

**A****Cohort 2 Weight Analysis**

```
Formula: weight_change ~ day * condition + (1 | new_ratid)
Data: data_no_baseline_2
```

REML criterion at convergence: 166

		R2m	R2c
		0.6576056	0.8143288

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.43230	-0.37062	0.00488	0.44989	1.61281

Random effects:

Groups	Name	Variance	Std.Dev.
new_ratid	(Intercept)	10.17	3.190
Residual		12.05	3.472

Number of obs: 30, groups: new\_ratid, 11

Correlation of Fixed Effects:

(Intr)	day	condinVEH	dy:cndtrnVEH
day	-0.682		
conditinVEH	-0.491	0.334	
dy:cndtrnVEH	0.333	-0.488	-0.723

Fixed effects:

Estimate	Std. Error	t value	
(Intercept)	1.9525	1.8490	1.056
day	-1.2228	0.1397	-8.756
conditionVEH	-3.7830	3.7689	-1.004
day:conditionVEH	1.2141	0.2862	4.242

**B****Female 3-Feature on Cohort 2**

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Formula: weight_change ~ p_Actinobacteria + p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales +
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus + (1 | new_ratid)
Data: data_no_baseline_2
```

REML criterion at convergence: 143.8

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.91850	-0.58403	-0.05095	0.66155	1.51589

Random effects:

Groups	Name	Variance	Std.Dev.
new_ratid	(Intercept)	11.49	3.389
Residual		38.00	6.164

Number of obs: 30, groups: new\_ratid, 11

Correlation of Fixed Effects:

(Intercept)	p_Act	p_A	
p_Actinobacteria	-5.996	2.120	-2.828
p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales	11703.733	57442.881	0.204
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus	-13734.435	57438.494	-0.239
	260.379	136.598	1.906

Fixed effects:

Estimate	Std. Error	t value	
(Intercept)	-5.996	2.120	-2.828
p_Actinobacteria	11703.733	57442.881	0.204
p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales	-13734.435	57438.494	-0.239
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus	260.379	136.598	1.906

Correlation of Fixed Effects:

(Intr)	p_Act	p_A	
p_Actinobacteria	-0.166		
p_Actinobacteria_c_Coriobacteriia_o_Coriobacteriales	0.160	-1.000	
p_Firmicutes_c_Bacilli_o_Lactobacillales_f_Lactobacillaceae_g_Lactobacillus	-0.434	-0.183	0.184

Pr(>Chisq)

model_null	1.711e-05 ***
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R2m R2c

0.3196729	0.4776002
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**C****Male 3-Feature on Female**

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Formula: weight_change ~ p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae +
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae +
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales + (1 | ratid)
Data: data_no_baseline_2
```

REML criterion at convergence: 304.7

Scaled residuals:

Min	1Q	Median	3Q	Max
-2.3647	-0.1419	0.1690	0.5632	1.3410

Random effects:

Groups	Name	Variance	Std.Dev.
ratid	(Intercept)	10.87	3.297
Residual		22.32	4.724

Number of obs: 55, groups: ratid, 12

Correlation of Fixed Effects:

(Intr)	p_F	p_B	p_P
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae	-0.582		
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae	-0.369	-0.251	
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales	0.134	-0.317	-0.052

Fixed effects:

Estimate	Std. Error	df	t value	Pr(> t )	
(Intercept)	-3.438	1.912	26.212	-1.798	0.0836
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae	4.176	27.723	50.931	0.151	0.8809
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae	7.577	46.181	50.765	0.164	0.8703
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales	81.183	179.692	46.889	0.452	0.6535

Pr(>Chisq)

model_null	0.01585 *
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R2m R2c

0.006264704	0.3317904
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**D****Male 3-Feature on Cohort 2 Females**

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Formula: weight_change ~ p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae +
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae +
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales + (1 | new_ratid)
Data: data_no_baseline_2
```

REML criterion at convergence: 148.3

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.47168	-0.59545	-0.05896	0.51798	1.72772

Random effects:

Groups	Name	Variance	Std.Dev.
new_ratid	(Intercept)	32.46	5.697
Residual		20.96	4.578

Number of obs: 30, groups: new\_ratid, 11

Correlation of Fixed Effects:

(Intr)	p_B	p_P	
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae	-0.417		
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae	-0.645	-0.133	
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales	-0.100	0.192	-0.256

Fixed effects:

Estimate	Std. Error	t value	
(Intercept)	10.062	3.563	2.824
p_Bacteroidetes_c_Bacteroidia_o_Bacteroidales_f_Rikenellaceae	-142.412	43.923	-3.242
p_Firmicutes_c_Clostridia_o_Clostridiales_f_Ruminococcaceae	-65.504	16.824	-3.893
p_Proteobacteria_c_Alphaproteobacteria_o_Rickettsiales	-43435.938	27303.651	-1.591

Pr(>Chisq)

model_null_2	0.0004609 ***
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R2m R2c

0.3724733	0.7538152
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**Supplementary Figure 6: R Summary Statistics Testing 3-Feature LME Models on a Second Female Mouse Cohort.** LME models predicting percent weight change from baseline in female mice. Results of summary(model) and of r.squaredGLMM(model) in R. Marginal R<sup>2</sup> (R2M) and conditional R<sup>2</sup> (R2C) are highlighted in the blue box. Result of likelihood ratio test against null model is isolated in the red boxes. **A)** Testing the female-specific 3-feature LME model in the second cohort of female mice. **B)** Testing the male-produced 3-feature LME model in the original female mice cohort. **C)** Testing the male-produced 3-feature LME model in the second female mice cohort.