The association of the Host Genome with Microbiome Composition and Growth Traits in Pigs

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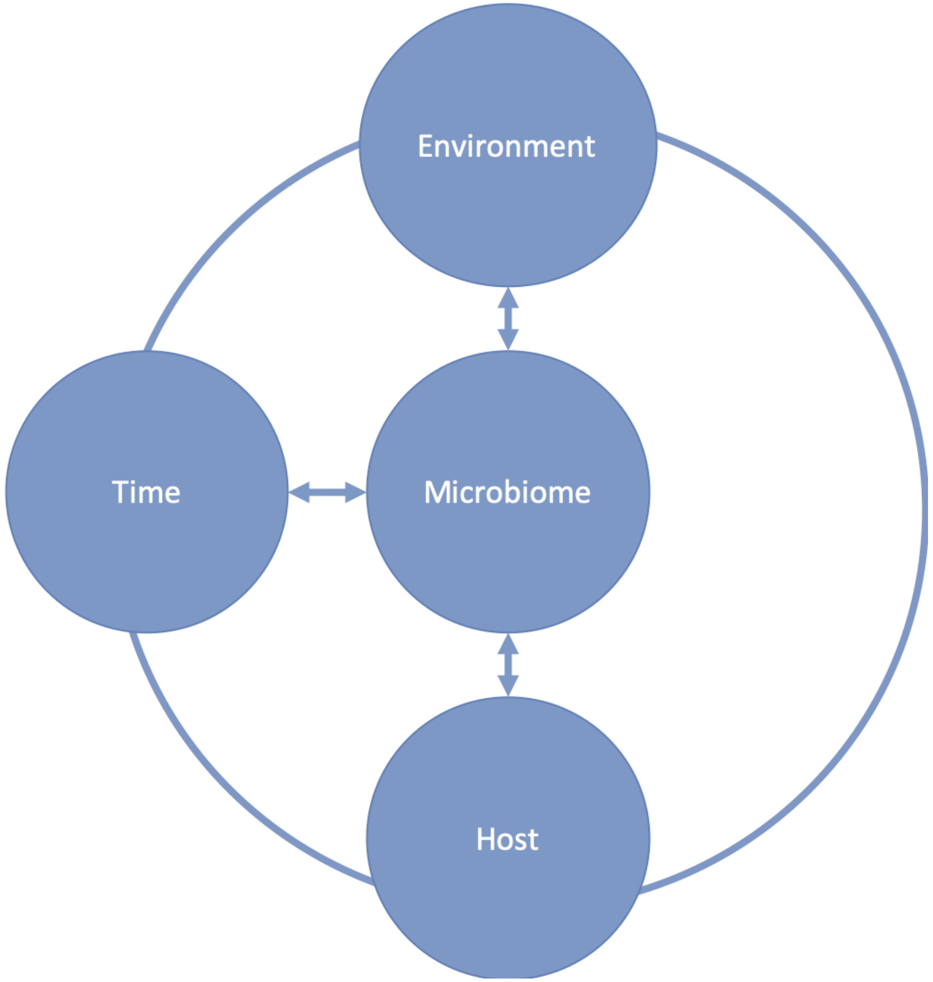
Introduction

Introduction

- The microbial community plays an important role inside each living body and profoundly influences health and disease
- The microorganisms residing in the gut live in intimal contact with each other and establish many mutualist or symbiotic relationships with the host
- These communities are influenced by many factors such as environment, age, sex, and diet



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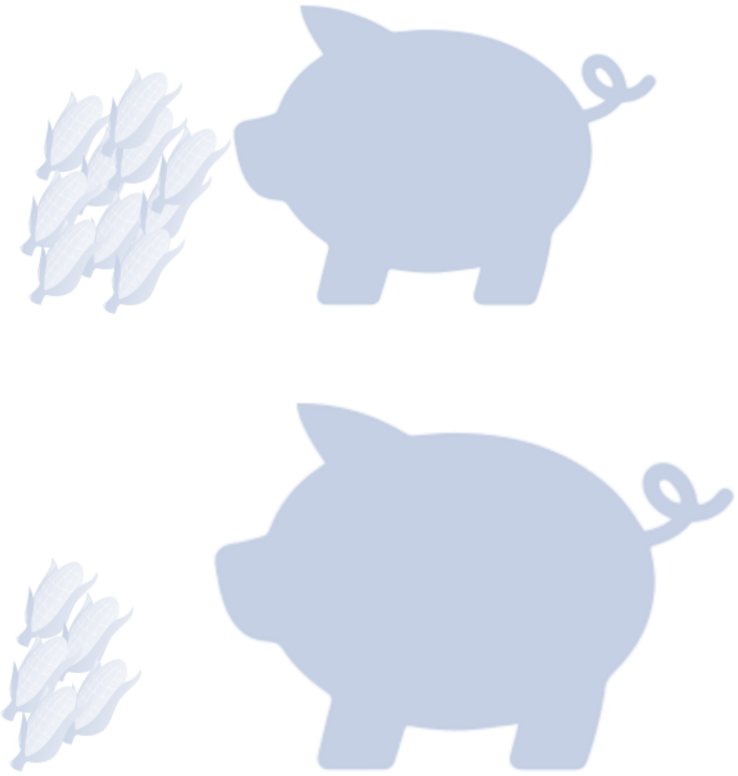
Introduction

Efficiency of producing meat determined:
- Feed Costs
- Quality of lean meat produced

Using feed resources more efficiently:
- Through diet
- Exploiting genomic variability for feed efficiency

Concentrating only on the pig variability
- Diminished marginal gains
- Losses of overall fitness



Introduction

The intestinal microbiome:

- Affects degradation of carbohydrates
- Provides short chain fatty acid
- Produces essential vitamins

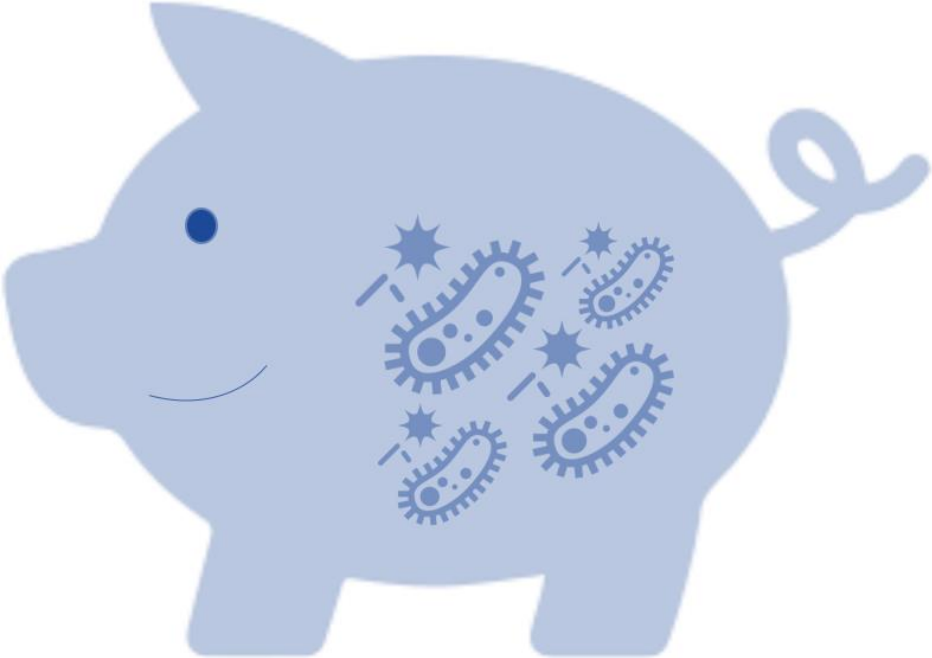
Different composition of gut microbiome:

- Alters ability of degrading enzymes
- Maintains population balance
- Influences overall health status
- Controls fatness and growth

Objectives

Objective

- Microbial diversity in pigs has been described to some extent.
- Composition and function of a healthy microbial population not yet employed as a tool to maximize animal health and performance



- Characterizing temporal changes in the microbiome community of pig feces with respect to both composition and diversity
- Investigating the potential influence of host genetics on this diversity.

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Objective(s)

- Association between microbiome extracted from fecal samples with host growth and fatness parameters
- Heritability estimates for taxa significantly linked to growth and fatness
- Genome-wide association between taxa significantly associated with growth parameters and pigs single nucleotide polymorphisms

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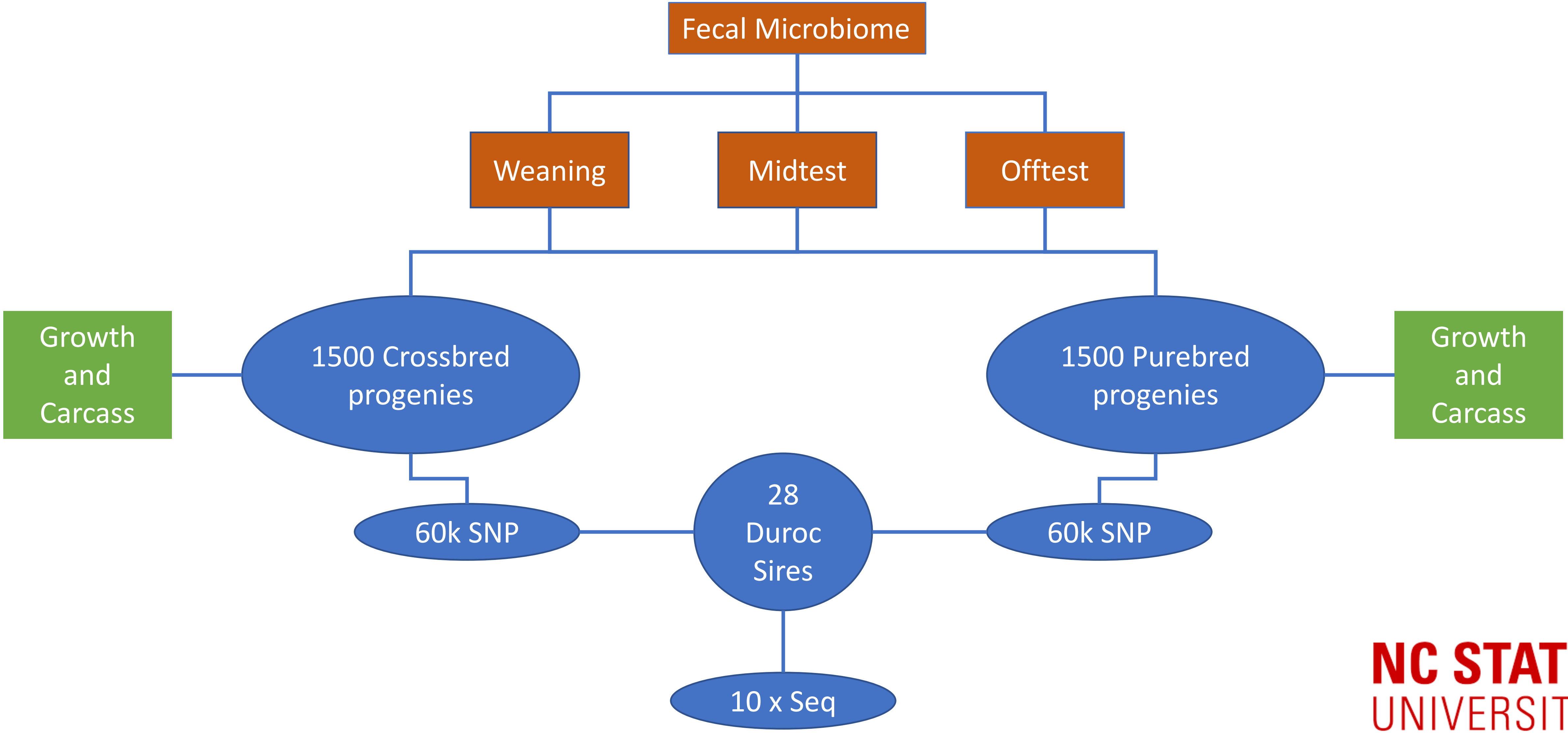
Materials and Methods

Experimental Design



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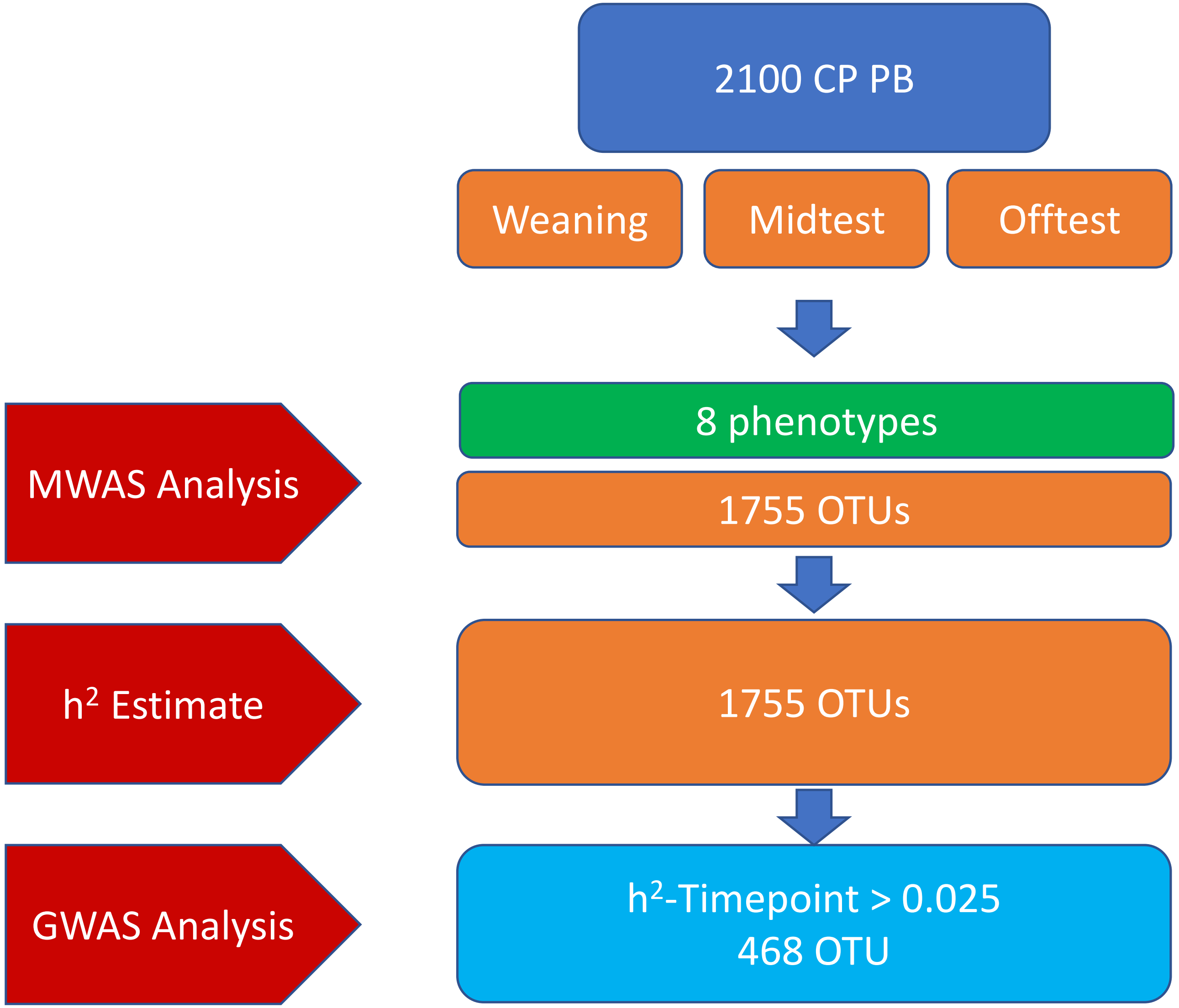
Analysis Design



2100 CP PB

Weaning

Midtest

Offtest

8 phenotypes

1755 OTUs

1755 OTUs

h^2-Timepoint > 0.025

468 OTU

MWAS Analysis

h^2 Estimate

GWAS Analysis

Extraction
- Bacterial DNA (gDNA) extracted from rectal swab

Amplification
- Amplification of V4 region sequences merged into a single sequence

QC and clustering
- Sequences with mean score quality below Q35 filtered and clustered into OTUs
- GreneGenes. The most abundant sequence as the representative for the OTU

Rarefication
- Sparse OTUs filtered minimum count of 1200.
- OTU table rarefied to 10,000 counts

Final data
- 1755 OTUs with complete phylogeny assigned retained for further analyses

Microbiome Phenotype Association

$$\boldsymbol{Phen} = \boldsymbol{X}b + \gamma OTU + \boldsymbol{W}p + \boldsymbol{e}$$

- Sex
- Sire
- Breed
- Contemporary group
- Pen

Phenotype	Mean	SD
ADG_{B14}, kg/d	0.57	0.08
ADG_{W14}, kg/d	0.64	0.10
ADG_{1422}, kg/d	0.87	0.16
ADG_{14MKT}, kg/d	0.89	0.14
BF_{14}, mm	12.5	2.81
BF_{22}, mm	20.1	5.36
LD_{14}, mm	42.3	4.80
LD_{22}, mm	55.8	5.15

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Taxa h^2 estimates

$$\boldsymbol{OTU} = \boldsymbol{X}b + \boldsymbol{Z}s + \boldsymbol{W}p + \boldsymbol{e}$$

- Sex
- Breed
- Contemporary group
- Sire
- Pen

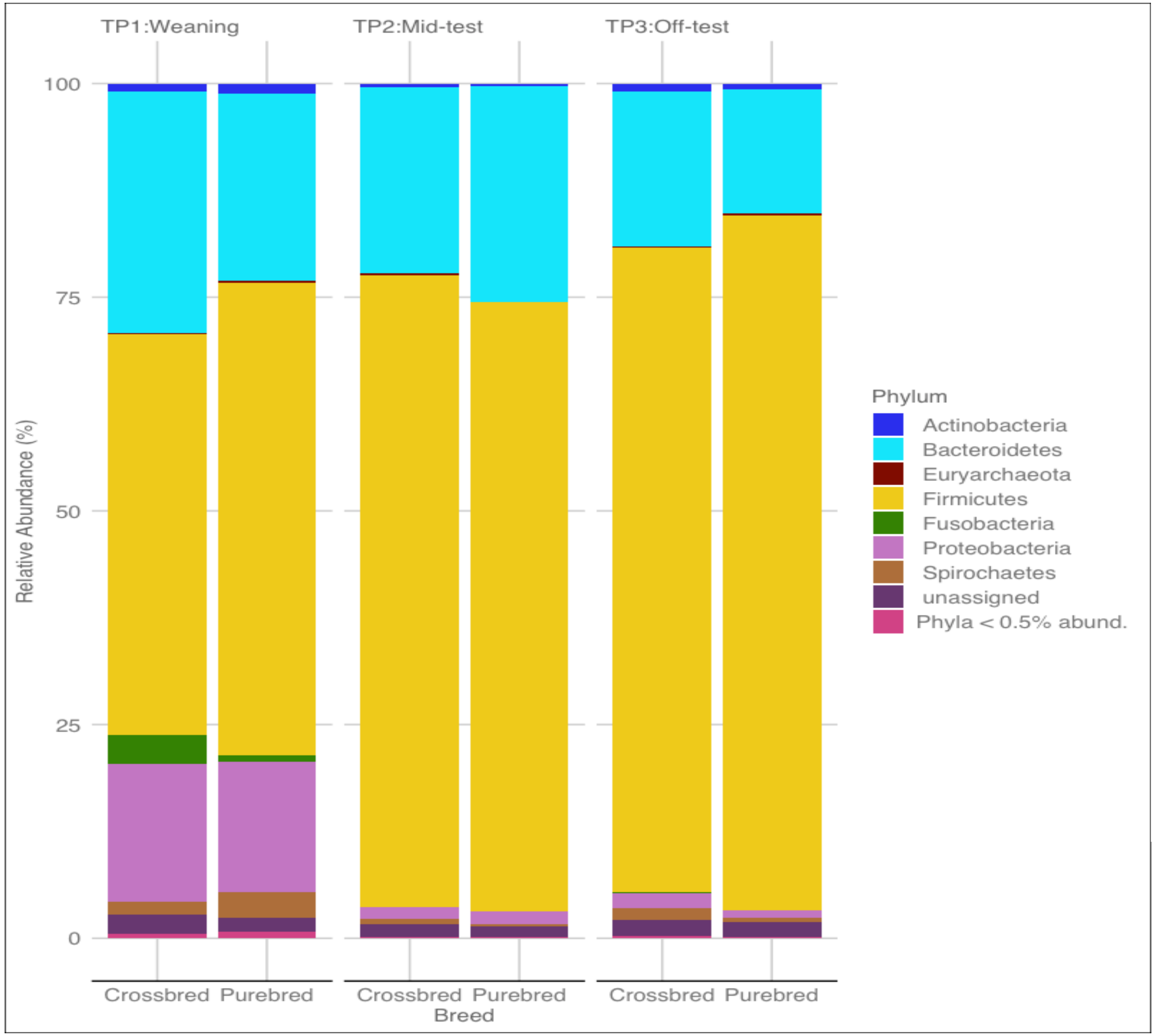
$$h^2 = \frac{4(Vs)}{Vt}$$

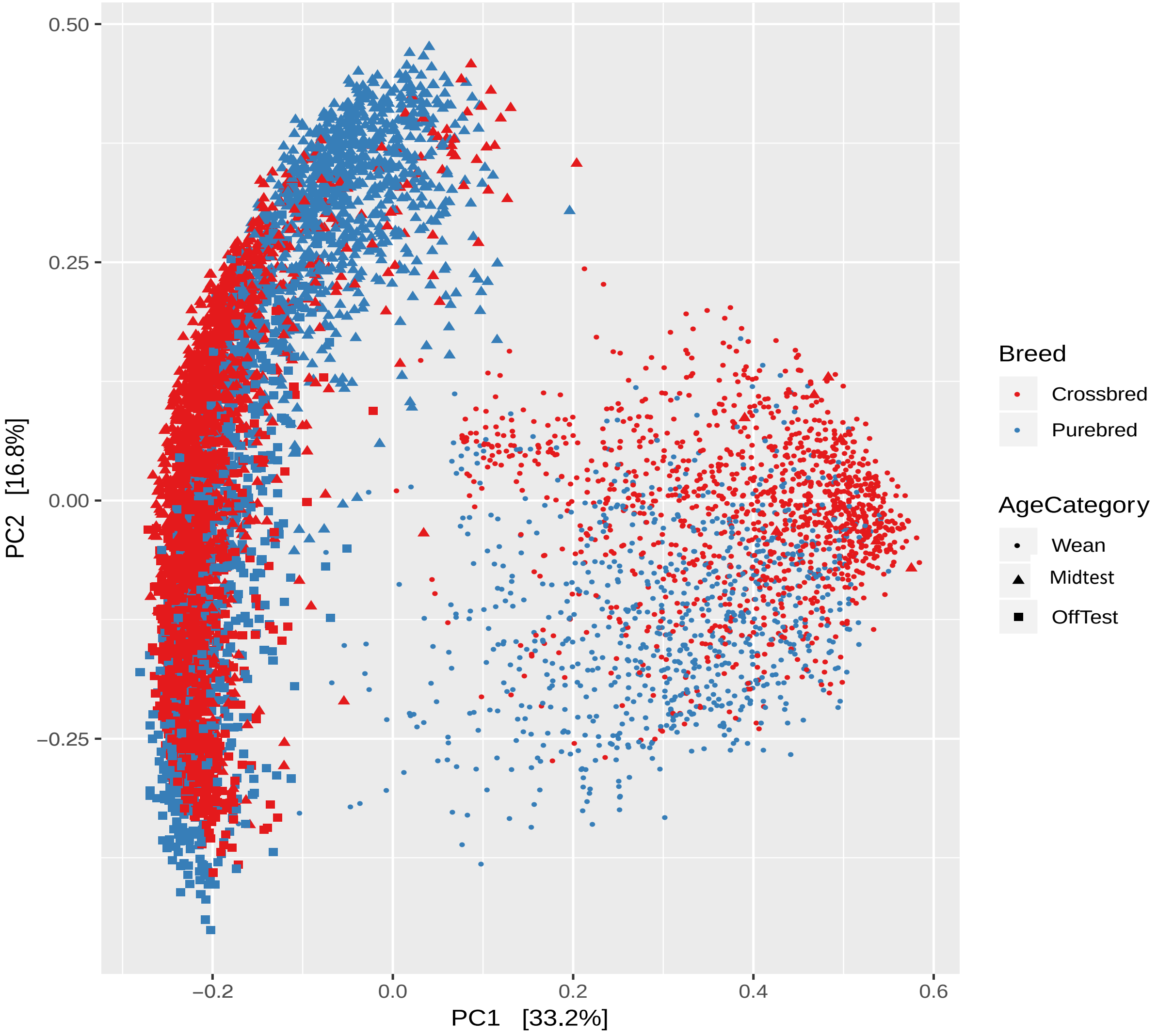
Taxa GWAS

$$\boldsymbol{OTU} = \boldsymbol{X}b + \boldsymbol{K}m + \boldsymbol{Z}s + \boldsymbol{W}p + \boldsymbol{e}$$

Results

Taxa Composition





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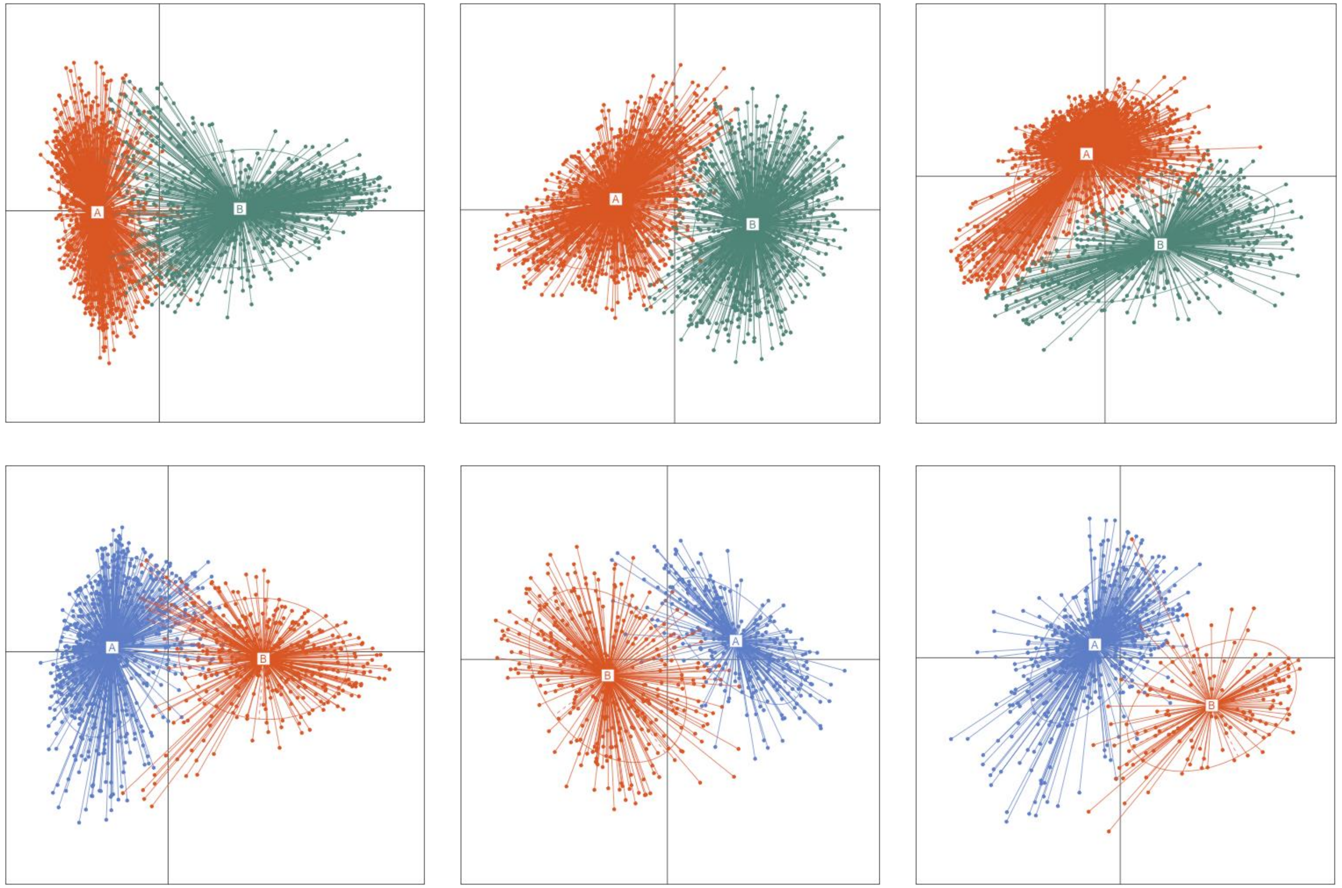
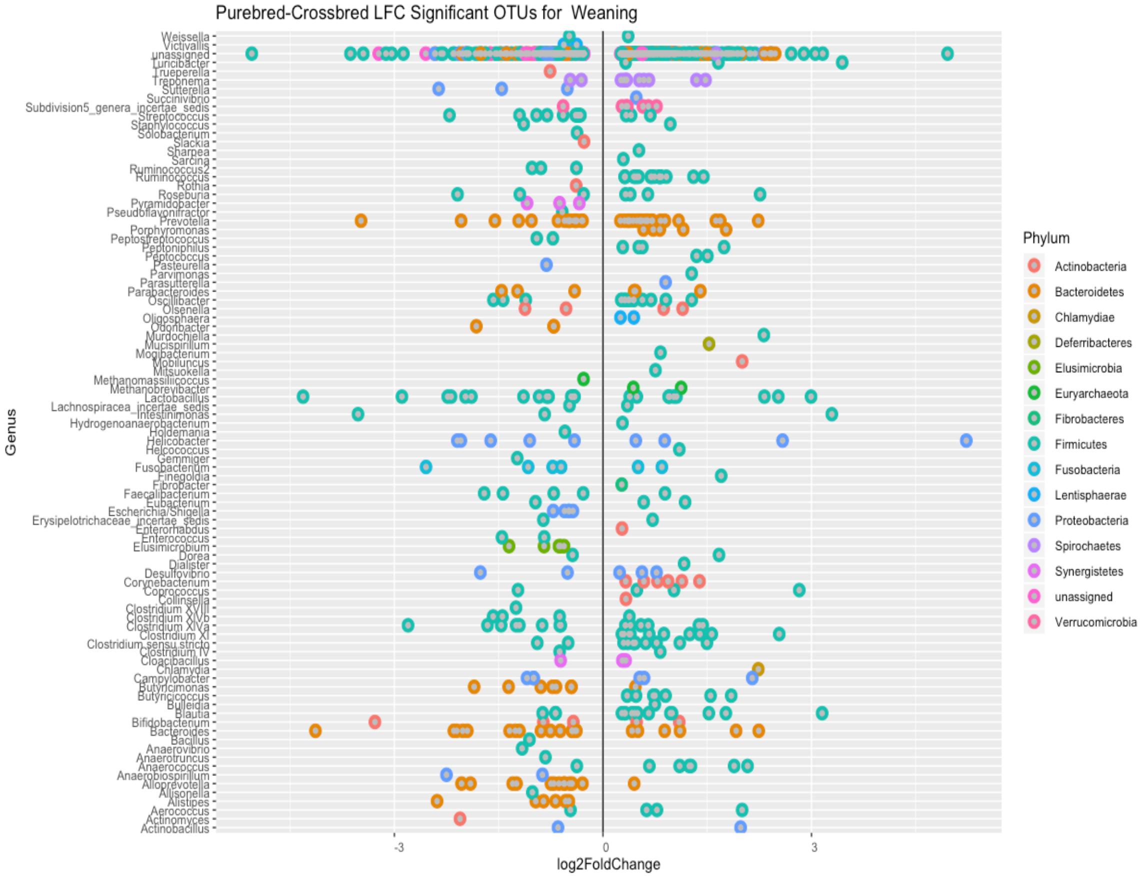
Taxa Composition





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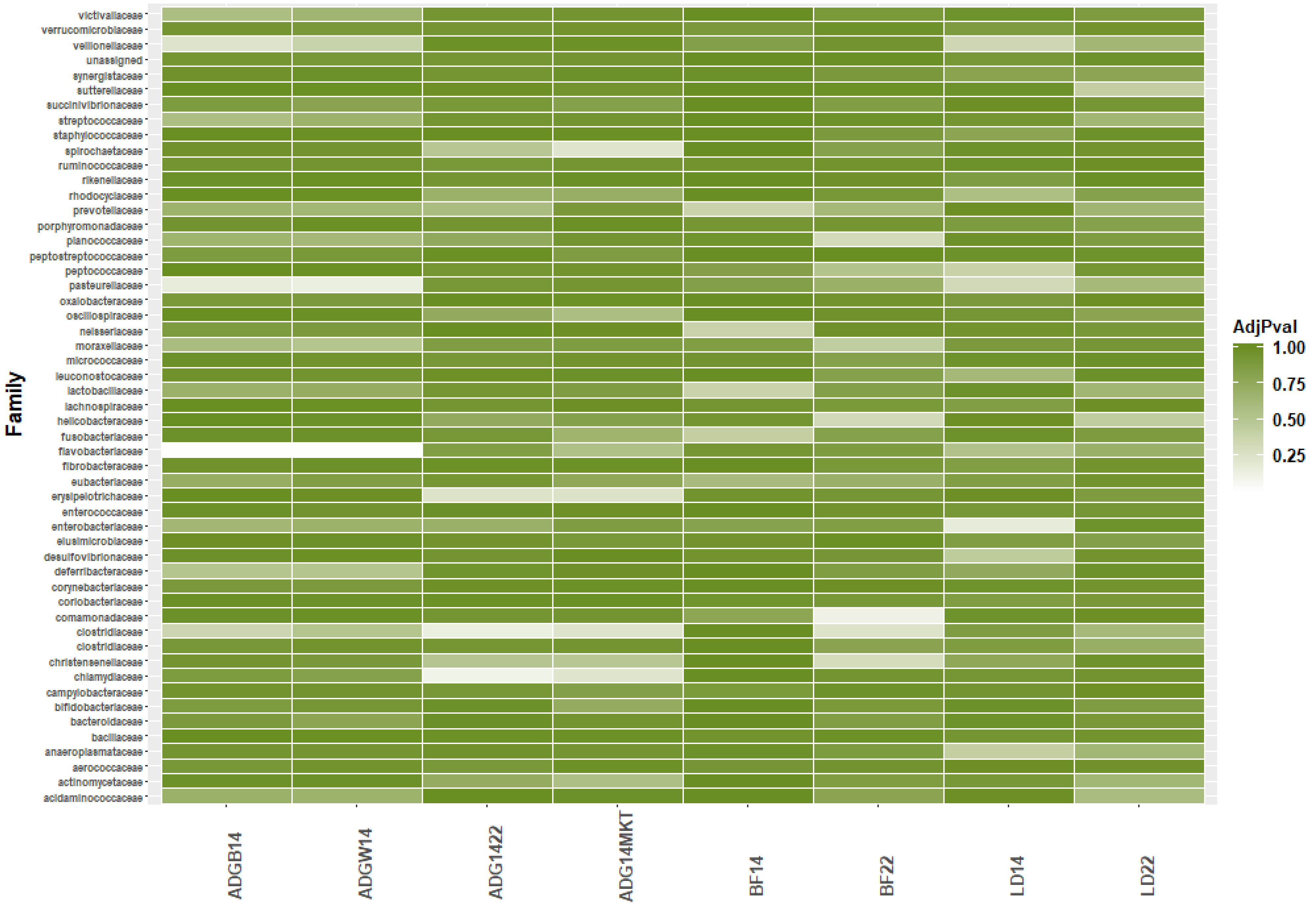
M-WAS

Weaning



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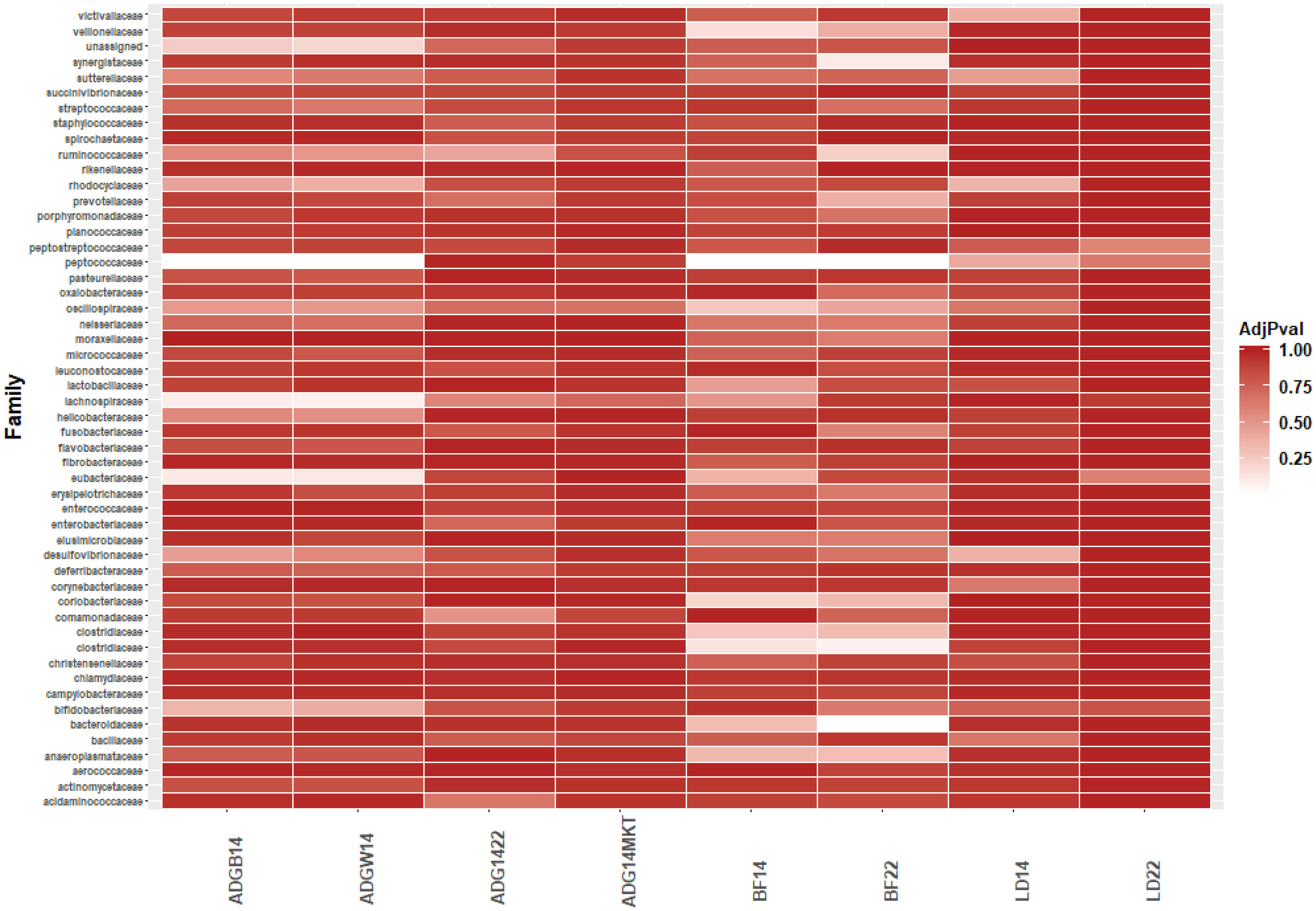
M-WAS

MidTest



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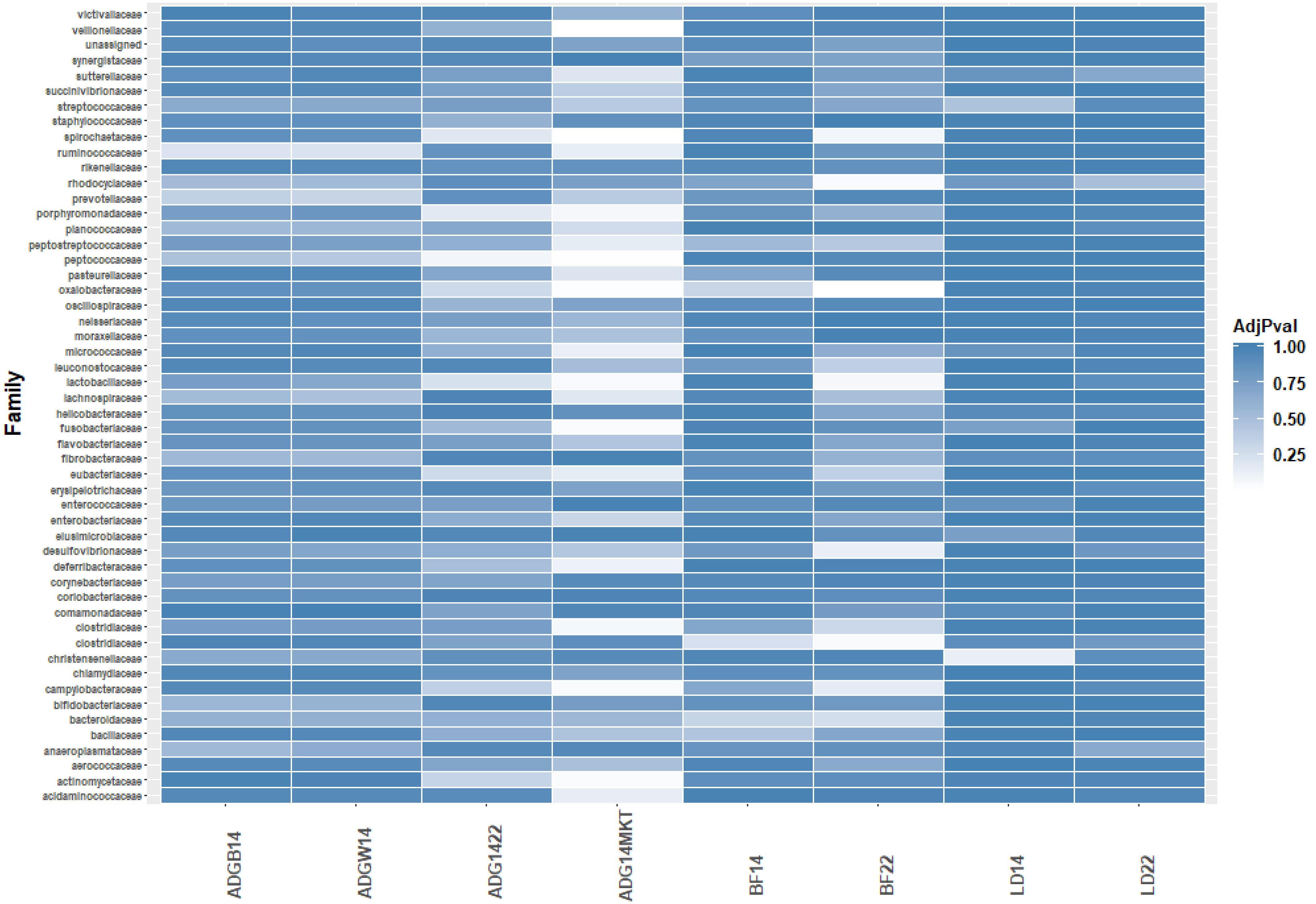
M-WAS

OffTest



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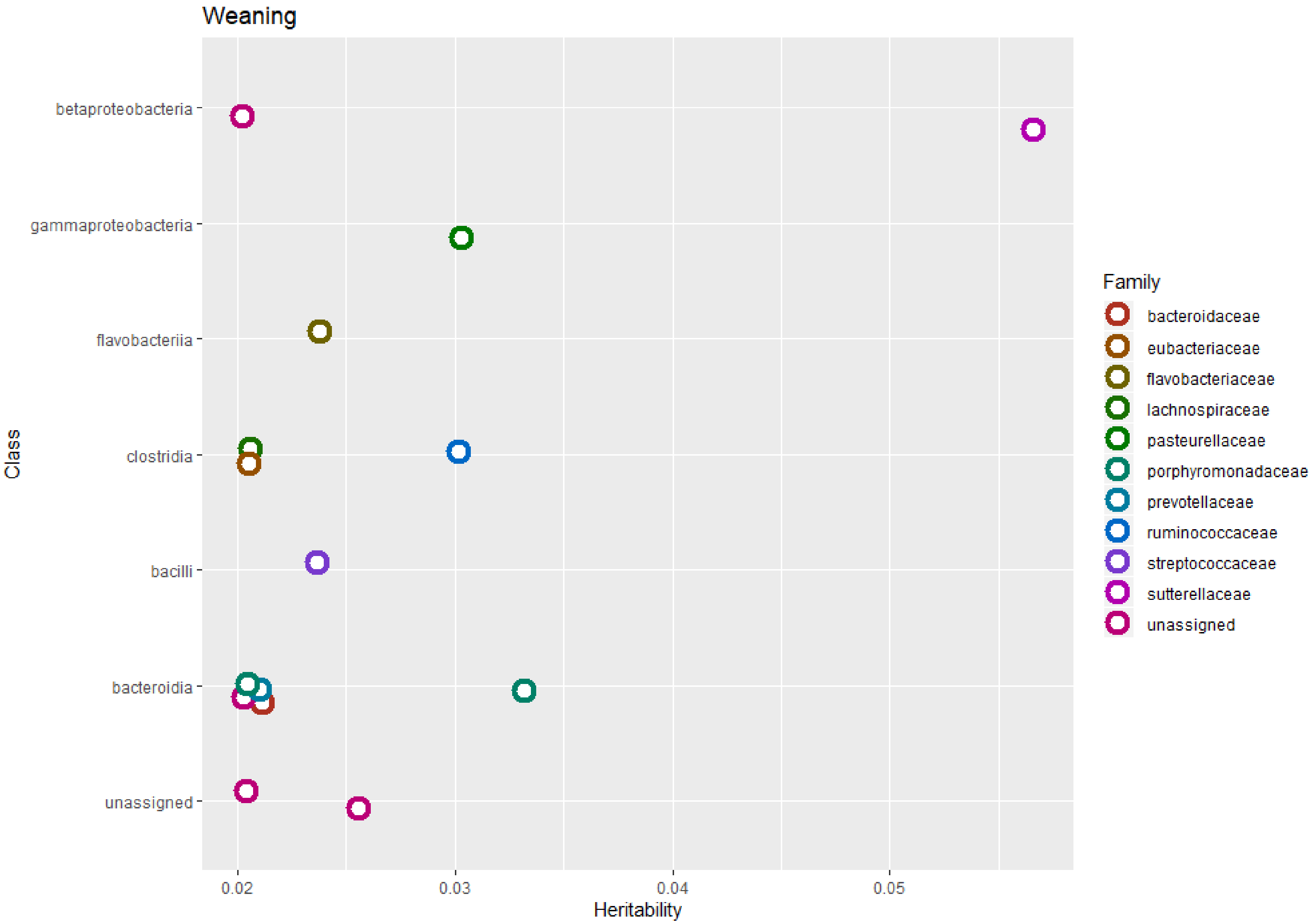
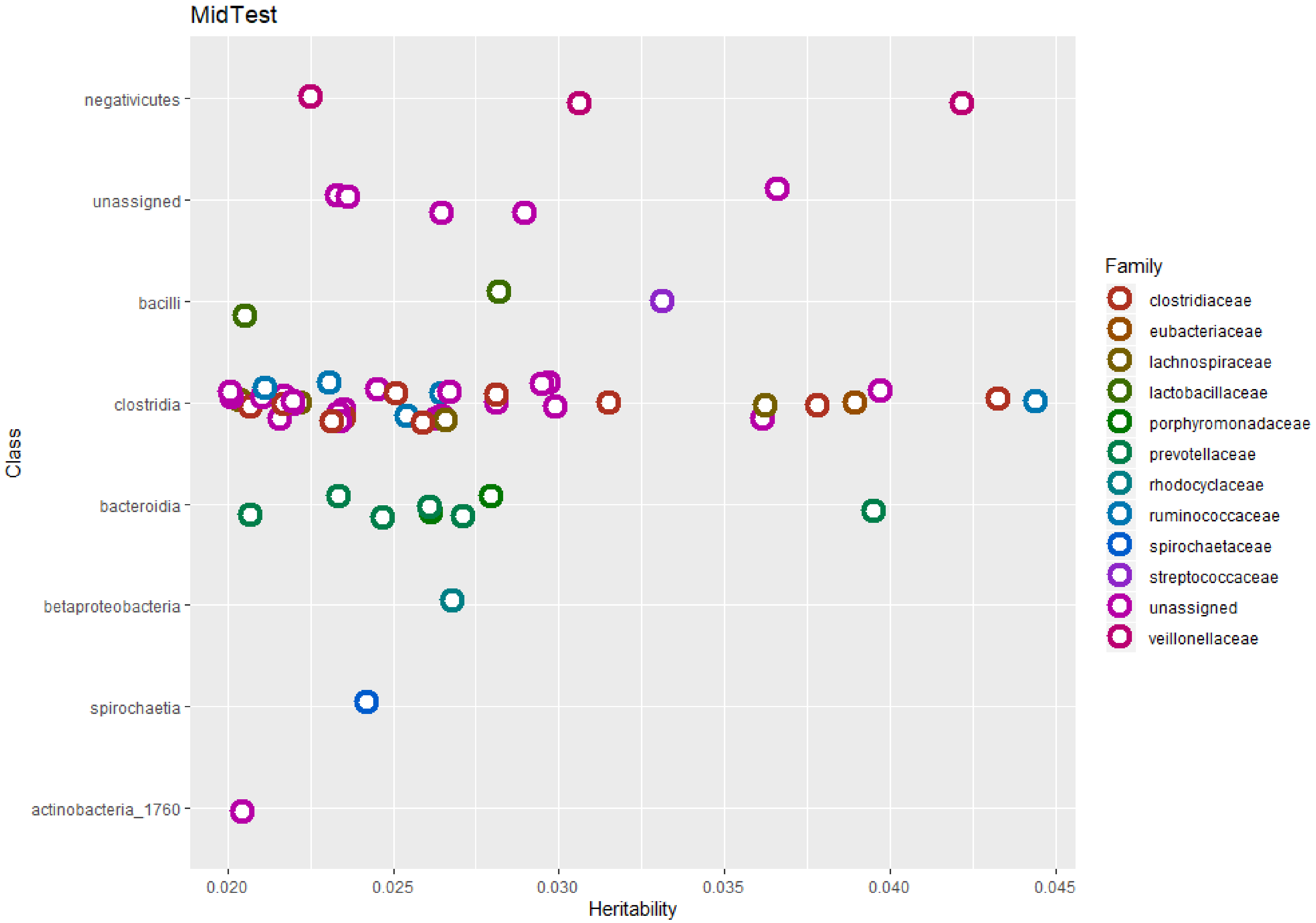
h^2 Estimates

Weaning



h^2 Estimates

MidTest



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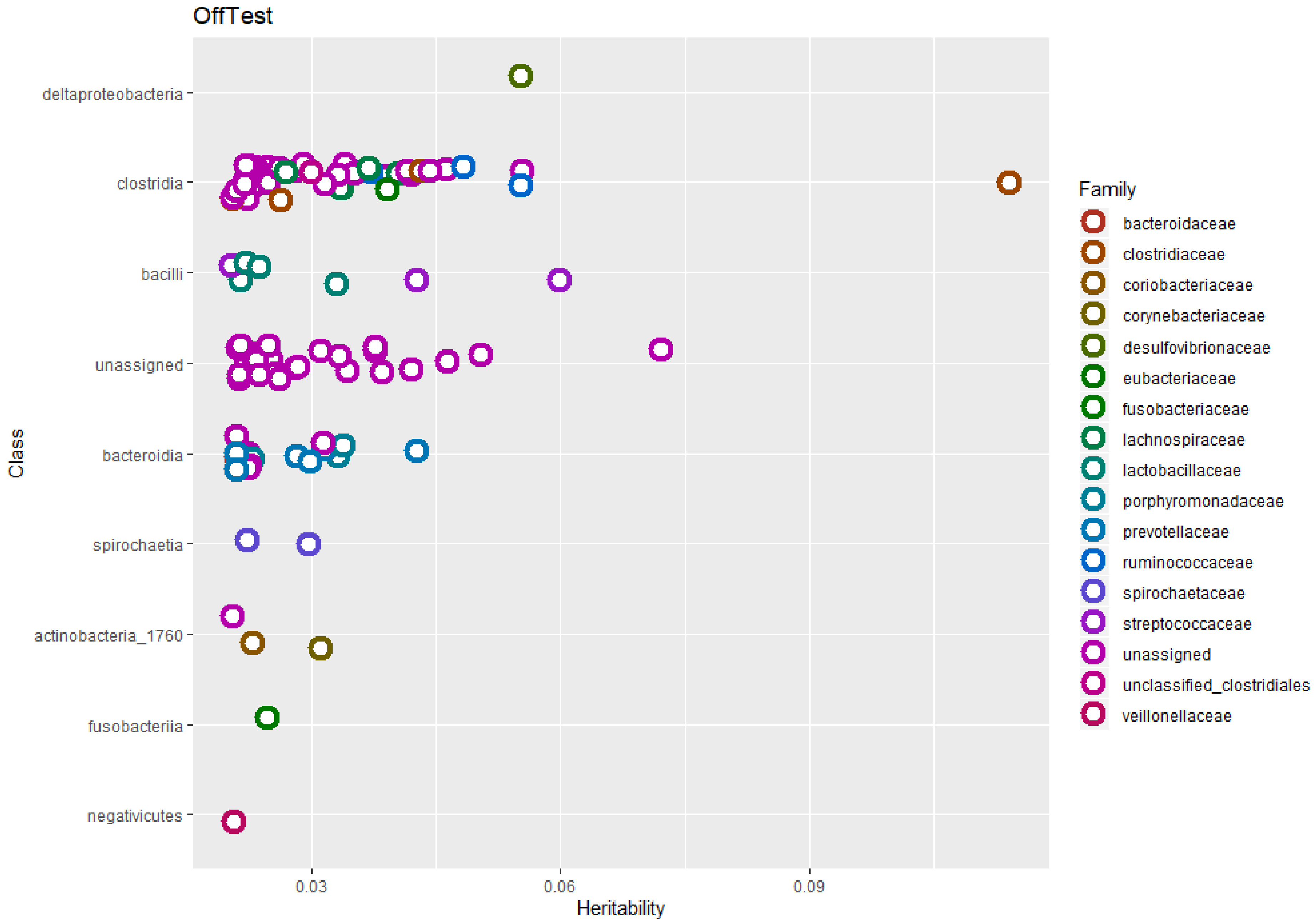
h^2 Estimates

OffTest



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h^2 Estimates

Phylum	Class	Order	Family	Genus	Species	MidTest	OffTest
actinobacteria	actinobacteria_1760	actinomycetales	unassigned	unassigned	unassigned	0.0205	0.0205
bacteroidetes	bacteroidia	bacteroidales	porphyromonadaceae	unassigned	unassigned	0.0262	0.0333
bacteroidetes	bacteroidia	bacteroidales	porphyromonadaceae	unassigned	unassigned	0.0280	0.0339
bacteroidetes	bacteroidia	bacteroidales	prevotellaceae	prevotella	unassigned	0.0395	0.0316
bacteroidetes	bacteroidia	bacteroidales	prevotellaceae	prevotella	copri	0.0271	0.0299
bacteroidetes	bacteroidia	bacteroidales	prevotellaceae	prevotella	copri	0.0261	0.0211
bacteroidetes	unassigned	unassigned	unassigned	unassigned	unassigned	0.0290	0.0228
bacteroidetes	unassigned	unassigned	unassigned	unassigned	unassigned	0.0265	0.0312
bacteroidetes	unassigned	unassigned	unassigned	unassigned	unassigned	0.0366	0.0421
firmicutes	bacilli	lactobacillales	lactobacillaceae	lactobacillus	reuteri	0.0205	0.0221
firmicutes	bacilli	lactobacillales	lactobacillaceae	lactobacillus	reuteri	0.0282	0.0238
firmicutes	bacilli	lactobacillales	streptococcaceae	streptococcus	gallolyticus	0.0331	0.0599
firmicutes	clostridia	clostridiales	clostridiaceae	clostridium	sp_shc10	0.0232	0.0433
firmicutes	clostridia	clostridiales	clostridiaceae	clostridium	butyricum	0.0433	0.1142
firmicutes	clostridia	clostridiales	lachnospiraceae	blautia	obeum	0.0362	0.0269
firmicutes	clostridia	clostridiales	ruminococcaceae	subdoligranulum	variabile	0.0231	0.0345
firmicutes	clostridia	clostridiales	ruminococcaceae	ruminococcus	sp_ce2	0.0212	0.0553
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0245	0.0554
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0297	0.0340
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0281	0.0211
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0397	0.0417
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0201	0.0226
firmicutes	clostridia	clostridiales	unassigned	unassigned	unassigned	0.0267	0.0444
firmicutes	negativicutes	selenomonadales	veillonellaceae	unassigned	unassigned	0.0306	0.0207
unassigned	unassigned	unassigned	unassigned	unassigned	unassigned	0.0233	0.0343

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GWAS

Weaning

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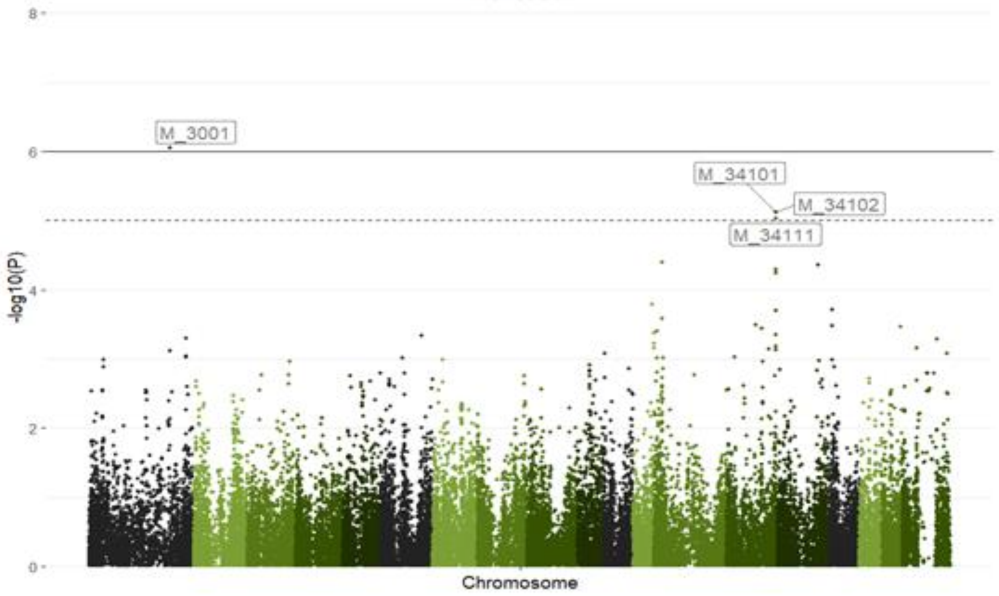

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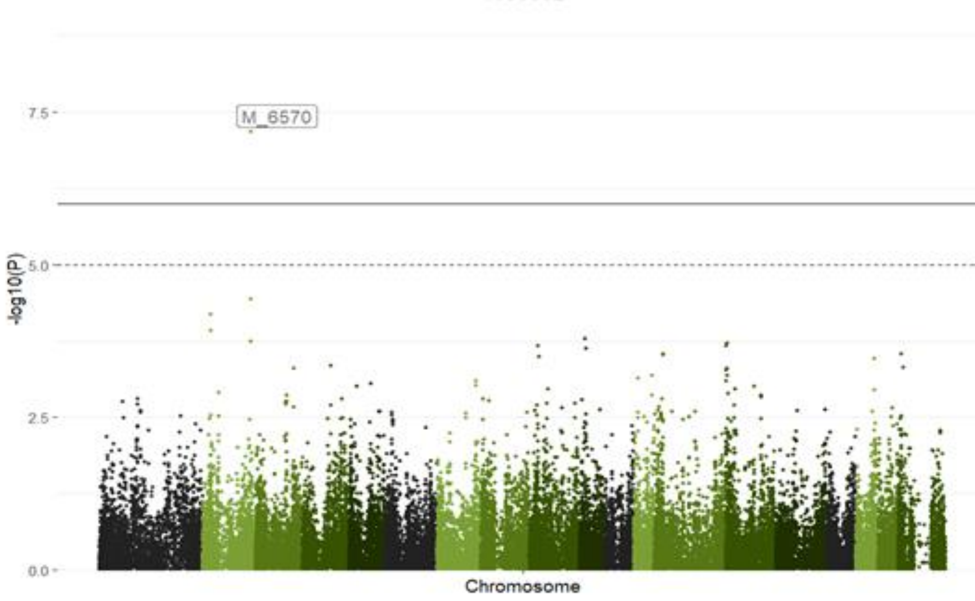

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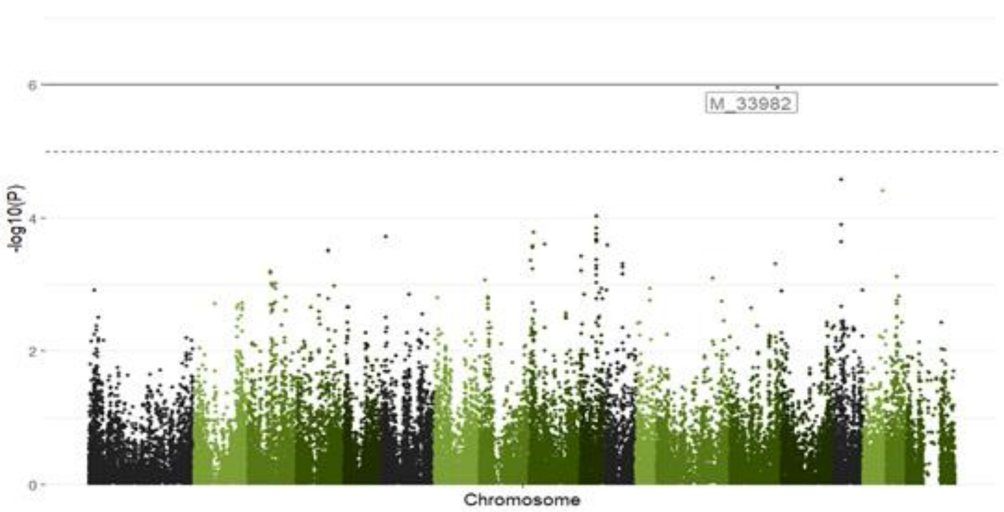

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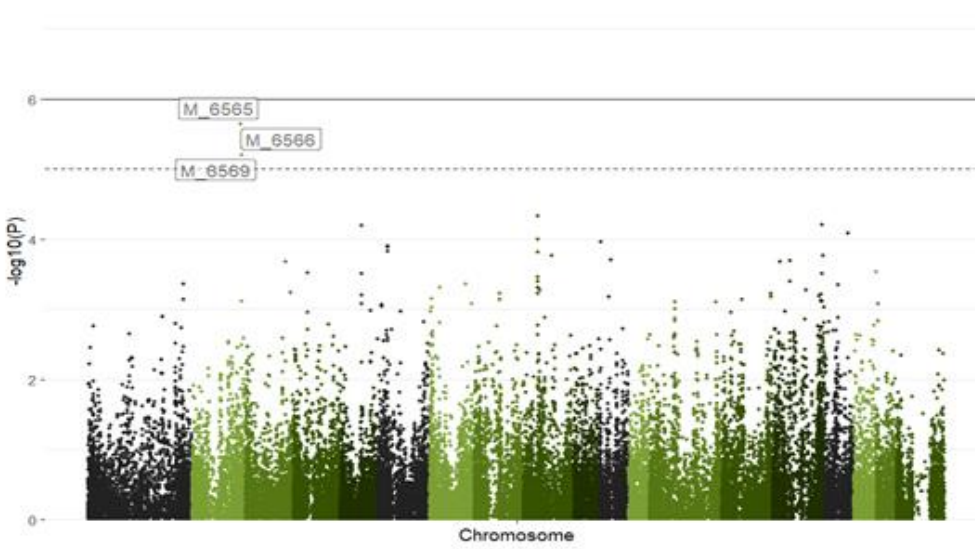

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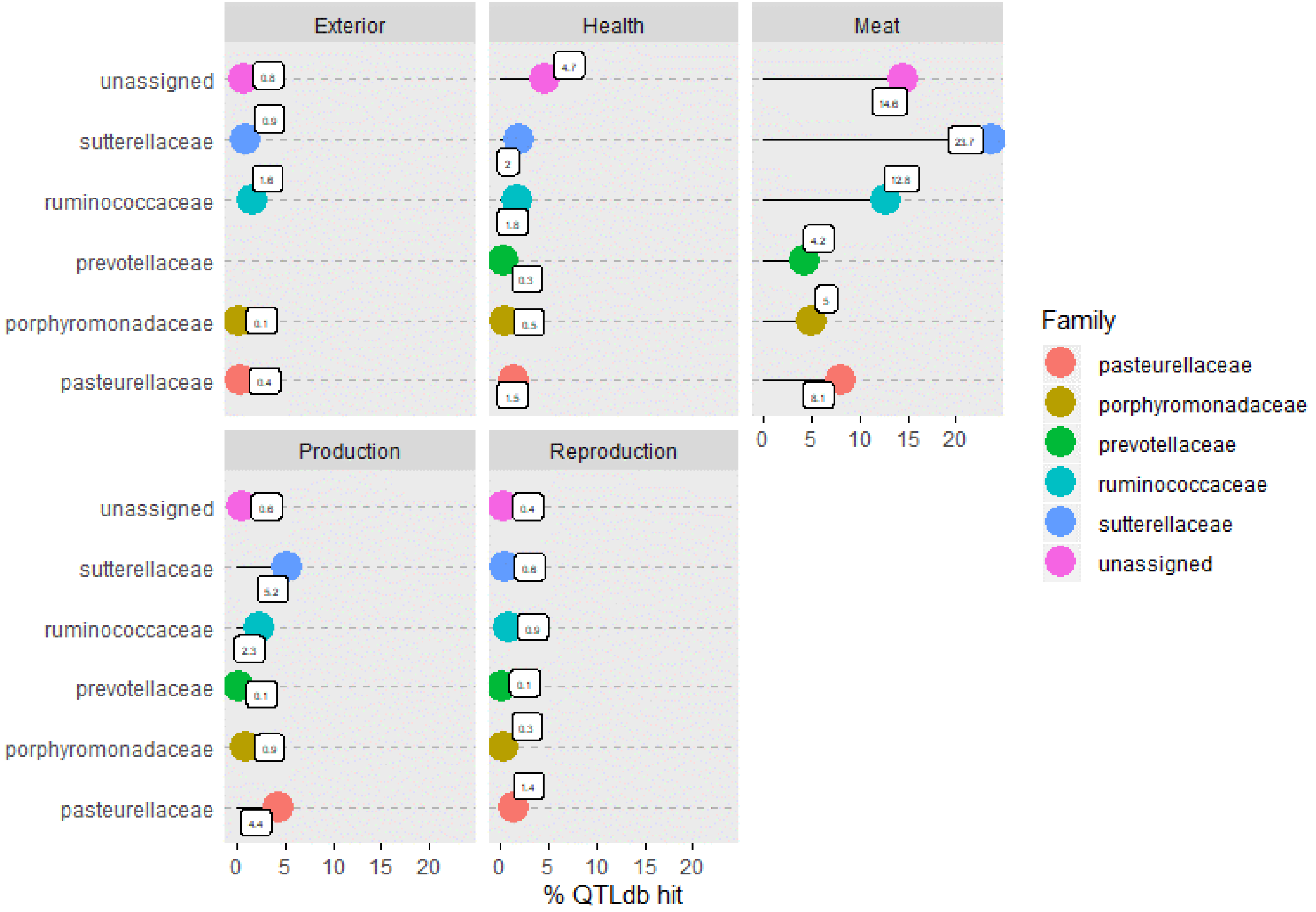
Weaning



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MidTest

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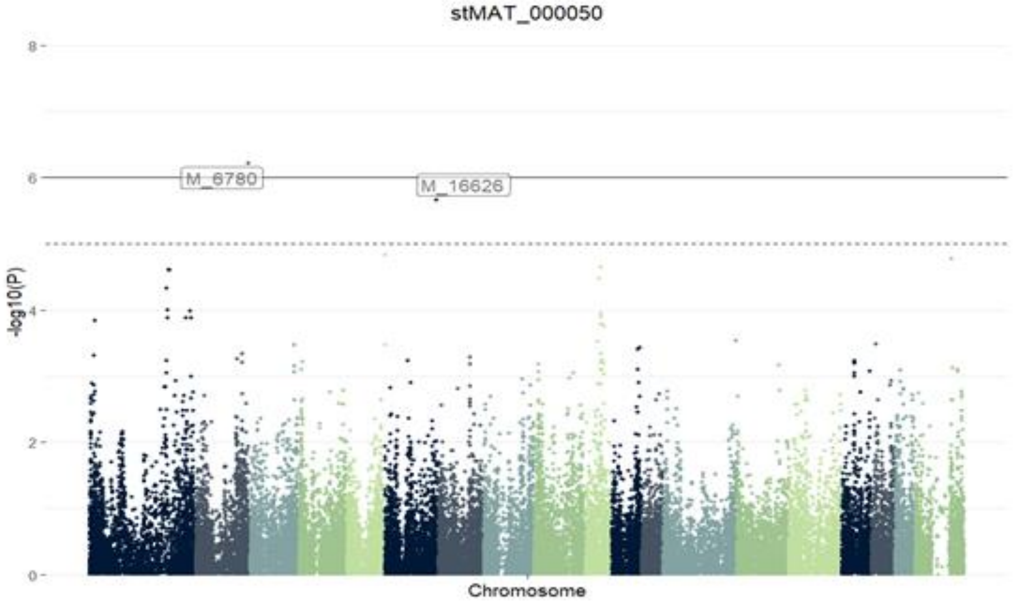

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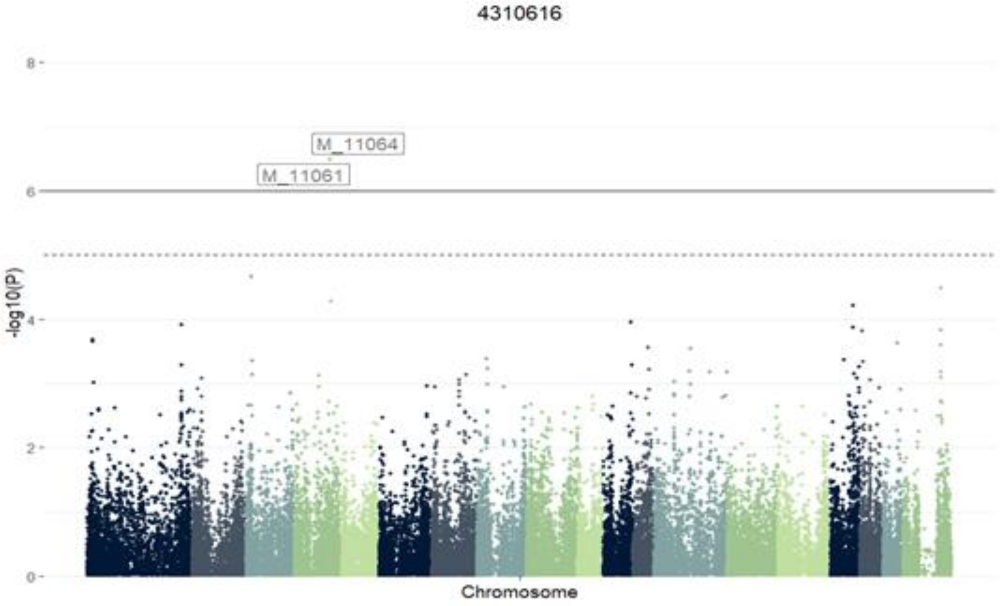

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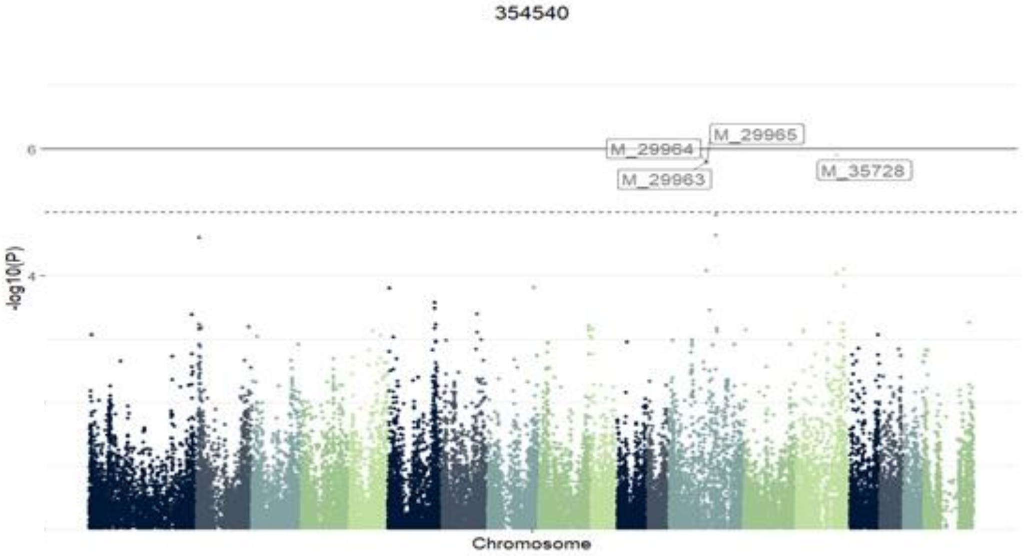

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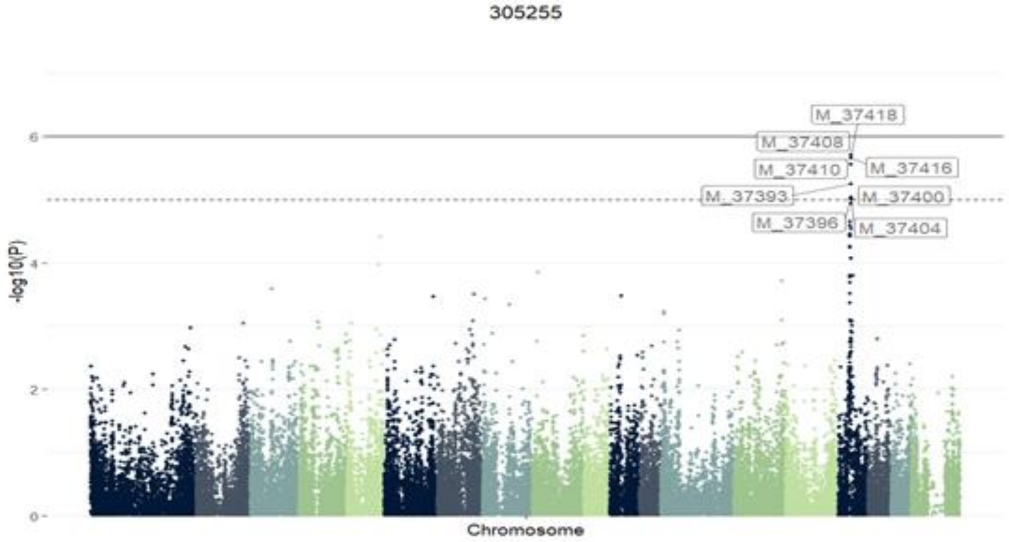

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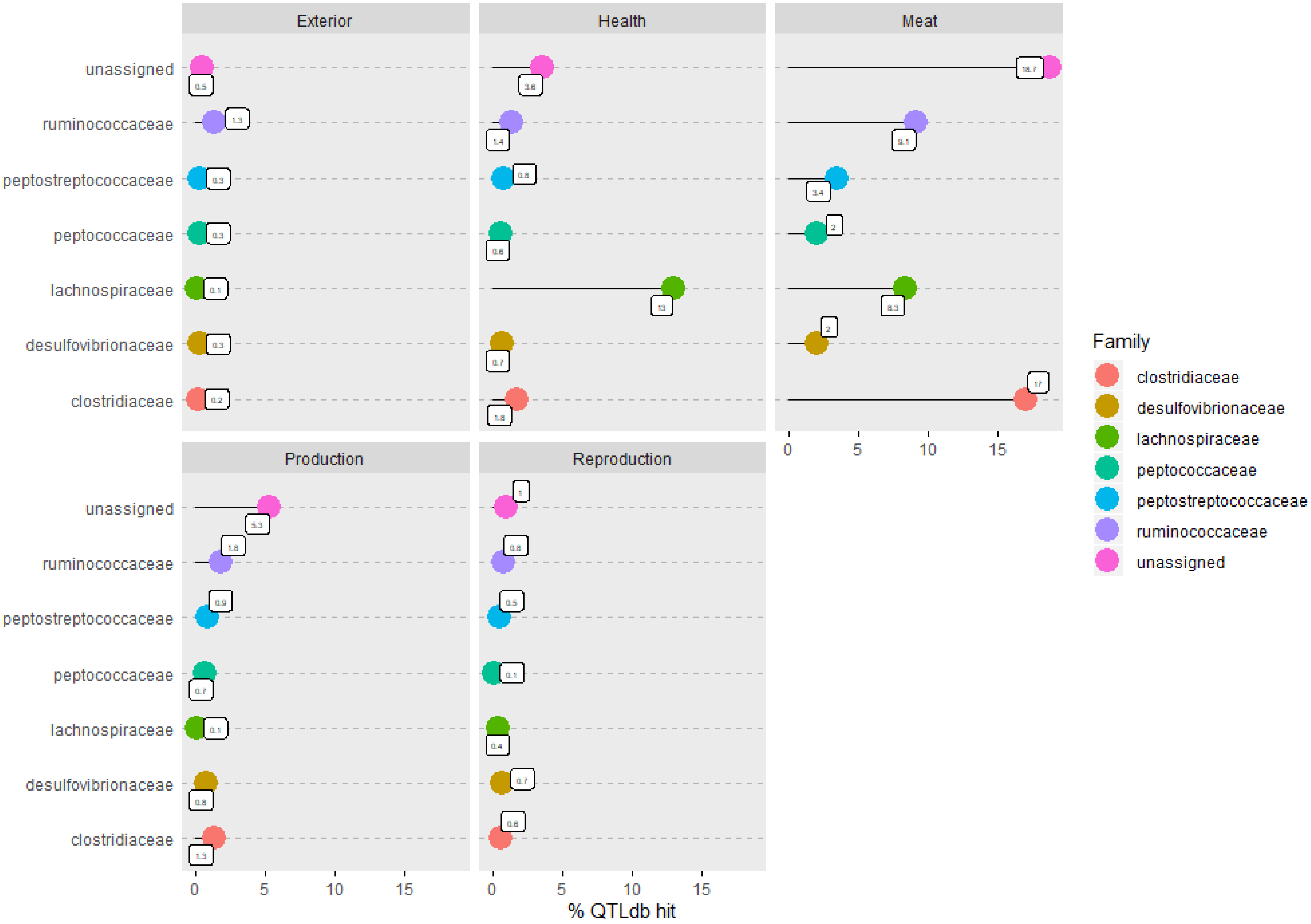
MidTest



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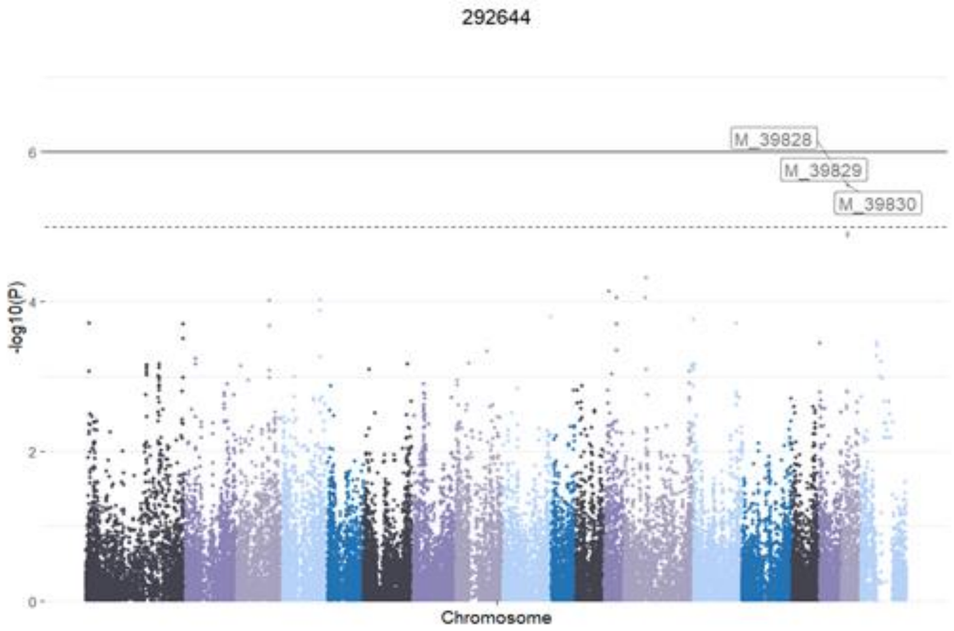
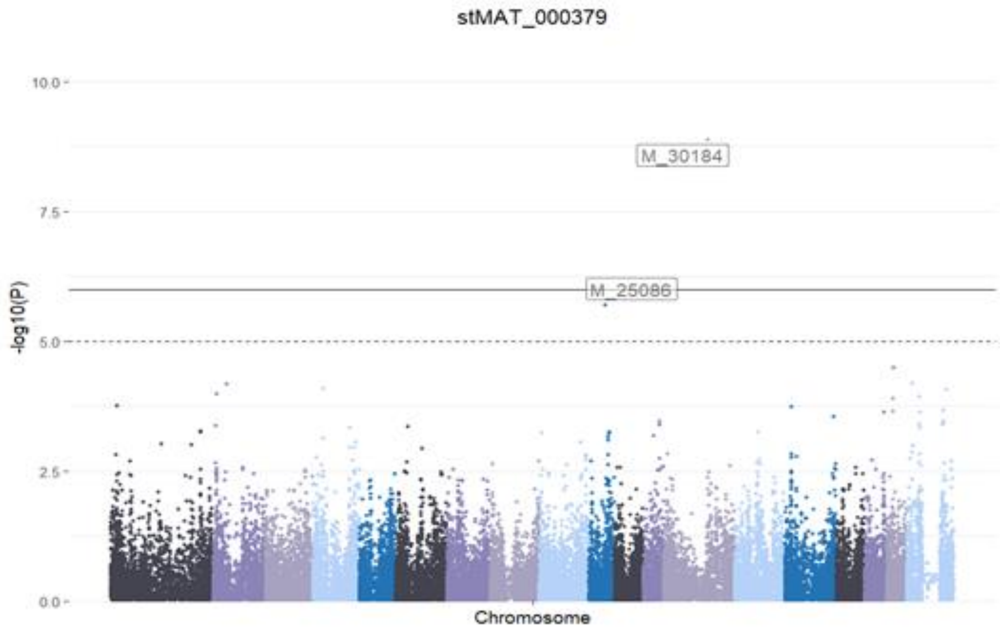
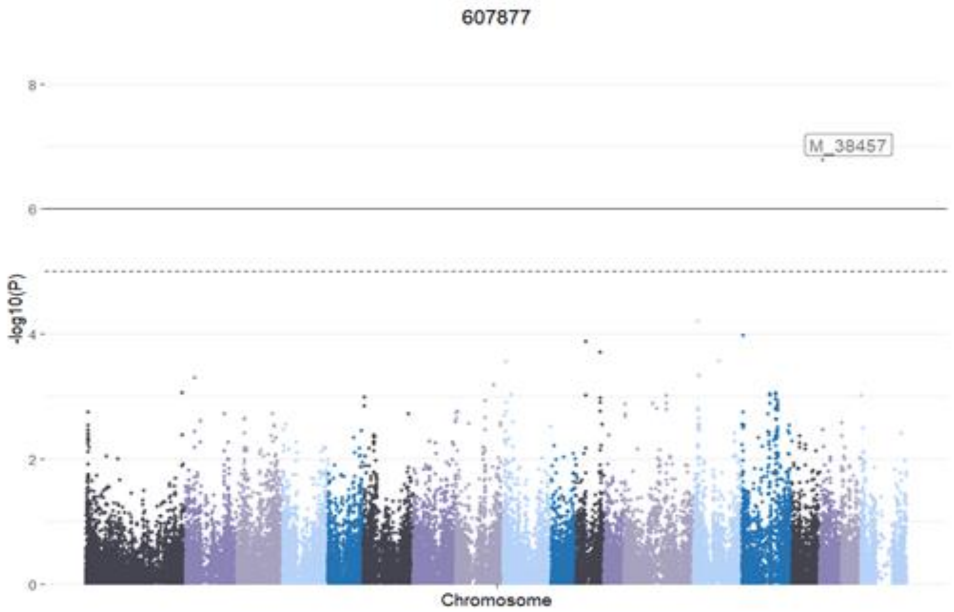
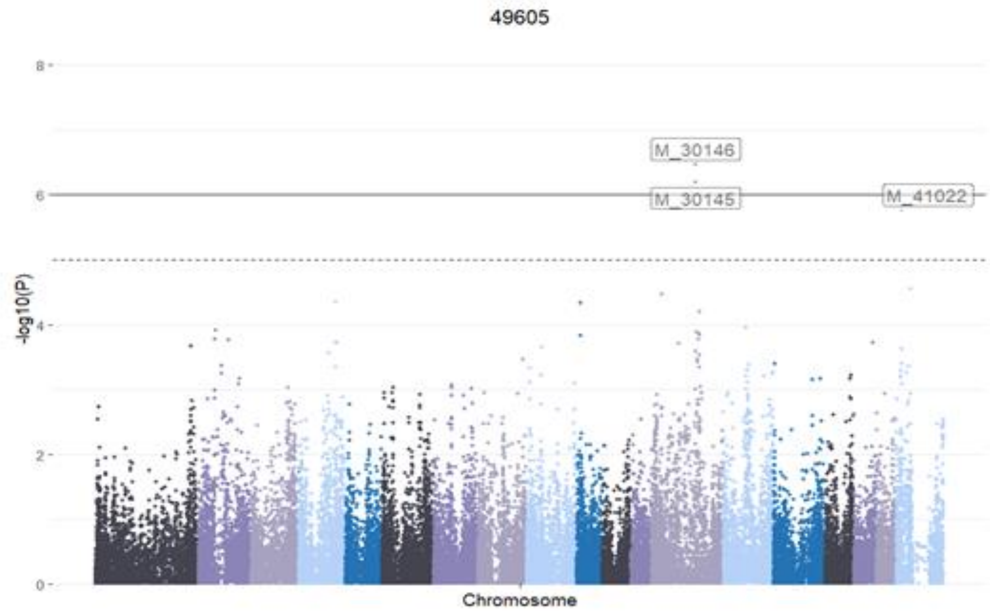
OffTest









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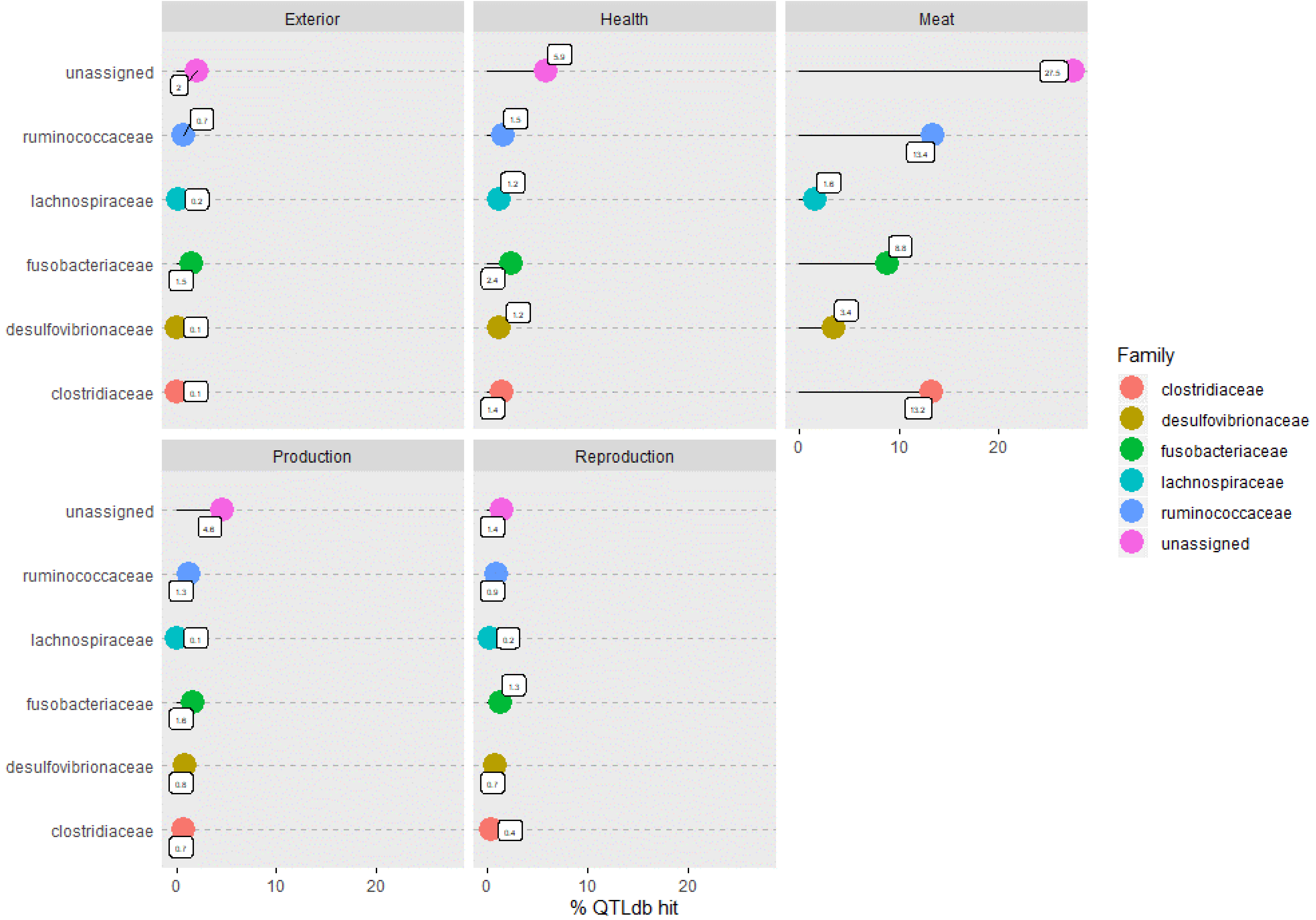
OffTest



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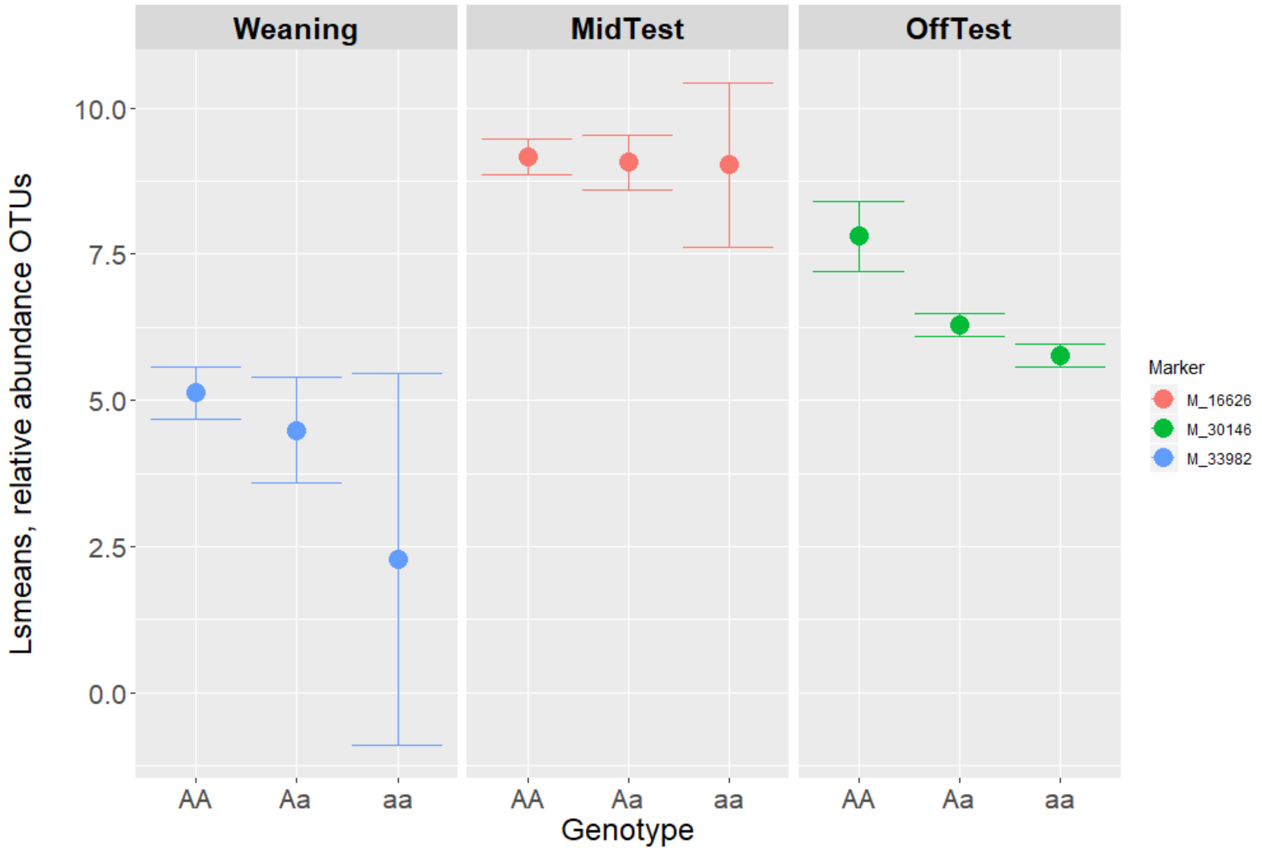
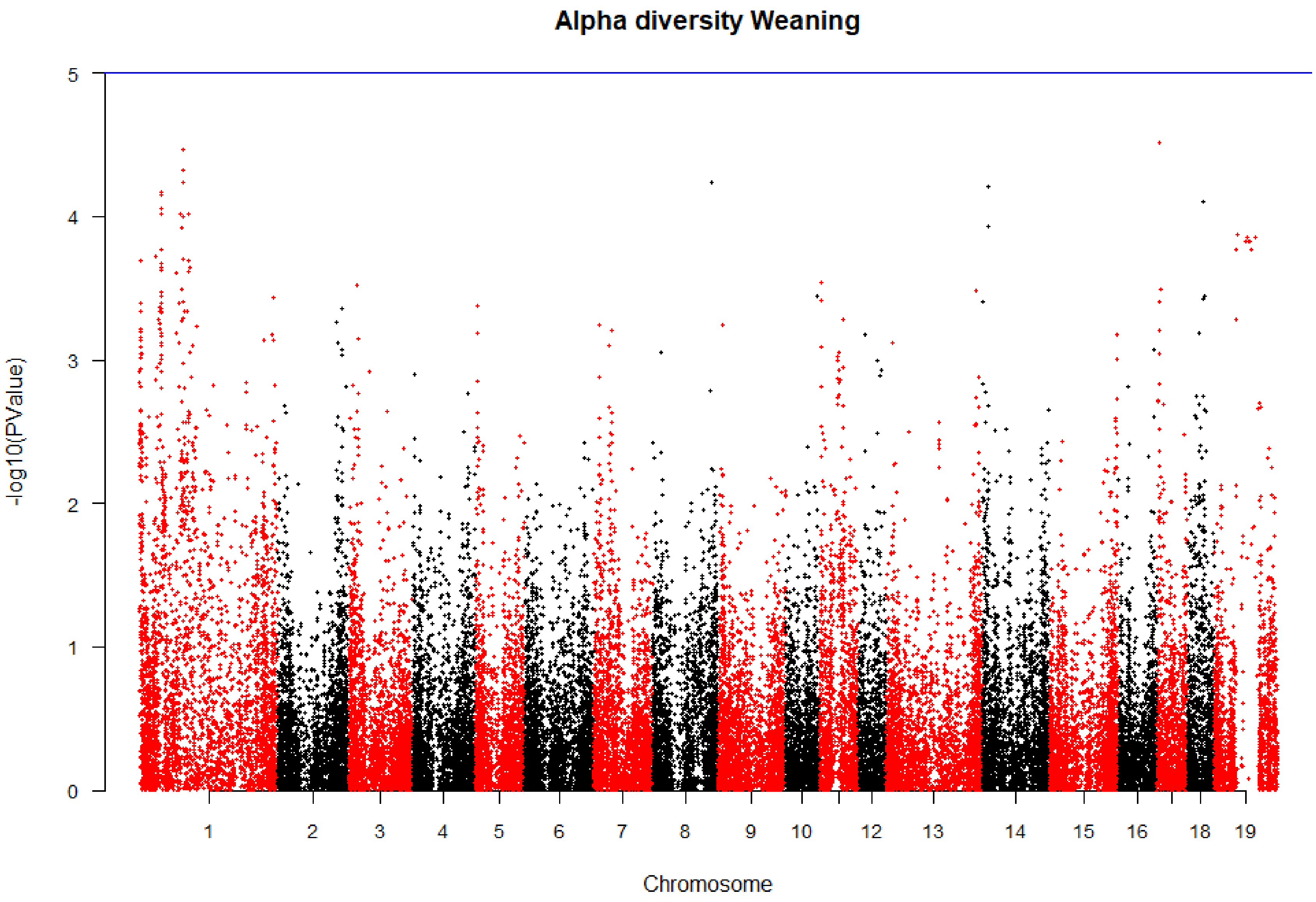


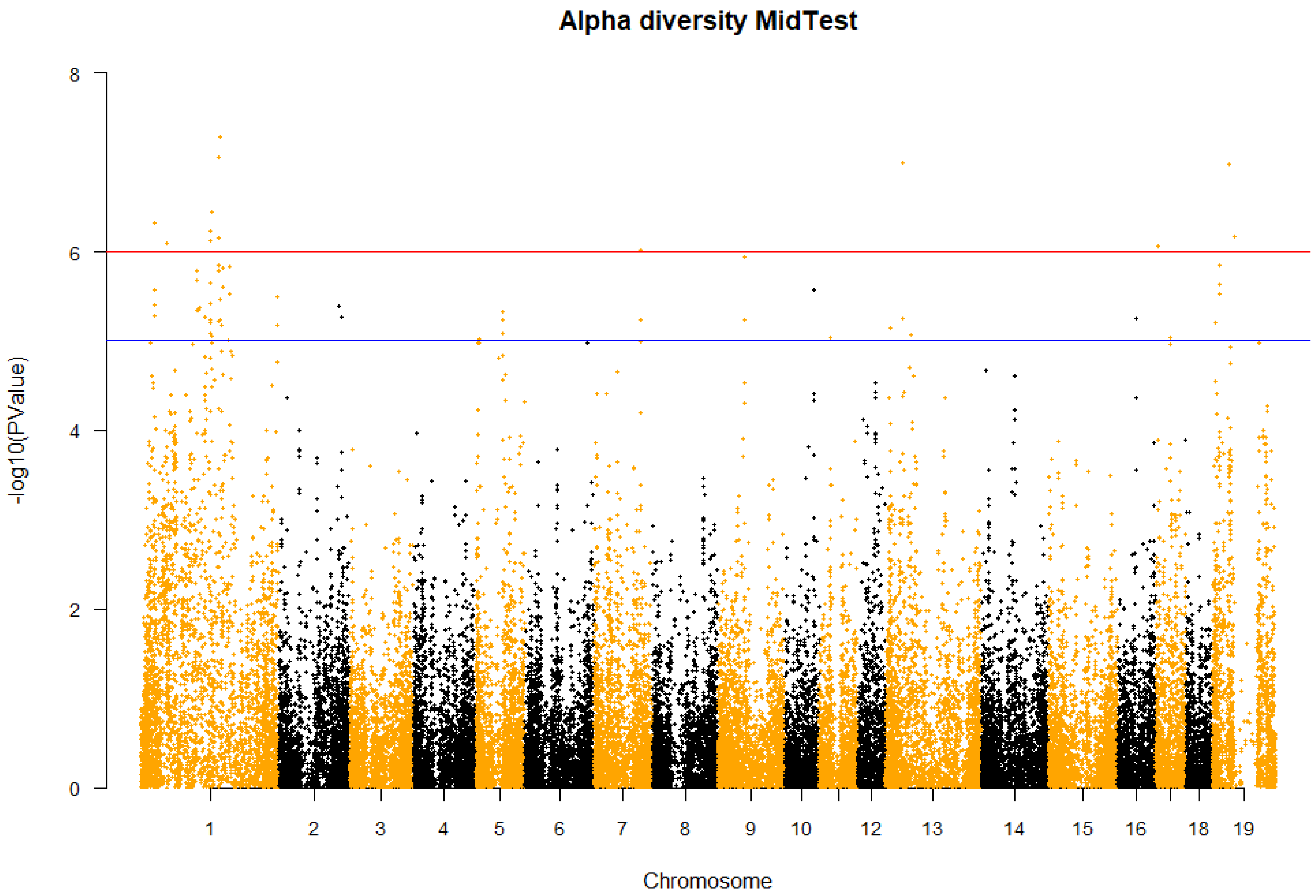
Phylum	Class	Order	Family	Genus	Species	hgnc_symbol
bacteroidetes	flavobacteriia	flavobacteriales	flavobacteriaceae	unassigned	unassigned	SCAF11
bacteroidetes	bacteroidia	bacteroidales	porphyromonadaceae	odoribacter	unassigned	PPFIA2
proteobacteria	betaproteobacteria	burkholderiales	sutterellaceae	parasutterella	secunda	KCNC4
firmicutes	clostridia	clostridiales	peptococcaceae	peptococcus	niger	TPPP
proteobacteria	deltaproteobacteria	desulfovibrionales	desulfovibrionaceae	desulfovibrio	unassigned	FAM114A1
bacteroidetes	unassigned	unassigned	unassigned	unassigned	unassigned	AP4B1
bacteroidetes	bacteroidia	bacteroidales	unassigned	unassigned	unassigned	CCDC6
unassigned	unassigned	unassigned	unassigned	unassigned	unassigned	PAPPA2
firmicutes	clostridia	unassigned	unassigned	unassigned	unassigned	DMC1

GWAS α Diversity
Weaning



GWAS α Diversity

MidTest



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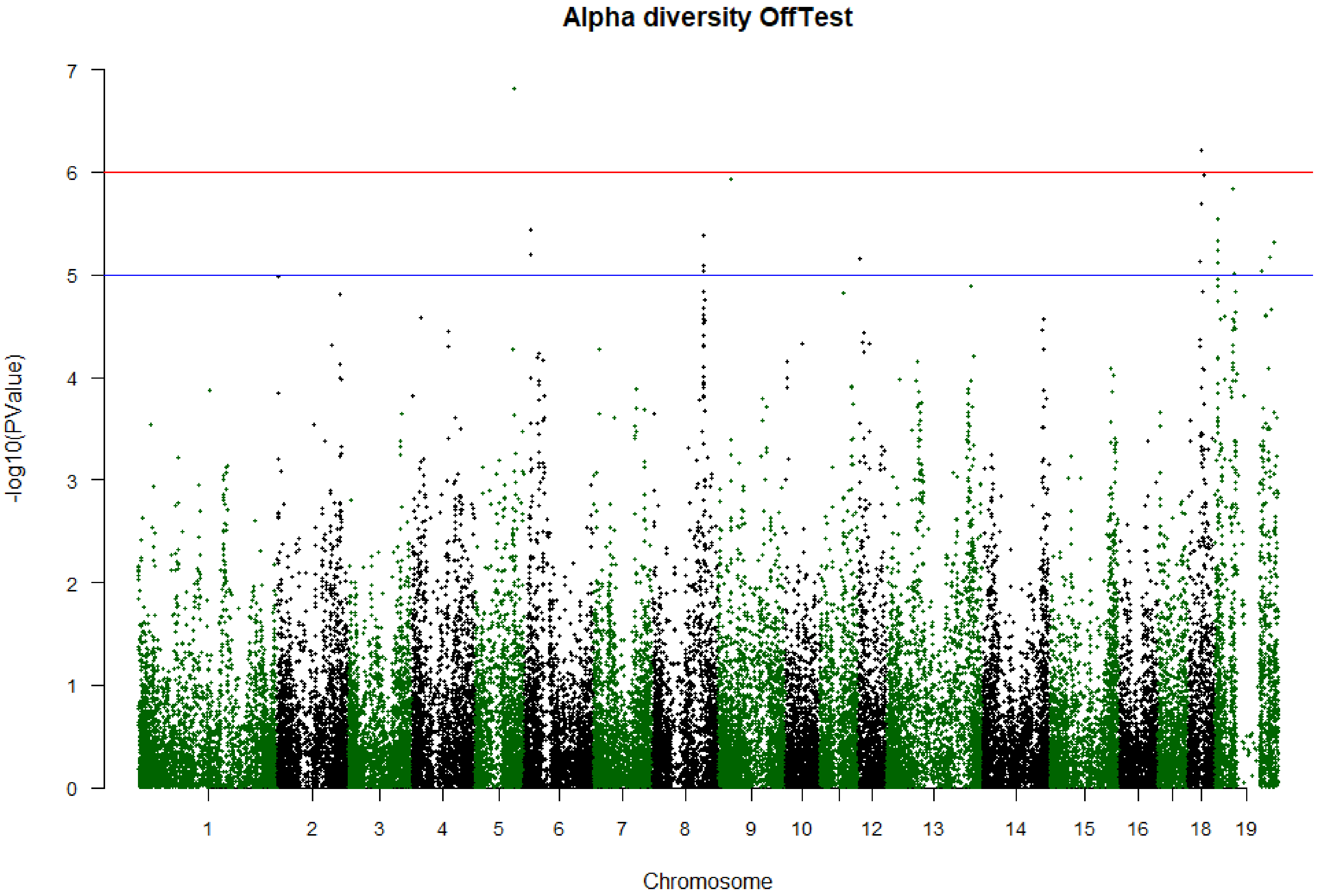
GWAS α Diversity

OffTest



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Summary

MWAS

- 5 taxa at weaning significantly associated with ADG
- 48 taxa from MidTest significantly associated with BF_{14}, BF_{22}, LD_{14}, and LD_{22};
- 19 taxa from OffTest were significantly associated with BF_{22} and ADG.

- Taxa with higher effect on ADG and carcass traits included
  - *Peptococcus niger*, *Rothia nasimurium*, *Coprococcus comes*, *Finegoldia magna, Faecalibacterium prausnitzii.*

h^2

- Heritability estimates for the significant taxa at weaning, MidTest, and OffTest were from 0.021 to 0.057, 0.020 to 0.072, and 0.020 to 0.136, respectively.

GWAS

- There were 15, 21, and 29 SNPs significantly associated with 9, 10, 18 taxa within Weaning, MidTest, and OffTest, respectively.

Acknowledgements

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Progressive Farming. Family Style.

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