Genotype by diet interactions in selection lines for residual feed intake in pigs

Mauch, Emily D.[1], N.V.L. Serão[2], J.M. Young[3], J.F. Patience[1], N.K. Gabler[1], and J.C.M. Dekkers[1]

[1] Department of Animal Science, Iowa State University, Ames 50011

[2]Department of Animal Science, North Carolina State University, Raleigh 27695

[3]Department of Animal Sciences, North Dakota State University, Fargo 58108

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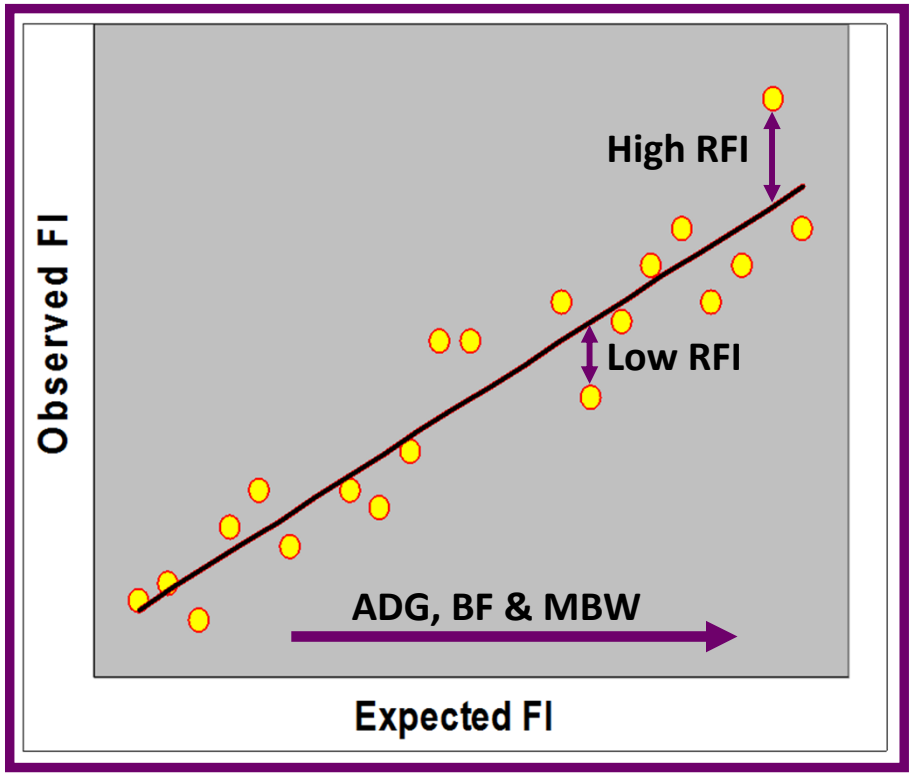
Residual Feed Intake

RFI =
Observed -Expected
Feed Intake

- Low RFI
  - More Feed Efficient
- High RFI
  - Less Feed Efficient

RFI = ADFI - b1*ADG - b2*BF - b3*MBW



RFI first proposed by Koch et al., 1963

ISU RFI Lines

Est. 2001

Fed Standard diet during selection

n = 1,359

Gen 5

n = 619

Low RFI
[More Feed Efficient]

High RFI
[Less Feed Efficient]

Diet Challenge of ISU RFI Lines

Est. 2001

Fed Standard diet during selection

n = 1,359

Gen 5

n = 619

Low RFI
[More Feed Efficient]

High RFI
[Less Feed Efficient]

Diet Challenge:
Generations 8, 9, & 10
n = 644

Standard
n = 172

Challenge
n = 157

Standard
n = 159

Challenge
n = 157

Diets:
Standard (n =2,309)
Challenge (n= 314) = ↓Energy [-18%], ↑Fiber [+175%]

Objective

Identify the impact of feeding a low energy, high fiber (**Challenge**) diet on

1) genetic parameters

2) response to selection

3) genomic regions associated with feed efficiency and component traits

in comparison to high energy, low fiber (**Standard**) diet

Phenotypes

1. Average Daily Gain (**ADG**), kg/d
   - Measured every 2 weeks
   - ~40kg- ~118 kg
2. Average Daily Feed Intake (**ADFI**), kg/d
   - FIRE© Feeders
3. Feed Conversion Ratio (**FCR**), kg/kg
4. Off-test Loin Muscle Area (**LMA**), cm^2
5. Off-test Backfat Depth (**BF**), mm
6. Residual Feed Intake (**RFI**), kg/d

n = 2,623

Genotypes

Illumina PorcineSNP60 Beadchip

Standard Diet

n = 1,692

- 51,098 SNP after quality control
- GWAS by Serão et al., 2016

Challenge Diet

n = 311

- 46, 347 SNP after quality control

Materials & Methods

1) Genetic Parameter Estimation (n = 2,623)

2) Response to Selection (n = 2,623)

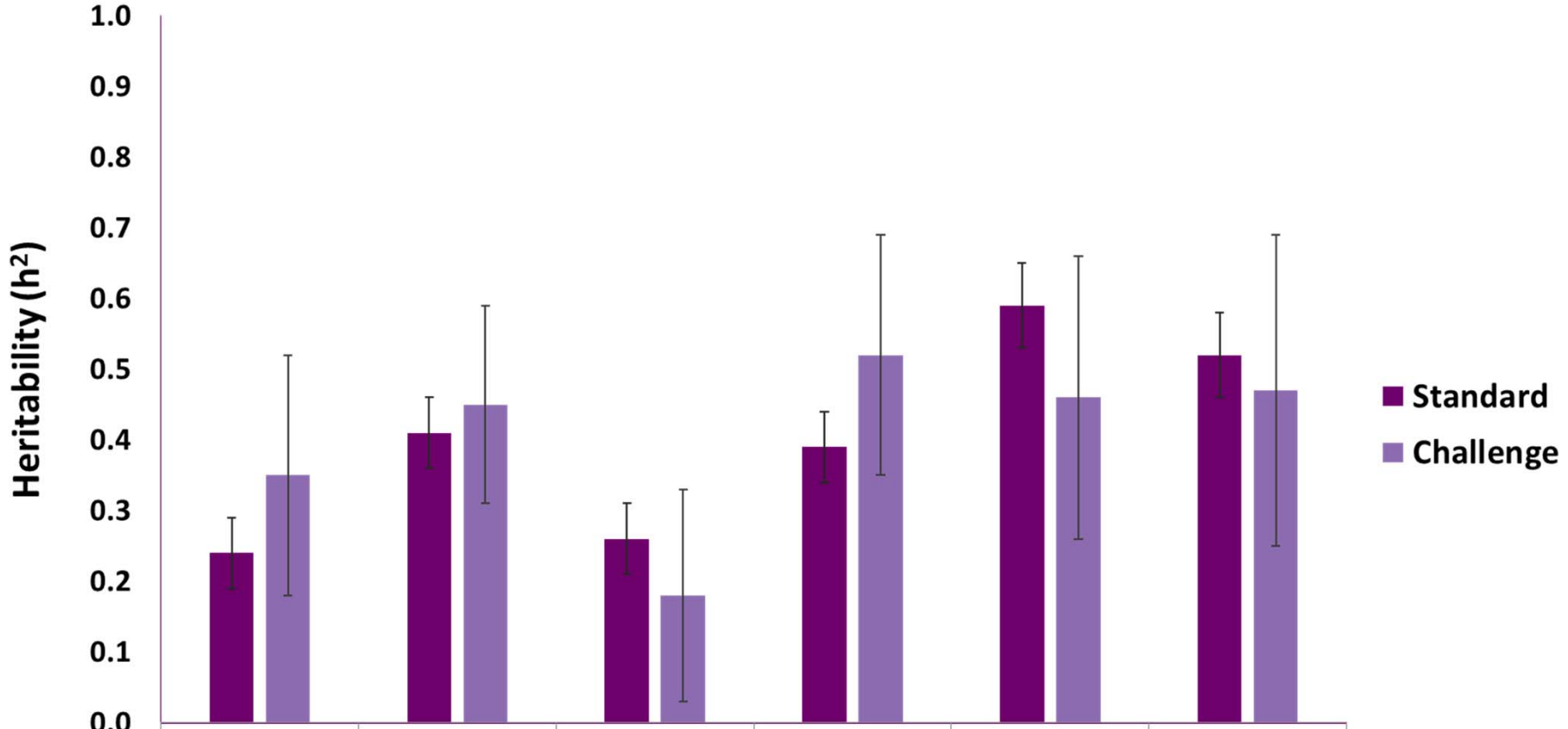
Bivariate Models in ASReml 3.0
- Traits separated by diet

3) Single-SNP Genome Wide Association Studies (GWAS)
   1. Pigs fed Standard diet reported by Serão et al., 2015 (n= 1,692)
   2. Pigs fed Challenge diet (n= 311)

Univariate Models in ASReml 4.0

1) Genetic Parameter Estimation

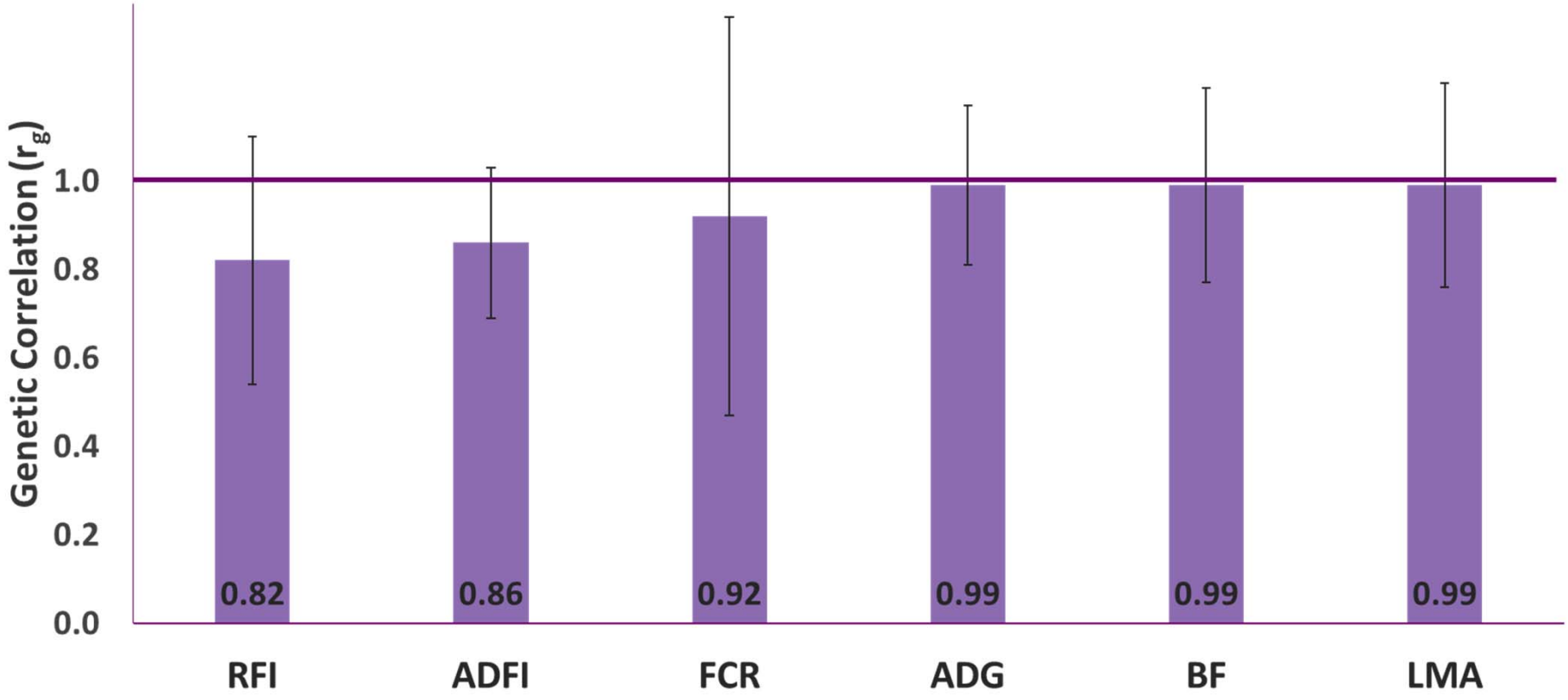
Heritability



	RFI	ADFI	FCR	ADG	BF	LMA
Standard	0.24	0.41	0.26	0.39	0.59	0.52
Challenge	0.35	0.45	0.18	0.52	0.46	0.47

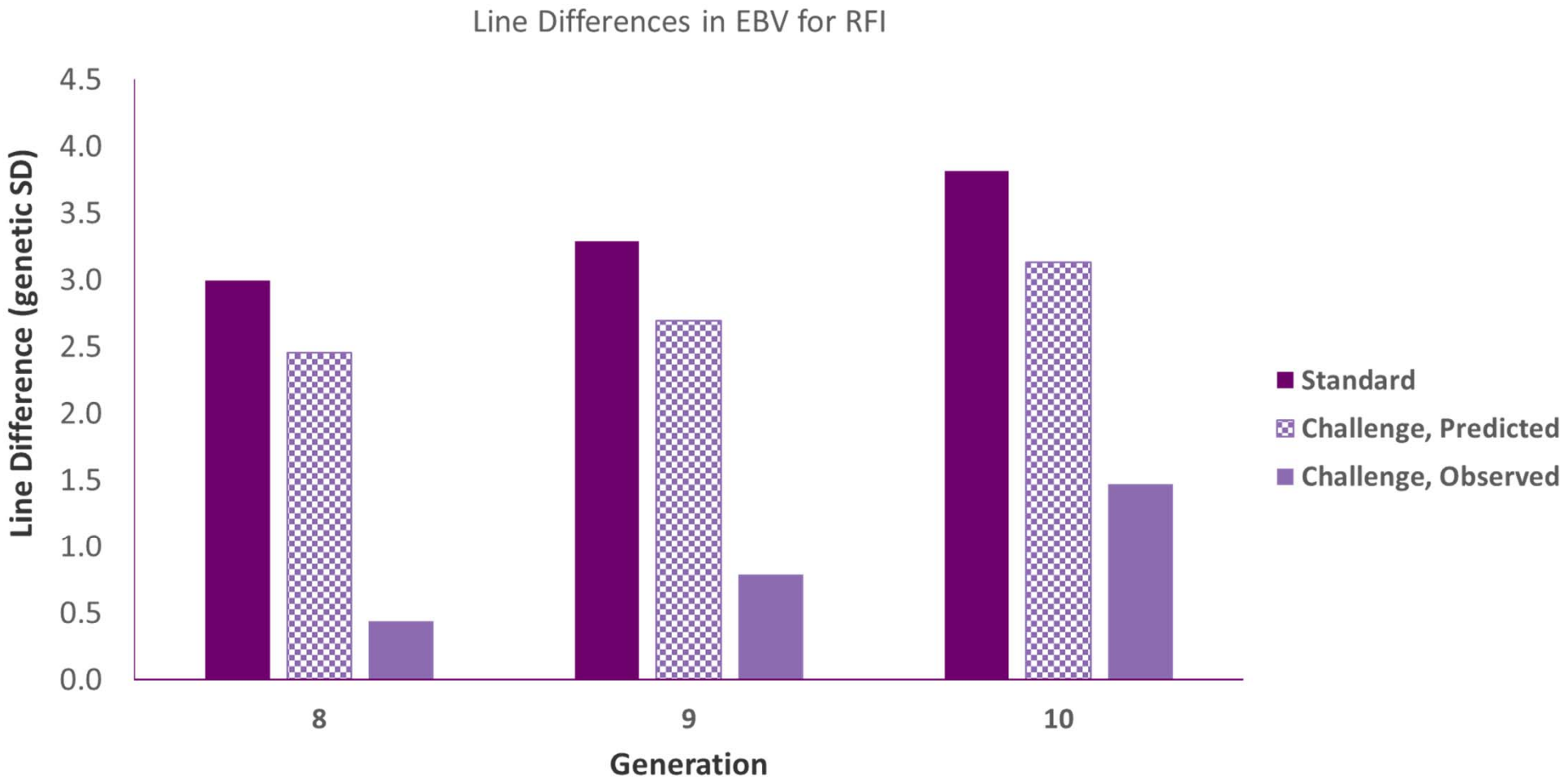
RFI = residual feed intake, ADFI = average daily feed intake, FCR = feed conversion ratio, ADG = average daily gain, BF = backfat depth, LMA = loin muscle area

Genetic Correlations between Diets

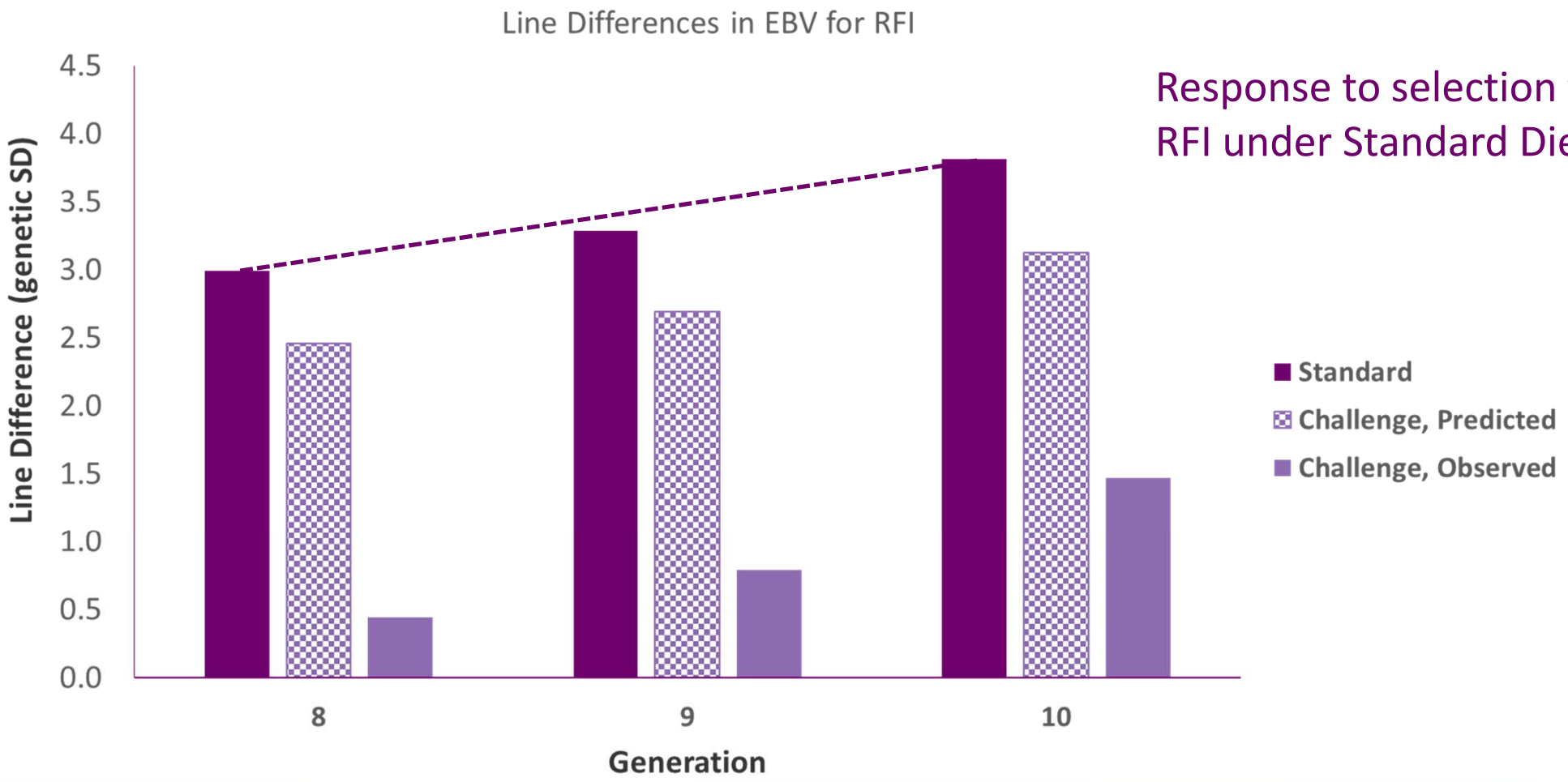


2) Response to Selection for RFI

Line Differences (High RFI minus Low RFI)

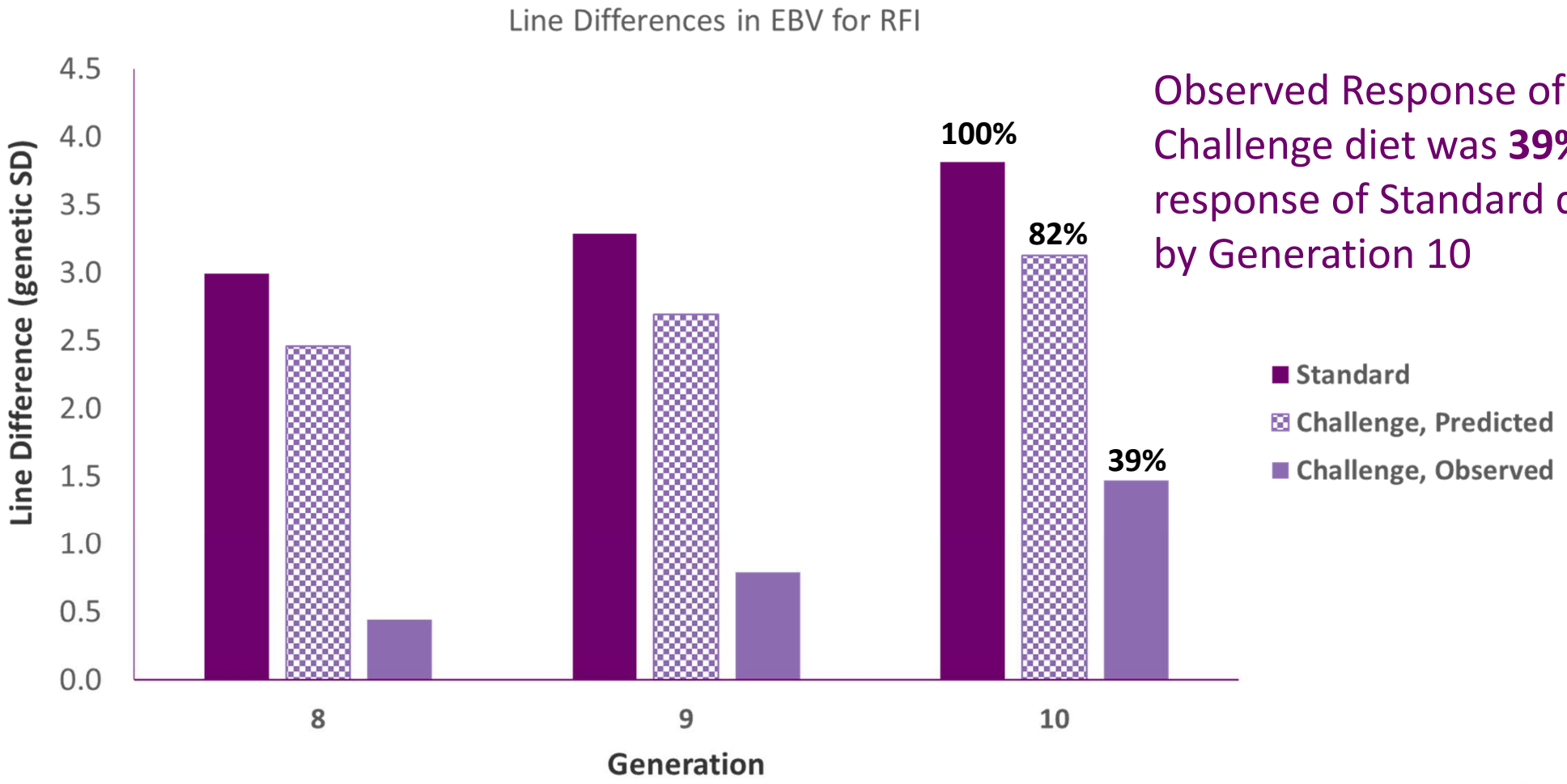


Line Differences (High RFI minus Low RFI)



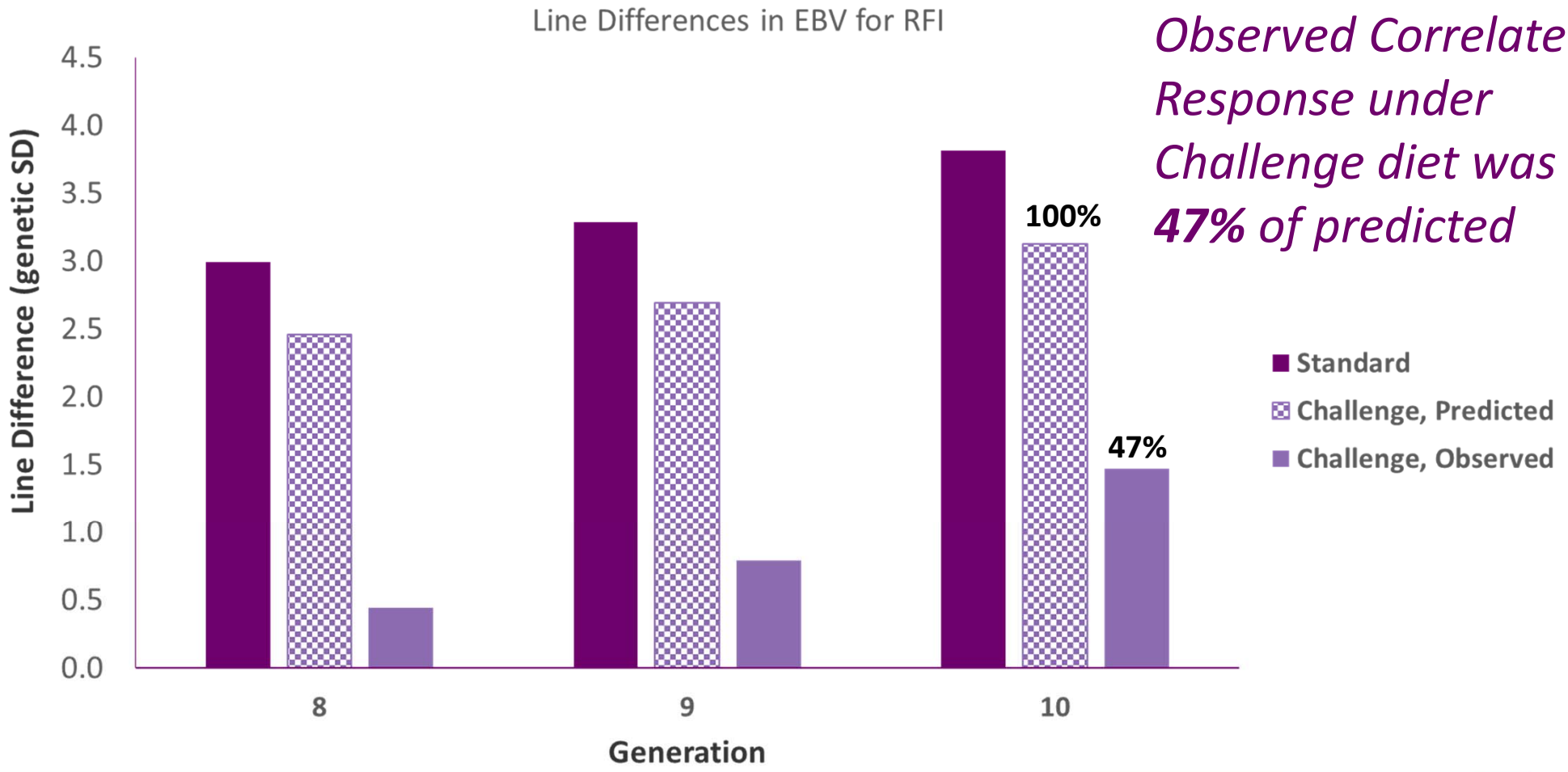
Response to selection for RFI under Standard Diet

Line Differences (High RFI minus Low RFI)



Observed Response of Challenge diet was **39%** of response of Standard diet by Generation 10

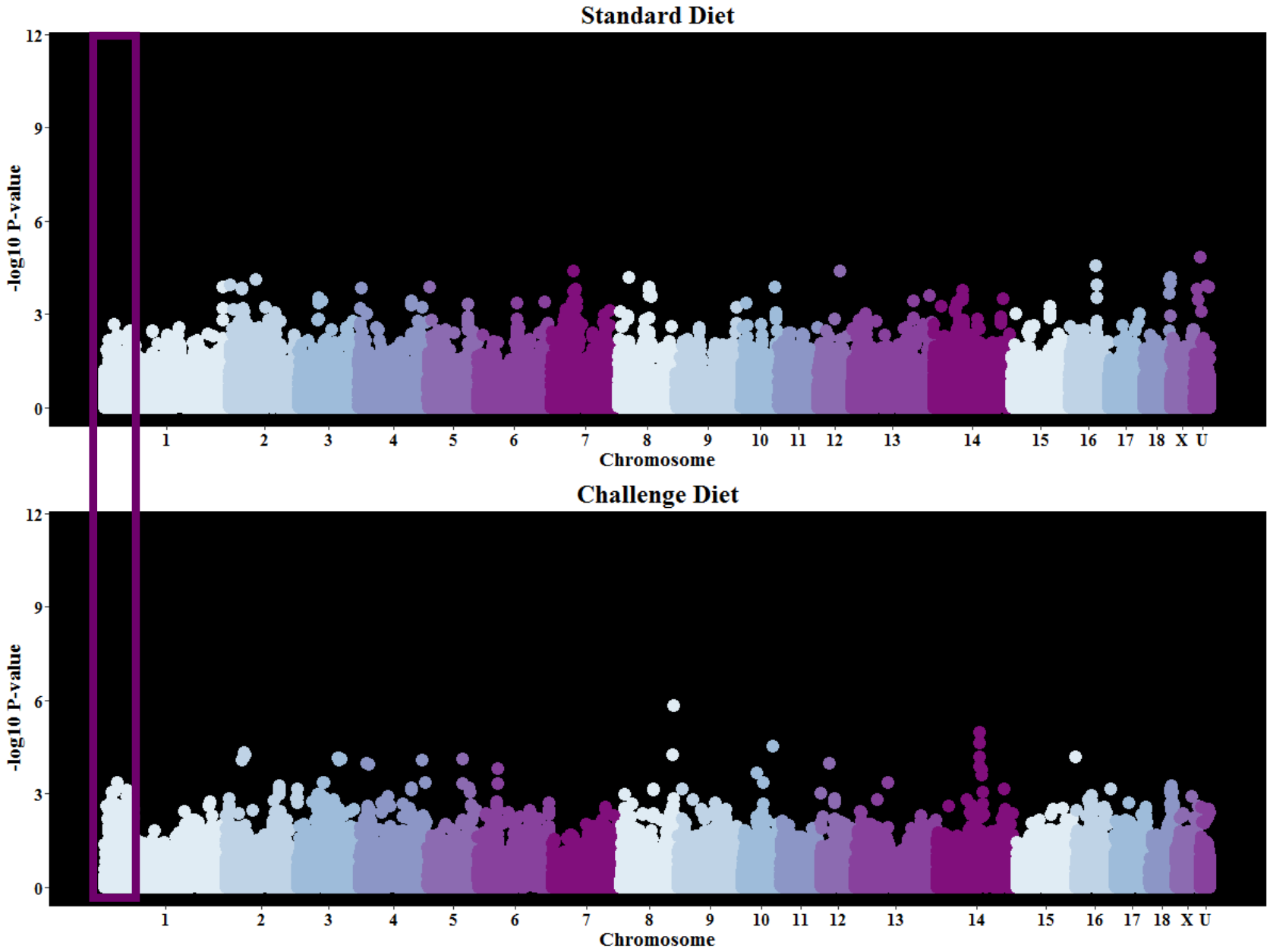
Line Differences (High RFI minus Low RFI)



*Observed Correlated Response under Challenge diet was **47%** of predicted*

3) Genome Wide Association Study (GWAS)

Residual Feed Intake



Genetic Parameter Conclusions

- RFI and component traits are **moderately to highly heritable** with similar estimates under Standard and Challenge diets
- RFI and component traits under Challenge diet have **high, positive genetic correlations** to the same trait under Standard diet
  - Genetic correlations for RFI, ADFI and FCR across diets tended to be lower
- The observed correlated response for RFI under the Challenge diet was **47% less than predicted** based on the genetic correlation across diets

GWAS Conclusions

- **RFI is a highly polygenic trait**
  - Affected by many genes with small effects
  - No clear overlap of regions identified in GWAS for RFI under Standard versus Challenge diet
- For component traits, some genomic regions overlap under Standard and Challenge diets
- Novel QTL for BF on SSC 2 at 162 Mb in ISU RFI lines

Overall Conclusions

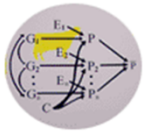
- RFI appears to be a genetically different trait depending on diet fed, suggesting **genotype by diet interactions**
  - $r_g = 0.82 \pm 0.28$
  - Lower response to selection under Challenge diet than predicted
  - No clear overlap in GWAS results between Standard & Challenge diets

- Diet may play a role in selection for feed efficiency pigs
  - Deviations from diet fed during selection may result in reduced response in feed efficiency

IOWA STATE UNIVERSITY

Acknowledgements

Animal Breeding & Genetics



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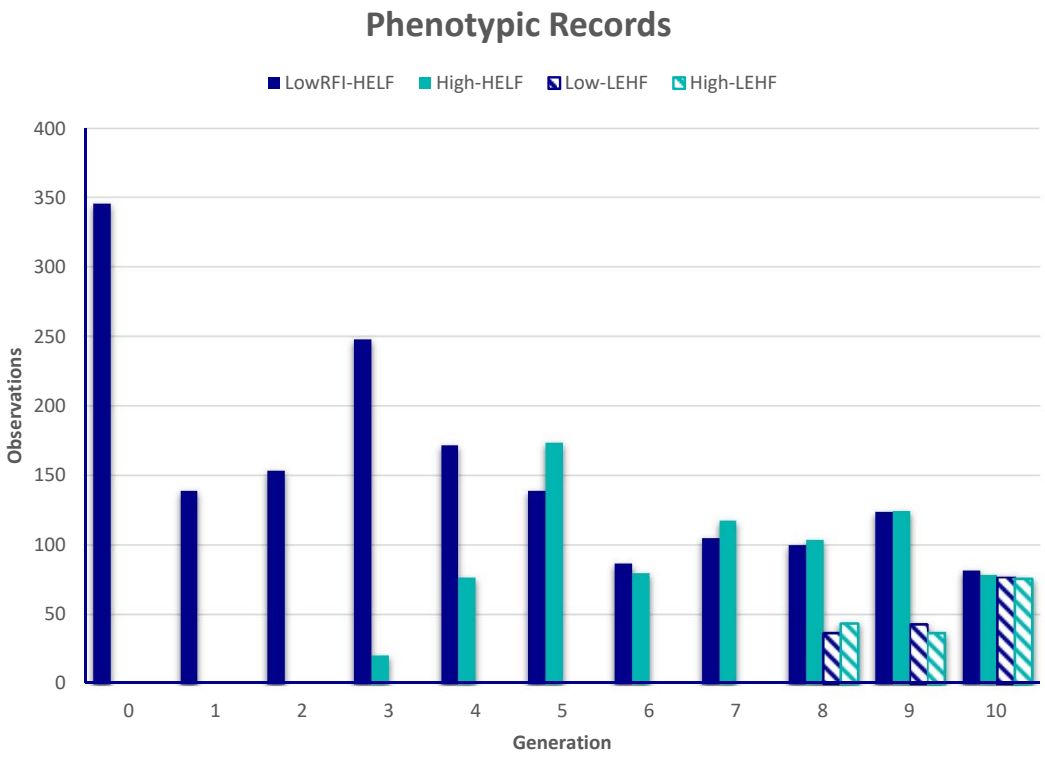
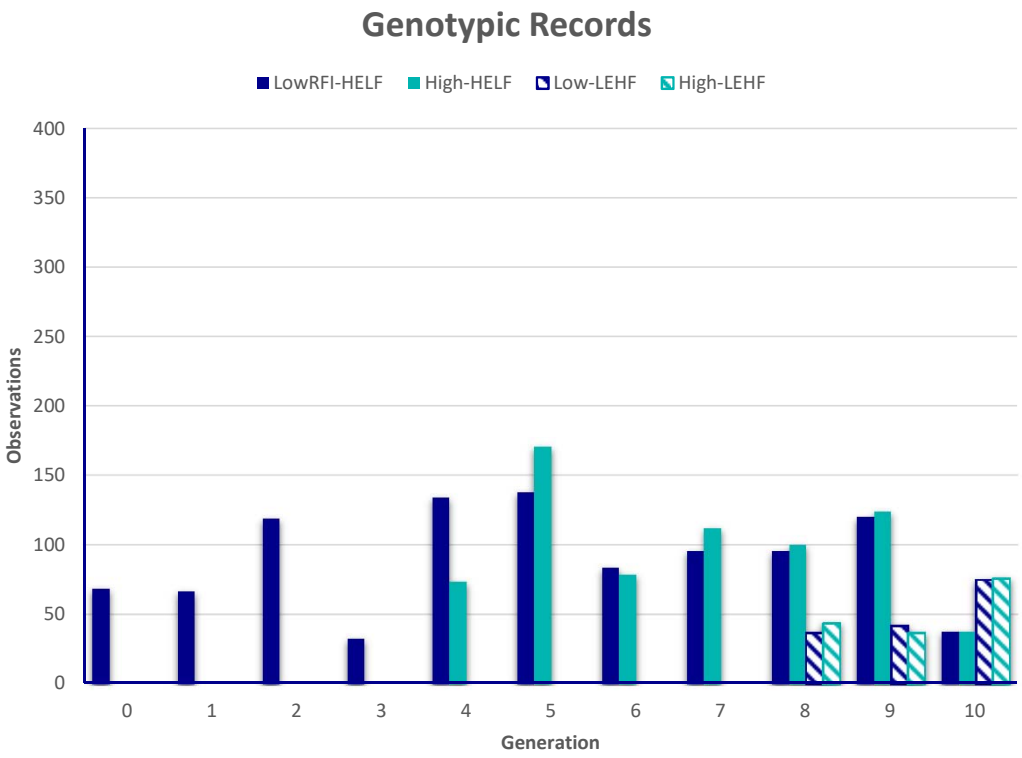
Appendix

Diet Differences

	Standard	Challenge	Difference
Net Energy, Mcal/kg	2.42	1.99	-18%
Acid Detergent Fiber (ADF), %	3.5%	12.5%	+257%
Neutral Detergent Fiber (NDF), %	9.4%	25.9%	+175%
Lysine:Metabolizable Energy (Lys:ME), g/Mcal	2.87	2.94	____

Phenotype & Genotype Records





Diet Standard & Challenge Bivariate Models, ASReml 3.0

Trait	line	sex	pen-cohort	onage	onwt	offwt	ADG*gen	offbf	metwt	litter	idpig
RFI, kg/d	X	X	X	X	X	X	X	X	X	X	X
ADFI, kg/d	X	X	X	X						X	X
FCR, kg/kg	X	X	X	X						X	X
ADG, kg/d	X	X	X	X						X	X
BF, mm	X	X	X			X				X	X
LMA, cm^2	X	X	X			X				X	X

RFI = residual feed intake, ADFI = average daily feed intake,
FCR = feed conversion ratio, ADG = average daily gain,
BF = backfat depth, LMA = loin muscle area

Genetic Parameters

1 = Standard Diet, 2 = Challenge Diet

Trait	N	Mean(SD)	h^2	c^2	σ_P	σ_g
RFI1, kg/d	2,309	------	0.24 ± 0.05	0.09 ± 0.03	0.13	0.06
RFI2, kg/d	313	------	0.35 ± 0.17	0.00 ± 0.00	0.22	0.13
ADFI1, kg/d	2,309	2.02 (0.30)	0.41 ± 0.05	0.02 ± 0.03	0. 20	0.13
ADFI2, kg/d	313	2.47 (0.38)	0.45 ± 0.14	0.00 ± 0.00	0.27	0.18
FCR1, kg/kg	2,309	2.78 (0.41)	0.26 ± 0.05	0.11 ± 0.03	0.26	0.13
FCR2, kg/kg	313	4.26 (0.62)	0.18 ± 0.15	0.04 ± 0.10	0.51	0.21

RFI = residual feed intake, ADFI = average daily feed intake, FCR = feed conversion ratio

c^2 = common litter effect

Genetic Parameters

1 = Standard Diet, 2 = Challenge Diet

Trait	N	Mean(SD)	h^2	c^2	σ_P	σ_g
ADG1, kg/d	2,309	0.73 (0.11)	0.39 ± 0.05	0.03 ± 0.03	0.09	0.05
ADG2, kg/d	314	0.59 (0.10)	0.52 ± 0.17	0.02 ± 0.09	0.08	0.06
BF1, mm	2,307	17.15 (4.86)	0.59 ± 0.06	0.08 ± 0.03	3.61	2.78
BF2, mm	314	19.16 (5.15)	0.46 ± 0.20	0.10 ± 0.09	4.10	2.78
LMA1, cm^2	2,306	42.82 (5.47)	0.52 ± 0.06	0.07 ± 0.03	4.65	3.36
LMA2, cm^2	314	43.26 (5.34)	0.47 ± 0.22	0.12 ± 0.10	4.92	3.37

ADG = average daily gain, BF = off-test backfat depth, LMA = loin muscle area

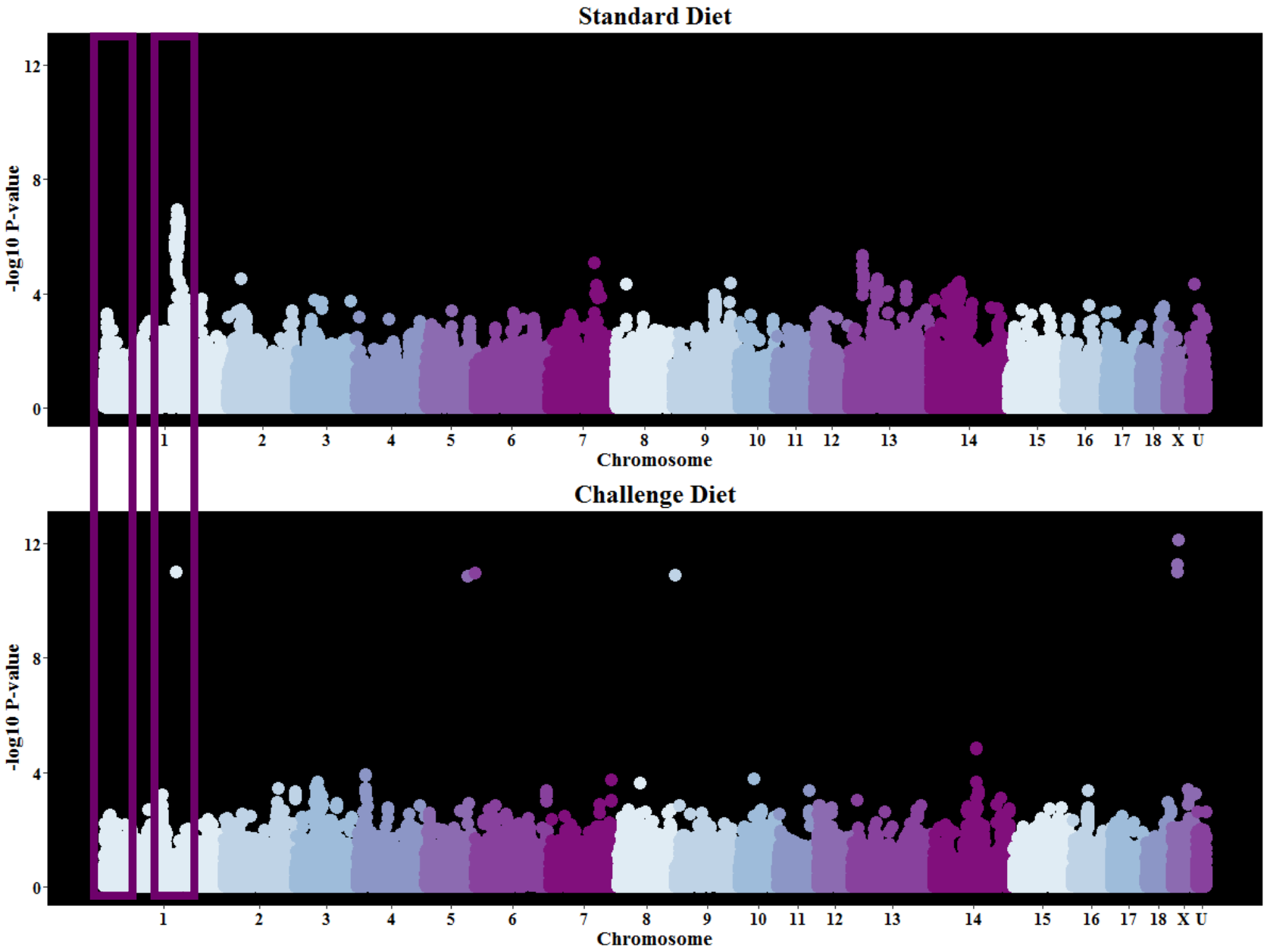
c^2 = common litter effect

Models for Single SNP GWAS

	Fixed Effects												Random Effects		
Trait	mu	line	sex	gen-par	scanner	onage	onwt	offwt	offbf	metwt	ADG*gen	SNP	pig	pen-cohort	litter
RFI, kg/d	X	X	X	X		X	X	X	X	X	X	X	X	X	X
ADFI, kg/d	X	X	X	X		X							X	X	X
FCR, kg/kg	X	X	X	X		X							X	X	X
ADG, kg/d	X	X	X	X		X							X	X	X
BF, mm	X	X	X	X	X			X					X	X	X
LMA, cm^2	X	X	X	X	X			X					X	X	X

RFI = residual feed intake, ADFI = average daily feed intake,
FCR = feed conversion ratio, ADG = average daily gain,
BF = backfat depth, LMA = loin muscle area

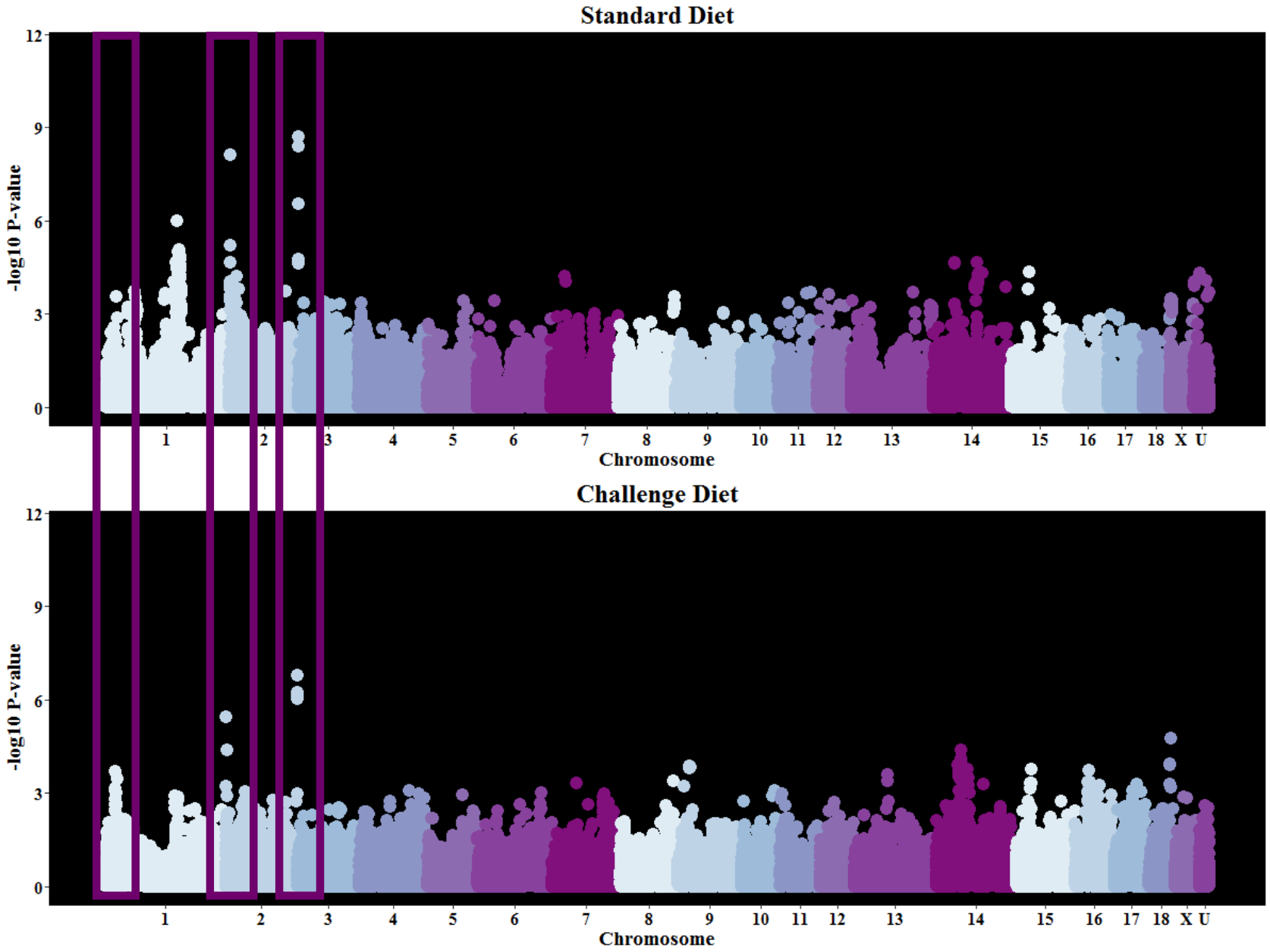
Average Daily Feed Intake



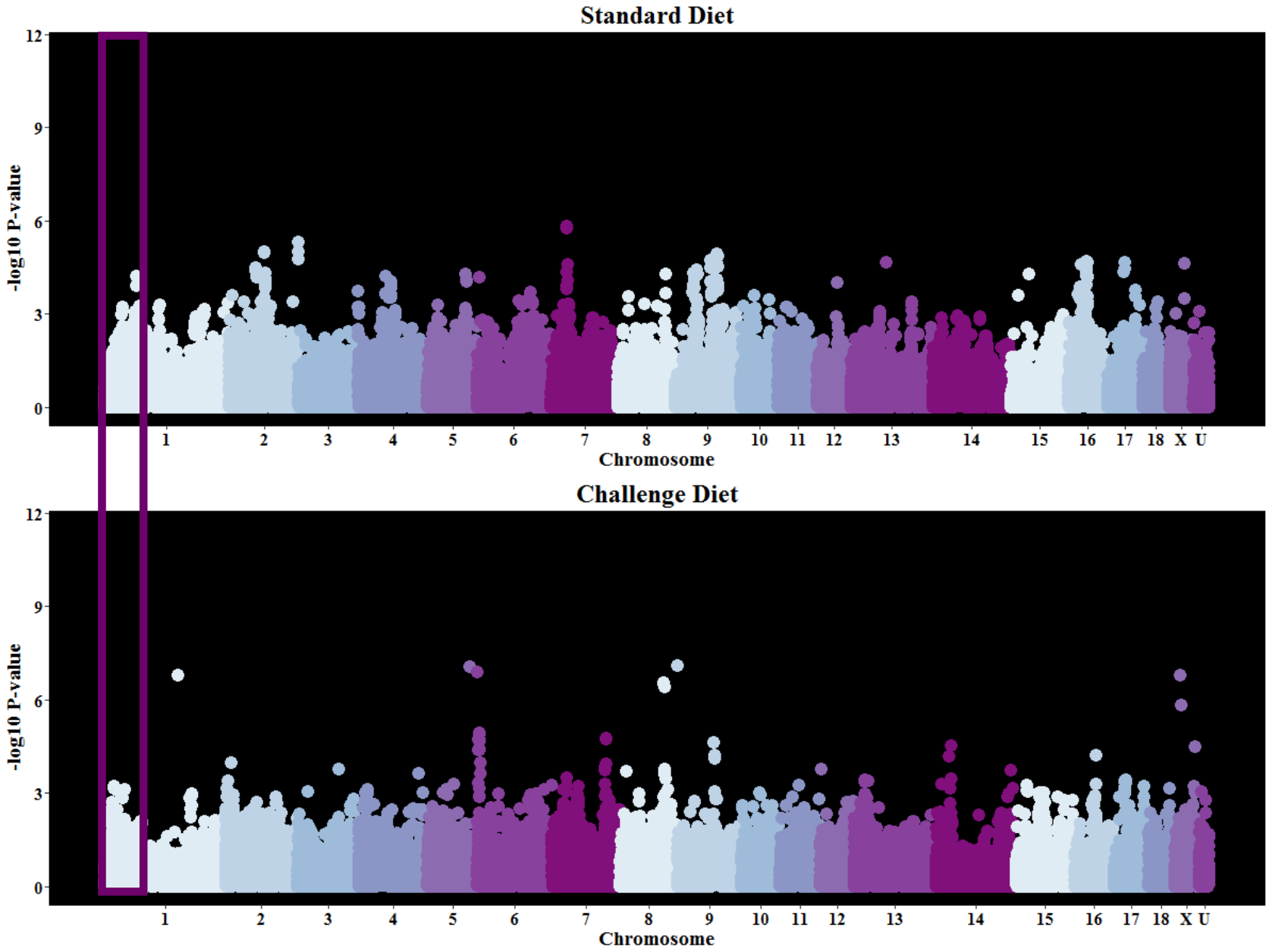
SSC1 180Mb

➔ MC4R

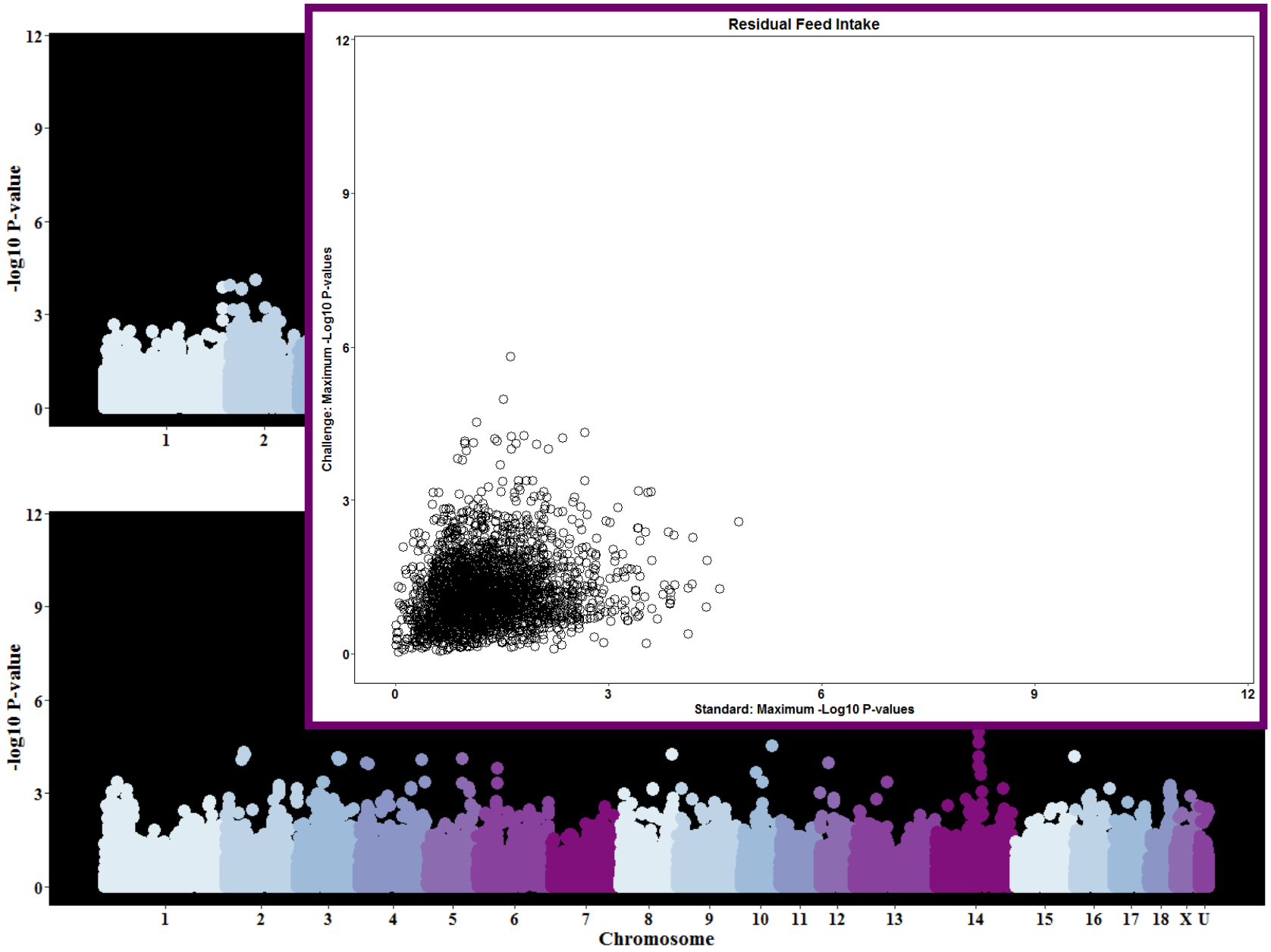
Feed Conversion Ratio



Loin Muscle Area



Residual Feed Intake



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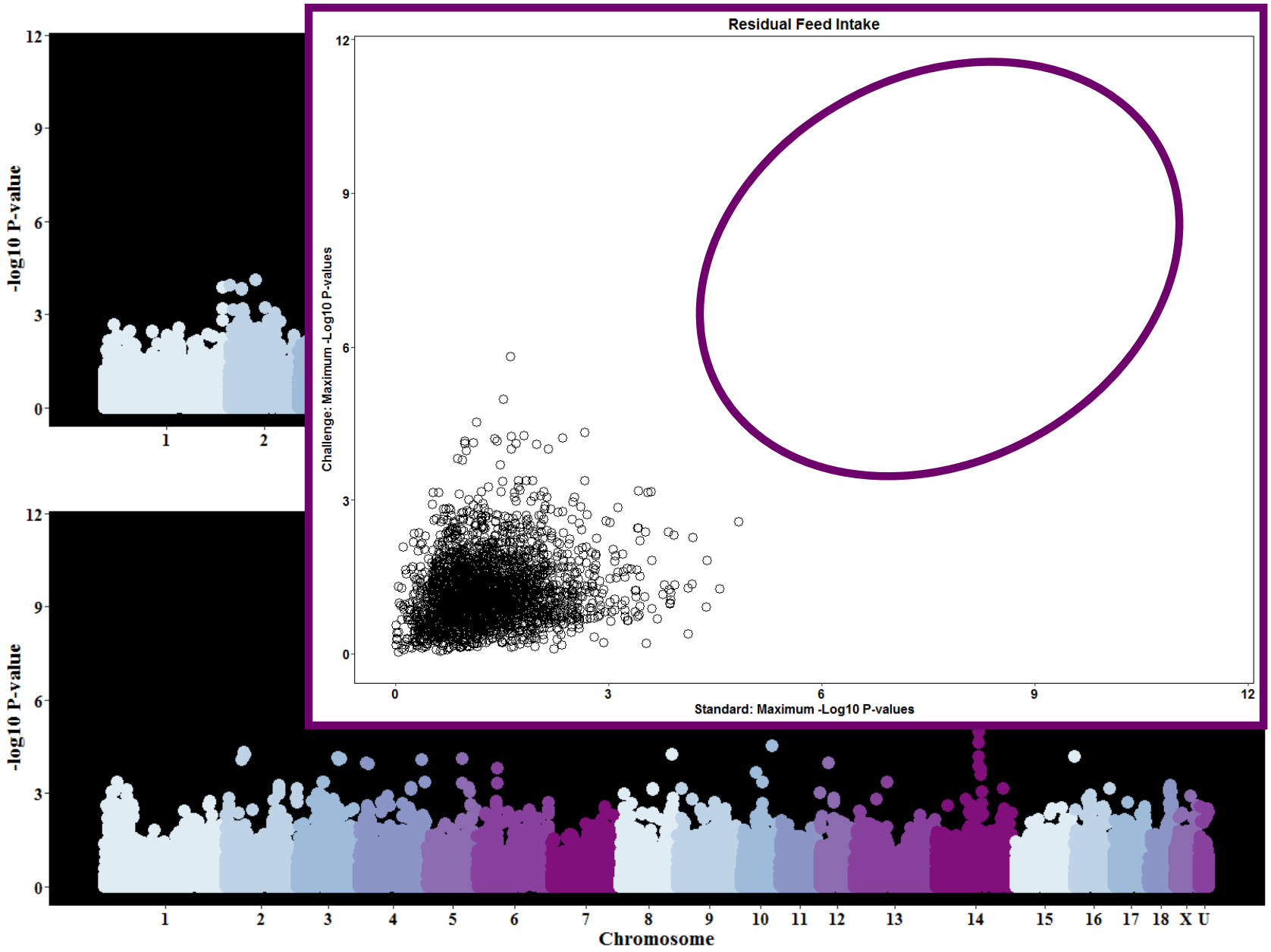

Residual Feed Intake