"Application of Genomic Information: The California Commercial Ranch Project"

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Objectives: “Integrating DNA information into beef cattle production systems”

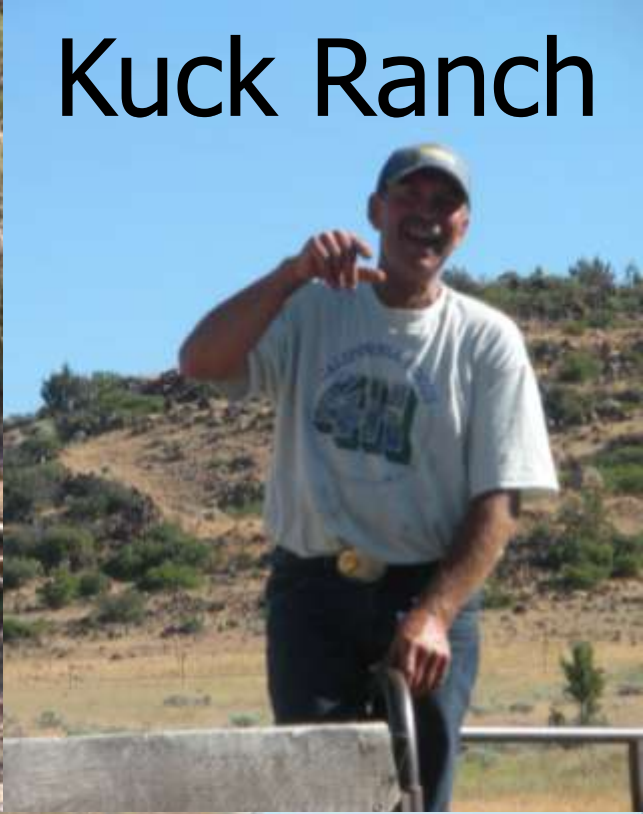
- The overall objective of this project is to develop a genotyped, phenotyped population to enable the evaluation and/or assessment of different DNA-enabled approaches for predicting the genetic merit of herd sires on commercial beef ranches.
- The research objective is to compare the current means of genetic prediction of herd sires (i.e. breed-based expected progeny differences) with DNA-assisted genetic predictions, and "commercial ranch" genetic evaluations based on the performance of their offspring under field conditions.
- An additional objective is to determine the costs and benefits associated with the application of DNA-based technologies on commercial beef operations

What does a California Commercial Ranch collaborator look like?

Photo taken in 1949 at Red Bluff Bull Sale, CA Generously provided by Cathy Maas from Crowe Hereford Ranch, Millville, CA.

Cowley Ranch

Kuck Ranch



Mole-Richardson Farms

UC Davis – Sierra foothills

Ranch resources/collaborators on "Integrating DNA information into beef cattle production systems"

- Four ranches on this project (UC Davis and 3 commercial cooperators in Siskiyou Co.)

– Cowley 900 (550 Spring; 350 Fall)	45
– Kuck 500 (200 Spring; 300 Fall)	16
– Mole-Richardson 700 (Fall)	40
– UC Davis 300 (Fall)	26

Approximately 125 Angus bulls, and 2,400 cows per year on project

Work flow and collaborators

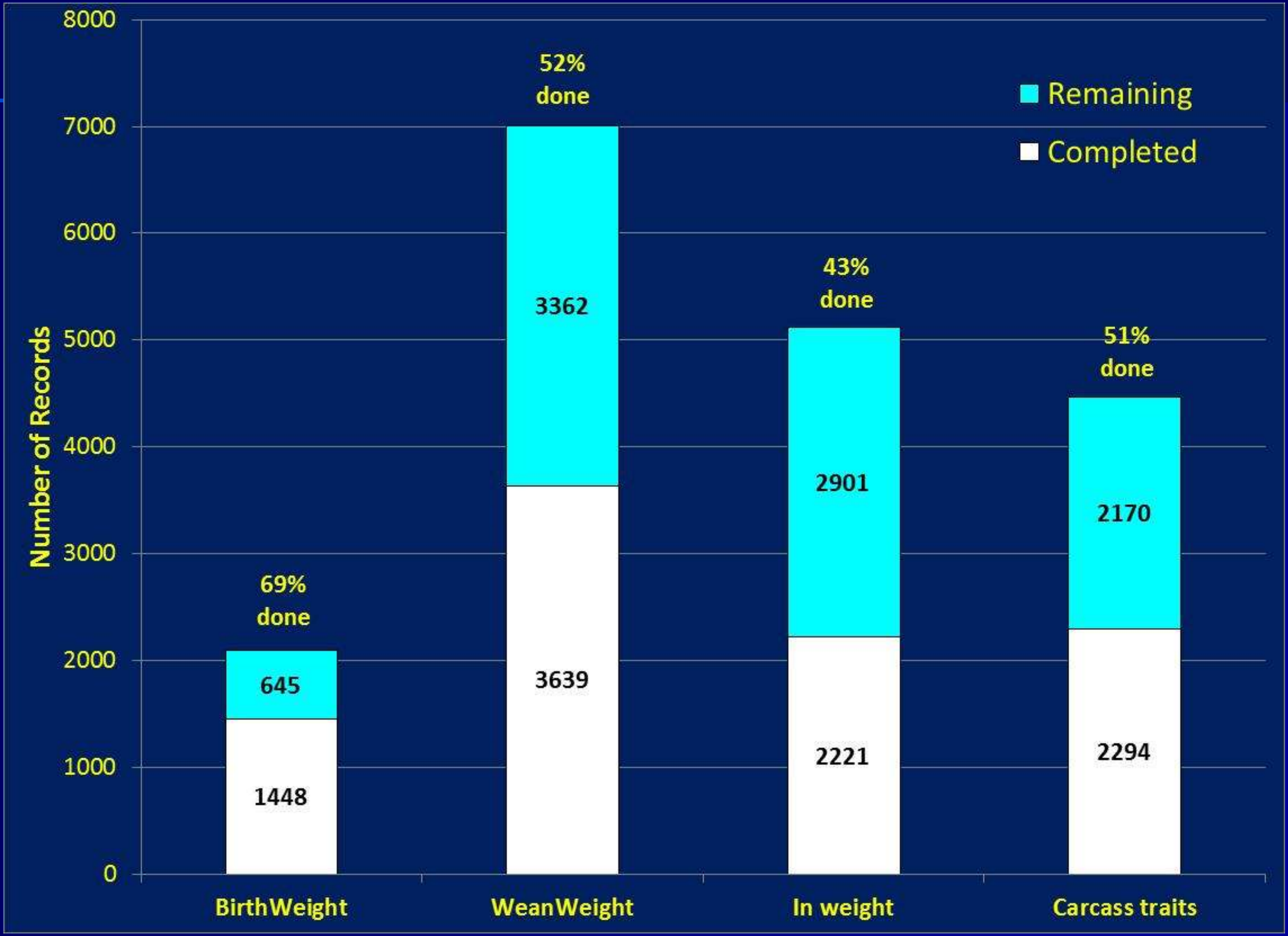
- DNA on all bulls goes for 50K whole genome scan – collaboration with Jerry Taylor (MO) and John Pollak (Meat Animal Research Center (NE)
- Molecular breeding value (MBV) prediction of genetic merit based on MARC training data set – collaboration with Dorian Garrick (IA) and Mark Thallman, U.S. Meat Animal Research Center (NE)
- Ranch data including sire groupings, birth dates and weaning weights on all calves, all EIDed, and "DNAed" for parentage determination – collaboration with Dan Drake and producers (CA)
- Steer feedlot in weights, treatments, and carcass traits (Hot weight, grading information and meat sample collected in the processing plant – collaboration with Harris Ranch (CA)
- Compile data and compare three sources of genetic estimates: breed EPDs (bEPDs), commercial ranch EPDs (rEPDs), and MBVs, **Kristina Weber, UC Davis, PhD student**

Commercial ranch sample collection

Problems experienced included

Tail should be here !????

Sampling Summary : Total Number of Records to date



Potential uses of genomic information for beef sectors

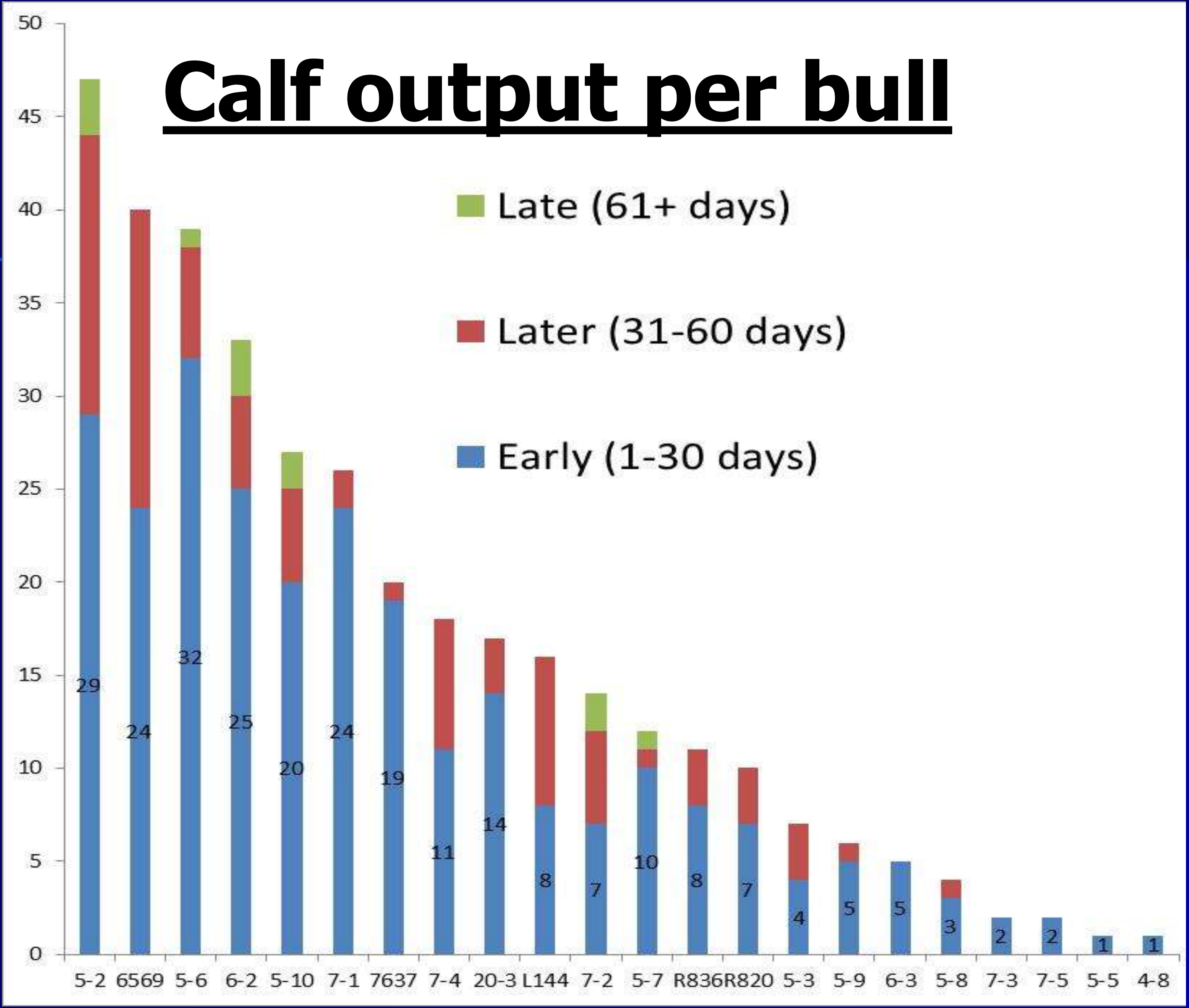
Use	Seedstock	Commercial	Feedlot	Processor
DNA-assisted selection	X	X		
Parentage	X	X		
Recessive allele testing	X	X		
Control of Inbreeding	X	X		
Mate selection	X	X		
DNA-assisted management	X	X	X	
Product differentiation				X
Traceability				X

Benefits of DNA-based parentage identification

- Correct pedigree errors so improve the rate of genetic gain
- Enables the use of multi-sire breeding pasture
  - Higher fertility
  - Elimination of sire failure
  - Tighter calving season
- Reduces the need for different breeding pastures
  - Allows for better pasture management
  - Less sorting and working of animals into different groups
- Enables the development of commercial-ranch genetic evaluations
  - Can determine which bull is causing calving problems

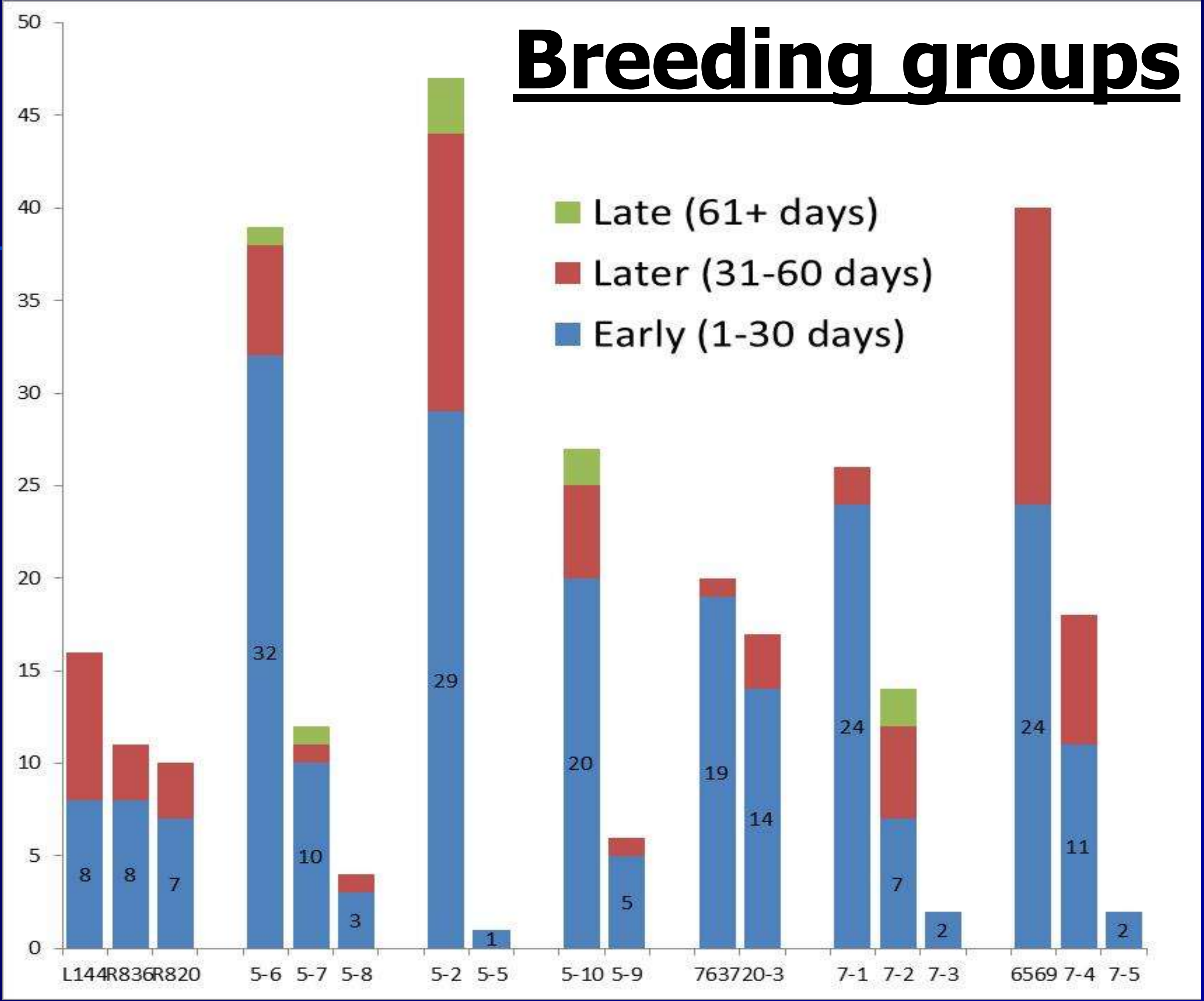
of calves born/bull – Fall 2009 calving

Calf output per bull



of calves born/bull – Fall 2009 calving

Breeding groups



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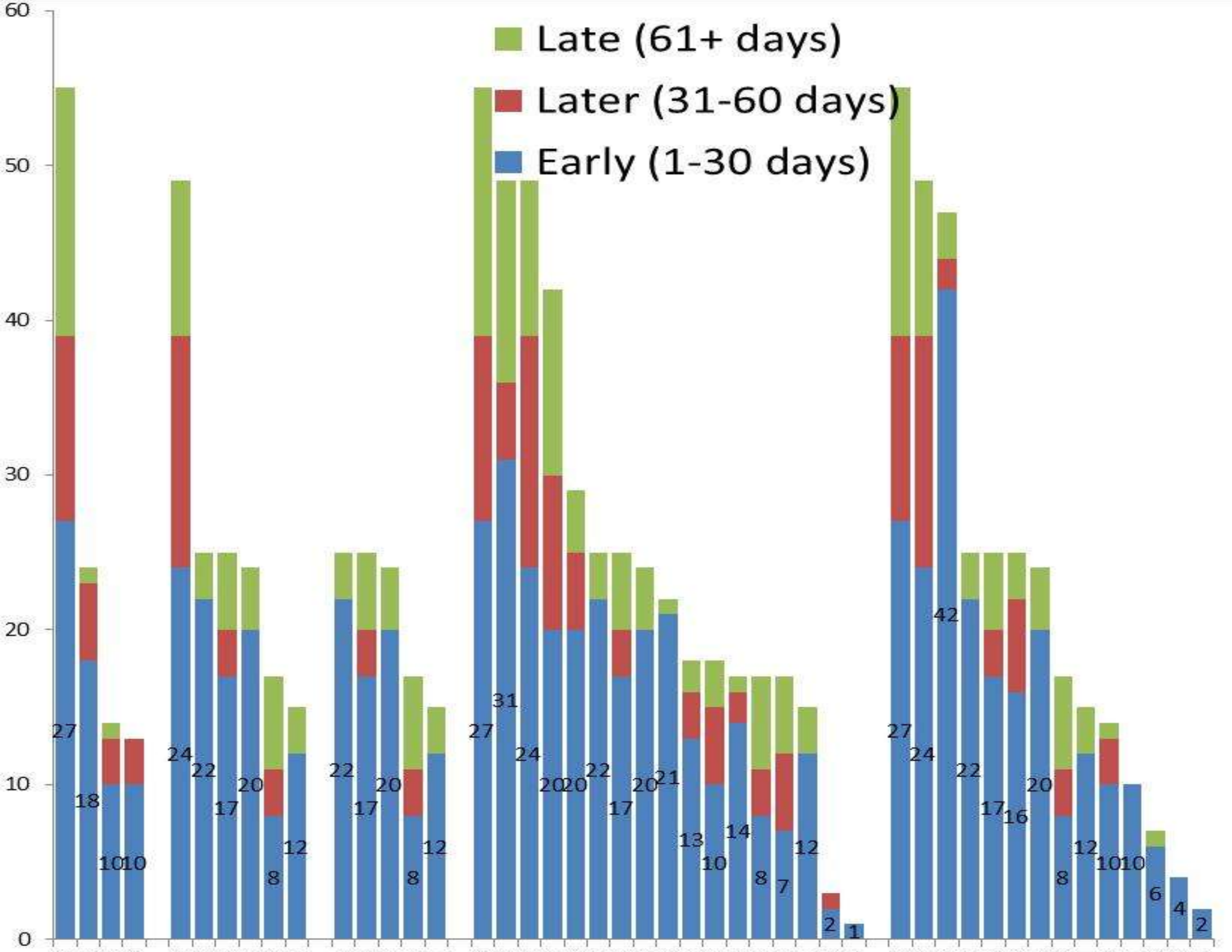
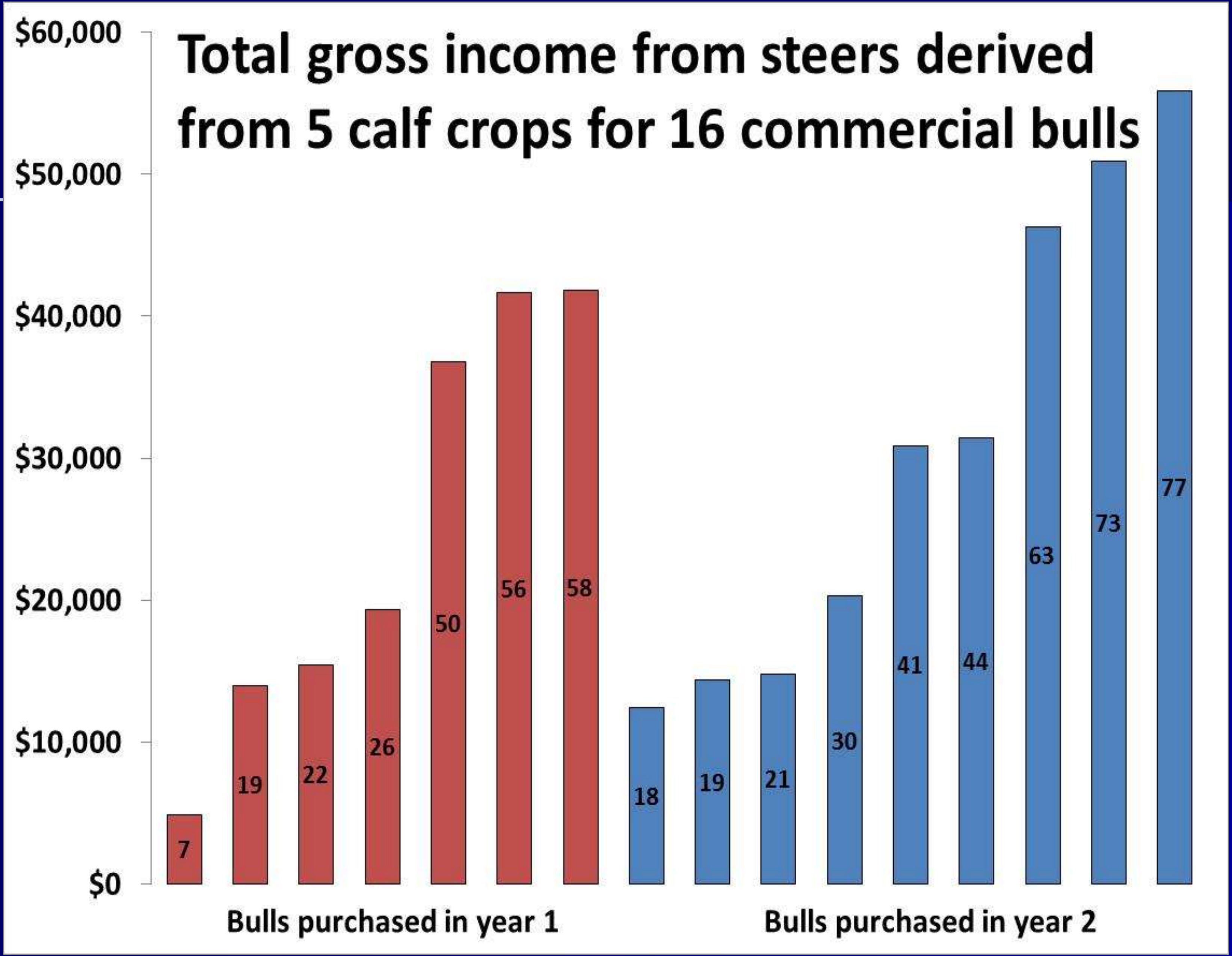
of calves born/bull – Fall 2009 calving

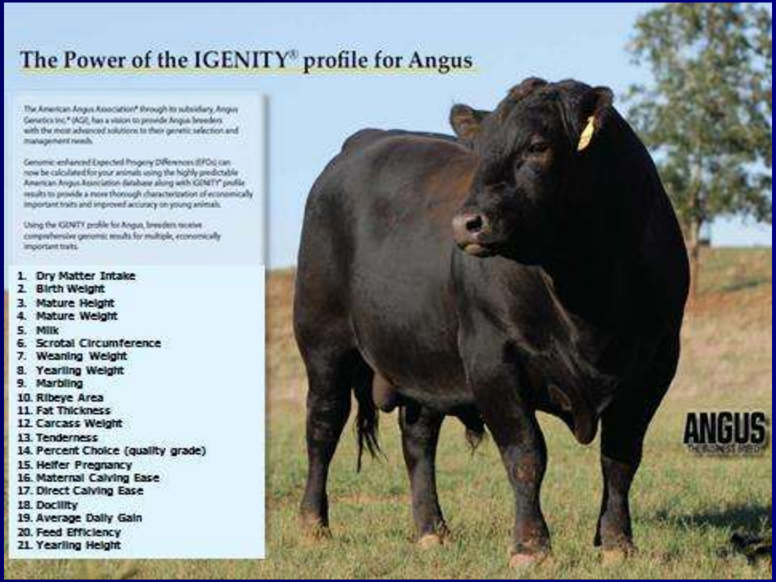


2004 (red) and 2005 (blue) born-bulls



Preliminary Assessment of Commercial Tests for Beef Cattle Production Traits

The objective of this study was to estimate the genetic correlation between DNA test results and target traits based on ranch genetic evaluations of herd bulls sourced from the Angus seedstock sector.



The Power of the IGENITY® profile for Angus

The American Angus Association® through its subsidiary Angus Genetics Inc.® (AGI), has a vision to provide Angus breeders with the most advanced solutions to their genetic selection and management needs.

Genomic-enhanced Expected Progeny Differences (EPDs) can now be calculated for your animals using the highly predictable American Angus Association database along with IGENITY® profile results to provide a more thorough characterization of economically important traits and improved accuracy on young animals.

Using the IGENITY profile for Angus, breeders receive comprehensive genomic results for multiple, economically important traits.

1. Dry Matter Intake
2. Birth Weight
3. Mature Height
4. Mature Weight
5. Milk
6. Scrotal Circumference
7. Weaning Weight
8. Yearling Weight
9. Marbling
10. Ribeye Area
11. Fat Thickness
12. Carcass Weight
13. Tenderness
14. Percent Choice (quality grade)
15. Heifer Pregnancy
16. Maternal Calving Ease
17. Direct Calving Ease
18. Docility
19. Average Daily Gain
20. Feed Efficiency
21. Yearling Height

Lead Today with 50K

1. Birth weight
2. Weaning weight
3. Weaning maternal (milk)
4. Calving ease direct
5. Calving ease maternal
6. Marbling
7. Backfat thickness
8. Ribeye area
9. Carcass weight
10. Tenderness
11. Postweaning average daily gain
12. Daily feed intake
13. Feed efficiency (net feed intake)

50K SNP chip assays 50,000 SNPs spread throughout genome

What was done?

- IGENITY and Pfizer MBV were purchased for 29 registered Angus bulls from 3 of the 4 ranches involved in this project. MBV evaluated were weaning weight, average daily gain, hot carcass weight, ribeye area, and marbling score. This set of bulls was selected based on number of progeny records available for analysis at this point (≥20 weaning weight or ≥10 ADG or carcass).
- Genetic correlations were estimated between IGENITY and Pfizer MBV and the genetic merit of 29 Angus bulls as estimated from performance of progeny produced on 3 commercial ranches since 2005.

Description of the records

- Progeny records of Angus bulls from calf cohorts beginning in 2006 (bulls bred 2005). Though the dataset currently includes over 3500 progeny records, only 1852 were direct progeny of the 29 analyzed bulls, though all were progeny of Angus bulls produced on those ranches and related by pedigree. Not all progeny had records for every trait.
- Of progeny of these particular sires, the most records were available for weaning weight (1734), then ADG (defined as rate of gain between weaning weight and entry weight into the feedlot (1356); then carcass traits HCWT, MRB, and REA (455).
- The pedigree included at least 4-generations on all registered Angus bulls.

Model used for analysis

Kachman SD (2008) Incorporation of marker scores into national genetic evaluations. Proc. 9thGenetic Prediction Workshop, Kansas City, MO, pp. 88-91. http://www.beefimprovement.org/PDFs/Kansas%20City%20Missouri%202008.pdf

A bivariate animal model was used to estimate the genetic correlations and EBV for bulls.

- MBV were treated as a second trait correlated with ranch performance.

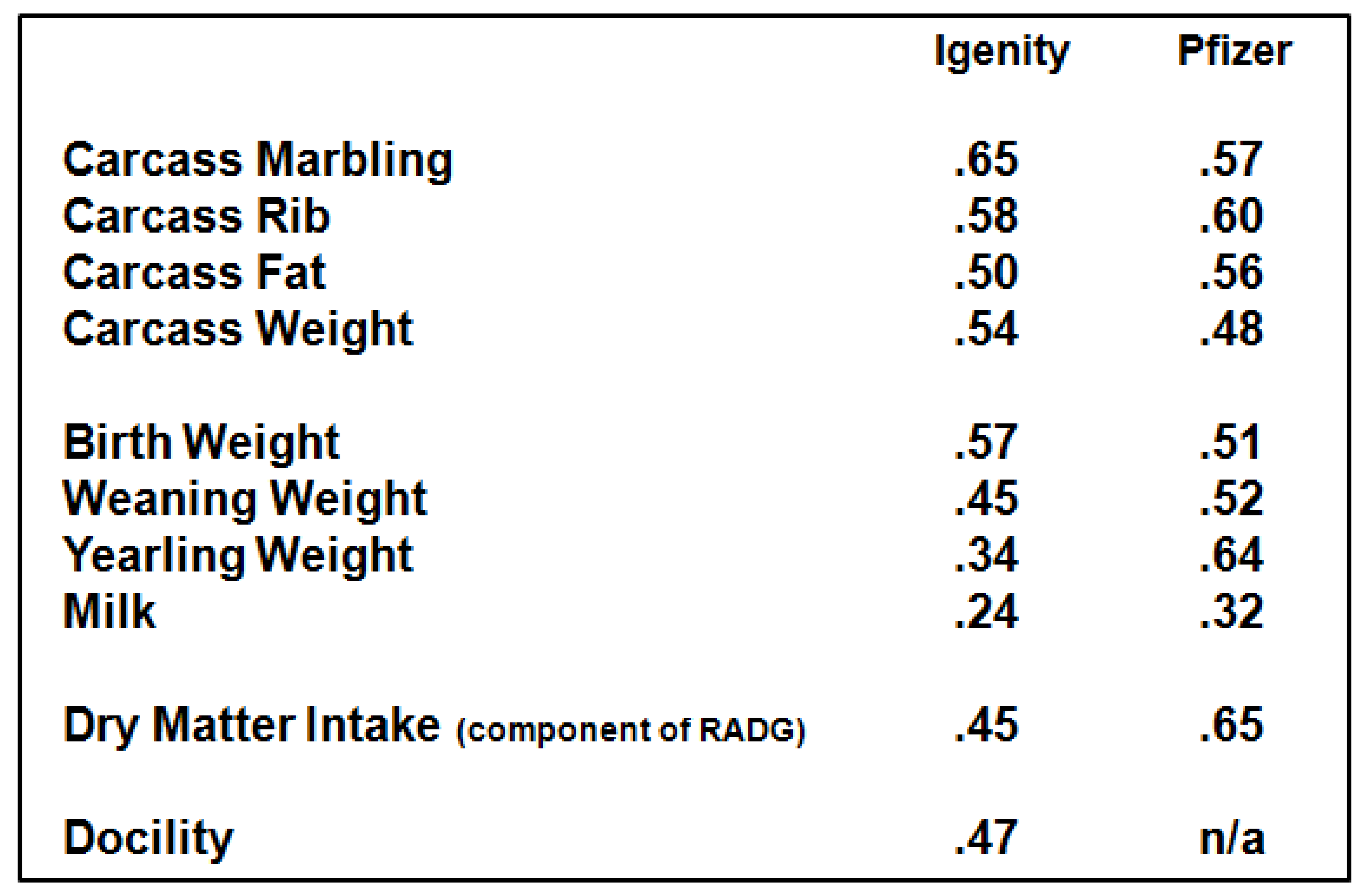
Results: Genetic correlations

	Bulls with ranch BIF acc > 0.05	# direct progeny in dataset	Pfizer estimated r	IGENITY estimated r
WWT	29	1734	0.51 (0.17)	0.12 (0.22)
ADG (FEEDLOT)	28	1356	0.10 (0.39)	-0.01 (0.42)
HCWT	20	455	0.08 (0.28)	0.33 (0.27)
REA	23	455	0.57 (0.21)	0.35 (0.24)
MRB	23	455	0.71 (0.17)	0.61 (0.19)

- MBVs had heritabilities near or equal to 1.
- Note large standard errors of the estimates

Genetic correlations for Angus National Cattle Evaluation traits by company

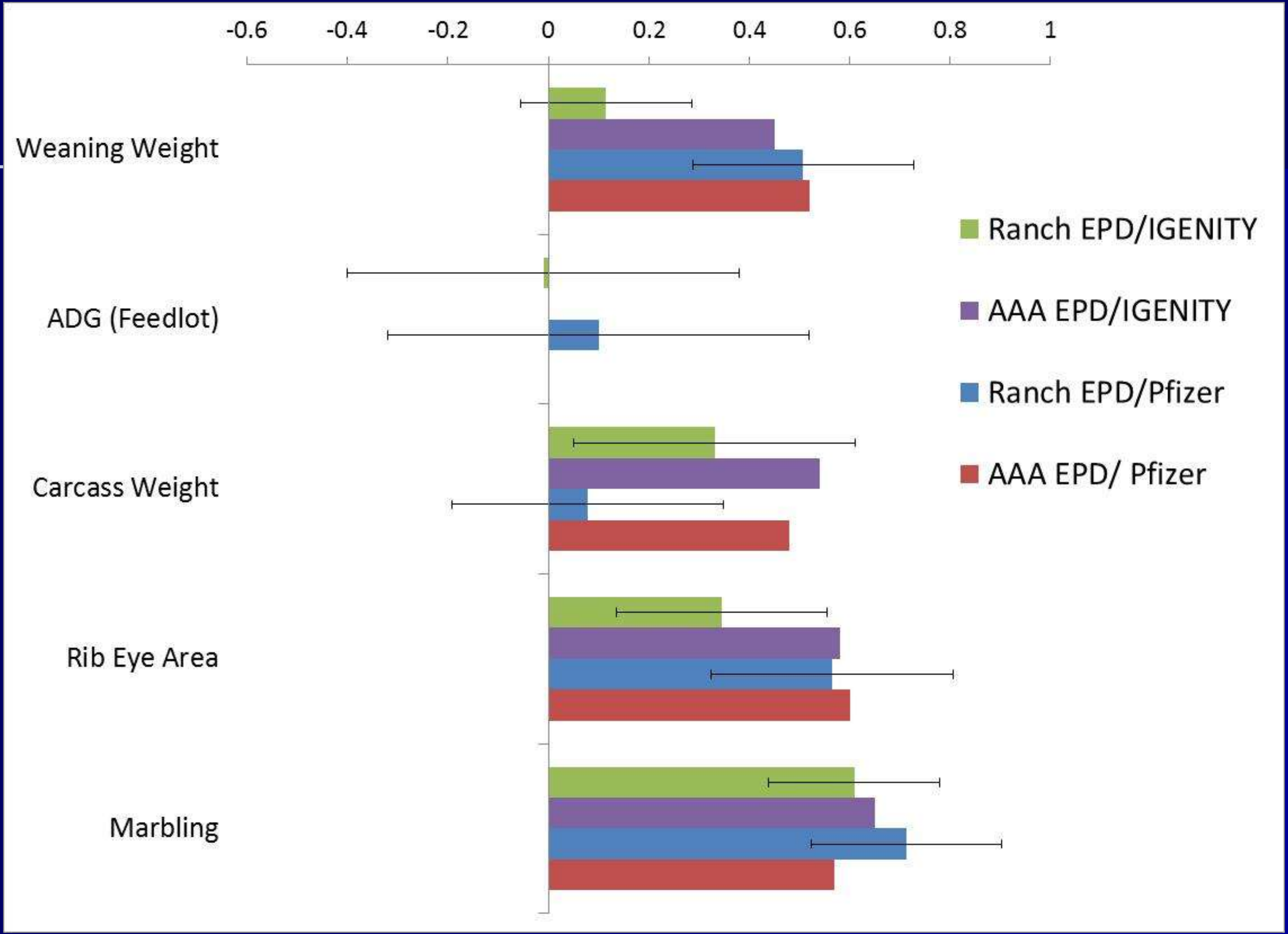
384 SNP 50K SNP



	Igenity	Pfizer
Carcass Marbling	.65	.57
Carcass Rib	.58	.60
Carcass Fat	.50	.56
Carcass Weight	.54	.48
Birth Weight	.57	.51
Weaning Weight	.45	.52
Yearling Weight	.34	.64
Milk	.24	.32
Dry Matter Intake (component of RADG)	.45	.65
Docility	.47	n/a

http://www.angus.org/AGI/GenomicChoiceApril2011.pdf

Est. genetic correlations (r)



GE-EPDs and Approximate Progeny Equivalents

Pfizer Animal Health
Animal Genetics

	AGI Heritability	AGI HD 50K Correlation	Avg. 50k Change in ACC - from .05[1]	Approximate Progeny Equivalents
BW	0.42	0.51	0.25	**8**
WW	0.20	0.52	0.23	**16**
YW[2]	0.20	0.64	0.27	**20**
RADG[3]	0.31	0.65	0.27	**13**
Milk	0.14	0.32	0.15	**12**
CW	0.31	0.48	0.17	**7**
Marb[4]	0.26	0.57	0.24	**12**
RE[4]	0.32	0.60	0.23	**9**
FAT[4]	0.26	0.56	0.23	**11**

[1] These changes are less for higher initial accuracy values
[2] Post-weaning ADG
[3] Dry matter intake
[4] Carcass progeny, not scanned progeny

Slide courtesy of Pfizer Animal Health

Relationship between genetic correlation (r) and progeny equivalents (for $h^2 = 0.2$ e.g. weaning weight)

Genetic Correlation (r)	Avg. Change in BIF ACC - from .05	Approximate Progeny Equivalents
0.1	0.006	0
0.2	0.02	0
0.3	0.04	1
0.4	0.07	3
0.5	0.12	6
0.6	0.18	10
0.7	0.26	18
0.8	0.36	34
0.9	0.52	81

Summary

- Genetic correlation estimates from this small preliminary dataset were generally positive and tended to be lower than the AAA values, although they were associated with large standard errors due to small sample size.
- As more records are added, these commercial ranch data will be used to assess genomic predictions from a variety of sources

“Integrating DNA information into Beef Cattle Production Systems” USDA Integrated Grant Collaborators

- Dr. Darrh Bullock, Extension Professor, University of Kentucky, KY
- Dr. Leslie “Bees” Butler, Extension Marketing Specialist, UC Davis, CA
- Dr. Daniel Drake, University of California Cooperative Extension Livestock Advisor, CA
- Dr. Dorian Garrick, Professor, Iowa State University, IA
- Dr. John Pollak, Professor, Cornell University, NY
- Dr. Mark Thallman, US Meat Animal Research Center, Clay Center, NE

Graduate Students

- Kristina Weber, Ph.D. Candidate, UC Davis, CA and Krista Cooprider, MS Candidate, UC Davis, CA

Producer Collaborators:

- Jack Cowley, Cowley Rancher, Siskiyou County, CA
- Dale, Greg, and Richard Kuck, Kuck Ranch, Siskiyou County, CA
- Matt Parker, Mole-Richardson Ranch, Siskiyou County, CA

Processor Collaborators:

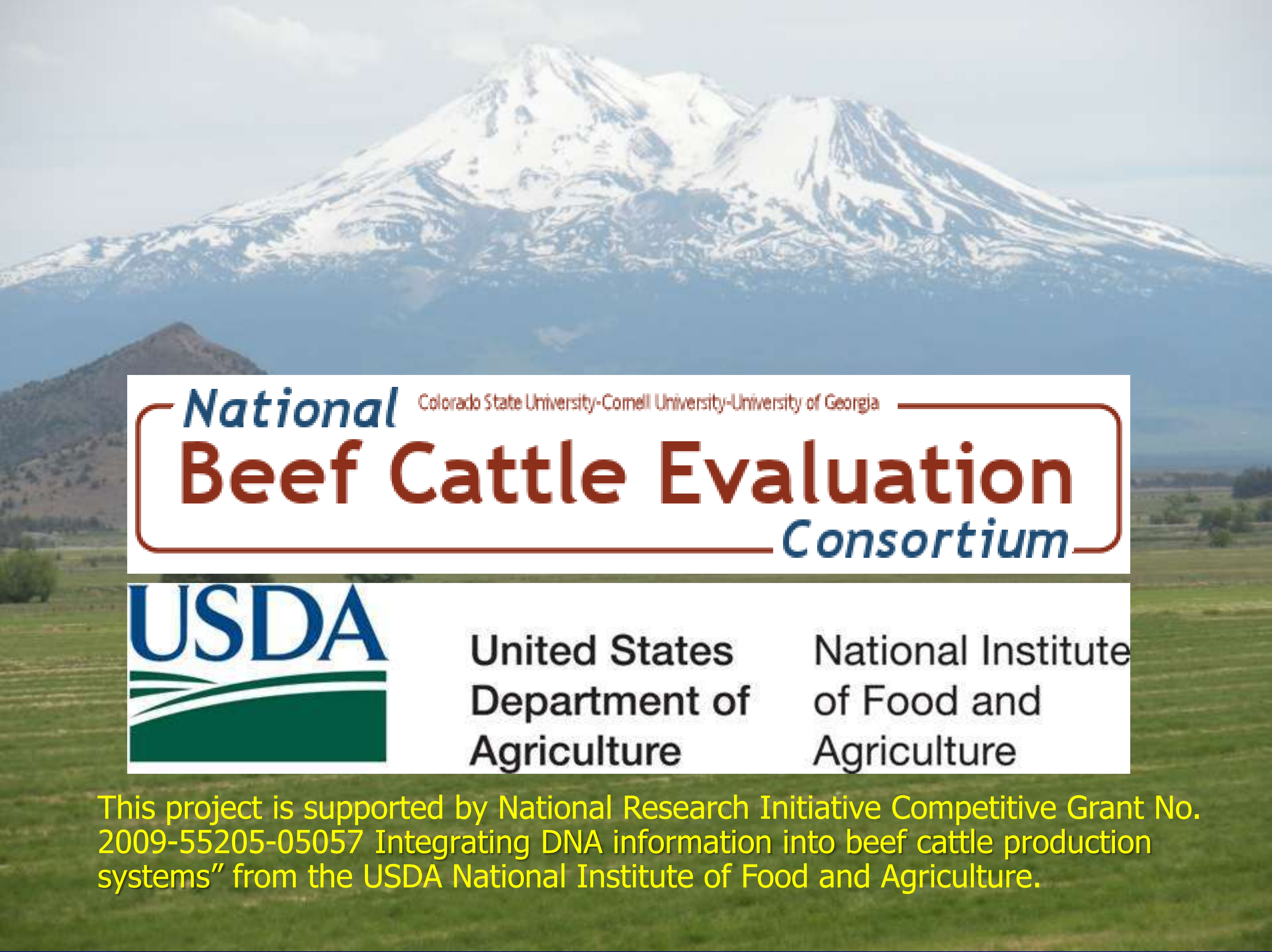
- Harris Ranch Beef Company, Coalinga, CA
- Los Banos Abattoir, Los Banos, CA

Software Collaborators:

- Jim Lowe, Cow Sense Herd Management Software, NE

Other Contributors/Collaborators

- Dr. Jerry Taylor, University of Missouri, MO
- Dr. Mike Goddard, University of Melbourne and Victorian DPI, Australia



National
Colorado State University-Cornell University-University of Georgia
Beef Cattle Evaluation
Consortium

USDA
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National Institute
of Food and
Agriculture

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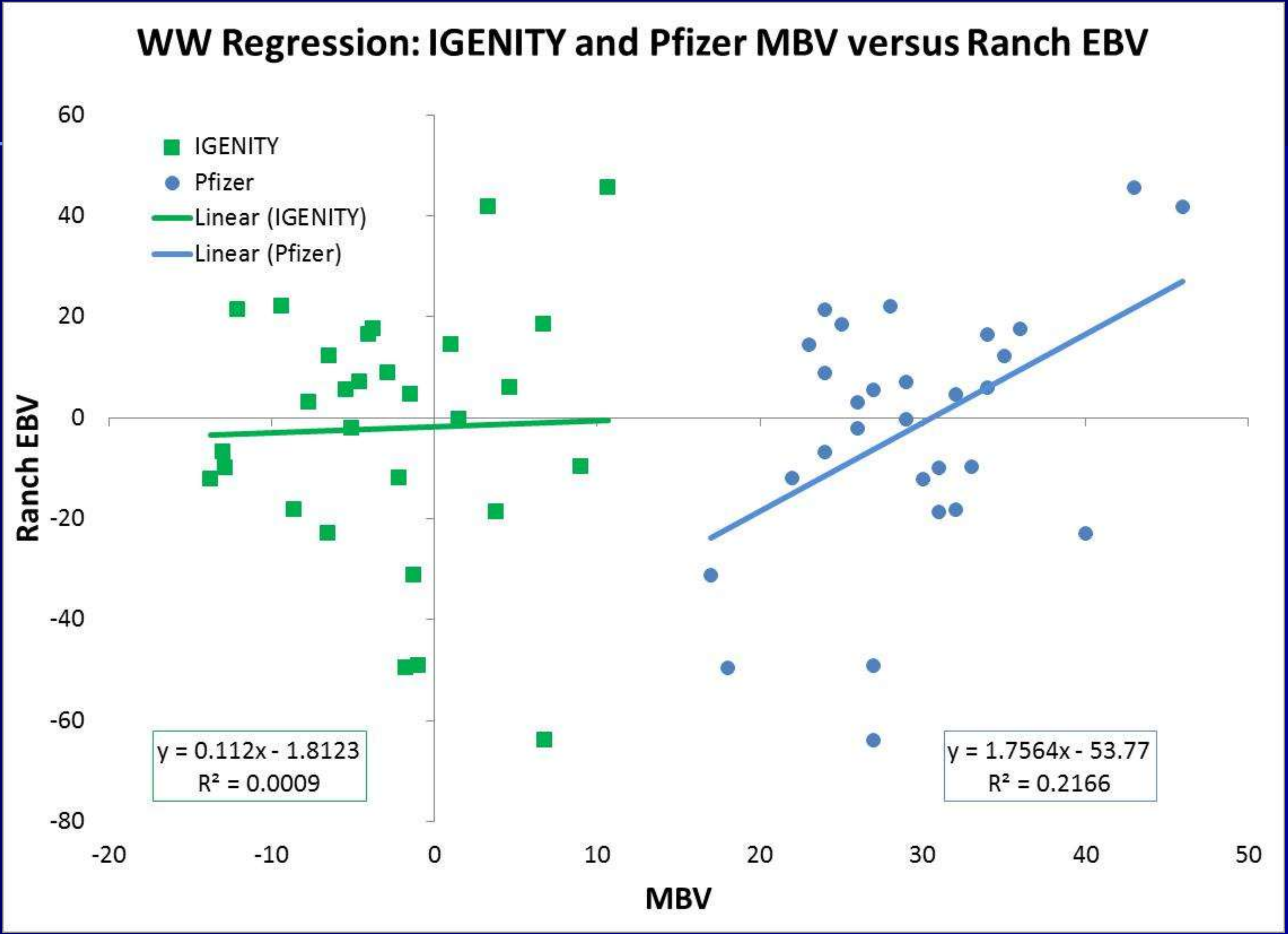
Questions?

Results: AAA Weaning weight

Results: Ranch Weaning weight



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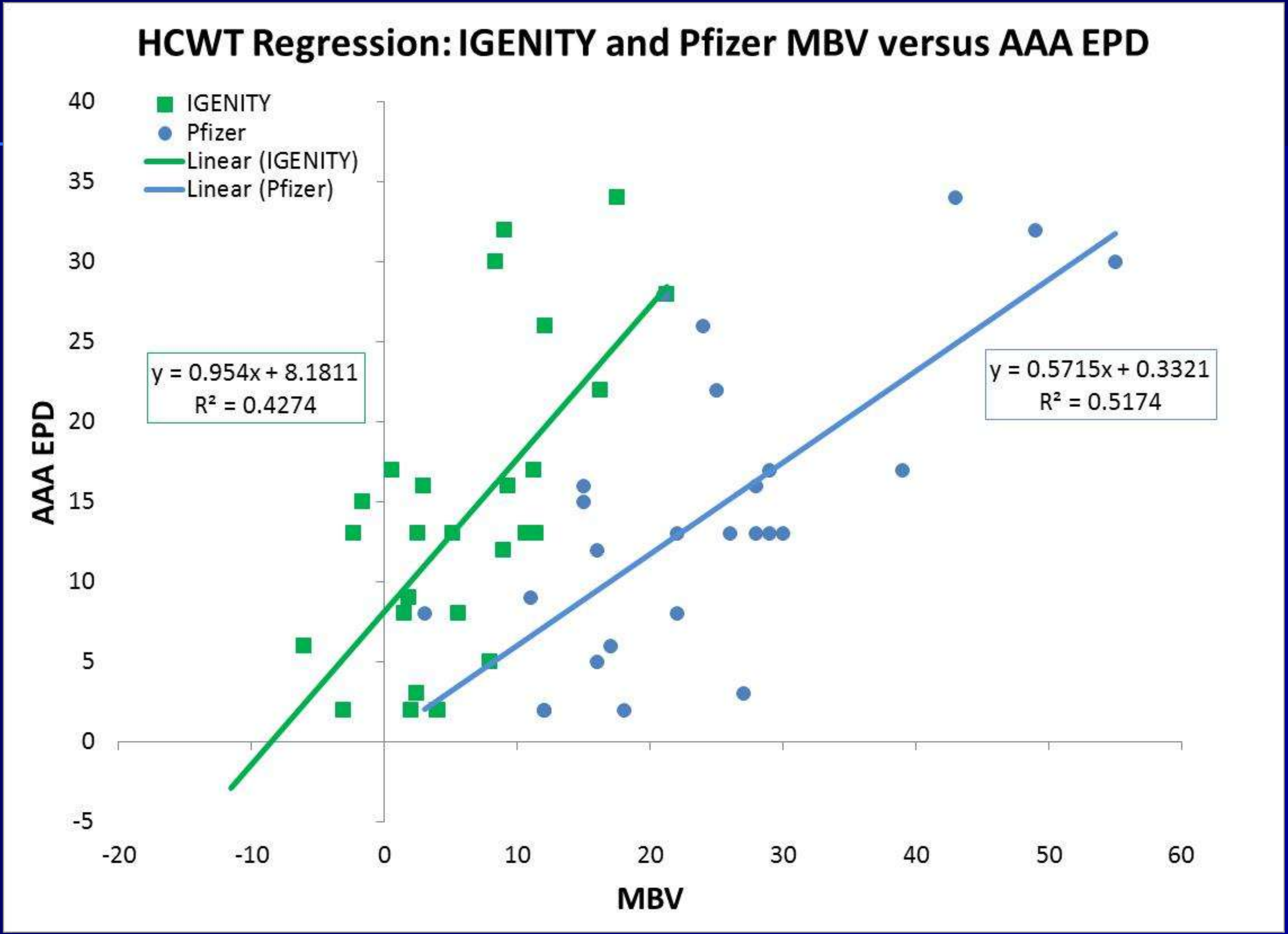
Results: AAA Hot Carcass Weight

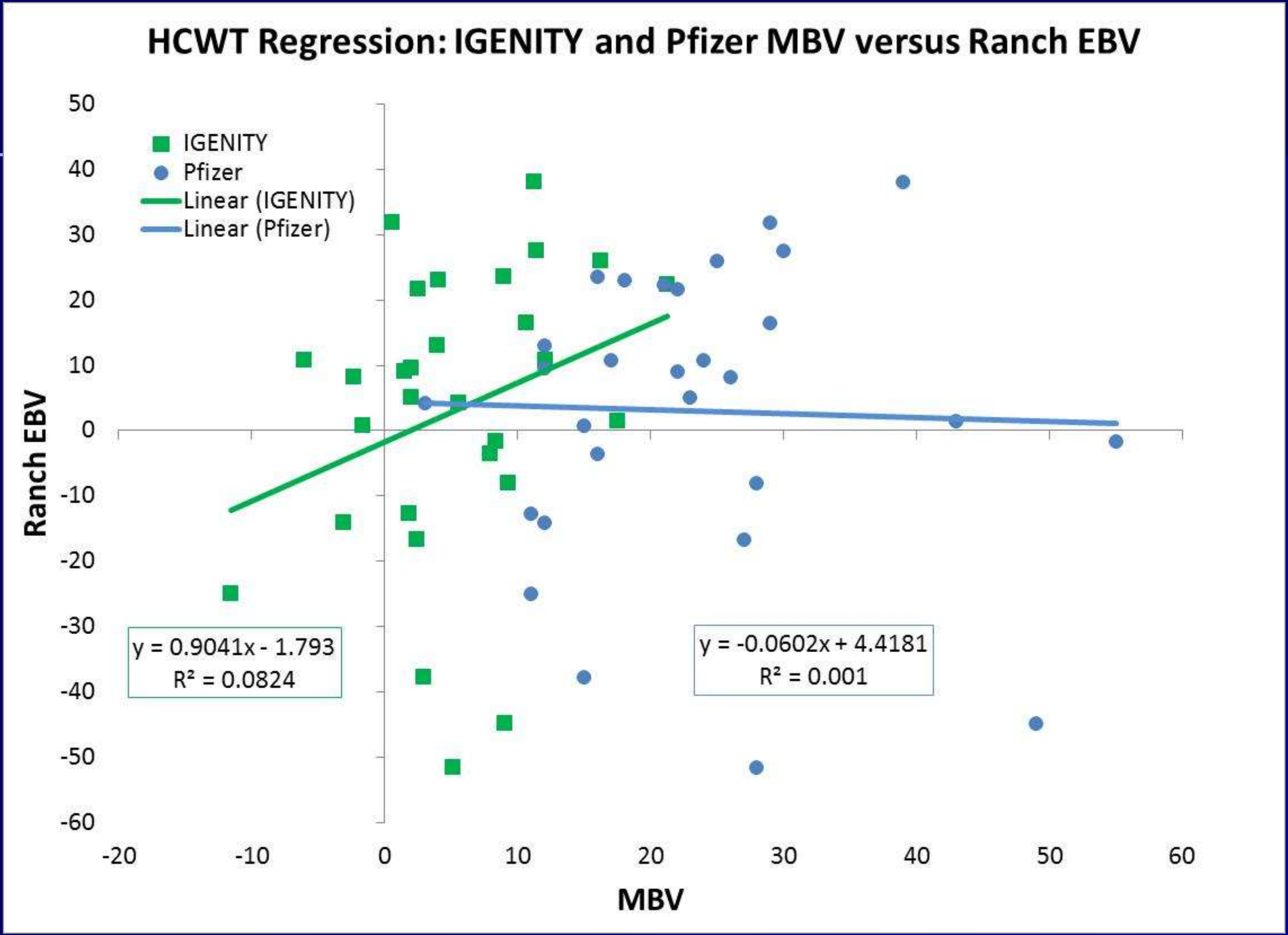


HCWT Regression: IGENITY and Pfizer MBV versus AAA EPD

$y = 0.954x + 8.1811$
$R^2 = 0.4274$

$y = 0.5715x + 0.3321$
$R^2 = 0.5174$

Results: Ranch Hot Carcass Weight



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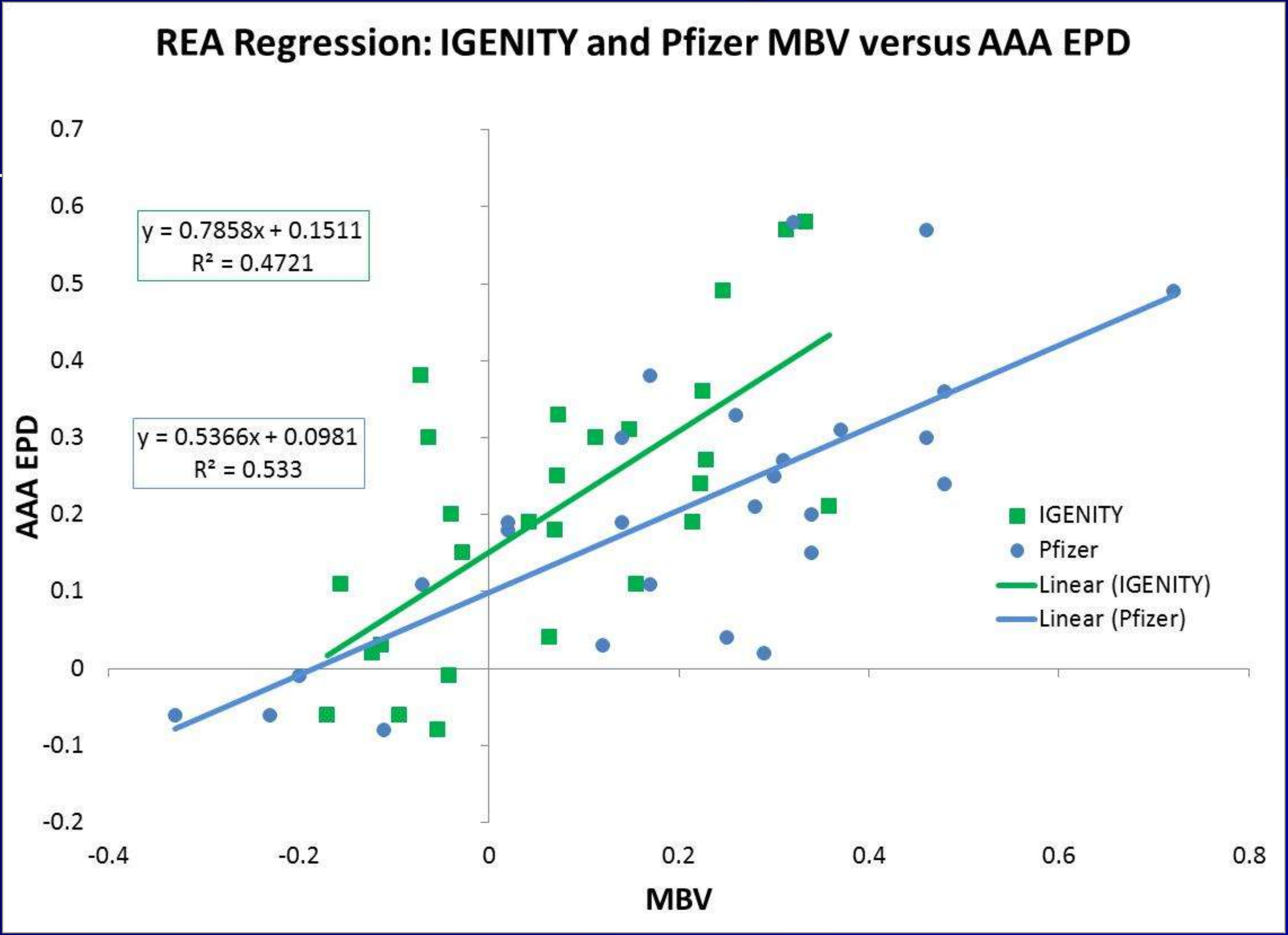
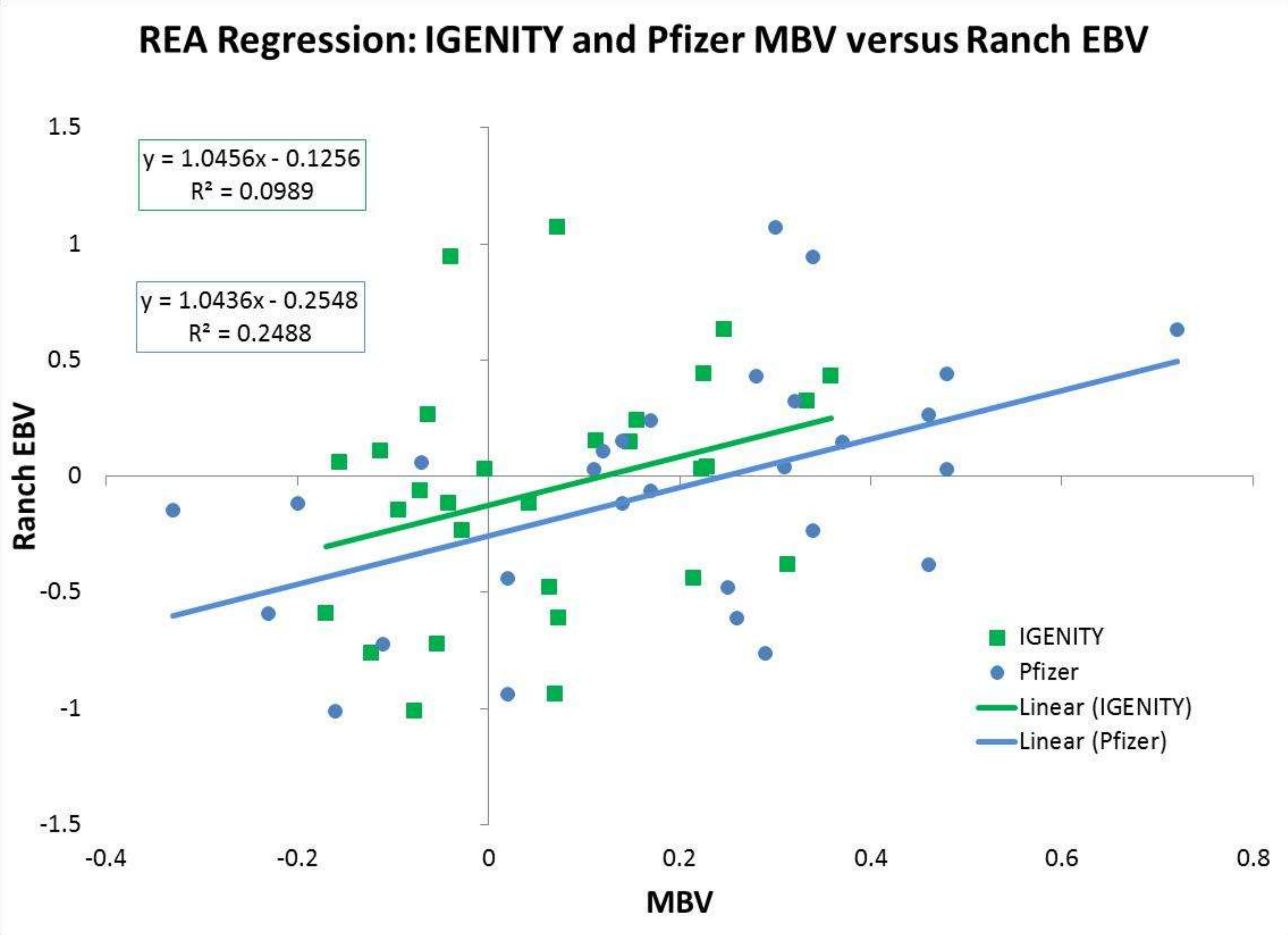
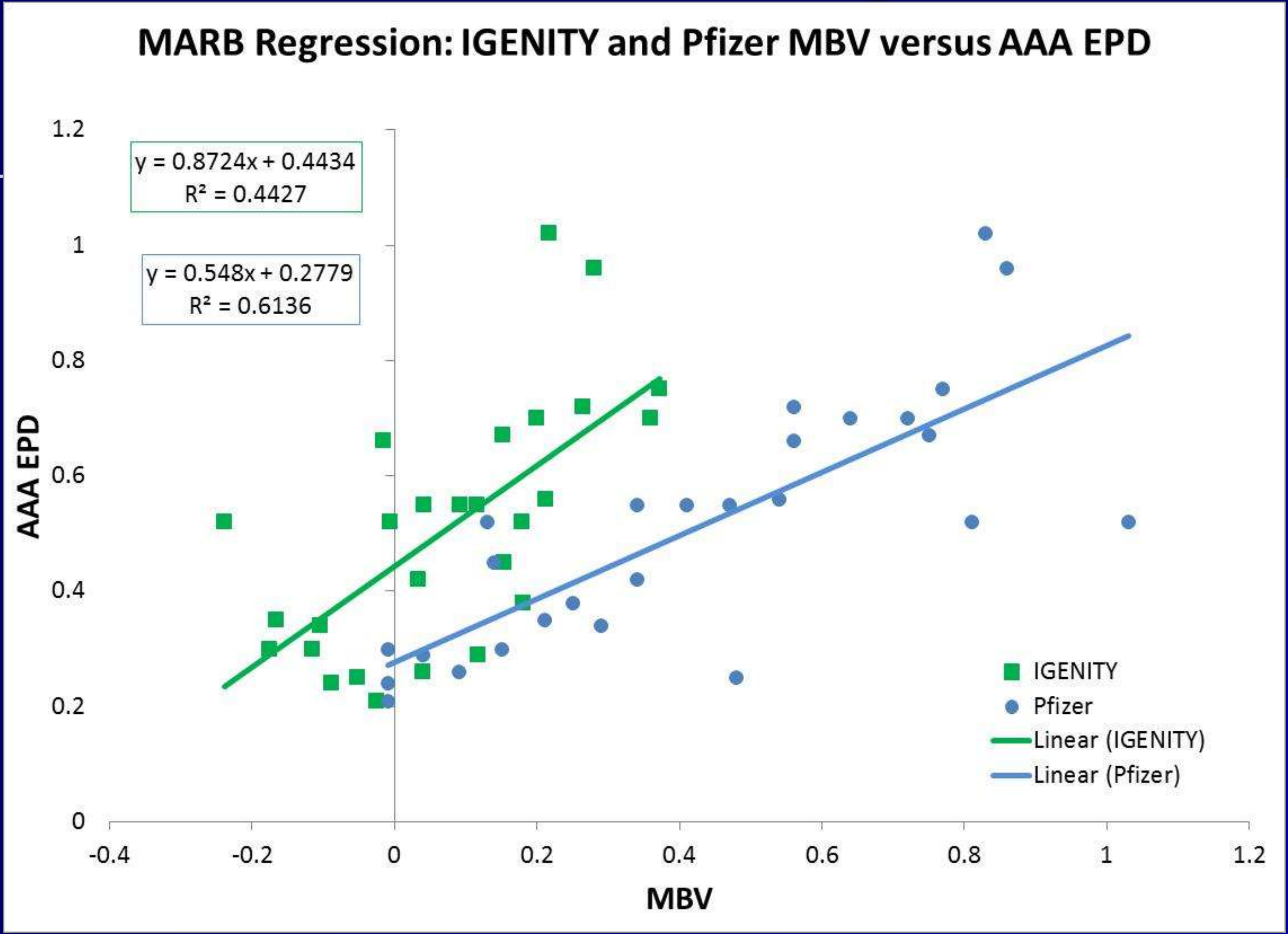
Results: AAA Ribeye Area



Results: Ranch Ribeye Area



Results: AAA Marbling



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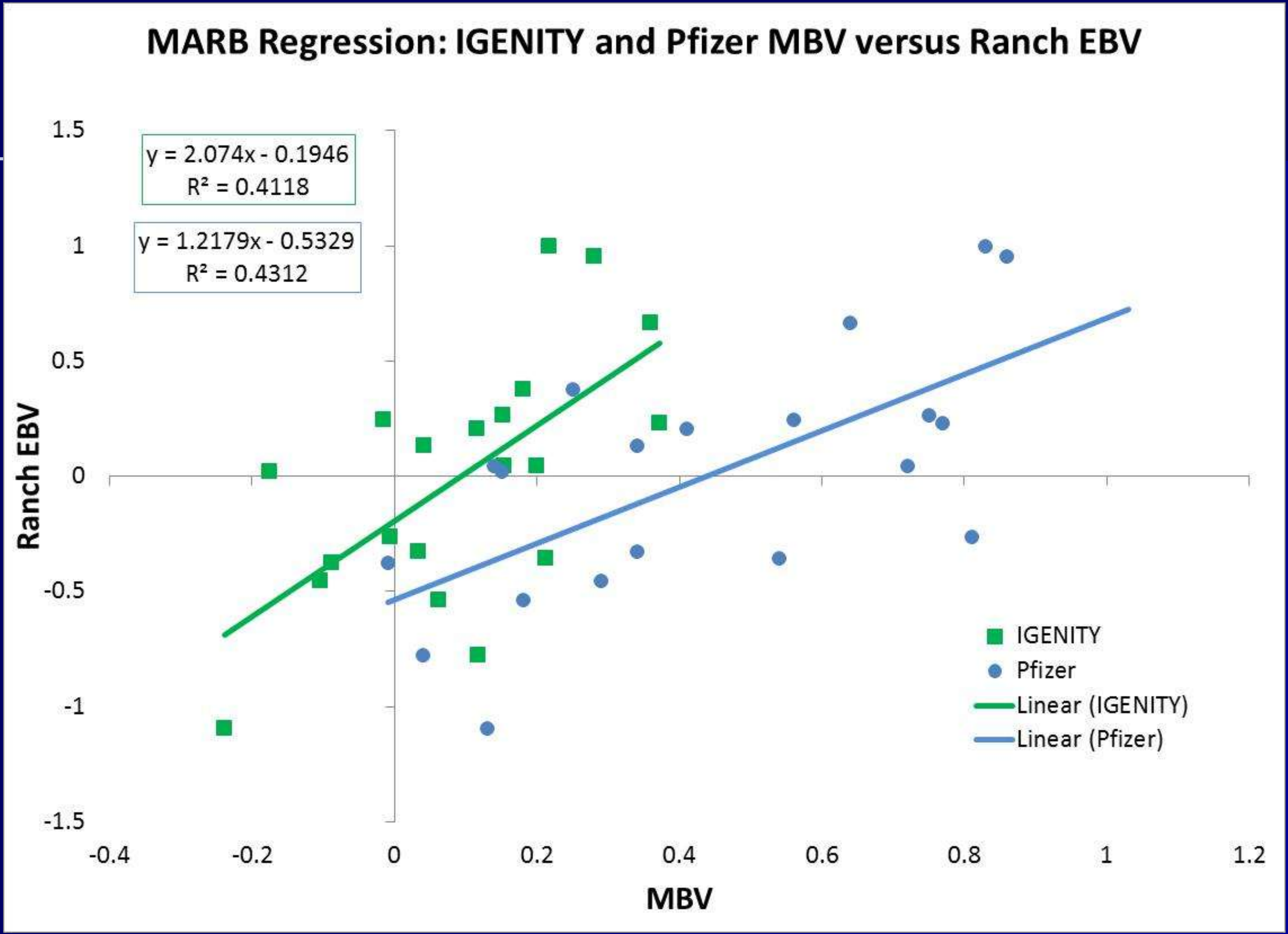
Results: Ranch Marbling



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