

Cardiac_CT HN: both diets

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01/17/23

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Data Summary

#We use microCT in mice on a HFD to compare cardiac metric for the following genotypes: APOE2HN, APOE3HN, APOE4HN, APOE-/-

```
## [1] "All data set"
```

```
## # A tibble: 27 x 4
## # Groups:   Diet, Genotype [14]
##   Diet Genotype Sex    count
##   <chr> <chr>    <chr> <int>
## 1 CTRL E22      Male     6
## 2 CTRL E2HN     Female   3
## 3 CTRL E2HN     Male     3
## 4 CTRL E33     Female   5
## 5 CTRL E33     Male     3
## 6 CTRL E3HN     Female   3
## 7 CTRL E3HN     Male     3
## 8 CTRL E44     Female   3
## 9 CTRL E44     Male     3
## 10 CTRL E4HN    Female   4
## # ... with 17 more rows
```

```
## [1] "Age <17"
```

```
## # A tibble: 27 x 4
## # Groups:   Diet, Genotype [14]
##   Diet Genotype Sex    count
##   <chr> <chr>    <chr> <int>
## 1 CTRL E22      Male     6
```

```
## 2 CTRL E2HN Female 3
## 3 CTRL E2HN Male 3
## 4 CTRL E33 Female 5
## 5 CTRL E33 Male 3
## 6 CTRL E3HN Female 3
## 7 CTRL E3HN Male 3
## 8 CTRL E44 Female 1
## 9 CTRL E44 Male 3
## 10 CTRL E4HN Female 2
## # ... with 17 more rows
```

```
## # A tibble: 27 x 4
## # Groups:   Diet, Genotype [14]
##   Diet Genotype Sex count
##   <chr> <chr> <chr> <int>
## 1 CTRL E22 Male 6
## 2 CTRL E2HN Female 3
## 3 CTRL E2HN Male 3
## 4 CTRL E33 Female 5
## 5 CTRL E33 Male 3
## 6 CTRL E3HN Female 3
## 7 CTRL E3HN Male 3
## 8 CTRL E44 Female 3
## 9 CTRL E44 Male 3
## 10 CTRL E4HN Female 4
## # ... with 17 more rows
```

Plots for all cardiac metrics

```
## 'summarise()' has grouped output by 'Diet', 'Genotype'. You can override using
## the '.groups' argument.
## Bin width defaults to 1/30 of the range of the data. Pick better value with
## 'binwidth'.
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```

