Genetic markers for beef quality traits

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USDA-ARS,

U.S. Meat Animal Research Center

# U.S. Meat Animal Research Center

- USDA-ARS in-house research agency

- USMARC

  - South central Nebraska

  - 7,000 brood cows – closed herd - only way in is a semen tank

  - 2,800 ewes

  - 1,000 litters of pigs/year

  - 35,000 acres

    - Pasture

    - Irrigated forage

    - Irrigated row crops

    - Feedlot

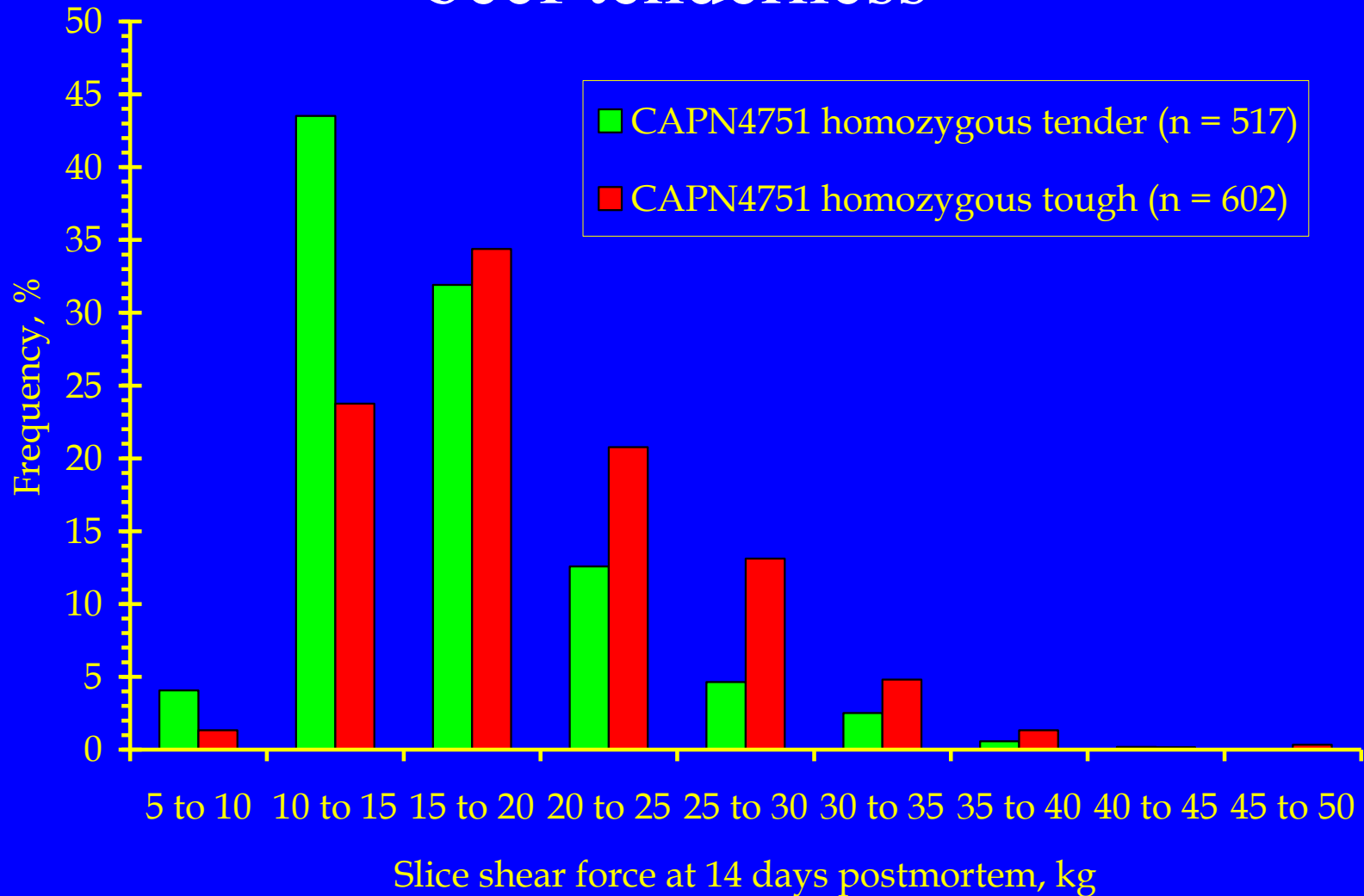# Test of tenderness SNP's in random test of U.S. Select carcasses

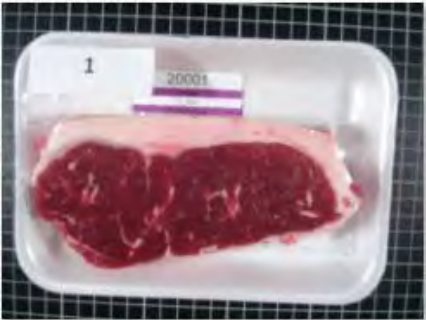# Effect of calpastatin genotype on beef tenderness
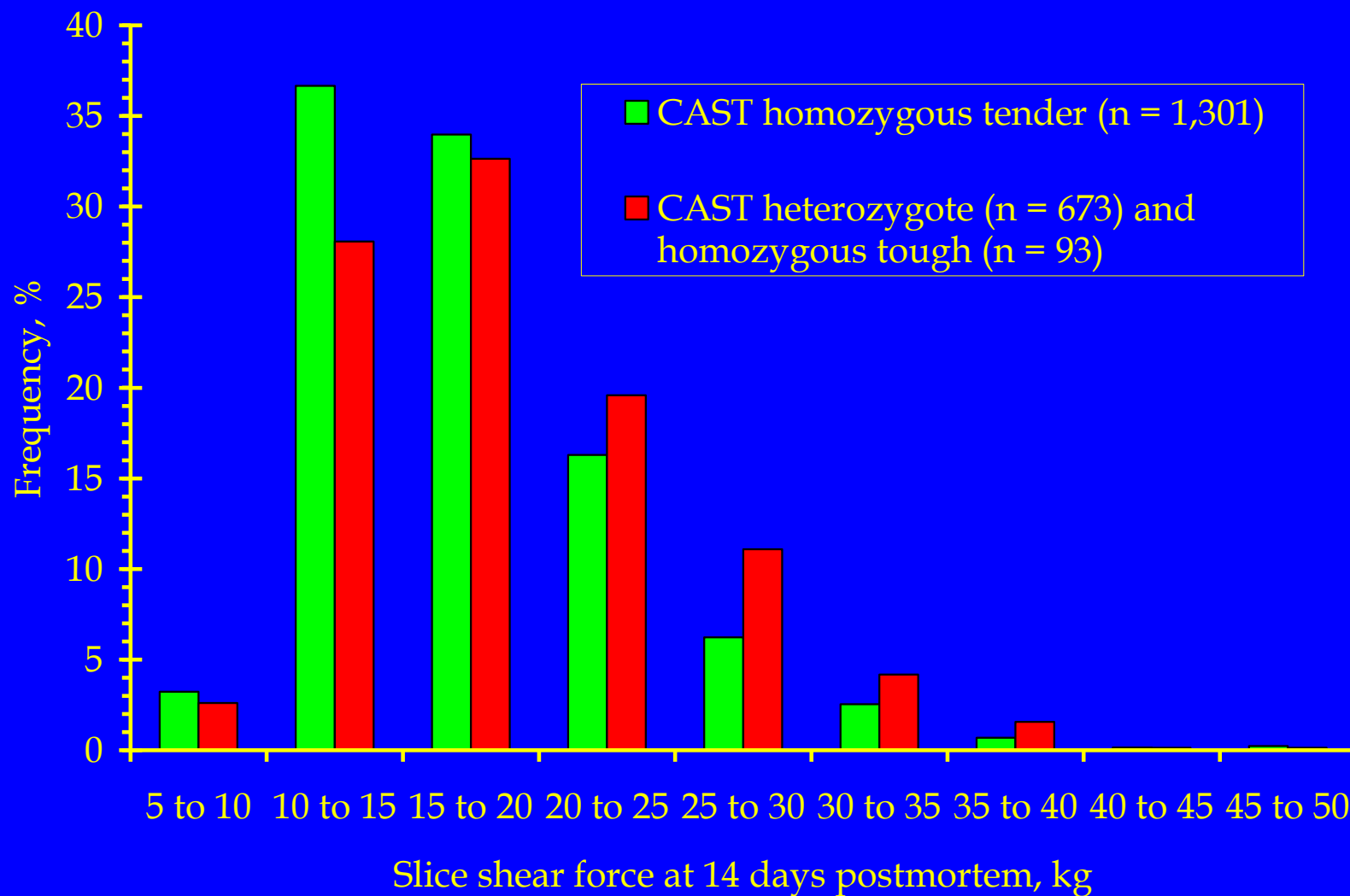
Effect of μ-calpain (CAPN316) genotype on beef tenderness
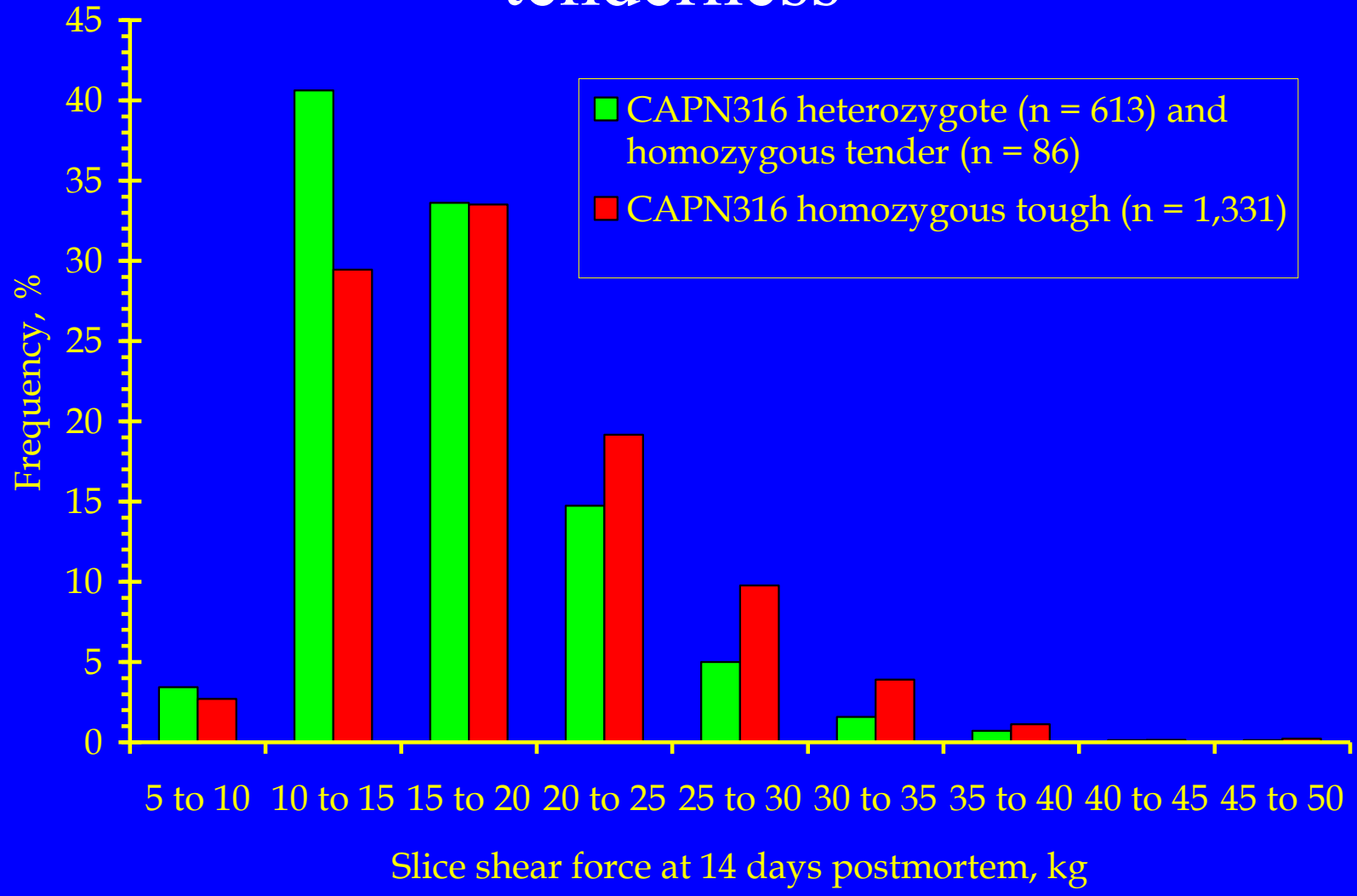
Effect of μ-calpain (CAPN4751) genotype on beef tenderness

Dark cutting condition

20001_Day_00.jpg

20002_Day_00.jpg

20003_Day_00.jpg

20004_Day_00.jpg

20005_Day_00.jpg

20006_Day_00.jpg

20007_Day_00.jpg

20008_Day_00.jpg

20009_Day_00.jpg

20010_Day_00.jpg

20011_Day_00.jpg

20012_Day_00.jpg

Dark cutting condition

- Abnormally high ultimate pH
- Due to exhaustion of glycogen reserves before slaughter
- Long-term stress
- Gender is a huge environment. Bulls, cryptorchids, heifers
- Estrus --- MGA
- Seasonality
    - Cold stress
    - Heat stress
   - Decreasing day length
    - ß-agonist ?

Dark cutting condition

- We were all taught, and accepted, that dark cutting happened because somebody messed up.
  - The packing plant blames the feeder
  - The feeder blames the plant
  - And, everybody blames the trucker

But, consider this.

- These are pen mate heifers. They, have lived the same life since they left their mother and traveled <10 miles to our feedlot.
- They, were harvested commercially within 2 minutes of each other.
- With the exception of permanent environment, the environment is the same.
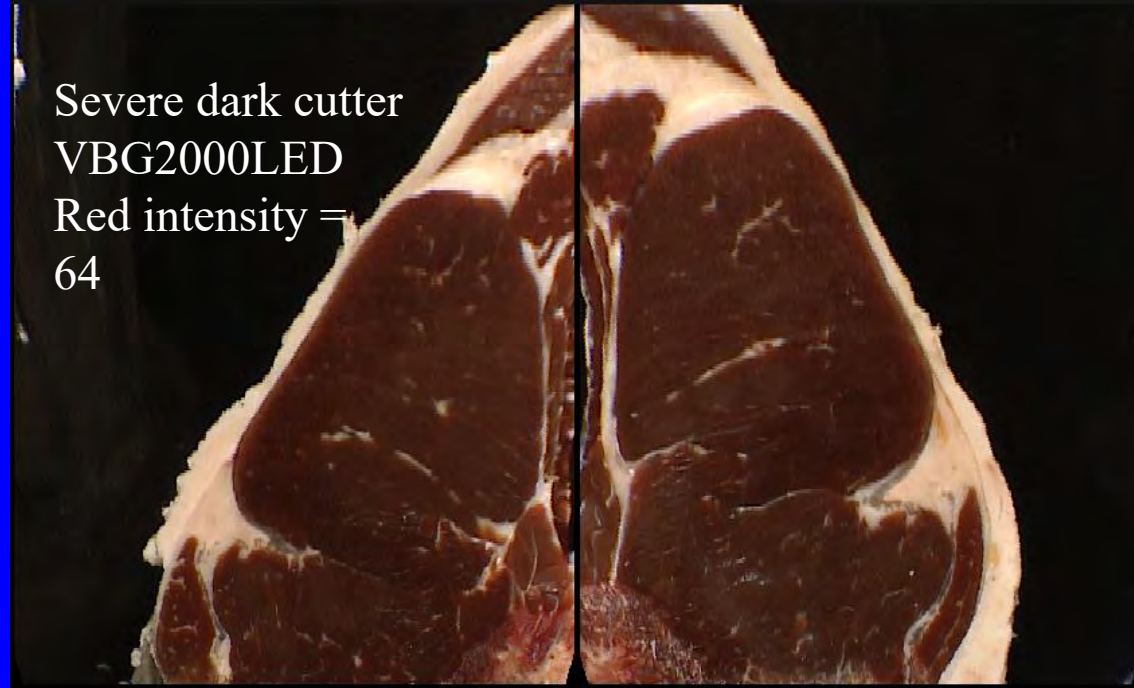
Severe dark cutter
VBG2000LED
Red intensity =
64

Pen mate heifers
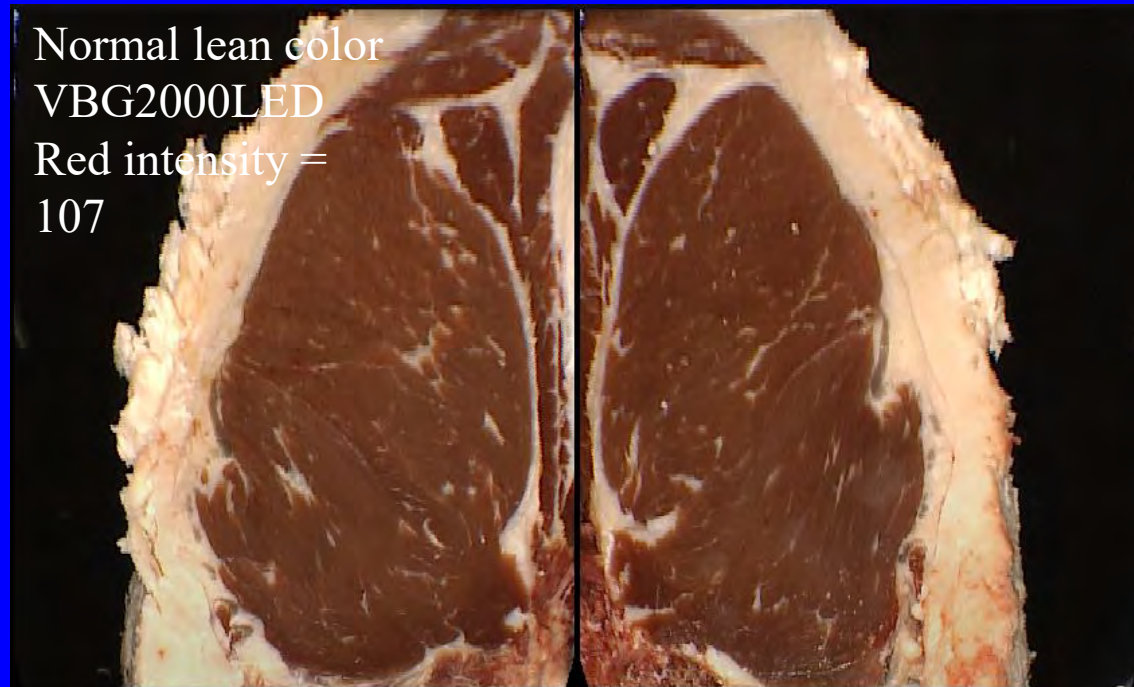
Normal lean color
VBG2000LED
Red intensity =
107

This, suggests that there is a genetic effect

VBG2000

File   Edit   Macro   Image   Video   Tools   Options   ID Reader   ?

C:\Documents and Settings\shackelford\My Documents\E+V\images\00183755.tif

183755

Image1

Image2

Weight: 815.0

Date: 02.03.06

Time: 09:47:42

REA: 16.81

CAL-YG: 1.87

Marb: Md 60

PYG: 3.2

Lean%:   64.0%

Height: 149.4
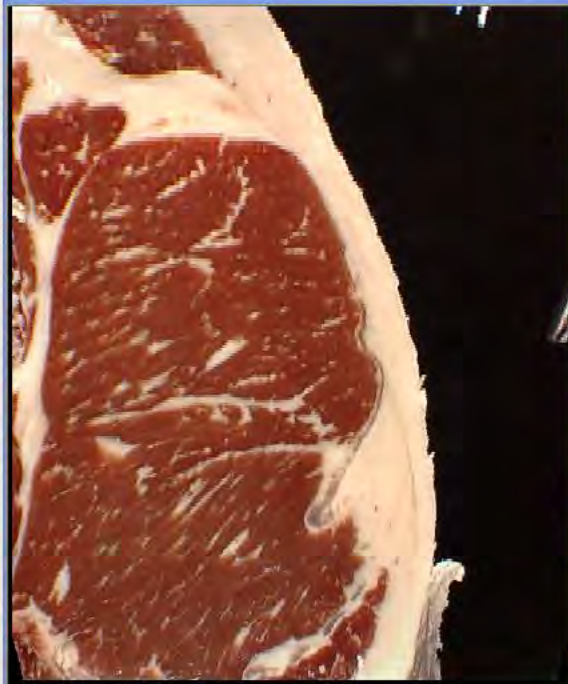
Broad: 99

with weight

Results

ID   183755

Wgt   815.0

PYG   3.2

ADJ   3.2

REA   16.8

YG   1.9

Marb Md 60

Evaluation: 0.72 s

Menue-Mode

Genomic control of dark cutting

- N = 7,355
- 60+ harvest days over 10 years
- contemporary groups
  - Heifer
  - Steer
  - Late-castrate
- Instrument evolution
- Color as a continuous variable. NOT categorical
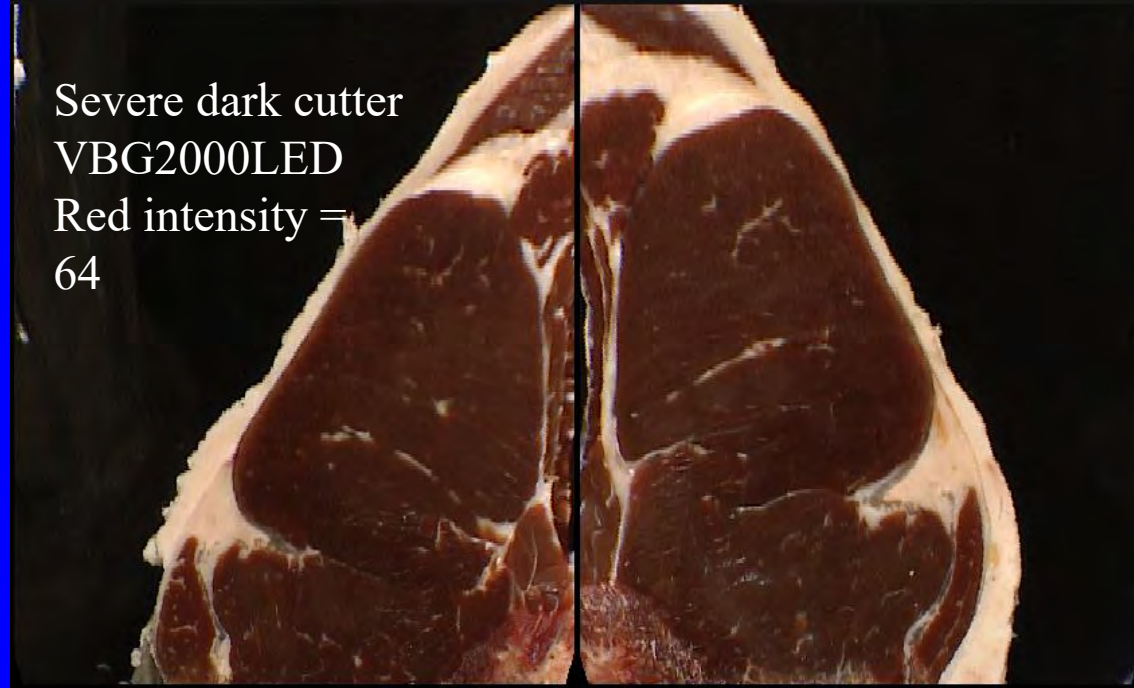
Severe dark cutter
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Pen mate heifers
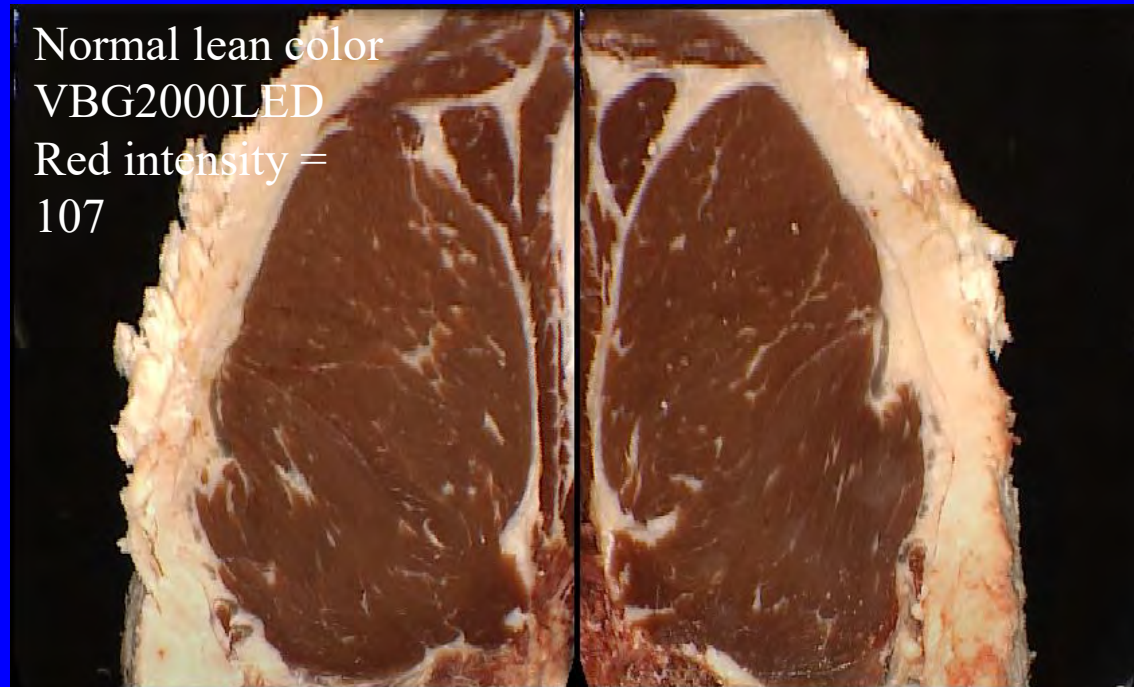
Normal lean color
VBG2000LED
Red intensity = 107

Not categorical because it isn't!

Imputation

- GPE, 18 beef breeds
- AI and multisire naturally-mated
- Every breed combination that you can imagine and many that you cannot.
- Smaller contribution from SFA and other projects (weight trait project)
- Imputed to F250

Ribeye_color_r

N = 7,355
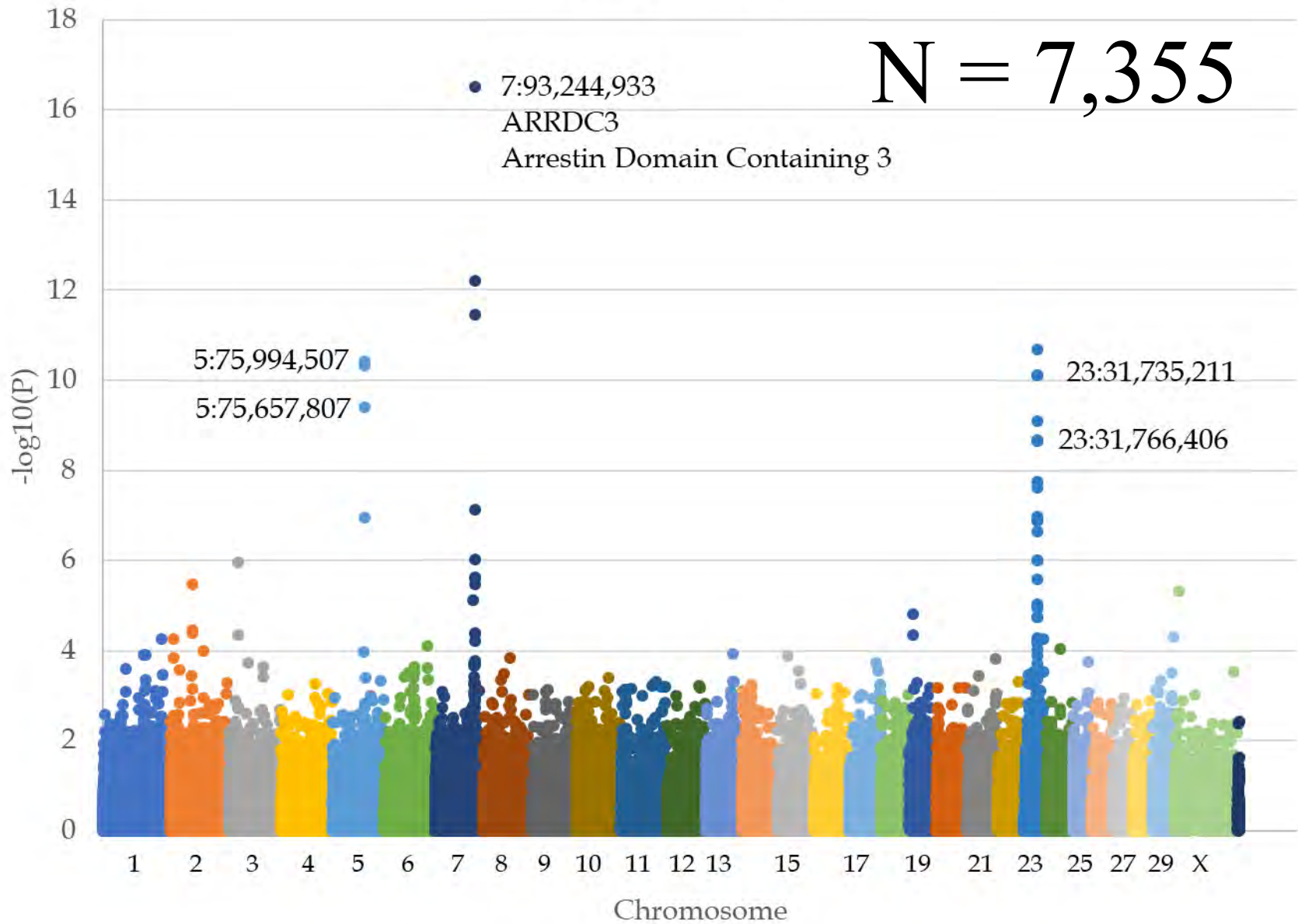
Chromosome 7 peak

- Functional mutation in a gene (ARRDC3) that regulates ß2 adrenergic agonist receptors

- This SNP is on many commercially-available SNP chips.

- Favorable allele is not fixed in any of the major beef breeds.
    - Highest frequency is ~ 0.7
    - For several breeds the frequency is less than 0.2
    - Originated in British breeds

Chromosome 7 peak

- Unfavorable allele is highly-conserved across species.

- Little change in sequence over 800 million years of evolution dating make to drosophila melanogaster.

- Similar among…

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Chromosome 7 peak

- Unfavorable allele is highly-conserved across species.

- Little change in sequence over 800 million years of evolution dating make to drosophila melanogaster.

- Similar among…

Ribeye_color_r
(0 to 255) lower value is darker..unfavorable
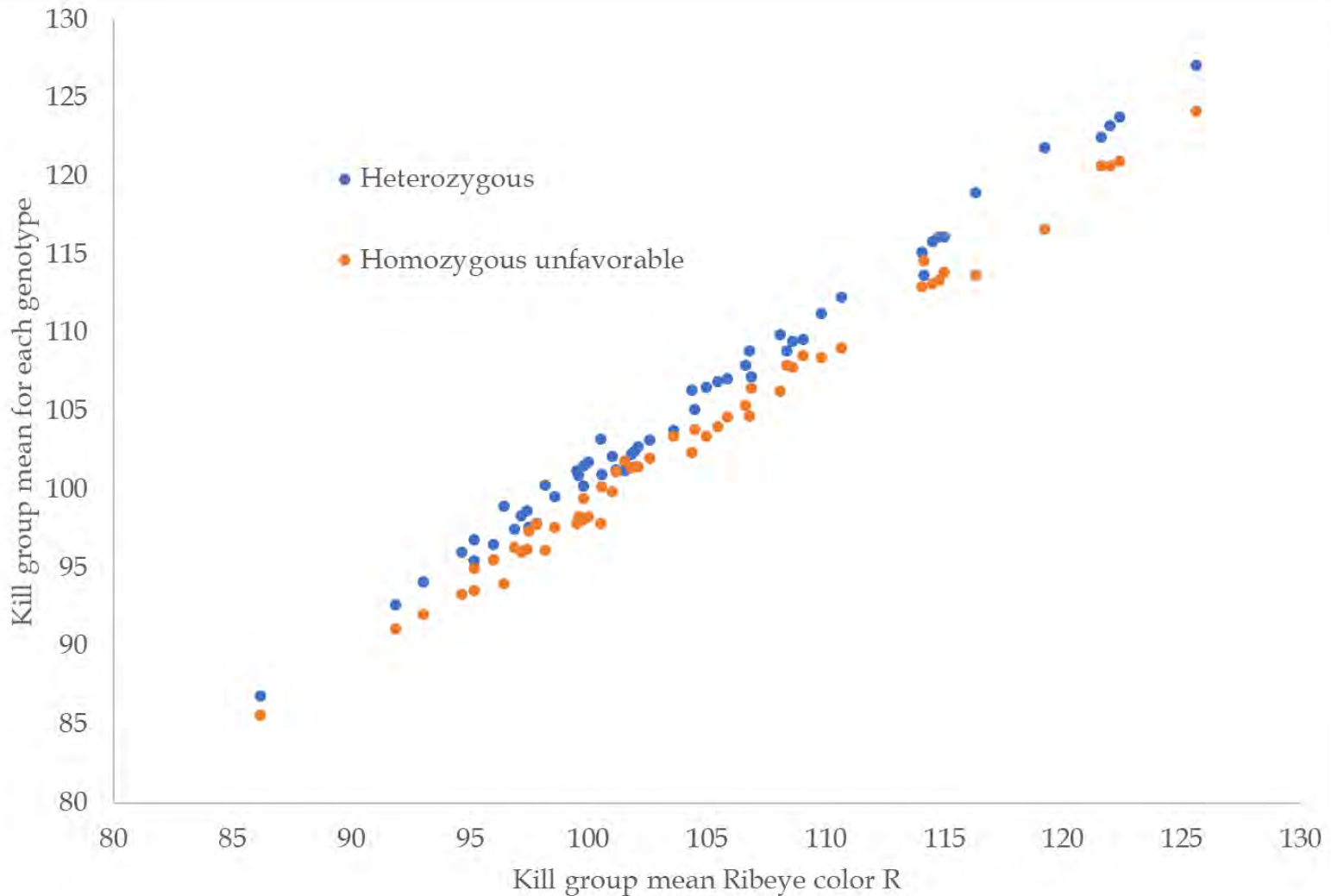
The blame game

- Turns out that maybe, the breeder is at fault.

Genetic correlation

- What happens if we select to decrease susceptibility to dark cutting?

- We are investigating

Dark cutting G × E

- Gary Bennett
  - Selecting Functional Alleles project
- Non-retained animals are fed for slaughter
  - And they have high density genotypes when they enter the feedlot at weaning!
- Blocked by Line (Angus and 3 composites), Pop (Control and select line), Sex (steers and heifers), and dark cutting genotype and assigned to
  - Natural (no life time implant)
  - Aggressive implant strategy
- Over the next 4 years, should be 1,500 to 2,000 head of excess steers and heifers in this study

Dark cutting G × E

– Natural (no life time implant)

– Aggressive implant strategy

Average of HCW Row Labels	Column Labels Implanted	Nonimplanted	
106	717.5	676.9	-41
125	716.5	669.4	-47
126	724.7	677.8	-47
127	693.0	614.7	-78
Grand Total	711.8	657.1	-55

Project	2_SFA		
Sex	(Multiple Items)		

Average of HCW Row Labels	Column Labels Implanted	Nonimplanted	
106	809.1	733.6	-75
125	855.6	765.9	-90
126	803.8	723.6	-80
127	795.5	703.6	-92
Grand Total	815.7	730.3	-85

Dark cutting G × E

Average of Marb Row Labels	Column Labels Implanted	Nonimplanted	Grand Total	
106	510	534	521.8	25
125	385	404	394.9	19
126	426	505	465.7	79
127	469	530	499.4	61
Grand Total	**443**	**489**	**466.0**	**46**

Project	2_SFA
Sex	(Multiple Items)

Average of Marb Row Labels	Column Labels Implanted	Nonimplanted	Grand Total	
106	450	529	488.2	80
125	369	387	377.8	17
126	417	450	434.0	33
127	452	531	490.8	80
Grand Total	**421**	**472**	**446.2**	**50**

Dark cutting G × E

Average of % Choice	Column Labels			
Row Labels	Implanted	Nonimplanted	Grand Total	
106	100	100	100.0	0
125	23	39	31.1	16
126	63	100	81.6	37
127	87	100	93.5	13
Grand Total	66	83	74.2	17

Project	2_SFA
Sex	(Multiple Items)

Average of % Choice	Column Labels			
Row Labels	Implanted	Nonimplanted	Grand Total	
106	72	89	80.4	16
125	12	28	19.8	15
126	53	69	61.0	17
127	67	93	79.8	27
Grand Total	50	69	59.4	19

Dark cutting G × E

Project	2_SFA			
Sex	(Multiple Items)			
Average of RibEyeColor_r	Column Labels			
Row Labels	Implanted	Nonimplanted	Grand Total	
0	104.9	104.8	104.8	-0.1
1	99.3	101.7	100.4	2.4
2	97.5	98.9	98.2	1.3
Grand Total	98.4	99.9	99.1	1.4

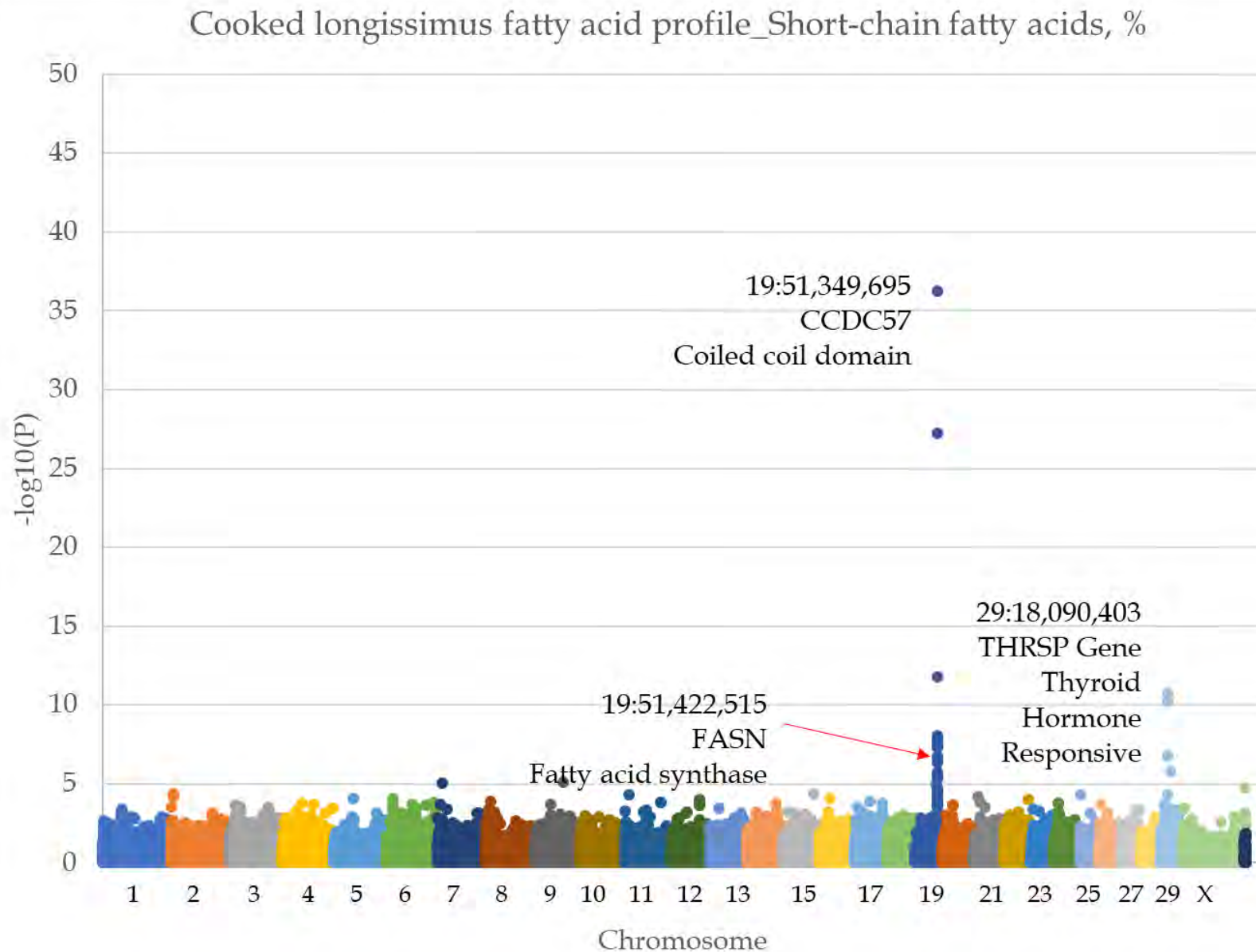| Project	2_SFA			
Sex	(Multiple Items)			
Average of RibEyeColor_r	Column Labels			
Row Labels	Implanted	Nonimplanted	Grand Total	
0	110.4	110.8	110.6	0.5
1	104.5	106.8	105.7	2.3
2	102.8	105.9	104.3	3.1
Grand Total	103.7	106.6	105.1	2.9

Fatty acid profile

- Cooked longissimus muscle

- Aged, cooked, trimmed, homogenized, fat extracted, GC-mass spectrometry

- Fatty acids expressed as a percentage of total fatty acids

- C14:0 C14:1 C15:0 C16:0 C16:1
  C17:0 C17:1 C18:0 C18:1t11 C18:1c9
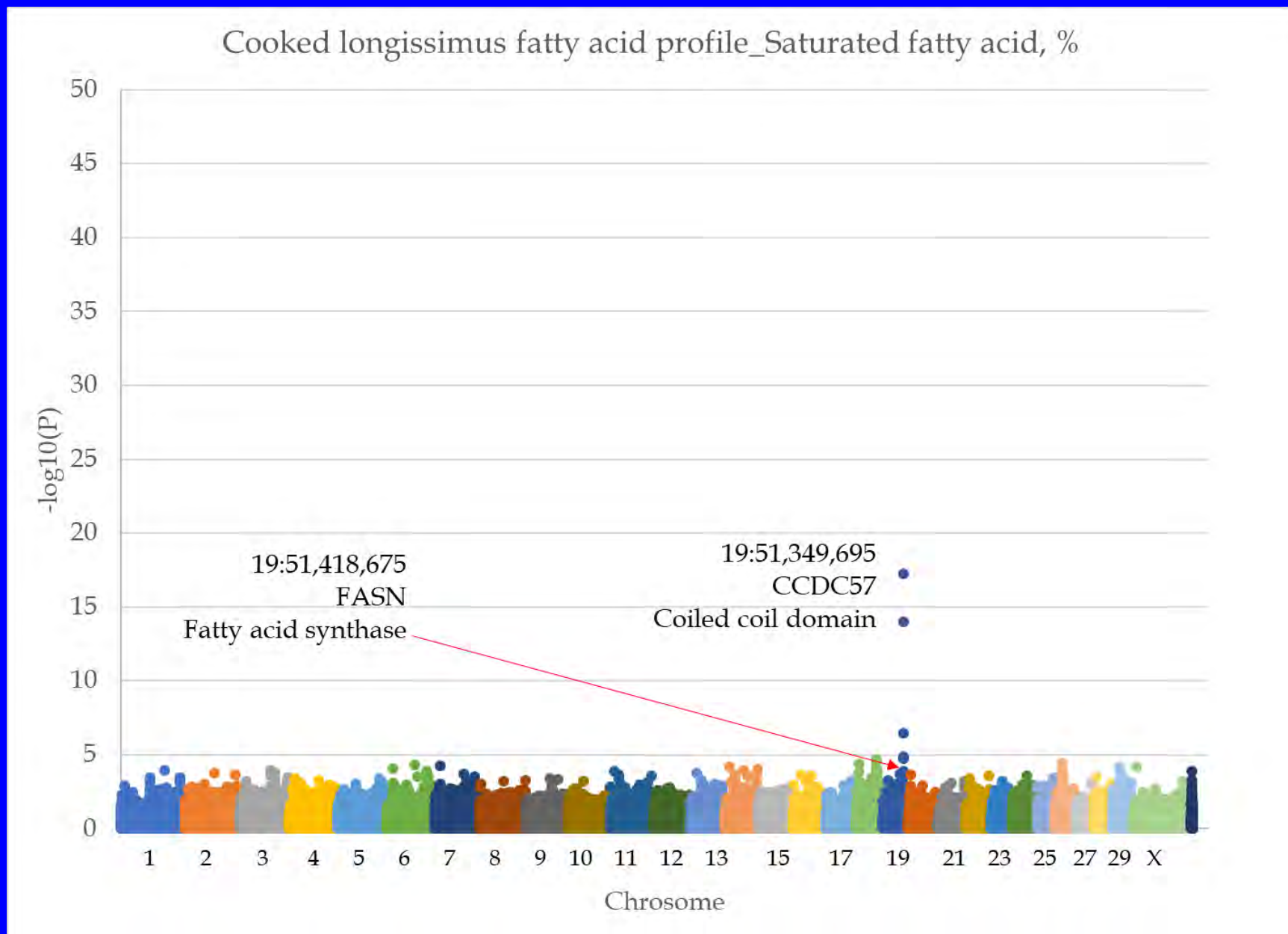 C18:1c11 C18:2t9,12 C18:2c9,12 C18:3
  CLA c9,t11 C20:3n6 C20:4n6

Genomic regulation of beef fatty acid profile traits
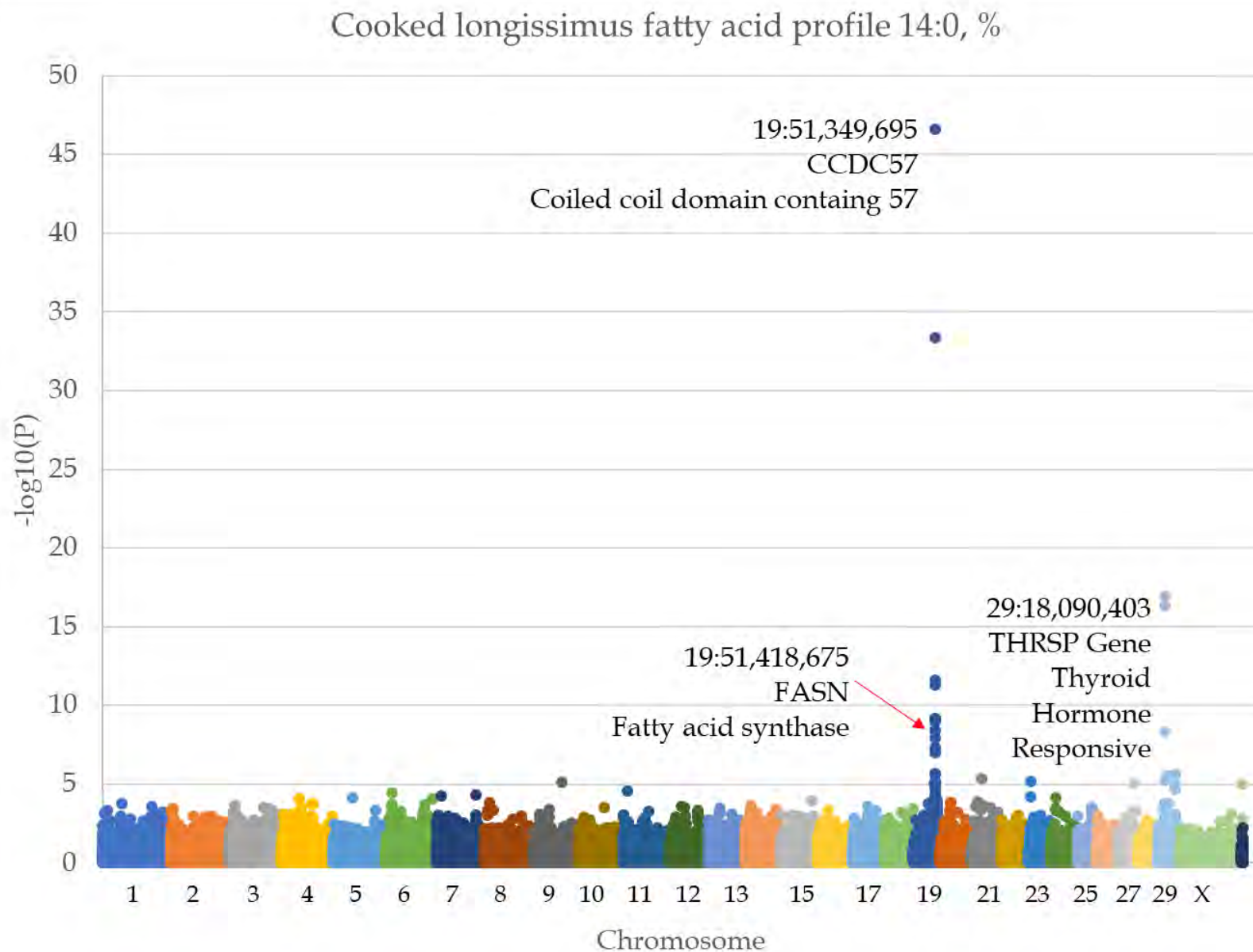
Cooked longissimus fatty acid profile 14:0, %

Genomic regulation of beef fatty acid profile traits

Cooked longissimus fatty acid profile_Short-chain fatty acids, %

19:51,349,695
CCDC57
Coiled coil domain

29:18,090,403
THRSP Gene
Thyroid
Hormone
Responsive

19:51,422,515
FASN
Fatty acid synthase

Genomic regulation of beef fatty acid profile traits

Cooked longissimus fatty acid profile_Saturated fatty acid, %

Biggest effect

- Myristic acid
  - The first fatty acid generated

Human health

- Muscle
- Ground beef
- Fat
  - Collecting data on s.c. fat
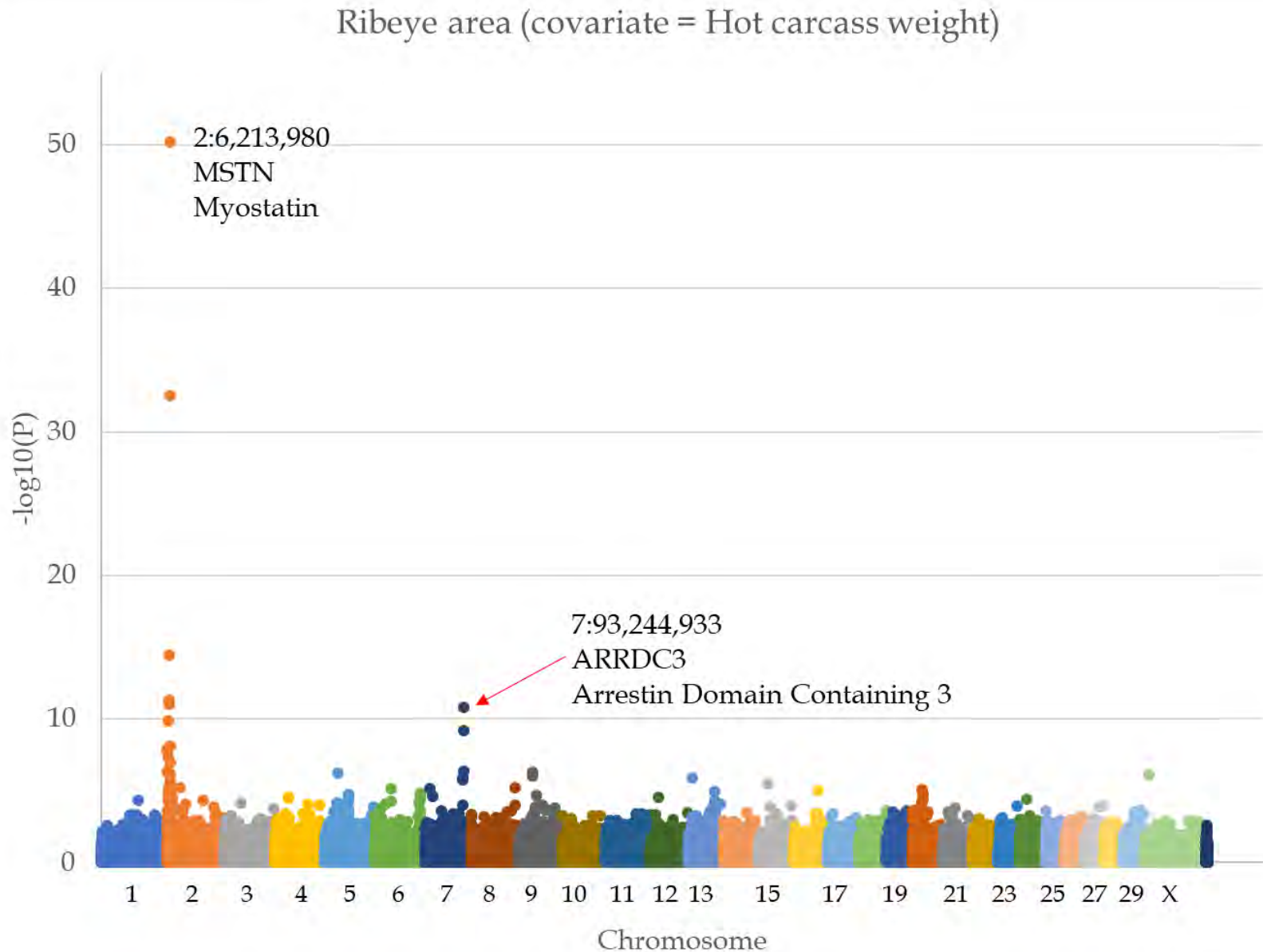- Next year's SFA carcasses
- Grand challenge

Genomic regulation of beef fatty acid profile traits

Cooked longissimus fatty acid profile_Polyunsaturated fatty acid, %

2:6,213,980
MSTN
Myostatin
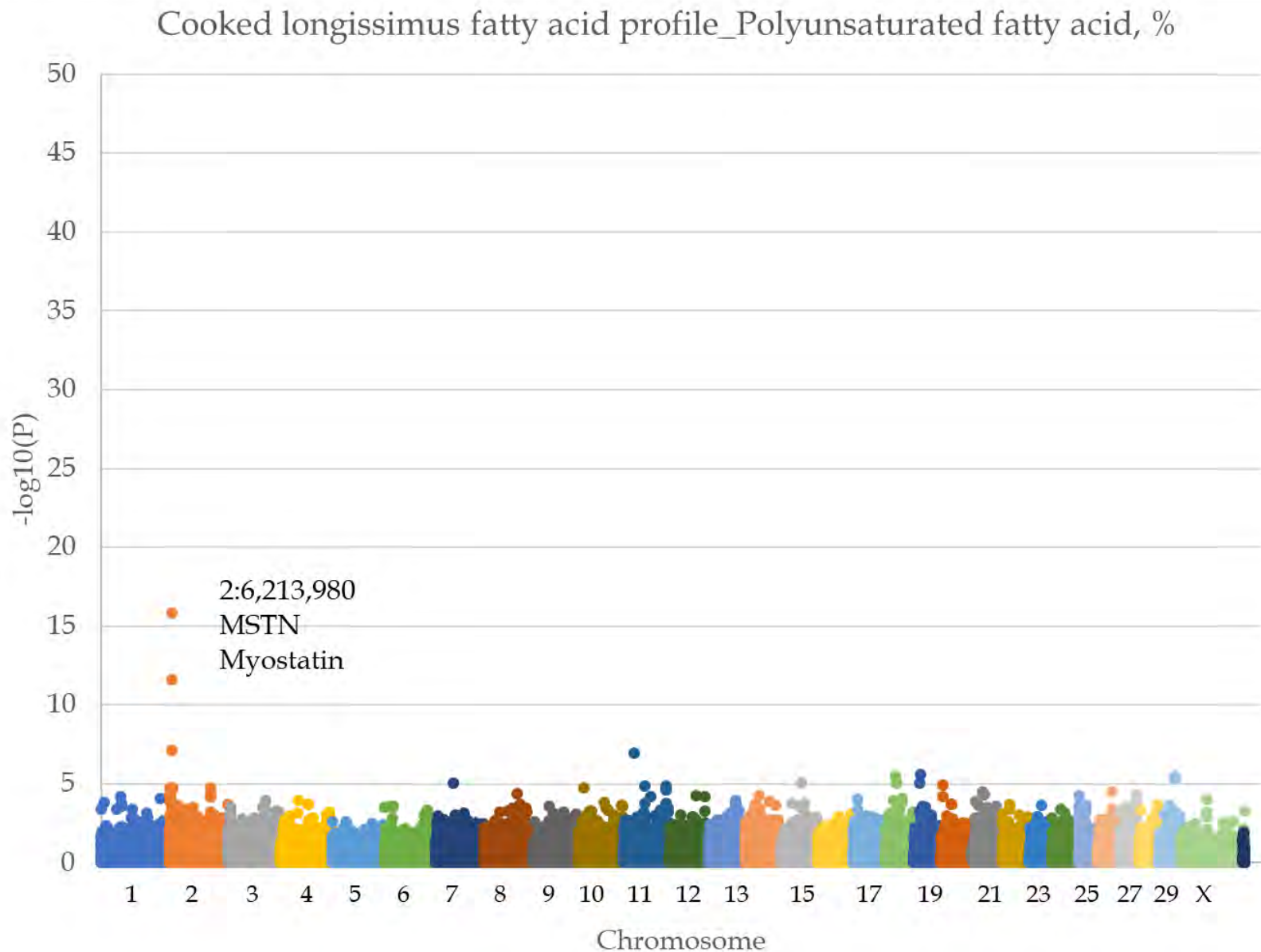
Myostatin effect

F94L Genotype	HCW	Calc_YG	PYG	ADJ PYG	REA	Marb	PUFA
LL	864.4	1.9	3.1	3.0	16.6	363	14.9
FL	831.7	2.8	3.5	3.4	14.3	366	12.1
FF	816.1	3.3	3.5	3.4	13.0	376	10.0

Genomic regulation of muscularity

Ribeye_color_r

N = 7,355

7:93,244,933
ARRDC3
Arrestin Domain Containing 3

5:75,994,507

5:75,657,807

23:31,735,211

23:31,766,406