

# SIS NMF Final: Diagnosis to DSD

December 9, 2014

## 1 Preparation

```
options(java.parameters = "-Xmx4G")

library(survival)

## Loading required package: splines

library(energy)
library(NMF)

## Loading required package: methods
## Loading required package: pkgmaker
## Loading required package: registry
## Loading required package: rngtools
## Loading required package: cluster
## NMF - BioConductor layer [OK] | Shared memory capabilities [OK] | Cores 7/8

library(nnlsl)

library(glmulti)

## Loading required package: rJava
##
## Attaching package: 'glmulti'
##
## The following object is masked from 'package:NMF':
##
##     consensus

library(glmnet)

## Loading required package: Matrix
## Loaded glmnet 1.9-8

library(RColorBrewer)
library(gplots)

##
## Attaching package: 'gplots'
##
## The following object is masked from 'package:stats':
##
##     lowess
```

```

library(xtable)
library(stargazer)

##
## Please cite as:
##
## Hlavac, Marek (2014). stargazer: LaTeX code and ASCII text for well-formatted regression
and summary statistics tables.
## R package version 5.1. http://CRAN.R-project.org/package=stargazer

load("image.rda")

```

## 2 Cohort characteristics

```

cpvs.diag_dsd$Path.TumourLocation[cpvs.diag_dsd$Path.TumourLocation == ""] = NA
cpvs.diag_dsd$Path.Nodes.Regional.Involved.Fraction = cpvs.diag_dsd$Path.Nodes.Regional.Involved/cpvs.d
cpvs.diag_dsd$Treat.Surgery.ExcisionStatus.Coarse = ordered(ifelse(cpvs.diag_dsd$Treat.Surgery.ExcisionS
"R0", "Clear", "Involved"), levels = c("Clear", "Involved"))
cpvs.diag_dsd$Path.Grade.Coarse = ordered(ifelse(cpvs.diag_dsd$Path.Grade %in%
c("1", "2"), "1or2", "3or4"), levels = c("1or2", "3or4"))
cpvs.diag_dsd$Path.TumourLocation.Coarse = factor(ifelse(cpvs.diag_dsd$Path.TumourLocation %in%
c("Head", "Head (Uncinate)", "Head", "Other")))

summary(cpvs.diag_dsd)

## Patient.ID Patient.Gender Patient.Ethnicity
## Length:110 Female:50 Asian : 5
## Class :character Male :60 Asian, White/Caucasian : 0
## Mode :character Black/African : 0
## Black/African, White/Caucasian: 0
## White/Caucasian :104
## NA's : 1
##
## Patient.Country History.LastFollowup.Date
## Australia :110 Min. :2007-06-29
## Italy : 0 1st Qu.:2011-08-19
## New Zealand : 0 Median :2013-03-12
## Puerto Rico : 0 Mean :2012-10-16
## United Kingdom : 0 3rd Qu.:2014-04-24
## United States of America: 0 Max. :2014-09-23
## NA's :1
## History.Smoking.PackYears History.Diagnosis.Date
## Min. : 0.75 Min. :2007-06-04
## 1st Qu.: 9.00 1st Qu.:2010-01-28
## Median :22.50 Median :2011-01-04
## Mean :26.89 Mean :2011-01-14
## 3rd Qu.:43.75 3rd Qu.:2012-02-15
## Max. :70.00 Max. :2012-10-17
## NA's :68
## History.Diagnosis.AgeAtYears History.Surgery.Date
## Min. :36.0 Min. :2007-05-29
## 1st Qu.:61.0 1st Qu.:2010-01-22

```

```

## Median :67.0           Median :2011-01-01
## Mean   :66.4           Mean   :2011-01-13
## 3rd Qu.:73.0           3rd Qu.:2012-02-13
## Max.   :87.0           Max.   :2012-10-17
##
##
##                               Treat.Surgery.Procedure
## Classic Whipple                               :79
## Splenectomy, Subtotal Panc/L sided Panc or distal Panc: 6
## Cholecystectomy, Classic Whipple              : 5
## Subtotal Panc/L sided Panc or distal Panc      : 4
## Classic Whipple, Exploratory laparotomy        : 3
## PPPD                                           : 3
## (Other)                                       :10
## Treat.Surgery.ExcisionStatus Treat.Surgery.Margin.Pancreatic
## R0:69                                         <2 mm   : 4
## R1:35                                         Clear    :88
## R2: 6                                         Involved: 9
##                                              NA's     : 9
##
##
##
## Treat.Surgery.MarginSizeMm.Pancreatic Treat.Surgery.Margin.Periunc
## Min.   : 0.0                               <2 mm   :20
## 1st Qu.: 5.0                               Clear    :52
## Median :10.0                              Involved:15
## Mean   :10.6                              NA's     :23
## 3rd Qu.:10.2
## Max.   :40.0
## NA's   :30
## Treat.Surgery.MarginSizeMm.Periunc Treat.Surgery.Margin.PVGroove
## Min.   : 0.00                             <2 mm   :23
## 1st Qu.: 1.00                             Clear    :55
## Median : 3.00                             Involved:12
## Mean   : 6.21                             NA's     :20
## 3rd Qu.:10.00
## Max.   :40.00
## NA's   :43
## Treat.Surgery.MarginSizeMm.PVGroove Treat.Surgery.Margin.Retrop
## Min.   : 0.00                             <2 mm   :21
## 1st Qu.: 1.00                             Clear    :68
## Median : 3.00                             Involved: 9
## Mean   : 4.08                             NA's     :12
## 3rd Qu.: 5.00
## Max.   :30.00
## NA's   :45
## Treat.Surgery.MarginSizeMm.Retrop Treat.Surgery.Margin.CBD
## Min.   : 0.10                             <2 mm   : 1
## 1st Qu.: 1.75                             Clear    :83
## Median : 3.00                             Involved: 0
## Mean   : 5.62                             NA's     :26
## 3rd Qu.:10.00
## Max.   :25.00
## NA's   :31
## Treat.Surgery.MarginSizeMm.CBD Treat.Surgery.Margin.Duodenal

```

```

## Min.      : 1.0                      Clear      :60
## 1st Qu.:11.8                      Involved: 1
## Median :20.0                      NA's       :49
## Mean    :23.6
## 3rd Qu.:32.5
## Max.    :55.0
## NA's    :47
## Treat.Surgery.MarginSizeMm.Duodenal Treat.Surgery.Margin.Gastric
## Min.      : 10.0                      Clear:59
## 1st Qu.: 40.0                      NA's :51
## Median : 80.0
## Mean    : 86.2
## 3rd Qu.:132.5
## Max.    :190.0
## NA's    :102
## Treat.Surgery.MarginSizeMm.Gastric Treat.Surgery.Margin.Comments
## Min.      : 10.0                      Length:110
## 1st Qu.: 50.0                      Class :character
## Median : 70.0                      Mode  :character
## Mean    : 67.9
## 3rd Qu.: 97.5
## Max.    :100.0
## NA's    :103
##
##                               Path.HistoType
## Pancreatic Ductal Adenocarcinoma:110
## Acinar Cell Carcinoma             : 0
## Ampullary Adenocarcinoma          : 0
## Carcinoid Tumour                  : 0
## Cholangiocarcinoma                : 0
## Clear Cell Carcinoma               : 0
## (Other)                           : 0
##
##                               Path.HistoType.Subtype Path.Grade
## Gastric                          : 0                1: 8
## Intestinal                       : 0                2:71
## Mixed                            : 0                3:30
## Not otherwise Specified (NOS):31                4: 1
## Pancreatobiliary                 :13
## Squamous                         : 0
## NA's                             :66
##
## Path.TumourLocation Path.TumourSizeMm Path.Invasion.PN
## Head                 :83             Min.    :10.0      Absent :13
## Head (Uncinate):10             1st Qu.:28.0      Present:96
## Tail                 : 9             Median :35.0      NA's   : 1
## Body                 : 7             Mean    :37.6
##                      : 0             3rd Qu.:45.0
## (Other)              : 0             Max.    :90.0
## NA's                 : 1             NA's    :1
##
## Path.Invasion.VS Path.Nodes.Regional.Total Path.Nodes.Regional.Involved
## Absent :34             Min.      : 0.0                      Min.      : 0.00
## Present:72             1st Qu.:11.0                      1st Qu.: 1.00
## NA's   : 4             Median :16.0                      Median : 2.00
##                      Mean    :18.1                      Mean    : 3.18
##                      3rd Qu.:24.0                      3rd Qu.: 4.00
##                      Max.    :46.0                      Max.    :18.00

```

```

##
## Path.Nodes.SepRec.Total Path.Nodes.SepRec.Involved
## Min. : 0.0 Min. : 0.00
## 1st Qu.:11.0 1st Qu.: 1.00
## Median :16.0 Median : 2.00
## Mean :18.1 Mean : 3.18
## 3rd Qu.:24.0 3rd Qu.: 4.00
## Max. :46.0 Max. :18.00
##
##
## Staging.Version Staging.pM Staging.pN
## pTNM AJCC 6th Ed 2002 :14 M0 : 2 N0 :25
## pTNM AJCC 7th Ed 2010 :96 M1 : 6 N1 :84
## pTNM AJCC 7th Ed 2010 (Ampulla) : 0 NA's:102 NA's: 1
## pTNM AJCC 7th Ed 2010 (Cholangiocarcinoma): 0
## pTNM AJCC 7th Ed 2010 (Neuroendocrine) : 0
##
##
## Staging.pT Staging.Stage History.Recurrence History.Recurrence.Date
## Tis : 0 IA : 0 Not observed:24 Min. :2007-10-14
## T1 : 0 IB : 3 Suspected : 4 1st Qu.:2010-12-11
## T2 : 6 IIA:20 Confirmed :78 Median :2012-02-22
## T3 :102 IIB:80 NA's : 4 Mean :2012-01-21
## T4 : 1 III: 1 3rd Qu.:2012-12-29
## NA's: 1 IV : 6 Max. :2014-08-27
## NA's :29
##
## History.Recurrence.Site.Stomach History.Recurrence.Site.Peritoneum
## Mode :logical Mode :logical
## FALSE:110 FALSE:94
## NA's :0 TRUE :16
## NA's :0
##
##
##
## History.Recurrence.Site.PancRemnant History.Recurrence.Site.PancBed
## Mode :logical Mode :logical
## FALSE:106 FALSE:91
## TRUE :4 TRUE :19
## NA's :0 NA's :0
##
##
##
## History.Recurrence.Site.Other History.Recurrence.Site.Omentum
## Mode :logical Mode :logical
## FALSE:102 FALSE:109
## TRUE :8 TRUE :1
## NA's :0 NA's :0
##
##
##
## History.Recurrence.Site.Mesentery History.Recurrence.Site.LymphNodes
## Mode :logical Mode :logical
## FALSE:108 FALSE:88
## TRUE :2 TRUE :22
## NA's :0 NA's :0

```

```

##
##
##
## History.Recurrence.Site.Lung History.Recurrence.Site.Liver
## Mode :logical Mode :logical
## FALSE:88 FALSE:72
## TRUE :22 TRUE :38
## NA's :0 NA's :0
##
##
##
## History.Recurrence.Site.Brain History.Recurrence.Site.Bone
## Mode :logical Mode :logical
## FALSE:109 FALSE:104
## TRUE :1 TRUE :6
## NA's :0 NA's :0
##
##
##
## History.Status History.Death.Date
## Alive - With Disease :15 Min. :2007-11-21
## Alive - Without Disease :22 1st Qu.:2011-01-14
## Deceased - Of Disease :70 Median :2012-03-07
## Deceased - Of Other Cause : 3 Mean :2012-02-21
## Deceased - Of Unknown Cause: 0 3rd Qu.:2013-03-17
## Max. :2014-06-17
## NA's :37
##
## History.Death.Cause Surv.Event.Death
## Cancer Death (Pancreatic) :69 Min. :0.000
## Cancer Death (Other) - Lung ca : 1 1st Qu.:0.000
## Died of Treatment Complication : 1 Median :1.000
## Other (please specify) : 1 Mean :0.664
## Other (please specify) - Suicide: 1 3rd Qu.:1.000
## (Other) : 0 Max. :1.000
## NA's :37
## Surv.EventTimeFromDiag.Death Surv.EventTimeFromSurg.Death
## Min. : 36 Min. : 36
## 1st Qu.: 402 1st Qu.: 406
## Median : 632 Median : 634
## Mean : 674 Mean : 676
## 3rd Qu.: 912 3rd Qu.: 917
## Max. :1778 Max. :1779
##
## Surv.EventTimeFromRec.Death Surv.Event.DSDeath
## Min. : 7 Min. :0.000
## 1st Qu.: 68 1st Qu.:0.000
## Median : 183 Median :1.000
## Mean : 250 Mean :0.636
## 3rd Qu.: 338 3rd Qu.:1.000
## Max. :1333 Max. :1.000
## NA's :29
## Surv.EventTimeFromDiag.DSDeath Surv.EventTimeFromSurg.DSDeath
## Min. : 36 Min. : 36
## 1st Qu.: 402 1st Qu.: 406

```



```

##      Treat.Surgery.ExcisionStatus
##                                0
##      Treat.Surgery.Margin.Comments
##                                0
##                                Path.HistoType
##                                0
##                                Path.Grade
##                                0
##      Path.Nodes.Regional.Total
##                                0
##      Path.Nodes.Regional.Involved
##                                0
##      Path.Nodes.SepRec.Total
##                                0
##      Path.Nodes.SepRec.Involved
##                                0
##      Staging.Version
##                                0
##      Staging.Stage
##                                0
##      History.Recurrence.Site.Stomach
##                                0
##      History.Recurrence.Site.Peritoneum
##                                0
##      History.Recurrence.Site.PancRemnant
##                                0
##      History.Recurrence.Site.PancBed
##                                0
##      History.Recurrence.Site.Other
##                                0
##      History.Recurrence.Site.Omentum
##                                0
##      History.Recurrence.Site.Mesentery
##                                0
##      History.Recurrence.Site.LymphNodes
##                                0
##      History.Recurrence.Site.Lung
##                                0
##      History.Recurrence.Site.Liver
##                                0
##      History.Recurrence.Site.Brain
##                                0
##      History.Recurrence.Site.Bone
##                                0
##      History.Status
##                                0
##      Surv.Event.Death
##                                0
##      Surv.EventTimeFromDiag.Death
##                                0
##      Surv.EventTimeFromSurg.Death
##                                0
##      Surv.Event.DSDeath
##                                0

```



```

##      Surv.EventTimeFromDiag.DSDeath
##                                0
##      Surv.EventTimeFromSurg.DSDeath
##                                0
##      Treat.Surgery.ExcisionStatus.Coarse
##                                0
##              Path.Grade.Coarse
##                                0
##      Path.TumourLocation.Coarse
##                                0
##              Patient.Ethnicity
##                                1
##      History.LastFollowup.Date
##                                1
##              Path.TumourLocation
##                                1
##              Path.TumourSizeMm
##                                1
##              Path.Invasion.PN
##                                1
##              Staging.pN
##                                1
##              Staging.pT
##                                1
## Path.Nodes.Regional.Involved.Fraction
##                                1
##              Path.Invasion.VS
##                                4
##              History.Recurrence
##                                4
##              Surv.Event.Recurrence
##                                4
##      Surv.EventTimeFromDiag.Recurrence
##                                6
##      Surv.EventTimeFromSurg.Recurrence
##                                6
##      Treat.Surgery.Margin.Pancreatic
##                                9
##      Treat.Surgery.Margin.Retrop
##                                12
##      Treat.Surgery.Margin.PVGroove
##                                20
##      Treat.Surgery.Margin.Periunc
##                                23
##      Treat.Surgery.Margin.CBD
##                                26
##      History.Recurrence.Date
##                                29
##      Surv.EventTimeFromRec.Death
##                                29
##      Surv.EventTimeFromRec.DSDeath
##                                29
##      Treat.Surgery.MarginSizeMm.Pancreatic
##                                30

```

```
##      Treat.Surgery.MarginSizeMm.Retrop
##                                31
##      History.Death.Date
##                                37
##      History.Death.Cause
##                                37
##      Treat.Surgery.MarginSizeMm.Periunc
##                                43
##      Treat.Surgery.MarginSizeMm.PVGroove
##                                45
##      Treat.Surgery.MarginSizeMm.CBD
##                                47
##      Treat.Surgery.Margin.Duodenal
##                                49
##      Treat.Surgery.Margin.Gastric
##                                51
##      Path.HistoType.Subtype
##                                66
##      History.Smoking.PackYears
##                                68
##      Treat.Surgery.MarginSizeMm.Duodenal
##                                102
##      Staging.pM
##                                102
##      Treat.Surgery.MarginSizeMm.Gastric
##                                103
```

### 3 Probe selection

```
table(cpss.sis$sel)

##
## FALSE  TRUE
## 12639   361

mean(cpss.sis$sel)

## [1] 0.02777

apply(cpss.sis.permuted, 2, sum)

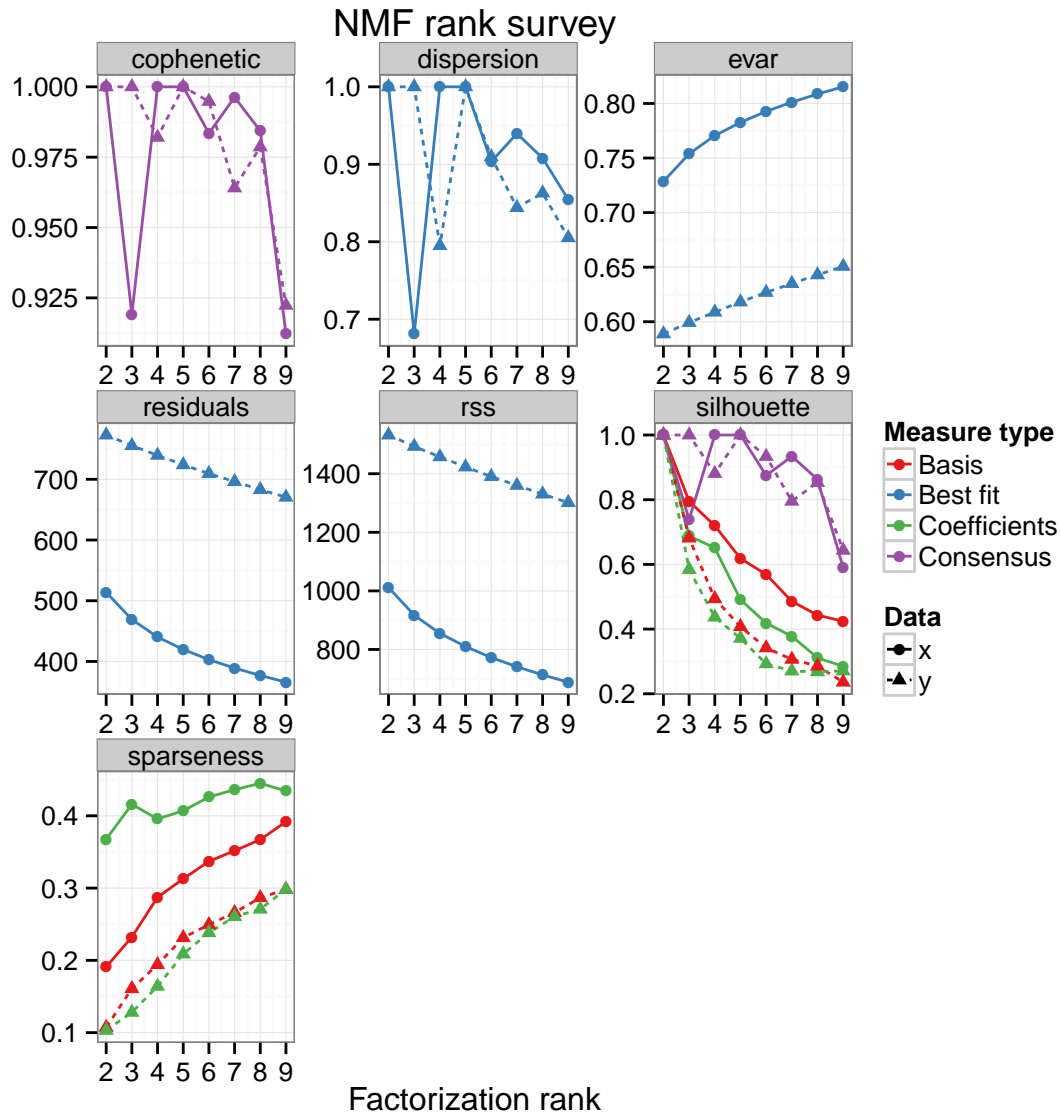
## [1] 37 175 92 32 298 49 47 138 43 173 98 86 207 102 147 41 28
## [18] 160 75 273 154 124 415 109 41 141 50 63 107 63 64 237 84 52
## [35] 40 203 88 55 98 87 57 231 54 48 81 186 114 43 58 347

median(apply(cpss.sis.permuted, 2, sum))

## [1] 87.5
```

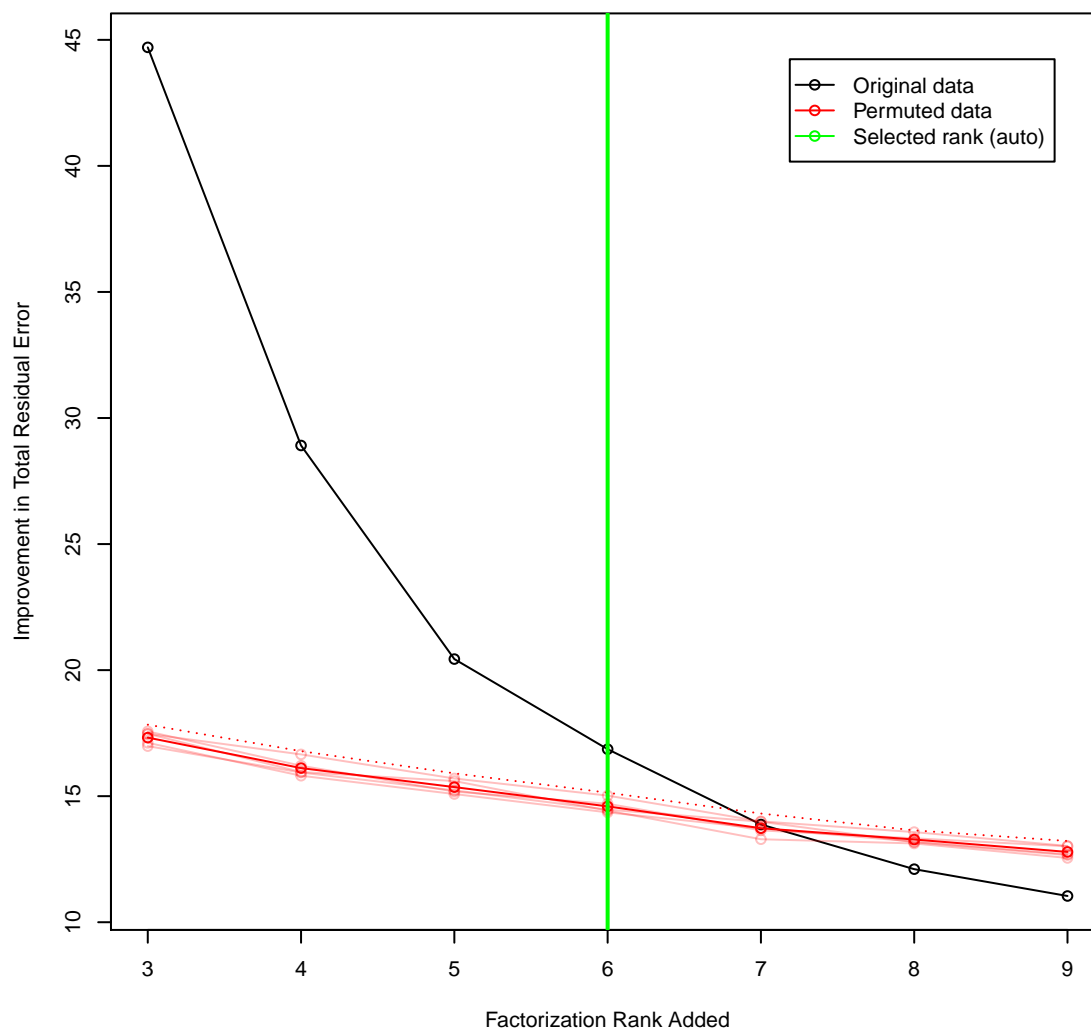
### 4 Factorization

```
plot(nmf.runs.rank, nmf.runs.rank.random[[1]])
```



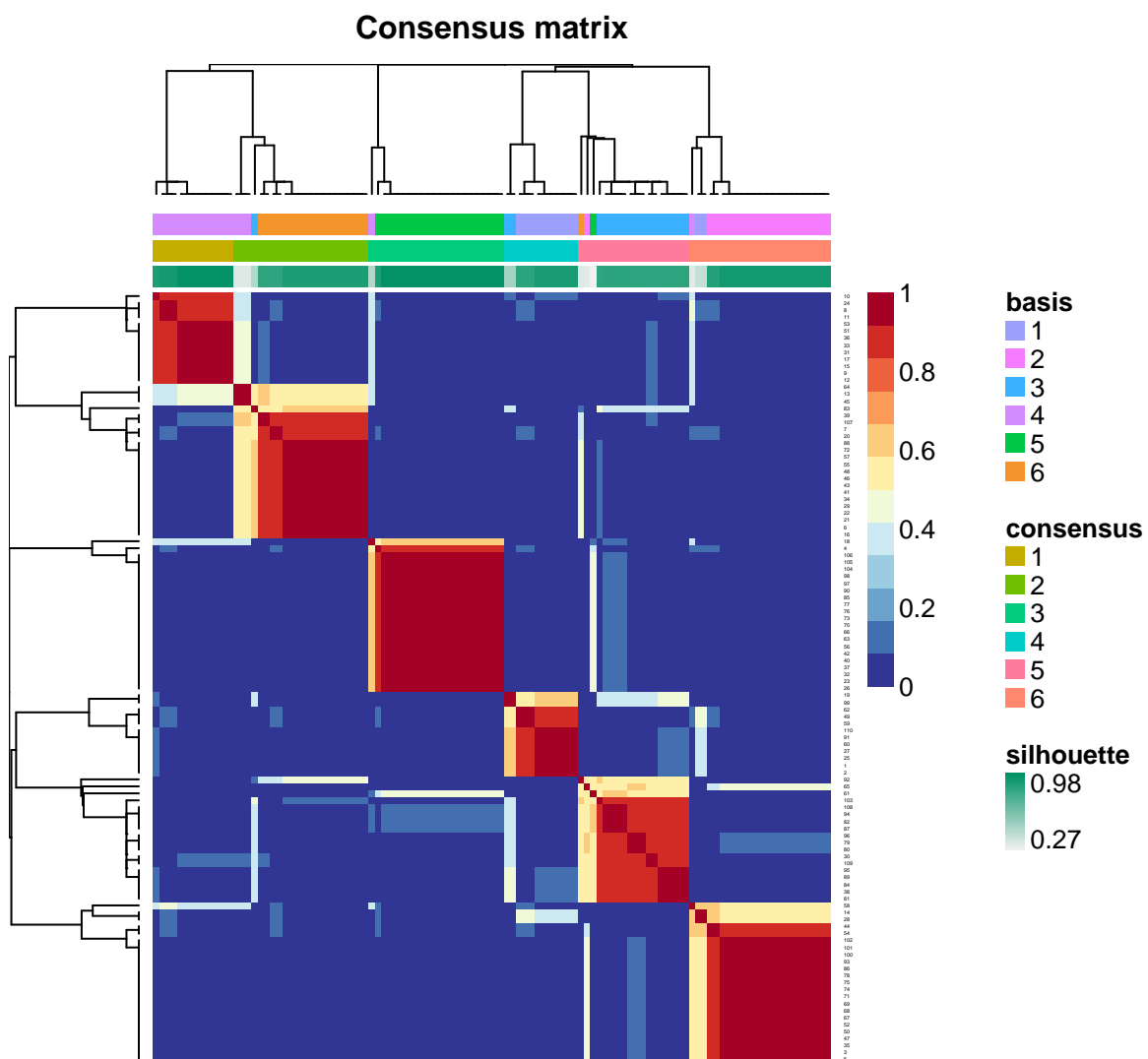
```
plot(nmf.rankrange[-1], -temp.orig_resids.delta, type = "o", col = "black",
     pch = 21, ylim = range(-c(temp.orig_resids.delta, temp.perm_resids.delta.mean)),
     xlab = "Factorization Rank Added", ylab = "Improvement in Total Residual Error")
lines(nmf.rankrange[-1], -temp.perm_resids.delta.mean, col = "red", type = "o",
      pch = 21, lwd = 1)
for (i in 1:ncol(temp.perm_resids)) {
  lines(nmf.rankrange[-1], -temp.perm_resids.delta[, i], type = "o", col = rgb(1,
    0, 0, 0.25))
}
lines(nmf.rankrange[-1], -temp.perm_resids.delta.threshold, col = "red", lty = "dotted")
if (nmf.rank.wasauto == TRUE) {
  temp.col = "green"
} else {
  temp.col = "blue"
}
```

```
abline(v = nmf.rank, col = temp.col, lwd = 2)
legend("topright", legend = c("Original data", "Permuted data", sprintf("Selected rank (%s)",
  ifelse(nmf.rank.wasauto == TRUE, "auto", "fixed"))), col = c("black", "red",
  temp.col), lty = "solid", pch = 21, inset = 0.05)
```

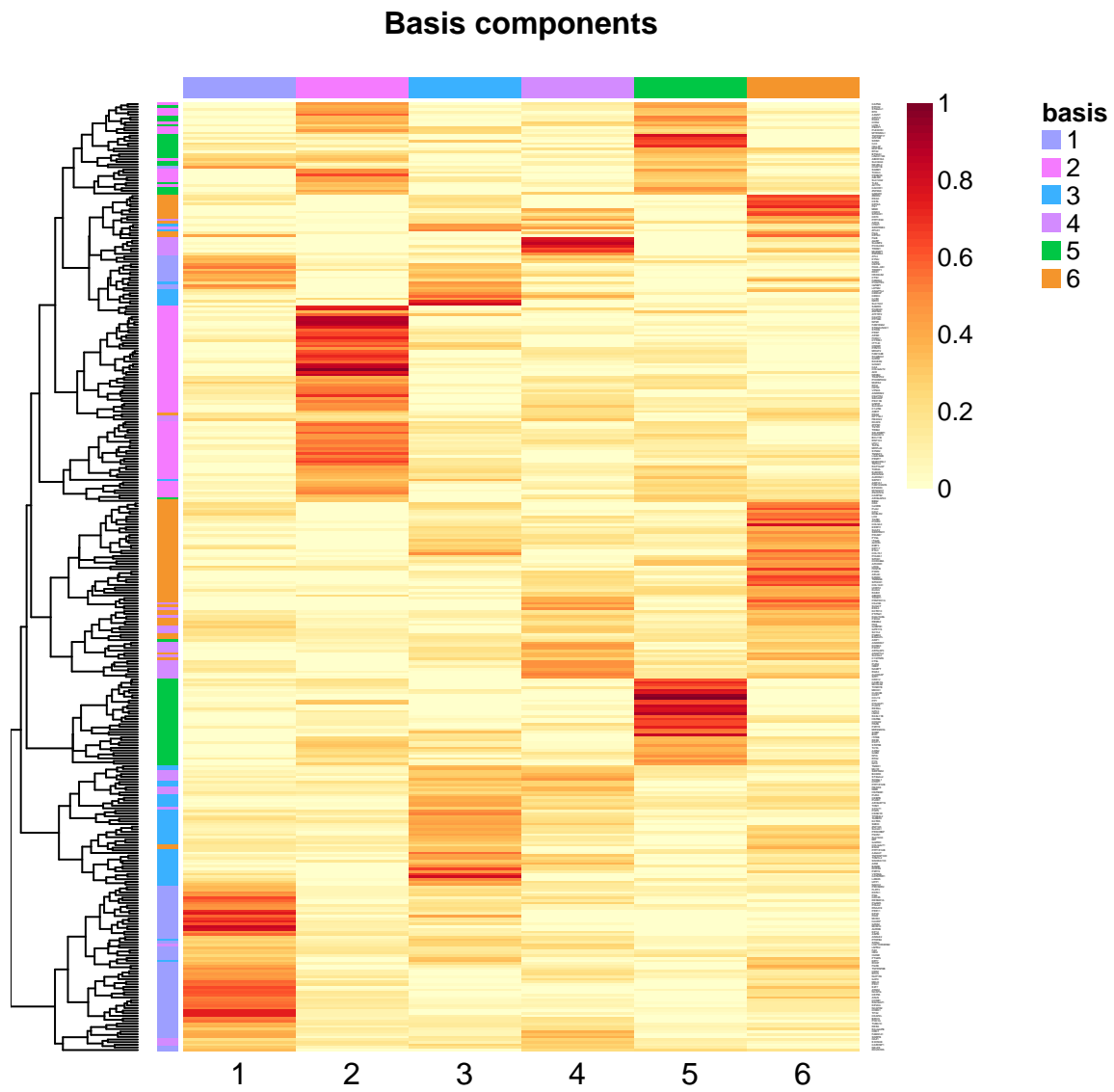


## 4.1 Fit

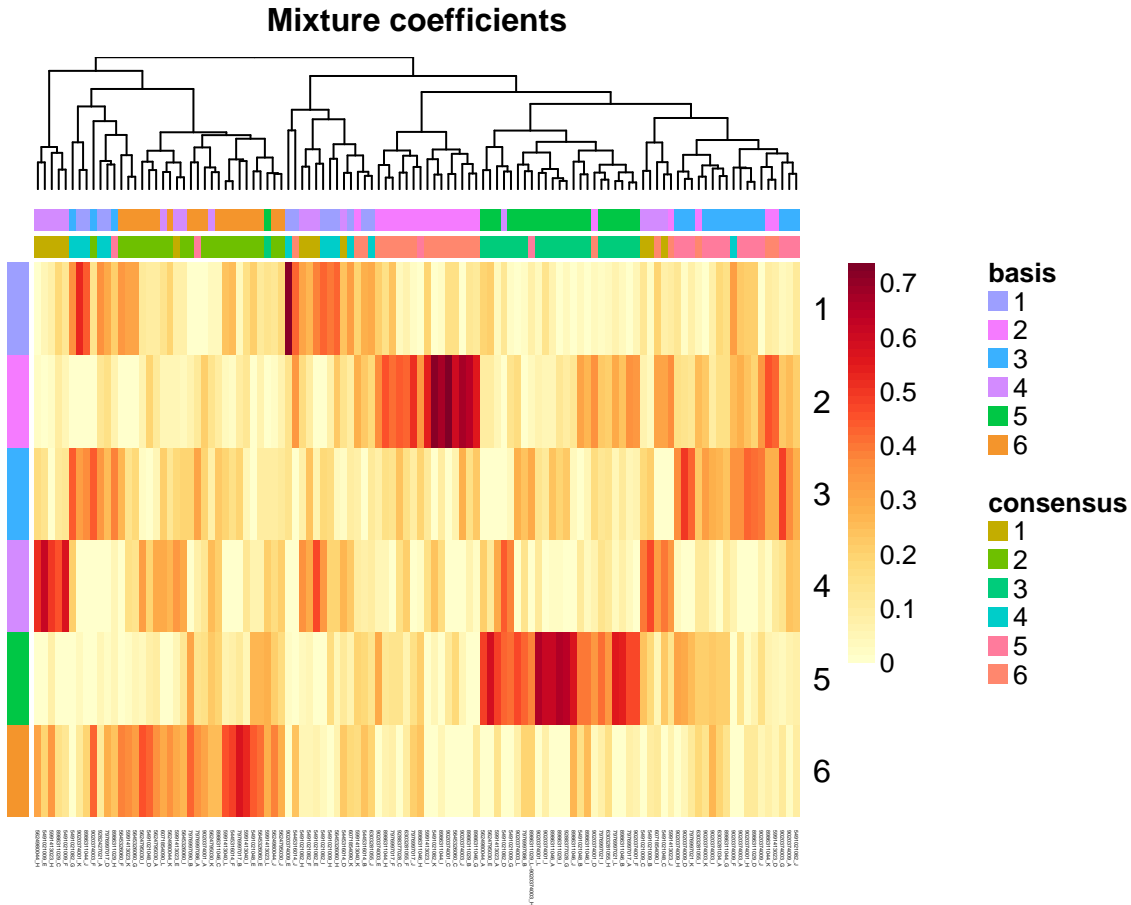
```
consensusmap(nmf.final)
```



```
basismap(nmf.final)
```



```
coefmap(nmf.final)
```



```

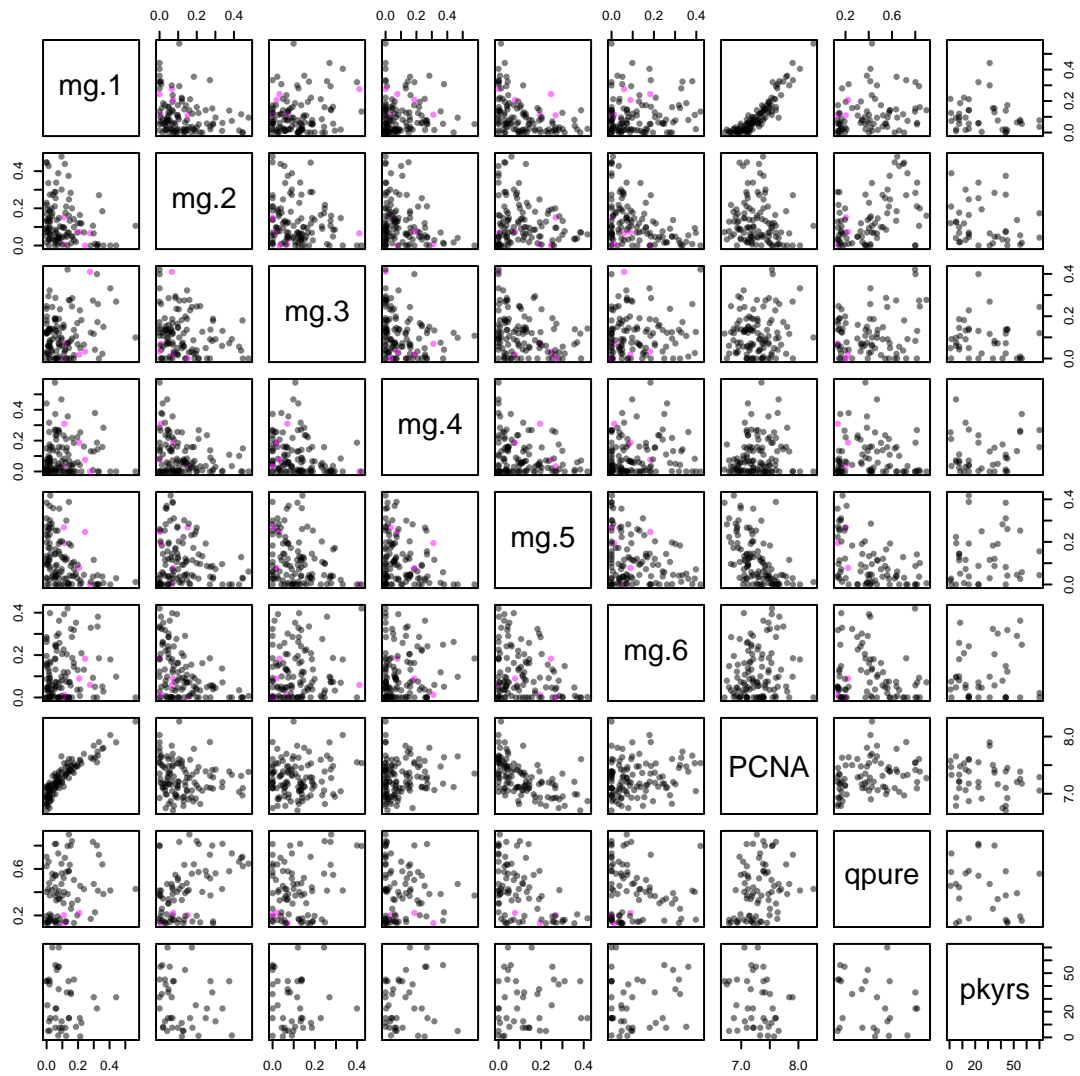
coefs.diag_dsd = apply(xlin.diag_dsd.sel, 2, function(xcol) nnls(basis(nmf.final),
xcol)$x)
coefs.diag_rec = apply(xlin.diag_rec.sel, 2, function(xcol) nnls(basis(nmf.final),
xcol)$x)
coefs.recr_dsd = apply(xlin.recr_dsd.sel, 2, function(xcol) nnls(basis(nmf.final),
xcol)$x)
coefs.pdac_au = apply(xlin.pdac_au.sel, 2, function(xcol) nnls(basis(nmf.final),
xcol)$x)

```

```

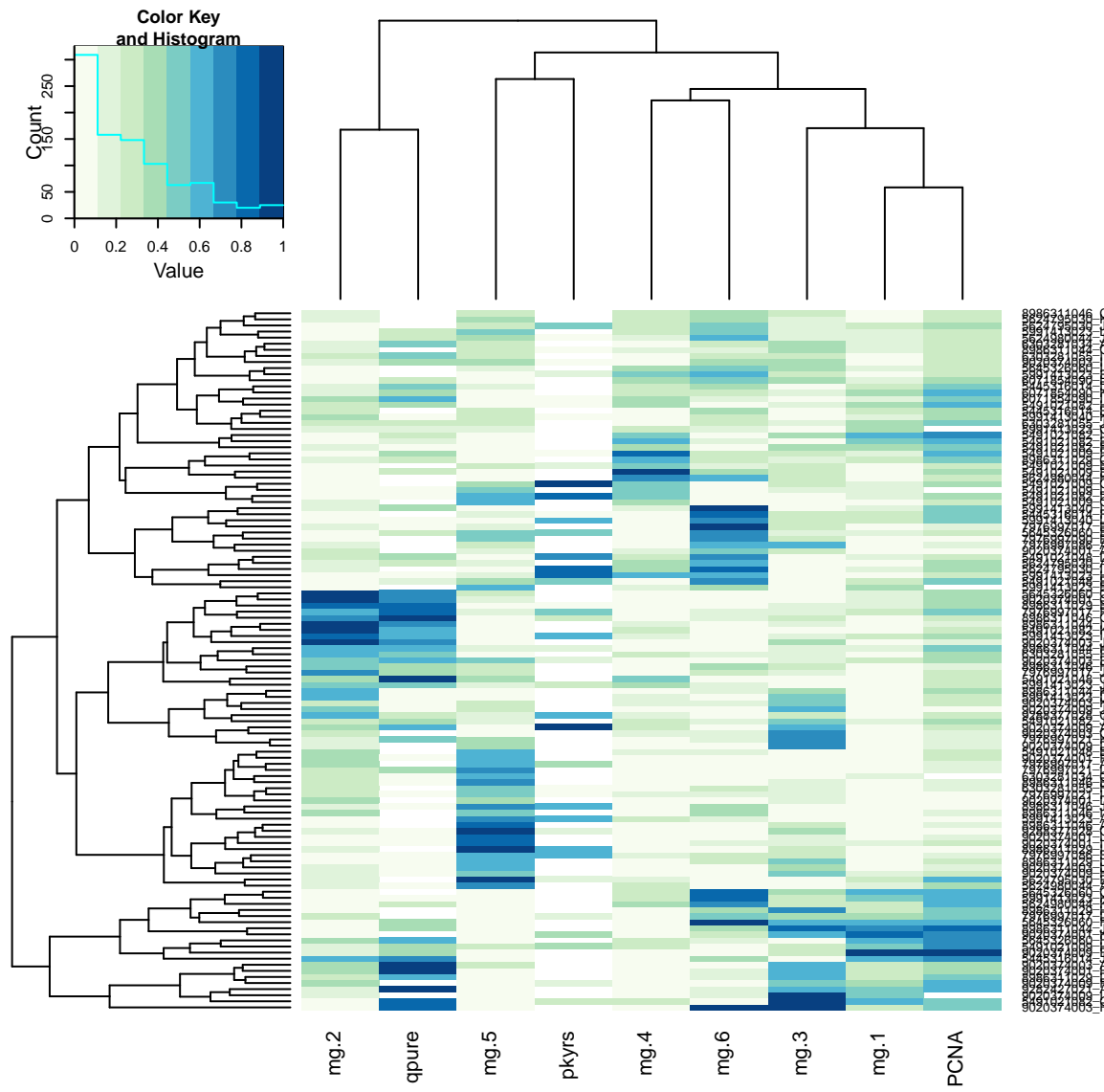
temp.pred.pairs = t(rbind(coefs.pdac_au, metapcna.scores[colnames(coefs.pdac_au)]))
colnames(temp.pred.pairs) = paste("mg", 1:ncol(temp.pred.pairs), sep = ".")
colnames(temp.pred.pairs)[ncol(temp.pred.pairs)] = "PCNA"
temp.pred.pairs = cbind(temp.pred.pairs, qpure = samp.pdac_au$purity_qpure,
pkys = cpvs.pdac_au$History.Smoking.PackYears)
pairs(temp.pred.pairs, pch = 16, cex = 1, col = ifelse(rownames(temp.pred.pairs) %in%
colnames(xlin.diag_dsd.sel), rgb(0, 0, 0, 0.5), rgb(1, 0, 1, 0.5)))

```

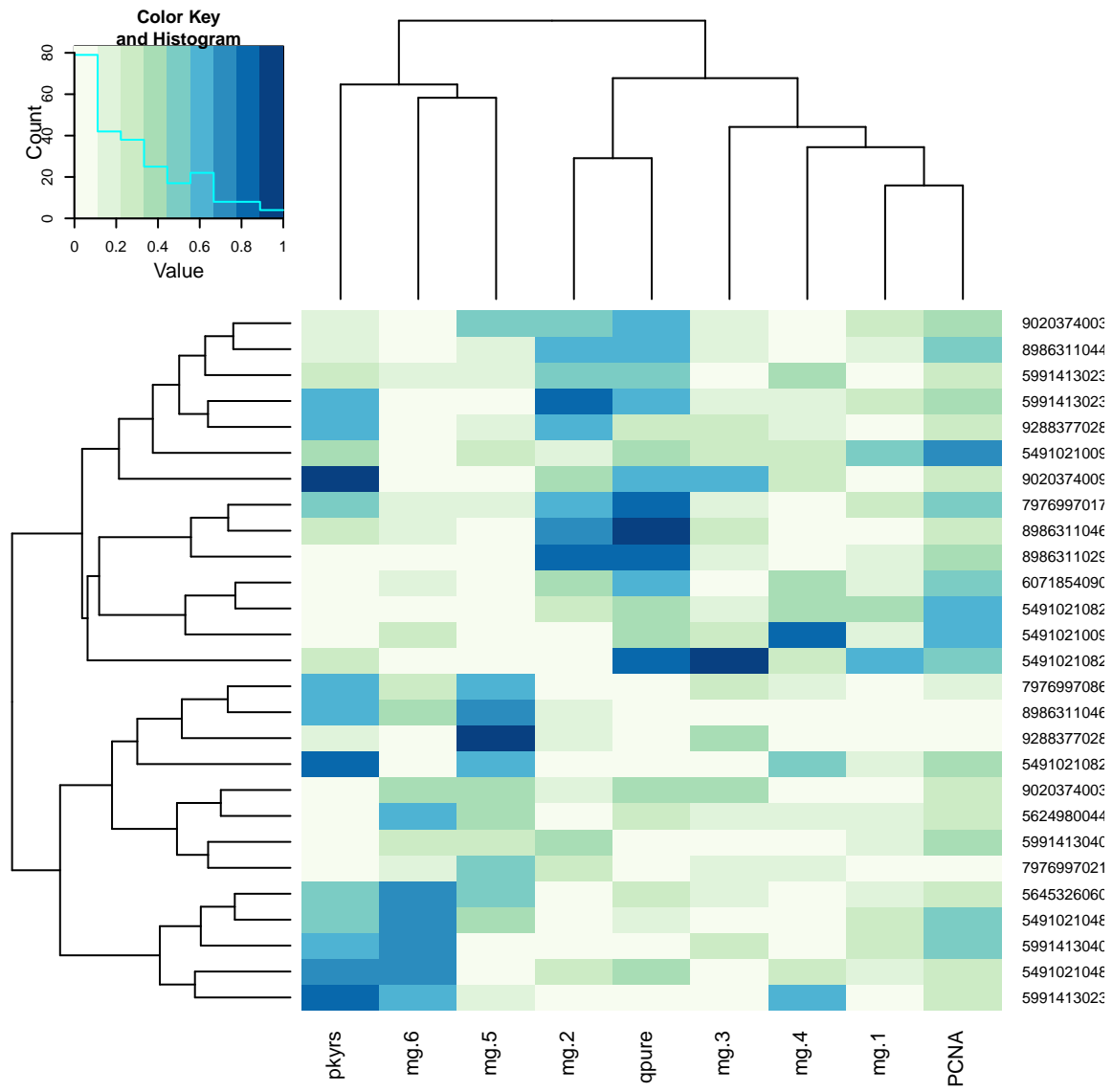


```
temp.pred.pairs.rescaled = t((t(temp.pred.pairs) - apply(temp.pred.pairs, 2,
  min, na.rm = TRUE))/(apply(temp.pred.pairs, 2, function(x) diff(range(x,
  na.rm = TRUE))))))
heatmap.2(temp.pred.pairs.rescaled, trace = "none", scale = "none", col = brewer.pal(9,
  "GnBu"))
```



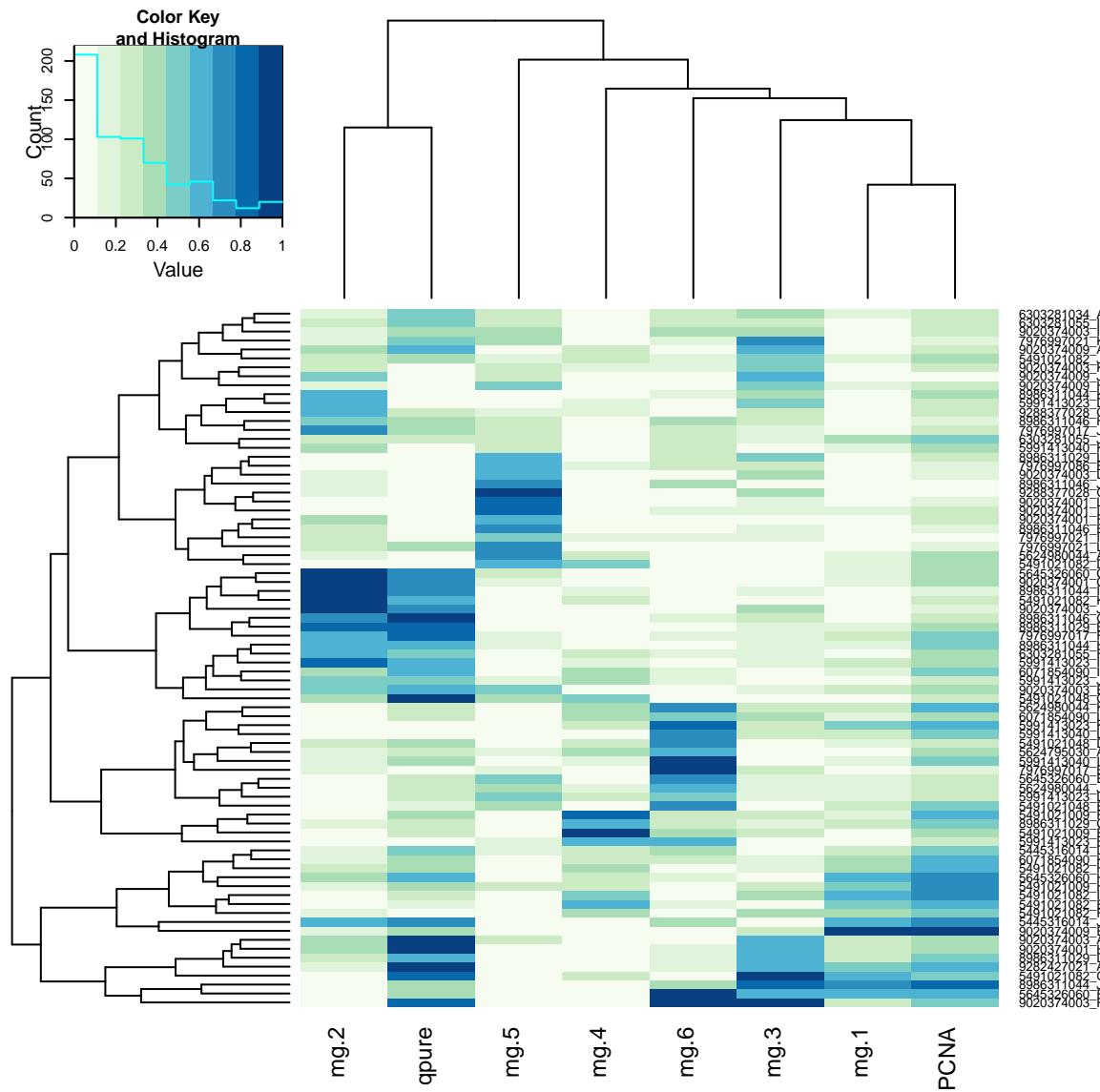


```
heatmap.2(temp.pred.pairs.rescaled[apply(!is.na(temp.pred.pairs.rescaled), 1,
all), ], trace = "none", scale = "none", col = brewer.pal(9, "GnBu"))
```

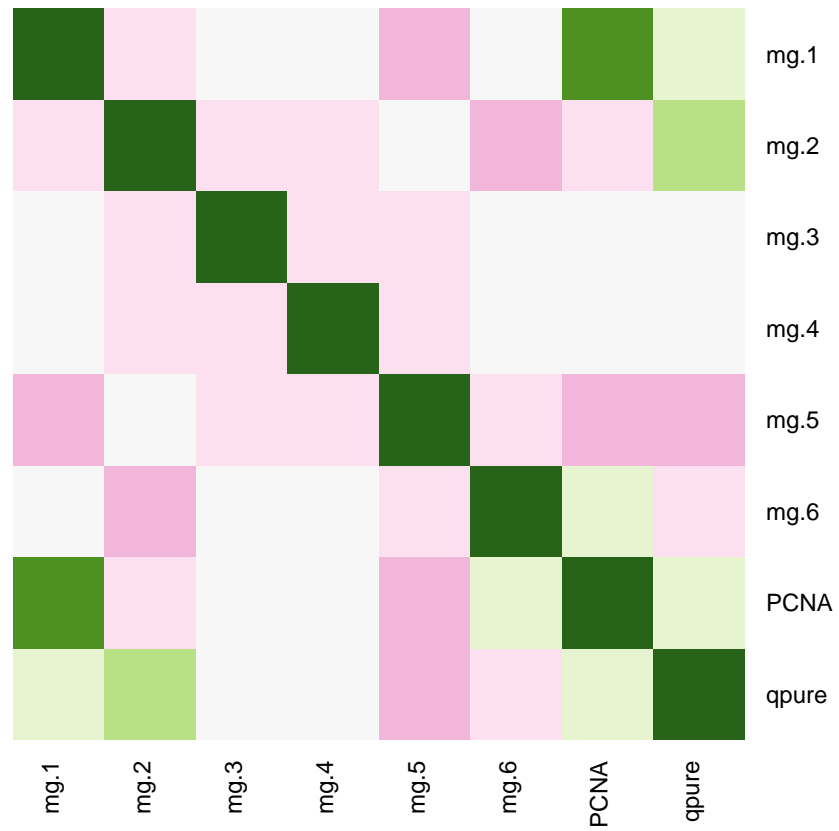
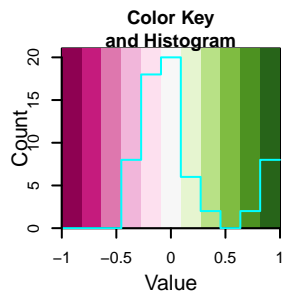


```
temp.pred.pairs.rescaled2 = temp.pred.pairs.rescaled[, colnames(temp.pred.pairs.rescaled) !=
"pkys"]
heatmap.2(temp.pred.pairs.rescaled2, trace = "none", scale = "none", col = brewer.pal(9,
"GnBu"))
```

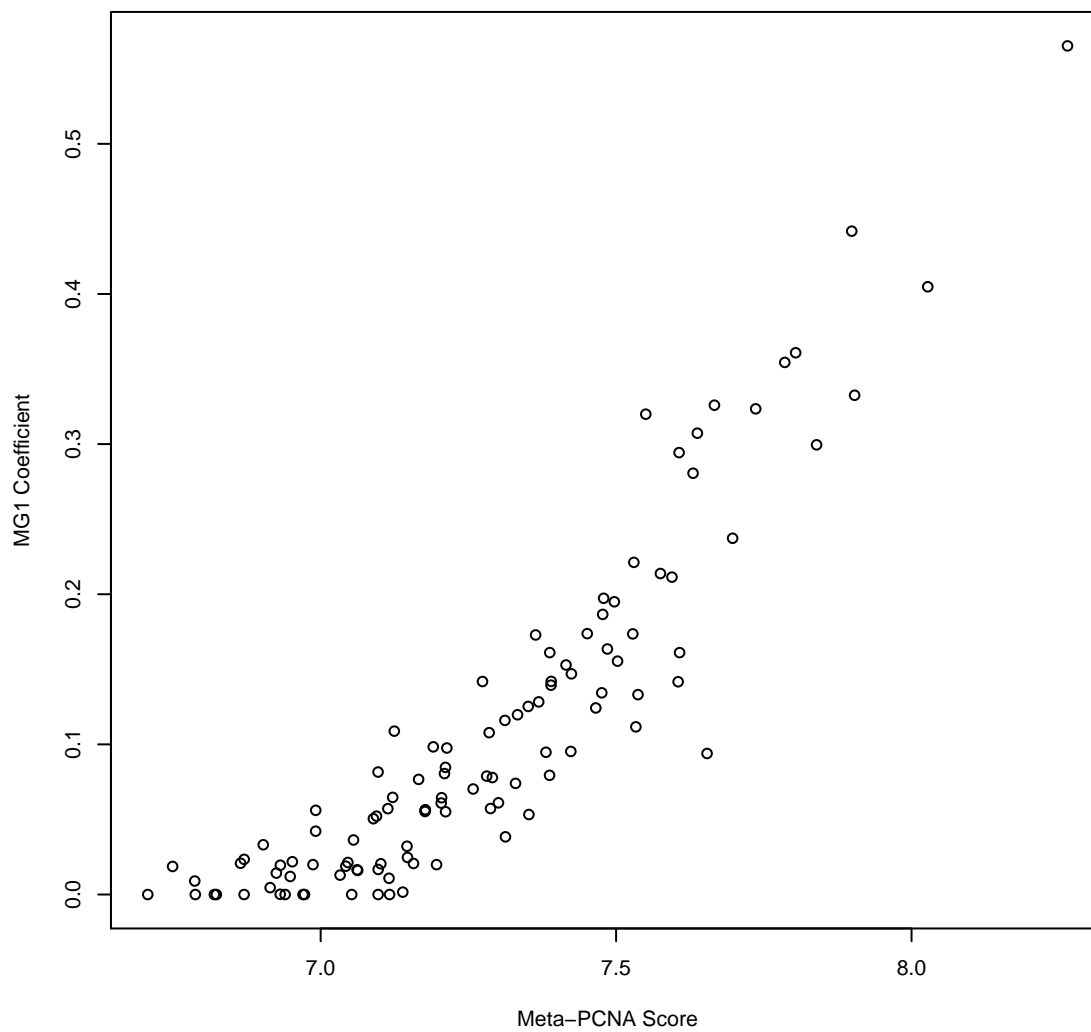




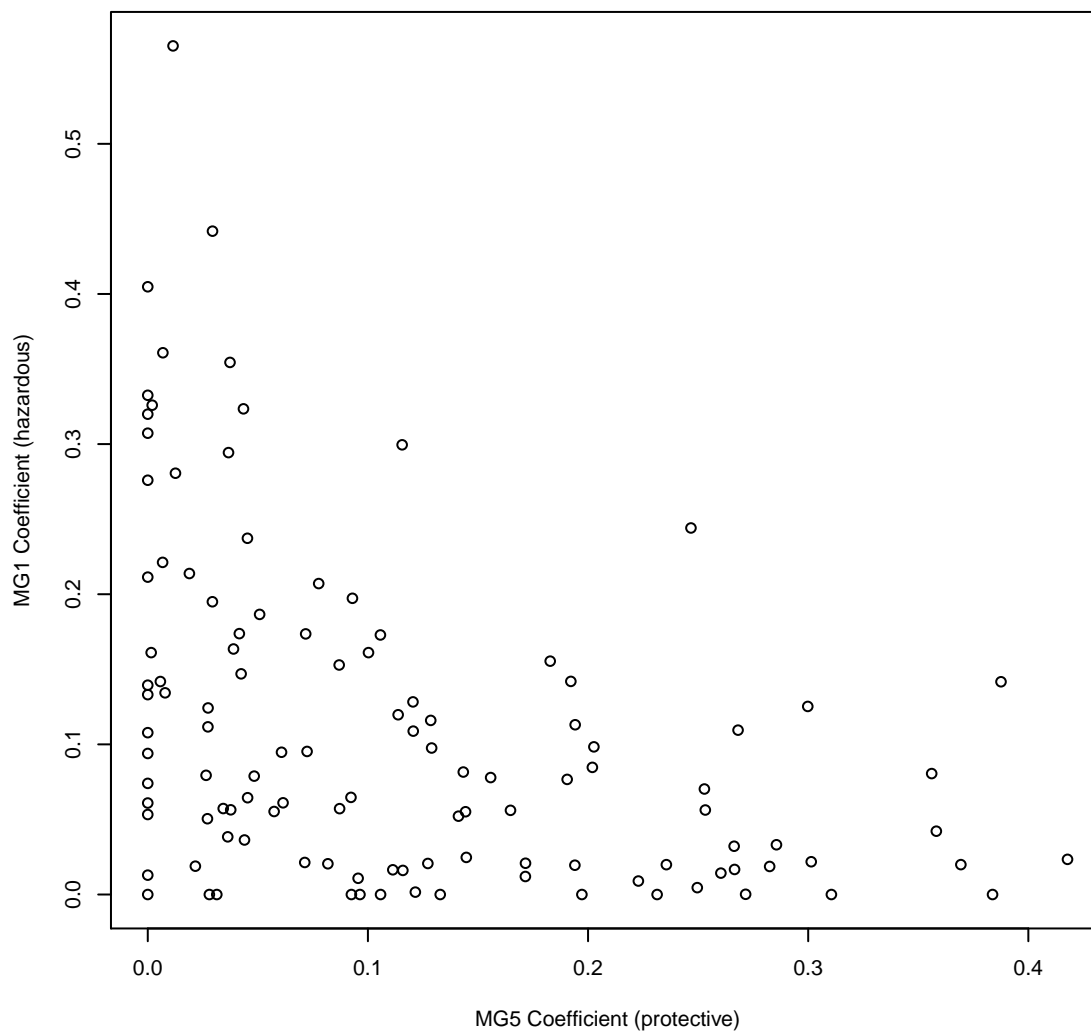
```
temp.cors = apply(temp.pred.pairs[, colnames(temp.pred.pairs) != "pkysr"], 2,
  function(x) apply(temp.pred.pairs[, colnames(temp.pred.pairs) != "pkysr"],
    2, function(y) {
      sel = !(is.na(x) | is.na(y))
      cor(x[sel], y[sel], method = "kendall")
    })
# diag(temp.cors) = NA
heatmap.2(temp.cors, trace = "none", Rowv = FALSE, Colv = FALSE, col = brewer.pal(11,
  "PiYG"), dendrogram = "none", scale = "none")
```



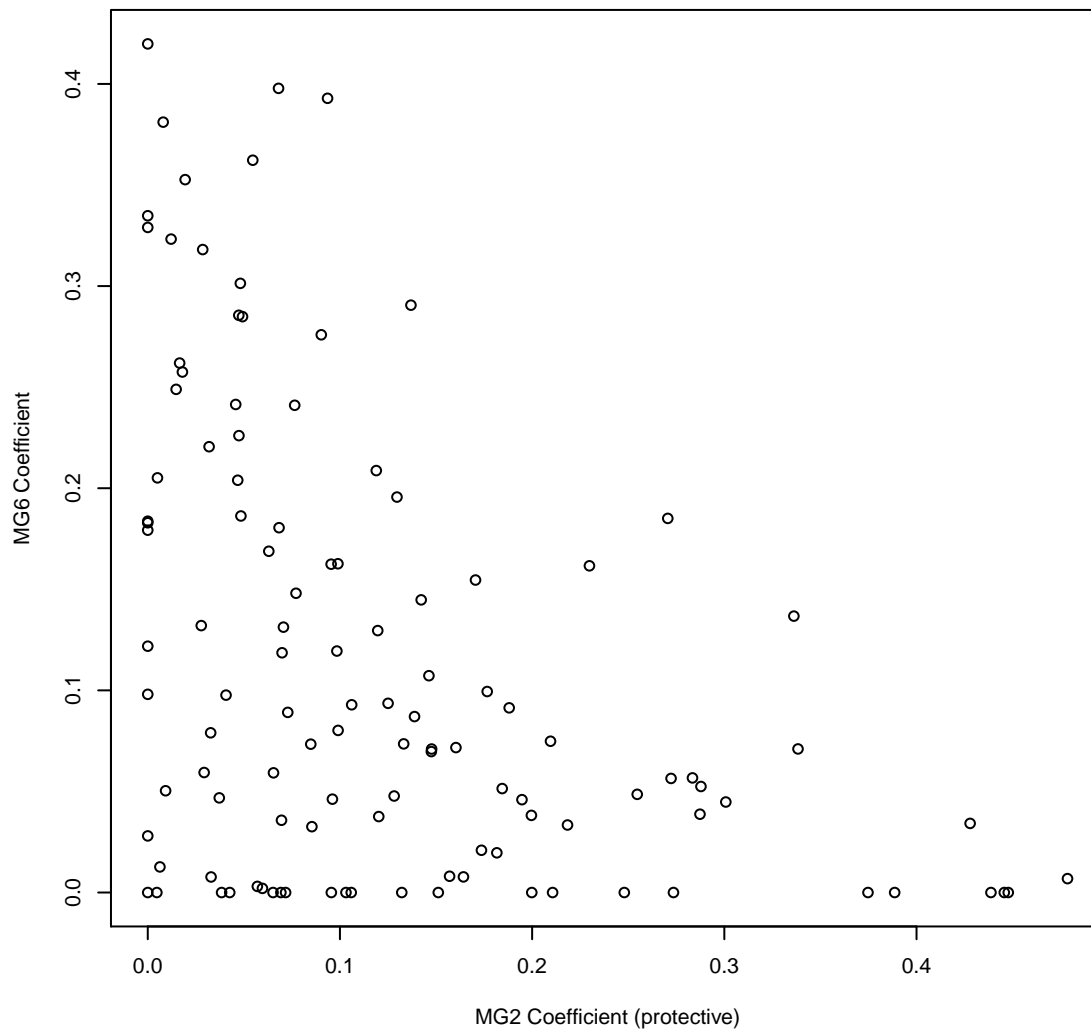
```
plot(temp.pred.pairs[, "mg.1"] ~ temp.pred.pairs[, "PCNA"], col = ifelse(rownames(temp.pred.pairs) %in%
  colnames(xlin.diag_dsd.sel), rgb(0, 0, 0, 1), rgb(0, 0, 0, 0)), xlab = "Meta-PCNA Score",
  ylab = "MG1 Coefficient")
```



```
plot(temp.pred.pairs[, "mg.5"], temp.pred.pairs[, "mg.1"], xlab = "MG5 Coefficient (protective)",  
      ylab = "MG1 Coefficient (hazardous)")
```



```
plot(temp.pred.pairs[, "mg.2"], temp.pred.pairs[, "mg.6"], xlab = "MG2 Coefficient (protective)",
      ylab = "MG6 Coefficient")
```



```
# scatter.smooth(temp.pred.pairs[, 'mg.5'], temp.pred.pairs[, 'mg.1'], xlab =
# 'MG5 Coefficient (protective)', ylab = 'MG1 Coefficient (hazardous)', span
# = 1/4, lpars = list(lwd = 2, col = rgb(0, 0, 0, 0.5)))
# scatter.smooth(temp.pred.pairs[, 'mg.2'], temp.pred.pairs[, 'mg.6'], xlab =
# 'MG2 Coefficient (protective)', ylab = 'MG6 Coefficient', span = 1/4,
# lpars = list(lwd = 2, col = rgb(0, 0, 1, 0.5)))
# smoothScatter(temp.pred.pairs[, 'mg.5'], temp.pred.pairs[, 'mg.1'], xlab =
# 'MG5 Coefficient (protective)', ylab = 'MG1 Coefficient (hazardous)')
# smoothScatter(temp.pred.pairs[, 'mg.2'], temp.pred.pairs[, 'mg.6'], xlab =
# 'MG2 Coefficient (protective)', ylab = 'MG6 Coefficient')

temp.coefs.pdcor = apply(coefs.diag_dsd, 1, function(x1) apply(coefs.diag_dsd,
1, function(x2) dcov.test(x1, x2, R = 9999)$p.value))
temp.coefs.pfisher = apply(coefs.diag_dsd, 1, function(x1) apply(coefs.diag_dsd,
1, function(x2) fisher.test(x1 > median(x1), x2 > median(x2))$p.value))
diag(temp.coefs.pdcor) = NA
temp.coefs.pdcor[lower.tri(temp.coefs.pdcor)] = NA
```



```

diag(temp.coefs.pfisher) = NA
temp.coefs.pfisher[lower.tri(temp.coefs.pfisher)] = NA
temp.coefs.pdcor.holm = matrix(p.adjust(temp.coefs.pdcor, "holm"), nrow = nrow(temp.coefs.pdcor))
temp.coefs.pfisher.holm = matrix(p.adjust(temp.coefs.pfisher, "holm"), nrow = nrow(temp.coefs.pfisher))
temp.coefs.pdcor.holm

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  NA 0.2016 0.4500 1.0000 0.0015 1.0000
## [2,]  NA      NA 0.3066 0.0130 0.1800 0.0015
## [3,]  NA      NA      NA 0.0336 0.0451 1.0000
## [4,]  NA      NA      NA      NA 0.0480 1.0000
## [5,]  NA      NA      NA      NA      NA 0.0480
## [6,]  NA      NA      NA      NA      NA      NA

temp.coefs.pfisher.holm

##      [,1] [,2] [,3] [,4] [,5] [,6]
## [1,]  NA      1 1.0000      1 0.03203 1.00000
## [2,]  NA      NA 0.7286      1 1.00000 0.03203
## [3,]  NA      NA      NA      1 1.00000 1.00000
## [4,]  NA      NA      NA      NA 0.72858 1.00000
## [5,]  NA      NA      NA      NA      NA 1.00000
## [6,]  NA      NA      NA      NA      NA      NA

dcov.test(coefs.diag_dsd[5, ], coefs.diag_dsd[1, ], R = 19999)

##
## dCov test of independence
##
## data: index 1, replicates 19999
## nV^2 = 0.1291, p-value = 5e-05
## sample estimates:
## dCov
## 0.03426

dcov.test(coefs.diag_dsd[2, ], coefs.diag_dsd[6, ], R = 19999)

##
## dCov test of independence
##
## data: index 1, replicates 19999
## nV^2 = 0.1396, p-value = 5e-05
## sample estimates:
## dCov
## 0.03562

cor.test(coefs.diag_dsd[5, ], coefs.diag_dsd[1, ], method = "kendall")

##
## Kendall's rank correlation tau
##
## data: coefs.diag_dsd[5, ] and coefs.diag_dsd[1, ]
## z = -4.97, p-value = 6.694e-07
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
## tau
## -0.3243

```

```

cor.test(coefs.diag_dsd[2, ], coefs.diag_dsd[6, ], method = "kendall")

##
## Kendall's rank correlation tau
##
## data:  coefs.diag_dsd[2, ] and coefs.diag_dsd[6, ]
## z = -4.931, p-value = 8.195e-07
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## -0.3236

temp.axis1 = coefs.diag_dsd[1, ] - coefs.diag_dsd[5, ]
temp.axis2 = coefs.diag_dsd[6, ] - coefs.diag_dsd[2, ]
dcov.test(temp.axis1, temp.axis2, R = 19999)

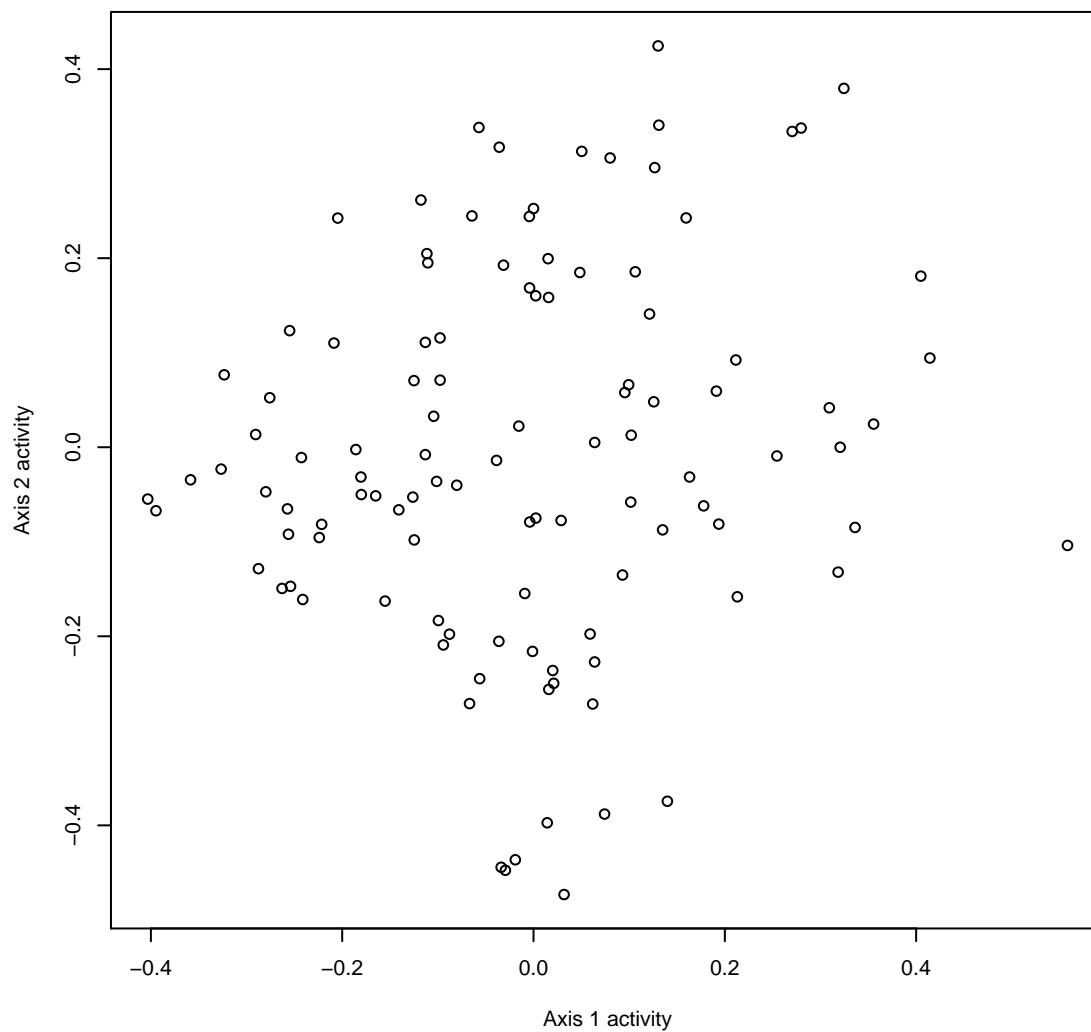
##
## dCov test of independence
##
## data:  index 1, replicates 19999
## nV^2 = 0.1074, p-value = 0.0197
## sample estimates:
##      dCov
## 0.03124

cor.test(temp.axis1, temp.axis2, method = "kendall")

##
## Kendall's rank correlation tau
##
## data:  temp.axis1 and temp.axis2
## z = 1.253, p-value = 0.2103
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## 0.0809

plot(temp.axis2 ~ temp.axis1, xlab = "Axis 1 activity", ylab = "Axis 2 activity")

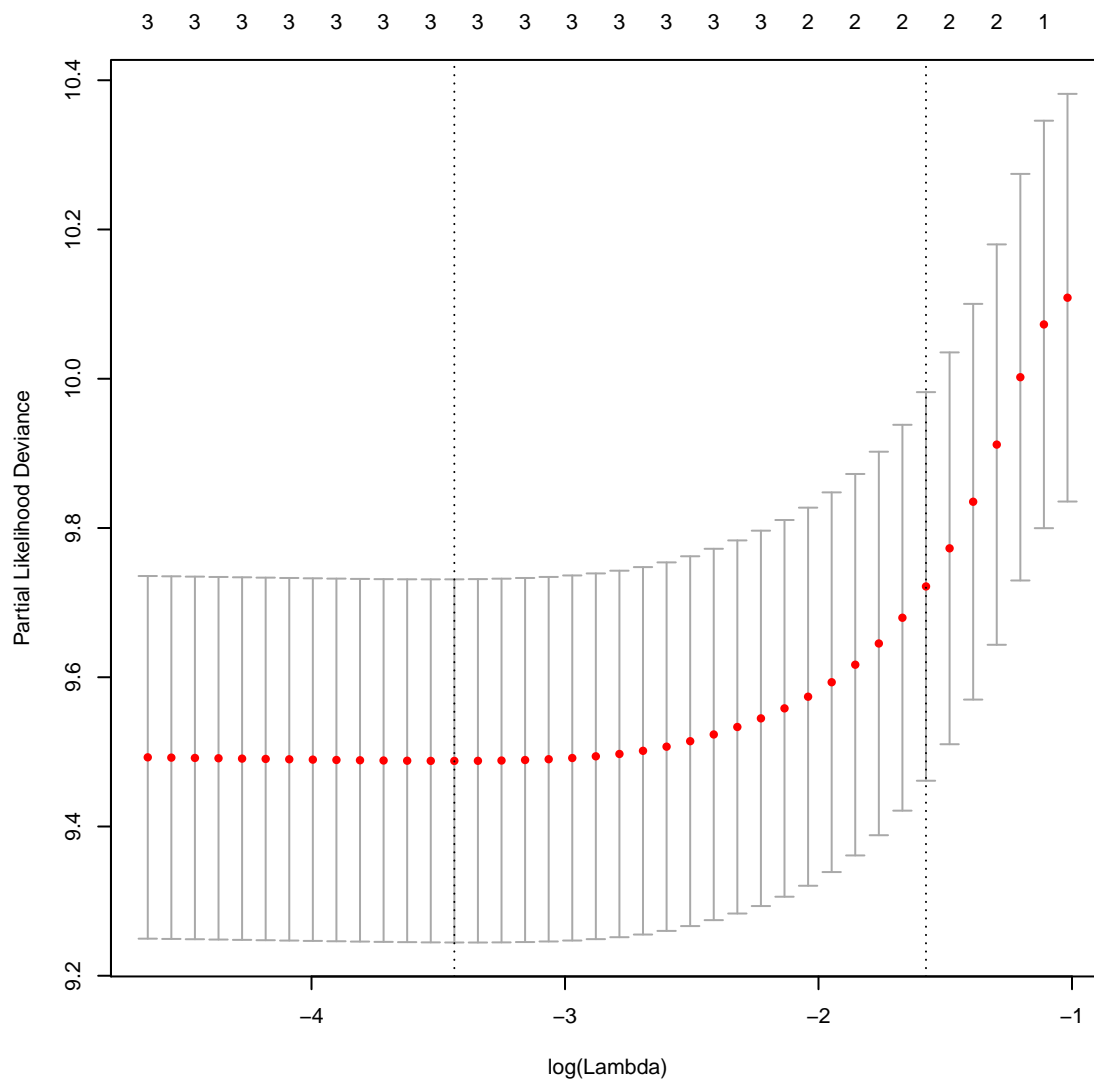
```



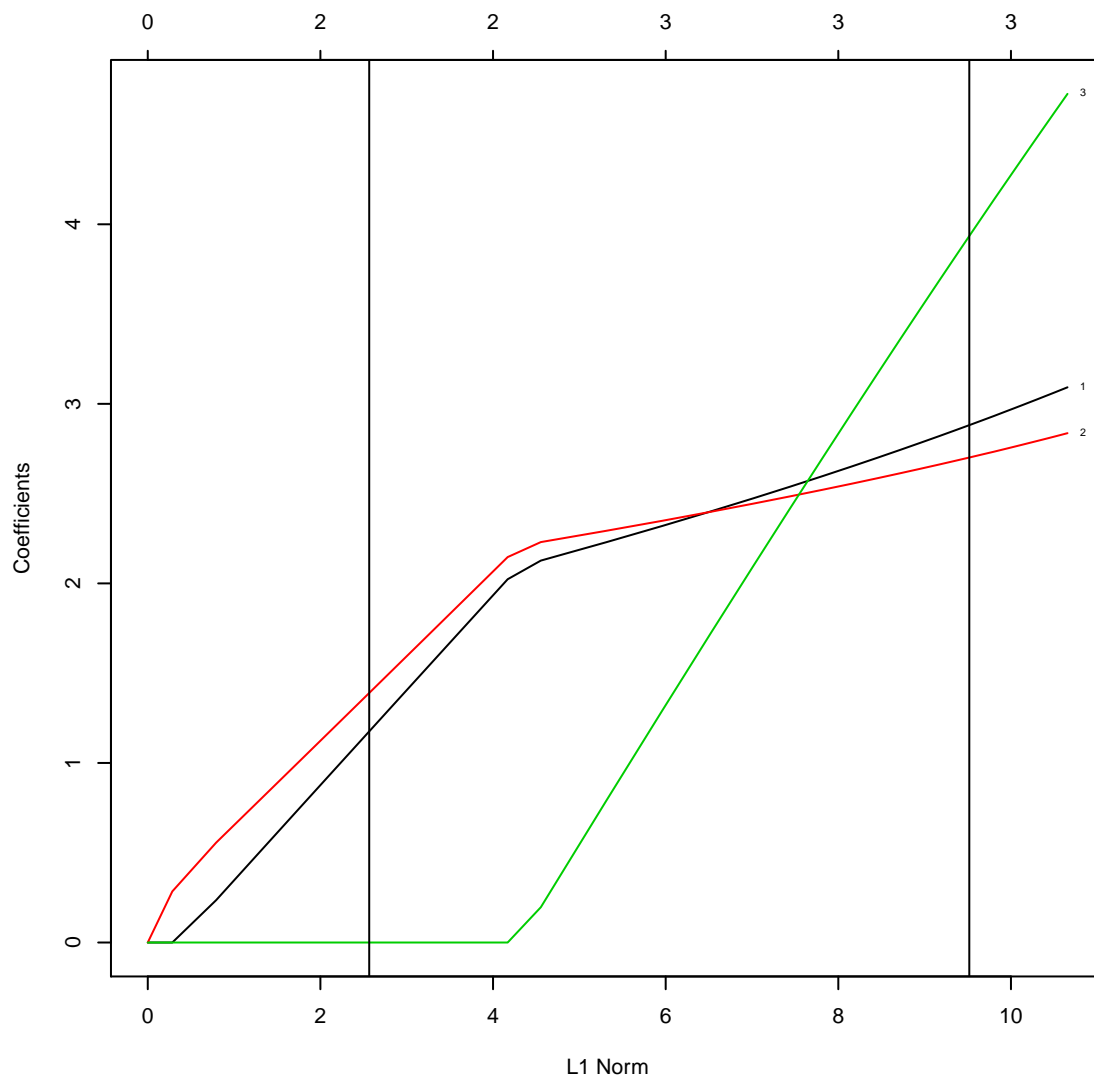
```
coxph(y.diag_dsd ~ temp.axis1 * temp.axis2)

## Call:
## coxph(formula = y.diag_dsd ~ temp.axis1 * temp.axis2)
##
##
##              coef exp(coef) se(coef)      z      p
## temp.axis1      3.19      24.2    0.676  4.72 2.4e-06
## temp.axis2      2.89      18.0    0.657  4.40 1.1e-05
## temp.axis1:temp.axis2 5.03     153.1    4.189  1.20 2.3e-01
##
## Likelihood ratio test=48 on 3 df, p=2.12e-10 n= 110, number of events= 70

temp = cv.glmnet(cbind(temp.axis1, temp.axis2, temp.axis1 * temp.axis2), y.diag_dsd,
  family = "cox", nfolds = 10)
plot(temp)
```



```
plot(temp$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(temp$glmnet.fit, s = temp$lambda.1se))))
abline(v = sum(abs(coef(temp$glmnet.fit, s = temp$lambda.min))))
```



```
coef(temp$glmnet.fit, s = temp$lambda.1se)

## 3 x 1 sparse Matrix of class "dgCMatrix"
##           1
## temp.axis1 1.176
## temp.axis2 1.390
##           .
```

## 4.2 LASSO on training set

```
glmnet.fit.cv.diag_dsd = cv.glmnet(t(coefs.diag_dsd), y.diag_dsd, family = "cox",
  nfolds = 10)
glmnet.fit.cv.diag_rec = cv.glmnet(t(coefs.diag_rec), y.diag_rec, family = "cox",
  nfolds = 10)
glmnet.fit.cv.recr_dsd = cv.glmnet(t(coefs.recr_dsd), y.recr_dsd, family = "cox",
```

```

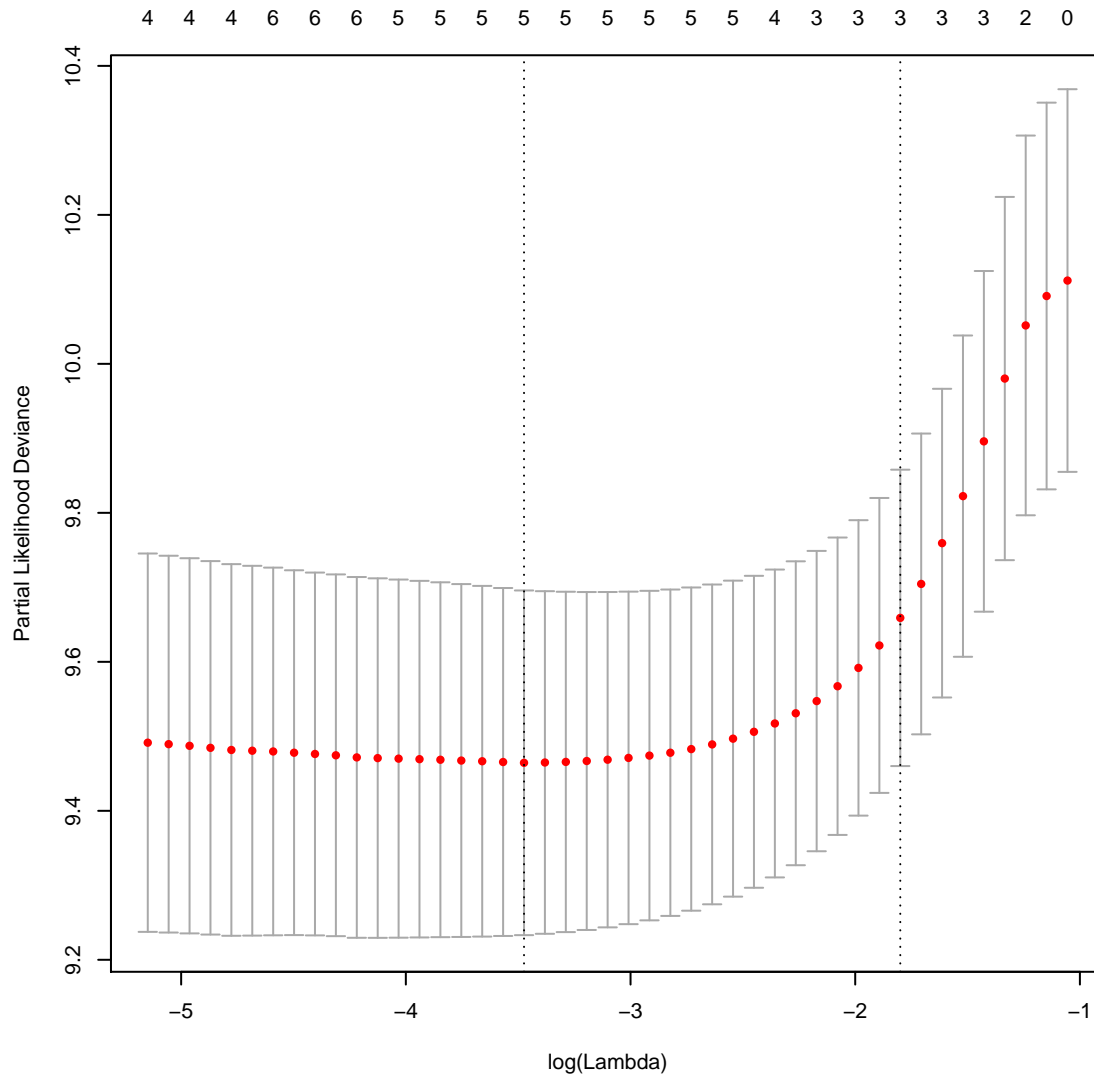
n folds = 10)
axis_coefs.diag_dsd = as.matrix(cbind(axis1 = coefs.diag_dsd[1, ] - coefs.diag_dsd[5,
], axis2 = coefs.diag_dsd[6, ] - coefs.diag_dsd[2, ]))

```

```

plot(glmnet.fit.cv.diag_dsd)

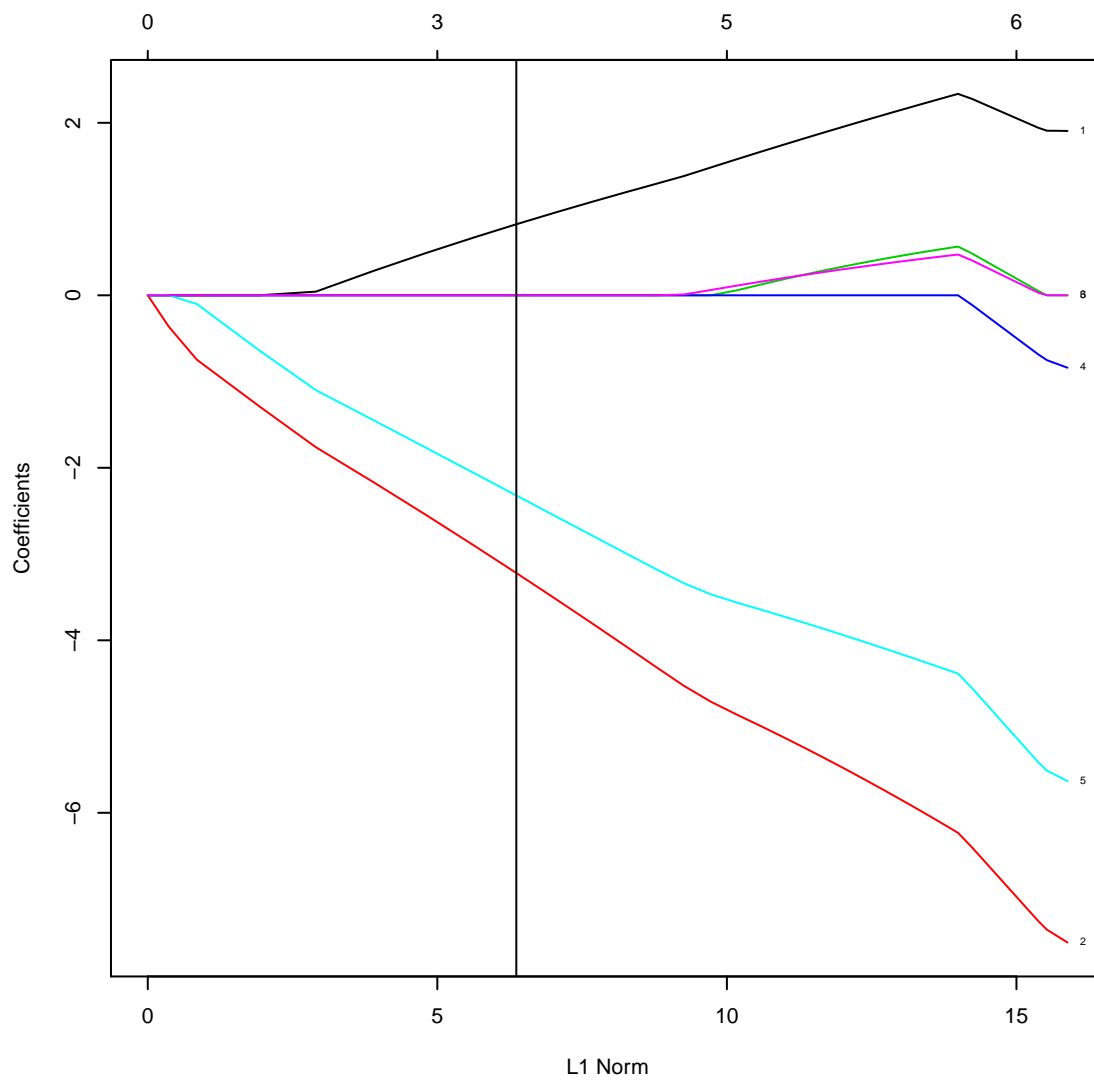
```



```

plot(glmnet.fit.cv.diag_dsd$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s = glmnet.fit.cv.diag_dsd$lambda.1se))))

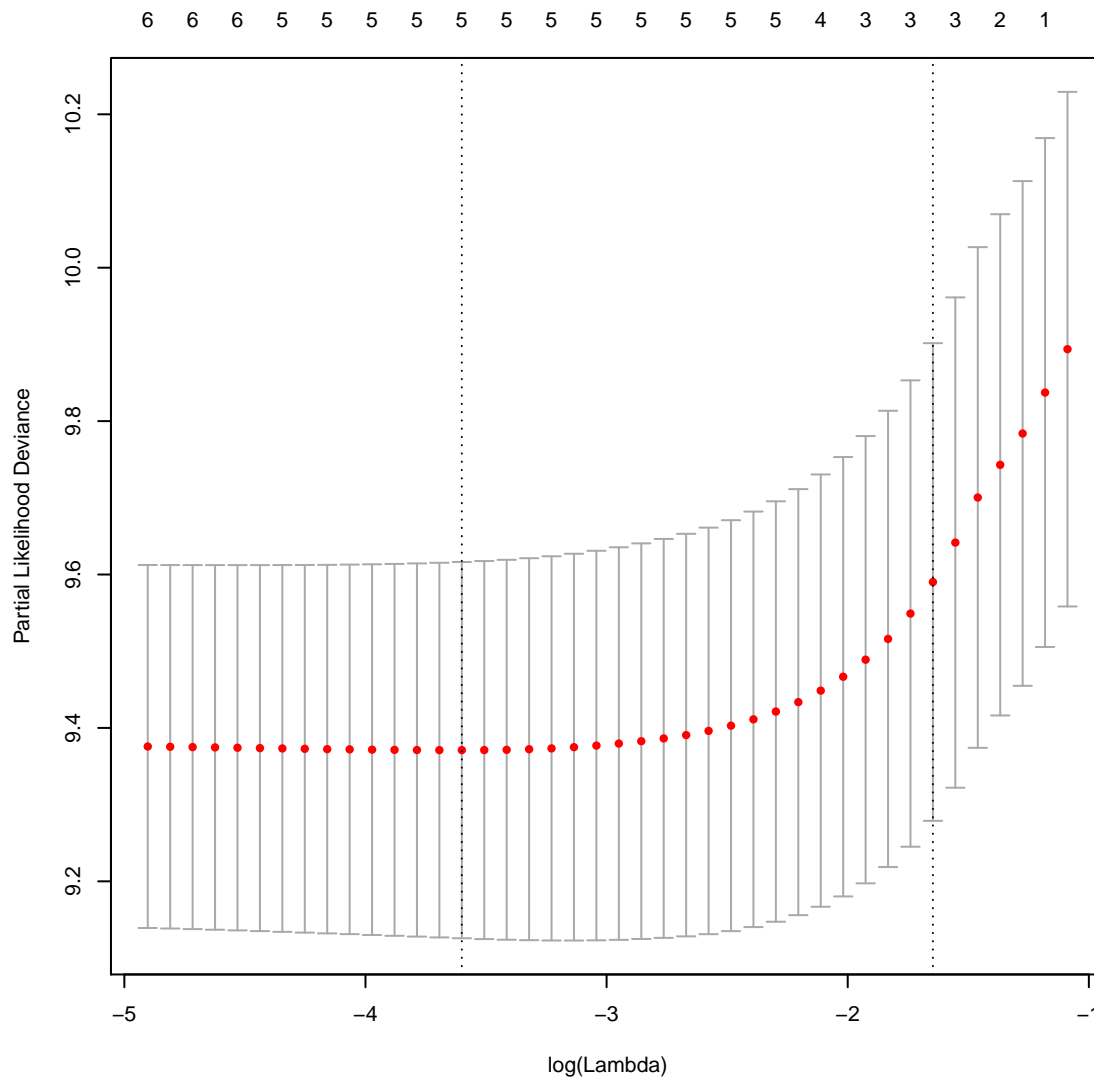
```



```
# abline(v = sum(abs(coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s =
# glmnet.fit.cv.diag_dsd$lambda.min))))
coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s = glmnet.fit.cv.diag_dsd$lambda.1se)

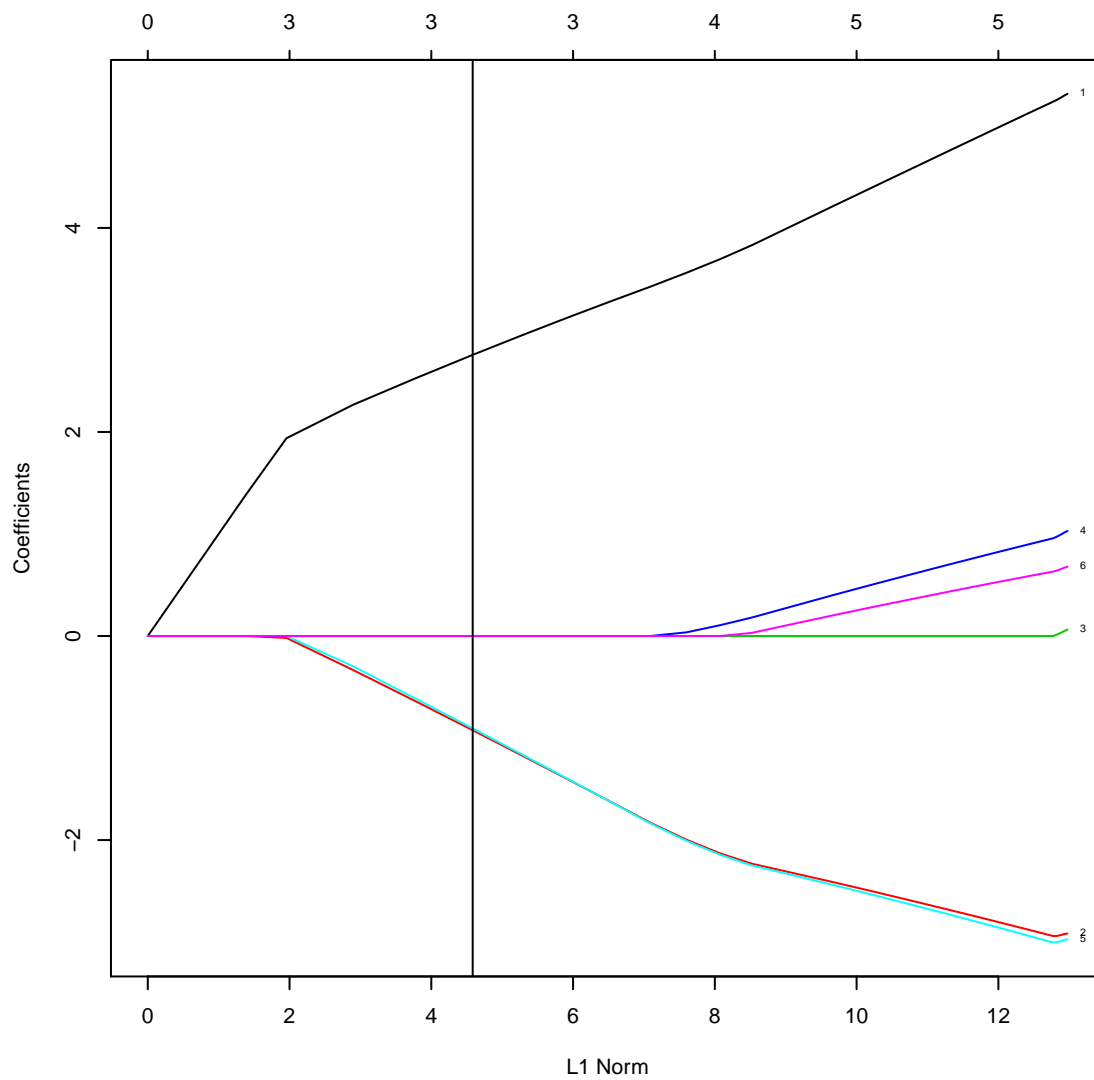
## 6 x 1 sparse Matrix of class "dgCMatrix"
##      1
## V1  0.8238
## V2 -3.2195
## V3  .
## V4  .
## V5 -2.3208
## V6  .

plot(glmnet.fit.cv.diag_rec)
```



```
plot(glmnet.fit.cv.diag_rec$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(glmnet.fit.cv.diag_rec$glmnet.fit, s = glmnet.fit.cv.diag_rec$lambda.1se))))
```

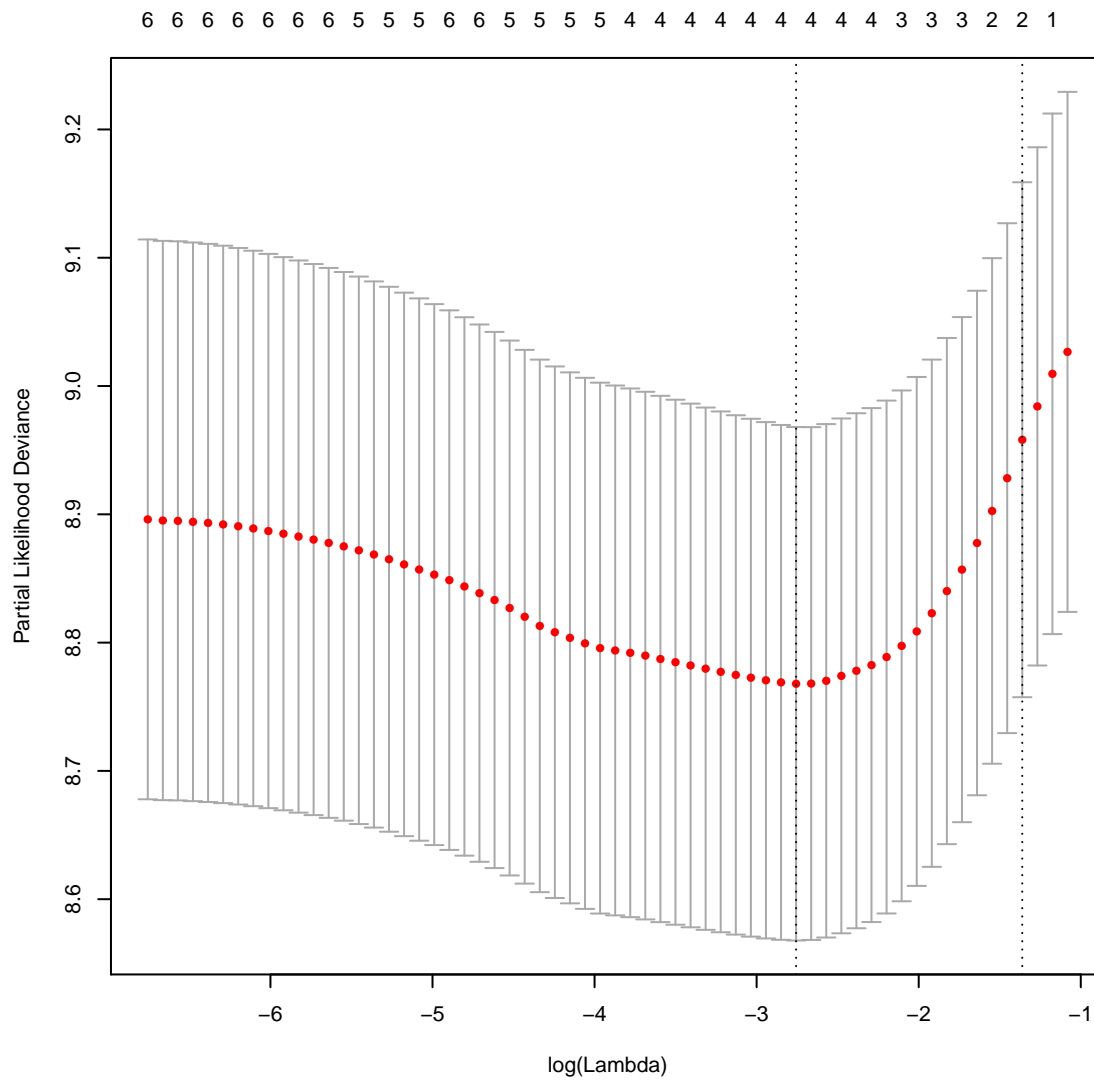




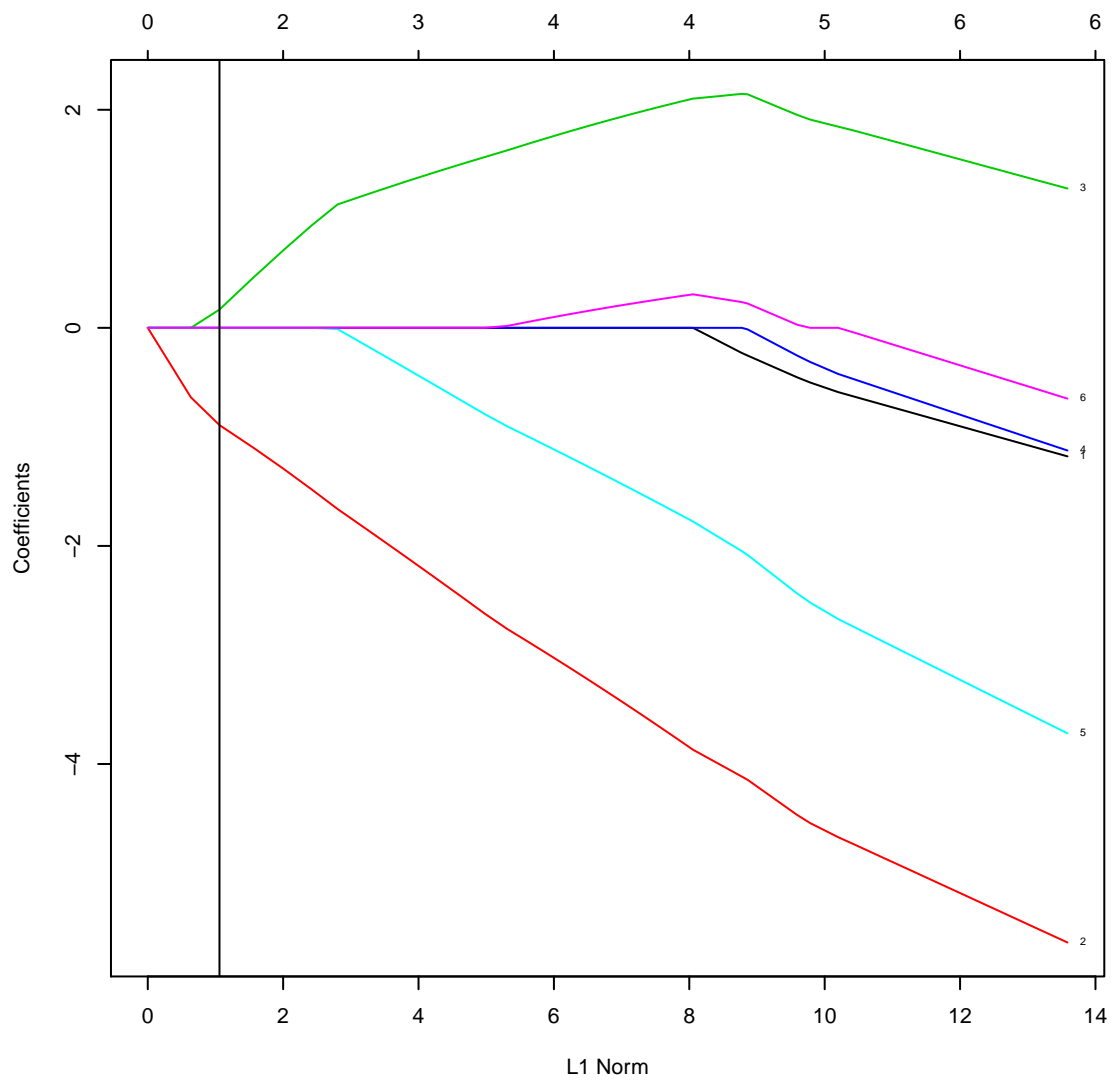
```
# abline(v = sum(abs(coef(glmnet.fit.cv.diag_rec$glmnet.fit, s =
# glmnet.fit.cv.diag_rec$lambda.min))))
coef(glmnet.fit.cv.diag_rec$glmnet.fit, s = glmnet.fit.cv.diag_rec$lambda.1se)

## 6 x 1 sparse Matrix of class "dgCMatrix"
##      1
## V1  2.7555
## V2 -0.9230
## V3  .
## V4  .
## V5 -0.9055
## V6  .

plot(glmnet.fit.cv.recr_dsd)
```



```
plot(glmnet.fit.cv.recr_dsd$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(glmnet.fit.cv.recr_dsd$glmnet.fit, s = glmnet.fit.cv.recr_dsd$lambda.1se))))
```



```
# abline(v = sum(abs(coef(glmnet.fit.cv.recr_dsd$glmnet.fit, s =
# glmnet.fit.cv.recr_dsd$lambda.min))))
coef(glmnet.fit.cv.recr_dsd$glmnet.fit, s = glmnet.fit.cv.recr_dsd$lambda.1se)

## 6 x 1 sparse Matrix of class "dgCMatrix"
##      1
## V1  .
## V2 -0.8920
## V3  0.1676
## V4  .
## V5  .
## V6  .
```

### 4.3 Prediction on validation sets

```
load("../data/15_validation.rda")
```

```
val.basis = basis(nmf.final)
rownames(GSE21501.lingex) = GSE21501.feats$Gene.symbol
rownames(GSE28735.lingex) = GSE28735.feats$Gene.symbol
GSE21501.lingex.for_basis = GSE21501.lingex[match(rownames(val.basis), rownames(GSE21501.lingex)),
]
GSE28735.lingex.for_basis = GSE28735.lingex[match(rownames(val.basis), rownames(GSE28735.lingex)),
]
GSE21501.lingex.for_basis[is.na(GSE21501.lingex.for_basis)] = 0
GSE28735.lingex.for_basis[is.na(GSE28735.lingex.for_basis)] = 0

GSE21501.coefs = apply(GSE21501.lingex.for_basis, 2, function(xcol) nnls(val.basis,
xcol)$x)
GSE28735.coefs = apply(GSE28735.lingex.for_basis, 2, function(xcol) nnls(val.basis,
xcol)$x)

GSE21501.axis1 = GSE21501.coefs[1, ] - GSE21501.coefs[5, ]
GSE21501.axis2 = GSE21501.coefs[6, ] - GSE21501.coefs[2, ]
GSE28735.axis1 = GSE28735.coefs[1, ] - GSE28735.coefs[5, ]
GSE28735.axis2 = GSE28735.coefs[6, ] - GSE28735.coefs[2, ]

GSE21501.score = 1.354 * GSE21501.axis1 + 1.548 * GSE21501.axis2
GSE28735.score = 1.354 * GSE28735.axis1 + 1.548 * GSE28735.axis2

GSE21501.pcna = apply(GSE21501.gex[match(metapcna.sig, GSE21501.feats$Gene.symbol),
], 2, median, na.rm = TRUE)
GSE28735.pcna = apply(GSE28735.gex[match(metapcna.sig, GSE28735.feats$Gene.symbol),
], 2, median, na.rm = TRUE)
```

```
temp = coxph(Surv(GSE21501.samp$time, GSE21501.samp$event) ~ GSE21501.score)
summary(temp)
```

```
## Call:
## coxph(formula = Surv(GSE21501.samp$time, GSE21501.samp$event) ~
##      GSE21501.score)
##
##      n= 102, number of events= 66
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## GSE21501.score 1.81      6.13    1.14 1.59    0.11
##
##              exp(coef) exp(-coef) lower .95 upper .95
## GSE21501.score    6.13    0.163    0.655    57.3
##
## Concordance= 0.577 (se = 0.042 )
## Rsquare= 0.024 (max possible= 0.993 )
## Likelihood ratio test= 2.49 on 1 df,  p=0.115
## Wald test              = 2.52 on 1 df,  p=0.112
## Score (logrank) test = 2.54 on 1 df,  p=0.111
```

```
temp = coxph(Surv(GSE28735.samp$time, GSE28735.samp$event) ~ GSE28735.score)
summary(temp)
```

```
## Call:
## coxph(formula = Surv(GSE28735.samp$time, GSE28735.samp$event) ~
##       GSE28735.score)
##
##      n= 42, number of events= 29
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## GSE28735.score 1.867      6.471    0.752 2.48   0.013
##
##              exp(coef) exp(-coef) lower .95 upper .95
## GSE28735.score      6.47      0.155      1.48     28.2
##
## Concordance= 0.655 (se = 0.064 )
## Rsquare= 0.132 (max possible= 0.981 )
## Likelihood ratio test= 5.92 on 1 df,  p=0.0149
## Wald test               = 6.17 on 1 df,  p=0.013
## Score (logrank) test = 6.46 on 1 df,  p=0.011

anova(coxph(Surv(GSE21501.samp$time, GSE21501.samp$event) ~ GSE21501.axis1 +
  GSE21501.axis2))

## Analysis of Deviance Table
## Cox model: response is Surv(GSE21501.samp$time, GSE21501.samp$event)
## Terms added sequentially (first to last)
##
##              loglik Chisq Df Pr(>|Chi|)
## NULL                -255
## GSE21501.axis1      -254  1.44  1      0.23
## GSE21501.axis2      -254  1.09  1      0.30

anova(coxph(Surv(GSE28735.samp$time, GSE28735.samp$event) ~ GSE28735.axis1 +
  GSE28735.axis2))

## Analysis of Deviance Table
## Cox model: response is Surv(GSE28735.samp$time, GSE28735.samp$event)
## Terms added sequentially (first to last)
##
##              loglik Chisq Df Pr(>|Chi|)
## NULL                -83.1
## GSE28735.axis1      -81.4  3.43  1      0.064
## GSE28735.axis2      -80.2  2.51  1      0.113
```

```
load("../data/validation/tcga-clin-gex.20141118.rda")
```

```
doValForSingleCancer = function(cancer_id) {
  # nevents, ntotal, score_p, anova_pcna, anova_score, anova_axis1,
  # anova_axis2
  message(cancer_id)
  cancer_data = data.merged[[cancer_id]]
  if (!"illuminahisec_rnaseqv2" %in% names(cancer_data$gex)) {
    return(c(0, 0, NA, NA, NA, NA, NA))
  }
}
```

```
gex = cancer_data$gex$Illuminahiseq_rnaseqv2
clin = cancer_data$clin

days_to_death = clin$days_to_death
days_to_death[days_to_death == "[Not Applicable]"] = NA
days_to_death = as.numeric(as.character(days_to_death))

days_to_initial_pathologic_diagnosis = clin$days_to_initial_pathologic_diagnosis
days_to_initial_pathologic_diagnosis[days_to_initial_pathologic_diagnosis ==
"[Not Applicable]"] = NA
days_to_initial_pathologic_diagnosis = as.numeric(as.character(days_to_initial_pathologic_diagnosis))

days_to_last_followup = clin$days_to_last_followup
days_to_last_followup[days_to_last_followup == "[Not Applicable]"] = NA
days_to_last_followup = as.numeric(as.character(days_to_last_followup))

time_event = days_to_death - days_to_initial_pathologic_diagnosis
time_lfu = days_to_last_followup - days_to_initial_pathologic_diagnosis
time_obs = time_event
time_obs[is.na(time_obs)] = time_lfu[is.na(time_obs)]
time_obs[!is.na(time_obs) & !is.na(time_lfu)] = pmin(time_obs[!is.na(time_obs) &
!is.na(time_lfu)], time_lfu[!is.na(time_obs) & !is.na(time_lfu)])
event = (time_event <= time_lfu & !is.na(time_event) & !is.na(time_lfu)) |
(!is.na(time_event) & is.na(time_lfu))

y = Surv(time_obs, event)

gex = gex[!grepl("^\\|?\\|\\|", rownames(gex)), ]
rownames(gex) = gsub("\\|\\.+", "", rownames(gex))

pcna = apply(log2(gex[rownames(gex) %in% metapcna.sig, ] + 1), 2, median)

gex.axes = gex[match(rownames(val.basis), rownames(gex)), ]
gex.axes[apply(is.na(gex.axes), 1, all), ] = 0
gex.axes = gex.axes - apply(gex.axes, 1, min, na.rm = TRUE)
gex.axes = gex.axes / apply(gex.axes, 1, max, na.rm = TRUE)
gex.axes[is.na(gex.axes)] = 0

coefs = apply(gex.axes, 2, function(xcol) nnls(val.basis, xcol)$x)

axis1 = coefs[1, ] - coefs[5, ]
axis2 = coefs[6, ] - coefs[2, ]
score = 1.354 * axis1 + 1.548 * axis2

valid = !is.na(score) & !is.na(pcna) & !is.na(y[, 1]) & !is.na(y[, 2])
axis1 = axis1[valid]
axis2 = axis2[valid]
score = score[valid]
pcna = pcna[valid]
y = y[valid, ]

nevents = sum(y[, 2])
ntotal = nrow(y)
```

```

    score_p = pchisq(2 * diff(coxph(y ~ score)$loglik), 1, lower.tail = FALSE)
    anova_pcna = anova(coxph(y ~ pcna + score))[, "Pr(>|Chi|)"][2]
    anova_score = anova(coxph(y ~ pcna + score))[, "Pr(>|Chi|)"][3]
    anova_axis1 = anova(coxph(y ~ axis1 + axis2))[, "Pr(>|Chi|)"][2]
    anova_axis2 = anova(coxph(y ~ axis1 + axis2))[, "Pr(>|Chi|)"][3]

    c(nevents, ntotal, score_p, anova_pcna, anova_score, anova_axis1, anova_axis2)
}

val_pvals = sapply(names(data.merged), doValForSingleCancer)

## acc
## blca
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## brca
## cesc
## coad
## dlbc
## Warning in fitter(X, Y, strats, offset, init, control, weights = weights, : Loglik converged
before variable 1,2 ; beta may be infinite.
## Warning in fitter(X, Y, strats, offset, init, control, weights = weights, : Loglik converged
before variable 1,2 ; beta may be infinite.
## gbm
## hnsc
## kich
## kirc
## kirp
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## lgg
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## lihc
## luad
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## lusc
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hnsc", : NAs introduced
by coercion
## meso
## ov
## paad
## prad
## Warning in fitter(X, Y, strats, offset, init, control, weights = weights, : Ran out of
iterations and did not converge
## Warning in fitter(X, Y, strats, offset, init, control, weights = weights, : Ran out of
iterations and did not converge

```

```
## read
## sarc
## skcm
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hns", : NAs introduced
by coercion
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hns", : NAs introduced
by coercion
## thca
## ucec
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hns", : NAs introduced
by coercion
## Warning in FUN(c("acc", "blca", "brca", "cesc", "coad", "dlbc", "gbm", "hns", : NAs introduced
by coercion
## ucs

rownames(val_pvals) = c("nevents", "ntotal", "p.score", "p.anova.pcna", "p.anova.pcna_score",
  "p.anova.axis1", "p.anova.axis1_axis2")
val_pvals = as.data.frame(t(val_pvals))

val_pvals[val_pvals$nevents >= 50 | rownames(val_pvals) == "paad", ]

##      nevents ntotal   p.score p.anova.pcna p.anova.pcna_score
## gbm         54    143 2.287e-01    8.185e-01         0.1587102
## hns         124    367 8.075e-03    4.719e-01         0.0107907
## kirc         153    497 2.034e-12    9.569e-11         0.0028892
## lgg          53    272 1.493e-05    6.316e-04         0.0078542
## luad         106    431 8.336e-06    7.205e-03         0.0001042
## lusc         117    395 9.624e-01    7.035e-02         0.4109578
## ov          115    251 2.380e-02    5.903e-01         0.0178108
## paad         17     58 4.952e-03    8.549e-02         0.0239990
##      p.anova.axis1 p.anova.axis1_axis2
## gbm      9.252e-01         6.877e-02
## hns       4.367e-02         8.341e-02
## kirc      2.673e-08         1.639e-05
## lgg       1.593e-04         3.350e-02
## luad      1.238e-03         1.543e-03
## lusc      1.597e-01         2.559e-01
## ov        3.655e-01         3.298e-02
## paad      1.562e-02         1.249e-01
```

```
plot_km_axes = function(axis1, axis2, y, mc = FALSE, ...) {
  t1 = t2 = 0
  if (mc == TRUE) {
    t1 = median(axis1, na.rm = TRUE)
    t2 = median(axis2, na.rm = TRUE)
  }

  class = paste(c("L", "H")[I(axis1 >= t1) + 1], c("L", "H")[I(axis2 >= t2) +
    1], sep = "")
  class = ordered(class, levels = c("LL", "LH", "HL", "HH"))
  fit = survfit(y ~ class)
  print(fit)
  print(survdiff(y ~ class))
}
```



```

pval = pchisq(survdiff(y ~ class)$chisq, 3, lower.tail = FALSE)
pal = brewer.pal(4, "Set2")
names(pal) = c("LL", "LH", "HL", "HH")
plot(axis2 ~ axis1, xlab = "A1 activity", ylab = "A2 activity", col = pal[class],
      pch = 16, cex = 1.5, ...)
abline(h = t2)
abline(v = t1)
plot(fit, col = pal, lwd = 2, xlab = "Time from diagnosis (days)", ylab = "Fraction surviving",
      sub = sprintf("P = %.3g", pval), ...)
}

plot_km_axes_tcga = function(code, mc) {
  if ("illumina_hiseq_rnaseqv2" %in% names(data.merged[[code]]$gex)) {
    temp.gex = data.merged[[code]]$gex$illumina_hiseq_rnaseqv2
    temp.gex = temp.gex[!grepl("^\\|\\?\\|\\|", rownames(temp.gex)), ]
    rownames(temp.gex) = gsub("\\|\\.+", "", rownames(temp.gex))
    temp.gex.axes = temp.gex[match(rownames(val.basis), rownames(temp.gex)),
                             ]
    temp.gex.axes[apply(is.na(temp.gex.axes), 1, all), ] = 0
    temp.gex.axes = temp.gex.axes - apply(temp.gex.axes, 1, min, na.rm = TRUE)
    temp.gex.axes = temp.gex.axes/apply(temp.gex.axes, 1, max, na.rm = TRUE)
    temp.gex.axes[is.na(temp.gex.axes)] = 0
    temp.coefs = apply(temp.gex.axes, 2, function(xcol) nnls(val.basis,
                                                             xcol)$x)
    temp.axis1 = temp.coefs[1, ] - temp.coefs[5, ]
    temp.axis2 = temp.coefs[6, ] - temp.coefs[2, ]

    temp.clin = data.merged[[code]]$clin
    temp.days_to_death = temp.clin$days_to_death
    temp.days_to_death[temp.days_to_death == "[Not Applicable]"] = NA
    temp.days_to_death = as.numeric(as.character(temp.days_to_death))
    temp.days_to_initial_pathologic_diagnosis = temp.clin$days_to_initial_pathologic_diagnosis
    temp.days_to_initial_pathologic_diagnosis[temp.days_to_initial_pathologic_diagnosis ==
                                              "[Not Applicable]"] = NA
    temp.days_to_initial_pathologic_diagnosis = as.numeric(as.character(temp.days_to_initial_pathologic_diagnosis))
    temp.days_to_last_followup = temp.clin$days_to_last_followup
    temp.days_to_last_followup[temp.days_to_last_followup == "[Not Applicable]"] = NA
    temp.days_to_last_followup = as.numeric(as.character(temp.days_to_last_followup))
    temp.time_event = temp.days_to_death - temp.days_to_initial_pathologic_diagnosis
    temp.time_lfu = temp.days_to_last_followup - temp.days_to_initial_pathologic_diagnosis
    temp.time_obs = temp.time_event
    temp.time_obs[is.na(temp.time_obs)] = temp.time_lfu[is.na(temp.time_obs)]
    temp.time_obs[!is.na(temp.time_obs) & !is.na(temp.time_lfu)] = pmin(temp.time_obs[!is.na(temp.time_obs) &
!is.na(temp.time_lfu)], temp.time_lfu[!is.na(temp.time_obs) & !is.na(temp.time_lfu)])
    temp.event = (temp.time_event <= temp.time_lfu & !is.na(temp.time_event) &
!is.na(temp.time_lfu)) | (!is.na(temp.time_event) & is.na(temp.time_lfu))
    temp.y = Surv(temp.time_obs, temp.event)

    plot_km_axes(temp.axis1, temp.axis2, temp.y, mc = FALSE, main = code)
  }
}

plot_km_axes(axis_coefs.diag_dsd[, 1], axis_coefs.diag_dsd[, 2], y.diag_dsd,

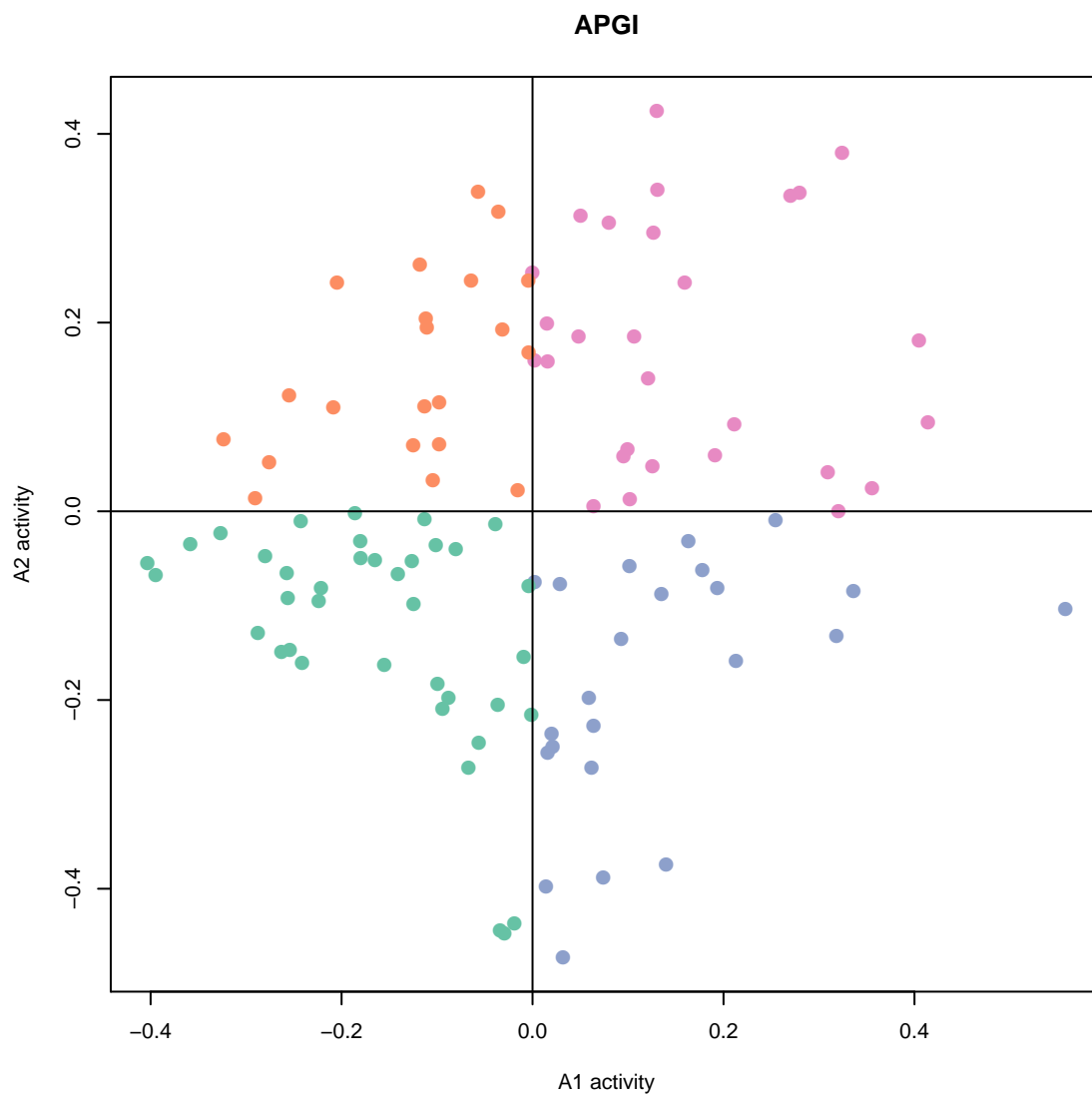
```

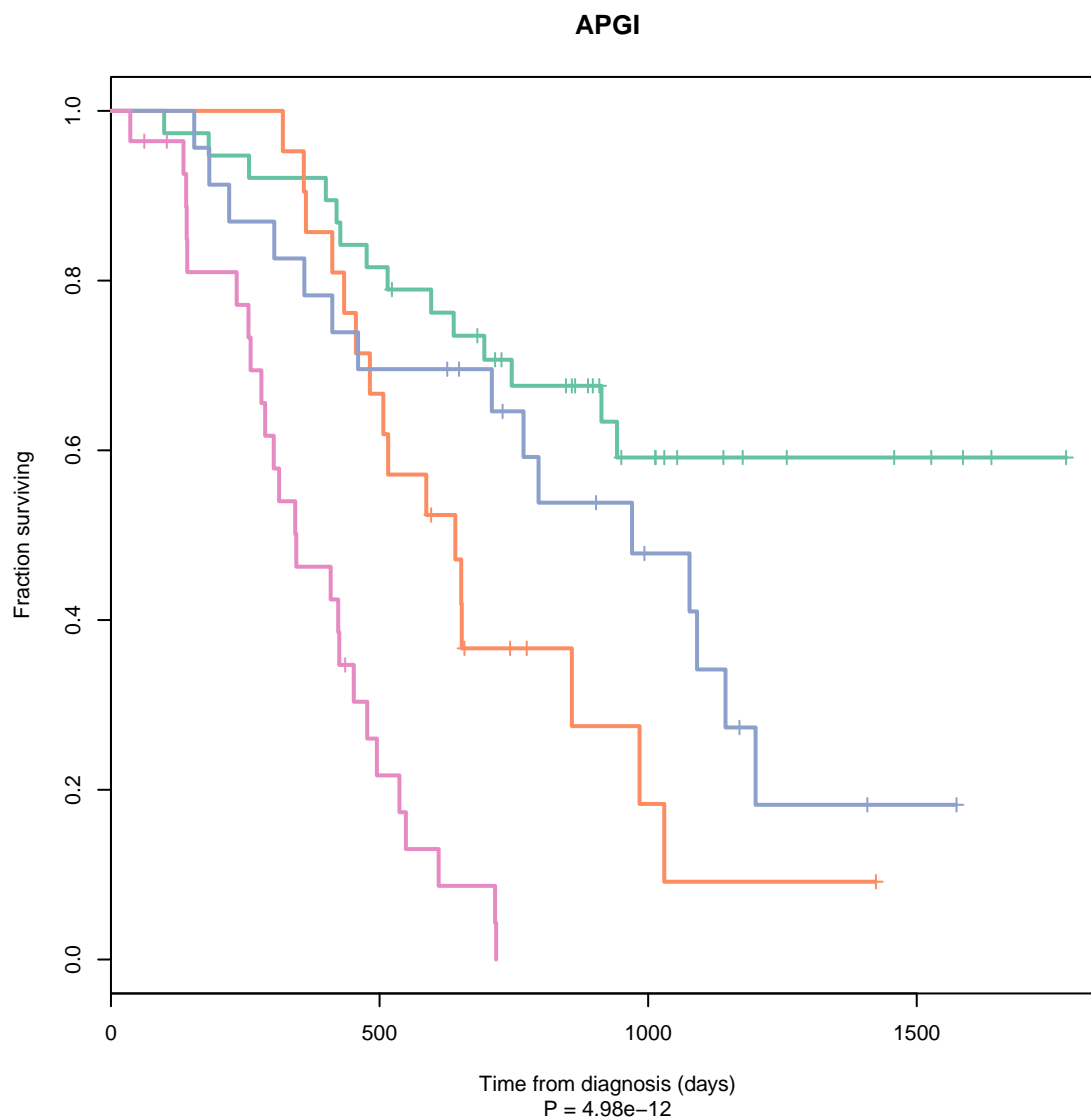
```

mc = FALSE, main = "APGI")

## Call: survfit(formula = y ~ class)
##
##           records n.max n.start events median 0.95LCL 0.95UCL
## class=LL      38    38     38     14     NA     913     NA
## class=LH      21    21     21     16    641     482     NA
## class=HL      23    23     23     15    970     709     NA
## class=HH      28    28     28     25    345     280    495
## Call:
## survdiff(formula = y ~ class)
##
##           N Observed Expected (O-E)^2/E (O-E)^2/V
## class=LL 38      14    31.77     9.942    18.645
## class=LH 21      16    13.02     0.683     0.852
## class=HL 23      15    17.66     0.401     0.543
## class=HH 28      25     7.55    40.376    48.292
##
## Chisq= 55.7  on 3 degrees of freedom, p= 4.98e-12

```





```
plot_km_axes(GSE21501.axis1, GSE21501.axis2, Surv(GSE21501.samp$time, GSE21501.samp$event),
  mc = FALSE, main = "GSE21501")
```

```
## Call: survfit(formula = y ~ class)
```

```
##
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
## class=LL	11	11	11	7	22	7	NA
## class=LH	50	50	50	33	19	15	25
## class=HL	5	5	5	4	14	14	NA
## class=HH	36	36	36	22	18	10	NA

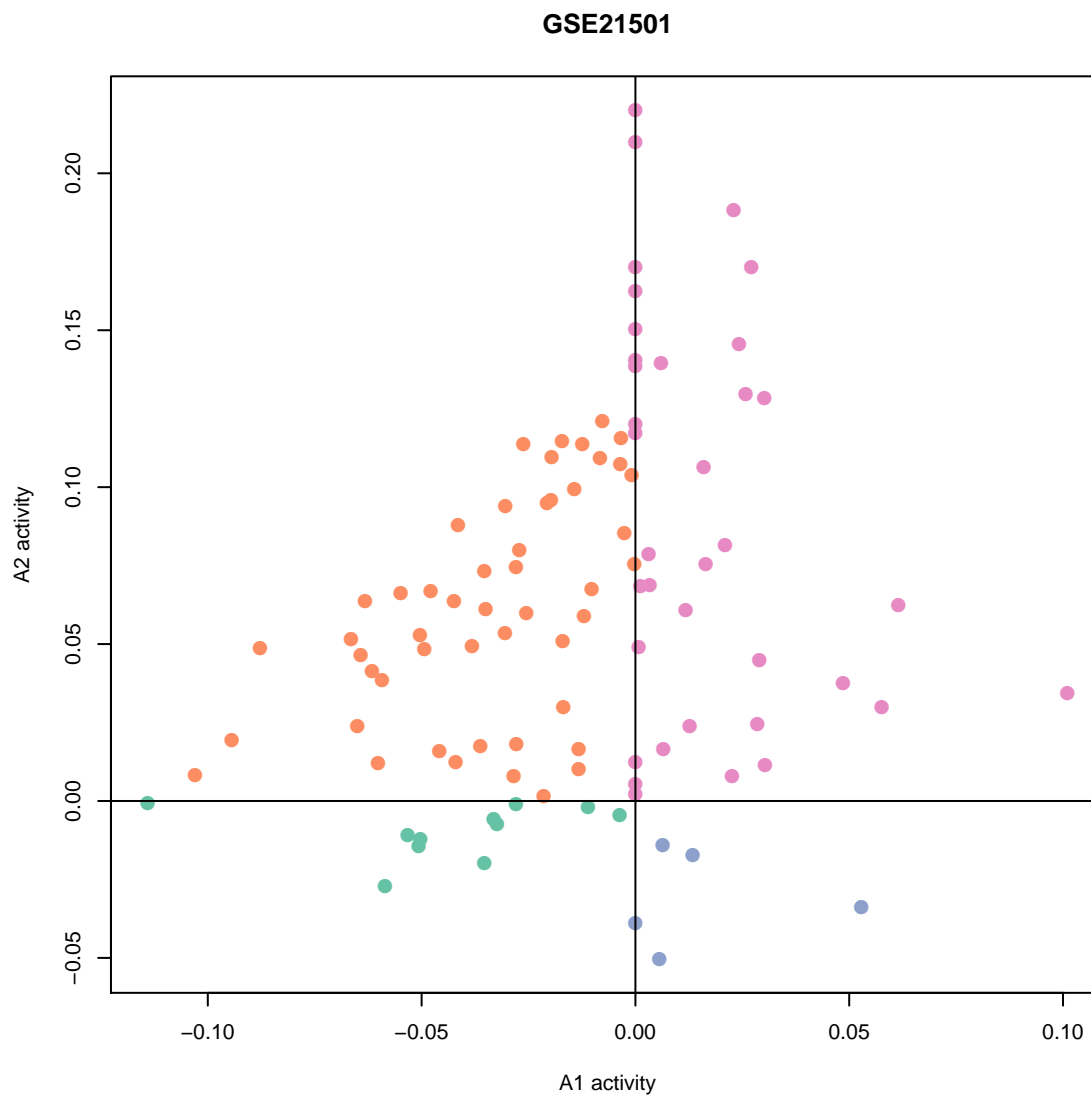
```
## Call:
```

```
## survdiff(formula = y ~ class)
```

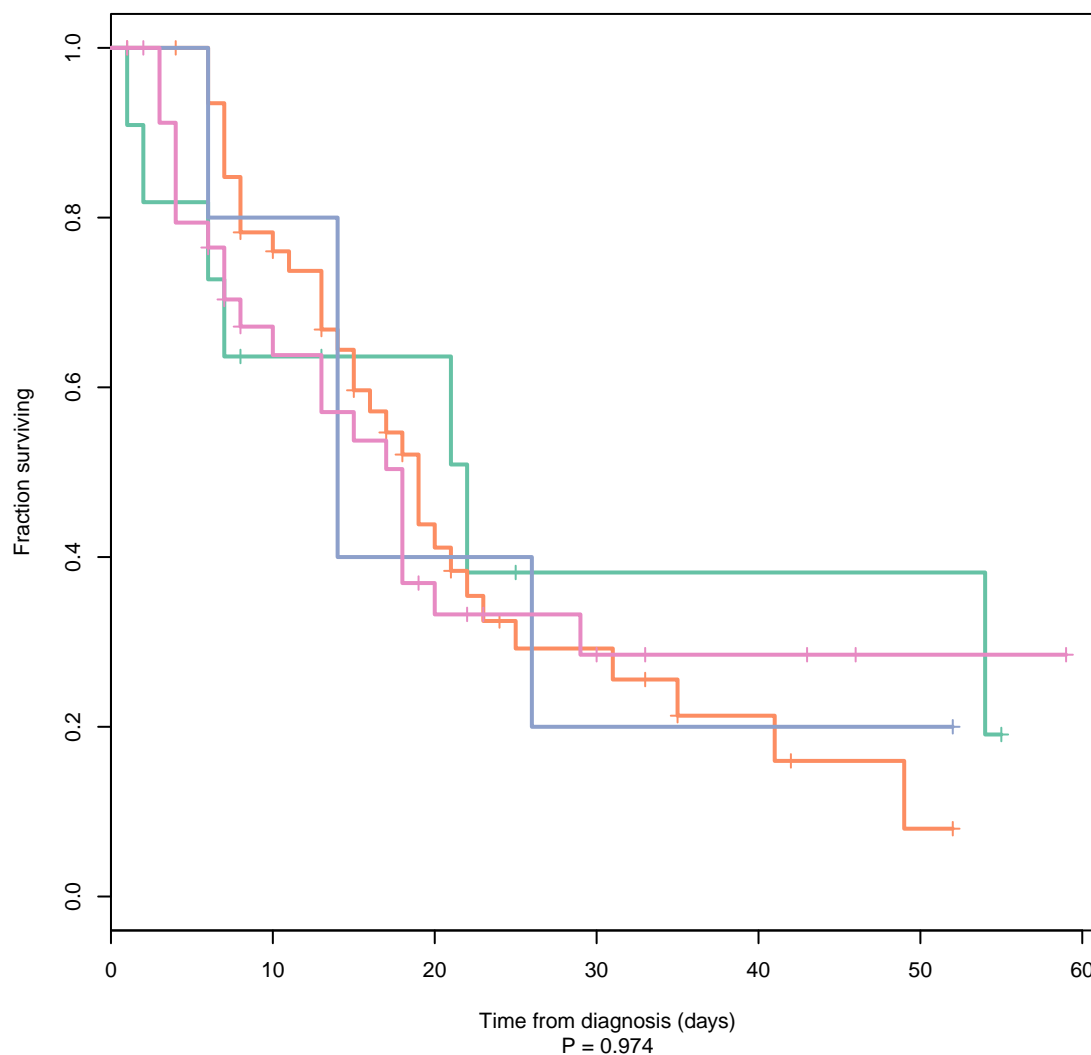
```
##
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
## class=LL	11	7	8.12	1.56e-01	1.95e-01
## class=LH	50	33	32.96	3.96e-05	8.43e-05
## class=HL	5	4	3.91	2.27e-03	2.53e-03

```
## class=HH 36      22      21.01  4.71e-02  7.23e-02
##
##  Chisq= 0.2  on 3 degrees of freedom, p= 0.974
```



## GSE21501



```
plot_km_axes(GSE28735.axis1, GSE28735.axis2, Surv(GSE28735.samp$time, GSE28735.samp$event),
  mc = FALSE, main = "GSE28735")
```

```
## Call: survfit(formula = y ~ class)
```

```
##
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
## class=LL	6	6	6	3	51	16	NA
## class=LH	13	13	13	9	25	13	NA
## class=HL	1	1	1	0	NA	NA	NA
## class=HH	22	22	22	17	13	8	NA

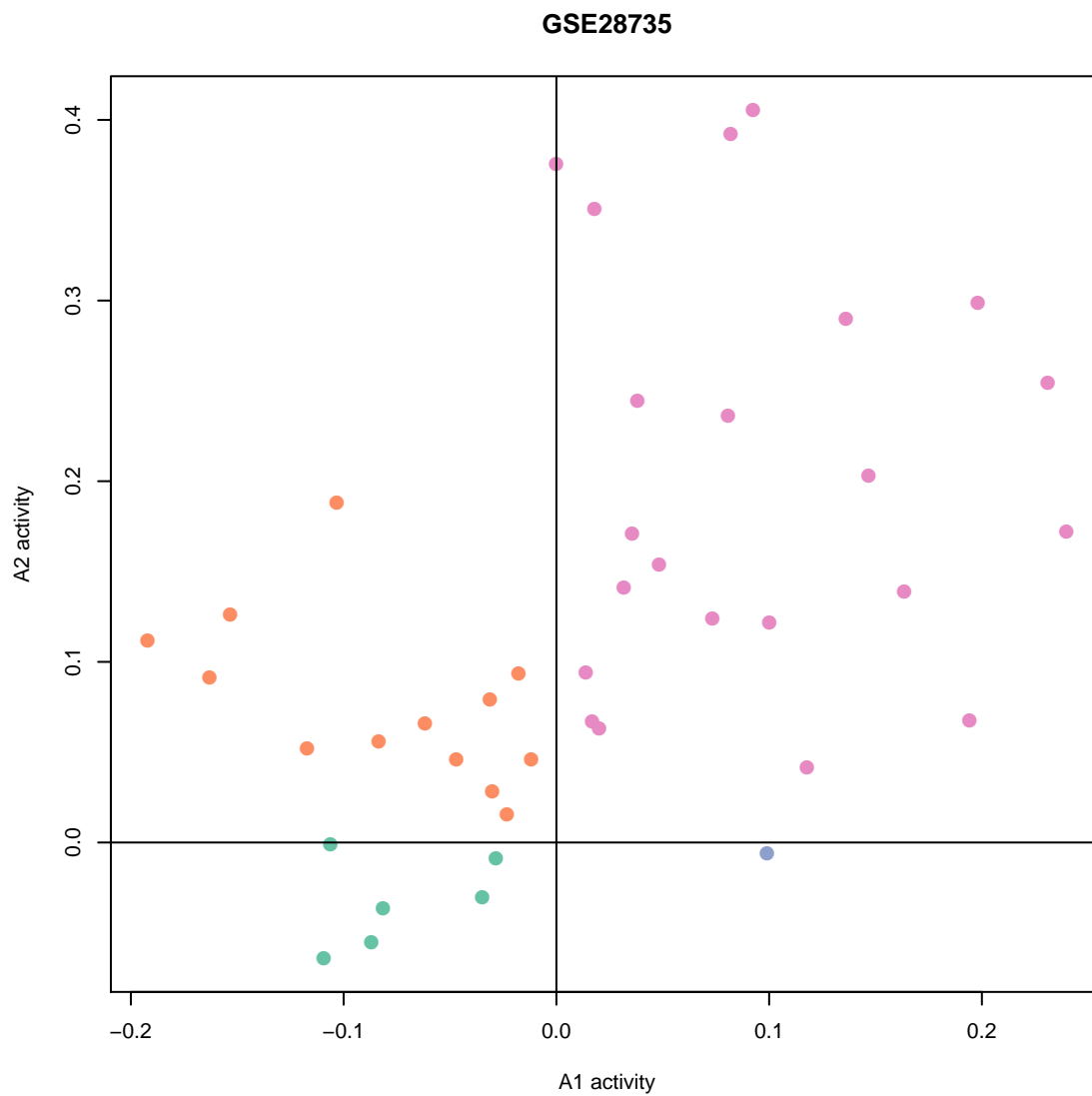
```
## Call:
```

```
## survdiff(formula = y ~ class)
```

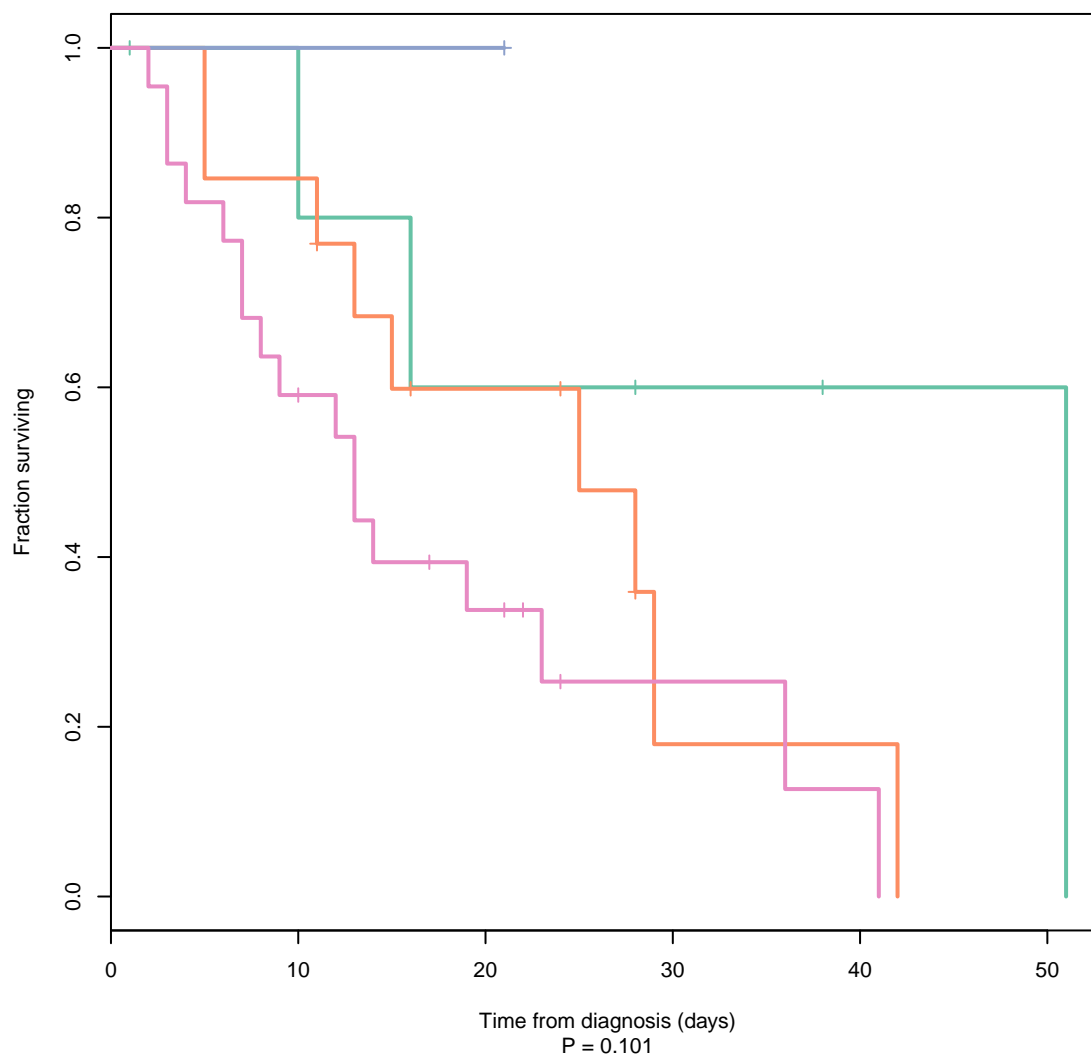
```
##
```

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
## class=LL	6	3	6.651	2.004	3.168
## class=LH	13	9	10.078	0.115	0.186
## class=HL	1	0	0.735	0.735	0.779

```
## class=HH 22      17   11.536    2.588    4.733
##
##  Chisq= 6.2  on 3 degrees of freedom, p= 0.101
```



# GSE28735

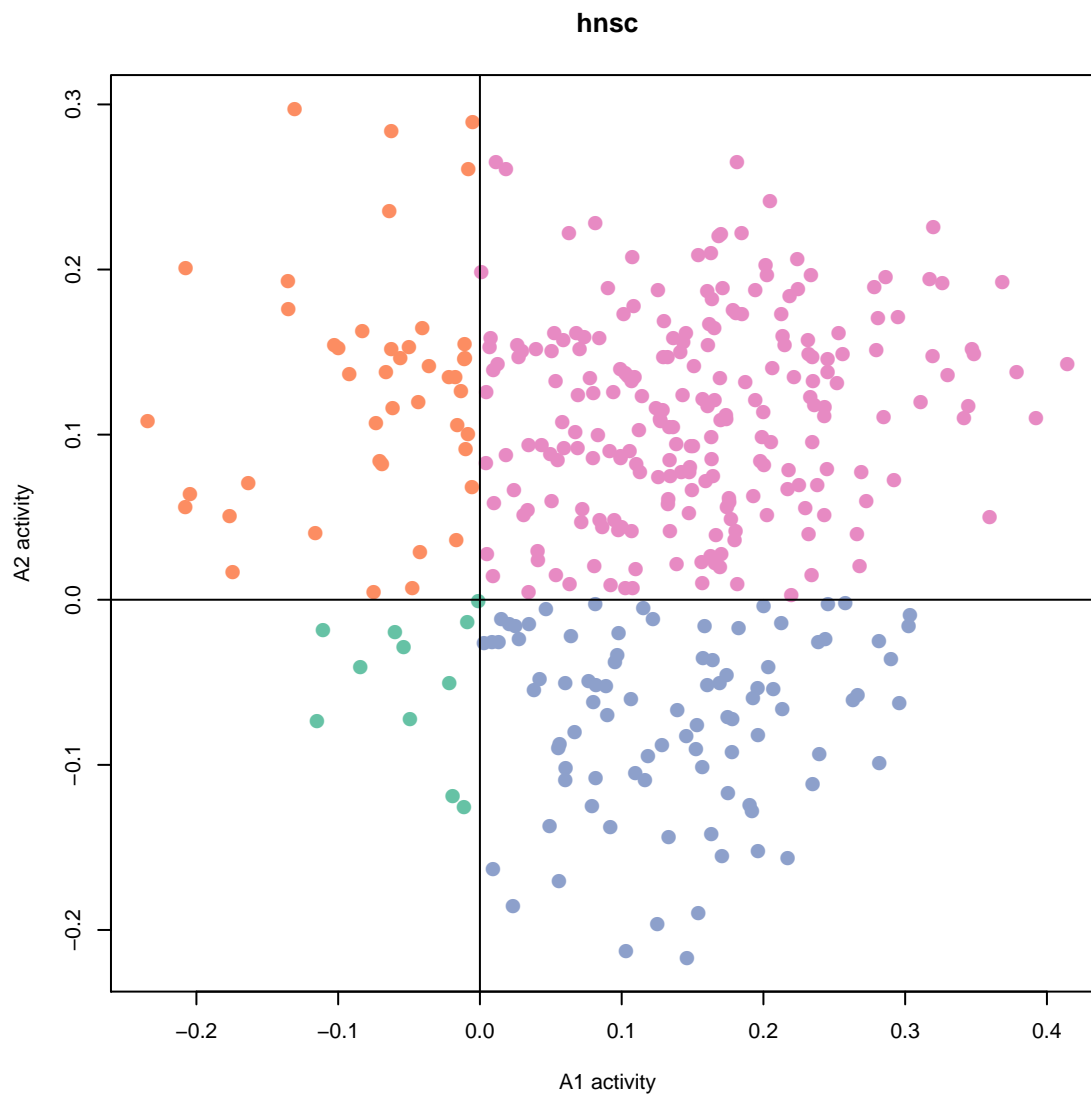


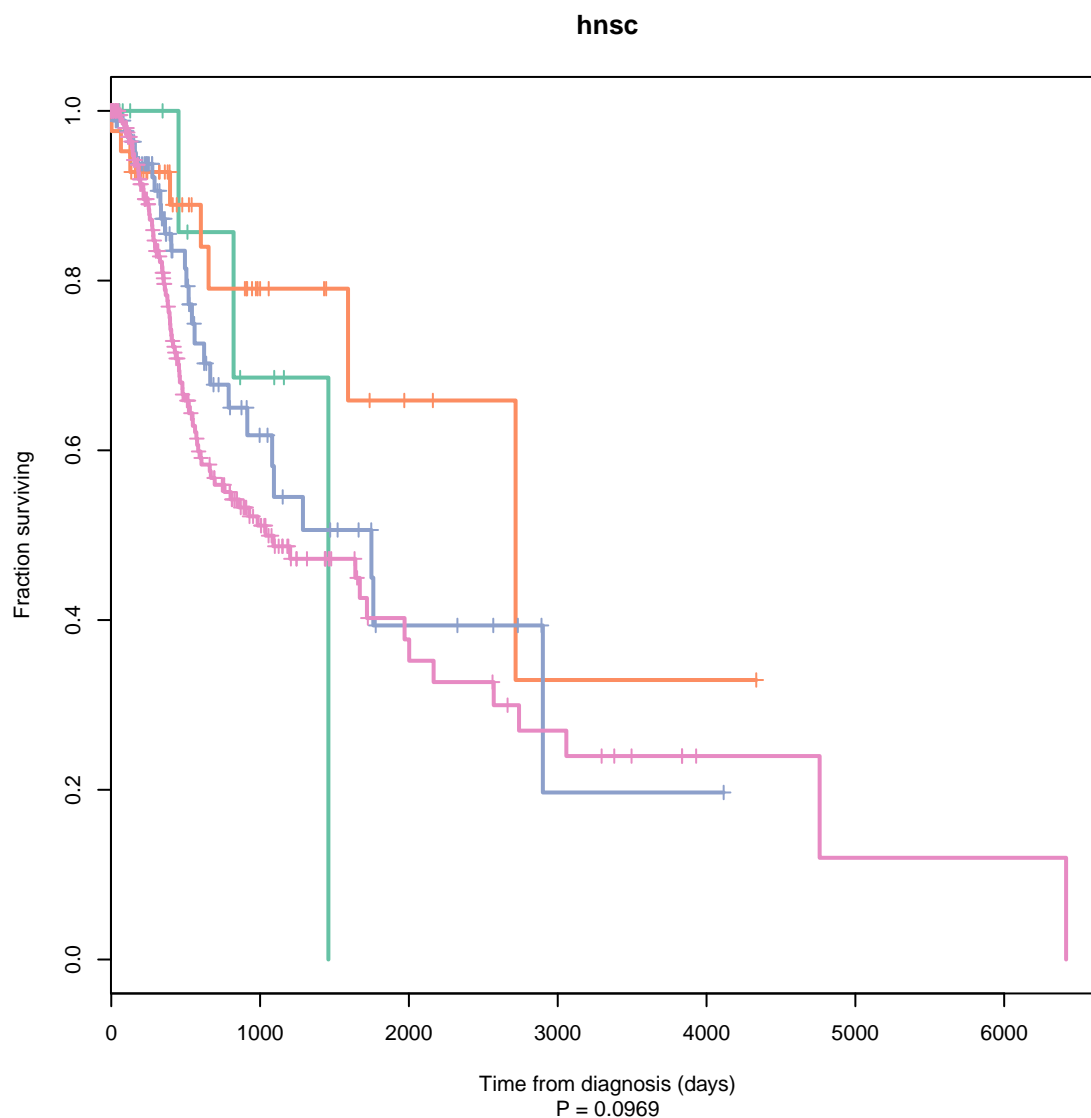
```
plot_km_axes_tcga("hnscl", mc = FALSE)

## Call: survfit(formula = y ~ class)
##
## 1 observation deleted due to missingness
##      records n.max n.start events median 0.95LCL 0.95UCL
## class=LL      11    11      11      3  1459      822     NA
## class=LH      43    43      43      8  2717     1591     NA
## class=HL      90    90      90     26  1748      914     NA
## class=HH     223   223     223     87  1037      669    2002
## Call:
## survdiff(formula = y ~ class)
##
## n=367, 1 observation deleted due to missingness.
##
##      N Observed Expected (O-E)^2/E (O-E)^2/V
## class=LL  11         3    3.77    0.156    0.162
```



```
## class=LH 43      8    15.60    3.700    4.249
## class=HL 90     26    29.68    0.457    0.606
## class=HH 223    87    74.95    1.936    4.969
##
## Chisq= 6.3  on 3 degrees of freedom, p= 0.0969
```





```
plot_km_axes_tcga("kirc", mc = FALSE)
```

```
## Call: survfit(formula = y ~ class)
```

```
##
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
## class=LL	77	77	77	17	2763	2385	NA
## class=LH	179	179	179	42	2600	2343	NA
## class=HL	96	96	96	25	2830	2190	NA
## class=HH	146	146	146	69	1432	1200	1964

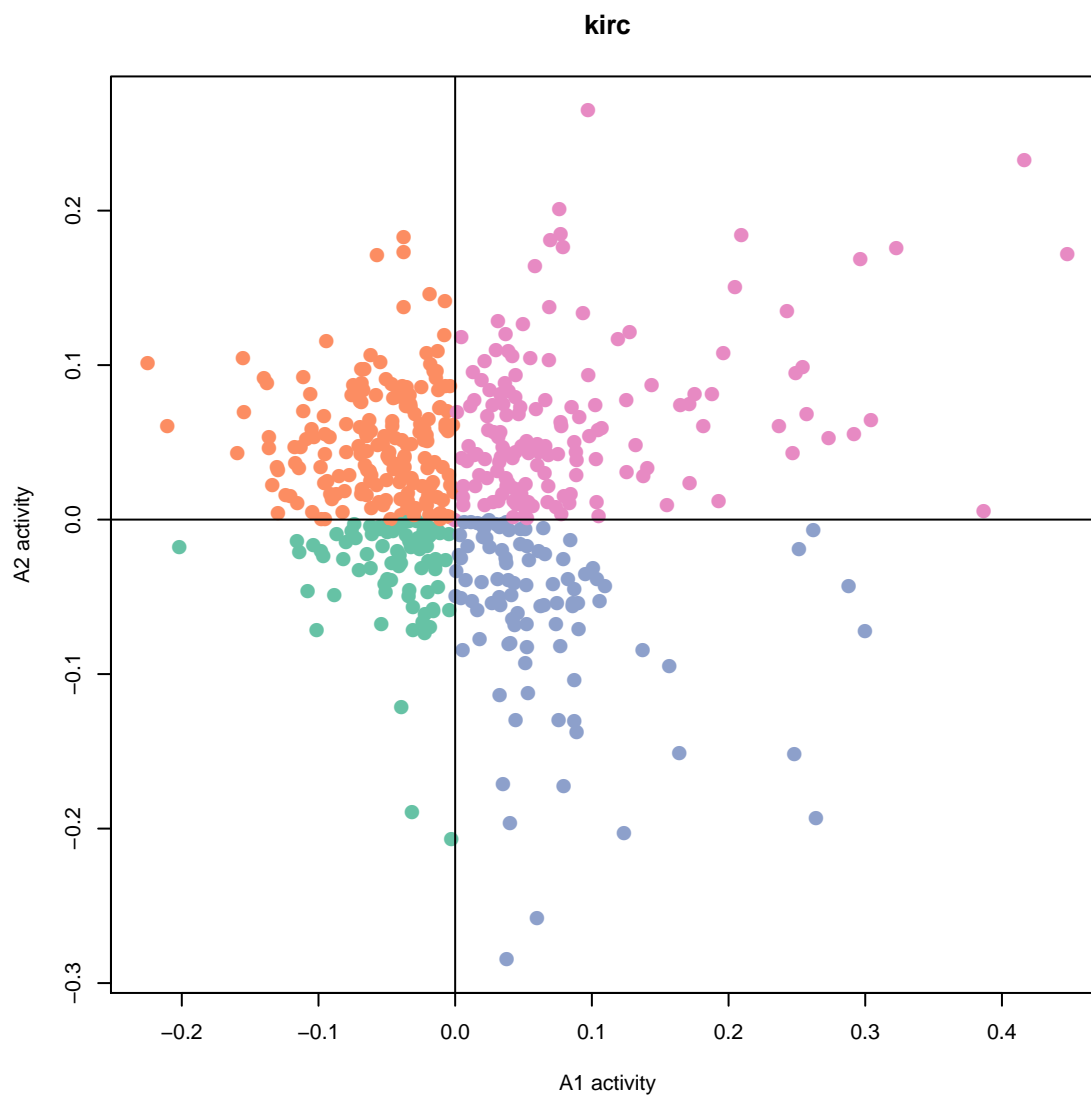
```
## Call:
```

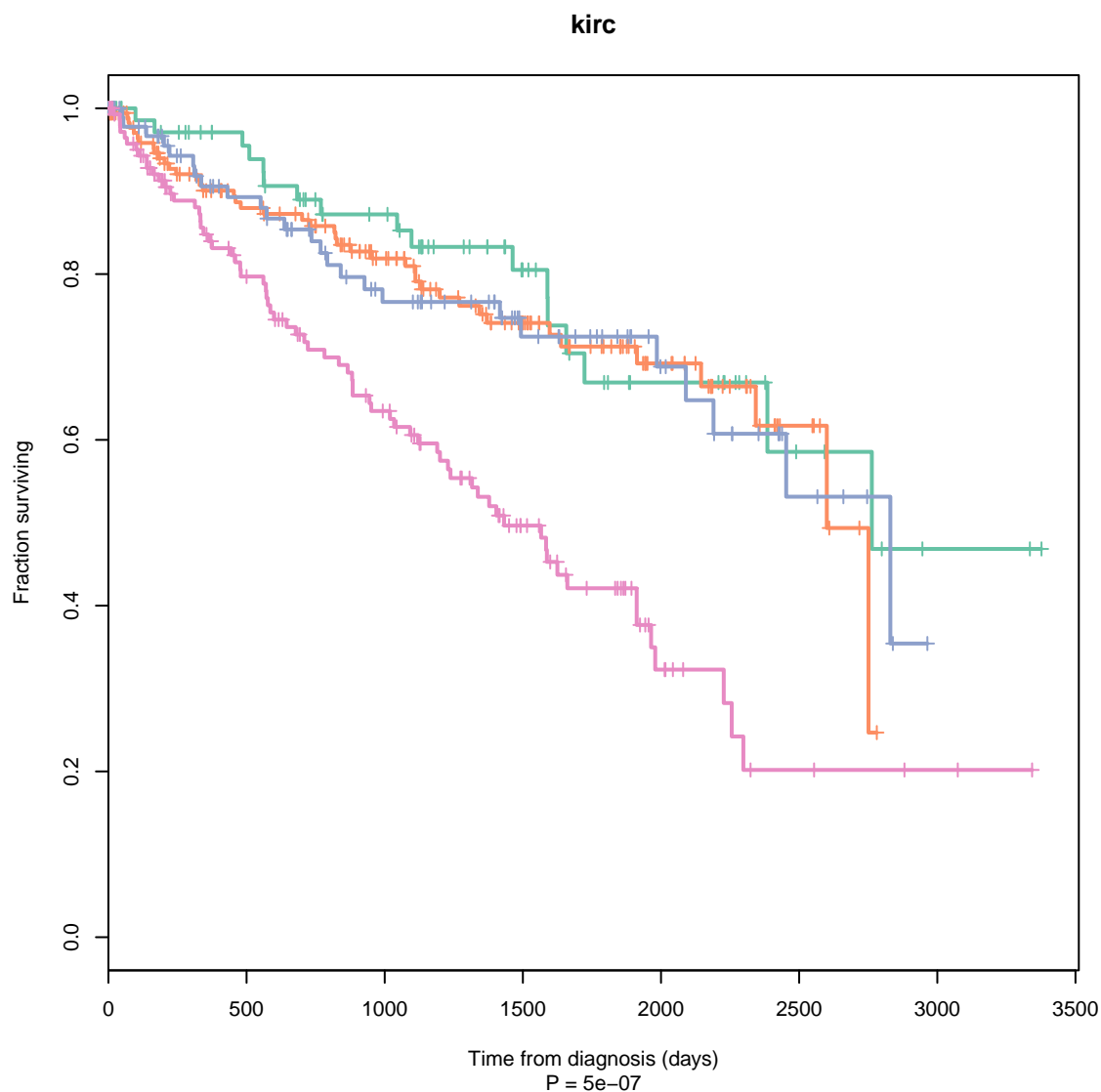
```
## survdiff(formula = y ~ class)
```

```
##
```

	N	Observed	Expected	(O-E) <sup>2</sup> /E	(O-E) <sup>2</sup> /V
## class=LL	77	17	26.8	3.59	4.39
## class=LH	179	42	55.3	3.21	5.08
## class=HL	96	25	32.0	1.54	1.96
## class=HH	146	69	38.8	23.44	31.71

```
##  
## Chisq= 32.1 on 3 degrees of freedom, p= 5e-07
```





```
plot_km_axes_tcga("lgg", mc = FALSE)
```

```
## Warning in plot_km_axes_tcga("lgg", mc = FALSE): NAs introduced by coercion
```

```
## Call: survfit(formula = y ~ class)
```

```
##
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
## class=LL	77	77	77	4	NA	1762	NA
## class=LH	32	32	32	3	2907	2660	NA
## class=HL	106	106	106	28	2051	1886	3978
## class=HH	57	57	57	18	1915	682	NA

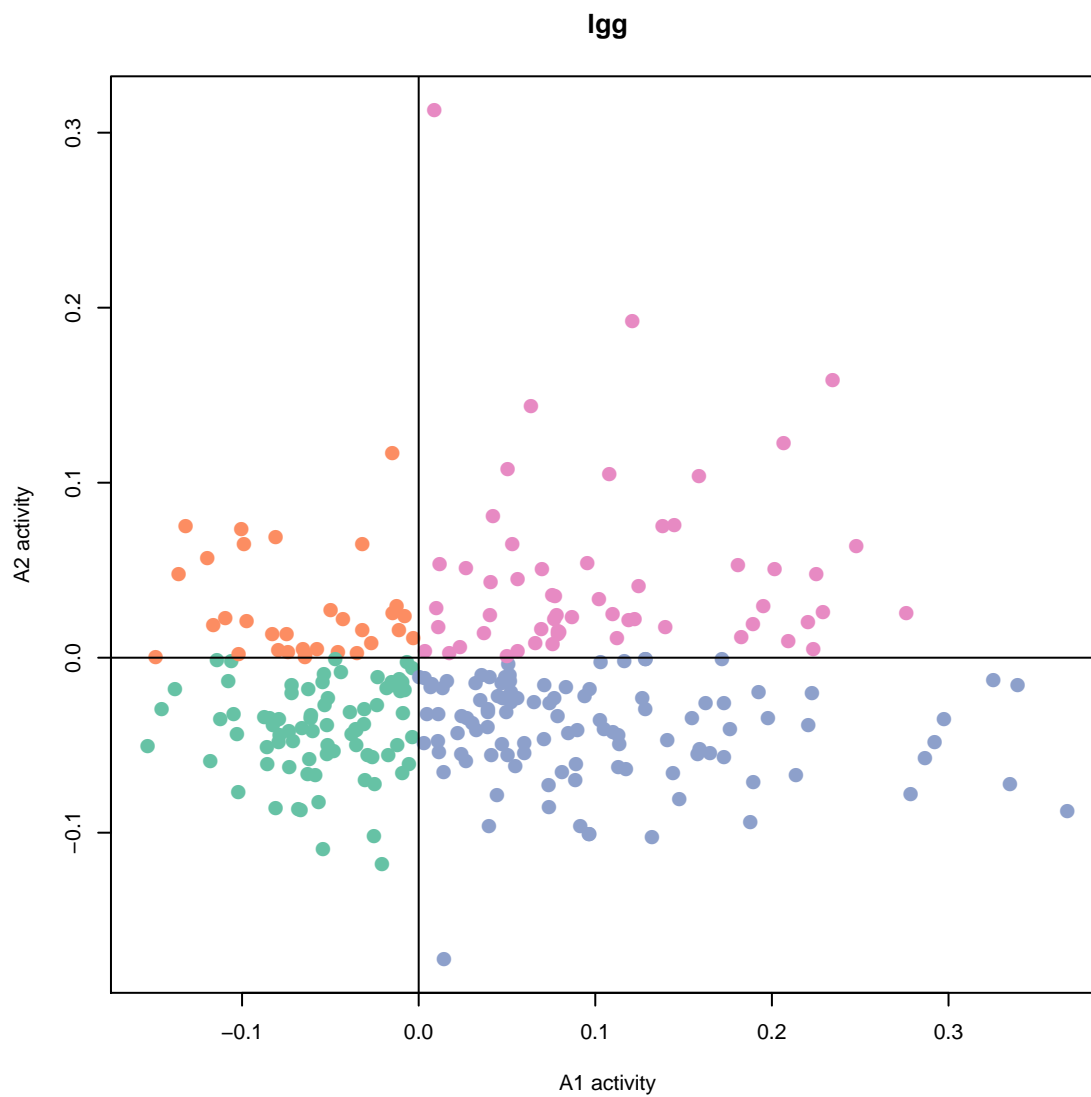
```
## Call:
```

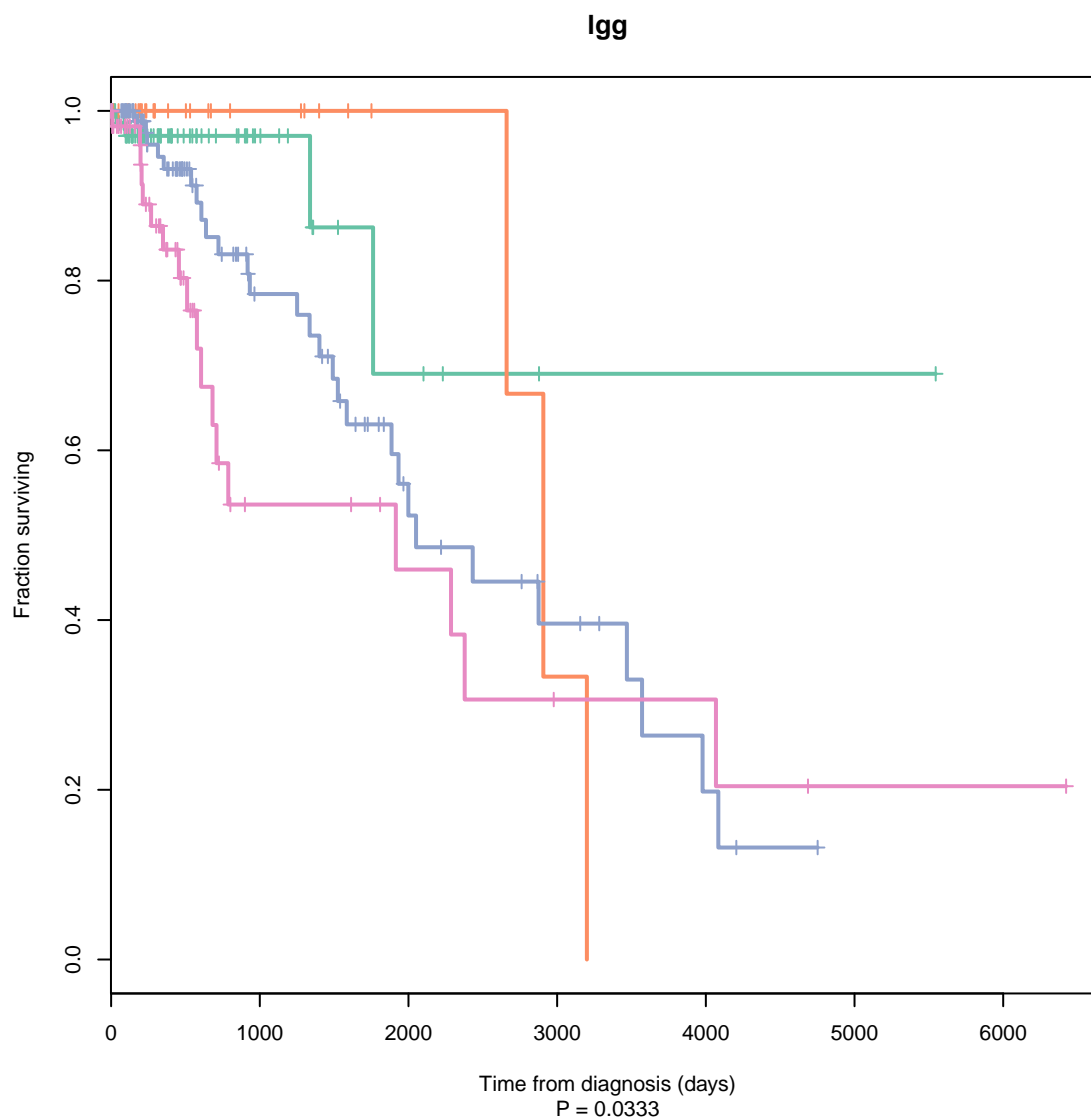
```
## survdiff(formula = y ~ class)
```

```
##
```

	N	Observed	Expected	(O-E) <sup>2</sup> /E	(O-E) <sup>2</sup> /V
## class=LL	77	4	9.86	3.479	4.389
## class=LH	32	3	5.38	1.055	1.191
## class=HL	106	28	26.36	0.102	0.207

```
## class=HH  57      18    11.40     3.815     4.950
##
##  Chisq= 8.7  on 3 degrees of freedom, p= 0.0333
```

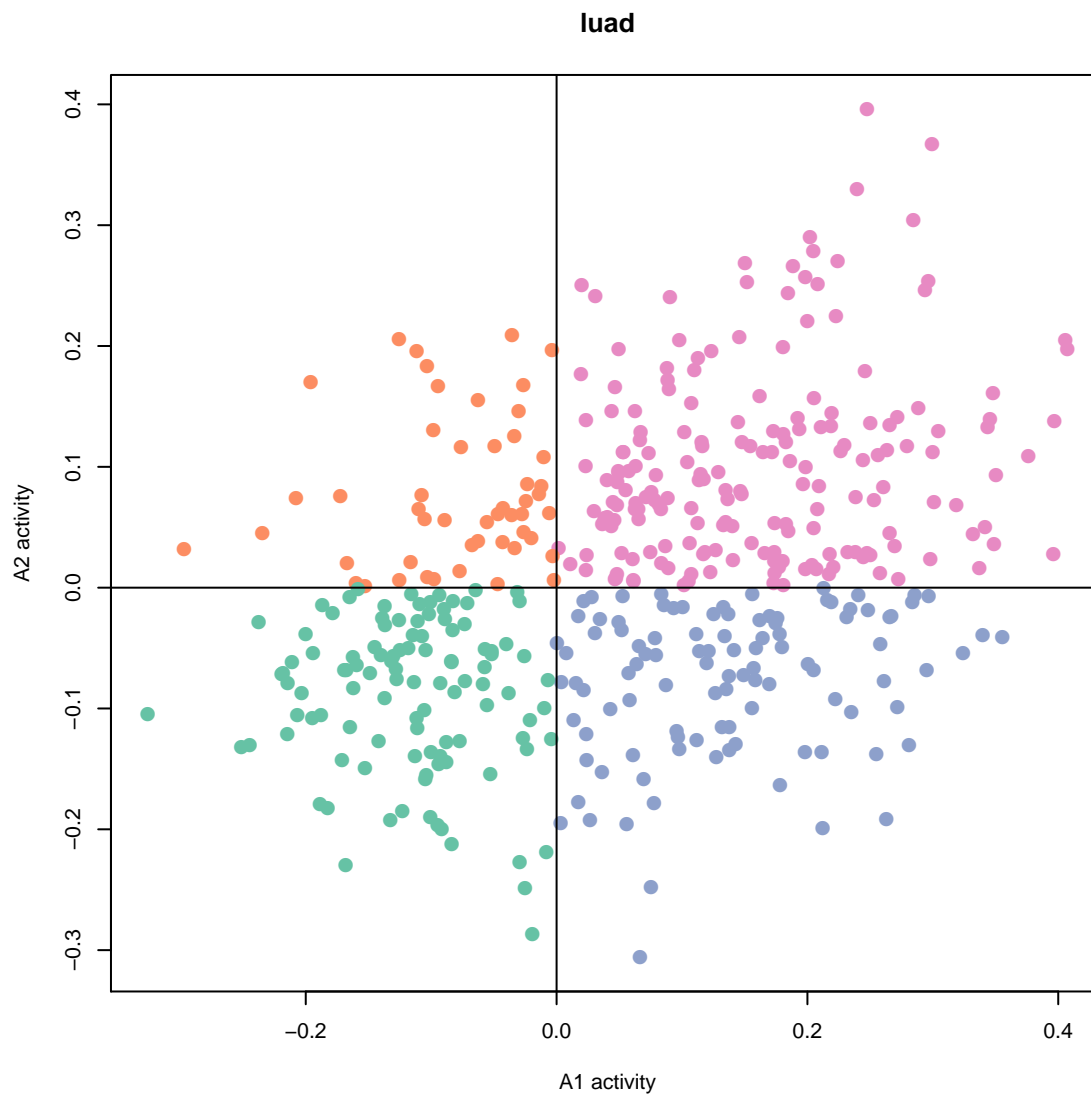


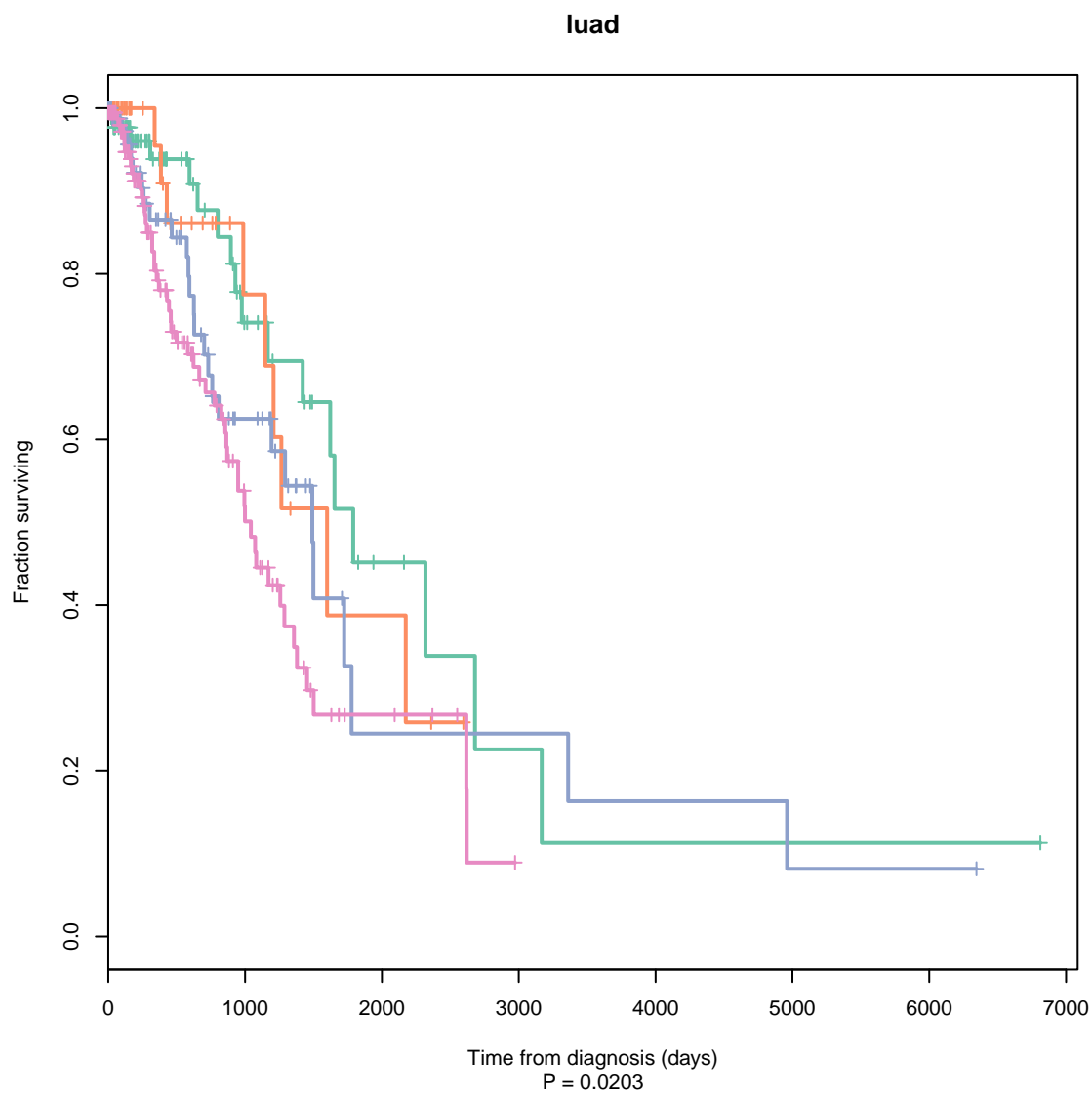


```
plot_km_axes_tcga("luad", mc = FALSE)

## Warning in plot_km_axes_tcga("luad", mc = FALSE): NAs introduced by coercion
## Call: survfit(formula = y ~ class)
##
##      19 observations deleted due to missingness
##           records n.max n.start events median 0.95LCL 0.95UCL
## class=LL      102   102    102     18   1790    1421      NA
## class=LH       49    49     49      9   1599    1147      NA
## class=HL       98    98     98     26   1491     807      NA
## class=HH      182   182    182     53   1042     863    1379
## Call:
## survdiff(formula = y ~ class)
##
## n=431, 19 observations deleted due to missingness.
##
##           N Observed Expected (O-E)^2/E (O-E)^2/V
```

```
## class=LL 102      18      28.0    3.5523    4.875
## class=LH  49       9      11.9    0.6911    0.786
## class=HL  98      26      27.5    0.0801    0.112
## class=HH 182     53      38.7    5.2967    8.567
##
## Chisq= 9.8  on 3 degrees of freedom, p= 0.0203
```





```
plot_km_axes_tcga("paad", mc = FALSE)
```

```
## Call: survfit(formula = y ~ class)
```

```
##
```

	records	n.max	n.start	events	median	0.95LCL	0.95UCL
## class=LL	9	9	9	2	906	480	NA
## class=LH	19	19	19	4	485	467	NA
## class=HL	9	9	9	2	665	334	NA
## class=HH	21	21	21	9	460	145	NA

```
## Call:
```

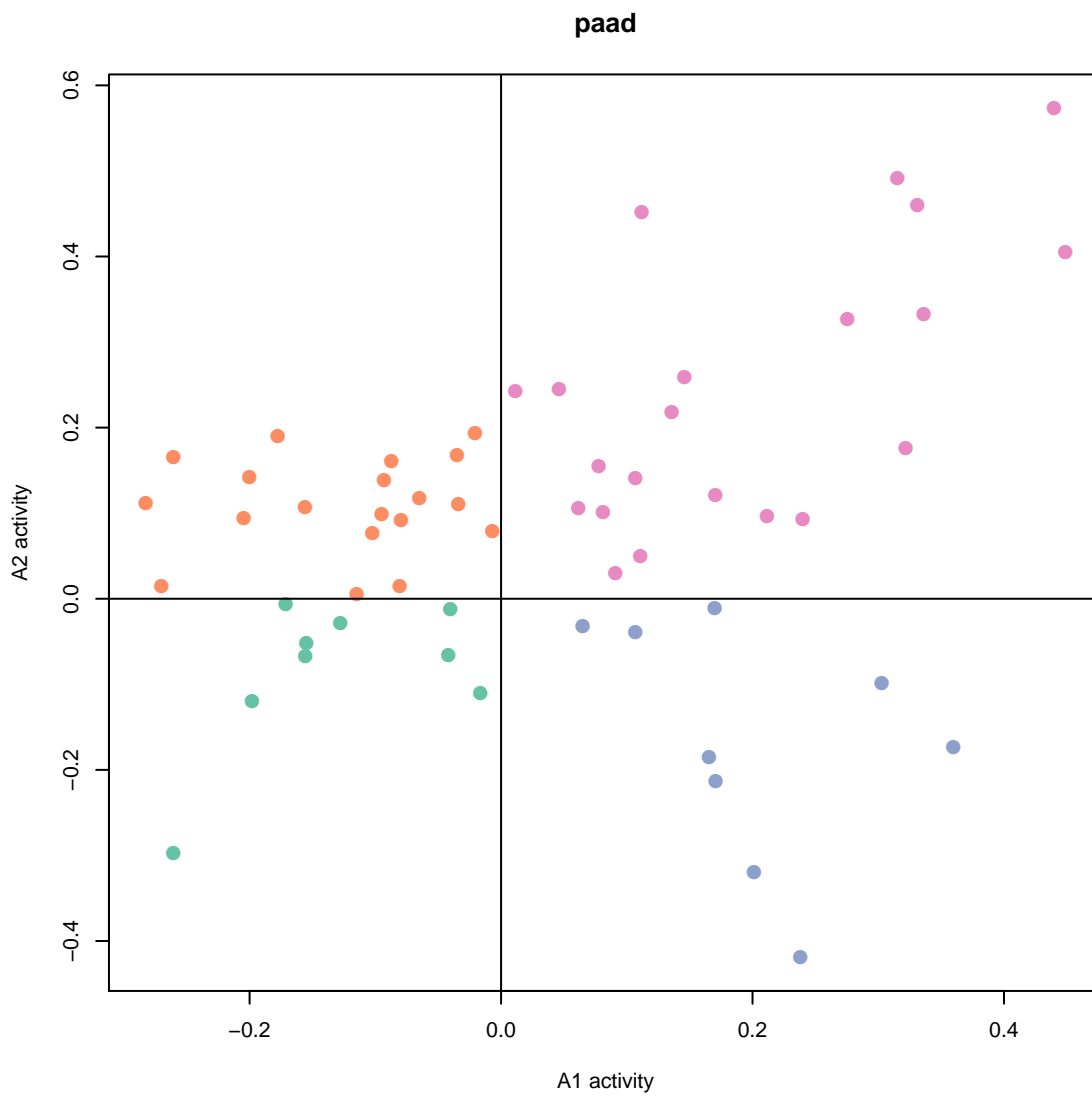
```
## survdiff(formula = y ~ class)
```

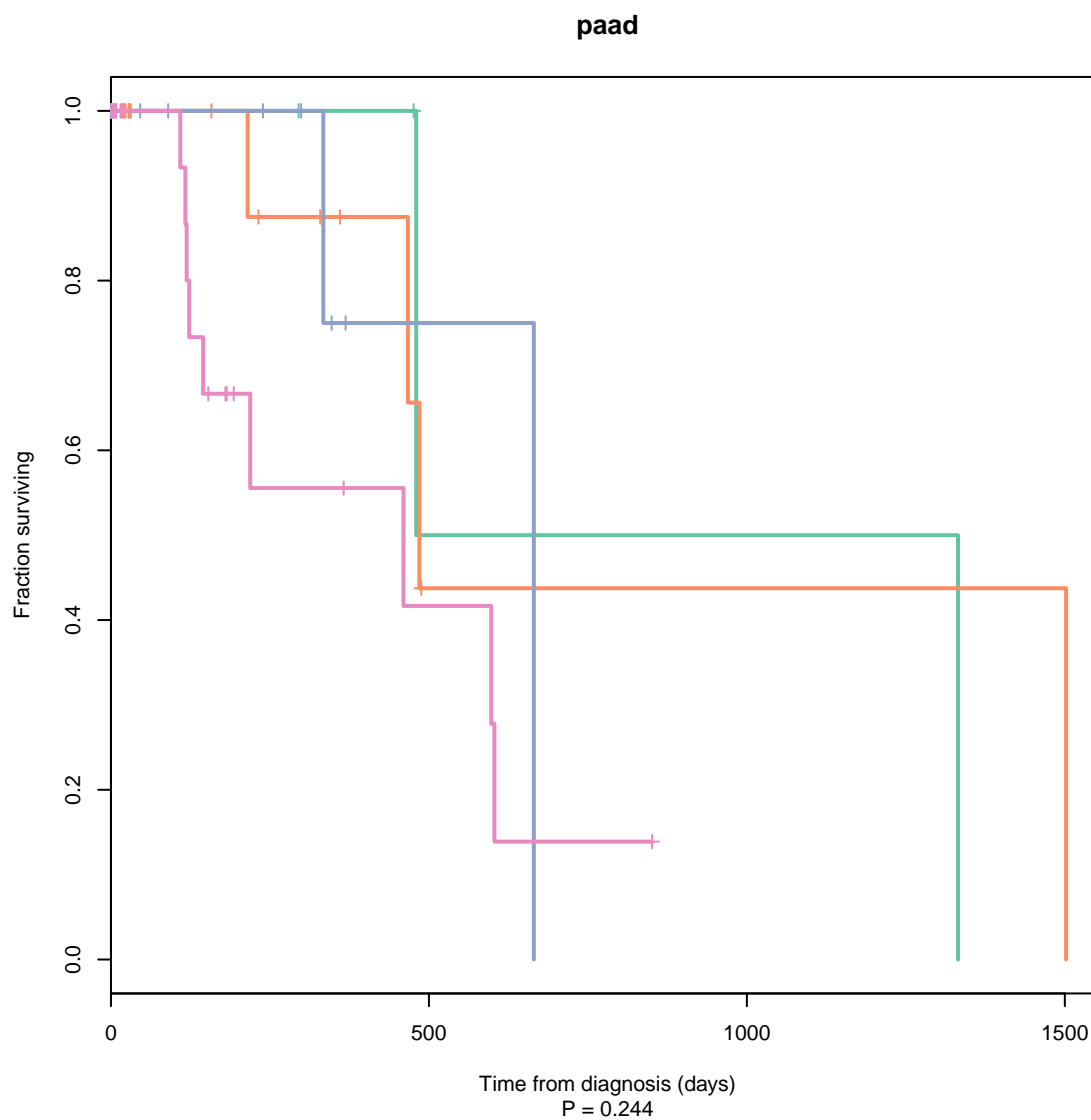
```
##
```

	N	Observed	Expected	(O-E) <sup>2</sup> /E	(O-E) <sup>2</sup> /V
## class=LL	9	2	3.13	0.408	0.536
## class=LH	19	4	5.86	0.592	1.052
## class=HL	9	2	2.71	0.187	0.233
## class=HH	21	9	5.29	2.593	4.105



```
##
##  Chisq= 4.2  on 3 degrees of freedom, p= 0.244
```

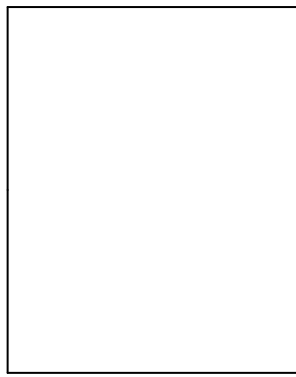
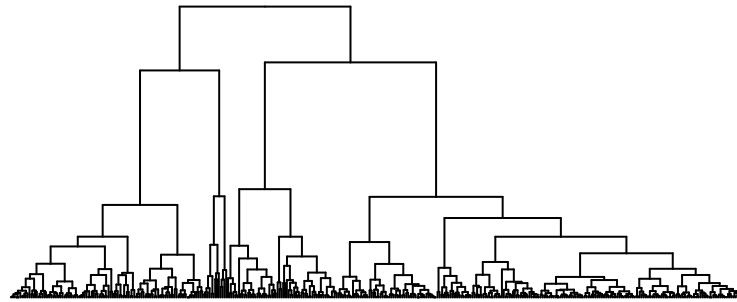
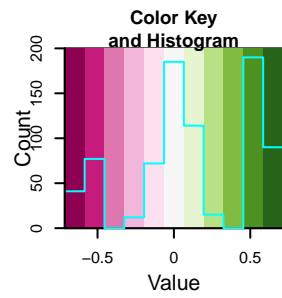




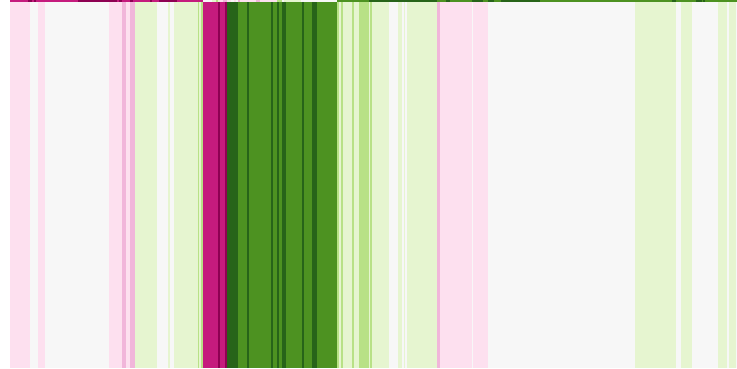
#### 4.4 MSigDB score correlation thresholding

```
axis_coefs.msigdb.corr = cor(axis_coefs.diag_dsd, t(sigs), method = "kendall")

temp.sel_cols = apply(abs(axis_coefs.msigdb.corr) >= sig.corr.threshold, 2,
  any)
heatmap.2(axis_coefs.msigdb.corr[, temp.sel_cols], trace = "none", scale = "none",
  useRaster = TRUE, col = brewer.pal(11, "PiYG"), symbreaks = TRUE)
```



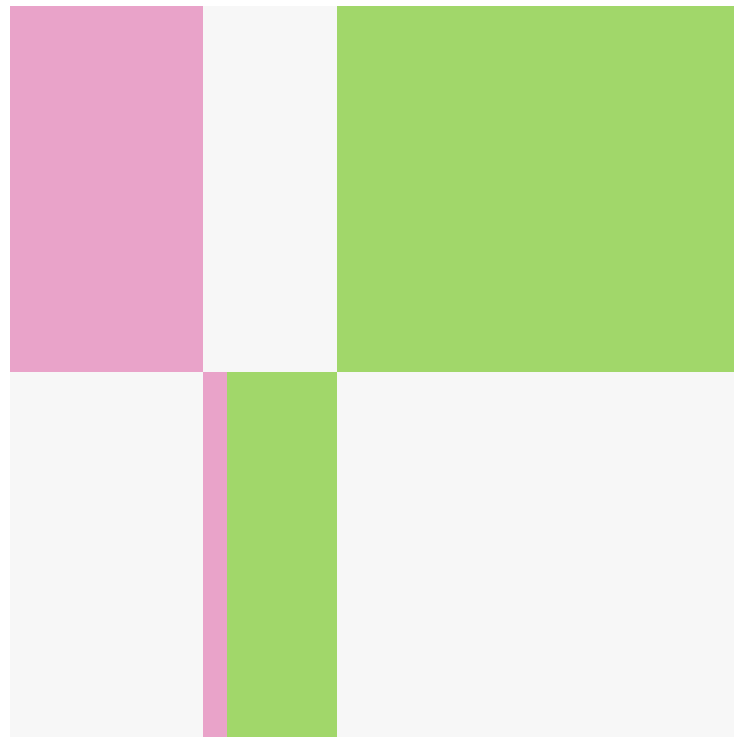
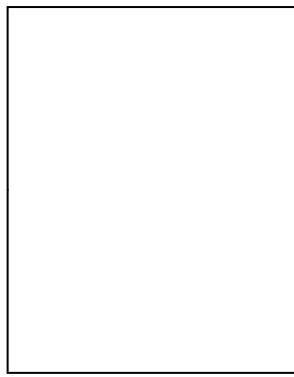
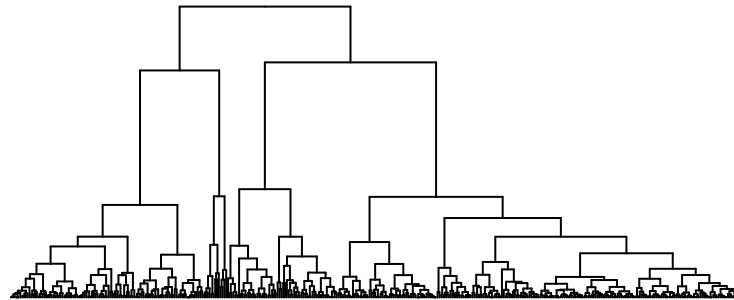
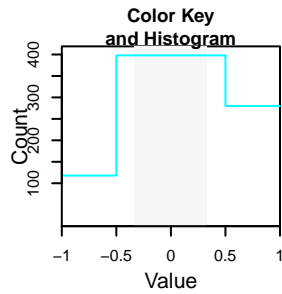
axis



axis



```
heatmap.2(axis_coefs.msigdb.corr[, temp.sel_cols], trace = "none", scale = "none",
  useRaster = TRUE, col = brewer.pal(3, "PiYG"), breaks = c(-1, -sig.corr.threshold,
    sig.corr.threshold, 1))
```



```
cpv.pvals = apply(axis_coefs.diag_dsd, 2, function(mg) sapply(cbind(cpv.diag_dsd,
purity = samp.diag_dsd$purity_qpure), function(x) {
  s = !is.na(mg) & !is.na(x)
  x = x[s]
  mg = mg[s]
  if (any(c("numeric", "integer") %in% class(x))) {
    return(cor.test(x, mg, method = "pearson")$p.value)
  } else if (any(c("factor", "ordered", "logical") %in% class(x)) && length(unique(x)) >
1) {
    return(anova(lm(mg ~ x))[, "Pr(>F)"][1])
  }
  NA
}))
cpv.pvals = cpv.pvals[!apply(is.na(cpv.pvals), 1, all), ]
cpv.pvals = cpv.pvals[!grepl("^Surv\\.", rownames(cpv.pvals)), ]
cpv.pvals = cpv.pvals[!grepl("^Treat\\.", rownames(cpv.pvals)), ]
cpv.pvals = cpv.pvals[!grepl("^Path\\.", rownames(cpv.pvals)), ]
```

```

cpv.pvals = cpv.pvals[!grepl("^Staging\\.Version", rownames(cpv.pvals)), ]
cpv.pvals = cpv.pvals[!grepl("^History\\.Recurrence$", rownames(cpv.pvals)),
]
cpv.pvals = cpv.pvals[!grepl("^History\\.Status$", rownames(cpv.pvals)), ]
cpv.pvals = cpv.pvals[!grepl("^History\\.Death\\.Cause$", rownames(cpv.pvals)),
]
cpv.pvals = cpv.pvals[!grepl("^Path\\.Grade$", rownames(cpv.pvals)), ]
cpv.pvals = cpv.pvals[!grepl("^Path\\.TumourLocation$", rownames(cpv.pvals)),
]

temp = as.vector(cpv.pvals)
temp = p.adjust(temp, "holm")
cpv.qvals = matrix(temp, nrow = nrow(cpv.pvals))
rownames(cpv.qvals) = rownames(cpv.pvals)
colnames(cpv.qvals) = colnames(cpv.pvals)

cpv.pvals

##                axis1    axis2
## Patient.Gender      0.1581541 0.0098535
## Patient.Ethnicity    0.7711156 0.1130046
## History.Smoking.PackYears 0.3562152 0.2753851
## History.Diagnosis.AgeAtYears 0.9250804 0.6658699
## Path.HistoType.Subtype 0.6966533 0.1569139
## Path.TumourSizeMm     0.8438715 0.1709600
## Path.Invasion.PN      0.0951996 0.2251091
## Path.Invasion.VS      0.6500594 0.0707968
## Staging.pM            0.4414498 0.4245233
## Staging.pN            0.2524195 0.2629997
## Staging.pT            0.2640385 0.4273685
## Staging.Stage         0.0605854 0.2355348
## History.Recurrence.Site.Peritoneum 0.9162045 0.0149891
## History.Recurrence.Site.PancRemnant 0.5341395 0.1839586
## History.Recurrence.Site.PancBed    0.8869735 0.5303110
## History.Recurrence.Site.Other      0.1930828 0.1614602
## History.Recurrence.Site.Omentum    0.1388378 0.0820434
## History.Recurrence.Site.Mesentery   0.9326763 0.1206991
## History.Recurrence.Site.LymphNodes 0.9332622 0.8703023
## History.Recurrence.Site.Lung        0.3900712 0.7130517
## History.Recurrence.Site.Liver       0.1596616 0.1046158
## History.Recurrence.Site.Brain       0.4296978 0.0621650
## History.Recurrence.Site.Bone        0.7889803 0.4128670
## Path.Grade.Coarse      0.0023854 0.0001297
## Path.TumourLocation.Coarse 0.1767526 0.1392750
## purity                 0.0002129 0.0004113

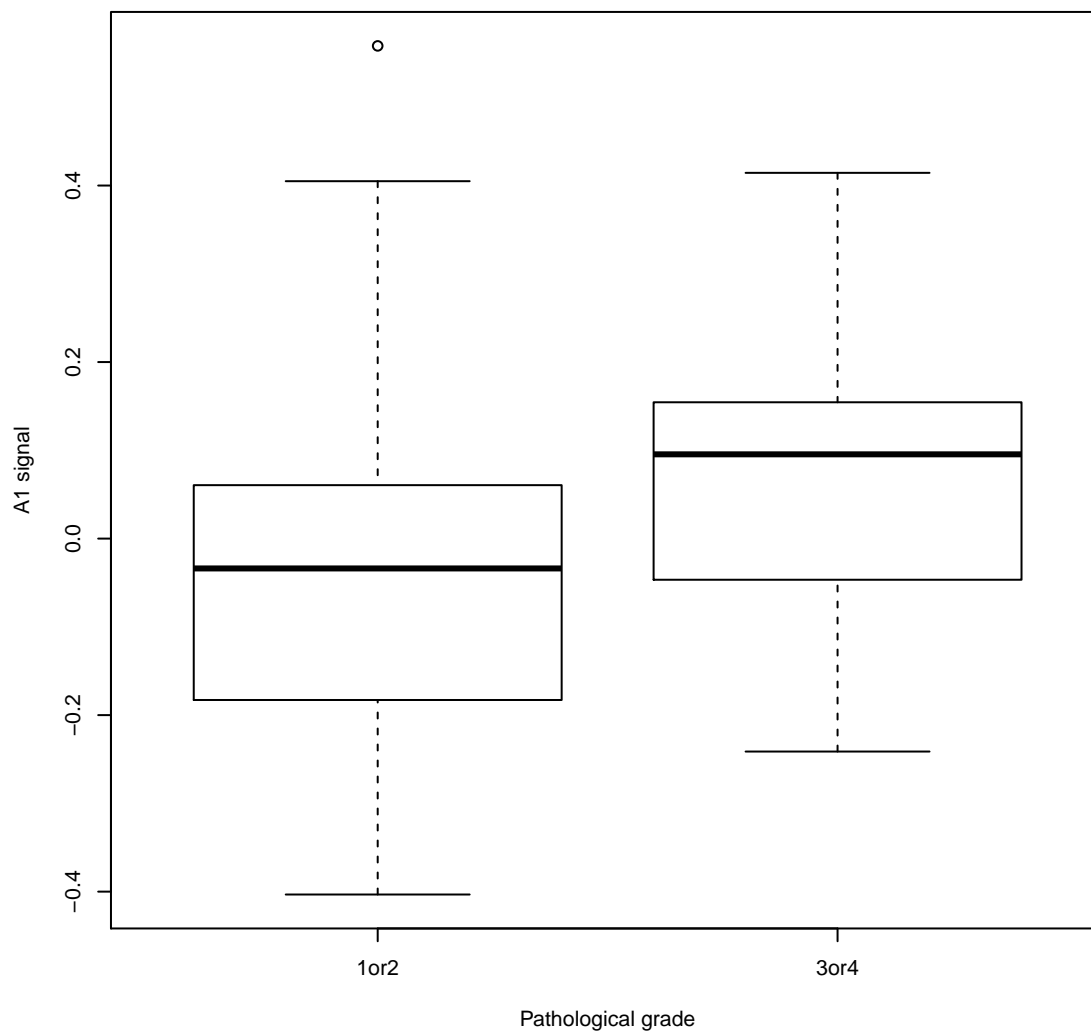
cpv.qvals

##                axis1    axis2
## Patient.Gender      1.00000 0.472968
## Patient.Ethnicity    1.00000 1.000000
## History.Smoking.PackYears 1.00000 1.000000
## History.Diagnosis.AgeAtYears 1.00000 1.000000
## Path.HistoType.Subtype 1.00000 1.000000

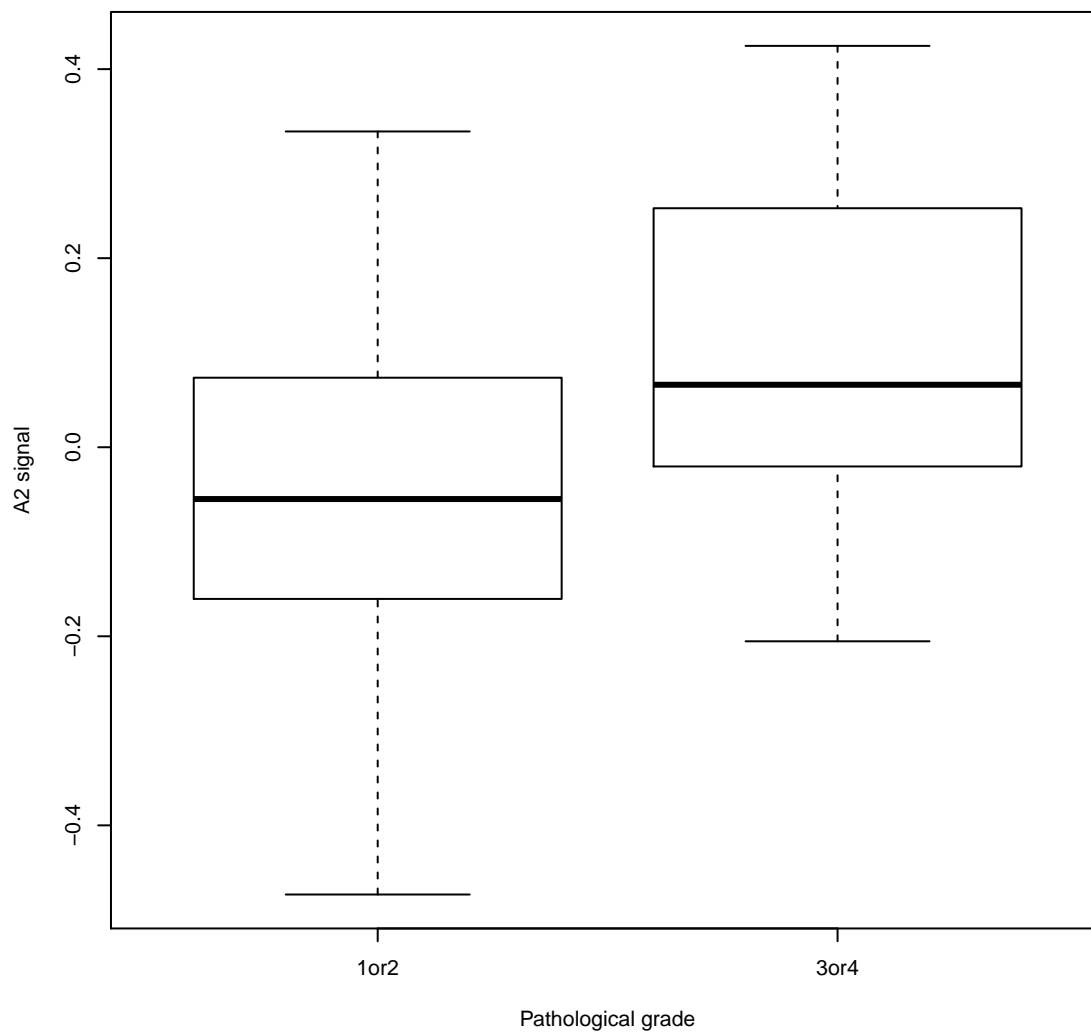
```

```
## Path.TumourSizeMm          1.00000 1.000000
## Path.Invasion.PN          1.00000 1.000000
## Path.Invasion.VS          1.00000 1.000000
## Staging.pM                1.00000 1.000000
## Staging.pN                1.00000 1.000000
## Staging.pT                1.00000 1.000000
## Staging.Stage             1.00000 1.000000
## History.Recurrence.Site.Peritoneum 1.00000 0.704486
## History.Recurrence.Site.PancRemnant 1.00000 1.000000
## History.Recurrence.Site.PancBed 1.00000 1.000000
## History.Recurrence.Site.Other 1.00000 1.000000
## History.Recurrence.Site.Omentum 1.00000 1.000000
## History.Recurrence.Site.Mesentery 1.00000 1.000000
## History.Recurrence.Site.LymphNodes 1.00000 1.000000
## History.Recurrence.Site.Lung 1.00000 1.000000
## History.Recurrence.Site.Liver 1.00000 1.000000
## History.Recurrence.Site.Brain 1.00000 1.000000
## History.Recurrence.Site.Bone 1.00000 1.000000
## Path.Grade.Coarse         0.11688 0.006743
## Path.TumourLocation.Coarse 1.00000 1.000000
## purity                    0.01086 0.020564

boxplot(axis_coefs.diag_dsd[, 1] ~ cpvs.diag_dsd$Path.Grade.Coarse, xlab = "Pathological grade",
        ylab = "A1 signal")
```



```
boxplot(axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse, xlab = "Pathological grade",
        ylab = "A2 signal")
```



```
lm(axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse)

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse)
##
## Coefficients:
##              (Intercept)  cpvs.diag_dsd$Path.Grade.Coarse.L
##                   0.0261                        0.1103

summary(lm(axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse))

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
```

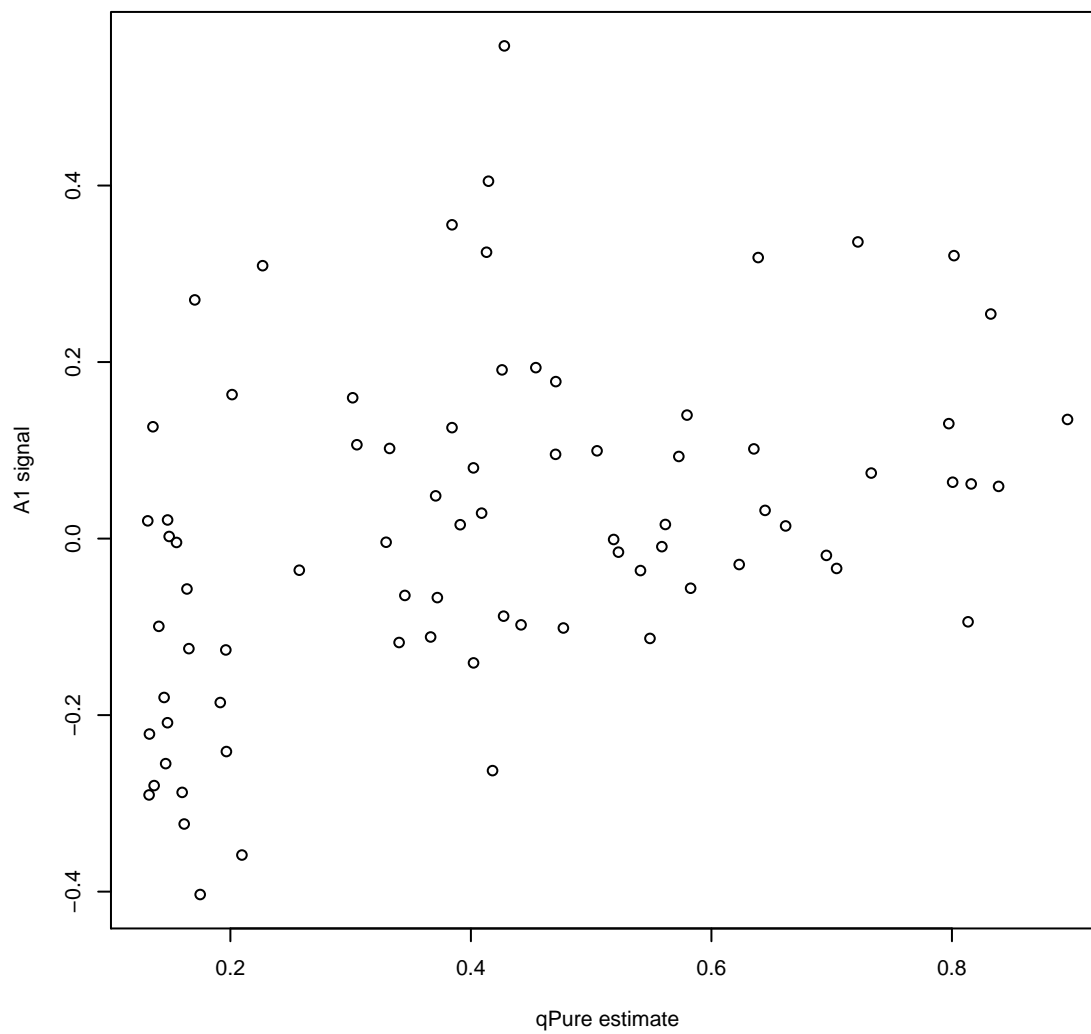


```
## -0.4212 -0.1130 -0.0137  0.1372  0.3860
##
## Coefficients:
##                      Estimate Std. Error t value Pr(>|t|)
## (Intercept)          0.0261     0.0197    1.33  0.18771
## cpvs.diag_dsd$Path.Grade.Coarse.L  0.1103     0.0278    3.97  0.00013
##
## Residual standard error: 0.185 on 108 degrees of freedom
## Multiple R-squared:  0.127, Adjusted R-squared:  0.119
## F-statistic: 15.8 on 1 and 108 DF,  p-value: 0.00013

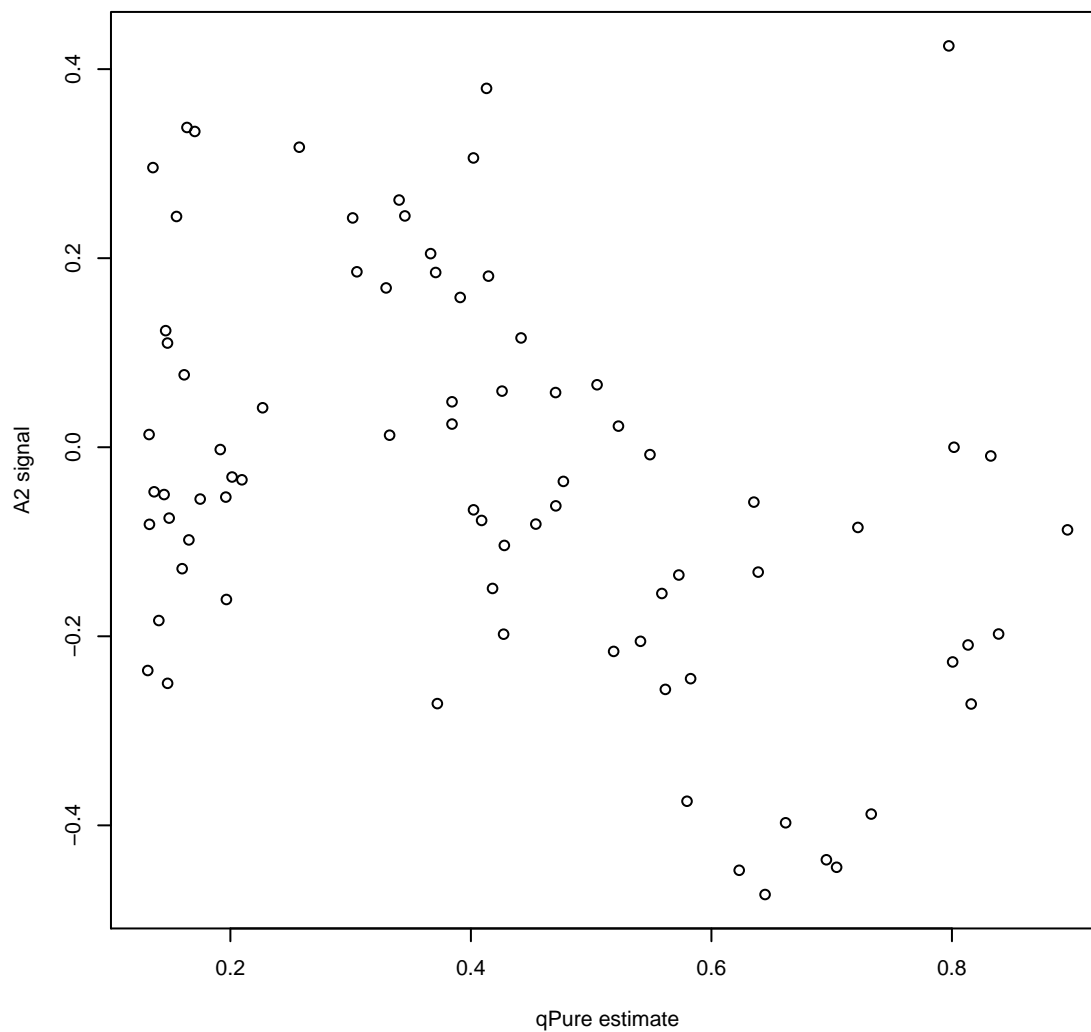
anova(lm(axis_coefs.diag_dsd[, 2] ~ cpvs.diag_dsd$Path.Grade.Coarse))

## Analysis of Variance Table
##
## Response: axis_coefs.diag_dsd[, 2]
##                      Df Sum Sq Mean Sq F value  Pr(>F)
## cpvs.diag_dsd$Path.Grade.Coarse    1    0.54    0.542    15.8 0.00013
## Residuals                      108    3.71    0.034

plot(axis_coefs.diag_dsd[, 1] ~ samps$purity_qpure, xlab = "qPure estimate",
      ylab = "A1 signal")
```



```
plot(axis_coefs.diag_dsd[, 2] ~ sampss$purity_qpure, xlab = "qPure estimate",
      ylab = "A2 signal")
```



```
cor.test(axis_coefs.diag_dsd[, 1], samps$purity_qpure, method = "kendall")

##
## Kendall's rank correlation tau
##
## data: axis_coefs.diag_dsd[, 1] and samps$purity_qpure
## z = 3.676, p-value = 0.0002369
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
## tau
## 0.2838

cor.test(axis_coefs.diag_dsd[, 2], samps$purity_qpure, method = "kendall")

##
## Kendall's rank correlation tau
##
## data: axis_coefs.diag_dsd[, 2] and samps$purity_qpure
```

```
## z = -3.598, p-value = 0.0003203
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## -0.2778

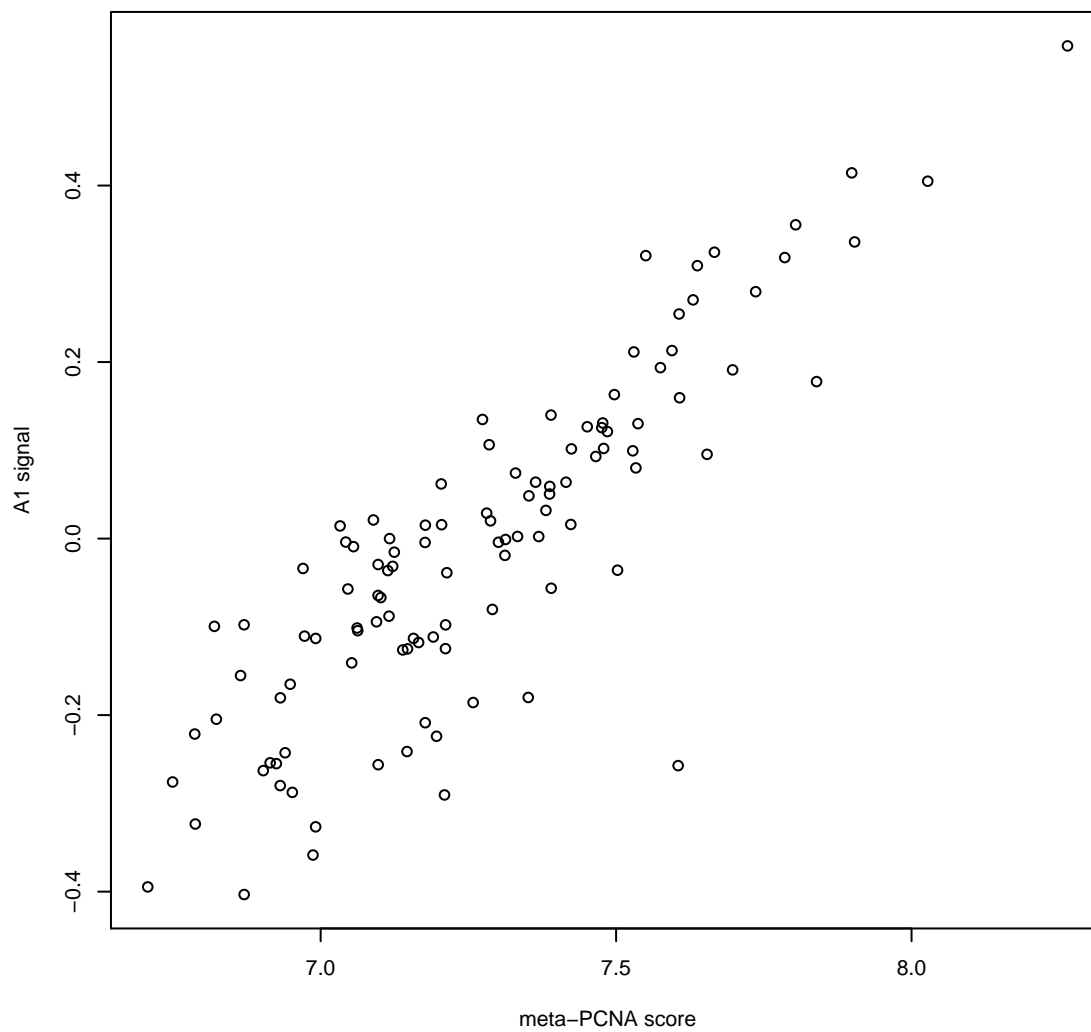
summary(lm(axis_coefs.diag_dsd[, 1] ~ samps$purity_qpure))

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 1] ~ samps$purity_qpure)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3318 -0.1172 -0.0469  0.1011  0.5422
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -0.132     0.042   -3.14  0.00240
## samps$purity_qpure  0.346     0.089    3.89  0.00021
##
## Residual standard error: 0.173 on 76 degrees of freedom
## (32 observations deleted due to missingness)
## Multiple R-squared:  0.166, Adjusted R-squared:  0.155
## F-statistic: 15.1 on 1 and 76 DF, p-value: 0.000213

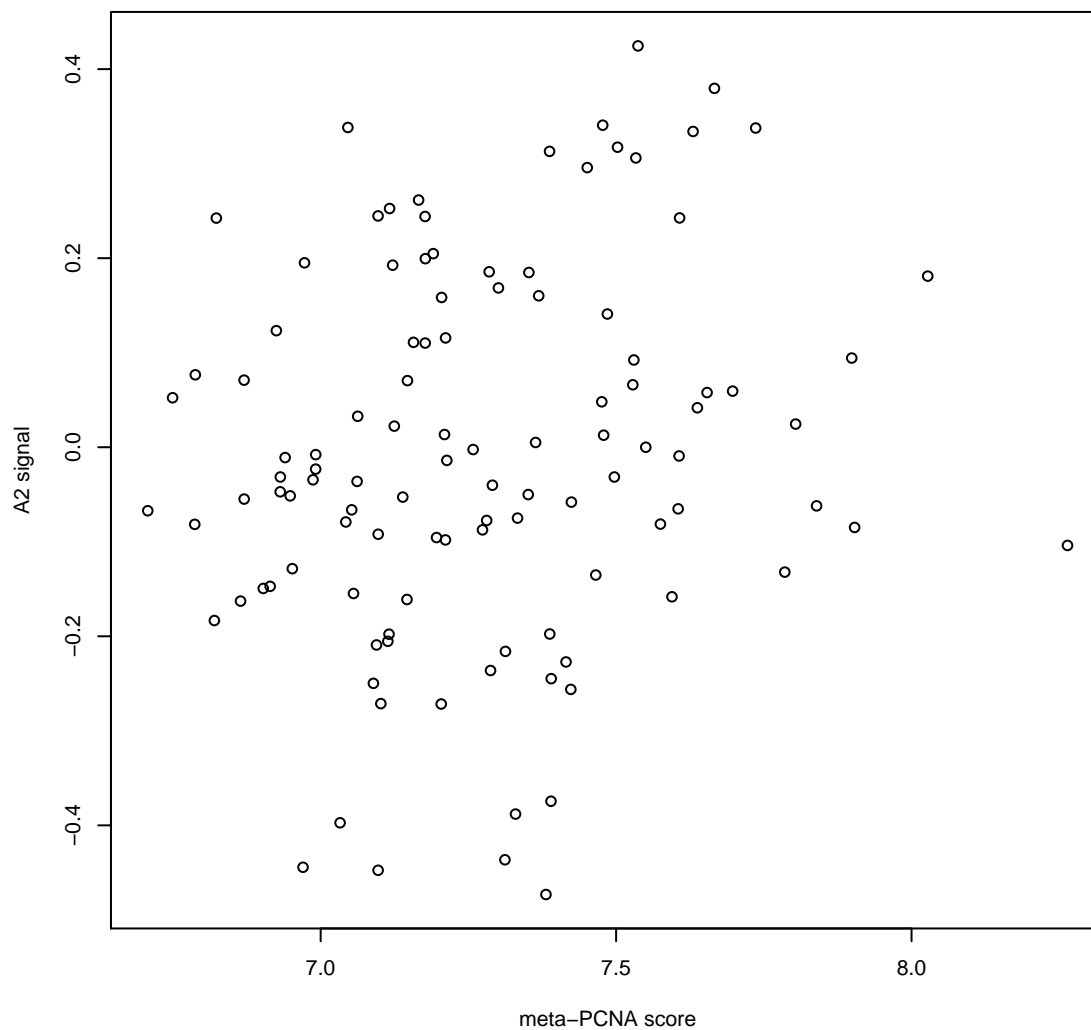
summary(lm(axis_coefs.diag_dsd[, 2] ~ samps$purity_qpure))

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 2] ~ samps$purity_qpure)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.3541 -0.1356 -0.0213  0.1531  0.6002
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.1195     0.0473   2.53  0.01363
## samps$purity_qpure -0.3701     0.1001  -3.70  0.00041
##
## Residual standard error: 0.195 on 76 degrees of freedom
## (32 observations deleted due to missingness)
## Multiple R-squared:  0.152, Adjusted R-squared:  0.141
## F-statistic: 13.7 on 1 and 76 DF, p-value: 0.000411

plot(axis_coefs.diag_dsd[, 1] ~ metapcna.scores, xlab = "meta-PCNA score", ylab = "A1 signal")
```



```
plot(axis_coefs.diag_dsd[, 2] ~ metapcna.scores, xlab = "meta-PCNA score", ylab = "A2 signal")
```



```
cor.test(axis_coefs.diag_dsd[, 1], metapcna.scores, method = "kendall")

##
## Kendall's rank correlation tau
##
## data: axis_coefs.diag_dsd[, 1] and metapcna.scores
## z = 10.27, p-value < 2.2e-16
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
## tau
## 0.6634

cor.test(axis_coefs.diag_dsd[, 2], metapcna.scores, method = "kendall")

##
## Kendall's rank correlation tau
##
## data: axis_coefs.diag_dsd[, 2] and metapcna.scores
```

```
## z = 1.899, p-value = 0.05762
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## 0.1226

summary(lm(axis_coefs.diag_dsd[, 1] ~ metapcna.scores))

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 1] ~ metapcna.scores)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.4295 -0.0477  0.0151  0.0622  0.1785
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -4.0135     0.2274   -17.6   <2e-16
## metapcna.scores  0.5504     0.0312    17.6   <2e-16
##
## Residual standard error: 0.0971 on 108 degrees of freedom
## Multiple R-squared:  0.742, Adjusted R-squared:  0.74
## F-statistic: 311 on 1 and 108 DF,  p-value: <2e-16

summary(lm(axis_coefs.diag_dsd[, 2] ~ metapcna.scores))

##
## Call:
## lm(formula = axis_coefs.diag_dsd[, 2] ~ metapcna.scores)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.478 -0.117  0.000  0.132  0.402
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -0.8487     0.4577   -1.85   0.066
## metapcna.scores  0.1156     0.0629    1.84   0.069
##
## Residual standard error: 0.195 on 108 degrees of freedom
## Multiple R-squared:  0.0303, Adjusted R-squared:  0.0214
## F-statistic: 3.38 on 1 and 108 DF,  p-value: 0.0688
```

```
temp.sig_id = colnames(axis_coefs.msigdb.corr)
temp.sig_class = gsub("\\\\.\\.*", "", temp.sig_id)
temp.nsig = length(temp.sig_id)
temp.nmeta = nrow(axis_coefs.msigdb.corr)
tables = lapply(1:temp.nmeta, function(metagene_i) {
  tapply(1:temp.nsig, temp.sig_class, function(sig_class_is) {
    all_cors = axis_coefs.msigdb.corr[, sig_class_is]
    this_cors = all_cors[metagene_i, ]
    this_ids = temp.sig_id[sig_class_is]
```

```

all_sig_cors = abs(all_cors) >= sig.corr.threshold
this_sig_cors = all_sig_cors[metagene_i, ]

sigs_to_report = which(this_sig_cors)

if (length(sigs_to_report) == 0) {
  table = data.frame(GeneSet = c(), Correlation = c(), Metagenes = c())
} else {
  table = data.frame(GeneSet = this_ids[sigs_to_report], Correlation = this_cors[sigs_to_report],
    Metagenes = apply(all_cors[, sigs_to_report, drop = FALSE],
      2, function(cors) {
        sel = abs(cors) >= sig.corr.threshold
        # A positive number implies that positive GSVA signal is associated with
        # worse prognosis
        paste(which(sel) * sign(cors[which(sel)]), collapse = ",")
      })
  table = table[order(-(table$Correlation)), ]
  rownames(table) <- NULL
}
table
}, simplify = FALSE)
})
tables

## [[1]]
## [[1]]$c1
## data frame with 0 columns and 0 rows
##
## [[1]]$c2
##
## 1
## 2
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## 24

```

c2.AMUNDSON\_GAMMA\_RADIATION\_RESPONSE/c4.GNF2\_CDC2

c2.EGUCHI\_CELL\_CYCLE\_RB1\_TARGETS/c2.ROSTY\_CERVIC



```

## 25
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## 54
## 55
## 56
## 57 c2.REACTOME_ACTIVATION_OF_THE_PRE_F
## 58
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## 60
## 61
## 62
## 63
## 64
## 65
## 66
## 67
## 68
## 69 c2.REACTOME_CELL_CYCLE_CHECKPOINTS/c2.REACTOME_G1_S_TRANSITION/c2.REACTOME_SYNTHESIS_OF_DNA/c2.RE
## 70
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```

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## 170
## 171
## 172
## 173
## 174
## 175
##      Correlation Metagenes
## 1      0.7141      1
## 2      0.6991      1
## 3      0.6981      1
## 4      0.6981      1
## 5      0.6964      1
## 6      0.6911      1
## 7      0.6894      1
## 8      0.6767      1
## 9      0.6767      1

```

## 10	0.6737	1
## 11	0.6711	1
## 12	0.6694	1
## 13	0.6617	1
## 14	0.6601	1
## 15	0.6584	1
## 16	0.6474	1
## 17	0.6470	1
## 18	0.6464	1
## 19	0.6460	1
## 20	0.6444	1
## 21	0.6440	1
## 22	0.6434	1
## 23	0.6404	1
## 24	0.6400	1
## 25	0.6344	1
## 26	0.6317	1
## 27	0.6294	1
## 28	0.6290	1
## 29	0.6287	1
## 30	0.6264	1
## 31	0.6257	1
## 32	0.6254	1
## 33	0.6230	1
## 34	0.6224	1
## 35	0.6180	1
## 36	0.6153	1
## 37	0.6143	1
## 38	0.6140	1
## 39	0.6123	1
## 40	0.6117	1
## 41	0.6073	1
## 42	0.6060	1
## 43	0.6053	1
## 44	0.6050	1
## 45	0.6047	1
## 46	0.6037	1
## 47	0.5993	1
## 48	0.5990	1
## 49	0.5963	1
## 50	0.5960	1
## 51	0.5950	1
## 52	0.5883	1
## 53	0.5870	1
## 54	0.5857	1
## 55	0.5853	1
## 56	0.5837	1
## 57	0.5833	1
## 58	0.5807	1
## 59	0.5807	1
## 60	0.5770	1
## 61	0.5756	1
## 62	0.5753	1
## 63	0.5750	1

## 64	0.5733	1
## 65	0.5730	1
## 66	0.5713	1
## 67	0.5683	1
## 68	0.5680	1
## 69	0.5660	1
## 70	0.5653	1
## 71	0.5650	1
## 72	0.5640	1
## 73	0.5620	1
## 74	0.5586	1
## 75	0.5586	1
## 76	0.5560	1
## 77	0.5536	1
## 78	0.5513	1
## 79	0.5500	1
## 80	0.5473	1
## 81	0.5466	1
## 82	0.5466	1
## 83	0.5463	1
## 84	0.5463	1
## 85	0.5456	1
## 86	0.5453	1
## 87	0.5336	1
## 88	0.5319	1
## 89	0.5313	1
## 90	0.5309	1
## 91	0.5306	1
## 92	0.5296	1
## 93	0.5279	1
## 94	0.5276	1
## 95	0.5273	1
## 96	0.5273	1
## 97	0.5246	1
## 98	0.5243	1
## 99	0.5239	1
## 100	0.5233	1
## 101	0.5226	1
## 102	0.5223	1
## 103	0.5199	1
## 104	0.5199	1
## 105	0.5196	1
## 106	0.5179	1
## 107	0.5179	1
## 108	0.5173	1
## 109	0.5173	1
## 110	0.5159	1
## 111	0.5146	1
## 112	0.5129	1
## 113	0.5103	1
## 114	0.5103	1
## 115	0.5099	1
## 116	0.5086	1
## 117	0.5073	1

## 118	0.5063	1
## 119	0.5059	1
## 120	0.5056	1
## 121	0.5056	1
## 122	0.5043	1
## 123	0.5029	1
## 124	0.5019	1
## 125	0.5019	1
## 126	0.5016	1
## 127	0.5013	1
## 128	0.5009	1
## 129	0.5003	1
## 130	0.5003	1
## 131	-0.5009	-1
## 132	-0.5033	-1
## 133	-0.5043	-1
## 134	-0.5056	-1
## 135	-0.5083	-1
## 136	-0.5089	-1
## 137	-0.5096	-1
## 138	-0.5243	-1
## 139	-0.5289	-1
## 140	-0.5316	-1
## 141	-0.5319	-1
## 142	-0.5393	-1
## 143	-0.5399	-1
## 144	-0.5416	-1
## 145	-0.5433	-1
## 146	-0.5516	-1
## 147	-0.5520	-1
## 148	-0.5570	-1
## 149	-0.5580	-1
## 150	-0.5583	-1
## 151	-0.5640	-1
## 152	-0.5646	-1
## 153	-0.5730	-1
## 154	-0.5733	-1
## 155	-0.5750	-1
## 156	-0.5893	-1
## 157	-0.5900	-1
## 158	-0.5913	-1
## 159	-0.5940	-1
## 160	-0.6047	-1
## 161	-0.6063	-1
## 162	-0.6147	-1
## 163	-0.6153	-1
## 164	-0.6217	-1
## 165	-0.6247	-1
## 166	-0.6260	-1
## 167	-0.6310	-1
## 168	-0.6347	-1
## 169	-0.6357	-1
## 170	-0.6370	-1
## 171	-0.6387	-1

```

## 172      -0.6454      -1
## 173      -0.6791      -1
## 174      -0.6894      -1
## 175      -0.6951      -1
##
## [[1]]$c3
##           GeneSet Correlation Metagenes
## 1          c3.V$ELK1_02      0.5740      1
## 2 c3.SCGGAAGY_V$ELK1_02      0.5580      1
## 3          c3.CTGCAGY_UNKNOWN -0.5046     -1
## 4          c3.V$OCT1_01      -0.5089     -1
## 5          c3.V$GATA_Q6       -0.5153     -1
## 6          c3.V$OCT1_04       -0.5313     -1
## 7          c3.V$OCT_C        -0.5436     -1
##
## [[1]]$c4
##                                           GeneSet
## 1 c4.GNF2_RFC3/c4.GNF2_RFC4/c4.GNF2_SMC2L1/c4.GNF2_CKS1B/c4.GNF2_CKS2/c4.GNF2_TTK
## 2                                           c4.MODULE_17
## 3                                           c4.MODULE_315
## 4                                           c4.MORF_BUB1B
## 5                                           c4.MODULE_244
## 6                                           c4.MODULE_337
## 7                                           c4.MORF_FEN1
## 8                                           c4.MODULE_126
## 9                                           c4.MODULE_124
## 10                                          c4.MORF_ESPL1
## 11                                          c4.MORF_BUB1
## 12                                          c4.MODULE_403
## 13                                          c4.MORF_BUB3/c4.MORF_RAD23A
## 14                                          c4.MORF_RFC4/c4.MORF_RRM1
## 15 c4.MODULE_98/c4.MODULE_198/c4.MODULE_252
## 16                                          c4.MODULE_125/c4.MODULE_158
## 17                                          c4.MORF_UNG
## 18                                          c4.MODULE_278
## 19                                          c4.MORF_GSPT1
## 20                                          c4.MODULE_320
## 21                                          c4.MODULE_8
## 22                                          c4.MORF_CCNF
## 23                                          c4.MORF_EI24
## 24 c4.GNF2_PA2G4/c4.GNF2_RAN
## 25                                          c4.MORF_PRKDC
## 26                                          c4.MORF_GMPS
## 27                                          c4.MODULE_219
## 28                                          c4.GNF2_MCM5
## 29                                          c4.MORF_DNMT1
## 30                                          c4.GNF2_MSH2
## 31                                          c4.MORF_CSNK2B
## 32                                          c4.MORF_PTPN11
## 33                                          c4.MORF_PPP1CC
## 34 c4.MORF_XRCC5/c4.MORF_GNB1
## 35                                          c4.MODULE_451
## 36                                          c4.MORF_SOD1
## 37                                          c4.MORF_HDAC1

```

```

## 38 c4.MODULE_51
## 39 c4.GNF2_MAPT
## 40 c4.MODULE_19
## 41 c4.MODULE_11/c4.MODULE_66/c4.MODULE_100/c4.MODULE_137
## Correlation Metagenes
## 1 0.6637 1
## 2 0.6510 1
## 3 0.6324 1
## 4 0.6307 1
## 5 0.6294 1
## 6 0.6244 1
## 7 0.5860 1
## 8 0.5817 1
## 9 0.5813 1
## 10 0.5656 1
## 11 0.5650 1
## 12 0.5640 1
## 13 0.5633 1
## 14 0.5606 1
## 15 0.5586 1
## 16 0.5586 1
## 17 0.5536 1
## 18 0.5536 1
## 19 0.5503 1
## 20 0.5490 1
## 21 0.5480 1
## 22 0.5436 1
## 23 0.5379 1
## 24 0.5313 1
## 25 0.5279 1
## 26 0.5279 1
## 27 0.5266 1
## 28 0.5249 1
## 29 0.5243 1
## 30 0.5206 1
## 31 0.5203 1
## 32 0.5163 1
## 33 0.5089 1
## 34 0.5039 1
## 35 0.5026 1
## 36 0.5019 1
## 37 0.5009 1
## 38 -0.5066 -1
## 39 -0.5259 -1
## 40 -0.5656 -1
## 41 -0.5967 -1
##
## [[1]]$c5
## GeneSet
## 1 c5.M_PHASE/c5.MITOSIS/c5.M_PHASE_OF_MITOTIC_CELL_CYCLE
## 2 c5.REGULATION_OF_MITOSIS
## 3 c5.CELL_CYCLE_PROCESS/c5.MITOTIC_CELL_CYCLE/c5.CELL_CYCLE_PHASE
## 4 c5.SPINDLE
## 5 c5.SPINDLE_POLE

```



```

## 6 c5.ORGANELLE_PART/c5.INTRACELLULAR_ORGANELLE_PART
## 7 c5.CHROMOSOME_SEGREGATION
## 8 c5.CELL_CYCLE_GO_0007049
## 9 c5.SPINDLE_MICROTUBULE
## 10 c5.MITOTIC_CELL_CYCLE_CHECKPOINT
## 11 c5.CONDENSED_CHROMOSOME
## 12 c5.MITOTIC_SISTER_CHROMATID_SEGREGATION/c5.SISTER_CHROMATID_SEGREGATION
## 13 c5.CELL_CYCLE_CHECKPOINT_GO_0000075
## 14 c5.MITOTIC_SPINDLE_ORGANIZATION_AND_BIOGENESIS/c5.SPINDLE_ORGANIZATION_AND_BIOGENESIS
## 15 c5.DOUBLE_STRAND_BREAK_REPAIR
## 16 c5.DNA_METABOLIC_PROCESS
## 17 c5.REGULATION_OF_MITOTIC_CELL_CYCLE
## 18 c5.RESPONSE_TO_ENDOGENOUS_STIMULUS/c5.RESPONSE_TO_DNA_DAMAGE_STIMULUS
## 19 c5.CHROMOSOME PERICENTRIC_REGION/c5.KINETOCHORE
## 20 c5.PORE_COMPLEX/c5.NUCLEAR_PORE
## 21 c5.DNA_REPAIR
## 22 c5.MACROMOLECULAR_COMPLEX/c5.PROTEIN_COMPLEX
## 23 c5.INTERPHASE/c5.INTERPHASE_OF_MITOTIC_CELL_CYCLE
## 24 c5.NON_MEMBRANE_BOUND_ORGANELLE/c5.INTRACELLULAR_NON_MEMBRANE_BOUND_ORGANELLE
## 25 c5.NUCLEAR_MEMBRANE/c5.NUCLEAR_MEMBRANE_PART
## 26 c5.CHROMOSOMAL_PART/c5.CHROMOSOME
## 27 c5.PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY
## 28 c5.CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166
## Correlation Metagenes
## 1 0.6894 1
## 2 0.6821 1
## 3 0.6527 1
## 4 0.6437 1
## 5 0.6280 1
## 6 0.6244 1
## 7 0.5883 1
## 8 0.5760 1
## 9 0.5726 1
## 10 0.5690 1
## 11 0.5620 1
## 12 0.5546 1
## 13 0.5426 1
## 14 0.5420 1
## 15 0.5369 1
## 16 0.5166 1
## 17 0.5156 1
## 18 0.5146 1
## 19 0.5136 1
## 20 0.5083 1
## 21 0.5063 1
## 22 0.5059 1
## 23 0.5033 1
## 24 0.5029 1
## 25 0.5013 1
## 26 0.5003 1
## 27 -0.5023 -1
## 28 -0.5176 -1
##

```

```

## [[1]]$c6
##               GeneSet Correlation Metagenes
## 1      c6.CSR_LATE_UP.V1_SIGNED      0.6297      1
## 2      c6.MTOR_UP.V1_SIGNED      0.5123      1
## 3 c6.GCNP_SHH_UP_EARLY.V1_SIGNED      0.5026      1
##
## [[1]]$c7
##
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22
## 23
## 24
## 25
## 26
## 27
## 28
## 29
## 30
## 31
## 32
## 33
## 34
## 35
## 36
## 37
## 38
## 39
## 40
## 41
## 42
## 43
## 44
## 45

```

c7.GSE15750\_DAY6\_VS\_I

c7.GSE24634\_TEFF\_VS\_TCONV\_

```

## 46
## 47
## 48
## 49
## 50
## 51
## 52
## 53
## 54 c7.GSE15930_NAIVE_VS_24H_IN_VITRO_STIM_CD8_TCELL_SIGNED/c7.GSE15930_NAIVE_VS_24H_IN_VITRO_STIM_IL1
## 55
## 56
## 57
## 58
## 59
## 60
## 61
## 62
## 63
## 64
## 65
## 66
## 67 c7.GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_T
## 68
## 69
## 70
## 71 c7.GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_T
##      Correlation Metagenes
## 1      0.6187      1
## 2      0.6160      1
## 3      0.6143      1
## 4      0.5880      1
## 5      0.5857      1
## 6      0.5756      1
## 7      0.5696      1
## 8      0.5653      1
## 9      0.5630      1
## 10     0.5623      1
## 11     0.5580      1
## 12     0.5553      1
## 13     0.5546      1
## 14     0.5476      1
## 15     0.5466      1
## 16     0.5423      1
## 17     0.5349      1
## 18     0.5336      1
## 19     0.5276      1
## 20     0.5186      1
## 21     0.5186      1
## 22     0.5036      1
## 23     -0.5039     -1
## 24     -0.5086     -1
## 25     -0.5109     -1
## 26     -0.5119     -1
## 27     -0.5119     -1

```

```

## 28      -0.5149      -1
## 29      -0.5179      -1
## 30      -0.5183      -1
## 31      -0.5223      -1
## 32      -0.5239      -1
## 33      -0.5269      -1
## 34      -0.5303      -1
## 35      -0.5316      -1
## 36      -0.5336      -1
## 37      -0.5343      -1
## 38      -0.5343      -1
## 39      -0.5426      -1
## 40      -0.5516      -1
## 41      -0.5520      -1
## 42      -0.5543      -1
## 43      -0.5560      -1
## 44      -0.5603      -1
## 45      -0.5603      -1
## 46      -0.5613      -1
## 47      -0.5630      -1
## 48      -0.5636      -1
## 49      -0.5650      -1
## 50      -0.5716      -1
## 51      -0.5743      -1
## 52      -0.5786      -1
## 53      -0.5830      -1
## 54      -0.5853      -1
## 55      -0.5860      -1
## 56      -0.5867      -1
## 57      -0.5920      -1
## 58      -0.5950      -1
## 59      -0.5953      -1
## 60      -0.6007      -1
## 61      -0.6010      -1
## 62      -0.6090      -1
## 63      -0.6190      -1
## 64      -0.6193      -1
## 65      -0.6254      -1
## 66      -0.6417      -1
## 67      -0.6500      -1
## 68      -0.6530      -1
## 69      -0.6637      -1
## 70      -0.6654      -1
## 71      -0.6667      -1
##
##
## [[2]]
## [[2]]$c1
## data frame with 0 columns and 0 rows
##
## [[2]]$c2
##
## 1
## 2

```

```

Ger
c2.PID_INTEGRIN1_PAT
c2.VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_SI

```

```

## 3 c2.LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_SI
## 4 c2.PID_INTEGRIN3_PAT
## 5 c2.SUZUKI_RESPONSE_TO_TSA_AND_DECITABIN
## 6 c2.HUANG_DASATINIB_RESISTANCE_SI
## 7 c2.WIEDERSCHAIN_TARGETS_OF_BMI1_AND_
## 8 c2.BURTON_ADIPOGENESIS
## 9 c2.POTTI_TOPOTECAN_SENSITI
## 10 c2.KARAKAS_TGFB1_SIGNA
## 11 c2.PID_UPA_UPAR_PAT
## 12 c2.CROMER_TUMORIGENESIS_SI
## 13 c2.ROZANOV_MMP14_TARGETS_SU
## 14 c2.WOO_LIVER_CANCER_RECURRENCE_SI
## 15 c2.KEGG_ECM_RECEPTOR_INTERAC
## 16 c2.FARMER_BREAST_CANCER_CLUSTER_5/c2.ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE/c4.GNF2_C
## 17 c2.PID_INTEGRIN5_PAT
## 18 c2.REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION/c2.REACTOME_COLLAGEN_FORMA
## 19 c2.ROY_WOUND_BLOOD_VESSEL_SI
## 20 c2.KEGG_FOCAL_ADHE
## 21 c2.CHICAS_RB1_TARGETS_CONFI
## 22 c2.YIH_RESPONSE_TO_ARSENIT
## 23 c2.PHONG_TNF_RESPONSE_VIA_P38_PAF
## 24 c2.SERVITJA_ISLET_HNF1A_TARGETS_SI
## 25 c2.LI_PROSTATE_CANCER_EPIGEN
## 26 c2.PID_SYNDECAN_1_PAT
## 27 c2.AGARWAL_AKT_PATHWAY_TAR
## 28 c2.REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACT
## 29 c2.PID_INTEGRIN_CS_PAT
## 30 c2.HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGEN
## 31 c2.MATTHEWS_AP1_TAR
## 32 c2.RODWELL_AGING_KIDNEY_NO_BLOOD_SI
## 33 c2.YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER
## 34 c2.WESTON_VEGFA_TAR
## 35 c2.WU_CELL_MIGRA
## 36 c2.SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_SI
## 37 c2.KAN_RESPONSE_TO_ARSENIC_TRIO
## 38 c2.VERHAAK_GLIOBLASTOMA_NE
## 39 c2.REACTOME_INTEGRIN_CELL_SURFACE_INTERACT
## 40 c2.GILDEA_METAST
## 41 c2.TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_SI
## 42 c2.HARRIS_HYPOXIA/c2.WINTER_HYPOXIA_META
## 43 c2.BIOCARTA_PLATELETAPP_PAT
## 44 c2.WANG_METHYLATED_IN_BREAST_CA
## 45 c2.RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_SI
## 46 c2.CHARAFE_BREAST_CANCER_LUMINAL_VS_BASAL_SI
## 47 c2.WALLACE_PROSTATE_CANCER_SI
## 48 c2.WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_SI
## 49 c2.SMID_BREAST_CANCER_RELAPSE_IN_BONE_SI
## 50 c2.MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_SI
## 51 c2.LIU_PROSTATE_CANCER_SI
## 52 c2.PASINI_SUZ12_TARGETS_SI
## 53 c2.NAKAMURA_ADIPOGENESIS_LATE_SI
## 54 c2.DOANE_BREAST_CANCER_CLASSES_SI
## 55 c2.CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_SI
## Correlation Metagenes

```

## 1	0.6544	2
## 2	0.6514	2
## 3	0.6454	2
## 4	0.6374	2
## 5	0.6370	2
## 6	0.6350	2
## 7	0.6250	2
## 8	0.6103	2
## 9	0.6017	2
## 10	0.5997	2
## 11	0.5970	2
## 12	0.5910	2
## 13	0.5907	2
## 14	0.5883	2
## 15	0.5817	2
## 16	0.5783	2
## 17	0.5766	2
## 18	0.5723	2
## 19	0.5676	2
## 20	0.5666	2
## 21	0.5643	2
## 22	0.5623	2
## 23	0.5590	2
## 24	0.5586	2
## 25	0.5543	2
## 26	0.5516	2
## 27	0.5486	2
## 28	0.5379	2
## 29	0.5363	2
## 30	0.5289	2
## 31	0.5279	2
## 32	0.5256	2
## 33	0.5239	2
## 34	0.5229	2
## 35	0.5209	2
## 36	0.5206	2
## 37	0.5206	2
## 38	0.5203	2
## 39	0.5179	2
## 40	0.5179	2
## 41	0.5146	2
## 42	0.5119	2
## 43	0.5056	2
## 44	0.5009	2
## 45	-0.5043	-2
## 46	-0.5209	-2
## 47	-0.5209	-2
## 48	-0.5443	-2
## 49	-0.5536	-2
## 50	-0.5563	-2
## 51	-0.5643	-2
## 52	-0.5663	-2
## 53	-0.5680	-2
## 54	-0.6010	-2

```

## 55      -0.6097      -2
##
## [[2]]$c3
## data frame with 0 columns and 0 rows
##
## [[2]]$c4
##      GeneSet Correlation Metagenes
## 1  c4.GNF2_PTX3      0.5933      2
## 2  c4.GNF2_MMP1      0.5750      2
## 3  c4.MODULE_412      0.5670      2
## 4  c4.MODULE_122      0.5600      2
## 5  c4.MODULE_47       0.5463      2
## 6  c4.MODULE_153      0.5426      2
## 7  c4.MODULE_321      0.5309      2
## 8  c4.MODULE_275      0.5253      2
## 9  c4.MODULE_562      0.5066      2
##
## [[2]]$c5
##                                     GeneSet
## 1                                     c5.AXON_GUIDANCE
## 2                                     c5.TISSUE_DEVELOPMENT
## 3                                     c5.COLLAGEN
## 4  c5.AXONOGENESIS/c5.CELLULAR_MORPHOGENESIS_DURING_DIFFERENTIATION
##      Correlation Metagenes
## 1      0.5710      2
## 2      0.5363      2
## 3      0.5313      2
## 4      0.5146      2
##
## [[2]]$c6
##                                     GeneSet Correlation Metagenes
## 1  c6.CORDENONSI_YAP_CONSERVED_SIGNATURE      0.5256      2
## 2                                     c6.LEF1_UP.V1_SIGNED      0.5193      2
## 3                                     c6.STK33_NOMO_SIGNED      0.5073      2
##
## [[2]]$c7
##                                     GeneSet
## 1                                     c7.GSE17721_CTRL_VS_CPG_12H_BMDM_SIGNED
## 2  c7.GSE1460_INTRATHYMIC_T_PROGENITOR_VS_THYMIC_STROMAL_CELL_SIGNED
##      Correlation Metagenes
## 1      -0.5076      -2
## 2      -0.5079      -2

for (subtable_index in 1:length(tables)) {
  write.csv(do.call(rbind, tables[[subtable_index]]), file = sprintf("A%d_corrs.csv",
    subtable_index))
}

```

## 5 Session information

```

session_info

## R version 3.1.1 (2014-07-10)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
## [1] LC_CTYPE=en_AU.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=en_AU.UTF-8      LC_COLLATE=en_AU.UTF-8
## [5] LC_MONETARY=en_AU.UTF-8  LC_MESSAGES=en_AU.UTF-8
## [7] LC_PAPER=en_AU.UTF-8     LC_NAME=en_AU.UTF-8
## [9] LC_ADDRESS=en_AU.UTF-8   LC_TELEPHONE=en_AU.UTF-8
## [11] LC_MEASUREMENT=en_AU.UTF-8 LC_IDENTIFICATION=en_AU.UTF-8
##
## attached base packages:
## [1] splines    parallel  methods    stats      graphics  grDevices  utils
## [8] datasets  base
##
## other attached packages:
## [1] doParallel_1.0.8    iterators_1.0.7    foreach_1.4.2
## [4] ahaz_1.14           survival_2.37-7    NMF_0.20.5
## [7] Biobase_2.26.0      BiocGenerics_0.12.1 cluster_1.15.3
## [10] rngtools_1.2.4      pkgmaker_0.22      registry_0.2
## [13] energy_1.6.2        glmnet_1.9-8       Matrix_1.1-4
## [16] glmulti_1.0.7       rJava_0.9-6
##
## loaded via a namespace (and not attached):
## [1] boot_1.3-13         codetools_0.2-9    colorspace_1.2-4
## [4] compiler_3.1.1      digest_0.6.4       ggplot2_1.0.0
## [7] grid_3.1.1          gridBase_0.4-7     gtable_0.1.2
## [10] lattice_0.20-29     MASS_7.3-35        munsell_0.4.2
## [13] plyr_1.8.1          proto_0.3-10       RColorBrewer_1.0-5
## [16] Rcpp_0.11.3         reshape2_1.4       scales_0.2.4
## [19] stringr_0.6.2       tools_3.1.1        xtable_1.7-4

sessionInfo()

## R version 3.1.1 (2014-07-10)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
## [3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=en_US.UTF-8     LC_NAME=en_US.UTF-8
## [9] LC_ADDRESS=en_US.UTF-8   LC_TELEPHONE=en_US.UTF-8
## [11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=en_US.UTF-8
##
## attached base packages:
## [1] parallel  methods    splines    stats      graphics  grDevices  utils
## [8] datasets  base
##
## other attached packages:
## [1] stargazer_5.1        xtable_1.7-4       gplots_2.14.2
## [4] RColorBrewer_1.0-5   glmnet_1.9-8       Matrix_1.1-4
## [7] glmulti_1.0.7       rJava_0.9-6       nnls_1.4

```



```
## [10] NMF_0.20.5          synchronicity_1.1.4 bigmemory_4.4.6
## [13] BH_1.54.0-5         bigmemory.sri_0.1.3 Biobase_2.26.0
## [16] BiocGenerics_0.12.1 cluster_1.15.3      rngtools_1.2.4
## [19] pkgmaker_0.22       registry_0.2        energy_1.6.2
## [22] survival_2.37-7     knitr_1.8
##
## loaded via a namespace (and not attached):
## [1] bitops_1.0-6        boot_1.3-13         caTools_1.17.1
## [4] codetools_0.2-9     colorspace_1.2-4    digest_0.6.4
## [7] doParallel_1.0.8    evaluate_0.5.5      foreach_1.4.2
## [10] formatR_1.0         gdata_2.13.3        ggplot2_1.0.0
## [13] grid_3.1.1          gridBase_0.4-7      gtable_0.1.2
## [16] gtools_3.4.1        highr_0.4            iterators_1.0.7
## [19] KernSmooth_2.23-13 labeling_0.3         lattice_0.20-29
## [22] MASS_7.3-35         munsell_0.4.2       plyr_1.8.1
## [25] proto_0.3-10        Rcpp_0.11.3         reshape2_1.4
## [28] scales_0.2.4        stringr_0.6.2       tools_3.1.1
```