

mTSC Food Intake Analysis

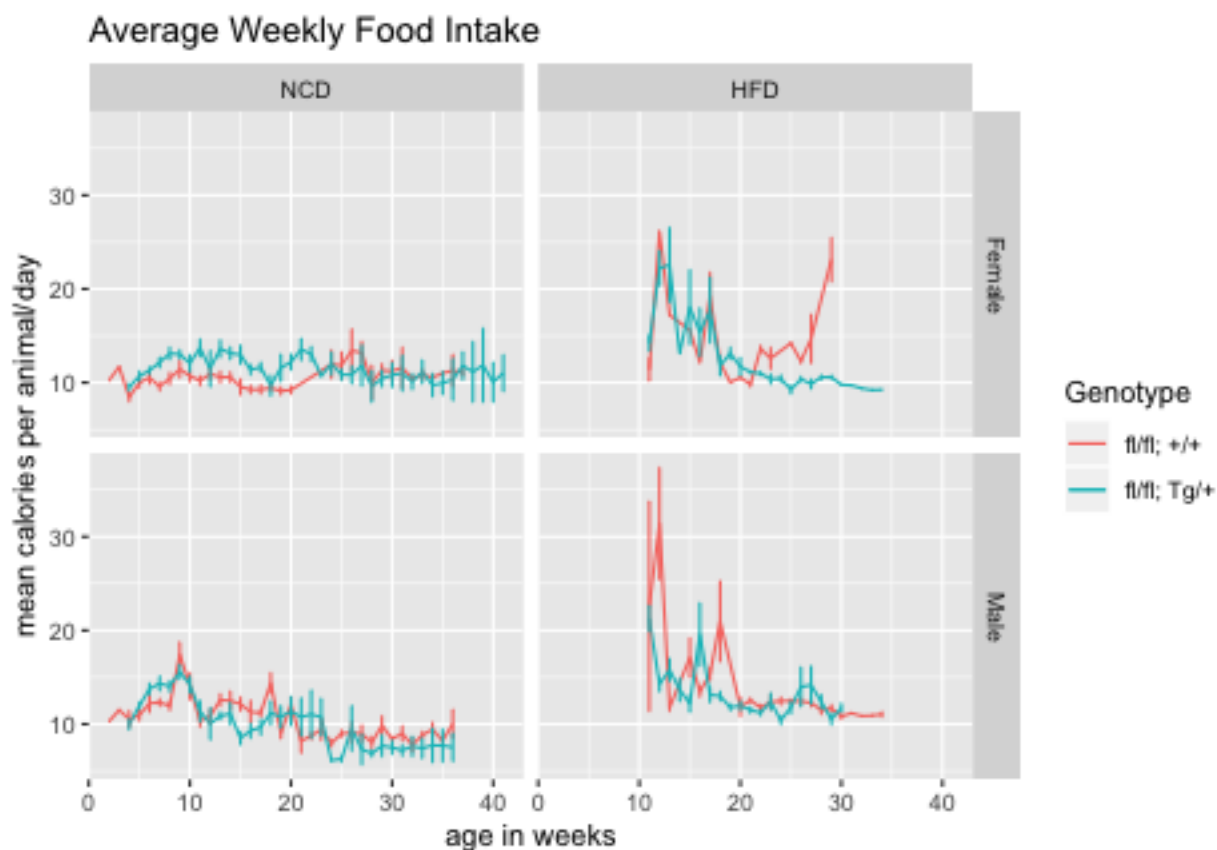
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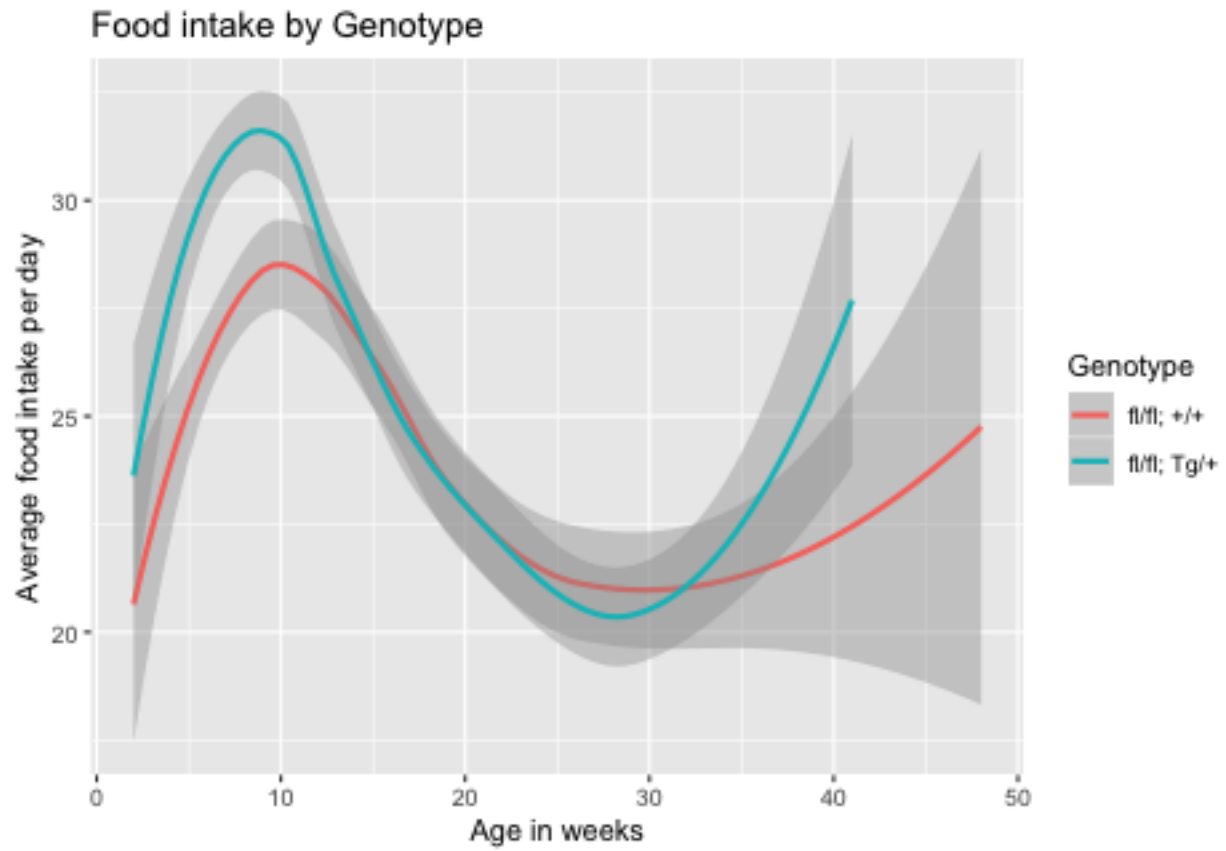
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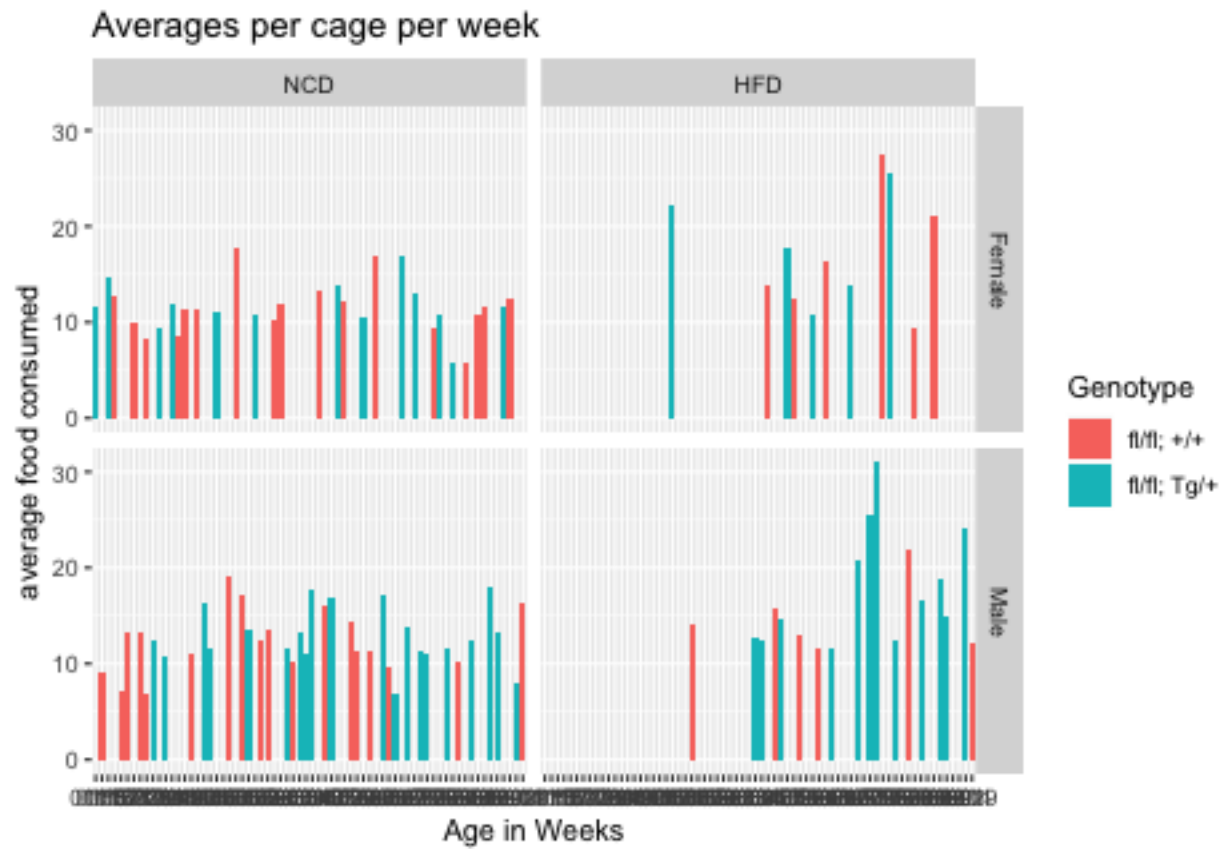
1 Raw Data

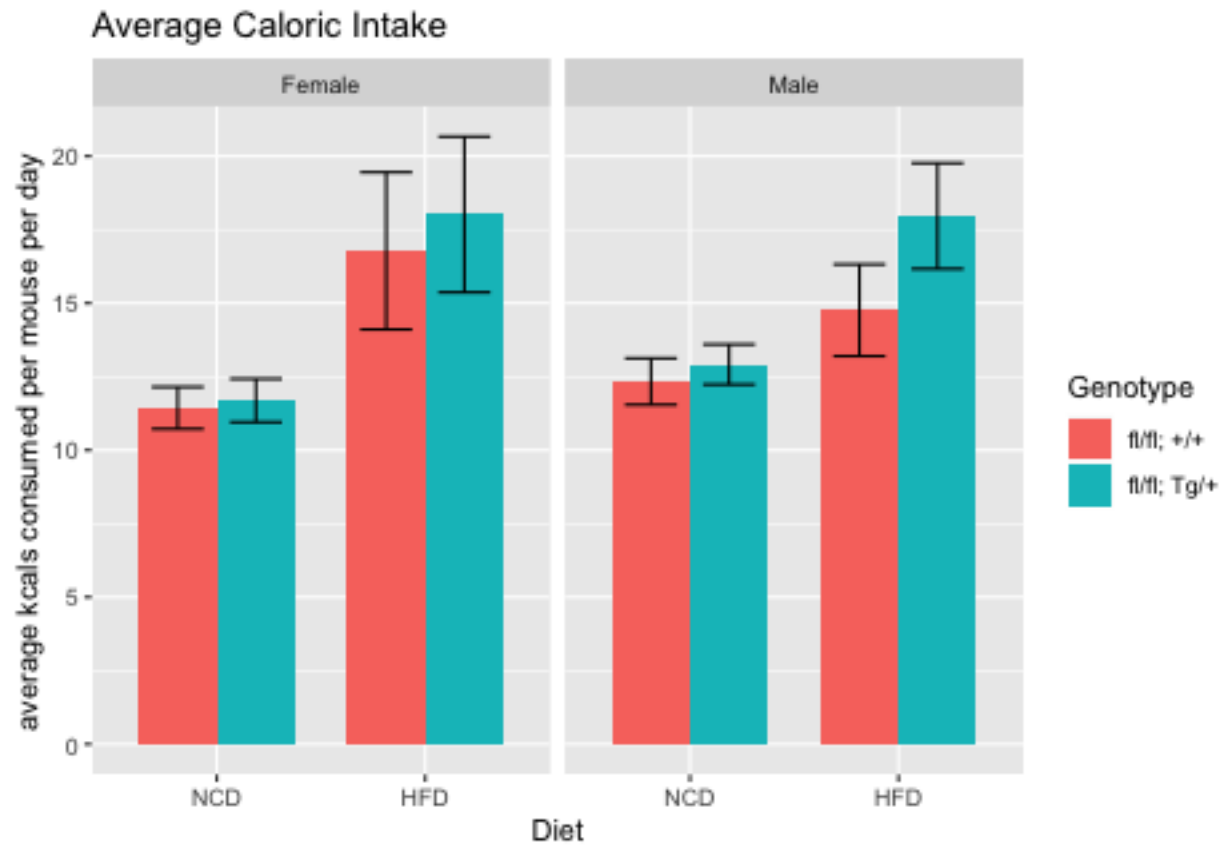


These data can be found in `/Users/davebrid/Documents/GitHub/TissueSpecificTscKnockouts/Mouse Data/Muscle Tsc1 Knockout` in a file named **Food Intake Log.csv**. This script was most recently updated on **Wed Apr 3 15:25:20 2019**. # Analysis

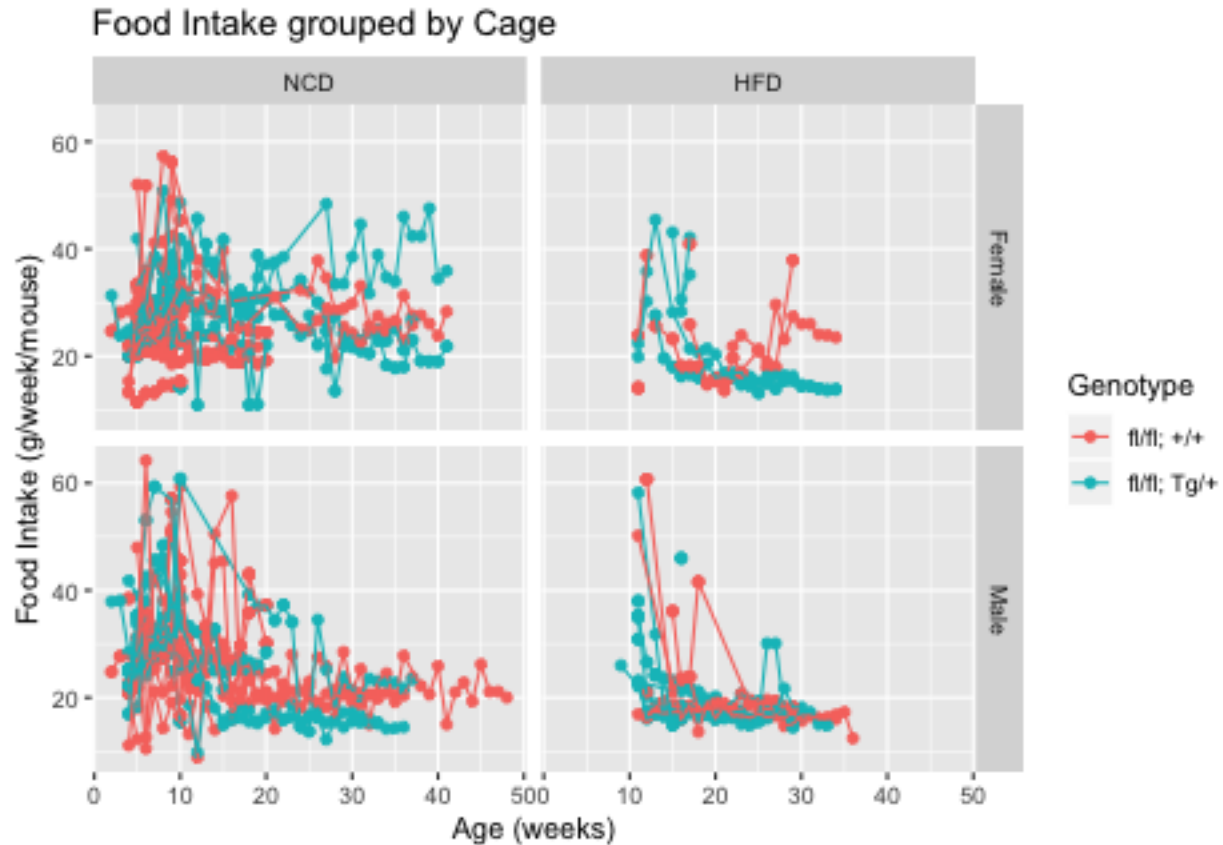








```
##           Df Sum Sq Mean Sq F value Pr(>F)
## Sex       1    0.0      0.0    0.00 0.9863
## HFD       1   45.8     45.8   38.02 0.0035 **
## Genotype  1    3.5      3.5    2.89 0.1644
## Residuals 4    4.8      1.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



1.1 Statistics

```
## Data: exp.data.22
## Models:
## intake.null: calorie.intake ~ 1 + (1 | Cage)
## intake.lme.hfd: calorie.intake ~ HFD + (1 | Cage)
##
##           Df  AIC  BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## intake.null    3 8611 8628  -4303     8605
## intake.lme.hfd  4 8542 8563  -4267     8534   71.8    1    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Data: exp.data.22
## Models:
## intake.lme.hfd: calorie.intake ~ HFD + (1 | Cage)
## intake.lme.age: calorie.intake ~ HFD + age + (1 | Cage)
##
##           Df  AIC  BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## intake.lme.hfd  4 8542 8563  -4267     8534
## intake.lme.age  5 8397 8424  -4194     8387   146    1    <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Data: exp.data.22
## Models:
## intake.lme.age: calorie.intake ~ HFD + age + (1 | Cage)
## intake.lme.sex: calorie.intake ~ HFD + age + Sex + (1 | Cage)
```

```
##           Df  AIC  BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## intake.lme.age  5 8397 8424  -4194      8387
## intake.lme.sex  6 8399 8431  -4194      8387  0.14      1      0.71
```

| | Df | AIC | BIC | logLik | deviance | Chisq | Chi Df | Pr(>Chisq) |
|-----------------|----|------|------|--------|----------|-------|--------|------------|
| intake.lme.sex | 6 | 8399 | 8431 | -4194 | 8387 | NA | NA | NA |
| intake.lme.geno | 7 | 8400 | 8438 | -4193 | 8386 | 0.678 | 1 | 0.41 |

| | Sum Sq | Mean Sq | NumDF | DenDF | F value | Pr(>F) |
|----------|---------|---------|-------|--------|---------|--------|
| HFD | 2033.65 | 2033.65 | 1 | 1361.7 | 174.135 | 0.000 |
| age | 1788.31 | 1788.31 | 1 | 1488.6 | 153.127 | 0.000 |
| Sex | 0.88 | 0.88 | 1 | 67.0 | 0.075 | 0.785 |
| Genotype | 7.49 | 7.49 | 1 | 59.3 | 0.642 | 0.426 |

Table 3: Pairwise contrasts from mixed linear model, for females on NCD. The random effect is the cage.

| | x |
|---------------------|--------|
| (Intercept) | 13.319 |
| HFDHFD | 4.451 |
| age | -0.166 |
| SexMale | 0.163 |
| Genotypefl/fl; Tg/+ | 0.487 |

| term | levels | Estimate | Std. Error | df | t value | Pr(> t) |
|----------|--------------------------|----------|------------|--------|---------|----------|
| HFD | NCD - HFD | -4.451 | 0.337 | 1361.7 | -13.196 | 0.000 |
| Sex | Female - Male | -0.163 | 0.594 | 67.0 | -0.274 | 0.785 |
| Genotype | fl/fl; +/+ - fl/fl; Tg/+ | -0.487 | 0.608 | 59.3 | -0.801 | 0.426 |

| Sex | HFD | Genotype | n |
|--------|-----|-------------|----|
| Female | NCD | fl/fl; +/+ | 17 |
| Female | NCD | fl/fl; Tg/+ | 13 |
| Female | HFD | fl/fl; +/+ | 5 |
| Female | HFD | fl/fl; Tg/+ | 5 |
| Male | NCD | fl/fl; +/+ | 18 |
| Male | NCD | fl/fl; Tg/+ | 20 |
| Male | HFD | fl/fl; +/+ | 6 |
| Male | HFD | fl/fl; Tg/+ | 12 |

2 Session Information

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
```

```

## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS 10.14.2
##
## Matrix products: default
## BLAS: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods    base
##
## other attached packages:
## [1] broom_0.5.1      lmerTest_3.0-1 lme4_1.1-19   Matrix_1.2-15
## [5] dbplyr_1.3.0     car_3.0-2       carData_3.0-2 nlme_3.1-137
## [9] ggplot2_3.1.0    bindrcpp_0.2.2 forcats_0.3.0 readr_1.3.1
## [13] dplyr_0.7.8      tidyr_0.8.2     knitr_1.21
##
## loaded via a namespace (and not attached):
## [1] tidyselect_0.2.5 xfun_0.4         purrr_0.2.5
## [4] reshape2_1.4.3   splines_3.5.0    haven_2.0.0
## [7] lattice_0.20-38  generics_0.0.2   colorspace_1.3-2
## [10] htmltools_0.3.6  yaml_2.2.0       rlang_0.3.1
## [13] nloptr_1.2.1     pillar_1.3.1     foreign_0.8-71
## [16] glue_1.3.0       withr_2.1.2      DBI_1.0.0
## [19] readxl_1.2.0     bindr_0.1.1      plyr_1.8.4
## [22] stringr_1.3.1    munsell_0.5.0    gtable_0.2.0
## [25] cellranger_1.1.0 zip_1.0.0         evaluate_0.12
## [28] labeling_0.3     rio_0.5.16       curl_3.2
## [31] highr_0.7        Rcpp_1.0.0       backports_1.1.3
## [34] scales_1.0.0     abind_1.4-5      hms_0.4.2
## [37] digest_0.6.18    stringi_1.2.4    openxlsx_4.1.0
## [40] numDeriv_2016.8-1 grid_3.5.0        tools_3.5.0
## [43] magrittr_1.5     lazyeval_0.2.1   tibble_2.0.0
## [46] crayon_1.3.4     pkgconfig_2.0.2  MASS_7.3-51.1
## [49] data.table_1.11.8 minqa_1.2.4       assertthat_0.2.0
## [52] rmarkdown_1.11   R6_2.3.0         compiler_3.5.0

```