

SIS NMF Final: Diagnosis to DSD

December 4, 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 [NO: bigmemory] | Cores 31/32
## To enable shared memory capabilities, try: install.extras('
## NMF
## ')

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)

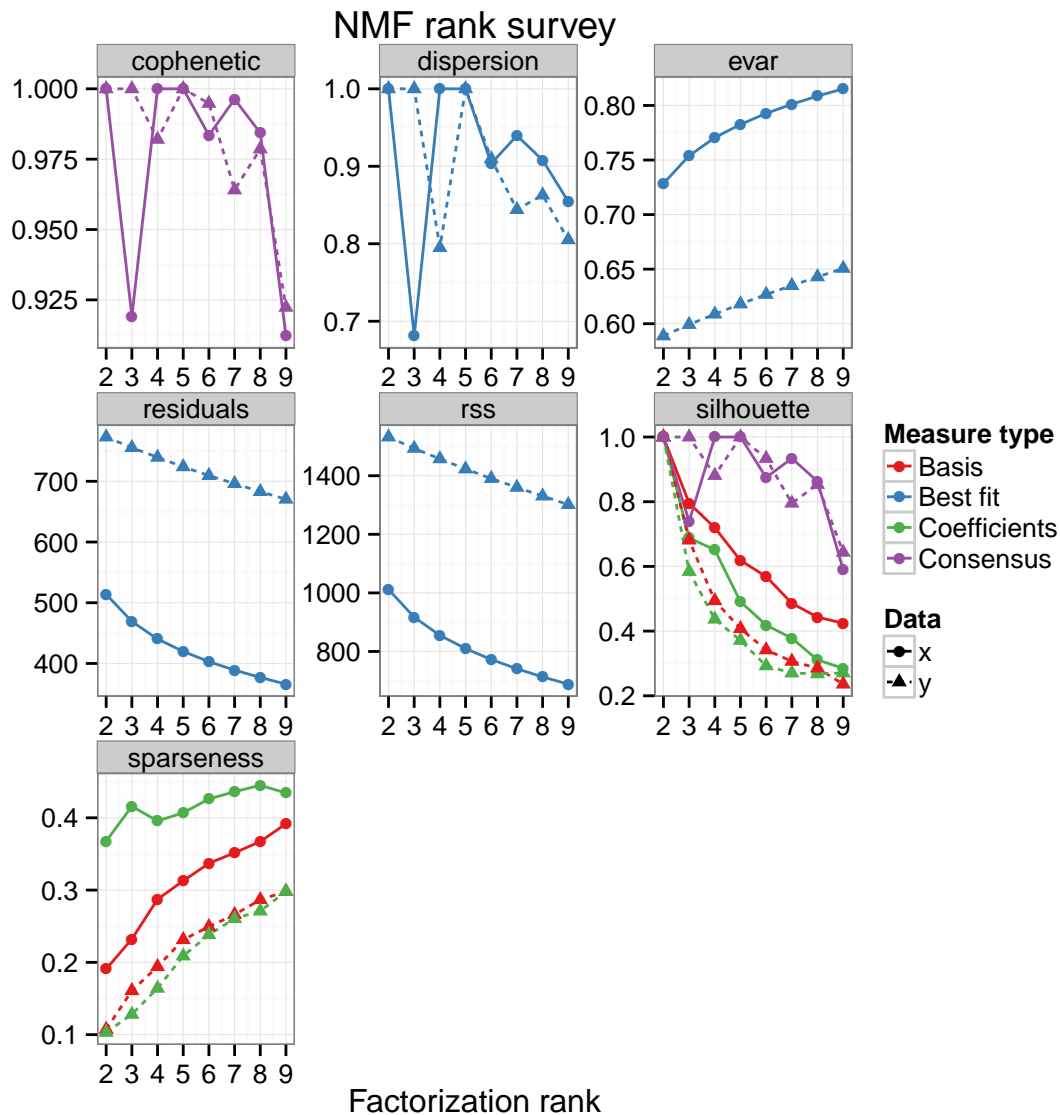
## [1] 37 175 92 32 298 49 47 138 43 173 98 86 207 102 147 41 28
## [18] 160 75 273 154 124 415 109 41 141 50 63 107 63 64 237 84 52
## [35] 40 203 88 55 98 87 57 231 54 48 81 186 114 43 58 347

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

## [1] 87.5
```

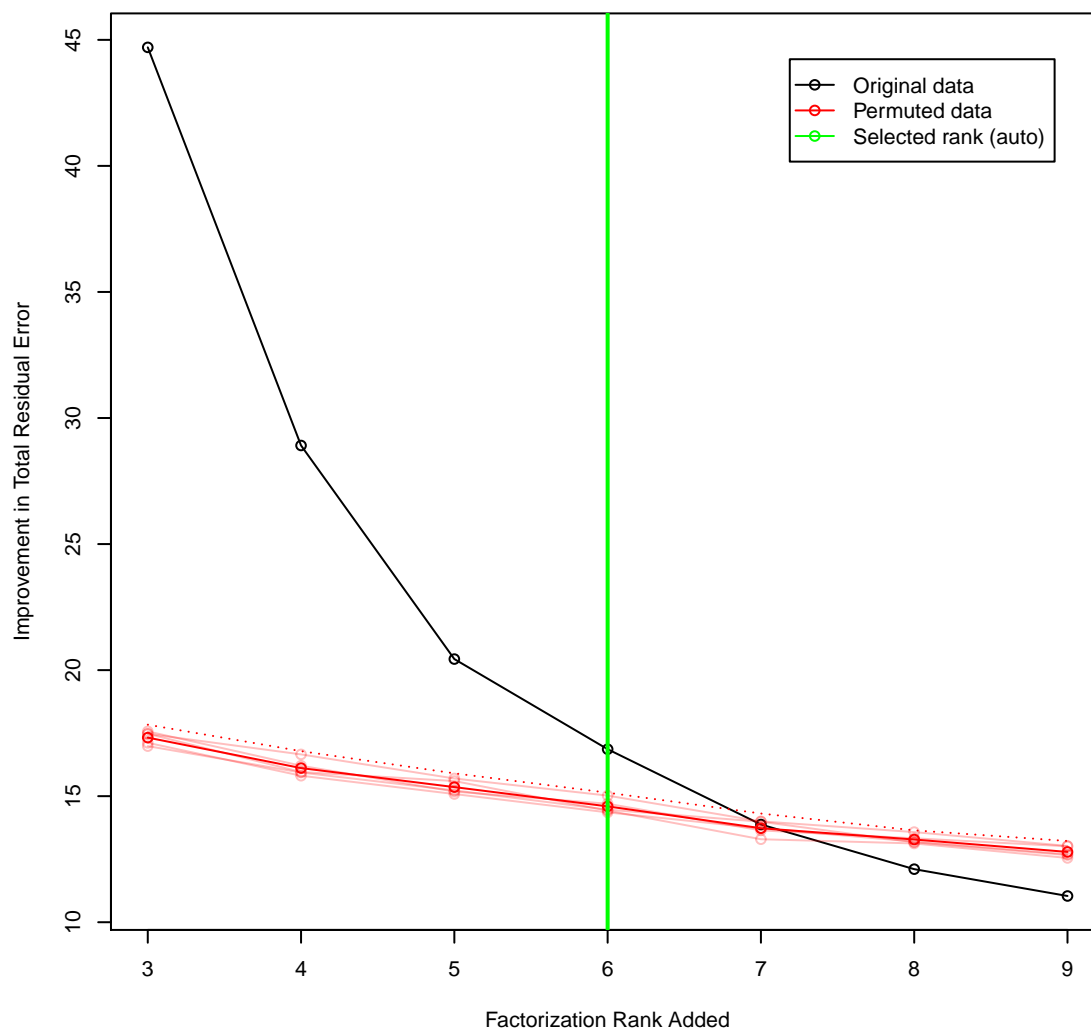
4 Factorization

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



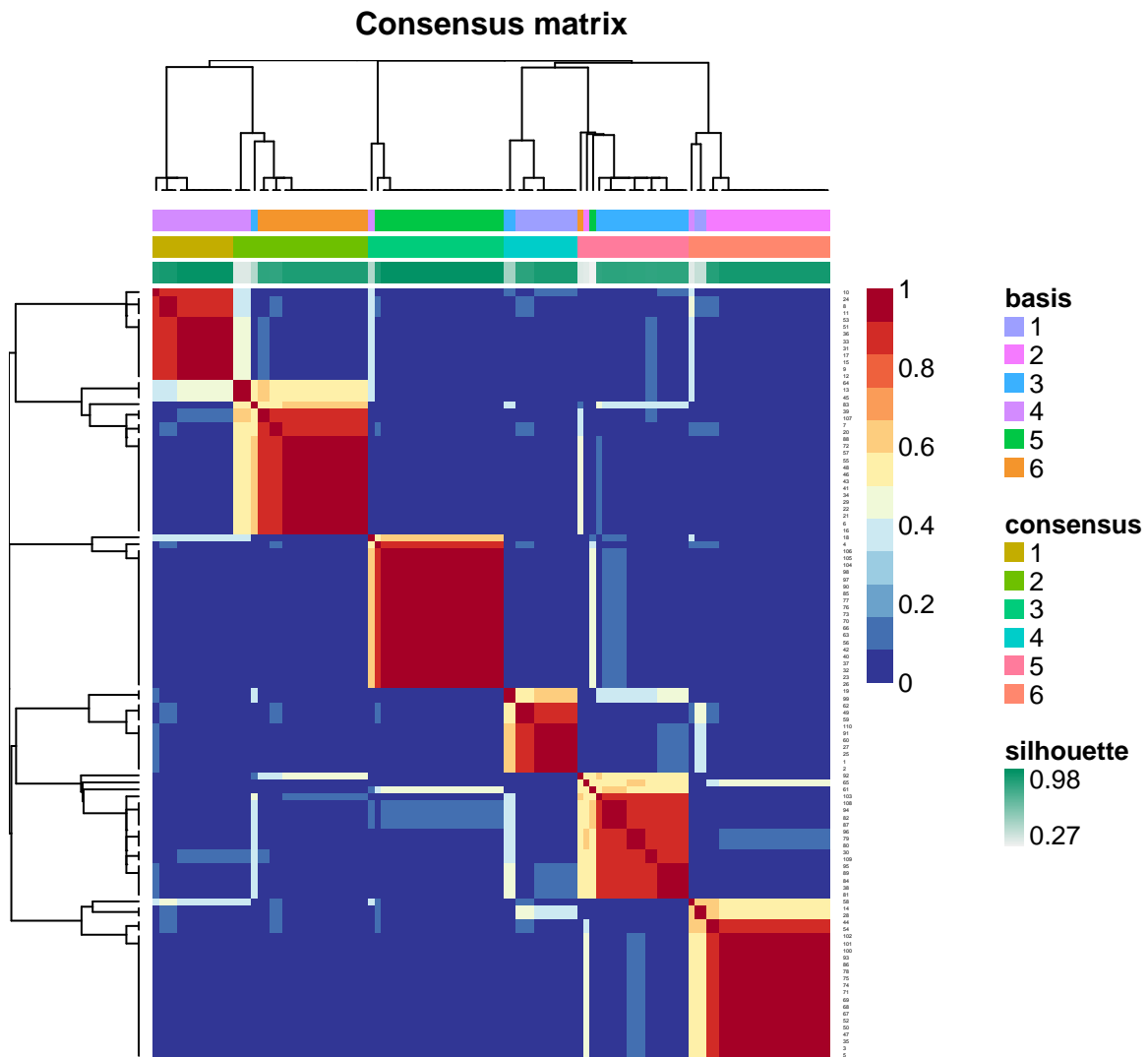
```
plot(nmf.rankrange[-1], -temp.orig_resids.delta, type = "o", col = "black",
     pch = 21, ylim = range(-c(temp.orig_resids.delta, temp.perm_resids.delta.mean)),
     xlab = "Factorization Rank Added", ylab = "Improvement in Total Residual Error")
lines(nmf.rankrange[-1], -temp.perm_resids.delta.mean, 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)
```

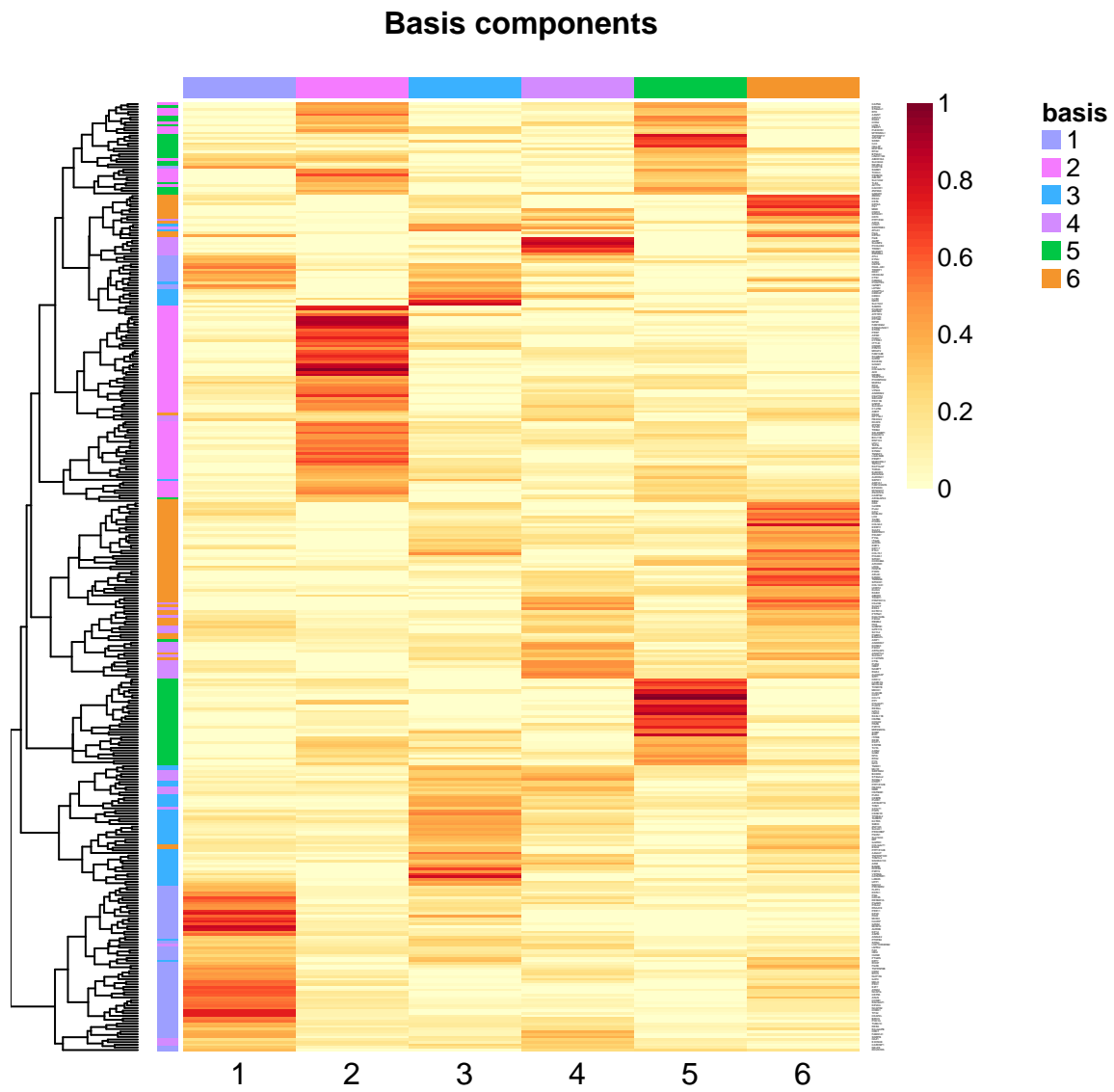


4.1 Fit

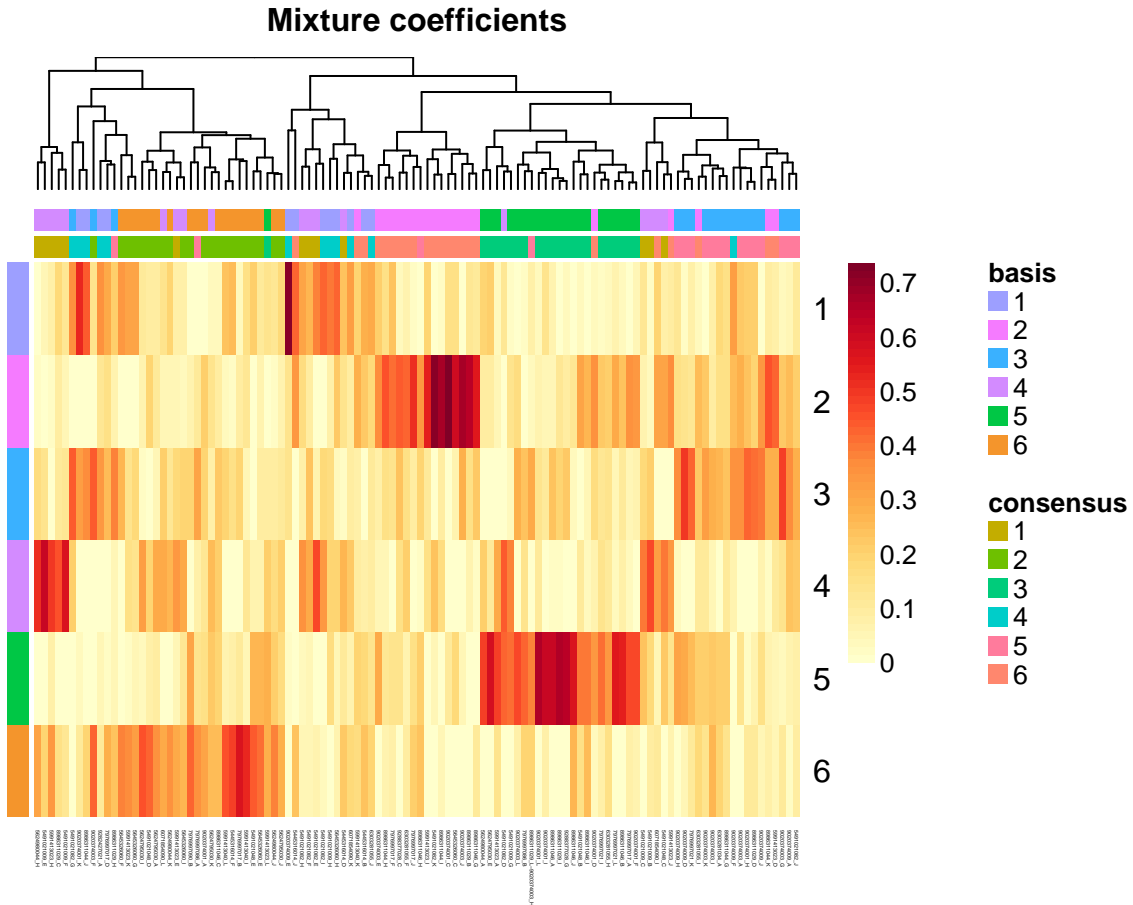
```
consensusmap(nmf.final)
```



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



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



```

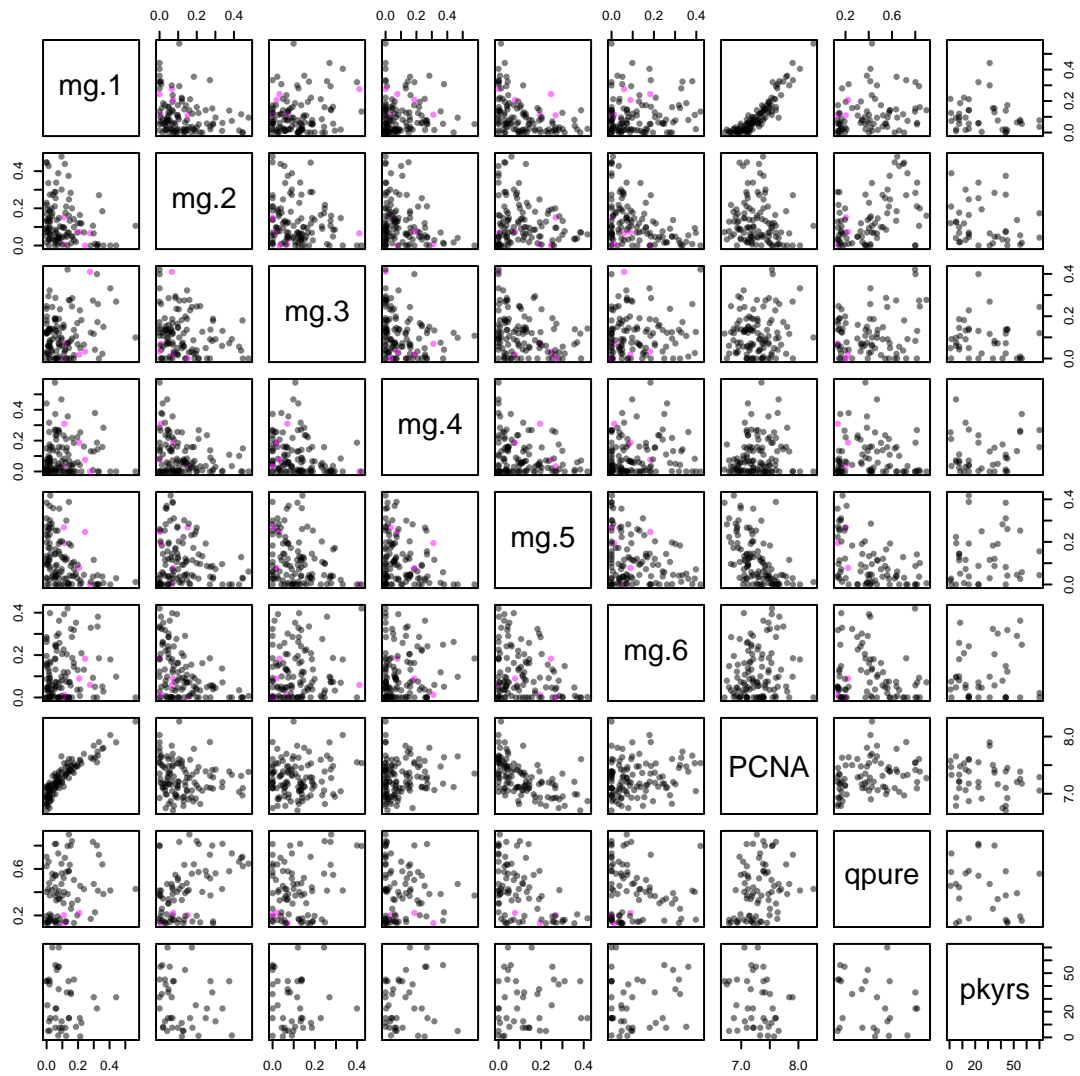
coefs.diag_dsd = apply(xlin.diag_dsd.sel, 2, function(xcol) nnls(basis(nmf.final),
  xcol)$x)
coefs.diag_rec = apply(xlin.diag_rec.sel, 2, function(xcol) nnls(basis(nmf.final),
  xcol)$x)
coefs.recr_dsd = apply(xlin.recr_dsd.sel, 2, function(xcol) nnls(basis(nmf.final),
  xcol)$x)
coefs.pdac_au = apply(xlin.pdac_au.sel,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

```

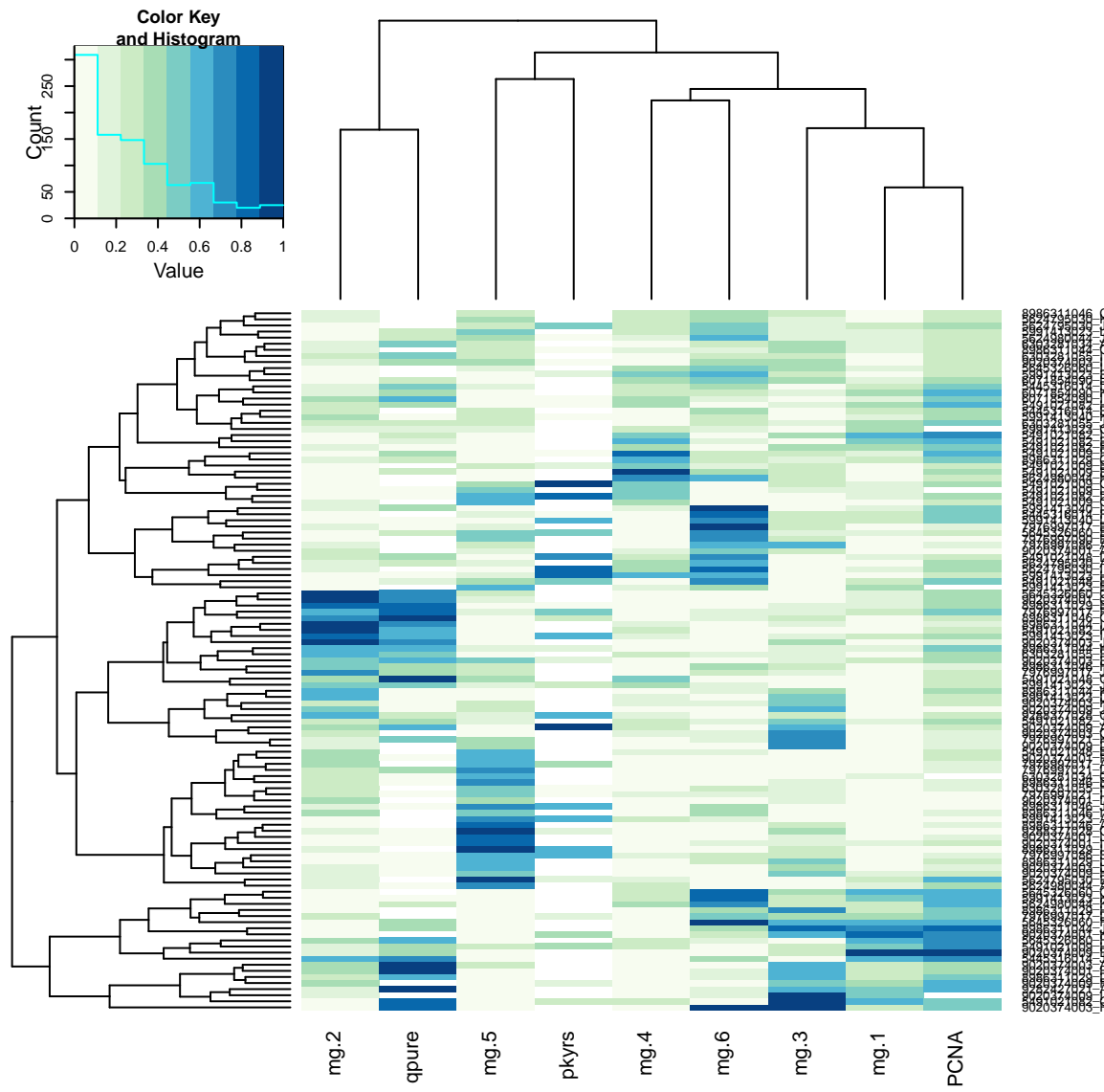
```

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$purity_qpure,
  pkyrs = cpvs.pdac_au$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)))

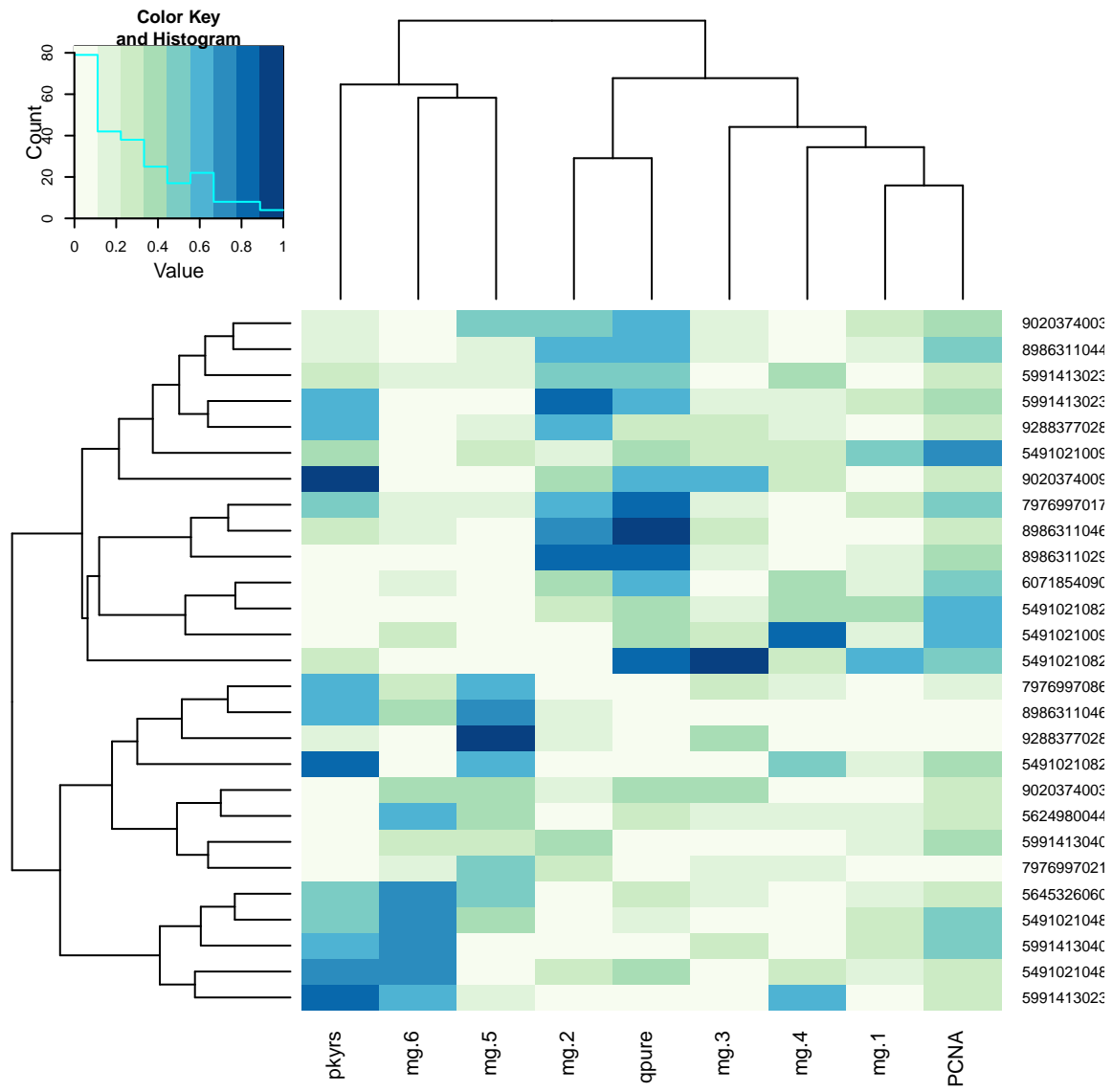
```



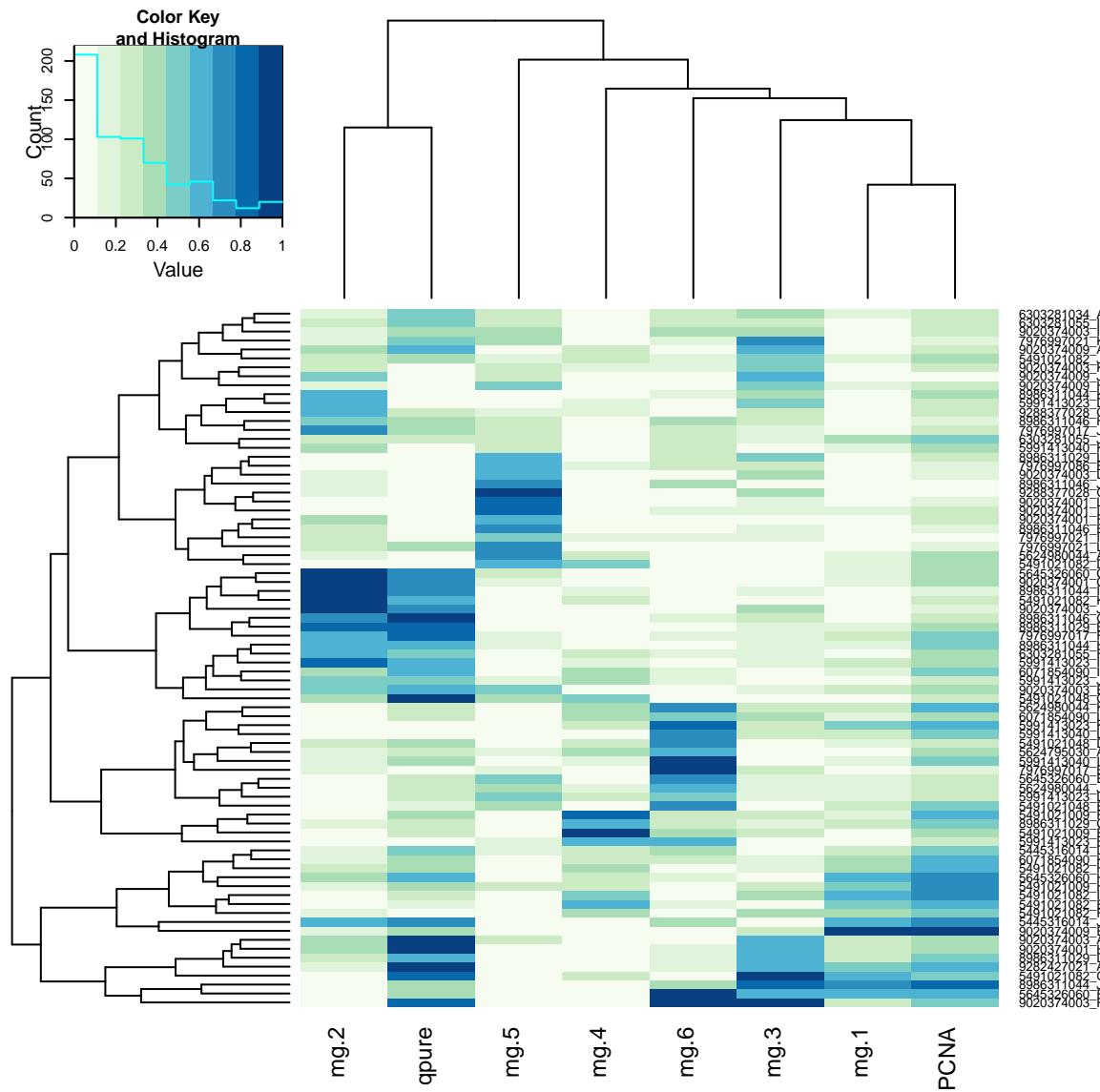
```
temp.pred.pairs.rescaled = t((t(temp.pred.pairs) - apply(temp.pred.pairs, 2,
  min, na.rm = TRUE))/(apply(temp.pred.pairs, 2, function(x) diff(range(x,
  na.rm = TRUE))))))
heatmap.2(temp.pred.pairs.rescaled, trace = "none", scale = "none", col = brewer.pal(9,
  "GnBu"))
```

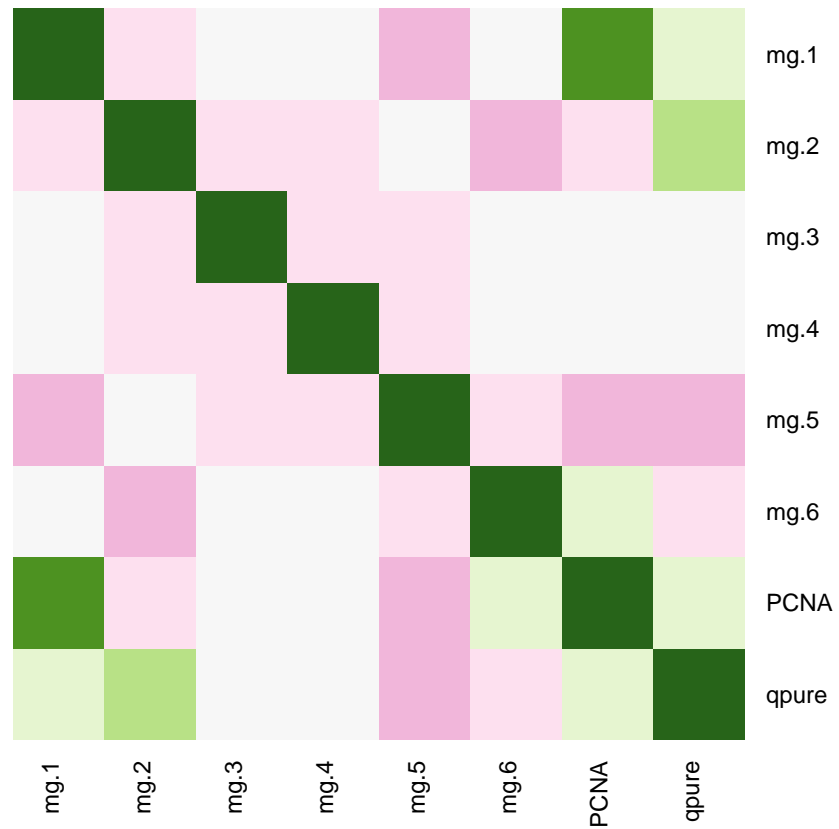
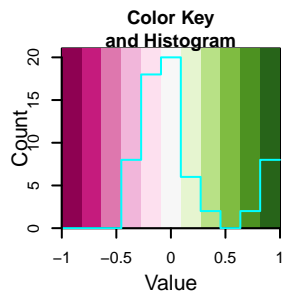
```
heatmap.2(temp.pred.pairs.rescaled[apply(!is.na(temp.pred.pairs.rescaled), 1,
all), ], trace = "none", scale = "none", col = brewer.pal(9, "GnBu"))
```



```
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"))
```

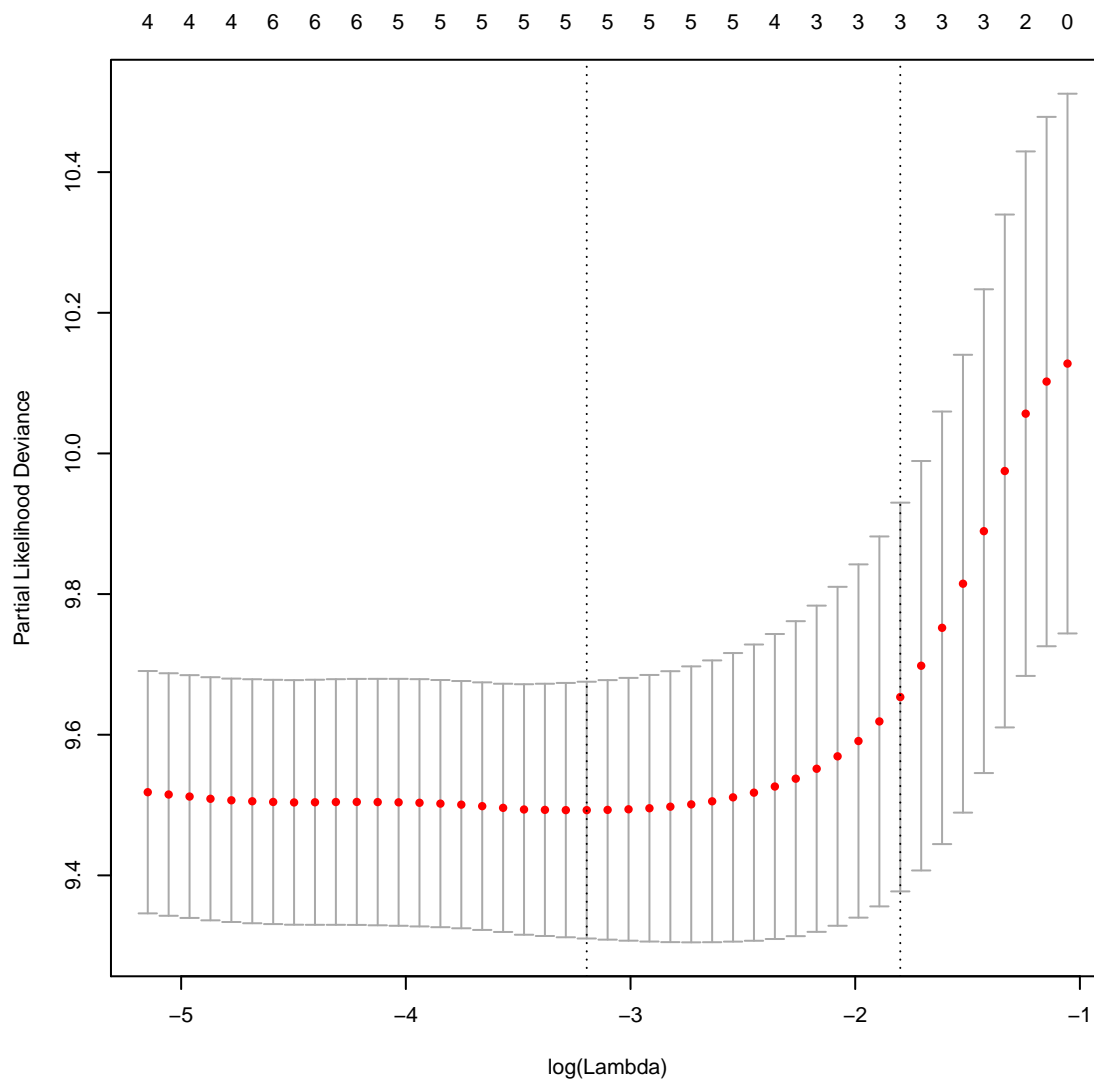
```
temp.cors = apply(temp.pred.pairs[, colnames(temp.pred.pairs) != "pkysr"], 2,
  function(x) apply(temp.pred.pairs[, colnames(temp.pred.pairs) != "pkysr"],
    2, function(y) {
      sel = !(is.na(x) | is.na(y))
      cor(x[sel], y[sel], method = "kendall")
    })
# diag(temp.cors) = NA
heatmap.2(temp.cors,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



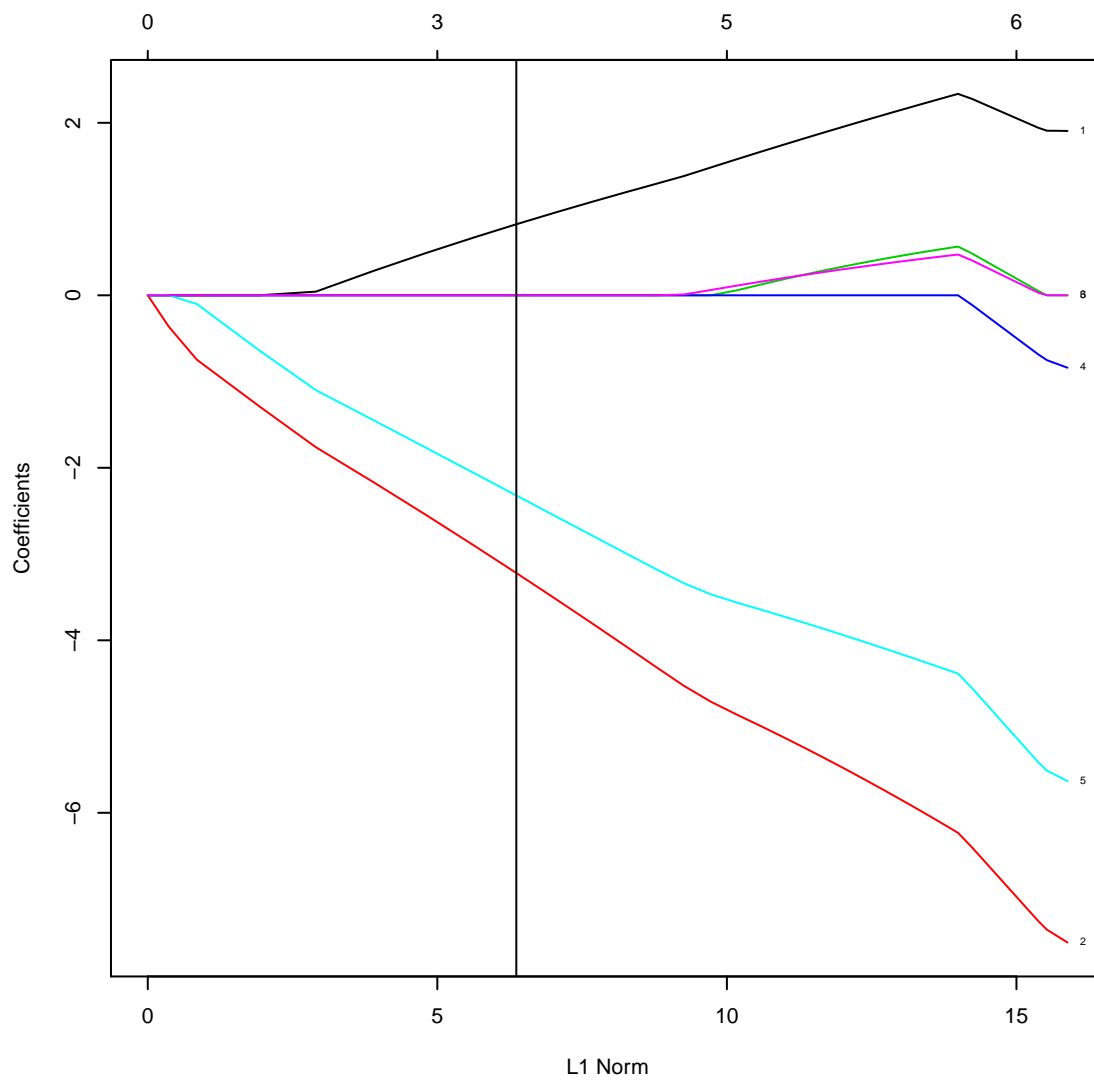
4.2 LASSO on training set

```
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",
  nfolds = 10)
```

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



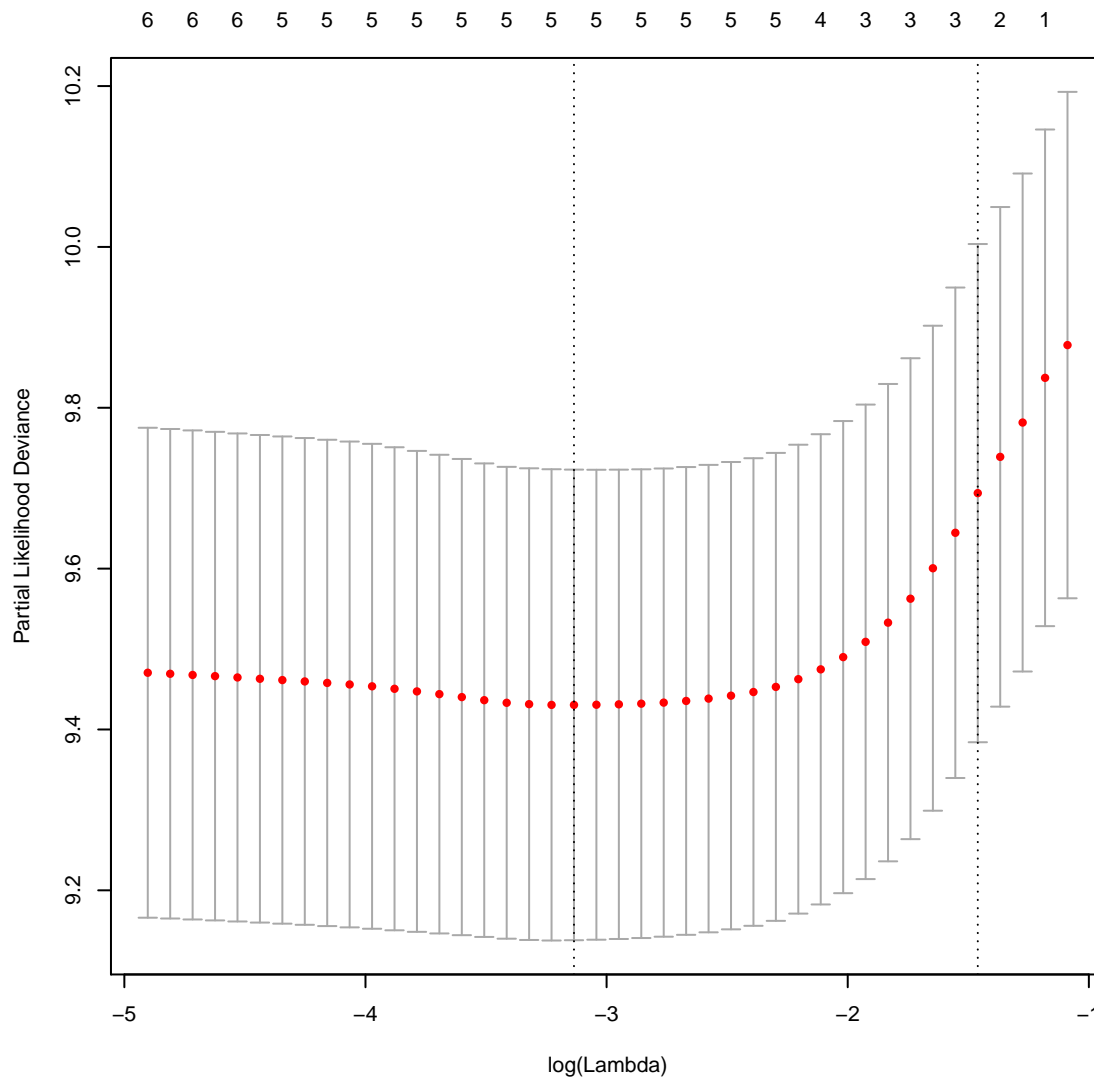
```
plot(glmnet.fit.cv.diag_dsd$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s = glmnet.fit.cv.diag_dsd$lambda.1se))))
```



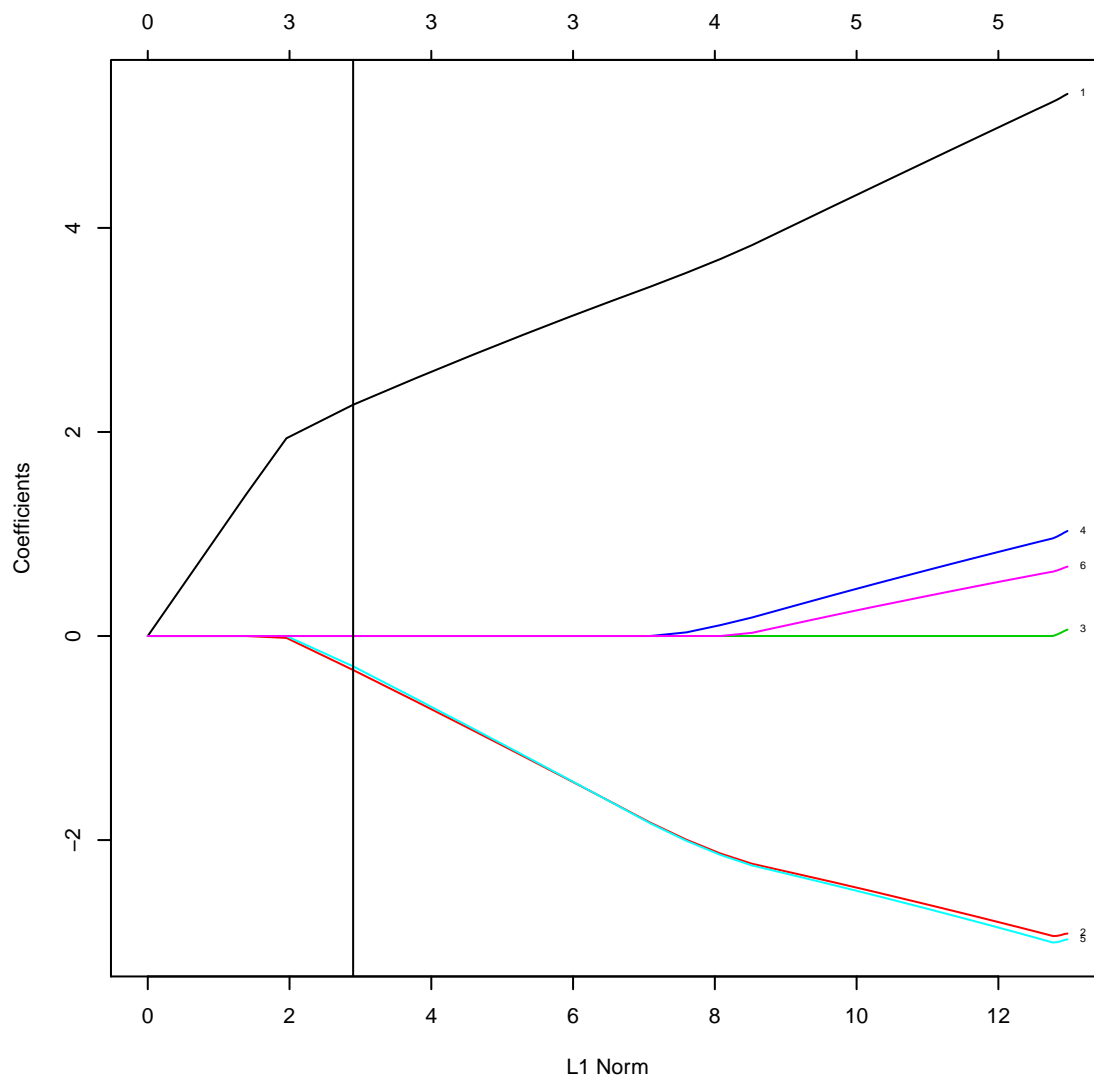
```
# abline(v = sum(abs(coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s =
# glmnet.fit.cv.diag_dsd$lambda.min))))
coef(glmnet.fit.cv.diag_dsd$glmnet.fit, s = glmnet.fit.cv.diag_dsd$lambda.1se)

## 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)
```



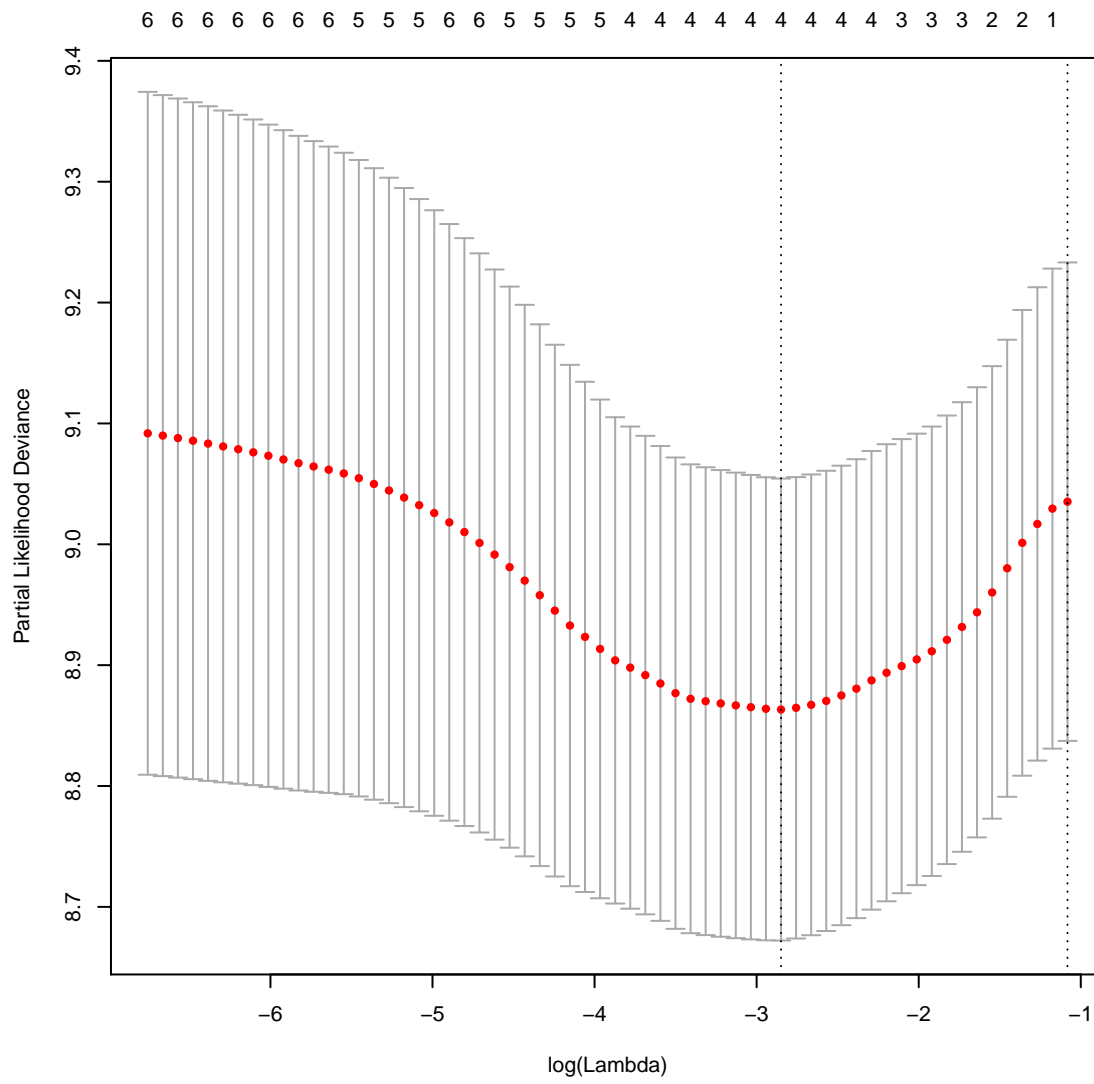
```
plot(glmnet.fit.cv.diag_rec$glmnet.fit, label = TRUE)
abline(v = sum(abs(coef(glmnet.fit.cv.diag_rec$glmnet.fit, s = glmnet.fit.cv.diag_rec$lambda.1se))))
```

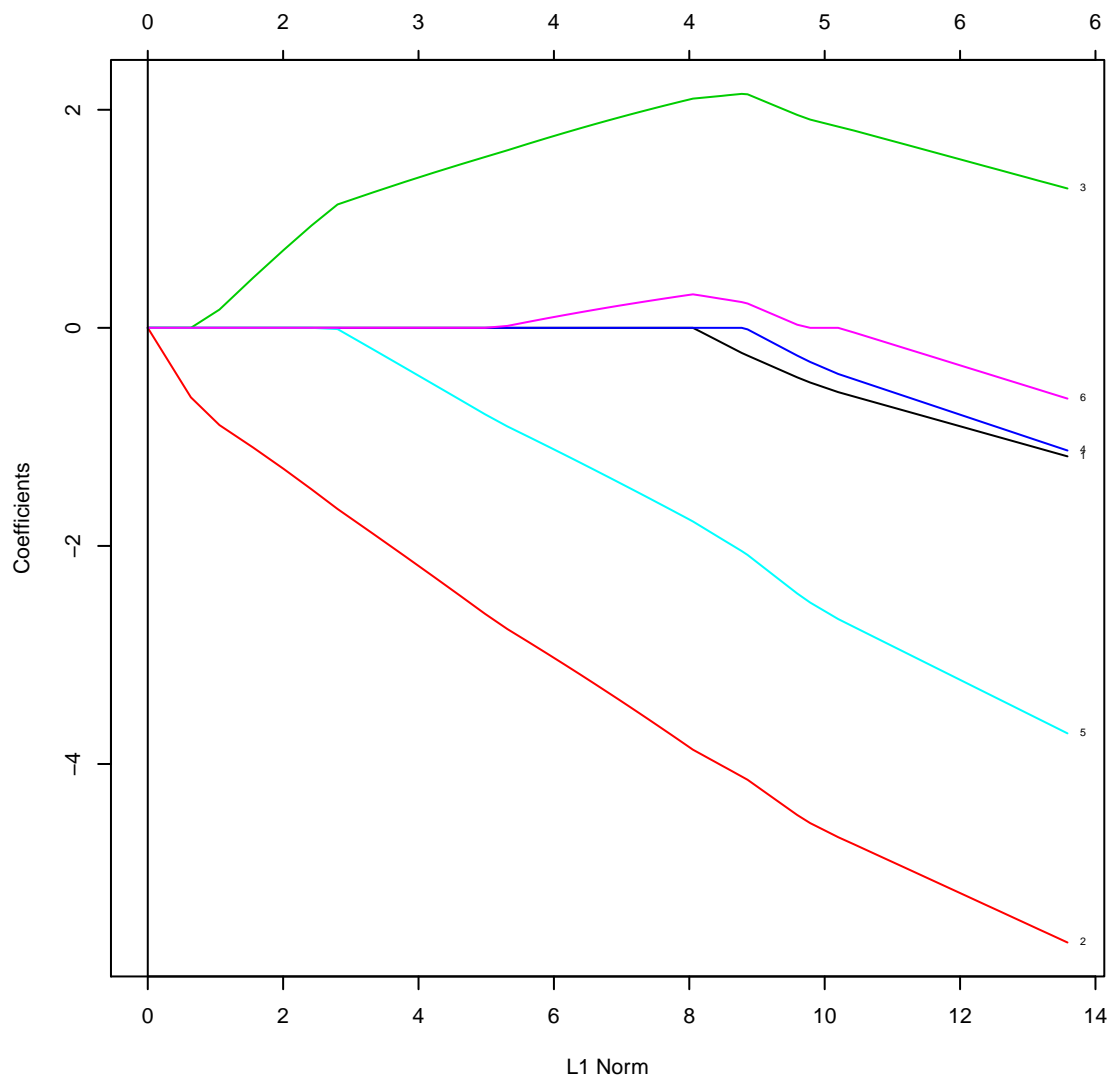
```
# abline(v = sum(abs(coef(glmnet.fit.cv.diag_rec$glmnet.fit, s =
# glmnet.fit.cv.diag_rec$lambda.min))))
coef(glmnet.fit.cv.diag_rec$glmnet.fit, s = glmnet.fit.cv.diag_rec$lambda.1se)

## 6 x 1 sparse Matrix of class "dgCMatrix"
##      1
## V1  2.2667
## V2 -0.3332
## V3   .
## V4   .
## V5 -0.2974
## 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 .
## V3 .
## V4 .
## V5 .
## V6 .
```

4.3 Prediction on 10-fold CV

```
cv_preds = readRDS("../analysis/14_SIS_NMF_CV_results.rds")
```

```
summary(coxph(y.diag_dsd ~ cv_preds["lasso.1se", ]))

## Call:
## coxph(formula = y.diag_dsd ~ cv_preds["lasso.1se", ])
##
##      n= 110, number of events= 70
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## cv_preds["lasso.1se", ] 0.606      1.833      0.200 3.03   0.0024
##
##              exp(coef) exp(-coef) lower .95 upper .95
## cv_preds["lasso.1se", ]      1.83      0.545      1.24      2.71
##
## Concordance= 0.594 (se = 0.038 )
## Rsquare= 0.078 (max possible= 0.995 )
## Likelihood ratio test= 8.91 on 1 df,  p=0.00284
## Wald test               = 9.18 on 1 df,  p=0.00244
## Score (logrank) test = 9.07 on 1 df,  p=0.0026
```

4.4 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.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.samps$time, GSE21501.samps$event) ~ predict(glmnet.fit.cv.diag_dsd$glmnet.fit,
newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se))
summary(temp)
```

```

## Call:
## coxph(formula = Surv(GSE21501.samp$time, GSE21501.samp$event) ~
##       predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs),
##       s = glmnet.fit.cv.recr_dsd$lambda.1se))
##
## n= 102, number of events= 66
##
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE21501.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## Concordance= 0.499 (se = 0.039 )
## Rsquare= 0 (max possible= 0.993 )
## Likelihood ratio test= 0.04 on 1 df, p=0.849
## Wald test = 0.04 on 1 df, p=0.849
## Score (logrank) test = 0.04 on 1 df, p=0.849

temp = coxph(Surv(GSE28735.samp$time, GSE28735.samp$event) ~ predict(glmnet.fit.cv.diag_dsd$glmnet.fit,
newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se))
summary(temp)

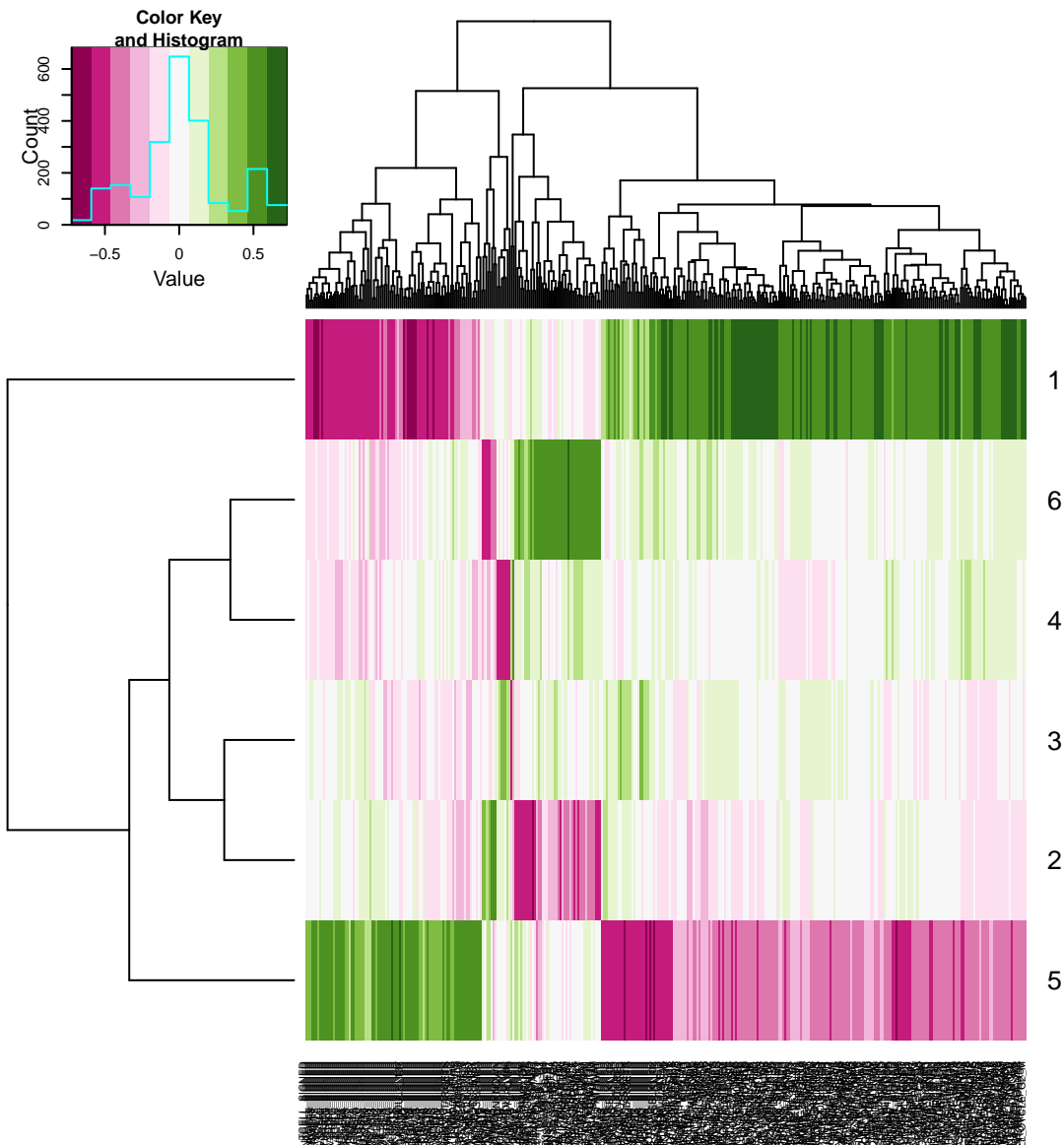
## Call:
## coxph(formula = Surv(GSE28735.samp$time, GSE28735.samp$event) ~
##       predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs),
##       s = glmnet.fit.cv.recr_dsd$lambda.1se))
##
## n= 42, number of events= 29
##
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda.1se)

```

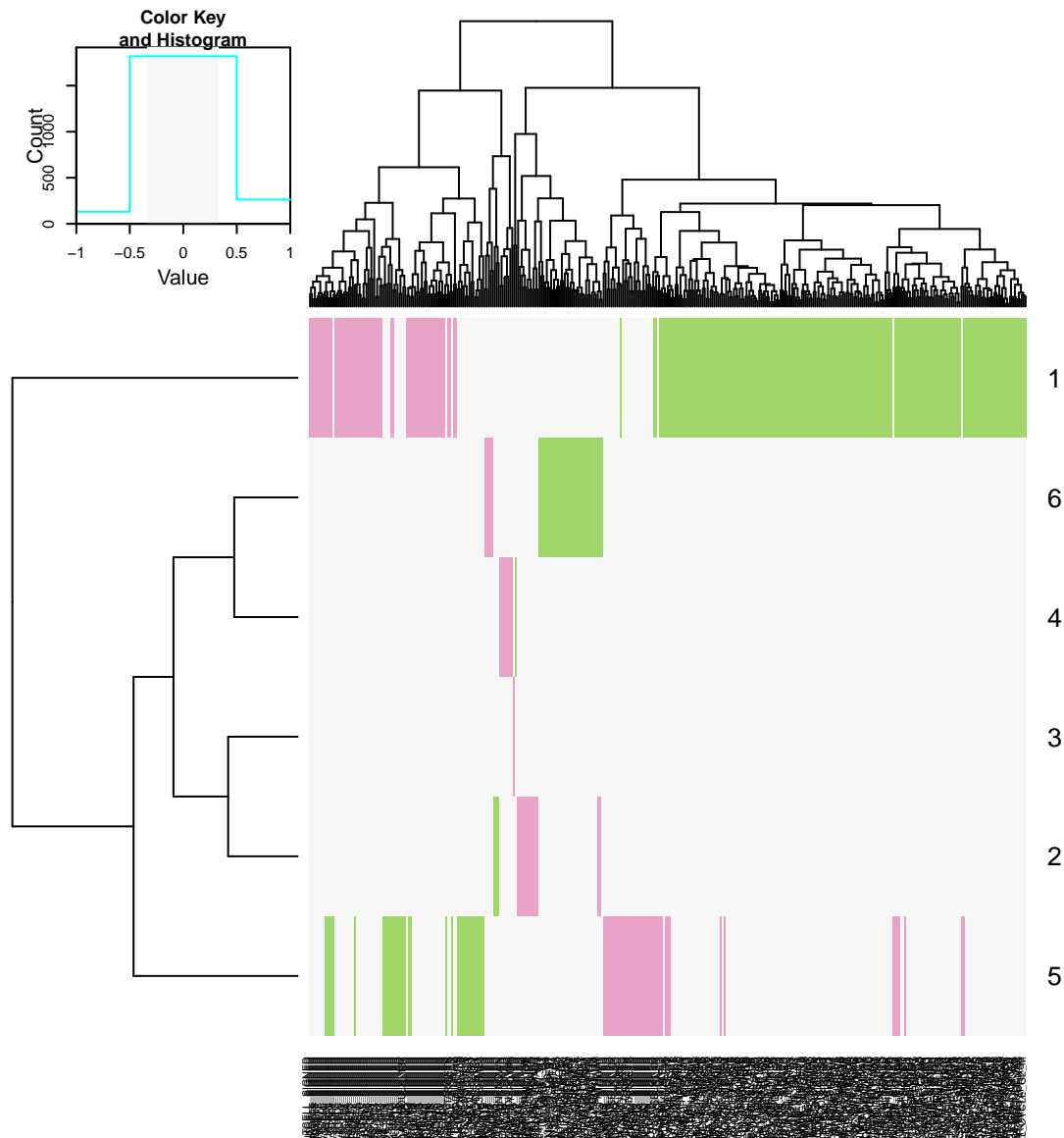
```
##
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda)
##
## predict(glmnet.fit.cv.diag_dsd$glmnet.fit, newx = t(GSE28735.coefs), s = glmnet.fit.cv.recr_dsd$lambda)
##
## Concordance= 0.693 (se = 0.064 )
## Rsquare= 0.134 (max possible= 0.981 )
## Likelihood ratio test= 6.06 on 1 df, p=0.0139
## Wald test = 5.71 on 1 df, p=0.0169
## Score (logrank) test = 6.04 on 1 df, p=0.014
```

4.5 MSigDB score correlation thresholding

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



```
heatmap.2(nmf.final.msigsdb.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(coef(nmf.final), 1, function(mg) sapply(cpv.diag_dsd, 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\\.Nodes", 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, "BH")
cpv.qvals = matrix(temp, nrow = nrow(cpv.pvals))
rownames(cpv.qvals) = rownames(cpv.pvals)
colnames(cpv.qvals) = colnames(cpv.pvals)

cpv.pvals

##              [,1]      [,2]      [,3]      [,4]
## Patient.Gender      0.138407 0.020688 0.72732 0.135009
## Patient.Ethnicity    0.622781 0.724384 0.18976 0.765995
## History.Smoking.PackYears 0.348090 0.260413 0.73136 0.321908
## History.Diagnosis.AgeAtYears 0.881590 0.681555 0.49230 0.914690
## Path.HistoType.Subtype 0.893359 0.561977 0.22914 0.104016
## Path.TumourSizeMm     0.940836 0.135210 0.70907 0.215133
## Path.Invasion.PN      0.326270 0.064524 0.89694 0.509692
## Path.Invasion.VS      0.626581 0.174550 0.93410 0.631215
## Staging.pM            0.396481 0.362385 0.85889 0.135211
## Staging.pN            0.731239 0.181076 0.62403 0.751373
## Staging.pT            0.137691 0.552980 0.34901 0.064967
## Staging.Stage        0.038185 0.219511 0.60239 0.089545
## History.Recurrence.Site.Peritoneum 0.958146 0.052848 0.61695 0.281081
## History.Recurrence.Site.PancRemnant 0.551611 0.239884 0.01780 0.914636
## History.Recurrence.Site.PancBed    0.869281 0.325053 0.66994 0.475247
## History.Recurrence.Site.Other      0.682468 0.295969 0.70889 0.003592
## History.Recurrence.Site.Omentum    0.120811 0.279015 0.95417 0.784937
## History.Recurrence.Site.Mesentery  0.502274 0.277140 0.78581 0.707436
## History.Recurrence.Site.LymphNodes 0.331799 0.986548 0.63649 0.014826
## History.Recurrence.Site.Lung       0.488661 0.297865 0.55622 0.748563
## History.Recurrence.Site.Liver      0.129400 0.046927 0.06894 0.547538
## History.Recurrence.Site.Brain      0.774503 0.029872 0.63502 0.971582
## History.Recurrence.Site.Bone       0.782178 0.804715 0.98003 0.854252
## Path.Grade.Coarse      0.006438 0.005655 0.36879 0.129514
## Path.TumourLocation.Coarse 0.469811 0.230100 0.07124 0.567640
##              [,5]      [,6]
## Patient.Gender      0.37328 0.0387623
## Patient.Ethnicity    0.99392 0.0191721
## History.Smoking.PackYears 0.50609 0.4738379
## History.Diagnosis.AgeAtYears 0.75115 0.7515763
## Path.HistoType.Subtype 0.56598 0.0595163
## Path.TumourSizeMm     0.81538 0.4037090
## Path.Invasion.PN      0.06422 0.8347923
## Path.Invasion.VS      0.78060 0.0862062
## Staging.pM            0.78029 0.2488073
## Staging.pN            0.11243 0.5892122

```

## Staging.pT	0.60510	0.4778634
## Staging.Stage	0.19216	0.4591937
## History.Recurrence.Site.Peritoneum	0.80851	0.0275532
## History.Recurrence.Site.PancRemnant	0.66211	0.2693233
## History.Recurrence.Site.PancBed	0.93894	0.9235058
## History.Recurrence.Site.Other	0.06915	0.1710832
## History.Recurrence.Site.Omentum	0.33922	0.0596320
## History.Recurrence.Site.Mesentery	0.40568	0.1203379
## History.Recurrence.Site.LymphNodes	0.39631	0.7818857
## History.Recurrence.Site.Lung	0.02854	0.0896567
## History.Recurrence.Site.Liver	0.37247	0.4265668
## History.Recurrence.Site.Brain	0.28099	0.3088652
## History.Recurrence.Site.Bone	0.46048	0.0952863
## Path.Grade.Coarse	0.01468	0.0001869
## Path.TumourLocation.Coarse	0.10923	0.1813727

cpv.qvals

##	[,1]	[,2]	[,3]	[,4]	[,5]
## Patient.Gender	0.5190	0.3448	0.9209	0.5190	0.7777
## Patient.Ethnicity	0.9093	0.9209	0.6266	0.9209	0.9939
## History.Smoking.PackYears	0.7699	0.7269	0.9209	0.7647	0.8688
## History.Diagnosis.AgeAtYears	0.9723	0.9209	0.8688	0.9800	0.9209
## Path.HistoType.Subtype	0.9749	0.8963	0.6903	0.5190	0.8963
## Path.TumourSizeMm	0.9800	0.5190	0.9209	0.6860	0.9336
## Path.Invasion.PN	0.7647	0.4453	0.9749	0.8688	0.4453
## Path.Invasion.VS	0.9093	0.6183	0.9800	0.9093	0.9209
## Staging.pM	0.8007	0.7777	0.9614	0.5190	0.9209
## Staging.pN	0.9209	0.6183	0.9093	0.9209	0.5190
## Staging.pT	0.5190	0.8963	0.7699	0.4453	0.9093
## Staging.Stage	0.4153	0.6860	0.9093	0.4981	0.6266
## History.Recurrence.Site.Peritoneum	0.9844	0.4453	0.9093	0.7269	0.9329
## History.Recurrence.Site.PancRemnant	0.8963	0.7055	0.3448	0.9800	0.9209
## History.Recurrence.Site.PancBed	0.9659	0.7647	0.9209	0.8636	0.9800
## History.Recurrence.Site.Other	0.9209	0.7447	0.9209	0.2414	0.4453
## History.Recurrence.Site.Omentum	0.5190	0.7269	0.9844	0.9209	0.7699
## History.Recurrence.Site.Mesentery	0.8688	0.7269	0.9209	0.9209	0.8007
## History.Recurrence.Site.LymphNodes	0.7657	0.9932	0.9093	0.3448	0.8007
## History.Recurrence.Site.Lung	0.8688	0.7447	0.8963	0.9209	0.3734
## History.Recurrence.Site.Liver	0.5190	0.4453	0.4453	0.8963	0.7777
## History.Recurrence.Site.Brain	0.9209	0.3734	0.9093	0.9914	0.7269
## History.Recurrence.Site.Bone	0.9209	0.9329	0.9932	0.9614	0.8636
## Path.Grade.Coarse	0.2414	0.2414	0.7777	0.5190	0.3448
## Path.TumourLocation.Coarse	0.8636	0.6903	0.4453	0.8963	0.5190
##	[,6]				
## Patient.Gender	0.41531				
## Patient.Ethnicity	0.34480				
## History.Smoking.PackYears	0.86361				
## History.Diagnosis.AgeAtYears	0.92087				
## Path.HistoType.Subtype	0.44526				
## Path.TumourSizeMm	0.80069				
## Path.Invasion.PN	0.94863				
## Path.Invasion.VS	0.49809				
## Staging.pM	0.71771				

```

## Staging.pN                                0.90927
## Staging.pT                                0.86361
## Staging.Stage                             0.86361
## History.Recurrence.Site.Peritoneum        0.37340
## History.Recurrence.Site.PancRemnant       0.72693
## History.Recurrence.Site.PancBed           0.98004
## History.Recurrence.Site.Other              0.61832
## History.Recurrence.Site.Omentum           0.44526
## History.Recurrence.Site.Mesentery         0.51902
## History.Recurrence.Site.LymphNodes        0.92087
## History.Recurrence.Site.Lung              0.49809
## History.Recurrence.Site.Liver             0.83097
## History.Recurrence.Site.Brain             0.75950
## History.Recurrence.Site.Bone              0.51046
## Path.Grade.Coarse                         0.02804
## Path.TumourLocation.Coarse                0.61832

apply(coef(nmf.final), 1, function(c1) cor.test(c1, samps$purity_qpure, method = "kendall"))$p.value)

## [1] 1.233e-02 9.044e-05 7.890e-01 4.713e-01 2.043e-04 3.156e-02

p.adjust(apply(coef(nmf.final), 1, function(c1) cor.test(c1, samps$purity_qpure,
method = "kendall"))$p.value), "BH")

## [1] 0.0246544 0.0005426 0.7889577 0.5655481 0.0006128 0.0473439

apply(coef(nmf.final), 1, function(c1) cor(c1, samps$purity_qpure, method = "kendall",
na.rm = TRUE))

## Error in cor(c1, samps$purity_qpure, method = "kendall", na.rm = TRUE): unused argument (na.rm
= TRUE)

# termplot(lm(coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse), se =
# TRUE, rug = TRUE)
lm(coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse)

##
## Call:
## lm(formula = coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse)
##
## Coefficients:
##                (Intercept)  cpvs.diag_dsd$Path.Grade.Coarse.L
##                0.1353                0.0623

summary(lm(coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse))

##
## Call:
## lm(formula = coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.1793 -0.0878 -0.0365  0.0655  0.2979
##
## Coefficients:
##
##                Estimate Std. Error t value Pr(>|t|)

```

```
## (Intercept)                0.1353      0.0114    11.89 < 2e-16
## cpvs.diag_dsd$Path.Grade.Coarse.L  0.0623      0.0161     3.87 0.00019
##
## Residual standard error: 0.107 on 108 degrees of freedom
## Multiple R-squared:  0.122, Adjusted R-squared:  0.114
## F-statistic: 15 on 1 and 108 DF, p-value: 0.000187
```

```
anova(lm(coef(nmf.final)[6, ] ~ cpvs.diag_dsd$Path.Grade.Coarse))
```

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

```
##
```

```
## Response: coef(nmf.final)[6, ]
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## cpvs.diag_dsd$Path.Grade.Coarse  1  0.173   0.1727      15 0.00019
## Residuals                108  1.245   0.0115
```

```
temp.sig_id = colnames(nmf.final.msigdb.corr)
temp.sig_class = gsub("\\.\\.*", "", temp.sig_id)
temp.nsig = length(temp.sig_id)
temp.nmeta = nrow(nmf.final.msigdb.corr)
tables = lapply(1:temp.nmeta, function(metagene_i) {
  tapply(1:temp.nsig, temp.sig_class, function(sig_class_is) {
    all_cors = nmf.final.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
    }
  }, simplify = FALSE)
})
tables

## [[1]]
## [[1]]$c1
## data frame with 0 columns and 0 rows
##
```

```
## [[1]]$c2
##
## 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
## 46
## 47
## 48
## 49
## 50
## 51
```

```
## 52
## 53
## 54
## 55
## 56
## 57
## 58
## 59
## 60
## 61
## 62
## 63
## 64
## 65
## 66
## 67
## 68
## 69
## 70
## 71
## 72
## 73
## 74
## 75
## 76
## 77
## 78
## 79 c2.REACTOME_CYCLIN_E_ASSOCIATED_EVENTS_DURING_G1_S_TRANSITION_/c2.REACTOME_REGULATION_OF_MITOTIC_
## 80
## 81
## 82
## 83
## 84
## 85
## 86
## 87
## 88
## 89
## 90
## 91
## 92
## 93
## 94
## 95
## 96
## 97
## 98
## 99
## 100
## 101
## 102
## 103
## 104
## 105
```

```

## 106
## 107
## 108
## 109
## 110
## 111
## 112
## 113
## 114
## 115
## 116
## 117
## 118
## 119
## 120
## 121
## 122
## 123
## 124
## 125
## 126
## 127
## 128
## 129
## 130
## 131
## 132
## 133
## 134
## 135
## 136
## 137
## 138
## 139
## 140
## 141
## 142
## 143
## 144
## 145
## 146
## 147
## 148
## 149
## 150
## 151
## 152
## 153
## 154
## 155
## 156
## 157
##      Correlation Metagenes
## 1      0.7237      1

```

## 2	0.7139	1
## 3	0.7106	1
## 4	0.7103	1
## 5	0.7019	1
## 6	0.7002	1
## 7	0.6945	1
## 8	0.6858	1
## 9	0.6828	1
## 10	0.6825	1
## 11	0.6818	1
## 12	0.6808	1
## 13	0.6784	1
## 14	0.6748	1,-5
## 15	0.6691	1
## 16	0.6654	1
## 17	0.6597	1
## 18	0.6567	1
## 19	0.6537	1
## 20	0.6523	1
## 21	0.6500	1
## 22	0.6476	1
## 23	0.6473	1
## 24	0.6436	1,-5
## 25	0.6399	1,-5
## 26	0.6366	1
## 27	0.6359	1
## 28	0.6309	1
## 29	0.6188	1
## 30	0.6175	1
## 31	0.6172	1
## 32	0.6158	1
## 33	0.6158	1
## 34	0.6128	1
## 35	0.6128	1
## 36	0.6121	1
## 37	0.6115	1
## 38	0.6101	1
## 39	0.6095	1
## 40	0.6088	1
## 41	0.6088	1
## 42	0.6081	1
## 43	0.6068	1
## 44	0.6065	1
## 45	0.6048	1
## 46	0.6014	1
## 47	0.5981	1
## 48	0.5967	1
## 49	0.5964	1
## 50	0.5957	1
## 51	0.5941	1
## 52	0.5937	1
## 53	0.5937	1
## 54	0.5914	1
## 55	0.5904	1

## 56	0.5887	1
## 57	0.5854	1
## 58	0.5850	1
## 59	0.5820	1
## 60	0.5817	1
## 61	0.5813	1
## 62	0.5807	1
## 63	0.5800	1
## 64	0.5770	1
## 65	0.5766	1
## 66	0.5753	1,-5
## 67	0.5753	1
## 68	0.5746	1
## 69	0.5743	1,-5
## 70	0.5720	1
## 71	0.5713	1
## 72	0.5706	1
## 73	0.5679	1
## 74	0.5673	1
## 75	0.5666	1
## 76	0.5663	1
## 77	0.5612	1,-5
## 78	0.5612	1
## 79	0.5606	1
## 80	0.5602	1
## 81	0.5582	1
## 82	0.5552	1,-5
## 83	0.5552	1
## 84	0.5545	1
## 85	0.5529	1
## 86	0.5502	1
## 87	0.5489	1
## 88	0.5472	1
## 89	0.5468	1
## 90	0.5455	1
## 91	0.5425	1
## 92	0.5408	1
## 93	0.5385	1
## 94	0.5381	1
## 95	0.5375	1
## 96	0.5361	1
## 97	0.5348	1
## 98	0.5338	1
## 99	0.5318	1,-5
## 100	0.5311	1
## 101	0.5301	1
## 102	0.5291	1,-5
## 103	0.5281	1
## 104	0.5274	1
## 105	0.5271	1
## 106	0.5241	1,-5
## 107	0.5224	1
## 108	0.5221	1
## 109	0.5217	1

```

## 110      0.5187      1
## 111      0.5184      1
## 112      0.5177      1,-5
## 113      0.5174      1
## 114      0.5170      1
## 115      0.5167      1
## 116      0.5160      1
## 117      0.5150      1
## 118      0.5120      1
## 119      0.5113      1,-5
## 120      0.5113      1,-5
## 121      0.5113      1
## 122      0.5110      1
## 123      0.5100      1
## 124      0.5097      1
## 125      0.5090      1
## 126      0.5083      1
## 127     -0.5053     -1
## 128     -0.5080     -1
## 129     -0.5090     -1
## 130     -0.5100     -1
## 131     -0.5134     -1
## 132     -0.5134     -1
## 133     -0.5150     -1,5
## 134     -0.5187     -1
## 135     -0.5201     -1
## 136     -0.5274     -1
## 137     -0.5318     -1
## 138     -0.5351     -1
## 139     -0.5475     -1
## 140     -0.5495     -1
## 141     -0.5556     -1
## 142     -0.5582     -1
## 143     -0.5586     -1
## 144     -0.5699     -1,5
## 145     -0.5780     -1
## 146     -0.5877     -1
## 147     -0.5884     -1
## 148     -0.5954     -1
## 149     -0.5961     -1
## 150     -0.5994     -1
## 151     -0.6105     -1
## 152     -0.6128     -1
## 153     -0.6138     -1
## 154     -0.6165     -1
## 155     -0.6570     -1
## 156     -0.6594     -1
## 157     -0.6979     -1
##
## [[1]]$c3
##
##           GeneSet Correlation Metagenes
## 1      c3.V$E2F_Q4_01      0.5401      1
## 2      c3.V$E2F_Q6_01      0.5284      1
## 3 c3.V$E2F_Q3_01/c3.V$E2F1_Q4_01      0.5167      1

```

```

## 4      c3.SGCGSSAAA_V$E2F1DP2_01      0.5093      1
##
## [[1]]$c4
##                                     GeneSet
## 1  c4.GNF2_RFC3/c4.GNF2_RFC4/c4.GNF2_SMC2L1/c4.GNF2_CKS1B/c4.GNF2_CKS2/c4.GNF2_TTK
## 2                                     c4.MORF_BUB1B
## 3                                     c4.MODULE_403
## 4                                     c4.MORF_FEN1
## 5                                     c4.MODULE_125/c4.MODULE_158
## 6                                     c4.MODULE_17
## 7                                     c4.MODULE_320
## 8                                     c4.MODULE_126
## 9                                     c4.MORF_ESPL1
## 10                                    c4.MODULE_315
## 11                                    c4.MODULE_124
## 12                                    c4.MODULE_244
## 13                                    c4.GNF2_MSH2
## 14                                    c4.MODULE_98/c4.MODULE_198/c4.MODULE_252
## 15                                    c4.GNF2_MCM5
## 16                                    c4.MODULE_451
## 17                                    c4.MORF_BUB1
## 18                                    c4.MODULE_278
## 19                                    c4.MORF_CCNF
## 20                                    c4.GNF2_PA2G4/c4.GNF2_RAN
## 21                                    c4.MORF_RFC4/c4.MORF_RRM1
## 22                                    c4.GNF2_MSH6
## 23                                    c4.MORF_UNG
## 24                                    c4.MORF_DNMT1
## 25                                    c4.MORF_BUB3/c4.MORF_RAD23A
## 26                                    c4.MORF_PCNA
## 27                                    c4.MODULE_337
## 28                                    c4.MODULE_8
##      Correlation Metagenes
## 1      0.7032      1
## 2      0.6517      1
## 3      0.6245      1
## 4      0.6239      1
## 5      0.6212      1
## 6      0.6175      1
## 7      0.6078      1
## 8      0.6061      1
## 9      0.6048      1
## 10     0.5998      1
## 11     0.5904      1
## 12     0.5904      1
## 13     0.5820      1
## 14     0.5787      1
## 15     0.5713      1
## 16     0.5643      1
## 17     0.5602      1
## 18     0.5545      1
## 19     0.5425      1
## 20     0.5348      1

```

```

## 21      0.5278      1
## 22      0.5244      1
## 23      0.5154      1
## 24      0.5117      1
## 25      0.5093      1
## 26      0.5063      1
## 27      0.5030      1,-5
## 28      0.5006      1
##
## [[1]]$c5
##
##                                     GeneSet
## 1                                c5.M_PHASE/c5.MITOSIS/c5.M_PHASE_OF_MITOTIC_CELL_CYCLE
## 2                                c5.CELL_CYCLE_PROCESS/c5.MITOTIC_CELL_CYCLE/c5.CELL_CYCLE_PHASE
## 3                                c5.REGULATION_OF_MITOSIS
## 4                                c5.SPINDLE
## 5                                c5.CELL_CYCLE_G0_0007049
## 6                                c5.CELL_CYCLE_CHECKPOINT_G0_0000075
## 7  c5.MITOTIC_SPINDLE_ORGANIZATION_AND_BIOGENESIS/c5.SPINDLE_ORGANIZATION_AND_BIOGENESIS
## 8                                c5.MITOTIC_CELL_CYCLE_CHECKPOINT
## 9                                c5.SPINDLE_POLE
## 10                               c5.CHROMOSOMAL_PART/c5.CHROMOSOME
## 11                               c5.DNA_METABOLIC_PROCESS
## 12                               c5.SPINDLE_MICROTUBULE
## 13                               c5.REGULATION_OF_CELL_CYCLE
## 14                               c5.ORGANELLE_PART/c5.INTRACELLULAR_ORGANELLE_PART
## 15                               c5.CHROMOSOMEPERICENTRIC_REGION/c5.KINETOCHORE
## 16                               c5.MICROTUBULE_CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS
## 17                               c5.DNA_REPLICATION
## 18                               c5.MITOTIC_SISTER_CHROMATID_SEGREGATION/c5.SISTER_CHROMATID_SEGREGATION
## 19                               c5.INTERPHASE/c5.INTERPHASE_OF_MITOTIC_CELL_CYCLE
## 20                               c5.DNA_POLYMERASE_ACTIVITY/c5.DNA_DIRECTED_DNA_POLYMERASE_ACTIVITY
## 21                               c5.RESPONSE_TO_ENDOGENOUS_STIMULUS/c5.RESPONSE_TO_DNA_DAMAGE_STIMULUS
## 22                               c5.CHROMOSOME_SEGREGATION
##      Correlation Metagenes
## 1      0.6808      1
## 2      0.6798      1
## 3      0.6543      1
## 4      0.6496      1
## 5      0.6493      1
## 6      0.6316      1
## 7      0.6195      1
## 8      0.6162      1
## 9      0.5827      1
## 10     0.5740      1
## 11     0.5706      1
## 12     0.5612      1
## 13     0.5458      1
## 14     0.5432      1
## 15     0.5301      1
## 16     0.5284      1
## 17     0.5281      1
## 18     0.5207      1
## 19     0.5201      1
## 20     0.5157      1

```

```

## 21      0.5137      1
## 22      0.5124      1
##
## [[1]]$c6
##           GeneSet Correlation Metagenes
## 1 c6.CSR_LATE_UP.V1_SIGNED      0.5612      1
## 2      c6.E2F1_UP.V1_SIGNED      0.5274      1
##
## [[1]]$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 c7.GSE15930_NAIVE_VS_24H_IN_VITRO_STIM_CD8_TCELL_SIGNED/c7.GSE15930_NAIVE_VS_24H_IN_VITRO_STIM_IL1
## 28
## 29
## 30
## 31
## 32
## 33
## 34
## 35
## 36
## 37
## 38
## 39
## 40
##           Correlation Metagenes
## 1      0.6664      1
## 2      0.6131      1
## 3      0.5847      1

```

```

## 4      0.5710      1
## 5      0.5468      1
## 6      0.5224      1
## 7      0.5217      1,-5
## 8      0.5204      1
## 9     -0.5057     -1
## 10     -0.5060     -1
## 11     -0.5080     -1
## 12     -0.5083     -1
## 13     -0.5097     -1
## 14     -0.5097     -1
## 15     -0.5130     -1
## 16     -0.5134     -1
## 17     -0.5147     -1
## 18     -0.5170     -1
## 19     -0.5234     -1
## 20     -0.5254     -1
## 21     -0.5314     -1,5
## 22     -0.5358     -1
## 23     -0.5361     -1,5
## 24     -0.5391     -1,5
## 25     -0.5415     -1
## 26     -0.5445     -1
## 27     -0.5458     -1
## 28     -0.5489     -1
## 29     -0.5505     -1
## 30     -0.5509     -1
## 31     -0.5519     -1
## 32     -0.5582     -1,5
## 33     -0.5639     -1
## 34     -0.5649     -1
## 35     -0.5656     -1
## 36     -0.5696     -1
## 37     -0.5854     -1
## 38     -0.5900     -1,5
## 39     -0.5964     -1,5
## 40     -0.6051     -1,5
##
##
## [[2]]
## [[2]]$c1
## data frame with 0 columns and 0 rows
##
## [[2]]$c2
##
##                                     GeneSet Correlation
## 1  c2.CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_SIGNED      0.5520
## 2                                     c2.LIU_PROSTATE_CANCER_SIGNED      0.5175
## 3  c2.WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_SIGNED      0.5105
## 4                                     c2.SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A -0.5008
## 5                                     c2.PID_INTEGRIN1_PATHWAY -0.5014
## 6                                     c2.SERVITJA_ISLET_HNF1A_TARGETS_SIGNED -0.5021
## 7  c2.SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_SIGNED -0.5074
## 8                                     c2.ROY_WOUND_BLOOD_VESSEL_SIGNED -0.5332
## 9  c2.VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_SIGNED -0.5352

```

```

## 10          c2.KARAKAS_TGFB1_SIGNALING      -0.5493
## 11          c2.HUANG_DASATINIB_RESISTANCE_SIGNED -0.5523
## 12          c2.KAN_RESPONSE_TO_ARSENIC_TRIOXIDE -0.5546
## 13 c2.LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_SIGNED -0.6035
##      Metagenes
## 1          2
## 2          2
## 3          2
## 4         -2,6
## 5         -2,6
## 6          -2
## 7          -2
## 8          -2
## 9          -2
## 10         -2
## 11         -2
## 12         -2
## 13         -2
##
## [[2]]$c3
## data frame with 0 columns and 0 rows
##
## [[2]]$c4
##      GeneSet Correlation Metagenes
## 1 c4.MODULE_488      -0.5085      -2
##
## [[2]]$c5
## data frame with 0 columns and 0 rows
##
## [[2]]$c6
##      GeneSet Correlation Metagenes
## 1          c6.LEF1_UP.V1_SIGNED      -0.5259      -2
## 2 c6.CORDENONSI_YAP_CONSERVED_SIGNATURE      -0.5319      -2
##
## [[2]]$c7
## data frame with 0 columns and 0 rows
##
## [[3]]
## [[3]]$c1
## data frame with 0 columns and 0 rows
##
## [[3]]$c2
##      GeneSet Correlation Metagenes
## 1 c2.ZHENG_BOUND_BY_FOXP3      -0.5047      -3
##
## [[3]]$c3
## data frame with 0 columns and 0 rows
##
## [[3]]$c4
## data frame with 0 columns and 0 rows
##
## [[3]]$c5
## data frame with 0 columns and 0 rows

```

```

##
## [[3]]$c6
## data frame with 0 columns and 0 rows
##
## [[3]]$c7
## data frame with 0 columns and 0 rows
##
##
## [[4]]
## [[4]]$c1
## data frame with 0 columns and 0 rows
##
## [[4]]$c2
##
##                                     GeneSet
## 1 c2.MARTINEZ_RB1_AND_TP53_TARGETS_SIGNED/c2.MARTINEZ_TP53_TARGETS_SIGNED
## 2                                     c2.FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_SIGNED
## 3                                     c2.DASU_IL6_SIGNALING_SCAR_SIGNED
## 4                                     c2.FAELT_B_CLL_WITH_VH3_21_SIGNED
## Correlation Metagenes
## 1      0.5081      4
## 2     -0.5020     -4
## 3     -0.5050     -4
## 4     -0.5146     -4
##
## [[4]]$c3
##
## GeneSet Correlation Metagenes
## 1 c3.GATGKMRGCG_UNKNOWN      -0.5321      -4
##
## [[4]]$c4
##
## GeneSet Correlation Metagenes
## 1 c4.MODULE_486      -0.5016      -4
##
## [[4]]$c5
## data frame with 0 columns and 0 rows
##
## [[4]]$c6
## data frame with 0 columns and 0 rows
##
## [[4]]$c7
##
## GeneSet Correlation
## 1      c7.GSE20366_CD103_KLRG1_DP_VS_DN_TREG_SIGNED      -0.5057
## 2 c7.GSE1448_CTRL_VS_ANTI_VALPHA2_DP_THYMOCYTE_SIGNED      -0.5109
## Metagenes
## 1      -4
## 2      -4
##
## [[5]]
## [[5]]$c1
## data frame with 0 columns and 0 rows
##
## [[5]]$c2
##
## 1
c2.REACTOME_G_ALPHA_S_SIGNALING

```


## 2		c2.ZHAN_MULTIPLE_MYELOMA_C
## 3		c2.GENTLES_LEUKEMIC_STEM_CE
## 4		c2.SMID_BREAST_CANCER_NORMAL_LI
## 5		c2.BROWNE_HCMV_INFECTION_2
## 6		c2.TERAMOTO_OPN_TARGETS
## 7		c2.LE_NEURONAL_DIFFERENTIATI
## 8		c2.TARTE_PLASMA_CELL_VS_PLASMABLA
## 9		c2.KATSANOUELAVL1_TARGE
## 10		c2.MIKKELSEN_MCV6_ICP_WITH
## 11	c2.BENPORATH_SUZ12_TARGETS/c2.BENPORATH_EED_TARGETS/c2.BENPORATH_ES_WITH_H3K27ME3/c2.BENPORATH_PRO	
## 12		c2.ONDER_CDH1_TARGETS
## 13		c2.AIGNER_ZEE
## 14		c2.WONG_ENDMETRIUM_CANC
## 15		c2.SHEDDEN_LUNG_CANCER_POOR_SU
## 16	c2.TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORM	
## 17		c2.ZHAN_MULTIPLE_MYELOMA
## 18		c2.CHANG_CORE_SERUM_RESPON
## 19		c2.LI_AMPLIFIED_IN_LU
## 20		c2.AKL_HTLV1_INFECTI
## 21		c2.FOURNIER_ACINAR_DEVELOPME
## 22		c2.CAIRO_HEPATOBLASTOMA_CLASS
## 23		c2.NADERI_BREAST_CANCER_PROGNOS
## 24		c2.DELYS_THYROID_CANC
## 25	c2.RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIAT	
## 26		c2.BOYVAULT_LIVER_CANCER_SUBCLASS_C
## 27		c2.BOQUEST_STEM_CELL_CULTURED_VS_FRE
## 28		c2.LI_WILMS_TUMOR_ANAPLAST
## 29		c2.YU_MYC_TARGE
## 30		c2.RODRIGUES_THYROID_CARCINOMA_ANAPLAST
## 31		c2.REACTOME_METABOLISM_OF_NU
## 32		c2.MILICIC_FAMILIAL_ADENOMATOUS_POLYPOS
## 33		c2.GRADE_COLON_AND_RECTAL_CANC
## 34		c2.BOYVAULT_LIVER_CANCER_SUBCLASS
## 35	c2.CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC	
## 36		c2.GREENBAUM_E2A_TARGE
## 37		c2.INAMURA_LUNG_CANCER_S
## 38		c2.VECCHI_GASTRIC_CANCER_EAR
## 39		c2.LEE_EARLY_T_LYMPHOCY
## 40		c2.SWEET_LUNG_CANCER_KF
## 41		c2.HOELZEL_NF1_TARGE
## 42		c2.WINTER_HYPOX
## 43		c2.HAHTOLA_SEZARY_SYNDR
## 44		c2.NAKAYAMA_SOFT_TISSUE_TUMORS_PO
## 45		c2.SABATES_COLORECTAL_ADENOC
## 46	c2.MARTORIATI_MDM4_TARGETS_NEUROEPITHEL	
## 47		c2.WEST_ADRENOCORTICAL_TUM
## 48		c2.SHIPP_DLBCL_VS_FOLLICULAR_LYMPHO
##	Correlation Metagenes	
## 1	0.5493	5
## 2	0.5456	5
## 3	0.5423	5
## 4	0.5409	5
## 5	0.5369	5
## 6	0.5359	5

```

## 7      0.5339      -1,5
## 8      0.5262      -1,5
## 9      0.5208        5
## 10     0.5161        5
## 11     0.5151        5
## 12     0.5014        5
## 13     -0.5004       -5
## 14     -0.5014       -5
## 15     -0.5084      1,-5
## 16     -0.5088       -5
## 17     -0.5111      1,-5
## 18     -0.5151      1,-5
## 19     -0.5158       -5
## 20     -0.5168       -5
## 21     -0.5171      1,-5
## 22     -0.5181       -5
## 23     -0.5198       -5
## 24     -0.5215       -5
## 25     -0.5225      1,-5
## 26     -0.5238      1,-5
## 27     -0.5252       -5
## 28     -0.5269       -5
## 29     -0.5292       -5
## 30     -0.5336      1,-5
## 31     -0.5376       -5
## 32     -0.5419       -5
## 33     -0.5500      1,-5
## 34     -0.5560      1,-5
## 35     -0.5564       -5
## 36     -0.5657       -5
## 37     -0.5694       -5
## 38     -0.5728      1,-5
## 39     -0.5734      1,-5
## 40     -0.5734       -5
## 41     -0.5838       -5
## 42     -0.5885       -5
## 43     -0.5905       -5
## 44     -0.5925      1,-5
## 45     -0.5959       -5
## 46     -0.6053       -5
## 47     -0.6140      1,-5
## 48     -0.6324       -5
##
## [[5]]$c3
##           GeneSet Correlation Metagenes
## 1      c3.V$STAT5A_01      0.5181      5
## 2      c3.V$ELK1_02      -0.5007     -5
## 3 c3.SCGGAAGY_V$ELK1_02      -0.5181     -5
##
## [[5]]$c4
##           GeneSet Correlation
## 1 c4.MODULE_11/c4.MODULE_66/c4.MODULE_100/c4.MODULE_137      0.5530
## 2                        c4.MODULE_51      0.5403
## 3                        c4.MODULE_19      0.5232

```

```

## 4          c4.MODULE_361      0.5091
## 5          c4.MODULE_200      0.5027
## 6          c4.MODULE_337     -0.5215
##   Metagenes
## 1          5
## 2          5
## 3          5
## 4          5
## 5          5
## 6          1,-5
##
## [[5]]$c5
##
## 1 c5.3_5_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY/c5.CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY
## 2                                     c5.PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY
##   Correlation Metagenes
## 1          0.5165      5
## 2          0.5161      5
##
## [[5]]$c6
##
##           GeneSet Correlation Metagenes
## 1 c6.SINGH_KRAS_DEPENDENCY_SIGNATURE_      -0.5051      -5
## 2                c6.AKT_UP.V1_SIGNED      -0.5218      -5
##
## [[5]]$c7
##
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14 c7.GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_YOUNG_SIGNED/c7.GSE36476_CTRL_VS_TSST_ACT_72H_ME
## 15
## 16 c7.GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_OLD_SIGNED/c7.GSE36476_CTRL_VS_TSST_ACT_72H_ME
## 17
## 18
##           Correlation Metagenes
## 1          0.6033      5
## 2          0.5956      5
## 3          0.5503     -1,5
## 4          0.5383     -1,5
## 5          0.5339      5
## 6          0.5285      5
## 7          0.5282      5
## 8          0.5188      5
## 9          0.5185      5

```

```

## 10      0.5181      -1,5
## 11      0.5151       5
## 12      0.5141      -1,5
## 13      0.5098       5
## 14      0.5078      -1,5
## 15      0.5024      -1,5
## 16      0.5000      -1,5
## 17     -0.5175      1,-5
## 18     -0.5309      -5
##
##
## [[6]]
## [[6]]$c1
## data frame with 0 columns and 0 rows
##
## [[6]]$c2
##
## 1
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9
## 10
## 11
## 12
## 13
## 14
## 15
## 16
## 17
## 18
## 19
## 20
## 21
## 22 c2.FARMER_BREAST_CANCER_CLUSTER_5/c2.ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE/c4.GNF2_
## 23
## 24
## 25
## 26
## 27
## 28
##
## Correlation Metagenes
## 1      0.5952       6
## 2      0.5667       6
## 3      0.5606       6
## 4      0.5555       6
## 5      0.5521       6
## 6      0.5518       6
## 7      0.5504       6
## 8      0.5450      -2,6

```

```
## 9      0.5402      6
## 10     0.5318      6
## 11     0.5291      6
## 12     0.5257     -2,6
## 13     0.5253      6
## 14     0.5250      6
## 15     0.5185      6
## 16     0.5175      6
## 17     0.5148      6
## 18     0.5107      6
## 19     0.5087      6
## 20     0.5080      6
## 21     0.5067      6
## 22     0.5053      6
## 23     0.5013      6
## 24    -0.5141     -6
## 25    -0.5152     -6
## 26    -0.5165     -6
## 27    -0.5419     -6
## 28    -0.5887     -6
##
## [[6]]$c3
##           GeneSet Correlation Metagenes
## 1 c3.TGANTCA_V$AP1_C      0.5891      6
## 2      c3.V$AP1_Q4      0.5379      6
## 3      c3.V$AP1_Q6      0.5365      6
## 4      c3.V$AP1_Q6_01     0.5023      6
##
## [[6]]$c4
##           GeneSet Correlation Metagenes
## 1 c4.MODULE_321      0.5616      6
## 2 c4.MODULE_562      0.5301      6
## 3 c4.MODULE_153      0.5287      6
## 4  c4.GNF2_MMP1      0.5257      6
##
## [[6]]$c5
##           GeneSet Correlation Metagenes
## 1      c5.COLLAGEN      0.5138      6
## 2 c5.AXON_GUIDANCE      0.5101      6
##
## [[6]]$c6
## data frame with 0 columns and 0 rows
##
## [[6]]$c7
## data frame with 0 columns and 0 rows
```

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_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] 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           Biobase_2.26.0     BiocGenerics_0.12.1
## [13] cluster_1.15.3       rngtools_1.2.4     pkgmaker_0.22
## [16] registry_0.2         energy_1.6.2       survival_2.37-7
```

```
## [19] 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
```