|  |  |  |  |
| --- | --- | --- | --- |
| Model: Depletion | Df | F | P value |
| Lean mass (W – W30) |  |  |  |
| * Strain | 18.73 | 5.9635 | 0.0247 \* |
| * Sample Day | 21.21 | 8.7666 | 0.0002 \* |
| * Strain x Sample Day | 9.81 | 1.1885 | 0.3744 |
| Final model:  lme4::lmer(formula = lean\_mass ~ strain + sample\_day + (1 | rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list( strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |
| Model: Depletion | Df | F | P value |
| Lipid mass (W – W30) |  |  |  |
| * Strain | 25.31 | 17.4790 | 0.0003 \* |
| * Sample Day | 20.36 | 63.8745 | <1e-07 \* |
| * Lean Mass | 37.93 | 1.3748 | 0.2483 |
| * Strain x Sample Day | 16.13 | 2.0535 | 0.1346 |
| Final model:  lme4::lmer(formula = lipid\_mass ~ strain + sample\_day + (1 |  rep/cohort), data = model.frame(object), REML = TRUE, contrasts = list(  strain = "contr.SAS", sample\_day = "contr.SAS")) | | | |