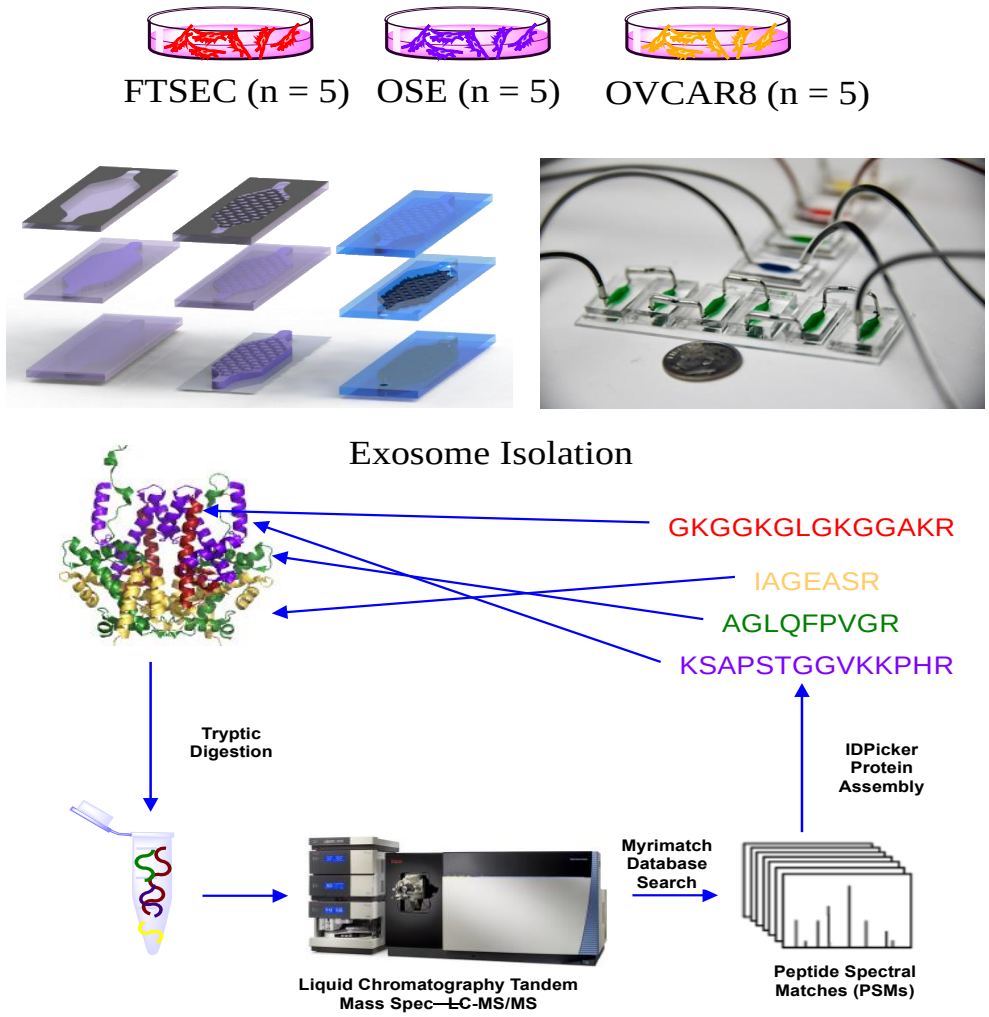
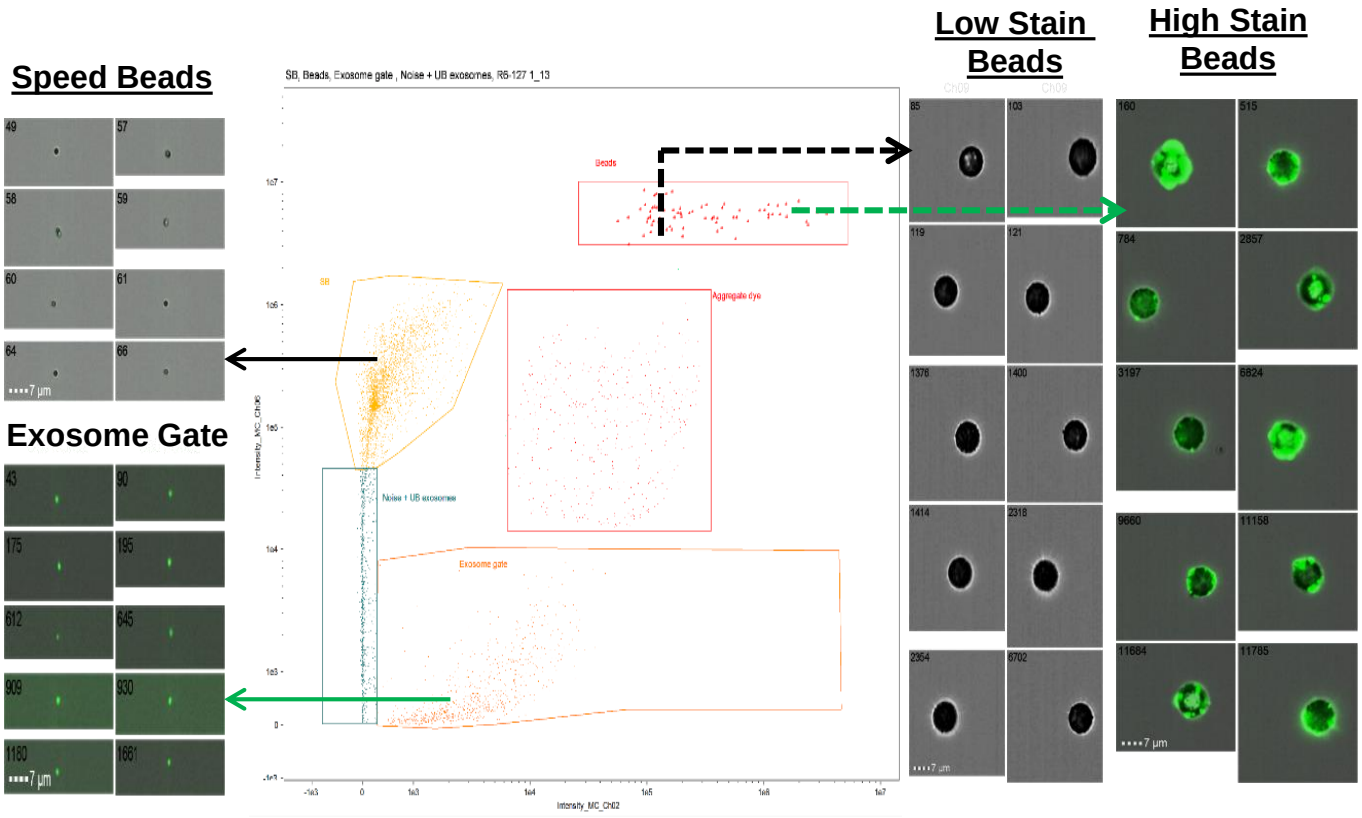
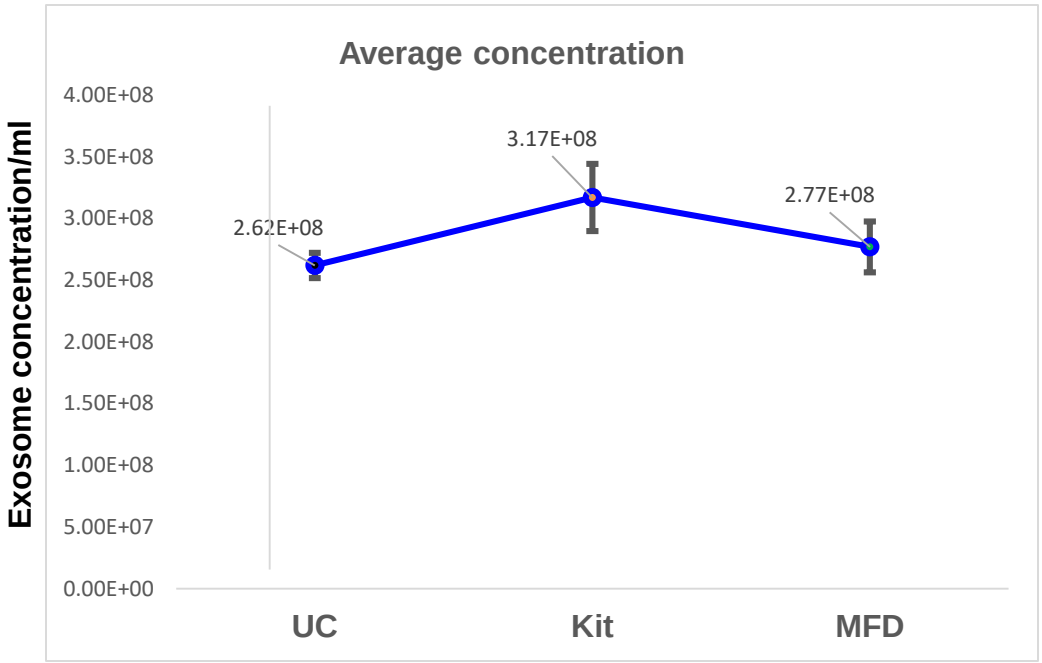


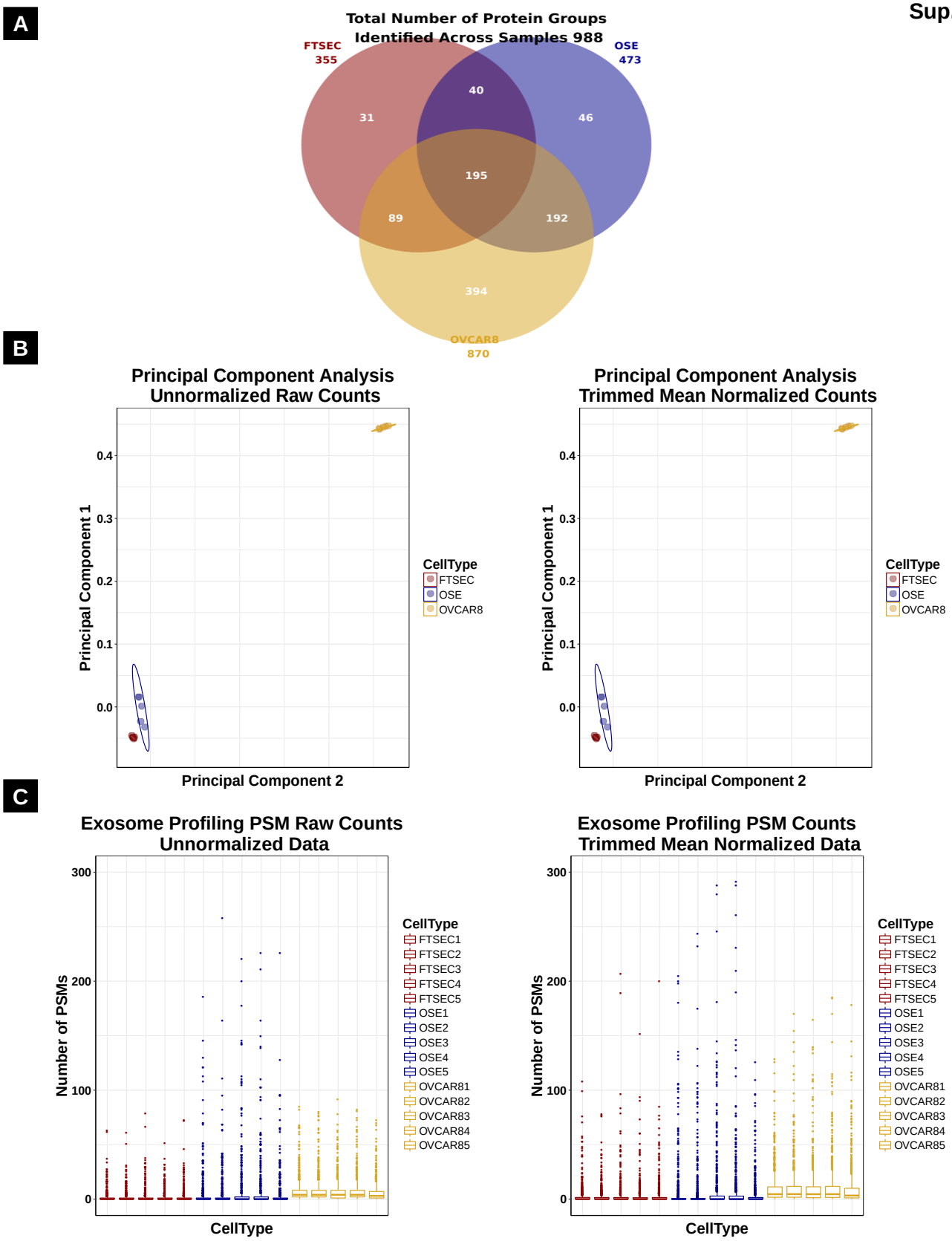
Sup. Fig. 1A: Work flow of our current study starting from isolation of exosomes using our microfluidics device from the culture media of five biological replicates from a HGSOC cell line (OVCAR8) and its precursor cells: ovarian surface epithelial cells (OSE) and fallopian tube secretory epithelial cells. The proteomic profiling by LCMS/MS was performed, followed by identification, and then subjected to different bioinformatics analyses to find out the upregulated pathways associated with the proteome data.



Sup. Fig. 1B: The intensity of the fluorescence on the magnetic beads bound for EpCAM-positive exosomes that are stained with CFSE dye are referred to as the low- and the highly-stained beads. Image stream analysis showing the gating of the speed beads (yellow), unbound exosomes (orange), low and high FITC beads (red).

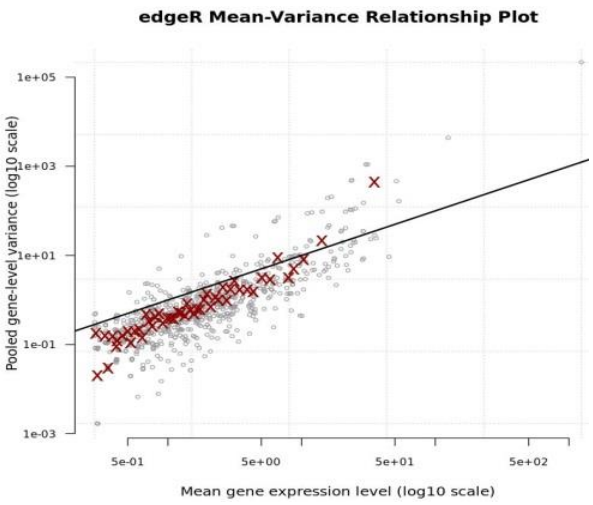


Sup. Fig. 1C: Average concentration of the vesicles captured in Ultracentrifugation (UC), Commercial Kit and microfluidics device (MFD) methods (n=3)

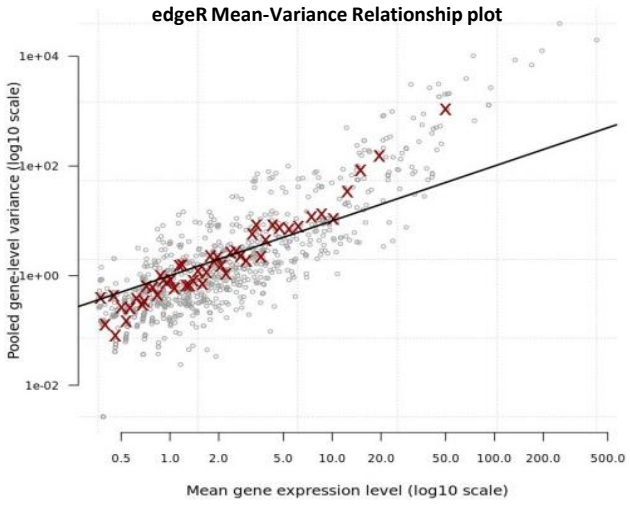


Sup. Fig. 2A: Total number of protein groups identified following protein assembly in IDPicker, prior to applying a filter threshold value of PSM > 8. **B:** Principal component analysis of data, pre- and post-normalization (n=5). **C:** Boxplot showing count distribution of data, pre- and post-normalization in the exosomes from all the three cell lines (n=5).

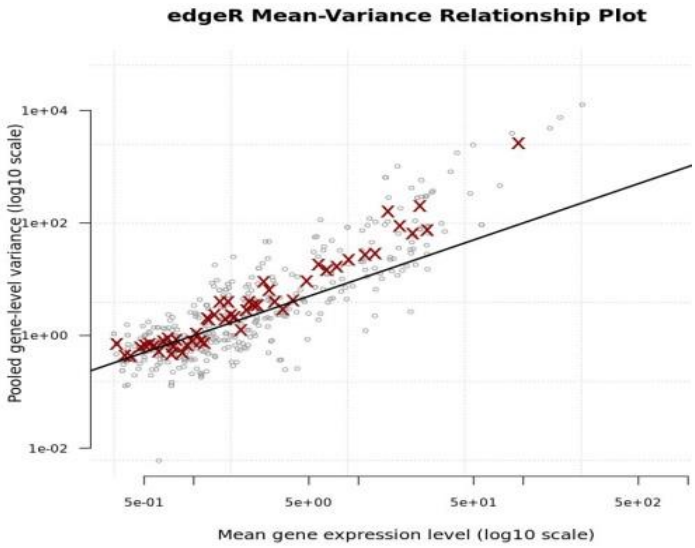
A **FTSEC vs. OVCAR8**



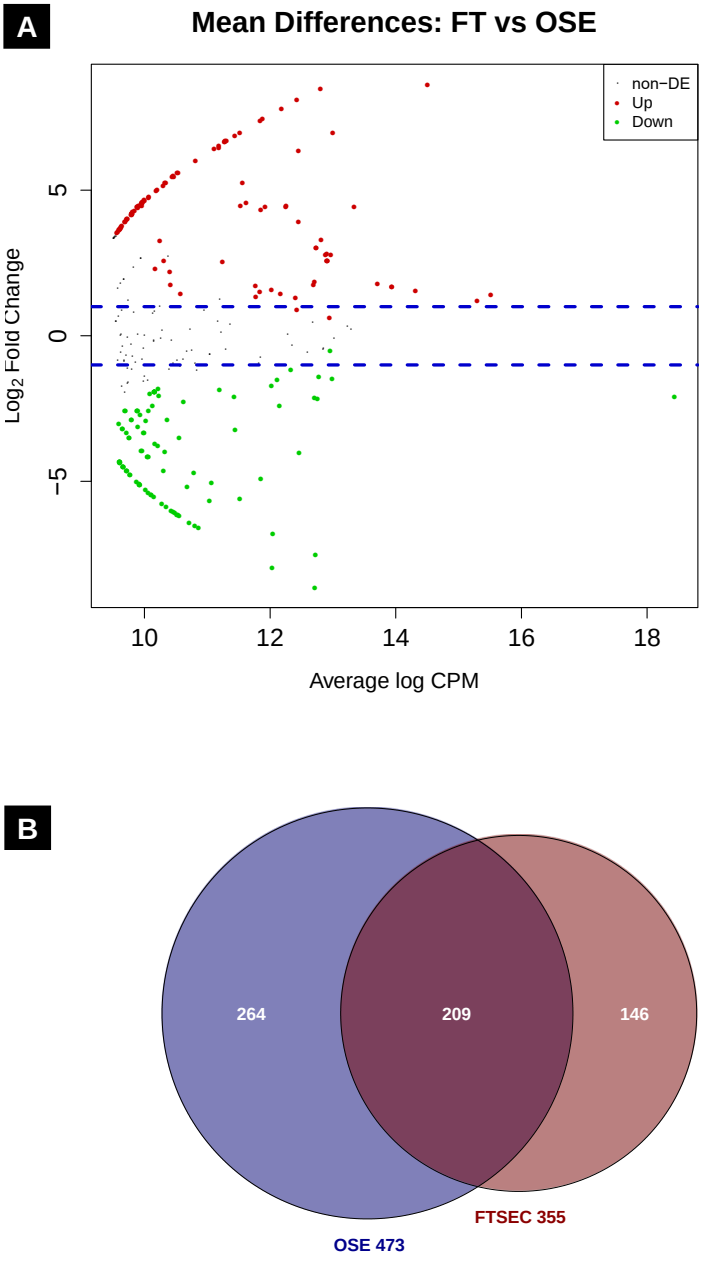
B **OSE vs. OVCAR8**



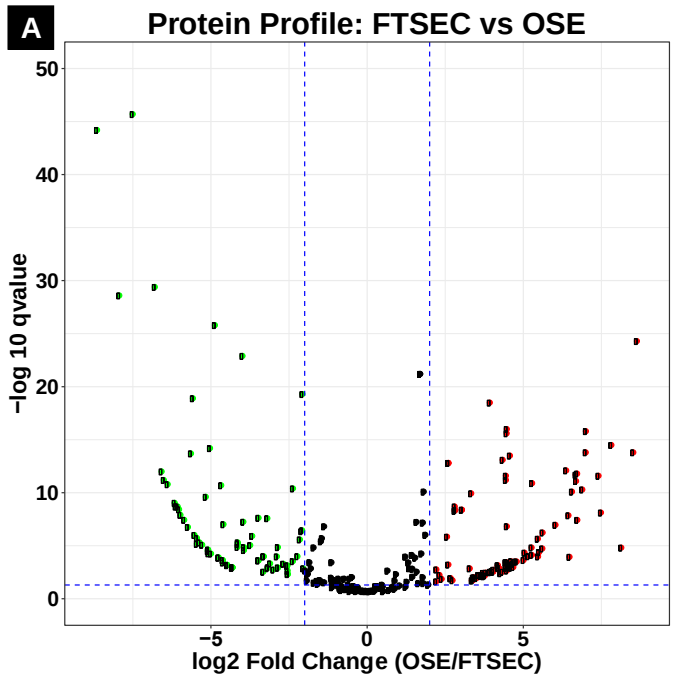
C **FTSEC vs. OSE**

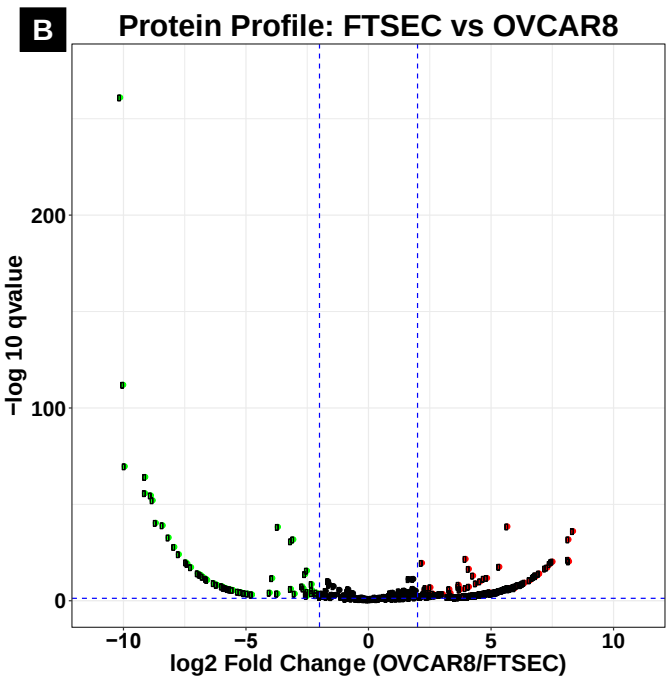


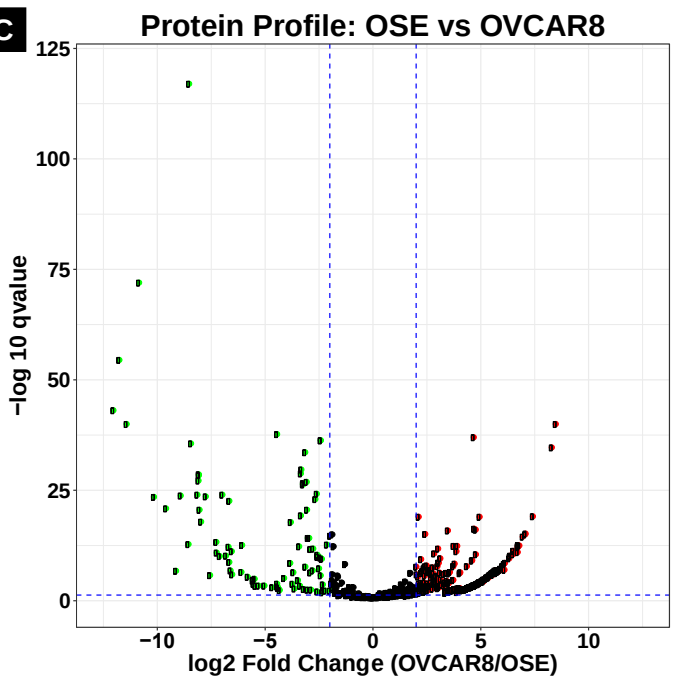
Sup. Fig. 3A-C: The relationship between mean protein expression and pooled protein level variance across each protein for FTSEC vs. OVCAR8, OSE vs. OVCAR8, and FTSEC vs. OSE exosomes is plotted showing a higher degree of positive correlation.



Sup. Fig. 4A: MA plot from EdgeR analysis. The blue ablines represent log $_2$ FC values with greater than 2-fold difference in expression. Proteins in red are upregulated in OSE, and those in green are upregulated in FTSEC. **B:** Venn Diagram where overlap of 209 is the total number of differentially expressed proteins in the OSE/FTSEC comparison.

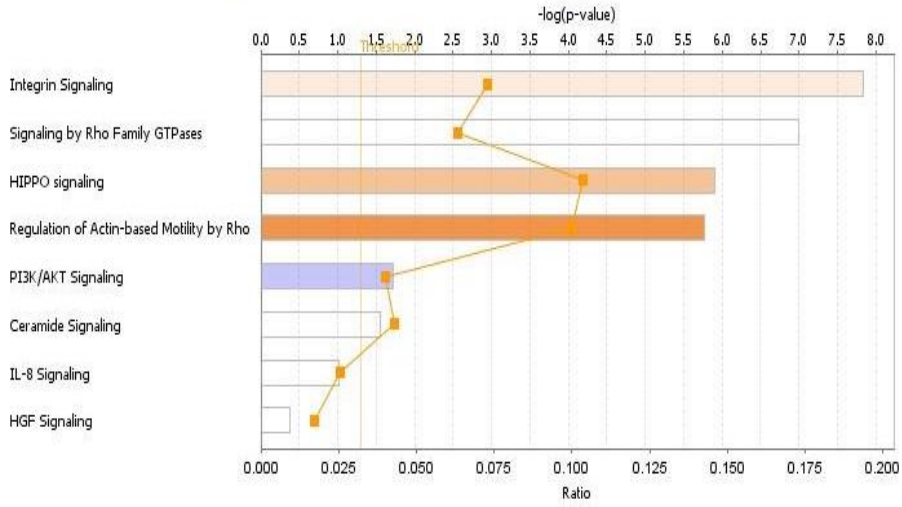




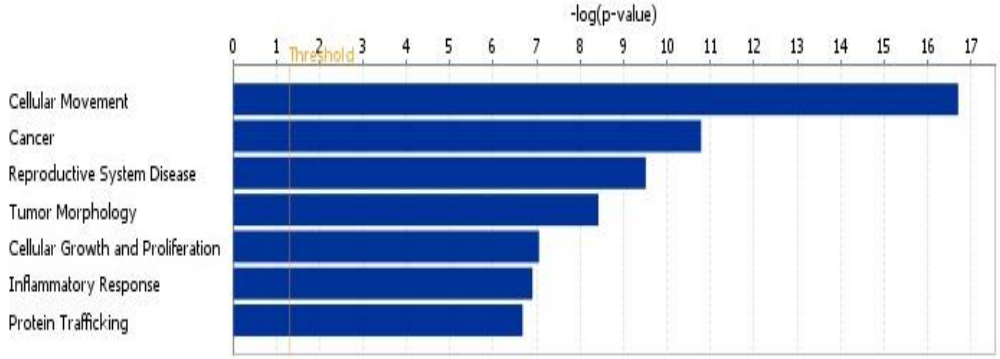


Sup. Fig. 5A-C: Volcano plots representing the protein profile in exosomes isolated from FTSEC, OSE, and OVCAR8. Vertical ablines is a log $_2$ Fold Change of 2 or four-fold difference in expression, while horizontal abline is a qvalue threshold of < 0.05. Proteins in red are upregulated in OSE (top) or OVCAR8 (bottom) and proteins in green are upregulated in FTSEC (top and bottom left) or OSE (bottom right).

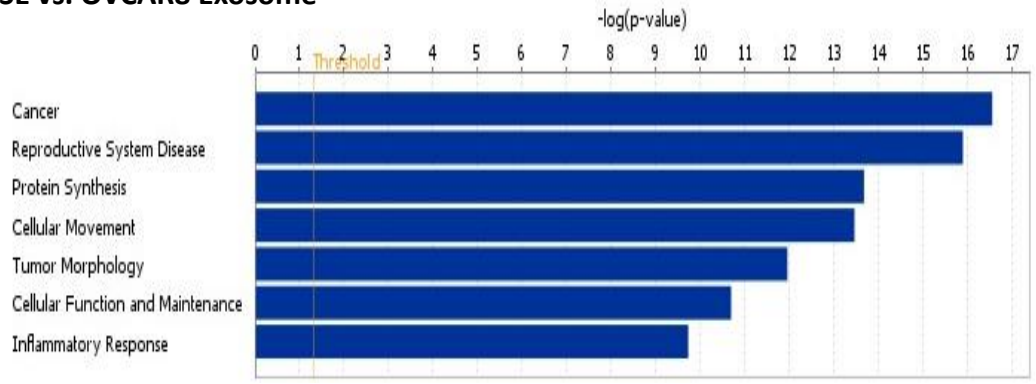
A **FTSEC vs. OSE Exosome**



B **FTSEC vs. OVCAR8 Exosome**

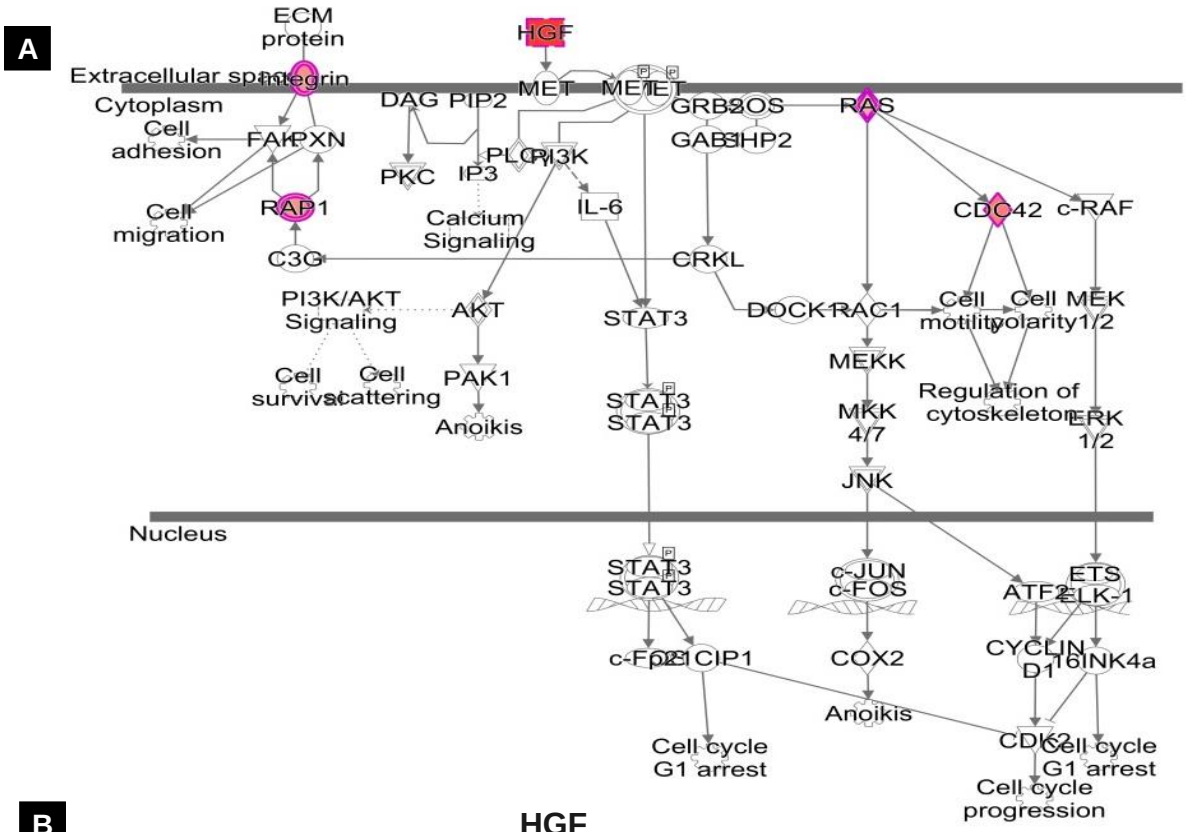


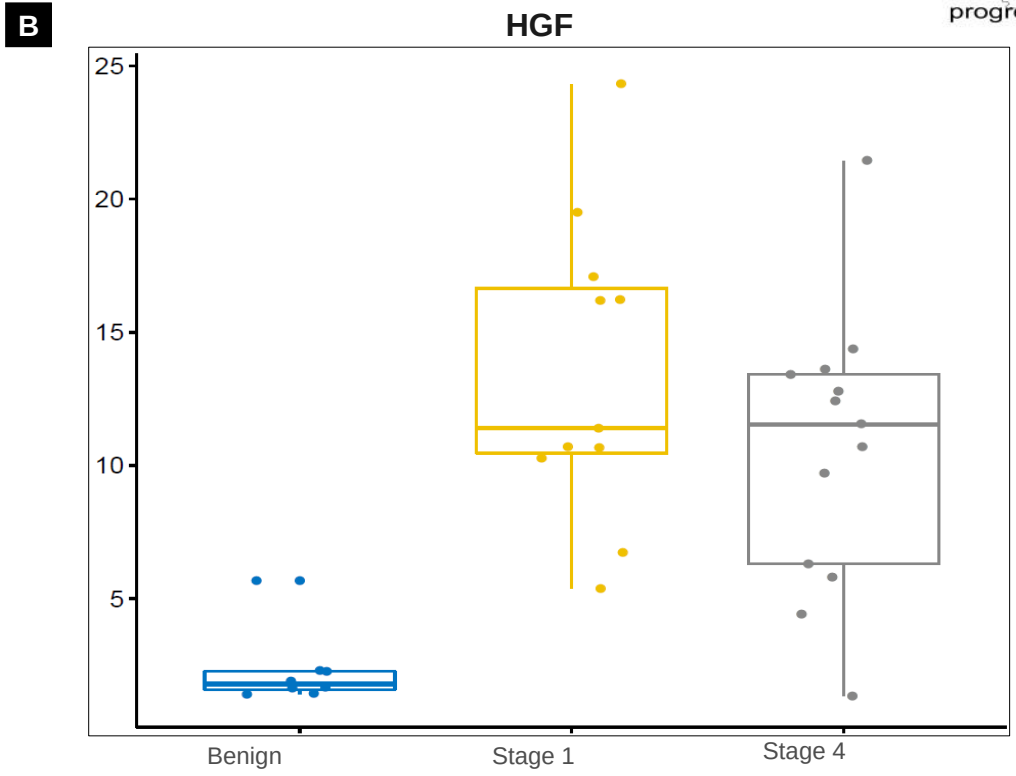
C **OSE vs. OVCAR8 Exosome**



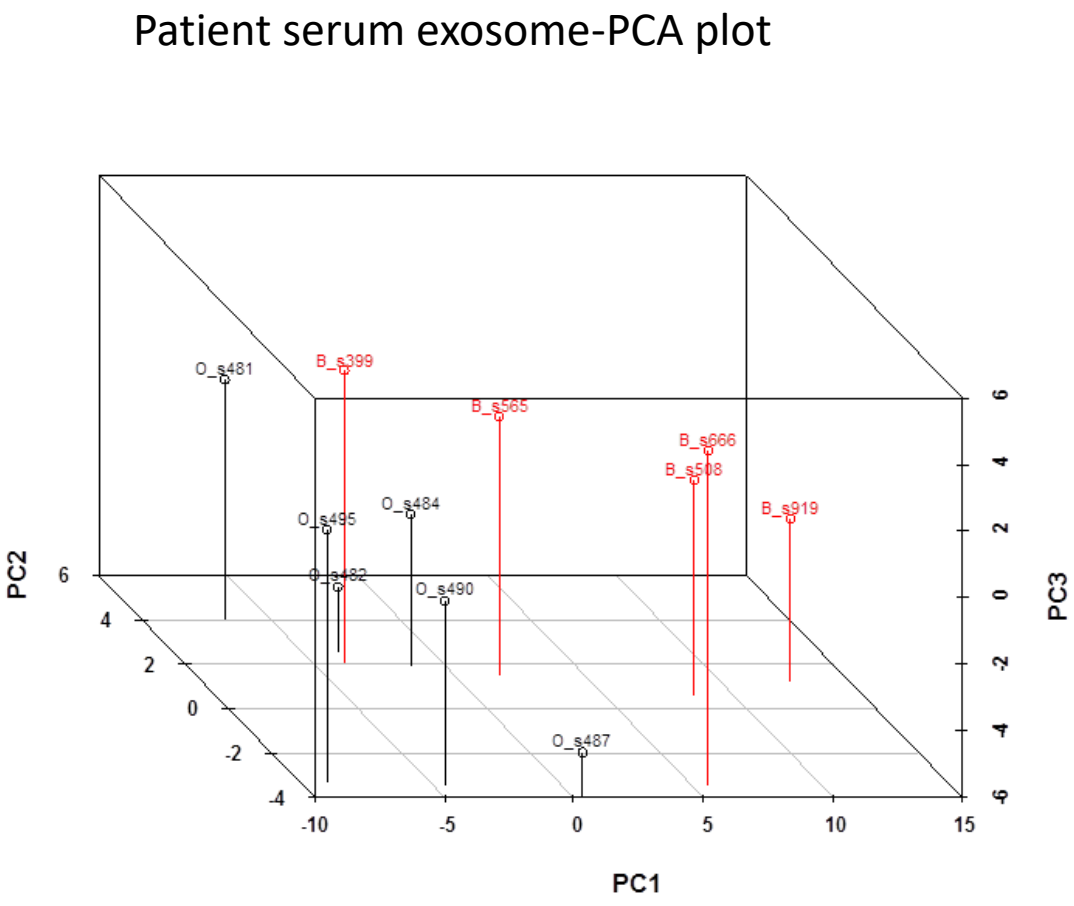
Sup. Fig. 6: **A)** The top Canonical pathways identified in the exosome protein data for FTSEC vs. OSE comparison based on Fishers exact test and selected based on their significance threshold above $p < 0.05$, show molecules involved in HGF signaling pathway to be upregulated in cancer exosomes. (Orange bars= positive Z- scores; blue bars= negative Z-scores; colourless bars= 0 Z- score). **B&C)** Top diseases and functions associated with the exosome protein data comparison between FTSEC vs. OVCAR8 and OSE vs. OVCAR8 based on Fishers exact test and selected based on their significance threshold above $p < 0.05$.

HGF signaling and Integrin signaling Pathway:





Sup. Fig. 7: A. HGF, the top molecule to be upregulated in our data set, shows the downstream proteins involved in the signaling network that predicts IL6 and STAT3 among its downstream effector molecules. **B**. Levels of HGF expression in benign (n=8), Stage-1 and IV serum exosomes (n=13; $p < 0.05$)



Sup. Fig. 8: Principal Component Analysis (PCA plot) on the filtered panel of immuno-oncology proteins in benign and HGSOC patient serum exosome samples. Linear model with variance smoothing method was used to test the group difference. FC 1.5 and P<0.02 were used as the cutoff for identifying the top proteins.