

# SIS NMF surg rec

November 23, 2014

## 1 Preparation

```
##### LIBRARIES
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 63/64

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

setwd(data_dir)
load("image.rda")
```

## 2 Probe selection

```
table(cpss.sis$sel)

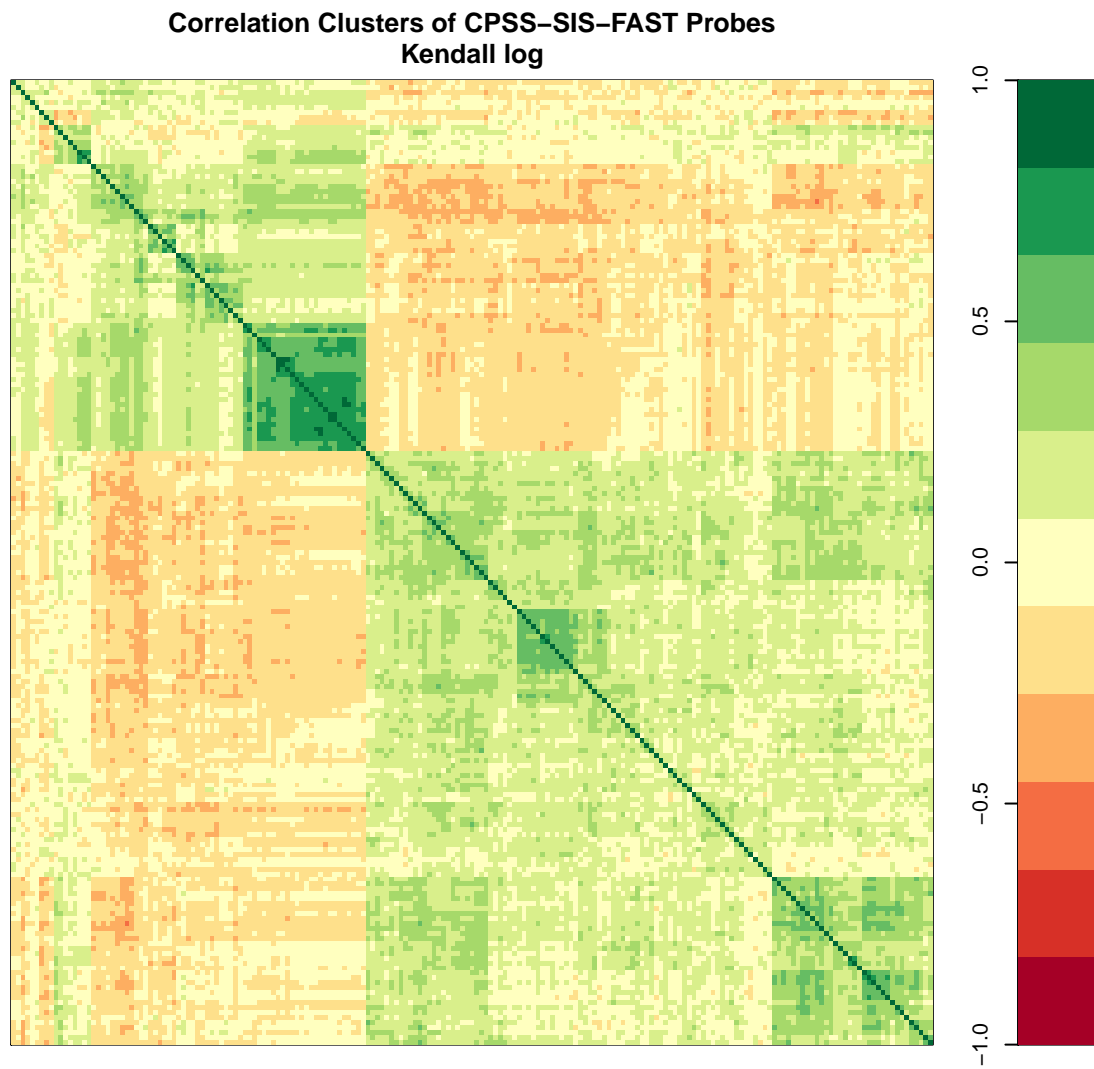
##
## FALSE  TRUE
## 12805   195

mean(cpss.sis$sel)

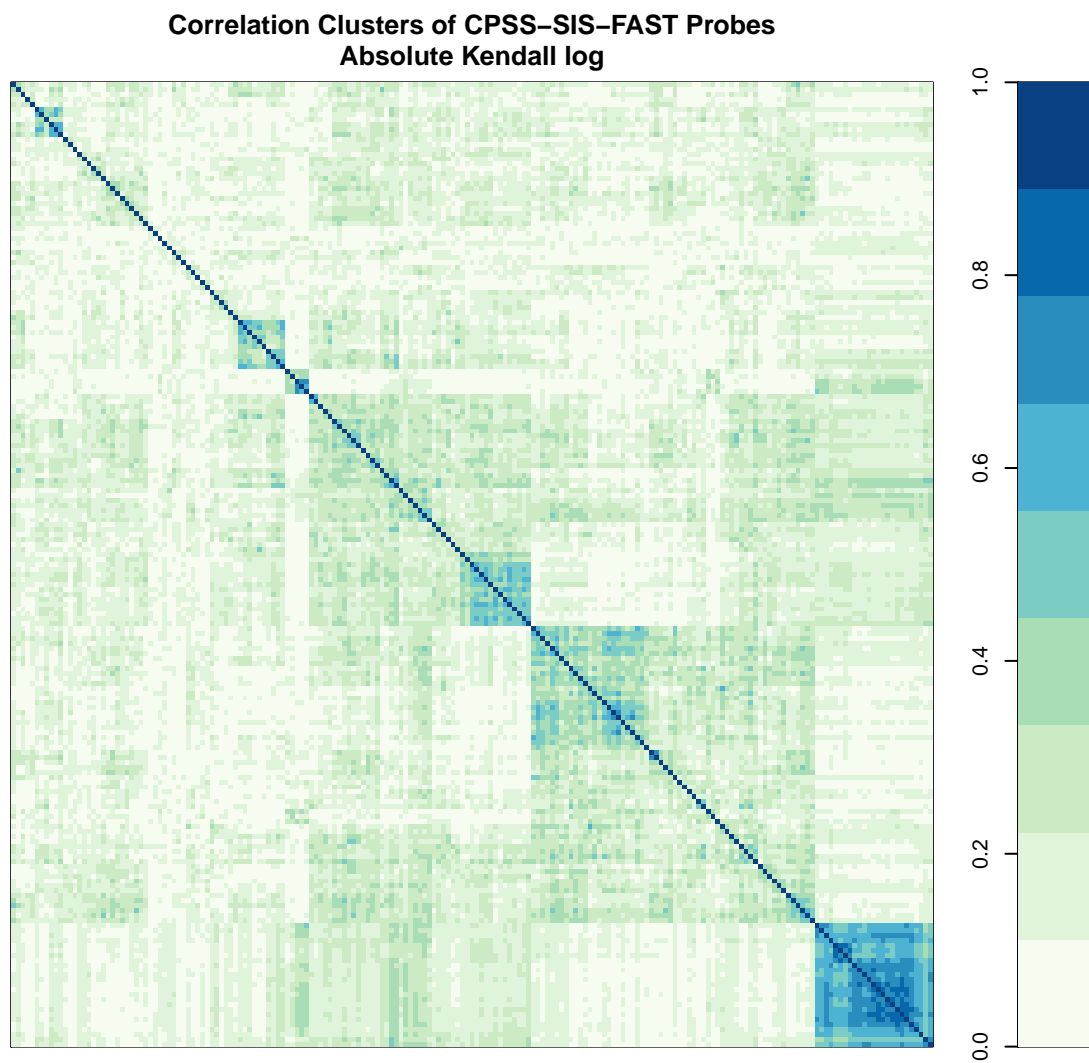
## [1] 0.015
```

## 3 Expression correlation

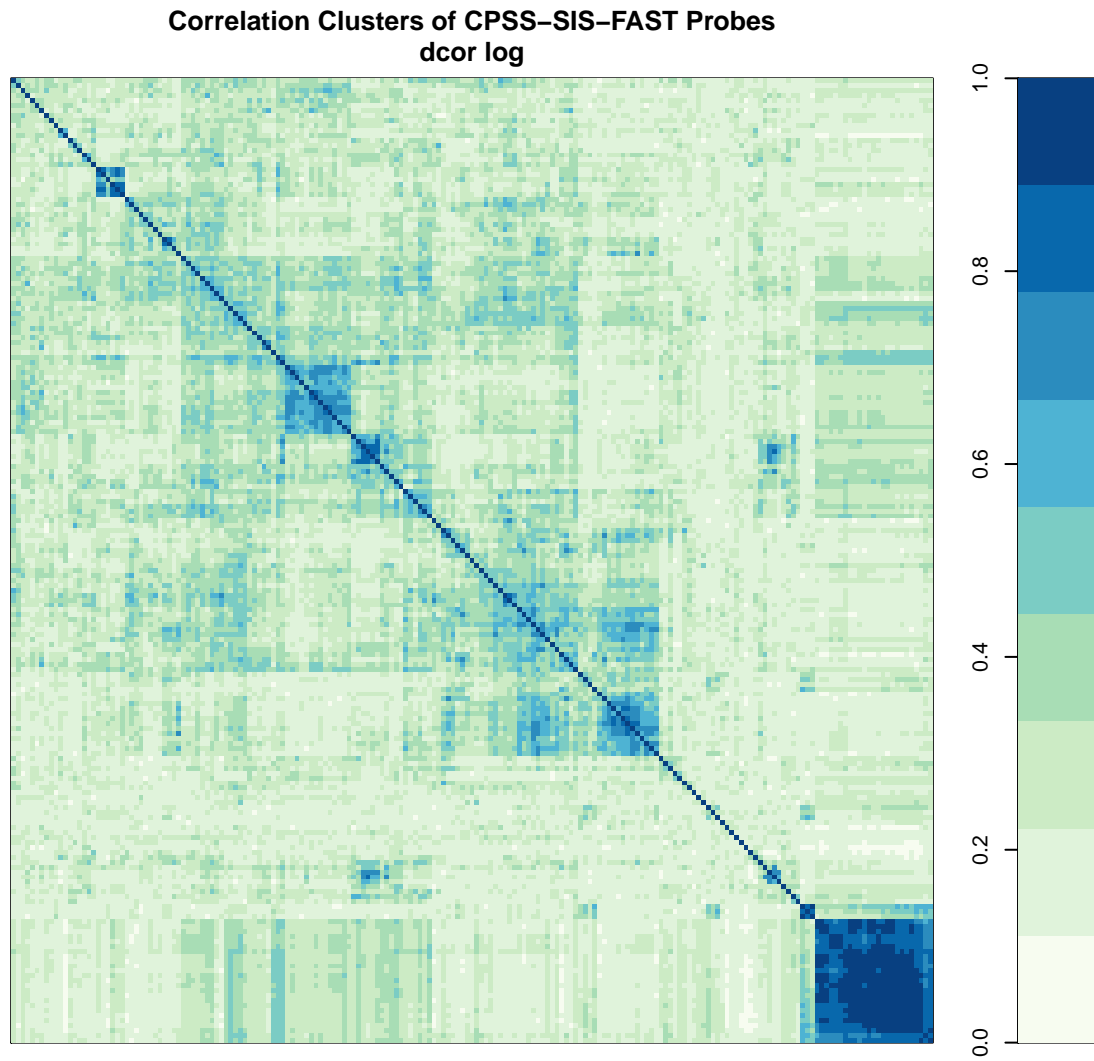
```
corPlot(x.sel.kcor, main = "Correlation Clusters of CPSS-SIS-FAST Probes\nKendall log",
        useRaster = FALSE)
```



```
corPlot(abs(x.sel.kcor), zlim = c(0, 1), pal = "GnBu", main = "Correlation Clusters of CPSS-SIS-FAST Probes",
        useRaster = FALSE)
```



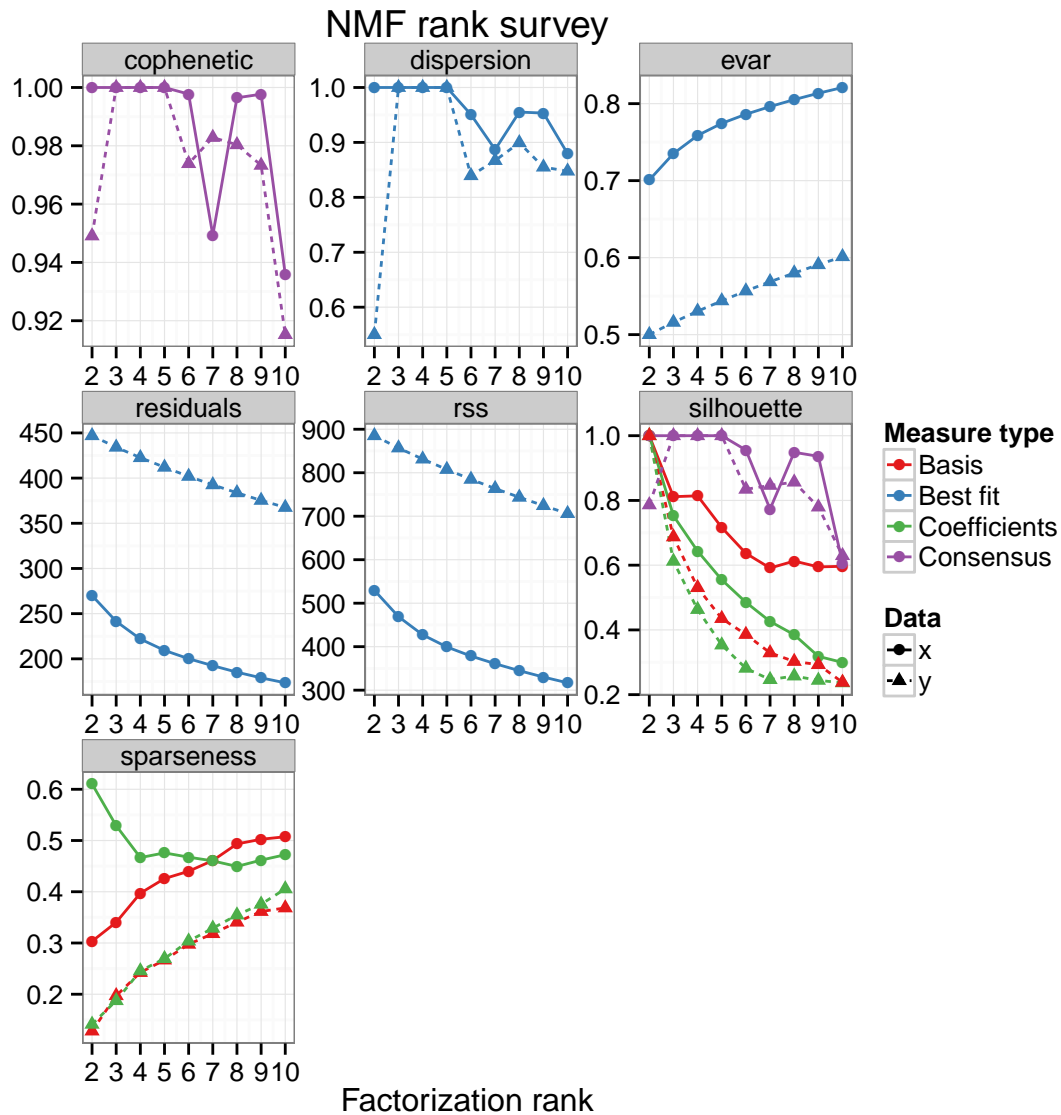
```
corPlot(x.sel.dcor, zlim = c(0, 1), pal = "GnBu", main = "Correlation Clusters of CPSS-SIS-FAST Probes",
        useRaster = FALSE)
```



## 4 Factorization

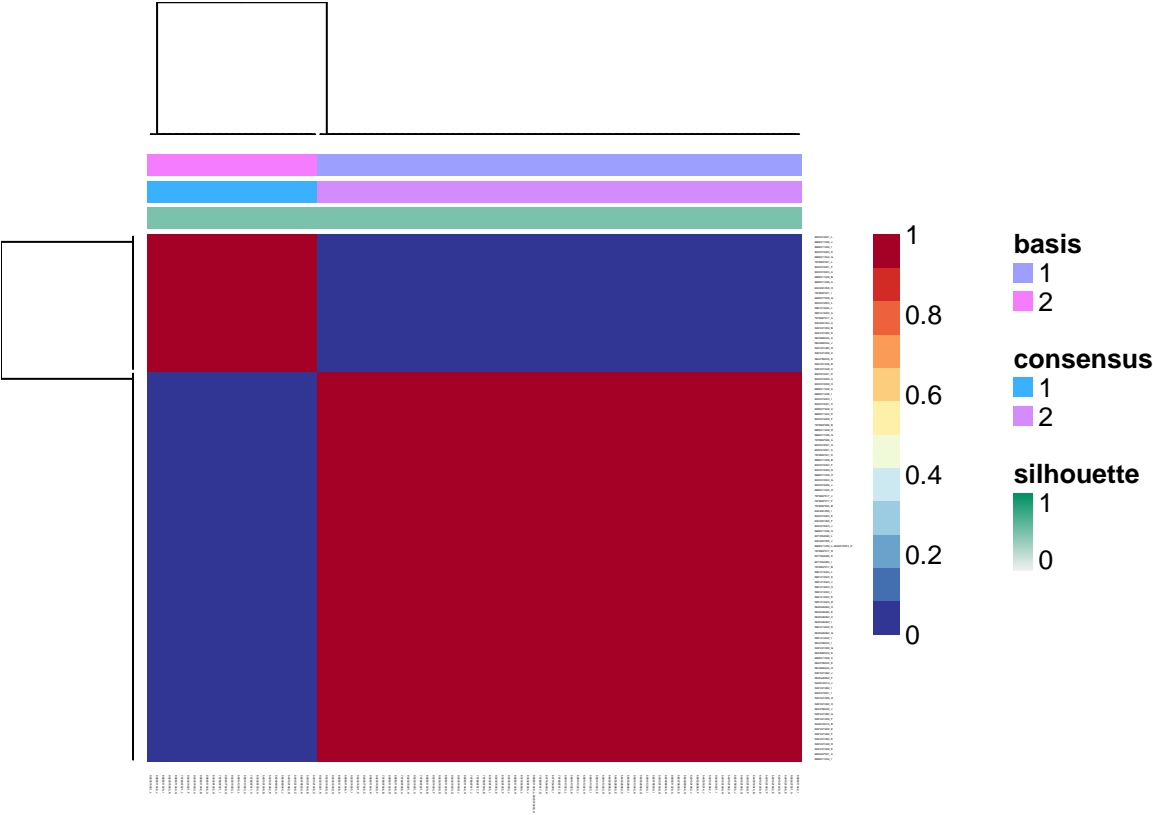
### 4.1 Rank estimation

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

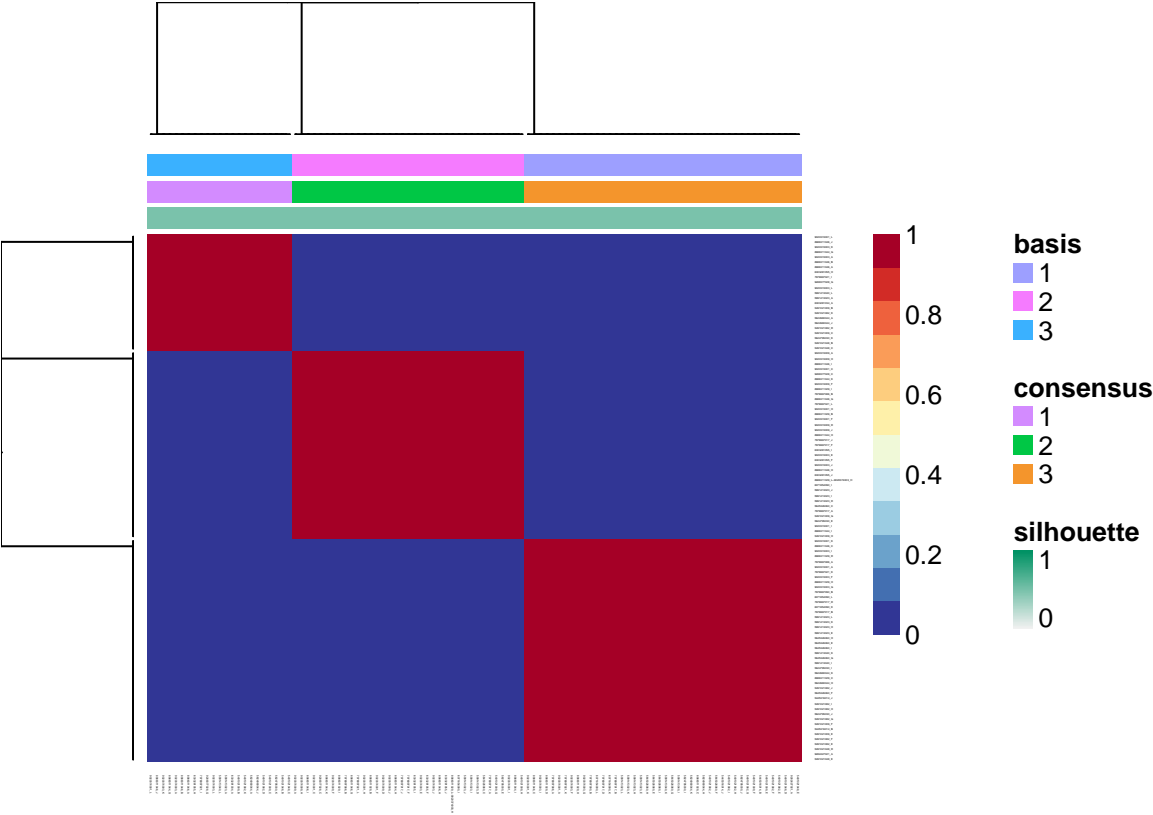


```
for (i in 1:length(temp.nmf.rank$fit)) {
  consensusmap(temp.nmf.rank$fit[[i]])
}
```

Consensus matrix

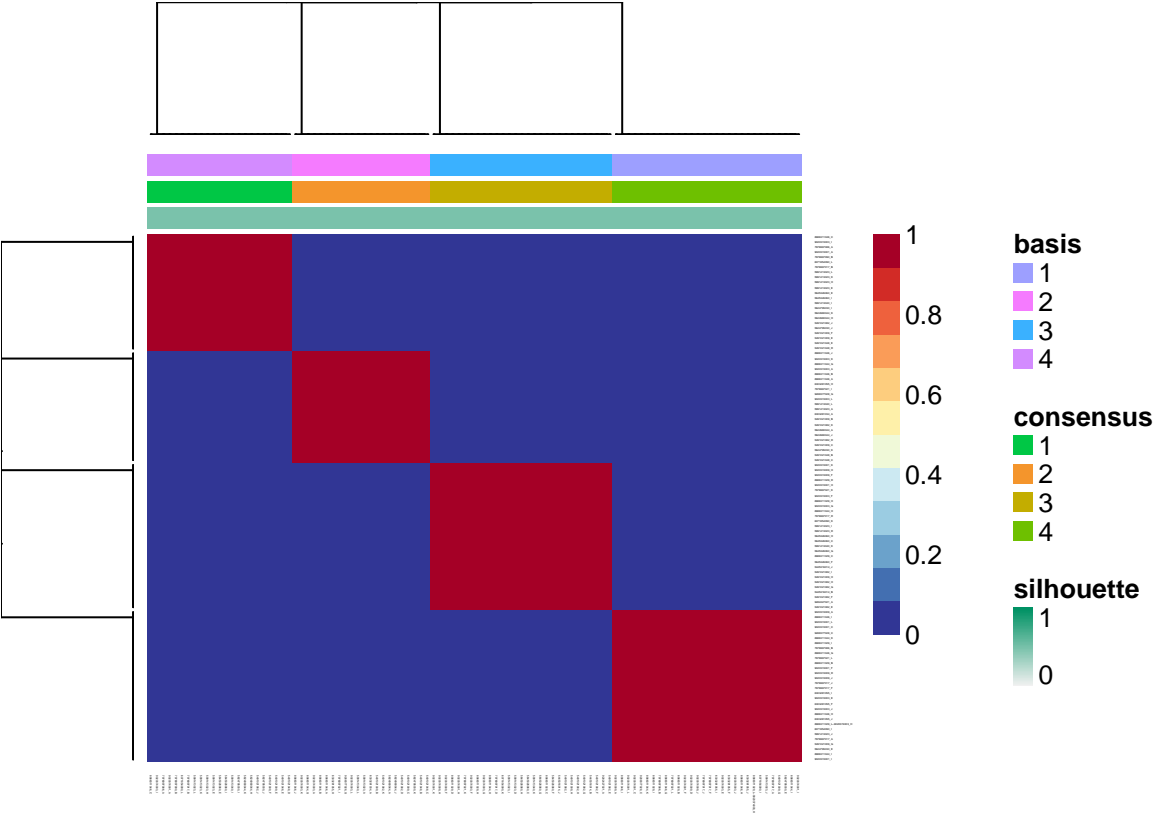


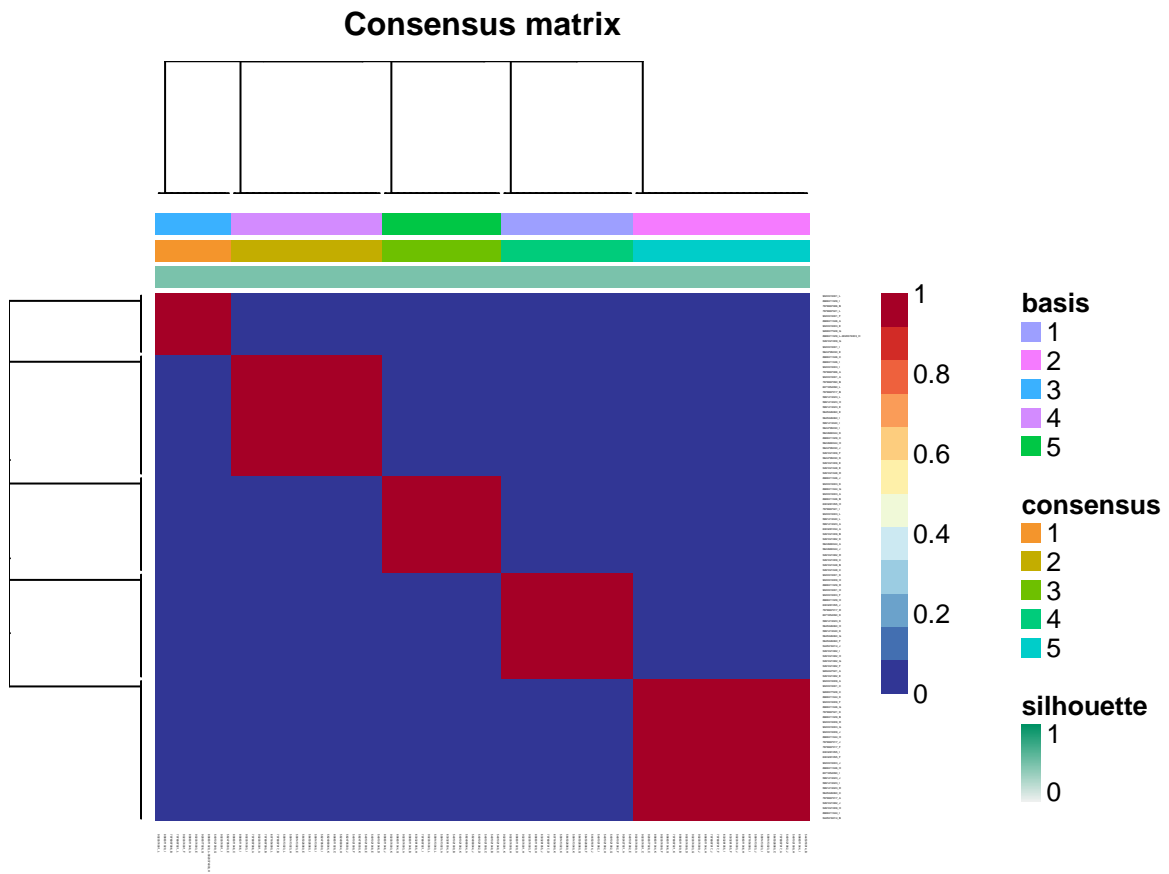
Consensus matrix

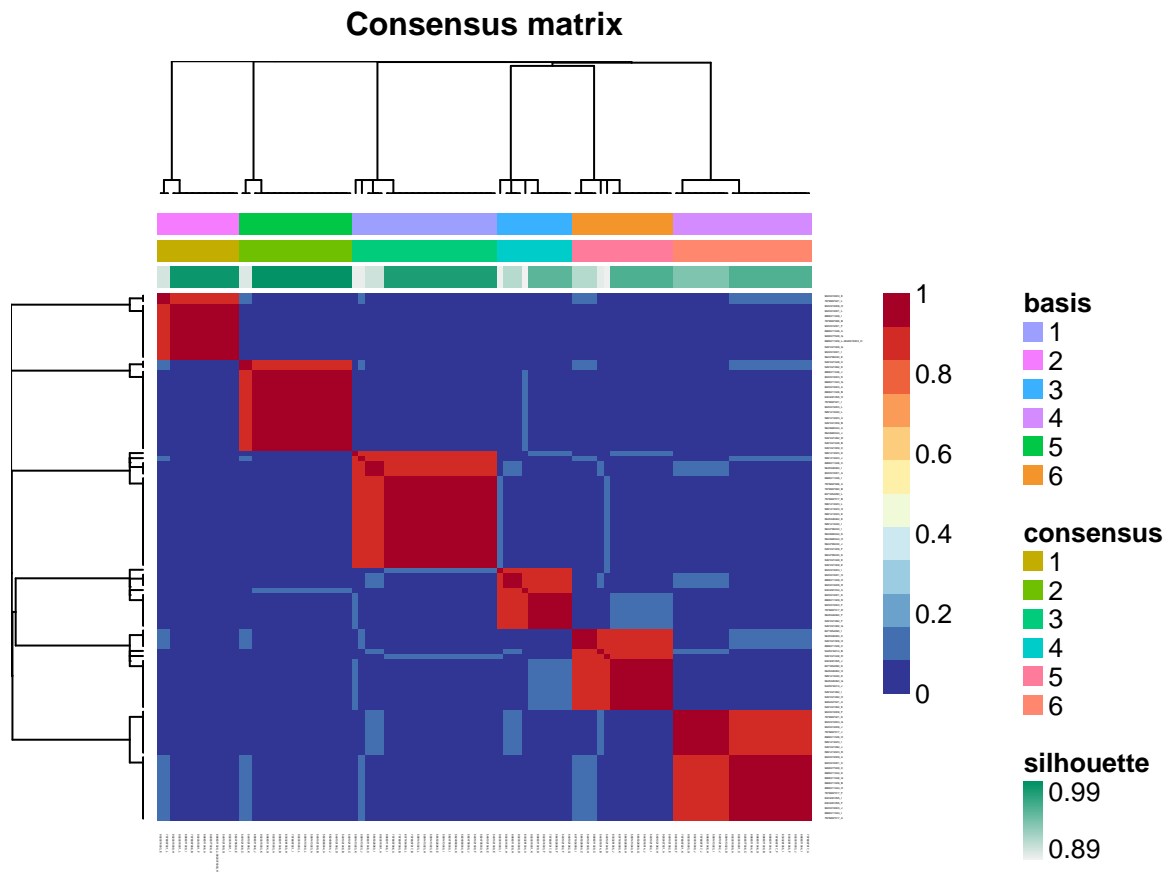


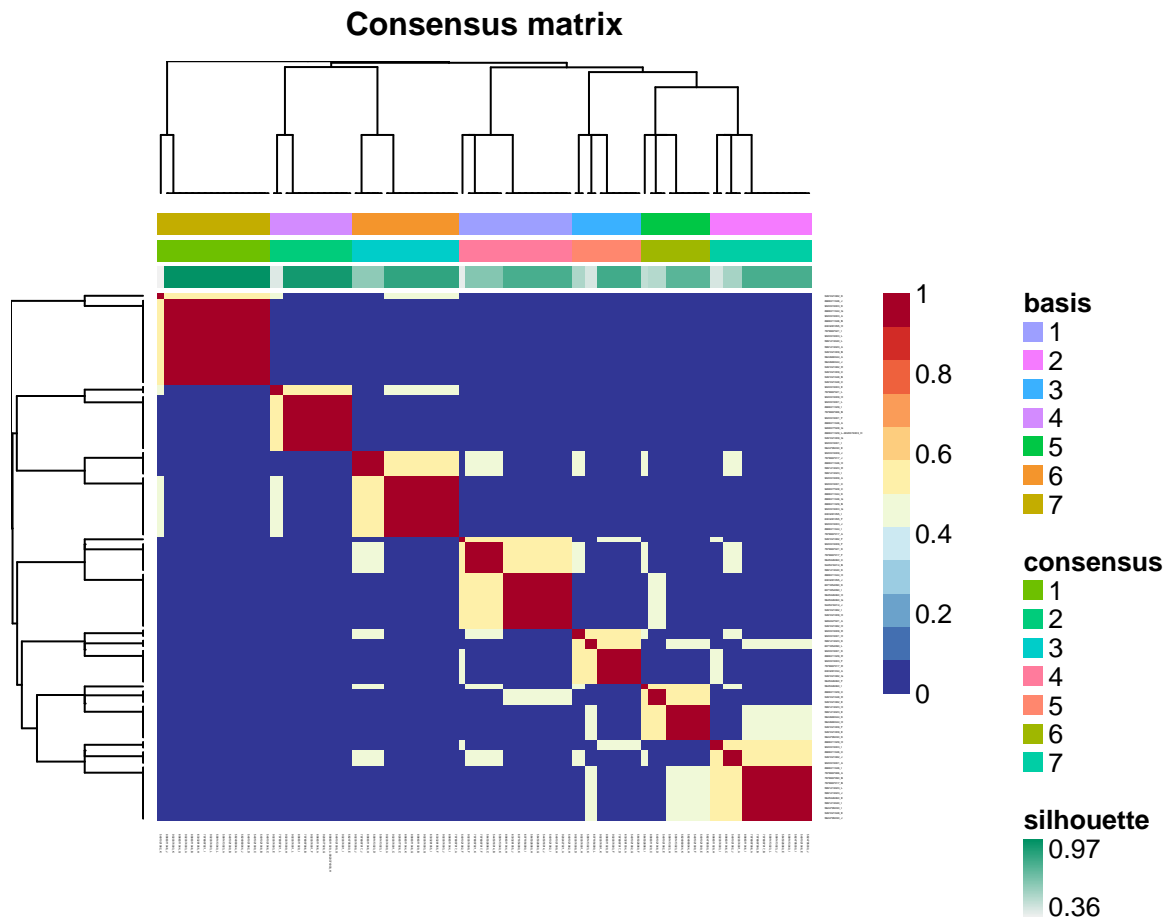


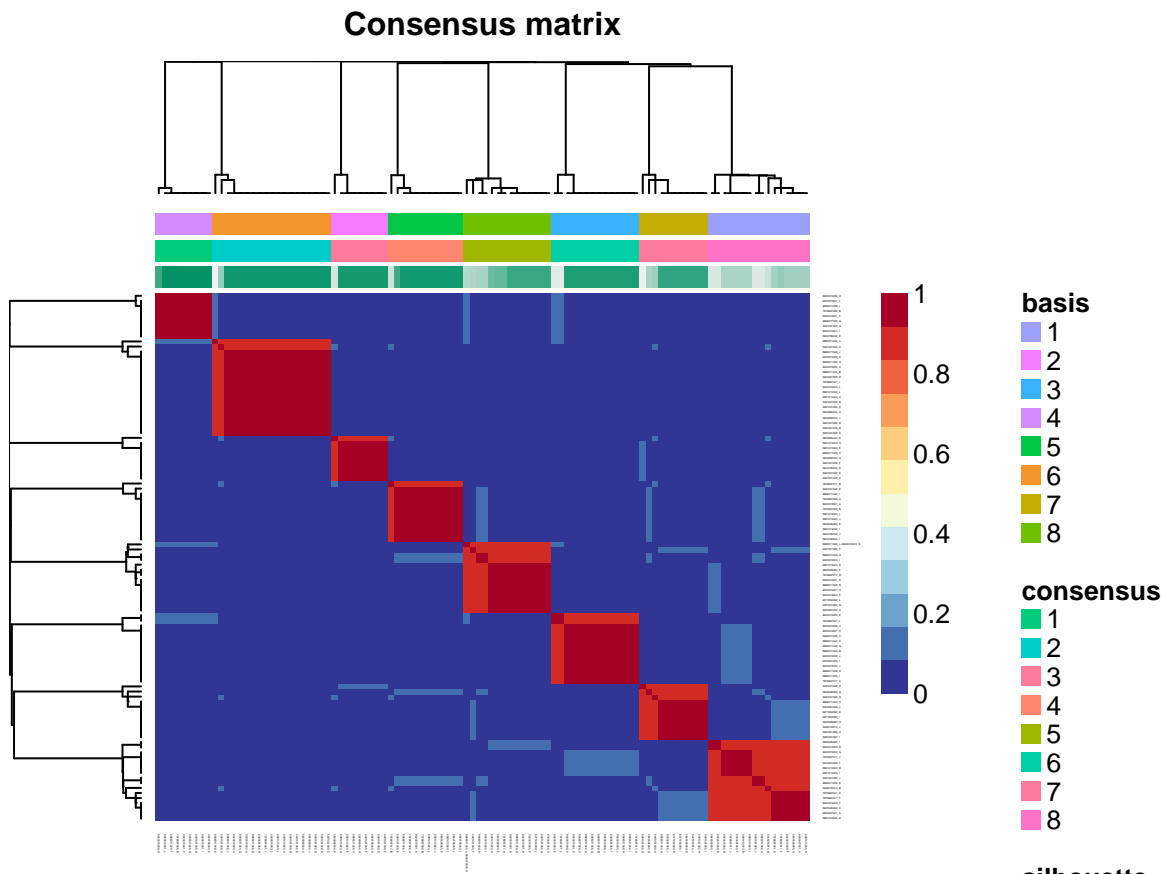
Consensus matrix

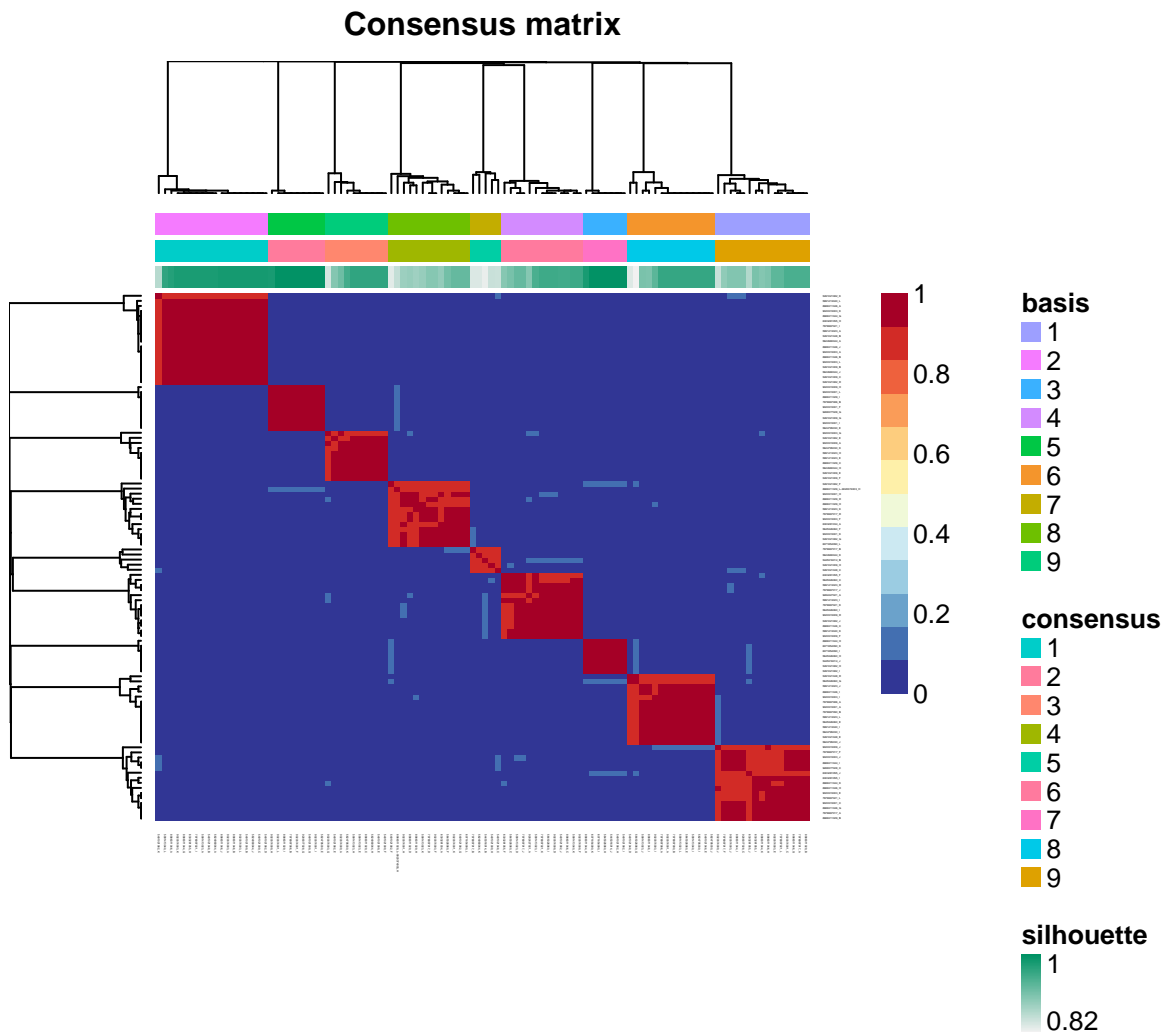


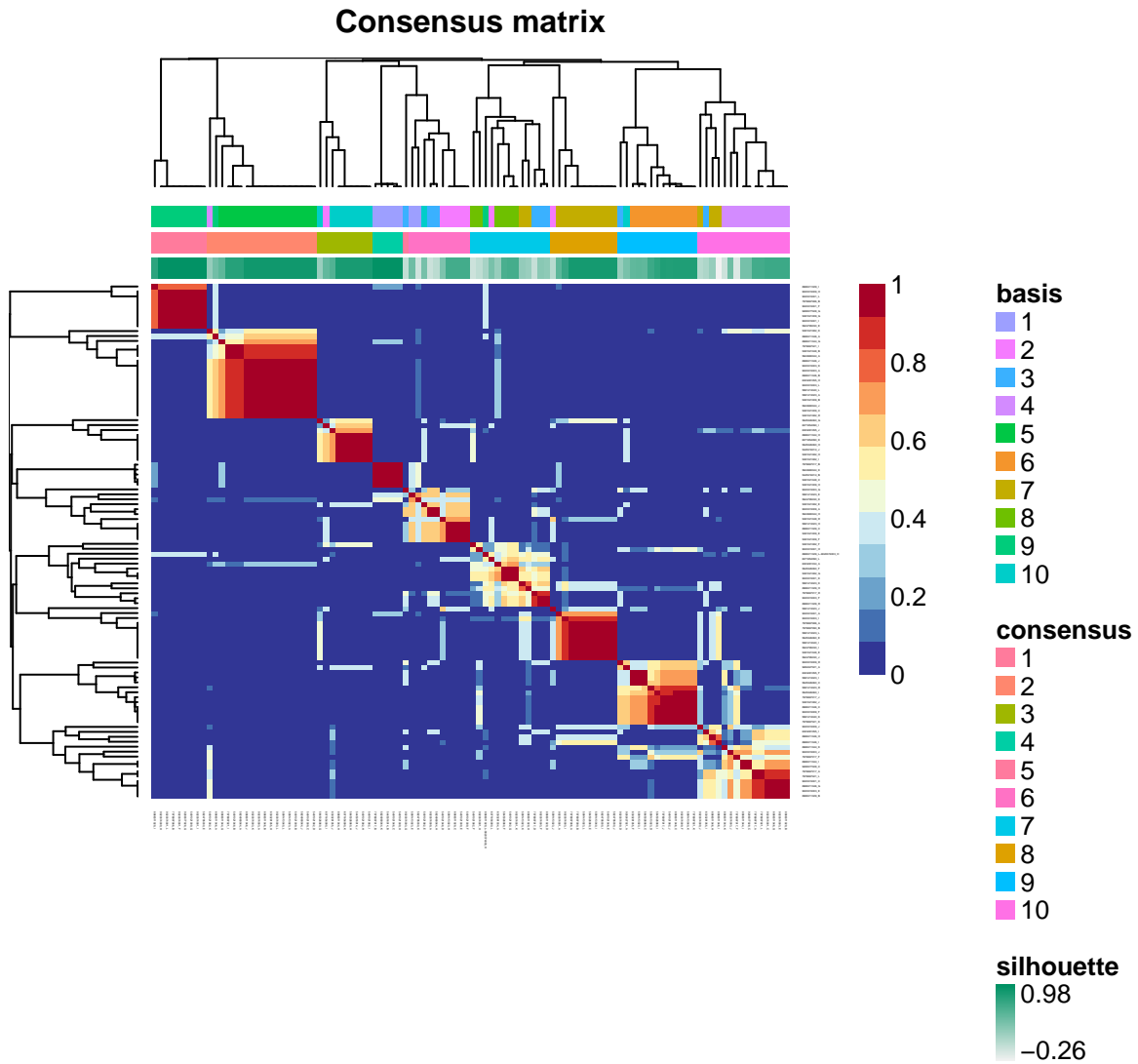








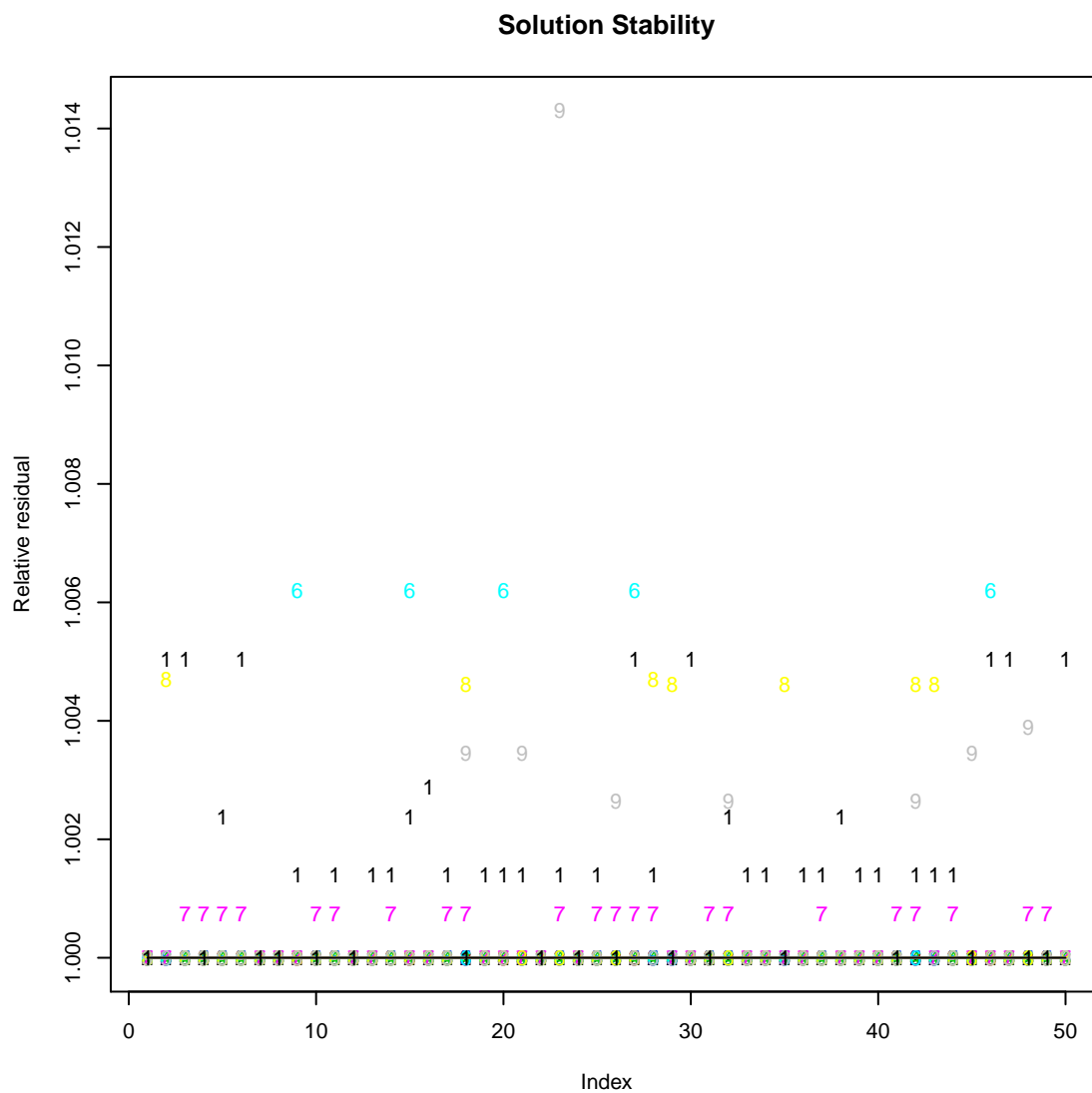




```

plot(0 ~ 0, type = "n", xlim = c(1, nrow(temp.resids)), ylim = range(temp.resids_rel),
     ylab = "Relative residual", main = "Solution Stability")
for (i in 1:ncol(temp.resids)) {
  points(temp.resids_rel[, i], col = i, pch = colnames(temp.resids)[i])
  lines(cummin(temp.resids_rel[, i]), col = i)
}

```

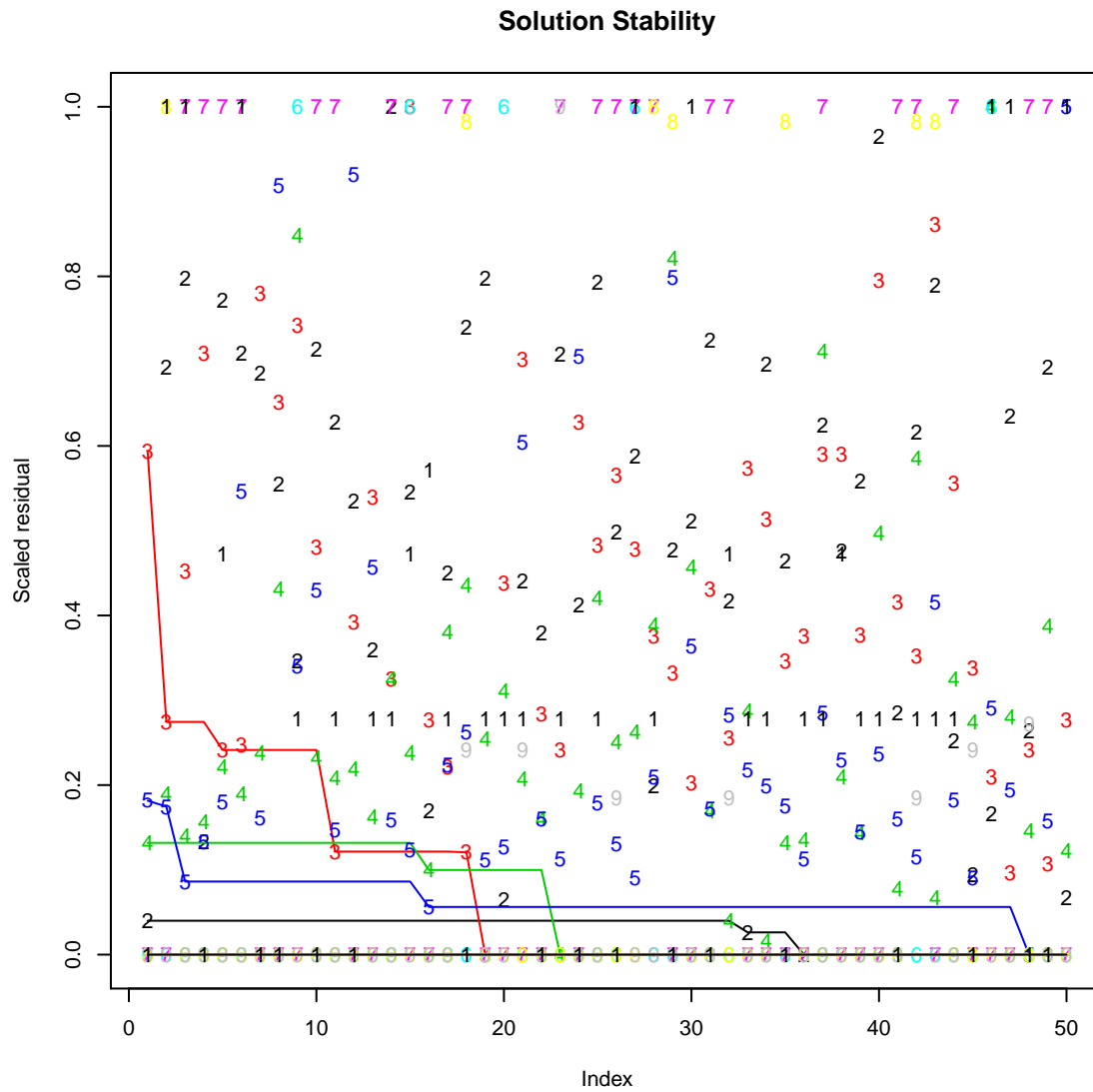


```

plot(0 ~ 0, type = "n", xlim = c(1, nrow(temp.resids)), ylim = range(temp.resids_scaled),
     ylab = "Scaled residual", main = "Solution Stability")
for (i in 1:ncol(temp.resids)) {
  points(temp.resids_scaled[, i], col = i, pch = colnames(temp.resids)[i])
  lines(cummin(temp.resids_scaled[, i]), col = i)
}

```





```

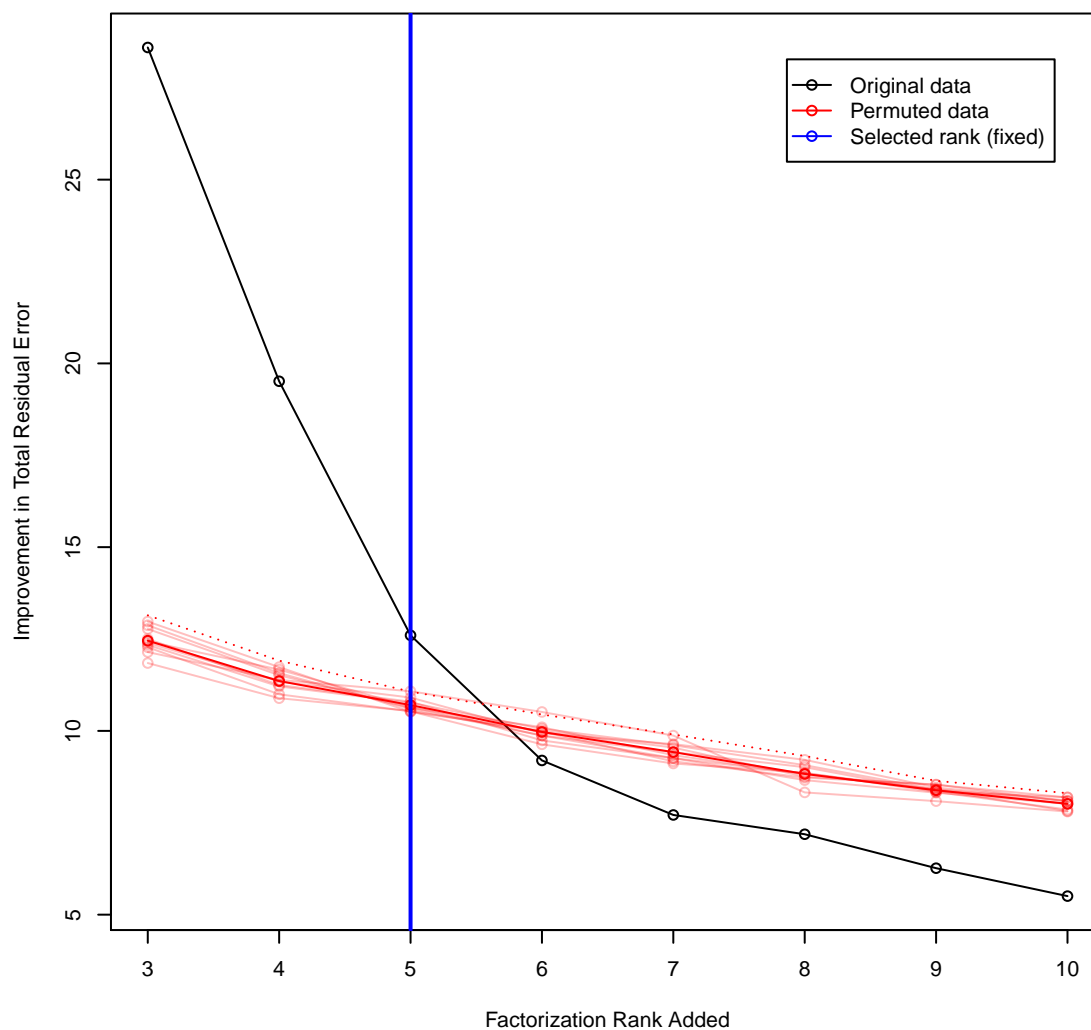
plot(nmf.rankrange[-1], -temp.orig_resids.delta, type = "o", col = "black",
     pch = 21, ylim = range(-c(temp.orig_resids.delta, temp.perm_resids.delta.mean)),
     xlab = "Factorization Rank Added", ylab = "Improvement in Total Residual Error")
lines(nmf.rankrange[-1], -temp.perm_resids.delta.mean, 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 == "auto") {
  temp.col = "green"
  nmf.rank = nmf.rank.auto
} 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(temp.col == "green", "auto", "fixed"))), col = c("black", "red",
temp.col), lty = "solid", pch = 21, inset = 0.05)

```

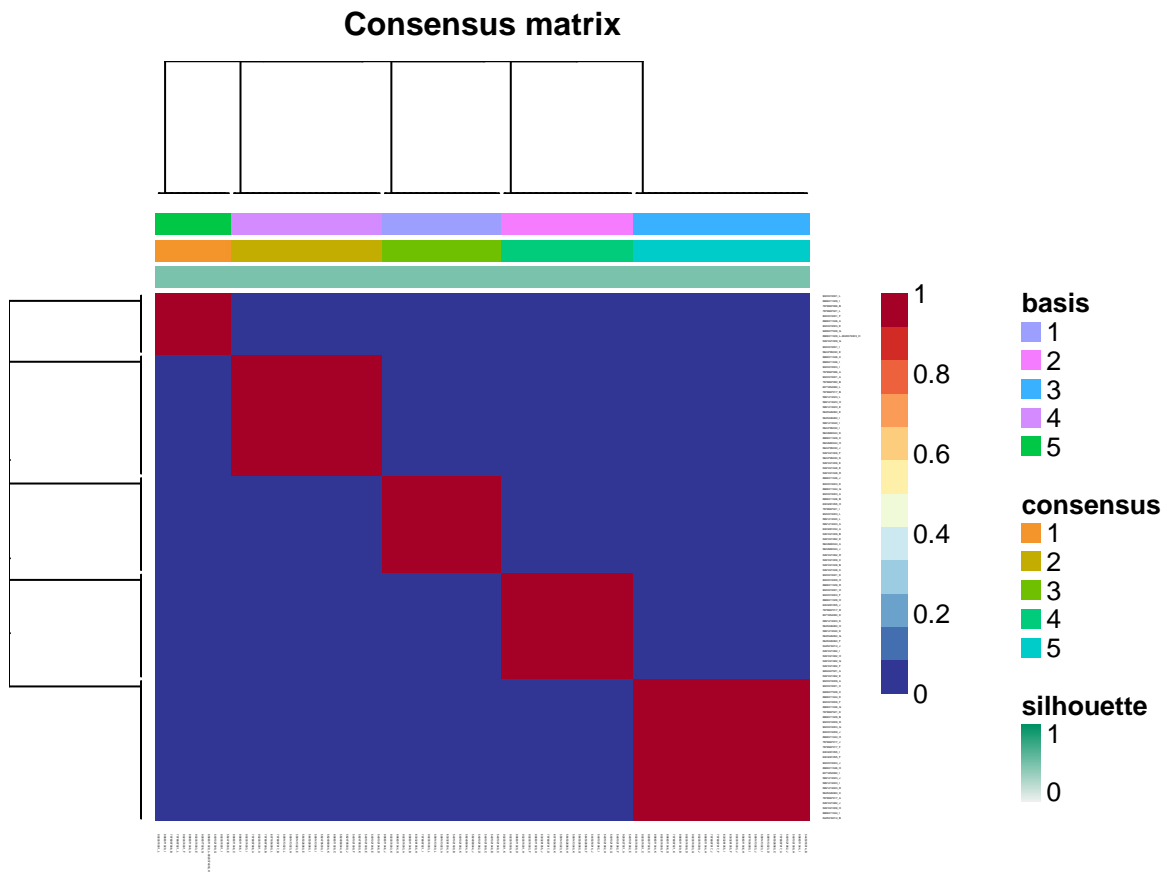


## 4.2 Fit

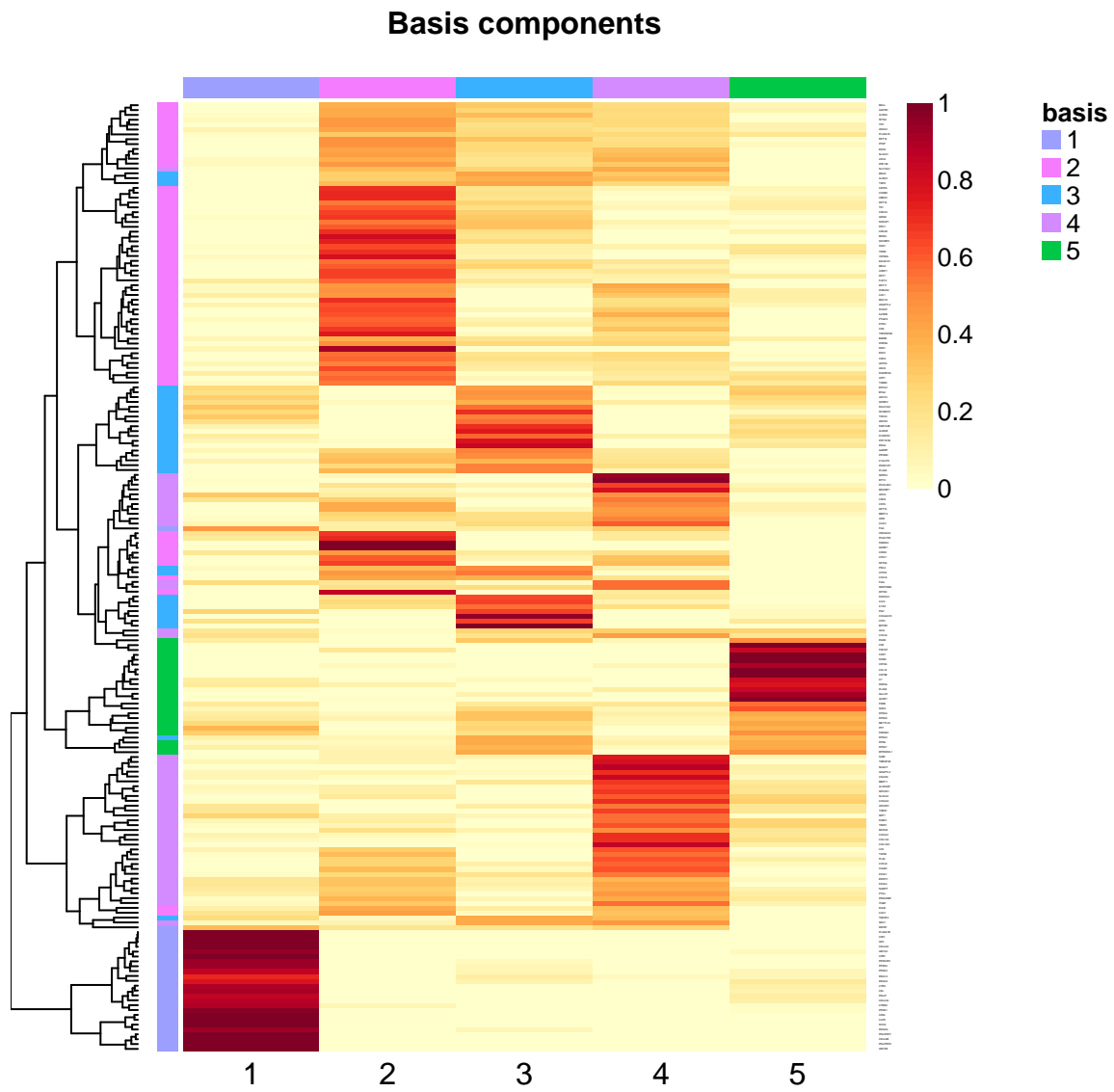
```

consensusmap(xlin.scaled.sel.nmf)

```

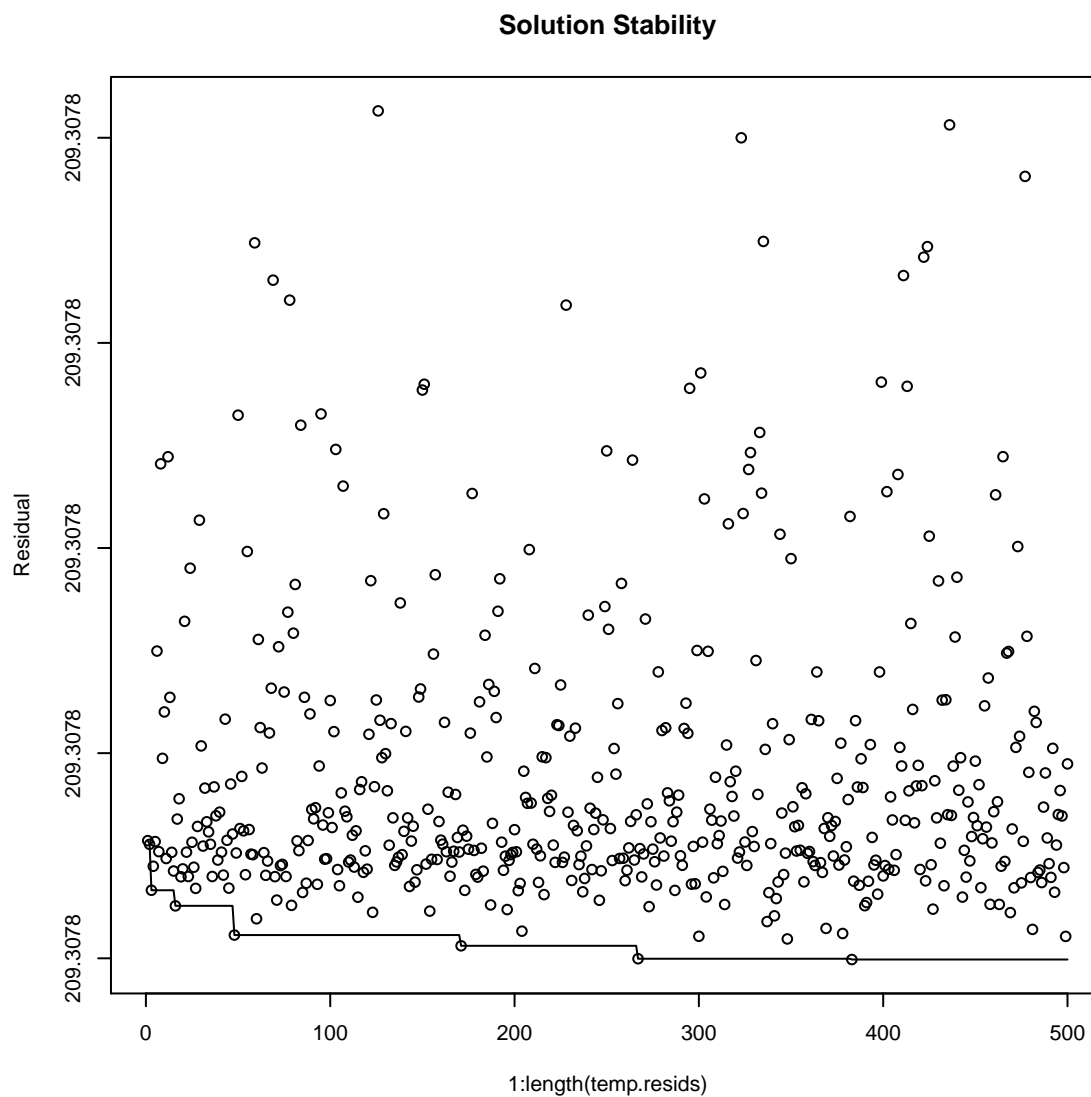


```
basimap(xlin.scaled.sel.nmf)
```



```
coefmap(xlin.scaled.sel.nmf)
```





## 4.3 Component CPV associations

### 4.3.1 Survival: Diagnosis to disease-specific death

```
for (i in 1:nrow(coef(xlin.scaled.sel.nmf))) {
  print(summary(coxph(y ~ coef(xlin.scaled.sel.nmf)[i, ])))
}
```

## Call:  
## coxph(formula = y ~ coef(xlin.scaled.sel.nmf)[i, ])  
##  
## n= 104, number of events= 77  
##

	coef	exp(coef)	se(coef)	z	Pr(> z )
## coef(xlin.scaled.sel.nmf)[i, ]	-1.224	0.294	1.045	-1.17	0.24

##

	exp(coef)	exp(-coef)	lower .95	upper .95
##				

Table 1:

	<i>Dependent variable:</i>
	y
coef(xlin.scaled.sel.nmf)[i, ]	-1.224 (1.045)
Observations	104
R <sup>2</sup>	0.014
Max. Possible R <sup>2</sup>	0.997
Log Likelihood	-307.100
Wald Test	1.370 (df = 1)
LR Test	1.473 (df = 1)
Score (Logrank) Test	1.383 (df = 1)
<i>Note:</i>	*p<0.1; **p<0.05; ***p<0.01

Table 2:

	<i>Dependent variable:</i>
	y
coef(xlin.scaled.sel.nmf)[i, ]	7.725*** (1.319)
Observations	104
R <sup>2</sup>	0.252
Max. Possible R <sup>2</sup>	0.997
Log Likelihood	-292.800
Wald Test	34.310*** (df = 1)
LR Test	30.140*** (df = 1)
Score (Logrank) Test	36.300*** (df = 1)
<i>Note:</i>	*p<0.1; **p<0.05; ***p<0.01

Table 3:

	<i>Dependent variable:</i>
	y
coef(xlin.scaled.sel.nmf)[i, ]	-1.441 (1.288)
Observations	104
R <sup>2</sup>	0.012
Max. Possible R <sup>2</sup>	0.997
Log Likelihood	-307.200
Wald Test	1.250 (df = 1)
LR Test	1.299 (df = 1)
Score (Logrank) Test	1.255 (df = 1)
<i>Note:</i>	*p<0.1; **p<0.05; ***p<0.01

Table 4:

	<i>Dependent variable:</i>
	y
coef(xlin.scaled.sel.nmf)[i, ]	4.362*** (1.177)
Observations	104
R <sup>2</sup>	0.115
Max. Possible R <sup>2</sup>	0.997
Log Likelihood	-301.500
Wald Test	13.730*** (df = 1)
LR Test	12.660*** (df = 1)
Score (Logrank) Test	14.210*** (df = 1)
<i>Note:</i>	*p<0.1; **p<0.05; ***p<0.01

Table 5:

	<i>Dependent variable:</i>
	y
coef(xlin.scaled.sel.nmf)[i, ]	-6.189*** (1.687)
Observations	104
R <sup>2</sup>	0.148
Max. Possible R <sup>2</sup>	0.997
Log Likelihood	-299.500
Wald Test	13.460*** (df = 1)
LR Test	16.640*** (df = 1)
Score (Logrank) Test	14.060*** (df = 1)
<i>Note:</i>	*p<0.1; **p<0.05; ***p<0.01



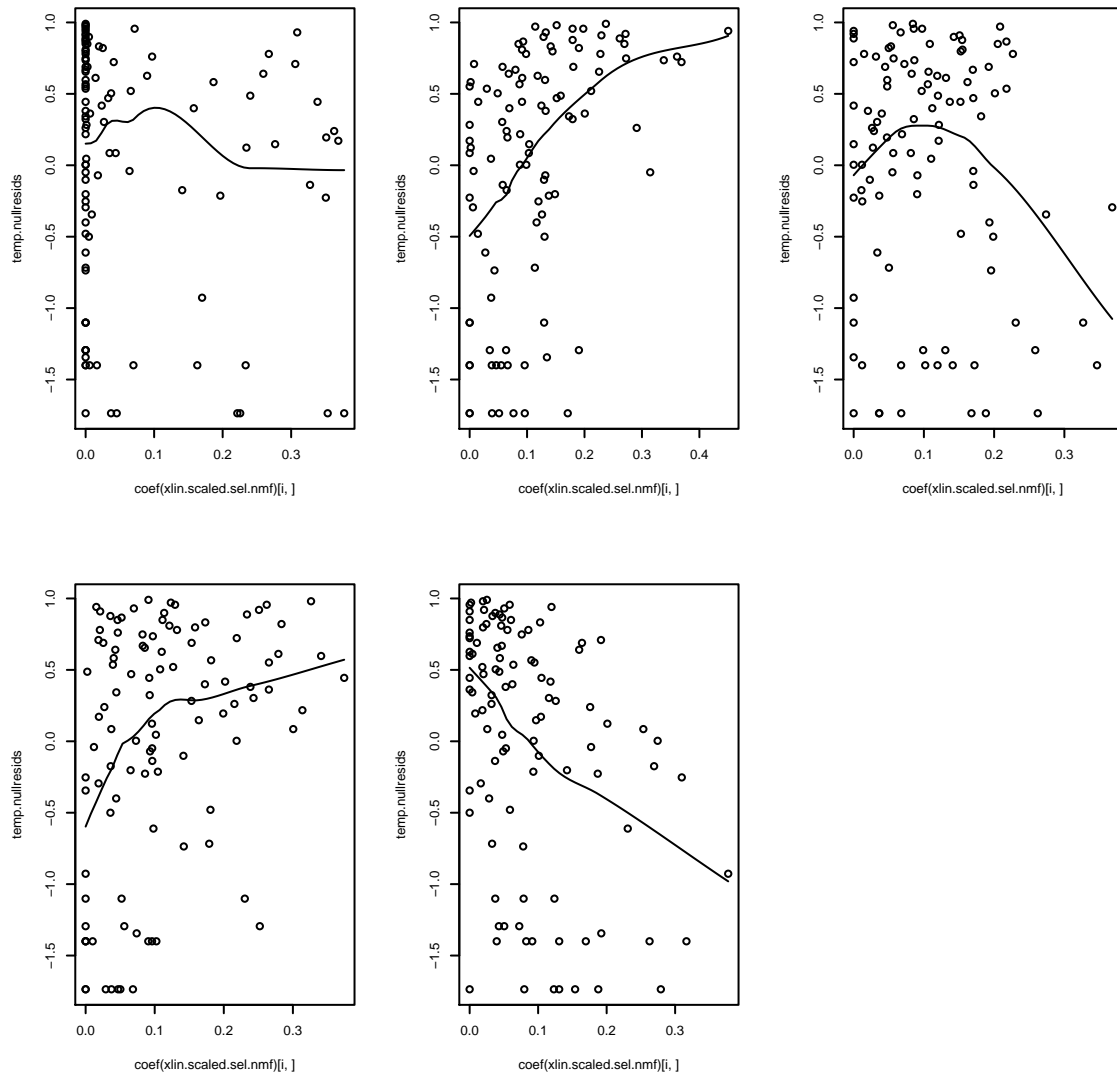
```

## coef(xlin.scaled.sel.nmf)[i, ]      0.294      3.4      0.0379      2.28
##
## Concordance= 0.546 (se = 0.035 )
## Rsquare= 0.014 (max possible= 0.997 )
## Likelihood ratio test= 1.47 on 1 df, p=0.225
## Wald test          = 1.37 on 1 df, p=0.241
## Score (logrank) test = 1.38 on 1 df, p=0.24
##
## Call:
## coxph(formula = y ~ coef(xlin.scaled.sel.nmf)[i, ])
##
## n= 104, number of events= 77
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## coef(xlin.scaled.sel.nmf)[i, ]    7.73  2264.99    1.32 5.86  4.7e-09
##
##              exp(coef) exp(-coef) lower .95 upper .95
## coef(xlin.scaled.sel.nmf)[i, ]    2265  0.000442    171  30045
##
## Concordance= 0.692 (se = 0.036 )
## Rsquare= 0.252 (max possible= 0.997 )
## Likelihood ratio test= 30.1 on 1 df, p=4.02e-08
## Wald test          = 34.3 on 1 df, p=4.71e-09
## Score (logrank) test = 36.3 on 1 df, p=1.69e-09
##
## Call:
## coxph(formula = y ~ coef(xlin.scaled.sel.nmf)[i, ])
##
## n= 104, number of events= 77
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## coef(xlin.scaled.sel.nmf)[i, ] -1.441    0.237    1.288 -1.12    0.26
##
##              exp(coef) exp(-coef) lower .95 upper .95
## coef(xlin.scaled.sel.nmf)[i, ]    0.237    4.23    0.0189    2.96
##
## Concordance= 0.508 (se = 0.036 )
## Rsquare= 0.012 (max possible= 0.997 )
## Likelihood ratio test= 1.3 on 1 df, p=0.254
## Wald test          = 1.25 on 1 df, p=0.263
## Score (logrank) test = 1.26 on 1 df, p=0.263
##
## Call:
## coxph(formula = y ~ coef(xlin.scaled.sel.nmf)[i, ])
##
## n= 104, number of events= 77
##
##              coef exp(coef) se(coef)      z Pr(>|z|)
## coef(xlin.scaled.sel.nmf)[i, ]  4.36    78.42    1.18 3.71  0.00021
##
##              exp(coef) exp(-coef) lower .95 upper .95
## coef(xlin.scaled.sel.nmf)[i, ]    78.4    0.0128    7.8    788
##

```

```
## Concordance= 0.616 (se = 0.036 )
## Rsquare= 0.115 (max possible= 0.997 )
## Likelihood ratio test= 12.7 on 1 df, p=0.000374
## Wald test = 13.7 on 1 df, p=0.000211
## Score (logrank) test = 14.2 on 1 df, p=0.000163
##
## Call:
## coxph(formula = y ~ coef(xlin.scaled.sel.nmf)[i, ])
##
## n= 104, number of events= 77
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## coef(xlin.scaled.sel.nmf)[i, ] -6.18940  0.00205  1.68734 -3.67  0.00024
##
##               exp(coef) exp(-coef) lower .95 upper .95
## coef(xlin.scaled.sel.nmf)[i, ]  0.00205      488 7.51e-05  0.056
##
## Concordance= 0.649 (se = 0.036 )
## Rsquare= 0.148 (max possible= 0.997 )
## Likelihood ratio test= 16.6 on 1 df, p=4.52e-05
## Wald test = 13.5 on 1 df, p=0.000244
## Score (logrank) test = 14.1 on 1 df, p=0.000177
```

```
temp.nullfit = coxph(y ~ 1)
temp.nullresids = residuals(temp.nullfit, type = "martingale")
par(mfrow = c(2, 3))
for (i in 1:nrow(coef(xlin.scaled.sel.nmf))) {
  scatter.smooth(temp.nullresids ~ coef(xlin.scaled.sel.nmf)[i, ])
}
par(mfrow = c(1, 1))
```



## 4.4 Purity

```
apply(coef(xlin.scaled.sel.nmf), 1, function(xc) cor.test(samps$purity_qpure,
  xc, method = "kendall"))

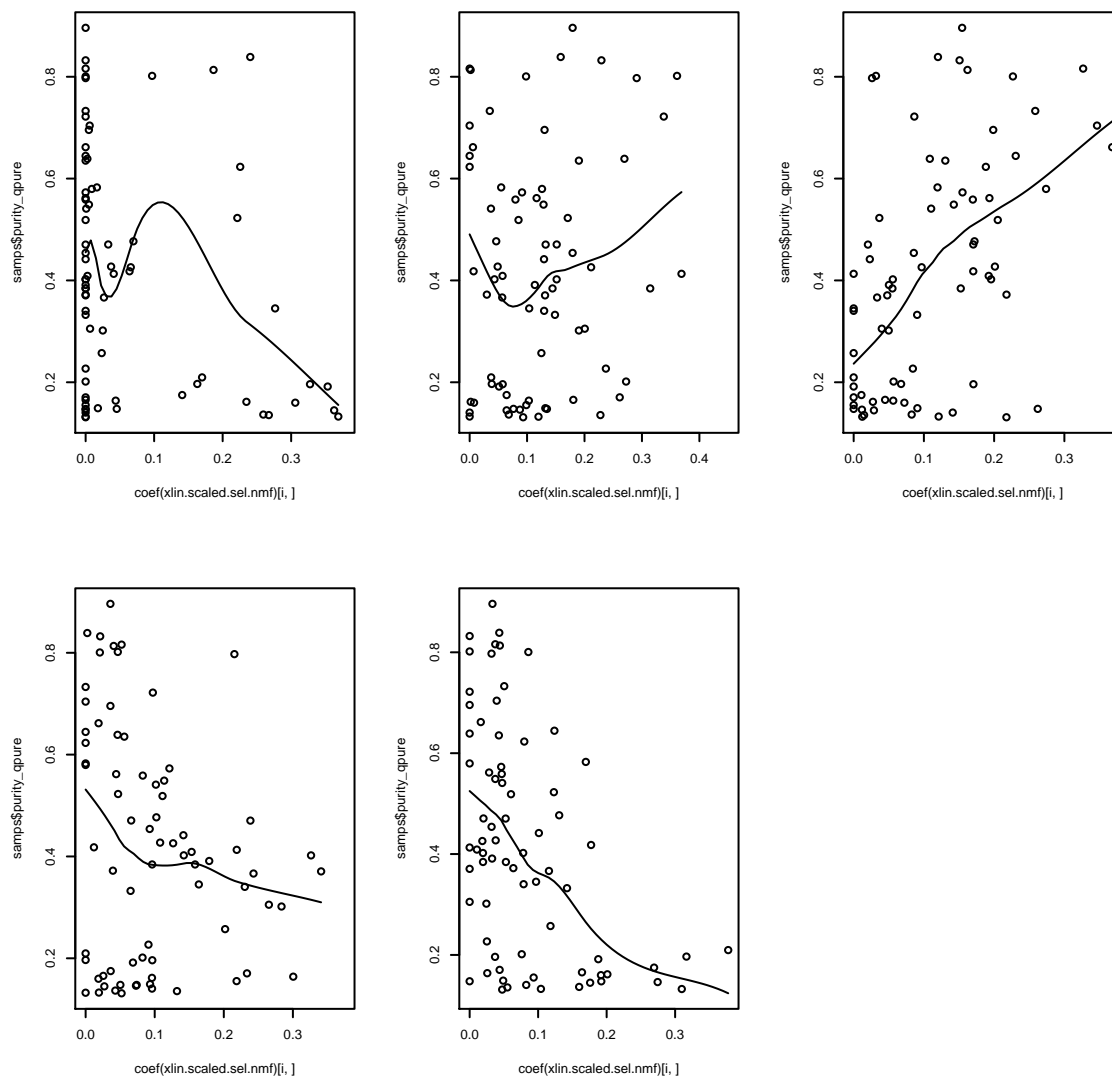
## [[1]]
##
## Kendall's rank correlation tau
##
## data: samps$purity_qpure and xc
## z = -1.903, p-value = 0.0571
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
## tau
## -0.162
##
```

```

##
## [[2]]
##
## Kendall's rank correlation tau
##
## data:  samps$purity_qpure and xc
## z = 0.5649, p-value = 0.5722
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## 0.04493
##
##
## [[3]]
##
## Kendall's rank correlation tau
##
## data:  samps$purity_qpure and xc
## z = 4.12, p-value = 3.785e-05
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## 0.3288
##
##
## [[4]]
##
## Kendall's rank correlation tau
##
## data:  samps$purity_qpure and xc
## z = -1.878, p-value = 0.06039
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## -0.1499
##
##
## [[5]]
##
## Kendall's rank correlation tau
##
## data:  samps$purity_qpure and xc
## z = -3.865, p-value = 0.0001112
## alternative hypothesis: true tau is not equal to 0
## sample estimates:
##      tau
## -0.3088

par(mfrow = c(2, 3))
for (i in 1:nrow(coef(xlin.scaled.sel.nmf))) {
  scatter.smooth(samps$purty_qpure ~ coef(xlin.scaled.sel.nmf)[i, ])
}
par(mfrow = c(1, 1))

```



## 4.5 MTC P-values

```
xlin.scaled.sel.nmf.cpv.pvals = data.frame(p.surv = apply(coef(xlin.scaled.sel.nmf),
  1, function(xc) pchisq(2 * diff(coxph(y ~ xc)$loglik), df = 1, lower.tail = FALSE)),
  p.pure = apply(coef(xlin.scaled.sel.nmf), 1, function(xc) cor.test(samps$purty_qpure,
    xc, method = "kendall")$p.value), d.surv = apply(coef(xlin.scaled.sel.nmf),
    1, function(xc) sign(coef(coxph(y ~ xc)))), d.pure = apply(coef(xlin.scaled.sel.nmf),
    1, function(xc) sign(cor.test(samps$purty_qpure, xc, method = "kendall")$statistic)))
temp.pvals.FWER = p.adjust(c(xlin.scaled.sel.nmf.cpv.pvals$p.surv, xlin.scaled.sel.nmf.cpv.pvals$p.pure),
  "holm")
temp.qvals.BY = p.adjust(c(xlin.scaled.sel.nmf.cpv.pvals$p.surv, xlin.scaled.sel.nmf.cpv.pvals$p.pure),
  "BY")
xlin.scaled.sel.nmf.cpv.pvals$p.surv.FWER = temp.pvals.FWER[1:(length(temp.pvals.FWER)/2)]
xlin.scaled.sel.nmf.cpv.pvals$p.pure.FWER = temp.pvals.FWER[(length(temp.pvals.FWER)/2 +
  1):length(temp.pvals.FWER)]
xlin.scaled.sel.nmf.cpv.pvals$q.surv.BY = temp.qvals.BY[1:(length(temp.qvals.BY)/2)]
```

```

xlin.scaled.sel.nmf.cpv.pvals$q.pure.BY = temp.qvals.BY[(length(temp.qvals.BY)/2 +
1):length(temp.qvals.BY)]
xlin.scaled.sel.nmf.cpv.pvals

##      p.surv    p.pure d.surv d.pure p.surv.FWER p.pure.FWER q.surv.BY
## 1 2.249e-01 5.710e-02    -1    -1 6.748e-01 0.2855120 8.235e-01
## 2 4.018e-08 5.722e-01     1     1 4.018e-07 0.6748161 1.177e-06
## 3 2.544e-01 3.785e-05    -1     1 6.748e-01 0.0003406 8.278e-01
## 4 3.739e-04 6.039e-02     1    -1 2.243e-03 0.2855120 2.190e-03
## 5 4.522e-05 1.112e-04    -1    -1 3.618e-04 0.0007786 4.415e-04
##      q.pure.BY
## 1 0.2526892
## 2 1.0000000
## 3 0.0004415
## 4 0.2526892
## 5 0.0008145

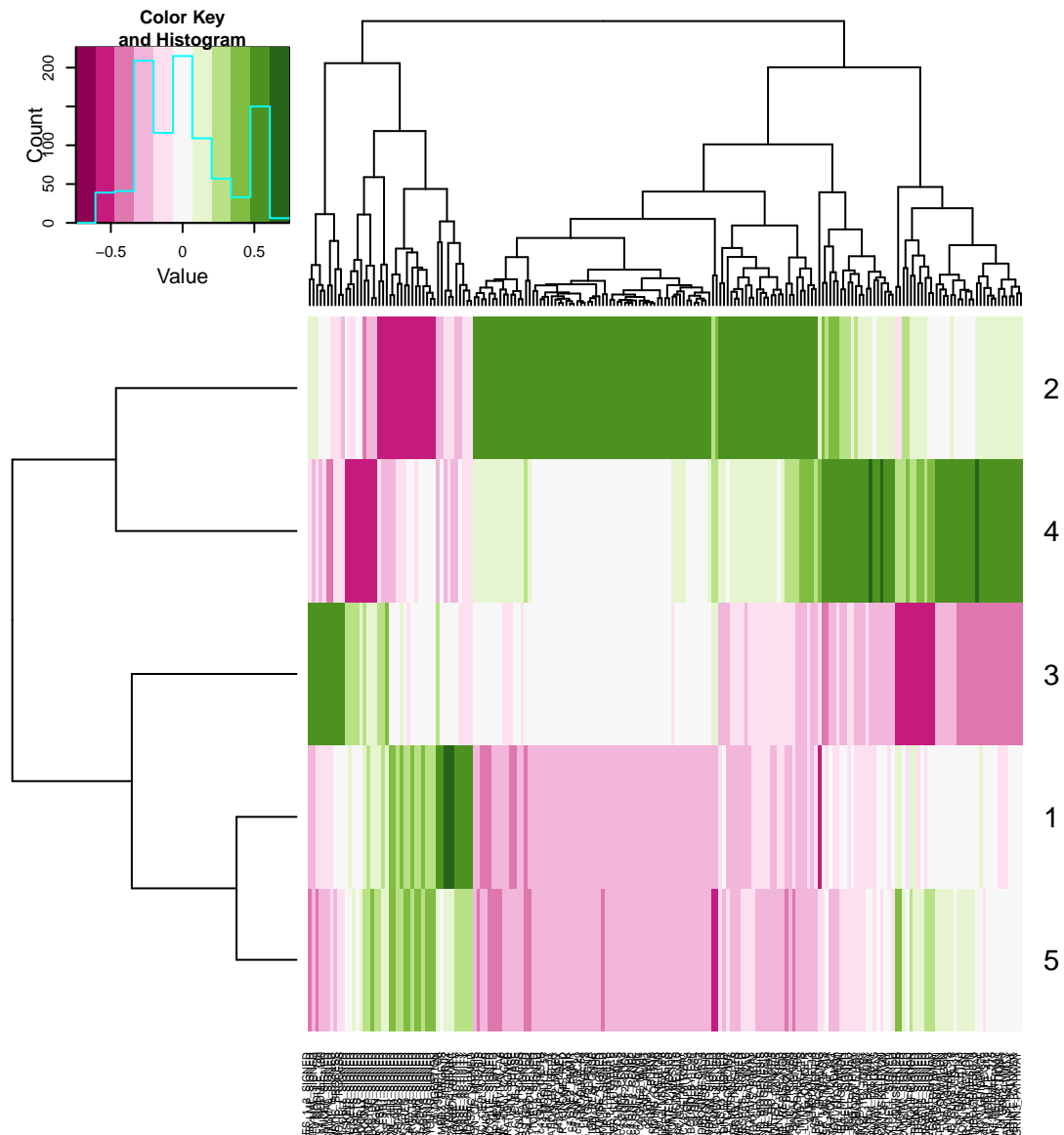
```

## 4.6 MSigDB score correlation thresholding

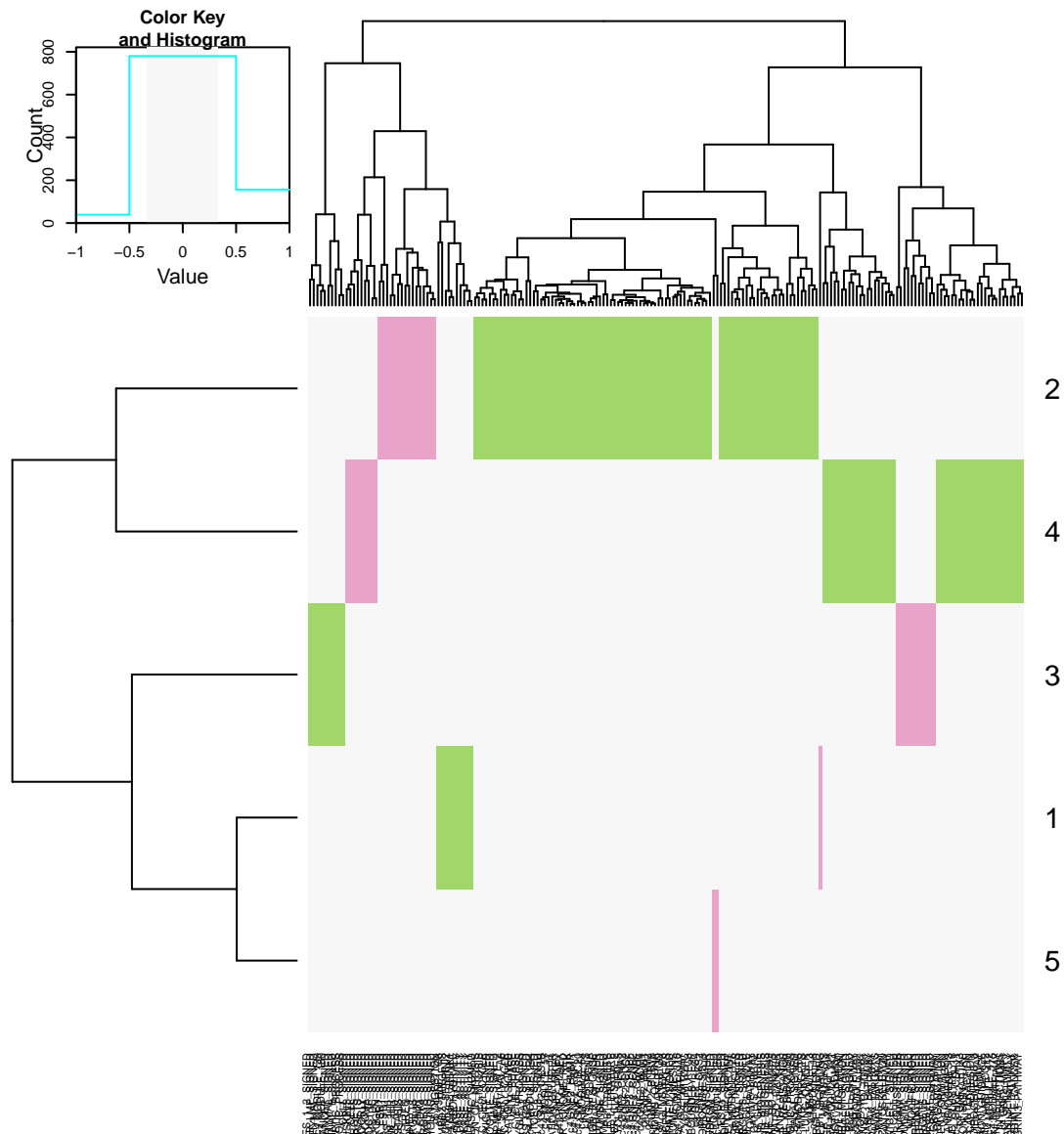
```

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

```



```
heatmap.2(xlin.scaled.sel.nmf.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))
```



```
temp.sig_id = colnames(xlin.scaled.sel.nmf.msigdb.corr)
temp.sig_class = gsub("\\\\.*", "", temp.sig_id)
temp.nsig = length(temp.sig_id)
temp.nmeta = nrow(xlin.scaled.sel.nmf.msigdb.corr)
tables = lapply(1:temp.nmeta, function(metagene_i) {
  tapply(1:temp.nsig, temp.sig_class, function(sig_class_is) {
    all_cors = xlin.scaled.sel.nmf.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)]) * sign(xlin.scaled.sel.nmf.cpv.pvals$d.surrogate),
              collapse = ",")
          })
      table = table[order(-(table$Correlation)), ]
      rownames(table) <- NULL
    }
  }
  table
}, simplify = FALSE)
})
tables

## [[1]]
## [[1]]$c1
## data frame with 0 columns and 0 rows
##
## [[1]]$c2
##
##          GeneSet Correlation Metagenes
## 1          c2.BERGER_MBD2_TARGETS      0.6714      -1
## 2 c2.REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE      0.5204      -1
## 3          c2.IGLESIAS_E2F_TARGETS_SIGNED     -0.5144       1
##
## [[1]]$c3
##          GeneSet Correlation Metagenes
## 1 c3.V$HNF1_Q6      0.5144      -1
##
## [[1]]$c4
##          GeneSet Correlation Metagenes
## 1   c4.GNF2_SPINK1      0.7429      -1
## 2   c4.GNF2_SERPINI2      0.7223      -1
##
## [[1]]$c5
##          GeneSet Correlation Metagenes
## 1   c5.CARBOXYPEPTIDASE_ACTIVITY      0.5204      -1
## 2   c5.SERINE_TYPE_PEPTIDASE_ACTIVITY      0.5191      -1
## 3 c5.SERINE_TYPE_ENDOPEPTIDASE_ACTIVITY      0.5153      -1
## 4   c5.SERINE_HYDROLASE_ACTIVITY      0.5140      -1
## 5          c5.DIGESTION      0.5093      -1
##
## [[1]]$c6
## data frame with 0 columns and 0 rows
##
## [[1]]$c7
## data frame with 0 columns and 0 rows
##
## [[2]]
## [[2]]$c1

```

```

## data frame with 0 columns and 0 rows
##
## [[2]]$c2
##                                     GeneSet
## 1                                c2.FOURNIER_ACINAR_DEVELOPMENT_LATE_2
## 2                                c2.WHITEFORD_PEDIATRIC_CANCER_MARKERS
## 3                                c2.SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
## 4                                c2.BASAKI_YBX1_TARGETS_SIGNED
## 5                                c2.WU_APOPTOSIS_BY_CDKN1A_VIA_TP53
## 6                                c2.GAVIN_FOXP3_TARGETS_CLUSTER_P6
## 7                                c2.CHIANG_LIVER_CANCER_SUBCLASS_PROLIFERATION_SIGNED
## 8                                c2.RHODES_UNDIFFERENTIATED_CANCER
## 9                                c2.SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_SIGNED
## 10                               c2.REACTOME_KINESINS
## 11                               c2.ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
## 12                               c2.SMID_BREAST_CANCER_BASAL_SIGNED
## 13                               c2.BURTON_ADIPOGENESIS_PEAK_AT_24HR
## 14                               c2.OHASHI_AURKB_TARGETS
## 15                               c2.LOPEZ_MESOTELIOMA_SURVIVAL_TIME_SIGNED
## 16                               c2.BIOCARTA_G2_PATHWAY
## 17                               c2.ZHOU_CELL_CYCLE_GENES_IN_IR_RESPONSE_24HR
## 18                               c2.RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_SIGNED
## 19                               c2.HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_SIGNED
## 20                               c2.WANG_METASTASIS_OF_BREAST_CANCER_ESR1_SIGNED
## 21                               c2.FARMER_BREAST_CANCER_CLUSTER_2
## 22                               c2.FINETTI_BREAST_CANCER_KINOME_RED
## 23                               c2.ZHAN_MULTIPLE_MYELOMA_PR_SIGNED
## 24                               c2.NAKAYAMA_SOFT_TISSUE_TUMORS_PCA2_SIGNED
## 25                               c2.REACTOME_PYRIMIDINE_METABOLISM
## 26                               c2.AMUNDSON_GAMMA_RADIATION_RESPONSE
## 27                               c2.BURTON_ADIPOGENESIS_3
## 28                               c2.REN_BOUND_BY_E2F
## 29                               c2.CHANG_CYCLING_GENES
## 30                               c2.CHANG_CORE_SERUM_RESPONSE_SIGNED
## 31                               c2.PID_FOXM1PATHWAY
## 32                               c2.MONTERO_THYROID_CANCER_POOR_SURVIVAL_SIGNED
## 33                               c2.WHITFIELD_CELL_CYCLE_LITERATURE
## 34                               c2.REACTOME_CELL_CYCLE_MITOTIC
## 35                               c2.REICHERT_MITOSIS_LIN9_TARGETS
## 36                               c2.EGUCHI_CELL_CYCLE_RB1_TARGETS
## 37                               c2.HONMA_DOCETAXEL_RESISTANCE
## 38                               c2.BOYALT_LIVER_CANCER_SUBCLASS_G23_SIGNED
## 39                               c2.RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_SIGNED
## 40 c2.REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION
## 41                               c2.HONRADO_BREAST_CANCER_BRCA1_VS_BRCA2
## 42                               c2.CHUNG_BLISTER_CYTOTOXICITY_SIGNED
## 43                               c2.LEI_MYB_TARGETS
## 44                               c2.REACTOME_UNWINDING_OF_DNA
## 45                               c2.CHEMNITZ_RESPONSE_TO_PROSTAGLANDIN_E2_SIGNED
## 46                               c2.KEGG_CELL_CYCLE
## 47                               c2.LI_LUNG_CANCER
## 48                               c2.VANTVEER_BREAST_CANCER_ESR1_SIGNED
## 49                               c2.DOANE_BREAST_CANCER_ESR1_SIGNED
## 50                               c2.BROWNE_HCMV_INFECTION_2HR_SIGNED

```

```

## 51          c2.LI_WILMS_TUMOR_VS_FETAL_KIDNEY_1_SIGNED
## 52          c2.MOLENAAR_TARGETS_OF_CCND1_AND_CDK4_SIGNED
## 53          c2.RUIZ_TNC_TARGETS_SIGNED
## 54          c2.KOBAYASHI_EGFR_SIGNALING_24HR_SIGNED
## 55          c2.VANTVEER_BREAST_CANCER_METASTASIS_SIGNED
## 56          c2.STEIN_ESRRA_TARGETS_RESPONSIVE_TO_ESTROGEN_SIGNED
## 57          c2.TANG_SENESCENCE_TP53_TARGETS_SIGNED
##      Correlation Metagenes
## 1      0.6067      2
## 2      0.5977      2
## 3      0.5947      2
## 4      0.5917      2
## 5      0.5831      2
## 6      0.5808      2
## 7      0.5636      2
## 8      0.5613      2
## 9      0.5595      2
## 10     0.5493      2
## 11     0.5493      2
## 12     0.5433      2
## 13     0.5407      2
## 14     0.5399      2
## 15     0.5377      2
## 16     0.5369      2
## 17     0.5343      2
## 18     0.5336      2
## 19     0.5328      2
## 20     0.5302      2
## 21     0.5268      2
## 22     0.5264      2
## 23     0.5234      2
## 24     0.5227      2
## 25     0.5227      2
## 26     0.5223      2
## 27     0.5215      2
## 28     0.5212      2
## 29     0.5212      2
## 30     0.5197      2
## 31     0.5189      2
## 32     0.5178      2
## 33     0.5118      2
## 34     0.5095      2
## 35     0.5088      2
## 36     0.5080      2
## 37     0.5080      2
## 38     0.5065      2
## 39     0.5050      2
## 40     0.5050      2
## 41     0.5047      2
## 42     0.5043      2
## 43     0.5024      2
## 44     0.5009      2
## 45     0.5005      2
## 46     0.5005      2

```

```

## 47      0.5001      2
## 48     -0.5058     -2
## 49     -0.5084     -2
## 50     -0.5167     -2
## 51     -0.5234     -2
## 52     -0.5377     -2
## 53     -0.5508     -2
## 54     -0.5640     -2
## 55     -0.5745     -2
## 56     -0.5842     -2
## 57     -0.6075     -2
##
## [[2]]$c3
## data frame with 0 columns and 0 rows
##
## [[2]]$c4
##      GeneSet Correlation Metagenes
## 1  c4.MODULE_54      0.5696      2
## 2  c4.GNF2_ESPL1      0.5677      2
## 3  c4.GNF2_CDC20      0.5606      2
## 4  c4.GNF2_H2AFX      0.5467      2
## 5  c4.GNF2_CKS1B      0.5456      2
## 6  c4.GNF2_MKI67      0.5441      2
## 7   c4.GNF2_HMMR      0.5407      2
## 8  c4.GNF2_CCNB2      0.5388      2
## 9  c4.MODULE_105      0.5384      2
## 10 c4.MODULE_57      0.5377      2
## 11 c4.GNF2_CENPF      0.5366      2
## 12 c4.GNF2_CCNA2      0.5358      2
## 13   c4.GNF2_TTK      0.5351      2
## 14 c4.MODULE_253      0.5336      2
## 15 c4.GNF2_CDC2      0.5328      2
## 16 c4.MODULE_126      0.5324      2
## 17 c4.MODULE_18      0.5290      2
## 18 c4.GNF2_RFC4      0.5230      2
## 19 c4.MODULE_17      0.5219      2
## 20 c4.GNF2_BUB1      0.5200      2
## 21 c4.GNF2_MCM4      0.5148      2
## 22   c4.MODULE_3      0.5148      2
## 23 c4.GNF2_BUB1B      0.5110      2
## 24 c4.GNF2_CENPE      0.5099      2
## 25 c4.GNF2_RFC3      0.5092      2
## 26 c4.GNF2_RRM2      0.5077      2
## 27 c4.GNF2_PCNA      0.5065      2
## 28 c4.GNF2_CKS2      0.5047      2
## 29 c4.MODULE_315      0.5043      2
## 30 c4.MODULE_244      0.5032      2
##
## [[2]]$c5
##      GeneSet Correlation Metagenes
## 1  c5.M_PHASE_OF_MITOTIC_CELL_CYCLE      0.5790      2
## 2      c5.CELL_CYCLE_G0_0007049      0.5771      2
## 3      c5.M_PHASE      0.5745      2
## 4      c5.MITOSIS      0.5733      2

```

```

## 5          c5.MITOTIC_CELL_CYCLE      0.5628      2
## 6          c5.REGULATION_OF_MITOSIS    0.5576      2
## 7          c5.CELL_CYCLE_PROCESS       0.5489      2
## 8          c5.CELL_CYCLE_CHECKPOINT_G0_0000075 0.5471      2
## 9          c5.CELL_CYCLE_PHASE         0.5414      2
## 10         c5.SPINDLE_ORGANIZATION_AND_BIOGENESIS 0.5260      2
## 11         c5.REGULATION_OF_CELL_CYCLE    0.5230      2
## 12         c5.MITOTIC_CELL_CYCLE_CHECKPOINT 0.5215      2
## 13         c5.NUCLEOTIDE_METABOLIC_PROCESS 0.5099      2
## 14 c5.MITOTIC_SPINDLE_ORGANIZATION_AND_BIOGENESIS 0.5077      2
##
## [[2]]$c6
## data frame with 0 columns and 0 rows
##
## [[2]]$c7
##                                     GeneSet
## 1 c7.GSE30962_PRIMARY_VS_SECONDARY_ACUTE_LCMV_INF_CD8_TCELL_SIGNED
## 2 c7.GSE24634_NAIVE_CD4_TCELL_VS_DAY3_IL4_CONV_TREG_SIGNED
## 3 c7.GSE3982_CENT_MEMORY_CD4_TCELL_VS_TH2_SIGNED
## 4 c7.GSE36476_CTRL_VS_TSST_ACT_72H_MEMORY_CD4_TCELL_YOUNG_SIGNED
## 5 c7.GSE3982_MEMORY_CD4_TCELL_VS_TH1_SIGNED
## 6 c7.GSE3982_BCELL_VS_TH1_SIGNED
## 7 c7.GSE36476_CTRL_VS_TSST_ACT_40H_MEMORY_CD4_TCELL_YOUNG_SIGNED
## Correlation Metagenes
## 1      0.5715      2
## 2     -0.5009     -2
## 3     -0.5043     -2
## 4     -0.5275     -2
## 5     -0.5298     -2
## 6     -0.5448     -2
## 7     -0.5598     -2
##
##
## [[3]]
## [[3]]$c1
## data frame with 0 columns and 0 rows
##
## [[3]]$c2
##                                     GeneSet Correlation
## 1 c2.CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_SIGNED      0.5843
## 2 c2.SMID_BREAST_CANCER_LUMINAL_B_SIGNED      0.5677
## 3 c2.CHARAFE_BREAST_CANCER_BASAL_VS_MESENCHYMAL_SIGNED      0.5178
## 4 c2.LIU_PROSTATE_CANCER_SIGNED      0.5129
## 5 c2.WAMUNYOKOLI_OVARIAN_CANCER_LMP_SIGNED      0.5129
## 6 c2.WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_SIGNED      0.5072
## 7 c2.SENGUPTA_NASOPHARYNGEAL_CARCINOMA_SIGNED     -0.5042
## 8 c2.LINDGREN_BLADDER_CANCER_CLUSTER_2B     -0.5102
## 9 c2.WOO_LIVER_CANCER_RECURRENCE_SIGNED     -0.5208
## 10 c2.SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_SIGNED     -0.5373
## 11 c2.LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_SIGNED     -0.5493
## 12 c2.LIM_MAMMARY_STEM_CELL_SIGNED     -0.5497
## 13 c2.ROY_WOUND_BLOOD_VESSEL_SIGNED     -0.5580
## 14 c2.VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_SIGNED     -0.5689
## 15 c2.SERVITJA_ISLET_HNF1A_TARGETS_SIGNED     -0.5771

```

```

##      Metagenes
## 1      -3
## 2      -3
## 3      -3
## 4      -3
## 5      -3
## 6      -3
## 7       3
## 8       3
## 9       3
## 10      3
## 11      3
## 12      3
## 13      3
## 14      3
## 15      3
##
## [[3]]$c3
## data frame with 0 columns and 0 rows
##
## [[3]]$c4
##      GeneSet Correlation Metagenes
## 1 c4.MODULE_180      0.5813      -3
## 2 c4.MODULE_139      0.5369      -3
##
## [[3]]$c5
##      GeneSet Correlation Metagenes
## 1 c5.GLYCOPROTEIN_BIOSYNTHETIC_PROCESS      0.5238      -3
## 2 c5.GLYCOPROTEIN_METABOLIC_PROCESS      0.5125      -3
## 3 c5.PEPTIDYL_TYROSINE_MODIFICATION      -0.5016       3
##
## [[3]]$c6
##      GeneSet Correlation Metagenes
## 1 c6.LEF1_UP.V1_SIGNED      -0.5937       3
##
## [[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.PID_INTEGRIN5_PATHWAY
## 2 c2.PID_SYNDECAN_1_PATHWAY
## 3 c2.BURTON_ADIPOGENESIS_8
## 4 c2.ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE
## 5 c2.KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC
## 6 c2.PID_INTEGRIN1_PATHWAY
## 7 c2.PID_UPA_UPAR_PATHWAY
## 8 c2.PID_INTEGRIN3_PATHWAY
## 9 c2.POTTI_TOPOTECAN_SENSITIVITY

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```

## 10          c2.KEGG_FOCAL_ADHESION
## 11          c2.REACTOME_COLLAGEN_FORMATION
## 12          c2.KEGG_ECM_RECEPTOR_INTERACTION
## 13          c2.REACTOME_CELL_EXTRACELLULAR_MATRIX_INTERACTIONS
## 14          c2.YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_16
## 15          c2.VERRECCHIA_EARLY_RESPONSE_TO_TGFB1
## 16          c2.HELLEBREKERS_SILENCED_DURING_TUMOR_ANGIOGENESIS
## 17          c2.PID_INTEGRIN_A9B1_PATHWAY
## 18          c2.REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION
## 19          c2.PID_INTEGRIN_CS_PATHWAY
## 20          c2.KEGG_REGULATION_OF_ACTIN_CYTOSKELETON
## 21          c2.PID_FAK_PATHWAY
## 22          c2.GILDEA_METASTASIS
## 23          c2.PID_AVB3_INTEGRIN_PATHWAY
## 24          c2.PID_SYNDECAN_4_PATHWAY
## 25          c2.WU_CELL_MIGRATION
## 26          c2.KARAKAS_TGFB1_SIGNALING
## 27          c2.WIEDERSCHAIN_TARGETS_OF_BMI1_AND_PCGF2
## 28          c2.AGARWAL_AKT_PATHWAY_TARGETS
## 29          c2.YAMASHITA_METHYLATED_IN_PROSTATE_CANCER
## 30          c2.AMIT_SERUM_RESPONSE_240_MCF10A
## 31          c2.KRIEG_HYPOXIA_NOT_VIA_KDM3A
## 32          c2.ELVIDGE_HIF1A_AND_HIF2A_TARGETS_SIGNED
## 33          c2.REN_ALVEOLAR_RHABDOMYOSARCOMA_SIGNED
## 34          c2.PASINI_SUZ12_TARGETS_SIGNED
## 35          c2.MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_SIGNED
## 36          c2.RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_SIGNED
##      Correlation Metagenes
## 1      0.6182      4
## 2      0.6088      4
## 3      0.6080      4
## 4      0.6002      4
## 5      0.5930      4
## 6      0.5852      4
## 7      0.5642      4
## 8      0.5600      4
## 9      0.5597      4
## 10     0.5481      4
## 11     0.5481      4
## 12     0.5473      4
## 13     0.5451      4
## 14     0.5357      4
## 15     0.5278      4
## 16     0.5244      4
## 17     0.5233      4
## 18     0.5196      4
## 19     0.5192      4
## 20     0.5177      4
## 21     0.5132      4
## 22     0.5124      4
## 23     0.5106      4
## 24     0.5106      4
## 25     0.5076      4
## 26     0.5061      4

```

```

## 27      0.5034      4
## 28      0.5019      4
## 29      0.5016      4
## 30      0.5004      4
## 31      0.5004      4
## 32     -0.5132     -4
## 33     -0.5211     -4
## 34     -0.5496     -4
## 35     -0.5803     -4
## 36     -0.5870     -4
##
## [[4]]$c3
## data frame with 0 columns and 0 rows
##
## [[4]]$c4
##      GeneSet Correlation Metagenes
## 1  c4.GNF2_MMP1      0.5904      4
## 2  c4.MODULE_321      0.5694      4
## 3  c4.MODULE_562      0.5526      4
## 4  c4.GNF2_CDH11      0.5439      4
## 5   c4.GNF2_PTX3      0.5376      4
## 6  c4.MODULE_275      0.5124      4
## 7  c4.MODULE_412      0.5019      4
##
## [[4]]$c5
##      GeneSet Correlation Metagenes
## 1      c5.COLLAGEN      0.5316      4
## 2      c5.AXON_GUIDANCE      0.5237      4
## 3  c5.TISSUE_DEVELOPMENT      0.5233      4
##
## [[4]]$c6
## data frame with 0 columns and 0 rows
##
## [[4]]$c7
##
##      GeneSet
## 1      c7.GSE3982_DC_VS_BCELL_SIGNED
## 2      c7.GSE3982_MAC_VS_BCELL_SIGNED
## 3      c7.GSE27786_NKCELL_VS_NKTCELL_SIGNED
## 4      c7.GSE22886_NAIVE_TCELL_VS_DC_SIGNED
## 5      c7.GSE29618_BCELL_VS_MONOCYTE_SIGNED
## 6      c7.GSE1460_CD4_THYMOCYTE_VS_THYMIC_STROMAL_CELL_SIGNED
## 7  c7.GSE1460_INTRATHYMIC_T_PROGENITOR_VS_THYMIC_STROMAL_CELL_SIGNED
##      Correlation Metagenes
## 1      0.5417      4
## 2      0.5083      4
## 3      0.5016      4
## 4     -0.5012     -4
## 5     -0.5031     -4
## 6     -0.5514     -4
## 7     -0.6043     -4
##
##
## [[5]]
## [[5]]$c1

```



```
## data frame with 0 columns and 0 rows
##
## [[5]]$c2
##                               GeneSet Correlation Metagenes
## 1 c2.HAHTOLA_SEZARY_SYNDROM_SIGNED      -0.5089          5
## 2          c2.WINTER_HYPOXIA_SIGNED      -0.5300          5
##
## [[5]]$c3
## data frame with 0 columns and 0 rows
##
## [[5]]$c4
## data frame with 0 columns and 0 rows
##
## [[5]]$c5
## data frame with 0 columns and 0 rows
##
## [[5]]$c6
## data frame with 0 columns and 0 rows
##
## [[5]]$c7
## data frame with 0 columns and 0 rows
```

```
print(asreg.result)
```

```
## glmulti.analysis
## Method: h / Fitting: coxph / IC used: bic
## Level: 2 / Marginality: TRUE
## From 100 models:
## Best IC: 586.982783576264
## Best model:
## [1] "Surv(time, event) ~ 1 + mg.2 + mg.4"
## Evidence weight: 0.178839068714947
## Worst IC: 598.680887369867
## 4 models within 2 IC units.
## 47 models to reach 95% of evidence weight.
```

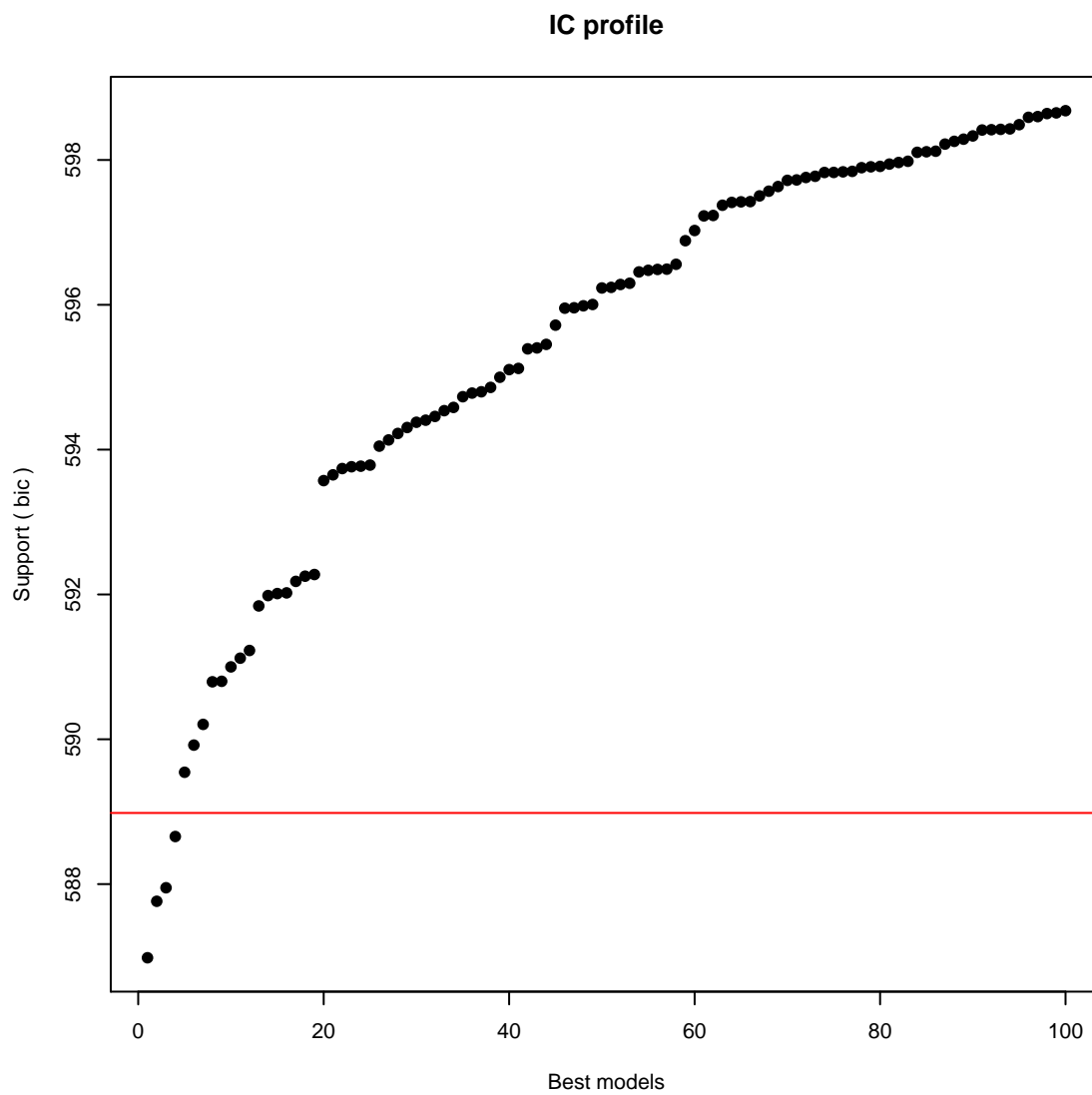
```
coef(asreg.result)
```

##	Estimate	Uncond. variance	Nb models	Importance	+/- (alpha=0.05)
## mg.1:mg.5	-0.04305	0.01590	3	0.004536	0.2501
## mg.1:mg.3	0.06329	0.02841	5	0.005286	0.3344
## mg.1:mg.4	0.08138	0.06786	8	0.010086	0.5168
## mg.3:mg.5	0.13560	0.19571	8	0.010353	0.8776
## mg.1:mg.2	-0.32611	0.61494	12	0.019221	1.5556
## mg.4:mg.5	0.05730	0.30744	6	0.021360	1.0999
## mg.2:mg.5	-0.44153	2.68816	13	0.046133	3.2525
## mg.3:mg.4	1.29553	7.77189	17	0.053343	5.5303
## mg.2:mg.3	1.52913	11.06376	20	0.062866	6.5984
## mg.2:mg.4	-2.69795	29.94018	25	0.143015	10.8546
## mg.1	0.12389	0.12171	53	0.154331	0.6921
## mg.3	0.18971	1.30123	66	0.330022	2.2629
## mg.5	-1.79547	5.65647	58	0.467331	4.7180
## mg.4	2.72919	5.25524	72	0.720460	4.5476
## mg.2	7.27130	4.08075	96	0.990789	4.0073

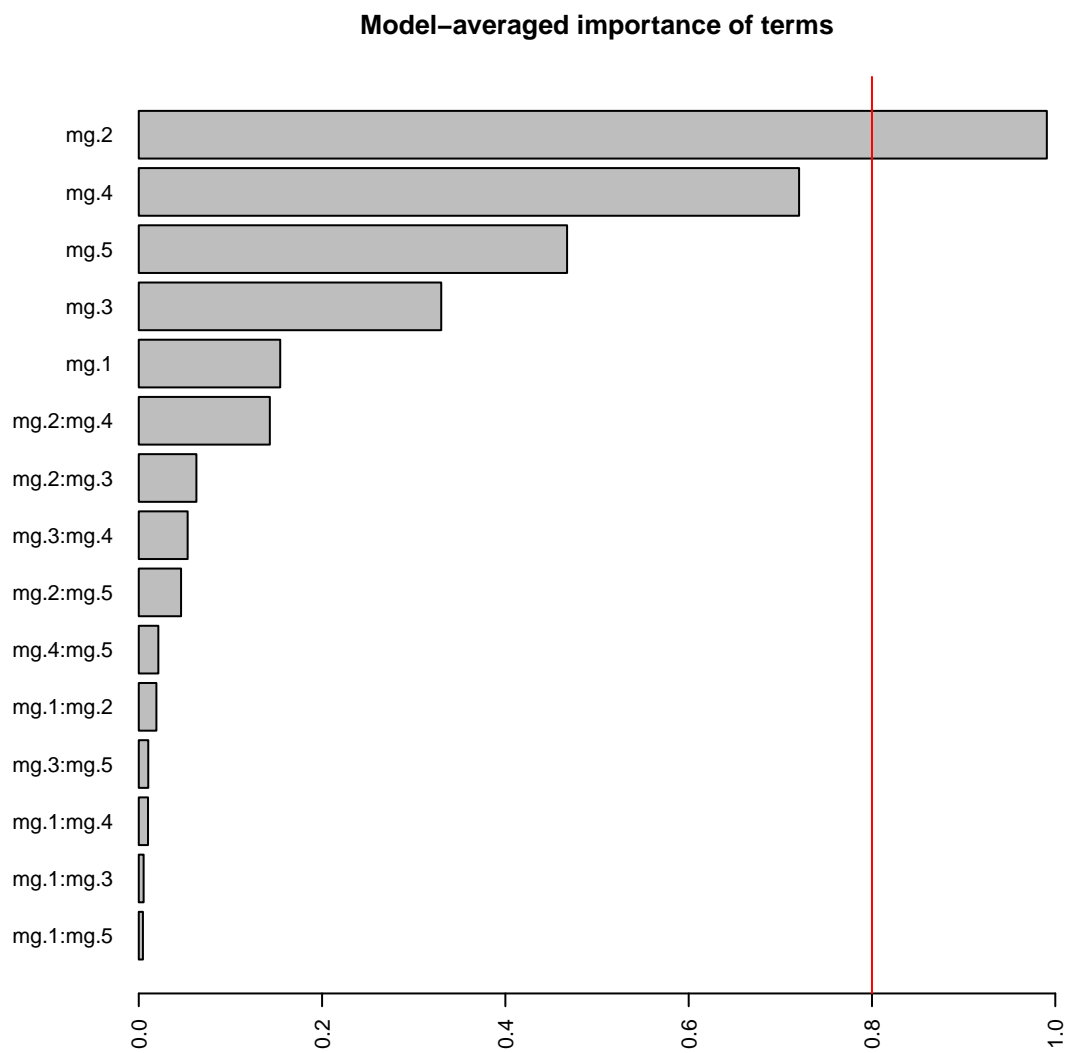
```
summary(asreg.result@objects[[1]])

## Call:
## fitfunc(formula = as.formula(x), data = data)
##
## n= 104, number of events= 77
##
##      coef exp(coef) se(coef)    z Pr(>|z|)
## mg.2   7.21  1350.26    1.35 5.33 9.6e-08
## mg.4   3.47   32.26    1.25 2.78 0.0054
##
##      exp(coef) exp(-coef) lower .95 upper .95
## mg.2   1350.3   0.000741    95.53   19085
## mg.4    32.3   0.031001     2.79     374
##
## Concordance= 0.706 (se = 0.036 )
## Rsquare= 0.302 (max possible= 0.997 )
## Likelihood ratio test= 37.4 on 2 df, p=7.48e-09
## Wald test = 40.3 on 2 df, p=1.81e-09
## Score (logrank) test = 42.5 on 2 df, p=5.8e-10
```

```
plot(asreg.result, type = "p")
```

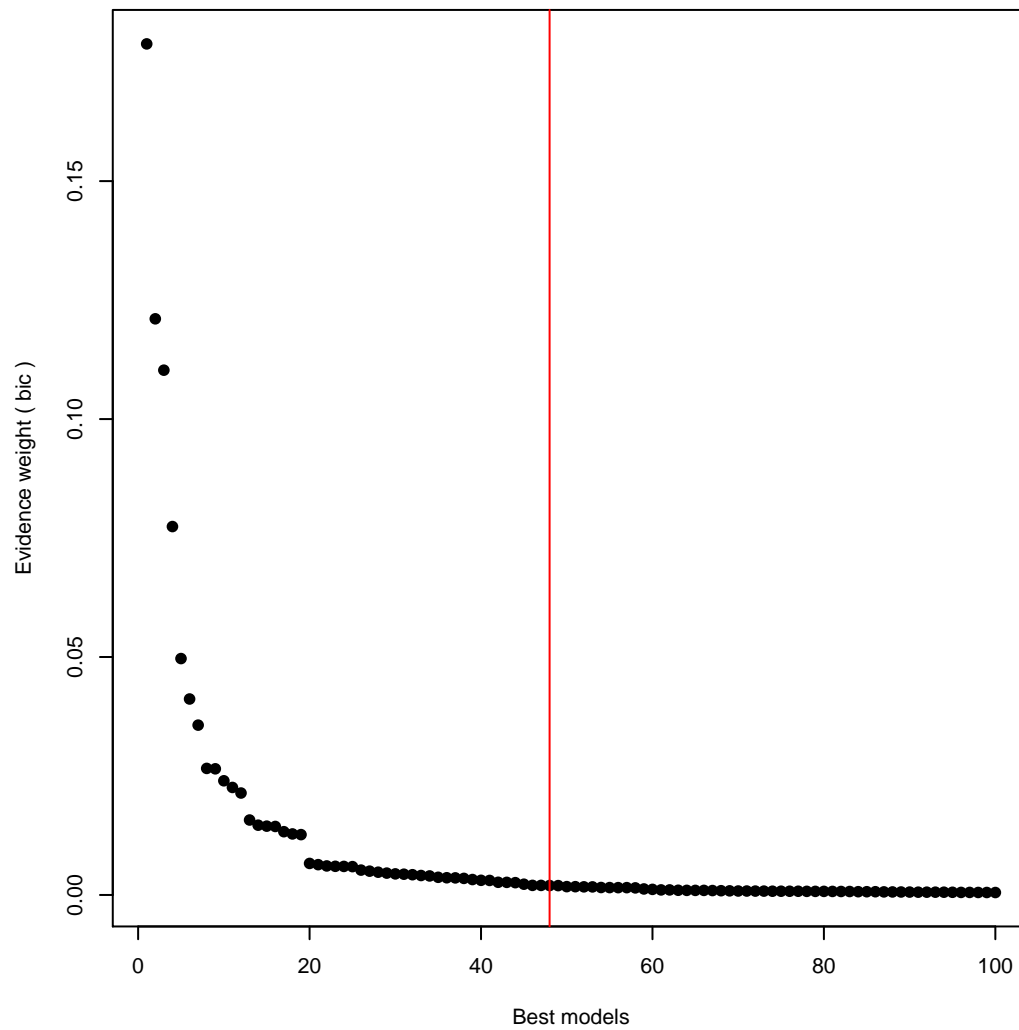


```
plot(asreg.result, type = "s")
```



```
plot(asreg.result, type = "w")
```

Profile of model weights

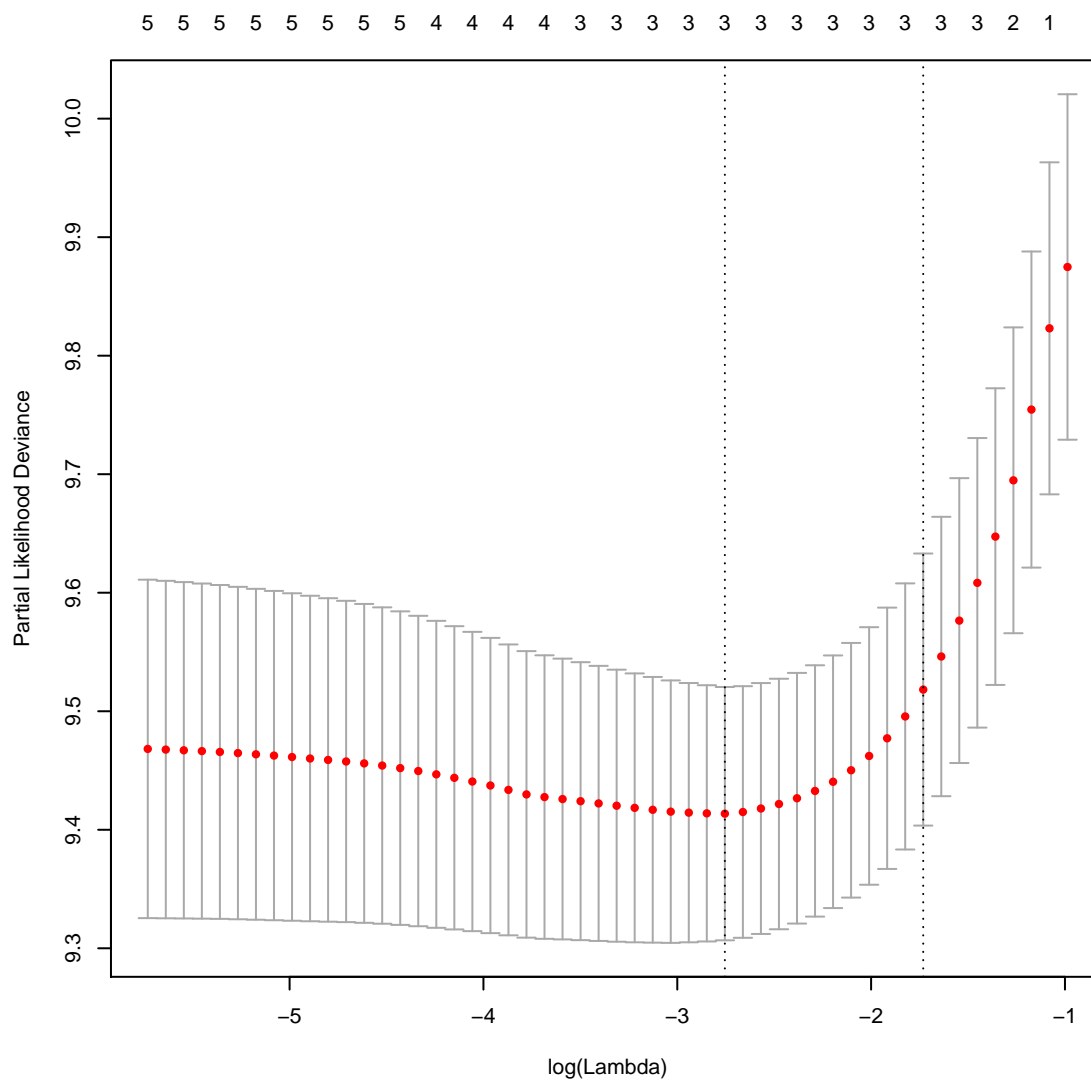


```
glmnet.coef.1se
## 5 x 1 sparse Matrix of class "dgCMatrix"
##           1
## mg.1  .
## mg.2  3.9181
## mg.3  .
## mg.4  0.7573
## mg.5 -1.3025

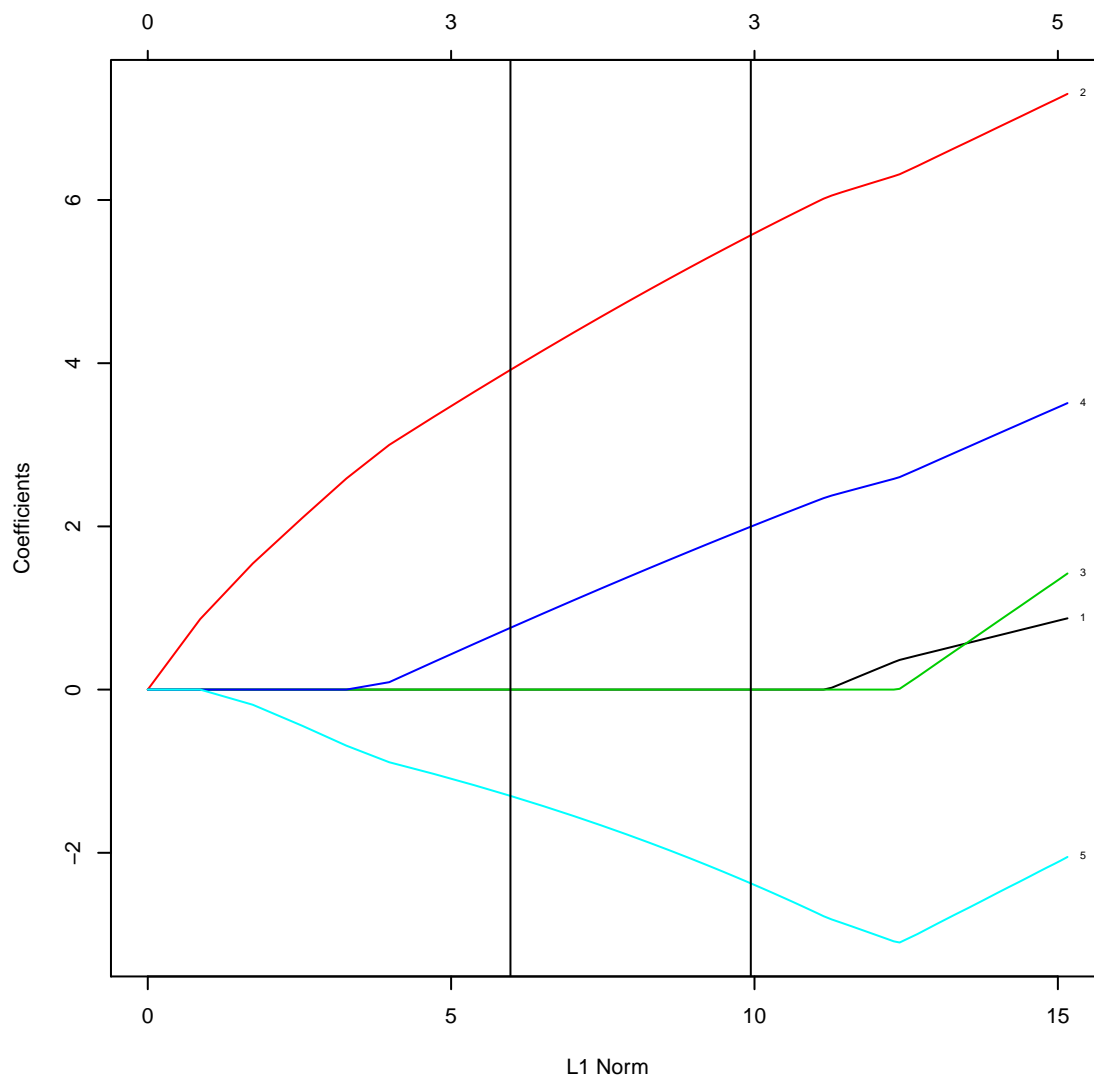
glmnet.coef.min
## 5 x 1 sparse Matrix of class "dgCMatrix"
##           1
## mg.1  .
## mg.2  5.568
## mg.3  .
## mg.4  1.997
```

```
## mg.5 -2.374
```

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



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



```
adaglmnet.coef.1se/adaglmnet.weights

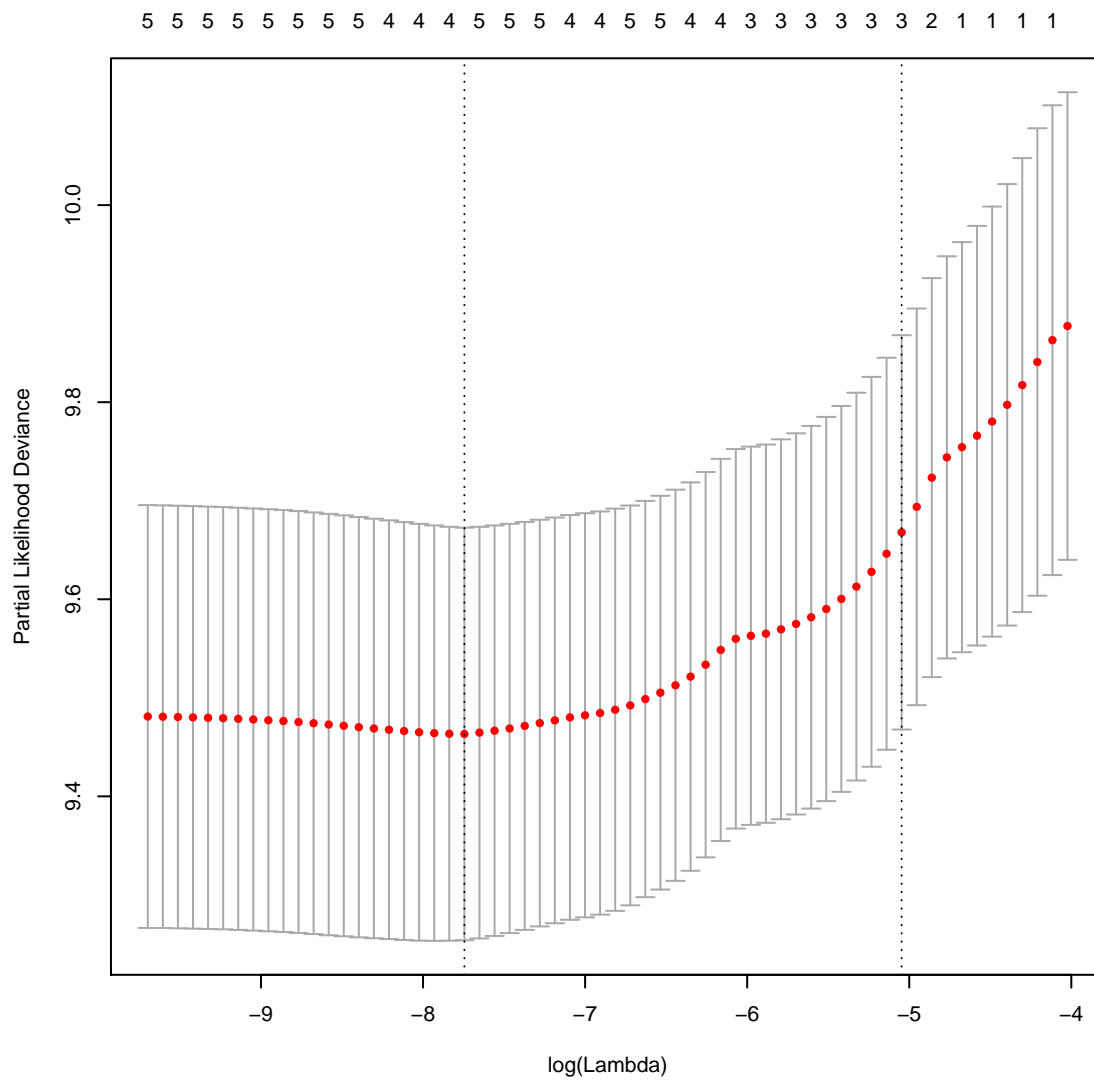
## 5 x 1 sparse Matrix of class "dgCMatrix"
##           1
## mg.1  -0.09148
## mg.2    .
## mg.3  -5.40187
## mg.4    .
## mg.5 -10.99728

adaglmnet.coef.min/adaglmnet.weights

## 5 x 1 sparse Matrix of class "dgCMatrix"
##           1
## mg.1   0.5029
## mg.2 346.6484
## mg.3    .
## mg.4  38.0964
```

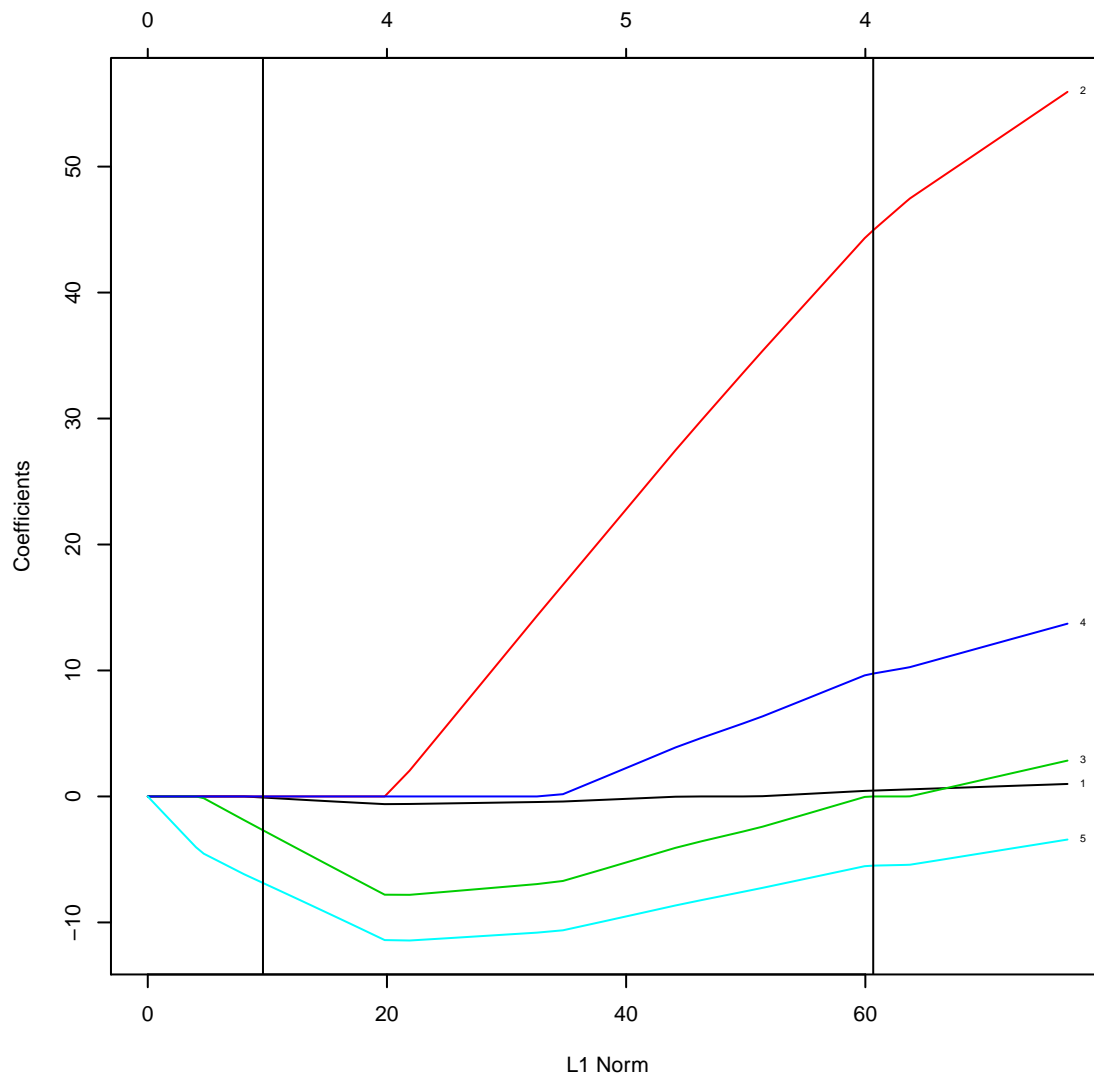
```
## mg.5 -8.7940
```

```
plot(adaglmnet.fit.cv)
```



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





## 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_US.iso885915      LC_NUMERIC=C
##  [3] LC_TIME=en_US.iso885915      LC_COLLATE=en_US.iso885915
##  [5] LC_MONETARY=en_US.iso885915  LC_MESSAGES=en_US.iso885915
##  [7] LC_PAPER=en_US.iso885915     LC_NAME=en_US.iso885915
##  [9] LC_ADDRESS=en_US.iso885915   LC_TELEPHONE=en_US.iso885915
## [11] LC_MEASUREMENT=en_US.iso885915 LC_IDENTIFICATION=en_US.iso885915
##
## 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 stargazer_5.1
## [7] gplots_2.14.2 NMF_0.20.4 synchronicity_1.1.4
## [10] bigmemory_4.4.6 BH_1.54.0-5 bigmemory.sri_0.1.3
## [13] Biobase_2.26.0 BiocGenerics_0.12.1 cluster_1.15.3
## [16] rngtools_1.2.4 pkgmaker_0.22 registry_0.2
## [19] RColorBrewer_1.0-5 energy_1.6.2 glmnet_1.9-8
## [22] Matrix_1.1-4 glmulti_1.0.7 rJava_0.9-6
## [25] xtable_1.7-4
##
## 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 compiler_3.1.1
## [7] digest_0.6.4 gdata_2.13.3 ggplot2_1.0.0
## [10] grid_3.1.1 gridBase_0.4-7 gtable_0.1.2
## [13] gtools_3.4.1 KernSmooth_2.23-13 lattice_0.20-29
## [16] MASS_7.3-35 munsell_0.4.2 plyr_1.8.1
## [19] proto_0.3-10 Rcpp_0.11.3 reshape2_1.4
## [22] scales_0.2.4 stringr_0.6.2 tools_3.1.1

sessionInfo()

## R version 3.1.1 (2014-07-10)
## Platform: x86_64-unknown-linux-gnu (64-bit)
##
## locale:
## [1] LC_CTYPE=en_US.iso885915 LC_NUMERIC=C
## [3] LC_TIME=en_US.iso885915 LC_COLLATE=en_US.iso885915
## [5] LC_MONETARY=en_US.iso885915 LC_MESSAGES=en_US.iso885915
## [7] LC_PAPER=en_US.iso885915 LC_NAME=en_US.iso885915
## [9] LC_ADDRESS=en_US.iso885915 LC_TELEPHONE=en_US.iso885915
## [11] LC_MEASUREMENT=en_US.iso885915 LC_IDENTIFICATION=en_US.iso885915
##
## 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 NMF_0.20.4
## [10] synchronicity_1.1.4 bigmemory_4.4.6 BH_1.54.0-5
## [13] bigmemory.sri_0.1.3 Biobase_2.26.0 BiocGenerics_0.12.1
## [16] cluster_1.15.3 rngtools_1.2.4 pkgmaker_0.22
## [19] registry_0.2 energy_1.6.2 survival_2.37-7
## [22] 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
```