

Cardiac_CT Basic: both diets

Alex Badea

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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: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>    <chr> <int>
## 1 CTRL E22      Male     6
## 2 CTRL E33      Female   5
## 3 CTRL E33      Male     3
## 4 CTRL E44      Female   3
## 5 CTRL E44      Male     3
## 6 CTRL K0       Female   4
## 7 CTRL K0       Male     2
## 8 HFD  E22      Female   4
## 9 HFD  E22      Male     5
## 10 HFD  E33      Female   6
## 11 HFD  E33      Male    10
## 12 HFD  E44      Female   2
## 13 HFD  E44      Male     4
## 14 HFD  K0       Female   5
## 15 HFD  K0       Male     4

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

```
## # A tibble: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>   <chr> <int>
## 1 CTRL E22     Male     6
## 2 CTRL E33     Female   5
## 3 CTRL E33     Male     3
## 4 CTRL E44     Female   1
## 5 CTRL E44     Male     3
## 6 CTRL K0      Female   4
## 7 CTRL K0      Male     1
## 8 HFD  E22     Female   4
## 9 HFD  E22     Male     5
## 10 HFD E33     Female   6
## 11 HFD E33     Male    10
## 12 HFD E44     Female   1
## 13 HFD E44     Male     1
## 14 HFD K0      Female   5
## 15 HFD K0      Male     4
```

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## # A tibble: 15 x 4
## # Groups:   Diet, Genotype [8]
##   Diet Genotype Sex    count
##   <chr> <chr>   <chr> <int>
## 1 CTRL E22     Male     6
## 2 CTRL E33     Female   5
## 3 CTRL E33     Male     3
## 4 CTRL E44     Female   3
## 5 CTRL E44     Male     3
## 6 CTRL K0      Female   4
## 7 CTRL K0      Male     2
## 8 HFD  E22     Female   4
## 9 HFD  E22     Male     5
## 10 HFD E33     Female   6
## 11 HFD E33     Male    10
## 12 HFD E44     Female   2
## 13 HFD E44     Male     4
## 14 HFD K0      Female   5
## 15 HFD K0      Male     4
```

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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