Proteomics profiles of *Longissimus thoracis* muscle of *Arouquesa* cattle under different production systems

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Session “Omics and integrative analyses towards understanding inter-organ cross-talk and whole body physiology of livestock”

29th August 2023

Introduction

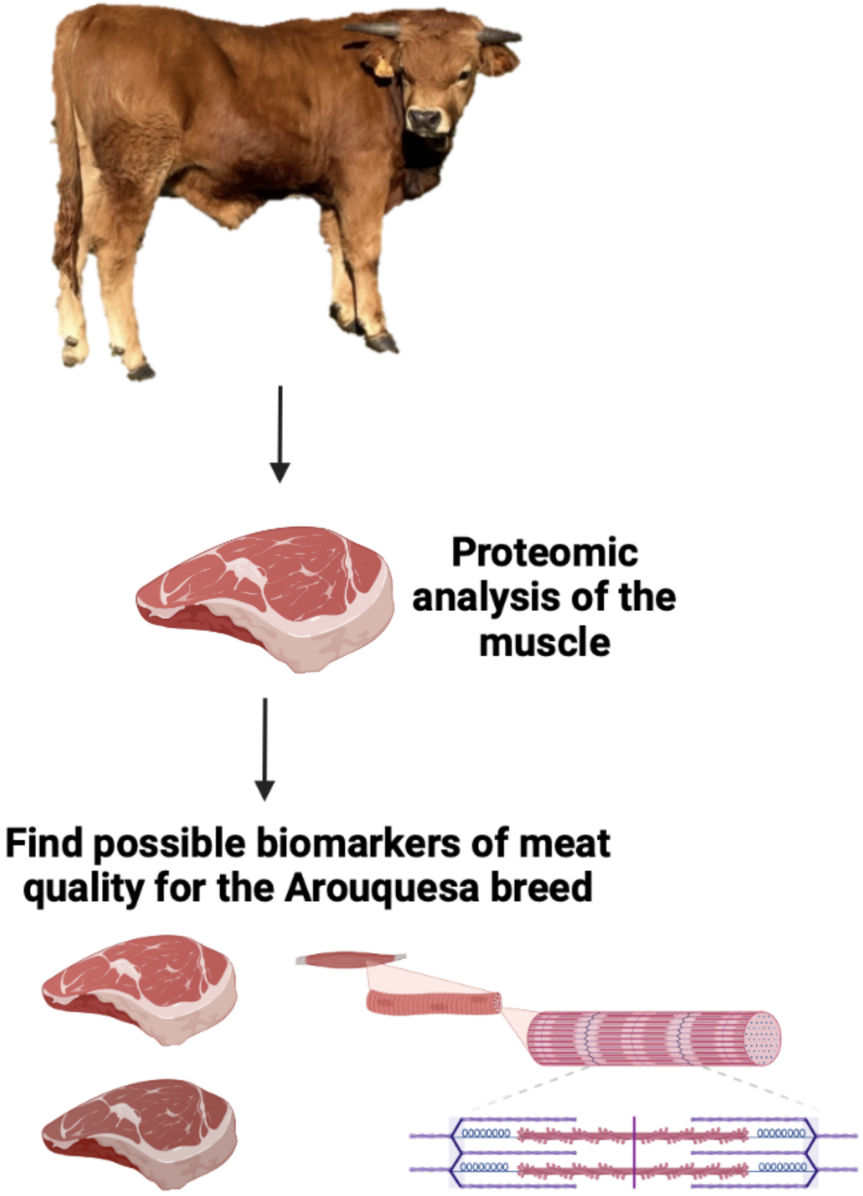
- The consumers' awareness about quality and the products' origin is increasing.
- The production in sustainable systems need to be improved and supported.
- Traditional systems are associated with sustainability and with the production of high-quality products.

Introduction

- Arouquesa breed is well known for the Arouquesa PDO beef
- Animals produced in a traditional mountain system with harsh climatic conditions
- Problems with nutritional restrictions
- Need to apply new systems without affecting the beef quality

Introduction

- Omics technologies are gaining interest in animal production
- Proteomics can be used to improve meat quality parameters and to establish biomarkers
- It can be a powerful tool to ensure compliance with the certification specifications
- There are lack of studies using omics in Portuguese autochthonous breeds



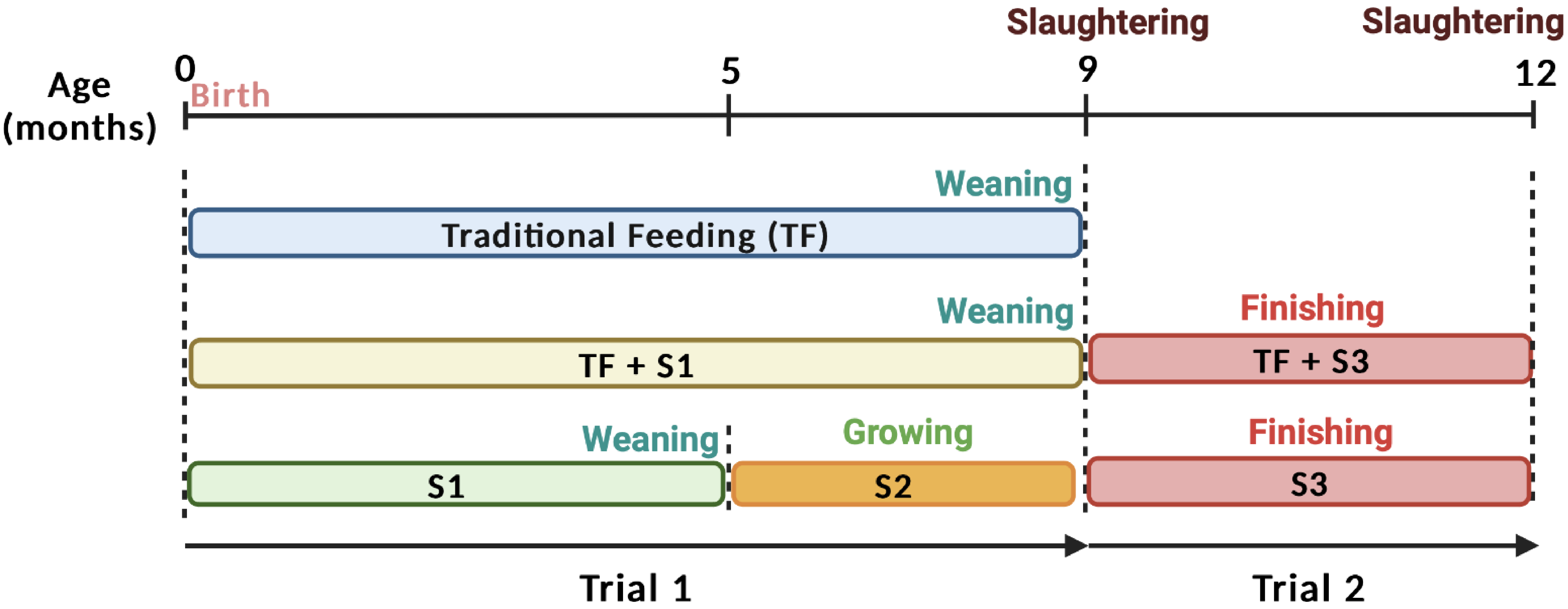
Proteomic analysis of the muscle

Find possible biomarkers of meat quality for the Arouquesa breed

Objectives

The aim of this work is to compare proteomic profiles of Arouquesa beef produced under traditional and improved production systems using label-free proteomics.

Experimental design



Age (months)

0 Birth

5

9 Slaughtering

12 Slaughtering

Weaning

Traditional Feeding (TF)

Weaning

TF + S1

Finishing

TF + S3

Weaning

S1

Growing

S2

Finishing

S3

Trial 1

Trial 2

Previous results

animals

MDPI

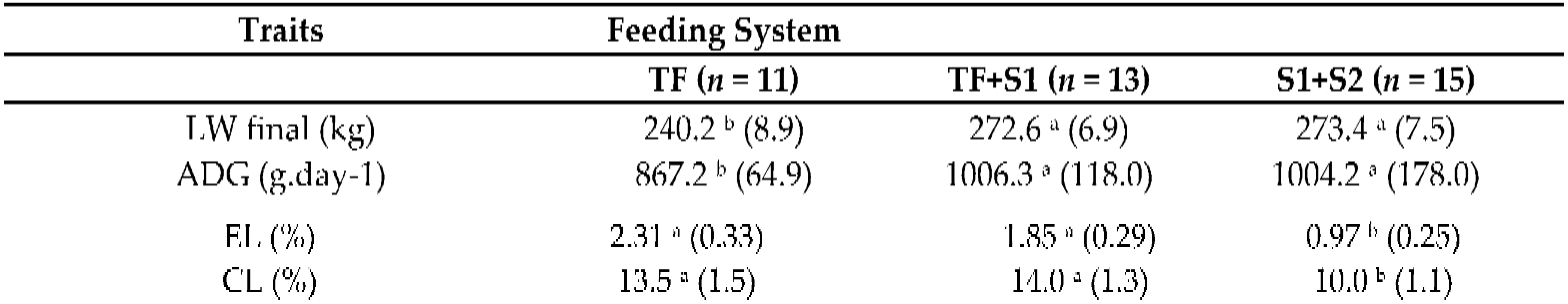
Article

Growth Performance, Carcass and Meat Traits of Autochthonous *Arouquesa* Weaners Raised on Traditional and Improved Feeding Systems

Laura Sacarrão-Birrento [1,*], Maria José Gomes [2,3], Severiano R. Silva [2,3], José A. Silva [2], Duarte Moreira [3], Raquel Vieira [4], Luis Mendes Ferreira [3,4], Pedro Pereira [5], André M. de Almeida [1], José Carlos Almeida [2,3] and Carlos Venâncio [3,4,*]

Previous results

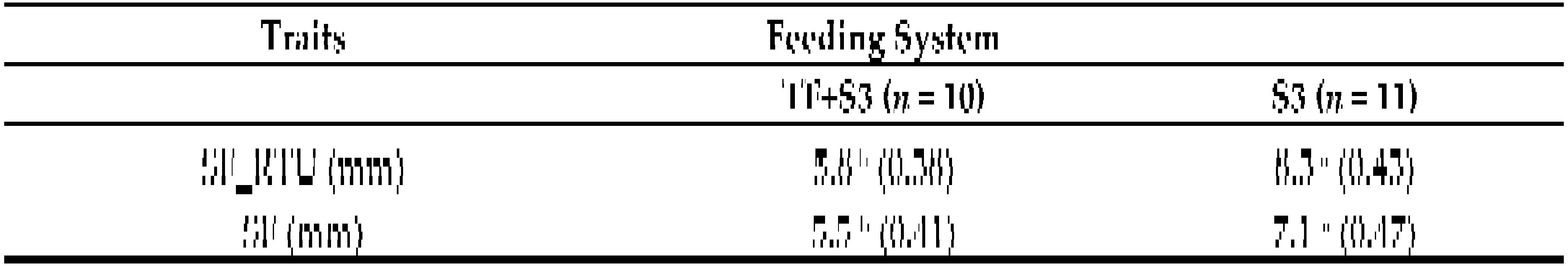
TRIAL 1



Traits	Feeding System		
	TF (n = 11)	TF+S1 (n = 13)	S1+S2 (n = 15)
LW final (kg)	240.2 ^{b} (8.9)	272.6 ^{a} (6.9)	273.4 ^{a} (7.5)
ADG (g.day-1)	867.2 ^{b} (64.9)	1006.3 ^{a} (118.0)	1004.2 ^{a} (178.0)
EL (%)	2.31 ^{a} (0.33)	1.85 ^{a} (0.29)	0.97 ^{b} (0.25)
CL (%)	13.5 ^{a} (1.5)	14.0 ^{a} (1.3)	10.0 ^{b} (1.1)

^{a,b} Rows with different superscripts indicate statistical differences ($p < 0.05$) LW—live weight; ADG—average daily gain EL—exudative losses measured at day 7 post mortem; CL—cooking losses measured at day 7 post mortem

TRIAL 2

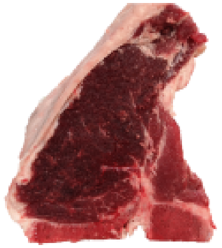


Traits	Feeding System	
	TF+S3 (n = 10)	S3 (n = 11)
SF_RTU (mm)	5.8 ^{b} (0.38)	8.3 ^{a} (0.43)
SF (mm)	5.5 ^{b} (0.41)	7.1 ^{a} (0.47)

^{a,b} Rows with different superscripts indicate statistical differences ($p < 0.05$) SF_RTU—subcutaneous fat thickness obtained with ultrasound SF—subcutaneous fat depth

No diferences in the other parameters measured as the carcass yield and weight, lumbar measurements, color, pH and shear force.

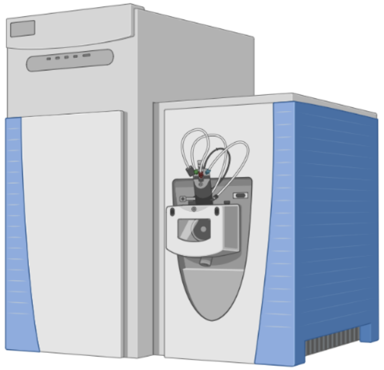
Methods



Longissimus thoracis muscle samples

Protein extraction

Trypsin digestion



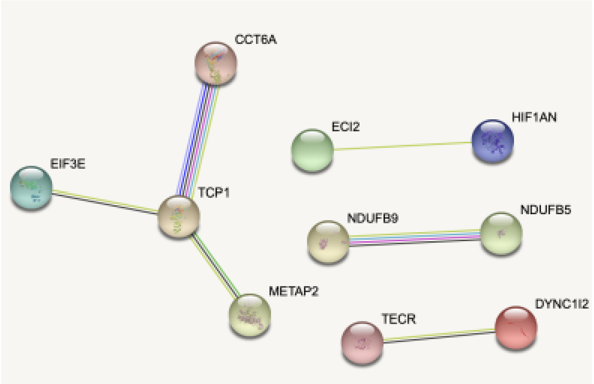
LC-MS/MS analysis

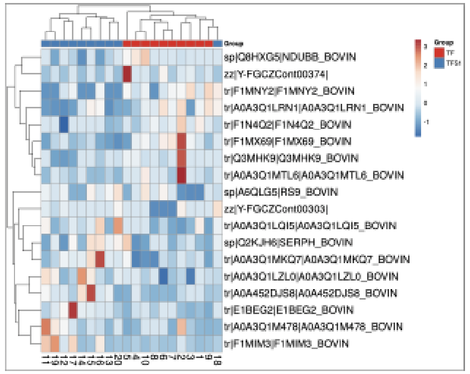
MaxQuant analysis

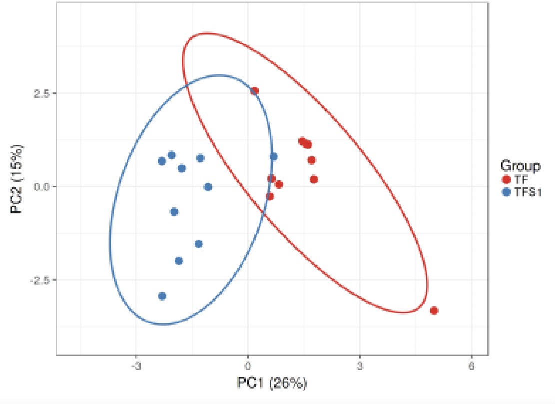
Identification Quantification

Bioinformatics analysis

GO and pathway analysis



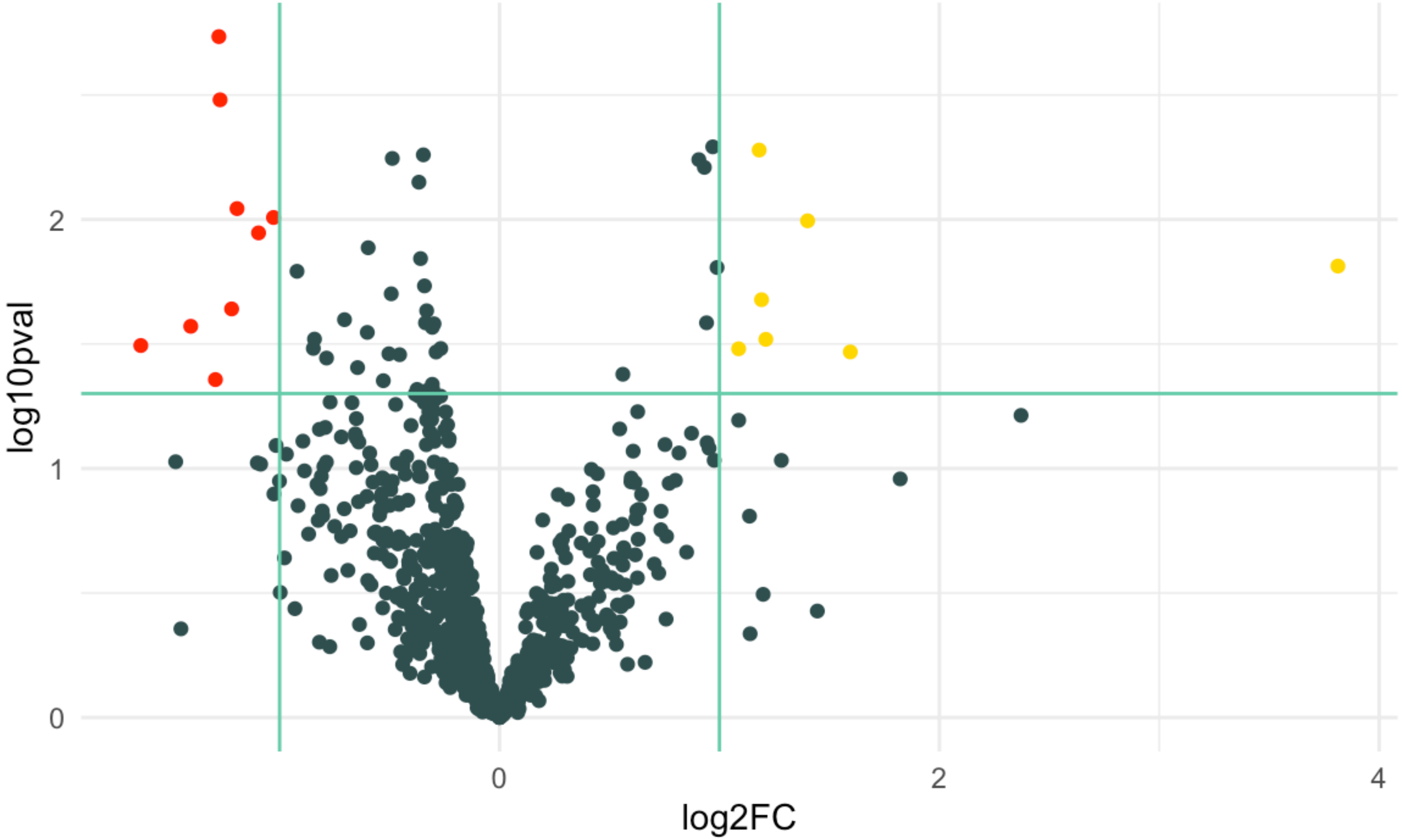




Results and discussion

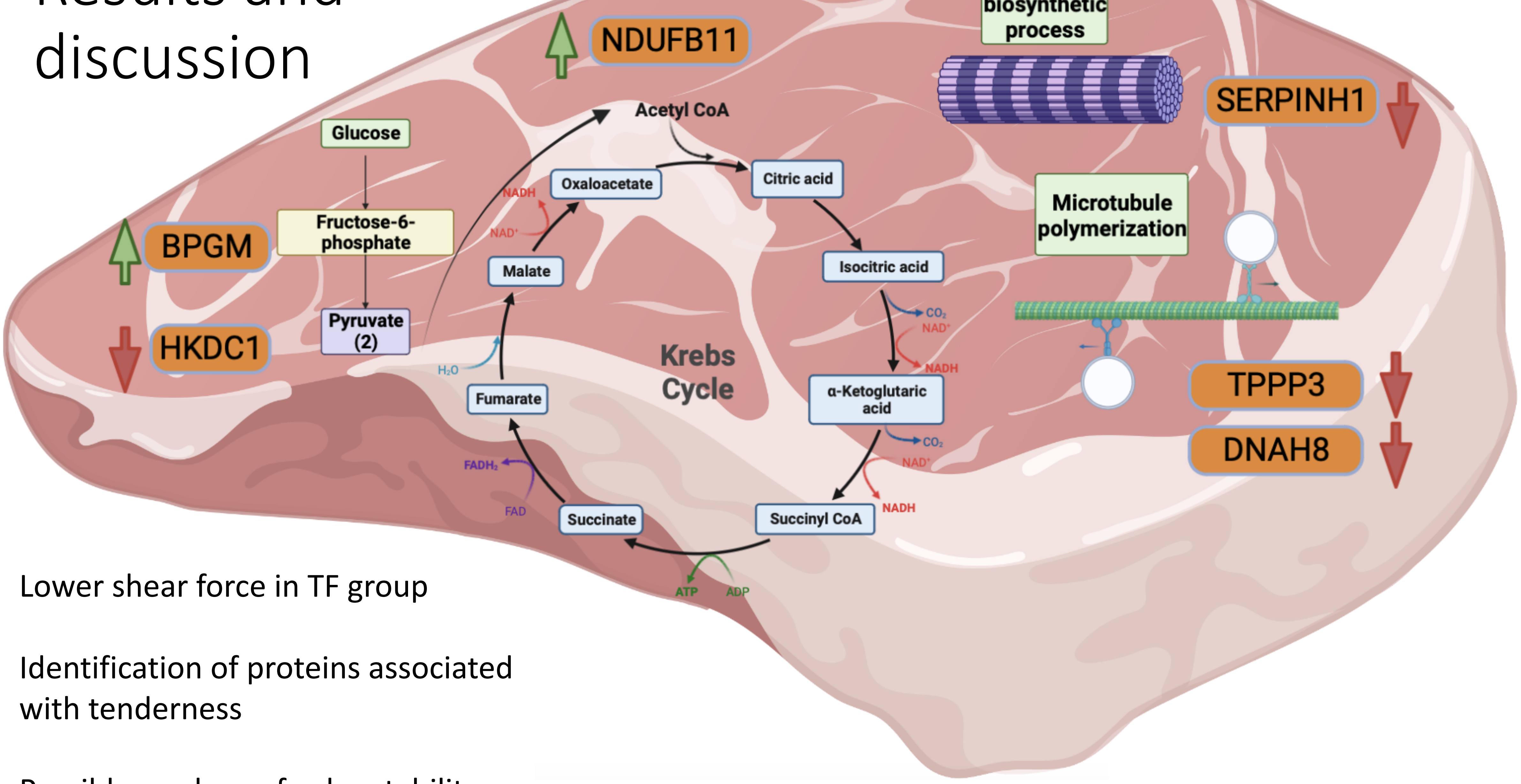
TF vs. TF+S1

- 16 proteins differentially abundant
- 9 proteins down-regulated (red)
- 7 proteins up-regulated (yellow)



Results and discussion

TF vs. TF+S1



NDUFB11

Acetyl CoA

Glucose

Fructose-6-phosphate

Pyruvate (2)

BPGM

HKDC1

Oxaloacetate

Citric acid

Isocitric acid

CO_2

NAD^+

NADH

α-Ketoglutaric acid

CO_2

NAD^+

NADH

Succinyl CoA

ATP

ADP

Succinate

FAD

$FADH_2$

Fumarate

H_2O

Malate

NAD^+

NADH

Krebs Cycle

Collagen biosynthetic process

SERPINH1

Microtubule polymerization

TPPP3

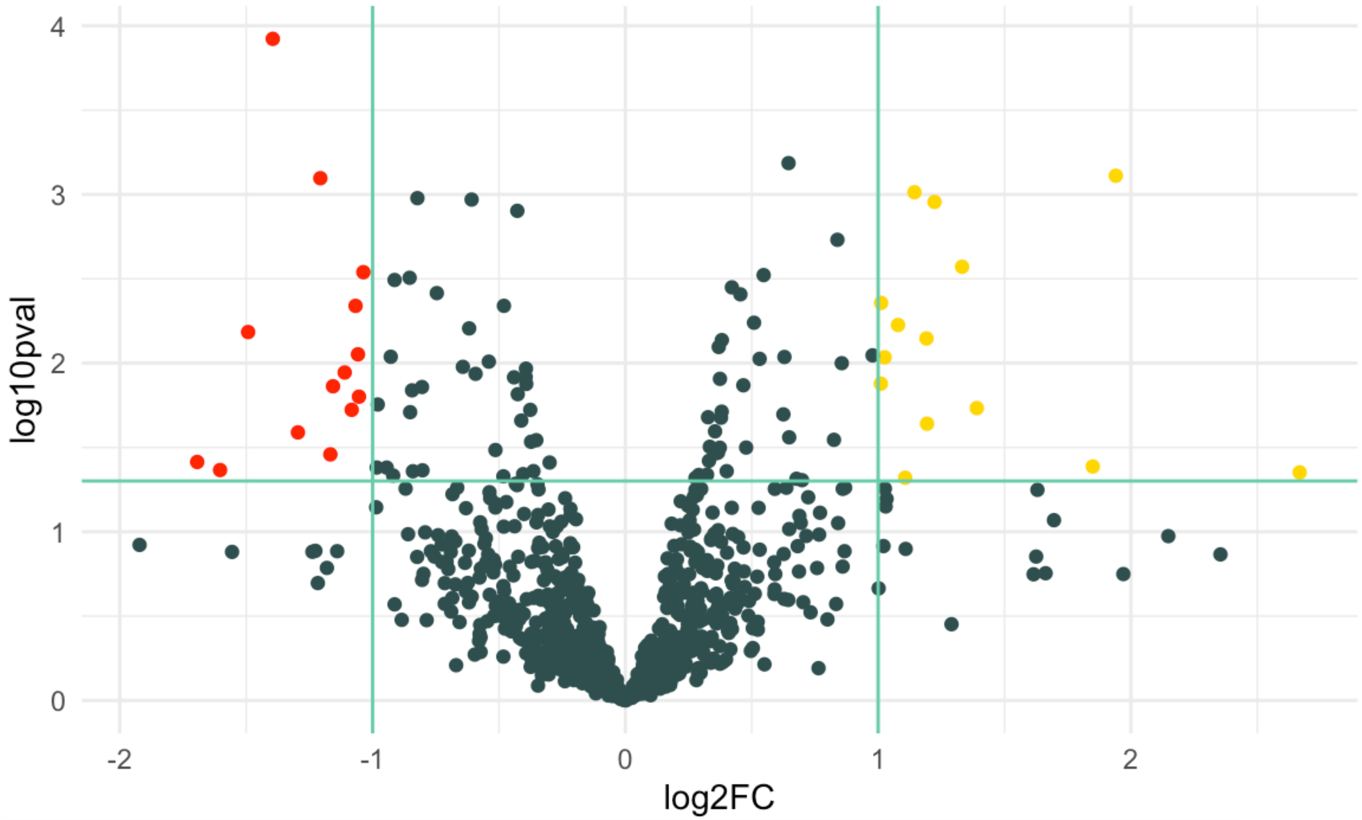
DNAH8

- Lower shear force in TF group
- Identification of proteins associated with tenderness
- Possible markers of color stability

Results and discussion

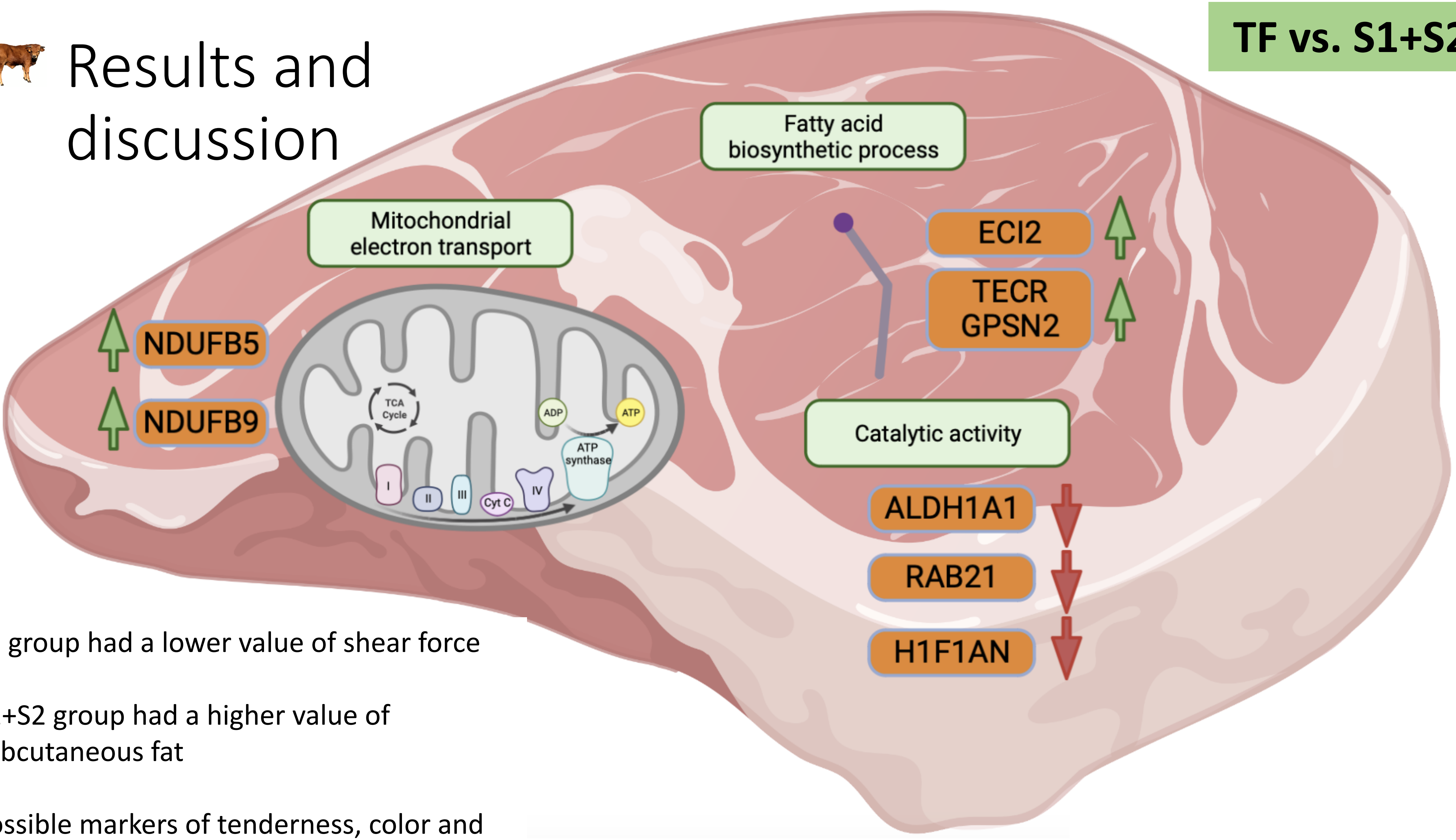
TF vs. S1+S2

- 28 proteins differentially abundant
- 14 proteins down-regulated (red)
- 14 proteins up-regulated (yellow)



Results and discussion

TF vs. S1+S2



Mitochondrial electron transport

- NDUFB5 ↑
- NDUFB9 ↑

Fatty acid biosynthetic process

- ECI2 ↑
- TECR GPSN2 ↑

Catalytic activity

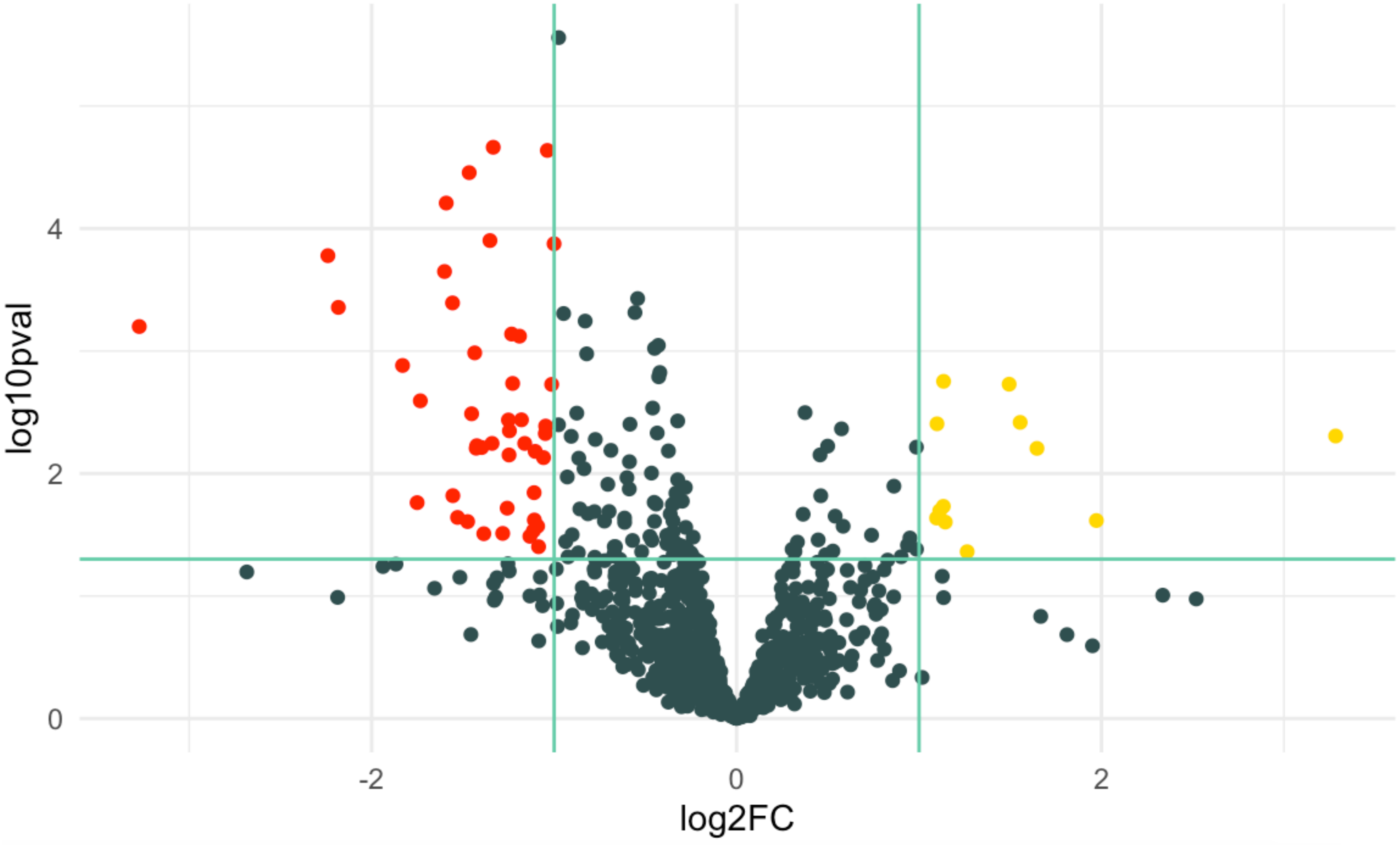
- ALDH1A1 ↓
- RAB21 ↓
- H1F1AN ↓

- TF group had a lower value of shear force
- S1+S2 group had a higher value of subcutaneous fat
- Possible markers of tenderness, color and fat deposition

Results and discussion

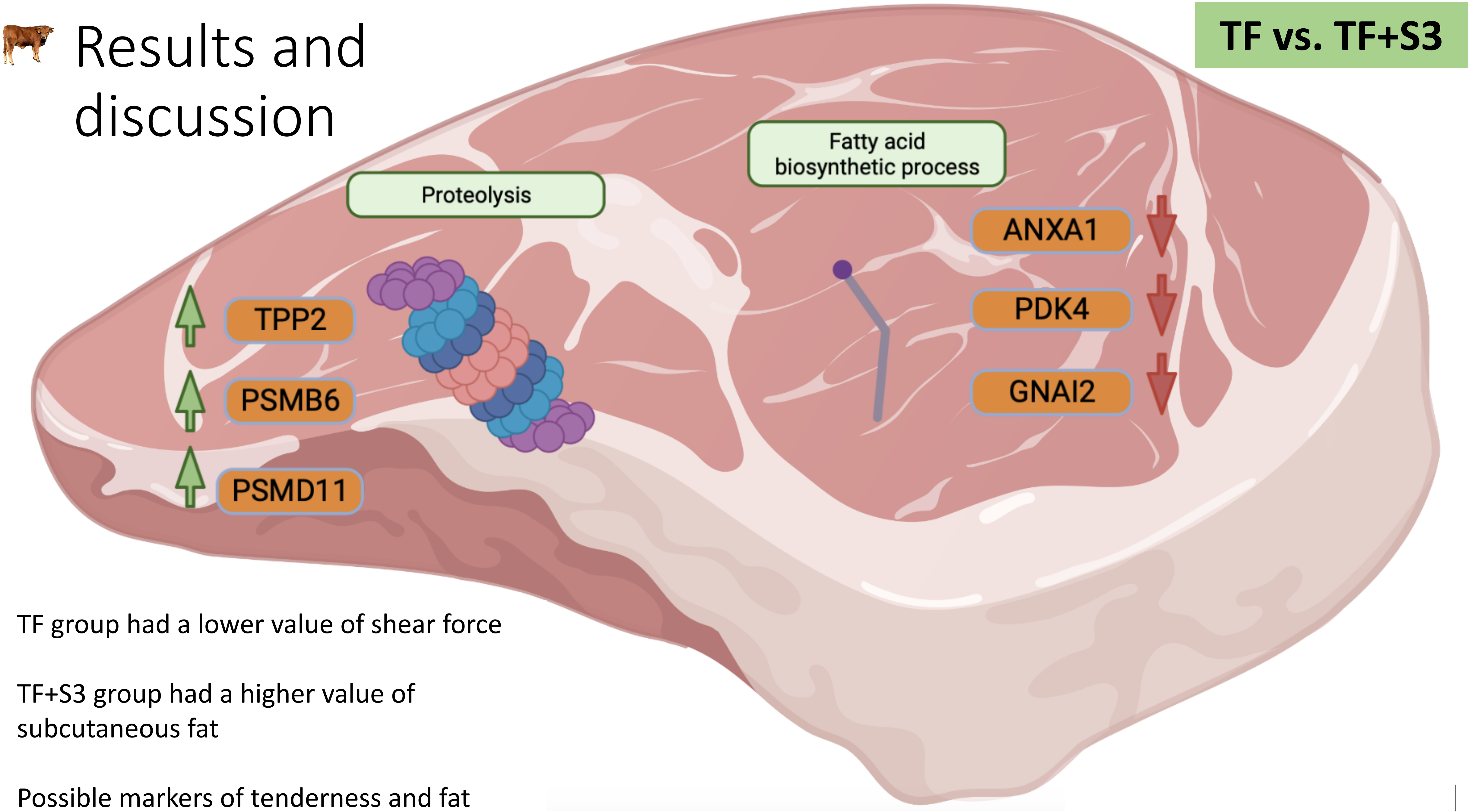
TF vs. TF+S3

- 57 proteins differentially abundant
- 45 proteins down-regulated (red)
- 12 proteins up-regulated (yellow)



Results and discussion

TF vs. TF+S3

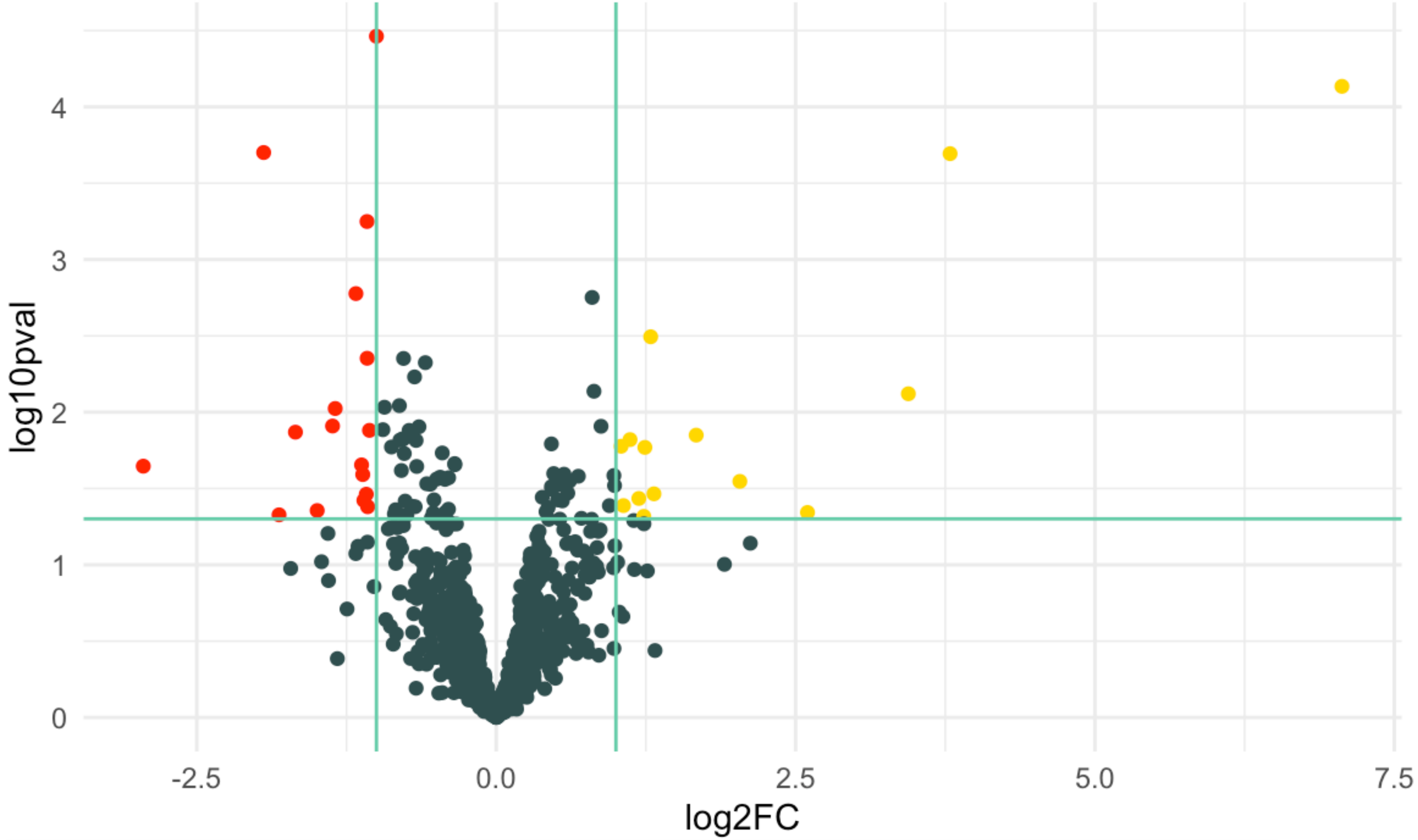


- TF group had a lower value of shear force
- TF+S3 group had a higher value of subcutaneous fat
- Possible markers of tenderness and fat accumulation

Results and discussion

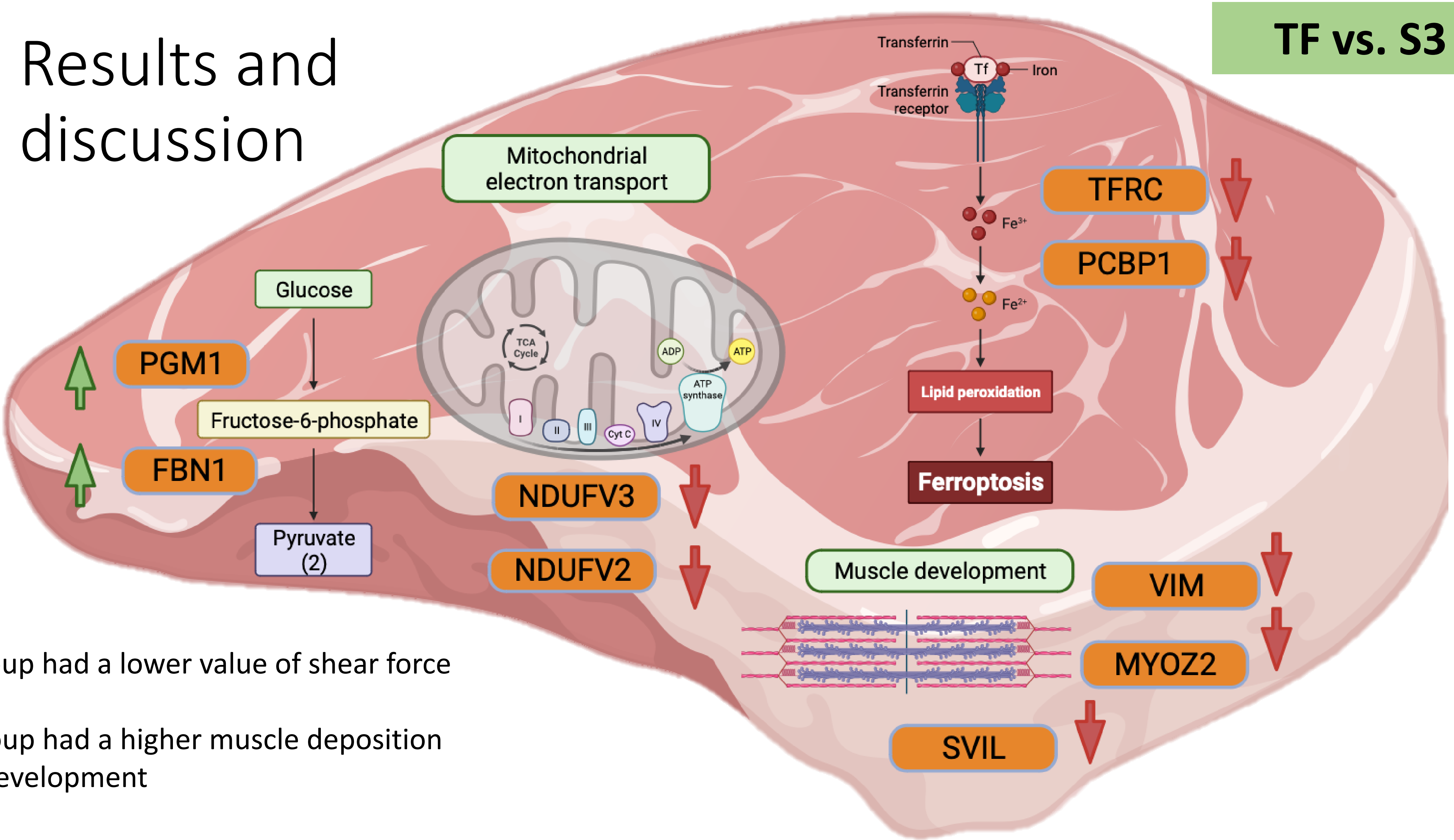
TF vs. S3

- 31 proteins differentially abundant
- 17 proteins down-regulated (red)
- 14 proteins up-regulated (yellow)



Results and discussion

TF vs. S3



- TF group had a lower value of shear force
- S3 group had a higher muscle deposition and development
- Possible markers of tenderness, color and muscle development

Conclusion

- There were proteins with high abundance involved in mechanisms that affect the color, tenderness and water holding capacity of meat.

- We found some putative biomarkers of meat quality for the Arouquesa breed.

- It was possible to distinguish different metabolisms up-regulated among the different systems.

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cevargado
Os resultados confirmam a diferença.