

NP101 Food Animal Production



Jeffrey Vallet

National Program Leader

Team Members:

Cyril Gay

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Vision

ARS will provide the scientific community and food animal industries with scientific information, biotechnologies, and best management practices that ensure consumers an abundant supply of competitively priced, high quality animal products that enhance human health, while ensuring domestic food security, and enhancing the efficiency, competitiveness and environmental sustainability of the food animal industry.



Mission

Conduct research to improve food animal production efficiency, industry sustainability, animal welfare, product quality and nutritional value while safeguarding animal genetic resources.



Program Components

Component 1: Increasing Production and Production Efficiencies while Enhancing Animal Well-Being across Diverse Food Animal Production Systems

Component 2: Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

Component 3: Measuring and Enhancing Product Quality and Enhancing the Healthfulness of Meat Animal Products

❖ NP101 Overall Statistics (2019):

❖ 94 SYs (75 Sys and 19 vacancies)

14 locations

❖ 26 projects Appropriated funding = \$51.6M



Clay Center NE



Dubois ID



Miles City MT



Madison WI



Fort Collins CO



El Reno OK



Beltsville MD



Lexington KY



Ames IA



Columbia MO



Lubbock TX



West Lafayette IN



East Lansing MI, Athens GA



Mississippi State MI

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Genomics in Beef



Clay Center NE



Dubois ID

Beef Range Management



Miles City MT

Dairy Systems



Madison WI

Beef and Dairy germplasm



Fort Collins CO

Beef Pasture Ecology



EI Reno OK

Dairy Genomics



Beltsville MD

Beef Fescue toxicosis



Lexington KY



Ames IA



Columbia MO

Beef Animal Welfare



Lubbock TX

Dairy animal welfare



West Lafayette IN



East Lansing MI, Athens GA



Mississippi State MI

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Genomics, Female
Reproduction Swine



Clay Center NE



Dubois ID



Miles City MT



Madison WI

Swine
germplasm



Fort Collins CO



El Reno OK

Swine Male
Reproduction,
mycobiome,
gene editing

Beltsville MD



Lexington KY

Swine nutrition



Ames IA

Swine gene
editing



Columbia MO

Swine Animal Welfare



Lubbock TX

Swine
animal
welfare



West Lafayette IN



East Lansing
MI, Athens GA



Mississippi State MI

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Genomics Sheep



Clay Center NE

Sheep Range Management



Dubois ID



Miles City MT



Madison WI

Sheep
germplasm



Fort Collins CO

Sheep pasture ecology



EI Reno OK

Goat genomics



Beltsville MD

Sheep Fescue
toxicosis



Lexington KY



Ames IA



Columbia MO



Lubbock TX



West Lafayette IN



East Lansing
MI, Athens GA



Mississippi State MI

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Clay Center NE



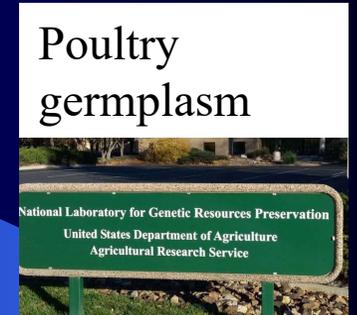
Dubois ID



Miles City MT



Madison WI



Fort Collins CO



El Reno OK



Beltsville MD



Lexington KY



Ames IA



Columbia MO



Lubbock TX



West Lafayette IN



East Lansing MI, Athens GA



Mississippi State MI

Animal Welfare



Meat Quality

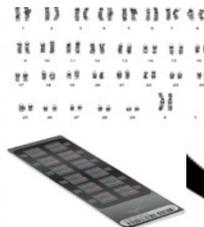


Meat Healthfulness

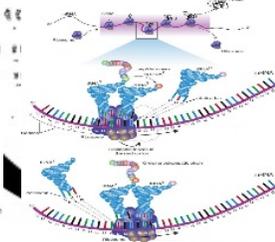


Genomics

Genomic Tools



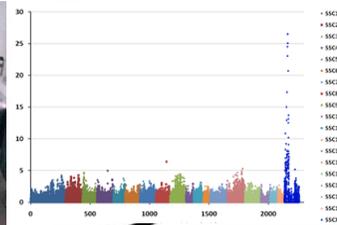
Functional Genomics



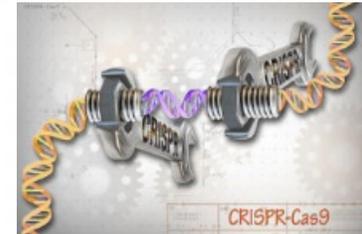
Preserve Germplasm



Genomic Selection



Gene Editing



Reproductive Efficiency



Nutritional Efficiency



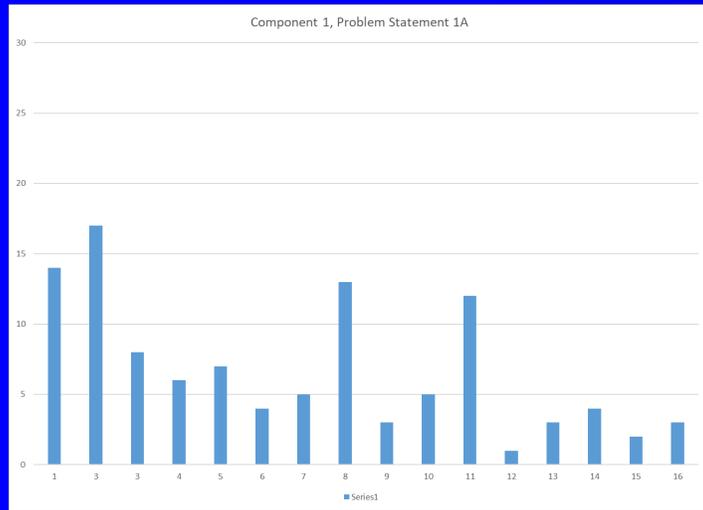
Component 1: Increasing Production and Production Efficiencies while Enhancing Animal Well-Being across Diverse Food Animal Production Systems

Problem Statement 1A: Improving the Efficiency of Growth and Nutrient Utilization

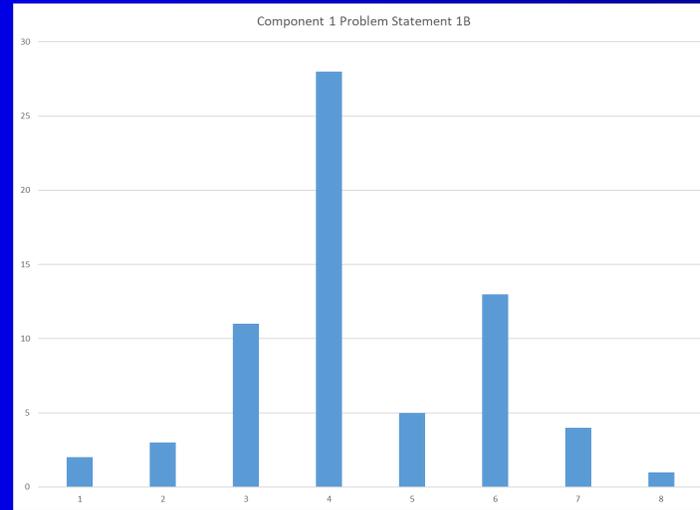
- 1) Elucidation of the genes and metabolic pathways that contribute to growth and developmental performance and nutrient utilization efficiency of livestock.
- 2) Biological markers that are useful in predicting and improving growth performance and nutrient utilization efficiency of livestock.
- 3) Strategies that alter metabolic pathways to improve growth performance and nutrient utilization efficiency in livestock.
- 4) Best management practices and genetic selection parameters that improve the rate of improvement for growth and feed efficiency for producers.
- 5) Comprehensive characterization of digestive system microflora in livestock species, including the organisms present and their prevalence, and identification of those species that are correlated with improved performance, nutrient utilization efficiency, and reduced environmental impact.
- 6) Strategies that can be used to alter digestive system microflora populations resulting in improved nutrient utilization efficiency in livestock species.
- 7) Effective strategies for determination of consumption and improved use of forages to meet livestock nutrient needs.
- 8) Identification of alternative feeds that can be used to provide nutrients for livestock while maintaining production and production efficiencies and meat quality.
- 9) Precision feeding systems for livestock and poultry that optimize nutrient availability to the animal while minimizing nutrient losses to the environment.
- 10) Development of refined methodology allowing precise real time nutrient evaluation of forages including improved sampling procedures.
- 11) Strategies to reduce the negative effects of fescue toxicosis in grazing livestock and realize the potential benefits of endophytes in forages.
- 12) Development of optimized year-round forage-based beef finishing systems, including the use of crop residues, cover crops and summer/fall annuals.
- 13) Identification of alternatives to antibiotics for improving growth performance in livestock.
- 14) Management strategies and programs for improving grazing-land health and sustainability and conservation/return of natural ecosystem services.
- 15) Reducing stress and the severity of disease through the use of pre-, pro- and para-probiotics.
- 16) Identification and development of alternatives to antibiotics to decrease pathogens and improve growth performance in livestock and poultry.

Component 1. Increasing Production and Production Efficiencies while Enhancing Animal Well-Being across Diverse Food Animal Production Systems

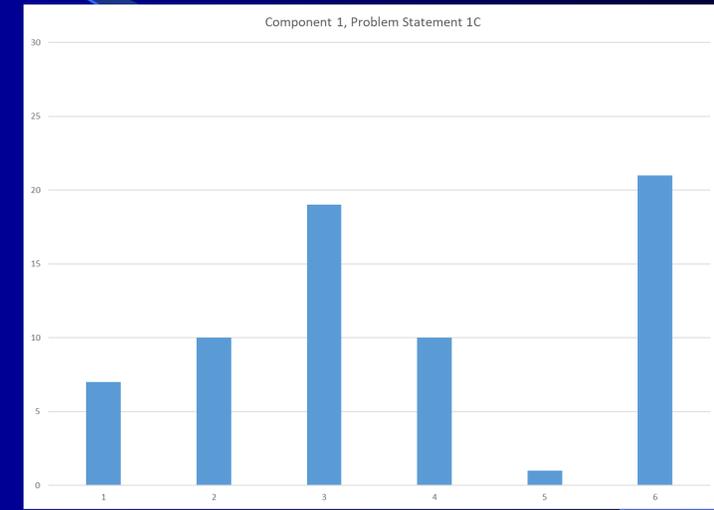
Nutrition



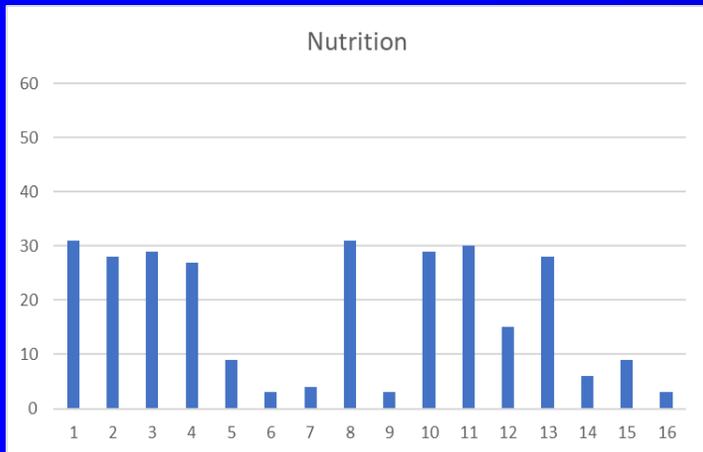
Reproduction



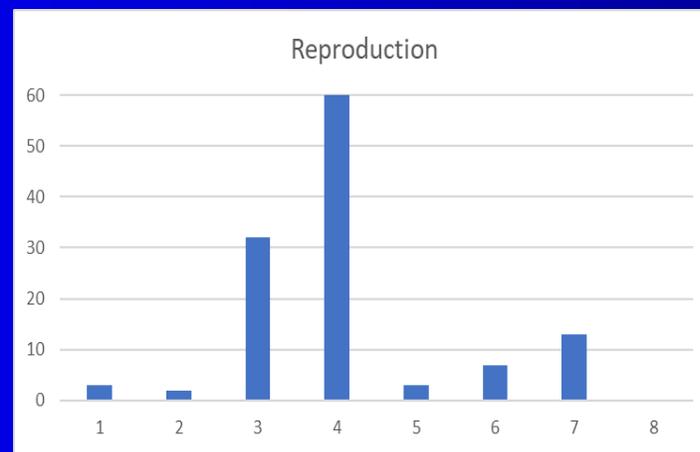
Welfare



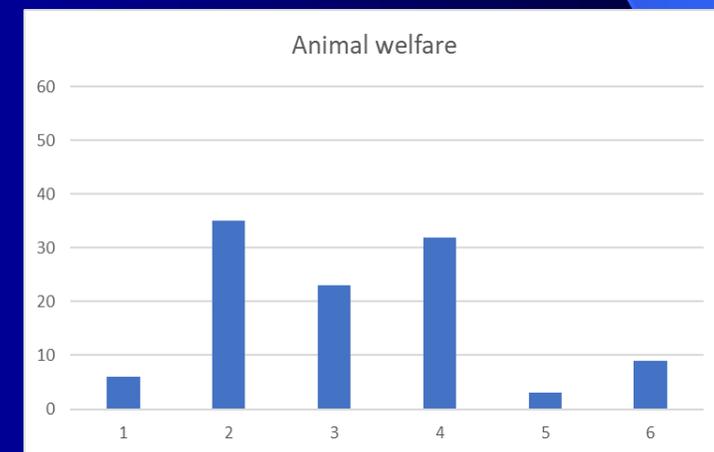
Nutrition



Reproduction

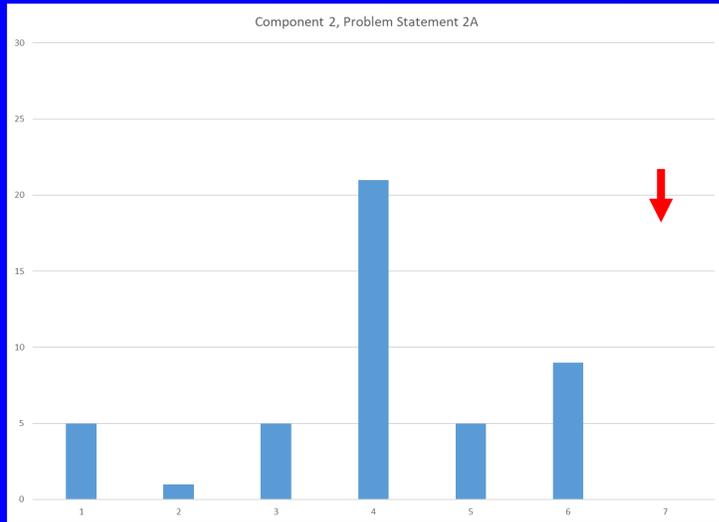


Animal welfare

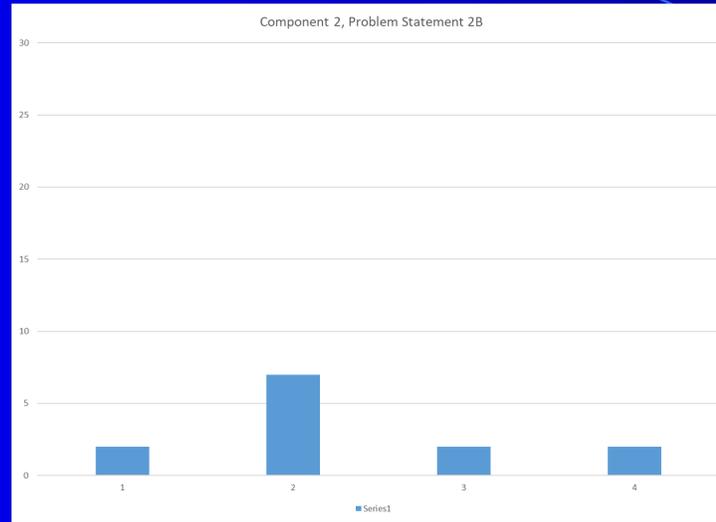


Component 2 Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

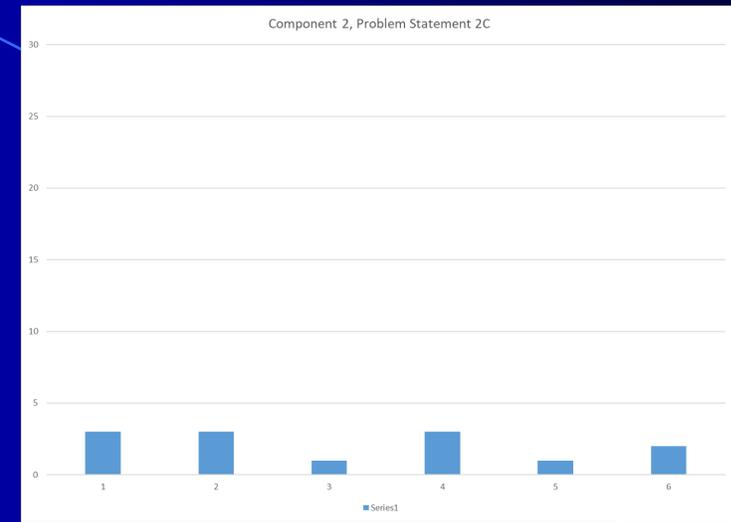
Genomic Tools



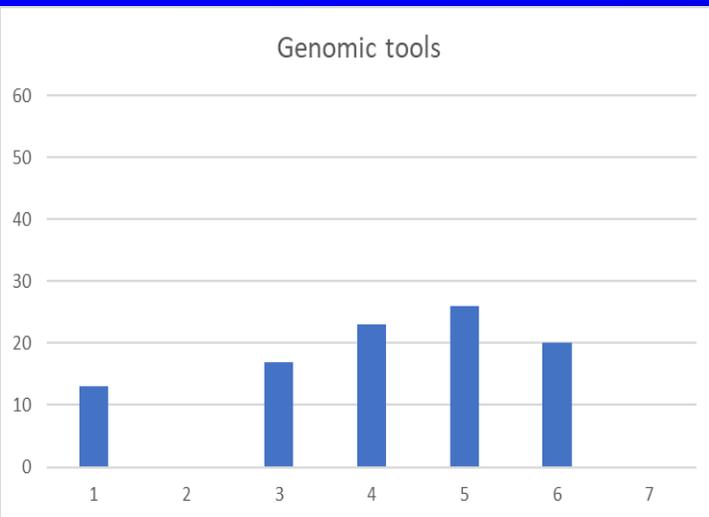
Functional genomics



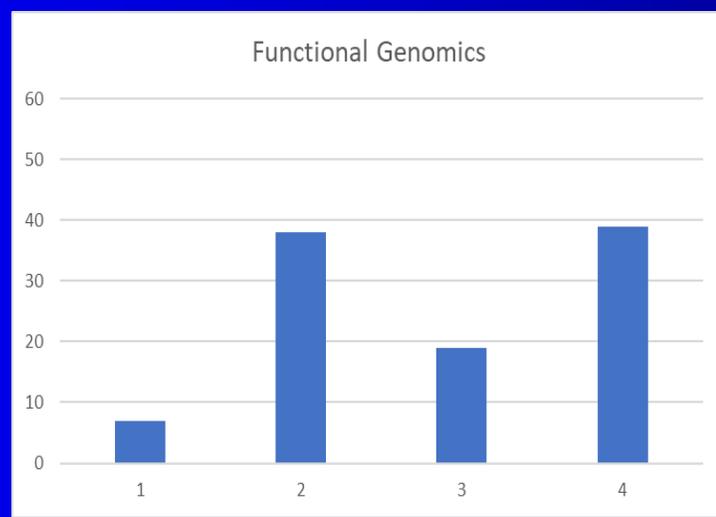
Germplasm preservation



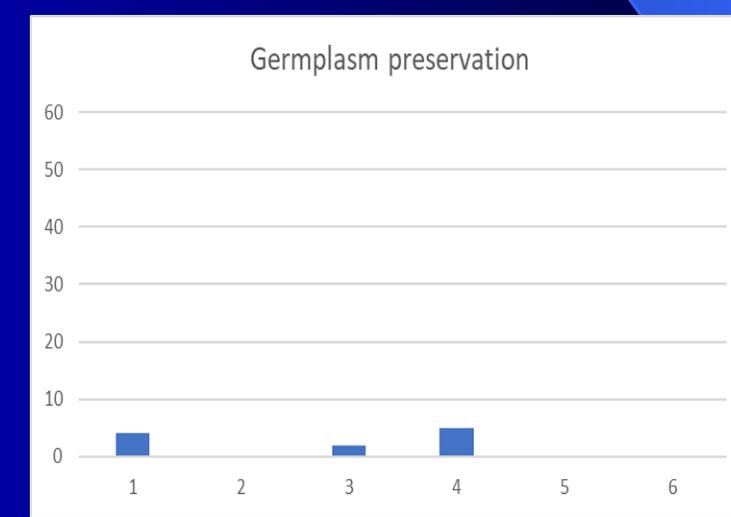
Genomic tools



Functional Genomics

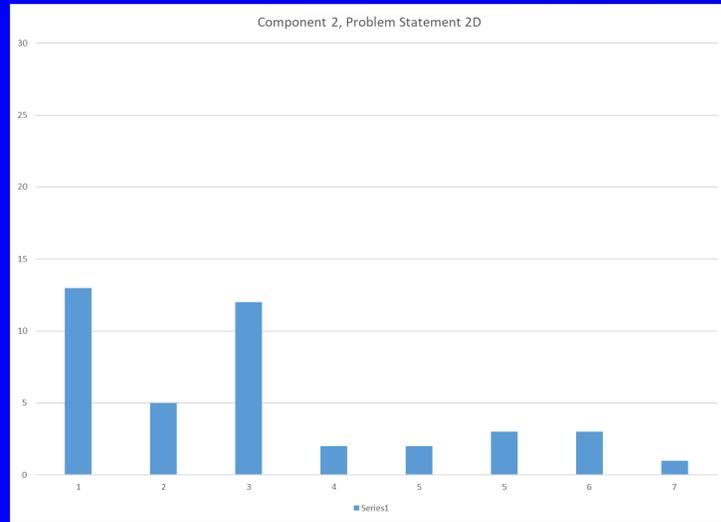


Germplasm preservation

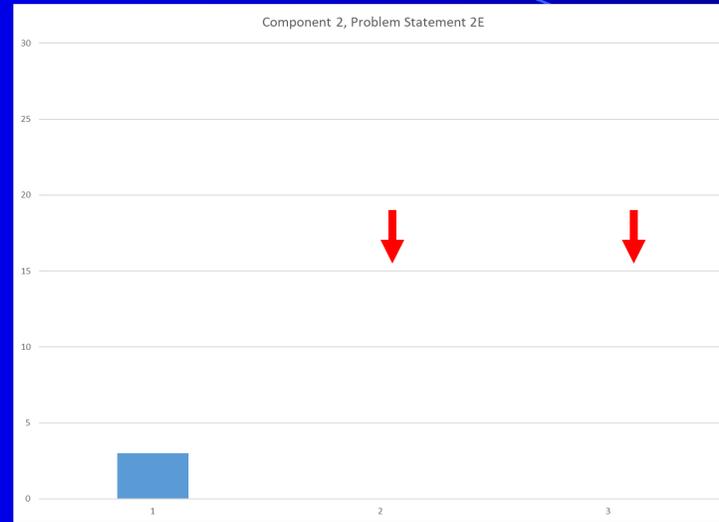


Component 2 Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

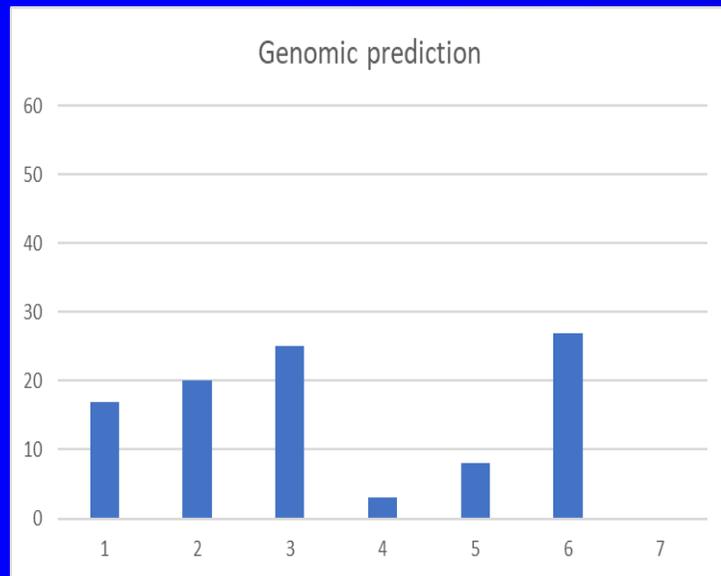
Genomic selection



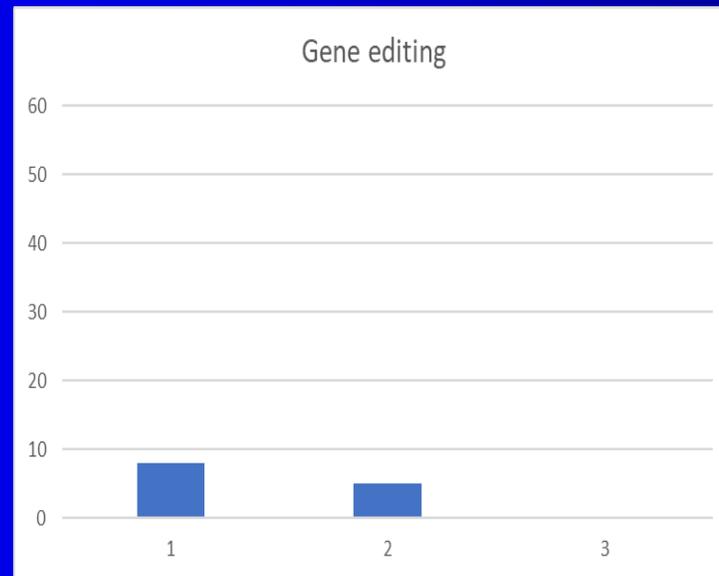
Gene editing



Genomic prediction

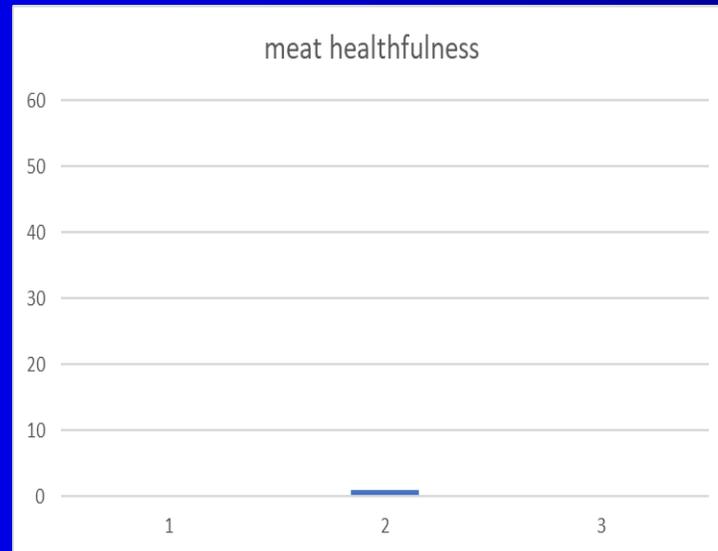
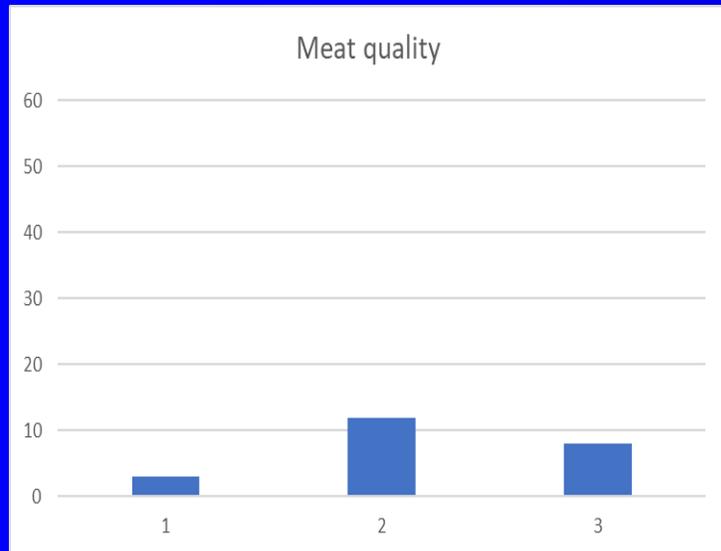
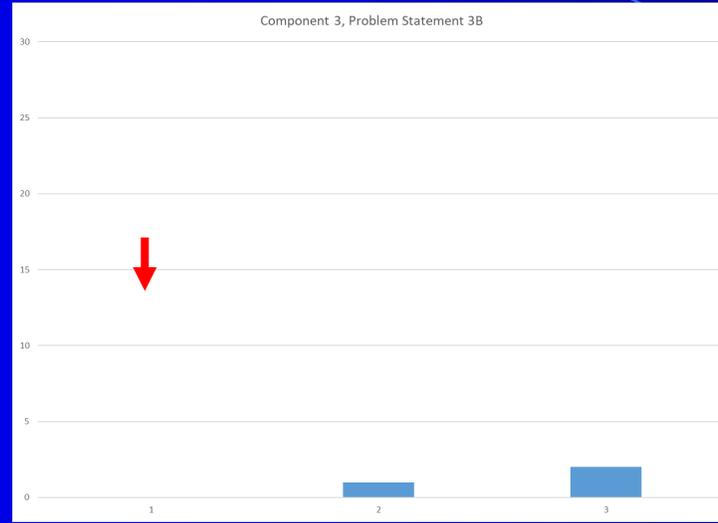
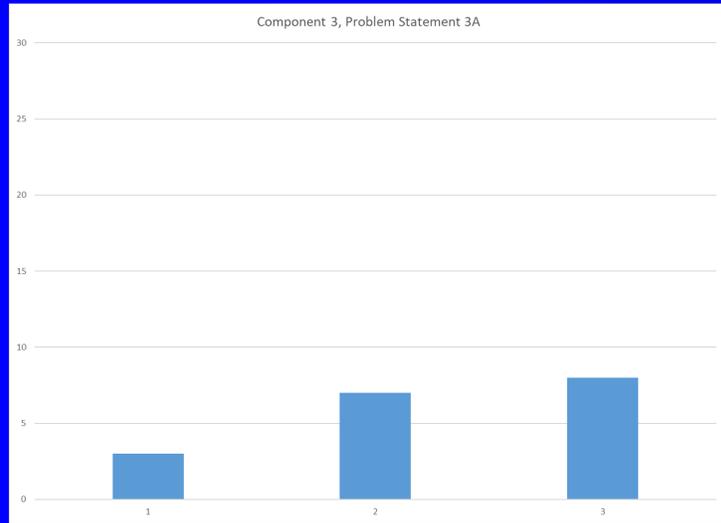


Gene editing



- Improved tissue/body fluid based phenotypes based on broad spectrum protein and metabolite analysis.
- Strategies to elucidate the genetic, protein and metabolic pathways that translate genotypes into phenotypes in food animals to inform gene modification design.
- Scientific data for use in the decision-making process regarding the nutritional value, healthfulness and animal well-being impact of genetically modified animals in meat animal production systems.

Component 3: Measuring and Enhancing Product Quality and Enhancing the Healthfulness of Meat Animal Products



- Improved meat products that enhance the health of consumers and promote increased demand

Component 1: Increasing Production and Production Efficiencies while Enhancing Animal Well-Being across Diverse Food Animal Production Systems

Problem Statement 1A: Improving the Efficiency of Growth and Nutrient Utilization

Anticipated product: Biological markers that are useful in predicting and improving growth performance and nutrient utilization efficiency of livestock.

- Ghrelin, leptin and endocannabinoids in beef cattle
- Acid 1 glycoprotein in pigs
- Growth and gut epithelial proteins in poultry during Eimeria infection

Anticipated product: Elucidation of the genes and metabolic pathways that contribute to growth and developmental performance and nutrient utilization efficiency of livestock.

- Cattle transcriptomic analysis of rumen, liver, spleen, small intestine, muscle, between high and low feed efficiency cattle
- Butyrate metabolism and responses in sheep and cattle

Table 3. Standardized coefficients (SC) and relative contribution (RC; %) of each independent variable toward the total variance accounted for in the multivariate regression model

Dependent variable	Active ghrelin		Total ghrelin		Ghrelin ratio ¹		NEFA		Lactate		Glucose		Sex ²		R ²
	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	SC	RC	
DMI	0.14 ^a	6.22	–	–	–	–	-0.11	3.49	-0.03	0.27	-0.22 ^a	14.79	0.49 ^a	75.23	0.33
DMI	–	–	-0.08	2.43	–	–	-0.10	3.39	-0.03	0.31	-0.19 ^a	13.01	0.47 ^a	80.87	0.32
DMI	–	–	–	–	0.18 ^a	10.16	-0.09	2.79	-0.04	0.46	-0.21 ^a	13.52	0.48 ^a	73.06	0.35
ADG	0.10 ^a	2.16	–	–	–	–	-0.10 ^a	2.32	-0.12 ^a	3.47	-0.05	0.56	0.63 ^a	91.48	0.47
ADG	–	–	-0.16 ^a	6.33	–	–	-0.09	1.77	-0.13 ^a	4.35	-0.02	0.07	0.60 ^a	87.48	0.48
ADG	–	–	–	–	0.16 ^a	6.02	-0.09	1.84	-0.13 ^a	3.99	-0.04	0.43	0.62 ^a	87.72	0.48
G:F	-0.01	0.04	–	–	–	–	-0.03	0.52	-0.15 ^a	10.37	0.17 ^a	13.05	0.41 ^a	76.02	0.21
G:F	–	–	-0.15 ^a	10.24	–	–	-0.02	0.20	-0.17 ^a	11.90	0.19 ^a	14.76	0.38 ^a	62.89	0.25
G:F	–	–	–	–	0.05	1.20	-0.03	0.45	-0.16 ^a	11.01	0.16 ^a	12.36	0.41 ^a	74.98	0.22

¹Ghrelin ratio = active ghrelin/total ghrelin.

²Sex value is the difference between steers and heifers (steers – heifers).

^aParameter estimate differed from 0 ($P < 0.05$).

Ghrelin, leptin and endocannabinoids as biological markers for production traits in beef cattle

	Anandamide	2-AG
DMI	-0.11	-0.04
ADG	0.07	-0.07
RFI	-0.07	0.04
G:F	0.20**	-0.02
YG	-0.15*	-0.08
Marb	0.06	-0.03
Fat	-0.17*	-0.05

Artegoitia et al., 2016

Table 5. Pseudo- R^2 values for mixed model analysis of production and carcass traits including or excluding serum leptin concentrations and the amount of the variance explained by leptin concentrations

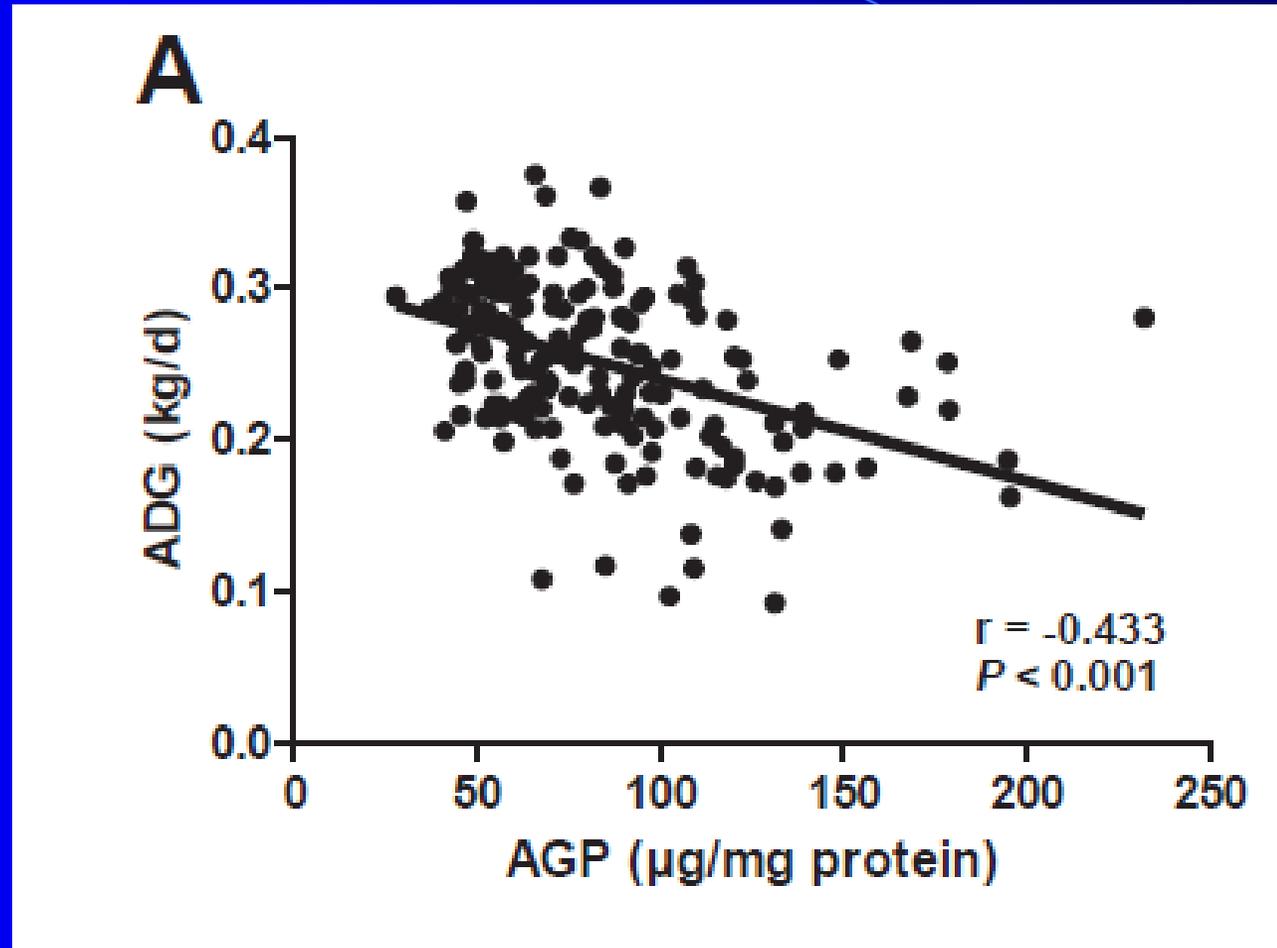
Variable	Covariates included	Pseudo- R^2 including leptin	Pseudo- R^2 excluding leptin	Percent of variance explained by leptin
DMI	Breed percentage ¹	0.165	0.154	1.10
DMI	Initial BW, YG, ² and breed percentage	0.494	0.488	0.54
ADG	Initial BW and breed percentage	0.088	0.061	2.62
G:F	Breed percentage	0.161	0.082	7.87
RFI ³	Breed percentage	0.074	0.062	1.20
12th-rib fat	Breed percentage	0.451	0.304	14.74
LM Area	Initial BW and breed percentage	0.451	0.399	5.17
HCW	Breed percentage	0.168	0.147	2.03
YG	HCW and breed percentage	0.494	0.366	12.74
Marbling score	Breed percentage	0.231	0.161	6.99

¹Breed percentage refers to a set of covariates for each of the 18 breeds.

²YG = USDA calculated yield grade.

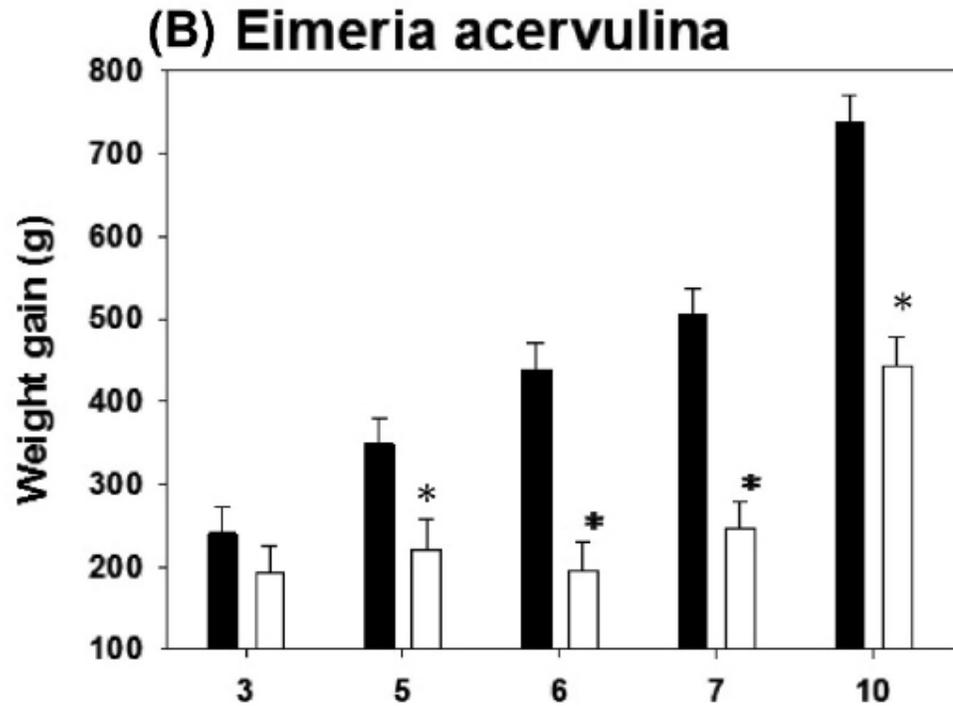
³RFI = residual feed intake.

Acid 1 Glycoprotein and growth in piglets

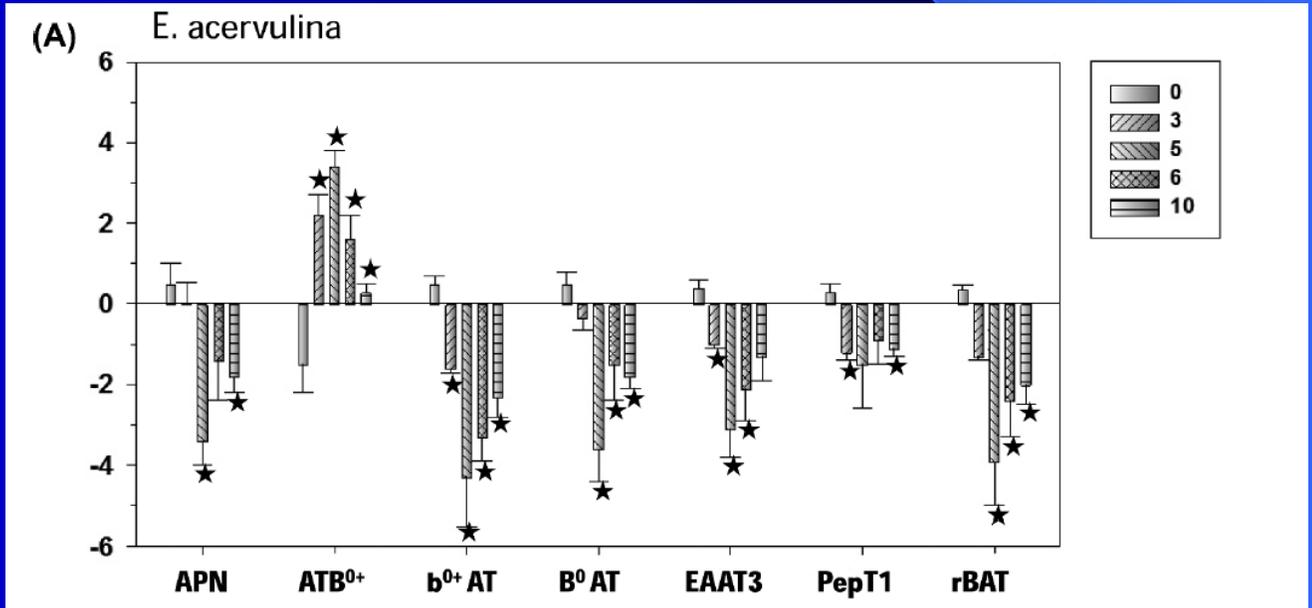
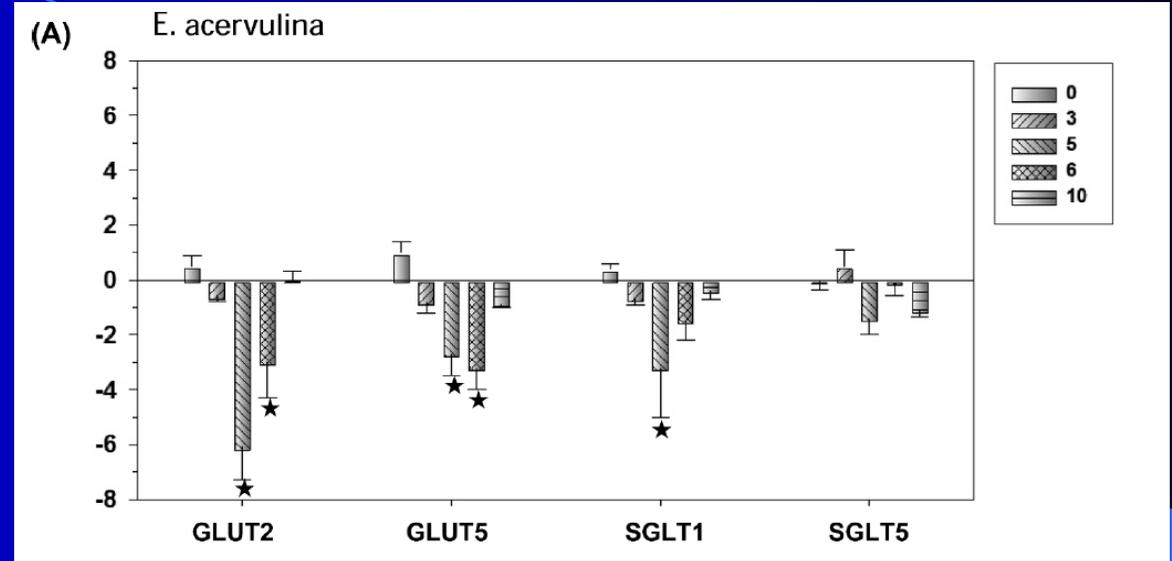


Caperna et al., 2017

Growth and gut gene expression during *Eimeria* infection



Miska and Fetterer, 2017



Differential expression in the gut from steers differing in feed efficiency, Lindholm-Perry et al., 2016

Table 1 Average, minimum and maximum values for the total gain and feed intake for 16 steers over 84 days on study.

Group ¹	Average gain (kg) ²	Min		Max		
		Min	Max	Min	Max	
High gain–high intake	187	162	204	1210	1389	
High gain–low intake	166	159	174	763	838	
Low gain–low intake	135	112	158	743	792	
Low gain–high intake	124	86	154	1135	1254	
High gain	176	159	204			
Low gain	130	86	158			
High intake				1172	1013	1389
Low intake				753	631	838

¹High gain group (n = 8) includes the high gain-high intake and high gain-low intake animals. Low gain group (n = 8) includes low gain-low intake and low gain-high intake animals. High intake group (n = 8) includes high gain-high intake and low gain-high intake animals. Low intake group (n = 8) includes high gain-low intake and low gain-low intake animals.

²Gain is in kilograms gained over the duration of the study.

³Intake units are kilograms of dry matter intake over the duration of the study.

Analysis ¹	Transcript ID ²	A ³	B ³	Fold change ⁴	P-value ⁵	FDR ⁶	Gene symbol	Description
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Differential expression in the duodenum

High gain–low intake vs. low gain–low intake	12767029	10.2	8.61	3.02	0.01	0.999	<i>CCL8</i>	chemokine (C-C motif) ligand 8
	12824902	8.35	6.91	2.7	0.006	0.999	<i>DEFB1</i>	defensin, beta 1
	12709591	8.99	7.86	2.19	0.005	0.999	<i>FLT3</i>	fms-related tyrosine kinase 3
	12755331	6.65	5.61	2.05	0.01	0.999	<i>IL-29</i>	interleukin-29 (interferon, lambda 1)
	12778544	10.78	11.79	-2.02	0.01	0.999	<i>MARCKSL1</i>	MARCKS-like 1
	12737596	13.35	14.41	-2.07	0.01	0.999	<i>CACYBP</i>	calyculin-binding protein
	12737877	4.32	5.44	-2.18	0.001	0.999	<i>MIR29B-2</i>	microRNA mir-29b-2
	12828142	9.41	10.6	-2.28	0.01	0.999	<i>P4HA1</i>	prolyl 4-hydroxylase, alpha polypeptide 1
	12709282	13.22	15.01	-3.46	0.004	0.999	<i>HSPH1</i>	heat-shock protein family H (Hsp110) member 1

Differential expression in the jejunum

High gain–low intake vs. low gain–low intake	12832009	9.08	8.03	2.07	0.01	0.99996	<i>LOC618367</i>	uncharacterized LOC618367
	12741933	9.89	11.02	-2.19	0.01	0.99996	<i>PRID</i>	peptidylprolyl isomerase D
	12737596	12.78	13.99	-2.3	0.005	0.99996	<i>CACYBP</i>	calyculin-binding protein
	12691128	11.25	12.71	-2.76	0.006	0.99996	<i>AHA1</i>	AHA1, activator of heat-shock 90-kDa protein ATPase homolog 1 (yeast)
	12813899	9.23	11.28	-4.13	0.007	0.99996	<i>ZFAND2A</i>	zinc finger, AN1-type domain 2A
	12804546	15.54	17.74	-4.61	0.003	0.99996	<i>HSPA1A</i>	heat-shock 70-kDa protein 1A
	12709282	12.63	15.02	-5.25	0.003	0.99996	<i>HSPH1</i>	heat-shock protein family H (Hsp110) member 1

Differential expression in the ileum

High gain–low intake vs. low gain–low intake	12803493	5.29	6.44	-2.23	0.01	0.99996	<i>LOC618064</i>	olfactory receptor 2G3
	12755462	6.45	7.62	-2.25	0.01	0.99996	<i>MIR2326</i>	microRNA mir-2326
	12841663	6.03	7.22	-2.29	0.008	0.99996	<i>LOC782190</i>	olfactory receptor 12
	12880985	11.99	13.69	-3.24	0.01	0.99996	<i>DNAJB1</i>	Dnal (Hsp40) homolog, subfamily B, member 1
	12804546	13.6	16.89	-9.78	0.01	0.99996	<i>HSPA1A</i>	heat-shock 70-kDa protein 1A

Butyrate effects on glucose flux across the gastrointestinal tract in wethers. Foote and Freetly, 2016. Butyrate stimulates glucose uptake.

Table 4. Effect of an abomasal pulse dose infusion of butyrate (10 mg·kg BW⁻¹·d⁻¹) or a control buffer on area under the flux rate × time curve for net nutrient flux across the portal-drained viscera of growing wether lambs (n = 9)

Item	Treatment		SEM	P-value
	Butyrate	Control		
O ₂ , mmol	-1,164	-1,060	116	0.24
Glucose, mmol	-27.1	35.0	24.3	0.006
Lactate, mmol	60.9	51.4	18.4	0.53
Glutamate, mmol	-11.3	-7.3	3.5	0.25
Glutamine, mmol	-13.1	-7.0	3.2	0.20
Urea nitrogen, mmol	-64	-125	55	0.27
α-Amino N, mmol	214	136	46	0.21
β-Hydroxybutyrate, mmol	170	157	20	0.55
Acetate, mmol	953	949	78	0.97
Propionate, mmol	322	307	22	0.64
Butyrate, mmol	98	102	10	0.77
Isobutyrate, mmol	13.7	13.7	0.93	0.95
Isovalerate, mmol	7.3	7.8	0.92	0.59
Valerate, mmol	16.1	16.0	2.23	0.99
Energy net flux, kcal	624	615	68	0.88
Energy flux, % DE intake	19.5	19.1	1.9	0.81
Energy flux, % ME intake	24.0	23.5	2.4	0.81

Rumen epithelium response to butyrate in dairy cattle, Baldwin et al., 2018. Increased protein transcription, indicated by EIF2 signaling.

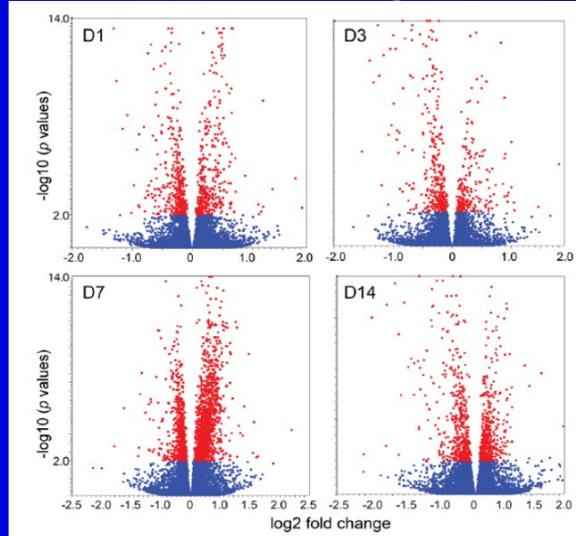


Figure 1. Volcano plots: the differentially expressed genes at different sampling time points after butyrate infusion (red dots indicate differentially expressed genes at cutoff of FDR < 0.01).

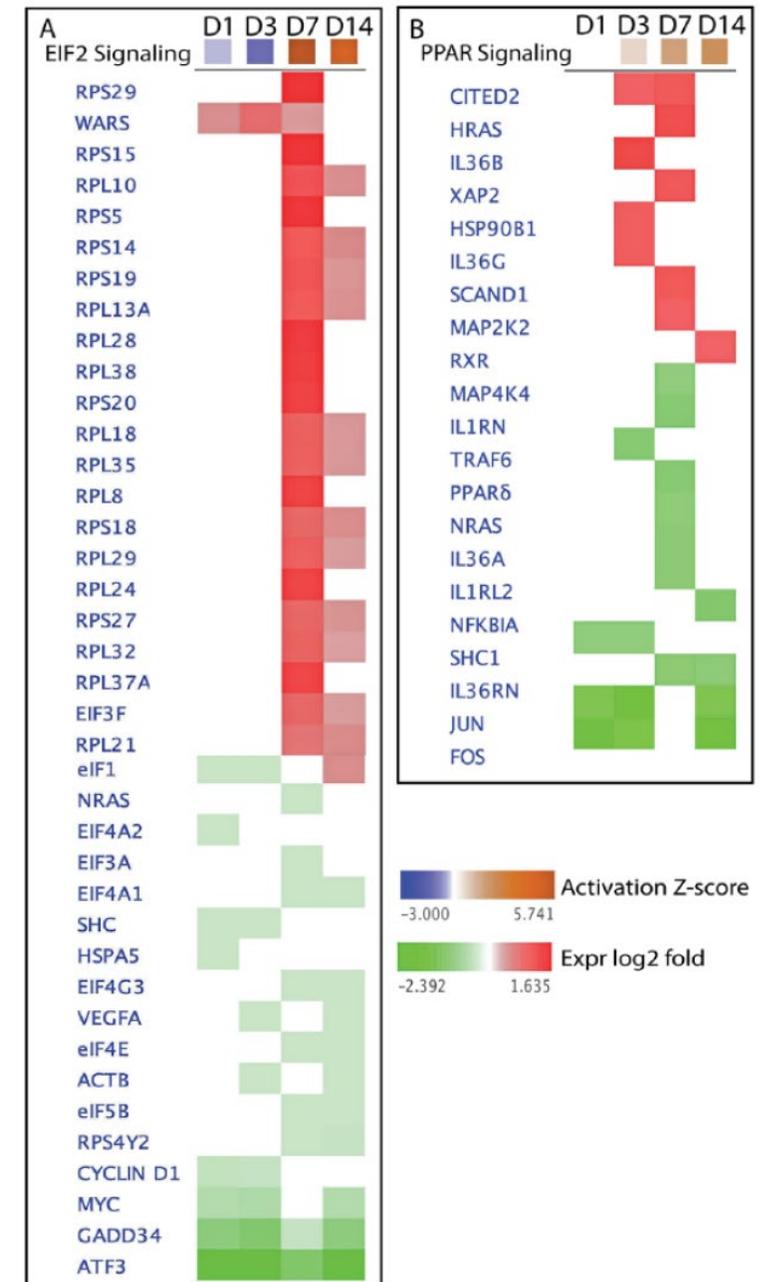
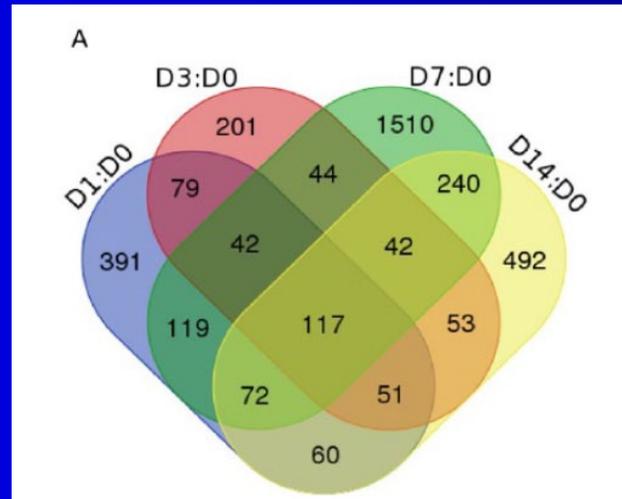


Figure 5. Heat map: effects of butyrate on the canonical pathways of EIF2 and PPAR, and genes in the pathway's network.



Anticipated product: Identification of alternative feeds that can be used to provide nutrients for livestock while maintaining production and production efficiencies and meat quality.

- Distillers grains in poultry
- Canola meal in dairy diets

Dried distillers grains incorporated into poultry diets. Kim et al., 2016. Progressive decrease in carcass yield when processed day 43, gone by day 57.

Table 5: Effect of LF-DDGS inclusion level on carcass composition of 43 and 57 d male broilers

% LF DDGS	D 43						D 57				
	Absolute wt (g)						Yield, relative to liveweight (%)				
	Live ²	Carcass ³	Fat	Fillet ⁴	Tender ⁵	Total breast ⁶	Carcass	Fat	Fillet	Tender	Total breast
0	2625	1920	27	461	98	559	73.46 ^a	0.98	17.49	3.73	21.22
6	2699	1970	28	481	100	581	73.21 ^{ab}	1.04	17.77	3.69	21.48
12	2623	1914	28	471	98	569	73.52 ^a	1.03	17.87	3.71	21.61
18	2722	1975	28	483	98	581	72.89 ^{abc}	1.02	17.66	3.59	21.26
24	2577	1870	25	458	96	553	72.75 ^{bc}	0.95	17.71	3.68	21.41
30	2598	1872	29	461	94	554	72.29 ^c	1.08	17.61	3.59	21.22
Pooled SEM	52	38	1	12	2	14	0.176	0.145	0.156	0.084	0.158
p-value	0.1740	0.1156	0.3066	0.3862	0.4101	0.3778	0.0084	0.5241	0.8284	0.3109	0.7764
0	4614	3508	79	976	179	1155	75.57	1.63	20.94	3.83	24.79
8	4665	3467	77	964	178	1142	75.18	1.63	20.81	3.84	24.65
16	4595	3490	78	972	180	1152	75.74	1.67	20.98	3.89	24.88
24	4659	3520	80	988	182	1170	76.12	1.69	21.25	3.91	25.17
Pooled SEM	47	37	3	16	4	19	0.01	0.00	0.00	0.00	0.00
Main	0.6313	0.7719	0.7817	0.7684	0.9380	0.7830	0.8084	0.7958	0.8045	0.8647	0.7879
Linear	0.7217	0.7592	0.5971	0.5597	0.5789	0.5374	0.4717	0.3233	0.4445	0.4017	0.4010
Quadratic	0.9060	0.3389	0.3198	0.3799	0.7842	0.4155	0.5682	0.8766	0.5327	0.9760	0.5660

^{a-c}Means without common superscripts are significantly different ($p \leq 0.05$). ¹6 replicate pens of 6 birds processed, ²After a 12 h overnight fast,

³Hot carcasses without fat pad, giblets and neck, ⁴Pectoralis major, ⁵Pectoralis minor, ⁶Summation of the pectoralis major and minor muscles

Canola meal as a protein source in dairy cattle increases milk production and decreases nitrogen excretion Broderick et al., 2015

Table 4. Effects of source of dietary protein, CP concentration, and supplemental rumen-protected Met plus Lys (RPML) on least squares means for production and urinary excretion in lactating dairy cows¹

Trait	Protein source		Formulated [CP]		SEM ²	RPML ³			Probability ⁴					
	SBM	CM	15%	17%		–	+	SEM ²	Source	[CP]	RPML	Source × [CP]	Source × RPML	[CP] × RPML
Production														
DMI, kg/d	24.8	25.2	24.9	25.0	0.39	24.1	25.9	0.53	0.05	0.47	0.01	0.91	0.51	0.17
BW gain, kg/d	0.38	0.47	0.41	0.45	0.067	0.46	0.39	0.067	0.32	0.67	0.43	0.07	0.61	0.73
Milk, kg/d	39.3	40.3	39.5	40.1	0.84	38.9	40.7	1.16	<0.01	0.07	0.26	0.33	0.87	0.21
Milk:DMI	1.59	1.60	1.59	1.60	0.026	1.61	1.58	0.035	0.11	0.14	0.44	0.17	0.43	0.88
ECM, kg/d	38.5	39.5	38.6	39.3	0.82	38.2	39.7	1.11	0.04	0.11	0.34	0.39	0.74	0.36
ECM:DMI	1.55	1.57	1.55	1.57	0.023	1.58	1.54	0.030	0.21	0.16	0.27	0.14	0.96	0.98
Fat, %	3.99	4.02	3.99	4.02	0.062	4.00	4.01	0.081	0.49	0.50	0.95	0.51	0.58	0.59
Fat, kg/d	1.56	1.61	1.56	1.61	0.039	1.55	1.63	0.052	0.06	0.05	0.32	0.34	0.94	0.44
True protein, %	3.04	3.06	3.05	3.05	0.033	3.08	3.03	0.044	0.51	0.80	0.43	0.99	0.57	0.50
True protein, kg/d	1.19	1.22	1.19	1.22	0.021	1.19	1.22	0.029	0.02	0.14	0.34	0.47	0.58	0.30
Lactose, %	4.88	4.87	4.91	4.84	0.032	4.93	4.83	0.039	0.71	0.03	0.06	0.76	0.89	0.91
Lactose, kg/d	1.92	1.95	1.93	1.94	0.043	1.90	1.96	0.059	0.13	0.72	0.47	0.62	0.50	0.39
SNF, %	8.81	8.81	8.85	8.77	0.056	8.90	8.72	0.066	1.00	0.18	0.06	0.85	0.88	0.61
SNF, kg/d	3.45	3.53	3.47	3.51	0.069	3.44	3.54	0.093	0.07	0.39	0.42	0.54	0.51	0.30
SCC, ×10 ³ cells/mL	277	384	274	388	73.7	336	325	84.4	0.22	0.19	0.93	0.83	0.90	0.72
MUN, mg/dL	11.5	10.3	9.3	12.5	0.17	10.7	11.2	0.22	<0.01	<0.01	0.11	0.63	0.56	0.40
Milk-N:N intake, %	30.0	30.8	32.1	28.8	0.38	31.1	29.8	0.51	<0.01	<0.01	0.07	0.32	0.78	0.80
Urinary excretion⁵														
Urine volume, L/d	27.7	26.3	24.8	29.2	0.75	26.1	27.9	0.91	0.07	<0.01	0.15	0.70	0.21	0.81
Urea-N, g/d	138	119	96	161	3.4	122	135	4.0	<0.01	<0.01	0.02	0.95	0.10	0.25
Total-N, g/d	229	206	180	254	4.4	208	226	5.6	<0.01	<0.01	0.02	0.67	0.47	0.67
Urea-N:total-N, %	60.4	56.7	52.7	64.4	1.07	58.0	59.1	1.11	0.01	<0.01	0.49	0.49	0.21	0.16

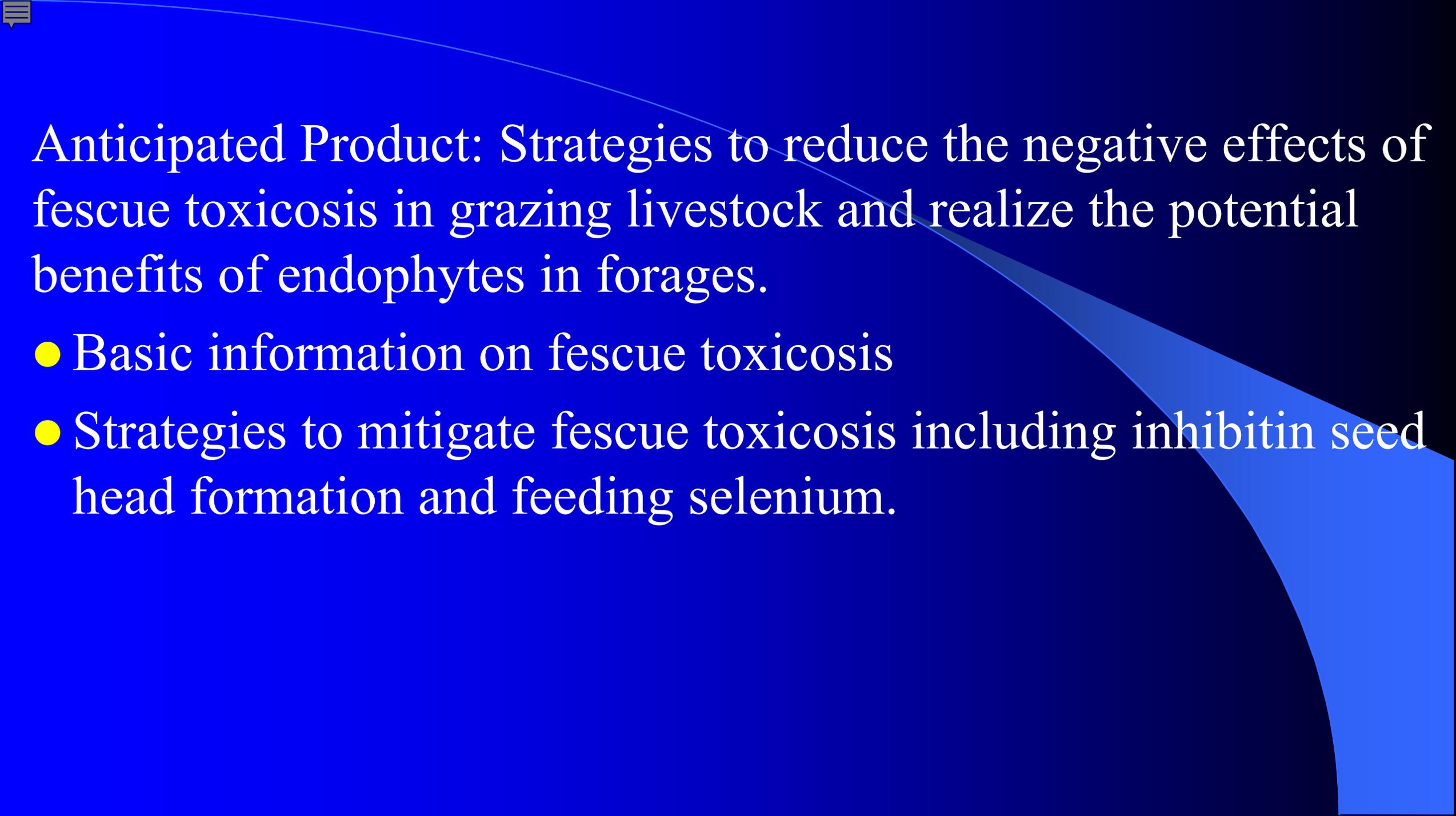
¹Sources of supplemental CP: CM = canola meal, SBM = solvent soybean meal; RPML = rumen-protected Met plus Lys.

²Standard error of the least squares means determined using statistical model 2; SEM for protein source and [CP] were identical.

³Minus (–) indicates no RPML supplement; plus (+) indicates supplementation with RPML.

⁴Probability of dietary treatment effects: Source = SBM versus CM; [CP] = 15% versus 17% CP; RPML = no RPML versus plus RPML; Source × [CP] = interaction of protein source and CP concentration; Source × RPML = interaction of protein source and RPML supplement; [CP] × RPML = interaction of CP concentration and RPML supplement.

⁵Estimated from urinary excretion of creatinine according to Valadares et al. (1999).

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Anticipated Product: Strategies to reduce the negative effects of fescue toxicosis in grazing livestock and realize the potential benefits of endophytes in forages.

- Basic information on fescue toxicosis
- Strategies to mitigate fescue toxicosis including inhibiting seed head formation and feeding selenium.

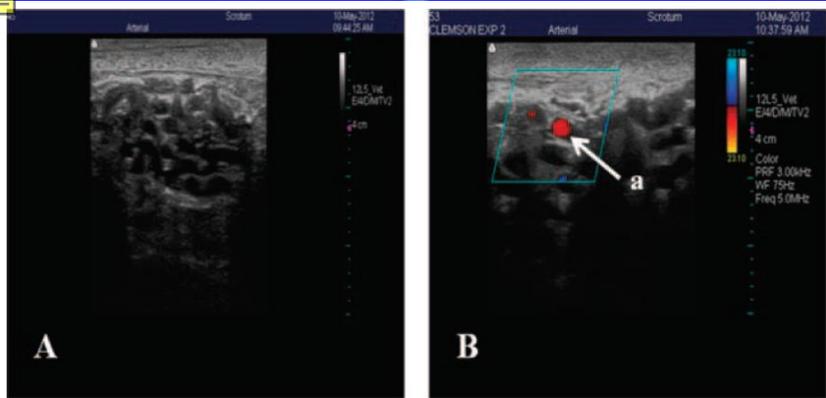


Figure 1. Cross-sectional B-mode (A) and color Doppler (B) ultrasound images of the intertwined testicular artery and pampiniform plexus (i.e., testicular vein). The arrow is pointing to a cross-section of a testicular artery (a) with color that delineates blood flow within the lumen.

Klotz et al., 2016; up to 7 weeks for vascular recovery from endophyte poisoning

Table 1. Inside and outside diameters of lateral saphenous veins biopsied on Days 0, 7, 14, and 28 for Experiment 1 and on Days 0, 21, 42, and 63 for Experiment 2.

Variable ¹	Days on Non-Toxic Diet				SEM	p-Value ²
Experiment 1	0	7	14	28	-	-
i.d., mm	0.69 ^{bc}	0.74 ^b	1.00 ^a	0.63 ^c	0.04	<0.01
o.d., mm	2.72	2.57	2.82	2.81	0.08	0.07
Experiment 2	0	21	42	63	-	-
i.d., mm	0.71 ^c	0.85 ^b	0.89 ^b	1.02 ^a	0.03	<0.01
o.d., mm	2.90	2.94	2.92	2.85	0.04	0.50

¹ i.d. = inside diameter and o.d. = outside diameter; ² Probability of a greater F-statistic for the effect of days off of pasture. Significant at $p < 0.05$; ^{abc} Means within a row not containing like superscripts are different ($p < 0.05$).

Aiken et al., 2015, endophyte infested fescue effects on testis artery

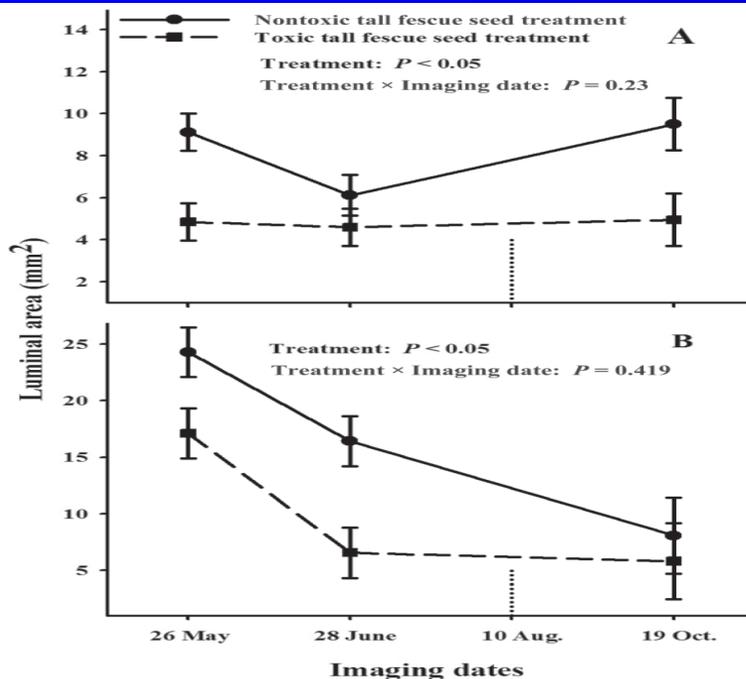
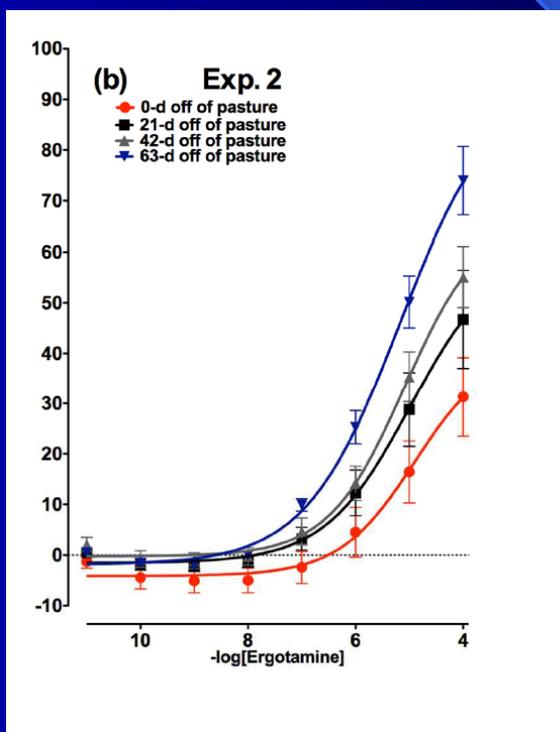


Figure 2. Mean \pm SE for luminal areas of the medial caudal (A) and testicular (B) arteries for 3 imaging dates in bulls fed toxic endophyte-infested (*Neotyphodium coenophialum*; $n = 6$) or endophyte-free tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh.] seed ($n = 7$). Probability values are provided below the regression lines for predicted differences among least squares means for pasture treatments. The dotted vertical line designates the date when bulls fed toxic endophyte-infested seed were switched to endophyte-free seed.



Comparison of novel endophyte fescue varieties with toxic endophyte varieties Review by Aiken and Strickland, 2013

Table 1. Differences in ADG and serum prolactin concentrations for different livestock classes between novel endophyte tall fescues and control treatments (toxic, endophyte, and endophyte-free tall fescues)¹

Livestock/class	Novel endophyte/ Tall fescue cultivar	Difference from control treatments				Reference
		ADG, kg		Serum prolactin, ng/mL		
		Toxic endophyte	Endophyte-free	Toxic endophyte	Endophyte-free	
Steers	AR542/Jesup	+0.35 ²	NS ³	+129	NS	Parish et al. (2003)
Postpartum cows	AR542/Jesup	+0.17 ²		+102		Watson et al. (2004)
Suckling calves	AR542/Jesup	+0.16 ²		+300		Watson et al. (2004)
Lambs	AR542/Jesup	+0.06 ²	NS	+292	NS	Parish et al. (2003)
Heifers	AR542/Jesup	+0.34 ²	NS			Franzluebbers and Stuedemann (2006)
Steers	Strain 4/HiMag	+0.26 ⁴	NS	+138	NS	Nihsen et al. (2004)
Steers	AR542-Georgia 5	+0.38 ⁴	NS	+6	NS	Hopkins and Alison (2006)
Steers	BarOptima PLUS E-34	+0.57 ⁴	NS	+126	NS	Beck et al. (2009)
Steers	AR584-KYFA9301	+0.18 ⁴	NS	+125	NS	Johnson et al. (2012)

¹Results are for those collected during spring and early summer grazing.

²Toxic control was toxic endophyte-infected Jesup tall fescue.

³No significant difference between novel endophyte-infested and endophyte-free tall fescues.

⁴Toxic control was toxic endophyte Kentucky 31 tall fescue.

Improved weight gain in cattle by suppressing seedheads Aiken et al., 2012

Table 4. Least square means for weight gain and physiological measures of steers' grazing mixtures of endophyte-infected tall fescue [*Lolium arundinaceum* (Schreb.) Darbysh] and Kentucky bluegrass (*Poa pratensis* L.) in 2009 and 2010 that were either treated with Chaparral herbicide to suppress seedhead emergence in tall fescue or left untreated.

Herbicide treatment	Average daily gain [†]	Rectal temperature	Serum prolactin [†]
	kg d ⁻¹	°C	Ng mL ⁻¹
2009			
Treated	0.91	40.5	58.3
Untreated	0.55	41.2	8.8
SEM	0.06	0.1	11.9
2010			
Treated	0.95	41.0	143
Untreated	0.79	41.3	86
SEM	0.06	0.1	11.9

[†]Year effect, $P < 0.05$; herbicide treatment effect, $P < 0.01$; year × herbicide treatment, $P > 0.10$.

Biochanin A (from red clover) effects on ergotamine induced contraction of mesenteric artery. Jia et al., 2015

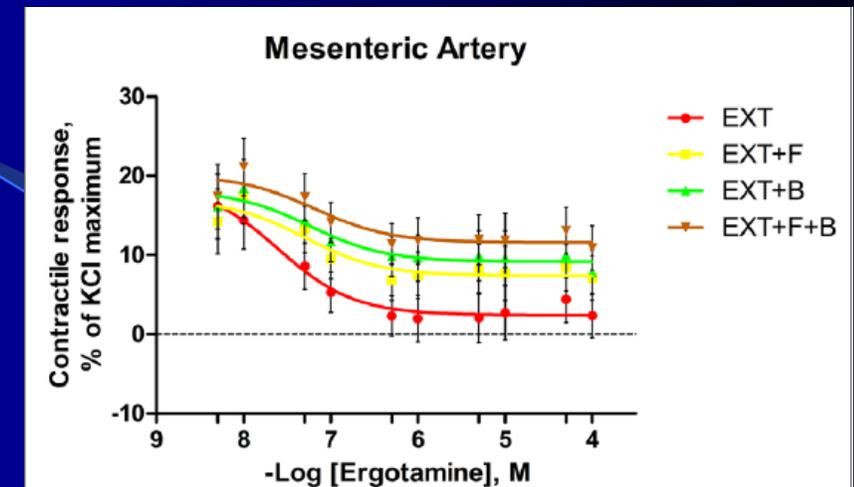


FIGURE 4 | Mean contractile response, as % KCl maximum of mesenteric artery to increasing concentrations of ergotamine for pretreatments with tall fescue seed extract: 1×10^{-6} M ergovaline-containing tall fescue seed extract (EXT); combinations of 1×10^{-6} M EXT and 1×10^{-6} M F (EXT + F); 1×10^{-6} M EXT and 1×10^{-6} M B (EXT + B); or 1×10^{-6} M EXT and 1×10^{-6} M F and 1×10^{-6} M B (EXT + F + B). The regression lines were plotted for each treatment using a non-linear regression with fixed slope, and the sigmoidal concentration response curves were calculated by the following equation: $y = \text{bottom} + \left[\frac{\text{top} - \text{bottom}}{1 + 10^{(\log EC_{50} - x)}} \right]$ where top and bottom are the plateaus of contractile response as percentage of 120 mM KCl maximum response. EC_{50} is the molar concentration of ergotamine inducing 50% of the KCl maximum response.



Anticipated Product: Strategies that alter metabolic pathways to improve growth performance and nutrient utilization efficiency in livestock.

- Zilpaterol studies in cattle

Zilpaterol effects on carcass composition in beef cattle. Boyd et al., 2015

Table 2. Main-effect means of zilpaterol hydrochloride (ZH) feeding and housing type on performance and carcass characteristics of finishing beef steers

Item	Open		Shade		P-value			SEM ³
	Control	ZH	Control	ZH	Diet ¹	Housing ²	Diet × housing	
Performance								
Initial BW, kg	360	362	358	359	0.37	0.24	0.72	3.1
Final BW, kg	645	649	635	640	0.43	0.08	0.90	7.6
DMI, kg/d	9.9	9.6	9.6	9.7	0.61	0.55	0.26	0.21
ADG, kg	1.58	1.58	1.52	1.55	0.56	0.10	0.68	0.034
G:F, kg/kg	0.160	0.164	0.159	0.160	0.44	0.39	0.53	0.0020
Carcass characteristic								
HCW, kg	410	425	406	418	<0.01	0.17	0.61	8.1
Dressing %	63.5	65.6	63.9	65.3	<0.01	0.78	0.29	0.30
LM area, cm ²	89.0	96.12	88.3	93.9	<0.01	0.27	0.59	0.20
12th Rib Fat, cm	1.64	1.59	1.63	1.52	0.15	0.39	0.54	0.020
Marbling score ⁴	473	470	478	466	0.50	0.92	0.67	10.0
USDA yield grade ⁵	3.6	3.2	3.5	3.2	<0.01	0.89	0.68	0.09
Nonperformance characteristics								
Respiration, breaths/min	92.9	99.7	91.8	101.9	0.05	0.88	0.69	5.82
Panting score ⁶	0.59	0.64	0.52	0.72	0.10	0.99	0.31	0.107

¹Main effect of ZH inclusion.

²Main effect of housing type.

³Pooled standard error of simple effects means; $n = 4$ pens/mean.

⁴300 = slight; 400 = small; 500 = modest.

⁵Calculated as $2.5 + (6.35 \times 12\text{th rib fat}) + (0.2 \times 2.5[\text{KPH}]) + (0.0017 \times \text{HCW}) - (2.06 \times \text{LM area})$ (USDA, 1997).

⁶Panting scores based on 0 to 4 scale with 0 = no panting and 4 = severe distress.

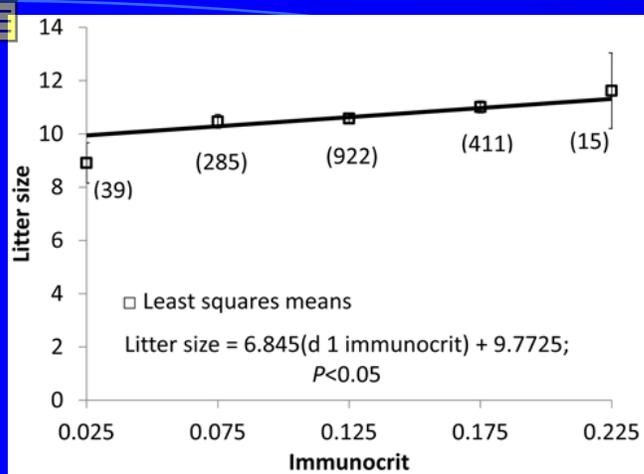
Problem Statement 1B: Improving Reproductive Efficiency

Anticipated product: Identification of critical control points limiting improvements in reproductive rate in food animals including physiological and management factors.

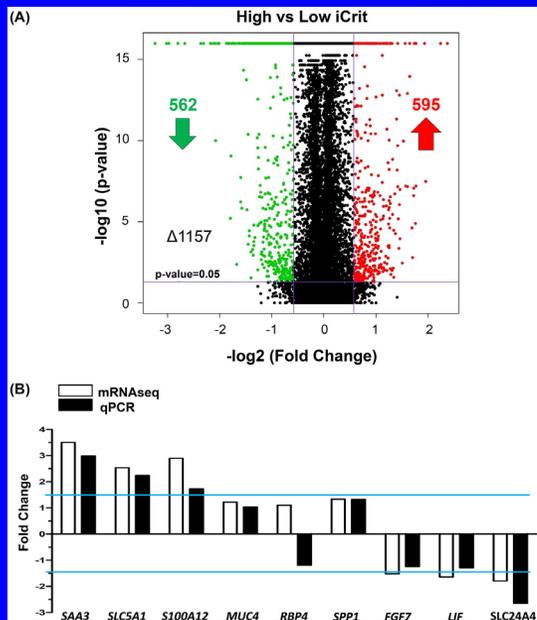
- Colostrum, glucosamine, feed restriction and sow posture in pigs
- Ovarian and uterine interactions in cattle
- Fertilized egg storage and fertility assessments in turkeys

Anticipated product: Strategies based on physiological data and biological markers for increasing longevity and lifetime productivity of breeding females in livestock systems.

- Metabolic factors and return to estrus in pigs
- Antral follicle counts and relations to fertility in cattle



Immunocrit effects on litter size Vallet et al., 2015



Immunocrit effects on endometrial gene expression George et al., 2015

Table 2 Treatment effects on placental morphometry from Experiment 1

Variable	Glucosamine ^a		Glucose	
	Large	Small	Large	Small
Fold Width, μm^b	778 \pm 37	818 \pm 37	716 \pm 36	731 \pm 36
Stromal Width, μm^c	236 \pm 28	142 \pm 28	140 \pm 27	146 \pm 27
Total Width, μm^b	1014 \pm 47	961 \pm 47	856 \pm 46	876 \pm 46
Interface length/unit placental length ^c	7470 \pm 403	7546 \pm 403	6969 \pm 389	6727 \pm 389

^aNumber of observations is 16 for glucosamine and 17 for glucose. Least squares means for bilayer fold width, stromal width above the folded bilayer, total placental width and placental bilayer interface length per unit placental length from Exp. 1 are presented

^bEffect of treatment ($P \leq 0.05$)

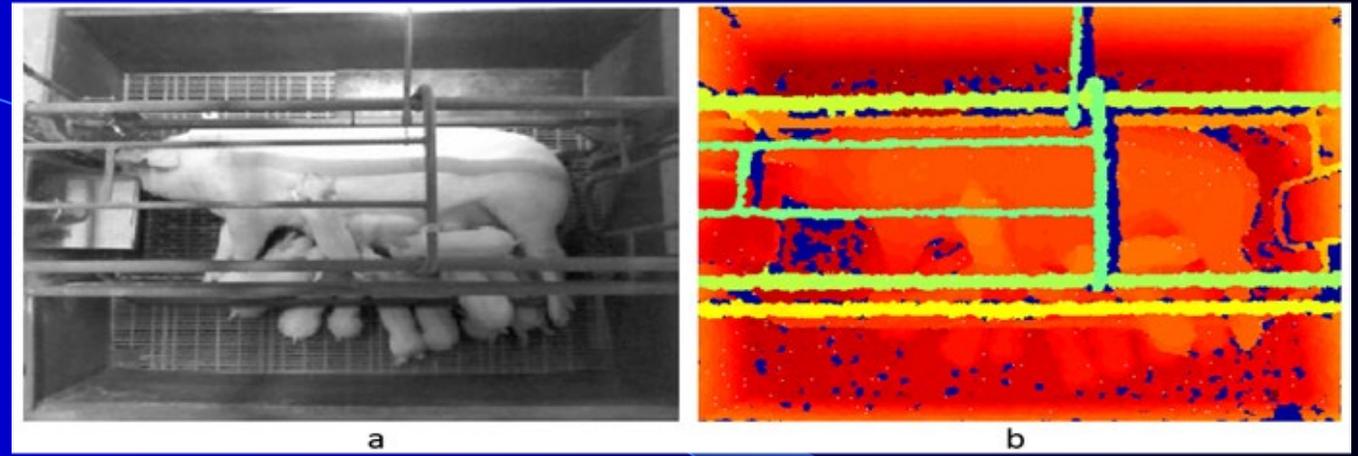
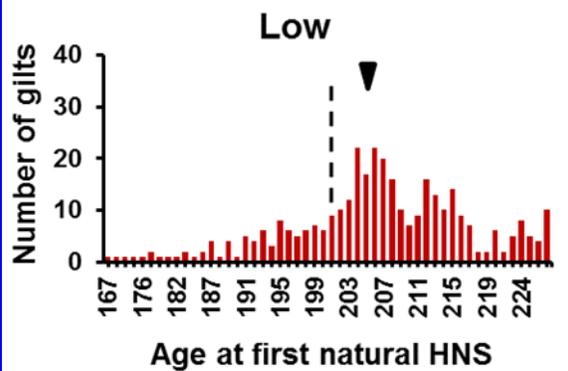
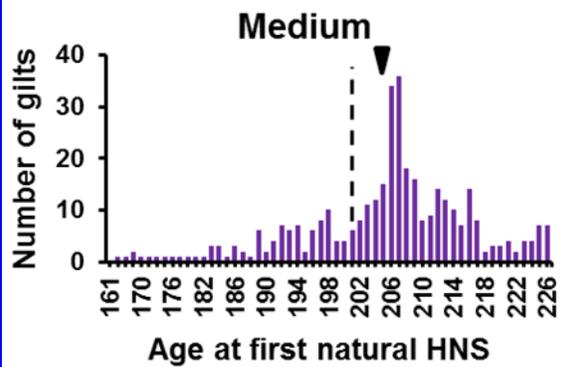
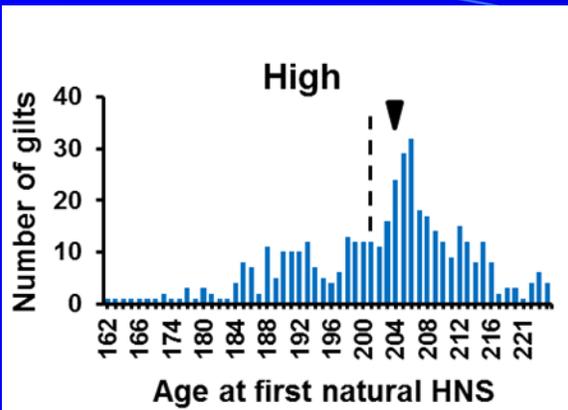
^cEffect of treatment by fetal size ($P = 0.07$)

Table 6 Treatment by parity effects on litter traits from experiment 3

Treatment	Total born ^a	Born alive ^a	Stillborns	Mummies	Birth weight	Weaning weight	Prewaning mortality
Glucosamine							
Parity 3	17.9 \pm 0.7	15.9 \pm 0.7	1.3 \pm 0.3	0.8 \pm 0.2	1.40 \pm 0.04	5.0 \pm 0.1	0.11 \pm 0.02
Parity 4	16.8 \pm 0.9	14.9 \pm 0.8	1.3 \pm 0.3	0.5 \pm 0.2	1.41 \pm 0.05	4.9 \pm 0.1	0.15 \pm 0.02
Parity 5	20.0 \pm 1.2	17.2 \pm 1.0	1.7 \pm 0.5	1.1 \pm 0.3	1.26 \pm 0.06	5.1 \pm 0.2	0.16 \pm 0.03
Parity 6	18.7 \pm 1.2	17.2 \pm 1.1	0.5 \pm 0.5	1.0 \pm 0.3	1.32 \pm 0.07	5.1 \pm 0.2	0.17 \pm 0.03
Parity 7	16.2 \pm 1.0	14.3 \pm 0.9	1.5 \pm 0.4	0.3 \pm 0.2	1.37 \pm 0.06	5.2 \pm 0.2	0.11 \pm 0.02
Glucose							
Parity 3	17.6 \pm 0.8	16.0 \pm 0.7	1.0 \pm 0.3	0.6 \pm 0.2	1.36 \pm 0.04	5.1 \pm 0.1	0.11 \pm 0.03
Parity 4	17.9 \pm 0.9	15.8 \pm 0.8	1.5 \pm 0.4	0.6 \pm 0.2	1.41 \pm 0.05	4.8 \pm 0.2	0.18 \pm 0.03
Parity 5	15.8 \pm 1.1	14.7 \pm 1.0	0.9 \pm 0.4	0.2 \pm 0.3	1.42 \pm 0.06	4.8 \pm 0.2	0.12 \pm 0.03
Parity 6	15.1 \pm 1.1	12.1 \pm 1.0	2.4 \pm 0.4	0.6 \pm 0.3	1.30 \pm 0.06	5.0 \pm 0.2	0.24 \pm 0.04
Parity 7	15.8 \pm 1.1	14.3 \pm 0.9	1.1 \pm 0.4	0.5 \pm 0.3	1.41 \pm 0.06	4.8 \pm 0.2	0.08 \pm 0.02

^aA treatment by parity interaction was present. Orthogonal contrasts indicated that total born and born alive were greater in later parities (5 and 6) in glucosamine treated sows compared to glucose treated sows, but were not different in early parities or in parity 7. Litter size trait, birth and weaning weight least squares means for glucosamine- and glucose-supplemented sows for each parity from Exp. 3 are presented

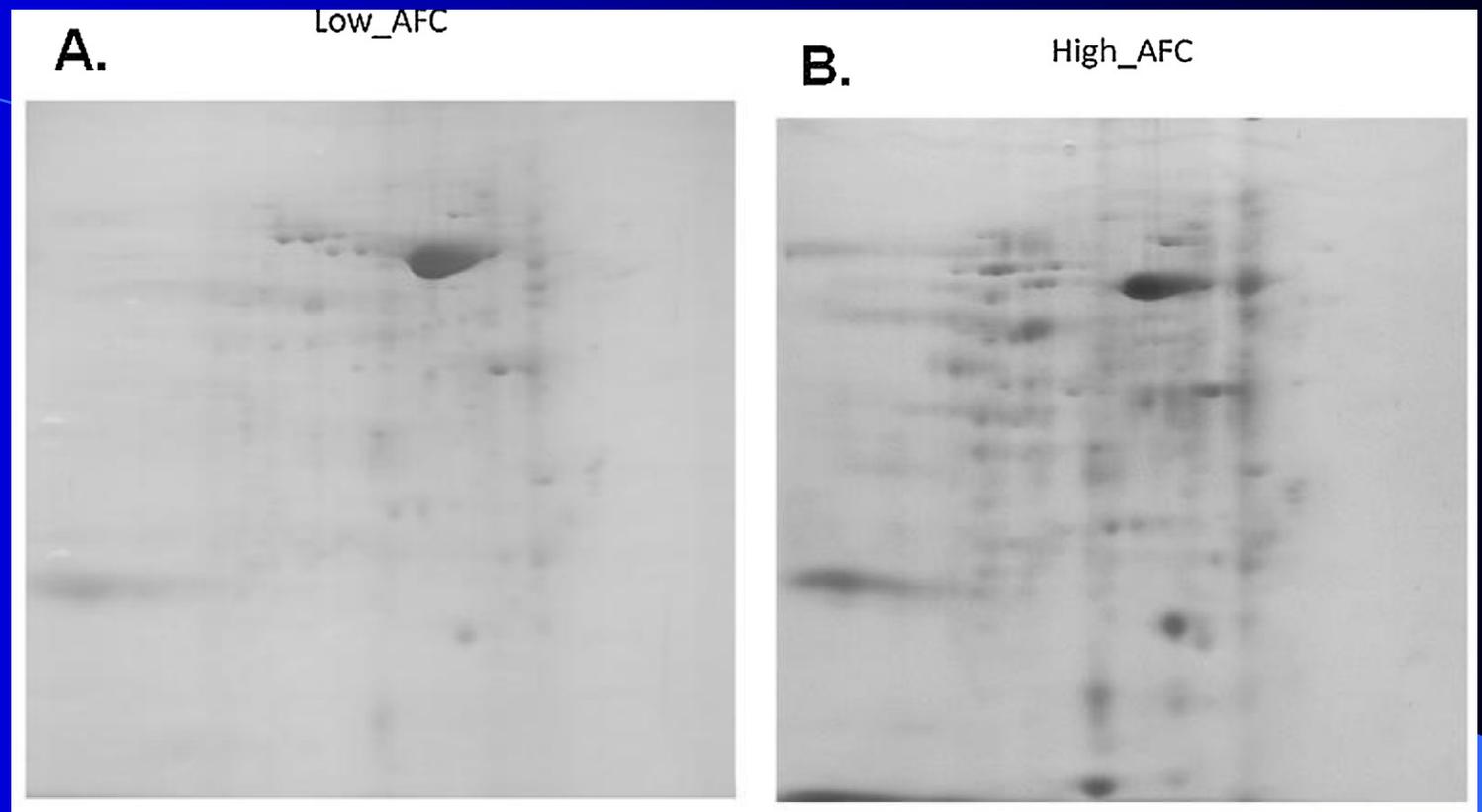
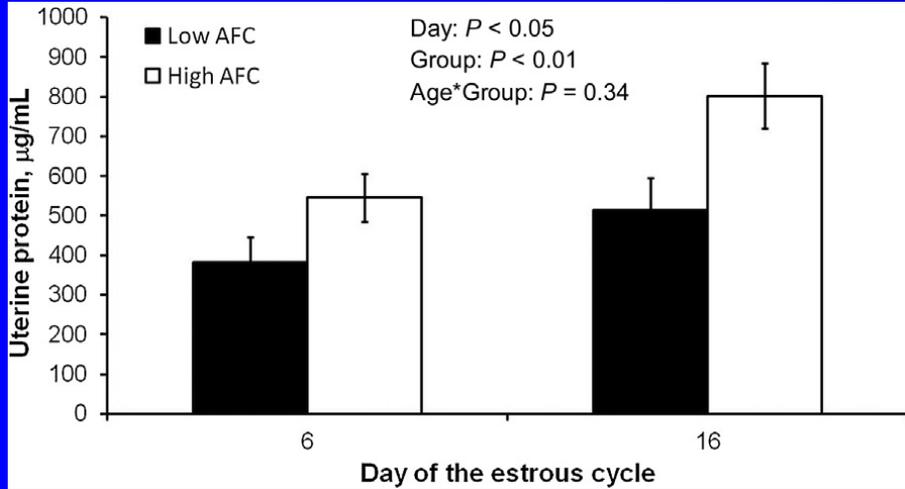
Glucosamine effects on placental development and litter size Vallet et al., 2017



Reduction in dietary protein reduces the rate of puberty attainment

Posture	Total #	Accuracy
Lying	36,384	99.9%
Standing	5,141	99.2%
Sitting	1,818	96.4%
Kneeling	37	78.1%

Brown-Brandl unpublished



Lower Antral follicles associated with less uterine protein
McNeel et al., 2017

Turkey egg storage for longer than 6 days reduces development and embryo weights when incubation is resumed Bakst et al., 2016 (correlates with increased mortality)

Table 1. Stages of embryos from eggs stored for varying time periods and incubated for 8 d.

Storage d ¹ (n)	Stage (Hamburger and Hamilton, 1951)						mean
	25	26	27	28	29	30	
<5 ^a (40)	0	2	1	15	15	7	28.6
6 to 10 ^b (41)	0	5	11	20	4	1	27.7
11 to 15 ^c (31)	1	7	17	4	2	0	27.0
16 to 20 ^c (31)	2	9	13	7	0	0	26.9
21 to 27 ^c (43)	5	12	19	7	0	0	26.6

¹Storage treatment intervals with different letters (a, b, c) are different at the 0.05 significance level.

Table 2. Weight (mg) means and means comparisons of embryos from eggs stored for varying time periods and incubated for 8 d.

Storage d	Mean ¹ (n)
< 5	504.6 ^a (40)
6 to 10	437.5 ^b (41)
11 to 15	406.0 ^b (31)
16 to 20	372.9 ^{b,c} (31)
21 to 27	336.8 ^c (42)

¹Weight means with different letters (a, b, c) are different at the 0.05 significance level.

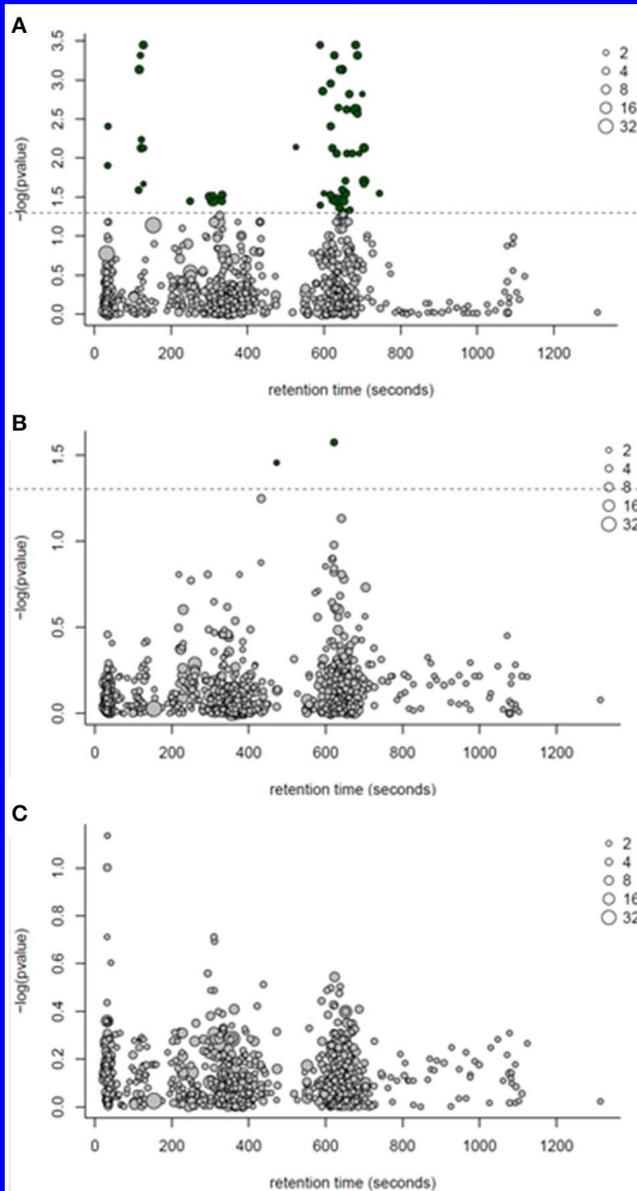


TABLE 5 | Log₂ fold-change (FC) differences between post-farrow and weaning following ANOVA analyses ($P \leq 0.05$), among detected compounds or features by LC-MS.

Annotated compound	FC	p-value	Score ^a	RT (s)	Mass
Caprolactam	-3.65	0.0257	1	115.0588	113.084
Phenylacetylglucine	-1.74	0.0058	2	122.3187	193.074
1,2-dioleoyl-sn-glycero-3-phosphoethanolamine	-1.54	0.0011	1	616.9482	743.547
PC(36:2).2	-1.29	0.0007	2	647.313	772.5867
Hippuric acid	-1.28	0.0007	1	116.7797	179.058
lysoPC(18:2).2	-1.13	0.0311	2	300.192	520.3399
lysoPC(18:2)	-0.95	0.0347	2	309.5405	520.3402
C16-20:3 PC	-0.73	0.0024	1	659.0428	769.599
PC(36:3).3	-0.73	0.0255	2	648.0042	784.5853
PC(36:3)	-0.64	0.0007	2	641.6088	784.5871
Betaine	-0.64	0.0125	1	34.17233	117.079
PC(32:2)	-0.60	0.0345	2	622.7085	732.5558
1,2-dilinolenoyl-sn-glycero-3-phosphocholine	-0.56	0.0343	1	632.0548	777.531
PC(O-34:3)	-0.53	0.0356	2	650.9358	742.5767
SM(24:1)	0.82	0.0197	3	704.4908	813.6867
PC(40:4)	1.01	0.0024	2	682.2406	838.6347

FC, log₂ fold-change; PF, post-farrow; WN, weaning; ANOVA, analysis of variance; LC-MS, liquid chromatography-mass spectrometry; m/z, mass value of compound or base peak; PC, phosphatidylcholine; SM, sphingomyelin.

^aAnnotation confidence score (scale of 1–4) based on guidelines provided by the Metabolomics Standards Initiative (Sumner et al., 2007).

TABLE 6 | Log₂ fold-change (FC) differences between maximal (Hi) and minimal (Lo) body condition loss following ANOVA analyses ($P \leq 0.05$), among detected features by LC-MS.

Compound identifier ^a	FC (Hi vs. Lo)	p-value (Hi vs. Lo)	Score ^b	RT (s)	Mass
C345	-0.77	0.0267	4	621.778	599.5044
C487	1.35	0.0350	4	472.369	203.0535

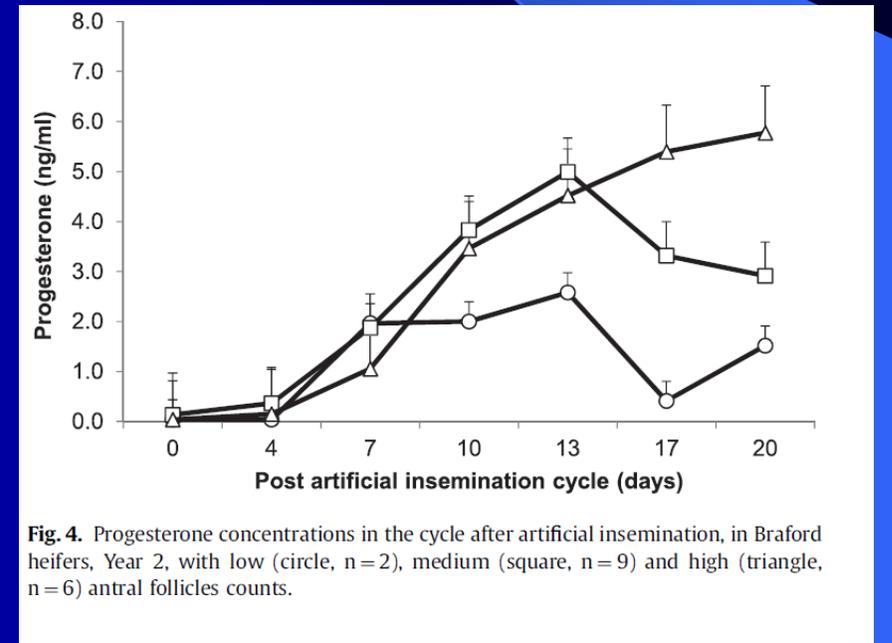
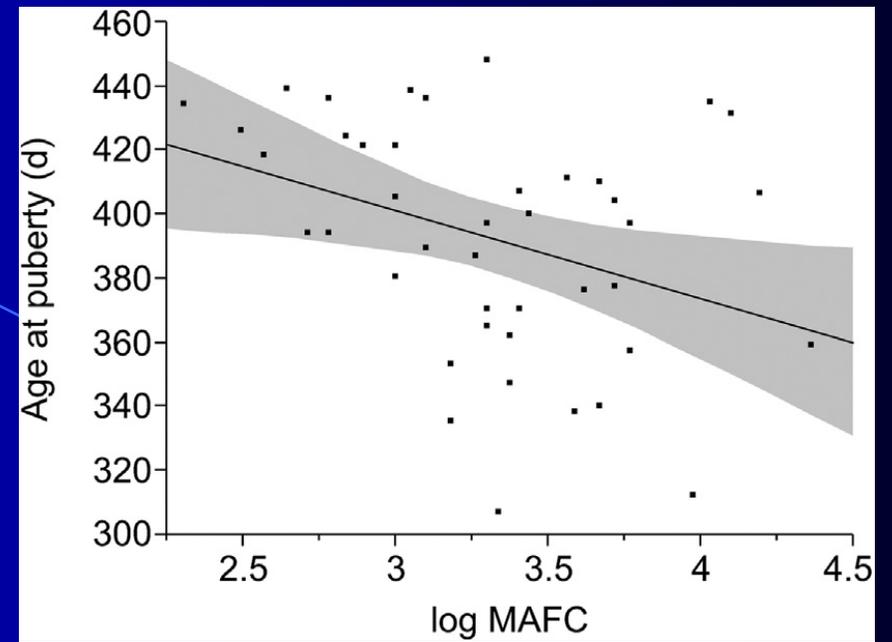
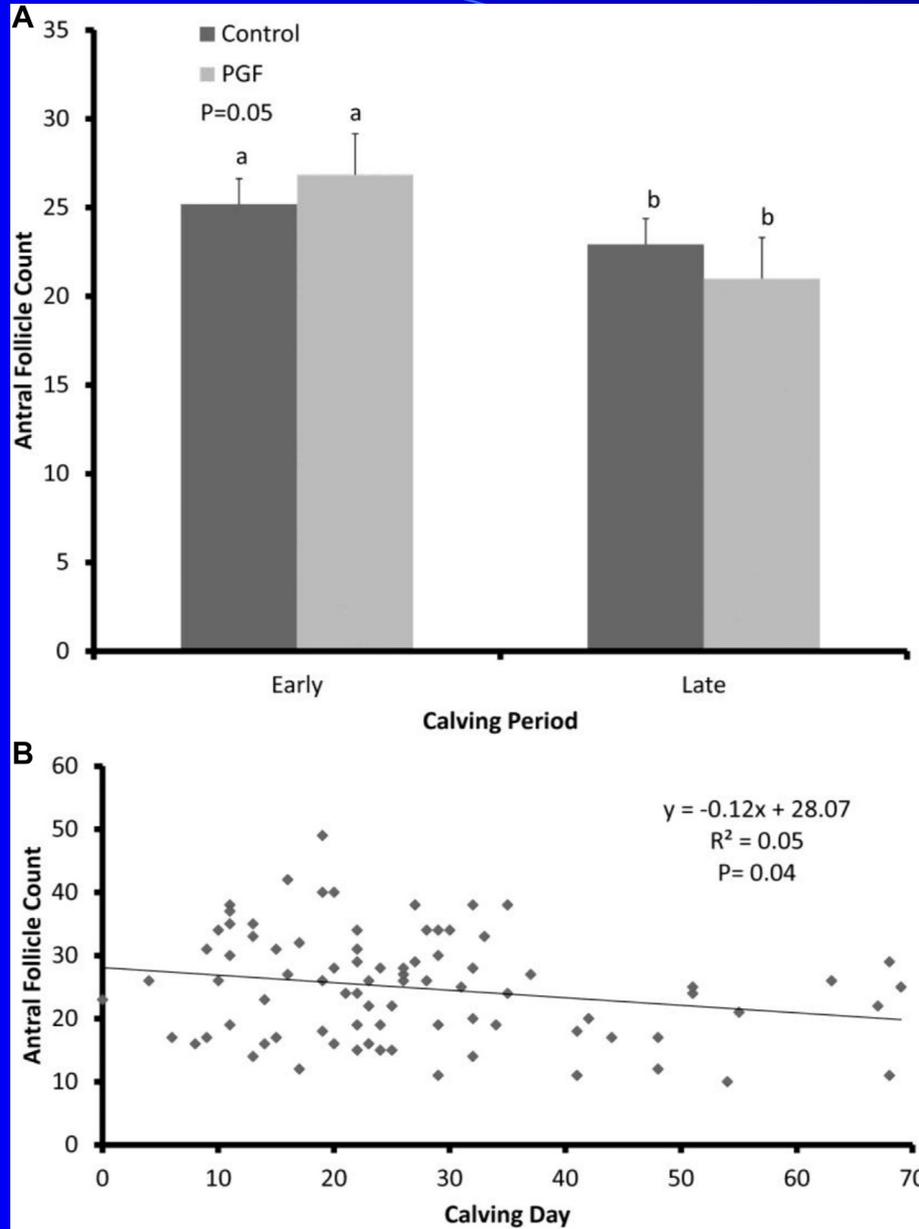
FC, log₂ fold-change; PF, post-farrow; WN, weaning; ANOVA, analysis of variance; LC-MS, liquid chromatography-mass spectrometry.

^aUnidentified feature denoted as C###.

^bAnnotation confidence score (scale of 1–4) based on guidelines provided by the Metabolomics Standards Initiative (Sumner et al., 2007).

Metabolic screening of sows indicated many differences in weaned versus post-farrowed sows, but only two unidentified metabolites between high and low weight loss sows. Rempel et al., 2016

High antral follicle counts are associated with improved fertility





Anticipated product: Strategies that optimize male and female contributions to reproductive efficiency.

- GNRHR2 and varicocele in boar fertility
- Bull contributions to calving
- Possible additions to semen extenders in turkeys

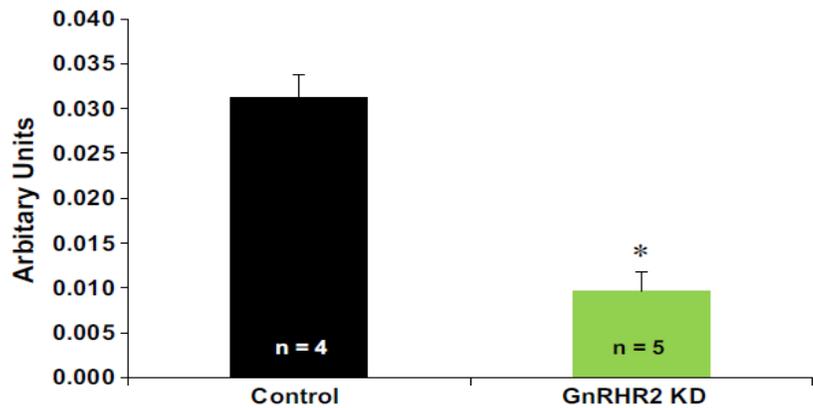
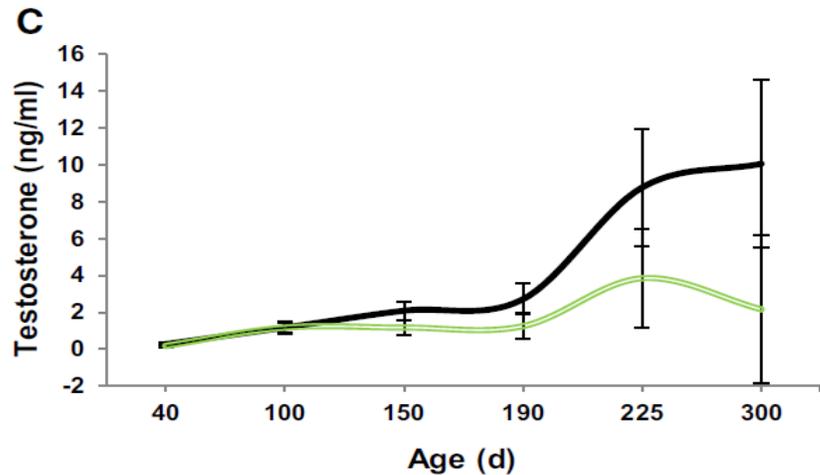


Fig. 3 Relative *GNRHR2* mRNA levels are significantly reduced within the testes of *GNRHR2* KD versus littermate control boars. Digital Droplet PCR revealed a 69% reduction in *GNRHR2* mRNA levels (normalized to *ACTB* mRNA levels) in the testes of transgenic (n = 5) compared to littermate control (n = 4) boars. Data are presented as the LSMEANS ± SEM. **P* < 0.001



From Desaulniers et al., 2017; GnRH2 receptor knockdown reduces testosterone in boars

Varicocele in boars, Gruhot et al., 2018; In humans, varicocele is associated with reduced fertility. Heritability is about 0.25

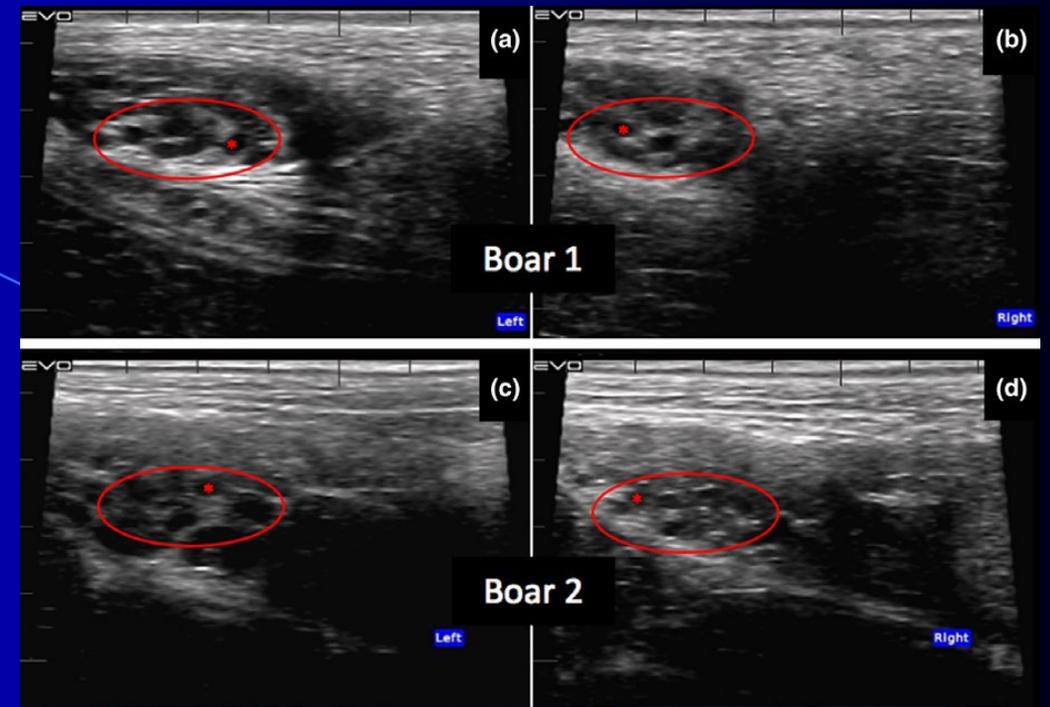
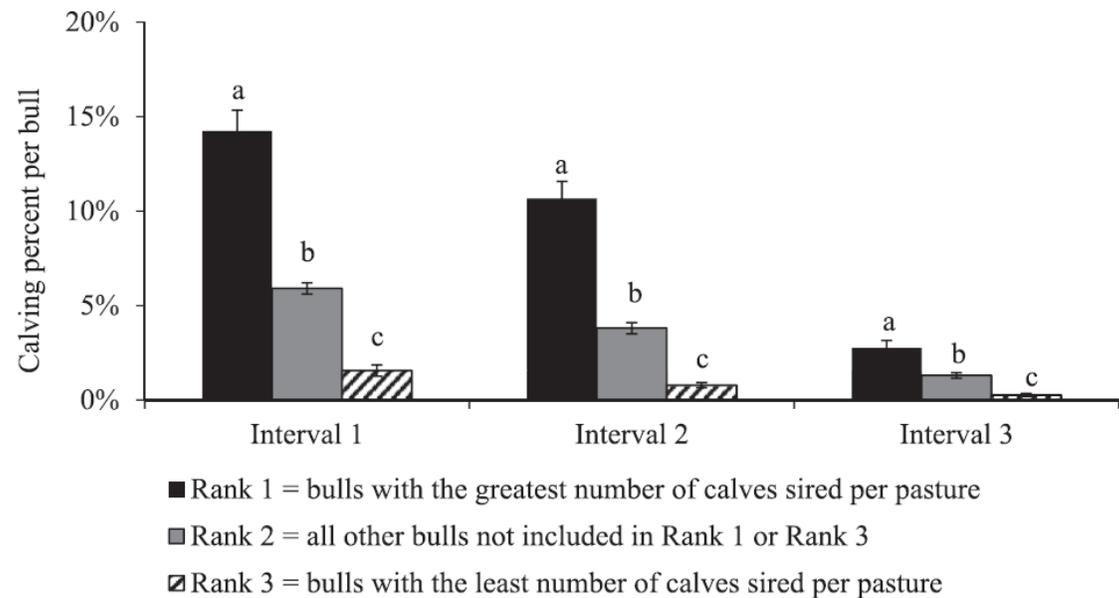


TABLE 2 Percentage of boars determined to be suspect varicocele using two methods of varicocele diagnosis

Method	Percentage
L/R ^a	18.89
R/L ^b	4.28
L/Lpop ^c	9.66
R/Rpop ^d	9.92
Method 1 ^e	23.17
Method 2 ^f	15.1
Method 2: bilateral ^g	4.4
Method 1 & 2 overlap ^h	4.7

Bulls in multisire pastures differ in their fertility, and rankings appear to be consistent over time, although the difference decreases as the breeding season advances; Abell et al., 2017.



Interval 1 = days 0 to 21

Interval 2 = days 22 to 43

Interval 3 = greater than 43 days

Table 2

Rank by year for individual bull counts. Breeding years correspond to the number of years a bull was used in a breeding season.

Rank change	Number of breeding years						Total
	1	2	3	4	5	6	
No change	47	92	5	15	0	1	160
1-2	0	0	1	3	0	0	4
1-3	0	0	0	1	0	0	1
2-1	0	0	4	2	0	0	6
2-3	0	1	2	2	0	0	5
3-2	0	0	2	3	0	0	5
Total	47	93	14	26	0	1	181

Table 2. Lectin labeling^a in chicken UVJ and SST grouped by preferred oligosaccharide moiety.

Preferred sugar lectin ^b	UVJ			SST			
	Apical surface	Cytoplasm	Basement membrane	Basement membrane	Cytoplasm	Lateral membranes	Apical surface
<u>Fucose</u>							
LTL	+	-	+/-	+/-	-	-	-
<u>Galactose / N-acetylgalactosamine</u>							
ECL	-	-, +/-	+/-, +	+/-	-, ++	-, +	+/-, ++
PNA	+/-	+/-	+/-	+/-, +	+	+/-, +	-, +/-
RCA-II	+/-	++	+	+	+/-	+/-, +	+/-
SBA	+	++	+/-	+/-	+	+/-	+/-, ++
WBA-I	+	-	+/-	+/-	-	-	-
WFL	-	-	-	+/-, ++	++	+/-, ++	++
<u>Mannose</u>							
Con-A	+/-	+/-, +	-	-, +/-	+/-, +	+	-, +/-
<u>N-acetylglucosamine</u>							
GSL-II	+/-	+/-	-, +/-	-, +/-	++	-	+/-
WGA	++	+	-, +/-	+/-, ++	+	-, +/-	++
<u>N-acetylneuraminic acid</u>							
SNA	+/-	+/-	+	-, +/-	+/-, +	-/+	-

^aLectin labeling intensity was visually scored as negative (-) with no fluorescence, (+/-) with inconsistent fluorescence with the same cell type, positive (+) when fluorescence was consistently discernible, and (++) with intense, consistent fluorescence.

^bSee Table 1 for full lectin names.

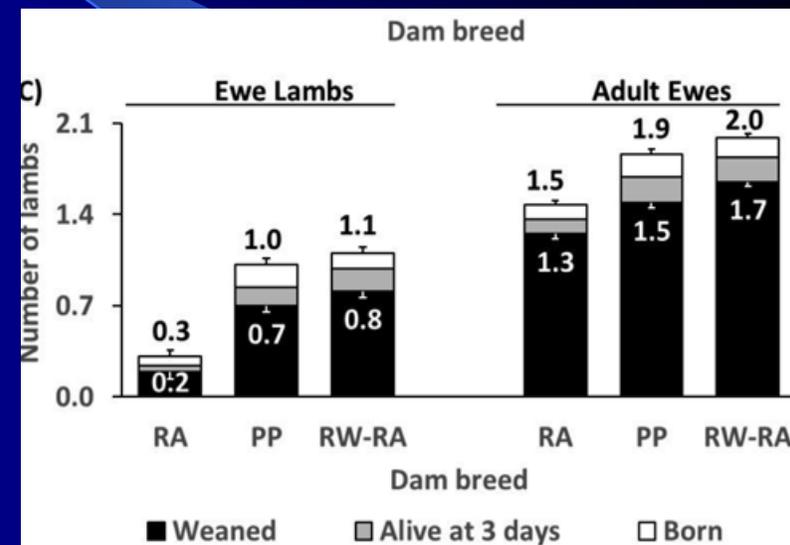
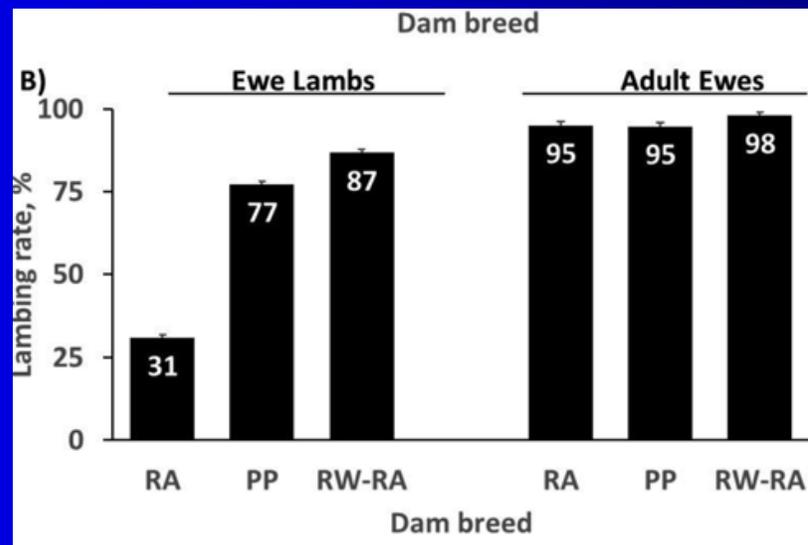
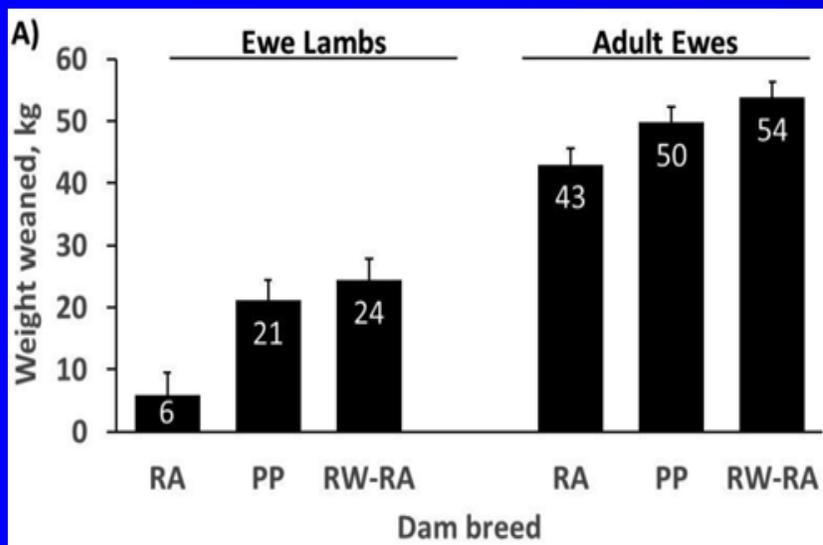
Differential lectin binding suggests that sugar moieties on the sperm storage tubules may contribute to the storage and continued fertility of sperm, Bakst and Bauchan, 2017



Anticipated product: Data to facilitate appropriate matching of management and production resources with genetic potential of breeding animals with the goal of increasing reproductive rate.

- Matching sheep breeds and composites to range conditions in the west

Crosses with greater fecundity are more profitable in rangeland conditions, Romanov-White Dorper crosses developed at USMARC, tested at USSES; Notter et al., 2017



Problem Statement 1C: Enhancing Animal Well-Being and Reducing Stress

Anticipated product: Development of specific management strategies (e.g., time of animal processing and vaccination, use of non-antibiotic supplements, etc.) targeted at reducing animal stress and improving immunity.

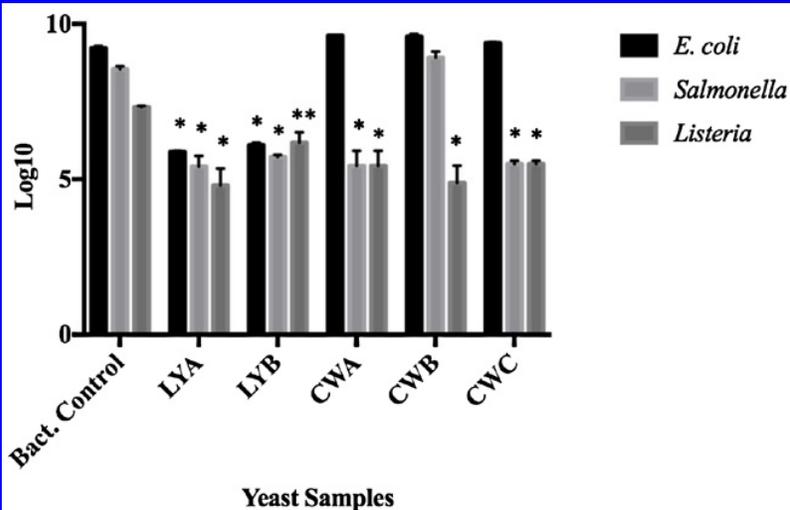
- Yeast and yeast product supplementation
- Pre and probiotics (glutamine, lactobacillus)

Anticipated product: Enhanced understanding of genetic, physiological, immunological, microbial and behavioral responses of food animals to management and environmental stressors.

- Heat stress
- BRD

Table 2. Scanning electron microscopy averages for adherence of pathogenic bacteria to yeast probiotics LYA and LYB and paraprobiotics CWA, CWB and CWC

Bacteria	LYA % Adhere	LYB % Adhere	CWA % Adhere	CWB % Adhere	CWC % Adhere
<i>A. pyogenes</i>	39.05	17.11	0.00	0.00	0.00
<i>B. fragilis</i>	55.32	13.51	37.50	15.22	4.55
<i>C. difficile</i>	17.24	20.97	0.00	5.00	0.00
<i>C. perfringens</i>	35.61	37.32	41.23	30.09	75.00
<i>E. coli</i> O157:H7	10.76	9.93	15.04	1.49	12.04
<i>F. necrophorum</i>	13.51	55.32	37.50	15.22	4.55
<i>L. monocytogenes</i>	8.69	6.25	1.96	9.37	5.88
<i>P. assacharolytica</i>	85.63	31.79	0.00	0.00	0.00
<i>S. Dublin</i>	34.00	9.09	12.00	0.00	6.00
<i>S. Enteritidis</i>	49.09	55.22	16.67	0.00	11.90
<i>S. Heidelberg</i>	29.30	30.43	24.99	46.43	22.22
<i>S. Typhi</i>	65.08	58.83	21.53	59.32	50.00
<i>S. Typhimurium</i>	92.31	96.67	88.89	85.71	98.11
Average	41.20%	34.03%	22.87%	20.60%	22.33%



Posadas et al., 2017

Table 7. Source 1 heifer performance following an immune challenge¹

Item	Control	YCW A, 2.5 g/(heifer·d)	YCW C, 2.5 g/(heifer·d)	SED	P-value, Trt
ADG, kg	1.72 ^a	1.73 ^a	2.25 ^b	0.075	<0.01
DMI, kg	8.82	8.88	9.22	0.273	0.10
G:F	0.196 ^a	0.196 ^a	0.244 ^b	0.0093	0.01

^{a,b}Means in a row without a common superscript differ ($P < 0.05$).

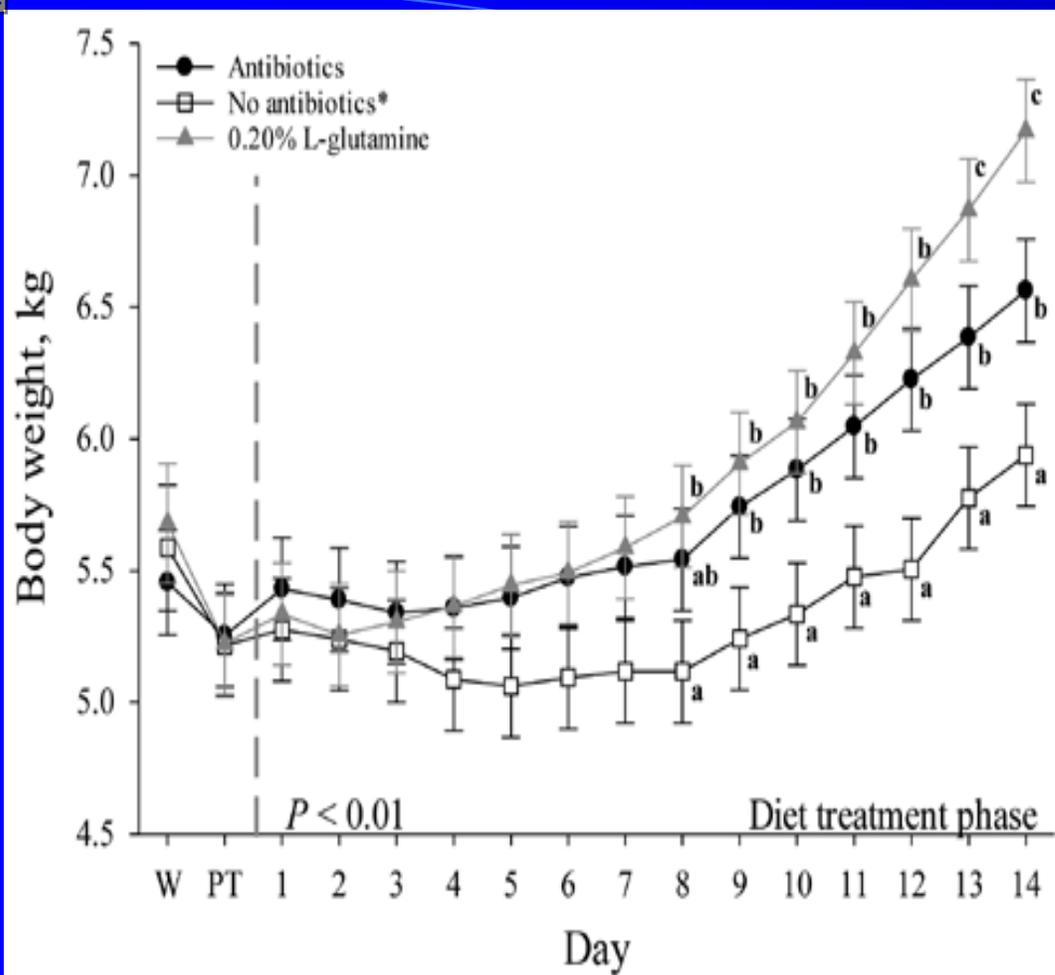
¹YCW = yeast cell wall; SED = SE of the difference between the treatment means; Trt = treatment.

Table 8. Source 2 heifer performance following an immune challenge¹

Item	Control	YCW A, 2.5 g/(heifer·d)	YCW C, 2.5 g/(heifer·d)	SED	P-value, Trt
ADG, kg	1.44	1.59	1.63	0.224	0.82
DMI, kg	7.25	8.02	7.60	0.536	0.62
G:F	0.198	0.199	0.215	0.0243	0.86

¹YCW = yeast cell wall; SED = SE of the difference between the treatment means; Trt = treatment.

Young et al, 2017, Variability in effects on growth under challenge conditions depending on source of material



Johnson and Lay, 2017. Glutamine increases weight gain in pigs treated with simulated transport stress

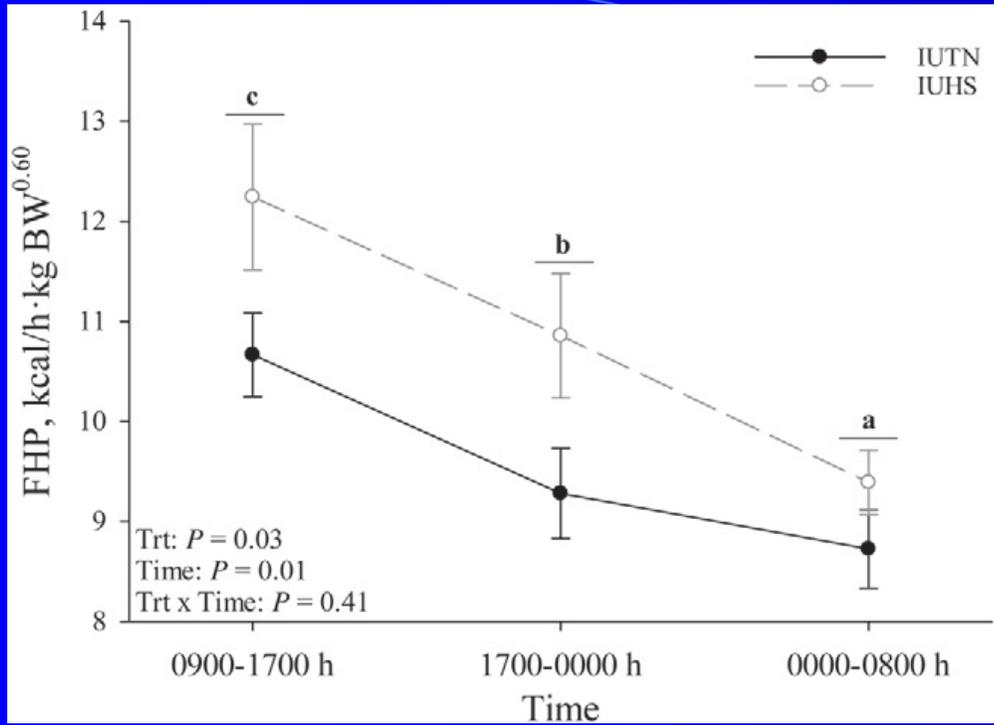
Lactobacillus fermentation products increase weight gain in piglets. Sanchez et al., 2019

Table 2 Performance parameters measured in pigs fed a control (Control) diet or supplemented with *Lactobacillus acidophilus* fermentation product (SynGenX) at 1 (SGX1) or 2 kg/metric ton (SGX2) for 18 days, with administration of an i.v. lipopolysaccharide challenge (25 µg/kg BW) on day 15

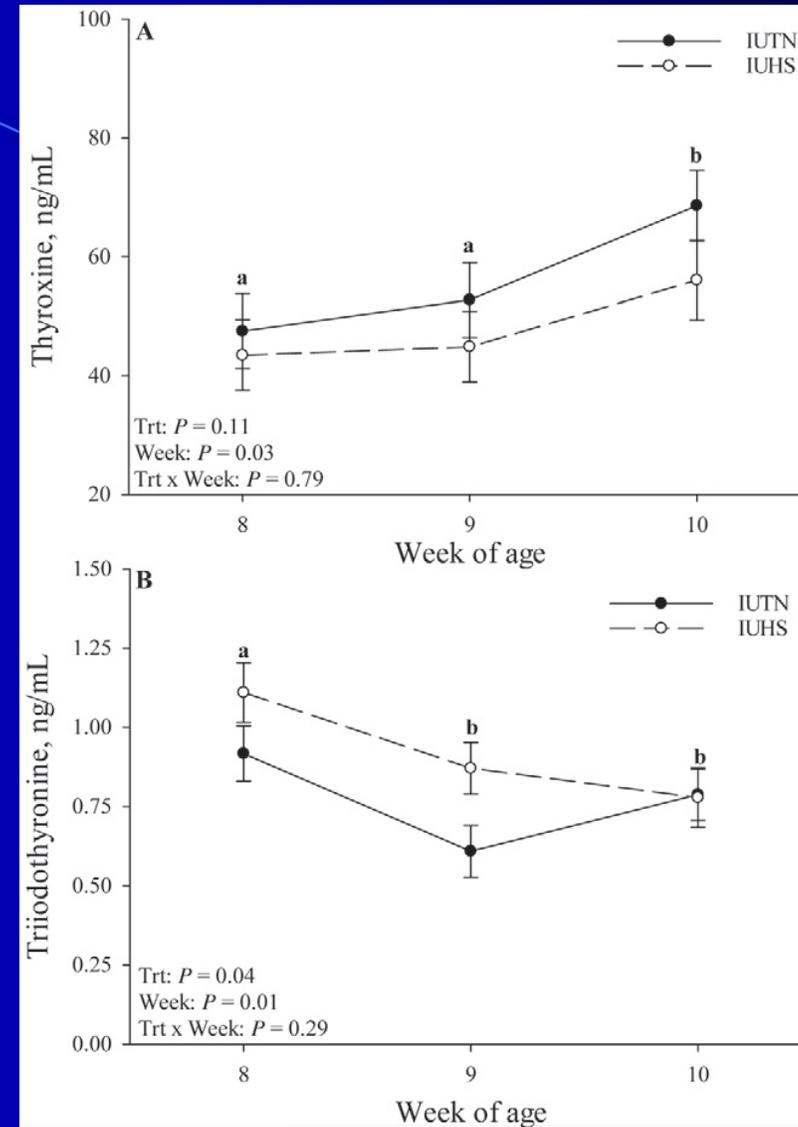
Variables	TRT	Day of study				SEM	P-value		
		0	7	14	18		TRT	Time	Interaction
Weight (kg)	Control	6.34	6.86 ^{ab}	8.66 ^b	9.58	0.31	0.08	<0.001	<0.001
	SGX1	6.72	7.46 ^a	10.05 ^a	10.28	0.31			
	SGX2	6.16	6.49 ^b	8.95 ^b	9.66	0.28			
ADG (kg/day)	Control		0.07	0.26 ^b	0.23 ^a	0.03	0.81	<0.001	<0.001
	SGX1		0.11	0.37 ^a	0.06 ^b	0.03			
	SGX2		0.05	0.35 ^a	0.18 ^a	0.02			
Feed disappearance (kg)	Control		0.84	2.08 ^b	1.45	0.15	0.41	<0.001	<0.001
	SGX1		0.98	2.80 ^a	1.23	0.16			
	SGX2		0.68	2.41 ^b	1.63	0.13			
G : F (kg)	Control		0.47	0.87	0.65 ^a	0.11	0.53	<0.001	0.03
	SGX1		0.73	0.94	0.16 ^b	0.13			
	SGX2		0.64	1.04	0.43 ^{ab}	0.10			

TRT = treatment; Interaction = treatment × time; ADG = average daily gain; G : F = gain to feed.

^{ab}Treatments with different superscripts within columns differ ($P \leq 0.05$).



From Chapel et al., 2017. Fasting heat production and triiodothyronine are increased after gestation during heat stress. Suggests an increase in heat production that could reduce the use of nutrients for growth etc.



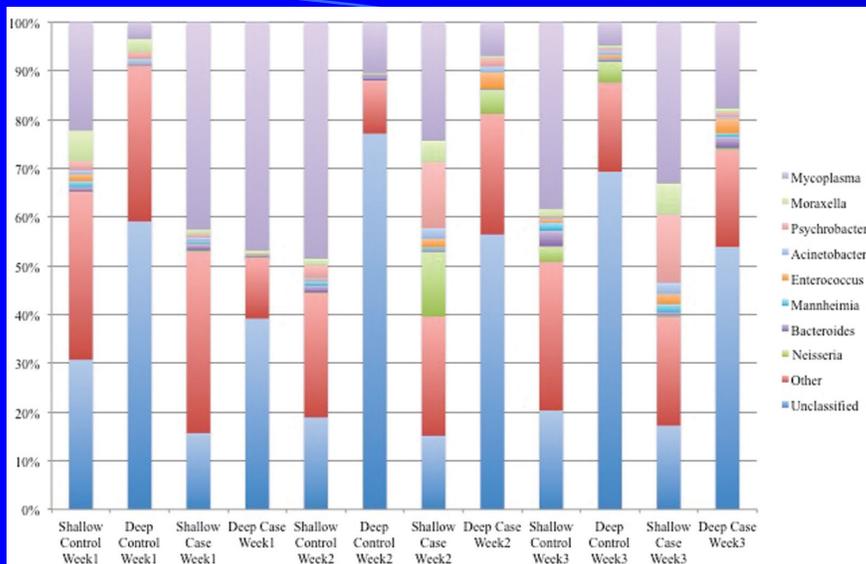


Table 2 Averages (SD) for the complete blood count for crossbred beef calves for diagnosed with BRD and for asymptomatic, healthy controls at each time point

Parameter	Asymptomatic control animals (n = 71)			Animals with BRD (n = 16)		
	Time 1 average (SD) ^a	Time 2	Time 3	Time 1	Time 2	Time 3
WBC	11.3 (0.29)	11.2 (0.32)	10.2 (0.29)	11.5 (0.59)	11.4 (0.65)	11.5 (0.58)
NEU	3.7 (0.14)	3.6 (0.17)	2.8 (0.17)	3.4 (0.29)	3.7 (0.35)	4.9 (0.35)
LYM	6.8 (0.21)	6.8 (0.25)	6.7 (0.21)	7.2 (0.42)	7 (0.5)	5.9 (0.43)
MONO	0.57 (0.02)	0.61 (0.022)	0.42 (0.019)	0.57 (0.04)	0.47 (0.044)	0.46 (0.038)
EOS	0.19 (0.013)	0.16 (0.007)	0.18 (0.018)	0.16 (0.027)	0.14 (0.015)	0.14 (0.036)
BAS	0.08 (0.005)	0.1 (0.004)	0.1 (0.005)	0.09 (0.01)	0.09 (0.009)	0.07 (0.011)
NEU%	32.1 (0.87)	32.1 (1.13)	27.4 (1.11)	30.2 (1.78)	31.5 (2.3)	40.8 (2.26)
LYM%	60.4 (0.88)	60.1 (1.17)	65.6 (1.1)	62.7 (1.78)	62.2 (0.38)	53 (2.23)
MONO%	5.1 (0.16)	5.5 (0.18)	4.2 (0.2)	4.9 (0.32)	4.2 (0.36)	4.3 (0.4)
EOS%	1.7 (0.11)	1.4 (0.06)	1.8 (0.16)	1.4 (0.23)	1.3 (0.12)	1.3 (0.33)
BAS%	0.73 (0.04)	0.87 (0.04)	0.99 (0.049)	0.79 (0.081)	0.77 (0.081)	0.64 (0.101)

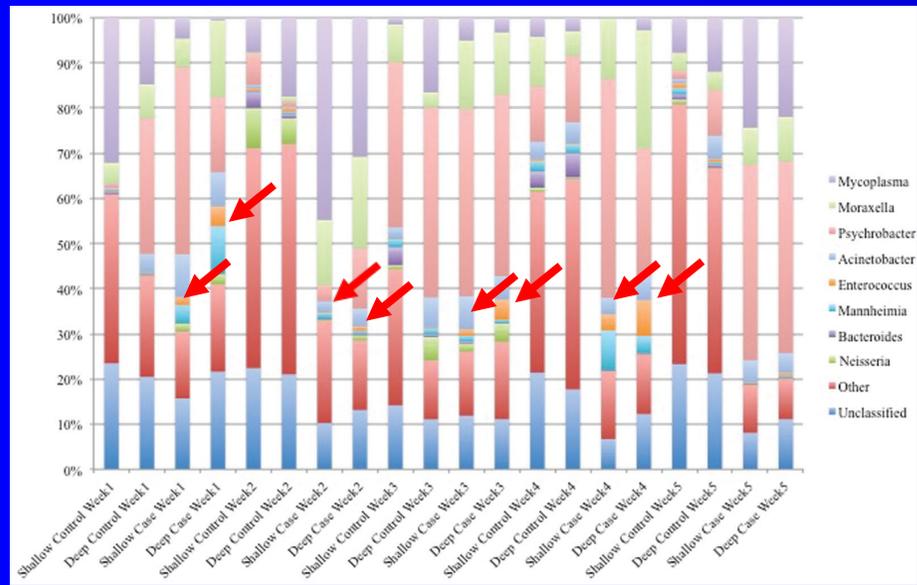


Table 3 Cytokine genes and receptors associated with bovine respiratory disease in calves

Gene	Effect	SE	F	Nominal P	P _{corrected}	Time point
CCL16	5.15	0.727	50.14	0.00010	0.0087	Diagnosis
CXCR1	8.71	1.706	26.09	0.00092	0.077	Diagnosis
CCR1	4.56	0.901	25.65	0.00097	0.081	Diagnosis

Comparison of sites of sampling and some evidence of bacteria associated with disease onset, McDanel et al., 2018

Blood cells and cytokines associated with BRD, Lindholm-Perry et al., 2018. Used Bovine Inflammatory Cytokine and Receptor PCR Array (Catalog #PABT-011Z; Qiagen)



Anticipated product: Objective, science-based criteria for assessment of animal stress and well-being in production systems in response to various management techniques.

- Tear stain, heart rate, intestinal permeability as measures of stress

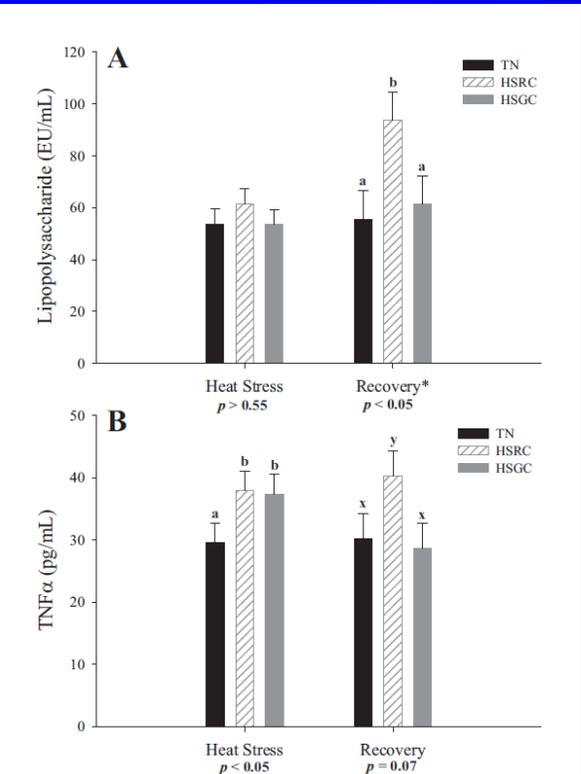
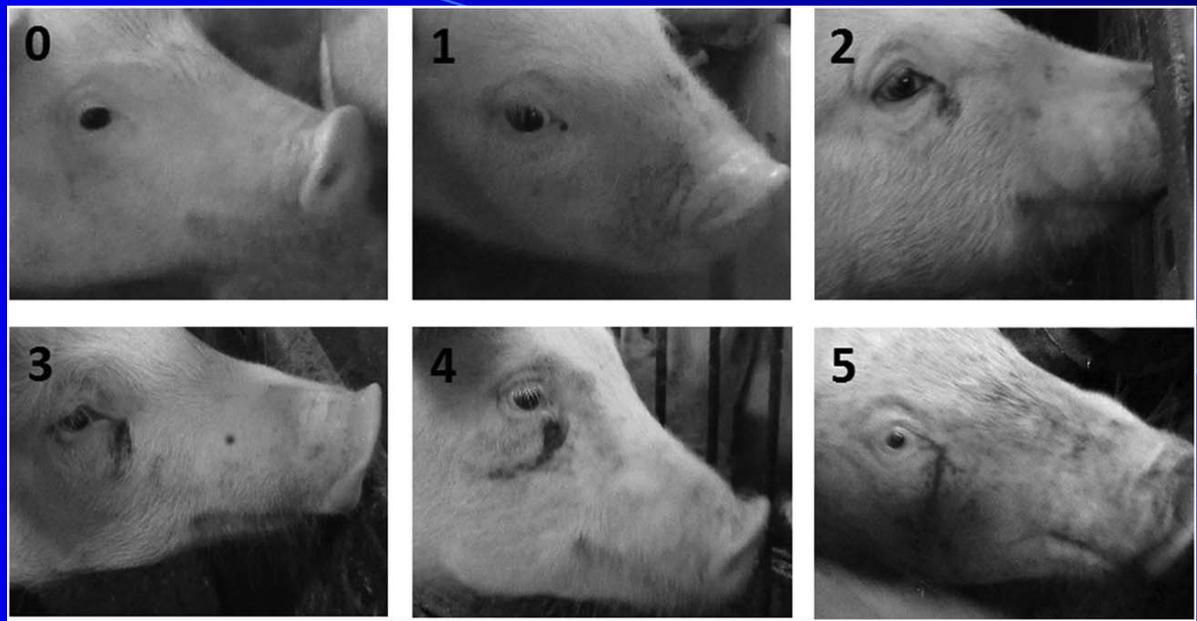


Fig. 4. Effects of heatstroke recovery treatments on circulating lipopolysaccharide (LPS; A) and tumor necrosis factor- α (TNF- α ; B) concentrations during heat stress and recovery periods. EU, endotoxin units. Error bars indicate \pm SE. Letters a < b indicate differences ($P < 0.05$) and letters x < y indicate tendencies ($0.05 < P \leq 0.10$) between recovery treatments. Asterisk indicates difference between periods.



Tear staining in pigs Telkanranta et al., 2016. Low but significant correlation with tail and ear damage

Heat stress increases intestinal permeability to lipopolysaccharides, Johnson et al., 2016

Table 4 Least squares means \pm SE for nonlinear heart rate variability measures. Heart rate variability collection occurred over three phases, where HS pigs were exposed to an acute heat episode during phase 2 while TN pigs remained in thermoneutral conditions. Phases 1 and 3 occurred under thermoneutral conditions and served as baseline and post-treatment measurement periods for all pigs. Parameter definitions can be found in Table 1

Parameter	Phase	TN	HS	Trt*Phase
SampEn	1	1.18 \pm 0.09 ^x	1.29 \pm 0.09 ^x	<0.0001
	2	1.46 \pm 0.12 ^{a,x,y}	0.90 \pm 0.09 ^{b,y}	
	3	1.52 \pm 0.09 ^y	1.11 \pm 0.09 ^{x,y}	
DFA α_1	1	1.54 \pm 0.06	1.38 \pm 0.06	ns
	2	1.41 \pm 0.07	1.54 \pm 0.05	
	3	1.40 \pm 0.06	1.51 \pm 0.05	
%REC ¹ , %	1	2.44 \pm 0.33	4.75 \pm 0.48	ns
	2	3.71 \pm 0.47	3.10 \pm 0.32	
	3	3.25 \pm 0.35	4.36 \pm 0.44	
%DET, %	1	61.9 \pm 5.0	64.3 \pm 4.5	0.05
	2	53.6 \pm 5.7	73.5 \pm 4.5	
	3	47.6 \pm 4.7 ^a	68.1 \pm 4.5 ^b	
Lmean ¹ , beats	1	3.35 \pm 0.12	3.07 \pm 0.10	ns
	2	2.81 \pm 0.12	3.83 \pm 0.13	
	3	2.76 \pm 0.10	3.70 \pm 0.12	

HS = heat stress; TN = thermoneutral control; Trt = experimental treatment; ns = non-significant; $P > 0.05$.
^{a,b} Differences between TN and HS treatments within phase ($P \leq 0.05$).
^{x,y} Differences between phases (1, 2, 3) within treatment ($P \leq 0.05$).
¹ Variable was transformed for analysis. Back-transformed least squares means \pm approximated SE are presented.

Heart rate variability and heat stress, Byrd et al., 2020



Anticipated product: Species-specific, cost-effective strategies to mitigate animal stress and improve animal well-being and longevity in conventional production systems.

- Heat stress mitigation
- Piglet euthanasia

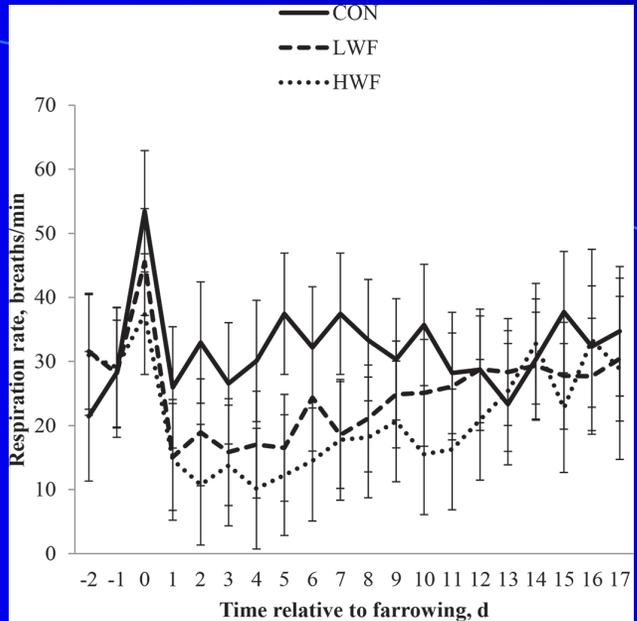
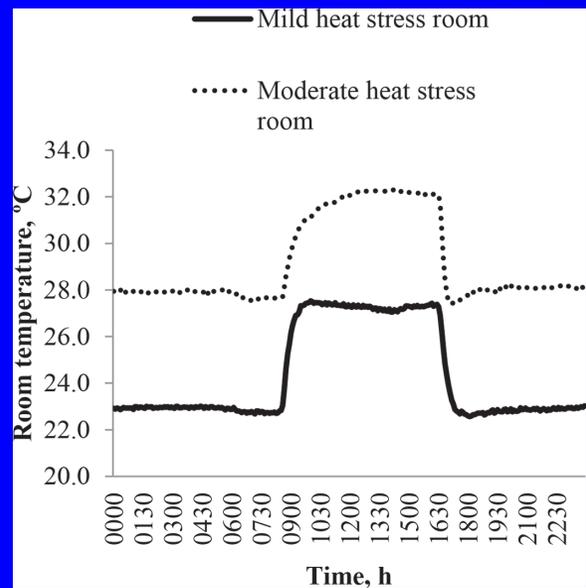
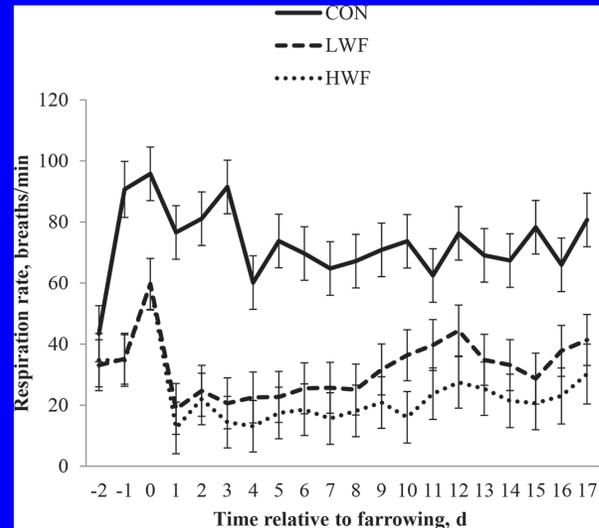
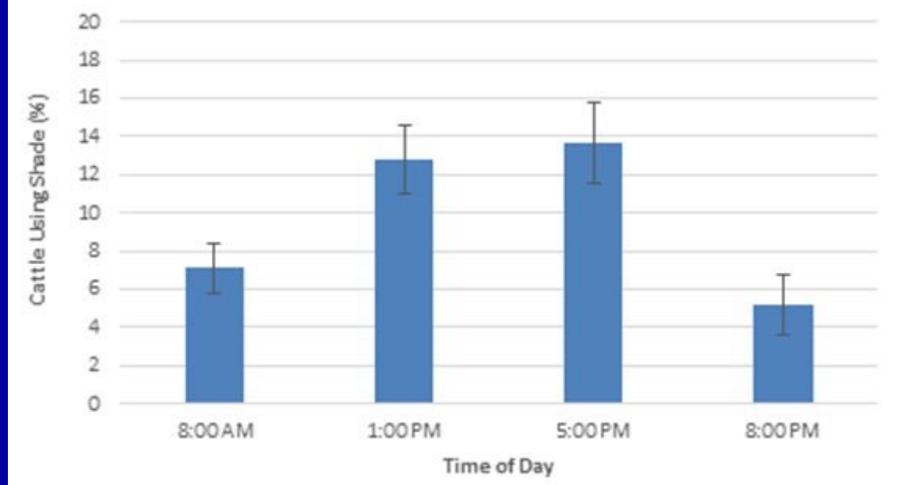


Figure 1. Photograph of the shade structures used during the experiment. The shades were incorporated into the fence line of each pen and the pens were north-south oriented. Each pen contained 2 shade structures, 1 on the west fence line and 1 on the east fence line.



Effects of low and high water flow through sow cooling pads on sow respiration rates during farrowing and lactation. Upper graph is mild heat stress, lower graph is moderate heat stress. Maskal et al., 2018



From Boyd et al., 2015 and Hayes et al., 2017

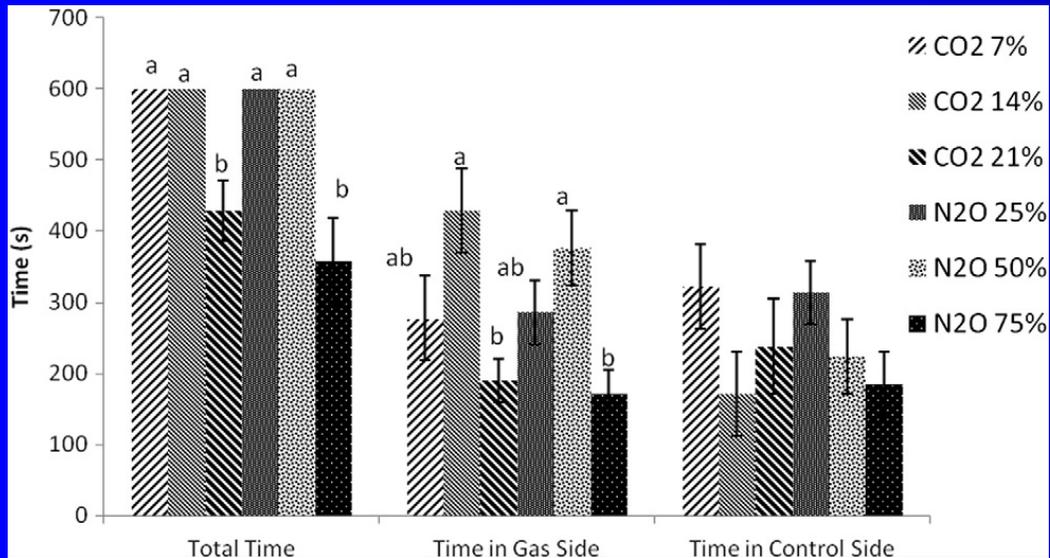
Table 2

Location and behavior (sec \pm SE) using the prefill method in Experiment 1 in piglets exposed to either 60% N₂O/30% O₂ in air (60N) or 90% N₂O in air (90N). The total duration of the test correspond to the time at which the pig entered the test chamber until 10 min or until it was removed when it started flailing.

Gas treatment	60N	90N	P-value
Treatment side	375.9 \pm 36.3	99.5 \pm 35.0	<0.001
Control side	224.1 \pm 36.3	155.9 \pm 44.6	0.24
Normal behavior	58.2 \pm 9.6	18.3 \pm 6.8	0.004
Ataxia	120.8 \pm 48.9	83.2 \pm 32.0	0.04
Flail	- ^a	4.4 \pm 1.6	-
Total duration of the test ^b	600.0 \pm 0.0	255.4 \pm 65.5	<0.001

^a Behavior not observed in that treatment.

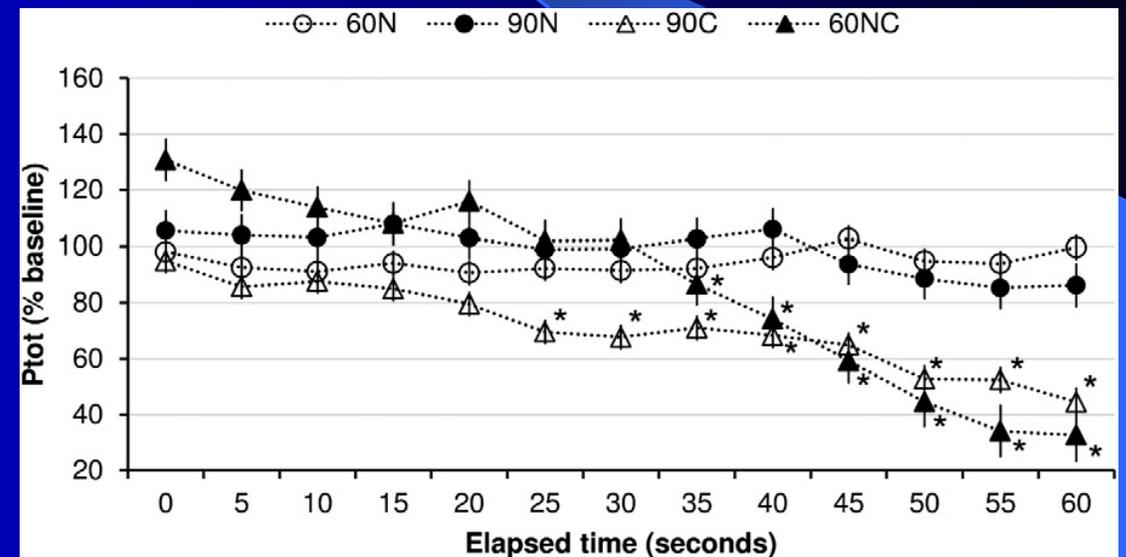
^b For ethical reasons, if the piglet fell recumbent and unresponsive or flailed, the test was terminated.

**Table 4**

Mean (\pm SE) latency (s) and range of latency (s) in brackets to the onset of transitional and isoelectric EEG in Experiment 3 in piglets exposed to either 90% N₂O in air (90N), 90% CO₂ in air (90C) or 90% CO₂ subsequent to the 15 min exposure to 60% N₂O/30% O₂ in air (60NC).

Variables	90N	90C	60NC	P-value
Transitional EEG	62.10 \pm 4.80 ^y [40–87]	45.49 \pm 5.23 [39–54]	41.82 \pm 5.18 ^x [15–51]	0.07
Isoelectric EEG	71.49 \pm 7.47 [55–94]	58.66 \pm 8.14 [46–68]	48.83 \pm 8.07 [33–73]	0.19

^{x,y}Values within a row with different superscripts tended to differ ($P < 0.10$).



Series of experiments to determine whether nitrous oxide provides a better euthanasia method than using carbon dioxide alone. Table on the upper left indicates that nitrous oxide is effective at rendering animals ataxic. Graph indicates that 75% nitrous is not aversive to piglets. Table on the right indicates that 90% nitrous reduces brain activity to zero slightly longer than 90% Carbon dioxide, and there is some evidence in the graph on the lower right that pretreatment with 60% nitrous before carbon dioxide is less aversive to piglets



Anticipated product: Comprehensive production system best management practices that improve production efficiencies while also maintaining or improving animal well-being, product quality, and economic competitiveness and sustainability.

- Poultry housing innovations

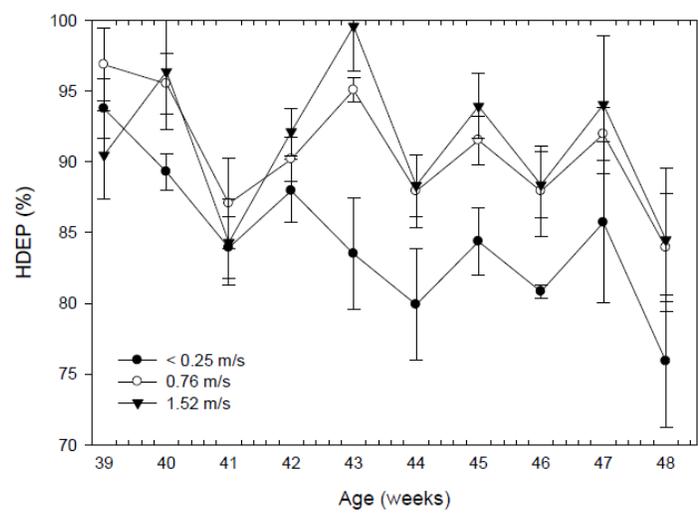


Figure 1. Weekly hen-day egg production (HDEP) over 10-week study period. Values are means and associated standard errors ($n = 4$).

Table 1: Influence of Photoperiod, light-intensity and their interaction on live body weights, eye weights, relative eye weight to BW and clinical corneal lesion (CLS) at 42 d of age^{1,A}

Treatments	Live BW (Kg)	Eye WT (g)	Eye WT:BW (g/kg)	CLS ⁴
Photoperiod				
Long	3.340 ^a	7.378 ^a	2.174	0.01
Reg-Inter	3.400 ^a	7.616 ^a	2.250	0.01
Short-Non-Inter	3.080 ^b	6.378 ^b	2.078	0.02
Intensity				
0.5 lx	3.238	7.585	2.345	0.00
5.0 lx	3.284	6.681	2.046	0.00
10.0 lx	3.294	6.935	2.111	0.01
SEM ²	0.081	0.286	0.112	0.012

Table 4: Influence of photoperiod, light-intensity and their interaction on body weight (BW) and footpad of broilers grown to heavy weights at 56 d of age¹

Treatments	Kg BW	Food pad	
		Left	Right
Photoperiod			
Long	4.204 ^a	1.33 ^c	1.33 ^b
Reg-Inter	4.262 ^a	1.62 ^b	1.52 ^b
Short-Non-inter	3.710 ^b	2.58 ^a	2.60 ^a
Light Intensity			
0.5 lx	4.058	1.88	1.90
5.0 lx	4.142	1.92	1.88
10 lx	3.974	1.73	1.67
SEM ²	0.069	0.120	0.113

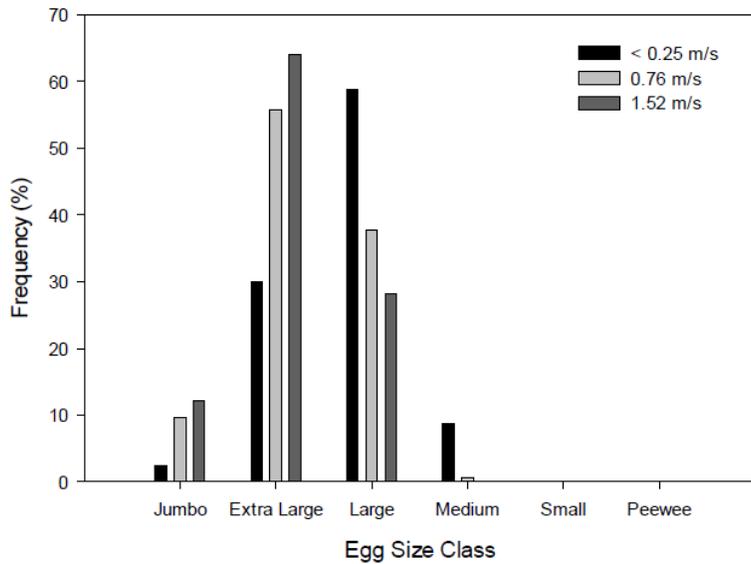


Figure 7. Size class distribution of eggs for all eggs assessed for quality attributes.

Increased air flow increases egg production and the size of eggs is larger, Purswell et al., 2015

Long (23L:1D) and intermittent (2L:2D) photoperiod increased growth rate of heavy broilers and decreased footpad lesions (3 is the largest score on this scale), compared to short (8L:16D) photoperiod

Component 2: Understanding, Improving, and Effectively Using Animal Genetic and Genomic Resources

Problem Statement 2A: Develop Bioinformatic and other Required Capacities for Research in Genomics and Metagenomics

Anticipated product: Improved annotation of genome sequence assemblies for food animals, including participation in the Functional Annotation of Animal Genomes consortium.

- FAANG efforts
- Improved genomes
- Trio binning

Anticipated product: Enhanced metagenomic characterization and analysis of the gut microbiome to develop better understanding of the relationship between the microbiome and the health, productivity and environmental impact of food animals.

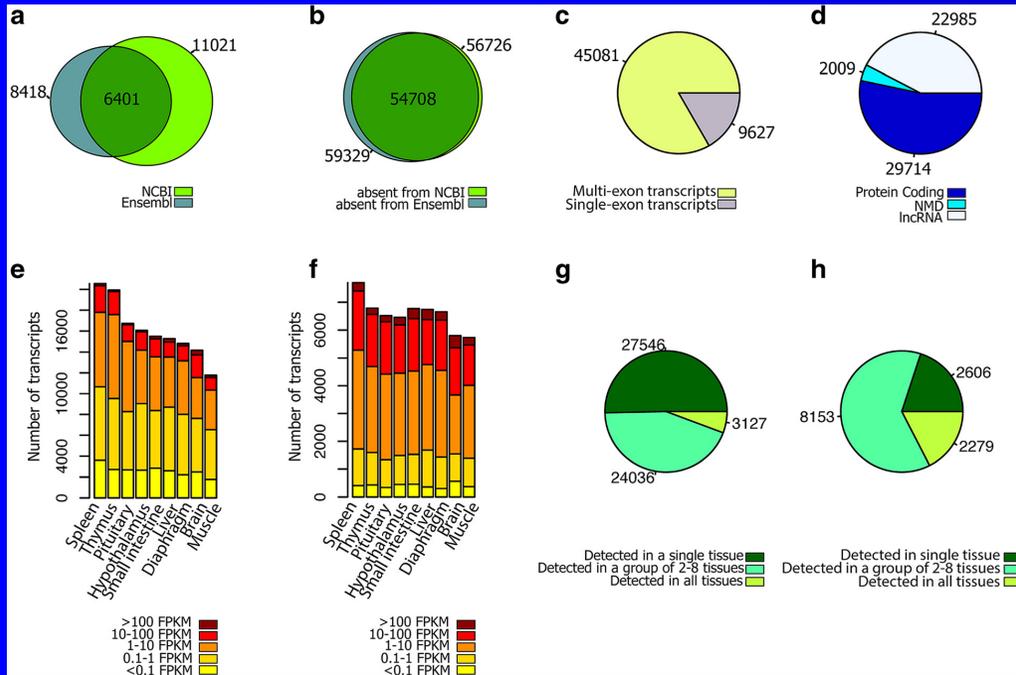
- Rumen microbiome
- Piglet mycobiome

Table 1 Sequencing and mapping summary

Tissue ID	Tissue name	Clean reads	Unique mapped reads	Unique mapping rate (%)	CG methylation (%)	Non-CG methylation (%)	Bisulfite conversion rate (%)
BGA13	Skeletal muscle near cesarian	62,431,346	27,615,411	44.23	33.87	1.45	99.38
BGA14	Whole testes ^a	65,883,038	23,323,753	35.40	37.00	0.94	99.45
BGA19	Mammary/parenchyma ^a	61,978,584	27,862,415	44.95	30.50	1.31	99.28
BGA22	Uterus intercaruncular ^a	62,431,548	26,830,069	42.98	33.22	1.45	99.41
BGA47	Frontal cortex ^a	63,601,202	22,808,676	35.86	30.89	1.48	99.30
BGA60	Abomasum ^a	62,173,874	28,496,274	45.83	38.06	1.04	99.25
BGA62	Ileum ^a	65,228,026	23,666,863	36.28	33.54	1.50	99.04
BGA81	Rumen ^a	62,646,332	25,923,247	41.38	29.87	1.44	99.28
BGA135	Nucleated blood cells ^a	63,611,924	23,184,841	36.45	36.03	1.54	99.07
BGA173	D 90 lactating mammary gland	62,474,748	28,581,463	45.75	32.04	1.36	99.33

^aTissues with RNA-seq data

Bisulfite sequencing on tissues, Zhou et al., 2016



RNA seq to annotate the genome in pigs, Beiki et al., 2019

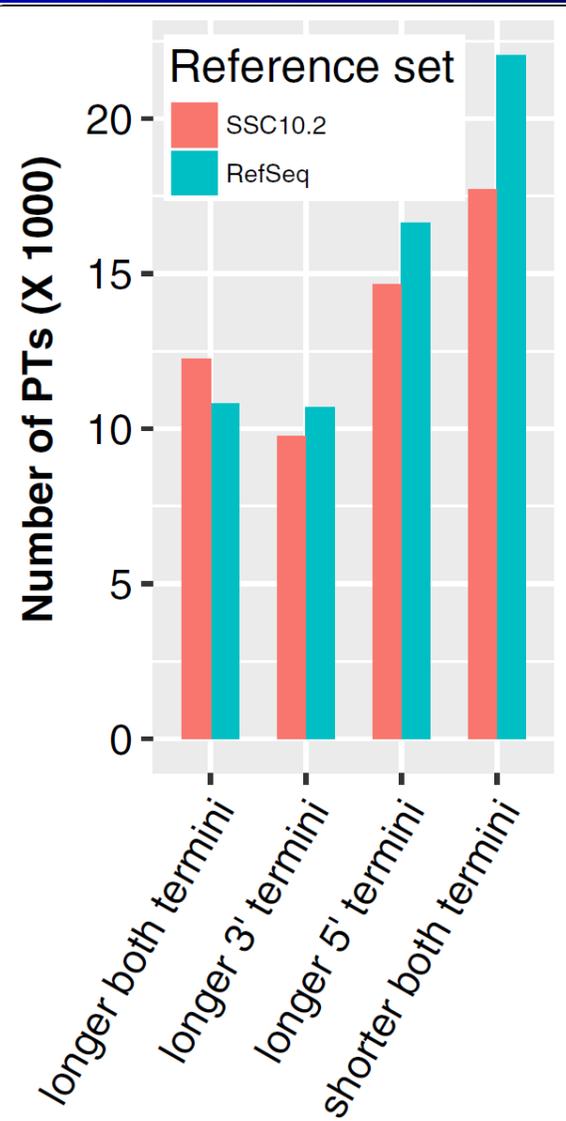


Fig. 5 Length comparison between PTs and transcripts in the reference sets. The lengths of uniquely mapping spliced PTs were compared with those of SSC10.2 transcripts and pig RefSeq mRNAs. The number of PTs with longer 5' and 3', only longer 3', and only longer 5' termini, or neither terminus than their maximally overlapping reference transcripts in SSC10.2 annotation (red) and RefSeq mRNA collection (blue), respectively is as displayed

Blood transcriptome improved the genome and refseq resources for pigs, Liu et al., 2017

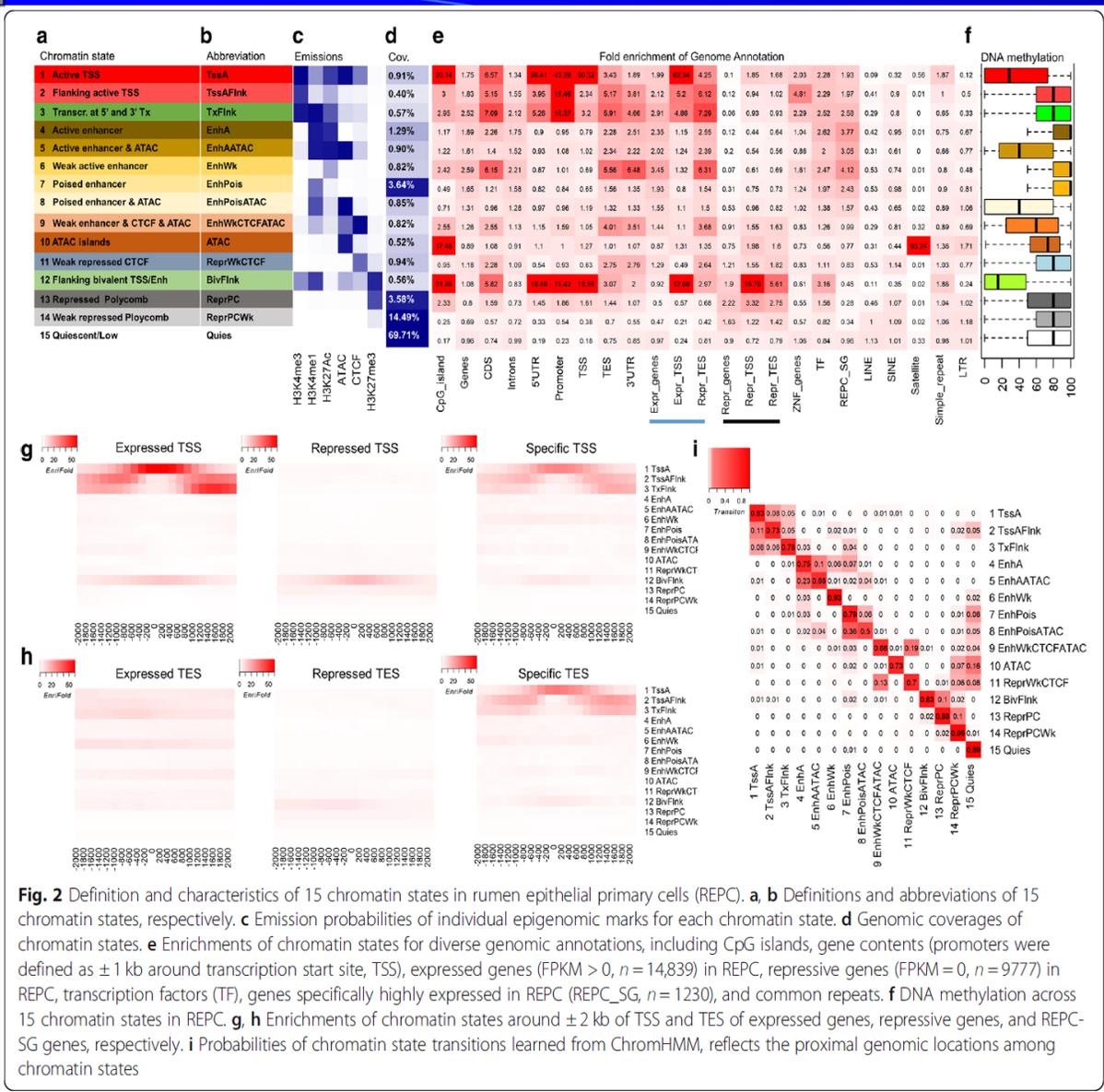
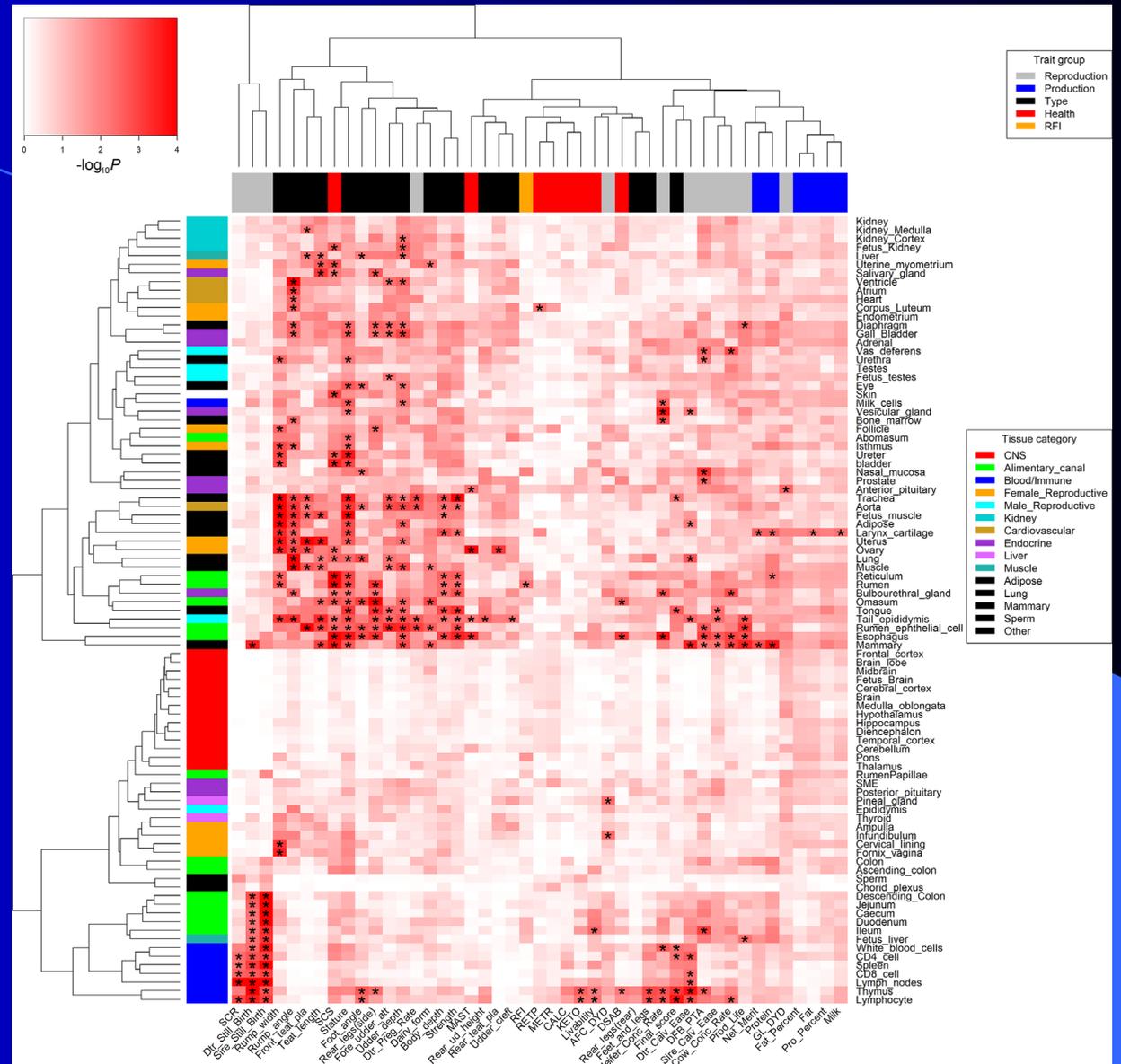
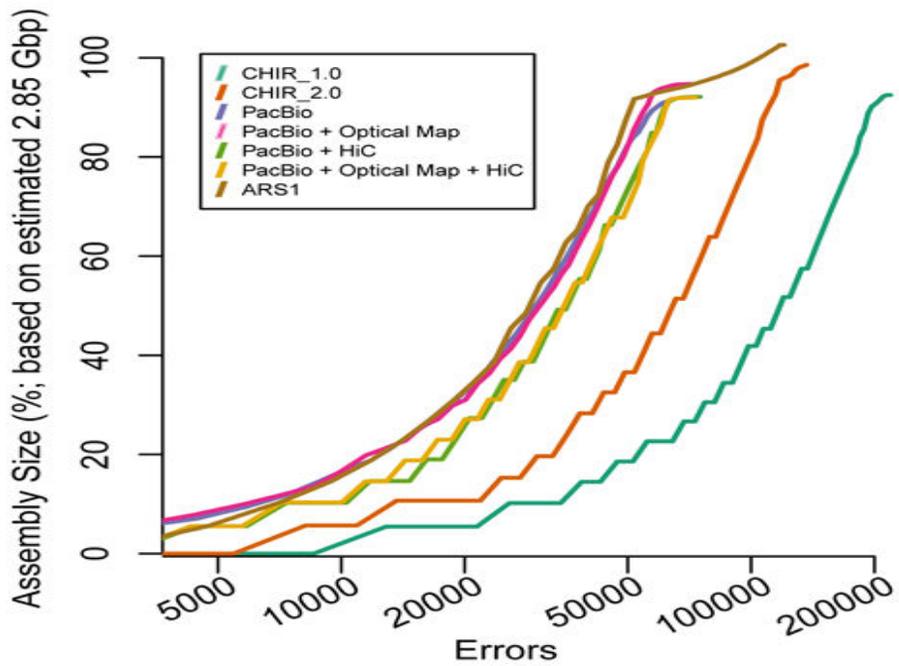


Fig. 2 Definition and characteristics of 15 chromatin states in rumen epithelial primary cells (REPC). **a, b** Definitions and abbreviations of 15 chromatin states, respectively. **c** Emission probabilities of individual epigenomic marks for each chromatin state. **d** Genomic coverages of chromatin states. **e** Enrichments of chromatin states for diverse genomic annotations, including CpG islands, gene contents (promoters were defined as ± 1 kb around transcription start site, TSS), expressed genes (FPKM > 0 , $n = 14,839$) in REPC, repressive genes (FPKM = 0, $n = 9,777$) in REPC, transcription factors (TF), genes specifically highly expressed in REPC (REPC_SG, $n = 1,230$), and common repeats. **f** DNA methylation across 15 chromatin states in REPC. **g, h** Enrichments of chromatin states around ± 2 kb of TSS and TES of expressed genes, repressive genes, and REPC-15 genes, respectively. **i** Probabilities of chromatin state transitions learned from ChromHMM, reflects the proximal genomic locations among chromatin states

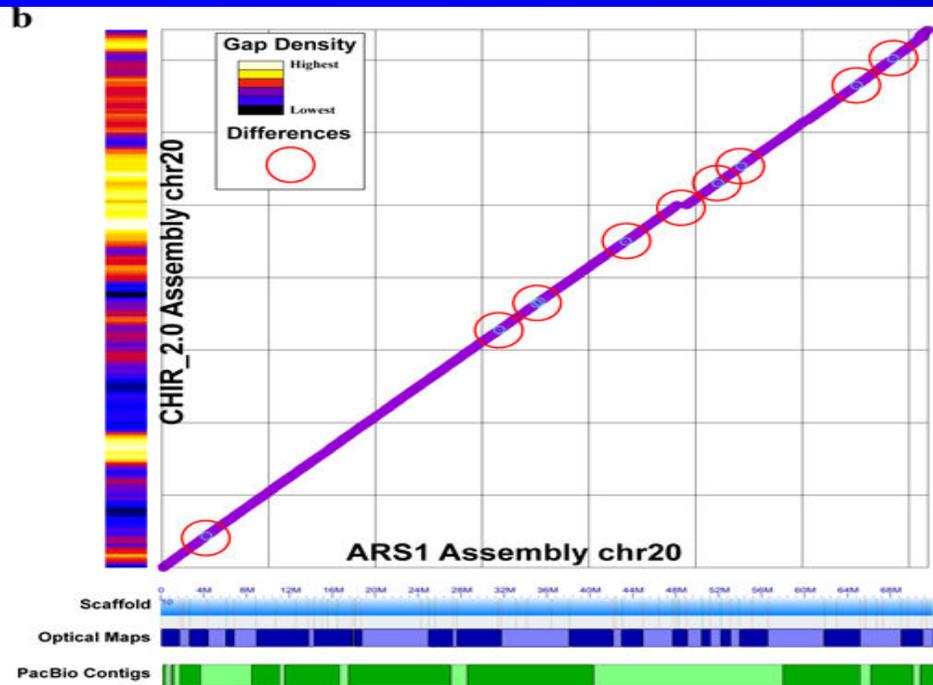
Butyrate induced changes in methylation in cattle, Fang et al., 2019



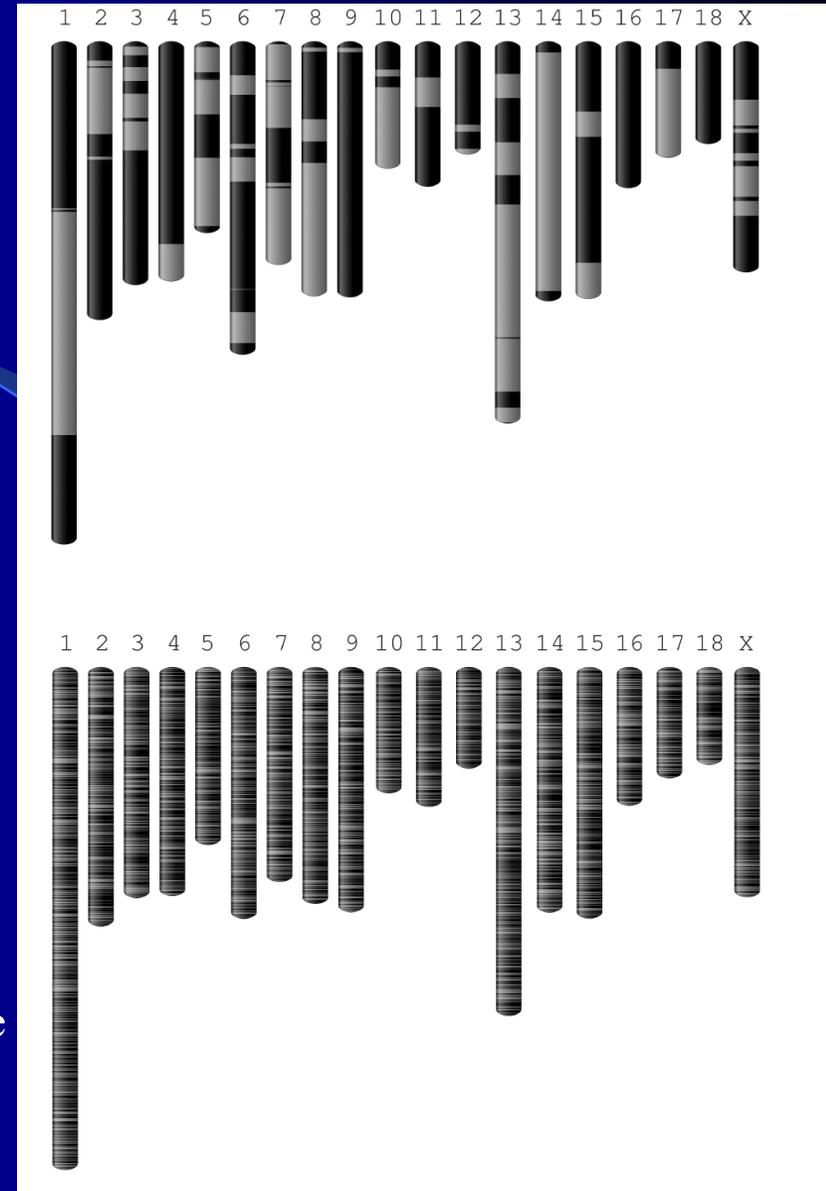
Cattle tissue atlas integrating GWAS loci, genes, tissues and chromatin changes, Fang et al., 2020



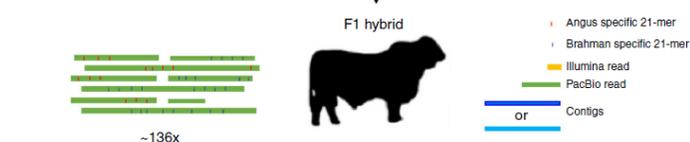
ARS goat genome compared to previous goat sequence. Resolved several problems and removed many gaps. Bickhart et al., 2017



New more contiguous pig assembly (top) compared to the old assembly, alternating black and grey indicate contigs



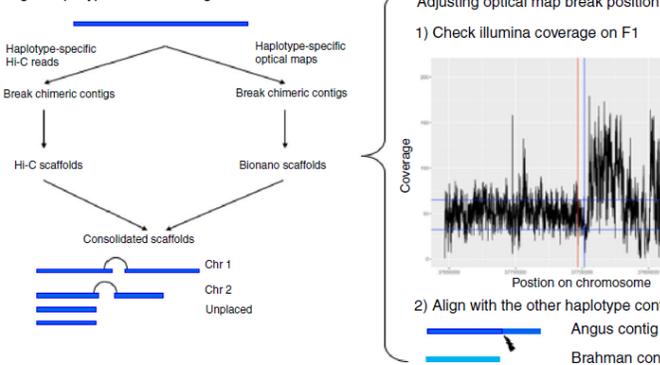
Binning long reads based on unique parental kmer



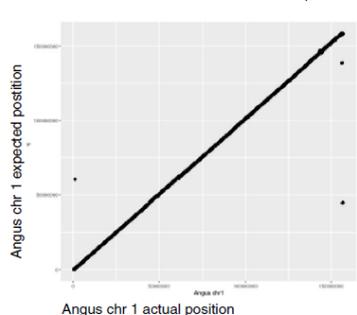
Contig assembly of haplotype-specific reads



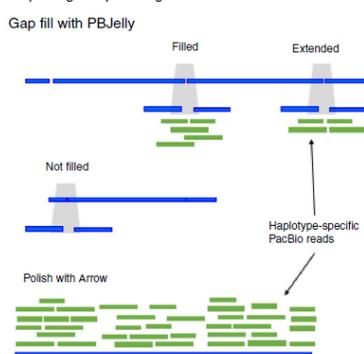
Scaffolding of haplotype-resolved contigs



Scaffolds validation with recombination map



Gap filling and polishing



Trio binning strategy, Angus versus Brahman, haplotype resolved sequences, Low et al., 2020. Two complete genomes

Trio binning yak and cattle hybrid, haplotype resolved sequence better than the current human genome. Rice et al., 2020. Chromosome 1 is a single contig

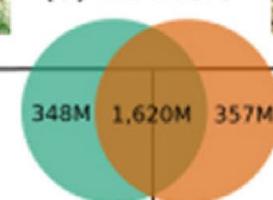
(a) Molly
♀ *Bos grunniens*
30x short reads



(b) Duke
♂ *Bos taurus*
43x short reads



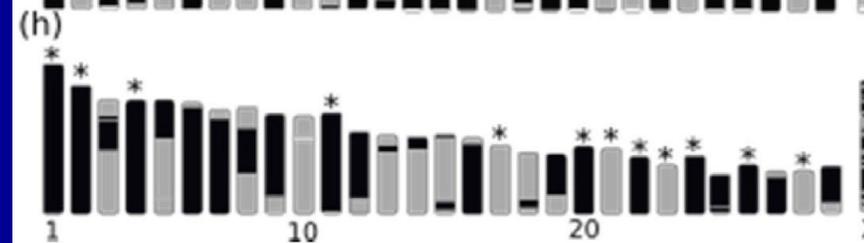
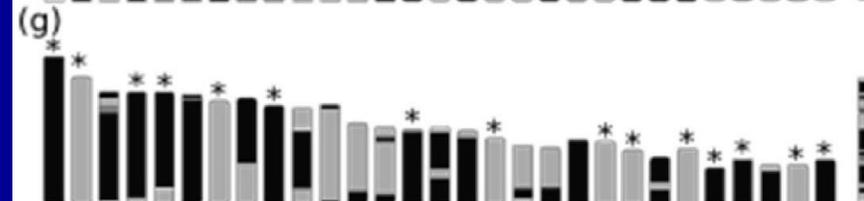
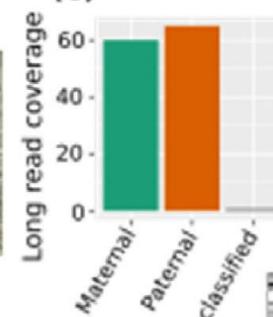
(d) 21-mers

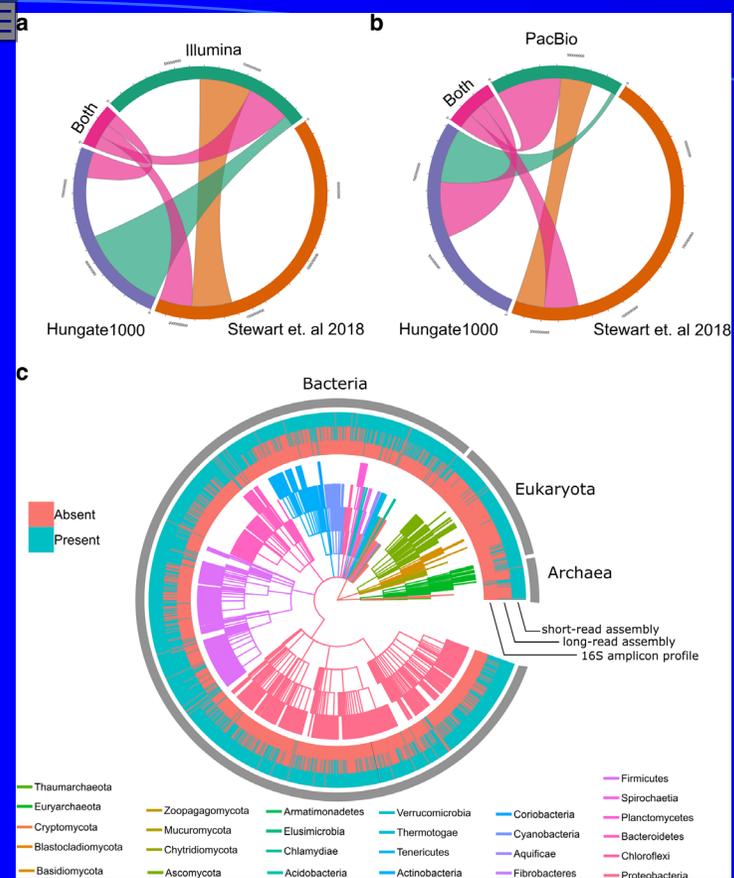


(c) Esperanza
♀ F1 hybrid
125x long reads

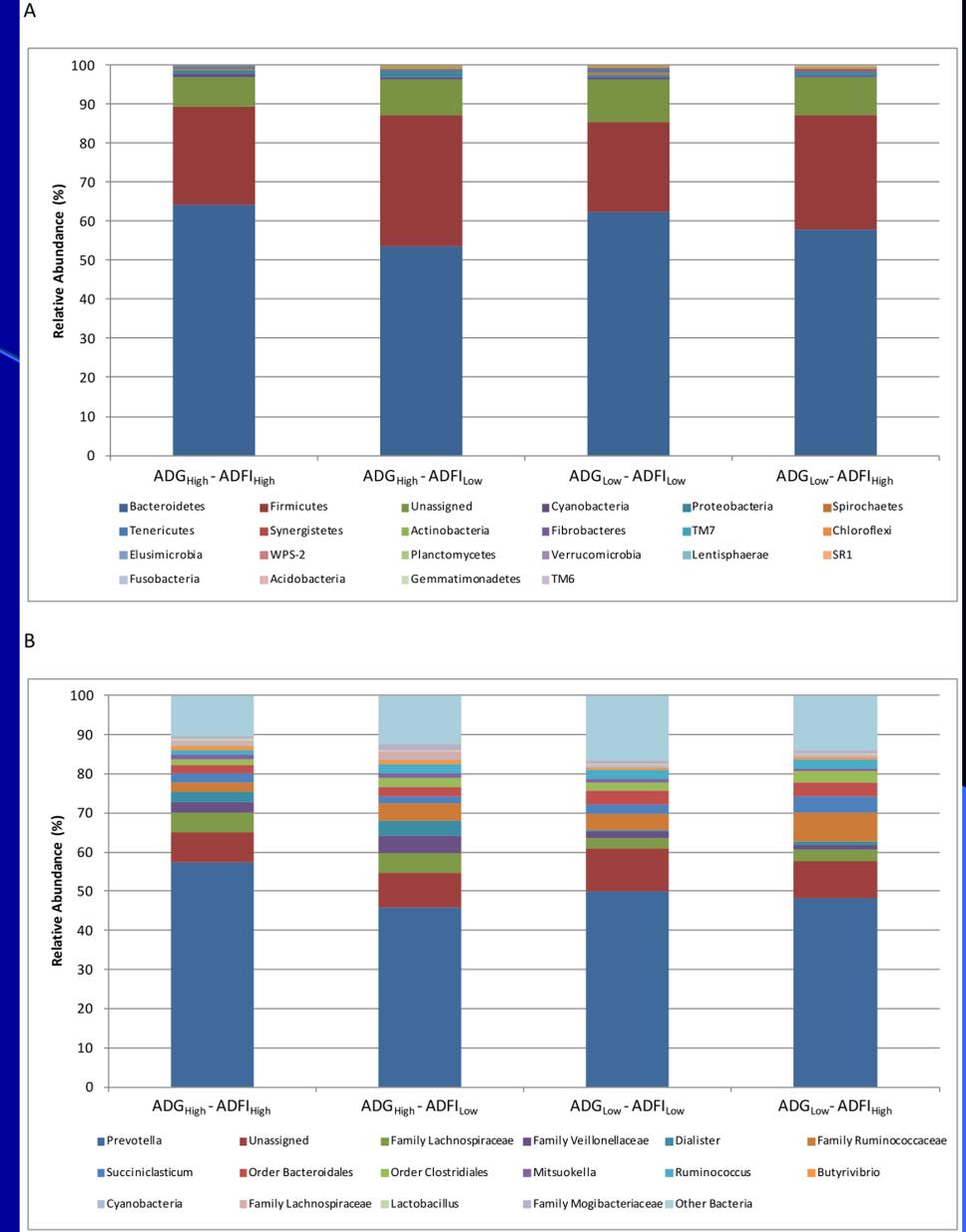
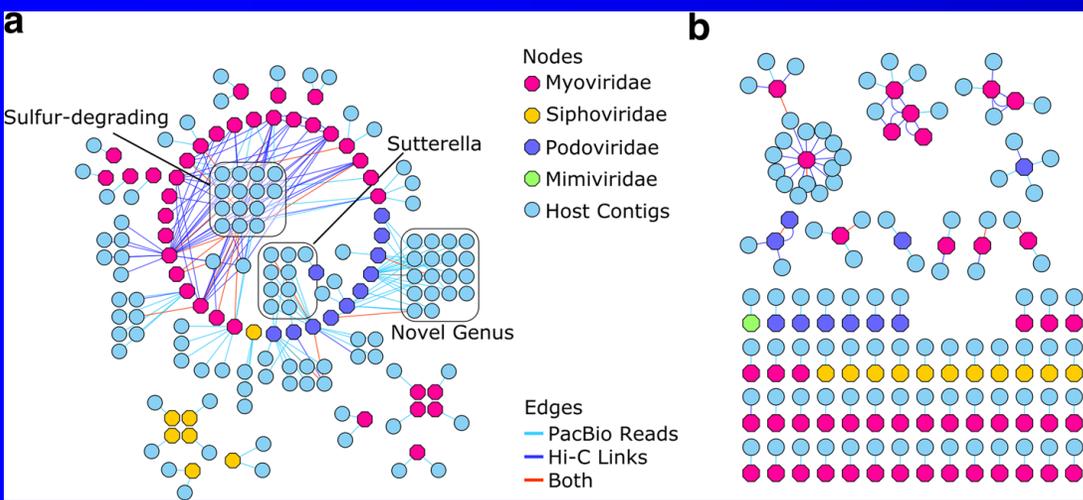


(e)

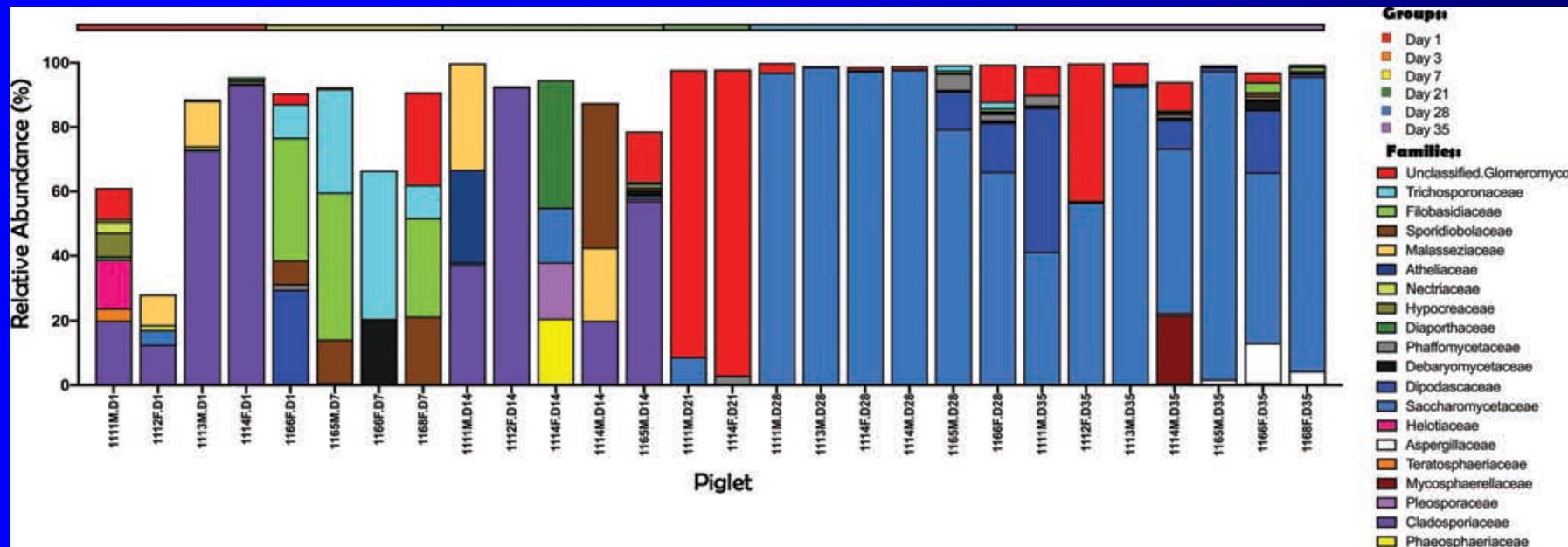
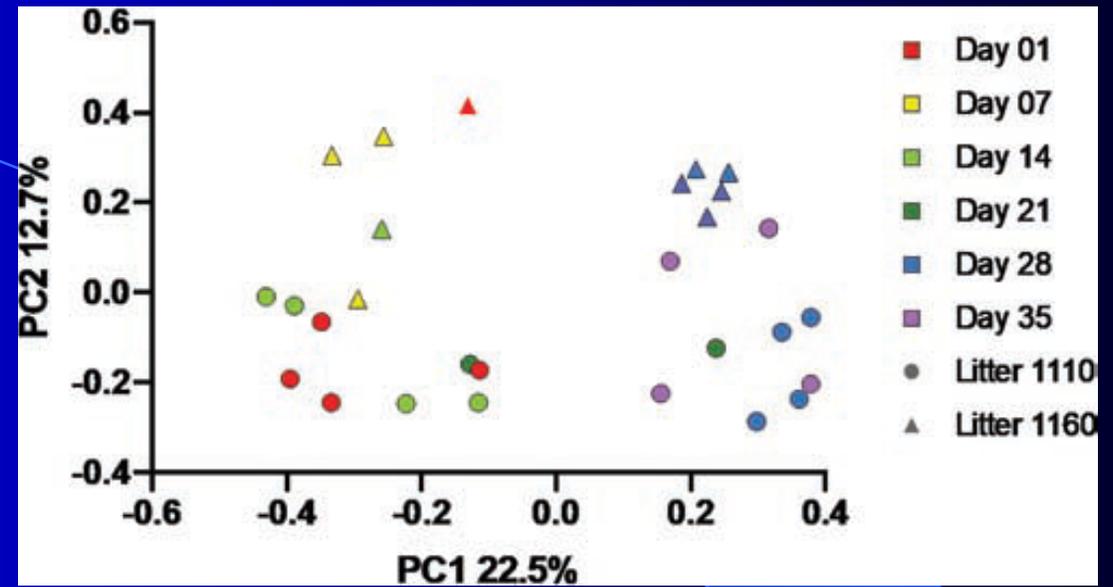
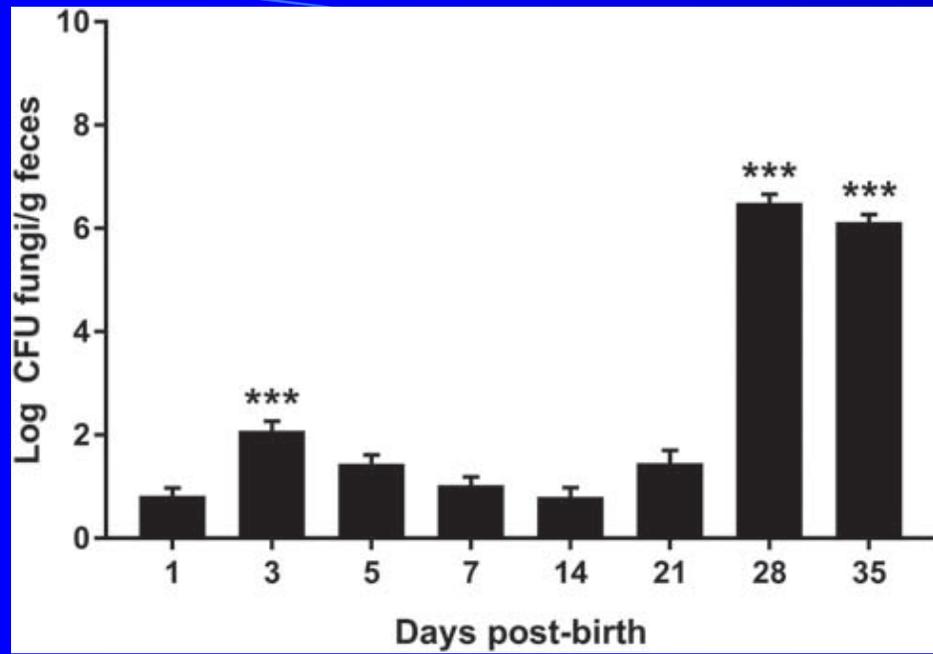




The combination of long- and short-range sequencing was effective at generating full sequences for numerous bacteria found in the rumen. Surprisingly, many viruses were found and Hi-C was effective in assigning the viruses to hosts. These viruses could be used to modify various components of the rumen, or possibly be used as a vector to introduce novel genes where they are desired. Bickhart et al., 2019



Microbiome analysis of feed efficiency in cattle, Myer et al., 2015

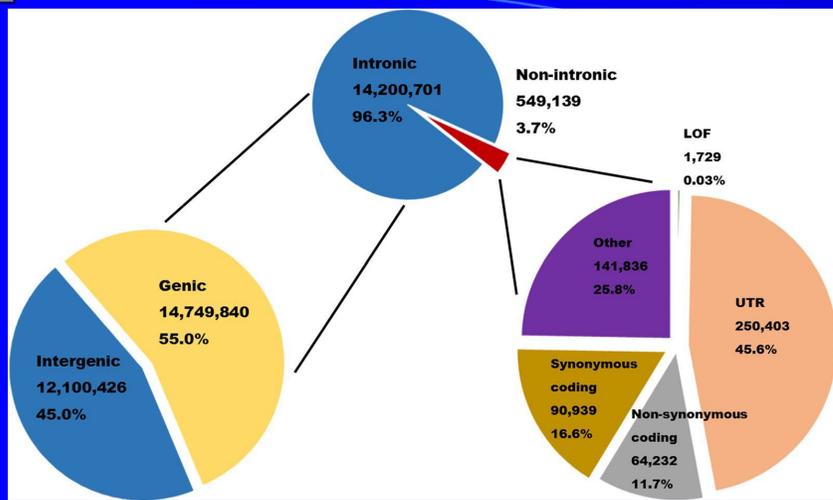


Very clear transition from very little fetal fungi to huge amounts of fetal fungi at weaning. Many questions to answer from this work, and lots of possible implications. Summers et al., 2019



Anticipated product: Association of genetic and genomic effects with economically important traits, including but not limited to growth, feed efficiency, reproductive efficiency, and production efficiency.

- Loss of function, number of mammary glands, liver abscesses, feeding behavior in heat stress, heifer fertility GWAS analyses



Determined loss of function and non-synonymous snp in pig sequence, Keel et al., 2018

Table 5 One-Mb windows that explained more than 1% of the genetic variance for each temperature-humidity index (THI) category comparisons

THI category comparison ^a	Chromosome	Position ^b (Mb)	% of genetic variance explained	Number of SNPs
<i>Normal-Alert</i>	5	68	11.9	26
	7	53	13.2	28
	10	44	12.7	24
<i>Normal-Emergency</i>	14	11	8.3	42

GWAS for feeding behavior changes during heat stress, Cross et al., 2018

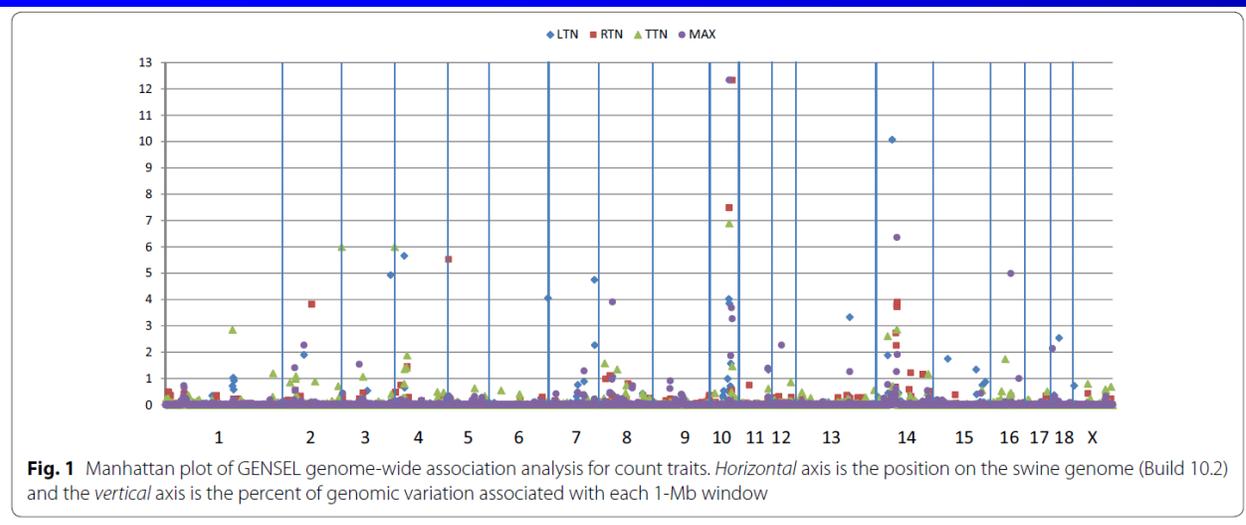
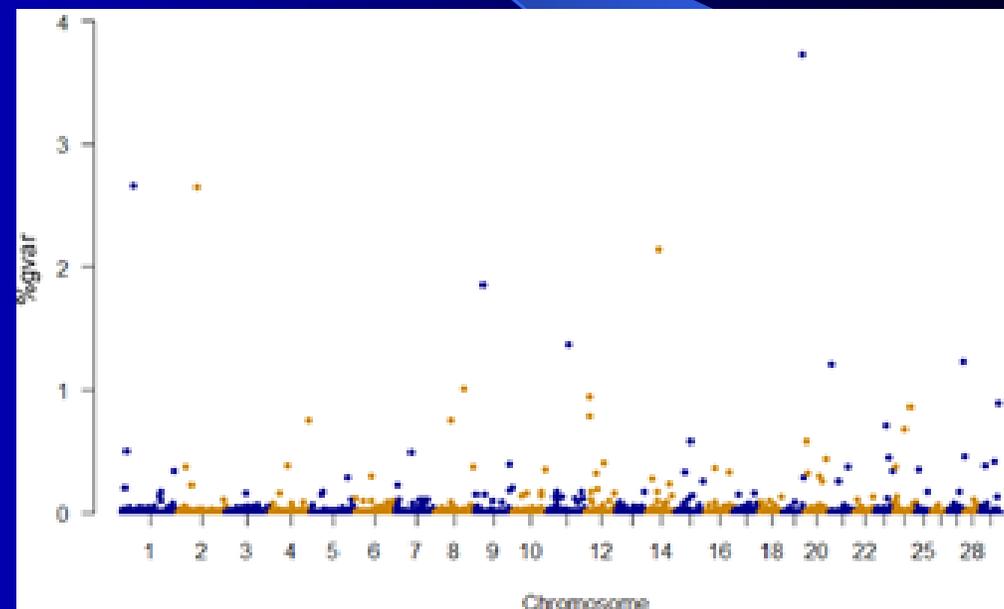


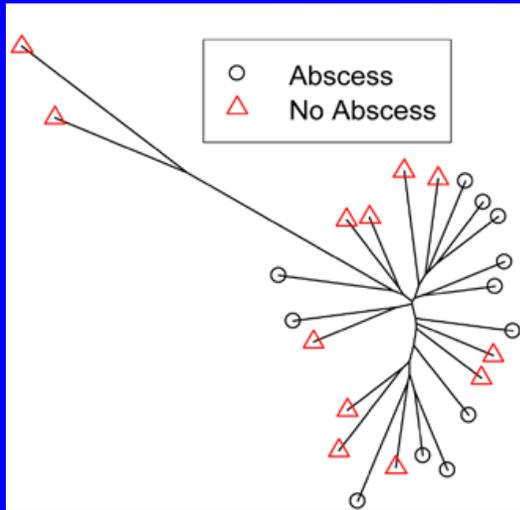
Fig. 1 Manhattan plot of GENSEL genome-wide association analysis for count traits. *Horizontal axis* is the position on the swine genome (Build 10.2) and the *vertical axis* is the percent of genomic variation associated with each 1-Mb window

GWAS for teat number in pigs, Rohrer and Nonneman, 2017

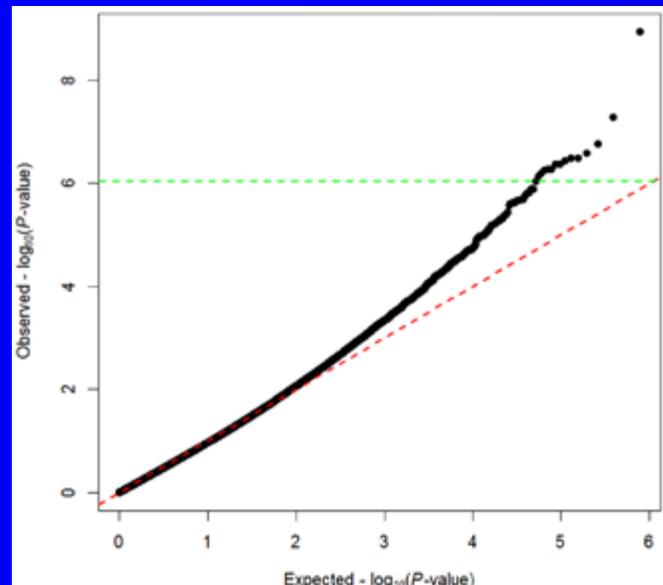


GWAS for longevity in cattle, Hay and Roberts, 2017

Genotyping after sample pooling- liver abscess, Keele et al., 2016



Clustering analysis indicates some population structure among pools (samples collected from slaughterhouse). These relationships were accounted for in the analysis



Loci above the green line were greater than the false discovery rate threshold. This graph shows pooling allele frequency, similar results, but completely different loci, were found for total intensity

Table 1. Associations between SNP pooling allele frequency¹ (PAF) and liver abscesses achieving false discovery rate of 5%

BTA	Position, bp	SNP ²	PAF		MSE ³	<i>t</i> -distribution	<i>P</i> -value	Gene	Gene ⁴	
			Abscess	No abscess					Starting position, bp	Ending position, bp
1	90,138,593	rs43248252	0.19	0.12	0.053	6.98	5.27×10^{-7}	XR_804373.1	90,120,141	90,121,253
1	117,247,146	rs137456530	0.16	0.11	0.029	7.50	1.70×10^{-7}	LOC782298	117,222,990	117,223,951
2	47,326,757	rs135856611	0.40	0.30	0.098	7.21	3.19×10^{-7}	KIF5C	47,311,871	47,472,004
2	107,508,288	rs43315181	0.40	0.26	0.200	6.96	5.54×10^{-7}	PRKAG3	107,507,841	107,517,485
7	21,558,133	rs136477409	0.23	0.14	0.083	7.07	4.30×10^{-7}	TBXA2R	21,556,155	21,569,886
8	24,743,994	rs133269746	0.16	0.09	0.055	6.84	7.16×10^{-7}	SLC24A2	24,487,108	24,779,293
15	47,296,349	rs109184225	0.51	0.37	0.184	7.16	3.58×10^{-7}	LOC786995	47,310,391	47,313,308
15	57,340,890	rs41776932	0.50	0.31	0.286	8.06	5.25×10^{-8}	MYO7A	57,315,857	57,419,715
15	80,515,623	rs134787048	0.15	0.09	0.016	10.03	1.15×10^{-9}	OR8J1	80,515,014	80,515,961
16	11,424,152	rs42601618	0.28	0.21	0.042	7.30	2.58×10^{-7}	LOC104970159	12,355,176	12,378,333
18	48,806,574	rs41885703	0.25	0.40	0.206	-7.07	4.29×10^{-7}	LGALS4	48,803,147	48,810,095
21	68,600,417	rs109014822	0.35	0.25	0.107	6.89	6.35×10^{-7}	HSP90AA1	68,595,870	68,601,237
22	50,708,448	rs42019238	0.18	0.12	0.045	6.97	5.42×10^{-7}	SLC38A3	50,702,769	50,717,523
X	16,094,115	rs135306367	0.31	0.19	0.164	6.74	9.03×10^{-7}	MBNL3	16,104,214	16,224,696
X	148,694,034	rs134648412	0.38	0.24	0.205	7.20	3.26×10^{-7}	LOC505052	148,690,204	148,703,791

¹Pooling allele frequency is red dye intensity divided by the sum of red and green dye intensities.

²SNP shown in bold are missense (nonsynonymous) mutations; all others are intron or intergenic mutations.

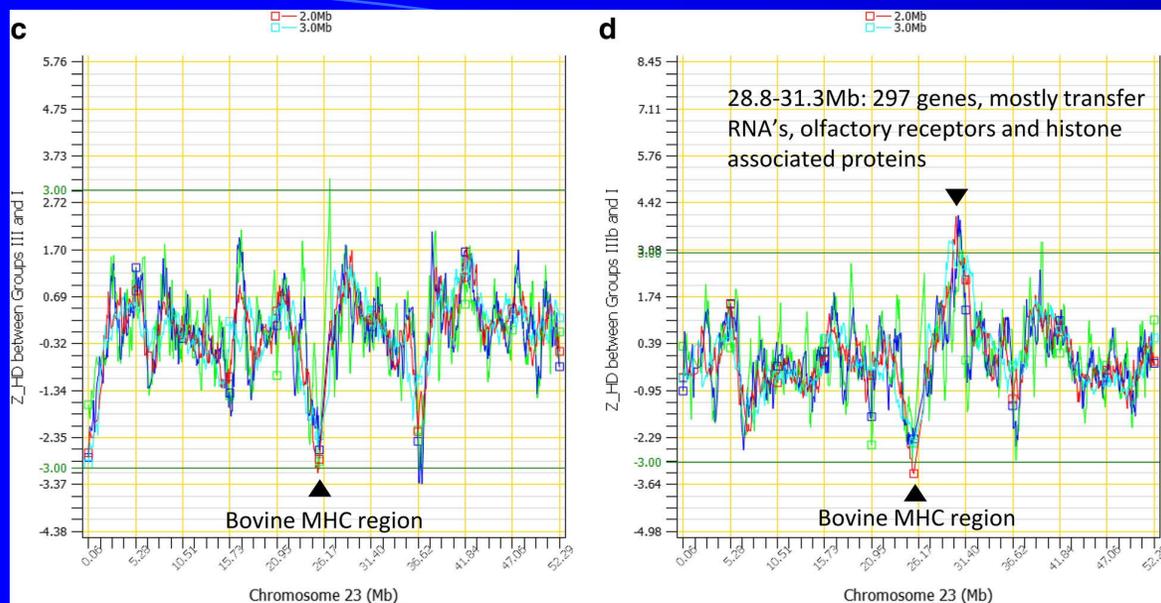
³MSE = mean squared error.

Significant loci obtained for pooling allele frequency. Separate loci were found for total intensity.



Anticipated product: Development of comprehensive intensive and extensive phenomic and analytical tools to relate genomic and phenotypic data for development of improved genome based estimates of genetic merit including well- characterized and deeply phenotyped ARS, field and other research food animal populations.

- New algorithms and traits for dairy
- New chips for turkey and swine



Heterozygosity decreases and increases in Holsteins due to selection for 40 years. Ma et al., 2019

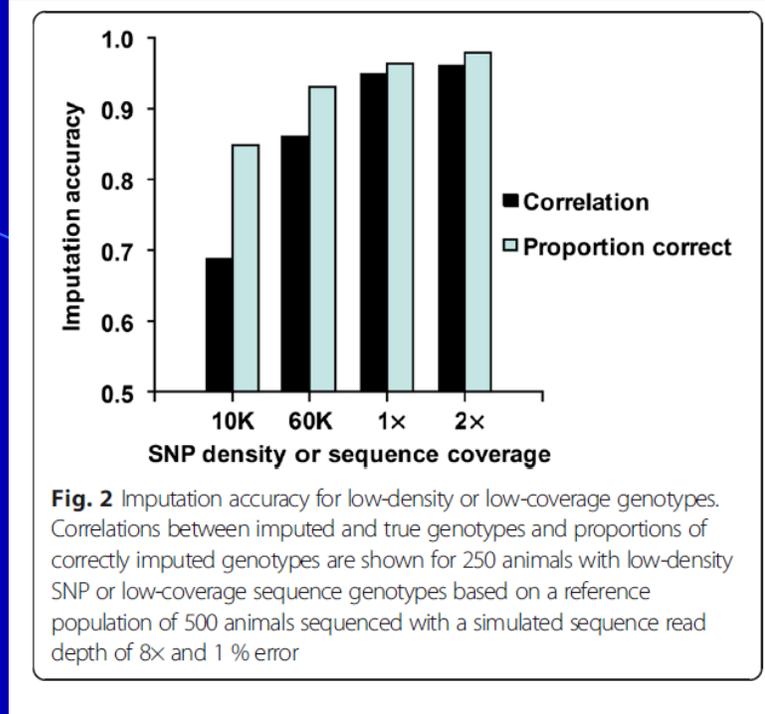


Fig. 2 Imputation accuracy for low-density or low-coverage genotypes. Correlations between imputed and true genotypes and proportions of correctly imputed genotypes are shown for 250 animals with low-density SNP or low-coverage sequence genotypes based on a reference population of 500 animals sequenced with a simulated sequence read depth of 8x and 1 % error

Developed new algorithms for imputation of genotypes from low coverage genotyping, Van Raden et al., 2015

Table 10. Correlations of truncated and current evaluations using previous and new software for bulls with no daughter records in July 2008 and bulls that gained daughter records after July 2008 by trait

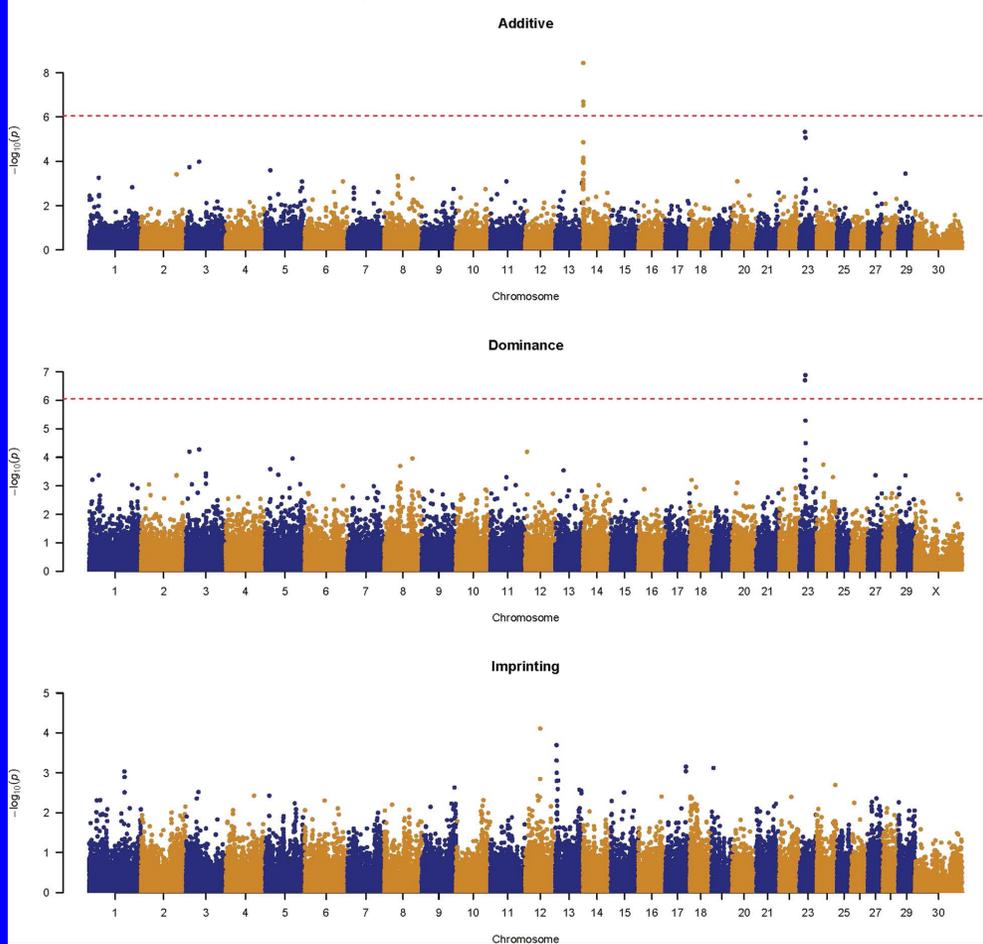
Breed	Trait	Bulls with no daughter records ¹			Bulls that gained daughter records ²		
		Previous	New single-trait	New multi-trait	Previous	New single-trait	New multi-trait
Holstein	Milk yield	0.579	0.577	0.584	0.792	0.812	0.820
	Fat yield	0.523	0.506	0.508	0.795	0.823	0.813
	Protein yield	0.559	0.560	0.561	0.792	0.827	0.813
	SCS	0.552	0.561	0.561	0.789	0.797	0.798
	Daughter pregnancy rate	0.528	0.606	0.601	0.659	0.694	0.704
Jersey	Productive life	0.661	0.641	0.658	0.818	0.744	0.790
	Milk yield	0.648	0.670	0.672	0.843	0.874	0.875
	Fat yield	0.616	0.637	0.641	0.692	0.687	0.681
	Protein yield	0.599	0.630	0.627	0.769	0.794	0.792
	SCS	0.458	0.478	0.465	0.652	0.700	0.688
	Daughter pregnancy rate	0.556	0.591	0.545	0.678	0.704	0.699
	Productive life	0.558	0.544	0.569	0.743	0.591	0.690

¹Included 4,059 Holstein and 415 Jersey bulls with 0 daughters in 2008 and >50 in 2012.

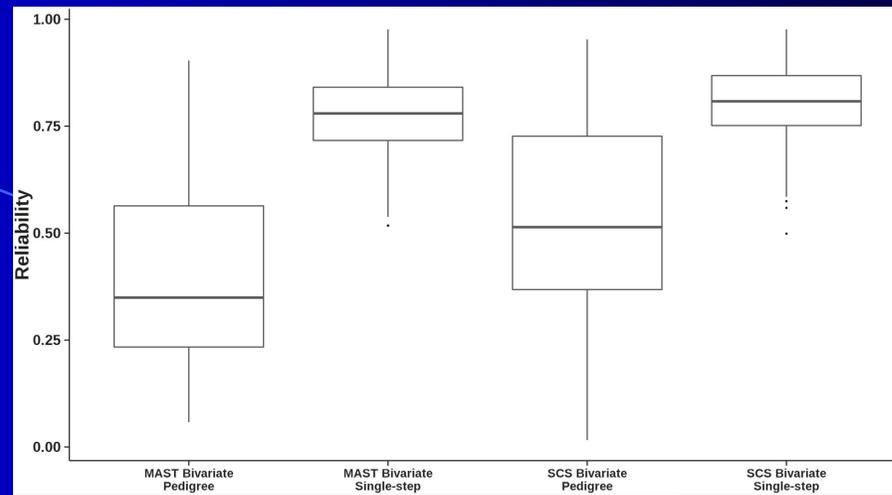
²Included 444 Holstein and 66 Jersey bulls with 10 to 200 daughters in 2008 and >500 daughters in 2012.

New algorithms improved prediction of traits, particularly for conception rates. Van Raden et al., 2014

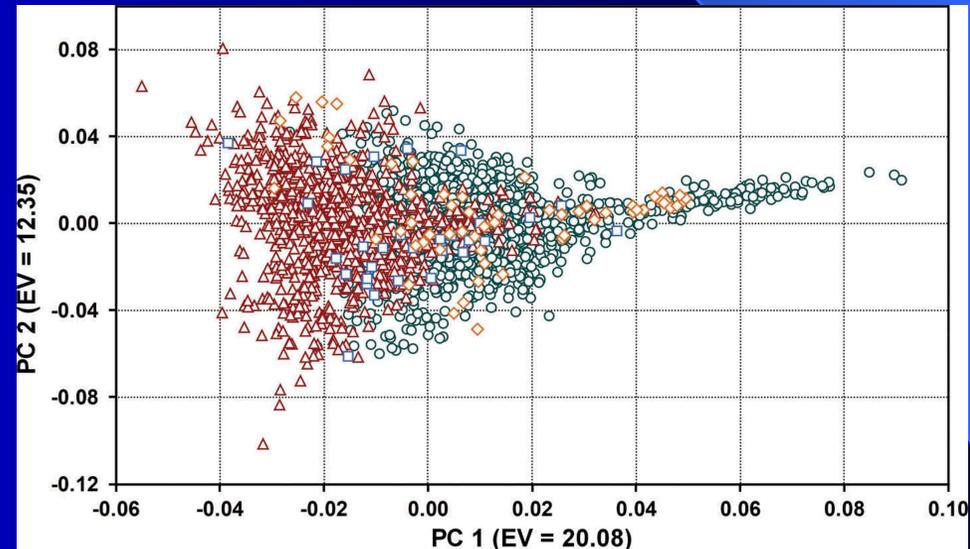
Manhattan plots for association of SNPs with Milk



Genomic decomposition of additive, dominance and imprinting effects for milk yield in Holsteins, Jiang et al., 2017.



Improvements in reliability in mastitis and somatic cell counts using genotypes in the analysis, Parker Gaddis et al., 2015



Population analysis of Guernsey cattle from different countries indicates that U.S. and other populations are distinct. 2016

Table 1. Number of SNP and overlapping genes included in *SowPro90*

SNP category	Number of SNP	Number of genes
SNP in genes and regulatory regions (RNA and genome sequencing)		
42 QTL for age at puberty (UNL)	11,474	788
222 QTL for age at puberty (USMARC)	21,490	1,500
Adaptive and immunity genes	16,271	1,015
Differentially expressed genes in hypothalamic arcuate nucleus	107	17
Upstream regulatory genes of differentially expressed genes	308	31
11 selection sweep regions for litter size	1,286	220
Structural soundness genes	607	224
Predicted loss-of-function SNP	617	376
SNP from commercial genotyping platforms		
Illumina <i>Porcine SNP60 BeadArray</i>	49,710	
Neogen <i>Porcine GGPHD Array</i>	1,012	
Affymetrix <i>Axiom PigHD Array</i>	594	
Total	103,476	4,171

UNL = University of Nebraska-Lincoln; USMARC = U.S. Meat Animal Research Center.



Affymetrix introduces Axiom Turkey Genotyping Array, developed in collaboration with the United States Department of Agriculture – Agricultural Research Service (USDA-ARS) along with Aviagen and Hendrix Genetics. December, 2015

New Affymetrix chip that includes LOF snp from Keel et al., Wijesena et al., 2019



Anticipated product: Improved bioinformatic tools for data movement, access, curation, annotation and analysis of extremely large genotypic, sequence and phenotypic data sets.

- Improved sequence data analysis
- Structural/copy number variation

Table 4. Alignment status percentages using Burrows–Wheeler alignment (BWA; Li and Durbin, 2009), SNAP,¹ or Findmap² with simulated cattle sequence

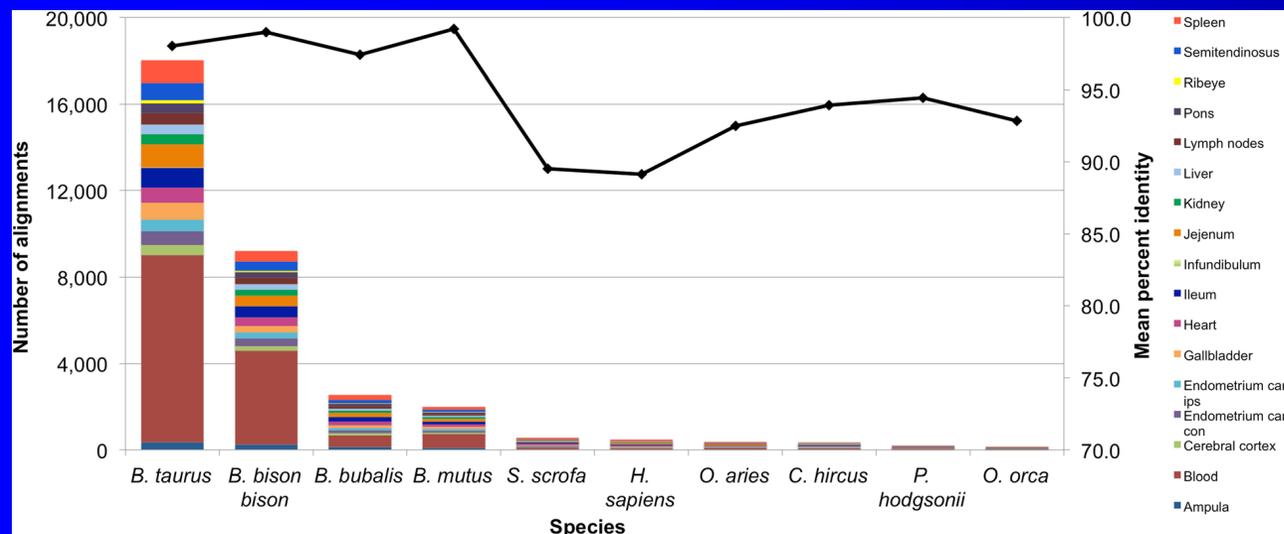
Alignment status	BWA	SNAP	Findmap
Correctly placed segments overall	90.5	92.6	92.9
Both ends of pair correctly placed	87.2	87.7	87.6
One end correct, one end wrong	6.4	10.0	10.6
Both ends wrong	6.2	2.3	1.8

¹<https://arxiv.org/abs/1111.5572>.

²<https://aipl.arsusda.gov/software/findmap/>.

Nonsynonymous SNPs display much less linkage disequilibrium when they are close to markers on the current chips, indicating that the markers chosen may not actually be very good at tracking functional SNPs

Findmap much more efficient in processing sequences for alignment and identifying SNP, Van Raden et al., 2019



An exploration of assembled, unmapped reads from RNA-seq data suggests that a single assembled reference genome may be incomplete, Whitacre et al., 2015

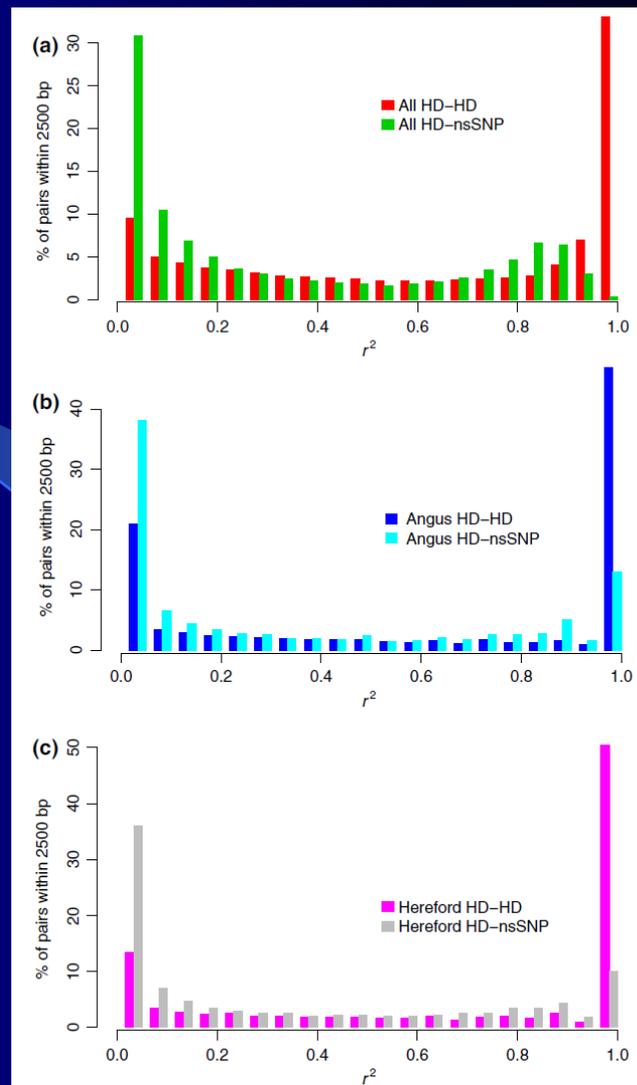
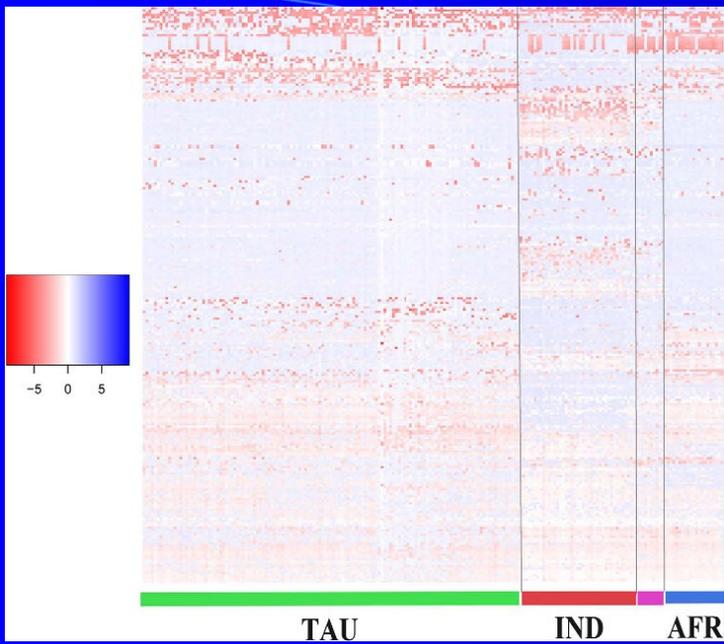
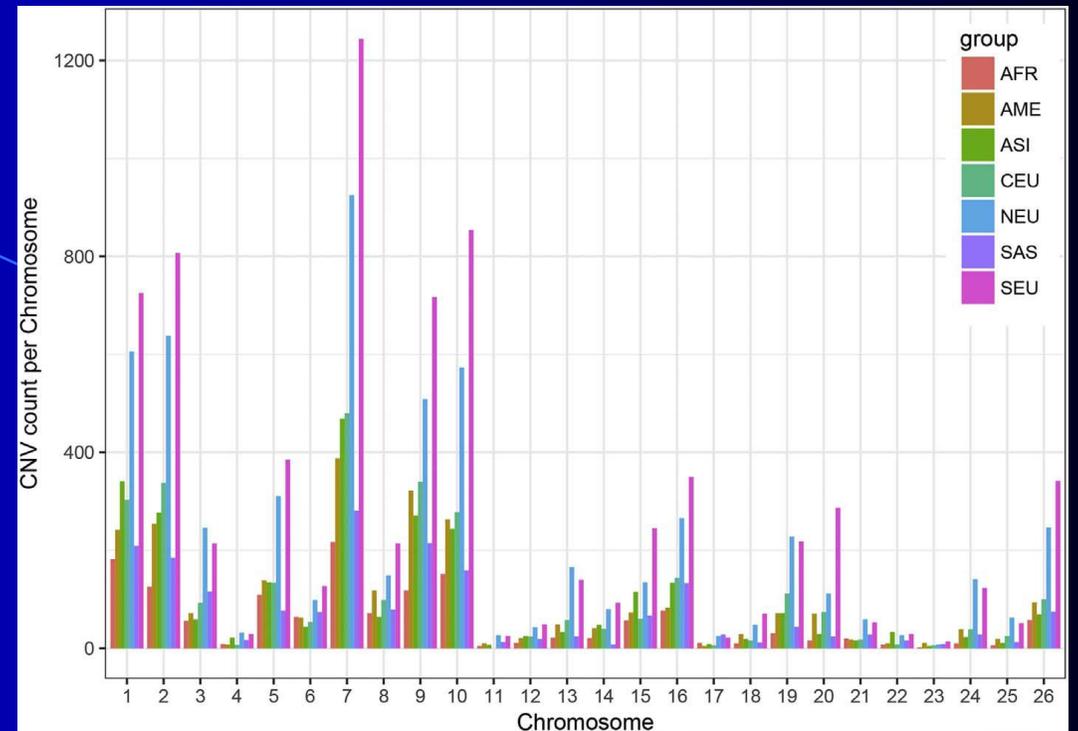


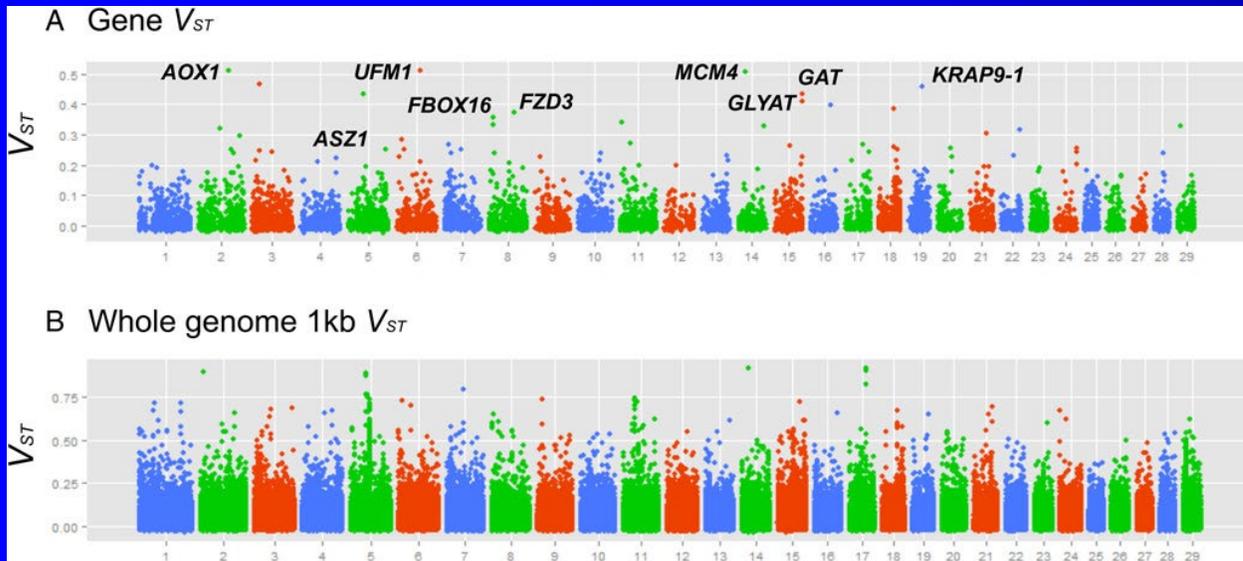
Figure 2 Distribution of linkage disequilibrium (r^2) values for BovineHD SNPs (HD) and non-synonymous SNPs (nsSNPs) separated by less than 2500 bp. Pairwise r^2 values were computed with genotypes of HD and nsSNPs called on purebred and F_1 crossbred sires of a multibreed population, using the complete set of bulls (panel a) and only purebred Angus (panel b) and Hereford (panel c) bulls.



Clear differences exist between breeds on the existence of copy number variation in cattle. Xu et al., 2016



Copy number variation in breeds of sheep, Yang et al., 2018



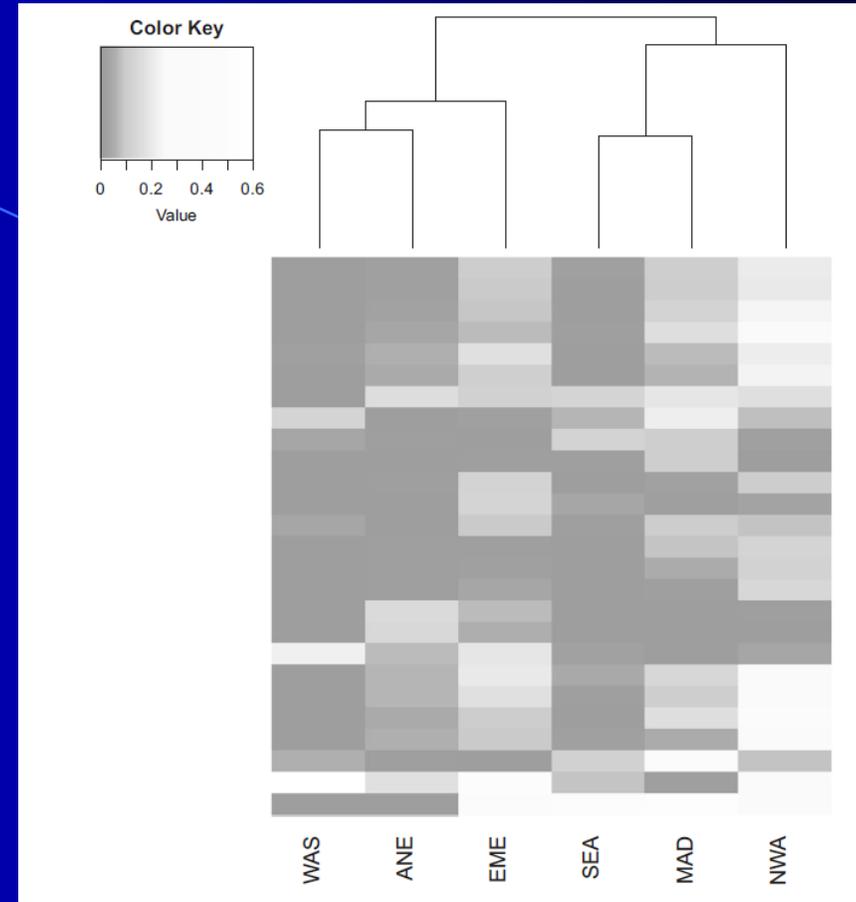
V_{st} is zero for same alleles and 1 for completely different alleles for copy number variation. As in Xu et al., different breeds of cattle clearly have differences in copy number variations and here the genes are identified, Bickhart et al., 2016

Table 1. Summary of the CNVR content of each autosome and the frequency of overlap with genes.

Chr	Length	CNVR length	Coverage	# CNVR	avg length (Kb)	# Genes	% Genes
1	315321320	36925232	0.117	59	629	44	75
2	162569373	37201656	0.229	31	1200	29	94
3	144787320	18957457	0.131	20	948	16	80
4	143465941	5322451	0.037	16	333	12	81
5	111506439	8337930	0.075	21	397	16	76
6	157765591	34634623	0.22	21	16496	16	76
7	134764509	4102732	0.03	18	228	15	83
8	148491824	19480680	0.131	20	974	14	70
9	153670195	44313723	0.288	15	2954	13	87
10	79102372	14048002	0.178	24	585	23	92
11	87690580	53738586	0.613	27	1990	23	85
12	63588570	27230880	0.428	20	1361	20	100
13	218635233	53013240	0.242	63	841	52	83
14	153851968	56829302	0.369	43	1321	36	84
15	157681620	38702927	0.245	42	921	38	90
16	86898990	30933018	0.356	33	937	29	88
17	69701580	7402936	0.106	22	336	19	86
18	61220070	4111482	0.067	7	587	5	71

doi:10.1371/journal.pone.0133529.t001

Copy number variation in pigs. Wiedmann et al., 2015



Types of CNV by pig breed, Keel et al., 2019

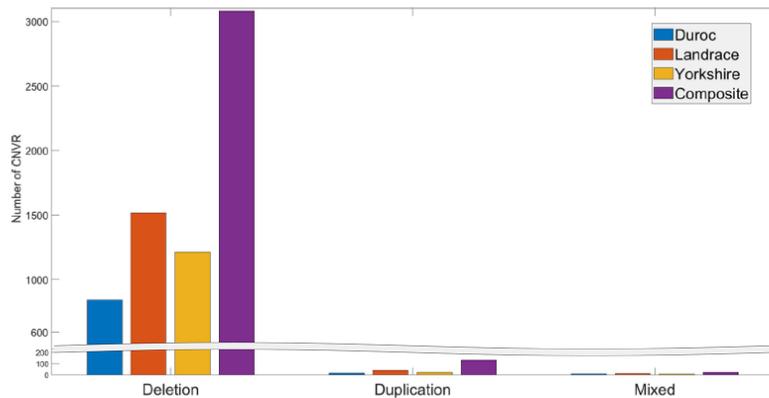


FIGURE 2 | Distribution of CNVR types across breeds.

CNV diversity in goats, Liu et al., 2019

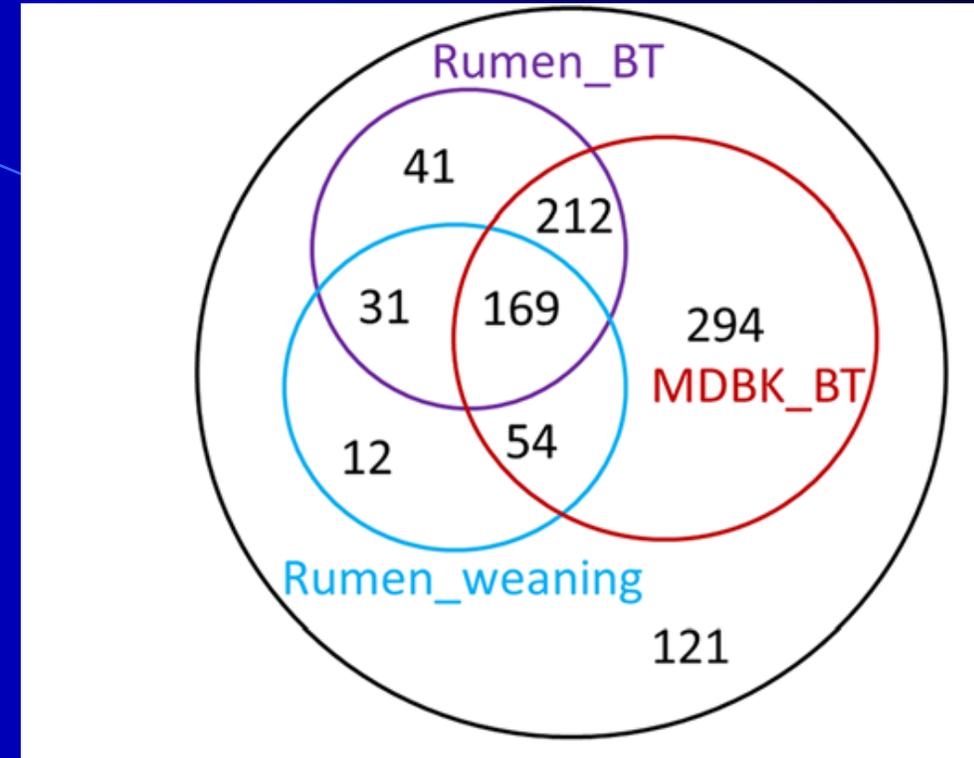
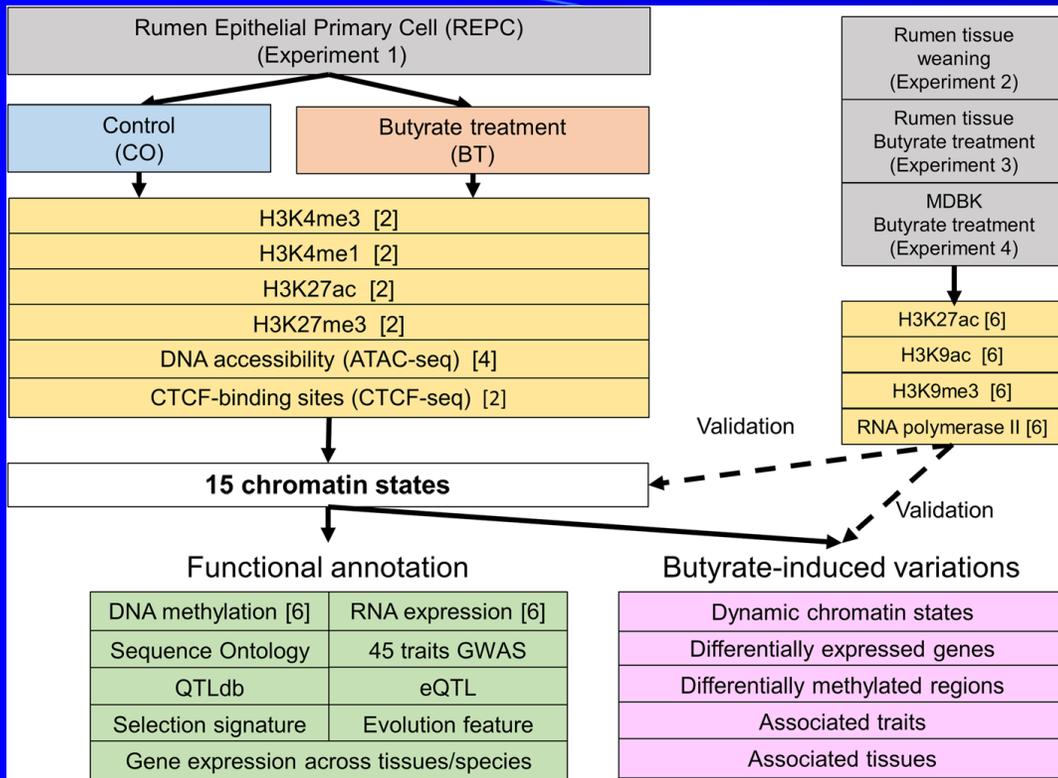
Problem Statement 2B: Characterize Functional Genomic Pathways and their Interactions

Anticipated product: Genetic prediction tools for traits in food animals related to health, production efficiencies, adaptability, and functionality in varied domestic and international production systems.

- Genes affecting ruminal maturation in dairy cattle

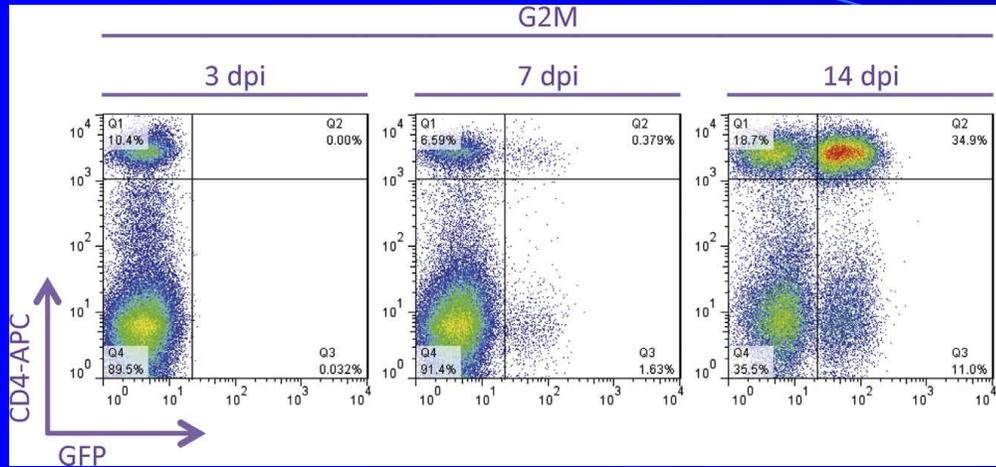
Anticipated product: Information relating the function and regulation of individual genes and their interaction with environmental and epigenetic effects contributing to economically important traits in food animals.

- Resistance to Mareks disease tumors

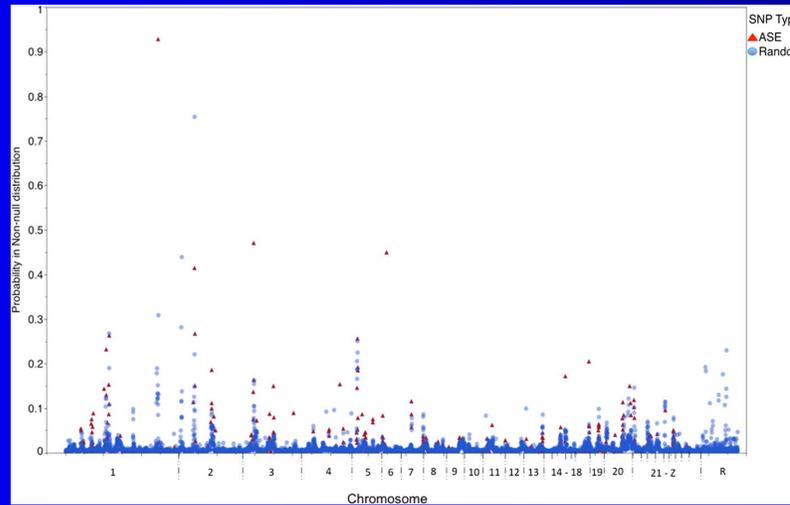
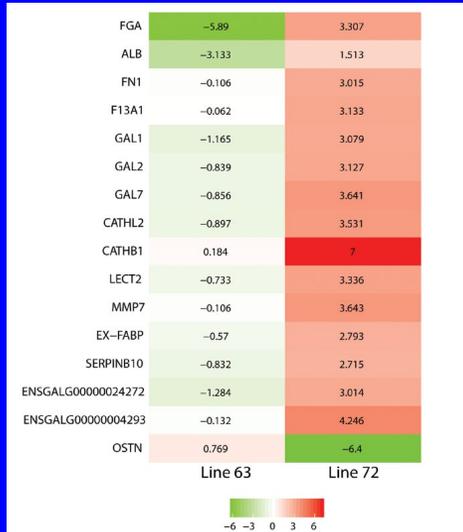
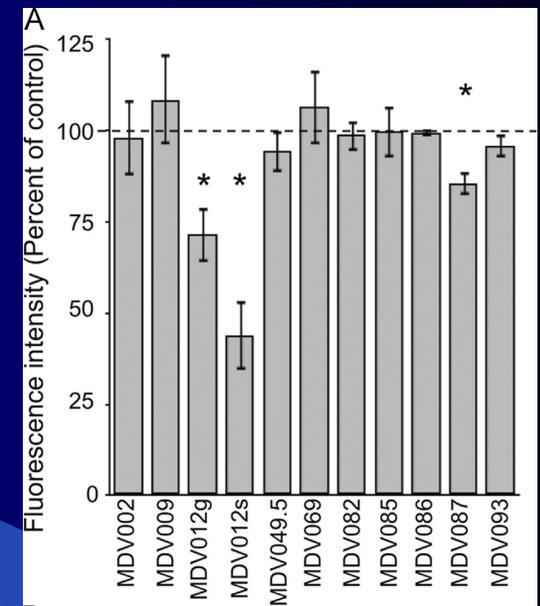


Genes that have both increased expression and changes in chromatin between rumen treated with butyrate, rumen changes after weaning, and MDBK cells treated with butyrate.
Fang et al., 2019

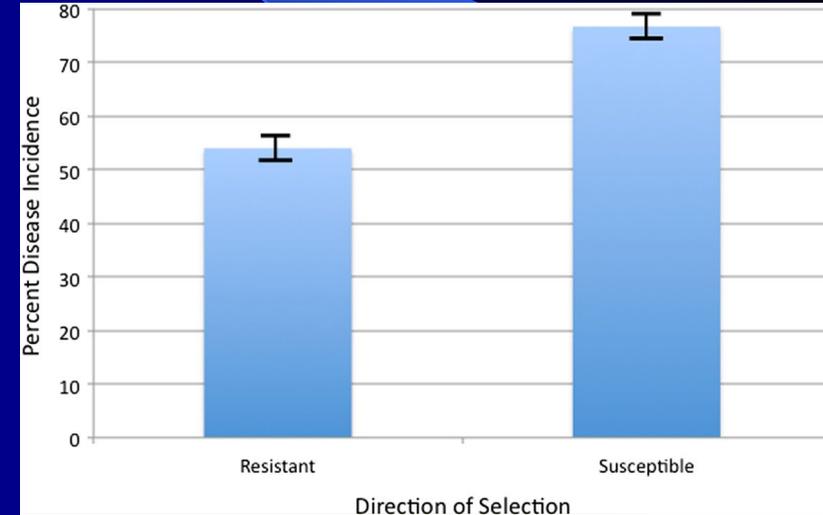
Meq oncogene expression corresponds with latency onset of Marek's virus. Meq expression transforms cells into tumors. Tai et al., 2017



MDV012 gene from Marek's disease prevents MHC class 1 antigen presentation, Hearn et al., 2015



Allele specific expression identifies many loci affecting resistance to Marek's disease when resistant and susceptible lines are mated and progeny are evaluated for resistance. Cheng et al., 2015



ASE based selection resulted in resistance differences after one generation. Cheng et al., 2015

Transcriptomic analysis between resistant and susceptible lines, Dong et al., 2017

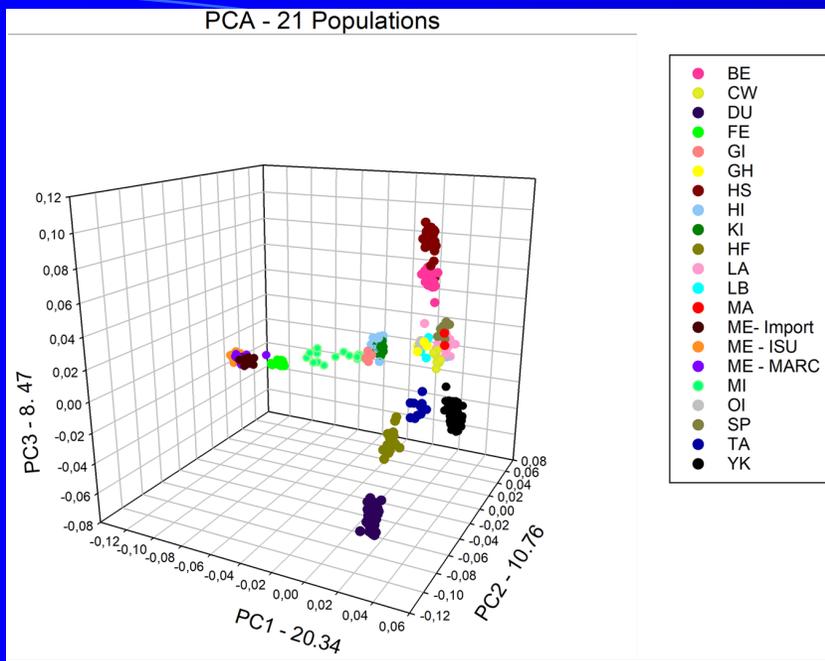
Problem Statement 2c: Preserve, Characterize and Curate Food Animal Genetic Resources

Anticipated product: A broad spectrum of genetic diversity in the form of viable and well documented livestock and poultry germplasm conserved.

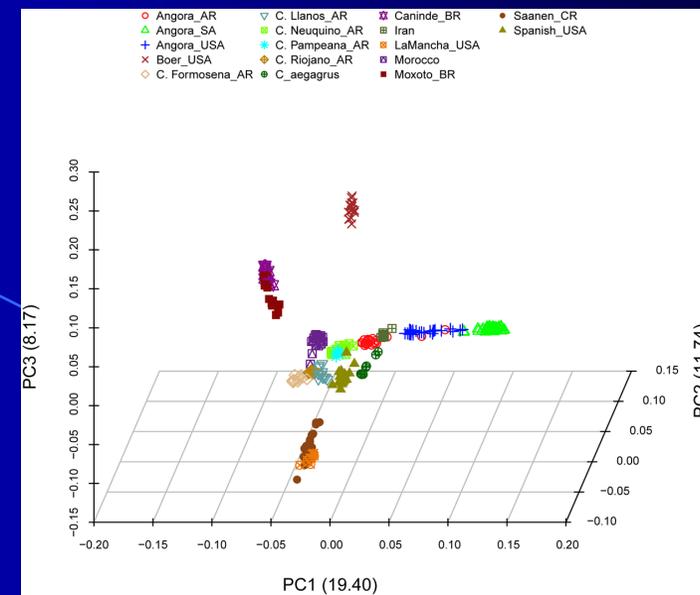
- Diversity and use of animal collection

Anticipated product: A publicly available database providing germplasm sample, phenotypic, and genomic information to industry and the research community.

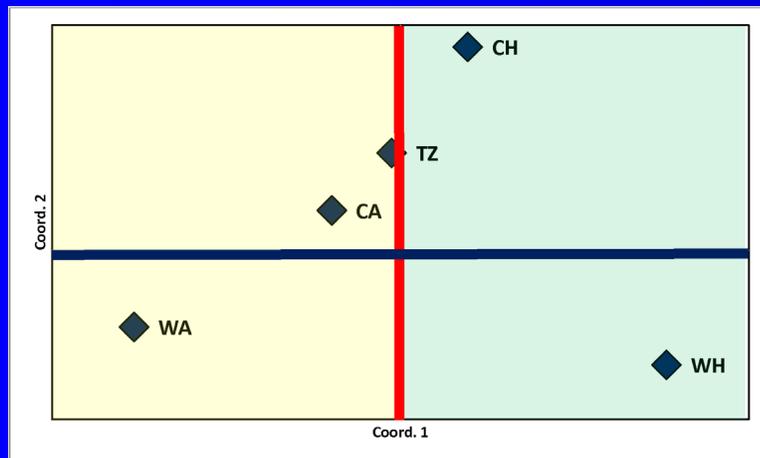
- Animal GRIN database development



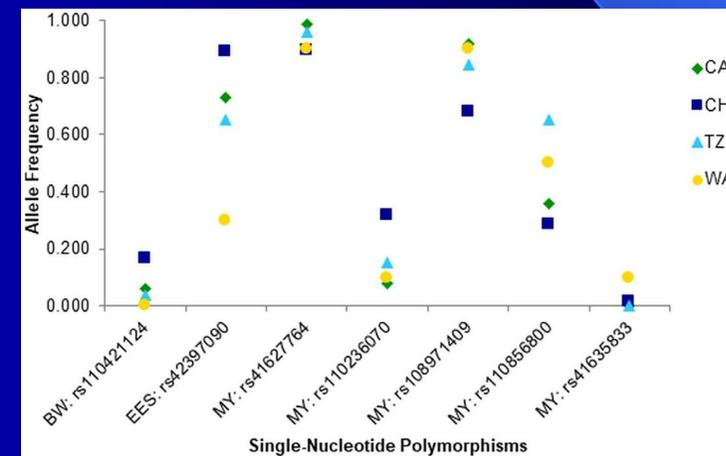
Diversity in pig breeds of samples at the NAGP, Faria et al., 2019



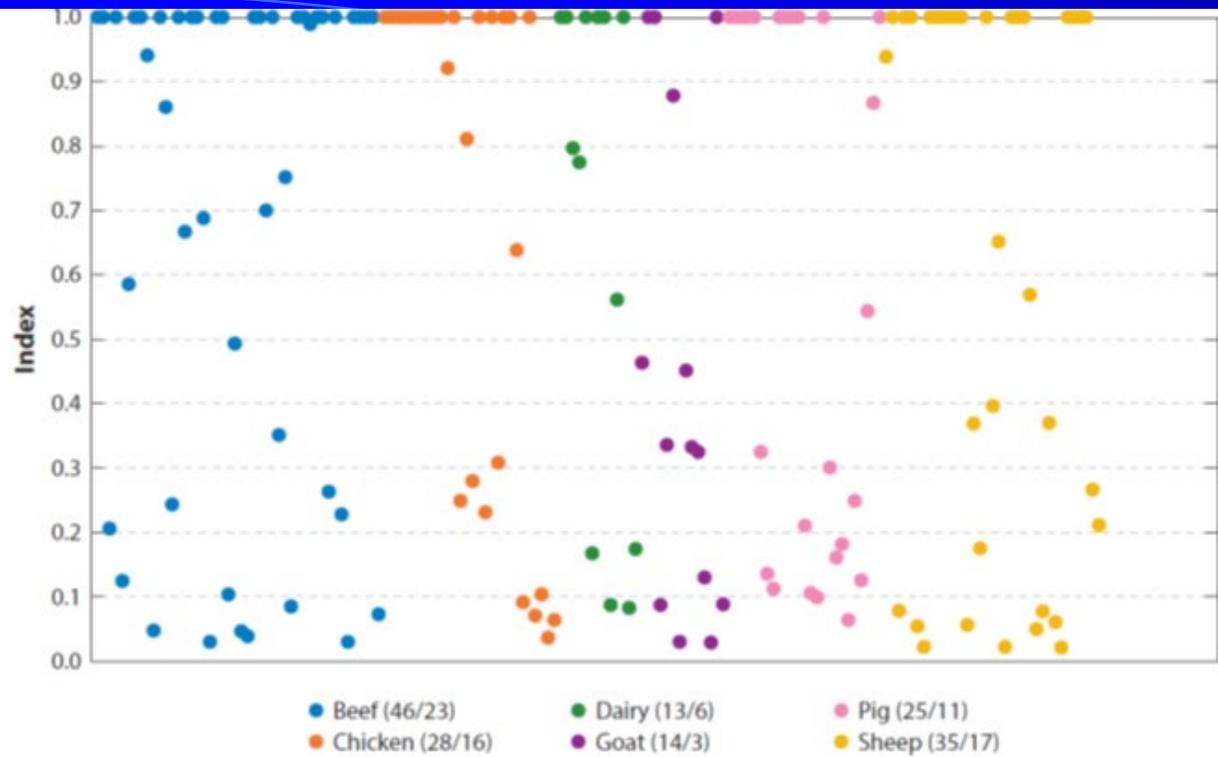
Diversity in goat breeds, Paim et al., 2018. Krehbiel et al., 2019



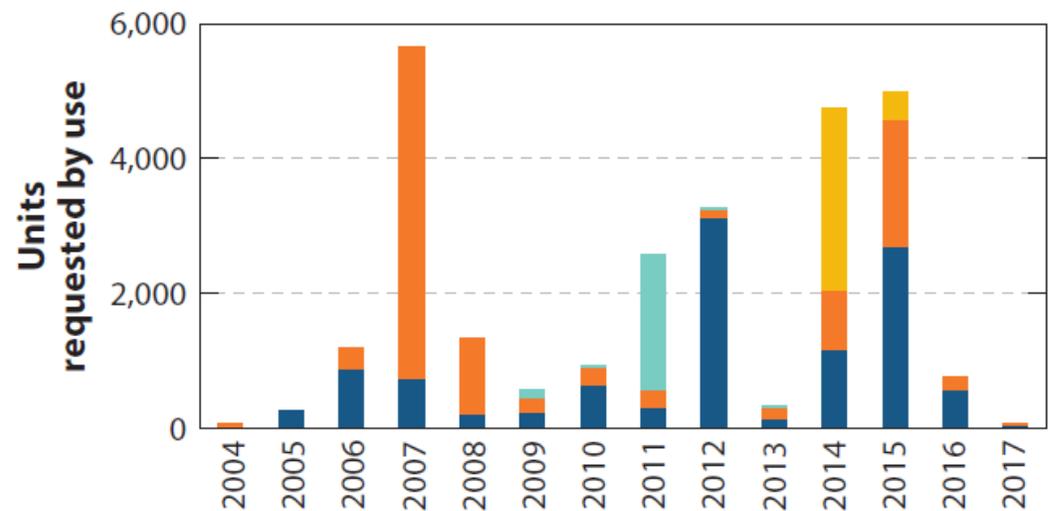
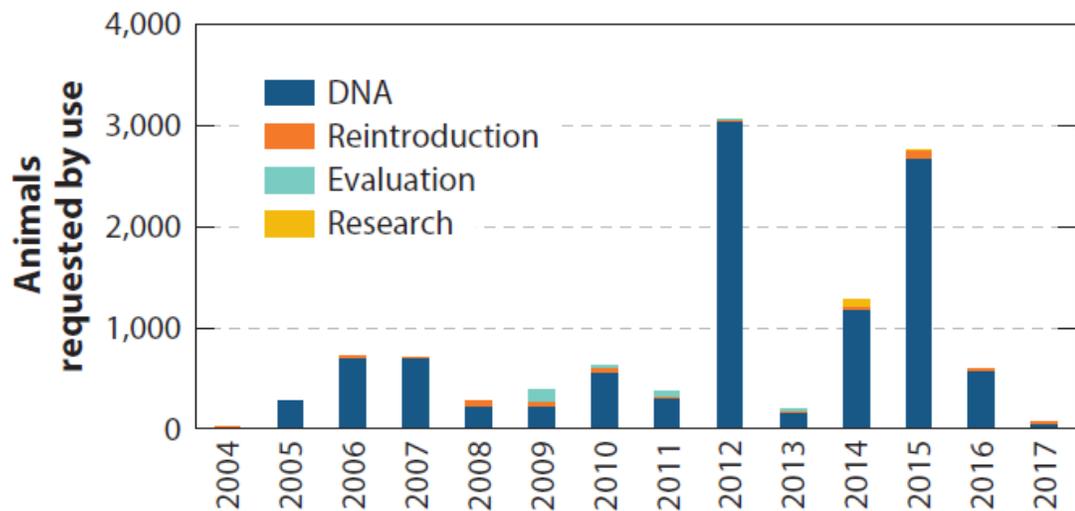
Diversity in Herefords according to climate regions, Blackburn et al., 2017



Diversity in Red Angus at specific loci in different zones of the U.S., Krehbiel et al., 2019



Completeness of collections by breed for various livestock, and use of resources for various purposes, Blackburn, 2018





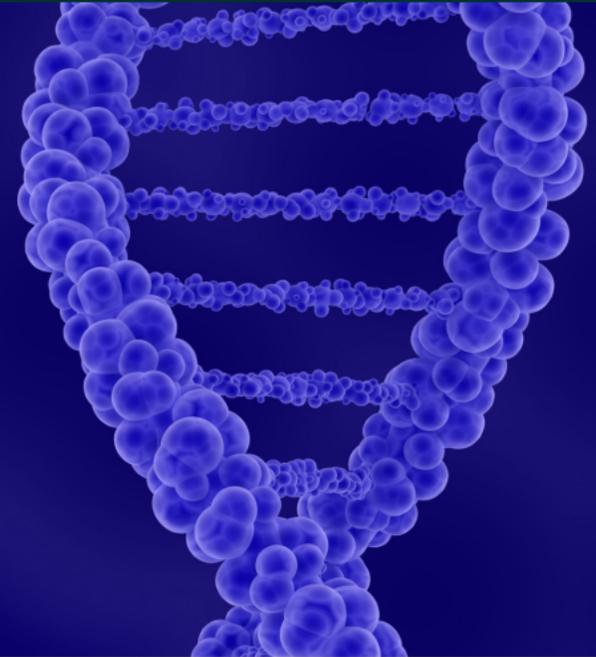
- Research
- People & Locations
- Newsroom
- Careers

National Animal Germplasm Program

- Home
- Explore Inventory
- Genomic Data
- Tools
- Germplasm Donation
- Germplasm Request
- Collection Security
- Select Country/Language

National Animal Germplasm Program

The Agricultural Research Service's National Animal Germplasm Program operates a gene bank for livestock, aquatic, poultry and insect genetic resources. Exploring these pages you will find information concerning the genetic resources collection and other issues related to genetic resources and how the program operates.



Explore Inventory

Uses a drilldown format that allows you to see the collection by species

Genomic Data Submission & Request

Allows the user to search for animals that meet their criteria in order to

Tools for Decision Support

Allows the user to search for animals that meet their criteria in order to

Germplasm Donation & Request

Provides an overview of how germplasm can be donated and

Problem Statement 2D: Develop and Implement Genetic Improvement Programs using Genomic Tools

Anticipated product: Improved genetic evaluation and genetic selection programs for the food animal industries.

- Dairy Improvements in net merit, health traits, crossbred incorporation
- Beef cattle improvements in genomic selection
- Crossbreed calving difficulty estimates
- Sheep improvements in fecundity, value of litter size in range conditions

Anticipated product: Genetic prediction tools for traits in food animals related to health, production efficiencies, adaptability, and functionality in varied domestic and international production systems.

- Age at puberty in pigs
- Inbreeding based on runs in homozygosity

Trait	Inbreeding depression/1%	Trait value in NM\$	\$ Value /1% F
Milk	-63.9	-0.004	0.3
Fat	-2.37	3.56	-8.4
Protein	-1.89	3.81	-7.2
Productive life	-0.26	21	-5.5
Somatic cell score	0.004	-117	-0.5
Daughter pregnancy rate	-0.13	11	-1.4
Cow conception rate	-0.16	2.2	-0.4
Heifer conception rate	-0.08	2.2	-0.2
Cow livability	-0.08	12	-1.0
Net merit \$	-25	1	-25

Health trait	Protein	PL	LIV	SCS	DPR	CCR	HCR
Hypocalcemia (MFEV)	0.18	0.15	0.19	-0.29*	0.003	0.01	0.02
Displaced abomasum (DA)	0.23	0.35*	0.47*	-0.13	0.32*	0.28*	0.24
Ketosis (KETO)	0.03	0.33	0.27	-0.19	0.59*	0.49*	0.07
Mastitis (MAST)	0.06	0.39*	0.22*	-0.68*	0.20*	0.21*	0.06
Metritis (METR)	0.05	0.32*	0.26*	-0.09	0.46*	0.41*	0.23*
Retained placenta (RETP)	-0.03	0.17*	0.13*	-0.10	0.14*	0.13*	0.12*

*Significant at P < 0.05

New health traits added to net merit, from the CDCB website

Net merit index adjustment for inbreeding, Van Raden et al., 2017

Crossbred EPDs for dairy cattle

April 2020 across breed base adjustment parameters

Breeding value (2*PTA) differences from Holstein

Breed	Milk	Fat	Protein	Productive Life	Somatic Cell Score	Daughter Pregnancy Rate	Heifer Conception Rate	Cow Conception Rate	Livability
Ayrshire	-5972	-194	-168	-3.6	0.06	1.5	-8.4	0.0	2.4
Brown Swiss	-4782	-131	-100	-3.8	0.19	-1.9	-9.7	-6.2	-0.8
Guernsey	-6842	-131	-179	-9.2	0.38	-0.5	-11.0	-7.6	-12.6
Jersey	-5597	-55	-94	1.9	0.40	3.9	-0.8	3.0	0.5
Milking Shorthorn	-6594	-256	-204	-3.3	0.27	3.5	-2.6	1.7	4.0

Trait means for base cows

Breed	Milk	Fat	Protein	Productive Life	Somatic Cell Score	Daughter Pregnancy Rate	Heifer Conception Rate	Cow Conception Rate	Livability
Ayrshire	19252	769	613	26.1	2.51	26.9	44.8	40.3	88.5
Brown Swiss	23060	943	774	25.9	2.51	24.7	45.9	30.8	83.2
Guernsey	17603	807	585	25.3	3.01	23.7	41.9	29.6	74.4
Holstein	28072	1077	871	27.4	2.31	31.4	55.3	38.7	85.7
Jersey	21288	1031	780	28.4	2.90	34.7	49.4	39.2	84.6
Milking Shorthorn	19113	730	597	26.6	2.88	29.1	52.0	41.8	84.9

FT Best Fit Analysis Comparisons

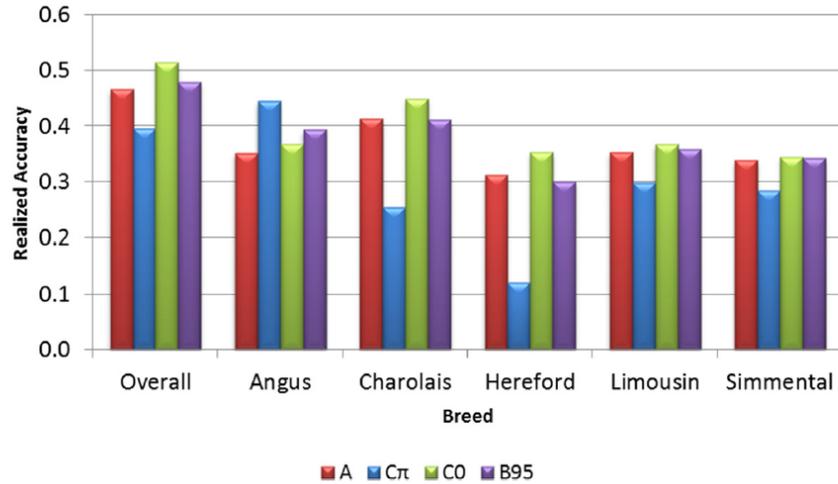


Figure 3 Mean DGV realized accuracies for FT over 20 bootstraps for BayesA (red), BayesC π (blue), BayesC0 (green) analyses, and BayesB95 (purple). An across-breed estimate of heritability from the BayesC0 analysis was used for the calculation of overall accuracy and within-breed realized accuracies were calculated from within-breed estimates of heritability obtained through GBLUP.

REA Best Fit Analysis Comparisons

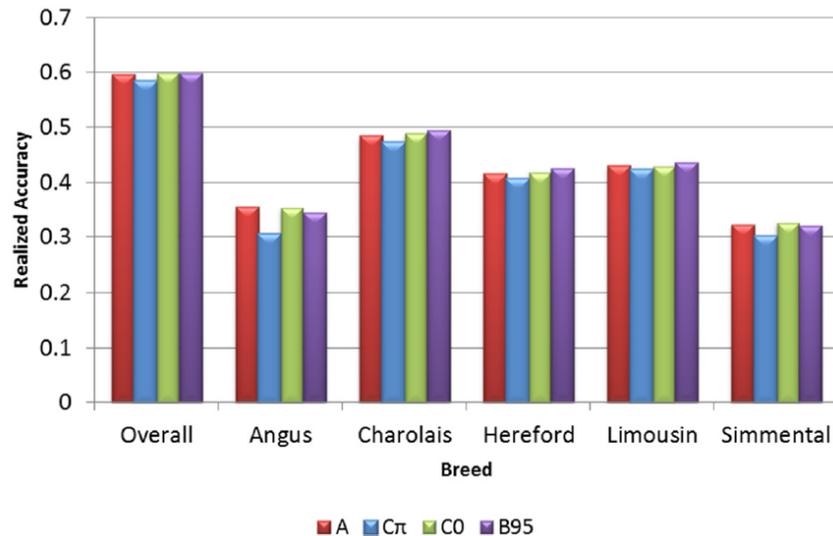


Figure 4 Mean DGV realized accuracies for REA over 20 bootstraps for BayesA (red), BayesC π (blue), BayesC0 (green) analyses, and BayesB95 (purple). An across-breed estimate of heritability from the BayesC0 analysis was used for the calculation of overall accuracy and within-breed realized accuracies were calculated from within-breed estimates of heritability obtained through GBLUP.

From Rolf et al., 2015. Comparison of accuracies of different approaches to genome selection in beef cattle. Best analyses were obtained using 60-70% training, remainder prediction population. Allowing large SNP effects provided better accuracies for traits where large SNP effects were known or expected (Fat thickness). Estimating the prior estimate of the proportion of SNPs that do not affect the trait (π) based on knowledge of the trait generally improved accuracies of estimates. Traits with large expected SNP effects did not do very well predicting across breeds when π was estimated beforehand, traits expected to better fit the infinitesimal model performed better across breed.

Table 5. Calving difficulty score direct breed differences estimated from USMARC data adjusted for sire sampling

Breed	Average base EBV		Additive genetic SD ³	BreedSoln at USMARC	BY 2012 breed difference ⁵
	Breed 2012 ¹	USMARC bulls ²		(vs. Angus) ⁴	
	(1)	(2)	(3)	(4)	(5)
Angus	-10.0	-4.1	9.4	0.00	0.00
Hereford	-1.6	8.1	8.3	0.06 (0.18)	-0.13 (0.06)
Red Angus	-8.0	-10.5	9.0	0.12 (0.26)	0.43 (0.09)
Brangus	-10.2	-9.8	8.4	-0.04 (0.60)	0.16 (0.21)
Charolais	-6.0	-3.9	14.2	0.59 (0.18)	0.76 (0.06)
Chiangus	-11.0	-14.4	7.8	0.27 (0.38)	0.64 (0.13)
Gelbvieh	-19.4	-14.2	7.8	0.17 (0.26)	0.16 (0.09)
Limousin	-18	-18.8	8.6	0.52 (0.18)	0.77 (0.06)
Maine-Anjou	-18.4	-13.7	7.8	0.40 (0.37)	0.41 (0.13)
Simmental	-18.6	-10.5	7.8	0.41 (0.20)	0.27 (0.07)

¹The average within-breed EBV for each breed for birth year 2012 as reported by each respective breed association.

²The weighted average EBV as reported by each respective breed association of bulls for each breed having descendants with records at the U.S. Meat Animal Research Center (USMARC).

³The additive genetic SD for calving difficulty direct for each breed.

⁴BreedSoln = estimated breed effect solutions (SE) from analysis of USMARC data (Z-scores) with Angus set as the base.

⁵Estimated breed effects (SE) corrected for sire sampling and reported on the USMARC scale (Z-scores) for birth year (BY) 2012. Calculations: (5) = $((4)/\sigma_a + \{(1) - (2)\}/(3)) - \{(1) - (2)\}/(3)_{Angus} \times \sigma_a$, in which σ_a is the direct additive genetic SD for calving difficulty estimated from the current analysis. Standard errors are the scaled SE from (4).

Calving difficulty score breed differences from the germplasm evaluation effort at USMARC. Ahlberg et al., 2016

Table 2. Least-squares means and SE for average numbers of lambs present at various times between birth and weaning, numbers of lambs orphaned or fostered, and weights of lambs weaned per ewe lambing by litter size and triplet-management treatment for ewes that produced single, twin, or triplet litters

Litter size and triplet management	No. of litters	No. present at:				No. orphaned or fostered	Weight weaned, kg
		3 d	14 d	30 d	Weaning		
<i>--Experiment 1--</i>							
1	81	0.98 ± 0.02 ^a	0.96 ± 0.03 ^a	0.95 ± 0.03 ^a	0.94 ± 0.03 ^a	0.00	40.4 ± 1.5 ^a
2	269	1.89 ± 0.03 ^b	1.86 ± 0.03 ^b	1.81 ± 0.03 ^b	1.77 ± 0.04 ^b	0.05 ± 0.01 ^b	58.9 ± 1.2 ^{bc}
3R ¹	94	2.08 ± 0.07 ^c	1.96 ± 0.07 ^b	1.91 ± 0.07 ^b	1.79 ± 0.07 ^b	0.76 ± 0.10 ^c	55.0 ± 2.2 ^b
3A ¹	89	2.72 ± 0.08 ^d	2.48 ± 0.08 ^c	2.25 ± 0.08 ^c	2.13 ± 0.08 ^c	0.02 ± 0.01 ^b	62.9 ± 2.2 ^c
<i>--Experiment 2, Generation 1--</i>							
1	42	0.95 ± 0.06 ^a	0.98 ± 0.07 ^a	0.91 ± 0.07 ^a	0.89 ± 0.08 ^a	0.00	36.1 ± 3.2 ^a
2	212	1.83 ± 0.04 ^b	1.74 ± 0.05 ^b	1.65 ± 0.05 ^b	1.55 ± 0.05 ^b	0.03 ± 0.01 ^a	51.4 ± 1.6 ^b
3	153	2.57 ± 0.06 ^c	2.21 ± 0.06 ^c	1.94 ± 0.06 ^c	1.65 ± 0.06 ^b	0.10 ± 0.03 ^b	50.8 ± 1.7 ^b
<i>--Experiment 2, Generation 2--</i>							
1	155	0.97 ± 0.02 ^a	0.98 ± 0.03 ^a	0.96 ± 0.03 ^a	0.96 ± 0.03 ^a	0.00	41.2 ± 1.3 ^a
2	644	1.92 ± 0.02 ^b	1.91 ± 0.02 ^b	1.88 ± 0.02 ^b	1.81 ± 0.02 ^b	0.01 ± 0.01 ^a	59.3 ± 0.7 ^b
3	164	2.60 ± 0.04 ^c	2.38 ± 0.04 ^c	2.20 ± 0.04 ^c	1.93 ± 0.04 ^c	0.06 ± 0.03 ^b	57.7 ± 1.3 ^b

¹Ewes with triplet lambs were either required to rear all their lambs (A) or had their litters reduced to 2 lambs (R).

^{abc}Means within a row with different superscripts differ ($P < 0.05$) based on the Tukey-Kramer mean-separation procedure.

Tests of various crossbred sheep at USSES indicated that range conditions cannot support a lambing rate much beyond 2 lambs per ewe. Triplets can be fostered, but triplets still have increased mortality and reduced weaning weights. In addition, litter sizes of ewes from triplet litters themselves have reduced fecundity.

Table 5. Least-squares means and SE for effects of litter size and triplet management on performance of Polypay replacement ewe lambs in Exp. 1

Item	Litter size and triplet management ¹			
	1	2	3R	3A
Percentage retained, 2007 ²	83.5 ± 10.7 ^{ab}	88.8 ± 3.3 ^a	66.9 ± 6.9 ^b	81.0 ± 6.7 ^{ab}
Percentage retained, 2008 ²	5.3 ± 5.2 ^a	36.6 ± 4.6 ^{ab}	57.6 ± 9.2 ^b	46.7 ± 6.9 ^b
Fleece weight, kg ³	2.67 ± 0.15 ^a	2.07 ± 0.04 ^b	1.95 ± 0.06 ^{bc}	1.86 ± 0.06 ^c
Percentage that lambed	91.1 ± 8.5	76.6 ± 3.8	71.1 ± 5.9	64.4 ± 6.7
Litter size	1.72 ± 0.46	1.48 ± 0.12	1.41 ± 0.19	1.33 ± 0.20

¹Ewes with triplet lambs were either required to rear all their lambs (A) or had their litters reduced to 2 lambs (R).

²Percentage of weaned ewe lambs retained as replacements. The total percentages retained were 82.1% in 2007 and 41.1% in 2008.

³In February, at approximately 10 mo of age.

^{abc}Means within a row with different superscripts differ ($P < 0.05$) based on the Tukey-Kramer mean-separation procedure.

Table 2 Most significant QTL for age at puberty in pigs

SSC	Start ¹	End ¹	Marker 1	Marker 5	GenVar (%)	Rank ²	p-value	-log(p)	Gene	Human trait or function
12	14,910,939	15,006,310	M1GA0016274	ASGA0053410	9.7332	1	0.0001	4.000	GH1	growth/height ←
6	68,823,187	68,890,361	ASGA0091283	ALGA0035583	0.3064	35	0.001	3.000	TMEM51	
1	291,202,322	291,277,150	ALGA0009830	M1GA0001507	0.6121	10	0.003	2.523	BRINP1	
3	26,517,667	26,631,496	MARCD007734	ALGA0018104	0.5091	15	0.003	2.523	GPR139	
7	43,190,587	43,400,560	ALGA0040857	ASGA0033098	0.1673	75	0.003	2.523	UBR2	obesity
7	75,121,635	75,460,294	INRA0026429	HBGA0022045	7.1362	2	0.003	2.523	C14orf23, PRKD1	BM/obesity ←
15	42,527,231	43,052,985	H3GA0044224	ALGA0114567	1.7467	3	0.003	2.523	ANGPT2	ovulation
3	11,143,547	11,286,978	H3GA0008684	ASGA0013430	0.5400	13	0.004	2.398	GTF2IRD1	
9	142,232,369	142,338,853	ASGA0044888	ASGA0044901	1.4283	4	0.004	2.398	SMYD2	
10	18,347,386	18,665,600	ASGA0046792	DRGA0010326	0.3992	24	0.004	2.398	SDCCAG8	obesity
3	11,960,567	12,093,180	ALGA0017578	ALGA0017611	1.0870	6	0.005	2.301	GATSL2	
14	138,428,984	138,850,067	DRGA0014684	ALGA0082115	0.4572	19	0.005	2.301	SLC18A2	dopamine transport
1	121,626,075	121,978,687	M1GA0001099	ASGA0004239	0.4196	21	0.006	2.222	RORA	menarche
3	21,596,232	22,794,763	ASGA0013855	ASGA0094123	0.1765	70	0.006	2.222	AQP8	menarche
3	27,054,931	27,208,960	MARCD085816	ALGA0124353	1.1368	5	0.006	2.222	GPRC5B	BM/obesity
6	127,194,648	127,655,907	MARCD001714	ASGA00029572	0.3900	25	0.006	2.222	ACADM	metabolite levels
15	148,542,045	148,722,557	ASGA0071543	ASGA0071569	0.1564	83	0.007	2.155	HUURP	
8	15,600,021	15,671,195	DRGA0008334	ASGA0037920	0.2543	41	0.008	2.097	SLIT2	
8	109,067,052	109,213,652	H3GA0025237	MARCD017963	0.2658	39	0.008	2.097	TRPC3	
11	55,668,610	55,844,999	ALGA0062350	ALGA0062355	0.3136	34	0.008	2.097	RNF219	
16	44,362,264	44,481,215	ALGA0090494	MARCD073104	0.2123	50	0.008	2.097	IPO11	
18	50,837,228	51,030,054	DRGA0017050	ASGA0105879	0.5142	14	0.008	2.097	SNX10	visceral adipose tissue
2	133,313,068	133,376,955	INRA0009763	MARCD038747	0.2935	36	0.009	2.046	ZNF608	BM/obesity
10	40,710,979	40,868,229	MARCD038064	ALGA0058443	0.0985	149	0.009	2.046	LINGO2	BM/obesity
15	142,893,866	142,992,475	MARCD112236	ALGA0087841	0.3401	29	0.009	2.046	KPNA4	
2	157,110,989	157,223,320	MARCD039166	M1GA0003373	0.2571	40	0.01	2.000	ABLIM3	
2	157,270,386	157,362,402	H3GA0008275	ALGA0017005	0.4738	17	0.01	2.000	AFAP1L1	obesity

¹Start and End refer to SNP position in *Sus scrofa* Build 10.2²Windows are ranked by % genetic variance

A couple of large variance loci for age at puberty in pigs. GH1 and PRKD1 genes are nearest to the loci, affecting growth and fat deposition. Nonneman et al., 2016

Table 5. Correlations between pedigree- and genomic-based inbreeding coefficients using genotyped animals

Inbreeding ¹	Correlation	CI ²
(F_{PED}, F_{GRM})	0.250	0.183 to 0.314
$(F_{PED}, F_{GRM0.5})$	0.434	0.376 to 0.490
(F_{PED}, F_{ROH})	0.661	0.620 to 0.700
$(F_{GRM}, F_{GRM0.5})$	0.804	0.777 to 0.827
(F_{GRM}, F_{ROH})	0.567	0.518 to 0.613
$(F_{GRM0.5}, F_{ROH})$	0.827	0.804 to 0.848

¹Pairwise correlation between different measures of inbreeding: F_{PED} = pedigree-based inbreeding; F_{GRM} = genomic relationship matrix (GRM)-based inbreeding using estimated allele frequencies; $F_{GRM0.5}$ = GRM-based inbreeding with allele frequencies fixed at 0.5; F_{ROH} = runs of homozygosity-based inbreeding.

²CI = 95% confidence interval.

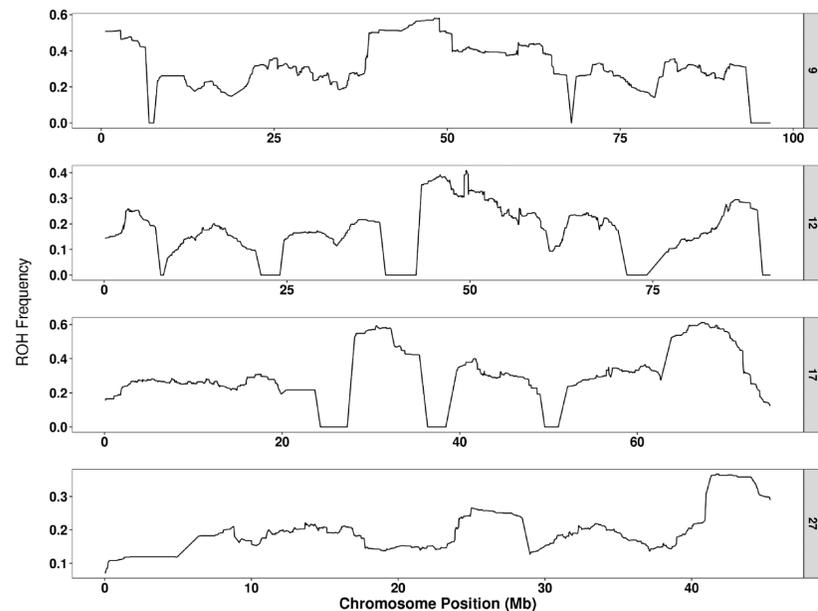


Figure 6. Frequency of ROH segments along chromosomes 9, 12, 17, and 27.

Data from Line 1 Herefords. Only some regions of homozygosity contribute to inbreeding depression. Others may be fixed long term and may not be detrimental. From Sumreddee et al., 2018

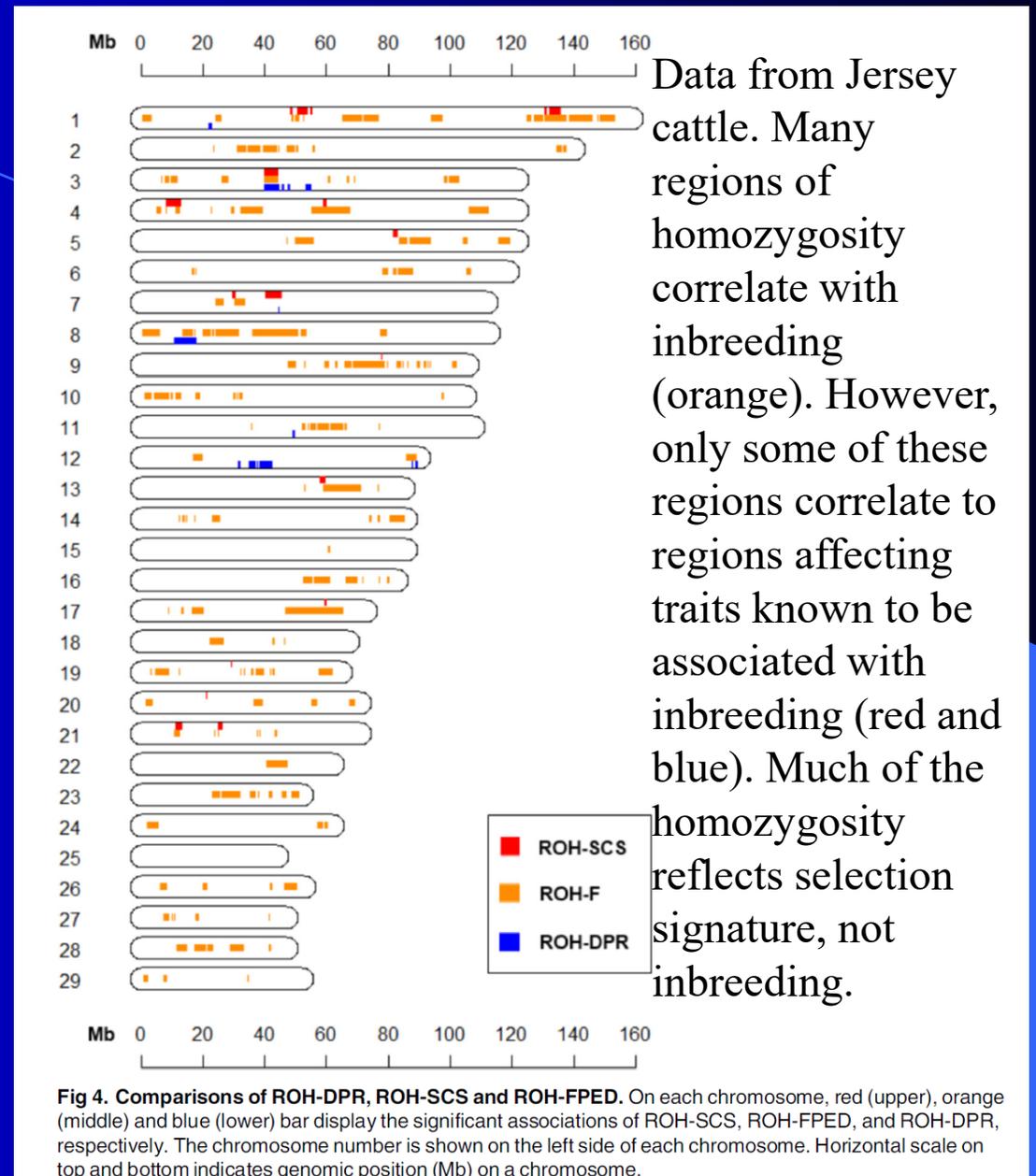


Fig 4. Comparisons of ROH-DPR, ROH-SCS and ROH-FPED. On each chromosome, red (upper), orange (middle) and blue (lower) bar display the significant associations of ROH-SCS, ROH-FPED, and ROH-DPR, respectively. The chromosome number is shown on the left side of each chromosome. Horizontal scale on top and bottom indicates genomic position (Mb) on a chromosome.

Data from Jersey cattle. Many regions of homozygosity correlate with inbreeding (orange). However, only some of these regions correlate to regions affecting traits known to be associated with inbreeding (red and blue). Much of the homozygosity reflects selection signature, not inbreeding.



Anticipated product: Development of DNA-based diagnostics to provide genotypic information for use in centralized genetic evaluation and improvement systems particularly for novel traits.

- GWAS for number of vertebrae in pigs

Table 1 Descriptive statistics for phenotypic data analyzed in the study. Genomic variation is the amount of phenotypic variation associated with genotypic data and genomic heritability is the ratio of genomic to phenotypic variation

Trait	Mean	Range	Genomic Variation	Phenotypic variation	Genomic heritability
Thoracic vertebrae (RIB)	15.42	14 to 17	0.0203	0.1258	0.1610
Lumbar vertebrae (LVN)	6.12	4 to 8	0.0200	0.1656	0.1202
Thoracolumbar vertebrae (TLV)	21.55	19 to 23	0.0405	0.1677	0.2412
Kyphosis	0.33	0 to 3	0.0699	0.4222	0.1655

Table 2 Results from GWAS for vertebral traits including chromosome, one megabase window and percent of genomic variation associated with the one megabase window for all significant associations (>1.0 %). Significant regions which were also suggestive (>0.4 %) for other traits are also listed. Potential candidate genes are presented in the last column

Chromosome	Mb	Thoracic variation	Lumbar variation	Thoracolumbar variation	Potential candidate gene symbol
6	99	8.99		2.38	GATA6
12	24			10.26	HOXB
12	26		8.59	4.76	COL1A1
12	27			3.66	CHAD
12	34			6.21	MSI2
16	18		4.80		CDH6
16	19			3.80	C5orf22
16	29		8.26		FGF10

Number of vertebrae in pigs varies, changing the body conformation of the pig (loin and bacon). Chromosomal regions were identified that controlled the variation of this trait. Rohrer et al., 2015



Problem Statement 2E: Improved Techniques for Genetic Modification and Genetic Engineering of Food Animals

Anticipate product: Programs to evaluate specific DNA modification techniques (i.e., Gene editing) to determine the effects of natural mutations and rationally designed modifications on economically important traits in food animals.

- Development of universal boars

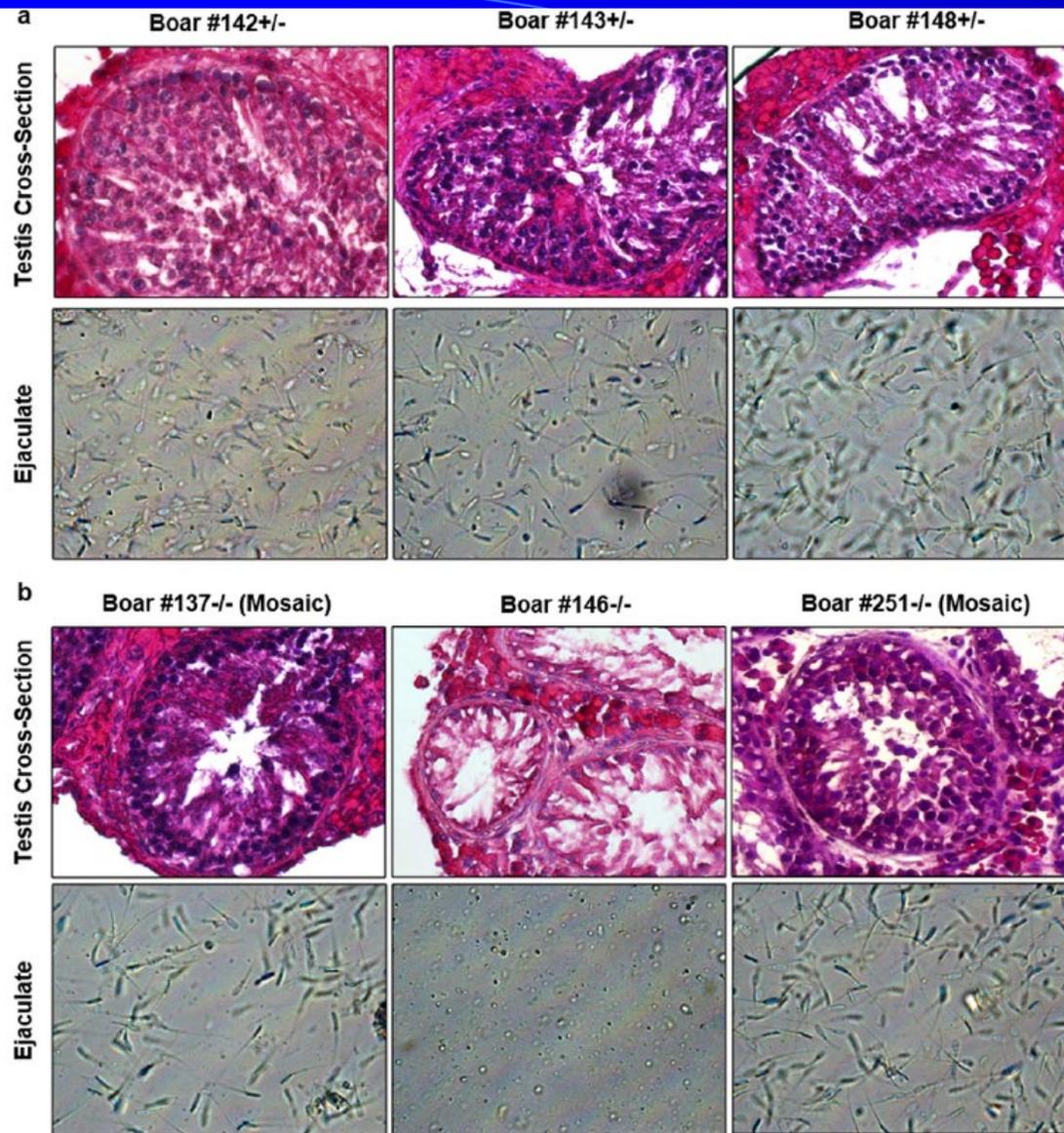


Figure 3. Testicular phenotype of NANOS2 gene edited male pigs. (a and b) Representative images of cross-sections from testicular parenchyma (upper panels) and ejaculates (lower panels) from NANOS2 mono-allelic (a) and bi-allelic (b) edited pigs at adulthood (6–8 months of age). Note that the cross-section of testicular tissue from bi-allelic knockout pig #146 lacks germline and the ejaculate is devoid of sperm.

NANOS2 deleted boars lack stem cells and do not generate viable sperm. Boars like this can be used to transfer stem cells from high genetic value boars to generate sperm. The blood testis-barrier prevents tissue rejection. Park et al., 2017

Component 3: Measuring and Enhancing Product Quality and Enhancing the Healthfulness of Meat Animal Products

Problem Statement 3a: Systems to Improve Product Quality and Reduce Variation in Meat Animal Products

Anticipated Product: Better understanding of the biological mechanisms that control and influence meat product quality, color stability and consistency.

- Lean color stability in beef
- Ham halo effect

Anticipate product: Identification of supply chain critical control points which can be targeted for increasing product quality.

- Pork loin grading camera

Table 2. Least squares means and SEM for longissimus lumborum slice shear force, sensory tenderness, and juiciness ratings of lean color classes

Degree ¹	Slice shear force ²		Tenderness ³		Juiciness ³	
	Mean	SEM	Mean	SEM	Mean	SEM
Severe DC	16.6 ^b	1.12	6.5 ^a	0.11	5.9 ^a	0.10
Moderate DC	19.2 ^b	1.12	6.1 ^b	0.11	5.7 ^b	0.09
Mild DC	22.8 ^a	1.12	5.2 ^c	0.11	5.4 ^c	0.09
Shady DC	25.2 ^a	1.12	4.7 ^e	0.11	5.2 ^d	0.10
Normal	17.6 ^b	0.76	5.0 ^d	0.07	5.3 ^d	0.08

^{a-e}Means lacking a common superscript within a column are different ($P < 0.05$).

¹DC = dark cutter.

²Expressed in kilograms.

³1 = extremely tough/dry; 2 = very tough/dry; 3 = moderately tough/dry; 4 = slightly tough/dry; 5 = slightly tender/juicy; 6 = moderately tender/juicy; 7 = very tender/juicy; 8 = extremely tender/juicy.

Dark cutters are unacceptable to consumers, even though results show these steaks are more tender and juicy than regular meat. McKeith et al., 2016

Table 4

Least squares means (standard error) for biochemical traits of longissimus lumborum from carcasses classified by dark cutting severity.

Dark cutter classification	Protein solubility, %	Mitochondrial abundance ¹	Myoglobin, mg/g	Protein carbonyls ² , μmol/mg	Electron loss ³	Bloomed Omb ⁴ , %	Initial MMB ⁵ , %
Control ⁶	21.12 ^b (0.48)	0.60 ^d (0.01)	4.36 ^c (0.10)	2.18 (0.17)	11.02 ^b (5.35)	91.54 ^a (1.08)	70.60 ^a (0.93)
Shady ⁷	22.77 ^a (0.56)	0.60 ^{cd} (0.01)	4.78 ^a (0.14)	2.30 (0.24)	19.91 ^a (5.97)	79.56 ^b (1.40)	59.47 ^b (1.07)
Mild ⁸	23.43 ^a (0.56)	0.61 ^c (0.01)	4.91 ^a (0.14)	2.20 (0.24)	18.33 ^a (6.00)	72.97 ^c (1.40)	55.78 ^c (1.07)
Moderate ⁹	22.91 ^a (0.56)	0.63 ^b (0.01)	4.68 ^{ab} (0.14)	2.21 (0.24)	17.84 ^a (5.89)	67.07 ^d (1.40)	51.25 ^d (1.07)
Severe ¹⁰	22.94 ^a (0.56)	0.64 ^a (0.01)	4.46 ^{bc} (0.14)	2.60 (0.24)	18.66 ^a (5.85)	63.25 ^c (1.40)	49.35 ^e (1.07)
$P > F$	<0.001	<0.001	<0.001	0.38	0.007	<0.001	<0.001

^{abcd}Least squares means, within a column, lacking common superscripts, differ ($P < 0.05$).

¹ Ratio of abundance of mitochondrial DNA to abundance of genomic DNA detected by real-time PCR.

² Carbonyls detected in the sarcoplasmic fraction.

³ Electrons lost during incubation with succinate as an energy substrate. Reactive oxygen species were converted to H₂O₂. Data are expressed as the percentage increase in fluorescence units.

⁴ Percentage of surface myoglobin present in the oxymyoglobin state following 2 h at 4 °C exposed to atmospheric oxygen.

⁵ Percentage of surface myoglobin in the metmyoglobin state following incubation in 0.3% NaNO₂ at 20 °C for 30 min.

⁶ n = 160 for all variables except electron loss; n = 91 for electron loss.

⁷ n = 40 for all variables except electron loss; n = 20 for electron loss.

⁸ n = 40 for all variables except electron loss; n = 19 for electron loss.

⁹ n = 40 for all variables except electron loss; n = 22 for electron loss.

¹⁰ n = 40 for all variables except electron loss; n = 24 for electron loss.

Dark Cutters are associated with greater mitochondria and less oxy and met myoglobin, contributing to their poor acceptance by consumers.

Table 3

Functional roles of the differentially abundant sarcoplasmic proteins in color-stable and color-labile beef *Longissimus lumborum* steaks.

Spot ^a	Protein	Function	Over-abundant category	Spot ratio
1	Phosphoglucosmutase-1	Glycolytic enzyme	Color-stable	1.8 ^b
2	Phosphoglucosmutase-1	Glycolytic enzyme	Color-stable	2.1 ^b
3	Glyceraldehyde-3-phosphate dehydrogenase	Glycolytic enzyme	Color-stable	1.9 ^b
4	Glyceraldehyde-3-phosphate dehydrogenase	Glycolytic enzyme	Color-stable	2.0 ^b
5	Glyceraldehyde-3-phosphate dehydrogenase	Glycolytic enzyme	Color-stable	2.4 ^b
6	Pyruvate kinase M2	Glycolytic enzyme	Color-stable	1.7 ^b
7	Creatine kinase M-type	ATP regeneration	Color-stable	1.8 ^b
8	Myosin regulatory light chain 2	Muscle contraction	Color-stable	2.4 ^b
9	Myosin light chain 1/3	Muscle contraction	Color-stable	2.0 ^b
10	Adenylate kinase isoenzyme 1	Adenosine phosphate metabolism	Color-labile	1.6 ^c
11	Phosphatidylethanolamine-binding protein 1	Signaling	Color-labile	1.7 ^c
12	Myoglobin	Oxygen transport	Color-labile	2.3 ^c

^a Spot number refers to the numbered spots in gel image (Fig. 1).

^b Spot ratio of color-stable/color-labile.

^c Spot ratio of color-labile/color-stable.

Color stability is associated with increased glycolytic enzymes in the meat (Canto et al., 2015).

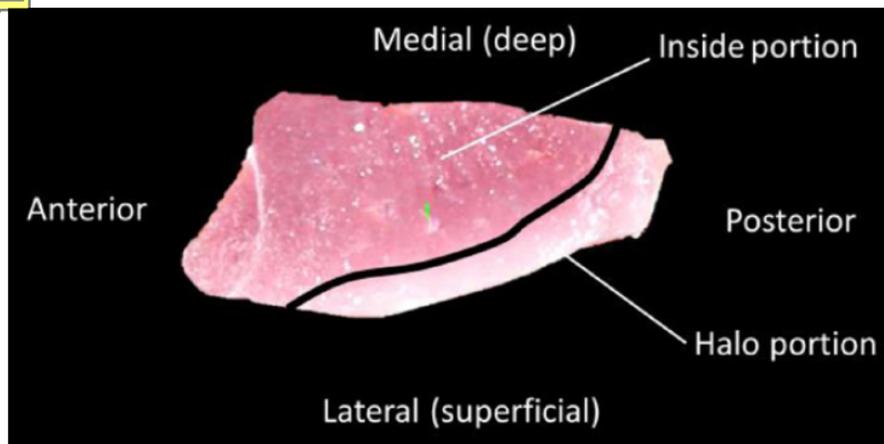


Figure 1. Picture of pork *biceps femoris* cross-section depicting the halo condition. Picture is of slice 6 of a muscle with a severe halo. Black curve depicts approximate separation during dissection between the halo sample and the sample of the unaffected portion.

Recently a ham “halo” effect was described, where regions of hams were pale compared to the remainder, which were rejected by consumers. Subsequent studies indicated lack of myoglobin in regions affected by the halo, and a GWAS analysis provided markers associated with myoglobin content

Table 1. Least-squares means for color traits, pH, and myoglobin concentration for the inside (medial) and halo (lateral) portions of pork biceps femoris muscles

Location	L^*	a^*	b^*	Hue angle	Chroma	pH	Myoglobin, mg/g
Inside	53.09	23.2	18.46	35.43	29.66	5.70	1.97
Halo	63.42	15.34	15.42	41.75	21.77	5.53	0.85
SEM	0.2	0.13	0.1	0.13	0.16	0.01	0.02
$P > F$	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001	< 0.001

King et al., 2018

Table 1. Windows identified in the GenSel analysis that explain at least 1.0% of genetic variation in myoglobin concentration

Chromosome	Position ¹ , Mb	% of genetic variance explained	Number of SNPs	Frequency of iterations with, $P > 0$
7	4	36.97	9	0.89
16	77	5.98	3	0.24
X	11	4.66	4	0.20
14	146	4.52	2	0.19
14	82	2.03	3	0.11
14	108	2.03	3	0.10
4	14	1.59	4	0.08
1	86	1.51	3	0.07
15	141	1.40	5	0.08
14	54	1.19	3	0.06
1	140	1.10	3	0.05

¹Positions are based on the Sscrofa 10.2 genome.

Cross et al., 2018

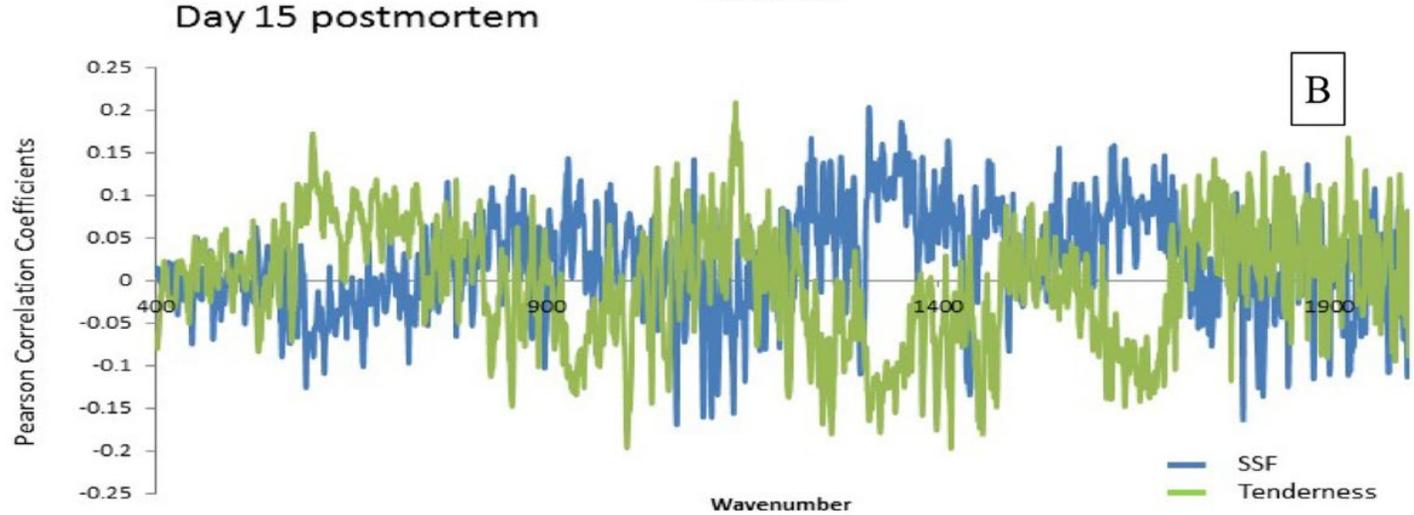
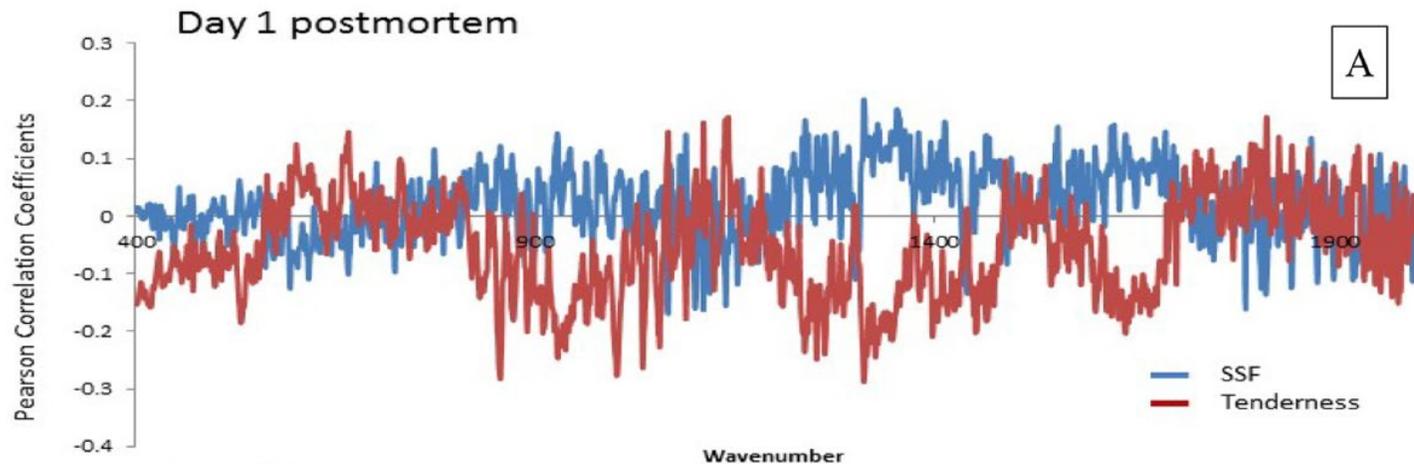
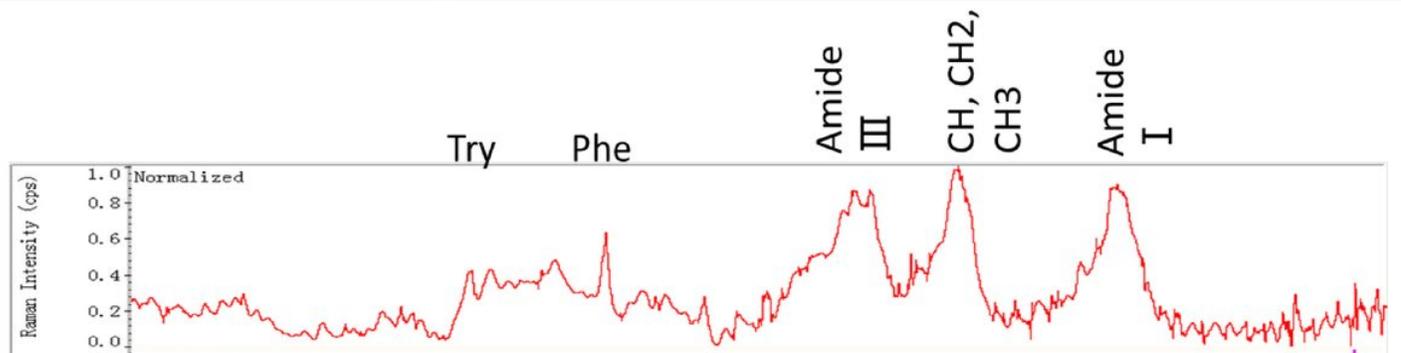


Table 4

The average classification accuracies for pork Raman (iRaman, B&W Tek, Newark, DE) spectra ($n = 800$) between Poor (SSF > 15), Medium ($10 < \text{SSF} < 15$) and Good (SSF < 10). The average accuracies are calculated from 10 training and testing using Support Vector Machine.

Grouping	Good	Medium	Poor
Day 1	71.7%	67.2%	78.6%
Day 15	92.7%	85.8%	97.5%

Table 3

The average classification accuracies for pork Raman (iRaman, B&W Tek, Newark, DE) spectra between Poor (1st 25% percentile for tenderness) and Good (4th 25% percentile for tenderness), for samples at day 1 and day 15 postmortem. The average accuracies are calculated from 10 training and testing using Support Vector Machine.

		Poor	Good
Classified as "poor"	Day 1	76.3%	5.1%
	Day 15	93.5%	1.5%
Classified as "good"	Day 1	4.8%	68.6%
	Day 15	2.3%	95.5%

Raman spectroscopy provided some discrimination between good and poor tenderness using slice shear force and panel tenderness evaluation as measures. It has potential for use in discriminating pork quality in real time during processing.



Problem Statement 3B: Improving the Healthfulness and Nutritional Value of Meat Products from Traditional and Non-Traditional Production Systems

Anticipated product: Identification of strategies for improving nutritional composition of meat products that will result in positive impact on human health.

- Modeling fat in beef to determine the potential for meeting saturated fat guidelines

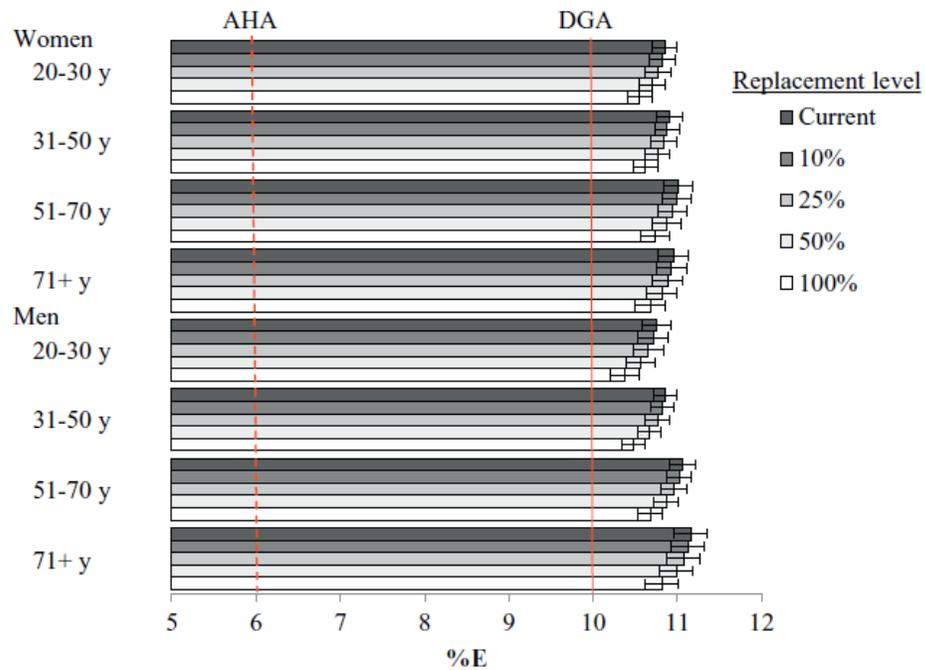


Fig. 2. Current and modeled saturated fat intake relative to energy intake under different scenarios of American Wagyu beef consumption, 2001–2016 (n = 39,758). Modeled SFA intake assuming 10%, 25%, 50%, and 100% replacement of the current fatty acid composition of beef fat with beef fat from American Wagyu. Error bars represent 95% confidence intervals. Red solid line represents Dietary Guidelines for Americans (DGA) recommendation for dietary saturated fat intake (Department of Health and Human Services, 2015). Red dashed line represents American Heart Association (AHA) recommendation for dietary saturated fat intake for individuals at increased risk for CVD (Eckel et al., 2014). All values are statistically different than current intake at $P < .001$. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Modeling fat effects in human diets resulting from replacement of beef with a more beneficial breed (Wagyu, left) or diet (flax, right) on saturated fat levels for various genders and age ranges. These manipulations can contribute to meeting the recommended saturated fat level, but even 100% replacement does not reduce saturated fats to the recommended level.

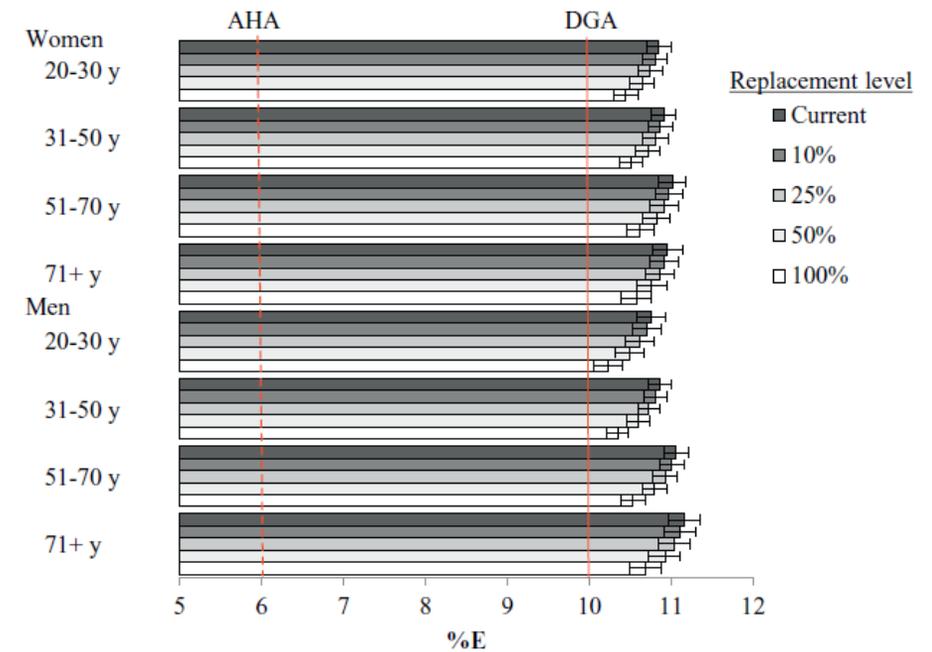


Fig. 3. Current and modeled saturated fat intake relative to energy intake under different scenarios of consuming beef from cattle fed a diet supplemented with flaxseed, 2001–2016 (n = 39,758). Modeled saturated fat intake assuming 10%, 25%, 50%, and 100% replacement of the current fatty acid composition of beef fat with beef fat from cattle fed a diet supplemented with 15% flaxseed. Error bars represent 95% confidence intervals. Red solid line represents Dietary Guidelines for Americans (DGA) recommendation for dietary saturated fat intake (Department of Health and Human Services, 2015). Red dashed line represents American Heart Association (AHA) recommendation for dietary saturated fat intake for individuals at increased risk for CVD (Eckel et al., 2014). All values are statistically different than current intake at $P < .001$. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Conclusions

- Significant nutritional accomplishments include exploring alternative feeds, transcriptomic analyses of various tissues in animals that differ in growth and feed efficiency, and the role of the microbiome in livestock
- Significant reproductive accomplishments include defining the roles of colostrum, ovary, placenta and uterus in reproductive efficiency
- Significant welfare accomplishments include improvements in stress detection, improved euthanasia, and inroads into alternatives to antibiotics

- Significant genomic tools include improved genomes, mapping of copy number variation, characterization of the rumen microbiome and better sequence imputation methods
- Significant functional annotation includes building a cattle genome tissue atlas and numerous transcriptomic analyses of various tissues
- Significant germplasm preservation includes the development of the animal GRIN database and improvement in livestock collections
- Significant genetic selection program progress includes numerous updates to dairy cattle genome enhanced breeding, and genome wide analyses of beef cattle and swine for various traits
- Significant gene editing includes development of universal boars

- Significant improvements in meat quality include include research to define biological mechanisms affecting lean color and ham halo
- Significant research in meat healthfulness includes modeling to determine the feasibility of improving health through changes in meat characteristics