

# Analysis of Tissue Weights from HFD/Dexamethasone Studies

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## Data Entry

This script generates figures from the tissue weights found in ../../data/raw/HFD and Chow Tissue Weights.csv. This file is located in /Users/davebrid/Documents/GitHub/CushingAcromegalyStudy/scripts/scripts-obesity and was most recently updated on Tue Aug 8 20:00:50 2017.

## Number of Animals

Table 1: Number of mice in each group

Status	Diet	Treatment	Number
Fasted	NCD	Water	8
Fasted	NCD	Dexamethasone	8
Fasted	HFD	Water	22
Fasted	HFD	Dexamethasone	12
Fed	NCD	Water	4
Fed	NCD	Dexamethasone	4

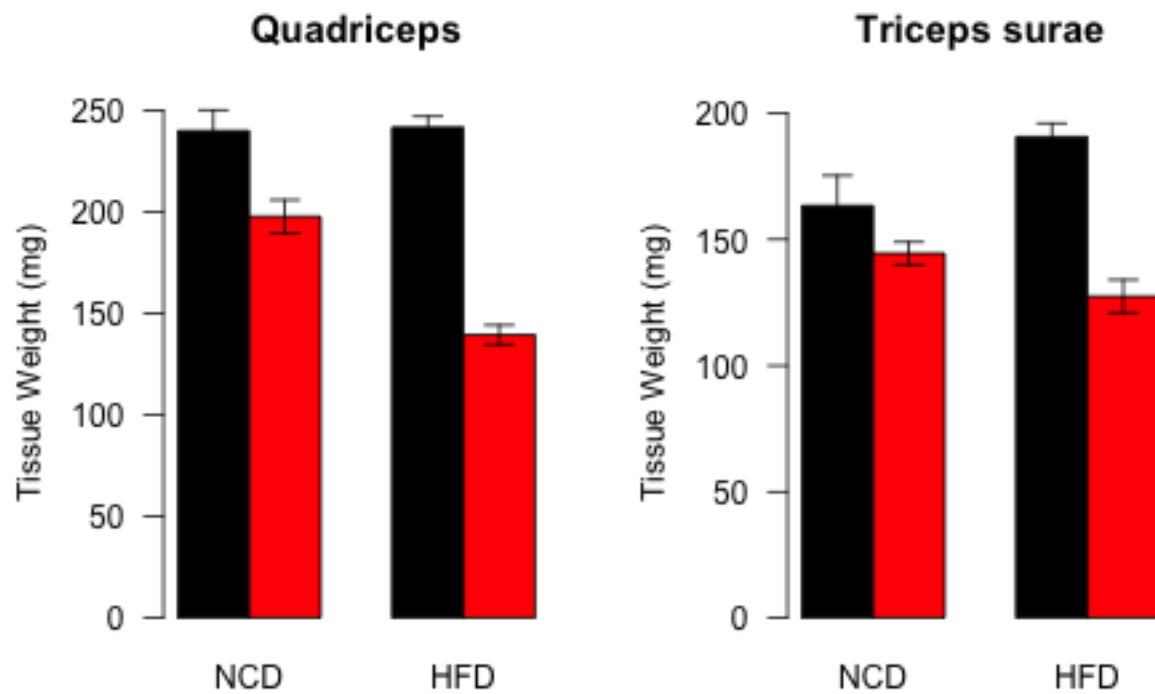
## Summary Data

The remainder of this analysis is only for Fasted animals

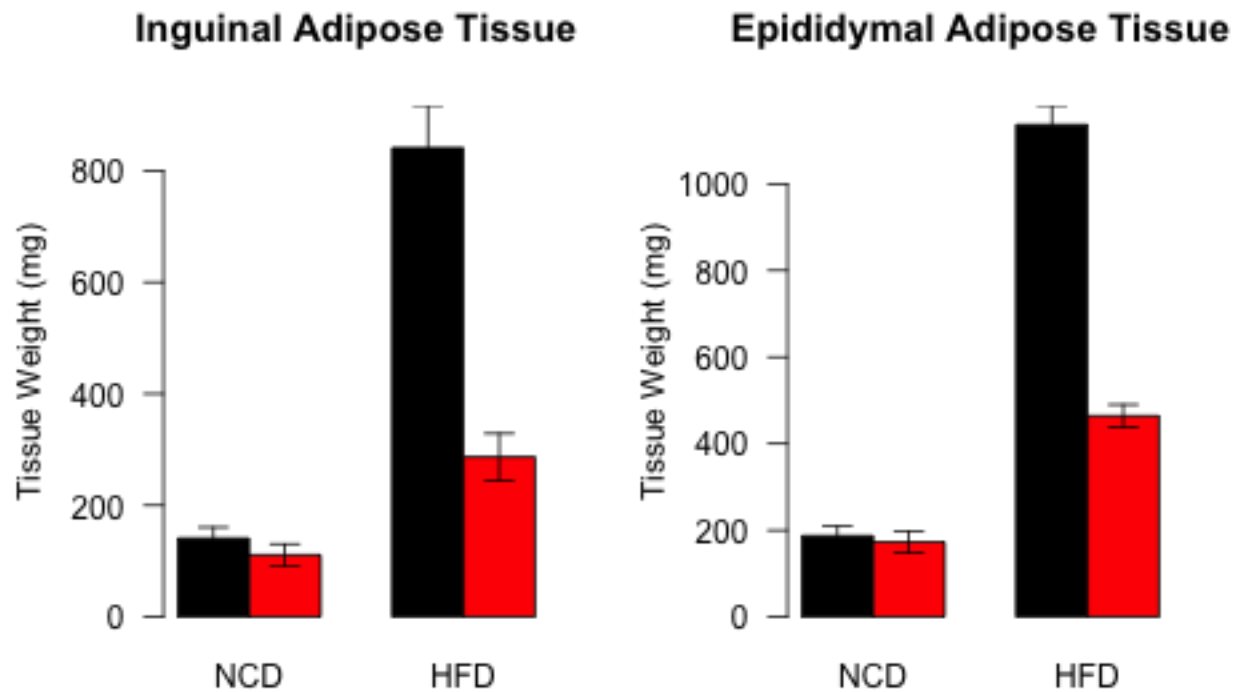
Table 2: Averaged Values

Diet	Treatment	iWAT_mean.na	eWAT_mean.na	TS_mean.na	Quad_mean.na
NCD	Water	140.9750	187.1125	163.3750	240.0250
NCD	Dexamethasone	111.0625	173.1875	144.5000	197.8250
HFD	Water	840.7545	1136.3773	190.6905	241.7727
HFD	Dexamethasone	286.8000	464.1000	127.4417	139.5000

## Muscle Barplots



## Adipose Barplots



### Analysis of Adipose Tissue Weights

We observed reductions in both iWAT and eWAT with HFD/Dexamethasone.

#### Inguinal Adipose Tissue

This included a 65.8877848% reduction in iWAT mass in the HFD mice. A Shapiro-Wilk test of the iWAT values had a p-value of  $>0.0621229$ , so normality could be assumed. To test for equal variance, Levene's tests were performed.

The p-value from the Levene's test were 0.0041061 for HFD. Based on this a Welch's  $t$  test was performed with a p-value of  $4.4777019 \times 10^{-7}$ .

For NCD the Levene's test had a p-value of 0.2829918, so equal variance could be assumed. Based on this, a Student's  $t$ -test had a p-value of **0.4967434** for NCD.

There was only a 21.2183011% reduction in iWAT mass in the NCD mice.

Based on a 2-way ANOVA with Diet and Group as the interacting covariates there was a significant interaction between diet and treatment:

Table 3: Two Way ANOVA with Interaction between treatment and diet.

term	df	sumsq	meansq	statistic	p.value
Diet	1	3579646.8	3579646.80	65.49123	0.00e+00
Group	1	1400297.4	1400297.44	25.61906	5.20e-06
Diet:Group	1	983744.2	983744.15	17.99804	8.73e-05
Residuals	54	2951554.4	54658.42	NA	NA

The p-value for the interaction was  $8.7281221 \times 10^{-5}$ . The residuals of this model, passed through a Shapiro-Wilk test had a p-value of 0.0015701, so normality could not be assumed.

### Epididimal Adipose Tissue

This included a 59.1596901% reduction in eWAT mass in the HFD mice.

There was only a 7.4420469% reduction in eWAT mass in the NCD mice.

The p-value from the Levene's test were 0.0298476 for HFD. Based on this a Welch's  $t$  test was performed with a p-value of  $3.7377627 \times 10^{-14}$ .

For NCD the Levene's test had a p-value of and 0.8965011, so equal variance could be assumed. Based on this, a Student's  $t$ -test had a p-value of  $0.5452112$  for NCD.

Based on a 2-way ANOVA with Diet and Group as the interacting covariates there was a significant interaction between diet and treatment:

Table 4: Two Way ANOVA with Interaction between treatment and diet.

term	df	sumsq	meansq	statistic	p.value
Diet	1	6924250	6924250.12	342.62891	0
Group	1	2055412	2055411.62	101.70682	0
Diet:Group	1	1455533	1455532.97	72.02335	0
Residuals	54	1091296	20209.18	NA	NA

The p-value for the interaction was  $1.6294353 \times 10^{-11}$ . The residuals of this model, passed through a Shapiro-Wilk test had a p-value of 0.0049698, so normality could not be assumed.

### Session Information

```
## R version 3.3.0 (2016-05-03)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.12.6 (unknown)
##
## 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_0.4.2    car_2.1-4      forcats_0.2.0 readr_1.1.0    dplyr_0.5.0
## [6] tidyr_0.6.1    knitr_1.15.1
##
## loaded via a namespace (and not attached):
## [1] Rcpp_0.12.10      nloptr_1.0.4      highr_0.6
## [4] plyr_1.8.4        tools_3.3.0       digest_0.6.12
## [7] lme4_1.1-12       evaluate_0.10     tibble_1.3.0
## [10] nlme_3.1-131      lattice_0.20-35   mgcv_1.8-17
## [13] Matrix_1.2-8      psych_1.7.3.21    DBI_0.6-1
## [16] yaml_2.1.14       parallel_3.3.0    SparseM_1.76
## [19] stringr_1.2.0     MatrixModels_0.4-1 hms_0.3
## [22] rprojroot_1.2     nnet_7.3-12       grid_3.3.0
## [25] R6_2.2.0          foreign_0.8-67    rmarkdown_1.6
## [28] minqa_1.2.4       reshape2_1.4.2    magrittr_1.5
## [31] backports_1.0.5   htmltools_0.3.5   MASS_7.3-45
## [34] splines_3.3.0     assertthat_0.1    pbkrtest_0.4-7
## [37] mnormt_1.5-5      quantreg_5.29     stringi_1.1.3
## [40] lazyeval_0.2.0

```