

A**Final Treatment + Timepoint**

```
Formula: weight_change ~ day + final_treatment + (1 | ratid)
Data: data_no_baseline

REML criterion at convergence: 246.6

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.3885 -0.4695  0.1949  0.4994  2.6236

Random effects:
    Groups Name      Variance Std.Dev.
    ratid  (Intercept) 0.9716  0.9857
    Residual              10.7682  3.2815
Number of obs: 47, groups: ratid, 16

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    0.4062    1.1880 42.9970   0.342   0.734
day            -0.9794    0.1128 29.4333  -8.684 1.29e-09 ***
final_treatmentVEH -1.2263    2.0373 42.9999  -0.602   0.550
day:final_treatmentVEH  0.9664    0.1904 30.4625   5.076 1.81e-05 ***
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Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) day    fn_VEH
day           -0.823
fn1_trtmVEH  -0.583  0.480
dy:fn1_tVEH   0.487 -0.592 -0.835
```

	R2m	R2C
	0.7166616	0.7401111

B**Male 3-Feature LME Model**

```
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 | new_ratid)

REML criterion at convergence: 245.3

Scaled residuals:
    Min       1Q   Median       3Q      Max
-2.54749 -0.47413  0.02667  0.60731  1.95694

Random effects:
    Groups Name      Variance Std.Dev.
    new_ratid (Intercept) 0.0  0.000
    Residual              25.8  5.079
Number of obs: 47, groups: new_ratid, 16

Fixed effects:
              Estimate Std. Error    df t value Pr(>|t|)
(Intercept)    2.091    1.878
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae -51.615    19.879
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae -36.747    10.592
p__Proteobacteria_c__Alphaproteobacteria_o__Rickettsiales -36393.037    16840.178
(Intercept)    43.000    1.114
p__Firmicutes_c__Clostridia_o__Clostridiales_f__Ruminococcaceae 43.000    2.596
p__Bacteroidetes_c__Bacteroidia_o__Bacteroidales_f__Rikenellaceae 43.000    3.469
p__Proteobacteria_c__Alphaproteobacteria_o__Rickettsiales 43.000    2.161
```

	R2m	R2C
	0.3905489	0.3905489

	Pr(>Chisq)
model_null_2	2.283e-05 ***
new_model	

	Correlation of Fixed Effects:
	(Intr) p__F__ p__B__
p__F__C	-0.829
p__B__B	-0.267 -0.050
p__P__A	-0.141 -0.041 -0.213

Supplementary Figure 4: R Summary Statistics Testing the Male-Produced 3-Feature LME Model on a Second Male Mouse Cohort. **A)** Results of summary(model) in R for an LME model of final treatment with temporal effects. **B)** Results of summary(model) in R for the 3-feature model in the second mouse cohort. Result of likelihood ratio test against null model is highlighted in the red box. Marginal R² (R2M) and conditional R² (R2C) are highlighted in the blue boxes.