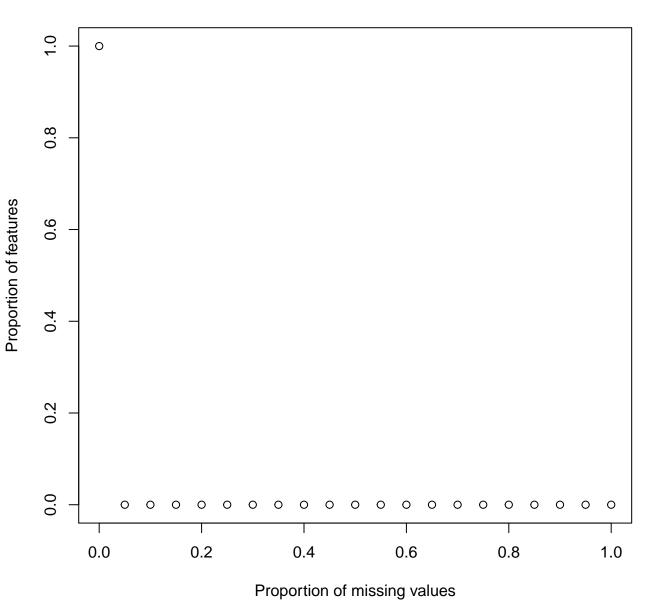
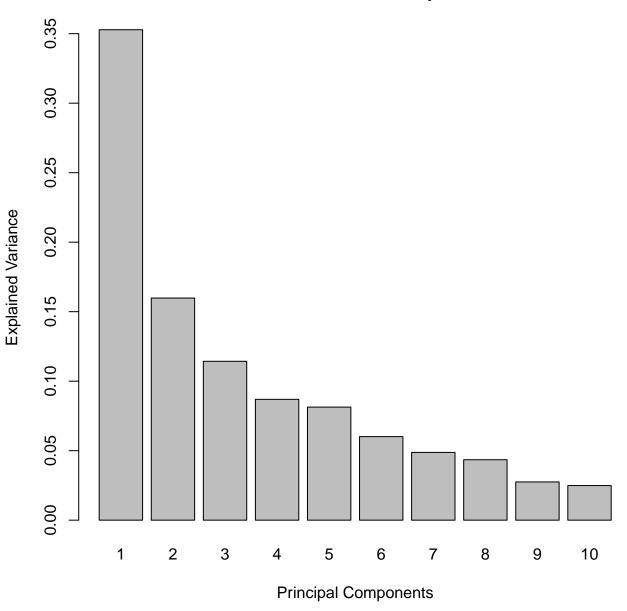
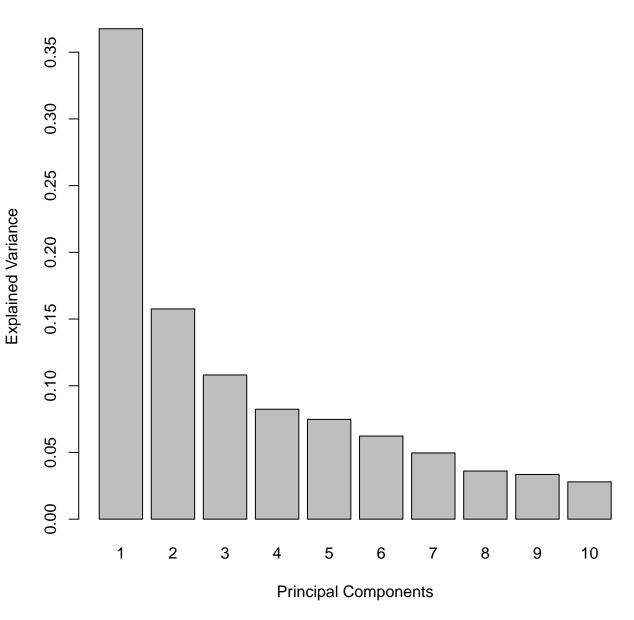
RNA_Seq missing value proportions for unfiltered data



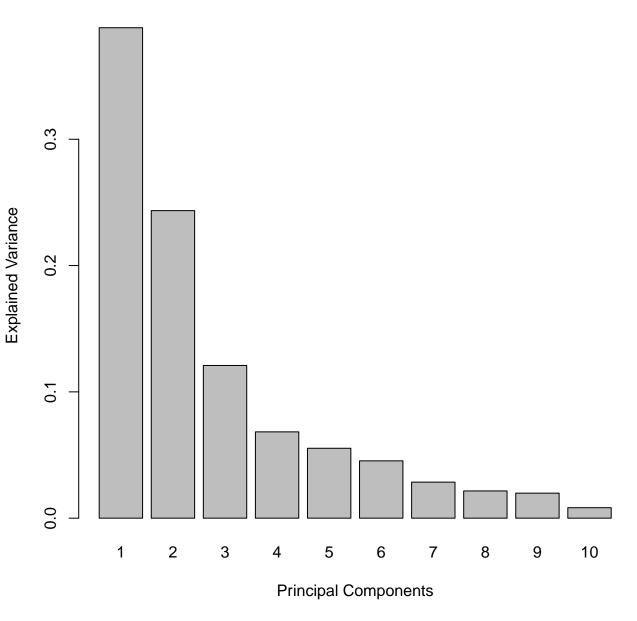
Metabolomics screeplot

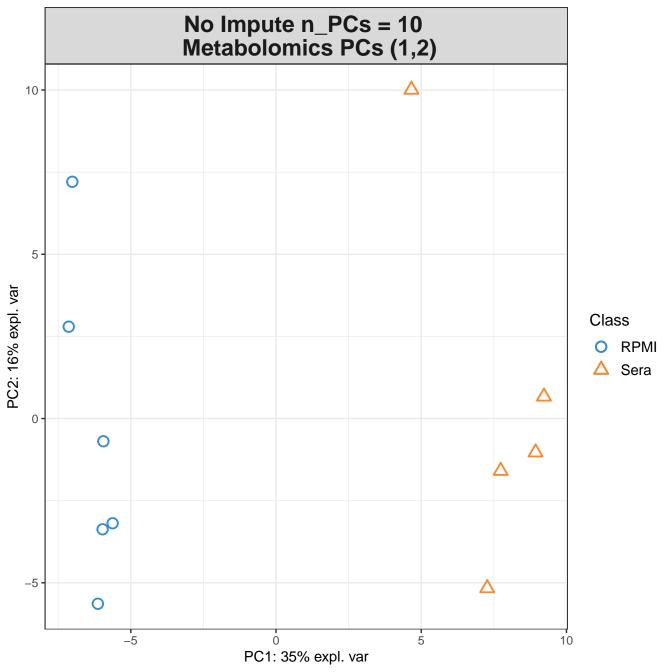


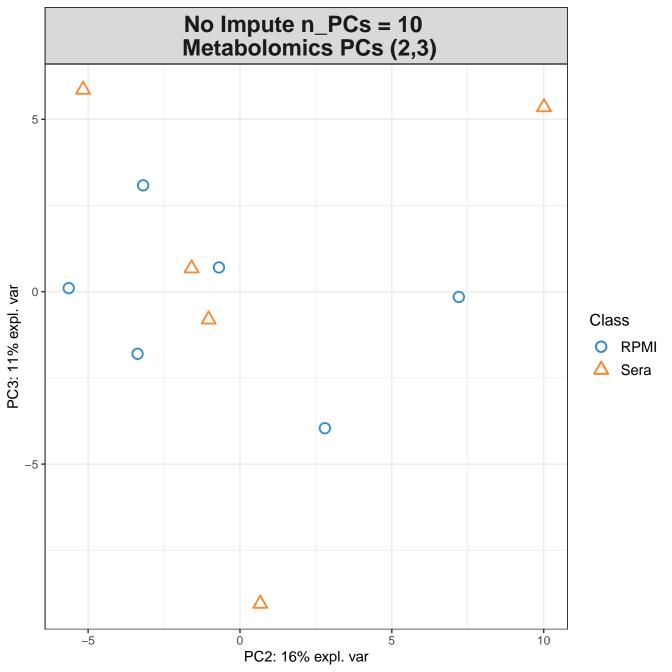
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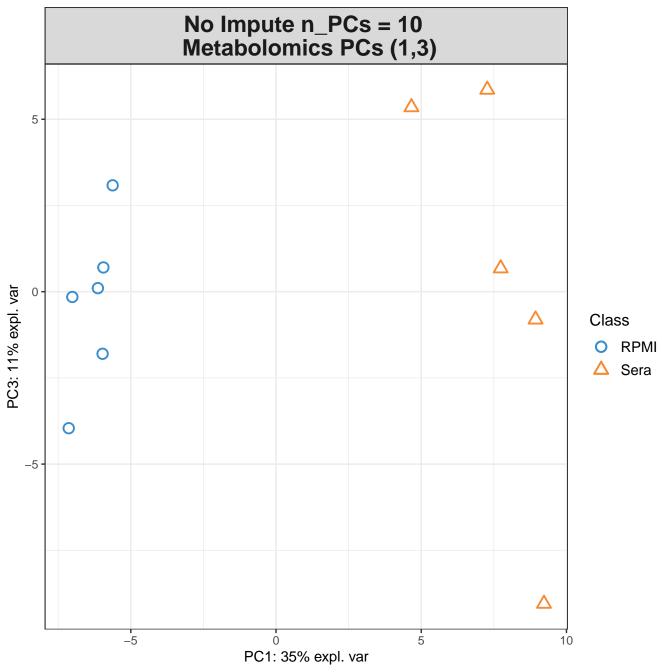


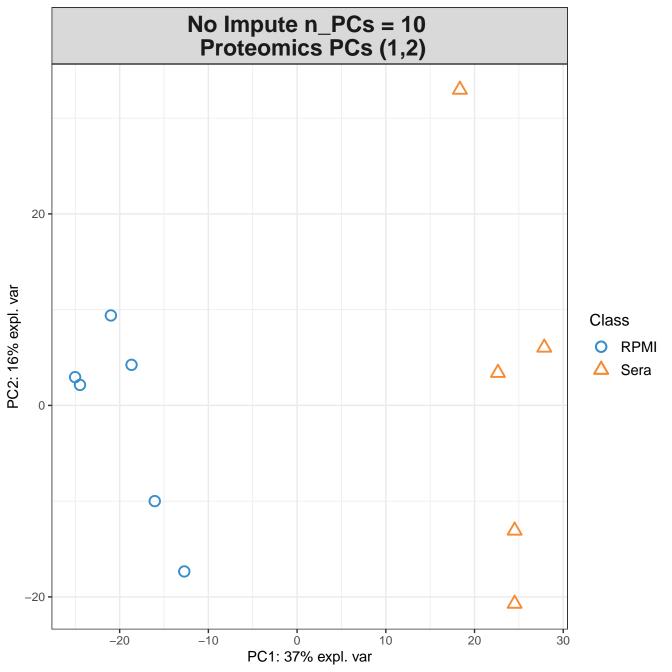


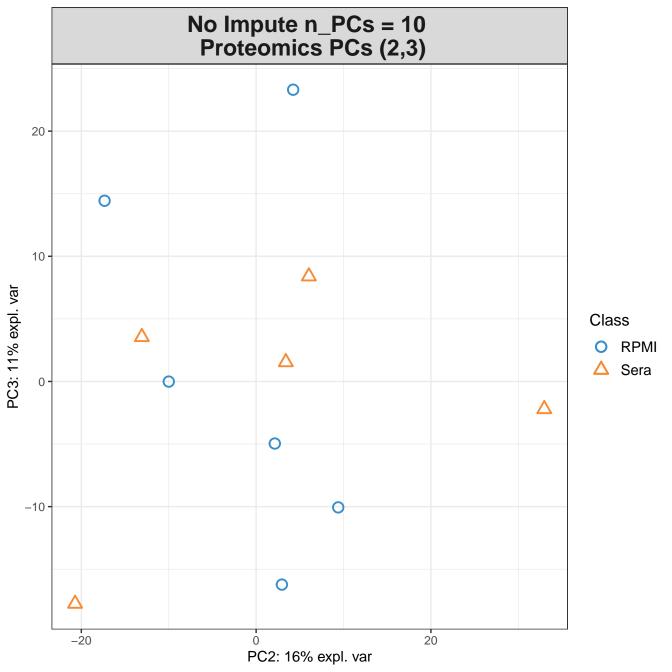


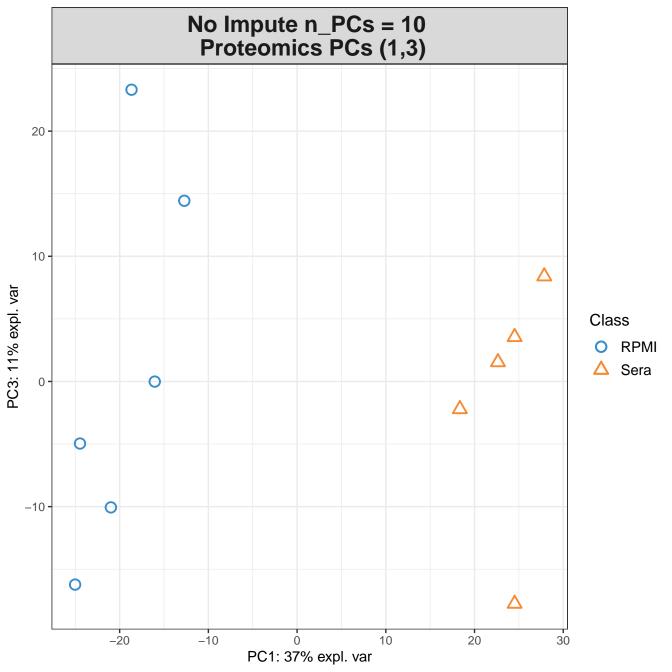


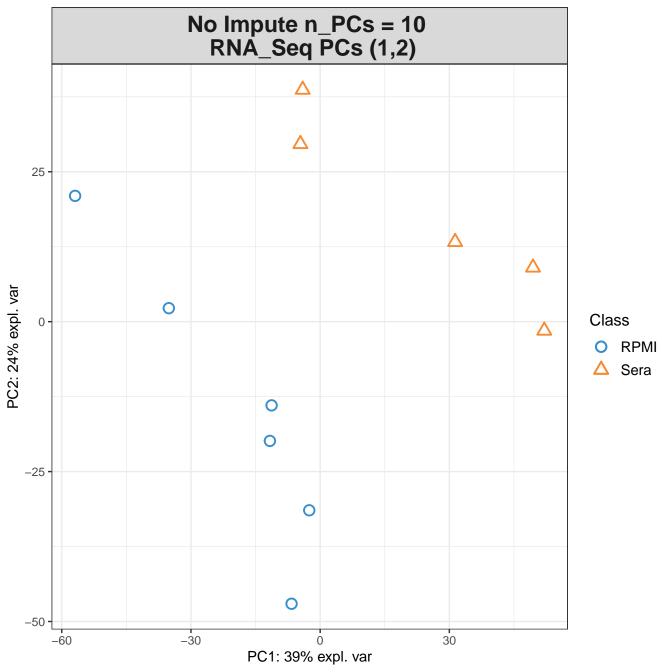


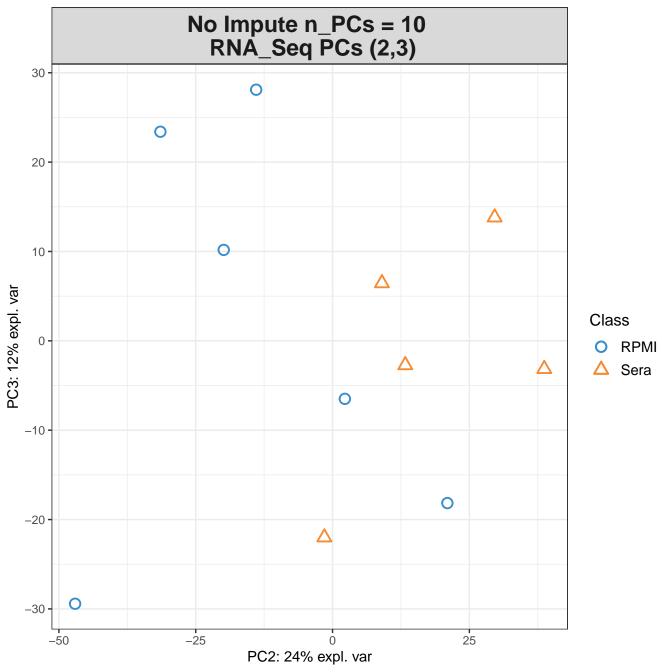


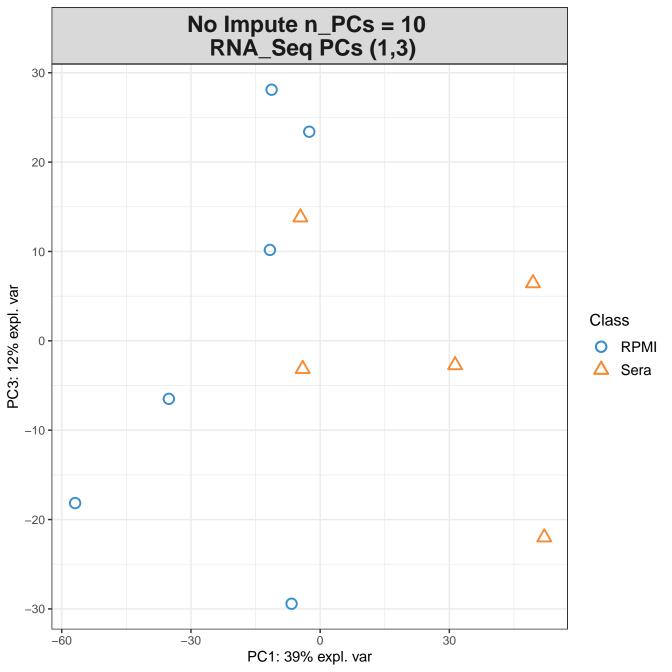




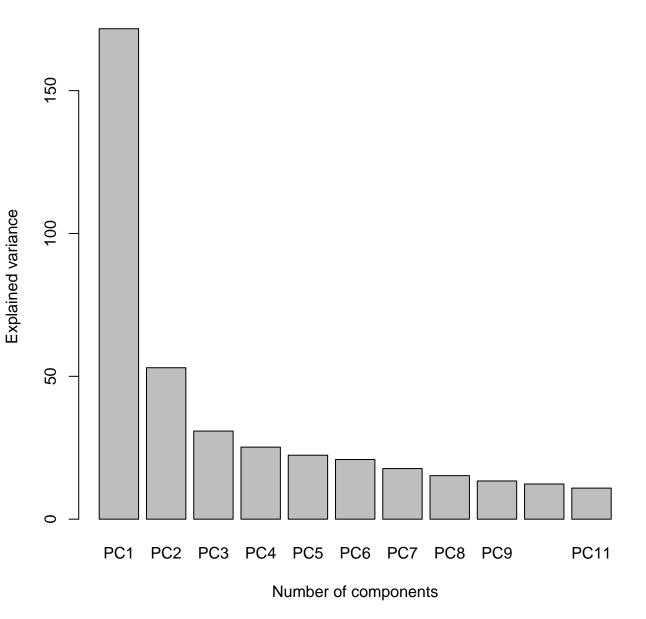




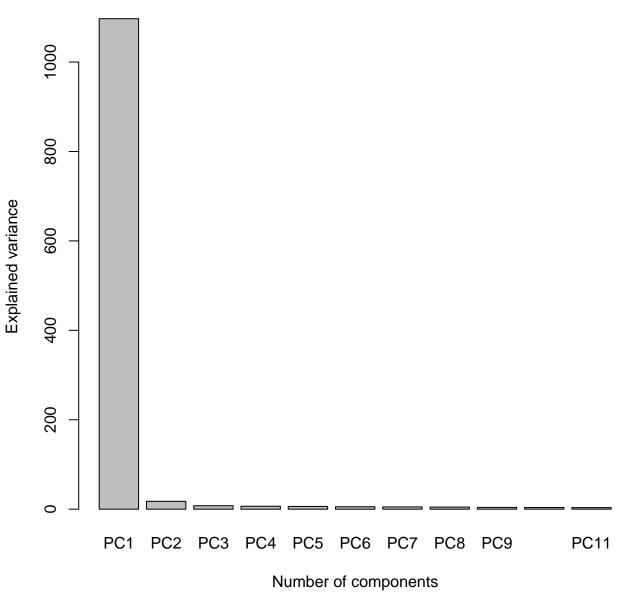




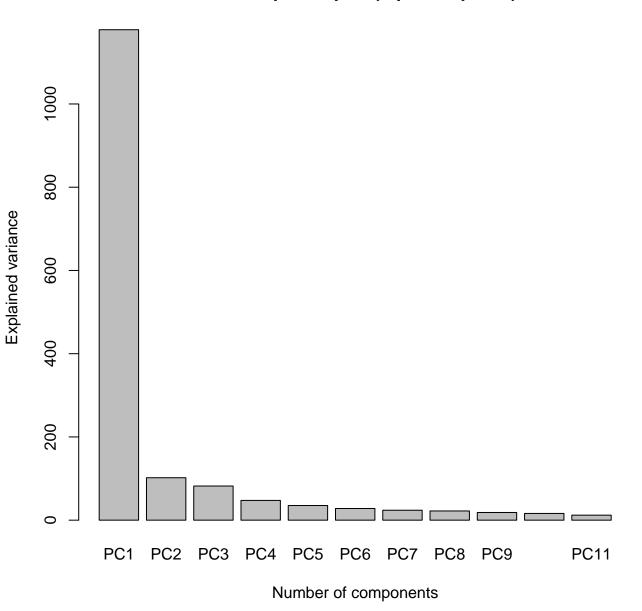
Metabolomics Screeplot (nipals imputed)



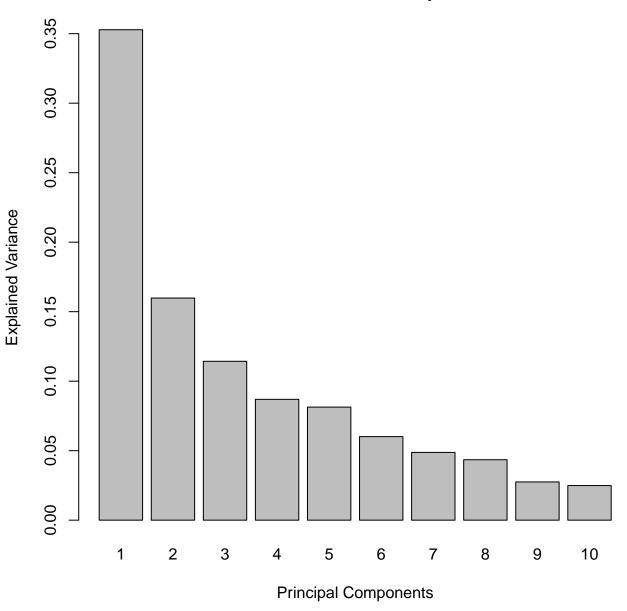
Proteomics Screeplot (nipals imputed)



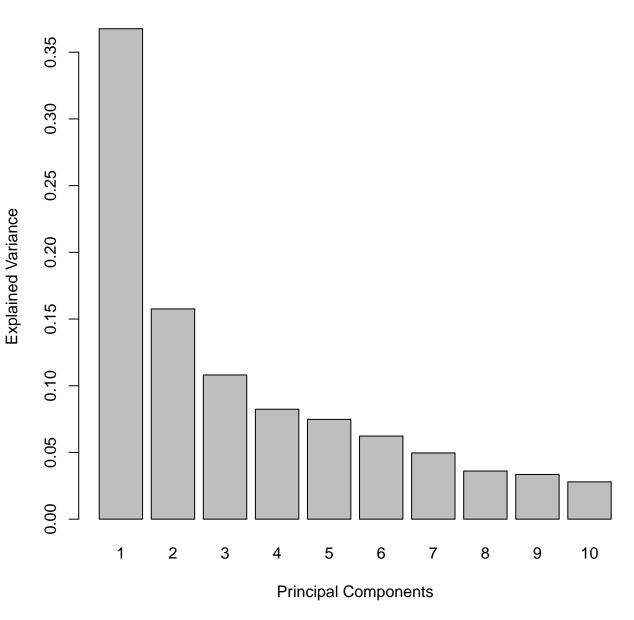
RNA_Seq Screeplot (nipals imputed)



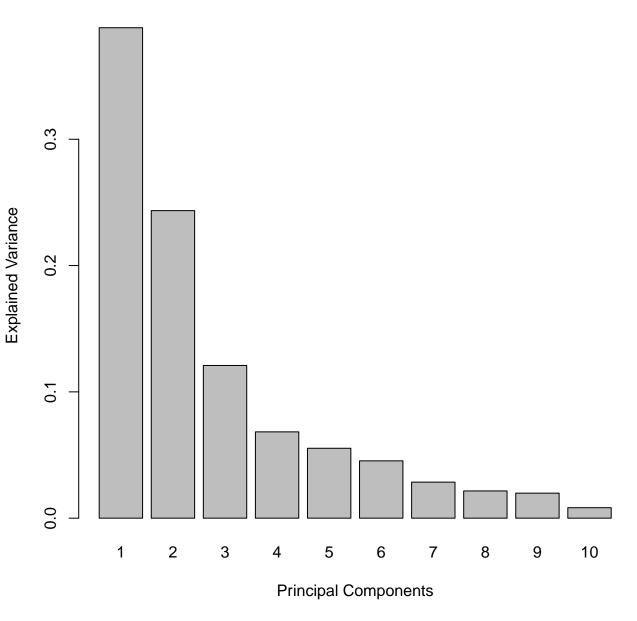
Metabolomics screeplot

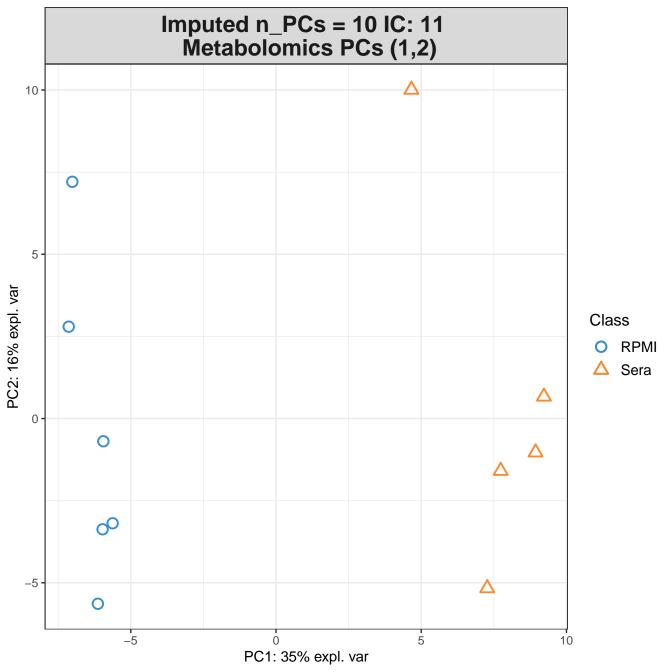


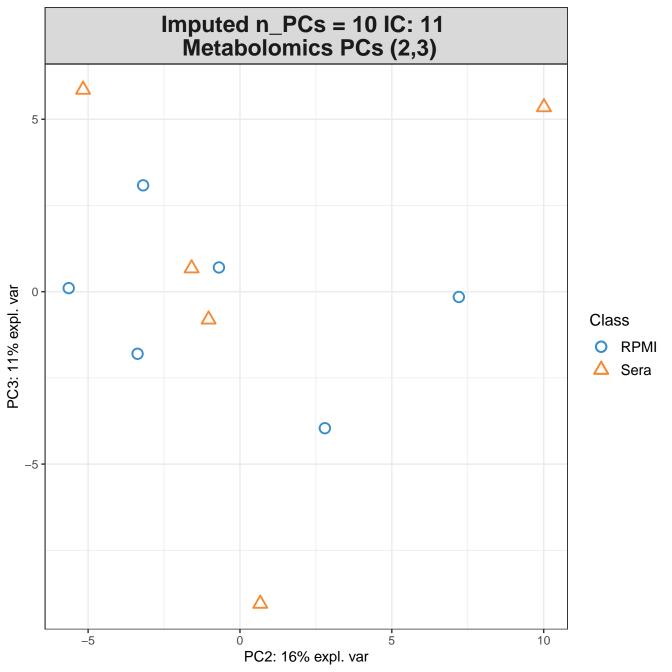
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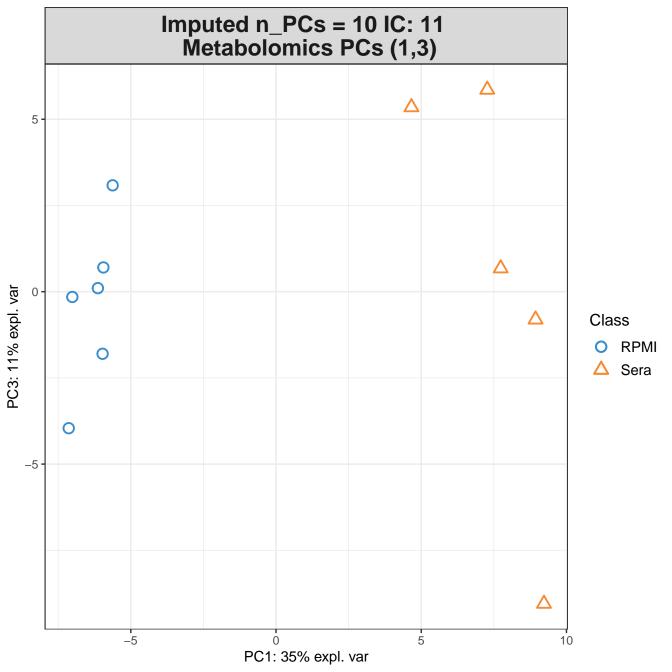


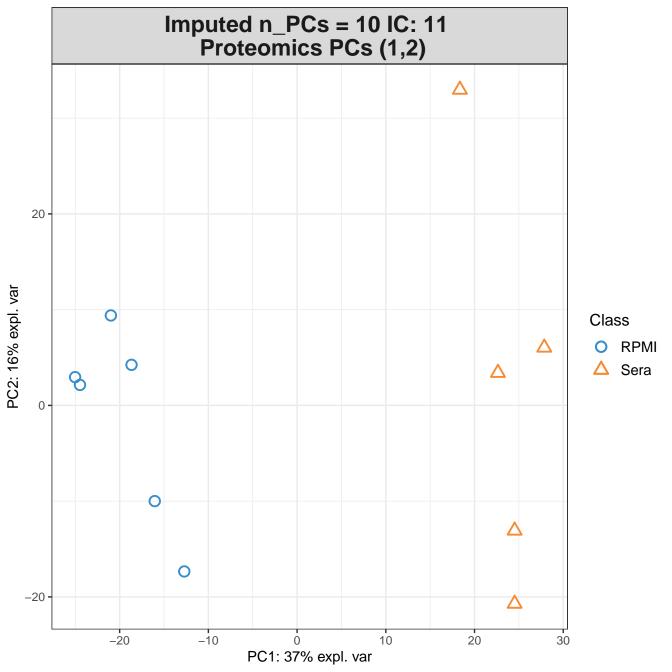


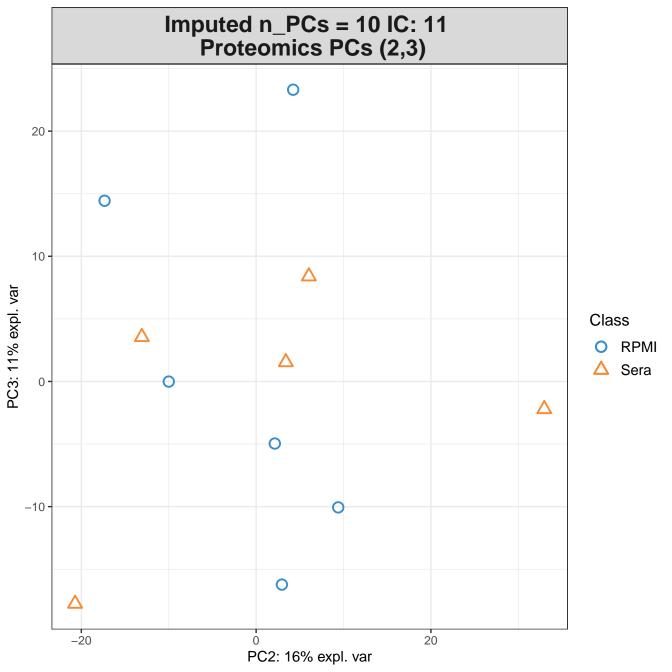


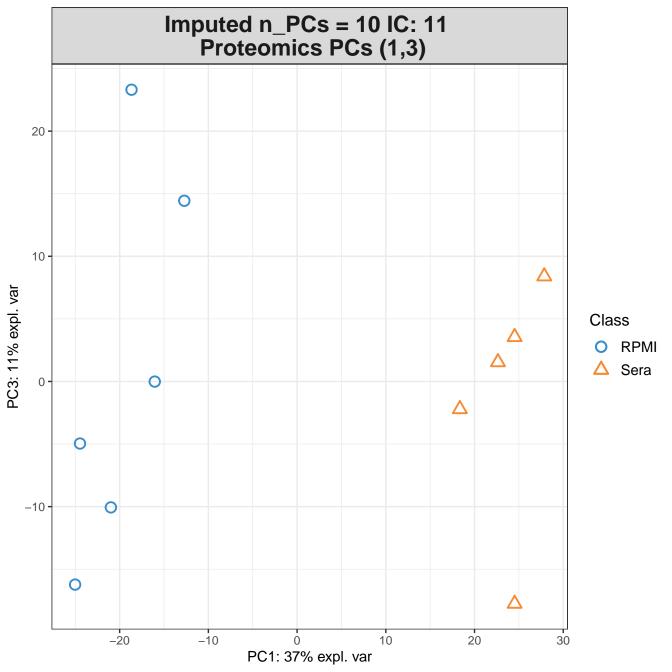


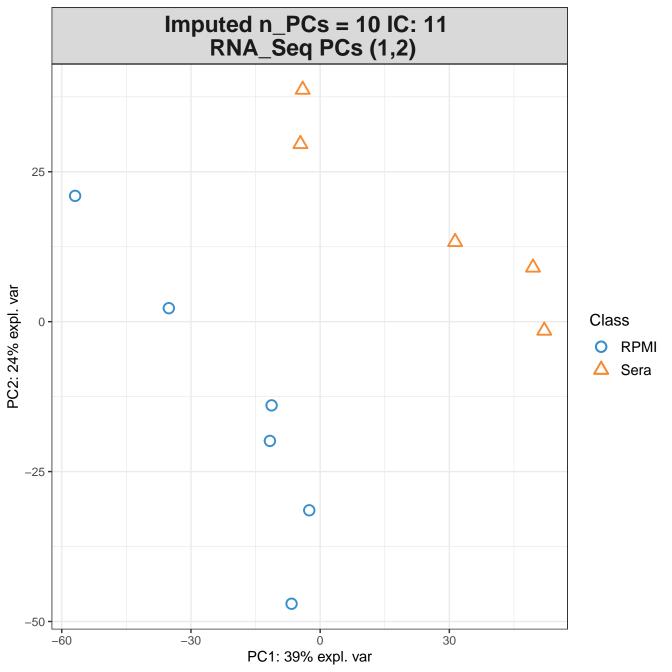


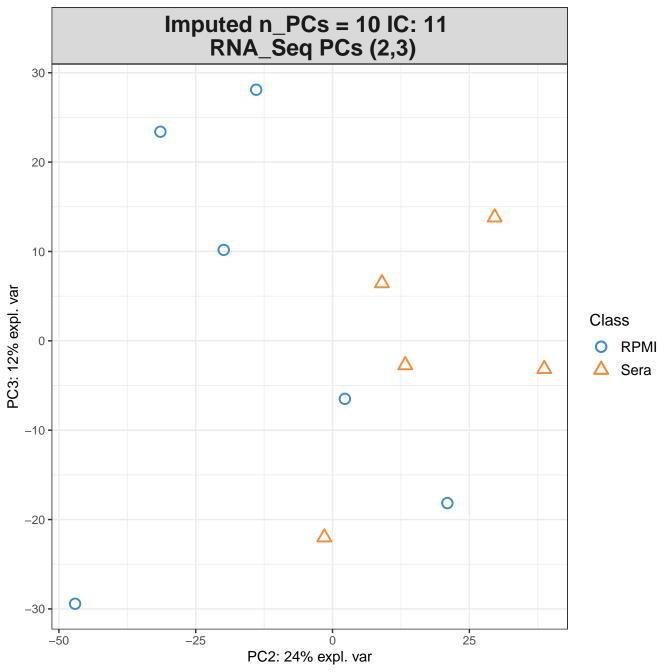


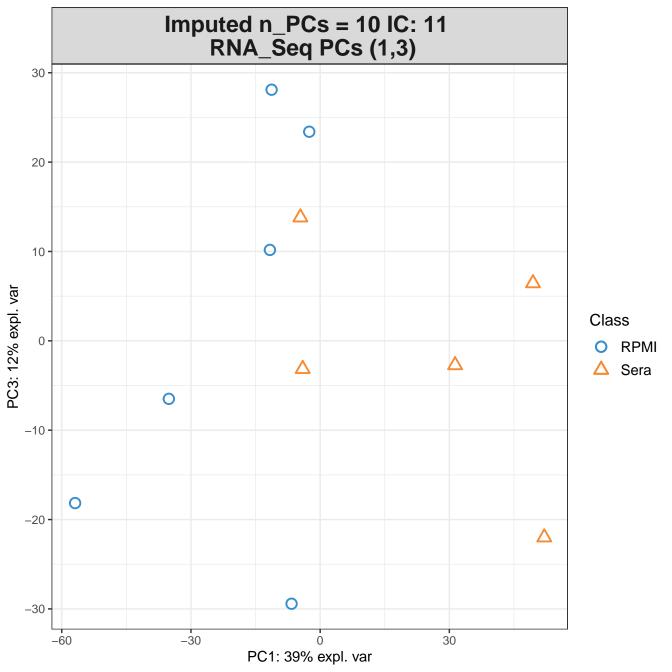


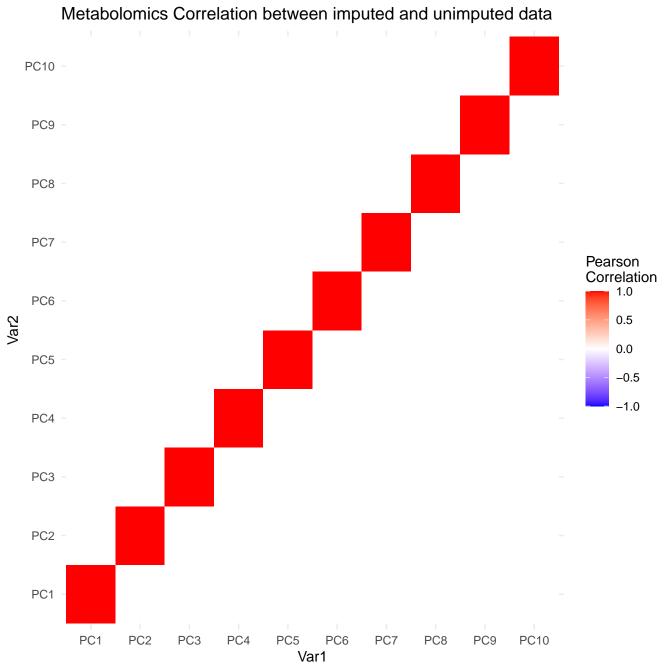


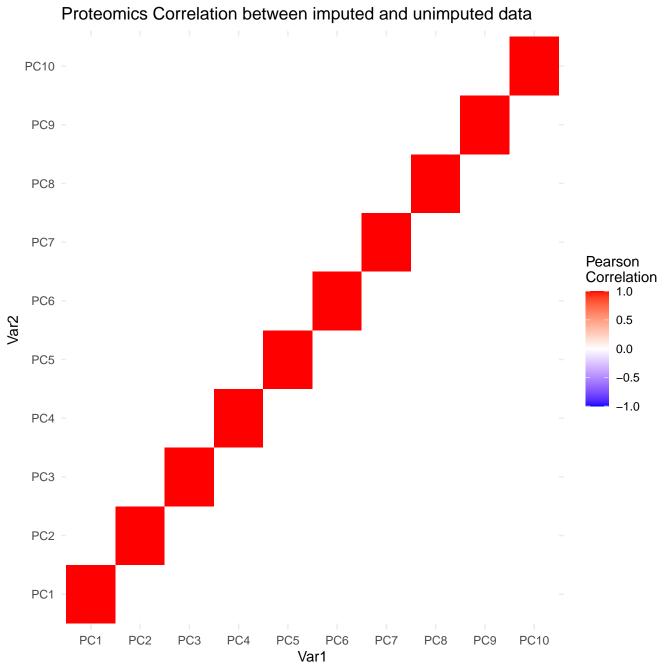


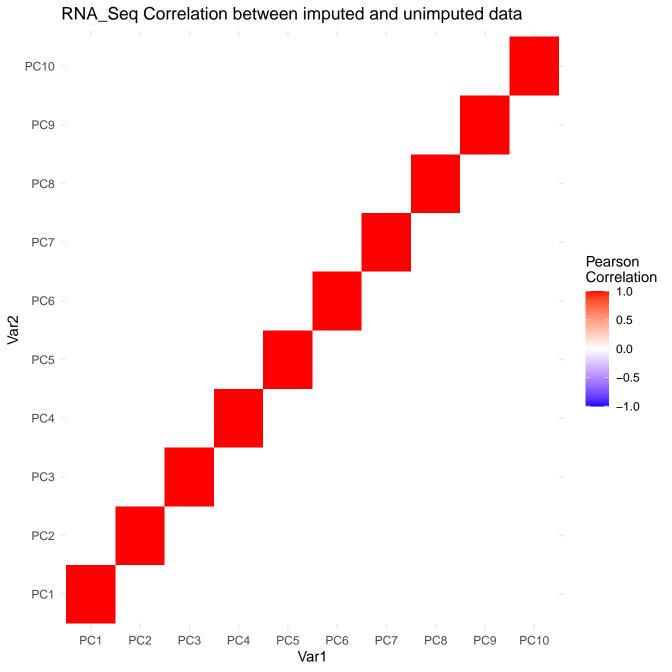




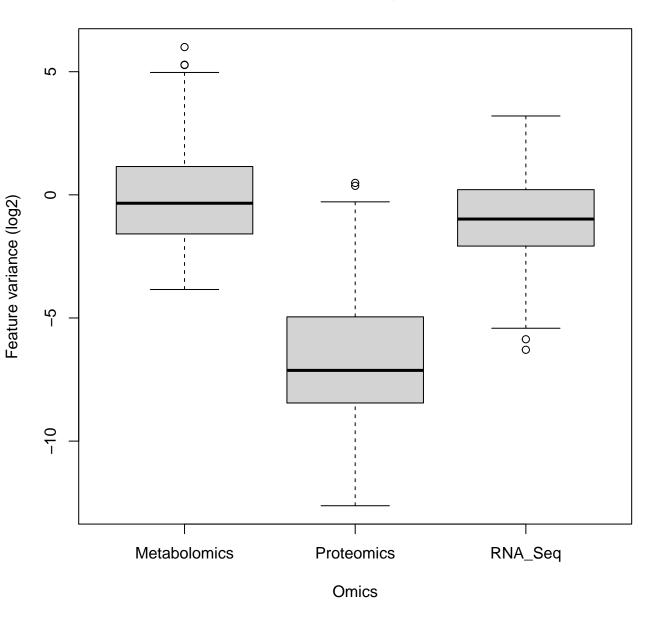


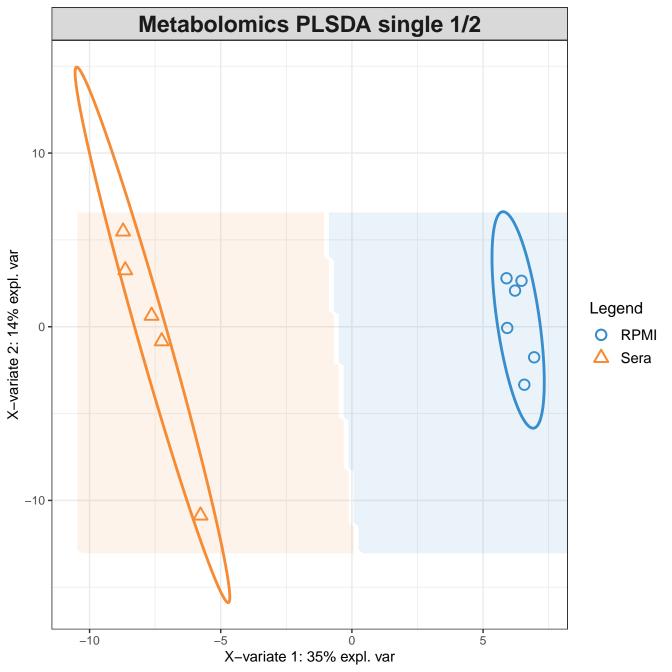


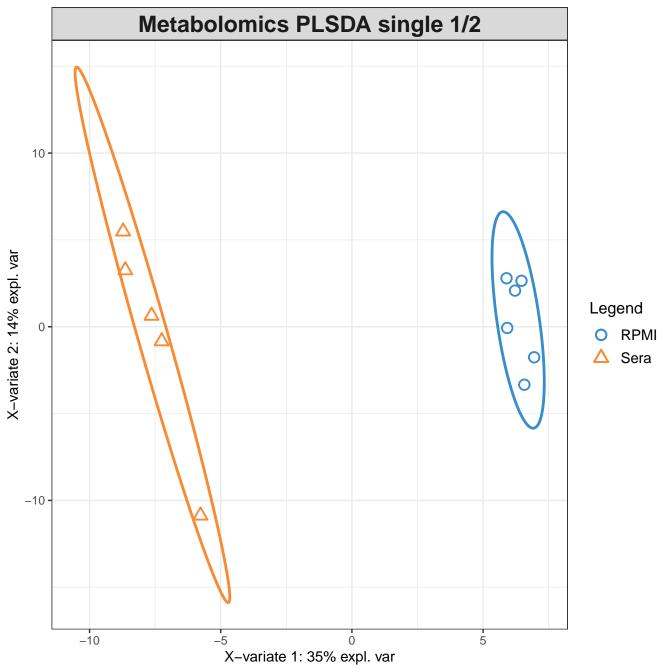


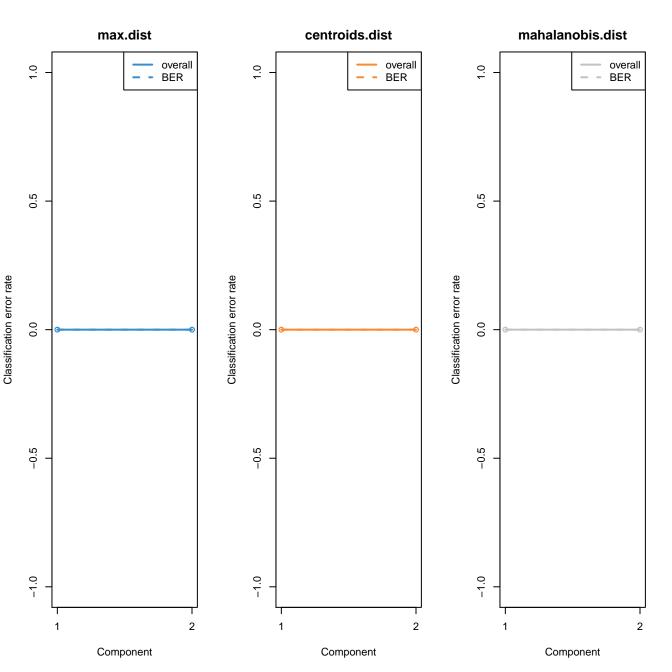


Feature variances (log2) per omics

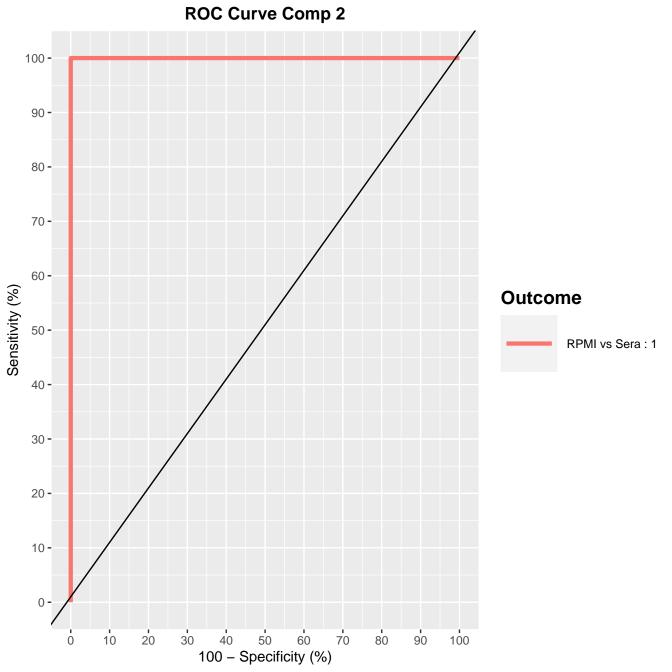


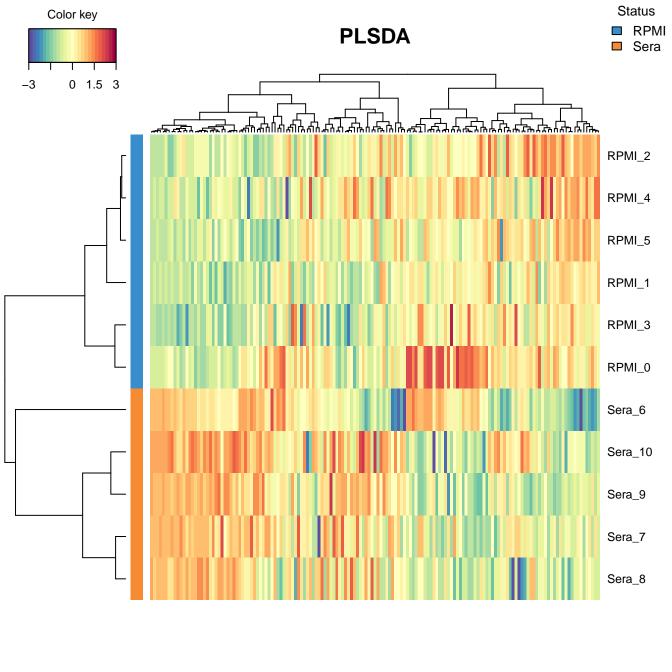


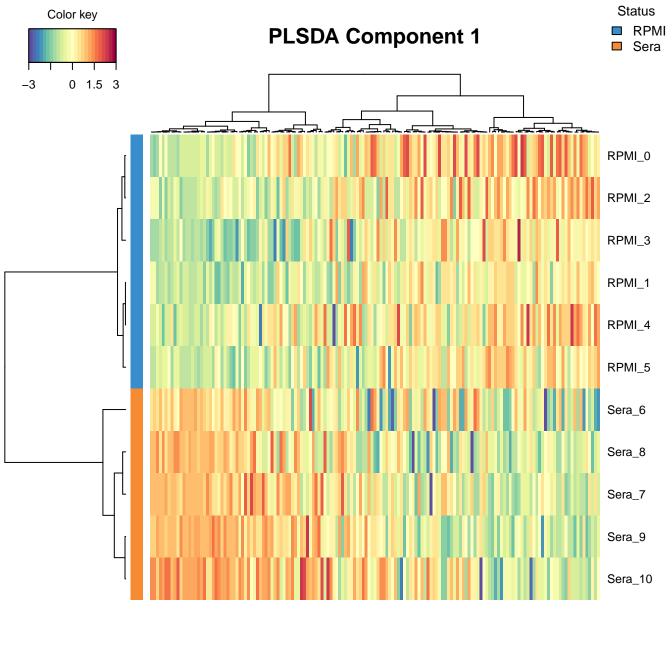




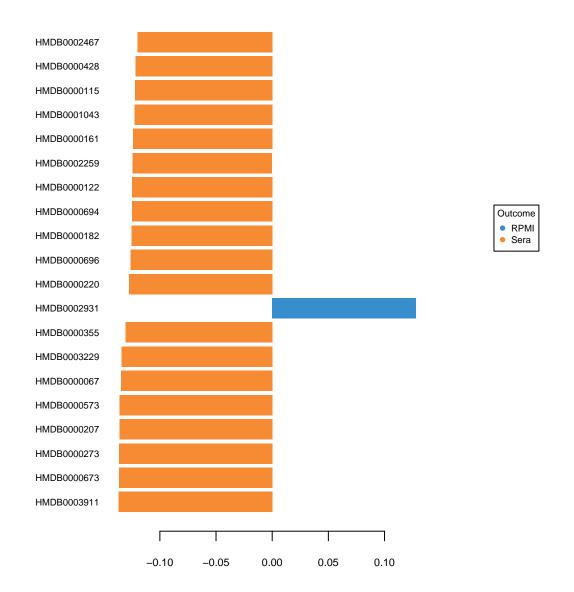




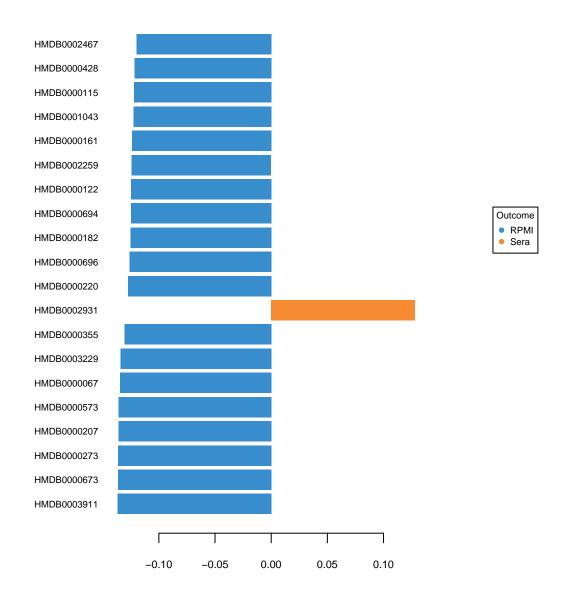


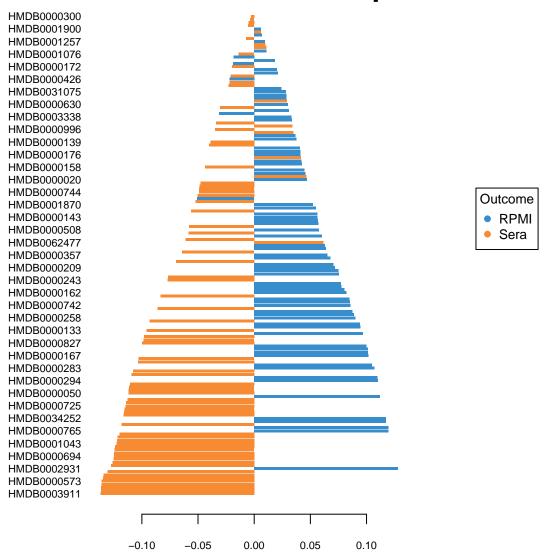


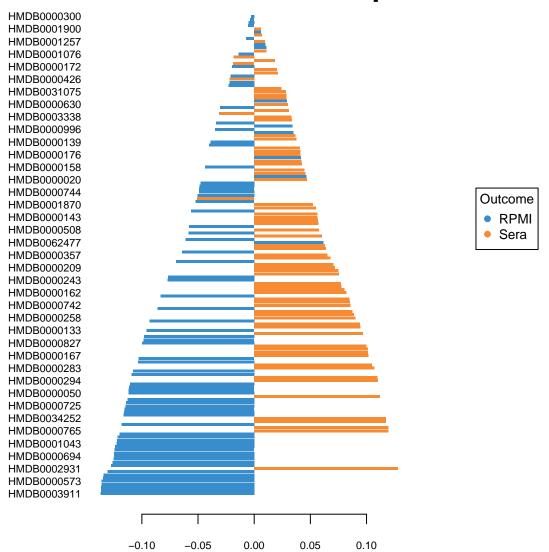
Metabolomics 1 PLSDA max load

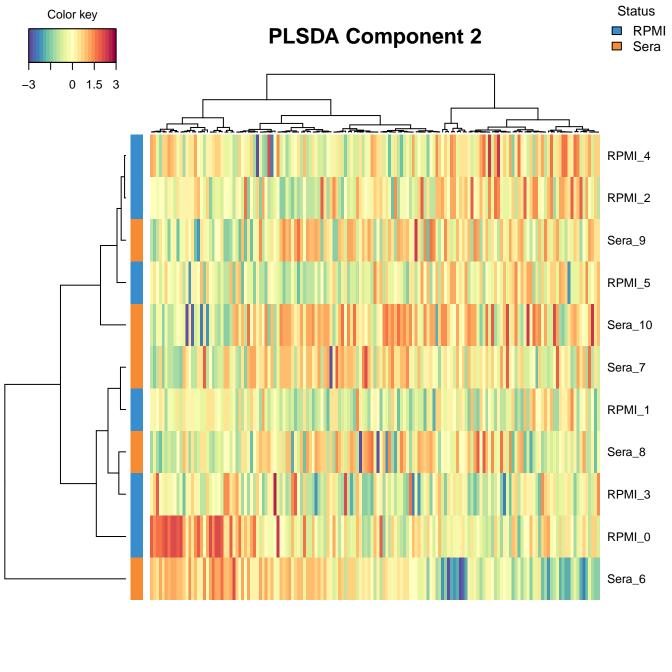


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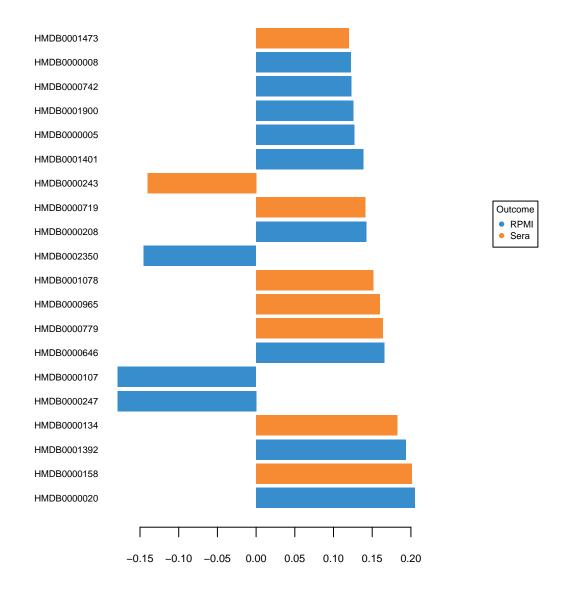




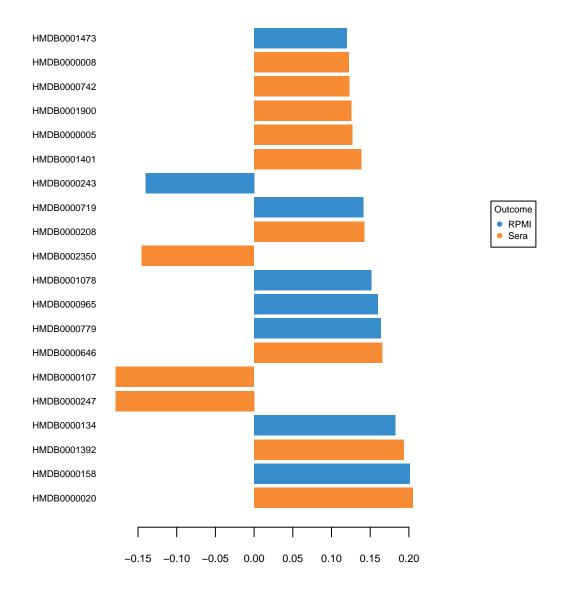


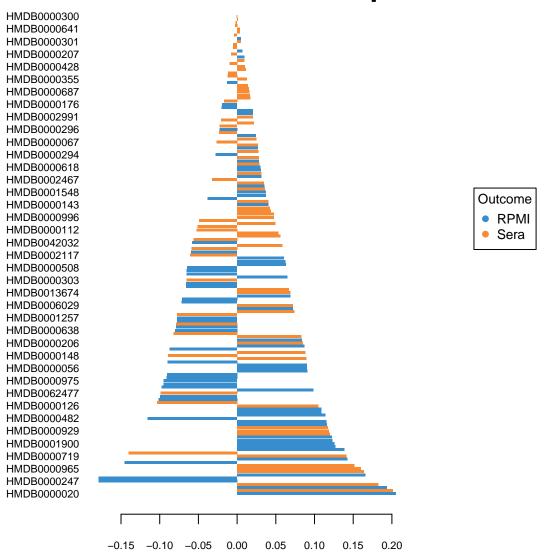


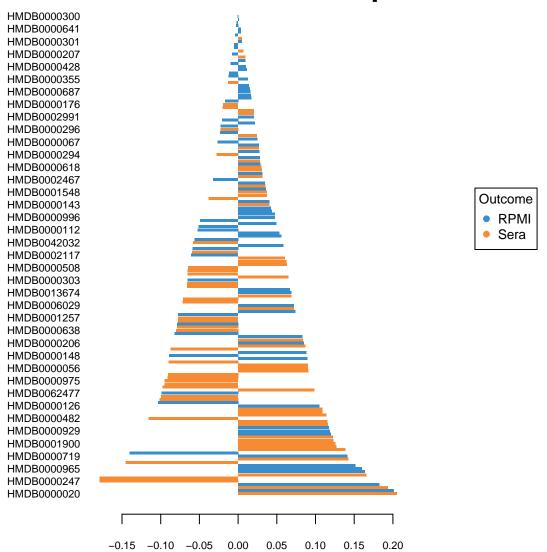
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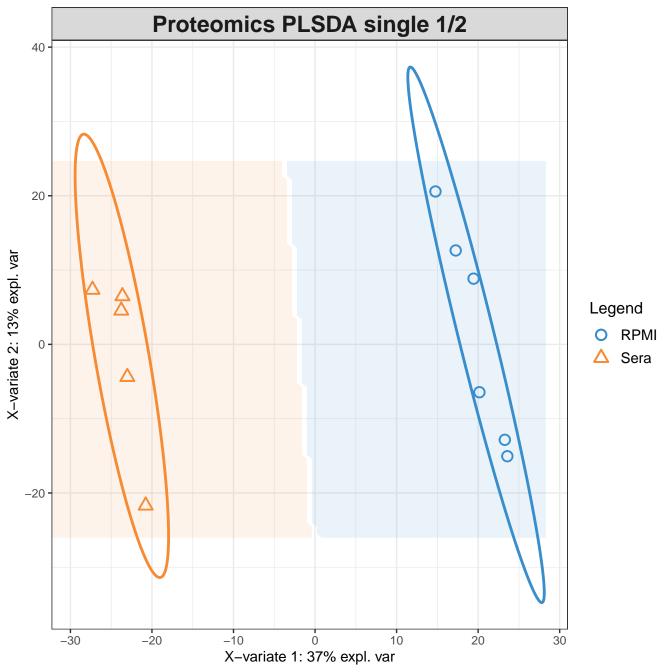


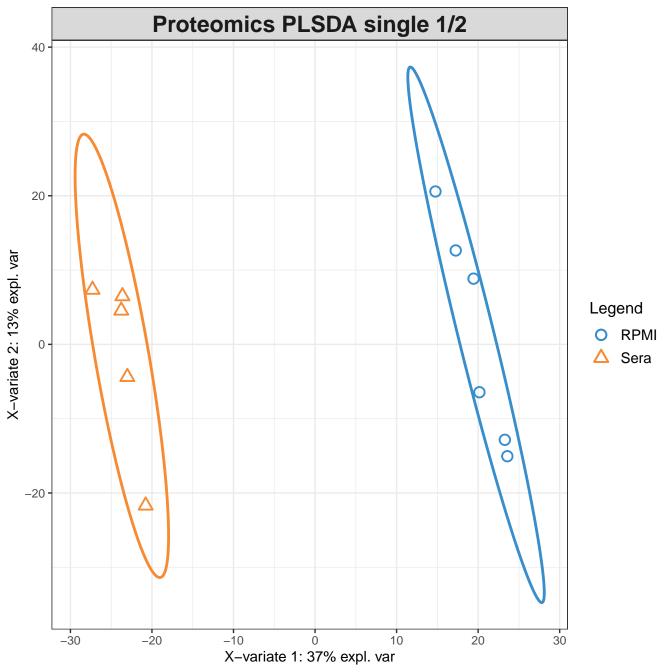
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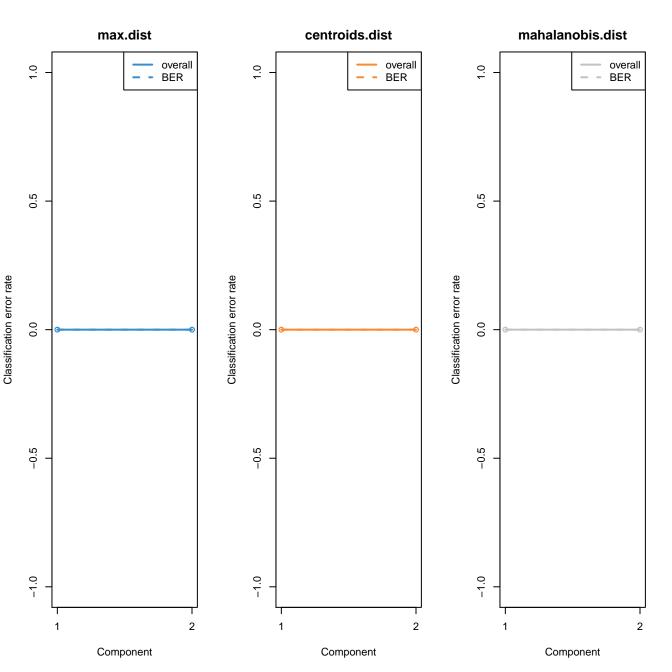




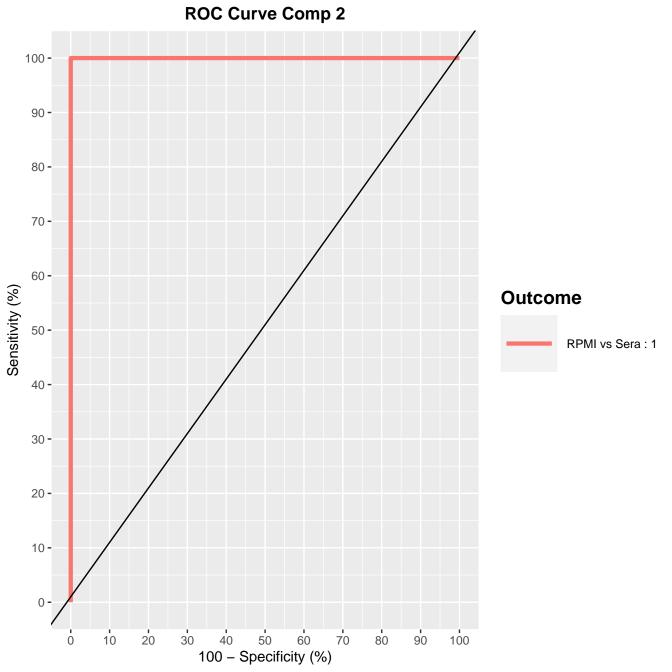


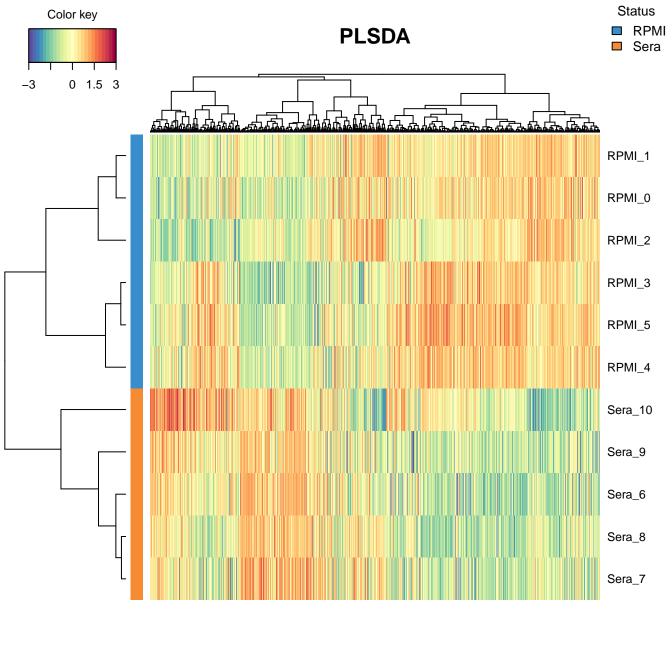


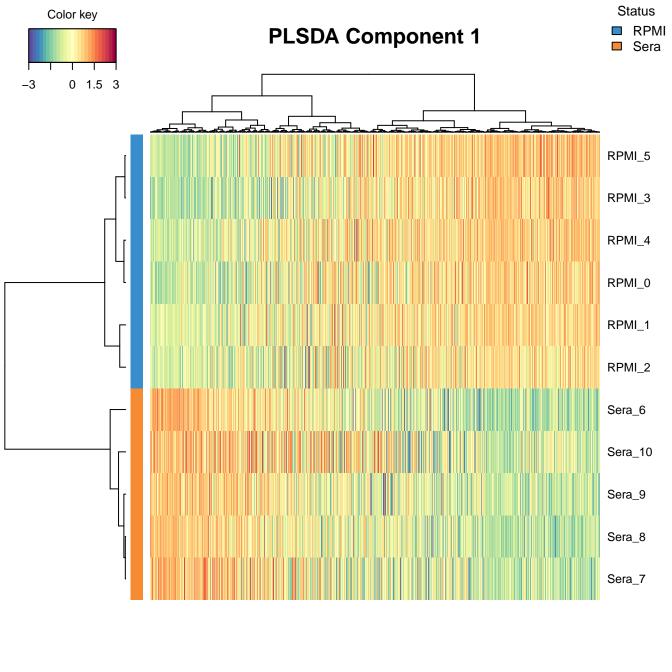




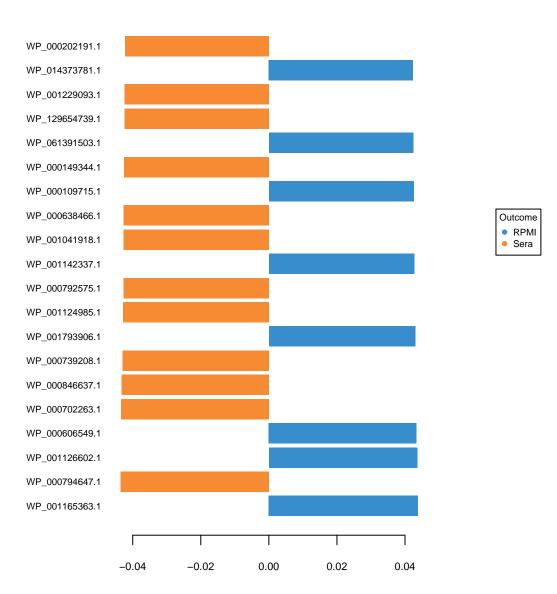




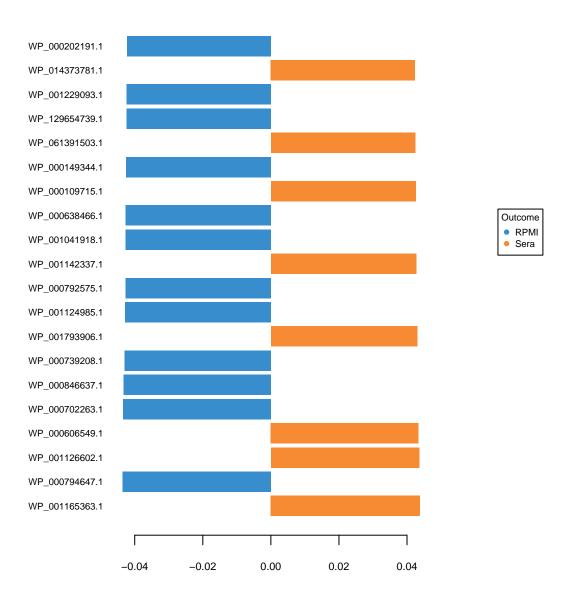


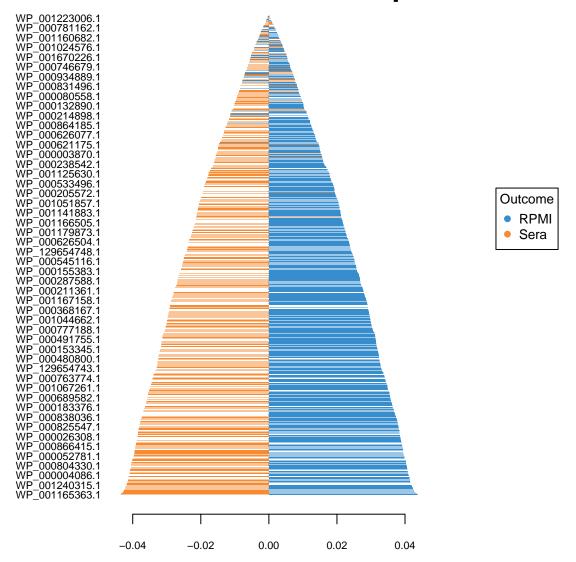


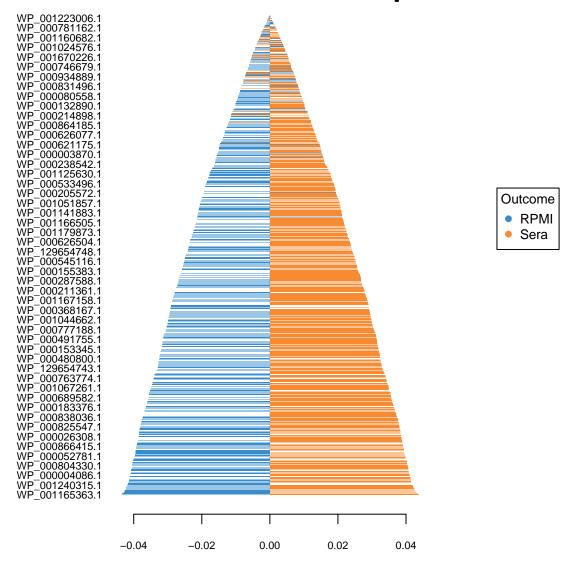
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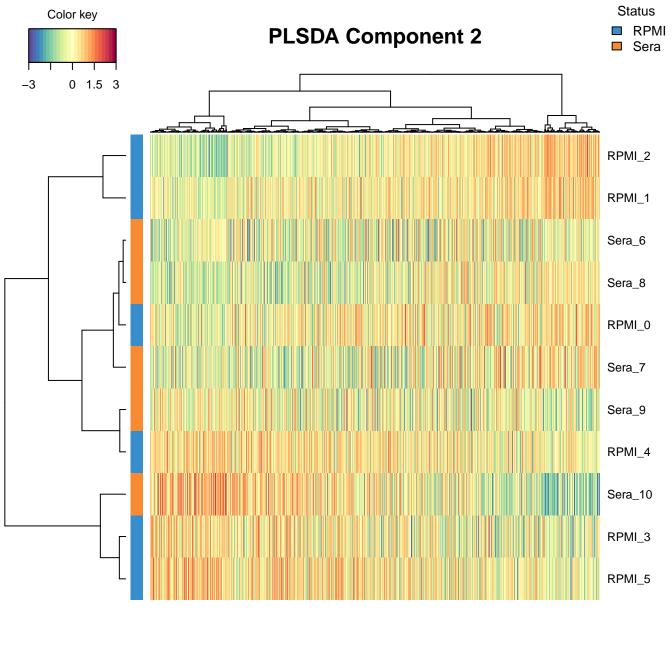


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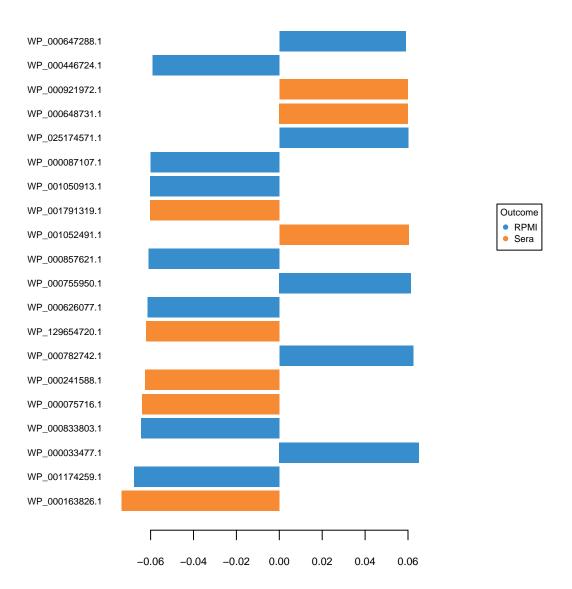




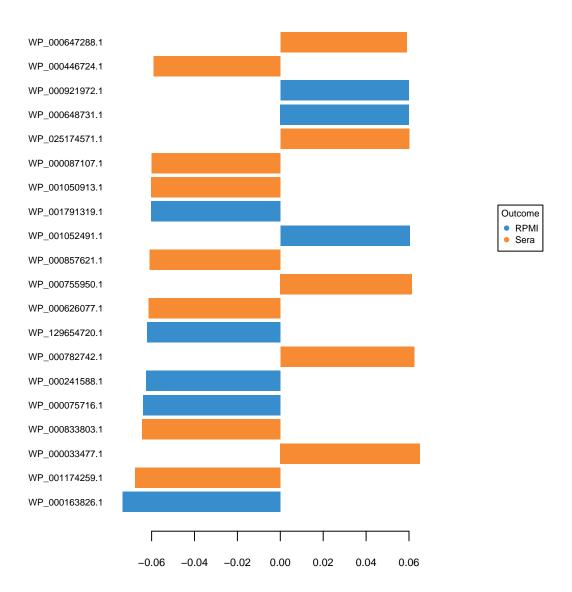


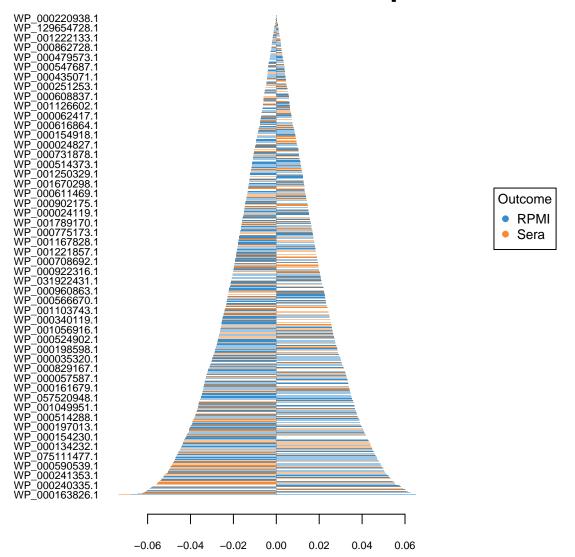


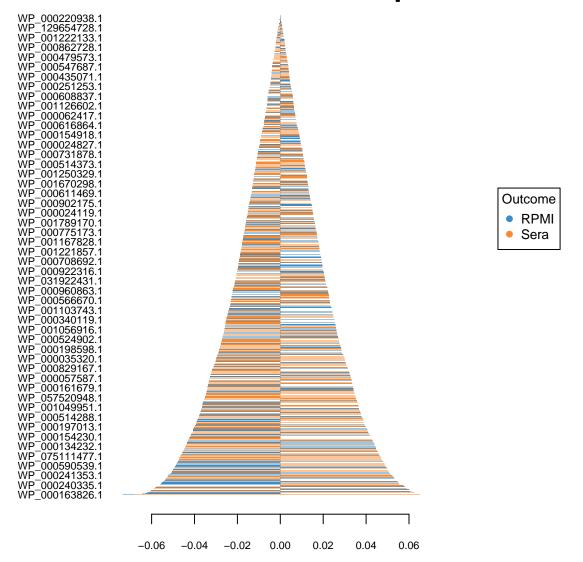
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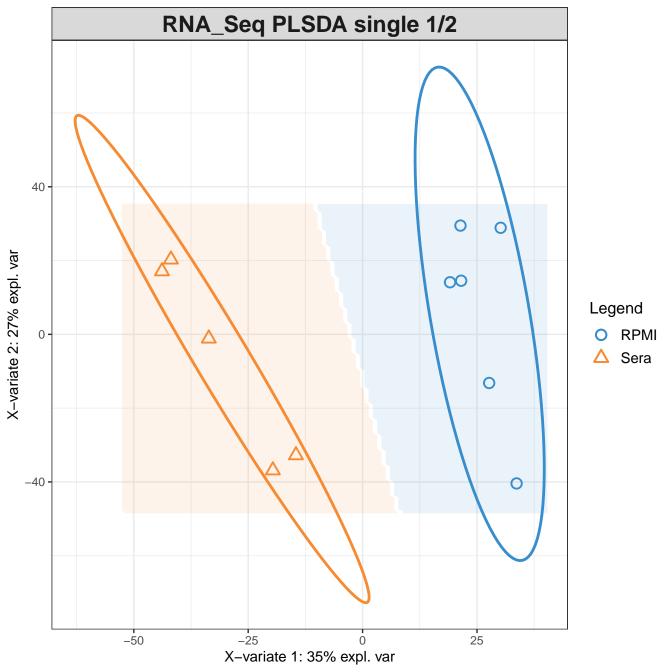


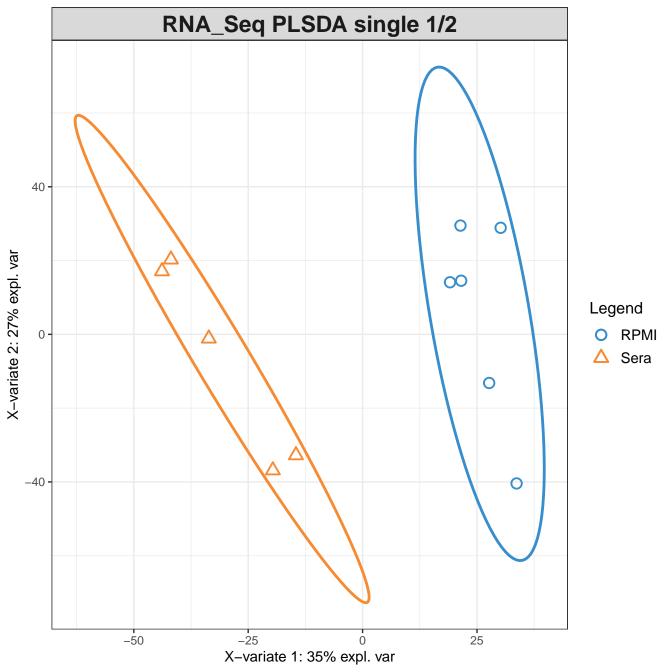
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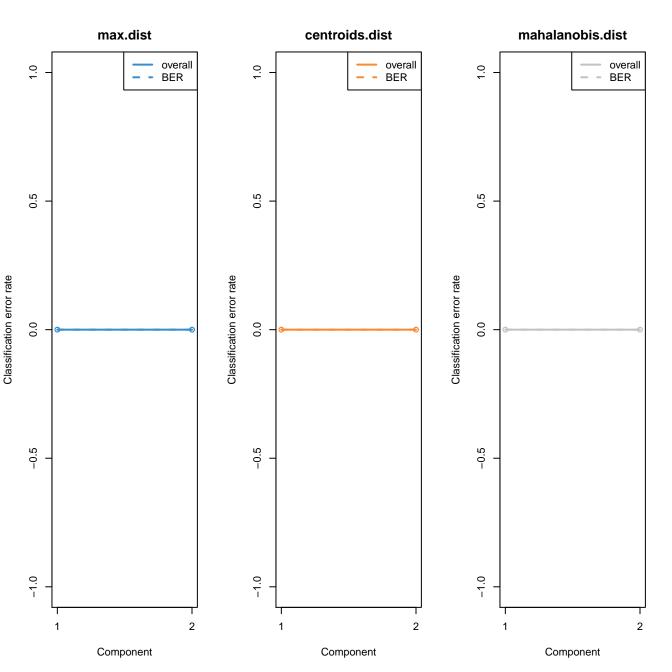




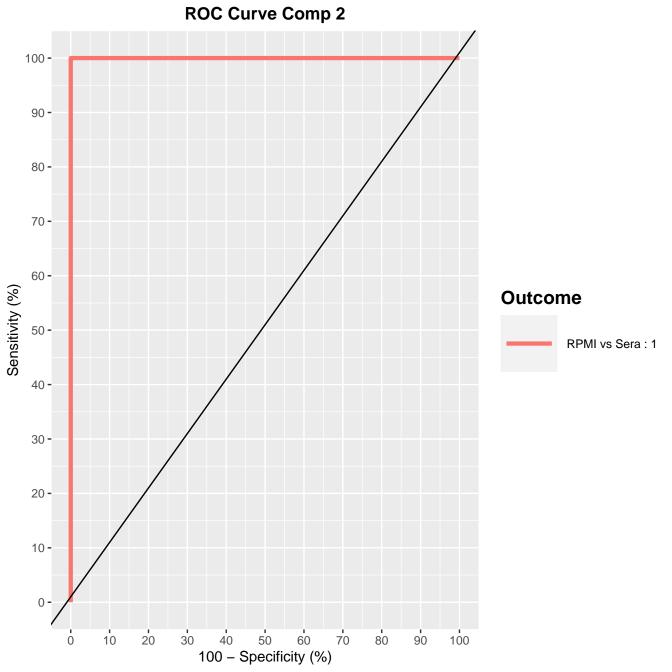


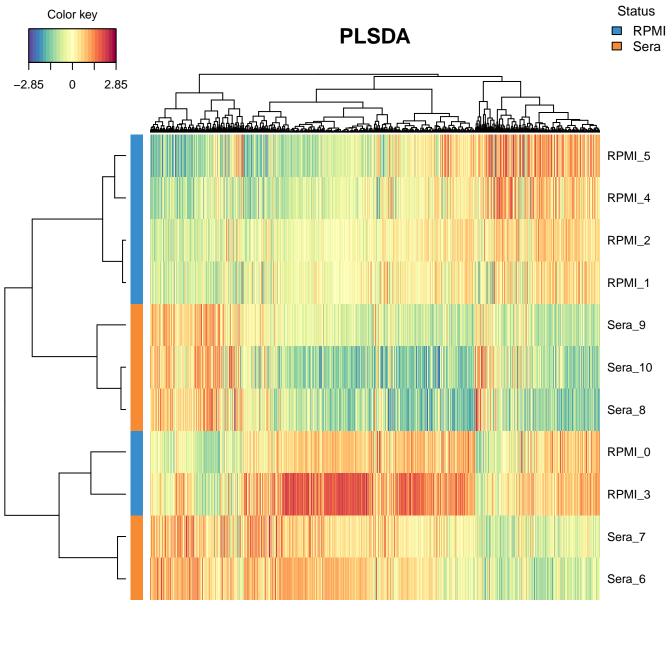


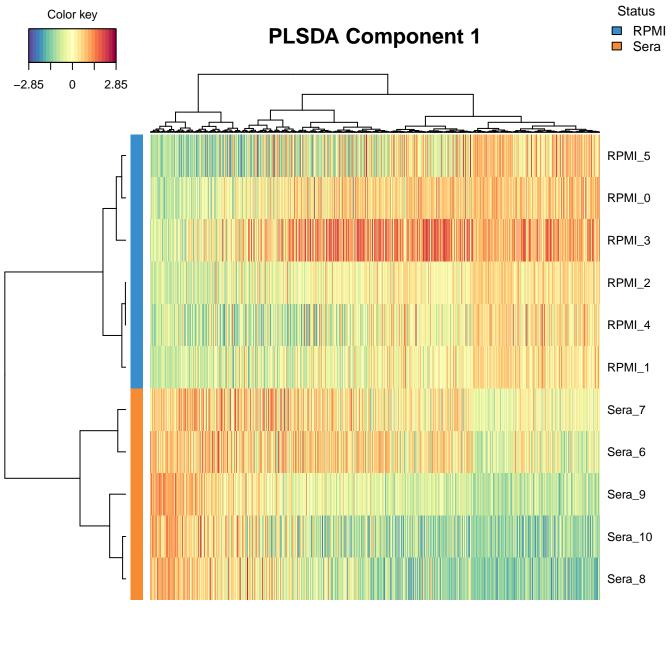




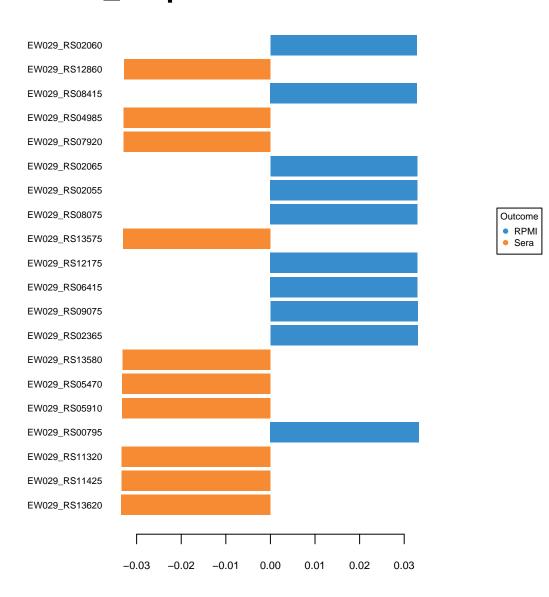




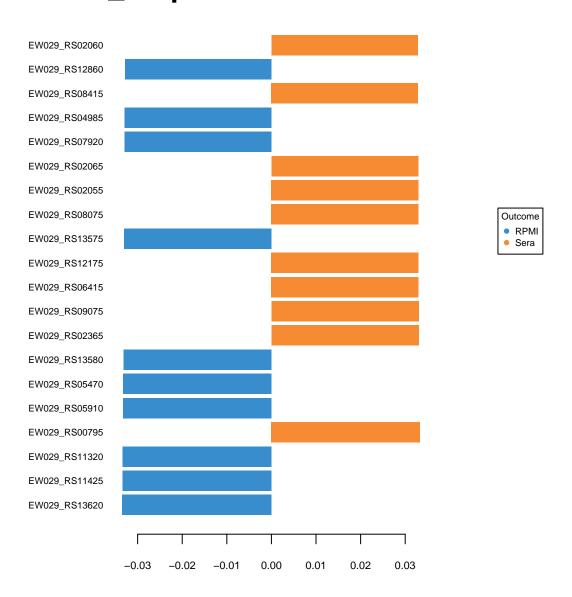


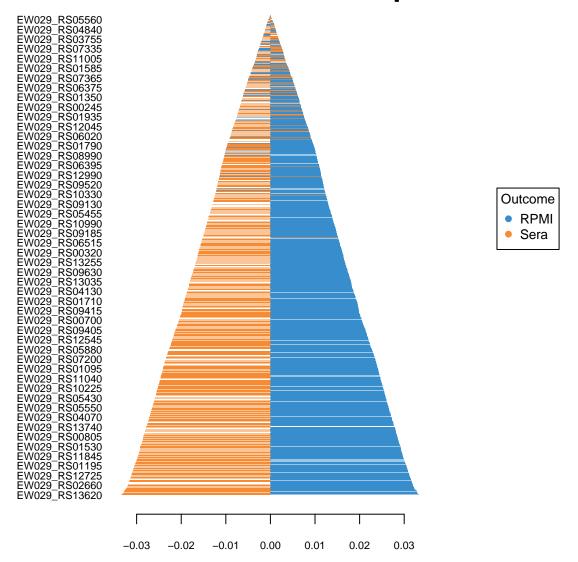


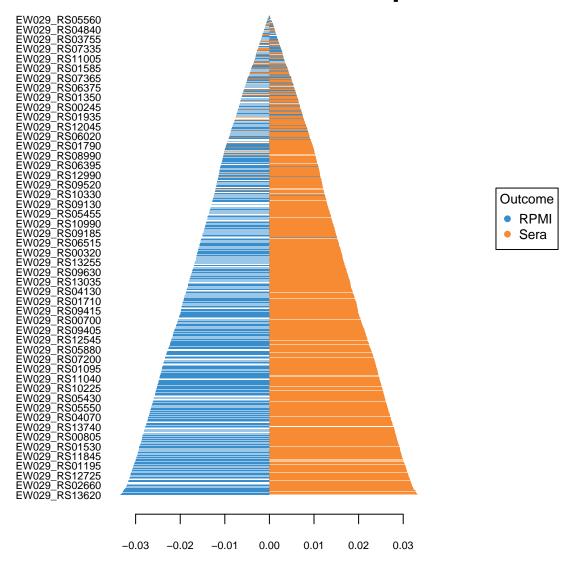
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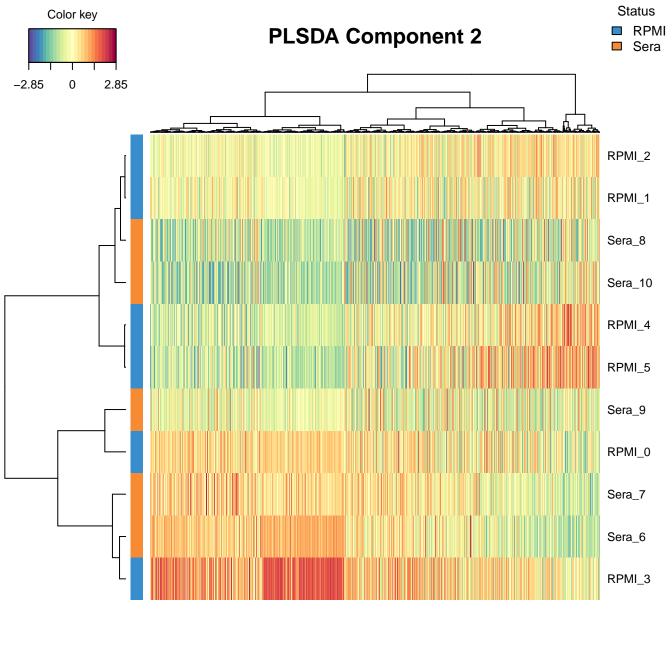


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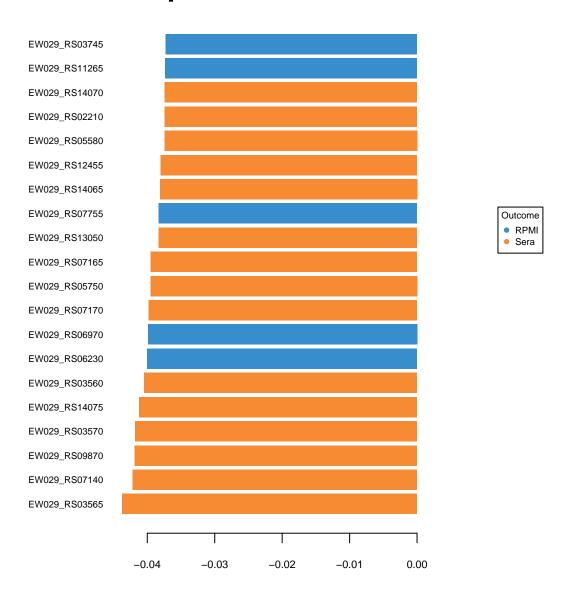




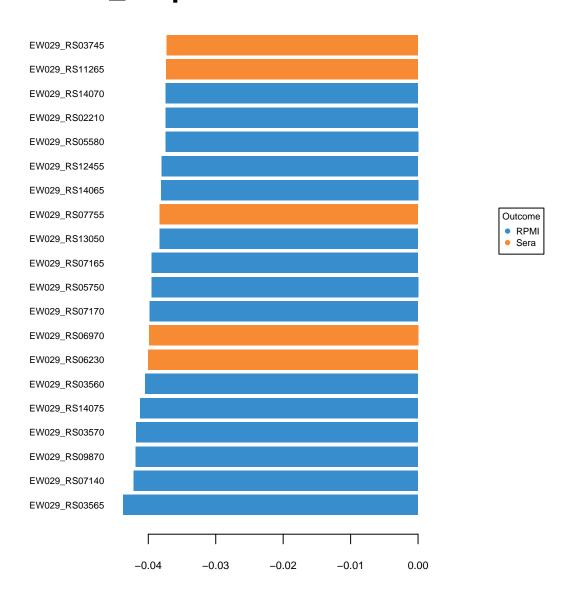


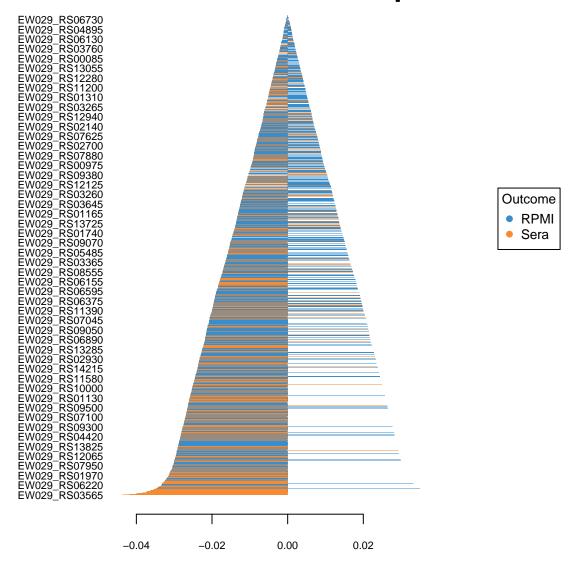


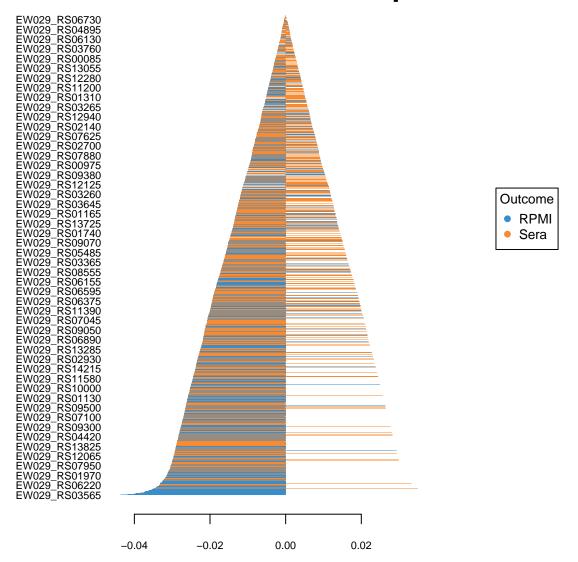
RNA_Seq 2 PLSDA max loadir

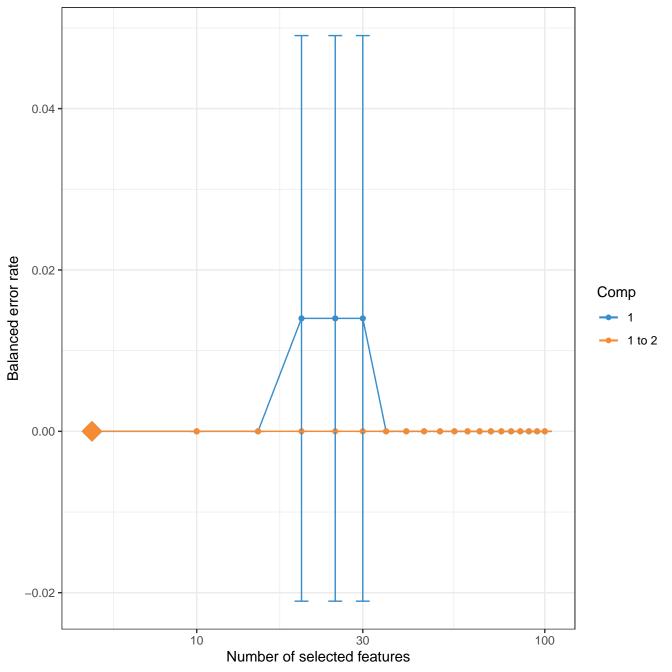


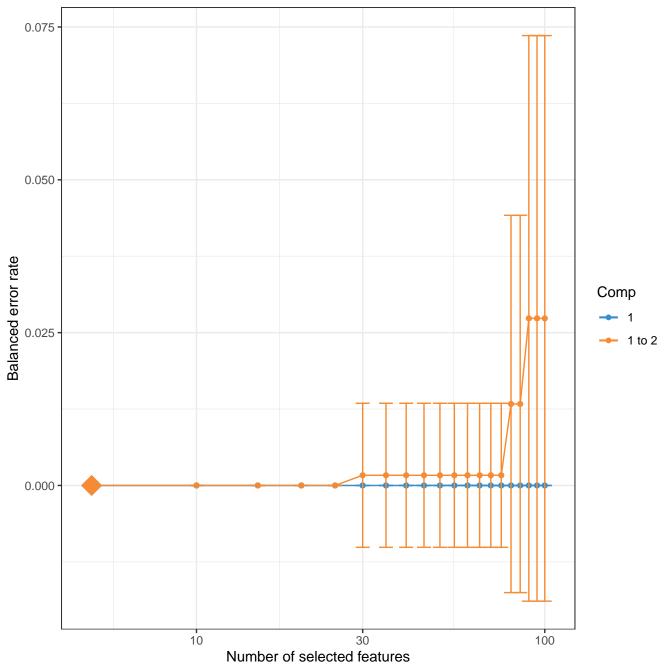
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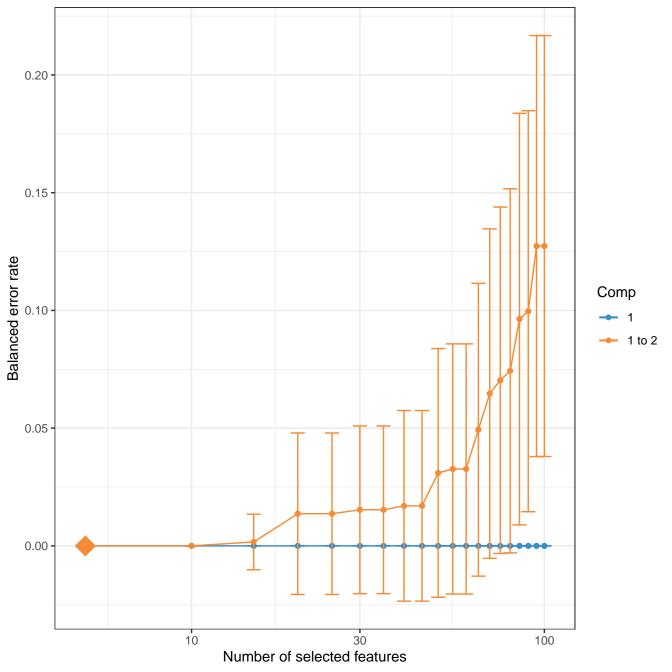


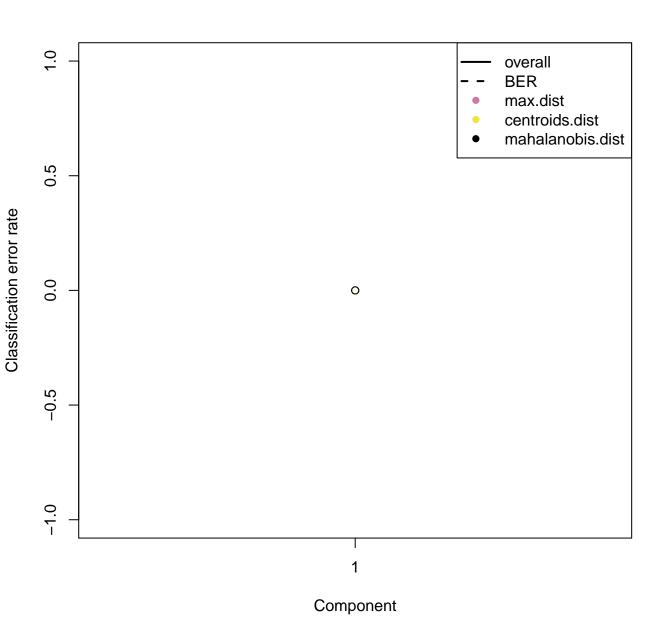




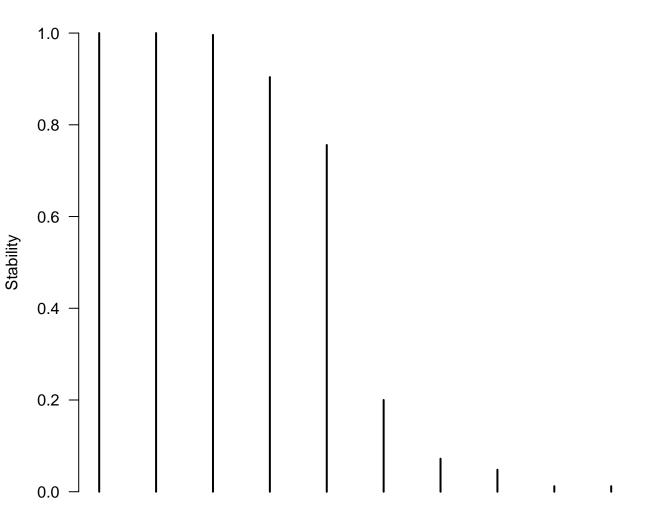






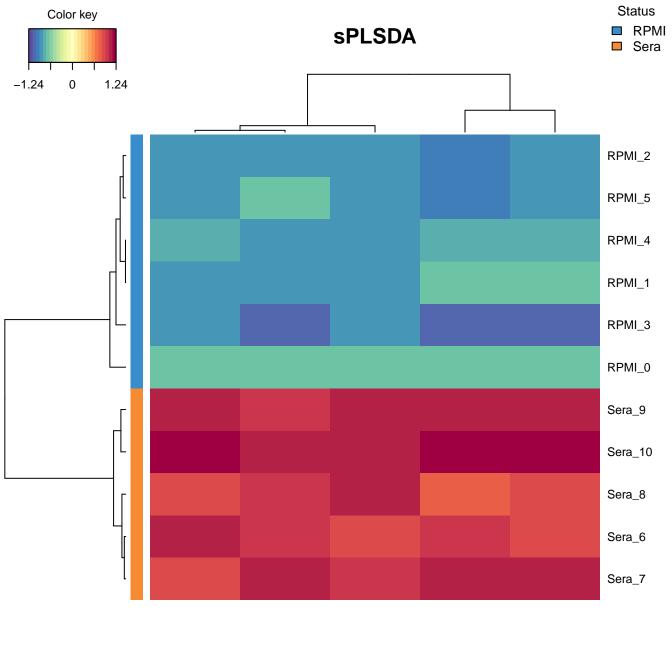


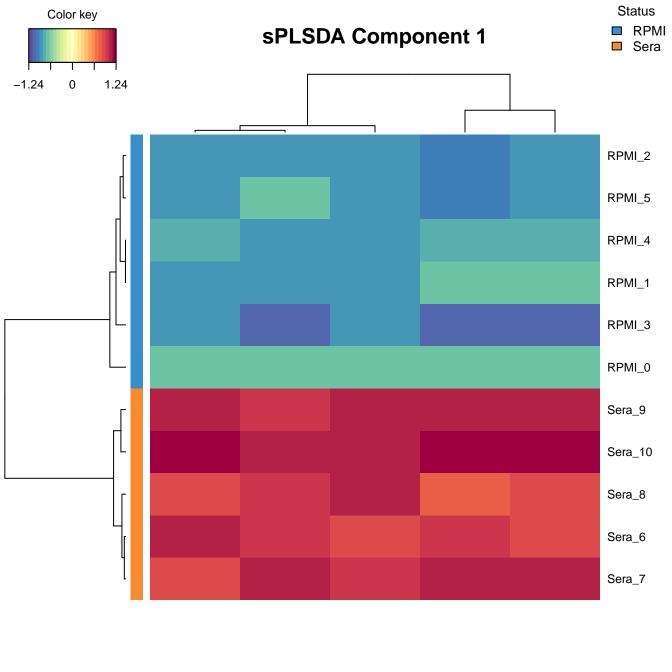




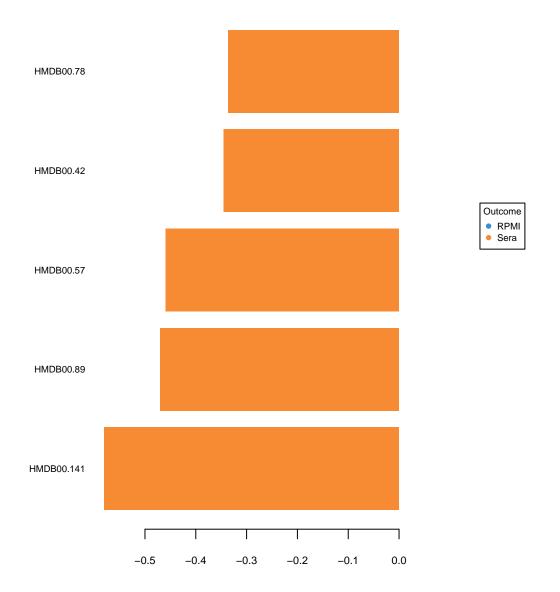
Features



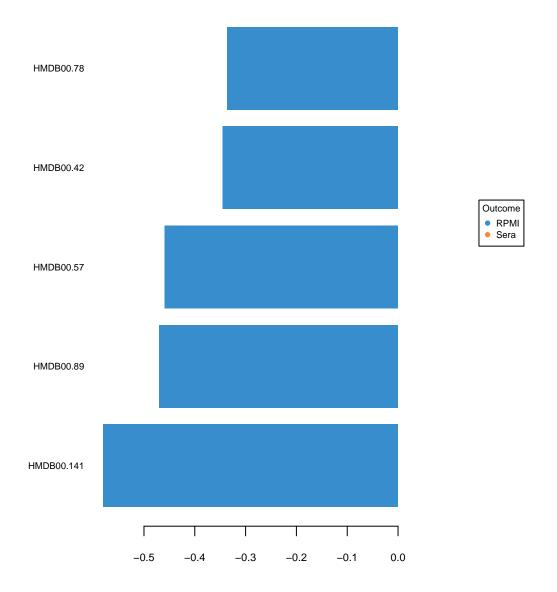


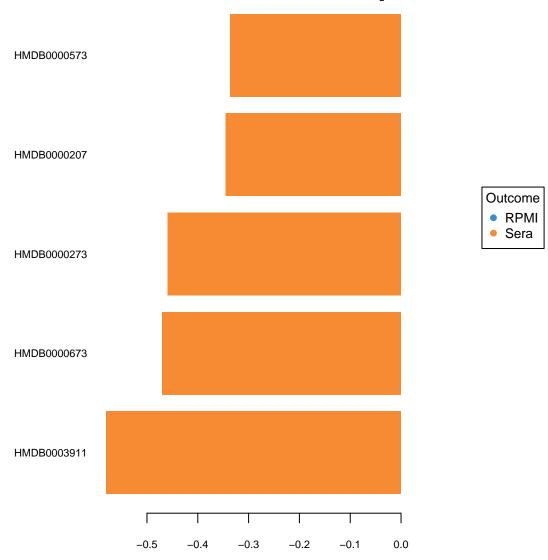


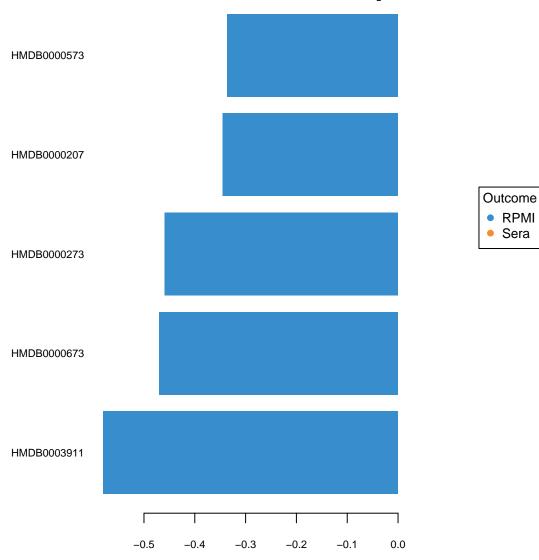
Metabolomics 1 sPLSDA max loa

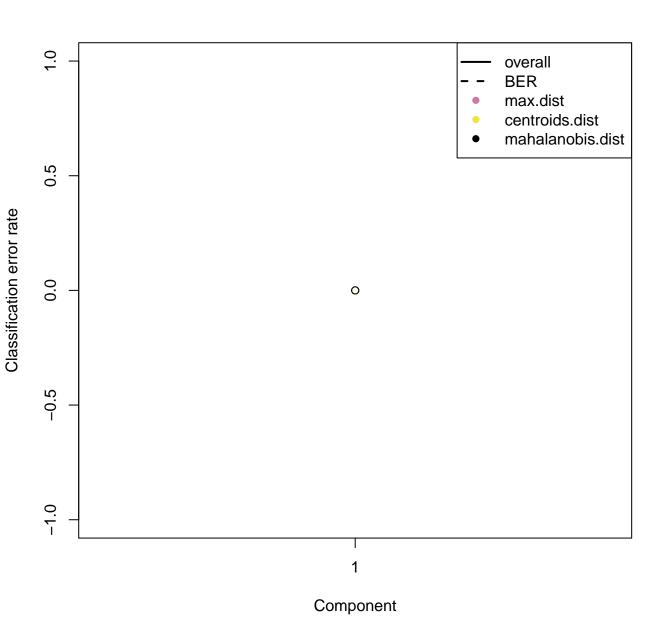


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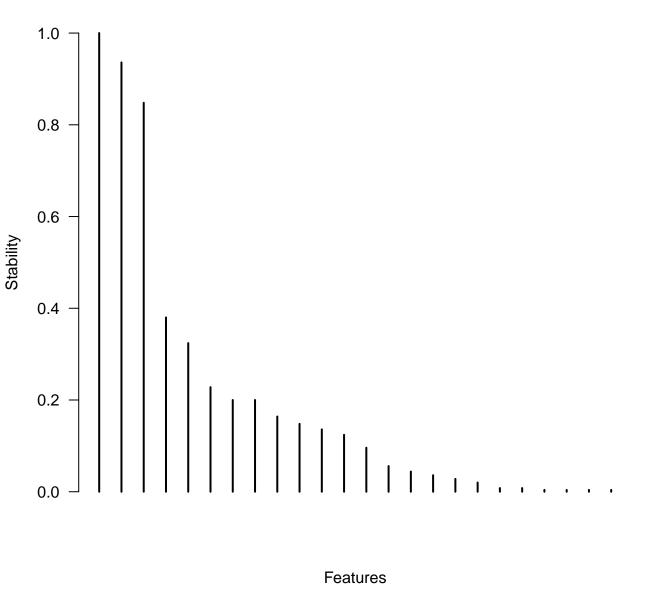




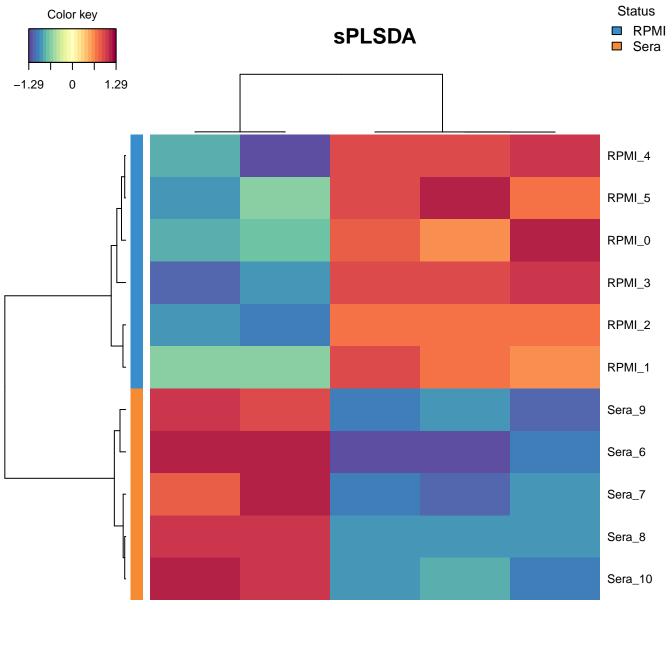


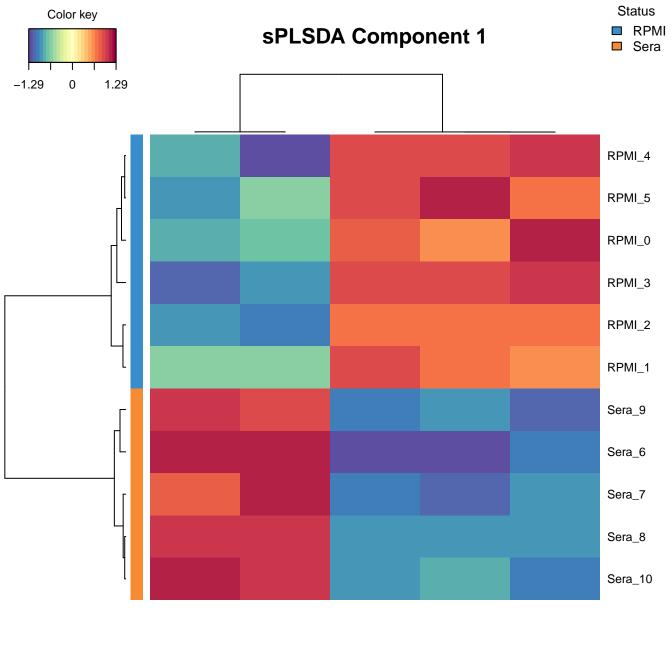




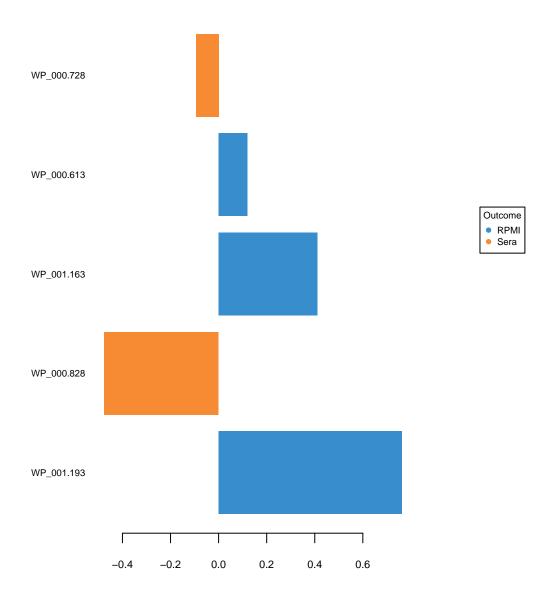




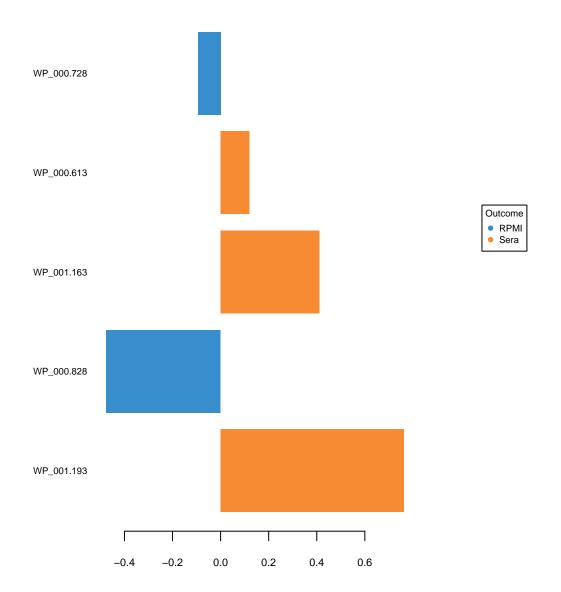


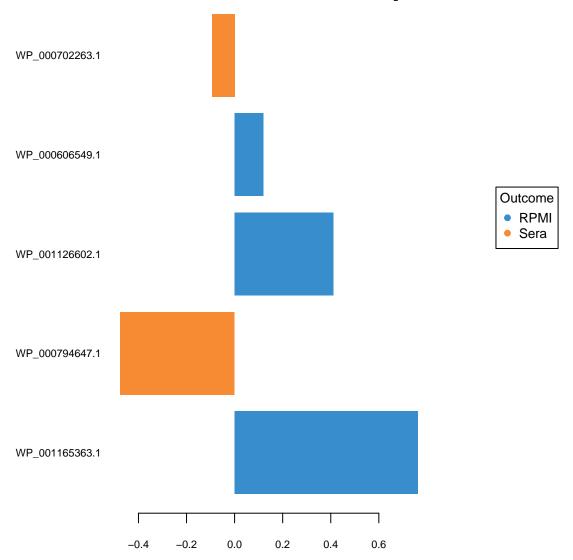


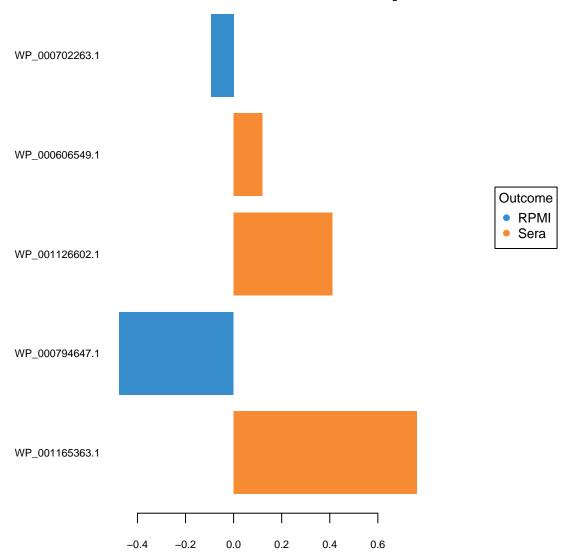
Proteomics 1 sPLSDA max load

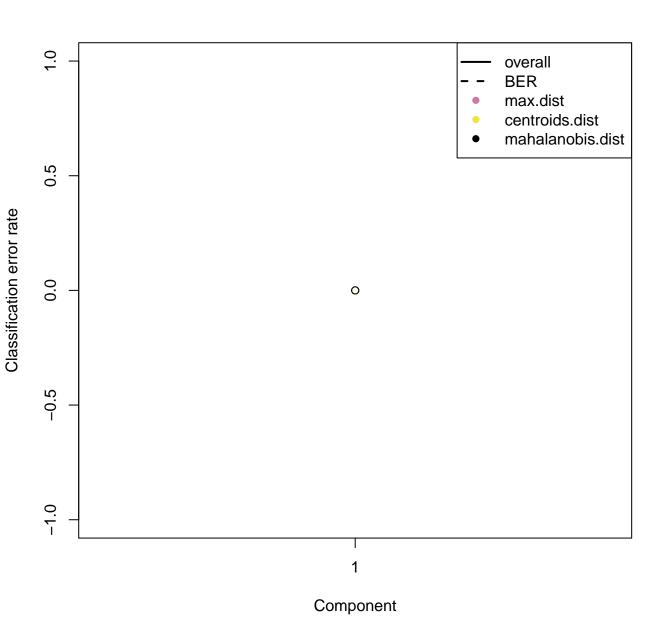


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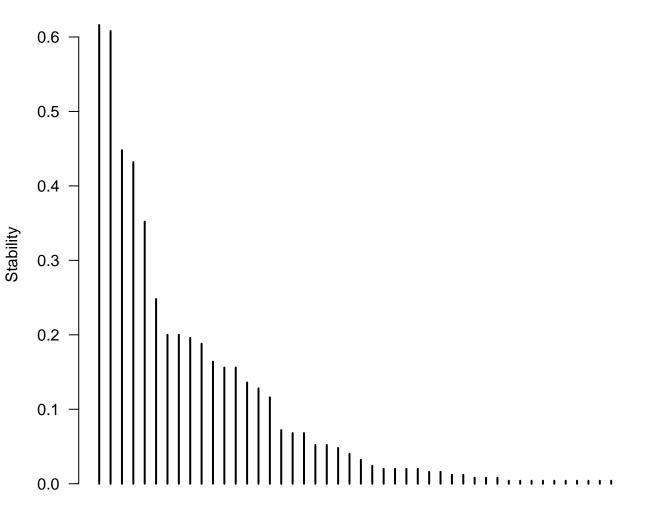






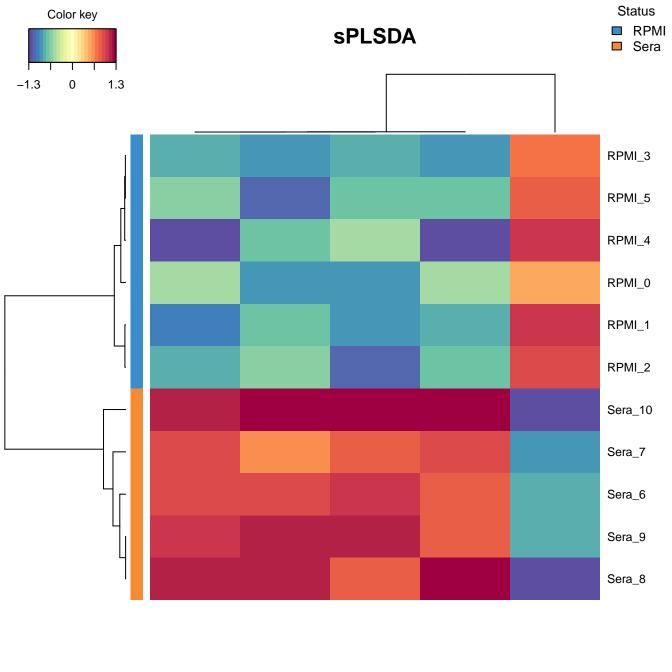


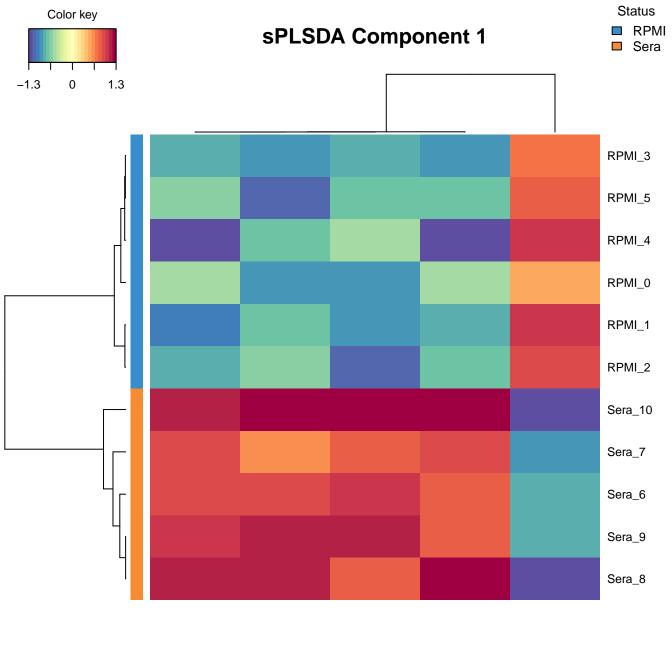
Comp 1



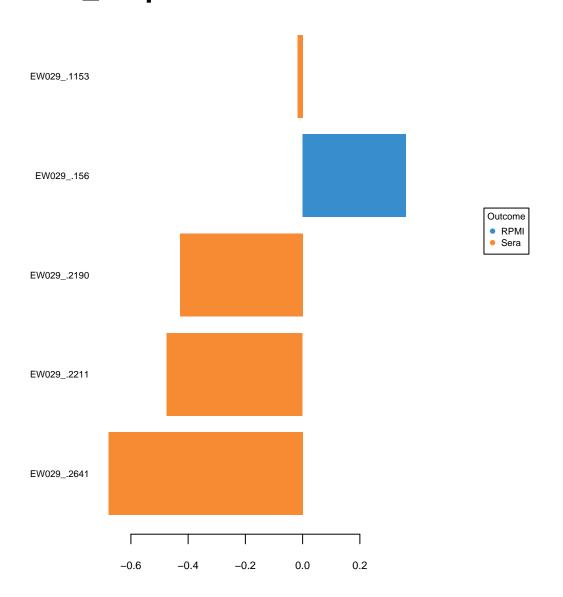
Features



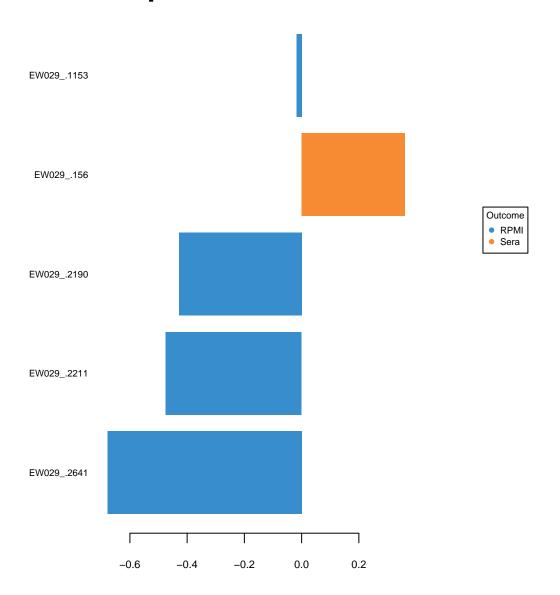


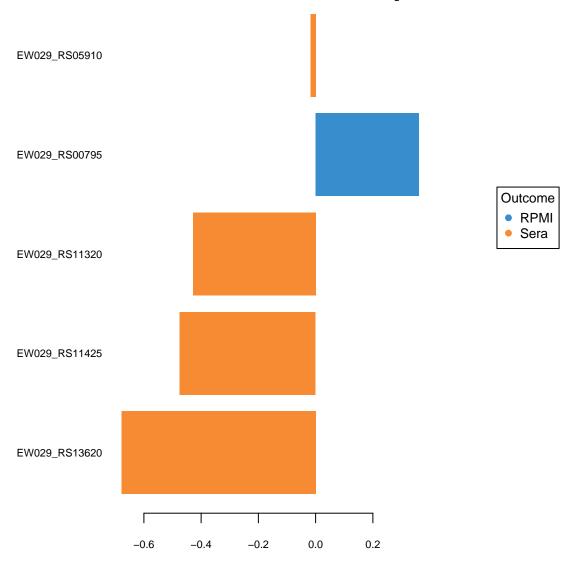


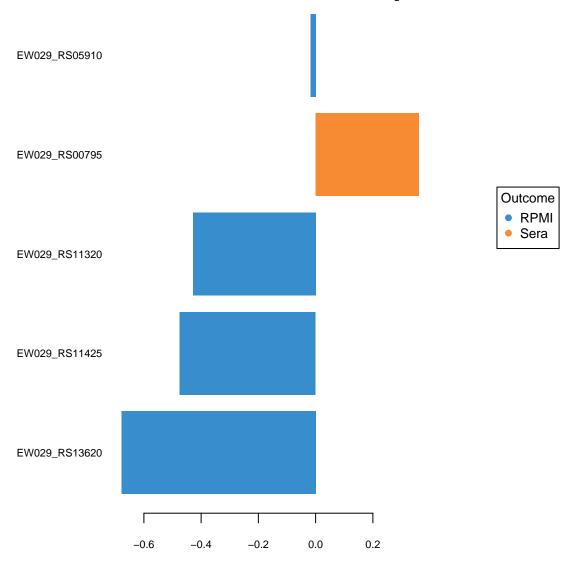
RNA_Seq 1 sPLSDA max loadi

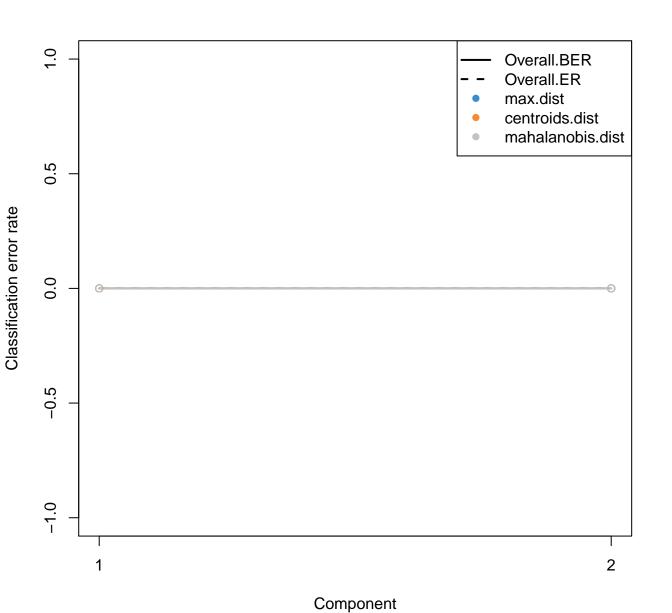


RNA_Seq 1 sPLSDA min loadii

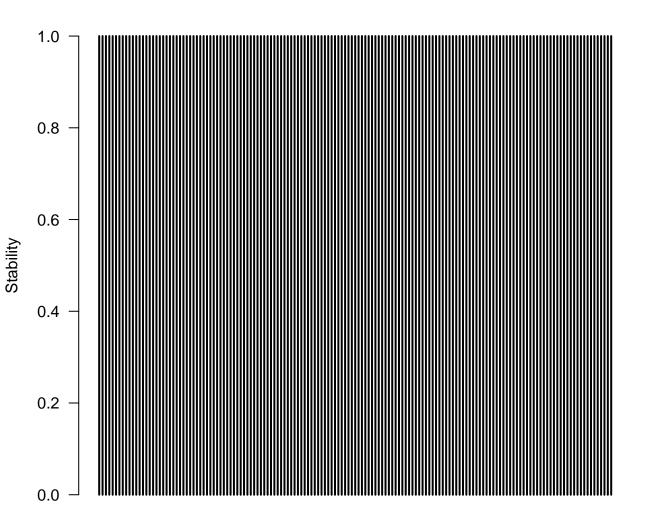






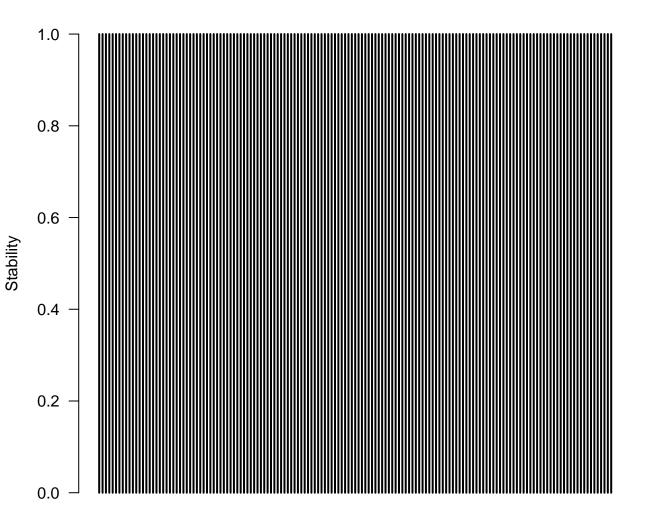


Metabolomics Comp 1

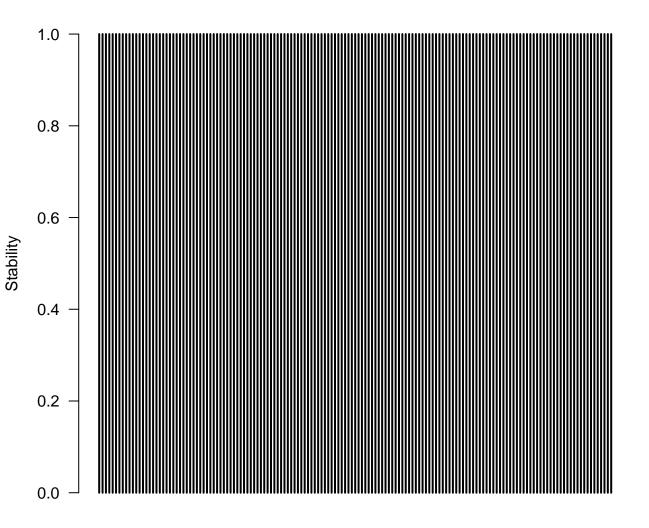


Features

Metabolomics Comp 2

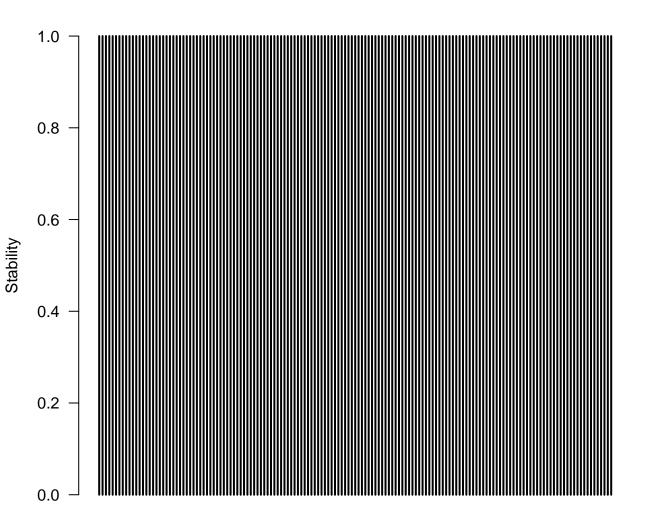


Proteomics Comp 1

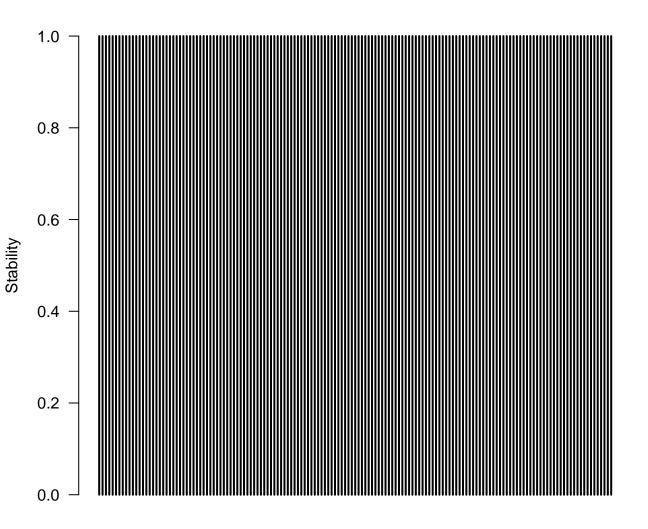


Features

Proteomics Comp 2

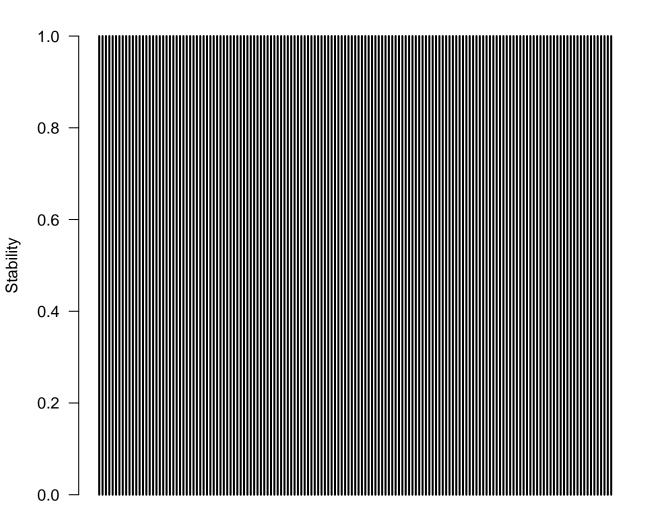


RNA_Seq Comp 1



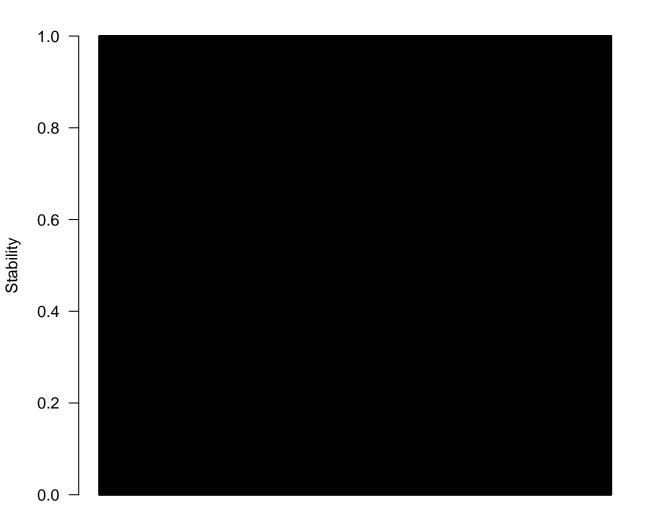
Features

RNA_Seq Comp 2



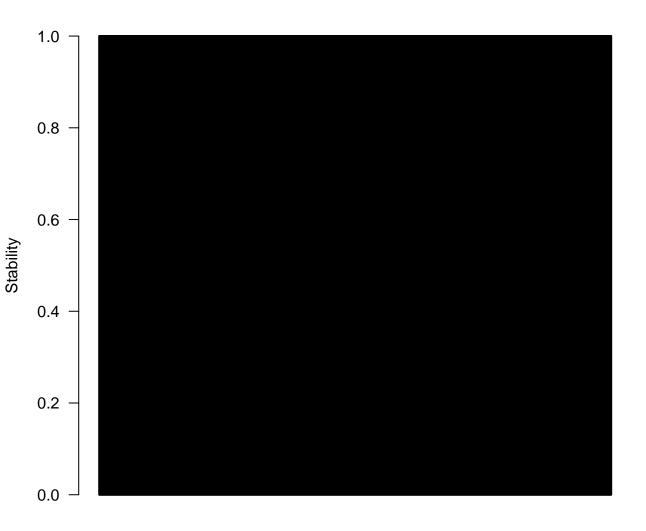
Features

Metabolomics Comp 1



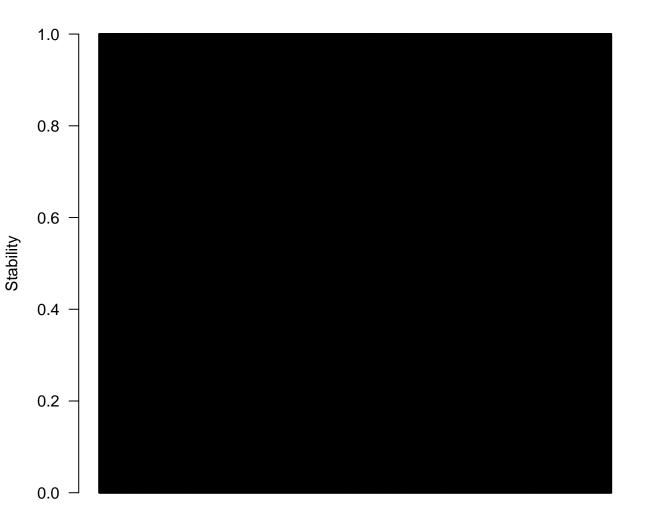
Features

Metabolomics Comp 2



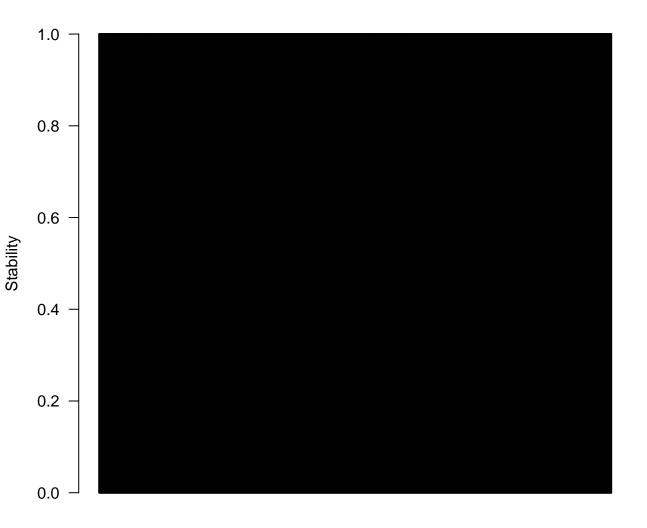
Features

Proteomics Comp 1



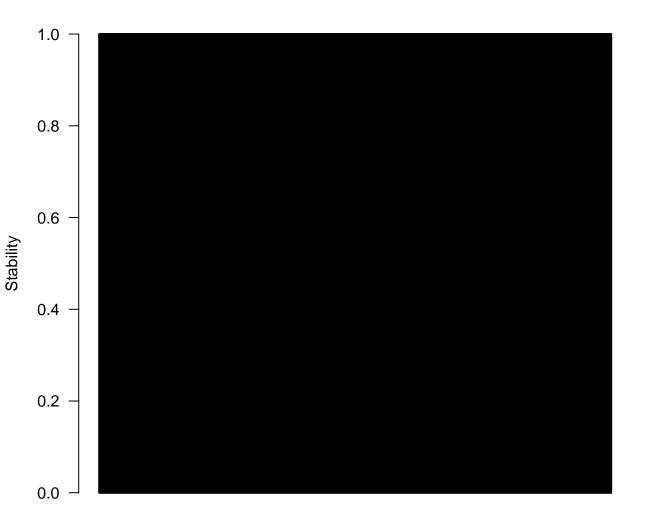
Features

Proteomics Comp 2



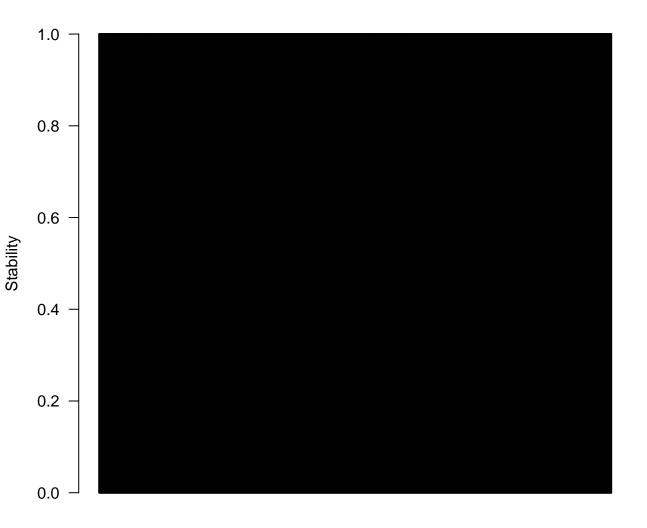
Features

RNA_Seq Comp 1



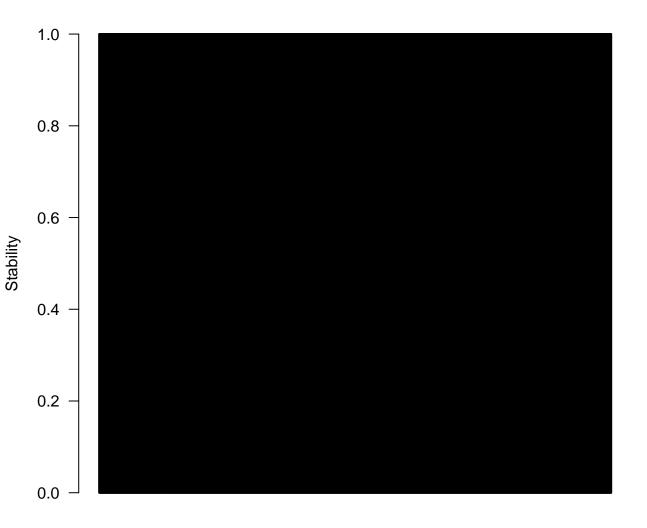
Features

RNA_Seq Comp 2



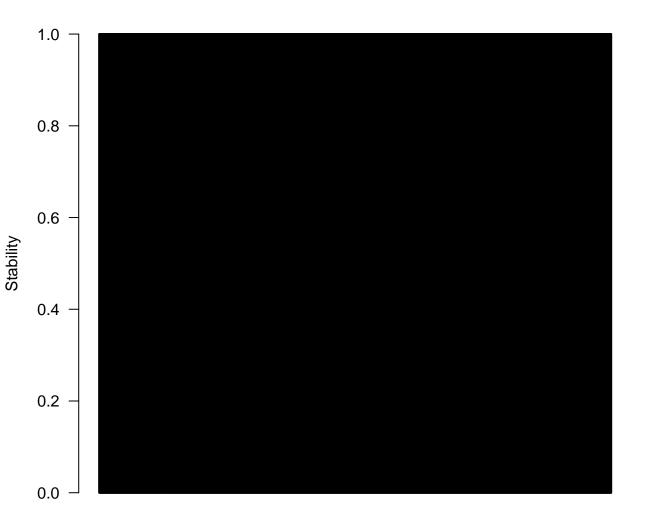
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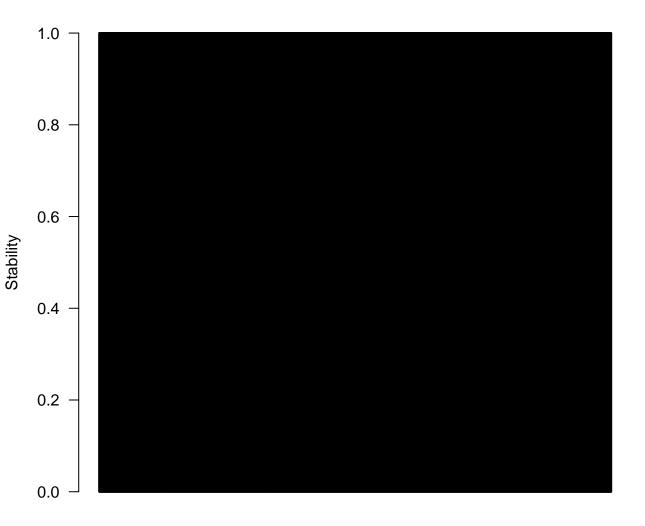
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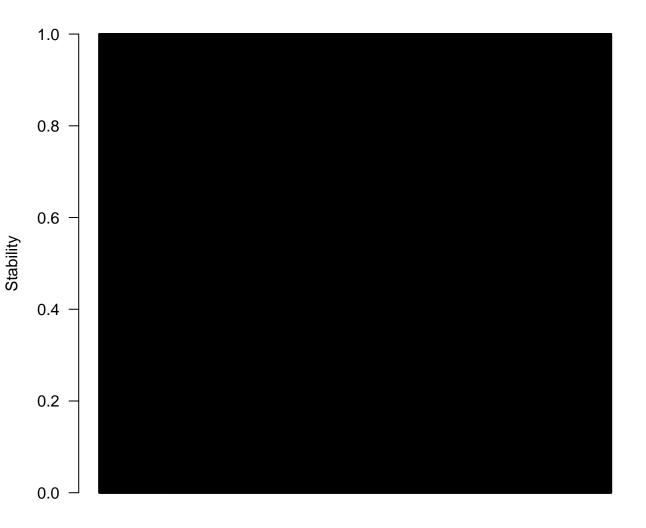
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Proteomics Comp 1



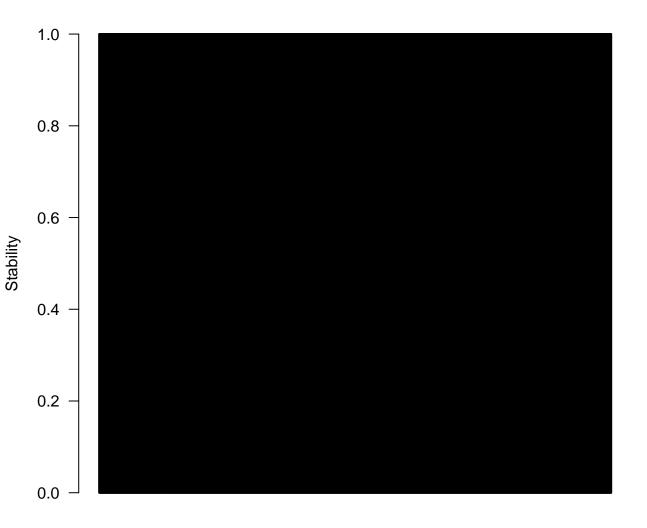
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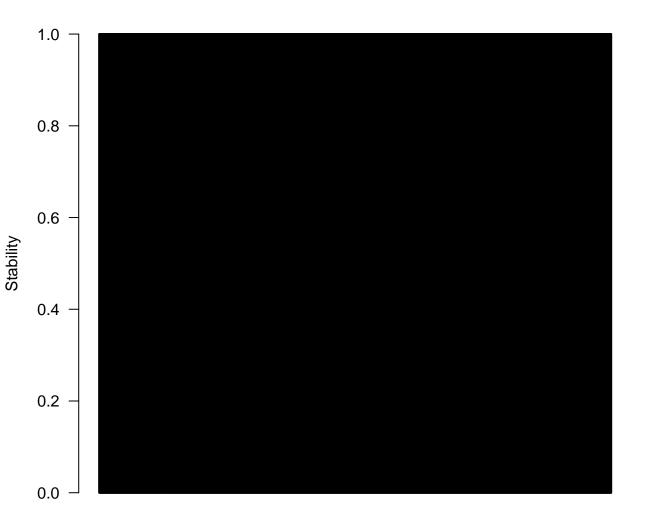
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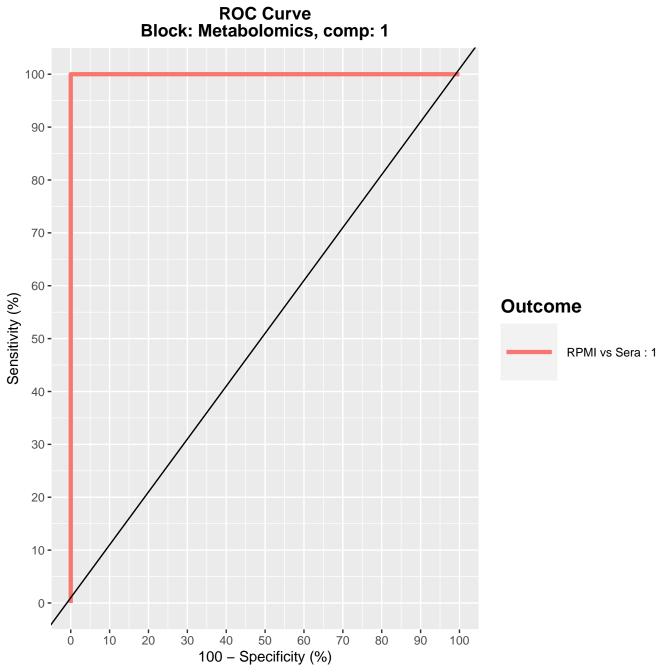


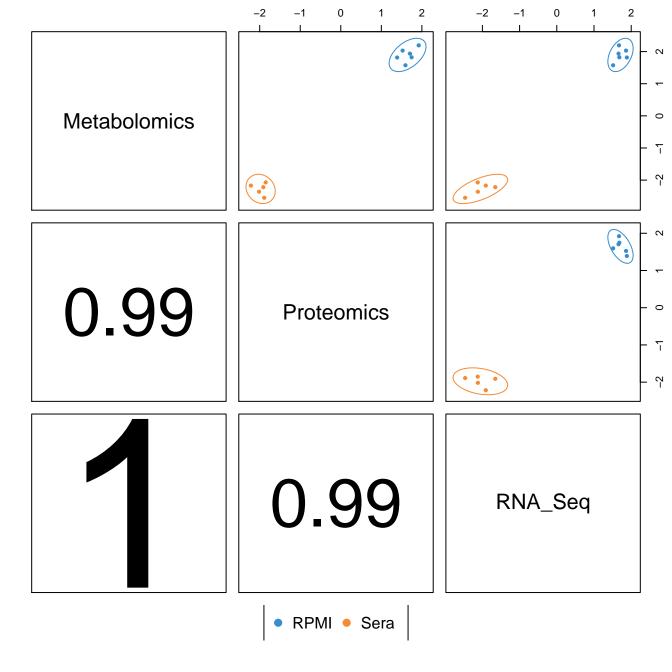
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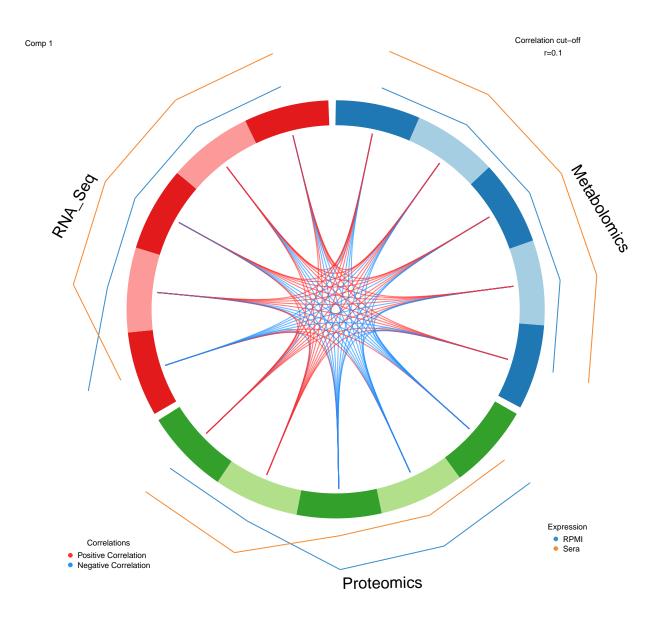
RNA_Seq Comp 2

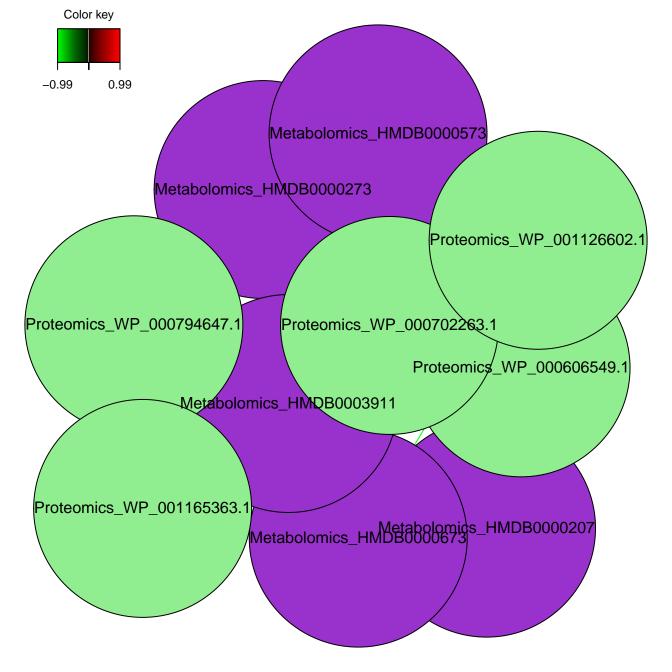


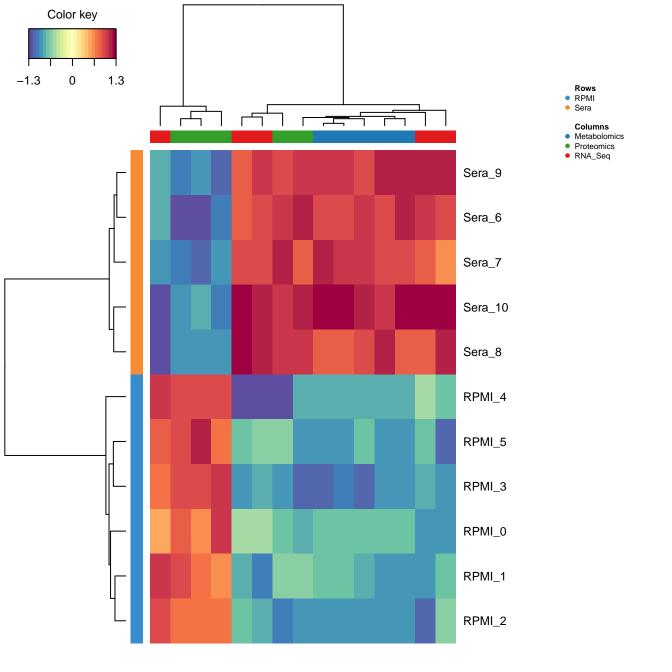
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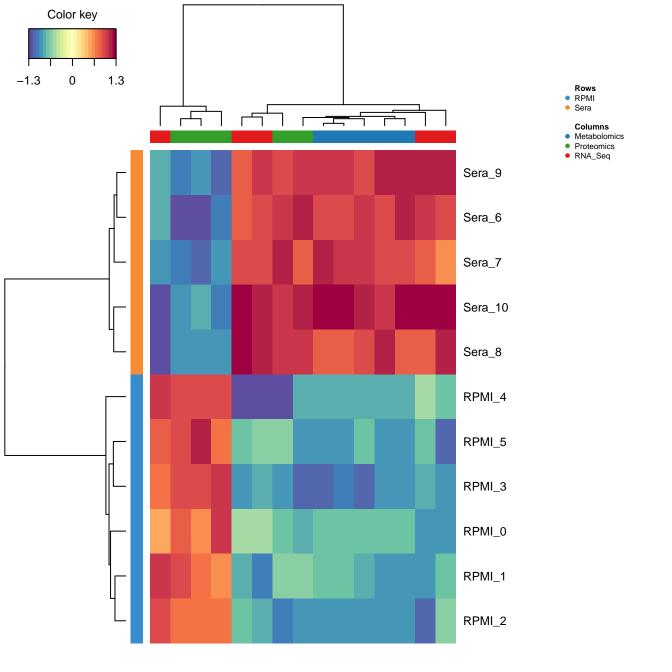




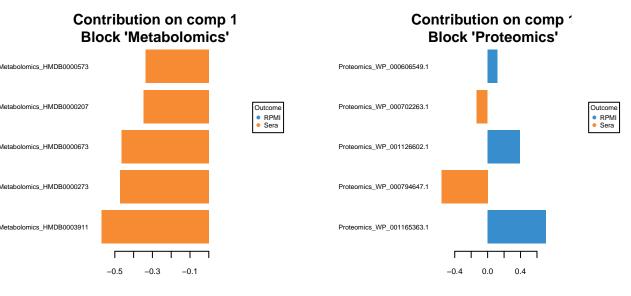


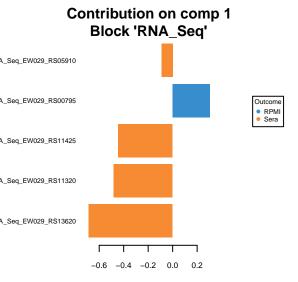




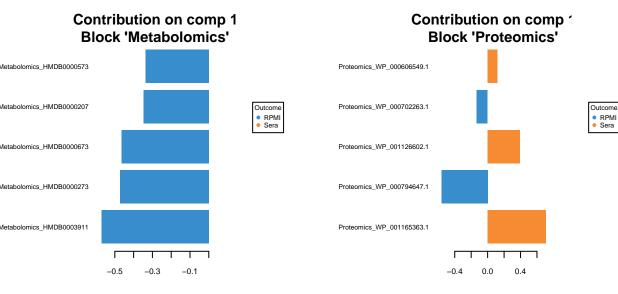


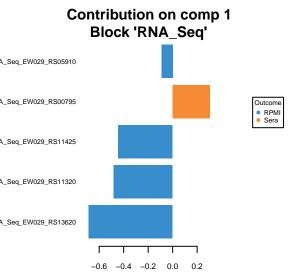
1 DIABLO max loadings



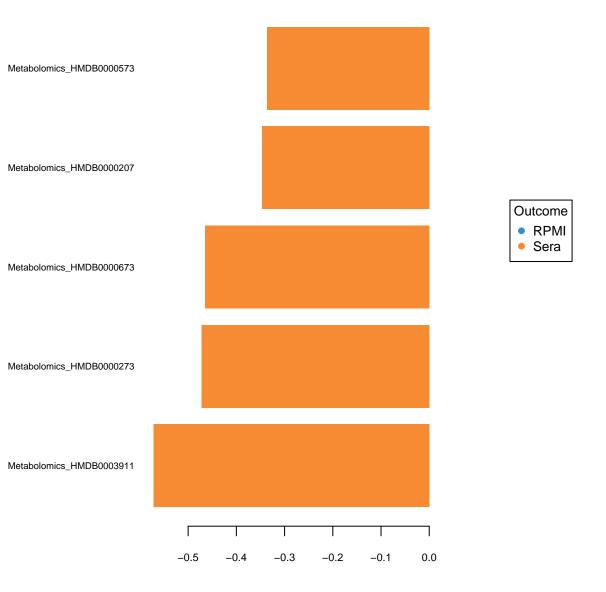


1 DIABLO min loadings

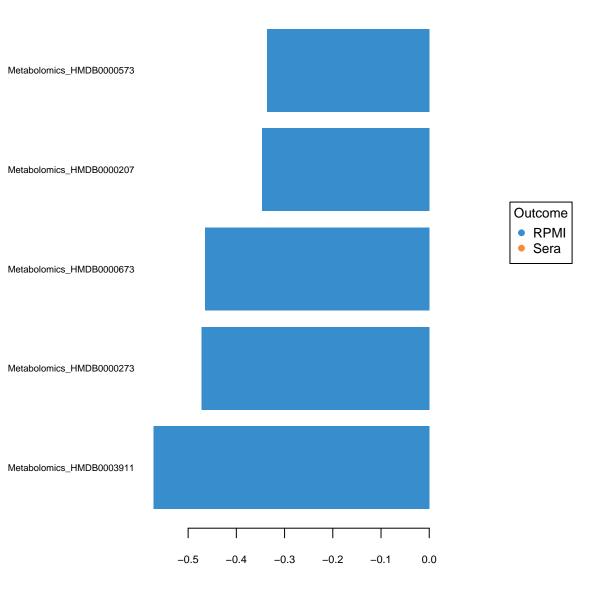


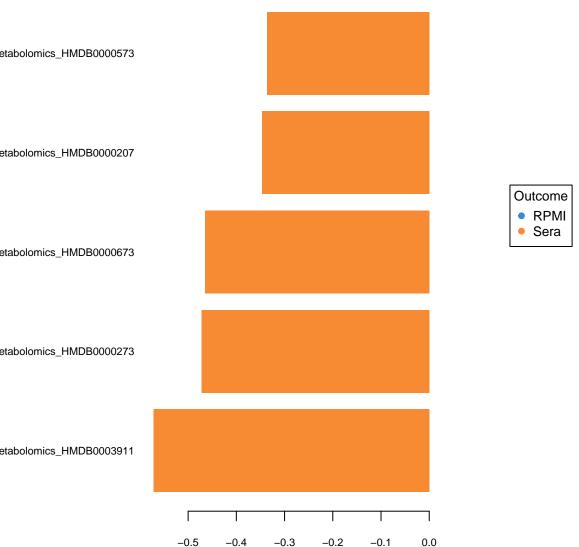


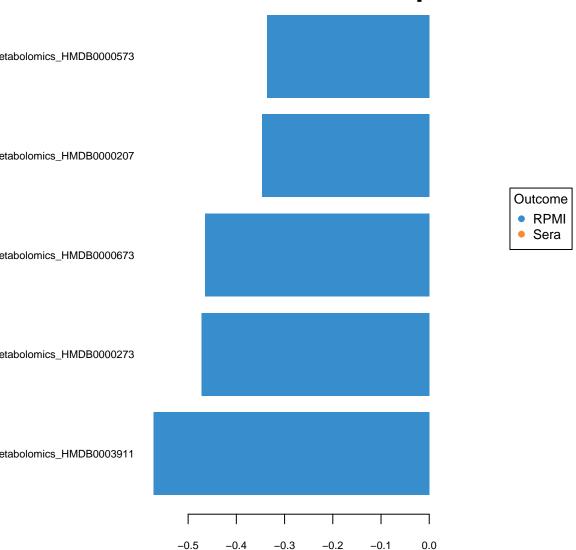
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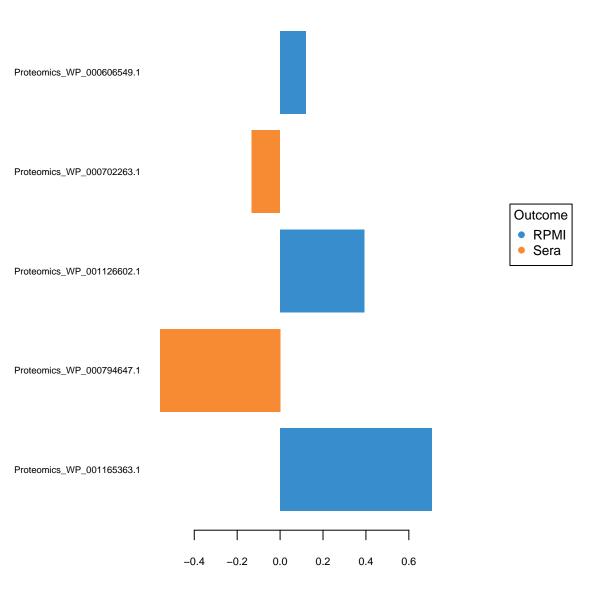
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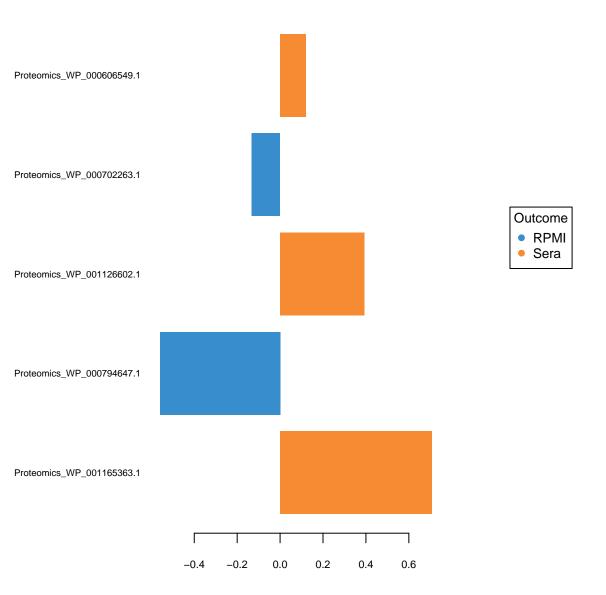


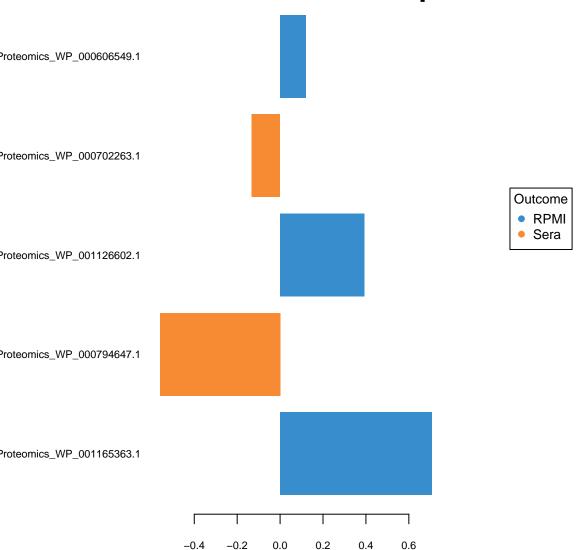


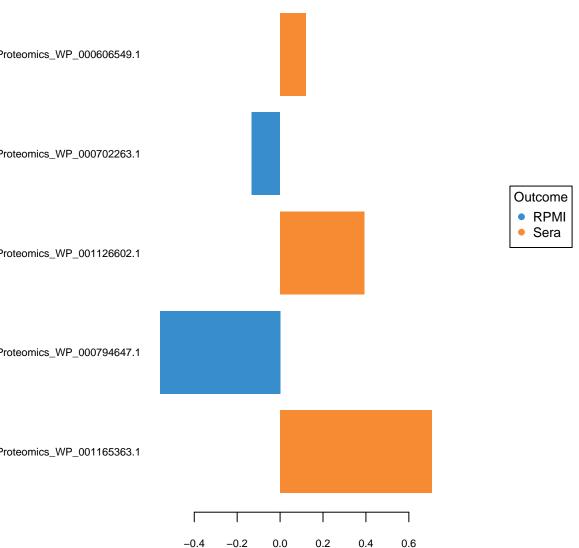
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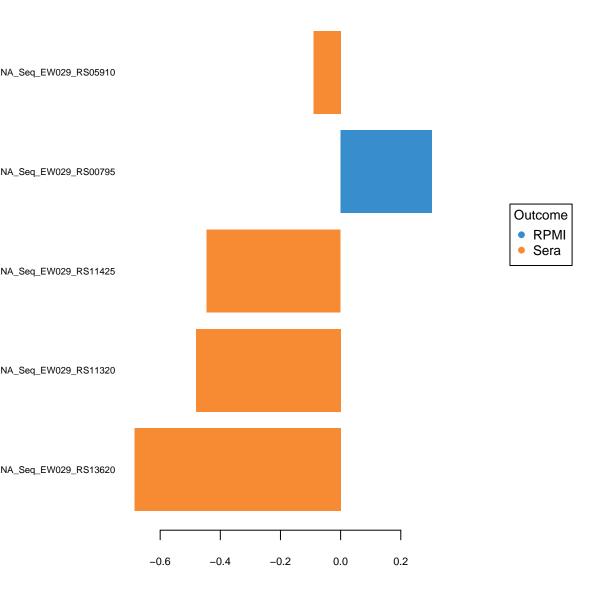
1 Proteomics DIABLO min load







1 RNA_Seq DIABLO max loadi



1 RNA_Seq DIABLO min loadii

