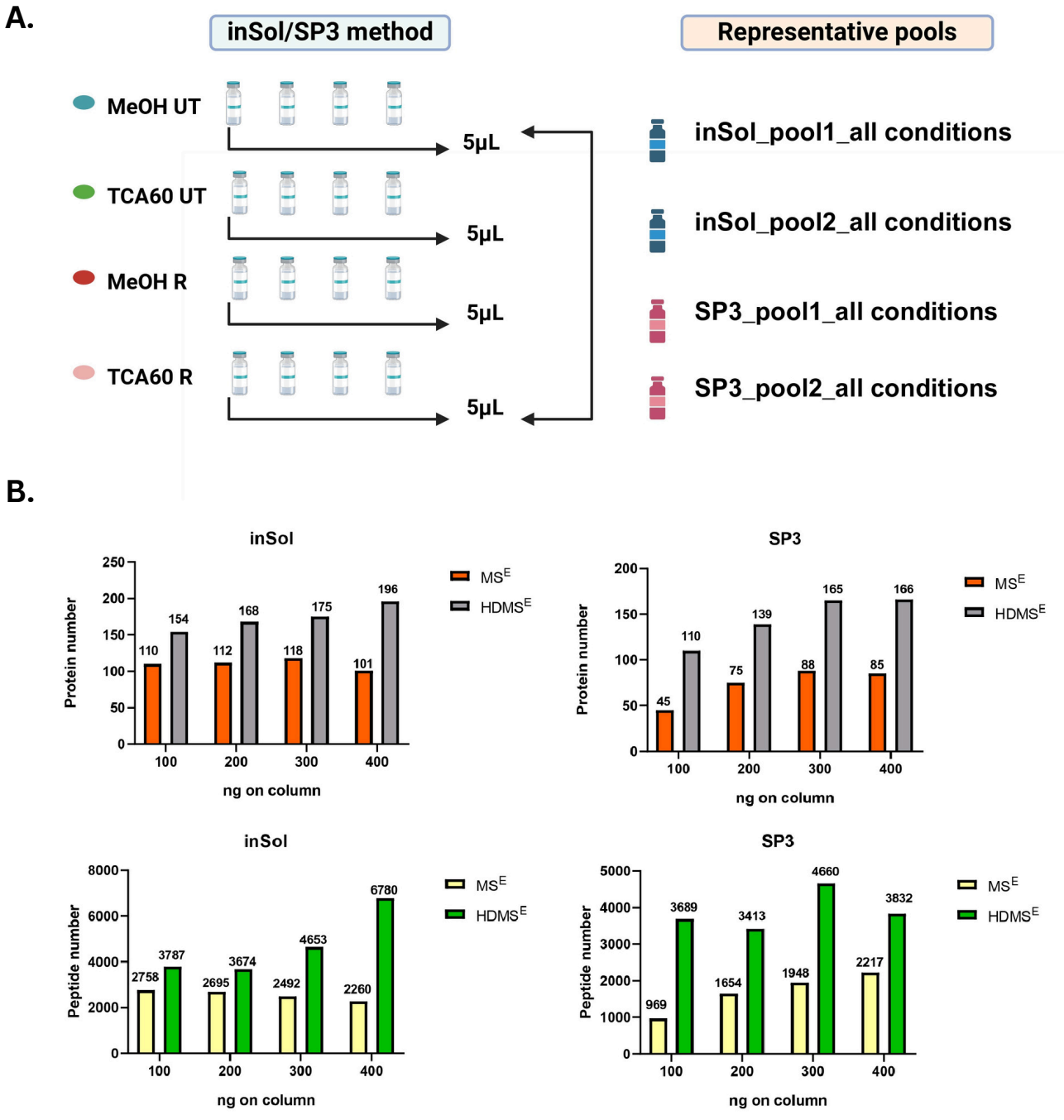


Figure S1: Optimal column load determination. A. Representative sample pools - experimental design B. Protein and peptide number for inSol and SP3 in MSE and HDMSE.

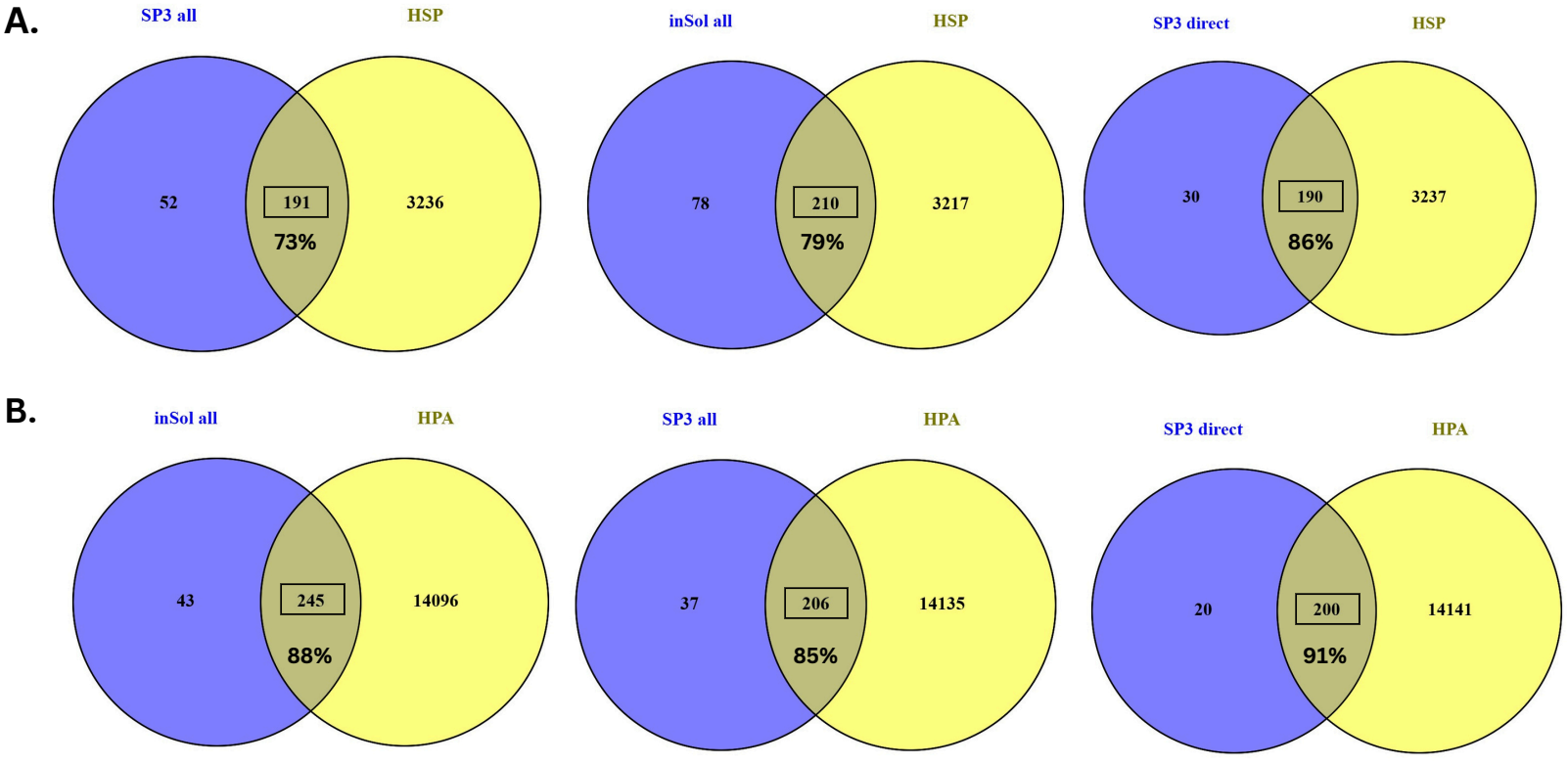


Figure S2: Venn diagram showing the overlap of protein identifications across the methods compared to salivary databases. A. Human Salivary Proteome; B. Human Protein Atlas.

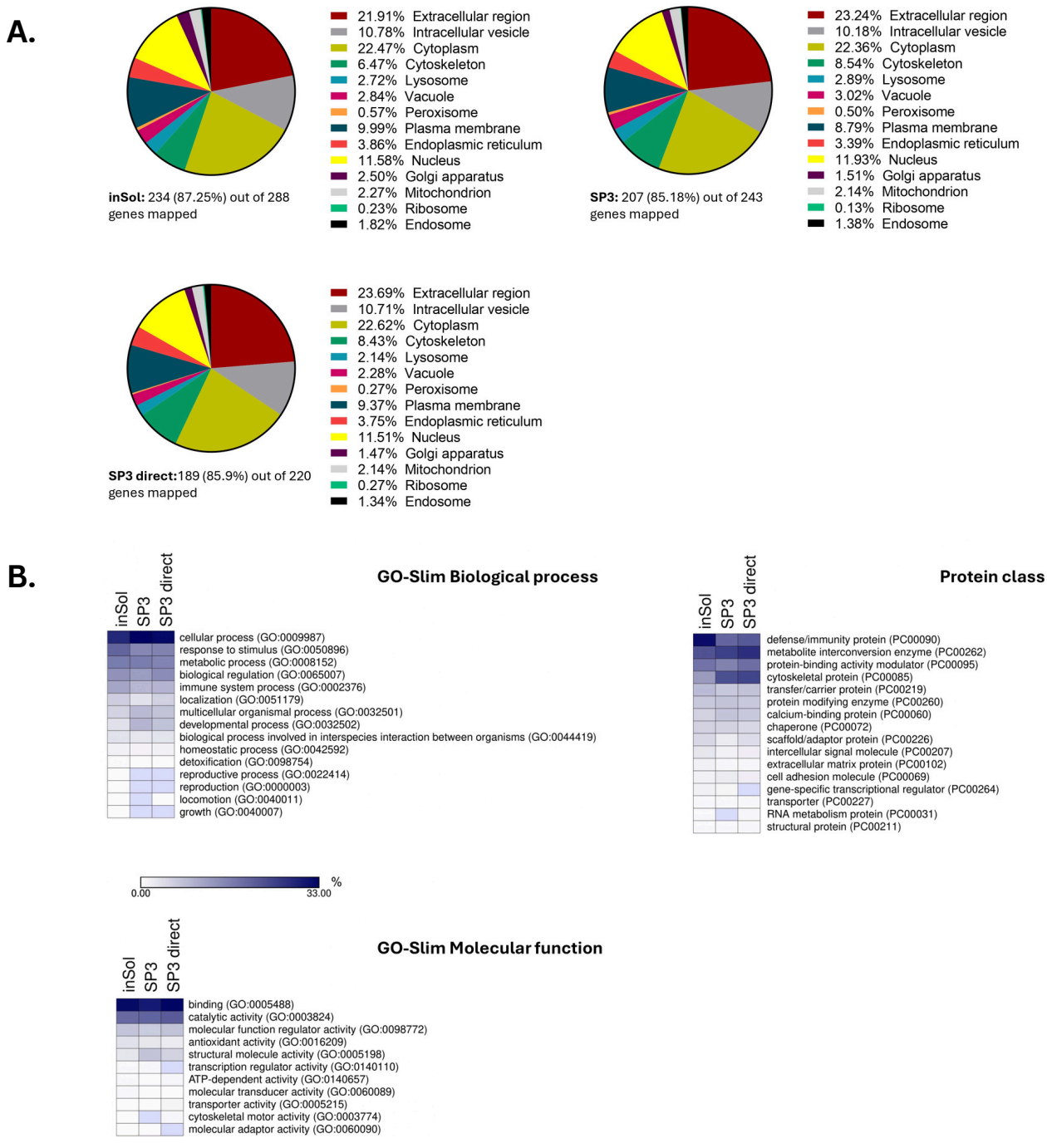


Figure S3: Functional analysis using SubCellularRVis and PantherDB. A. Cellular component gene function analysis for tested methods using SubCellularRVis; B. Gene function analysis using Panther Classification system v.17.0 for tested methods.

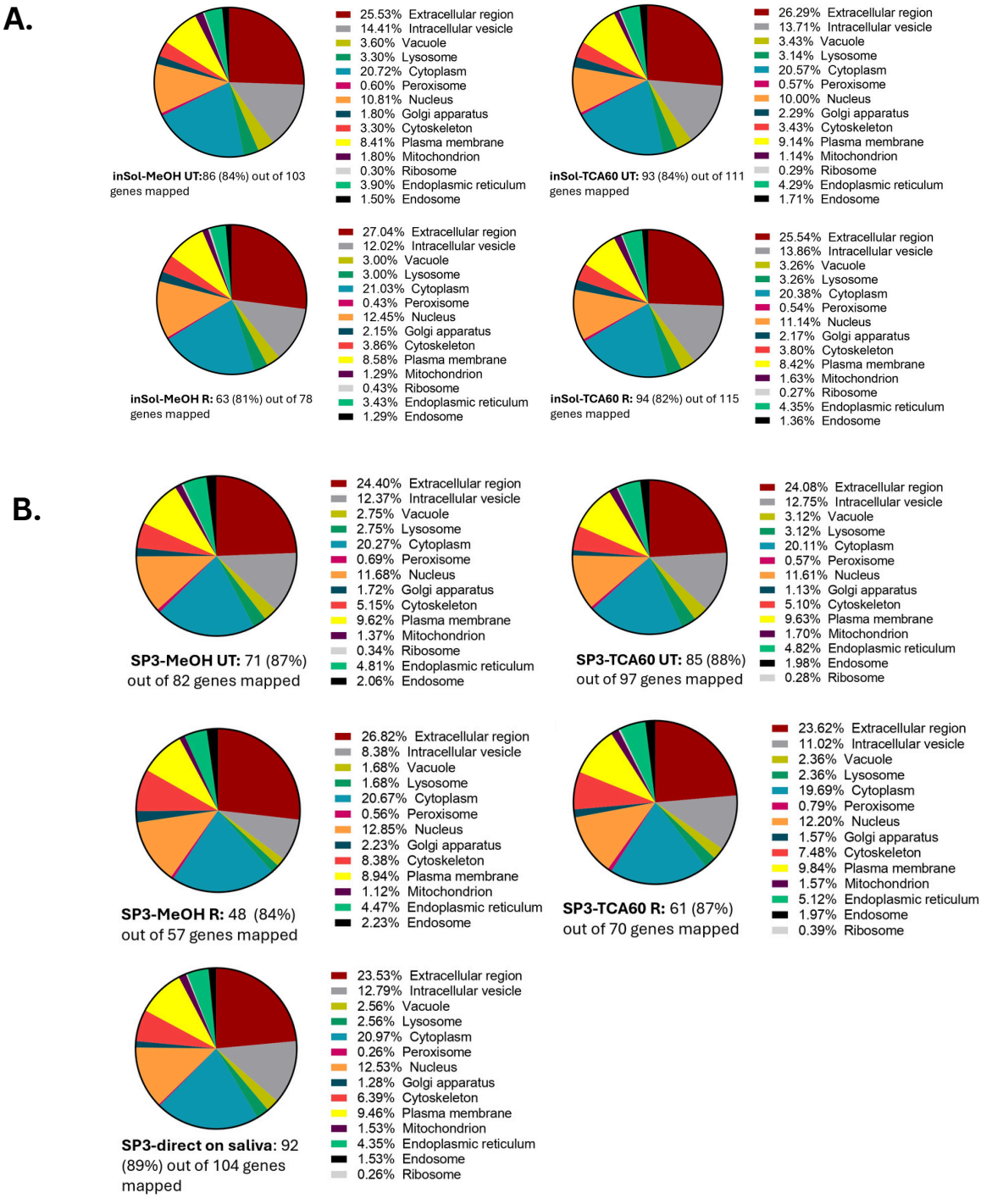


Figure S4: Cellular component gene function analysis using SubCellularRVis for A. in-solution and B. SP3 conditions. Graphical representations were obtained using GraphPad Prism v.8.

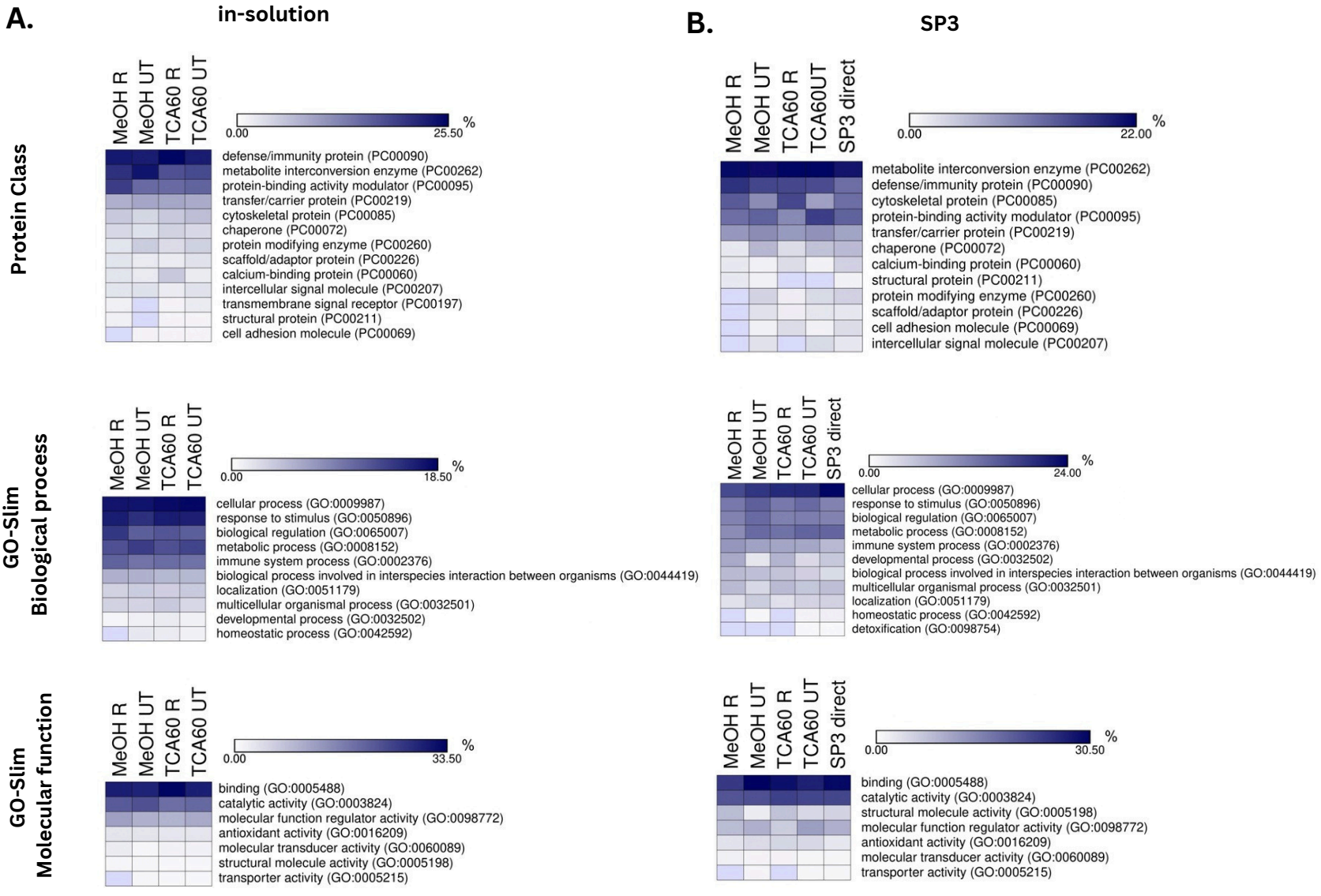
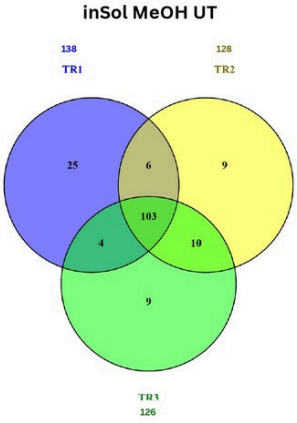
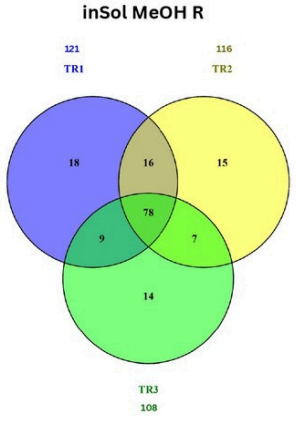


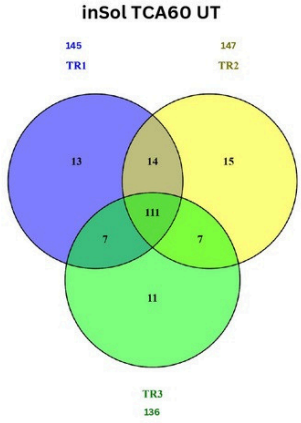
Figure S5: Gene function analysis using PantherDB for A. in-solution and B. SP3 strategies. Graphical representations were obtained using Morpheus.



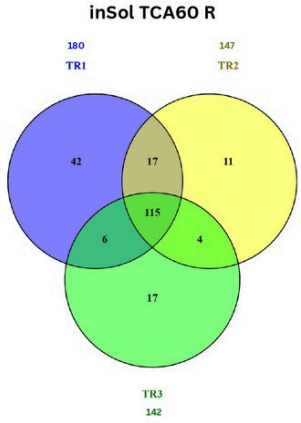
% of common proteins in		
TR1	TR2	TR3
75	80	82



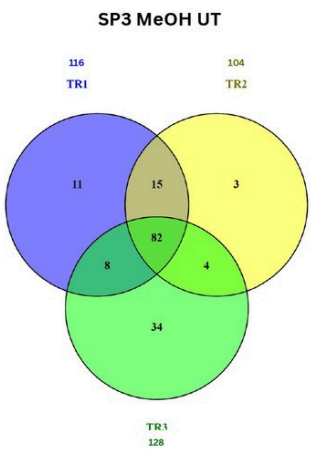
% of common proteins in		
TR1	TR2	TR3
65	67	72



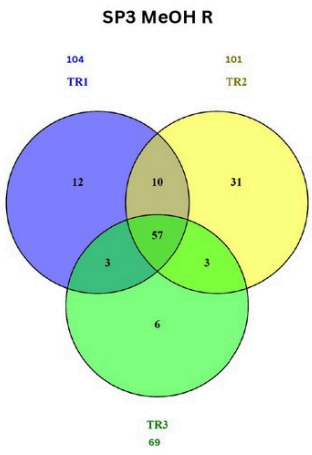
% of common proteins in		
TR1	TR2	TR3
77	76	82



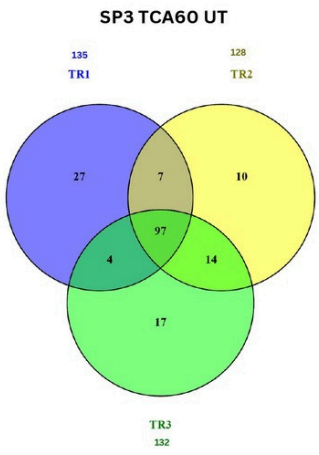
% of common proteins in		
TR1	TR2	TR3
64	78	81



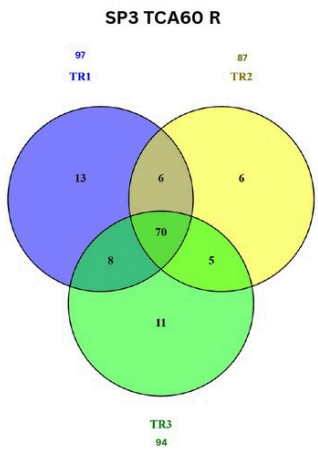
% of common proteins in		
TR1	TR2	TR3
71	79	64



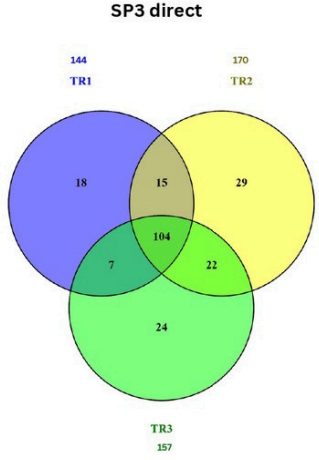
% of common proteins in		
TR1	TR2	TR3
70	56	83



% of common proteins in		
TR1	TR2	TR3
72	76	73



% of common proteins in		
TR1	TR2	TR3
72	80	74



% of common proteins in		
TR1	TR2	TR3
72	61	66

Figure S6: Protein overlap among replicates using different in-solution and SP3 strategies.

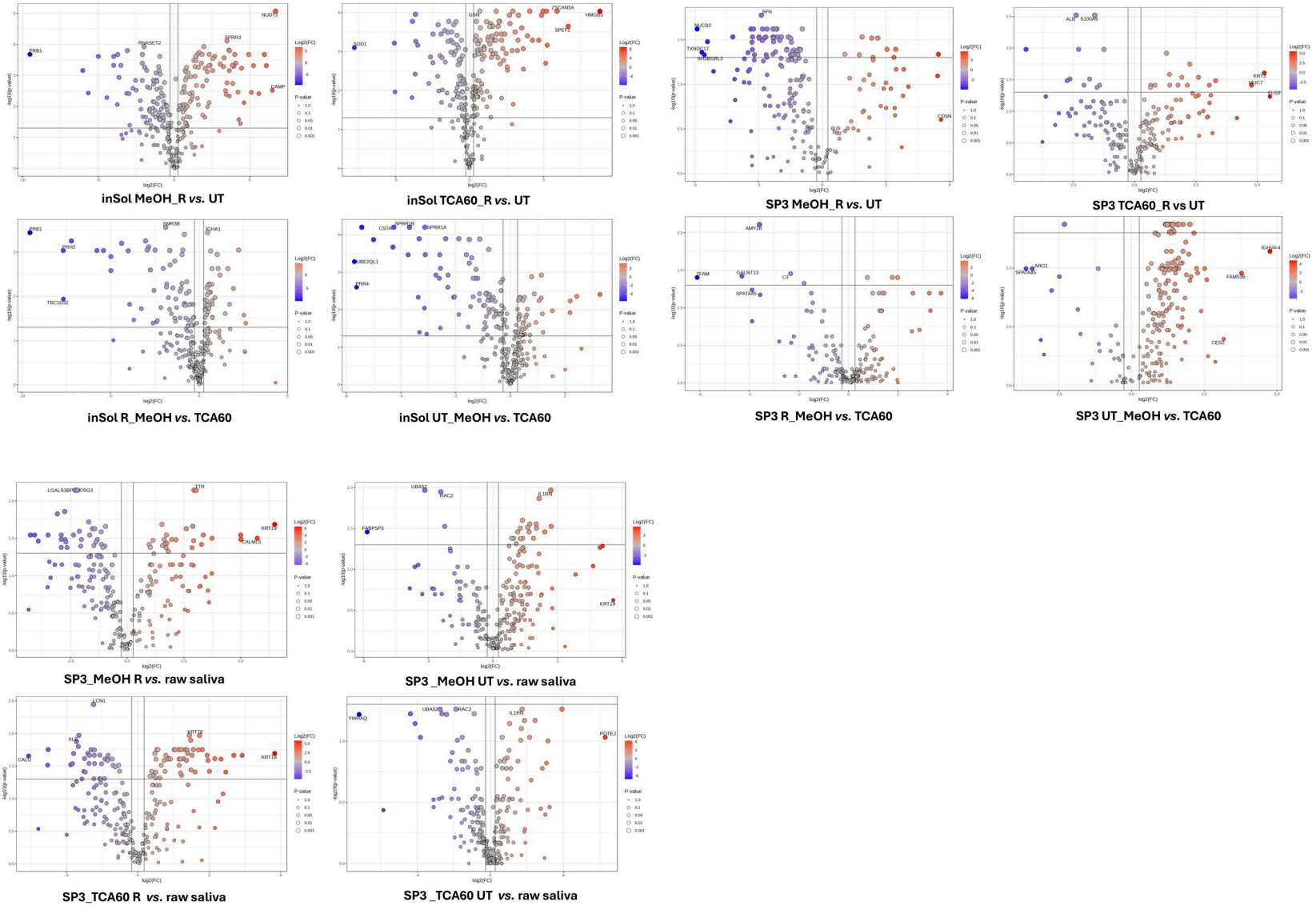


Figure S7: Volcano plots displaying the statistical p-value with the magnitude of abundance changes between each condition for in-solution and SP3 methods.