Demographic and Longitudinal Phenotype Analyses

Analysis of demographic and longitudinal phenotype data

Setup

```r
library(easypackages)
libraries("ggplot2","psych","here")
source(here("code","spaghettiPlot.R"))
options(stringsAsFactors=FALSE)

ndigits2use = 4

# function to grab intake or outcome timepoints from longitudinal data
findIntakeOutcomeData <- function(D, type2find, sublist) {
# D = data frame
# type2find = "intake" or "outcome"
# sublist = list of subjects to use
#

    result = data.frame(matrix(nrow=length(sublist), ncol = dim(D)[2]))
    colnames(result) = colnames(D)

    # loop over subjects and grab their data
    for (isub in 1:length(sublist)) {
      submask = is.element(D$subjectId,sublist[isub])
      tmp_data = subset(D,submask)

      if (dim(tmp_data)[1]!=0) {
          if (type2find=="intake"){
            result[isub,] = tmp_data[1,]
          } else if (type2find=="outcome"){
          result[isub,] = tmp_data[dim(tmp_data)[1],]
          }
      }
    }
    result$subjectId = sublist
    result
}# function findIntakeOutcomeData
```

Read in data

```r
# read in longitudinal clinical data
lwdata_flat = read.csv(here("data","tidy","tidy_longpheno_flat.csv"))

# read in demographic data
labelfile = here("data","tidy","tidy_demographic_data.csv")
labels = read.csv(labelfile)
sublist = labels$subjectId
```

Descriptive statistics on demographic data

```
describeBy(labels, group="subgrp2")
```

```
##
##  Descriptive statistics by group
## group: Good
##               vars  n   mean    sd median trimmed    mad   min    max
## subjectId*       1 40    NaN    NA     NA     NaN     NA   Inf   -Inf
## Dx*              2 40    NaN    NA     NA     NaN     NA   Inf   -Inf
## subgrp2*         3 40    NaN    NA     NA     NaN     NA   Inf   -Inf
## scan_age         4 40  29.79  8.41  29.95   30.13   8.16 12.62  45.14
## sex*             5 40    NaN    NA     NA     NaN     NA   Inf   -Inf
## gex_age          6 40  26.47  8.31  26.46   26.28   8.06 12.62  42.25
## batch*           7 40   1.15  0.36   1.00    1.07   0.00  1.00   2.00
## exprColNames*    8 40 218.32 92.90 238.50  218.54 114.16 69.00 376.00
## RIN              9 37   8.24  1.28   8.50    8.45   0.44  2.60   9.60
## meanFD          10 40   0.11  0.23   0.05    0.06   0.03  0.02   1.49
## meanDVARS       11 40   8.81  2.85   8.17    8.45   1.47  5.26  23.04
##               range  skew kurtosis    se
## subjectId*     -Inf    NA       NA    NA
## Dx*            -Inf    NA       NA    NA
## subgrp2*       -Inf    NA       NA    NA
## scan_age      32.53 -0.25    -0.67  1.33
## sex*           -Inf    NA       NA    NA
## gex_age       29.63  0.18    -0.90  1.31
## batch*         1.00  1.91     1.68  0.06
## exprColNames* 307.00 -0.09   -1.21 14.69
## RIN            7.00 -2.77     8.93  0.21
## meanFD         1.47  5.21    27.75  0.04
## meanDVARS     17.78  3.07    12.91  0.45
## -----------------------------------------------------------
## group: Poor
##               vars  n   mean     sd median trimmed    mad   min    max
## subjectId*       1 41    NaN     NA     NA     NaN     NA   Inf   -Inf
## Dx*              2 41    NaN     NA     NA     NaN     NA   Inf   -Inf
## subgrp2*         3 41    NaN     NA     NA     NaN     NA   Inf   -Inf
## scan_age         4 41  29.70   7.88  27.89   29.74   6.62 12.48  46.95
## sex*             5 41    NaN     NA     NA     NaN     NA   Inf   -Inf
## gex_age          6 41  25.46   7.23  25.13   25.19   5.06 12.16  41.82
## batch*           7 41   1.15   0.36   1.00    1.06   0.00  1.00   2.00
## exprColNames*    8 41 219.93 101.71 236.50  219.06 137.88 47.00 377.00
## RIN              9 39   8.28   1.47   8.80    8.57   0.59  2.40   9.50
## meanFD          10 41   0.07   0.08   0.05    0.05   0.03  0.02   0.45
## meanDVARS       11 41   8.61   2.57   8.17    8.28   1.74  4.84  19.05
##               range  skew kurtosis    se
## subjectId*     -Inf    NA       NA    NA
## Dx*            -Inf    NA       NA    NA
## subgrp2*       -Inf    NA       NA    NA
## scan_age      34.47  0.08    -0.42  1.23
## sex*           -Inf    NA       NA    NA
## gex_age       29.67  0.37    -0.16  1.13
## batch*         1.00  1.89     1.60  0.06
## exprColNames* 330.00 0.03    -1.43 15.89
```

```
## RIN              7.10 -2.40     5.89  0.24
## meanFD          0.43  3.65    14.28  0.01
## meanDVARS      14.21  1.75     4.47  0.40
## ----------------------------------------------------------
## group: TD
##              vars  n   mean     sd median trimmed    mad    min     max
## subjectId*      1 37    NaN     NA     NA     NaN     NA    Inf    -Inf
## Dx*             2 37    NaN     NA     NA     NaN     NA    Inf    -Inf
## subgrp2*        3 37    NaN     NA     NA     NaN     NA    Inf    -Inf
## scan_age        4 37  26.20  10.21  23.91   25.71  12.62  12.12   45.37
## sex*            5 37    NaN     NA     NA     NaN     NA    Inf    -Inf
## gex_age         6 37  22.95   9.87  22.54   21.88  11.20  12.12   44.62
## batch*          7 37   1.16   0.37   1.00    1.08   0.00   1.00    2.00
## exprColNames*   8 37 203.81  78.79 193.00  196.24  57.82  92.00  388.00
## RIN             9 28   8.39   1.06   8.65    8.55   0.37   4.40    9.90
## meanFD         10 37   0.07   0.03   0.06    0.07   0.02   0.03    0.15
## meanDVARS      11 37   7.75   2.01   7.21    7.56   1.35   4.81   16.10
##              range  skew kurtosis    se
## subjectId*    -Inf    NA       NA    NA
## Dx*           -Inf    NA       NA    NA
## subgrp2*      -Inf    NA       NA    NA
## scan_age     33.25  0.29    -1.21  1.68
## sex*          -Inf    NA       NA    NA
## gex_age      32.49  0.88    -0.34  1.62
## batch*        1.00  1.75     1.11  0.06
## exprColNames* 296.00 0.81     0.08 12.95
## RIN           5.50 -2.21     5.36  0.20
## meanFD        0.13  1.09     0.34  0.01
## meanDVARS    11.30  1.92     5.79  0.33
```

Descriptive statistics at the intake timepoint

```
intake_data = findIntakeOutcomeData(D = lwdata_flat,
                                     type2find = "intake",
                                     sublist=sublist)


intake_data = merge(x = intake_data,
                    y = labels[,c("subjectId","scan_age","gex_age")],
                    by.x = "subjectId",
                    by.y = "subjectId")


describeBy(intake_data, group = "subgrp2")
```

```
##
##  Descriptive statistics by group
## group: Good
##                       vars  n  mean     sd median trimmed    mad    min
## subjectId*              1 40   NaN     NA     NA     NaN     NA    Inf
## sex*                    2 40   NaN     NA     NA     NaN     NA    Inf
## Dx*                     3 40   NaN     NA     NA     NaN     NA    Inf
## subgrp2*                4 40   NaN     NA     NA     NaN     NA    Inf
## vine_agemo              5 40 24.93   7.77  25.49   24.53   7.60  12.55
## vine_ComTotal_DomStd    6 40 81.05  11.69  80.50   80.38  11.12  60.00
```

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```
## vine_DlyTotal_DomStd    7 40 88.15  9.78  86.00   87.78 10.38 69.00
## vine_SocTotal_DomStd    8 40 85.47  9.03  86.00   85.75  9.64 66.00
## vine_MtrTotal_DomStd    9 40 93.28  9.19  93.00   92.88  5.19 74.00
## vine_AdapBehav_DomStd  10 40 84.30  7.74  83.00   83.84  7.41 68.00
## ados_ageMo            11 40 25.12  7.79  25.61   24.70  7.92 12.62
## ados_CoSoTot          12 40 12.68  4.58  13.00   12.66  5.93  3.00
## ados_RRTot            13 40  3.83  2.01   4.00    3.72  1.48  0.00
## ados_CoSoTotRRTot     14 40 16.50  5.45  16.50   16.69  6.67  4.00
## mullen_ageMo          15 40 24.97  7.74  25.49   24.55  7.65 12.62
## mullen_VRT            16 40 46.33 10.57  44.50   45.72  9.64 25.00
## mullen_FMT            17 40 42.98 10.14  43.50   43.09  8.15 20.00
## mullen_RLT            18 40 34.10 11.88  34.50   33.00 14.08 20.00
## mullen_ELT            19 40 36.52 10.70  35.00   35.72  8.15 20.00
## mullen_ELC_Std        20 40 81.35 16.18  80.00   79.94 16.31 56.00
## scan_age              21 40 29.79  8.41  29.95   30.13  8.16 12.62
## gex_age               22 40 26.47  8.31  26.46   26.28  8.06 12.62
##                          max range  skew kurtosis   se
## subjectId*              -Inf  -Inf    NA       NA   NA
## sex*                    -Inf  -Inf    NA       NA   NA
## Dx*                     -Inf  -Inf    NA       NA   NA
## subgrp2*                -Inf  -Inf    NA       NA   NA
## vine_agemo             41.79 29.24  0.31    -0.70 1.23
## vine_ComTotal_DomStd  109.00 49.00  0.41    -0.46 1.85
## vine_DlyTotal_DomStd  111.00 42.00  0.34    -0.77 1.55
## vine_SocTotal_DomStd  104.00 38.00 -0.20    -0.71 1.43
## vine_MtrTotal_DomStd  118.00 44.00  0.39     0.40 1.45
## vine_AdapBehav_DomStd 103.00 35.00  0.44    -0.30 1.22
## ados_ageMo             42.25 29.63  0.33    -0.70 1.23
## ados_CoSoTot           21.00 18.00 -0.05    -0.89 0.72
## ados_RRTot              8.00  8.00  0.25    -0.46 0.32
## ados_CoSoTotRRTot      25.00 21.00 -0.26    -0.66 0.86
## mullen_ageMo           41.79 29.17  0.32    -0.71 1.22
## mullen_VRT             69.00 44.00  0.38    -0.54 1.67
## mullen_FMT             69.00 49.00 -0.08     0.18 1.60
## mullen_RLT             72.00 52.00  0.77     0.62 1.88
## mullen_ELT             76.00 56.00  1.31     3.03 1.69
## mullen_ELC_Std        133.00 77.00  0.92     1.09 2.56
## scan_age               45.14 32.53 -0.25    -0.67 1.33
## gex_age                42.25 29.63  0.18    -0.90 1.31
## -------------------------------------------------------
## group: Poor
##                       vars  n  mean    sd median trimmed   mad  min
## subjectId*              1 41   NaN    NA     NA     NaN    NA  Inf
## sex*                    2 41   NaN    NA     NA     NaN    NA  Inf
## Dx*                     3 41   NaN    NA     NA     NaN    NA  Inf
## subgrp2*                4 41   NaN    NA     NA     NaN    NA  Inf
## vine_agemo              5 41 25.21  7.30  24.97   24.90  5.94 12.16
## vine_ComTotal_DomStd    6 41 73.59 15.45  69.00   72.55 11.86 49.00
## vine_DlyTotal_DomStd    7 41 85.12 12.49  83.00   84.76 11.86 62.00
## vine_SocTotal_DomStd    8 41 82.44 12.75  80.00   81.58 10.38 61.00
## vine_MtrTotal_DomStd    9 41 92.78 12.73  93.00   92.24 16.31 74.00
## vine_AdapBehav_DomStd  10 41 80.80 12.56  80.00   79.73 10.38 60.00
## ados_ageMo            11 41 25.46  7.35  25.17   25.14  5.94 12.39
## ados_CoSoTot          12 41 16.78  2.95  18.00   17.18  1.48  7.00
```

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```
## ados_RRTot              13 41  4.78  1.94   5.00    4.82  1.48  1.00
## ados_CoSoTotRRTot       14 41 21.56  4.06  22.00   22.12  2.97  9.00
## mullen_ageMo            15 41 25.22  7.37  24.84   24.87  5.99 12.16
## mullen_VRT              16 41 37.44 10.27  37.00   37.42 10.38 20.00
## mullen_FMT              17 41 36.95 14.19  38.00   36.06 17.79 20.00
## mullen_RLT              18 41 23.12 10.10  20.00   22.64  4.45  1.00
## mullen_ELT              19 41 25.17 11.21  27.00   25.12  8.90  1.00
## mullen_ELC_Std          20 41 65.59 15.60  63.00   64.33 17.79 42.00
## scan_age                21 41 29.70  7.88  27.89   29.74  6.62 12.48
## gex_age                 22 41 25.46  7.23  25.13   25.19  5.06 12.16
##                          max range  skew kurtosis   se
## subjectId*              -Inf  -Inf    NA       NA   NA
## sex*                    -Inf  -Inf    NA       NA   NA
## Dx*                     -Inf  -Inf    NA       NA   NA
## subgrp2*                -Inf  -Inf    NA       NA   NA
## vine_agemo             41.53 29.37  0.40    -0.26 1.14
## vine_ComTotal_DomStd  128.00 79.00  1.06     1.78 2.41
## vine_DlyTotal_DomStd  125.00 63.00  0.68     0.76 1.95
## vine_SocTotal_DomStd  123.00 62.00  0.83     0.82 1.99
## vine_MtrTotal_DomStd  122.00 48.00  0.21    -1.08 1.99
## vine_AdapBehav_DomStd 127.00 67.00  1.17     2.59 1.96
## ados_ageMo             41.95 29.57  0.41    -0.22 1.15
## ados_CoSoTot           20.00 13.00 -1.27     1.37 0.46
## ados_RRTot              8.00  7.00 -0.24    -0.93 0.30
## ados_CoSoTotRRTot      27.00 18.00 -1.18     0.94 0.63
## mullen_ageMo           41.95 29.80  0.44    -0.19 1.15
## mullen_VRT             59.00 39.00  0.03    -0.75 1.60
## mullen_FMT             68.00 48.00  0.21    -1.11 2.22
## mullen_RLT             62.00 61.00  1.14     4.23 1.58
## mullen_ELT             61.00 60.00  0.42     1.45 1.75
## mullen_ELC_Std        120.00 78.00  1.02     1.58 2.44
## scan_age               46.95 34.47  0.08    -0.42 1.23
## gex_age                41.82 29.67  0.37    -0.16 1.13
## -------------------------------------------------------
## group: TD
##                       vars  n   mean    sd median trimmed   mad   min
## subjectId*               1 35    NaN    NA     NA     NaN    NA   Inf
## sex*                     2 35    NaN    NA     NA     NaN    NA   Inf
## Dx*                      3 35    NaN    NA     NA     NaN    NA   Inf
## subgrp2*                 4 35    NaN    NA     NA     NaN    NA   Inf
## vine_agemo               5 35  19.54  8.45  14.92   18.53  3.51  9.59
## vine_ComTotal_DomStd     6 35 104.31 11.33 102.00  104.07 10.38 87.00
## vine_DlyTotal_DomStd     7 35 101.40 11.08 100.00  101.62 13.34 77.00
## vine_SocTotal_DomStd     8 35 104.03  9.03 104.00  104.00  8.90 82.00
## vine_MtrTotal_DomStd     9 35 101.09  8.07 102.00  101.17  5.93 84.00
## vine_AdapBehav_DomStd   10 35 103.09 10.09 102.00  102.97 11.86 82.00
## ados_ageMo              11 35  20.10  8.35  16.23   19.06  5.36 12.12
## ados_CoSoTot            12 35   1.86  1.56   2.00    1.72  1.48  0.00
## ados_RRTot              13 35   0.23  0.73   0.00    0.07  0.00  0.00
## ados_CoSoTotRRTot       14 35   2.09  1.65   2.00    1.97  1.48  0.00
## mullen_ageMo            15 35  19.50  8.45  14.92   18.49  3.75  9.59
## mullen_VRT              16 35  58.31  8.81  58.00   58.14  8.90 40.00
## mullen_FMT              17 35  58.74  9.43  59.00   58.83  7.41 38.00
## mullen_RLT              18 35  52.11  8.22  52.00   52.10 10.38 35.00
```

```
## mullen_ELT               19 35  55.34  8.93  56.00   55.10  7.41 41.00
## mullen_ELC_Std           20 35 112.17 13.27 113.00  112.31 13.34 83.00
## scan_age                 21 35  25.12  9.39  23.79   24.75 12.42 12.12
## gex_age                  22 35  21.71  8.61  19.78   20.66  8.04 12.12
##                          max range  skew kurtosis   se
## subjectId*              -Inf  -Inf    NA       NA   NA
## sex*                    -Inf  -Inf    NA       NA   NA
## Dx*                     -Inf  -Inf    NA       NA   NA
## subgrp2*                -Inf  -Inf    NA       NA   NA
## vine_agemo             39.66 30.06  0.94    -0.36 1.43
## vine_ComTotal_DomStd  124.00 37.00  0.15    -1.03 1.92
## vine_DlyTotal_DomStd  121.00 44.00 -0.16    -0.95 1.87
## vine_SocTotal_DomStd  121.00 39.00 -0.06    -0.51 1.53
## vine_MtrTotal_DomStd  118.00 34.00 -0.20    -0.61 1.36
## vine_AdapBehav_DomStd 121.00 39.00  0.10    -0.99 1.71
## ados_ageMo             40.02 27.89  0.92    -0.41 1.41
## ados_CoSoTot            6.00  6.00  0.73    -0.21 0.26
## ados_RRTot             4.00  4.00  4.03    17.39 0.12
## ados_CoSoTotRRTot       6.00  6.00  0.51    -0.78 0.28
## mullen_ageMo           39.66 30.06  0.95    -0.35 1.43
## mullen_VRT             75.00 35.00  0.03    -0.60 1.49
## mullen_FMT             80.00 42.00  0.01     0.15 1.59
## mullen_RLT             66.00 31.00  0.03    -1.05 1.39
## mullen_ELT             73.00 32.00  0.21    -0.93 1.51
## mullen_ELC_Std        138.00 55.00 -0.15    -0.63 2.24
## scan_age               44.52 32.39  0.26    -1.25 1.59
## gex_age                44.52 32.39  0.93     0.02 1.46
```

Descriptive statistics at the outcome timepoint

```r
outcome_data = findIntakeOutcomeData(D = lwdata_flat,
                                     type2find = "outcome",
                                     sublist=sublist)

outcome_data = merge(x = outcome_data,
                     y = labels[,c("subjectId","scan_age","gex_age")],
                     by.x = "subjectId",
                     by.y = "subjectId")

describeBy(outcome_data, group = "subgrp2")
```

```
##
##  Descriptive statistics by group
## group: Good
##                       vars  n  mean    sd median trimmed   mad   min
## subjectId*               1 40   NaN    NA     NA     NaN    NA   Inf
## sex*                     2 40   NaN    NA     NA     NaN    NA   Inf
## Dx*                      3 40   NaN    NA     NA     NaN    NA   Inf
## subgrp2*                 4 40   NaN    NA     NA     NaN    NA   Inf
## vine_agemo               5 40 36.58  6.48  35.61   36.44  6.19 22.93
## vine_ComTotal_DomStd     6 40 91.17 11.29  89.00   90.62 13.34 72.00
## vine_DlyTotal_DomStd     7 40 89.28 10.81  87.00   88.66 13.34 75.00
## vine_SocTotal_DomStd     8 40 86.85 11.90  86.00   86.34 14.08 65.00
```

```
## vine_MtrTotal_DomStd     9 40 91.08  9.61  91.00   91.09  9.64 74.00
## vine_AdapBehav_DomStd   10 40 87.58 10.13  86.50   86.97 12.60 72.00
## ados_ageMo              11 40 36.82  6.52  35.63   36.67  6.48 23.16
## ados_CoSoTot            12 40 12.90  3.34  13.00   12.84  2.97  7.00
## ados_RRTot              13 40  3.45  1.43   3.00    3.44  1.48  1.00
## ados_CoSoTotRRTot       14 40 16.35  3.75  16.00   16.06  2.97 10.00
## mullen_ageMo            15 40 36.53  6.46  35.45   36.37  6.19 22.93
## mullen_VRT              16 40 50.67 11.02  49.00   49.94  9.64 30.00
## mullen_FMT              17 40 42.90 10.69  44.00   42.78 11.12 20.00
## mullen_RLT              18 40 43.40  9.78  42.00   43.09  7.41 25.00
## mullen_ELT              19 40 46.00  9.17  43.50   45.28  5.19 28.00
## mullen_ELC_Std          20 40 91.95 15.61  89.50   90.69 11.86 68.00
## scan_age                21 40 29.79  8.41  29.95   30.13  8.16 12.62
## gex_age                 22 40 26.47  8.31  26.46   26.28  8.06 12.62
##                           max range  skew kurtosis   se
## subjectId*               -Inf  -Inf    NA      NA   NA
## sex*                     -Inf  -Inf    NA      NA   NA
## Dx*                      -Inf  -Inf    NA      NA   NA
## subgrp2*                 -Inf  -Inf    NA      NA   NA
## vine_agemo              51.78 28.85  0.23   -0.13 1.02
## vine_ComTotal_DomStd   116.00 44.00  0.36   -0.63 1.79
## vine_DlyTotal_DomStd   111.00 36.00  0.40   -1.08 1.71
## vine_SocTotal_DomStd   112.00 47.00  0.34   -0.80 1.88
## vine_MtrTotal_DomStd   108.00 34.00 -0.11   -0.79 1.52
## vine_AdapBehav_DomStd  109.00 37.00  0.41   -0.98 1.60
## ados_ageMo              52.73 29.57  0.25   -0.08 1.03
## ados_CoSoTot            20.00 13.00  0.04   -0.79 0.53
## ados_RRTot               6.00  5.00  0.12   -0.79 0.23
## ados_CoSoTotRRTot       25.00 15.00  0.60   -0.24 0.59
## mullen_ageMo            51.78 28.85  0.26   -0.10 1.02
## mullen_VRT              77.00 47.00  0.54   -0.16 1.74
## mullen_FMT              67.00 47.00 -0.01   -0.32 1.69
## mullen_RLT              72.00 47.00  0.44    0.46 1.55
## mullen_ELT              76.00 48.00  0.92    1.45 1.45
## mullen_ELC_Std         133.00 65.00  0.79    0.16 2.47
## scan_age                45.14 32.53 -0.25   -0.67 1.33
## gex_age                 42.25 29.63  0.18   -0.90 1.31
## -----------------------------------------------------------
## group: Poor
##                         vars  n  mean    sd median trimmed   mad   min
## subjectId*                1 41   NaN    NA     NA     NaN    NA   Inf
## sex*                      2 41   NaN    NA     NA     NaN    NA   Inf
## Dx*                       3 41   NaN    NA     NA     NaN    NA   Inf
## subgrp2*                  4 41   NaN    NA     NA     NaN    NA   Inf
## vine_agemo                5 41 37.01  6.38  36.80   37.18  5.11 19.75
## vine_ComTotal_DomStd      6 41 71.44 15.27  74.00   71.21 17.79 42.00
## vine_DlyTotal_DomStd      7 41 79.76 11.91  83.00   79.94  8.90 56.00
## vine_SocTotal_DomStd      8 41 75.20 10.35  76.00   75.00  8.90 57.00
## vine_MtrTotal_DomStd      9 41 84.98 10.80  85.00   84.55  8.90 56.00
## vine_AdapBehav_DomStd    10 41 74.34 11.52  75.00   74.27  8.90 47.00
## ados_ageMo               11 41 37.25  6.42  37.16   37.41  4.87 19.78
## ados_CoSoTot             12 41 15.88  2.84  16.00   15.88  4.45  8.00
## ados_RRTot               13 41  4.41  1.20   4.00    4.39  1.48  2.00
## ados_CoSoTotRRTot        14 41 20.29  3.15  20.00   20.27  2.97 14.00
```

```
## mullen_ageMo              15 41 37.00  6.41  36.80   37.17  5.11 19.75
## mullen_VRT                16 41 33.07 10.90  33.00   32.18 13.34 20.00
## mullen_FMT                17 41 31.98 10.09  31.00   31.27 16.31 20.00
## mullen_RLT                18 41 23.00  9.78  20.00   23.70 10.38  1.00
## mullen_ELT                19 41 20.05 11.50  22.00   20.39 13.34  1.00
## mullen_ELC_Std            20 41 61.63 12.25  60.00   61.48 11.86 37.00
## scan_age                  21 41 29.70  7.88  27.89   29.74  6.62 12.48
## gex_age                   22 41 25.46  7.23  25.13   25.19  5.06 12.16
##                             max range  skew kurtosis    se
## subjectId*                 -Inf  -Inf    NA       NA    NA
## sex*                       -Inf  -Inf    NA       NA    NA
## Dx*                        -Inf  -Inf    NA       NA    NA
## subgrp2*                   -Inf  -Inf    NA       NA    NA
## vine_agemo                51.81 32.07 -0.30     0.96  1.00
## vine_ComTotal_DomStd     108.00 66.00  0.15    -0.56  2.38
## vine_DlyTotal_DomStd     111.00 55.00 -0.05     0.07  1.86
## vine_SocTotal_DomStd     104.00 47.00  0.28    -0.10  1.62
## vine_MtrTotal_DomStd     122.00 66.00  0.52     2.33  1.69
## vine_AdapBehav_DomStd    104.00 57.00  0.00     0.19  1.80
## ados_ageMo                53.03 33.25 -0.23     0.98  1.00
## ados_CoSoTot              21.00 13.00 -0.25    -0.40  0.44
## ados_RRTot                 8.00  6.00  0.36     0.45  0.19
## ados_CoSoTotRRTot         26.00 12.00  0.12    -1.02  0.49
## mullen_ageMo              51.81 32.07 -0.28     0.89  1.00
## mullen_VRT                56.00 36.00  0.43    -0.90  1.70
## mullen_FMT                54.00 34.00  0.29    -1.02  1.58
## mullen_RLT                38.00 37.00 -0.48    -0.18  1.53
## mullen_ELT                39.00 38.00 -0.32    -1.21  1.80
## mullen_ELC_Std            89.00 52.00  0.22    -0.71  1.91
## scan_age                  46.95 34.47  0.08    -0.42  1.23
## gex_age                   41.82 29.67  0.37    -0.16  1.13
## -------------------------------------------------------
## group: TD
##                          vars  n    mean    sd median trimmed   mad   min
## subjectId*                  1 35     NaN    NA     NA     NaN    NA   Inf
## sex*                        2 35     NaN    NA     NA     NaN    NA   Inf
## Dx*                         3 35     NaN    NA     NA     NaN    NA   Inf
## subgrp2*                    4 35     NaN    NA     NA     NaN    NA   Inf
## vine_agemo                  5 35   30.42  5.18  29.86   30.47  4.92 14.98
## vine_ComTotal_DomStd        6 35  103.97 11.21 101.00  103.34 10.38 86.00
## vine_DlyTotal_DomStd        7 35  103.37 13.21 100.00  102.55 13.34 85.00
## vine_SocTotal_DomStd        8 35  105.11 10.82 103.00  104.66 11.86 90.00
## vine_MtrTotal_DomStd        9 35  100.77  9.52 100.00  100.52 10.38 88.00
## vine_AdapBehav_DomStd      10 35  103.71 11.80 101.00  103.24 13.34 86.00
## ados_ageMo                 11 35   31.18  5.39  30.32   31.10  4.38 16.59
## ados_CoSoTot               12 35    1.91  1.88   1.00    1.69  1.48  0.00
## ados_RRTot                 13 35    0.09  0.28   0.00    0.00  0.00  0.00
## ados_CoSoTotRRTot          14 35    2.00  1.88   1.00    1.79  1.48  0.00
## mullen_ageMo               15 35   30.42  5.20  29.86   30.46  4.92 14.98
## mullen_VRT                 16 35   61.83  9.63  62.00   61.83  8.90 43.00
## mullen_FMT                 17 35   55.54  9.24  54.00   55.24 10.38 38.00
## mullen_RLT                 18 35   54.94  8.37  55.00   55.10  7.41 39.00
## mullen_ELT                 19 35   55.49  8.93  57.00   55.55 11.86 41.00
## mullen_ELC_Std             20 35  113.80 12.94 116.00  113.90 14.83 90.00
```

```
## scan_age                21 35  25.12  9.39  23.79   24.75 12.42 12.12
## gex_age                 22 35  21.71  8.61  19.78   20.66  8.04 12.12
##                         max range  skew kurtosis   se
## subjectId*             -Inf  -Inf    NA       NA   NA
## sex*                   -Inf  -Inf    NA       NA   NA
## Dx*                    -Inf  -Inf    NA       NA   NA
## subgrp2*               -Inf  -Inf    NA       NA   NA
## vine_agemo             39.66 24.67 -0.27     0.56 0.88
## vine_ComTotal_DomStd  135.00 49.00  0.61    -0.19 1.90
## vine_DlyTotal_DomStd  129.00 44.00  0.56    -1.06 2.23
## vine_SocTotal_DomStd  125.00 35.00  0.38    -1.23 1.83
## vine_MtrTotal_DomStd  117.00 29.00  0.25    -1.29 1.61
## vine_AdapBehav_DomStd 127.00 41.00  0.39    -1.28 2.00
## ados_ageMo             42.35 25.76  0.00     0.06 0.91
## ados_CoSoTot            7.00  7.00  0.94    -0.01 0.32
## ados_RRTot              1.00  1.00  2.83     6.21 0.05
## ados_CoSoTotRRTot       7.00  7.00  0.88    -0.14 0.32
## mullen_ageMo           39.66 24.67 -0.27     0.54 0.88
## mullen_VRT             80.00 37.00  0.03    -0.71 1.63
## mullen_FMT             80.00 42.00  0.32    -0.21 1.56
## mullen_RLT             72.00 33.00 -0.10    -0.81 1.42
## mullen_ELT             71.00 30.00 -0.14    -1.27 1.51
## mullen_ELC_Std        138.00 48.00 -0.11    -1.12 2.19
## scan_age               44.52 32.39  0.26    -1.25 1.59
## gex_age                44.52 32.39  0.93     0.02 1.46
```

Chi-square test on sex by subgroup

```
tab2use = table(labels$sex, labels$subgrp2)
res = chisq.test(tab2use)
knitr::kable(tab2use)
```

	Good	Poor	TD
F	10	7	16
M	30	34	21

```
res
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab2use
## X-squared = 6.8763, df = 2, p-value = 0.03212
```

ANOVA on age at MRI scan

```
# scan age
mod2use = lm(scan_age ~ subgrp2, data = labels)
anova(mod2use)
```

```
## Analysis of Variance Table
```

```
##
## Response: scan_age
##              Df Sum Sq Mean Sq F value Pr(>F)
## subgrp2      2  318.8 159.380  2.0387 0.1349
## Residuals 115 8990.3  78.177
```

ANOVA on meanFD

```
mod2use = lm(meanFD ~ subgrp2, data = labels)
anova(mod2use)
```

```
## Analysis of Variance Table
##
## Response: meanFD
##              Df  Sum Sq  Mean Sq F value Pr(>F)
## subgrp2      2 0.04643 0.023217  1.1206 0.3296
## Residuals 115 2.38269 0.020719
```

ANOVA on meanDVARS

```
mod2use = lm(meanDVARS ~ subgrp2, data = labels)
anova(mod2use)
```

```
## Analysis of Variance Table
##
## Response: meanDVARS
##              Df Sum Sq Mean Sq F value Pr(>F)
## subgrp2      2  24.37  12.187  1.9313 0.1496
## Residuals 115 725.65   6.310
```

ANOVA on age at blood sample

```
# gex age
mod2use = lm(gex_age ~ subgrp2, data = labels)
anova(mod2use)
```

```
## Analysis of Variance Table
##
## Response: gex_age
##              Df Sum Sq Mean Sq F value Pr(>F)
## subgrp2      2  251.2 125.596  1.7423 0.1797
## Residuals 115 8289.8  72.085
```

ANOVA on RIN

```
mod2use = lm(RIN ~ subgrp2, data = labels)
anova(mod2use)
```

```
## Analysis of Variance Table
##
```

```
## Response: RIN
##            Df  Sum Sq Mean Sq F value Pr(>F)
## subgrp2     2   0.342 0.17111  0.1007 0.9043
## Residuals 101 171.654 1.69955
```

Mullen EL trajectory

```
plot_xlim = c(0,60)

fname2save = NULL
p2 = spaghettiPlot(df = lwdata_flat,
                   x_var = "mullen_ageMo",
                   y_var = "mullen_ELT",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Mullen Expressive Language",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p2$lme_model)
```

```
##                      numDF denDF  F-value p-value
## (Intercept)             1   172 3281.946  <.0001
## mullen_ageMo            1   172   11.656   8e-04
## subgrp2                 2   113  157.792  <.0001
## mullen_ageMo:subgrp2    2   172   20.217  <.0001
```

```
p2$p
```
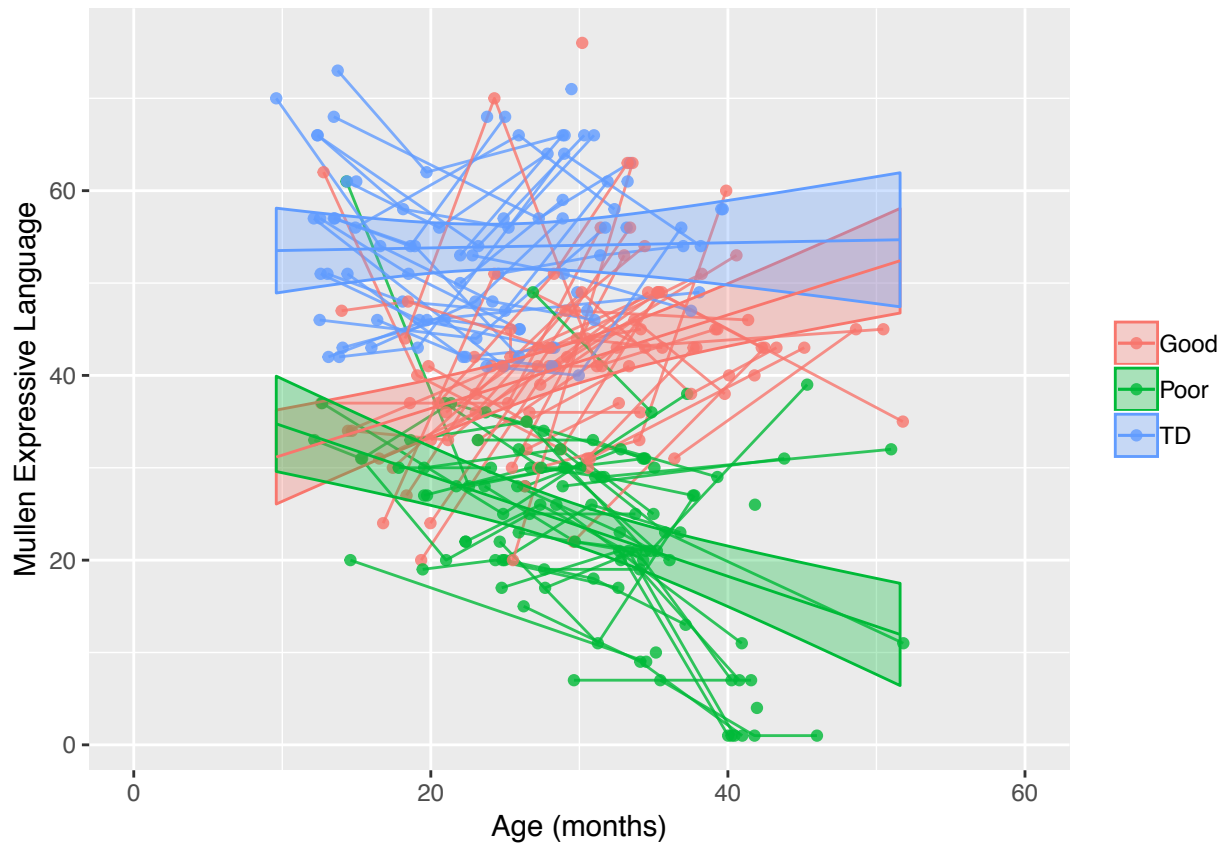
Mullen EL - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_ELT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Expressive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF   F-value p-value
## (Intercept)         1   113 2024.0359  <.0001
```

```
## mullen_ageMo                1   113   39.8851   <.0001
## subgrp2                      1    74  257.9090   <.0001
## mullen_ageMo:subgrp2         1   113   11.0625   0.0012
```

Mullen EL - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_ELT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Expressive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                   numDF denDF  F-value  p-value
## (Intercept)          1   109 3850.190   <.0001
## mullen_ageMo         1   109    0.174   0.6775
## subgrp2              1    73   69.464   <.0001
## mullen_ageMo:subgrp2 1   109    4.630   0.0336
```

Mullen EL - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_ELT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Expressive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                    xLimits = plot_xlim,
                    yLimits = NULL)
anova(p$lme_model)
```

```
##                   numDF denDF   F-value p-value
## (Intercept)           1   122 1633.0668  <.0001
## mullen_ageMo          1   122    0.4210  0.5176
## subgrp2               1    79  110.0302  <.0001
## mullen_ageMo:subgrp2  1   122   36.4114  <.0001
```

Mullen RL trajectory

```
fname2save = NULL
p3 = spaghettiPlot(df = lwdata_flat,
                   x_var = "mullen_ageMo",
                   y_var = "mullen_RLT",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Mullen Receptive Language",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p3$lme_model)
```

```
##                   numDF denDF  F-value p-value
## (Intercept)           1   172 3940.156  <.0001
## mullen_ageMo          1   172   14.191    2e-04
## subgrp2               2   113  177.665  <.0001
## mullen_ageMo:subgrp2  2   172    9.552    1e-04
```

```
p3$p
```
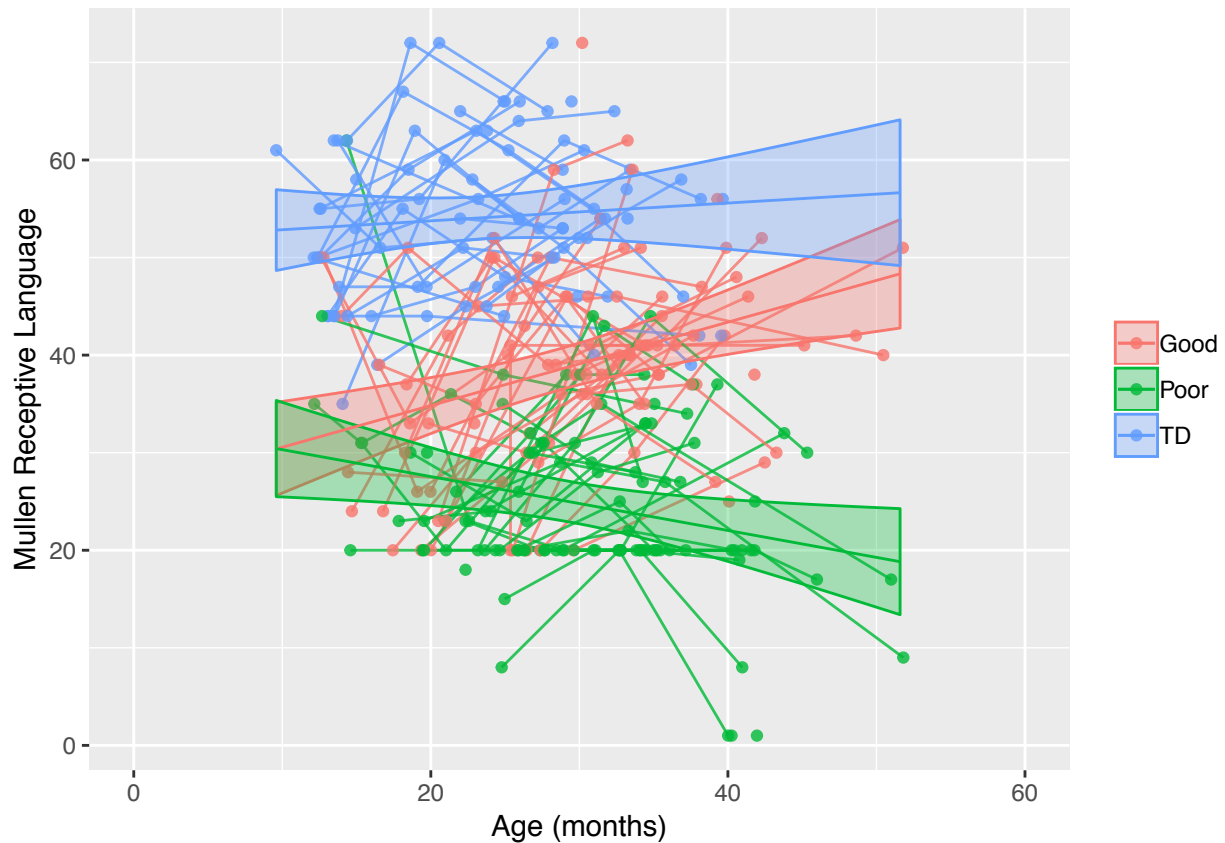
Mullen RL - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_RLT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Receptive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF   F-value p-value
## (Intercept)         1   113 2753.0452  <.0001
```

```
## mullen_ageMo                1    113    32.1775  <.0001
## subgrp2                      1     74   346.4340  <.0001
## mullen_ageMo:subgrp2         1    113     4.1855  0.0431
```

Mullen RL - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_RLT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Receptive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                        numDF denDF   F-value p-value
## (Intercept)                1   109  3722.598  <.0001
## mullen_ageMo               1   109     0.107  0.7444
## subgrp2                    1    73   108.897  <.0001
## mullen_ageMo:subgrp2       1   109     3.485  0.0646
```

Mullen RL - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_RLT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Receptive Language",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                    xLimits = plot_xlim,
                    yLimits = NULL)
anova(p$lme_model)
```

```
##                     numDF denDF   F-value p-value
## (Intercept)            1   122 1773.7876  <.0001
## mullen_ageMo           1   122    0.4747  0.4922
## subgrp2                1    79   82.8545  <.0001
## mullen_ageMo:subgrp2   1   122   15.6651  0.0001
```

Mullen VR trajectory

```
fname2save = NULL
p4 = spaghettiPlot(df = lwdata_flat,
                   x_var = "mullen_ageMo",
                   y_var = "mullen_VRT",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Mullen Visual Reception",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p4$lme_model)
```

```
##                     numDF denDF  F-value p-value
## (Intercept)            1   172 4375.491  <.0001
## mullen_ageMo           1   172    9.313  0.0026
## subgrp2                2   113   64.932  <.0001
## mullen_ageMo:subgrp2   2   172   11.684  <.0001
```

```
p4$p
```
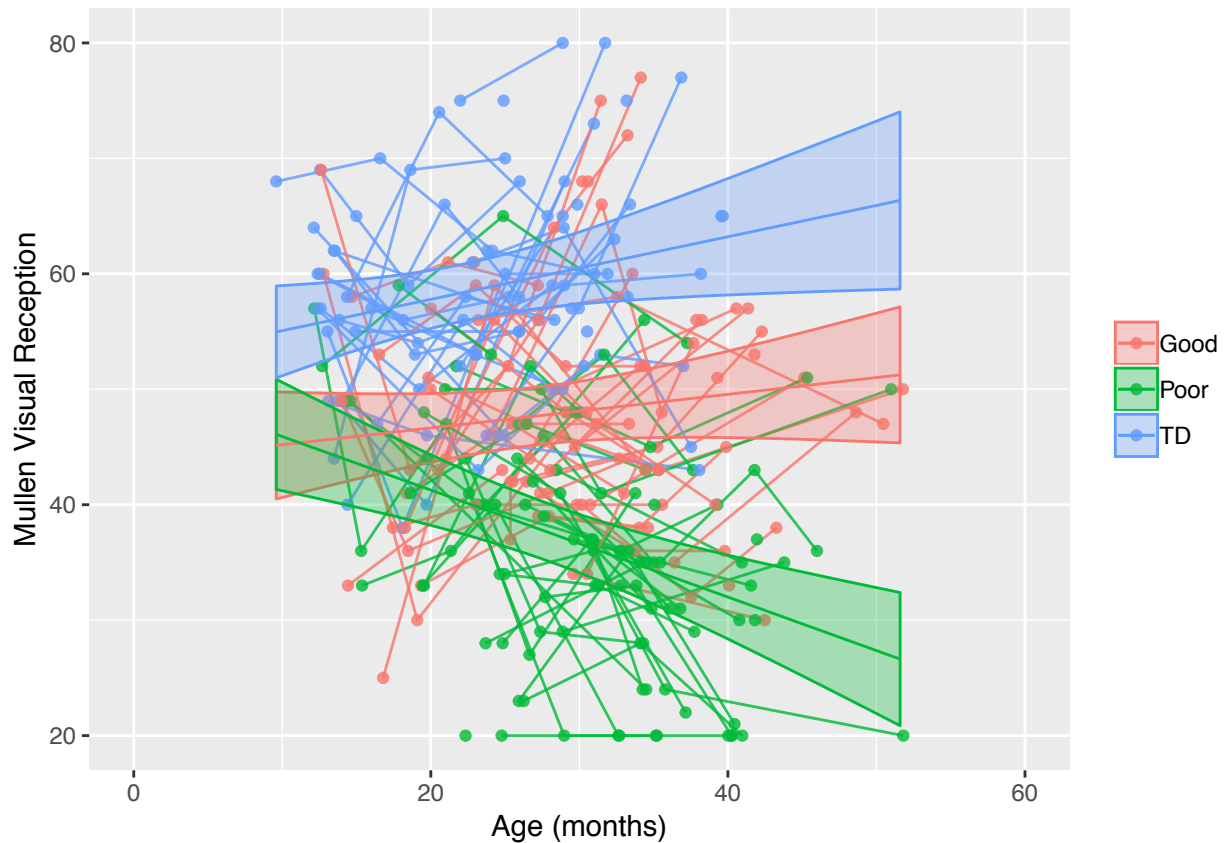
Mullen VR - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_VRT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Visual Reception",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##               numDF denDF   F-value p-value
## (Intercept)       1   113 3152.4818  <.0001
```

```
## mullen_ageMo              1   113   20.3477  <.0001
## subgrp2                   1    74  124.5595  <.0001
## mullen_ageMo:subgrp2      1   113   20.3821  <.0001
```

Mullen VR - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_VRT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Visual Reception",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                       numDF denDF  F-value p-value
## (Intercept)              1   109 3688.649  <.0001
## mullen_ageMo             1   109    0.036  0.8495
## subgrp2                  1    73   42.833  <.0001
## mullen_ageMo:subgrp2     1   109    0.759  0.3856
```

Mullen VR - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_VRT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Visual Reception",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                    numDF denDF   F-value p-value
## (Intercept)            1   122 2135.4719  <.0001
## mullen_ageMo           1   122    4.2869  0.0405
## subgrp2                1    79   29.6819  <.0001
## mullen_ageMo:subgrp2   1   122   15.3252  0.0001
```

Mullen FM trajectory

```
fname2save = NULL
p5 = spaghettiPlot(df = lwdata_flat,
                   x_var = "mullen_ageMo",
                   y_var = "mullen_FMT",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Mullen Fine Motor",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p5$lme_model)
```

```
##                    numDF denDF  F-value p-value
## (Intercept)            1   172 3234.230  <.0001
## mullen_ageMo           1   172   29.553  <.0001
## subgrp2                2   113   56.443  <.0001
## mullen_ageMo:subgrp2   2   172    2.980  0.0534
```

```
p5$p
```
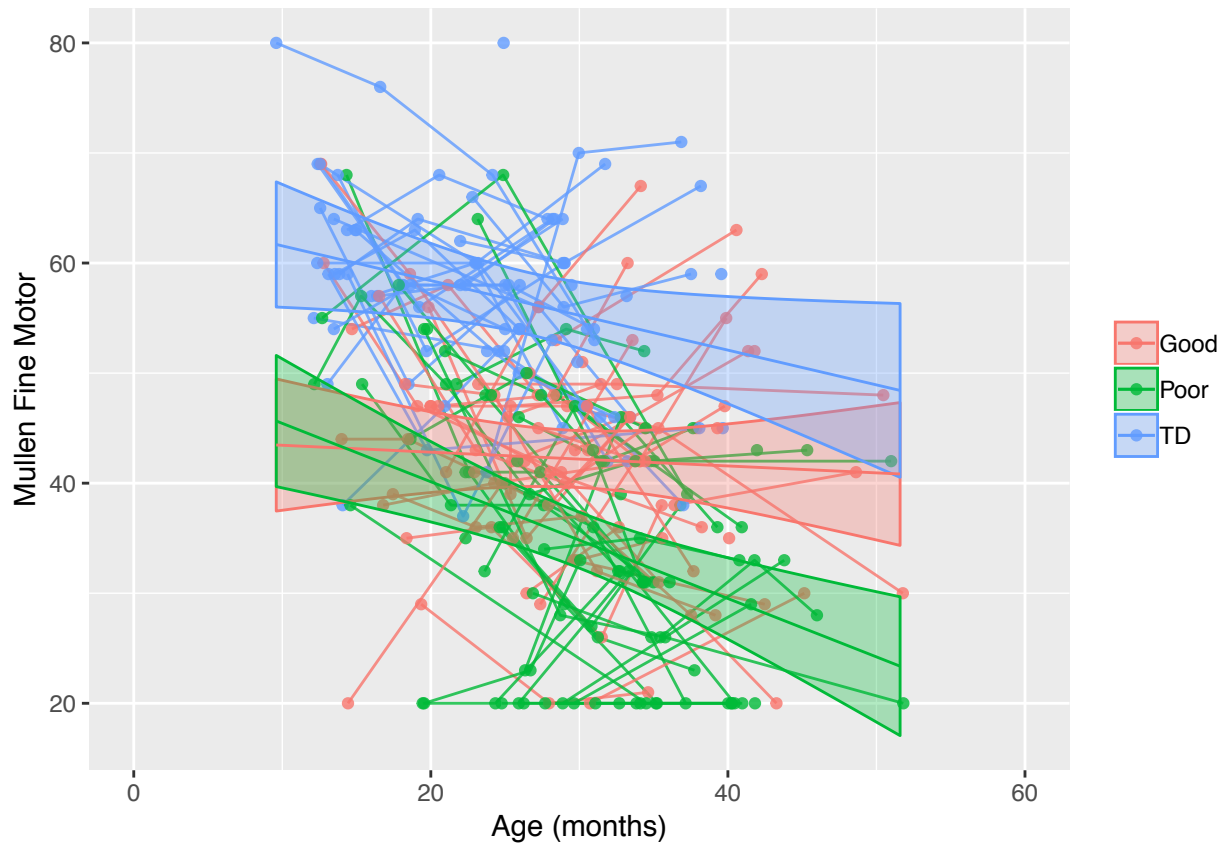
Mullen FM - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_FMT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Fine Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF   F-value p-value
## (Intercept)         1   113 2129.4100  <.0001
```

```
## mullen_ageMo               1   113    48.0224  <.0001
## subgrp2                     1    74   101.4430  <.0001
## mullen_ageMo:subgrp2        1   113     1.2713  0.2619
```

Mullen FM - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_FMT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Fine Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                      numDF denDF  F-value p-value
## (Intercept)              1   109 3482.348  <.0001
## mullen_ageMo             1   109   10.373  0.0017
## subgrp2                  1    73   67.170  <.0001
## mullen_ageMo:subgrp2     1   109    1.543  0.2169
```

Mullen FM - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "mullen_ageMo",
                  y_var = "mullen_FMT",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Mullen Fine Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                 xLimits = plot_xlim,
                 yLimits = NULL)
anova(p$lme_model)
```

```
##                 numDF denDF   F-value p-value
## (Intercept)         1   122 1498.7637  <.0001
## mullen_ageMo        1   122    6.8570  0.0099
## subgrp2             1    79   15.8318  0.0002
## mullen_ageMo:subgrp2 1  122    5.0849  0.0259
```

Vineland Communication trajectory

```
fname2save = NULL
p6 = spaghettiPlot(df = lwdata_flat,
                   x_var = "vine_agemo",
                   y_var = "vine_ComTotal_DomStd",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Vineland Communication",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p6$lme_model)
```

```
##                 numDF denDF  F-value p-value
## (Intercept)         1   172 9364.749  <.0001
## vine_agemo          1   172    0.242  0.6234
## subgrp2             2   113   98.875  <.0001
## vine_agemo:subgrp2  2   172   13.447  <.0001
```

```
p6$p
```
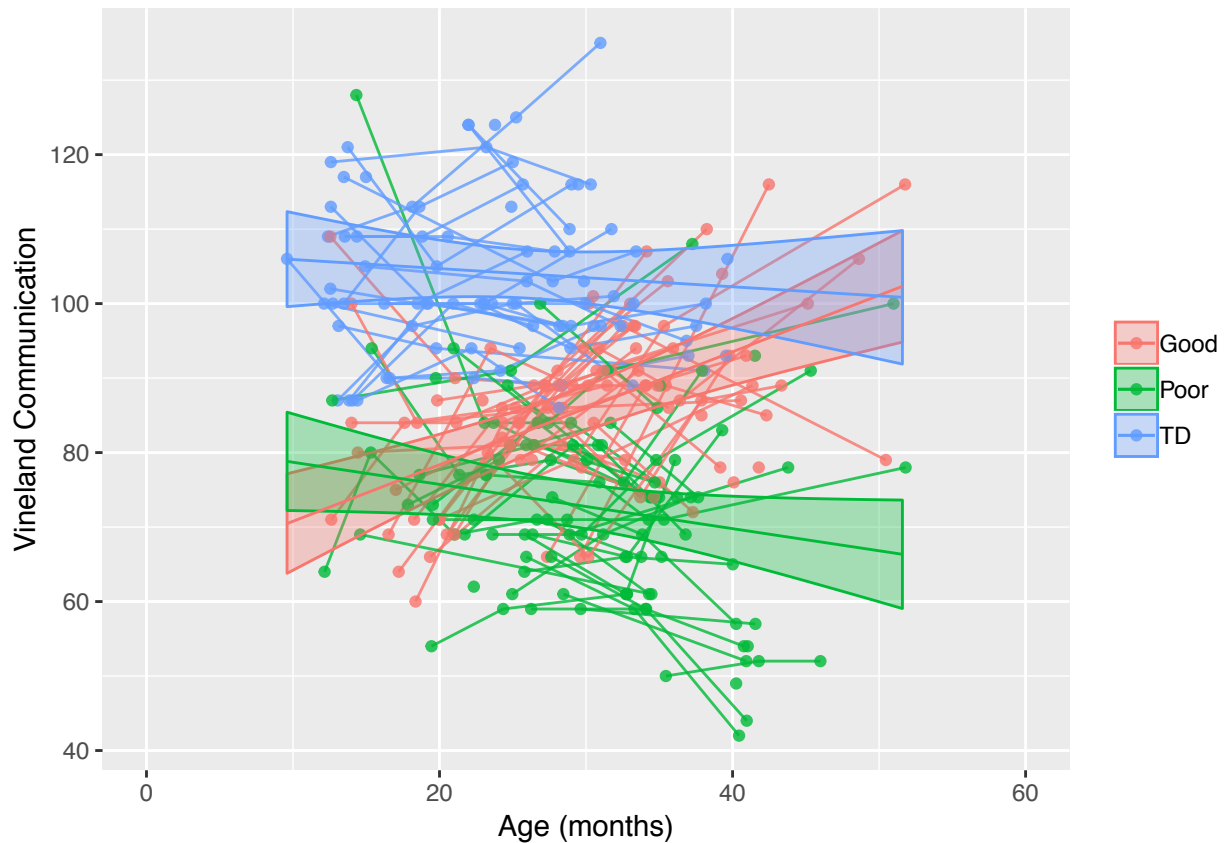
Vineland Communication - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_ComTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Communication",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF  F-value p-value
## (Intercept)        1    113 4999.857  <.0001
```

```
## vine_agemo            1   113   10.629  0.0015
## subgrp2               1    74  148.705  <.0001
## vine_agemo:subgrp2     1   113    0.720  0.3978
```

Vineland Communication - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_ComTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Communication",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                    numDF denDF  F-value  p-value
## (Intercept)           1   109 9544.539   <.0001
## vine_agemo            1   109    1.797   0.1828
## subgrp2               1    73   89.267   <.0001
## vine_agemo:subgrp2     1   109   16.495   0.0001
```

Vineland Communication - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_ComTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Communication",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                        xLimits = plot_xlim,
                        yLimits = NULL)
anova(p$lme_model)

## numDF denDF  F-value p-value
## (Intercept)      1   122 5815.862  <.0001
## vine_agemo       1   122    2.769  0.0987
## subgrp2          1    79   36.077  <.0001
## vine_agemo:subgrp2   1   122   20.109  <.0001
```

Vineland Socialization trajectory

```
fname2save = NULL
p7 = spaghettiPlot(df = lwdata_flat,
                   x_var = "vine_agemo",
                   y_var = "vine_SocTotal_DomStd",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Vineland Socialization",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p7$lme_model)

## numDF denDF   F-value p-value
## (Intercept)      1   172 11913.739  <.0001
## vine_agemo       1   172    28.817  <.0001
## subgrp2          2   113    64.343  <.0001
## vine_agemo:subgrp2   2   172   11.041  <.0001
```

```
p7$p
```

Vineland Socialization - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_SocTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Socialization",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF  F-value p-value
## (Intercept)         1   113 7700.000  <.0001
```

```
## vine_agemo            1  113   38.900  <.0001
## subgrp2               1   74  117.875  <.0001
## vine_agemo:subgrp2    1  113   17.944  <.0001
```

Vineland Socialization - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_SocTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Socialization",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                   numDF denDF  F-value p-value
## (Intercept)          1   109 9136.616  <.0001
## vine_agemo           1   109    3.857  0.0521
## subgrp2              1    73   64.846  <.0001
## vine_agemo:subgrp2   1   109    0.515  0.4745
```

Vineland Socialization - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_SocTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Socialization",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                xLimits = plot_xlim,
                yLimits = NULL)
anova(p$lme_model)
```

```
##              numDF denDF  F-value p-value
## (Intercept)      1   122 7640.169  <.0001
## vine_agemo       1   122   13.797   3e-04
## subgrp2          1    79   14.407   3e-04
## vine_agemo:subgrp2  1  122   15.092   2e-04
```

Vineland Daily Living trajectory

```
fname2save = NULL
p8 = spaghettiPlot(df = lwdata_flat,
                x_var = "vine_agemo",
                y_var = "vine_DlyTotal_DomStd",
                subgrp_var = "subgrp2",
                xLabel = "Age (months)",
                yLabel = "Vineland Daily Living",
                modelType = "linear",
                fname2save = fname2save,
                plot_dots = TRUE,
                plot_lines = TRUE,
                ci_band = TRUE,
                pi_band = FALSE,
                dot_alpha = 8/10,
                line_alpha = 8/10,
                band_alpha = 3/10,
                xLimits = plot_xlim,
                yLimits = NULL)
anova(p8$lme_model)
```

```
##              numDF denDF   F-value p-value
## (Intercept)      1   172 10470.861  <.0001
## vine_agemo       1   172    14.593  0.0002
## subgrp2          2   113    37.161  <.0001
## vine_agemo:subgrp2  2  172     6.915  0.0013
```

```
p8$p
```
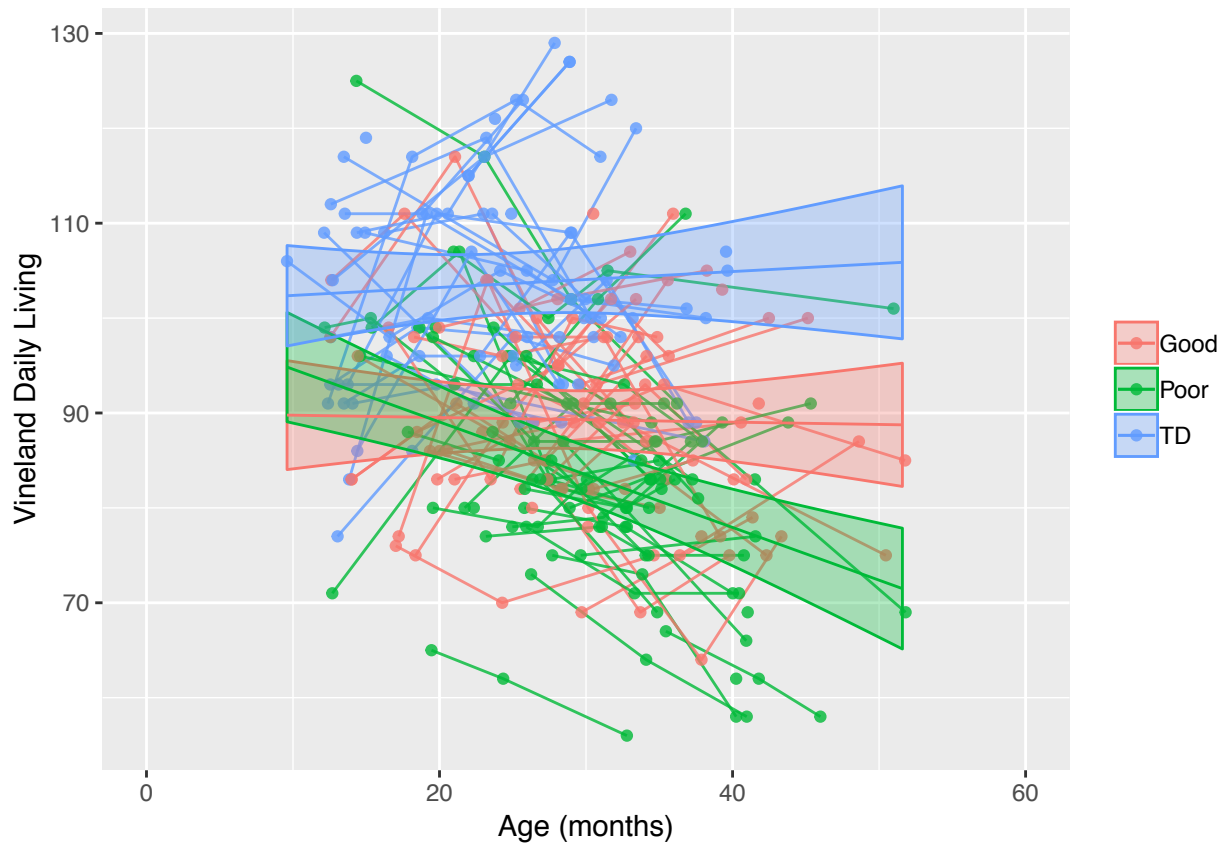
Vineland Daily Living - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_DlyTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Daily Living",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                numDF denDF  F-value p-value
## (Intercept)        1   113 6510.344  <.0001
```
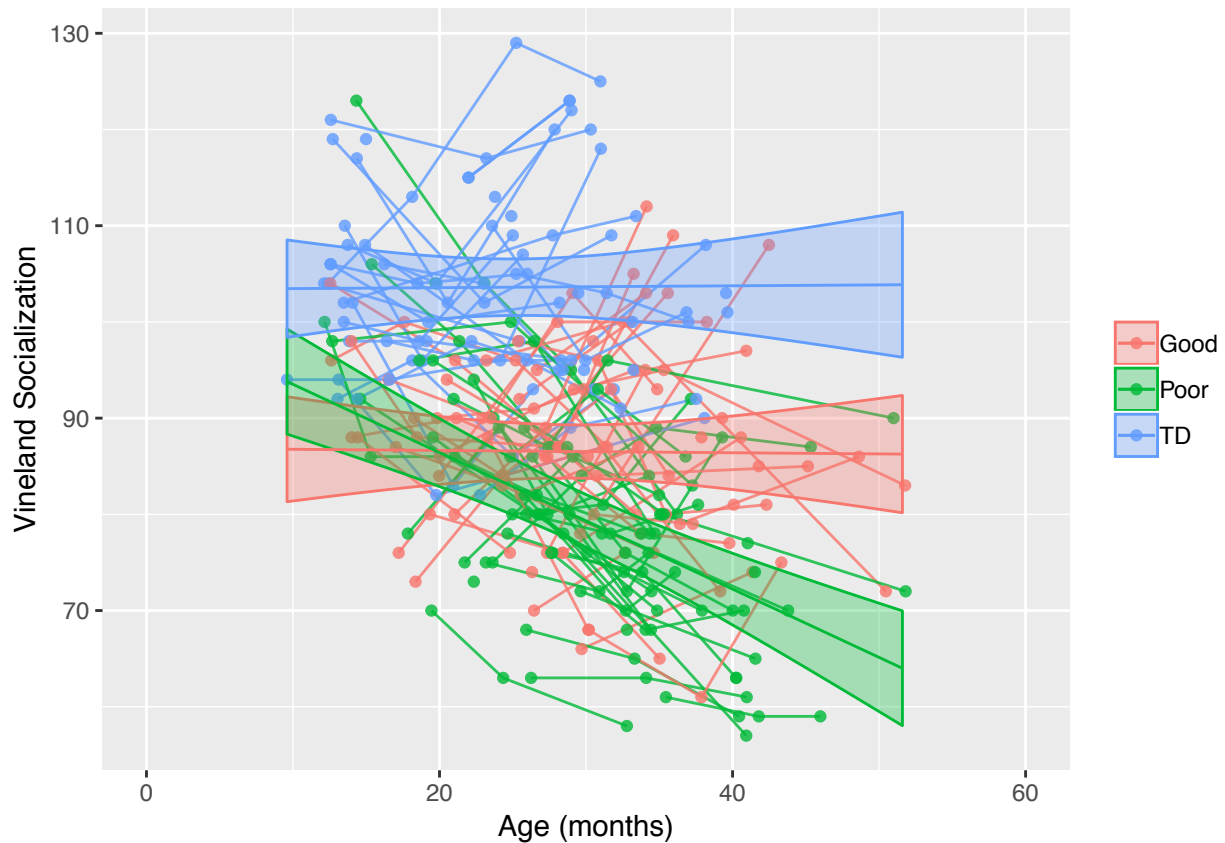
```
## vine_agemo            1   113   17.119   1e-04
## subgrp2               1    74   61.672   <.0001
## vine_agemo:subgrp2    1   113   11.480   1e-03
```

Vineland Daily Living - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_DlyTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Daily Living",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                     numDF denDF   F-value p-value
## (Intercept)            1   109  8030.416  <.0001
## vine_agemo             1   109     1.623  0.2054
## subgrp2                1    73    40.679  <.0001
## vine_agemo:subgrp2     1   109     0.806  0.3713
```

Vineland Daily Living - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_DlyTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Daily Living",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                        xLimits = plot_xlim,
                        yLimits = NULL)
anova(p$lme_model)
```

```
##                    numDF denDF  F-value p-value
## (Intercept)            1   122 6868.838  <.0001
## vine_agemo             1   122    8.810  0.0036
## subgrp2                1    79    7.407  0.0080
## vine_agemo:subgrp2     1   122    8.719  0.0038
```

Vineland Motor trajectory

```
fname2save = NULL
p9 = spaghettiPlot(df = lwdata_flat,
                    x_var = "vine_agemo",
                    y_var = "vine_MtrTotal_DomStd",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "Vineland Motor",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p9$lme_model)
```

```
##                    numDF denDF   F-value p-value
## (Intercept)            1   172 15563.259  <.0001
## vine_agemo             1   172    59.493  <.0001
## subgrp2                2   113    11.849  <.0001
## vine_agemo:subgrp2     2   172     8.320   4e-04
```

```
p9$p
```
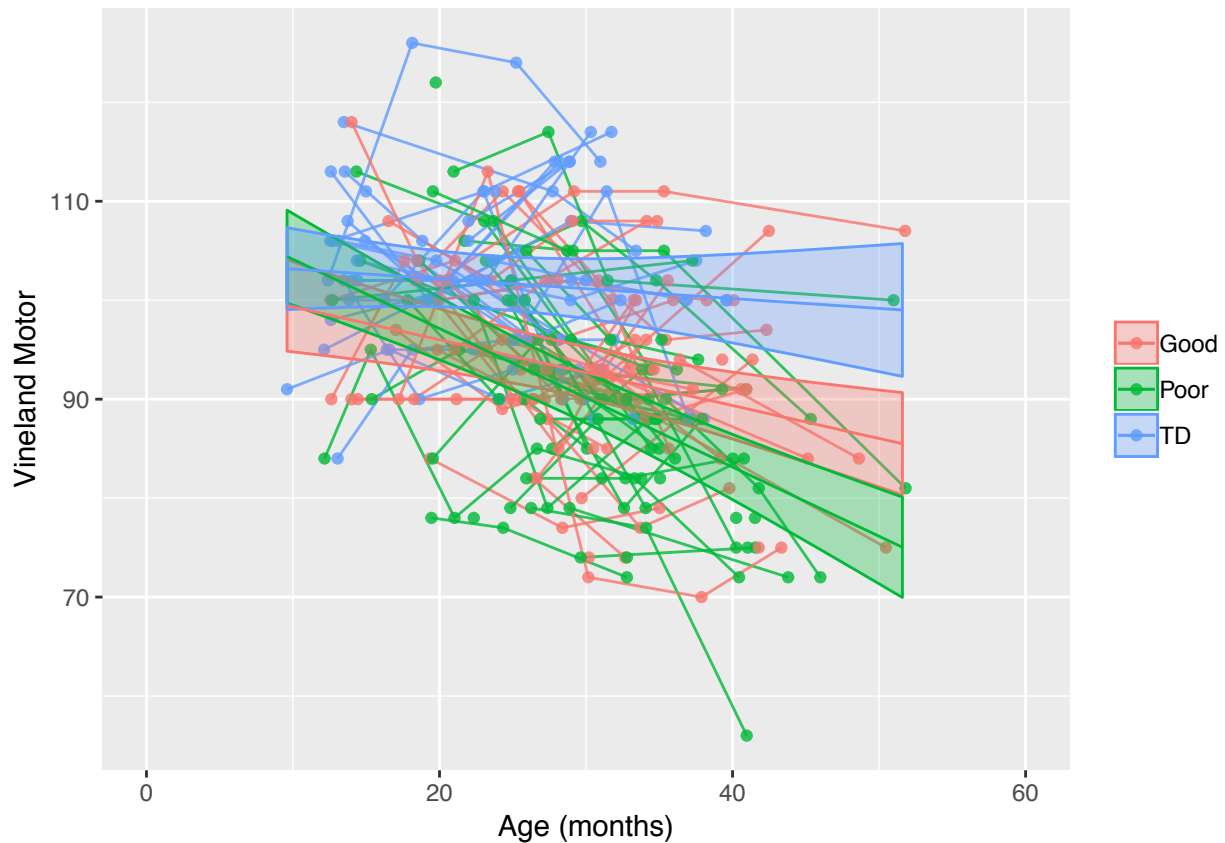
Vineland Motor - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_MtrTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF  F-value p-value
## (Intercept)         1   113 9650.565  <.0001
```

```
## vine_agemo             1   113   50.865  <.0001
## subgrp2                1    74   22.186  <.0001
## vine_agemo:subgrp2     1   113   18.007  <.0001
```

Vineland Motor - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_MtrTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                     numDF denDF    F-value p-value
## (Intercept)            1   109  13453.684  <.0001
## vine_agemo             1   109     17.292  0.0001
## subgrp2                1    73     16.965  0.0001
## vine_agemo:subgrp2     1   109      2.329  0.1299
```

Vineland Motor - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_MtrTotal_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Motor",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                    xLimits = plot_xlim,
                    yLimits = NULL)
anova(p$lme_model)
```

```
##                    numDF denDF  F-value p-value
## (Intercept)           1   122 9025.338  <.0001
## vine_agemo            1   122   48.146  <.0001
## subgrp2               1    79    1.818  0.1814
## vine_agemo:subgrp2    1   122    6.488  0.0121
```

Vineland Adaptive Behavior trajectory

```
fname2save = NULL
p10 = spaghettiPlot(df = lwdata_flat,
                    x_var = "vine_agemo",
                    y_var = "vine_AdapBehav_DomStd",
                    subgrp_var = "subgrp2",
                    xLabel = "Age (months)",
                    yLabel = "Vineland Adaptive Behavior",
                    modelType = "linear",
                    fname2save = fname2save,
                    plot_dots = TRUE,
                    plot_lines = TRUE,
                    ci_band = TRUE,
                    pi_band = FALSE,
                    dot_alpha = 8/10,
                    line_alpha = 8/10,
                    band_alpha = 3/10,
                    xLimits = plot_xlim,
                    yLimits = NULL)
anova(p10$lme_model)
```

```
##                    numDF denDF   F-value p-value
## (Intercept)           1   172 11747.689  <.0001
## vine_agemo            1   172    17.291   1e-04
## subgrp2               2   113    70.622  <.0001
## vine_agemo:subgrp2    2   172    12.431  <.0001
```

```
p10$p
```
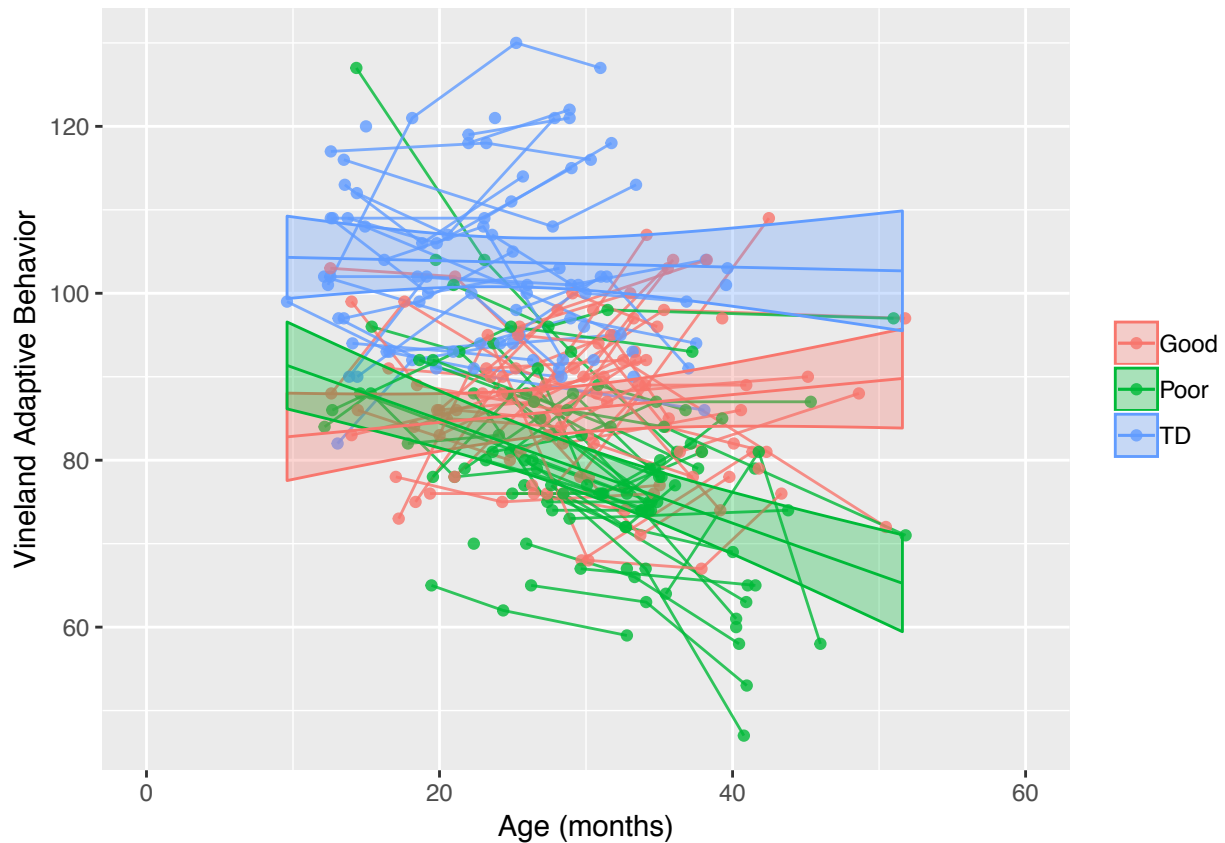
Vineland Adaptive Behavior - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_AdapBehav_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Adaptive Behavior",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF  F-value p-value
## (Intercept)         1   113 6895.113  <.0001
```

```
## vine_agemo              1   113   30.349   <.0001
## subgrp2                 1    74  109.685   <.0001
## vine_agemo:subgrp2      1   113   12.706   5e-04
```

Vineland Adaptive Behavior - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_AdapBehav_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Adaptive Behavior",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                      numDF denDF  F-value p-value
## (Intercept)              1   109 8907.768  <.0001
## vine_agemo               1   109    0.474  0.4926
## subgrp2                  1    73   77.135  <.0001
## vine_agemo:subgrp2       1   109    0.694  0.4065
```

Vineland Adaptive Behavior - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "vine_agemo",
                  y_var = "vine_AdapBehav_DomStd",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "Vineland Adaptive Behavior",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                        xLimits = plot_xlim,
                        yLimits = NULL)
anova(p$lme_model)


##                  numDF denDF  F-value p-value
## (Intercept)          1   122 8243.749  <.0001
## vine_agemo           1   122    7.355  0.0077
## subgrp2              1    79   15.842  0.0002
## vine_agemo:subgrp2   1   122   20.605  <.0001
```

ADOS Social-Communication trajectory

```
fname2save = NULL
p = spaghettiPlot(df = lwdata_flat,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Communication-Social",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)


##                  numDF denDF   F-value p-value
## (Intercept)          1   172 2359.3059  <.0001
## ados_ageMo           1   172   18.0252  <.0001
## subgrp2              2   113  303.2900  <.0001
## ados_ageMo:subgrp2   2   172    0.3190  0.7273
```

```
p$p
```

ADOS Social-Communication - TD vs ASD Poor

```r
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Communication-Social",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                 numDF denDF   F-value p-value
## (Intercept)         1   113 1874.3664  <.0001
```

```
## ados_ageMo               1   113    33.2769  <.0001
## subgrp2                  1    74   862.5059  <.0001
## ados_ageMo:subgrp2       1   113     0.7523  0.3876
```

ADOS Social-Communication - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Communication-Social",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                      numDF denDF   F-value  p-value
## (Intercept)             1   109  731.8233  <.0001
## ados_ageMo              1   109   16.9792  0.0001
## subgrp2                 1    73  317.4491  <.0001
## ados_ageMo:subgrp2      1   109    0.0111  0.9164
```

ADOS Social-Communication - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Communication-Social",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                    xLimits = plot_xlim,
                    yLimits = NULL)
anova(p$lme_model)

##                  numDF denDF    F-value p-value
## (Intercept)          1   122 2386.8523  <.0001
## ados_ageMo           1   122    0.3716  0.5432
## subgrp2              1    79   32.3795  <.0001
## ados_ageMo:subgrp2   1   122    0.4039  0.5263
```

ADOS RRB trajectory

```
fname2save = NULL
p = spaghettiPlot(df = lwdata_flat,
                  x_var = "ados_ageMo",
                  y_var = "ados_RRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Restricted Repetitive Behaviors",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                  numDF denDF    F-value p-value
## (Intercept)          1   172 1019.8378  <.0001
## ados_ageMo           1   172    5.7976  0.0171
## subgrp2              2   113  165.9659  <.0001
## ados_ageMo:subgrp2   2   172    0.1045  0.9008

p$p
```
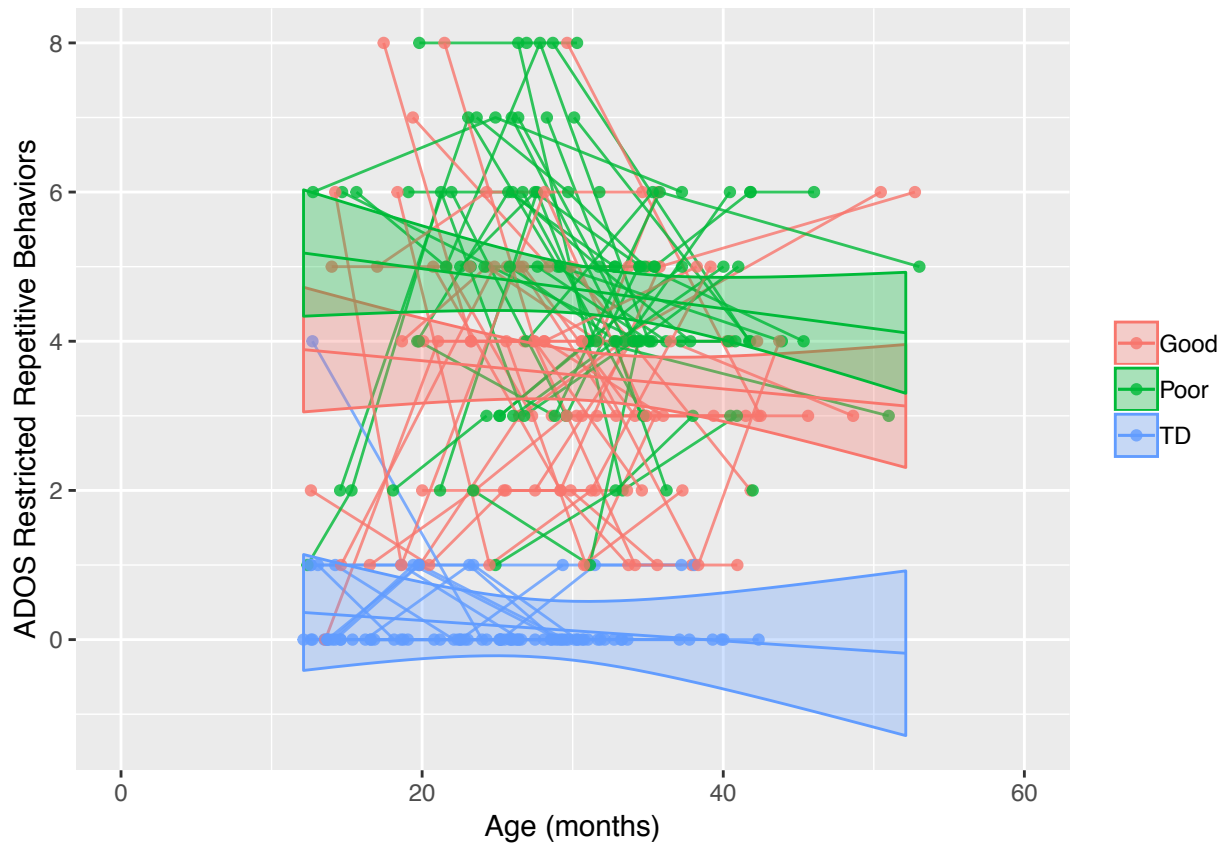
ADOS RRB - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_RRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Restricted Repetitive Behaviors",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##              numDF denDF  F-value p-value
## (Intercept)      1   113 664.9935  <.0001
```

```
## ados_ageMo              1  113  12.2156  0.0007
## subgrp2                 1   74 380.4118  <.0001
## ados_ageMo:subgrp2      1  113   0.2320  0.6310
```

ADOS RRB - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_RRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Restricted Repetitive Behaviors",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```
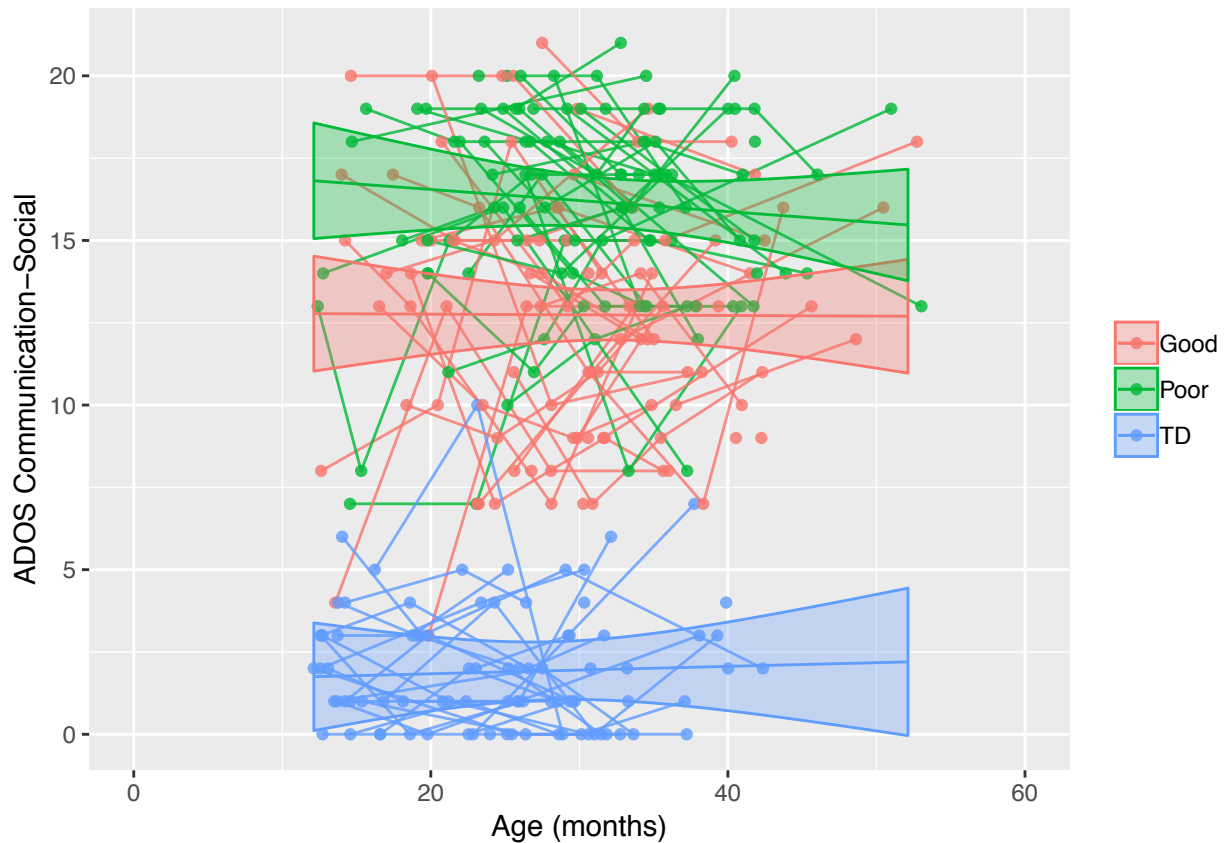
```
##                    numDF denDF  F-value p-value
## (Intercept)           1   109 357.7468  <.0001
## ados_ageMo            1   109   4.8277  0.0301
## subgrp2              1    73 233.5445  <.0001
## ados_ageMo:subgrp2   1   109   0.1365  0.7125
```

ADOS RRB - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_RRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Restricted Repetitive Behaviors",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                 xLimits = plot_xlim,
                 yLimits = NULL)
anova(p$lme_model)
```

```
##                numDF denDF  F-value p-value
## (Intercept)        1   122 985.6580  <.0001
## ados_ageMo         1   122   1.8220  0.1796
## subgrp2            1    79  18.9914  <.0001
## ados_ageMo:subgrp2 1   122   0.0681  0.7945
```

ADOS CoSo RR Total trajectory

```
fname2save = NULL
p1 = spaghettiPlot(df = lwdata_flat,
                   x_var = "ados_ageMo",
                   y_var = "ados_CoSoTotRRTot",
                   subgrp_var = "subgrp2",
                   xLabel = "Age (months)",
                   yLabel = "ADOS Total",
                   modelType = "linear",
                   fname2save = fname2save,
                   plot_dots = TRUE,
                   plot_lines = TRUE,
                   ci_band = TRUE,
                   pi_band = FALSE,
                   dot_alpha = 8/10,
                   line_alpha = 8/10,
                   band_alpha = 3/10,
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p1$lme_model)
```

```
##                numDF denDF  F-value p-value
## (Intercept)        1   172 3223.494  <.0001
## ados_ageMo         1   172   23.075  <.0001
## subgrp2            2   113  428.524  <.0001
## ados_ageMo:subgrp2 2   172    0.333  0.7174
```

```
p1$p
```
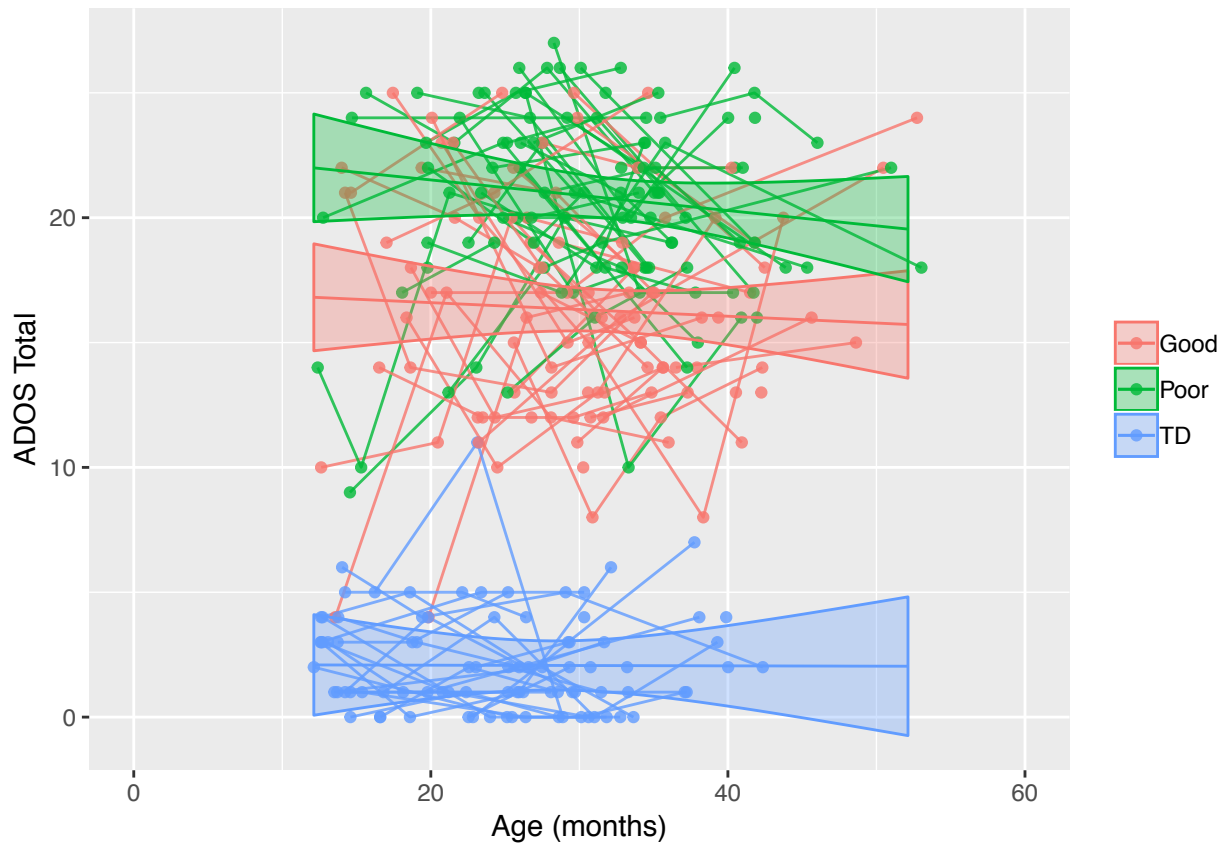
ADOS CoSo RR Total - TD vs ASD Poor

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Poor")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTotRRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Total",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)

##                  numDF denDF   F-value p-value
## (Intercept)          1   113 2625.5585  <.0001
```

```
## ados_ageMo          1   113   53.0554  <.0001
## subgrp2             1    74 1230.7989  <.0001
## ados_ageMo:subgrp2  1   113    0.7857  0.3773
```

ADOS CoSo RR Total - TD vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="TD" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTotRRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Total",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
                  xLimits = plot_xlim,
                  yLimits = NULL)
anova(p$lme_model)
```

```
##                     numDF denDF   F-value p-value
## (Intercept)            1   109  970.7358  <.0001
## ados_ageMo             1   109   18.6356  <.0001
## subgrp2                1    73  451.6558  <.0001
## ados_ageMo:subgrp2     1   109    0.0631  0.8022
```

ADOS CoSo RR Total - ASD Poor vs ASD Good

```
fname2save = NULL
tmp_data = subset(lwdata_flat,lwdata_flat$subgrp2=="Poor" | lwdata_flat$subgrp2=="Good")
p = spaghettiPlot(df = tmp_data,
                  x_var = "ados_ageMo",
                  y_var = "ados_CoSoTotRRTot",
                  subgrp_var = "subgrp2",
                  xLabel = "Age (months)",
                  yLabel = "ADOS Total",
                  modelType = "linear",
                  fname2save = fname2save,
                  plot_dots = TRUE,
                  plot_lines = TRUE,
                  ci_band = TRUE,
                  pi_band = FALSE,
                  dot_alpha = 8/10,
                  line_alpha = 8/10,
                  band_alpha = 3/10,
```

```
                   xLimits = plot_xlim,
                   yLimits = NULL)
anova(p$lme_model)
```

```
##                  numDF denDF  F-value p-value
## (Intercept)          1   122 3206.285  <.0001
## ados_ageMo           1   122    1.120  0.2921
## subgrp2              1    79   46.493  <.0001
## ados_ageMo:subgrp2   1   122    0.262  0.6099
```

ROI Analysis

ROI analysis

Setup

```
library(easypackages)
libraries("ggplot2","patchwork","here")
source(here("code","cohens_d.R"))
options(stringsAsFactors=FALSE)
```

Read in data

```
# read in ROI data
fname = file.path(here("data","tidy","tidy_roidata.csv"))
data = read.csv(fname)
```

Run analyses on each ROI

```
# names of ROIs
roiname = c("LHfrontal","LHtemporal","RHfrontal","RHtemporal")

# pre-allocate data frame for storing subtype model results
res_colnames = c("fstat","pval","fdr",
  "d_TD_vs_ASDGood","t_TD_vs_ASDGood","p_TD_vs_ASDGood",
  "d_TD_vs_ASDPoor","t_TD_vs_ASDPoor","p_TD_vs_ASDPoor",
  "d_ASDGood_vs_ASDPoor","t_ASDGood_vs_ASDPoor","p_ASDGood_vs_ASDPoor")
res = data.frame(matrix(nrow = length(roiname), ncol = length(res_colnames)))
colnames(res) = res_colnames
rownames(res) = roiname

# pre-allocate data frame for storing case-control model results
res_colnames = c("fstat","pval","fdr",
                 "d_TD_vs_ASD","t_TD_vs_ASD","p_TD_vs_ASD")
res_casecontrol = data.frame(matrix(nrow = length(roiname),
                                    ncol = length(res_colnames)))
colnames(res_casecontrol) = res_colnames
rownames(res_casecontrol) = roiname

for (i in 1:length(roiname)){
  # run subtype model
  form2use = as.formula(sprintf("%s ~ subgrp + sex",roiname[i]))
  mod2use = lm(formula = form2use, data = data)
  tmp_res = anova(mod2use)
  res$fstat[i] = tmp_res[1,4]
  res$pval[i] = tmp_res[1,5]

  # run case-control model
```

```r
form2use = as.formula(sprintf("%s ~ Dx + sex",roiname[i]))
mod2use = lm(formula = form2use, data = data)
tmp_res = anova(mod2use)
res_casecontrol$fstat[i] = tmp_res[1,4]
res_casecontrol$pval[i] = tmp_res[1,5]

# remove sex variation from data to compute effect sizes
form2use = as.formula(sprintf("%s ~ subgrp + sex",roiname[i]))
residmod = lm(formula = form2use, data = data)
full_model = model.matrix(~0+as.factor(subgrp) + as.factor(sex), data=data)
colnames(full_model) = c("Good","Poor","TD","sex")
cov_columns = c("sexM")
beta1 = residmod$coefficients[cov_columns, drop = FALSE]
beta1[is.na(beta1)] = 0
cov_columns = c("sex")
reduced_model = full_model[,cov_columns]
data$resid2use = t(data[,roiname[i]] - beta1 %*% t(reduced_model))

# case-control t-stats and effect sizes
mask1 = data$subgrp=="TD"
mask2 = data$subgrp=="Good" | data$subgrp=="Poor"
res_casecontrol$d_TD_vs_ASD[i] = cohens_d(data$resid2use[mask1],
                                          data$resid2use[mask2])
res_casecontrol$t_TD_vs_ASD[i] = t.test(data$resid2use[mask1],
                                        data$resid2use[mask2])$statistic
res_casecontrol$p_TD_vs_ASD[i] = t.test(data$resid2use[mask1],
                                        data$resid2use[mask2])$p.value


# subtype t-tstats and effect sizes
res$d_TD_vs_ASDGood[i] = cohens_d(data$resid2use[data$subgrp=="TD"],
                                  data$resid2use[data$subgrp=="Good"])
res$d_TD_vs_ASDPoor[i] = cohens_d(data$resid2use[data$subgrp=="TD"],
                                  data$resid2use[data$subgrp=="Poor"])
res$d_ASDGood_vs_ASDPoor[i] = cohens_d(data$resid2use[data$subgrp=="Good"],
                                       data$resid2use[data$subgrp=="Poor"])

res$t_TD_vs_ASDGood[i] = t.test(data$resid2use[data$subgrp=="TD"],
                                data$resid2use[data$subgrp=="Good"])$statistic
res$t_TD_vs_ASDPoor[i] = t.test(data$resid2use[data$subgrp=="TD"],
                                data$resid2use[data$subgrp=="Poor"])$statistic
res$t_ASDGood_vs_ASDPoor[i] = t.test(data$resid2use[data$subgrp=="Good"],
                                     data$resid2use[data$subgrp=="Poor"])$statistic

res$p_TD_vs_ASDGood[i] = t.test(data$resid2use[data$subgrp=="TD"],
                                data$resid2use[data$subgrp=="Good"])$p.value
res$p_TD_vs_ASDPoor[i] = t.test(data$resid2use[data$subgrp=="TD"],
                                data$resid2use[data$subgrp=="Poor"])$p.value
res$p_ASDGood_vs_ASDPoor[i] = t.test(data$resid2use[data$subgrp=="Good"],
                                     data$resid2use[data$subgrp=="Poor"])$p.value

# fill in effect size matrix
names2use = c("TD","ASD Good","ASD Poor")
es_mat = matrix(nrow = length(names2use), ncol = length(names2use))
```

```
colnames(es_mat) = names2use
rownames(es_mat) = colnames(es_mat)
es_mat[1,1] = NA
es_mat[2,2] = NA
es_mat[3,3] = NA

es_mat[1,2] = res$d_TD_vs_ASDGood[i]
es_mat[2,1] = res$d_TD_vs_ASDGood[i]
es_mat[1,3] = res$d_TD_vs_ASDPoor[i]
es_mat[3,1] = res$d_TD_vs_ASDPoor[i]
es_mat[2,3] = res$d_ASDGood_vs_ASDPoor[i]
es_mat[3,2] = res$d_ASDGood_vs_ASDPoor[i]

#plot the effect size matrix as a heatmap
  WGCNA::labeledHeatmap(Matrix = es_mat,
      xLabels = rownames(es_mat), yLabels = colnames(es_mat),
      ySymbols = NULL, colorLabels = FALSE,
      colors = WGCNA::blueWhiteRed(50), textMatrix = round(es_mat,digits=2),
      setStdMargins = FALSE, cex.text = 3, zlim = c(0,0.75),
      main = sprintf("%s Effect Size (Cohen's d)",roiname[i]))
} # for (i in 1:length(roiname))
```

LHfrontal Effect Size (Cohen's d)

LHtemporal Effect Size (Cohen's d)

	TD	ASD Good	ASD Poor
TD		0.27	0.73
ASD Good	0.27		0.46
ASD Poor	0.73	0.46	

RHfrontal Effect Size (Cohen's d)

	TD	ASD Good	ASD Poor
TD		0.08	0.59
ASD Good	0.08		0.48
ASD Poor	0.59	0.48	
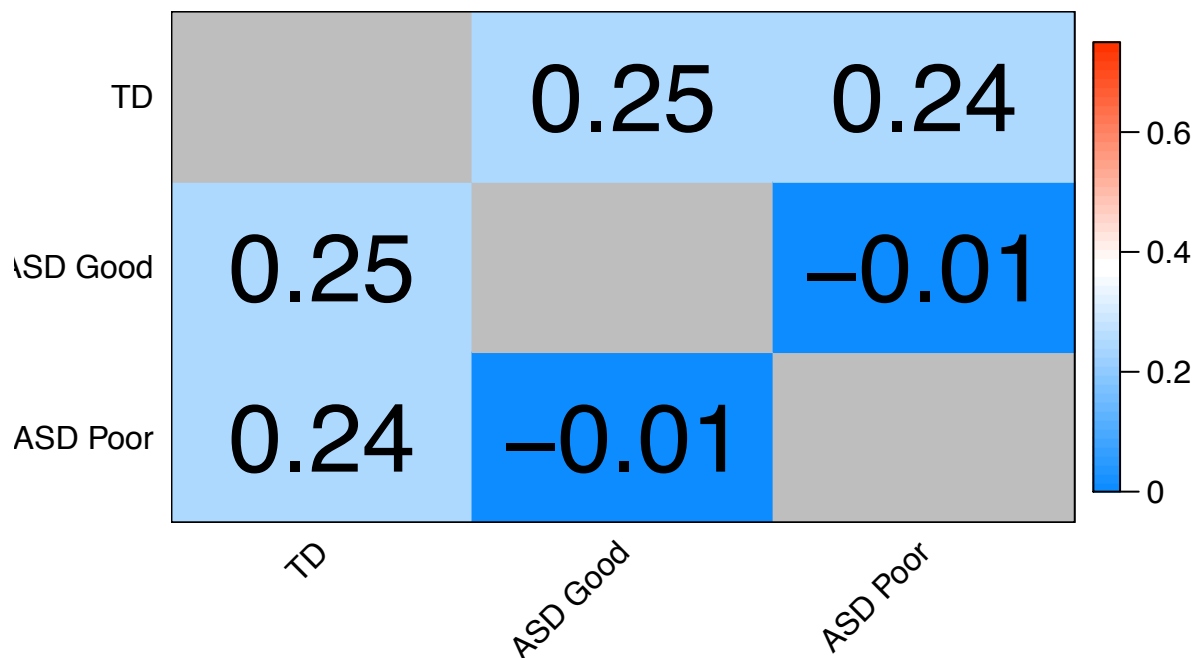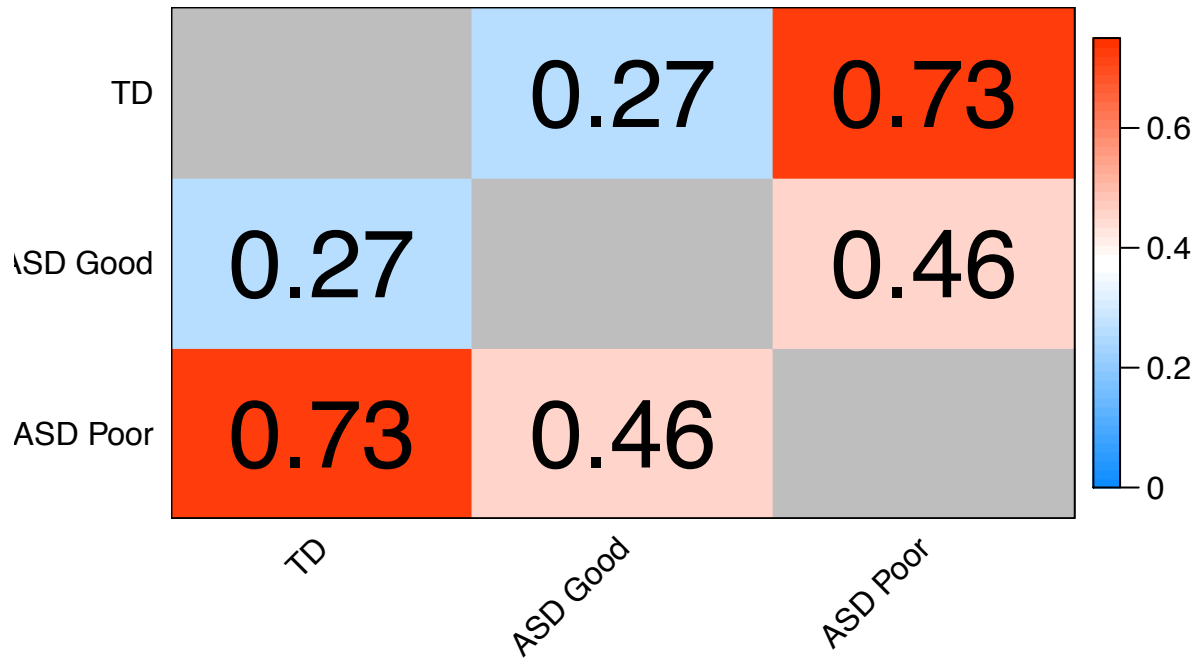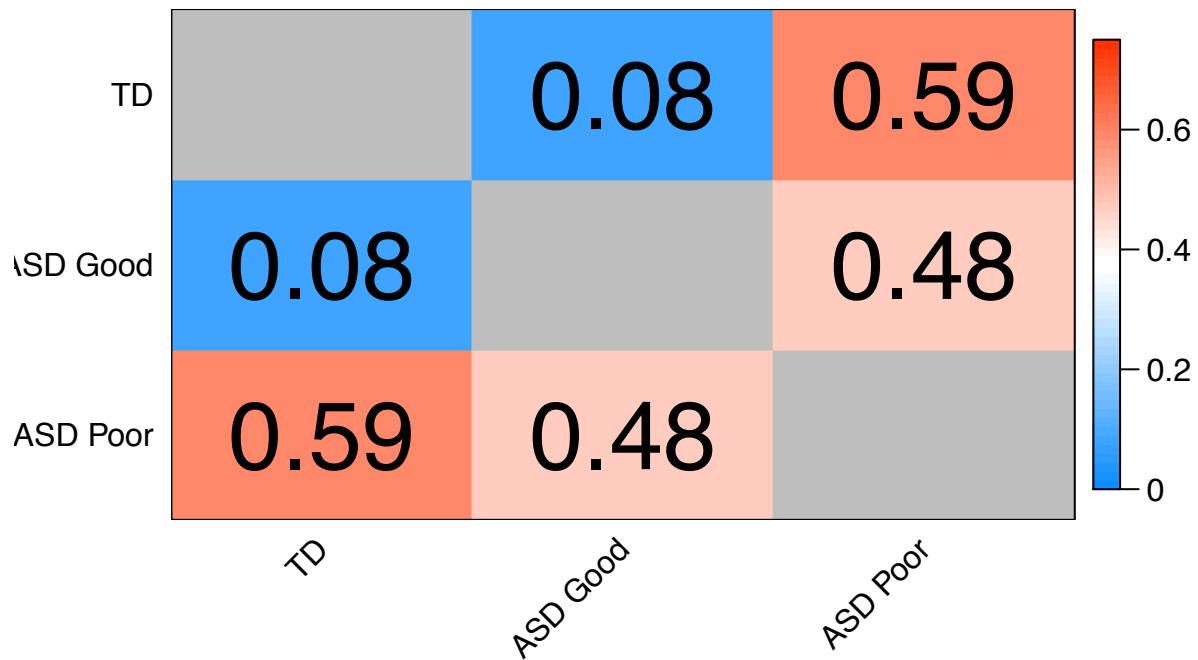
RHtemporal Effect Size (Cohen's d)
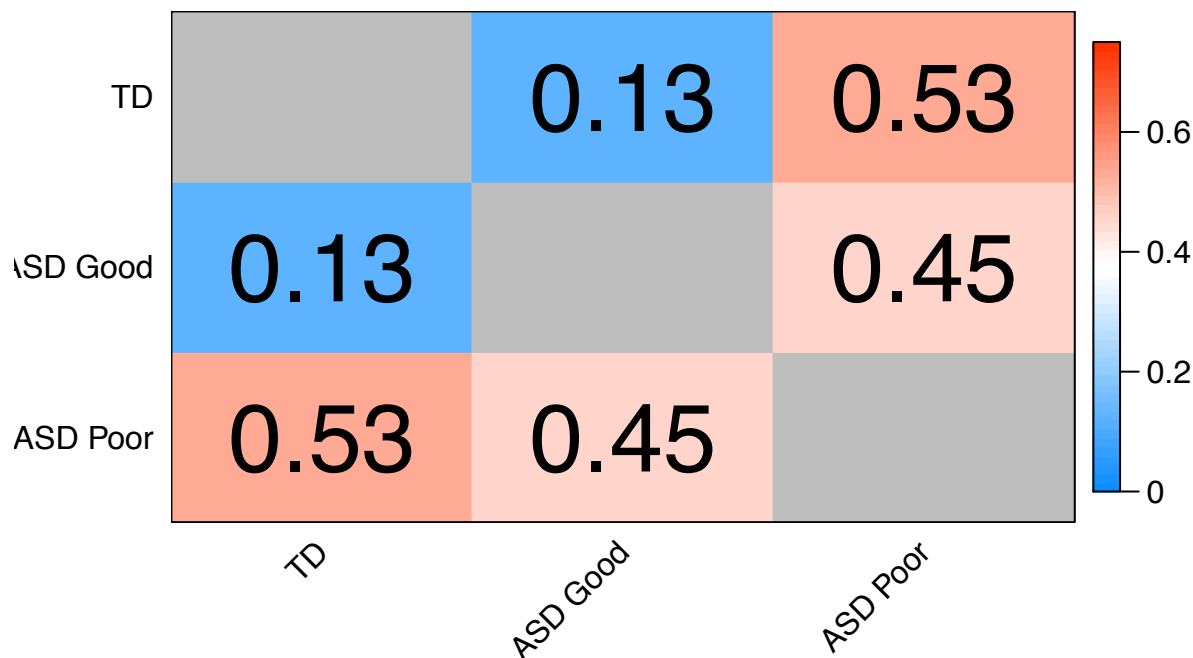

```
# compute FDR
res_casecontrol$fdr = p.adjust(res_casecontrol$pval, method = "fdr")
res$fdr = p.adjust(res$pval, method = "fdr")
```

Results from subtype model

```
knitr::kable(res[,c("fstat","pval","fdr")], digits = 4)
```

	fstat	pval	fdr
LHfrontal	0.7500	0.4747	0.4747
LHtemporal	6.1688	0.0029	0.0114
RHfrontal	3.6576	0.0289	0.0385
RHtemporal	4.5552	0.0125	0.0250

Results from case-control model

```
knitr::kable(res_casecontrol, digits = 4)
```

	fstat	pval	fdr	d_TD_vs_ASD	t_TD_vs_ASD	p_TD_vs_ASD
LHfrontal	1.5121	0.2213	0.2213	0.2475	1.2306	0.2227
LHtemporal	7.2353	0.0082	0.0328	0.4887	2.5954	0.0112
RHfrontal	2.4242	0.1222	0.1630	0.3202	1.7009	0.0929
RHtemporal	4.5727	0.0346	0.0692	0.3419	1.6850	0.0967

Make plots

```r
dotSize = 1
yLabel = "Delta % Signal Change"
xLabel = "Group"
black.bold.italic.text = element_text(face = "bold",
                                      colour = "black")
black.bold.axis.title = element_text(face="bold",
                                     size = 12,
                                     colour = "black")
bold.axis.text = element_text(face="bold",
                              size = 10)

data$plotOrder = factor(data$plotOrder)

p1 = ggplot(data = data, aes(x = reorder(subgrp, as.numeric(plotOrder)),
                             y = LHtemporal, colour = subgrp))
p1 = p1 + geom_jitter(size = dotSize) +
  geom_boxplot(fill = NA, colour = "#000000", outlier.shape = NA) +
  guides(colour = FALSE)
p1 = p1 + xlab(xLabel) + ylab(yLabel) + labs(title = "LH Temporal") +
  theme(plot.title = element_text(hjust = 0.5))
p1 = p1 + theme(title = black.bold.italic.text) +
  theme(axis.title = black.bold.axis.title) +
  theme(axis.text.x = bold.axis.text) +
  theme(axis.text.y = bold.axis.text)

p2 = ggplot(data = data, aes(x = reorder(subgrp, as.numeric(plotOrder)),
                             y = RHtemporal, colour = subgrp))
p2 = p2 + geom_jitter(size = dotSize) +
  geom_boxplot(fill = NA, colour = "#000000", outlier.shape = NA) +
  guides(colour = FALSE)
p2 = p2 + xlab(xLabel) + ylab(yLabel) + labs(title = "RH Temporal") +
  theme(plot.title = element_text(hjust = 0.5))
p2 = p2 + theme(title = black.bold.italic.text) +
  theme(axis.title = black.bold.axis.title) +
  theme(axis.text.x = bold.axis.text) +
  theme(axis.text.y = bold.axis.text)

p3 = ggplot(data = data, aes(x = reorder(subgrp, as.numeric(plotOrder)),
                             y = LHfrontal, colour = subgrp))
p3 = p3 + geom_jitter(size = dotSize) +
  geom_boxplot(fill = NA, colour = "#000000", outlier.shape = NA) +
  guides(colour = FALSE)
p3 = p3 + xlab(xLabel) + ylab(yLabel) + labs(title = "LH Frontal") +
  theme(plot.title = element_text(hjust = 0.5))
p3 = p3 + theme(title = black.bold.italic.text) +
  theme(axis.title = black.bold.axis.title) +
  theme(axis.text.x = bold.axis.text) +
  theme(axis.text.y = bold.axis.text)

p4 = ggplot(data = data, aes(x = reorder(subgrp, as.numeric(plotOrder)),
                             y = RHfrontal, colour = subgrp))
```

```
p4 = p4 + geom_jitter(size = dotSize) +
  geom_boxplot(fill = NA, colour = "#000000", outlier.shape = NA) +
  guides(colour = FALSE)
p4 = p4 + xlab(xLabel) + ylab(yLabel) + labs(title = "RH Frontal") +
  theme(plot.title = element_text(hjust = 0.5))
p4 = p4 + theme(title = black.bold.italic.text) +
  theme(axis.title = black.bold.axis.title) +
  theme(axis.text.x = bold.axis.text) +
  theme(axis.text.y = bold.axis.text)

p_final = p1 + p2 + p3 + p4 + plot_layout(nrow = 2, ncol = 2)
p_final
```
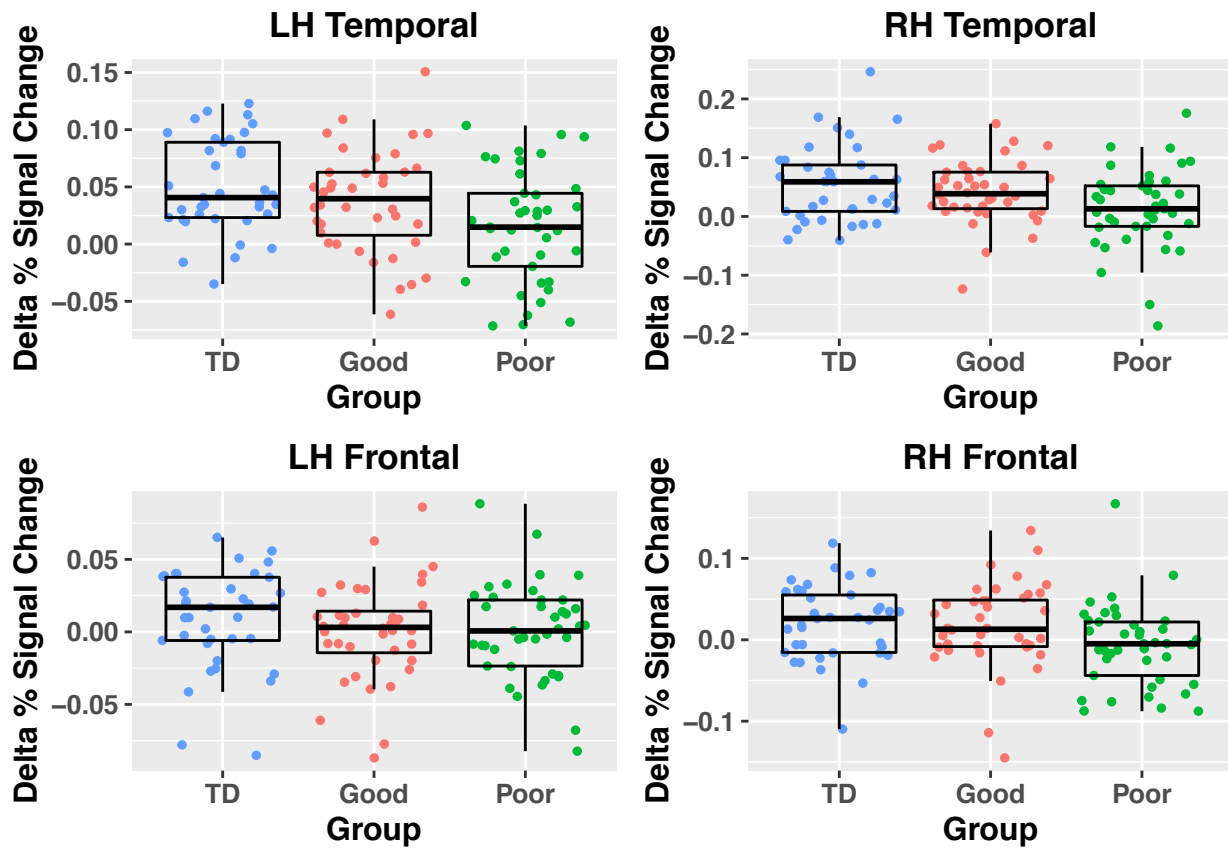
Covariate Adjustment of Expression Data

Adjust gene expression data by batch, sex, and RIN and analyze cell type surrogate proportion variables

The analysis for cell type surrogate proportion variables uses the CellCODE library(https://github.com/mchikina/CellCODE) based on Chikina, Zaslavsky, & Sealfon, (2015) Bioinformatics, 10, 1584-1591. Paper can be found here: https://academic.oup.com/bioinformatics/article/31/10/1584/177237.

Setup

```
# load libraries
library(here)
install.packages(here("code","CellCODE"), repos=NULL, type="source")
library(easypackages)
libraries("limma","CellCODE")
options(stringsAsFactors = FALSE)
```

Read in data

```
# load gene expression data, gene information, and labels
load(here("data","tidy","exprData.Rdata"))

# construct model
cov_columns = c("batch2","batchWG6","sex","RIN")
full_model = model.matrix(~0+as.factor(Dx) +
                            as.factor(batch) +
                            as.factor(sex) +
                           RIN,
                         data=labelData)
colnames(full_model) = c("ASD", "TD",cov_columns)

# fit model -------------------------------------------------------
fit = lmFit(exprData,full_model)

# remove batch, sex, and RIN
beta1 = fit$coefficients[, cov_columns, drop = FALSE]
beta1[is.na(beta1)] = 0
exprDataAdj = exprData - beta1 %*% t(full_model[,cov_columns])

# save adjusted expression data
save(exprDataAdj,geneInfo,labelData,
     file = here("data","processed","exprDataAdj.Rdata"))
```

Estimate surrogate proportion variables for leukocyte cell types

```r
data("IRIS")

ref_data = exprDataAdj
rownames(ref_data) = geneInfo$geneSymbol

cellTypes2use = c("Neutrophil-Resting","CD4Tcell-N0",
                  "Monocyte-Day0", "Bcell-naïve","NKcell-control")
cellTypeNames = c("Neutrophil","Tcell", "Monocyte","Bcell", "NKcell")
irisTag = tagData(IRIS[,cellTypes2use],
                  cutoff = 2,
                  max = 50,
                  ref = ref_data,
                  ref.mean = F)
colnames(irisTag)= cellTypeNames

SPVs=getAllSPVs(data = ref_data,
                grp = labelData$subgrp2,
                dataTag = irisTag,
                method =  "mixed" ,
                plot = TRUE)
```
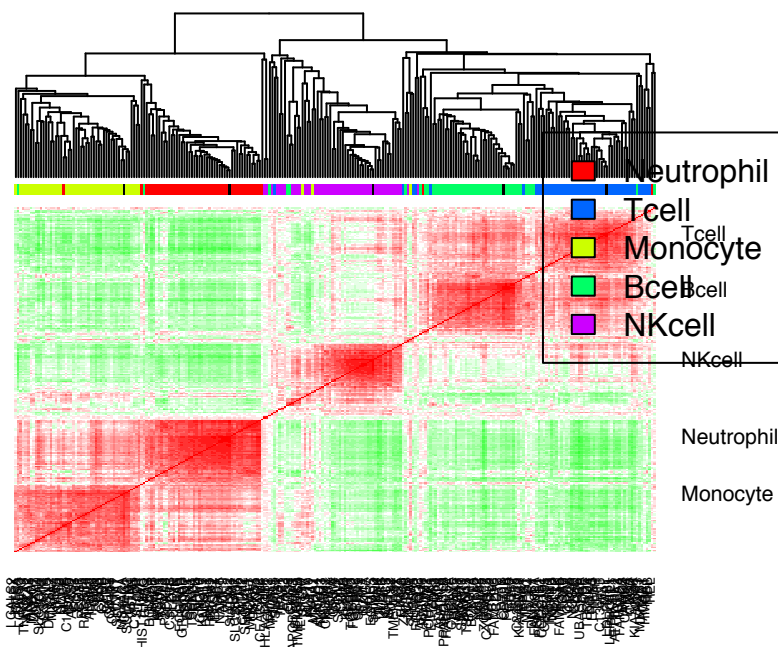

Test SPVs for group-difference

```r
SPVs = data.frame(SPVs)
labelData$Neutrophil = SPVs$Neutrophil
labelData$Tcell = SPVs$Tcell
labelData$Monocyte = SPVs$Monocyte
labelData$Bcell = SPVs$Bcell
labelData$NKcell = SPVs$NKcell
```

```r
cols2use = c("Fstat","pval")
aov_res = data.frame(matrix(nrow = length(cellTypeNames),
                            ncol = length(cols2use)))
rownames(aov_res) = cellTypeNames
colnames(aov_res) = cols2use

for (i in 1:length(cellTypeNames)){
  form2use = as.formula(sprintf("%s ~ subgrp2",cellTypeNames[i]))
  mod2use = lm(formula = form2use, data = labelData)
  res = anova(mod2use)
  aov_res[cellTypeNames[i],"Fstat"] = res["subgrp2","F value"]
  aov_res[cellTypeNames[i],"pval"] = res["subgrp2","Pr(>F)"]
}
aov_res
```

```
##               Fstat      pval
## Neutrophil 1.2569308 0.2884049
## Tcell      0.8111317 0.4468806
## Monocyte   1.9553526 0.1461911
## Bcell      1.3541728 0.2622459
## NKcell     1.0345787 0.3586596
```

Differential Expression Analyses

Differential expression analysis on gene expression data.

Setup and read in data

```r
# load libraries
library(easypackages)
libraries("limma","qvalue","here")
options(stringsAsFactors = FALSE)

# create directory to save results in
dir.create(here("DEresults"))

# Read in data
load(here("data","processed","exprDataAdj.Rdata"))
```

DE analysis ASD subtypes vs TD

```r
fdr_thresh = 0.05

# construct model
full_model = model.matrix(~0+as.factor(subgrp2), data=labelData)
colnames(full_model) <- c("Good","Poor", "TD")

# make contrast matrix
contrast.matrix <- makeContrasts(TD-Poor,TD-Good,Good-Poor,
                                 levels=full_model)

# fit DE limma model
fit = lmFit(exprDataAdj,full_model)

# fit contrasts
fitContrasts = contrasts.fit(fit,contrast.matrix)

# use empirical bayes
eb = eBayes(fitContrasts)
pvals_pairwise_comps = eb$p.value

# get table of DE results
DEresults = topTable(eb, number = dim(geneInfo)[1], adjust.method = "fdr")
pvals_pairwise_comps = pvals_pairwise_comps[rownames(DEresults),]
geneInfo2 = geneInfo[rownames(DEresults),]
DEresults = cbind(GeneSymbols = geneInfo2$geneSymbol, DEresults, pvals_pairwise_comps)
colnames(DEresults)[2:4] = c("TD_vs_ASDPoor.tstat",
                             "TD_vs_ASDGood.tstat",
                             "ASDGood_vs_ASDPoor.tstat")
colnames(DEresults)[9:11] = c("TD_vs_ASDPoor.pval",
```

```r
                              "TD_vs_ASDGood.pval",
                              "ASDGood_vs_ASDPoor.pval")

# compute FDR on pairwise group comparisons
DEresults$TD_vs_ASDPoor.fdr = p.adjust(DEresults$TD_vs_ASDPoor.pval,
                                       method = "fdr")
DEresults$TD_vs_ASDGood.fdr = p.adjust(DEresults$TD_vs_ASDGood.pval,
                                       method = "fdr")
DEresults$ASDGood_vs_ASDPoor.fdr = p.adjust(DEresults$ASDGood_vs_ASDPoor.pval,
                                            method = "fdr")

# save results to csv file
write.csv(DEresults, file = here("DEresults","DEresults_gene.csv"))

# show top 20 genes
knitr::kable(head(DEresults[,c("GeneSymbols","F","P.Value","adj.P.Val")],20), digits = 4)
```

	GeneSymbols	F	P.Value	adj.P.Val
ILMN_1805636	PGAP3	12.4505	0e+00	0.0968
ILMN_1673275	TRAPPC2	12.3410	0e+00	0.0968
ILMN_1740903	C7orf49	11.3902	0e+00	0.1222
ILMN_2073012	TMEM203	11.1560	0e+00	0.1222
ILMN_1661888	MEF2A	10.9644	0e+00	0.1222
ILMN_1765332	TIMM10	10.7507	1e-04	0.1222
ILMN_1668752	FLJ20850	10.4846	1e-04	0.1224
ILMN_1748529	RLN2	10.2888	1e-04	0.1224
ILMN_1769783	ZDHHC2	10.2710	1e-04	0.1224
ILMN_1764380	GLTP	9.7212	1e-04	0.1764
ILMN_1761058	ACAD11	9.4124	2e-04	0.1848
ILMN_1775743	BTG1	9.3052	2e-04	0.1848
ILMN_1738229	NDRG3	9.2666	2e-04	0.1848
ILMN_2154566	RPL10A	9.1465	2e-04	0.1848
ILMN_1689189	ZBTB3	9.0809	2e-04	0.1848
ILMN_1701914	CD274	9.0166	2e-04	0.1848
ILMN_1706645	C6orf150	8.9635	2e-04	0.1848
ILMN_1656682	AZIN1	8.9334	2e-04	0.1848
ILMN_2047599	TMEM50B	8.9133	2e-04	0.1848
ILMN_1812250	LOC644642	8.8201	3e-04	0.1848

WGCNA Analyses

Run WGCNA

Setup and read in data

```r
# Libraries
library(easypackages)
libraries("WGCNA","gplots","here","ggplot2")
```

```
## =============================================================================
## *
## *  Package WGCNA 1.63 loaded.
## *
## *    Important note: It appears that your system supports multi-threading,
## *    but it is not enabled within WGCNA in R.
## *    To allow multi-threading within WGCNA with all available cores, use
## *
## *            allowWGCNAThreads()
## *
## *    within R. Use disableWGCNAThreads() to disable threading if necessary.
## *    Alternatively, set the following environment variable on your system:
## *
## *            ALLOW_WGCNA_THREADS=<number_of_processors>
## *
## *    for example
## *
## *            ALLOW_WGCNA_THREADS=24
## *
## *    To set the environment variable in linux bash shell, type
## *
## *             export ALLOW_WGCNA_THREADS=24
## *
## *     before running R. Other operating systems or shells will
## *     have a similar command to achieve the same aim.
## *
## =============================================================================
```

```r
# Allow multi-threading within WGCNA
allowWGCNAThreads()
```

```
## Allowing multi-threading with up to 24 threads.
```

```r
options(stringsAsFactors = FALSE)

# WGCNA parameters
networkType = 'signed'
tomType = 'signed'
corrType = 'bicor'
maxBlockSize = 30000
minModSize = 100
modMergeCutHeight = 0.20
```

```
deepSplit = 4

resultpath = here("WGCNAresults")
dir.create(resultpath)

# Read in data
load(here("data","processed","exprDataAdj.Rdata"))

datExpr = t(exprDataAdj)
datTraits = as.data.frame(labelData[,c("subgrp2",
                                       "gex_age",
                                       "sex",
                                       "batch",
                                       "RIN")])
rownames(datTraits) = labelData$exprColNames
datTraits$sex = as.numeric(factor(datTraits$sex))
datTraits$subgrp2 = as.numeric(factor(datTraits$subgrp2))
datTraits$batch = as.numeric(factor(datTraits$batch))
```

Choose soft-threshold power

```
powers = c(1:30)
if (corrType=="pearson"){
  corFnc2use = "cor"
}else if (corrType=="bicor"){
  corFnc2use = corrType
}
sft = pickSoftThreshold(datExpr,
                        powerVector = powers,
                        verbose = 5,
                        networkType = networkType,
                        corFnc = corrType)
```

```
## pickSoftThreshold: will use block size 3125.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 3125 of 14313
##     ..working on genes 3126 through 6250 of 14313
##     ..working on genes 6251 through 9375 of 14313
##     ..working on genes 9376 through 12500 of 14313
##     ..working on genes 12501 through 14313 of 14313
##    Power SFT.R.sq  slope truncated.R.sq  mean.k. median.k. max.k.
## 1      1    0.066   8.57          0.958 7190.000  7.19e+03 7550.0
## 2      2    0.420 -12.20          0.833 3730.000  3.68e+03 4300.0
## 3      3    0.780 -10.90          0.935 1990.000  1.95e+03 2610.0
## 4      4    0.833  -7.76          0.972 1090.000  1.06e+03 1680.0
## 5      5    0.843  -5.94          0.984  617.000  5.88e+02 1120.0
## 6      6    0.839  -4.80          0.983  358.000  3.34e+02  771.0
## 7      7    0.834  -4.06          0.980  214.000  1.93e+02  547.0
## 8      8    0.836  -3.49          0.978  131.000  1.14e+02  397.0
## 9      9    0.822  -3.11          0.965   82.500  6.86e+01  294.0
## 10    10    0.831  -2.75          0.963   53.300  4.20e+01  221.0
## 11    11    0.856  -2.45          0.974   35.400  2.62e+01  169.0
```

```
## 12      12      0.876  -2.25              0.984     24.000  1.66e+01  132.0
## 13      13      0.874  -2.20              0.984     16.700  1.06e+01  109.0
## 14      14      0.875  -2.14              0.981     11.900  6.89e+00   90.5
## 15      15      0.876  -2.07              0.975      8.640  4.52e+00   75.9
## 16      16      0.900  -1.95              0.985      6.400  2.99e+00   64.1
## 17      17      0.917  -1.89              0.990      4.820  2.01e+00   55.8
## 18      18      0.865  -1.99              0.956      3.690  1.36e+00   51.7
## 19      19      0.876  -1.99              0.965      2.870  9.34e-01   48.1
## 20      20      0.876  -1.99              0.965      2.270  6.43e-01   44.9
## 21      21      0.889  -1.96              0.968      1.810  4.47e-01   41.9
## 22      22      0.902  -1.93              0.972      1.460  3.14e-01   39.2
## 23      23      0.910  -1.89              0.971      1.200  2.22e-01   36.7
## 24      24      0.918  -1.85              0.969      0.987  1.57e-01   34.5
## 25      25      0.927  -1.81              0.974      0.822  1.12e-01   32.4
## 26      26      0.927  -1.78              0.973      0.691  8.02e-02   30.4
## 27      27      0.932  -1.75              0.972      0.586  5.76e-02   28.6
## 28      28      0.935  -1.71              0.970      0.500  4.18e-02   27.0
## 29      29      0.939  -1.68              0.969      0.430  3.03e-02   25.4
## 30      30      0.942  -1.65              0.967      0.372  2.22e-02   23.9
```

```r
makeSoftPowerPlot <- function(sft, powers, cex1 = 0.9){
  # Scale-free topology fit index as a function of the soft-thresholding power
  par(mfrow = c(1,2))
  plot(sft$fitIndices[,1],
       -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
       xlab = "Soft Threshold (power)",
       ylab = "Scale Free Topology Model Fit,signed R^2",
       type = "n",
       main = paste("Scale independence"))
  text(sft$fitIndices[,1],
       -sign(sft$fitIndices[,3])*sft$fitIndices[,2],
       labels = powers,
       cex = cex1,
       col = "red")
  abline(h = 0.90, col = "red")
  ## Mean connectivity as a function of the soft-thresholding power
  plot(sft$fitIndices[,1],
       sft$fitIndices[,5],
       xlab="Soft Threshold (power)",
       ylab="Mean Connectivity",
       type="n",
       main = "Mean connectivity")
  text(sft$fitIndices[,1],
       sft$fitIndices[,5],
       labels=powers,
       cex=cex1,
       col="red")
}

makeSoftPowerPlot(sft = sft, powers = powers)
```
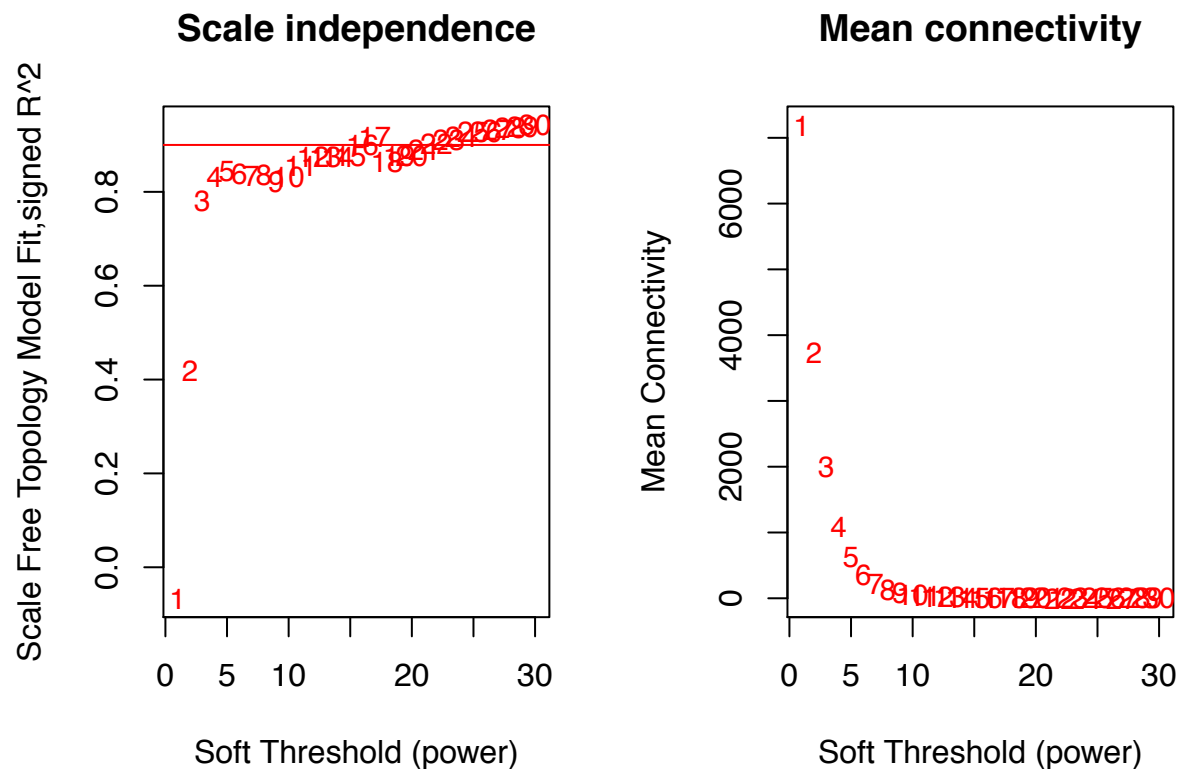
Run blockwiseModules

```
softPower = 16

## Run an automated network analysis
net3 = blockwiseModules(datExpr,
                        power = softPower,
                        deepSplit = deepSplit,
                        minModuleSize = minModSize,
                        mergeCutHeight = modMergeCutHeight,
                        detectCutHeight = 0.9999,
                        corType = corrType,
                        networkType = networkType,
                        pamStage = FALSE,
                        pamRespectsDendro = TRUE,
                        verbose = 3,
                        saveTOMs = FALSE,
                        maxBlockSize = maxBlockSize,
                        numericLabels = TRUE)
```

```
##  Calculating module eigengenes block-wise from all genes
##    Flagging genes and samples with too many missing values...
##     ..step 1
##  ..Working on block 1 .
##    TOM calculation: adjacency..
##    ..will use 24 parallel threads.
##     Fraction of slow calculations: 0.000000
##    ..connectivity..
```

```
##     ..matrix multiplication (system BLAS)..
##     ..normalization..
##     ..done.
##   ....clustering..
##   ....detecting modules..
##   ....calculating module eigengenes..
##   ....checking kME in modules..
##       ..removing 62 genes from module 1 because their KME is too low.
##       ..removing 226 genes from module 2 because their KME is too low.
##       ..removing 1 genes from module 3 because their KME is too low.
##       ..removing 49 genes from module 4 because their KME is too low.
##       ..removing 7 genes from module 5 because their KME is too low.
##       ..removing 46 genes from module 6 because their KME is too low.
##       ..removing 1 genes from module 7 because their KME is too low.
##       ..removing 27 genes from module 8 because their KME is too low.
##       ..removing 4 genes from module 9 because their KME is too low.
##       ..removing 15 genes from module 11 because their KME is too low.
##       ..removing 27 genes from module 13 because their KME is too low.
##       ..removing 10 genes from module 14 because their KME is too low.
##       ..removing 1 genes from module 18 because their KME is too low.
##   ..reassigning 42 genes from module 1 to modules with higher KME.
##   ..reassigning 2 genes from module 2 to modules with higher KME.
##   ..reassigning 18 genes from module 3 to modules with higher KME.
##   ..reassigning 9 genes from module 4 to modules with higher KME.
##   ..reassigning 13 genes from module 5 to modules with higher KME.
##   ..reassigning 3 genes from module 6 to modules with higher KME.
##   ..reassigning 3 genes from module 7 to modules with higher KME.
##   ..reassigning 9 genes from module 8 to modules with higher KME.
##   ..reassigning 8 genes from module 9 to modules with higher KME.
##   ..reassigning 8 genes from module 10 to modules with higher KME.
##   ..reassigning 7 genes from module 11 to modules with higher KME.
##   ..reassigning 1 genes from module 12 to modules with higher KME.
##   ..reassigning 2 genes from module 14 to modules with higher KME.
##   ..reassigning 2 genes from module 15 to modules with higher KME.
##   ..reassigning 5 genes from module 16 to modules with higher KME.
##   ..reassigning 3 genes from module 17 to modules with higher KME.
##   ..reassigning 1 genes from module 19 to modules with higher KME.
##   ..reassigning 4 genes from module 20 to modules with higher KME.
##   ..reassigning 3 genes from module 22 to modules with higher KME.
##   ..merging modules that are too close..
##       mergeCloseModules: Merging modules whose distance is less than 0.2
##         Calculating new MEs...
```

```r
net3$moduleNumbers = net3$colors
net3$colors = labels2colors(net3$moduleNumbers)

moduleLabels = net3$moduleNumbers
moduleColors = net3$colors
modNum_tab = data.frame(table(moduleLabels))
modCol_tab = data.frame(table(moduleColors))
modColNum_tab = cbind(moduleLabels = modNum_tab$moduleLabels,
                      modCol_tab[order(-modCol_tab$Freq),])
knitr::kable(modColNum_tab)
```

	moduleLabels	moduleColors	Freq
8	0	grey	7523
21	1	turquoise	1678
2	2	blue	590
3	3	brown	495
22	4	yellow	383
6	5	green	367
17	6	red	344
1	7	black	323
15	8	pink	292
13	9	magenta	264
16	10	purple	262
7	11	greenyellow	244
20	12	tan	241
19	13	salmon	231
4	14	cyan	159
14	15	midnightblue	147
9	16	grey60	140
10	17	lightcyan	140
11	18	lightgreen	128
12	19	lightyellow	126
18	20	royalblue	123
5	21	darkred	113

```r
rownames(net3$MEs) = labelData$subjectId
tmp_MEs = net3$MEs
# rename columns in net3$MEs
for (i in 1:dim(tmp_MEs)[2]){
  tmp_mnum = substr(colnames(tmp_MEs)[i], 3, nchar(colnames(tmp_MEs)[i]))
  if (nchar(tmp_mnum)==1){
    new_mnum = sprintf("M0%s",tmp_mnum)
  } else if (nchar(tmp_mnum)==2){
    new_mnum = sprintf("M%s",tmp_mnum)
  }
  colnames(tmp_MEs)[i] = new_mnum
}
net3$MEs_colreordered = tmp_MEs[,sort(colnames(tmp_MEs))]
nums2use = 0:(dim(tmp_MEs)[2]-1)
for (i in 1:length(nums2use)){
  colnames(net3$MEs_colreordered)[i] = sprintf("M%d",nums2use[i])
}
if (sum(colnames(net3$MEs_colreordered)=="M0")>0){
  net3$MEs_colreordered = net3$MEs_colreordered[,2:ncol(net3$MEs_colreordered)]
}

# order rows by subgrp2 and then subjectId
new_label_data = labelData
new_label_data2 = new_label_data[order(new_label_data$subgrp2,
                            order(new_label_data$subjectId)),]
net3$MEs_colreordered = net3$MEs_colreordered[new_label_data2$subjectId,]

# rename columns in net3$MEs
```

```
for (i in 1:dim(net3$MEs)[2]){
  tmp_mnum = substr(colnames(net3$MEs)[i], 3, nchar(colnames(net3$MEs)[i]))
  new_mnum = sprintf("M%s",tmp_mnum)
  colnames(net3$MEs)[i] = new_mnum
}
```

Make TOM plot

```
plotDendroAndColors(net3$dendrograms[[1]],
                    net3$colors, "Dynamic Tree Cut",
                    dendroLabels = FALSE,
                    hang = 0.03,
                    addGuide = TRUE,
                    guideHang = 0.05,
                    main = "Gene dendrogram and module colors")
```
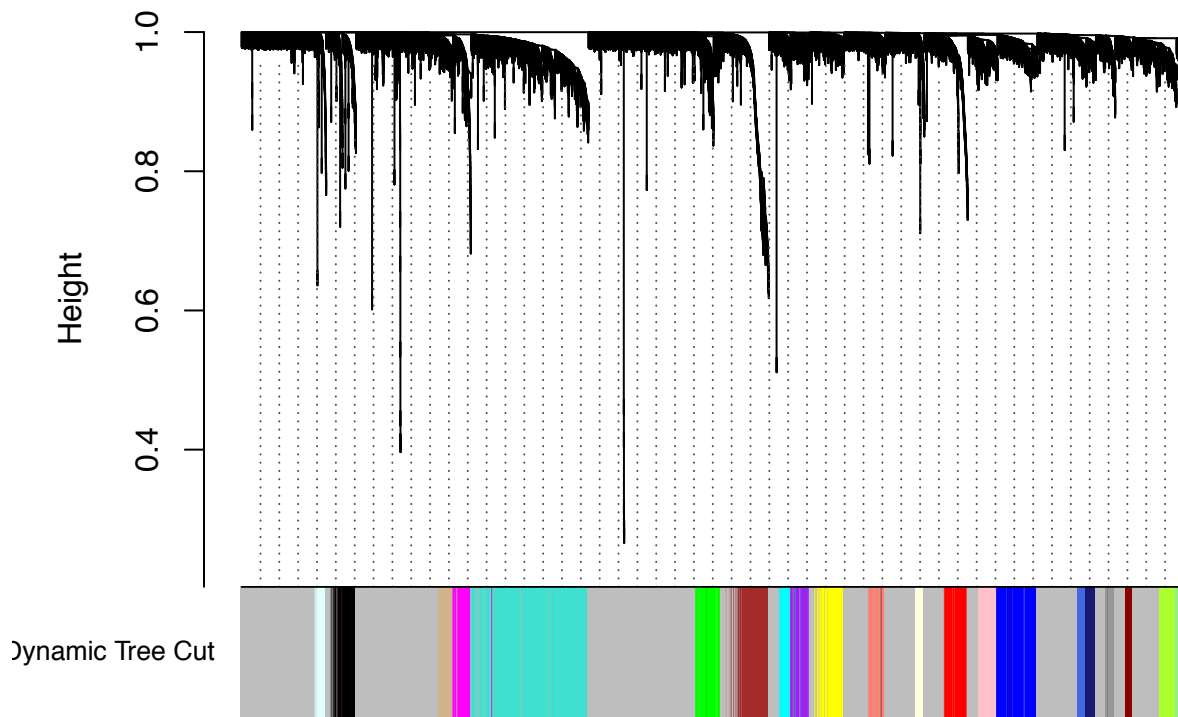

Make eigengene network plot

```
MEcorMat = data.frame(cor(net3$MEs))
MEcorMat = MEcorMat[!(names(MEcorMat) %in% "M0"),
                    !(names(MEcorMat) %in% "M0")]

heatmap.2(as.matrix(MEcorMat),
          col = blueWhiteRed(50),
          Rowv = TRUE,
```

```r
        trace = "none",
        cellnote= round(as.matrix(MEcorMat),digits = 2),
        notecol = "black",
        notecex=0.5,
        density.info = "none",
        key.xlab ="ME Correlation (r)")
```

Color Key

ME Correlation (r)

	M12	M9	M1	M2	M21	M11	M18	M4	M5	M19	M6	M8	M3	M7	M16	M13	M10	M14	M17	M20	M15	
	−0.46	−0.4	−0.56	0.34	0.76	0.5	0.76	−0.23	0.14	0.31	−0.02	0.04	0.18	−0.1	0.07	0.59	0.49	0.24	0.49	0.78	1	M15
	−0.58	−0.48	−0.52	0.03	0.41	0.51	0.58	0.09	0.28	0.22	−0.11	0.12	0.06	−0.15	0.06	0.04	0.74	0.38	0.6	1	0.78	M20
	−0.52	−0.56	−0.46	0.23	0.57	0.68	0.44	0	0.34	−0.04	−0.28	0.16	−0.01	−0.07	0.21	0.16	0.2	0.13	1	0.6	0.49	M17
	−0.09	−0.05	−0.18	−0.1	0.02	0.17	0.21	0.37	−0.22	0.08	−0.05	0.1	−0.24	0	−0.03	−0.09	0.46	1	0.13	0.38	0.24	M14
	−0.12	−0.14	0.08	−0.52	−0.07	−0.08	0.04	0.13	−0.09	−0.04	−0.36	−0.36	0.13	−0.09	0.07	−0.04	1	0.46	0.2	0.74	0.49	M10
	0.06	−0.15	−0.09	0.42	0.76	0.21	0.39	−0.58	−0.21	0.11	−0.16	−0.25	0.16	0.13	0.15	1	−0.04	−0.09	0.16	0.04	0.59	M13
	−0.07	−0.24	0.07	−0.08	0.1	0.04	−0.07	−0.06	−0.02	−0.15	−0.21	−0.18	−0.02	0.16	1	0.15	0.07	−0.03	0.21	0.06	0.07	M16
	0.21	−0.01	0.18	0.07	0.06	0.04	−0.16	−0.32	−0.38	−0.13	−0.28	−0.22	−0.22	1	0.16	0.13	−0.09	0	−0.07	−0.15	−0.1	M7
	−0.06	0	0.14	−0.26	0.02	−0.36	−0.12	−0.41	0.27	−0.14	−0.19	−0.46	1	−0.22	−0.02	0.16	0.13	−0.24	−0.01	0.06	0.18	M3
	−0.37	−0.05	−0.77	0.65	0.18	0.56	0.59	0.49	0.29	0.44	0.71	1	−0.46	−0.22	−0.18	−0.25	−0.36	0.1	0.16	0.12	0.04	M8
	−0.24	0.13	−0.47	0.51	−0.04	0.08	0.45	0.23	0.11	0.48	1	0.71	−0.19	−0.28	−0.21	−0.16	−0.36	−0.05	−0.28	−0.11	−0.02	M6
	−0.4	−0.2	−0.49	0.44	0.26	0.31	0.62	0.13	0.06	1	0.48	0.44	−0.14	−0.13	−0.15	0.11	−0.04	0.08	−0.04	0.22	0.31	M19
	−0.47	−0.35	−0.39	0.04	0.14	0.32	0.25	0.14	1	0.06	0.11	0.29	0.27	−0.38	−0.02	−0.21	−0.09	−0.22	0.34	0.28	0.14	M5
	−0.15	0.08	−0.22	−0.23	−0.37	0.06	−0.01	1	0.14	0.13	0.23	0.49	−0.41	−0.32	−0.06	−0.58	0.13	0.37	0	0.09	−0.23	M4
	−0.64	−0.44	−0.85	0.74	0.77	0.76	1	−0.01	0.25	0.62	0.45	0.59	−0.12	−0.16	−0.07	0.39	0.04	0.21	0.44	0.58	0.76	M18
	−0.64	−0.66	−0.71	0.66	0.74	1	0.76	0.06	0.32	0.31	0.08	0.56	−0.36	0.04	0.04	0.21	−0.08	0.17	0.68	0.51	0.5	M11
	−0.42	−0.49	−0.58	0.69	1	0.74	0.77	−0.37	0.14	0.26	−0.04	0.18	0.02	0.06	0.1	0.76	−0.07	0.02	0.57	0.41	0.76	M21
	−0.28	−0.19	−0.7	1	0.69	0.66	0.74	−0.23	0.04	0.44	0.51	0.65	−0.26	0.07	−0.08	0.42	−0.52	−0.1	0.23	0.03	0.34	M2
	0.51	0.21	1	−0.7	−0.58	−0.71	−0.85	−0.22	−0.39	−0.49	−0.47	−0.77	0.14	0.18	0.07	−0.09	0.08	−0.18	−0.46	−0.52	−0.56	M1
	0.73	1	0.21	−0.19	−0.49	−0.66	−0.44	0.08	−0.35	−0.2	0.13	−0.05	0	−0.01	−0.24	−0.15	−0.14	−0.05	−0.56	−0.48	−0.4	M9
	1	0.73	0.51	−0.28	−0.42	−0.64	−0.64	−0.15	−0.47	−0.4	−0.24	−0.37	−0.06	0.21	−0.07	0.06	−0.12	−0.09	−0.52	−0.58	−0.46	M12

Write out results files

```r
# write ME files
fname2write = here("WGCNAresults","module_eigengenes.csv")
write.csv(net3$MEs,file = fname2write)
write.table(net3$MEs_colreordered,
            file = here("WGCNAresults","data4pls.txt"),
            quote = FALSE,
            row.names = FALSE,
            sep="\t",
            col.names = FALSE)

# compute module membership and write out to file
kme_data = signedKME(datExpr = datExpr, datME = net3$MEs)
for (i in 1:dim(net3$MEs)[2]){
  colnames(kme_data)[i] = sprintf("kME.%s",colnames(net3$MEs)[i])
}
geneInfo2use = geneInfo[,c("PROBE_ID","geneSymbol")]

wgcna_res_data = cbind(geneInfo2use,
```

```
                        data.frame(moduleLabels, moduleColors),
                        kme_data)
write.csv(wgcna_res_data,
          file = here("WGCNAresults", "wgcna_results_summary.csv"),
          quote = FALSE,
          col.names = FALSE,
          row.names = FALSE)
```

Run DE analysis on module eigengenes

```
medata = net3$MEs
nmods = dim(medata)[2]
medata$group = factor(labelData$subgrp2)
medata$sex = factor(labelData$sex)
medata$age = labelData$age
medata$Dx = factor(labelData$Dx)
medata$batch = factor(labelData$batch)
medata$RIN = labelData$RIN
covs2use = "group"

res_colnames = c("Module",
                 "Group.Fstat",
                 "Group.pval",
                 "Group.fdr",
                 "TD_vs_ASDPoor.tstat",
                 "TD_vs_ASDPoor.pval",
                 "TD_vs_ASDPoor.fdr",
                 "TD_vs_ASDGood.tstat",
                 "TD_vs_ASDGood.pval",
                 "TD_vs_ASDGood.fdr",
                 "ASDGood_vs_ASDPoor.tstat",
                 "ASDGood_vs_ASDPoor.pval",
                 "ASDGood_vs_ASDPoor.fdr")
group_diff_res = data.frame(matrix(nrow = nmods-1,
                                   ncol = length(res_colnames)))
colnames(group_diff_res) = res_colnames

for (imod in 1:(nmods-1)){
  module2use = sprintf("M%d",imod)
  group_diff_res$Module[imod] = module2use

  # test for subgroup effect
  form2use = as.formula(sprintf("%s ~ %s",module2use,covs2use))
  mod2use = lm(formula = form2use, data = medata)
  res = anova(mod2use)
  group_diff_res$Group.Fstat[imod] = res["group","F value"]
  group_diff_res$Group.pval[imod] = res["group","Pr(>F)"]

  # test for TD vs ASD Poor effect
  mask = medata$group=="TD" | medata$group=="Poor"
  tmp_data = subset(medata, mask)
  form2use = as.formula(sprintf("%s ~ %s",module2use,covs2use))
```

```
    mod2use = t.test(formula = form2use, data = tmp_data)
    group_diff_res$TD_vs_ASDPoor.tstat[imod] = mod2use$statistic
    group_diff_res$TD_vs_ASDPoor.pval[imod] = mod2use$p.value

    # test for TD vs ASD Good effect
    mask = medata$group=="TD" | medata$group=="Good"
    tmp_data = subset(medata, mask)
    form2use = as.formula(sprintf("%s ~ %s",module2use,covs2use))
    mod2use = t.test(formula = form2use, data = tmp_data)
    group_diff_res$TD_vs_ASDGood.tstat[imod] = mod2use$statistic
    group_diff_res$TD_vs_ASDGood.pval[imod] = mod2use$p.value

    # test for ASD Good vs ASD Poor effect
    mask = medata$group=="Good" | medata$group=="Poor"
    tmp_data = subset(medata, mask)
    form2use = as.formula(sprintf("%s ~ %s",module2use,covs2use))
    mod2use = t.test(formula = form2use, data = tmp_data)
    group_diff_res$ASDGood_vs_ASDPoor.tstat[imod] = mod2use$statistic
    group_diff_res$ASDGood_vs_ASDPoor.pval[imod] = mod2use$p.value
}#for (imod in 1:(nmods-1)){
rownames(group_diff_res) = group_diff_res$Module

# compute FDR
group_diff_res$Group.fdr = p.adjust(group_diff_res$Group.pval,
                                    method = "fdr")
group_diff_res$TD_vs_ASDPoor.fdr = p.adjust(group_diff_res$TD_vs_ASDPoor.pval,
                                            method = "fdr")
group_diff_res$TD_vs_ASDGood.fdr = p.adjust(group_diff_res$TD_vs_ASDGood.pval,
                                            method = "fdr")
group_diff_res$ASDGood_vs_ASDPoor.fdr = p.adjust(group_diff_res$ASDGood_vs_ASDPoor.pval,
                                                method = "fdr")

group_diff_res
```

```
##      Module Group.Fstat Group.pval Group.fdr TD_vs_ASDPoor.tstat
## M1       M1  0.85466832 0.42810844 0.5993518          -1.3077840
## M2       M2  2.21274318 0.11403738 0.3204154           1.9583960
## M3       M3  3.48452314 0.03394472 0.1425678          -2.3282604
## M4       M4  0.99199585 0.37398634 0.5609795          -0.7802731
## M5       M5  0.15349680 0.85787894 0.9007729          -0.3953875
## M6       M6  1.23334291 0.29514108 0.5164969           1.0178269
## M7       M7  0.60950713 0.54536534 0.6673585           1.0717799
## M8       M8  0.56130056 0.57202155 0.6673585           0.8370422
## M9       M9  4.67901867 0.01112702 0.1366466          -1.9749269
## M10     M10  0.09927062 0.90557513 0.9055751           0.4028410
## M11     M11  4.50985599 0.01301396 0.1366466           2.5044641
## M12     M12  1.77808444 0.17357485 0.3645072          -1.5280577
## M13     M13  1.12424957 0.32844036 0.5305575           1.4686285
## M14     M14  0.45444935 0.63593248 0.7028727           0.6495977
## M15     M15  1.80609348 0.16892359 0.3645072           1.6993953
## M16     M16  0.63403431 0.53229143 0.6673585           1.0884492
## M17     M17  2.14668001 0.12153188 0.3204154           1.3515302
## M18     M18  3.67200087 0.02845258 0.1425678           2.4916716
## M19     M19  2.14215664 0.12206301 0.3204154           2.0033869
## M20     M20  1.26492125 0.28615870 0.5164969           1.5494964
```

```
## M21    M21  3.69217556 0.02791818 0.1425678          2.3337542
##     TD_vs_ASDPoor.pval TD_vs_ASDPoor.fdr TD_vs_ASDGood.tstat
## M1          0.19490314         0.3148435          -0.7133109
## M2          0.05391260         0.1617378           1.4702005
## M3          0.02257705         0.1185295          -2.3035095
## M4          0.43766928         0.5106142           0.5774464
## M5          0.69367516         0.6936752          -0.5418886
## M6          0.31201017         0.4095134          -0.3542066
## M7          0.28723281         0.4021259           0.5502798
## M8          0.40521200         0.5005560           0.9952571
## M9          0.05299963         0.1617378          -2.6683263
## M10         0.68823574         0.6936752           0.1001046
## M11         0.01459805         0.1185295           2.6205969
## M12         0.13148716         0.2761230          -1.5304563
## M13         0.14633954         0.2793755           1.0096012
## M14         0.51803237         0.5725621           1.0172965
## M15         0.09334369         0.2450272           0.7945324
## M16         0.27984237         0.4021259           0.3609575
## M17         0.18065763         0.3148435           2.0288055
## M18         0.01492681         0.1185295           1.9561098
## M19         0.04870371         0.1617378           1.7747514
## M20         0.12567776         0.2761230           0.9181648
## M21         0.02225434         0.1185295           2.3564695
##     TD_vs_ASDGood.pval TD_vs_ASDGood.fdr ASDGood_vs_ASDPoor.tstat
## M1          0.47787535         0.6690255              0.605344288
## M2          0.14594251         0.3405325             -0.631508970
## M3          0.02403018         0.1261584              0.007879917
## M4          0.56554160         0.6878272              1.394010742
## M5          0.58956615         0.6878272             -0.128465624
## M6          0.72440050         0.7606205             -1.587045747
## M7          0.58380490         0.6878272             -0.577615462
## M8          0.32287520         0.5650316              0.132805503
## M9          0.01005985         0.1115294             -0.914398070
## M10         0.92054642         0.9205464             -0.343384180
## M11         0.01062185         0.1115294              0.431908102
## M12         0.13071826         0.3405325             -0.042657185
## M13         0.31593678         0.5650316             -0.581530532
## M14         0.31247684         0.5650316              0.313983191
## M15         0.42985018         0.6447753             -1.208229109
## M16         0.71914725         0.7606205             -0.742428674
## M17         0.04632505         0.1905484              0.649485776
## M18         0.05444241         0.1905484             -0.743318261
## M19         0.08015987         0.2404796             -0.045094533
## M20         0.36158682         0.5841018             -0.670069422
## M21         0.02133914         0.1261584             -0.357707051
##     ASDGood_vs_ASDPoor.pval ASDGood_vs_ASDPoor.fdr
## M1                0.5466854              0.9890597
## M2                0.5295575              0.9890597
## M3                0.9937327              0.9937327
## M4                0.1677955              0.9890597
## M5                0.8981105              0.9937327
## M6                0.1171290              0.9890597
## M7                0.5651770              0.9890597
## M8                0.8946860              0.9937327
```

```
## M9                      0.3633331                  0.9890597
## M10                     0.7322268                  0.9900994
## M11                     0.6670684                  0.9900994
## M12                     0.9660831                  0.9937327
## M13                     0.5626257                  0.9890597
## M14                     0.7543615                  0.9900994
## M15                     0.2310813                  0.9890597
## M16                     0.4600424                  0.9890597
## M17                     0.5179341                  0.9890597
## M18                     0.4595420                  0.9890597
## M19                     0.9641492                  0.9937327
## M20                     0.5047740                  0.9890597
## M21                     0.7216176                  0.9900994
```

Run WGCNA on TD only

```r
# run on TD
grp2use = "TD"
datExpr_grp = datExpr[labelData$subgrp2==grp2use,]
datTraits_grp = datTraits[labelData$subgrp2==grp2use,]

# Choose a soft-threshold power
powers = c(1:30)
if (corrType=="pearson"){
  corFnc2use = "cor"
}else if (corrType=="bicor"){
  corFnc2use = corrType
}
sft = pickSoftThreshold(datExpr_grp,
                        powerVector = powers,
                        verbose = 5,
                        networkType = networkType,
                        corFnc = corrType)
```

```
## pickSoftThreshold: will use block size 3125.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 3125 of 14313
##     ..working on genes 3126 through 6250 of 14313
##     ..working on genes 6251 through 9375 of 14313
##     ..working on genes 9376 through 12500 of 14313
##     ..working on genes 12501 through 14313 of 14313
##     Power SFT.R.sq  slope truncated.R.sq  mean.k. median.k. max.k.
## 1      1    0.108   8.77          0.937 7190.000  7200.000 7580.0
## 2      2    0.479 -10.80          0.858 3800.000  3760.000 4440.0
## 3      3    0.696  -8.20          0.905 2100.000  2050.000 2800.0
## 4      4    0.779  -6.09          0.950 1210.000  1170.000 1860.0
## 5      5    0.800  -4.79          0.970  723.000   688.000 1290.0
## 6      6    0.819  -3.95          0.986  446.000   416.000  929.0
## 7      7    0.821  -3.50          0.986  284.000   257.000  687.0
## 8      8    0.828  -3.16          0.989  185.000   163.000  522.0
## 9      9    0.834  -2.91          0.990  124.000   105.000  404.0
## 10    10    0.836  -2.73          0.988   85.600    69.400  318.0
## 11    11    0.832  -2.60          0.987   60.100    46.500  253.0
```

```
## 12   12   0.832   -2.49      0.983   43.100   31.600   205.0
## 13   13   0.829   -2.40      0.980   31.500   21.900   167.0
## 14   14   0.820   -2.34      0.976   23.500   15.300   138.0
## 15   15   0.813   -2.28      0.973   17.700   10.800   115.0
## 16   16   0.808   -2.22      0.969   13.600    7.700    96.7
## 17   17   0.808   -2.14      0.965   10.600    5.560    81.8
## 18   18   0.815   -2.05      0.961    8.320    4.040    69.6
## 19   19   0.865   -1.90      0.978    6.630    2.960    59.6
## 20   20   0.894   -1.84      0.991    5.340    2.180    52.7
## 21   21   0.884   -1.90      0.990    4.340    1.620    49.3
## 22   22   0.895   -1.91      0.996    3.560    1.220    46.3
## 23   23   0.907   -1.91      0.998    2.950    0.916    43.6
## 24   24   0.919   -1.91      0.999    2.460    0.696    41.1
## 25   25   0.927   -1.90      0.998    2.070    0.530    38.8
## 26   26   0.933   -1.89      0.997    1.750    0.406    36.7
## 27   27   0.942   -1.86      0.996    1.490    0.313    34.7
## 28   28   0.947   -1.84      0.995    1.280    0.241    32.9
## 29   29   0.955   -1.82      0.997    1.100    0.189    31.2
## 30   30   0.960   -1.80      0.996    0.958    0.147    29.6
```

```r
makeSoftPowerPlot(sft = sft, powers = powers)
```



```r
softPower = 16
```

```r
## Run an automated network analysis
net_tmp = blockwiseModules(datExpr,
                           power = softPower,
                           deepSplit = deepSplit,
                           minModuleSize = minModSize,
                           mergeCutHeight = modMergeCutHeight,
```

```
                              detectCutHeight = 0.9999,
                              corType = corrType,
                              networkType = networkType,
                              pamStage = FALSE,
                              pamRespectsDendro = TRUE,
                              verbose = 3,
                              saveTOMs = FALSE,
                              maxBlockSize = maxBlockSize,
                              numericLabels = TRUE)
```

```
##  Calculating module eigengenes block-wise from all genes
##    Flagging genes and samples with too many missing values...
##      ..step 1
##  ..Working on block 1 .
##     TOM calculation: adjacency..
##     ..will use 24 parallel threads.
##      Fraction of slow calculations: 0.000000
##     ..connectivity..
##     ..matrix multiplication (system BLAS)..
##     ..normalization..
##     ..done.
##  ....clustering..
##  ....detecting modules..
##  ....calculating module eigengenes..
##  ....checking kME in modules..
##      ..removing 62 genes from module 1 because their KME is too low.
##      ..removing 226 genes from module 2 because their KME is too low.
##      ..removing 1 genes from module 3 because their KME is too low.
##      ..removing 49 genes from module 4 because their KME is too low.
##      ..removing 7 genes from module 5 because their KME is too low.
##      ..removing 46 genes from module 6 because their KME is too low.
##      ..removing 1 genes from module 7 because their KME is too low.
##      ..removing 27 genes from module 8 because their KME is too low.
##      ..removing 4 genes from module 9 because their KME is too low.
##      ..removing 15 genes from module 11 because their KME is too low.
##      ..removing 27 genes from module 13 because their KME is too low.
##      ..removing 10 genes from module 14 because their KME is too low.
##      ..removing 1 genes from module 18 because their KME is too low.
##    ..reassigning 42 genes from module 1 to modules with higher KME.
##    ..reassigning 2 genes from module 2 to modules with higher KME.
##    ..reassigning 18 genes from module 3 to modules with higher KME.
##    ..reassigning 9 genes from module 4 to modules with higher KME.
##    ..reassigning 13 genes from module 5 to modules with higher KME.
##    ..reassigning 3 genes from module 6 to modules with higher KME.
##    ..reassigning 3 genes from module 7 to modules with higher KME.
##    ..reassigning 9 genes from module 8 to modules with higher KME.
##    ..reassigning 8 genes from module 9 to modules with higher KME.
##    ..reassigning 8 genes from module 10 to modules with higher KME.
##    ..reassigning 7 genes from module 11 to modules with higher KME.
##    ..reassigning 1 genes from module 12 to modules with higher KME.
##    ..reassigning 2 genes from module 14 to modules with higher KME.
##    ..reassigning 2 genes from module 15 to modules with higher KME.
##    ..reassigning 5 genes from module 16 to modules with higher KME.
##    ..reassigning 3 genes from module 17 to modules with higher KME.
```

```
##    ..reassigning 1 genes from module 19 to modules with higher KME.
##    ..reassigning 4 genes from module 20 to modules with higher KME.
##    ..reassigning 3 genes from module 22 to modules with higher KME.
##   ..merging modules that are too close..
##      mergeCloseModules: Merging modules whose distance is less than 0.2
##        Calculating new MEs...
```

```r
td_colors = labels2colors(net_tmp$colors)
datExpr_td = datExpr_grp
```

Run WGCNA on ASD Good only

```r
# run on ASD Good
grp2use = "Good"
datExpr_grp = datExpr[labelData$subgrp2==grp2use,]
datTraits_grp = datTraits[labelData$subgrp2==grp2use,]

# Choose a soft-threshold power
powers = c(1:30)
if (corrType=="pearson"){
  corFnc2use = "cor"
}else if (corrType=="bicor"){
  corFnc2use = corrType
}
sft = pickSoftThreshold(datExpr_grp,
                        powerVector = powers,
                        verbose = 5,
                        networkType = networkType,
                        corFnc = corrType)
```

```
## pickSoftThreshold: will use block size 3125.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 3125 of 14313
##     ..working on genes 3126 through 6250 of 14313
##     ..working on genes 6251 through 9375 of 14313
##     ..working on genes 9376 through 12500 of 14313
##     ..working on genes 12501 through 14313 of 14313
##    Power SFT.R.sq  slope truncated.R.sq  mean.k. median.k. max.k.
## 1      1   0.0473   7.65          0.929 7180.000  7.18e+03 7490.0
## 2      2   0.5400 -15.70          0.823 3780.000  3.73e+03 4380.0
## 3      3   0.7300 -10.50          0.905 2080.000  2.03e+03 2780.0
## 4      4   0.7880  -7.49          0.937 1190.000  1.14e+03 1880.0
## 5      5   0.8090  -5.81          0.950  704.000  6.59e+02 1320.0
## 6      6   0.8170  -4.68          0.957  430.000  3.92e+02  965.0
## 7      7   0.8190  -4.03          0.958  271.000  2.39e+02  726.0
## 8      8   0.7980  -3.68          0.948  176.000  1.48e+02  559.0
## 9      9   0.7960  -3.37          0.947  117.000  9.42e+01  439.0
## 10    10   0.7910  -3.15          0.944   79.500  6.07e+01  350.0
## 11    11   0.7840  -2.98          0.945   55.300  3.99e+01  282.0
## 12    12   0.7890  -2.79          0.945   39.300  2.66e+01  231.0
## 13    13   0.7950  -2.63          0.946   28.500  1.80e+01  190.0
## 14    14   0.8160  -2.47          0.953   21.000  1.23e+01  158.0
## 15    15   0.8320  -2.35          0.961   15.700  8.52e+00  133.0
```

```
## 16   16   0.8520   -2.23          0.972   11.900   5.98e+00   112.0
## 17   17   0.8610   -2.15          0.977    9.200   4.22e+00    95.1
## 18   18   0.8750   -2.06          0.981    7.170   3.02e+00    81.3
## 19   19   0.8830   -2.02          0.984    5.660   2.16e+00    71.0
## 20   20   0.8850   -1.99          0.988    4.520   1.57e+00    62.6
## 21   21   0.8890   -1.96          0.990    3.640   1.14e+00    55.4
## 22   22   0.8900   -1.93          0.990    2.960   8.38e-01    49.2
## 23   23   0.8880   -1.91          0.989    2.420   6.23e-01    43.8
## 24   24   0.8870   -1.89          0.988    2.000   4.66e-01    39.1
## 25   25   0.8820   -1.88          0.985    1.670   3.49e-01    35.0
## 26   26   0.8870   -1.85          0.986    1.390   2.64e-01    31.4
## 27   27   0.9000   -1.80          0.988    1.180   2.00e-01    28.3
## 28   28   0.9030   -1.78          0.987    0.997   1.52e-01    25.5
## 29   29   0.9130   -1.74          0.989    0.850   1.16e-01    23.1
## 30   30   0.9070   -1.75          0.989    0.729   8.92e-02    21.8
```

```
makeSoftPowerPlot(sft = sft, powers = powers)
```



```
softPower = 16
```

```
## Run an automated network analysis
net_tmp = blockwiseModules(datExpr,
                           power = softPower,
                           deepSplit = deepSplit,
                           minModuleSize = minModSize,
                           mergeCutHeight = modMergeCutHeight,
                           detectCutHeight = 0.9999,
                           corType = corrType,
                           networkType = networkType,
                           pamStage = FALSE,
```

```
                        pamRespectsDendro = TRUE,
                        verbose = 3,
                        saveTOMs = FALSE,
                        maxBlockSize = maxBlockSize,
                        numericLabels = TRUE)
```

```
##  Calculating module eigengenes block-wise from all genes
##    Flagging genes and samples with too many missing values...
##      ..step 1
##  ..Working on block 1 .
##      TOM calculation: adjacency..
##      ..will use 24 parallel threads.
##       Fraction of slow calculations: 0.000000
##      ..connectivity..
##      ..matrix multiplication (system BLAS)..
##      ..normalization..
##      ..done.
##  ....clustering..
##  ....detecting modules..
##  ....calculating module eigengenes..
##  ....checking kME in modules..
##      ..removing 62 genes from module 1 because their KME is too low.
##      ..removing 226 genes from module 2 because their KME is too low.
##      ..removing 1 genes from module 3 because their KME is too low.
##      ..removing 49 genes from module 4 because their KME is too low.
##      ..removing 7 genes from module 5 because their KME is too low.
##      ..removing 46 genes from module 6 because their KME is too low.
##      ..removing 1 genes from module 7 because their KME is too low.
##      ..removing 27 genes from module 8 because their KME is too low.
##      ..removing 4 genes from module 9 because their KME is too low.
##      ..removing 15 genes from module 11 because their KME is too low.
##      ..removing 27 genes from module 13 because their KME is too low.
##      ..removing 10 genes from module 14 because their KME is too low.
##      ..removing 1 genes from module 18 because their KME is too low.
##  ..reassigning 42 genes from module 1 to modules with higher KME.
##  ..reassigning 2 genes from module 2 to modules with higher KME.
##  ..reassigning 18 genes from module 3 to modules with higher KME.
##  ..reassigning 9 genes from module 4 to modules with higher KME.
##  ..reassigning 13 genes from module 5 to modules with higher KME.
##  ..reassigning 3 genes from module 6 to modules with higher KME.
##  ..reassigning 3 genes from module 7 to modules with higher KME.
##  ..reassigning 9 genes from module 8 to modules with higher KME.
##  ..reassigning 8 genes from module 9 to modules with higher KME.
##  ..reassigning 8 genes from module 10 to modules with higher KME.
##  ..reassigning 7 genes from module 11 to modules with higher KME.
##  ..reassigning 1 genes from module 12 to modules with higher KME.
##  ..reassigning 2 genes from module 14 to modules with higher KME.
##  ..reassigning 2 genes from module 15 to modules with higher KME.
##  ..reassigning 5 genes from module 16 to modules with higher KME.
##  ..reassigning 3 genes from module 17 to modules with higher KME.
##  ..reassigning 1 genes from module 19 to modules with higher KME.
##  ..reassigning 4 genes from module 20 to modules with higher KME.
##  ..reassigning 3 genes from module 22 to modules with higher KME.
##  ..merging modules that are too close..
```

```
##       mergeCloseModules: Merging modules whose distance is less than 0.2
##          Calculating new MEs...
```

```r
asdgood_colors = labels2colors(net_tmp$colors)
datExpr_asdgood = datExpr_grp
```

Run WGCNA on ASD Poor only

```r
# run on ASD Poor
grp2use = "Poor"
datExpr_grp = datExpr[labelData$subgrp2==grp2use,]
datTraits_grp = datTraits[labelData$subgrp2==grp2use,]

# Choose a soft-threshold power
powers = c(1:30)
if (corrType=="pearson"){
  corFnc2use = "cor"
}else if (corrType=="bicor"){
  corFnc2use = corrType
}
sft = pickSoftThreshold(datExpr_grp,
                        powerVector = powers,
                        verbose = 5,
                        networkType = networkType,
                        corFnc = corrType)
```

```
## pickSoftThreshold: will use block size 3125.
##  pickSoftThreshold: calculating connectivity for given powers...
##     ..working on genes 1 through 3125 of 14313
##     ..working on genes 3126 through 6250 of 14313
##     ..working on genes 6251 through 9375 of 14313
##     ..working on genes 9376 through 12500 of 14313
##     ..working on genes 12501 through 14313 of 14313
##     Power SFT.R.sq  slope truncated.R.sq  mean.k. median.k.  max.k.
## 1      1   0.0746   9.00          0.957 7190.000  7.19e+03  7560.0
## 2      2   0.3890 -13.00          0.902 3770.000  3.74e+03  4330.0
## 3      3   0.5440 -10.00          0.900 2050.000  2.02e+03  2650.0
## 4      4   0.6890  -8.20          0.952 1160.000  1.13e+03  1690.0
## 5      5   0.7600  -6.84          0.977  674.000  6.51e+02  1130.0
## 6      6   0.7670  -5.52          0.985  404.000  3.85e+02   776.0
## 7      7   0.7740  -4.63          0.987  249.000  2.34e+02   548.0
## 8      8   0.7800  -4.04          0.986  158.000  1.45e+02   396.0
## 9      9   0.7900  -3.57          0.983  102.000  9.15e+01   292.0
## 10    10   0.8010  -3.19          0.982   67.800  5.88e+01   219.0
## 11    11   0.8350  -2.81          0.988   46.000  3.84e+01   167.0
## 12    12   0.8130  -2.89          0.970   31.800  2.56e+01   137.0
## 13    13   0.7860  -2.96          0.953   22.400  1.72e+01   114.0
## 14    14   0.8050  -2.85          0.964   16.100  1.17e+01    95.7
## 15    15   0.7950  -2.83          0.963   11.800  8.08e+00    81.0
## 16    16   0.8070  -2.73          0.966    8.760  5.64e+00    69.1
## 17    17   0.8150  -2.62          0.963    6.600  3.98e+00    59.3
## 18    18   0.8210  -2.51          0.956    5.050  2.83e+00    51.2
## 19    19   0.8250  -2.39          0.945    3.910  2.03e+00    44.4
```

```
## 20    20    0.9010    -2.16        0.975    3.070    1.46e+00    38.7
## 21    21    0.9340    -2.03        0.986    2.440    1.07e+00    33.9
## 22    22    0.9440    -1.97        0.987    1.960    7.85e-01    30.7
## 23    23    0.9490    -1.95        0.988    1.590    5.82e-01    28.6
## 24    24    0.9510    -1.92        0.987    1.300    4.33e-01    26.7
## 25    25    0.9570    -1.88        0.990    1.070    3.25e-01    24.9
## 26    26    0.9560    -1.86        0.988    0.893    2.45e-01    23.3
## 27    27    0.9630    -1.83        0.991    0.750    1.85e-01    21.8
## 28    28    0.9640    -1.80        0.990    0.634    1.41e-01    20.4
## 29    29    0.9630    -1.77        0.987    0.540    1.08e-01    19.1
## 30    30    0.9640    -1.74        0.986    0.463    8.28e-02    18.0
```

```r
makeSoftPowerPlot(sft = sft, powers = powers)
```



```r
softPower = 16
```

```r
## Run an automated network analysis
net_tmp = blockwiseModules(datExpr,
                           power = softPower,
                           deepSplit = deepSplit,
                           minModuleSize = minModSize,
                           mergeCutHeight = modMergeCutHeight,
                           detectCutHeight = 0.9999,
                           corType = corrType,
                           networkType = networkType,
                           pamStage = FALSE,
                           pamRespectsDendro = TRUE,
                           verbose = 3,
                           saveTOMs = FALSE,
                           maxBlockSize = maxBlockSize,
```

```
                                numericLabels = TRUE)
```

```
## Calculating module eigengenes block-wise from all genes
##     Flagging genes and samples with too many missing values...
##       ..step 1
##  ..Working on block 1 .
##     TOM calculation: adjacency..
##     ..will use 24 parallel threads.
##      Fraction of slow calculations: 0.000000
##     ..connectivity..
##     ..matrix multiplication (system BLAS)..
##     ..normalization..
##     ..done.
##  ....clustering..
##  ....detecting modules..
##  ....calculating module eigengenes..
##  ....checking kME in modules..
##       ..removing 62 genes from module 1 because their KME is too low.
##       ..removing 226 genes from module 2 because their KME is too low.
##       ..removing 1 genes from module 3 because their KME is too low.
##       ..removing 49 genes from module 4 because their KME is too low.
##       ..removing 7 genes from module 5 because their KME is too low.
##       ..removing 46 genes from module 6 because their KME is too low.
##       ..removing 1 genes from module 7 because their KME is too low.
##       ..removing 27 genes from module 8 because their KME is too low.
##       ..removing 4 genes from module 9 because their KME is too low.
##       ..removing 15 genes from module 11 because their KME is too low.
##       ..removing 27 genes from module 13 because their KME is too low.
##       ..removing 10 genes from module 14 because their KME is too low.
##       ..removing 1 genes from module 18 because their KME is too low.
##   ..reassigning 42 genes from module 1 to modules with higher KME.
##   ..reassigning 2 genes from module 2 to modules with higher KME.
##   ..reassigning 18 genes from module 3 to modules with higher KME.
##   ..reassigning 9 genes from module 4 to modules with higher KME.
##   ..reassigning 13 genes from module 5 to modules with higher KME.
##   ..reassigning 3 genes from module 6 to modules with higher KME.
##   ..reassigning 3 genes from module 7 to modules with higher KME.
##   ..reassigning 9 genes from module 8 to modules with higher KME.
##   ..reassigning 8 genes from module 9 to modules with higher KME.
##   ..reassigning 8 genes from module 10 to modules with higher KME.
##   ..reassigning 7 genes from module 11 to modules with higher KME.
##   ..reassigning 1 genes from module 12 to modules with higher KME.
##   ..reassigning 2 genes from module 14 to modules with higher KME.
##   ..reassigning 2 genes from module 15 to modules with higher KME.
##   ..reassigning 5 genes from module 16 to modules with higher KME.
##   ..reassigning 3 genes from module 17 to modules with higher KME.
##   ..reassigning 1 genes from module 19 to modules with higher KME.
##   ..reassigning 4 genes from module 20 to modules with higher KME.
##   ..reassigning 3 genes from module 22 to modules with higher KME.
##   ..merging modules that are too close..
##       mergeCloseModules: Merging modules whose distance is less than 0.2
##         Calculating new MEs...
```

```
asdpoor_colors = labels2colors(net_tmp$colors)
datExpr_asdpoor = datExpr_grp
```

Function for reporting module preservation results

```
modulePreservationReport <- function(mp){
  ref = 1
  test = 2

  modColors = rownames(mp$preservation$observed[[ref]][[test]])
  moduleSizes = mp$preservation$Z[[ref]][[test]][, 1]
  plotMods = !(modColors %in% c("grey", "gold"))
  text = modColors[plotMods]
  plotData = cbind(mp$preservation$observed[[ref]][[test]][, 2],
                   mp$preservation$Z[[ref]][[test]][, 2])
  mains = c("Preservation Median rank", "Preservation Zsummary")

  # Start the plot
  par(mfrow = c(1,2))
  par(mar = c(4.5,4.5,2.5,1))
  for (p in 1:2){
    min = min(plotData[, p], na.rm = TRUE)
    max = max(plotData[, p], na.rm = TRUE)
    # Adjust ploting ranges appropriately
    if (p==2){
      if (min > -max/10) min = -max/10
      ylim = c(min - 0.1 * (max-min), max + 0.1 * (max-min))
    } else
      ylim = c(max + 0.1 * (max-min), min - 0.1 * (max-min))
    plot(moduleSizes[plotMods],
         plotData[plotMods, p],
         col = 1,
         bg = modColors[plotMods],
         pch = 21,
         main = mains[p],
         cex = 2.4,
         ylab = mains[p],
         xlab = "Module size",
         log = "x",
         ylim = ylim,
         xlim = c(10, 2000),
         cex.lab = 1.2,
         cex.axis = 1.2,
         cex.main =1.4)
    #labelPoints(moduleSizes[plotMods],
    #            plotData[plotMods, p],
    #            text,
    #            cex = 1,
    #            offs = 0.08);

    # For Zsummary, add threshold lines
    if (p==2) {
```

```
      abline(h=0)
      abline(h=2, col = "blue", lty = 2)
      abline(h=10, col = "darkgreen", lty = 2)
    } # if
  } # for

  statsObs = cbind(mp$quality$observed[[ref]][[test]][,-1],
                   mp$preservation$observed[[ref]][[test]][,-1])
  statsZ = cbind(mp$quality$Z[[ref]][[test]][,-1],
                 mp$preservation$Z[[ref]][[test]][,-1])

  sumTable = cbind(statsObs[, c("medianRank.pres", "medianRank.qual")],
              signif(statsZ[, c("Zsummary.pres", "Zsummary.qual")], 2))
  sumTable
} # function modulePreservationReport
```

TD - ASD Good module preservation results

```
nperm = 1000
rand_seed = 1

setLabels = c("TD","ASDGood")
multiExpr = list(TD = list(data = datExpr_td),
                 ASDGood = list(data = datExpr_asdgood))
multiColor = list(TD = td_colors)

mp_td_asdgood = modulePreservation(multiExpr,
                                   multiColor,
                                   networkType = networkType,
                                   corFnc = corFnc2use,
                                   referenceNetworks = 1,
                                   nPermutations = nperm,
                                   randomSeed = rand_seed,
                                   quickCor = 0,
                                   verbose = 0)

mp_res = modulePreservationReport(mp_td_asdgood)
```

Preservation Median rank   **Preservation Zsummary**
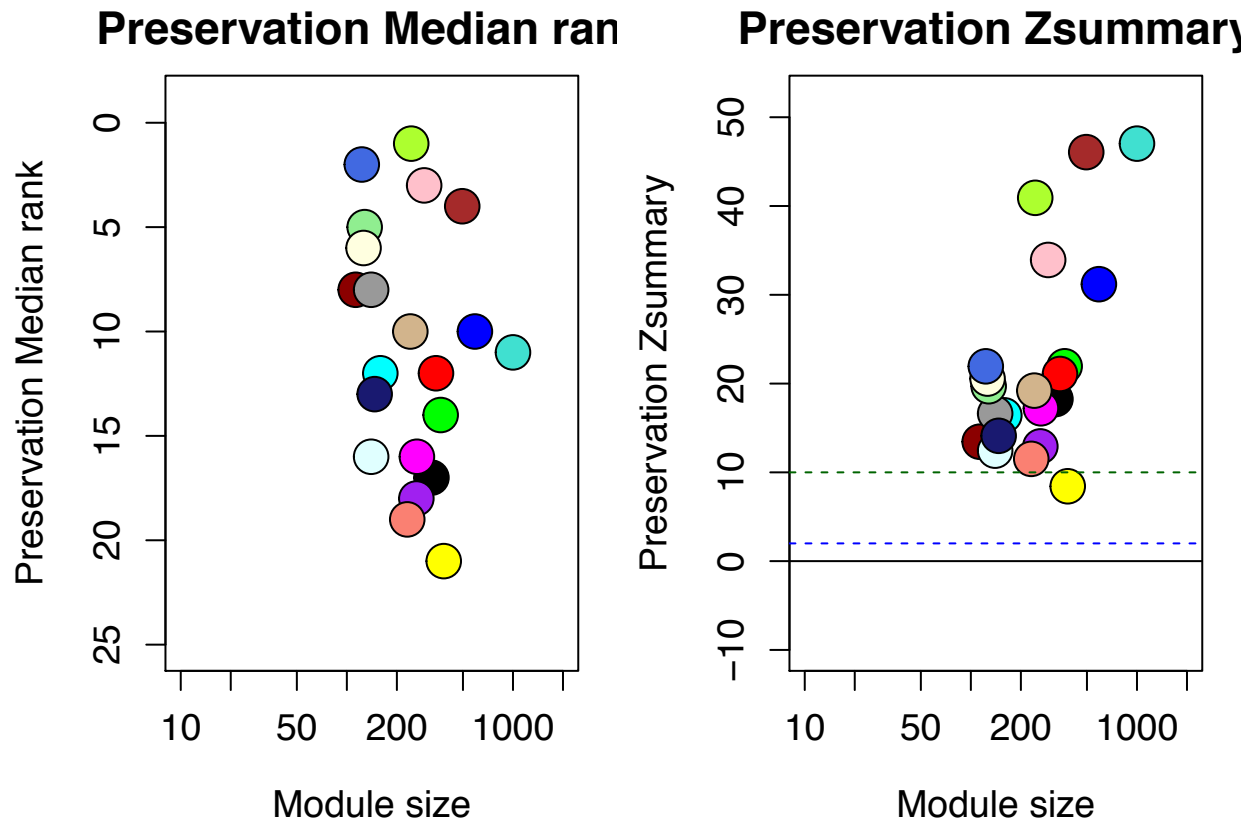
mp_res

```
##              medianRank.pres medianRank.qual Zsummary.pres Zsummary.qual
## black                     17            18.0          18.0         28.00
## blue                      10            11.0          31.0         68.00
## brown                      4            13.0          46.0         74.00
## cyan                      12            20.5          16.0          7.40
## darkred                    8             7.0          13.0         45.00
## gold                      22            22.0          22.0          0.34
## green                     14            13.5          22.0         41.00
## greenyellow                1             1.0          41.0         81.00
## grey                      23            23.0          11.0        -15.00
## grey60                     8             6.0          17.0         54.00
## lightcyan                 16            16.0          12.0         23.00
## lightgreen                 5             4.5          20.0         54.00
## lightyellow                6            12.5          21.0         27.00
## magenta                   16             5.5          17.0         76.00
## midnightblue              13             4.0          14.0         57.00
## pink                       3             8.5          34.0         70.00
## purple                    18            15.0          13.0         25.00
## red                       12            10.5          21.0         64.00
## royalblue                  2             2.5          22.0         55.00
## salmon                    19            20.5          12.0          8.90
## tan                       10             5.5          19.0         74.00
## turquoise                 11            16.5          47.0         56.00
## yellow                    21            19.0           8.4         23.00
```

TD - ASD Poor module preservation results

```
nperm = 1000
rand_seed = 1

setLabels = c("TD","ASDPoor");
multiExpr = list(TD = list(data = datExpr_td),
                 ASDPoor = list(data = datExpr_asdpoor))
multiColor = list(TD = td_colors)

# Calculate module preservation stats
mp_td_asdpoor = modulePreservation(multiExpr,
                                   multiColor,
                                   networkType = networkType,
                                   corFnc = corFnc2use,
                                   referenceNetworks = 1,
                                   nPermutations = nperm,
                                   randomSeed = rand_seed,
                                   quickCor = 0,
                                   verbose = 0)

mp_res = modulePreservationReport(mp_td_asdpoor)
```



```
mp_res
```
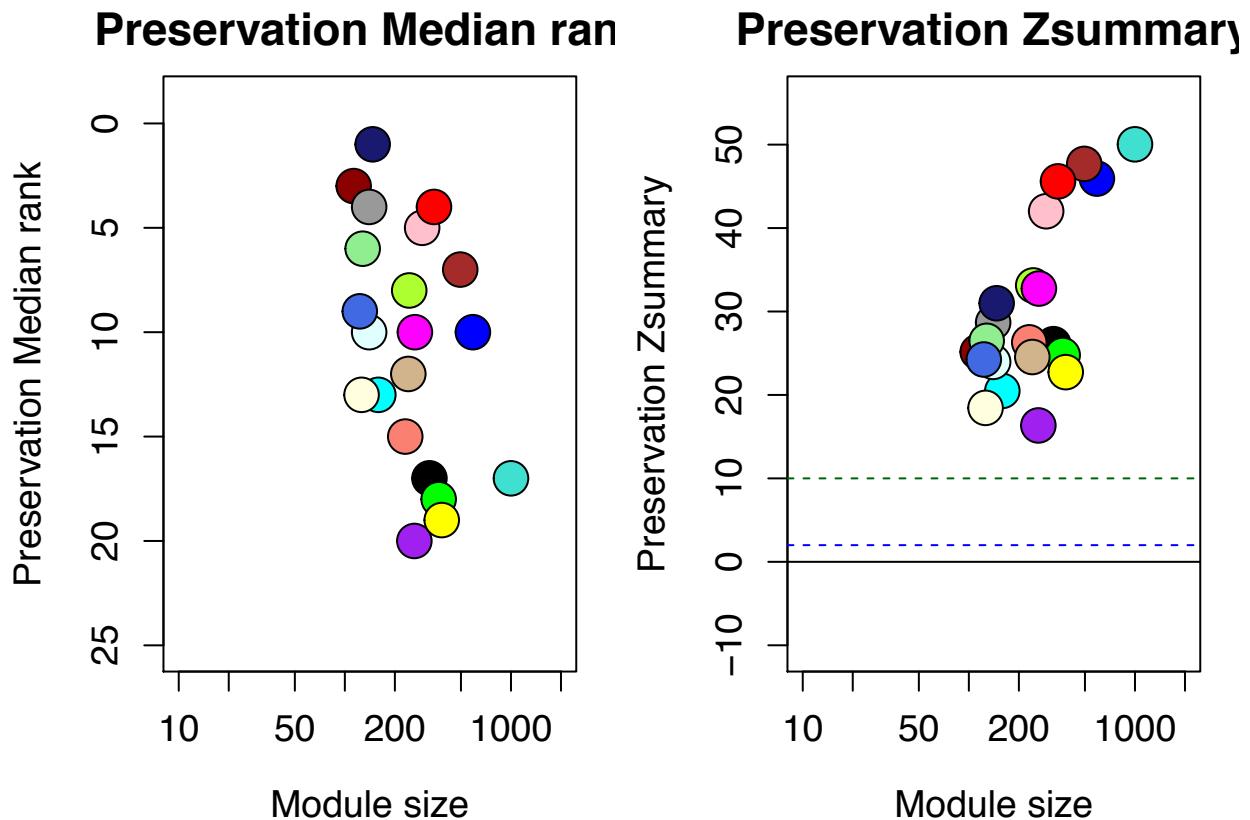
```
##          medianRank.pres medianRank.qual Zsummary.pres Zsummary.qual
## black              17            18.0          26.0         28.00
## blue               10            11.0          46.0         68.00
```

```
## brown                 7    13.0   48.0   74.00
## cyan                 13    20.5   20.0    7.40
## darkred               3     7.0   25.0   45.00
## gold                 22    22.0   24.0    0.34
## green                18    13.5   25.0   41.00
## greenyellow           8     1.0   33.0   81.00
## grey                 23    23.0    9.9  -15.00
## grey60                4     6.0   29.0   54.00
## lightcyan            10    16.0   24.0   23.00
## lightgreen            6     4.5   26.0   54.00
## lightyellow          13    12.5   18.0   27.00
## magenta              10     5.5   33.0   76.00
## midnightblue          1     4.0   31.0   57.00
## pink                  5     8.5   42.0   70.00
## purple               20    15.0   16.0   25.00
## red                   4    10.5   46.0   64.00
## royalblue             9     2.5   24.0   55.00
## salmon               15    20.5   26.0    8.90
## tan                  12     5.5   25.0   74.00
## turquoise            17    16.5   50.0   56.00
## yellow               19    19.0   23.0   23.00
```

ASD Good - ASD Poor module preservation results

```r
nperm = 1000
rand_seed = 1

setLabels = c("ASDGood","ASDPoor")
multiExpr = list(ASDGood = list(data = datExpr_asdgood),
                 ASDPoor = list(data = datExpr_asdpoor))
multiColor = list(ASDGood = asdgood_colors)

# Calculate module preservation stats
mp_asdgood_asdpoor = modulePreservation(multiExpr,
                                        multiColor,
                                        networkType = networkType,
                                        corFnc = corFnc2use,
                                        referenceNetworks = 1,
                                        nPermutations = nperm,
                                        randomSeed = rand_seed,
                                        quickCor = 0,
                                        verbose = 0)

mp_res = modulePreservationReport(mp_asdgood_asdpoor)
```

```
mp_res
```
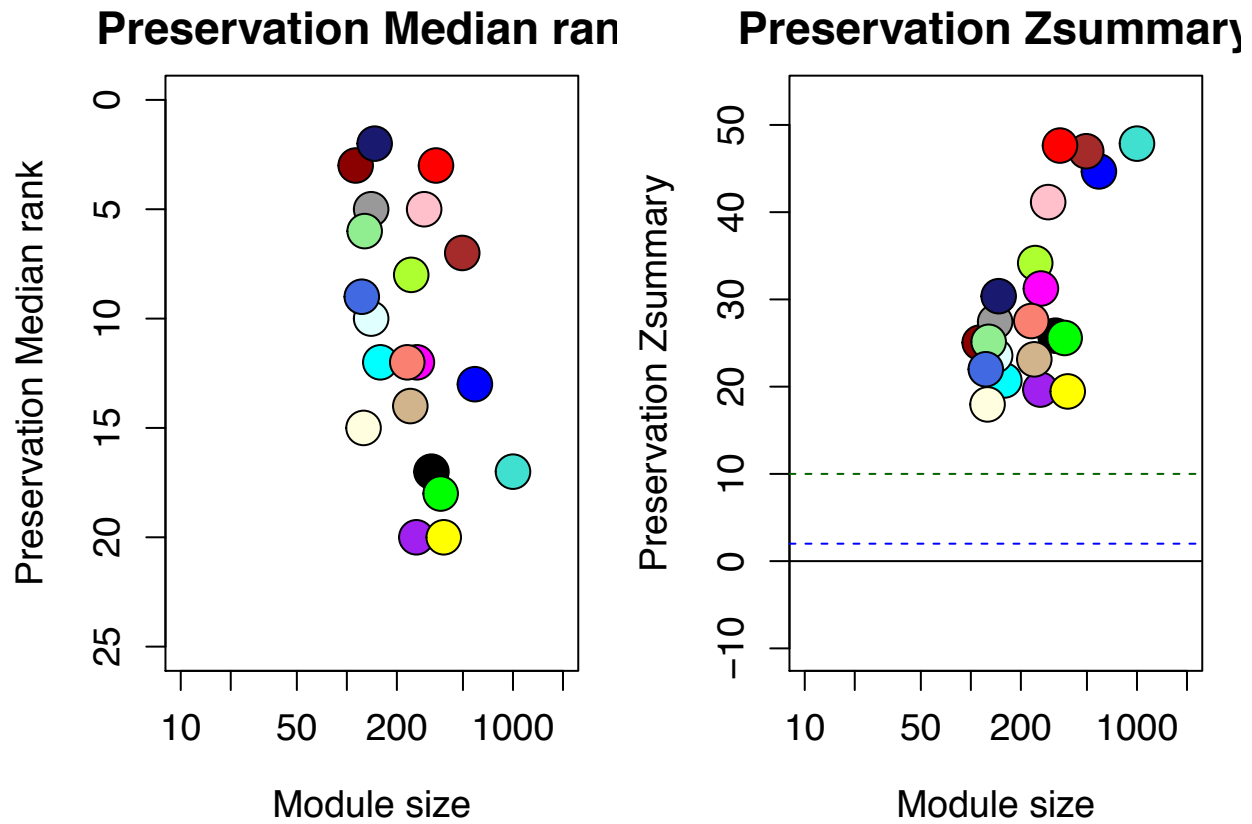
```
##                medianRank.pres medianRank.qual Zsummary.pres Zsummary.qual
## black                       17            17.5          26.0         23.00
## blue                        13            10.5          45.0         55.00
## brown                        7            11.0          47.0         84.00
## cyan                        12             8.0          21.0         32.00
## darkred                      3             5.5          25.0         27.00
## gold                        22            22.0          26.0         -0.61
## green                       18            14.0          26.0         35.00
## greenyellow                  8             1.0          34.0        110.00
## grey                        23            23.0           7.5        -13.00
## grey60                       5             8.0          27.0         29.00
## lightcyan                   10            16.5          24.0         17.00
## lightgreen                   6             4.0          25.0         43.00
## lightyellow                 15             9.0          18.0         38.00
## magenta                     12            18.5          31.0         24.00
## midnightblue                 2            11.0          30.0         25.00
## pink                         5             3.0          41.0         79.00
## purple                      20            19.0          20.0         18.00
## red                          3            17.0          48.0         30.00
## royalblue                    9             2.0          22.0         56.00
## salmon                      12            15.5          28.0         20.00
## tan                         14             6.5          23.0         40.00
## turquoise                   17            11.0          48.0         78.00
## yellow                      20            21.0          19.0         15.00
```

Songbird Differential Expression Analysis

Differential expression analysis on Hilliard et al., 2012, Neuron, microarray data from songbird Area X

See here for the actual Hilliard et al., 2012, Neuron paper: https://www.sciencedirect.com/science/article/pii/S0896627312000463

Uses preprocessed data from Hilliard et al.,'s preprocessing pipeline: https://www.ibp.ucla.edu/research/white/micorarray_preprocessing.R

```
library(easypackages)
libraries("limma","here")
options(stringsAsFactors = FALSE)

# load in the preprocessed data
load(here("data","tidy","exprData_songbird.Rdata"))
```

Run differential expression analysis

```
fdr_thresh = 0.05

# construct model
full_model = model.matrix(~as.factor(SingerGrp), data=labelData)

# make contrast matrix
contrast.matrix = "C1"=c(0,1)

# fit DE limma model
fit = lmFit(exprData,full_model)

# fit contrasts
fitContrasts = contrasts.fit(fit,contrast.matrix)

# use empirical bayes
eb = eBayes(fitContrasts)

# tabulate results
DEresults = topTable(eb,
                     number = dim(geneInfo)[1],
                     adjust.method = "fdr")
geneInfo2 = geneInfo[rownames(DEresults),]

# bind gene information to the results
DEresults = cbind(geneInfo2,DEresults)

# show FDR q<0.05 genes
DEres_subset = DEresults[DEresults$adj.P.Val<=fdr_thresh,]
cols2display = c("gene_symbols","t","P.Value","adj.P.Val")
# DEres_subset[,cols2display]
knitr::kable(DEres_subset[,cols2display], digits = 4)
```

	gene_symbols	t	P.Value	adj.P.Val
2762789	FAM8A1	-10.1482	0.0000	0.0000
2782731	FAM8A1	-10.0031	0.0000	0.0000
2760214	PRKRIP1	-9.0904	0.0000	0.0000
2789549	CYB5A	-9.0838	0.0000	0.0000
2778767	SEC11C	-8.3863	0.0000	0.0000
2764091		-8.3246	0.0000	0.0000
2778745		-8.2966	0.0000	0.0000
2785048		-8.1257	0.0000	0.0000
2766135	PTPRR	-8.0767	0.0000	0.0000
2790887	DGCR6	-7.9775	0.0000	0.0001
2759469	PSMF1	-7.9515	0.0000	0.0001
2760249	FAM8A1	-7.9225	0.0000	0.0001
2785462	ACTG1	7.8145	0.0000	0.0001
2793415	C8ORF76	-7.7777	0.0000	0.0001
2787195	YPEL5	-7.7711	0.0000	0.0001
2781472	STK25	-7.6830	0.0000	0.0001
2770308	YPEL5	-7.6511	0.0000	0.0001
2761007		-7.5679	0.0000	0.0001
2774919	DLG1	7.5423	0.0000	0.0001
2795786	PEX6	-7.4741	0.0000	0.0001
2797656	VPS8	-7.3849	0.0000	0.0001
2788991	ACTG1	7.3298	0.0000	0.0001
2758703	ACTB	7.3183	0.0000	0.0001
2767187	C2ORF44	-7.2686	0.0000	0.0001
2761030	SRF	7.2598	0.0000	0.0001
2798497		-7.2401	0.0000	0.0001
2778600	MBNL2	7.2318	0.0000	0.0001
2794279	MBNL2	7.2224	0.0000	0.0001
2771535	WIPI1	-7.1990	0.0000	0.0001
2789773	ACTB	7.1915	0.0000	0.0001
2762047	ACTB	7.1082	0.0000	0.0001
2791541	C22ORF36	-7.1072	0.0000	0.0001
2772502	C22ORF36	-7.0978	0.0000	0.0001
2767208	RRAGC	-7.0836	0.0000	0.0001
2796075	SS18L1	-7.0815	0.0000	0.0001
2775354	SRF	7.0439	0.0000	0.0001
2799655	EPB41L4A	-7.0220	0.0000	0.0001
2791730	AMFR	-7.0051	0.0000	0.0001
2787360	TTC7B	-6.9900	0.0000	0.0001
2774662	YPEL5	-6.9727	0.0000	0.0001
2761172	EIF5	-6.9717	0.0000	0.0001
2761511	PEX6	-6.9702	0.0000	0.0001
2766623	GBAS	-6.9605	0.0000	0.0001
2791367	KPNA4	-6.9598	0.0000	0.0001
2768421	ZFR	6.9548	0.0000	0.0001
2783885	ZFYVE27	-6.9423	0.0000	0.0001
2758434	PIK3IP1	-6.8525	0.0000	0.0002
2768744		6.8439	0.0000	0.0002
2782488	UBE3B	-6.8402	0.0000	0.0002
2760427	ACTB	6.8056	0.0000	0.0002
2763345	FUSIP1	-6.7312	0.0000	0.0002
2799969		-8.0344	0.0000	0.0001

	gene_symbols	t	P.Value	adj.P.Val
2766681	C10ORF32	-6.7157	0.0000	0.0002
2780655		-6.6951	0.0000	0.0002
2798919	PEX6	-6.6661	0.0000	0.0002
2780492		-6.6456	0.0000	0.0002
2772472		-6.6300	0.0000	0.0002
2763942	SEC11C	-6.6115	0.0000	0.0002
2769182	TAF13	-6.5962	0.0000	0.0002
2766671		-6.5696	0.0000	0.0002
2794373	DERL1	-6.5653	0.0000	0.0002
2785325		6.5652	0.0000	0.0002
2790902	TAF13	-6.5466	0.0000	0.0002
2777980	SUB1	6.5437	0.0000	0.0002
2769232	DGKI	6.4929	0.0000	0.0003
2761443	NTRK2	6.4828	0.0000	0.0003
2765168	UTP15	6.4695	0.0000	0.0003
2783376	ACTN1	6.4670	0.0000	0.0003
2789946	AP3M2	-6.4648	0.0000	0.0003
2759937	TMEM171	-6.4624	0.0000	0.0003
2789415	C22ORF36	-6.4437	0.0000	0.0003
2788978		-6.4435	0.0000	0.0003
2787072	WDR1	6.4323	0.0000	0.0003
2773523	ACTN1	6.4276	0.0000	0.0003
2771893		-6.4086	0.0000	0.0003
2795026	C5ORF41	-6.3856	0.0000	0.0003
2799037	ZFR	6.3735	0.0000	0.0003
2788275	FBXL20	-6.3538	0.0000	0.0003
2788249	SDHD	-6.7051	0.0000	0.0002
2761611	POF1B	-6.3408	0.0000	0.0003
2765874	PEX6	-6.3321	0.0000	0.0003
2769976	C22ORF36	-6.3153	0.0000	0.0003
2767779	COL4A3BP	-6.2967	0.0000	0.0004
2764293	AMACR	-6.2832	0.0000	0.0004
2791542	UPF1	-6.2649	0.0000	0.0004
2773456	PDDC1	-6.2517	0.0000	0.0004
2798158	DLG1	6.2270	0.0000	0.0004
2767126	SHC3	6.2175	0.0000	0.0004
2778404	RPS24	-6.2112	0.0000	0.0004
2774627	PSMF1	-6.2067	0.0000	0.0004
2790259	RORA	-6.2023	0.0000	0.0004
2794871	KPNA4	-6.1864	0.0000	0.0004
2781729	PTCH1	-6.1860	0.0000	0.0004
2765153	SYMENSTGUG00000017592	-6.1799	0.0000	0.0004
2779184	ACTR3	6.1652	0.0000	0.0004
2775685	RRAGC	-6.1588	0.0000	0.0004
2785826	ATXN3	-6.1584	0.0000	0.0004
2768389	NTRK2	6.1559	0.0000	0.0004
2799010		6.1546	0.0000	0.0004
2791392	SHC3	6.1307	0.0000	0.0004
2792208	SUB1	6.1303	0.0000	0.0004
2774234	TPM1	6.1290	0.0000	0.0004
2768948	ATXN7L1	-6.1141	0.0000	0.0004
2788306	FAM8A1	-6.1108	0.0000	0.0004

	gene_symbols	t	P.Value	adj.P.Val
2795154	XP_002188032.1	-6.1019	0.0000	0.0004
2793580	RUSC2	-6.1012	0.0000	0.0004
2799555	WDR1	6.0954	0.0000	0.0004
2787767	ETF1	6.0942	0.0000	0.0004
2780156	ACTG2	6.0856	0.0000	0.0004
2766264	NBN	-6.0853	0.0000	0.0004
2778298	C10ORF32	-6.0787	0.0000	0.0004
2767181	BRD3	-6.0751	0.0000	0.0004
2791025	PLK2	6.0694	0.0000	0.0004
2783284	CUGBP2-1	6.0617	0.0000	0.0004
2768989	NTRK2	6.0503	0.0000	0.0004
2797078		-6.0361	0.0000	0.0005
2795973	RNF19B	6.3370	0.0000	0.0004
2780656	PCSK1	6.0263	0.0000	0.0005
2771640	RAB11FIP4	6.3318	0.0000	0.0004
2767511	AMFR	-6.0227	0.0000	0.0005
2792897	EIF5	-6.0174	0.0000	0.0005
2792908	SERTAD2	6.0099	0.0000	0.0005
2782585	SUB1	6.0082	0.0000	0.0005
2766176	FBXL20	-6.0068	0.0000	0.0005
2797270	ACTB	5.9950	0.0000	0.0005
2775903	PLLP	-5.9929	0.0000	0.0005
2758206	FRAT1	-5.9904	0.0000	0.0005
2789763	KIAA1462	5.9880	0.0000	0.0005
2784646		-5.9874	0.0000	0.0005
2760072		-5.9831	0.0000	0.0005
2767198	HIVEP2	5.9731	0.0000	0.0005
2763783		-5.9691	0.0000	0.0005
2781789	HNRNPD	5.9673	0.0000	0.0005
2796749	C22ORF32	-5.9665	0.0000	0.0005
2786646	PTDSS2	-5.9622	0.0000	0.0005
2793984	NR4A1	6.2592	0.0000	0.0004
2786318	ETF1	5.9583	0.0000	0.0005
2785854	HIVEP2	5.9440	0.0000	0.0005
2778302	ASB3	-5.9435	0.0000	0.0005
2800048		-5.9400	0.0000	0.0005
2774092	ZC3H7A	-5.9373	0.0000	0.0005
2781604	UBXN2A	5.9241	0.0000	0.0005
2772307	SERTAD2	6.2119	0.0000	0.0004
2793291	LIN52	-5.9184	0.0000	0.0005
2769526	MBNL2	5.9169	0.0000	0.0005
2794711	ACTB	5.9061	0.0000	0.0005
2780013	DENND2A	-5.8990	0.0000	0.0005
2761700	SGSM2	5.8892	0.0000	0.0005
2759394		-5.8744	0.0000	0.0005
2770736	NTRK2	5.8693	0.0000	0.0005
2783121	MBNL2	5.8690	0.0000	0.0005
2789669	C1ORF96	-5.8451	0.0000	0.0006
2762021	TXNDC12	-5.8267	0.0000	0.0006
2781527	UCP2	-5.8219	0.0000	0.0006
2789062	MED13	-5.8195	0.0000	0.0006
2765825		-5.8131	0.0000	0.0006

	gene_symbols	t	P.Value	adj.P.Val
2792452	C15ORF40	-5.8092	0.0000	0.0006
2767203	BSDC1	-5.8045	0.0000	0.0006
2757076	NTRK2	5.8007	0.0000	0.0006
2785702	WDYHV1	-5.7907	0.0000	0.0006
2793598	C10ORF104-2	-5.7765	0.0000	0.0006
2763675	ATG12	-5.7668	0.0000	0.0006
2762591		-5.7599	0.0000	0.0006
2759567	SHC3	5.7536	0.0000	0.0007
2782515		-5.7531	0.0000	0.0007
2787596		6.0192	0.0000	0.0005
2773554	DNAJB14	-5.7296	0.0000	0.0007
2765801	PIK3IP1	-5.7255	0.0000	0.0007
2765851	C15ORF40	-5.7225	0.0000	0.0007
2784772	TSR1	5.7210	0.0000	0.0007
2798662	RABL3	-5.7202	0.0000	0.0007
2783128	RAB11FIP4	5.9801	0.0000	0.0005
2760295	NCBP2	-5.7112	0.0000	0.0007
2767394	RAB11FIP4	5.9599	0.0000	0.0005
2790190		5.6957	0.0000	0.0007
2772818	RCAN1	-5.6954	0.0000	0.0007
2762752	HIVEP2	5.6918	0.0000	0.0007
2759966	MED10	-5.6878	0.0000	0.0007
2765488	ZFR	5.6822	0.0000	0.0007
2758456	TANC2	5.6813	0.0000	0.0007
2783040	TMEM111	-5.6803	0.0000	0.0007
2776506	CCT2	5.6802	0.0000	0.0007
2796655	CDC2L6	-5.6774	0.0000	0.0007
2771553	THUMPD1	-5.6768	0.0000	0.0007
2760821	TMCC2	-5.6737	0.0000	0.0007
2789211	DEK	-5.6723	0.0000	0.0007
2761268	KIAA1462	5.6676	0.0000	0.0007
2760096	HN1L	-5.6657	0.0000	0.0007
2776511	NOL8	-5.6624	0.0000	0.0007
2789937	BSDC1	-5.6418	0.0000	0.0008
2775565	DLG1	5.6382	0.0000	0.0008
2761495	C14ORF83	-5.6326	0.0000	0.0008
2766052	TPM4	5.6323	0.0000	0.0008
2774758	XP_002188032.1	-5.6297	0.0000	0.0008
2769137	PELI1	5.6234	0.0000	0.0008
2782659	RNF19B	5.6216	0.0000	0.0008
2784605		-5.6201	0.0000	0.0008
2777552	SYMENSTGUG00000017592	-5.6184	0.0000	0.0008
2770568	LOC422221	-5.6156	0.0000	0.0008
2780693	ACTR3	5.5988	0.0000	0.0008
2760224	HIVEP2	5.5938	0.0000	0.0008
2790875	BAI3	-5.5900	0.0000	0.0008
2768206	GPR12	5.5879	0.0000	0.0008
2763350	REEP3	-5.5833	0.0000	0.0008
2776040	B3GALT6	-5.5814	0.0000	0.0008
2765456	SUB1	5.5795	0.0000	0.0008
2779868	HOMER1	5.5757	0.0000	0.0008
2799286	SHC3	5.5744	0.0000	0.0008

	gene_symbols	t	P.Value	adj.P.Val
2792142	NCBP2	-5.5676	0.0000	0.0008
2775953	SF3B14	-5.5586	0.0000	0.0008
2799559	EGR1	5.5559	0.0000	0.0008
2788164	TRPV1	-5.5540	0.0000	0.0008
2772405	GFM2	-5.5469	0.0000	0.0009
2783111	FEM1C	-5.5459	0.0000	0.0009
2787375	PM20D1	-5.5441	0.0000	0.0009
2766722	COL4A3BP	-5.5416	0.0000	0.0009
2790332	PAFAH1B2	-5.5394	0.0000	0.0009
2796310	PTCH1	-5.5362	0.0000	0.0009
2777308		-6.2856	0.0000	0.0004
2767701	NUP188	-5.5302	0.0000	0.0009
2763381	SLC6A6	5.5252	0.0000	0.0009
2797196		-5.5237	0.0000	0.0009
2789938	RRAGC	-5.5220	0.0000	0.0009
2766587		-5.5211	0.0000	0.0009
2794357		-6.2594	0.0000	0.0004
2790393	RCJMB04_31O3	-5.4920	0.0000	0.0009
2769883	TAF13	-5.4822	0.0000	0.0010
2790600	HMGN2	-5.4810	0.0000	0.0010
2777016	KCNK2	-5.4737	0.0000	0.0010
2770773	THUMPD1	-6.1979	0.0000	0.0004
2791298	SYT14	-5.4658	0.0000	0.0010
2776018	FAM8A1	-5.4527	0.0000	0.0010
2784556	SIK2	5.4496	0.0000	0.0010
2781522	EGR1	5.4434	0.0000	0.0010
2783004	ACTR3	5.4424	0.0000	0.0010
2776200	C15ORF41	-5.4344	0.0000	0.0010
2769348	FAM92A1	-5.4318	0.0000	0.0010
2783041	PELI1	5.4292	0.0000	0.0010
2773875	C15ORF41	-5.4286	0.0000	0.0010
2794375	EGR1	5.4281	0.0000	0.0010
2787420	CDKN1B	-5.4275	0.0000	0.0010
2772110		-5.4274	0.0000	0.0010
2782928	ZFR	5.4235	0.0000	0.0010
2759065	FOSL2	5.4168	0.0000	0.0010
2797543	ZC3H8	-6.1047	0.0000	0.0005
2795192	UBE2L3	-6.1038	0.0000	0.0005
2796554	TRIM23	-5.3894	0.0000	0.0011
2786303	MBNL2	5.3873	0.0000	0.0011
2763809	CXCL14	5.3839	0.0000	0.0011
2776120	ACTR3	5.3798	0.0000	0.0011
2798094	EGR1	5.3749	0.0000	0.0011
2763747	ABL2	-5.3715	0.0000	0.0011
2757328	SIK2	5.3708	0.0000	0.0011
2782785	WDR5	-5.3688	0.0000	0.0011
2781238	GDAP1	-5.5892	0.0000	0.0009
2790793	CLDN12	-5.3651	0.0000	0.0011
2781237		5.3623	0.0000	0.0011
2766669	GBAS	-6.0549	0.0000	0.0005
2781445		-5.3533	0.0000	0.0012
2758847	PTPRJ	5.3500	0.0000	0.0012

	gene_symbols	t	P.Value	adj.P.Val
2761518		-5.3470	0.0000	0.0012
2795936	PABPC1	-5.3444	0.0000	0.0012
2780227	C15ORF40	-5.3443	0.0000	0.0012
2788781		5.3411	0.0000	0.0012
2762225	MAPK1IP1L	-5.3373	0.0000	0.0012
2776532	TAF13	-5.3358	0.0000	0.0012
2788987	LPCAT1	-5.3305	0.0000	0.0012
2784218	ACVR2A	-5.3180	0.0000	0.0012
2764711	SIRT1	-5.3158	0.0000	0.0012
2762294	CXCL14	5.3108	0.0000	0.0012
2771140		5.5114	0.0000	0.0010
2760380	EGR1	5.2941	0.0000	0.0013
2759501	ABCC5	-5.2940	0.0000	0.0013
2770794		5.5007	0.0000	0.0010
2795713	HIVEP2	5.2865	0.0000	0.0013
2787962	SYMENSTGUG00000003396	5.2827	0.0000	0.0013
2800014	C8ORF76	-5.2817	0.0000	0.0013
2760115		-5.2817	0.0000	0.0013
2768899		-5.2782	0.0000	0.0013
2792589	KIAA1462	5.2714	0.0000	0.0013
2781896	NR4A3	5.7404	0.0000	0.0008
2783513	EGR1	5.2670	0.0000	0.0013
2789690	ANAPC2	-5.2647	0.0000	0.0013
2764693	DRP2	-5.2633	0.0000	0.0013
2760493	SHROOM2	-5.2626	0.0000	0.0013
2778991		-5.4696	0.0000	0.0010
2794149	RNF145	-5.2535	0.0000	0.0014
2793863	ATG12	-5.2477	0.0000	0.0014
2794917	NINL	-5.2468	0.0000	0.0014
2785087	TRIM23	-5.2466	0.0000	0.0014
2793097	P4HA1	-5.2451	0.0000	0.0014
2769964	USP37	5.2442	0.0000	0.0014
2785864	DDX3X	5.2348	0.0000	0.0014
2763330	PTPRJ	5.2291	0.0000	0.0014
2778798	NUP188	-5.2197	0.0000	0.0014
2786511	ZFYVE21	-5.2184	0.0000	0.0014
2786906	NUP88	-5.2160	0.0000	0.0014
2761221	BSDC1	-5.2134	0.0000	0.0015
2793887	SLC38A2	-5.2109	0.0000	0.0015
2798599	RAB11FIP4	5.4126	0.0000	0.0011
2783778	SMEK2	5.2068	0.0000	0.0015
2776828	TMCC2	-5.2027	0.0000	0.0015
2765635	NTRK2	5.2026	0.0000	0.0015
2791590	RBM14	-5.1994	0.0000	0.0015
2775590	CPNE1	-5.1984	0.0000	0.0015
2799568		-5.8331	0.0000	0.0006
2771791	LANCL1	-5.1908	0.0000	0.0015
2762738		-5.1870	0.0000	0.0015
2766676	ORC5L	-5.1823	0.0000	0.0015
2791028	TTC33	5.1731	0.0000	0.0015
2769284	BPGM	-5.1725	0.0000	0.0015
2767212	CPEB3	-5.1713	0.0000	0.0015

	gene_symbols	t	P.Value	adj.P.Val
2790205	AGTPBP1	5.1668	0.0000	0.0015
2781017	C2ORF44	-5.7834	0.0000	0.0007
2766933	FOSL2	5.1505	0.0000	0.0016
2771023		5.1455	0.0000	0.0016
2791183	PELI1	5.1451	0.0000	0.0016
2758601	PTPRR	-5.1444	0.0000	0.0016
2758022	PAM	5.1437	0.0000	0.0016
2782601	TET2	5.1424	0.0000	0.0016
2785977		-5.1414	0.0000	0.0016
2776367	DLG3	5.1397	0.0000	0.0016
2781399	SFPQ	5.1396	0.0000	0.0016
2759852	TRIP13	-5.1387	0.0000	0.0016
2789433		-5.7569	0.0000	0.0007
2765876	GBAS	-5.7562	0.0000	0.0007
2799313	NTRK2	5.1350	0.0000	0.0016
2785358	EIF2AK3	-5.1340	0.0000	0.0016
2789183	SERTAD2	5.1338	0.0000	0.0016
2770625	TRIM36-1	-5.1322	0.0000	0.0016
2764626	JARID2	-5.1300	0.0000	0.0016
2767927	CUGBP2-1	5.1284	0.0000	0.0016
2784768	ANKS3	-5.1280	0.0000	0.0016
2790899	SETBP1	5.1248	0.0000	0.0016
2776868	EGR2	5.1147	0.0000	0.0017
2764795	ISL1	5.1141	0.0000	0.0017
2770904	DDX18	5.1107	0.0000	0.0017
2772859	SLC25A25	5.1097	0.0000	0.0017
2757971	GBAS	-5.7221	0.0000	0.0007
2778230	HINT3	-5.1057	0.0000	0.0017
2795259	EGR1	5.1037	0.0000	0.0017
2784175	RAB11FIP4	5.2952	0.0000	0.0014
2780198	KCNC1	-5.2905	0.0000	0.0014
2799219	HS3ST4	-5.0969	0.0000	0.0017
2778389	EGR1	5.0959	0.0000	0.0017
2791016	MEA1	-5.0955	0.0000	0.0017
2793447	C1ORF57	-5.0910	0.0000	0.0017
2774782		-5.0909	0.0000	0.0017
2766314	PSPC1	5.0867	0.0000	0.0017
2775938	SYMENSTGUG00000017606	-5.0861	0.0000	0.0017
2762629		5.0814	0.0000	0.0017
2763017	HMGB3	-5.0736	0.0000	0.0018
2776710	UPRT	-5.0730	0.0000	0.0018
2784060	ASAP1	5.0685	0.0000	0.0018
2781138	TXNDC12	-5.0642	0.0000	0.0018
2766842		-5.0629	0.0000	0.0018
2791372	DEK	-5.2433	0.0000	0.0015
2780630	KCNAB2	-5.0391	0.0000	0.0019
2763570	ANAPC13	-5.0382	0.0000	0.0019
2776390	TET2	5.0378	0.0000	0.0019
2761140	ZBTB17	5.0372	0.0000	0.0019
2787029		-5.2215	0.0000	0.0015
2796466	DCLK1	5.0348	0.0000	0.0019
2784506	REV3L	-5.2155	0.0000	0.0015

	gene_symbols	t	P.Value	adj.P.Val
2799759	EGR1	5.0269	0.0000	0.0019
2760709	LRRTM1	-5.0265	0.0000	0.0019
2781345	GSTO1	-5.0260	0.0000	0.0019
2790713	DUSP6	5.0220	0.0000	0.0019
2798375	KCNC1	-5.0217	0.0000	0.0019
2773512	CUGBP2-1	5.0136	0.0000	0.0020
2779351	TRIM37	5.0124	0.0000	0.0020
2778938	ABCC5	-5.0093	0.0000	0.0020
2766259		-5.0093	0.0000	0.0020
2792710	FSCN1	-5.0045	0.0000	0.0020
2779726	VPS39	-5.0023	0.0000	0.0020
2797698	TRIM9	4.9971	0.0000	0.0020
2787300	TMEM123	-5.1750	0.0000	0.0016
2776778	SUB1	4.9839	0.0000	0.0021
2788989	GDAP1	-4.9827	0.0000	0.0021
2793033	PPP2CA	4.9812	0.0000	0.0021
2793725		-4.9779	0.0000	0.0021
2763494	RYBP	-4.9767	0.0000	0.0021
2777527	PTPN9	5.1513	0.0000	0.0017
2766441	GSTO1	-5.1484	0.0000	0.0017
2788137	ILK	-4.9653	0.0000	0.0021
2759489	UNC80	-4.9641	0.0000	0.0021
2776693	RRP9	4.9570	0.0000	0.0022
2778345	CXCL14	4.9560	0.0000	0.0022
2785723	TCTE1	-4.9489	0.0000	0.0022
2799153		-4.9472	0.0000	0.0022
2777802		-5.5096	0.0000	0.0010
2779689	BZW2	4.9427	0.0000	0.0022
2787101	TET2	4.9417	0.0000	0.0022
2797439	RPS6KA6	4.9414	0.0000	0.0022
2768243	CPEB1	-4.9394	0.0000	0.0022
2775630	RAB4A	-4.9277	0.0000	0.0023
2792108	CCDC53	-5.4862	0.0000	0.0010
2783512	MCAT	-4.9259	0.0000	0.0023
2757294	PPIG	4.9254	0.0000	0.0023
2772008	SLMO1	5.0962	0.0000	0.0018
2779605	C9ORF89	-4.9208	0.0000	0.0023
2777316	XP_002200388.1	-4.9207	0.0000	0.0023
2762698	SGSM2	4.9115	0.0000	0.0024
2757463	DCLK1	4.9090	0.0000	0.0024
2790019	SLC25A25	4.9075	0.0000	0.0024
2765597	FBXW11	-4.9061	0.0000	0.0024
2784323	NETO1	4.8987	0.0001	0.0024
2765138	EIF2C3	4.8980	0.0001	0.0024
2791651	CDC2L6	-4.8921	0.0001	0.0024
2795403	UBFD1	-5.4403	0.0000	0.0011
2765330		5.0595	0.0000	0.0020
2765280	KLC4	-4.8862	0.0001	0.0025
2794916	IRS2	4.8849	0.0001	0.0025
2795281	SMPD3	-4.8847	0.0001	0.0025
2771546		5.0511	0.0000	0.0020
2784956	ACTA2	4.8772	0.0001	0.0025

	gene_symbols	t	P.Value	adj.P.Val
2784593	IRS4	-4.8753	0.0001	0.0025
2793695		-4.8709	0.0001	0.0025
2792060	WNK1	4.8697	0.0001	0.0025
2795822	RBM14	-4.8692	0.0001	0.0025
2795022	CREM	4.8691	0.0001	0.0025
2761950		-4.8662	0.0001	0.0025
2792280	KIAA0652	-4.8659	0.0001	0.0025
2761589	PLK2	4.8649	0.0001	0.0025
2773061	SF3B14	-4.8648	0.0001	0.0025
2778224		-4.8627	0.0001	0.0025
2792167	INO80C	-4.8613	0.0001	0.0025
2762777	FBXO21	-4.8611	0.0001	0.0025
2784178	TRAPPC10	-4.8601	0.0001	0.0025
2780362	RAC3	-4.8576	0.0001	0.0026
2797472	PROSC	-4.8542	0.0001	0.0026
2768730	IRS2	4.8537	0.0001	0.0026
2792667		-4.8511	0.0001	0.0026
2775598	BAIAP2	4.8482	0.0001	0.0026
2762128	DNAJB5	4.8443	0.0001	0.0026
2774097	NLK	4.8431	0.0001	0.0026
2758217		-4.8415	0.0001	0.0026
2788506	PLEKHA3	-4.8411	0.0001	0.0026
2780095	JHDM1D	5.0086	0.0000	0.0021
2757981	NTRK2	4.8384	0.0001	0.0026
2798063	ETF1	4.8344	0.0001	0.0027
2799855	KIAA1462	4.8322	0.0001	0.0027
2792713	PTPN9	4.9936	0.0000	0.0022
2761494	MCAT	-4.8239	0.0001	0.0027
2772623	ACTB	4.8239	0.0001	0.0027
2761150	ZBTB8OS	-4.8213	0.0001	0.0027
2793201	TELO2	-4.8201	0.0001	0.0027
2778756		-4.8187	0.0001	0.0027
2769109	SOX11	-4.8151	0.0001	0.0027
2758261		4.8138	0.0001	0.0027
2769608	FBXO7	-4.8127	0.0001	0.0027
2757108	DHDDS	4.8079	0.0001	0.0028
2790865	MRAS	-4.8027	0.0001	0.0028
2783737	FNDC4	-4.7966	0.0001	0.0028
2758693	DBC1	4.7952	0.0001	0.0029
2775585	MKL1	4.7884	0.0001	0.0029
2764391	CREM	4.7860	0.0001	0.0029
2798876	DLG3	4.7857	0.0001	0.0029
2773636	ARPP19	4.7815	0.0001	0.0029
2778885	KIAA0895L	-4.7808	0.0001	0.0029
2791199	CUGBP2-1	4.7803	0.0001	0.0029
2770721	C5ORF41	-4.7794	0.0001	0.0029
2770621	WNT5A	-5.5123	0.0000	0.0011
2783429	TMEM111	-4.7752	0.0001	0.0029
2759705	BBX	-4.7727	0.0001	0.0030
2761770		-4.7703	0.0001	0.0030
2786357	EGR2	4.7685	0.0001	0.0030
2759761	TRIM9	4.7678	0.0001	0.0030

	gene_symbols	t	P.Value	adj.P.Val
2763130	NPDC1	-4.7652	0.0001	0.0030
2759201	ACTR3	4.7646	0.0001	0.0030
2770783	FOXO3	-4.7635	0.0001	0.0030
2794530	TLN2	4.7631	0.0001	0.0030
2777718		-4.7576	0.0001	0.0030
2778070	AQP7	-4.7546	0.0001	0.0030
2785518	B5FZ53_TAEGU	-4.7527	0.0001	0.0030
2781397	TTC38	-4.7475	0.0001	0.0031
2791346	TTC32	-4.7467	0.0001	0.0031
2799537	BCL9L	-4.9013	0.0001	0.0025
2781032	CDH11	4.7402	0.0001	0.0031
2797086	MED9	-4.7382	0.0001	0.0031
2765294	DIP2C	4.7359	0.0001	0.0031
2784095	CDK8	4.7352	0.0001	0.0031
2763318	CUL4B	-4.7326	0.0001	0.0032
2763895	NFE2L2	-4.7252	0.0001	0.0032
2779508	PCDH19	-4.7239	0.0001	0.0032
2766632		-5.2241	0.0000	0.0015
2760814	LGR4	-4.7206	0.0001	0.0032
2788543		-4.7184	0.0001	0.0032
2795117	KCNC1	-4.7173	0.0001	0.0033
2781439	KIAA1462	4.7149	0.0001	0.0033
2772114	ABL2	-4.7149	0.0001	0.0033
2773979	DDX3X	4.7083	0.0001	0.0033
2799751	SPAST	-4.7078	0.0001	0.0033
2792392	SNX4	-4.7073	0.0001	0.0033
2761497	CPSF6	4.7012	0.0001	0.0033
2758076	AGFG1	-4.6984	0.0001	0.0034
2791765	PELI1	4.6944	0.0001	0.0034
2799343		4.6908	0.0001	0.0034
2766443	ETV3	4.6892	0.0001	0.0034
2760265	XKR8	-4.6855	0.0001	0.0034
2796738	CRYL1	-4.6853	0.0001	0.0034
2774636		4.6853	0.0001	0.0034
2760646	LRRC4C	4.6837	0.0001	0.0034
2769575		-4.6812	0.0001	0.0035
2783549	SGK1	-4.6803	0.0001	0.0035
2785314	ANKMY2	4.6801	0.0001	0.0035
2759618	GRAMD1B	4.6798	0.0001	0.0035
2767192		-4.6769	0.0001	0.0035
2778881	SYMENSTGUG00000011132	4.6717	0.0001	0.0035
2773479	RUNX1T1	-4.8230	0.0001	0.0029
2796733		-4.6706	0.0001	0.0035
2786275		-4.6689	0.0001	0.0035
2788225	DDX3X	4.6668	0.0001	0.0035
2797162	TRIM37	4.6647	0.0001	0.0035
2758083	SLC9A7	-4.6597	0.0001	0.0036
2779757	DLGAP2	4.6594	0.0001	0.0036
2773975	DDX3X	4.6578	0.0001	0.0036
2788769	BSDC1	-4.6562	0.0001	0.0036
2788157	OSBPL6	4.6551	0.0001	0.0036
2789568		-4.6536	0.0001	0.0036

	gene_symbols	t	P.Value	adj.P.Val
2762143		-4.6514	0.0001	0.0036
2767847	KLHL12	-4.6500	0.0001	0.0036
2768240	ST3GAL3	-4.6494	0.0001	0.0036
2791315	CABC1	-4.6491	0.0001	0.0036
2773782	MPPE1	-4.6465	0.0001	0.0036
2768709		-4.6450	0.0001	0.0036
2772105	CDK2AP1	-4.6446	0.0001	0.0036
2796631	UPB1	-4.6445	0.0001	0.0036
2781859	C1ORF144	-4.6404	0.0001	0.0036
2778393	C19ORF44	-5.1191	0.0000	0.0018
2779202	MBNL1	-4.6367	0.0001	0.0037
2771417	YPEL2	-4.6343	0.0001	0.0037
2762806	PDCD4	-4.6331	0.0001	0.0037
2765008		4.6307	0.0001	0.0037
2757547	ARC	4.7776	0.0001	0.0031
2799179	STRADB	-4.6283	0.0001	0.0037
2794775	TCF20	-4.6253	0.0001	0.0037
2767369		4.6142	0.0001	0.0038
2790740	PNLDC1	-4.6138	0.0001	0.0038
2763593	ERMP1	-4.6136	0.0001	0.0038
2784274	TMEM5	-4.6122	0.0001	0.0038
2759848	PTDSS1	-4.6120	0.0001	0.0038
2766043		4.6101	0.0001	0.0038
2791267	KCNC1	-4.6095	0.0001	0.0038
2792545	METTL9	-4.6064	0.0001	0.0039
2773908	ARPP19	4.6054	0.0001	0.0039
2790296		-4.6043	0.0001	0.0039
2778643	PPP3CA	-4.6026	0.0001	0.0039
2791729	DNAJB5	4.6001	0.0001	0.0039
2774949		4.5997	0.0001	0.0039
2768655	DUSP5	4.5971	0.0001	0.0039
2760601	DIP2C	4.5952	0.0001	0.0039
2777674	HEXDC	-4.5925	0.0001	0.0039
2798598	DNAJB5	4.5903	0.0001	0.0039
2760980	CDAN1	-4.5902	0.0001	0.0039
2771419	CEBPZ	-4.5896	0.0001	0.0039
2787096	SOD1	-4.5844	0.0001	0.0040
2766488	RANBP2	4.5814	0.0001	0.0040
2762406		-4.5771	0.0001	0.0040
2776476	RUSC2	-4.5746	0.0001	0.0040
2787309	SUB1	4.5739	0.0001	0.0040
2771712	FAR1	-4.5727	0.0001	0.0041
2785966	CNNM1	-4.5694	0.0001	0.0041
2764704	SAMD14	-4.5595	0.0001	0.0042
2774870	SLC38A7	-4.5578	0.0001	0.0042
2769510	RUFY3	-4.5575	0.0001	0.0042
2763398	SYT4	4.5544	0.0001	0.0042
2768113	BOC	4.5517	0.0001	0.0042
2765011	ARHGEF18	-4.5509	0.0001	0.0042
2772555	DDX26B	-5.0099	0.0000	0.0021
2759463	SHC3	4.5482	0.0001	0.0042
2784875	GABBR2	-4.5482	0.0001	0.0042

	gene_symbols	t	P.Value	adj.P.Val
2775794	MAPK1IP1L	-4.5468	0.0001	0.0042
2787743	R3HDM1	4.5415	0.0001	0.0043
2788342	XKR8	-4.5406	0.0001	0.0043
2781112	TCF20	-4.5379	0.0001	0.0043
2798679	GAD2	4.5373	0.0001	0.0043
2792951		-4.6776	0.0001	0.0036
2788173	CUGBP2	4.5343	0.0001	0.0043
2775355	R3HDM1	4.5342	0.0001	0.0043
2775836	TMEM97	4.5319	0.0001	0.0043
2797912		4.6720	0.0001	0.0037
2763953	TAGLN	4.6674	0.0001	0.0037
2774454	TIMM9	-4.5253	0.0001	0.0044
2790025	C10ORF104	-4.9673	0.0000	0.0023
2789471	SMEK2	4.5129	0.0001	0.0045
2789273	SLC38A7	-4.5103	0.0001	0.0046
2791294	CHD9	4.5094	0.0001	0.0046
2792752		-4.5074	0.0001	0.0046
2782094	C13ORF37	-4.5067	0.0001	0.0046
2767539	LOC415511	4.5052	0.0001	0.0046
2759373	UBXN4	4.5051	0.0001	0.0046
2780628		-4.5048	0.0001	0.0046
2796879	SOD1	-4.5044	0.0001	0.0046
2789277	EZH1	-4.5024	0.0001	0.0046
2768028		4.6401	0.0001	0.0039
2784083	SYBL1	-4.5018	0.0001	0.0046
2798999	MBNL2	4.4966	0.0001	0.0046
2757233	YARS	-4.4960	0.0001	0.0046
2797742		-4.4949	0.0001	0.0046
2764661	FAM173B	-4.4943	0.0001	0.0046
2787814	SETMAR	-4.4932	0.0001	0.0046
2760896	MRPL23	-4.4916	0.0001	0.0046
2782046	RYBP	-4.4877	0.0001	0.0047
2766566	LRRC4C	4.6197	0.0001	0.0040
2796267	TDP1	-4.4818	0.0001	0.0047
2761846	FAM65A	-4.4816	0.0001	0.0047
2797297	SLC35F4	-4.4809	0.0001	0.0047
2766821	FBXW7	4.4787	0.0001	0.0047
2796246	NR4A1	4.6135	0.0001	0.0040
2771785	RNPC3	-4.4769	0.0001	0.0048
2782184	NFKBIE	-4.4727	0.0002	0.0048
2775871	KPNA4	-4.4719	0.0002	0.0048
2779151	EFNB1	4.6069	0.0001	0.0041
2786794	CFH	-4.4703	0.0002	0.0048
2758839	A2BP1	-4.4688	0.0002	0.0048
2783844	UBASH3B	4.4623	0.0002	0.0049
2776711		-4.4584	0.0002	0.0049
2785874	BZW2	4.4560	0.0002	0.0050
2762966		4.5868	0.0001	0.0042
2763987		-4.4524	0.0002	0.0050
2786530	BAIAP2	4.4518	0.0002	0.0050
2795481	ZC3H7B	-4.4514	0.0002	0.0050
2791058	PEX14	-4.5845	0.0001	0.0042

	gene_symbols	t	P.Value	adj.P.Val
2799624	ACOX1	-4.4507	0.0002	0.0050
2770852	RALGAPB	4.4494	0.0002	0.0050
2796227	RTCD1	4.4452	0.0002	0.0050
2762561	DDX3X	4.4430	0.0002	0.0051
2779780	ADRM1	4.4421	0.0002	0.0051
2791461	RBM16	4.4421	0.0002	0.0051
2761205	CKB	-4.4412	0.0002	0.0051
2782807	LRRC4C	4.4382	0.0002	0.0051
2759764	MAPK10	-4.4381	0.0002	0.0051
2783899	DHDDS	4.4371	0.0002	0.0051
2794669	GRM4	-4.4344	0.0002	0.0051
2791976		4.4344	0.0002	0.0051
2764277	ACVR1B	-4.4339	0.0002	0.0051
2758674	KCNAB2	-4.4318	0.0002	0.0051
2794595	ARL4C	4.4316	0.0002	0.0051
2793238	TCF12	-4.4289	0.0002	0.0051
2773748	NAA25	4.4283	0.0002	0.0051
2790055		4.4247	0.0002	0.0052
2790165		-4.8532	0.0001	0.0027
2788930	SIK2	4.4219	0.0002	0.0052
2787447	SGK1	-4.5527	0.0001	0.0045
2798729	TBC1D9B	-4.4170	0.0002	0.0053
2760067	TIMM22	-4.4169	0.0002	0.0053
2792651	SYMENSTGUG00000017592	-4.4158	0.0002	0.0053
2790021	VLDLR	-4.4151	0.0002	0.0053
2782125	SORBS1	4.4124	0.0002	0.0053
2759270		4.4116	0.0002	0.0053
2783850	ANKRD10	-4.4103	0.0002	0.0053
2769267	GRAMD4	4.4099	0.0002	0.0053
2768909	SGSM2	4.5383	0.0001	0.0046
2762484	DTD1	-4.4024	0.0002	0.0054
2796685	TBC1D24	-4.4019	0.0002	0.0054
2795165	TMEM151B	-4.4019	0.0002	0.0054
2799150		-4.4012	0.0002	0.0054
2781795	LFNG	4.5291	0.0001	0.0046
2773002	EIF2C3	4.3991	0.0002	0.0054
2779356		-4.3990	0.0002	0.0054
2788686	TAF7	-4.3977	0.0002	0.0054
2767588	PPP1R16B	4.3961	0.0002	0.0054
2795349	COG4	-4.3956	0.0002	0.0054
2762131	LOC418729	-4.3920	0.0002	0.0055
2771111	KIAA1462	4.3894	0.0002	0.0055
2769870	ABTB2	-4.3868	0.0002	0.0055
2786907	SLITRK2	4.3858	0.0002	0.0055
2779734		-4.3856	0.0002	0.0055
2776609	CALM1	-4.3833	0.0002	0.0055
2764716	ZC4H2	-4.6648	0.0001	0.0039
2798271	NFKBIE	-4.3809	0.0002	0.0055
2780372	RRP9	4.3786	0.0002	0.0056
2784942	EIF5	-4.3764	0.0002	0.0056
2757366		-4.3753	0.0002	0.0056
2778170		-4.3750	0.0002	0.0056

	gene_symbols	t	P.Value	adj.P.Val
2787172	TBC1D30	4.3747	0.0002	0.0056
2791737	MBNL1	-4.3744	0.0002	0.0056
2793246	RBBP6	-4.3731	0.0002	0.0056
2779582	EEFSEC	-4.3705	0.0002	0.0056
2770579	SETBP1	4.3694	0.0002	0.0056
2768482	LOC421379	-4.3639	0.0002	0.0057
2788446	DDX18	4.4897	0.0002	0.0050
2791228	TET2	4.3626	0.0002	0.0057
2777449	RGS7	-4.3611	0.0002	0.0057
2772221		-4.3602	0.0002	0.0057
2777663	SNTG1	4.3601	0.0002	0.0057
2793784	CD164	4.3598	0.0002	0.0057
2776924	TRIM37	4.3579	0.0002	0.0057
2764032	PSME4	4.3559	0.0002	0.0057
2761388		4.3549	0.0002	0.0057
2764477	GRSF1	-4.3540	0.0002	0.0057
2759273	TIMM9	-4.3511	0.0002	0.0058
2772541	UAP1	4.3506	0.0002	0.0058
2788296	TIMM22	-4.3467	0.0002	0.0058
2765642	BZW2	4.3466	0.0002	0.0058
2766194	NEDD1	-4.4711	0.0002	0.0051
2786998	TRIM9	4.3404	0.0002	0.0059
2799748	ARPC1A	4.3394	0.0002	0.0059
2772060	PHIP	-4.3357	0.0002	0.0059
2775757	CORO1C	4.3307	0.0002	0.0060
2761496	C7ORF20	-4.3300	0.0002	0.0060
2766425	KIAA0922	4.3273	0.0002	0.0060
2765228	SERPINB8	4.3260	0.0002	0.0060
2798136	CPSF6	4.3236	0.0002	0.0061
2759029	NCKIPSD	-4.3228	0.0002	0.0061
2788276	CAT	-4.3215	0.0002	0.0061
2790819	KDSR	-4.3201	0.0002	0.0061
2783529		-4.3169	0.0002	0.0061
2760929	EGR1	4.3156	0.0002	0.0061
2764353	ADRM1	4.3152	0.0002	0.0061
2757748	FAM43A	-4.4384	0.0002	0.0054
2798710	MCAT	-4.3142	0.0002	0.0061
2796232		-4.3138	0.0002	0.0061
2796507	MRAS	-4.3113	0.0002	0.0062
2786670	IRS2	4.4328	0.0002	0.0054
2765584	LMO7	4.3092	0.0002	0.0062
2758691	C14ORF102	-4.3069	0.0002	0.0062
2778924	C11ORF73	-4.4280	0.0002	0.0054
2758927	FOXP2	-4.3051	0.0002	0.0062
2758373		-4.3037	0.0002	0.0062
2790013	MED12	-4.3032	0.0002	0.0062
2793650	ARHGEF12	-4.7065	0.0001	0.0035
2759861	LRRTM1	-4.3023	0.0002	0.0062
2770808	LIFR	-4.3022	0.0002	0.0062
2774002	PALM2	-4.3008	0.0002	0.0062
2760941	SORBS1	4.2992	0.0002	0.0063
2776186		4.4196	0.0002	0.0055

	gene_symbols	t	P.Value	adj.P.Val
2776661	SMEK2	4.2975	0.0002	0.0063
2797534	PIK3C2A	-4.6991	0.0001	0.0036
2790643	A2BP1	-4.2962	0.0002	0.0063
2797200	UNC80	-4.2961	0.0002	0.0063
2761338	SYMENSTGUG00000010594	-4.2952	0.0002	0.0063
2777022	LANCL1	-4.2945	0.0002	0.0063
2757997	NCBP2	-4.2942	0.0002	0.0063
2782280	CIDEC	-4.4144	0.0002	0.0055
2778635	EFNB1	4.4095	0.0002	0.0056
2784580	CUGBP2-1	4.2877	0.0002	0.0064
2762434	R3HDM1	4.2856	0.0002	0.0064
2785965		-4.6844	0.0001	0.0036
2769862	KCNK5	4.4054	0.0002	0.0056
2779765	CALM1	-4.2837	0.0002	0.0064
2762153	MBD3	-4.2814	0.0002	0.0064
2788316	REV3L	-4.2803	0.0002	0.0064
2789296	SYMENSTGUG00000017925	-4.4000	0.0002	0.0056
2792014	COG4	-4.2794	0.0002	0.0064
2770372	CCT5	4.2773	0.0002	0.0065
2766554	RUFY2	-4.3975	0.0002	0.0057
2769066	UBE2A	4.2764	0.0002	0.0065
2783804	AKAP7	-4.2762	0.0002	0.0065
2772163	CEP170	4.2738	0.0003	0.0065
2774331	GSTO2	-4.2726	0.0003	0.0065
2757886	USP39	4.2726	0.0003	0.0065
2798687		-4.2722	0.0003	0.0065
2789659	MBNL1	-4.2708	0.0003	0.0065
2794031	HINT3	-4.2686	0.0003	0.0065
2791359	ILK	-4.2671	0.0003	0.0065
2781771	ARPP19	4.2665	0.0003	0.0065
2791679	SPAST	-4.2648	0.0003	0.0066
2769654	ADRM1	4.2643	0.0003	0.0066
2778341		-4.3832	0.0002	0.0058
2774236		-4.2628	0.0003	0.0066
2763421		4.2622	0.0003	0.0066
2763131	PKIA	-4.2620	0.0003	0.0066
2794006	PHF6	-4.2614	0.0003	0.0066
2769540	DRP2	-4.2606	0.0003	0.0066
2761540	SYMENSTGUG00000008883	-4.2593	0.0003	0.0066
2791485	B3GNT1	4.2569	0.0003	0.0066
2768156	SRGAP2	-4.3743	0.0002	0.0059
2784154	C9ORF72	-4.2547	0.0003	0.0066
2798907	ARPC1A	4.2545	0.0003	0.0066
2777569	URB1	4.2541	0.0003	0.0066
2799686	EGR1	4.2530	0.0003	0.0067
2760550	MNT	-4.2516	0.0003	0.0067
2770681	PSME4	4.2495	0.0003	0.0067
2770740	SLC25A5	4.2482	0.0003	0.0067
2771619	GRB10	-4.2479	0.0003	0.0067
2782469	P4HA1	-4.2479	0.0003	0.0067
2758109	BTF3L4	4.2478	0.0003	0.0067
2759909	PTPN9	4.3659	0.0002	0.0059

	gene_symbols	t	P.Value	adj.P.Val
2794642		-4.2477	0.0003	0.0067
2771851	PCMT1	-4.2469	0.0003	0.0067
2794826	CAPZA2	4.2464	0.0003	0.0067
2769373	IAPP	4.2450	0.0003	0.0067
2767938	SYMENSTGUG00000010884	-4.2448	0.0003	0.0067
2782762	PPP2R5C	4.2422	0.0003	0.0067
2761974		4.2418	0.0003	0.0067
2792098	ATIC	-4.2413	0.0003	0.0067
2782740	DEGS1	4.2409	0.0003	0.0067
2799403	ADPRHL2	-4.2403	0.0003	0.0067
2779261	IAPP	4.2397	0.0003	0.0067
2764928	ANKRD10	-4.2392	0.0003	0.0067
2799819	MAPK8IP1	4.2386	0.0003	0.0067
2788499	ING1	-4.6280	0.0001	0.0039
2771282	NETO1	4.2378	0.0003	0.0067
2789653	ARPP21	4.2353	0.0003	0.0068
2768154	TMEM189	-4.2325	0.0003	0.0068
2765196	EGR1	4.3456	0.0002	0.0061
2783840	C1ORF149	-4.2285	0.0003	0.0069
2777495	CPSF6	4.2273	0.0003	0.0069
2767052	DGKI	4.2260	0.0003	0.0069
2790406	PSMD9	-4.2260	0.0003	0.0069
2760378	NECAB1	4.2251	0.0003	0.0069
2764196	CSNK1G1	4.2250	0.0003	0.0069
2777694	EIF2C3	4.2238	0.0003	0.0069
2767412		-4.2230	0.0003	0.0069
2779068	KDSR	-4.2227	0.0003	0.0069
2764507	TMEM69	-4.2224	0.0003	0.0069
2768965	HS6ST1	4.2211	0.0003	0.0069
2761184		4.3348	0.0002	0.0062
2770786	NETO1	4.2185	0.0003	0.0069
2789322	NFYA	-4.2176	0.0003	0.0070
2771455	NAB1	4.2161	0.0003	0.0070
2795485	KIAA0895L	-4.2150	0.0003	0.0070
2792044		-4.2145	0.0003	0.0070
2799422	TIAL1	-4.2144	0.0003	0.0070
2757686	APOA1BP	-4.2139	0.0003	0.0070
2767010	MAP3K3	-4.2139	0.0003	0.0070
2758014	TPM2	4.3288	0.0002	0.0063
2777214		4.2127	0.0003	0.0070
2776955	XP_002194193.1	-4.2125	0.0003	0.0070
2794416	C20ORF4	-4.2118	0.0003	0.0070
2762832	PNPT1	4.2114	0.0003	0.0070
2769250		-4.2106	0.0003	0.0070
2758609	G3BP2	4.2105	0.0003	0.0070
2770348	FAF2	4.2095	0.0003	0.0070
2760266	TMX2	-4.2085	0.0003	0.0070
2771909	ISL1	4.2073	0.0003	0.0070
2767777	TRIM9	4.2069	0.0003	0.0070
2778696	CD164	4.2069	0.0003	0.0070
2774723	PHLDA1	-4.2046	0.0003	0.0070
2779171	DGKI	4.3195	0.0002	0.0063

	gene_symbols	t	P.Value	adj.P.Val
2793734	C1ORF174	-4.3173	0.0002	0.0064
2767704	HSPE1	-4.1977	0.0003	0.0071
2786351	BAZ2B	-4.1970	0.0003	0.0071
2786553	CALM1	-4.1961	0.0003	0.0071
2771978	CKS1B	-4.1960	0.0003	0.0071
2798315	COL11A1	-4.1955	0.0003	0.0071
2762497	SP9	-4.1953	0.0003	0.0071
2774619	ZBTB47	-4.1951	0.0003	0.0071
2788572	WNK1	4.1947	0.0003	0.0071
2778804	ARPC1A	4.1928	0.0003	0.0072
2791582	8-Mar	-4.1924	0.0003	0.0072
2778458	PDE7B	-4.5721	0.0001	0.0043
2793589	CRK	-4.1890	0.0003	0.0072
2789027	SLMO1	4.1879	0.0003	0.0072
2799449	UFD1L	-4.1876	0.0003	0.0072
2798506	H3F3B	4.1872	0.0003	0.0072
2772152	MRAS	-4.1871	0.0003	0.0072
2774845	XP_002194412.1	-4.1850	0.0003	0.0072
2764760	ARPP19	4.1849	0.0003	0.0072
2772187		-4.1843	0.0003	0.0072
2797762	SOD1	-4.1812	0.0003	0.0073
2758096		-4.1810	0.0003	0.0073
2794935		4.1801	0.0003	0.0073
2792561	R3HDM1	4.1797	0.0003	0.0073
2797173	ASB3	-4.1790	0.0003	0.0073
2786728	AAMP	-4.1785	0.0003	0.0073
2789561	CYGB	-4.1775	0.0003	0.0073
2766393	SYMENSTGUG00000017248	-4.1772	0.0003	0.0073
2778642	ZC3H7A	-4.1765	0.0003	0.0073
2771728	ST3GAL3	-4.1763	0.0003	0.0073
2775442		-4.1755	0.0003	0.0073
2771059	PPP3CA	-4.1731	0.0003	0.0073
2775971		-4.1715	0.0003	0.0073
2788436	PSME4	4.1702	0.0003	0.0074
2762882	WNT5A	-4.5448	0.0001	0.0046
2786081	ZMYND8	-4.1644	0.0003	0.0074
2782069	PPP3CA	-4.1644	0.0003	0.0074
2781833	UBE2A	4.1644	0.0003	0.0074
2798171	SLC2A3	4.1634	0.0003	0.0075
2789983	MRPL38	-4.1595	0.0003	0.0075
2793061	BRI3	-4.1586	0.0003	0.0075
2772335		-4.5305	0.0001	0.0046
2770795		-4.1571	0.0003	0.0075
2767613	GRSF1	-4.1545	0.0003	0.0076
2791675	KCNAB2	-4.1526	0.0003	0.0076
2786933	XP_002195769.1	-4.5234	0.0001	0.0047
2798139	EGR1	4.1515	0.0003	0.0076
2778788	SF3B3	-4.1508	0.0003	0.0076
2798033	ANKMY2	4.1506	0.0003	0.0076
2771744	RAD51	-4.5190	0.0001	0.0047
2775457	SRP54	4.1427	0.0004	0.0077
2758457	NUS1	4.1423	0.0004	0.0077

	gene_symbols	t	P.Value	adj.P.Val
2770876	ZNF827	-4.1420	0.0004	0.0077
2795412		4.1415	0.0004	0.0077
2779079		4.1407	0.0004	0.0077
2774479		-4.2472	0.0003	0.0069
2794710	UAP1	4.1364	0.0004	0.0078
2775665	CSNK1G1	4.1344	0.0004	0.0079
2790167	PROSC	-4.1341	0.0004	0.0079
2789668	NSUN2	4.1335	0.0004	0.0079
2775059	ZMYND8	-4.1327	0.0004	0.0079
2778119	SPAST	-4.1317	0.0004	0.0079
2765155	GNG3	-4.1309	0.0004	0.0079
2758972	A2BP1	-4.1304	0.0004	0.0079
2776633	ZBTB6	-4.1295	0.0004	0.0079
2760504	WDR43	4.1277	0.0004	0.0079
2774956	A2BP1	-4.1241	0.0004	0.0080
2793400	BNIP3L	-4.1240	0.0004	0.0080
2764165	C1ORF55	4.1239	0.0004	0.0080
2791005	NCOA2	-4.1228	0.0004	0.0080
2783673	PPP2CA	4.1216	0.0004	0.0080
2758495	PAM	4.1211	0.0004	0.0080
2760818	TLE2	-4.4853	0.0002	0.0050
2780454	HINT3	-4.1200	0.0004	0.0080
2769658	KIAA0922	4.1200	0.0004	0.0080
2795509	TNRC18	-4.1199	0.0004	0.0080
2780498	GRM4	-4.1168	0.0004	0.0081
2771669	NXT2	-4.1167	0.0004	0.0081
2764958	PLK2	4.1157	0.0004	0.0081
2767407	TIMM9	-4.1144	0.0004	0.0081
2795999		4.1116	0.0004	0.0081
2766120		-4.1114	0.0004	0.0081
2779568	RNF126	4.1111	0.0004	0.0081
2790166	SYT4	4.1104	0.0004	0.0081
2790872		-4.1097	0.0004	0.0081
2796971	SYMENSTGUG00000002805	4.2180	0.0003	0.0072
2783316	SYNE1	4.1082	0.0004	0.0082
2792888		-4.1073	0.0004	0.0082
2766925	SERTAD2	4.2151	0.0003	0.0072
2764699		4.1033	0.0004	0.0082
2793679	ACTB	4.0985	0.0004	0.0083
2778590	C14ORF159	-4.0983	0.0004	0.0083
2793867	EIF2AK3	-4.2049	0.0003	0.0073
2763203	SERTAD2	4.2048	0.0003	0.0073
2793588	LFNG	4.2032	0.0003	0.0073
2777792		-4.0940	0.0004	0.0084
2777335	NTRK2	4.0927	0.0004	0.0084
2768420	C10ORF2	4.0917	0.0004	0.0084
2793121	MYL12A	4.0885	0.0004	0.0085
2790709		-4.0877	0.0004	0.0085
2794597	RIMS1	4.0866	0.0004	0.0085
2794783	CACNB4	4.0860	0.0004	0.0085
2762776	MBNL1	-4.0848	0.0004	0.0085
2780956	PPP2R2A	4.0842	0.0004	0.0085

	gene_symbols	t	P.Value	adj.P.Val
2782348	2/2/11	-4.0837	0.0004	0.0085
2777085	C9ORF125	-4.4378	0.0002	0.0054
2771000	CAT	-4.0807	0.0004	0.0086
2778030	ARHGEF18	-4.0802	0.0004	0.0086
2787522	CXCL14	4.0792	0.0004	0.0086
2779867	PPP3CA	-4.0785	0.0004	0.0086
2794062	FBXL10	-4.0783	0.0004	0.0086
2790112	ARPP-21	4.0758	0.0004	0.0086
2776371	ATG5	-4.0753	0.0004	0.0086
2796848	NSUN2	4.0743	0.0004	0.0087
2769403	NLK	4.0739	0.0004	0.0087
2776264	POLR1D-2	-4.0734	0.0004	0.0087
2769251	LFNG	4.1789	0.0003	0.0076
2797711	DEGS1	4.0714	0.0004	0.0087
2788994	SLC6A6	4.0714	0.0004	0.0087
2796957	NCKIPSD	-4.0712	0.0004	0.0087
2776398	MYL12A	4.0693	0.0004	0.0087
2781578	CEBPZ	-4.0683	0.0004	0.0087
2769488	CDK8	4.0662	0.0004	0.0088
2777640	CHST11	4.0650	0.0004	0.0088
2775376	PPP2CA	4.0643	0.0004	0.0088
2781412	NAA25	4.0639	0.0004	0.0088
2797915	NUCKS1	-4.0629	0.0004	0.0088
2759791	MBNL1	-4.0604	0.0004	0.0088
2765858	DGKZ	4.0604	0.0004	0.0088
2770042	TAOK1	-4.0558	0.0004	0.0089
2797569	C3ORF37	-4.0554	0.0004	0.0089
2799527	ASAP1	4.0538	0.0004	0.0090
2784960	AOF1	4.0517	0.0004	0.0090
2785785	PDCD4	-4.0505	0.0004	0.0090
2779542	A2BP1	-4.0493	0.0004	0.0090
2779804	RPP38	4.0491	0.0004	0.0090
2796511	FAM110B	4.0486	0.0004	0.0090
2772768	MRPL17	-4.0452	0.0005	0.0091
2784519		-4.0451	0.0005	0.0091
2779708	ATP1B4-2	-4.0447	0.0005	0.0091
2796790	XRN1	4.0444	0.0005	0.0091
2774151	PSMD11	4.0440	0.0005	0.0091
2760092	TBC1D30	4.0426	0.0005	0.0091
2799802	ZNF326	4.0422	0.0005	0.0091
2798251	SLC36A1	-4.0418	0.0005	0.0091
2784228		-4.0415	0.0005	0.0091
2794048		-4.3897	0.0002	0.0057
2789142	RANBP9	-4.0383	0.0005	0.0092
2790328	FBXO21	-4.0359	0.0005	0.0092
2778704	HS6ST1	4.0356	0.0005	0.0092
2762767	SIK2	4.0352	0.0005	0.0092
2757524	DCLK1	4.1376	0.0004	0.0081
2770677		4.0341	0.0005	0.0092
2795042	TMEM93	-4.0339	0.0005	0.0092
2779396	FAM134C	-4.0311	0.0005	0.0093
2765929	BOC	4.1338	0.0004	0.0082

	gene_symbols	t	P.Value	adj.P.Val
2775490	LUC7L2	4.0302	0.0005	0.0093
2795268	DEGS1	4.0288	0.0005	0.0093
2793068	FOS	4.0285	0.0005	0.0093
2784726	IQGAP1	-4.0269	0.0005	0.0094
2762378	NR1D2	-4.0230	0.0005	0.0094
2785409		-4.3680	0.0002	0.0059
2793758	TTC39C	-4.0225	0.0005	0.0094
2796072		-4.3678	0.0002	0.0059
2771505		-4.0223	0.0005	0.0094
2764412	KIAA0895L	-4.0221	0.0005	0.0094
2757840	TET2	4.0170	0.0005	0.0095
2772289		4.1191	0.0004	0.0084
2793383	CLIC3	-4.3596	0.0002	0.0060
2768121		-4.0145	0.0005	0.0096
2799812	FTSJD2	-4.0143	0.0005	0.0096
2761381	RIMS1	4.0119	0.0005	0.0096
2789532	MNAT1	-4.0098	0.0005	0.0097
2795671	SYNCRIP	4.0093	0.0005	0.0097
2775054	KIAA1107	4.0083	0.0005	0.0097
2794442	ST5	-4.0060	0.0005	0.0097
2776399	ATIC	-4.0057	0.0005	0.0097
2799175	TSC22D3	-4.0055	0.0005	0.0097
2784941		-4.0050	0.0005	0.0097
2777265	TGFBR1	-4.0044	0.0005	0.0097
2795286		4.0024	0.0005	0.0098
2782981	TESK1	-4.0015	0.0005	0.0098
2776168	H3F3B	4.0015	0.0005	0.0098
2764612	SESN2	-3.9997	0.0005	0.0098
2761142		-4.3394	0.0002	0.0062
2773372	HSPE1	-3.9973	0.0005	0.0099
2778819	HARS	-3.9971	0.0005	0.0099
2758807	CCT2	3.9971	0.0005	0.0099
2792353	EGR3	3.9942	0.0005	0.0099
2763982		3.9935	0.0005	0.0099
2785856	PHF20	3.9934	0.0005	0.0099
2784800	CARS	3.9921	0.0005	0.0099
2781249	LONRF1	-4.3316	0.0002	0.0062
2783701	MMACHC	-4.0925	0.0004	0.0088
2771230	RAB8B	-3.9907	0.0005	0.0099
2765762	RNF126	3.9894	0.0005	0.0100
2763117	KIAA0895L	-3.9881	0.0005	0.0100
2786368	NEDD4L	-3.9877	0.0005	0.0100
2787571	KCTD21	-4.3259	0.0002	0.0063
2774275	TMCC3	-3.9860	0.0005	0.0100
2767578	RAC1	-3.9857	0.0005	0.0100
2780462	PPP2CA	3.9848	0.0005	0.0100
2760613	MPST	-3.9833	0.0005	0.0100
2763765	ZNF398	-3.9827	0.0005	0.0101
2763602	ING3	-3.9822	0.0005	0.0101
2776961	C17ORF28	-3.9813	0.0005	0.0101
2781121	DEGS1	3.9802	0.0005	0.0101
2784723	SLC25A5	3.9801	0.0005	0.0101

	gene_symbols	t	P.Value	adj.P.Val
2770254	UBXN4	3.9795	0.0005	0.0101
2790064	TLN2	3.9787	0.0005	0.0101
2791546		-4.3158	0.0002	0.0064
2784461		-3.9774	0.0005	0.0101
2772991	ZMYND8	-3.9764	0.0005	0.0101
2790524	NLK	3.9756	0.0005	0.0101
2764563	CCDC85C	-3.9756	0.0005	0.0101
2785558		3.9731	0.0005	0.0102
2793464	ROMO1	-3.9727	0.0005	0.0102
2781060	NRG2	-3.9714	0.0005	0.0102
2763871	KCTD15	-4.3059	0.0002	0.0065
2780018	CKB	-3.9684	0.0005	0.0103
2795785	TNRC6A	-3.9674	0.0005	0.0103
2795889	MARK1	3.9665	0.0006	0.0103
2770413	TMEM171	-4.3000	0.0003	0.0065
2791747	HNRPDL	3.9643	0.0006	0.0104
2761122	BRD3	-3.9618	0.0006	0.0104
2796541	C1ORF91	-3.9617	0.0006	0.0104
2777946	DMAP1	3.9616	0.0006	0.0104
2770519	CSNK1G1	3.9604	0.0006	0.0104
2760143	MEIS1	-4.2934	0.0003	0.0066
2773637	MFSD10	-3.9586	0.0006	0.0105
2788003	BTAF1	-3.9585	0.0006	0.0105
2787672	STRA13	-3.9570	0.0006	0.0105
2763818	TARS	3.9569	0.0006	0.0105
2794984	FOS	3.9567	0.0006	0.0105
2776469	RBMX	3.9545	0.0006	0.0105
2764759		-3.9539	0.0006	0.0105
2778340	FBXO33	-3.9537	0.0006	0.0105
2783241		-3.9535	0.0006	0.0105
2784591	DEGS1	3.9525	0.0006	0.0105
2790563	HNRPDL	3.9522	0.0006	0.0105
2781296	DGCR6	-3.9521	0.0006	0.0105
2780909	EGR1	3.9519	0.0006	0.0105
2774169	PCSK1	3.9512	0.0006	0.0105
2762508	S100B	-3.9511	0.0006	0.0105
2768405		-3.9476	0.0006	0.0106
2773026	KIAA0753	-3.9474	0.0006	0.0106
2770510	DDX26B	-4.2751	0.0003	0.0067
2797664	ATP5D	-3.9445	0.0006	0.0107
2792629	MAN1C1	-3.9441	0.0006	0.0107
2772301	CPNE1	-3.9437	0.0006	0.0107
2784084	KIAA1377	-4.0404	0.0005	0.0096
2777202	NONO	-3.9426	0.0006	0.0107
2788042	SYMENSTGUG00000017707	3.9421	0.0006	0.0107
2795928	C3ORF39	-3.9416	0.0006	0.0107
2764237		3.9406	0.0006	0.0107
2765620	CALM1	-3.9400	0.0006	0.0107
2787217	AMOTL2	3.9398	0.0006	0.0107
2778810	POLD3	-3.9398	0.0006	0.0107
2785110	KCNS2	-3.9390	0.0006	0.0107
2796651	LYRM2	-3.9389	0.0006	0.0107

	gene_symbols	t	P.Value	adj.P.Val
2762493	MBTPS1	-3.9363	0.0006	0.0108
2761250	LRRTM1	-3.9356	0.0006	0.0108
2765587	SPTLC1	-3.9319	0.0006	0.0109
2771334	AMOTL2	3.9314	0.0006	0.0109
2771523	ZC3H7A	-3.9311	0.0006	0.0109
2770545	MAN2B2	3.9302	0.0006	0.0109
2779691		-3.9290	0.0006	0.0109
2795102	SOD1	-3.9290	0.0006	0.0109
2789425	CPSF6	3.9288	0.0006	0.0109
2776830	TRIM3	-3.9278	0.0006	0.0109
2775338	RORA	-3.9269	0.0006	0.0109
2780819	C13ORF37	-4.2525	0.0003	0.0069
2761990	FOS	3.9231	0.0006	0.0110
2791277	BAIAP2	3.9217	0.0006	0.0111
2785974	DEGS1	3.9215	0.0006	0.0111
2767265	COIL	-3.9209	0.0006	0.0111
2774817	DDB2	-3.9204	0.0006	0.0111
2766356	URB1	-3.9199	0.0006	0.0111
2777530		3.9199	0.0006	0.0111
2760985	MAP3K7	3.9197	0.0006	0.0111
2760138	MYL12A	3.9194	0.0006	0.0111
2795273	MXD4	-3.9189	0.0006	0.0111
2772269		-3.9184	0.0006	0.0111
2783112		4.0140	0.0005	0.0100
2761779	C4ORF44	3.9156	0.0006	0.0111
2776586		-4.3597	0.0002	0.0063
2763189	RAP2A	3.9153	0.0006	0.0111
2799842	SLC38A2	-3.9143	0.0006	0.0111
2757942	HNRNPH3	3.9142	0.0006	0.0111
2776227	KCNG1	-4.0092	0.0005	0.0100
2776676	OAZ1	-3.9136	0.0006	0.0111
2784982	MSH4	-3.9119	0.0006	0.0112
2774715		-3.9116	0.0006	0.0112
2776992	STARD5	3.9094	0.0006	0.0112
2783887	IFT140	-3.9082	0.0006	0.0113
2787779	XP_002194193.1	-3.9079	0.0006	0.0113
2787324	DLGAP2	3.9076	0.0006	0.0113
2766929	RIMS1	3.9057	0.0006	0.0113
2788903	MAFF	3.9045	0.0006	0.0113
2776631	FAM8A1	-4.2267	0.0003	0.0071
2772228	HDAC4	3.9019	0.0006	0.0114
2792698	EFHA2	-3.9014	0.0007	0.0114
2774778	CCT2	3.9012	0.0007	0.0114
2785359	PDCL	3.9011	0.0007	0.0114
2767712	RANBP2	3.9009	0.0007	0.0114
2784020	SS18L1	-3.9003	0.0007	0.0114
2788581	DPH1	3.8995	0.0007	0.0114
2771696	TRIB1	3.8993	0.0007	0.0114
2777808	SOD1	-3.8990	0.0007	0.0114
2764333	MEF2C	-3.8989	0.0007	0.0114
2759606	MRAS	-3.8987	0.0007	0.0114
2792865	DGKZ	3.8982	0.0007	0.0114

	gene_symbols	t	P.Value	adj.P.Val
2769367	RRAD	3.8978	0.0007	0.0114
2790457	CD164	3.8961	0.0007	0.0114
2791722	ACOX1	-3.8950	0.0007	0.0114
2774217	RNF145	-3.8948	0.0007	0.0114
2765596	EGR3	3.8944	0.0007	0.0114
2788820		3.8937	0.0007	0.0114
2765954	ETV3	3.8932	0.0007	0.0115
2761379	TAGLN3	-3.8916	0.0007	0.0115
2788801	MAFK	3.8911	0.0007	0.0115
2765500	UBE4B	-3.8910	0.0007	0.0115
2783807	MXD4	-3.8907	0.0007	0.0115
2788460		3.8875	0.0007	0.0116
2767667	DNAJB14	-3.8868	0.0007	0.0116
2783957		-3.8863	0.0007	0.0116
2785935		3.8855	0.0007	0.0116
2773541	ACBD3	3.8849	0.0007	0.0116
2788759	RAD54L	-3.8813	0.0007	0.0117
2759928		3.8803	0.0007	0.0117
2784846	PSPC1	3.8803	0.0007	0.0117
2768793	WDR48	-3.8793	0.0007	0.0117
2773776	PTPN2	3.8789	0.0007	0.0117
2768834	FRMD3	-3.8776	0.0007	0.0117
2796602	EXTL3	3.8771	0.0007	0.0117
2794030	MEAF6	-3.8759	0.0007	0.0118
2774019	PLCXD3	-3.8747	0.0007	0.0118
2780950		-3.8741	0.0007	0.0118
2778222	MRPL36	-3.8738	0.0007	0.0118
2771032	KCNS1	-3.8722	0.0007	0.0118
2767622	HNRNPK	3.8717	0.0007	0.0118
2757961	N6AMT2	-3.8713	0.0007	0.0118
2793262	SHISA5	3.8712	0.0007	0.0118
2772466	JARID2	3.8706	0.0007	0.0118
2782898	TOMM34	-3.8702	0.0007	0.0118
2788039	SLC2A3	3.8687	0.0007	0.0119
2767880		-4.1848	0.0003	0.0075
2774759	ZNF830	3.8642	0.0007	0.0120
2774239	RNF126	3.8642	0.0007	0.0120
2770244		-4.1795	0.0003	0.0076
2799872	C3ORF37	-3.8632	0.0007	0.0120
2785046		-3.8616	0.0007	0.0120
2775282	XP_002188032.1	-4.1757	0.0003	0.0076
2776895	FECH	-3.8602	0.0007	0.0121
2787724	DLX1	-3.8584	0.0007	0.0121
2776580	TANC2	3.8579	0.0007	0.0121
2782804	FAR1	-3.8579	0.0007	0.0121
2763084	KLHDC4	-3.8570	0.0007	0.0121
2769542		-3.8564	0.0007	0.0121
2791860	RAB14	-3.8555	0.0007	0.0121
2783295		3.9475	0.0006	0.0110
2763990	LMBRD1	-3.8552	0.0007	0.0121
2787113	UQCR11	-4.1689	0.0004	0.0077
2787584	PRRG3	3.8546	0.0007	0.0122

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	gene_symbols	t	P.Value	adj.P.Val
2793338	CLCA2	-3.8541	0.0007	0.0122
2794772	KCNC1	-3.8517	0.0007	0.0122
2768242	FOS	3.8510	0.0007	0.0122
2766099		3.8497	0.0007	0.0123
2770698	PTPN2	3.8488	0.0007	0.0123
2760750	ACTC1	3.8484	0.0007	0.0123
2761222	STAG2	-3.8467	0.0007	0.0123
2796621	CAPZB	3.8408	0.0008	0.0125
2780743	NETO1	3.8403	0.0008	0.0125
2768874	LMO7	3.8379	0.0008	0.0125
2767917	ARIH2	3.8377	0.0008	0.0125
2777314	CTCF	-3.8373	0.0008	0.0125
2773181	SYTL4	-3.8371	0.0008	0.0125
2782972	P2RY1	-3.8368	0.0008	0.0125
2769944	R3HDM2	3.8366	0.0008	0.0125
2763881		-3.8363	0.0008	0.0125
2794561	IKBKAP	3.9269	0.0006	0.0113
2795222	RAB32	-3.8360	0.0008	0.0125
2766382	CAT	-3.8348	0.0008	0.0126
2762252	SYT4	3.8335	0.0008	0.0126
2781113		-3.8330	0.0008	0.0126
2794705	TCF12	-3.8325	0.0008	0.0126
2785245	TSC22D3	-3.8309	0.0008	0.0126
2761643	GPM6B	-3.8276	0.0008	0.0127
2765493	RAC1	3.8274	0.0008	0.0127
2766989	DCUN1D5	3.8271	0.0008	0.0127
2766411	JARID2	3.8267	0.0008	0.0127
2783018	WDR5	-3.8267	0.0008	0.0127
2762070	CORO1C	3.8260	0.0008	0.0127
2777965	DDX3X	3.8253	0.0008	0.0127
2772210	SEC61A1	3.8208	0.0008	0.0129
2770022		3.9104	0.0007	0.0116
2776438	CAMK2A	-3.8197	0.0008	0.0129
2799583	TCP11L2	-3.8194	0.0008	0.0129
2771736	CTCF	-3.8182	0.0008	0.0129
2798344	H3F3B	3.8175	0.0008	0.0129
2781913	FEZ1	-4.2351	0.0003	0.0073
2786705	IMPAD1	-3.8172	0.0008	0.0129
2778816	GAD2	3.8166	0.0008	0.0129
2764208	NCOA7	-3.8166	0.0008	0.0129
2789510	PMEPA1	-3.8165	0.0008	0.0129
2789187		-3.8158	0.0008	0.0129
2770807	UBE2D3	3.8153	0.0008	0.0129
2768692	NSBP1	-3.8148	0.0008	0.0129
2790938	KIAA1919	-3.8146	0.0008	0.0129
2773019		-3.8145	0.0008	0.0129
2771678	PDE4DIP	-3.8142	0.0008	0.0129
2789562	BMI1	-3.8139	0.0008	0.0129
2783924	KLF11	-3.9029	0.0007	0.0117
2786451	WASF3	-3.8135	0.0008	0.0129
2792707		3.8123	0.0008	0.0130
2775697	TLN2	3.8121	0.0008	0.0130

	gene_symbols	t	P.Value	adj.P.Val
2771567	PCOLCE2	-3.8115	0.0008	0.0130
2784266		3.8110	0.0008	0.0130
2784707	PCSK1	3.8102	0.0008	0.0130
2796745	NKRF	3.8101	0.0008	0.0130
2789645		-3.8099	0.0008	0.0130
2760053	PTCH1	-3.8097	0.0008	0.0130
2786734	PLK2	3.8982	0.0007	0.0118
2793549	PMEPA1	-3.8059	0.0008	0.0131
2799516	C1ORF149	-3.8054	0.0008	0.0131
2758365		-3.8052	0.0008	0.0131
2784975	DNAJB14	-3.8049	0.0008	0.0131
2763042	HS6ST1	3.8037	0.0008	0.0131
2775574	TMEM8B	3.8020	0.0008	0.0132
2790230		-4.1057	0.0004	0.0086
2778564	TMEM5	-3.8001	0.0008	0.0132
2791723	SSB	3.7988	0.0008	0.0132
2758200	TLN2	3.7986	0.0008	0.0132
2770866		3.7985	0.0008	0.0132
2786886	NDUFAF2	-3.7982	0.0008	0.0132
2757750		3.7974	0.0008	0.0133
2781241		-3.8857	0.0007	0.0120
2773244	MIPEP	3.7949	0.0009	0.0133
2787716	FAM109B	-3.7931	0.0009	0.0134
2777650	FAM46A	3.7927	0.0009	0.0134
2783620	RCBTB1	-3.7926	0.0009	0.0134
2766245	XP_002194193.1	-3.7925	0.0009	0.0134
2761600	PHC3	-3.7922	0.0009	0.0134
2760721	KCTD1	-3.7914	0.0009	0.0134
2769117	AP4E1	-3.7912	0.0009	0.0134
2775397	EFHA2	-3.7899	0.0009	0.0134
2762101	PPP2CA	3.7898	0.0009	0.0134
2795540	NCOA7	-3.7882	0.0009	0.0134
2765066	NUP160	-3.7879	0.0009	0.0134
2761604	MRAS	-3.7864	0.0009	0.0135
2788487	SS18L1	-3.7856	0.0009	0.0135
2781827		3.8733	0.0007	0.0122
2759348	ACTC1	3.7837	0.0009	0.0135
2784972	MAGI2	-3.7825	0.0009	0.0136
2764288	OXNAD1	-3.7824	0.0009	0.0136
2782847	POLD3	-3.7817	0.0009	0.0136
2758377	LOC421379	-3.7814	0.0009	0.0136
2781470	CPEB3	-3.7814	0.0009	0.0136
2760783	HS6ST1	3.7791	0.0009	0.0136
2764187	PCNX	3.7787	0.0009	0.0136
2781139	GTLF3B	-3.7785	0.0009	0.0136
2799963	PPP2R2A	3.7763	0.0009	0.0137
2777799	DDX3X	3.7743	0.0009	0.0138
2794601	DEGS1	3.7737	0.0009	0.0138
2797198		-3.7733	0.0009	0.0138
2762108		3.8597	0.0008	0.0125
2796559	RPRD1B	-3.7709	0.0009	0.0138
2761526	UQCRQ	-3.7704	0.0009	0.0139

	gene_symbols	t	P.Value	adj.P.Val
2796119	PM20D1	-3.7681	0.0009	0.0139
2795588	RBBP6	-3.7665	0.0009	0.0140
2768230		-3.7649	0.0009	0.0140
2787185	ZBTB44	-3.8473	0.0008	0.0127
2761780	TMEM135	-3.7607	0.0009	0.0141
2776447	PCSK1	3.7604	0.0009	0.0141
2757259	ARPC1A	3.7587	0.0009	0.0142
2764531	MAFK	3.7575	0.0009	0.0142
2796076	LBH	-4.0538	0.0005	0.0093
2771860	C15ORF40	-3.7564	0.0009	0.0142
2796231	DPF3	-3.7552	0.0009	0.0143
2797251	PTPN5	3.7540	0.0009	0.0143
2763279		3.7539	0.0009	0.0143
2797751	RCCD1	-3.7518	0.0010	0.0144
2762909		-3.7509	0.0010	0.0144
2783698	PDE7B	-3.7506	0.0010	0.0144
2797417	RAB8B	-3.7496	0.0010	0.0144
2761427	PPP3CA	-3.7484	0.0010	0.0145
2760582	DSTN	3.7455	0.0010	0.0145
2781021	PNLDC1	-3.7446	0.0010	0.0146
2757869	RYBP	-3.7432	0.0010	0.0146
2766558	IRF2BP2	3.7426	0.0010	0.0146
2759896	ING2	3.7419	0.0010	0.0146
2772427	FGD4	-3.7411	0.0010	0.0146
2795667	CUGBP2-1	3.7404	0.0010	0.0147
2780015	STARD5	3.7390	0.0010	0.0147
2760893	THAP4	-3.7388	0.0010	0.0147
2796196	CUGBP2-1	3.7382	0.0010	0.0147
2767106	NKRF	3.7379	0.0010	0.0147
2763308	AFF4	3.7375	0.0010	0.0147
2799118	H3F3B	3.7371	0.0010	0.0147
2781759	C7ORF20	-3.7371	0.0010	0.0147
2781026	FAM84A	-3.8209	0.0008	0.0132
2761155	SLC2A3	3.8206	0.0008	0.0132
2780400	DYNC1LI2	-3.7342	0.0010	0.0148
2789355	ROCK2	3.7328	0.0010	0.0148
2792389	PDXK	3.7323	0.0010	0.0148
2792264	LRRN3	-4.0246	0.0005	0.0098
2757297		-3.7315	0.0010	0.0149
2796249		3.7296	0.0010	0.0149
2761858		-4.0200	0.0005	0.0099
2761949	PKIA	-3.7261	0.0010	0.0150
2788177	DUSP11	-3.8104	0.0009	0.0134
2795951	SAAL1	-3.7257	0.0010	0.0150
2758289		3.7251	0.0010	0.0150
2774345	SFRP1	-4.0162	0.0005	0.0099
2793638	TNFAIP2	-3.7249	0.0010	0.0150
2776080	CKB	-3.7242	0.0010	0.0151
2787972	XP_002188089.1	-3.7240	0.0010	0.0151
2793958	CRTC1	-3.8066	0.0009	0.0135
2760688	SYMENSTGUG00000017592	-3.7221	0.0010	0.0151
2762006	RMND1	-3.7212	0.0010	0.0151

	gene_symbols	t	P.Value	adj.P.Val
2762431	KPNA4	-3.7208	0.0010	0.0151
2778588	NONO	-3.7206	0.0010	0.0151
2769892	NFRKB	-3.7203	0.0010	0.0151
2788787	C22ORF13	-3.7202	0.0010	0.0151
2759914	EIF2B3	3.7179	0.0010	0.0152
2780683	PTPN5	3.7175	0.0010	0.0152
2792906	SLC25A5	3.7156	0.0010	0.0153
2772345	AKTIP	-3.7148	0.0010	0.0153
2782688	SEC11A	3.7148	0.0010	0.0153
2795757	VMA21	-3.7110	0.0011	0.0154
2783692	SLC2A3	3.7107	0.0011	0.0154
2766224	SMEK2	3.7104	0.0011	0.0154
2763598		3.7089	0.0011	0.0155
2794177	BCL7A	-3.7089	0.0011	0.0155
2773611	PPP1R12A	3.7060	0.0011	0.0155
2773913	SOAT1	-3.7060	0.0011	0.0155
2792977	SYT4	3.7060	0.0011	0.0155
2770090	NUP153	3.7039	0.0011	0.0156
2784903	TET2	3.7029	0.0011	0.0156
2777132	CHUK	-3.7026	0.0011	0.0156
2768198	GTPBP2	-3.7026	0.0011	0.0156
2766081	PTPRT	-3.7023	0.0011	0.0156
2785784	RB1CC1	-3.7021	0.0011	0.0156
2772338	XRN1	3.7007	0.0011	0.0156
2767457	SFPQ	3.6975	0.0011	0.0157
2799523	ZBED4	3.6954	0.0011	0.0158
2771687	TMEM229B	-3.6931	0.0011	0.0159
2757132		3.6927	0.0011	0.0159
2772454	SMAD7	3.6926	0.0011	0.0159
2765602	CEP57	3.6925	0.0011	0.0159
2758137		-3.6895	0.0011	0.0160
2793144		3.6892	0.0011	0.0160
2799703	CD2	3.6887	0.0011	0.0160
2770055	MAF	3.6879	0.0011	0.0160
2766815	TLK1	-3.6876	0.0011	0.0160
2790389	H3F3B	3.6875	0.0011	0.0160
2765917	AKAP7	-3.9718	0.0006	0.0106
2786171	UBE2A	3.6866	0.0011	0.0160
2799588	RPS6KC1	-3.6860	0.0011	0.0160
2766610		-3.6833	0.0011	0.0161
2763138	TBC1D15	-3.6830	0.0011	0.0161
2764631	HMG20A	-3.6828	0.0011	0.0161
2780832		-3.7639	0.0010	0.0146
2779293		-3.6810	0.0011	0.0162
2790862	PCMT1	-3.6798	0.0011	0.0162
2782508	RCAN2	3.6792	0.0011	0.0163
2796452	SLTM	3.6765	0.0012	0.0163
2784174	ZNF462	-3.7580	0.0010	0.0147
2772403	KCNC1	-3.6760	0.0012	0.0164
2762675		3.7572	0.0010	0.0147
2774375	FAM44B	-3.9584	0.0006	0.0108
2774468	PIGU	3.6732	0.0012	0.0164

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	gene_symbols	t	P.Value	adj.P.Val
2772733		3.6703	0.0012	0.0165
2768312	YTHDF3	3.6702	0.0012	0.0165
2763188		3.6701	0.0012	0.0165
2772096	CUGBP2-1	3.6700	0.0012	0.0165
2774586	ZC3H6	-3.6699	0.0012	0.0165
2794712	TSR1	3.6674	0.0012	0.0166
2764679	PITPNM1	3.6671	0.0012	0.0166
2784979	RIMS2	-3.6667	0.0012	0.0166
2786037	CPEB3	-3.6662	0.0012	0.0166
2771510	TNRC18	-3.6653	0.0012	0.0166
2771009	BAIAP2	3.6642	0.0012	0.0167
2769204	KBTBD11	3.6627	0.0012	0.0167
2797242	C16ORF62	-3.6615	0.0012	0.0167
2768433	CCT8	3.6613	0.0012	0.0167
2766721	TAF4	-3.6606	0.0012	0.0167
2783016	CKB	-3.6606	0.0012	0.0167
2757433	SOX4	-3.6602	0.0012	0.0168
2787178	TOMM7	-3.9400	0.0006	0.0111
2790965	PBP	-3.6593	0.0012	0.0168
2788569	FAM120A	3.6576	0.0012	0.0168
2792143	RCJMB04_3A6	-3.6574	0.0012	0.0168
2768644	TMEM120B	3.6561	0.0012	0.0169
2776824	TNRC6C	-3.6548	0.0012	0.0169
2777549	LRRC4C	3.6511	0.0012	0.0171
2768364	RPRD1A	3.6492	0.0012	0.0171
2760594	CHST1	3.7290	0.0011	0.0155
2771564	C10ORF118	-3.6489	0.0012	0.0171
2782134	TBL1XR1	-3.6485	0.0012	0.0171
2770029	CHRAC1	-3.7282	0.0011	0.0155
2771911		-3.6478	0.0012	0.0171
2788924	EXT2	-3.6476	0.0012	0.0171
2778504	TAOK1	-3.6470	0.0012	0.0172
2761679	FAM117B	-3.6467	0.0012	0.0172
2767871	ZNF622	-3.6462	0.0012	0.0172
2759646	PPP2R5C	3.6461	0.0012	0.0172
2768342	RUFY2	-3.6452	0.0012	0.0172
2789196	TSC22D1	-3.6447	0.0012	0.0172
2779411	STIL	-3.6441	0.0012	0.0172
2773470	AP1S2	-3.6425	0.0013	0.0173
2798748	RAD51C	-3.6420	0.0013	0.0173
2769235	RRN3	3.6410	0.0013	0.0173
2796237	GAD2	3.6406	0.0013	0.0173
2783849	SEC63	-3.6393	0.0013	0.0173
2799344		-3.6383	0.0013	0.0174
2777722	ZYG11A	-3.6378	0.0013	0.0174
2775003	TMEM8B	3.6373	0.0013	0.0174
2781362	LBH	-3.9113	0.0007	0.0116
2781423	ETF1	3.6346	0.0013	0.0175
2763718	CSRNP3	-3.8065	0.0009	0.0141
2775160	PPP3CA	-3.6338	0.0013	0.0175
2783647	RHPN1	3.6337	0.0013	0.0175
2773729	STMN2	-3.6305	0.0013	0.0176

	gene_symbols	t	P.Value	adj.P.Val
2782501	ZNF326	3.6298	0.0013	0.0177
2771030	CSNK1G1	3.6287	0.0013	0.0177
2761206		-3.6273	0.0013	0.0177
2757810		3.6264	0.0013	0.0177
2776162	EFNB2	-3.6259	0.0013	0.0177
2796811	CEP63	-3.6256	0.0013	0.0177
2790752	C15ORF40	-3.6255	0.0013	0.0177
2786630	TRIM37	3.6251	0.0013	0.0177
2785701	FBXO31	-3.6251	0.0013	0.0177
2758589	LOC772206	-3.6246	0.0013	0.0177
2774513	STMN2	-3.6236	0.0013	0.0177
2772531	SETD3	3.6234	0.0013	0.0177
2759589	GPR146	3.6234	0.0013	0.0177
2763569	MAP3K7IP3	-3.6233	0.0013	0.0177
2768395		3.6209	0.0013	0.0178
2788505	CACNB4	3.6205	0.0013	0.0178
2778195	PDE2A	3.6199	0.0013	0.0178
2776444	EXT2	-3.6199	0.0013	0.0178
2757260	CDKN1B	-3.6193	0.0013	0.0179
2765432	LRRN3	-3.6186	0.0013	0.0179
2778722		3.6969	0.0011	0.0163
2786344	OGT	-3.6177	0.0013	0.0179
2757157	EED	3.6157	0.0013	0.0180
2773437	GATAD1	-3.6154	0.0013	0.0180
2765819	SHC3	3.6141	0.0013	0.0180
2760807	ST5	-3.6088	0.0014	0.0182
2777881	C19ORF26	3.6071	0.0014	0.0183
2769828	MRPS18A	3.6054	0.0014	0.0183
2790497	SGSM2	3.6829	0.0012	0.0167
2770861	KCTD1	-3.6041	0.0014	0.0184
2776077	FANCL	-3.6040	0.0014	0.0184
2773438	H3F3B	3.6040	0.0014	0.0184
2799371	COX6A1	-3.6040	0.0014	0.0184
2789751	MEF2C	-3.6024	0.0014	0.0184
2767157	SLC25A16	-3.6020	0.0014	0.0184
2787530	C11ORF73	-3.6791	0.0012	0.0168
2793783	SPATA20	-3.6015	0.0014	0.0184
2764358	FCHSD2	3.6010	0.0014	0.0184
2797149	FPGS	-3.6009	0.0014	0.0184
2777997	NPEPL1	-3.8710	0.0007	0.0123
2777772	TGFB2	-3.5998	0.0014	0.0185
2764819	SGMS1	3.5993	0.0014	0.0185
2780838	MPST	-3.5992	0.0014	0.0185
2773199	CHSY1	3.5991	0.0014	0.0185
2773792	PPHLN1	3.5983	0.0014	0.0185
2793098	LBR	-3.5977	0.0014	0.0185
2775332	LOC418040	3.5952	0.0014	0.0186
2772313	HEATR1	3.5948	0.0014	0.0186
2757182	GGA3	-3.5937	0.0014	0.0186
2776169	ZFP36L2	-3.5935	0.0014	0.0186
2770939	UHRF2	-3.5929	0.0014	0.0186
2758432		3.5911	0.0014	0.0187

	gene_symbols	t	P.Value	adj.P.Val
2793631	POLE4	-3.5887	0.0014	0.0188
2771831	KLHL20	-3.5870	0.0014	0.0189
2766976		-3.5869	0.0014	0.0189
2770843	MARK1	3.5865	0.0014	0.0189
2783961	EIF4A2	3.5863	0.0014	0.0189
2796661	TUBGCP4	-3.5862	0.0014	0.0189
2759725	TMEM8B	3.5849	0.0014	0.0189
2760689		-3.5848	0.0014	0.0189
2785621	POLR2D	-3.8504	0.0008	0.0127
2799025	CXORF15	-3.5825	0.0015	0.0190
2787329	BHLHE40	3.5822	0.0015	0.0190
2773657	ZDHHC4	-3.5809	0.0015	0.0190
2788056	RRAGD	3.5797	0.0015	0.0191
2779933	PCSK1	3.5790	0.0015	0.0191
2790502	PDDC1	-3.5756	0.0015	0.0192
2789545	CETN3	-3.5754	0.0015	0.0192
2780508	ZNF326	3.5746	0.0015	0.0192
2785495	ERRFI1	3.5745	0.0015	0.0192
2759100	HOMER1	3.6491	0.0013	0.0177
2770373	TIMM9	-3.5729	0.0015	0.0193
2792187	ETV3	3.6483	0.0013	0.0177
2757301		3.6478	0.0013	0.0177
2796153	GPATCH8	-3.5708	0.0015	0.0194
2783560	SERTAD2	3.6464	0.0013	0.0177
2780038	ABI1	3.5695	0.0015	0.0194
2781551	HINT2	-3.5693	0.0015	0.0194
2785473	STK3	3.6440	0.0013	0.0177
2777511	FBXL10	-3.5679	0.0015	0.0195
2790234	JPH1	-3.9223	0.0007	0.0118
2781051	GGA3	-3.5661	0.0015	0.0195
2768473	PDE3A	3.5659	0.0015	0.0195
2759182	BEND5	3.5656	0.0015	0.0195
2785763	RFX3	-3.5645	0.0015	0.0196
2788445	C15ORF42	3.6392	0.0013	0.0178
2793988	AKR1B1	-3.5634	0.0015	0.0196
2781851		-3.5628	0.0015	0.0196
2764222	PDXK	3.5627	0.0015	0.0196
2779424		-3.5623	0.0015	0.0196
2764482	RAB22A	-3.5623	0.0015	0.0196
2781594	KCNV1	-3.5620	0.0015	0.0196
2770213	DCLK1	3.5612	0.0015	0.0197
2763777	IFNGR1	3.5600	0.0015	0.0197
2783300		3.6350	0.0013	0.0180
2791339	TMEM229B	-3.5591	0.0015	0.0197
2777020	TMEM97	3.5583	0.0015	0.0197
2766708	C14ORF159	-3.5582	0.0015	0.0197
2791074		3.5553	0.0016	0.0199
2785851		-3.5549	0.0016	0.0199
2797435	DNAJC3	3.5547	0.0016	0.0199
2772528	NPAL3	-3.5543	0.0016	0.0199
2784432	LOC416755	-3.5541	0.0016	0.0199
2770115	ANAPC7	-3.5540	0.0016	0.0199

	gene_symbols	t	P.Value	adj.P.Val
2794267	SYMENSTGUG00000003816	-3.5522	0.0016	0.0199
2789198	TNPO1	-3.5516	0.0016	0.0200
2772002	ERI1	-3.5509	0.0016	0.0200
2798379	C16ORF63	-3.5508	0.0016	0.0200
2763862	TP53BP1	-3.5477	0.0016	0.0201
2769133	GATAD1	-3.5469	0.0016	0.0201
2793442		-3.5467	0.0016	0.0201
2787773	NUDT8	-3.5463	0.0016	0.0201
2776560	RND2	-3.5463	0.0016	0.0201
2788884	TMEM170B	-3.5457	0.0016	0.0201
2758147	SORBS1	3.6161	0.0014	0.0185
2767610	LNX2	3.5416	0.0016	0.0203
2761738		3.5414	0.0016	0.0203
2757983	GRIA1	-3.6154	0.0014	0.0185
2762198		3.5396	0.0016	0.0204
2787734	CNKSR2	3.5368	0.0016	0.0205
2794142	WDYHV1	-3.5344	0.0016	0.0206
2764791		3.5341	0.0016	0.0206
2800022		3.5320	0.0017	0.0207
2781873	KIAA0652	-3.5296	0.0017	0.0208
2786307	H3F3A	-3.5291	0.0017	0.0208
2783653	TNRC18	-3.5289	0.0017	0.0208
2768010	FNDC3A	3.6020	0.0015	0.0190
2799024	EIF6	-3.5279	0.0017	0.0208
2766080	ASF1A	-3.5277	0.0017	0.0208
2757994	HEBP2	-3.6001	0.0015	0.0190
2797341	VAC14	-3.5264	0.0017	0.0209
2768425	TPM1	3.5257	0.0017	0.0209
2798062	FAIM2	-3.5255	0.0017	0.0209
2764161	IQCG	3.5247	0.0017	0.0209
2767869	ARSA	-3.7824	0.0009	0.0141
2792163	MGLL	-3.5240	0.0017	0.0209
2769921	FKBP4	-3.5239	0.0017	0.0209
2771512		-3.5964	0.0015	0.0191
2781204	AKAP8	-3.5215	0.0017	0.0210
2786892	TSPAN12	-3.5210	0.0017	0.0210
2791815	PDE4B	-3.5207	0.0017	0.0210
2768401	KIF5B	3.5207	0.0017	0.0210
2790425	ORAI1	3.5937	0.0015	0.0192
2776029		3.5204	0.0017	0.0210
2769660	MRAS	-3.5192	0.0017	0.0211
2759298	TERF2	-3.5189	0.0017	0.0211
2765088	COG4	-3.5188	0.0017	0.0211
2767908	RRAGD	3.5184	0.0017	0.0211
2757789		-3.5183	0.0017	0.0211
2791149	C7ORF20	-3.5172	0.0017	0.0211
2774477	HS6ST1	3.5162	0.0017	0.0211
2773751	HARBI1	-3.5160	0.0017	0.0211
2765111	TMTC3	3.5158	0.0017	0.0211
2775823	VLDLR	-3.5149	0.0017	0.0212
2760324		3.5129	0.0017	0.0213
2789086	C3ORF21	-3.5125	0.0017	0.0213

	gene_symbols	t	P.Value	adj.P.Val
2757857	CKB	-3.5122	0.0017	0.0213
2764260	MGA	-3.5116	0.0017	0.0213
2774596	UHRF2	-3.5114	0.0017	0.0213
2793133		3.5108	0.0017	0.0213
2781063	H3F3B	3.5073	0.0018	0.0215
2797388		3.5057	0.0018	0.0216
2770006	SNX24	-3.5054	0.0018	0.0216
2774878	GALE	-3.5777	0.0015	0.0197
2769115	DNAJB14	-3.5037	0.0018	0.0216
2784917	CABIN1	-3.5758	0.0016	0.0198
2769389		-3.5031	0.0018	0.0216
2793228	TAX1BP1	3.5031	0.0018	0.0216
2777855	PEX1	-3.5016	0.0018	0.0217
2790073	SOX4	-3.5000	0.0018	0.0218
2762057	C21ORF70	-3.4993	0.0018	0.0218
2769764		3.4975	0.0018	0.0219
2795547	MSH4	-3.4972	0.0018	0.0219
2776403	FMNL1	3.4968	0.0018	0.0219
2785187	DACH2	3.6521	0.0014	0.0181
2778782	TDG	3.5673	0.0016	0.0200
2767494		-3.4945	0.0018	0.0220
2773084	BHLHE41	-3.4933	0.0018	0.0220
2780338	MAGT1	3.4932	0.0018	0.0220
2766907	GABPA	-3.4931	0.0018	0.0220
2781694	MARK1	3.4931	0.0018	0.0220
2792105	NCOA7	-3.4931	0.0018	0.0220
2776470	CPNE1	-3.5642	0.0016	0.0201
2767813	NIPBL	-3.4918	0.0018	0.0221
2786071	ADAM11	-3.4916	0.0018	0.0221
2763688	MPV17	-3.4911	0.0018	0.0221
2799104	SIN3B	-3.4910	0.0018	0.0221
2799806	BRS3	-3.7417	0.0010	0.0151
2774752	MIPEP	3.4884	0.0018	0.0222
2778513	NEDD4-1	3.4875	0.0018	0.0222
2786083	RIMS1	3.4858	0.0019	0.0223
2768566		3.4851	0.0019	0.0223
2778388		-3.4848	0.0019	0.0223
2792727	DLGAP2	3.4833	0.0019	0.0224
2767861	LUC7L3	-3.5543	0.0016	0.0205
2762677	PIK3R1	3.4828	0.0019	0.0224
2782048	KLHDC4	-3.4816	0.0019	0.0224
2757730	KCNJ4	3.4815	0.0019	0.0224
2771721	EEF1A1	-3.4812	0.0019	0.0224
2781620	EPM2A	-3.5504	0.0017	0.0207
2789398	MCM3AP	-3.4774	0.0019	0.0226
2778900	LONRF1	-3.4771	0.0019	0.0227
2766803	AGR2	3.5475	0.0017	0.0208
2767467	WNT5A	-3.7275	0.0011	0.0155
2774781	WDR7	-3.5474	0.0017	0.0208
2785567	EPHA5	-3.4757	0.0019	0.0227
2772960		-3.4739	0.0019	0.0228
2795469	SYMENSTGUG00000000772	-3.4729	0.0019	0.0228

	gene_symbols	t	P.Value	adj.P.Val
2784361		-3.4729	0.0019	0.0228
2766196	ACTR8	3.4720	0.0019	0.0229
2773950		-3.4717	0.0019	0.0229
2771761		-3.7182	0.0011	0.0157
2759211	EIF3E	3.4682	0.0019	0.0231
2786535	RORA	-3.4678	0.0019	0.0231
2763177	RRP15	3.4671	0.0019	0.0231
2780437	XP_002194193.1	-3.4667	0.0019	0.0231
2761265	JOSD1	-3.4658	0.0020	0.0231
2784504	C9ORF61	-3.4658	0.0020	0.0231
2789873		3.4657	0.0020	0.0231
2792069	UBE2J2	-3.4640	0.0020	0.0232
2773649	FAM117B	-3.4634	0.0020	0.0232
2785449	TRIM3	-3.4632	0.0020	0.0232
2762360	CTCF	-3.5328	0.0017	0.0212
2784351	ITCH	-3.4623	0.0020	0.0232
2790088	ACOT7	-3.4617	0.0020	0.0233
2787446	ODC1	3.4609	0.0020	0.0233
2799000	BRD1	-3.4590	0.0020	0.0233
2798978	XP_002194193.1	-3.4589	0.0020	0.0233
2785640	DCLK1	3.4586	0.0020	0.0233
2785468	STMN2	-3.4586	0.0020	0.0233
2797976	C19ORF70	-3.4585	0.0020	0.0233
2778547	SEC11A	3.4583	0.0020	0.0233
2766769	EIF6	-3.4577	0.0020	0.0234
2776242	LHFPL4	-3.4569	0.0020	0.0234
2791862		3.4563	0.0020	0.0234
2799054	DHX15	3.4561	0.0020	0.0234
2776048	SYNE1	3.4558	0.0020	0.0234
2798303	FAM46A	3.4555	0.0020	0.0234
2788494	HYOU1	3.4532	0.0020	0.0236
2790102	PLCL2	-3.4528	0.0020	0.0236
2791204	CABP1	3.4514	0.0020	0.0236
2770093	EXTL3	3.4498	0.0020	0.0237
2766305		-3.4488	0.0020	0.0238
2776205	KCNJ9	-3.4483	0.0020	0.0238
2781068	LOC395611	-3.4482	0.0020	0.0238
2787613	NOL8	-3.6944	0.0012	0.0164
2762172	MED13	-3.4468	0.0020	0.0238
2757244	SEC23B	-3.6926	0.0012	0.0165
2776173	DCLK1	3.4455	0.0021	0.0239
2767135	TMEM120B	3.4453	0.0021	0.0239
2779721	LGR4	-3.6896	0.0012	0.0165
2786850	AAMP	-3.4435	0.0021	0.0240
2768109	SLC38A7	-3.4434	0.0021	0.0240
2790962	SLC7A6	-3.4428	0.0021	0.0240
2796193	NAA25	3.4426	0.0021	0.0240
2759982	C6ORF129	-3.4422	0.0021	0.0240
2783228	GALNT10	3.4421	0.0021	0.0240
2781908	GSPT1	3.4421	0.0021	0.0240
2771464	GPR175	-3.4420	0.0021	0.0240
2762593	THAP11	-3.4414	0.0021	0.0240

	gene_symbols	t	P.Value	adj.P.Val
2763585		-3.4413	0.0021	0.0240
2788220	HERC4	3.5101	0.0018	0.0220
2793152	KIAA0895	-3.4406	0.0021	0.0240
2795665	SERPINC1	-3.4377	0.0021	0.0242
2795778		-3.4353	0.0021	0.0243
2781318	HIST2H2AB	-3.4351	0.0021	0.0243
2779157	AOF1	3.4339	0.0021	0.0243
2779611	MXI1	-3.4328	0.0021	0.0244
2758025	SGSM2	3.5002	0.0019	0.0224
2762449	CTGF	3.4311	0.0021	0.0244
2762227		3.4309	0.0021	0.0244
2799764	RELN	3.4307	0.0021	0.0244
2785907	SLTM	3.4303	0.0021	0.0244
2767891	BCAS3	-3.4296	0.0021	0.0245
2798420		-3.4282	0.0021	0.0246
2792828	CCT8	3.4275	0.0021	0.0246
2776838		3.4274	0.0021	0.0246
2758437	MED13L	-3.4272	0.0021	0.0246
2783400	MORN4	-3.4256	0.0022	0.0247
2793753	PALM2	-3.4227	0.0022	0.0248
2763763		3.4222	0.0022	0.0248
2790488	RGL1	-3.6634	0.0012	0.0172
2794317	GAD2	3.4197	0.0022	0.0249
2793673	TAX1BP1	3.4192	0.0022	0.0249
2757849	SLC30A1	3.4192	0.0022	0.0249
2757772	WDR37	3.4188	0.0022	0.0249
2772089	CCDC6	-3.4183	0.0022	0.0250
2796574	NAIF1	-3.4178	0.0022	0.0250
2773689	SPG7	-3.4174	0.0022	0.0250
2765188	MYEF2	3.4172	0.0022	0.0250
2799809	RBBP6	-3.4167	0.0022	0.0250
2778990	MXI1	-3.4160	0.0022	0.0250
2785188	KANK1	-3.4159	0.0022	0.0250
2784324	REXO2	-3.4152	0.0022	0.0251
2759895	TPRKB	-3.4134	0.0022	0.0251
2797557	DCLK1	3.4119	0.0022	0.0252
2778347		-3.4114	0.0022	0.0252
2797607		-3.4107	0.0022	0.0252
2785224	FAM84A	-3.4782	0.0020	0.0233
2757827		3.4098	0.0022	0.0253
2759977	SEMA4G	-3.4094	0.0022	0.0253
2770113	UBP1	-3.4094	0.0022	0.0253
2776481	DDX3X	3.4072	0.0023	0.0254
2775638	CKB	-3.4069	0.0023	0.0254
2778574	GTF2A1	-3.4068	0.0023	0.0254
2762581	TLE4	-3.4058	0.0023	0.0254
2761252	PCMT1	-3.4051	0.0023	0.0255
2790913	LCOR	-3.4041	0.0023	0.0255
2759910	JHDM1D	3.4036	0.0023	0.0255
2775050	GPM6B	-3.4027	0.0023	0.0256
2782227	ATP1B4-2	-3.4027	0.0023	0.0256
2773547	ATXN3	-3.4015	0.0023	0.0256

	gene_symbols	t	P.Value	adj.P.Val
2761431	NSD1	-3.4004	0.0023	0.0257
2787844	ZDHHC17	3.3999	0.0023	0.0257
2769059	AFF4	3.3997	0.0023	0.0257
2767505	TTC33	3.3996	0.0023	0.0257
2761301		3.3996	0.0023	0.0257
2771932	SLMO1	3.3995	0.0023	0.0257
2798075		-3.6383	0.0013	0.0179
2758690	BTBD1	-3.3967	0.0023	0.0258
2777884		3.3963	0.0023	0.0258
2794701	ACOT7	-3.3940	0.0023	0.0259
2792096	ACBD3	3.3938	0.0023	0.0259
2782003	ARNT2	-3.3937	0.0023	0.0259
2787086	PPP3CA	-3.6308	0.0014	0.0181
2788053	ATG3	3.3924	0.0023	0.0260
2796261	FAM92A1	-3.3924	0.0023	0.0260
2758135	ACVR1B	-3.3920	0.0023	0.0260
2790983	MAP3K1	3.3916	0.0023	0.0260
2798921	CHD3	-3.3907	0.0024	0.0260
2789482	RNASET2	-3.3906	0.0024	0.0260
2795901	C5ORF41	-3.4566	0.0021	0.0241
2775226	GPR146	3.3898	0.0024	0.0261
2763893	OTUD7A	3.3893	0.0024	0.0261
2786785	PPRC1	3.3889	0.0024	0.0261
2782302		3.3887	0.0024	0.0261
2786484	MRPS6	-3.3880	0.0024	0.0261
2769249	KIAA0100	-3.3865	0.0024	0.0262
2797405		-3.6225	0.0014	0.0184
2773970	APBA1	-3.4512	0.0021	0.0243
2799871	DNAJC13	-3.4510	0.0021	0.0243
2788545	RIMS1	3.3831	0.0024	0.0264
2780235	C20ORF142	-3.3829	0.0024	0.0264
2770067	WSB1	3.3827	0.0024	0.0264
2779498		-3.3820	0.0024	0.0264
2770381	PUM1	-3.3814	0.0024	0.0264
2793272	LHFPL5	-3.3806	0.0024	0.0265
2787154	PPP2R2A	3.3805	0.0024	0.0265
2788540		3.3803	0.0024	0.0265
2793334		-3.3795	0.0024	0.0265
2764905	RNF170	-3.3774	0.0024	0.0266
2757514	PIM3	3.3765	0.0024	0.0266
2797025	DLG2	3.3764	0.0024	0.0266
2786547	TM2D1	-3.3761	0.0024	0.0266
2767473	MED30	3.3755	0.0024	0.0267
2779129	AP2B1	-3.6888	0.0012	0.0171
2778603	PPP2R2A	3.3737	0.0025	0.0268
2794146	FAM135A	3.3736	0.0025	0.0268
2793532	NCOA2	-3.3734	0.0025	0.0268
2780231	KCNAB2	-3.3724	0.0025	0.0268
2792497		3.3715	0.0025	0.0268
2766035	ASAP1	3.4368	0.0022	0.0249
2762184	PRRG3	3.3709	0.0025	0.0268
2777203	ACSL1	3.3708	0.0025	0.0268

	gene_symbols	t	P.Value	adj.P.Val
2763471	BANP	-3.3705	0.0025	0.0268
2790817	TMCC3	-3.3703	0.0025	0.0268
2765359	SYF2	-3.3675	0.0025	0.0270
2791241	GOLGA7	-3.3669	0.0025	0.0270
2785413	HMGB3	-3.3669	0.0025	0.0270
2791113	GPM6B	-3.3663	0.0025	0.0270
2760350	FAM110B	3.3651	0.0025	0.0271
2776684	ZYG11A	-3.3634	0.0025	0.0272
2770741	ZNF362	-3.3620	0.0025	0.0273
2765033	ETF1	3.3618	0.0025	0.0273
2777654		-3.3608	0.0025	0.0273
2774228	ASF1A	-3.3607	0.0025	0.0273
2767746	MAPK8IP1	3.3605	0.0025	0.0273
2763102	CCDC53	-3.5927	0.0015	0.0192
2790589	TSR1	3.3576	0.0026	0.0275
2779789	CPSF6	3.3571	0.0026	0.0275
2758415	ARGLU1	-3.3570	0.0026	0.0275
2780590	TMEM199	-3.5896	0.0015	0.0194
2787371	SH3BP1	-3.3551	0.0026	0.0276
2782093	UBE3A	3.3528	0.0026	0.0277
2795651	DEPDC6-1	-3.3524	0.0026	0.0277
2784968	ERBB2IP	-3.3522	0.0026	0.0277
2784799	SETMAR	-3.3521	0.0026	0.0277
2778842	SENP6	3.3520	0.0026	0.0277
2796588	C16ORF63	-3.3505	0.0026	0.0278
2789702	WDR43	3.4140	0.0023	0.0258
2795825	AURKAIP1	-3.4131	0.0023	0.0258
2773151	RTCD1	3.3485	0.0026	0.0279
2786179	PALM2	-3.3476	0.0026	0.0279
2781173	RRAGD	3.3454	0.0026	0.0281
2767736	ST3GAL3	-3.3449	0.0026	0.0281
2761003	HS3ST4	-3.4089	0.0023	0.0260
2763539	CCDC88A	3.3442	0.0026	0.0281
2793085	RPRD1B	-3.3428	0.0026	0.0282
2798722	C7ORF20	-3.3424	0.0026	0.0282
2764258		-3.3419	0.0027	0.0283
2781857	MMADHC	-3.3416	0.0027	0.0283
2788242	GOLT1B	3.3413	0.0027	0.0283
2768773	STRAP	-3.3406	0.0027	0.0283
2795867	FBXO28	3.3404	0.0027	0.0283
2766068	STMN2	-3.3390	0.0027	0.0284
2797320	EFNB2	-3.3387	0.0027	0.0284
2757697		3.3382	0.0027	0.0284
2776998	DCAF10	-3.3381	0.0027	0.0284
2770600		-3.3381	0.0027	0.0284
2775883	SLITRK2	3.3371	0.0027	0.0284
2757235		-3.3364	0.0027	0.0285
2783599	LGR4	-3.5636	0.0016	0.0201
2778438	EML1	3.3329	0.0027	0.0287
2777492	C11ORF46	-3.3328	0.0027	0.0287
2784206	GSG1L	3.3325	0.0027	0.0287
2785237	C1ORF55	3.3325	0.0027	0.0287

	gene_symbols	t	P.Value	adj.P.Val
2772750	YPEL1	-3.3318	0.0027	0.0287
2759419	DMXL2	-3.3316	0.0027	0.0287
2769694		-3.6354	0.0014	0.0186
2762621	RPL11	-3.3309	0.0027	0.0287
2791324		3.3302	0.0027	0.0288
2765423	SYNE1	3.3935	0.0024	0.0266
2758069		-3.3294	0.0027	0.0288
2757189	PPP2R2A	3.3280	0.0027	0.0289
2794359	CCDC93	3.3278	0.0027	0.0289
2763237	CETN3	-3.3275	0.0027	0.0289
2780609	H3F3B	3.3265	0.0028	0.0289
2797727	FAM117B	-3.3264	0.0028	0.0289
2791569	B5G1C5_TAEGU	3.3263	0.0028	0.0289
2785708	ENO2	-3.3259	0.0028	0.0290
2792695	DACH2	3.3248	0.0028	0.0290
2793143	SOX1	3.3879	0.0025	0.0268
2784089		-3.5525	0.0016	0.0206
2792922	ARRDC3	-3.3873	0.0025	0.0268
2764296	FMNL1	3.3235	0.0028	0.0291
2758886	ZDHHC13	3.3234	0.0028	0.0291
2783411	FNDC3A	3.3232	0.0028	0.0291
2773141	STRN3	-3.3220	0.0028	0.0291
2787325	PPID	-3.3217	0.0028	0.0291
2777310		-3.3215	0.0028	0.0291
2763736	TPM1	3.3212	0.0028	0.0291
2778796	CSMD2	-3.3201	0.0028	0.0292
2778718	NDUFAF2	-3.5471	0.0017	0.0208
2793566	NETO1	3.3192	0.0028	0.0292
2768602		3.3190	0.0028	0.0292
2771121		3.3180	0.0028	0.0293
2764481	C4ORF44	3.3178	0.0028	0.0293
2785353	CHAF1A	-3.3173	0.0028	0.0293
2785312	EZH1	-3.3171	0.0028	0.0293
2798556	CSNK1A1	3.3167	0.0028	0.0293
2796762	AARS2	-3.5437	0.0017	0.0209
2777944	FREQ	3.3164	0.0028	0.0293
2783676	PIM3	3.3164	0.0028	0.0293
2766073	FLT1	-3.3137	0.0028	0.0295
2777758	ODC1	3.3127	0.0029	0.0295
2761073	MGEA5	-3.3125	0.0029	0.0295
2769497	GLP1R	-3.3120	0.0029	0.0296
2763873	SLC36A1	-3.5382	0.0017	0.0210
2776232	WDTC1	3.3115	0.0029	0.0296
2780045	CNOT10	3.3107	0.0029	0.0296
2759555	ADPRHL2	-3.3084	0.0029	0.0298
2777435	SHF	-3.3079	0.0029	0.0298
2781811	TBC1D15	-3.3078	0.0029	0.0298
2794417	MAP3K3	-3.3076	0.0029	0.0298
2767293		-3.3071	0.0029	0.0298
2763172	DGKI	3.3062	0.0029	0.0299
2799448	TAGLN2	3.3062	0.0029	0.0299
2771796	JHDM1D	3.3058	0.0029	0.0299

	gene_symbols	t	P.Value	adj.P.Val
2765177	CEBPE	-3.3057	0.0029	0.0299
2790232	BCL9L	-3.3675	0.0026	0.0277
2797564	FMNL1	3.3036	0.0029	0.0300
2787539	TSKU	-3.3034	0.0029	0.0300
2763031	STIM2	-3.3033	0.0029	0.0300
2799350	NARG1	3.3018	0.0029	0.0301
2778218	BRD3	-3.3015	0.0029	0.0301
2764144		3.3014	0.0029	0.0301
2787069	FNDC5	-3.3013	0.0029	0.0301
2767709		-3.3009	0.0029	0.0301
2783541		3.4355	0.0023	0.0256
2764261	ROCK2	3.2998	0.0029	0.0301
2779398	CRY1	3.2997	0.0029	0.0301
2793179	LYRM7	-3.2989	0.0029	0.0302
2759786	ACTR2	3.2987	0.0030	0.0302
2773179	EIF3I	3.2976	0.0030	0.0302
2799169	R3HDM1	3.2965	0.0030	0.0303
2797938	RABL2B	3.3569	0.0027	0.0283
2794735		-3.2947	0.0030	0.0304
2778352	SGK3	-3.2929	0.0030	0.0305
2784491		-3.2925	0.0030	0.0305
2779084	ANKRD10	-3.2912	0.0030	0.0306
2773230	SIRT6	-3.5117	0.0018	0.0220
2799079	PLCL2	-3.2870	0.0030	0.0309
2760139	TEX9	3.5078	0.0018	0.0221
2792844	SLC6A1	-3.2846	0.0031	0.0311
2780351	MYO5A	3.2840	0.0031	0.0311
2773310	CHSY1	3.2828	0.0031	0.0312
2778479	C1ORF149	-3.2822	0.0031	0.0312
2780648		-3.2785	0.0031	0.0315
2766219	B3GNT1	3.2782	0.0031	0.0315
2794974	SYMENSTGUG00000010312	-3.2778	0.0031	0.0315
2792134	DBC1	3.2775	0.0031	0.0315
2784528	GARS	3.2771	0.0031	0.0315
2785047	C14ORF23	3.3376	0.0028	0.0291
2775381	ODC1	3.2754	0.0031	0.0316
2783403	HNRPDL	3.2753	0.0031	0.0316
2790789	CHST1	3.2747	0.0031	0.0316
2764607	FOXP2	-3.2743	0.0031	0.0317
2782102	MRPL38	-3.2739	0.0031	0.0317
2787369		-3.2734	0.0031	0.0317
2794770	BTF3L4	3.2734	0.0031	0.0317
2760361	ANKMY2	3.2717	0.0032	0.0318
2759871	BACH1	3.2708	0.0032	0.0318
2783993	CSDC2	-3.2689	0.0032	0.0320
2768142	FEZ2	-3.4869	0.0019	0.0230
2786254		-3.2664	0.0032	0.0321
2793069	CUGBP2	3.2664	0.0032	0.0321
2790460	WTAP	-3.2647	0.0032	0.0322
2774037	SETBP1	3.2643	0.0032	0.0323
2771197		3.2638	0.0032	0.0323
2774725		-3.2624	0.0032	0.0324

	gene_symbols	t	P.Value	adj.P.Val
2785648	STAT5B	-3.2615	0.0032	0.0324
2780643	DIMT1L	3.2614	0.0032	0.0324
2799370	TP53INP1	-3.2608	0.0032	0.0324
2784495	ROD1	-3.4798	0.0020	0.0232
2783331	PI15	-3.2603	0.0032	0.0325
2758499	CPEB3	-3.2596	0.0032	0.0325
2783124	ZBTB44	-3.3197	0.0029	0.0299
2779158	ZDHHC13	3.2586	0.0033	0.0326
2774300	CTCF	-3.2583	0.0033	0.0326
2762221		-3.3171	0.0029	0.0301
2787979		-3.2563	0.0033	0.0327
2758410	RTN4RL1	3.2561	0.0033	0.0327
2763376	OPRL1	-3.2554	0.0033	0.0328
2799048	CNNM1	-3.2551	0.0033	0.0328
2773756	MAPK8IP1	3.2529	0.0033	0.0329
2767199	B3GNT1	3.2528	0.0033	0.0329
2798022	HMG20A	-3.2515	0.0033	0.0330
2779037		3.2515	0.0033	0.0330
2790176	NAT8L	-3.2483	0.0033	0.0332
2776014		3.2482	0.0033	0.0332
2761055	SOD1	-3.2479	0.0033	0.0332
2764690	TERF2	-3.2477	0.0033	0.0332
2790661	LOC416926	-3.2466	0.0034	0.0333
2785066	NUMB	-3.3063	0.0030	0.0306
2781150	CACNG3	3.2443	0.0034	0.0335
2794290	PLDN	3.2433	0.0034	0.0335
2757228	SLC6A8	-3.2429	0.0034	0.0335
2792118	PTP4A3	3.2426	0.0034	0.0335
2757392	HYOU1	3.2425	0.0034	0.0335
2761506	FOXP2	-3.2418	0.0034	0.0336
2796126	ZMAT4	-3.2405	0.0034	0.0337
2792791	BZW2	3.2399	0.0034	0.0337
2759115	NOL6	3.2395	0.0034	0.0337
2771377	ZFHX4	-3.2392	0.0034	0.0337
2763878	SMAP1	3.2383	0.0034	0.0338
2786696	CHST1	3.2960	0.0031	0.0313
2799342	SYMENSTGUG00000017777	-3.2366	0.0034	0.0339
2773467		-3.4512	0.0021	0.0243
2785073	BRCC3	-3.4506	0.0021	0.0243
2791257	CCT5	3.2349	0.0035	0.0340
2758174	C6ORF129	-3.2346	0.0035	0.0340
2784714	TAGLN2	3.2345	0.0035	0.0340
2770588	CDV3	3.3624	0.0027	0.0288
2785395		-3.2338	0.0035	0.0340
2777199		-3.2328	0.0035	0.0341
2775488	AIG1	-3.2327	0.0035	0.0341
2758702	CD164	3.2315	0.0035	0.0342
2793517	EIF2B3	3.2306	0.0035	0.0342
2782636	ACTG1	3.2299	0.0035	0.0343
2772326	AZI2	-3.2289	0.0035	0.0343
2760639	C7ORF30	-3.2279	0.0035	0.0344
2758024	ARPC2	3.2279	0.0035	0.0344

	gene_symbols	t	P.Value	adj.P.Val
2796488	MOSPD2	-3.2261	0.0035	0.0345
2782988	TXN2	-3.4399	0.0022	0.0248
2777579	RPRD1B	-3.2253	0.0035	0.0345
2791405	SRP72	3.2249	0.0035	0.0346
2776127	ATXN2	3.2245	0.0035	0.0346
2769917	C17ORF59	-3.2242	0.0035	0.0346
2780802	PLXNA1	-3.2235	0.0035	0.0346
2781125	DEGS1	3.2233	0.0035	0.0346
2795257	UGCGL1	3.2221	0.0036	0.0347
2772353	FLCN	-3.2805	0.0032	0.0322
2782000	ZSWIM6	3.2214	0.0036	0.0347
2772891	CREG2	-3.2207	0.0036	0.0348
2786010		3.2204	0.0036	0.0348
2763437	PLXNA1	-3.2204	0.0036	0.0348
2760870	LONRF2	3.2200	0.0036	0.0348
2798957	COL23A1	-3.2198	0.0036	0.0348
2798865	ARPC2	-3.2189	0.0036	0.0348
2783786	SENP6	3.2182	0.0036	0.0349
2767899	NDUFS5	-3.4309	0.0022	0.0251
2776786	HTR1D	3.2174	0.0036	0.0349
2796161		-3.2170	0.0036	0.0350
2790615	PPP2R2B	-3.2164	0.0036	0.0350
2780537	LINGO2	-3.2160	0.0036	0.0350
2797782	CTDP1	-3.4275	0.0022	0.0252
2766642	STARD5	3.2140	0.0036	0.0352
2772687	SAFB-1	3.2138	0.0036	0.0352
2765171	JAK2	-3.4237	0.0023	0.0254
2785222	PPM1G	3.2101	0.0037	0.0355
2781305	HS6ST1	3.2084	0.0037	0.0356
2781289		3.2074	0.0037	0.0357
2786650	UAP1	3.2647	0.0033	0.0331
2795174	TMEM121	-3.2060	0.0037	0.0358
2777299	SEC24B	-3.2057	0.0037	0.0358
2790220	EBAG9	3.2052	0.0037	0.0358
2765290	KCNJ3	-3.2047	0.0037	0.0358
2769398	RNF217	3.2047	0.0037	0.0358
2789529	LHFPL4	-3.2023	0.0037	0.0360
2782911	EHMT1	-3.2007	0.0038	0.0361
2778672	SKI	3.2002	0.0038	0.0361
2793781		-3.1998	0.0038	0.0362
2761481	WDR3	3.1995	0.0038	0.0362
2757340		-3.1986	0.0038	0.0362
2767464	DEK	-3.1974	0.0038	0.0363
2768128		-3.1973	0.0038	0.0363
2789302	LFNG	3.2541	0.0034	0.0337
2762897	CSMD2	-3.4067	0.0024	0.0260
2787667		3.1961	0.0038	0.0364
2758766	MEX3B	-3.1955	0.0038	0.0364
2777770	VTI1A	-3.4054	0.0024	0.0261
2797058	PARD6A	3.1951	0.0038	0.0365
2780915	SKI	3.1944	0.0038	0.0365
2782875	ZBTB1	-3.1944	0.0038	0.0365

	gene_symbols	t	P.Value	adj.P.Val
2758937	NDRG4	-3.2519	0.0034	0.0338
2792823	PSPC1	3.1941	0.0038	0.0365
2764624	CYB5R	-3.1931	0.0038	0.0365
2782066	MARK1	3.1929	0.0038	0.0365
2781548	ALDH5A1	-3.1914	0.0038	0.0367
2767726		-3.1911	0.0038	0.0367
2763647	PTP4A2	3.1906	0.0038	0.0367
2772655	JARID2	3.1900	0.0039	0.0367
2763683	CCDC58	3.1897	0.0039	0.0367
2777506	NAP1L1	3.1896	0.0039	0.0367
2791272	FZR1	-3.1894	0.0039	0.0367
2776935	PKIA	-3.1893	0.0039	0.0367
2758653	TARS	3.1880	0.0039	0.0368
2796625		-3.1871	0.0039	0.0369
2785355	SGK3	-3.1869	0.0039	0.0369
2778856	TANC2	3.1867	0.0039	0.0369
2778841	NIT2	-3.1866	0.0039	0.0369
2772777	JHDM1D	3.1859	0.0039	0.0369
2771884	EIF3I	3.1859	0.0039	0.0369
2788770	SLC8A3	-3.3939	0.0024	0.0266
2785406	GARS	3.1850	0.0039	0.0369
2783110	KCTD1	-3.1839	0.0039	0.0370
2759304	FMN2	-3.1835	0.0039	0.0370
2759284	MAPRE1	3.1826	0.0039	0.0371
2783137	UBE2D3	3.1826	0.0039	0.0371
2757406	CHD3	-3.1818	0.0039	0.0371
2796485	SCG2	3.1816	0.0039	0.0371
2774416		3.1816	0.0039	0.0371
2789312	MTMR12	-3.2383	0.0035	0.0346
2787222	YPEL1	-3.1799	0.0039	0.0372
2798697	CLIC3	-3.3878	0.0025	0.0268
2763069	RUNX1T1	-3.1797	0.0039	0.0372
2773021	ZFAND5	3.1792	0.0040	0.0373
2783434	STMN2	-3.1784	0.0040	0.0373
2794679	C11ORF58	-3.1767	0.0040	0.0374
2761745	DHRSX	-3.1765	0.0040	0.0374
2799228	BAI3	3.1759	0.0040	0.0375
2796854	PKIA	-3.1739	0.0040	0.0376
2781531	SOX4	-3.1731	0.0040	0.0377
2774143	CCRL2	3.1731	0.0040	0.0377
2782543	BHLHE41	-3.1717	0.0040	0.0378
2765169	NFS1	-3.1715	0.0040	0.0378
2796469	NSMAF	-3.1714	0.0040	0.0378
2782113	ADSS	3.1709	0.0040	0.0378
2780444		3.1707	0.0040	0.0378
2789104	RANBP2	3.1679	0.0041	0.0380
2776741	VTI1A	-3.3740	0.0025	0.0275
2778878		-3.1675	0.0041	0.0381
2791724		-3.1672	0.0041	0.0381
2793968	TBC1D9B	-3.3730	0.0026	0.0275
2771905	FCF1	3.1659	0.0041	0.0382
2784246	HDHD2	-3.1637	0.0041	0.0383

	gene_symbols	t	P.Value	adj.P.Val
2759103	HMGN3	-3.1636	0.0041	0.0383
2786090	ZNF292	-3.1632	0.0041	0.0384
2800040		-3.3686	0.0026	0.0277
2784401		-3.1627	0.0041	0.0384
2759016	SHISA5	3.1625	0.0041	0.0384
2792041	KLHL2	-3.1623	0.0041	0.0384
2789315	SLITRK5	-3.1622	0.0041	0.0384
2799329	BRS3	-3.3673	0.0026	0.0277
2785841	KCNMB4	-3.3673	0.0026	0.0277
2762246	SMTN	3.2167	0.0037	0.0360
2769025	R3HDM1	3.1590	0.0042	0.0387
2760872	SIK2	3.1569	0.0042	0.0388
2789401	FAM110B	3.1568	0.0042	0.0388
2761465	PCTK2	3.1548	0.0042	0.0390
2790659	TTLL5	-3.1532	0.0042	0.0391
2760611	MAP7	-3.1529	0.0042	0.0391
2771715	PRKCA	3.2080	0.0038	0.0365
2761792	LNX2	3.1520	0.0042	0.0392
2776881	FBXO3	-3.1516	0.0042	0.0392
2764176	SOX4	-3.1515	0.0042	0.0392
2761750	RUFY2	-3.1514	0.0042	0.0392
2792468	SYT4	3.1500	0.0042	0.0393
2788122	XP_002200388.1	-3.1476	0.0043	0.0395
2771767	BRWD3	3.1474	0.0043	0.0395
2780477	LRRN3	3.1465	0.0043	0.0396
2770417		-3.1455	0.0043	0.0397
2797505	CIAPIN1	3.1452	0.0043	0.0397
2761287		-3.1435	0.0043	0.0398
2798268	BLOC1S2	-3.1434	0.0043	0.0398
2788378	RNASET2	-3.1428	0.0043	0.0398
2773757	DDX3X	3.1424	0.0043	0.0399
2771238	CAMSAP1L1	3.1415	0.0043	0.0399
2789072	EFNB2	-3.1413	0.0043	0.0399
2798603	RUFY2	-3.1409	0.0043	0.0399
2758077	PIGT	3.1409	0.0043	0.0399
2763030	TBCA	-3.1405	0.0043	0.0400
2770451	NOLC1	3.1950	0.0039	0.0371
2789151	B3GNT1	3.1395	0.0044	0.0400
2797262		3.1395	0.0044	0.0400
2759706	MAP1D	3.1371	0.0044	0.0402
2782649	TNPO1	-3.3390	0.0028	0.0291
2796030	SETD1B	-3.1368	0.0044	0.0402
2758667		-3.1361	0.0044	0.0403
2780411	GNAL	-3.1909	0.0040	0.0374
2794881	MAPK8IP1	3.1357	0.0044	0.0403
2763713	CPSF6	3.1346	0.0044	0.0404
2777171	SNCAIP	3.1342	0.0044	0.0404
2758712	MAP3K7	3.1339	0.0044	0.0404
2792577	FSCN1	-3.1334	0.0044	0.0404
2761984		3.1317	0.0044	0.0405
2760566	KCNJ4	3.1312	0.0044	0.0406
2774162		3.1307	0.0044	0.0406

	gene_symbols	t	P.Value	adj.P.Val
2789795	COIL	-3.1303	0.0045	0.0406
2797545		-3.1299	0.0045	0.0407
2773373		-3.3301	0.0028	0.0294
2757870	RTCD1	3.1269	0.0045	0.0409
2779509	HDGFRP3	-3.1255	0.0045	0.0410
2777509	ZFYVE1	-3.1252	0.0045	0.0410
2798282	HNRNPH3	3.1252	0.0045	0.0410
2759080	NETO1	3.1241	0.0045	0.0411
2779609	MN1	3.1231	0.0045	0.0411
2760316	ZDHHC17	3.1230	0.0045	0.0411
2794108	KLHL32	-3.1230	0.0045	0.0411
2787813	ADAP1	-3.1228	0.0045	0.0411
2775351	BRIX1	3.1218	0.0045	0.0412
2792421	CLASP2	-3.1214	0.0045	0.0412
2773580	GAS1	-3.1210	0.0046	0.0412
2787866	PIP4K2A	-3.1209	0.0046	0.0412
2771073	MED14	3.1204	0.0046	0.0412
2763043	NIPBL	-3.1194	0.0046	0.0413
2790528		-3.1170	0.0046	0.0415
2774520	MAPRE1	3.1153	0.0046	0.0417
2765898	BRP44	-3.1145	0.0046	0.0417
2775076	BBX	-3.1142	0.0046	0.0418
2796826	TOR1AIP1	-3.1129	0.0046	0.0418
2773862	FOXQ1	-3.1121	0.0047	0.0419
2770088	C13ORF37	-3.3106	0.0030	0.0304
2759592	SYNE1	3.1104	0.0047	0.0420
2797225	MTMR7	-3.1103	0.0047	0.0420
2760372	PRDM15-1	3.1101	0.0047	0.0420
2768094	XBP1	3.1098	0.0047	0.0420
2790882	POLG	-3.1084	0.0047	0.0422
2785432	BRCC3	-3.1083	0.0047	0.0422
2777863	SRFBP1	3.1081	0.0047	0.0422
2765510	TMED10	3.1076	0.0047	0.0422
2778610	ACSL1	3.1070	0.0047	0.0422
2771963	ALDH3A2	-3.1056	0.0047	0.0424
2772572		-3.1052	0.0047	0.0424
2771575	MMP11	-3.1045	0.0047	0.0424
2784609		-3.1029	0.0048	0.0426
2788135		-3.1007	0.0048	0.0428
2783035	SPIN1	-3.1004	0.0048	0.0428
2786287	WASH1	-3.0992	0.0048	0.0429
2792297	CA7	-3.0988	0.0048	0.0429
2772890	LONP1	3.0985	0.0048	0.0429
2771615	NHSL1	-3.0983	0.0048	0.0429
2792489	ING2	3.0973	0.0048	0.0430
2769937	GRB2	-3.0968	0.0048	0.0430
2762075	C11ORF58	-3.0951	0.0048	0.0432
2786488	MAPKSP1	-3.0947	0.0049	0.0432
2758810	PPCS	3.0938	0.0049	0.0433
2776211	CHST1	3.1467	0.0044	0.0404
2770643	LRRTM2	-3.0934	0.0049	0.0433
2792104	BRD1	-3.0934	0.0049	0.0433

	gene_symbols	t	P.Value	adj.P.Val
2758271	MCM3AP	-3.0933	0.0049	0.0433
2757932	C6ORF125	-3.2891	0.0031	0.0317
2759510	NUP155	3.1457	0.0044	0.0405
2761880	AGGF1	3.0916	0.0049	0.0434
2778604	GABRG2	-3.0908	0.0049	0.0435
2786204	ETF1	3.0908	0.0049	0.0435
2787211	TMEM189	-3.0901	0.0049	0.0435
2794083	CTNNBIP1	-3.0883	0.0049	0.0437
2760440		-3.1403	0.0045	0.0409
2795892	SLITRK2	3.0869	0.0049	0.0438
2791608	ZFHX4	-3.0868	0.0049	0.0438
2784964	GNL3	3.0860	0.0050	0.0439
2777636	SEC24B	-3.0847	0.0050	0.0440
2772145	PKIA	-3.0841	0.0050	0.0440
2782672	RGS20	3.0839	0.0050	0.0440
2794944	HUNK	-3.0837	0.0050	0.0440
2759181	RUNX1T1	-3.0833	0.0050	0.0440
2773720	LIMK1	3.0824	0.0050	0.0441
2780153	TGFBR1	-3.0809	0.0050	0.0443
2792803	TRUB1	3.1334	0.0046	0.0412
2793637	GNA11	-3.1324	0.0046	0.0413
2781232	TSC22D1	-3.0792	0.0050	0.0444
2775735	NPM1	3.0789	0.0050	0.0444
2767166	WDR33	3.0789	0.0050	0.0444
2796071		-3.0784	0.0050	0.0444
2786791	FXC1	-3.0780	0.0051	0.0444
2778647	SPG7	-3.0779	0.0051	0.0444
2791357	DENND5B	-3.0779	0.0051	0.0444
2761862	DLG2	3.0771	0.0051	0.0445
2775666	CSNK1A1	3.0757	0.0051	0.0446
2776206	NARG1	3.0756	0.0051	0.0446
2768430	YPEL1	-3.0748	0.0051	0.0446
2757453	MYO5A	3.0746	0.0051	0.0446
2759518	TAX1BP1	3.1269	0.0046	0.0418
2761668	ROCK2	3.0744	0.0051	0.0446
2793905		-3.0739	0.0051	0.0446
2788333	FARSB	3.0739	0.0051	0.0446
2771348	MED9	-3.2672	0.0033	0.0329
2772090	LRRC8D	3.0731	0.0051	0.0447
2797697	HISPPD1	3.0729	0.0051	0.0447
2773246		-3.1242	0.0047	0.0420
2772275	TCHP	-3.0703	0.0051	0.0450
2762361	GTPBP2	-3.0701	0.0051	0.0450
2763977		-3.0691	0.0052	0.0450
2759525	VCL	3.0687	0.0052	0.0451
2782782	FRMPD3	-3.0686	0.0052	0.0451
2797721	GGT7	-3.0668	0.0052	0.0452
2769123	PPAPR3	-3.0657	0.0052	0.0453
2765307	FAM92A1	-3.0656	0.0052	0.0453
2775930	CREB3	3.0650	0.0052	0.0454
2774655	YWHAH	3.0648	0.0052	0.0454
2768337	MAPRE1	3.0647	0.0052	0.0454

	gene_symbols	t	P.Value	adj.P.Val
2772220	DHX15	3.0641	0.0052	0.0454
2759271	PPAPR3	-3.0639	0.0052	0.0454
2779756	TEX10	3.0639	0.0052	0.0454
2757080	USP16	3.0635	0.0052	0.0454
2767697	ANKRD17	3.0634	0.0052	0.0454
2792807	FXC1	-3.0617	0.0053	0.0456
2787097	CTTNBP2	3.0603	0.0053	0.0457
2777641	TCP11L2	-3.2523	0.0034	0.0338
2770000	LLPH	3.0597	0.0053	0.0457
2762338	LNX2	3.0591	0.0053	0.0458
2792447	PHIP	-3.1103	0.0048	0.0430
2764406	GPM6B	-3.0579	0.0053	0.0459
2763430	MTMR9	-3.0565	0.0053	0.0460
2778416	FANCL	-3.0564	0.0053	0.0460
2784082	ANP32B	3.0550	0.0053	0.0462
2774261	C11ORF74	-3.2459	0.0035	0.0342
2761428	ALG2	3.0543	0.0053	0.0462
2778253	UAP1	3.0543	0.0053	0.0462
2774168	EML1	3.0538	0.0054	0.0462
2759985	MYST4	-3.0536	0.0054	0.0462
2787973	CP	-3.0524	0.0054	0.0464
2797019	HMGB3	-3.0515	0.0054	0.0464
2760895	SLC35A1	-3.0513	0.0054	0.0464
2782761	PSME4	3.1027	0.0049	0.0435
2788659	LHFPL5	-3.0513	0.0054	0.0464
2789351	PYROXD1	-3.0511	0.0054	0.0464
2779768	FAM110B	3.0508	0.0054	0.0464
2770849		3.0505	0.0054	0.0464
2786938	RPS20	-3.0499	0.0054	0.0465
2799491	DACT2	3.0498	0.0054	0.0465
2768955	TBC1D20	-3.0497	0.0054	0.0465
2779951	C7ORF20	-3.2401	0.0035	0.0345
2794671	ALG2	3.0490	0.0054	0.0465
2784426	LARGE	3.0486	0.0054	0.0465
2774546	C18ORF51	3.0485	0.0054	0.0465
2758657	BTF3L4	3.0485	0.0054	0.0465
2767570	CTTNBP2	3.0482	0.0054	0.0465
2796139	NONO	-3.0475	0.0054	0.0466
2783760	UNC84A	-3.0471	0.0054	0.0466
2789737		3.0469	0.0054	0.0466
2779257	CAPZA2	3.0451	0.0055	0.0468
2765428	RMND1	3.0448	0.0055	0.0468
2786964	SYNCRIP	3.0436	0.0055	0.0469
2774392		3.0431	0.0055	0.0470
2784026	RELT	3.0420	0.0055	0.0470
2771638	GNAZ	-3.0919	0.0050	0.0444
2789358	AOF1	3.0407	0.0055	0.0472
2764438	RCJMB04_23A5	3.0913	0.0050	0.0444
2766128	KIAA0649	-3.0384	0.0056	0.0474
2781476	DLG3	3.0383	0.0056	0.0474
2780248	CNTNAP2	3.0374	0.0056	0.0475
2769863	SCG2	3.0369	0.0056	0.0475

	gene_symbols	t	P.Value	adj.P.Val
2793168	MXD4	-3.0365	0.0056	0.0475
2790797	ANKRD10	-3.0363	0.0056	0.0475
2766417	NRBF2	-3.0362	0.0056	0.0475
2781814	DYDC1	-3.0871	0.0051	0.0446
2795296	MSH3	-3.0359	0.0056	0.0475
2777072		-3.0354	0.0056	0.0476
2773391		3.0351	0.0056	0.0476
2761087	PTPN5	3.0338	0.0056	0.0477
2764753	B5G1C5_TAEGU	3.0334	0.0056	0.0477
2766486	CACNG4	3.0842	0.0051	0.0448
2798562		-3.0316	0.0056	0.0479
2783527		3.0316	0.0056	0.0479
2784087	VPS37D	-3.0313	0.0057	0.0479
2787431	C5ORF45	-3.0311	0.0057	0.0479
2796160	OPA1	-3.0310	0.0057	0.0479
2792182	HIPK2	-3.0306	0.0057	0.0479
2759941	ACBD3	3.0304	0.0057	0.0479
2794652	PAK1IP1	3.0296	0.0057	0.0480
2792204	TMX2	-3.0283	0.0057	0.0481
2771948	PKIA	-3.0277	0.0057	0.0481
2795429	LOC395251	3.0257	0.0057	0.0484
2765264	BBS10	-3.0253	0.0057	0.0484
2774075	ETF1	3.0250	0.0057	0.0484
2760589	SBK1	3.0747	0.0052	0.0455
2796707	ATF7IP	-3.0238	0.0058	0.0485
2770726	CPLX2	-3.0234	0.0058	0.0485
2791892	ZFYVE20	-3.0231	0.0058	0.0485
2782790	C19ORF29	-3.0216	0.0058	0.0487
2768792	CLMN-1	3.0206	0.0058	0.0488
2792325	ZBTB26	3.0200	0.0058	0.0488
2789656	TSKU	3.0192	0.0058	0.0489
2765870	CP	-3.0189	0.0058	0.0489
2796638	TMEM199	-3.0175	0.0058	0.0490
2795090	NUMB	-3.0174	0.0058	0.0490
2775106	GARS	3.0171	0.0058	0.0491
2764045	SYMENSTGUG00000017592	-3.0169	0.0059	0.0491
2792965	BRIX1	3.0160	0.0059	0.0491
2762686	KCTD8	3.0157	0.0059	0.0491
2771199	DPP7	-3.0154	0.0059	0.0492
2783941	SV2C	3.0149	0.0059	0.0492
2787755	PLEKHO1	3.0146	0.0059	0.0492
2758310	PHLDB2	-3.0143	0.0059	0.0492
2772663		-3.2004	0.0039	0.0369
2799463	UCHL3	3.0140	0.0059	0.0492
2767437	CHRNA4	-3.0128	0.0059	0.0494
2792524	TMEM128	-3.1987	0.0039	0.0369
2767449	RNF20	-3.0121	0.0059	0.0494
2799348	KCTD21	-3.4546	0.0022	0.0249
2759085		-3.0112	0.0059	0.0495
2770137		-3.0109	0.0059	0.0495
2764940	MLLT10	-3.0105	0.0059	0.0495
2788975	EXTL3	3.0104	0.0059	0.0495

	gene_symbols	t	P.Value	adj.P.Val
2760993	C5ORF30	-3.0095	0.0060	0.0496
2792385	VPS13D	3.0091	0.0060	0.0496
2762132	HDAC4	3.0088	0.0060	0.0496
2762291	UNC84B	-3.0084	0.0060	0.0497
2791513	CASP2	-3.0065	0.0060	0.0499
2772545	ADSS	3.0553	0.0055	0.0470
2774802	REEP2	-3.0055	0.0060	0.0500
2769256	RNPC3	-3.1902	0.0040	0.0374
2800049		3.0483	0.0056	0.0475
2763281	HS6ST1	3.0403	0.0057	0.0481
2777918		-3.1718	0.0042	0.0387
2767976	IRF2BP2	3.0370	0.0057	0.0484
2760293	MAFF	3.0316	0.0058	0.0489
2763218		-3.0287	0.0059	0.0491
2757527	NDUFA11	-3.2157	0.0039	0.0369
2796142	PABPC1	-3.1592	0.0043	0.0396
2799163	K60	-3.0247	0.0059	0.0494
2775392		-3.0227	0.0059	0.0495
2769067	XP_002198613.1	-3.1481	0.0044	0.0404
2783084	LOC427250	-3.1424	0.0045	0.0407
2785816	TCTA	-3.1376	0.0045	0.0411
2764639	WNT5B	-3.1373	0.0045	0.0411
2798265	TRIM63	-3.1138	0.0048	0.0428
2783431	HAX1	-3.1657	0.0044	0.0402
2793743	MAPK14	-3.0988	0.0050	0.0439
2772336	C2ORF77	-3.0879	0.0051	0.0446
2788745	ANUBL1	-3.0547	0.0055	0.0470
2780106	H3F3A	-3.0525	0.0055	0.0472

```r
# save results to csv file
write.csv(DEresults,
          file = here("DEresults","DEresults_gene_songbird_all.csv"))
write.csv(DEres_subset,
          file = here("DEresults","DEresults_gene_songbird_fdr.csv"))
```

Enrichment Analyses

Setup

```r
library(easypackages)
libraries("here")
options(stringsAsFactors = FALSE)

ndigits2use = 4

source(here("code","genelistOverlap.R"))
fdr_thresh = 0.05

# non-zero and zero modules
nmods = 21
nonzeromods = c(1,2,6,8,10,11,13,15,17,18,21)
zeromods = c(3,4,5,7,9,12,14,16,19,20)

# Load in gene lists for enrichment analyses
load(here("data","tidy","enrichment_data.Rdata"))
```

Read in data

```r
# read in WGCNA results
wgcna_res = read.csv(here("WGCNAresults","wgcna_results_summary.csv"))
backgroundTotal = dim(wgcna_res)[1]
bglist = wgcna_res$geneSymbol
M0_size = dim(subset(wgcna_res, wgcna_res$moduleLabels==0))[1]
```

Non-zero modules

Grab non-zero modules and report percentage of genes falling within those modules

```r
mask = is.element(wgcna_res$moduleLabels, nonzeromods)
nonzeromod_data = subset(wgcna_res, mask)
nz_genes = nonzeromod_data$geneSymbol
# percentage of clustered genes falling within those modules
nz_prop = dim(nonzeromod_data)[1]/(backgroundTotal-M0_size)
nz_prop
```

```
## [1] 0.6139912
```

Zero modules

Grab zero modules and report percentage of genes falling within those modules

```r
mask = is.element(wgcna_res$moduleLabels, zeromods)
zeromod_data = subset(wgcna_res, mask)
z_genes = zeromod_data$geneSymbol
```

```
# percentage of clustered genes falling within those modules
z_prop = dim(zeromod_data)[1]/(backgroundTotal-M0_size)
z_prop
```

```
## [1] 0.3860088
```

Annotate each module by enrichment in broadly expressed, blood, brain, or lymphocyte genes

```
mod_names = c("M1_turquoise","M2_blue","M3_brown","M4_yellow",
  "M5_green","M6_red","M7_black","M8_pink","M9_magenta",
  "M10_purple","M11_greenyellow","M12_tan","M13_salmon",
  "M14_cyan","M15_midnightblue","M16_lightcyan","M17_grey60",
  "M18_lightgreen","M19_lightyellow","M20_royalblue","M21_darkred")

geneclasses = c("BroadGenes","BloodGenes","BrainGenes","LymphocyteGenes")
outcols = c("OR","pval","fdr")

out_mats = vector(mode = "list", length = length(geneclasses))
names(out_mats) = geneclasses
for (igc in 1:length(geneclasses)){
  out_res = data.frame(matrix(nrow = length(mod_names),
                              ncol = length(outcols)))
  colnames(out_res) = outcols
  rownames(out_res) = mod_names

  # intersect genes2 list with background
  genes2 = eval(as.name(geneclasses[igc]))
  mask = is.element(genes2,bglist)
  genes2 = data.frame(genes2[mask])

  for (imod in 1:length(mod_names)){
    # filename for module list
    genes1 = wgcna_res$geneSymbol[wgcna_res$moduleLabels==imod]

    overlap_res = genelistOverlap(genes1,
                                  genes2,
                                  backgroundTotal,
                                  print_result = FALSE,
                                  header = FALSE)
    out_res[imod,1] = overlap_res[[1]]$OR
    out_res[imod,2] = overlap_res[[1]]$hypergeo_p
  }
  out_res[,3] = p.adjust(out_res[,2], method = "fdr")
  out_mats[[igc]] = out_res
}
```

Modules enriched for broadly expressed genes

out_mats[[1]]

```
##                          OR         pval          fdr
## M1_turquoise     1.4754869 7.384191e-05 2.215257e-04
## M2_blue          4.3473823 2.843457e-59 5.971260e-58
## M3_brown         0.4028520 1.000000e+00 1.000000e+00
## M4_yellow        1.0127503 5.891632e-01 1.000000e+00
## M5_green         0.8250661 9.591967e-01 1.000000e+00
## M6_red           0.6841978 9.982855e-01 1.000000e+00
## M7_black         0.6557372 9.990008e-01 1.000000e+00
## M8_pink          3.4594286 5.151937e-23 5.409534e-22
## M9_magenta       0.9673481 6.687839e-01 1.000000e+00
## M10_purple       1.7558107 6.361290e-05 2.215257e-04
## M11_greenyellow  2.8354308 5.456839e-14 2.864840e-13
## M12_tan          0.9602873 6.756651e-01 1.000000e+00
## M13_salmon       3.2416943 6.186578e-17 4.330604e-16
## M14_cyan         0.8460565 8.385310e-01 1.000000e+00
## M15_midnightblue 2.9259899 8.821725e-10 3.705125e-09
## M16_lightcyan    0.2184977 1.000000e+00 1.000000e+00
## M17_grey60       0.3078006 9.999977e-01 1.000000e+00
## M18_lightgreen   2.0544133 1.640082e-04 4.305215e-04
## M19_lightyellow  0.1180096 1.000000e+00 1.000000e+00
## M20_royalblue    0.8797679 7.608833e-01 1.000000e+00
## M21_darkred      1.8493827 2.375546e-03 5.542940e-03
```

Modules enriched for whole-blood-specific genes

out_mats[[2]]

```
##                           OR         pval          fdr
## M1_turquoise     11.5273292 4.658437e-56 9.782719e-55
## M2_blue           0.0000000 1.000000e+00 1.000000e+00
## M3_brown          0.4055741 9.808647e-01 1.000000e+00
## M4_yellow         0.0000000 1.000000e+00 1.000000e+00
## M5_green          0.0000000 1.000000e+00 1.000000e+00
## M6_red            0.0000000 1.000000e+00 1.000000e+00
## M7_black          4.7788779 8.944644e-08 9.391876e-07
## M8_pink           0.0000000 1.000000e+00 1.000000e+00
## M9_magenta        2.1295290 4.617022e-02 1.615958e-01
## M10_purple        0.0000000 1.000000e+00 1.000000e+00
## M11_greenyellow   0.2711242 9.758859e-01 1.000000e+00
## M12_tan           2.3397400 2.934126e-02 1.232333e-01
## M13_salmon        0.8751862 6.778683e-01 1.000000e+00
## M14_cyan          0.4169821 9.110777e-01 1.000000e+00
## M15_midnightblue  0.0000000 1.000000e+00 1.000000e+00
## M16_lightcyan     5.8975148 8.474162e-06 5.931914e-05
## M17_grey60        0.0000000 1.000000e+00 1.000000e+00
## M18_lightgreen    0.0000000 1.000000e+00 1.000000e+00
## M19_lightyellow   5.9327166 2.006122e-05 1.053214e-04
## M20_royalblue     0.0000000 1.000000e+00 1.000000e+00
```

```
## M21_darkred          0.0000000 1.000000e+00 1.000000e+00
```

Modules enriched for brain-specific genes

```
out_mats[[3]]
```

```
##                         OR        pval         fdr
## M1_turquoise      0.6372773 0.993733802 1.00000000
## M2_blue           0.1048834 0.999939871 1.00000000
## M3_brown          0.9104730 0.682859810 1.00000000
## M4_yellow         0.3257368 0.985882512 1.00000000
## M5_green          0.8687475 0.702908371 1.00000000
## M6_red            0.7366275 0.804434834 1.00000000
## M7_black          2.7368728 0.002137245 0.04488215
## M8_pink           0.0000000 1.000000000 1.00000000
## M9_magenta        0.2348909 0.986403449 1.00000000
## M10_purple        0.0000000 1.000000000 1.00000000
## M11_greenyellow   0.2542235 0.981117101 1.00000000
## M12_tan           1.0567651 0.540726528 1.00000000
## M13_salmon        0.0000000 1.000000000 1.00000000
## M14_cyan          0.7904823 0.725793834 1.00000000
## M15_midnightblue  0.0000000 1.000000000 1.00000000
## M16_lightcyan     1.3649312 0.388779322 1.00000000
## M17_grey60        0.4444339 0.896601020 1.00000000
## M18_lightgreen    0.0000000 1.000000000 1.00000000
## M19_lightyellow   2.5990629 0.051837402 0.54429272
## M20_royalblue     0.0000000 1.000000000 1.00000000
## M21_darkred       0.5515742 0.839551585 1.00000000
```

Modules enriched for lymphocyte-specific genes

```
out_mats[[4]]
```

```
##                          OR         pval          fdr
## M1_turquoise       0.1838656 1.000000e+00 1.000000e+00
## M2_blue            0.2589684 9.994031e-01 1.000000e+00
## M3_brown           0.9595463 6.359708e-01 1.000000e+00
## M4_yellow          1.3943998 2.186229e-01 7.651803e-01
## M5_green           0.5604264 9.315386e-01 1.000000e+00
## M6_red            18.3563827 1.246918e-55 2.618528e-54
## M7_black           0.3145521 9.880536e-01 1.000000e+00
## M8_pink            2.0437365 2.899534e-02 1.522256e-01
## M9_magenta         4.1752756 1.103923e-06 7.727462e-06
## M10_purple         0.7885069 7.575422e-01 1.000000e+00
## M11_greenyellow    0.2070003 9.922681e-01 1.000000e+00
## M12_tan            1.0815100 5.104906e-01 1.000000e+00
## M13_salmon         0.0000000 1.000000e+00 1.000000e+00
## M14_cyan           1.3124825 3.778501e-01 1.000000e+00
## M15_midnightblue   1.0556558 5.514536e-01 1.000000e+00
## M16_lightcyan      0.7316755 7.628255e-01 1.000000e+00
```

```
## M17_grey60       6.8665689 1.456634e-08 1.529466e-07
## M18_lightgreen   2.5198636 3.990386e-02 1.675962e-01
## M19_lightyellow  0.8142841 7.097983e-01 1.000000e+00
## M20_royalblue    1.2667870 4.333959e-01 1.000000e+00
## M21_darkred      0.9096507 6.520517e-01 1.000000e+00
```

At the level of modules, test non-zero and zero modules for enrichment in broadly expressed, blood, brain, or lymphocyte modules

```
fname = "Subgrp_STRUCTresultMEfMRIcorr_bootlim_data4plotting_LV1_ci95.csv"
fname = here("PLSresults",fname)
plsbootdata = read.csv(fname)

var2use = "nonzero"

td_tmp = subset(plsbootdata, plsbootdata$Grp=="TD")
rownames(td_tmp) = 1:nmods
poor_tmp = subset(plsbootdata, plsbootdata$Grp=="Poor")
rownames(poor_tmp) = 1:nmods
good_tmp = subset(plsbootdata, plsbootdata$Grp=="Good")
rownames(good_tmp) = 1:nmods

td_mods = as.numeric(rownames(td_tmp)[td_tmp[,var2use]==1])
asd_poor_mods = as.numeric(rownames(poor_tmp)[poor_tmp[,var2use]==1])
asd_good_mods = as.numeric(rownames(good_tmp)[good_tmp[,var2use]==1])
if (identical(td_mods,numeric(0))){
  td_mods = NA
} else if (identical(asd_poor_mods,numeric(0))){
  asd_poor_mods = NA
} else if (identical(asd_good_mods,numeric(0))){
  asd_good_mods = NA
}

mask = logical(length = nmods)
nonzero_mods = sort(unique(c(td_mods, asd_poor_mods, asd_good_mods)))
mask[nonzero_mods] = TRUE
zero_mods = 1:nrow(td_tmp)
zero_mods = zero_mods[!mask]

nz_mods = mod_names[nonzero_mods]
z_mods = mod_names[zero_mods]

# broadly expressed modules
broadmods = mod_names[out_mats$BroadGenes$fdr<=fdr_thresh]; broadmods
```

```
## [1] "M1_turquoise"    "M2_blue"        "M8_pink"
## [4] "M10_purple"      "M11_greenyellow" "M13_salmon"
## [7] "M15_midnightblue" "M18_lightgreen"  "M21_darkred"
```

```
# test enrichment between non-zero modules and broadly expressed modules
overlap_res = genelistOverlap(nz_mods,
                              broadmods,
```

```
                                   length(mod_names),
                                   print_result = TRUE)
```

[1] "OR = 184.500000, p = 0.000187"

```
# test enrichment between zero modules and broadly expressed modules
overlap_res = genelistOverlap(z_mods,
                              broadmods,
                              length(mod_names),
                              print_result = TRUE)
```

[1] "OR = 0.000000, p = 1.000000"

```
# blood modules
bloodmods = mod_names[out_mats$BloodGenes$fdr<=fdr_thresh]

# test enrichment between non-zero modules and blood modules
overlap_res = genelistOverlap(nz_mods,
                              bloodmods,
                              length(mod_names),
                              print_result = TRUE)
```

[1] "OR = 0.600000, p = 0.964912"

```
# test enrichment between zero modules and blood modules
overlap_res = genelistOverlap(z_mods,
                              bloodmods,
                              length(mod_names),
                              print_result = TRUE)
```

[1] "OR = 8.571429, p = 0.255639"

```
# brain expressed modules
brainmods = mod_names[out_mats$BrainGenes$fdr<=fdr_thresh]

# test enrichment between non-zero modules and brain modules
overlap_res = genelistOverlap(nz_mods,
                              brainmods,
                              length(mod_names),
                              print_result = TRUE)
```

[1] "OR = 0.000000, p = 1.000000"

```
# test enrichment between zero modules and brain modules
overlap_res = genelistOverlap(z_mods,
                              brainmods,
                              length(mod_names),
                              print_result = TRUE)
```

[1] "OR = 4.555556, p = 0.476190"

```
# lymphocyte modules
lymphocytemods = mod_names[out_mats$LymphocyteGenes$fdr<=fdr_thresh]

# test enrichment between non-zero modules and lymphocyte modules
overlap_res = genelistOverlap(nz_mods,
                              lymphocytemods,
                              length(mod_names),
```

```
                              print_result = TRUE)
```

`## [1] "OR = 4.444444, p = 0.537594"`
```
# test enrichment between zero modules and lymphocyte modules
overlap_res = genelistOverlap(z_mods,
                              lymphocytemods,
                              length(mod_names),
                              print_result = TRUE)
```

`## [1] "OR = 1.055556, p = 0.875940"`

At the level of modules, test for overlap between non-zero modules across groups

```
# show the ASD Poor modules
asd_poor_mods = mod_names[asd_poor_mods]

# show the ASD Good modules
asd_good_mods = mod_names[asd_good_mods]

# show the TD modules
td_mods = mod_names[td_mods]

# test overlap between ASD Poor and ASD Good
overlap_res = genelistOverlap(asd_poor_mods,
                              asd_good_mods,
                              length(mod_names),
                              print_result = TRUE)
```

`## [1] "OR = 0.000000, p = 1.000000"`
```
# test overlap between TD and ASD Good
overlap_res = genelistOverlap(td_mods,
                              asd_good_mods,
                              length(mod_names),
                              print_result = TRUE)
```

`## [1] "OR = 0.000000, p = 1.000000"`
```
# test overlap between TD and ASD Poor
overlap_res = genelistOverlap(td_mods,
                              asd_poor_mods,
                              length(mod_names),
                              print_result = TRUE)
```

`## [1] "OR = 1.666667, p = 0.655659"`

Examine enrichment at the gene-level between gene classes and non-zero or zero modules

```r
geneclasses = c("BroadGenes","BloodGenes","BrainGenes","LymphocyteGenes")
res_colnames = c("Non-Zero Modules","Zero Modules")

ORmat = data.frame(matrix(nrow = length(geneclasses),
                          ncol = length(res_colnames)))
logPmat = data.frame(matrix(nrow = length(geneclasses),
                            ncol = length(res_colnames)))
Pmat = data.frame(matrix(nrow = length(geneclasses),
                         ncol = length(res_colnames)))
FDRmat = data.frame(matrix(nrow = length(geneclasses),
                           ncol = length(res_colnames)))

colnames(ORmat) = res_colnames
colnames(logPmat) = res_colnames
colnames(Pmat) = res_colnames
colnames(FDRmat) = res_colnames
rownames(ORmat) = geneclasses
rownames(logPmat) = geneclasses
rownames(Pmat) = geneclasses
rownames(FDRmat) = geneclasses

for (i in 1:length(geneclasses)){
  # intersect genes2 with background list
  genes2 = eval(as.name(geneclasses[i]))
  mask = is.element(genes2,bglist)
  genes2 = data.frame(genes2[mask])

  overlap_res = genelistOverlap(nz_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,1] = overlap_res[[1]]$OR
  logPmat[i,1] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,1] = overlap_res[[1]]$hypergeo_p

  overlap_res = genelistOverlap(z_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,2] = overlap_res[[1]]$OR
  logPmat[i,2] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,2] = overlap_res[[1]]$hypergeo_p
}
for (i in 1:dim(Pmat)[2]){
  FDRmat[,i] = p.adjust(Pmat[,i], method = "fdr")
}
```

```r
zLIM = c(0,30)
par(mar = c(6, 8.5, 3, 3))
WGCNA::labeledHeatmap(Matrix = logPmat,
                      xLabels = colnames(ORmat),
                      yLabels = rownames(ORmat),
                      ySymbols = NULL,
                      colorLabels = FALSE,
                      colors = WGCNA::blueWhiteRed(100),
                      textMatrix = round(ORmat, digits = 2),
                      setStdMargins = FALSE,
                      cex.text = 3,
                      zlim = zLIM)
```



```r
# Enrichment Odds Ratios
ORmat
```
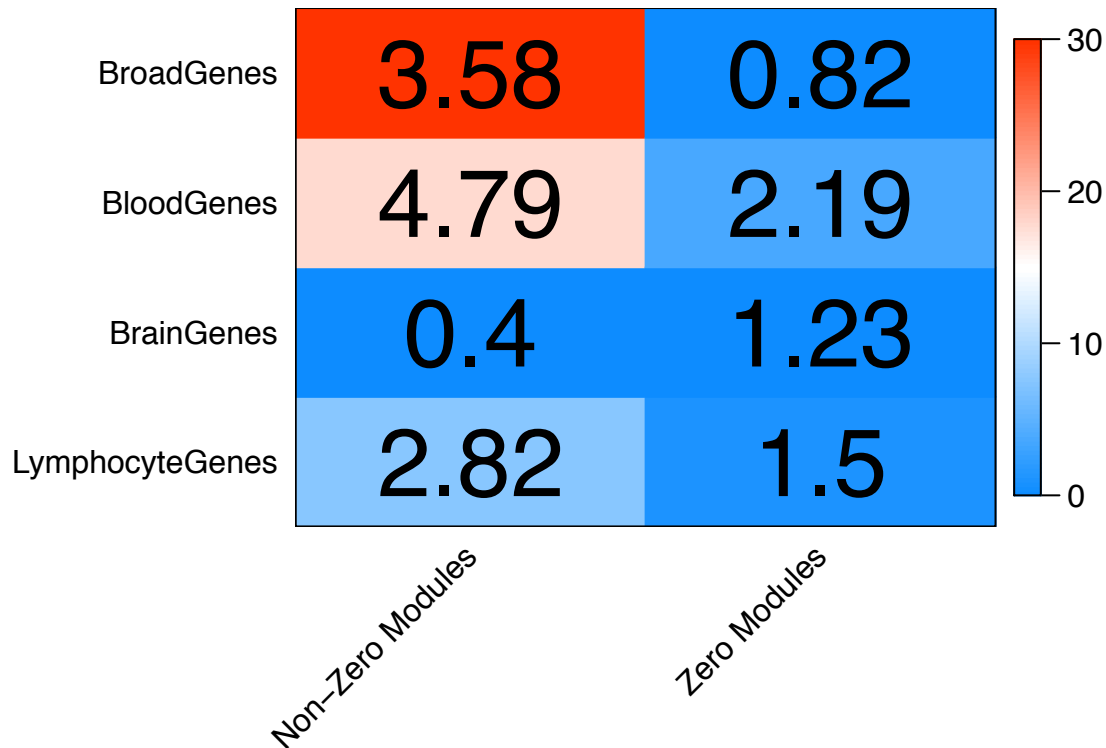
```
##                 Non-Zero Modules Zero Modules
## BroadGenes             3.5847421    0.8168439
## BloodGenes             4.7909589    2.1907949
## BrainGenes             0.3984724    1.2301995
## LymphocyteGenes        2.8233783    1.5007987
```

```r
# P-values
Pmat
```

```
##                 Non-Zero Modules Zero Modules
## BroadGenes          1.480874e-93 1.0000000000
## BloodGenes          1.573773e-18 0.0001826812
## BrainGenes          1.000000e+00 0.5228156458
## LymphocyteGenes     1.944252e-08 0.1012197835
```

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```
# FDR
FDRmat
```

```
##                    Non-Zero Modules Zero Modules
## BroadGenes          5.923497e-93 1.0000000000
## BloodGenes          3.147546e-18 0.0007307249
## BrainGenes          1.000000e+00 0.6970875277
## LymphocyteGenes     2.592336e-08 0.2024395670
```

Examine enrichment between non-zero or zero modules and song bird DE, Human Specific, ASD Prenatal, ASD CTX Dysregulated Modules, ASD PTVs, ASD SFARI, and FMRP and CHD8 targets

```
geneclasses = list(SongBirdDE,
                   HumanSpecific1,
                   HumanSpecific2,
                   ASDPrenatal1,
                   ASDPrenatal2,
                   ASDCTXDownreg,
                   ASDCTXUpreg,
                   ASDPTVs,
                   ASDPTVs_pLI,
                   SFARIASD,
                   FMRP1,
                   FMRP2,
                   CHD81,
                   CHD82)

geneclassnames = c("Song Bird DE",
                   "Human-Specific1",
                   "Human-Specific2",
                   "ASD Prenatal1",
                   "ASD Prenatal2",
                   "ASD CTX Downreg",
                   "ASD CTX Upreg",
                   "ASD dnPTVs",
                   "ASD dnPTVs + pLI >= 0.9",
                   "SFARI ASD",
                   "FMRP Targets1",
                   "FMRP Targets2",
                   "CHD8 Targets1",
                   "CHD8 Targets2")

res_colnames =  c("Broadly Expressed","Non-Zero Modules","Zero Modules")
ORmat = data.frame(matrix(nrow = length(geneclasses),
                      ncol = length(res_colnames)))
logPmat = data.frame(matrix(nrow = length(geneclasses),
                        ncol = length(res_colnames)))
Pmat = data.frame(matrix(nrow = length(geneclasses),
                     ncol = length(res_colnames)))
FDRmat = data.frame(matrix(nrow = length(geneclasses),
```

```r
                                       ncol = length(res_colnames)))
colnames(ORmat) = res_colnames
colnames(logPmat) = res_colnames
colnames(Pmat) = res_colnames
colnames(FDRmat) = res_colnames
rownames(ORmat) = geneclassnames
rownames(logPmat) = geneclassnames
rownames(Pmat) = geneclassnames
rownames(FDRmat) = geneclassnames

for (i in 1:length(geneclasses)){
  # intersect with background list
  genes2 = geneclasses[[i]]
  mask = is.element(genes2,bglist)
  genes2 = data.frame(genes2[mask])

  overlap_res = genelistOverlap(BroadGenes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,1] = overlap_res[[1]]$OR
  logPmat[i,1] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,1] = overlap_res[[1]]$hypergeo_p

  overlap_res = genelistOverlap(nz_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,2] = overlap_res[[1]]$OR
  logPmat[i,2] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,2] = overlap_res[[1]]$hypergeo_p

  overlap_res = genelistOverlap(z_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,3] = overlap_res[[1]]$OR
  logPmat[i,3] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,3] = overlap_res[[1]]$hypergeo_p
}
for (i in 1:dim(Pmat)[2]){
  FDRmat[,i] = p.adjust(Pmat[,i], method = "fdr")
}


zLIM = c(0,-log10(0.005))
par(mar = c(6, 8.5, 3, 3))
WGCNA::labeledHeatmap(Matrix = logPmat,
                      xLabels = colnames(ORmat),
                      yLabels = rownames(ORmat),
```

```
                    ySymbols = NULL,
                    colorLabels = FALSE,
                    colors = WGCNA::blueWhiteRed(50),
                    textMatrix = round(ORmat, digits = 2),
                    setStdMargins = FALSE,
                    cex.text = 1,
                    zlim = zLIM)
```

	Broadly Expressed	Non-Zero Modules	Zero Modules
Song Bird DE	2.31	1.77	1.37
Human–Specific1	1.63	1.85	1.1
Human–Specific2	1.84	1.74	1.11
ASD Prenatal1	0.93	1.7	1.19
ASD Prenatal2	1.67	1.72	1.03
ASD CTX Downreg	2.68	1.7	1.15
ASD CTX Upreg	1.29	1.64	1.79
ASD dnPTVs	1.52	2.58	1.82
dnPTVs + pLI >= 0.9	2.22	2.01	1.37
SFARI ASD	1.28	1.36	1.26
FMRP Targets1	1.8	1.99	1.16
FMRP Targets2	1.97	1.89	1.64
CHD8 Targets1	3.27	2.05	1.23
CHD8 Targets2	4.52	2.54	1.17
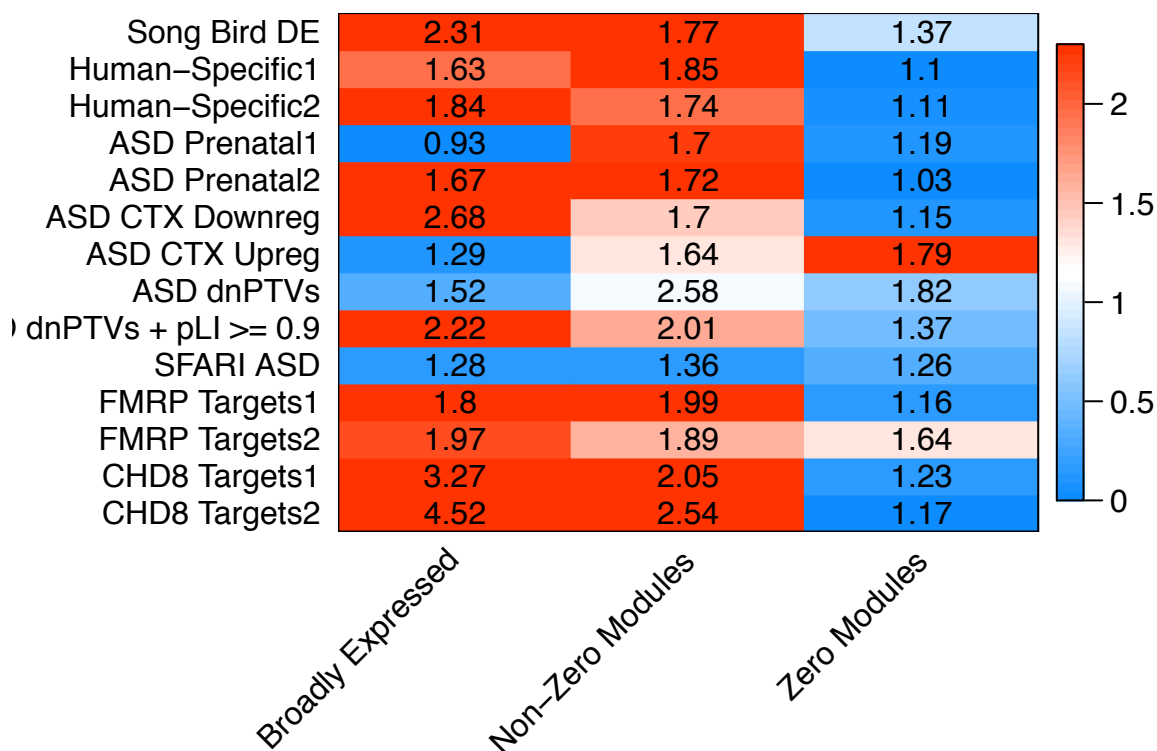
```
# Enrichment Odds Ratios
ORmat
```

```
##                        Broadly Expressed Non-Zero Modules Zero Modules
## Song Bird DE                    2.313688         1.766018     1.367557
## Human-Specific1                 1.631961         1.849270     1.098895
## Human-Specific2                 1.838675         1.737814     1.110486
## ASD Prenatal1                   0.926925         1.703069     1.188698
## ASD Prenatal2                   1.670964         1.723063     1.026814
## ASD CTX Downreg                 2.680746         1.698674     1.146462
## ASD CTX Upreg                   1.285018         1.643444     1.792725
## ASD dnPTVs                      1.518109         2.579444     1.822494
## ASD dnPTVs + pLI >= 0.9         2.224350         2.010678     1.369595
## SFARI ASD                       1.280636         1.357698     1.263160
## FMRP Targets1                   1.797595         1.988684     1.164068
## FMRP Targets2                   1.967917         1.891329     1.637426
## CHD8 Targets1                   3.270380         2.052746     1.233921
## CHD8 Targets2                   4.519513         2.543460     1.167394
```

```
# P-values
Pmat
```

```
##                 Broadly Expressed Non-Zero Modules Zero Modules
```

```
## Song Bird DE               1.207256e-12      2.931725e-03 0.1368211698
## Human-Specific1            1.121700e-02      1.454892e-04 0.9326513736
## Human-Specific2            3.930965e-04      1.157684e-02 0.8584468499
## ASD Prenatal1              1.000000e+00      5.633423e-03 0.7471413303
## ASD Prenatal2              3.797020e-03      4.664096e-03 0.9902083264
## ASD CTX Downreg            2.357339e-13      3.556493e-02 0.7510873768
## ASD CTX Upreg              8.001010e-01      5.025116e-02 0.0000280431
## ASD dnPTVs                 4.664012e-01      8.499079e-02 0.2420677095
## ASD dnPTVs + pLI >= 0.9    2.704798e-03      2.351178e-02 0.3230860055
## SFARI ASD                  7.123606e-01      6.624826e-01 0.4480139650
## FMRP Targets1              3.146039e-03      2.511948e-04 0.7045078476
## FMRP Targets2              7.574835e-03      2.692390e-02 0.0483558183
## CHD8 Targets1              2.526525e-66      1.922342e-11 0.6731317925
## CHD8 Targets2              3.046940e-176     5.203285e-35 0.9979914178
```

```
# FDR
FDRmat
```

```
##                           Broadly Expressed Non-Zero Modules Zero Modules
## Song Bird DE                   4.225398e-12      8.208830e-03 0.6384987923
## Human-Specific1                1.570380e-02      6.789495e-04 0.9979914178
## Human-Specific2                1.100670e-03      2.025946e-02 0.9979914178
## ASD Prenatal1                  1.000000e+00      1.126685e-02 0.9979914178
## ASD Prenatal2                  6.644784e-03      1.088289e-02 0.9979914178
## ASD CTX Downreg                1.100092e-12      4.526446e-02 0.9979914178
## ASD CTX Upreg                  8.616473e-01      5.862636e-02 0.0003926034
## ASD dnPTVs                     5.936015e-01      9.152854e-02 0.8472369833
## ASD dnPTVs + pLI >= 0.9        6.292077e-03      3.657388e-02 0.9046408153
## SFARI ASD                      8.310873e-01      6.624826e-01 0.9979914178
## FMRP Targets1                  6.292077e-03      8.791818e-04 0.9979914178
## FMRP Targets2                  1.178308e-02      3.769346e-02 0.3384907284
## CHD8 Targets1                  1.768568e-65      1.345639e-10 0.9979914178
## CHD8 Targets2                  4.265716e-175     7.284599e-34 0.9979914178
```

Assess enrichments with individual modules

```
geneclasses = list(SongBirdDE,
                   HumanSpecific1,
                   HumanSpecific2,
                   ASDPrenatal1,
                   ASDPrenatal2,
                   ASDCTXDownreg,
                   ASDCTXUpreg,
                   ASDPTVs,
                   ASDPTVs_pLI,
                   SFARIASD,
                   FMRP1,
                   FMRP2,
                   CHD81,
                   CHD82)

geneclassnames = c("Song Bird DE",
                   "Human-Specific1",
```

```r
                    "Human-Specific2",
                    "ASD Prenatal1",
                    "ASD Prenatal2",
                    "ASD CTX Downreg",
                    "ASD CTX Upreg",
                    "ASD dnPTVs",
                    "ASD dnPTVs + pLI >= 0.9",
                    "SFARI ASD",
                    "FMRP Targets1",
                    "FMRP Targets2",
                    "CHD8 Targets1",
                    "CHD8 Targets2")

ORmat = data.frame(matrix(nrow = length(mod_names),
                          ncol = length(geneclasses)))
colnames(ORmat) = geneclassnames
rownames(ORmat) = mod_names

Pmat = data.frame(matrix(nrow = length(mod_names),
                         ncol = length(geneclasses)))
colnames(Pmat) = geneclassnames
rownames(Pmat) = mod_names

FDRmat = data.frame(matrix(nrow = length(mod_names),
                           ncol = length(geneclasses)))
colnames(FDRmat) = geneclassnames
rownames(FDRmat) = mod_names

for (imod in 1:length(mod_names)){
  for (igc in 1:length(geneclasses)){
    # intersect geneclass list with background
    genes2 = geneclasses[[igc]]
    mask = is.element(genes2,bglist)
    genes2 = data.frame(genes2[mask])

    modulegenes = wgcna_res$geneSymbol[wgcna_res$moduleLabels==imod]

    overlap_res = genelistOverlap(modulegenes,
                                  genes2,
                                  backgroundTotal,
                                  print_result = FALSE,
                                  header = FALSE)
    ORmat[imod,igc] = overlap_res[[1]]$OR
    Pmat[imod,igc] = overlap_res[[1]]$hypergeo_p
  }
}
for (i in 1:dim(Pmat)[2]){
  FDRmat[,i] = p.adjust(Pmat[,i], method = "fdr")
}

# Enrichment Odds Ratios
ORmat

##               Song Bird DE Human-Specific1 Human-Specific2
```

```
## M1_turquoise         1.4445211        1.3602330        1.3827322
## M2_blue              0.7958297        1.4650369        1.2453501
## M3_brown             0.8860220        0.6767508        0.5936064
## M4_yellow            1.5090185        1.2511181        0.8326079
## M5_green             0.9253541        0.6903564        0.1652351
## M6_red               0.6901101        0.6560055        0.4810582
## M7_black             1.1156977        1.0673586        1.2112116
## M8_pink              1.6308335        1.2989832        0.6435447
## M9_magenta           0.5923608        1.1530506        1.5941173
## M10_purple           2.4734411        0.7101442        1.0631122
## M11_greenyellow      0.8497899        1.0677513        0.5077765
## M12_tan              0.7903243        1.4725596        1.9683535
## M13_salmon           1.0511399        2.2164479        2.1740584
## M14_cyan             1.5767099        0.9321128        0.9290233
## M15_midnightblue     1.3406242        1.6501061        1.8071866
## M16_lightcyan        0.9097010        0.9637196        1.3902530
## M17_grey60           0.6704924        0.3662373        1.0617409
## M18_lightgreen       1.4162710        1.6715831        1.3469630
## M19_lightyellow      1.5875813        0.6238701        0.6583452
## M20_royalblue        2.4333866        0.1017561        0.8521449
## M21_darkred          0.9900495        1.7789470        2.8840875
##                  ASD Prenatal1 ASD Prenatal2 ASD CTX Downreg ASD CTX Upreg
## M1_turquoise        1.3381209    1.21649298       1.1577181     2.6647637
## M2_blue             0.1370147    0.67341820       1.4019170     0.3555503
## M3_brown            1.2149589    1.01679360       0.5383083     0.4253381
## M4_yellow           0.6147053    1.18654720       0.9227490     1.1016428
## M5_green            0.7392235    0.69232381       0.8860065     0.3617998
## M6_red              0.3301020    0.62262775       0.5391205     0.6774242
## M7_black            0.2859428    0.45985351       0.9222863     1.9704467
## M8_pink             0.1732171    0.46607986       1.0240332     0.1920415
## M9_magenta          0.3930965    0.56751762       0.7069401     4.3941300
## M10_purple          8.2872987    3.79826082       1.7183441     1.2261200
## M11_greenyellow     0.3378921    1.07248377       0.7665975     0.3881439
## M12_tan             0.5707456    0.35478149       0.6613822     2.4172766
## M13_salmon          0.7978864    1.33216464       1.4362206     0.4104708
## M14_cyan            2.6667225    2.36212561       2.5407476     0.9872183
## M15_midnightblue    3.8293530    3.80990783       2.1158332     0.6532845
## M16_lightcyan       0.5241799    0.25869606       0.9575429     2.4324639
## M17_grey60          1.1131640    1.01525923       0.9575429     0.9793079
## M18_lightgreen      2.3316823    1.34855662       1.7337107     0.1452521
## M19_lightyellow     0.4108537    0.09432708       1.2952068     0.9290014
## M20_royalblue       8.6813664    2.92346826       2.0571087     0.6227430
## M21_darkred         0.8633273    0.54799867       1.4525683     0.5045455
##                  ASD dnPTVs ASD dnPTVs + pLI >= 0.9 SFARI ASD
## M1_turquoise       2.331068               1.8123249 1.0941257
## M2_blue            0.000000               0.0000000 0.5267210
## M3_brown           1.071075               0.9634694 1.2063686
## M4_yellow          1.385108               1.5128977 1.0624673
## M5_green           0.000000               0.5071179 0.6020550
## M6_red             0.000000               0.0000000 0.7762389
## M7_black           1.643202               0.8734169 0.8276617
## M8_pink            1.818251               0.6382691 0.4496127
## M9_magenta         0.000000               1.0708560 0.4978471
## M10_purple        12.087633               9.2202576 4.0020135
```

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```
## M11_greenyellow    0.000000          0.0000000 0.3568258
## M12_tan            4.598326          1.1743421 0.7333386
## M13_salmon         0.000000          1.2258483 0.1871304
## M14_cyan           3.348805          2.4203375 2.6490852
## M15_midnightblue   0.000000          0.6297367 2.5329171
## M16_lightcyan      0.000000          0.0000000 1.2779503
## M17_grey60         0.000000          0.6614501 1.6143994
## M18_lightgreen     0.000000          1.4690321 0.6853322
## M19_lightyellow    0.000000          0.0000000 1.0564072
## M20_royalblue      4.336976          4.0008475 1.8469824
## M21_darkred        0.000000          0.0000000 0.0000000
##                  FMRP Targets1 FMRP Targets2 CHD8 Targets1 CHD8 Targets2
## M1_turquoise        1.77837177     1.4218235     1.4026976     1.0273298
## M2_blue             0.09058257     0.4497145     0.9584927     2.2386635
## M3_brown            0.97644260     1.5487484     0.7002422     0.6495313
## M4_yellow           0.28219918     0.5176744     1.9441924     2.3620897
## M5_green            0.60067026     1.2995524     1.1431016     1.5181749
## M6_red              0.07748698     1.3882459     0.6686003     1.4838831
## M7_black            1.04856065     2.1665335     0.6734572     0.4274248
## M8_pink             0.18366396     0.2232252     1.3907819     4.0816199
## M9_magenta          0.10105717     1.2779379     0.6816482     0.5346531
## M10_purple          6.57738001     5.2056148     3.2020846     2.5922017
## M11_greenyellow     0.10937463     0.0000000     0.9915956     2.0356069
## M12_tan             1.29703596     1.4024827     0.5250000     0.4607735
## M13_salmon          1.89878988     0.5699903     1.7081370     1.5627897
## M14_cyan            1.23884272     1.7002110     2.2693241     2.4702393
## M15_midnightblue    4.61389446     3.8651593     2.3011600     2.0559087
## M16_lightcyan       0.78642271     0.9458535     0.3754422     0.2151048
## M17_grey60          0.78642271     0.0000000     0.8627102     0.2908104
## M18_lightgreen      0.86252813     1.5737302     1.5458041     2.0696739
## M19_lightyellow     0.65084682     1.0526434     0.4203669     0.3281622
## M20_royalblue       6.75317693     0.5324469     2.3867476     2.0317321
## M21_darkred         0.47984278     1.7883298     1.5658605     1.2546882
```

```
# P-values
Pmat
```

```
##                  Song Bird DE Human-Specific1 Human-Specific2
## M1_turquoise     1.135926e-02    0.0370449781    0.0531442710
## M2_blue          9.377147e-01    0.0126259601    0.1935379709
## M3_brown         8.102005e-01    0.9883005346    0.9896875497
## M4_yellow        2.728203e-02    0.1653906610    0.8194122762
## M5_green         7.092930e-01    0.9685538226    0.9999974945
## M6_red           9.528888e-01    0.9769653059    0.9937242112
## M7_black         3.840173e-01    0.4545384863    0.2818489779
## M8_pink          1.758832e-02    0.1449957535    0.9421794458
## M9_magenta       9.733735e-01    0.3256260624    0.0490572469
## M10_purple       8.148640e-06    0.9302965559    0.4831616424
## M11_greenyellow  7.730565e-01    0.4579170004    0.9778899554
## M12_tan          8.381252e-01    0.0586074419    0.0057577949
## M13_salmon       4.907752e-01    0.0001038944    0.0016049040
## M14_cyan         7.659553e-02    0.6472804680    0.6400846002
## M15_midnightblue 2.164513e-01    0.0469912857    0.0487215926
## M16_lightcyan    6.632690e-01    0.6040681500    0.2254255378
## M17_grey60       8.823591e-01    0.9941921806    0.5047795745
```

```
## M18_lightgreen      1.834003e-01    0.0540509708    0.2672967510
## M19_lightyellow     9.966779e-02    0.9159692459    0.8575415339
## M20_royalblue       1.805791e-03    0.9999309678    0.7045897102
## M21_darkred         5.741872e-01    0.0415247676    0.0009591607
##                      ASD Prenatal1 ASD Prenatal2 ASD CTX Downreg ASD CTX Upreg
## M1_turquoise        4.066360e-02  2.722458e-01    0.470344698   5.389578e-18
## M2_blue             1.000000e+00  9.949803e-01    0.084889985   9.999913e-01
## M3_brown            1.667206e-01  5.748241e-01    0.990974520   9.997226e-01
## M4_yellow           9.951909e-01  2.436432e-01    0.686673625   4.150673e-01
## M5_green            9.581872e-01  9.704682e-01    0.730193394   9.996131e-01
## M6_red              9.999970e-01  9.872932e-01    0.976308498   9.445452e-01
## M7_black            9.999990e-01  9.992359e-01    0.674084136   1.306131e-03
## M8_pink             1.000000e+00  9.985516e-01    0.540636871   9.999752e-01
## M9_magenta          9.997949e-01  9.880782e-01    0.872129944   1.299903e-14
## M10_purple          4.015611e-49  4.904733e-15    0.039073174   2.761094e-01
## M11_greenyellow     9.999203e-01  4.481913e-01    0.815924947   9.958920e-01
## M12_tan             9.893399e-01  9.996371e-01    0.894379052   1.211472e-04
## M13_salmon          8.610099e-01  1.381745e-01    0.161605388   9.932632e-01
## M14_cyan            6.180530e-06  2.535122e-04    0.002704974   5.780211e-01
## M15_midnightblue    1.866337e-10  1.788732e-09    0.022910114   8.807543e-01
## M16_lightcyan       9.771761e-01  9.991133e-01    0.609303240   2.277237e-03
## M17_grey60          4.086077e-01  5.399646e-01    0.609303240   5.863878e-01
## M18_lightgreen      5.444295e-04  2.012199e-01    0.109400839   9.988837e-01
## M19_lightyellow     9.922097e-01  9.999668e-01    0.336696478   6.359043e-01
## M20_royalblue       2.902982e-26  2.469850e-05    0.042274031   8.837559e-01
## M21_darkred         7.197188e-01  9.471181e-01    0.251699190   9.351176e-01
##                       ASD dnPTVs ASD dnPTVs + pLI >= 0.9    SFARI ASD
## M1_turquoise        0.1017431544            2.250048e-02 6.101846e-01
## M2_blue             1.0000000000            1.000000e+00 9.827665e-01
## M3_brown            0.6270976927            6.254016e-01 3.392103e-01
## M4_yellow           0.5324191633            2.356721e-01 5.098157e-01
## M5_green            1.0000000000            9.105677e-01 9.241632e-01
## M6_red              1.0000000000            1.000000e+00 7.996989e-01
## M7_black            0.4725612191            6.834226e-01 7.487100e-01
## M8_pink             0.4388050788            8.283296e-01 9.643412e-01
## M9_magenta          1.0000000000            5.474334e-01 9.422390e-01
## M10_purple          0.0001377041            7.743579e-13 6.135478e-07
## M11_greenyellow     1.0000000000            1.000000e+00 9.766108e-01
## M12_tan             0.0801795280            4.861569e-01 8.027132e-01
## M13_salmon          1.0000000000            4.583188e-01 9.953270e-01
## M14_cyan            0.2688111675            9.433107e-02 1.067048e-02
## M15_midnightblue    1.0000000000            7.998837e-01 1.936296e-02
## M16_lightcyan       1.0000000000            1.000000e+00 3.956264e-01
## M17_grey60          1.0000000000            7.838677e-01 2.149659e-01
## M18_lightgreen      1.0000000000            4.046924e-01 7.926736e-01
## M19_lightyellow     1.0000000000            1.000000e+00 5.502525e-01
## M20_royalblue       0.2148570594            1.085325e-02 1.495658e-01
## M21_darkred         1.0000000000            1.000000e+00 1.000000e+00
##                      FMRP Targets1 FMRP Targets2 CHD8 Targets1 CHD8 Targets2
## M1_turquoise        2.226484e-04  1.474974e-01  2.984251e-03  9.969544e-01
## M2_blue             1.000000e+00  9.810569e-01  7.951487e-01  1.781877e-18
## M3_brown            6.298647e-01  1.357062e-01  9.983422e-01  9.999986e-01
## M4_yellow           9.996186e-01  9.341598e-01  3.453303e-07  3.641500e-15
## M5_green            9.593074e-01  3.267190e-01  2.527031e-01  3.054372e-04
```

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```
## M6_red            9.999975e-01  2.712390e-01  9.960769e-01  8.703035e-04
## M7_black          5.102954e-01  2.641720e-02  9.943618e-01  1.000000e+00
## M8_pink           9.997783e-01  9.891998e-01  2.638276e-02  2.276259e-30
## M9_magenta        9.999479e-01  3.752907e-01  9.869745e-01  9.999973e-01
## M10_purple        7.335198e-21  1.061350e-07  2.968418e-16  1.466074e-13
## M11_greenyellow   9.998893e-01  1.000000e+00  5.910126e-01  1.147537e-07
## M12_tan           2.615079e-01  3.060536e-01  9.994199e-01  9.999999e-01
## M13_salmon        2.171335e-02  8.701578e-01  1.066555e-03  1.199621e-03
## M14_cyan          3.569345e-01  2.241826e-01  1.218388e-05  2.597814e-08
## M15_midnightblue  7.855050e-08  1.857350e-03  1.717384e-05  1.864293e-05
## M16_lightcyan     7.534806e-01  6.322221e-01  9.997070e-01  1.000000e+00
## M17_grey60        7.534806e-01  1.000000e+00  7.731854e-01  1.000000e+00
## M18_lightgreen    6.884989e-01  3.094799e-01  3.509229e-02  5.017636e-05
## M19_lightyellow   8.412809e-01  5.747735e-01  9.986039e-01  9.999997e-01
## M20_royalblue     1.216023e-11  8.498274e-01  3.321972e-05  1.035651e-04
## M21_darkred       9.204829e-01  2.474667e-01  3.948243e-02  1.581403e-01
```

```r
# FDR
FDRmat
```

```
##                  Song Bird DE Human-Specific1 Human-Specific2
## M1_turquoise     0.0795148525  0.175822326     0.18600495
## M2_blue          0.9733735451  0.132572581     0.58061391
## M3_brown         0.9733735451  0.999930968     0.99999749
## M4_yellow        0.1145845372  0.385911542     0.99999749
## M5_green         0.9733735451  0.999930968     0.99999749
## M6_red           0.9733735451  0.999930968     0.99999749
## M7_black         0.8064362451  0.801354751     0.59188285
## M8_pink          0.0923387045  0.380613853     0.99999749
## M9_magenta       0.9733735451  0.683814731     0.18600495
## M10_purple       0.0001711214  0.999930968     0.88336426
## M11_greenyellow  0.9733735451  0.801354751     0.99999749
## M12_tan          0.9733735451  0.175822326     0.04030456
## M13_salmon       0.9369344138  0.002181782     0.01685149
## M14_cyan         0.2680843478  0.970920702     0.99999749
## M15_midnightblue 0.5050529741  0.175822326     0.18600495
## M16_lightcyan    0.9733735451  0.970920702     0.59174204
## M17_grey60       0.9733735451  0.999930968     0.88336426
## M18_lightgreen   0.4814257997  0.175822326     0.59188285
## M19_lightyellow  0.2990033553  0.999930968     0.99999749
## M20_royalblue    0.0189608037  0.999930968     0.99999749
## M21_darkred      0.9733735451  0.175822326     0.01685149
##                  ASD Prenatal1 ASD Prenatal2 ASD CTX Downreg ASD CTX Upreg
## M1_turquoise     1.423226e-01  7.146452e-01     0.95837883  1.131811e-16
## M2_blue          1.000000e+00  9.999668e-01     0.35653794  9.999913e-01
## M3_brown         5.001619e-01  9.999668e-01     0.99097452  9.999913e-01
## M4_yellow        1.000000e+00  7.146452e-01     0.95837883  9.999913e-01
## M5_green         1.000000e+00  9.999668e-01     0.95837883  9.999913e-01
## M6_red           1.000000e+00  9.999668e-01     0.99097452  9.999913e-01
## M7_black         1.000000e+00  9.999668e-01     0.95837883  6.857185e-03
## M8_pink          1.000000e+00  9.999668e-01     0.95837883  9.999913e-01
## M9_magenta       1.000000e+00  9.999668e-01     0.98852422  1.364898e-13
## M10_purple       8.432784e-48  1.029994e-13     0.22193867  9.663829e-01
## M11_greenyellow  1.000000e+00  9.999668e-01     0.98852422  9.999913e-01
## M12_tan          1.000000e+00  9.999668e-01     0.98852422  8.480307e-04
```

```
## M13_salmon          1.000000e+00  5.803327e-01        0.48481616  9.999913e-01
## M14_cyan            3.244778e-05  1.330939e-03        0.05680446  9.999913e-01
## M15_midnightblue    1.306436e-09  1.878168e-08        0.22193867  9.999913e-01
## M16_lightcyan       1.000000e+00  9.999668e-01        0.95837883  9.564394e-03
## M17_grey60          1.000000e+00  9.999668e-01        0.95837883  9.999913e-01
## M18_lightgreen      2.286604e-03  7.042696e-01        0.38290294  9.999913e-01
## M19_lightyellow     1.000000e+00  9.999668e-01        0.78562512  9.999913e-01
## M20_royalblue       3.048131e-25  1.728895e-04        0.22193867  9.999913e-01
## M21_darkred         1.000000e+00  9.999668e-01        0.66071037  9.999913e-01
##                     ASD dnPTVs ASD dnPTVs + pLI >= 0.9     SFARI ASD
## M1_turquoise        0.712202081             1.575033e-01 1.0000000000
## M2_blue             1.000000000             1.000000e+00 1.0000000000
## M3_brown            1.000000000             1.000000e+00 1.0000000000
## M4_yellow           1.000000000             9.898230e-01 1.0000000000
## M5_green            1.000000000             1.000000e+00 1.0000000000
## M6_red              1.000000000             1.000000e+00 1.0000000000
## M7_black            1.000000000             1.000000e+00 1.0000000000
## M8_pink             1.000000000             1.000000e+00 1.0000000000
## M9_magenta          1.000000000             1.000000e+00 1.0000000000
## M10_purple          0.002891785             1.626152e-11 0.0000128845
## M11_greenyellow     1.000000000             1.000000e+00 1.0000000000
## M12_tan             0.712202081             1.000000e+00 1.0000000000
## M13_salmon          1.000000000             1.000000e+00 1.0000000000
## M14_cyan            1.000000000             4.952381e-01 0.1120399904
## M15_midnightblue    1.000000000             1.000000e+00 0.1355407283
## M16_lightcyan       1.000000000             1.000000e+00 1.0000000000
## M17_grey60          1.000000000             1.000000e+00 0.9028567788
## M18_lightgreen      1.000000000             1.000000e+00 1.0000000000
## M19_lightyellow     1.000000000             1.000000e+00 1.0000000000
## M20_royalblue       1.000000000             1.139592e-01 0.7852201971
## M21_darkred         1.000000000             1.000000e+00 1.0000000000
##                     FMRP Targets1 FMRP Targets2 CHD8 Targets1 CHD8 Targets2
## M1_turquoise         1.168904e-03  6.194891e-01  8.952754e-03  1.000000e+00
## M2_blue              1.000000e+00  1.000000e+00  9.997070e-01  1.870970e-17
## M3_brown             1.000000e+00  6.194891e-01  9.997070e-01  1.000000e+00
## M4_yellow            1.000000e+00  1.000000e+00  3.625968e-06  2.549050e-14
## M5_green             1.000000e+00  6.237362e-01  4.824332e-01  6.414182e-04
## M6_red               1.000000e+00  6.237362e-01  9.997070e-01  1.661489e-03
## M7_black             1.000000e+00  1.849204e-01  9.997070e-01  1.000000e+00
## M8_pink              1.000000e+00  1.000000e+00  6.925475e-02  4.780143e-29
## M9_magenta           1.000000e+00  6.567587e-01  9.997070e-01  1.000000e+00
## M10_purple           1.540392e-19  2.228834e-06  6.233677e-15  7.696889e-13
## M11_greenyellow      1.000000e+00  1.000000e+00  9.997070e-01  4.016379e-07
## M12_tan              9.152778e-01  6.237362e-01  9.997070e-01  1.000000e+00
## M13_salmon           9.119606e-02  1.000000e+00  3.732942e-03  2.099336e-03
## M14_cyan             1.000000e+00  6.237362e-01  8.528716e-05  1.091082e-07
## M15_midnightblue     5.498535e-07  1.950218e-02  9.016265e-05  5.592878e-05
## M16_lightcyan        1.000000e+00  9.483331e-01  9.997070e-01  1.000000e+00
## M17_grey60           1.000000e+00  1.000000e+00  9.997070e-01  1.000000e+00
## M18_lightgreen       1.000000e+00  6.237362e-01  8.188200e-02  1.317129e-04
## M19_lightyellow      1.000000e+00  9.284803e-01  9.997070e-01  1.000000e+00
## M20_royalblue        1.276825e-10  1.000000e+00  1.395228e-04  2.416519e-04
## M21_darkred          1.000000e+00  6.237362e-01  8.291310e-02  2.554575e-01
```

Examine enrichment between non-zero or zero modules after broadly expressed genes are removed and song bird DE, Human Specific, ASD Prenatal, ASD CTX Dysregulated Modules, ASD PTVs, ASD SFARI, and FMRP and CHD8 targets

```r
geneclasses = list(SongBirdDE_notBE,
                   HumanSpecific1_notBE,
                   HumanSpecific2_notBE,
                   ASDPrenatal1_notBE,
                   ASDPrenatal2_notBE,
                   ASDCTXDownreg_notBE,
                   ASDCTXUpreg_notBE,
                   ASDPTVs_pLI_notBE,
                   SFARIASD_notBE,
                   FMRP1_notBE,
                   FMRP2_notBE,
                   CHD81_notBE,
                   CHD82_notBE)

geneclassnames = c("Song Bird DE",
                   "Human-Specific1",
                   "Human-Specific2",
                   "ASD Prenatal1",
                   "ASD Prenatal2",
                   "ASD CTX Downreg",
                   "ASD CTX Upreg",
                   "ASD dnPTVs + pLI >= 0.9",
                   "SFARI ASD",
                   "FMRP Targets1",
                   "FMRP Targets2",
                   "CHD8 Targets1",
                   "CHD8 Targets2")

res_colnames = c("Non-Zero Modules","Zero Modules")
ORmat = data.frame(matrix(nrow = length(geneclasses),
                          ncol = length(res_colnames)))
logPmat = data.frame(matrix(nrow = length(geneclasses),
                            ncol = length(res_colnames)))
Pmat = data.frame(matrix(nrow = length(geneclasses),
                         ncol = length(res_colnames)))
FDRmat = data.frame(matrix(nrow = length(geneclasses),
                           ncol = length(res_colnames)))
colnames(ORmat) = res_colnames
colnames(logPmat) = res_colnames
colnames(Pmat) = res_colnames
colnames(FDRmat) = res_colnames
rownames(ORmat) = geneclassnames
rownames(logPmat) = geneclassnames
rownames(Pmat) = geneclassnames
rownames(FDRmat) = geneclassnames
```

```r
for (i in 1:length(geneclasses)){
  # intersect with background list
  genes2 = geneclasses[[i]]
  mask = is.element(genes2,bglist)
  genes2 = data.frame(genes2[mask])

  overlap_res = genelistOverlap(nz_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,1] = overlap_res[[1]]$OR
  logPmat[i,1] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,1] = overlap_res[[1]]$hypergeo_p

  overlap_res = genelistOverlap(z_genes,
                                genes2,
                                backgroundTotal,
                                print_result = FALSE,
                                header = FALSE)
  ORmat[i,2] = overlap_res[[1]]$OR
  logPmat[i,2] = -log10(overlap_res[[1]]$hypergeo_p)
  Pmat[i,2] = overlap_res[[1]]$hypergeo_p
}
for (i in 1:dim(Pmat)[2]){
  FDRmat[,i] = p.adjust(Pmat[,i], method = "fdr")
}

zLIM = c(0,-log10(0.005))
par(mar = c(6, 8.5, 3, 3))
WGCNA::labeledHeatmap(Matrix = logPmat,
                      xLabels = colnames(ORmat),
                      yLabels = rownames(ORmat),
                      ySymbols = NULL,
                      colorLabels = FALSE,
                      colors = WGCNA::blueWhiteRed(50),
                      textMatrix = round(ORmat, digits = 2),
                      setStdMargins = FALSE,
                      cex.text = 1,
                      zlim = zLIM)
```
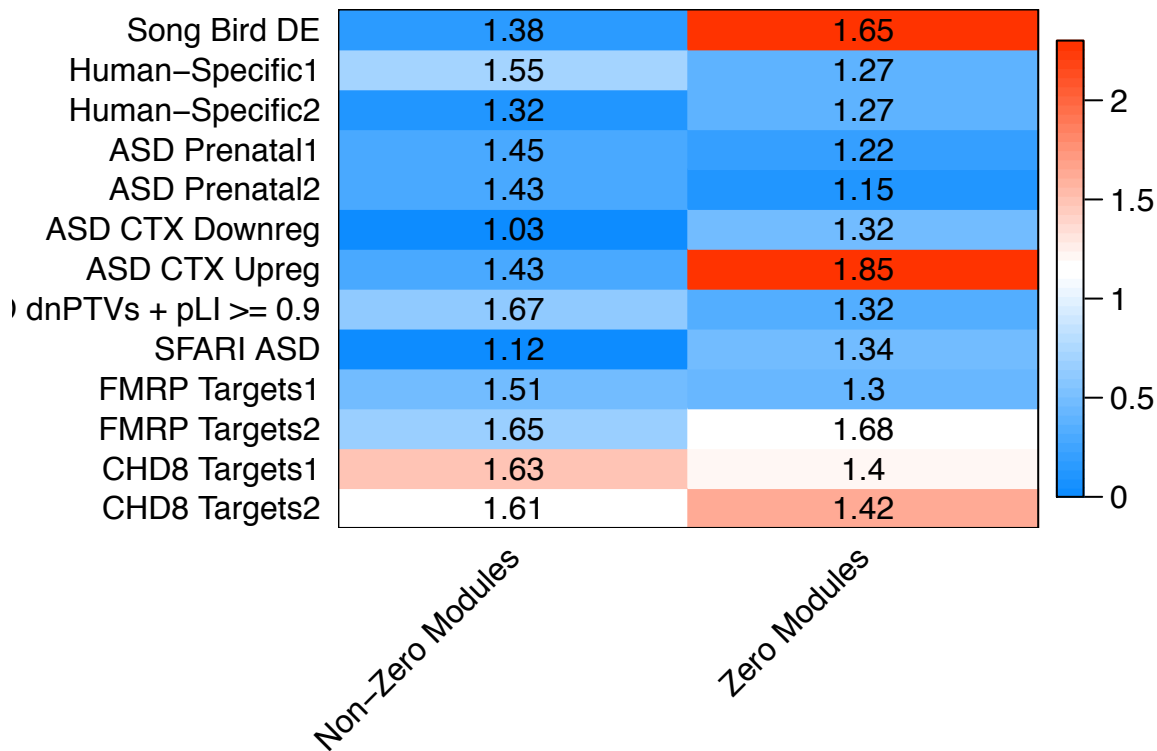
```
# Enrichment Odds Ratios
ORmat

##                        Non-Zero Modules Zero Modules
## Song Bird DE                   1.379753     1.651039
## Human-Specific1                1.546674     1.270655
## Human-Specific2                1.317637     1.269140
## ASD Prenatal1                  1.450761     1.216592
## ASD Prenatal2                  1.432734     1.148539
## ASD CTX Downreg                1.033342     1.319874
## ASD CTX Upreg                  1.430286     1.847027
## ASD dnPTVs + pLI >= 0.9        1.669721     1.315668
## SFARI ASD                      1.121266     1.343655
## FMRP Targets1                  1.514483     1.301697
## FMRP Targets2                  1.653905     1.681547
## CHD8 Targets1                  1.631681     1.402352
## CHD8 Targets2                  1.614453     1.423758

# P-values
Pmat

##                        Non-Zero Modules Zero Modules
## Song Bird DE                 0.65830774 2.955475e-03
## Human-Specific1              0.18486378 4.038351e-01
## Human-Specific2              0.78588124 4.213025e-01
## ASD Prenatal1                0.48435786 6.115897e-01
## ASD Prenatal2                0.52157849 7.921408e-01
## ASD CTX Downreg              0.99378945 3.313699e-01
## ASD CTX Upreg                0.50833829 6.246612e-05
## ASD dnPTVs + pLI >= 0.9      0.25215918 4.317354e-01
## SFARI ASD                    0.95180870 3.142967e-01
```

```
## FMRP Targets1              0.31184208 3.599767e-01
## FMRP Targets2              0.21524562 7.003694e-02
## CHD8 Targets1              0.03346473 5.806758e-02
## CHD8 Targets2              0.06733423 2.272613e-02
```

```
# FDR
FDRmat
```

```
##                    Non-Zero Modules Zero Modules
## Song Bird DE              0.8558001 0.0192105875
## Human-Specific1          0.6556139 0.5102327791
## Human-Specific2          0.9287687 0.5102327791
## ASD Prenatal1            0.7533912 0.6625555508
## ASD Prenatal2            0.7533912 0.7921408257
## ASD CTX Downreg          0.9937895 0.5102327791
## ASD CTX Upreg            0.7533912 0.0008120595
## ASD dnPTVs + pLI >= 0.9  0.6556139 0.5102327791
## SFARI ASD                0.9937895 0.5102327791
## FMRP Targets1            0.6756578 0.5102327791
## FMRP Targets2            0.6556139 0.1820960499
## CHD8 Targets1            0.4350414 0.1820960499
## CHD8 Targets2            0.4376725 0.0984798866
```

Blood Module Preservation in ASD Cortical Tissue

Module Preservation ASD Blood Leukocytes, ASD Post-Mortem Cortical Tissue

Setup and read in data

```r
library(easypackages)
libraries("WGCNA","here")
```

```
## ==============================================================================
## *
## *  Package WGCNA 1.63 loaded.
## *
## *    Important note: It appears that your system supports multi-threading,
## *    but it is not enabled within WGCNA in R.
## *    To allow multi-threading within WGCNA with all available cores, use
## *
## *          allowWGCNAThreads()
## *
## *    within R. Use disableWGCNAThreads() to disable threading if necessary.
## *    Alternatively, set the following environment variable on your system:
## *
## *          ALLOW_WGCNA_THREADS=<number_of_processors>
## *
## *    for example
## *
## *          ALLOW_WGCNA_THREADS=24
## *
## *    To set the environment variable in linux bash shell, type
## *
## *           export ALLOW_WGCNA_THREADS=24
## *
## *     before running R. Other operating systems or shells will
## *     have a similar command to achieve the same aim.
## *
## ==============================================================================
```

```r
options(stringsAsFactors=FALSE)

# Read in ASD brain data
load(here("data","tidy","asd_brain_data.Rdata"))

# Read in ASD blood data
load(here("data","processed","exprDataAdj.Rdata"))

# Read in WGCNA ASD blood results
wgcna_res = read.csv(here("WGCNAresults","wgcna_results_summary.csv"))
blood_colors = wgcna_res$moduleColors
asd_blood_data = exprDataAdj
asd_blood_geneAnno = geneInfo
```

Find common genes amongst the two datasets

```
gene_mask = is.element(asd_blood_geneAnno$geneSymbol, asd_brain_geneAnno$hgnc_symbol)
genes2use = asd_blood_geneAnno$geneSymbol[gene_mask]
asd_blood_geneAnno_subset = asd_blood_geneAnno[gene_mask,]

asd_blood_data_subset = asd_blood_data[gene_mask,]
rownames(asd_blood_data_subset) = asd_blood_geneAnno_subset$geneSymbol
blood_colors_subset = blood_colors[gene_mask]

geneAnno2 = subset(asd_brain_geneAnno,
                   is.element(asd_brain_geneAnno$hgnc_symbol,genes2use))
asd_brain_data_subset = subset(asd_brain_data,
                               is.element(asd_brain_geneAnno$hgnc_symbol, genes2use))
rownames(asd_brain_data_subset) = geneAnno2$hgnc_symbol
asd_brain_data_subset = asd_brain_data_subset[rownames(asd_blood_data_subset),]
```

Run modulePreservation

```
setLabels = c("ASDBlood","ASDBrain")
multiExpr = list(ASDBlood = list(data = t(asd_blood_data_subset)),
                 ASDBrain = list(data = t(asd_brain_data_subset)))
multiColor = list(ASDBlood = blood_colors_subset)

# Calculate module preservation stats
corFnc2use = "bicor"
networkType = "signed"
nperm = 1000
rand_seed = 1
mp = modulePreservation(multiExpr,
                        multiColor,
                        networkType = networkType,
                        corFnc= corFnc2use,
                        maxGoldModuleSize = 1000,
                        referenceNetworks = 1,
                        nPermutations = nperm,
                        randomSeed = rand_seed,
                        quickCor = 0,
                        verbose = 0)
```

Show module preservation results

```
ref = 1
test = 2
statsObs = cbind(mp$quality$observed[[ref]][[test]][,-1],
                 mp$preservation$observed[[ref]][[test]][,-1])
statsZ = cbind(mp$quality$Z[[ref]][[test]][,-1],
               mp$preservation$Z[[ref]][[test]][,-1])

# compute p-values from log10 pvalues in mp
```

```
Zsummary.log10pvals = mp$preservation$log.p$ref.ASDBlood$inColumnsAlsoPresentIn.ASDBrain$log.psummary.p:
Zsummary.pvals = 10^Zsummary.log10pvals
Zsummary.fdr = p.adjust(Zsummary.pvals, method = "fdr")

sumTable = cbind(statsObs[, c("medianRank.pres", "medianRank.qual")],
          signif(statsZ[, c("Zsummary.pres", "Zsummary.qual")], 2),
          Zsummary.pvals, Zsummary.fdr)

ModCols = c("black","blue","brown","cyan","darkred","gold","green",
          "greenyellow","grey","grey60","lightcyan","lightgreen",
          "lightyellow","magenta","midnightblue","pink","purple",
          "red","royalblue","salmon","tan","turquoise","yellow")
ModNums = c("M7","M2","M3","M14","M21",NA,"M5","M11","M0","M16","M17",
          "M18","M19","M9","M15","M8","M10","M6","M20","M13","M12",
          "M1","M4")
modinfo = data.frame(moduleColors = ModCols, moduleLabels = ModNums)
sumTable = cbind(moduleLabels = modinfo$moduleLabels, sumTable)
sumTable
```

```
##              moduleLabels medianRank.pres medianRank.qual Zsummary.pres
## black                  M7              17            18.0         0.240
## blue                   M2               2            11.0         8.100
## brown                  M3              19            10.0        -0.940
## cyan                  M14               9            15.0         0.900
## darkred               M21              16             5.0        -0.190
## gold                 <NA>              14            22.0         5.500
## green                  M5               9            18.0         1.300
## greenyellow           M11               3             1.0         4.100
## grey                   M0              18            23.0        -0.054
## grey60                M16              20             7.0        -1.200
## lightcyan             M17              18            17.0        -0.380
## lightgreen            M18               9             4.0         0.810
## lightyellow           M19              14            12.0        -0.190
## magenta                M9               1            12.0         6.500
## midnightblue          M15              14             3.5        -0.160
## pink                   M8               4             6.0         5.400
## purple                M10              11            20.0         1.700
## red                    M6              13             9.5        -0.940
## royalblue             M20              14             2.0         0.340
## salmon                M13              15            18.0        -0.240
## tan                   M12               5             8.0         2.500
## turquoise              M1              12            13.5         1.500
## yellow                 M4              10            21.0         2.400
##              Zsummary.qual Zsummary.pvals Zsummary.fdr
## black                   25   1.588561e-01 2.810530e-01
## blue                    56   3.402800e-19 7.826441e-18
## brown                   80   6.023294e-01 6.297080e-01
## cyan                    23   1.225806e-01 2.563049e-01
## darkred                 48   4.955699e-01 6.297080e-01
## gold                     1   2.483746e-10 1.904205e-09
## green                   22   7.677112e-02 1.765736e-01
## greenyellow             84   4.107692e-07 1.889538e-06
## grey                   -14   1.767056e-01 2.903021e-01
## grey60                  41   8.646665e-01 8.646665e-01
```

```
## lightcyan                 15    5.928797e-01 6.297080e-01
## lightgreen                55    1.413842e-01 2.709863e-01
## lightyellow               19    5.709222e-01 6.297080e-01
## magenta                   48    1.341995e-13 1.543294e-12
## midnightblue              62    5.573078e-01 6.297080e-01
## pink                      78    6.224280e-09 3.578961e-08
## purple                    19    2.293958e-02 5.862338e-02
## red                       53    4.692526e-01 6.297080e-01
## royalblue                 58    3.449277e-01 5.288892e-01
## salmon                    21    5.660540e-01 6.297080e-01
## tan                       47    6.357133e-03 2.088772e-02
## turquoise                 86    1.643211e-02 4.724230e-02
## yellow                    20    6.254077e-03 2.088772e-02
```

```r
# Plot results
modColors = rownames(mp$preservation$observed[[ref]][[test]])
moduleSizes = mp$preservation$Z[[ref]][[test]][,1]
plotMods = !(modColors %in% c("grey", "gold"));
text = modColors[plotMods]
plotData = cbind(mp$preservation$observed[[ref]][[test]][,2],
                 mp$preservation$Z[[ref]][[test]][,2])
mains = c("Preservation Median rank", "Preservation Zsummary")
par(mfrow = c(1,2))
par(mar = c(4.5,4.5,2.5,1))
for (p in 1:2)
{
  min = min(plotData[, p], na.rm = TRUE)
  max = max(plotData[, p], na.rm = TRUE)
  # Adjust ploting ranges appropriately
  if (p==2)
  {
    if (min > -max/10) min = -max/10
    # ylim = c(min - 0.1 * (max-min), max + 0.1 * (max-min))
    ylim = c(-2,12)
  } else
    ylim = c(max + 0.1 * (max-min), min - 0.1 * (max-min))
    # ylim = c(-2,12)
  plot(moduleSizes[plotMods],
       plotData[plotMods, p],
       col = 1,
       bg = modColors[plotMods],
       pch = 21,
       main = mains[p],
       cex = 2.4,
       ylab = mains[p],
       xlab = "Module size",
       log = "x",
       ylim = ylim,
       xlim = c(10, 2000),
       cex.lab = 1.2,
       cex.axis = 1.2,
       cex.main =1.4)
  # labelPoints(moduleSizes[plotMods],
  #           plotData[plotMods, p],
```

```
#                 text,
#                 cex = 1,
#                 offs = 0.08);

# For Zsummary, add threshold lines
if (p==2) {
  abline(h=0)
  abline(h=2, col = "blue", lty = 2)
  abline(h=10, col = "darkgreen", lty = 2)
}
}
```


Preservation Median ran   ## Preservation Zsummary