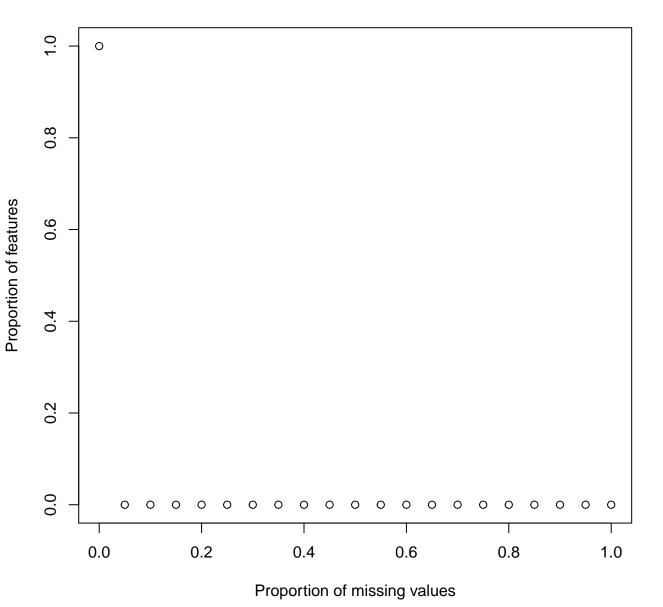
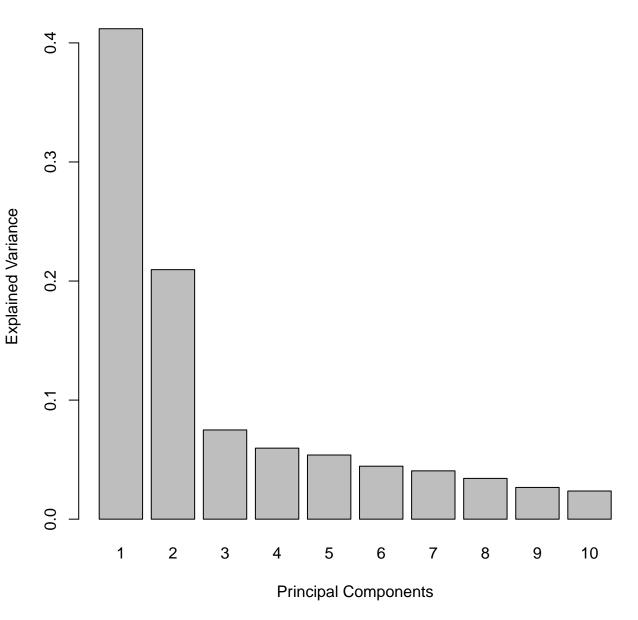
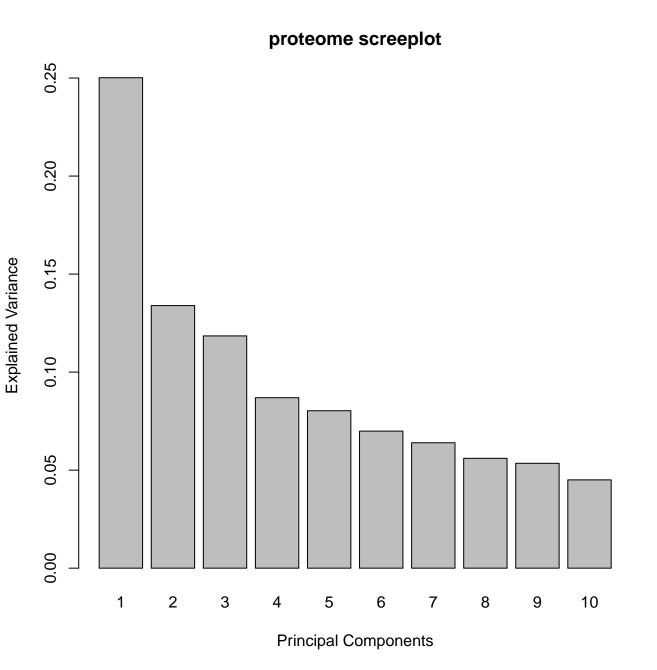
transcriptome missing value proportions for unfiltered data

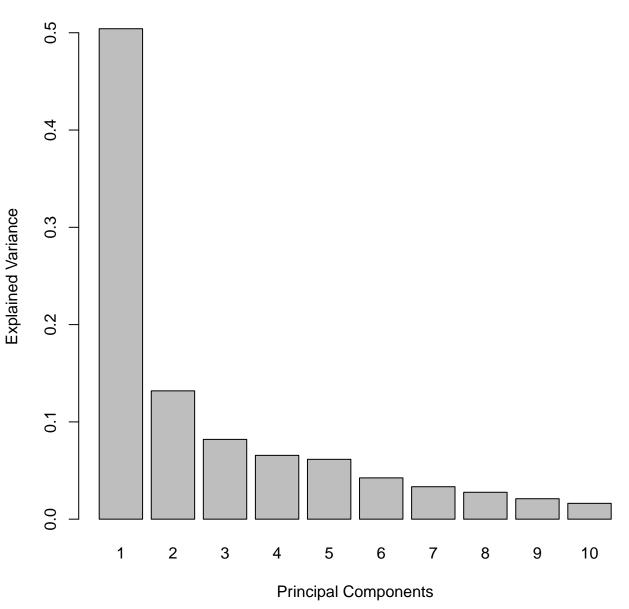


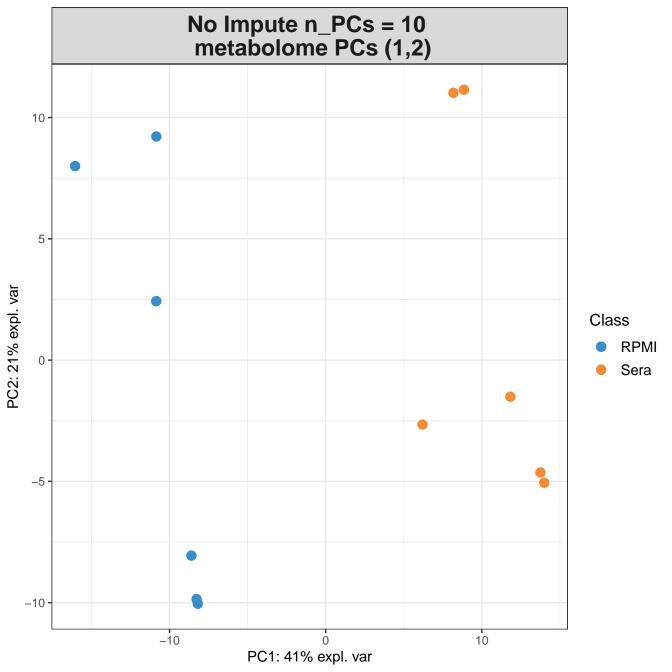
metabolome screeplot

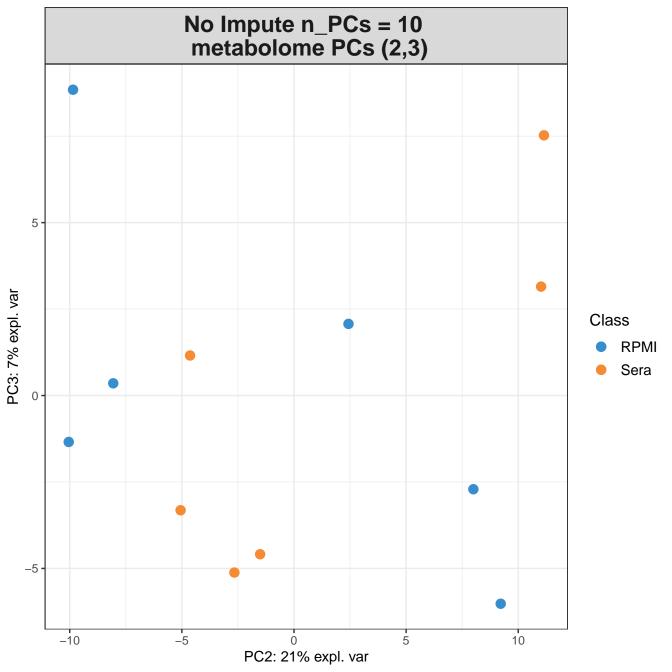


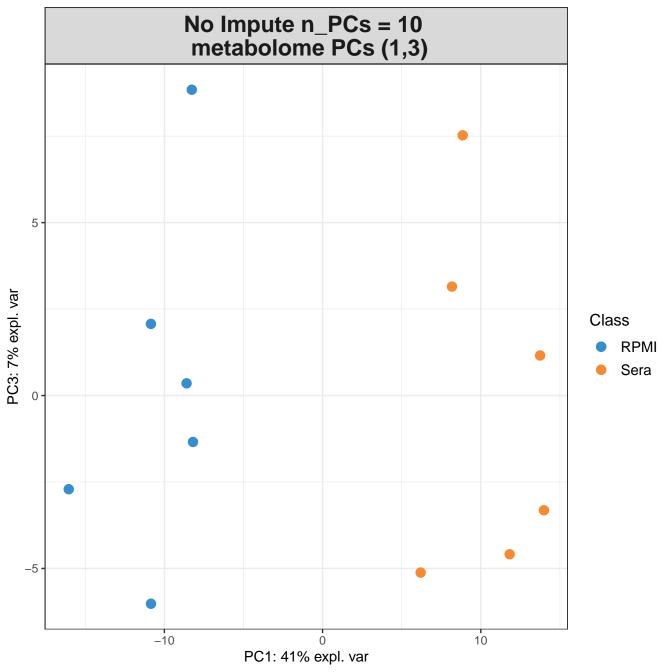


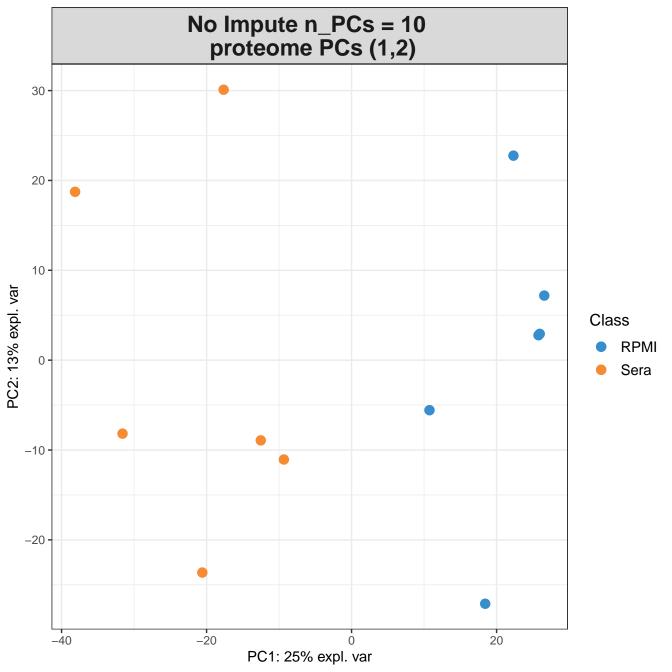
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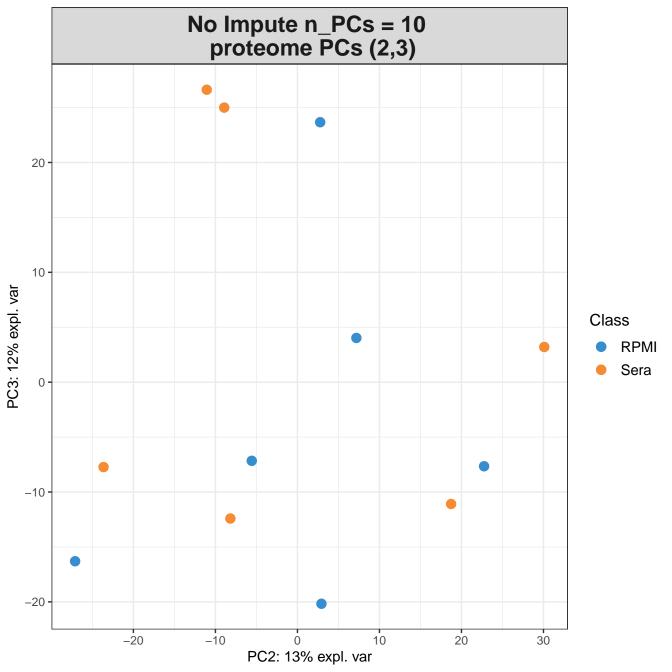


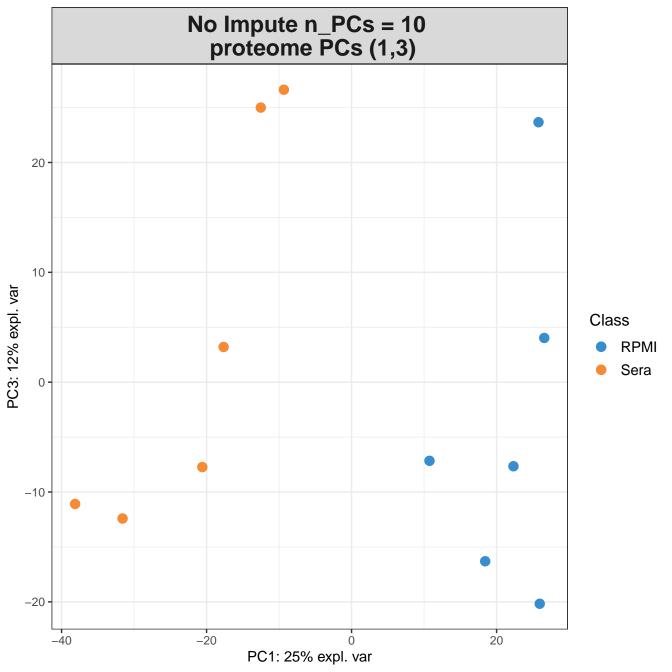


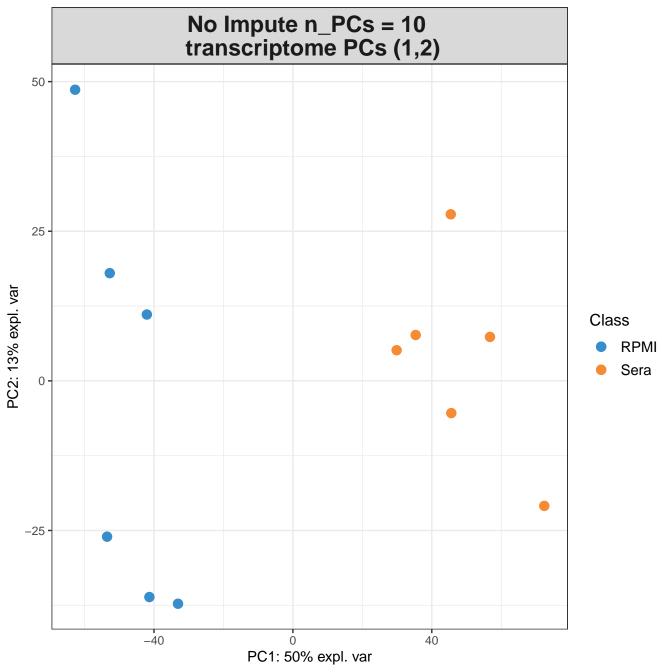


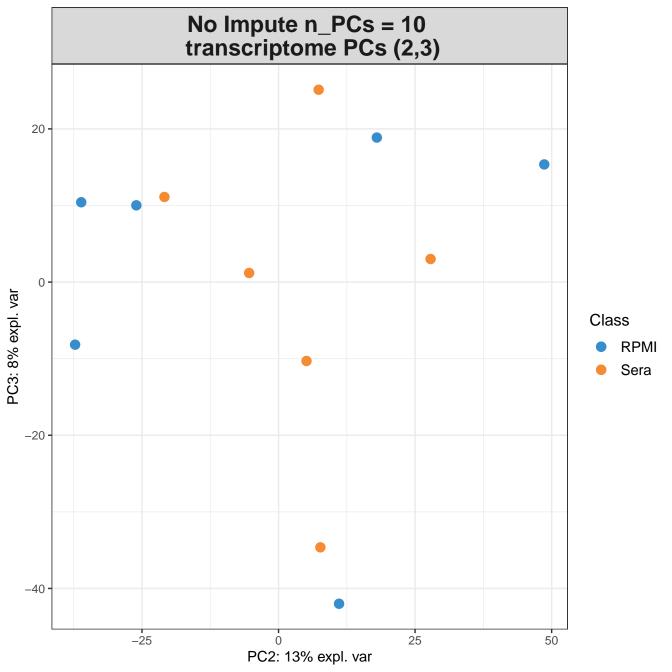


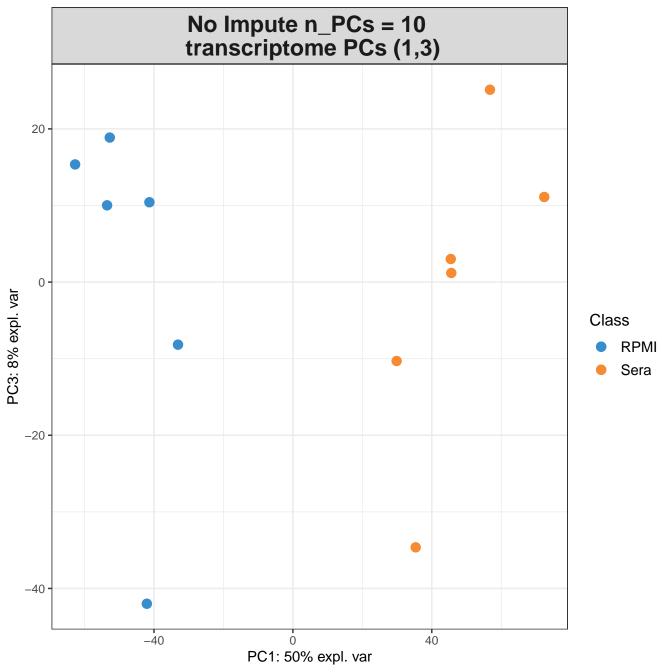




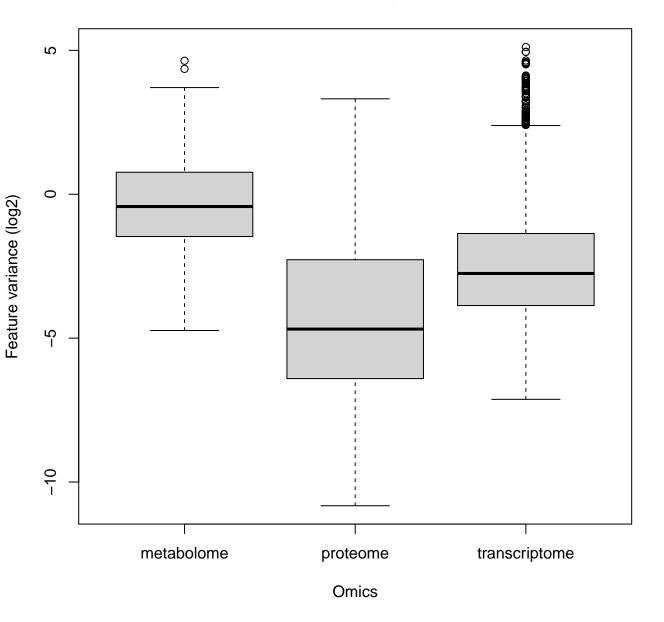


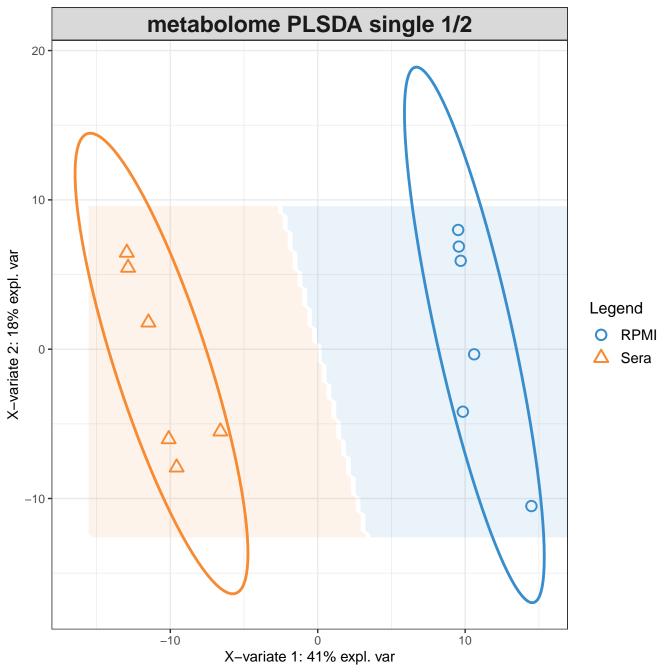


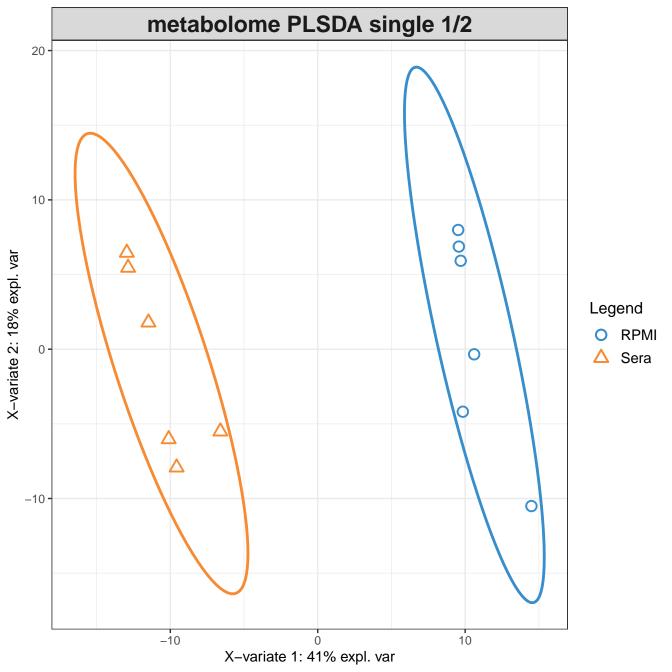


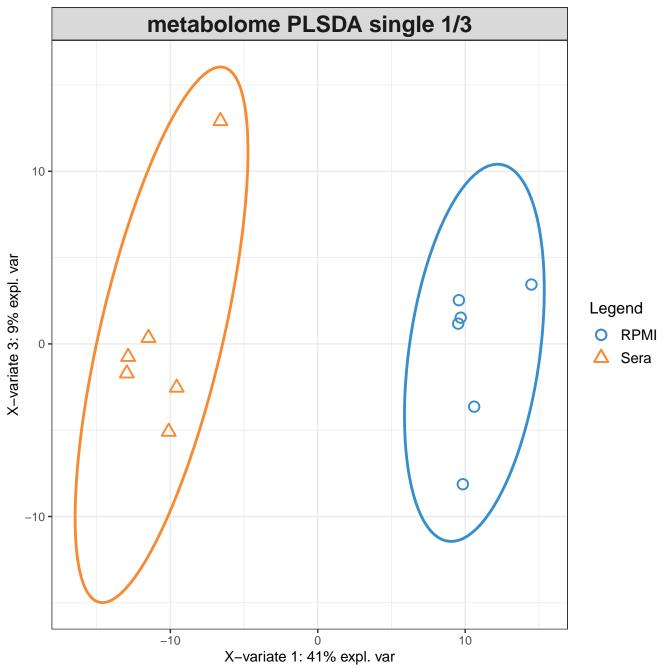


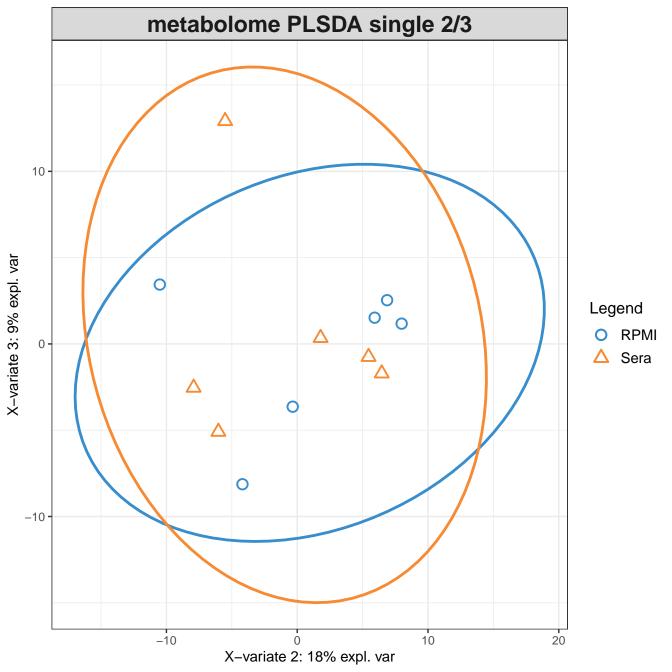
Feature variances (log2) per omics

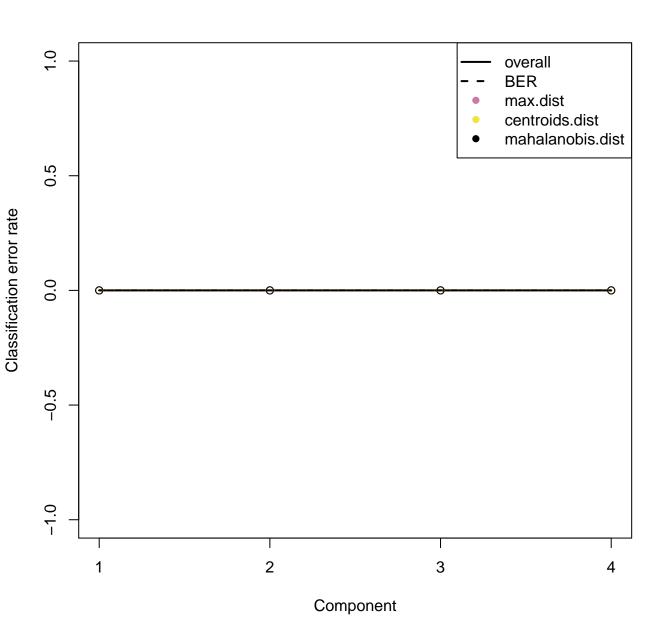




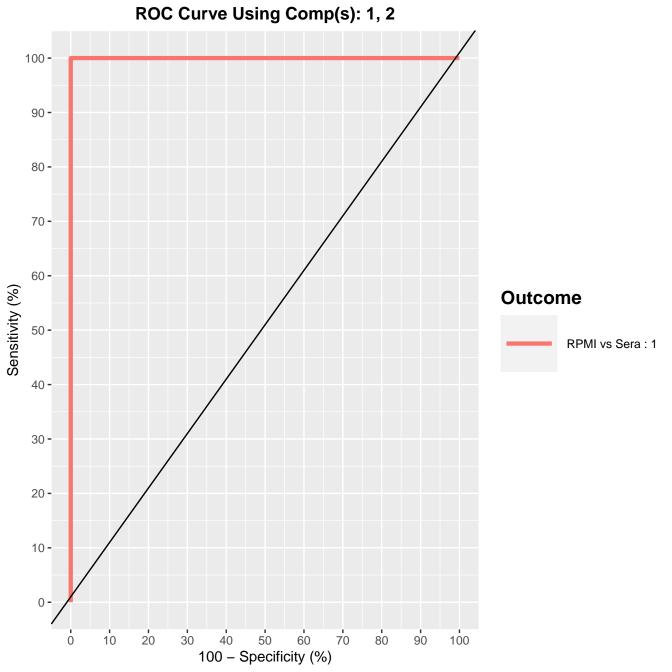


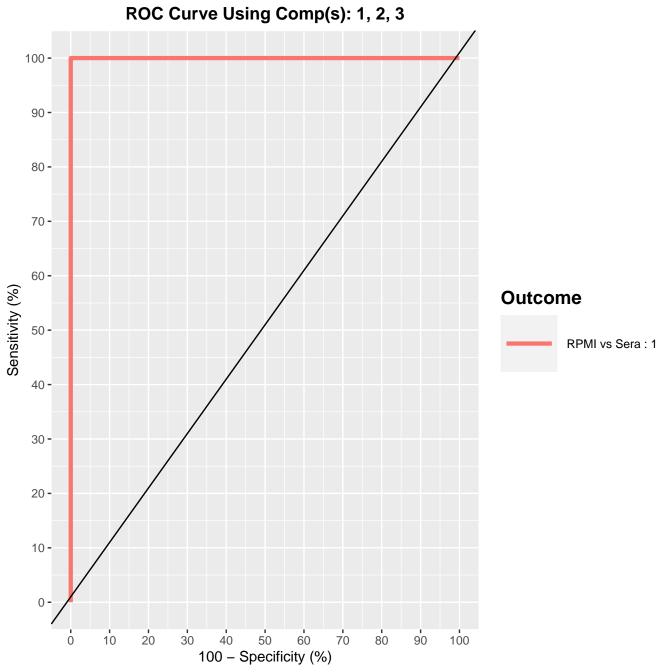


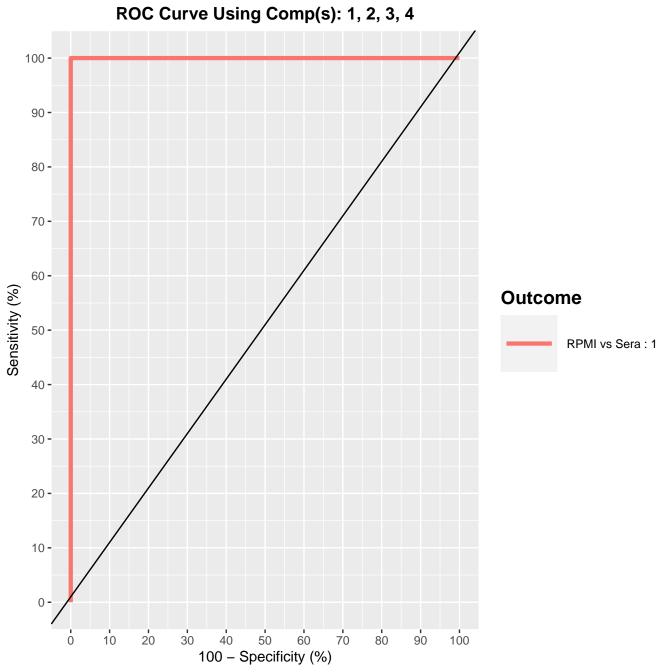


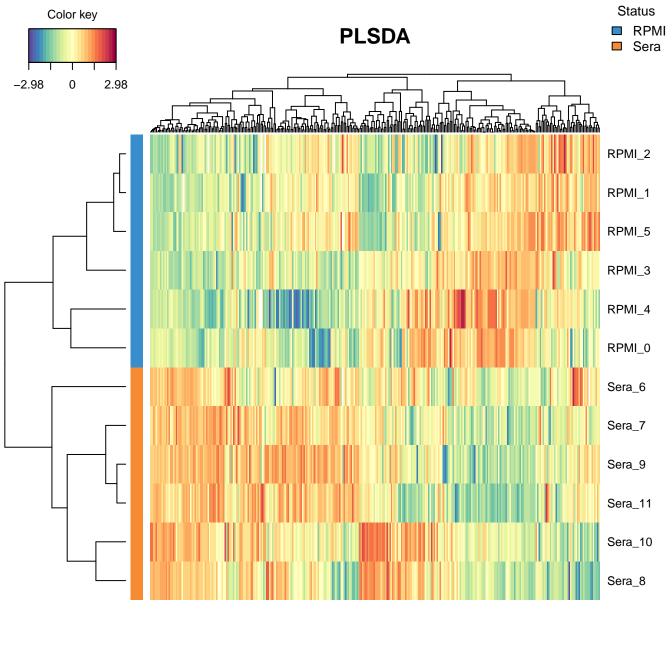


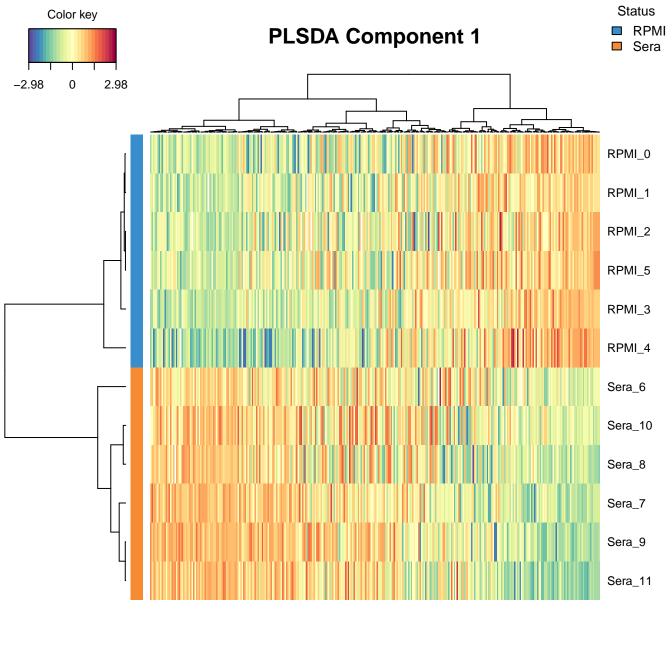




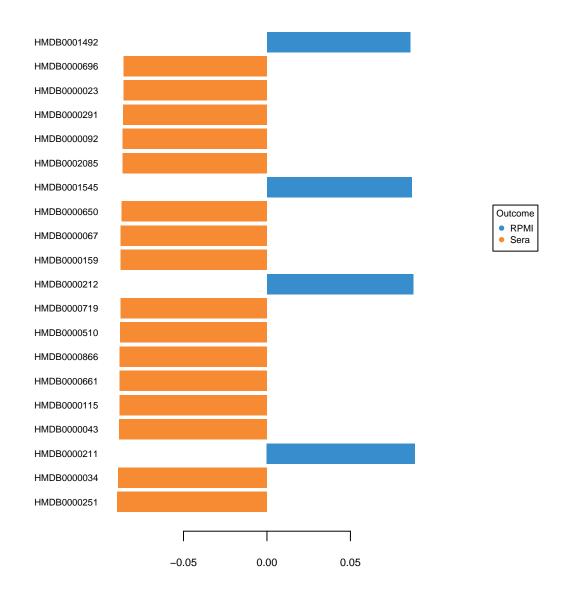




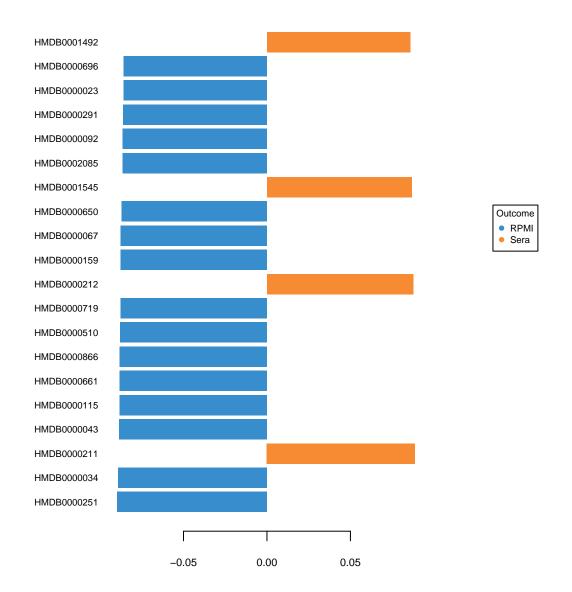


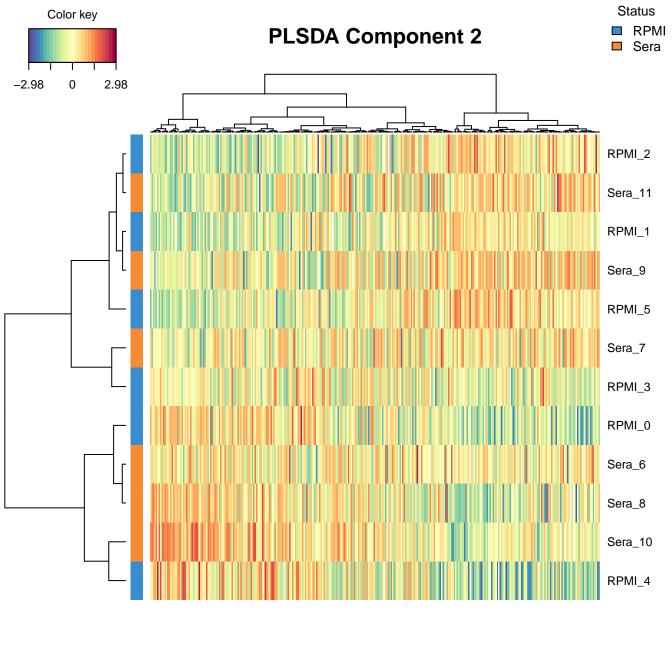


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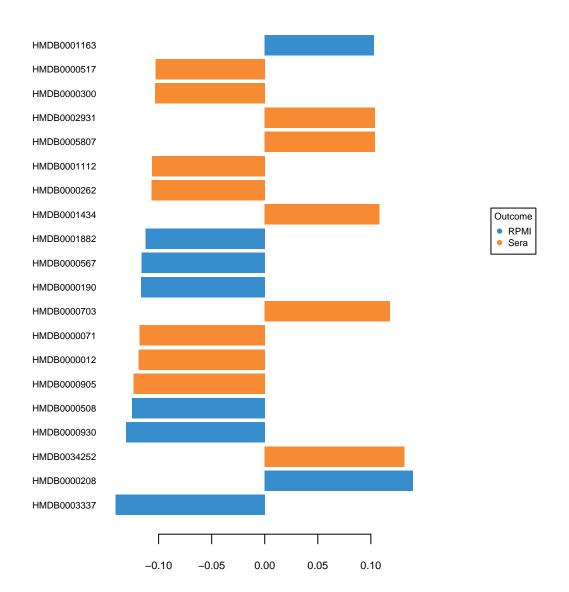


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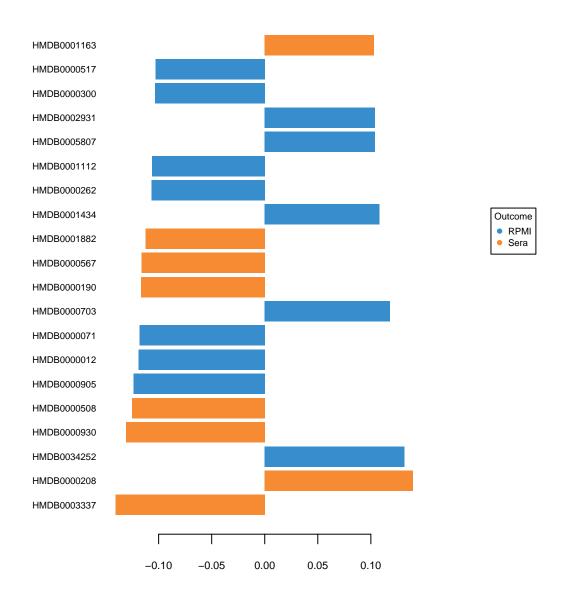


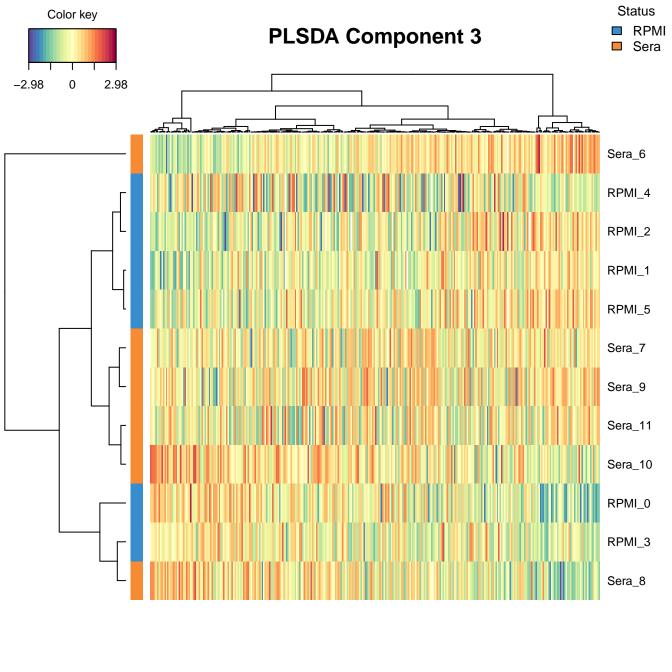


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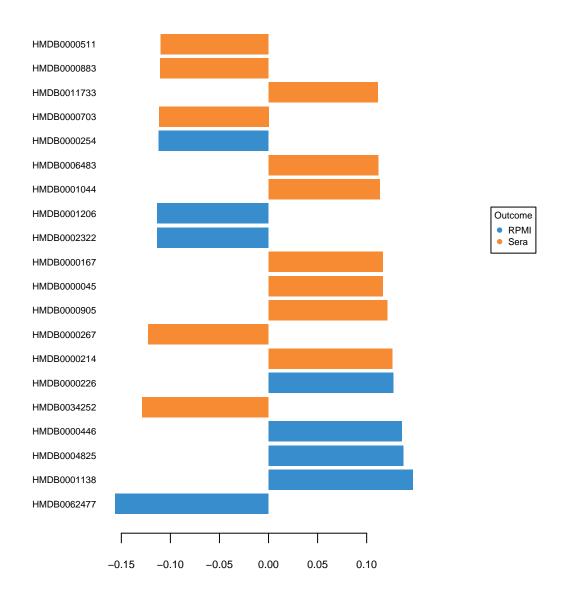


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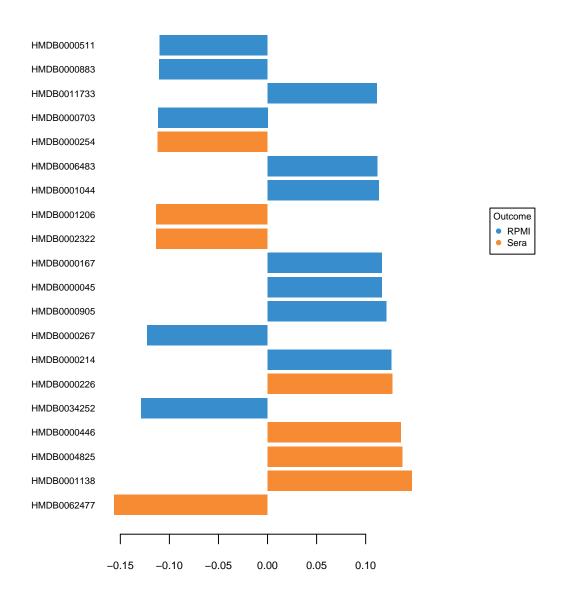


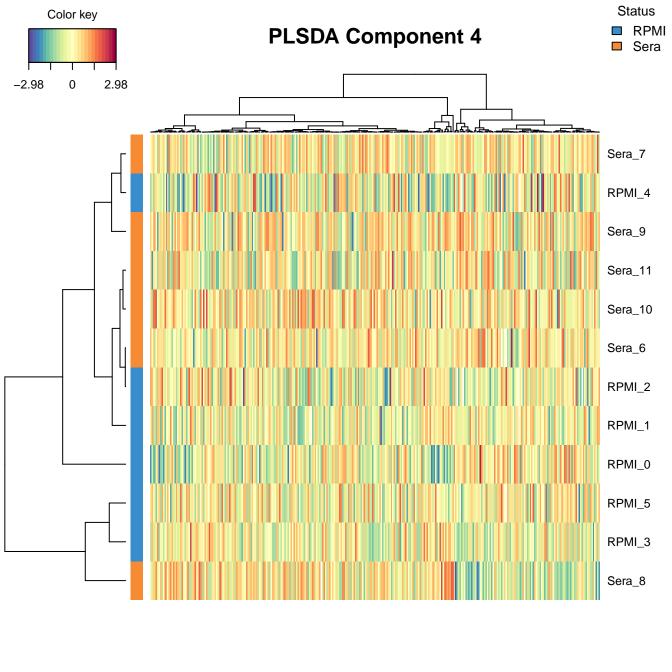


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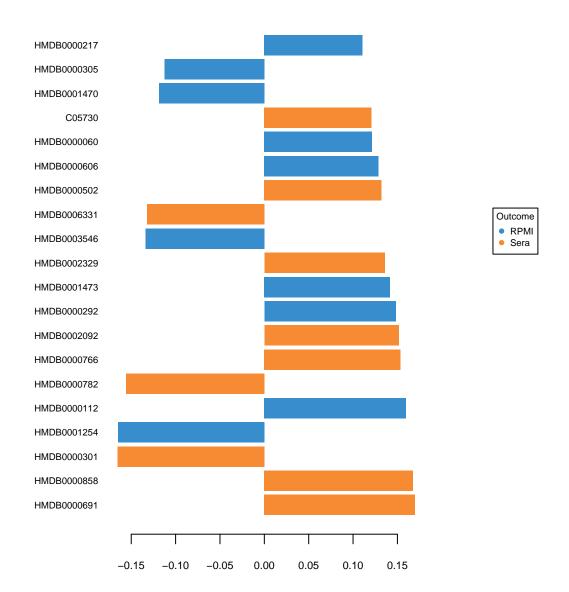


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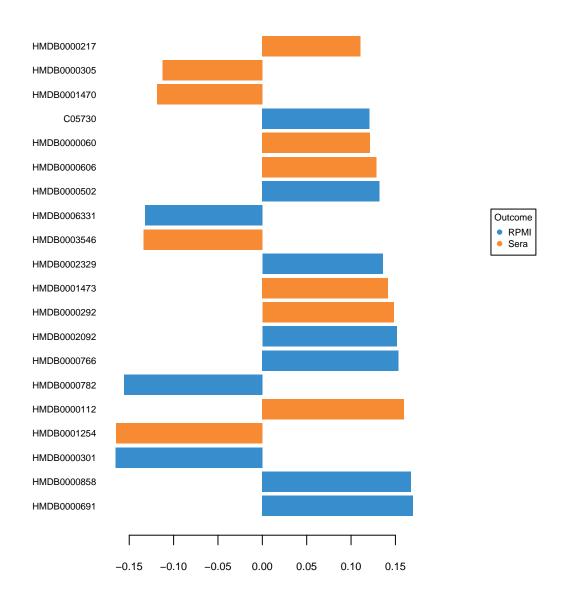


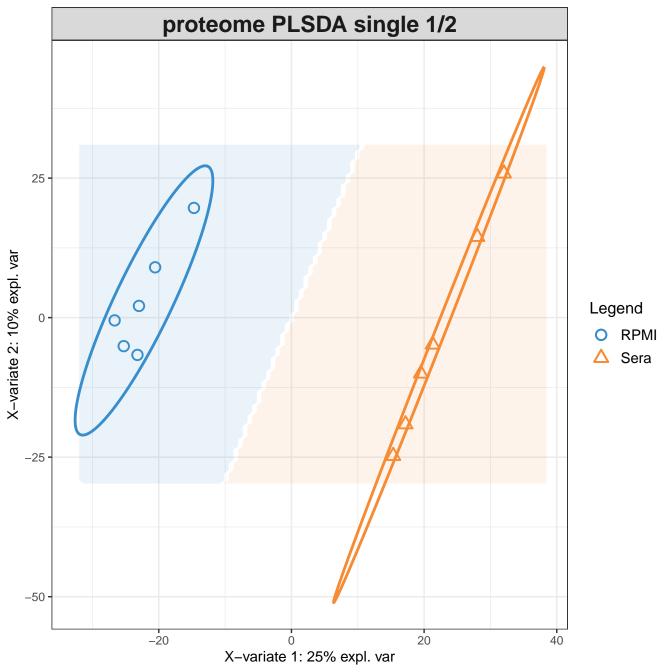


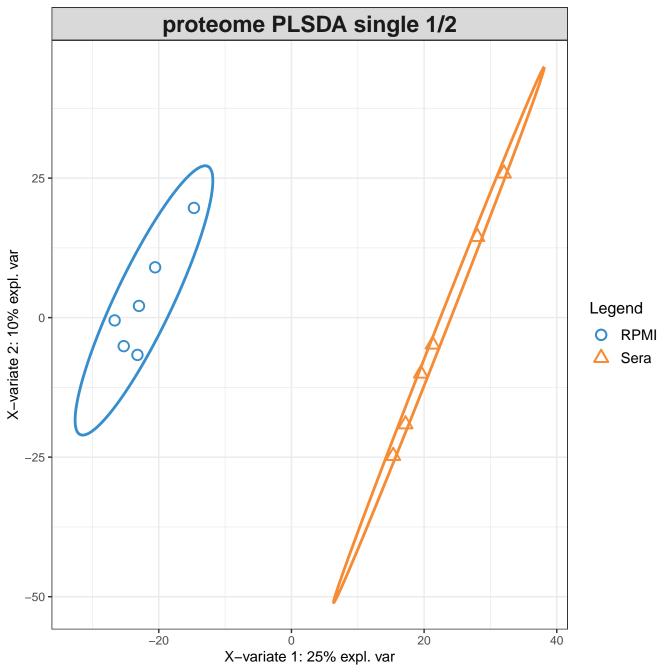
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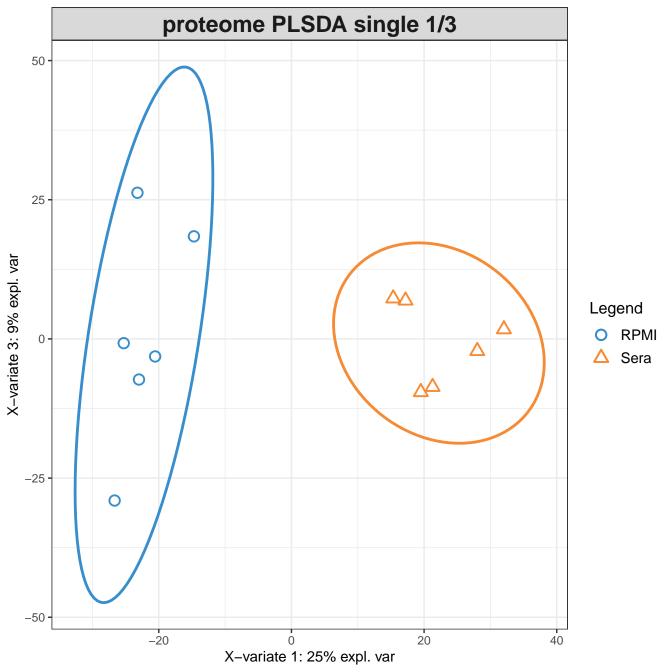


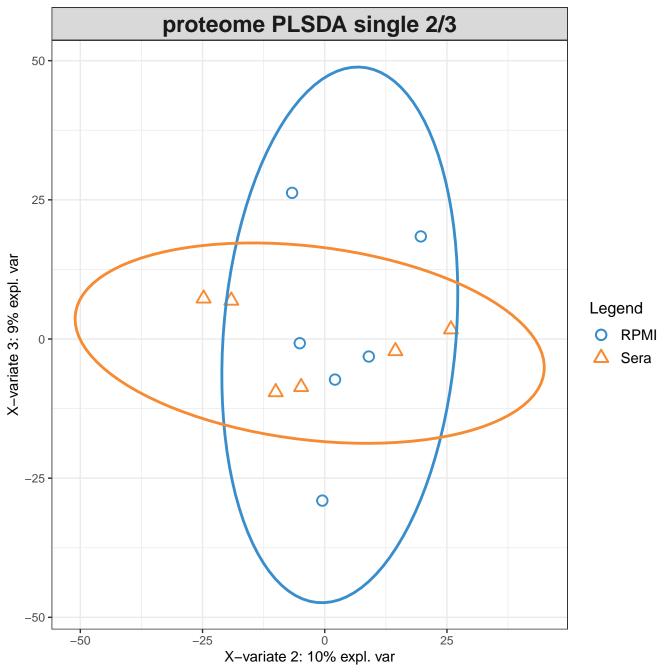
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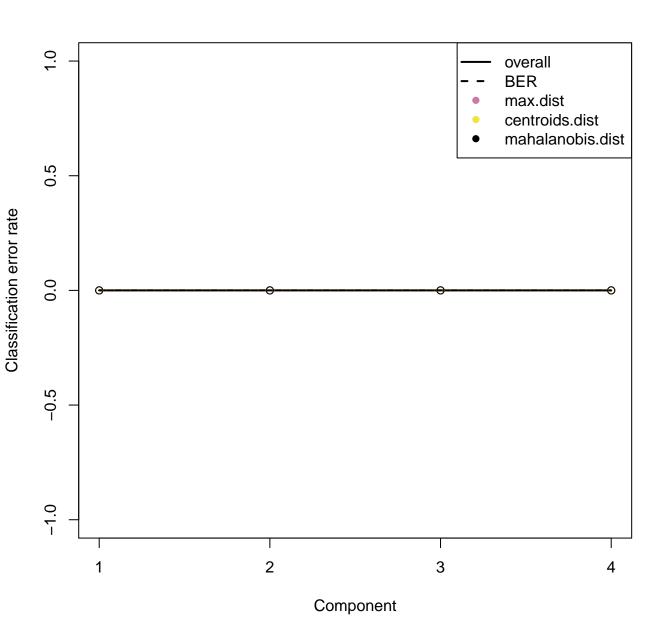




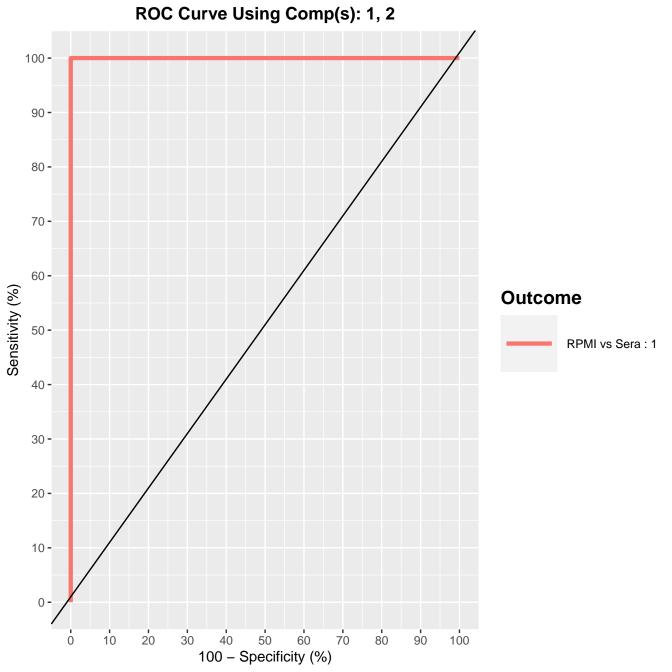


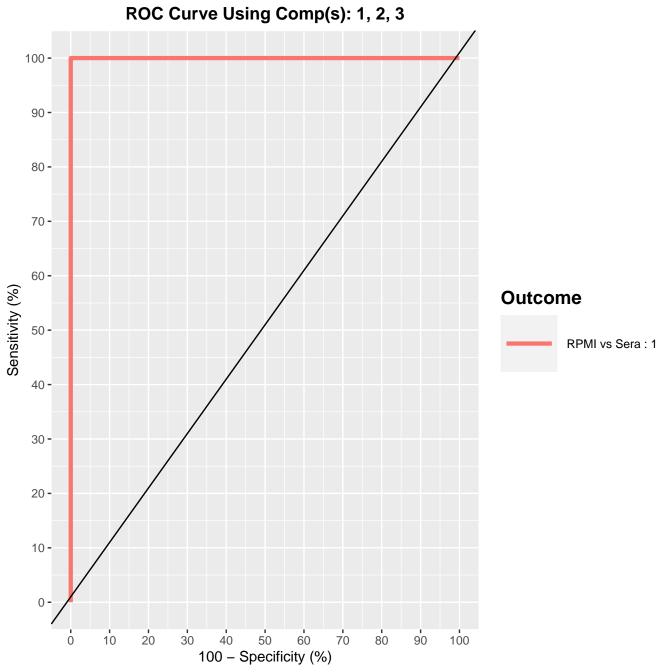


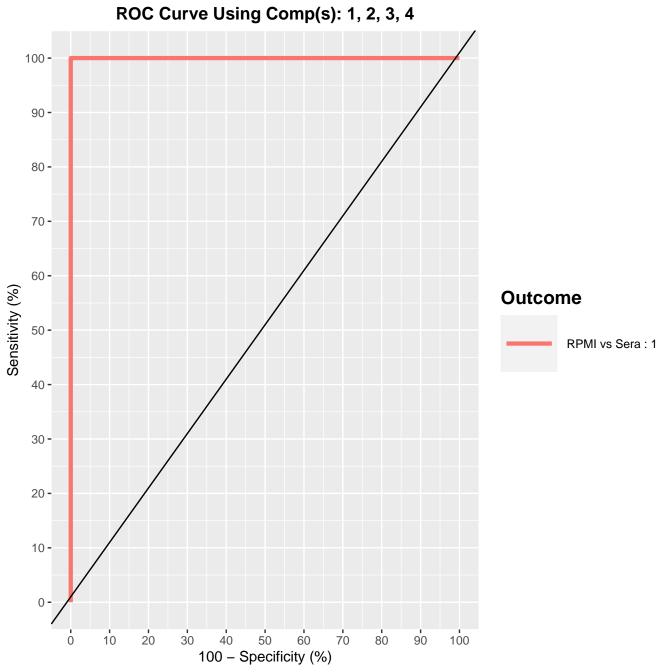


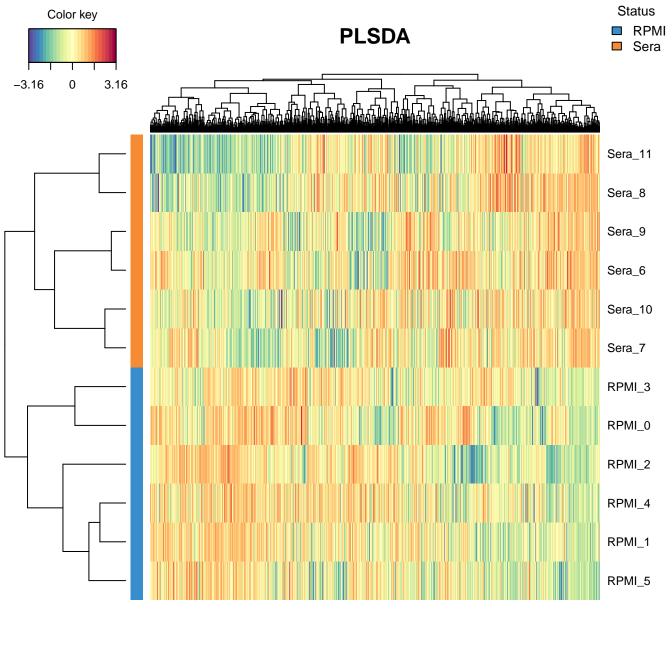


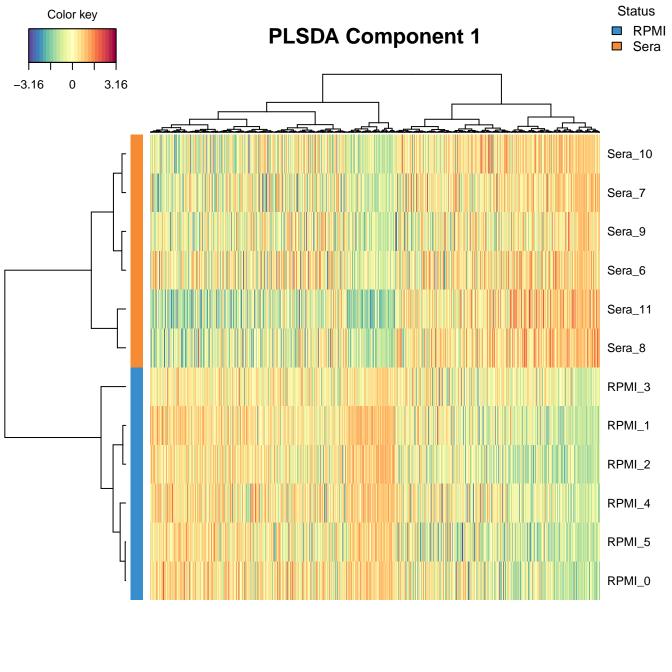




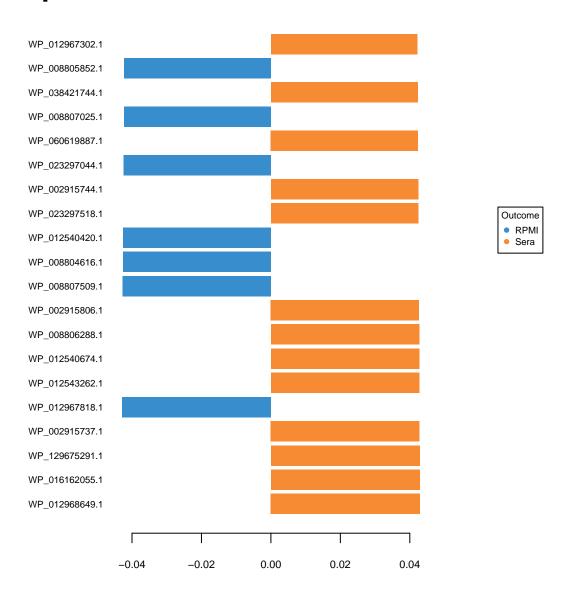




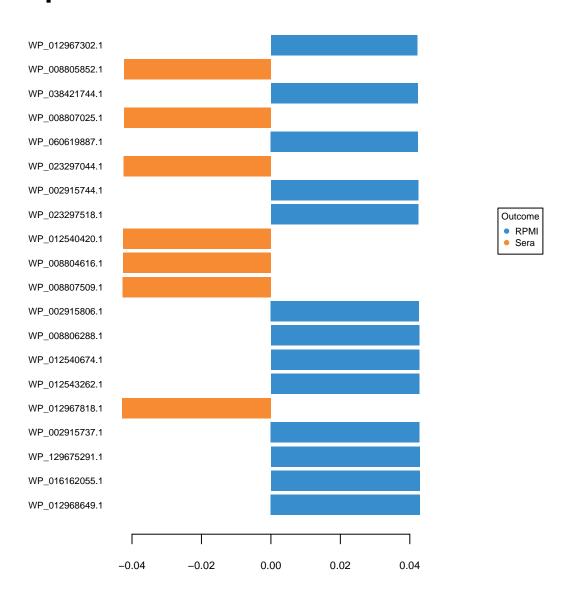


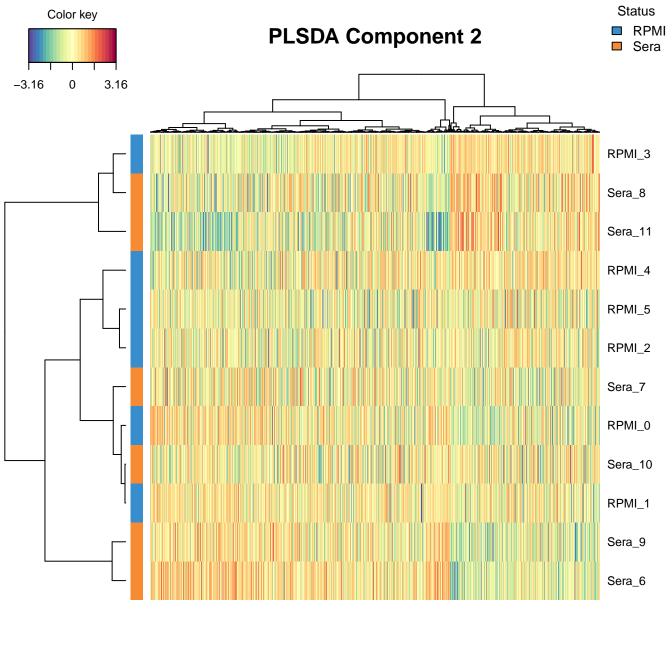


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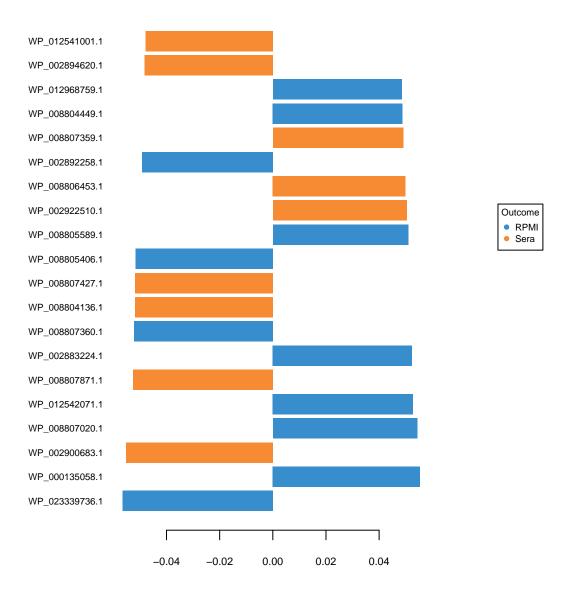


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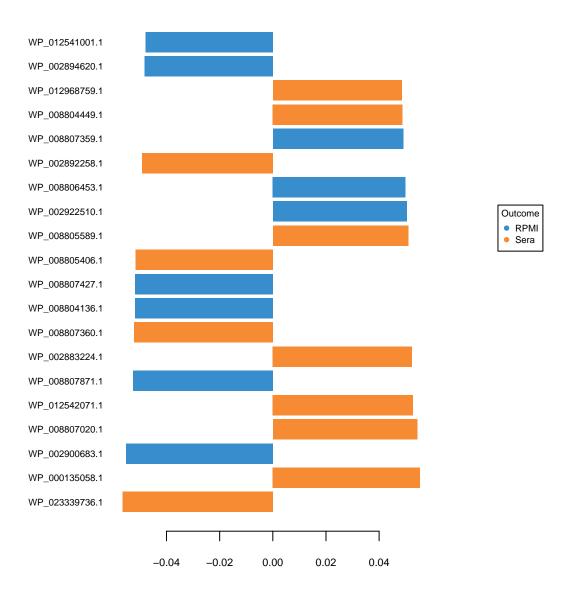


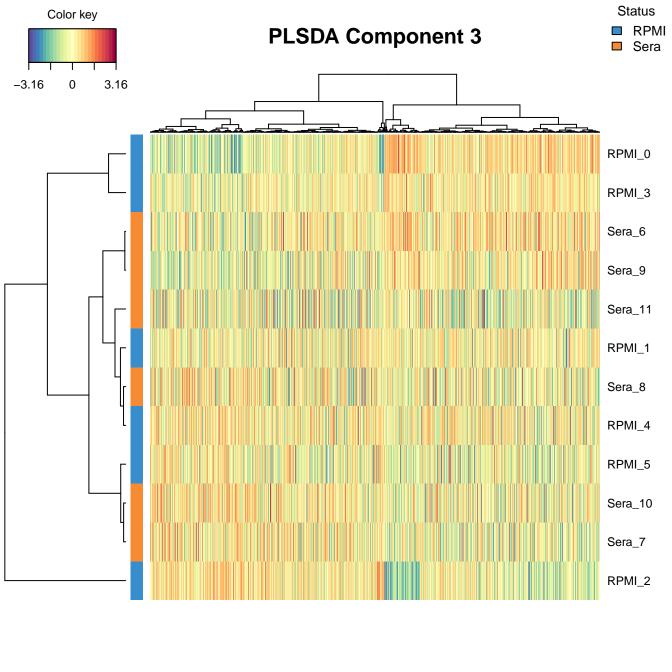


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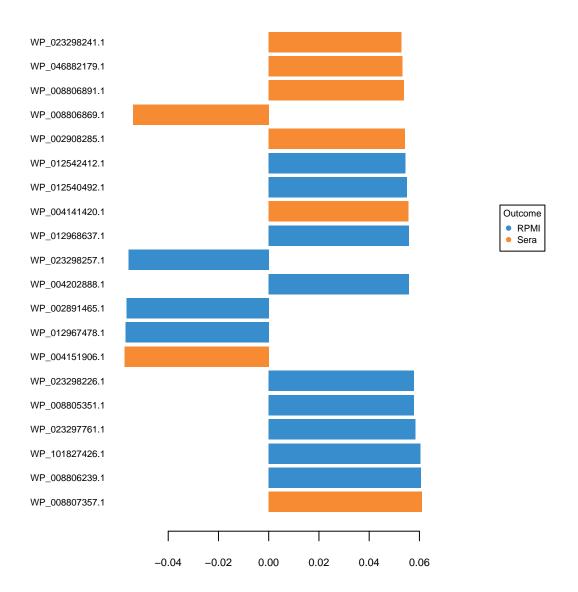


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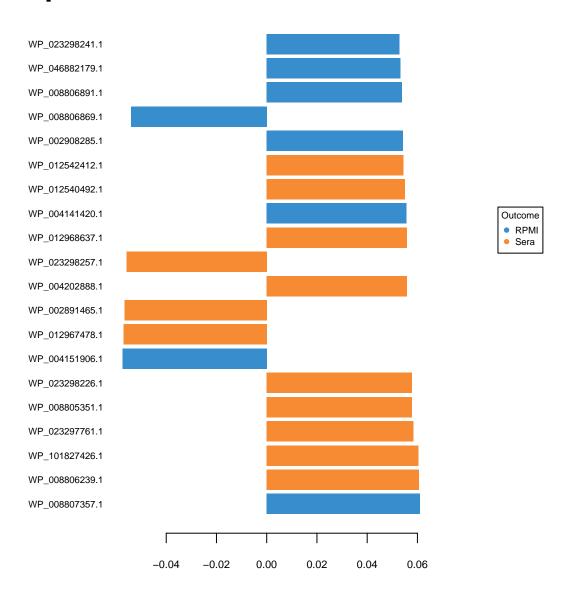


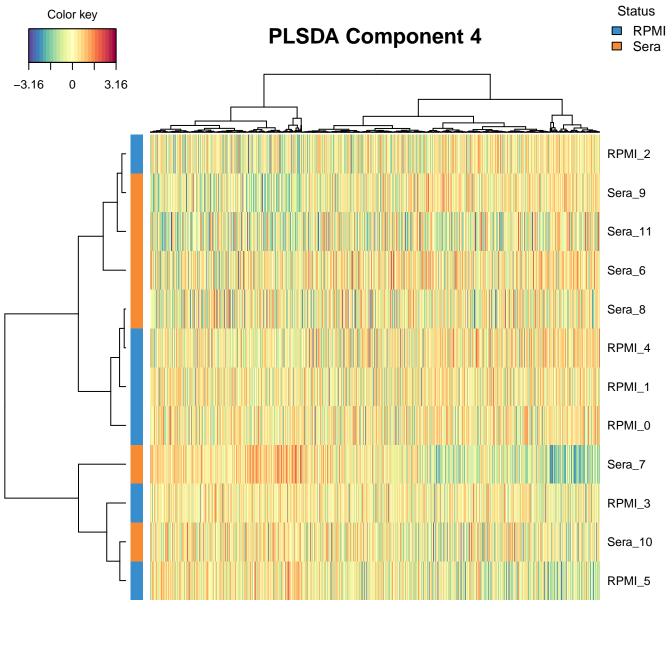


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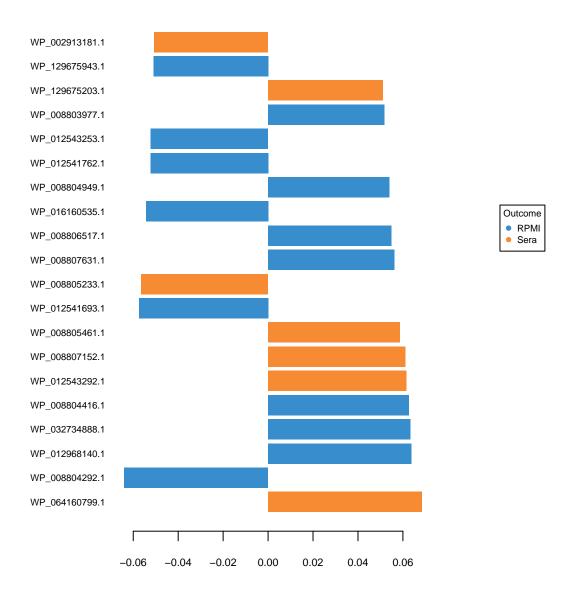


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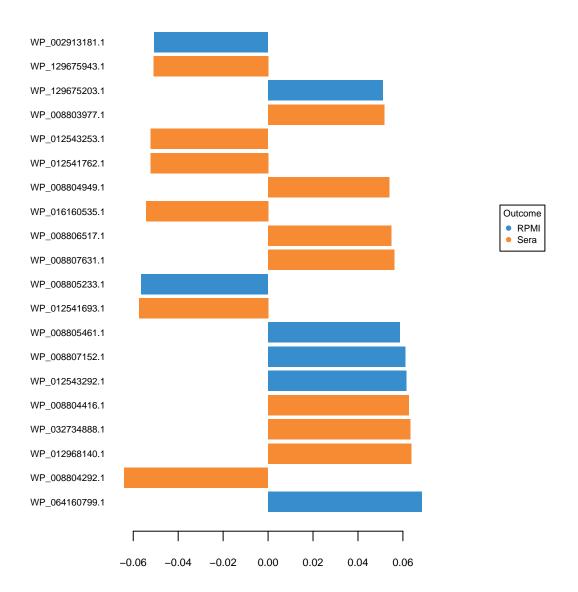


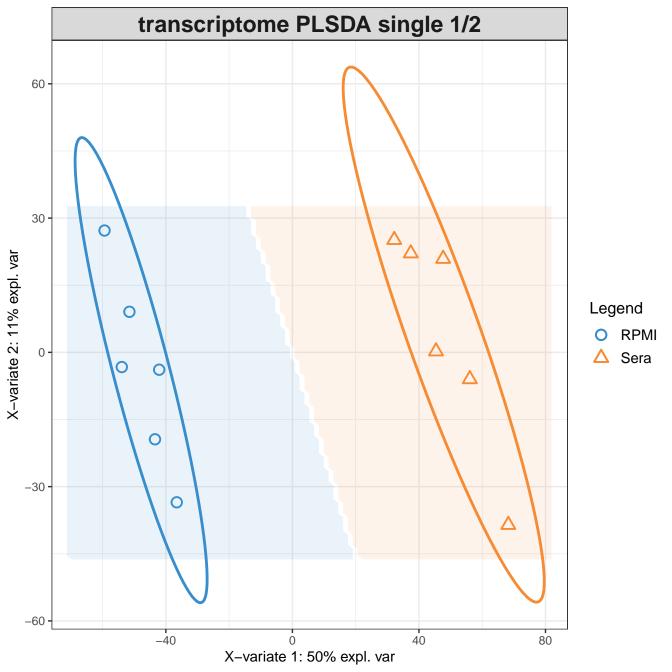


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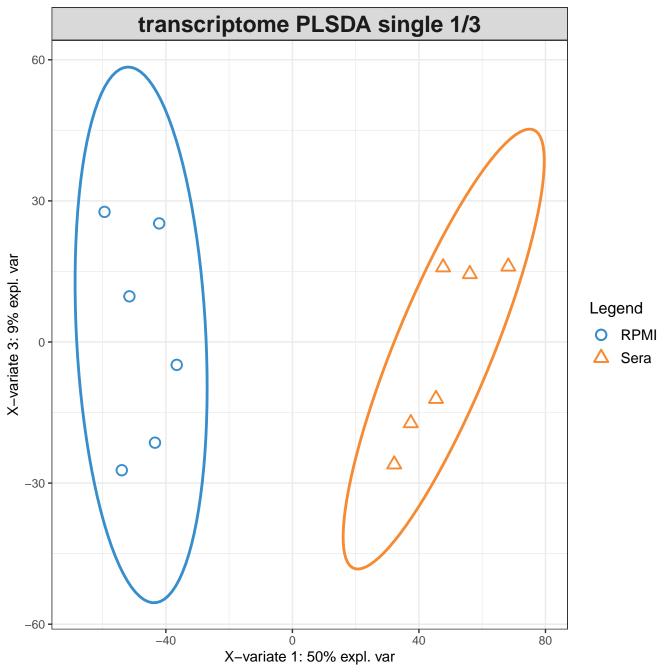


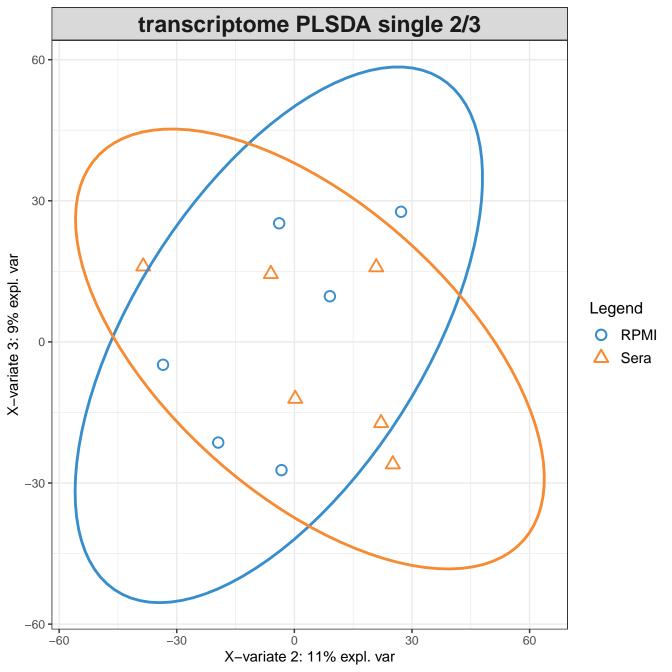
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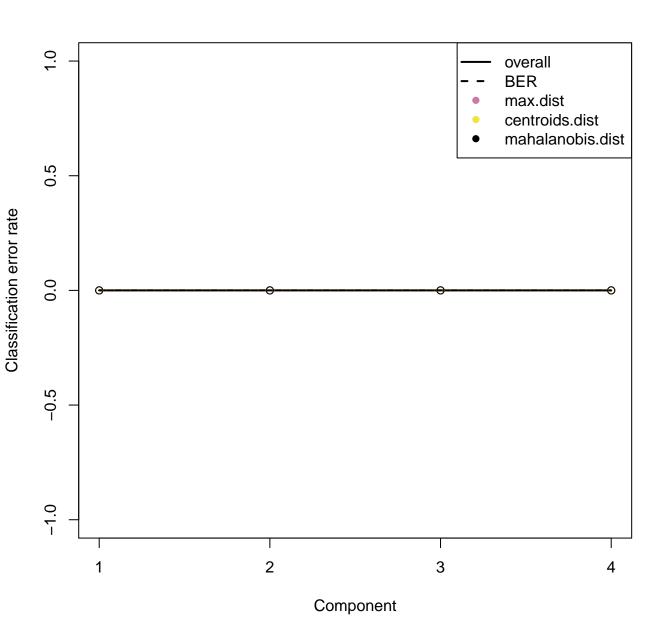




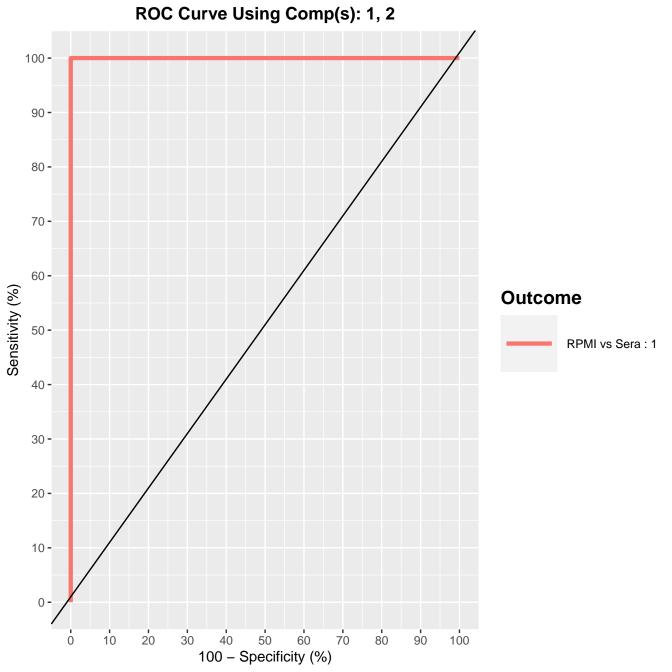


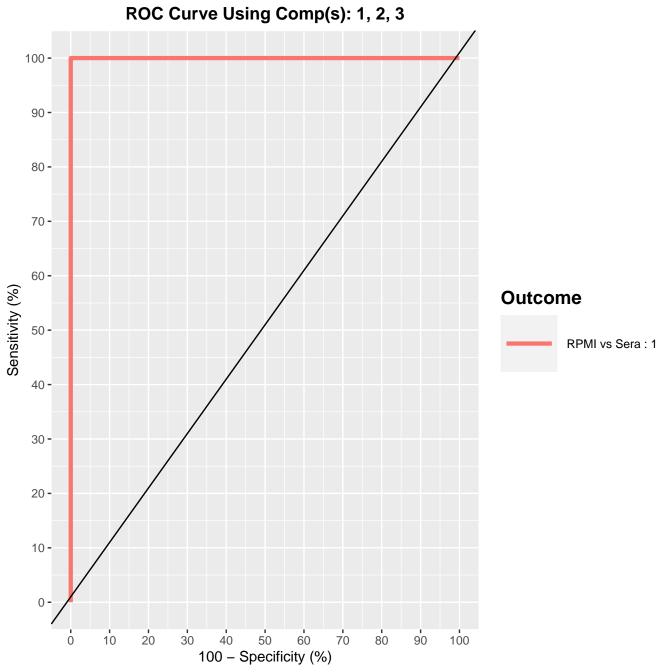


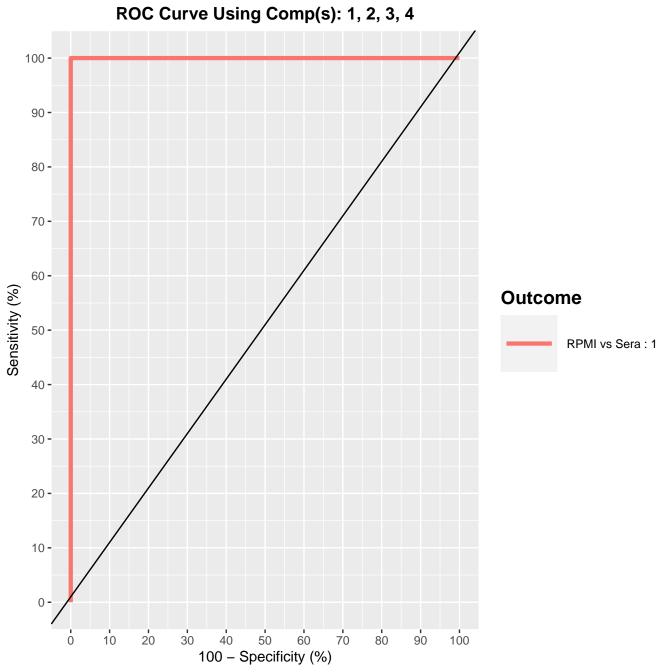


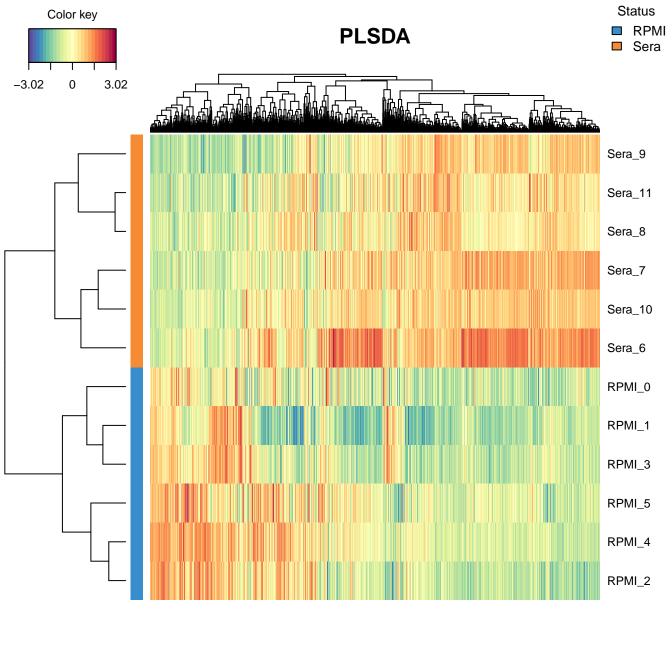


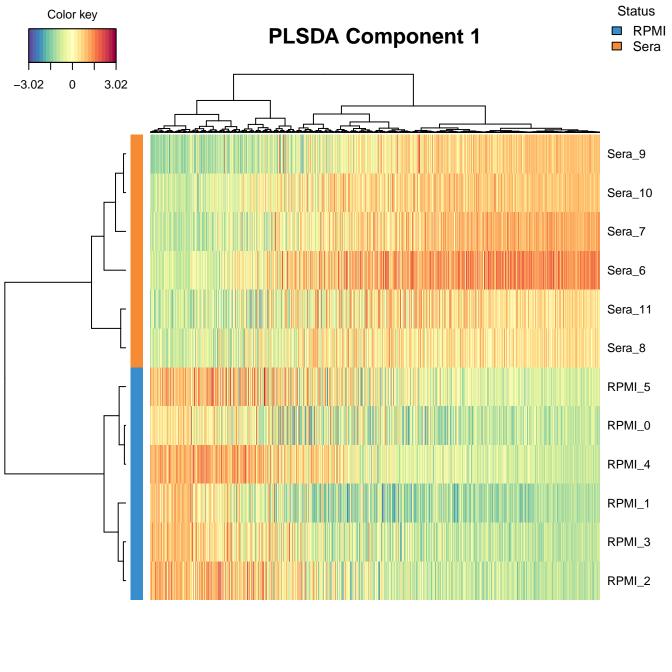




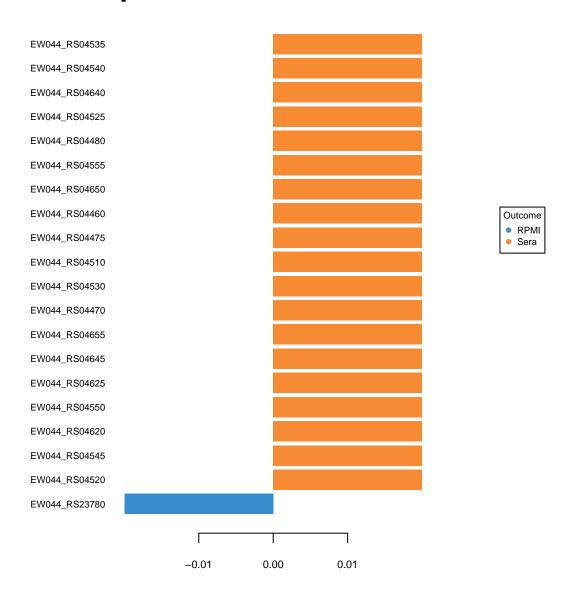




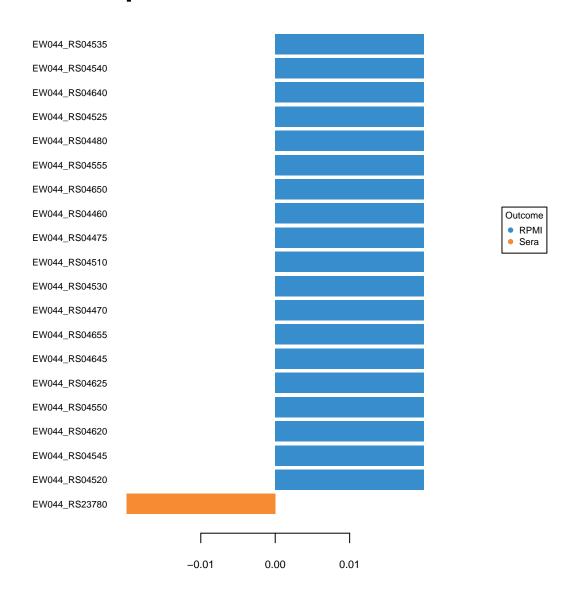


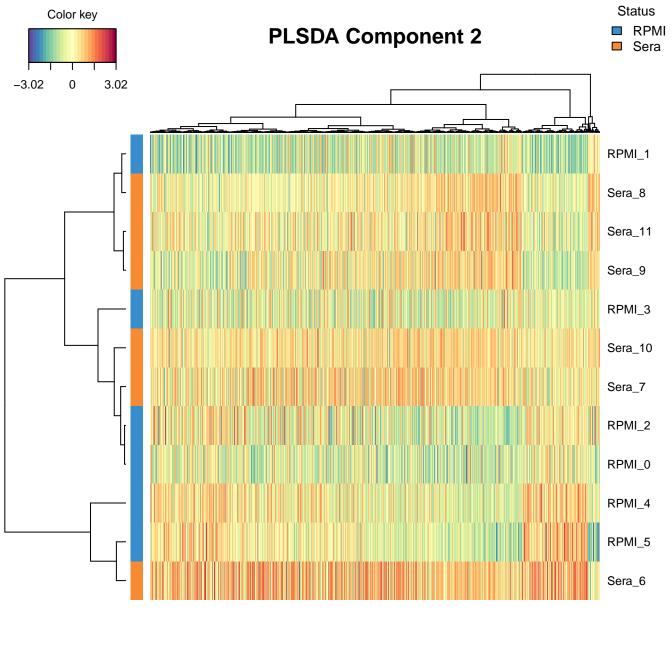


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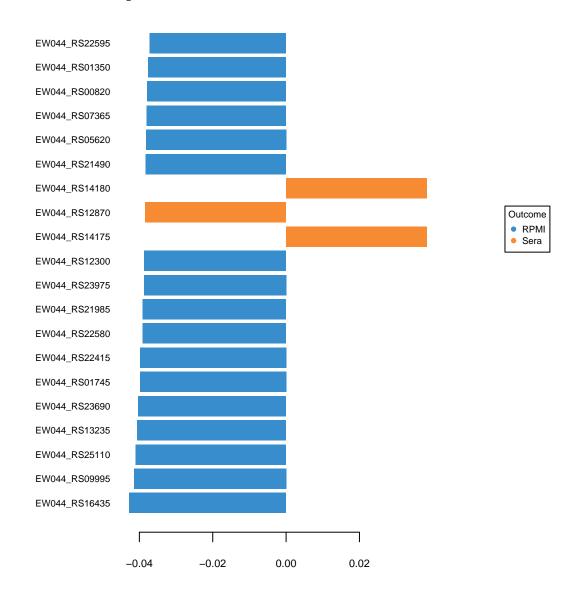


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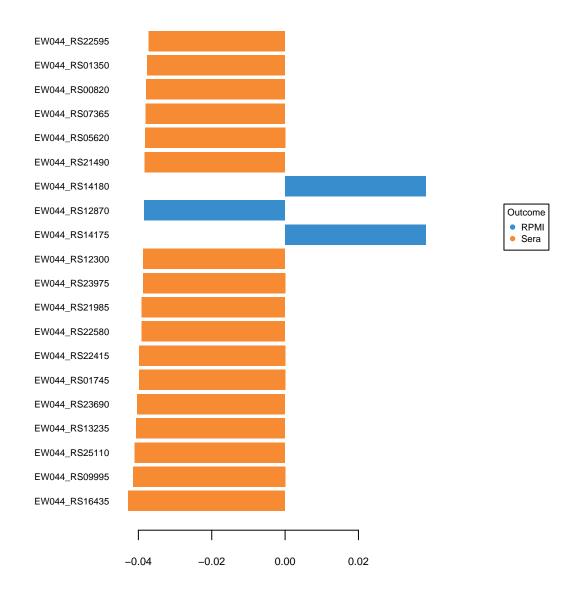


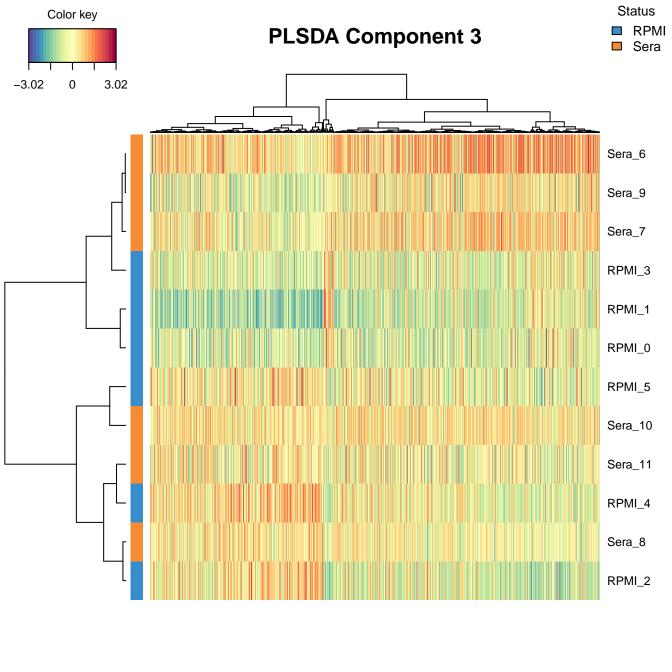


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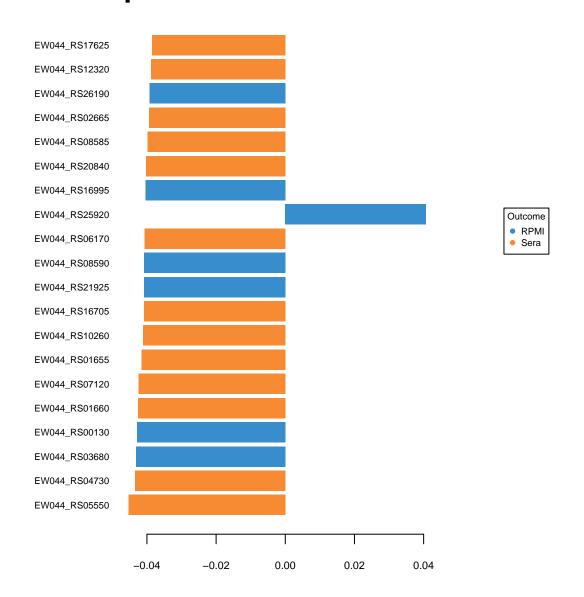


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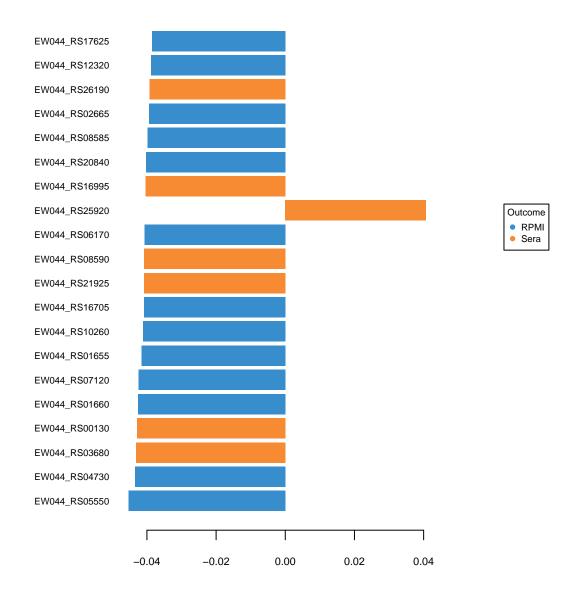


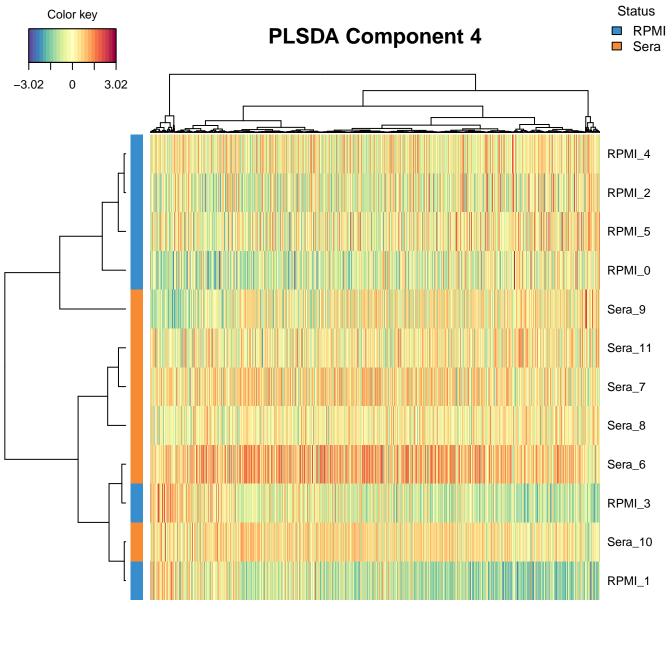


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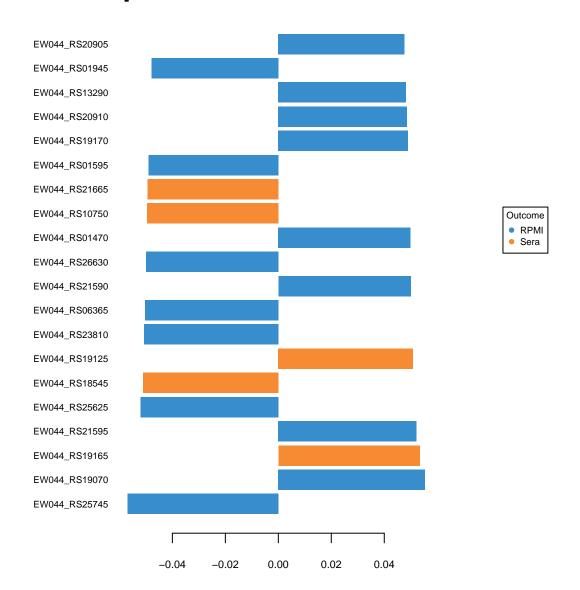


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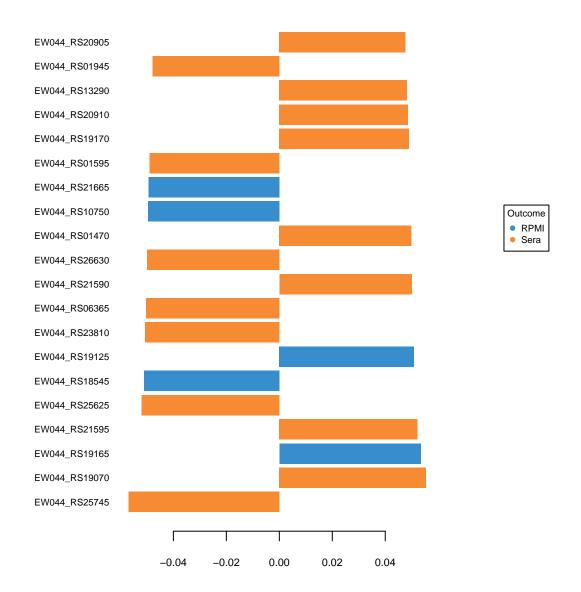


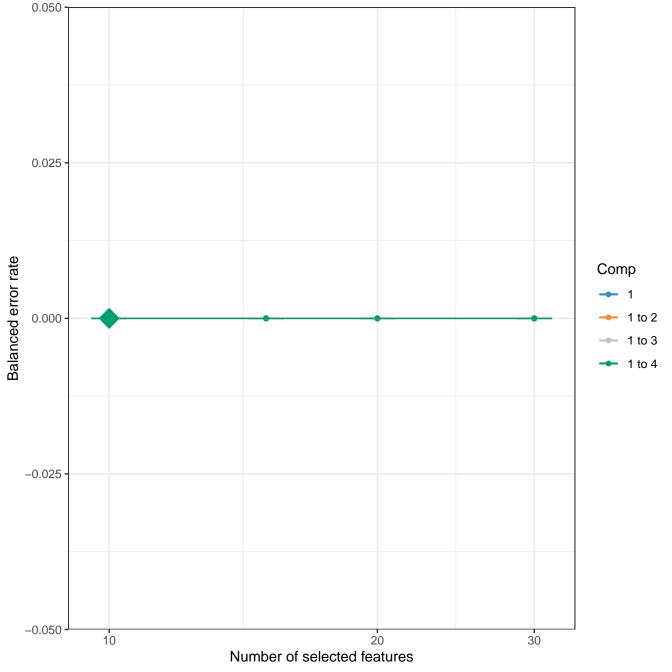


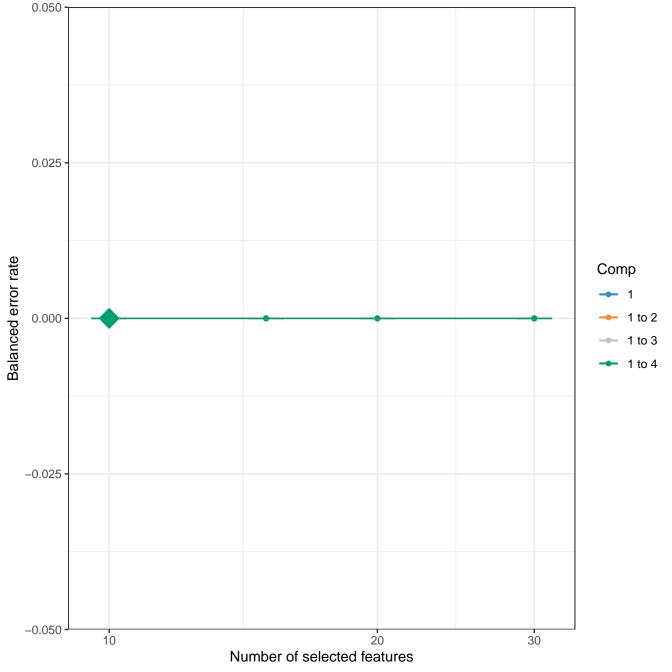
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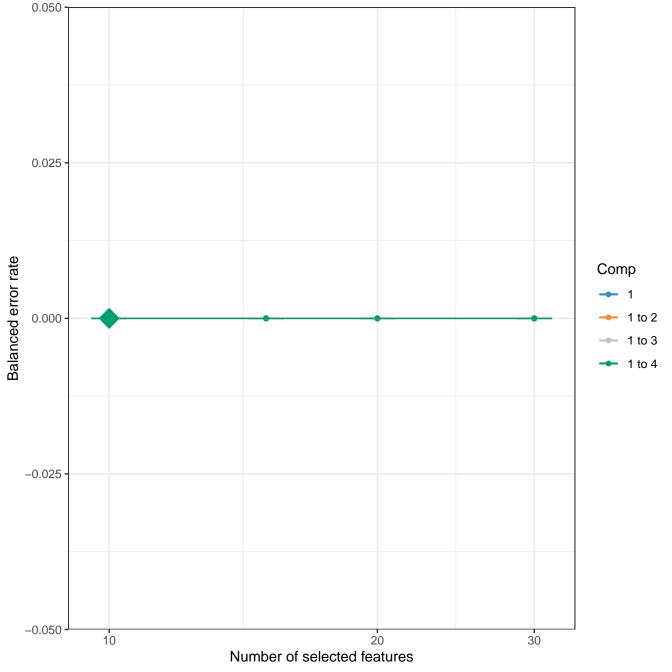


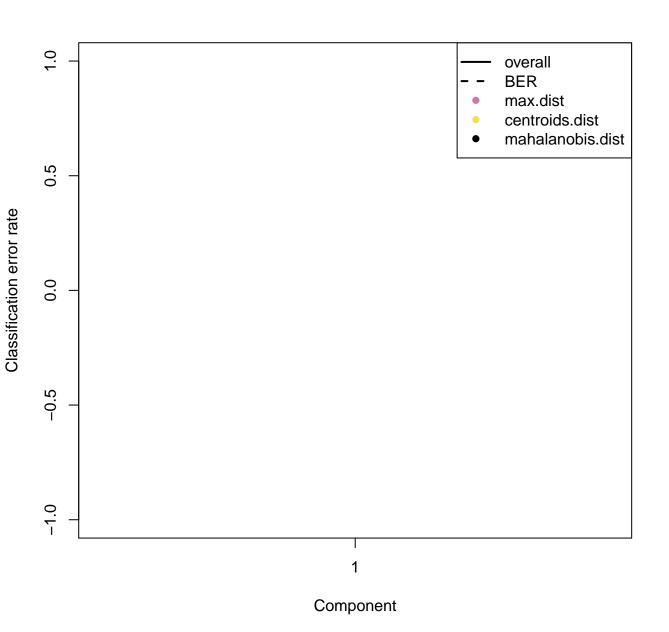
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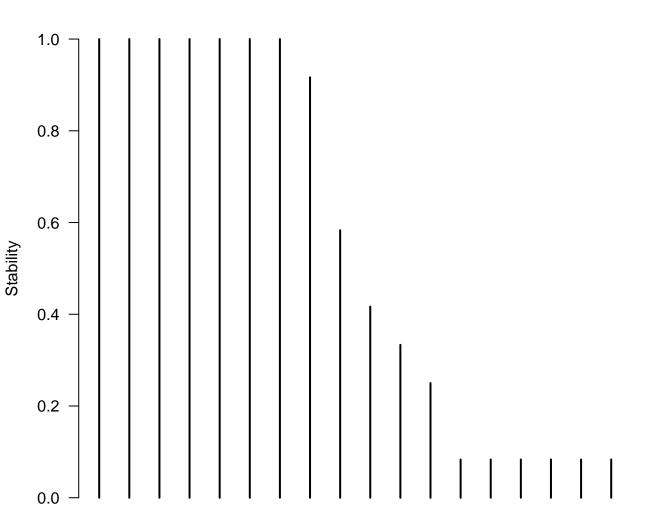




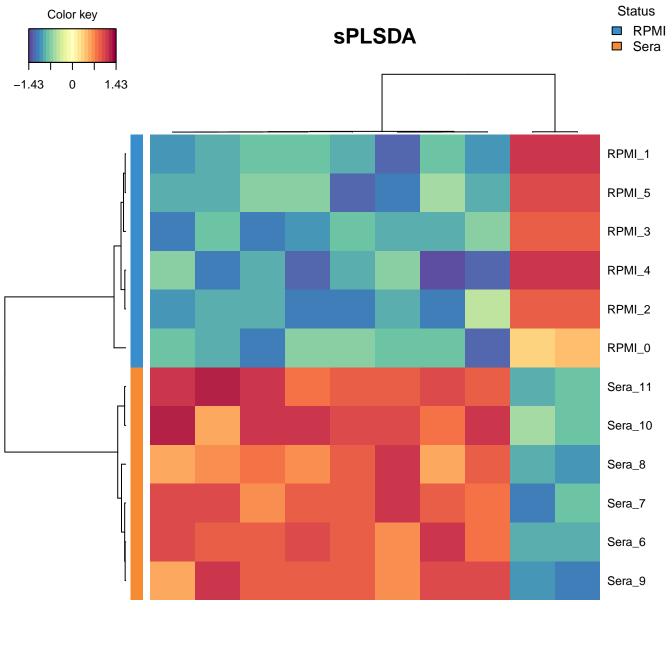


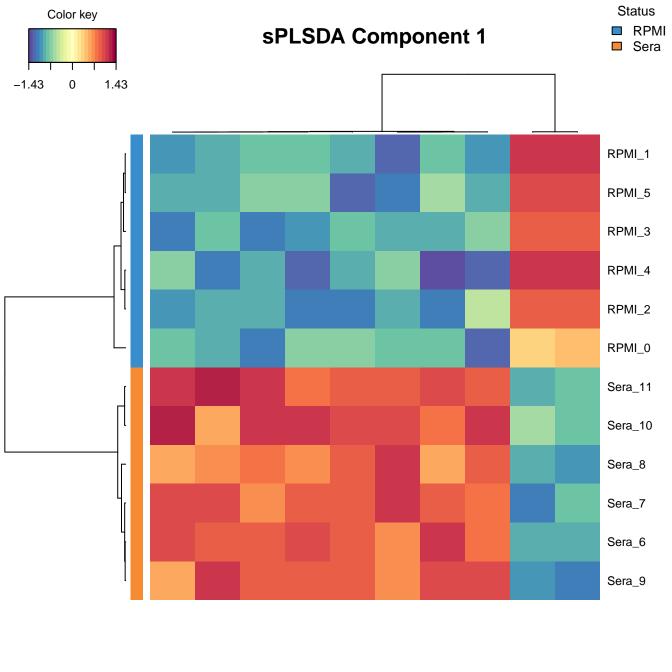




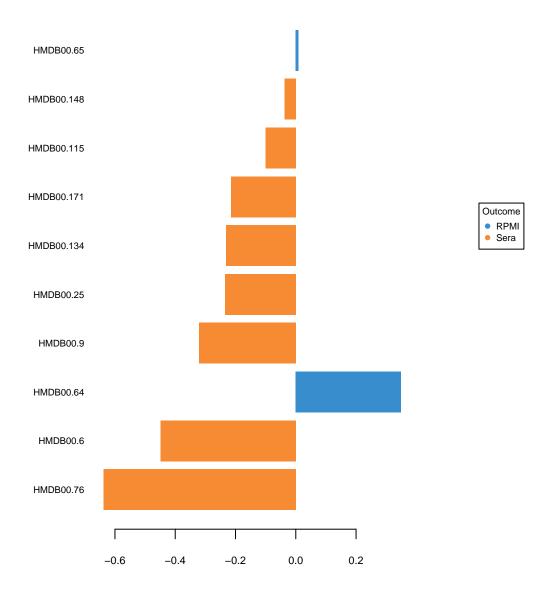




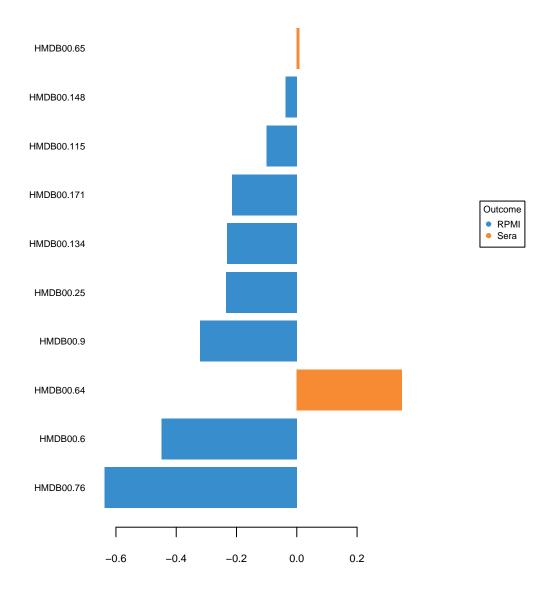


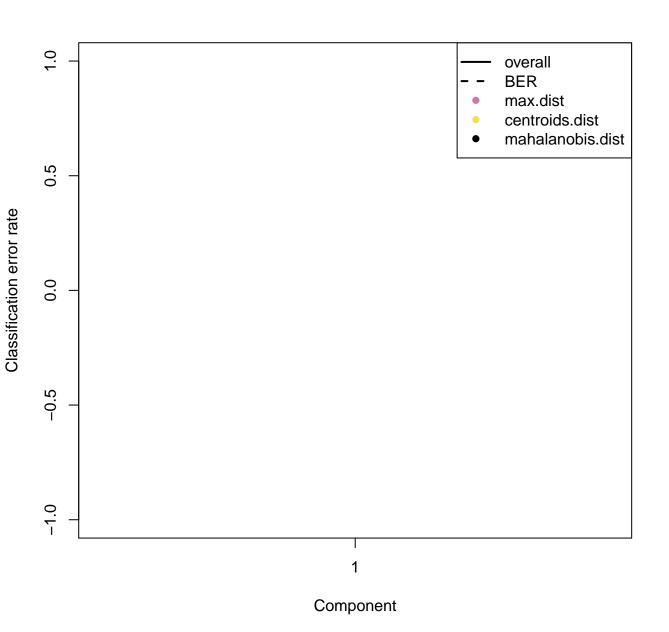


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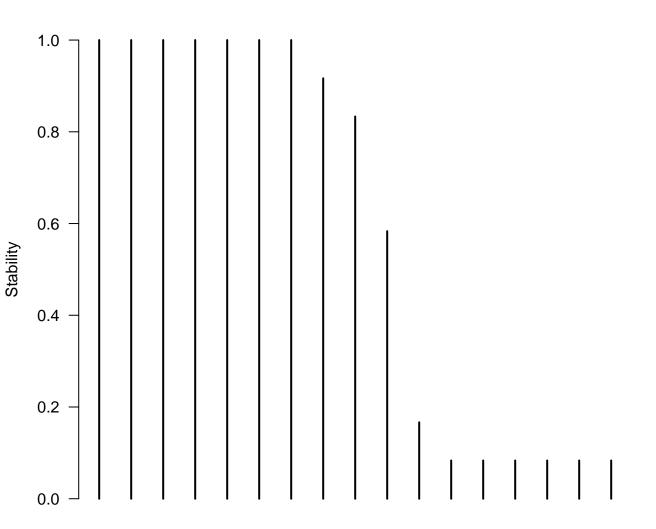


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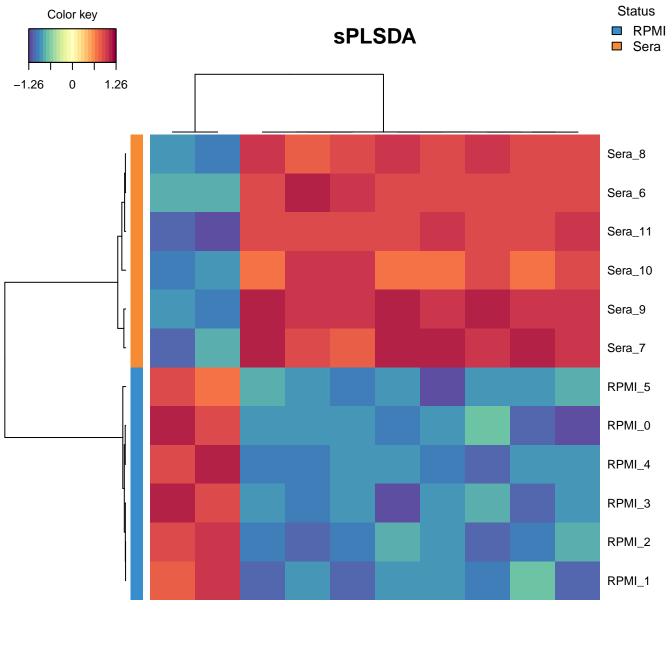


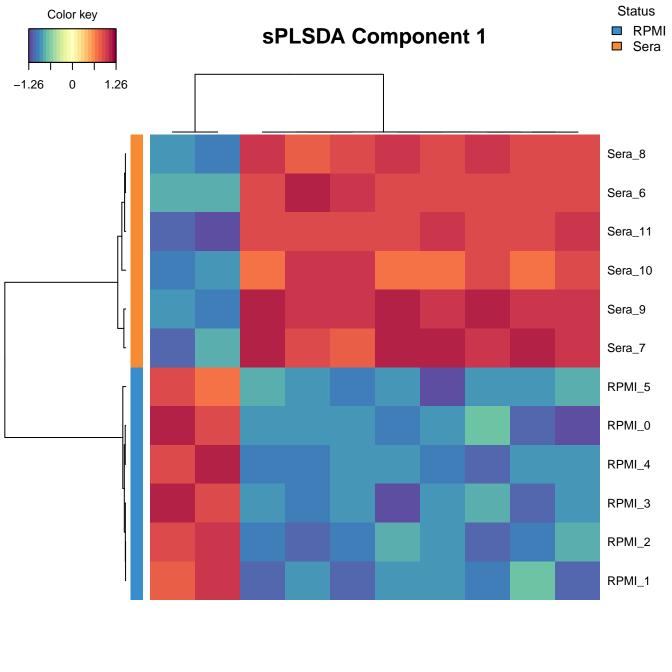




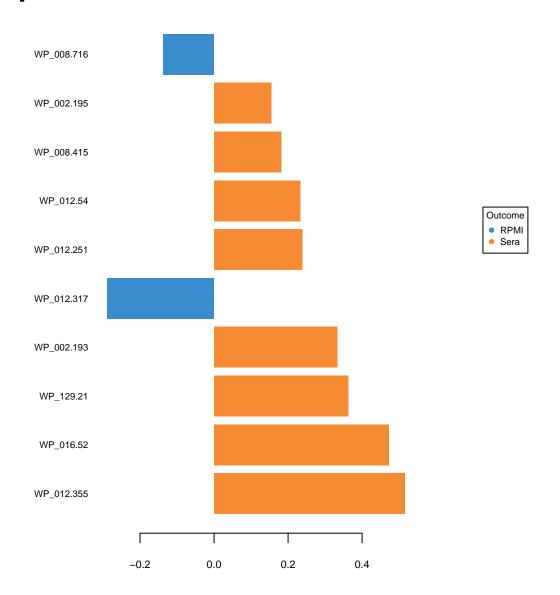
Features



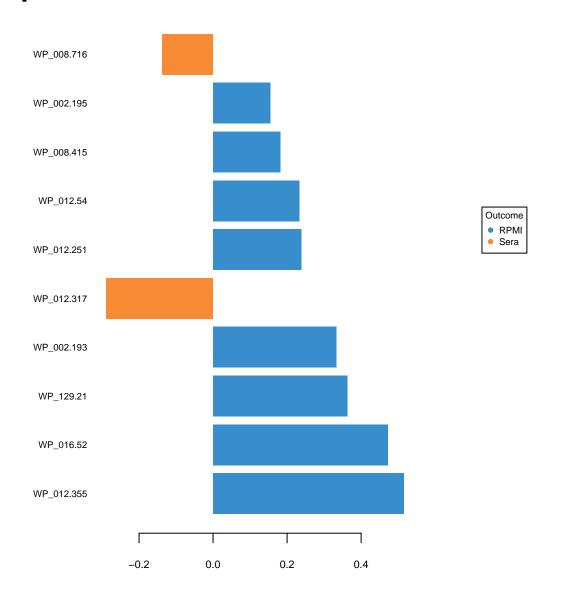


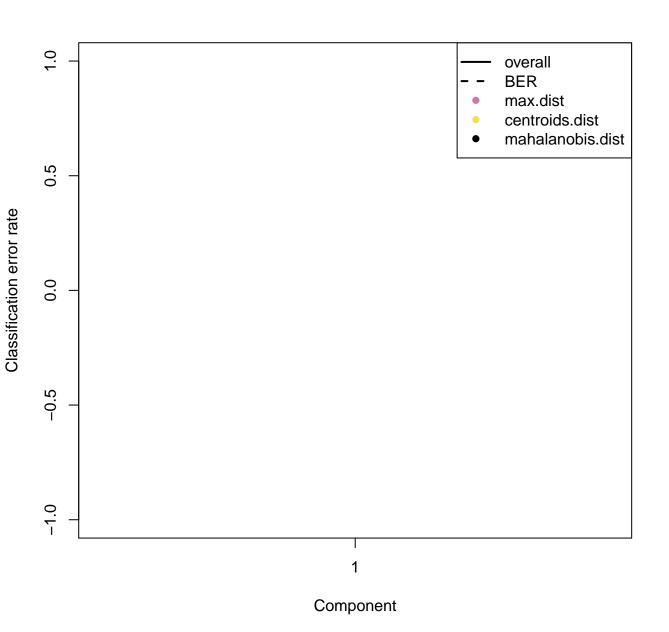


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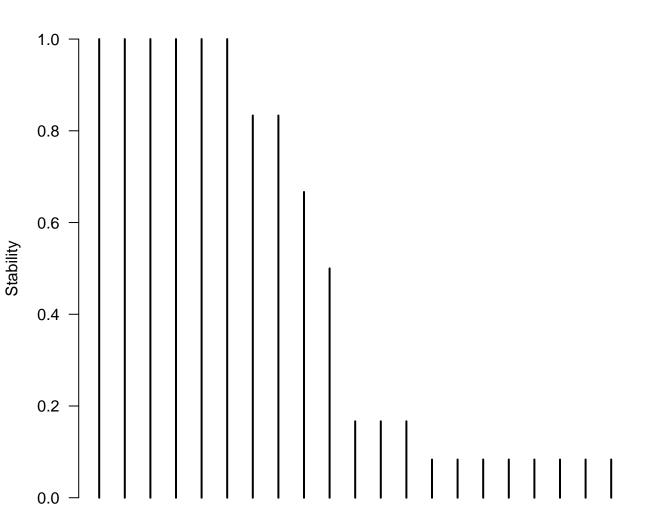


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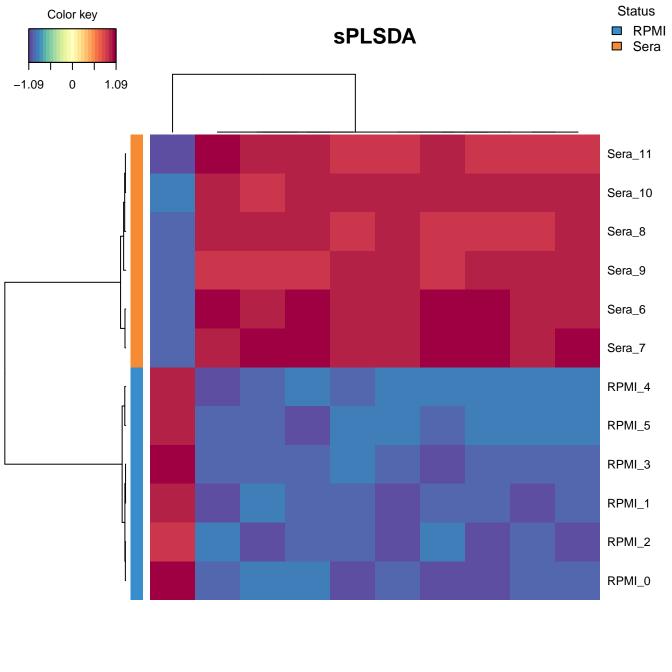


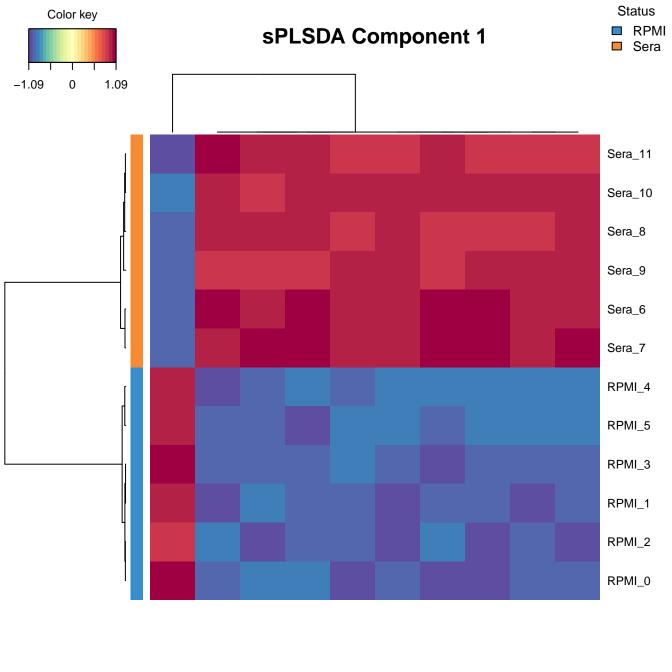




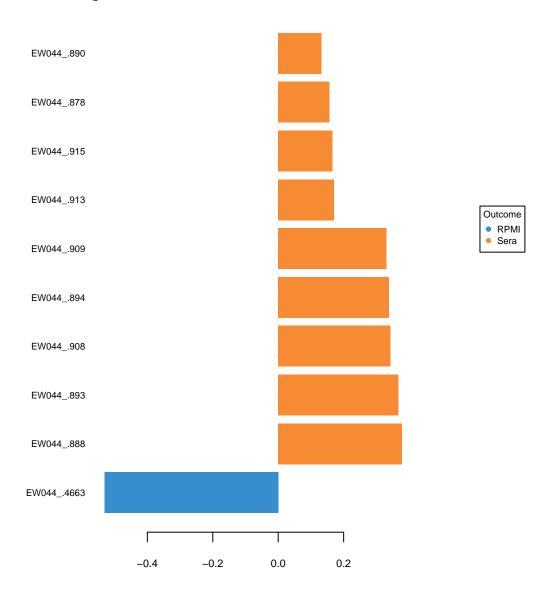




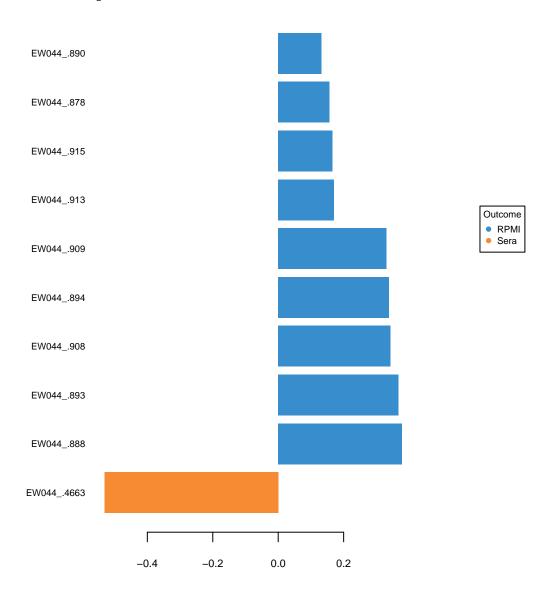


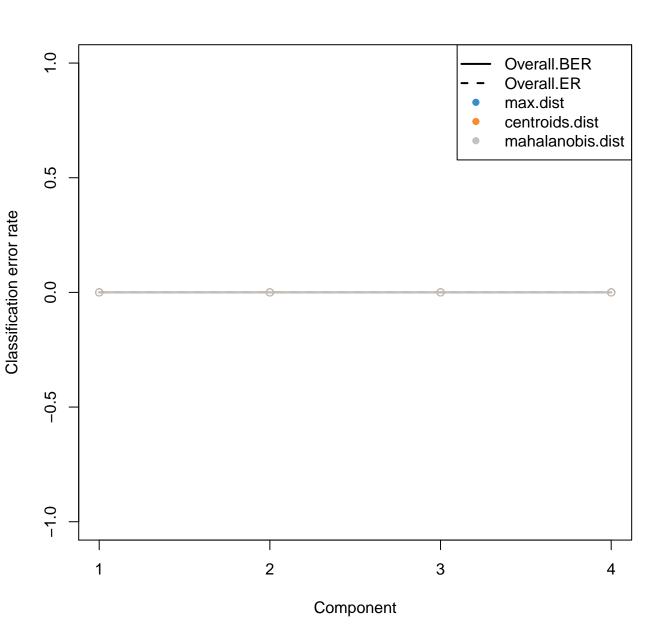


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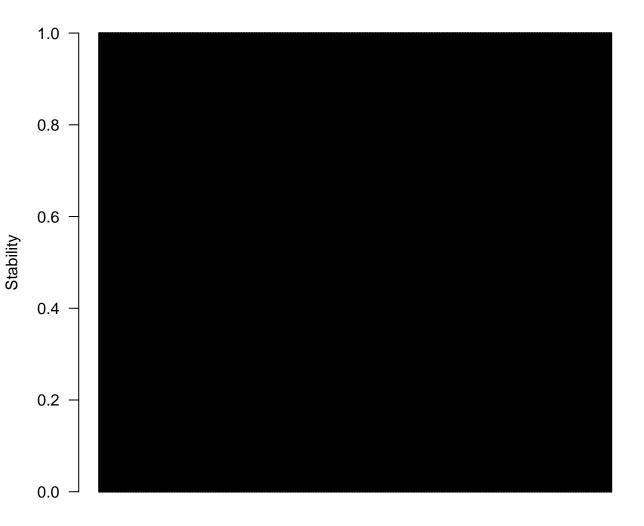


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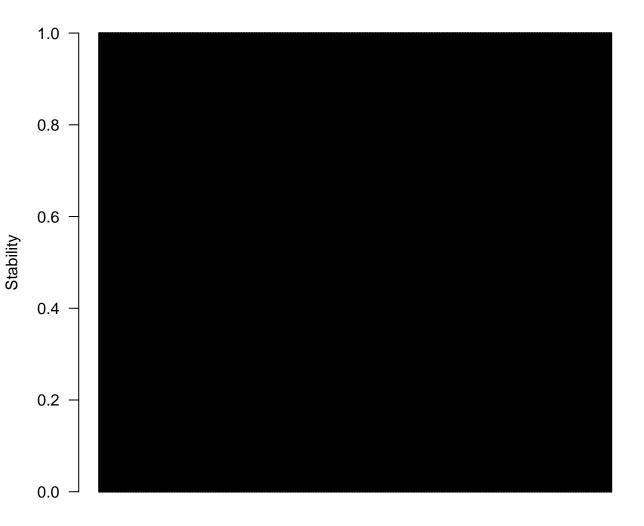


metabolome Comp 1



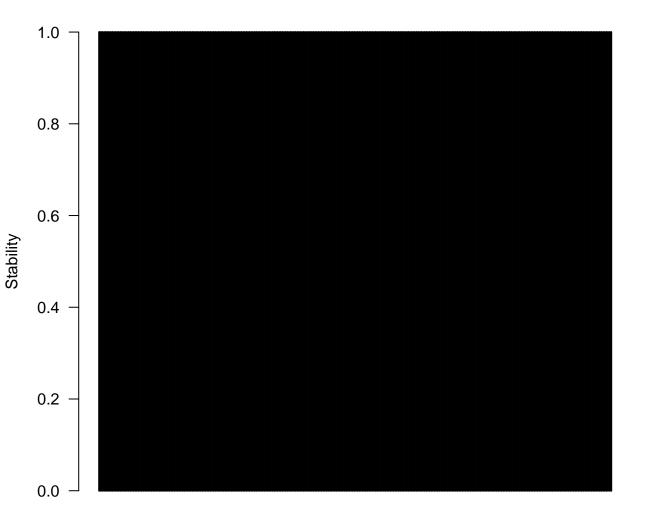
Features

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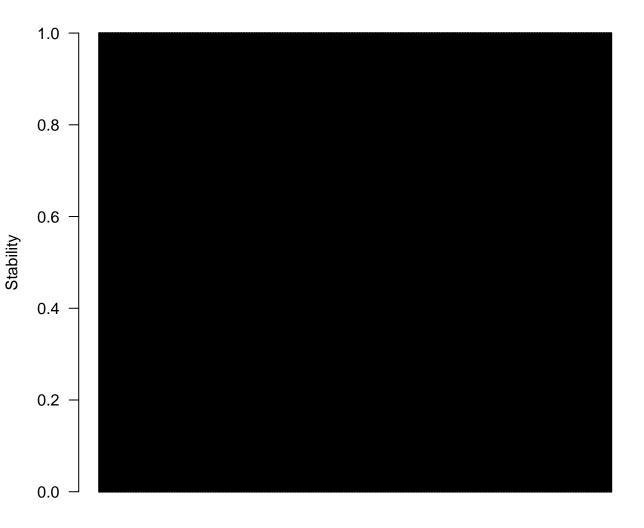


Features

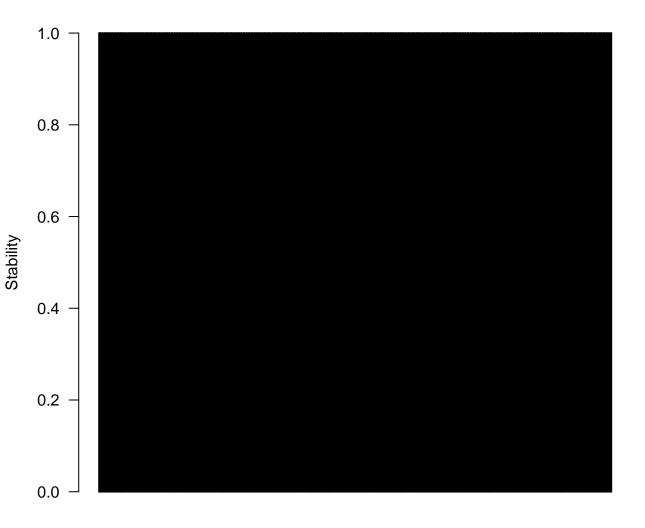
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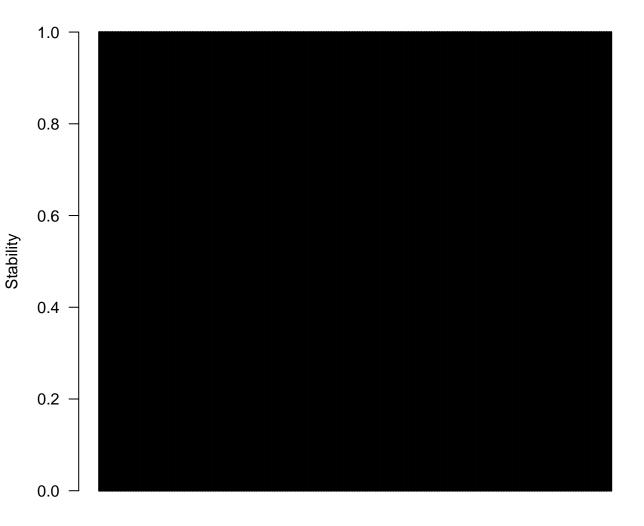
Features



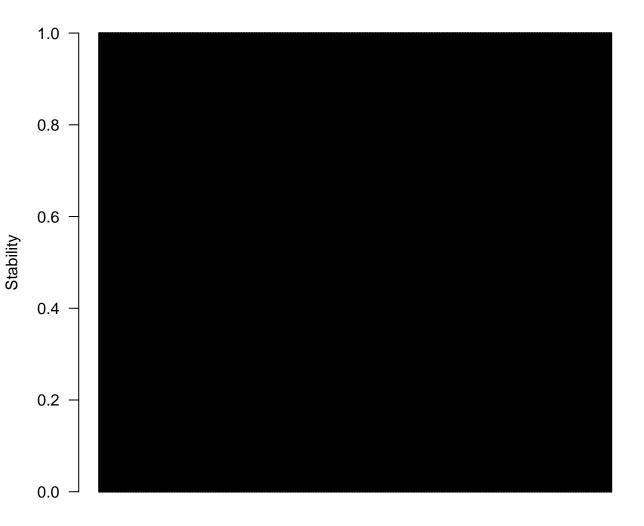
Features



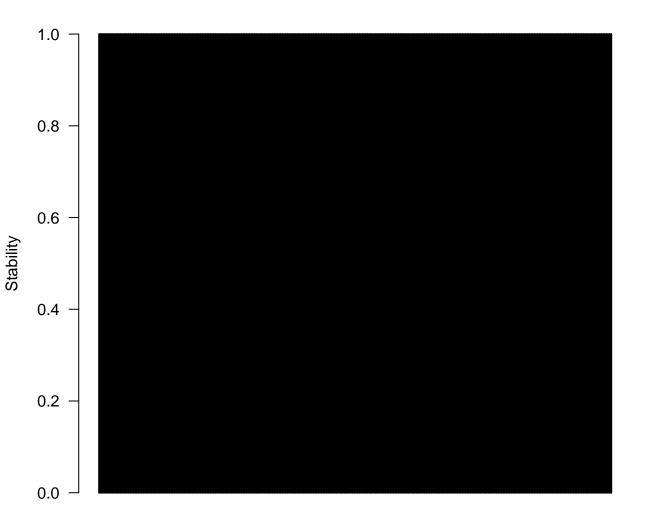
Features



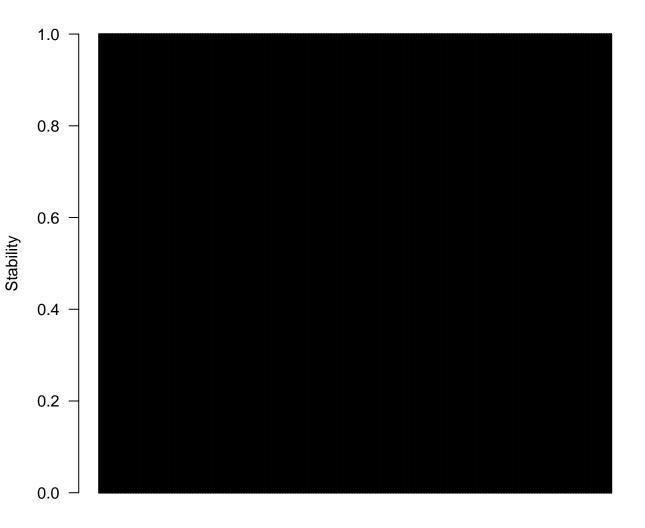
Features



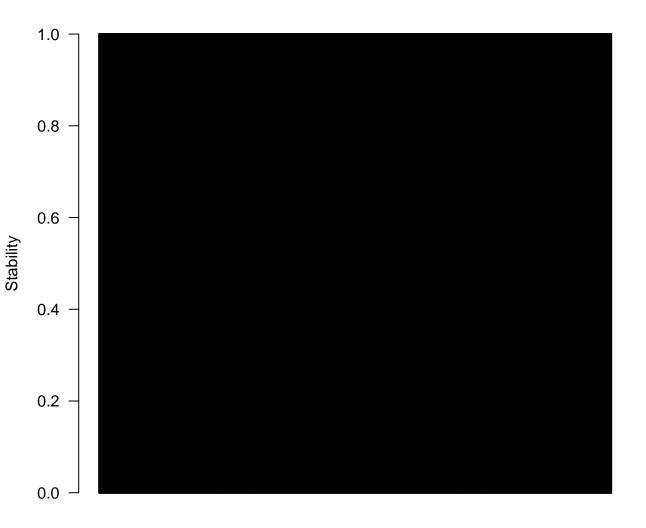
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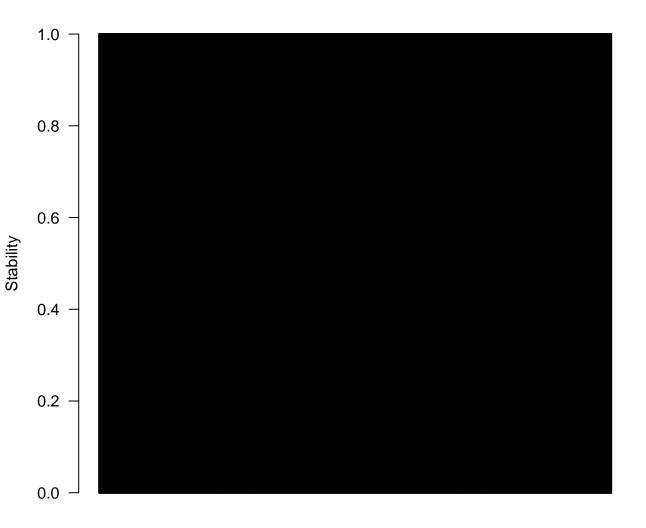
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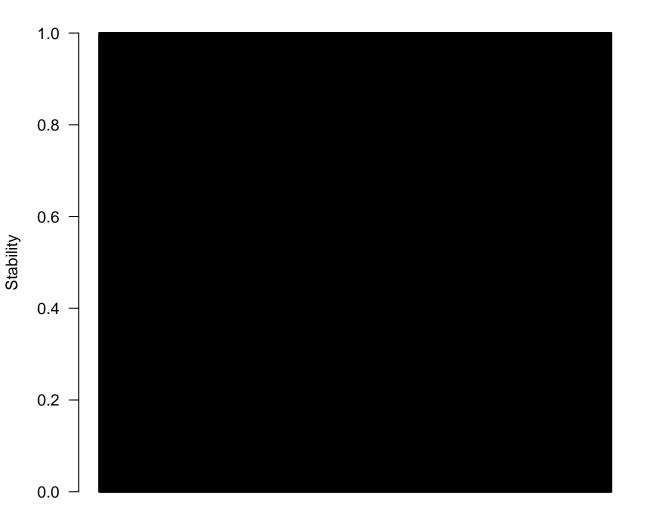
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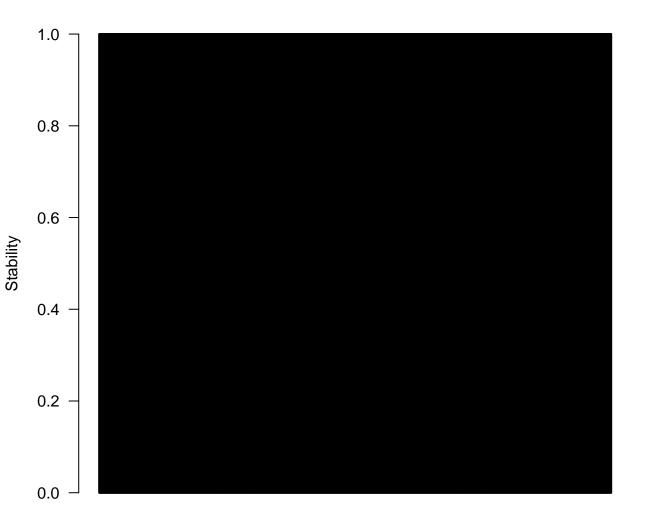
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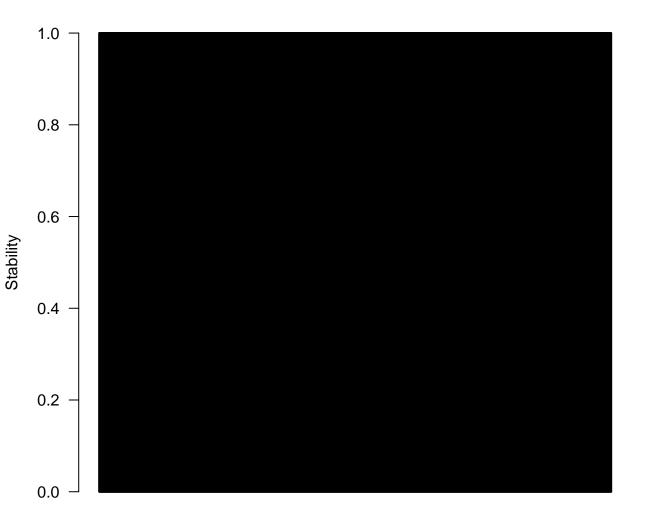
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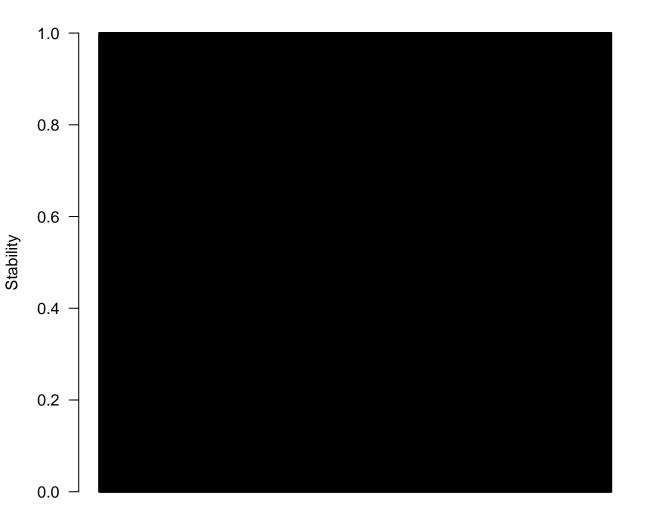
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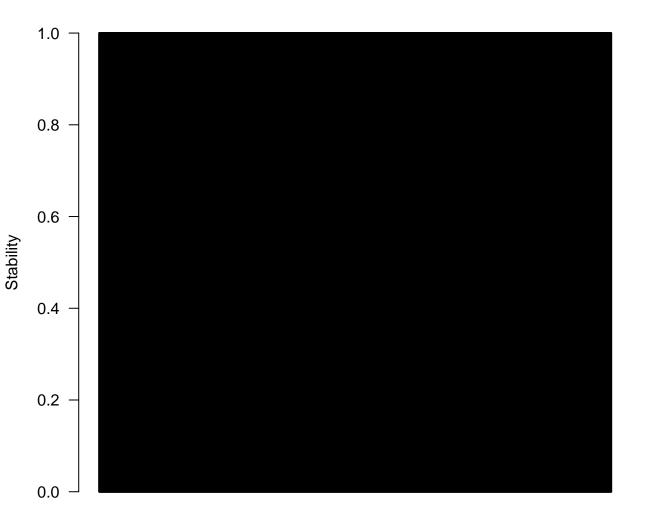
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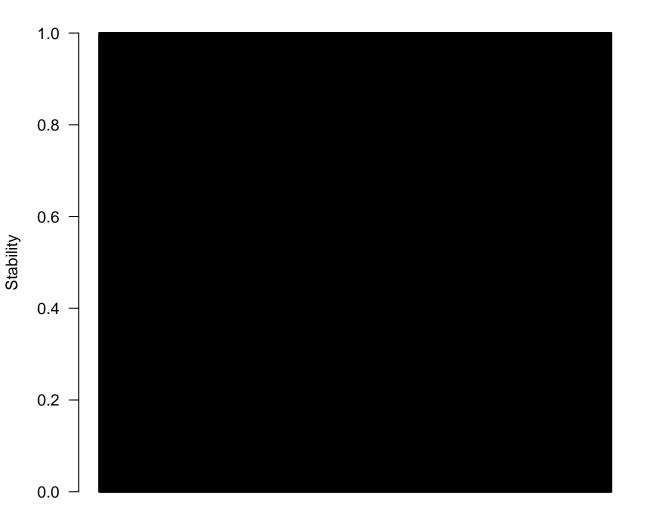
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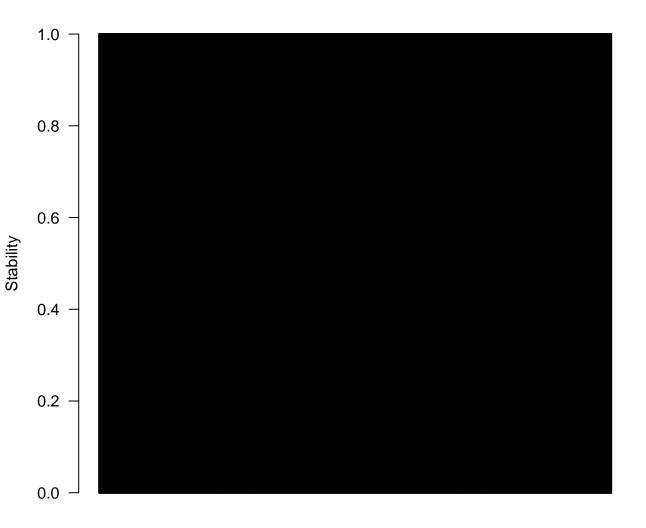
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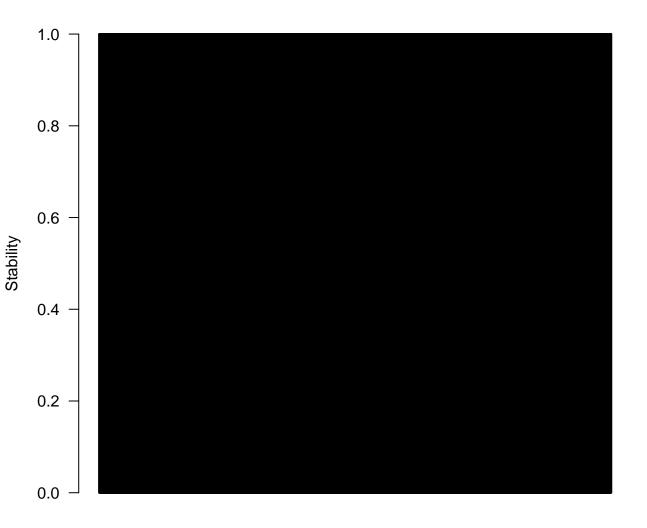
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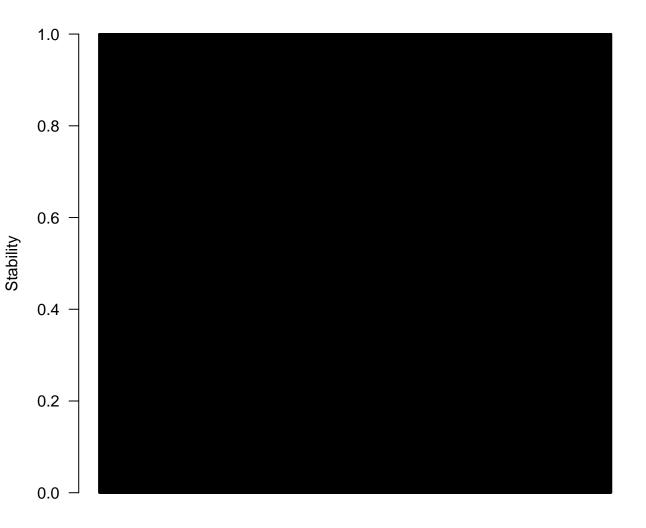
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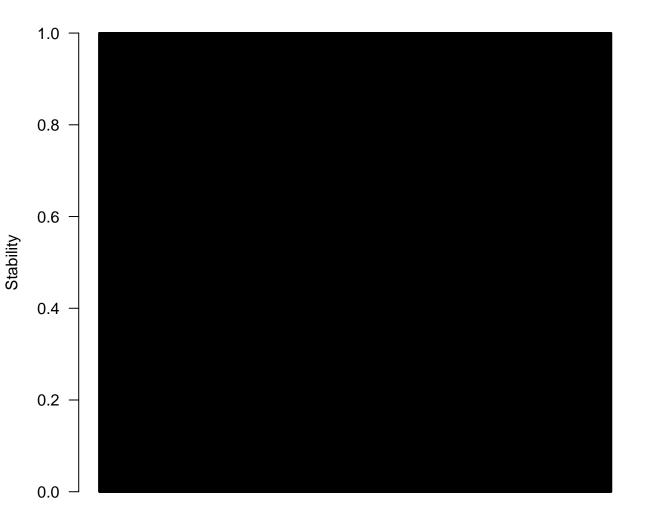
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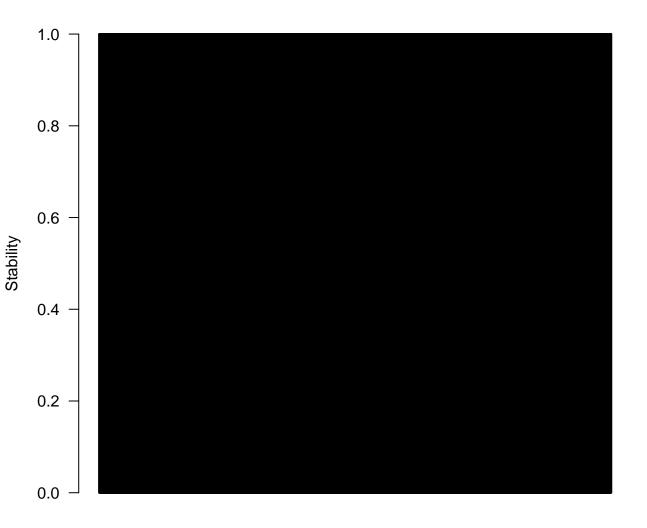
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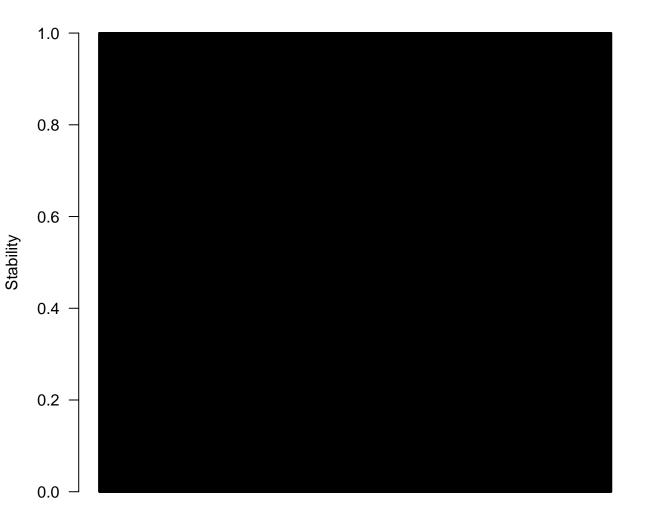
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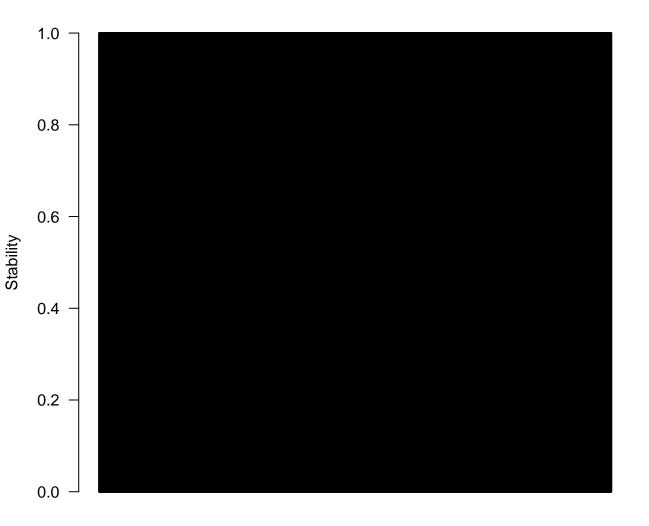
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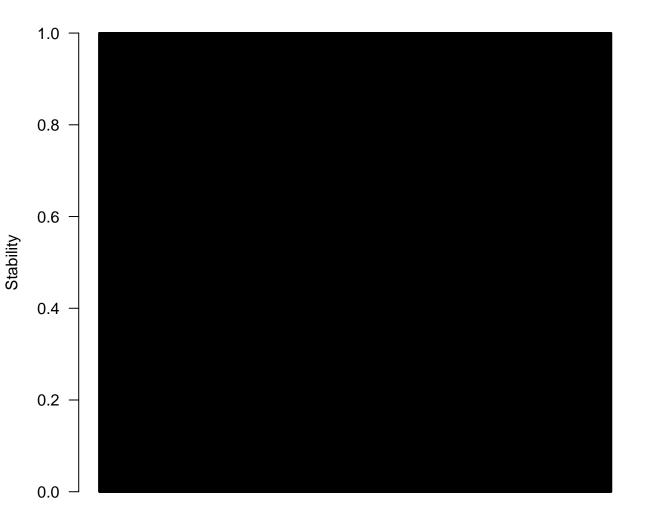
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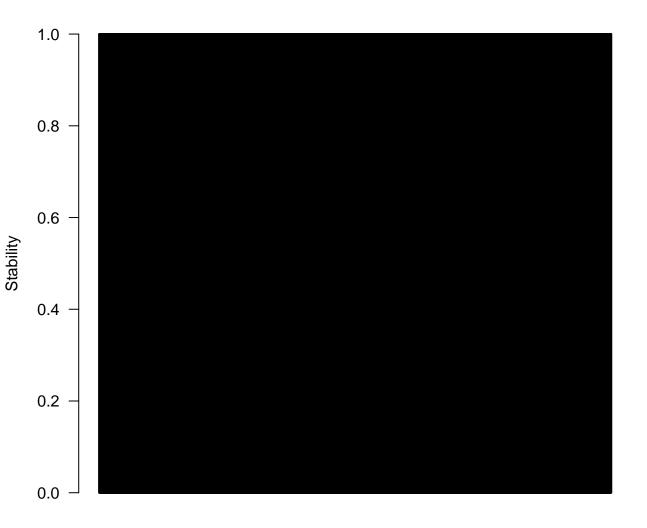
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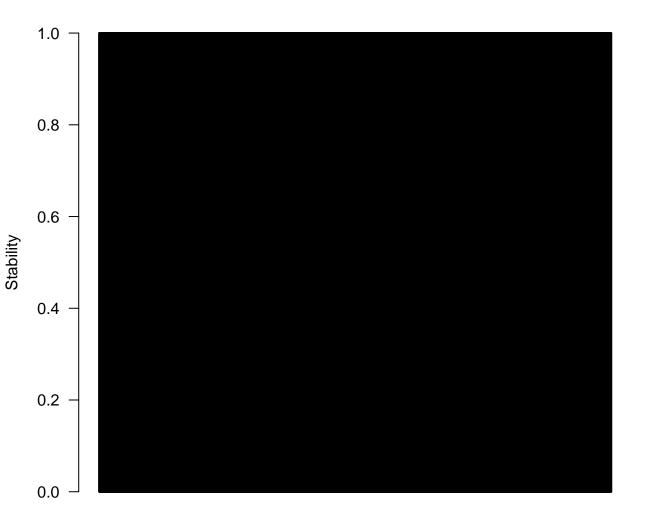
Features



Features

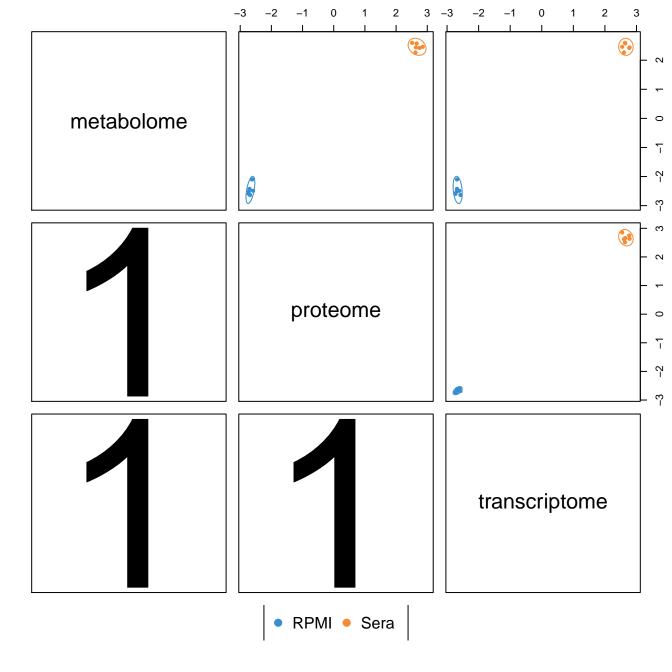


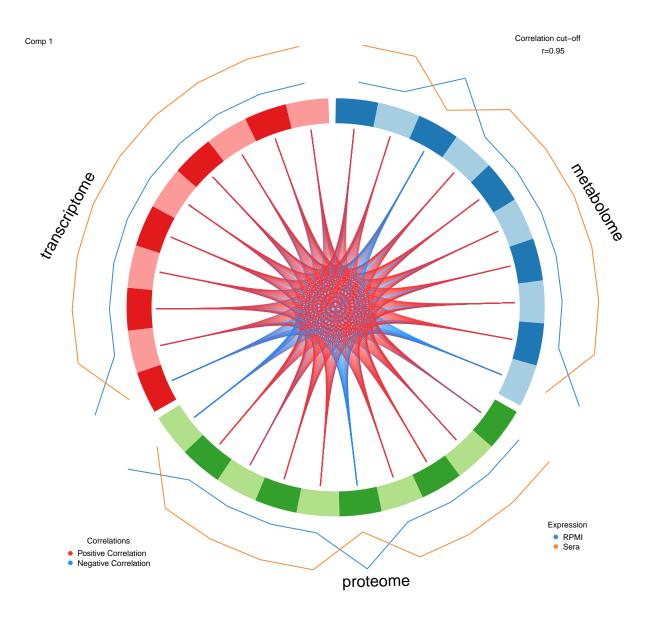
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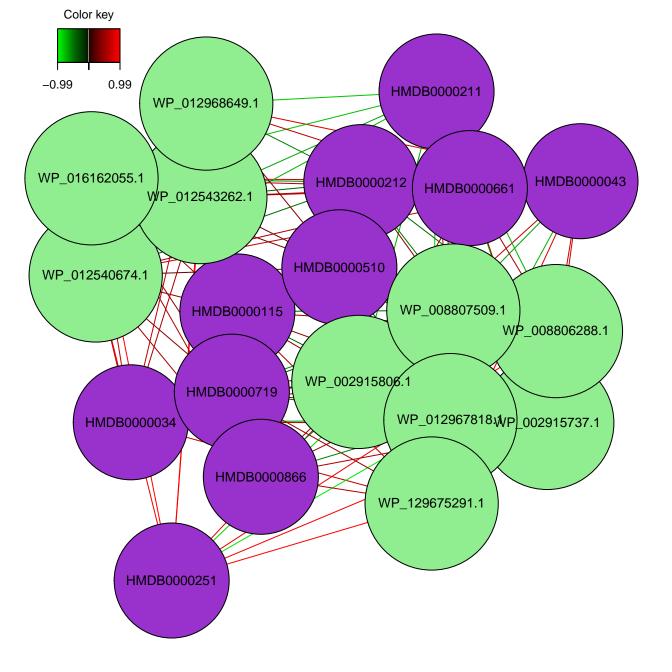


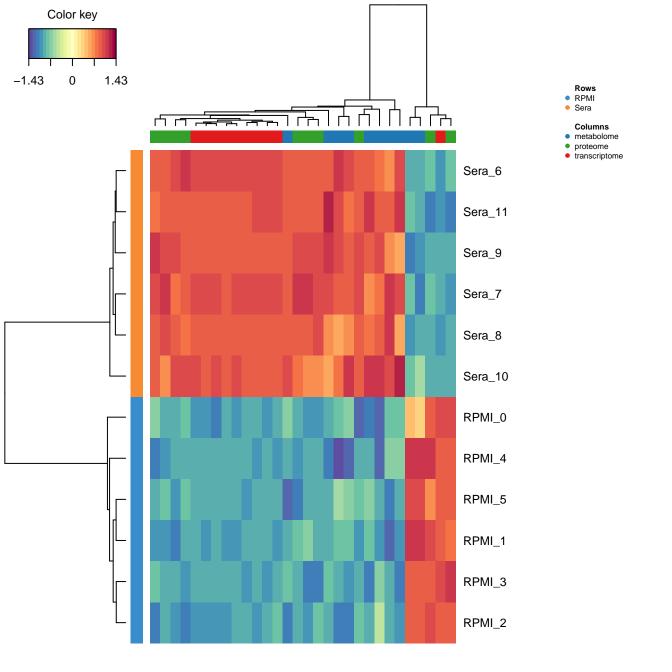
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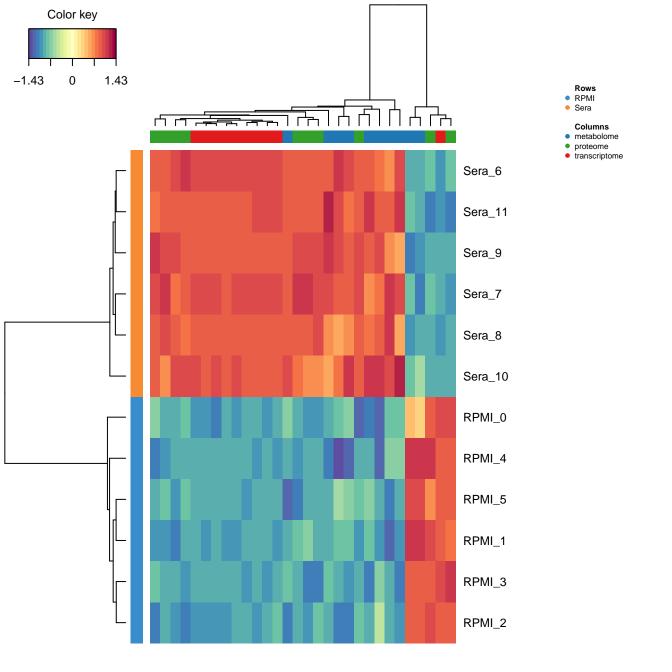
ROC Curve Block: metabolome, Using Comp(s): 1 100 -90 -80 -70 -60 -Sensitivity (%) **Outcome** 50 **-**RPMI vs Sera: 1 40 -30 -20 -10 -0 -10 20 30 70 80 40 50 60 100 90 100 - Specificity (%)



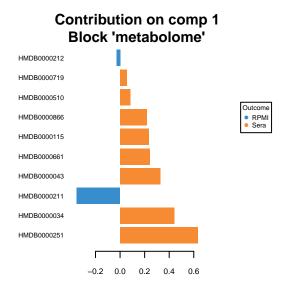


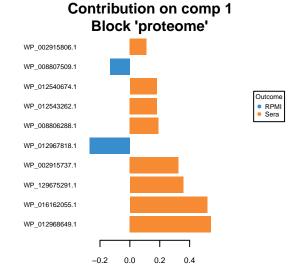




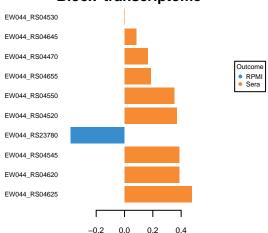


1 DIABLO max loadings

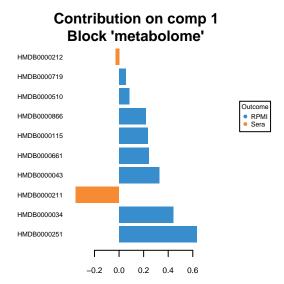


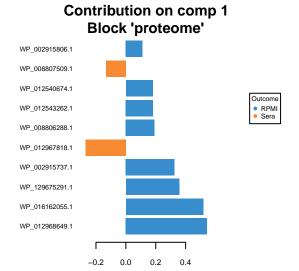


Contribution on comp 1 Block 'transcriptome'

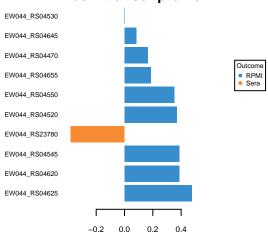


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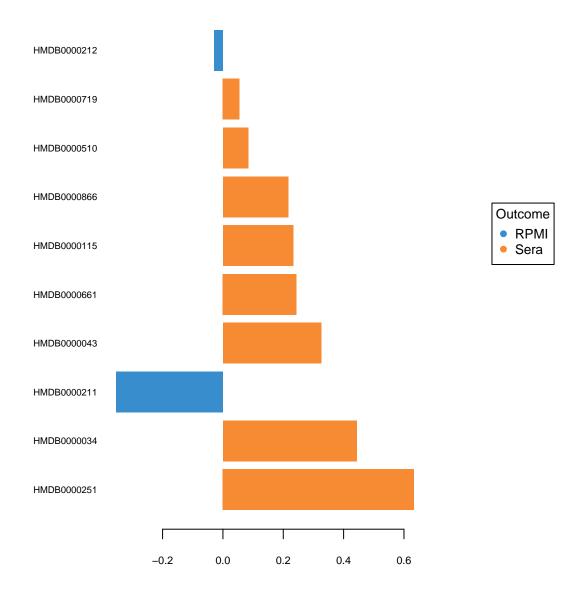




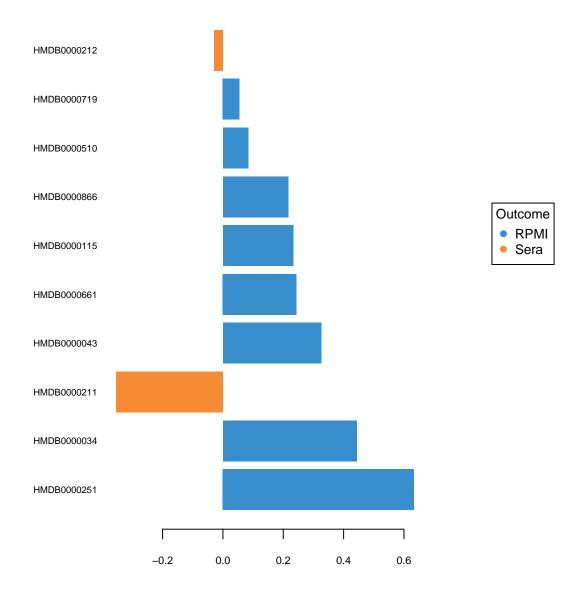
Contribution on comp 1 Block 'transcriptome'



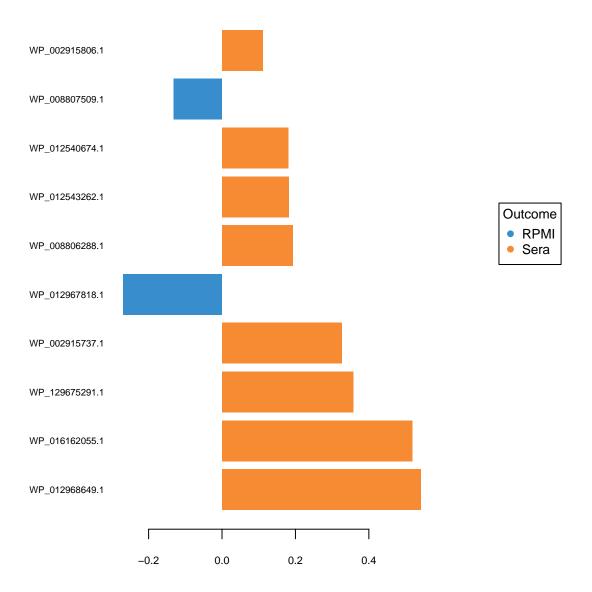
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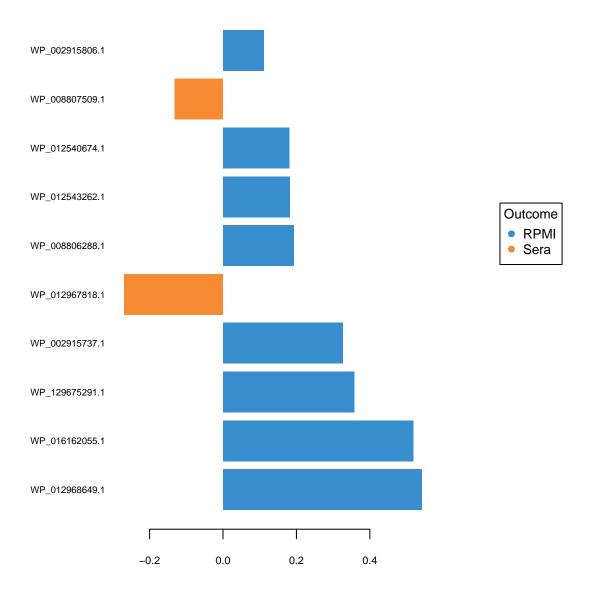
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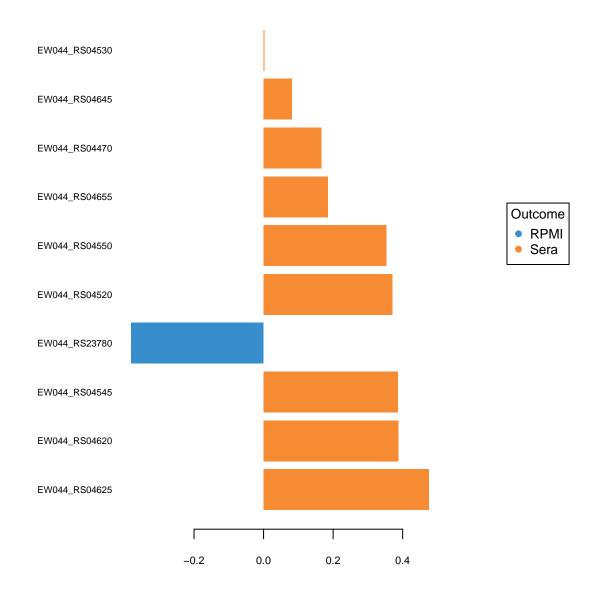
1 proteome DIABLO max loadi



1 proteome DIABLO min loadii



1 transcriptome DIABLO max loa



1 transcriptome DIABLO min loa

