

## SUPPLEMENTARY FIGURES

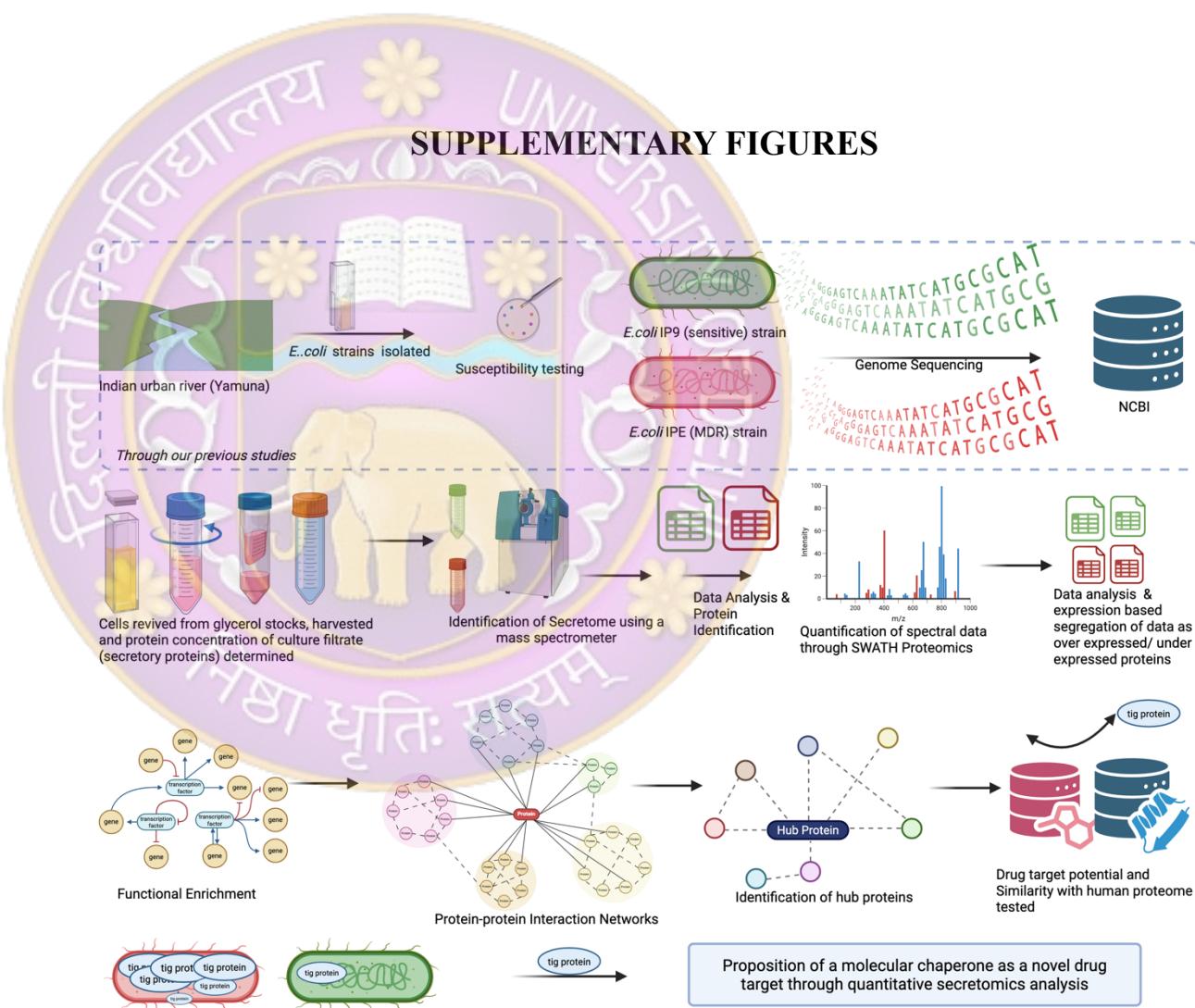


Fig. S1: Graphical abstract depicting the overall workflow of functional analysis of secretomic proteins of MDR and sensitive *E. coli* strains.

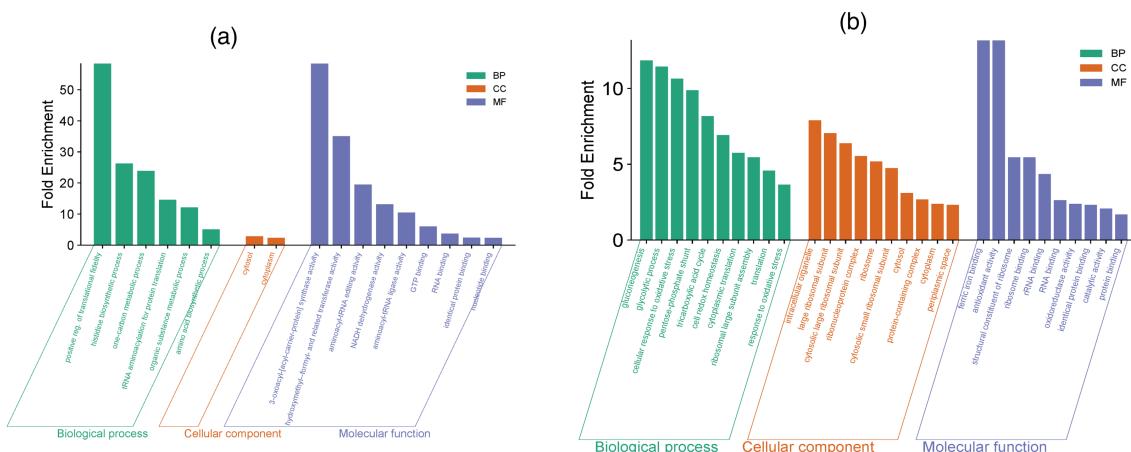
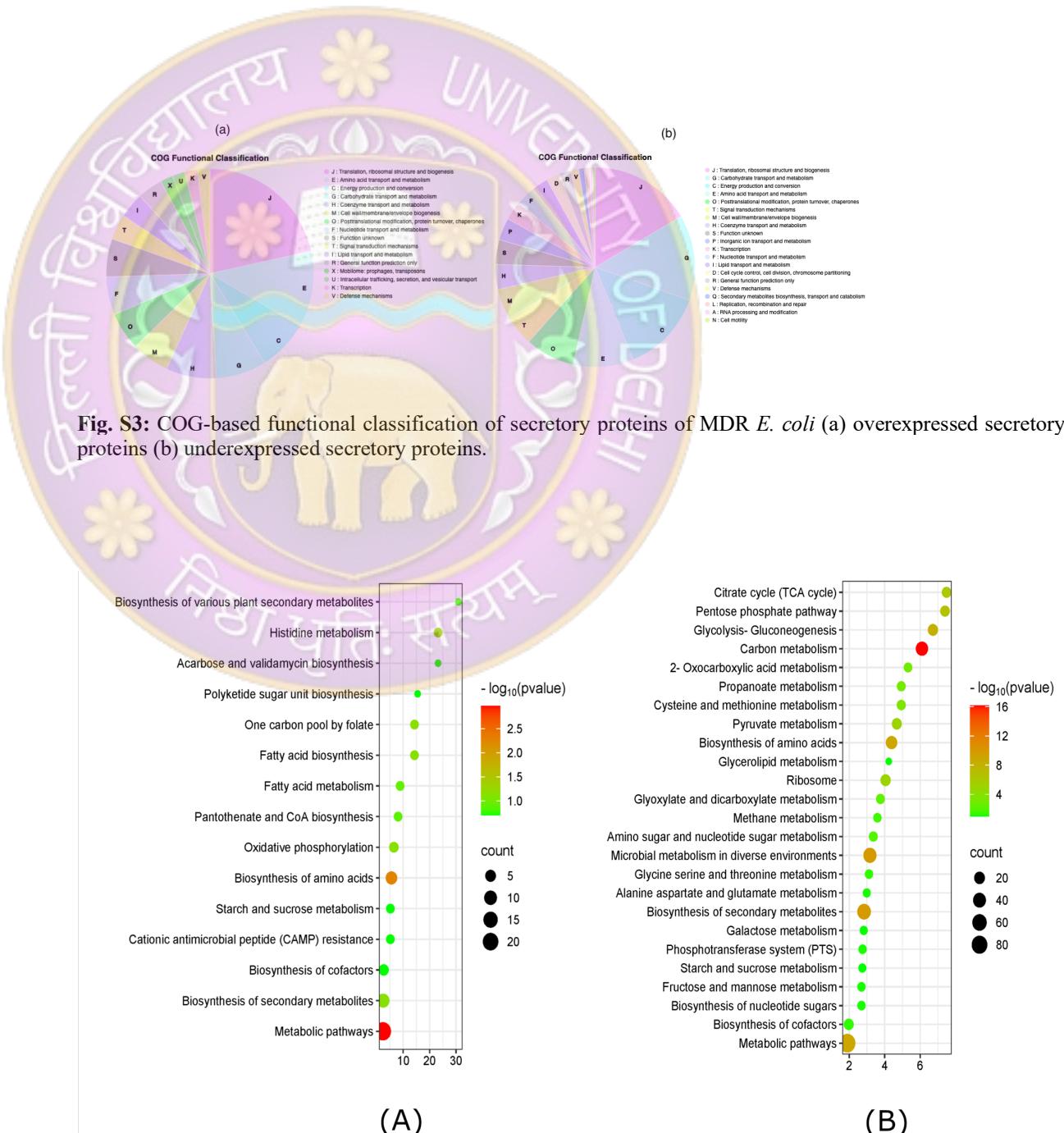
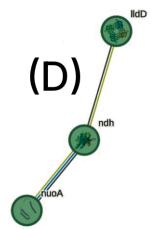
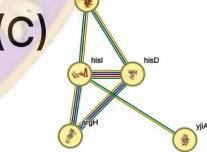
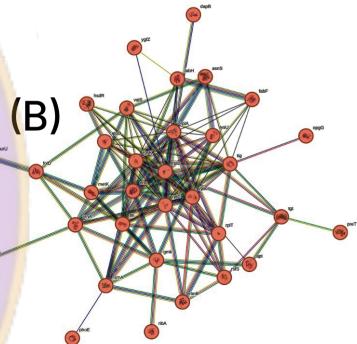
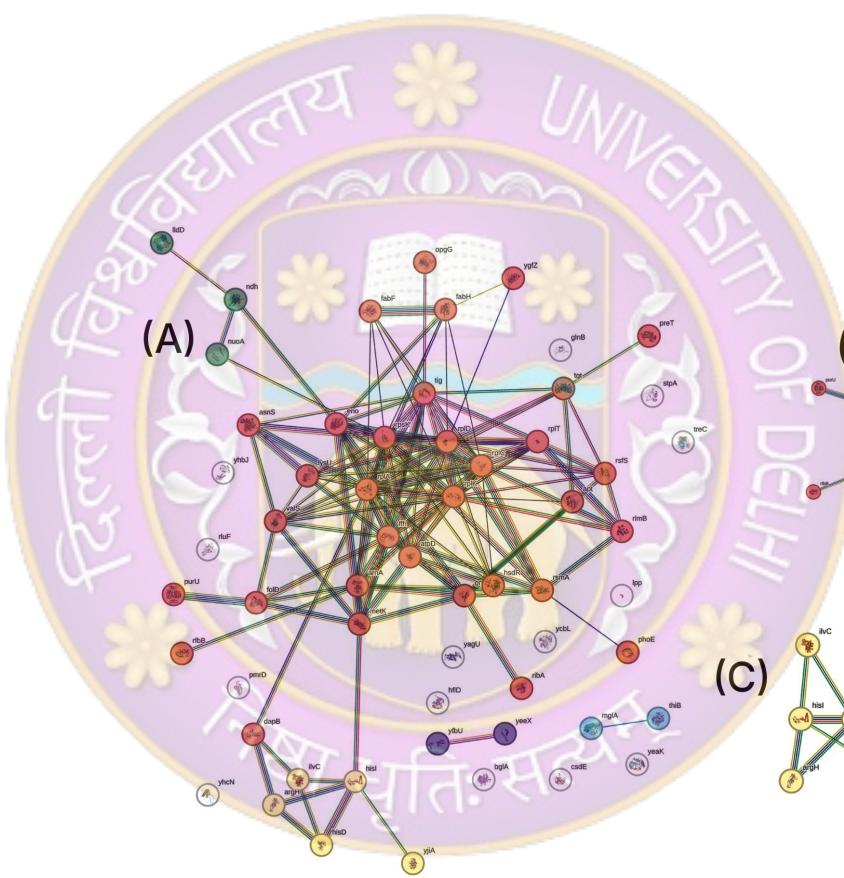


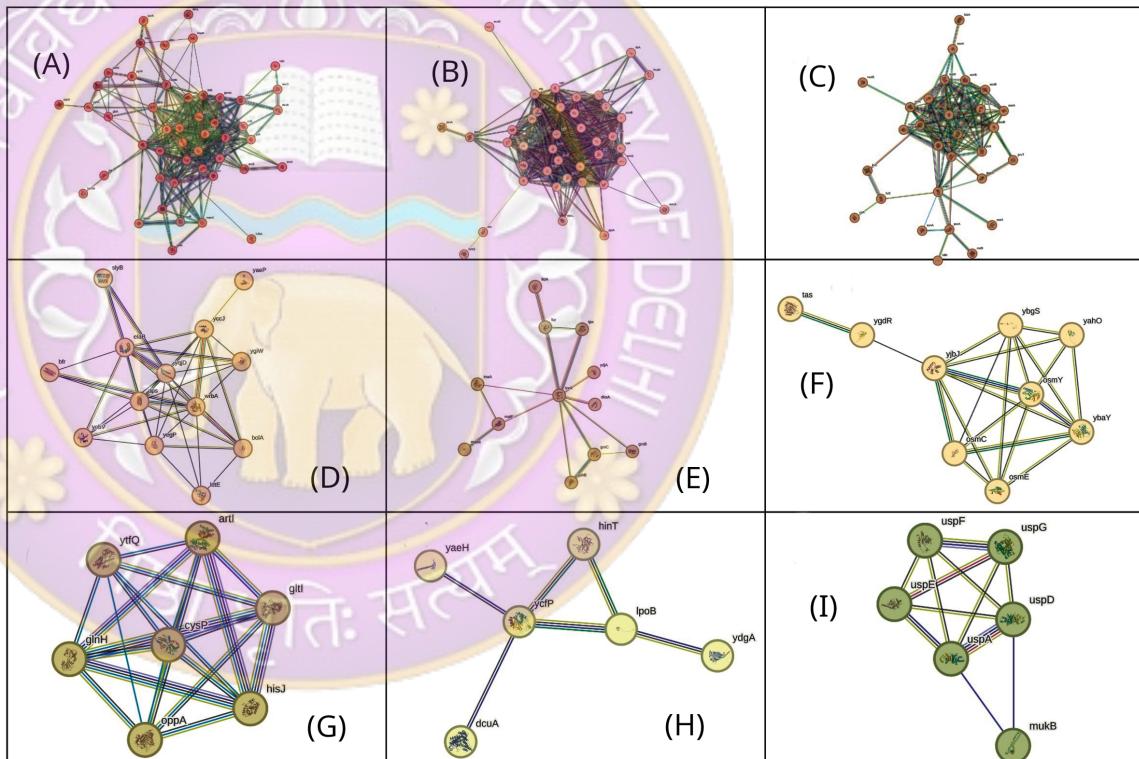
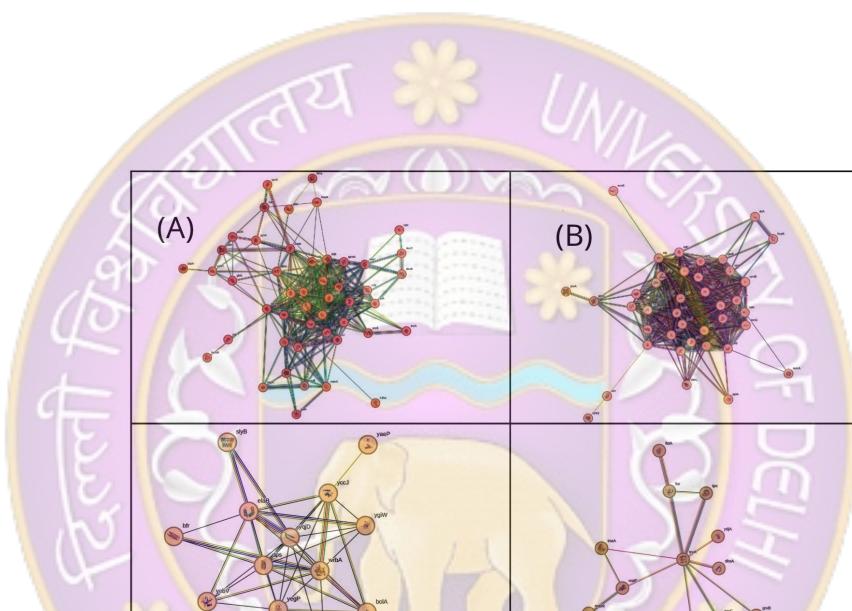
Fig. S2: GO-enriched terms associated with secretory proteins of MDR *E. coli* (a) overexpressed secretory proteins, (b) under expressed secretory proteins. The X-axis shows the GO-terms and the Y-axis shows the fold enrichment values associated with each GO-term.



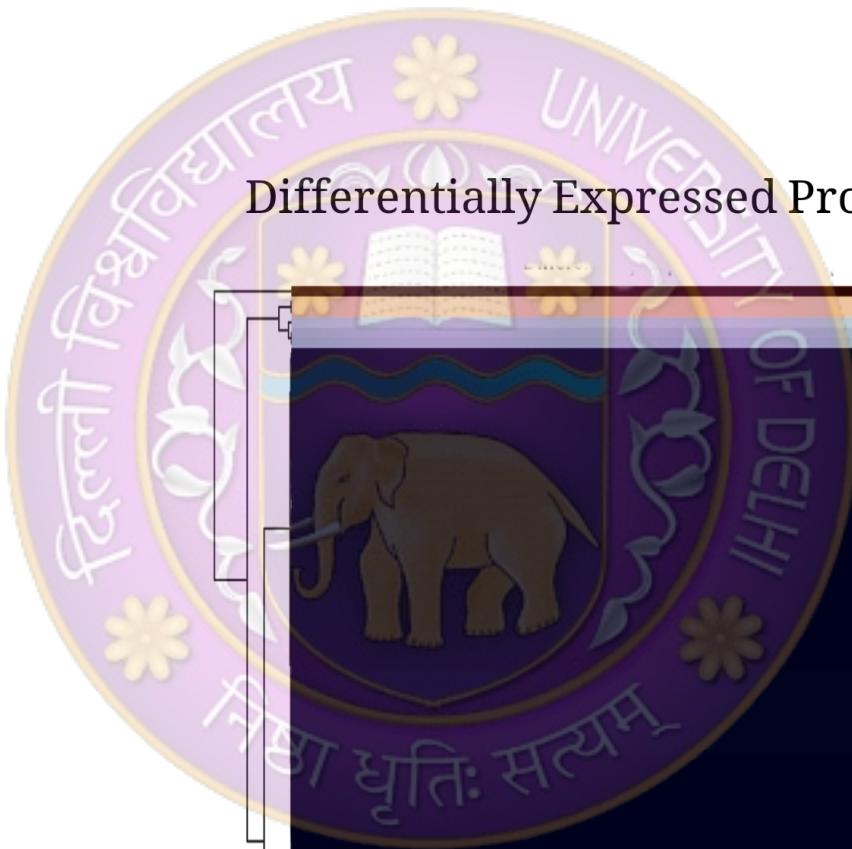
**Fig. S4:** KEGG-enriched pathways with the enrichment score of secretory proteins of MDR *E. coli* (a) overexpressed secretory proteins (b) under expressed secretory proteins.



**Fig. S5:** (a) PPI networks of overexpressed secretory proteins of MDR *E. coli*. Only the most significant clusters (b) cluster 1 formed by 33 proteins involved in ribosome biogenesis, translation and protein export (c) cluster 2 formed by 5 proteins involved in histidine metabolism (d) cluster 3 formed by 3 proteins involved in oxidative phosphorylation are shown.



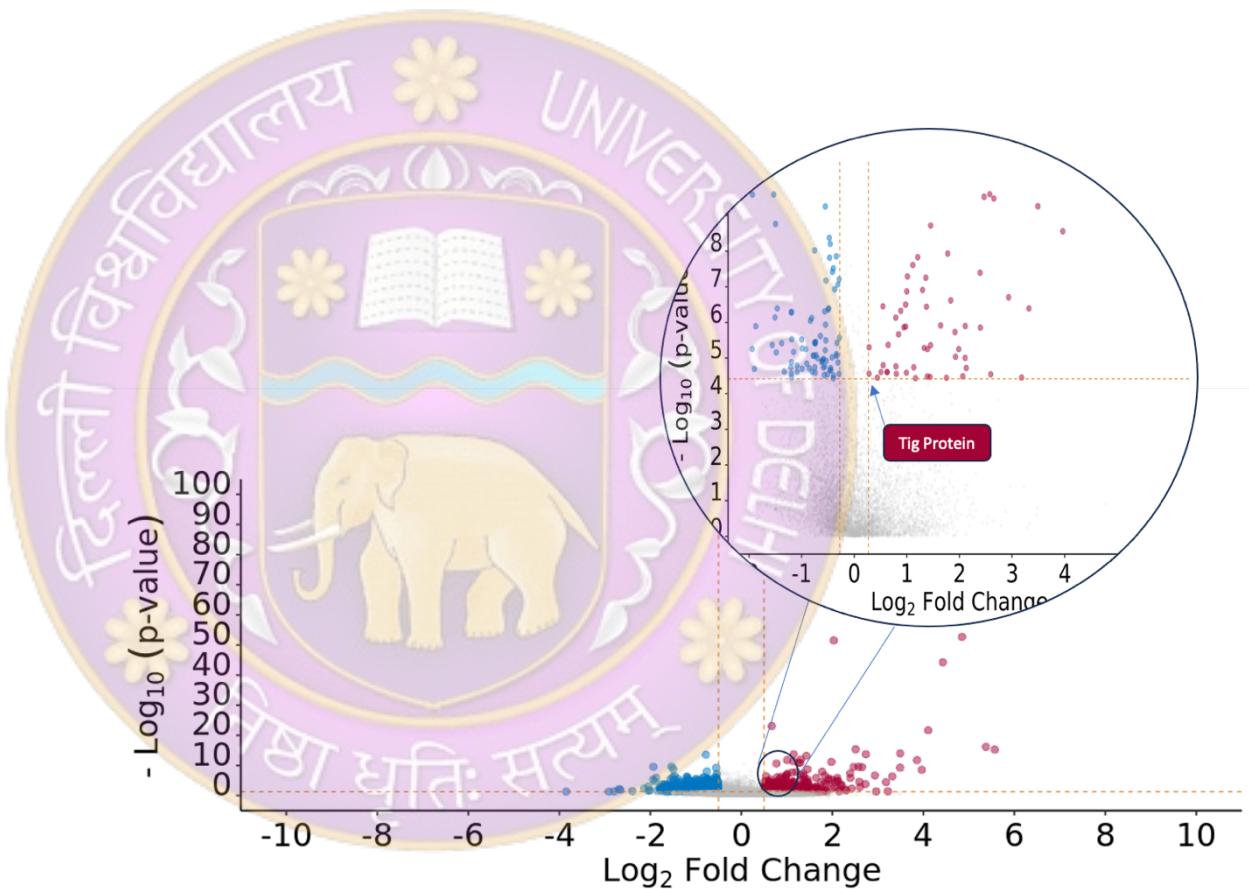
**Fig. S6:** PPI networks of underexpressed secretory proteins of MDR *E. coli*. Only the most significant clusters: (a) cluster 1 formed by 48 proteins involved in glycolysis/gluconeogenesis, (b) cluster 2 formed by 40 proteins involved in translation (c), cluster 3 formed by 29 proteins involved in tricarboxylic acid cycle, (d) cluster 4 formed by 13 proteins belonging to OsmC/Ohr family involved in response to multiple stress, (e) cluster 5 formed by 12 proteins involved in antioxidant activity, (f) cluster 6 formed by 9 proteins involved in response to osmotic stress, (g) cluster 7 formed by 7 proteins which are components of bacterial periplasmic substrate binding proteins, (h) cluster 8 formed by 6 proteins involved in D-alanine catabolism, (i) cluster 9 formed by 6 proteins called as the universal stress proteins are shown.



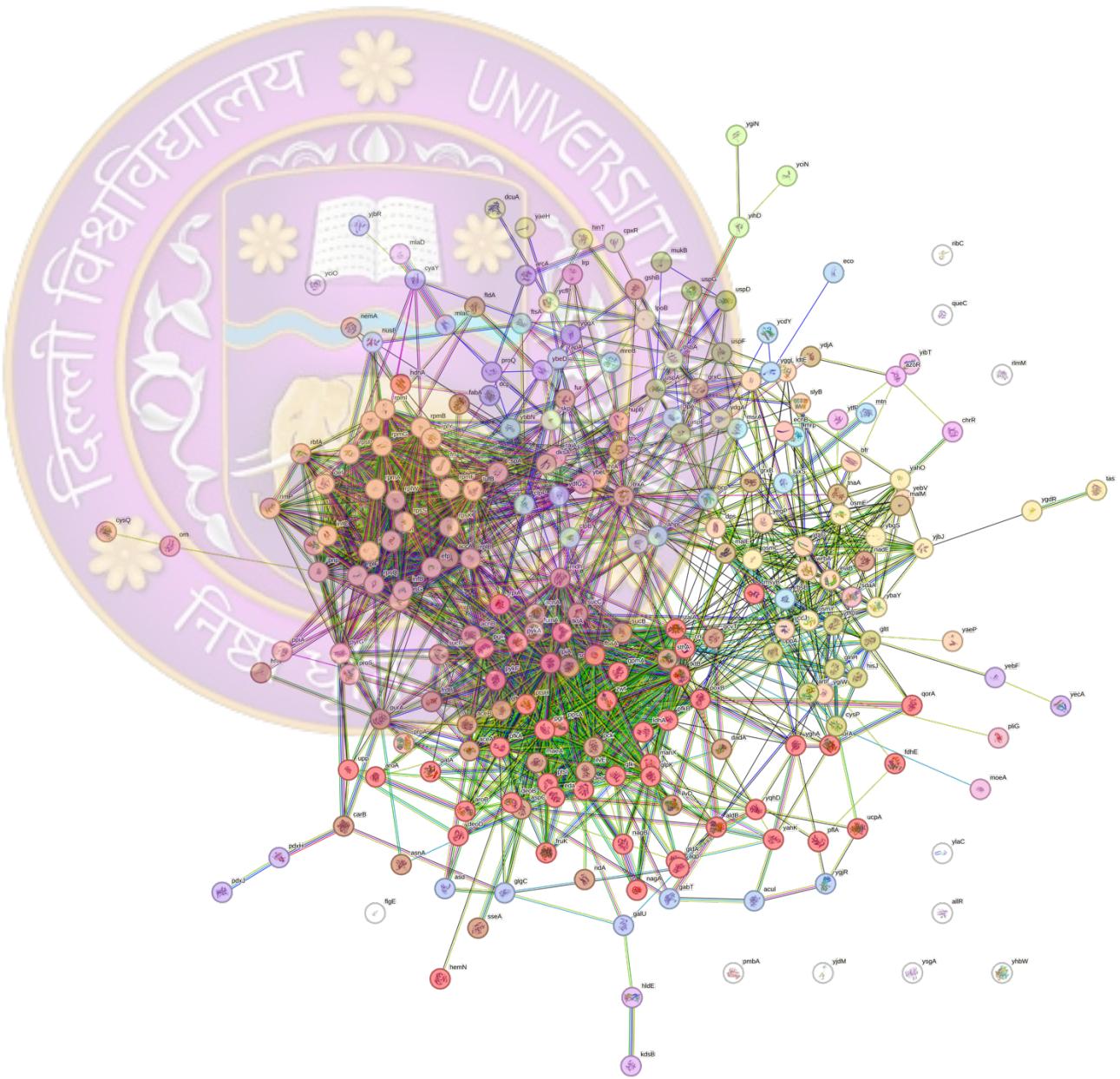
## Differentially Expressed Proteins(Fold Change)



**Fig. S7:** Clustered heatmap of differentially expressed secreted proteins. The overexpressed proteins are shown in red colour while the underexpressed proteins are shown in blue colour. For scalability, the top 54 underexpressed protein of the total 236 under expressed proteins were plotted against the 54 overexpressed proteins. The horizontal axis shows the fold change and the vertical axis on the right shows the UniProt ID of each protein. Each row represents a protein, and color intensity reflects the relative fold change values.



**Fig. S8:** Volcano plot depicting differential protein expressions at fold change beyond the defined threshold;  $p$ -value  $\leq 0.05$ . The over- and under-expressed proteins are shown in red and blue color, respectively. The plot was generated using ggvolcanoR (<https://ggvolcanor.erc.monash.edu/>). The zoomed in view highlights the exact position of the tig protein (UniProt ID P0A850) with  $\text{log}_2$  fold change value = 0.27 and  $p$  value of 3.81E-05 (0.0000381). Here,  $-\text{log}_{10} p$  value = 4.42 . Hence, the point at the intersection of  $x$  axis = 0.27 and  $y$  axis = 4.42 corresponds to the tig protein.



**Fig. S9:** PPI networks of underexpressed secretory proteins of MDR *E. coli*.