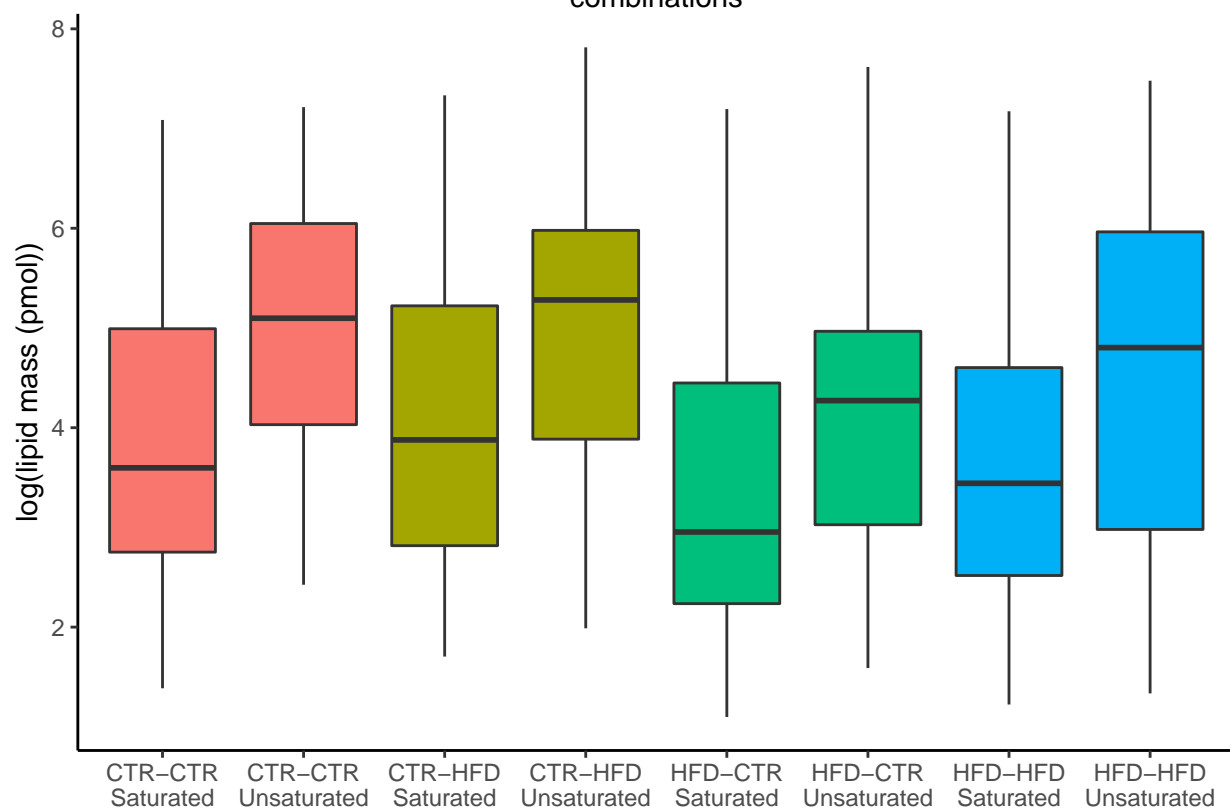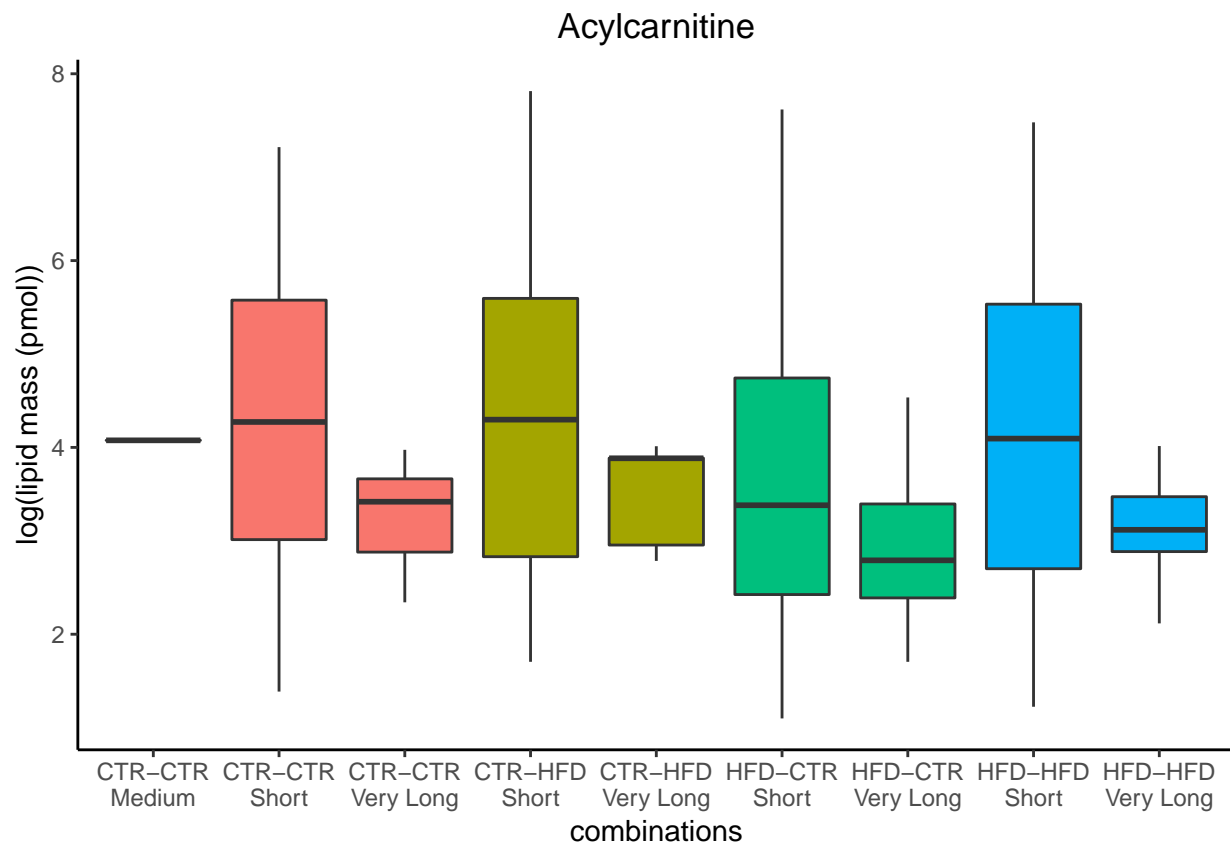# secondary anova

Alex Ostrovsky

1/17/2019

Acylcarnitine

Acylcarnitine

```
## [1] "Length as affected by combination"
## Analysis of Variance Table
##
## Response: acchain$value
##                         Df   Sum Sq Mean Sq F value  Pr(>F)
## acchain$combinations     8  1637322  204665  1.8926 0.06027 .
## Residuals              339 36659515  108140
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by maternal"
## Analysis of Variance Table
##
## Response: acchain$value
##                         Df   Sum Sq Mean Sq F value  Pr(>F)
## acchain$mcombinations    4  1290798  322700   2.991 0.01895 *
## Residuals              343 37006039  107889
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by juvenile"
## Analysis of Variance Table
##
## Response: acchain$value
##                         Df   Sum Sq Mean Sq F value  Pr(>F)
## acchain$jcombinations    4  1014203  253551  2.3327 0.05554 .
## Residuals              343 37282634  108696
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by combination"
## Analysis of Variance Table
##
## Response: acchain$value
##                          Df   Sum Sq Mean Sq F value    Pr(>F)
## acchain$satcombinations   7  2839136  405591  3.8892 0.0004307 ***
## Residuals               340 35457701  104287
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"
## Analysis of Variance Table
##
## Response: acchain$value
##                            Df   Sum Sq Mean Sq F value    Pr(>F)
## acchain$satmatcombinations  6  2798537  466423  4.4805 0.0002201 ***
## Residuals                 341 35498300  104101
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"
## Analysis of Variance Table
##
```

```
## Response: acchain$value
##                               Df  Sum Sq Mean Sq F value   Pr(>F)
## acchain$satjuvcombinations     6 2499026  416504  3.9675 0.0007494 ***
## Residuals                    341 35797811  104979
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = acchain$value ~ acchain$combinations)
##
## $`acchain$combinations`
##                                    diff        lwr        upr
## CTR.CTR.small-CTR.CTR.medium  171.99770115  -860.53254 1204.52794
## CTR.CTR.vlong-CTR.CTR.medium  -29.21250000 -1118.13590 1059.71090
## CTR.HFD.small-CTR.CTR.medium  202.45272727  -833.48521 1238.39066
## CTR.HFD.vlong-CTR.CTR.medium  -21.30000000 -1145.93525 1103.33525
## HFD.CTR.small-CTR.CTR.medium   64.59898990  -967.21989 1096.41787
## HFD.CTR.vlong-CTR.CTR.medium  -31.87777778 -1114.05855 1050.30300
## HFD.HFD.small-CTR.CTR.medium  149.88961039  -883.40225 1183.18147
## HFD.HFD.vlong-CTR.CTR.medium  -31.85714286 -1129.38877 1065.67448
## CTR.CTR.vlong-CTR.CTR.small  -201.21020115  -580.50619  178.08579
## CTR.HFD.small-CTR.CTR.small    30.45502612  -146.40279  207.31285
## CTR.HFD.vlong-CTR.CTR.small  -193.29770115  -665.43722  278.84182
## HFD.CTR.small-CTR.CTR.small  -107.39871125  -258.26782   43.47039
## HFD.CTR.vlong-CTR.CTR.small  -203.87547893  -563.35637  155.60541
## HFD.HFD.small-CTR.CTR.small   -22.10809076  -182.74229  138.52611
## HFD.HFD.vlong-CTR.CTR.small  -203.85484401  -607.19954  199.48985
## CTR.HFD.small-CTR.CTR.vlong   231.66522727  -156.81150  620.14195
## CTR.HFD.vlong-CTR.CTR.vlong     7.91250000  -577.36624  593.19124
## HFD.CTR.small-CTR.CTR.vlong    93.81148990  -283.54373  471.16671
## HFD.CTR.vlong-CTR.CTR.vlong    -2.66527778  -501.52597  496.19541
## HFD.HFD.small-CTR.CTR.vlong   179.10211039  -202.26231  560.46653
## HFD.HFD.vlong-CTR.CTR.vlong    -2.64464286  -533.98485  528.69557
## CTR.HFD.vlong-CTR.HFD.small  -223.75272727  -703.29881  255.79335
## HFD.CTR.small-CTR.HFD.small  -137.85373737  -310.51006   34.80259
## HFD.CTR.vlong-CTR.HFD.small  -234.33050505  -603.48525  134.82424
## HFD.HFD.small-CTR.HFD.small   -52.56311688  -233.81450  128.68827
## HFD.HFD.vlong-CTR.HFD.small  -234.30987013  -646.29975  177.68001
## HFD.CTR.small-CTR.HFD.vlong    85.89898990  -384.68282  556.48080
## HFD.CTR.vlong-CTR.HFD.vlong   -10.57777778  -583.21402  562.05846
## HFD.HFD.small-CTR.HFD.vlong   171.18961039  -302.61320  644.99242
## HFD.HFD.vlong-CTR.HFD.vlong   -10.55714286  -611.69997  590.58568
## HFD.CTR.vlong-HFD.CTR.small   -96.47676768  -453.90931  260.95578
## HFD.HFD.small-HFD.CTR.small    85.29062049   -70.70573  241.28697
## HFD.HFD.vlong-HFD.CTR.small   -96.45613276  -497.97632  305.06405
## HFD.HFD.small-HFD.CTR.vlong   181.76738817  -179.89528  543.43005
## HFD.HFD.vlong-HFD.CTR.vlong     0.02063492  -517.36073  517.40200
## HFD.HFD.vlong-HFD.HFD.small  -181.74675325  -587.03716  223.54366
##                                  p adj
## CTR.CTR.small-CTR.CTR.medium 0.9998635
## CTR.CTR.vlong-CTR.CTR.medium 1.0000000
```

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```
## CTR.HFD.small-CTR.CTR.medium 0.9995491
## CTR.HFD.vlong-CTR.CTR.medium 1.0000000
## HFD.CTR.small-CTR.CTR.medium 0.9999999
## HFD.CTR.vlong-CTR.CTR.medium 1.0000000
## HFD.HFD.small-CTR.CTR.medium 0.9999524
## HFD.HFD.vlong-CTR.CTR.medium 1.0000000
## CTR.CTR.vlong-CTR.CTR.small  0.7726168
## CTR.HFD.small-CTR.CTR.small  0.9998247
## CTR.HFD.vlong-CTR.CTR.small  0.9371201
## HFD.CTR.small-CTR.CTR.small  0.3934998
## HFD.CTR.vlong-CTR.CTR.small  0.7015844
## HFD.HFD.small-CTR.CTR.small  0.9999682
## HFD.HFD.vlong-CTR.CTR.small  0.8163287
## CTR.HFD.small-CTR.CTR.vlong  0.6405696
## CTR.HFD.vlong-CTR.CTR.vlong  1.0000000
## HFD.CTR.small-CTR.CTR.vlong  0.9974312
## HFD.CTR.vlong-CTR.CTR.vlong  1.0000000
## HFD.HFD.small-CTR.CTR.vlong  0.8703706
## HFD.HFD.vlong-CTR.CTR.vlong  1.0000000
## CTR.HFD.vlong-CTR.HFD.small  0.8744801
## HFD.CTR.small-CTR.HFD.small  0.2392220
## HFD.CTR.vlong-CTR.HFD.small  0.5572169
## HFD.HFD.small-CTR.HFD.small  0.9925850
## HFD.HFD.vlong-CTR.HFD.small  0.6983489
## HFD.CTR.small-CTR.HFD.vlong  0.9997285
## HFD.CTR.vlong-CTR.HFD.vlong  1.0000000
## HFD.HFD.small-CTR.HFD.vlong  0.9696620
## HFD.HFD.vlong-CTR.HFD.vlong  1.0000000
## HFD.CTR.vlong-HFD.CTR.small  0.9954469
## HFD.HFD.small-HFD.CTR.small  0.7420261
## HFD.HFD.vlong-HFD.CTR.small  0.9979838
## HFD.HFD.small-HFD.CTR.vlong  0.8209629
## HFD.HFD.vlong-HFD.CTR.vlong  1.0000000
## HFD.HFD.vlong-HFD.HFD.small  0.8973695
```

Ceramides

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: cerchain$value
##                         Df  Sum Sq Mean Sq F value Pr(>F)
## cerchain$combinations    4   18729  4682.3   0.493 0.7409
## Residuals              256 2431230  9497.0

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: cerchain$value
##                          Df  Sum Sq Mean Sq F value Pr(>F)
## cerchain$mcombinations    2   13848  6924.1  0.7333 0.4813
## Residuals               258 2436111  9442.3
```

```
## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: cerchain$value
##                        Df  Sum Sq Mean Sq F value Pr(>F)
## cerchain$jcombinations   2   11887  5943.5  0.6289  0.534
## Residuals              258 2438072  9449.9

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: cerchain$value
##                          Df  Sum Sq Mean Sq F value   Pr(>F)
## cerchain$satcombinations   7  236847   33835   3.868 0.000509 ***
## Residuals                253 2213112    8747
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: cerchain$value
##                             Df  Sum Sq Mean Sq F value    Pr(>F)
## cerchain$satmatcombinations   4  228097   57024  6.5703 4.771e-05 ***
## Residuals                   256 2221862    8679
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: cerchain$value
##                             Df  Sum Sq Mean Sq F value    Pr(>F)
## cerchain$satjuvcombinations   4  239567   59892  6.9364 2.574e-05 ***
## Residuals                   256 2210392    8634
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = cerchain$value ~ cerchain$combinations)
##
## $`cerchain$combinations`
##                                   diff        lwr       upr    p adj
## CTR.CTR.small-CTR.CTR.medium   89.723944 -179.88808 359.33597 0.8912462
## CTR.HFD.small-CTR.CTR.medium   89.406667 -181.28497 360.09830 0.8938900
## HFD.CTR.small-CTR.CTR.medium   93.253086 -176.12769 362.63386 0.8764645
## HFD.HFD.small-CTR.CTR.medium  104.985714 -164.86396 374.83538 0.8223511
## CTR.HFD.small-CTR.CTR.small    -0.317277  -51.33202  50.69747 1.0000000
## HFD.CTR.small-CTR.CTR.small     3.529143  -39.99721  47.05550 0.9994509
## HFD.HFD.small-CTR.CTR.small    15.261771  -31.07813  61.60167 0.8948807
```

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```
## HFD.CTR.small-CTR.HFD.small     3.846420  -45.93172  53.62456 0.9995460
## HFD.HFD.small-CTR.HFD.small    15.579048  -36.67712  67.83521 0.9246024
## HFD.HFD.small-HFD.CTR.small    11.732628  -33.24232  56.70757 0.9525429
```

DGs 1.2

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                         Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$combinations   4    650518  162629  0.6133 0.6532
## Residuals                691 183243635  265186

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                          Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$mcombinations   2    213858  106929  0.4034 0.6682
## Residuals                 693 183680294  265051

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                          Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$jcombinations   2     46050   23025  0.0868 0.9169
## Residuals                 693 183848103  265293

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                            Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$satcombinations   7   1013267  144752  0.5446 0.8008
## Residuals                   688 182880885  265815

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                               Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$satmatcombinations   4    630741  157685  0.5946 0.6667
## Residuals                      691 183263412  265215

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: DGs1.2chain$value
##                               Df    Sum Sq Mean Sq F value Pr(>F)
## DGs1.2chain$satjuvcombinations   4    444356  111089  0.4184 0.7954
```

```
## Residuals                        691 183449797   265485

## [1] "Tukey test"

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = DGs1.2chain$value ~ DGs1.2chain$combinations)
##
## $`DGs1.2chain$combinations`
##                                    diff        lwr        upr      p adj
## CTR.CTR.small-CTR.CTR.medium    250.68534 -1161.41559 1662.78627 0.9886841
## CTR.HFD.small-CTR.CTR.medium    197.09833 -1217.17668 1611.37335 0.9955186
## HFD.CTR.small-CTR.CTR.medium    177.32778 -1234.34747 1589.00302 0.9970044
## HFD.HFD.small-CTR.CTR.medium    226.12619 -1186.47809 1638.73047 0.9923652
## CTR.HFD.small-CTR.CTR.small     -53.58701  -217.64776  110.47374 0.8993788
## HFD.CTR.small-CTR.CTR.small     -73.35756  -213.24717   66.53205 0.6057007
## HFD.HFD.small-CTR.CTR.small     -24.55915  -173.53220  124.41390 0.9914579
## HFD.CTR.small-CTR.HFD.small     -19.77056  -180.12609  140.58498 0.9972143
## HFD.HFD.small-CTR.HFD.small      29.02786  -139.31038  197.36610 0.9898647
## HFD.HFD.small-HFD.CTR.small      48.79841   -96.08408  193.68090 0.8887339
```

DGs 1.3

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                           Df Sum Sq Mean Sq F value    Pr(>F)
## DGs1.3chain$combinations   4  35954  8988.5  5.1323 0.0005622 ***
## Residuals                227 397559  1751.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                            Df Sum Sq Mean Sq F value Pr(>F)
## DGs1.3chain$mcombinations   2   4515  2257.3  1.2049 0.3016
## Residuals                 229 428999  1873.4

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                            Df Sum Sq Mean Sq F value   Pr(>F)
## DGs1.3chain$jcombinations   2  24220 12110.2  6.7757 0.001384 **
## Residuals                 229 409293  1787.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by combination"
```

```
## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                                 Df Sum Sq Mean Sq F value    Pr(>F)
## DGs1.3chain$satcombinations    7  47014  6716.2  3.8925 0.0005044 ***
## Residuals                    224 386500  1725.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                                    Df Sum Sq Mean Sq F value Pr(>F)
## DGs1.3chain$satmatcombinations    4  14248  3561.9  1.9285 0.1066
## Residuals                       227 419265  1847.0

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: DGs1.3chain$value
##                                    Df Sum Sq Mean Sq F value    Pr(>F)
## DGs1.3chain$satjuvcombinations    4  34965  8741.2  4.9787 0.0007269 ***
## Residuals                       227 398548  1755.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = DGs1.3chain$value ~ DGs1.3chain$combinations)
##
## $`DGs1.3chain$combinations`
##                                 diff        lwr        upr      p adj
## CTR.CTR.small-CTR.CTR.long   26.536508  -89.451591 142.524607 0.9702431
## CTR.HFD.small-CTR.CTR.long   -7.595000 -124.102974 108.912974 0.9997676
## HFD.CTR.small-CTR.CTR.long    8.681944 -107.192829 124.556718 0.9995964
## HFD.HFD.small-CTR.CTR.long   -0.975000 -117.076313 115.126313 0.9999999
## CTR.HFD.small-CTR.CTR.small -34.131508  -57.396990 -10.866026 0.0007093
## HFD.CTR.small-CTR.CTR.small -17.854563  -37.707469   1.998342 0.1004603
## HFD.HFD.small-CTR.CTR.small -27.511508  -48.646540  -6.376476 0.0038217
## HFD.CTR.small-CTR.HFD.small  16.276944   -6.416817  38.970706 0.2829234
## HFD.HFD.small-CTR.HFD.small   6.620000  -17.203487  30.443487 0.9405724
## HFD.HFD.small-HFD.CTR.small  -9.656944  -30.160937  10.847048 0.6945085
```

Dihydrohceramide

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: dhchain$value
```

```
##                             Df  Sum Sq Mean Sq F value Pr(>F)
## dhchain$combinations    4   40.82   10.205  0.9097 0.4602
## Residuals             140 1570.48   11.218

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: dhchain$value
##                            Df  Sum Sq Mean Sq F value Pr(>F)
## dhchain$mcombinations   2   12.71   6.3532  0.5643   0.57
## Residuals             142 1598.59 11.2577

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: dhchain$value
##                            Df  Sum Sq Mean Sq F value Pr(>F)
## dhchain$jcombinations   2   33.12   16.561  1.4901 0.2288
## Residuals             142 1578.17   11.114

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: dhchain$value
##                              Df  Sum Sq Mean Sq F value    Pr(>F)
## dhchain$satcombinations   7  278.45   39.778  4.0887 0.0004174 ***
## Residuals               137 1332.85    9.729
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: dhchain$value
##                                 Df  Sum Sq Mean Sq F value    Pr(>F)
## dhchain$satmatcombinations   4  237.38   59.344  6.0471 0.0001616 ***
## Residuals                  140 1373.92    9.814
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: dhchain$value
##                                 Df  Sum Sq Mean Sq F value    Pr(>F)
## dhchain$satjuvcombinations   4  276.16   69.040  7.2394 2.502e-05 ***
## Residuals                  140 1335.13    9.537
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
```

```
## Fit: aov(formula = dhchain$value ~ dhchain$combinations)
##
## $`dhchain$combinations`
##                                   diff       lwr       upr      p adj
## CTR.CTR.small-CTR.CTR.long     2.6333333 -6.740839 12.007505 0.9370416
## CTR.HFD.small-CTR.CTR.long     3.9040000 -5.535563 13.343563 0.7833676
## HFD.CTR.small-CTR.CTR.long     3.1888889 -6.169646 12.547424 0.8800827
## HFD.HFD.small-CTR.CTR.long     3.6114286 -5.776125 12.998983 0.8249887
## CTR.HFD.small-CTR.CTR.small    1.2706667 -1.100832  3.642165 0.5766485
## HFD.CTR.small-CTR.CTR.small    0.5555556 -1.469497  2.580608 0.9419963
## HFD.HFD.small-CTR.CTR.small    0.9780952 -1.177091  3.133281 0.7194868
## HFD.CTR.small-CTR.HFD.small   -0.7151111 -3.024026  1.593804 0.9122954
## HFD.HFD.small-CTR.HFD.small   -0.2925714 -2.716427  2.131285 0.9973017
## HFD.HFD.small-HFD.CTR.small    0.4225397 -1.663583  2.508663 0.9805501
```

Glucosylceramide

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                      Df Sum Sq Mean Sq F value Pr(>F)
## Gluchain$combinations  4  188.9  47.222  1.5784 0.1815
## Residuals            198 5923.8  29.918

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                       Df Sum Sq Mean Sq F value  Pr(>F)
## Gluchain$mcombinations  2  154.7  77.338  2.5961 0.07708 .
## Residuals             200 5958.0  29.790
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                       Df Sum Sq Mean Sq F value Pr(>F)
## Gluchain$jcombinations  2    0.4  0.2059  0.0067 0.9933
## Residuals             200 6112.3 30.5614

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                         Df Sum Sq Mean Sq F value  Pr(>F)
## Gluchain$satcombinations  7  377.6  53.939   1.834 0.08273 .
## Residuals               195 5735.1  29.411
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                               Df Sum Sq Mean Sq F value  Pr(>F)
## Gluchain$satmatcombinations    4  344.1  86.031  2.9529 0.02121 *
## Residuals                    198 5768.6  29.134
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: Gluchain$value
##                               Df Sum Sq Mean Sq F value Pr(>F)
## Gluchain$satjuvcombinations    4  187.9  46.973  1.5698 0.1838
## Residuals                    198 5924.8  29.923

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Gluchain$value ~ Gluchain$combinations)
##
## $`Gluchain$combinations`
##                                  diff        lwr        upr     p adj
## CTR.CTR.small-CTR.CTR.long    1.4690909 -13.725851 16.6640329 0.9988893
## CTR.HFD.small-CTR.CTR.long    0.5171429 -14.755128 15.7894133 0.9999828
## HFD.CTR.small-CTR.CTR.long   -0.9825397 -16.160244 14.1951647 0.9997726
## HFD.HFD.small-CTR.CTR.long   -0.2489796 -15.460525 14.9625658 0.9999991
## CTR.HFD.small-CTR.CTR.small  -0.9519481  -4.208007  2.3041109 0.9288757
## HFD.CTR.small-CTR.CTR.small  -2.4516306  -5.230549  0.3272876 0.1119533
## HFD.HFD.small-CTR.CTR.small  -1.7180705  -4.676244  1.2401031 0.4998295
## HFD.CTR.small-CTR.HFD.small  -1.4996825  -4.674327  1.6749621 0.6911956
## HFD.HFD.small-CTR.HFD.small  -0.7661224  -4.098805  2.5665602 0.9695666
## HFD.HFD.small-HFD.CTR.small   0.7335601  -2.134756  3.6018766 0.9553740
```

Hexocylceramides

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: hexchain$value
##                         Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$combinations    4   3423  855.75  0.3061 0.8737
## Residuals              227 634639 2795.76

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: hexchain$value
```

```
##                            Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$mcombinations     2    1900  950.07   0.342 0.7107
## Residuals               229 636162 2778.00

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: hexchain$value
##                            Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$jcombinations     2    1763  881.74  0.3173 0.7284
## Residuals               229 636298 2778.59

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: hexchain$value
##                             Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$satcombinations    7  11793  1684.7  0.6026 0.7535
## Residuals                224 626269  2795.8

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: hexchain$value
##                               Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$satmatcombinations    4  10370  2592.6  0.9376 0.4429
## Residuals                   227 627691  2765.2

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: hexchain$value
##                               Df Sum Sq Mean Sq F value Pr(>F)
## hexchain$satjuvcombinations    4  10642  2660.6  0.9626 0.4288
## Residuals                   227 627419  2764.0

## [1] "Tukey test"

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = hexchain$value ~ hexchain$combinations)
##
## $`hexchain$combinations`
##                                   diff        lwr        upr      p adj
## CTR.CTR.small-CTR.CTR.long   27.9936508 -118.55298 174.54028 0.9847149
## CTR.HFD.small-CTR.CTR.long   27.0925000 -120.11097 174.29597 0.9867061
## HFD.CTR.small-CTR.CTR.long   25.9361111 -120.46733 172.33956 0.9884881
## HFD.HFD.small-CTR.CTR.long   19.0285714 -127.66110 165.71824 0.9965155
## CTR.HFD.small-CTR.CTR.small  -0.9011508  -30.29622  28.49392 0.9999885
## HFD.CTR.small-CTR.CTR.small  -2.0575397  -27.14094  23.02586 0.9994224
## HFD.HFD.small-CTR.CTR.small  -8.9650794  -35.66840  17.73824 0.8877202
## HFD.CTR.small-CTR.HFD.small  -1.1563889  -29.82911  27.51633 0.9999656
## HFD.HFD.small-CTR.HFD.small  -8.0639286  -38.16401  22.03616 0.9476876
## HFD.HFD.small-HFD.CTR.small  -6.9075397  -32.81357  18.99849 0.9485495
```

Lactosylceramide

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                        Df Sum Sq Mean Sq F value  Pr(>F)
## Lacchain$combinations   4  19554  4888.6  2.4111 0.04977 *
## Residuals             247 500796  2027.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                        Df Sum Sq Mean Sq F value  Pr(>F)
## Lacchain$mcombinations  2  14374  7187.2  3.5369 0.03057 *
## Residuals             249 505975  2032.0
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                        Df Sum Sq Mean Sq F value Pr(>F)
## Lacchain$jcombinations  2   4123  2061.5  0.9944 0.3714
## Residuals             249 516227  2073.2

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                         Df Sum Sq Mean Sq F value Pr(>F)
## Lacchain$satcombinations 7  23657  3379.5  1.6602 0.1194
## Residuals              244 496693  2035.6

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                            Df Sum Sq Mean Sq F value  Pr(>F)
## Lacchain$satmatcombinations 4  17790  4447.5  2.1859 0.07113 .
## Residuals                 247 502560  2034.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: Lacchain$value
##                            Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Lacchain$satjuvcombinations   4  11119  2779.8  1.3483 0.2526
## Residuals                    247 509231  2061.7

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = Lacchain$value ~ Lacchain$combinations)
##
## $`Lacchain$combinations`
##                                 diff        lwr        upr     p adj
## CTR.CTR.small-CTR.CTR.long   54.872727 -69.985363 179.73081797 0.7469341
## CTR.HFD.small-CTR.CTR.long   49.602857 -75.890648 175.09636207 0.8135589
## HFD.CTR.small-CTR.CTR.long   34.578571 -89.710869 158.86801140 0.9404816
## HFD.HFD.small-CTR.CTR.long   46.177551 -78.816972 171.17207383 0.8482145
## CTR.HFD.small-CTR.CTR.small  -5.269870 -32.025175  21.48543502 0.9829119
## HFD.CTR.small-CTR.CTR.small -20.294156 -40.667949   0.07963767 0.0514569
## HFD.HFD.small-CTR.CTR.small  -8.695176 -33.002733  15.61238035 0.8627719
## HFD.CTR.small-CTR.HFD.small -15.024286 -38.986098   8.93752618 0.4217064
## HFD.HFD.small-CTR.HFD.small  -3.425306 -30.810234  23.95962176 0.9969849
## HFD.HFD.small-HFD.CTR.small  11.598980  -9.594873  32.79283209 0.5608945
```

Sphingomyelin

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: myechain$value
##                         Df     Sum Sq Mean Sq F value Pr(>F)
## myechain$combinations    4    3075633  768908  0.2326   0.92
## Residuals              372 1229872480 3306109

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: myechain$value
##                          Df     Sum Sq Mean Sq F value Pr(>F)
## myechain$mcombinations    2    1734960  867480  0.2635 0.7685
## Residuals               374 1231213152 3292014

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: myechain$value
##                          Df     Sum Sq Mean Sq F value Pr(>F)
## myechain$jcombinations    2    2191460 1095730   0.333  0.717
## Residuals               374 1230756652 3290793

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: myechain$value
```

```
##                                Df     Sum Sq  Mean Sq F value    Pr(>F)
## myechain$satcombinations    7 271004278 38714897   14.851 < 2.2e-16 ***
## Residuals                 369 961943834  2606894
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: myechain$value
##                                 Df     Sum Sq  Mean Sq F value    Pr(>F)
## myechain$satmatcombinations   4 271419450 67854862   26.252 < 2.2e-16 ***
## Residuals                   372 961528663  2584754
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: myechain$value
##                                 Df     Sum Sq  Mean Sq F value    Pr(>F)
## myechain$satjuvcombinations   4 273875475 68468869   26.557 < 2.2e-16 ***
## Residuals                   372 959072638  2578152
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##    Tukey multiple comparisons of means
##      95% family-wise confidence level
##
## Fit: aov(formula = myechain$value ~ myechain$combinations)
##
## $`myechain$combinations`
##                                   diff        lwr       upr     p adj
## CTR.CTR.small-CTR.CTR.medium 1324.21650 -3684.1737 6332.6067 0.9506953
## CTR.HFD.small-CTR.CTR.medium 1293.06154 -3729.3858 6315.5089 0.9551236
## HFD.CTR.small-CTR.CTR.medium 1218.78889 -3786.7193 6224.2971 0.9632291
## HFD.HFD.small-CTR.CTR.medium 1378.27473 -3633.2897 6389.8392 0.9433960
## CTR.HFD.small-CTR.CTR.small    -31.15497  -820.7046  758.3947 0.9999690
## HFD.CTR.small-CTR.CTR.small   -105.42762  -778.8692  568.0139 0.9929134
## HFD.HFD.small-CTR.CTR.small     54.05822  -663.0120  771.1284 0.9995929
## HFD.CTR.small-CTR.HFD.small    -74.27265  -845.3291  696.7838 0.9989285
## HFD.HFD.small-CTR.HFD.small     85.21319  -724.2275  894.6539 0.9984810
## HFD.HFD.small-HFD.CTR.small    159.48584  -537.1698  856.1415 0.9705799
```

Sphingosine

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: sinechain$value
##                        Df  Sum Sq Mean Sq F value Pr(>F)
```

```
## sinechain$combinations  4  364.89  91.224  0.9604 0.4471
## Residuals             24 2279.56  94.982

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: sinechain$value
##                          Df  Sum Sq Mean Sq F value Pr(>F)
## sinechain$mcombinations  2    7.29   3.647   0.036 0.9647
## Residuals              26 2637.16 101.429

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: sinechain$value
##                          Df  Sum Sq Mean Sq F value Pr(>F)
## sinechain$jcombinations  2  115.39  57.695  0.5931 0.5599
## Residuals              26 2529.07  97.272

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: sinechain$value
##                           Df  Sum Sq Mean Sq F value Pr(>F)
## sinechain$satcombinations  3  341.36 113.788  1.2352 0.3179
## Residuals               25 2303.09  92.124

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: sinechain$value
##                              Df  Sum Sq Mean Sq F value Pr(>F)
## sinechain$satmatcombinations  2    7.29   3.647   0.036 0.9647
## Residuals                  26 2637.16 101.429

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: sinechain$value
##                              Df  Sum Sq Mean Sq F value Pr(>F)
## sinechain$satjuvcombinations  2  115.39  57.695  0.5931 0.5599
## Residuals                  26 2529.07  97.272

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = sinechain$value ~ sinechain$combinations)
##
## $`sinechain$combinations`
##                               diff        lwr       upr      p adj
## CTR.CTR.small-CTR.CTR.long   5.1858571 -25.50810 35.879811 0.9868077
## CTR.HFD.small-CTR.CTR.long  -5.8200000 -37.27194 25.631943 0.9815045
## HFD.CTR.small-CTR.CTR.long  -0.8888889 -31.15354 29.375758 0.9999863
```

```
## HFD.HFD.small-CTR.CTR.long    0.1571429 -30.53681 30.851096 1.0000000
## CTR.HFD.small-CTR.CTR.small -11.0058571 -27.81763  5.805914 0.3300014
## HFD.CTR.small-CTR.CTR.small  -6.0747460 -20.54401  8.394522 0.7304995
## HFD.HFD.small-CTR.CTR.small  -5.0287143 -20.37569 10.318263 0.8678761
## HFD.CTR.small-CTR.HFD.small   4.9311111 -11.08343 20.945657 0.8913575
## HFD.HFD.small-CTR.HFD.small   5.9771429 -10.83463 22.788914 0.8307884
## HFD.HFD.small-HFD.CTR.small   1.0460317 -13.42324 15.515300 0.9995073
```

Triacylglycerols

```
## [1] "Length as affected by combination"

## Analysis of Variance Table
##
## Response: TAGchain$value
##                         Df    Sum Sq   Mean Sq F value    Pr(>F)
## TAGchain$combinations    4 6.1038e+08 152593889  8.7835 6.146e-07 ***
## Residuals              778 1.3516e+10  17372784
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Length as affected by maternal"

## Analysis of Variance Table
##
## Response: TAGchain$value
##                          Df    Sum Sq  Mean Sq F value Pr(>F)
## TAGchain$mcombinations    2 4.3887e+06  2194351  0.1212 0.8859
## Residuals               780 1.4122e+10 18105144

## [1] "Length as affected by juvenile"

## Analysis of Variance Table
##
## Response: TAGchain$value
##                          Df    Sum Sq   Mean Sq F value    Pr(>F)
## TAGchain$jcombinations    2 5.8954e+08 294772264  16.985 6.021e-08 ***
## Residuals               780 1.3537e+10  17354945
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by combination"

## Analysis of Variance Table
##
## Response: TAGchain$value
##                            Df    Sum Sq   Mean Sq F value    Pr(>F)
## TAGchain$satcombinations    7 1.1195e+09 159926682   9.529 2.185e-11 ***
## Residuals                 775 1.3007e+10  16783116
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by maternal"

## Analysis of Variance Table
##
## Response: TAGchain$value
```

```
##                                  Df     Sum Sq   Mean Sq F value   Pr(>F)
## TAGchain$satmatcombinations    4 4.7201e+08 118002343  6.7235 2.539e-05 ***
## Residuals                    778 1.3654e+10  17550632
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Saturation as affected by juvenile"

## Analysis of Variance Table
##
## Response: TAGchain$value
##                                  Df     Sum Sq   Mean Sq F value   Pr(>F)
## TAGchain$satjuvcombinations    4 1.0985e+09 274622737    16.4 6.59e-13 ***
## Residuals                    778 1.3028e+10  16745386
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## [1] "Tukey test"

##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = TAGchain$value ~ TAGchain$combinations)
##
## $`TAGchain$combinations`
##                                 diff        lwr        upr      p adj
## CTR.CTR.vlong-CTR.CTR.small -1444.8070 -12867.5476  9977.9336 0.9969273
## CTR.HFD.small-CTR.CTR.small  1387.2804    135.8389  2638.7220 0.0211753
## HFD.CTR.small-CTR.CTR.small  -317.2502  -1384.2714   749.7710 0.9266776
## HFD.HFD.small-CTR.CTR.small  1731.8518    595.5250  2868.1785 0.0003304
## CTR.HFD.small-CTR.CTR.vlong  2832.0874  -8606.3115 14270.4863 0.9613790
## HFD.CTR.small-CTR.CTR.vlong  1127.5568 -10292.1367 12547.2502 0.9988339
## HFD.HFD.small-CTR.CTR.vlong  3176.6587  -8249.7188 14603.0362 0.9418292
## HFD.CTR.small-CTR.HFD.small -1704.5306  -2927.8463  -481.2149 0.0014094
## HFD.HFD.small-CTR.HFD.small   344.5713   -939.6426  1628.7853 0.9486246
## HFD.HFD.small-HFD.CTR.small  2049.1019    943.8265  3154.3773 0.0000050
```