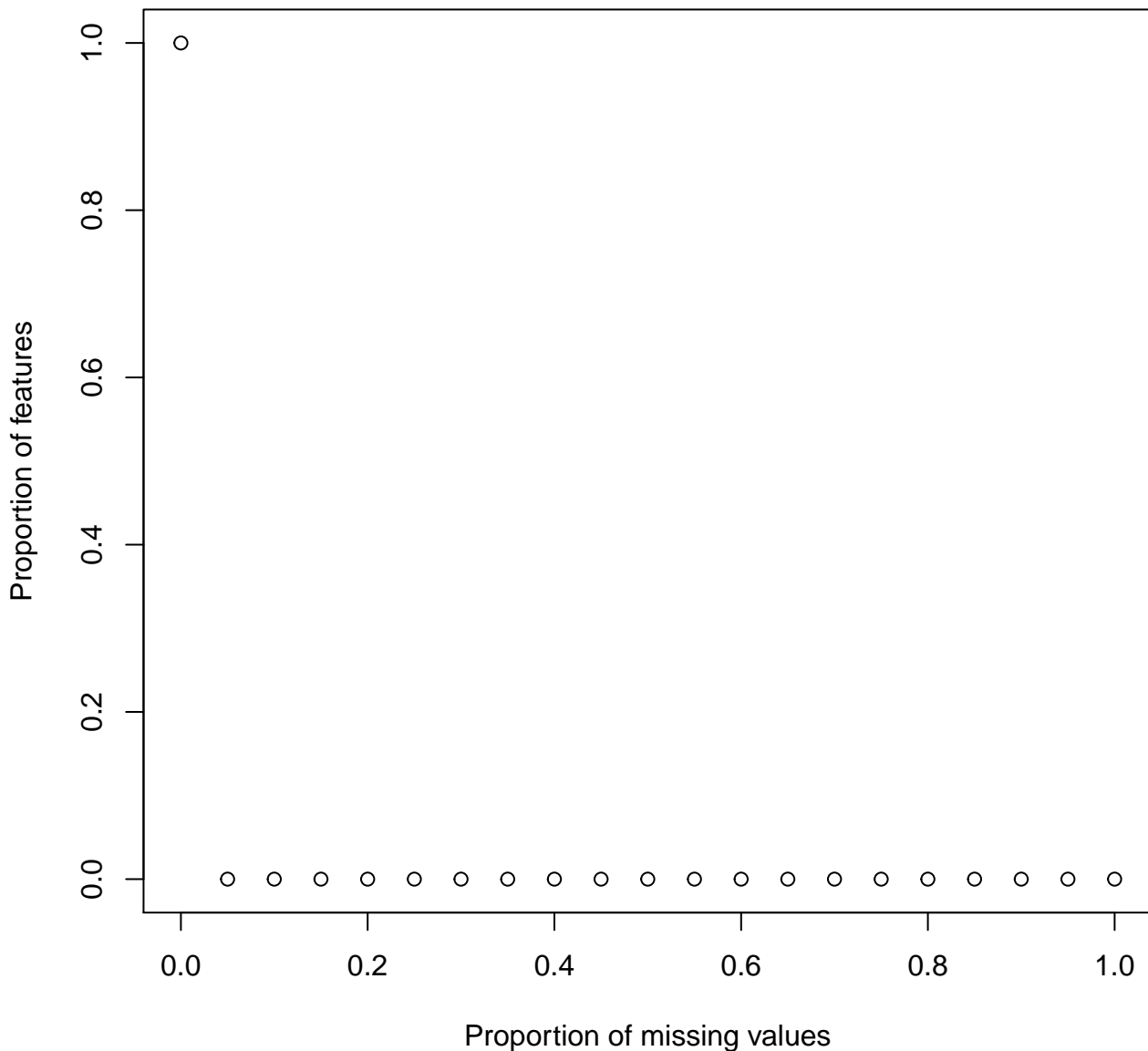
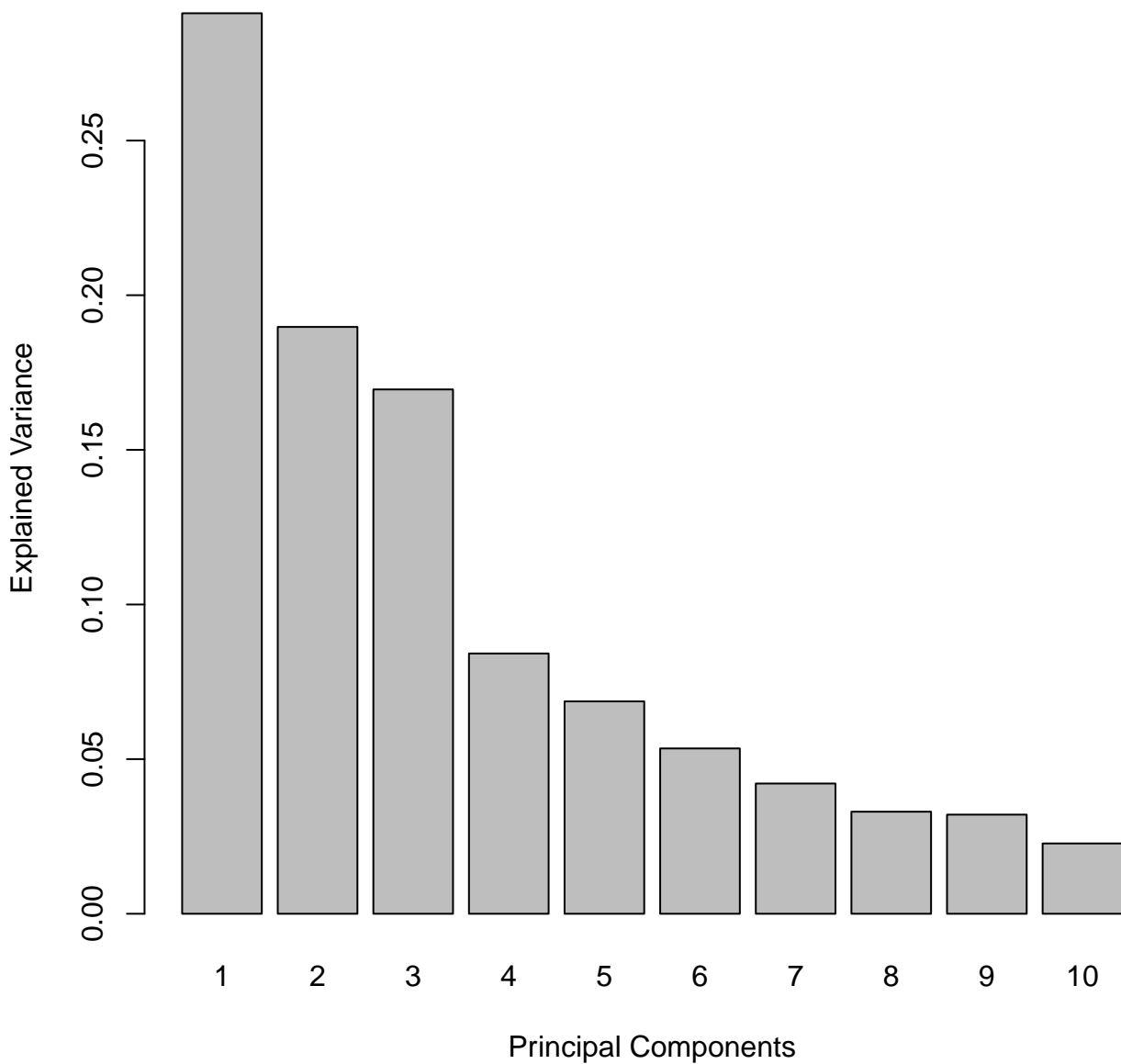


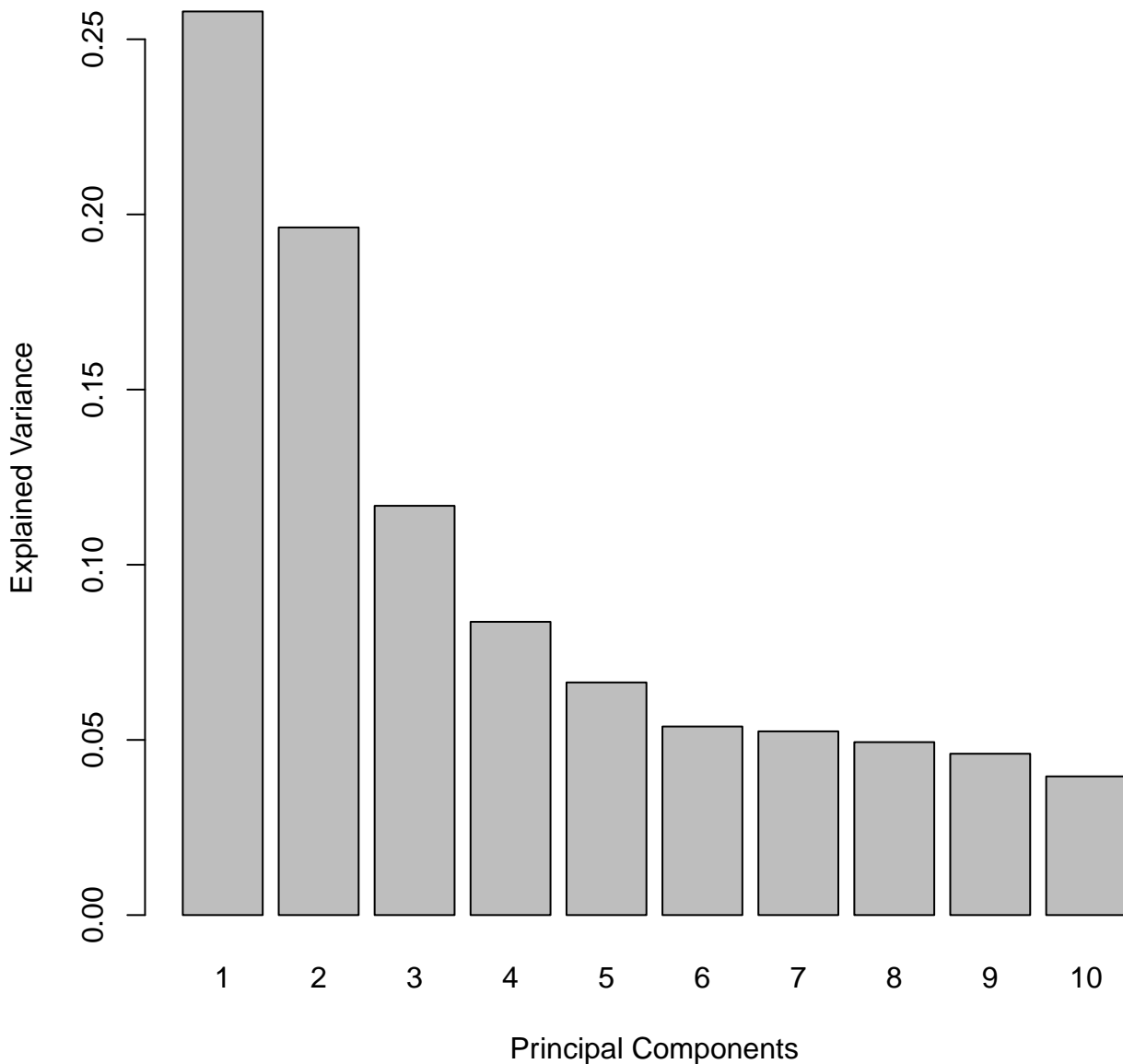
# transcriptome missing value proportions for unfiltered data



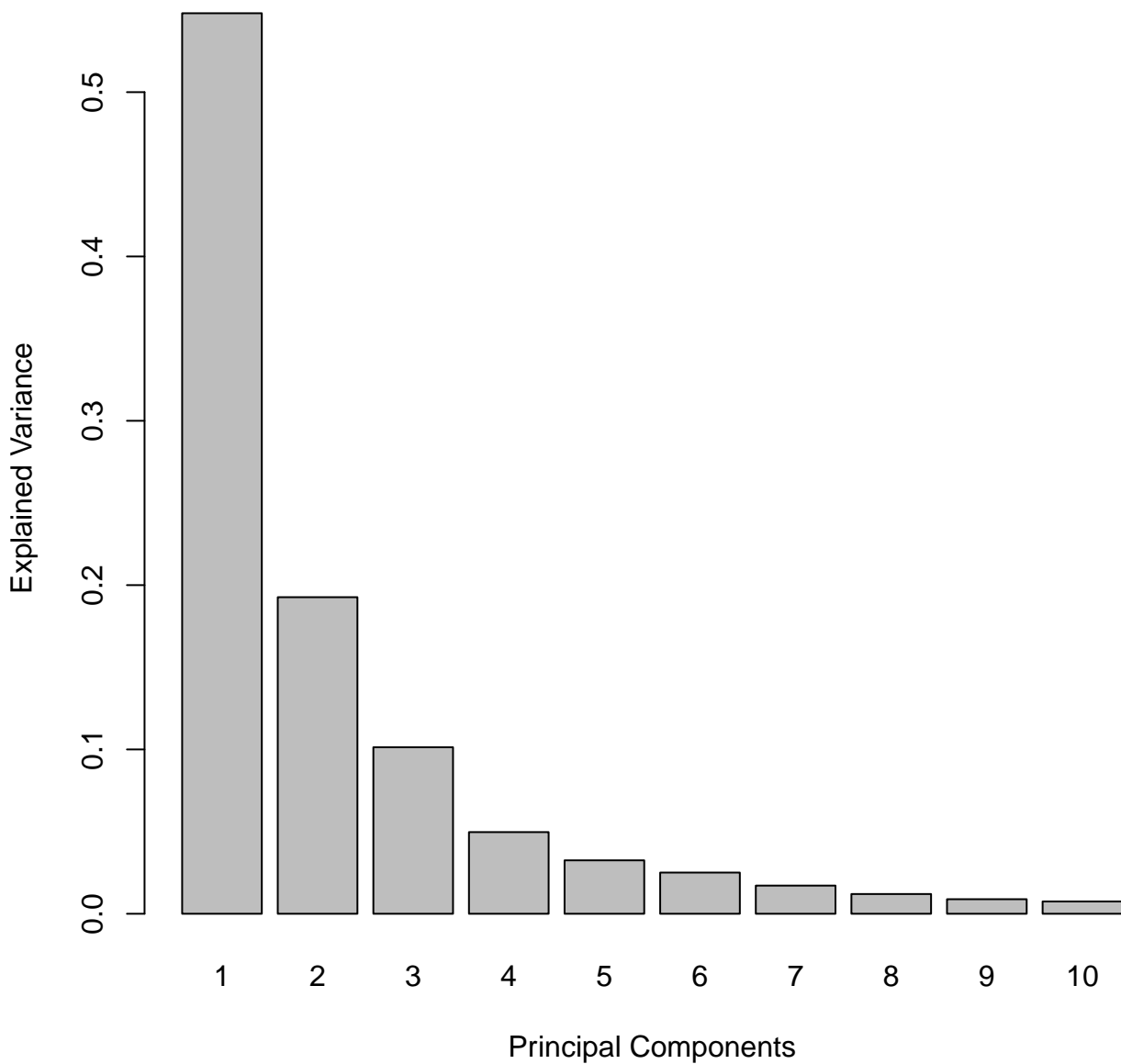
# metabolome screeplot



# proteome screeplot



**transcriptome screeplot**



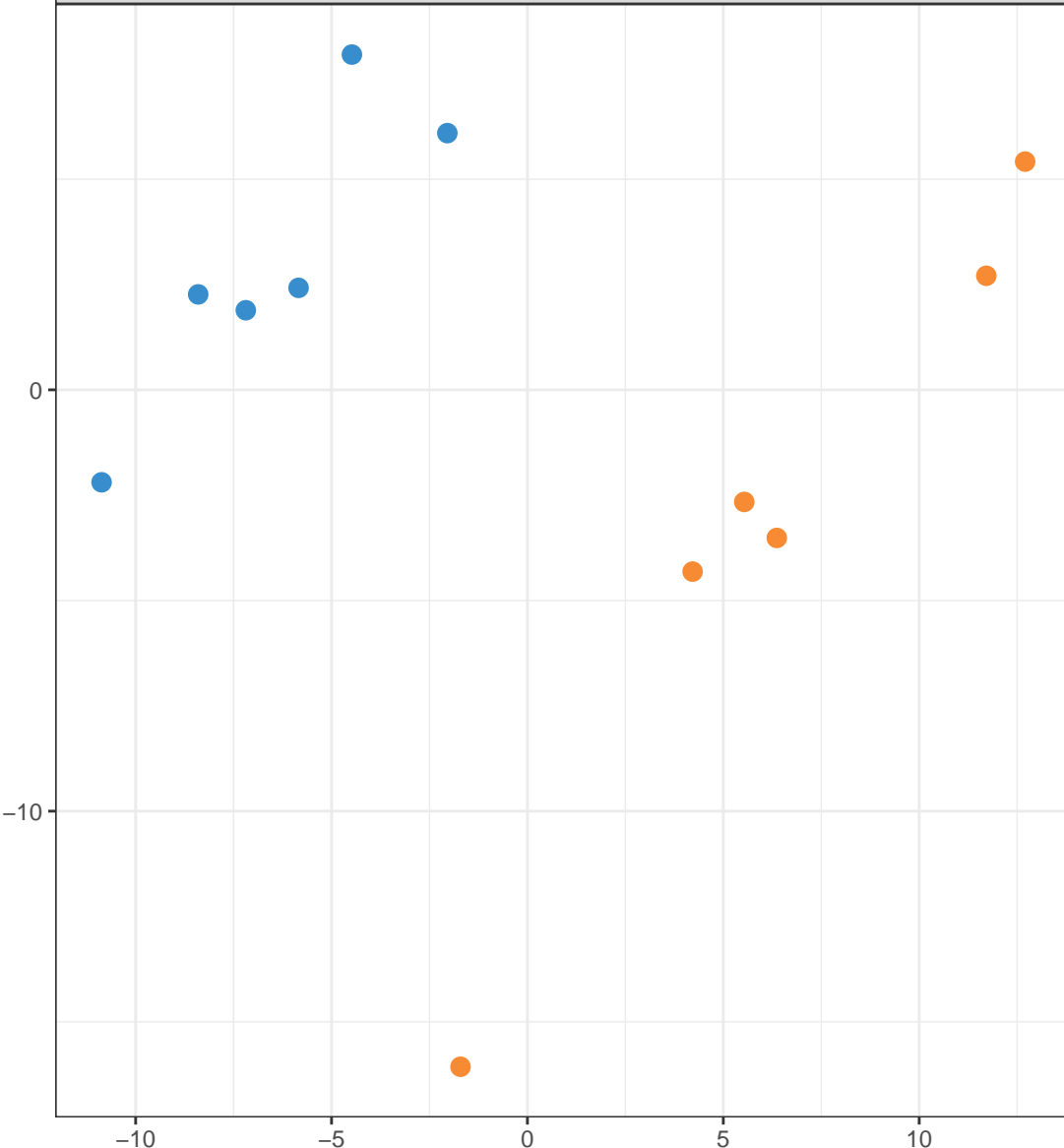
**No Impute n\_PCs = 10  
metabolome PCs (1,2)**

PC2: 19% expl. var

PC1: 29% expl. var

Class

● RPMI  
● Sera



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

PC3: 17% expl. var

-10

-5

0

5

10

-10

0

PC2: 19% expl. var

Class

● RPMI  
● Sera

-10

-5

0

5

10

-10

0

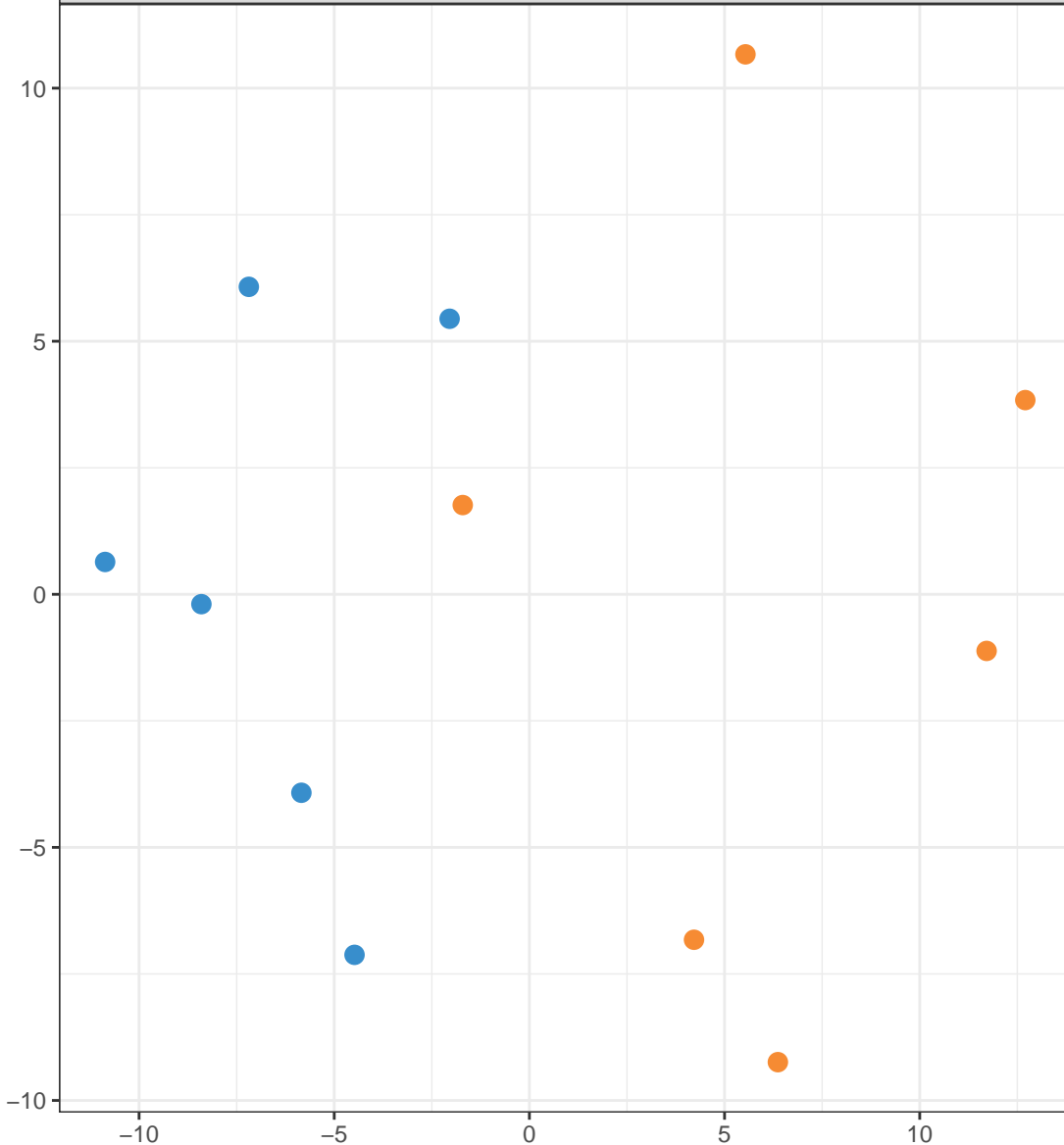
PC2: 19% expl. var

Class

● RPMI  
● Sera

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

PC3: 17% expl. var

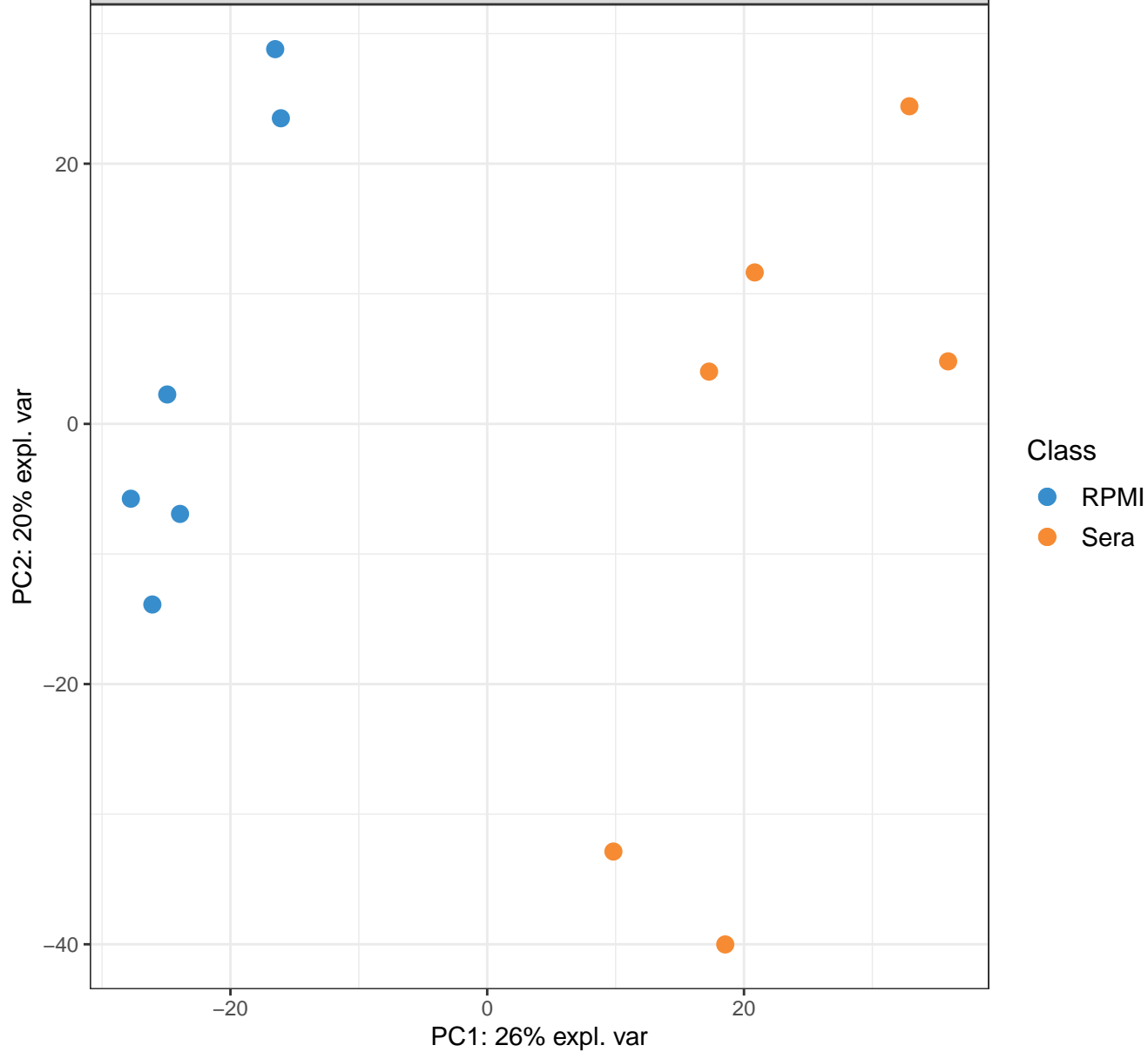


Class

● RPMI  
● Sera

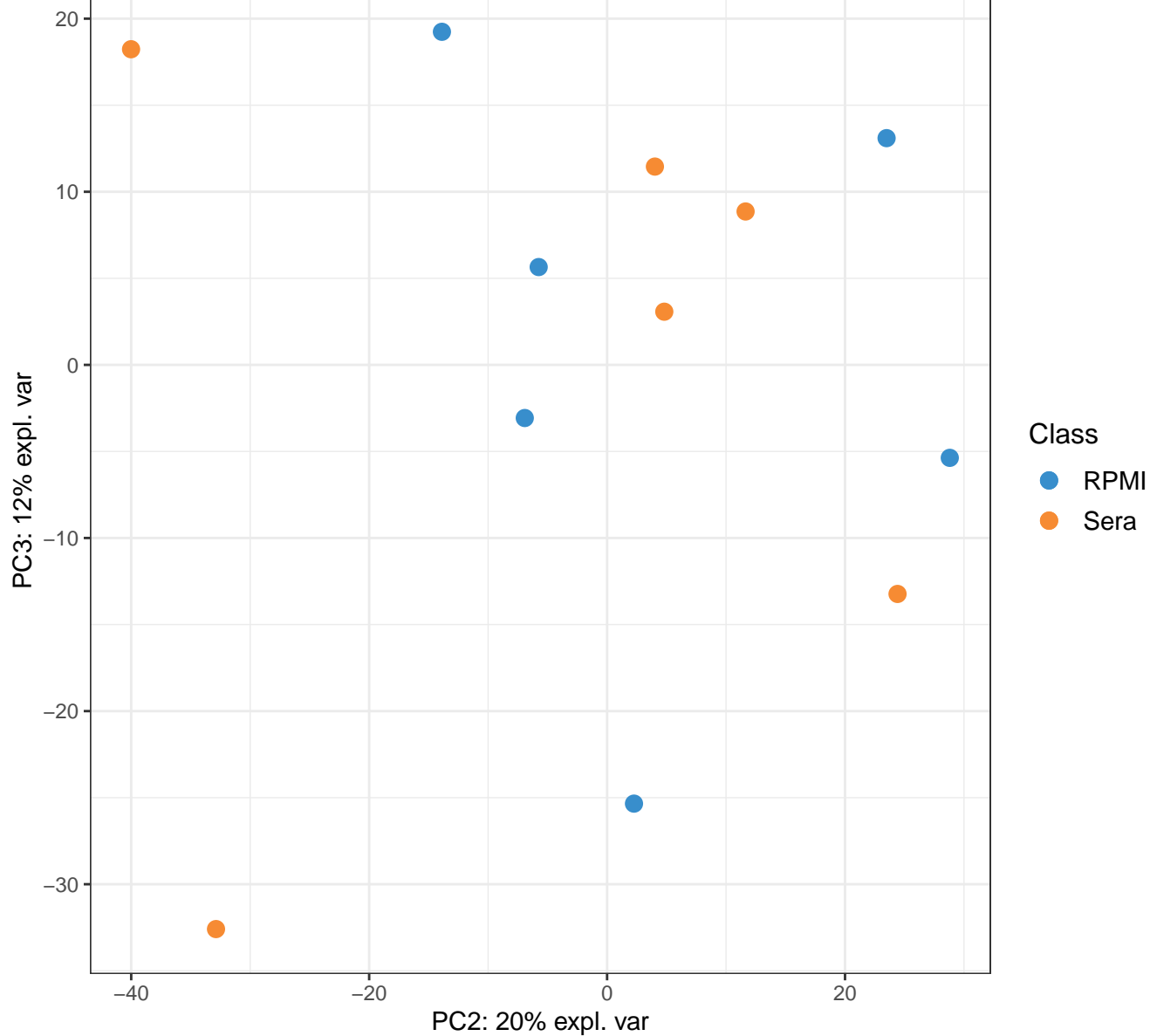
PC1: 29% expl. var

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

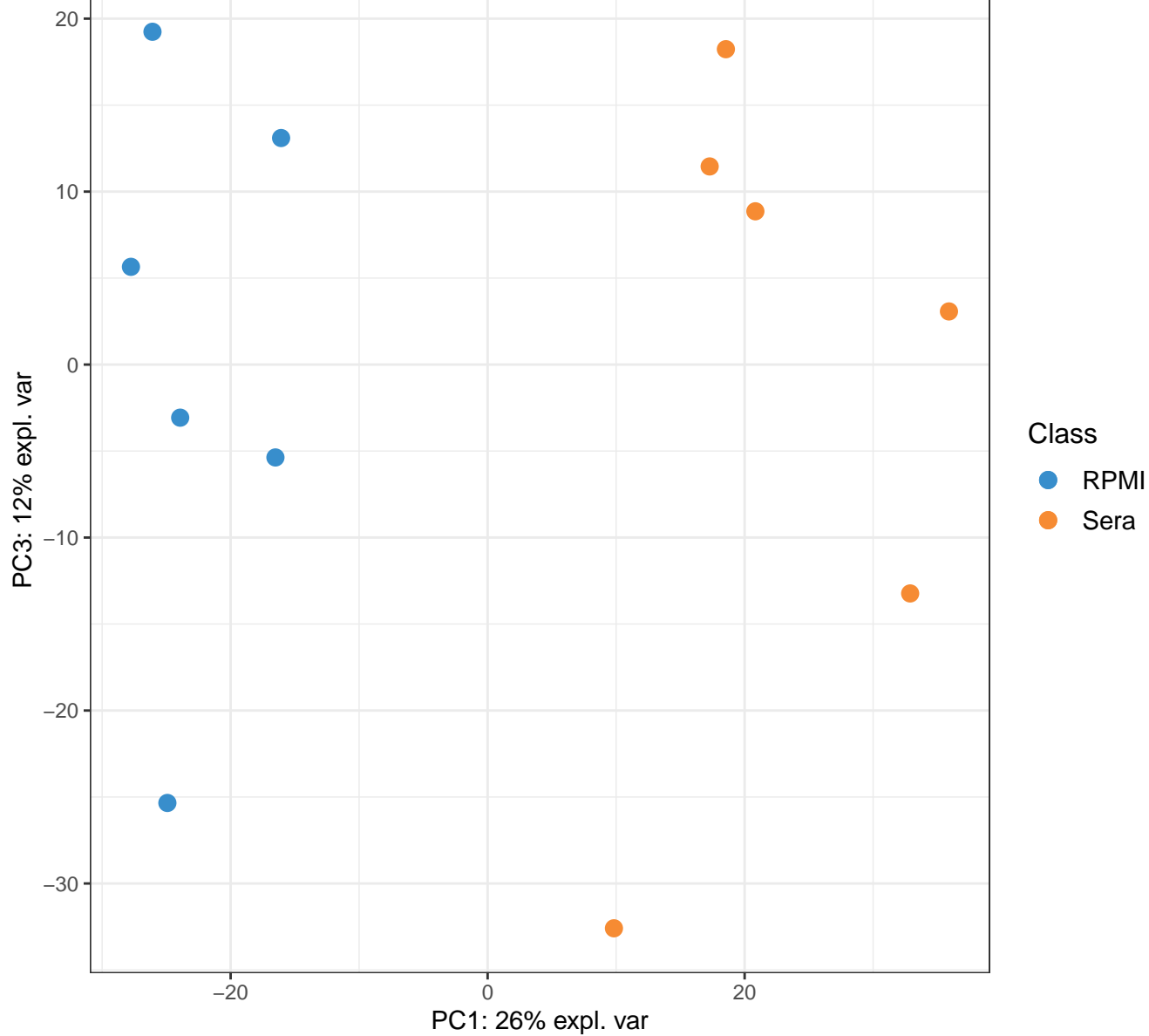




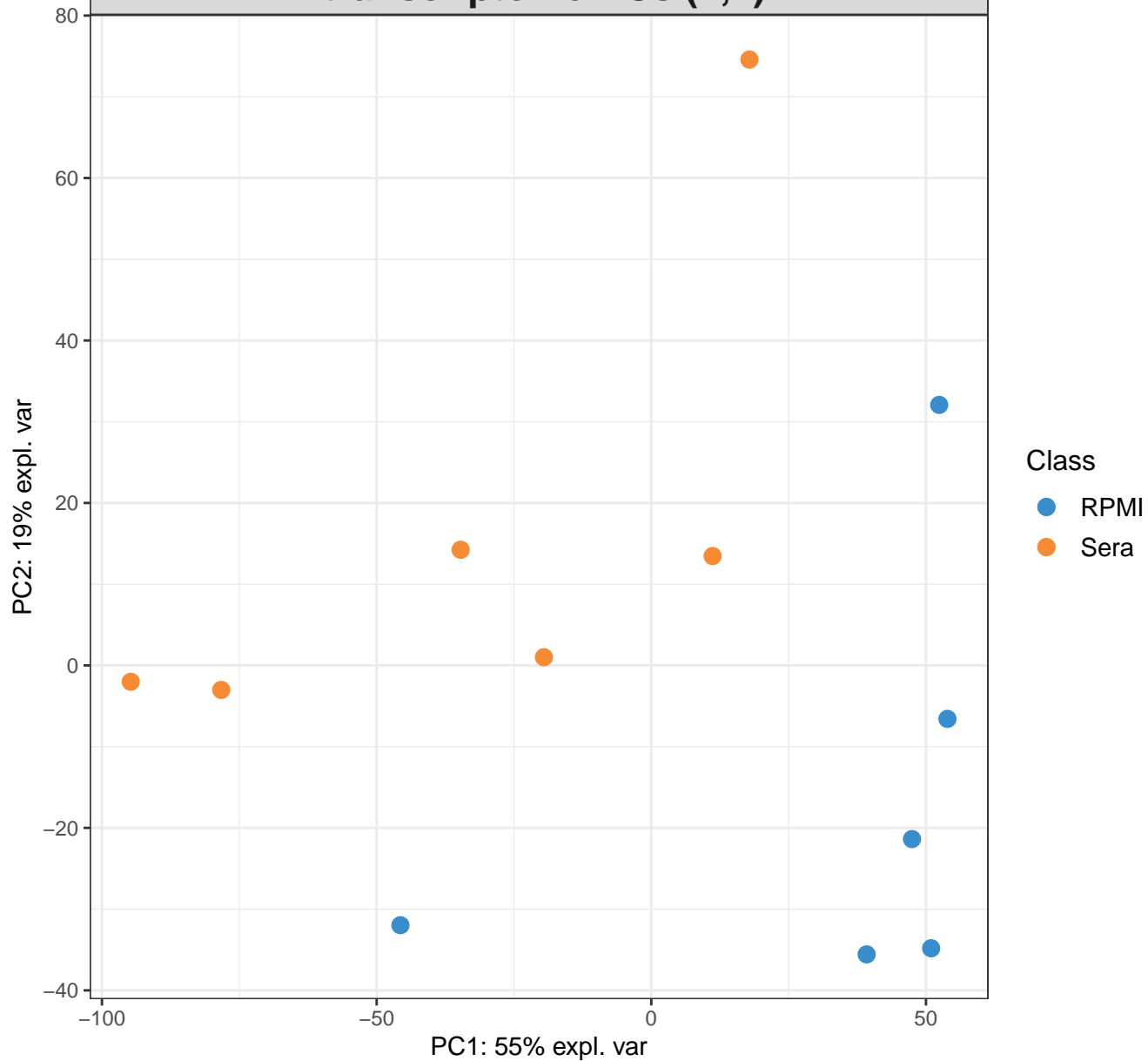
**No Impute n\_PCs = 10  
proteome PCs (2,3)**



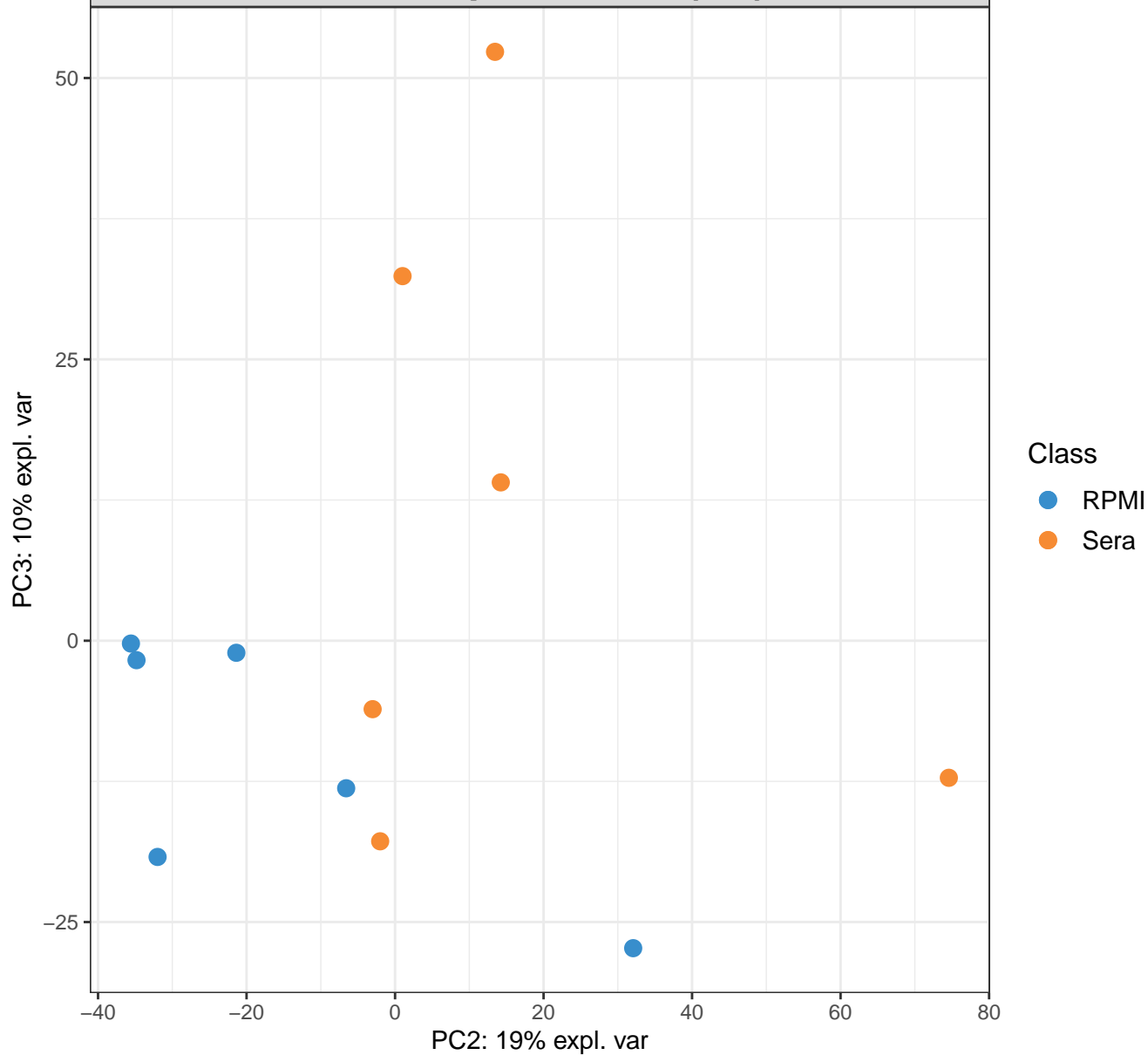
**No Impute n\_PCs = 10  
proteome PCs (1,3)**



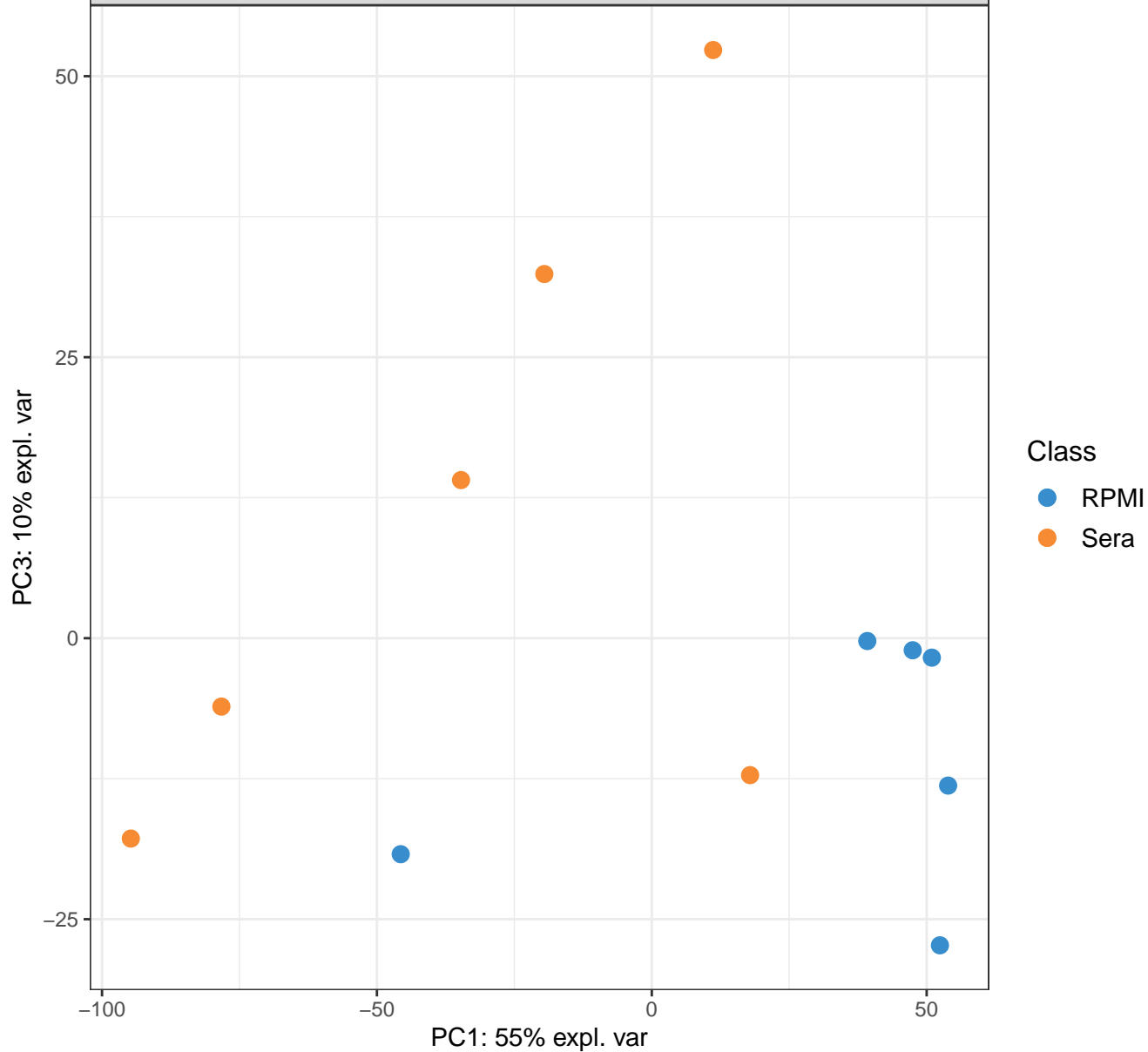
No Impute n\_PCs = 10  
transcriptome PCs (1,2)



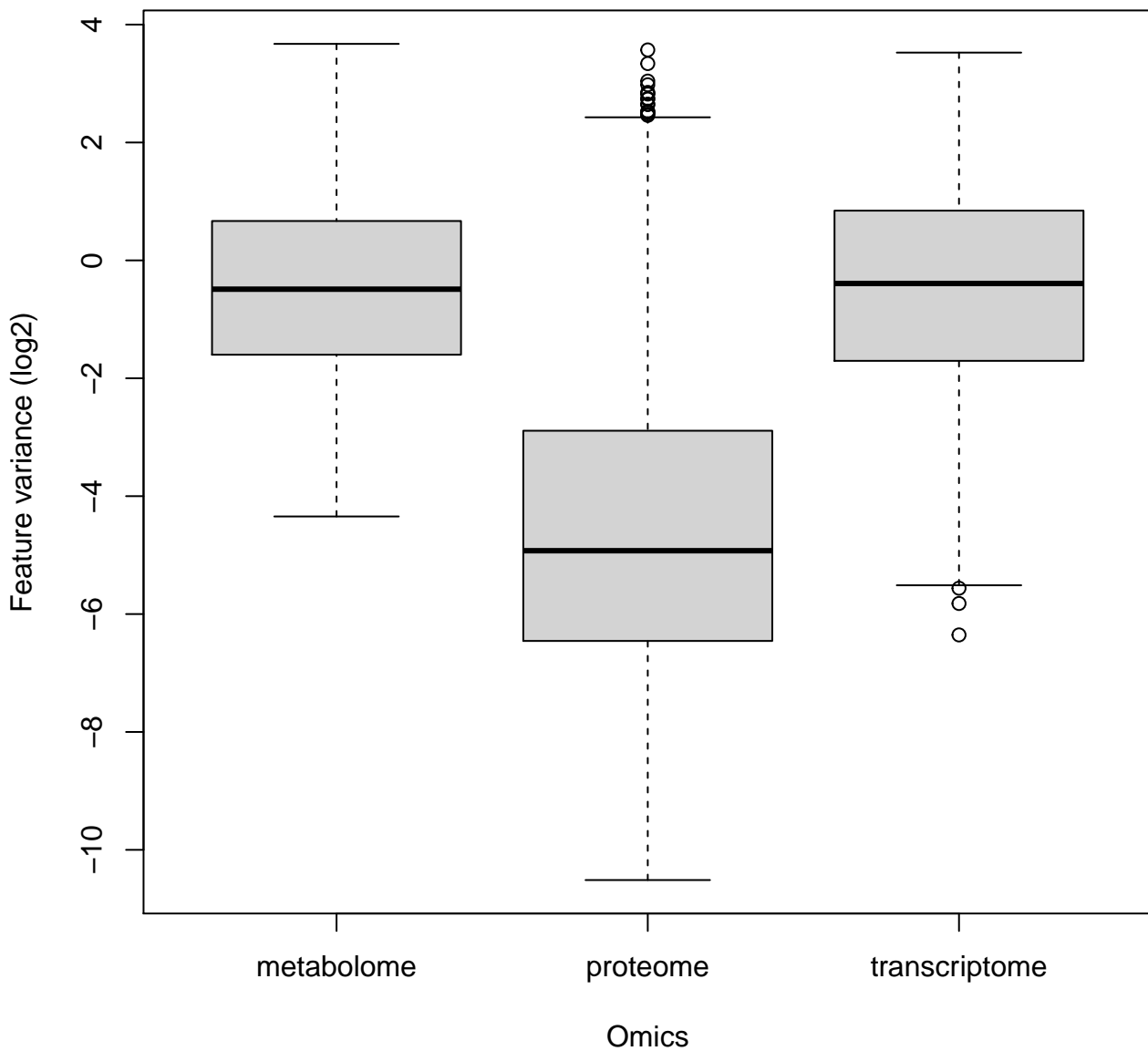
**No Impute n\_PCs = 10  
transcriptome PCs (2,3)**



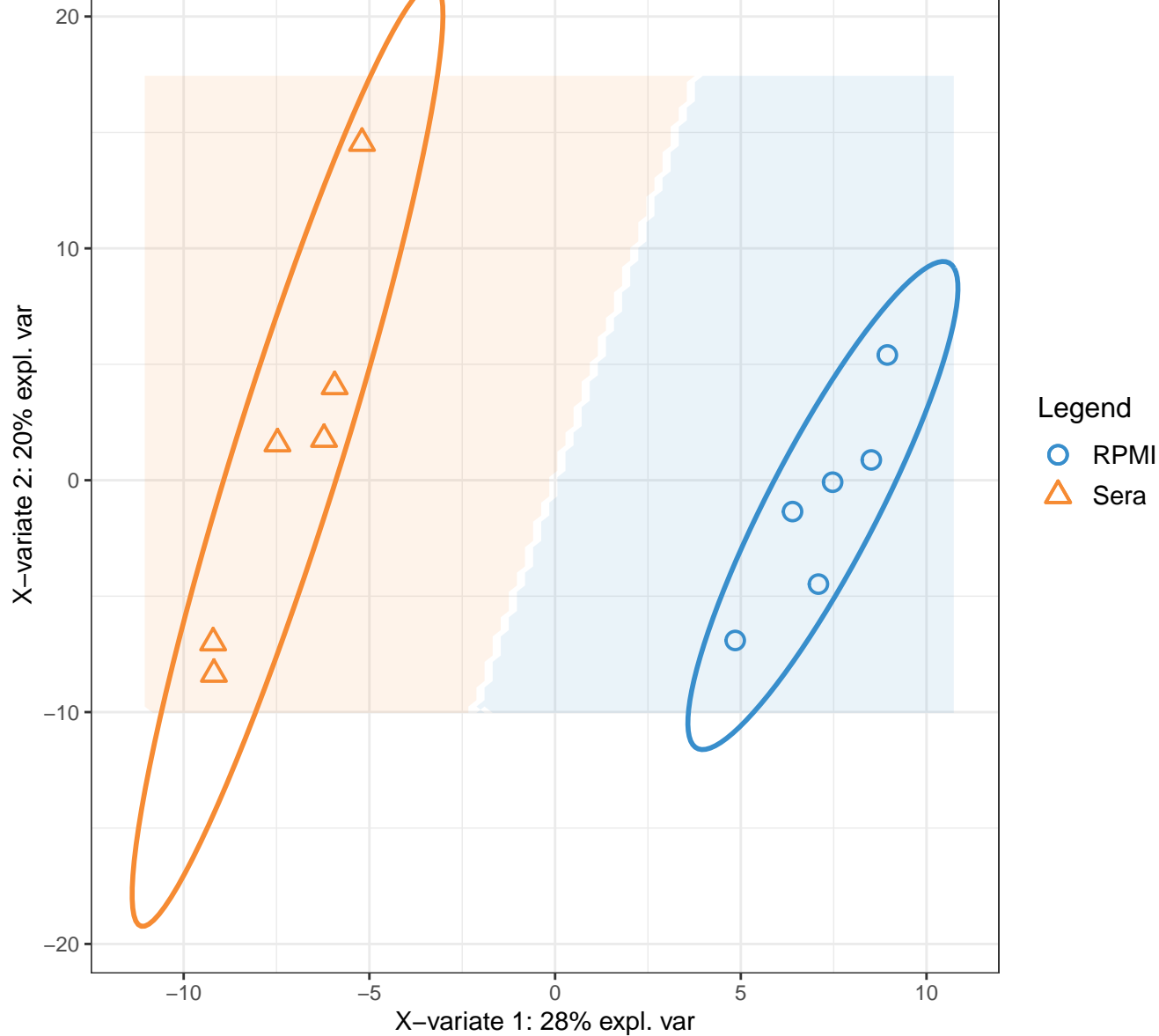
No Impute n\_PCs = 10  
transcriptome PCs (1,3)



**Feature variances (log2) per omics**



# metabolome PLSDA single 1/2



# metabolome PLSDA single 1/2

X-variate 2: 20% expl. var

X-variate 1: 28% expl. var

Legend

- RPMI
- △ Sera

20  
10  
0  
-10  
-20

-10

-5

0

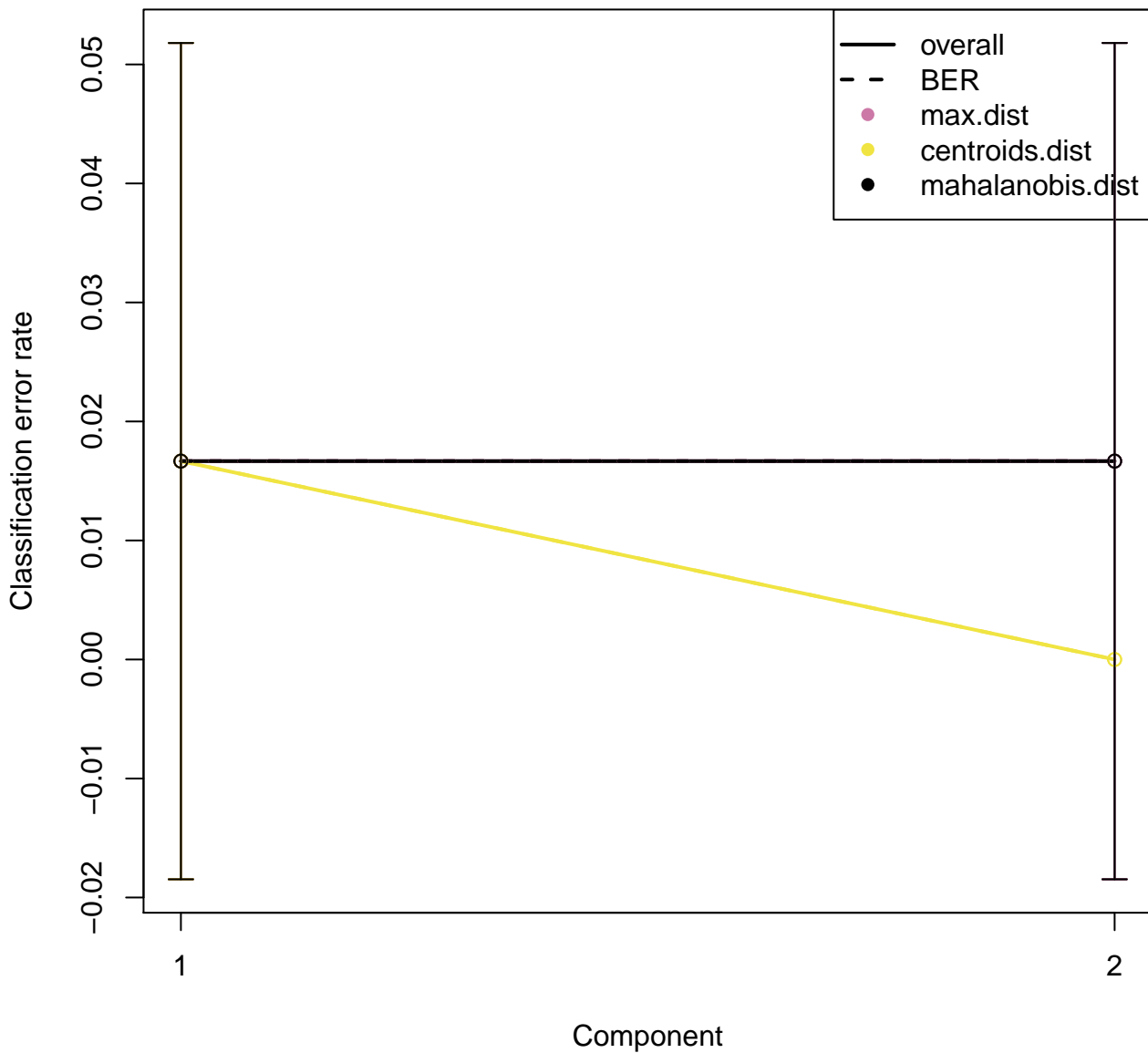
5

10

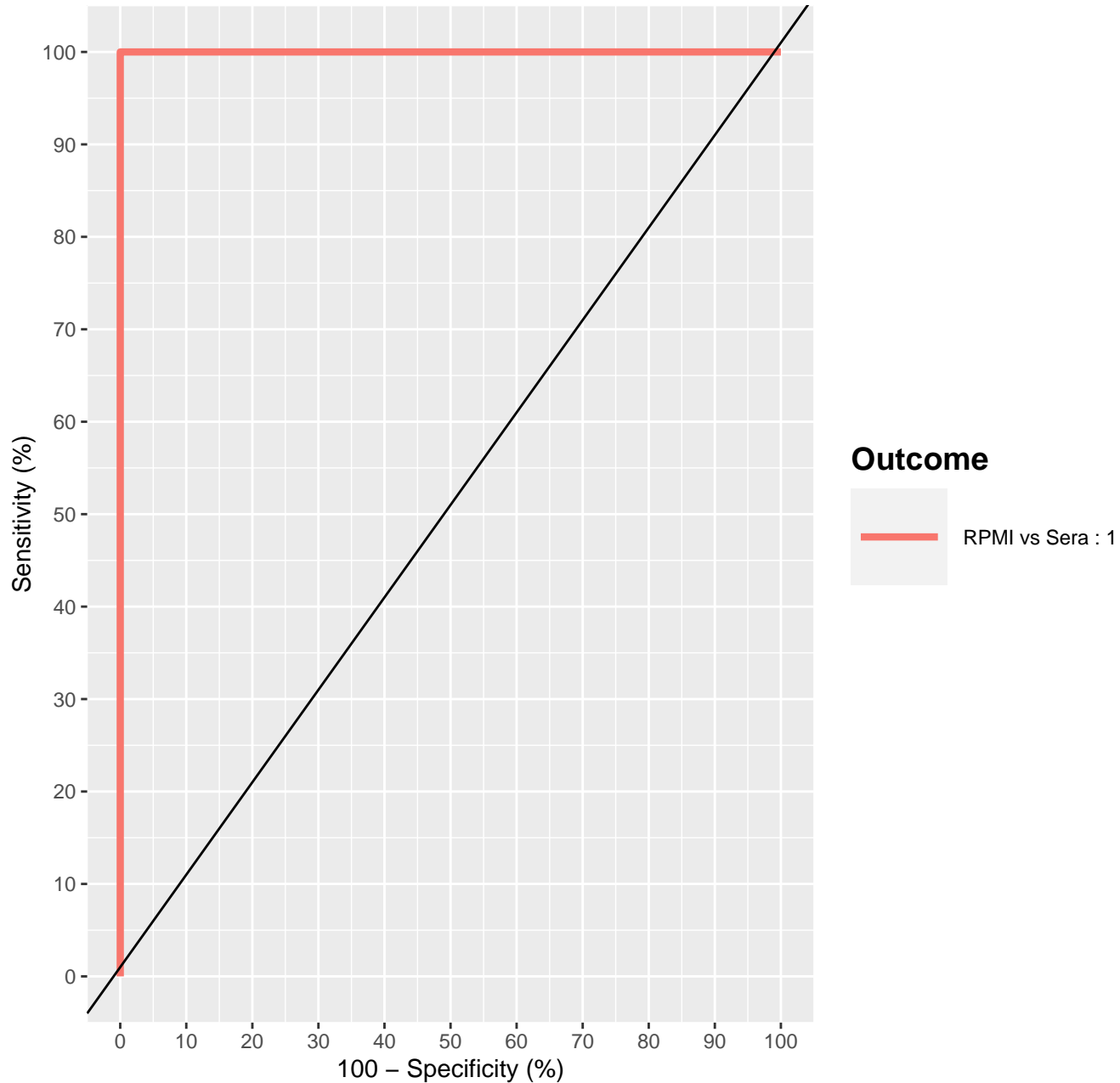
- RPMI
- △ Sera

20  
10  
0  
-10  
-20

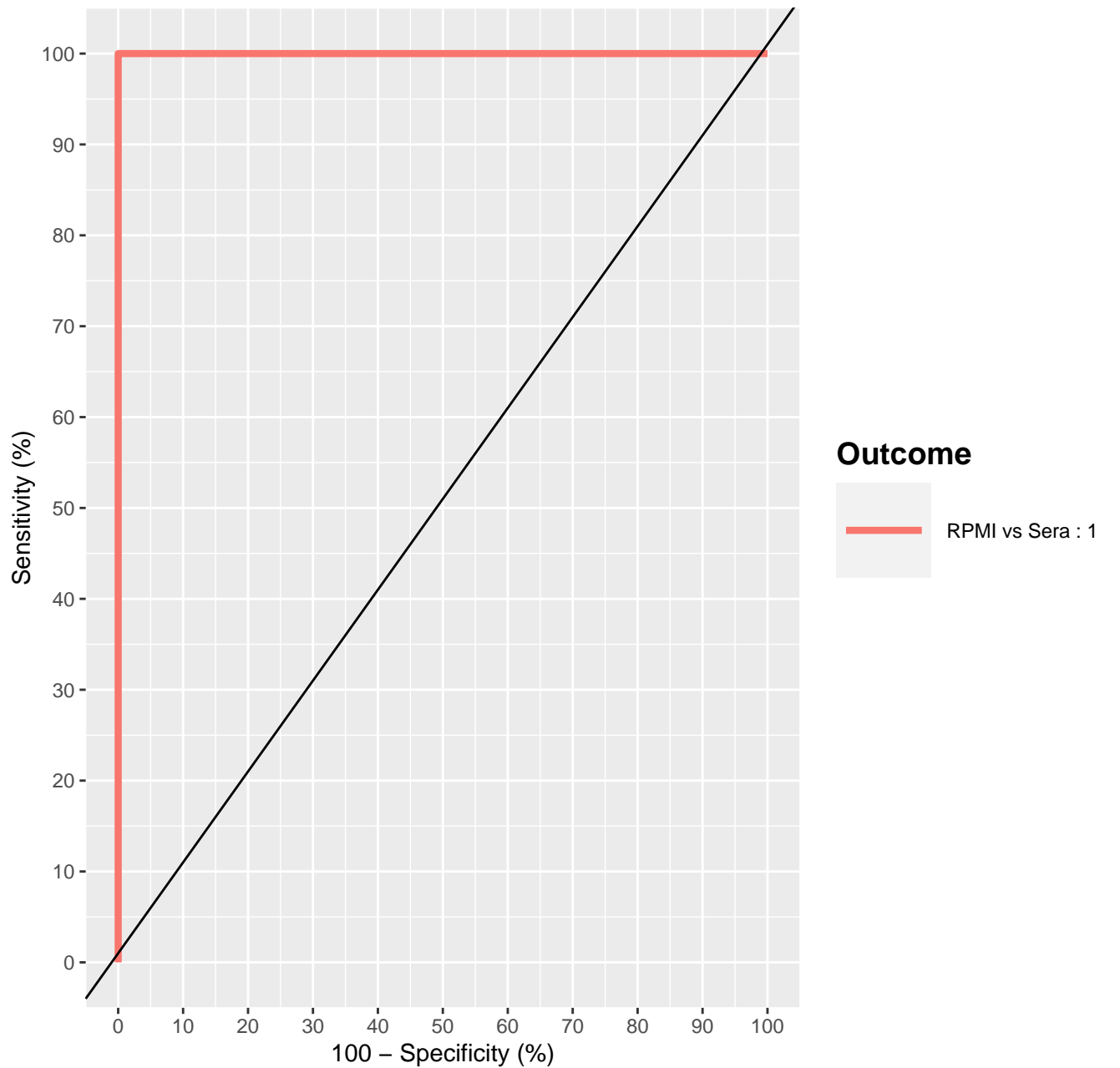




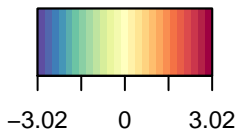
**ROC Curve Using Comp(s): 1**



ROC Curve Using Comp(s): 1, 2



Color key

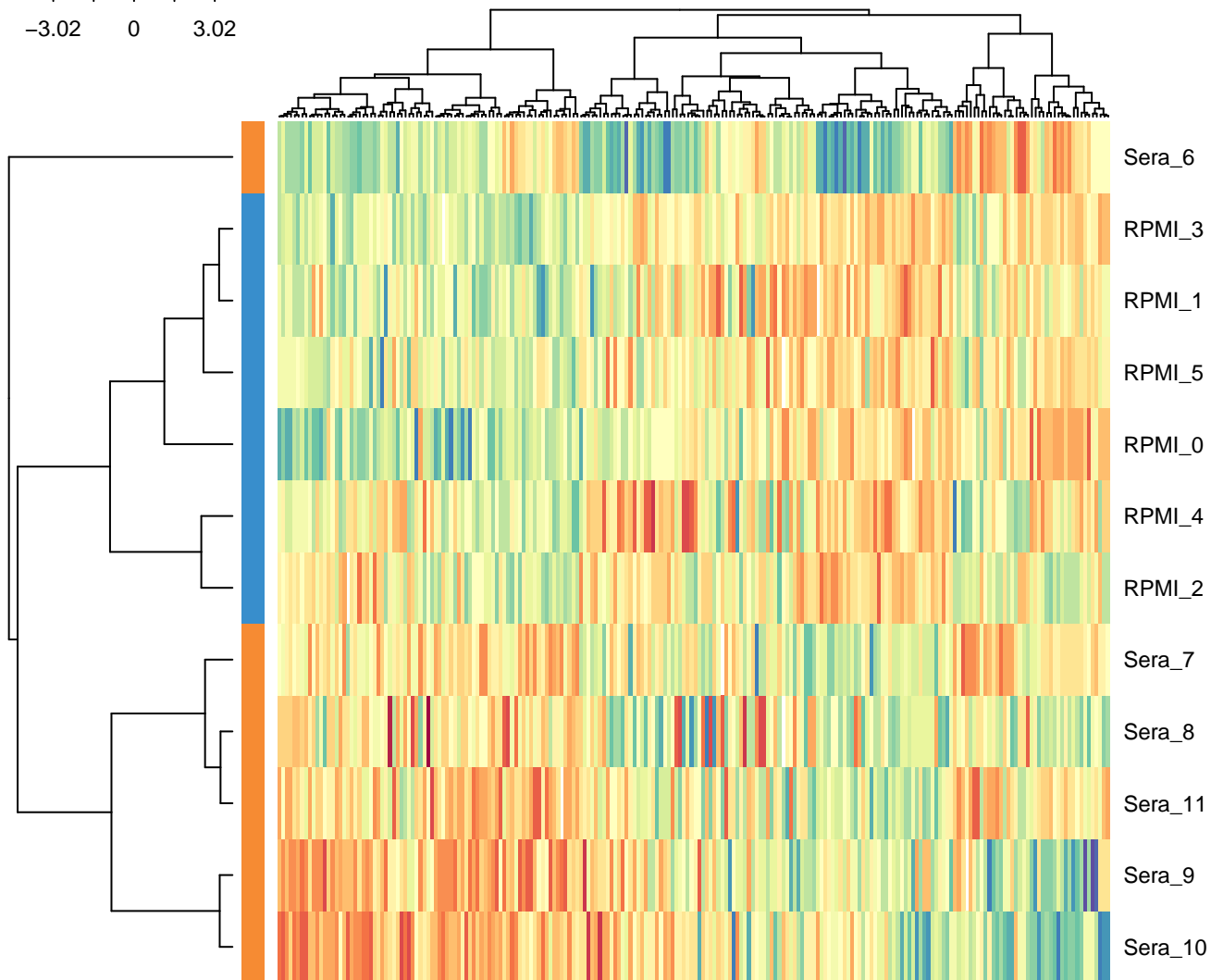


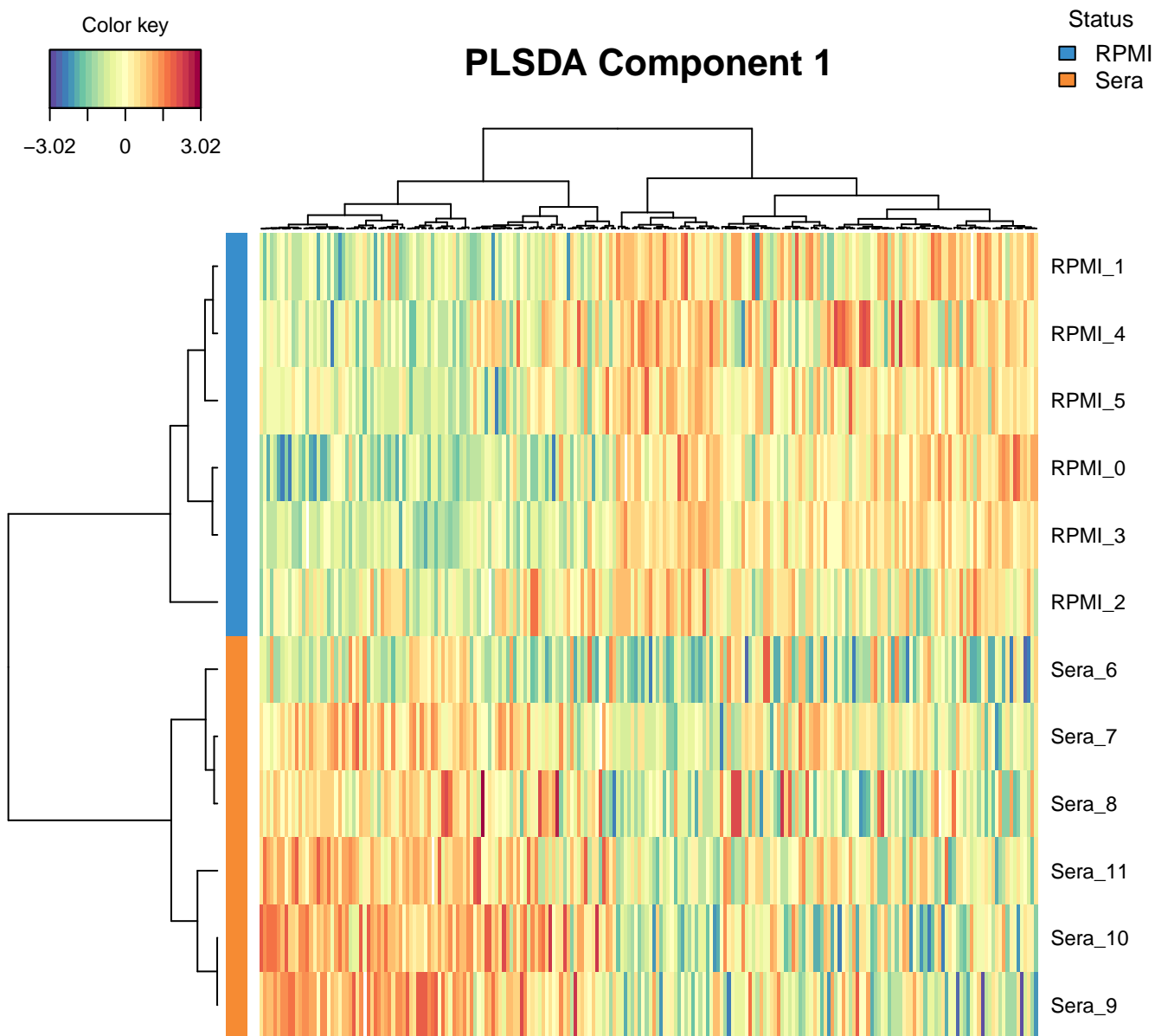
PLSDA

Status

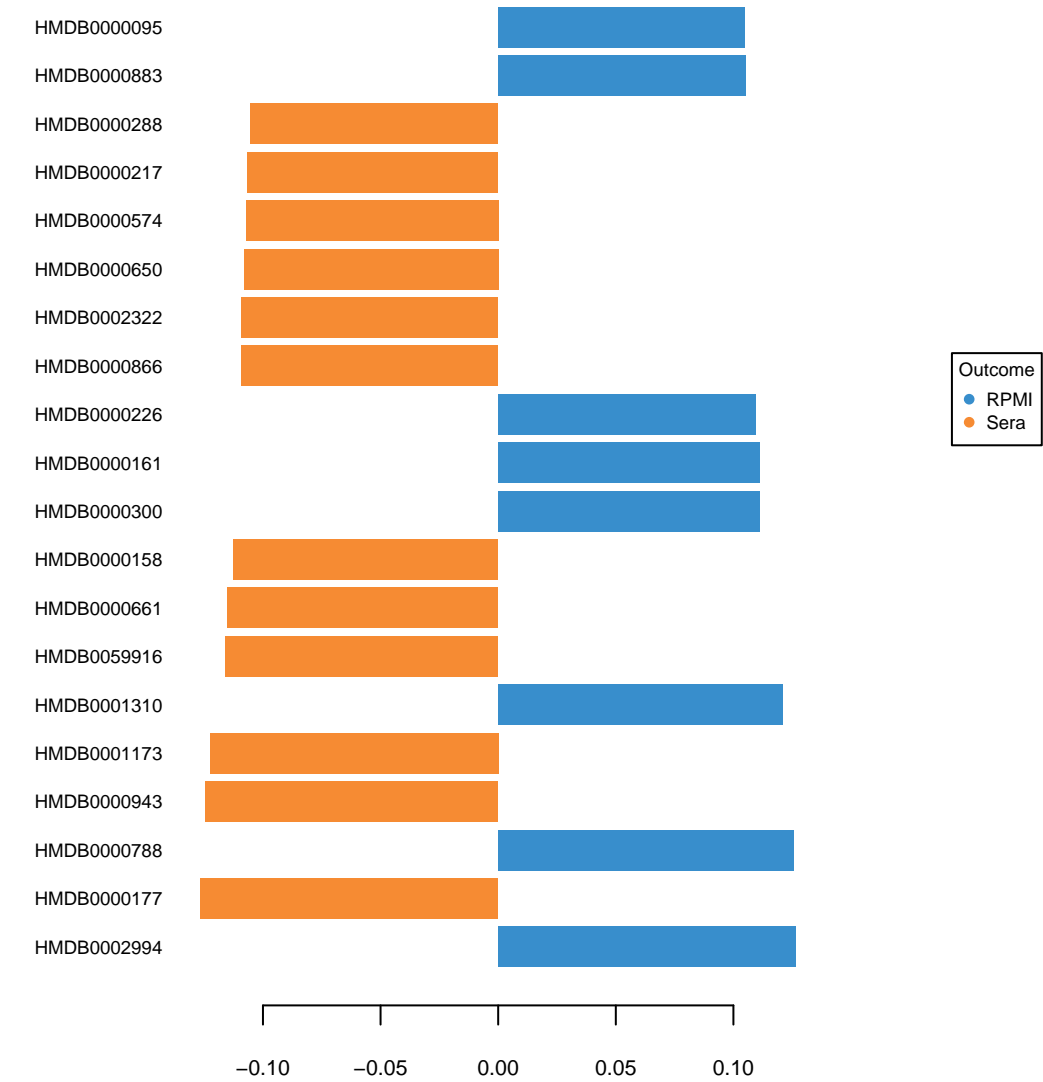
RPMI

Sera

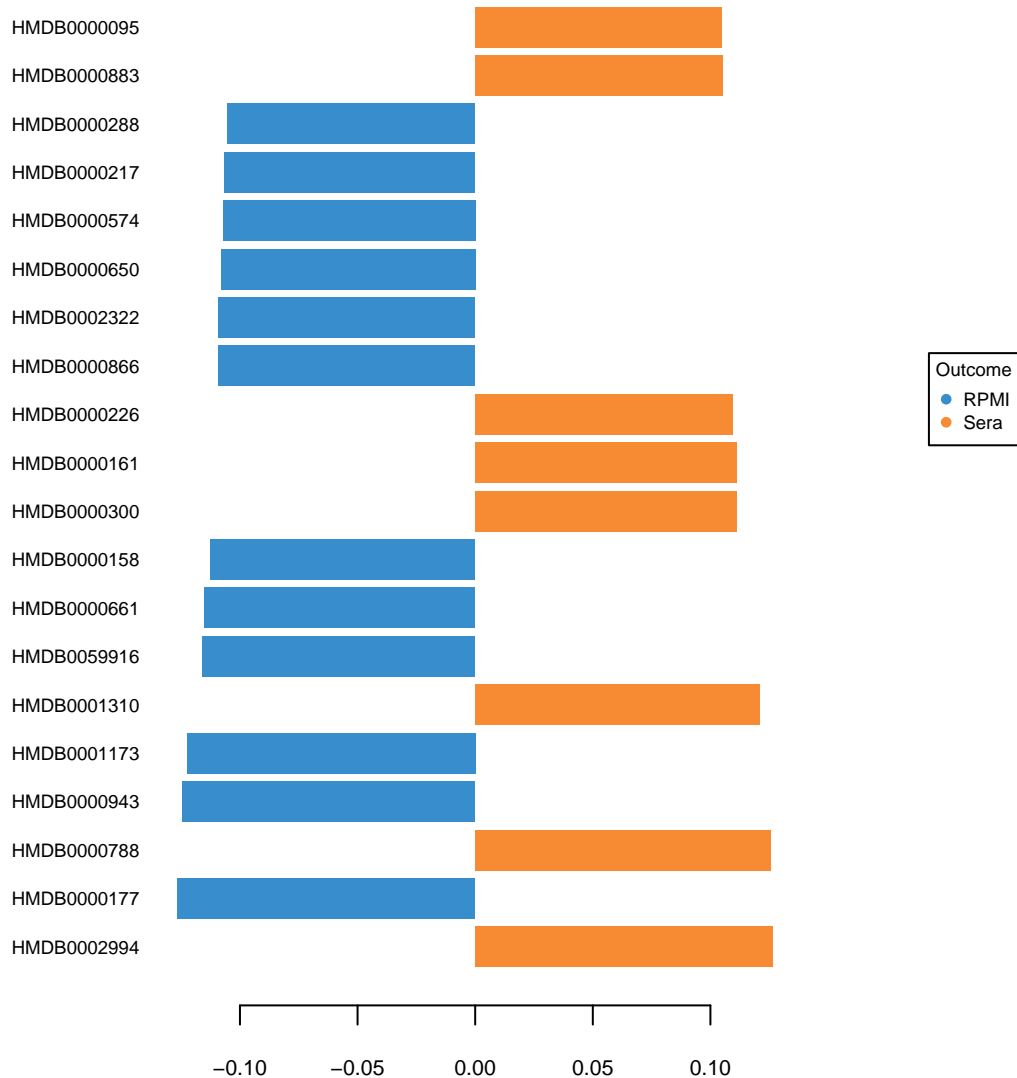




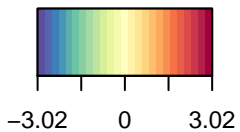
# metabolome 1 PLSDA max load



# metabolome 1 PLSDA min load



Color key

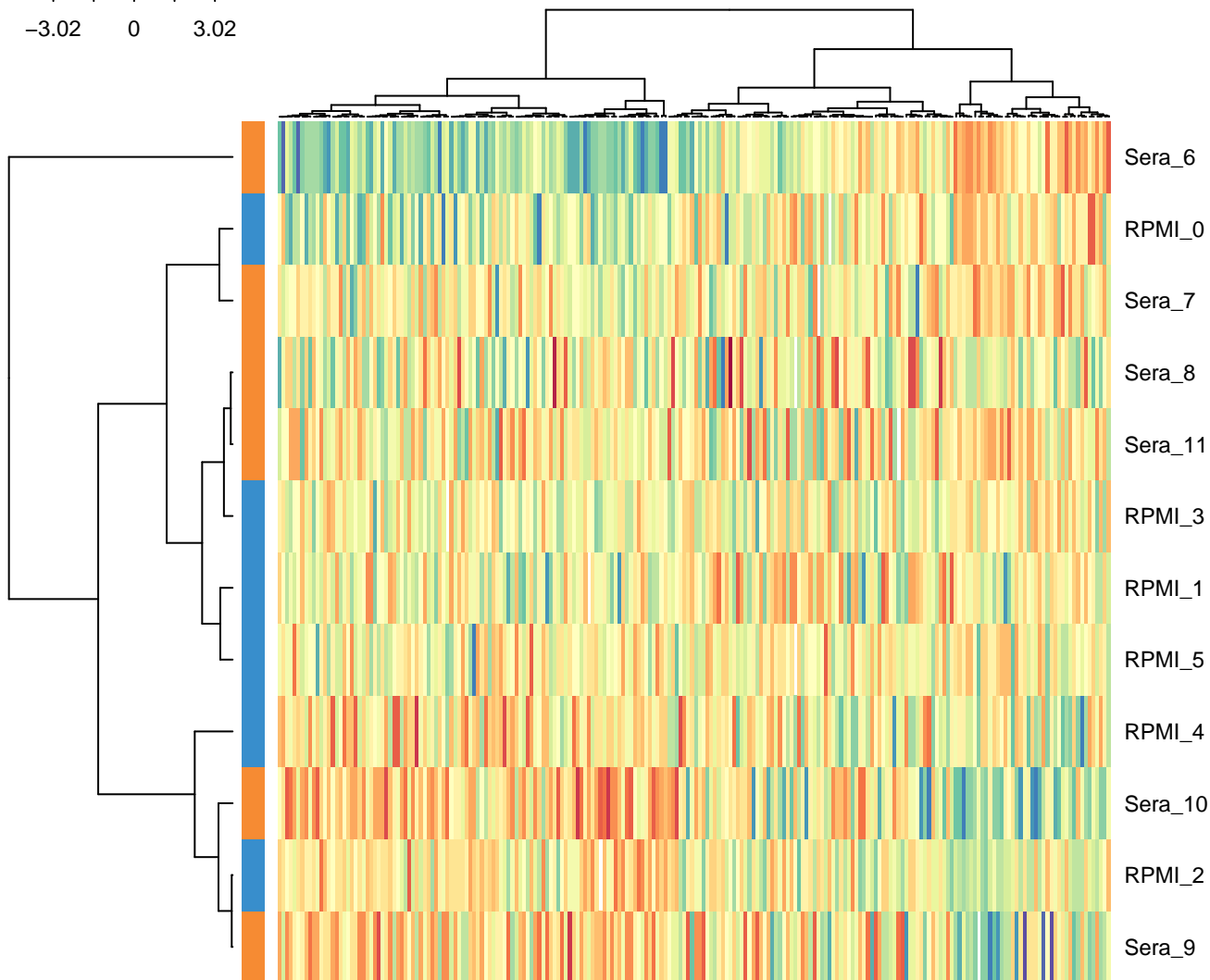


## PLSDA Component 2

Status

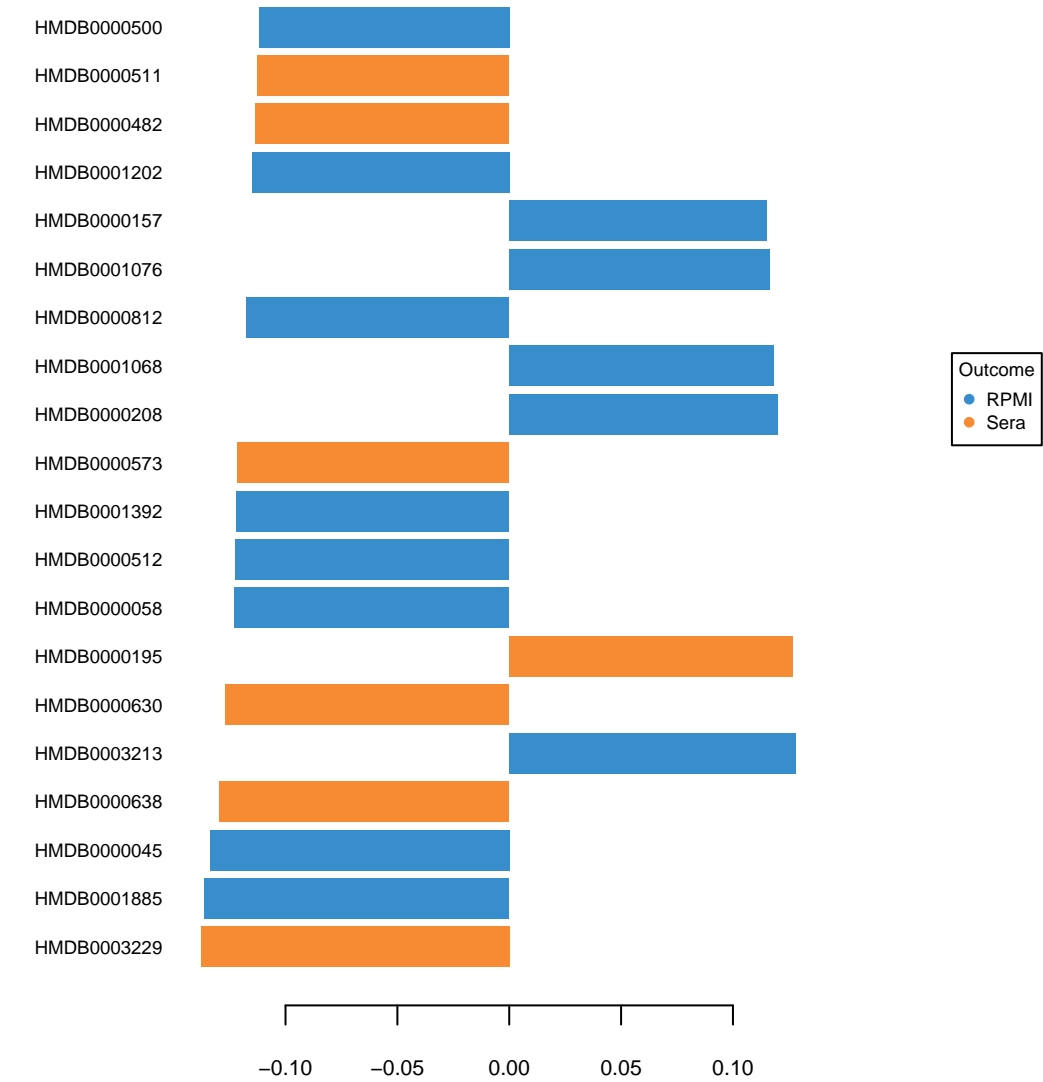
RPMI

Sera

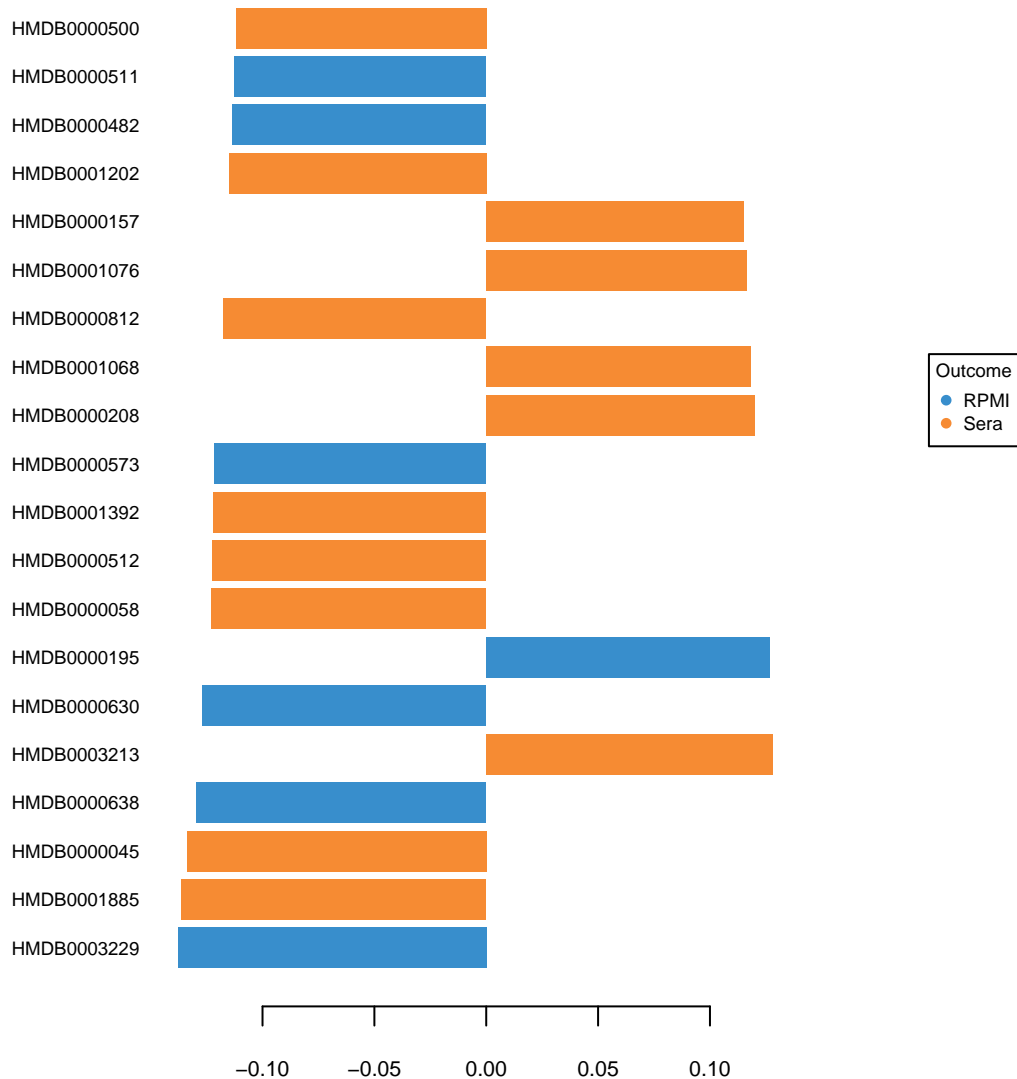




# metabolome 2 PLSDA max load



# metabolome 2 PLSDA min load



# proteome PLSDA single 1/2

X-variate 2: 14% expl. var

30

0

-30

-20

0

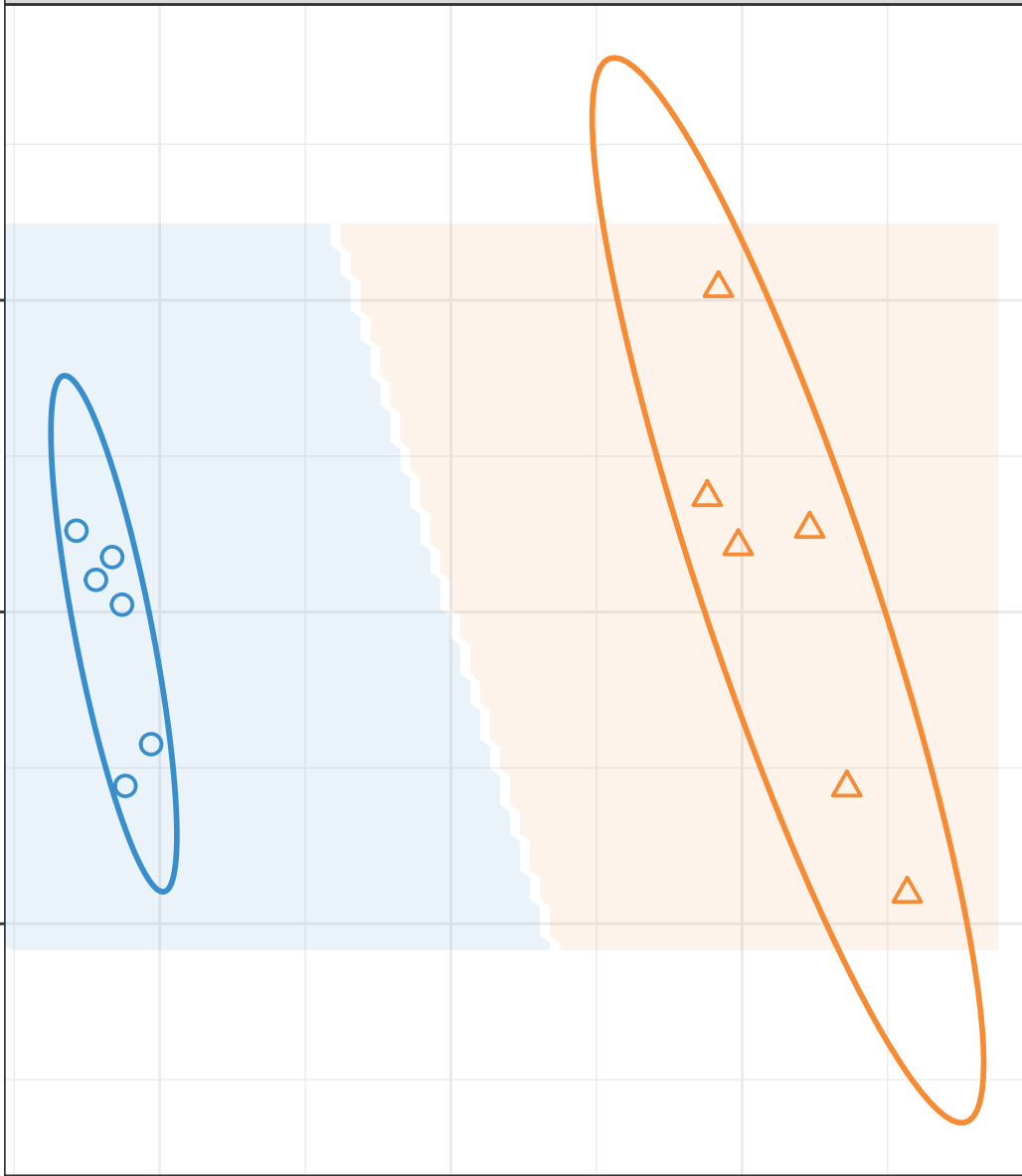
20

X-variate 1: 26% expl. var

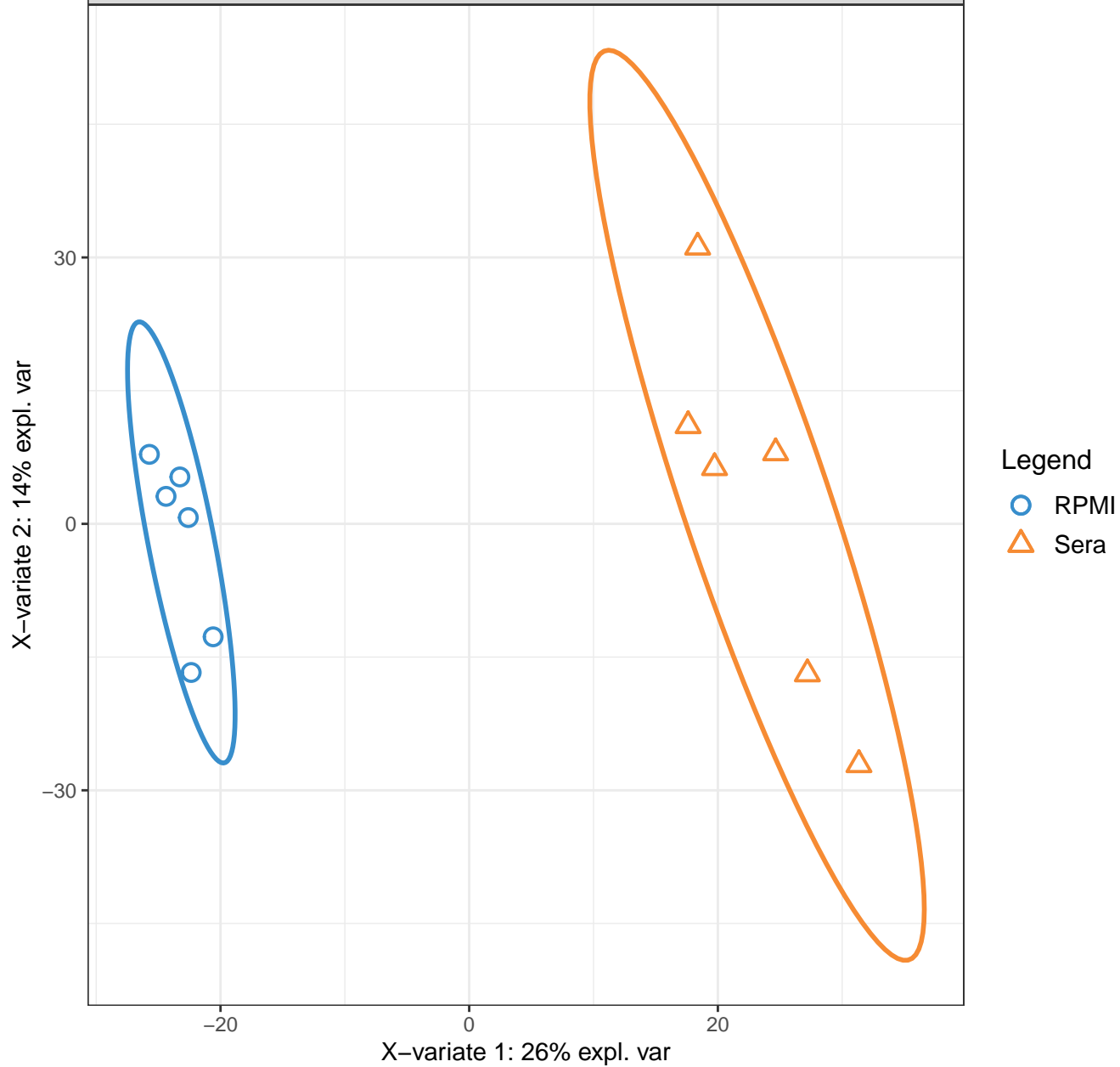
Legend

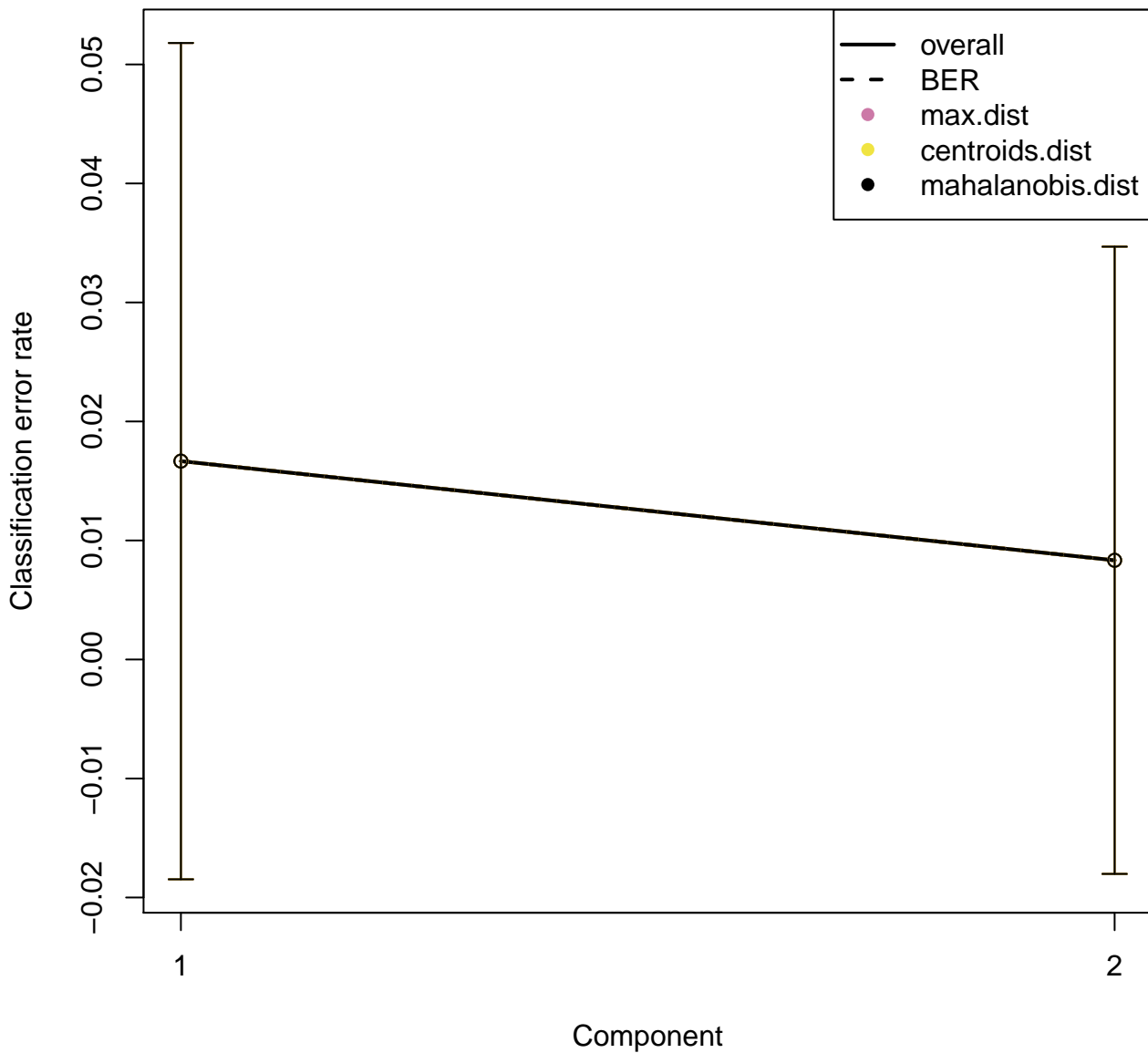
○ RPMI

△ Sera

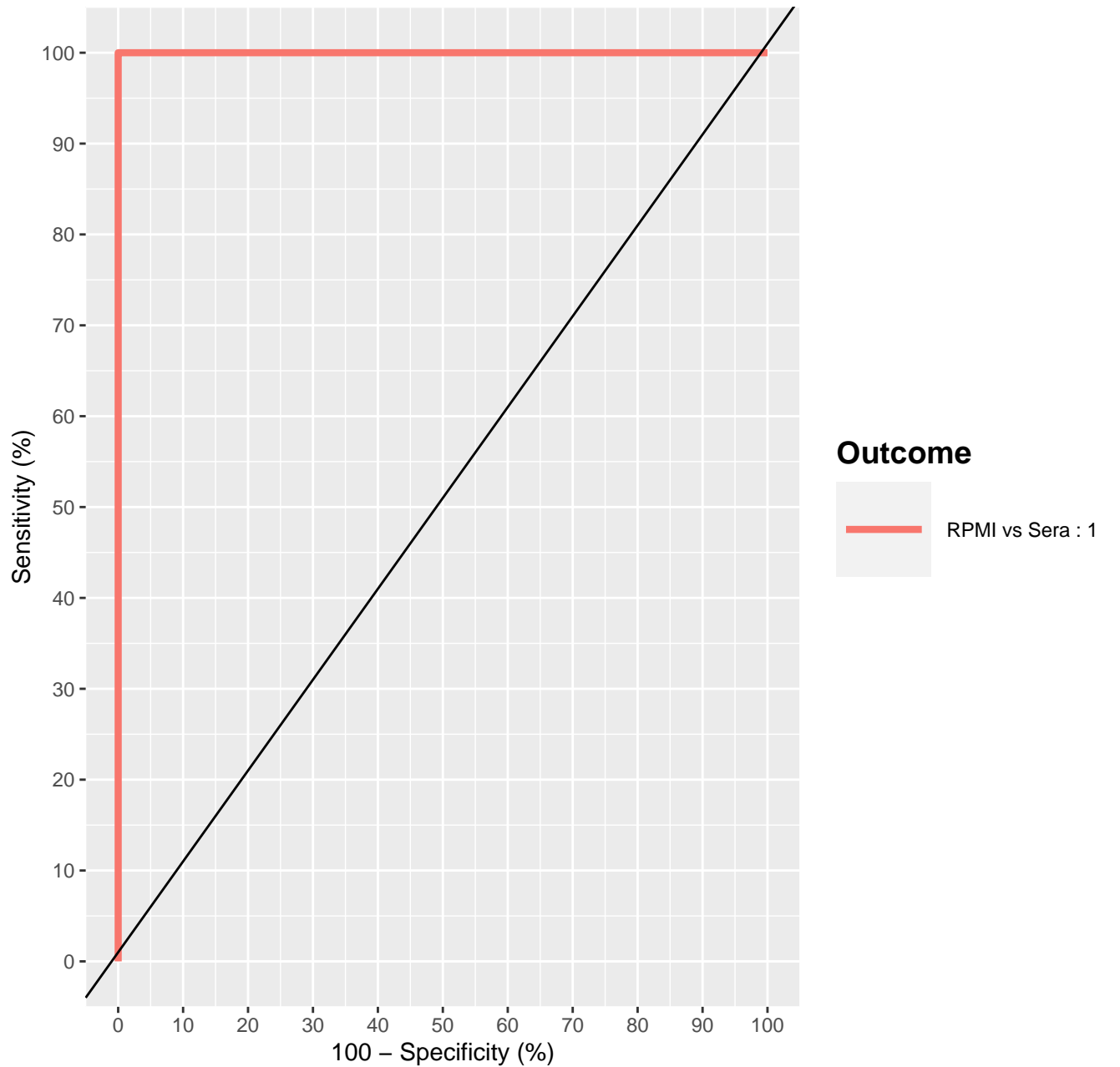


# proteome PLSDA single 1/2

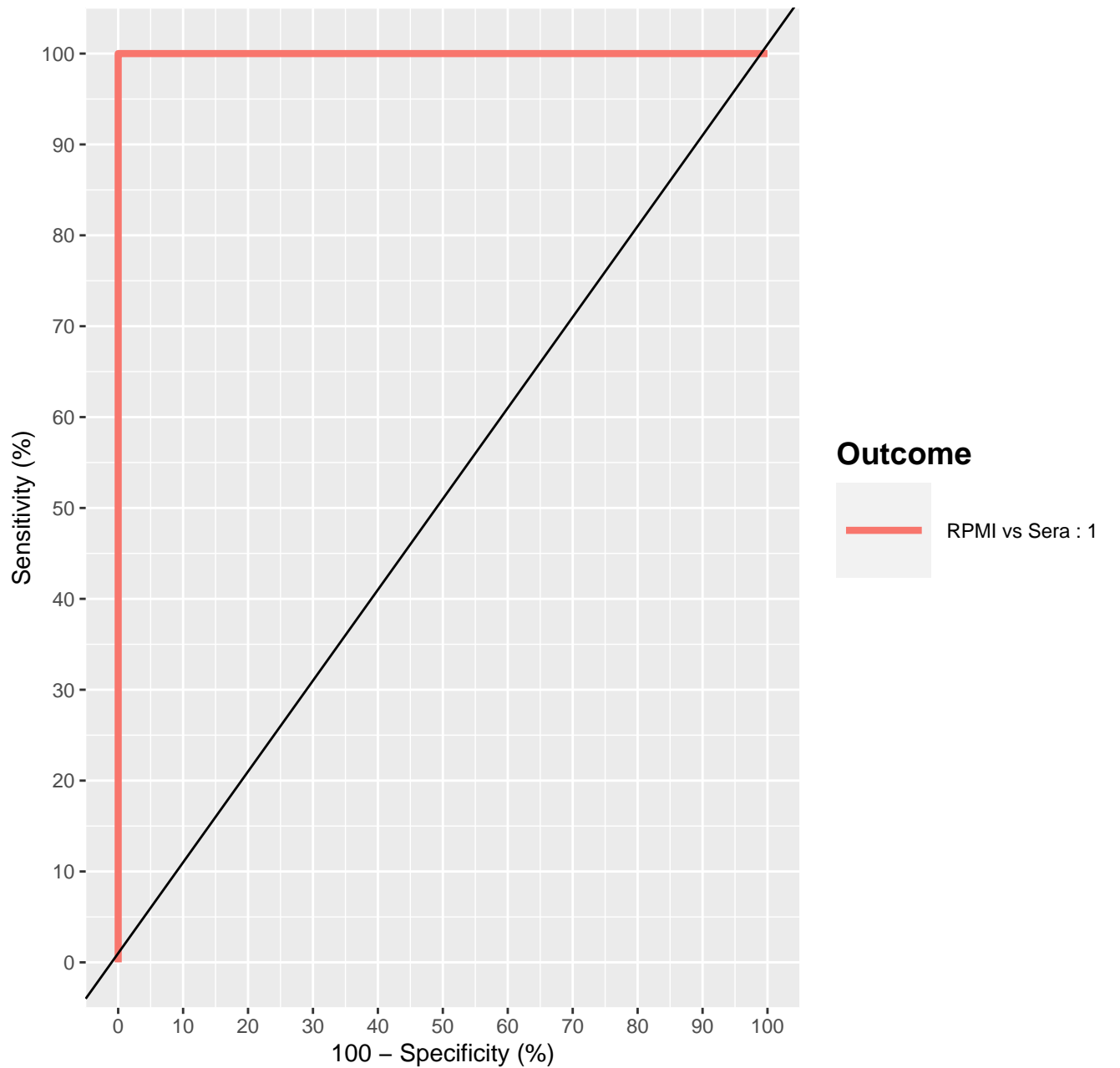




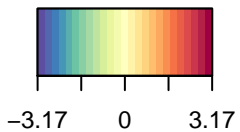
**ROC Curve Using Comp(s): 1**



ROC Curve Using Comp(s): 1, 2



Color key

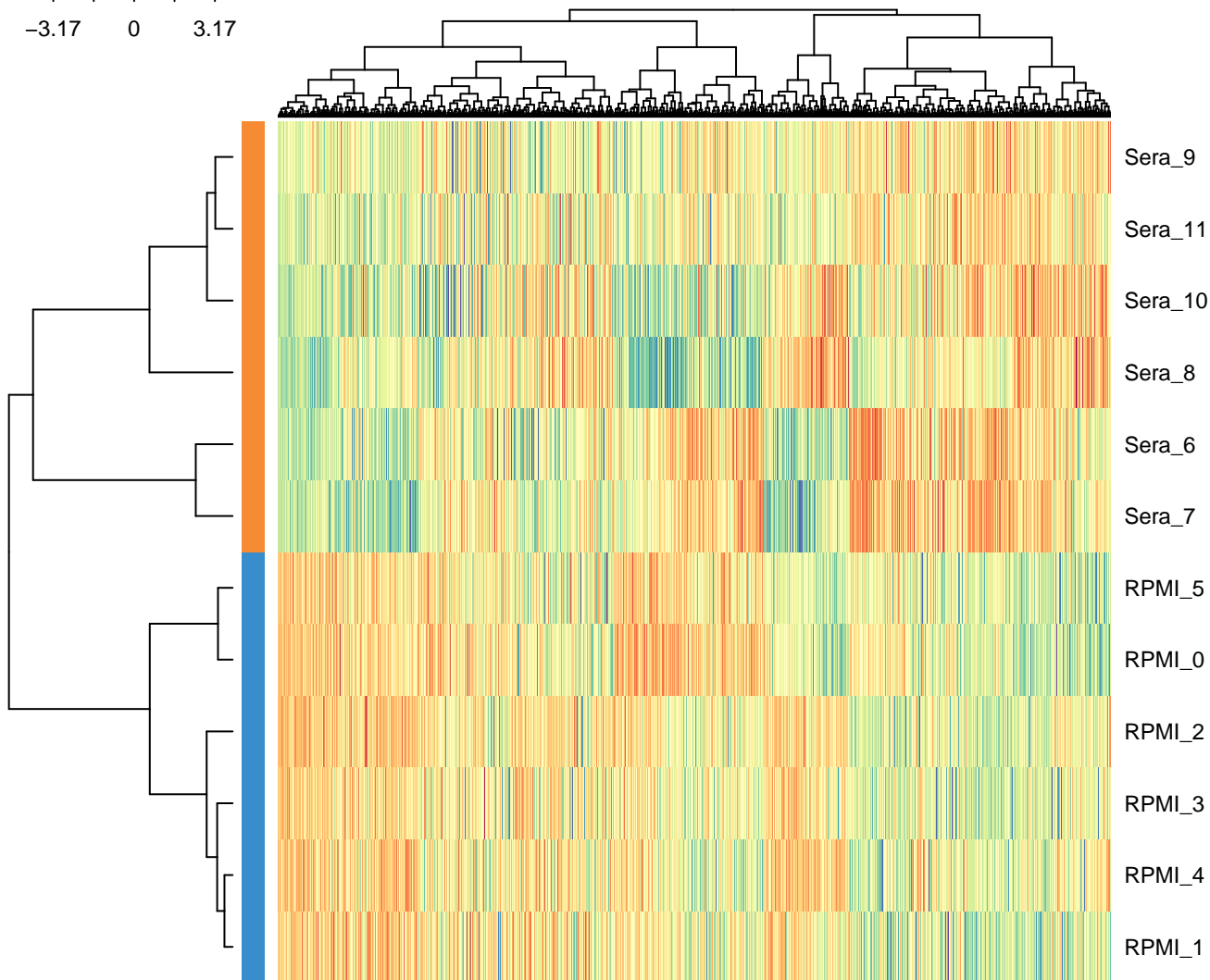


# PLSDA

Status

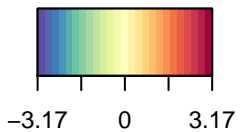
■ RPMI

■ Sera





Color key

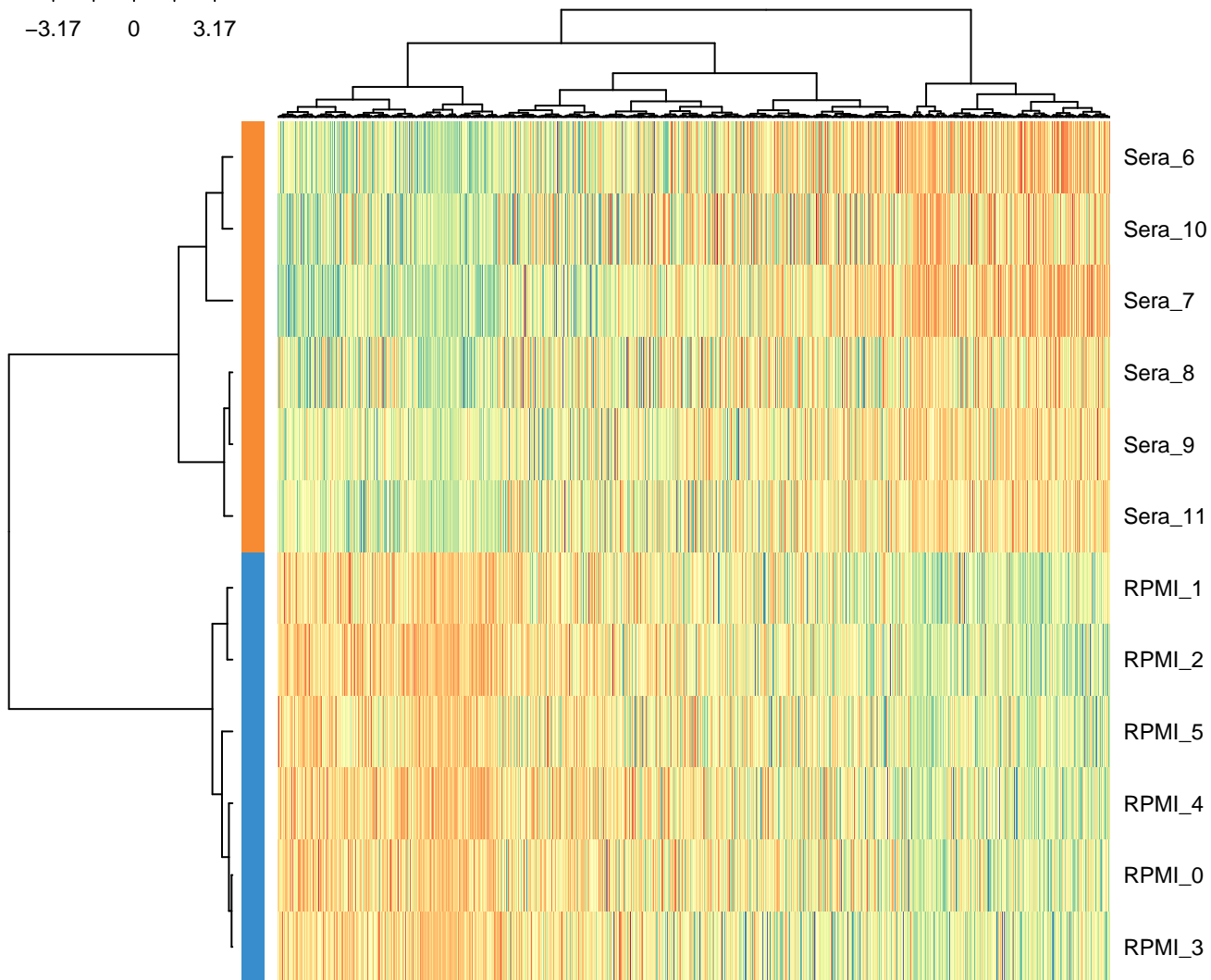


# PLSDA Component 1

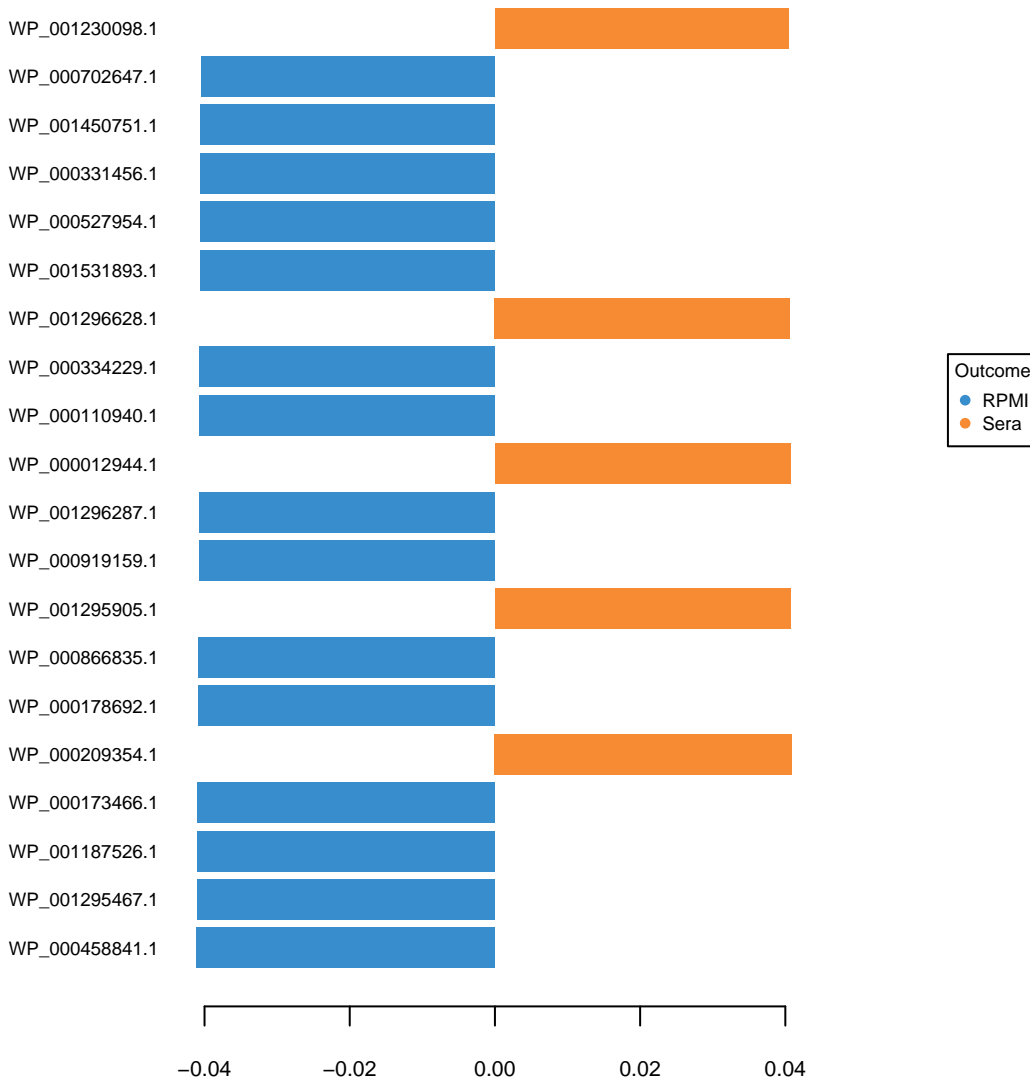
Status

RPMI

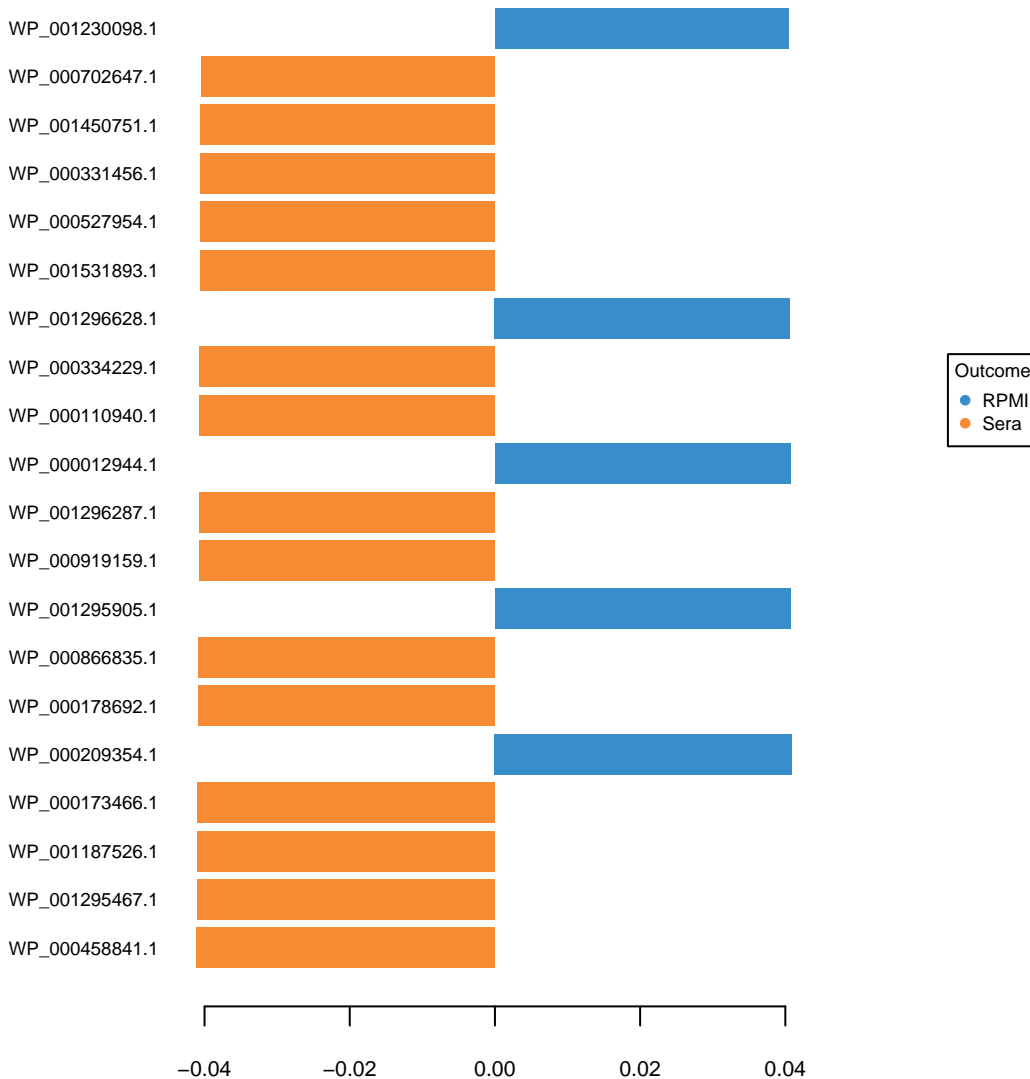
Sera



# proteome 1 PLSDA max loadir

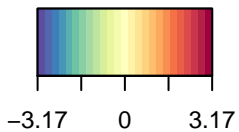


# proteome 1 PLSDA min loadin



# PLSDA Component 2

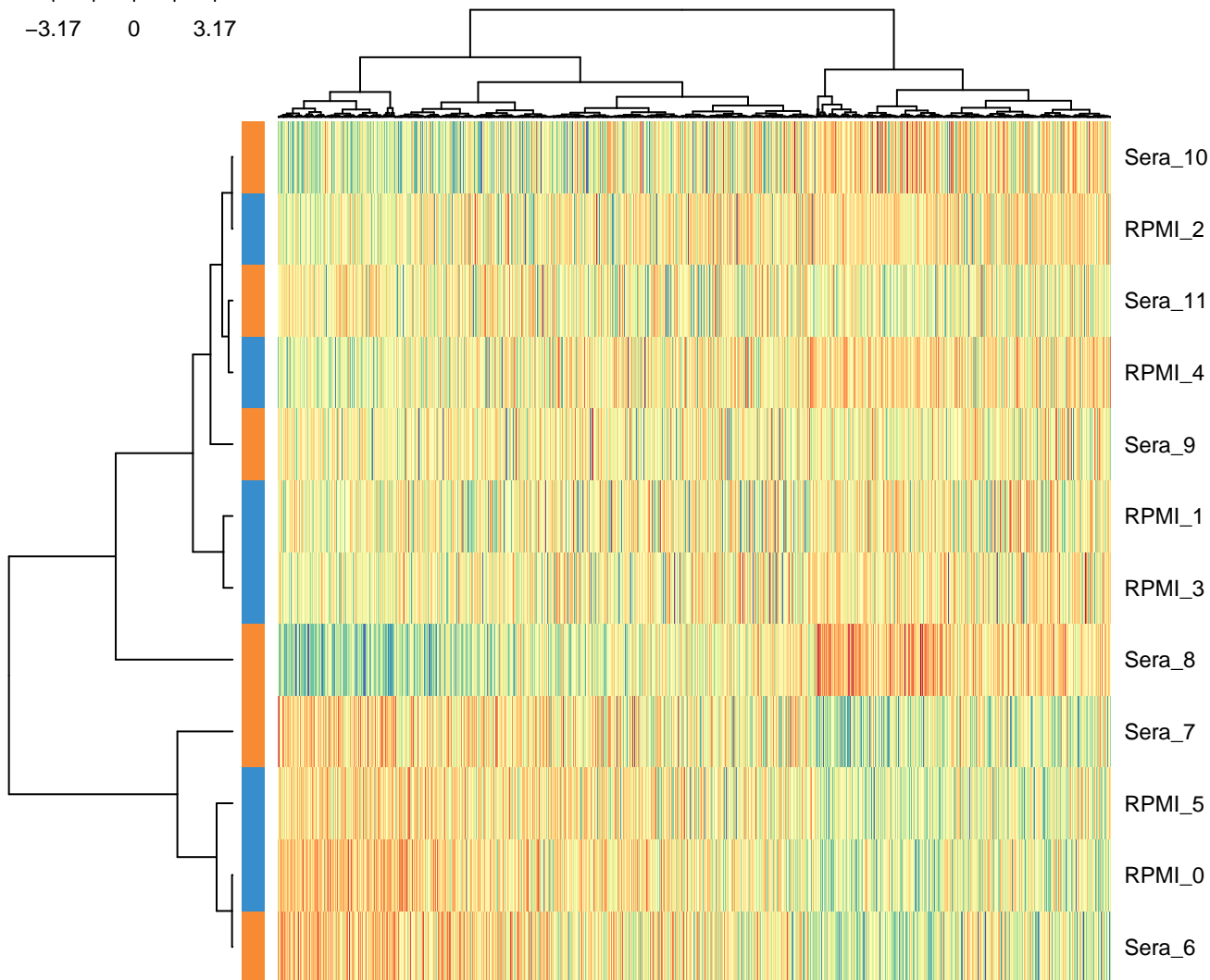
Color key



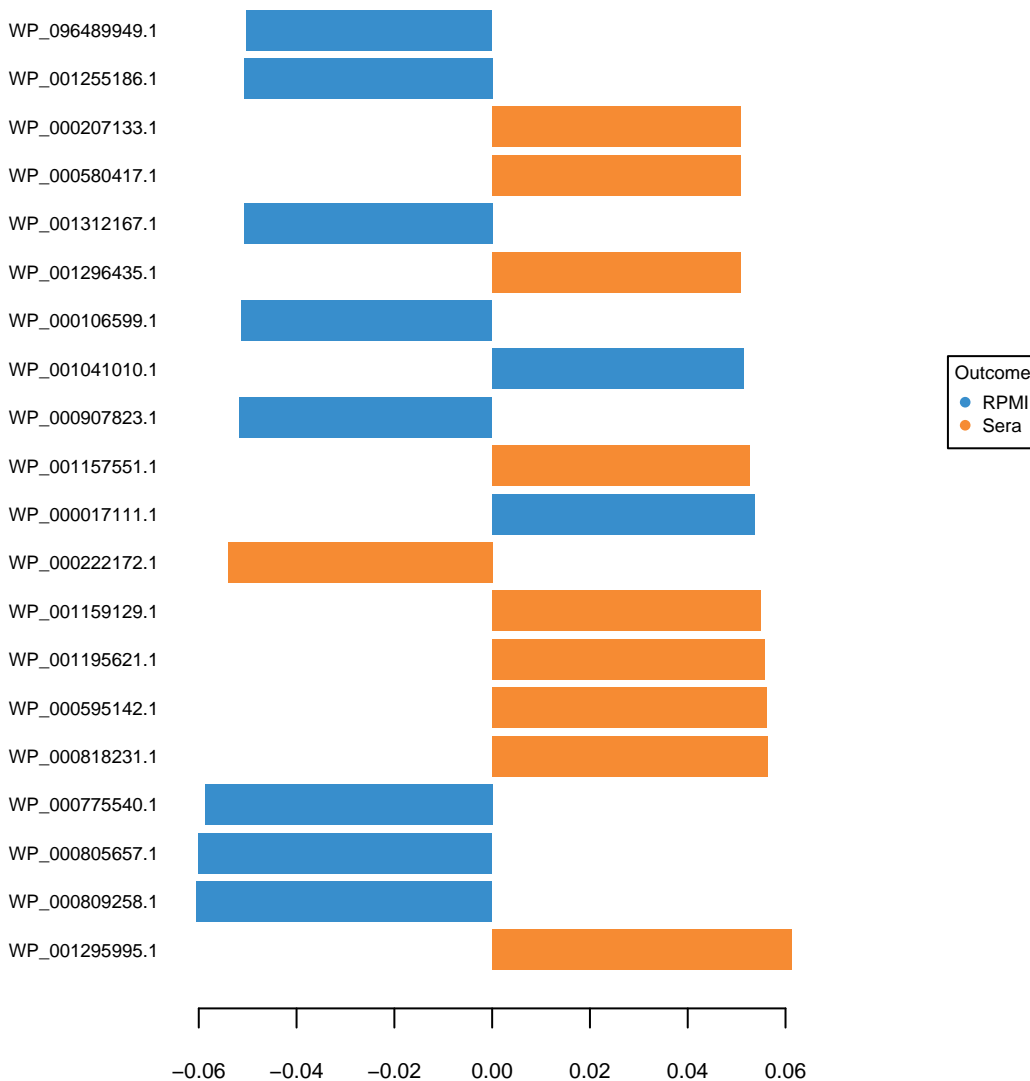
Status

RPMI

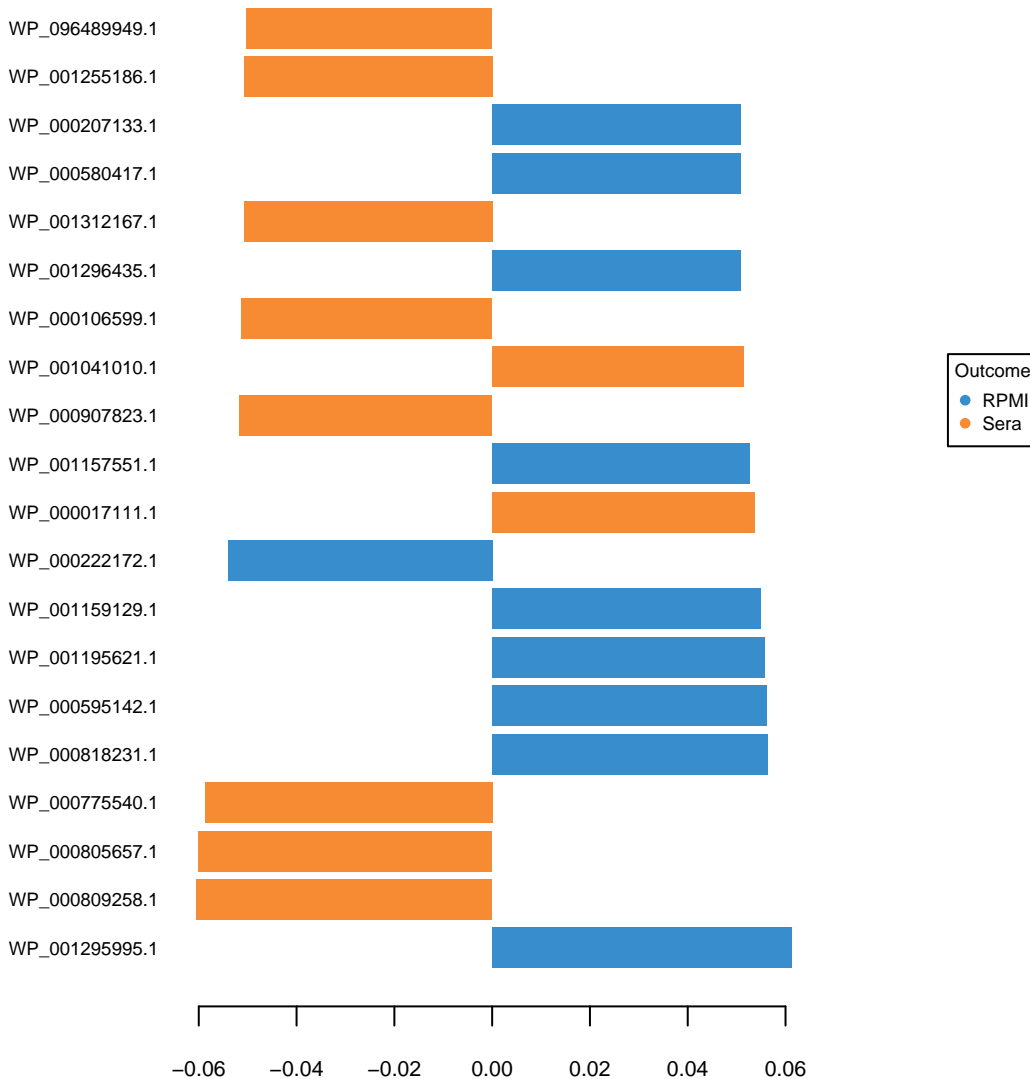
Sera



# proteome 2 PLSDA max loadir



# proteome 2 PLSDA min loadin



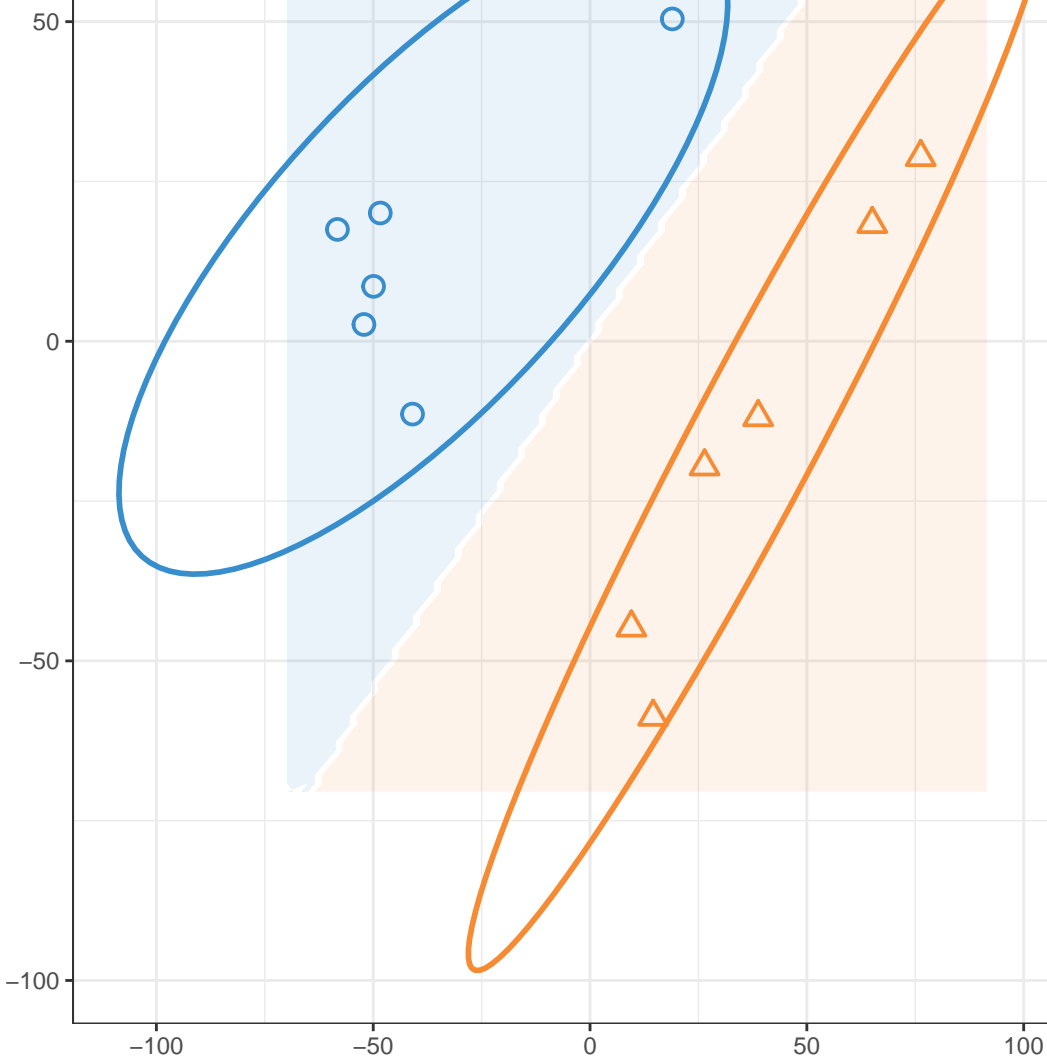
# transcriptome PLSDA single 1/2

X-variate 2: 20% expl. var

X-variate 1: 51% expl. var

Legend

- RPMI
- △ Sera



# transcriptome PLSDA single 1/2

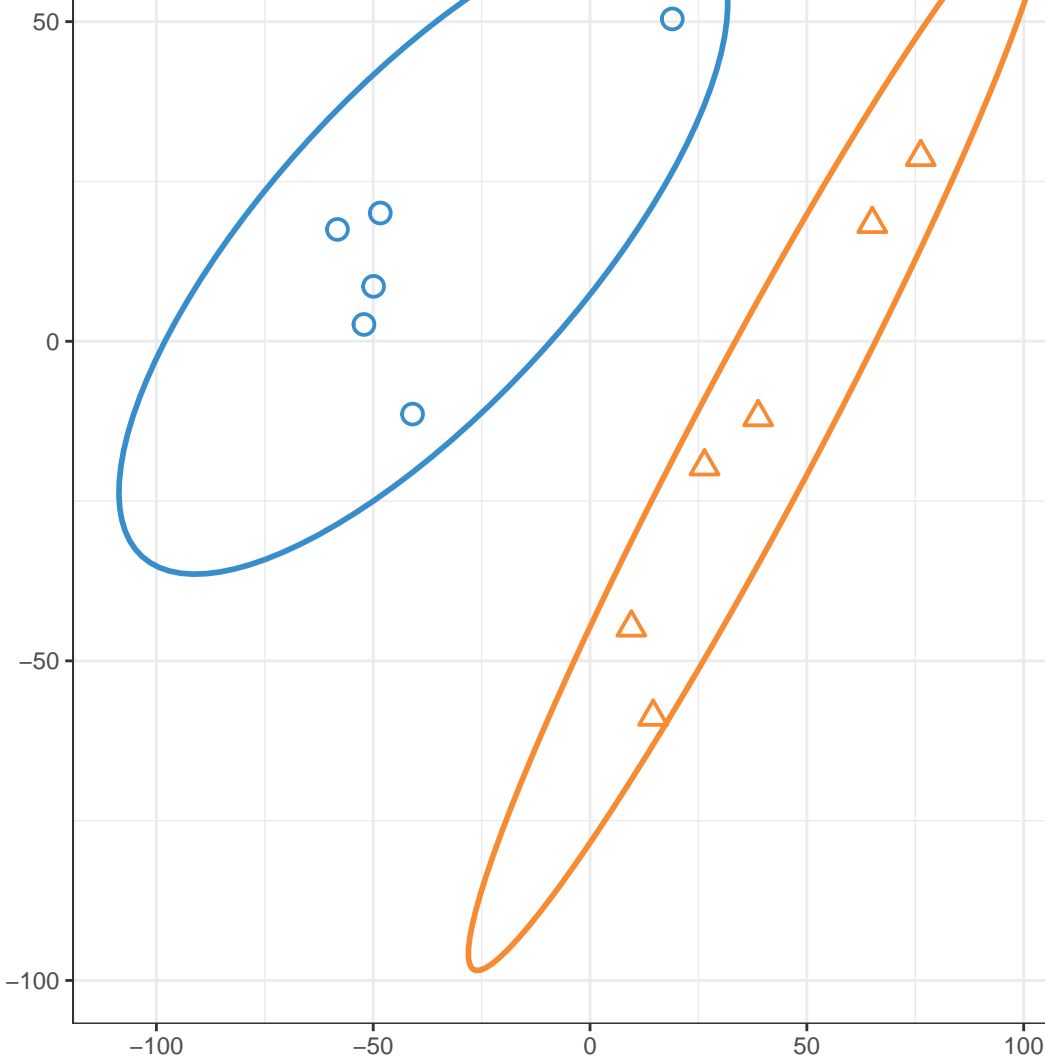
X-variate 2: 20% expl. var

X-variate 1: 51% expl. var

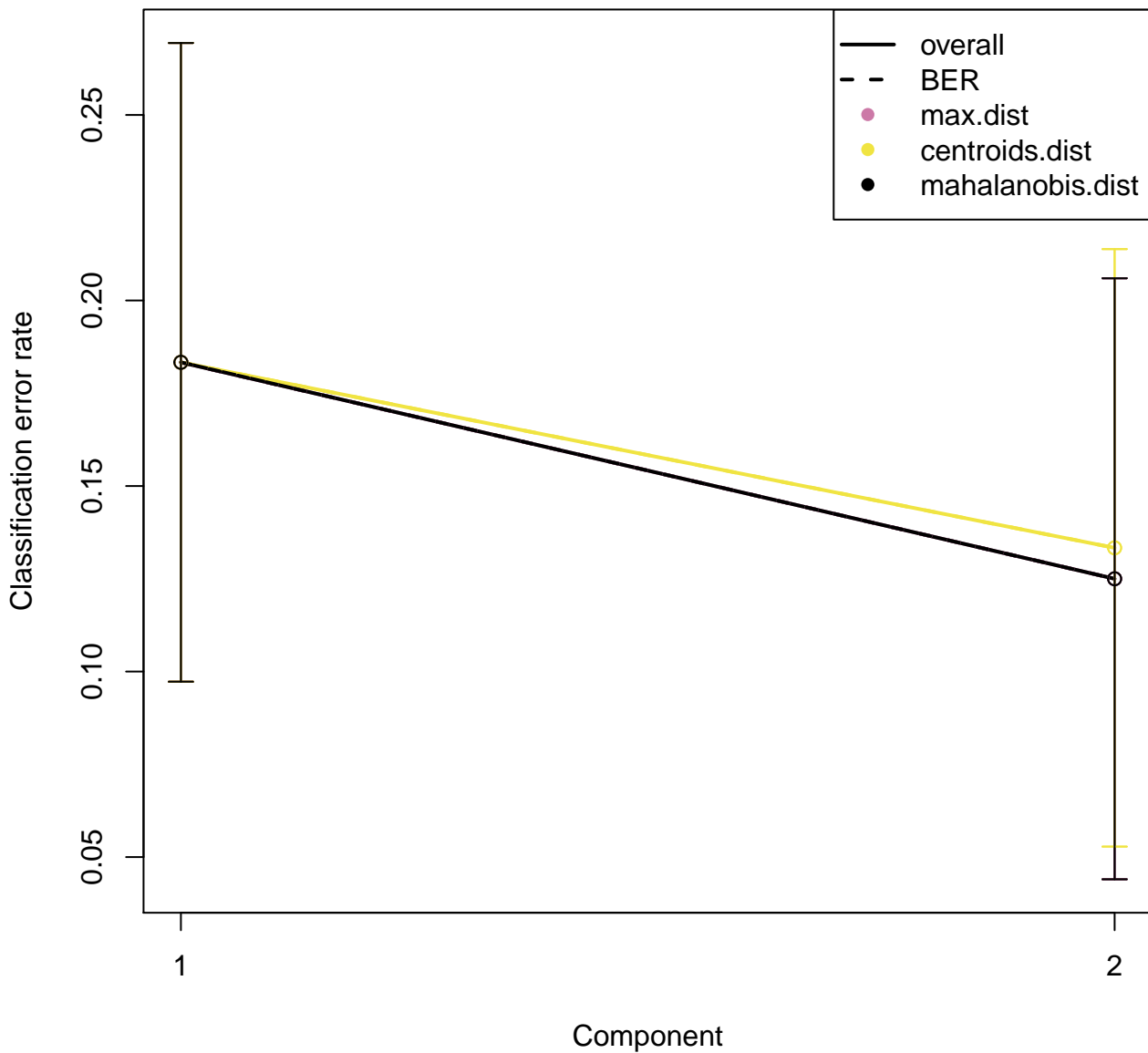
Legend

○ RPMI

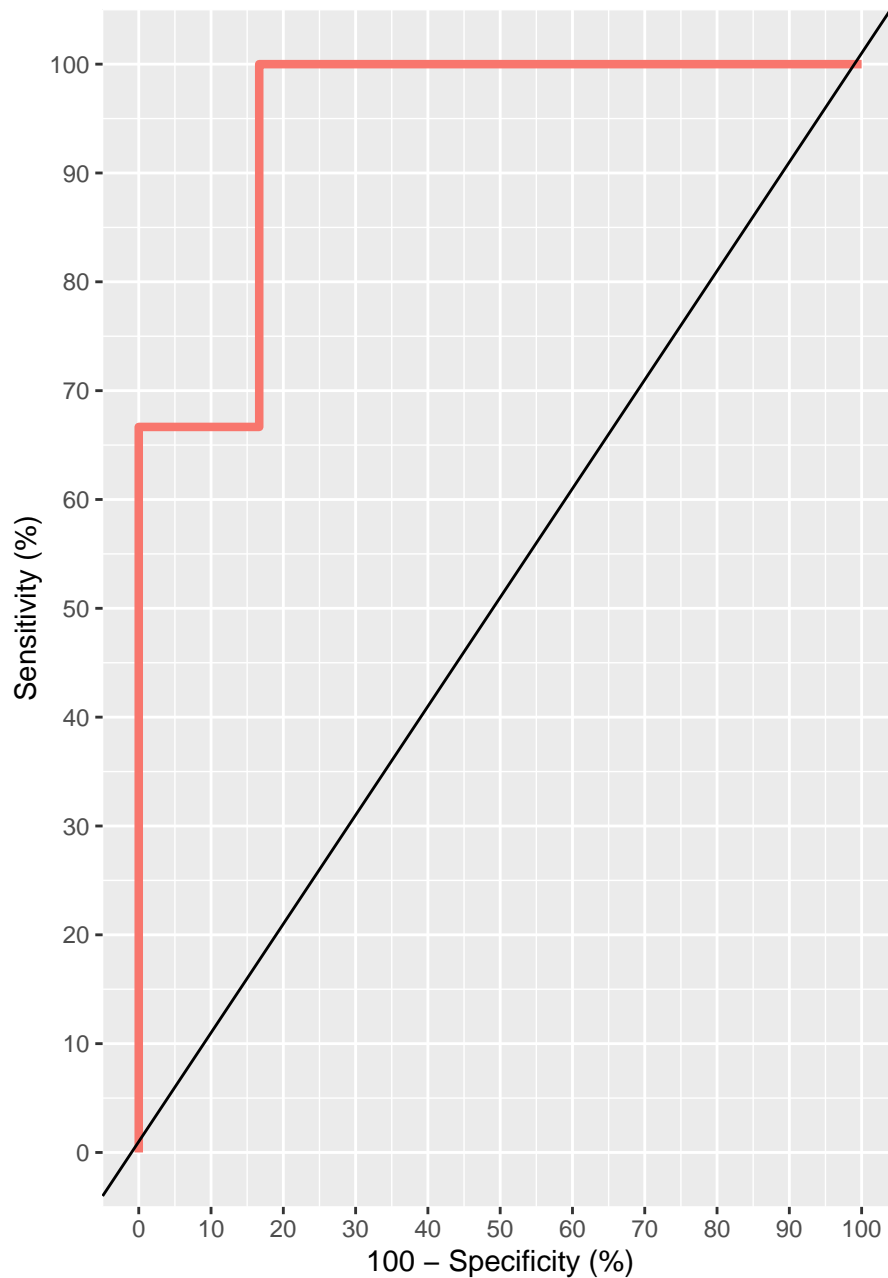
△ Sera







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

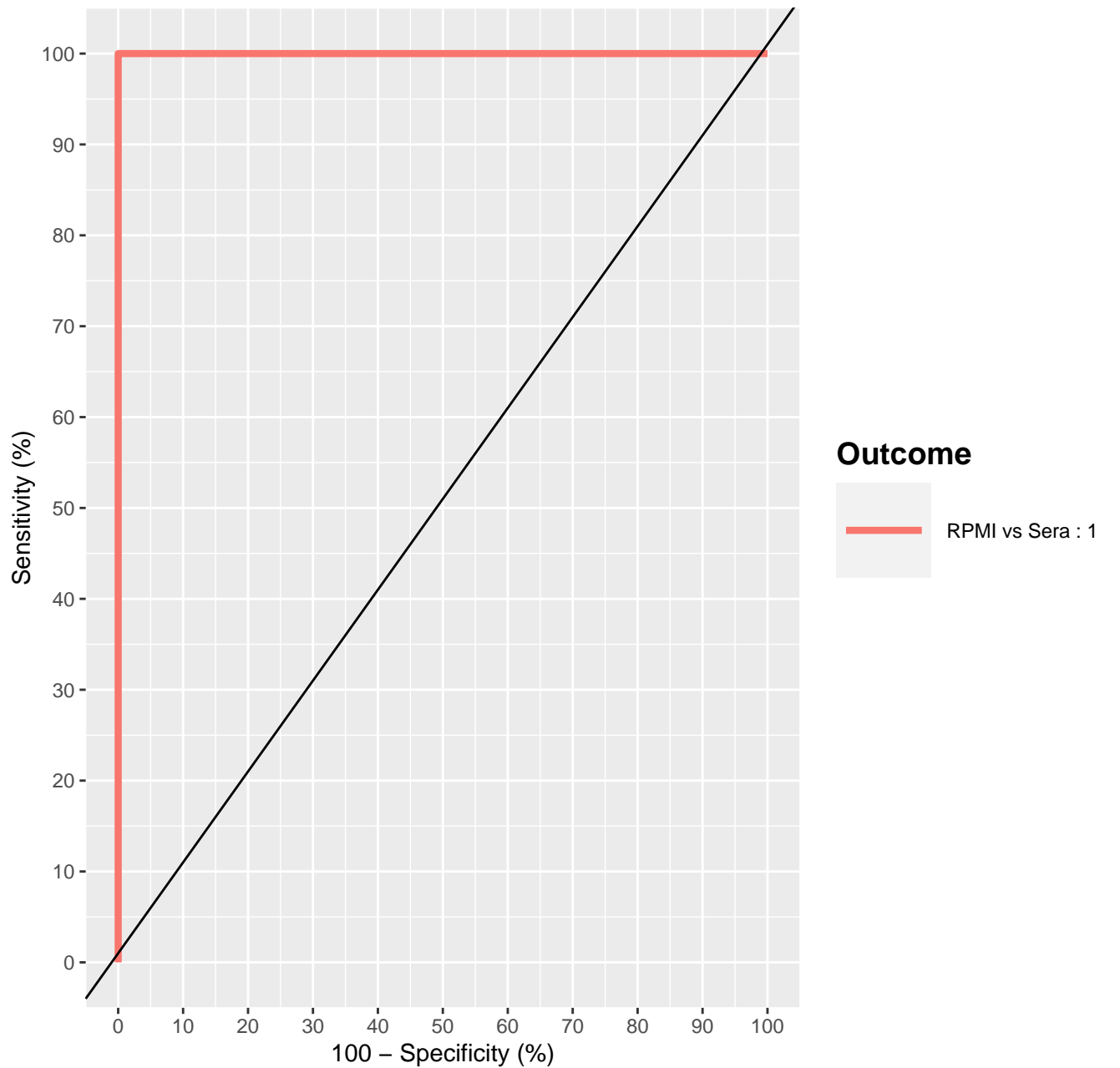


**Outcome**

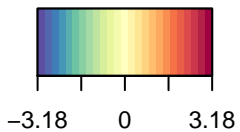


RPMI vs Sera : 0.9444

ROC Curve Using Comp(s): 1, 2



Color key

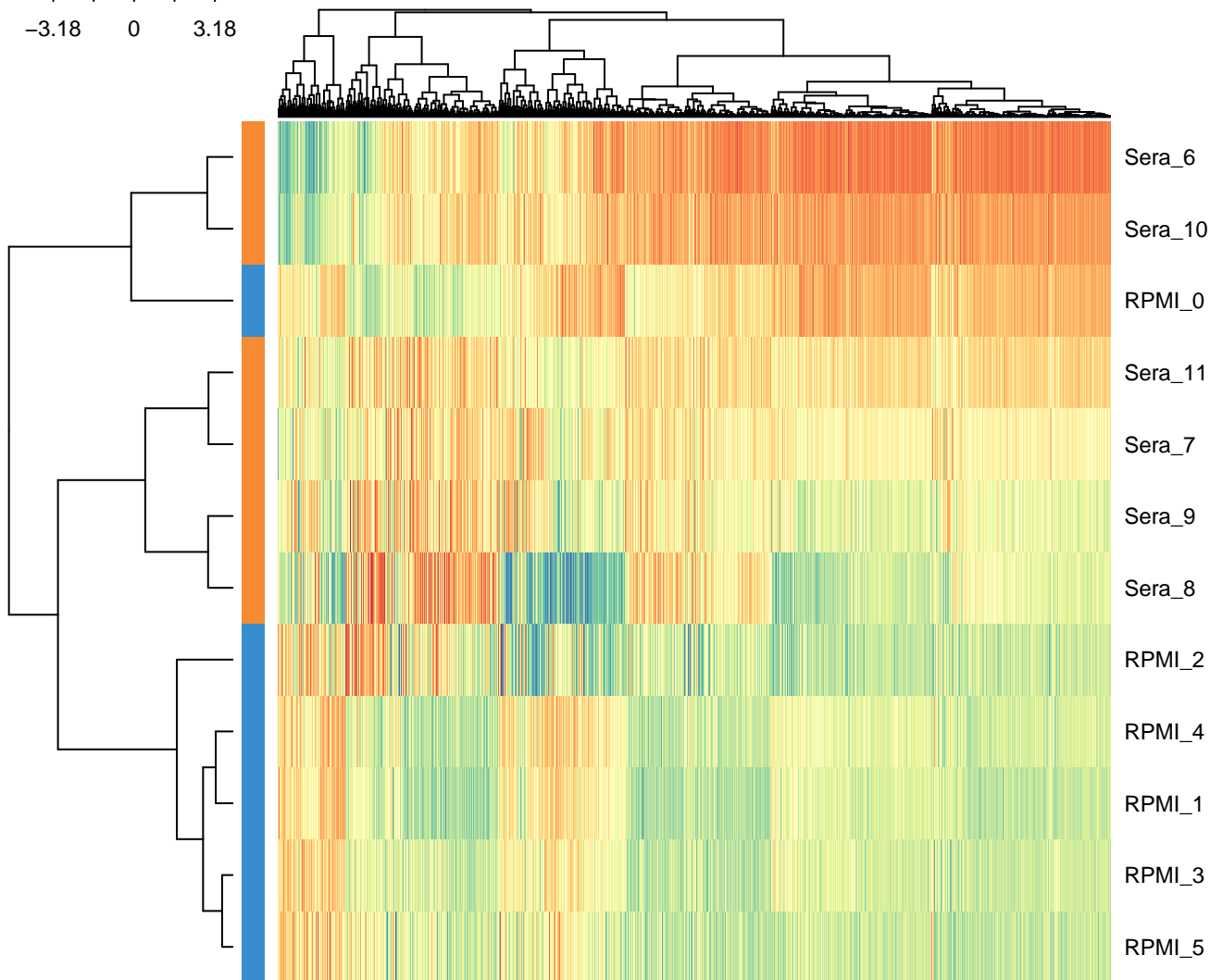


PLSDA

Status

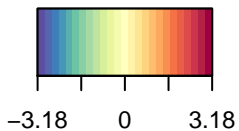
■ RPMI

■ Sera



# PLSDA Component 1

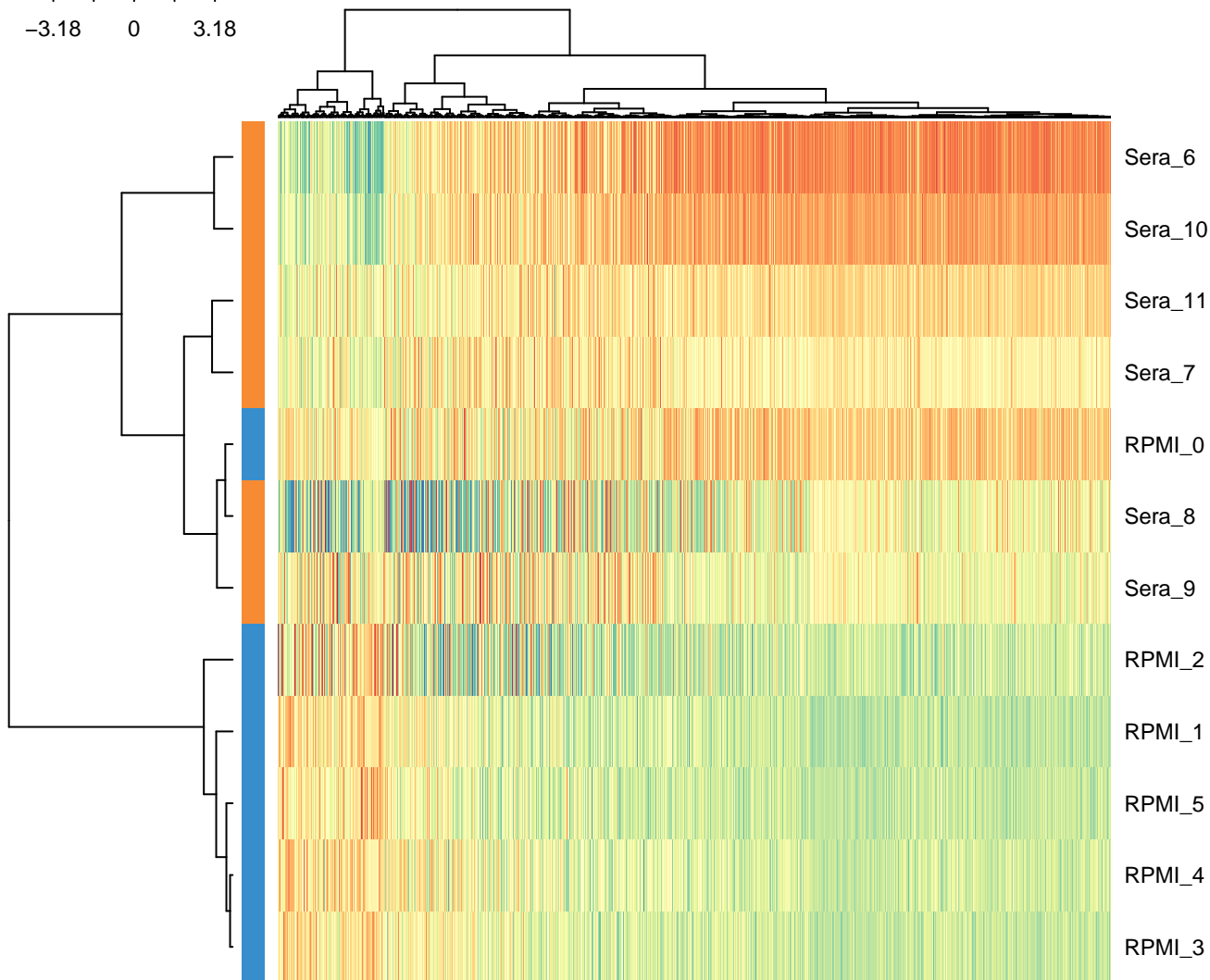
Color key



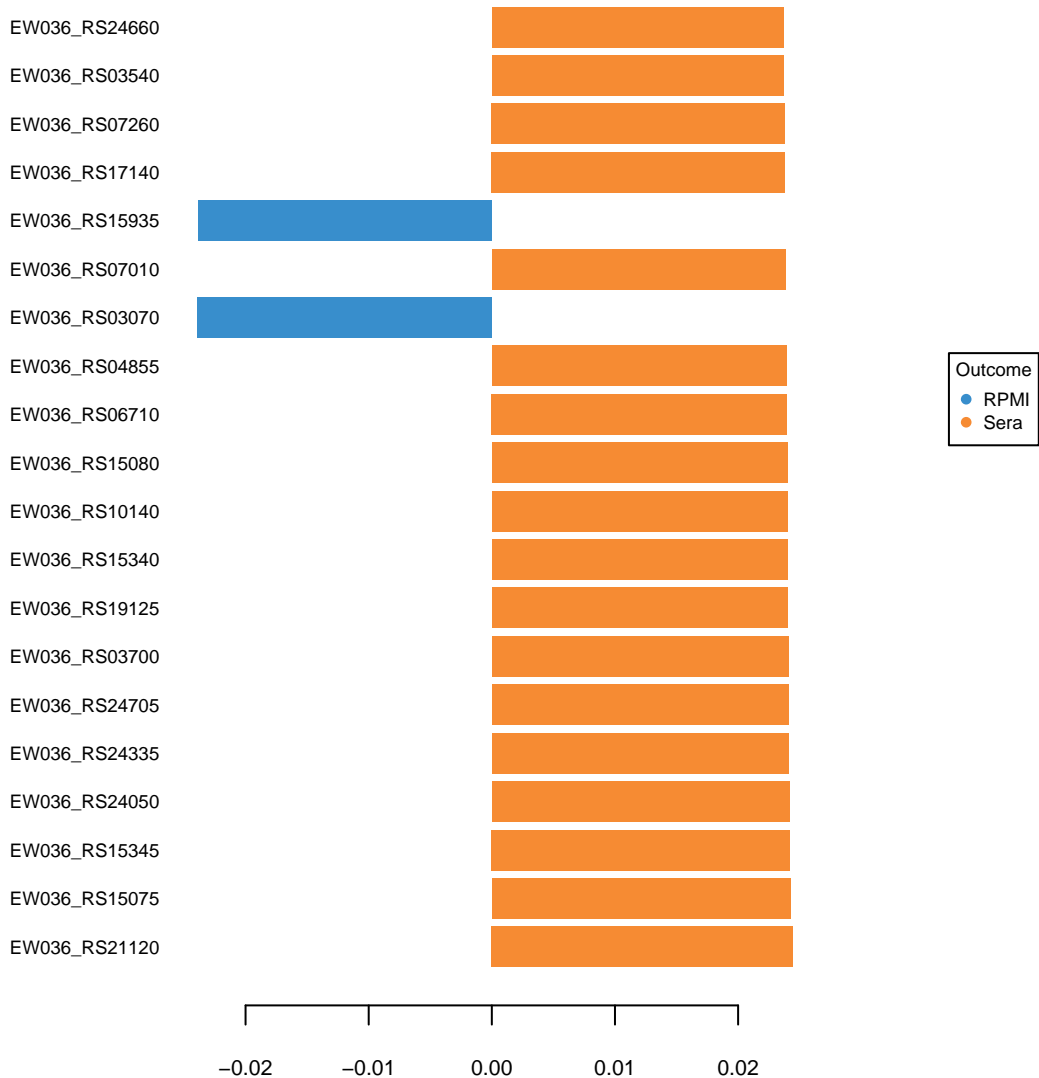
Status

RPMI

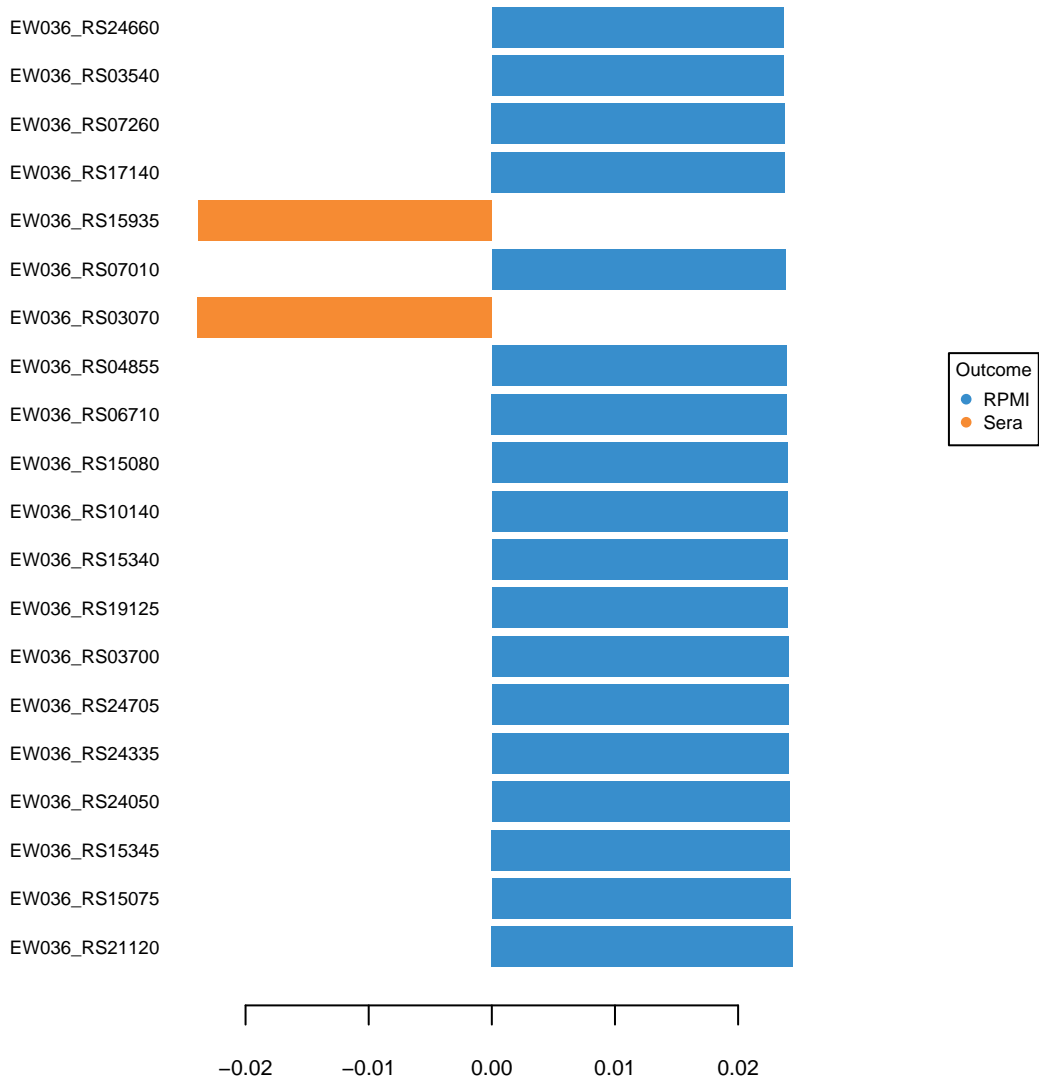
Sera



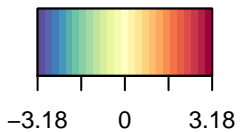
# transcriptome 1 PLSDA max load



# transcriptome 1 PLSDA min load



Color key

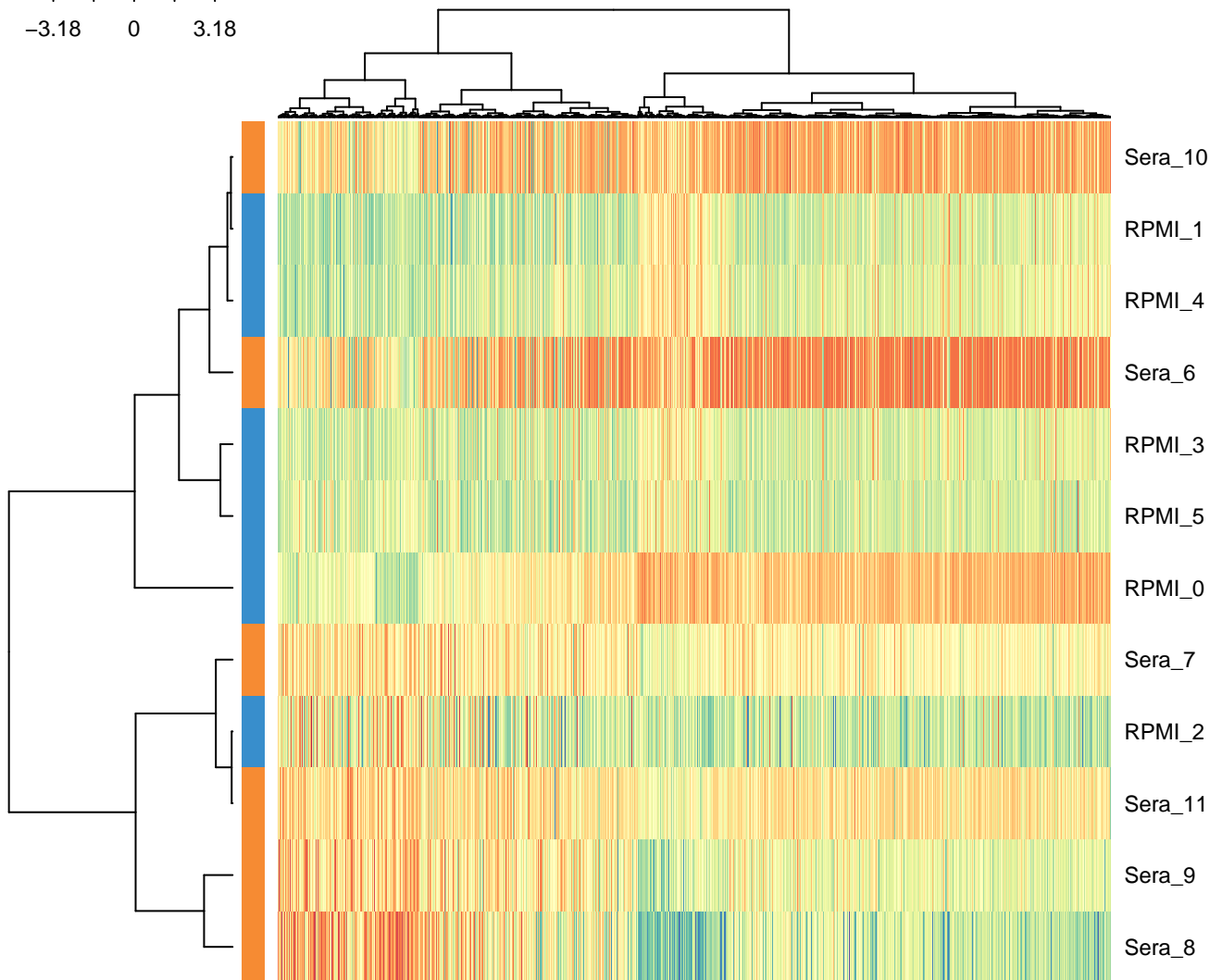


## PLSDA Component 2

Status

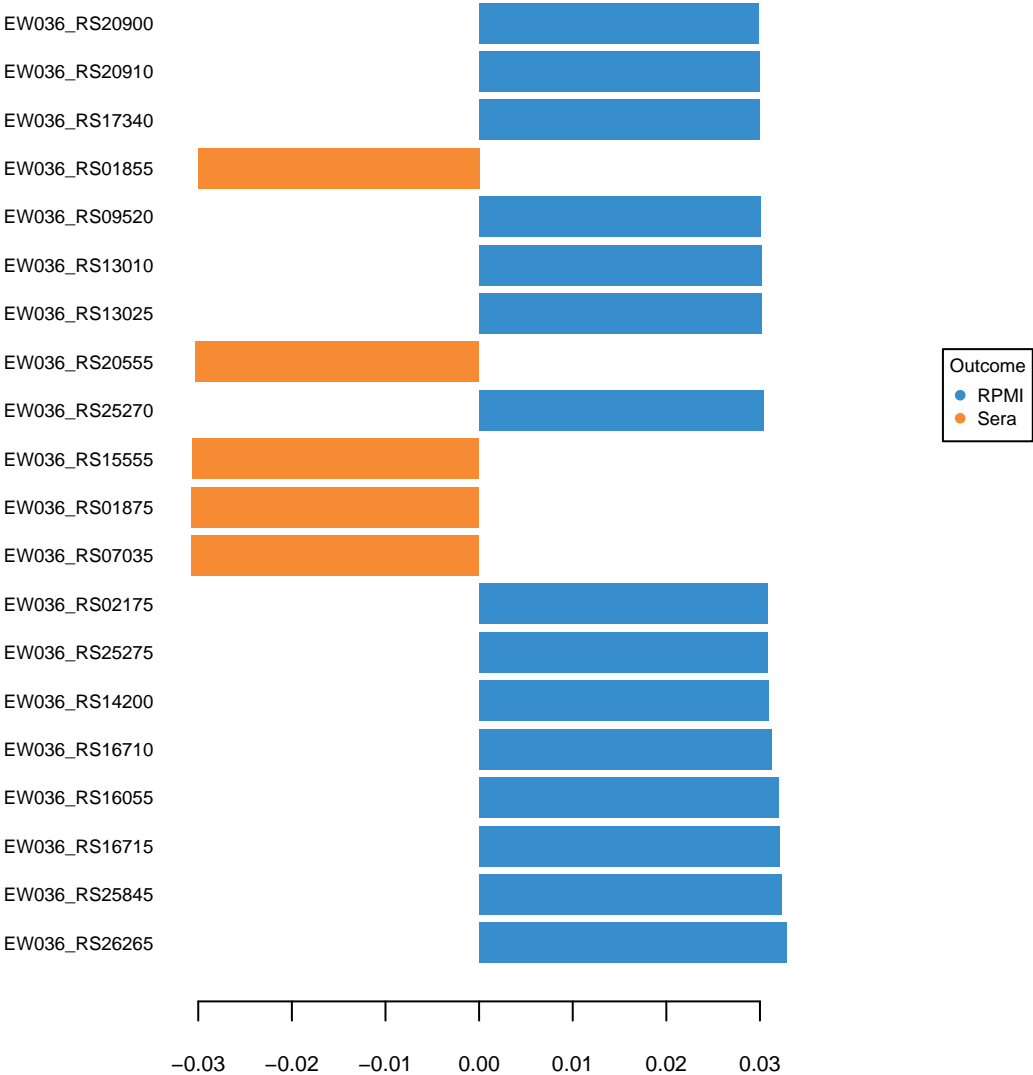
RPMI

Sera

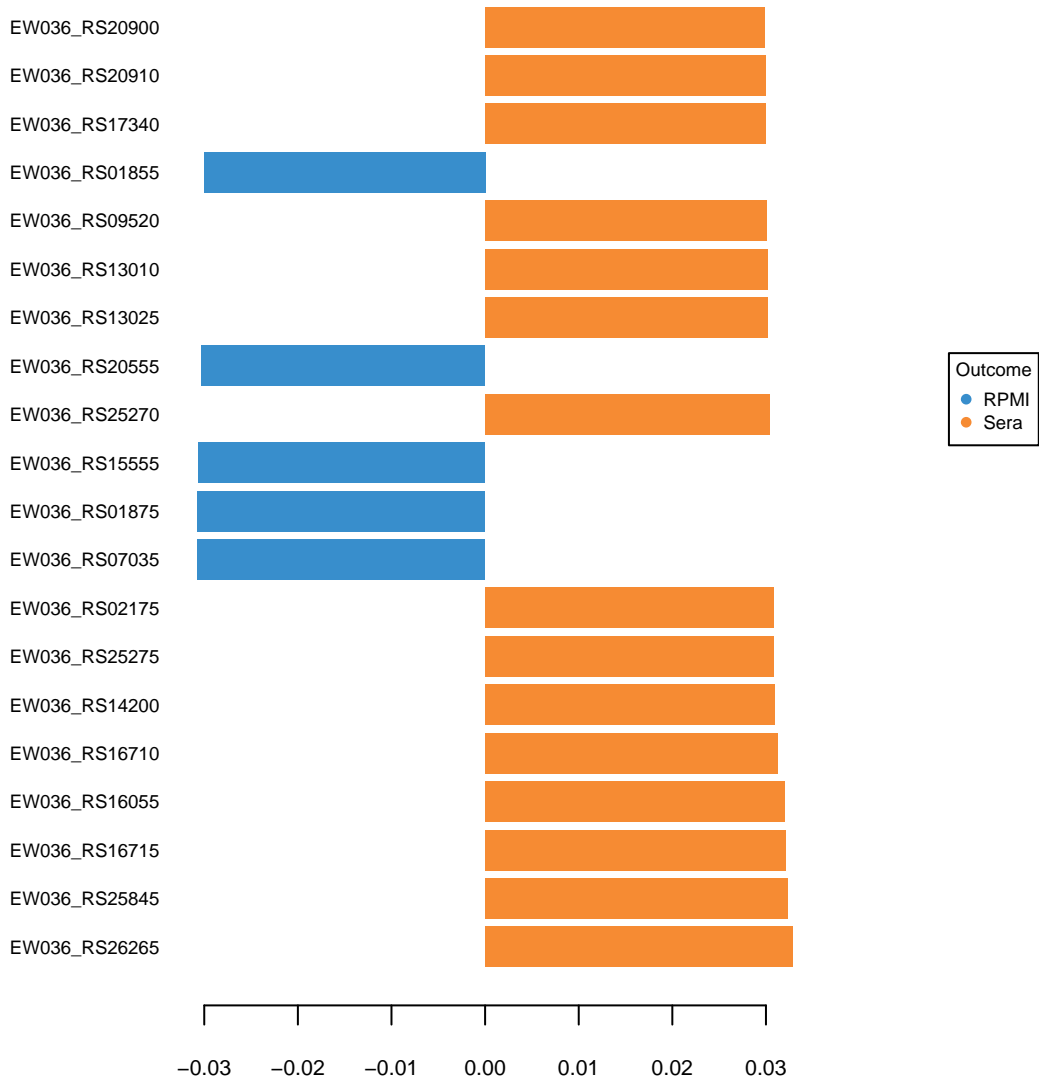


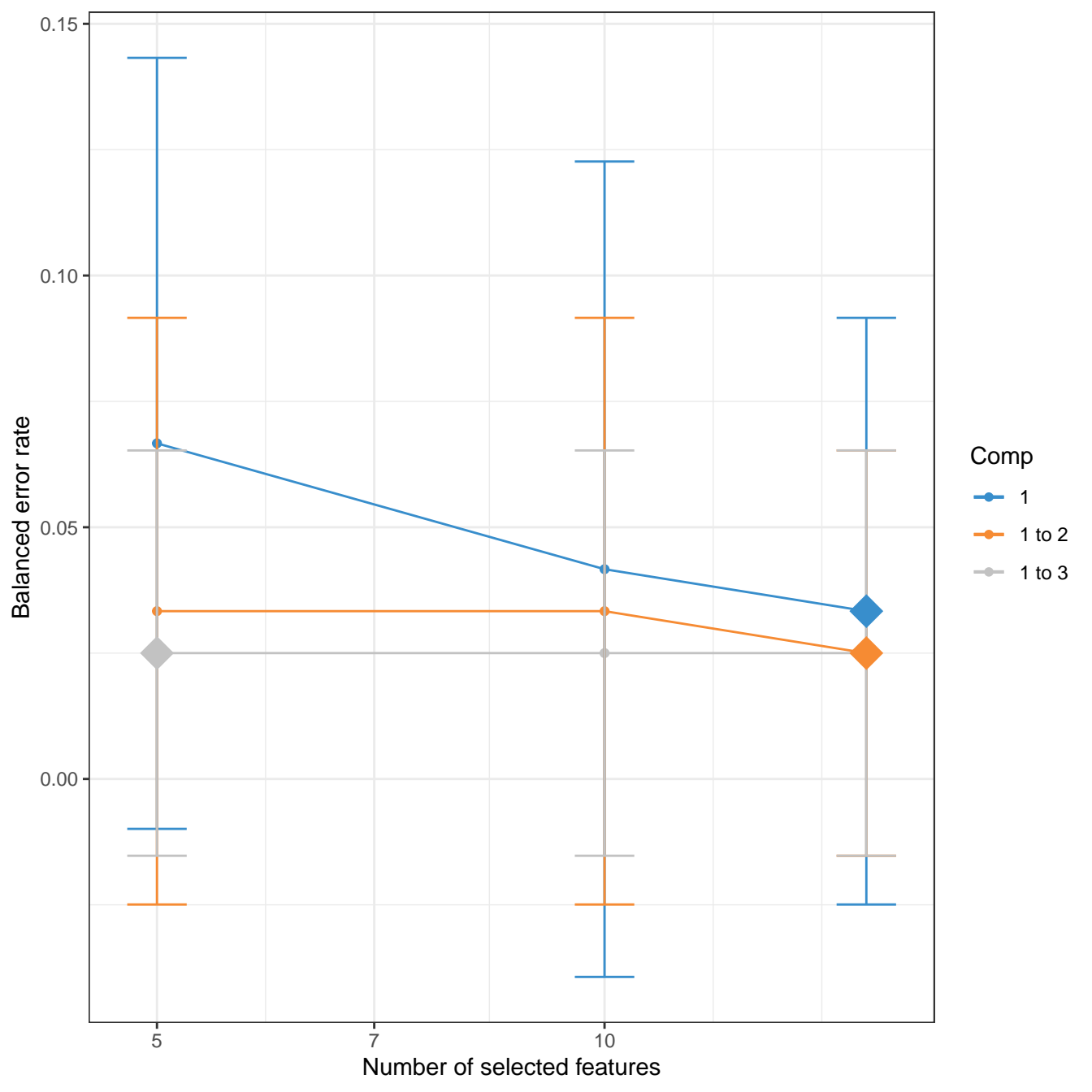


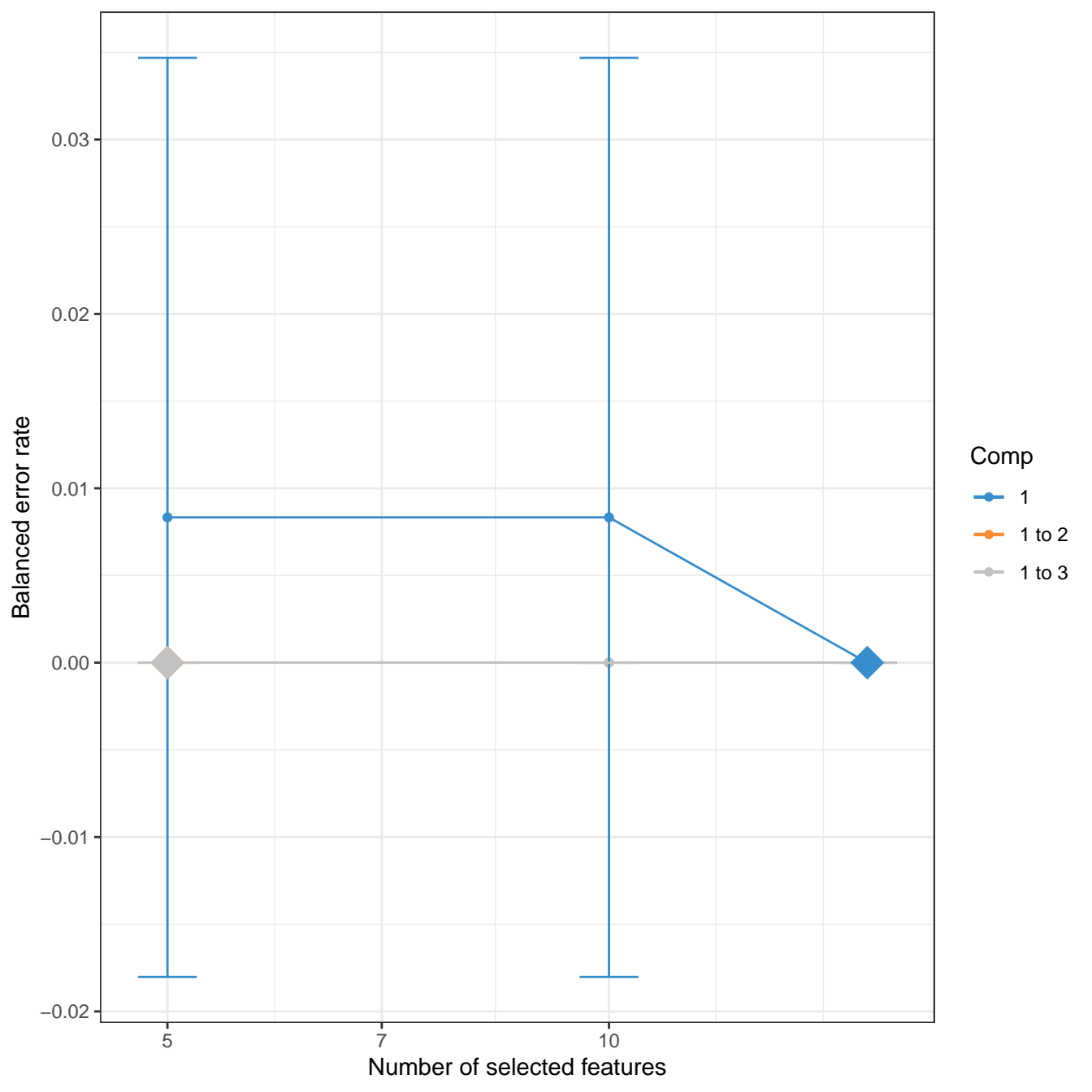
# transcriptome 2 PLSDA max load

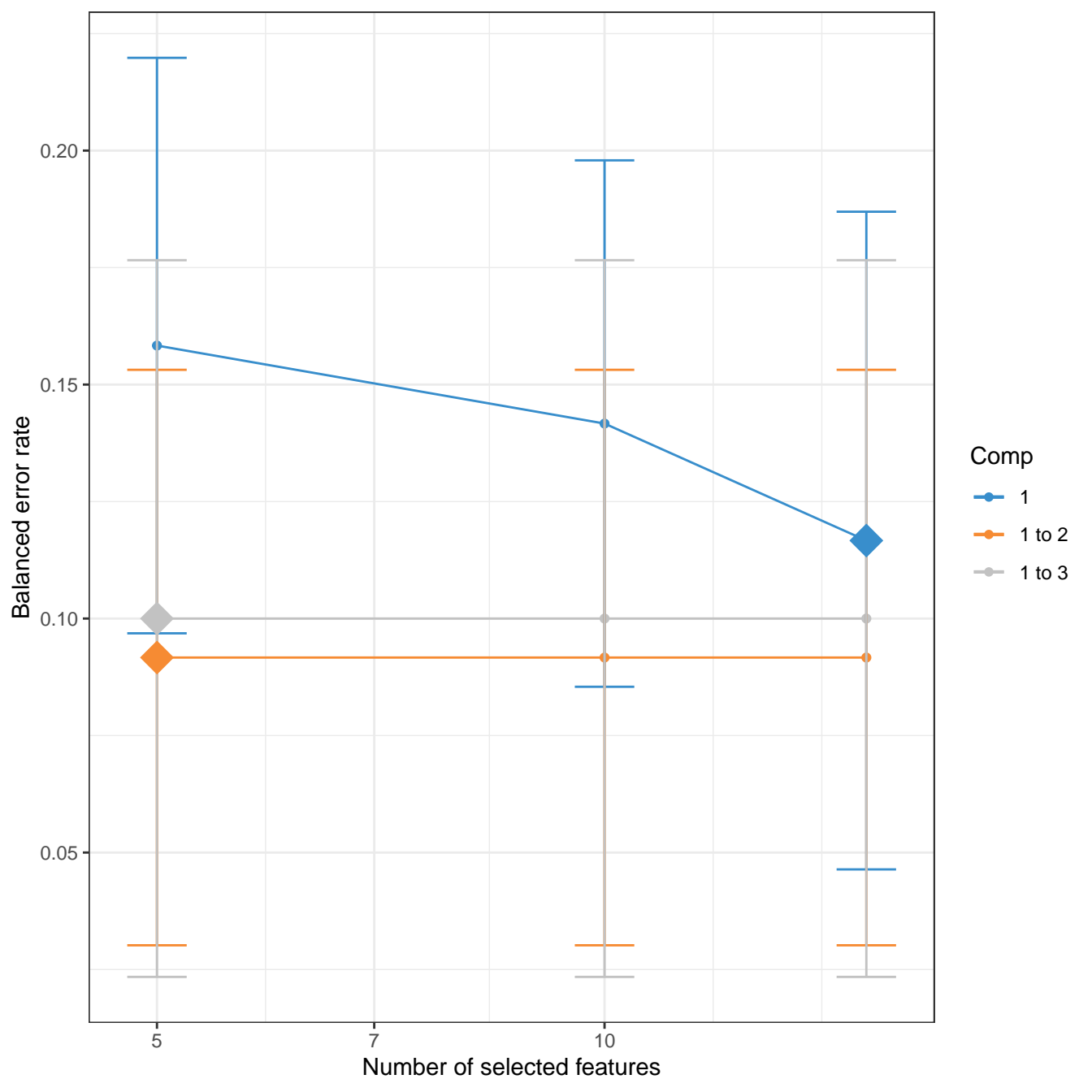


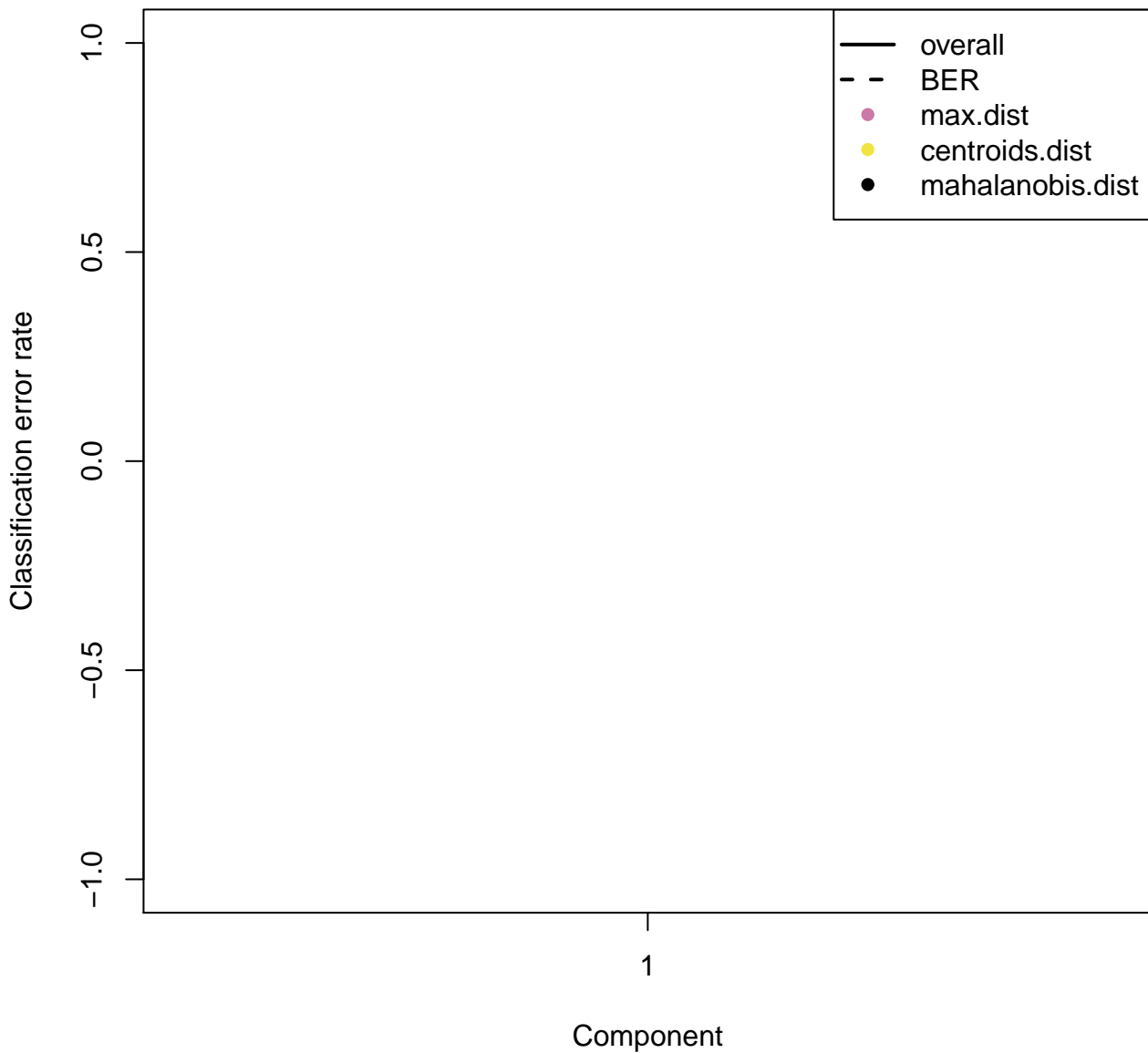
# transcriptome 2 PLSDA min load



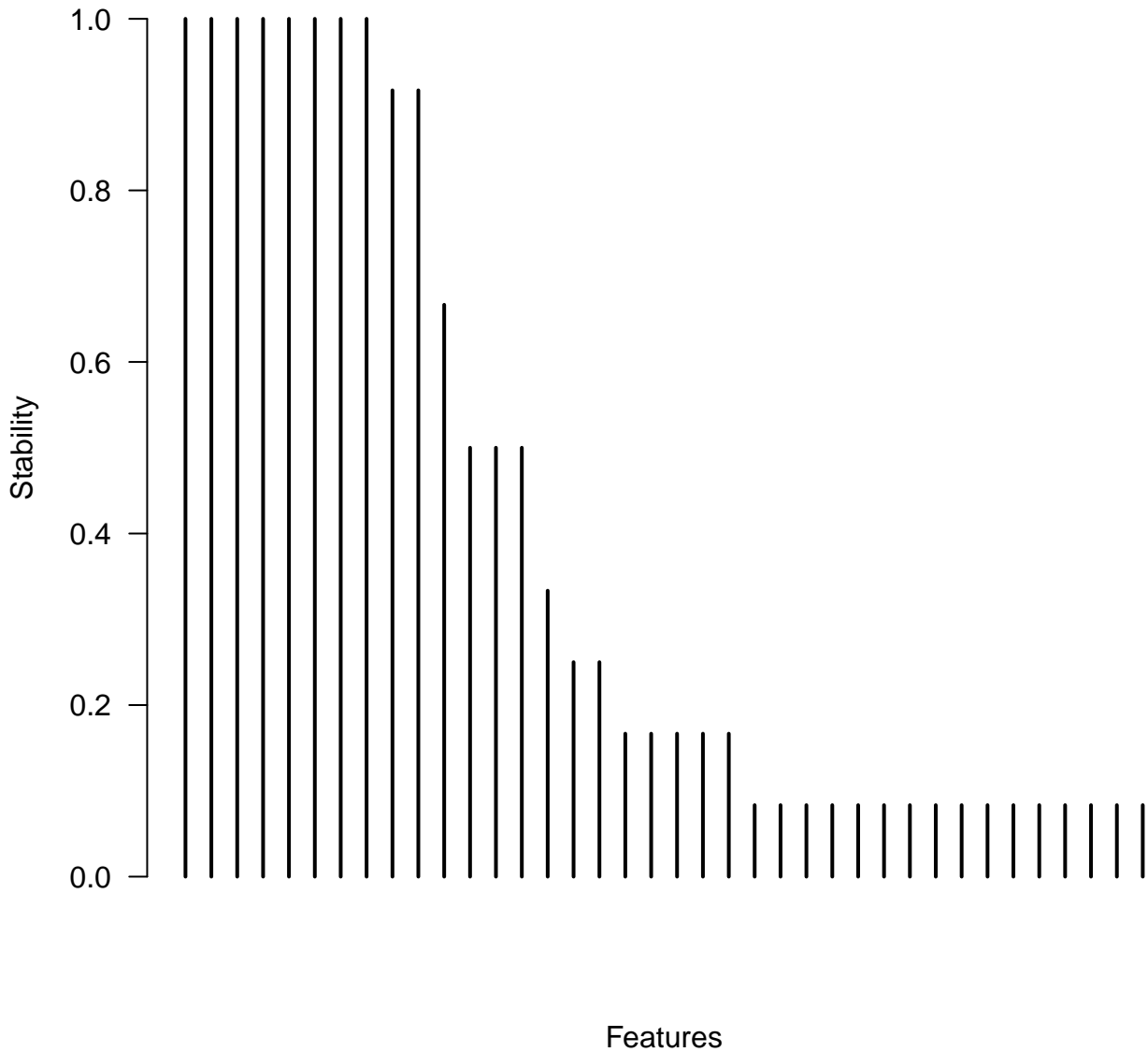




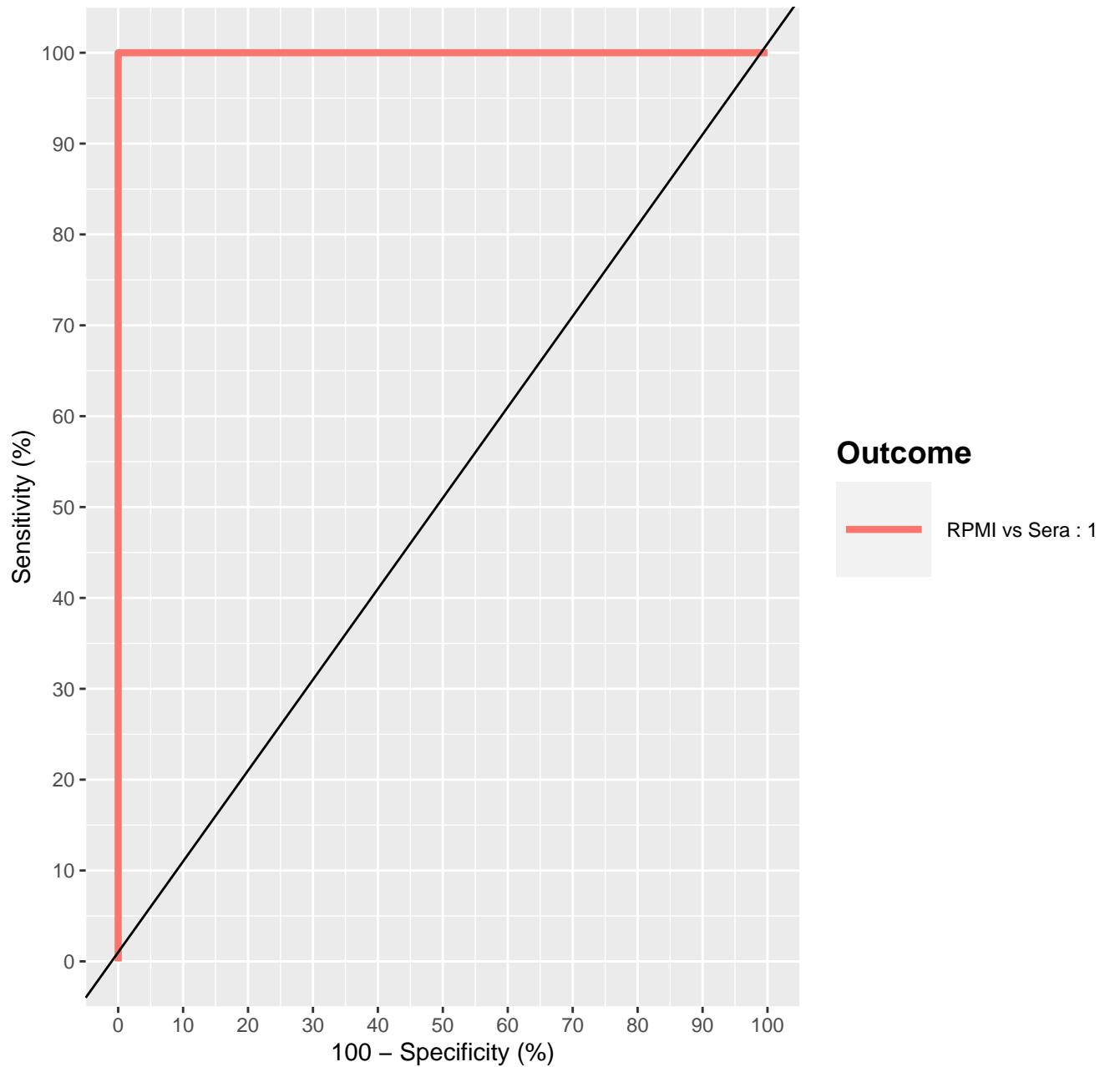




# Comp 1

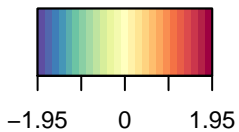


**ROC Curve Using Comp(s): 1**





Color key

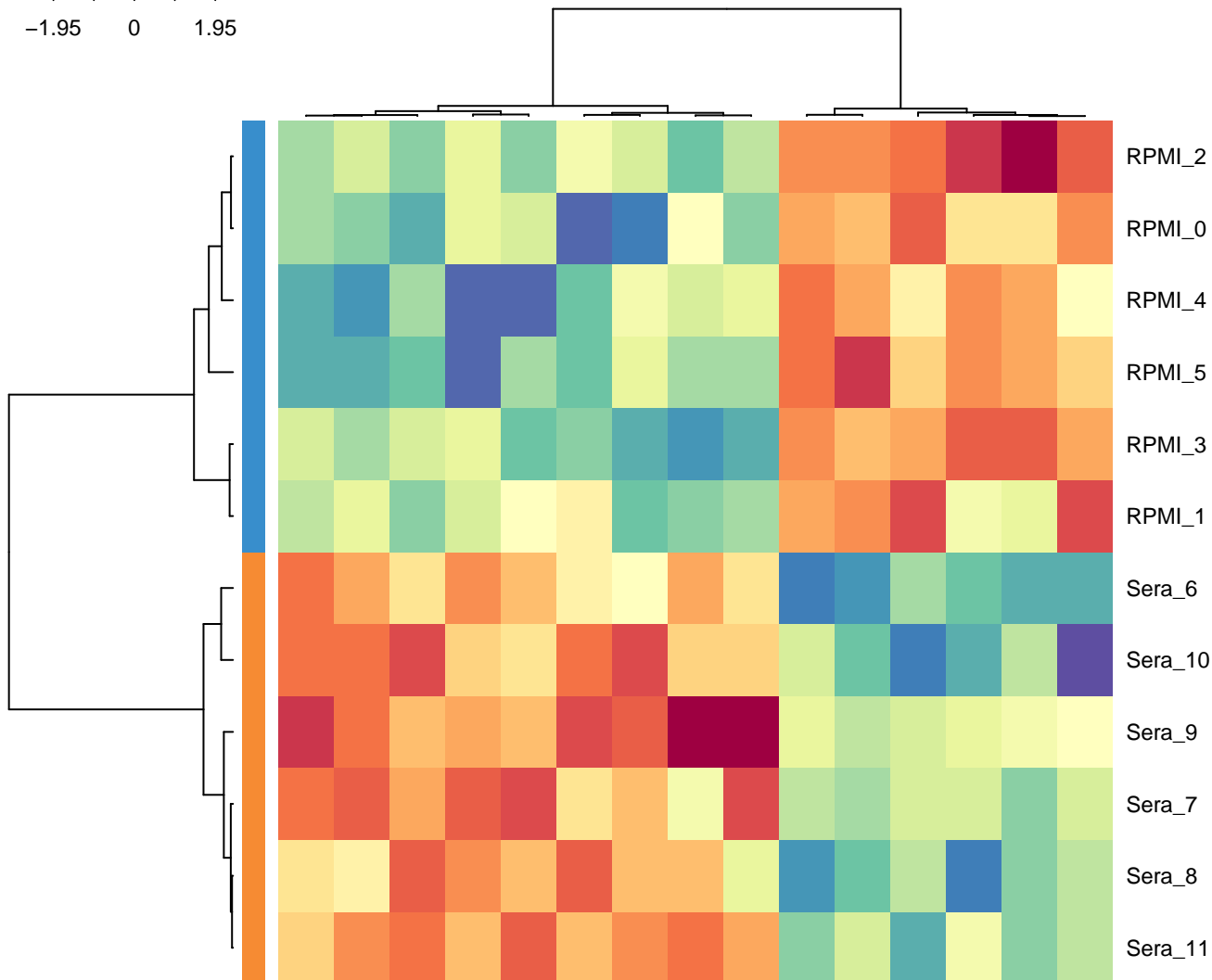


sPLSDA

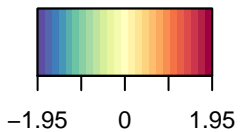
Status

RPMI

Sera



Color key

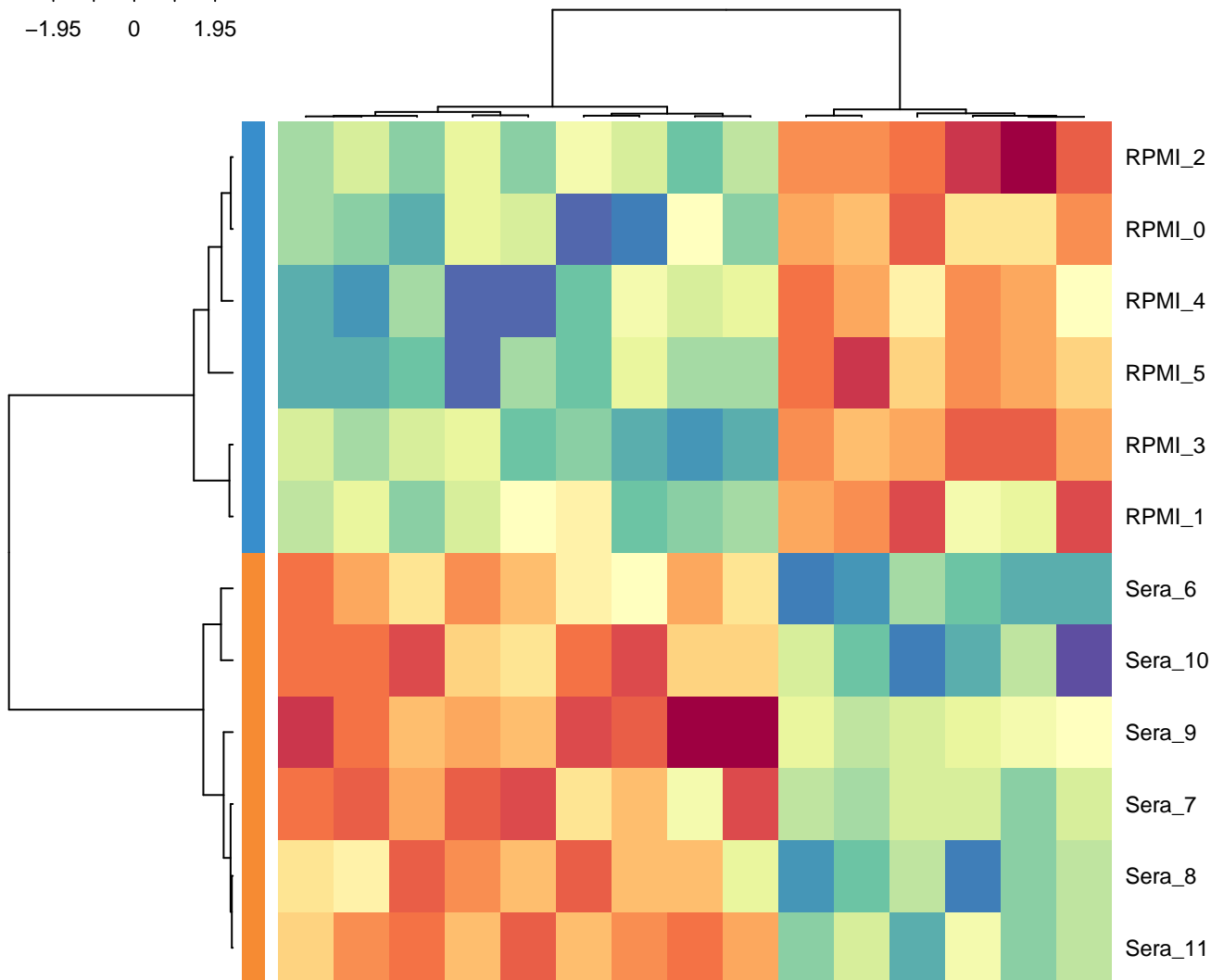


# sPLSDA Component 1

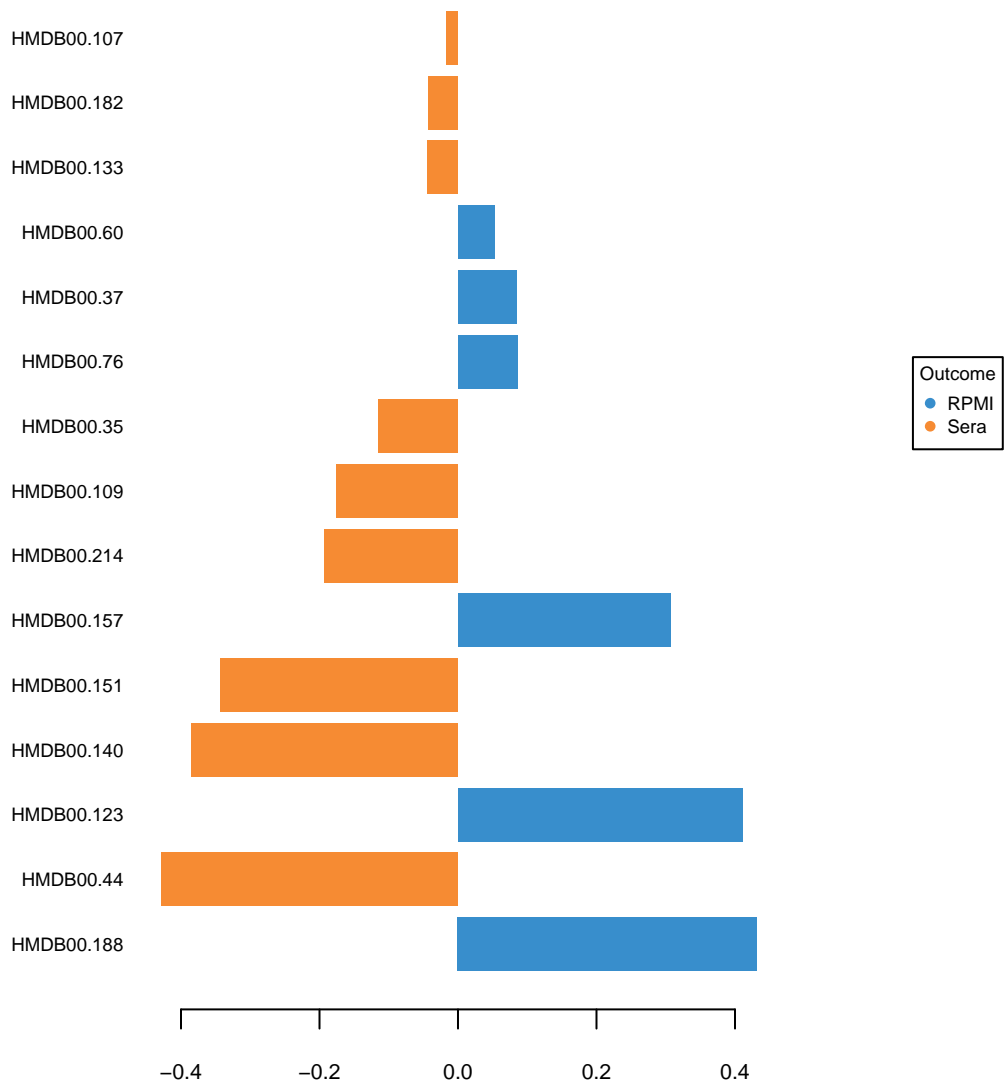
Status

RPMI

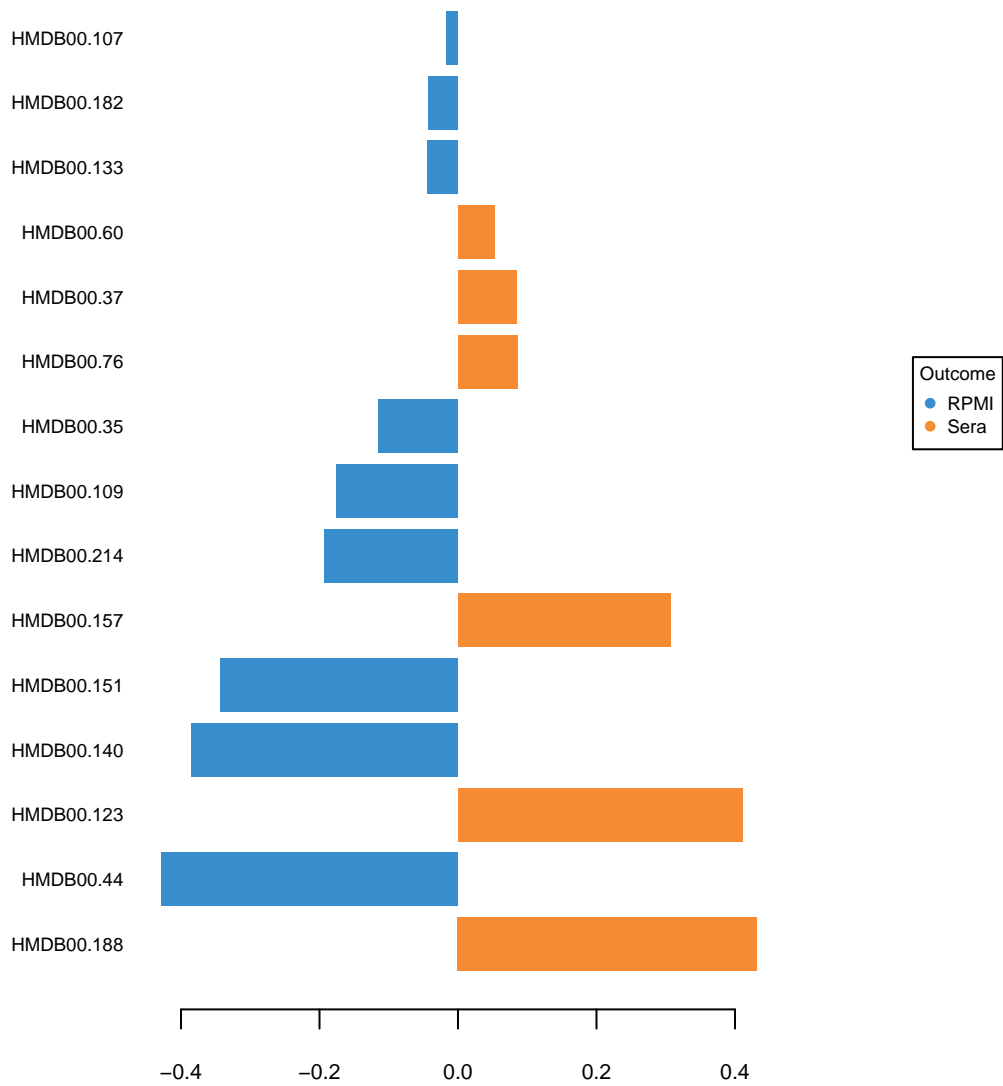
Sera

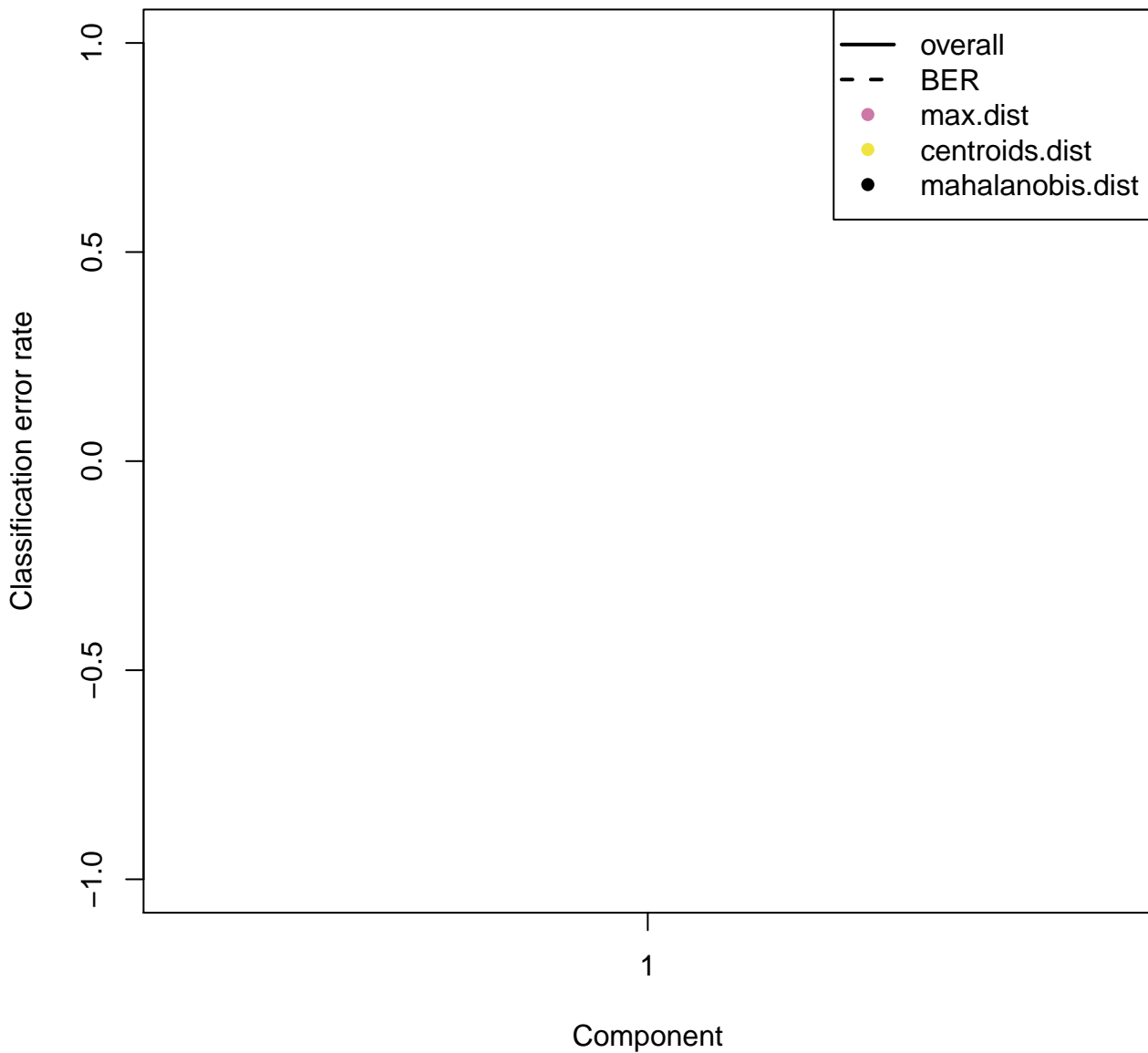


# metabolome 1 sPLSDA max load

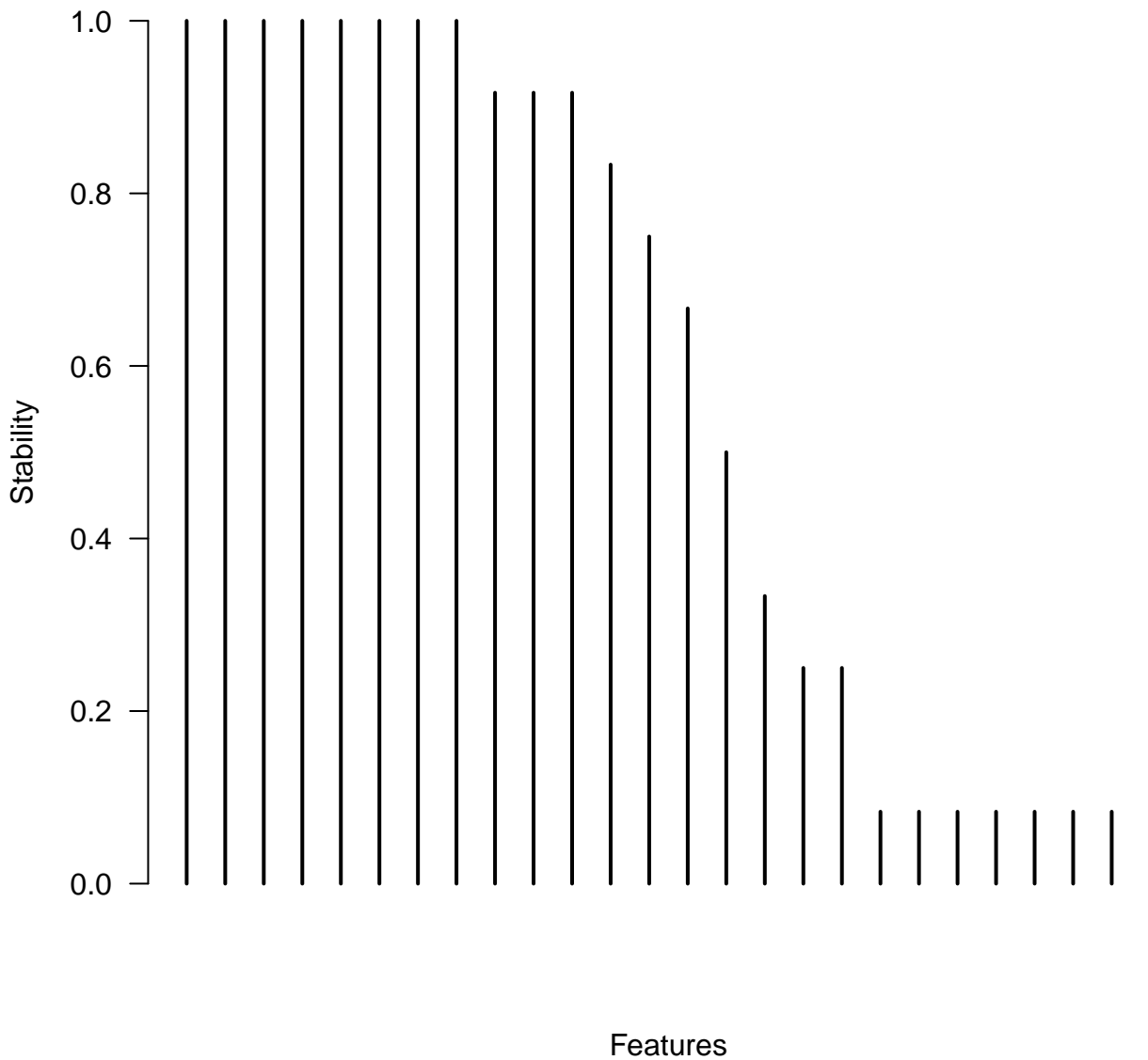


# metabolome 1 sPLSDA min loac

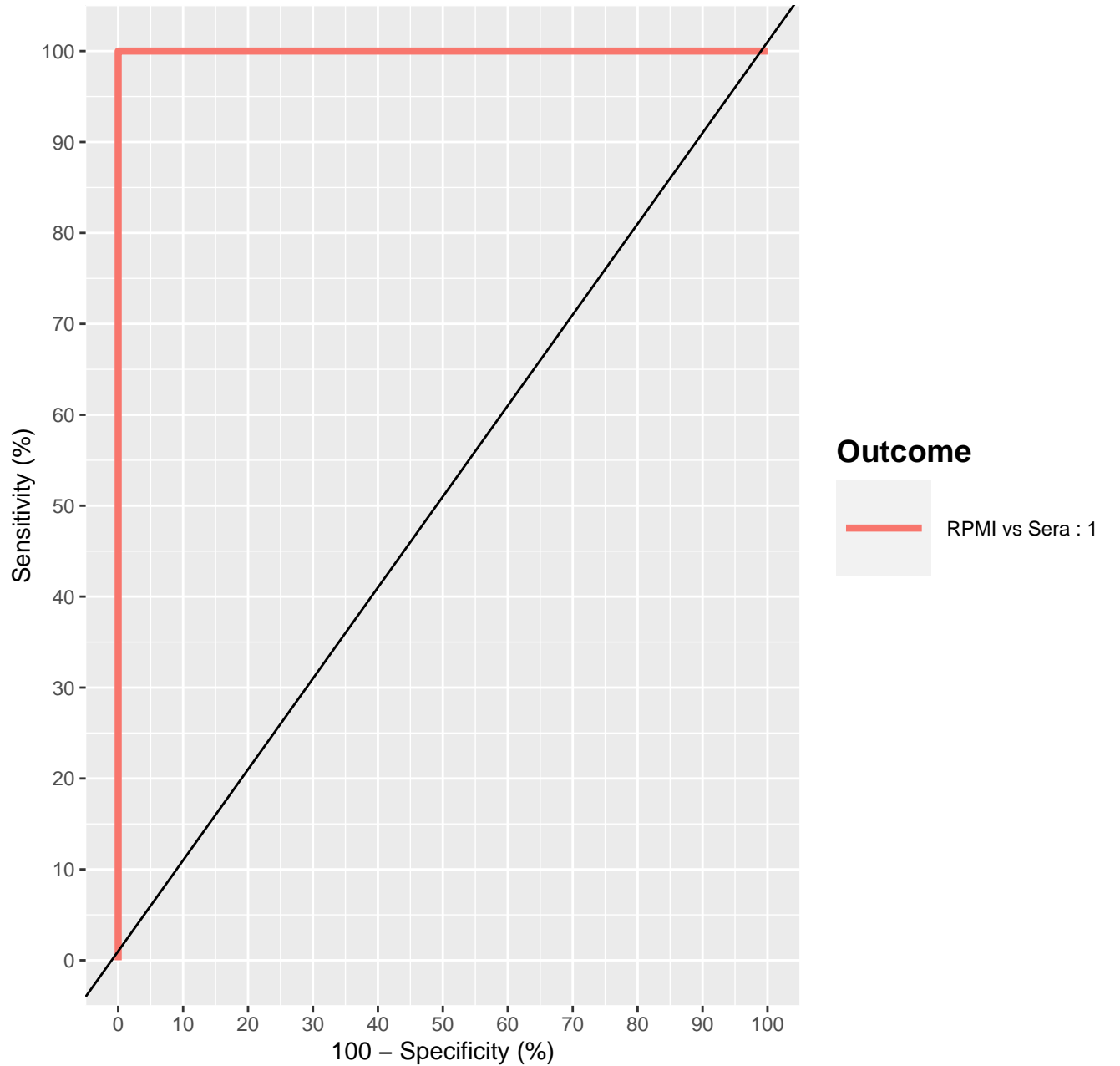




# Comp 1

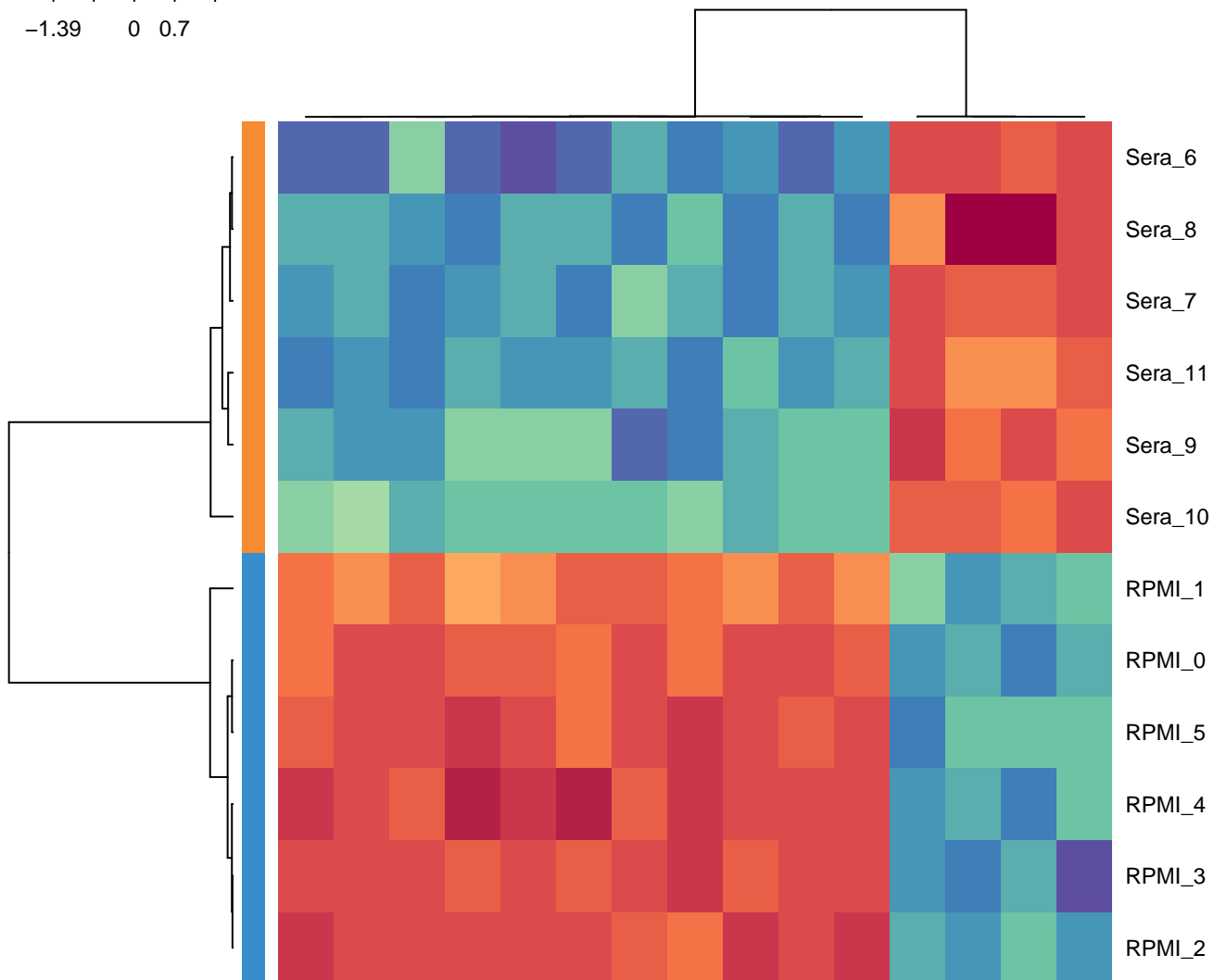


**ROC Curve Using Comp(s): 1**



## sPLSDA

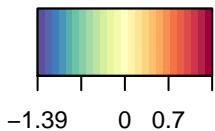
■ RPMI  
■ Sera





# sPLSDA Component 1

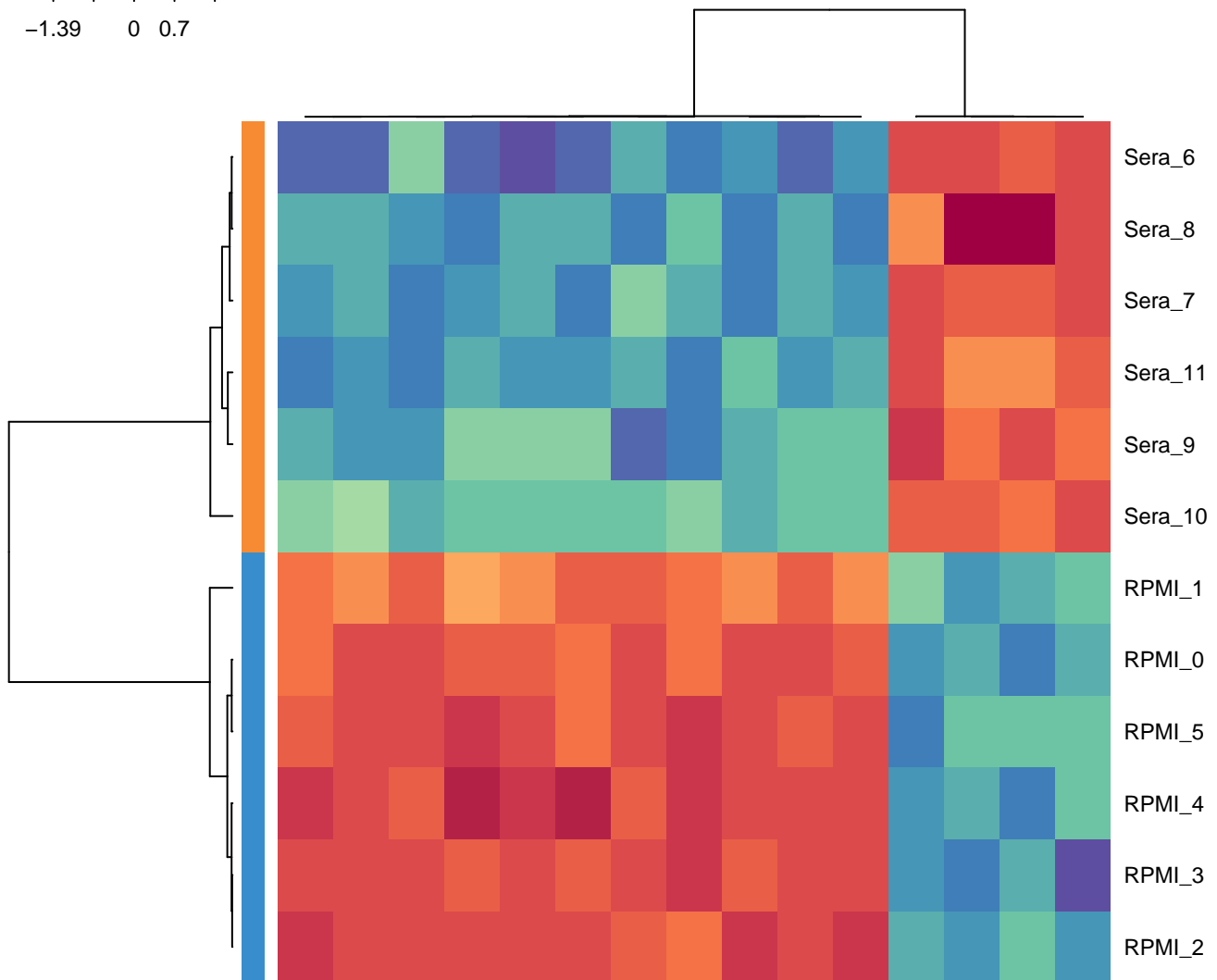
Color key



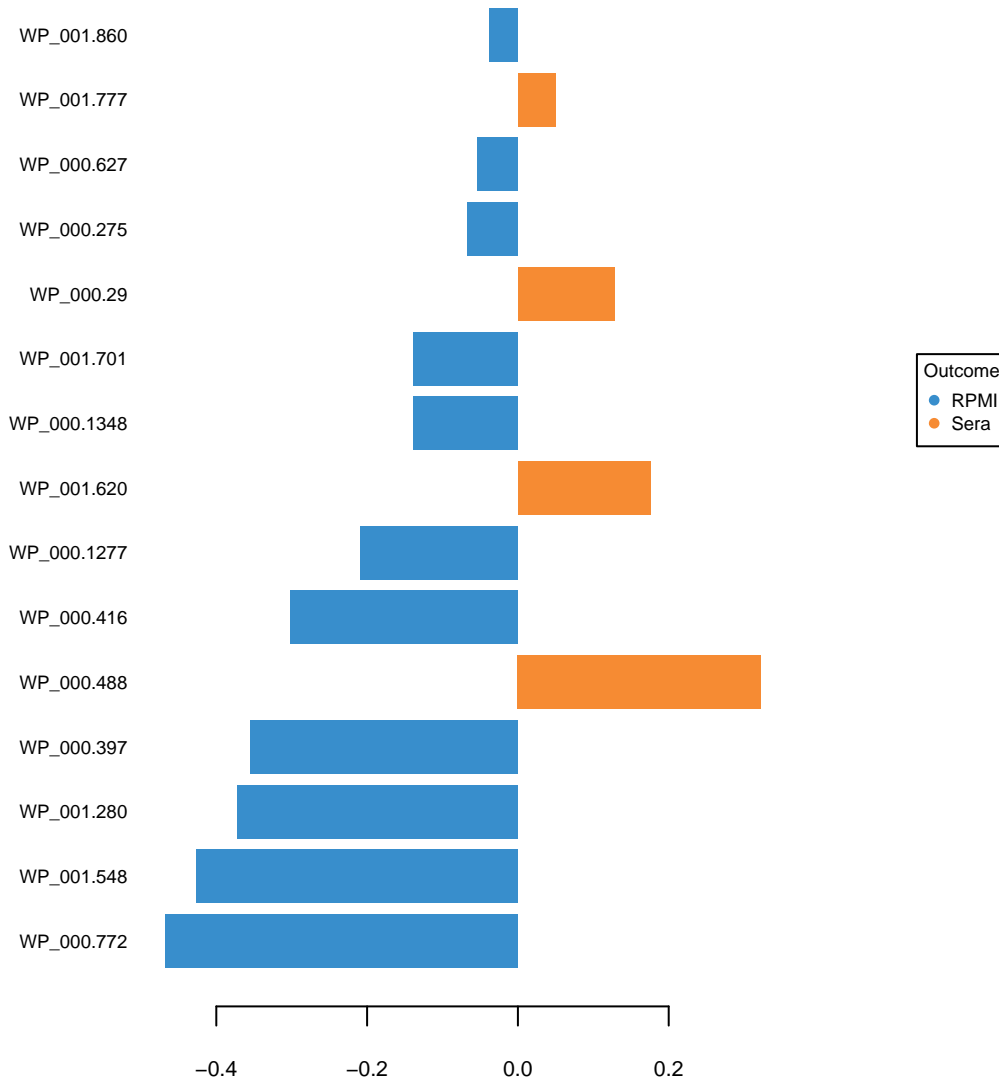
Status

RPMI

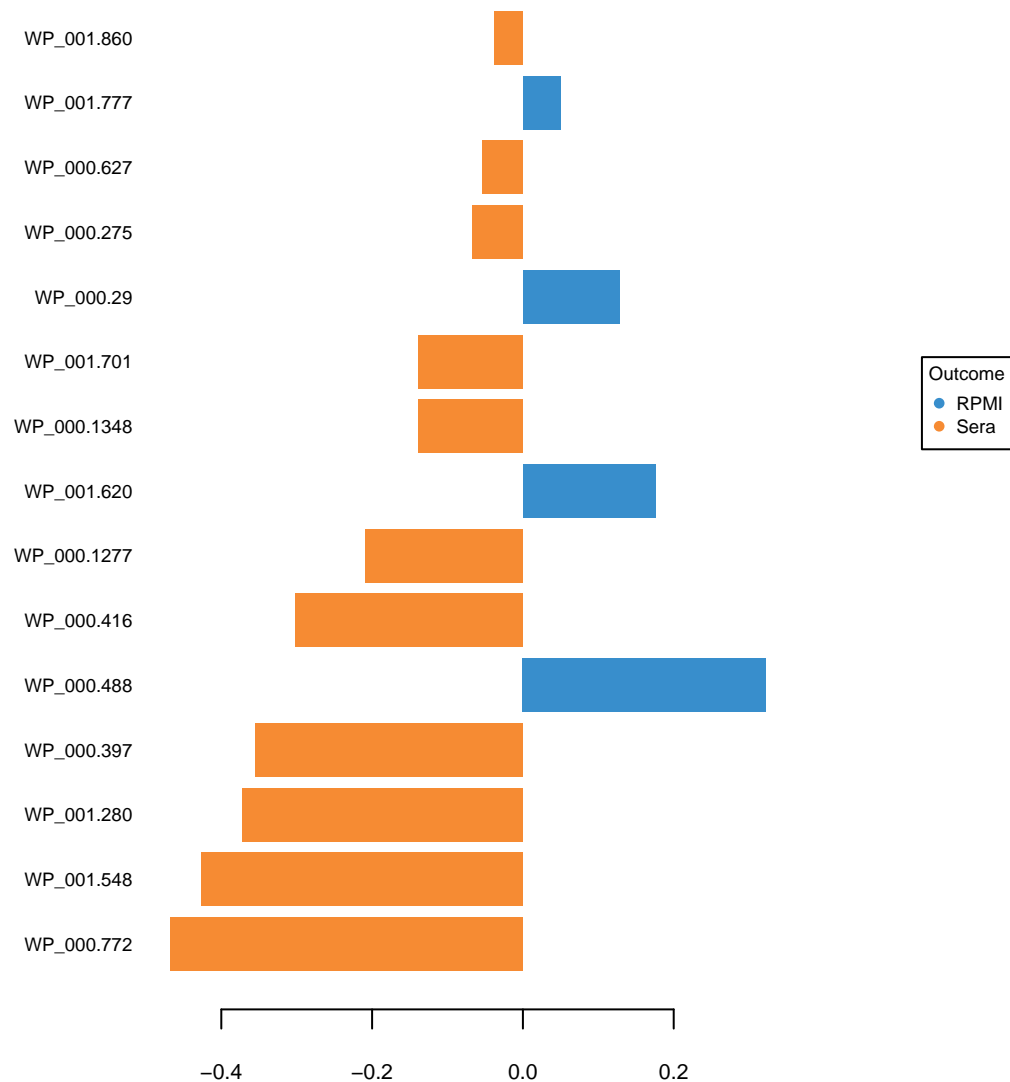
Sera

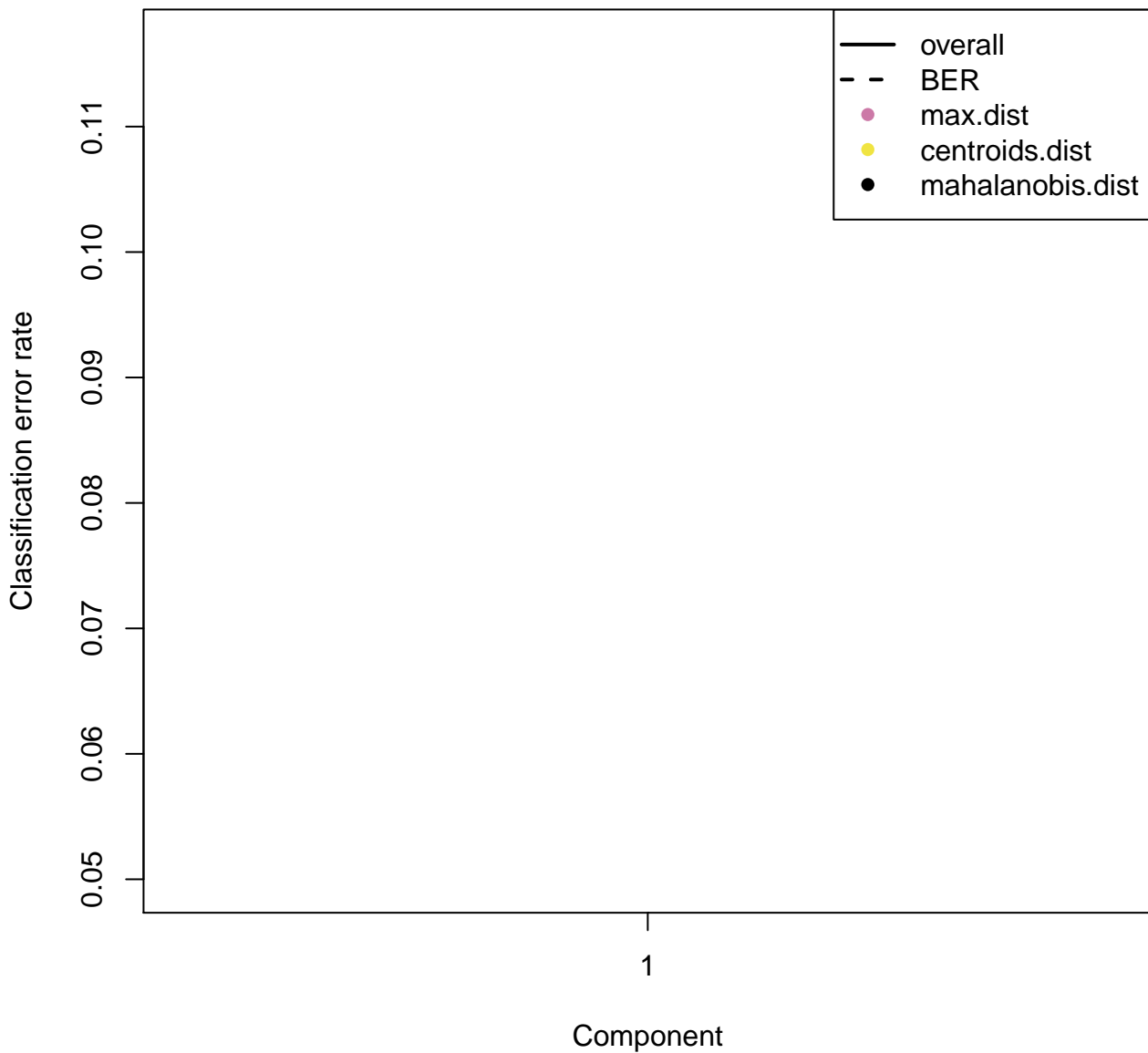


# proteome 1 sPLSDA max loadings

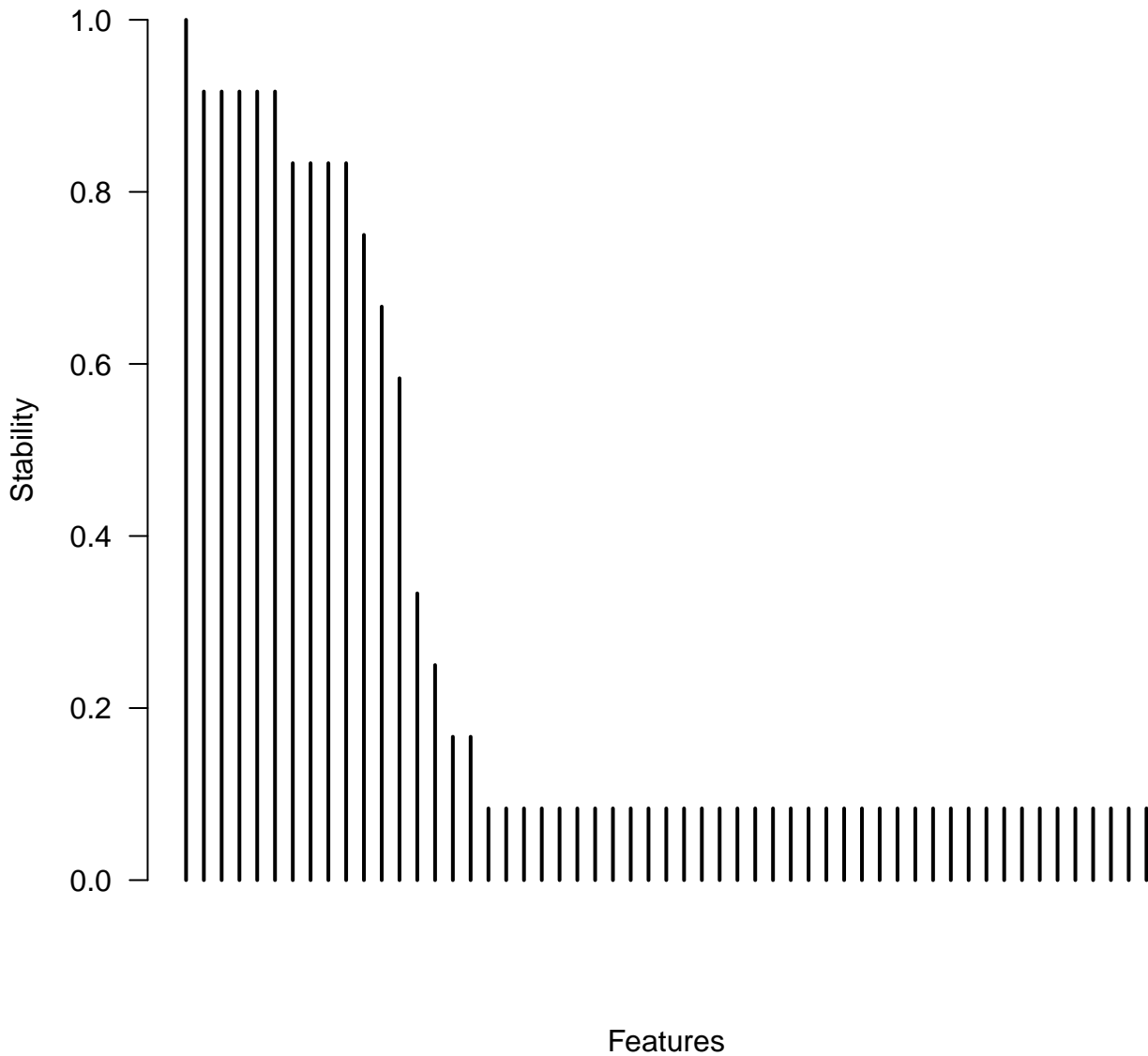


# proteome 1 sPLSDA min loadings

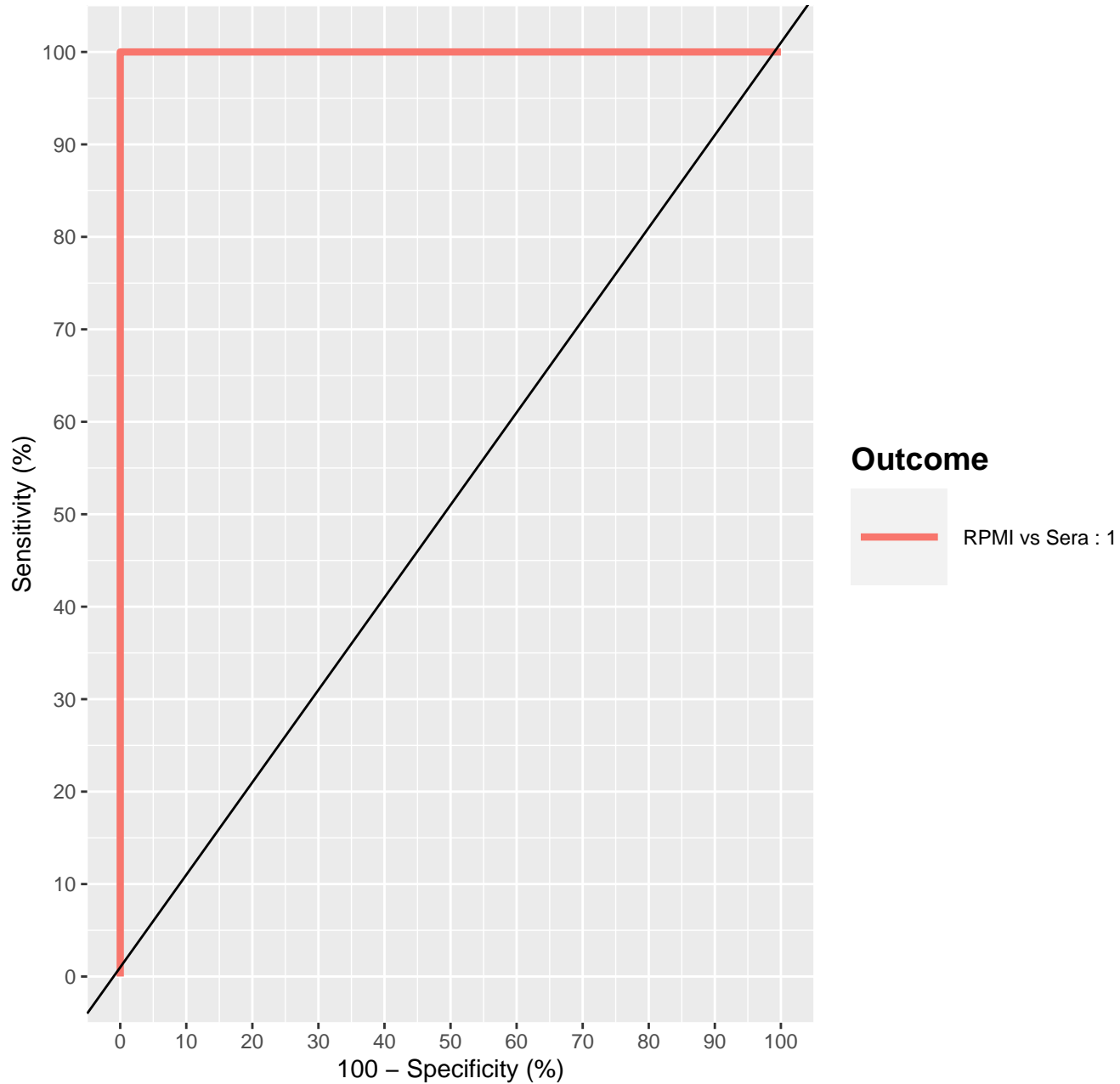




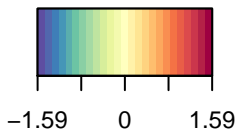
# Comp 1



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



Color key

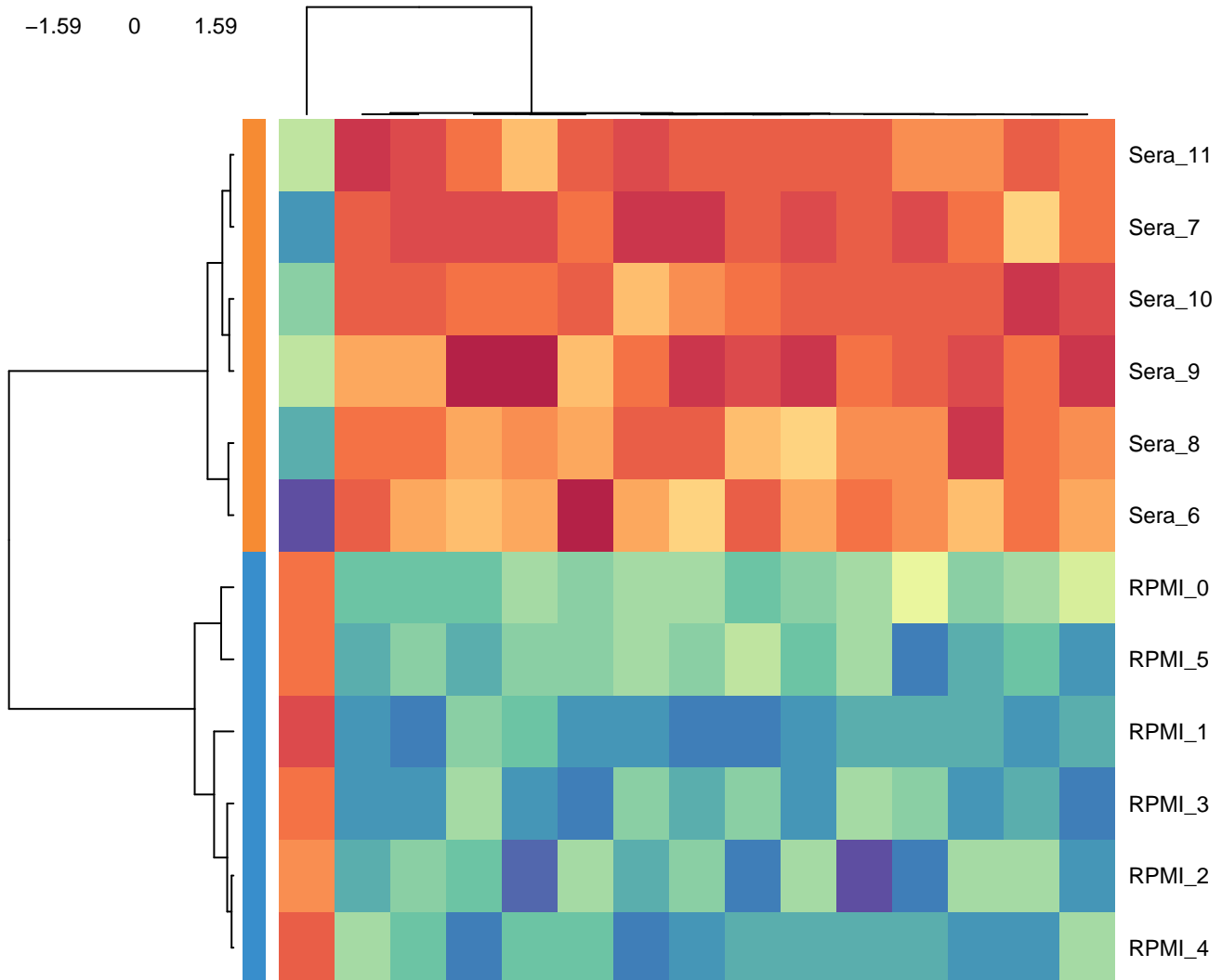


sPLSDA

Status

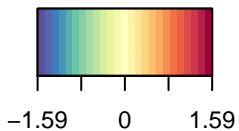
RPMI

Sera



# sPLSDA Component 1

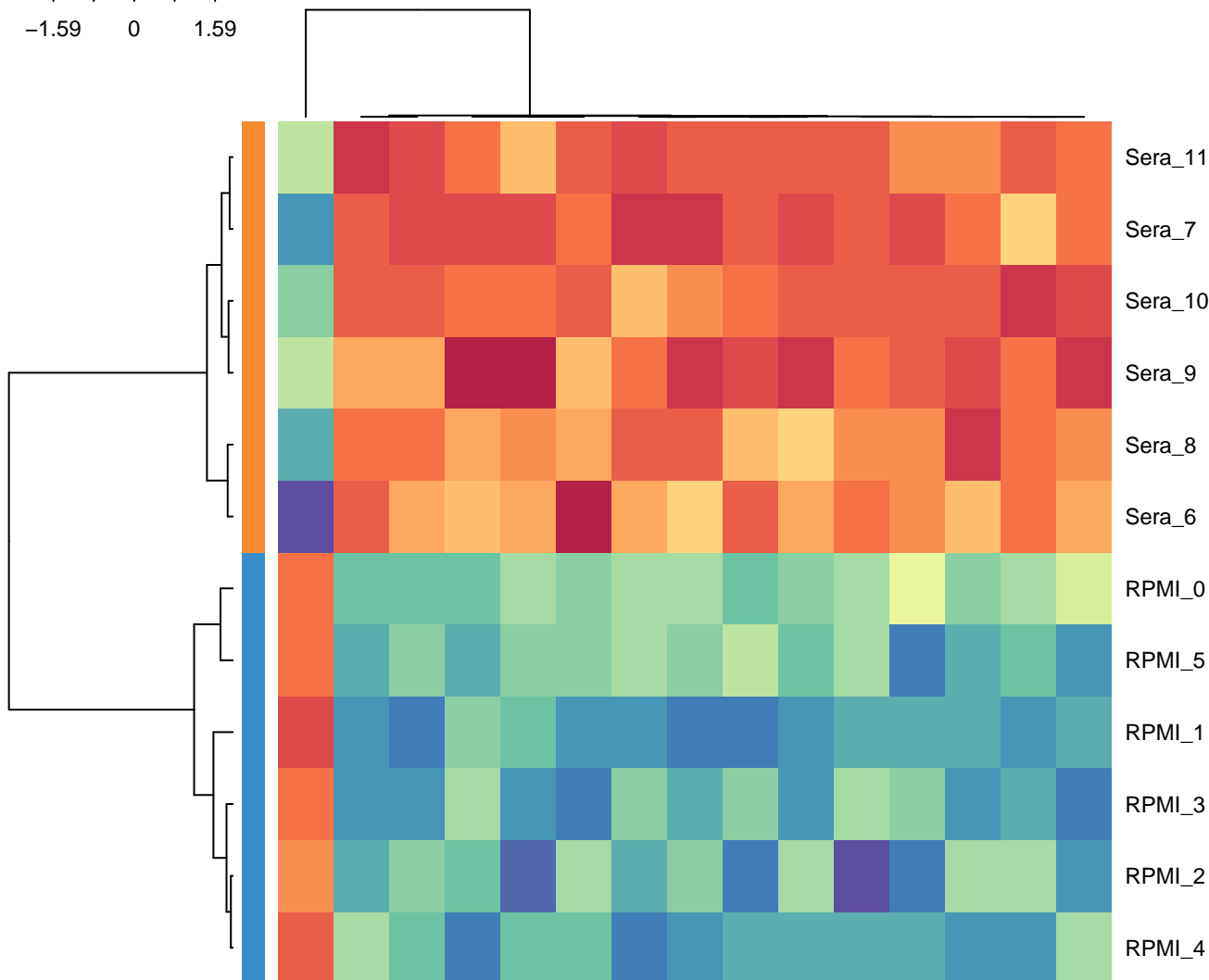
Color key



Status

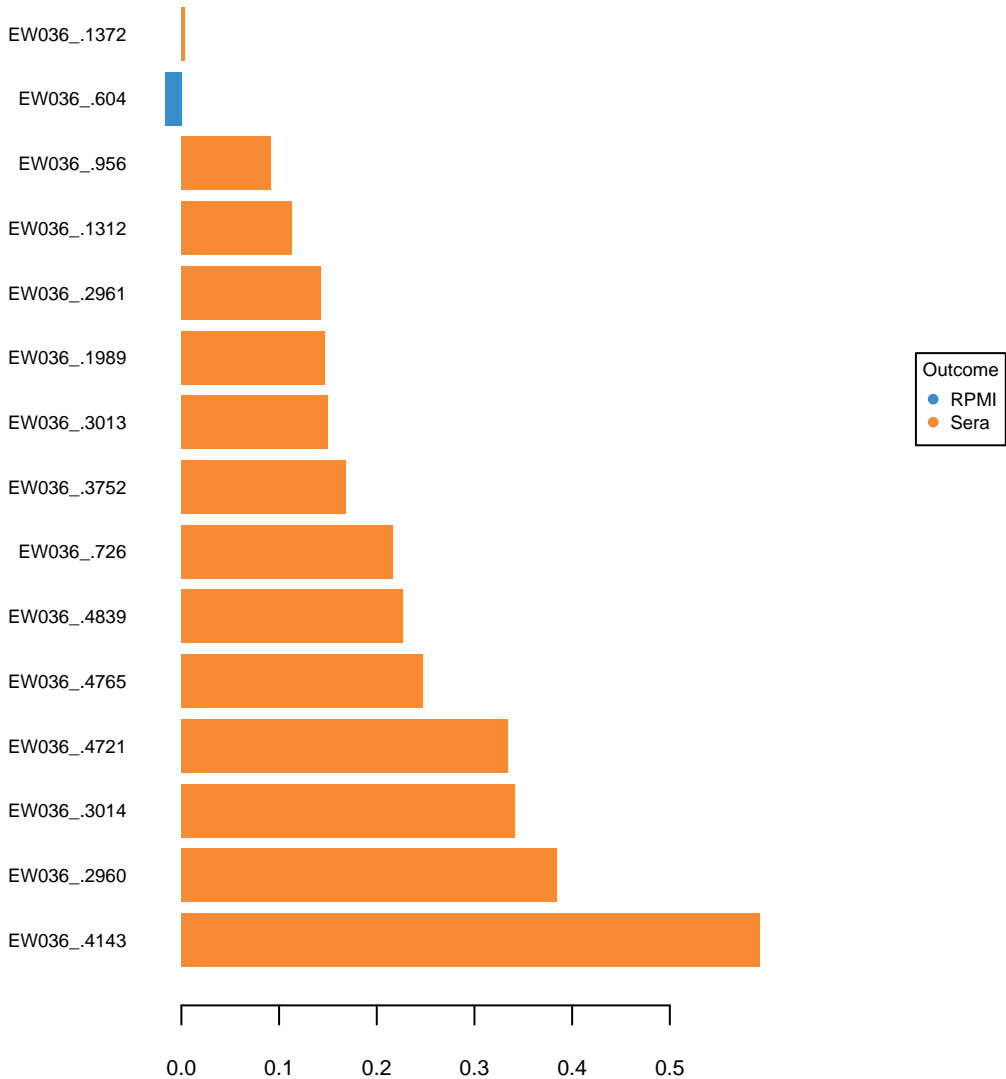
RPMI

Sera

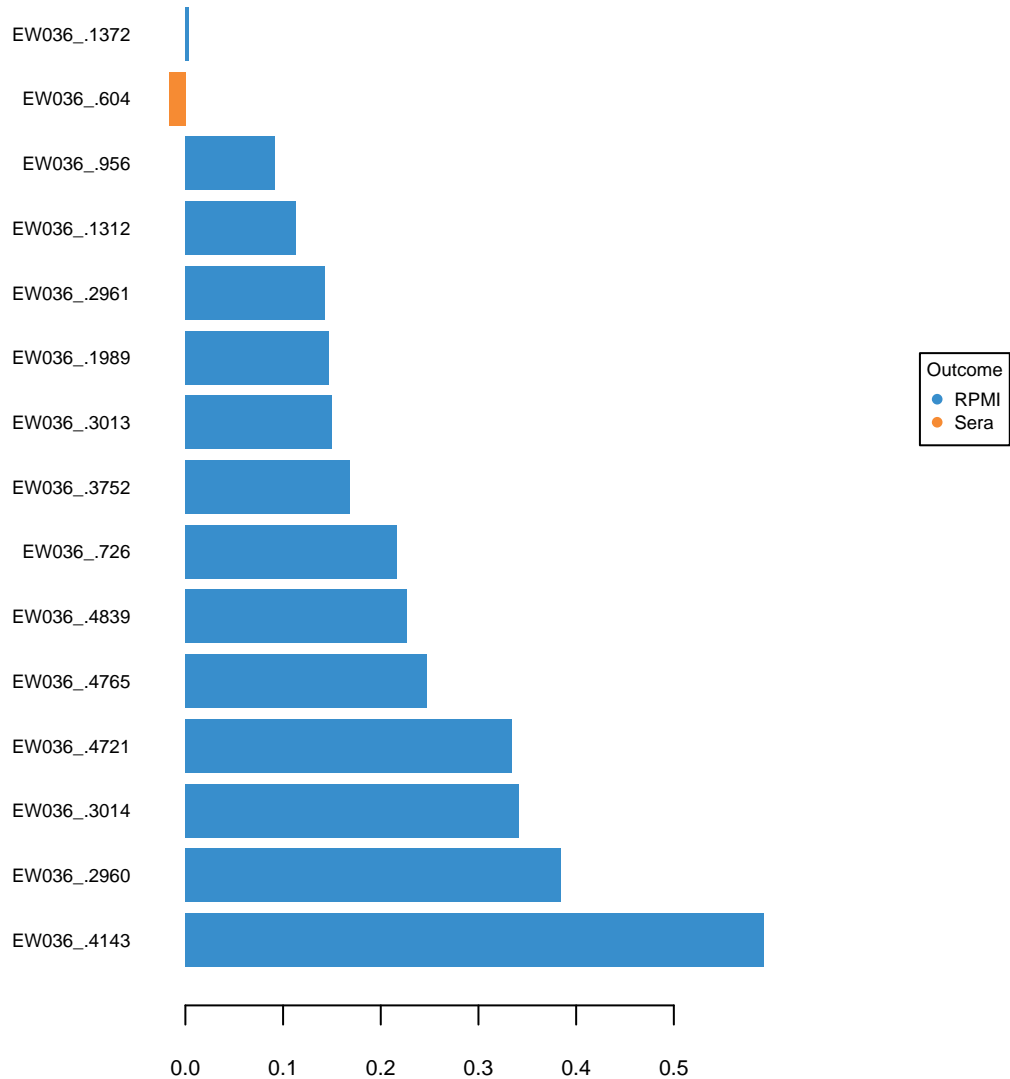


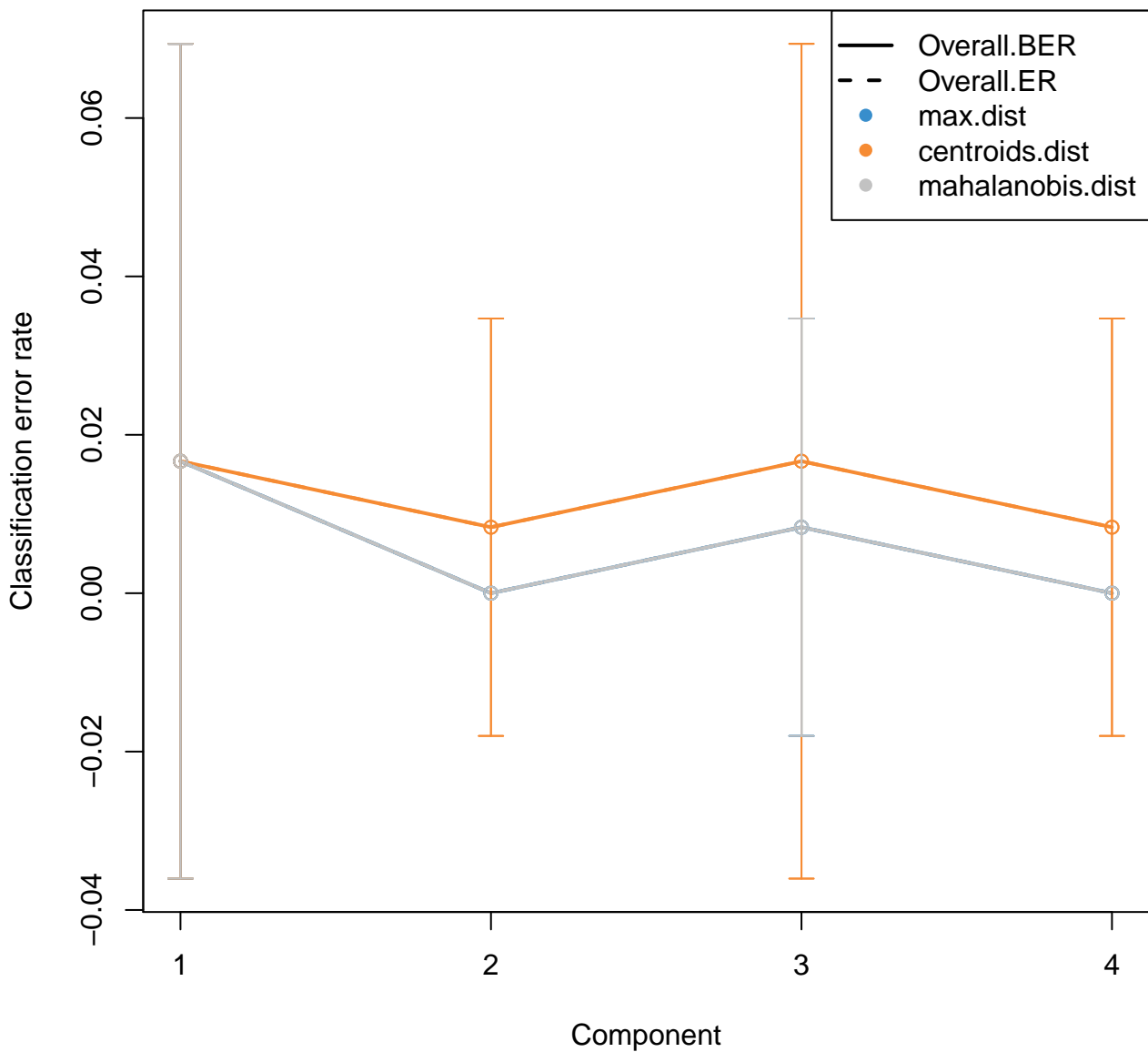


# transcriptome 1 sPLSDA max loa

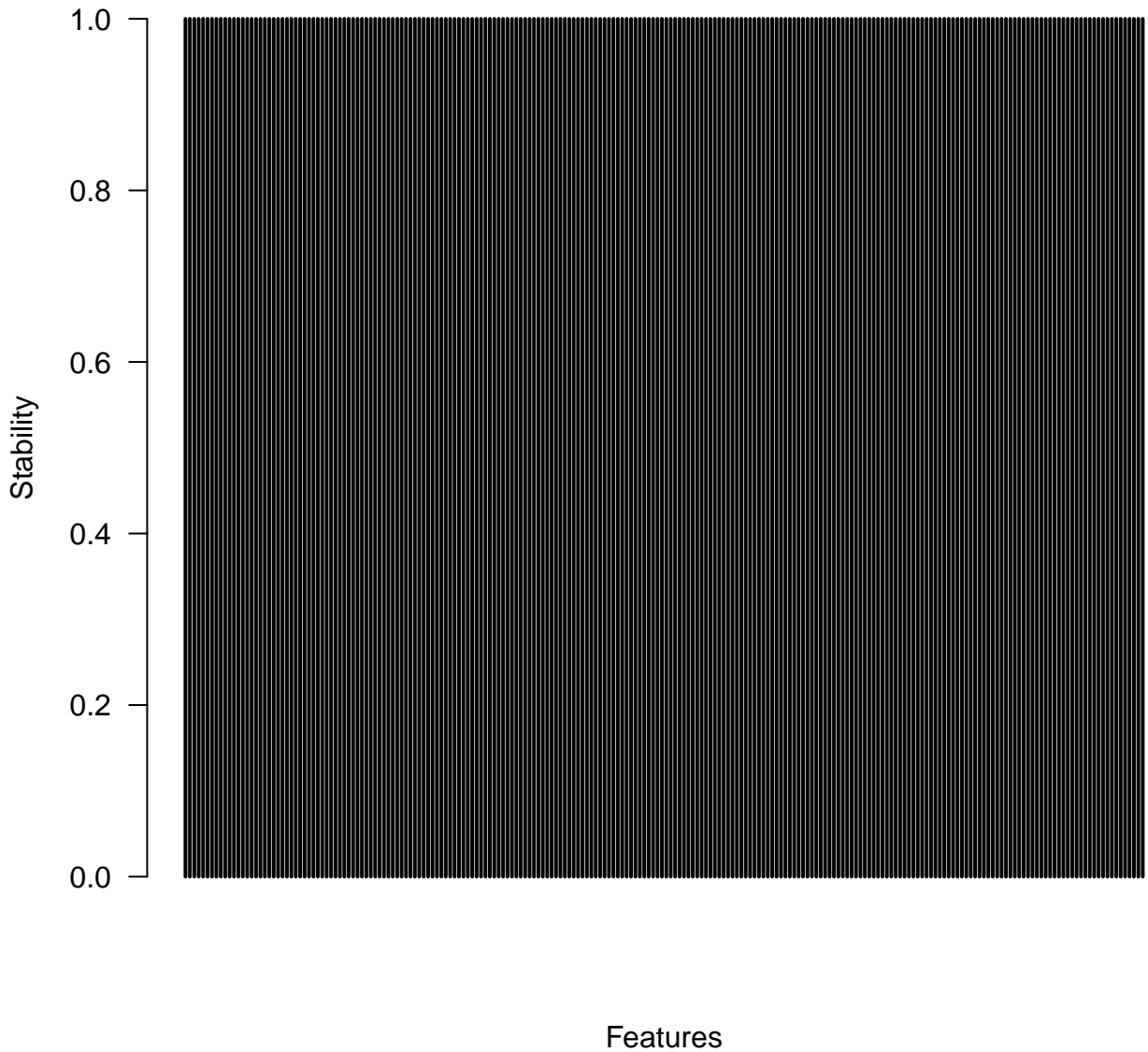


# transcriptome 1 sPLSDA min loa

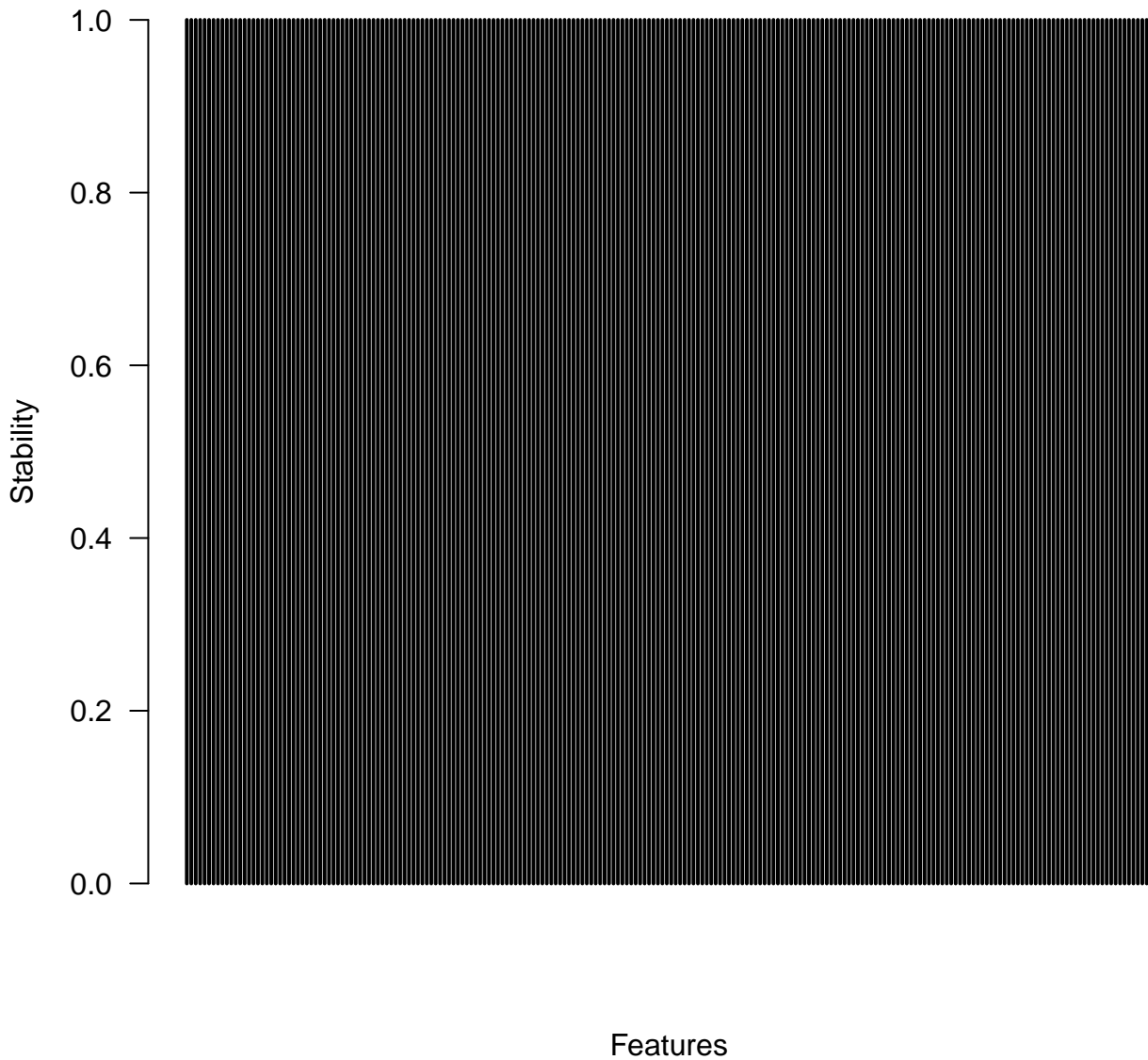




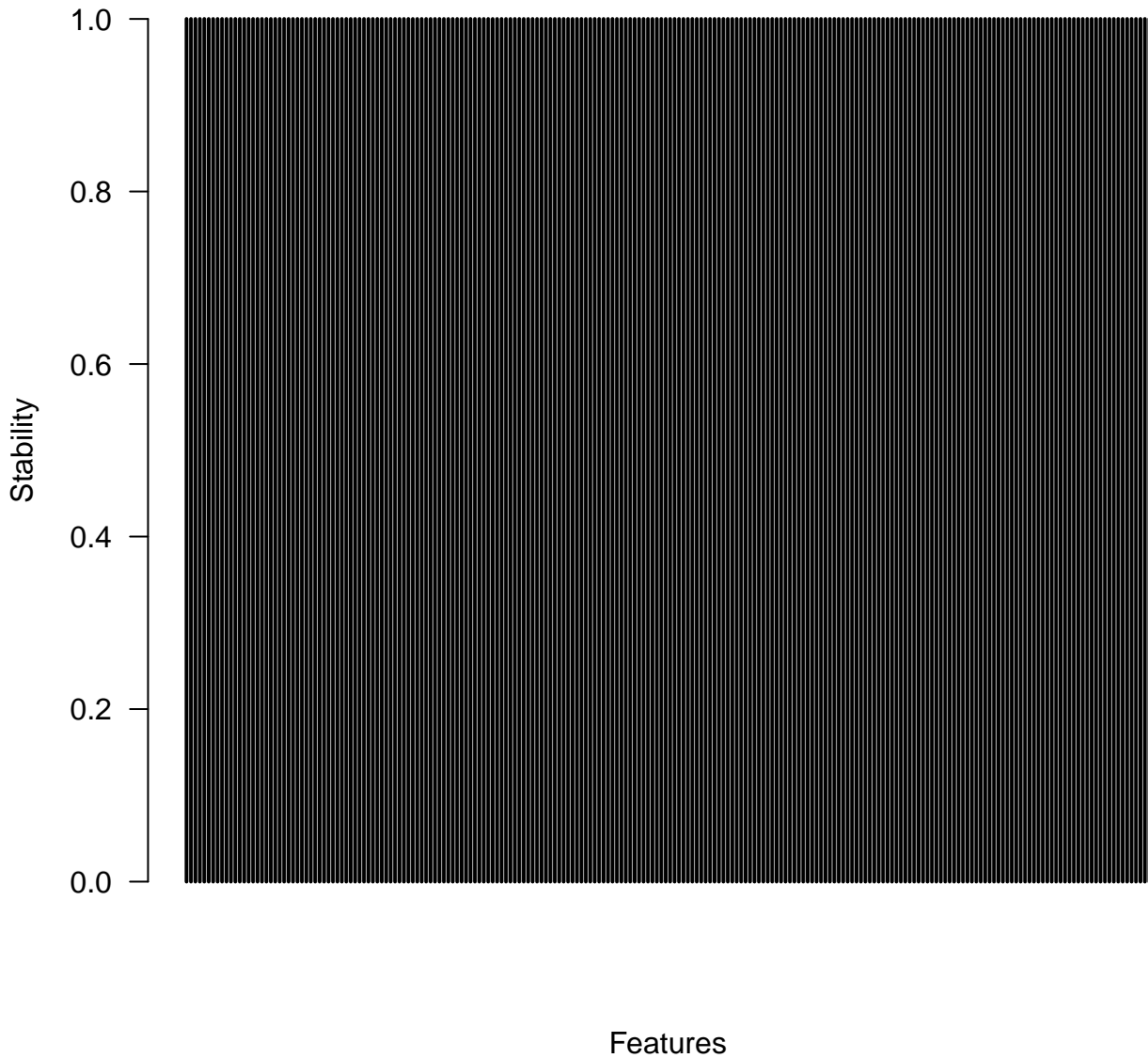
# metabolome Comp 1



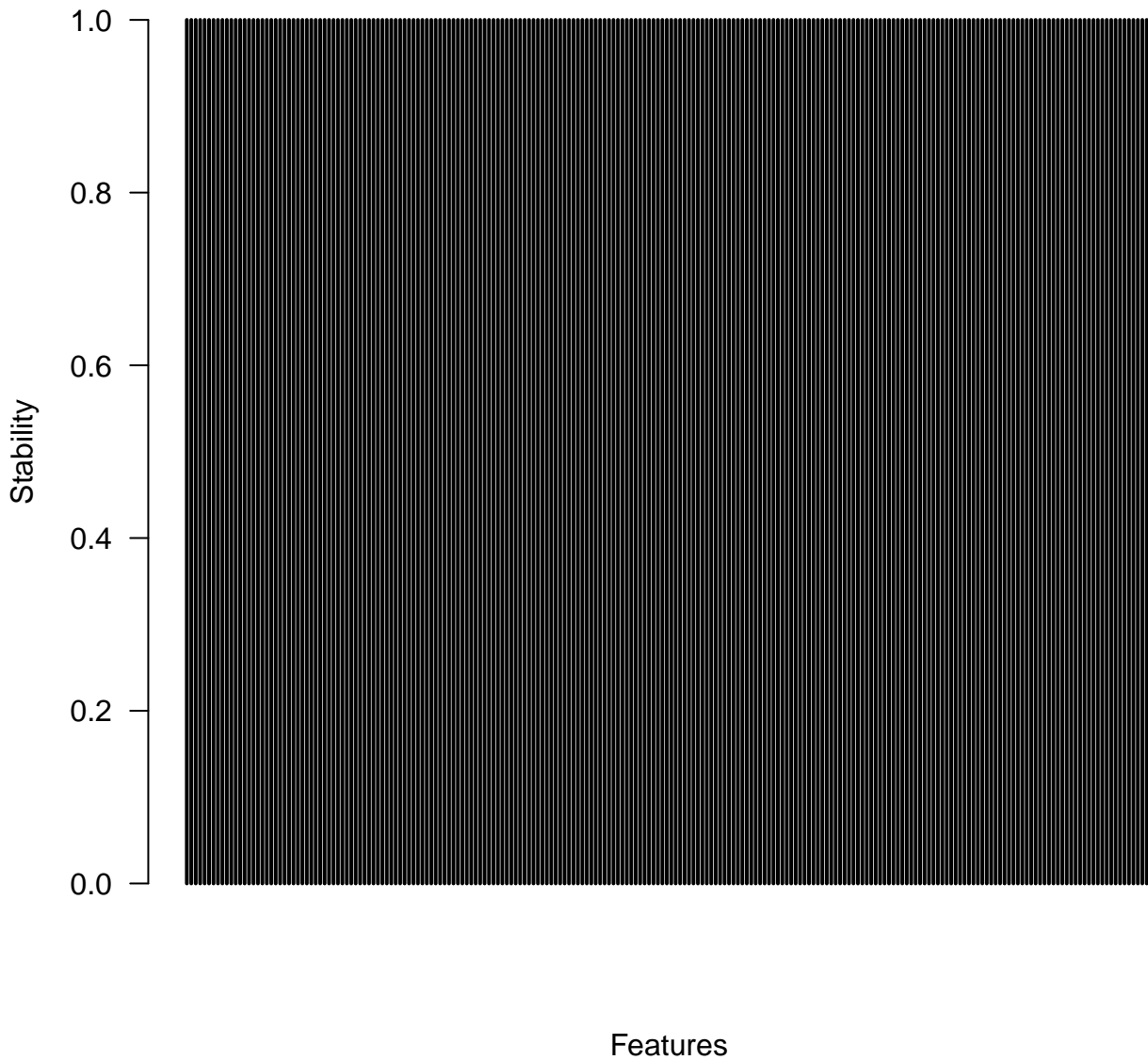
## metabolome Comp 2



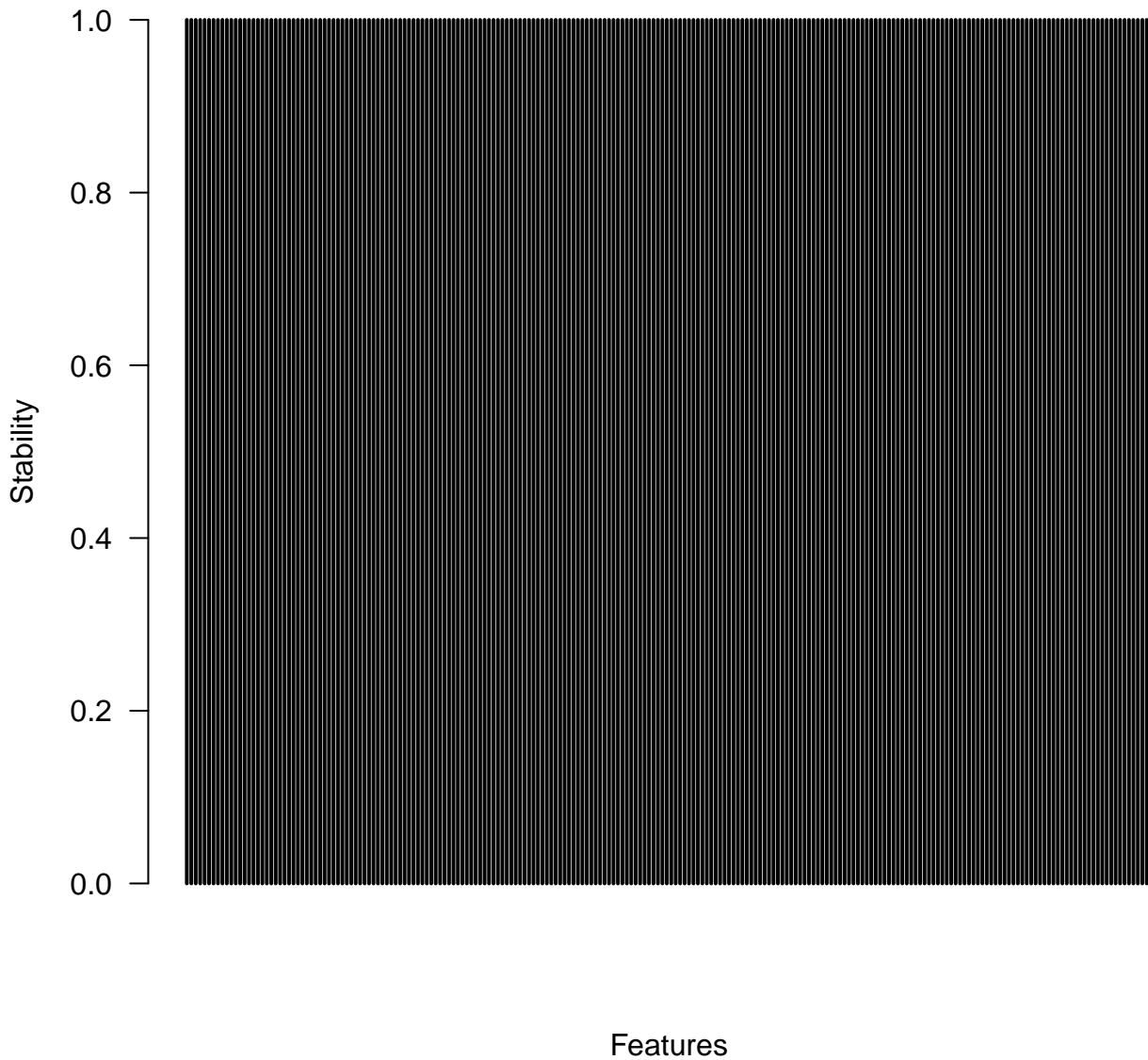
# metabolome Comp 3



# proteome Comp 1

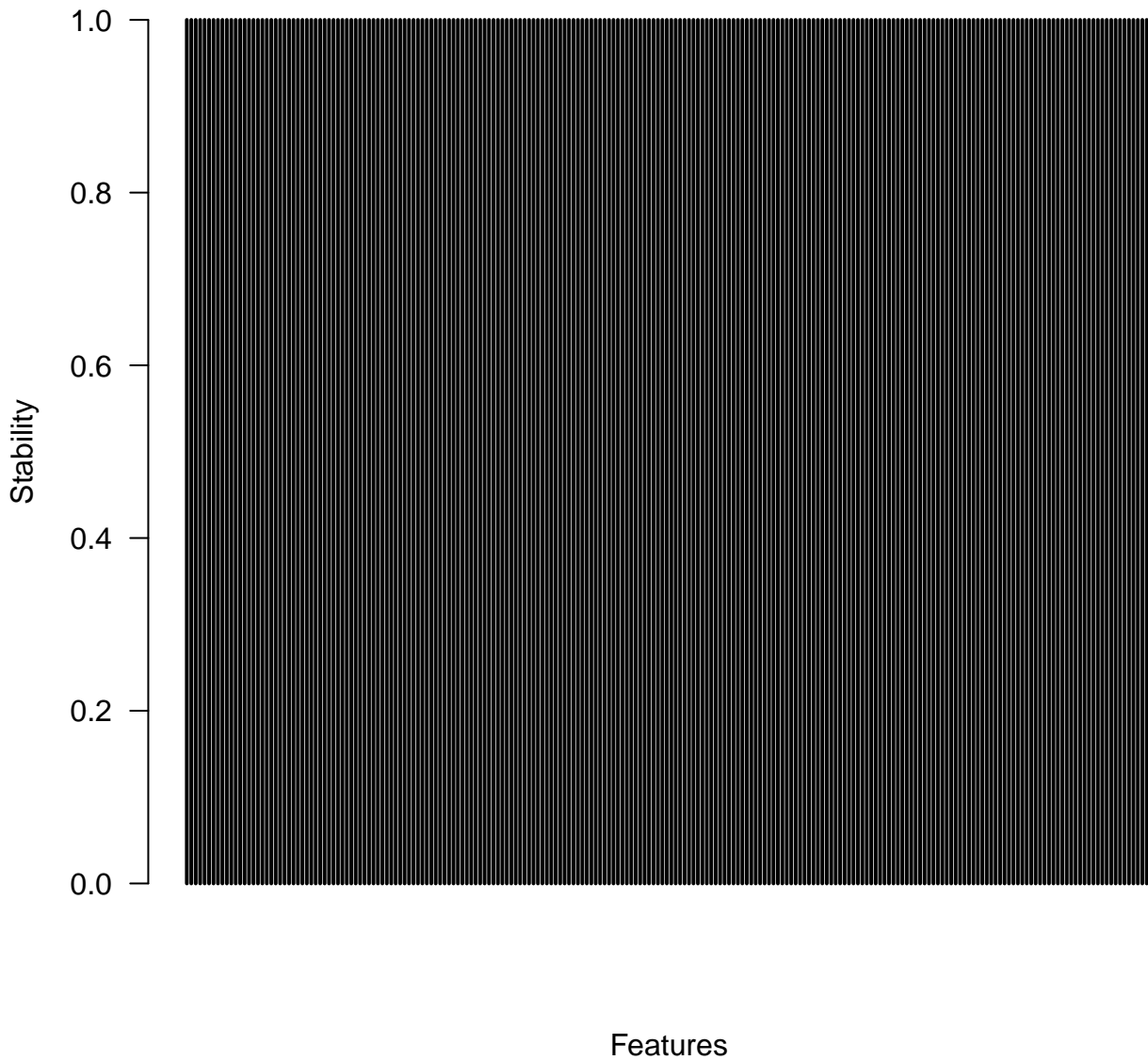


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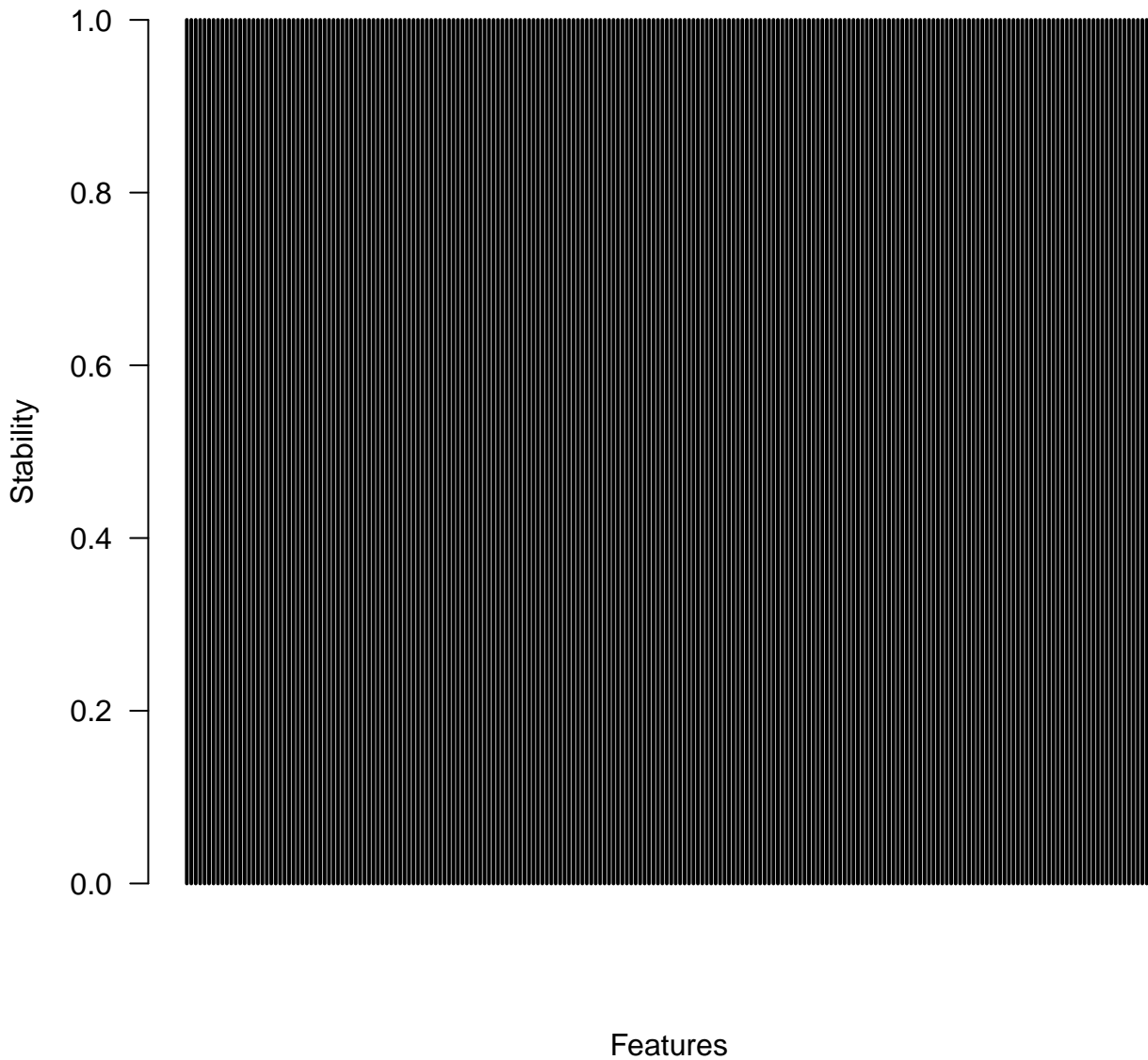




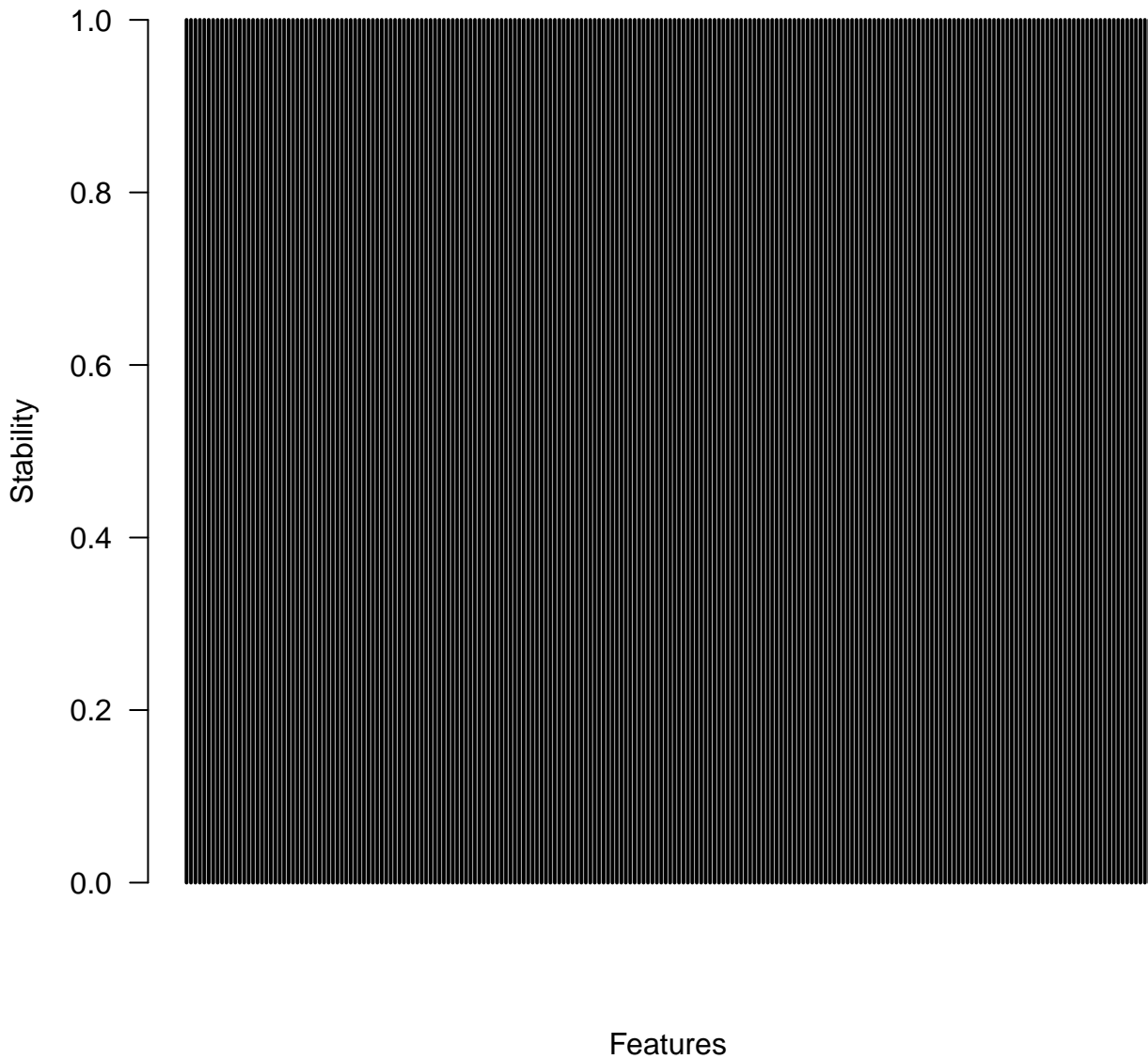
# proteome Comp 3



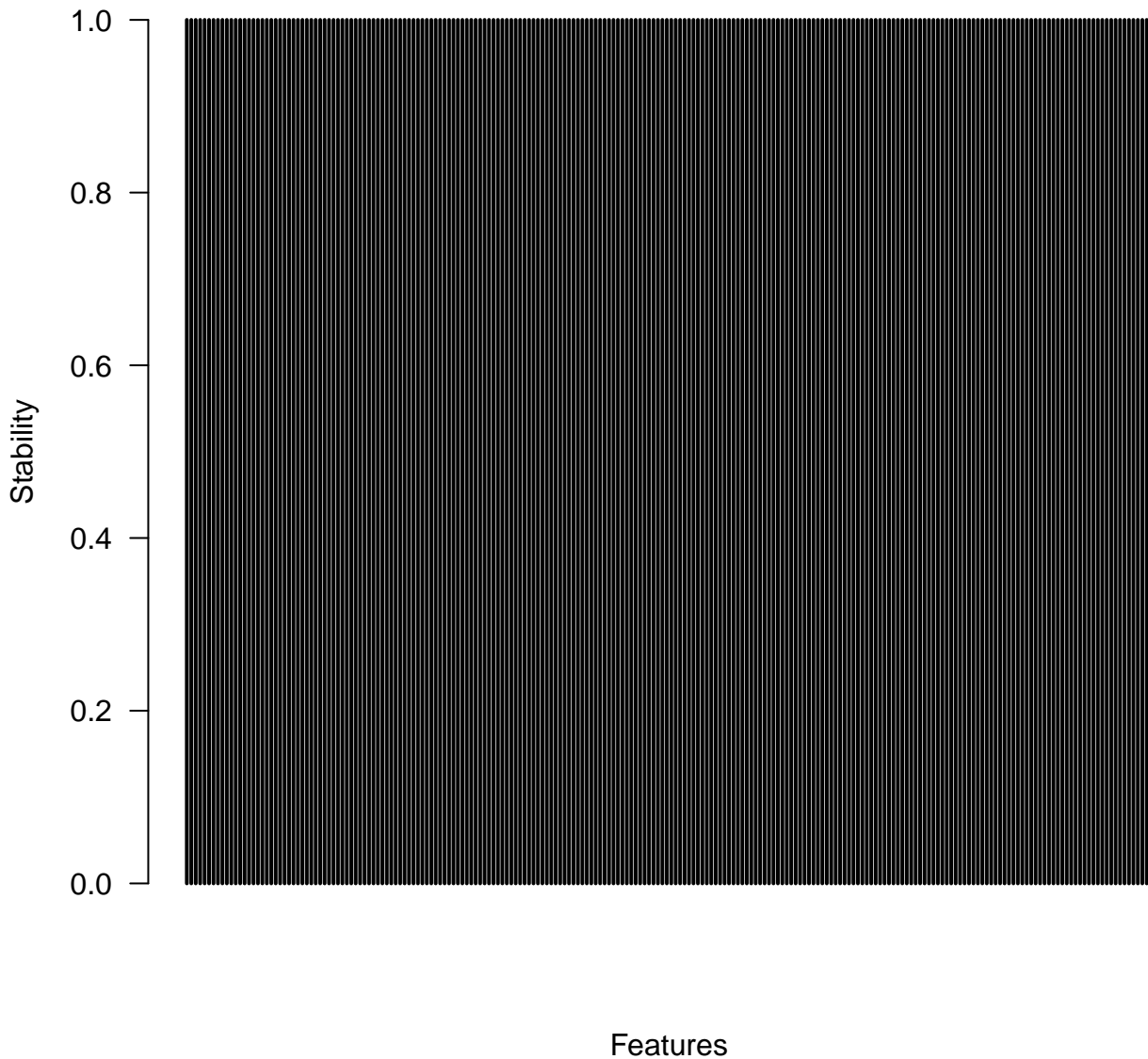
# transcriptome Comp 1



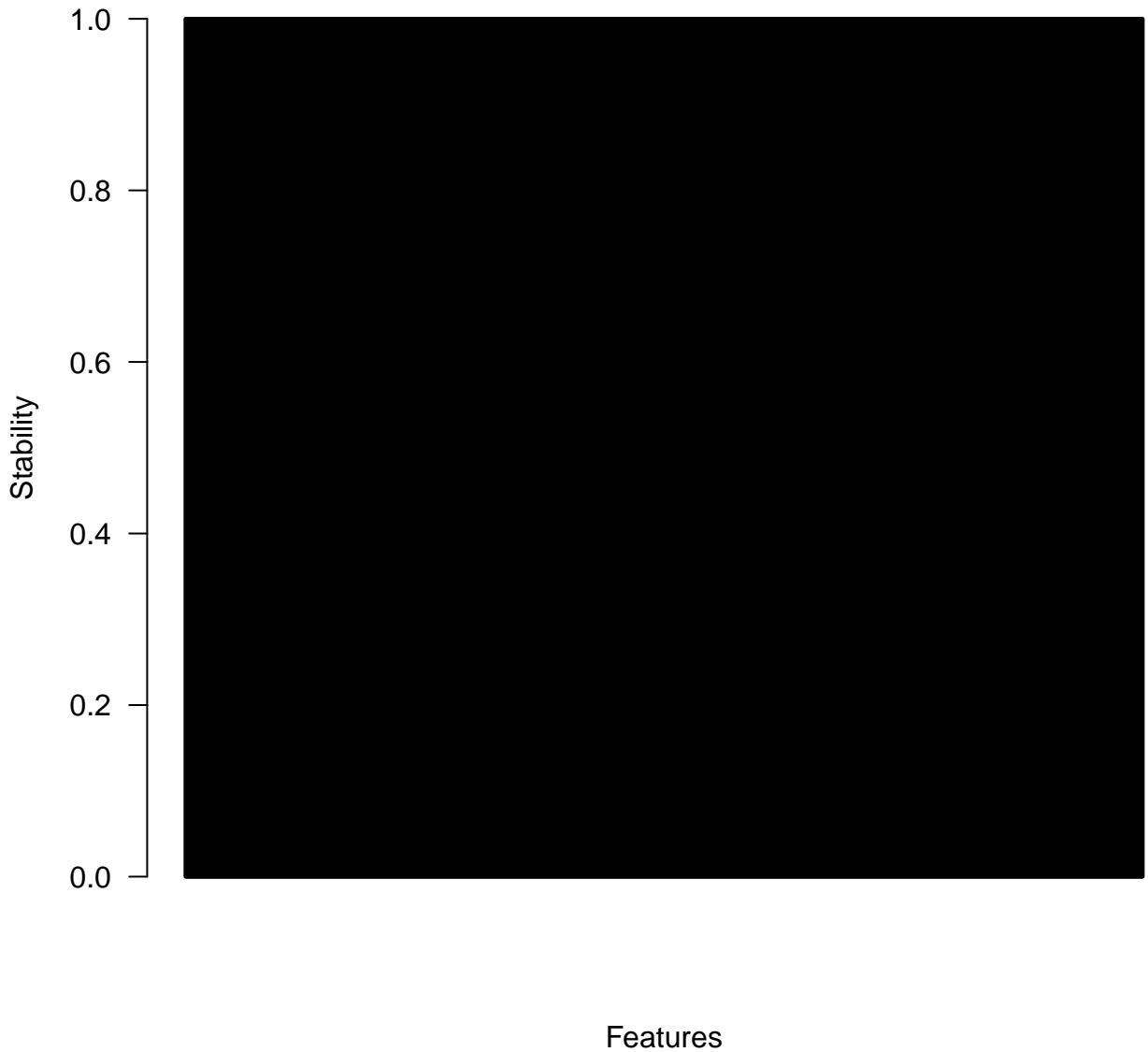
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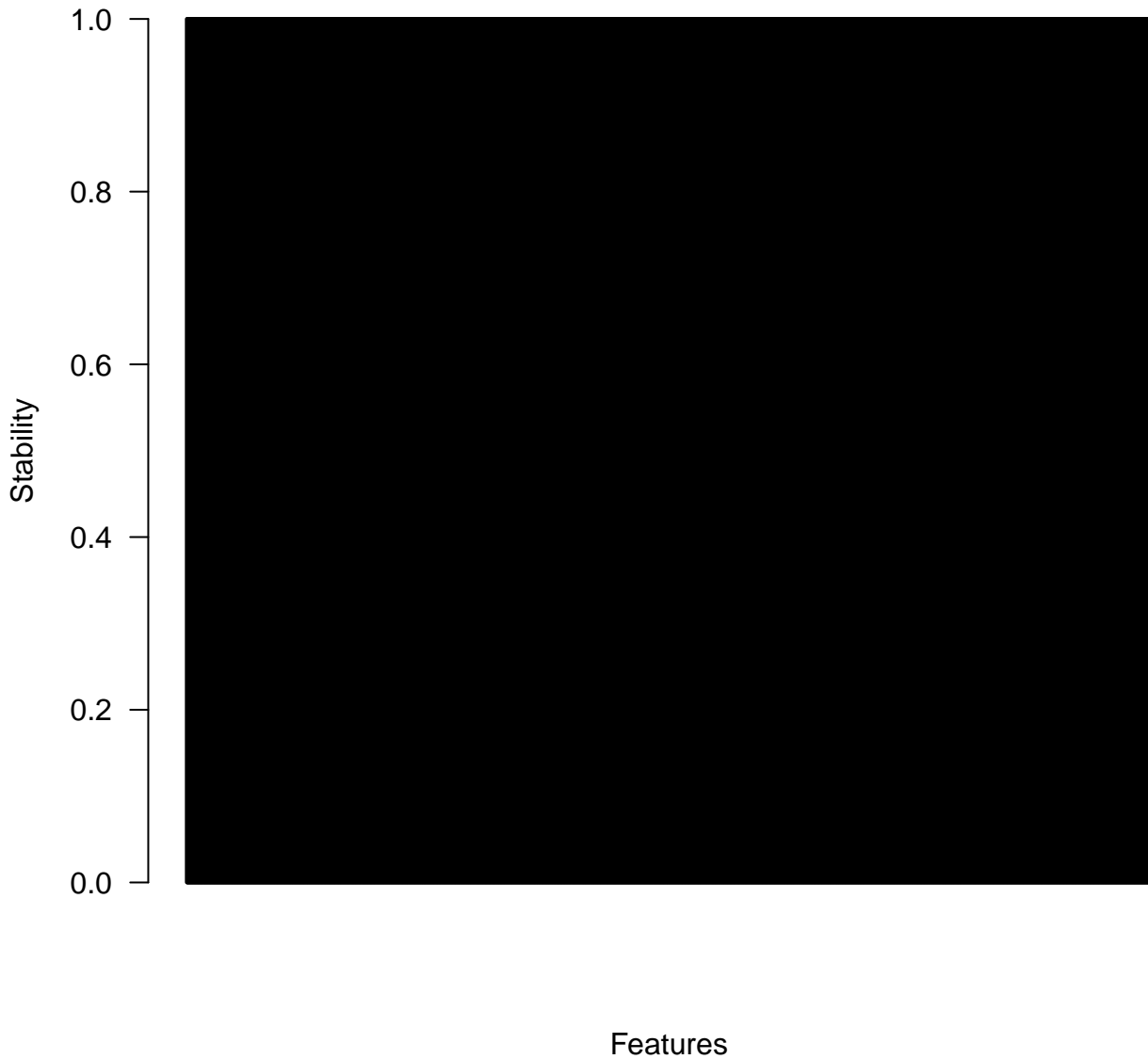
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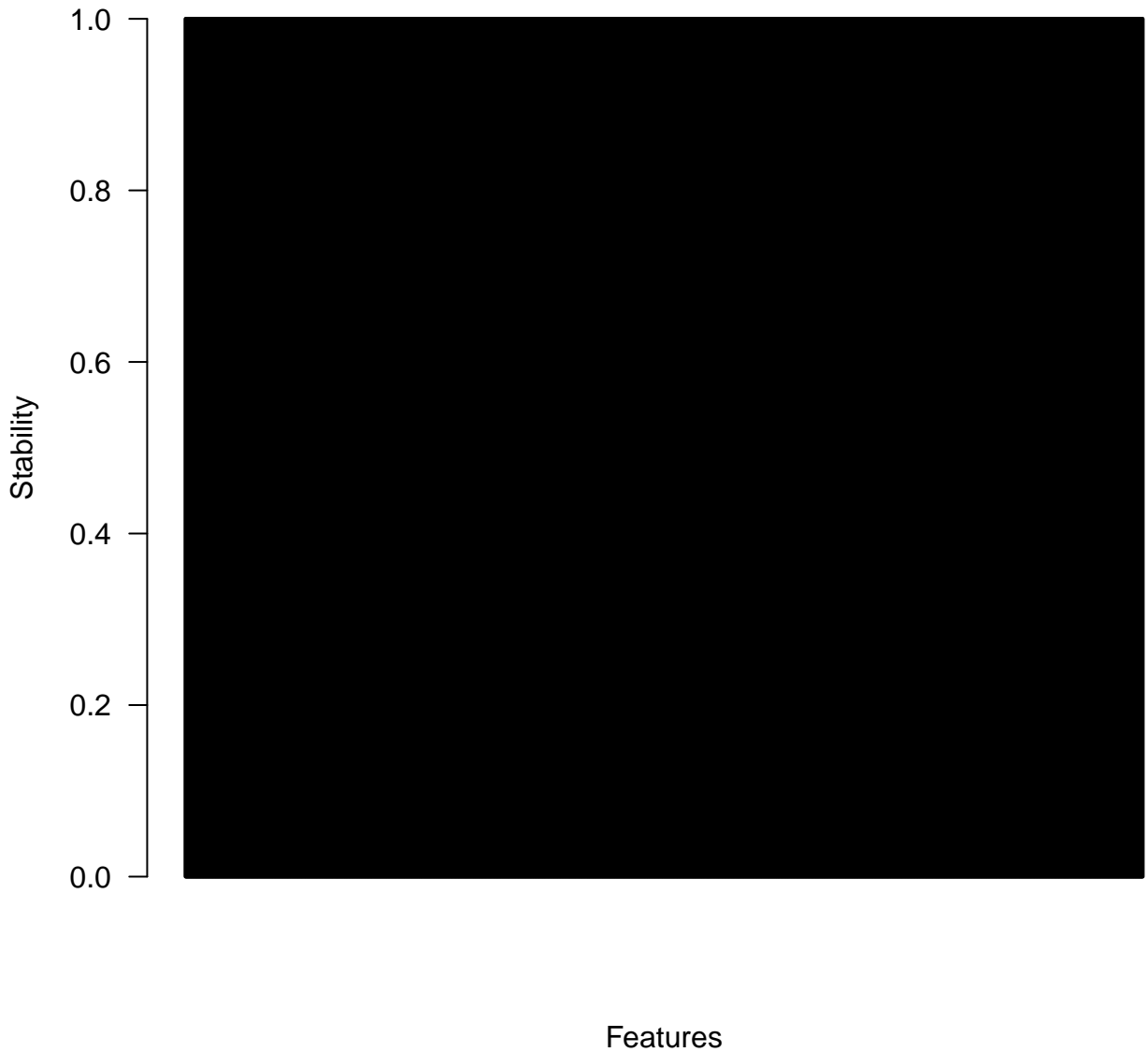
# metabolome Comp 1



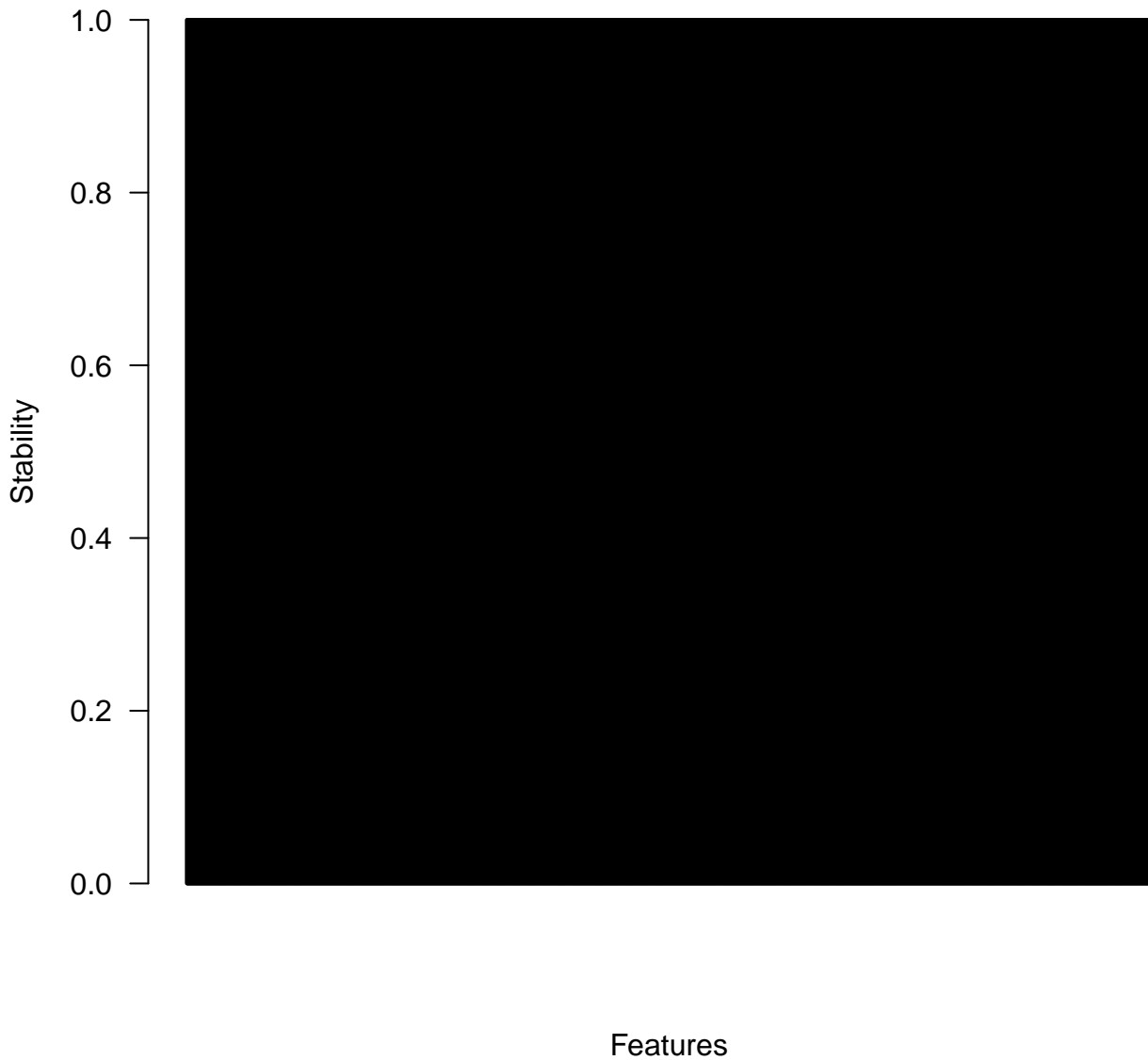
## metabolome Comp 2



# metabolome Comp 3

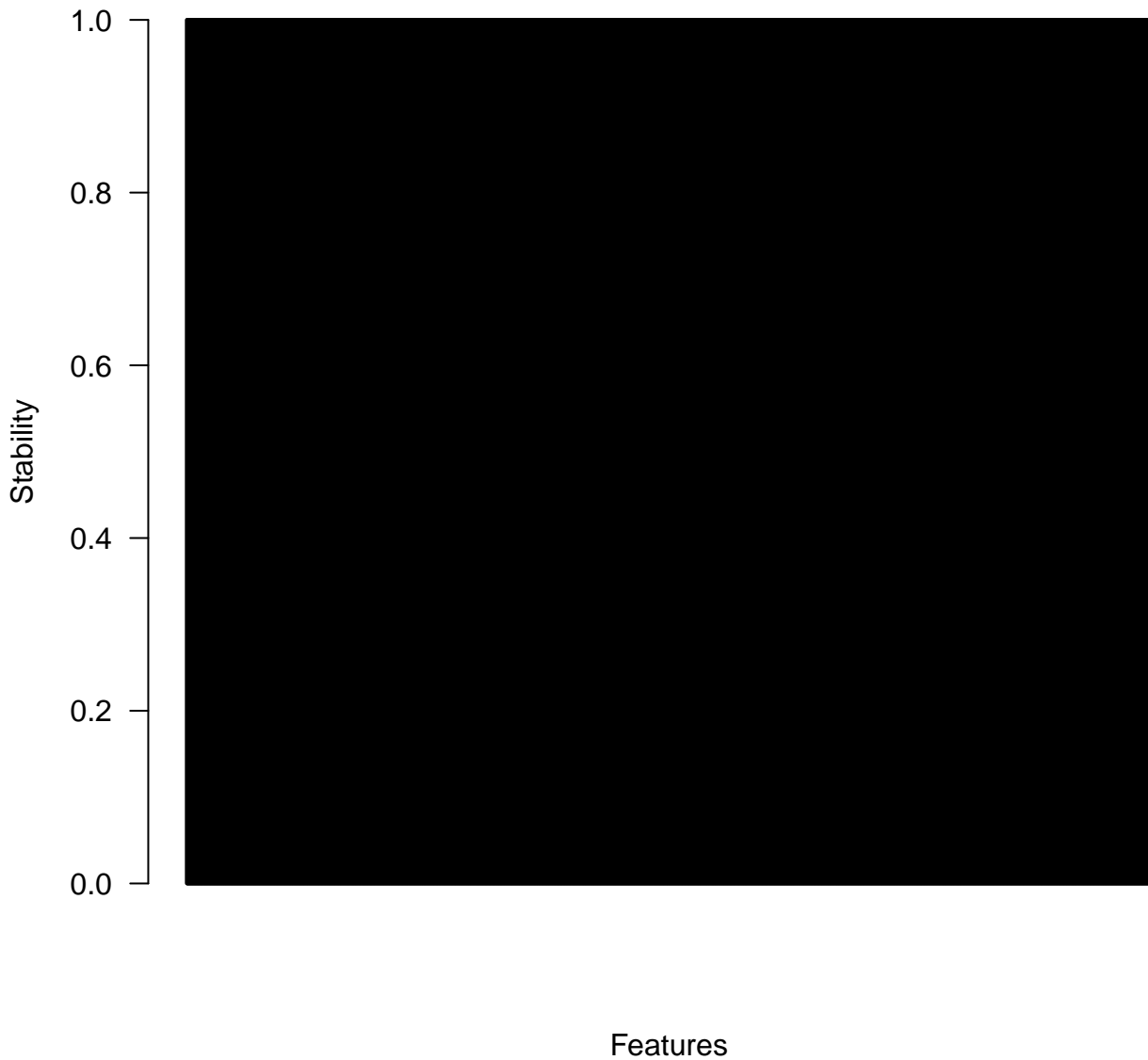


# proteome Comp 1

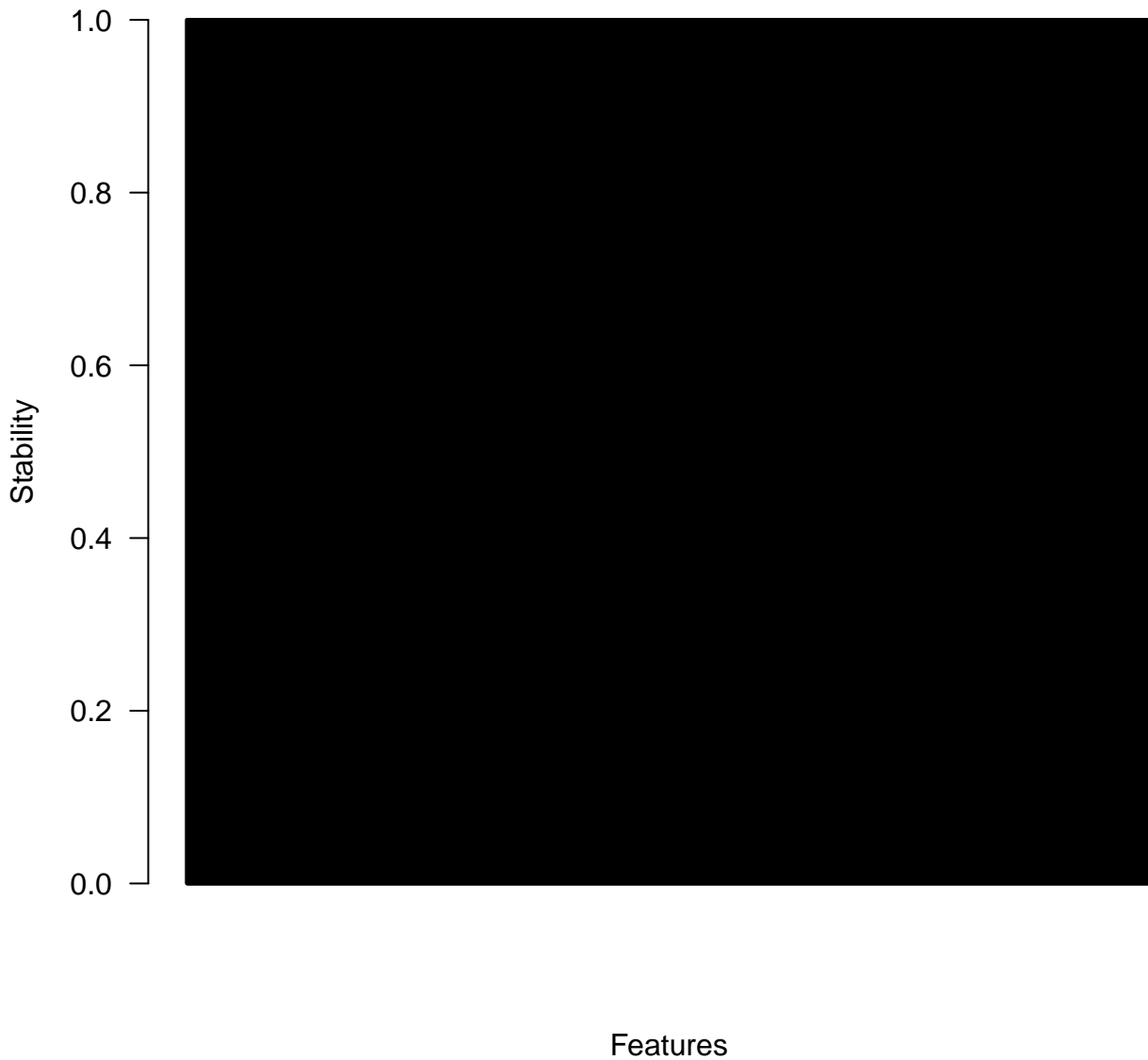




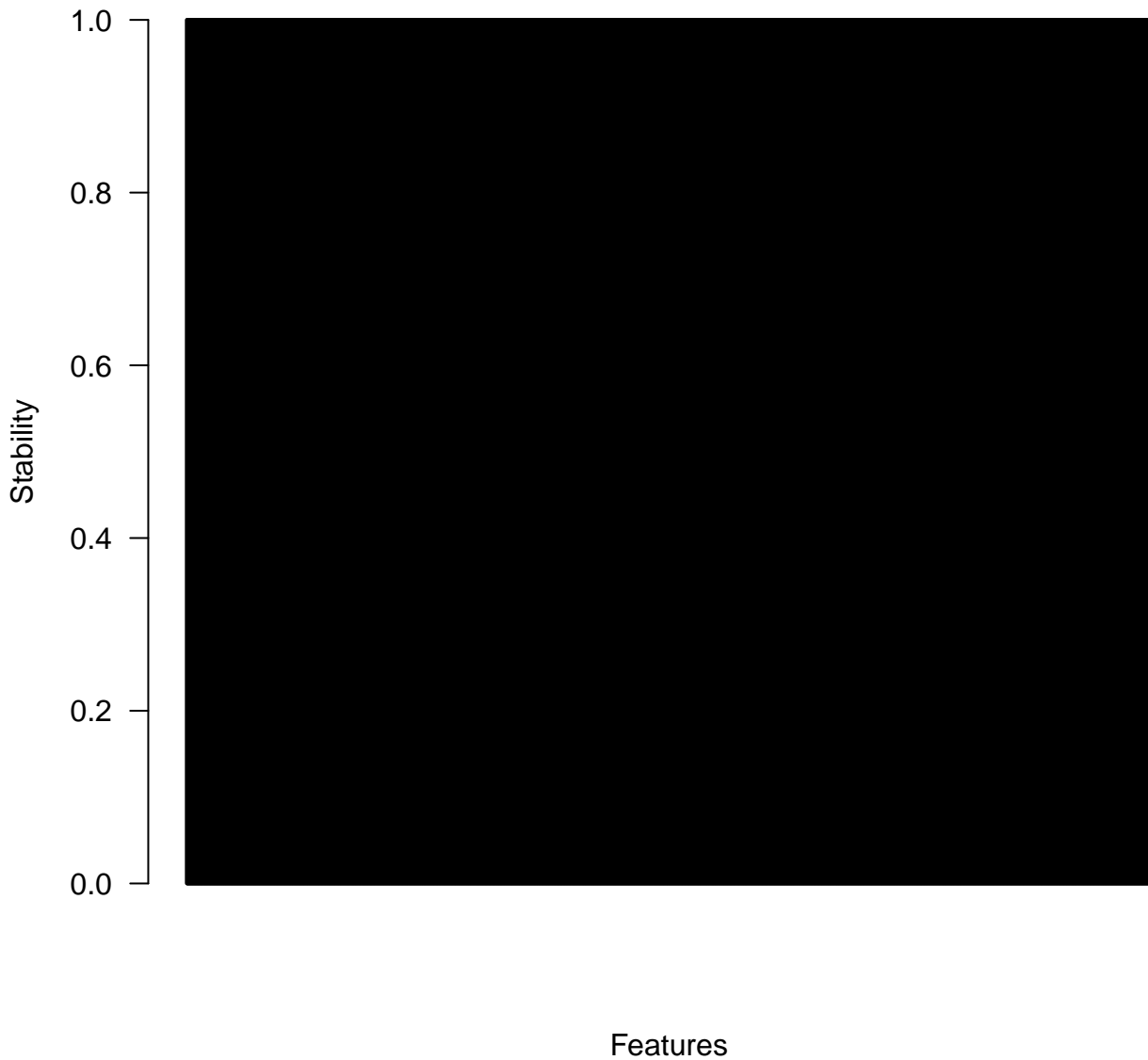
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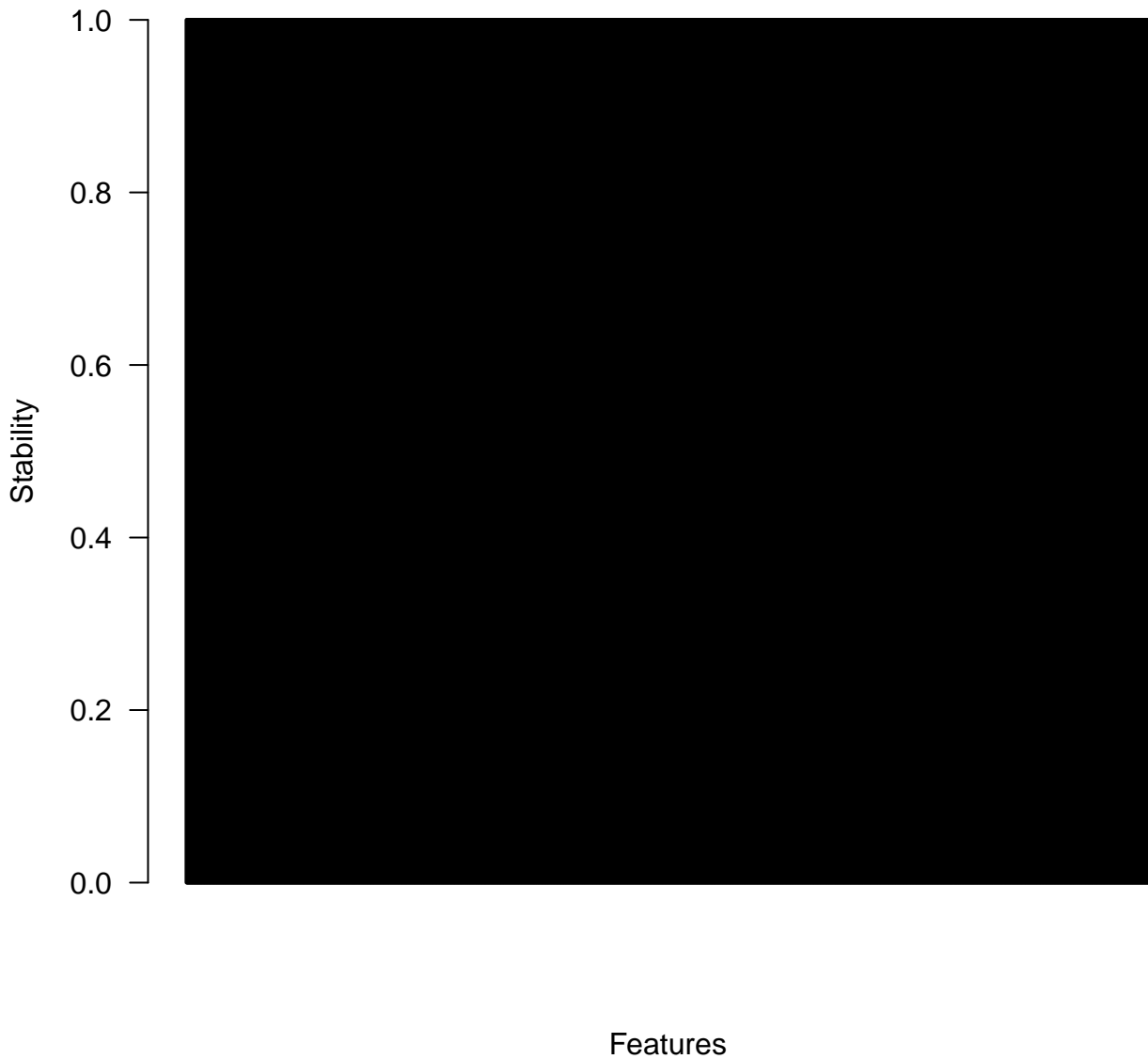
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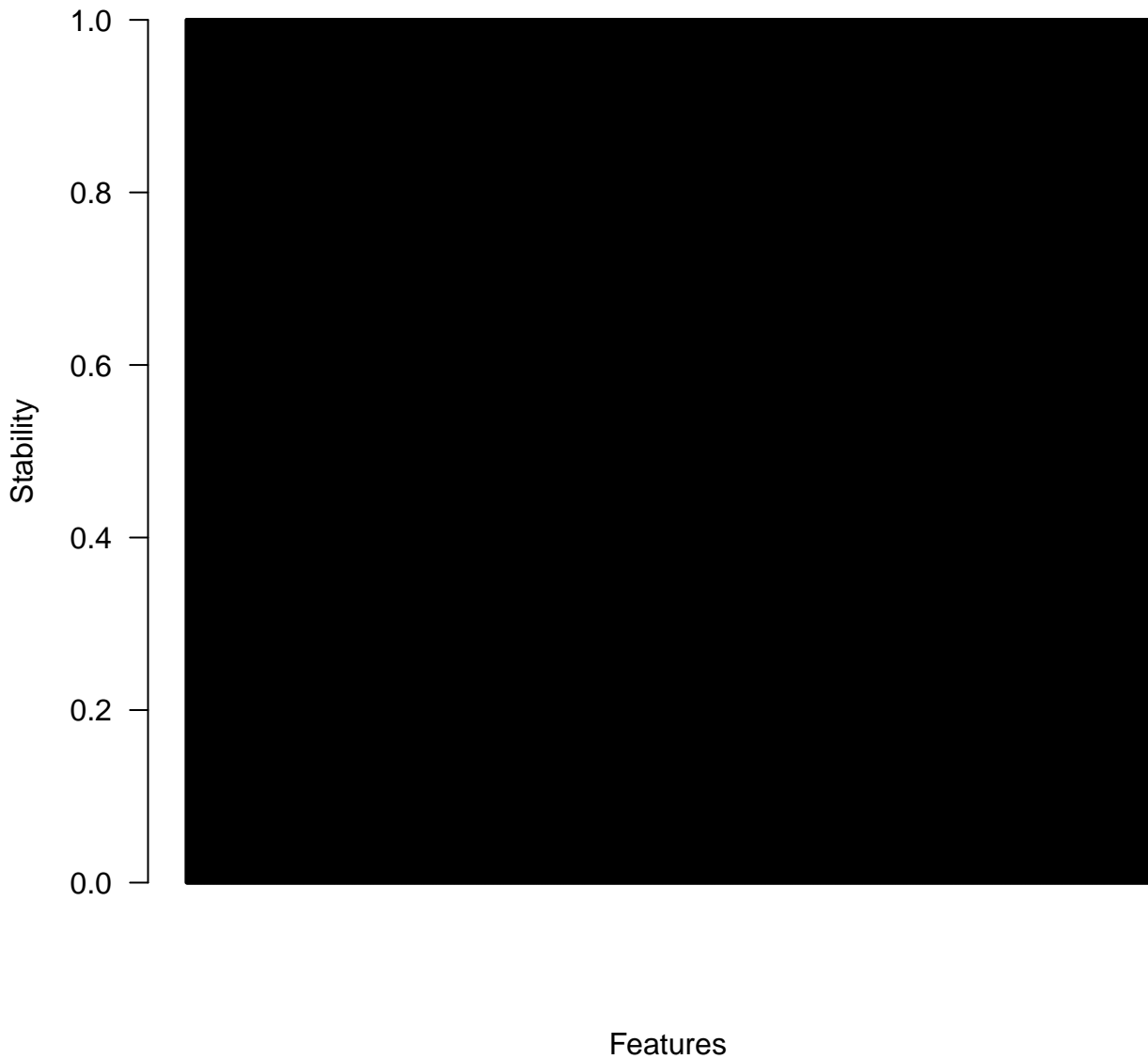
# transcriptome Comp 1



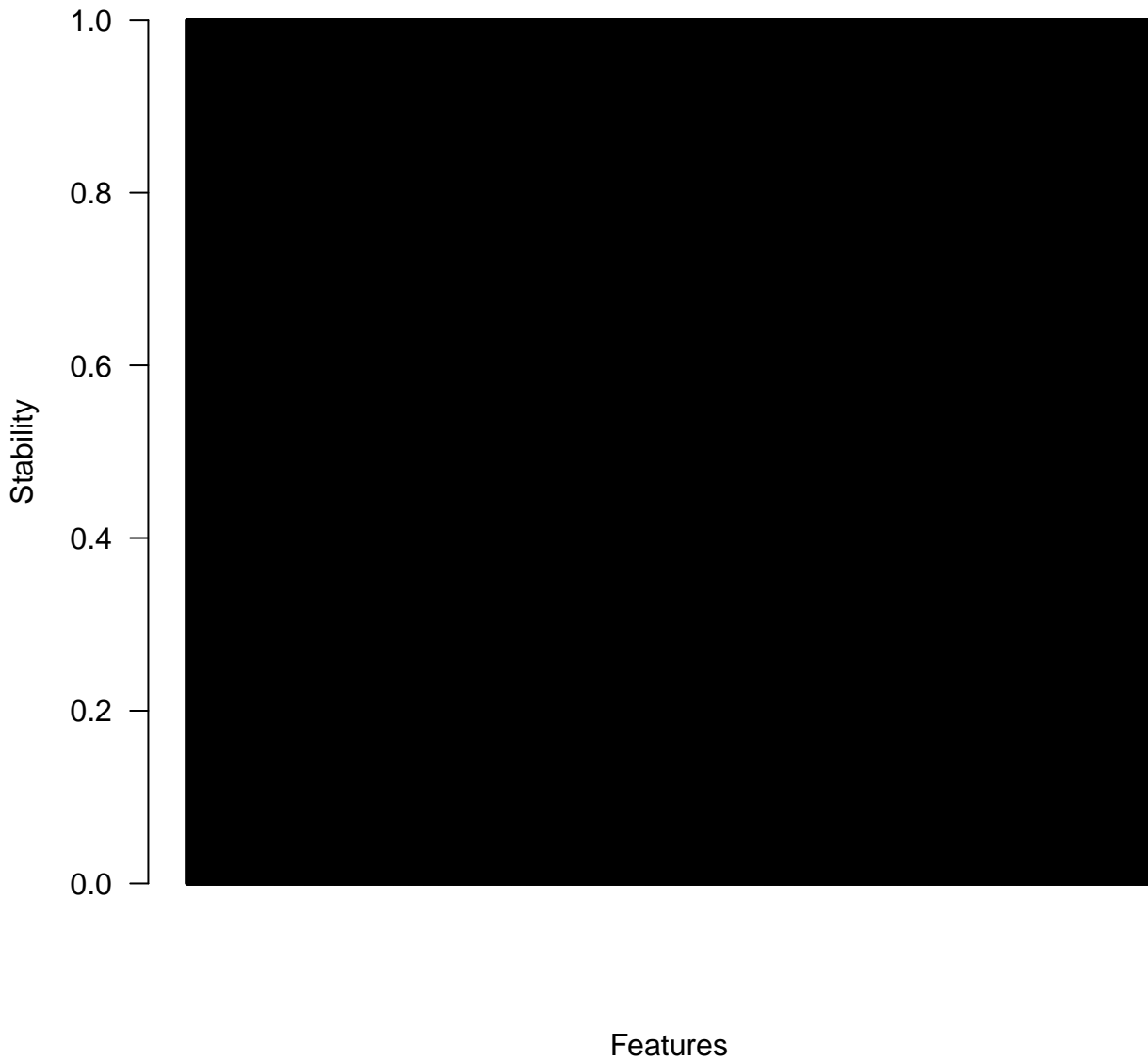
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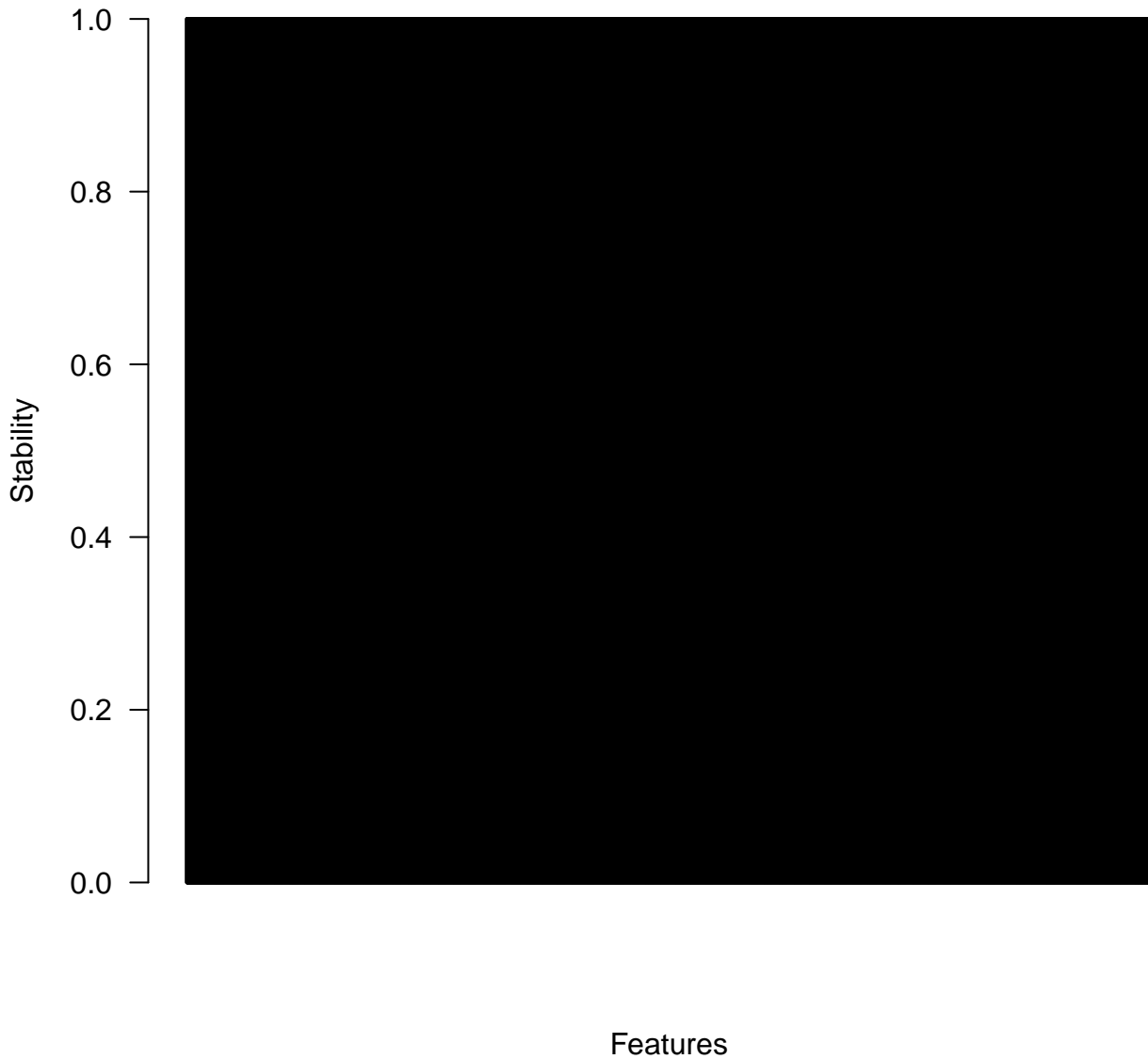
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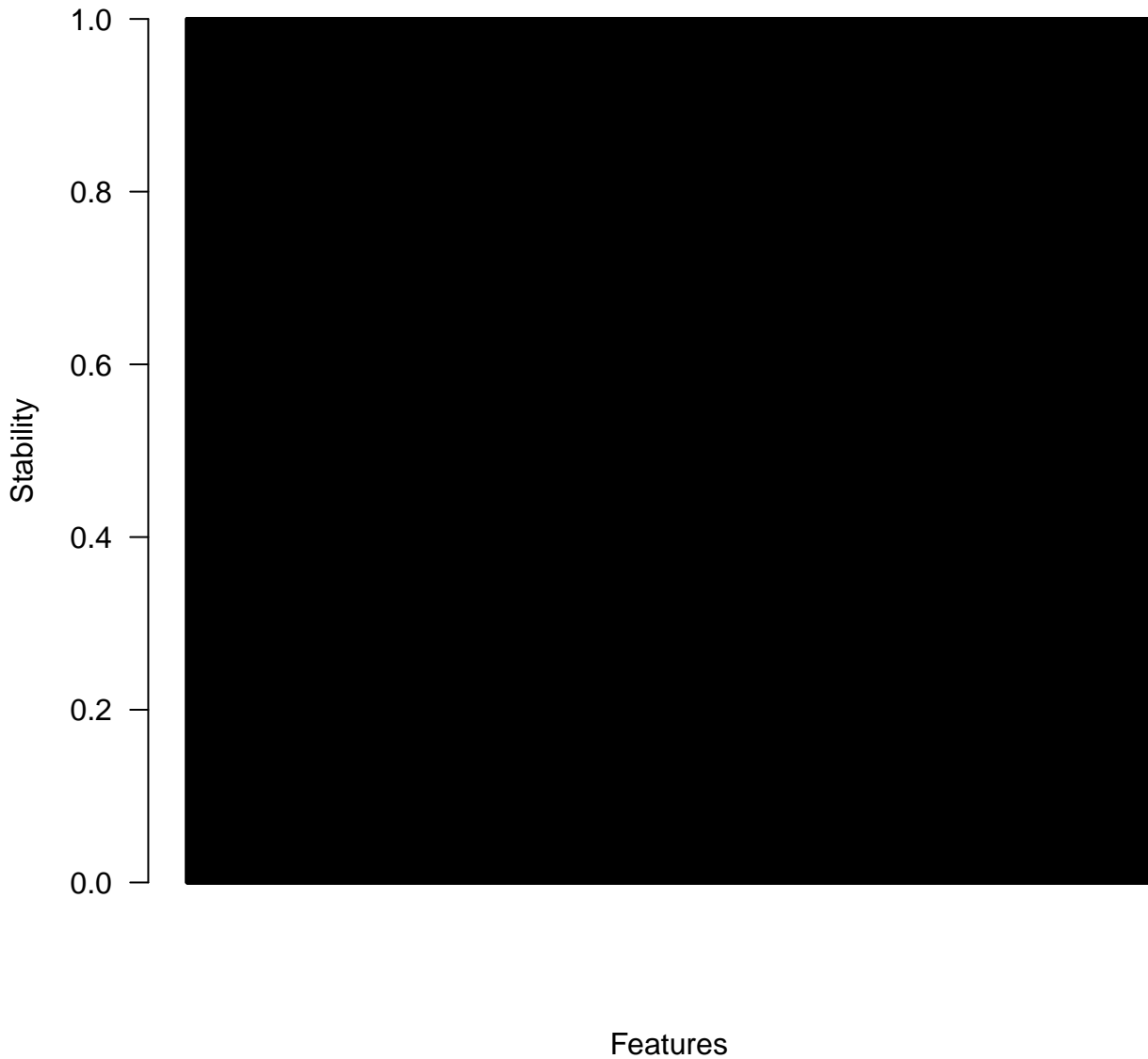
# metabolome Comp 1



## metabolome Comp 2

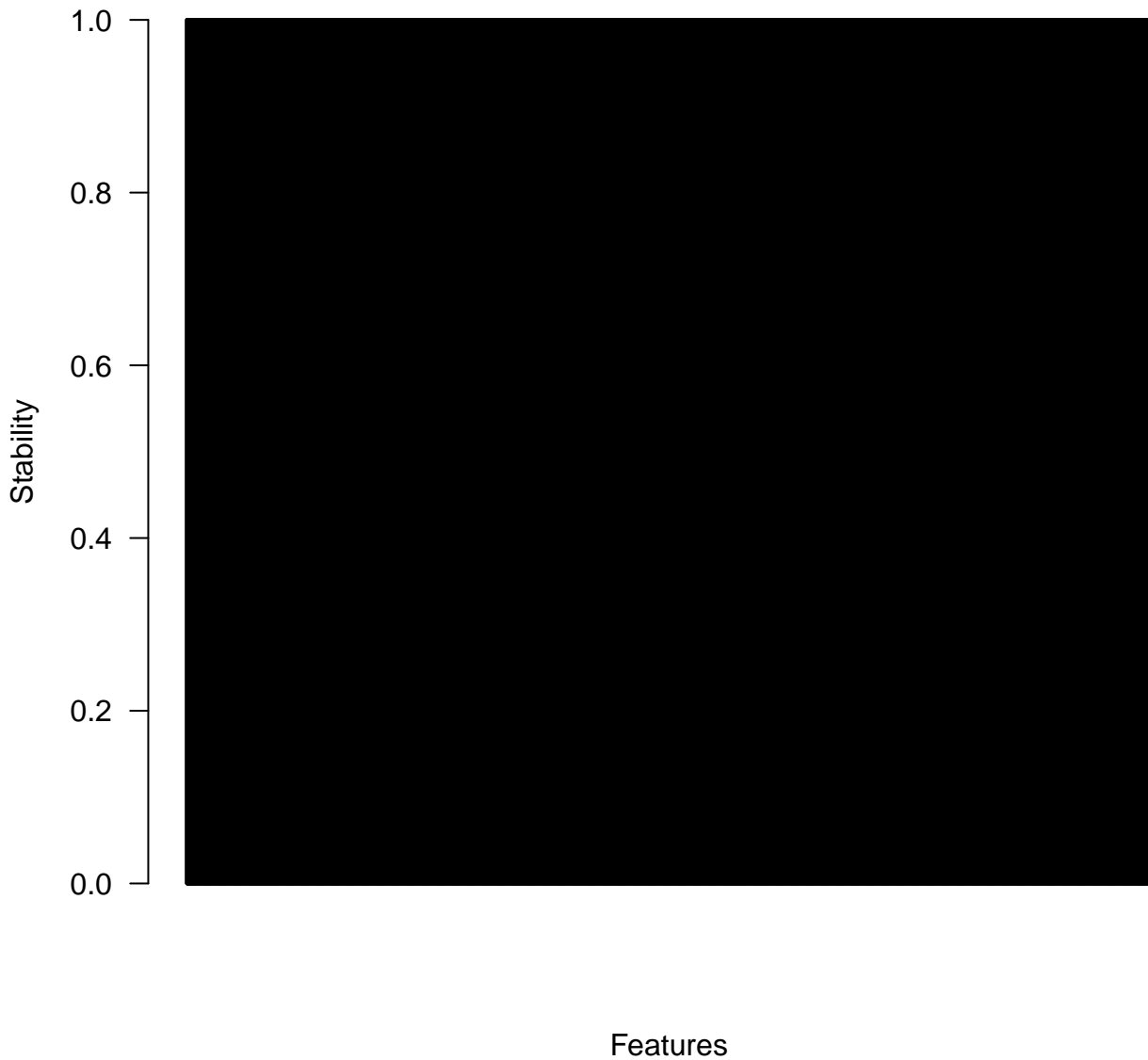


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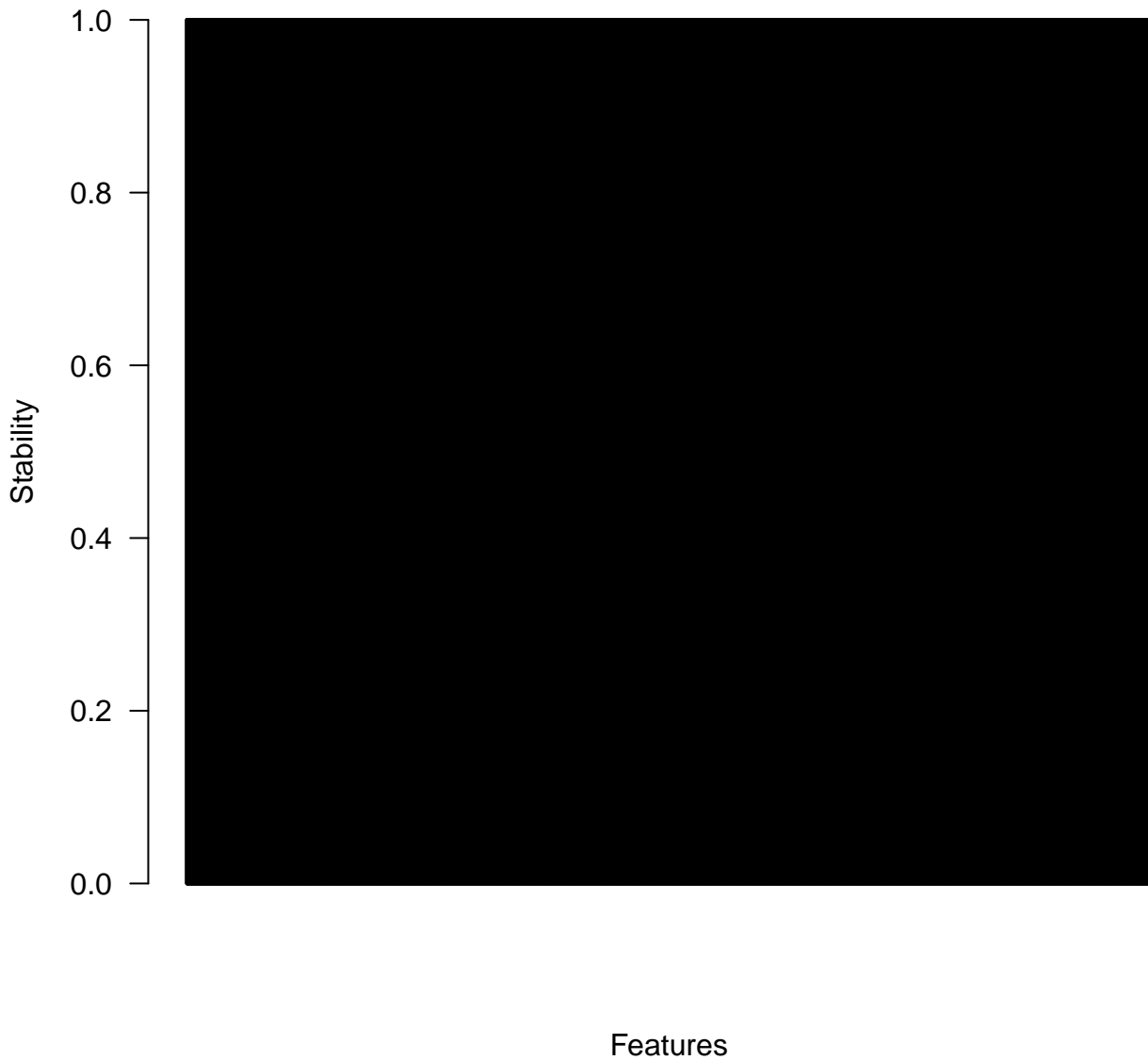




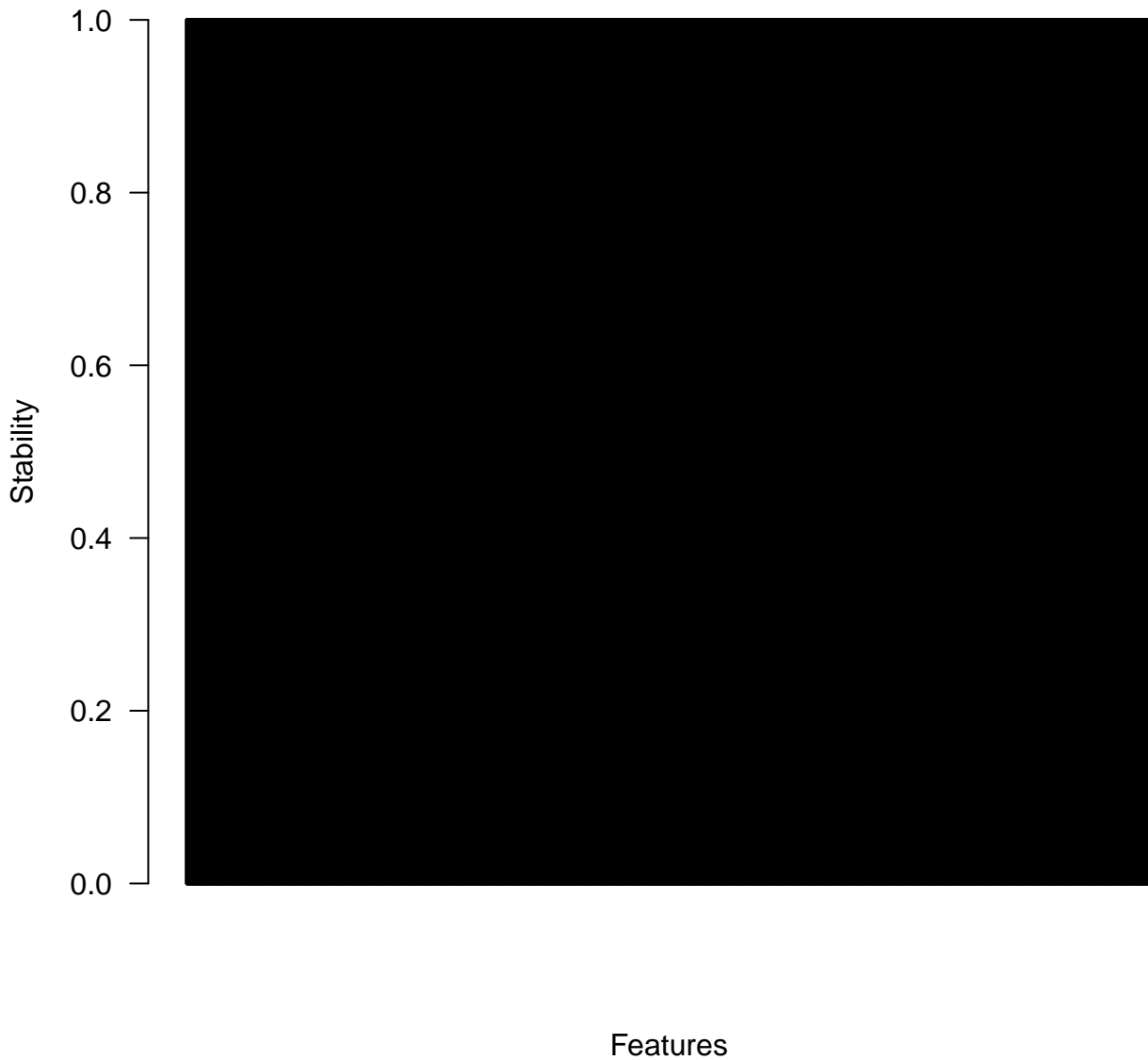
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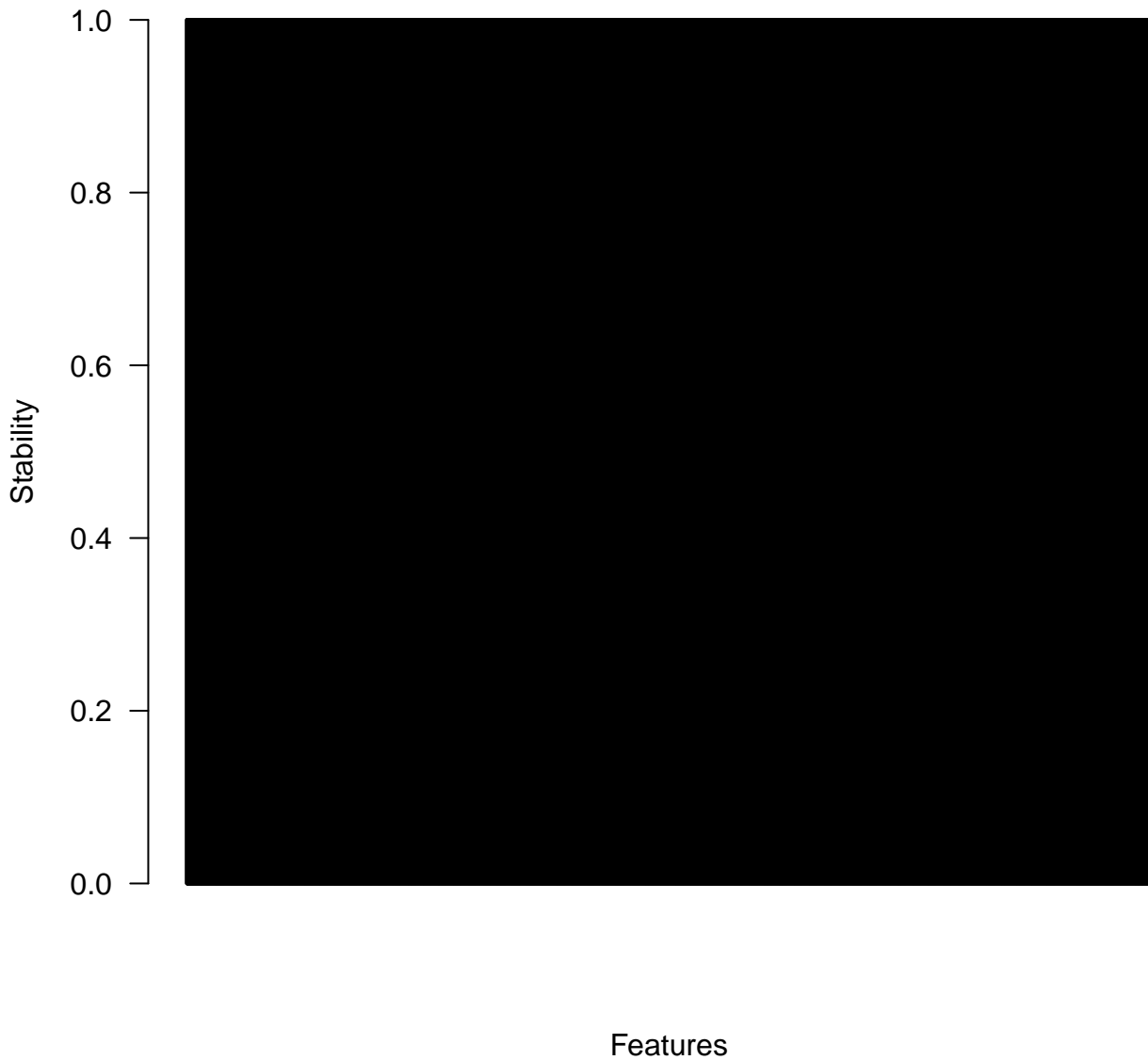
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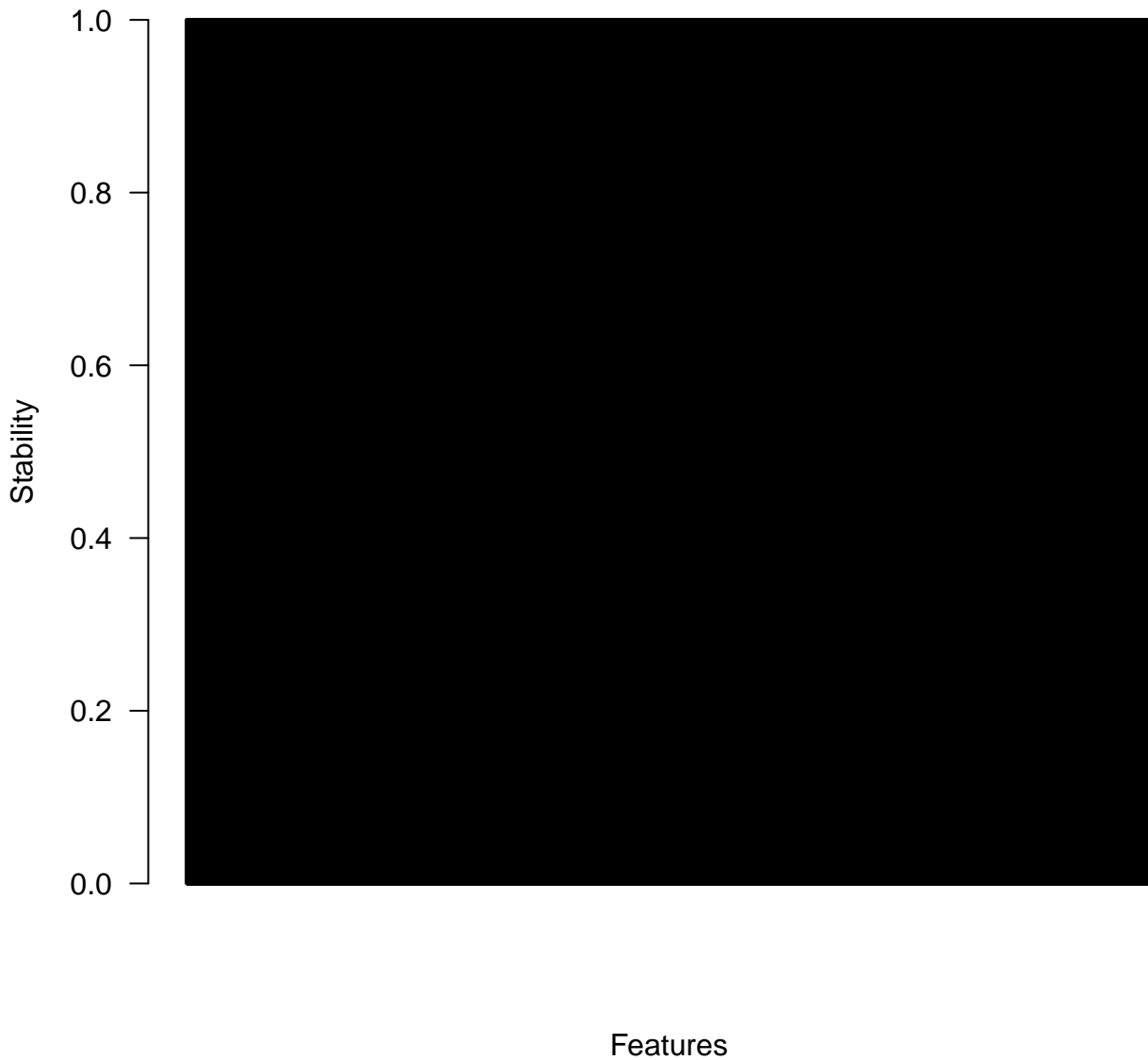
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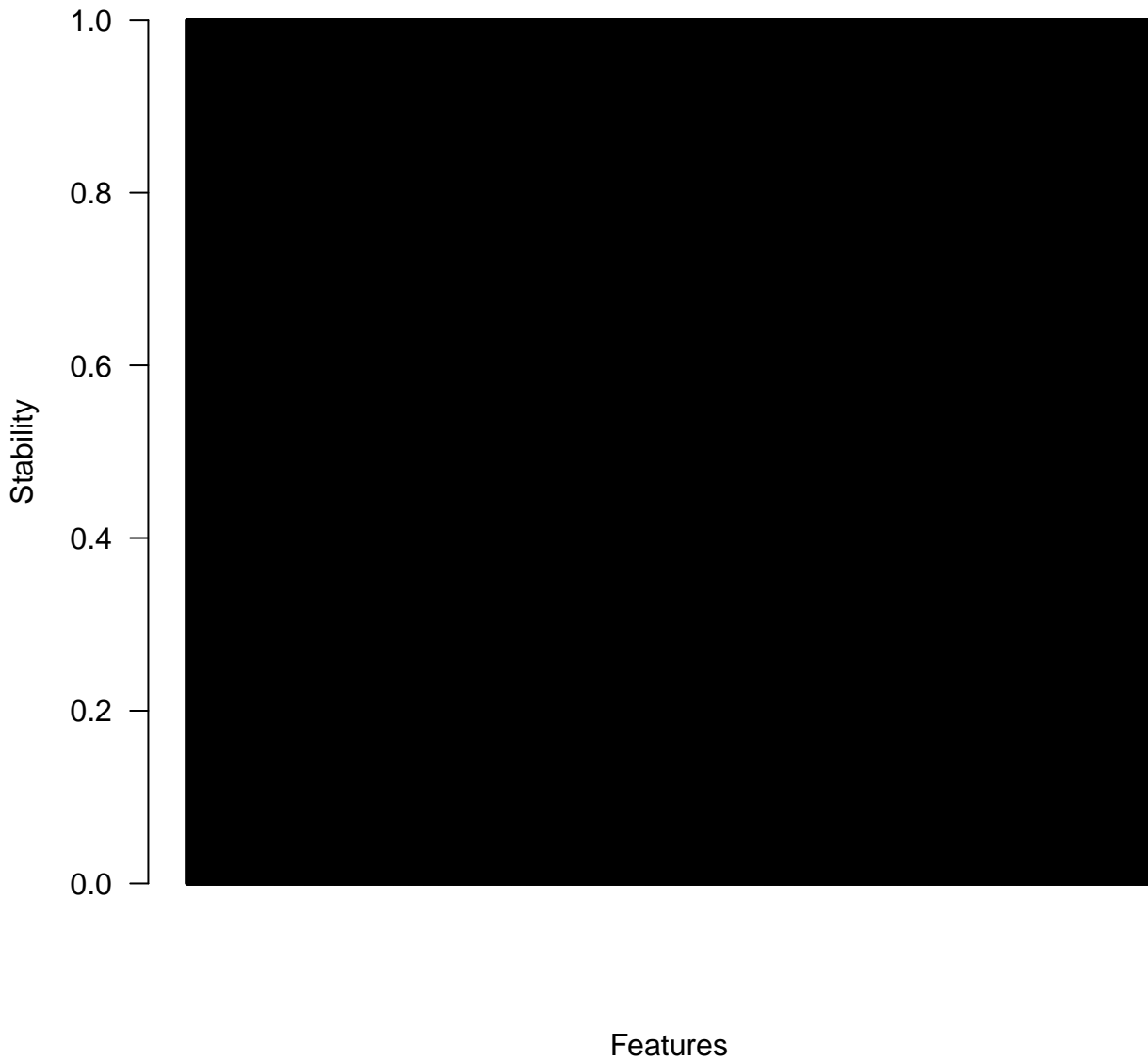
# transcriptome Comp 1



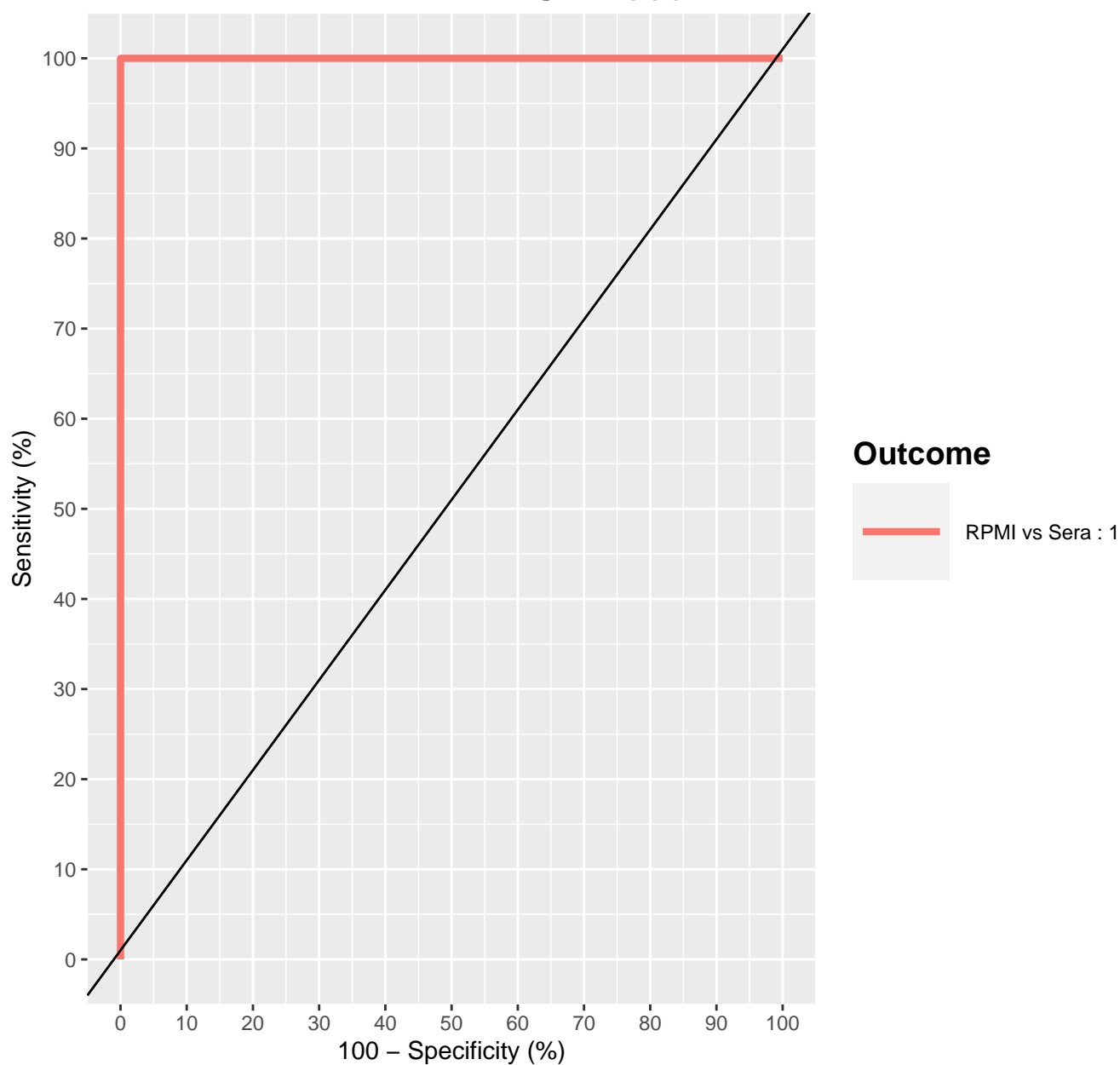
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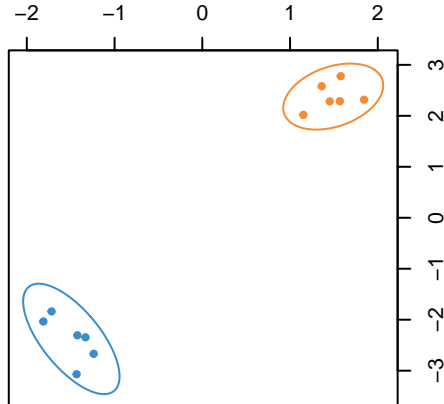
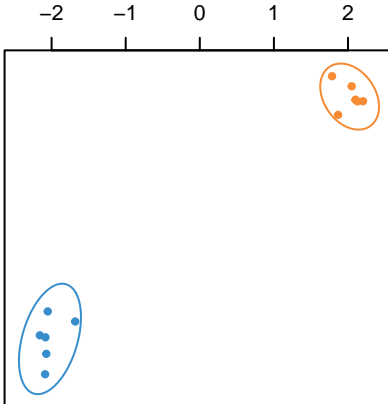
# transcriptome Comp 3



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

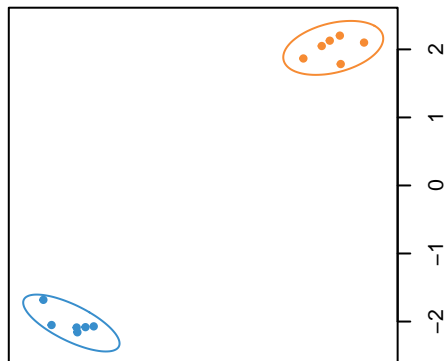


metabolome



0.99

proteome



0.98

0.99

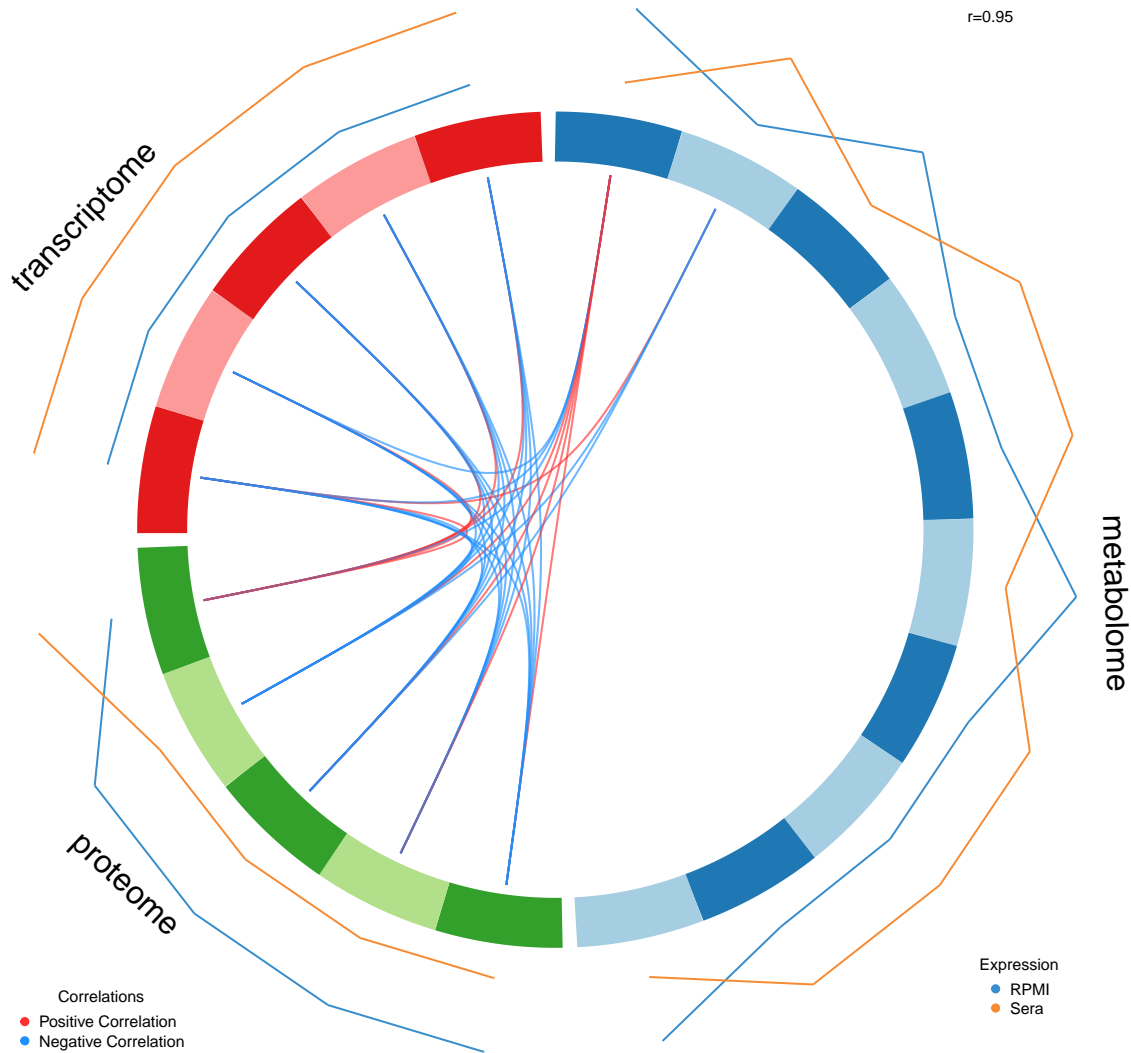
transcriptome





Comp 1

Correlation cut-off  
 $r=0.95$

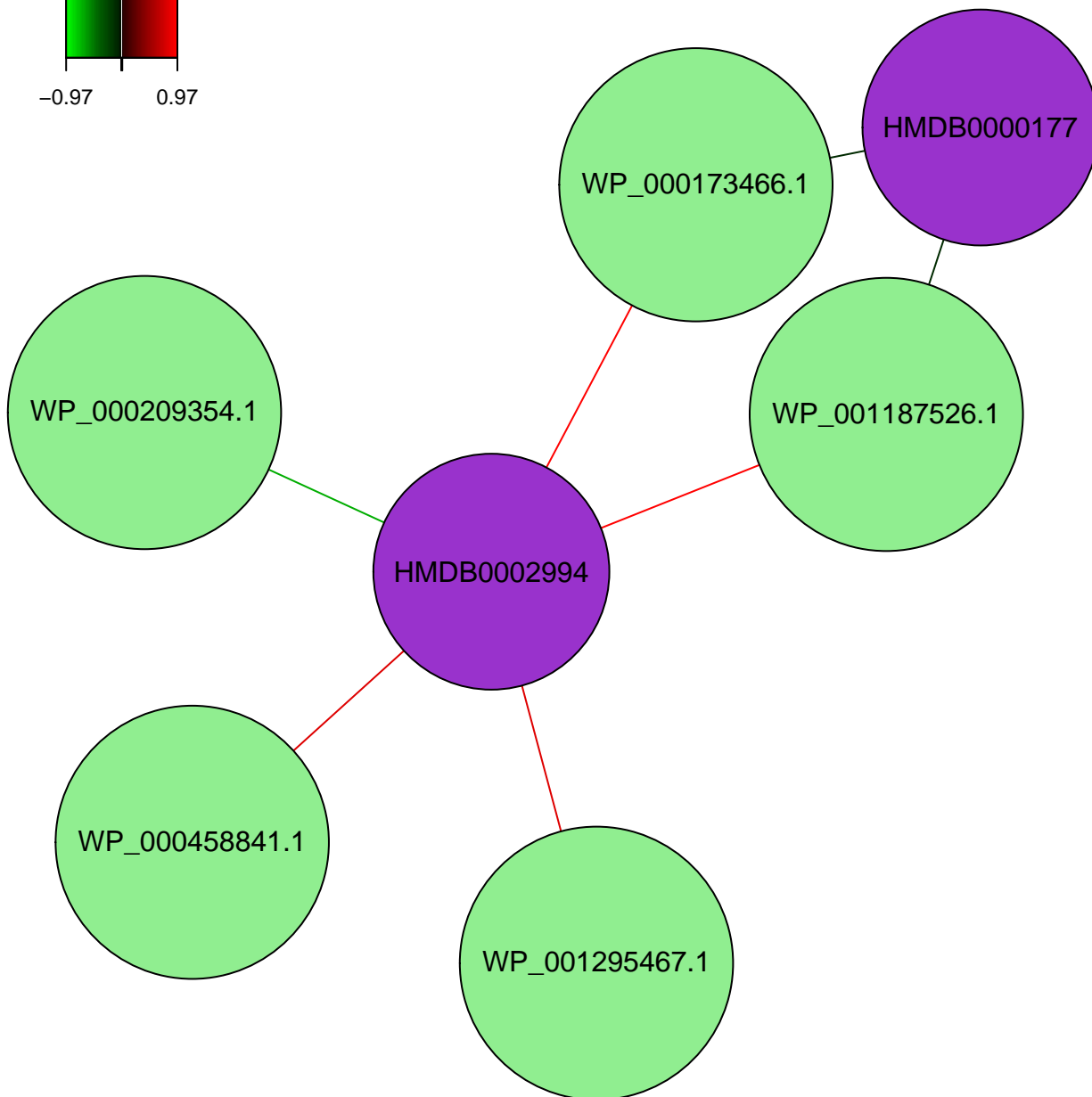


Color key

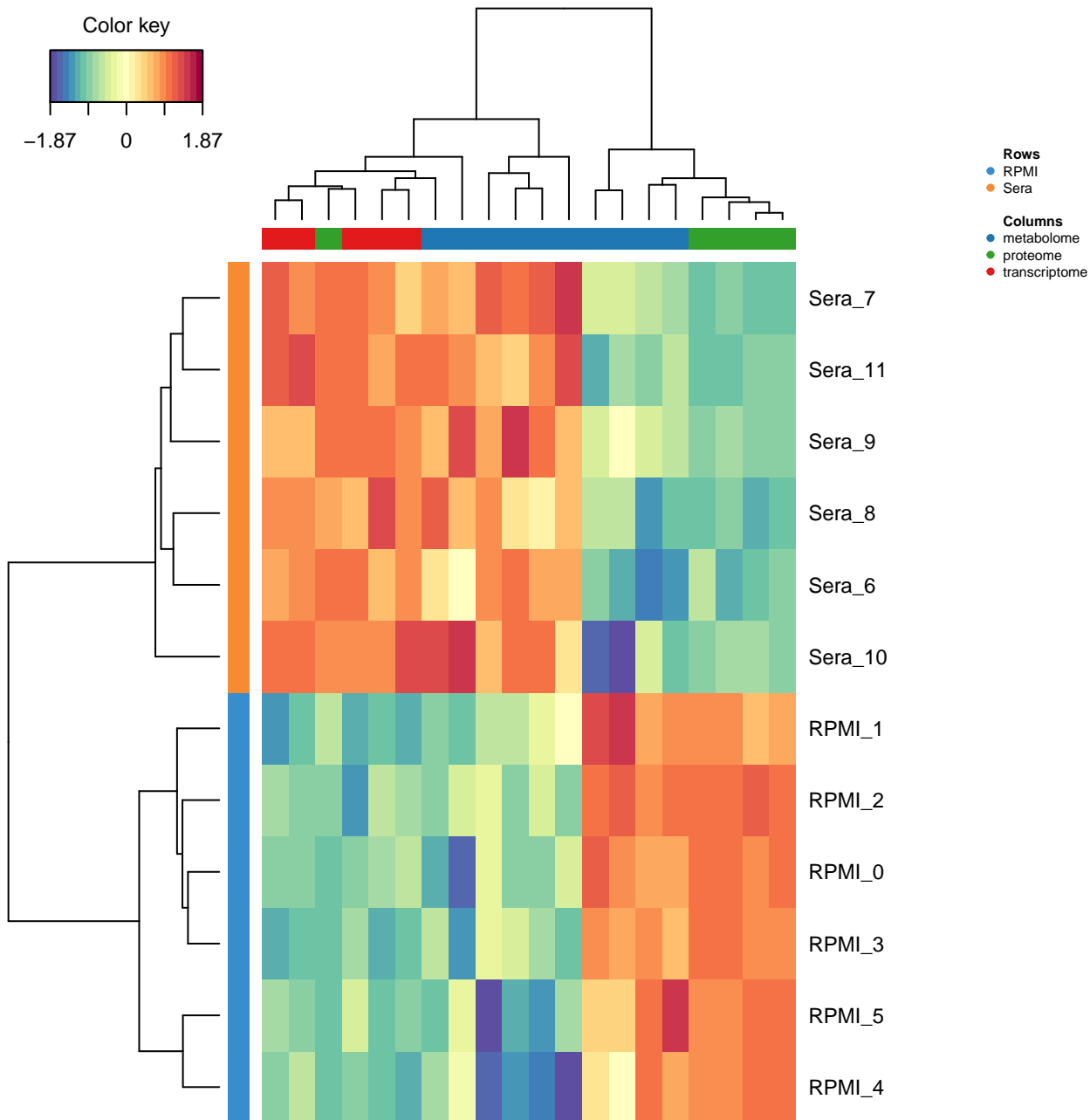
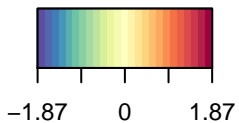


-0.97

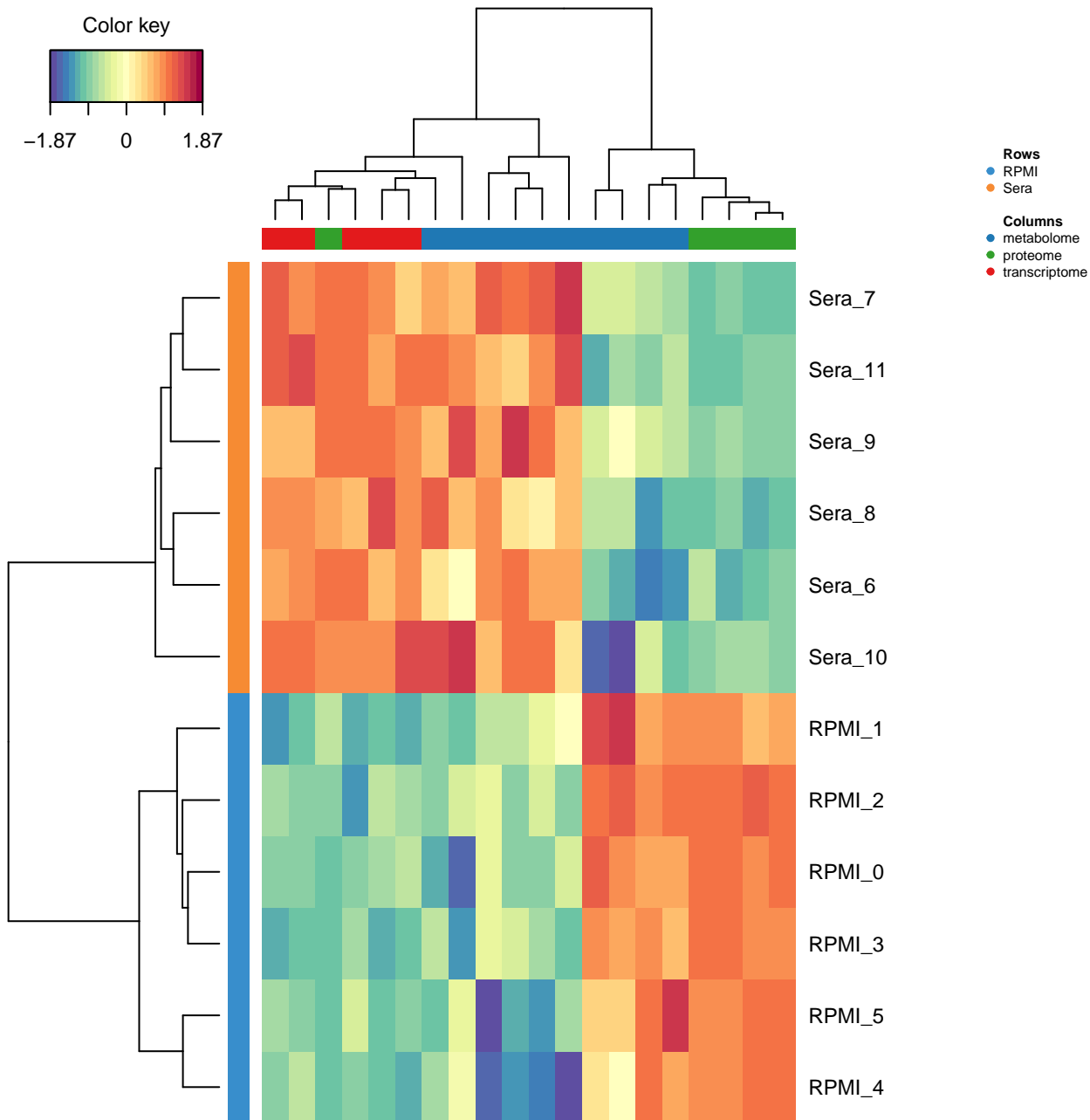
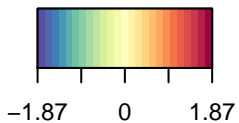
0.97



Color key

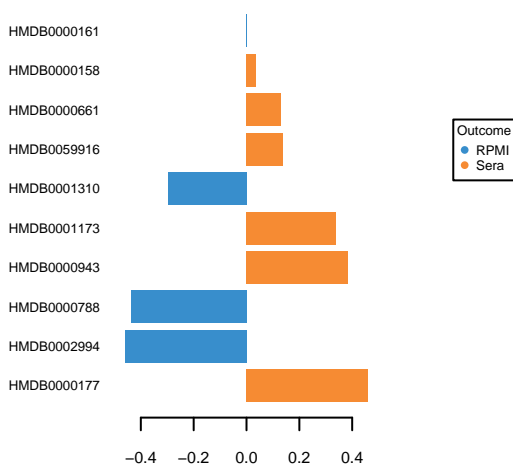


Color key

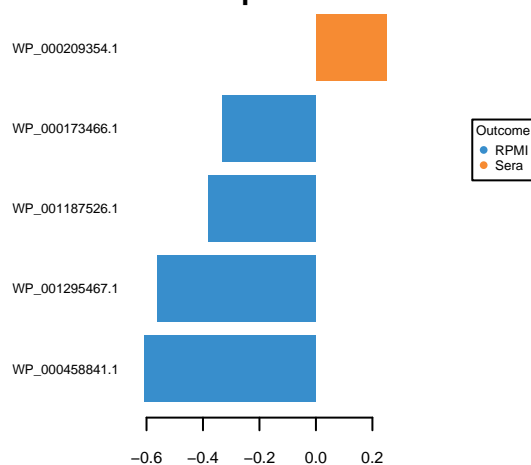


# 1 DIABLO max loadings

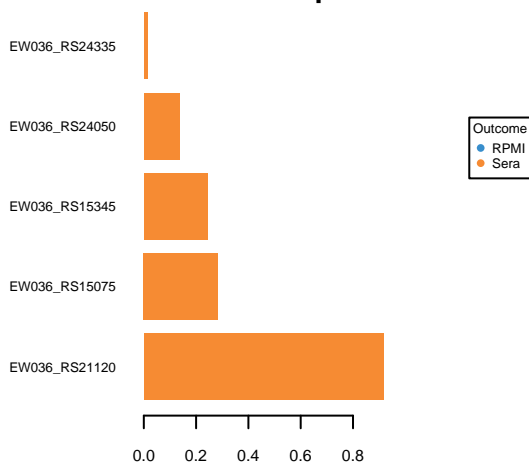
**Contribution on comp 1**  
**Block 'metabolome'**



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

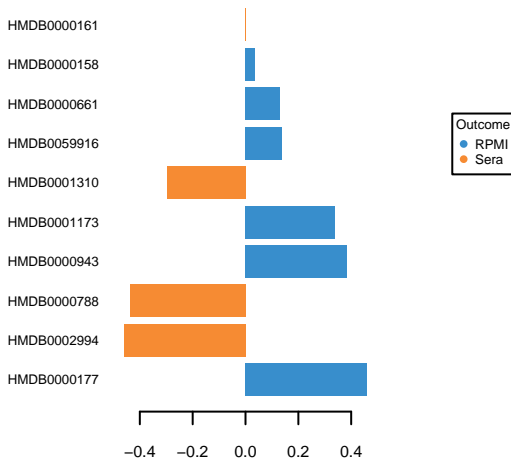


**Contribution on comp 1**  
**Block 'transcriptome'**

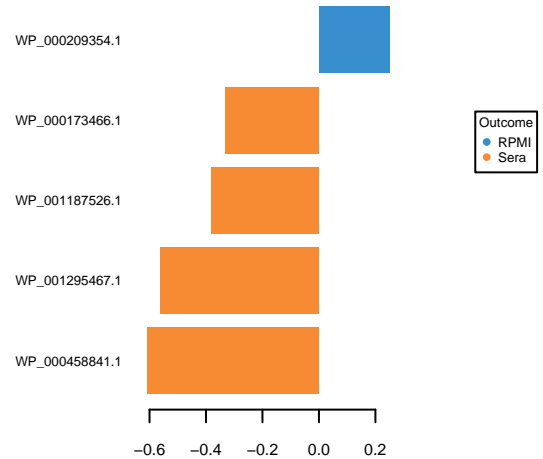


# 1 DIABLO min loadings

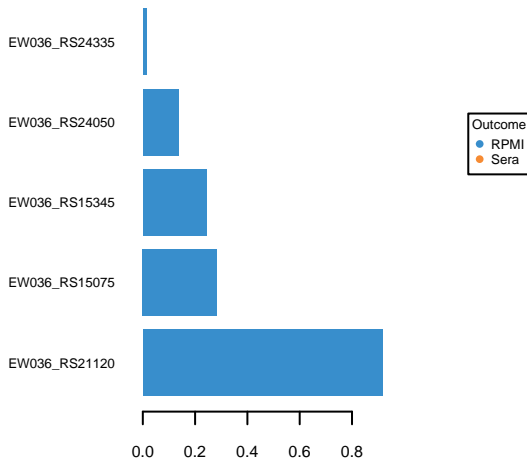
**Contribution on comp 1**  
**Block 'metabolome'**



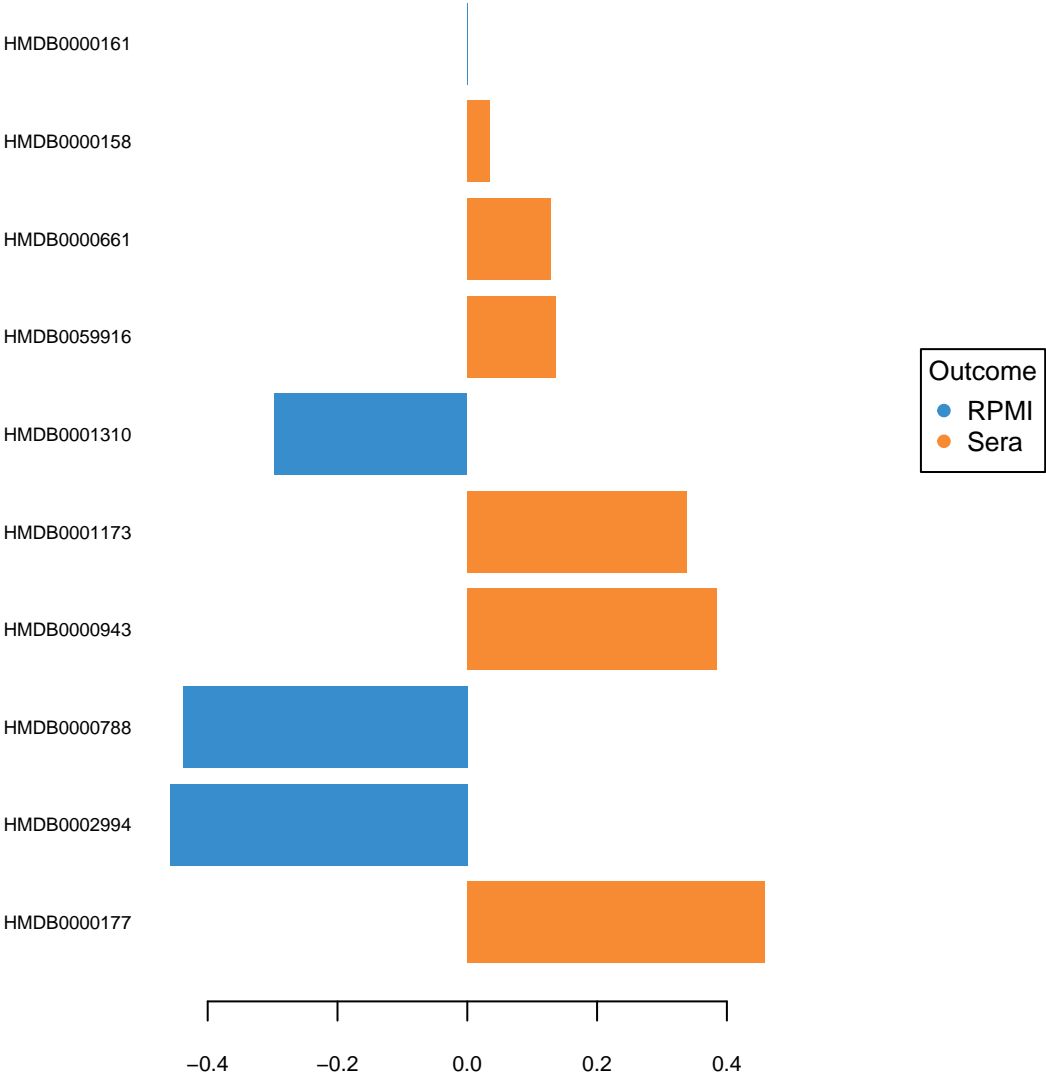
**Contribution on comp 1**  
**Block 'proteome'**



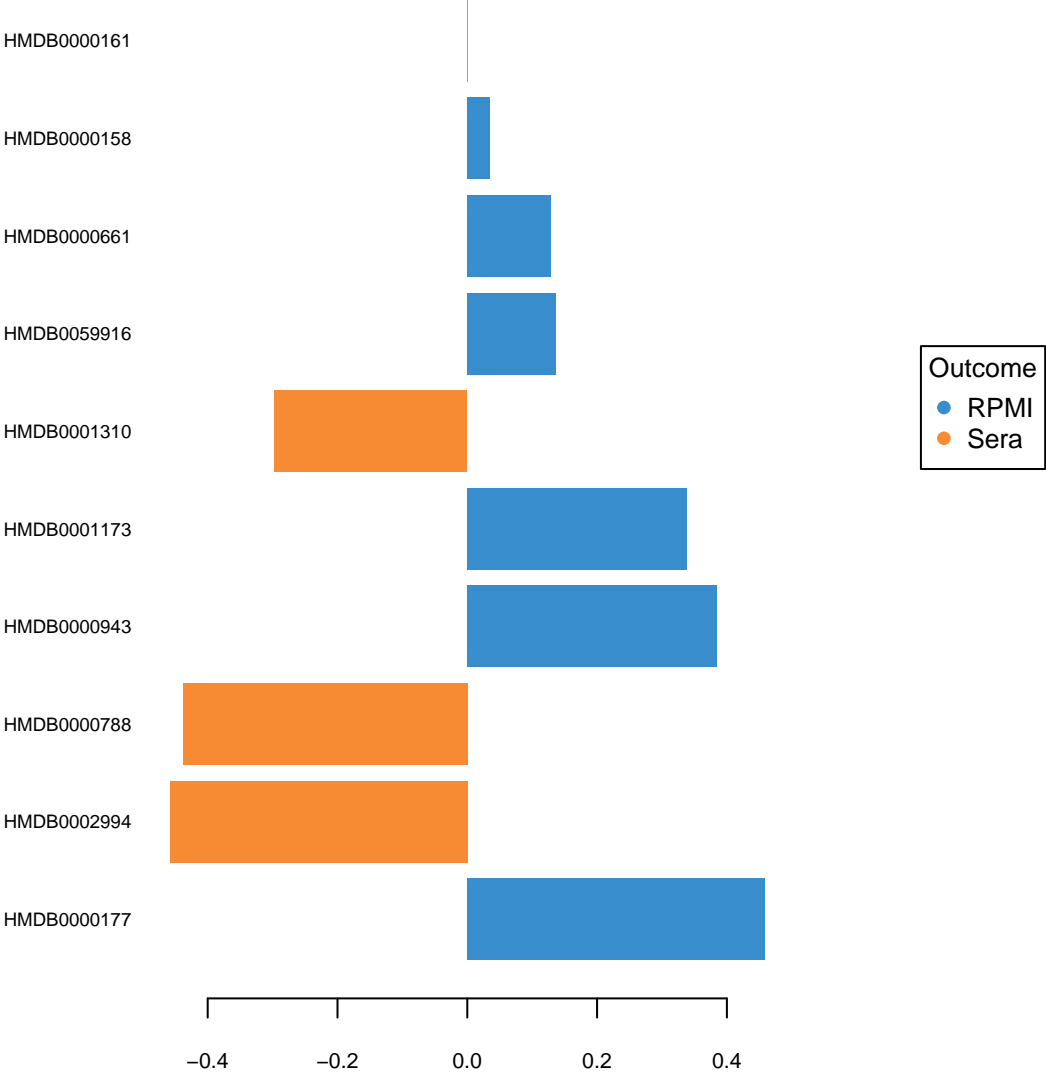
**Contribution on comp 1**  
**Block 'transcriptome'**



# 1 metabolome DIABLO max load

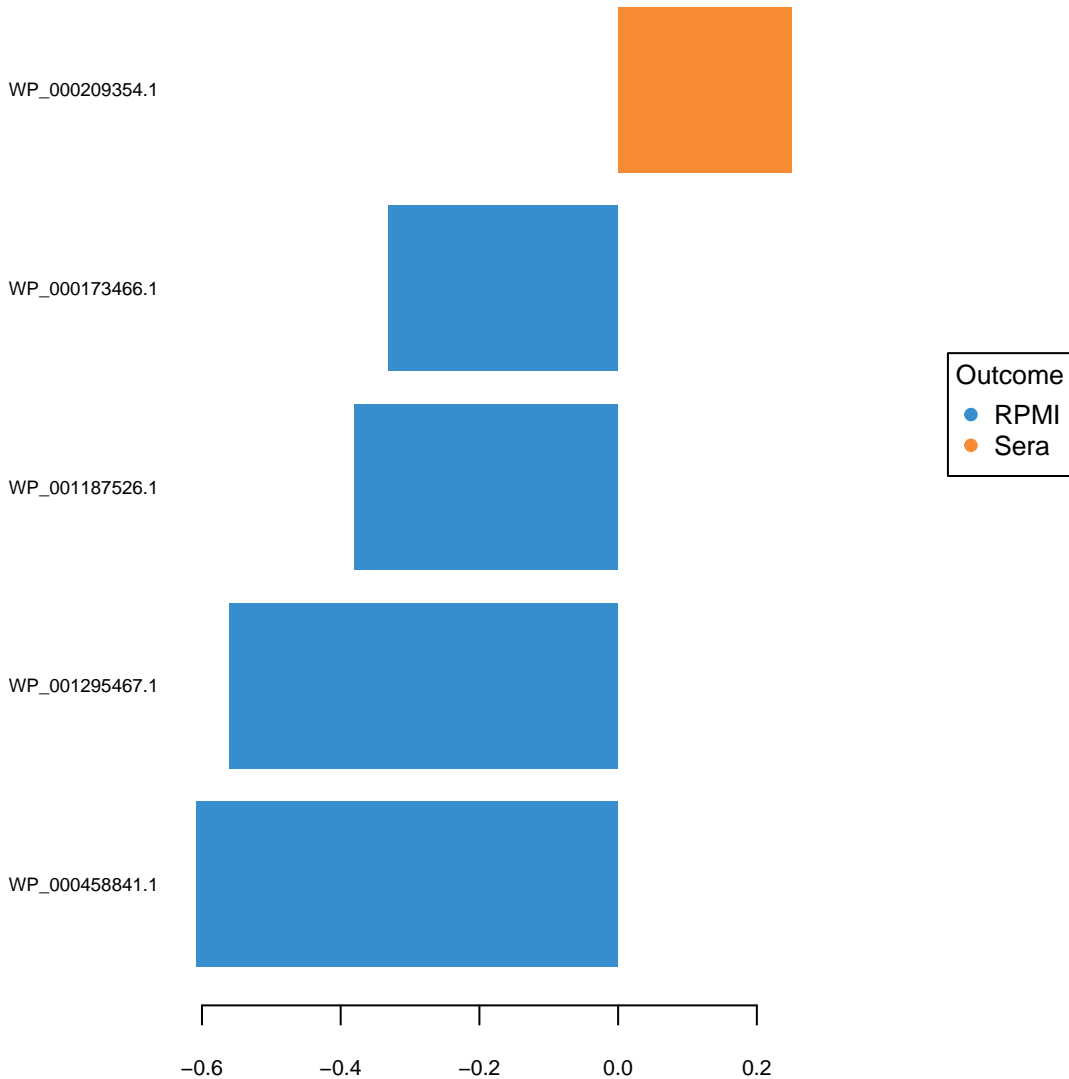


# 1 metabolome DIABLO min loac

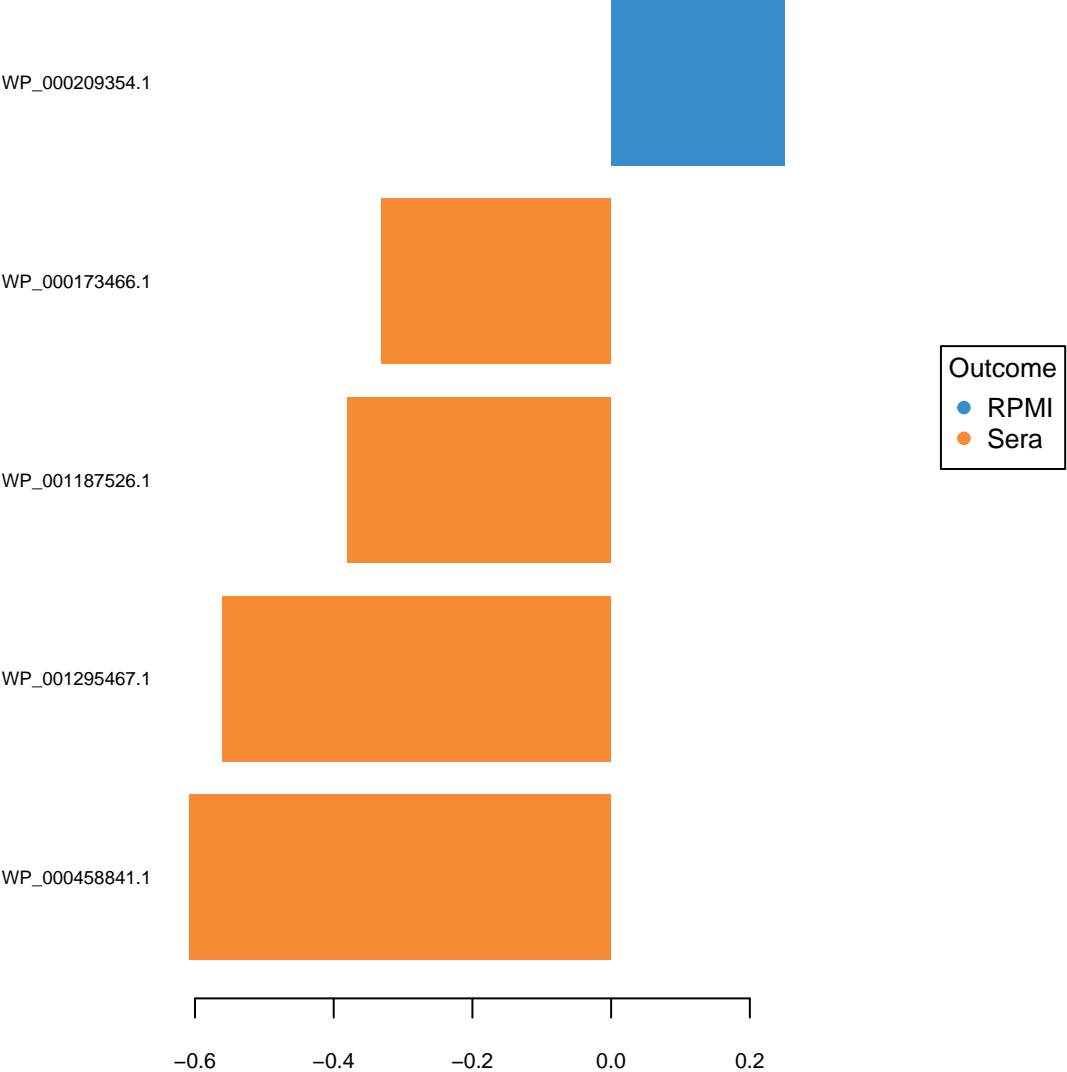




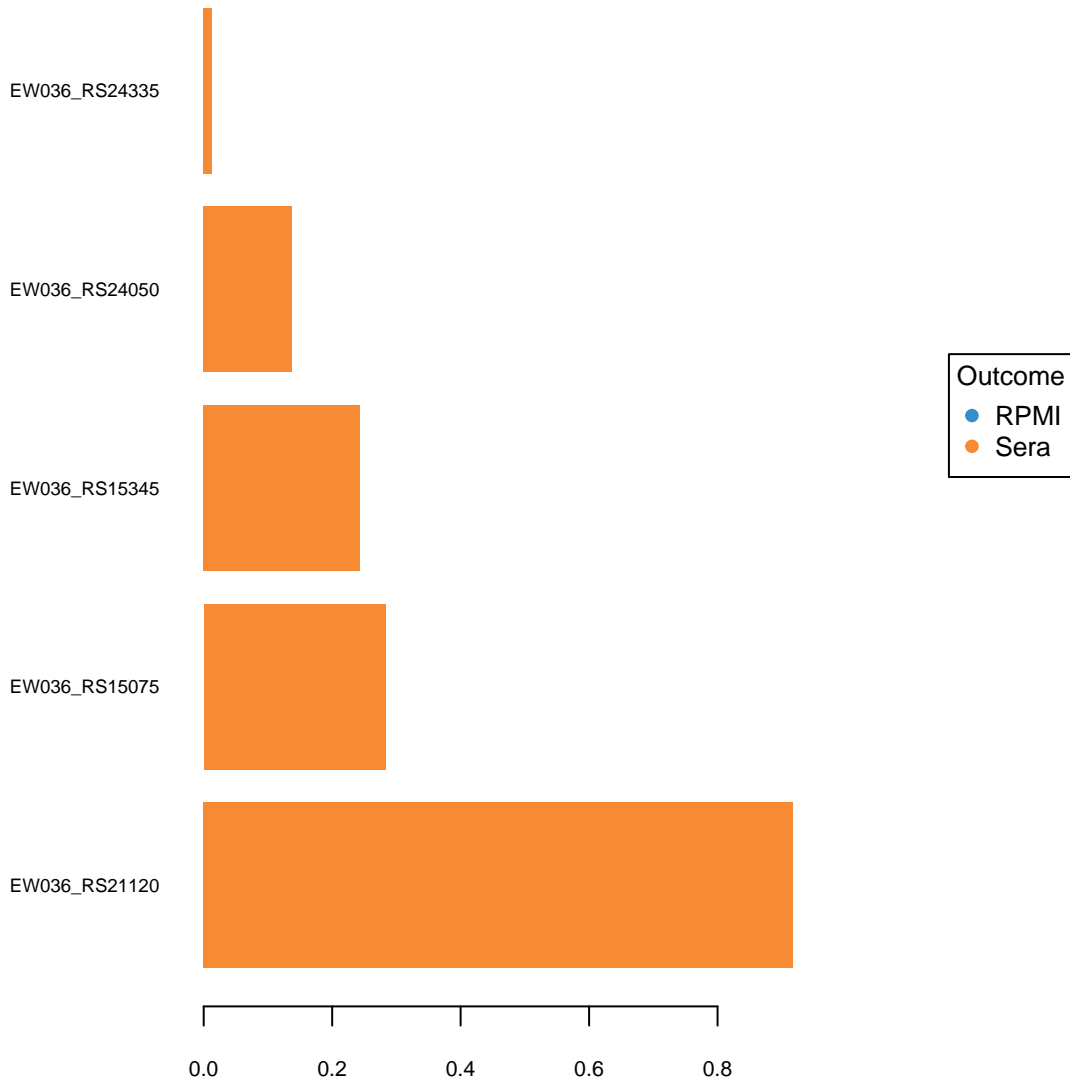
# 1 proteome DIABLO max load



# 1 proteome DIABLO min load



# 1 transcriptome DIABLO max loa



# 1 transcriptome DIABLO min loa

