

"WHAT ARE HERD BULLS ACCOMPLISHING IN MULTIPLE SIRE BREEDING PASTURES?"

Alison Van Eenennaam, Ph.D.

Cooperative Extension Specialist
Animal Biotechnology and Genomics

Department of Animal Science
University of California, Davis
alvaneennaam@ucdavis.edu

(530) 752-7942



<http://animalscience.ucdavis.edu/animalbiotech>



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*



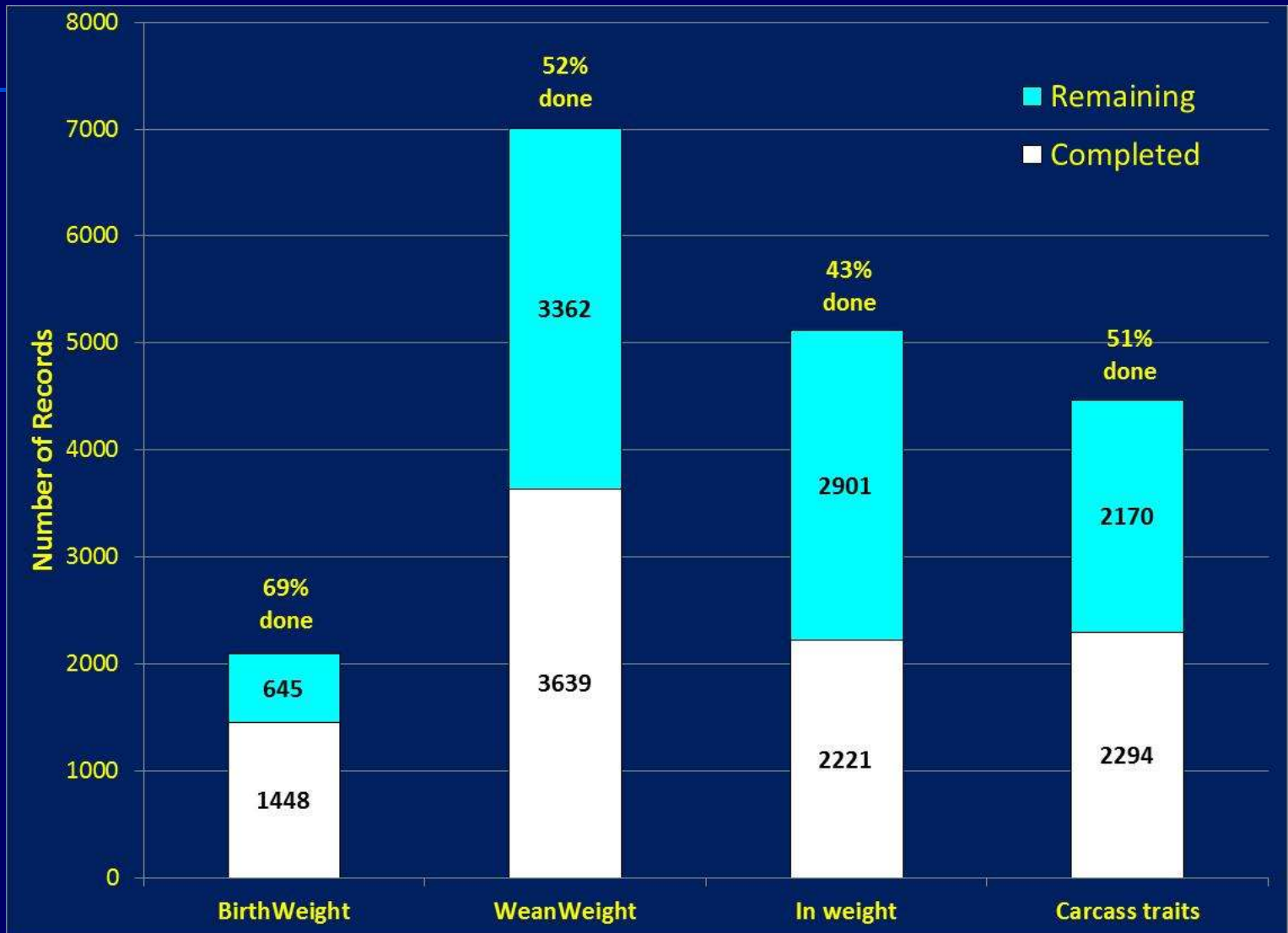
Work flow and collaborators



- 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**



Sampling Summary : Total Number of Records to date





Methods



- IGENITY and Pfizer MBV were purchased for 29 registered Angus bulls from 3 of the 4 ranches involved in this project. MBV evaluations 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 data

- Progeny records of Angus bulls from calf cohorts beginning in 2006 (bulls bred 2005). Though the dataset included 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



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. The only fixed effect fit was the mean.
- Ranch records were adjusted for contemporary group and progeny weaning weights were adjusted to 205-days of age.
- Random maternal effects were included in the weaning weight model but random permanent environmental effects were not included in the model due to the scarcity of information available on the dams.
- Residual covariance was assumed zero and for weaning weight, covariance between weaning weight MBV and weaning weight maternal was assumed zero.

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)	-0.0 (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.



Genetic correlations for National Cattle Evaluation traits by company



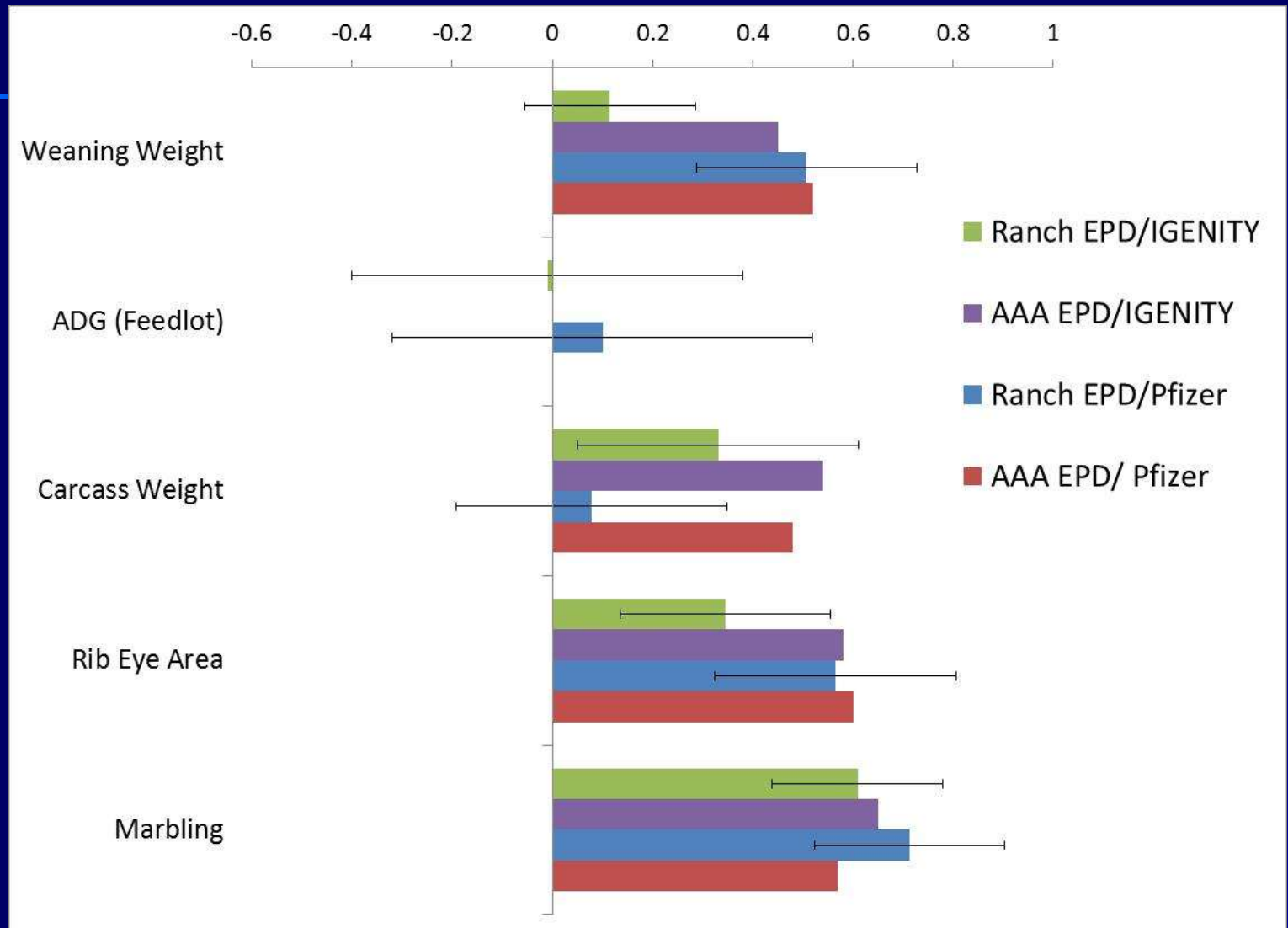
384 SNP 50K SNP

	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)



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 ¹	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



Results: Regression analyses



<u>Trait</u>	<u>Source of EPD</u>	<u>Test</u>	<u>Slope</u>	<u>Sterr</u>	<u>Prob</u>	<u>Significance</u>
WWT	AAA	IGENITY	0.03	0.20	0.87	
WWT	Ranch	IGENITY	0.13	0.74	0.86	
REA	AAA	IGENITY	0.79	0.17	0.0001	***
REA	Ranch	IGENITY	1.69	0.83	0.06	
MRB	AAA	IGENITY	0.87	0.20	0.0002	***
MRB	Ranch	IGENITY	2.07	0.58	0.0023	**
CW	AAA	IGENITY	0.95	0.22	0.0002	***
CW	Ranch	IGENITY	1.09	0.75	0.17	
ADG	AAA	IGENITY	--	--	--	
ADG	Ranch (PostWG)	IGENITY	-1.08	1.23	0.39	
WW	AAA	Pfizer	0.37	0.15	0.03	*
WW	Ranch	Pfizer	1.78	0.65	0.01	*
REA	AAA	Pfizer	0.54	0.10	0.00002	***
REA	Ranch	Pfizer	1.60	0.48	0.004	**
MRB	AAA	Pfizer	0.55	0.09	0.000001	***
MRB	Ranch	Pfizer	1.22	0.33	0.002	**
CW	AAA	Pfizer	0.57	0.11	0.00002	***
CW	Ranch	Pfizer	-0.04	0.47	0.94	
ADG	AAA	Pfizer	--	--	--	
ADG	Ranch (PostWG)	Pfizer	-0.39	0.45	0.39	



Correlation between ranch EBV when incorporating Pfizer or Merial MBVs as a correlated trait

- Ranch EBV were calculated in
 - a univariate analysis
 - a bivariate analysis with MBV
 - using the estimated genetic correlation and
 - using a fixed genetic correlation (the AAA standard)
- The correlation between EBV from each model was estimated.



Correlation between Ranch EBVs and MBV-adjusted Ranch EBVs using different r values



	Bulls with ranch bif acc > 0.05	# direct progeny in dataset	Pfizer-Estimated r	Pfizer-AAA r	IGENITY-Estimated r	IGENITY-AAA r
WWT	29	1734	0.9870	0.9861	0.9992	0.9828
ADG	28	1356	0.9921		0.9993	
HCWT	20	455	0.9985	0.9311	0.9727	0.7991
REA	23	455	0.9311	0.9206	0.9809	0.9389
MRB	23	455	0.9442	0.9715	0.9591	0.9512



WW EBV	Igenity Est.	Igentiy AAA	Pfizer Est.	Pfizer AAA	RANK	Igenity Est.	Igentiy AAA	Pfizer Est.	Pfizer AAA
43.6	1.0	2.6	3.8	3.9	1	0	0	0	0
40.7	0.4	0.1	5.2	5.3	2	0	0	0	0
20.9	-1.0	-6.1	-2.5	-2.7	3	0	-2	0	0
19.4	-1.1	-6.3	-5.7	-6.0	4	0	-4	-2	-2
16.4	-0.1	-1.6	1.7	1.7	5	-1	1	1	1
15.6	1.6	5.4	-3.7	-3.9	6	1	3	-2	-2
15.2	0.0	-1.2	1.7	1.8	7	0	1	2	2
13.5	0.3	0.0	-5.2	-5.5	8	0	1	-1	-1
11.1	-0.8	-4.6	1.8	1.8	9	0	-2	2	2
7.5	0.1	-0.6	-5.2	-5.4	10	0	0	-3	-3
5.6	-0.2	-1.0	0.4	0.4	11	-1	-1	0	0
4.1	-1.0	-4.6	-3.9	-4.1	12	-1	-3	-2	-2
3.8	1.6	6.5	3.9	4.0	13	2	4	3	3
2.4	0.2	-0.1	0.6	0.6	14	0	1	2	2
1.5	-0.9	-4.6	-3.6	-3.8	15	0	-2	-1	-1
-1.6	0.2	0.6	0.0	0.0	16	0	0	1	1
-3.0	-0.3	-2.0	-0.9	-0.9	17	0	-1	0	0
-7.7	-0.9	-3.5	-5.1	-5.3	18	-1	-2	-3	-3
-10.5	2.1	10.0	2.6	2.7	19	1	5	1	1
-11.3	-1.2	-5.4	2.3	2.4	20	0	-2	1	1
-13.3	-1.8	-7.5	1.5	1.6	21	-1	-2	1	1
-13.6	0.7	3.7	-5.1	-5.3	22	1	3	-3	-3
-20.5	0.9	4.6	3.0	3.2	23	0	2	-1	-1
-20.5	-0.6	-1.8	3.8	4.0	24	0	0	2	2
-24.1	-0.2	-0.9	6.9	7.1	25	0	0	2	2
-32.0	0.2	1.9	-6.5	-6.6	26	0	0	0	0
-48.8	0.1	1.2	1.6	1.7	27	0	0	0	0
-49.5	0.0	1.9	-7.1	-7.3	28	0	0	0	0
-66.4	2.2	12.0	5.4	5.6	29	0	0	0	0



Correlation between Pfizer and IGENITY MBVs (n=29)



Trait	Raw correlation between Pfizer and IGENITY MBV
WWT	0.22
ADG (WWT to INWT)	0.14
HCWT	0.45
REA	0.59
MRB	0.56





2011 Outreach progress and plans

- Abstract: **Genomic Selection in Beef Cattle: Training and Validation In Multibreed Populations.** Plant and Animal Genome
- Paper: **Accuracy of genomic breeding values in multi-breed beef cattle populations derived from deregressed breeding values and phenotypes**
- Beef magazine.Feb. **Improving the accuracy of EPDs with DNA information**
- ASAS Abstract/Paper: Comparison of different prediction equations (2000 bull, MARC trained, any one else that wants to be involved) versus Angus EPDs versus integrated ranch data (Years 1 and 2) – also have Pfizer MVPs and Igenity MBVs on bulls with at least 10 carcass trait records
- BIF paper: Economic analysis of value of emerging MBV for ERT for which no bEPD exist **“What weighting should be given to BRD resistance in selection decisions?”** (Collaboration with Mike MacNeil)
- Presentations: PAG January, Siskiyou January, Sierra Field Day April, SMO genomics conference May, Lincoln June, AAABG July, Missouri Reproduction Symposium August, Idaho September, California Cattlemen’s November, Oregon December



2012 workshop.....

- In-depth **NBCEC** stakeholder workshop entitled "*Integrating DNA information into beef cattle production systems*" will be held at a central location (eg. Kansas City) to report on the results and findings of this project, and detail the implications of the use of DNA technologies for various sectors of the beef cattle industry.
- In year 4, **\$10,000** to offset costs (facility room rental, speaker travel costs and accommodations, advertising, refreshments, supplies etc) associated with a national NBCEC workshop entitled "*Integrating DNA information into beef cattle production systems*" is requested.



“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 Coopriker, 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*



United States
Department of
Agriculture

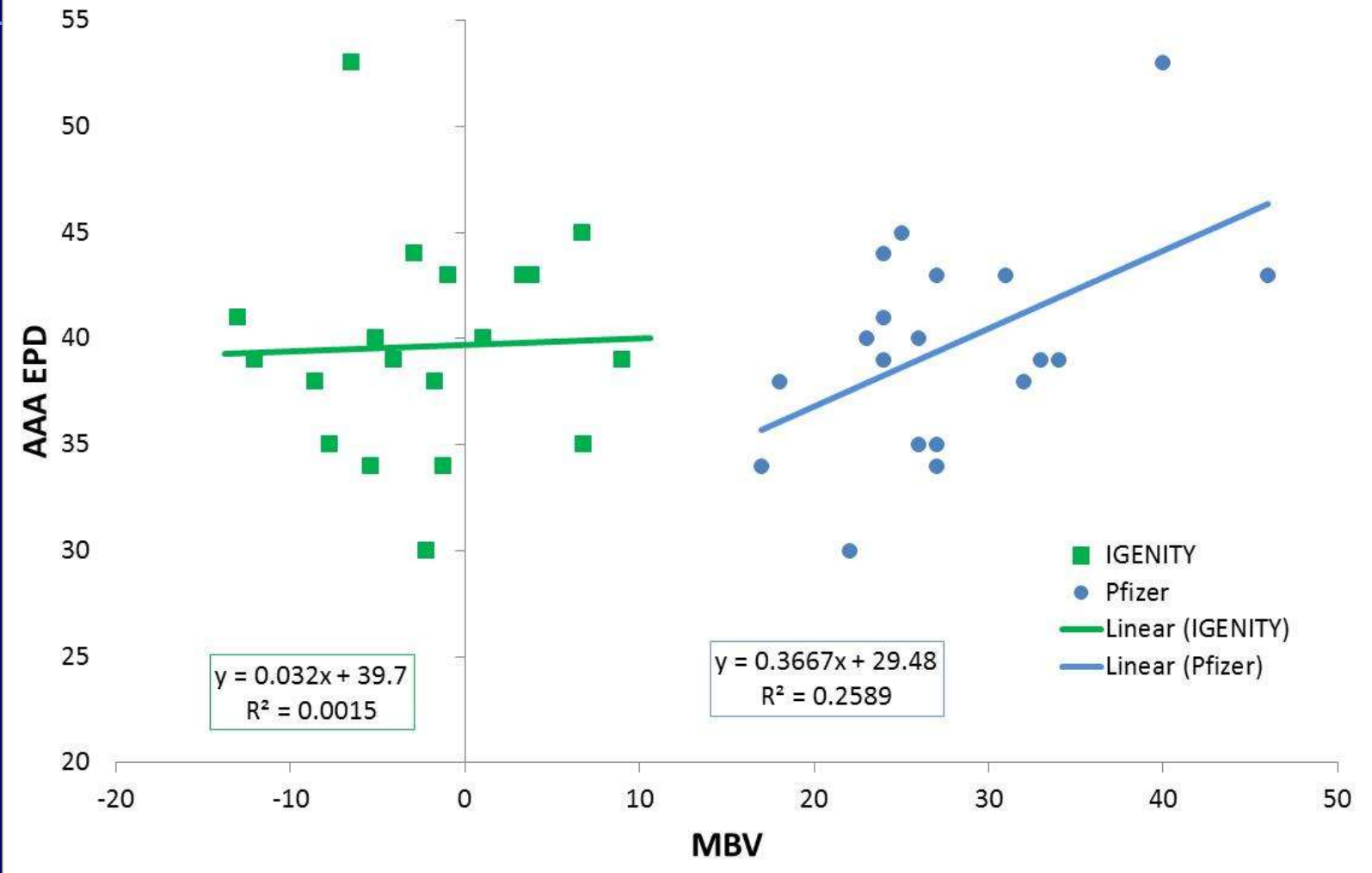
National Institute
of Food and
Agriculture

This project is supported by National Research Initiative Competitive Grant No. 2009-55205-05057 Integrating DNA information into beef cattle production systems" from the USDA National Institute of Food and Agriculture.



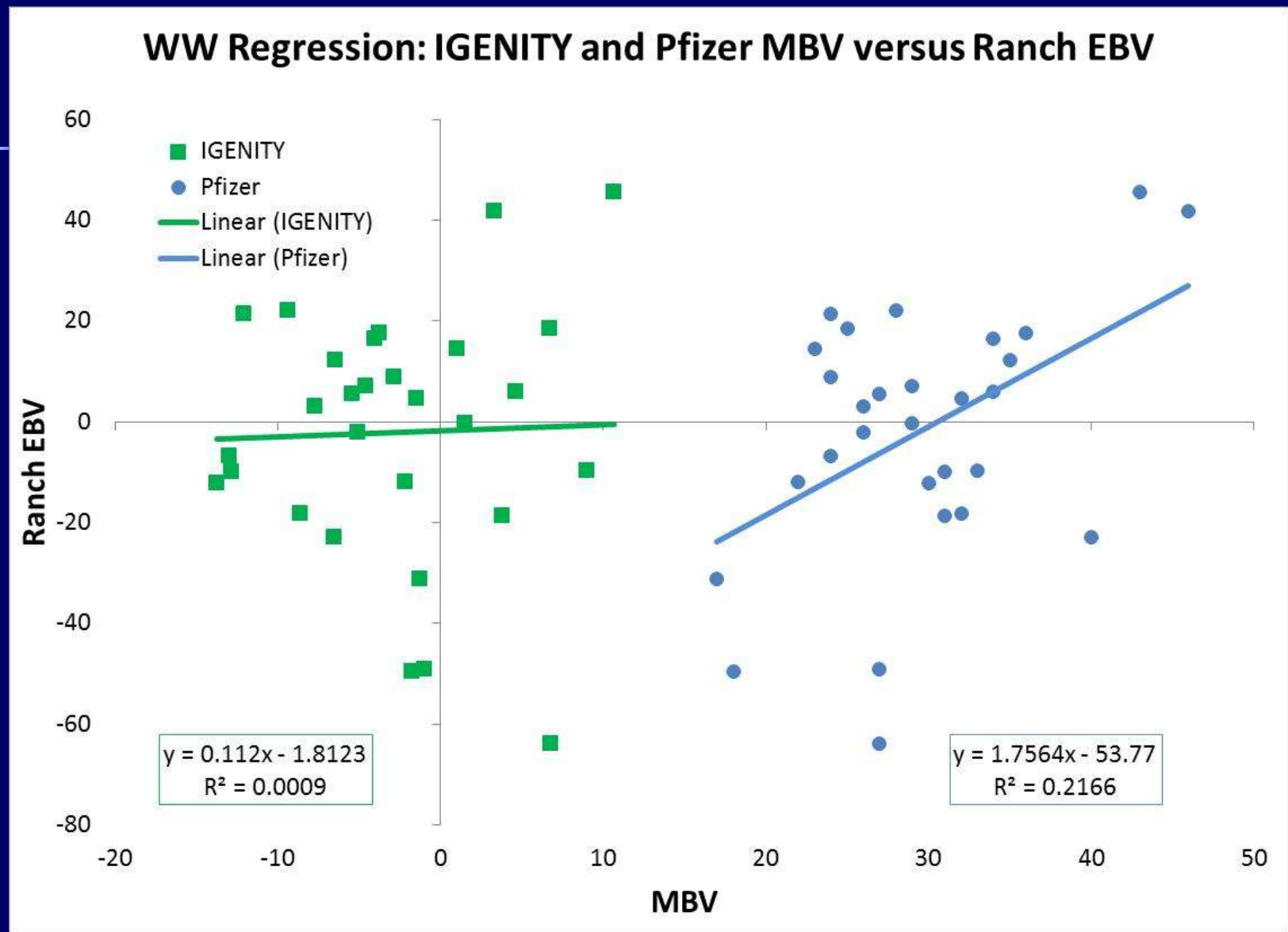
Results: AAA Weaning weight

WW Regression: IGENITY and Pfizer MBV versus AAA EPD



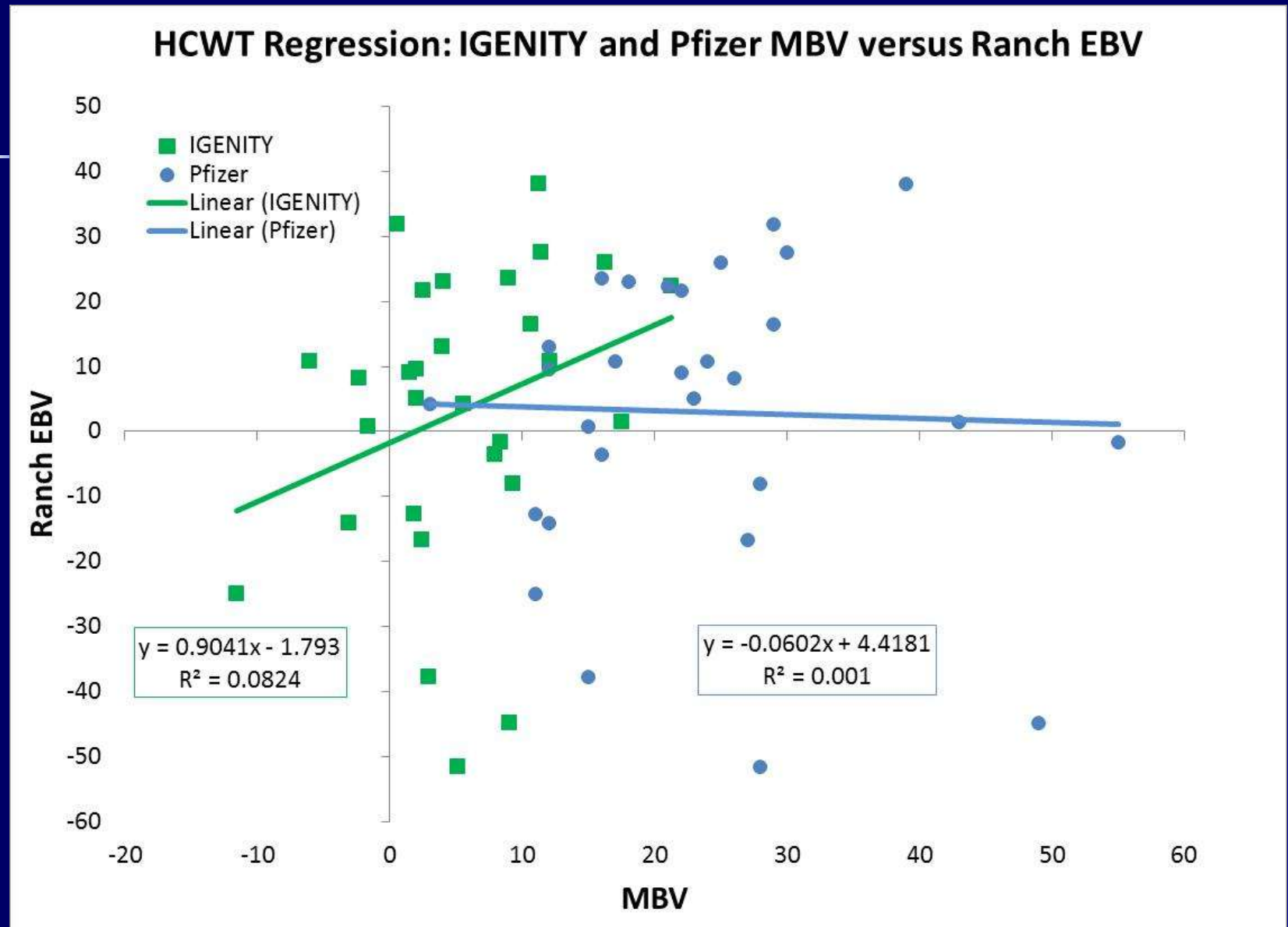


Results: Ranch Weaning weight





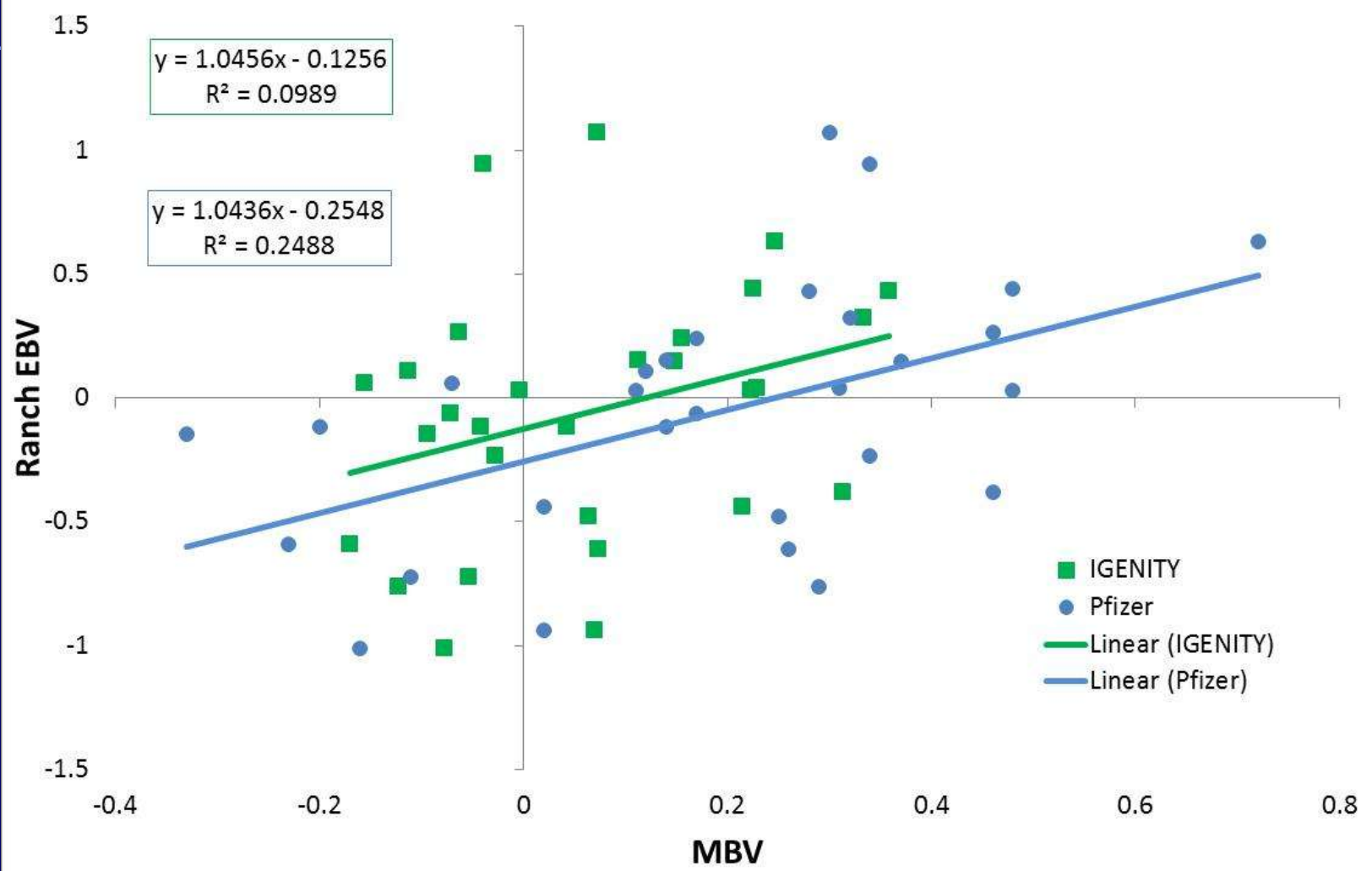
Results: Ranch Hot Carcass Weight





Results: Ranch Ribeye Area

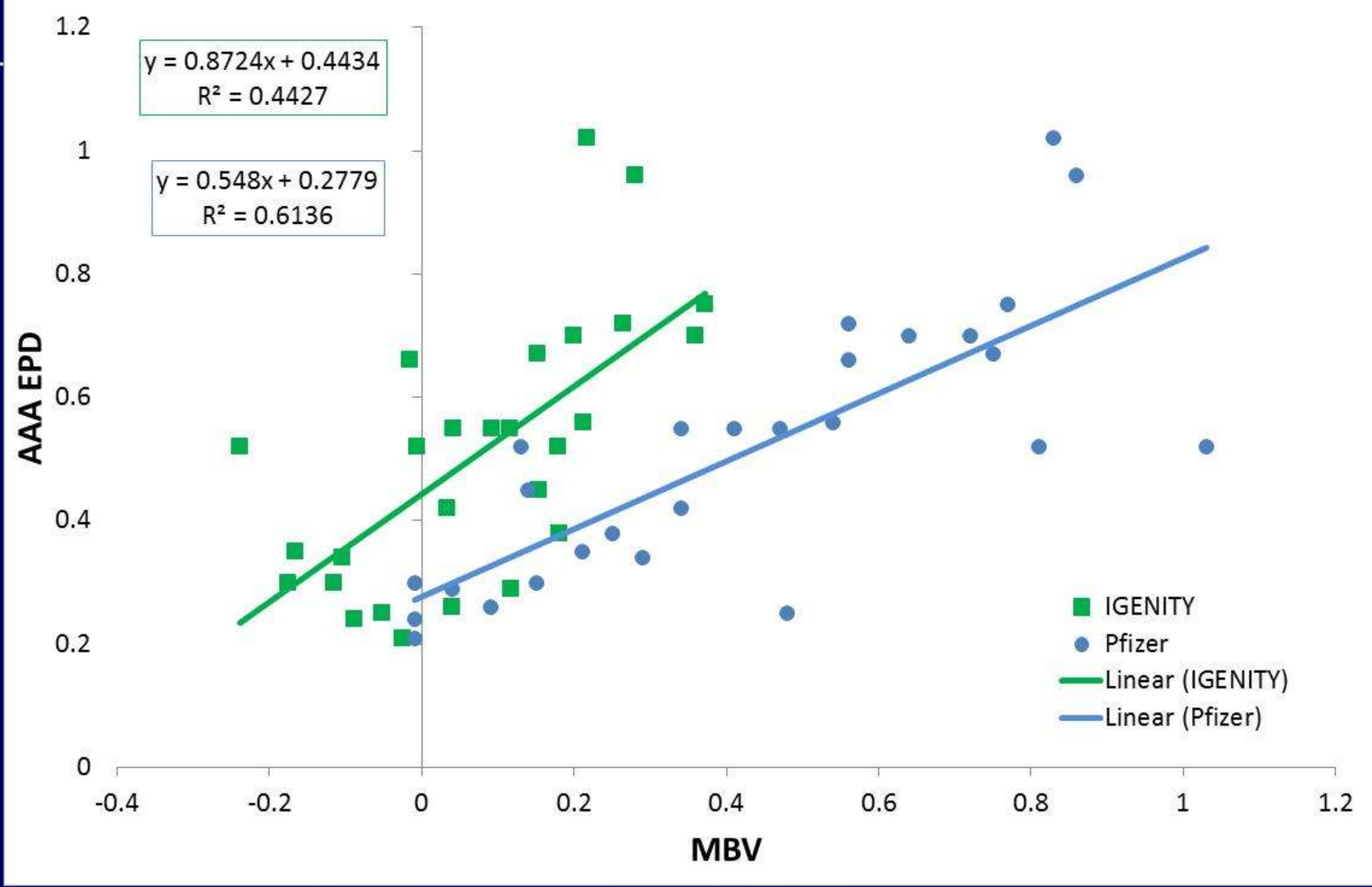
REA Regression: IGENITY and Pfizer MBV versus Ranch EBV





Results: AAA Marbling

MARB Regression: IGENITY and Pfizer MBV versus AAA EPD

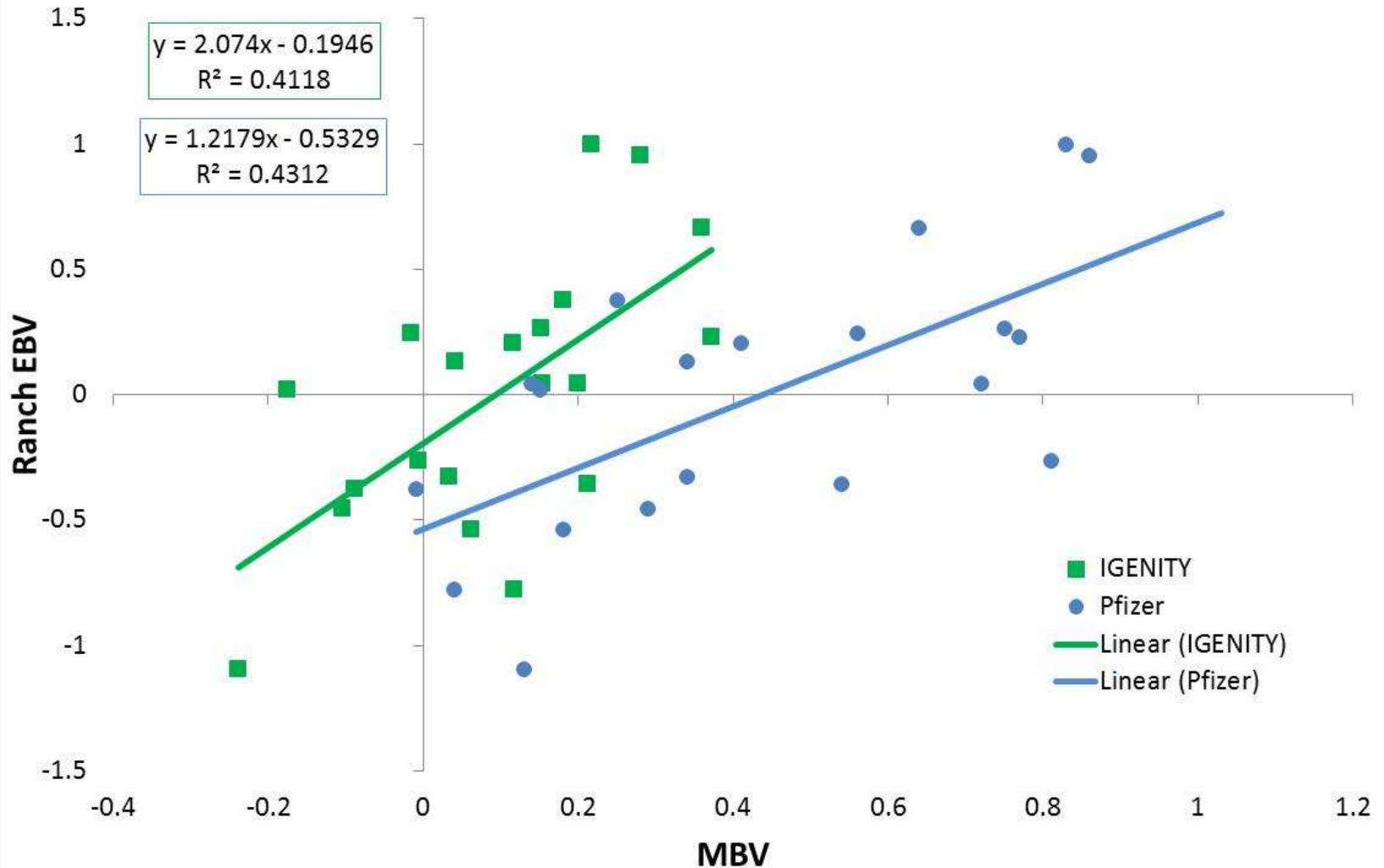




Results: Ranch Marbling



MARB Regression: IGENITY and Pfizer MBV versus Ranch EBV





Questions?