

PAG 2020

# Integrated -Omics Approaches for Meat Quality Improvement



**UF|IFAS**  
UNIVERSITY of FLORIDA

Department of  
Animal Sciences

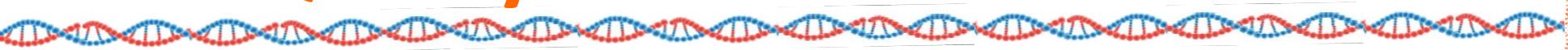
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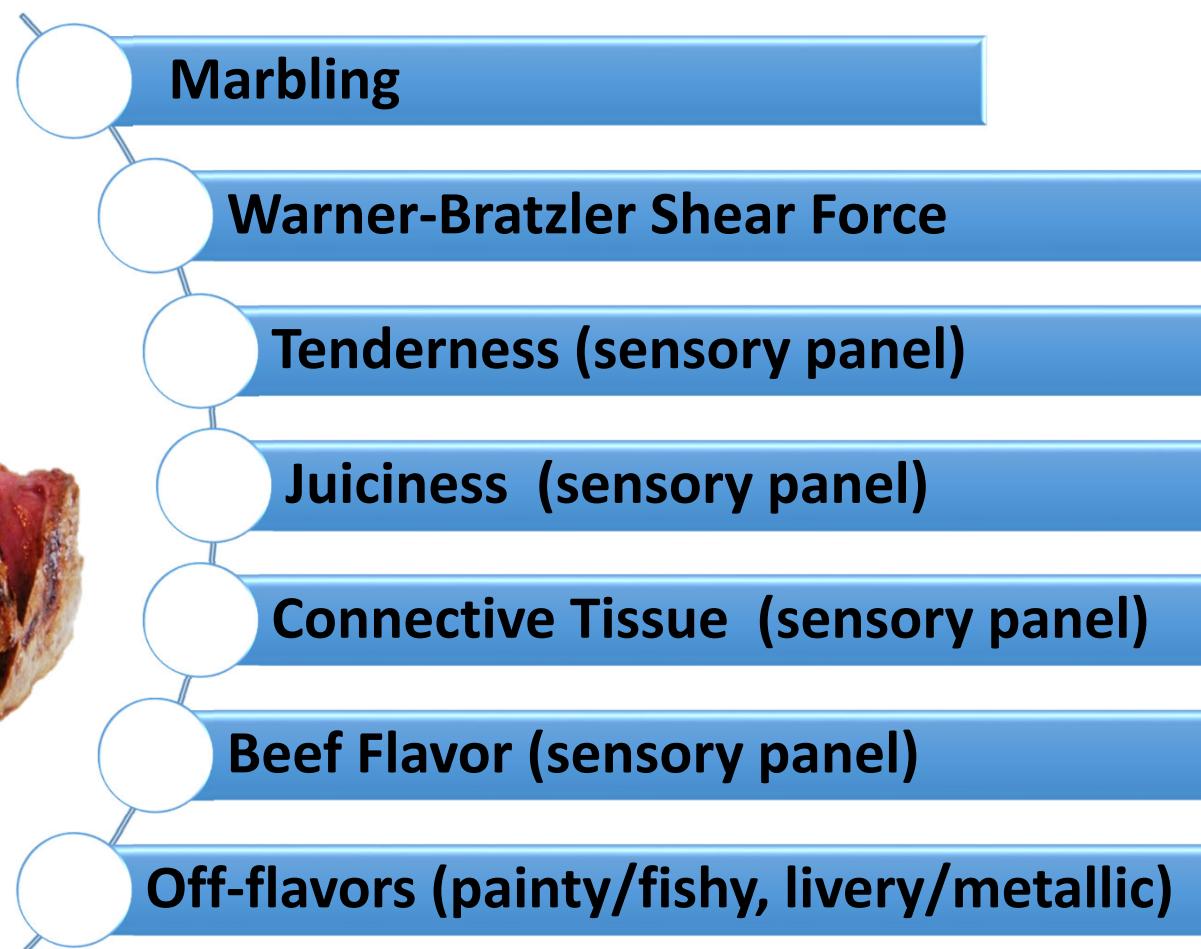
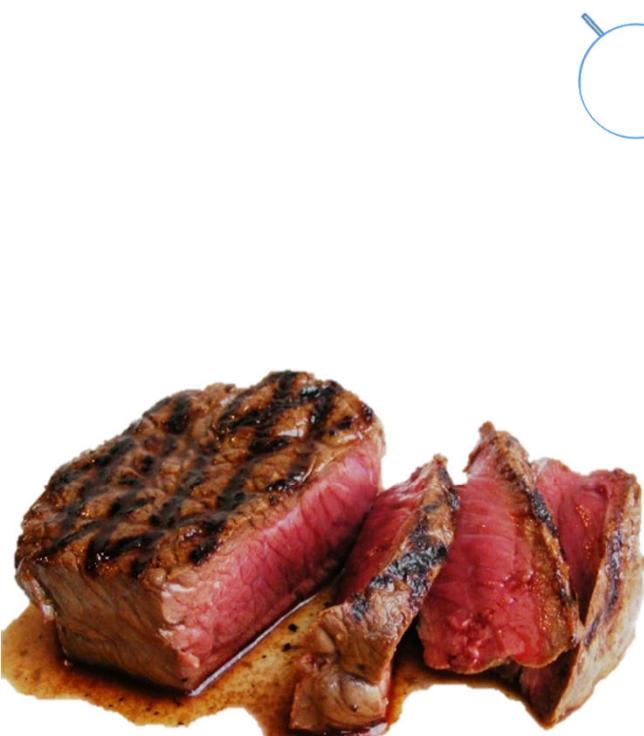
# Meat Quality



- Top priority for beef industry
  - Great power to influence demand
  - Can be improved
- Very important for *B. indicus* crosses
  - Routinely penalized for relatively **low marbling** score.
  - Routinely penalized for **perceived** inadequate **tenderness**

**Goal:** Develop genomic tools to select for superior meat quality in *Bos Indicus* influenced populations.

# Meat quality – complex of complex traits



# RNA Level - expressionQTL

# Gene expression - eQTL

## • Meat quality index:

- PCA on marbling, WBSF, cooking loss, juiciness, tenderness, connective tissue
- Used PC1, PC2 and PC3 to calculate a meat quality index
- Select **80** animals with **low** and **high** meat quality index
- Global gene expression (**RNAseq**)

**Goal:** Combine gene expression and genotypic information to understand the genetic architecture of meat quality.

### Low index

N = 40

Avg = **1.15**

Tougher  
Dryer  
More CT  
Less marbling

### High index

N = 40

Avg = **3.35**

More tender  
More juicy  
Less CT  
More marbling

- Illumina HiSeq 3000 PE100 platform
- Sequencing depth: **30X**
- Raw data: 101 bp **paired-end reads**

- **QC:** base + read filtering, single reads screening
- Mapping the reads: **Tophat & Bowtie**  
(genome guided transcriptome assembly)
- Gene counts (**HTSeq**) and Exon Counts (**DEXSeq**)

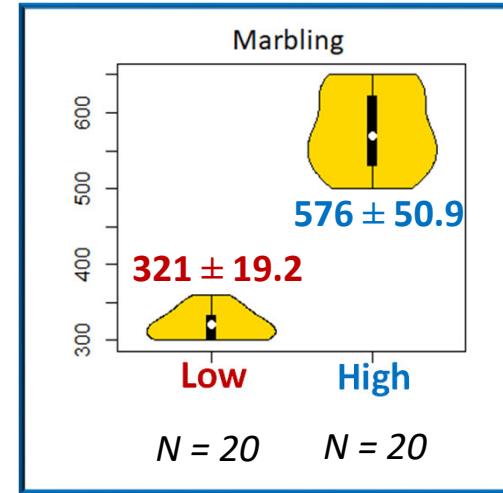
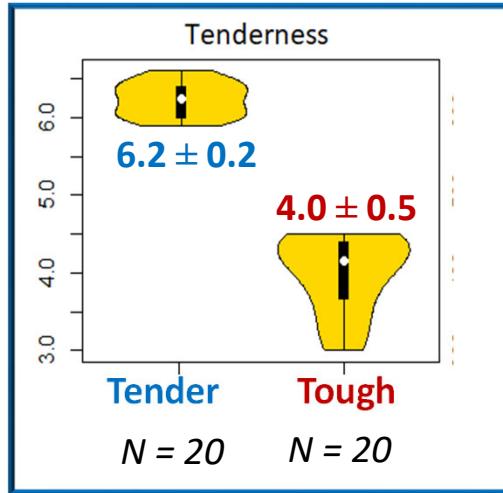
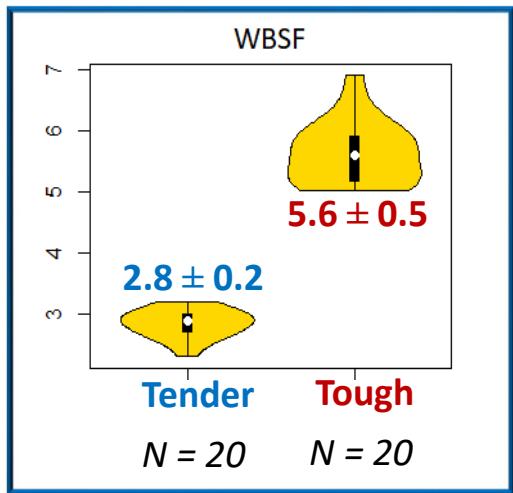
# RNA seq data analyses



## Differential Expression

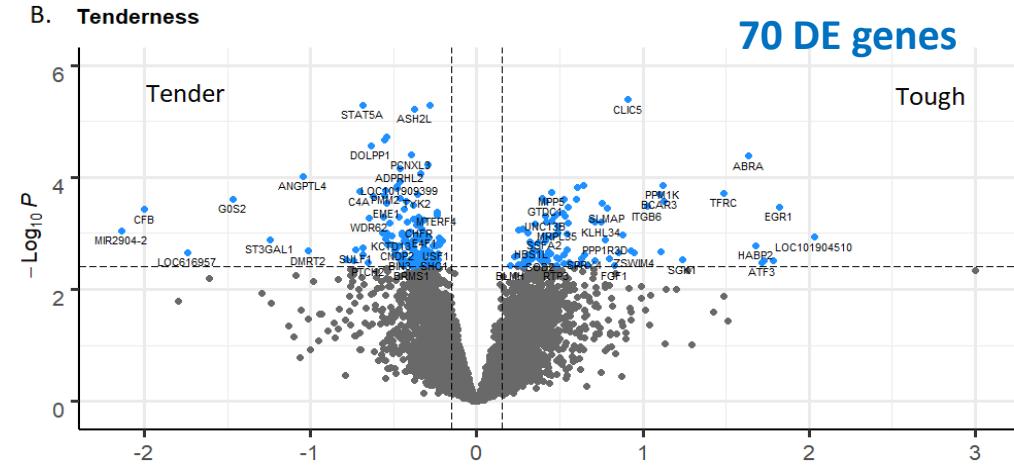
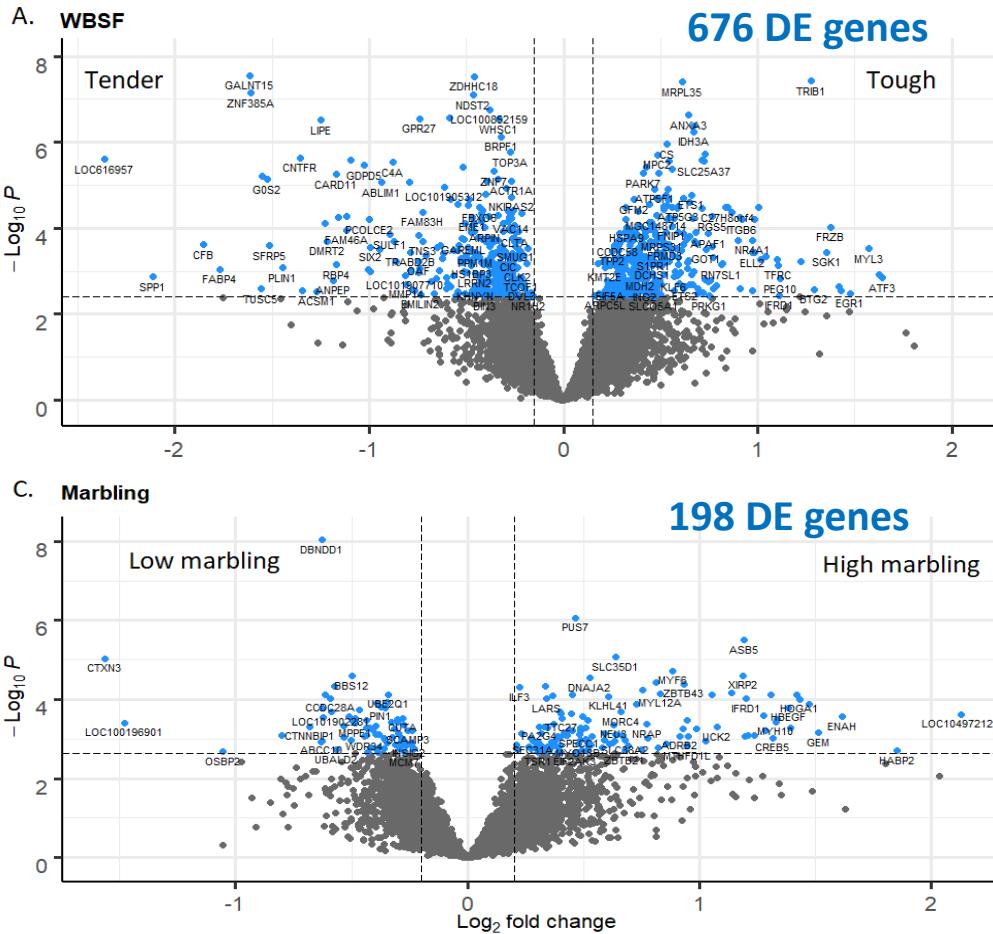
- Compare **two extreme groups** for WBSF, tenderness and marbling
- Selected **40** extreme animals: 20 high and 20 low performance
- Gene **counts** = **response** variable
- Regression using the negative binomial distribution (**DESeq2**)

# Differential Expression Analysis



- Used **DESeq2** to identify differentially expressed (DE) genes
- Gene counts = **response** variable
- Year of birth, breed group, category** (tender/tough, high/low marbling) = **fixed** effects
- Genes with Benjamini-Hochberg adjusted p-values < **0.05** for WBSF,  
< **0.1** for tenderness and marbling = **DE** genes.

# Differential Expression Analysis



- DE gene, adjPvalue < 0.05, 0.1

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# RNA seq data analyses

## Differential Expression

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## Gene Expression Association

- **Continuous** response variable (Meat quality index)
- Gene / exon **counts** = **predictor**
- All **80** animals
- Huber's M-estimator robust regression: less affected by outliers

- Meat Quality Index = response variable
- Gene/exon **counts** = **predictor**
- Year of birth, PC1 (pop structure) = **fixed effects**
- 8,799 genes and 96,645 exons were tested

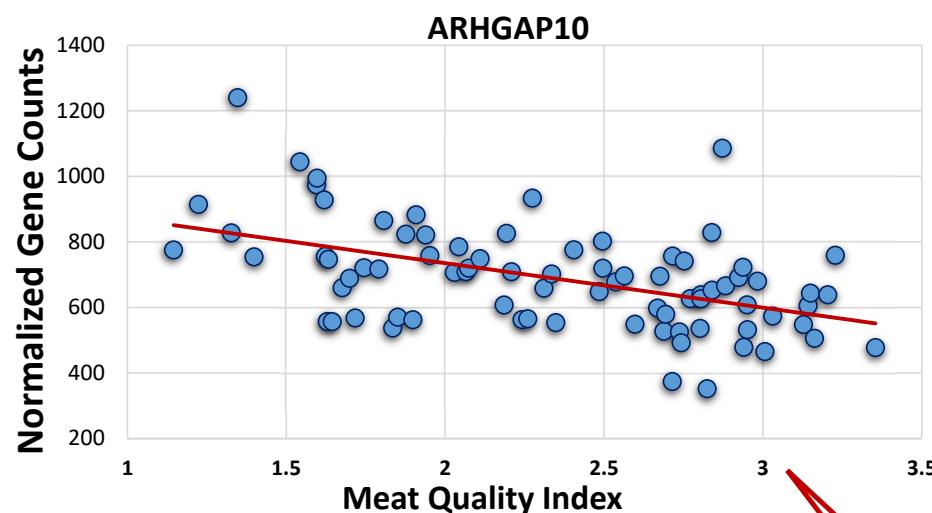
# Gene Expression Association Analysis



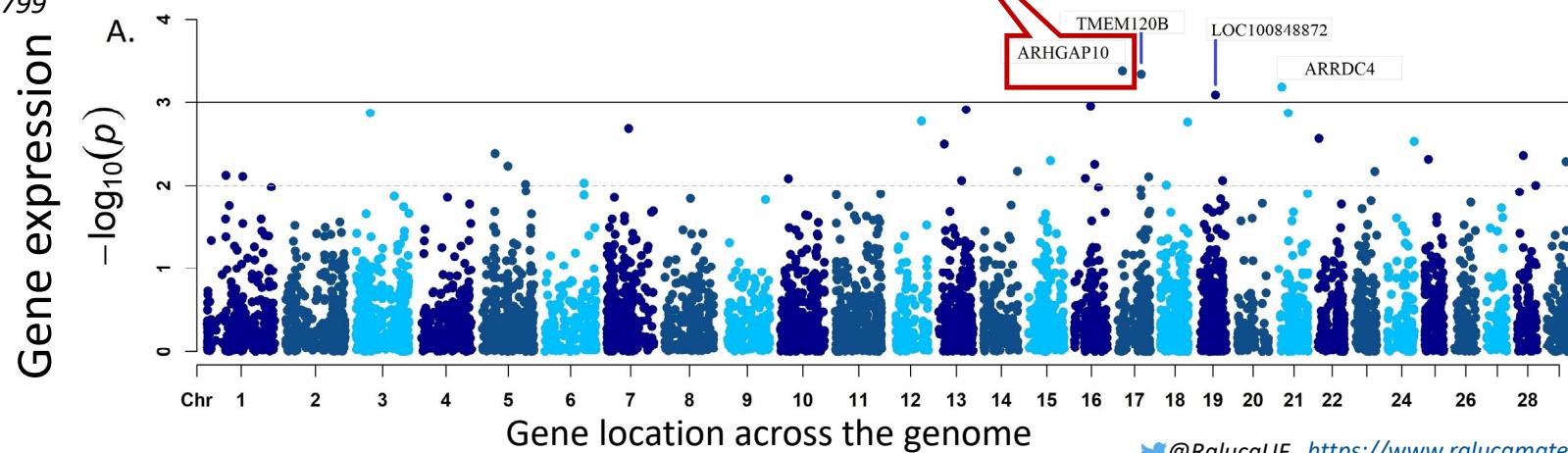
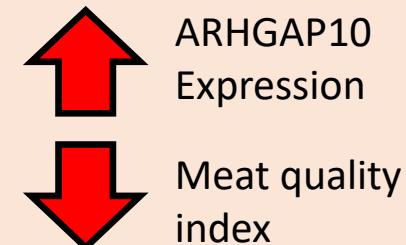
Associated genes = 208

P-value  $\leq 0.05$

Tested genes = 8,799



**ARHGAP10** - regulates actin cytoskeleton remodeling.  
↑ expression, more stable actin cytoskeleton structure.



# Genetical Genomics

# Map genomic regions for gene expression

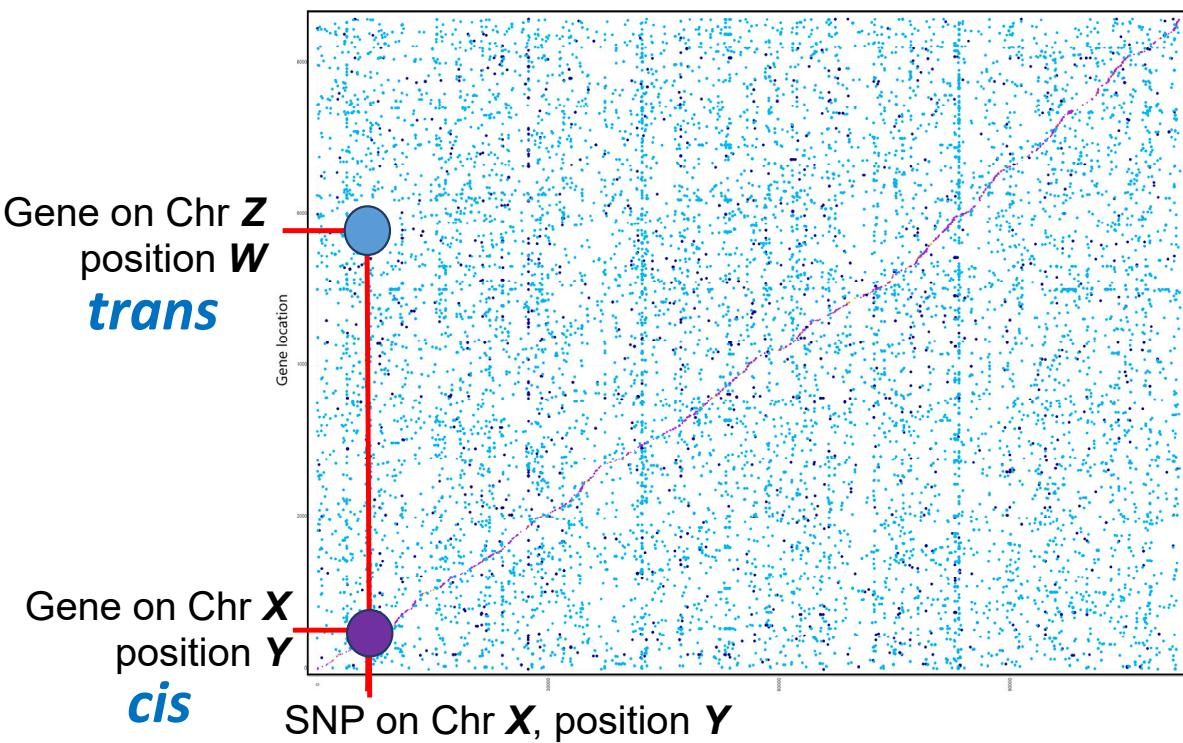
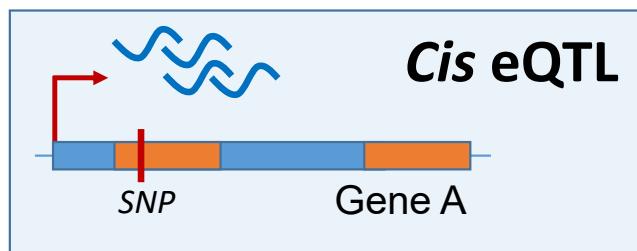
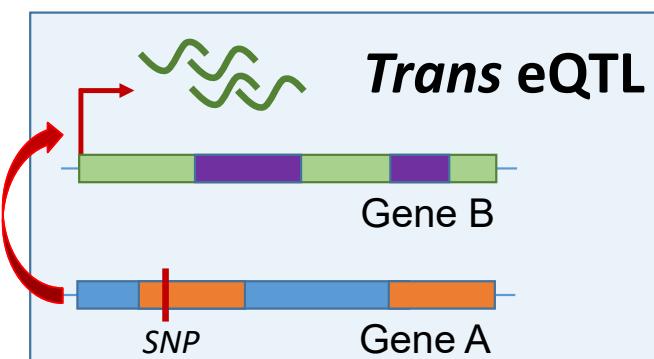
- Use gene expression as a trait, GWAS for each gene (250K)
  - 8,588 autosomal genes expressed in skeletal muscle

- Matrix eQTL
  - 112,042 **SNPs** and 8,588 **genes**
  - Gene **counts** = **response**
- SNP **genotype** and year of birth = **fixed effects**
- **PC1** = **covariate** (pop structure)

# Map genomic regions for gene expression

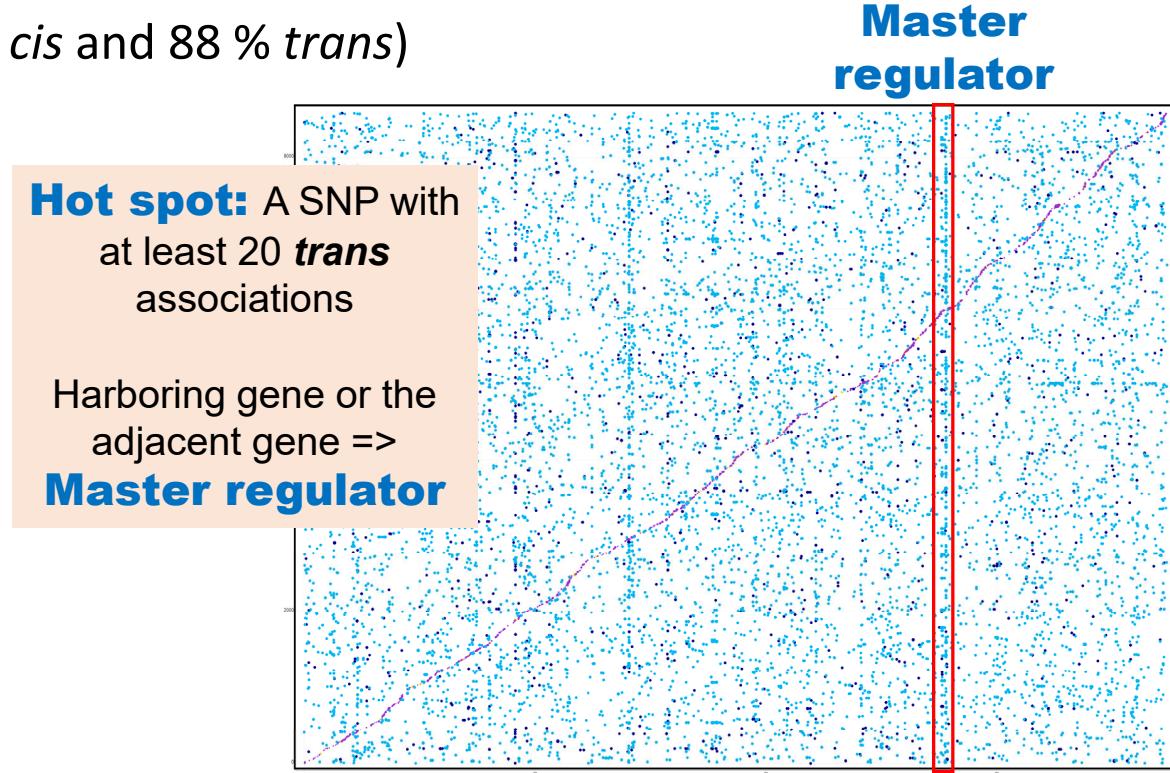
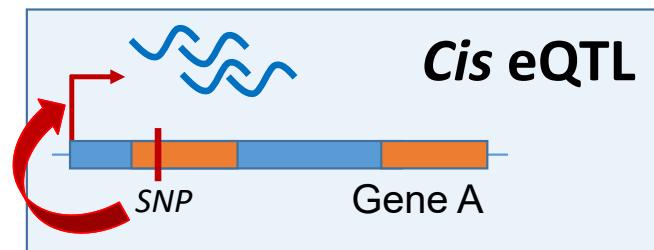
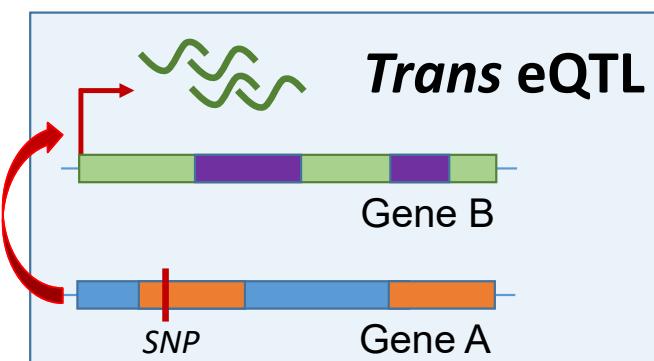
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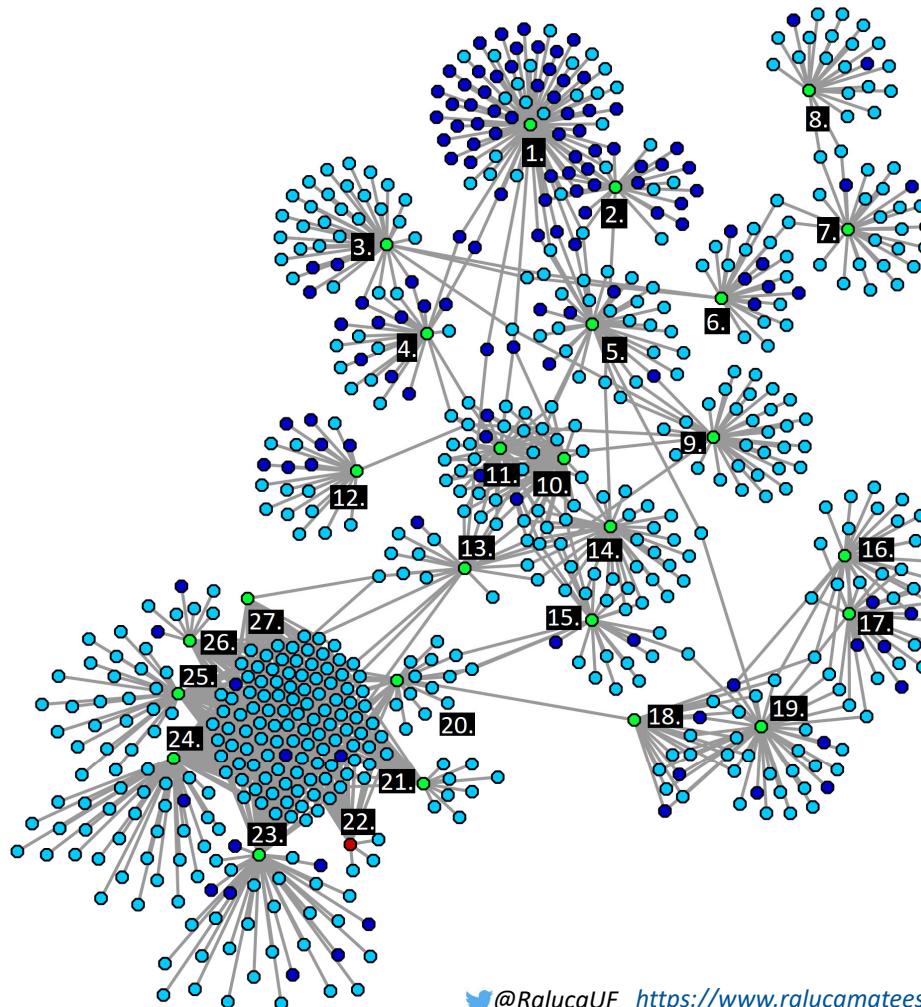


# Network of expression master regulators

Master regulator  
Diff master regulator

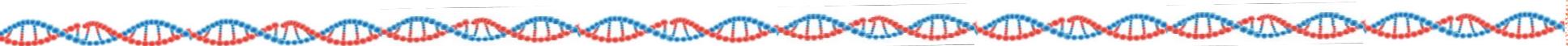
Regulated gene  
Diff regulated gene

- **27** expression **master regulators**
- Associated with **674** regulated **genes**
- Classified as membrane associated or cytoskeletal proteins, transcription factors and DNA methylases.



1	NTF3
2	PDE8B
3	GAD1
4	ZNF445
5	FAT4
6	PCGF5
7	ALAD
8	ZNF804A
9	ENSBTAG00000035487
10	PAX8
11	PSD4
12	OR4S1
13	RUNX1T1
14	TTC25
15	ENSBTAG00000011638
16	CSAD
17	KRT7
18	MYH14
19	KLK4
20	KCNU1
21	TOR1AIP1
22	KDM4A
23	OR13F1
24	ENSBTAG0000000336
25	TM4SF1
26	SIPA1L2
27	GPR98

# Conclusions



- Different types of analyses combined with multiple layers of omics information:
  - At the **phenotypic** level – structural equation modeling
  - At the **DNA** level – GWAS on individual traits and latent variables
  - At the **RNA** level – global gene expression in samples with extreme meat quality
- Provides new insight in the regulatory **network architecture** in LD muscle
- Positional identification of gene expression **master regulators**

**Goal:** Develop genomic tools to select for superior meat quality.

# Acknowledgements

@RalucaUF <https://www.ralucamateescu.com>

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