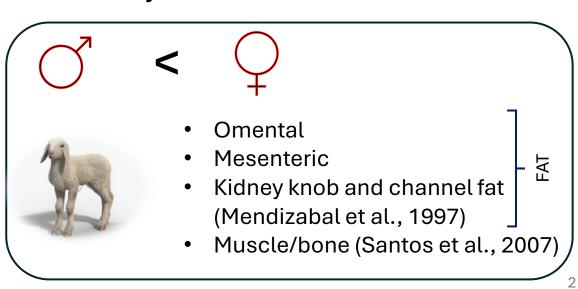


Suckling lamb carcass

- Suckling lamb meat is one of the most relevant products of the Mediterranean dairy sheep industry (Battacone et al., 2021).
- Suckling lamb carcass composition is a key determinant affecting both carcass quality and yield, and it is influenced by:
 - slaughter body weight
 - fatness level
 - diet
 - sex



(Sañudo et al., 1997; Velasco et al., 2000)



Previous studies

 Our group has previousely compared lamb perirenal fat transcriptome between:





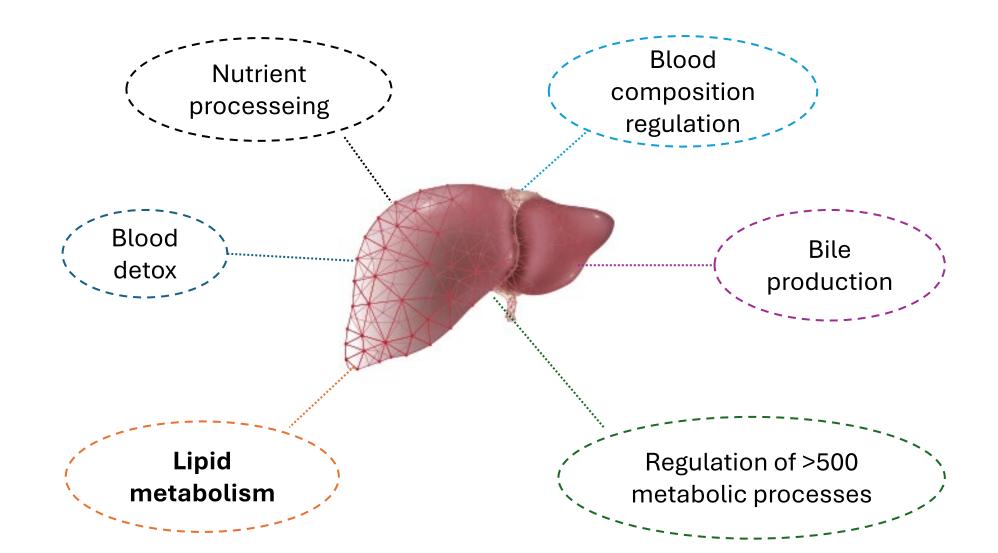


HighFat vs. LowFat (Alonso-García et al., 2023)



Males vs. females (Fonseca et al., 2022)

Liver functions



Objective



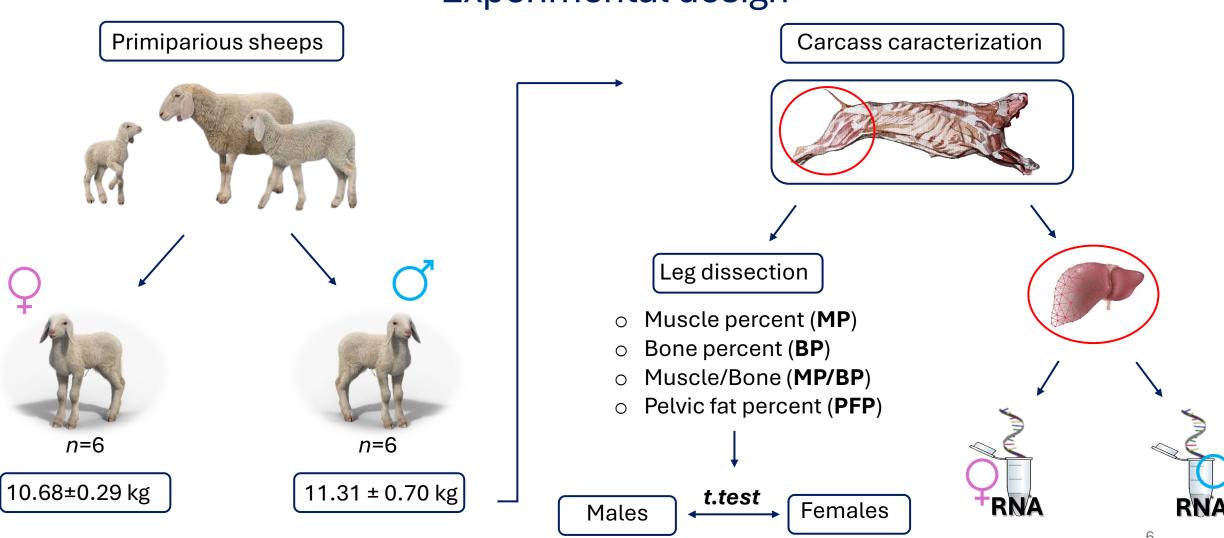
INTRODUCTION

Exploit the potential of Weighted Gene Co-expression Network Analysis (WGCNA) to better understand the link between liver transcriptome profiles and quantitative traits related to carcass quality in male and female suckling lambs.

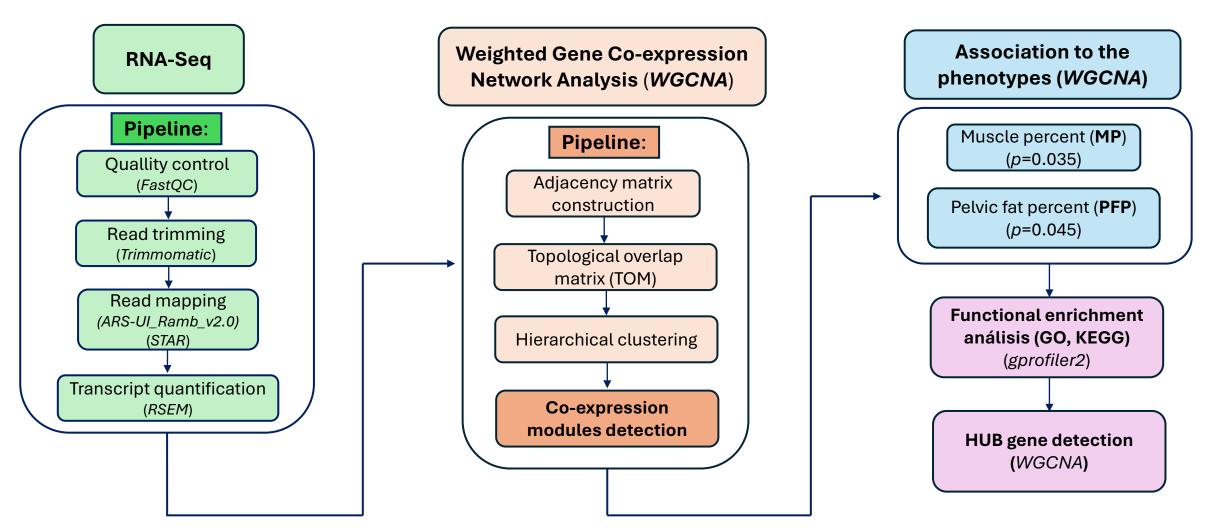
INTRODUCTION

Experimental design

RESULTS AND DISCUSSION



Bioinformatic workflow



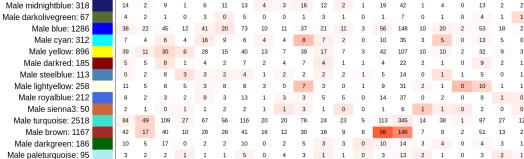
The analysis of the carcass phenotypes

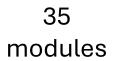
Leg tissue composition traits	Mean (±SD)		
	Male	Female	<i>p</i> -value ¹
Muscle percent (MP)	55.306	58.187	0.035
	(±0.861)	(±2.471)	
Bone percent (BP)	31.302	31.281	0.986
	(± 2.73)	(± 0.978)	
Muscle / Bone (MP/BP)	1.778	1.863	0.323
	(± 0.153)	(±0.131)	
Pelvic fat percent (PFP)	2.835	1.999	0.045
	(± 0.727)	(±0.487)	

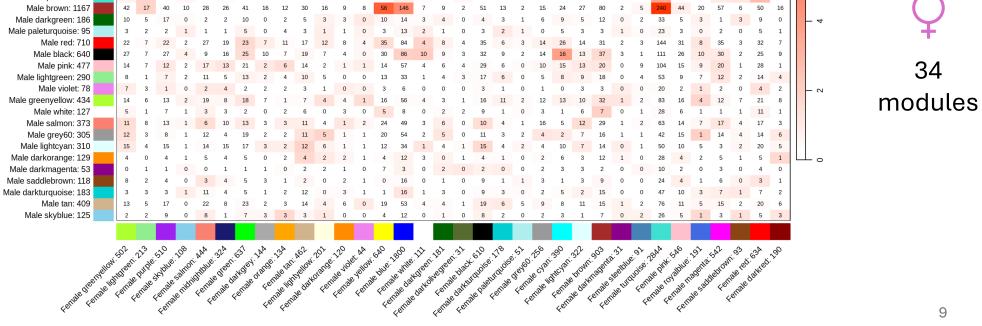
¹ t-student p-value

Male green: 795 Male orange: 170 Male magenta: 458 Male darkgrey: 169

Male and female co-expressed modules



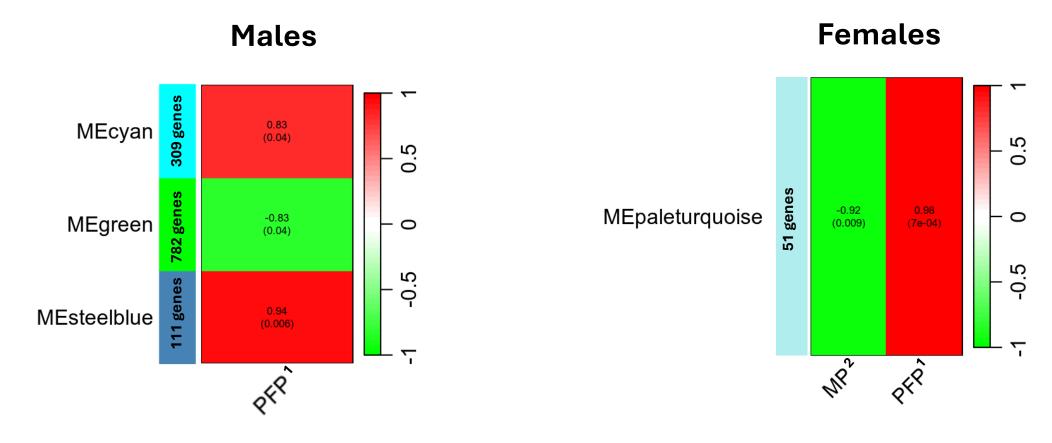




RESULTS AND

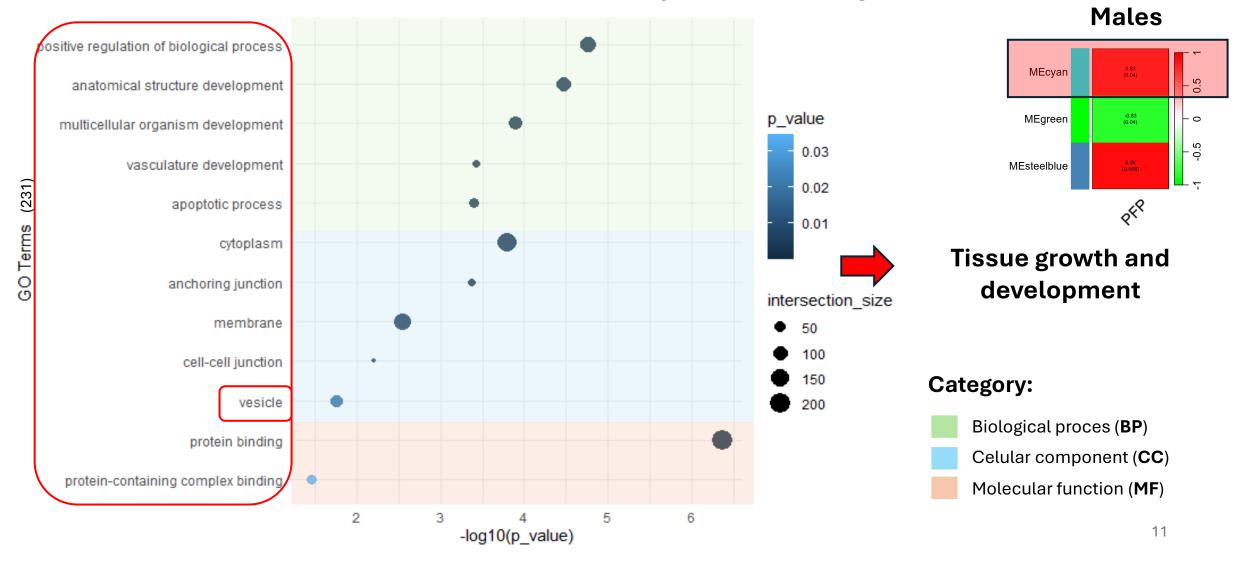
DISCUSSION

Male and female co-expressed modules associated to the traits

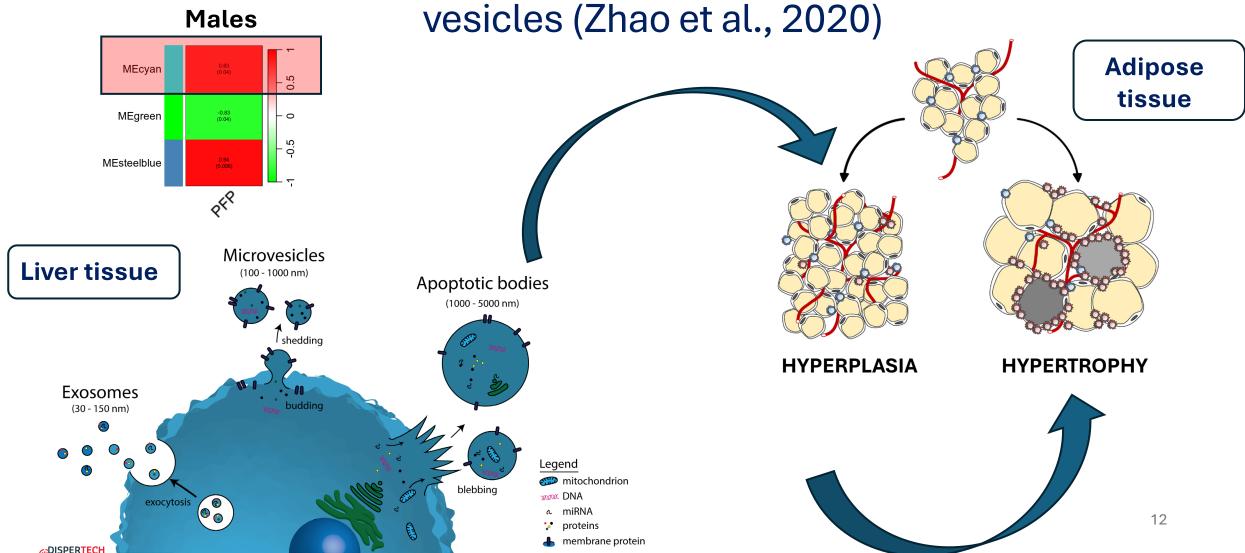


PFP-pelvic fat percent, MP-muscle percent

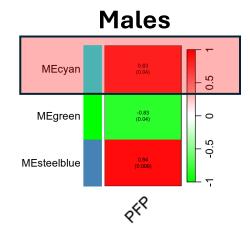
Functional enrichment analysis of the cyan module



Adipose tissue remodeling via extracellular

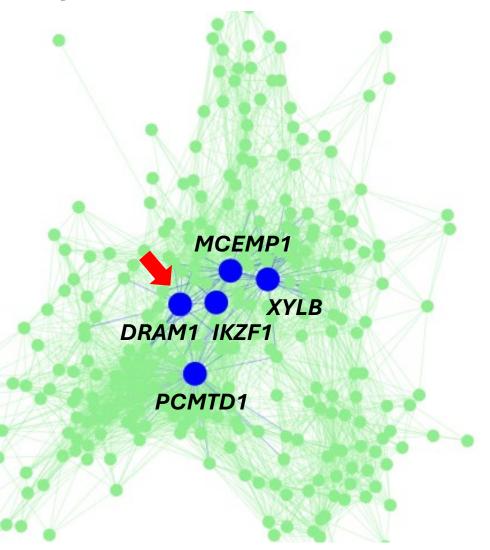


HUB genes identified in the male cyan module

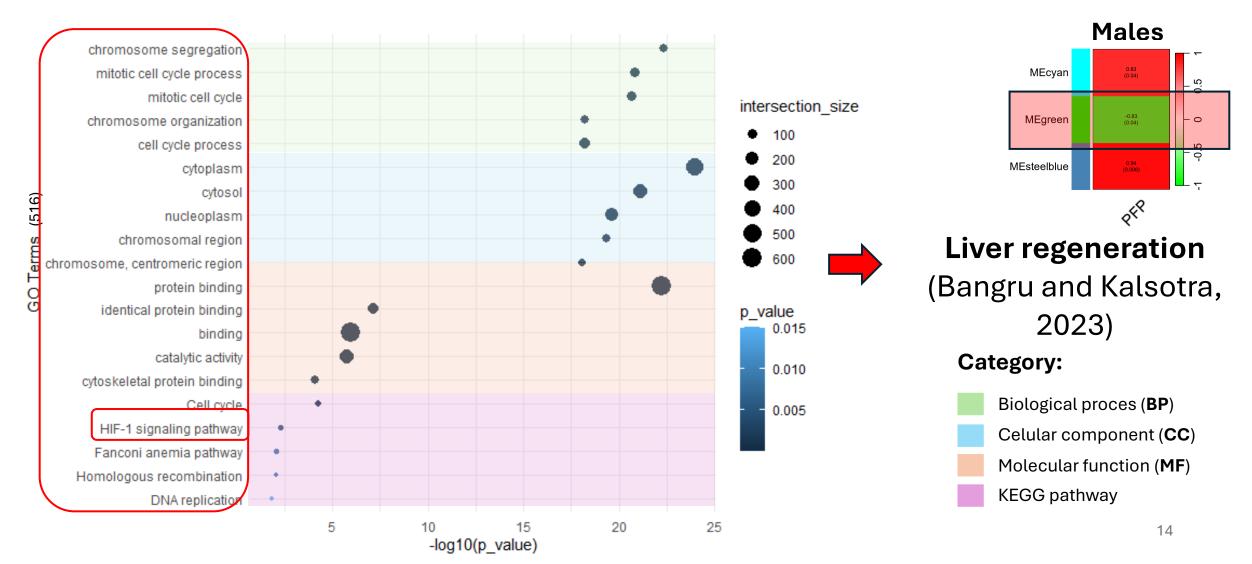


INTRODUCTION

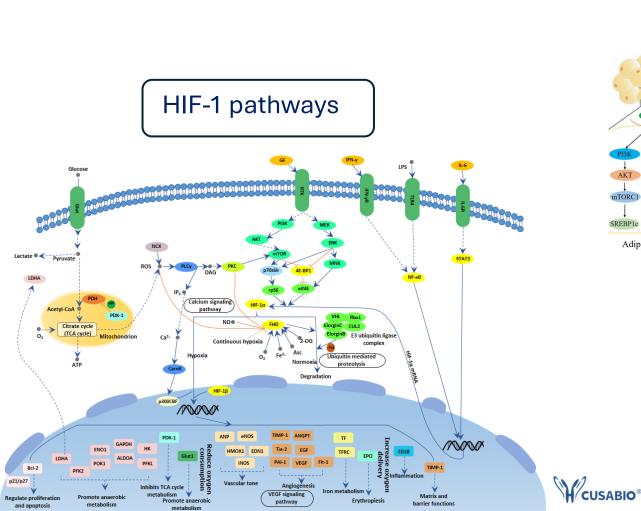
DRAM1 modulates insulin signaling and mTORC1 activity during adipogenesis (Beaumatin et al., 2019).



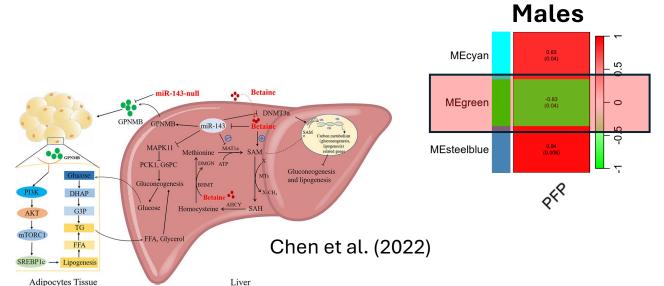
Functional enrichment analysis of the green module



Hypoxia inducible factor 1 pathway



INTRODUCTION



RESULTS AND

DISCUSSION

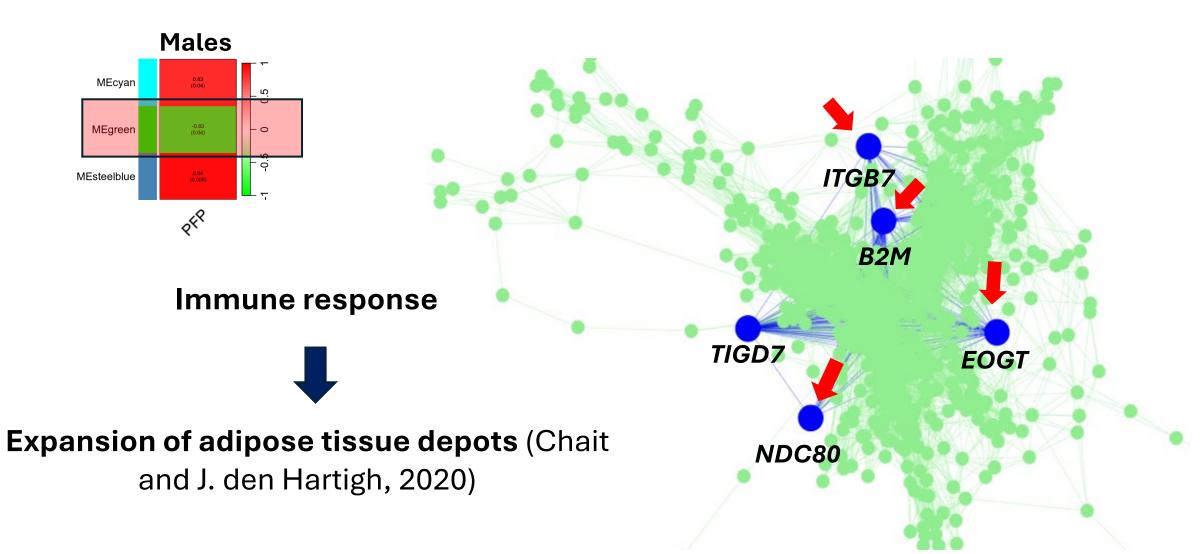
lipogenic and gluconeogenic pathways



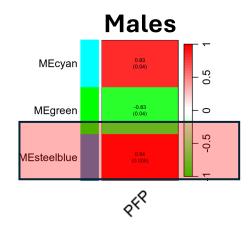
HUB genes identified in within green male module

RESULTS AND

DISCUSSION

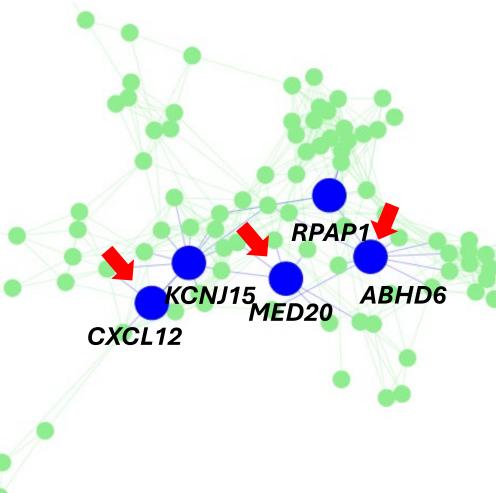


HUB genes identified within the steelblue male module

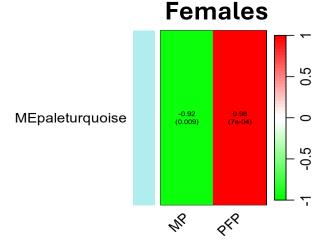


ABHD6 is a negative modulator of adaptive ^{CO}thermogenesis in visceral adipose tissue 🔮 under high-rat diet (Kurita et al., 2019)

- Regulated by hypoxia inducible factor

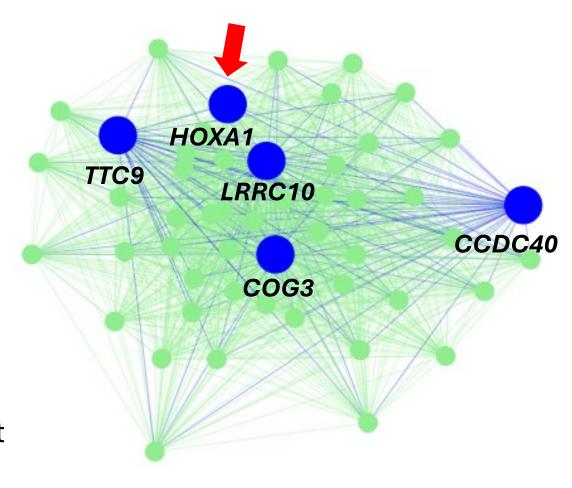


HUB genes identified within the *paleturquoise* female module



Expression of *Hox* genes is linked with **fat accumulation** in differentiated brown adipocytes (Singh et al., 2016).

Hox genes have an essential role in **skeletal** and connective tissue patterning (Pineault and Wellik, 2014)



INTRODUCTION

The results presented here highlight sex-dependent differences in the liver transcriptome associated with the molecular mechanisms underlying carcass trait:

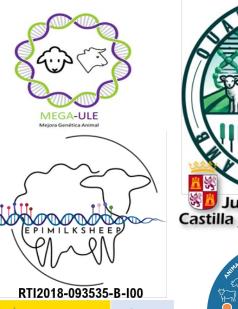
RESULTS AND DISCUSSION

- For males, these results underscore the importance of the vesicles and hypoxia pathways in fat deposition.
- For **females**, HUB genes, particularly, **HOX1** showed a clear **association to the muscle percent and pelvic fat percent,** traits that differentiate male and female carcasses.
- These findings emphasize the need for further analyses into the biological processes and pathways affecting muscle and adipose tissue growth and development.















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