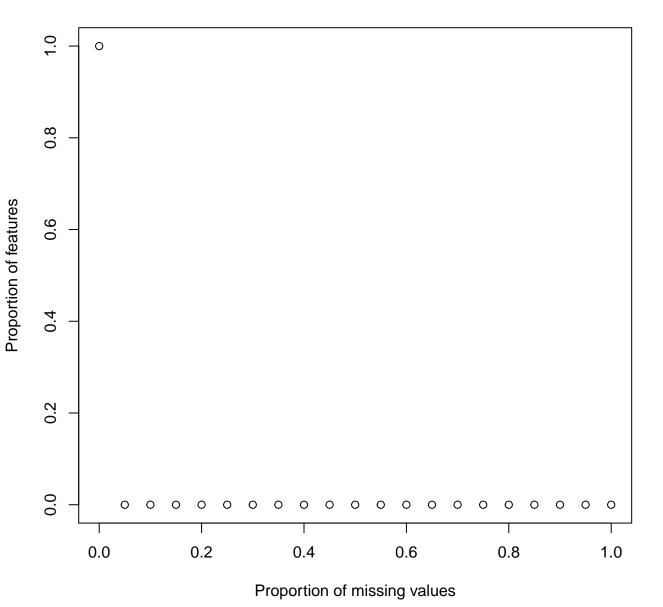
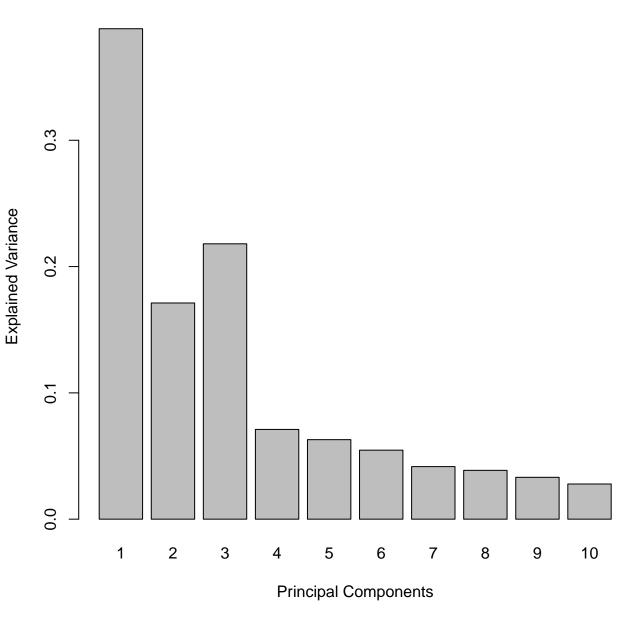
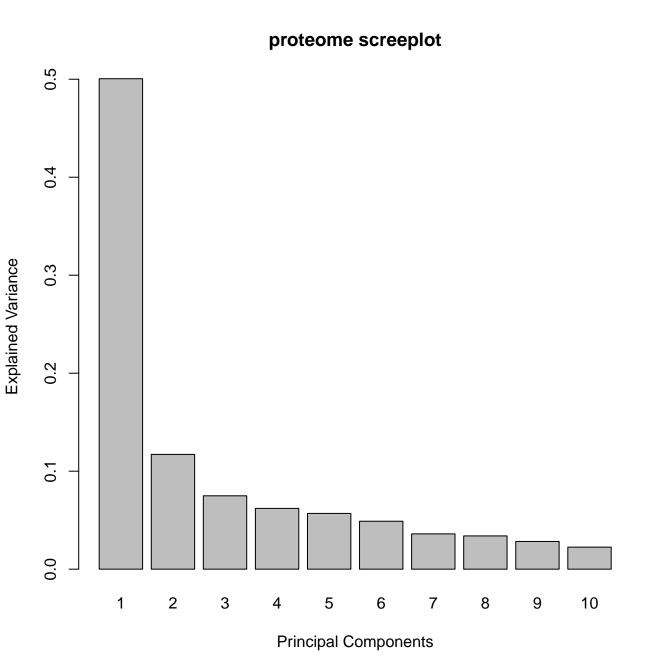
#### transcriptome missing value proportions for unfiltered data

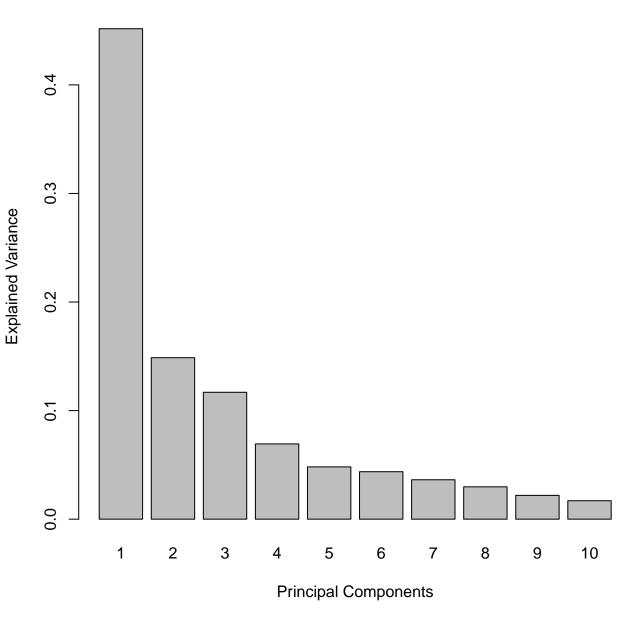


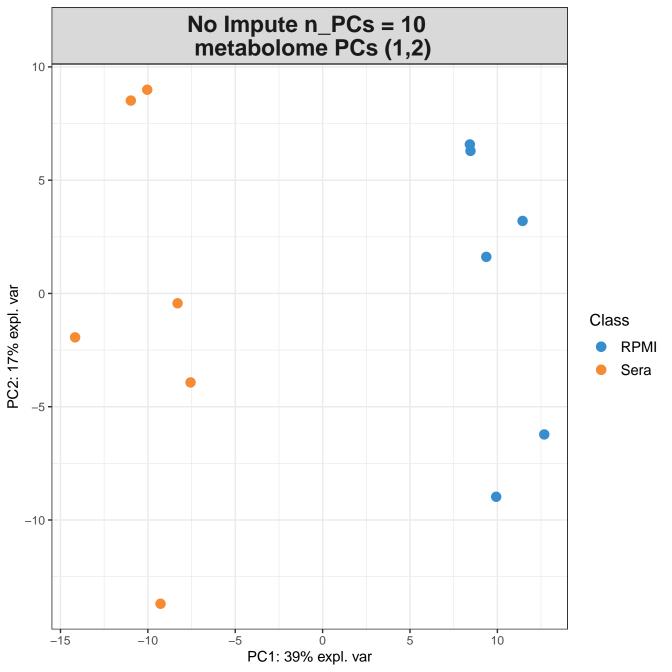
#### metabolome screeplot

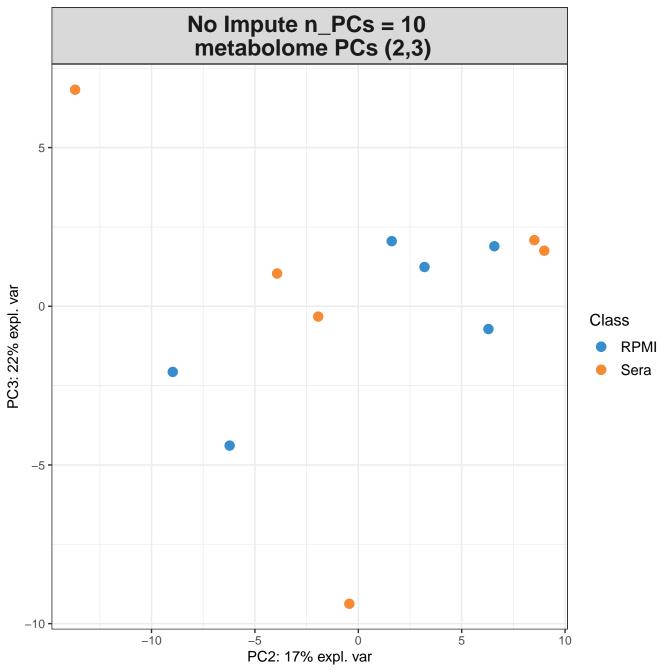


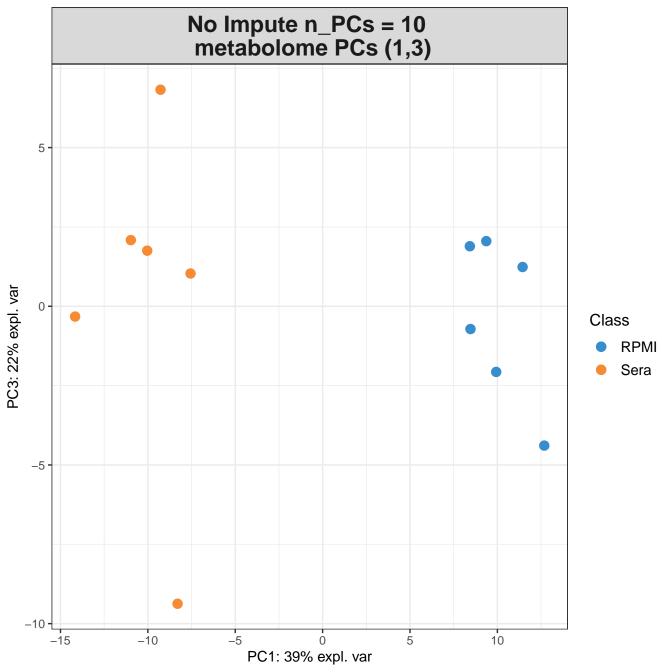


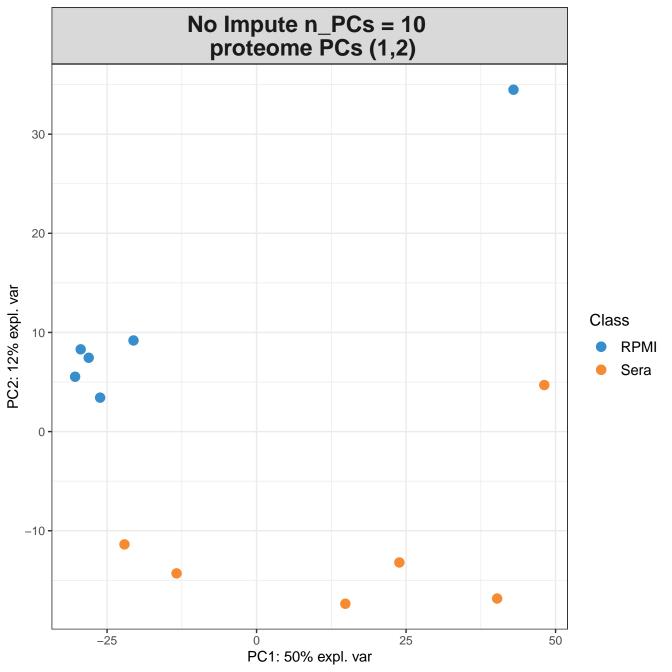
#### transcriptome screeplot

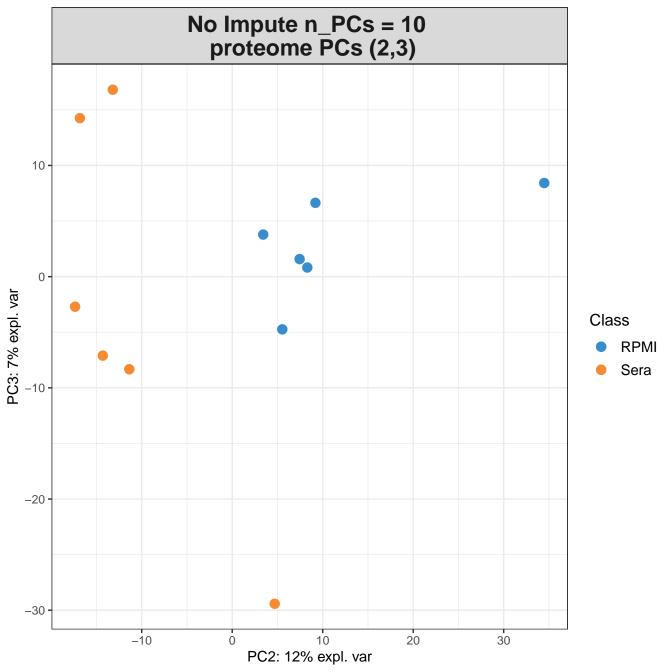


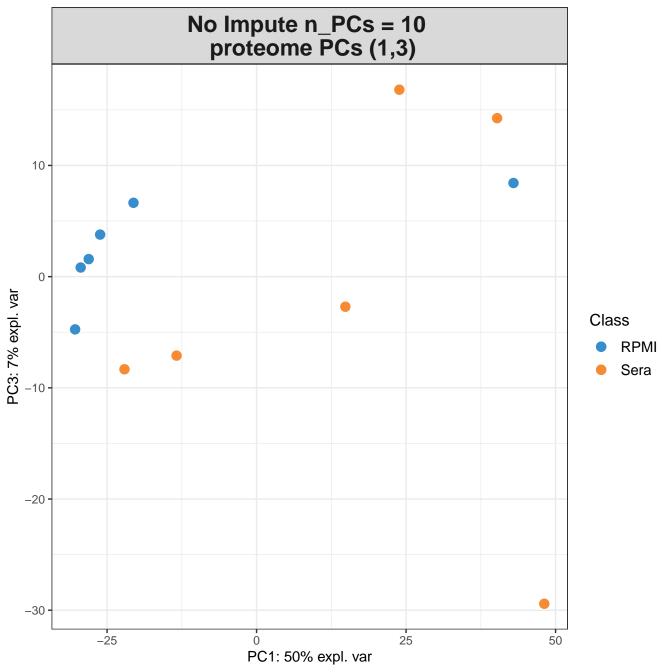


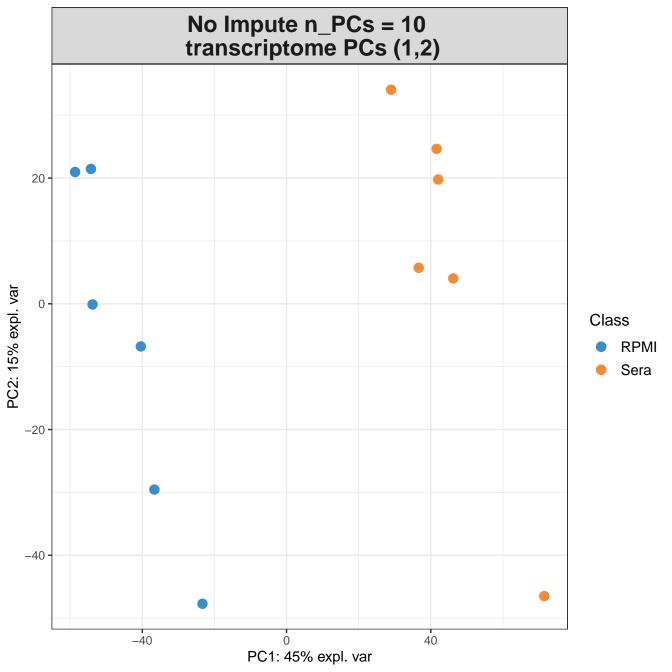


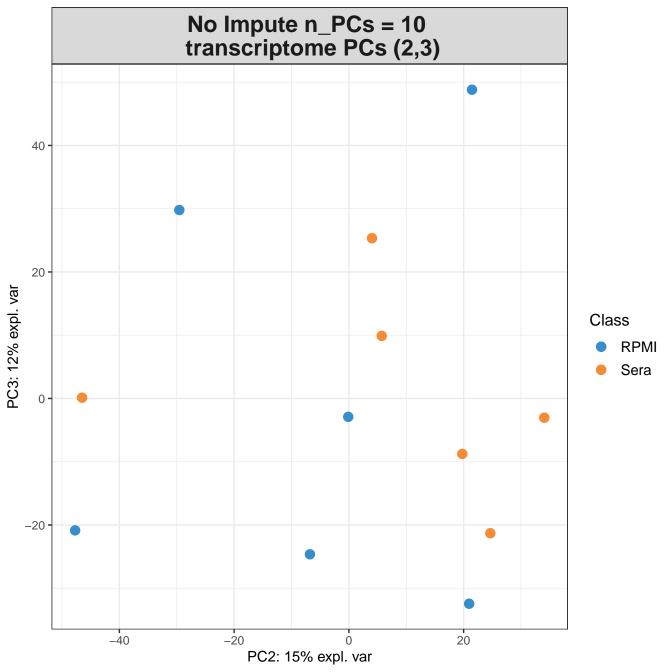


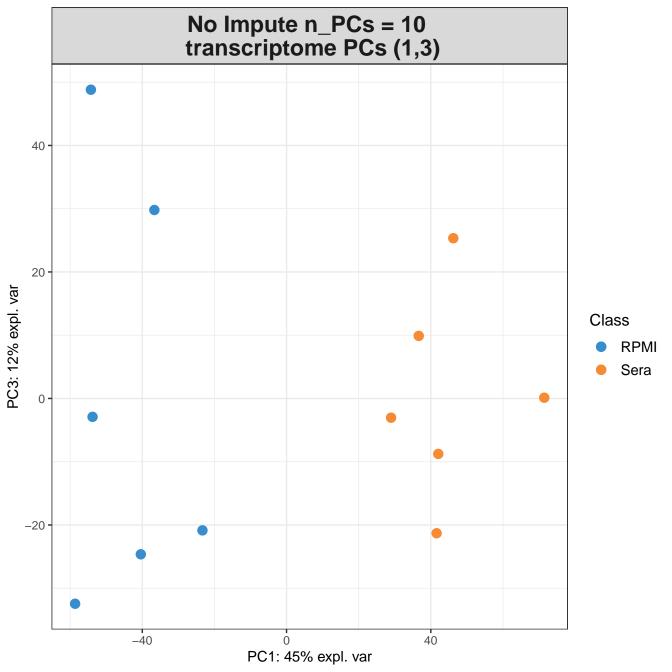




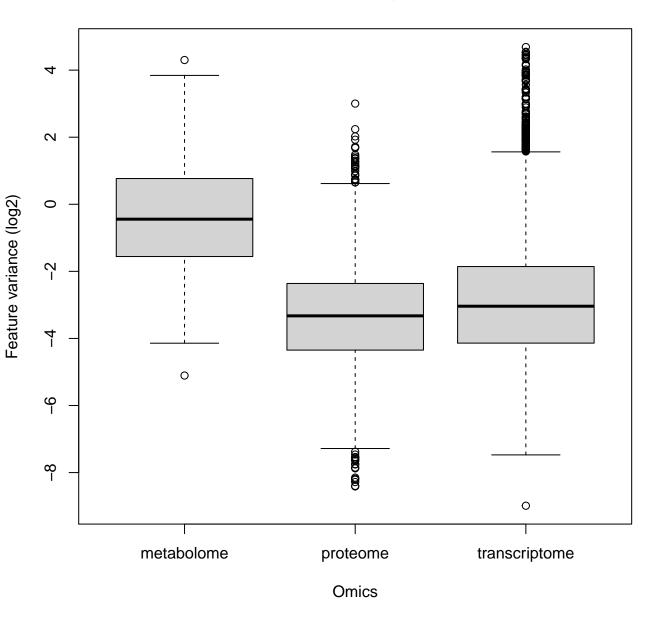


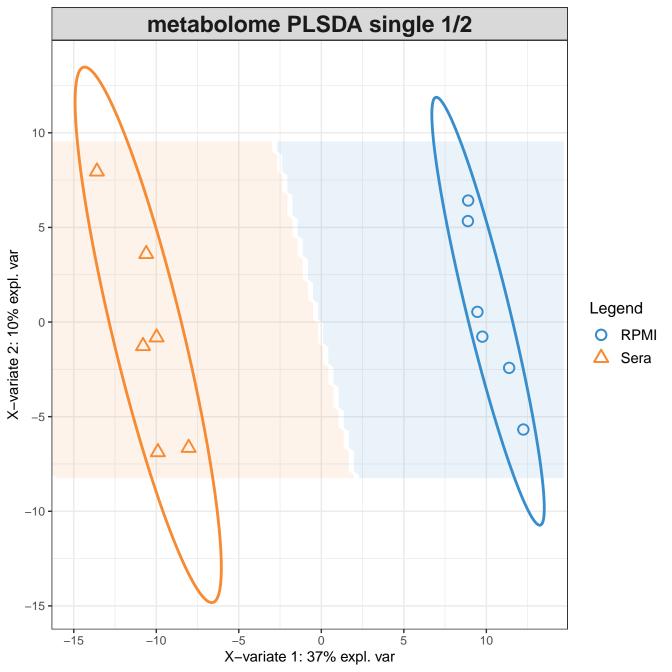


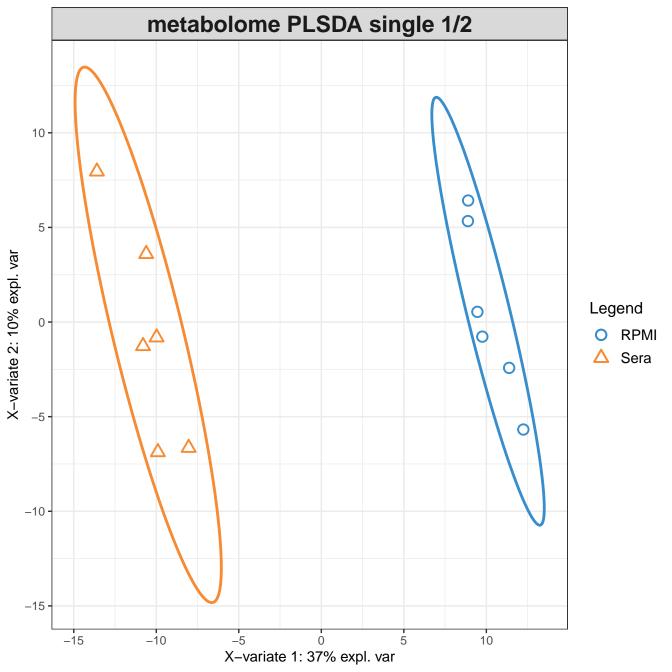


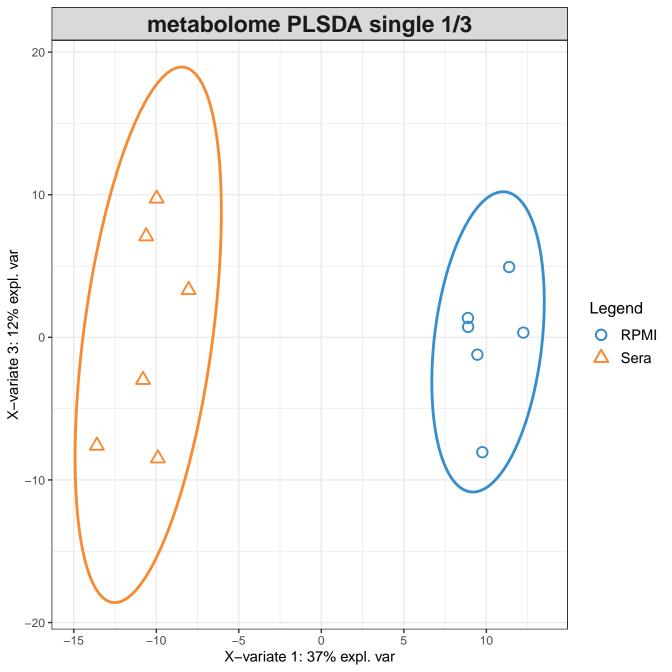


#### Feature variances (log2) per omics

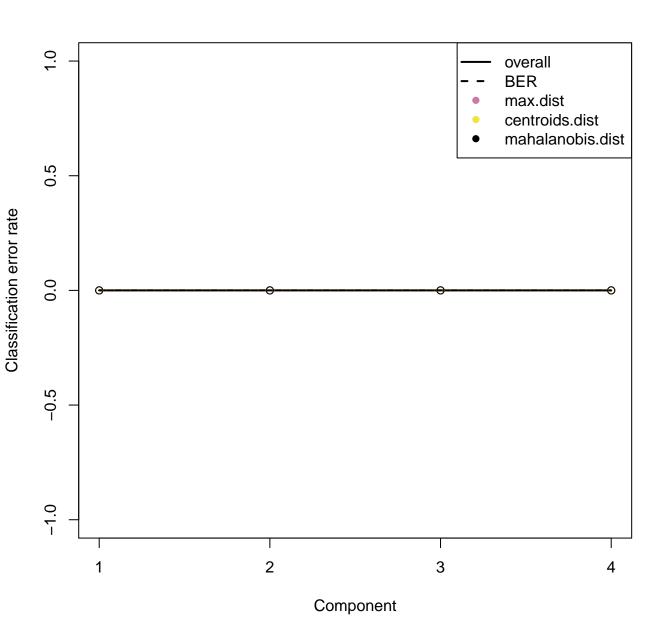




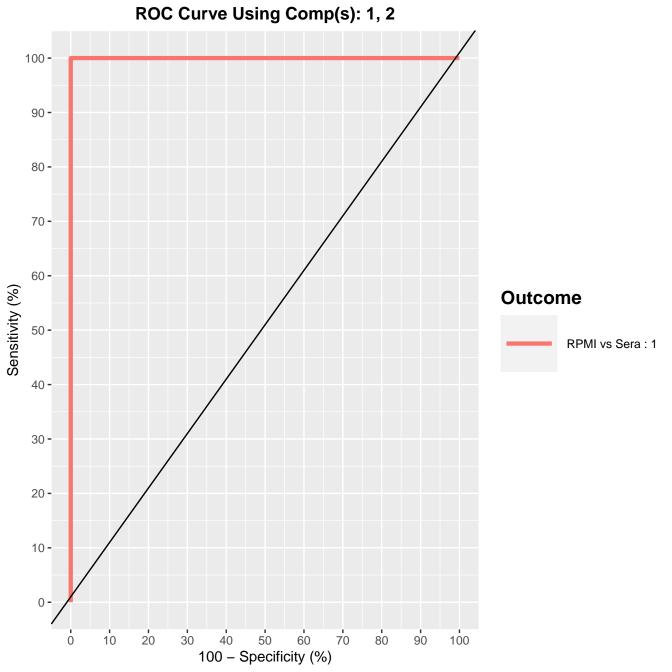


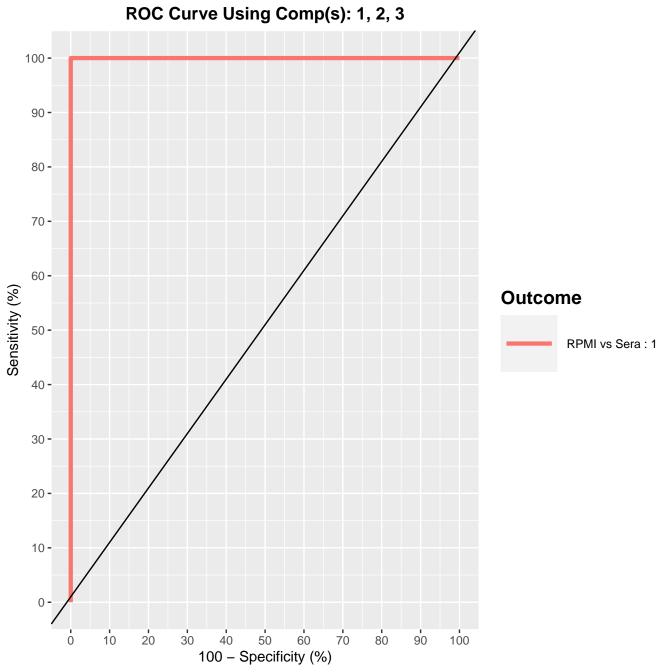


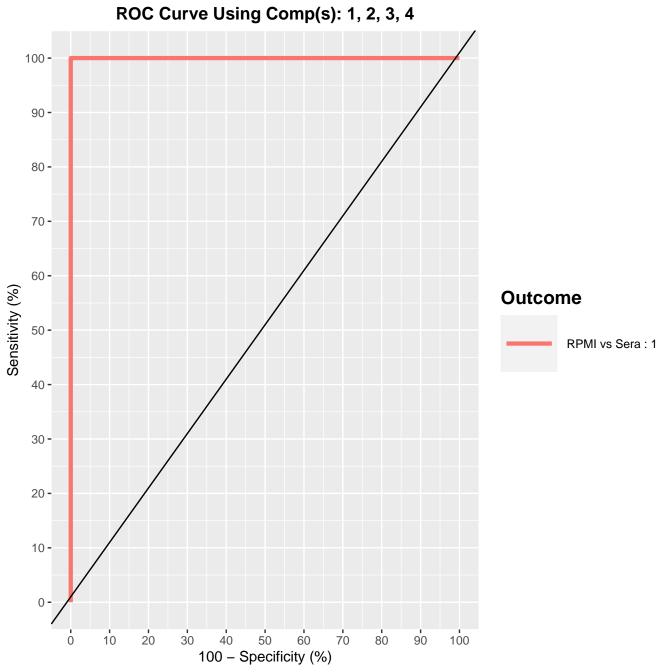


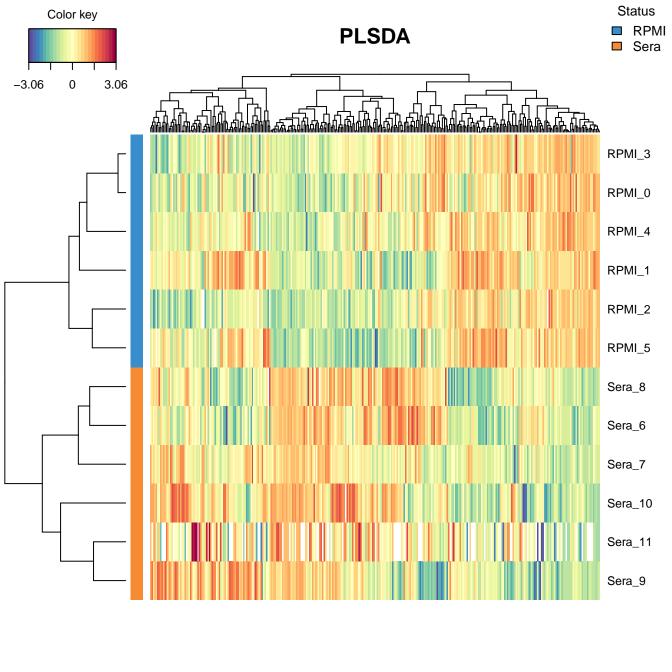


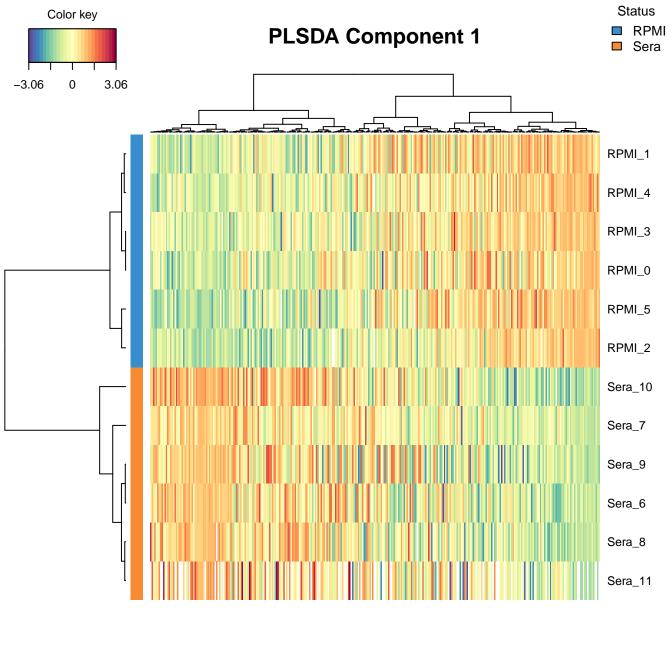




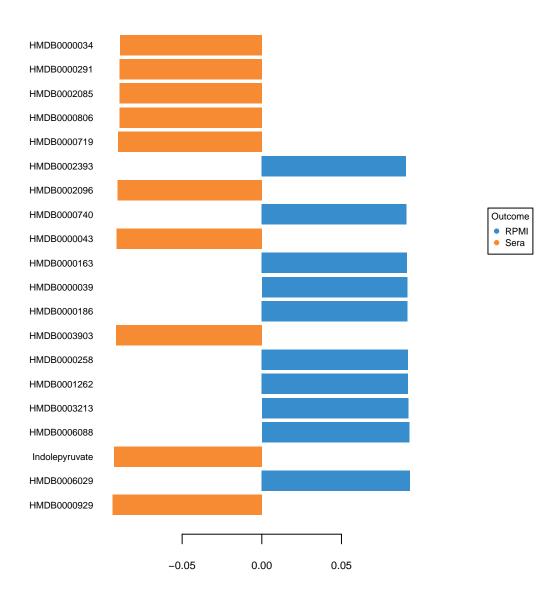




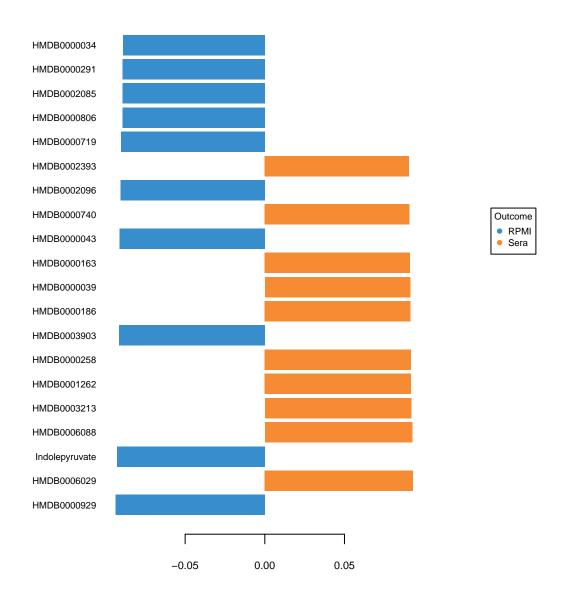


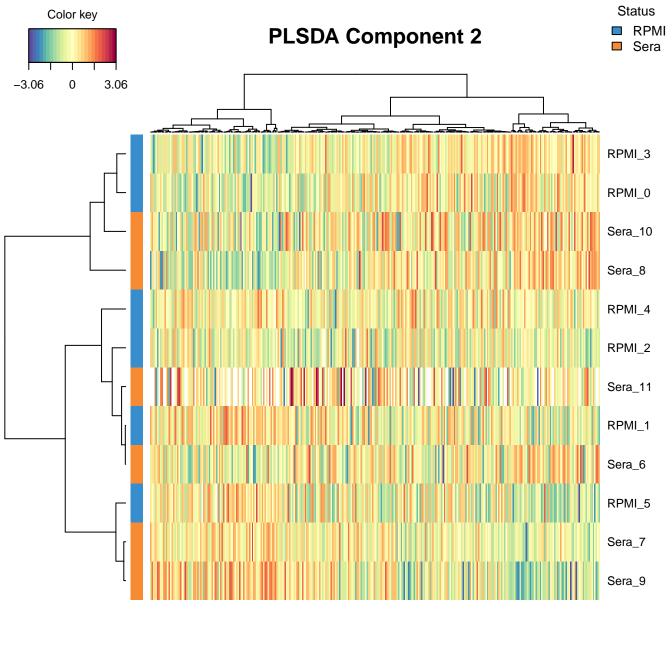


# metabolome 1 PLSDA max load

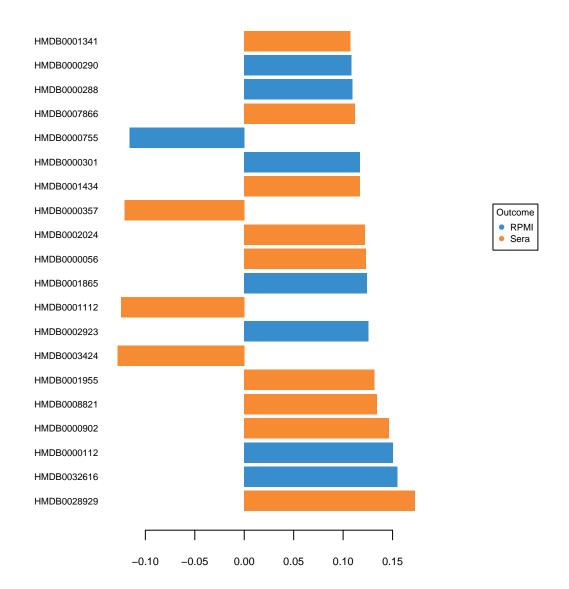


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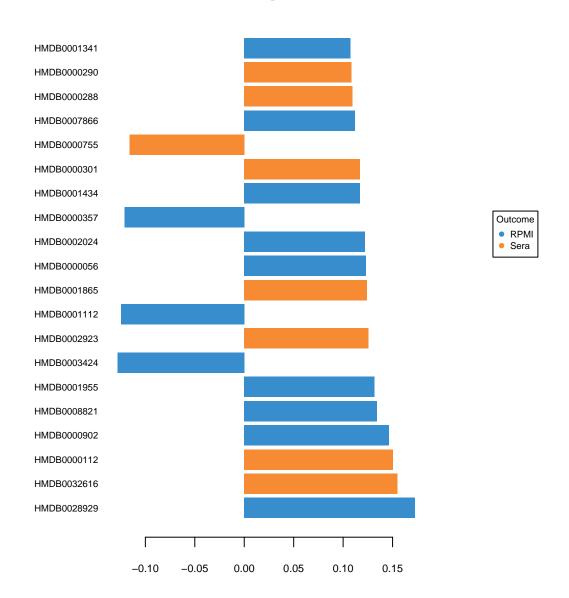


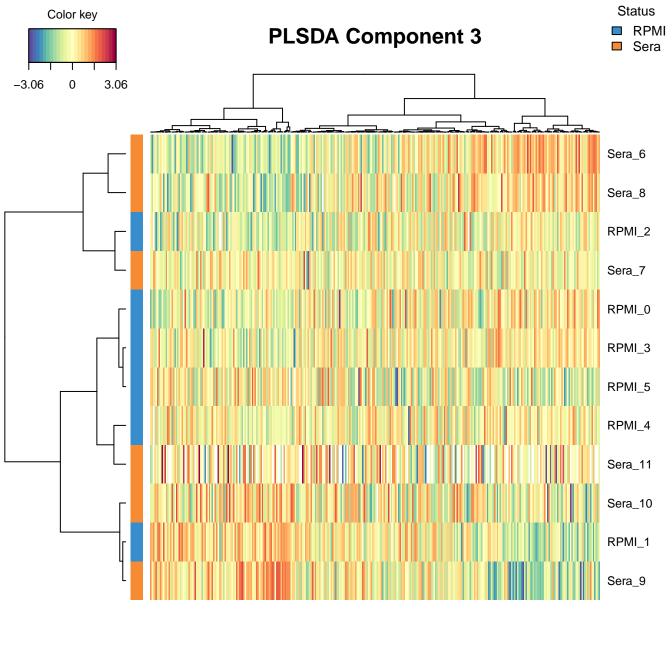


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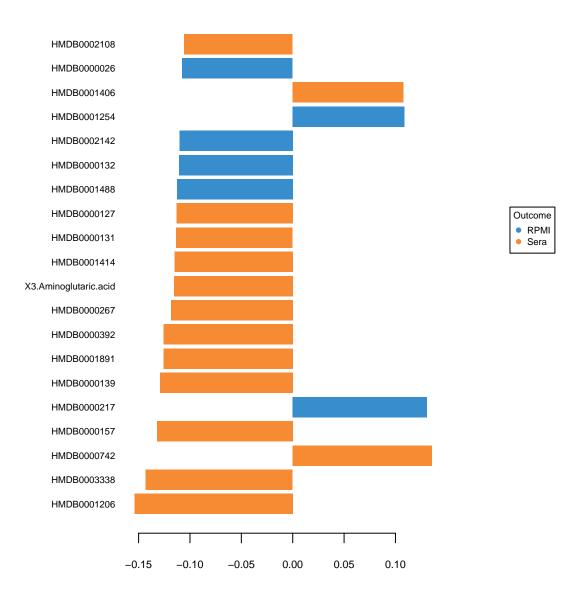


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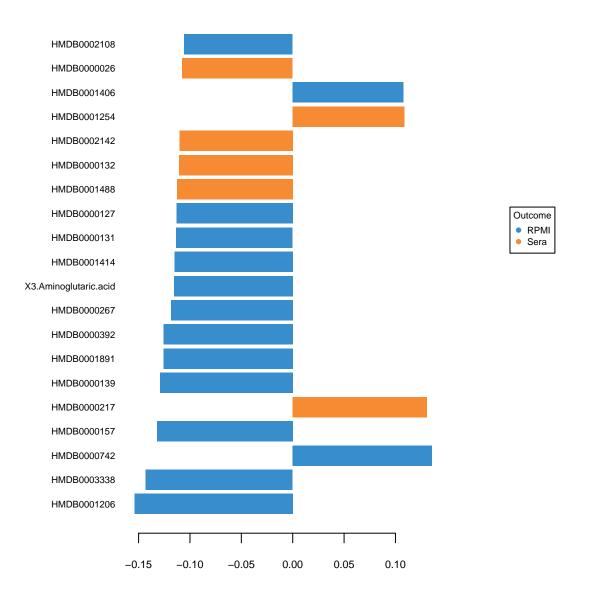


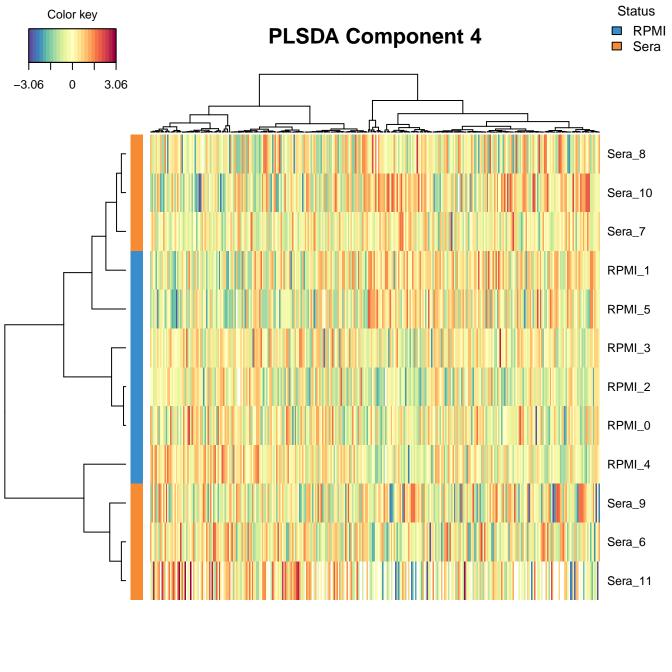


# metabolome 3 PLSDA max load

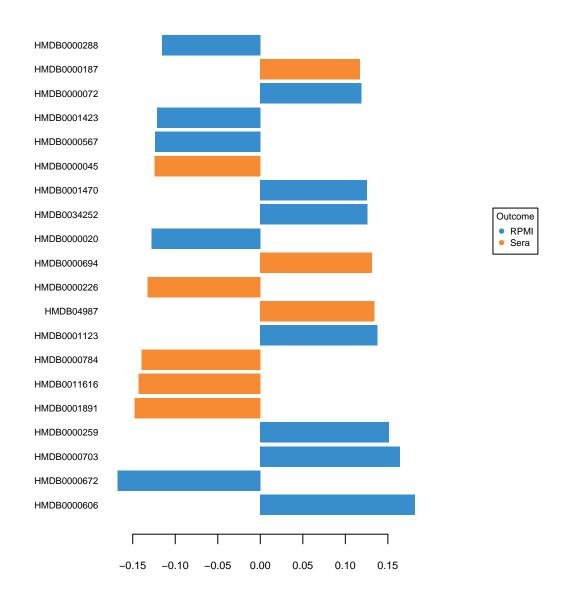


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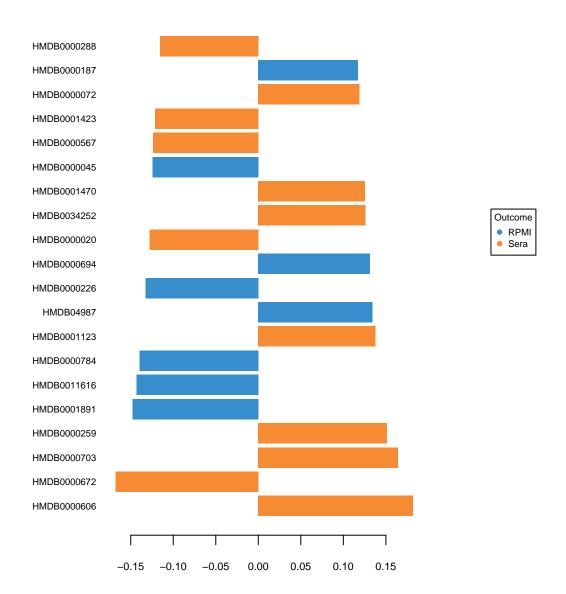


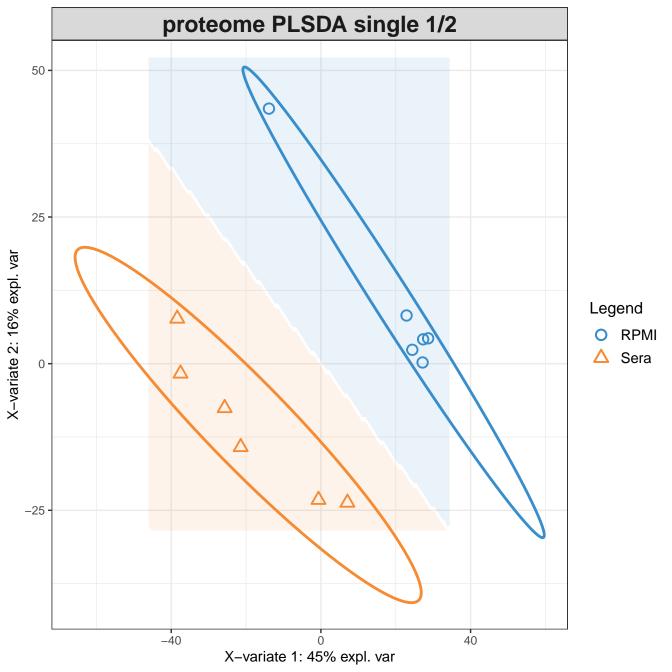


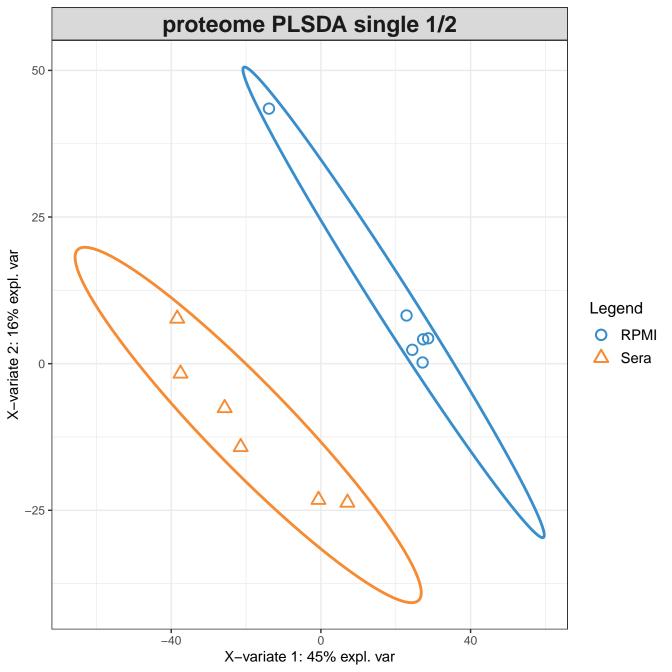
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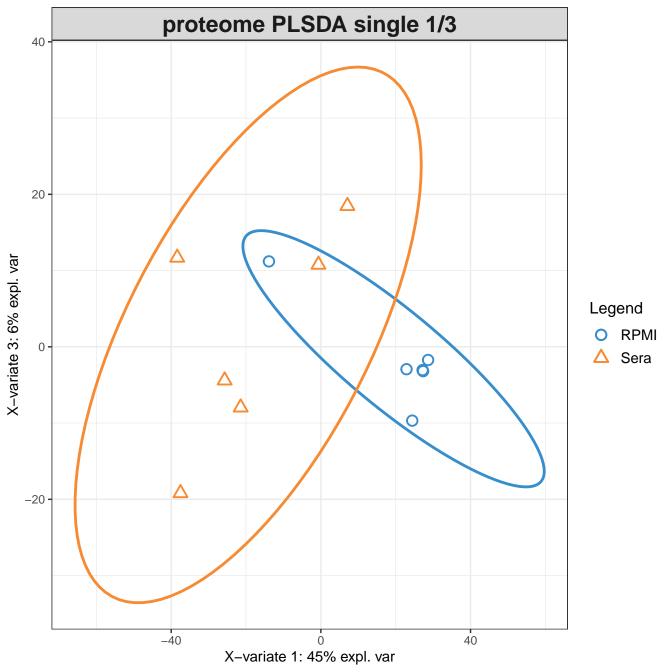


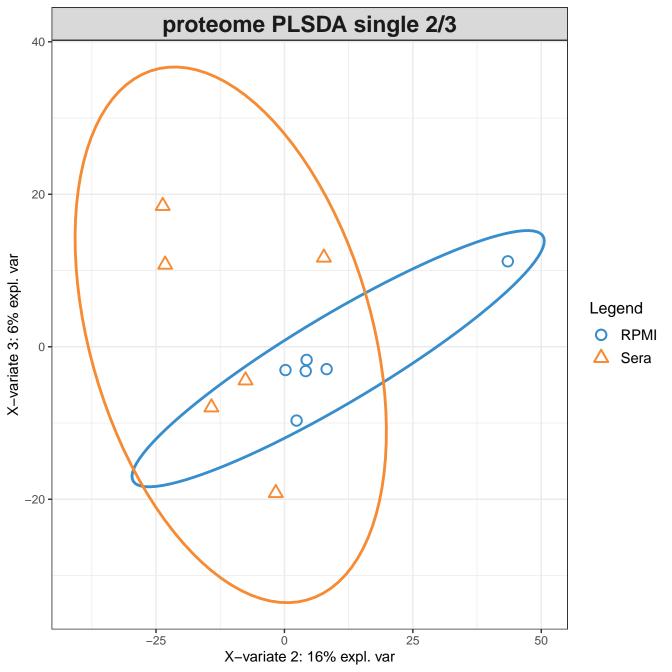
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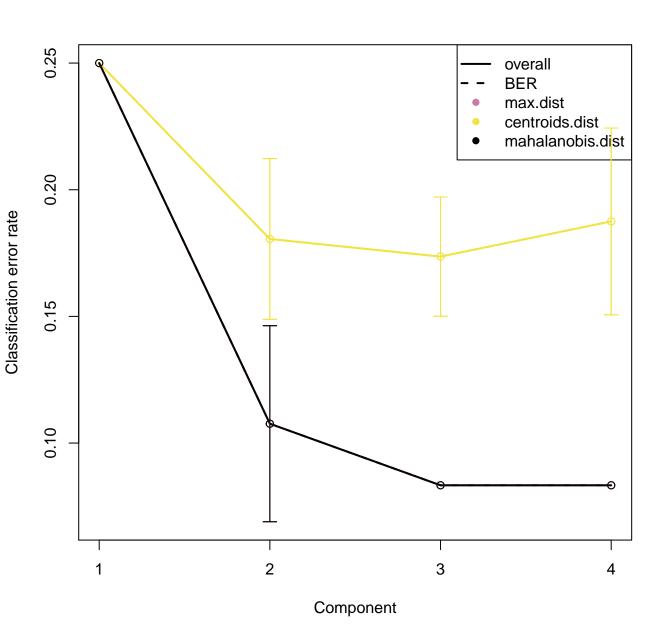


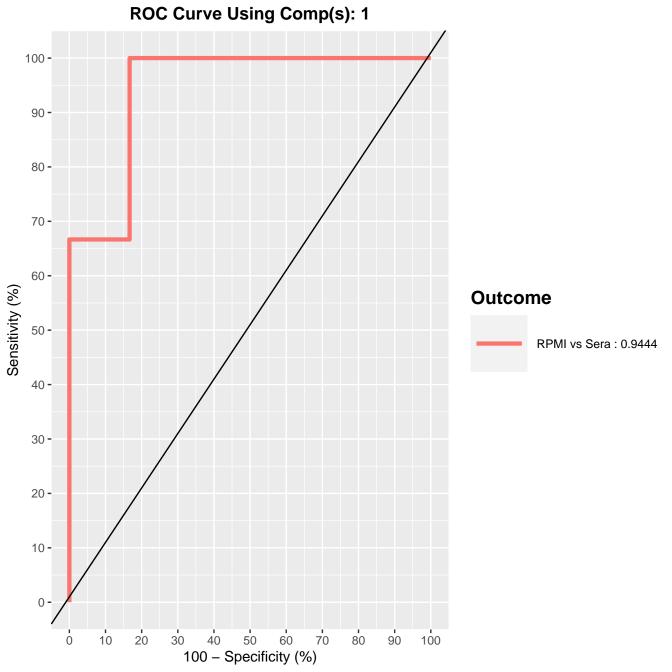


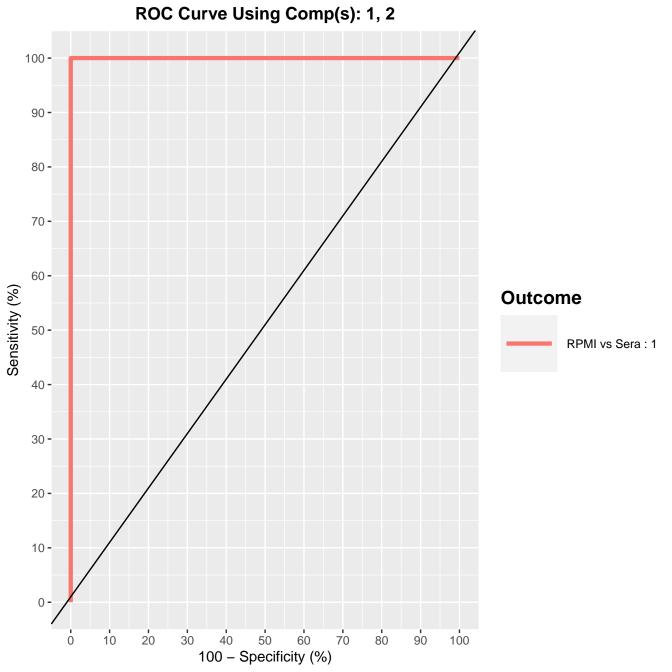


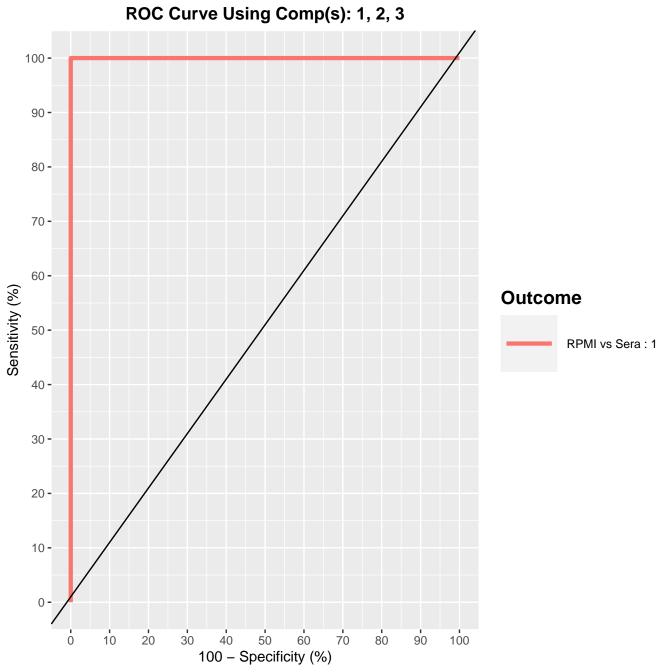


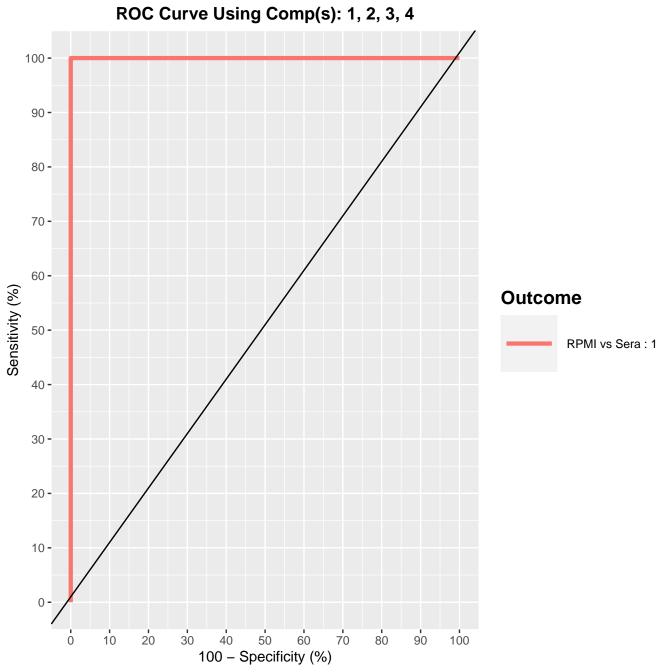


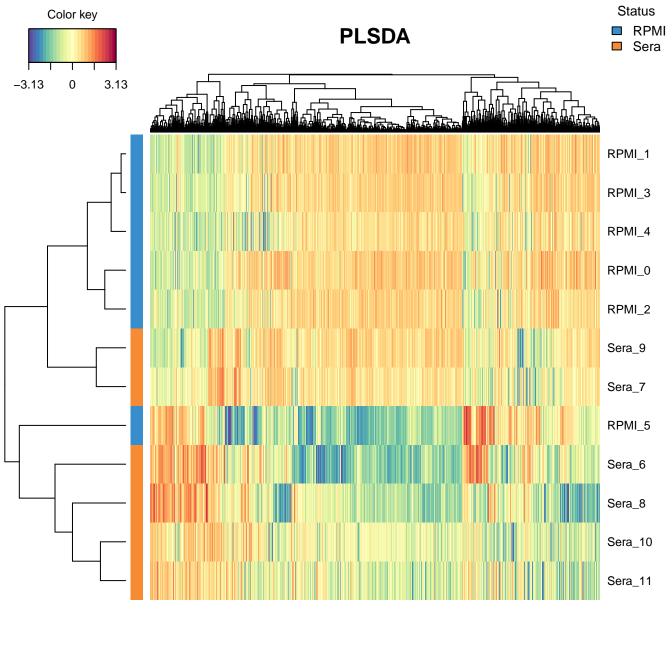


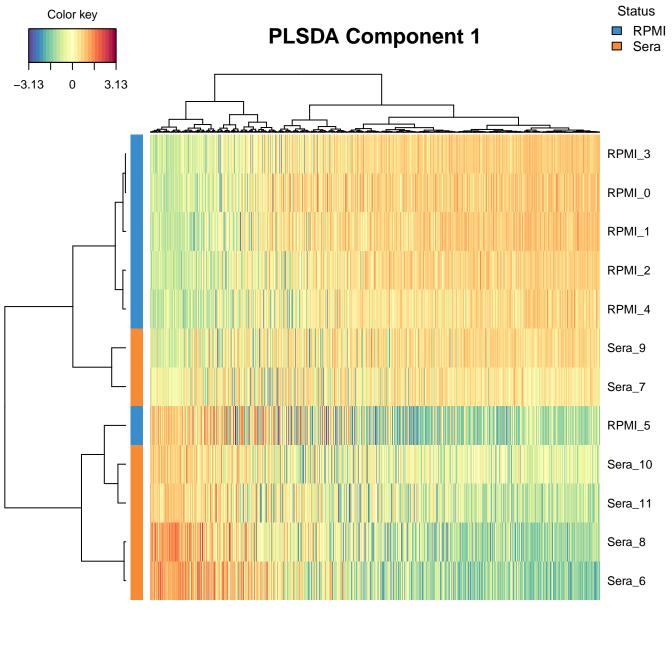




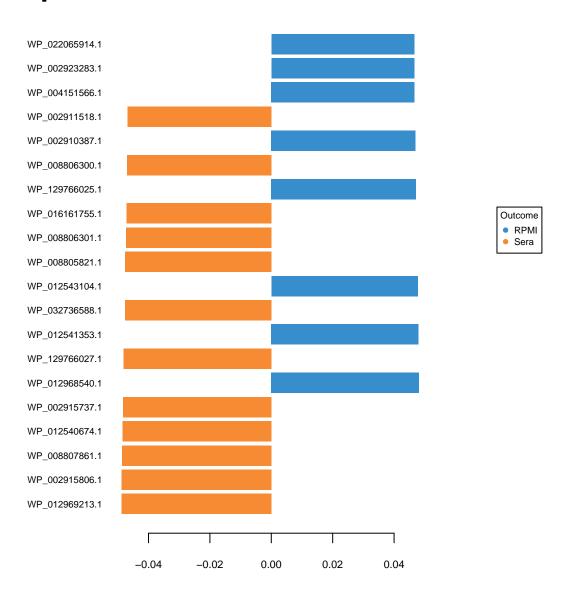




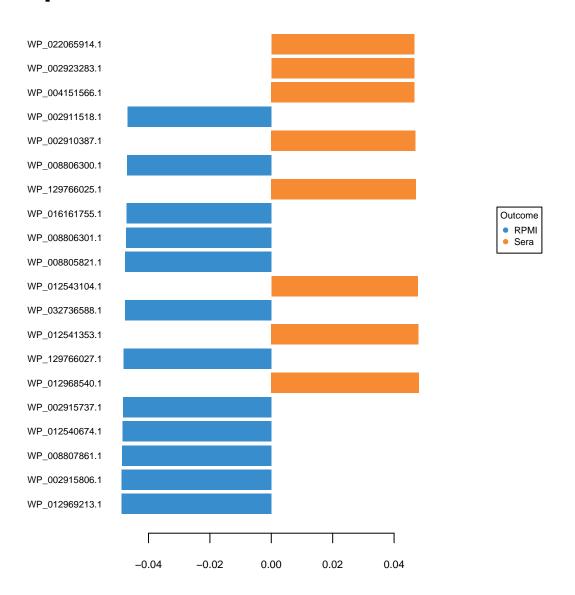


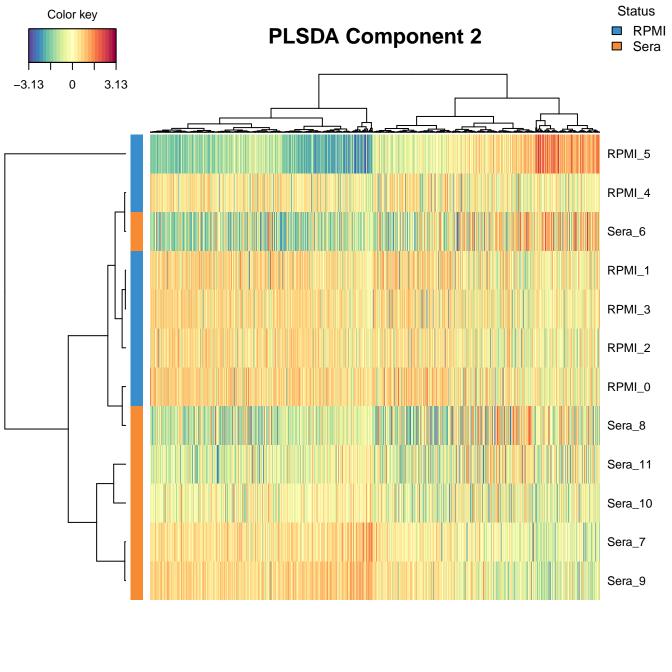


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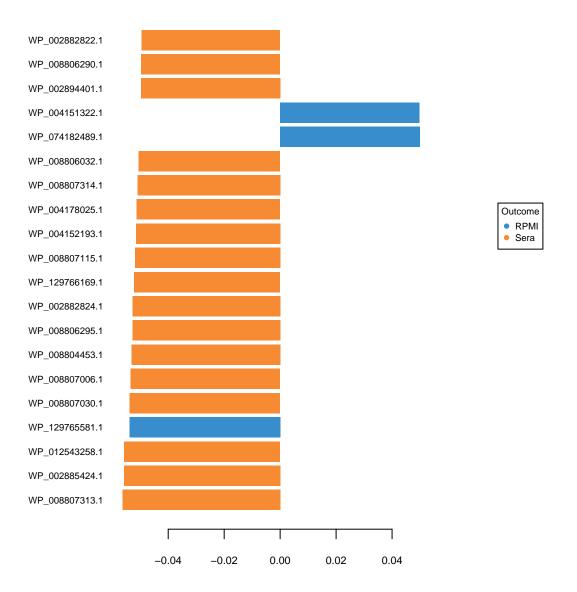


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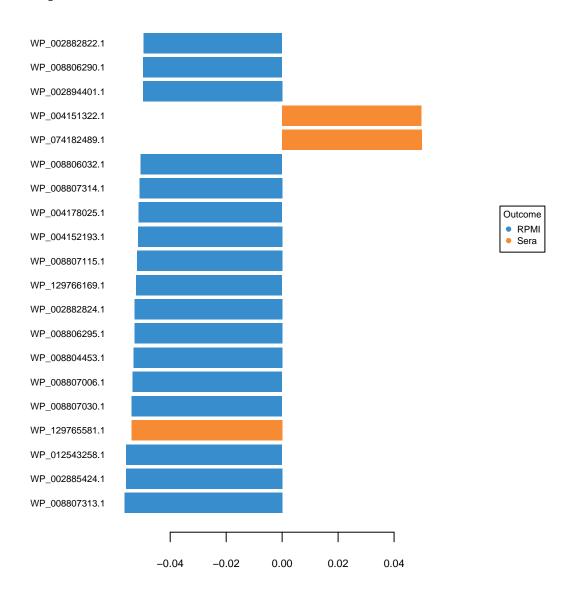


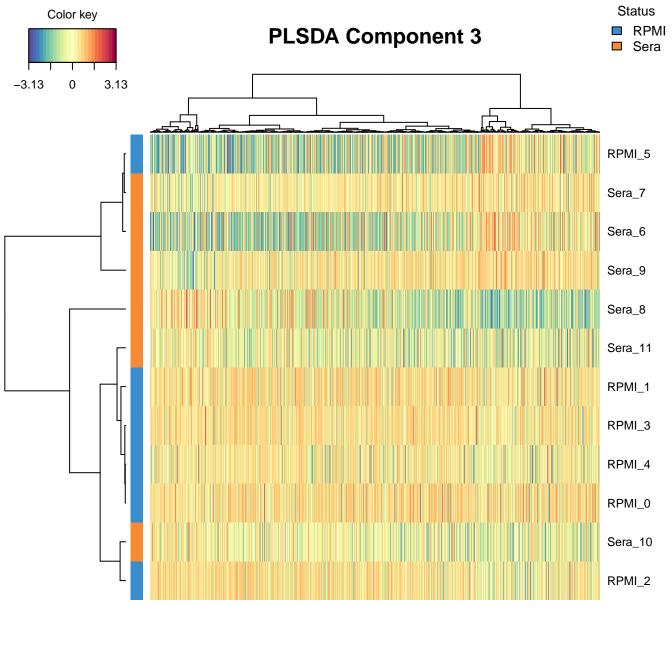


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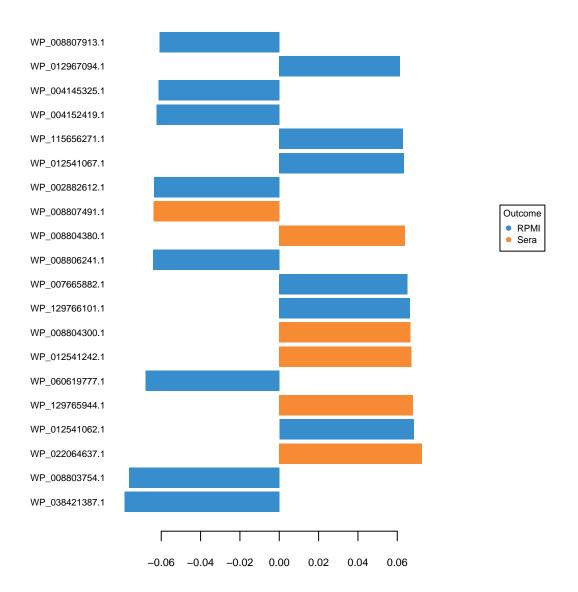


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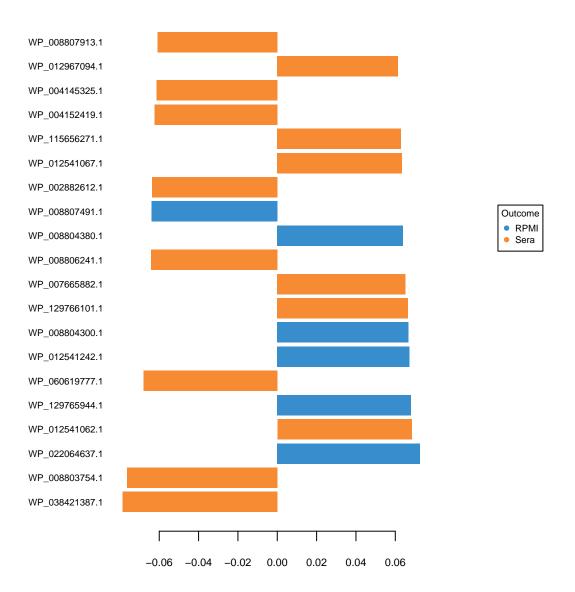




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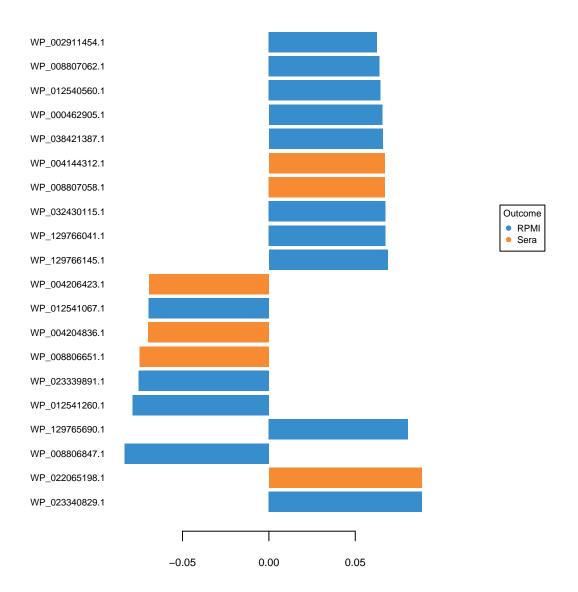


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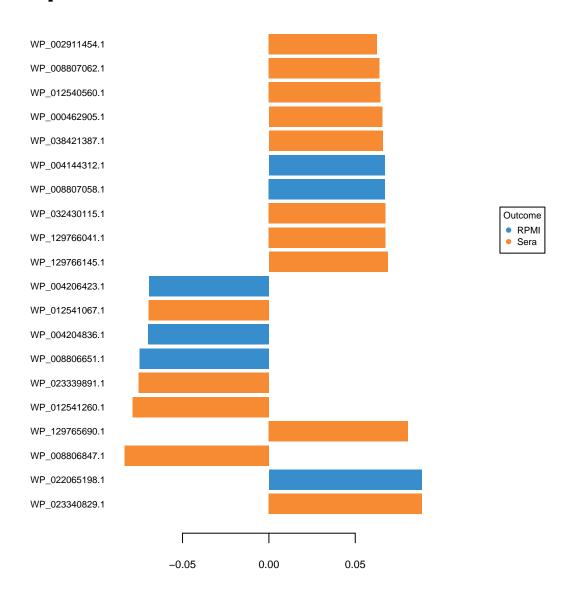




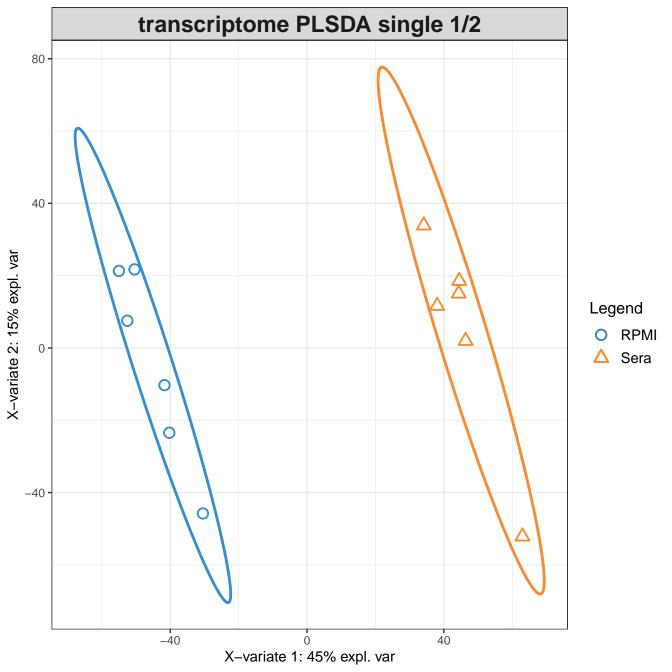
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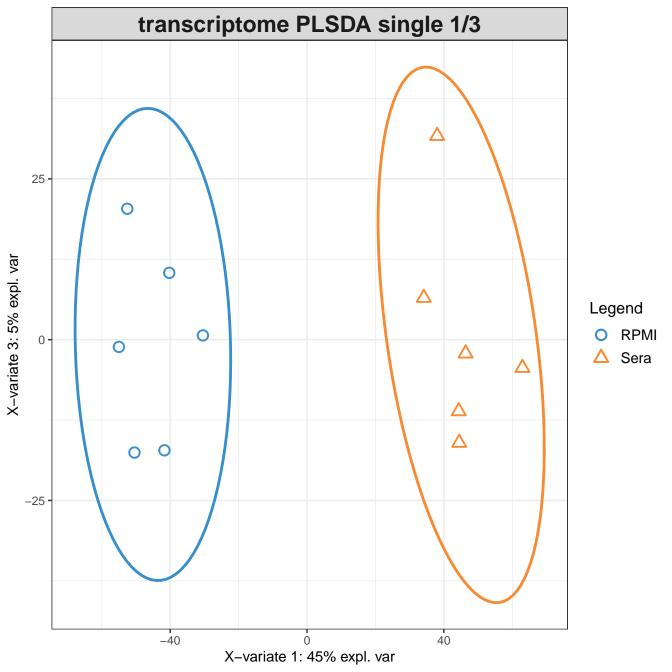


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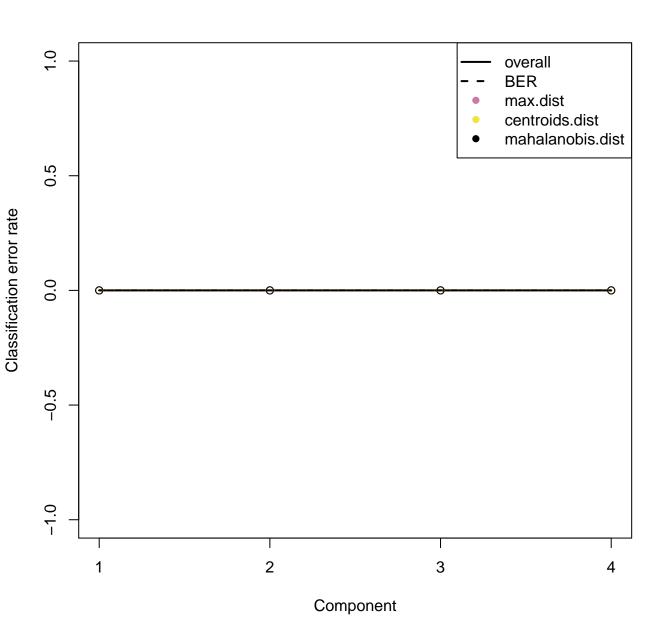




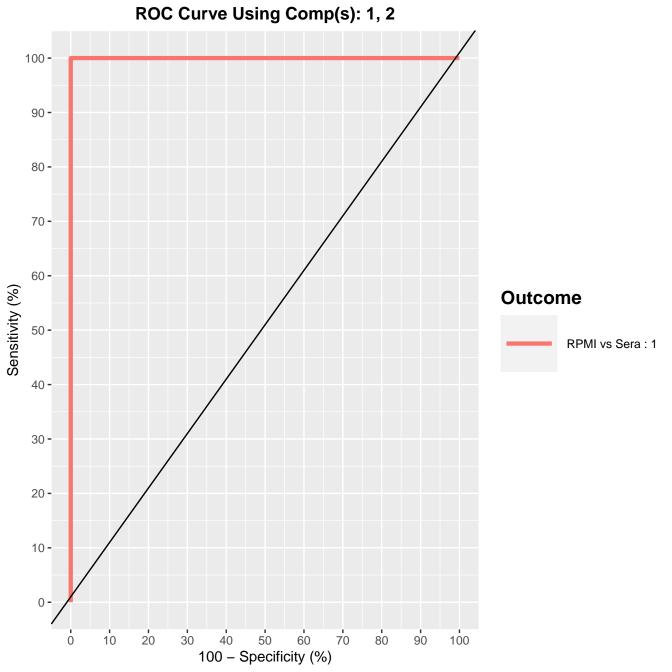


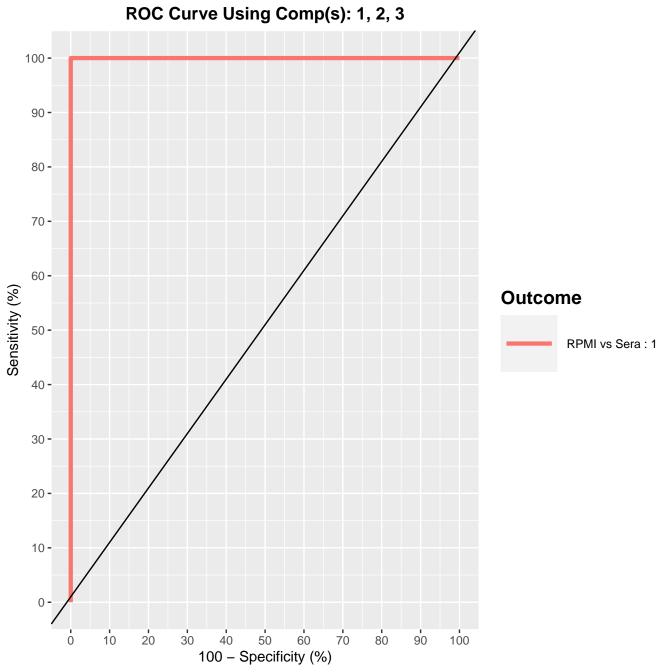


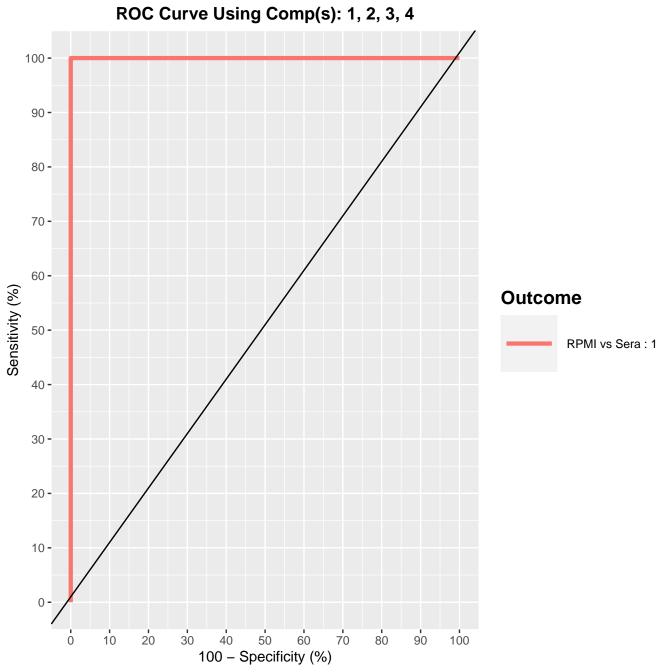


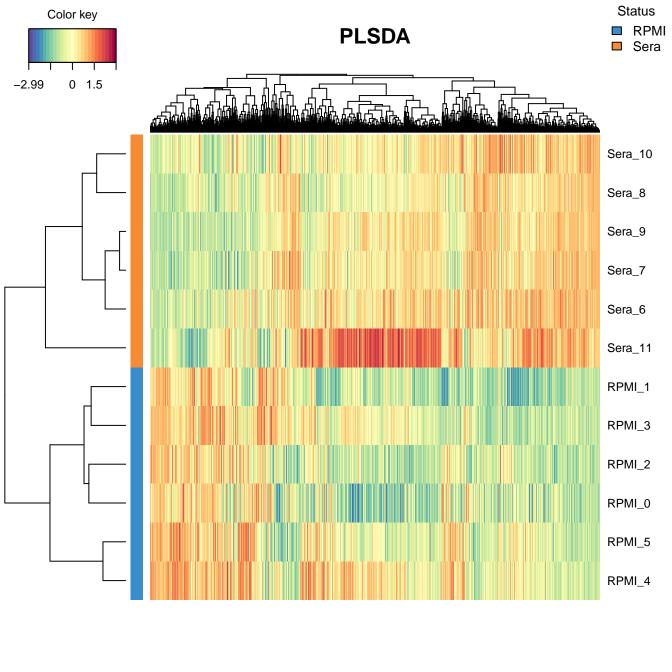


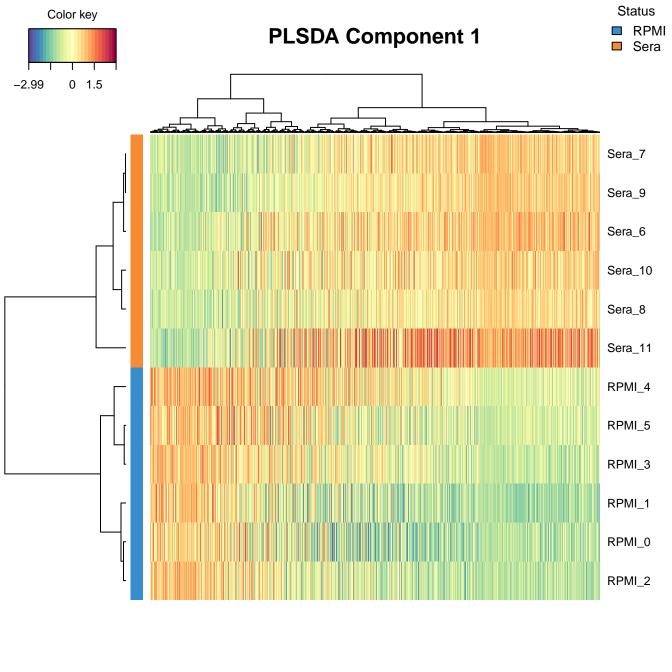




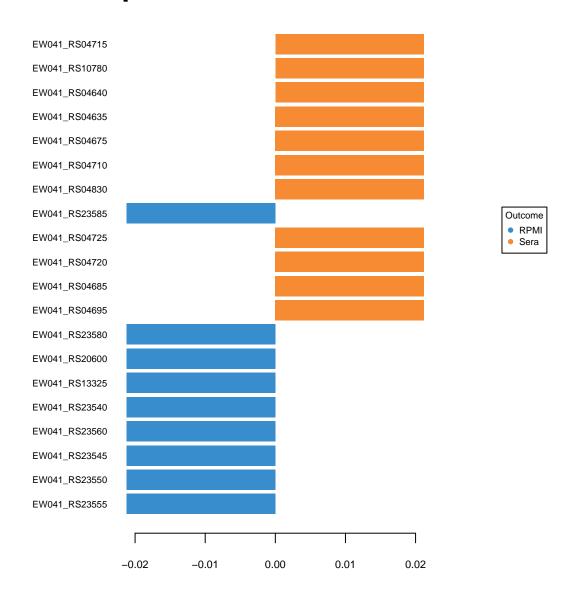




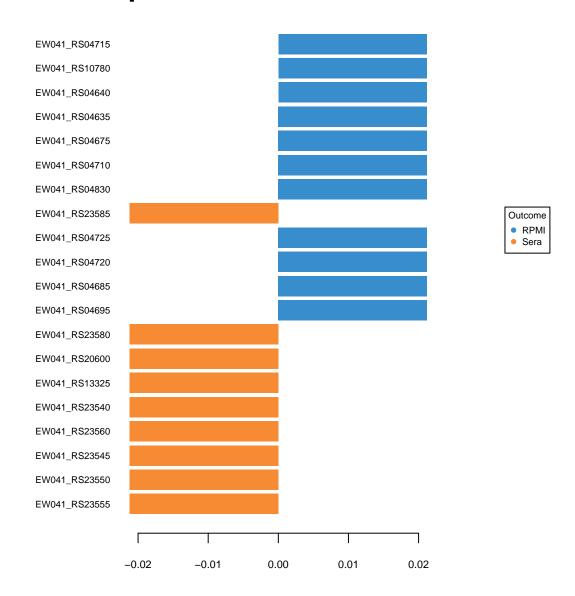


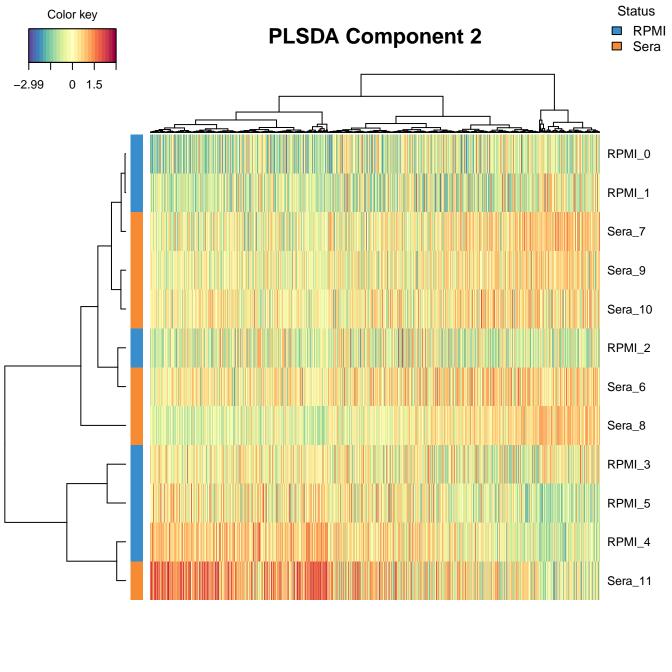


# transcriptome 1 PLSDA max load

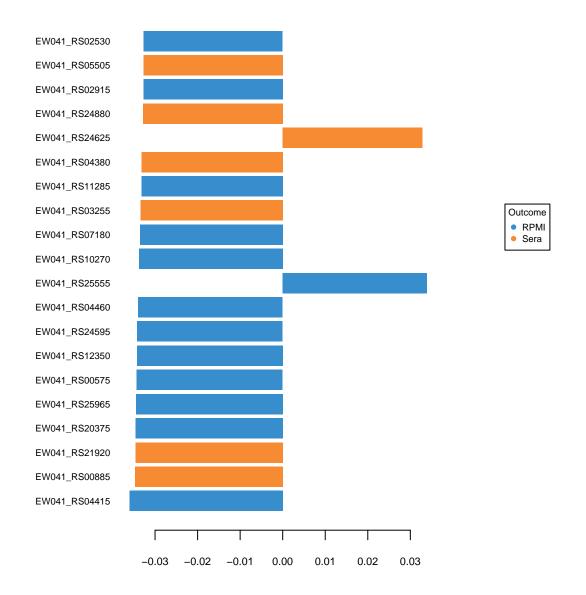


## transcriptome 1 PLSDA min load

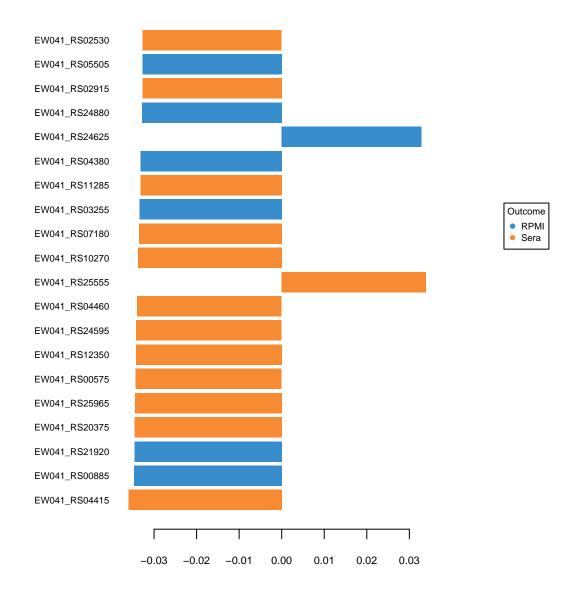


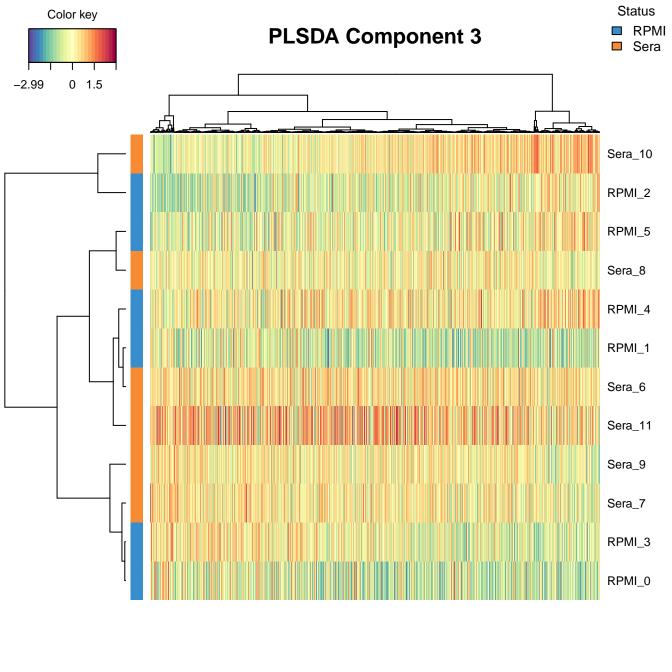


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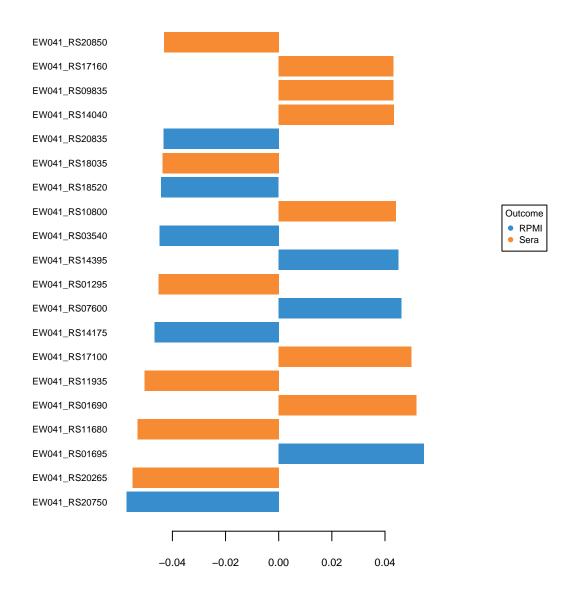


### transcriptome 2 PLSDA min load

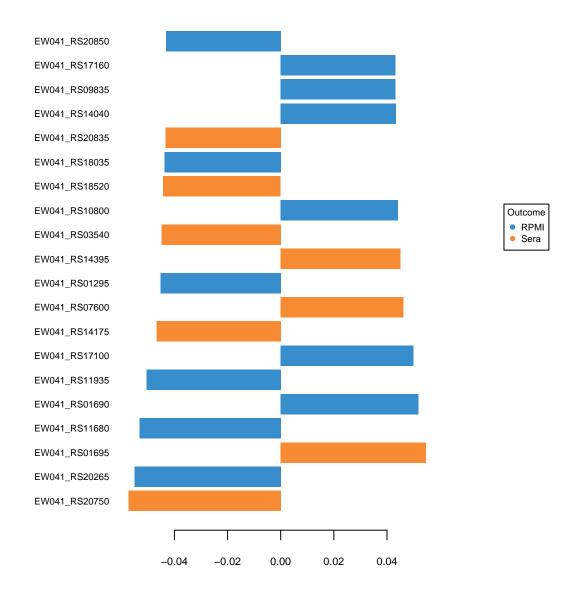


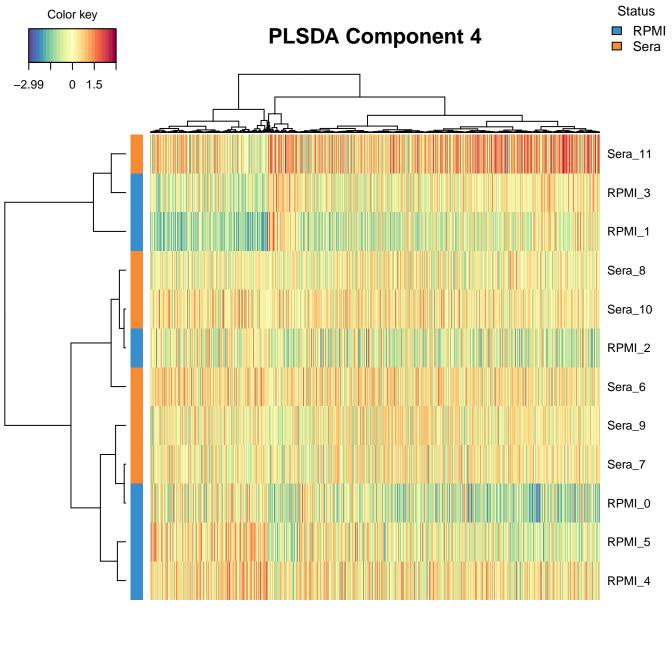


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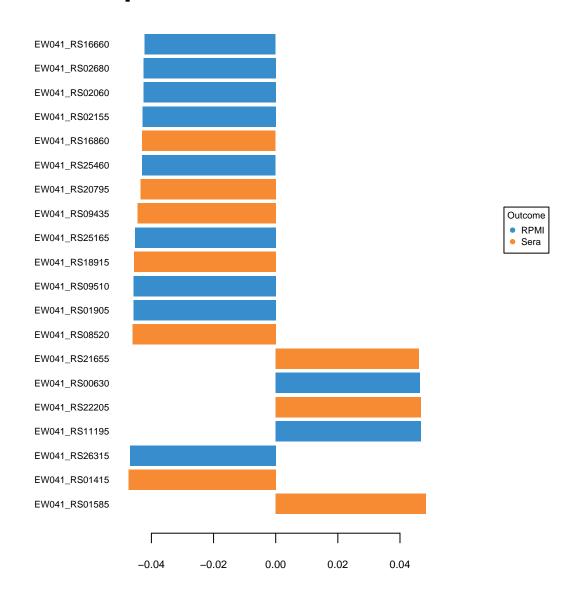


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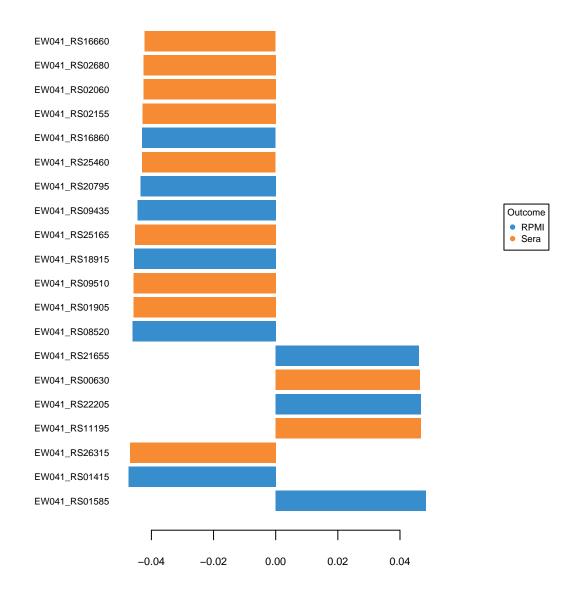


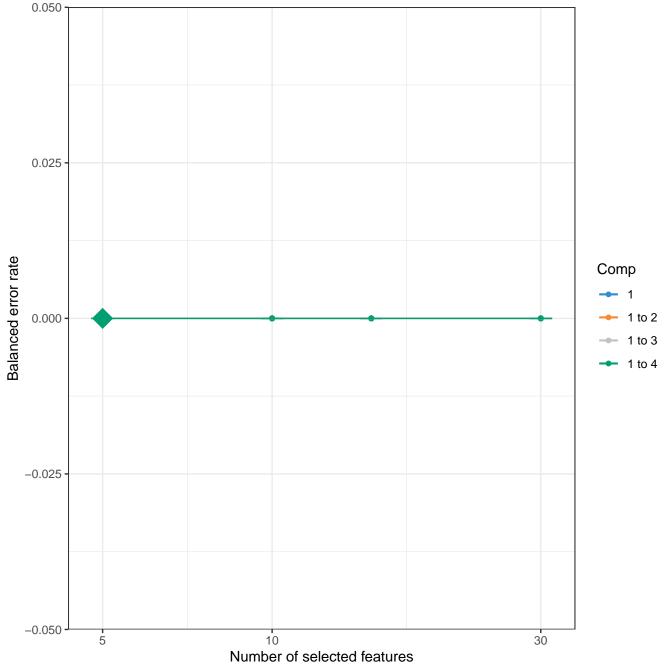


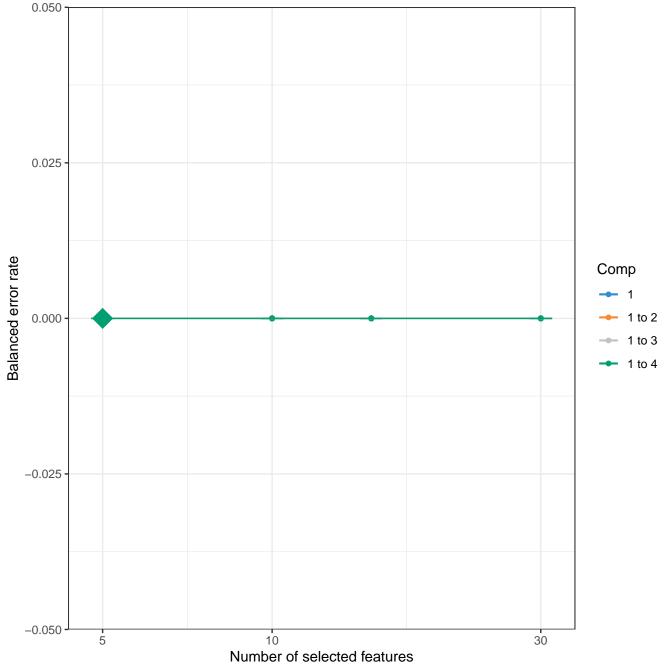
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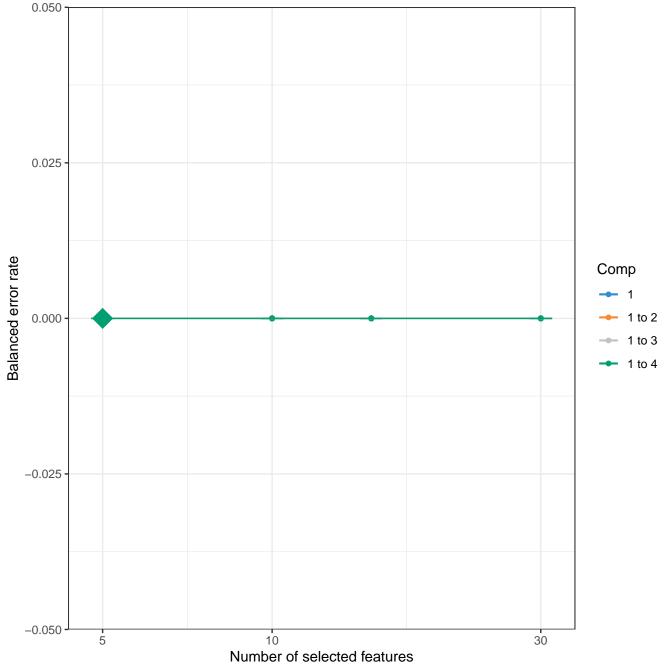


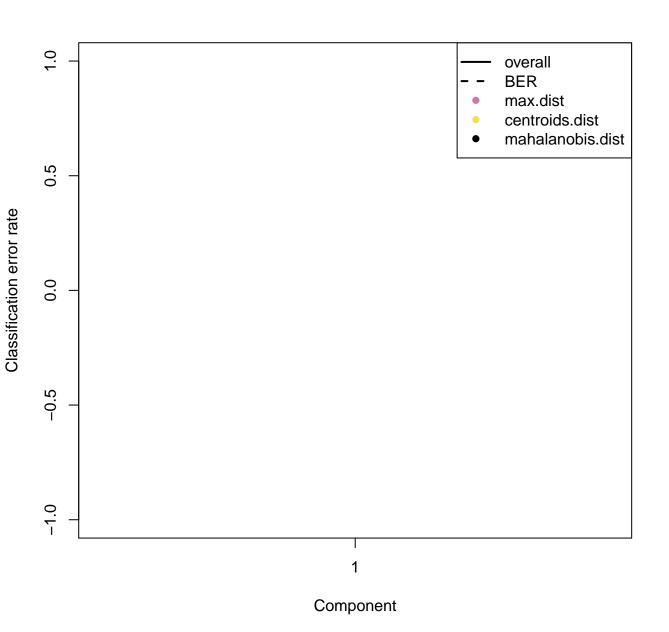
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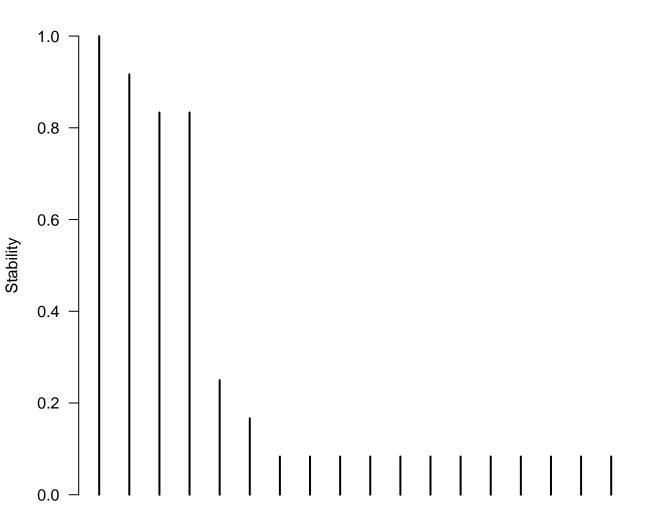




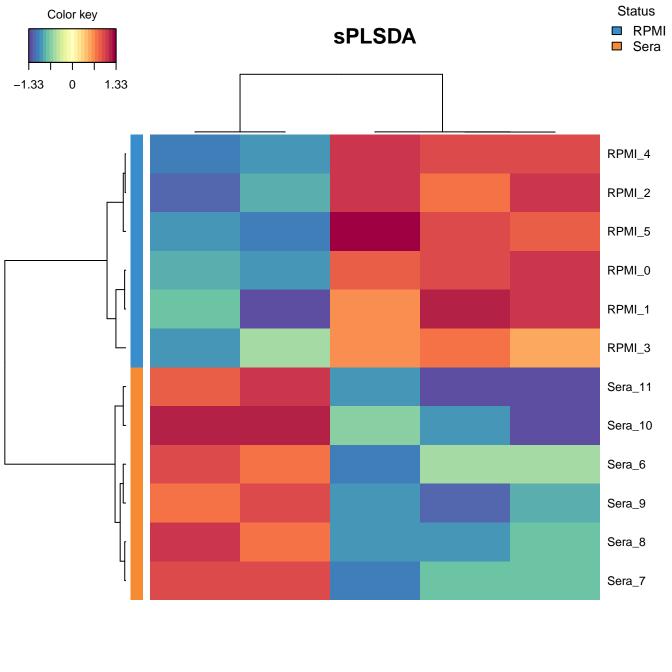


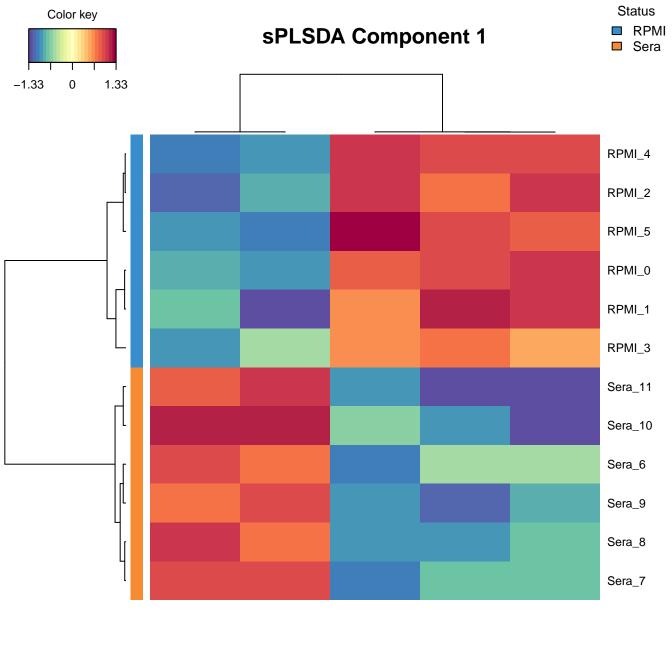




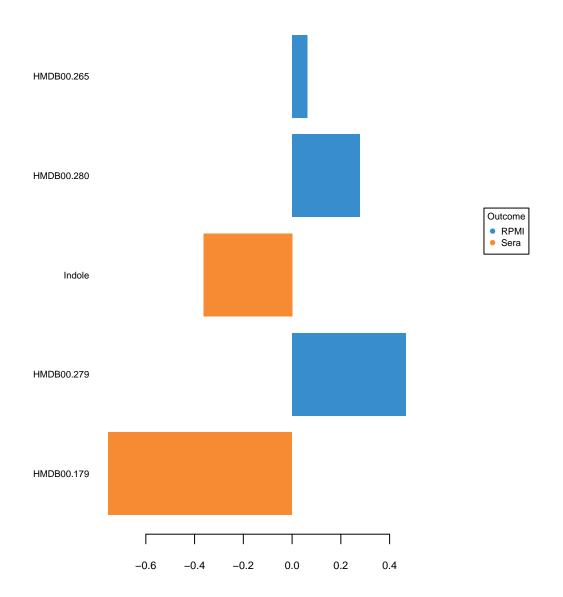




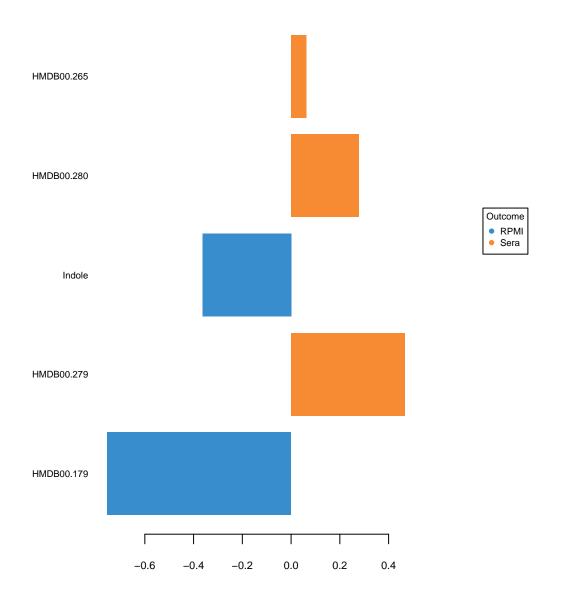


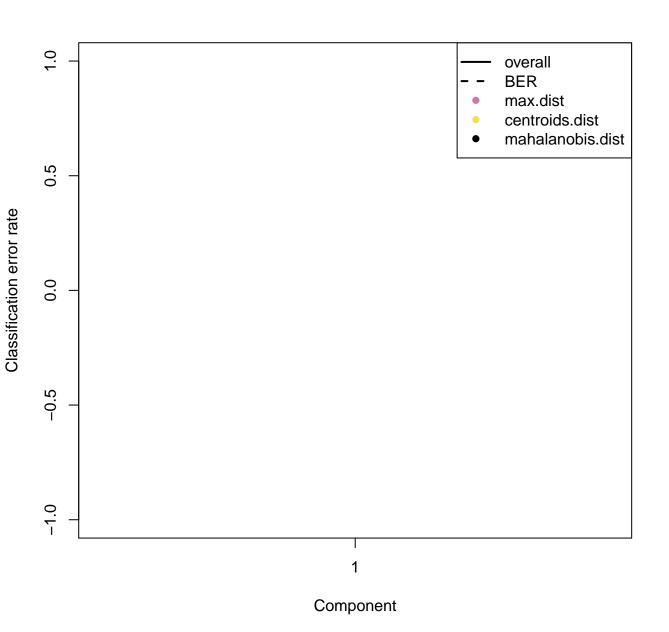


#### metabolome 1 sPLSDA max load

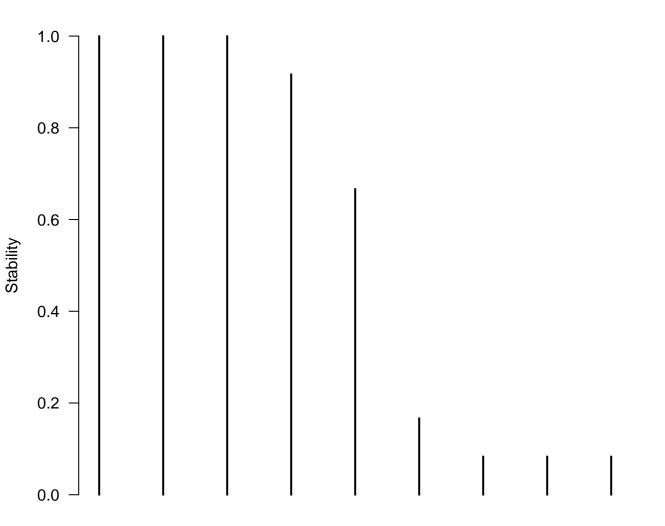


#### metabolome 1 sPLSDA min loac



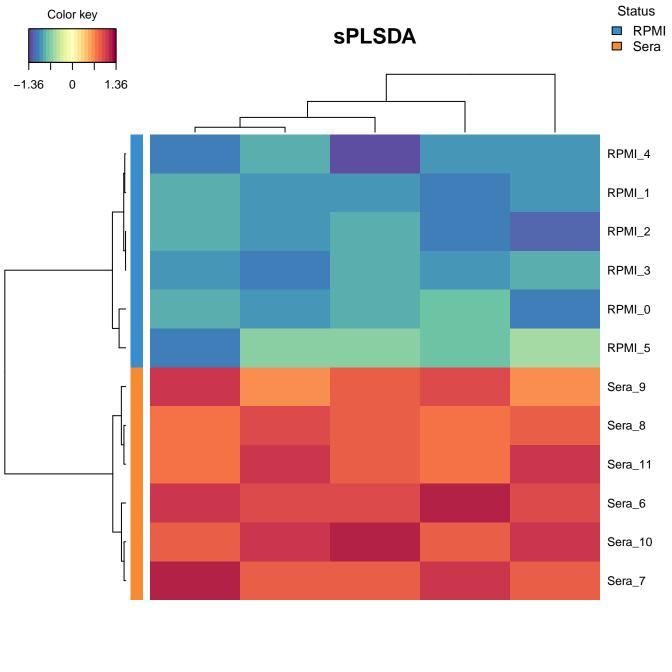


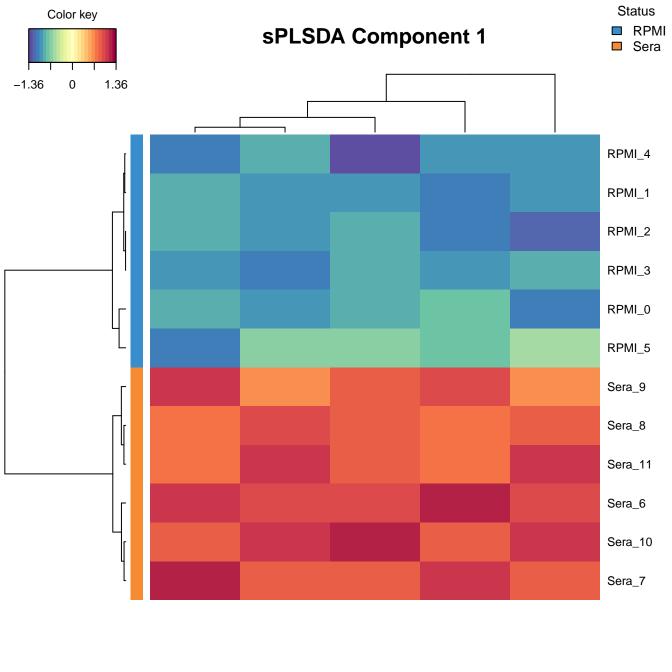




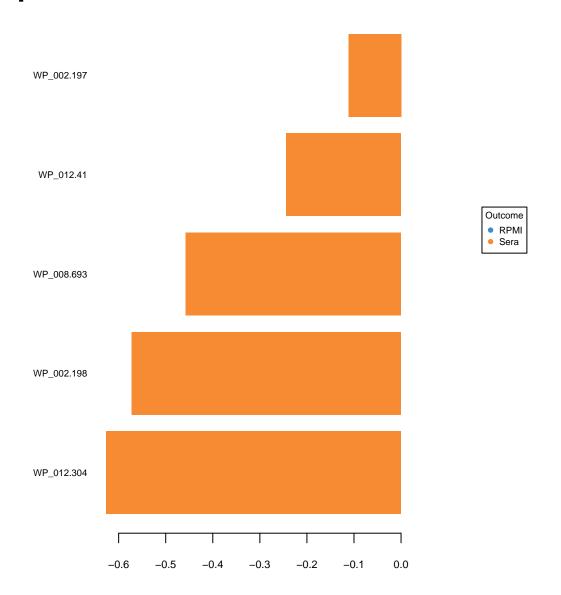
Features



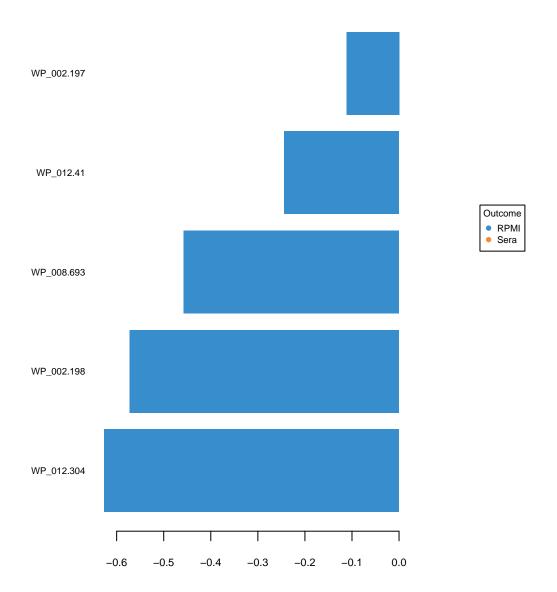


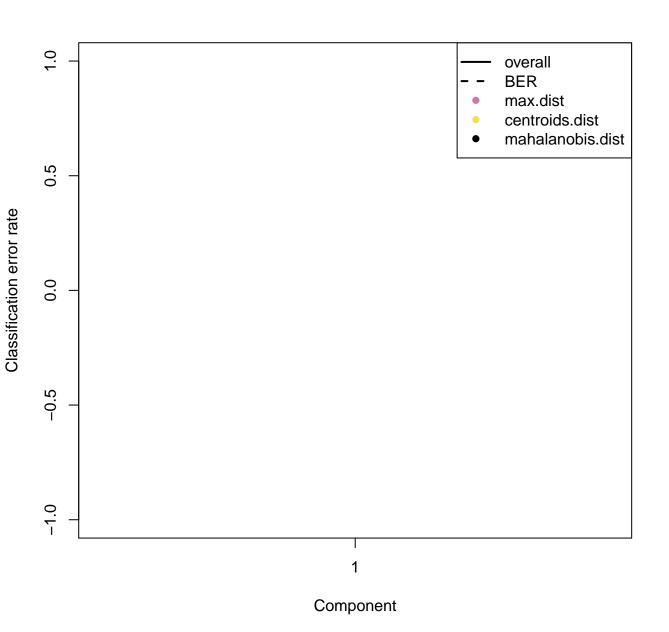


## proteome 1 sPLSDA max loadi

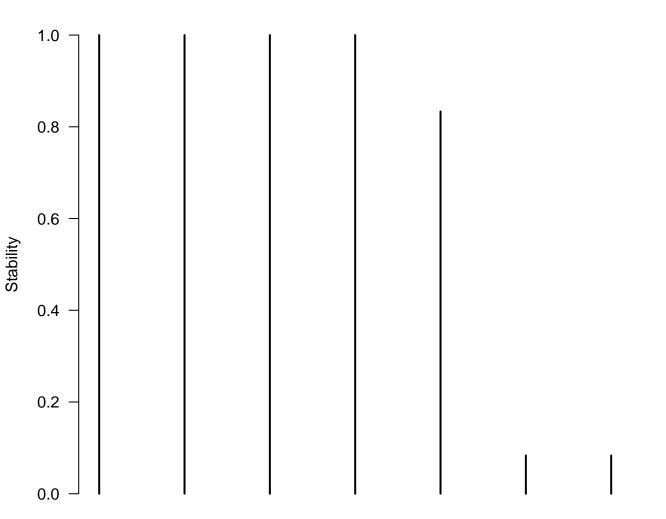


## proteome 1 sPLSDA min loadii



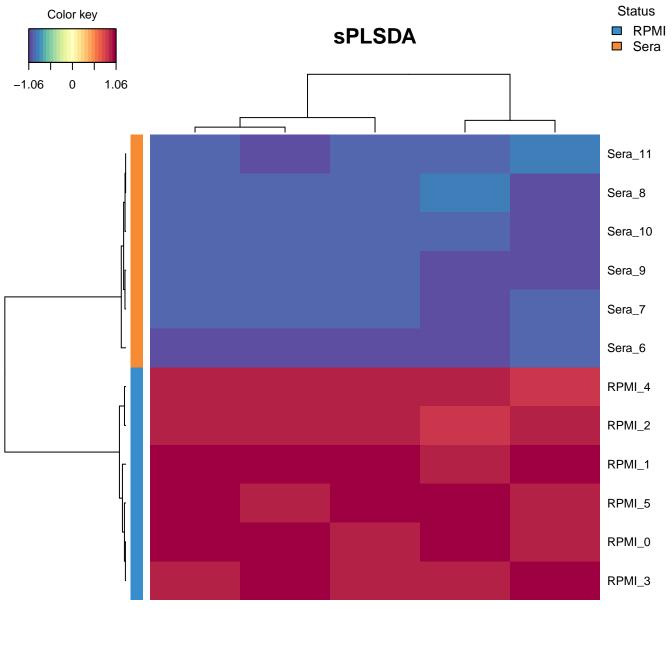


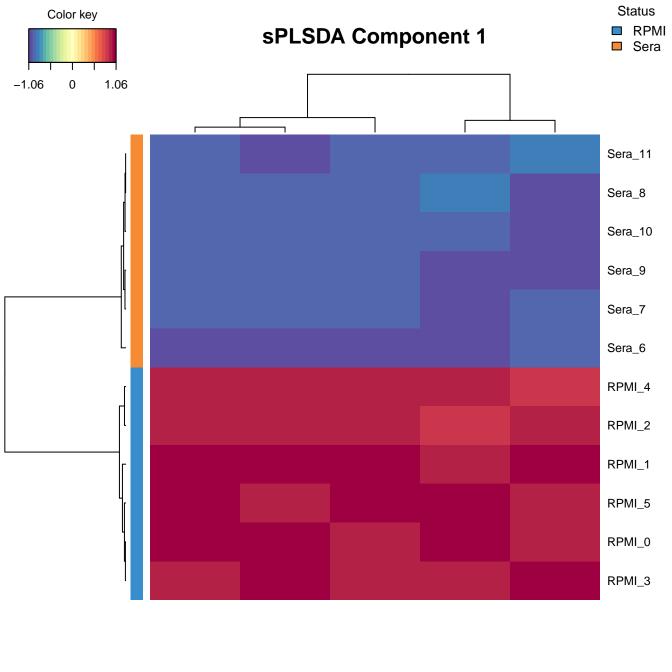




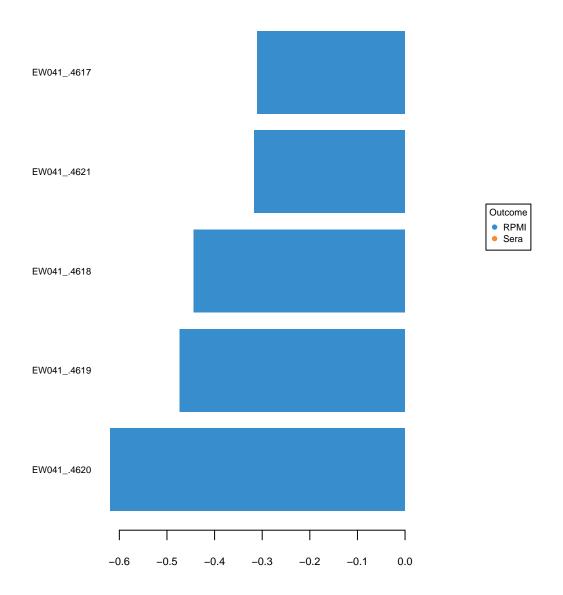
Features



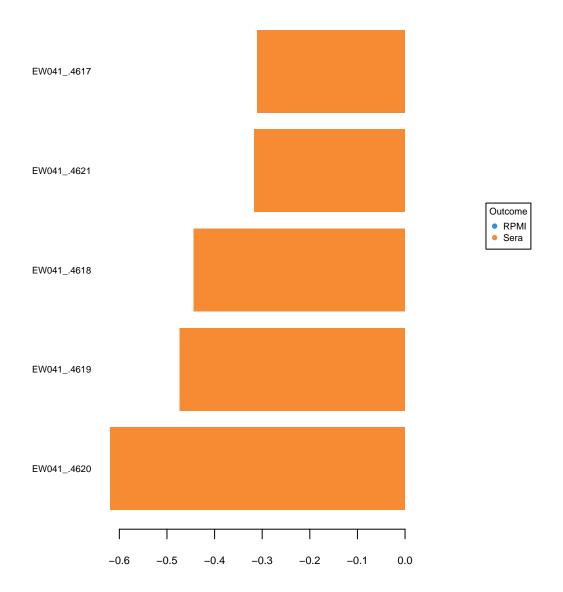


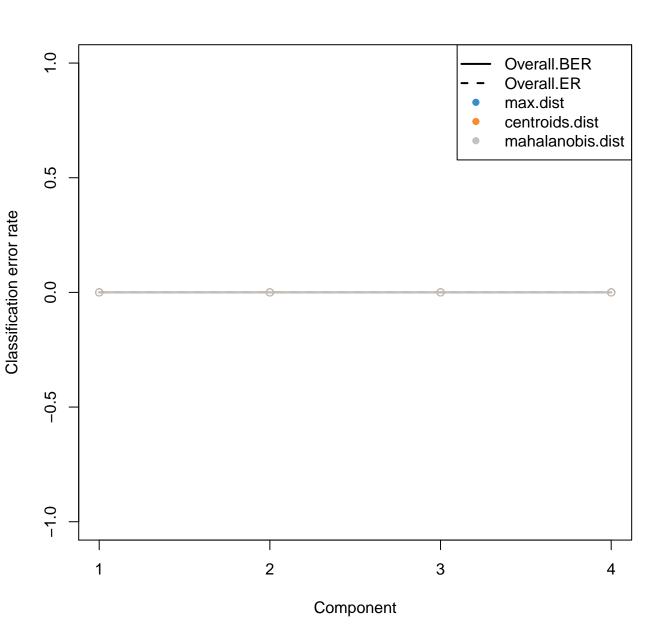


## transcriptome 1 sPLSDA max loa

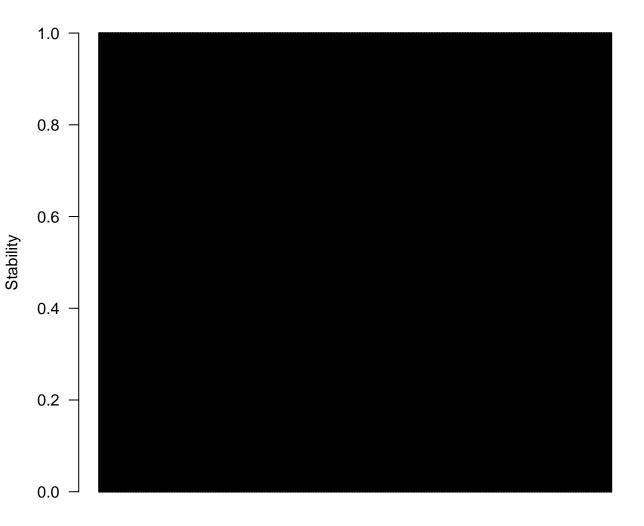


## transcriptome 1 sPLSDA min loa



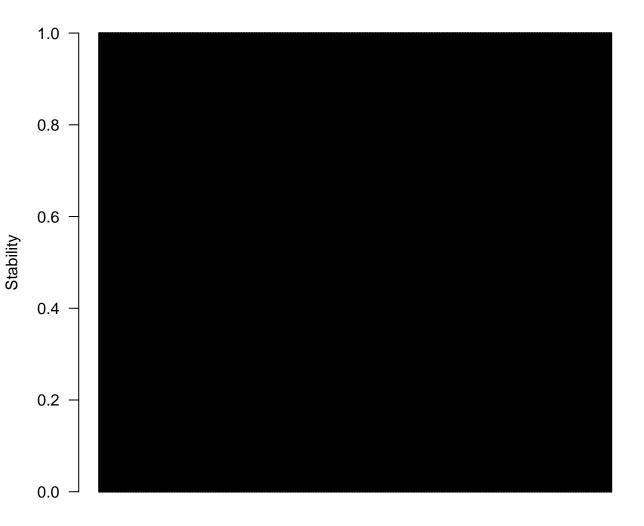


#### metabolome Comp 1



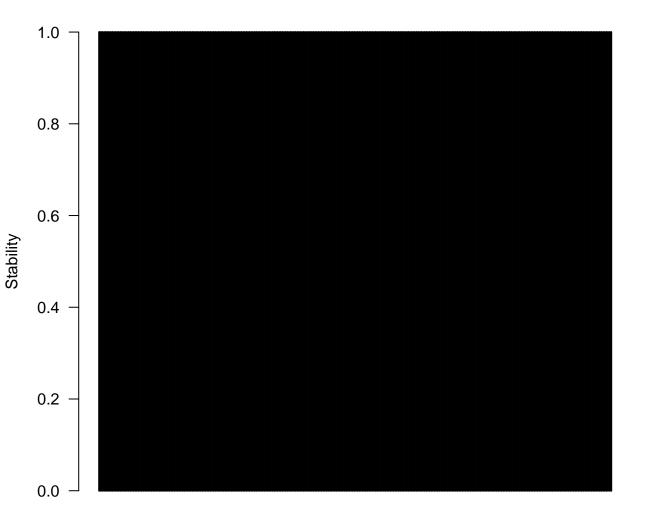
Features

#### metabolome Comp 2

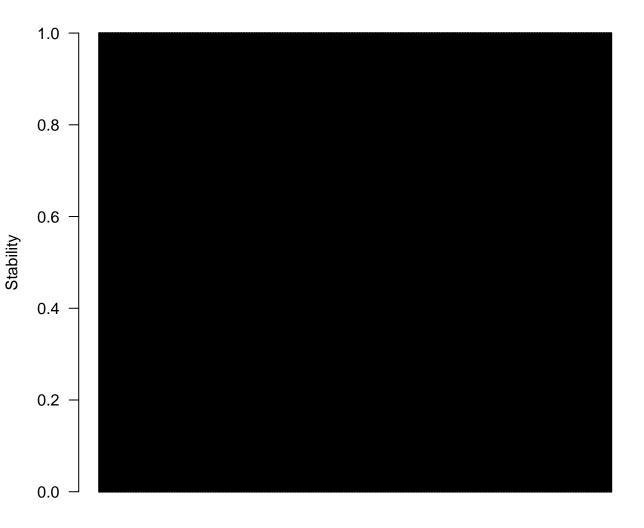


Features

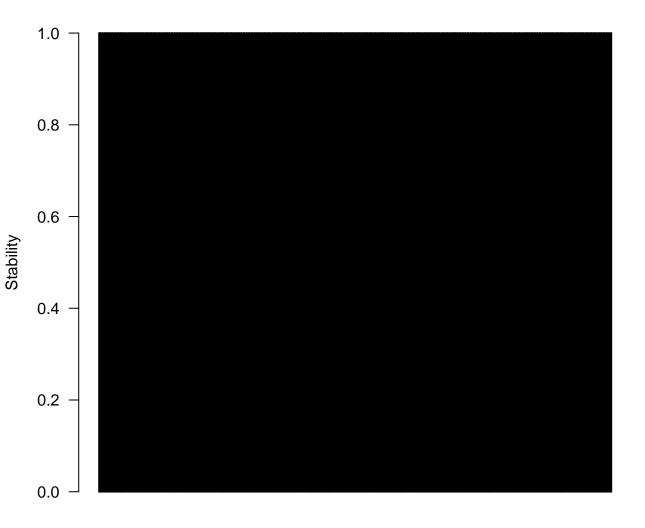
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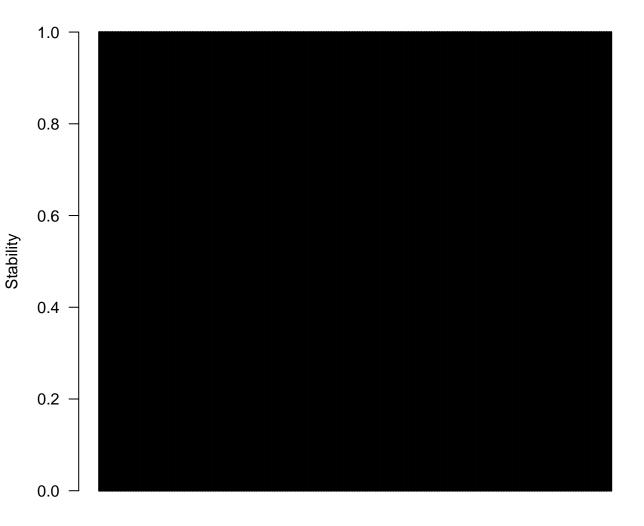
Features



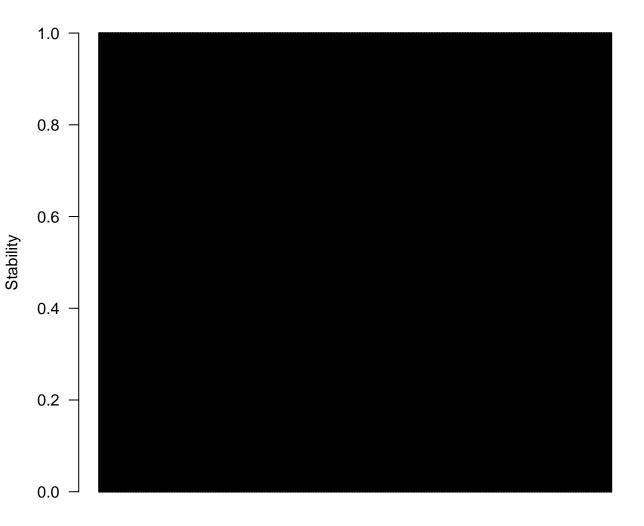
Features



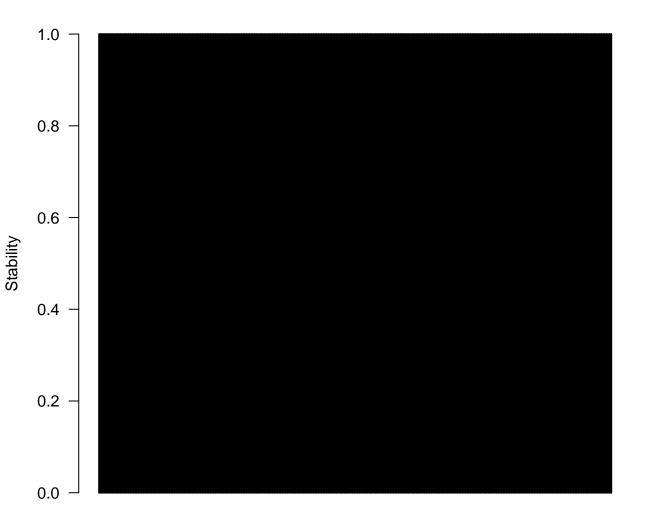
Features



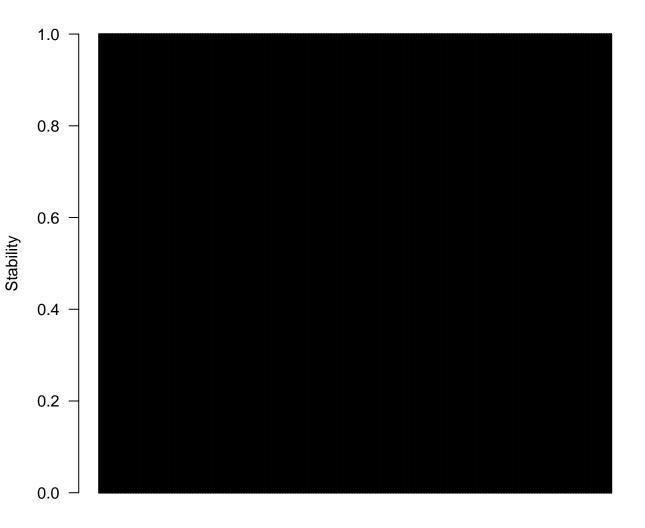
Features



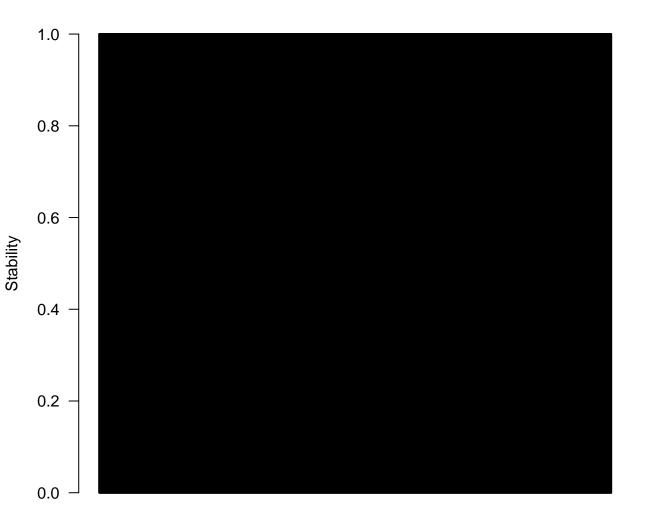
Features



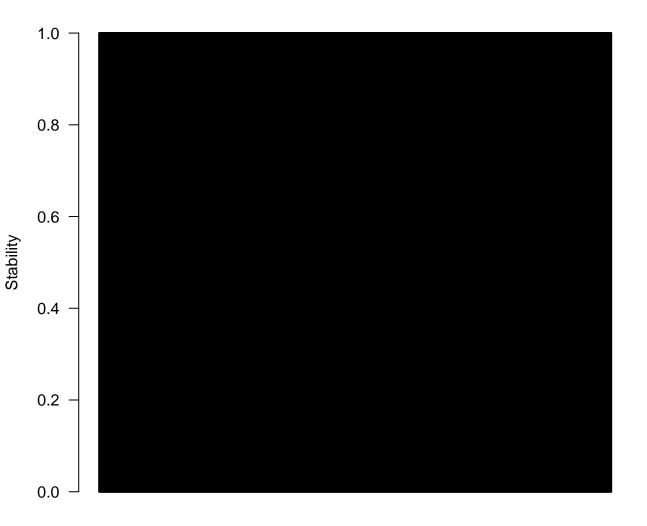
Features



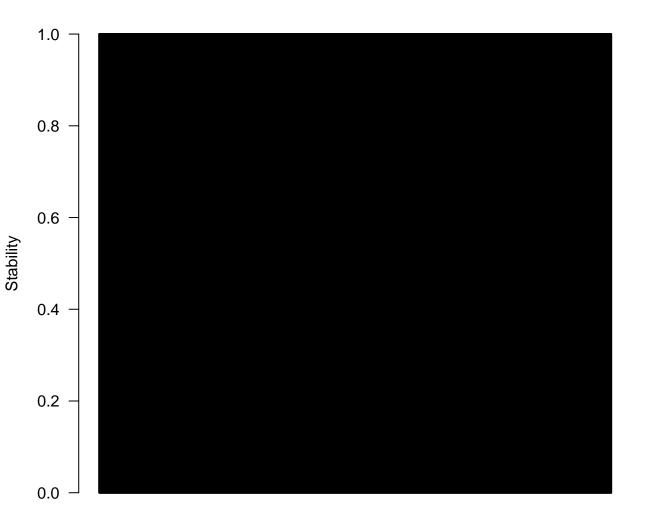
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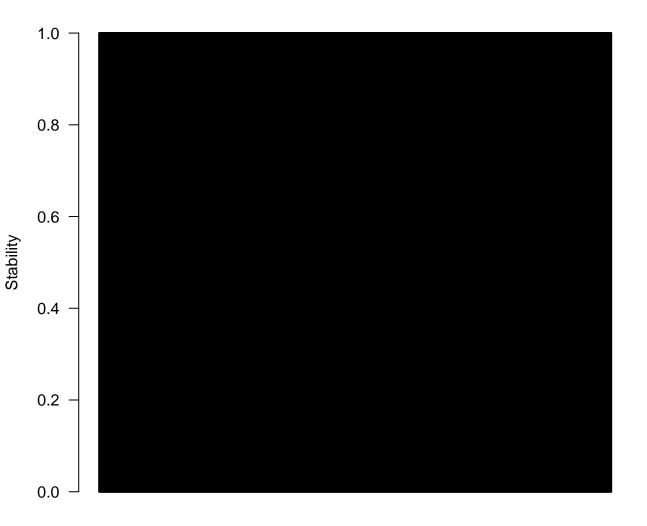
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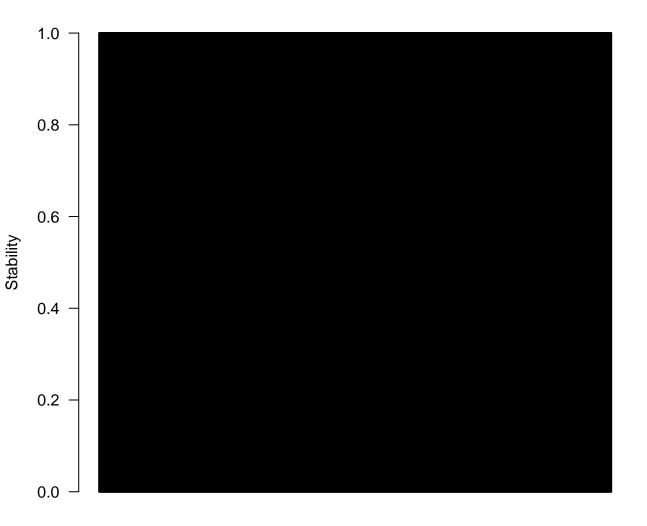
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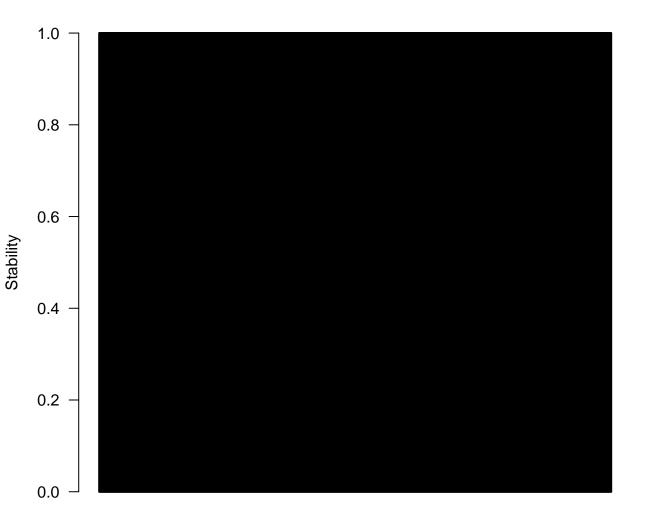
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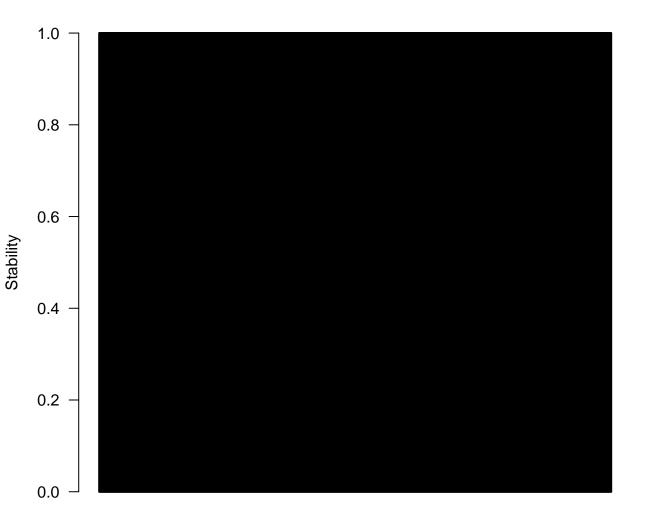
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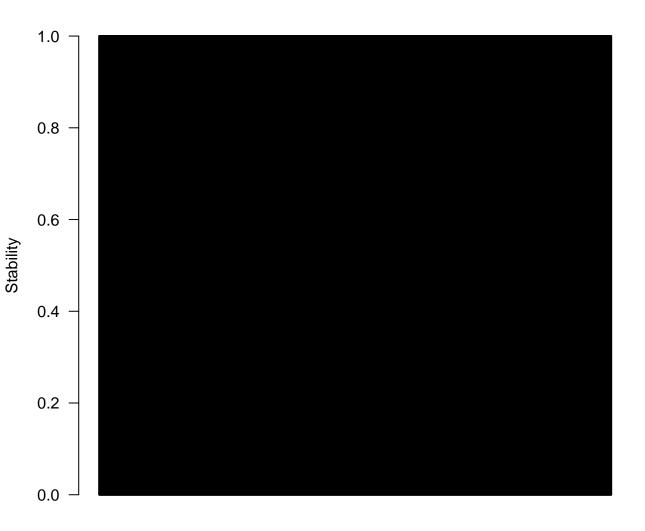
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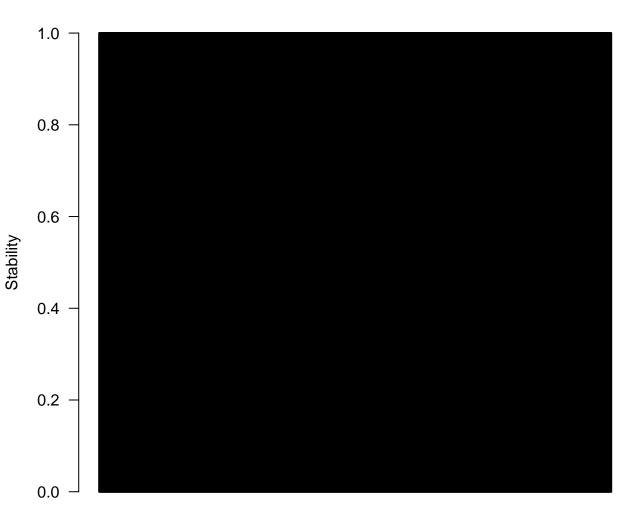
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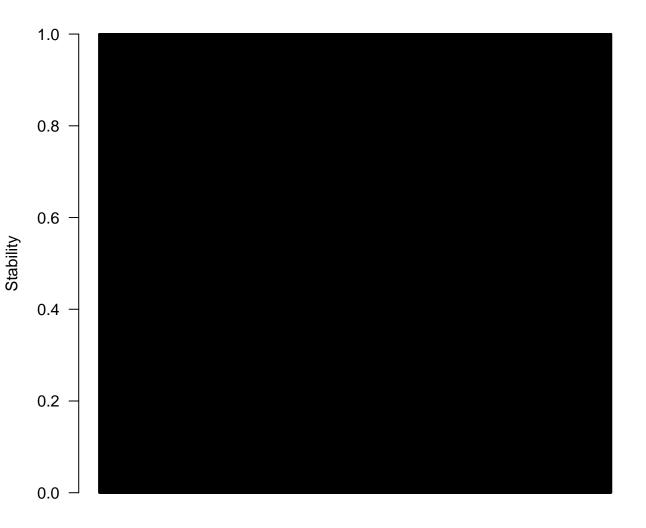
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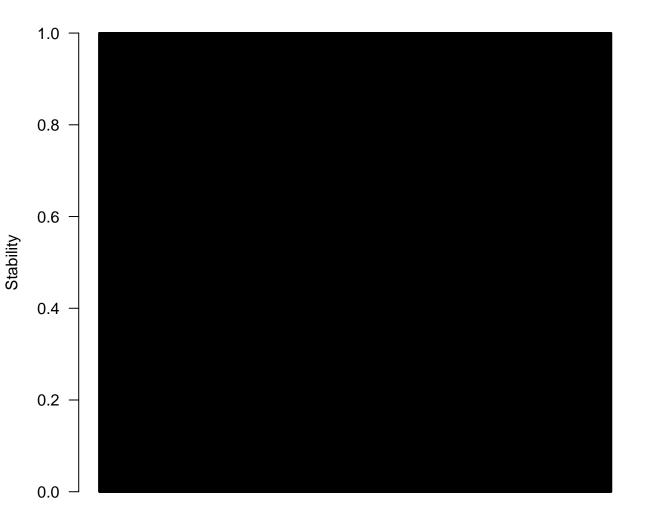
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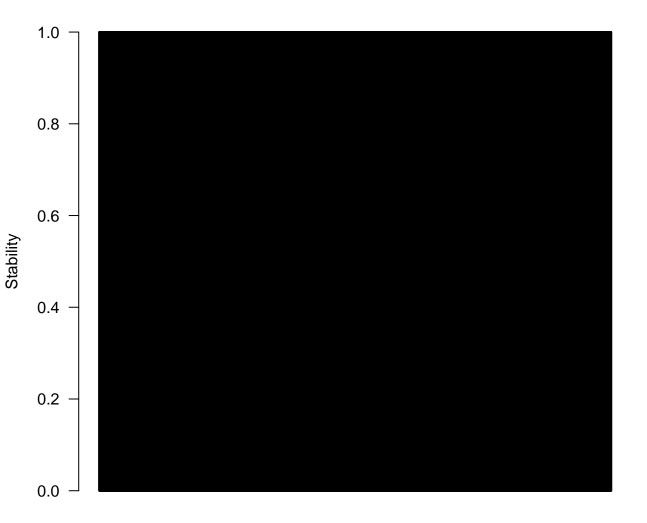
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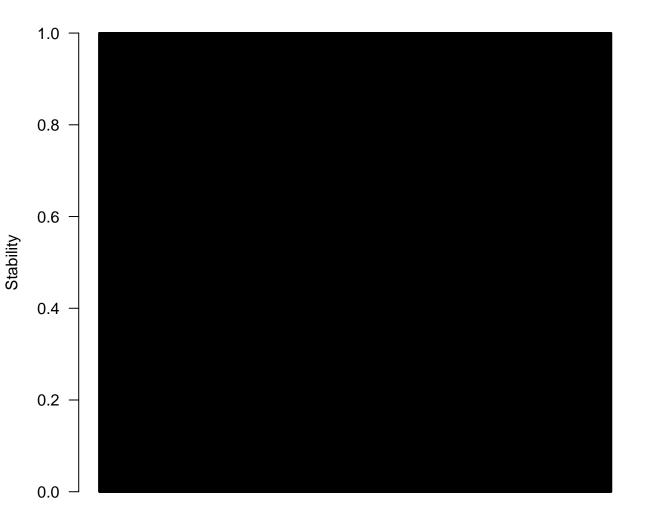
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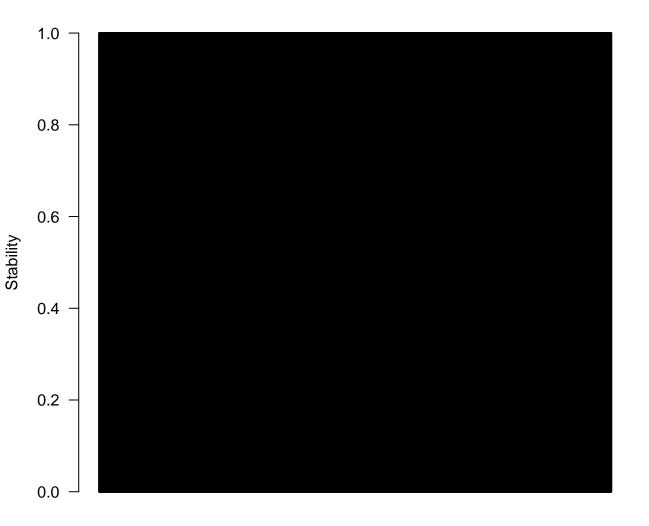
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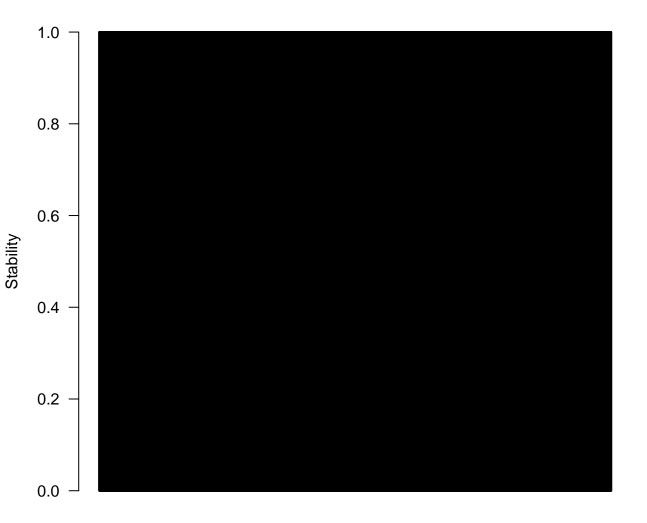
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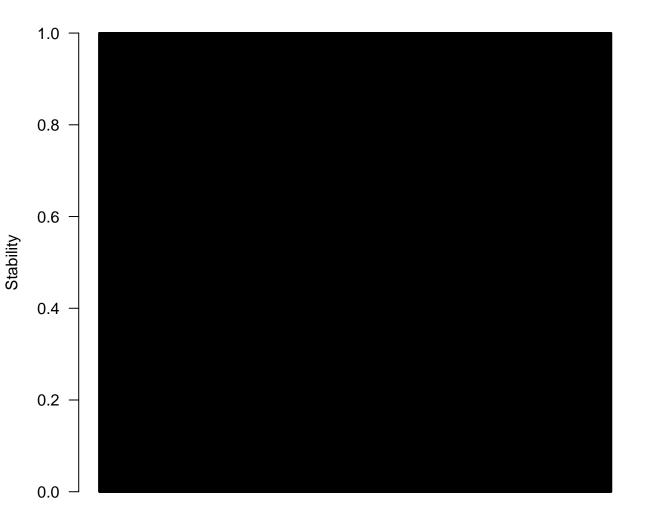
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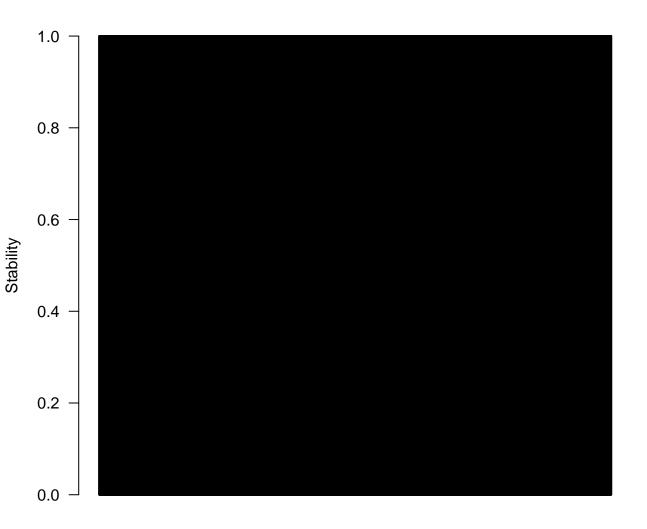
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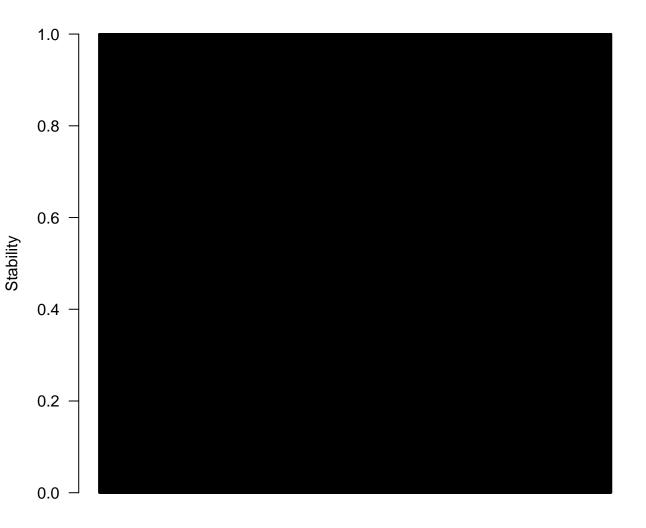
Features



Features

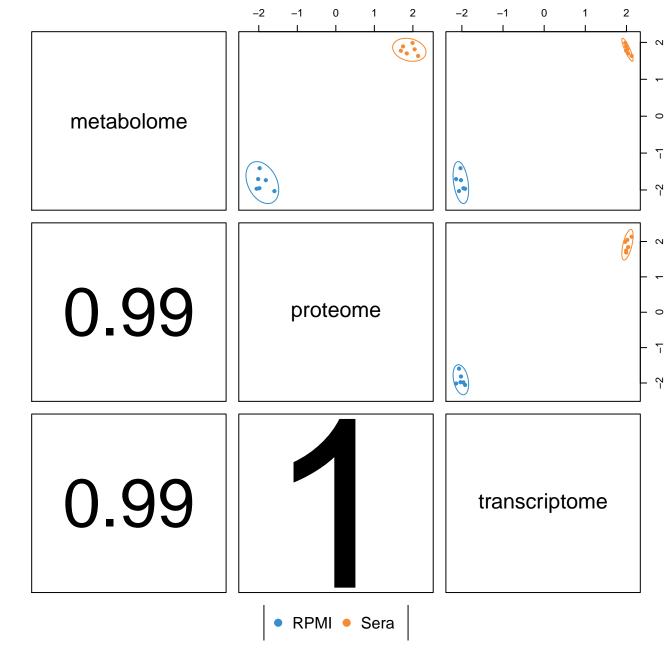


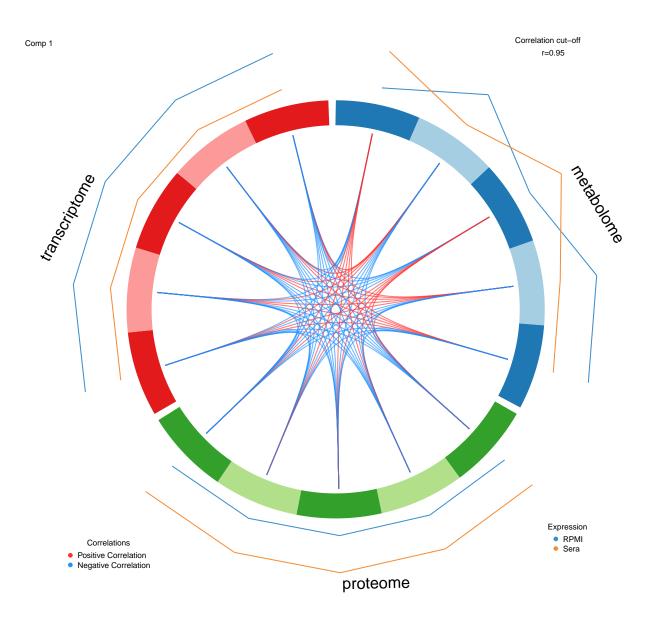
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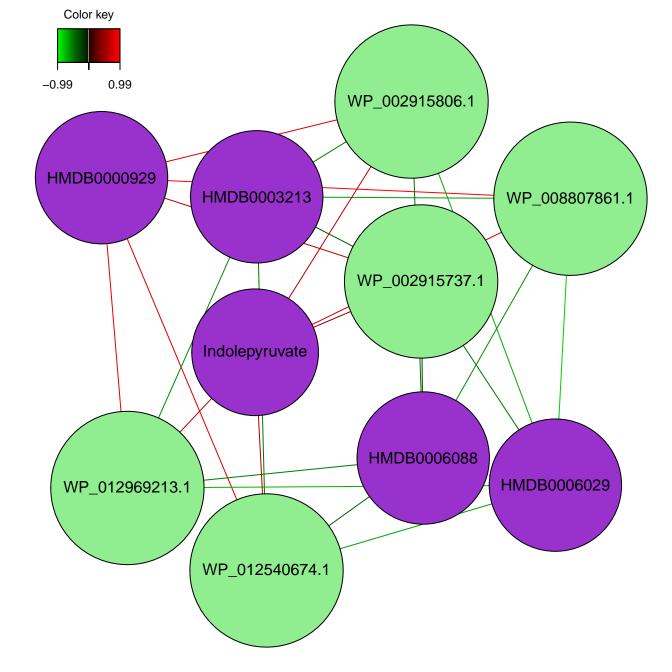


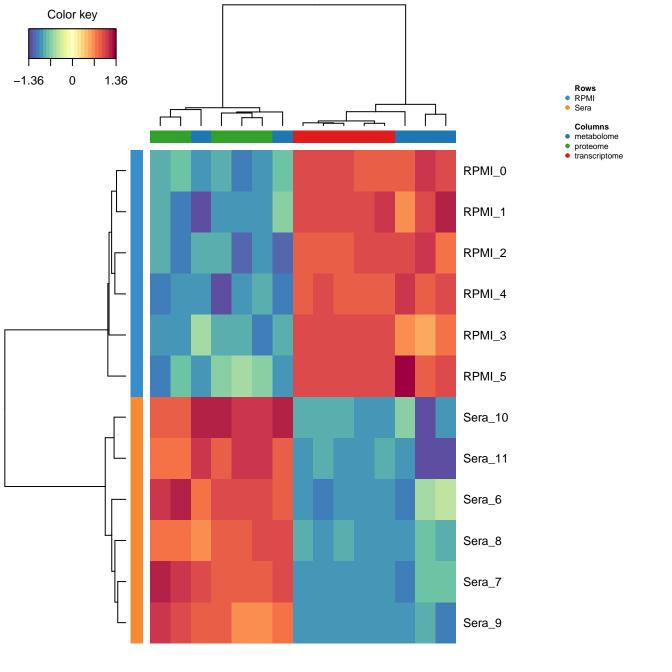
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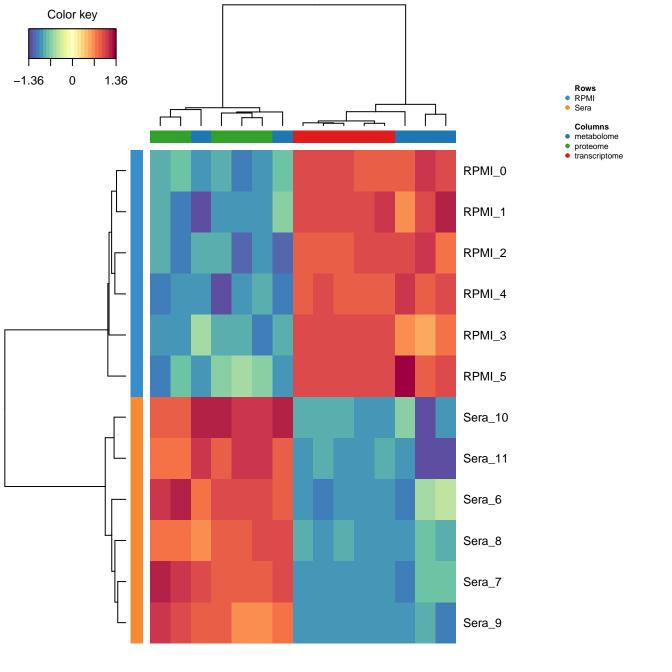
ROC Curve Block: metabolome, Using Comp(s): 1 100 -90 -80 -70 -60 -Sensitivity (%) **Outcome** 50 **-**RPMI vs Sera: 1 40 -30 -20 -10 -0 -10 20 30 70 80 40 50 60 100 90 100 - Specificity (%)



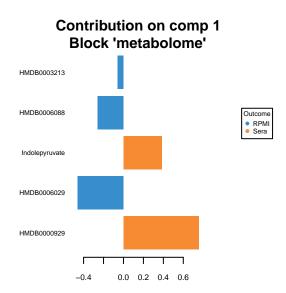


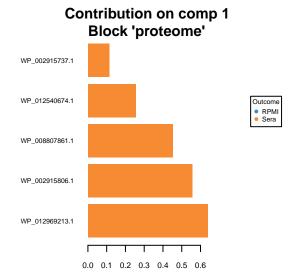


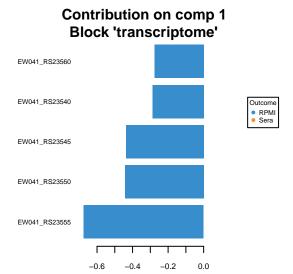




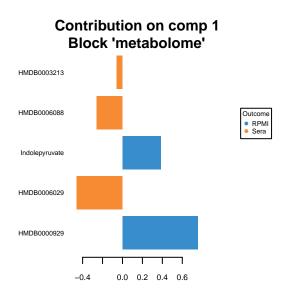
#### 1 DIABLO max loadings

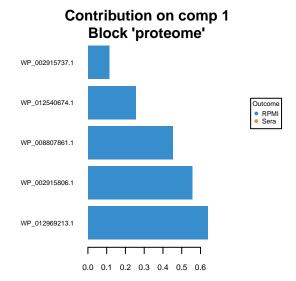


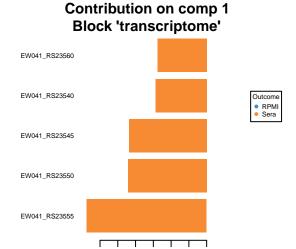




#### 1 DIABLO min loadings







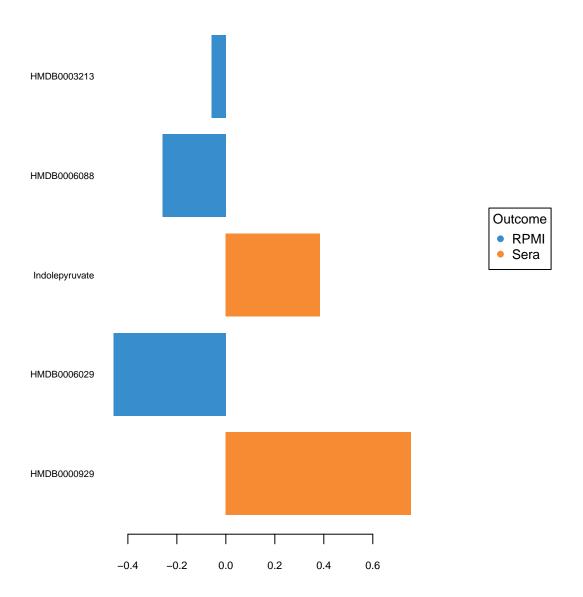
-0.6

-0.4

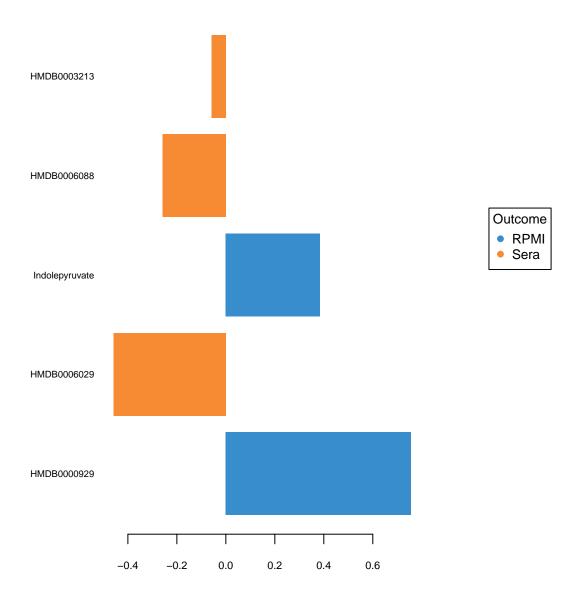
-0.2

0.0

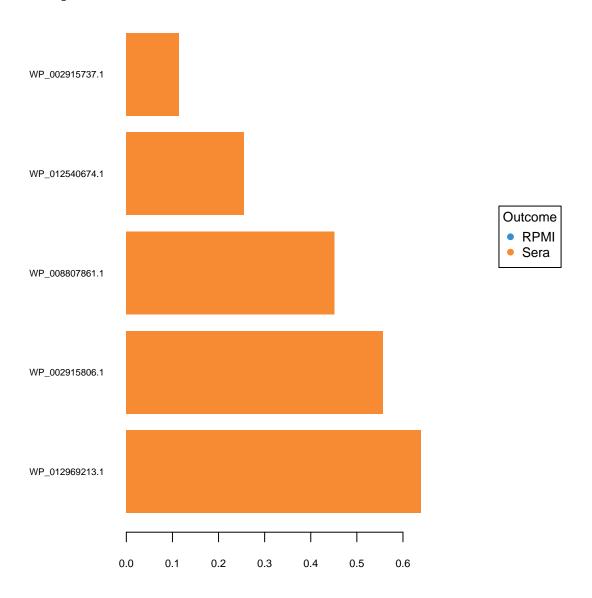
## 1 metabolome DIABLO max load



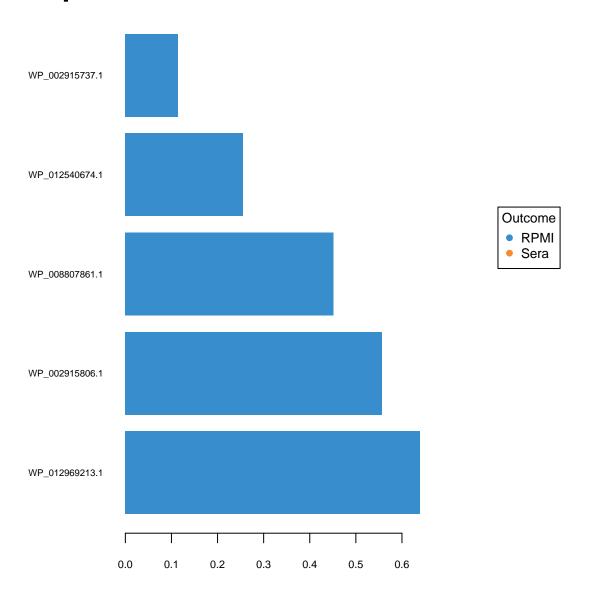
## 1 metabolome DIABLO min loac



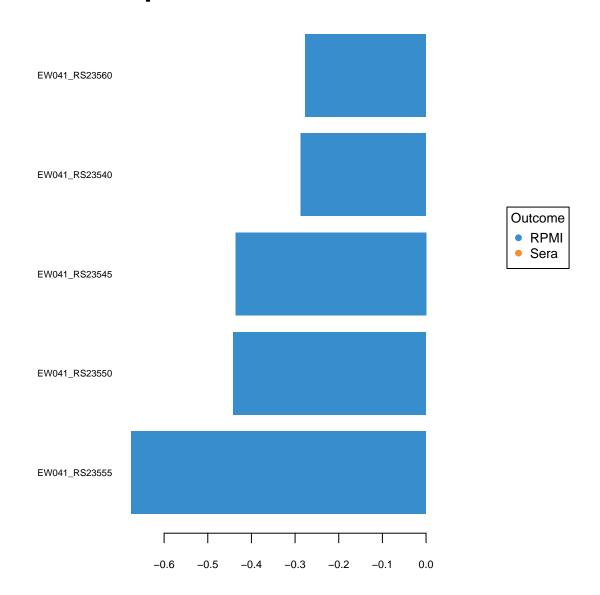
## 1 proteome DIABLO max loadi



## 1 proteome DIABLO min loadii



# 1 transcriptome DIABLO max loa



# 1 transcriptome DIABLO min loa

