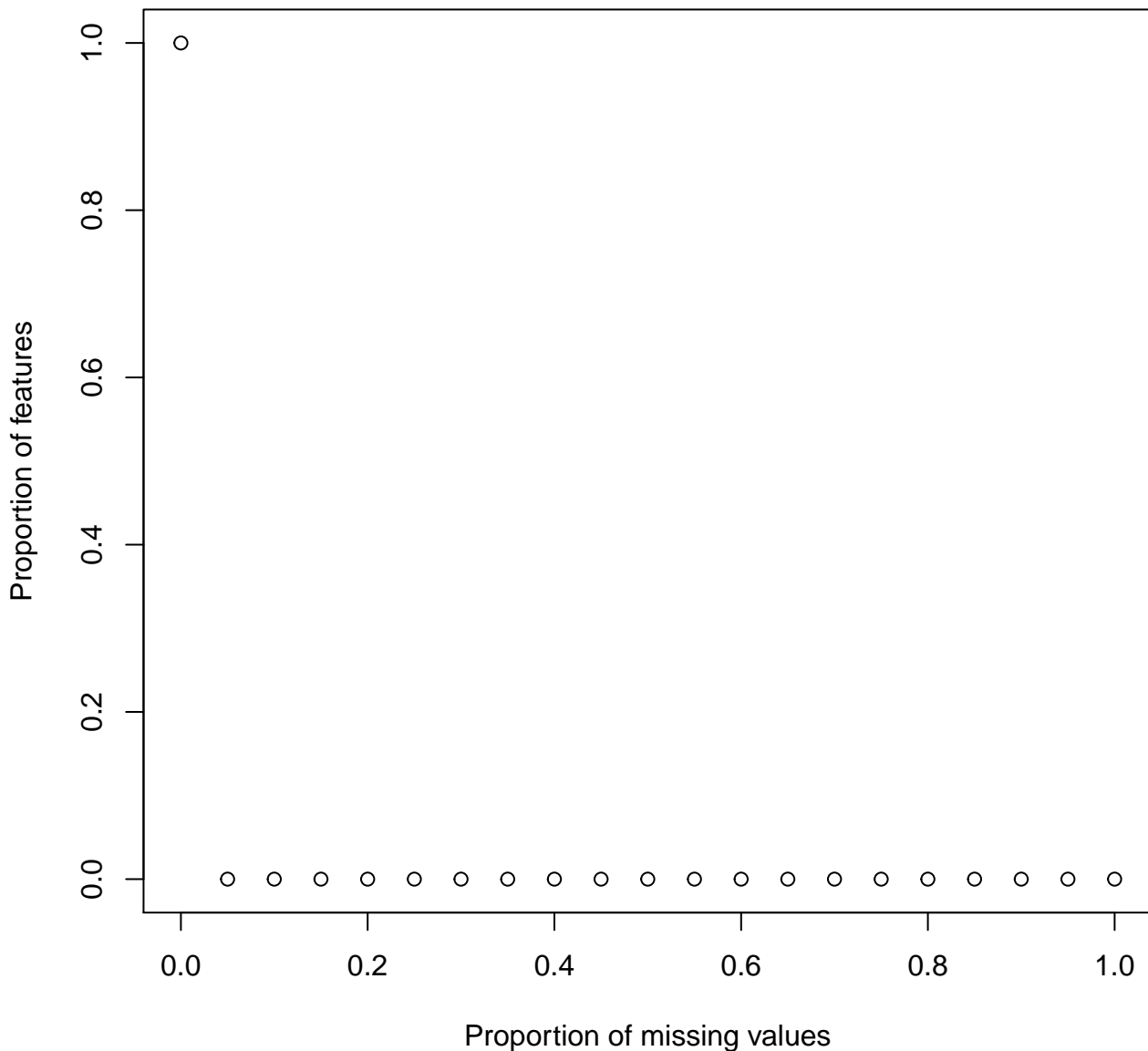
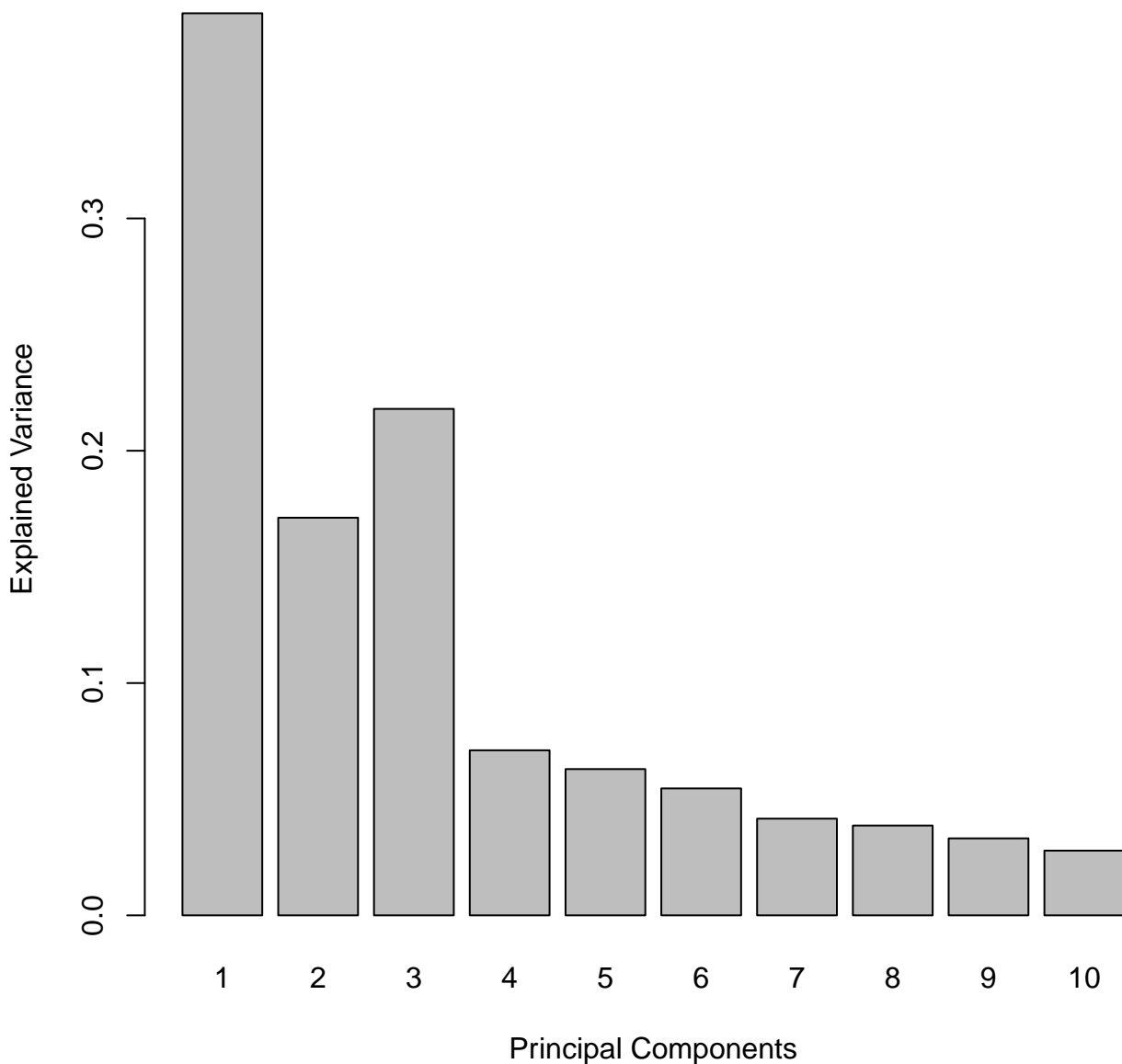


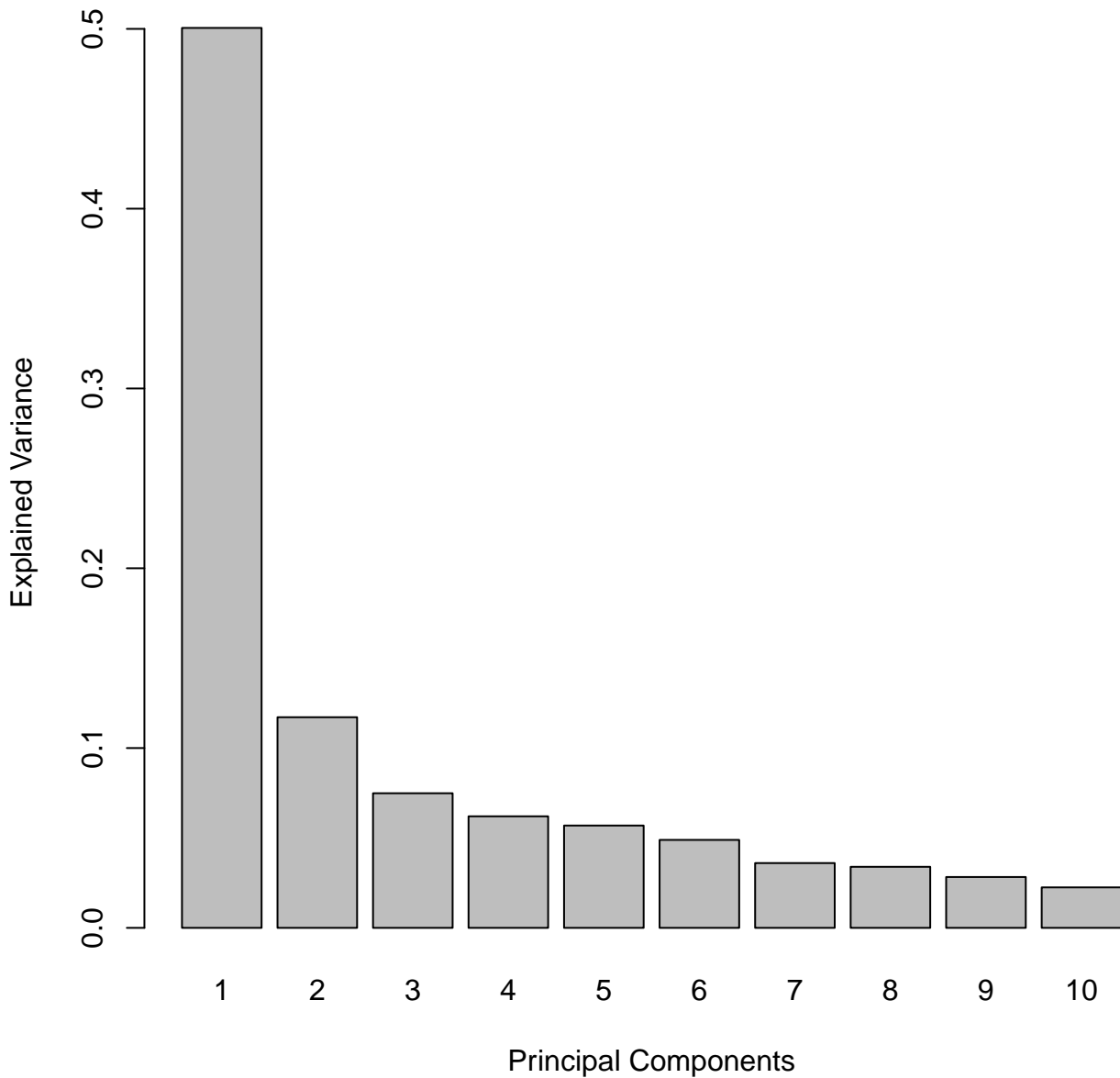
# transcriptome missing value proportions for unfiltered data



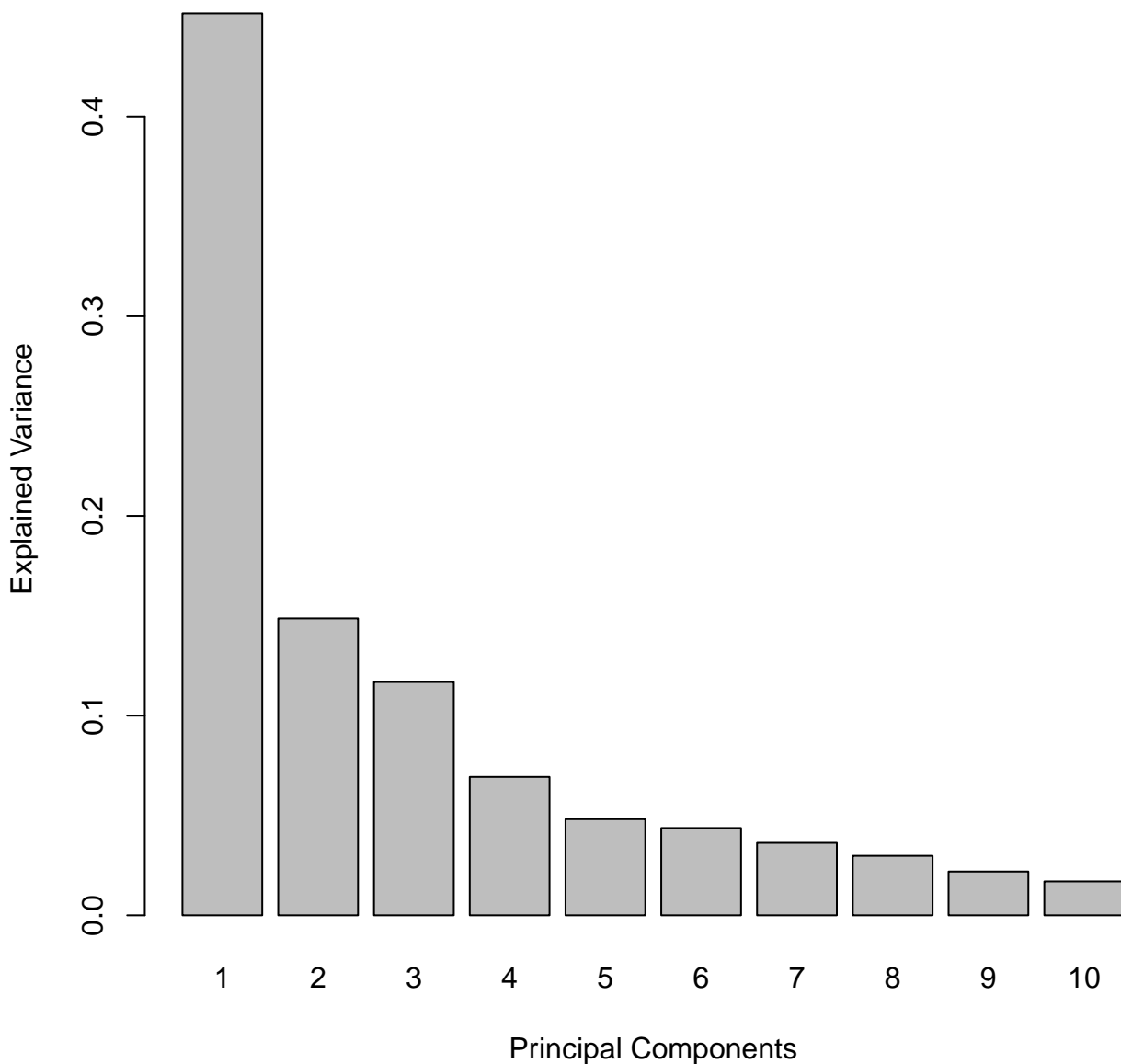
# metabolome screeplot



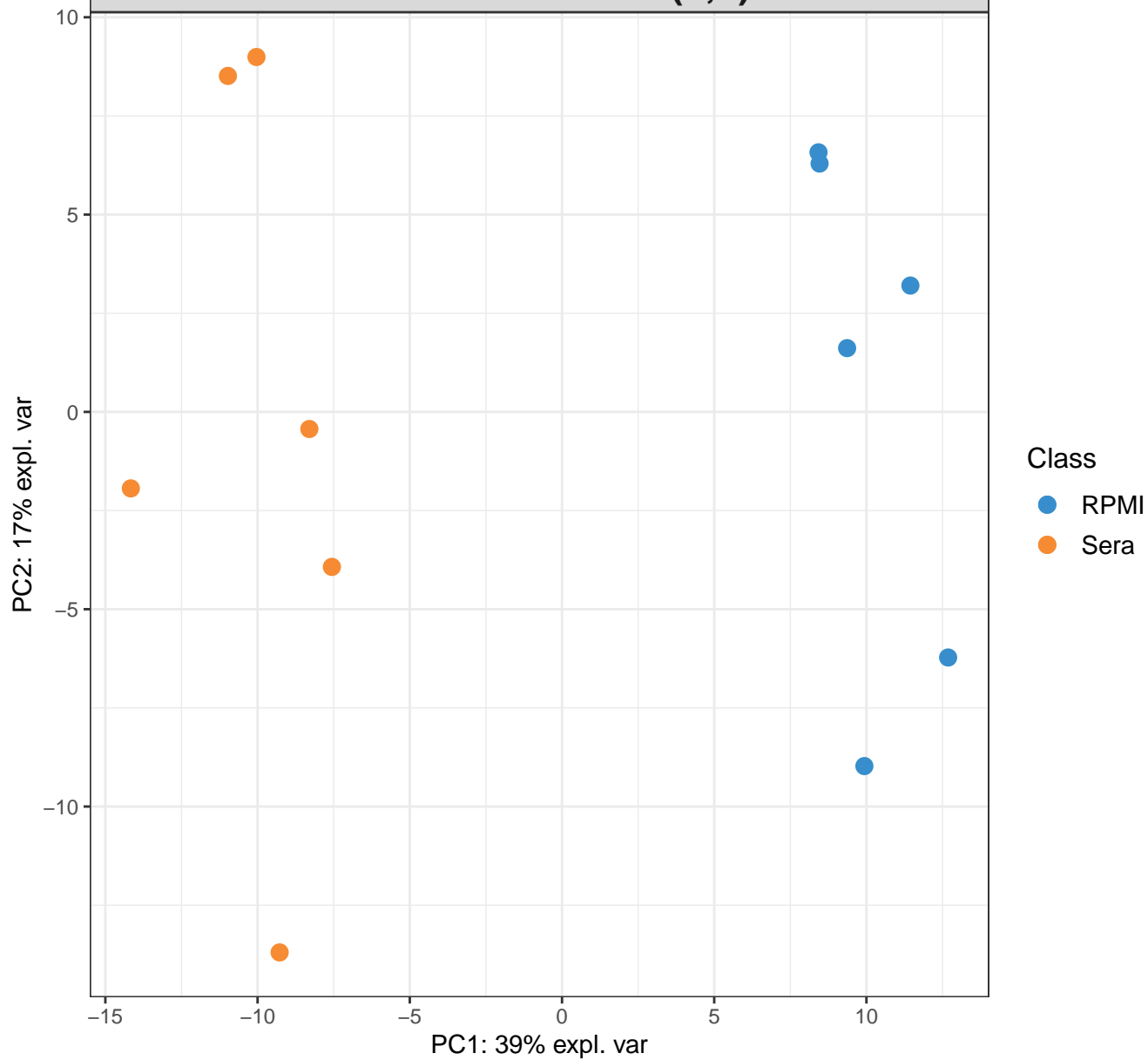
# proteome screeplot



# transcriptome screeplot

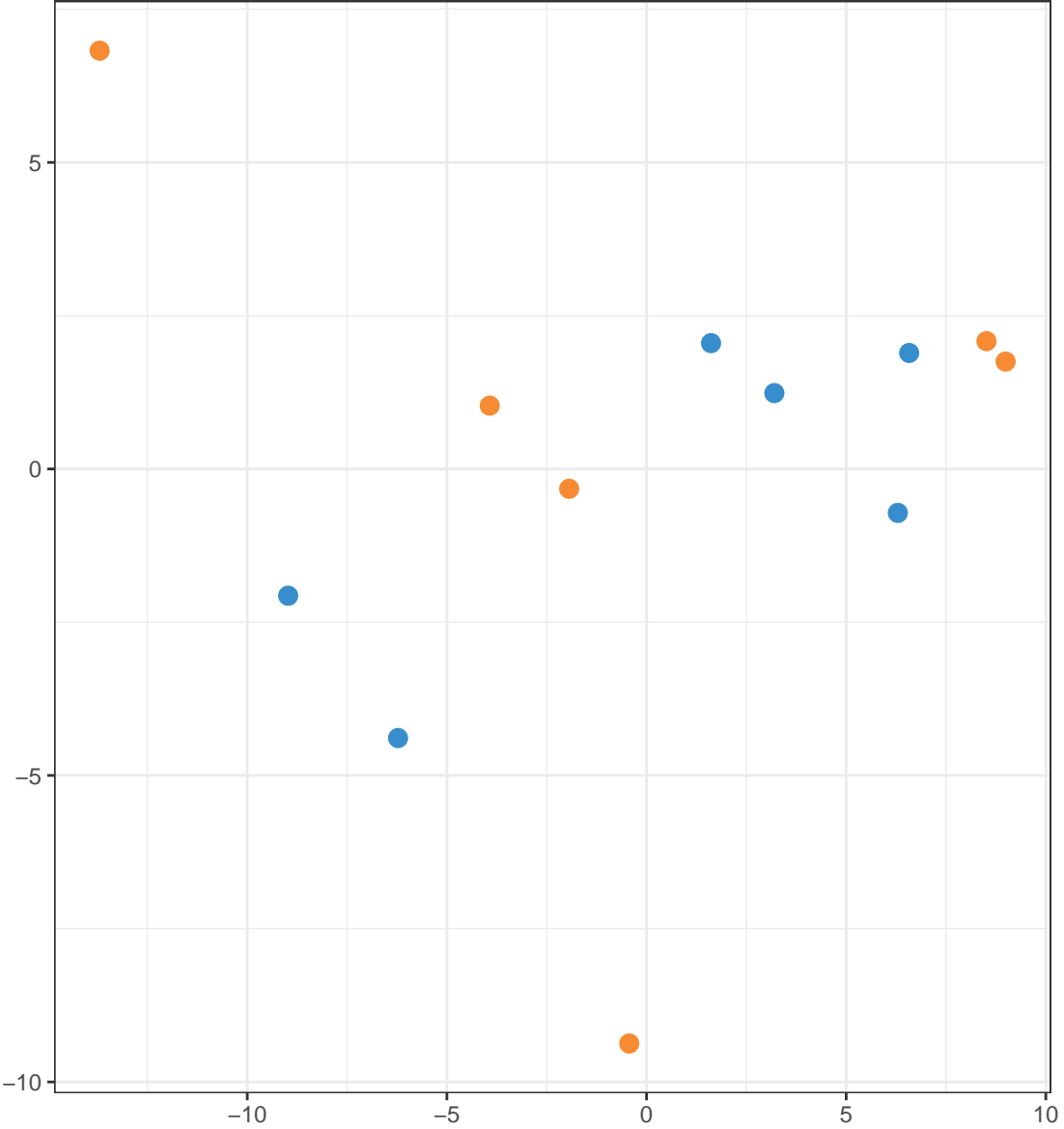


**No Impute n\_PCs = 10  
metabolome PCs (1,2)**



No Impute n\_PCs = 10  
metabolome PCs (2,3)

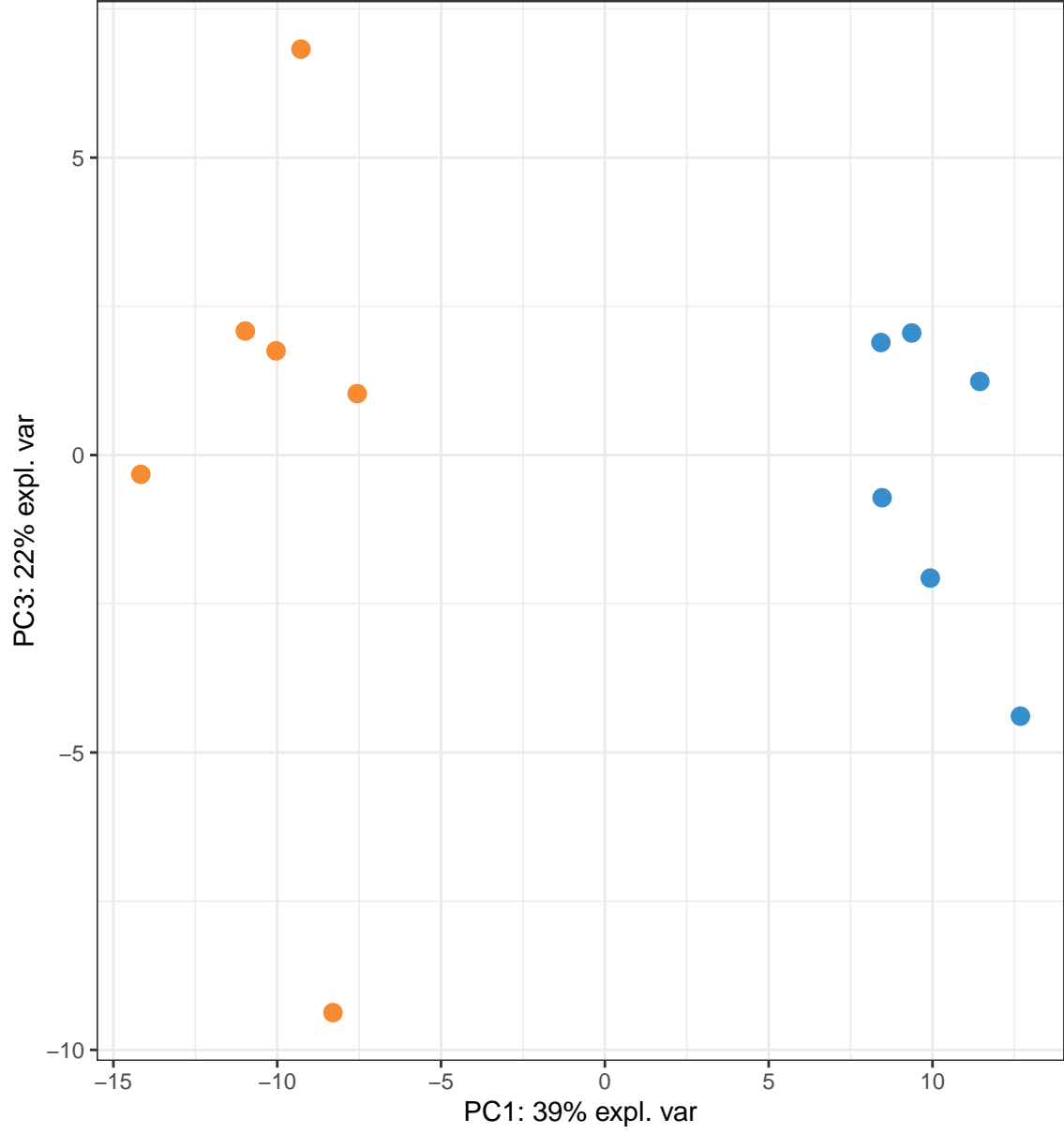
PC3: 22% expl. var



Class

- RPMI
- Sera

No Impute n\_PCs = 10  
metabolome PCs (1,3)

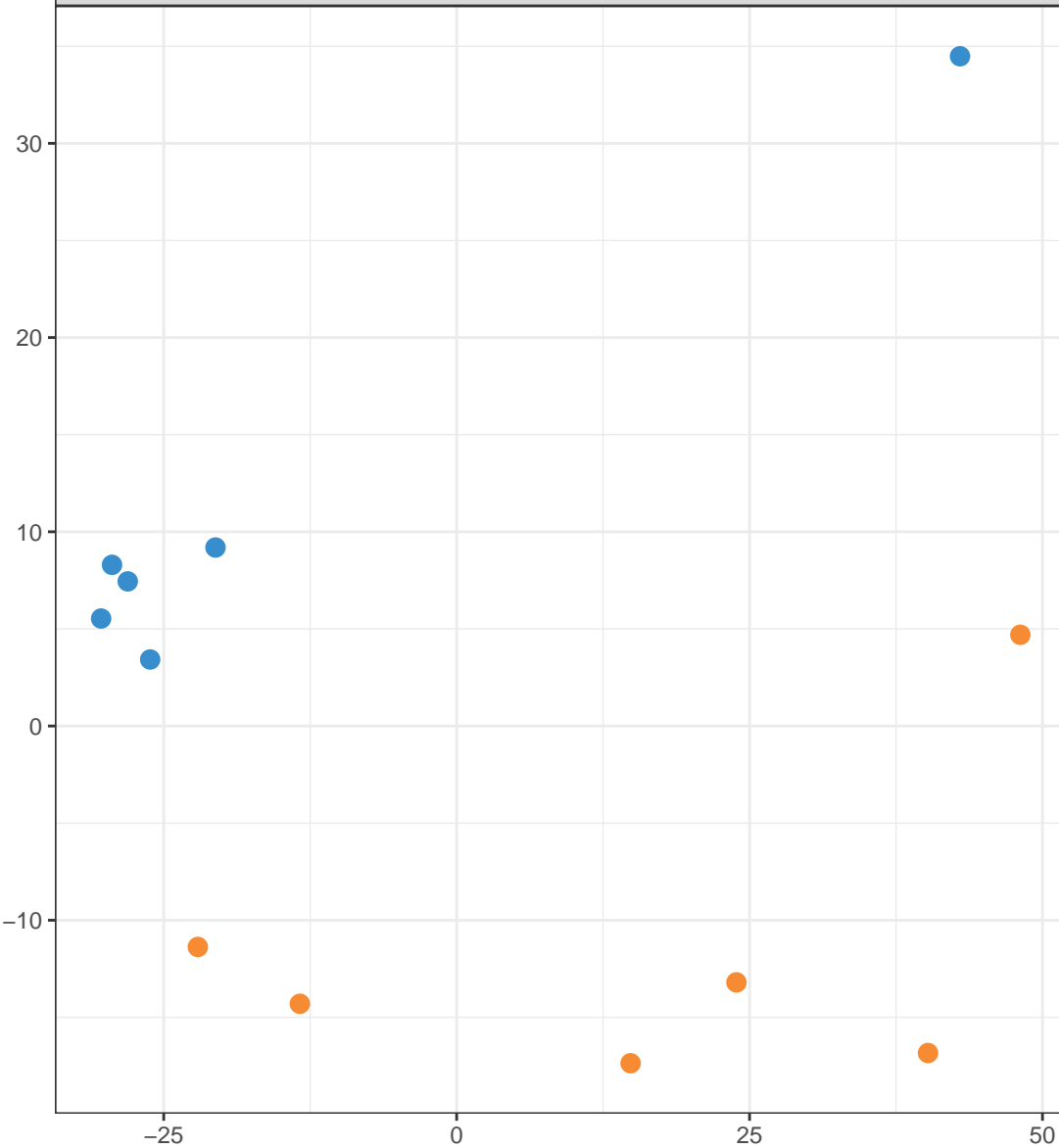


Class

- RPMI
- Sera

**No Impute n\_PCs = 10  
proteome PCs (1,2)**

PC2: 12% expl. var



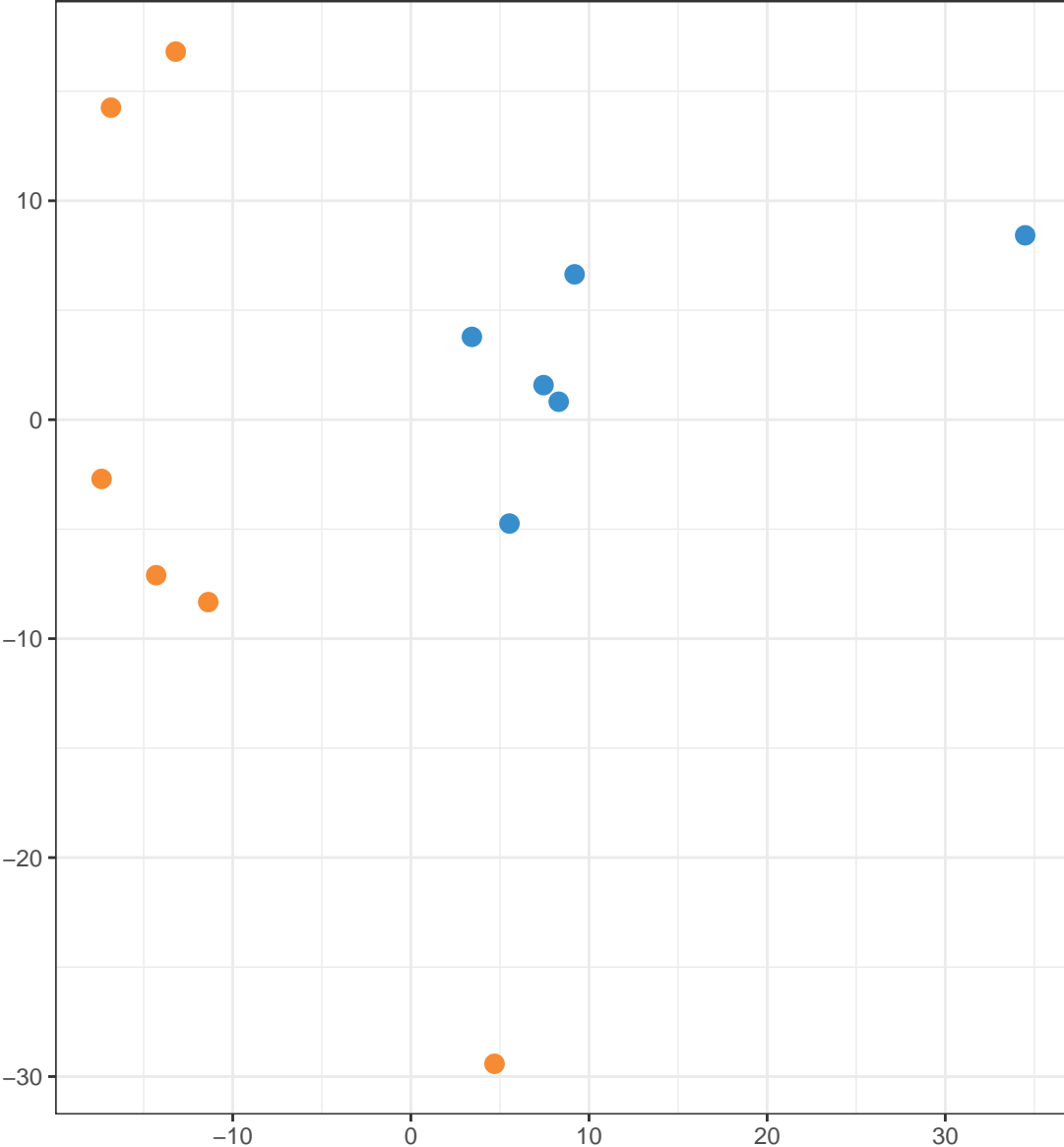
Class

● RPMI  
● Sera



**No Impute n\_PCs = 10  
proteome PCs (2,3)**

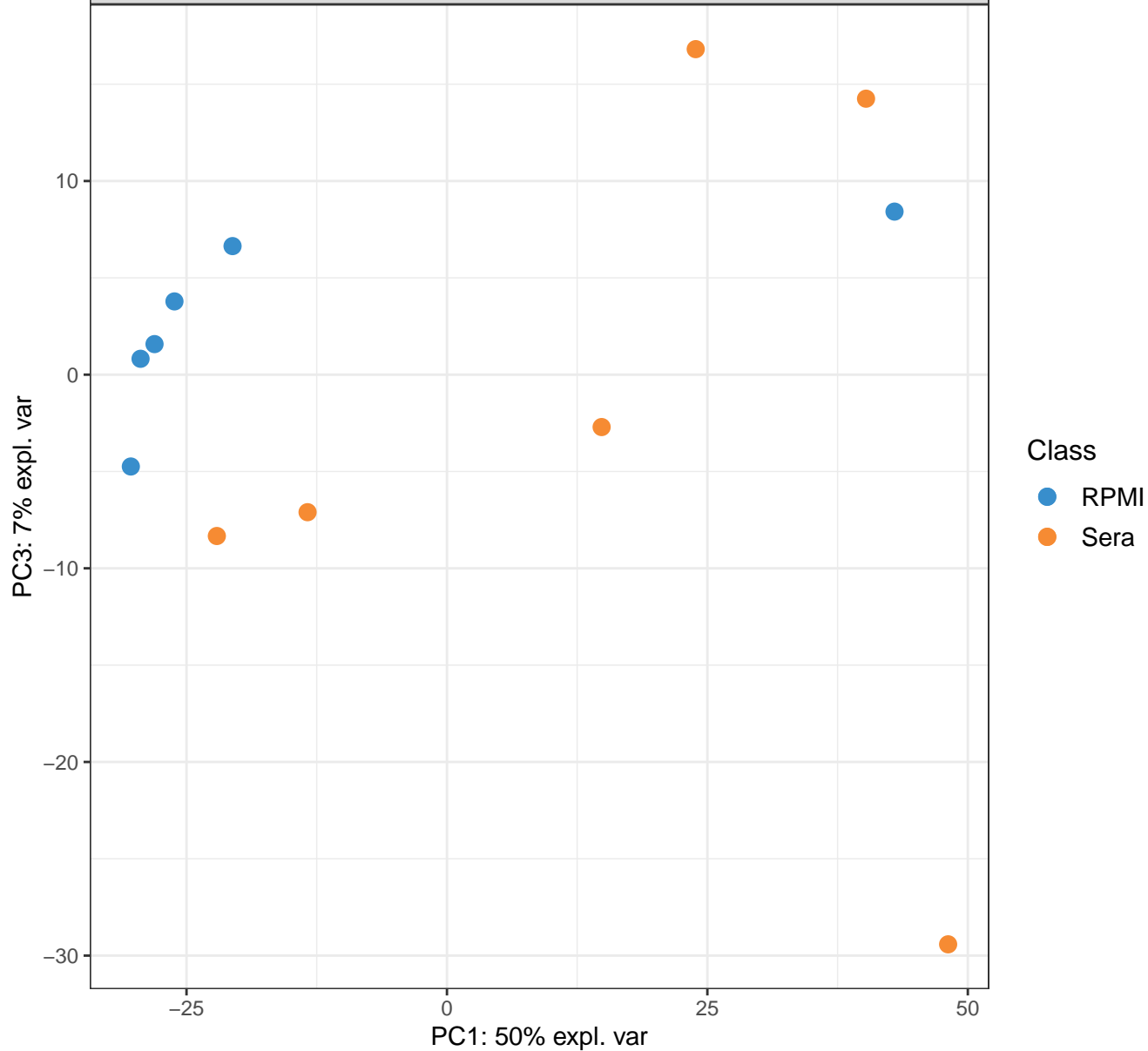
PC3: 7% expl. var



Class

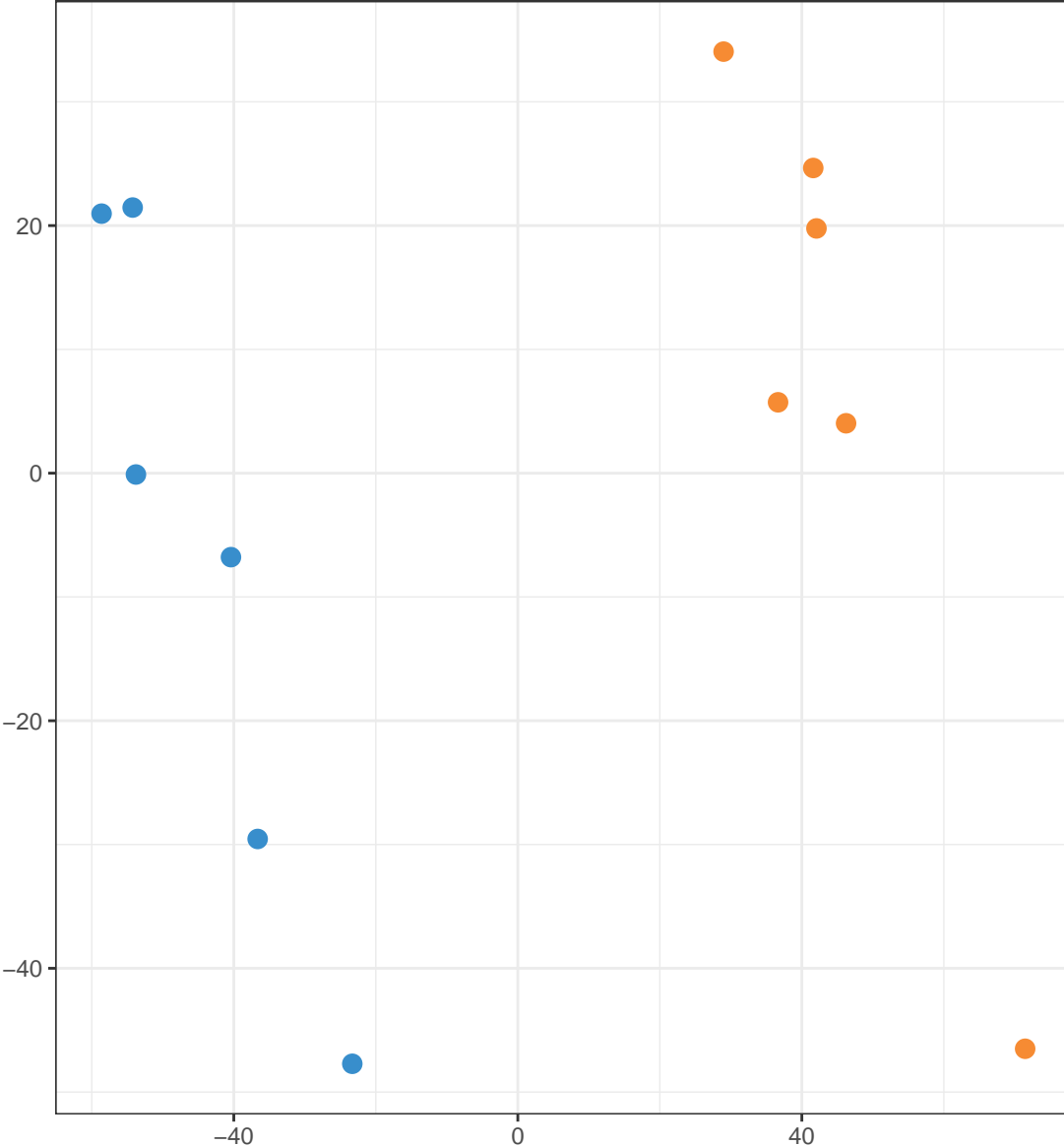
- RPMI
- Sera

**No Impute n\_PCs = 10  
proteome PCs (1,3)**



**No Impute n\_PCs = 10  
transcriptome PCs (1,2)**

PC2: 15% expl. var

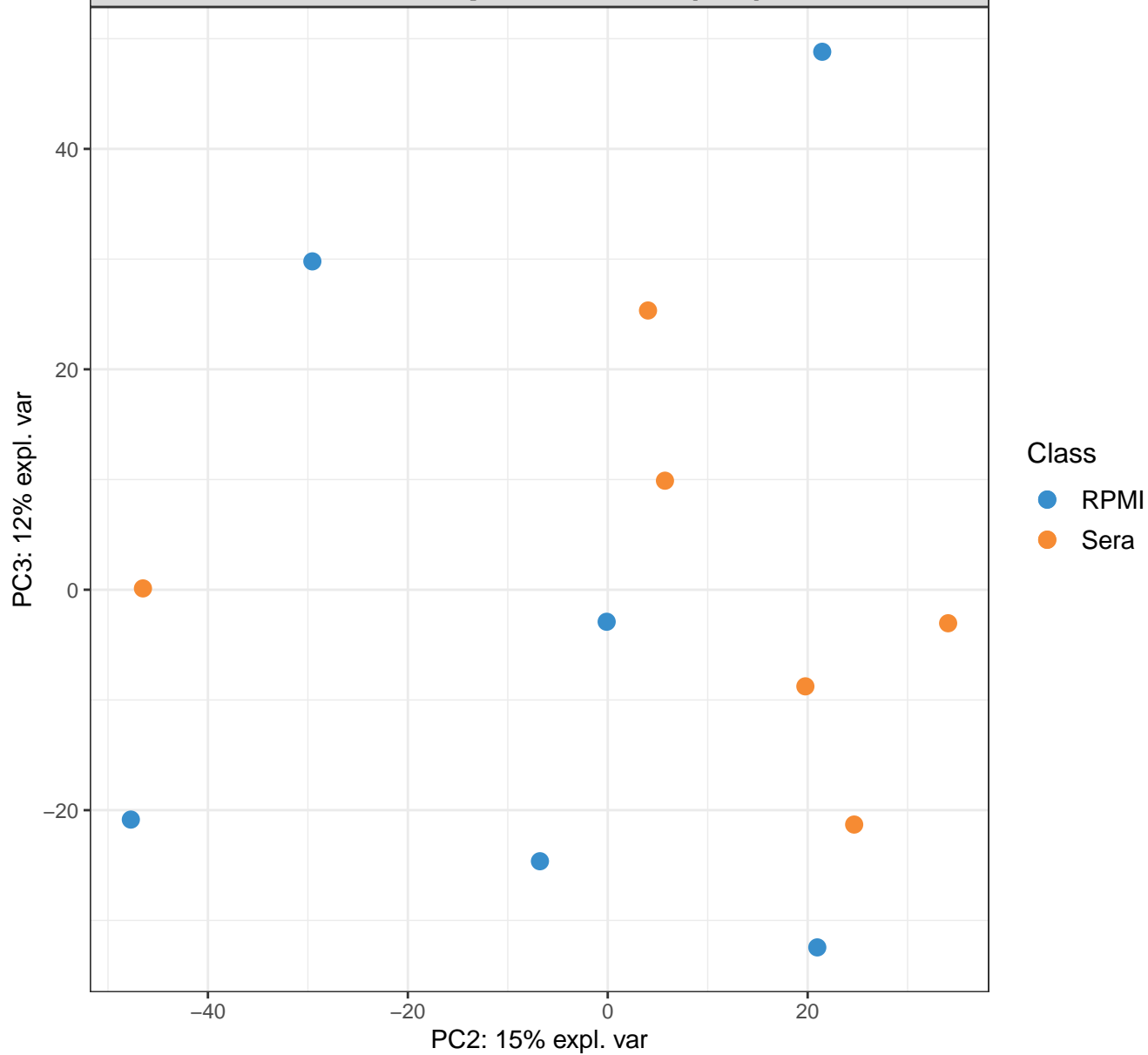


PC1: 45% expl. var

Class

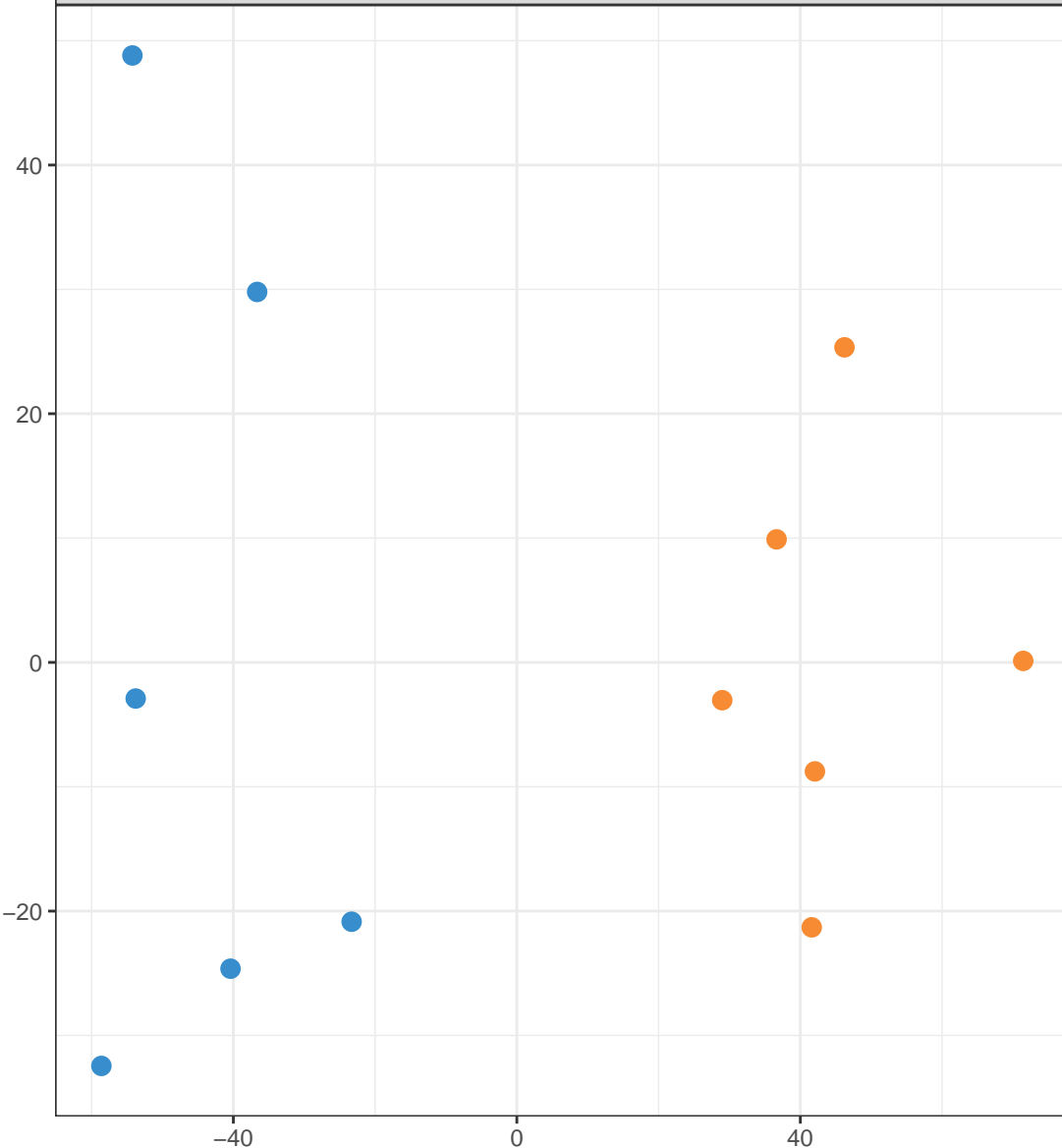
- RPMI
- Sera

**No Impute n\_PCs = 10  
transcriptome PCs (2,3)**



**No Impute n\_PCs = 10  
transcriptome PCs (1,3)**

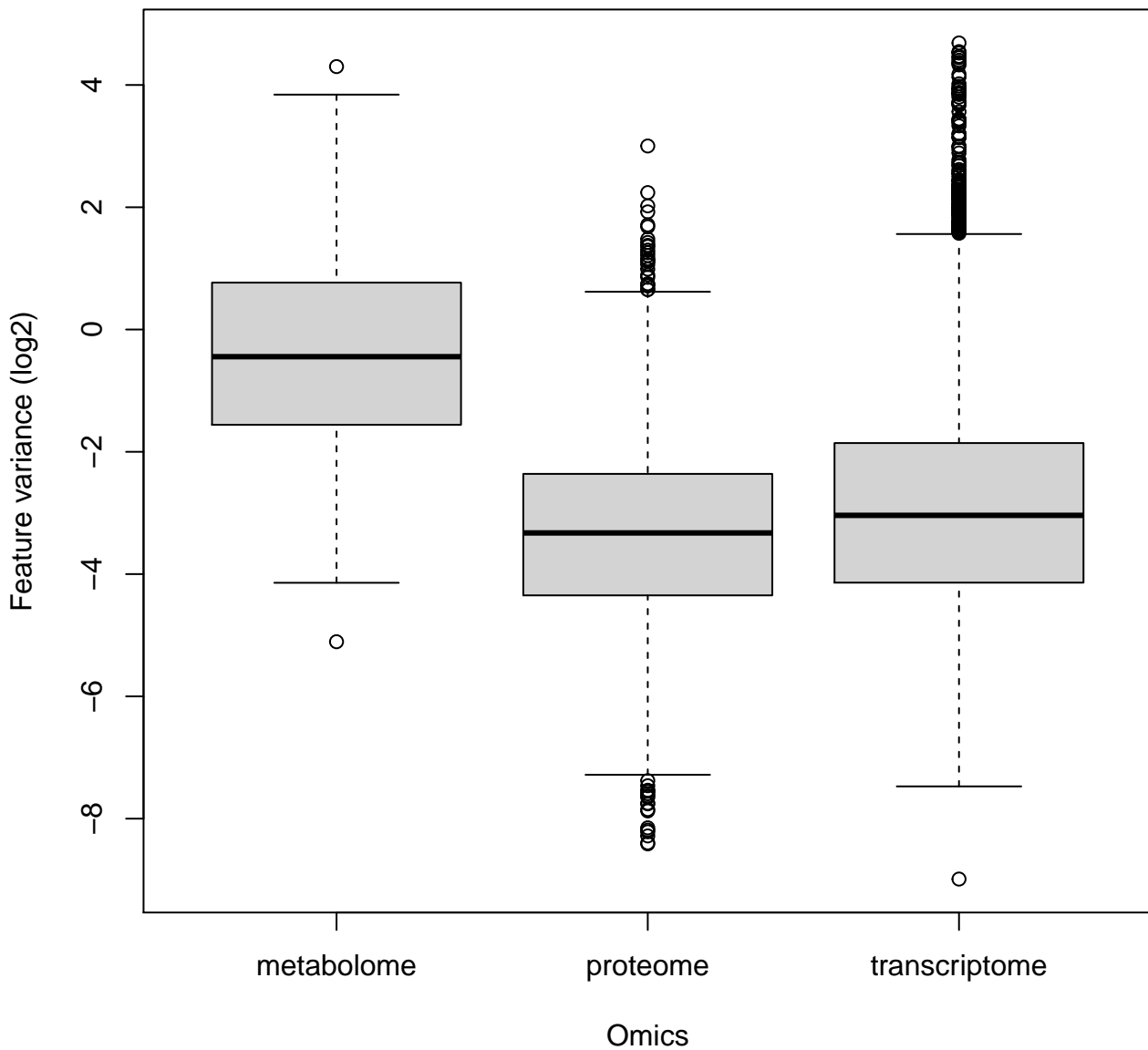
PC3: 12% expl. var



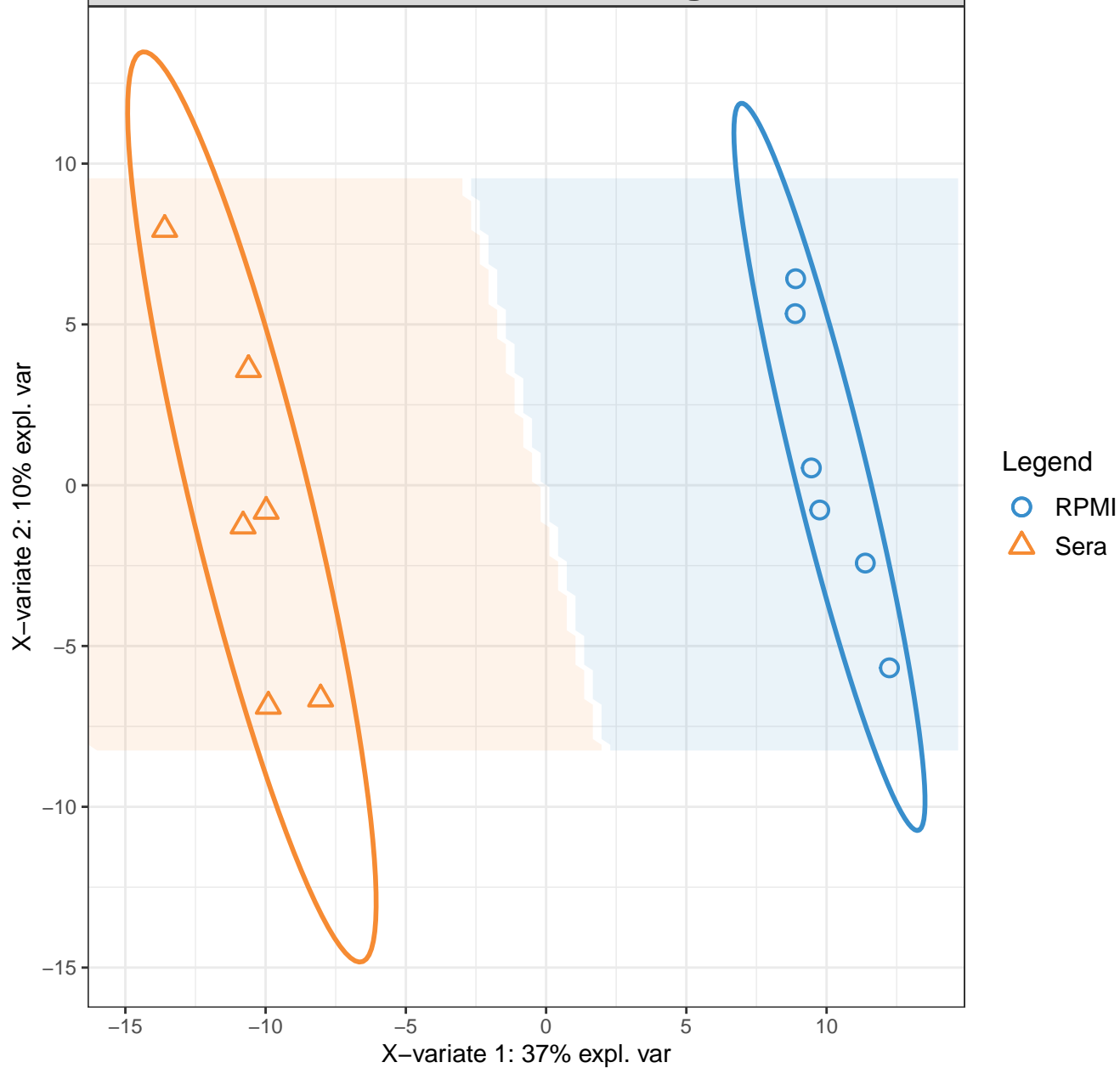
Class

- RPMI
- Sera

## Feature variances (log2) per omics

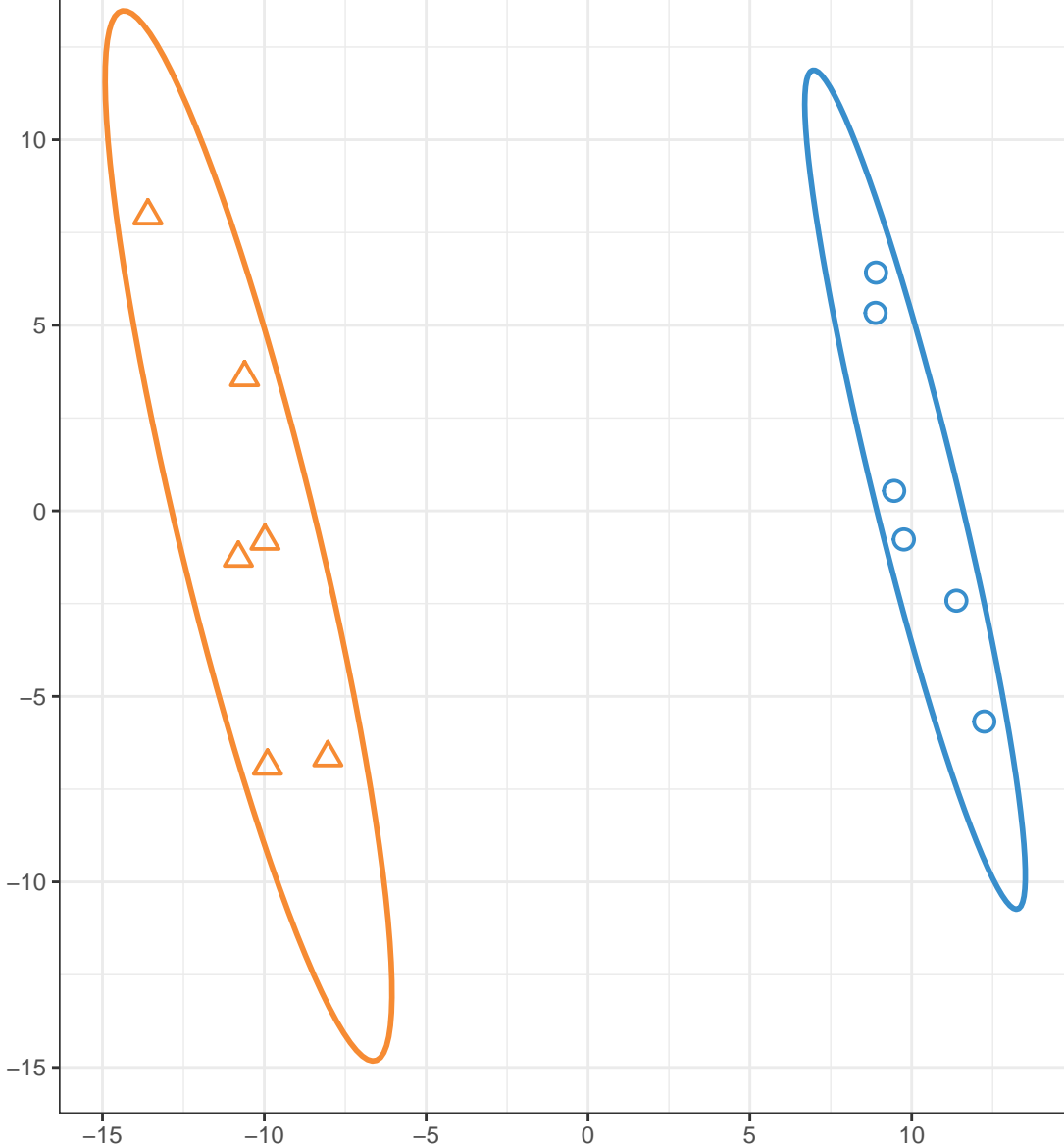


# metabolome PLSDA single 1/2



# metabolome PLSDA single 1/2

X-variate 2: 10% expl. var

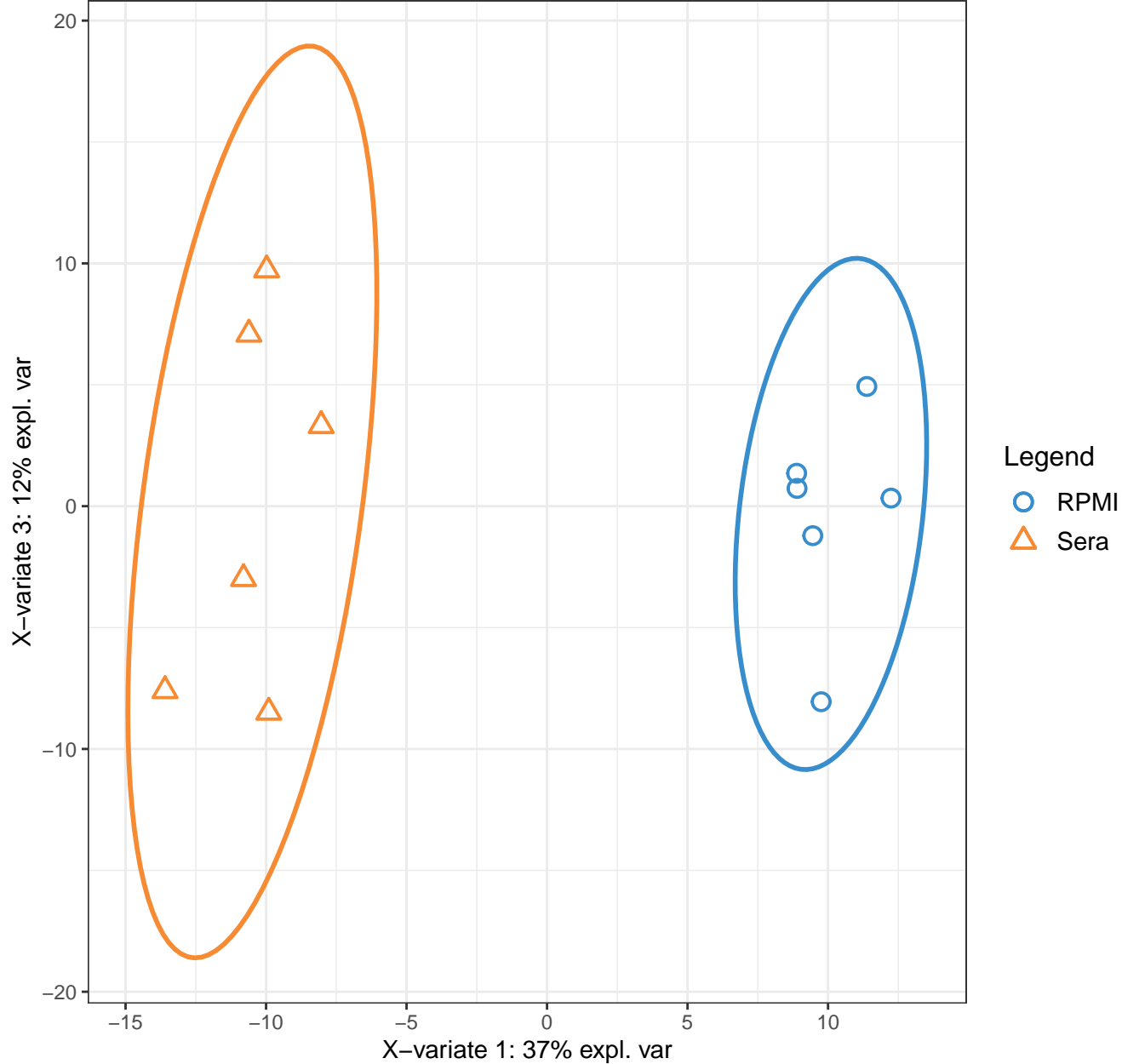


Legend

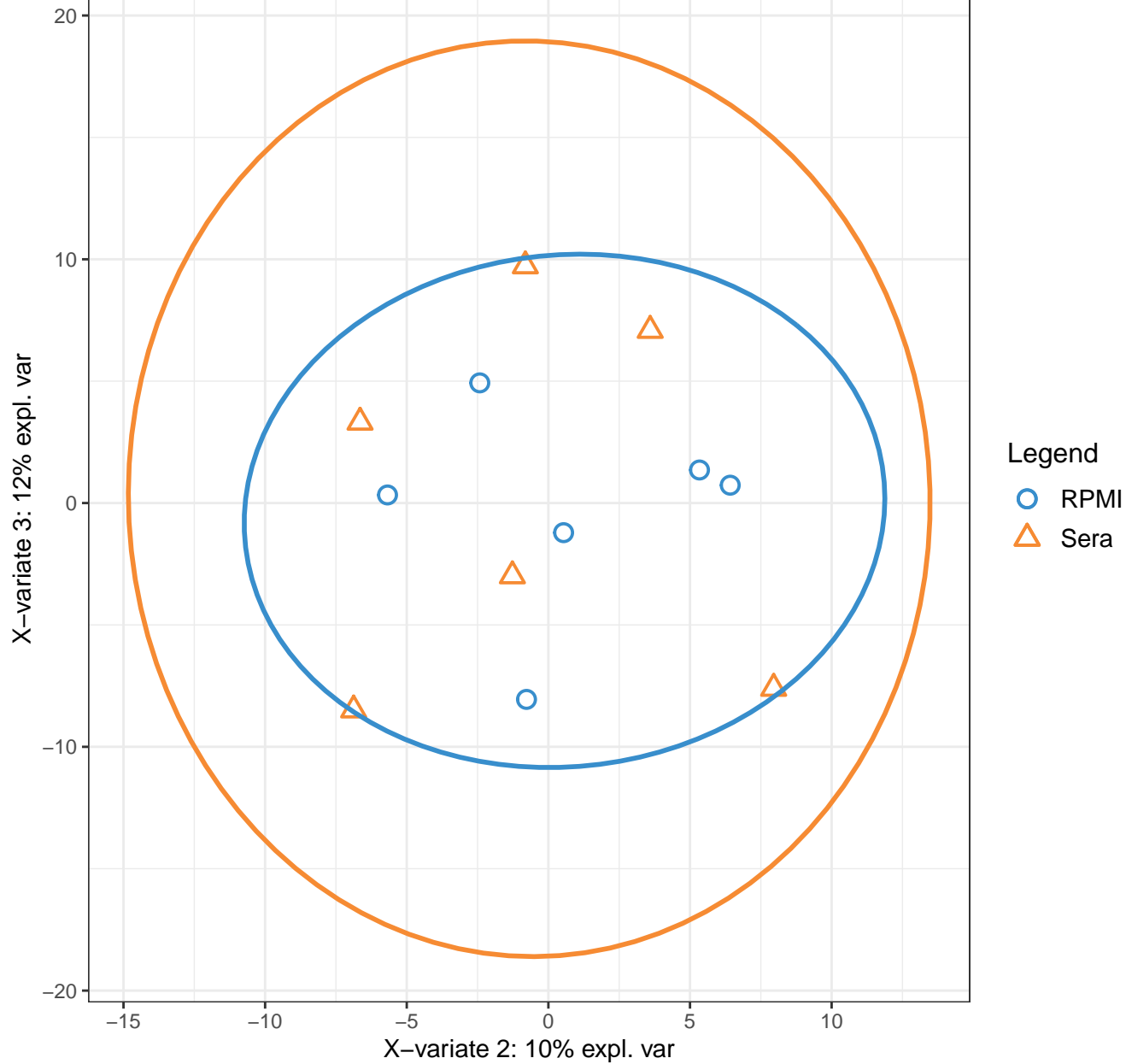
- RPMI
- △ Sera

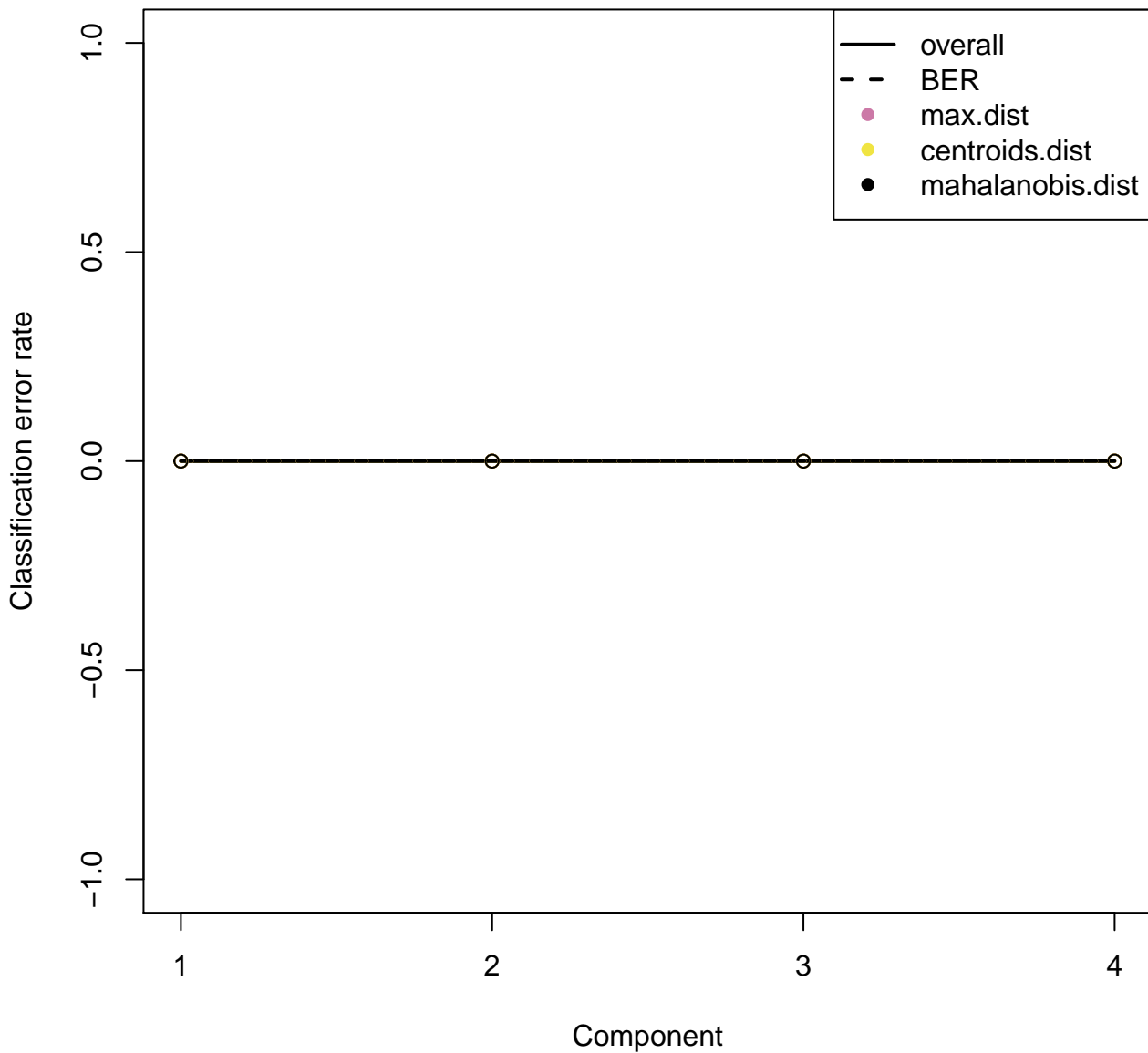


# metabolome PLSDA single 1/3

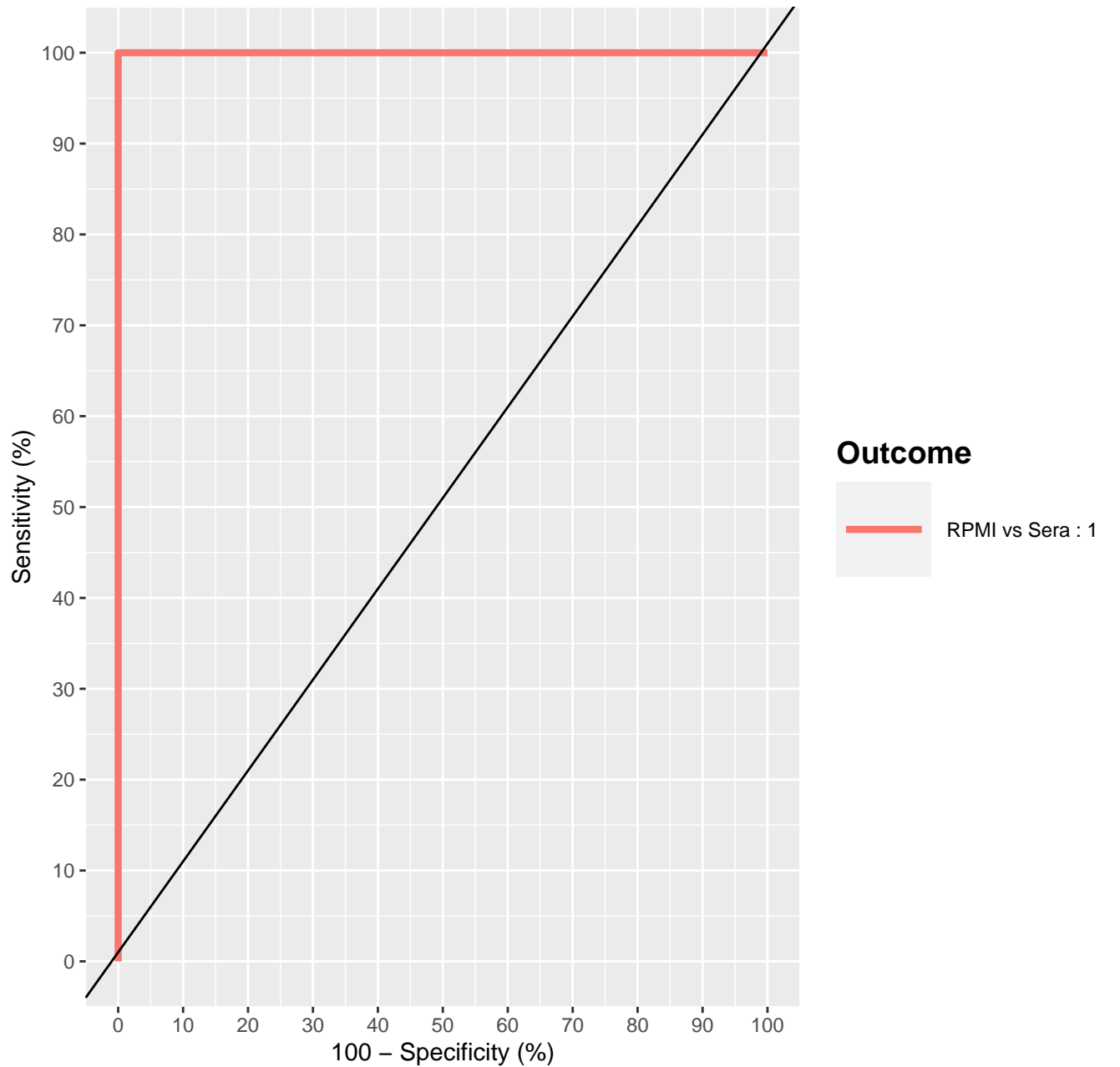


# metabolome PLSDA single 2/3

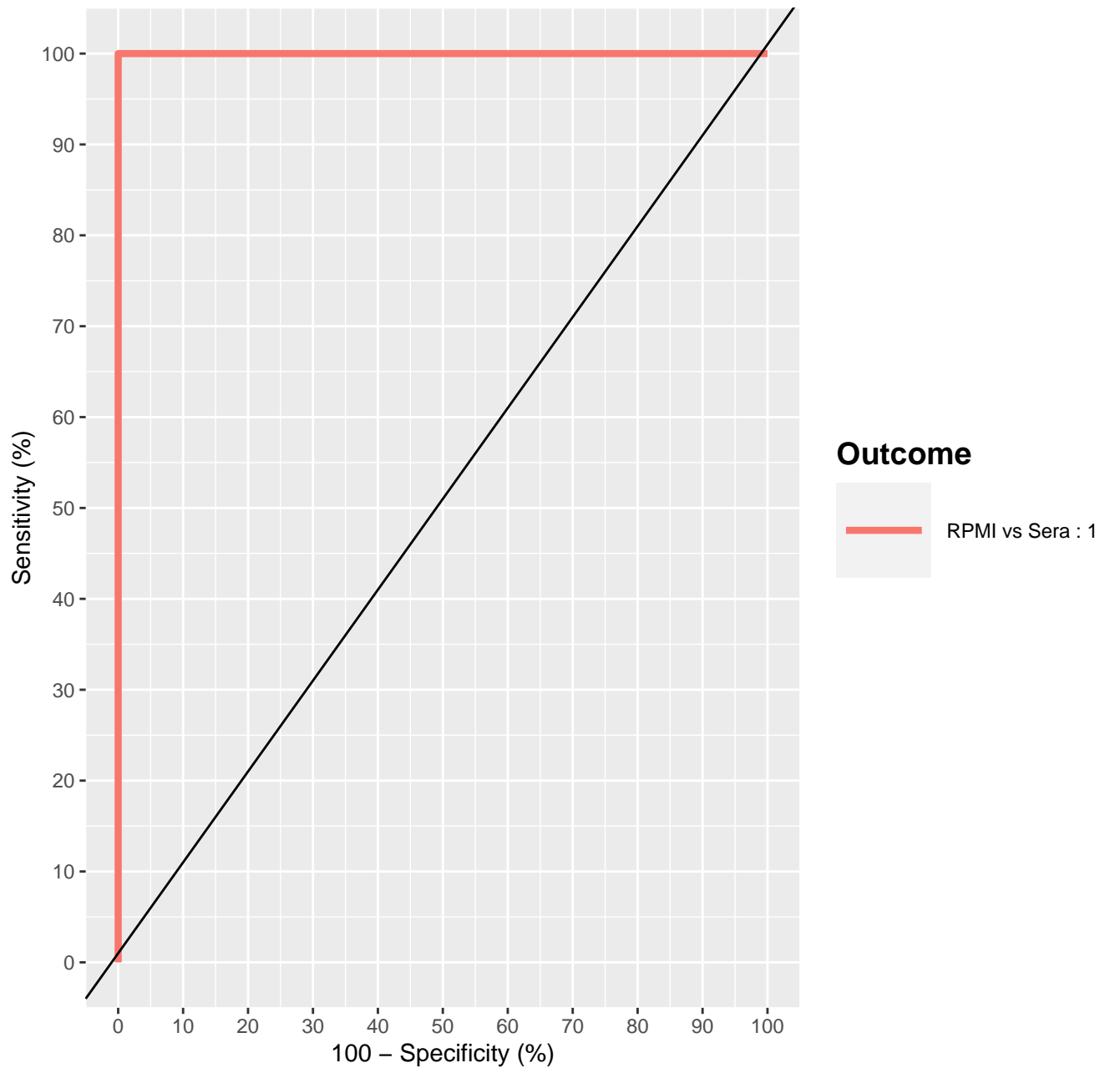




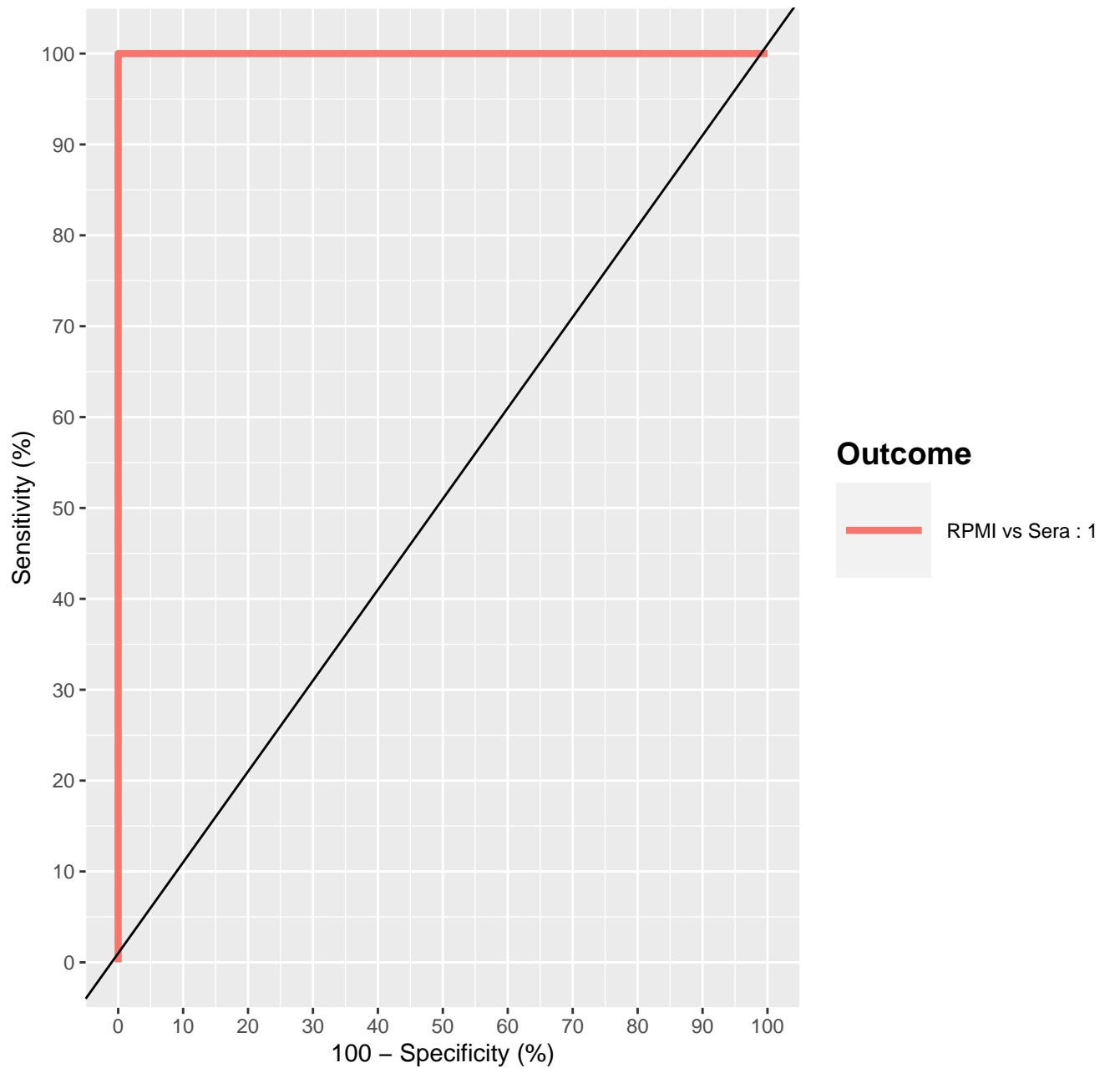
**ROC Curve Using Comp(s): 1**



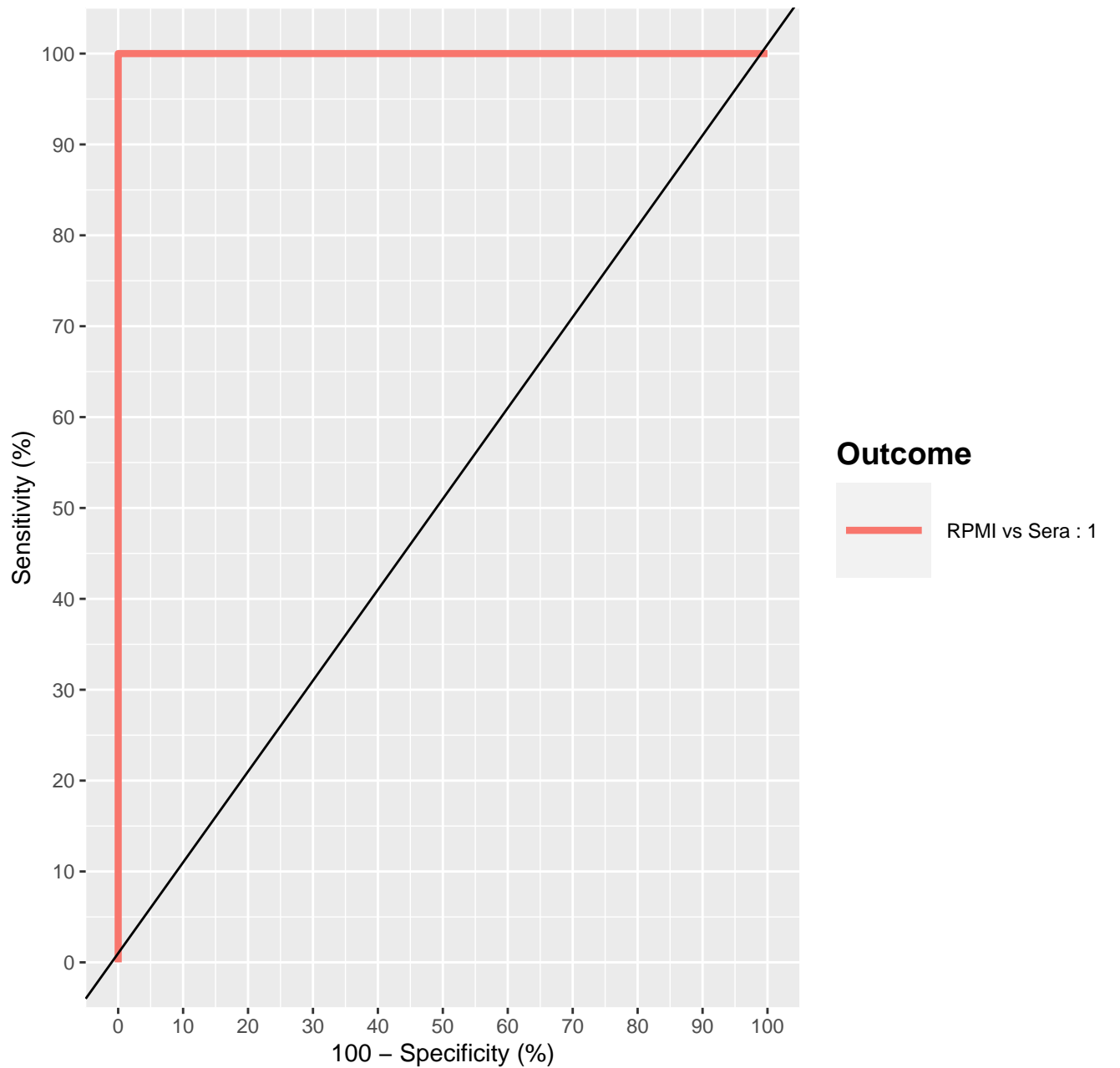
ROC Curve Using Comp(s): 1, 2



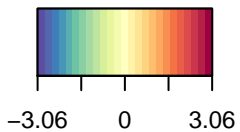
**ROC Curve Using Comp(s): 1, 2, 3**



**ROC Curve Using Comp(s): 1, 2, 3, 4**



Color key

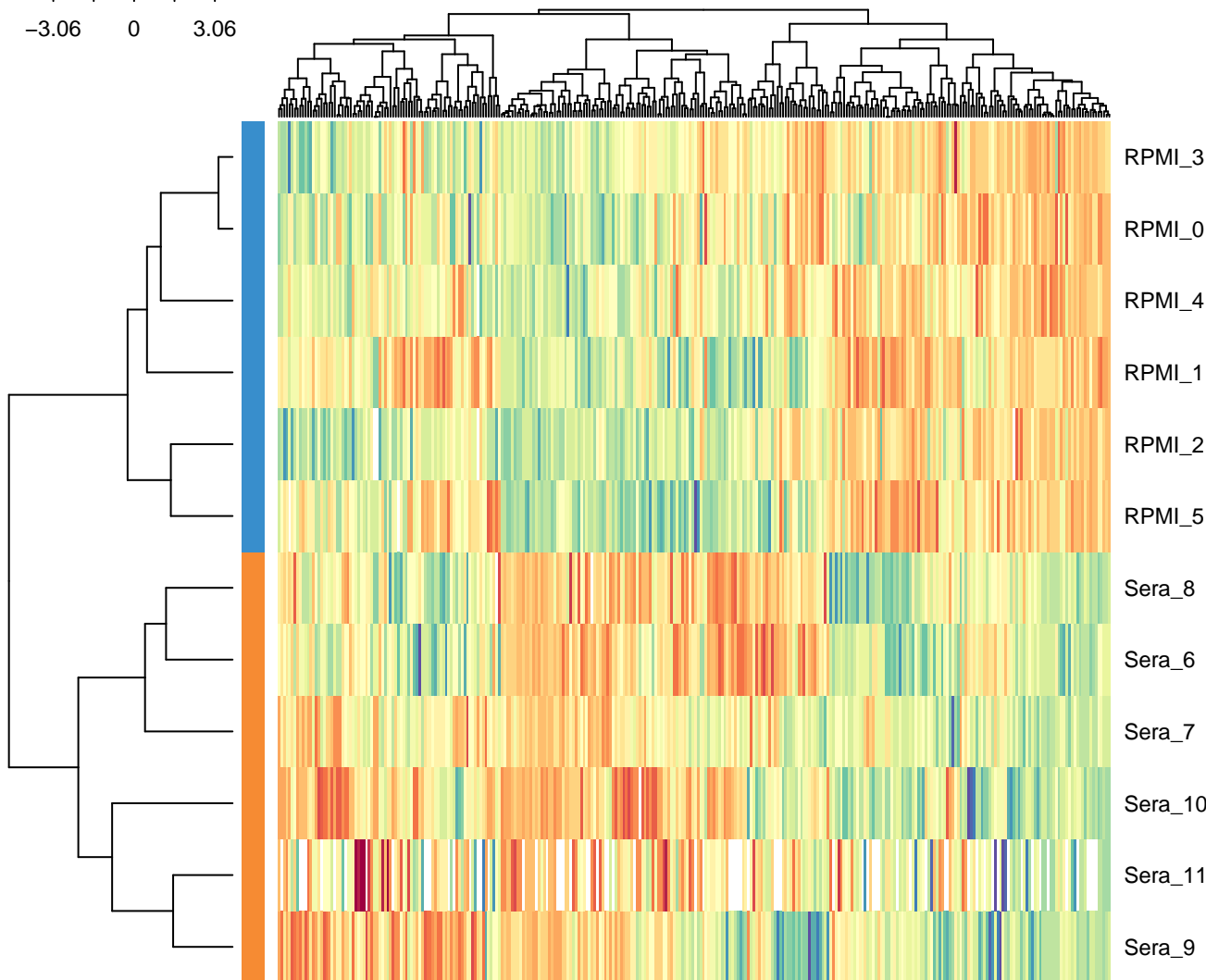


# PLSDA

Status

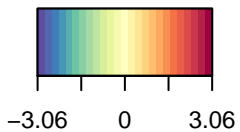
■ RPMI

■ Sera





Color key

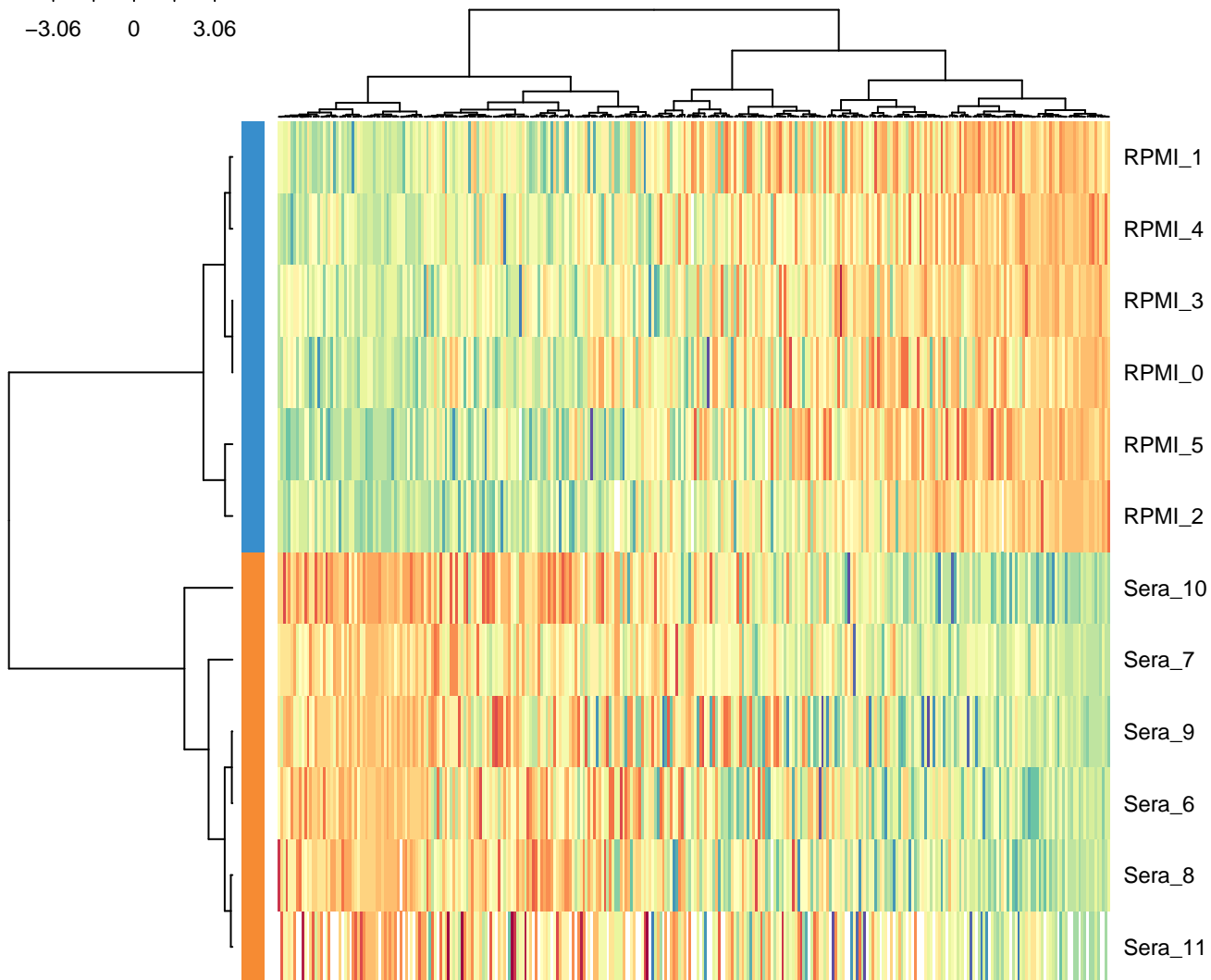


# PLSDA Component 1

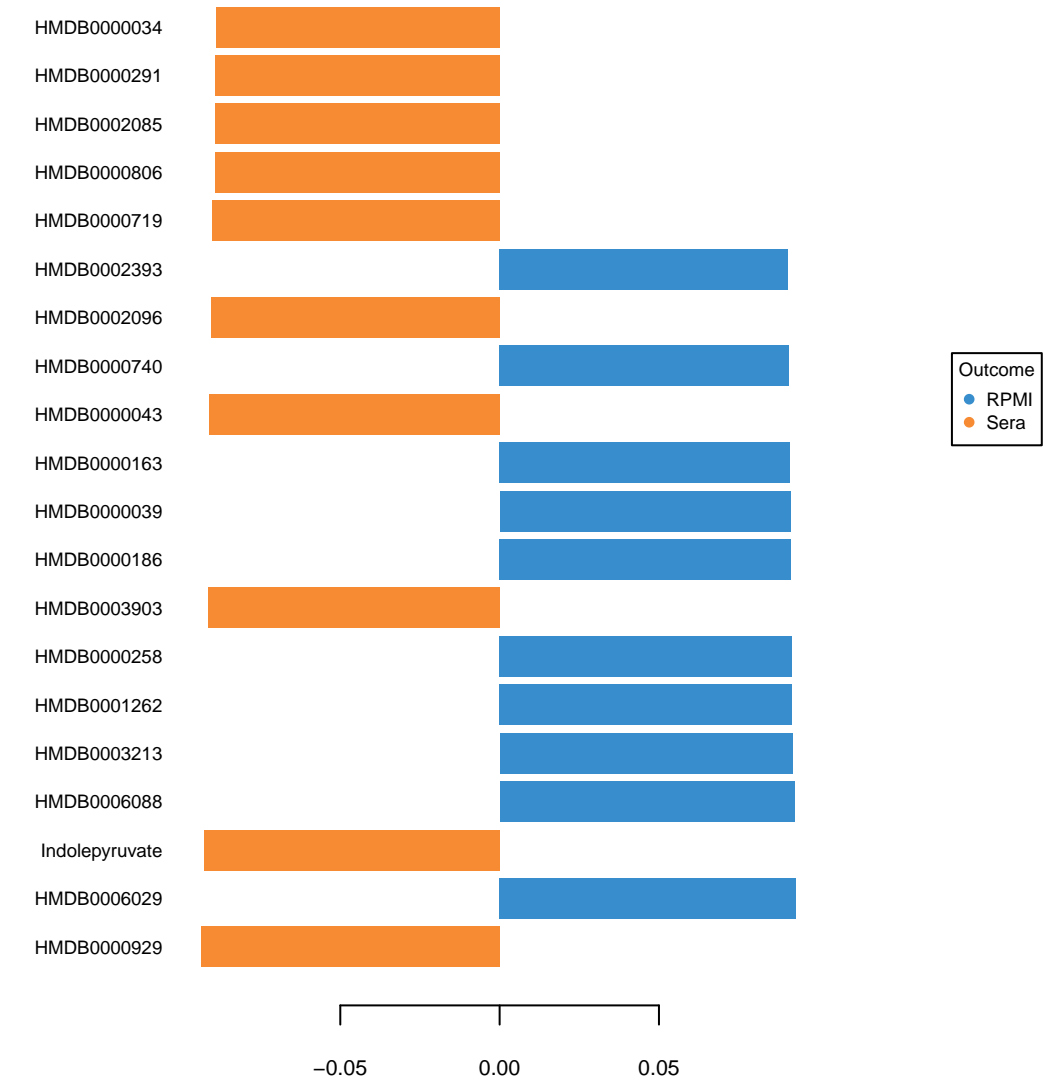
Status

RPMI

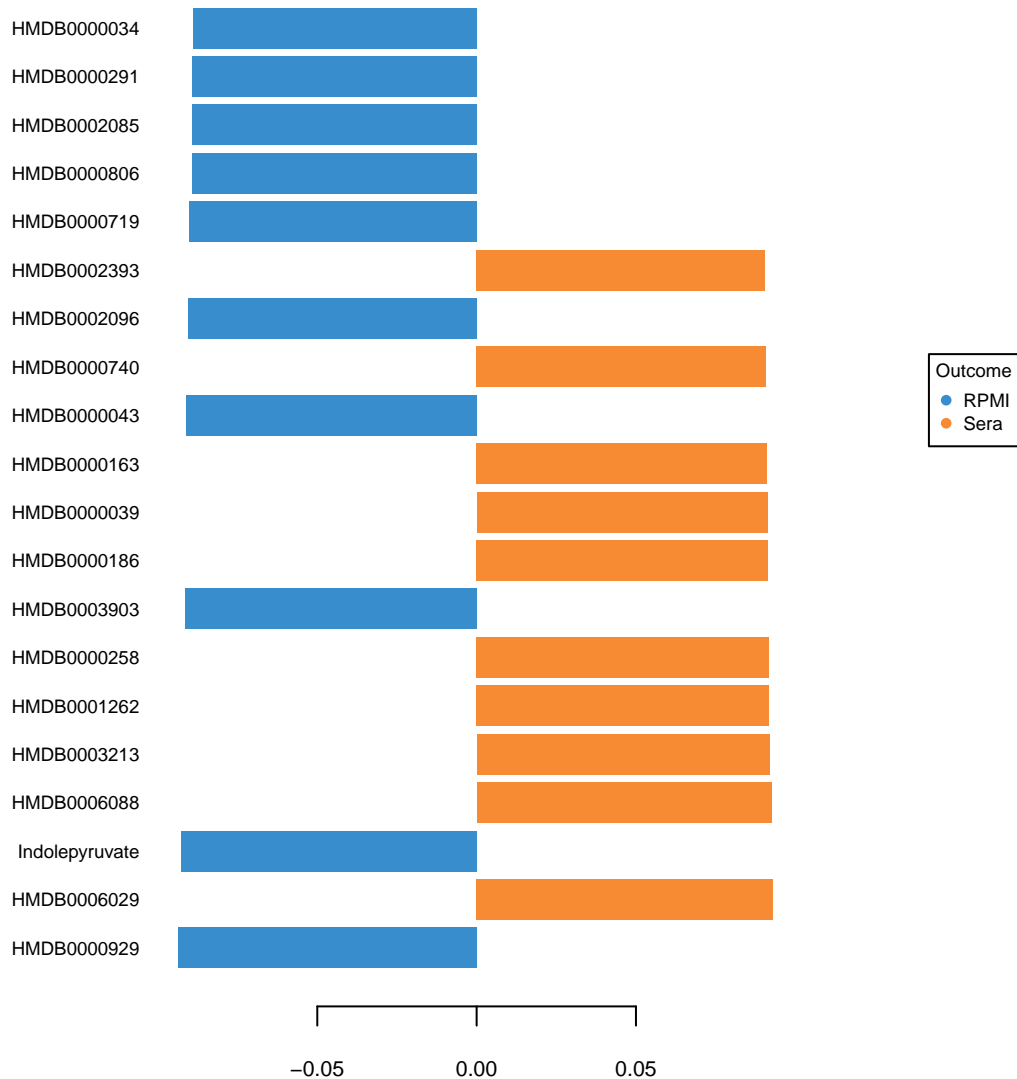
Sera



# metabolome 1 PLSDA max load

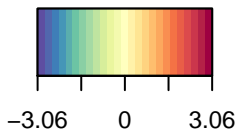


# metabolome 1 PLSDA min load



# PLSDA Component 2

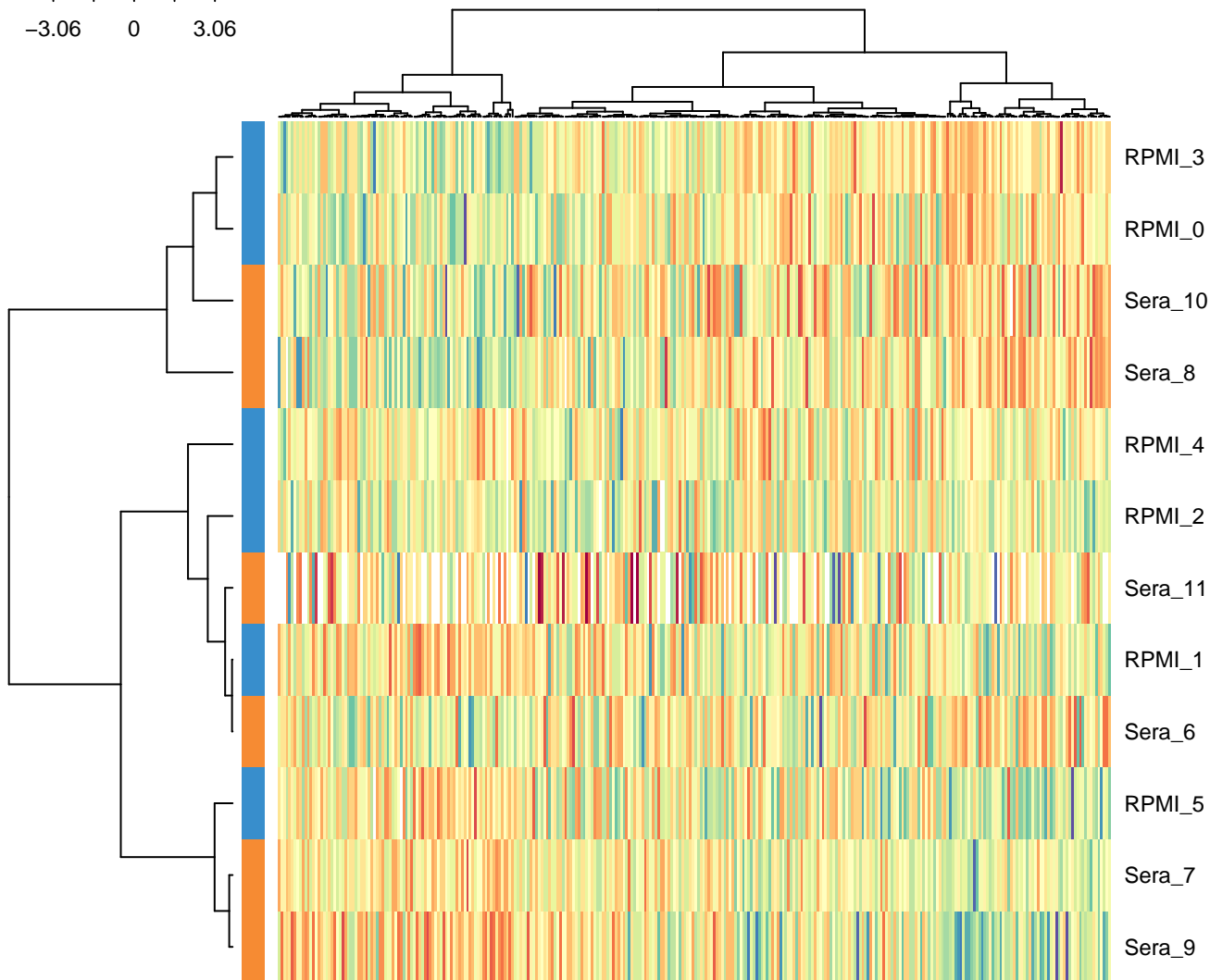
Color key



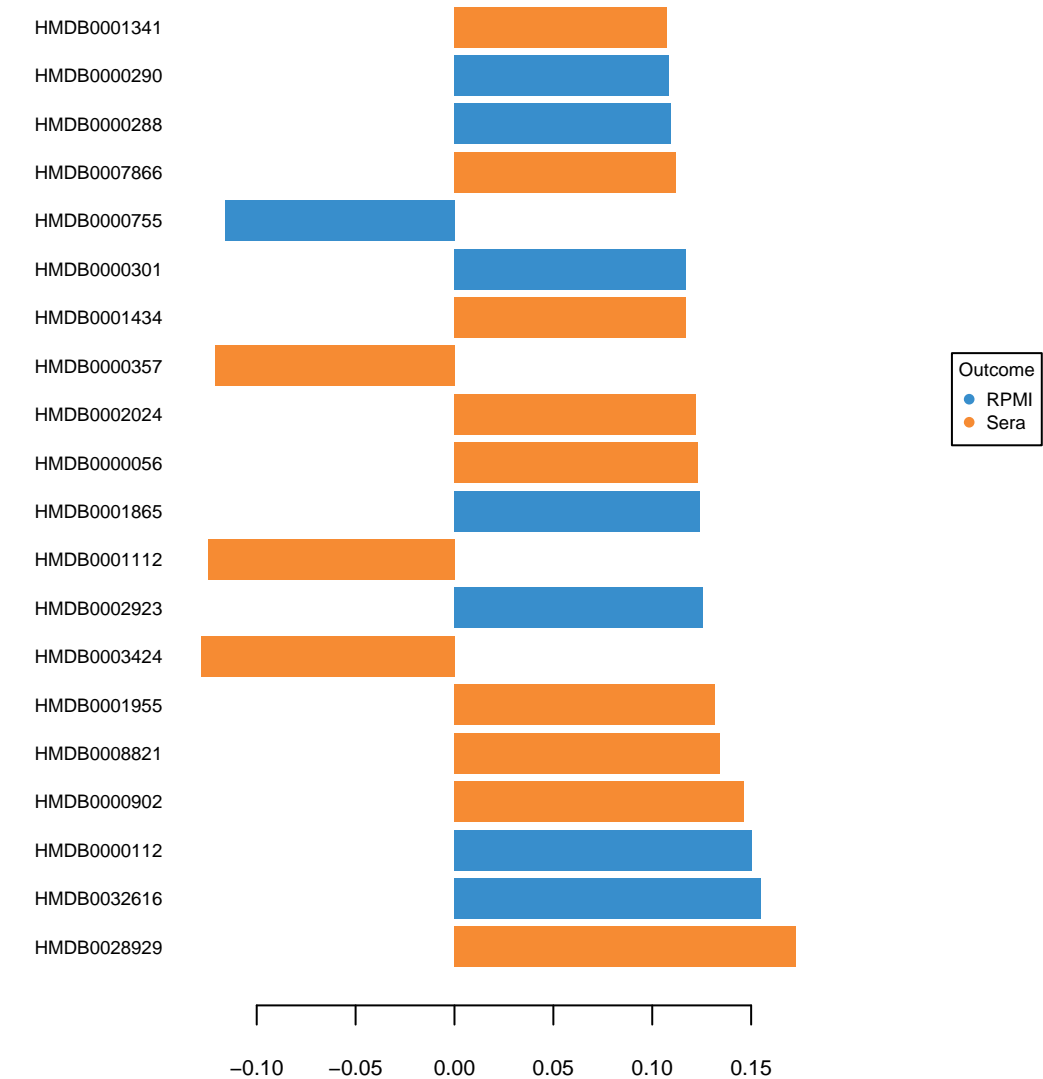
Status

RPMI

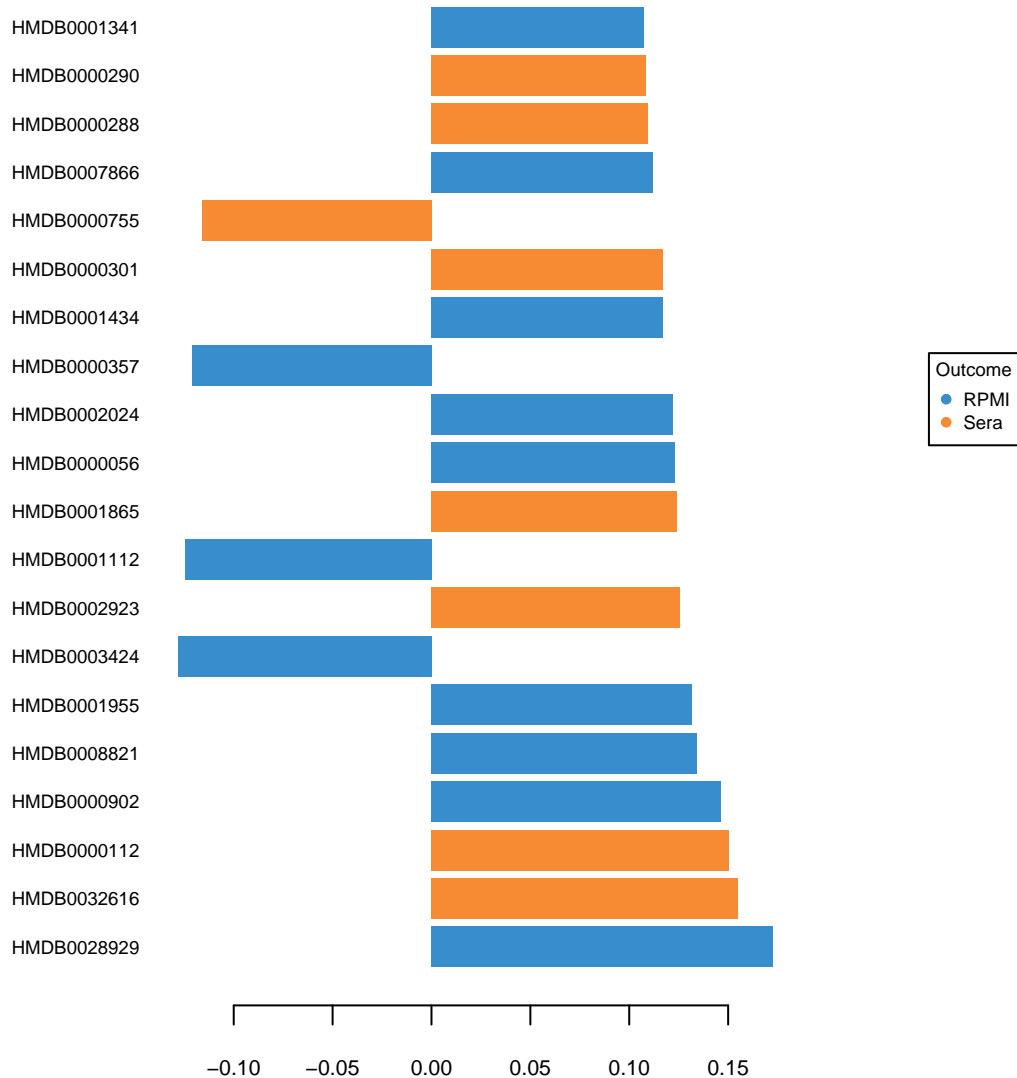
Sera



# metabolome 2 PLSDA max load

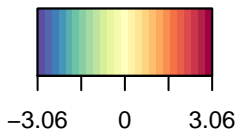


# metabolome 2 PLSDA min load



# PLSDA Component 3

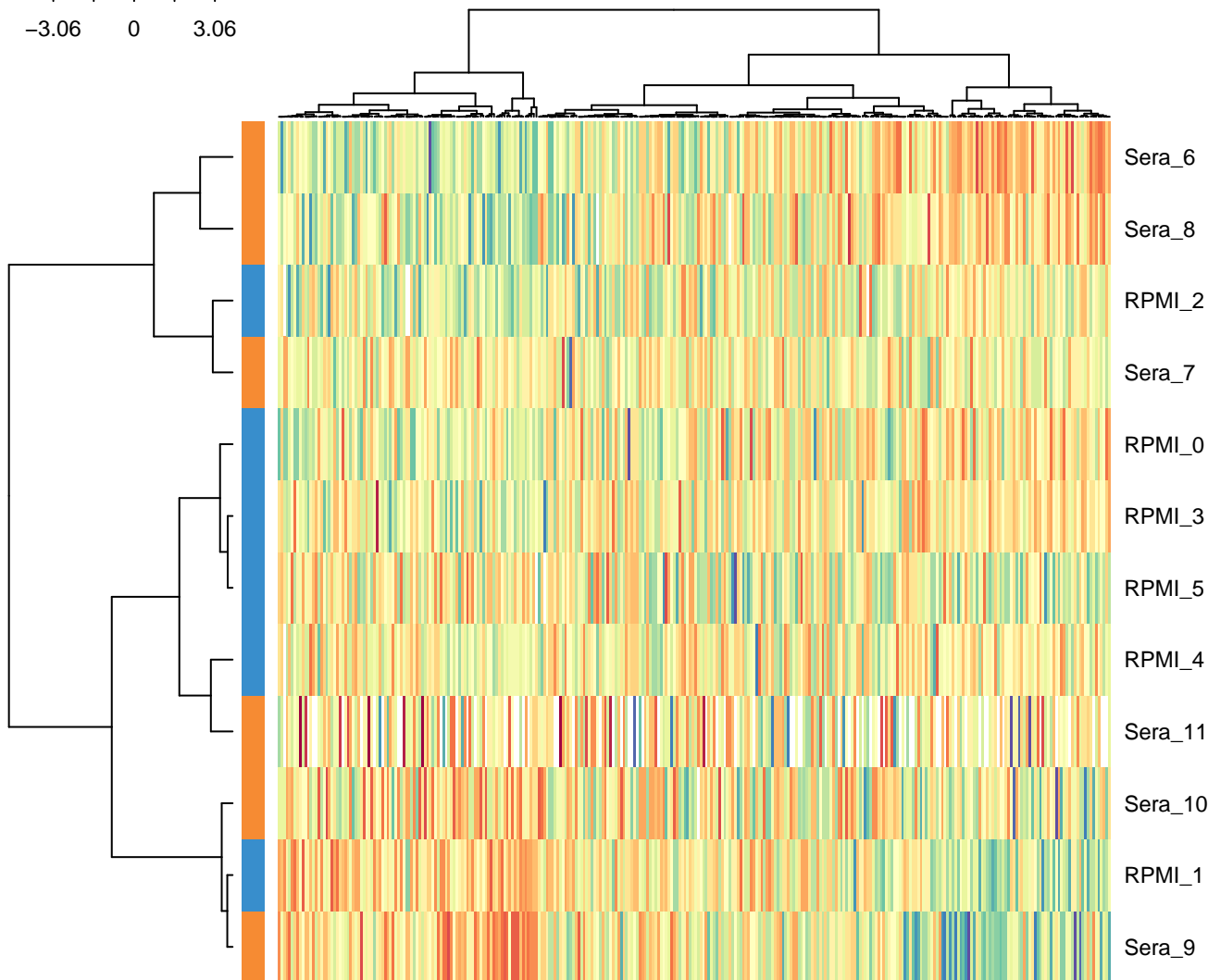
Color key



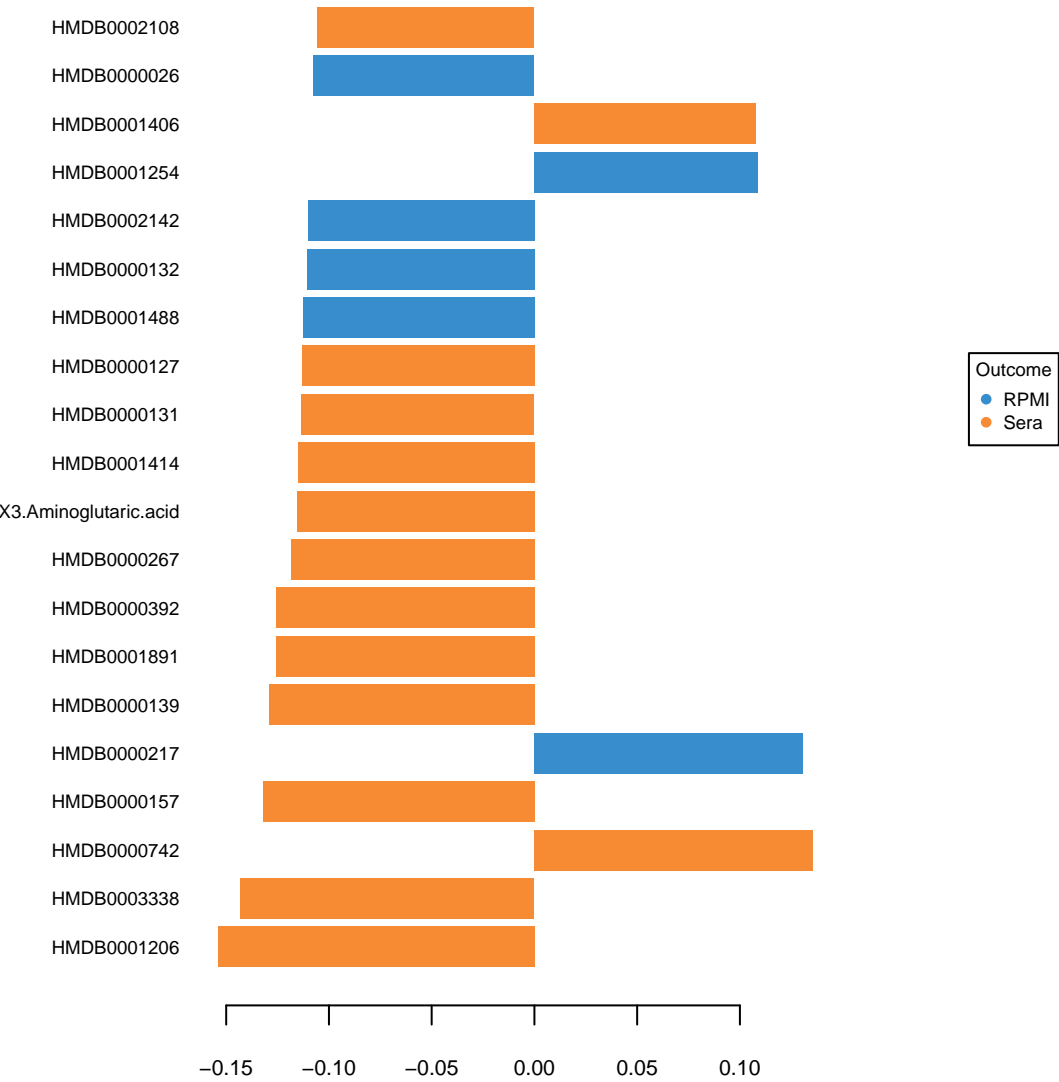
Status

RPMI

Sera

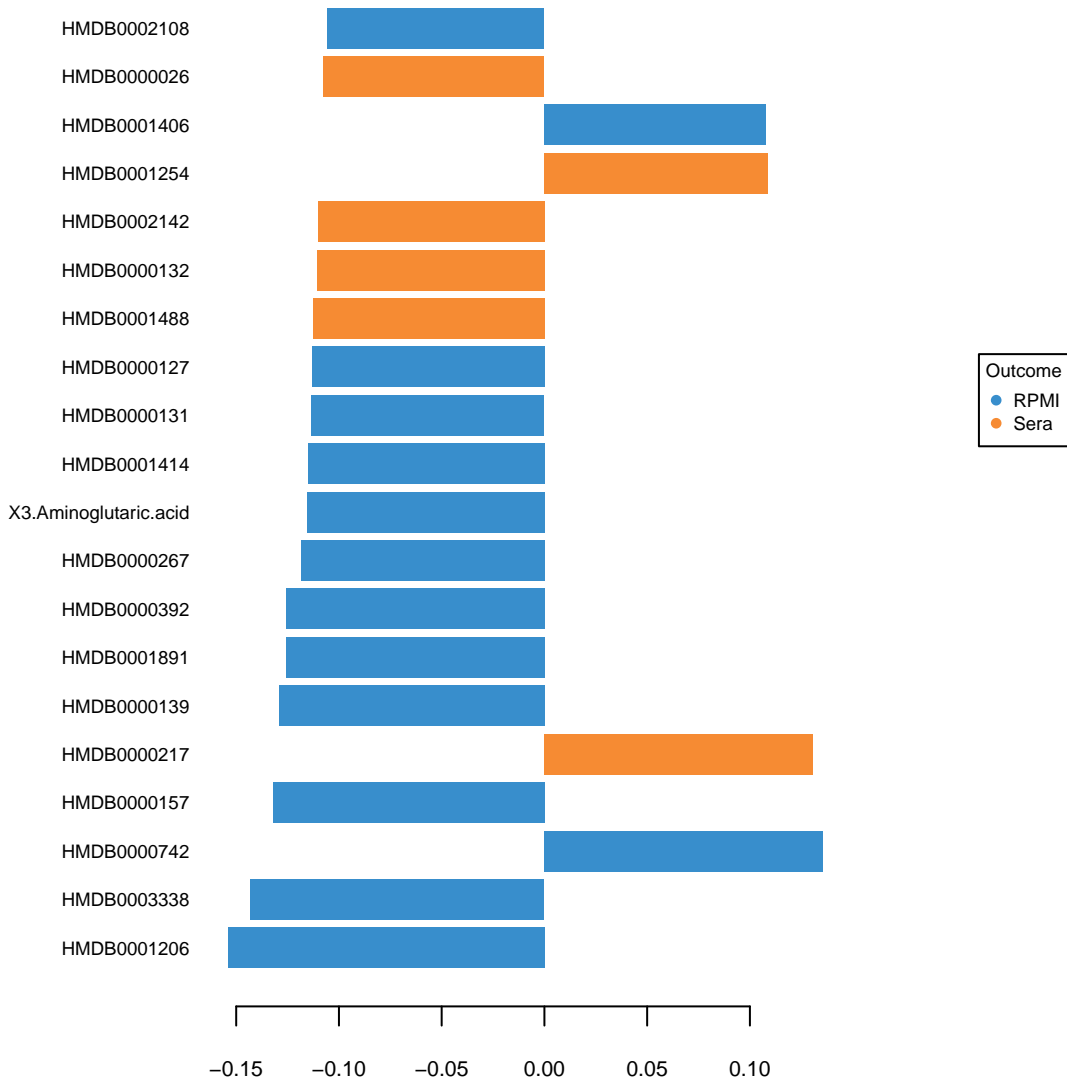


# metabolome 3 PLSDA max load



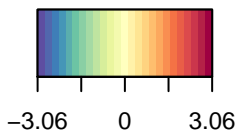


# metabolome 3 PLSDA min load



# PLSDA Component 4

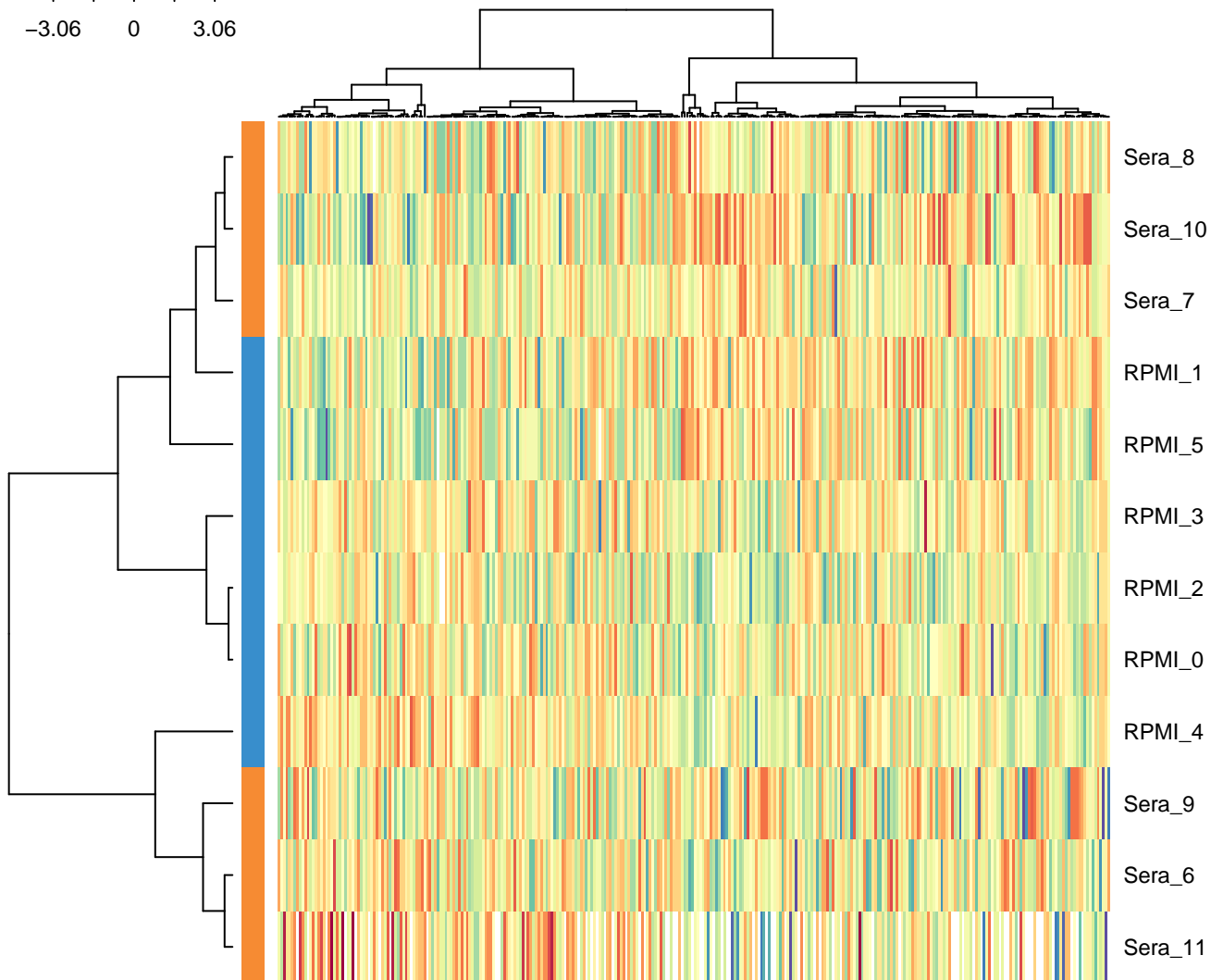
Color key



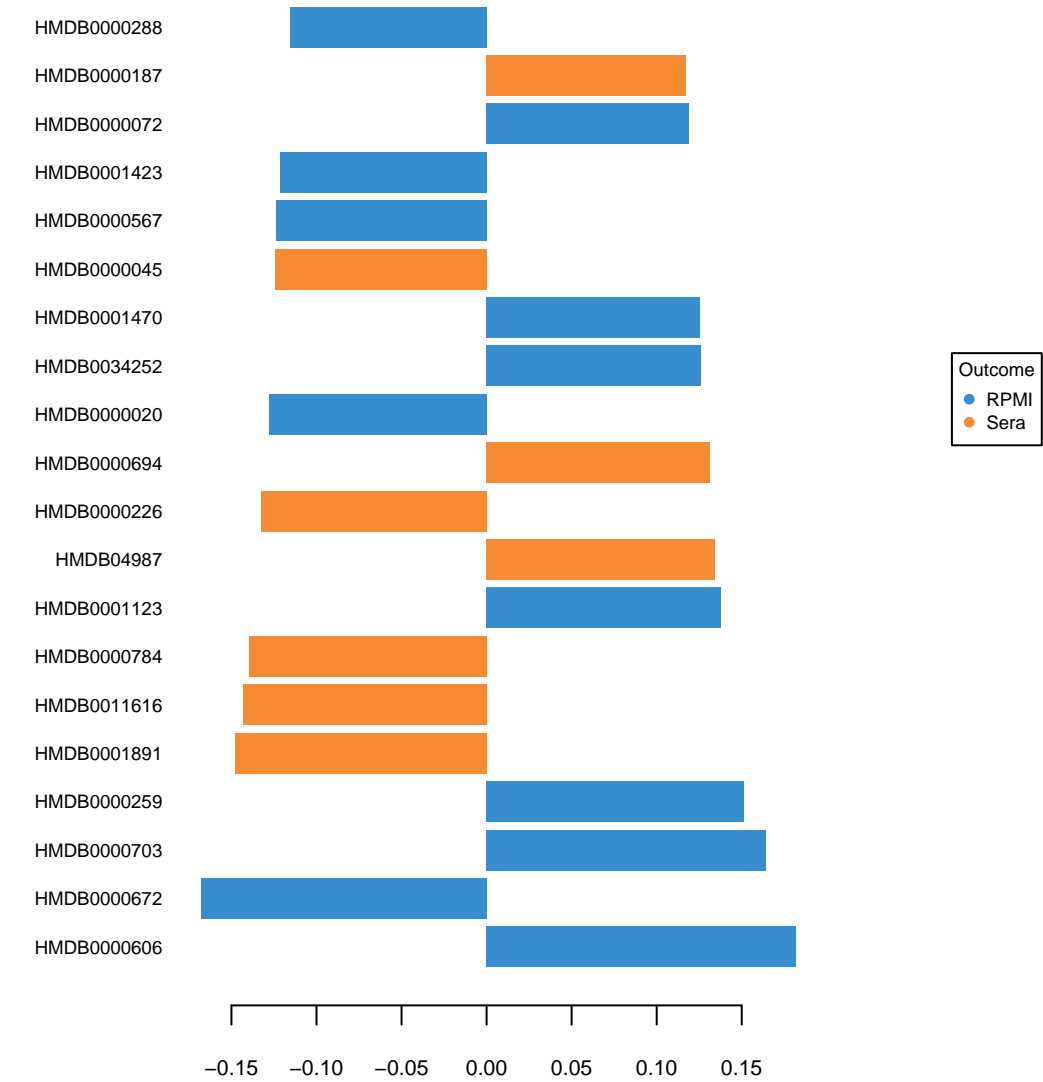
Status

RPMI

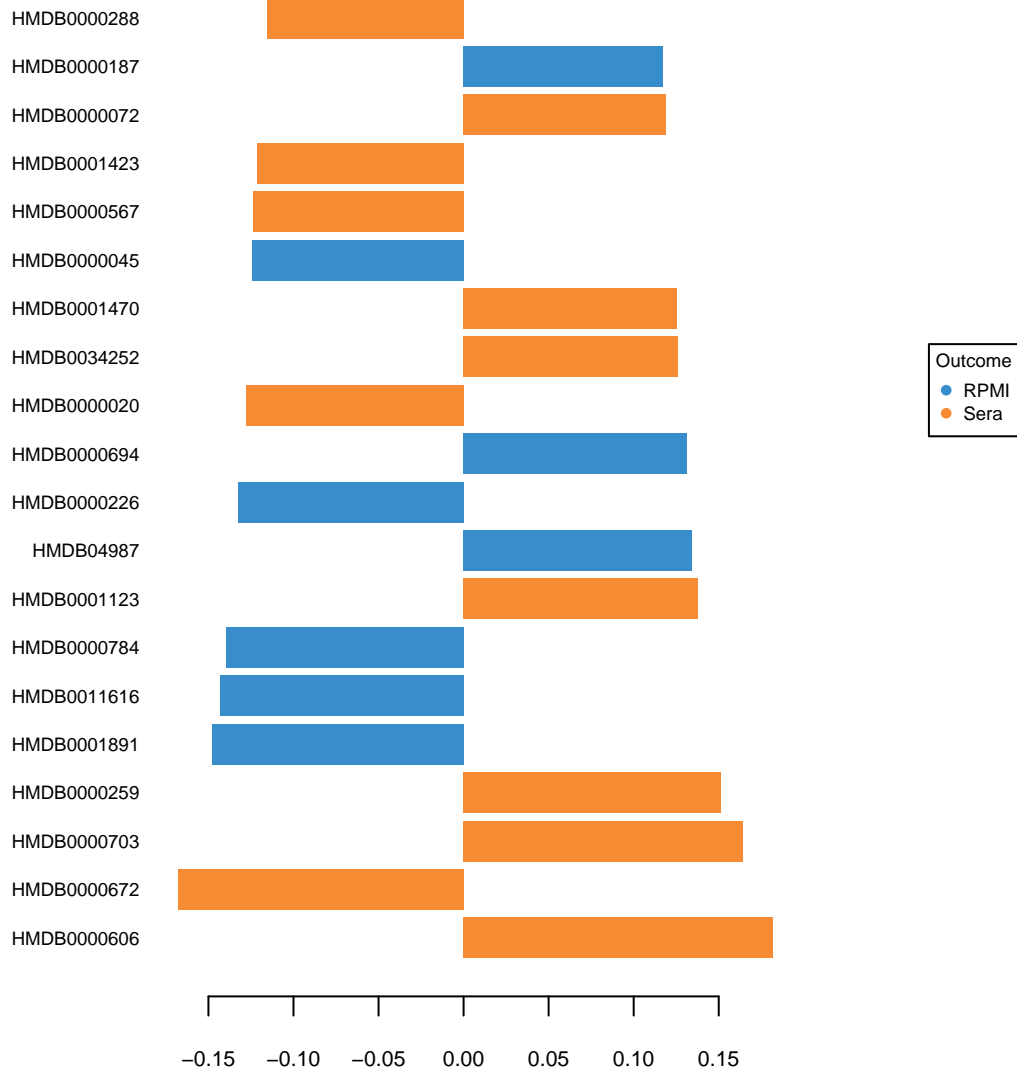
Sera



# metabolome 4 PLSDA max load



# metabolome 4 PLSDA min load



# proteome PLSDA single 1/2

X-variate 2: 16% expl. var

50

25

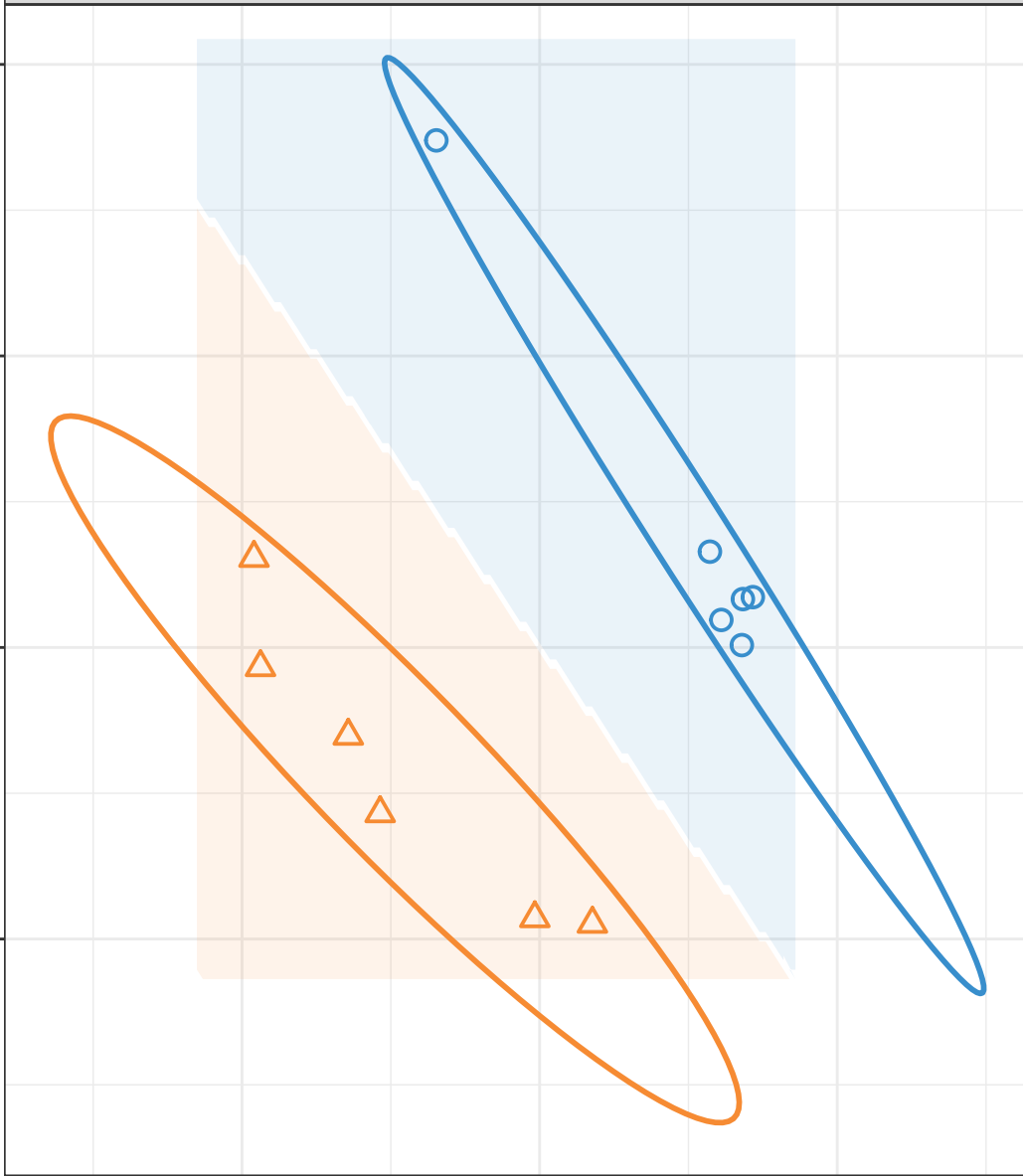
0

-25

X-variate 1: 45% expl. var

Legend

- RPMI
- △ Sera



# proteome PLSDA single 1/2

X-variate 2: 16% expl. var

50

25

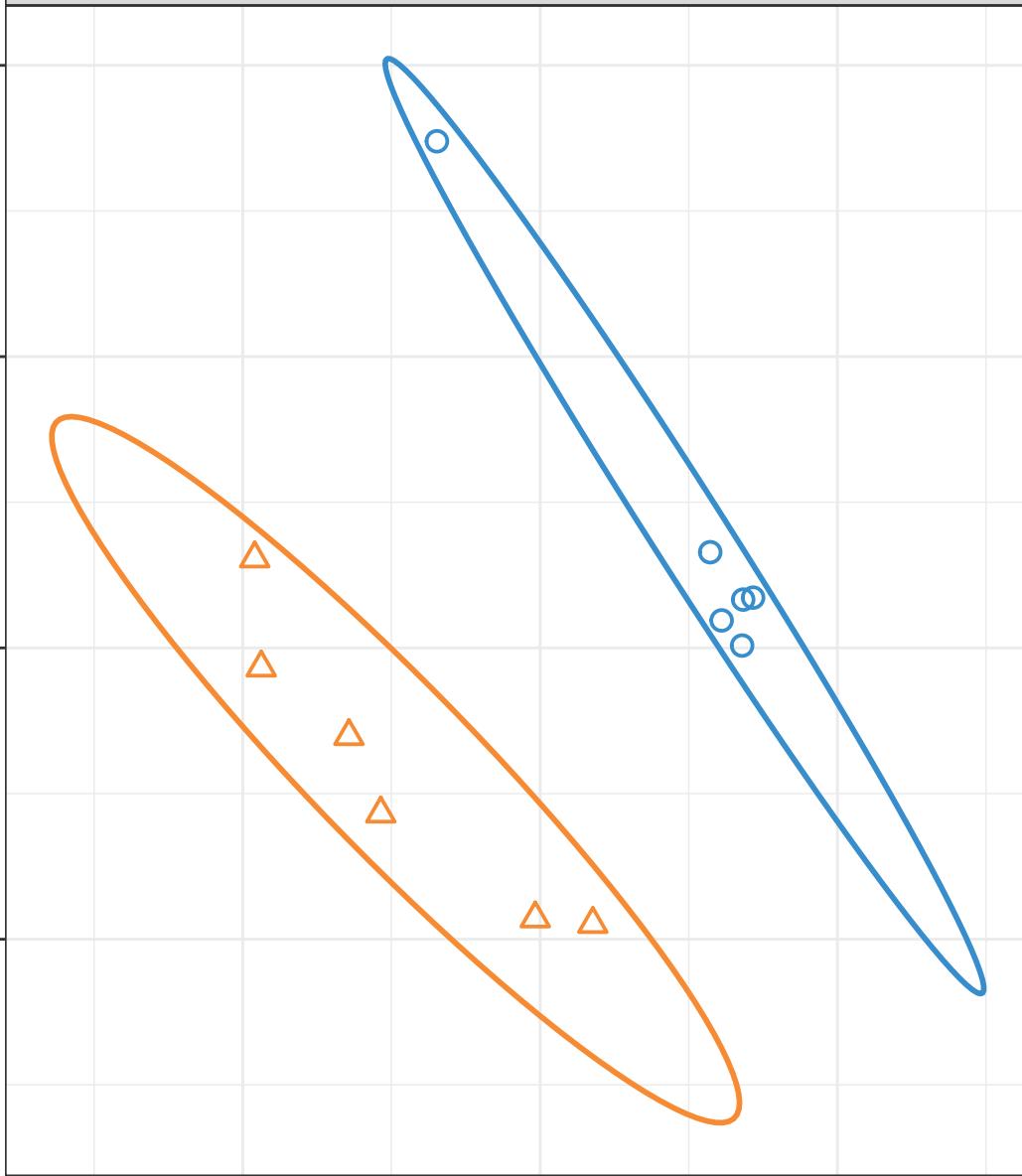
0

-25

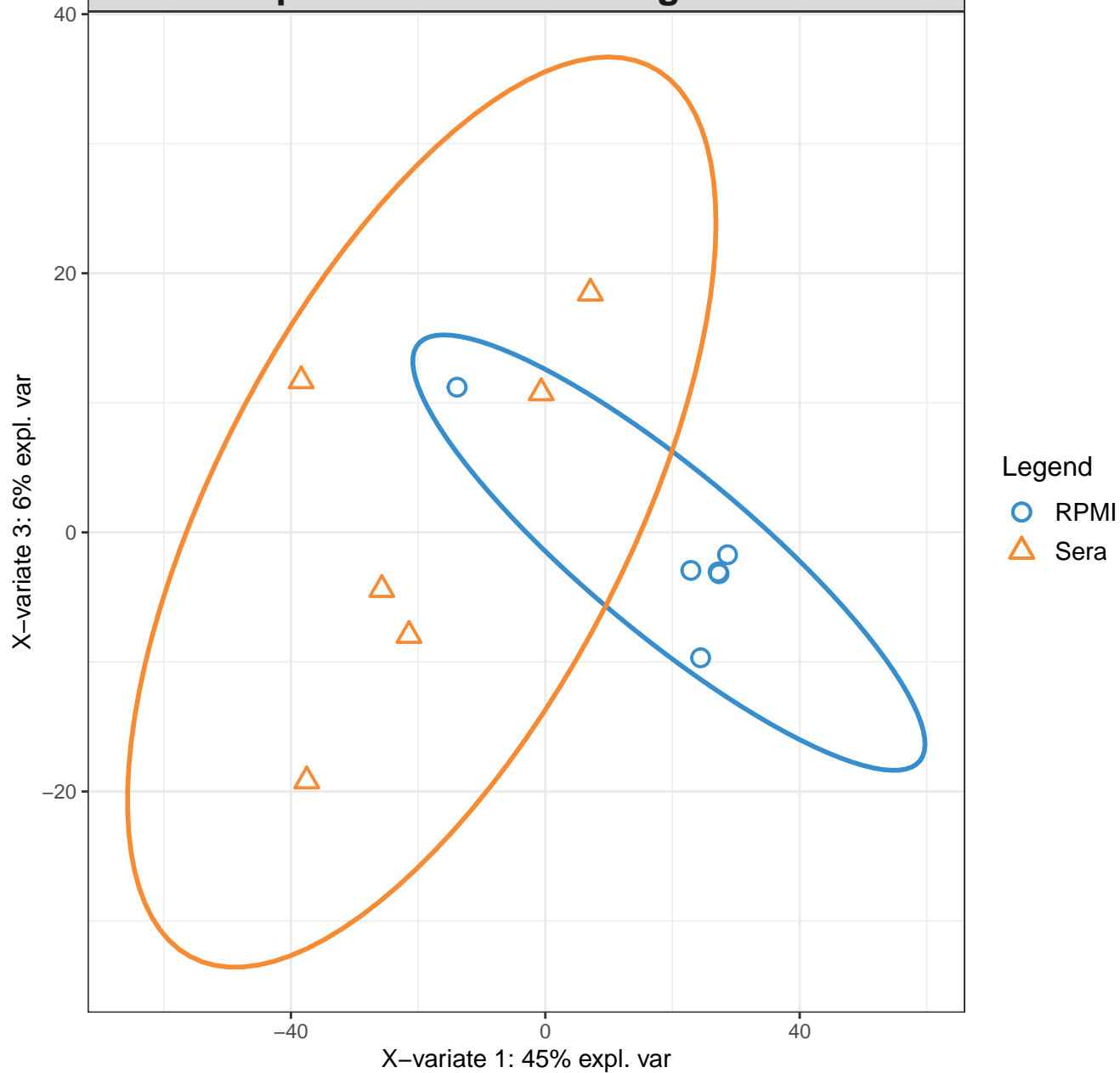
X-variate 1: 45% expl. var

Legend

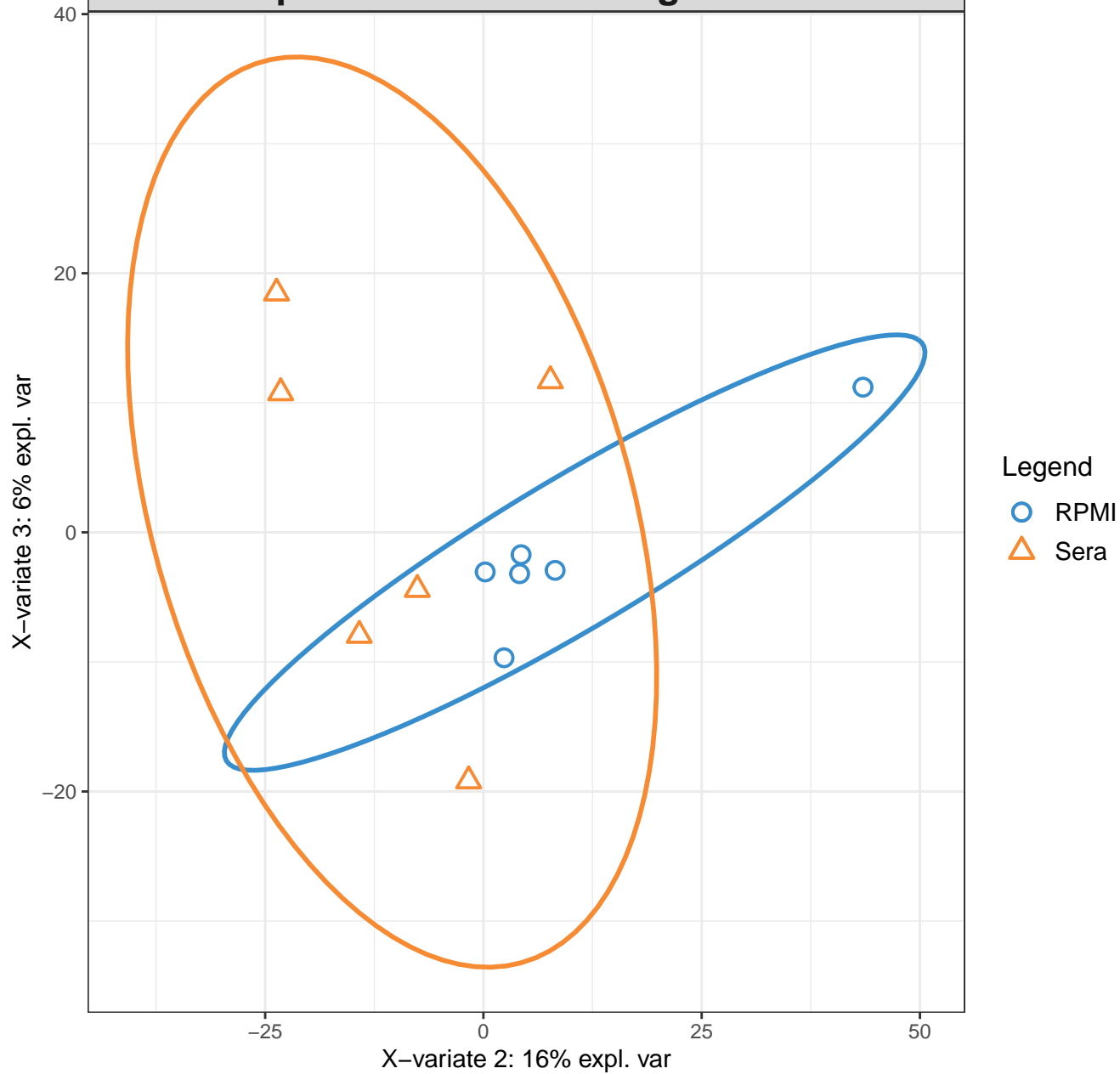
- RPMI
- △ Sera



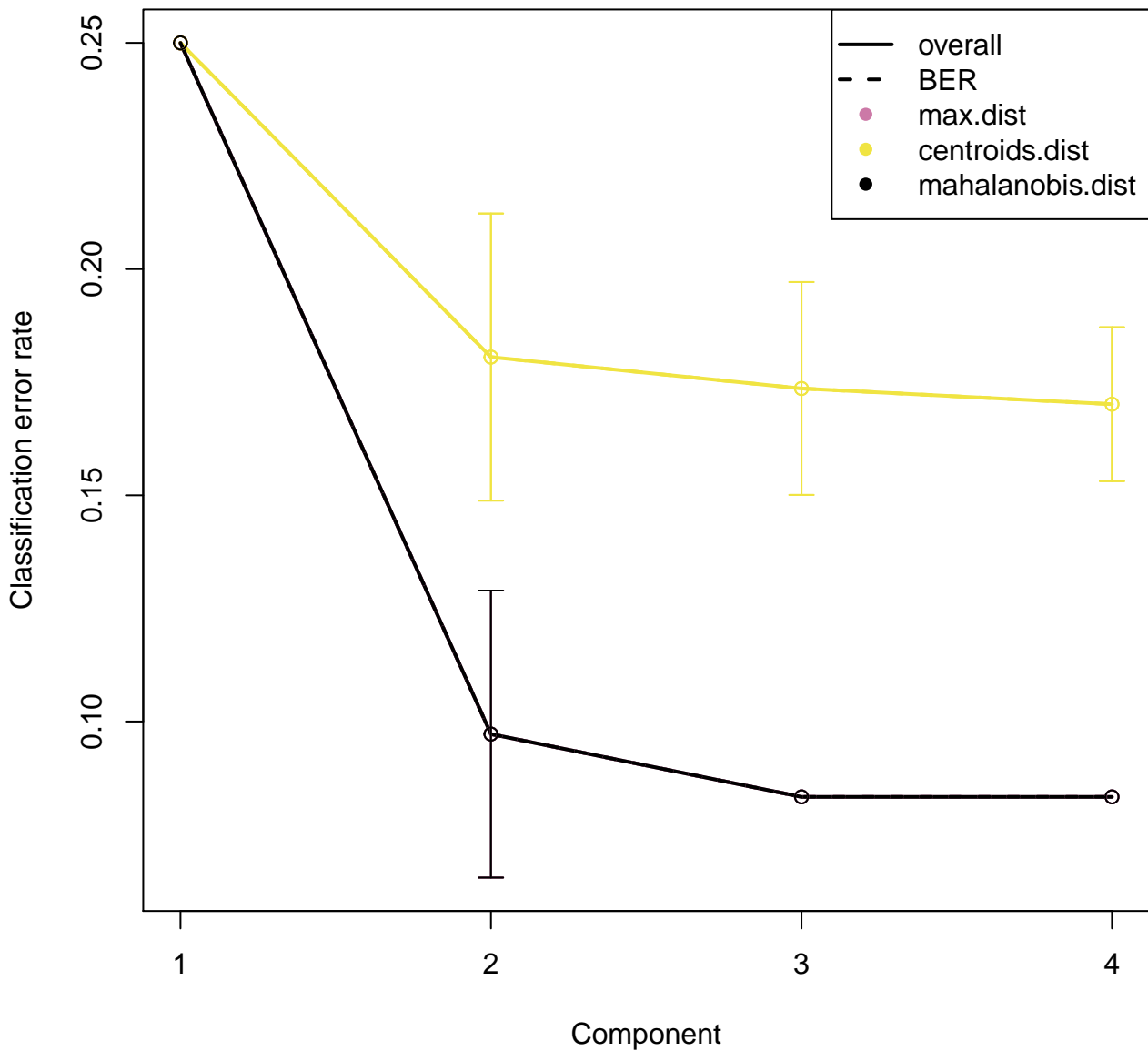
# proteome PLSDA single 1/3



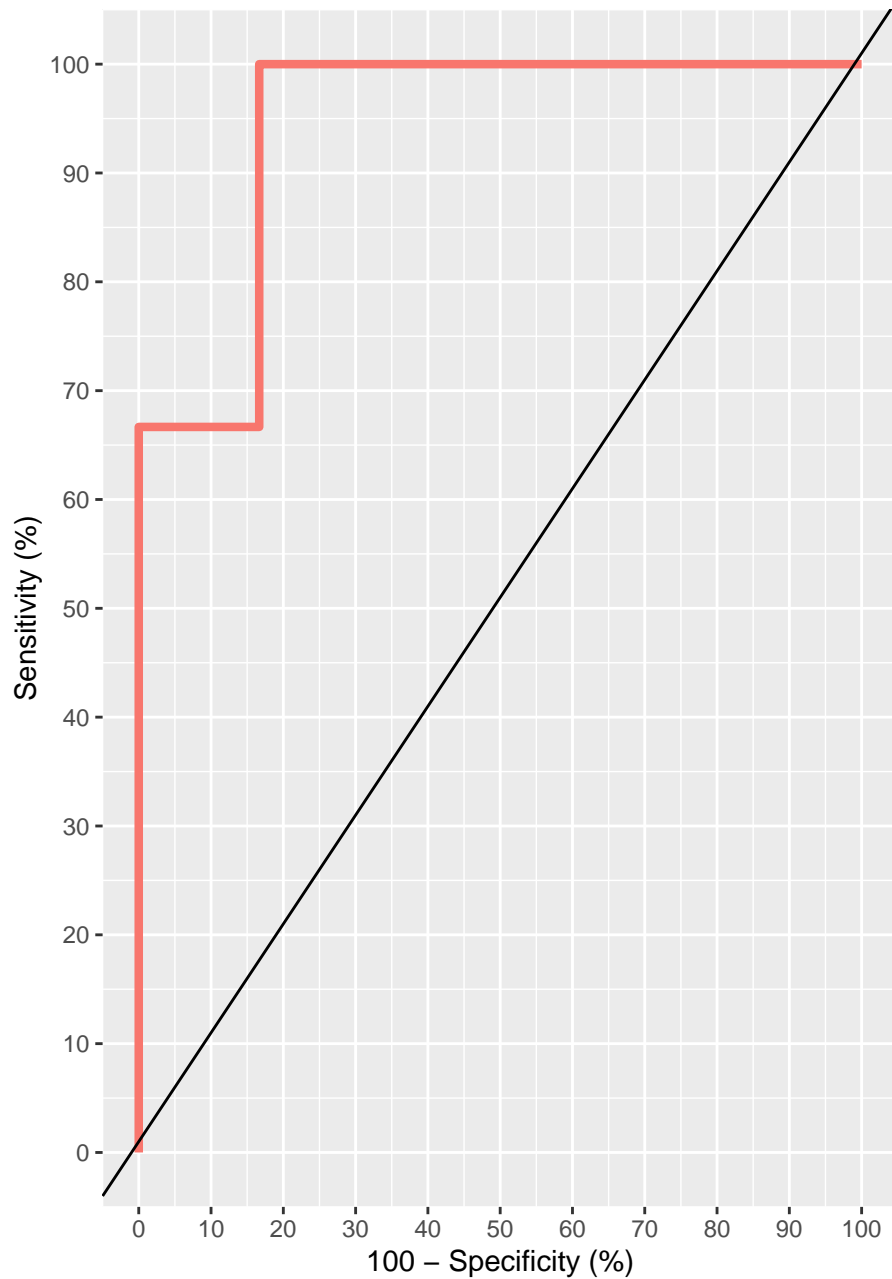
# proteome PLSDA single 2/3







**ROC Curve Using Comp(s): 1**

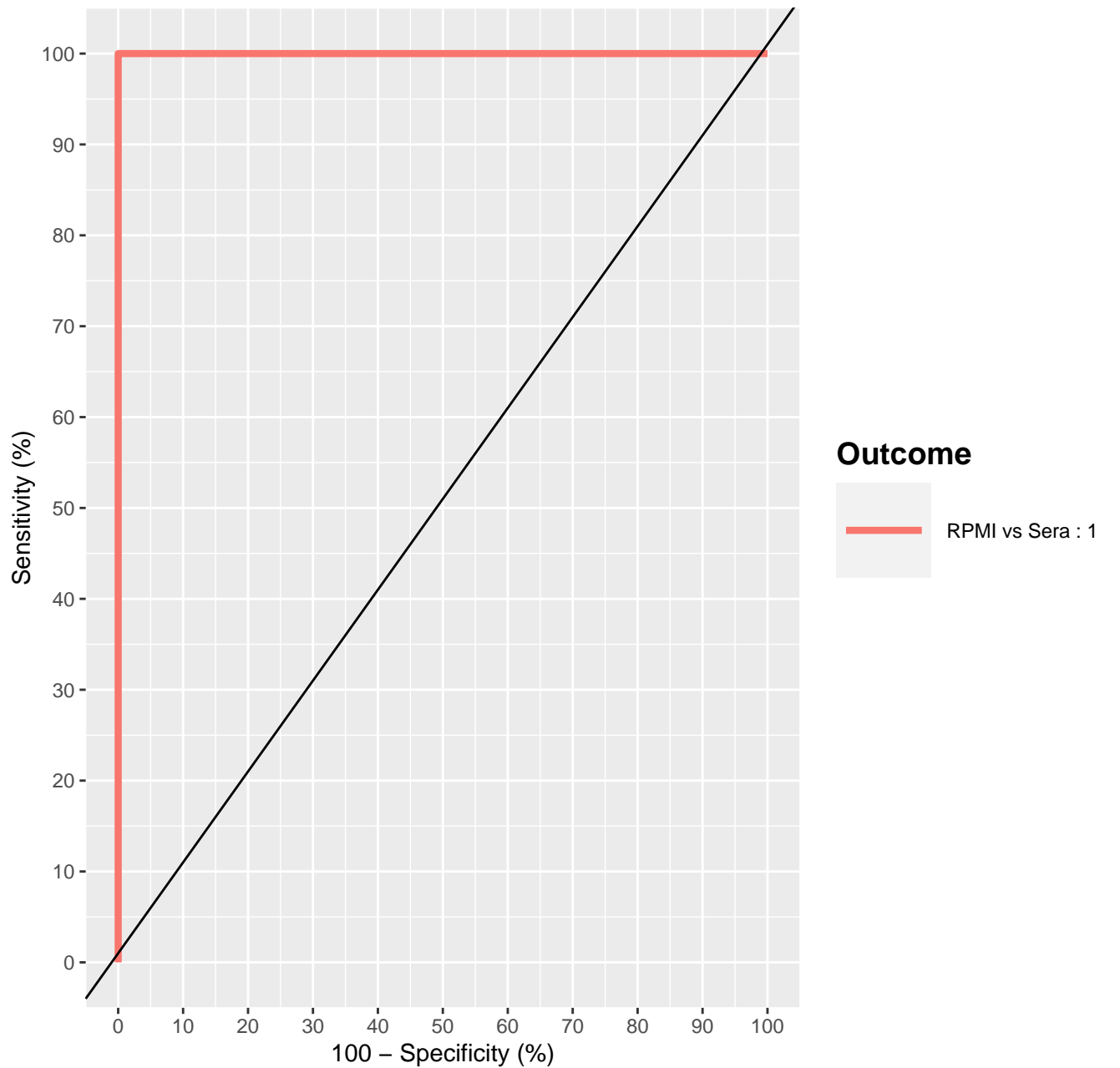


**Outcome**

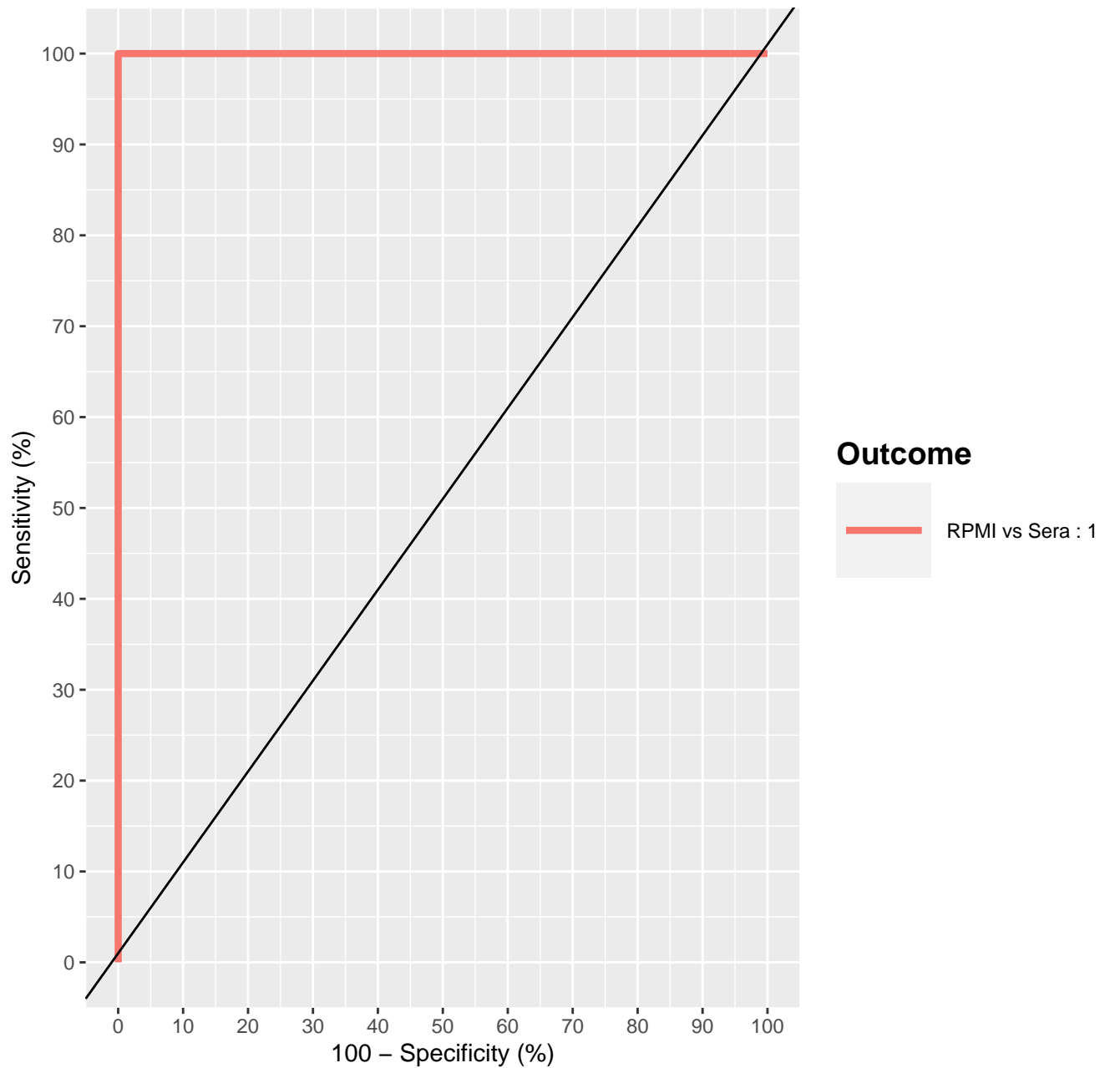


RPMI vs Sera : 0.9444

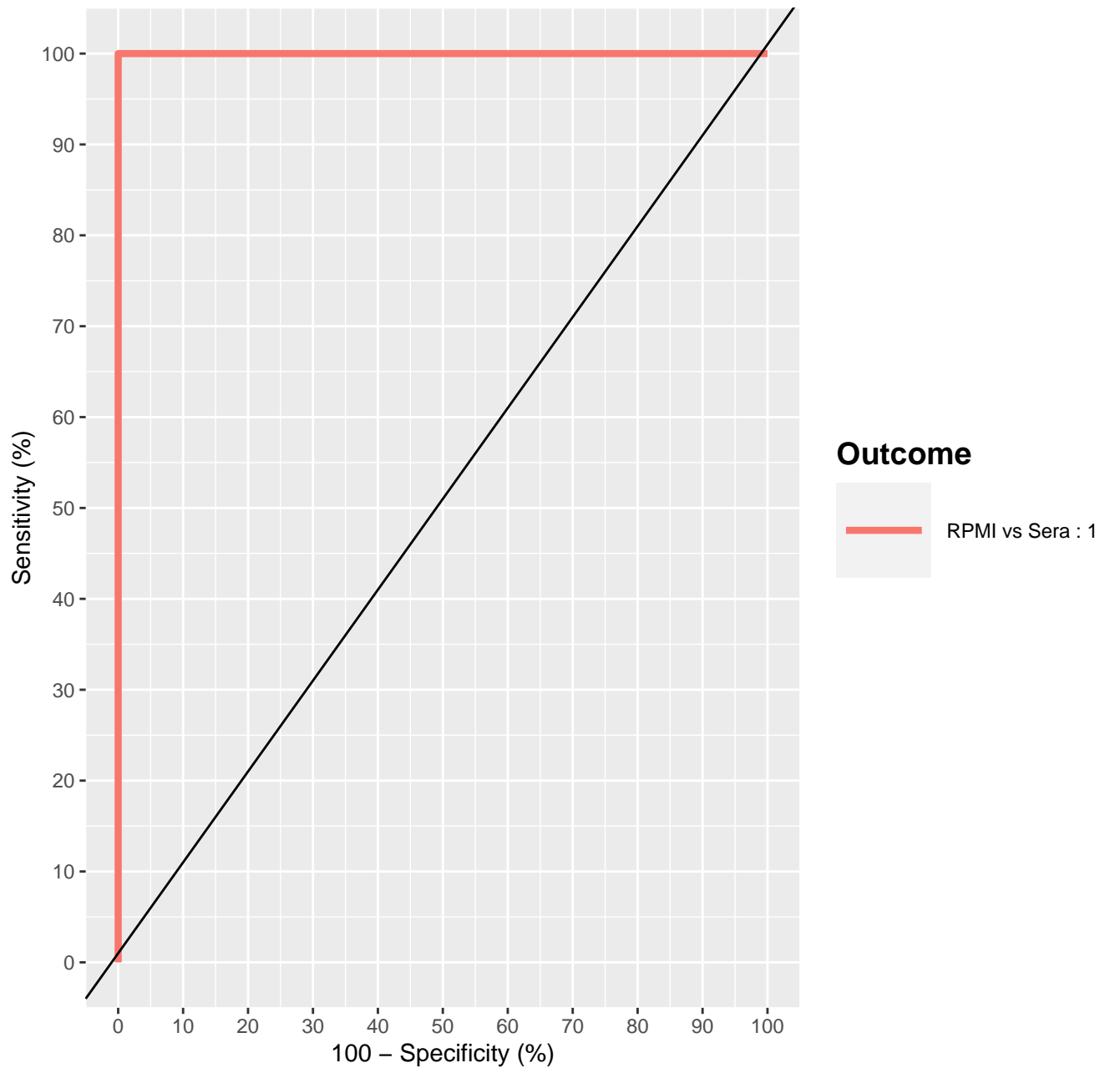
ROC Curve Using Comp(s): 1, 2



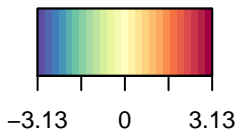
**ROC Curve Using Comp(s): 1, 2, 3**



ROC Curve Using Comp(s): 1, 2, 3, 4



Color key

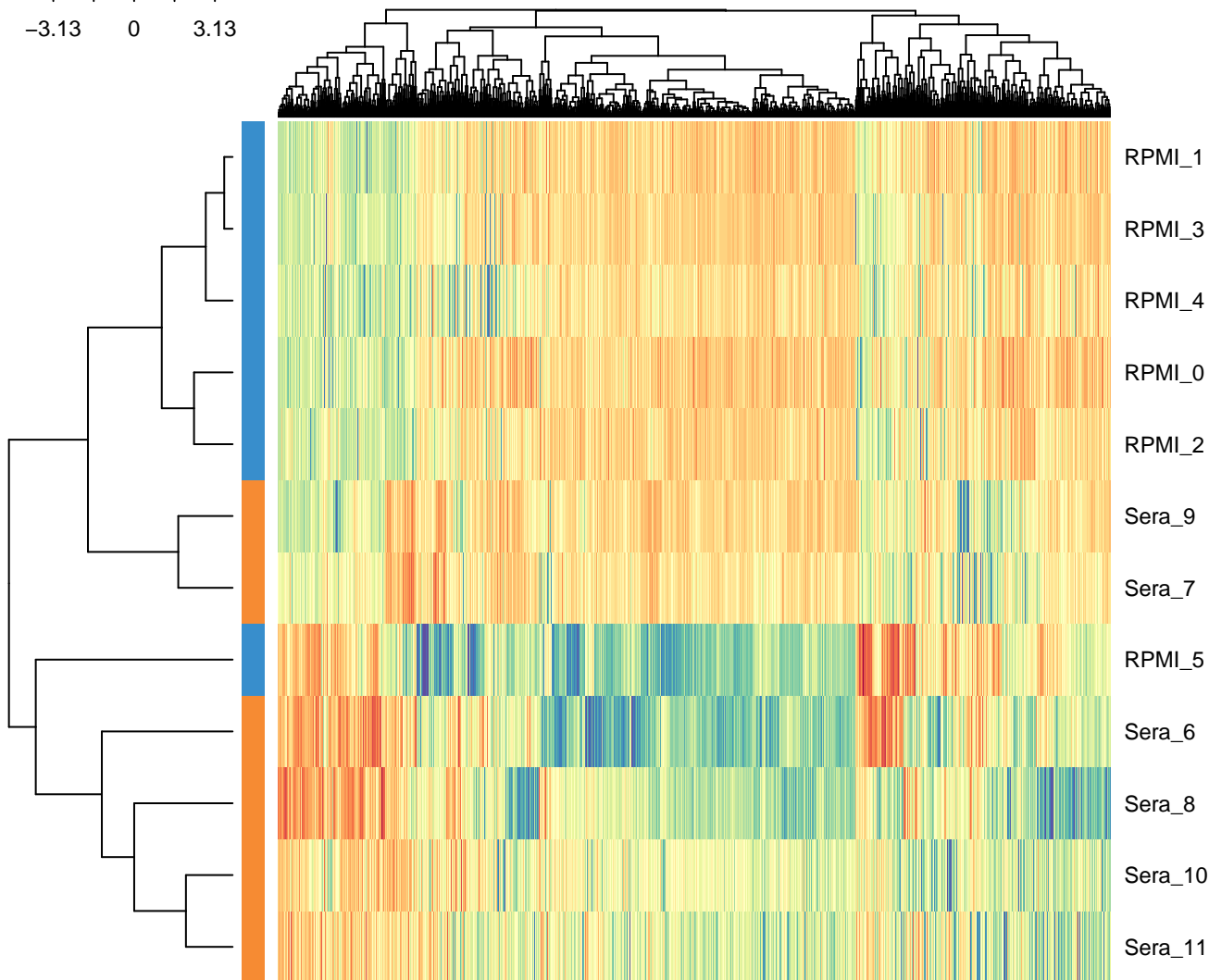


PLSDA

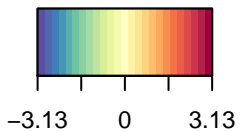
Status

■ RPMI

■ Sera



Color key

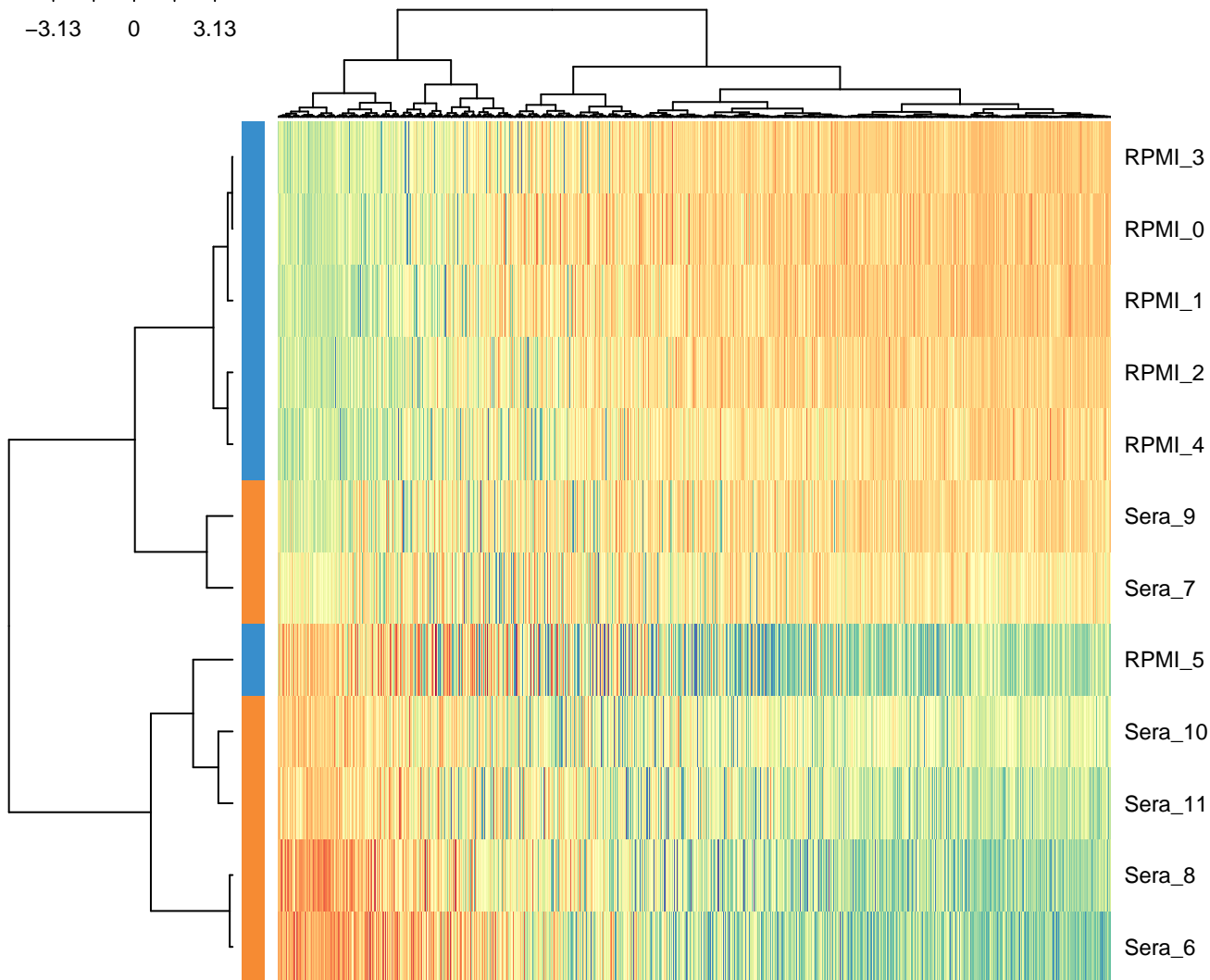


# PLSDA Component 1

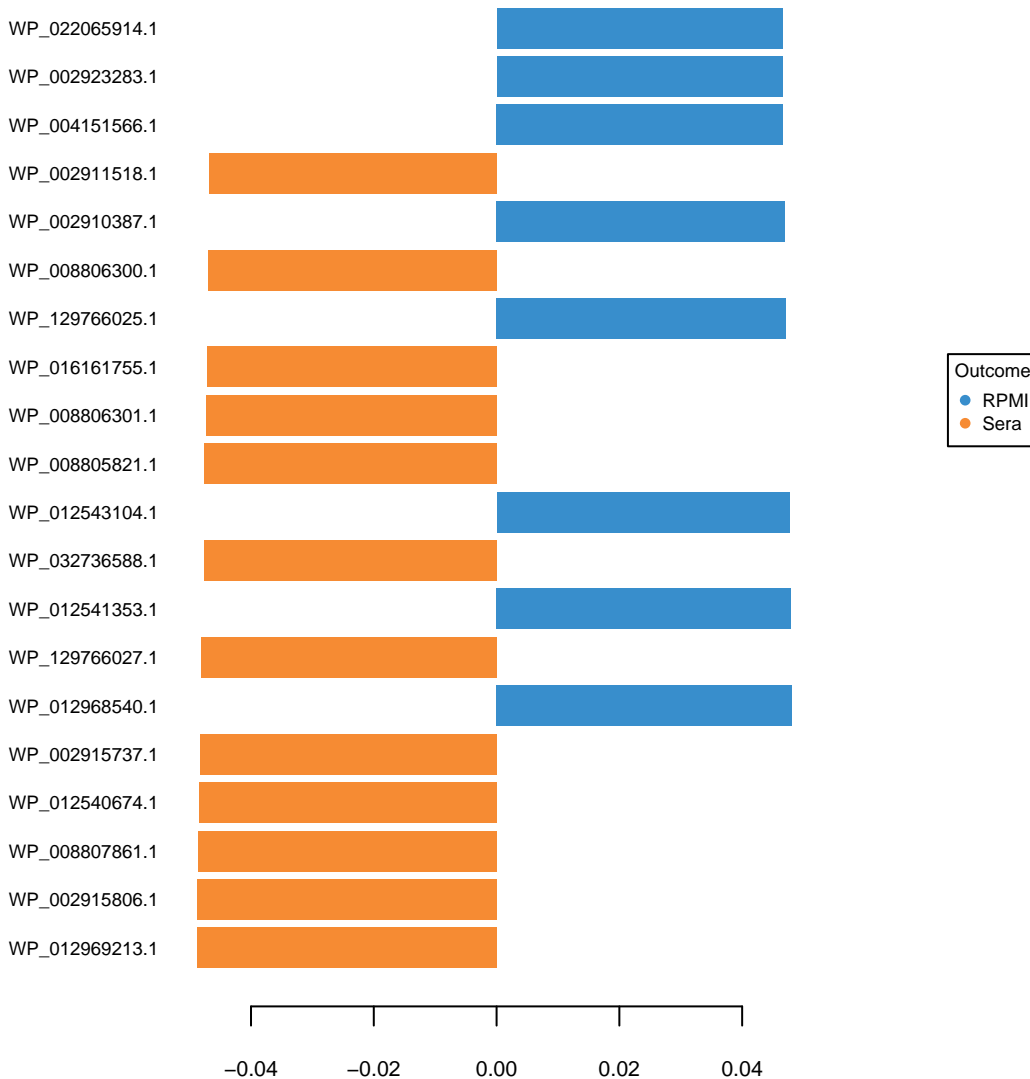
Status

RPMI

Sera

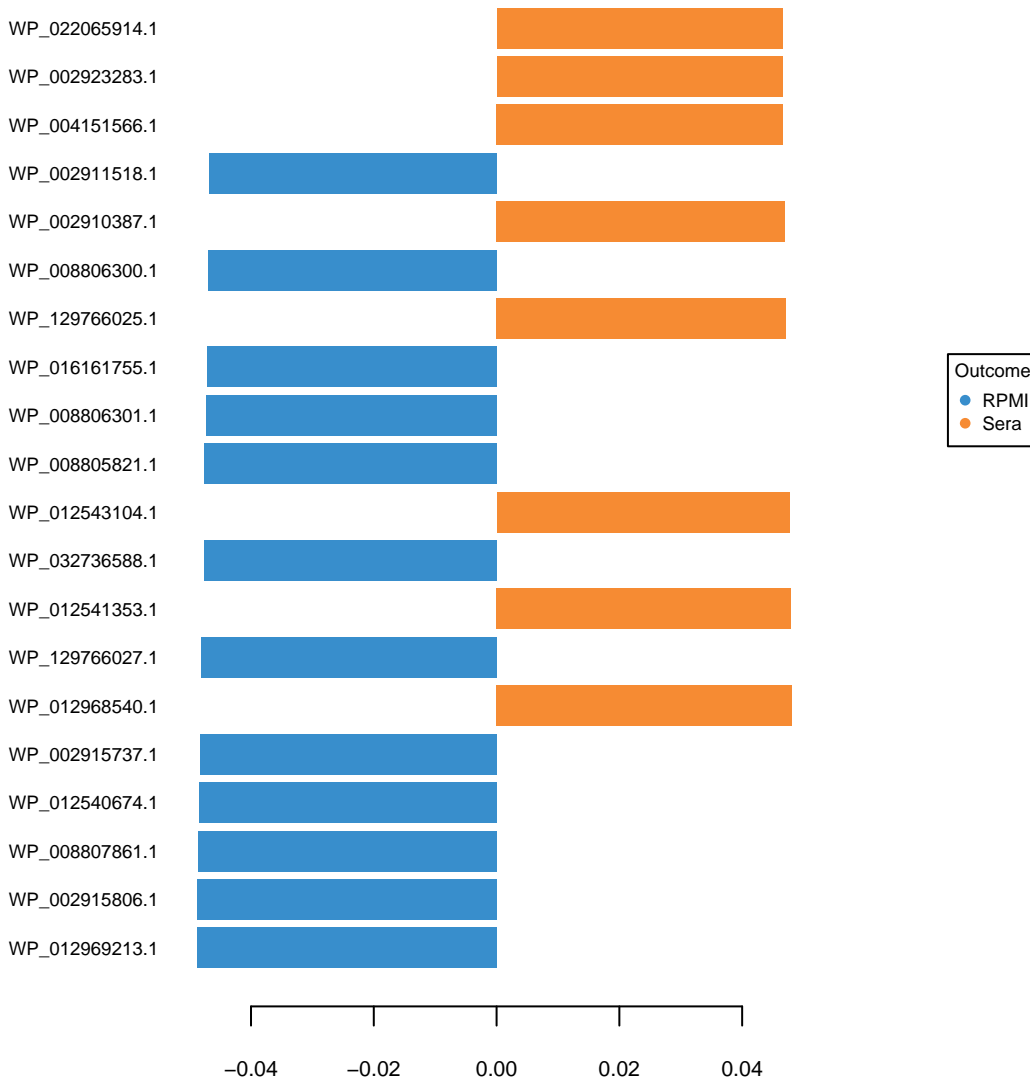


# proteome 1 PLSDA max loadir



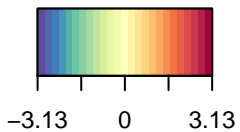


# proteome 1 PLSDA min loadin



# PLSDA Component 2

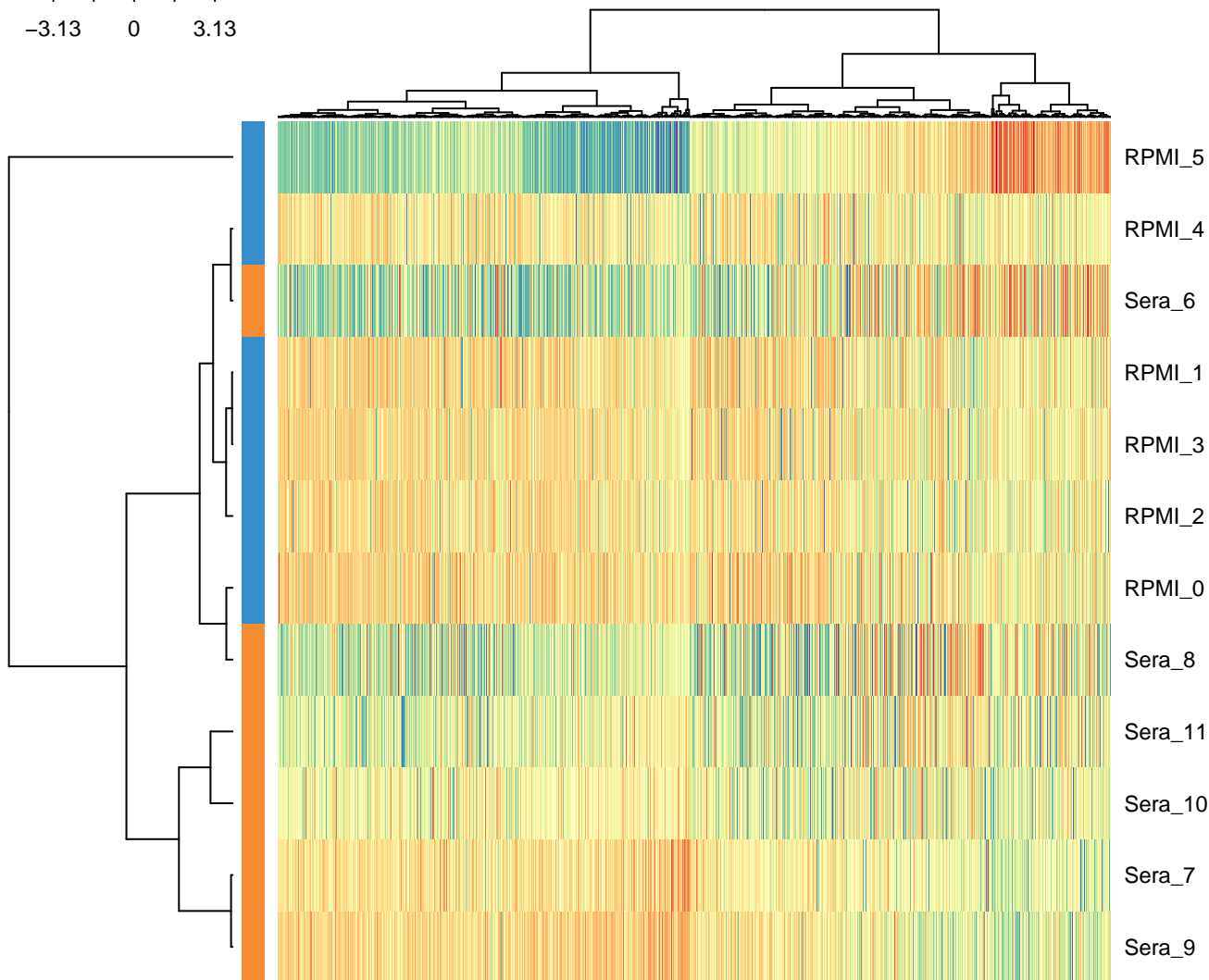
Color key



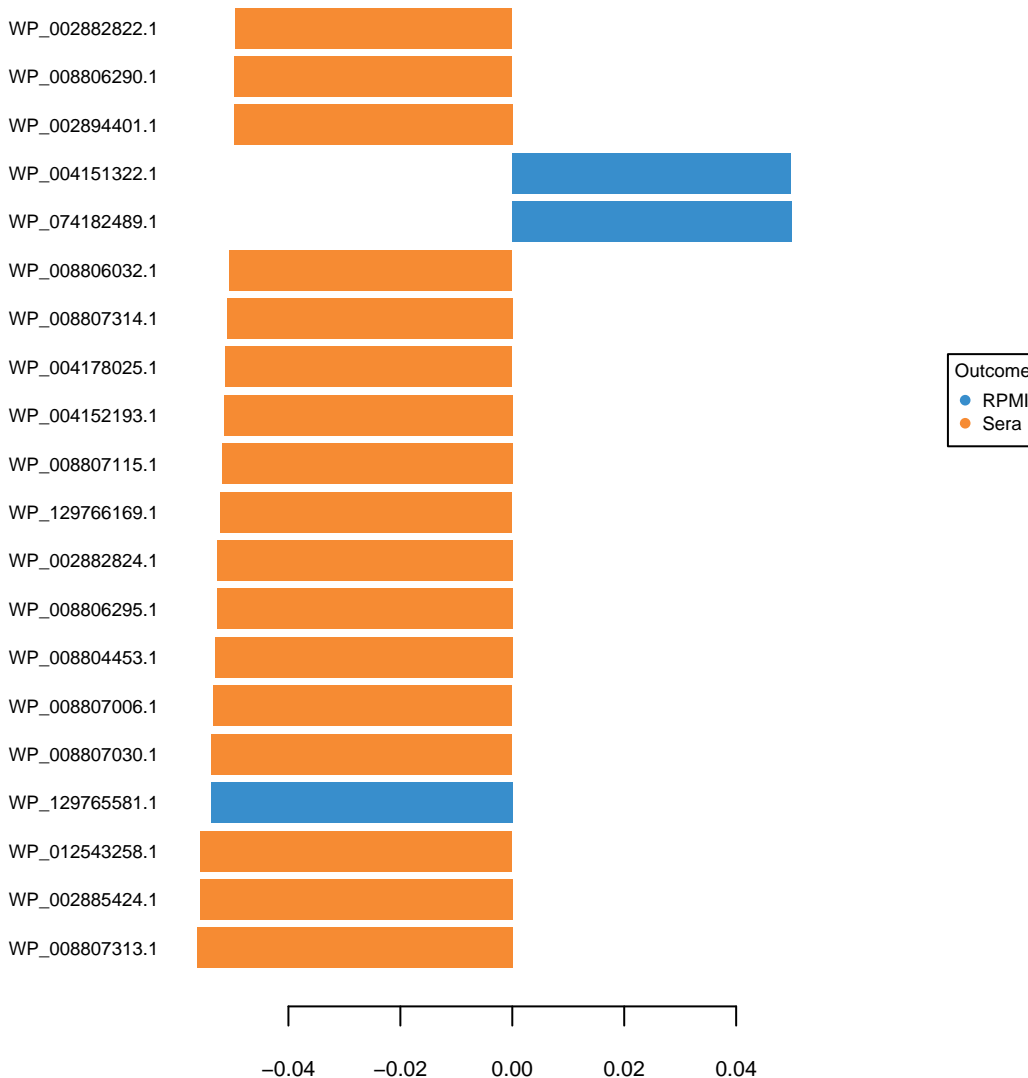
Status

RPMI

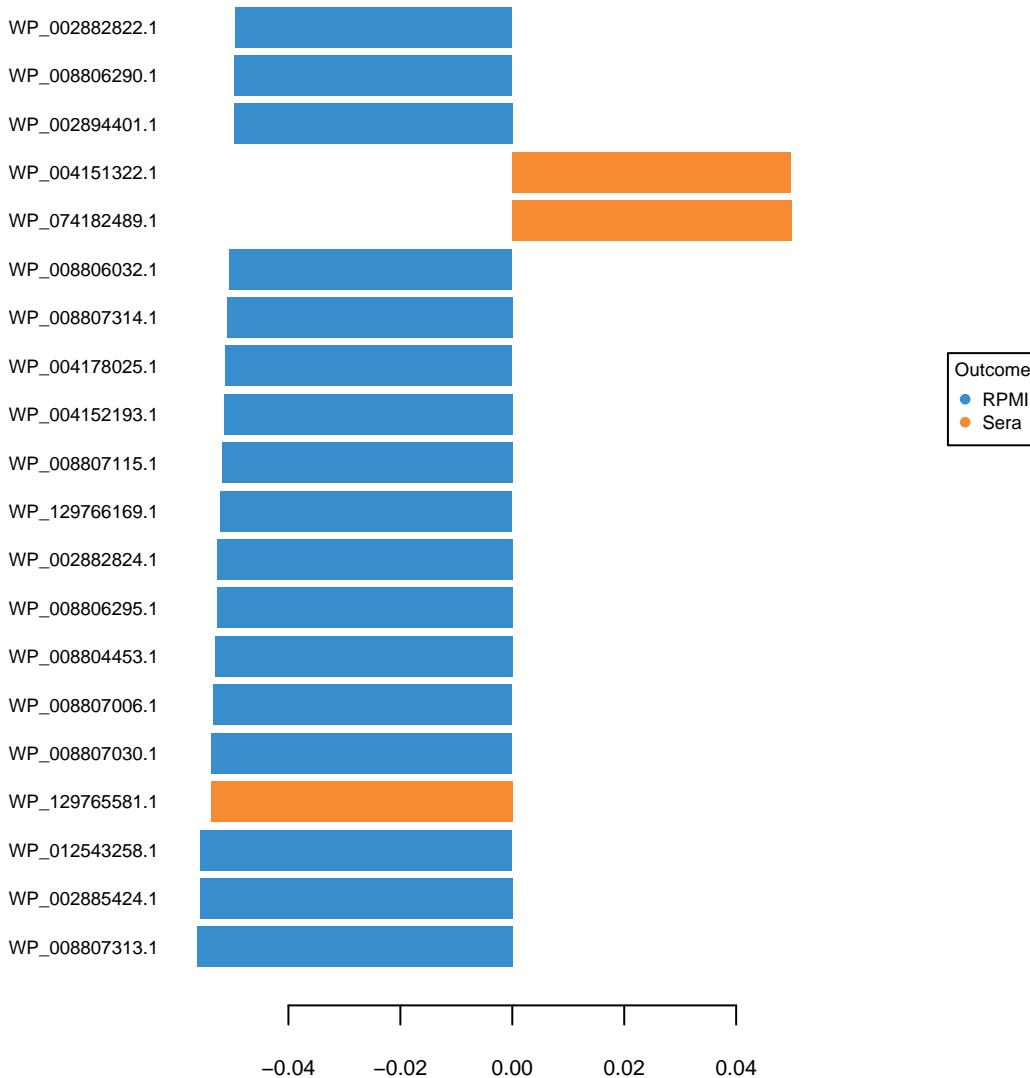
Sera



# proteome 2 PLSDA max loadir

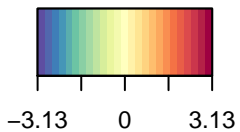


# proteome 2 PLSDA min loadin



# PLSDA Component 3

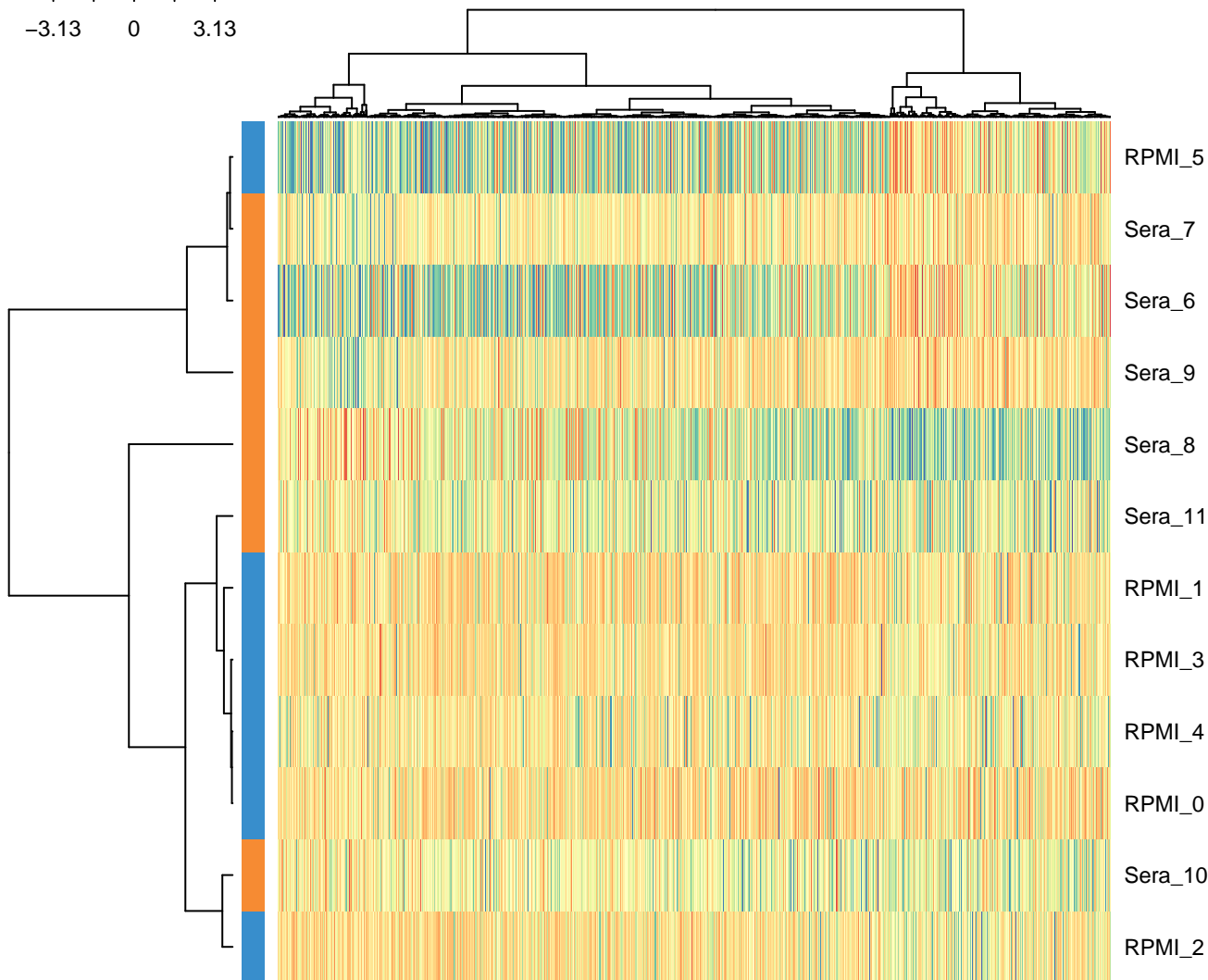
Color key



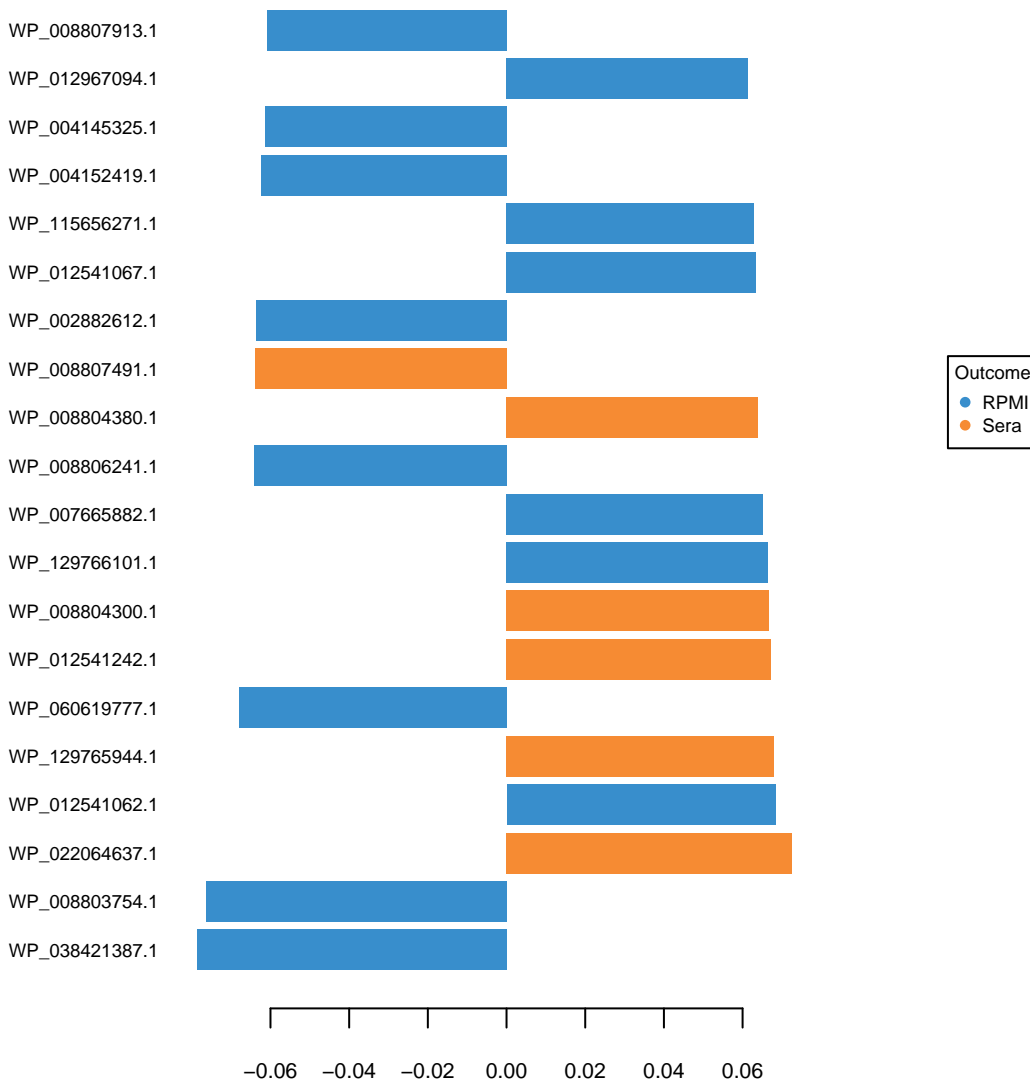
Status

RPMI

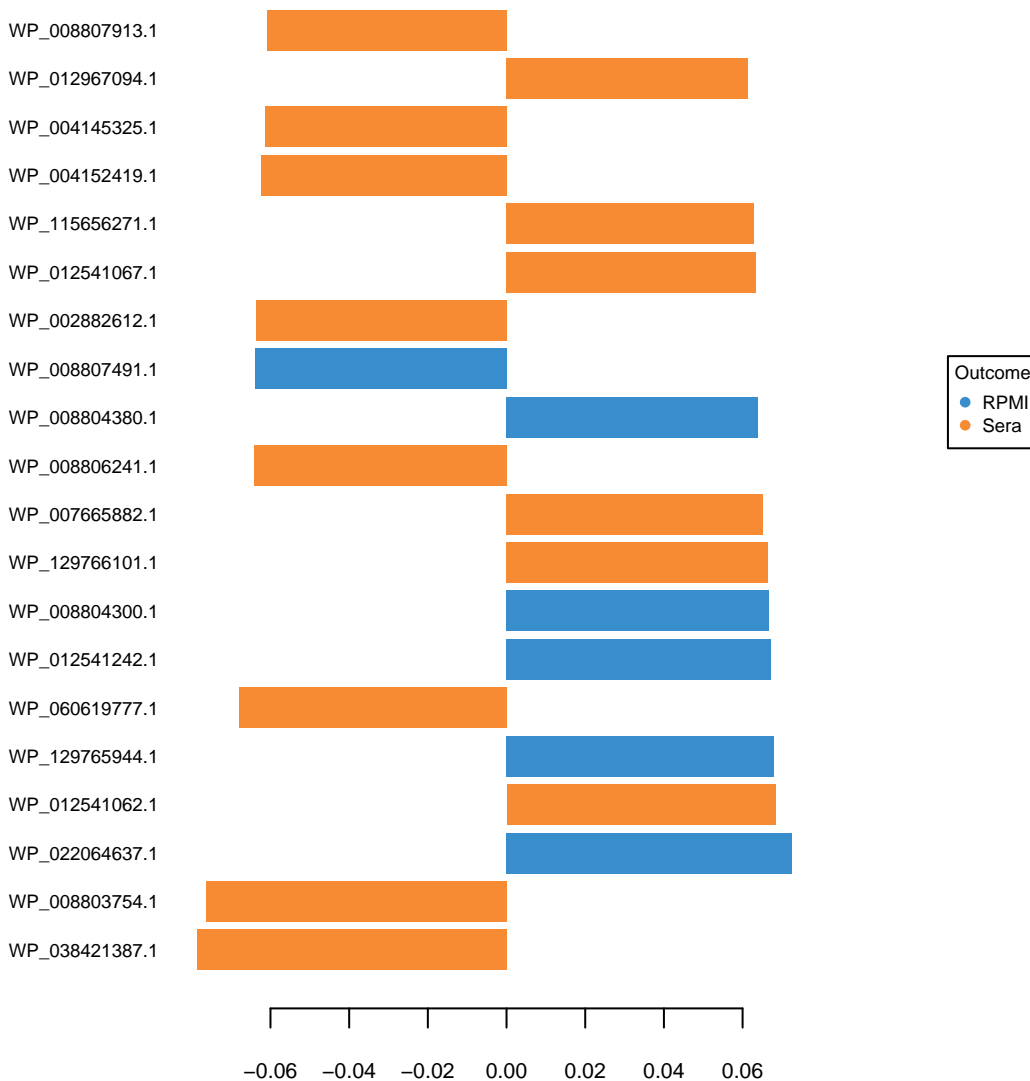
Sera



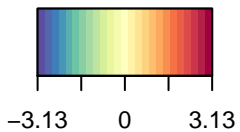
# proteome 3 PLSDA max loadir



# proteome 3 PLSDA min loadin



Color key

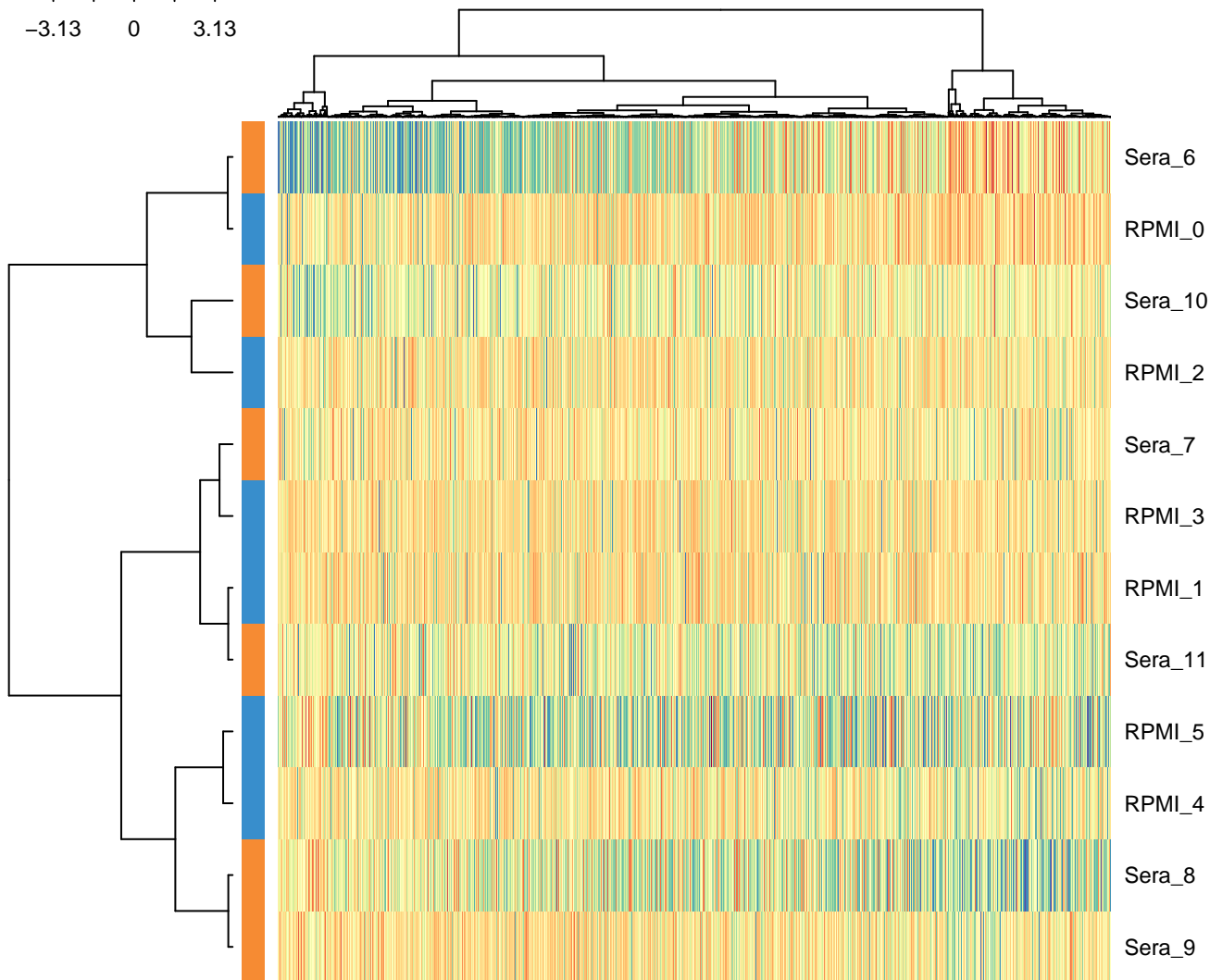


# PLSDA Component 4

Status

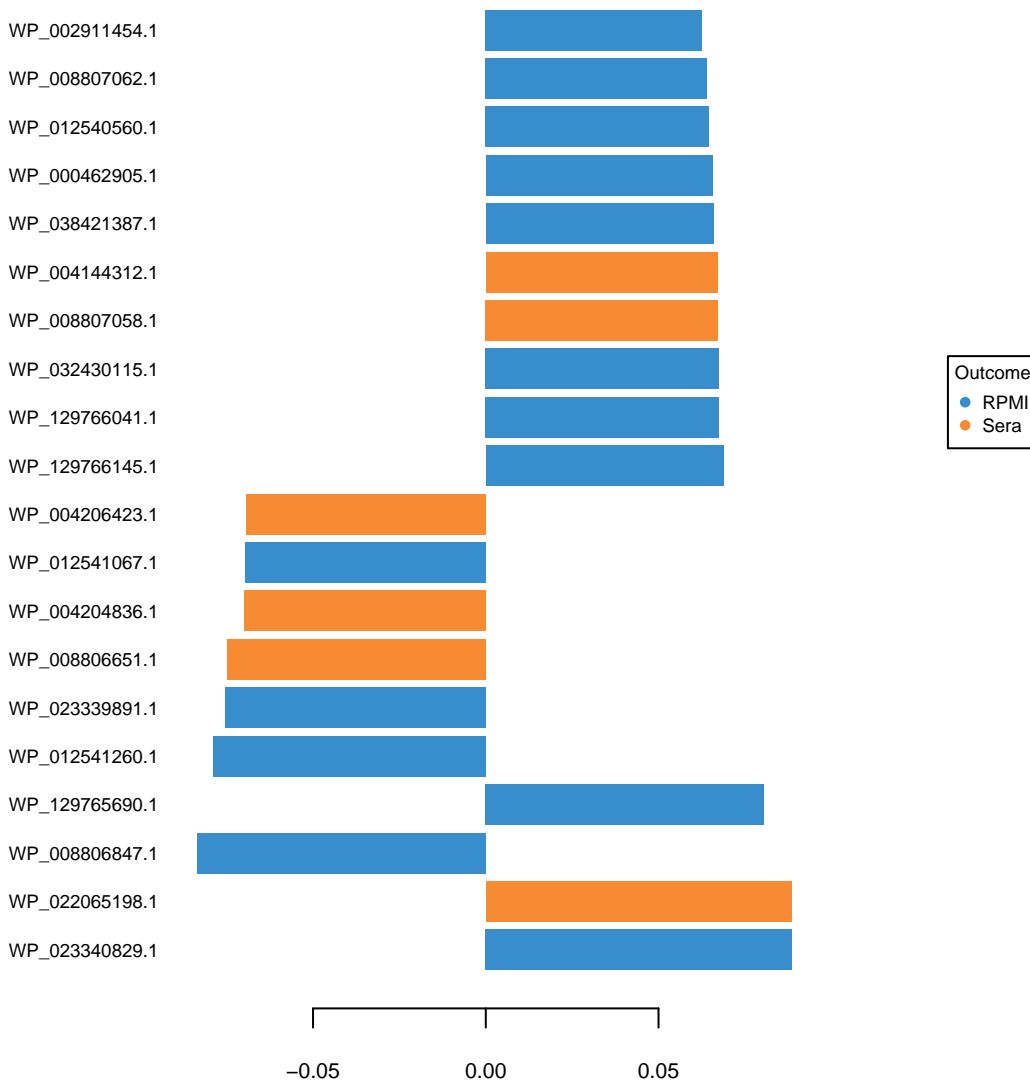
RPMI

Sera

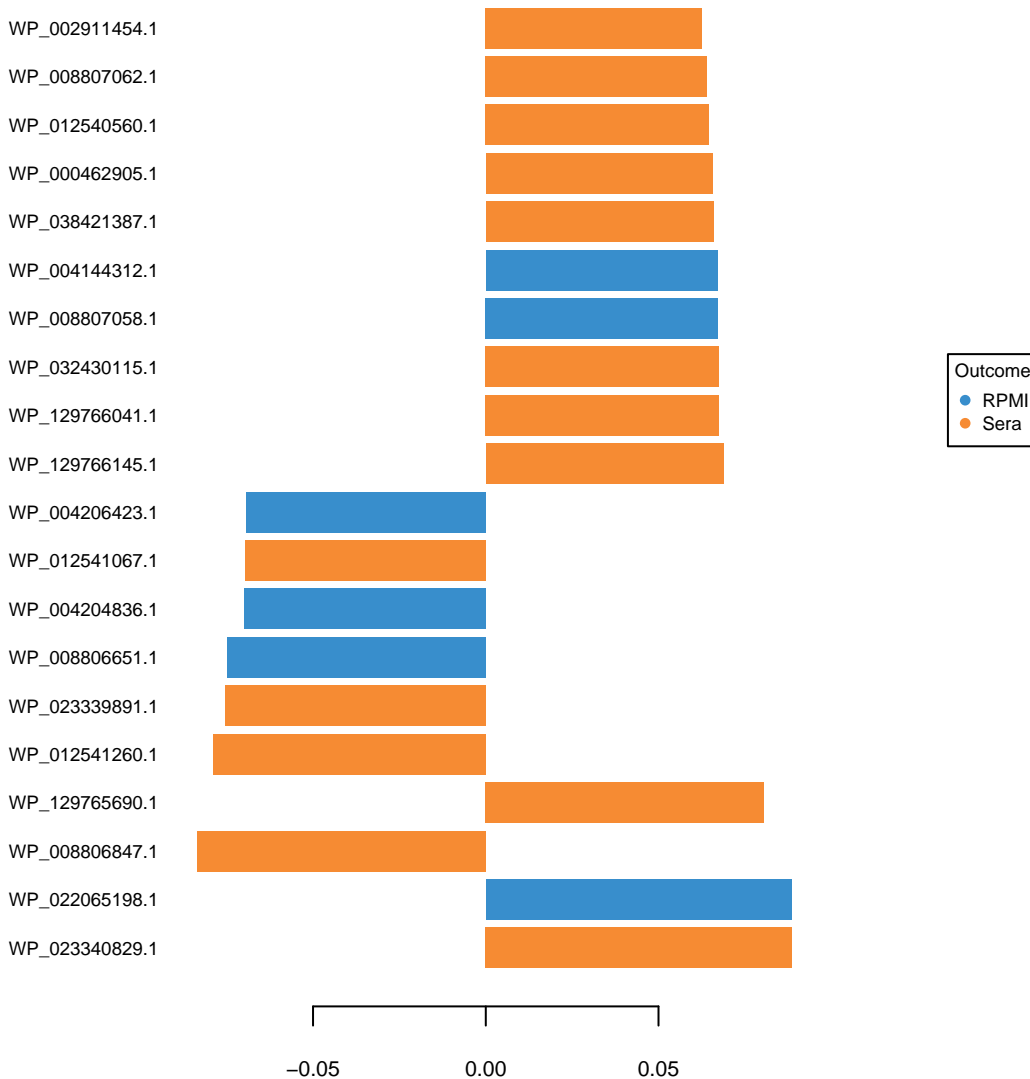




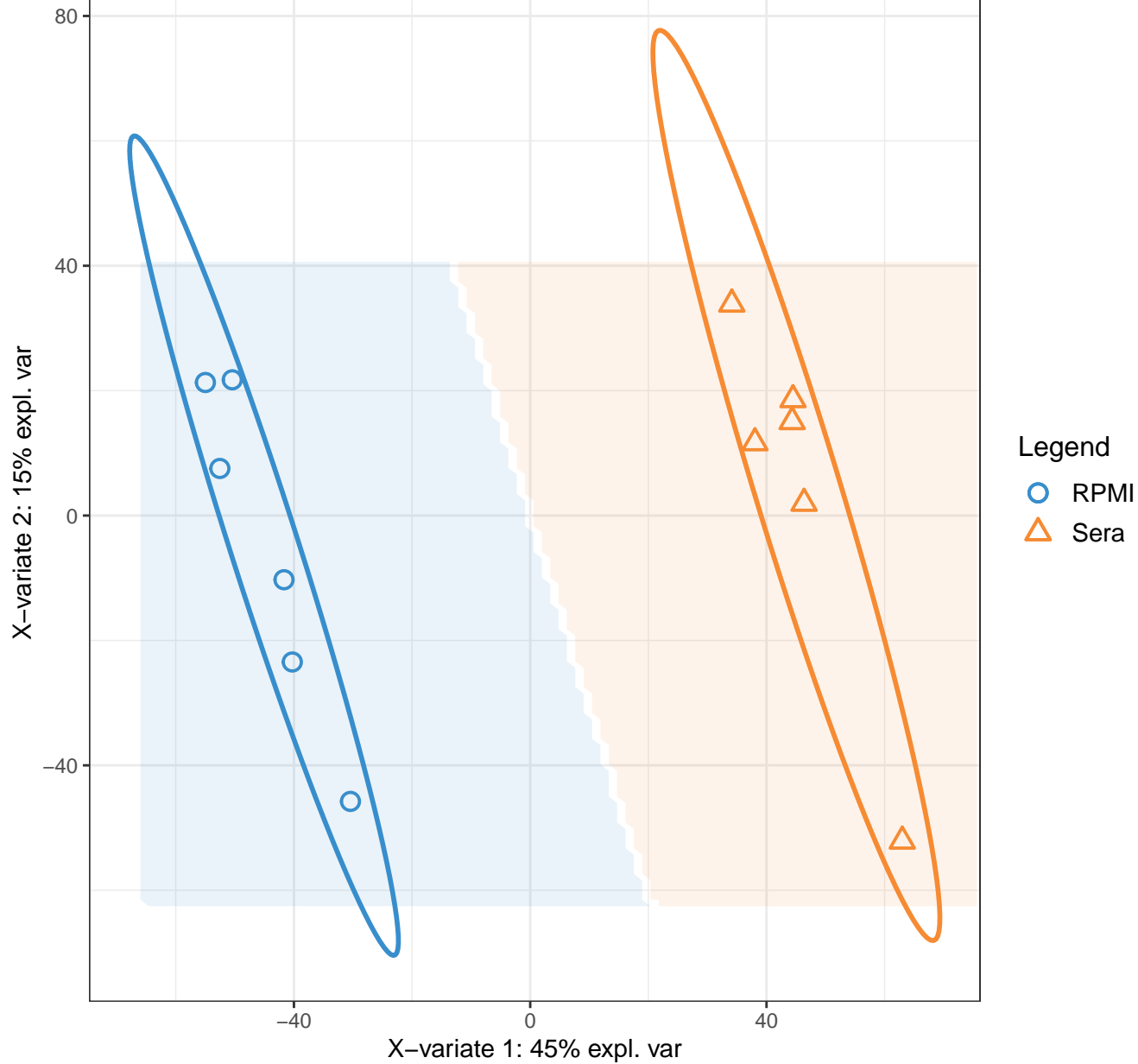
# proteome 4 PLSDA max loadir



# proteome 4 PLSDA min loadin



# transcriptome PLSDA single 1/2



# transcriptome PLSDA single 1/2

X-variate 2: 15% expl. var

80  
40  
0  
-40

-40

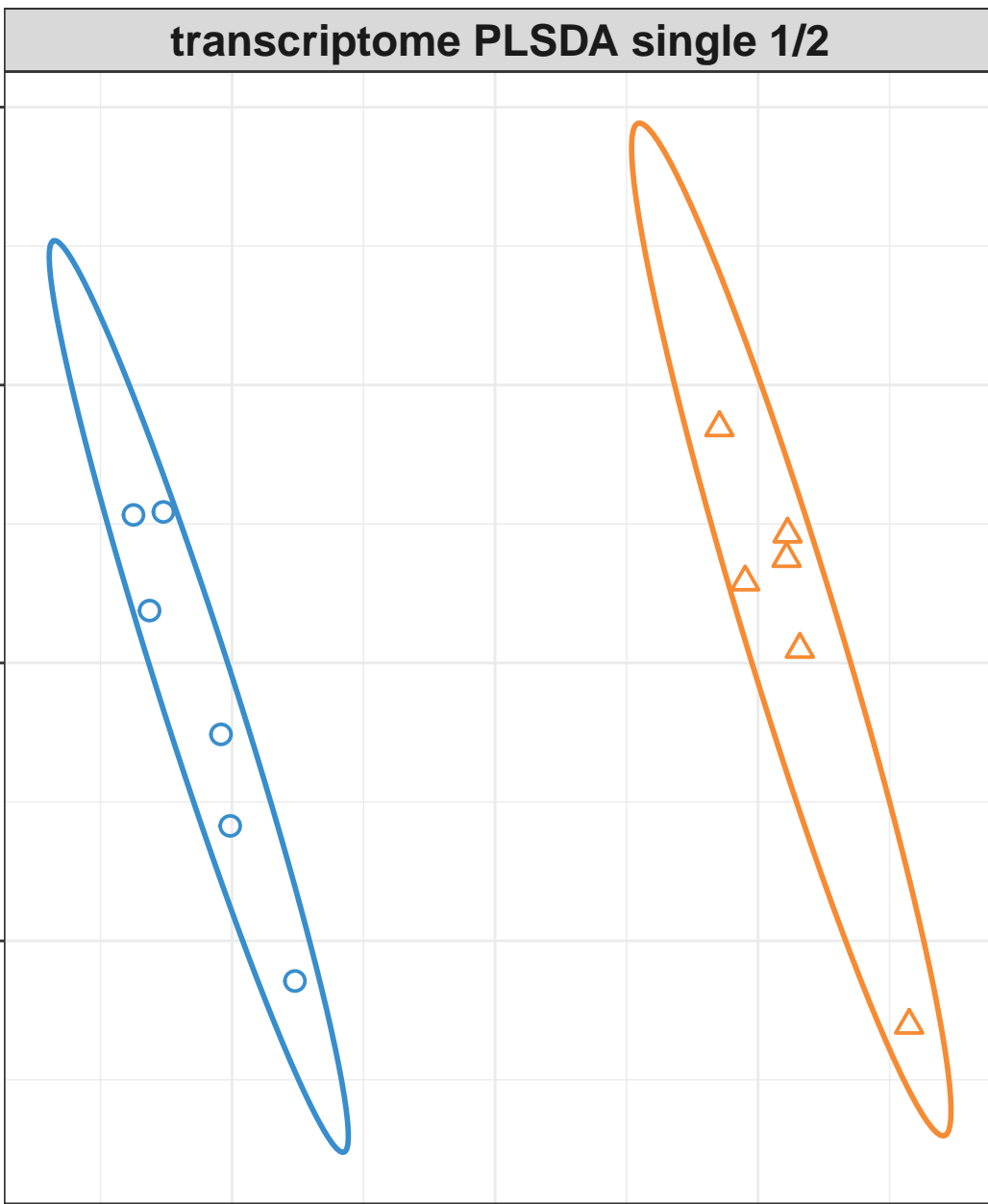
0

40

X-variate 1: 45% expl. var

Legend

- RPMI
- △ Sera



# transcriptome PLSDA single 1/3

X-variate 3: 5% expl. var

25

0

-25

-40

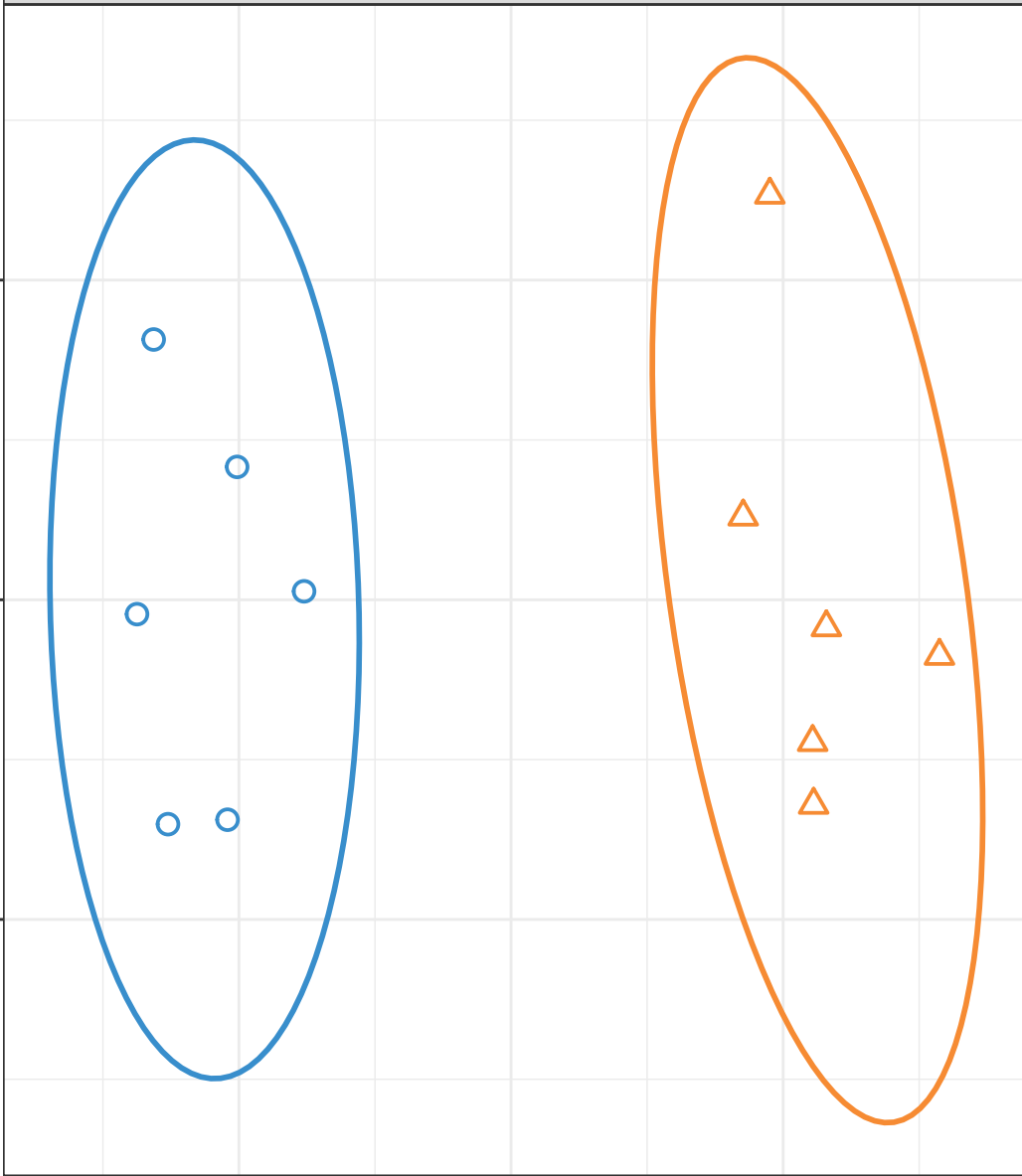
0

40

X-variate 1: 45% expl. var

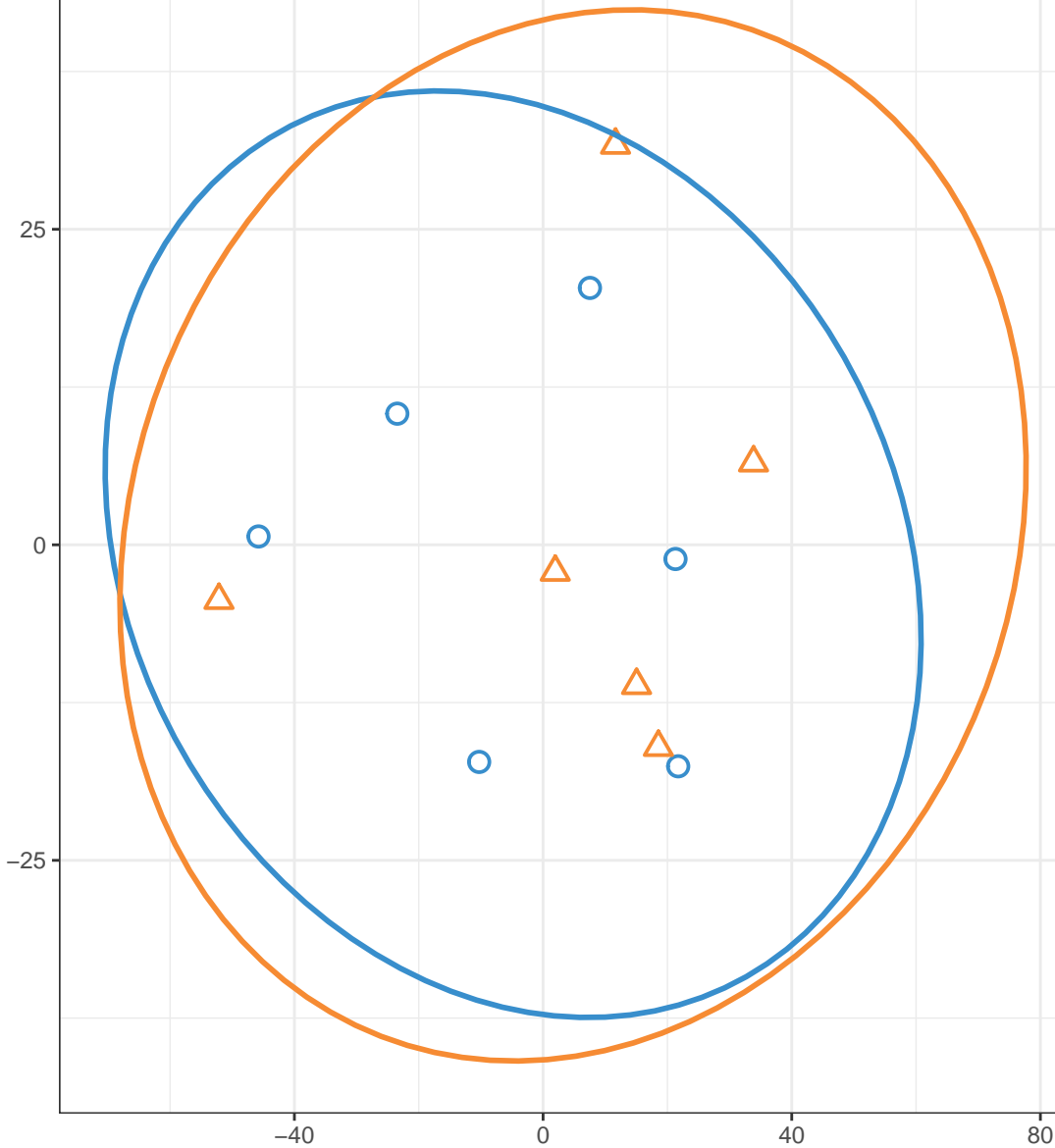
Legend

- RPMI
- △ Sera



# transcriptome PLSDA single 2/3

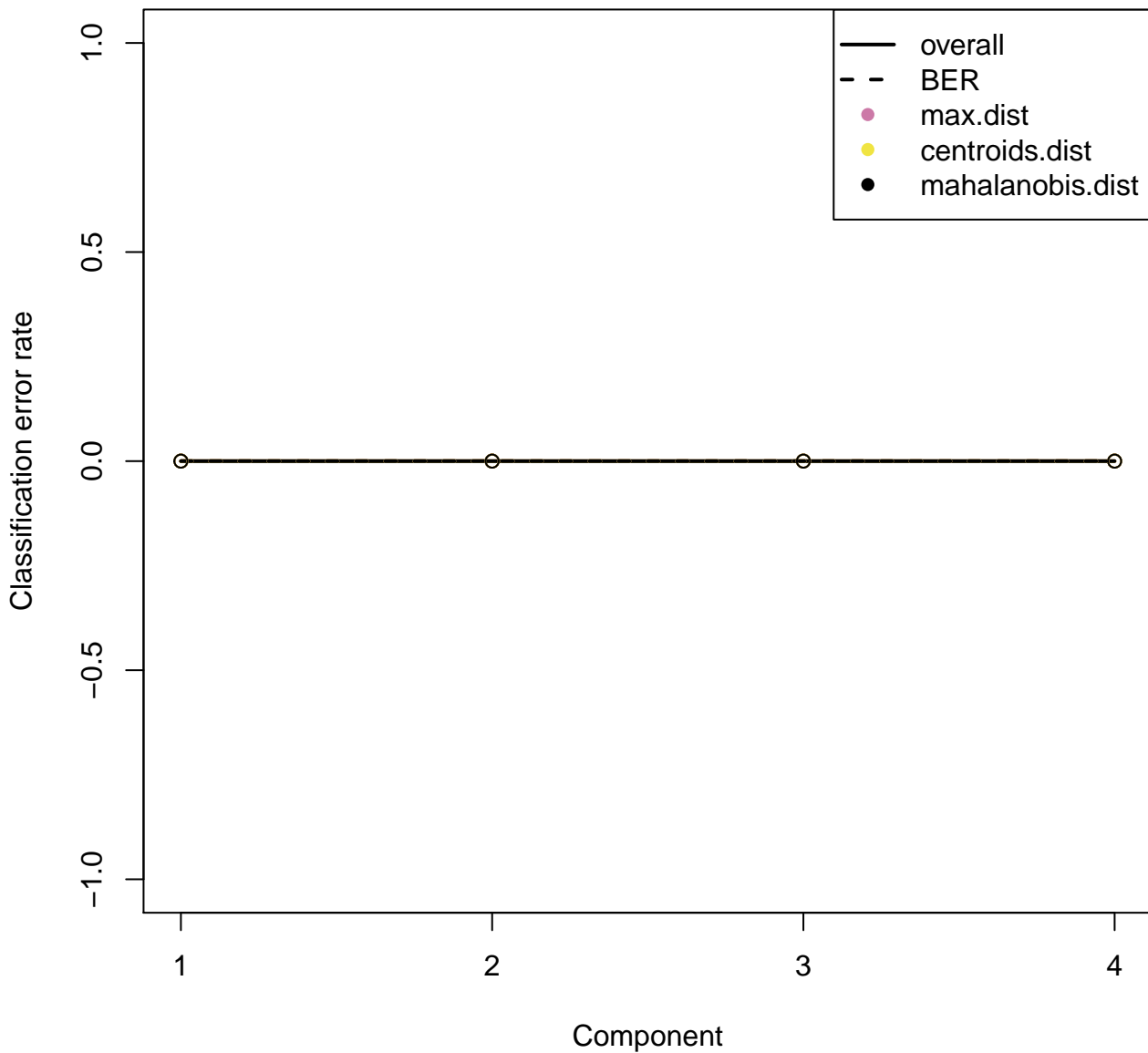
X-variate 3: 5% expl. var



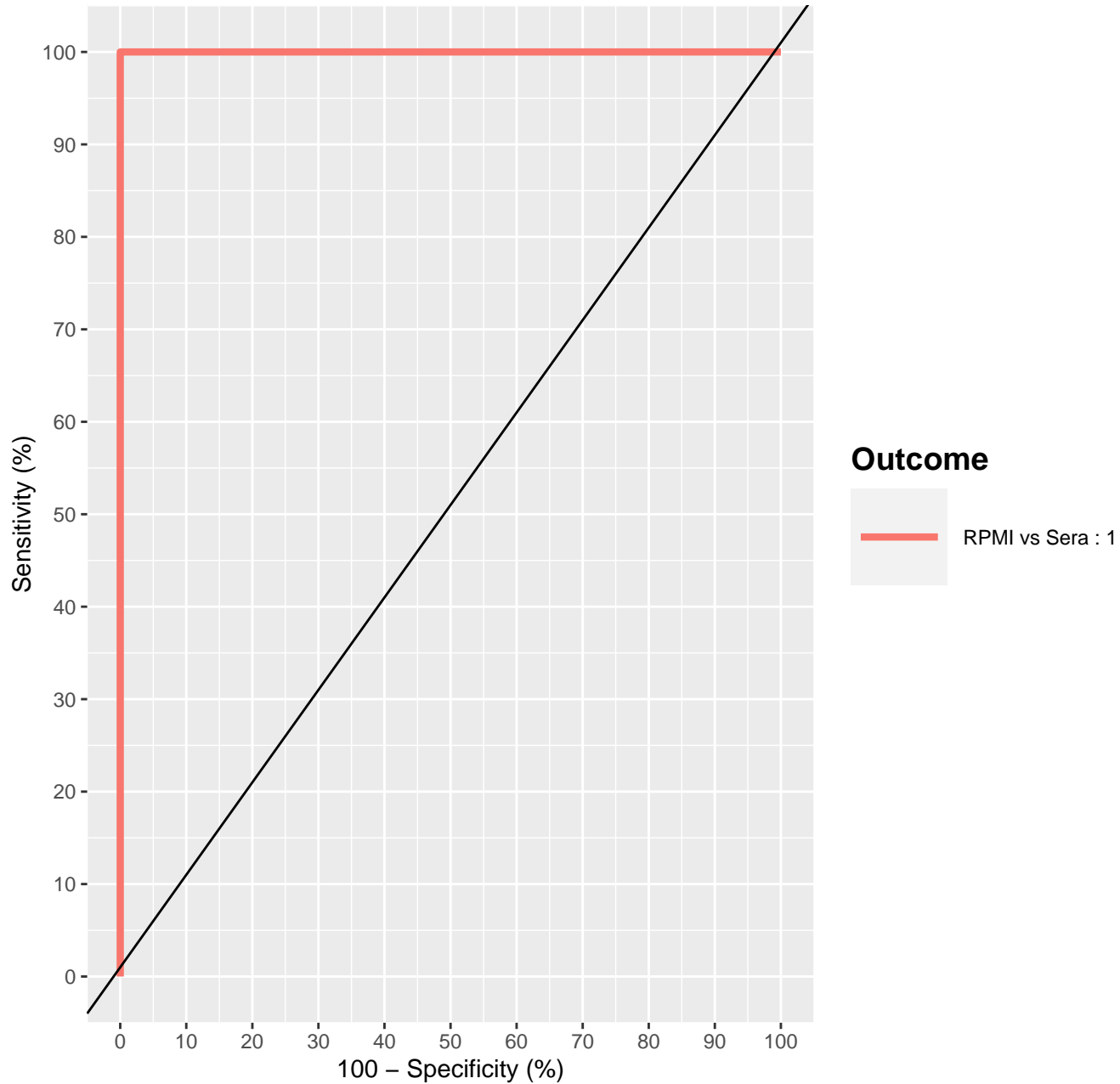
Legend

○ RPMI

△ Sera

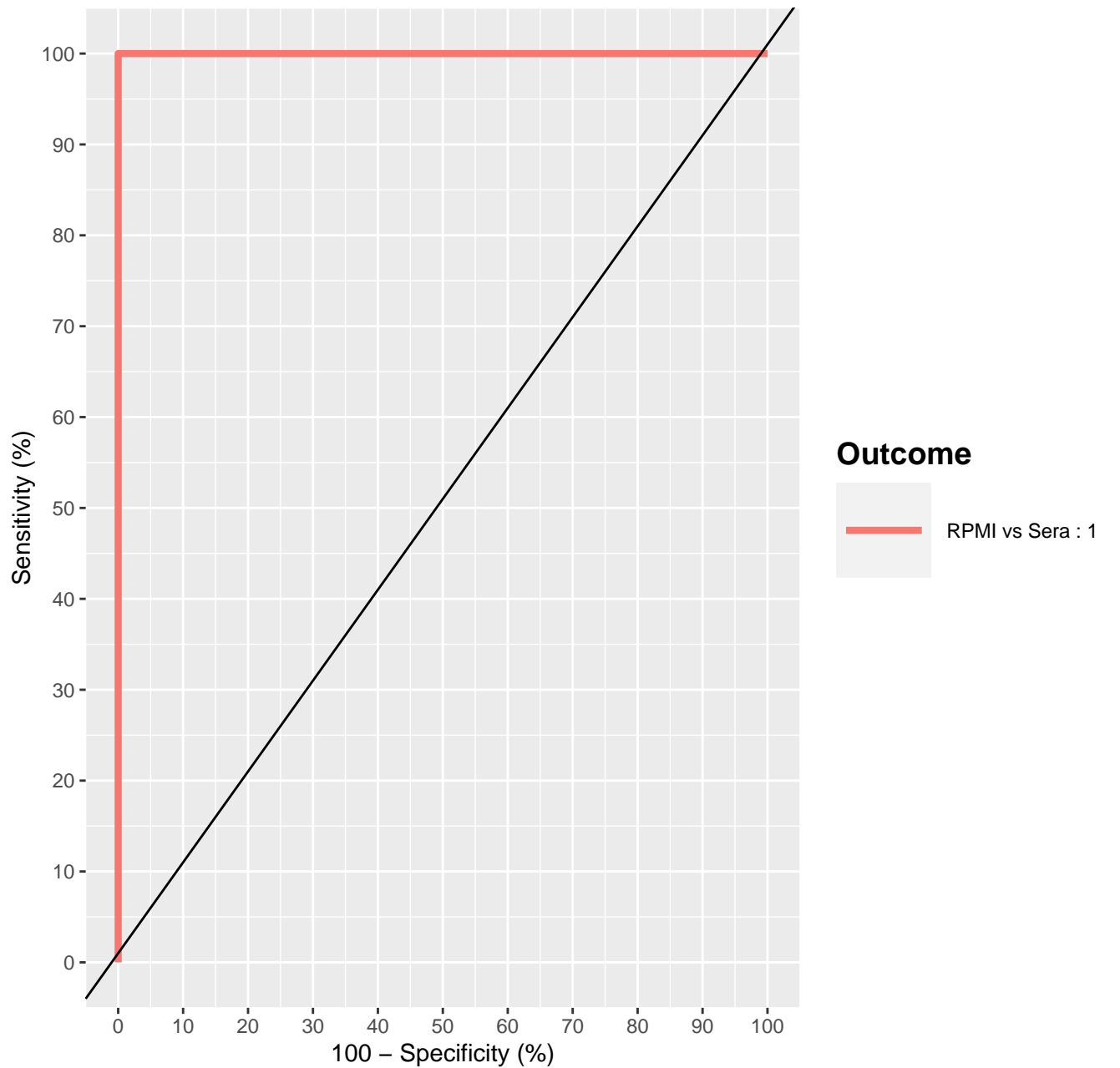


**ROC Curve Using Comp(s): 1**

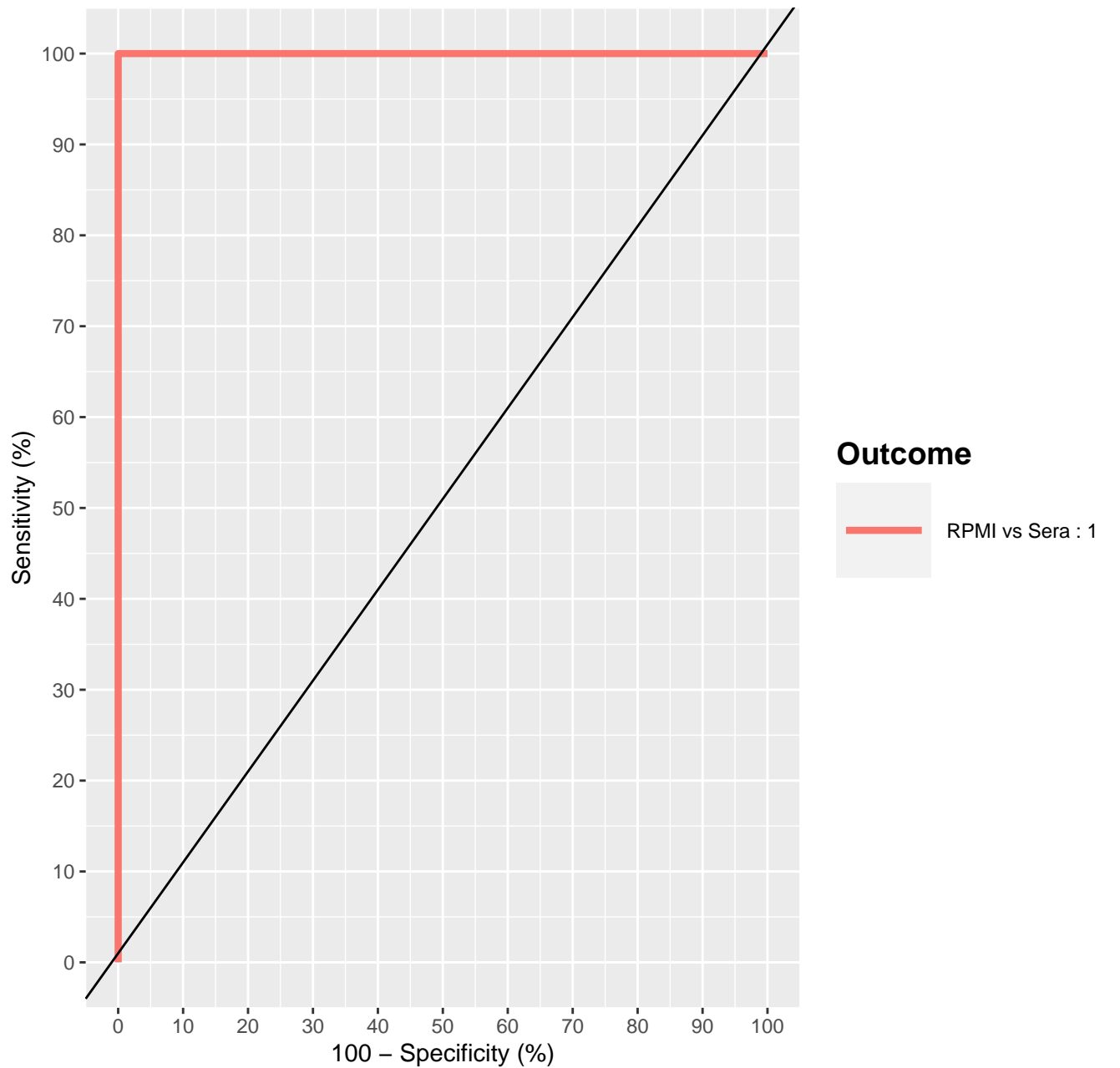




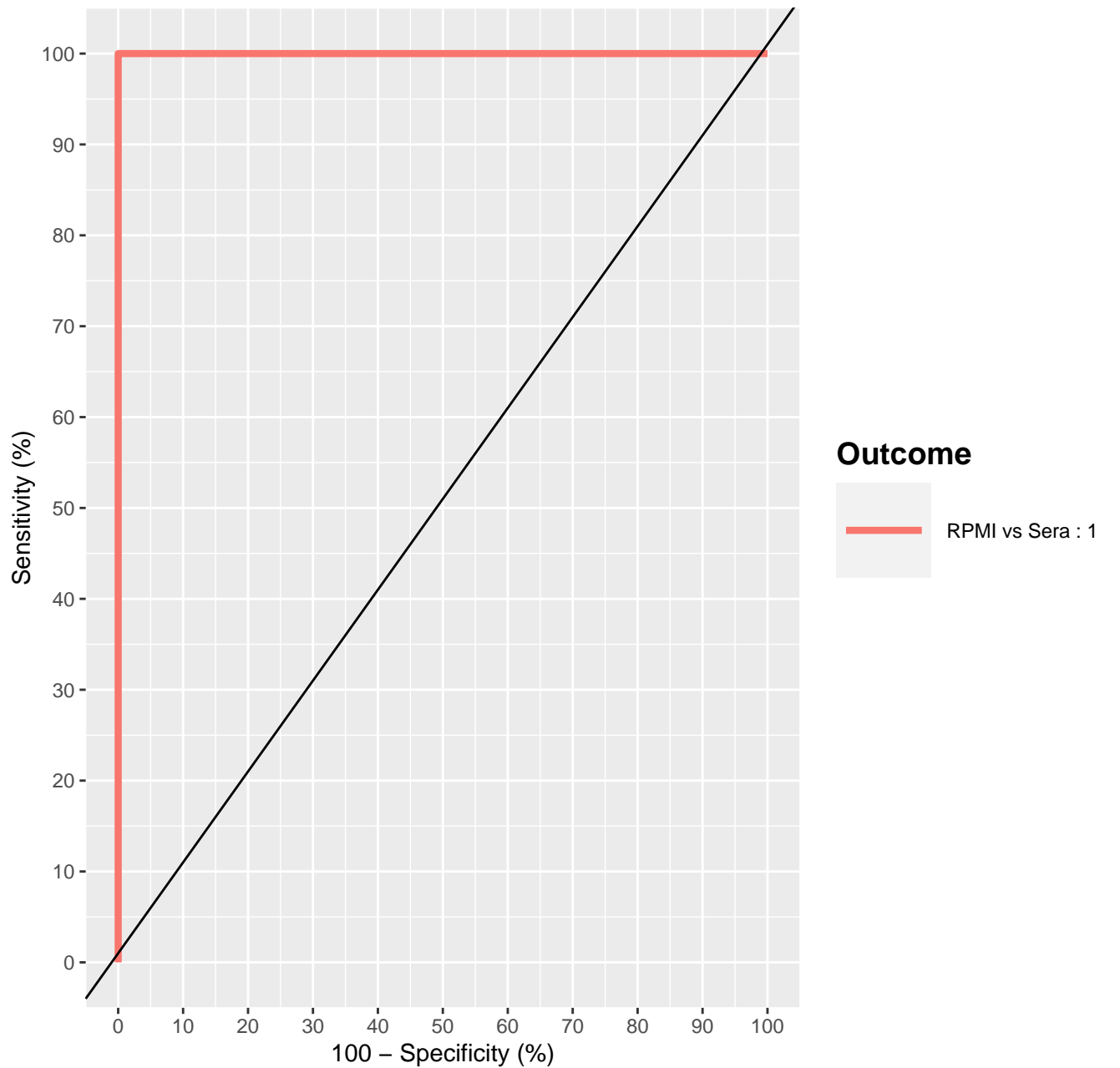
ROC Curve Using Comp(s): 1, 2



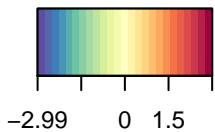
**ROC Curve Using Comp(s): 1, 2, 3**



**ROC Curve Using Comp(s): 1, 2, 3, 4**



Color key

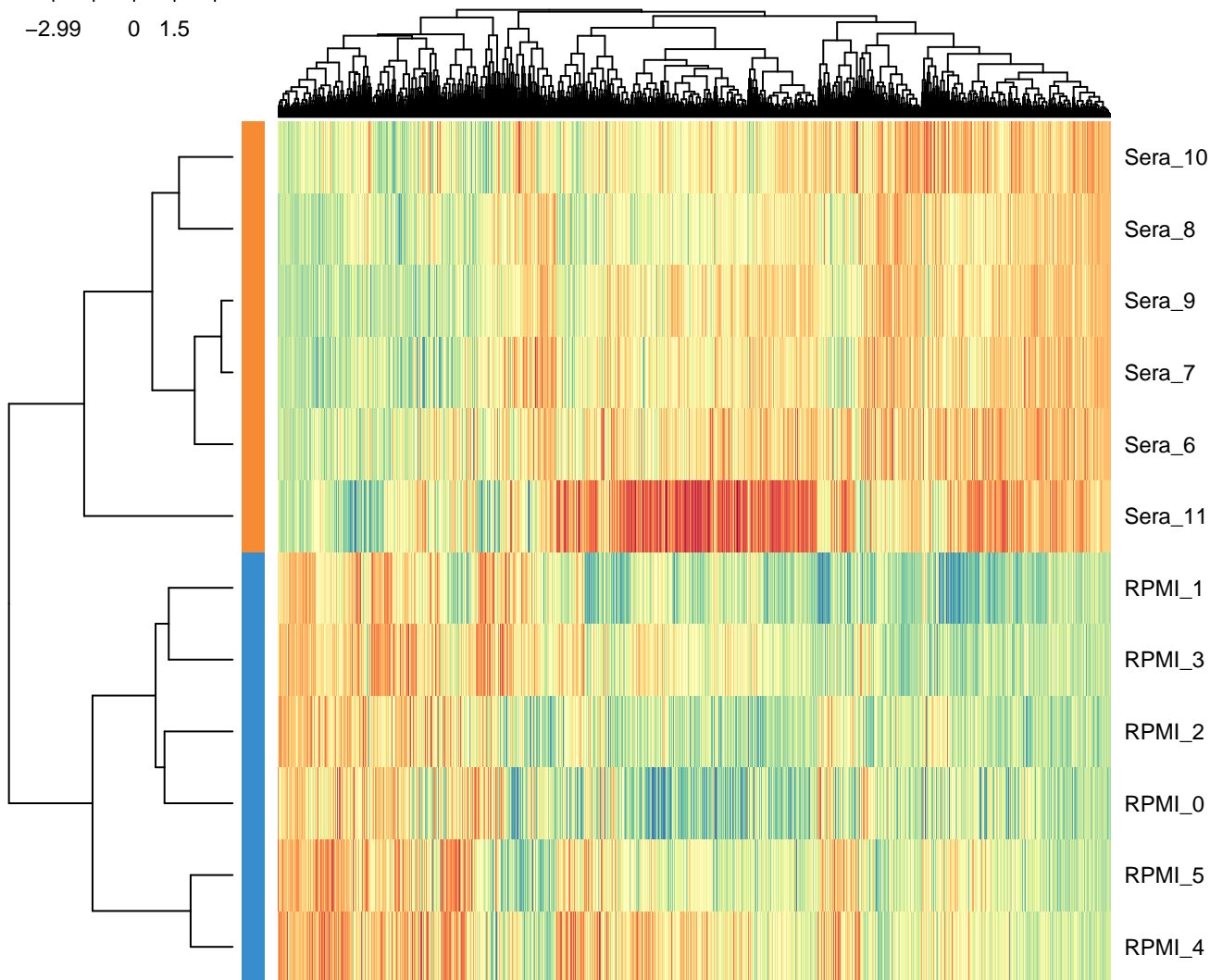


# PLSDA

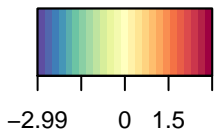
Status

■ RPMI

■ Sera



Color key

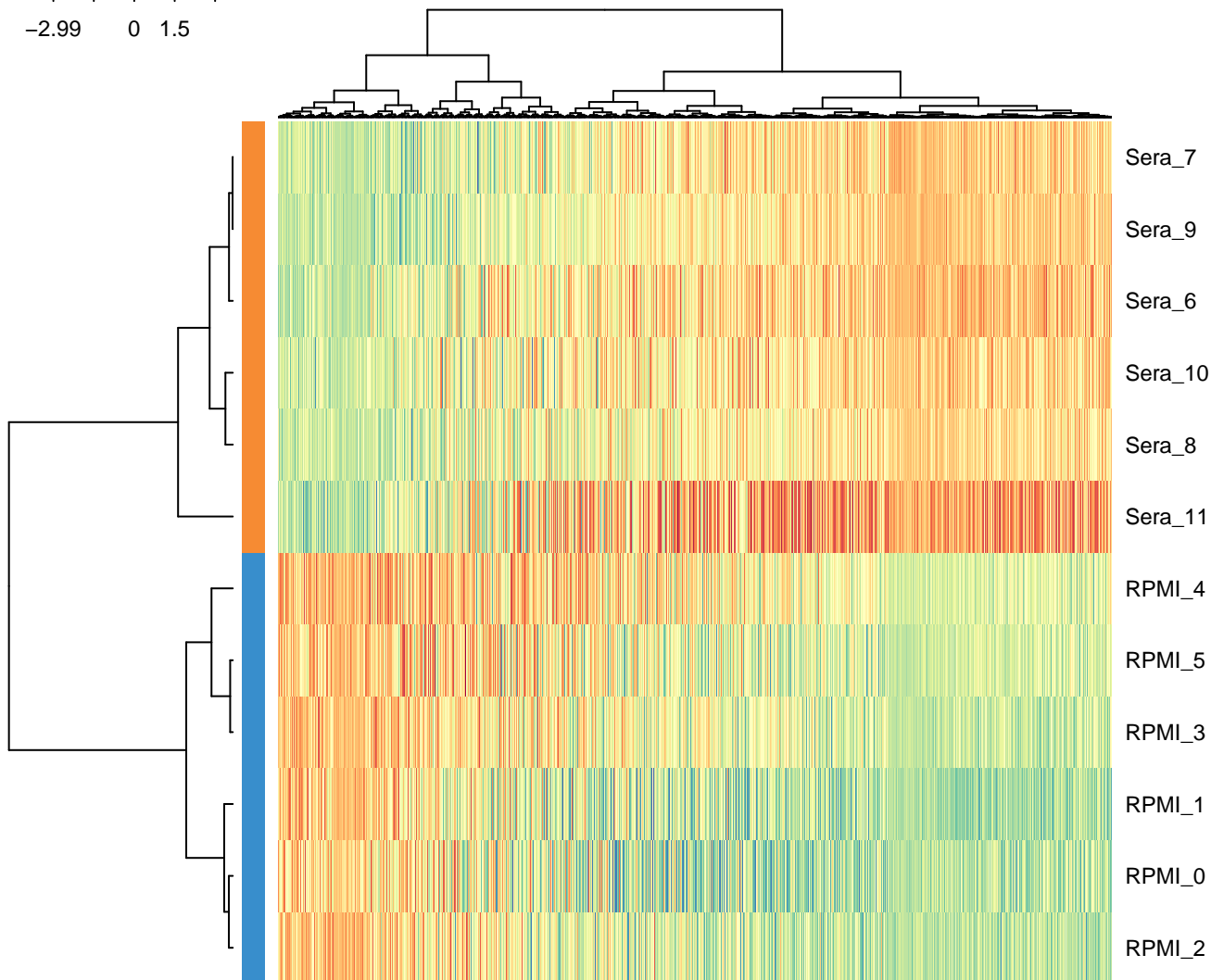


# PLSDA Component 1

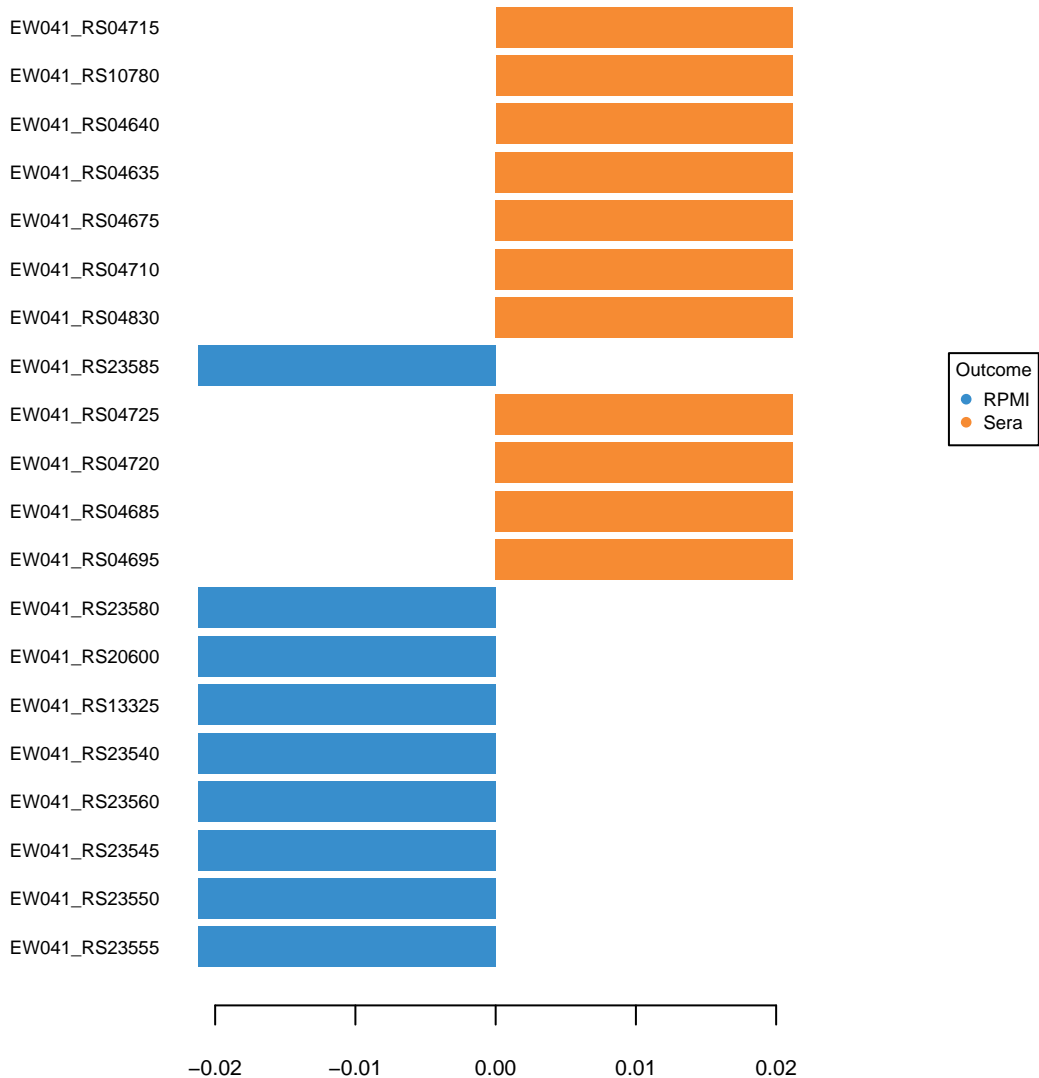
Status

RPMI

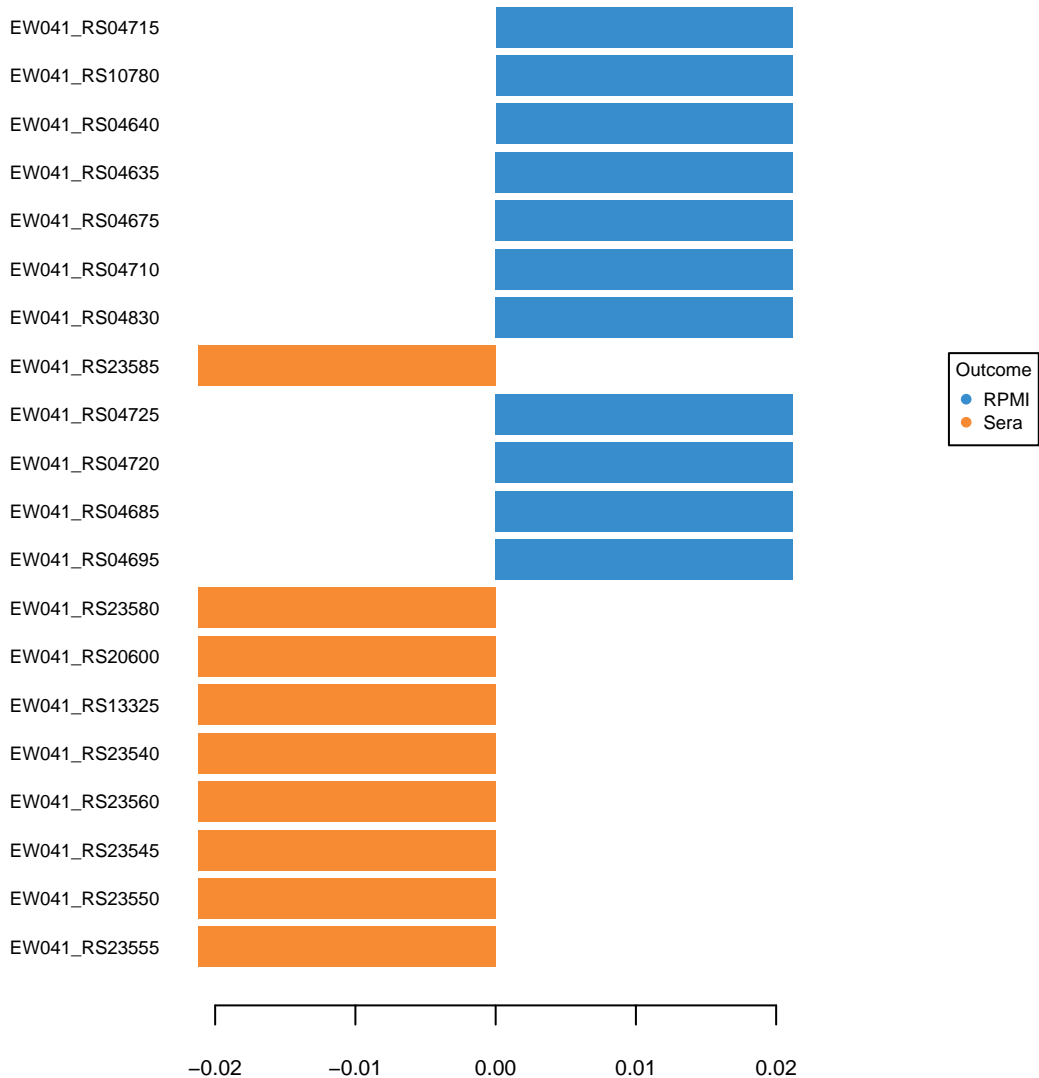
Sera



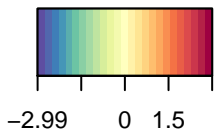
# transcriptome 1 PLSDA max load



# transcriptome 1 PLSDA min load



Color key

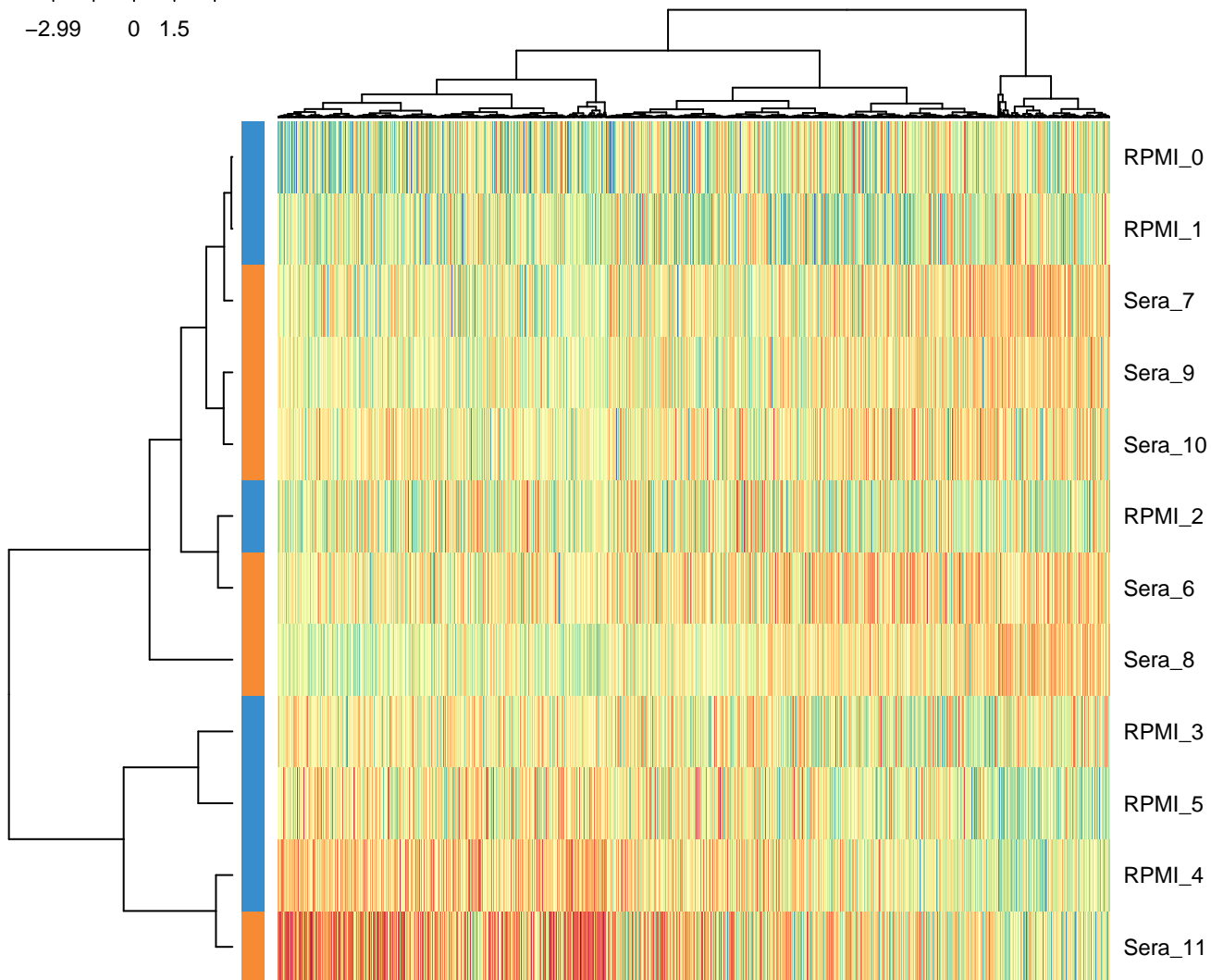


## PLSDA Component 2

Status

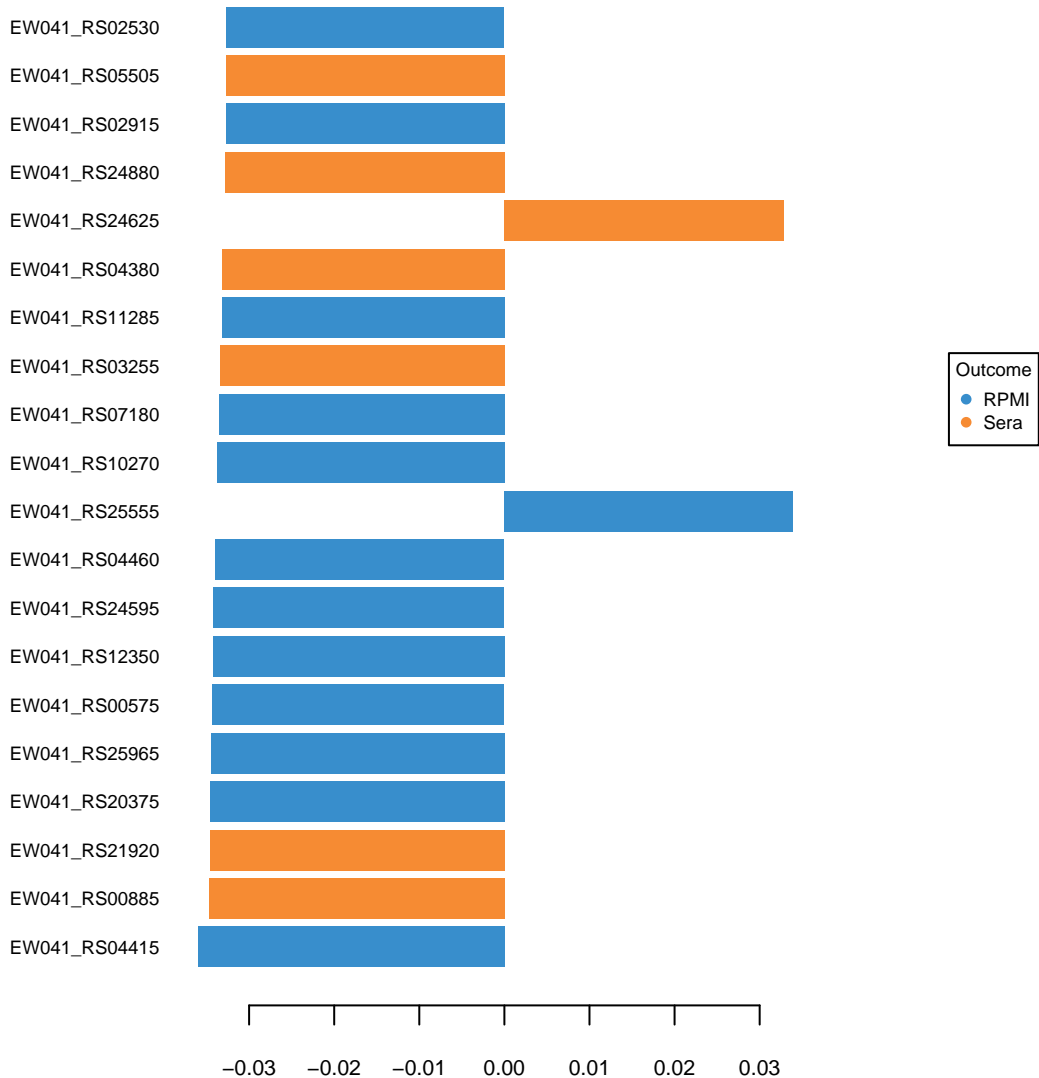
■ RPMI

■ Sera

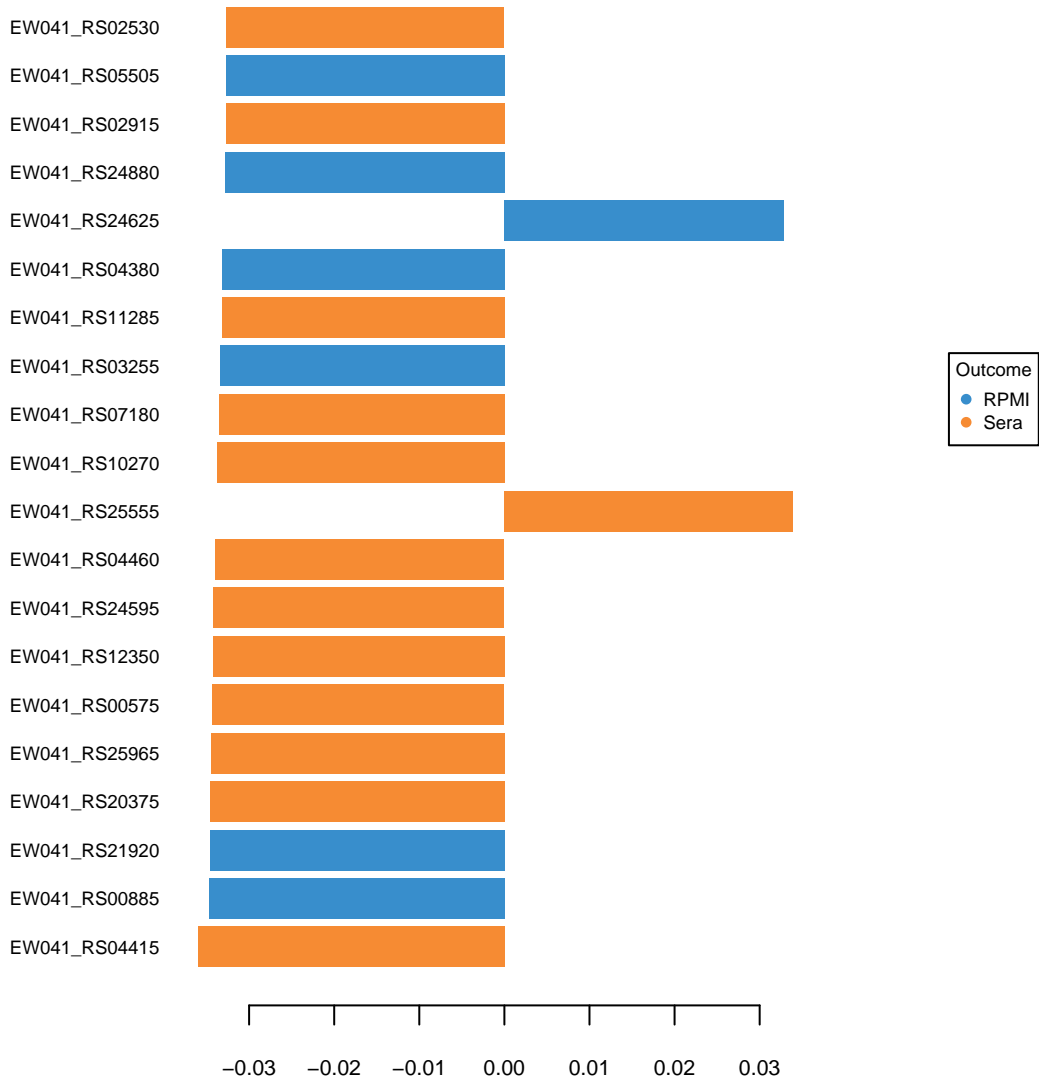




# transcriptome 2 PLSDA max load



# transcriptome 2 PLSDA min load



Color key

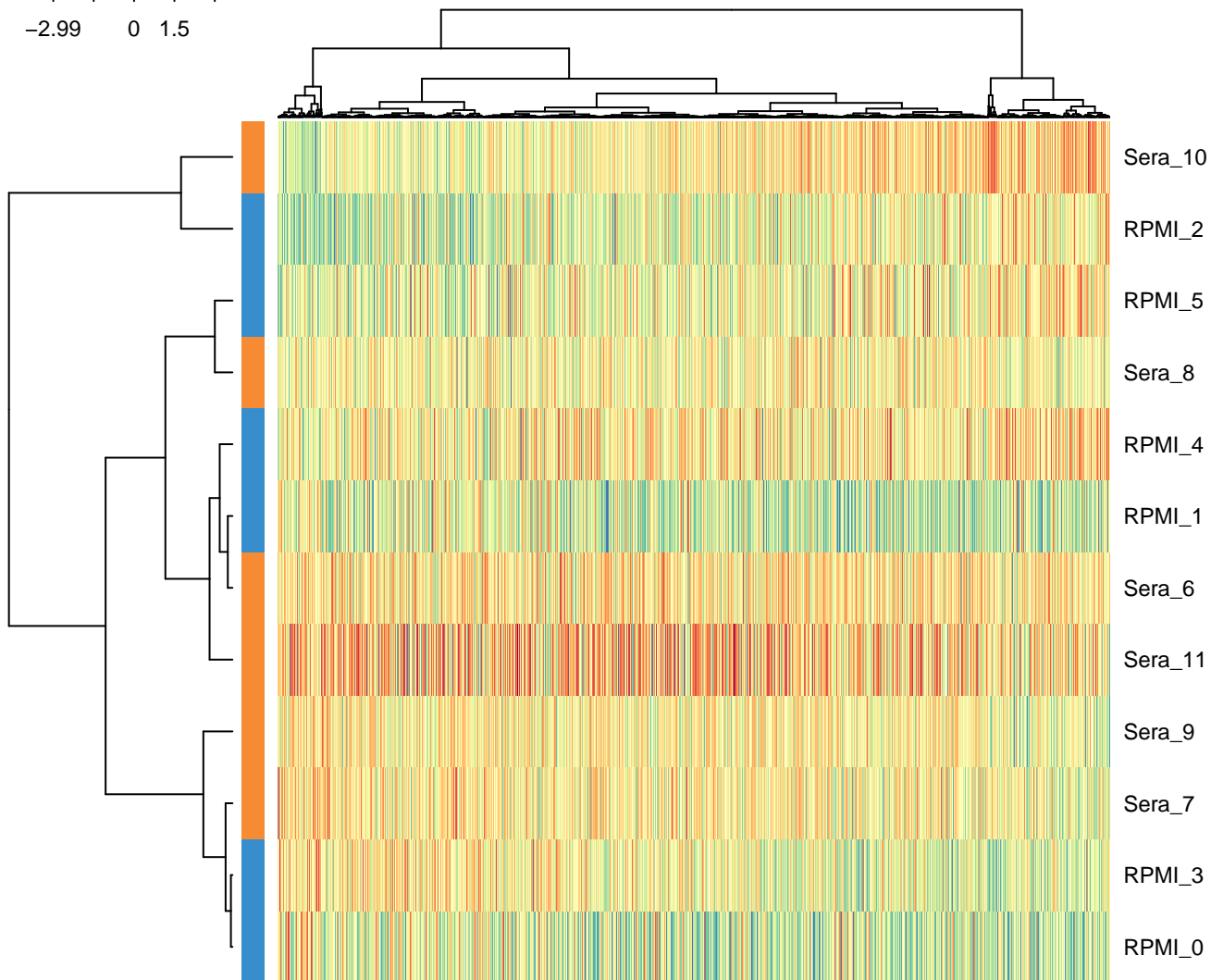
# PLSDA Component 3

Status

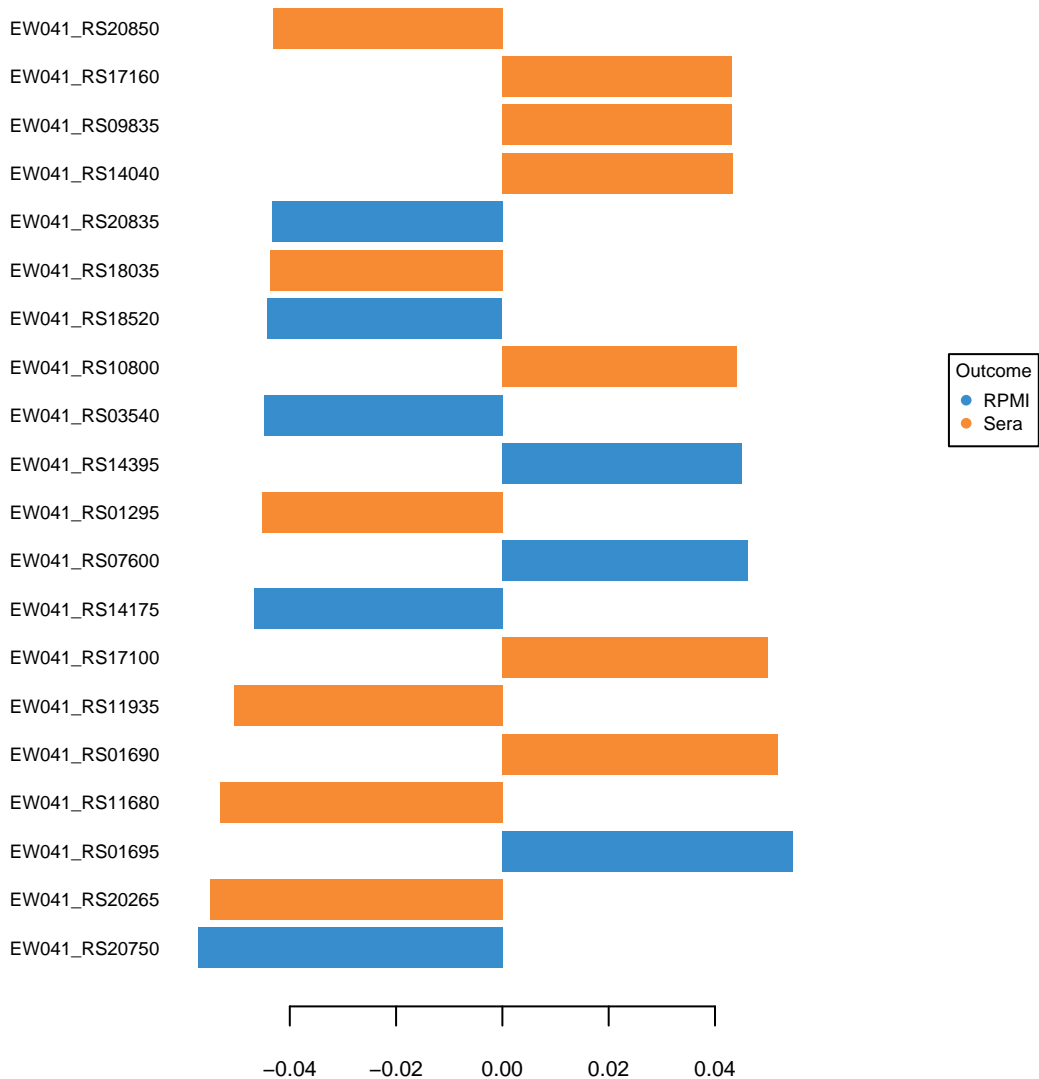
RPMI

Sera

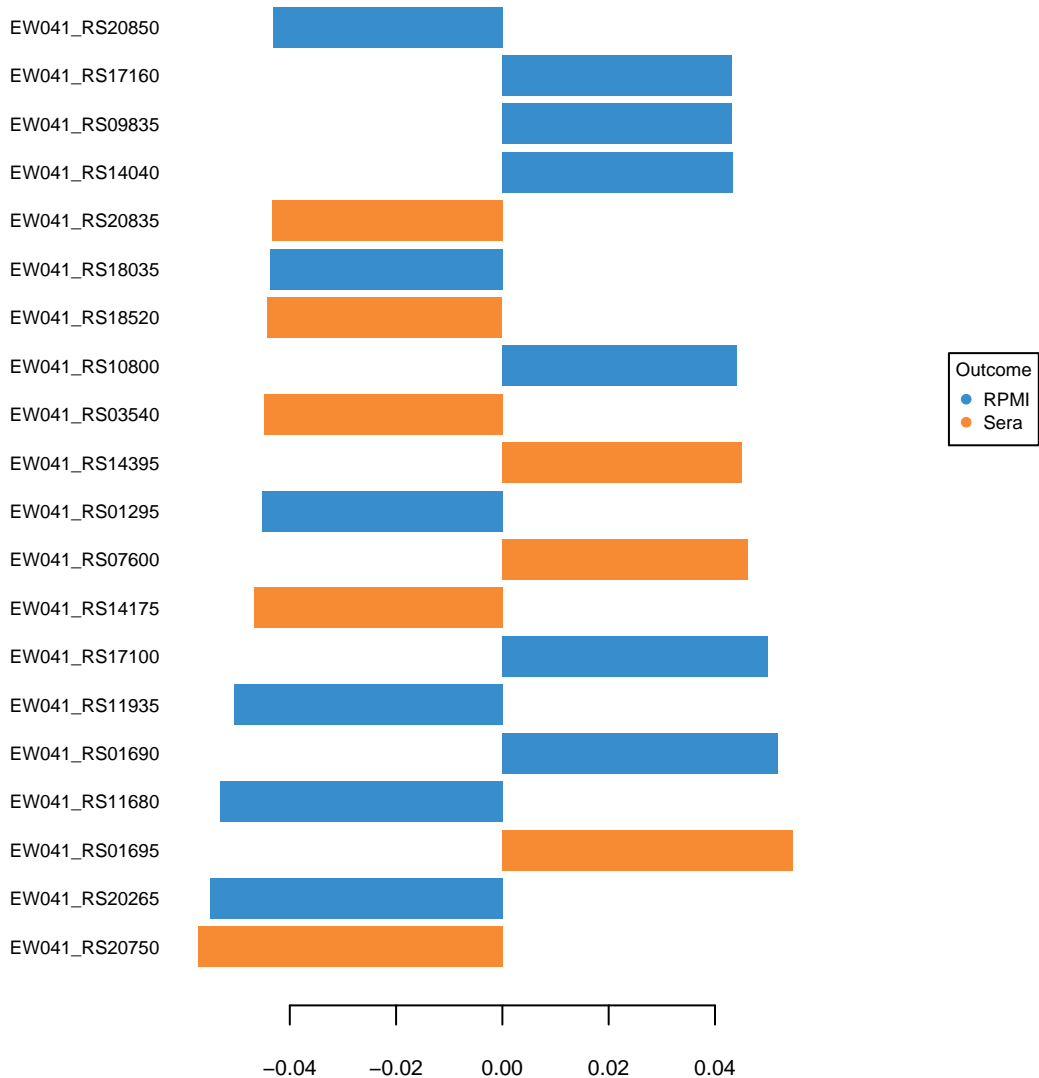
-2.99 0 1.5



# transcriptome 3 PLSDA max load

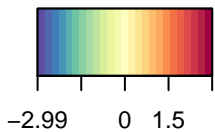


# transcriptome 3 PLSDA min load



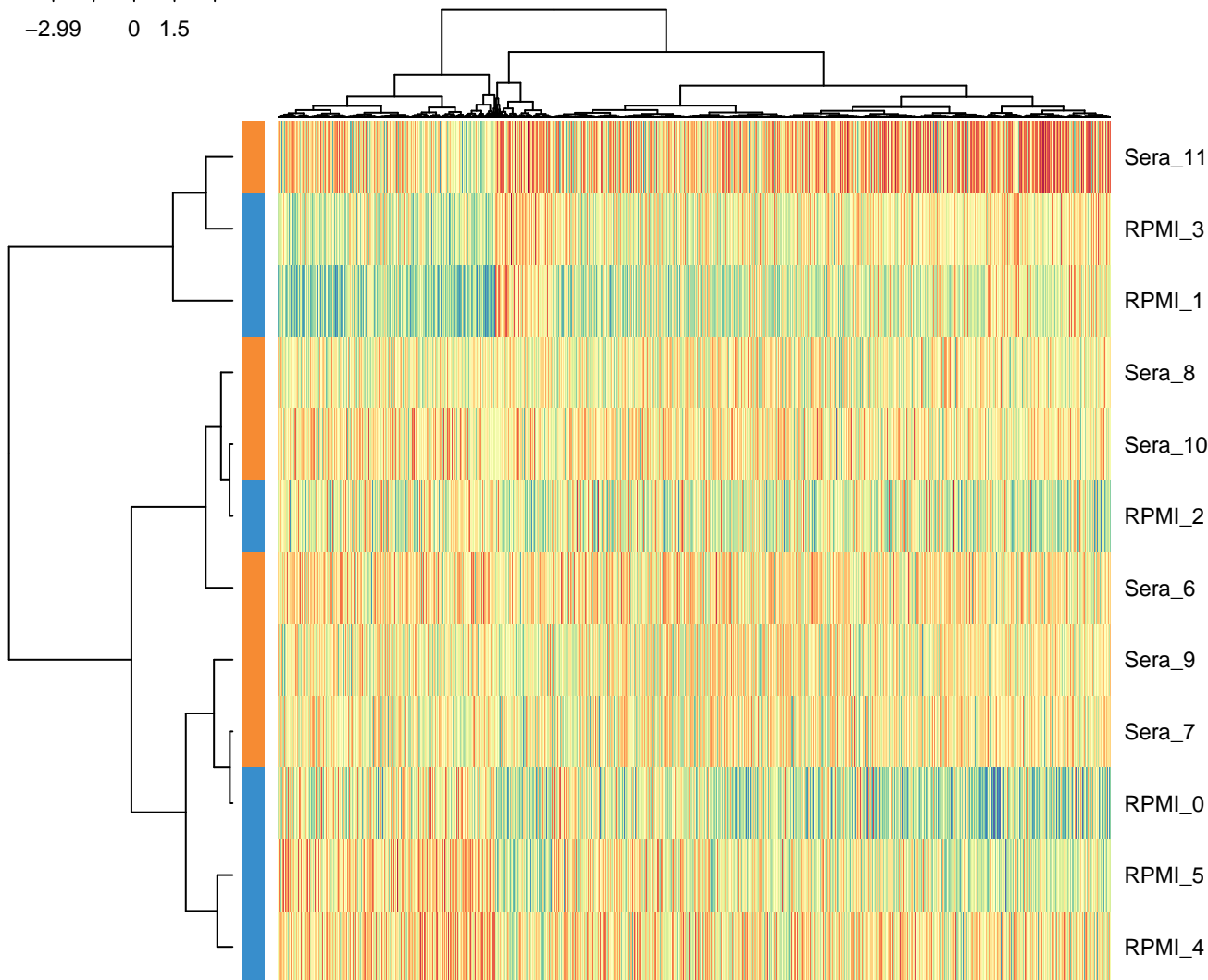
# PLSDA Component 4

Color key

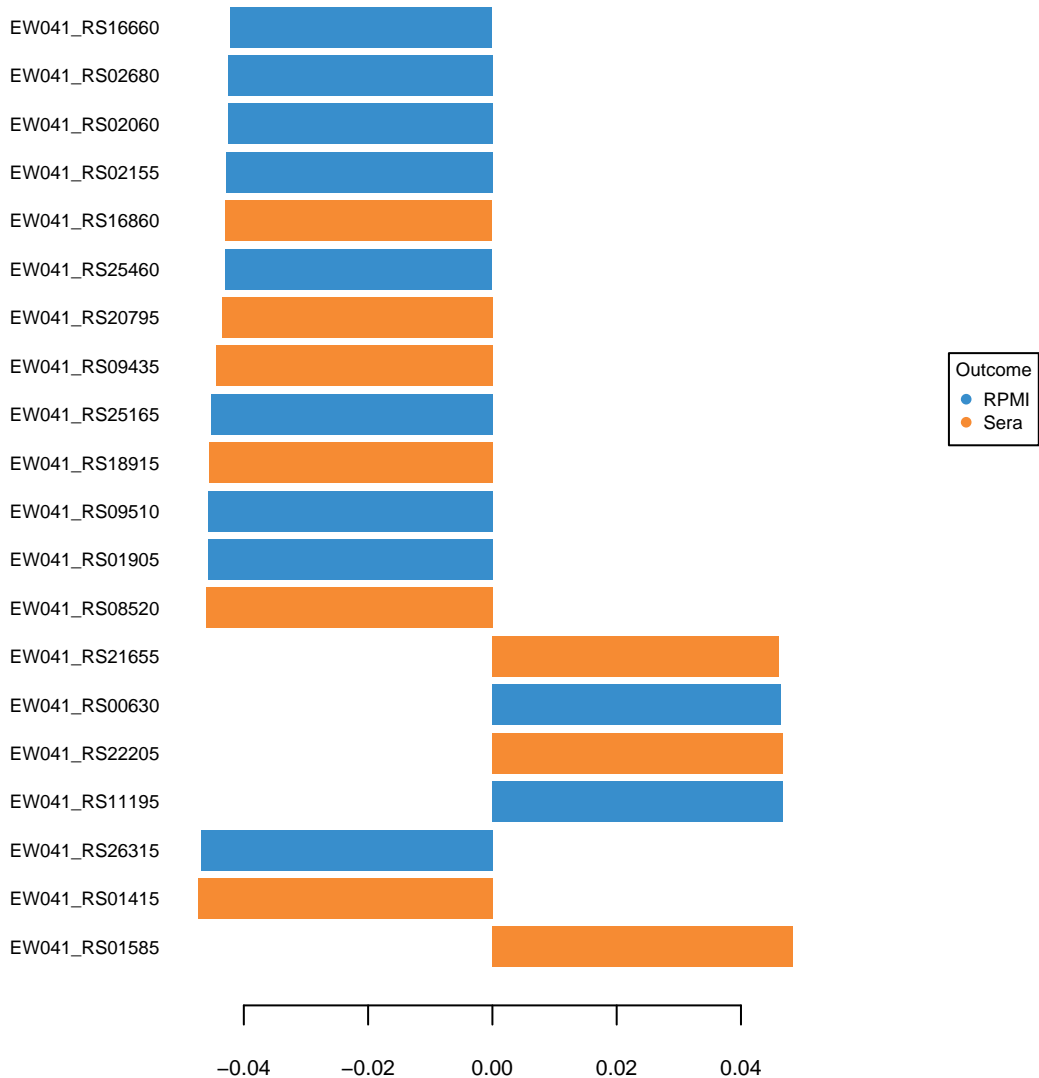


Status

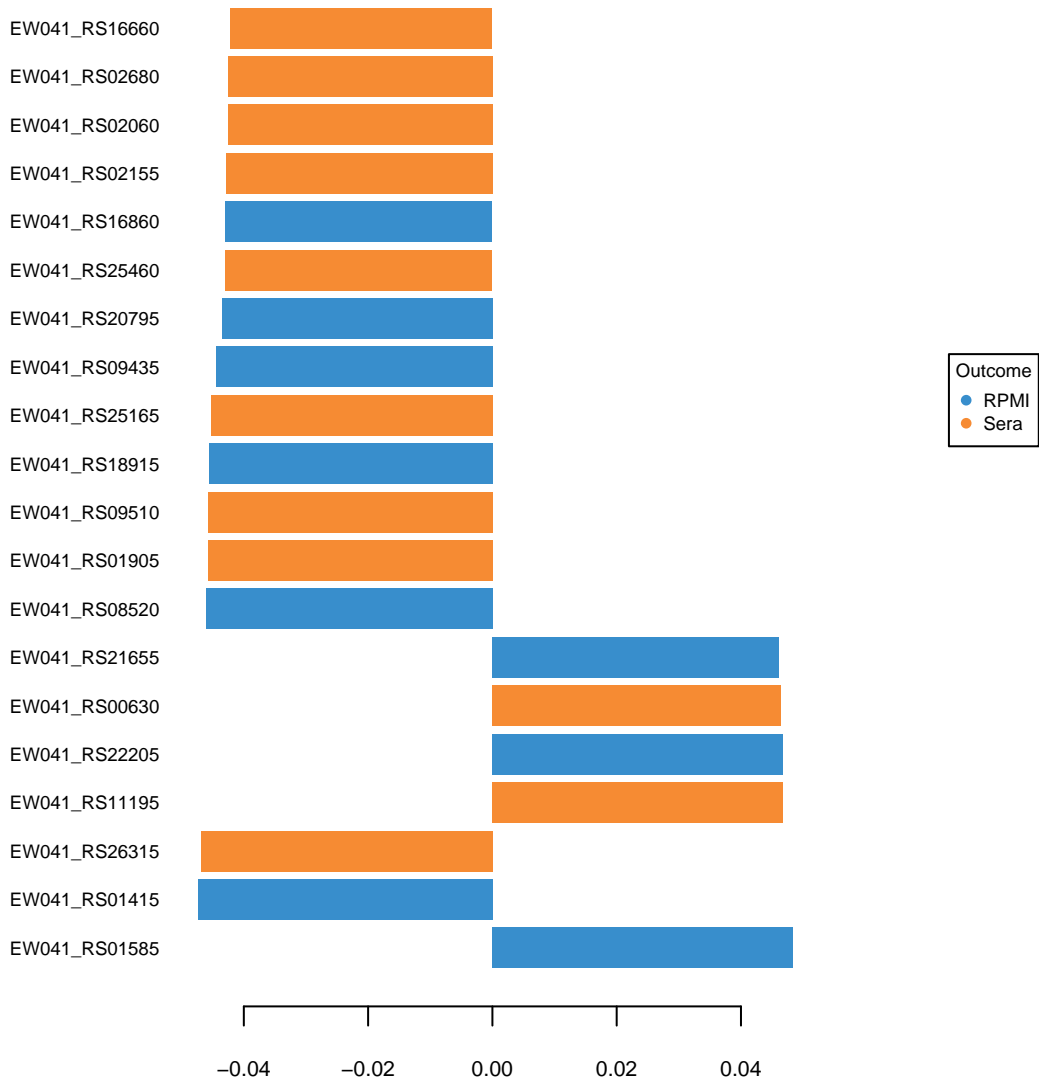
- RPMI
- Sera



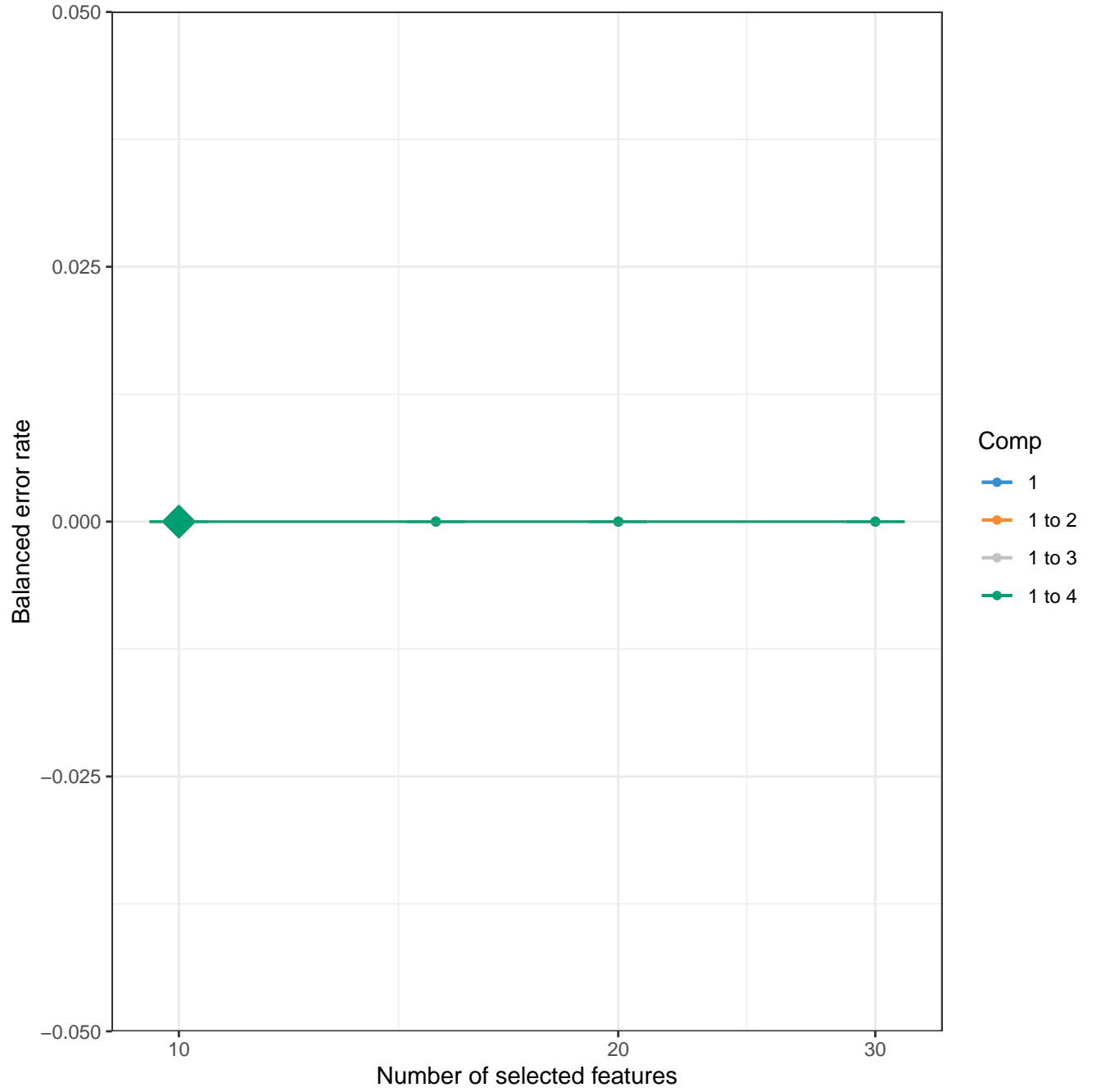
# transcriptome 4 PLSDA max load

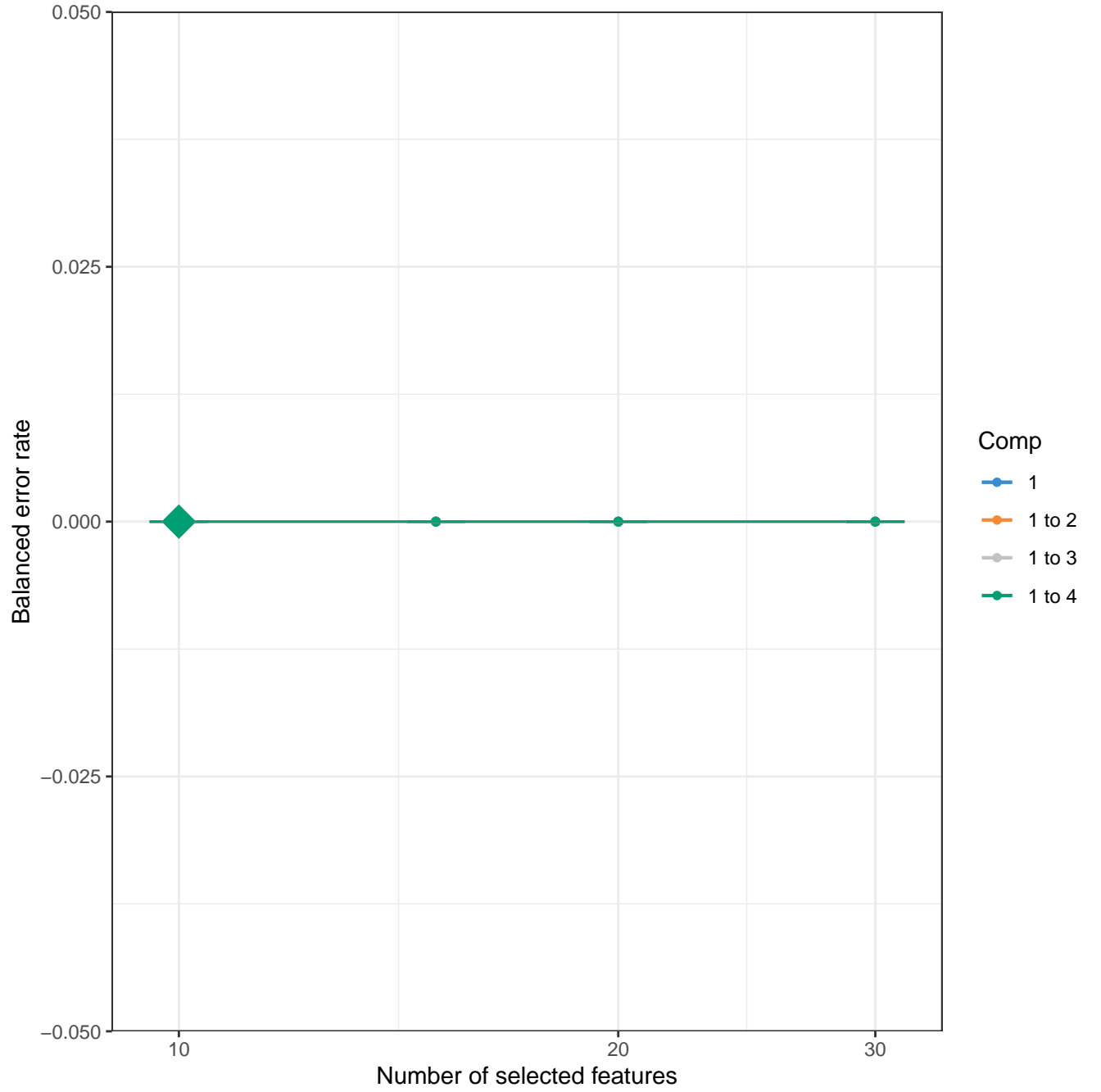


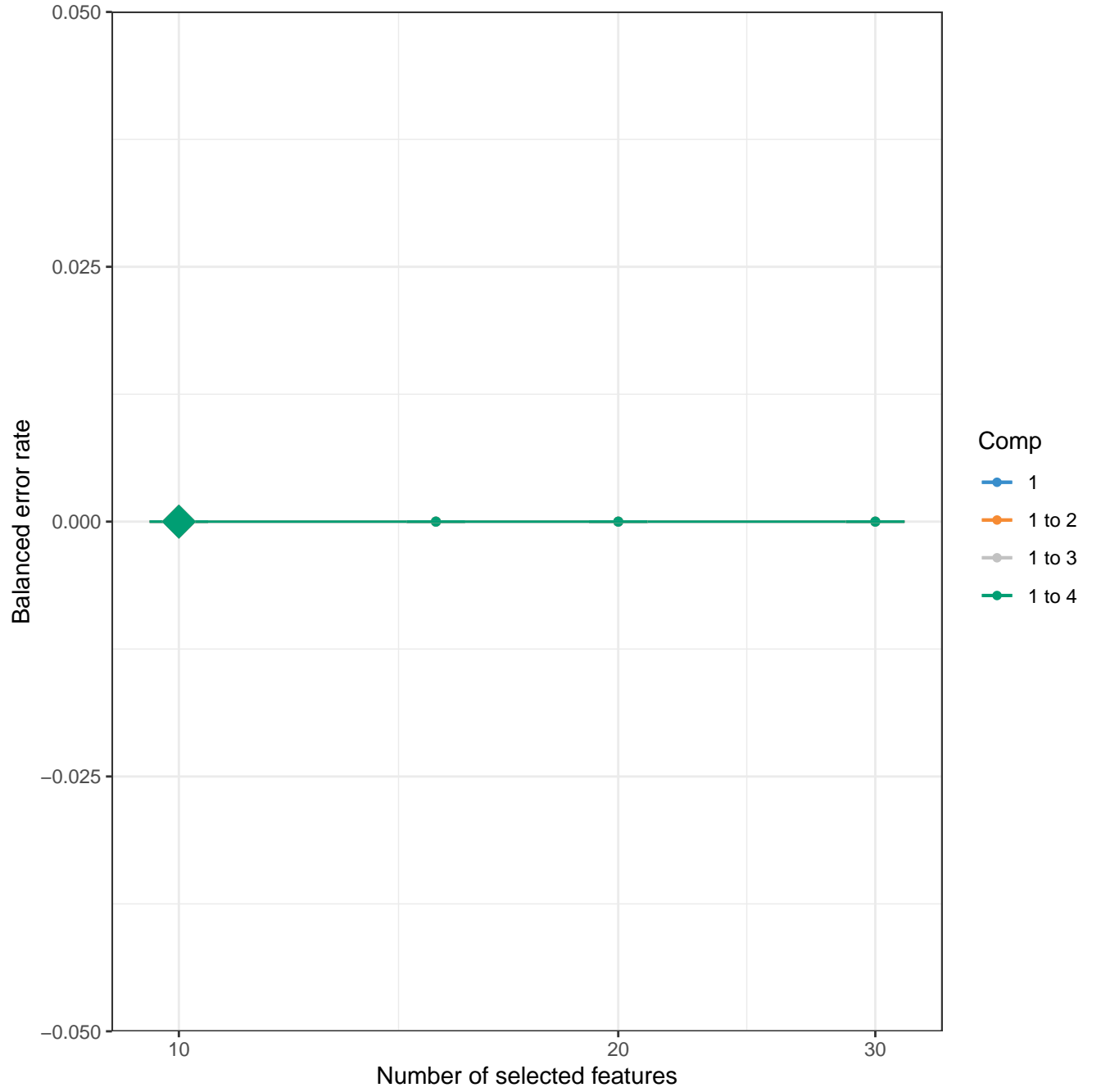
# transcriptome 4 PLSDA min load

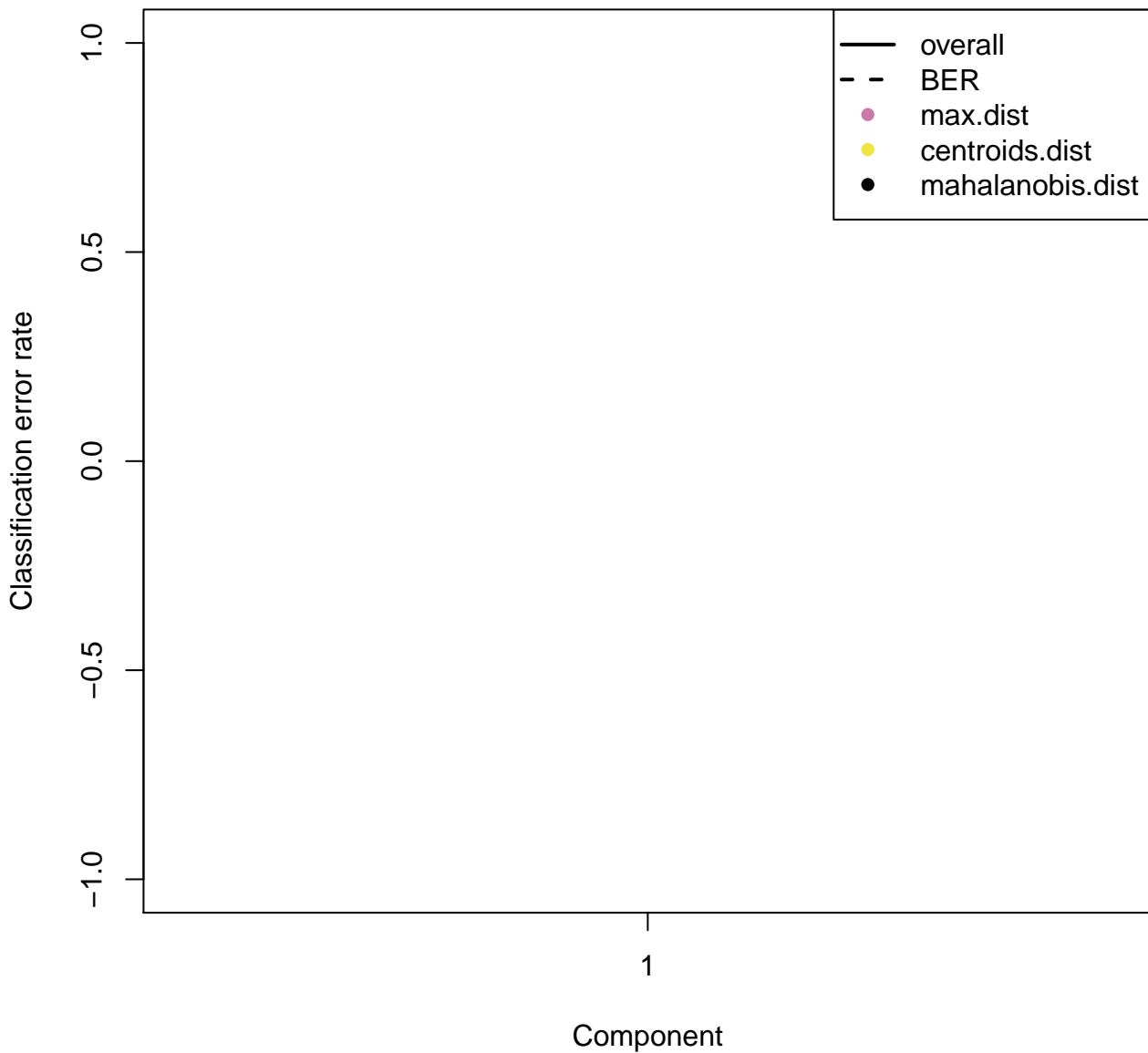




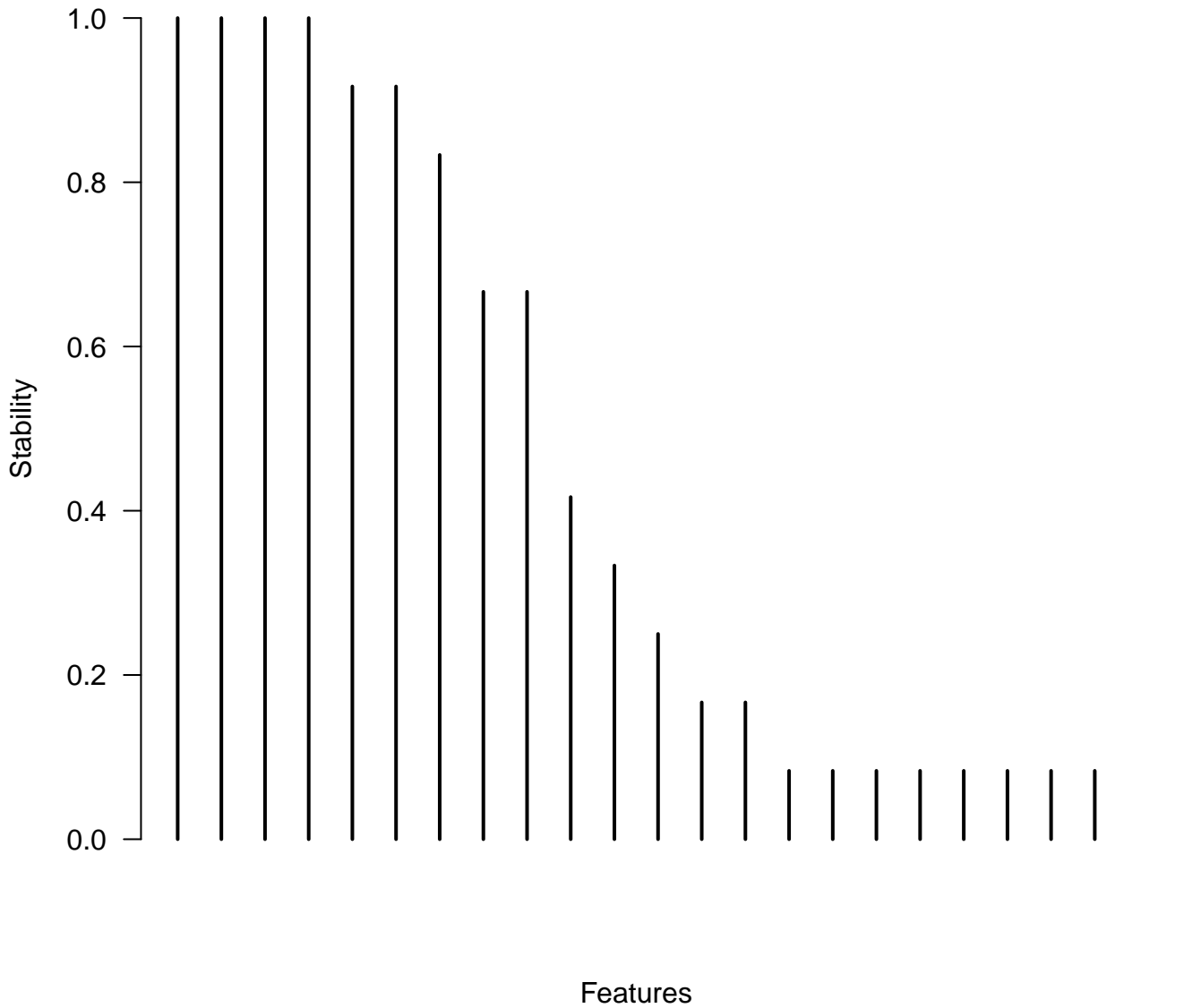




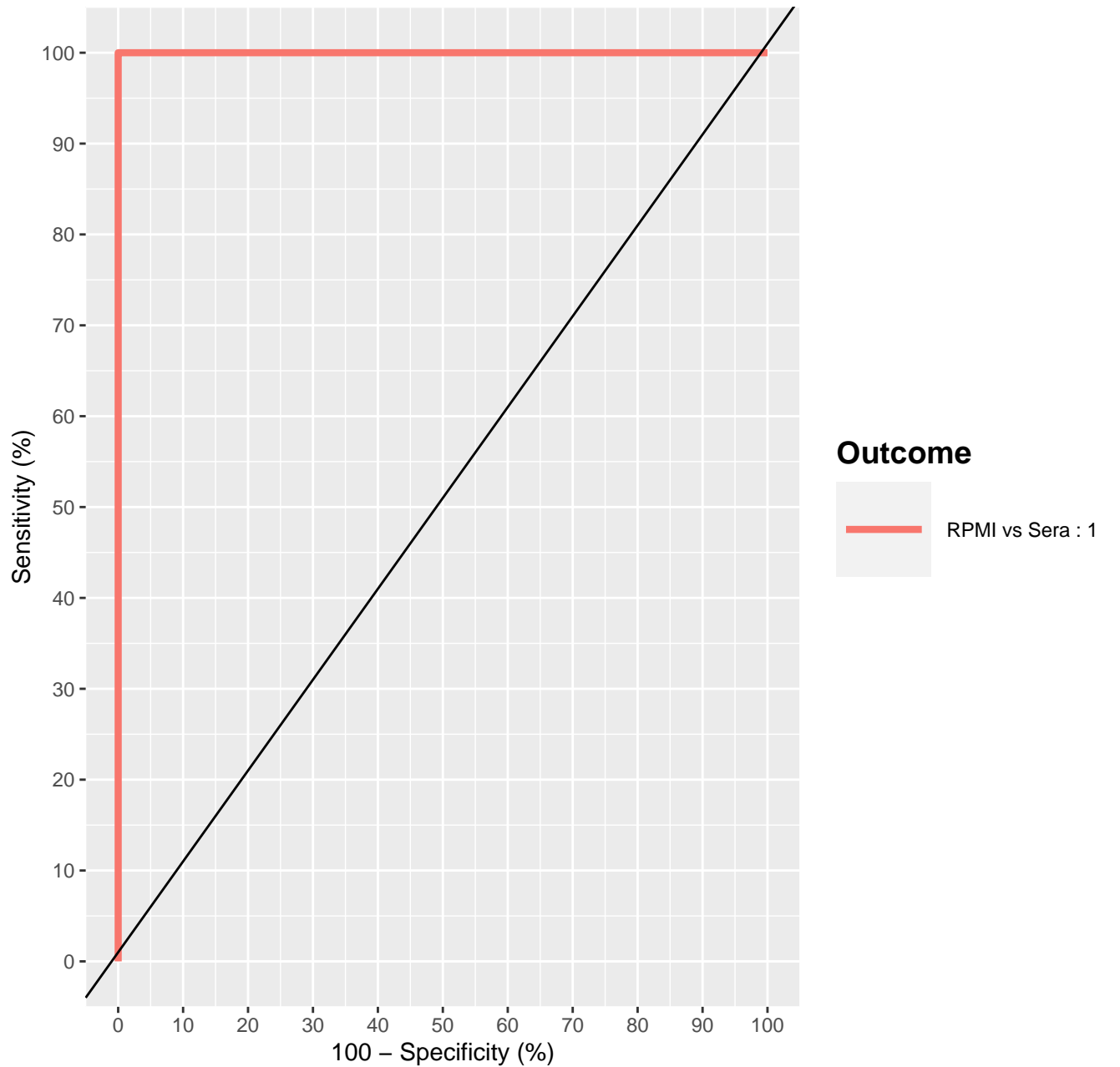




# Comp 1

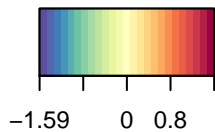


**ROC Curve Using Comp(s): 1**



# sPLSDA

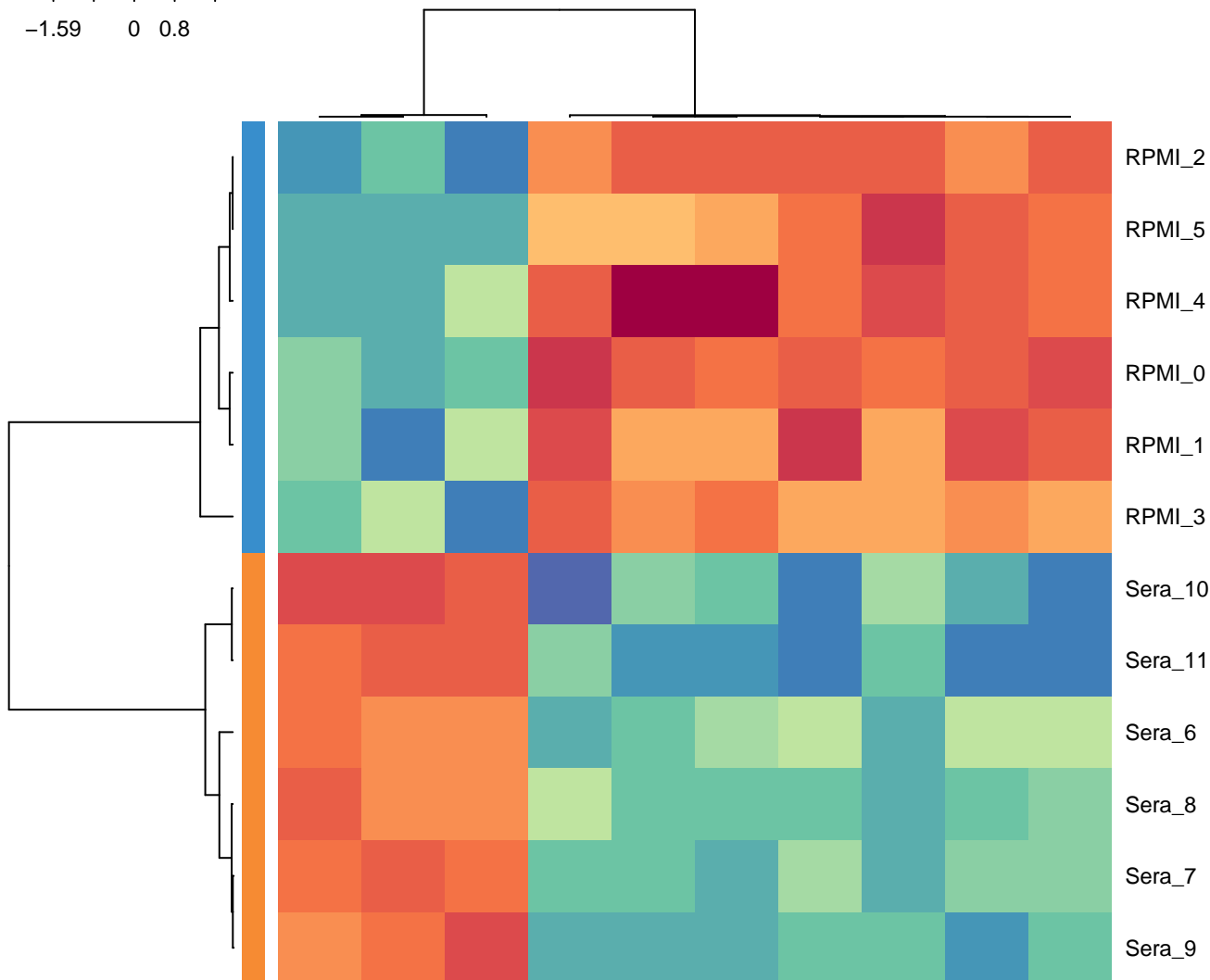
Color key



Status

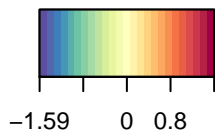
RPMI

Sera



# sPLSDA Component 1

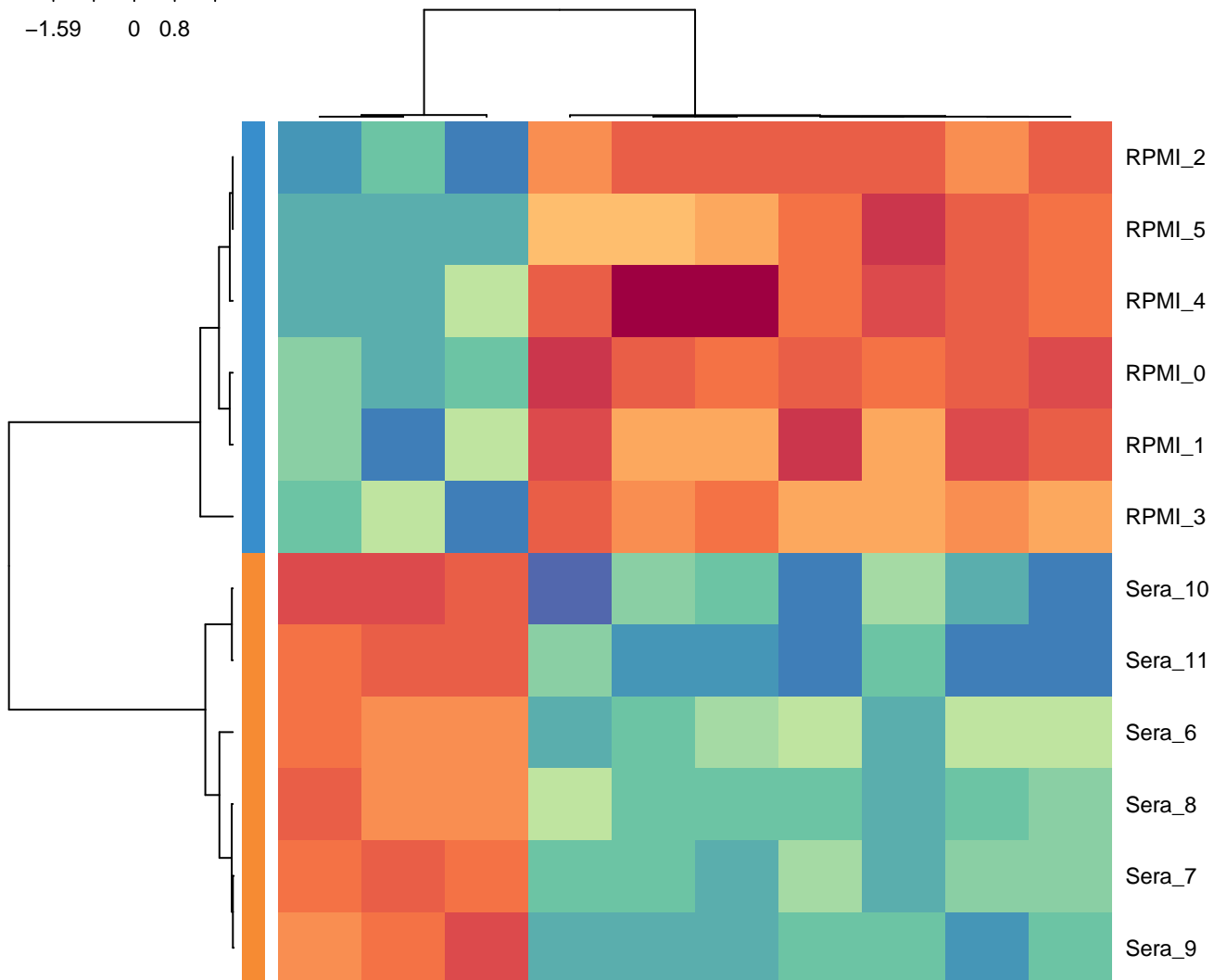
Color key



Status

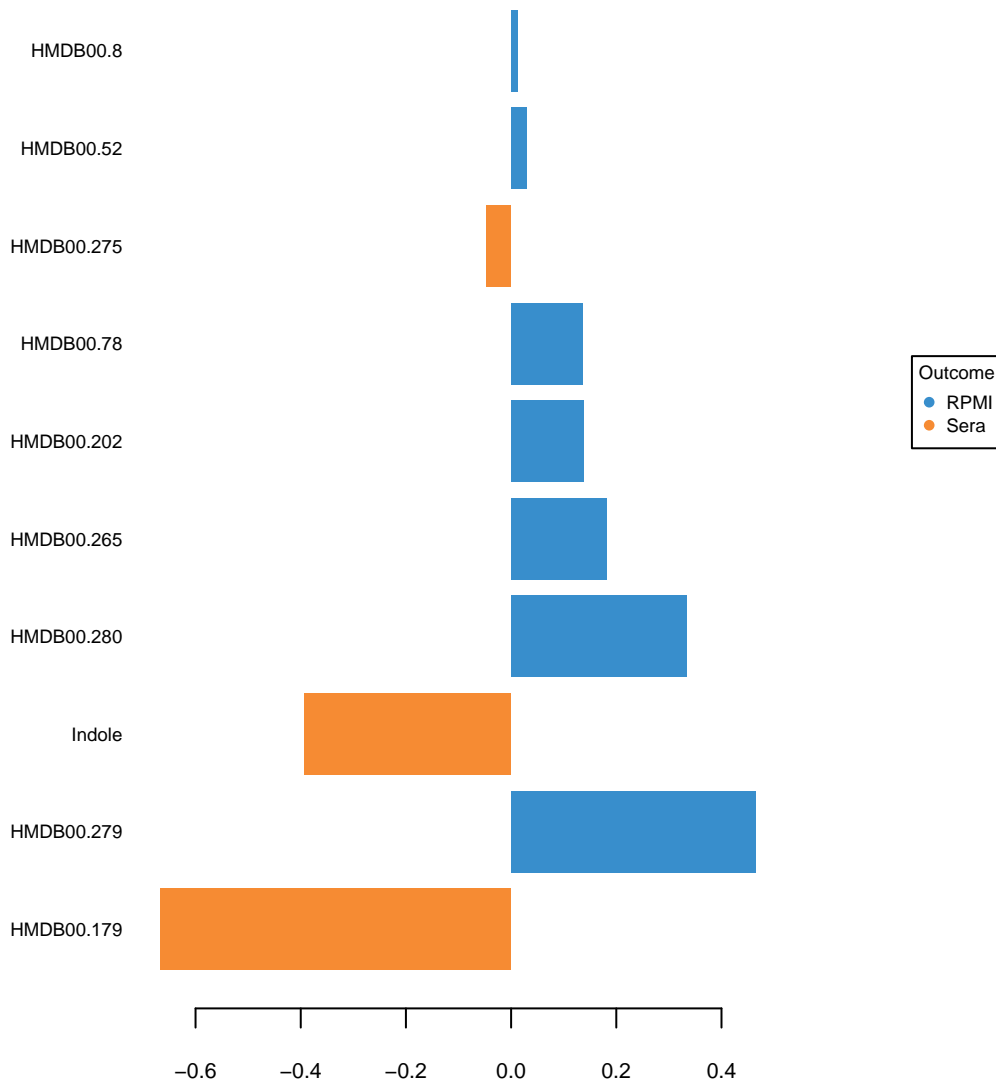
RPMI

Sera

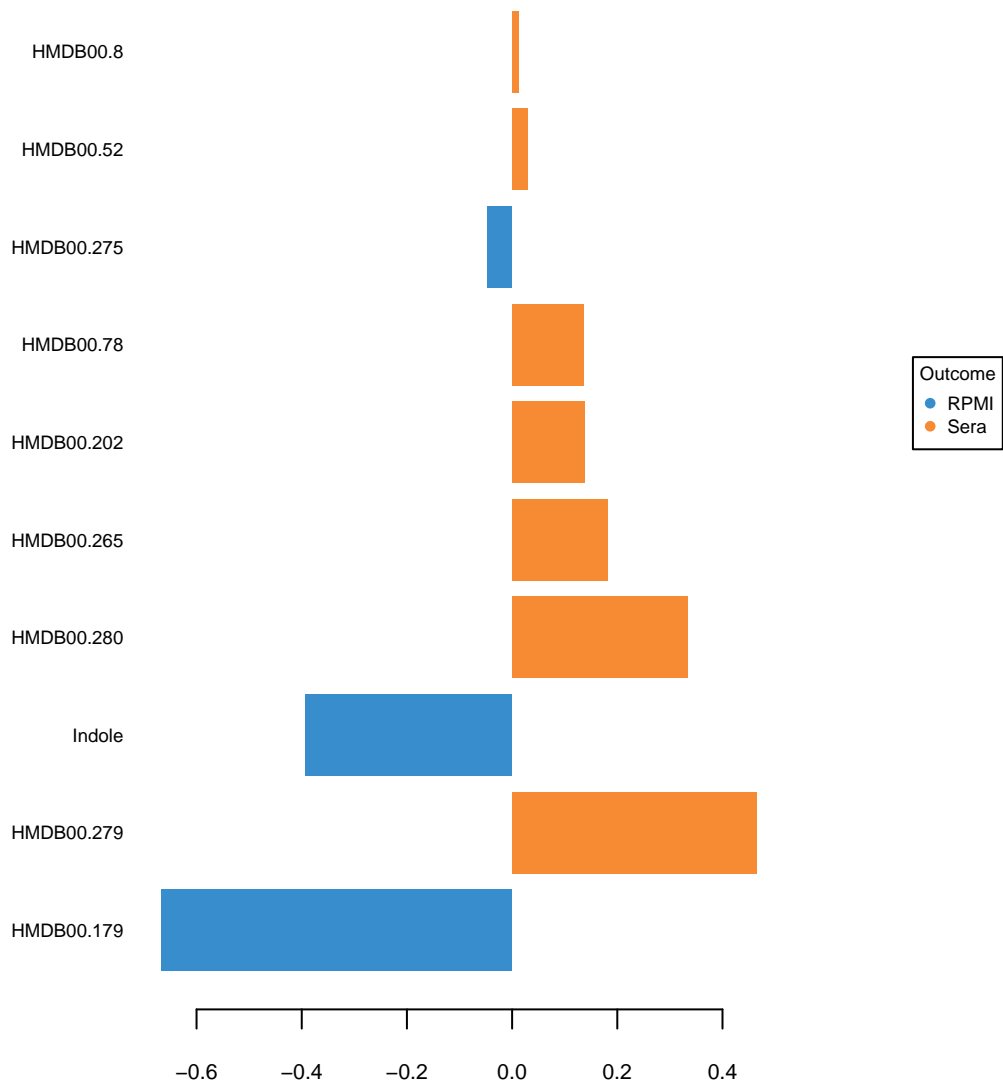


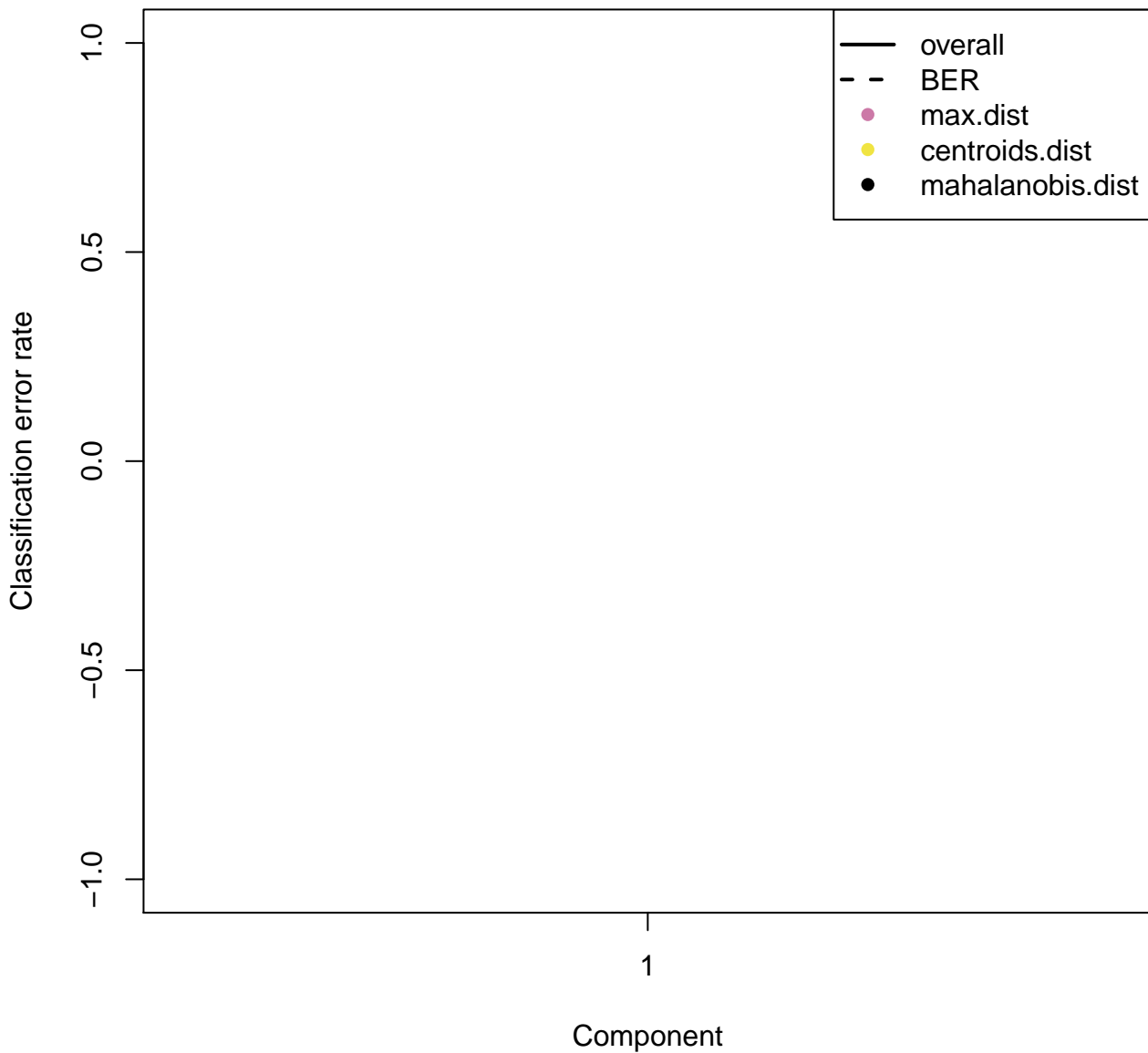


# metabolome 1 sPLSDA max load

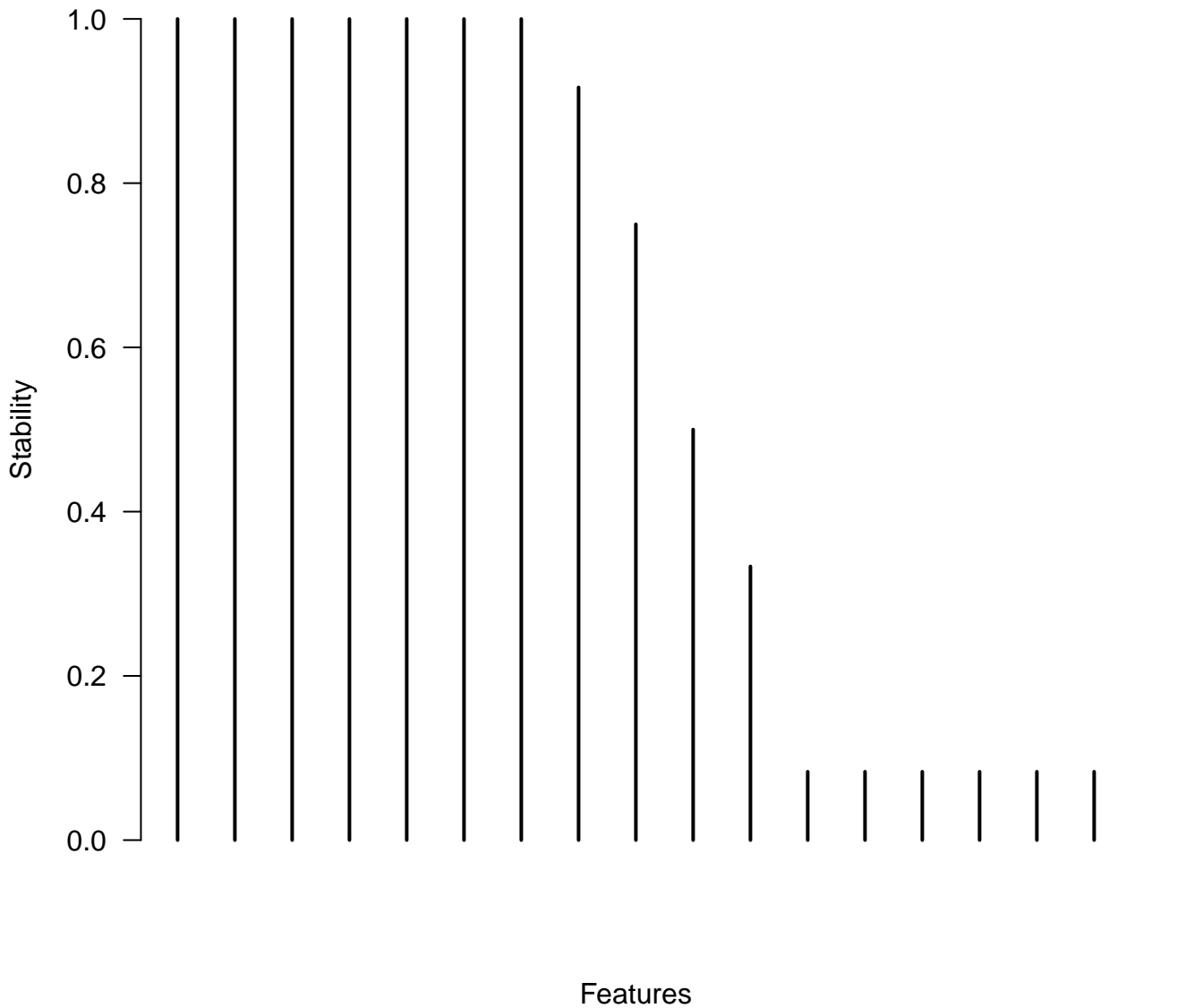


# metabolome 1 sPLSDA min loac

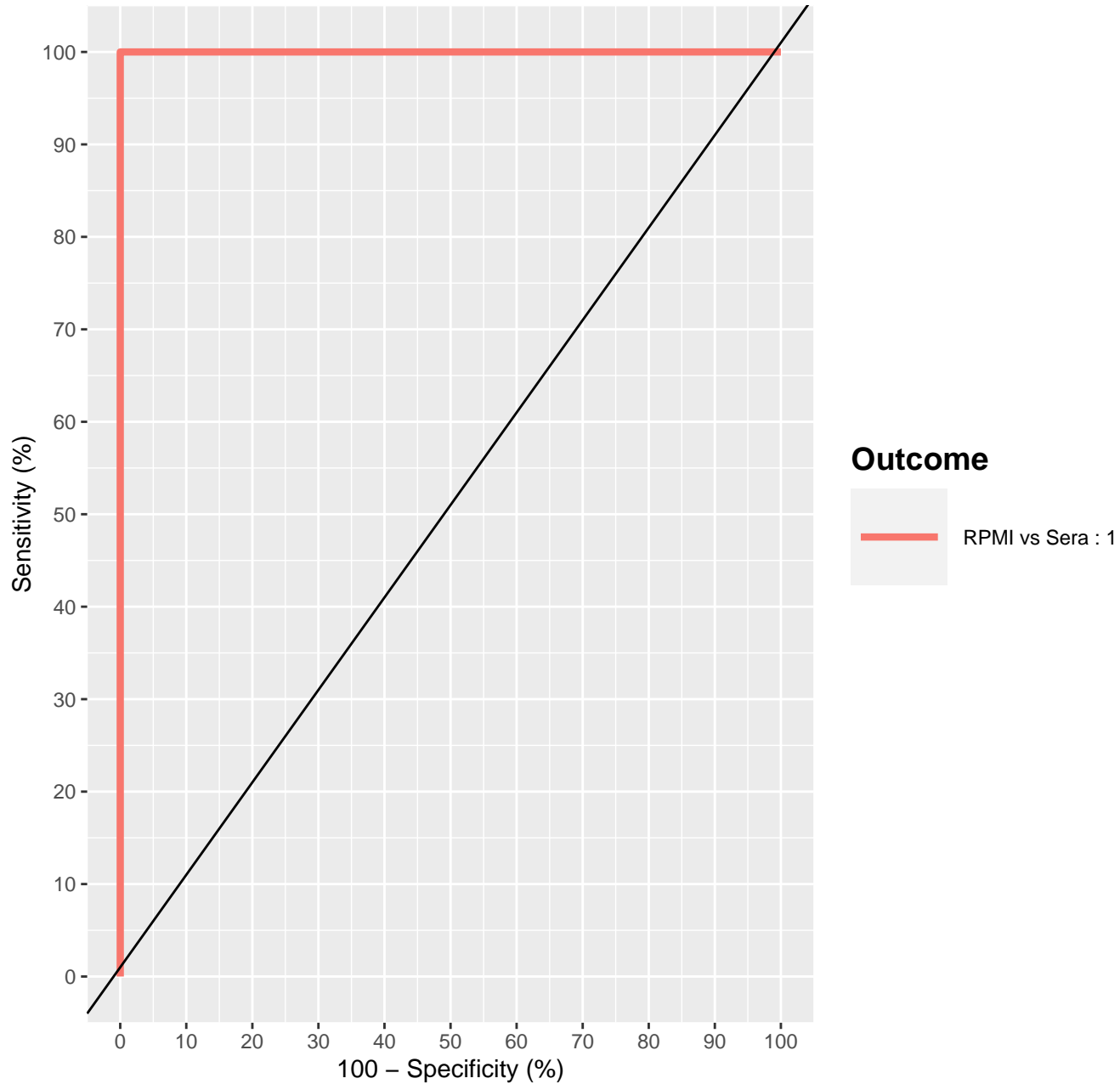




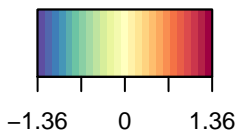
# Comp 1



**ROC Curve Using Comp(s): 1**



Color key

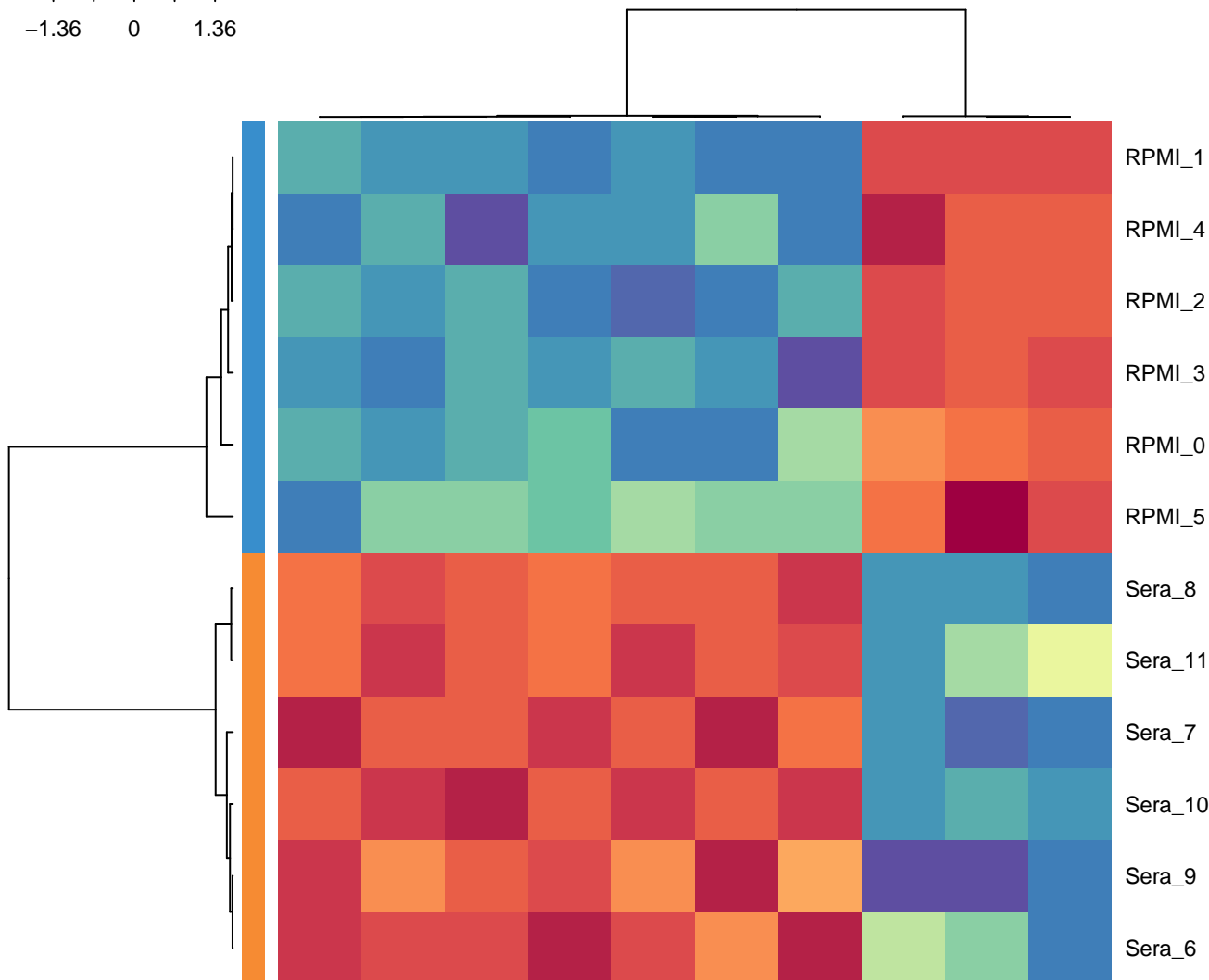


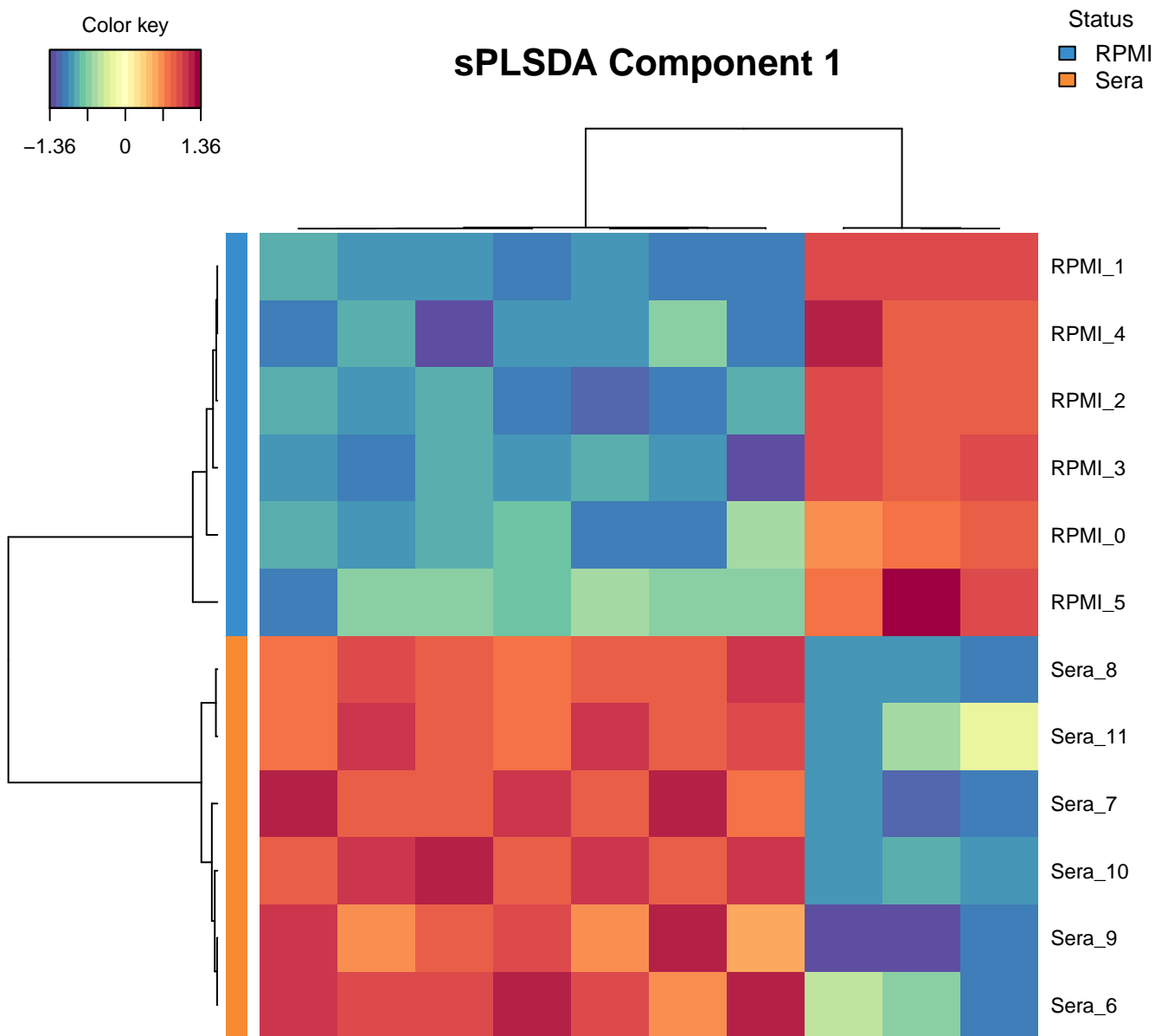
sPLSDA

Status

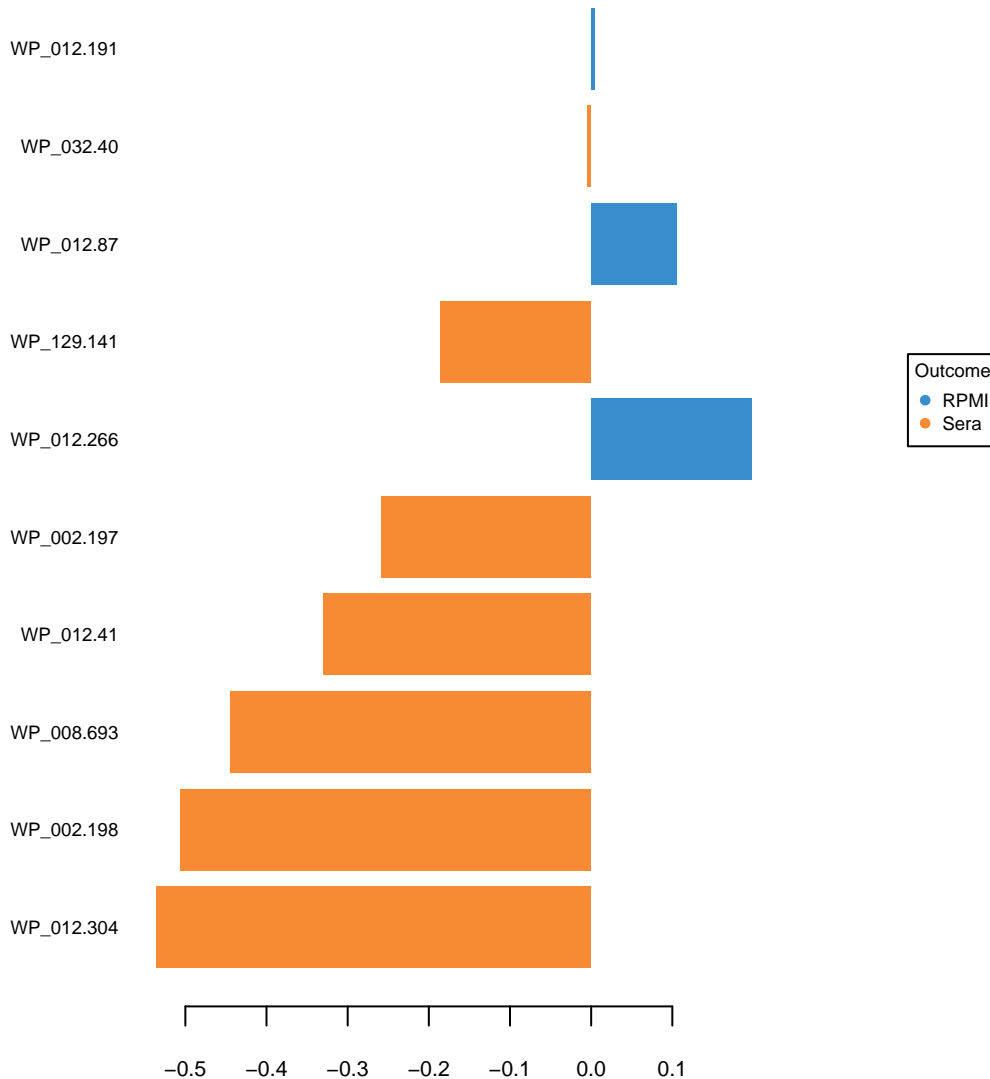
■ RPMI

■ Sera



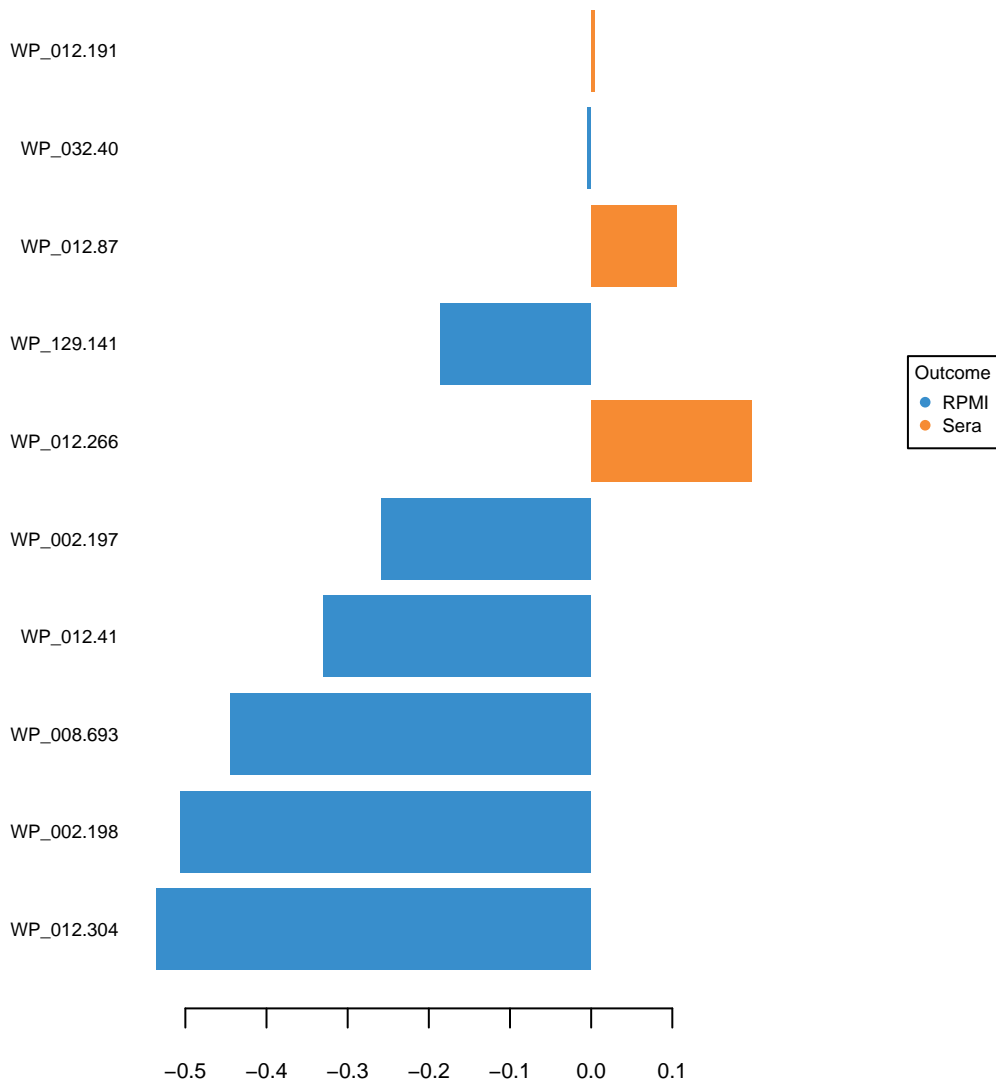


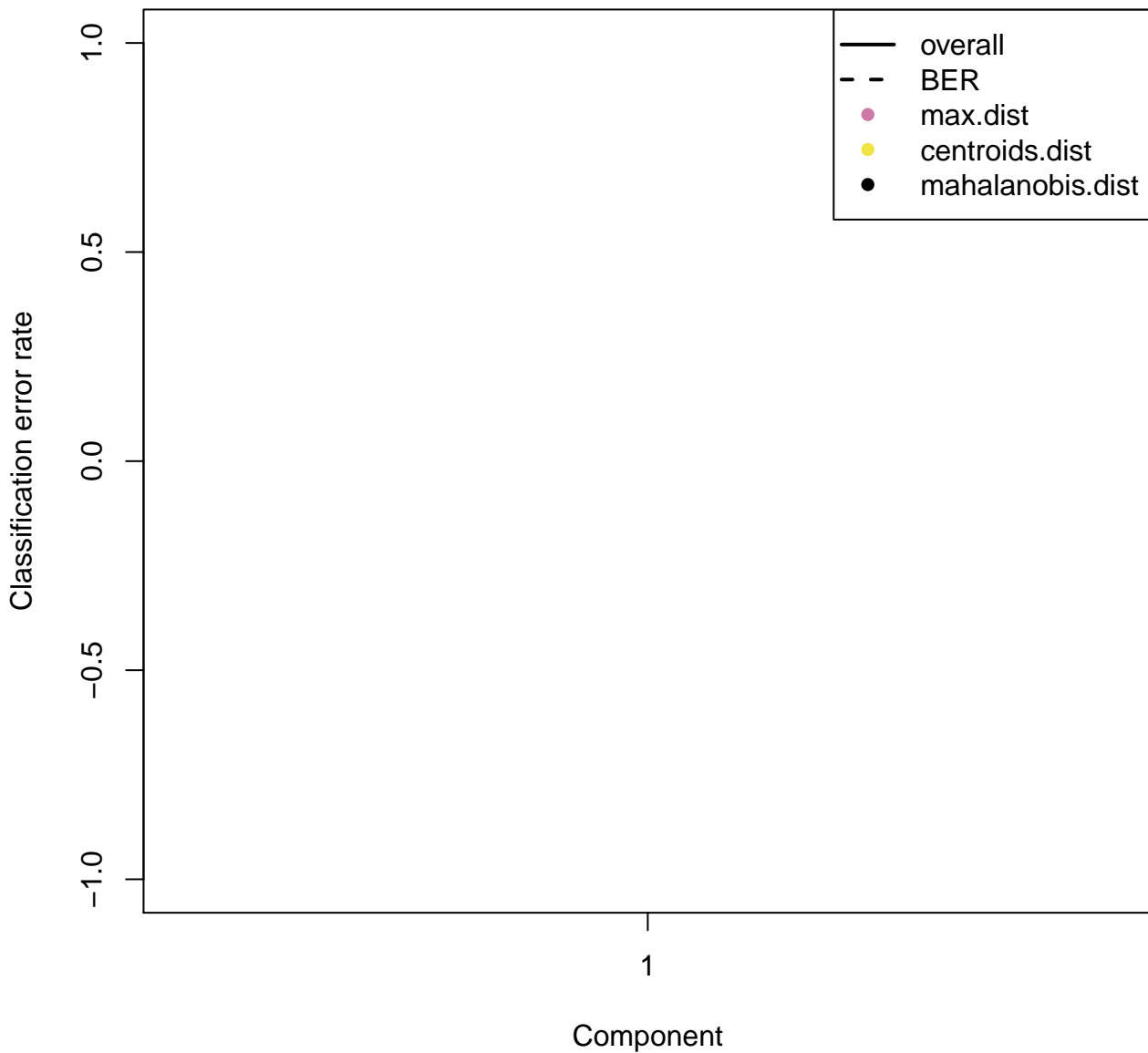
# proteome 1 sPLSDA max loadings



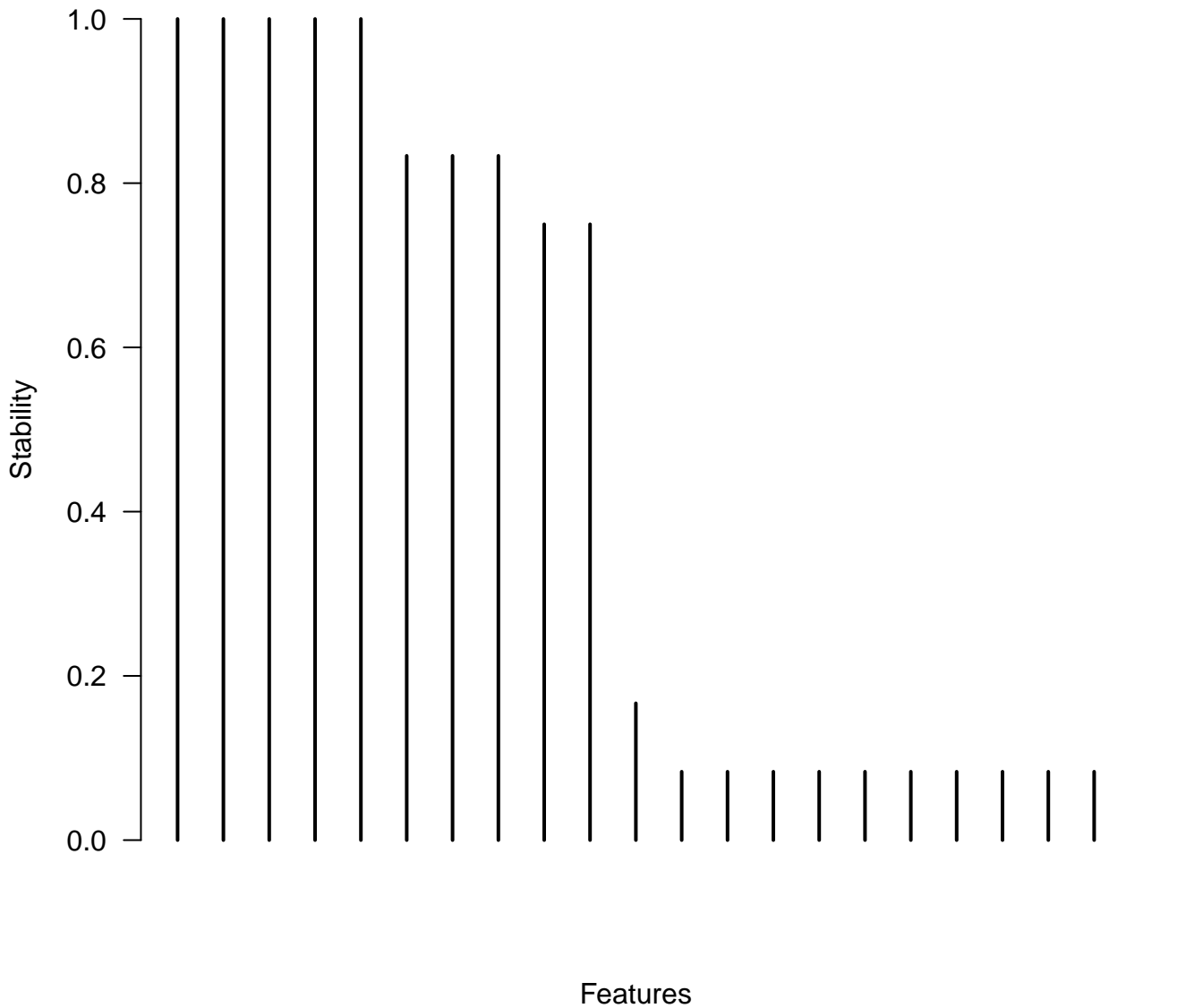


# proteome 1 sPLSDA min loadings

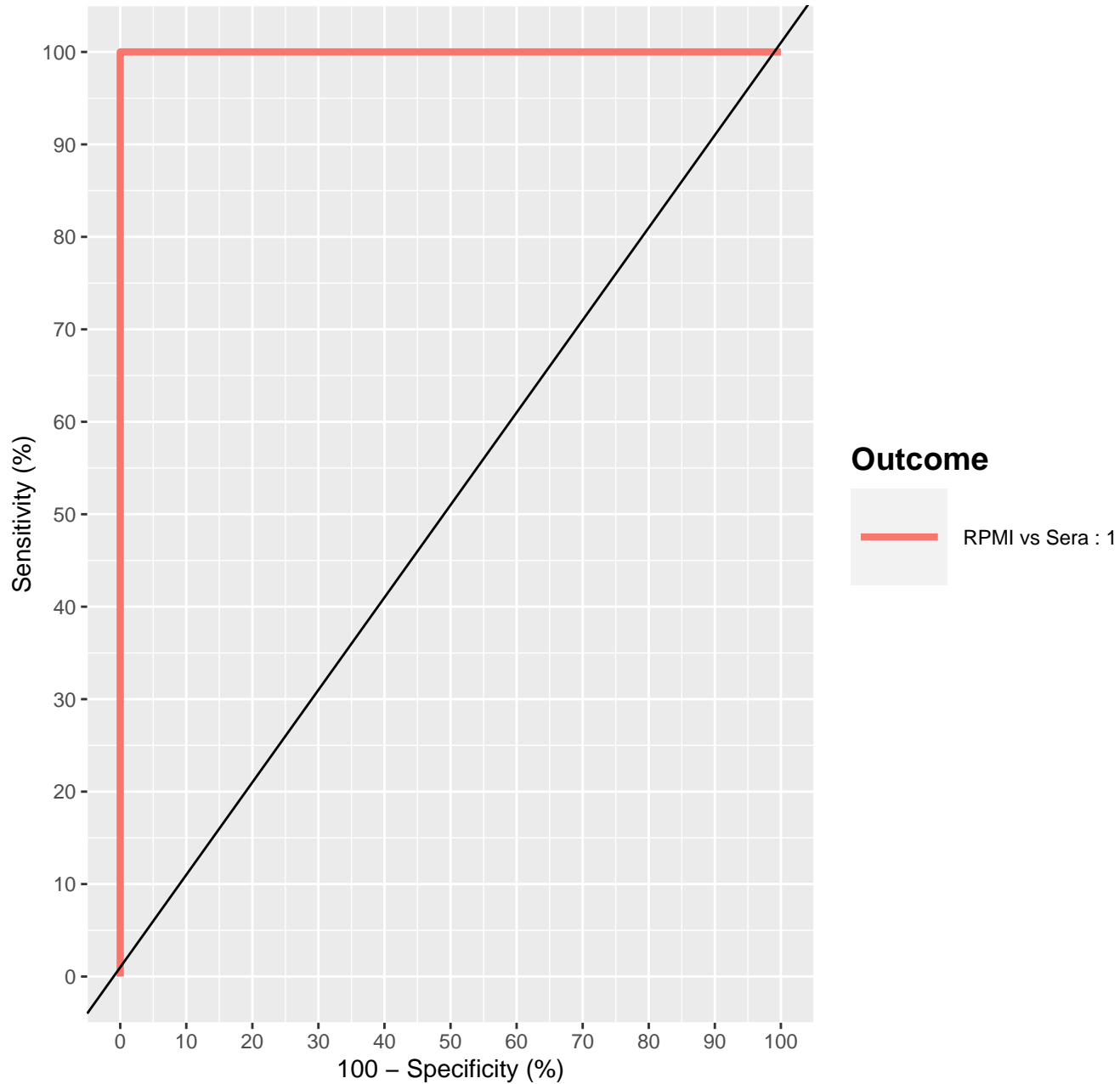




# Comp 1

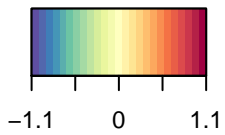


**ROC Curve Using Comp(s): 1**



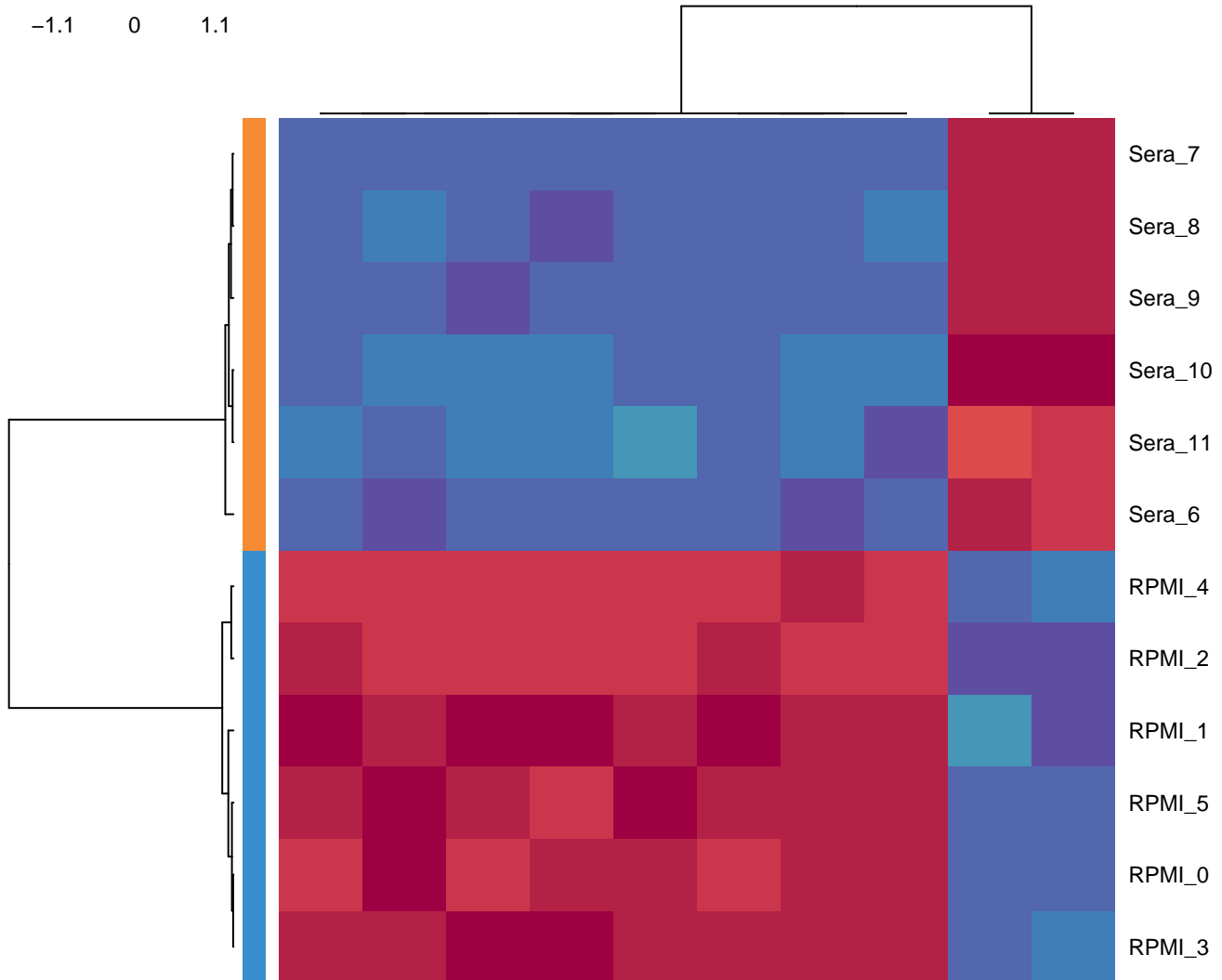
# sPLSDA

Color key



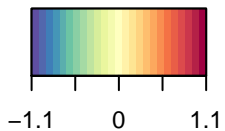
Status

- RPMI
- Sera



# sPLSDA Component 1

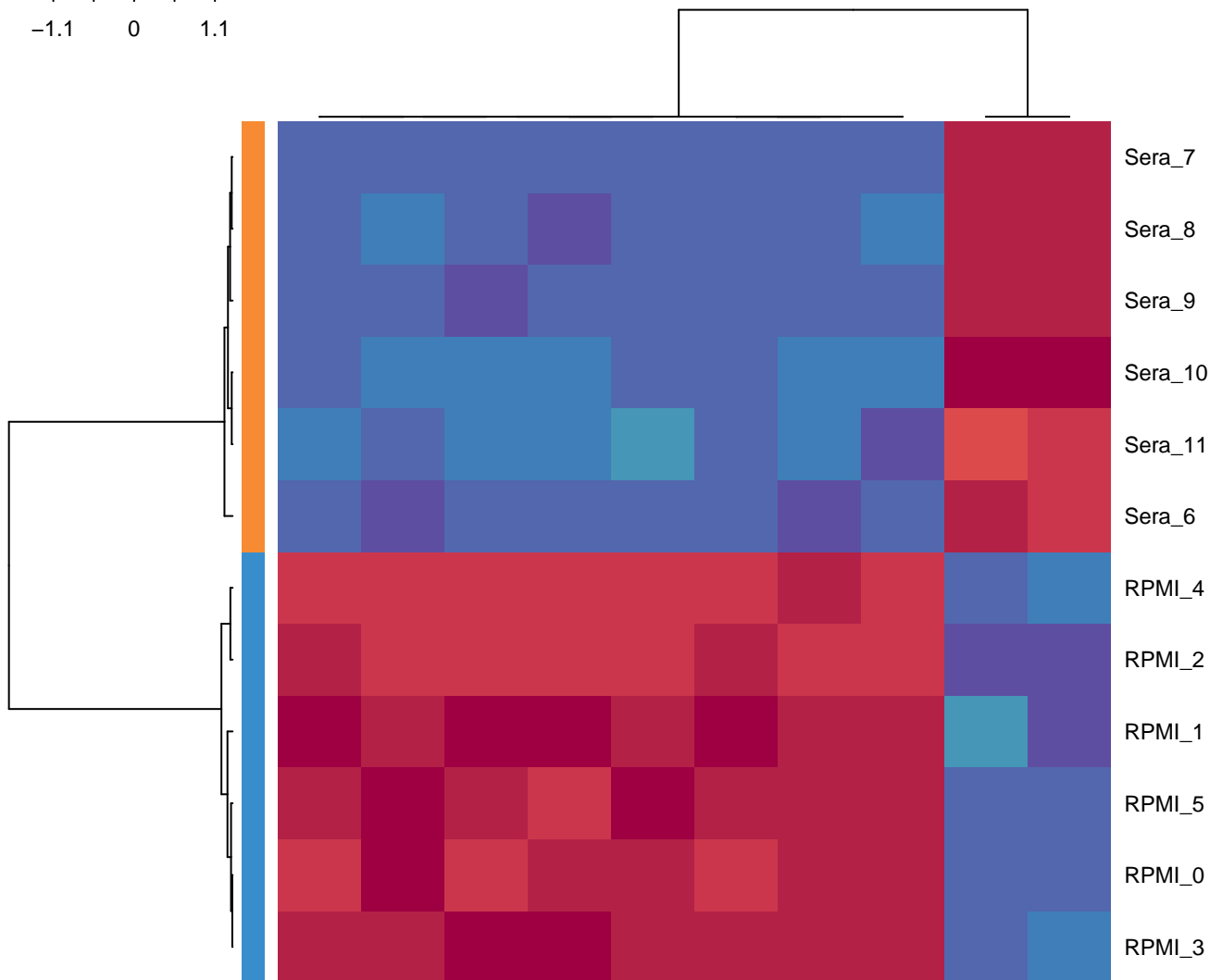
Color key



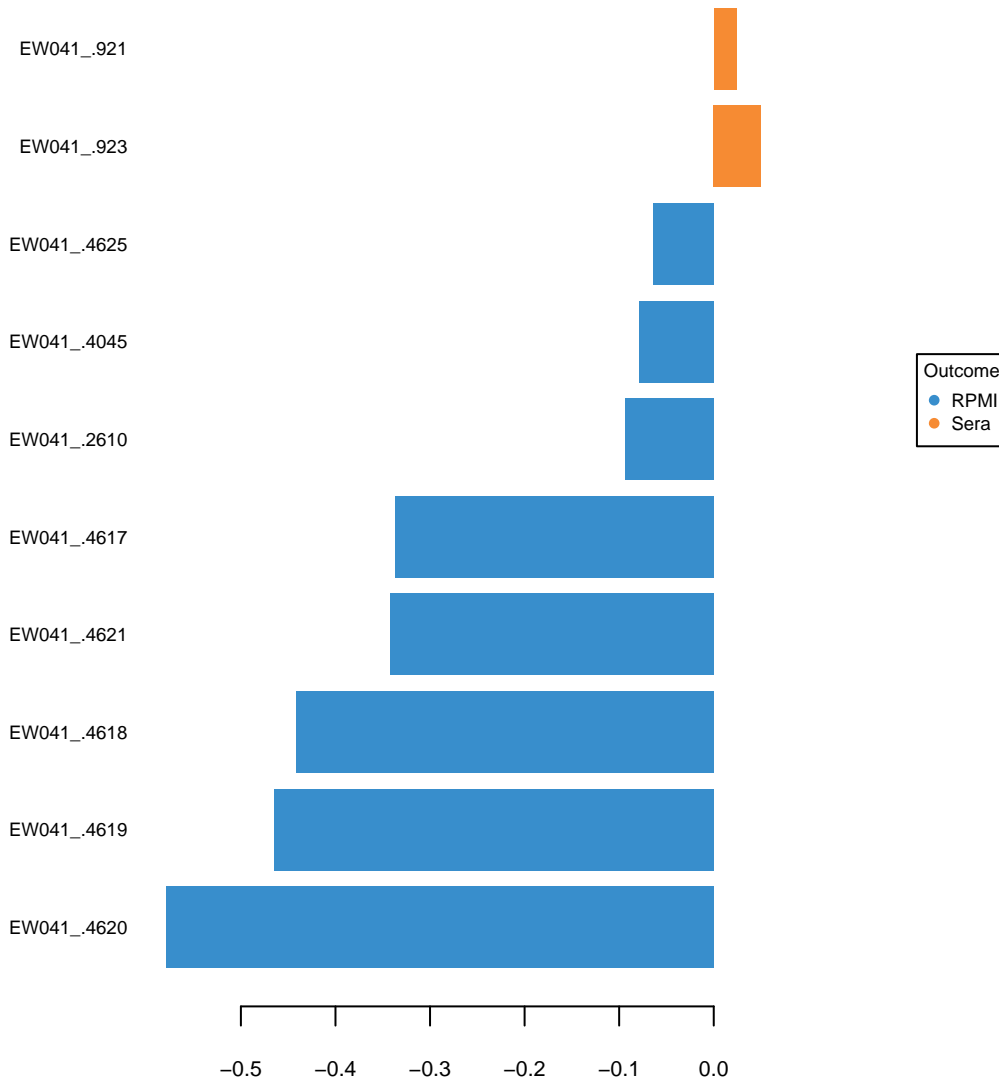
Status

RPMI

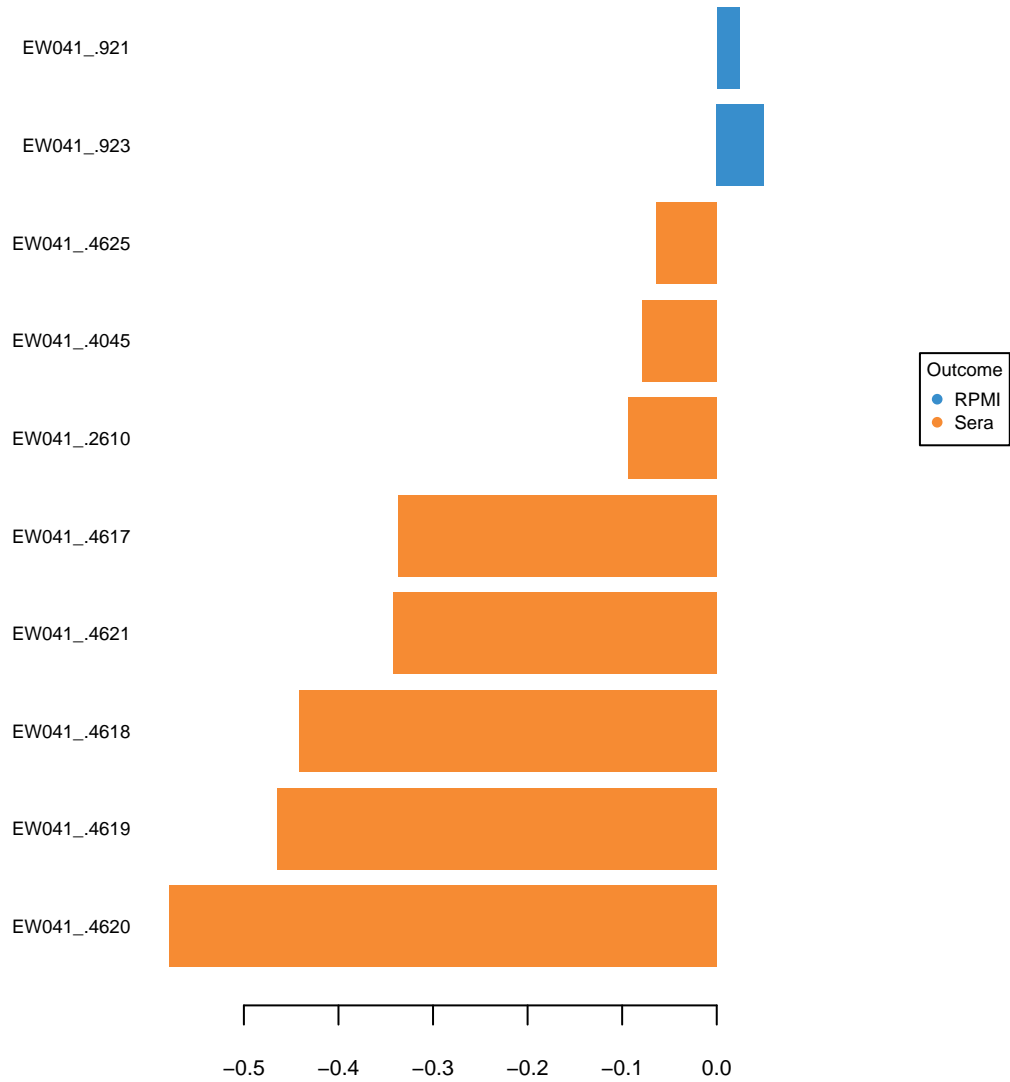
Sera



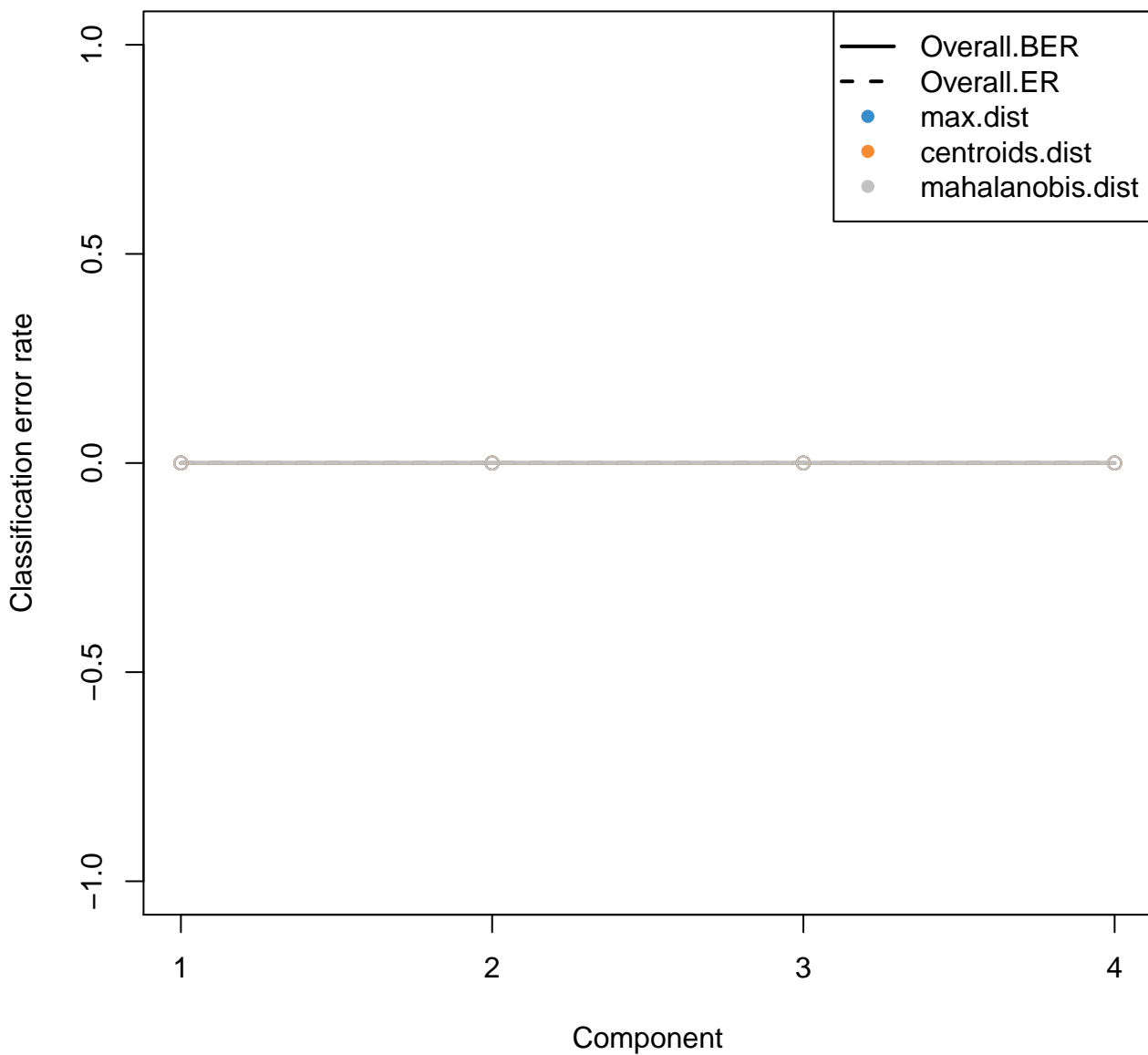
# transcriptome 1 sPLSDA max loa



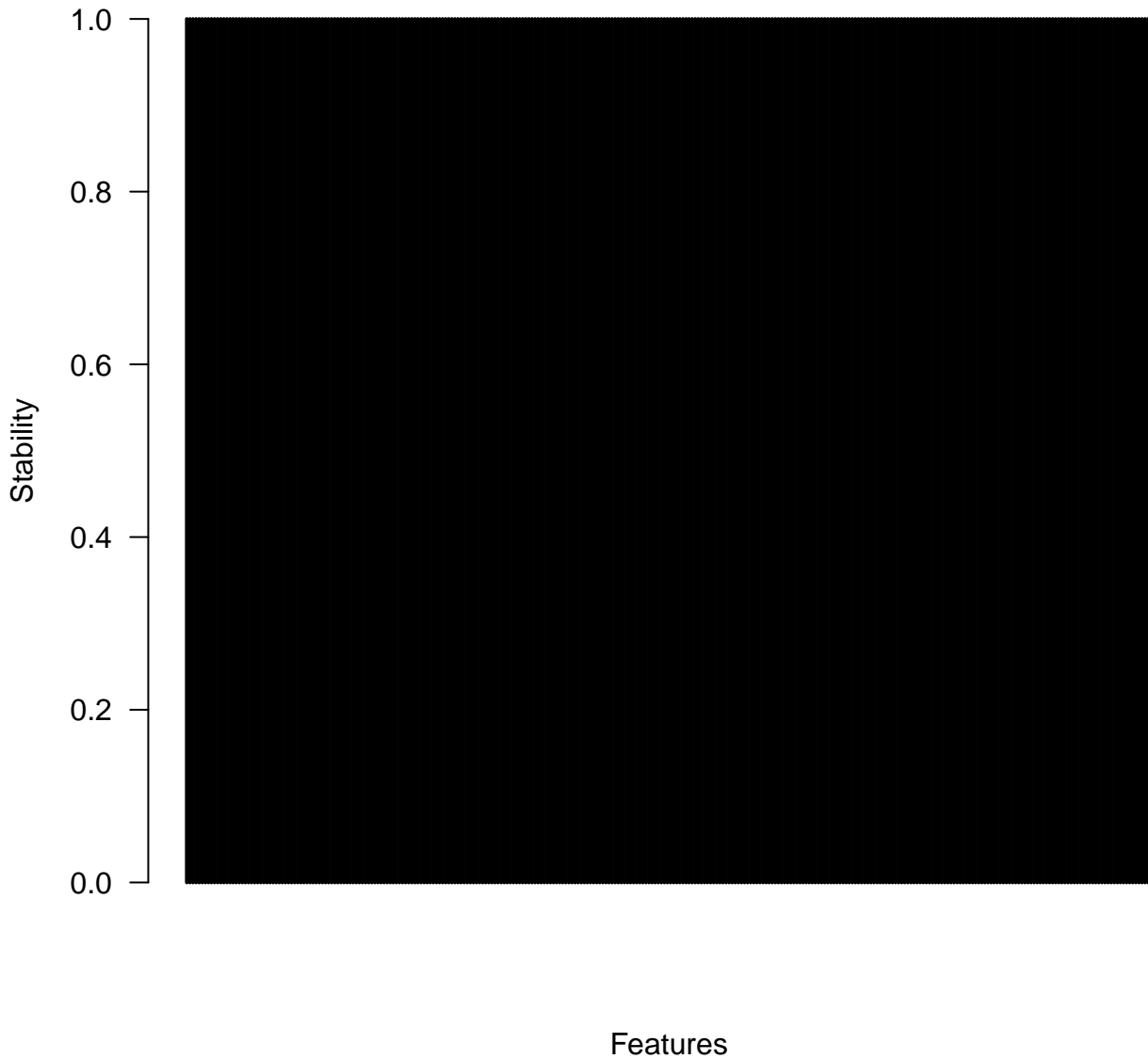
# transcriptome 1 sPLSDA min loa



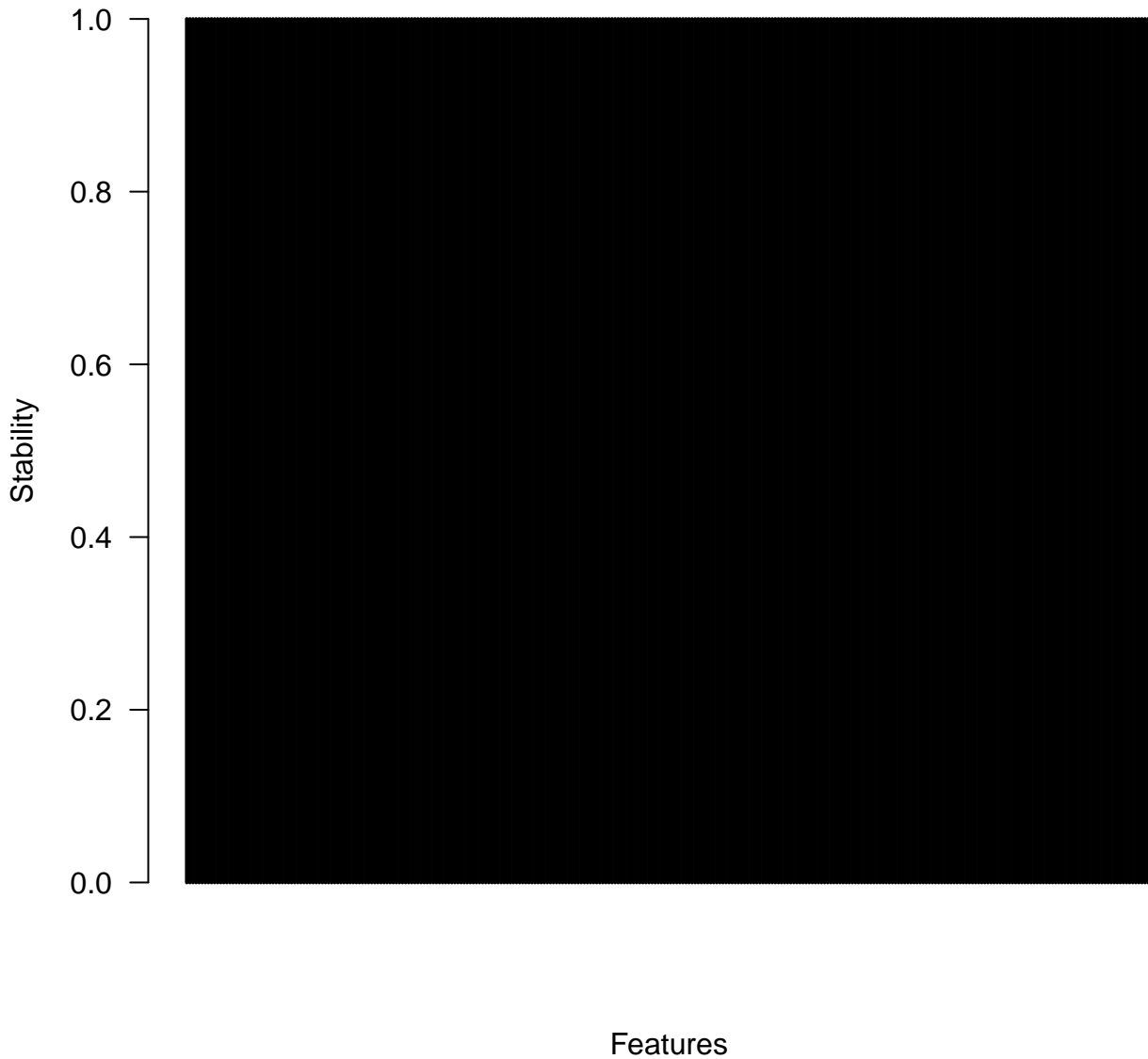




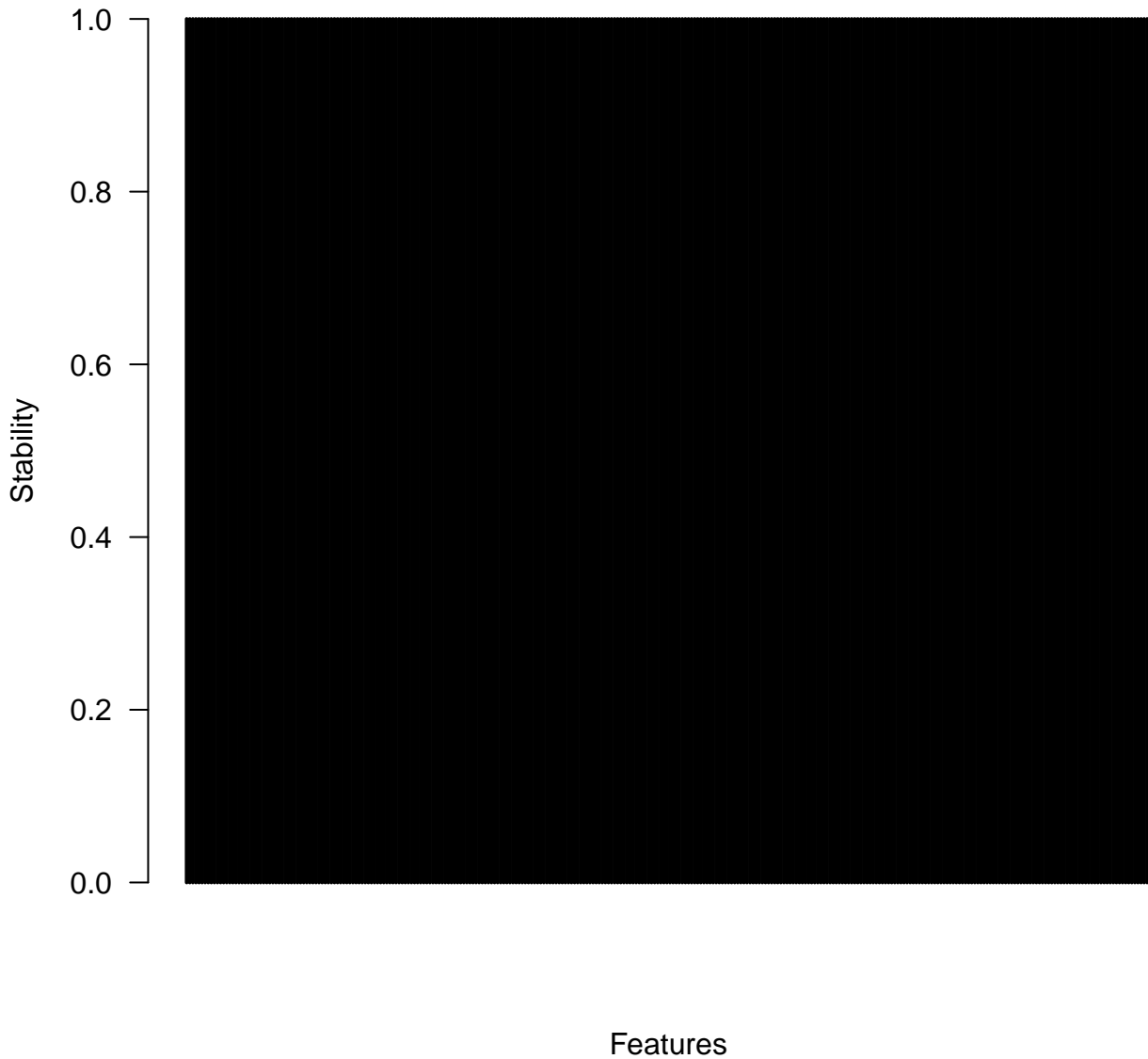
# metabolome Comp 1



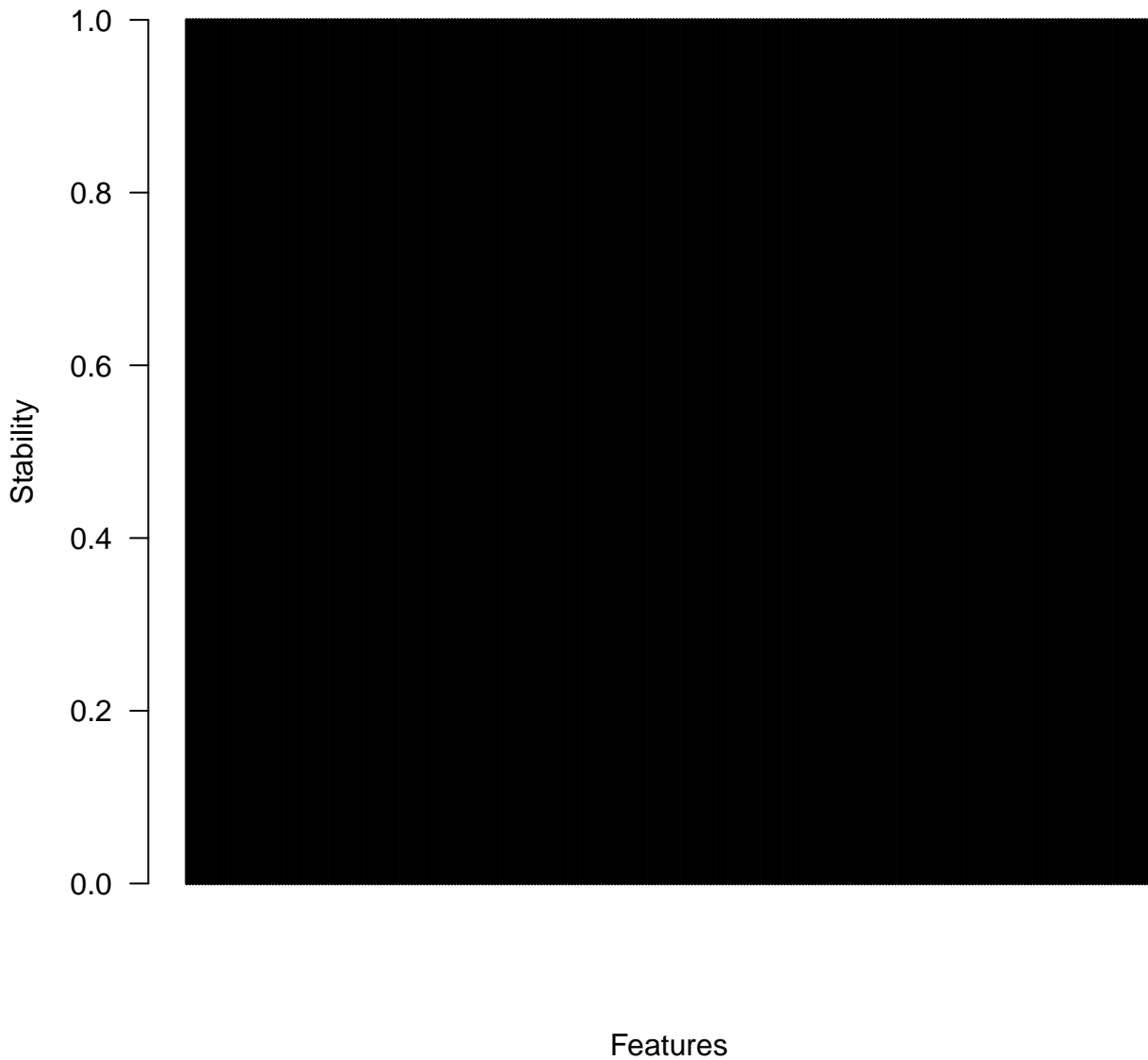
## metabolome Comp 2



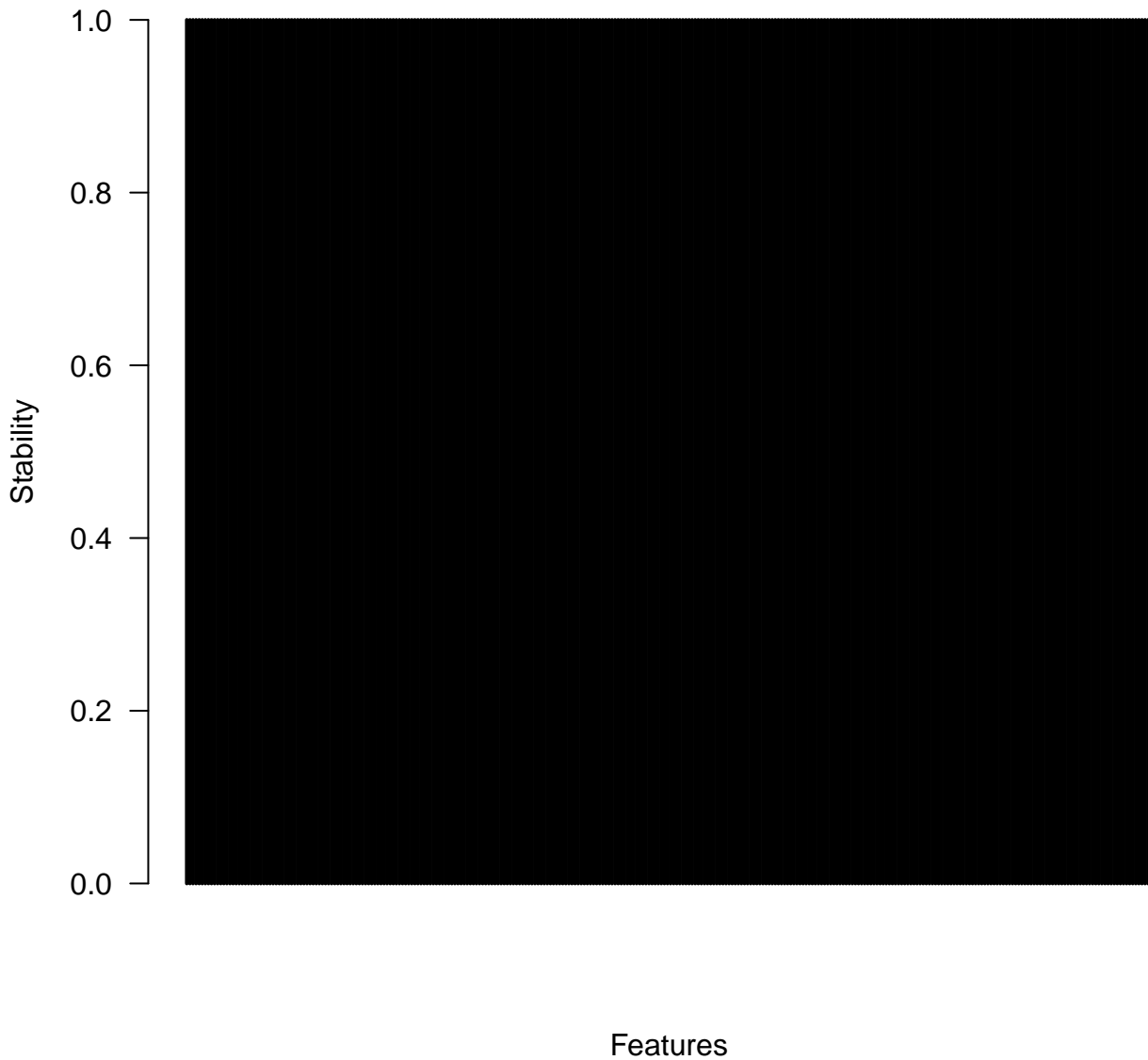
# metabolome Comp 3



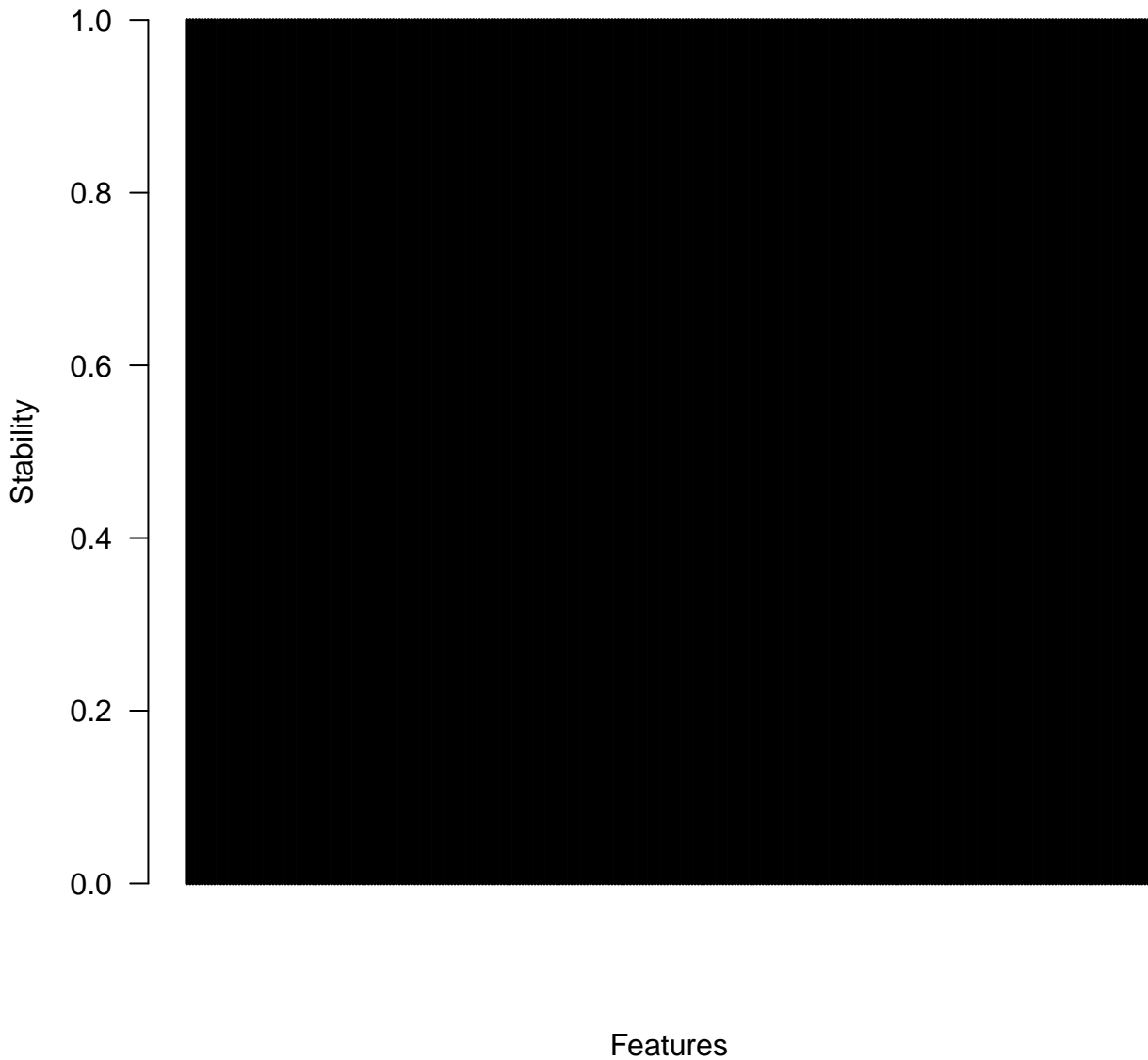
# proteome Comp 1



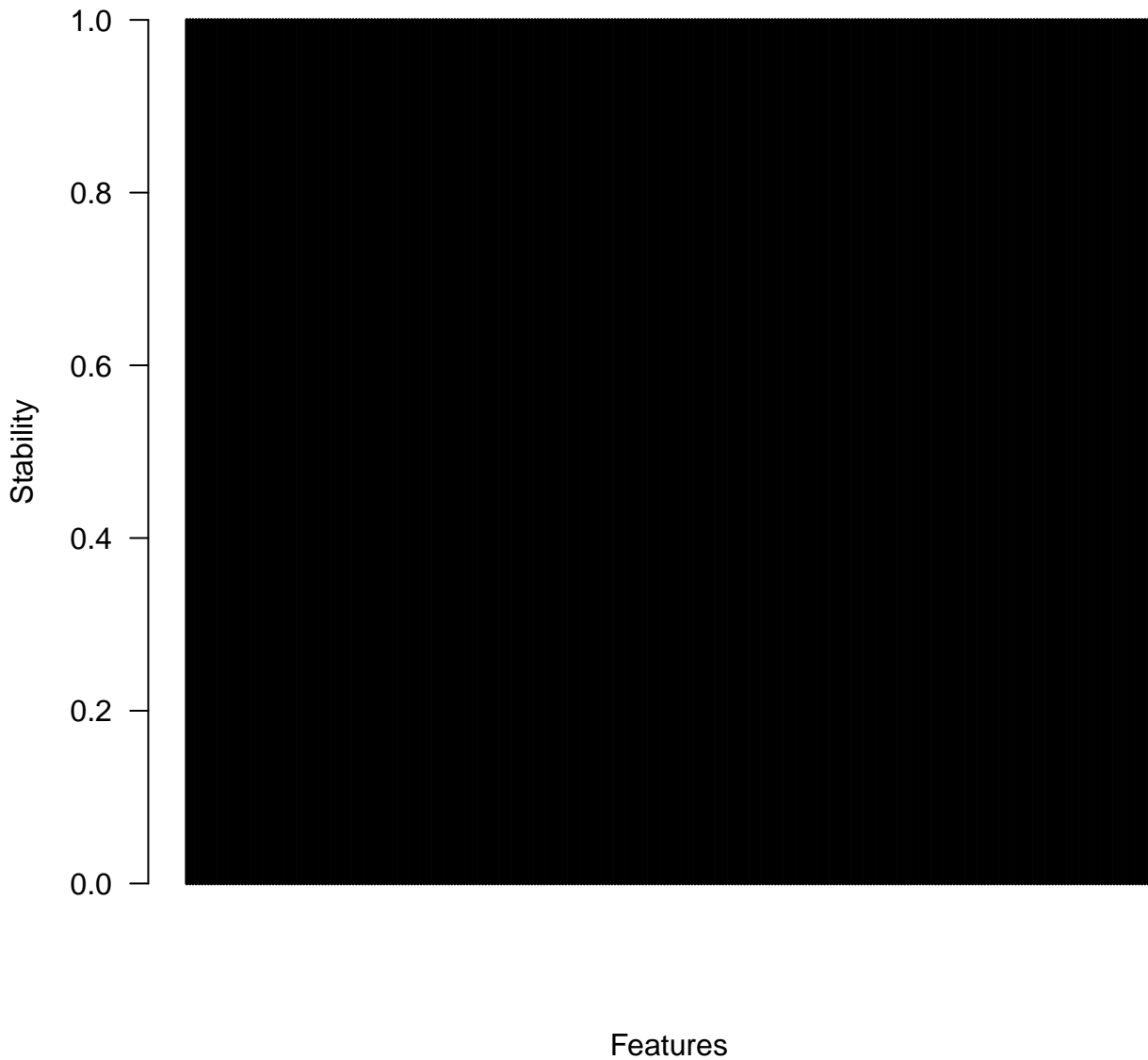
## proteome Comp 2



# proteome Comp 3

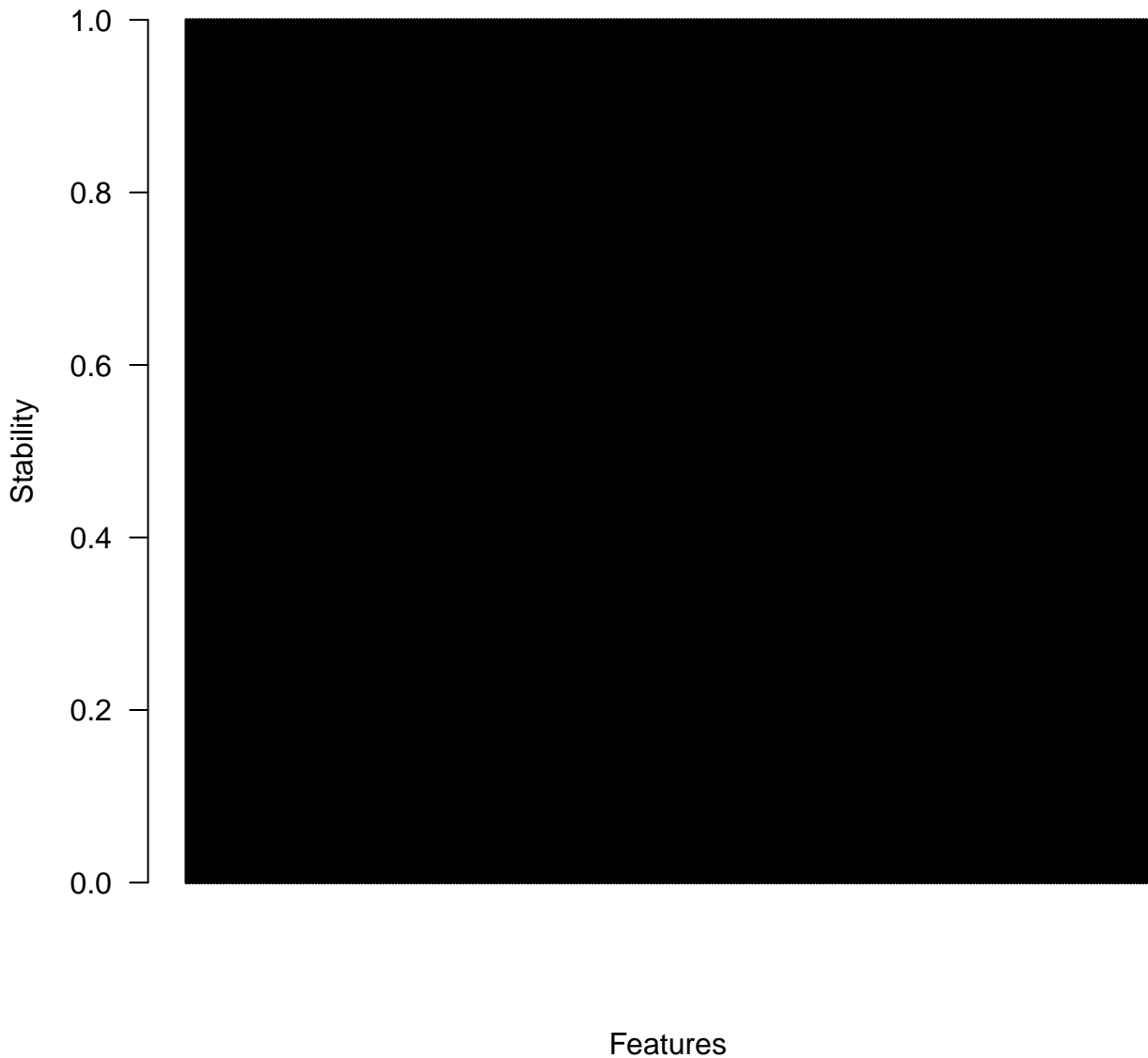


# transcriptome Comp 1

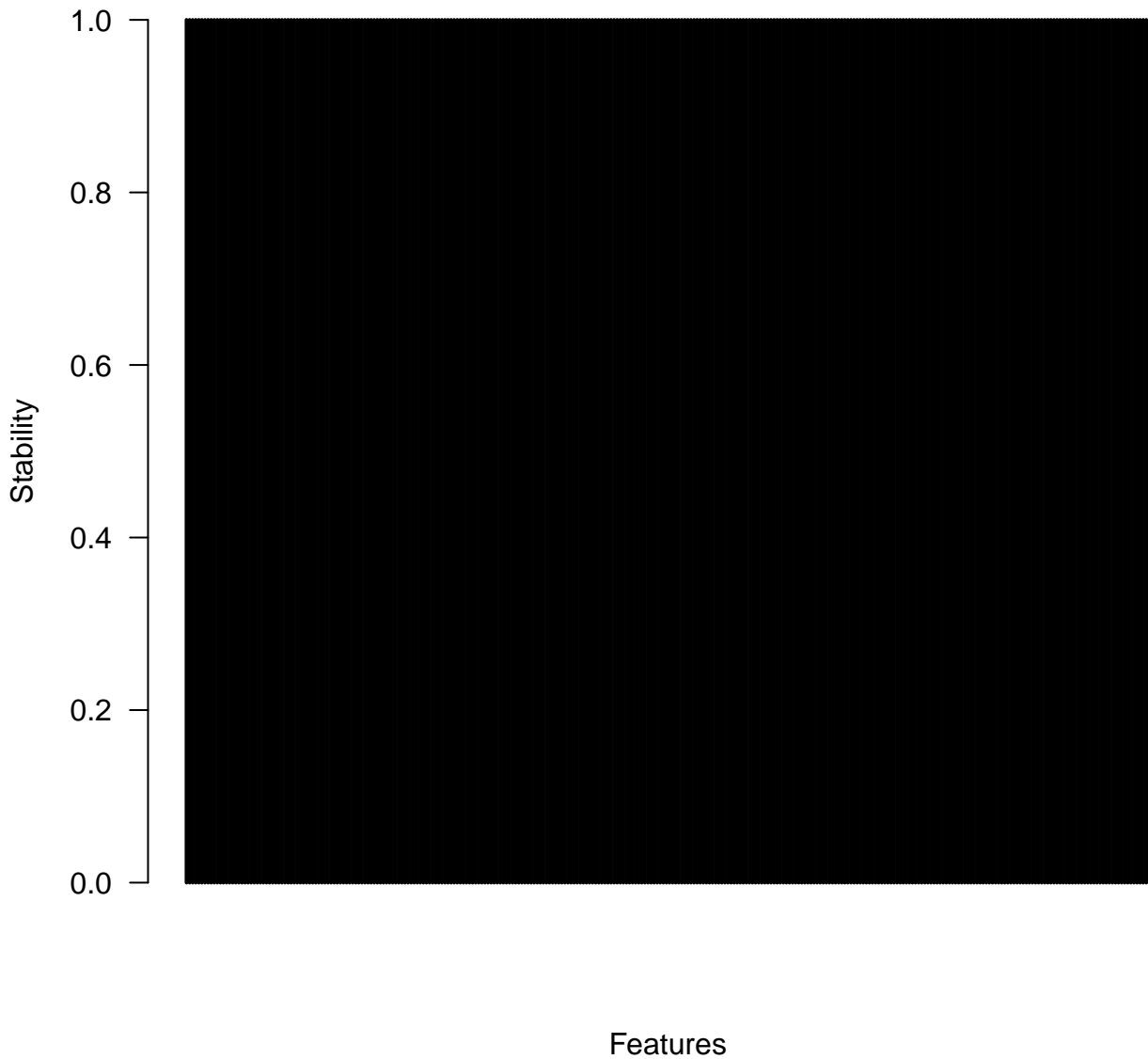




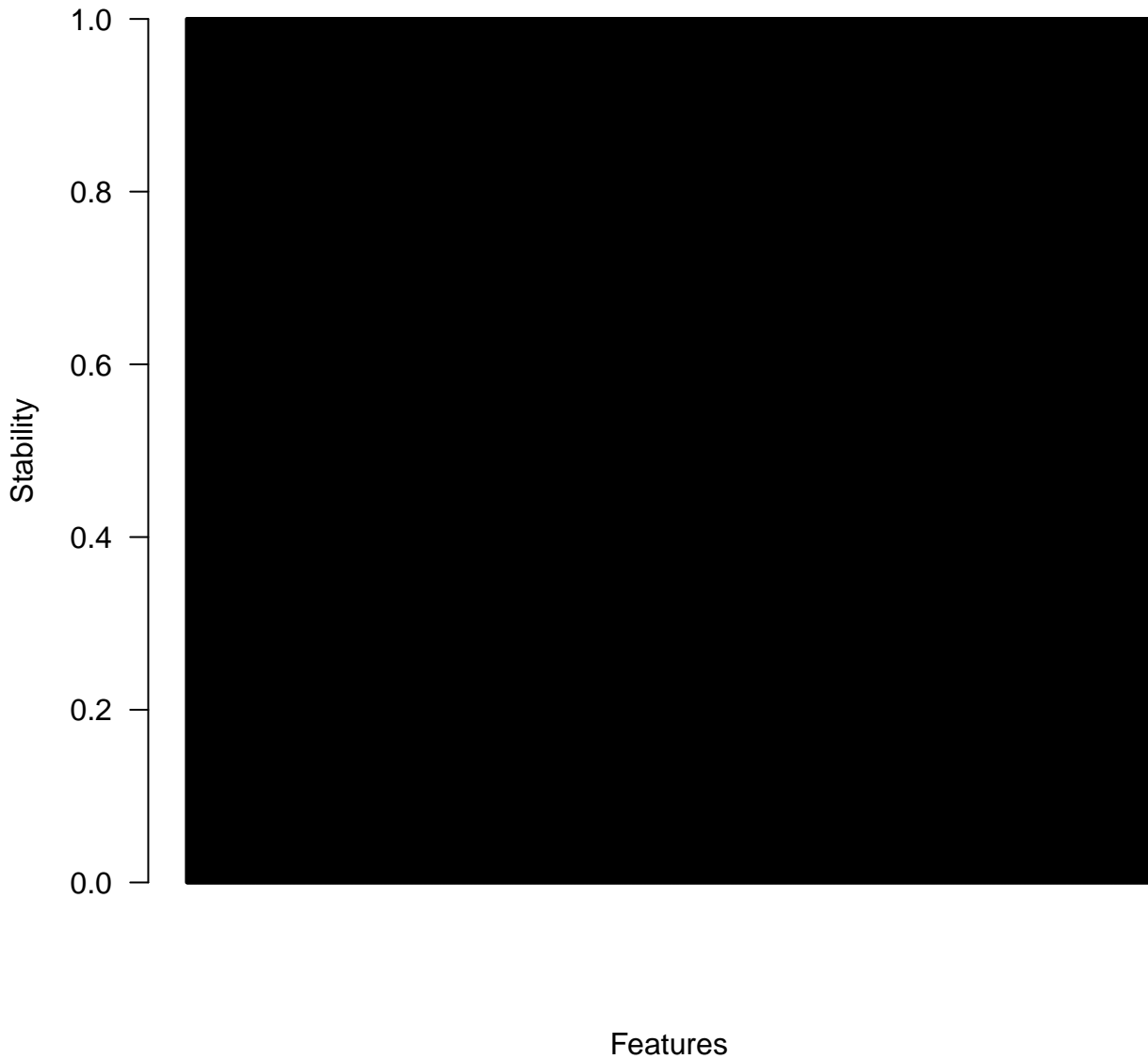
# transcriptome Comp 2



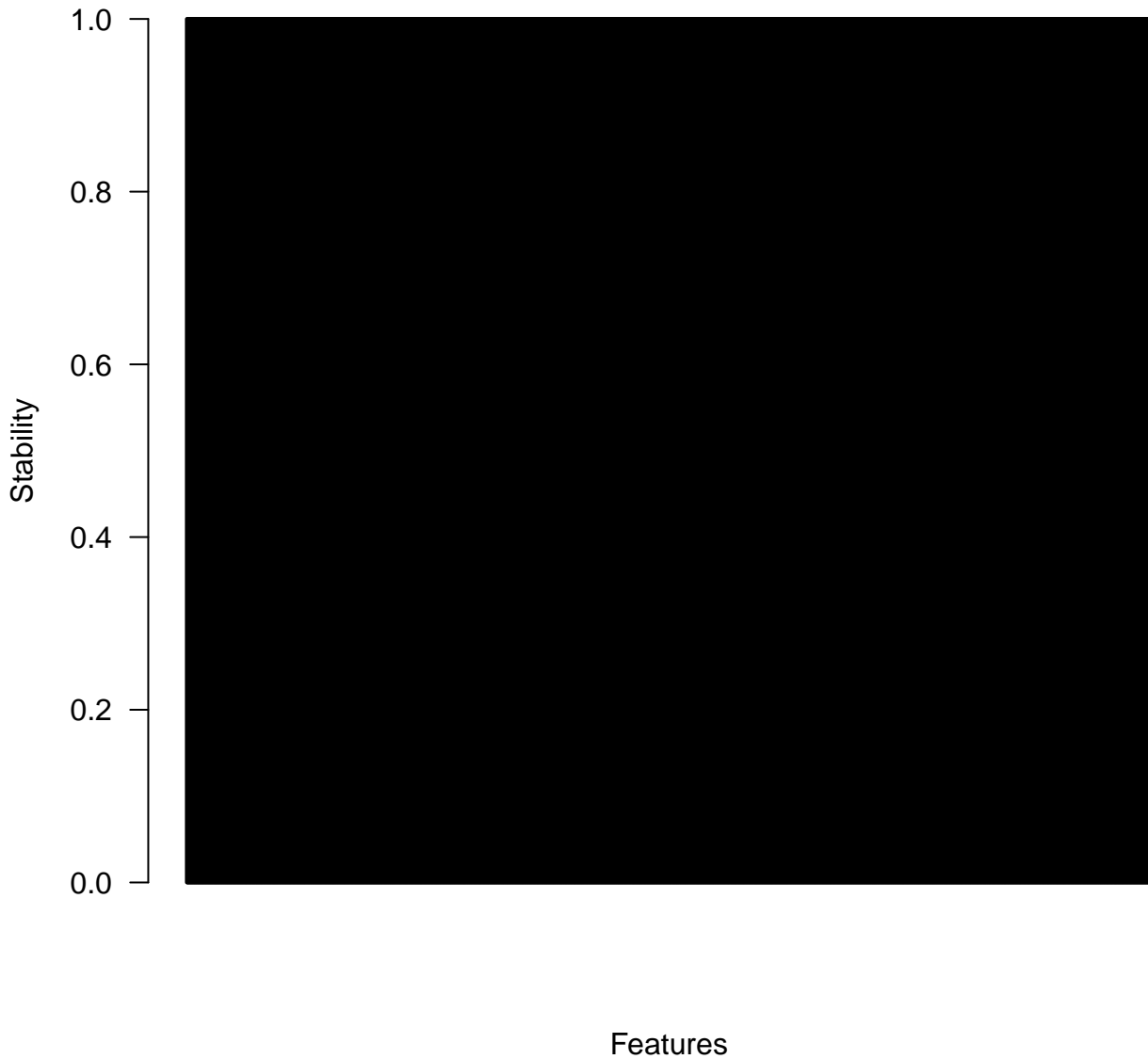
# transcriptome Comp 3



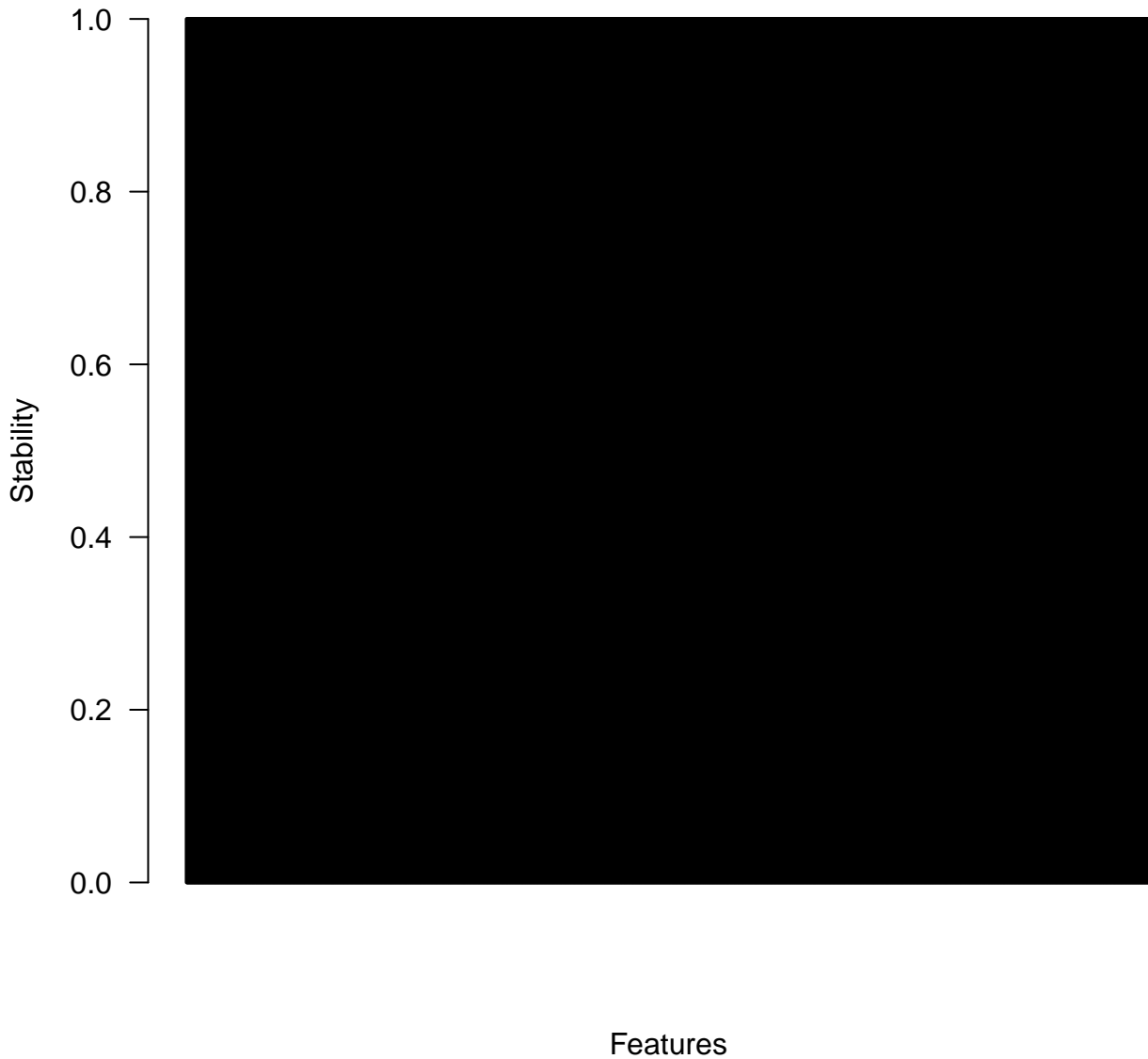
# metabolome Comp 1



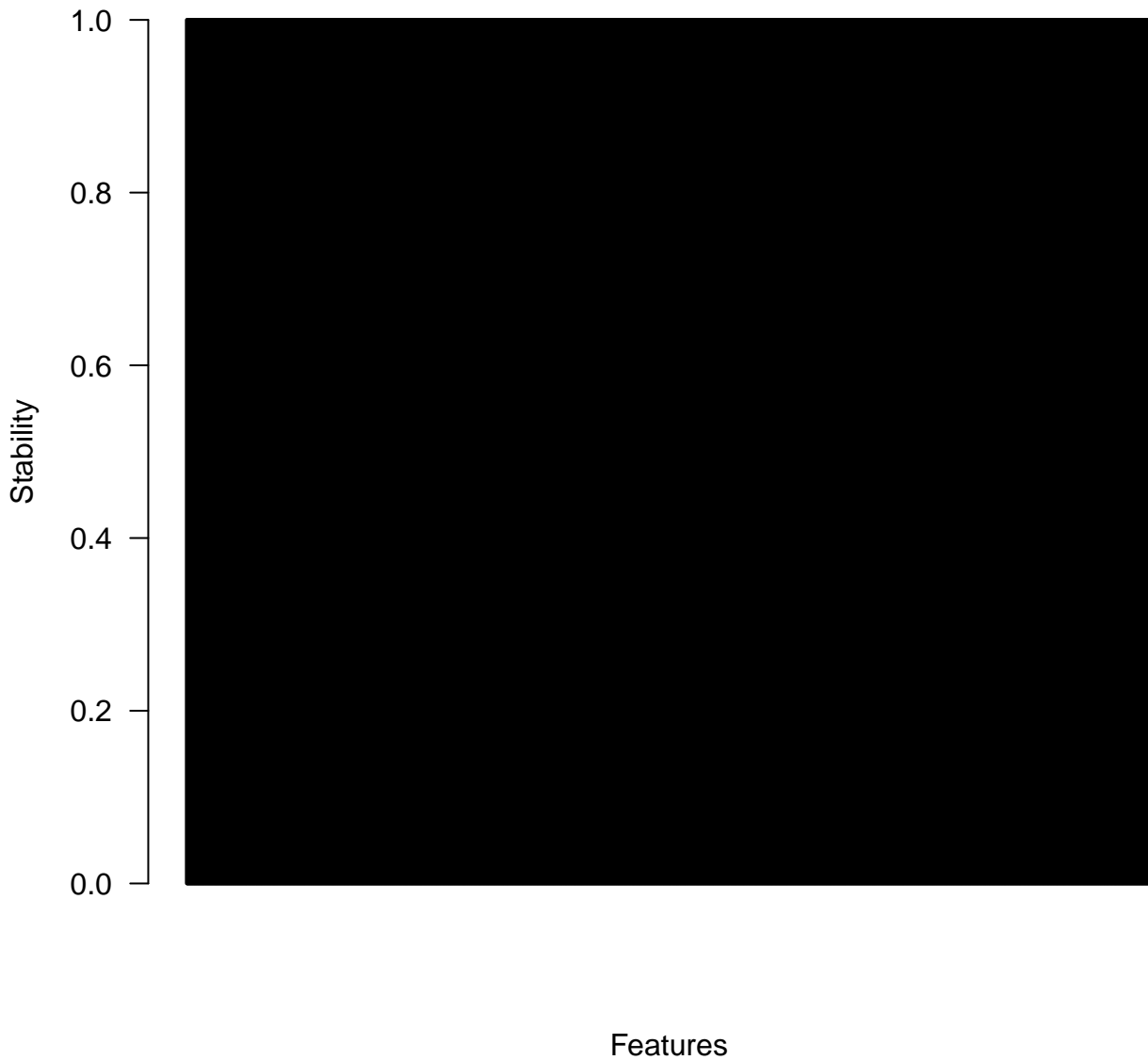
## metabolome Comp 2



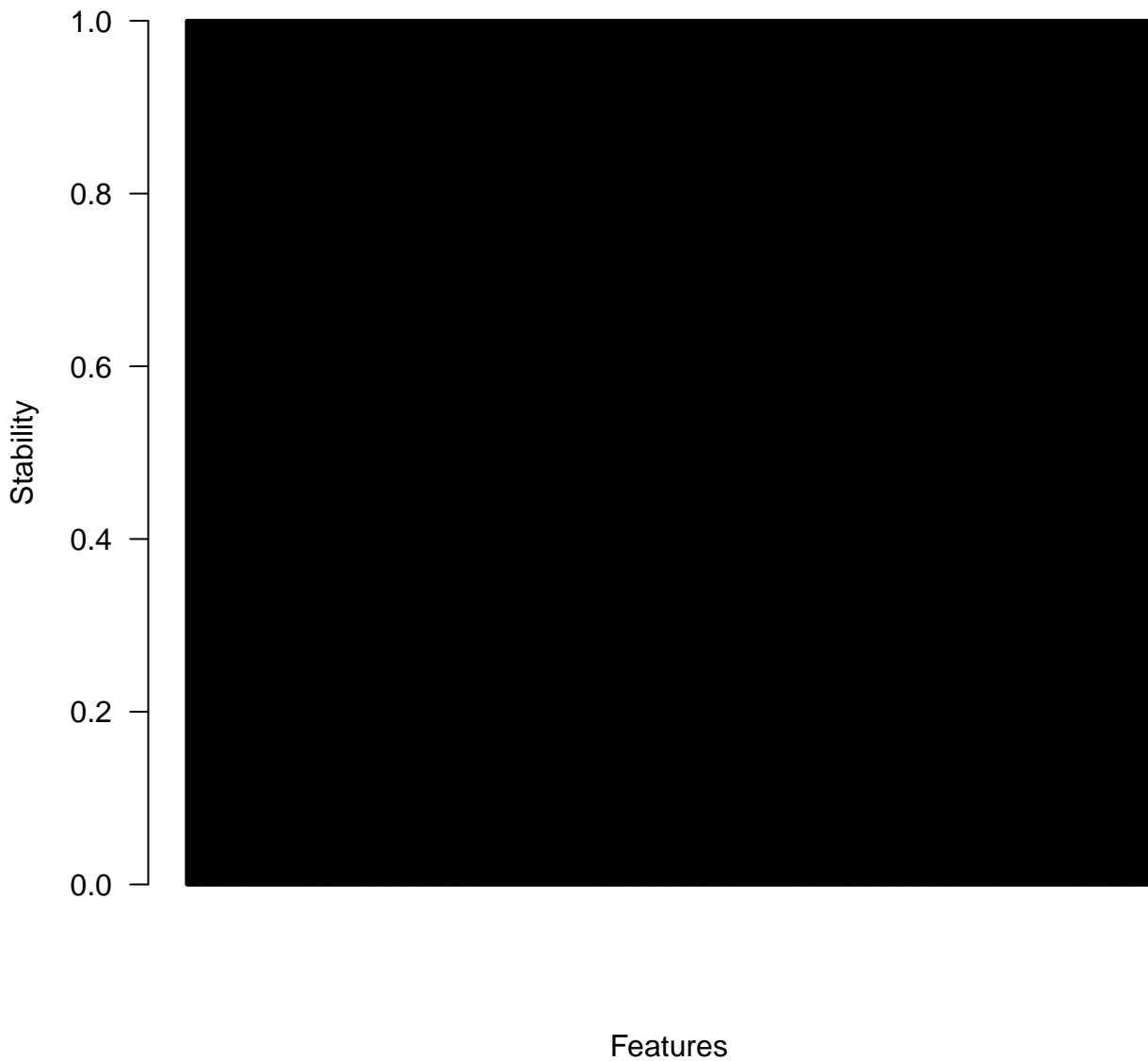
# metabolome Comp 3



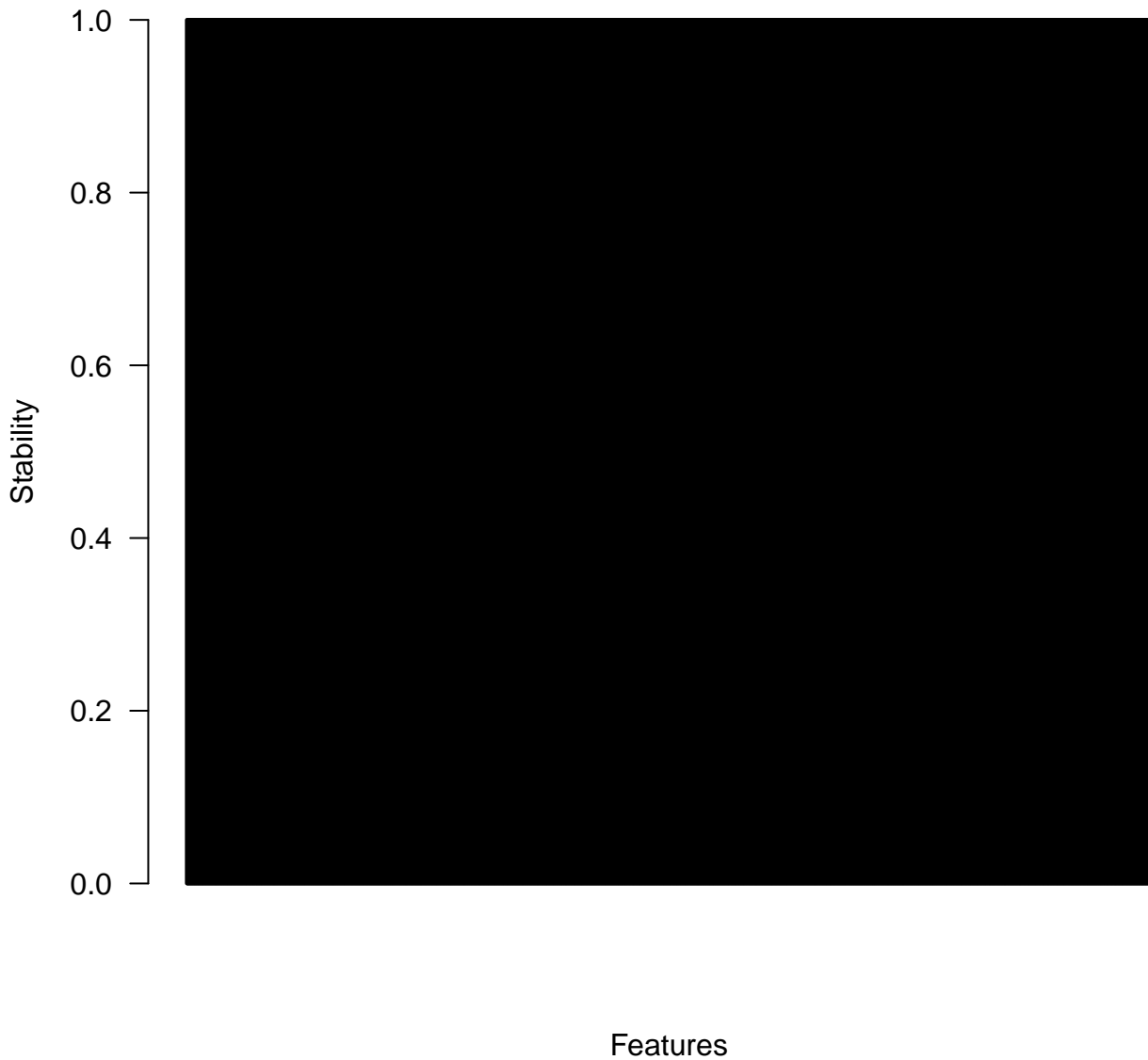
# proteome Comp 1



## proteome Comp 2

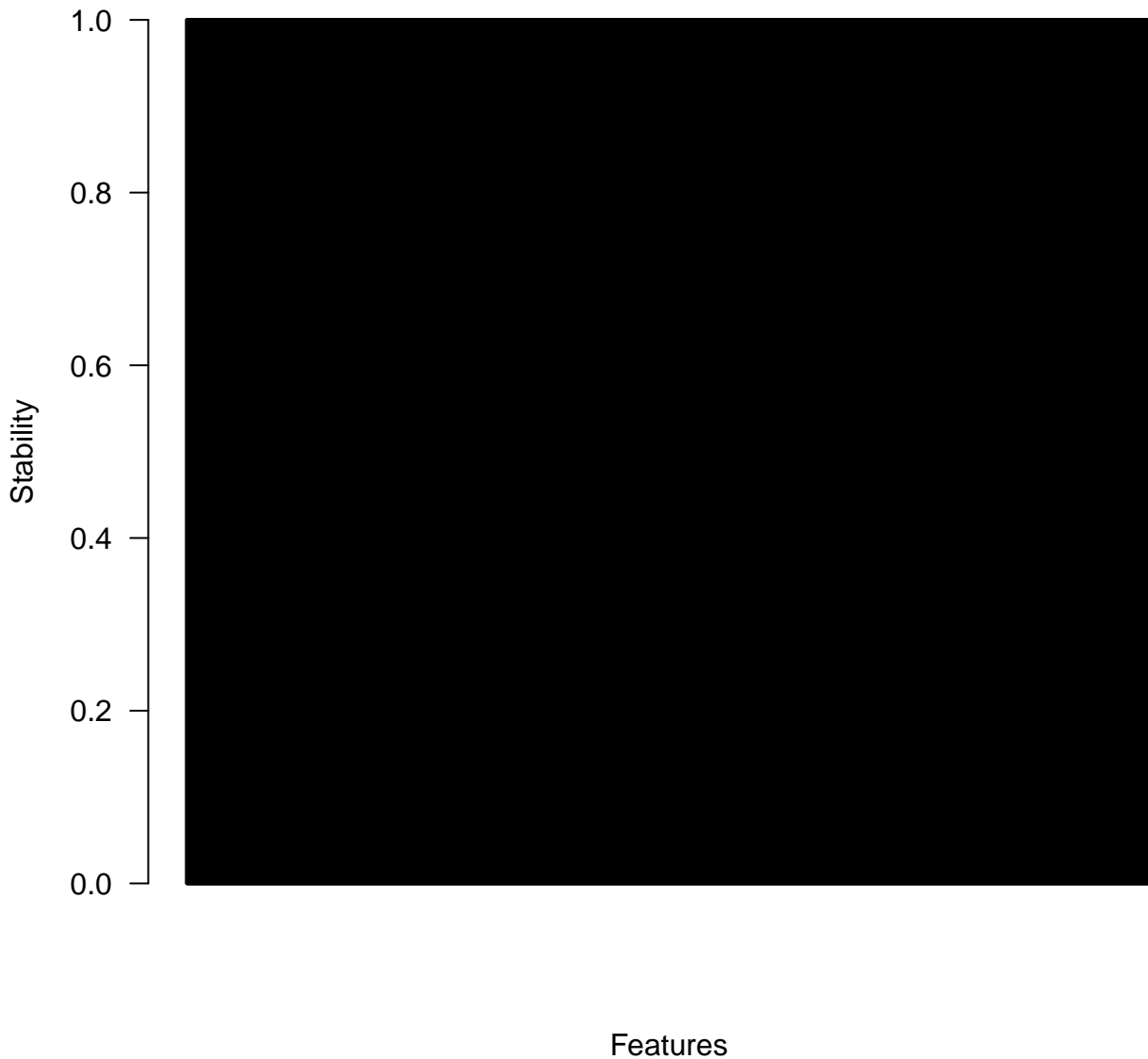


# proteome Comp 3

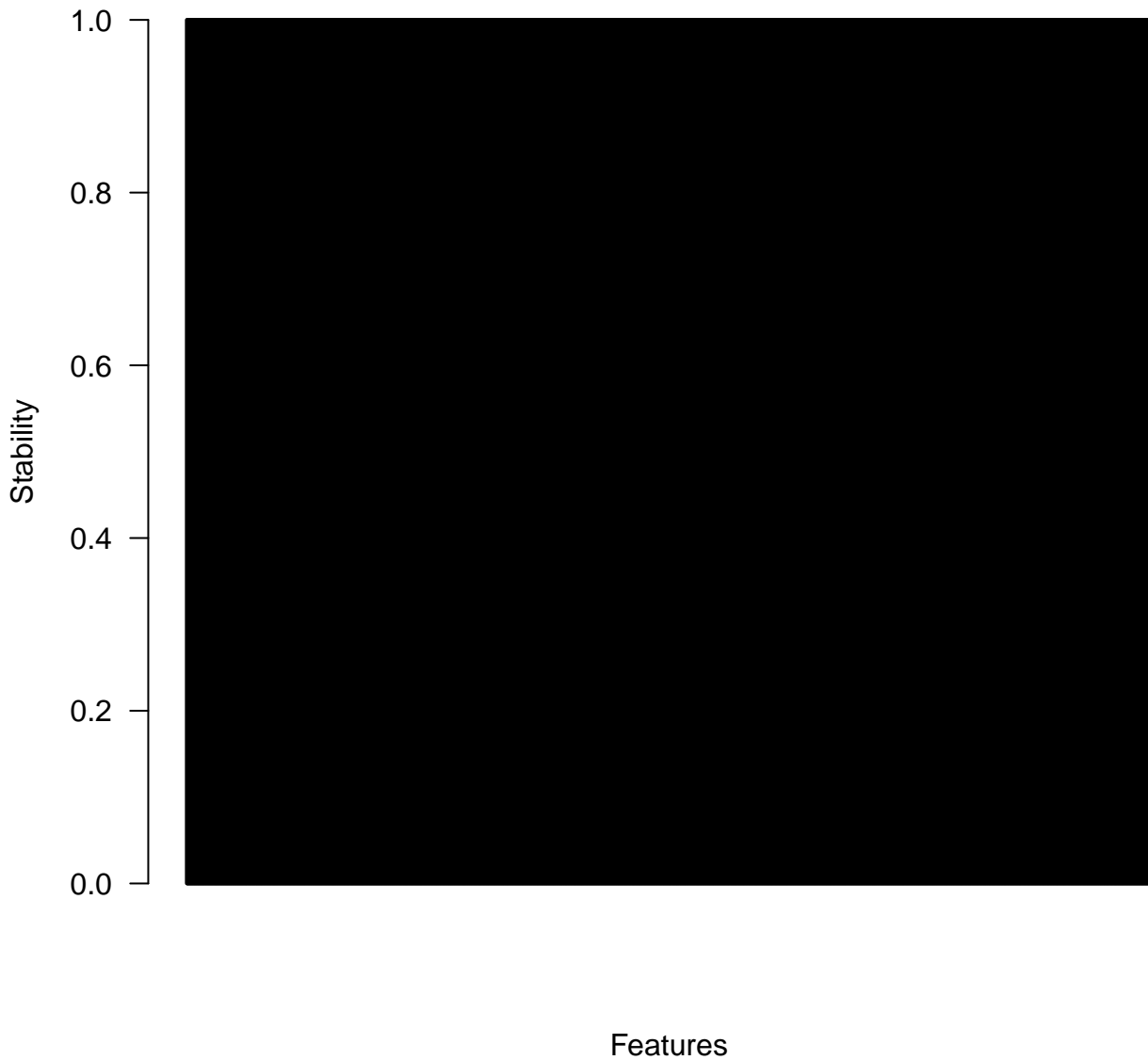




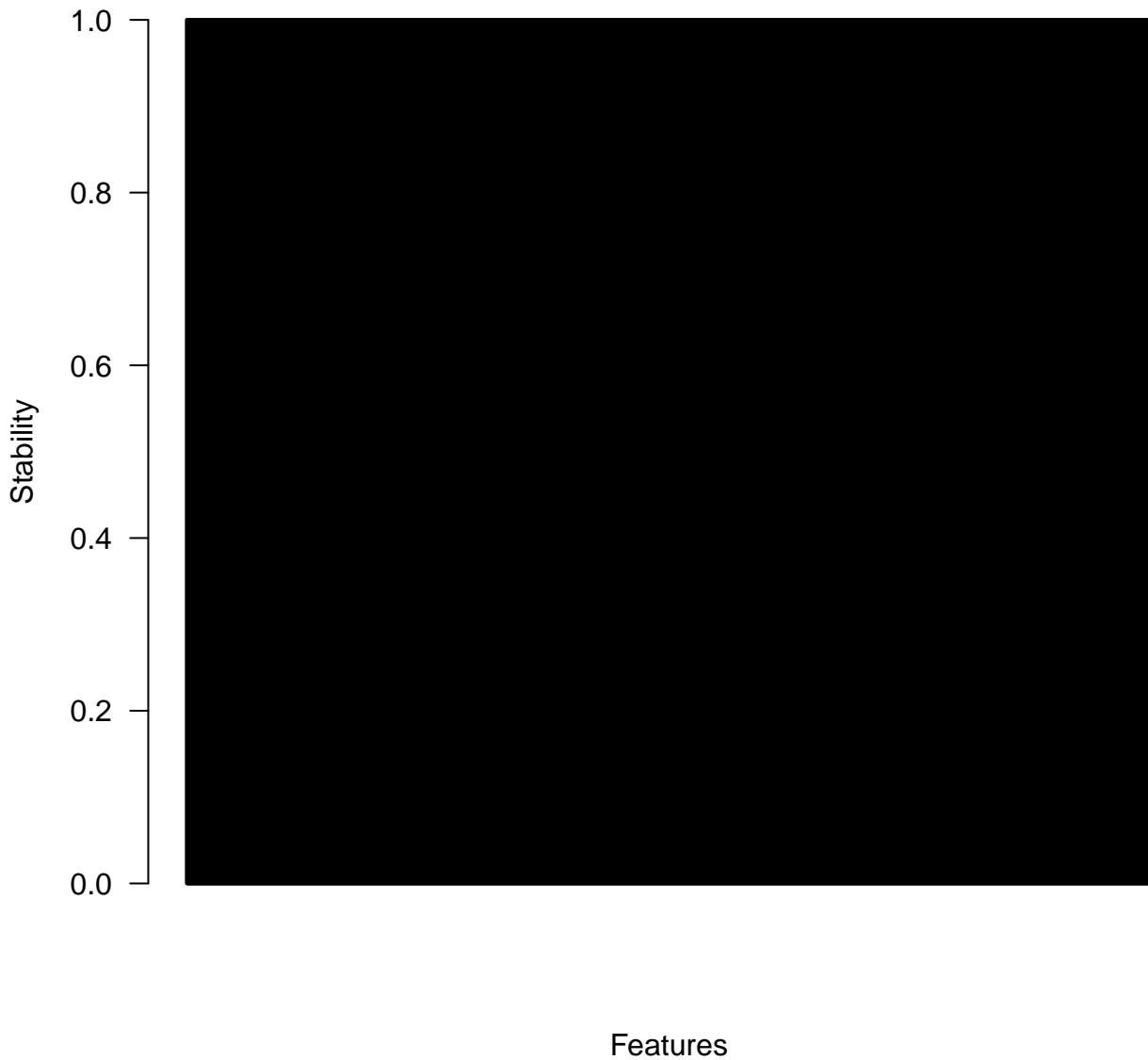
# transcriptome Comp 1



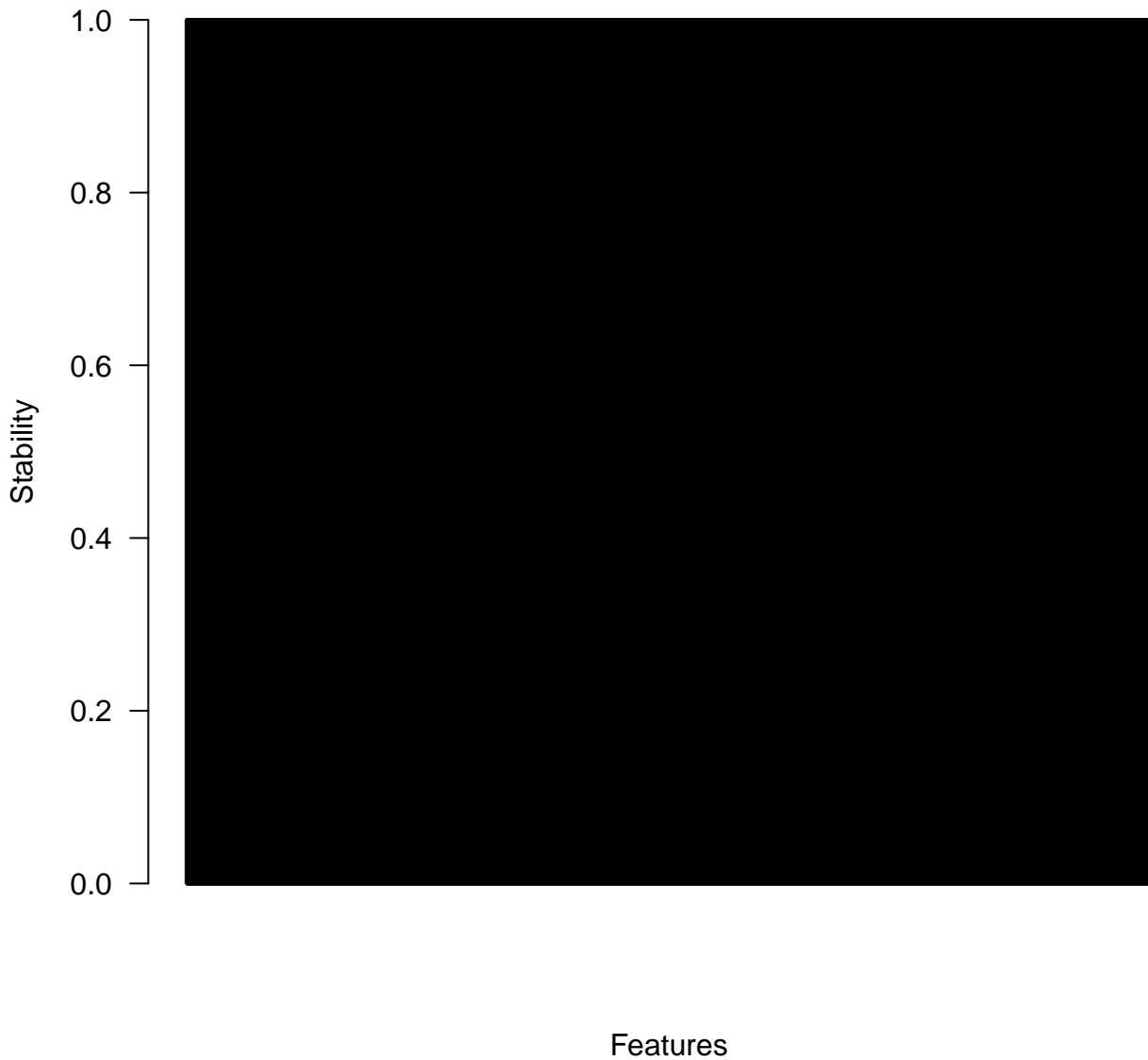
## transcriptome Comp 2



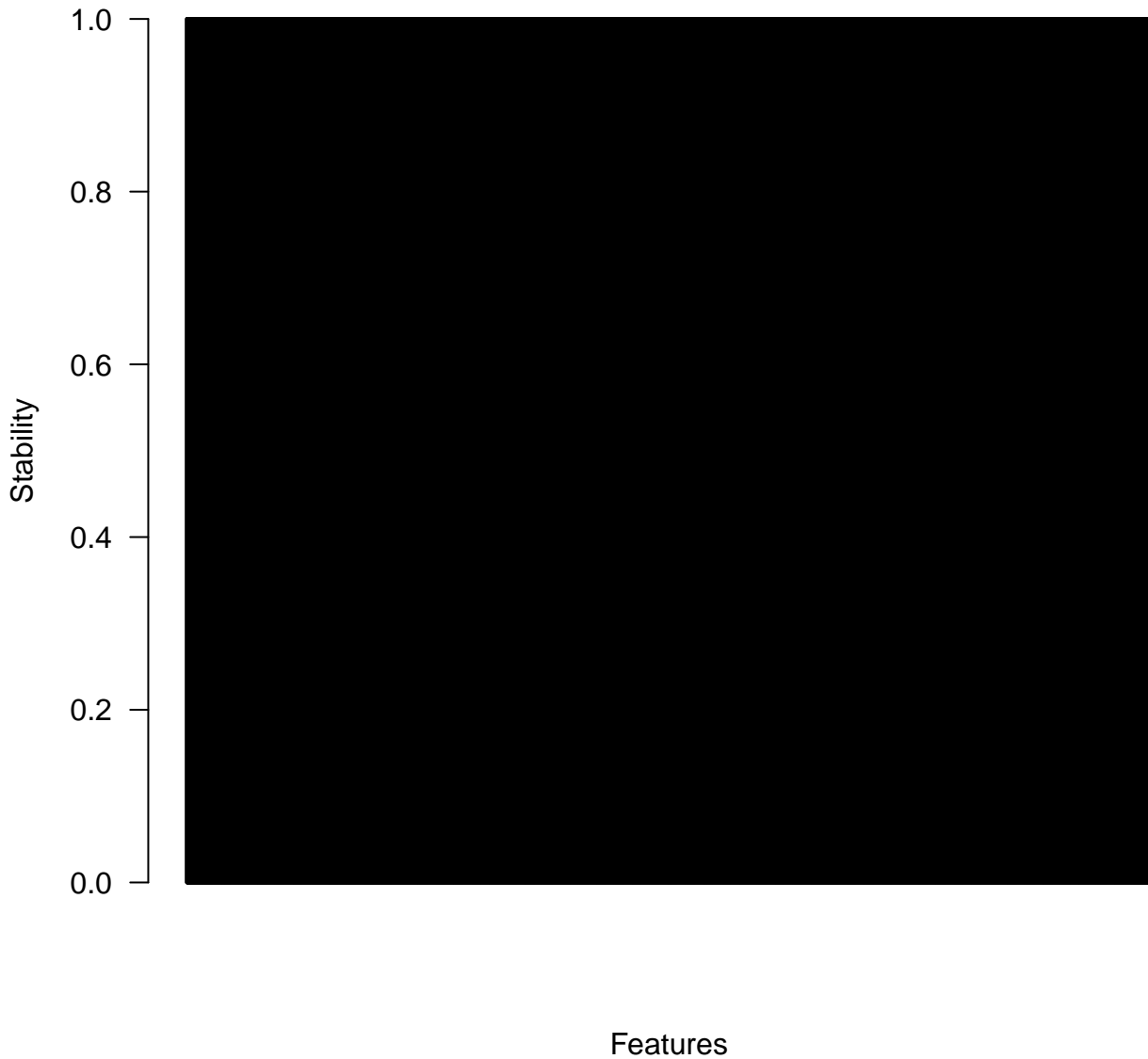
# transcriptome Comp 3



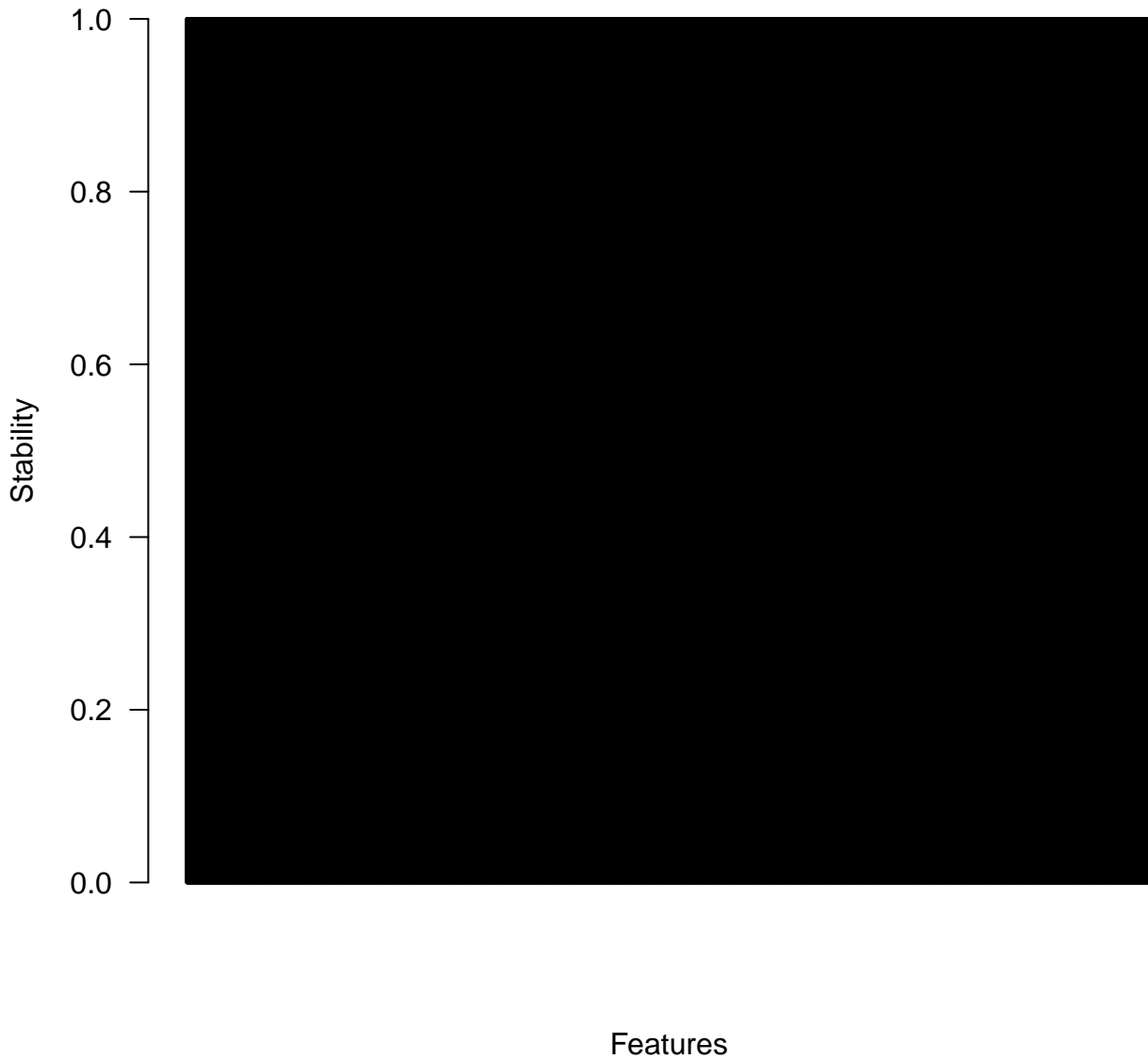
# metabolome Comp 1



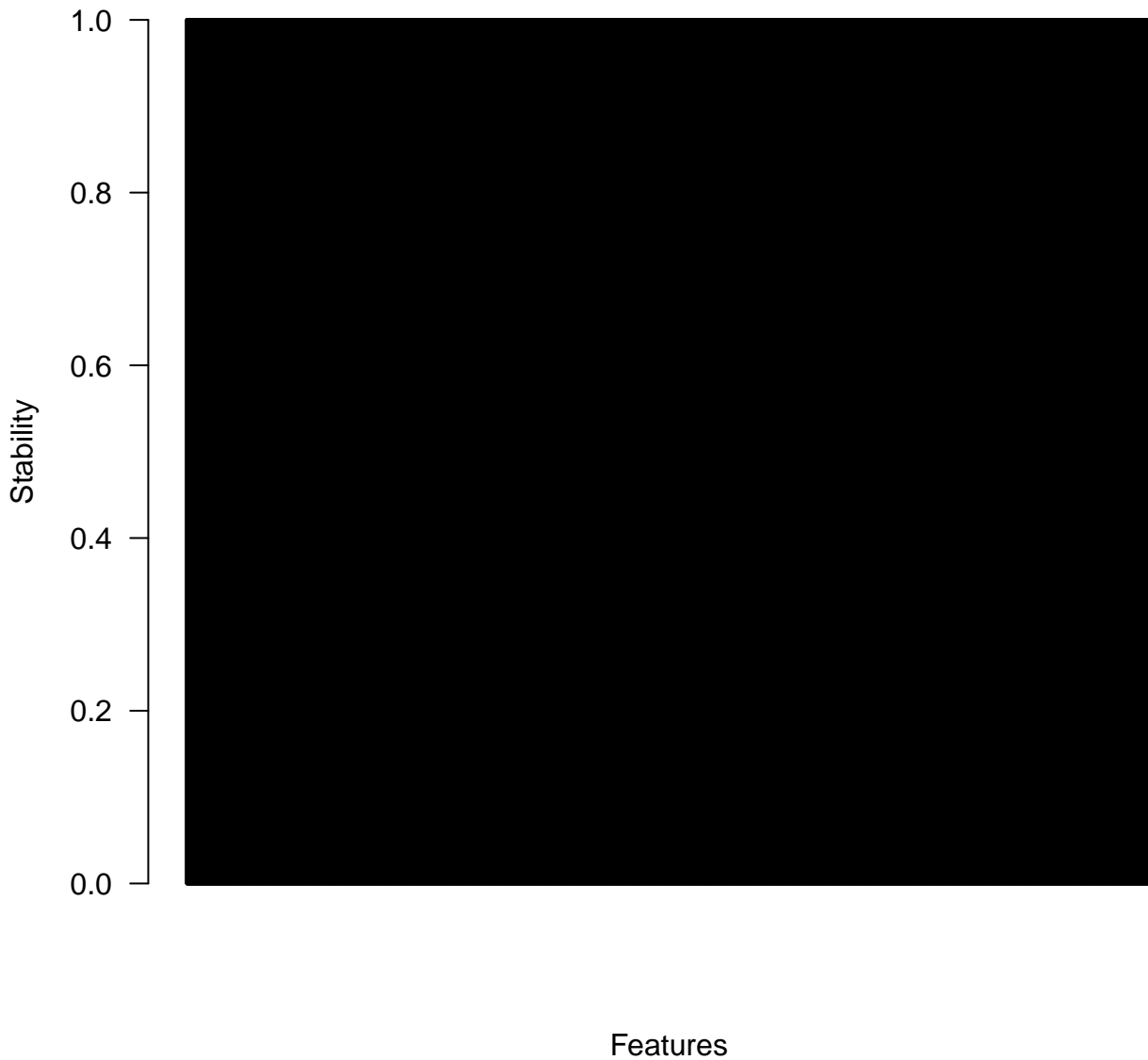
## metabolome Comp 2



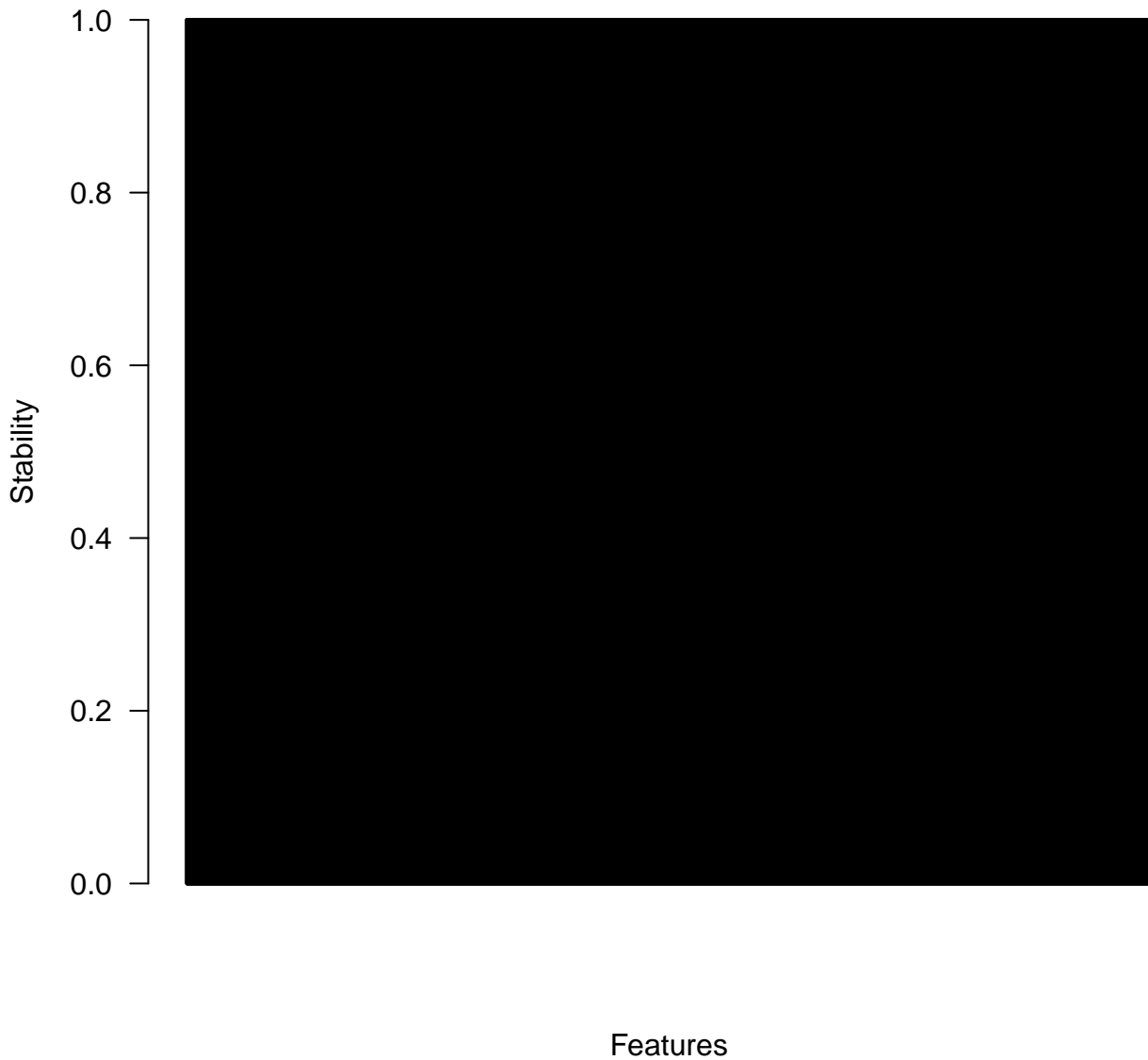
# metabolome Comp 3



# proteome Comp 1

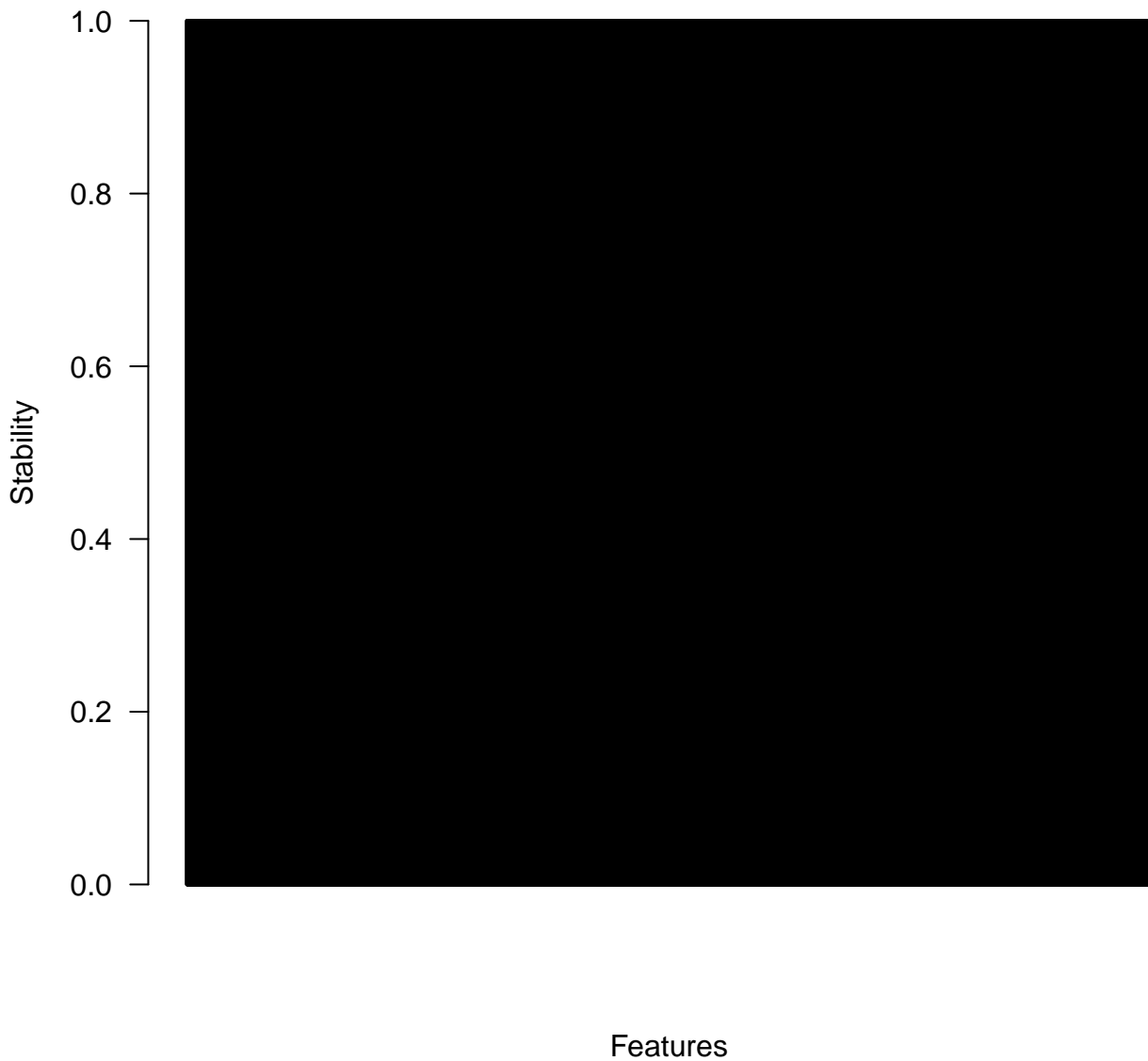


## proteome Comp 2

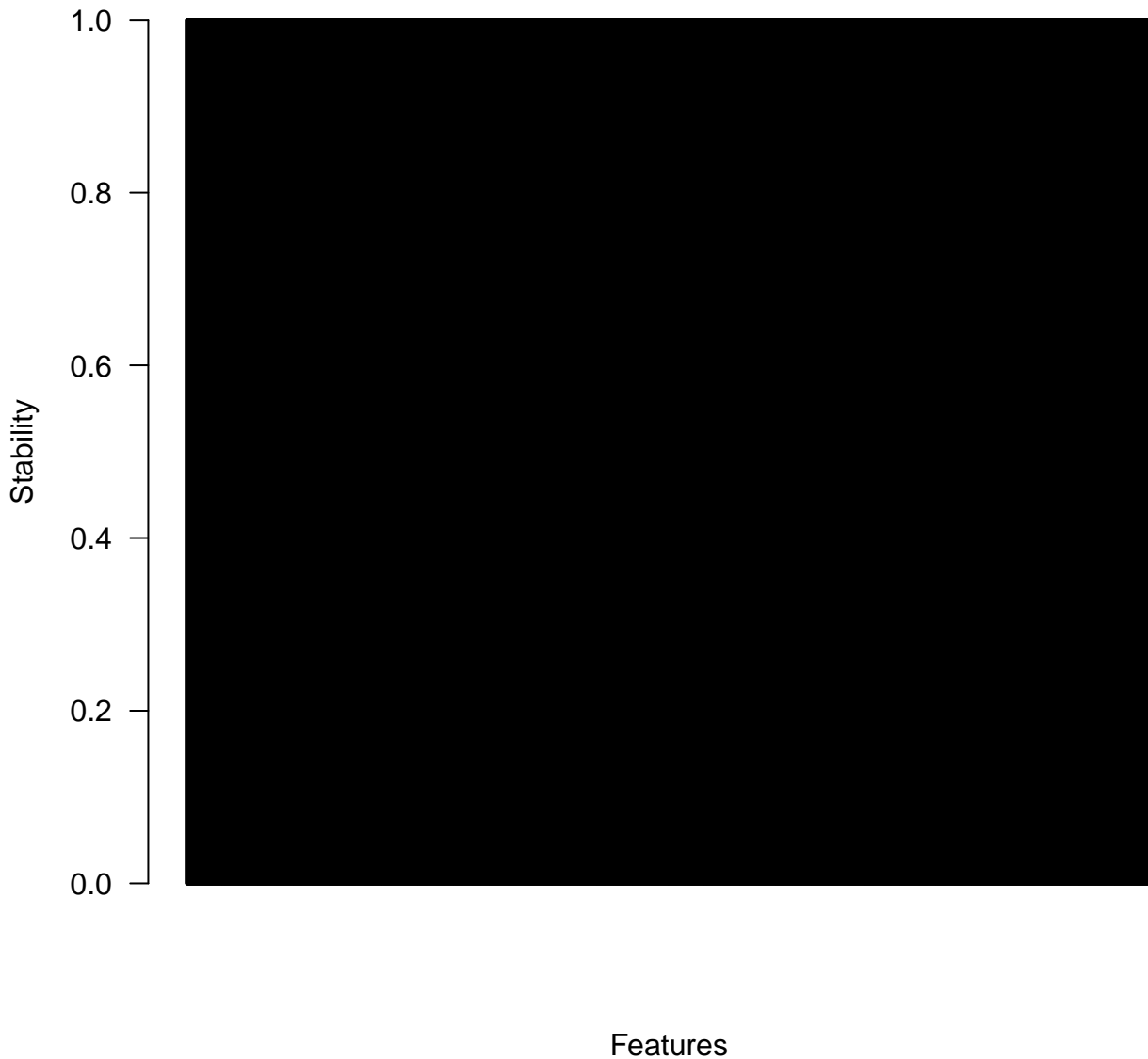




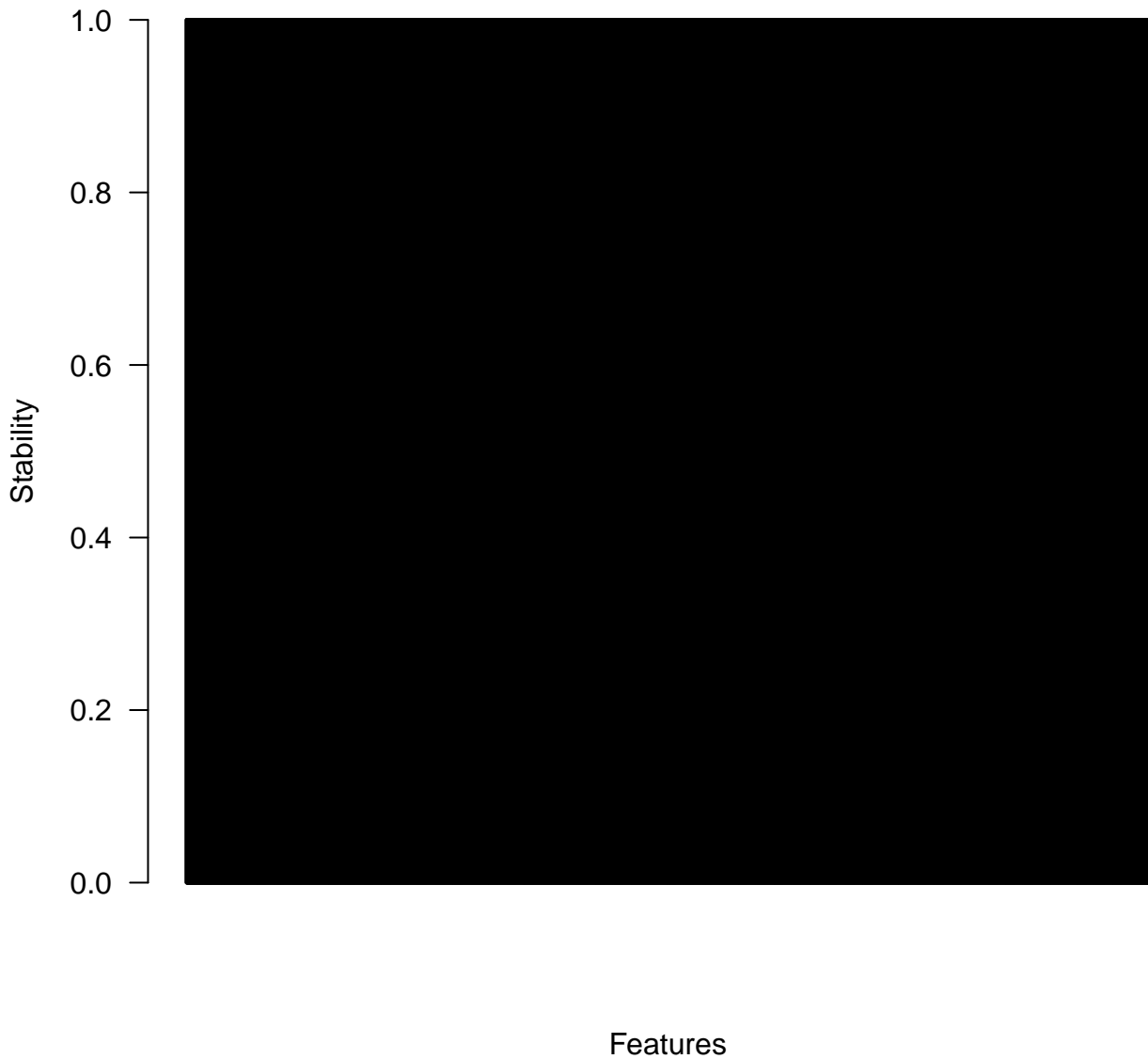
# proteome Comp 3



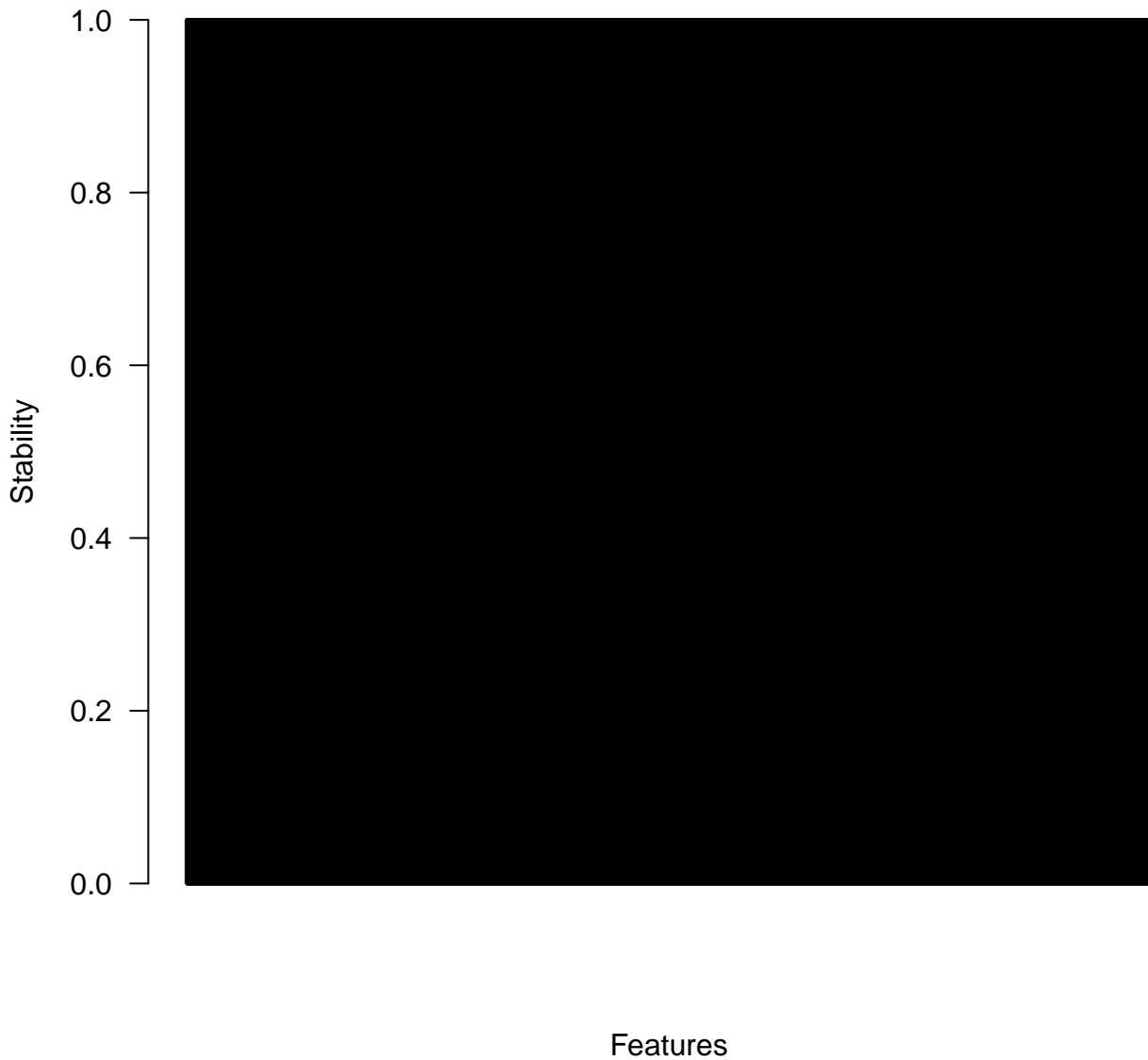
# transcriptome Comp 1



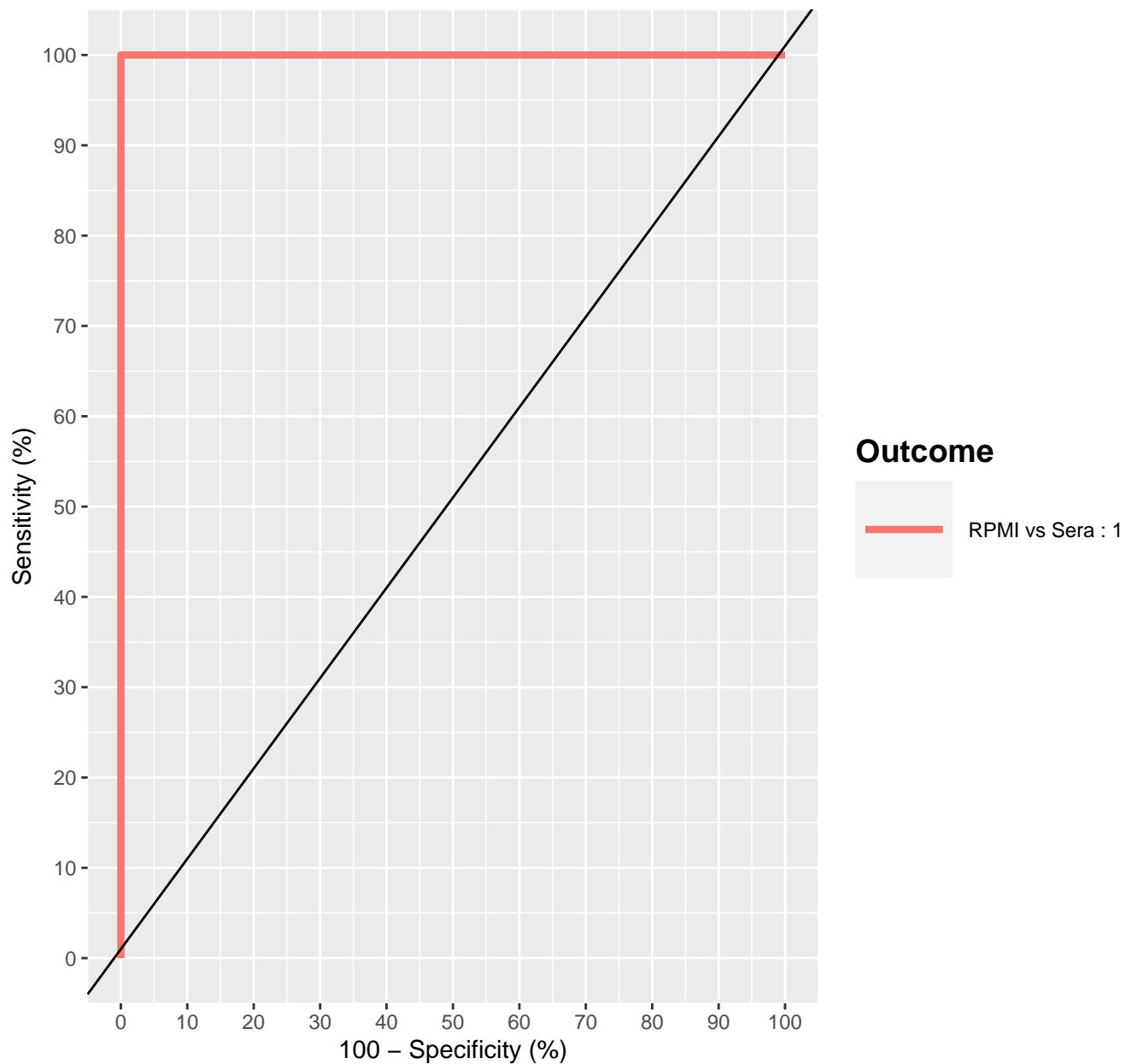
# transcriptome Comp 2



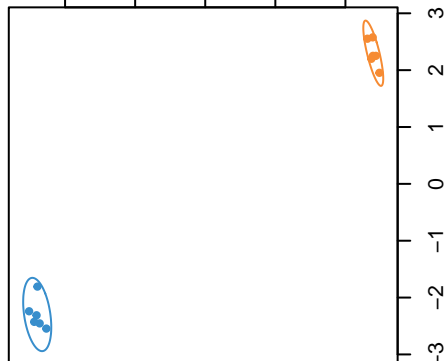
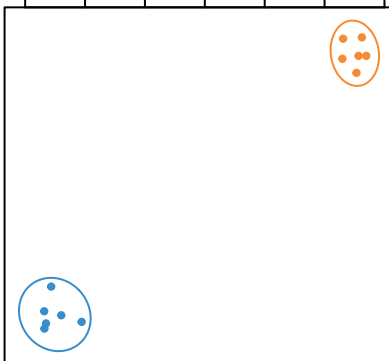
# transcriptome Comp 3



**ROC Curve**  
**Block: metabolome, Using Comp(s): 1**

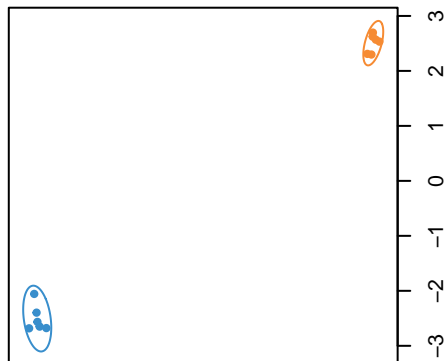


metabolome



0.99

proteome



0.99

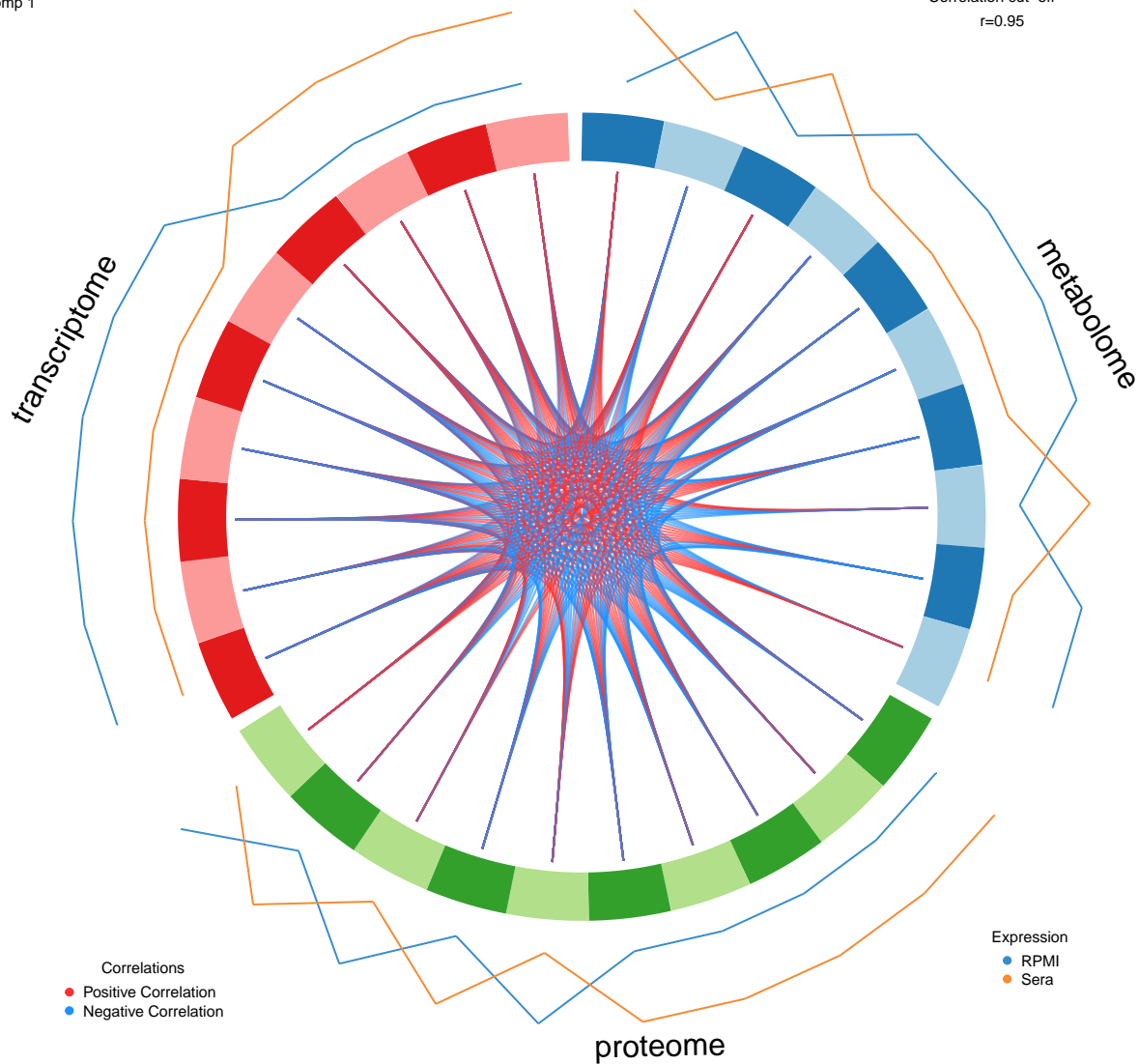
1

transcriptome

● RPMI ● Sera

Comp 1

Correlation cut-off  
 $r=0.95$

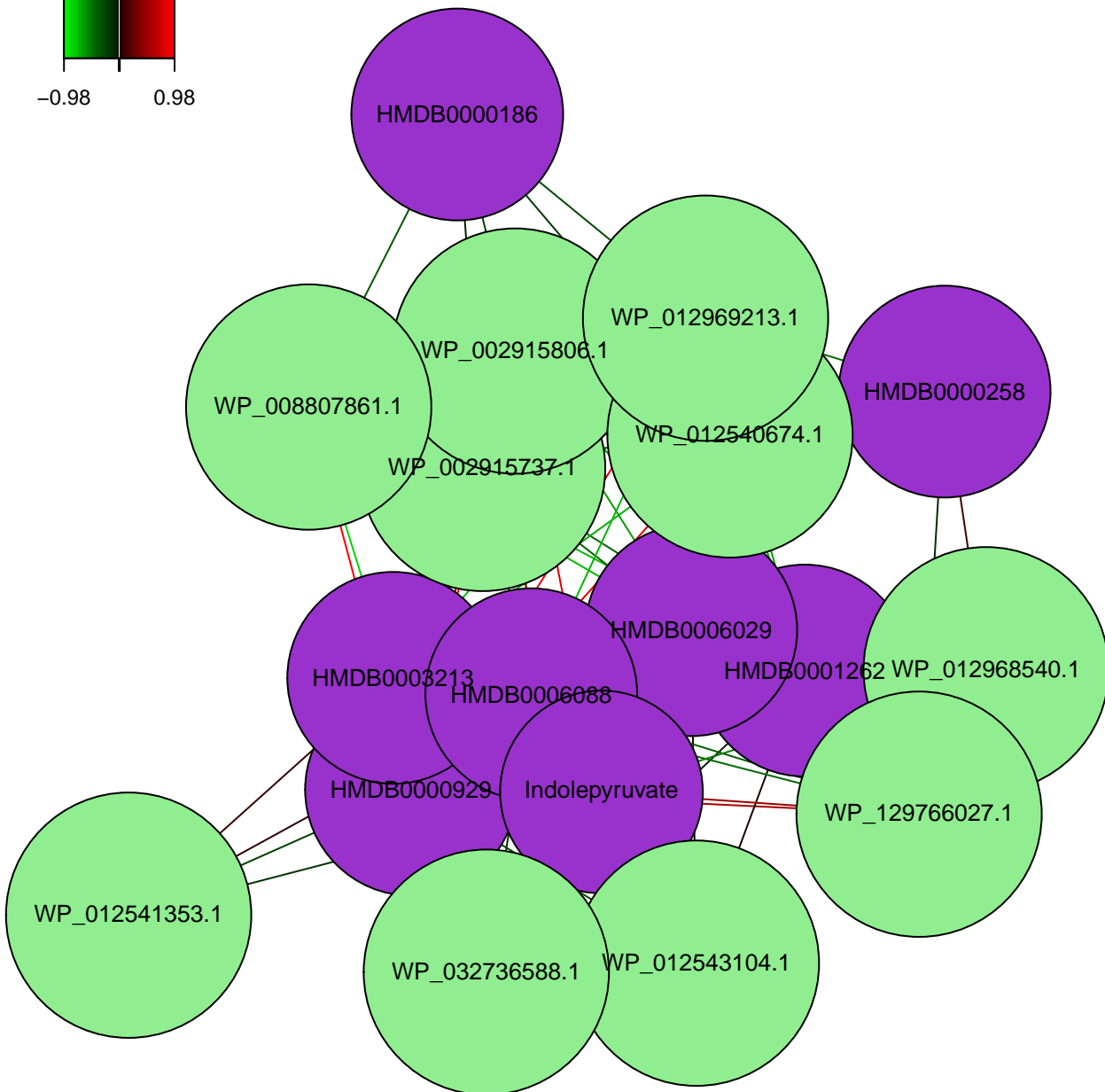


Color key



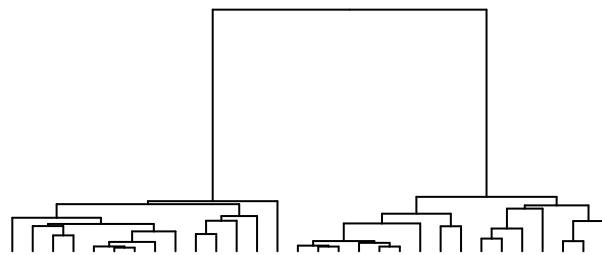
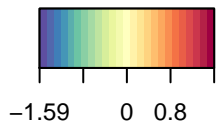
-0.98

0.98





Color key



Rows

● RPMI

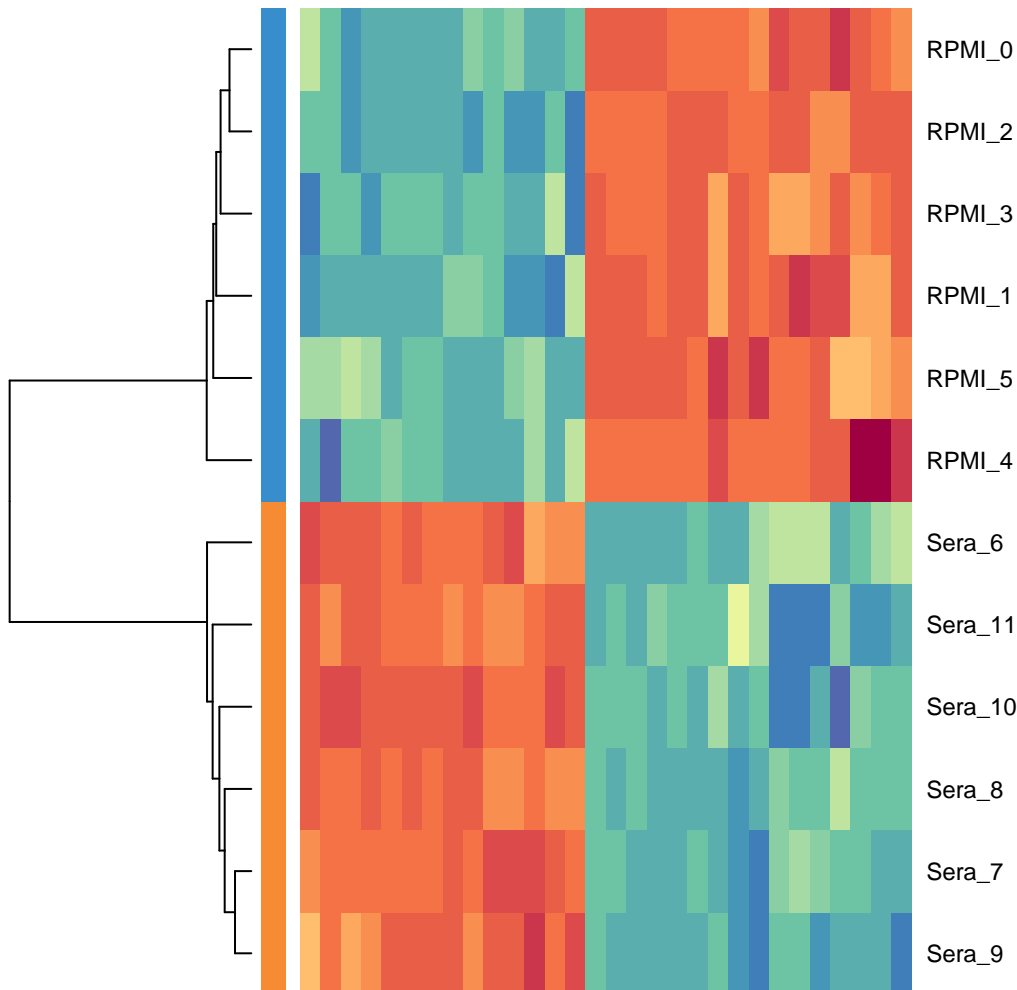
● Sera

Columns

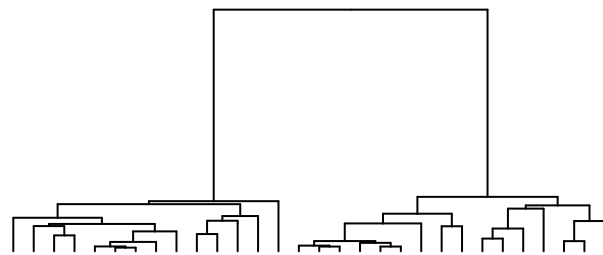
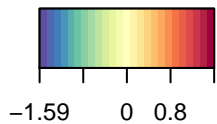
● metabolome

● proteome

● transcriptome



Color key



Rows

● RPMI

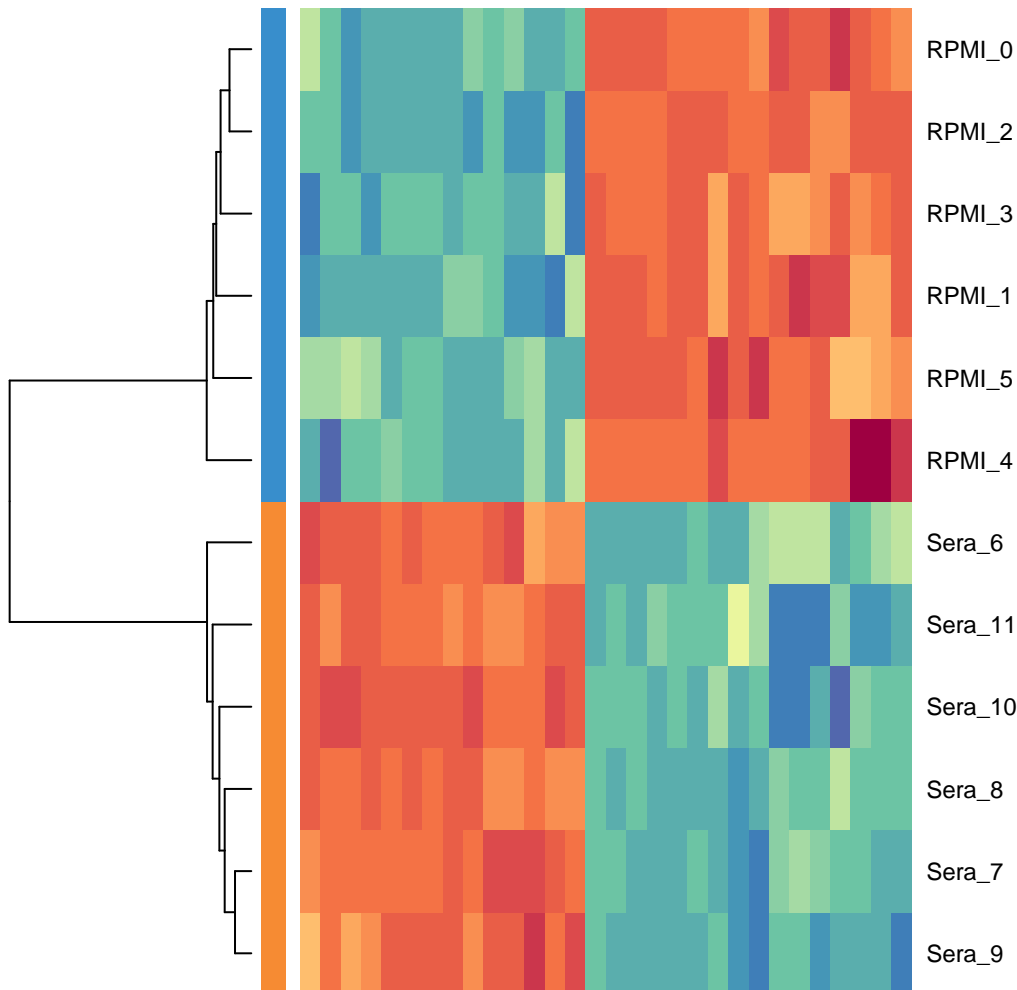
● Sera

Columns

● metabolome

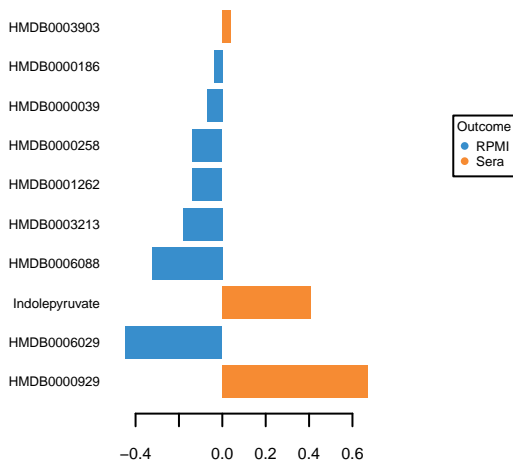
● proteome

● transcriptome

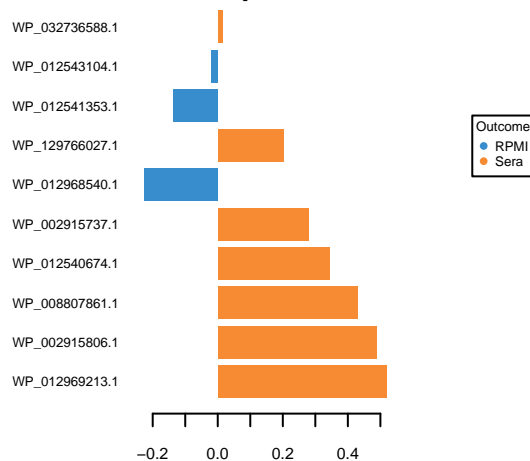


# 1 DIABLO max loadings

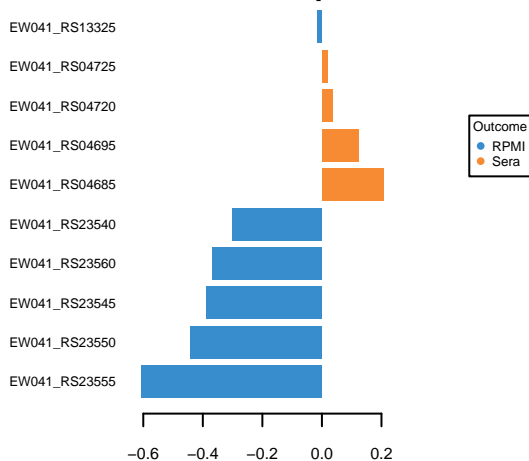
**Contribution on comp 1**  
**Block 'metabolome'**



**Contribution on comp 1**  
**Block 'proteome'**

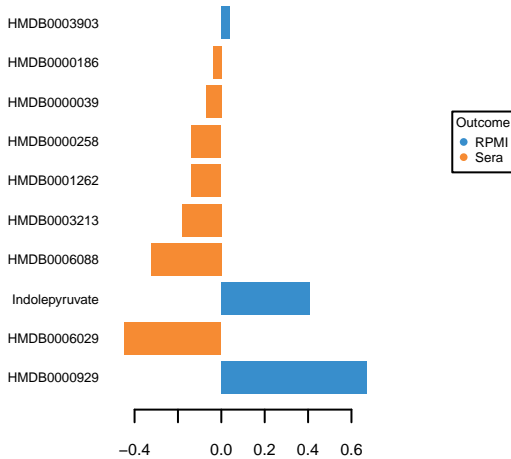


**Contribution on comp 1**  
**Block 'transcriptome'**

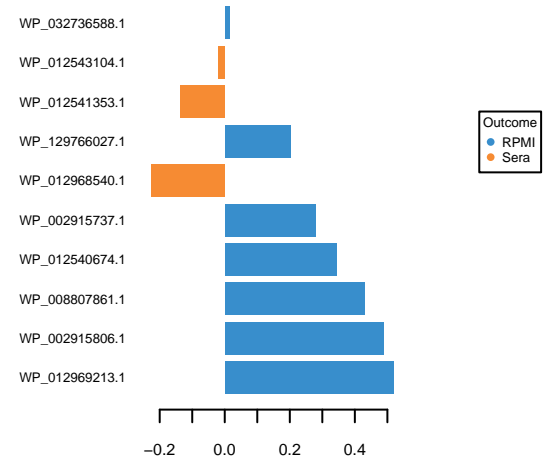


# 1 DIABLO min loadings

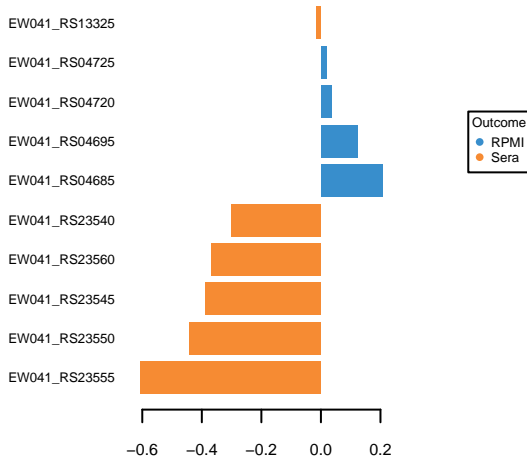
**Contribution on comp 1**  
**Block 'metabolome'**



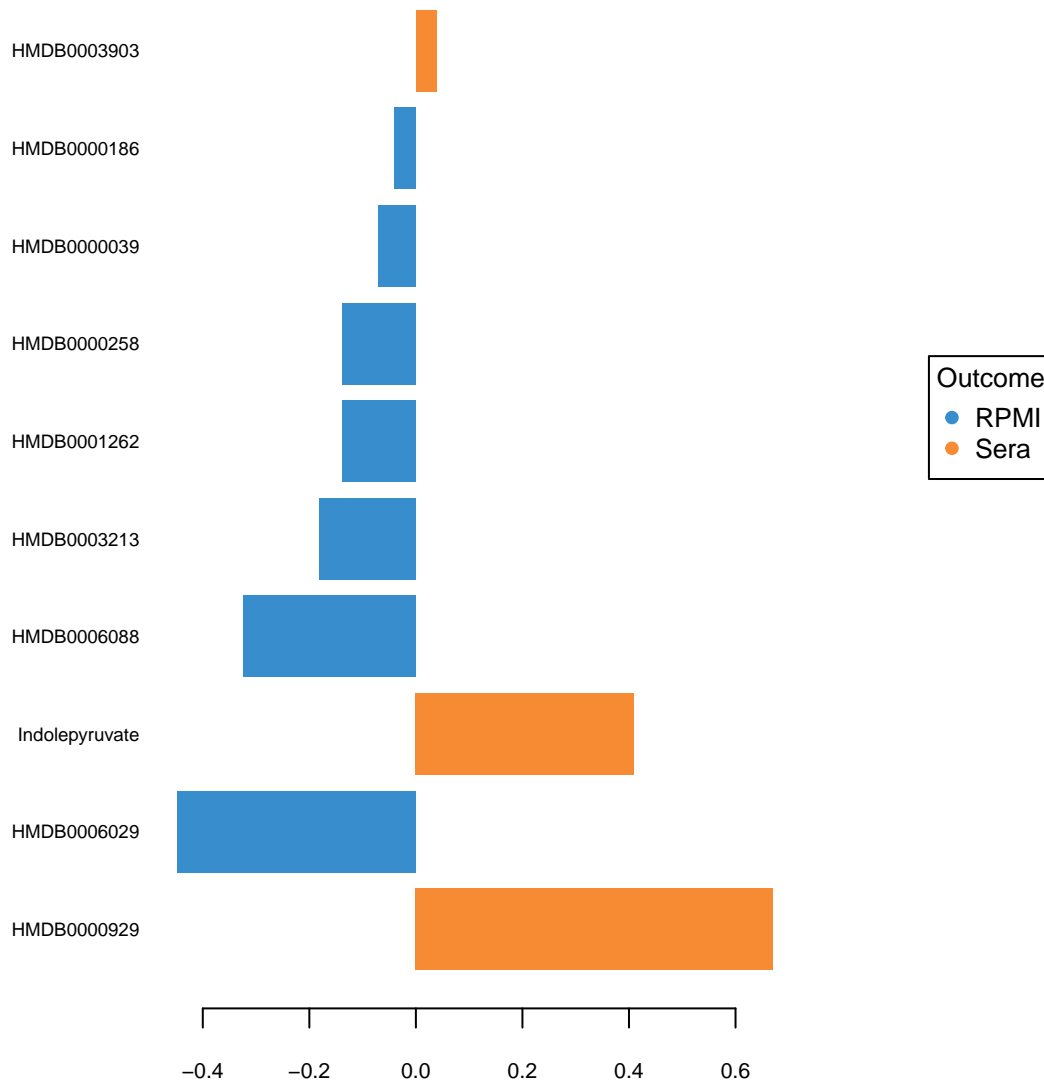
**Contribution on comp 1**  
**Block 'proteome'**



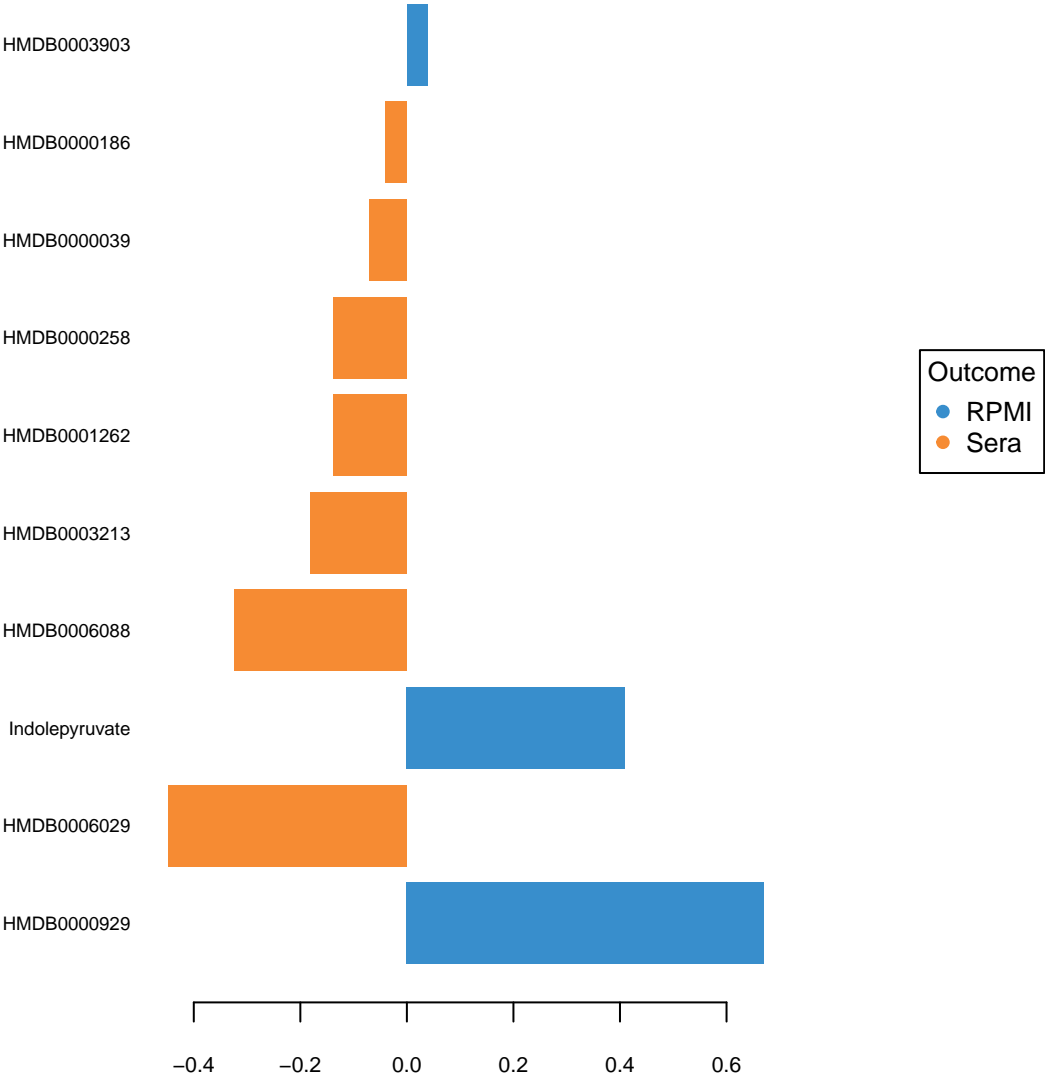
**Contribution on comp 1**  
**Block 'transcriptome'**



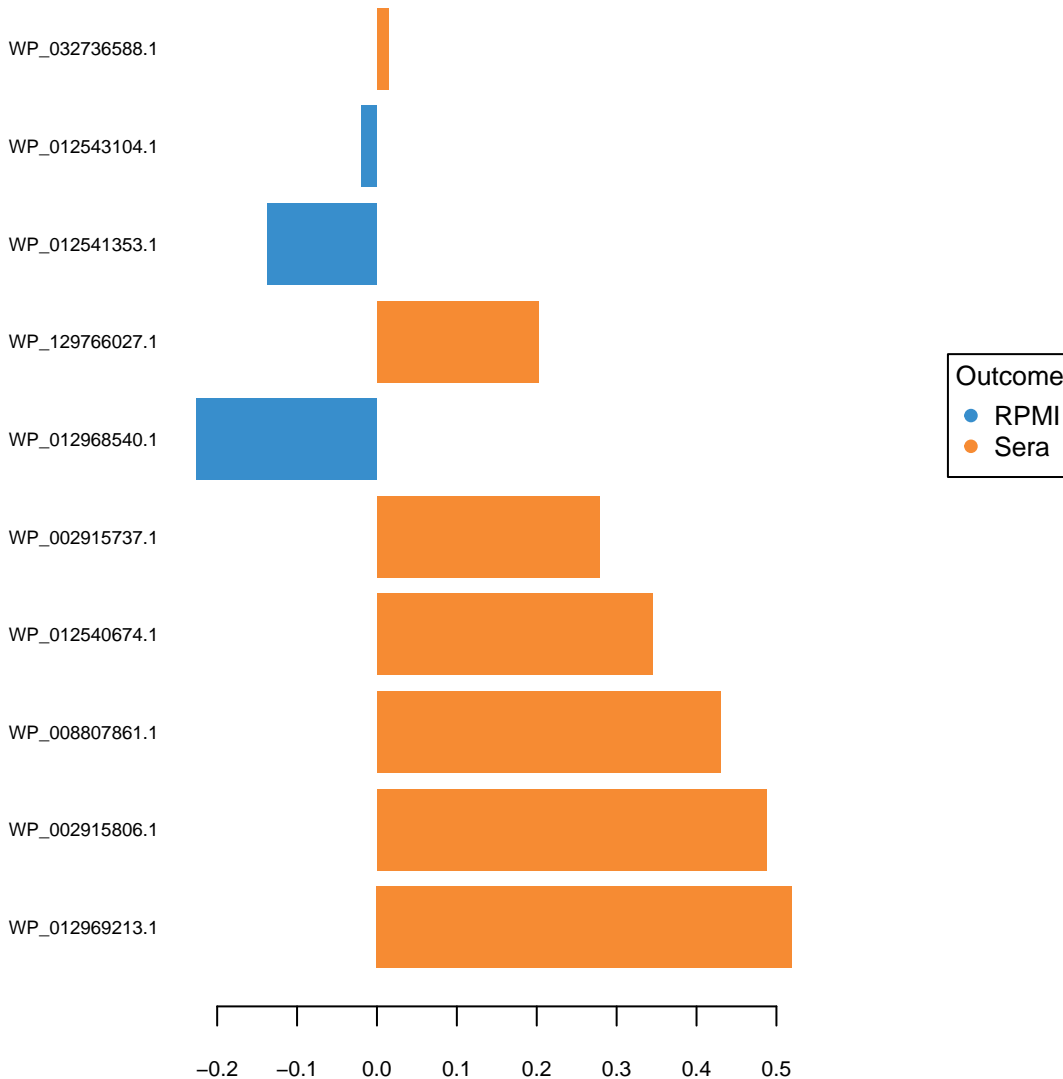
# 1 metabolome DIABLO max load



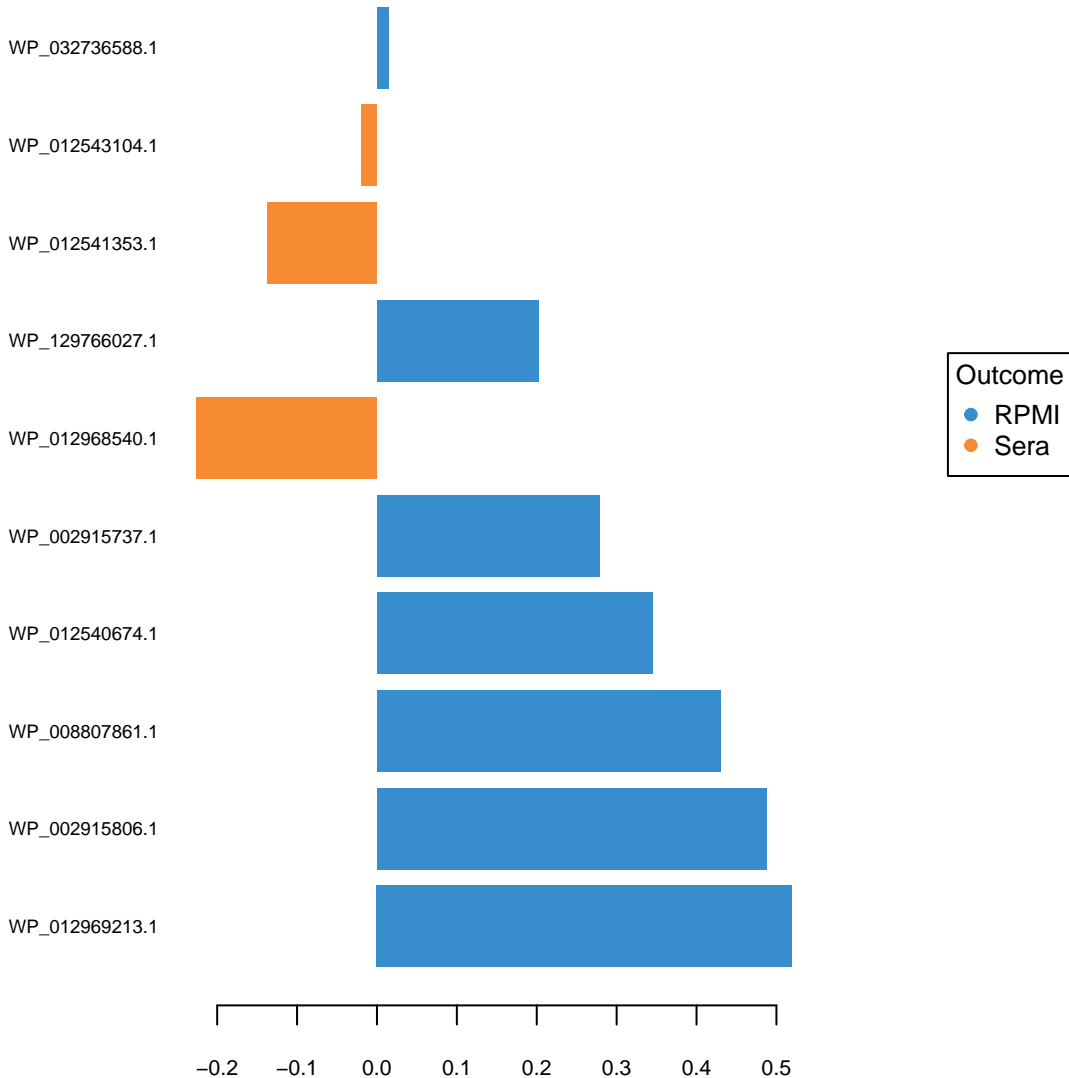
# 1 metabolome DIABLO min loac



# 1 proteome DIABLO max load

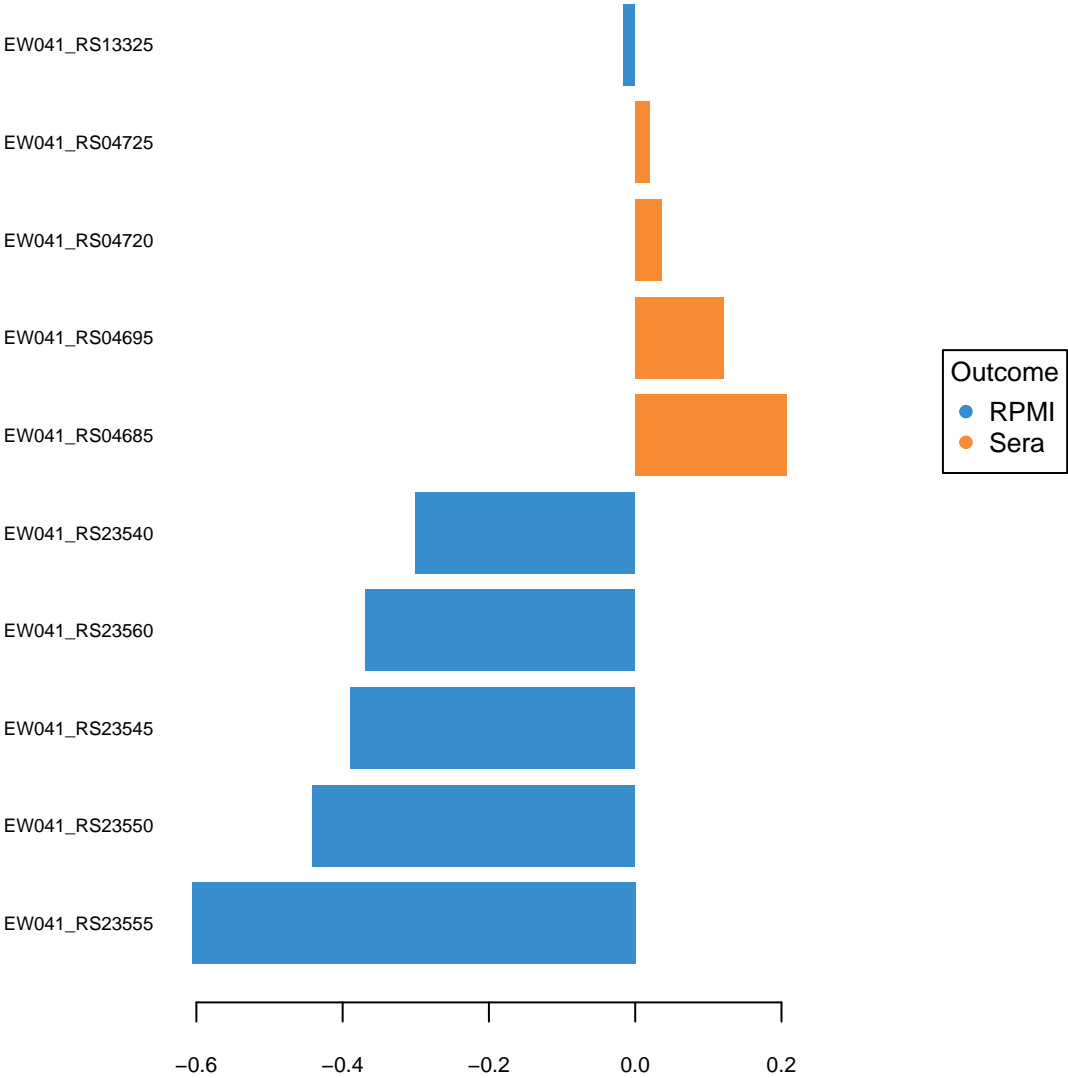


# 1 proteome DIABLO min load





# 1 transcriptome DIABLO max loa



# 1 transcriptome DIABLO min loa

