SIS NMF Final: Diagnosis to DSD

November 29, 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 [NO: bigmemory] | Cores 31/32
##  To enable shared memory capabilities, try:  install.extras('
## NMF
## ')

library(nnls)

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
```

```r
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
```

```r
load("image.rda")
```

2 Probe selection

```r
table(cpss.sis$sel)
```

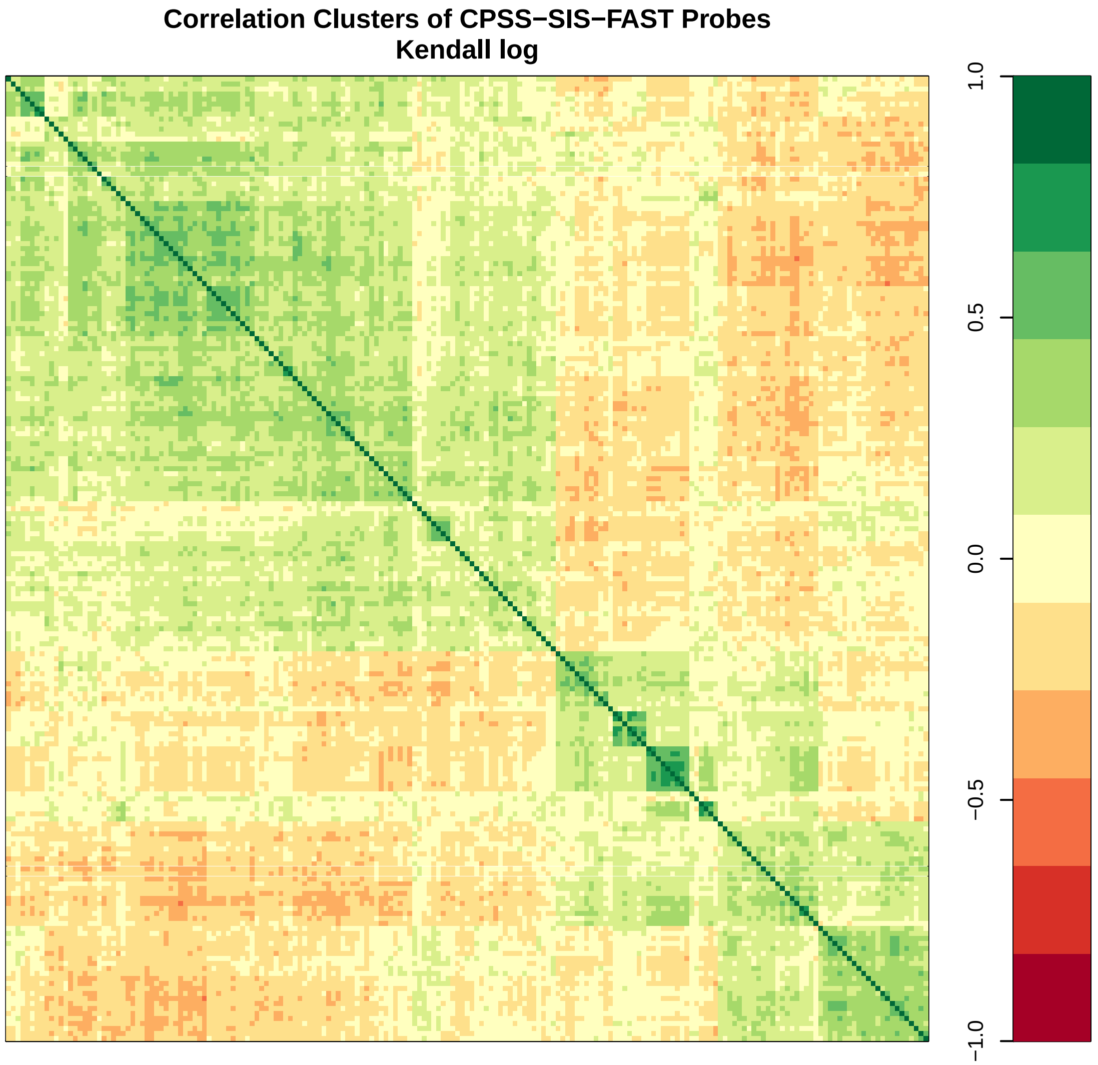
```
##
## FALSE  TRUE
## 12807   193
```

```r
mean(cpss.sis$sel)
```

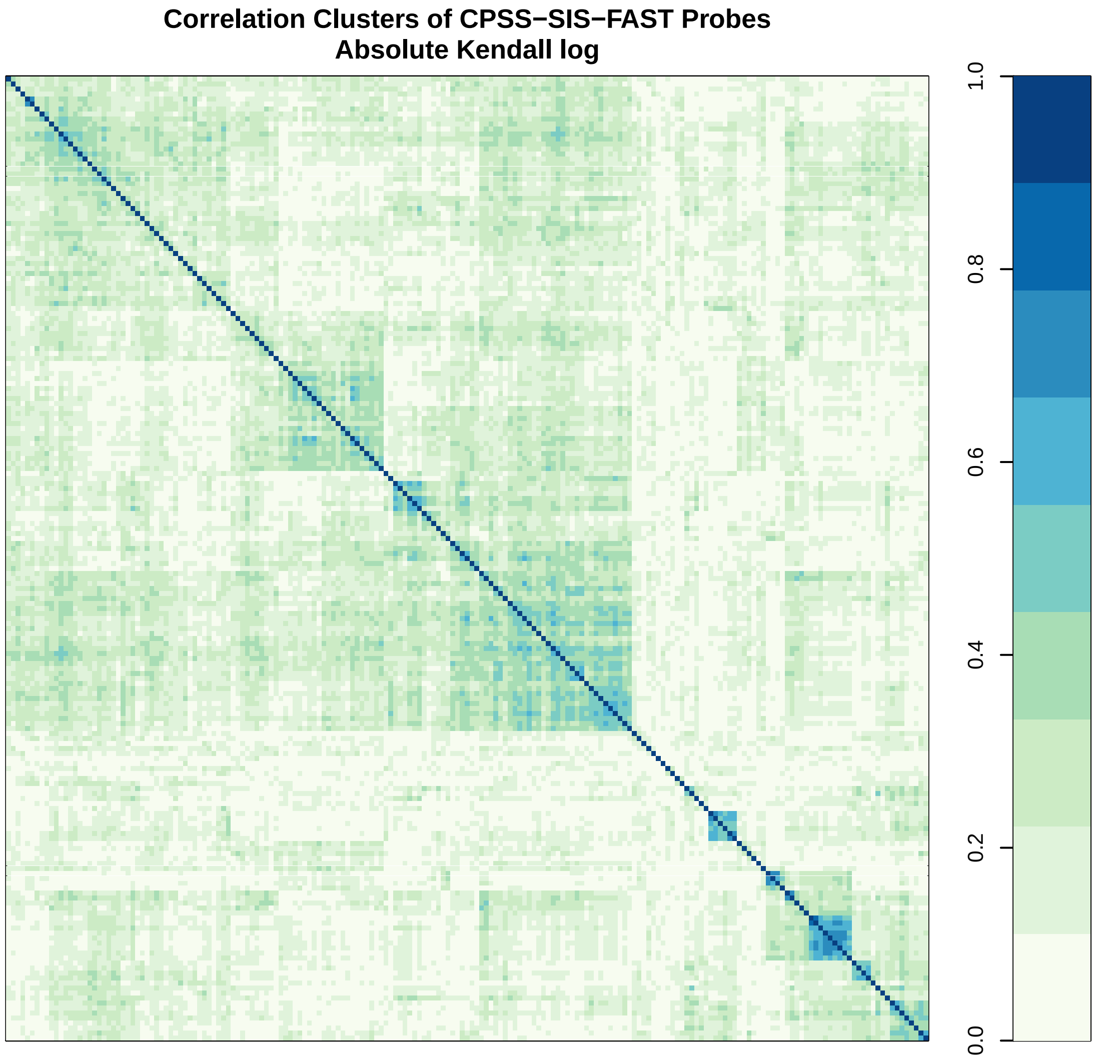
```
## [1] 0.01485
```

3 Expression correlation

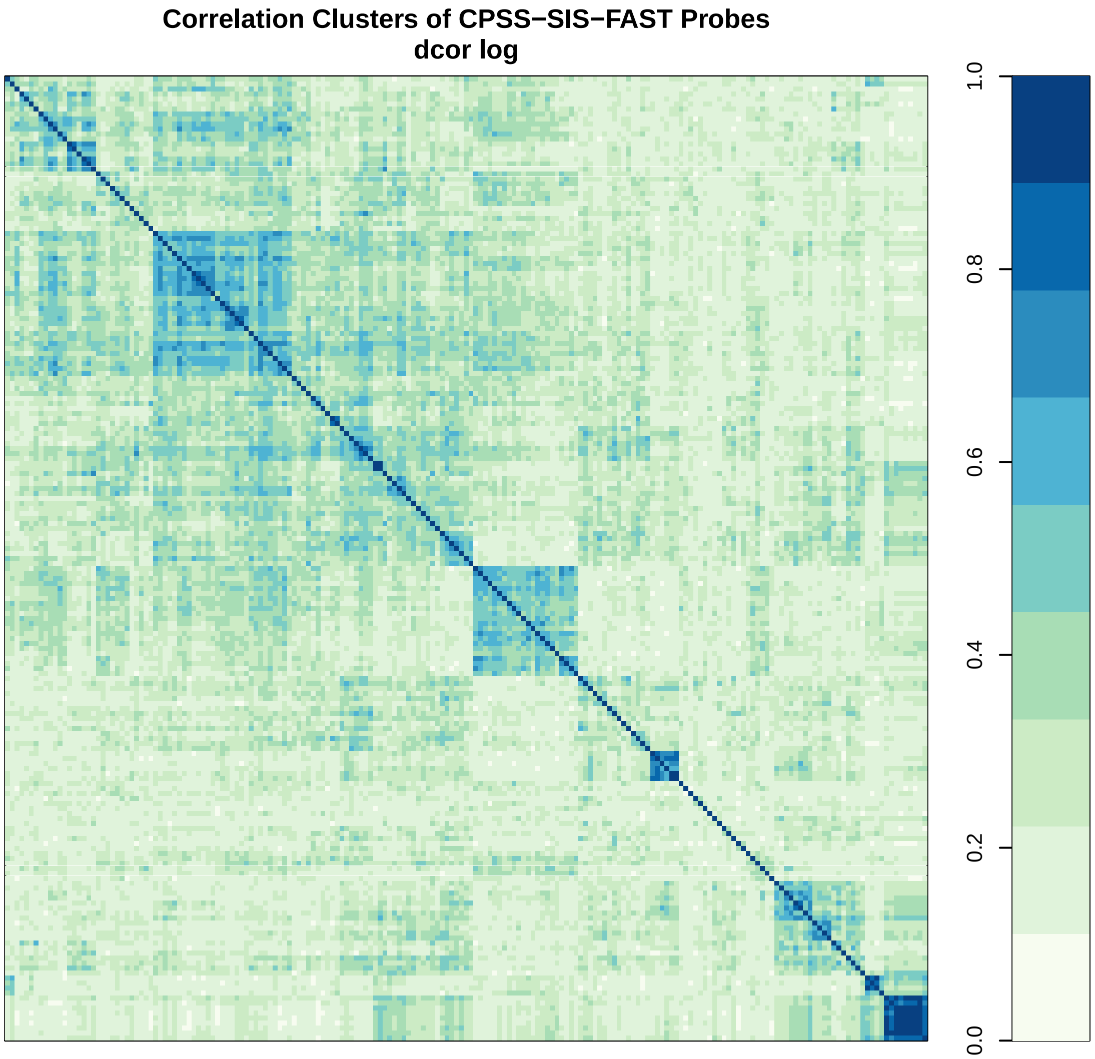
```r
corPlot(x.sel.kcor, main = "Correlation Clusters of CPSS-SIS-FAST Probes\nKendall log",
    useRaster = FALSE)
```



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

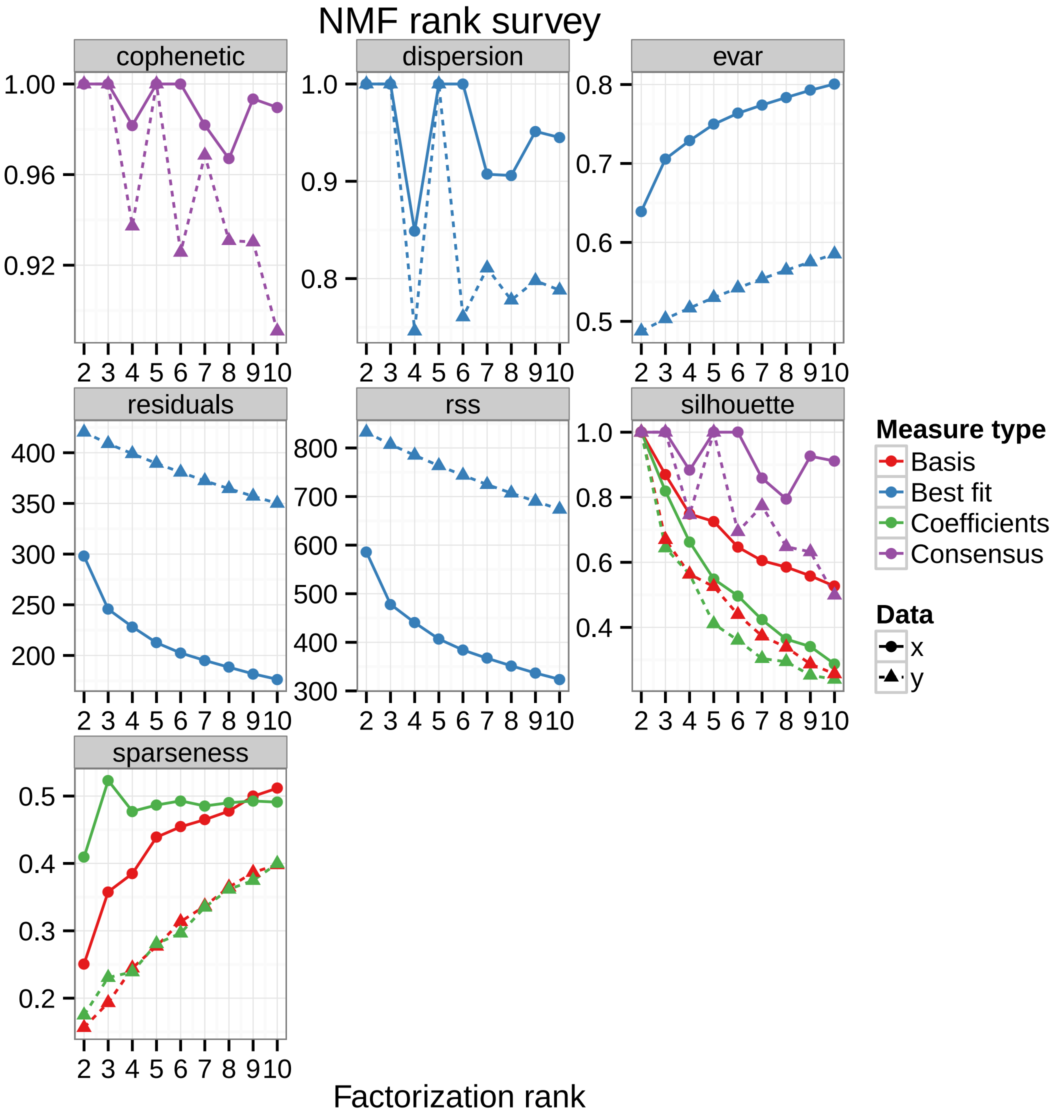


```
corPlot(x.sel.dcor, zlim = c(0, 1), pal = "GnBu", main = "Correlation Clusters of CPSS-SIS-FAST Probes\n
    useRaster = FALSE)
```

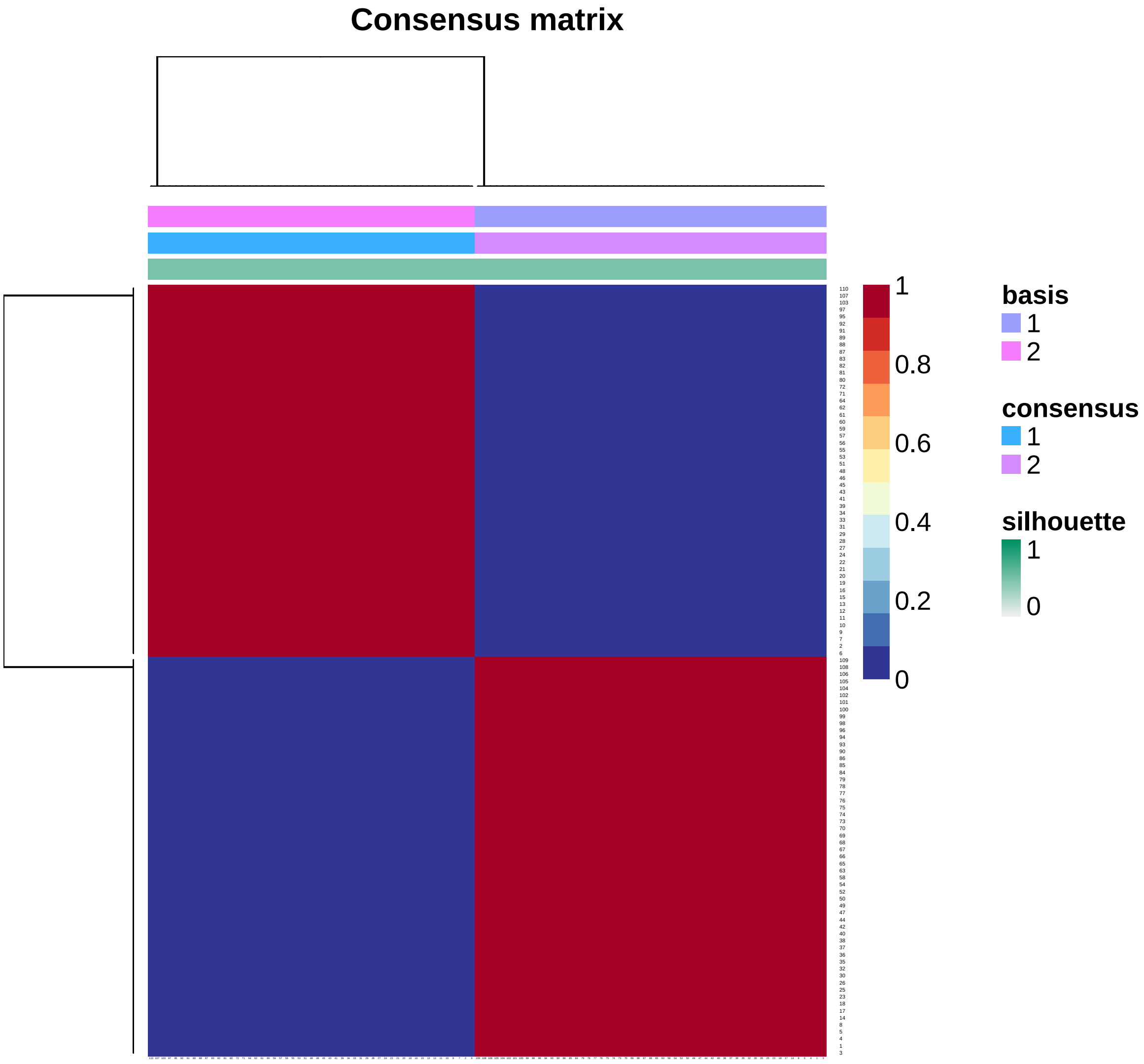


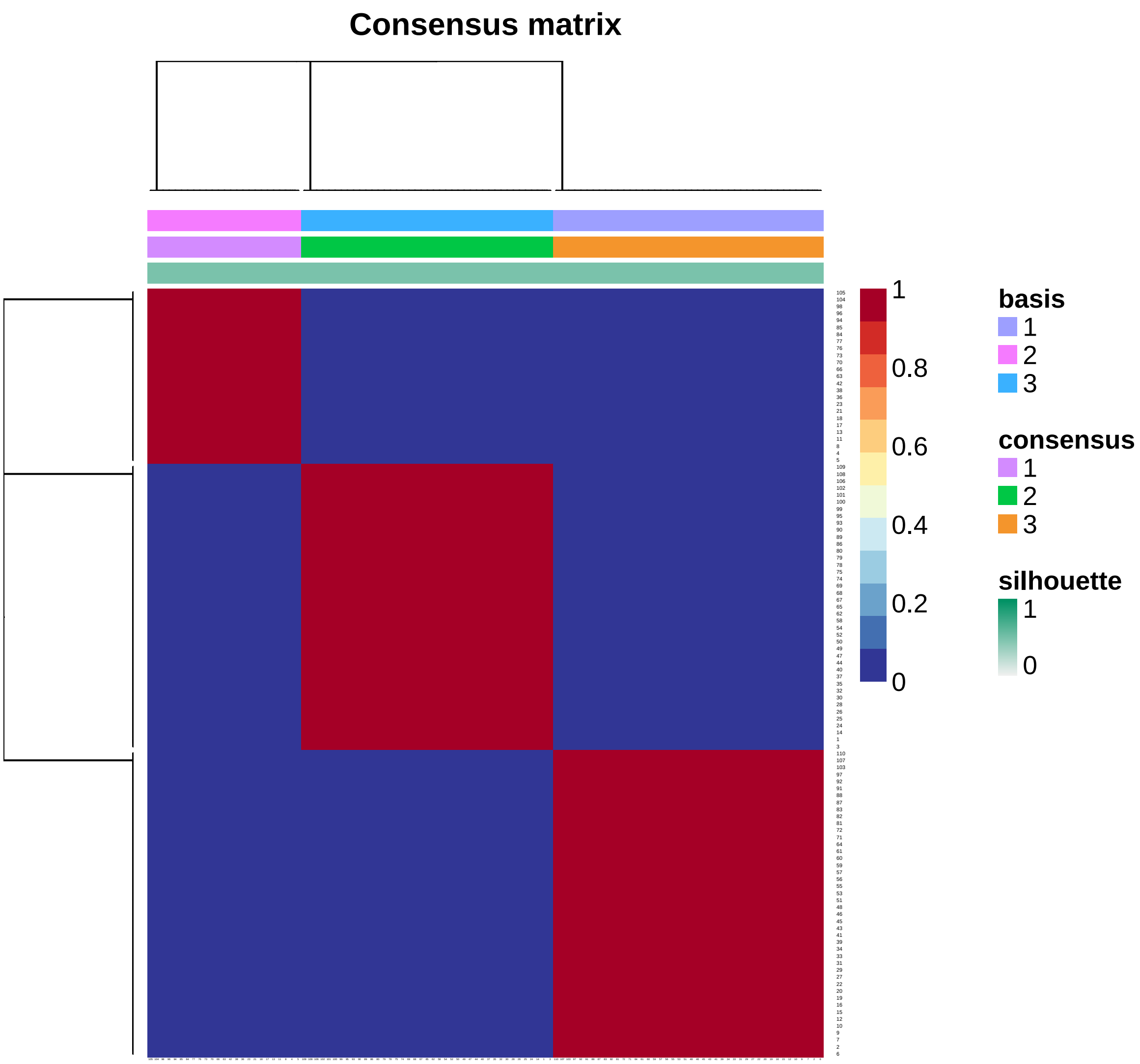
4 Factorization

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



```
for (i in nmf.runs.rank$fit) {
    consensusmap(i)
}
```


Consensus matrix
110
107
103
97
95
92
91
89
88
87
83
82
81
80
72
71
64
62
61
60
59
57
56
55
53
51
48
46
45
43
41
39
34
33
31
29
28
27
24
22
21
20
19
16
15
13
12
11
10
9
7
2
6
109
108
106
105
104
102
101
100
99
98
96
94
93
90
86
85
84
79
78
77
76
75
74
73
70
69
68
67
66
65
63
58
54
52
50
49
47
44
42
40
38
37
36
35
32
30
26
25
23
18
17
14
8
5
4
1
3
1
0.8
0.6
0.4
0.2
0
basis
1
2
consensus
1
2
silhouette
1
0


Consensus matrix
105
104
98
96
94
85
84
77
76
73
70
66
63
42
38
36
23
21
18
17
13
11
8
4
5
109
108
106
102
101
100
99
95
93
90
89
86
80
79
78
75
74
69
68
67
65
62
58
54
52
50
49
47
44
40
37
35
32
30
28
26
25
24
14
1
3
110
107
103
97
92
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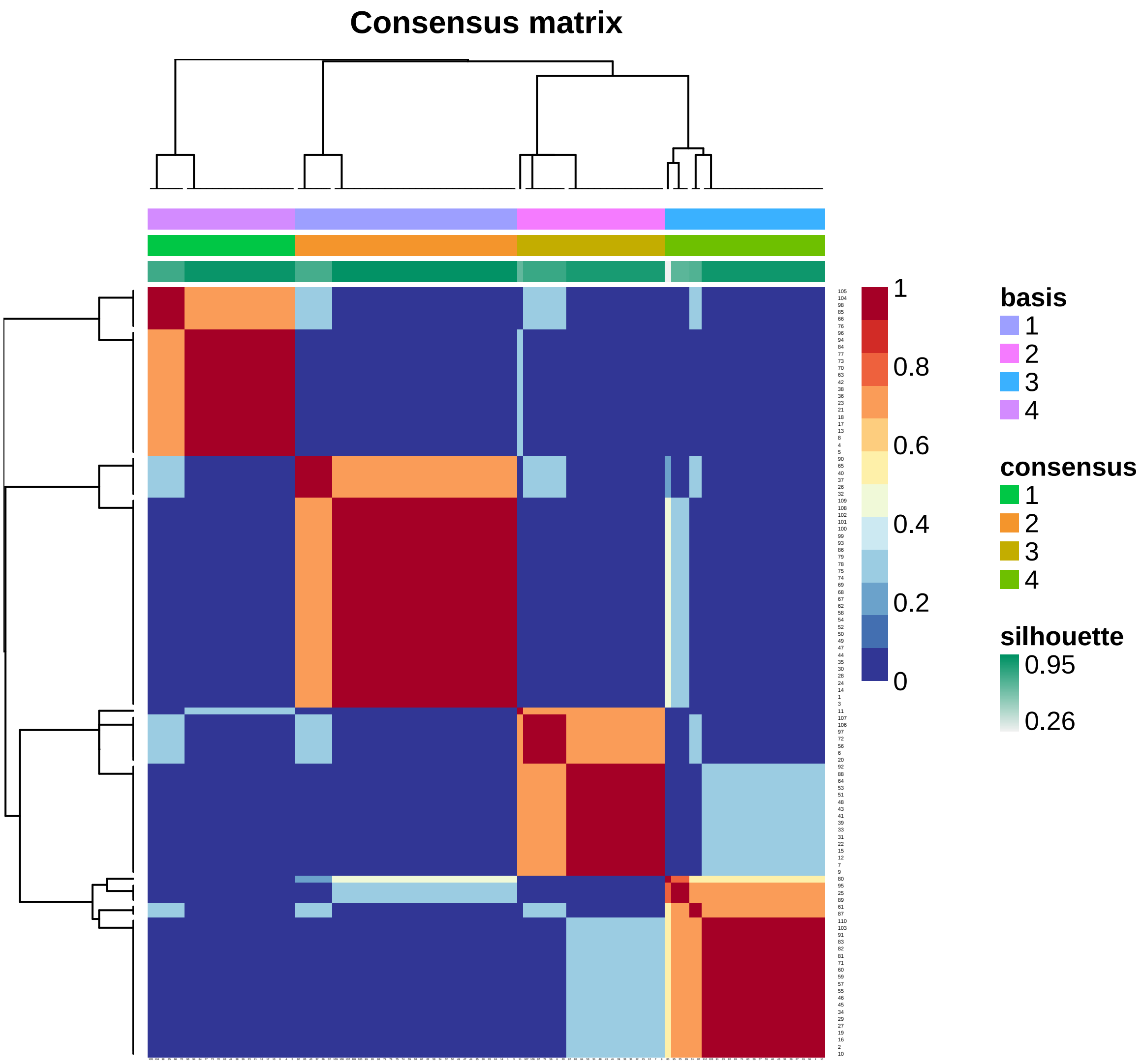
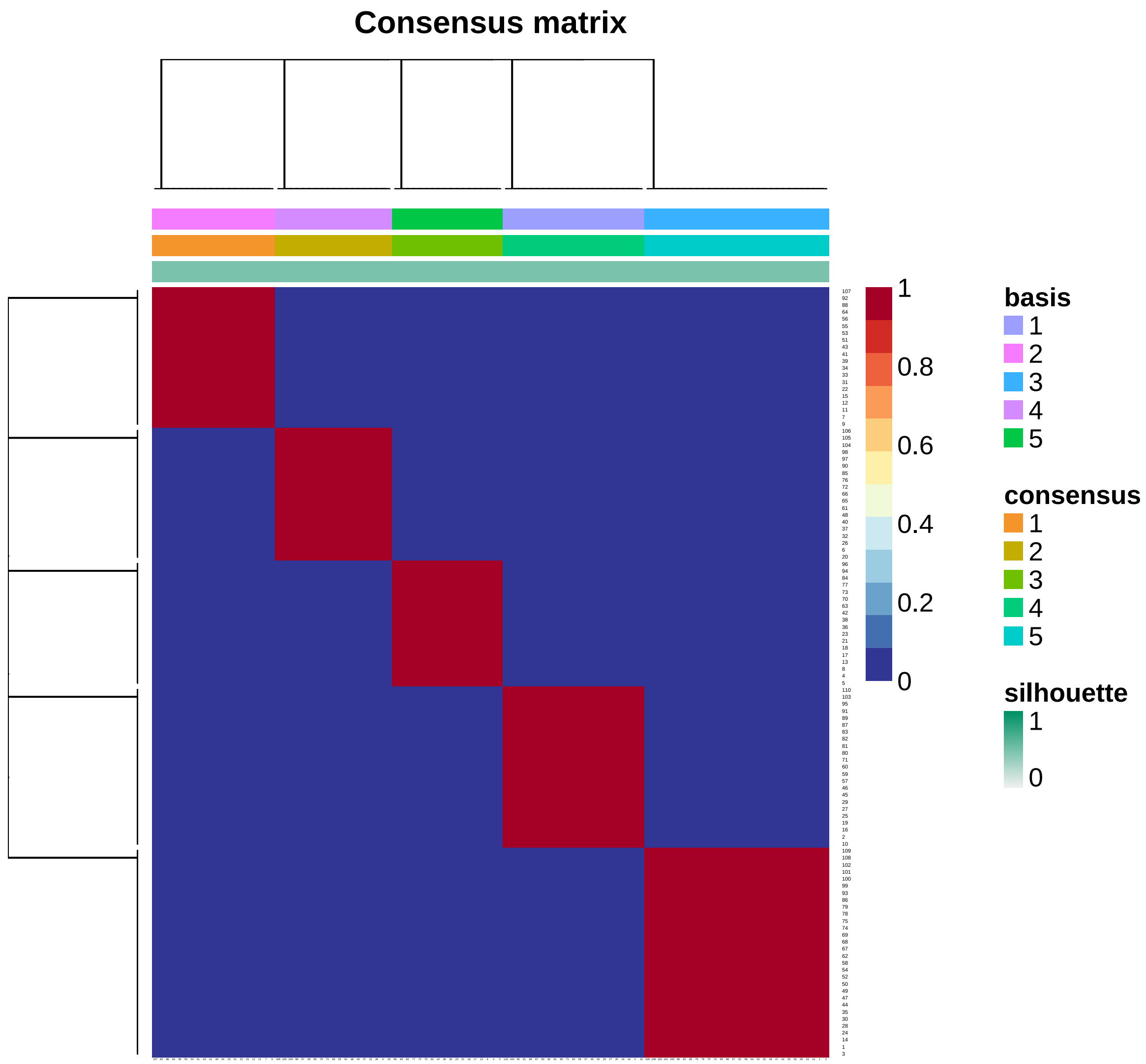
87
83
82
81
72
71
64
61
60
59
57
56
55
53
51
48
46
45
43
41
39
34
33
31
29
27
22
20
19
16
15
12
10
9
7
2
6
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
consensus
1
2
3
silhouette
1
0


Consensus matrix
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
4
consensus
1
2
3
4
silhouette
0.95
0.26


Consensus matrix
basis
1
2
3
4
5
consensus
1
2
3
4
5
silhouette
1
0
1
0.8
0.6
0.4
0.2
0
107
92
88
64
56
55
53
51
43
41
39
34
33
31
22
15
12
11
7
9
106
105
104
98
97
90
85
76
72
66
65
61
48
40
37
32
26
6
20
96
94
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77
73
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42
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36
23
21
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110
103
95
91
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82
81
80
71
60
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27
25
19
16
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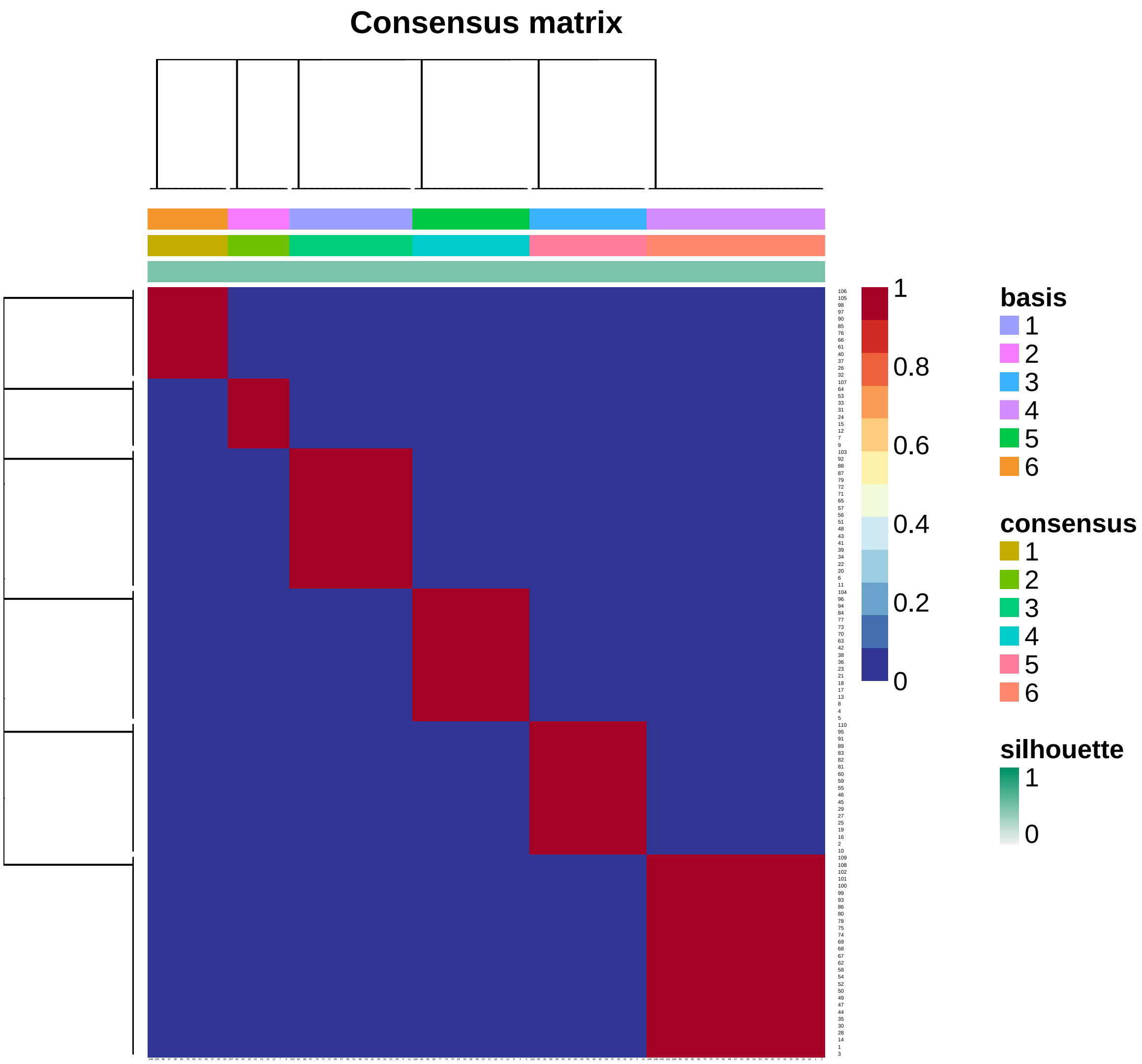
109
108
102
101
100
99
93
86
79
78
75
74
69
68
67
62
58
54
52
50
49
47
44
35
30
28
24
14
1
3


Consensus matrix
106
105
98
97
90
85
76
66
61
40
37
26
32
107
64
53
33
31
24
15
12
7
9
103
92
88
87
79
72
71
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43
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39
34
22
20
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104
96
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77
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42
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36
23
21
18
17
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4
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110
95
91
89
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81
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16
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108
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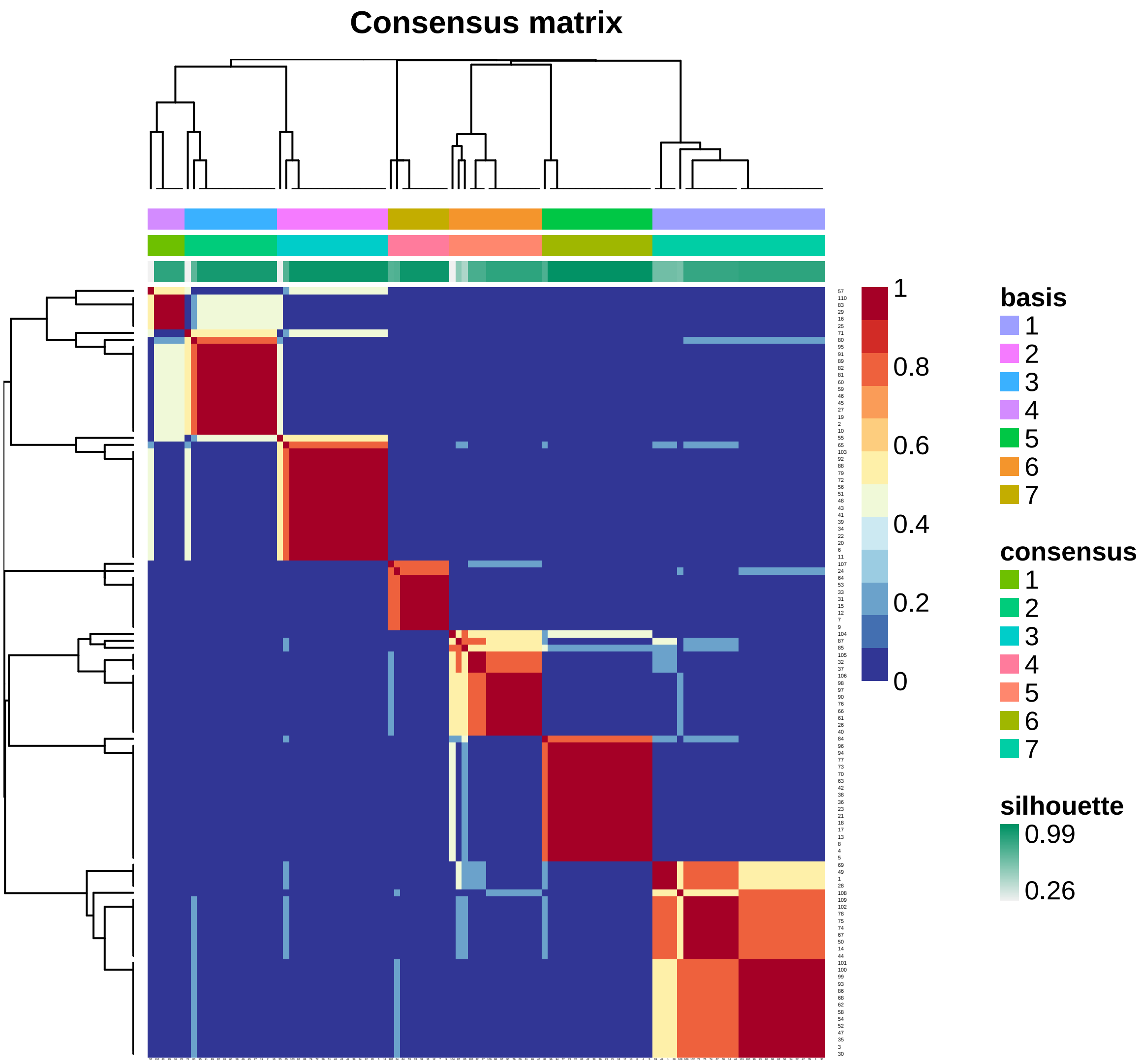
58
54
52
50
49
47
44
35
30
28
14
1
3
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
4
5
6
consensus
1
2
3
4
5
6
silhouette
1
0


Consensus matrix
57
110
83
29
16
25
71
80
95
91
89
82
81
60
59
46
45
27
19
2
10
55
65
103
92
88
79
72
56
51
48
43
41
39
34
22
20
6
11
107
24
64
53
33
31
15
12
7
9
104
87
85
105
32
37
106
98
97
90
76
66
61
26
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84
96
94
77
73
70
63
42
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36
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21
18
17
13
8
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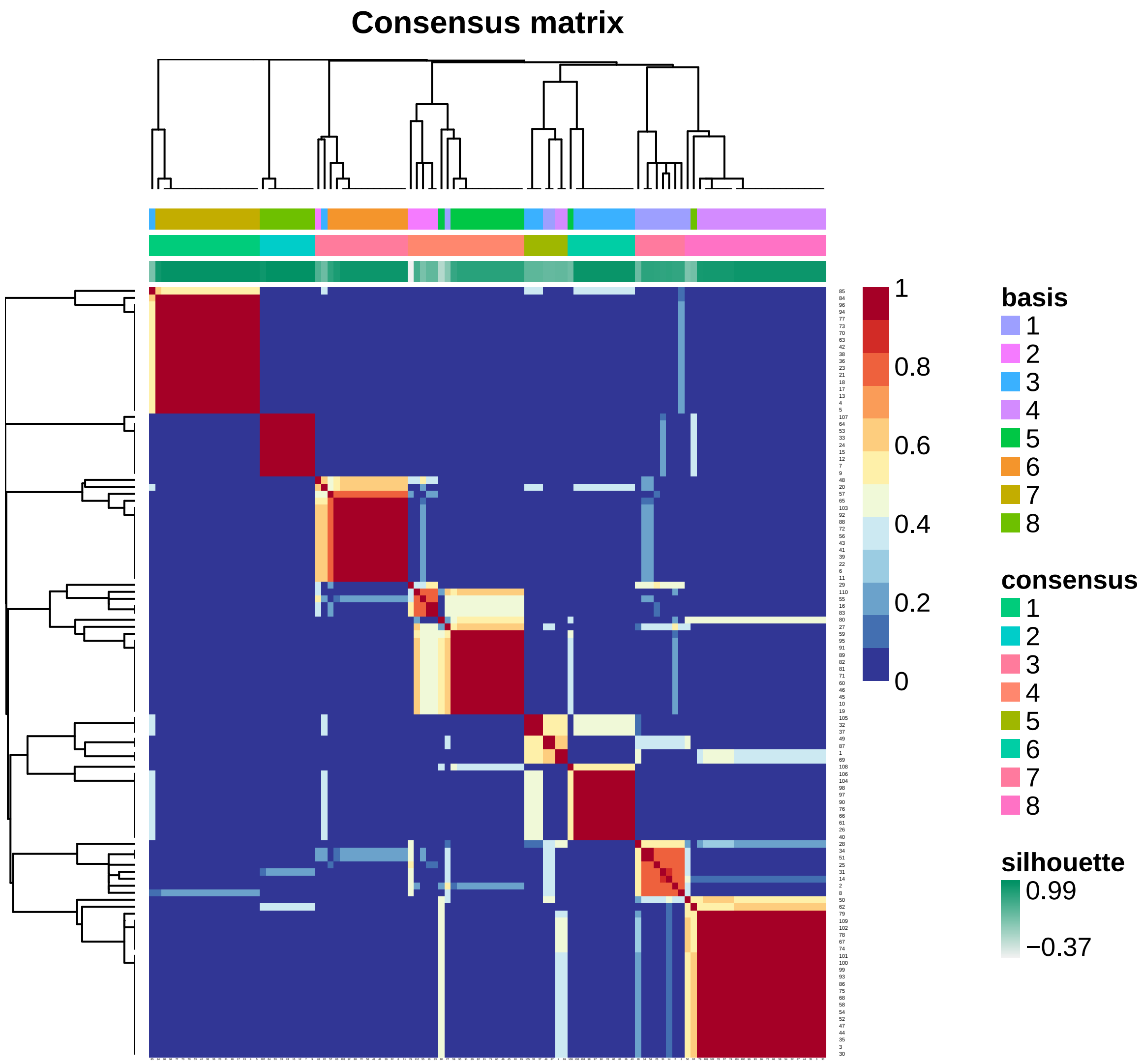
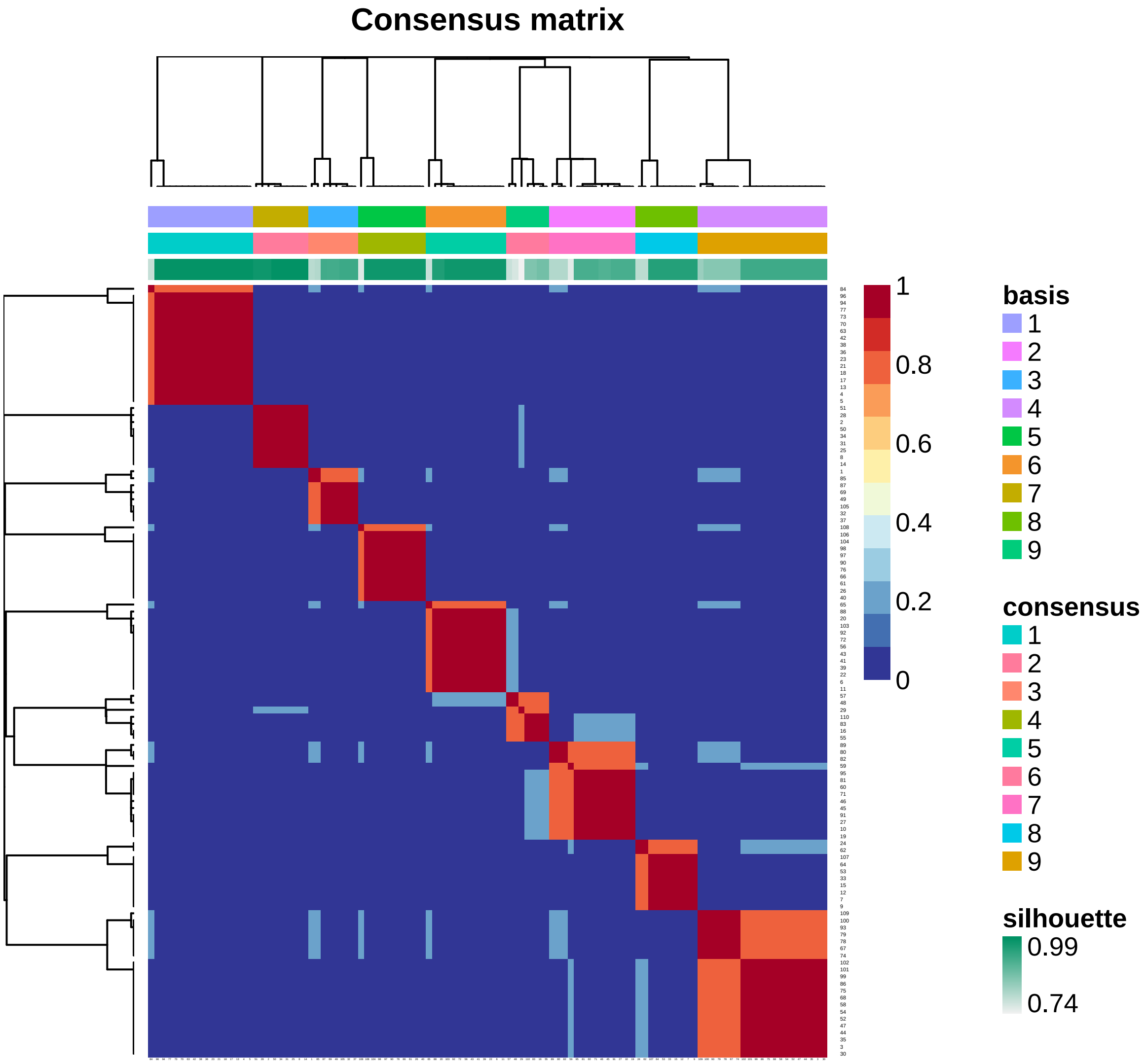
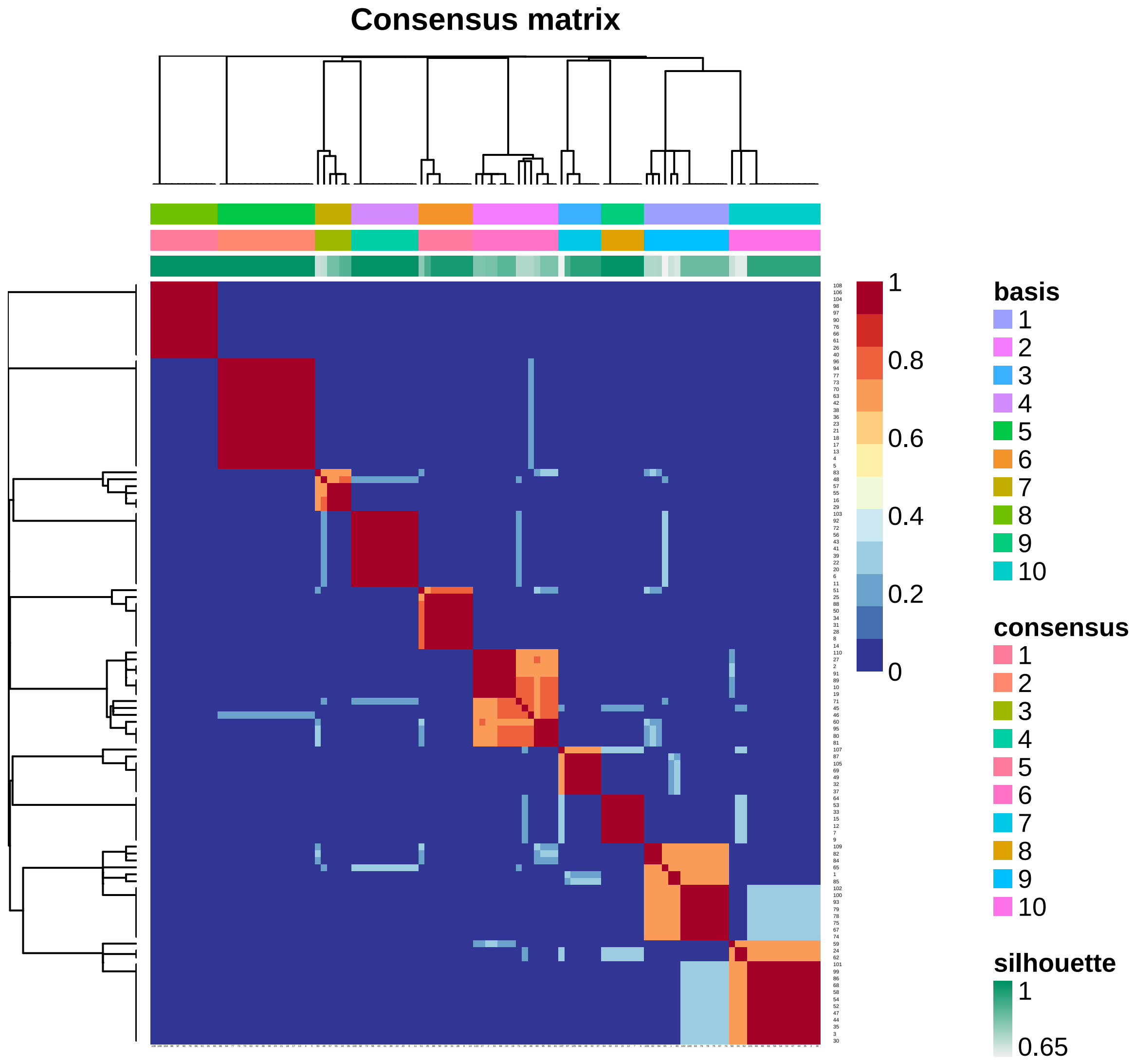
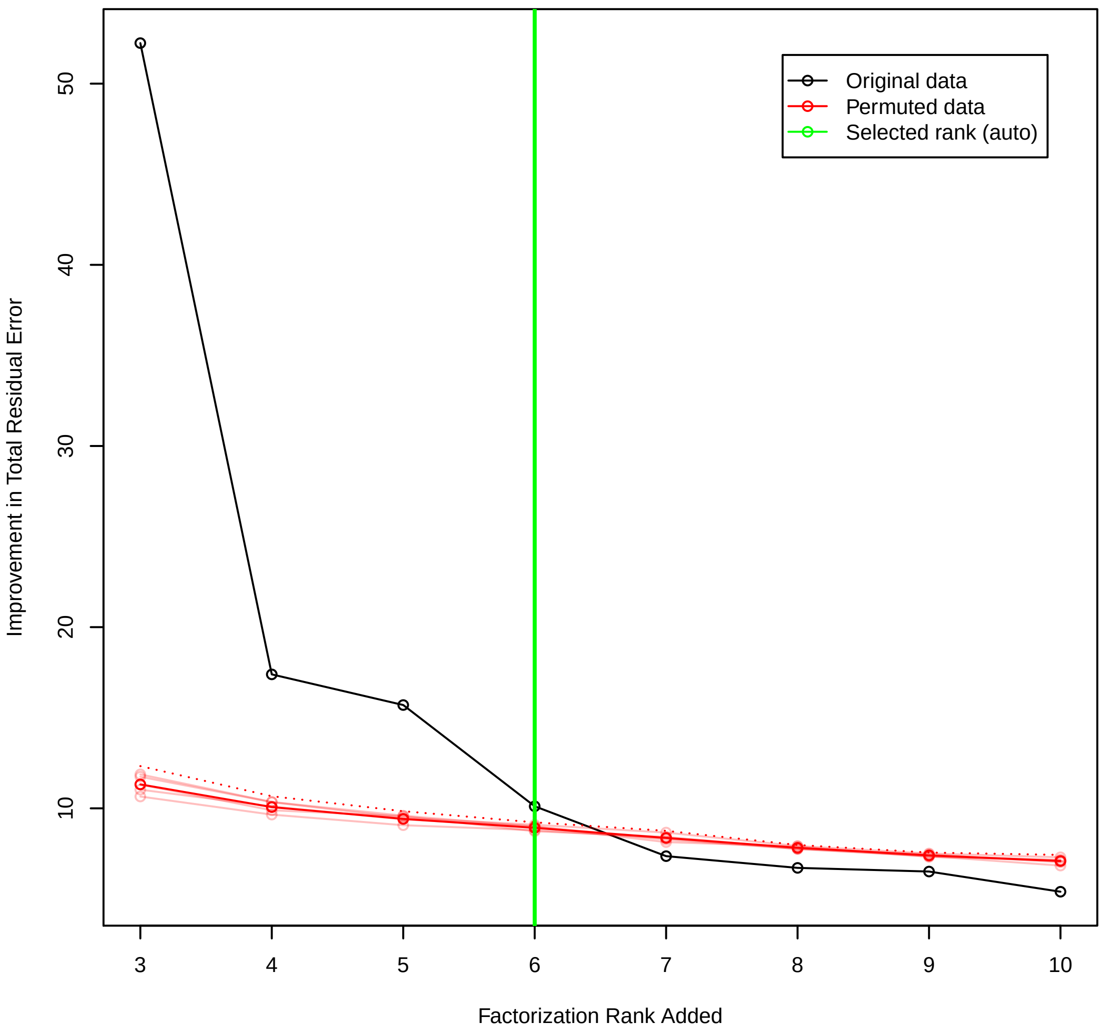
5
69
49
1
28
108
109
102
78
75
74
67
50
14
44
101
100
99
93
86
68
62
58
54
52
47
35
3
30
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
4
5
6
7
consensus
1
2
3
4
5
6
7
silhouette
0.99
0.26


Consensus matrix
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
4
5
6
7
8
consensus
1
2
3
4
5
6
7
8
silhouette
0.99
−0.37


Consensus matrix
1
0.8
0.6
0.4
0.2
0
basis
1
2
3
4
5
6
7
8
9
consensus
1
2
3
4
5
6
7
8
9
silhouette
0.99
0.74

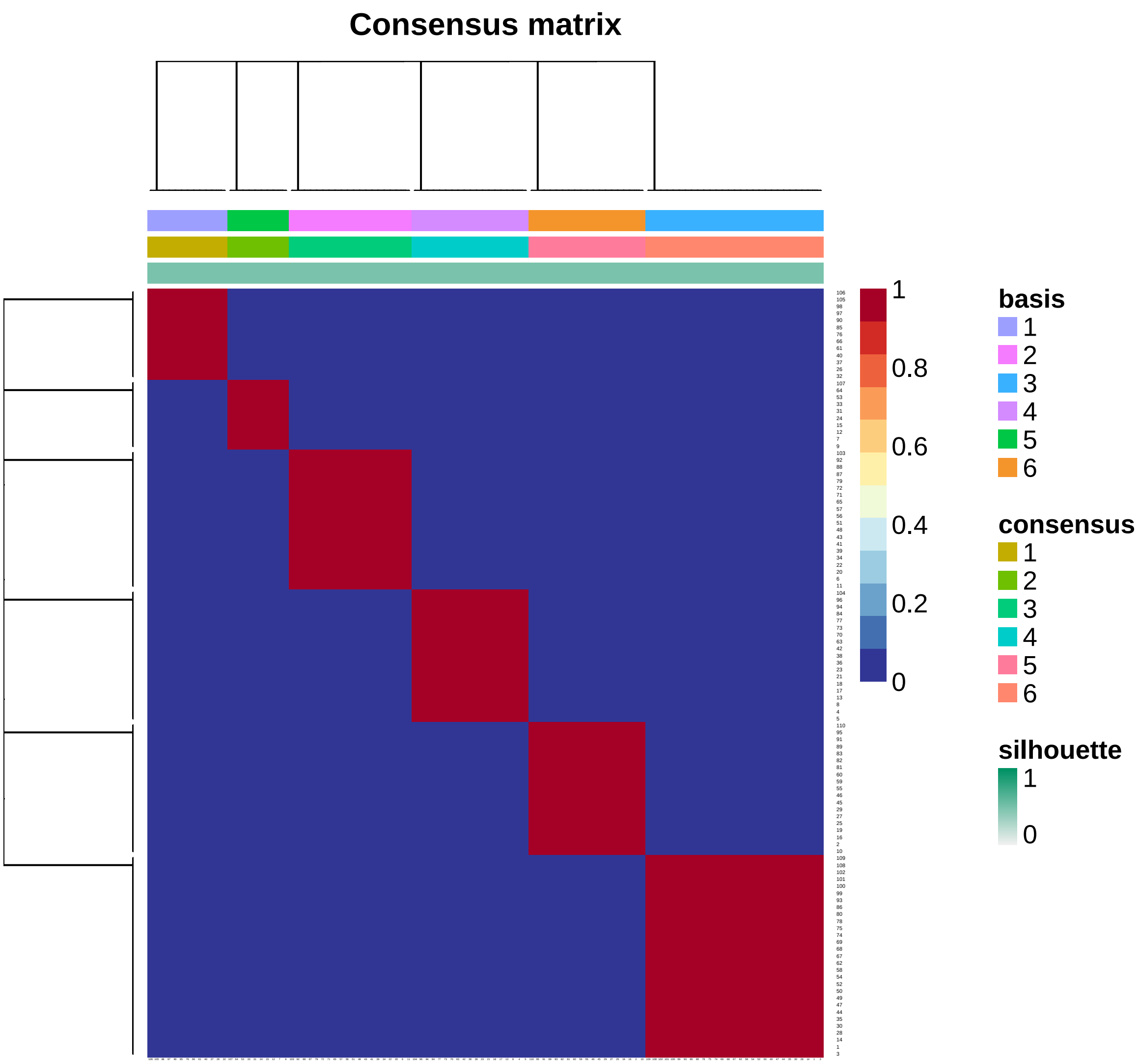


```
plot(nmf.rankrange[-1], -temp.orig_resids.delta, type = "o", col = "black",
    pch = 21, ylim = range(-c(temp.orig_resids.delta, temp.perm_resids.delta.mean)),
    xlab = "Factorization Rank Added", ylab = "Improvement in Total Residual Error")
lines(nmf.rankrange[-1], -temp.perm_resids.delta.mean,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

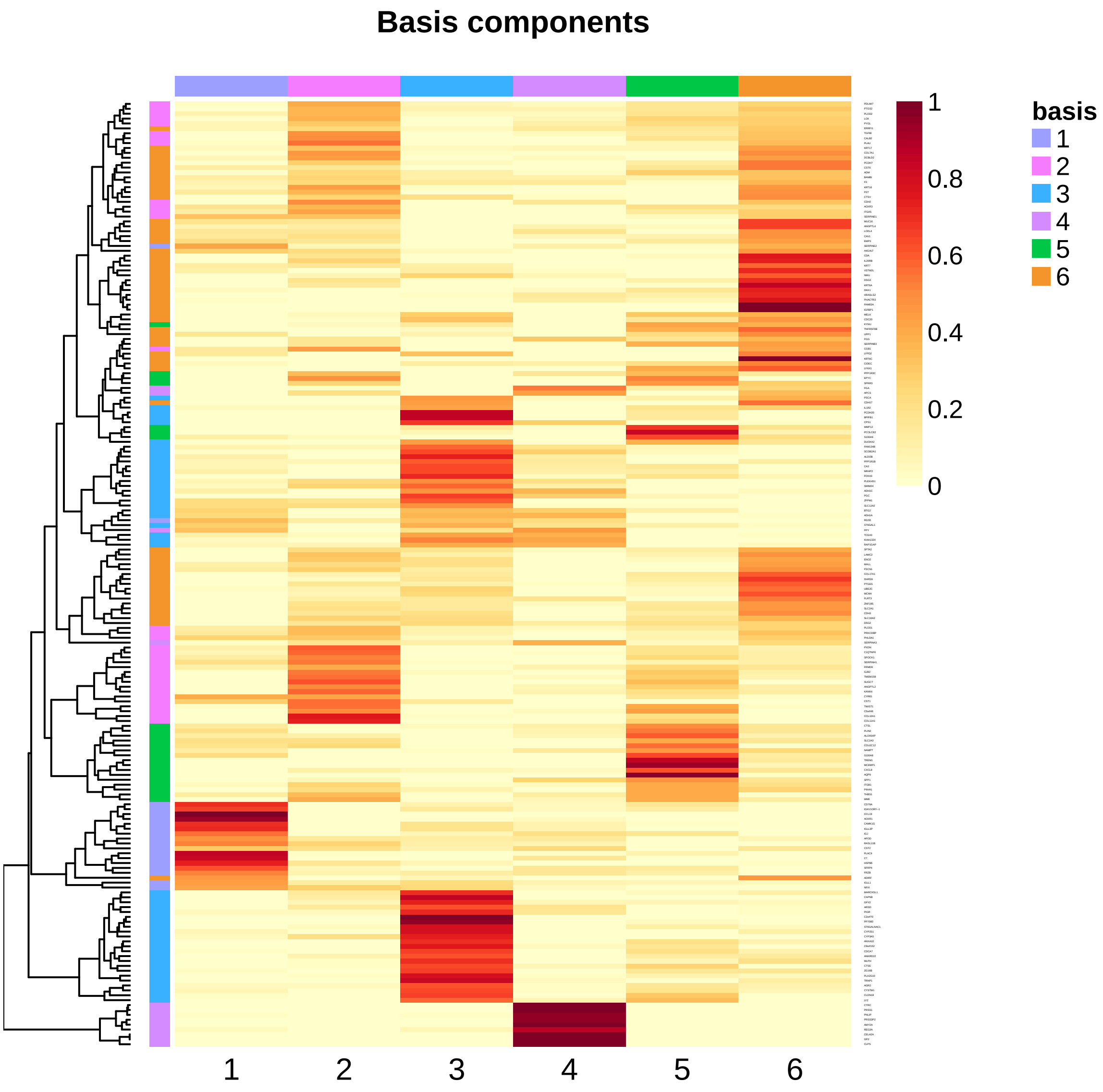


4.1 Fit

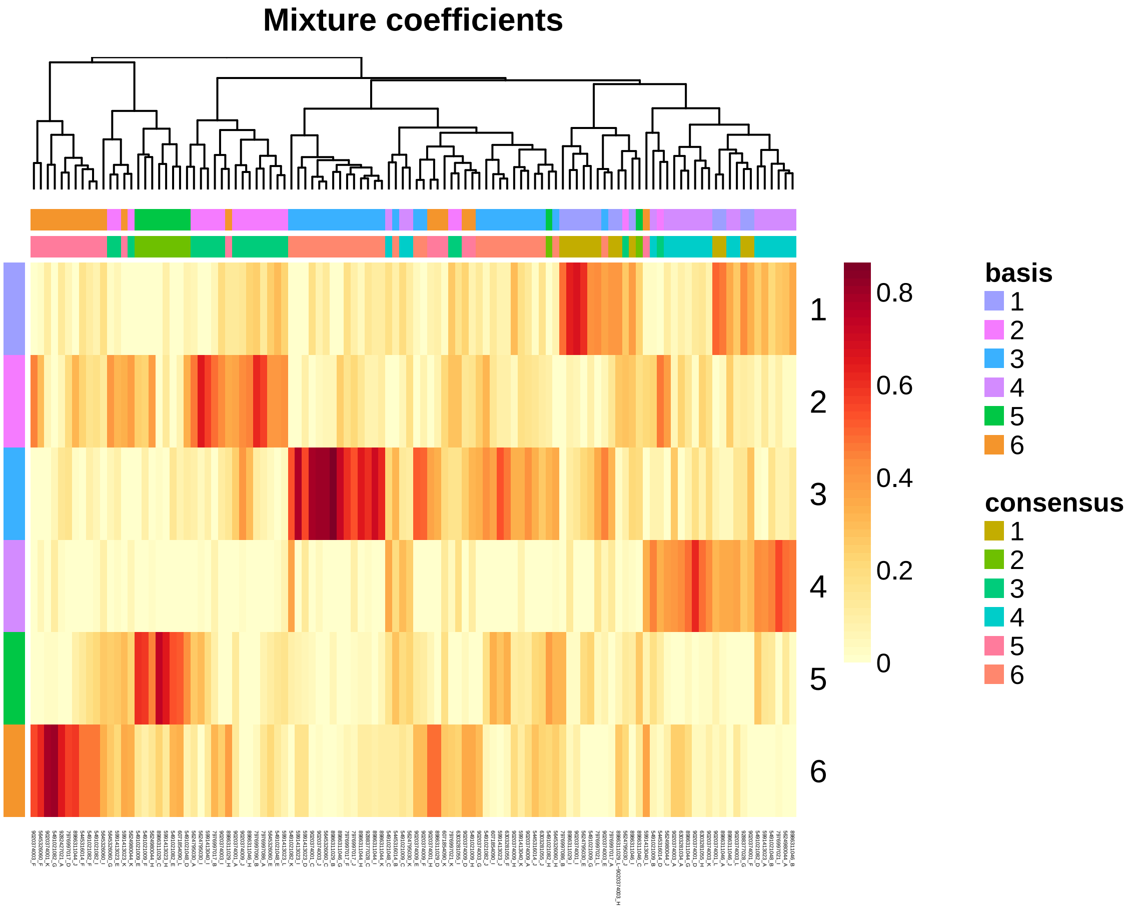
```
consensusmap(nmf.final)
```



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

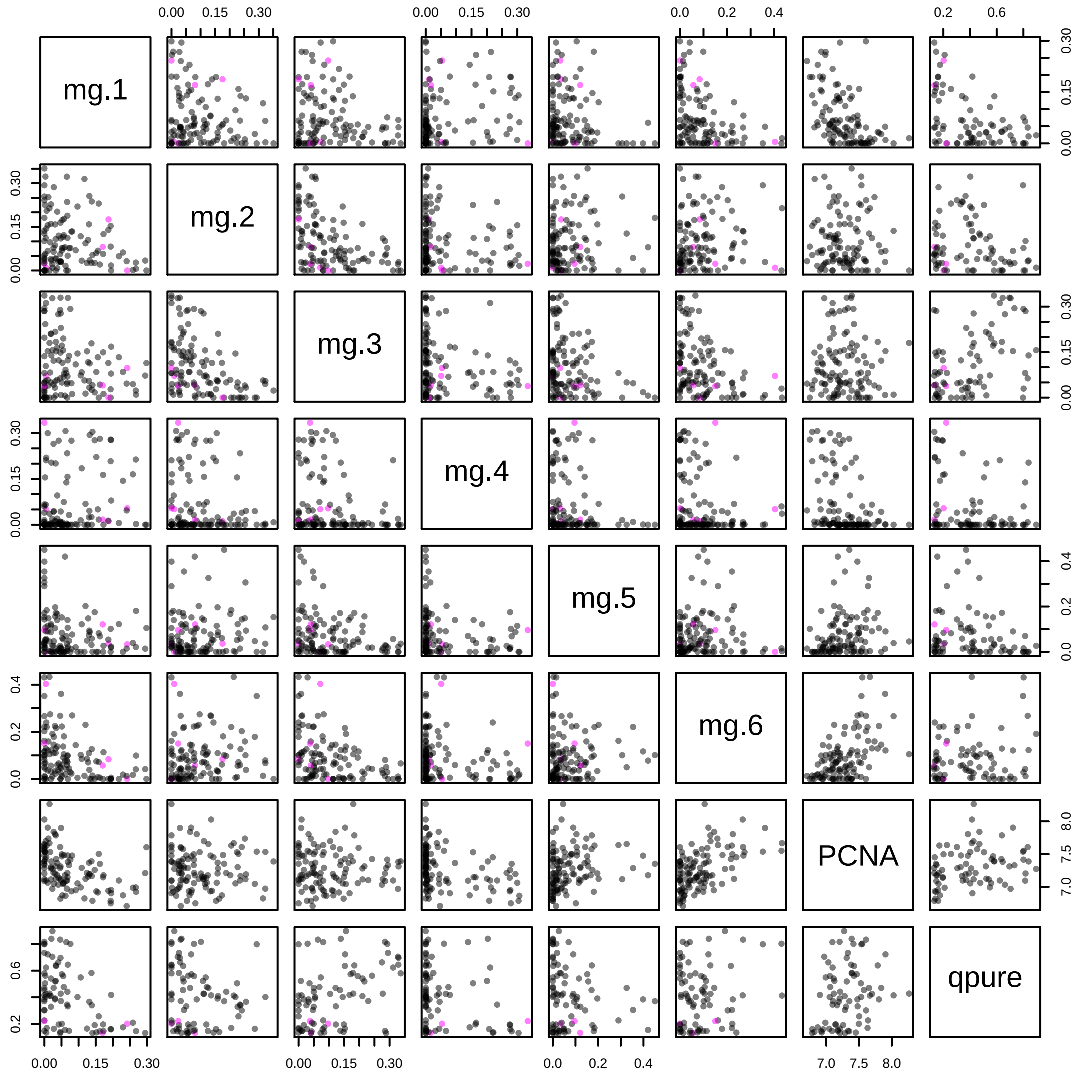


```
coefmap(nmf.final)
```



```
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 = samps.pdac_au$purity_qpure)
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)))
```



4.2 Prediction on training set

```
nmf.final.cpv.pvals = data.frame(surv.diag_rec.p = apply(coefs.diag_rec, 1,
    function(xc) pchisq(2 * diff(coxph(y.diag_rec ~ xc)$loglik), df = 1, lower.tail = FALSE)),
    surv.diag_rec.c = apply(coefs.diag_rec, 1, function(xc) coef(coxph(y.diag_rec ~
        xc))), surv.diag_dsd.p = apply(coefs.diag_dsd, 1, function(xc) pchisq(2 *
        diff(coxph(y.diag_dsd ~ xc)$loglik), df = 1, lower.tail = FALSE)), surv.diag_dsd.c = apply(coefs
        1, function(xc) coef(coxph(y.diag_dsd ~ xc))), surv.recr_dsd.p = apply(coefs.recr_dsd,
        1, function(xc) pchisq(2 * diff(coxph(y.recr_dsd ~ xc)$loglik), df = 1,
            lower.tail = FALSE)), surv.recr_dsd.c = apply(coefs.recr_dsd, 1,
        function(xc) coef(coxph(y.recr_dsd ~ xc))), pure.p = apply(coefs.pdac_au,
        1, function(xc) cor.test(samps.pdac_au$purity_qpure, xc, method = "kendall")$p.value),
    pure.s = apply(coefs.pdac_au, 1, function(xc) cor.test(samps.pdac_au$purity_qpure,
        xc, method = "kendall")$statistic))
temp.pvals = as.matrix(nmf.final.cpv.pvals[, grepl("\\.p$", colnames(nmf.final.cpv.pvals))])
temp.pvals.FWER = matrix(p.adjust(as.vector(temp.pvals), "holm"), nrow = nrow(temp.pvals))
colnames(temp.pvals.FWER) = paste(colnames(temp.pvals), "Holm", sep = ".")
temp.pvals.BY = matrix(p.adjust(as.vector(temp.pvals), "BY"), nrow = nrow(temp.pvals))
colnames(temp.pvals.BY) = paste(colnames(temp.pvals), "BY", sep = ".")
nmf.final.cpv.pvals = cbind(nmf.final.cpv.pvals, temp.pvals.FWER, temp.pvals.BY)
nmf.final.cpv.pvals = nmf.final.cpv.pvals[, order(colnames(nmf.final.cpv.pvals))]
```

	pure.p	pure.p.BY	pure.p.Holm	pure.s	surv.diag_dsd.c	surv.diag_dsd.p	surv.diag_dsd.p.BY	surv.diag_dsd.p.Holm	surv.diag_rec.c	surv.diag_rec.p	surv.diag_rec.p.BY	surv.diag_rec.p.Holm	surv.recr_dsd.c	surv.recr_dsd.p	surv.recr_dsd.p.BY	surv.recr_dsd.p.Holm
1	0.00	0.01	0.01	-3.42	-4.56	0.00	0.04	0.06	-3.78	0.01	0.07	0.11	-2.36	0.16	0.75	0.96
2	0.05	0.30	0.50	-1.96	3.10	0.02	0.15	0.25	1.99	0.11	0.55	0.77	2.62	0.06	0.35	0.56
3	0.00	0.00	0.00	3.91	-5.46	0.00	0.00	0.00	-2.64	0.03	0.19	0.33	-4.66	0.00	0.04	0.04
4	0.03	0.19	0.33	-2.19	-0.95	0.44	1.00	1.00	-1.68	0.16	0.75	0.96	0.56	0.68	1.00	1.00
5	0.07	0.38	0.57	-1.81	2.84	0.02	0.12	0.21	2.73	0.01	0.12	0.20	1.37	0.29	1.00	1.00
6	0.78	1.00	1.00	0.28	6.61	0.00	0.00	0.00	5.49	0.00	0.00	0.00	3.97	0.00	0.04	0.06

Table 1: Resubstitution prediction, all tests

	pure.p.Holm	pure.s	surv.diag_dsd.c	surv.diag_dsd.p.Holm	surv.diag_rec.c	surv.diag_rec.p.Holm	surv.recr_dsd.c	surv.recr_dsd.p.Holm
1	0.01	-3.42	-4.56	0.06	-3.78	0.11	-2.36	0.96
2	0.50	-1.96	3.10	0.25	1.99	0.77	2.62	0.56
3	0.00	3.91	-5.46	0.00	-2.64	0.33	-4.66	0.04
4	0.33	-2.19	-0.95	1.00	-1.68	0.96	0.56	1.00
5	0.57	-1.81	2.84	0.21	2.73	0.20	1.37	1.00
6	1.00	0.28	6.61	0.00	5.49	0.00	3.97	0.06

Table 2: Resubstitution prediction, Holm MTC only

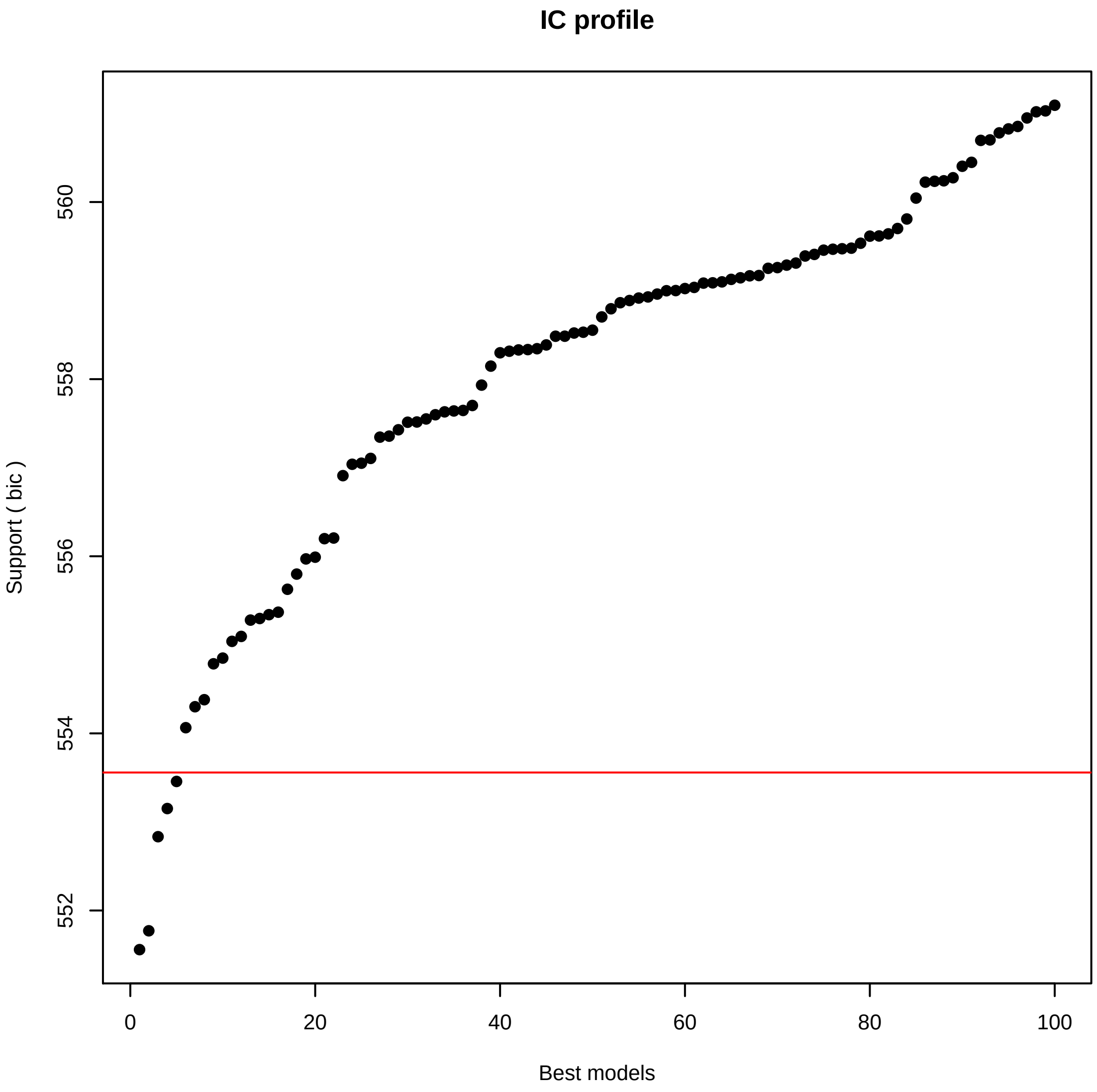
MTC P-values

```
print(asreg.result)

## glmulti.analysis
## Method: h / Fitting: coxph / IC used: bic
## Level: 2 / Marginality: TRUE
## From 100 models:
## Best IC: 551.558245978867
## Best model:
## [1] "Surv(time, event) ~ 1 + mg.5 + mg.6"
## Evidence weight: 0.121525761025609
## Worst IC: 561.093163081812
## 5 models within 2 IC units.
## 71 models to reach 95% of evidence weight.

coef(asreg.result)

##            Estimate Uncond. variance Nb models Importance +/- (alpha=0.05)
## mg.1:mg.4 -0.00342         0.001098         1   0.001595          0.06569
## mg.2:mg.4  0.06847         0.024924         2   0.003030          0.31297
## mg.4:mg.5 -0.05064         0.019737         1   0.003679          0.27850
## mg.4:mg.6  0.02227         0.015093         2   0.004699          0.24355
## mg.2:mg.3  0.08587         0.057059         3   0.004885          0.47354
## mg.1:mg.2  0.10761         0.069012         2   0.004997          0.52078
## mg.1:mg.5 -0.01322         0.015809         2   0.005116          0.24925
## mg.3:mg.4 -0.25668         0.347670         4   0.008845          1.16890
## mg.3:mg.5  0.01013         0.047858         3   0.009870          0.43368
## mg.2:mg.5  0.09367         0.064793         4   0.010069          0.50461
## mg.5:mg.6  0.10404         0.413552         8   0.036678          1.27485
## mg.1:mg.6  0.75549         3.893974         8   0.039107          3.91192
## mg.1:mg.3 -1.05886         7.166918         9   0.043683          5.30712
## mg.2:mg.6 -1.53508         9.333667        13   0.074749          6.05646
## mg.3:mg.6  2.60281        29.616218        14   0.097762         10.78842
## mg.4       0.09036         0.113089        33   0.136430          0.66666
## mg.2       0.33327         0.778397        42   0.219557          1.74902
## mg.1      -1.85625         6.374836        54   0.439670          5.00527
## mg.5       1.08749         2.127350        49   0.444550          2.89143
## mg.3      -2.66620         7.511723        65   0.592820          5.43329
## mg.6       5.31298         5.463222        90   0.932557          4.63359
```

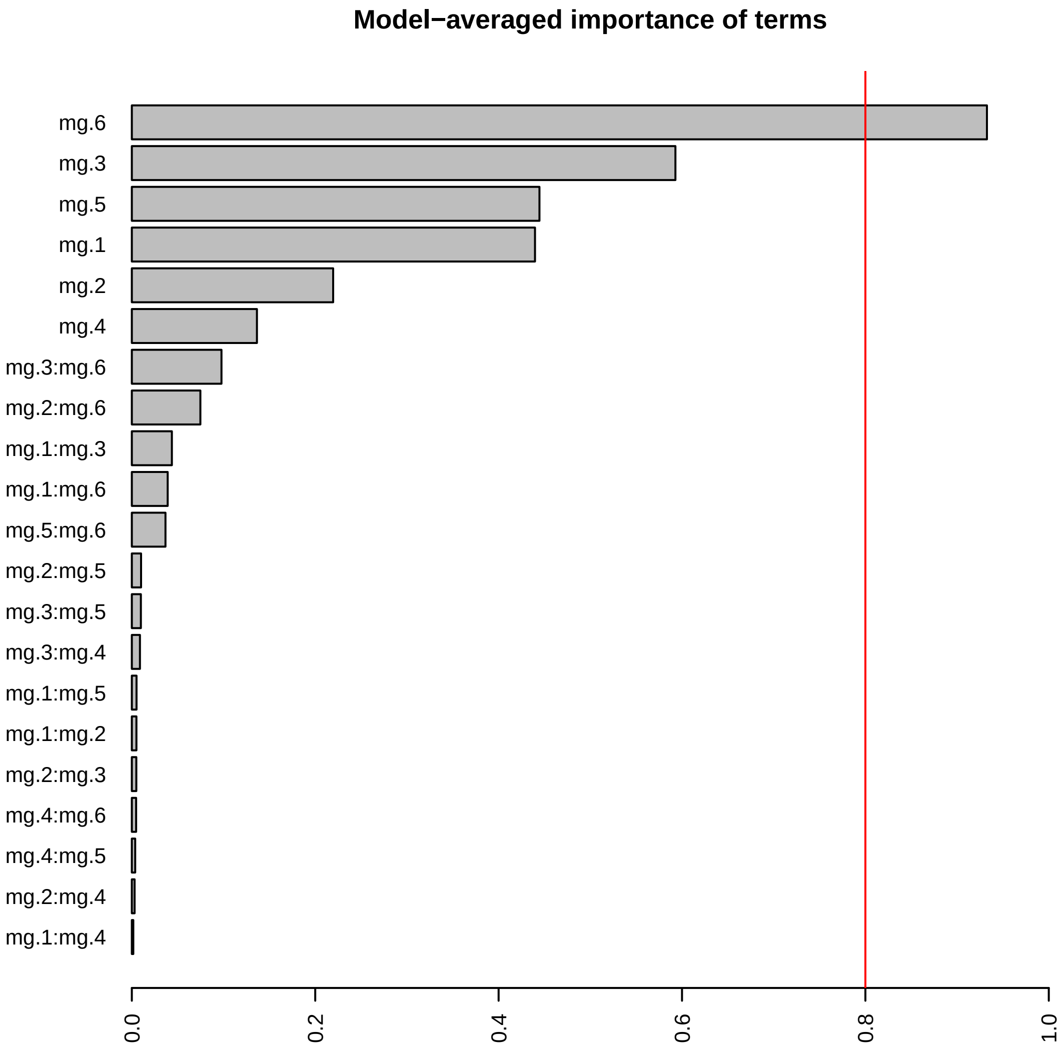
```
summary(asreg.result@objects[[1]])
```

```
## Call:
## fitfunc(formula = as.formula(x), data = data)
##
##   n= 110, number of events= 70
##
##         coef exp(coef) se(coef)    z Pr(>|z|)
## mg.5    2.81     16.65     1.08 2.60   0.0093
## mg.6    6.99   1089.19     1.19 5.87  4.4e-09
##
##      exp(coef) exp(-coef) lower .95 upper .95
## mg.5      16.7   0.060050         2       139
## mg.6    1089.2   0.000918       105     11264
##
## Concordance= 0.702  (se = 0.038 )
## Rsquare= 0.265   (max possible= 0.995 )
## Likelihood ratio test= 33.9  on 2 df,   p=4.29e-08
## Wald test            = 38.8  on 2 df,   p=3.77e-09
## Score (logrank) test = 42.9  on 2 df,   p=4.87e-10
```

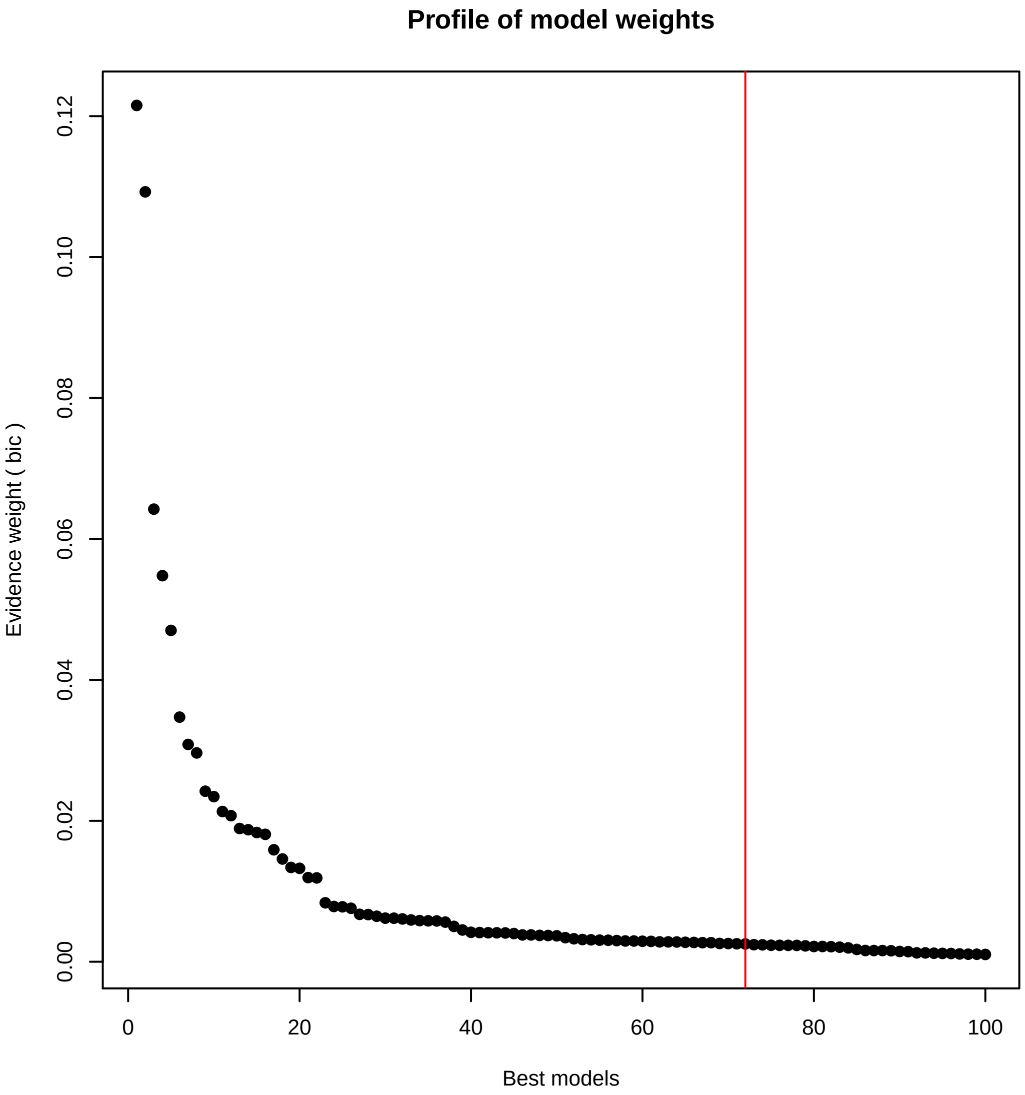
```
plot(asreg.result, type = "p")
```



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



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



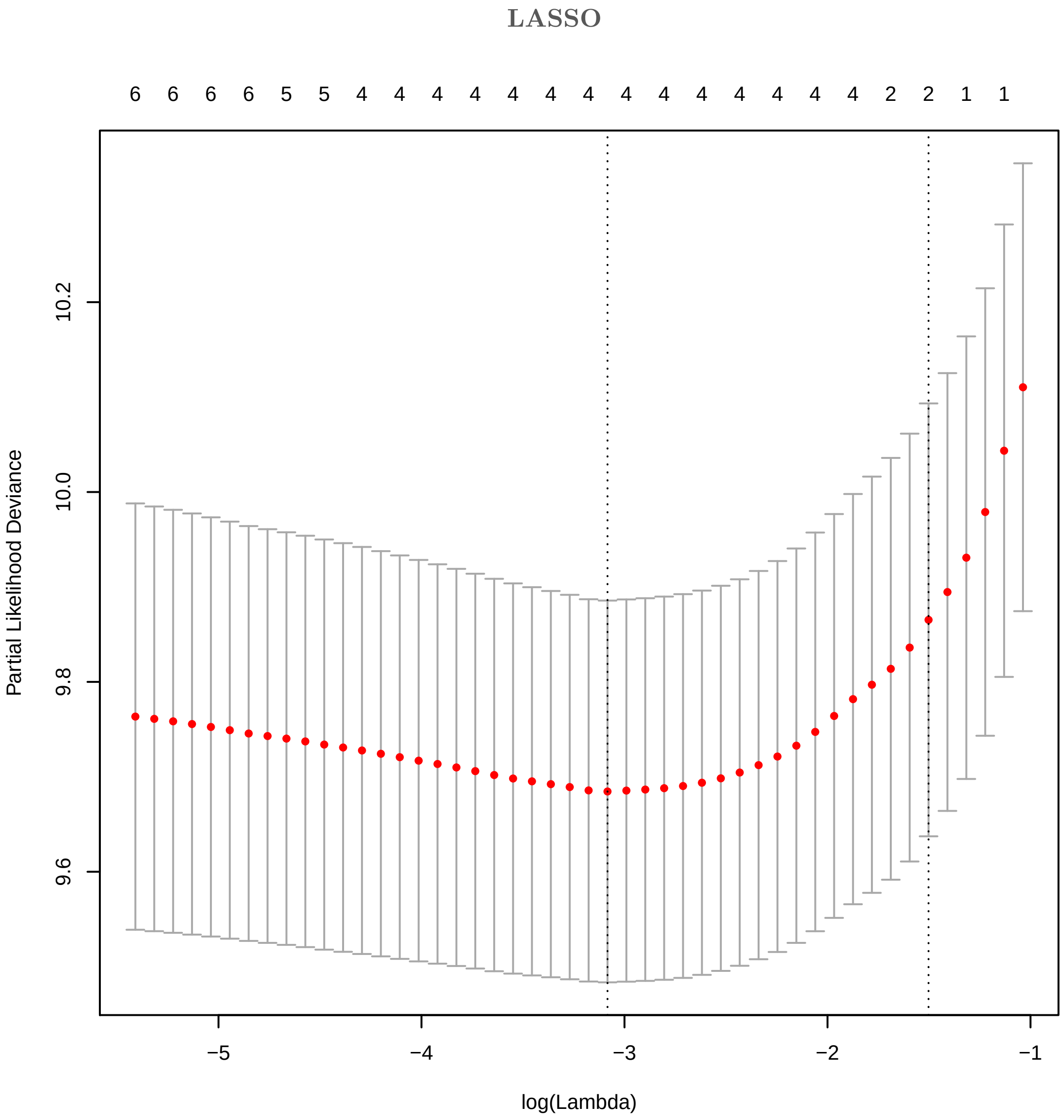
```
glmnet.coef.1se
```

```
## 6 x 1 sparse Matrix of class "dgCMatrix"
##             1
## mg.1  .
## mg.2  .
## mg.3 -0.1635
## mg.4  .
## mg.5  .
## mg.6  3.0808
```

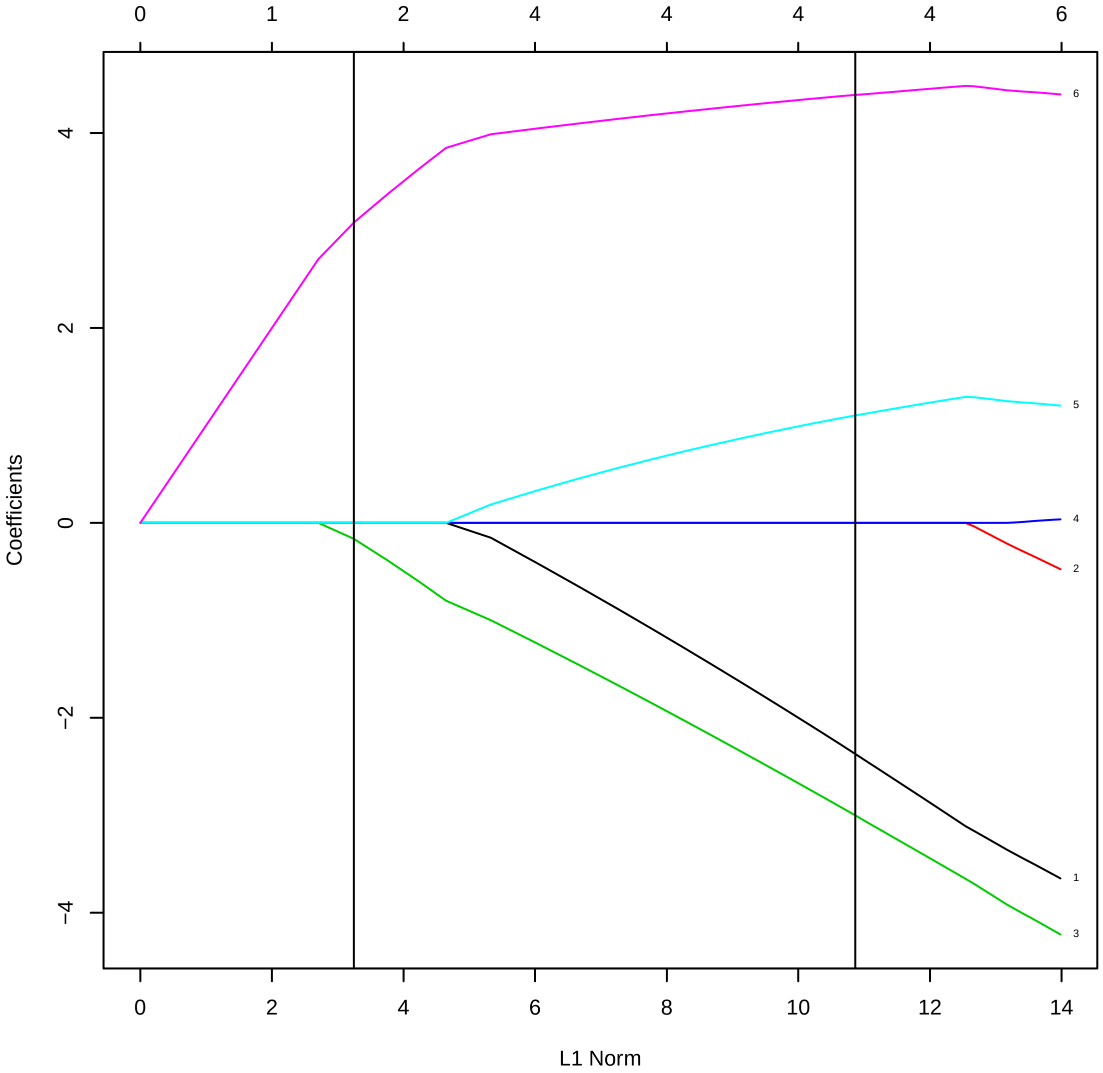
```
glmnet.coef.min
```

```
## 6 x 1 sparse Matrix of class "dgCMatrix"
##             1
## mg.1 -2.372
## mg.2  .
## mg.3 -3.002
## mg.4  .
## mg.5  1.102
## mg.6  4.391
```

```
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)))
```



4.3 Prediction on validation sets

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

```
val.basis = basis(nmf.final)
rownames(GSE21501.lingex) = GSE21501.feat$Gene.symbol
rownames(GSE28735.lingex) = GSE28735.feat$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)
```

```
apply(GSE21501.coefs, 1, function(xc) coxph(Surv(time, event) ~ xc, data = GSE21501.samp))

## [[1]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##     coef exp(coef) se(coef)     z    p
## xc -5.31   0.00495     3.44 -1.54 0.12
##
## Likelihood ratio test=2.57  on 1 df, p=0.109  n= 102, number of events= 66
##
## [[2]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##    coef exp(coef) se(coef)     z   p
## xc 2.17      8.79      2.6 0.836 0.4
##
## Likelihood ratio test=0.68  on 1 df, p=0.41  n= 102, number of events= 66
##
## [[3]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##     coef exp(coef) se(coef)      z    p
## xc -1.09     0.337     2.73 -0.399 0.69
##
## Likelihood ratio test=0.16  on 1 df, p=0.688  n= 102, number of events= 66
##
## [[4]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##      coef exp(coef) se(coef)       z    p
## xc -0.226     0.798     2.47 -0.0914 0.93
##
## Likelihood ratio test=0.01  on 1 df, p=0.927  n= 102, number of events= 66
##
## [[5]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##    coef exp(coef) se(coef)     z    p
## xc 2.17      8.75     3.04 0.713 0.48
```

```
##
## Likelihood ratio test=0.49  on 1 df, p=0.486  n= 102, number of events= 66
##
## [[6]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE21501.samp)
##
##
##    coef exp(coef) se(coef)    z    p
## xc 2.57      13.1     2.08 1.24 0.22
##
## Likelihood ratio test=1.45  on 1 df, p=0.229  n= 102, number of events= 66
```

```
apply(GSE21501.coefs, 1, function(xc) coxph(Surv(time, event) ~ tstage + nstage +
    xc, data = GSE21501.samp))
```

```
## [[1]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.166   0.84664    0.281 -0.593 0.550
## nstage  0.653   1.92135    0.315  2.074 0.038
## xc     -5.237   0.00532    3.545 -1.477 0.140
##
## Likelihood ratio test=7.13  on 3 df, p=0.0678  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
##
## [[2]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.161     0.851    0.287 -0.560 0.580
## nstage  0.643     1.903    0.316  2.039 0.041
## xc      1.025     2.788    2.658  0.386 0.700
##
## Likelihood ratio test=4.94  on 3 df, p=0.176  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
##
## [[3]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.153     0.858    0.286 -0.535 0.590
## nstage  0.659     1.933    0.314  2.097 0.036
## xc     -1.379     0.252    2.796 -0.493 0.620
##
## Likelihood ratio test=5.04  on 3 df, p=0.169  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
```

```
##
## [[4]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.158     0.854    0.285 -0.554 0.580
## nstage  0.678     1.970    0.319  2.126 0.034
## xc     -1.041     0.353    2.463 -0.423 0.670
##
## Likelihood ratio test=4.98  on 3 df, p=0.173  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
##
## [[5]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.179     0.836    0.289 -0.621 0.530
## nstage  0.641     1.898    0.315  2.033 0.042
## xc      1.878     6.543    3.313  0.567 0.570
##
## Likelihood ratio test=5.11  on 3 df, p=0.164  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
##
## [[6]]
## Call:
## coxph(formula = Surv(time, event) ~ tstage + nstage + xc, data = GSE21501.samp)
##
##
##          coef exp(coef) se(coef)      z     p
## tstage -0.110     0.896    0.284 -0.388 0.700
## nstage  0.657     1.928    0.316  2.077 0.038
## xc      2.510    12.310    2.164  1.160 0.250
##
## Likelihood ratio test=6.07  on 3 df, p=0.108  n= 97, number of events= 63
##    (5 observations deleted due to missingness)
```

```
apply(GSE21501.coefs, 1, function(xc) anova(coxph(Surv(time, event) ~ tstage +
    nstage + xc, data = GSE21501.samp)))
```

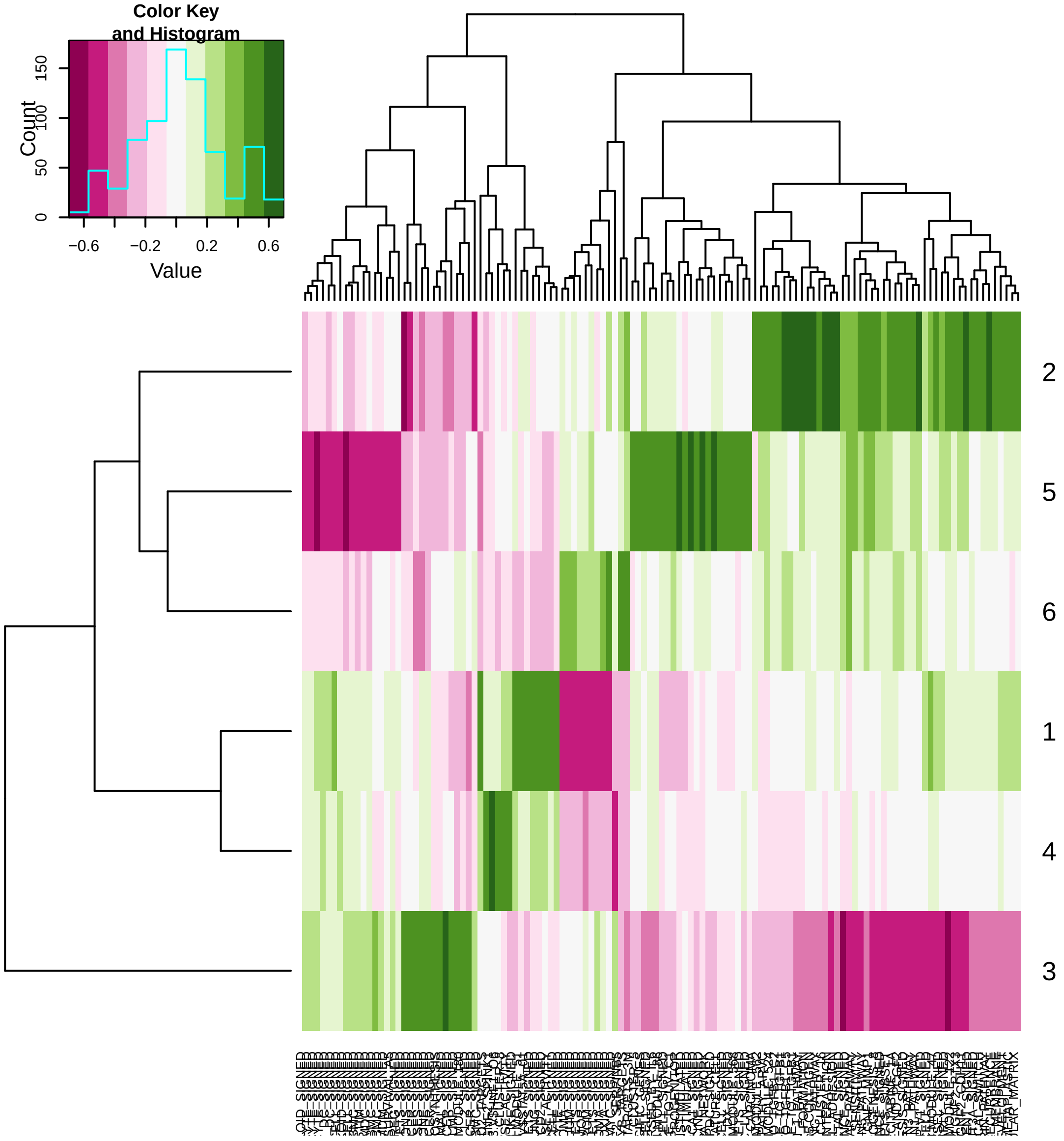
```
## [[1]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -238  2.34  1      0.126
##
```

```
## [[2]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -239  0.15  1      0.702
##
## [[3]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -239  0.25  1      0.619
##
## [[4]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -239  0.18  1      0.668
##
## [[5]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -239  0.31  1      0.577
##
## [[6]]
## Analysis of Deviance Table
##  Cox model: response is Surv(time, event)
## Terms added sequentially (first to last)
##
##        loglik Chisq Df Pr(>|Chi|)
## NULL     -242
## tstage   -242  0.01  1      0.928
## nstage   -239  4.79  1      0.029
## xc       -239  1.27  1      0.259

apply(GSE28735.coefs, 1, function(xc) coxph(Surv(time, event) ~ xc, data = GSE28735.samp))

## [[1]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##    coef exp(coef) se(coef)    z    p
## xc -4.5    0.0111     3.74 -1.2 0.23
##
## Likelihood ratio test=1.55  on 1 df, p=0.213  n= 42, number of events= 29
##
## [[2]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##    coef exp(coef) se(coef)    z    p
## xc 3.46      31.7     2.53 1.36 0.17
##
## Likelihood ratio test=1.63  on 1 df, p=0.201  n= 42, number of events= 29
##
## [[3]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##     coef exp(coef) se(coef)     z     p
## xc -7.79  0.000415     3.22 -2.42 0.015
##
## Likelihood ratio test=6.32  on 1 df, p=0.0119  n= 42, number of events= 29
##
## [[4]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##    coef exp(coef) se(coef)     z   p
## xc 0.72      2.05     2.81 0.256 0.8
##
## Likelihood ratio test=0.06  on 1 df, p=0.801  n= 42, number of events= 29
##
## [[5]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##      coef exp(coef) se(coef)     z    p
## xc -0.469     0.625     2.61 -0.18 0.86
##
## Likelihood ratio test=0.03  on 1 df, p=0.857  n= 42, number of events= 29
##
```

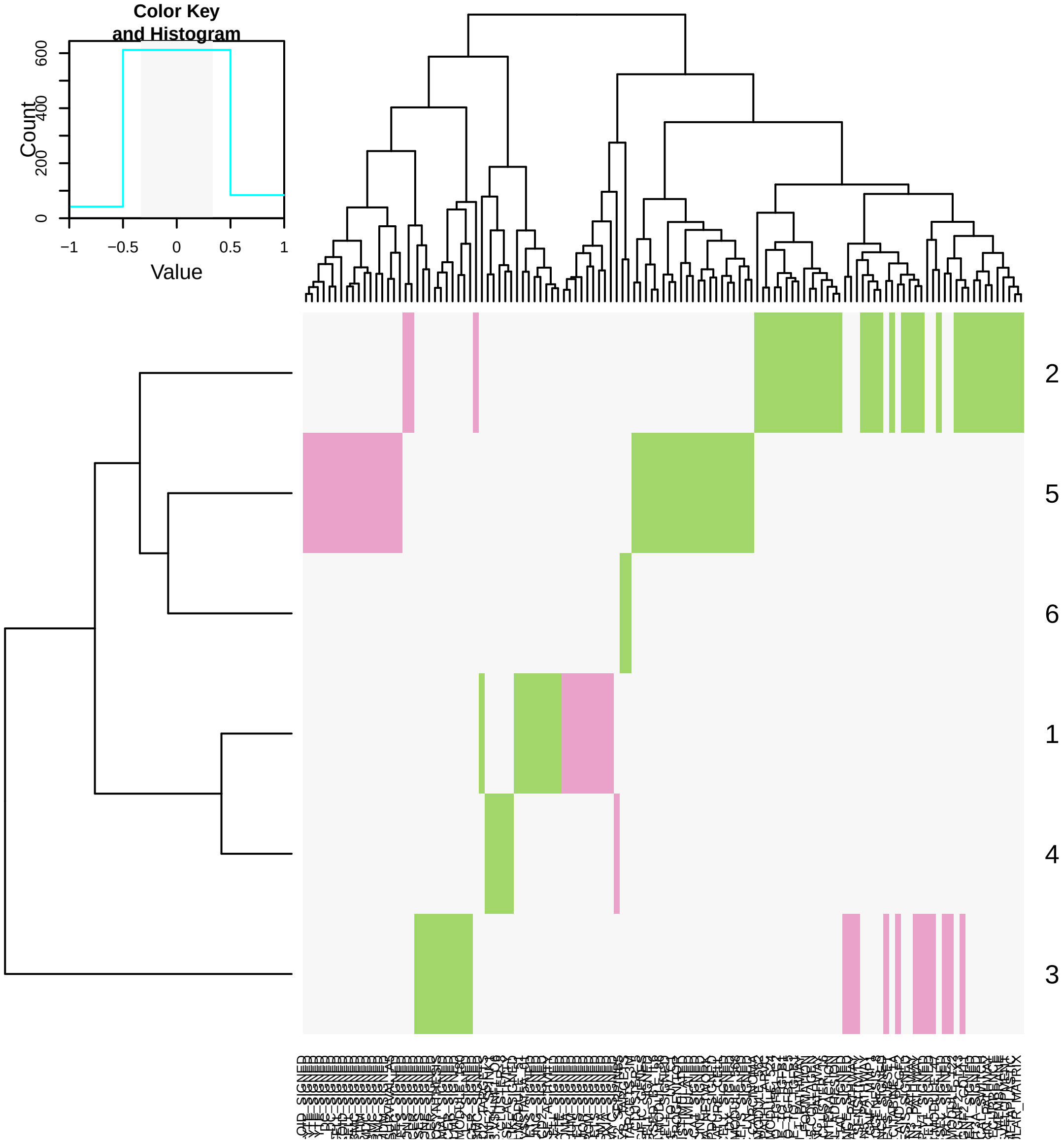
```
## [[6]]
## Call:
## coxph(formula = Surv(time, event) ~ xc, data = GSE28735.samp)
##
##
##    coef exp(coef) se(coef)    z     p
## xc 5.73       308     2.32 2.47 0.014
##
## Likelihood ratio test=5.68  on 1 df, p=0.0171  n= 42, number of events= 29
```

4.4 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)
```



```r
heatmap.2(nmf.final.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))
```



```r
temp.sig_id = colnames(nmf.final.msigdb.corr)
temp.sig_class = gsub("\\..*", "", temp.sig_id)
temp.nsigs = length(temp.sig_id)
temp.nmeta = nrow(nmf.final.msigdb.corr)
tables = lapply(1:temp.nmeta, function(metagene_i) {
    tapply(1:temp.nsigs, 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_repor
                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(nmf.final.cpv.pvals$surv.diag_dsd.c
                      collapse = ",")
                  }))
            table = table[order(-(table$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.KATSANOU_ELAVL1_TARGETS_SIGNED      0.5096        -1
## 2                 c2.ZHAN_MULTIPLE_MYELOMA_CD2_SIGNED      0.5086        -1
## 3            c2.SMID_BREAST_CANCER_NORMAL_LIKE_SIGNED      0.5080        -1
## 4                     c2.GREENBAUM_E2A_TARGETS_SIGNED     -0.5009         1
## 5  c2.MARTORIATI_MDM4_TARGETS_NEUROEPITHELIUM_SIGNED     -0.5012         1
## 6                            c2.YU_MYC_TARGETS_SIGNED     -0.5029         1
## 7                 c2.SABATES_COLORECTAL_ADENOMA_SIGNED     -0.5036         1
## 8                            c2.WINTER_HYPOXIA_SIGNED     -0.5241         1
## 9                 c2.WEST_ADRENOCORTICAL_TUMOR_SIGNED     -0.5416         1
## 10     c2.SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_SIGNED     -0.5500         1
## 11                  c2.LEE_EARLY_T_LYMPHOCYTE_SIGNED     -0.5517         1
## 12                  c2.HAHTOLA_SEZARY_SYNDROM_SIGNED     -0.5641         1
##
## [[1]]$c3
##          GeneSet Correlation Metagenes
## 1 c3.V$STAT5A_01      0.5234        -1
##
## [[1]]$c4
##        GeneSet Correlation Metagenes
## 1 c4.MODULE_51      0.5399        -1
##
## [[1]]$c5
##                                      GeneSet Correlation Metagenes
## 1 c5.PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY      0.5113        -1
##
## [[1]]$c6
## data frame with 0 columns and 0 rows
##
## [[1]]$c7
##                                                    GeneSet Correlation
## 1          c7.GSE20715_0H_VS_48H_OZONE_TLR4_KO_LUNG_SIGNED      0.5160
## 2 c7.GSE22886_IGM_MEMORY_BCELL_VS_BLOOD_PLASMA_CELL_SIGNED      0.5019
## 3        c7.GSE34205_HEALTHY_VS_RSV_INF_INFANT_PBMC_SIGNED      0.5002
##   Metagenes
## 1        -1
## 2        -1
## 3        -1
##
##
## [[2]]
## [[2]]$c1
## data frame with 0 columns and 0 rows
##
## [[2]]$c2
##                                                                                                   Gen
## 1                            c2.REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION/c2.REACTOME_COLLAGEN_FORMA
## 2                                                                                   c2.PID_SYNDECAN_1_PAT
## 3                                                                     c2.VERRECCHIA_DELAYED_RESPONSE_TO_T
## 4                                                                                    c2.PID_INTEGRIN1_PAT
## 5                                                                                c2.PID_AVB3_INTEGRIN_PAT
## 6  c2.FARMER_BREAST_CANCER_CLUSTER_5/c2.ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGNATURE/c4.GNF2_C
## 7                                                       c2.YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTE
## 8                                                                            c2.KEGG_ECM_RECEPTOR_INTERAC
## 9                                                                          c2.VERRECCHIA_RESPONSE_TO_TGF
## 10                                                                      c2.VERRECCHIA_EARLY_RESPONSE_TO_T
## 11                                                                                     c2.KEGG_FOCAL_ADH
## 12                                                                     c2.MAHADEVAN_GIST_MORPHOLOGICAL_SW
## 13                                                                          c2.CAIRO_LIVER_DEVELOPMENT_S
## 14                                                                                   c2.PID_INTEGRIN3_PAT
## 15                                                                               c2.KEGG_BASAL_CELL_CARC
## 16                                                                                   c2.BURTON_ADIPOGENE
## 17                                                                         c2.VERRECCHIA_RESPONSE_TO_TGF
## 18                                                                             c2.CROMER_TUMORIGENESIS_S
## 19                                                                  c2.WIEDERSCHAIN_TARGETS_OF_BMI1_AND_
## 20                                                                            c2.ROZANOV_MMP14_TARGETS_S
## 21                                                                               c2.PID_WNT_SIGNALING_PAT
## 22                                           c2.KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_
## 23                                                             c2.LABBE_TARGETS_OF_TGFB1_AND_WNT3A_S
## 24                                                                   c2.LIEN_BREAST_CARCINOMA_METAPL
## 25                                                                                   c2.PID_INTEGRIN5_PAT
## 26                                                             c2.LINDGREN_BLADDER_CANCER_HIGH_RECUR
## 27                                                                         c2.POTTI_TOPOTECAN_SENSIT
## 28                                                        c2.MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_S
## 29                                                   c2.BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_S
## 30                                                                         c2.PASINI_SUZ12_TARGETS_S
##    Correlation Metagenes
## 1       0.6490         2
## 2       0.6355         2
## 3       0.6178         2
## 4       0.6067      2,-3
## 5       0.6020         2
## 6       0.5990         2
## 7       0.5963         2
## 8       0.5953         2
## 9       0.5849         2
## 10      0.5829         2
## 11      0.5758         2
## 12      0.5587         2
## 13      0.5429         2
## 14      0.5409      2,-3
## 15      0.5396         2
## 16      0.5346         2
## 17      0.5312         2
## 18      0.5258         2
## 19      0.5242         2
## 20      0.5228         2
## 21      0.5171         2
## 22      0.5114         2
## 23      0.5081         2
## 24      0.5077         2
## 25      0.5074         2
## 26      0.5047         2
## 27      0.5017         2
## 28     -0.5087        -2
## 29     -0.5436        -2
## 30     -0.5916        -2
##
## [[2]]$c3
## data frame with 0 columns and 0 rows
##
## [[2]]$c4
##                       GeneSet Correlation Metagenes
## 1                c4.GNF2_PTX3      0.5533      2,-3
## 2               c4.MODULE_122      0.5369         2
## 3                c4.GNF2_MMP1      0.5366         2
## 4               c4.MODULE_562      0.5178         2
## 5 c4.MODULE_419/c4.MODULE_524      0.5128         2
## 6                c4.MODULE_47      0.5003         2
##
## [[2]]$c5
##                                                                                       GeneSet
## 1                                                                                 c5.COLLAGEN
## 2 c5.PROTEINACEOUS_EXTRACELLULAR_MATRIX/c5.EXTRACELLULAR_MATRIX_PART/c5.EXTRACELLULAR_MATRIX
## 3                                                                        c5.BASEMENT_MEMBRANE
## 4                                                                     c5.SKELETAL_DEVELOPMENT
##   Correlation Metagenes
## 1      0.6496         2
## 2      0.5336         2
## 3      0.5148         2
## 4      0.5101         2
##
## [[2]]$c6
## data frame with 0 columns and 0 rows
##
```

```
## [[2]]$c7
## data frame with 0 columns and 0 rows
##
##
## [[3]]
## [[3]]$c1
## data frame with 0 columns and 0 rows
##
## [[3]]$c2
##                                                   GeneSet Correlation
## 1  c2.CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL_SIGNED      0.5882
## 2            c2.REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS      0.5269
## 3            c2.SMID_BREAST_CANCER_RELAPSE_IN_BONE_SIGNED      0.5215
## 4                           c2.LIU_PROSTATE_CANCER_SIGNED      0.5202
## 5         c2.WAMUNYOKOLI_OVARIAN_CANCER_GRADES_1_2_SIGNED      0.5178
## 6  c2.WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_SIGNED      0.5175
## 7                c2.WAMUNYOKOLI_OVARIAN_CANCER_LMP_SIGNED      0.5165
## 8                       c2.WALLACE_PROSTATE_CANCER_SIGNED      0.5155
## 9                    c2.DOANE_BREAST_CANCER_CLASSES_SIGNED      0.5111
## 10                   c2.WOO_LIVER_CANCER_RECURRENCE_SIGNED     -0.5000
## 11                                 c2.PID_UPA_UPAR_PATHWAY     -0.5011
## 12           c2.SUZUKI_RESPONSE_TO_TSA_AND_DECITABINE_1A     -0.5141
## 13                    c2.HUANG_DASATINIB_RESISTANCE_SIGNED     -0.5145
## 14                         c2.LIM_MAMMARY_STEM_CELL_SIGNED     -0.5175
## 15                                c2.PID_INTEGRIN3_PATHWAY     -0.5175
## 16                        c2.ROY_WOUND_BLOOD_VESSEL_SIGNED     -0.5235
## 17                                c2.PID_INTEGRIN1_PATHWAY     -0.5248
## 18  c2.LIEN_BREAST_CARCINOMA_METAPLASTIC_VS_DUCTAL_SIGNED     -0.6110
## 19      c2.VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_SIGNED     -0.6217
##    Metagenes
## 1         -3
## 2         -3
## 3         -3
## 4         -3
## 5         -3
## 6         -3
## 7         -3
## 8         -3
## 9         -3
## 10         3
## 11         3
## 12         3
## 13         3
## 14         3
## 15      -2,3
## 16         3
## 17      -2,3
## 18         3
## 19         3
##
## [[3]]$c3
## data frame with 0 columns and 0 rows
##
```

```
## [[3]]$c4
##                       GeneSet Correlation Metagenes
## 1 c4.MODULE_139/c4.MODULE_180      0.5195        -3
## 2                c4.GNF2_PTX3     -0.5155      -2,3
##
## [[3]]$c5
## data frame with 0 columns and 0 rows
##
## [[3]]$c6
##                GeneSet Correlation Metagenes
## 1 c6.LEF1_UP.V1_SIGNED     -0.5597         3
##
## [[3]]$c7
## data frame with 0 columns and 0 rows
##
##
## [[4]]
## [[4]]$c1
## data frame with 0 columns and 0 rows
##
## [[4]]$c2
##                             GeneSet Correlation Metagenes
## 1            c2.BERGER_MBD2_TARGETS      0.5646        -4
## 2 c2.TERAMOTO_OPN_TARGETS_CLUSTER_8      0.5274        -4
## 3    c2.LEE_LIVER_CANCER_MYC_SIGNED     -0.5203         4
##
## [[4]]$c3
##        GeneSet Correlation Metagenes
## 1 c3.V$HNF1_Q6      0.5124        -4
##
## [[4]]$c4
##                           GeneSet Correlation Metagenes
## 1 c4.GNF2_SERPINI2/c4.GNF2_SPINK1      0.6959        -4
##
## [[4]]$c5
##                        GeneSet Correlation Metagenes
## 1 c5.CARBOXYPEPTIDASE_ACTIVITY      0.5342        -4
##
## [[4]]$c6
## data frame with 0 columns and 0 rows
##
## [[4]]$c7
## data frame with 0 columns and 0 rows
##
##
## [[5]]
## [[5]]$c1
## data frame with 0 columns and 0 rows
##
## [[5]]$c2
##                                                                    GeneSet
## 1                                 c2.IVANOVA_HEMATOPOIESIS_LATE_PROGENITOR
## 2                                      c2.MARSON_BOUND_BY_FOXP3_STIMULATED
## 3                                               c2.SESTO_RESPONSE_TO_UV_C1
## 4                                c2.NAKAYAMA_SOFT_TISSUE_TUMORS_PCA1_SIGNED
## 5                                      c2.IVANOVA_HEMATOPOIESIS_MATURE_CELL
## 6  c2.MARTINEZ_RB1_AND_TP53_TARGETS_SIGNED/c2.MARTINEZ_TP53_TARGETS_SIGNED
## 7                                         c2.KAMIKUBO_MYELOID_CEBPA_NETWORK
## 8                                     c2.MARSON_BOUND_BY_FOXP3_UNSTIMULATED
## 9                                                     c2.VALK_AML_CLUSTER_5
## 10                                  c2.RAGHAVACHARI_PLATELET_SPECIFIC_GENES
## 11                        c2.LIAN_LIPA_TARGETS_6M/c2.LIAN_LIPA_TARGETS_3M
## 12                                      c2.BROCKE_APOPTOSIS_REVERSED_BY_IL6
## 13                                  c2.SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A5
##    Correlation Metagenes
## 1       0.6114         5
## 2       0.5798         5
## 3       0.5491         5
## 4       0.5413         5
## 5       0.5410         5
## 6       0.5304         5
## 7       0.5280         5
## 8       0.5154         5
## 9       0.5134         5
## 10      0.5124         5
## 11      0.5005         5
## 12      0.5001         5
## 13     -0.5080        -5
##
## [[5]]$c3
## data frame with 0 columns and 0 rows
##
## [[5]]$c4
##                       GeneSet Correlation Metagenes
## 1                c4.MODULE_86      0.5240         5
## 2 c4.MODULE_491/c4.MODULE_568      0.5063         5
##
## [[5]]$c5
## data frame with 0 columns and 0 rows
##
## [[5]]$c6
## data frame with 0 columns and 0 rows
##
## [[5]]$c7
##                                                              GeneSet
## 1                               c7.GSE29618_MONOCYTE_VS_PDC_SIGNED
## 2              c7.GSE29618_MONOCYTE_VS_PDC_DAY7_FLU_VACCINE_SIGNED
## 3                                  c7.GSE3982_MAC_VS_NKCELL_SIGNED
## 4                             c7.GSE15767_MED_VS_SCS_MAC_LN_SIGNED
## 5              c7.GSE3982_BASOPHIL_VS_CENT_MEMORY_CD4_TCELL_SIGNED
## 6                         c7.GSE11057_PBMC_VS_MEM_CD4_TCELL_SIGNED
## 7  c7.GSE9006_HEALTHY_VS_TYPE_1_DIABETES_PBMC_4MONTH_POST_DX_SIGNED
## 8                   c7.GSE11057_NAIVE_CD4_VS_PBMC_CD4_TCELL_SIGNED
## 9                             c7.GSE3982_DC_VS_MAC_LPS_STIM_SIGNED
## 10                c7.GSE17721_POLYIC_VS_GARDIQUIMOD_1H_BMDM_SIGNED
## 11                                   c7.GSE29618_PDC_VS_MDC_SIGNED
## 12              c7.GSE6269_HEALTHY_VS_STREP_AUREUS_INF_PBMC_SIGNED
## 13                     c7.GSE20366_CD103_KLRG1_DP_VS_DN_TREG_SIGNED
## 14                         c7.GSE22886_NAIVE_CD8_TCELL_VS_DC_SIGNED
## 15                   c7.GSE22886_NAIVE_CD8_TCELL_VS_MONOCYTE_SIGNED
## 16                          c7.GSE11057_CD4_CENT_MEM_VS_PBMC_SIGNED
## 17                         c7.GSE22886_NAIVE_CD4_TCELL_VS_DC_SIGNED
## 18                     c7.GSE11057_NAIVE_VS_MEMORY_CD4_TCELL_SIGNED
## 19                           c7.GSE11057_CD4_EFF_MEM_VS_PBMC_SIGNED
## 20                              c7.GSE10325_BCELL_VS_MYELOID_SIGNED
## 21                       c7.GSE22886_NAIVE_TCELL_VS_MONOCYTE_SIGNED
## 22              c7.GSE10325_LUPUS_CD4_TCELL_VS_LUPUS_MYELOID_SIGNED
## 23                   c7.GSE22886_NAIVE_CD4_TCELL_VS_MONOCYTE_SIGNED
##    Correlation Metagenes
## 1       0.5760         5
## 2       0.5712         5
## 3       0.5573         5
## 4       0.5502         5
## 5       0.5352         5
## 6       0.5314         5
## 7       0.5209         5
## 8      -0.5042        -5
## 9      -0.5042        -5
## 10     -0.5076        -5
## 11     -0.5086        -5
## 12     -0.5086        -5
## 13     -0.5233        -5
## 14     -0.5267        -5
## 15     -0.5274        -5
## 16     -0.5352        -5
## 17     -0.5355        -5
## 18     -0.5379        -5
## 19     -0.5420        -5
## 20     -0.5519        -5
## 21     -0.5610        -5
## 22     -0.5699        -5
## 23     -0.5825        -5
##
##
## [[6]]
## [[6]]$c1
## data frame with 0 columns and 0 rows
##
## [[6]]$c2
##              GeneSet Correlation Metagenes
## 1 c2.LEI_MYB_TARGETS       0.509         6
##
## [[6]]$c3
## data frame with 0 columns and 0 rows
##
## [[6]]$c4
##                         GeneSet Correlation Metagenes
## 1 c4.GNF2_CDH3/c4.GNF2_SERPINB5      0.5532         6
##
## [[6]]$c5
## data frame with 0 columns and 0 rows
```

```
##
## [[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
```