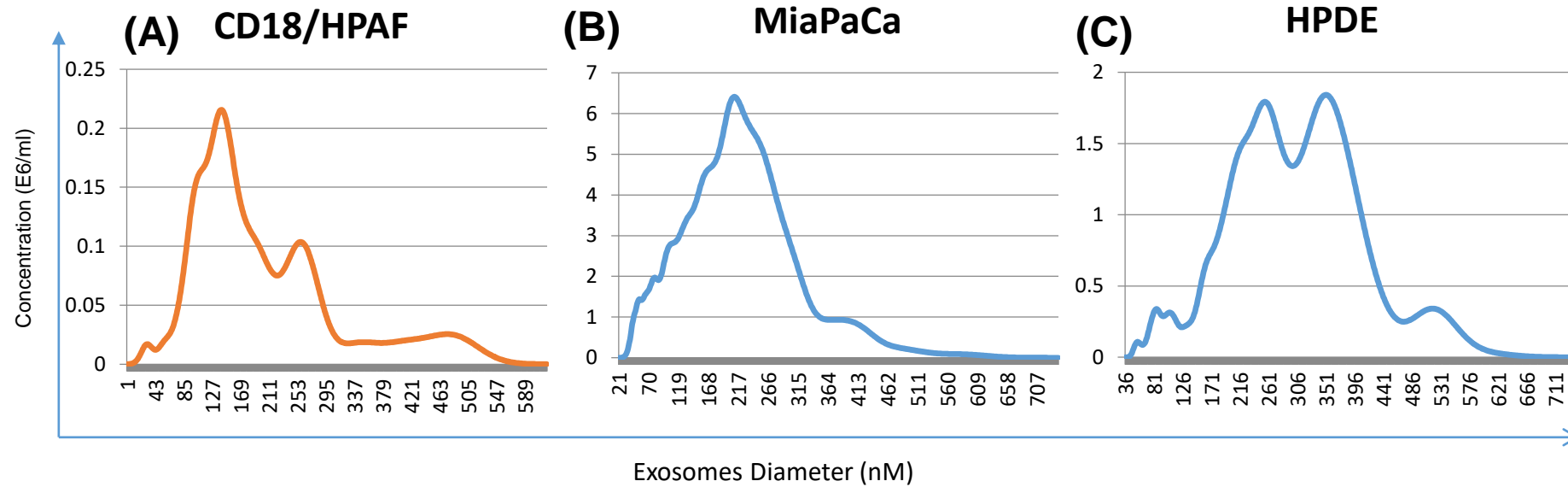
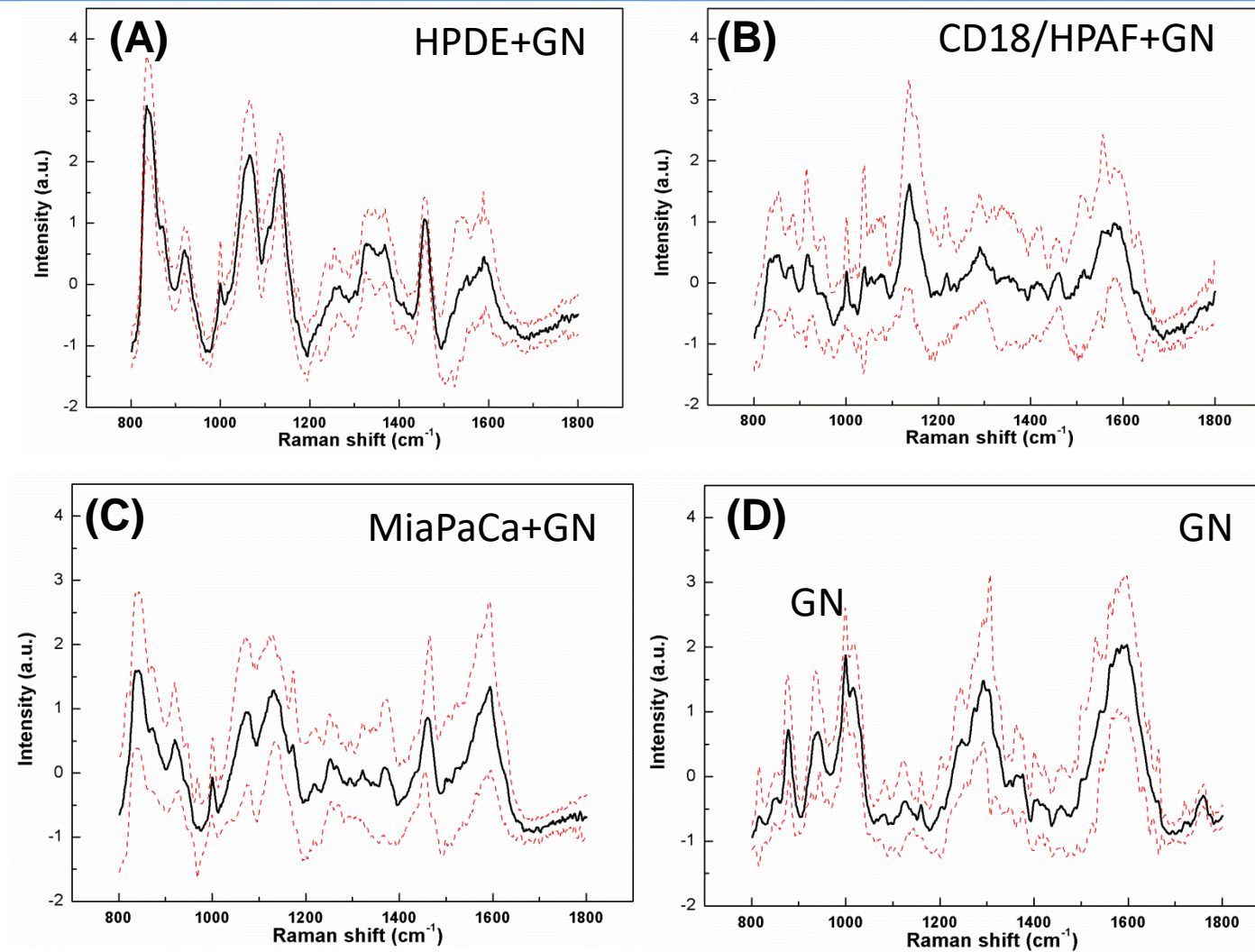


SUPPLEMENTARY FIGURE 1



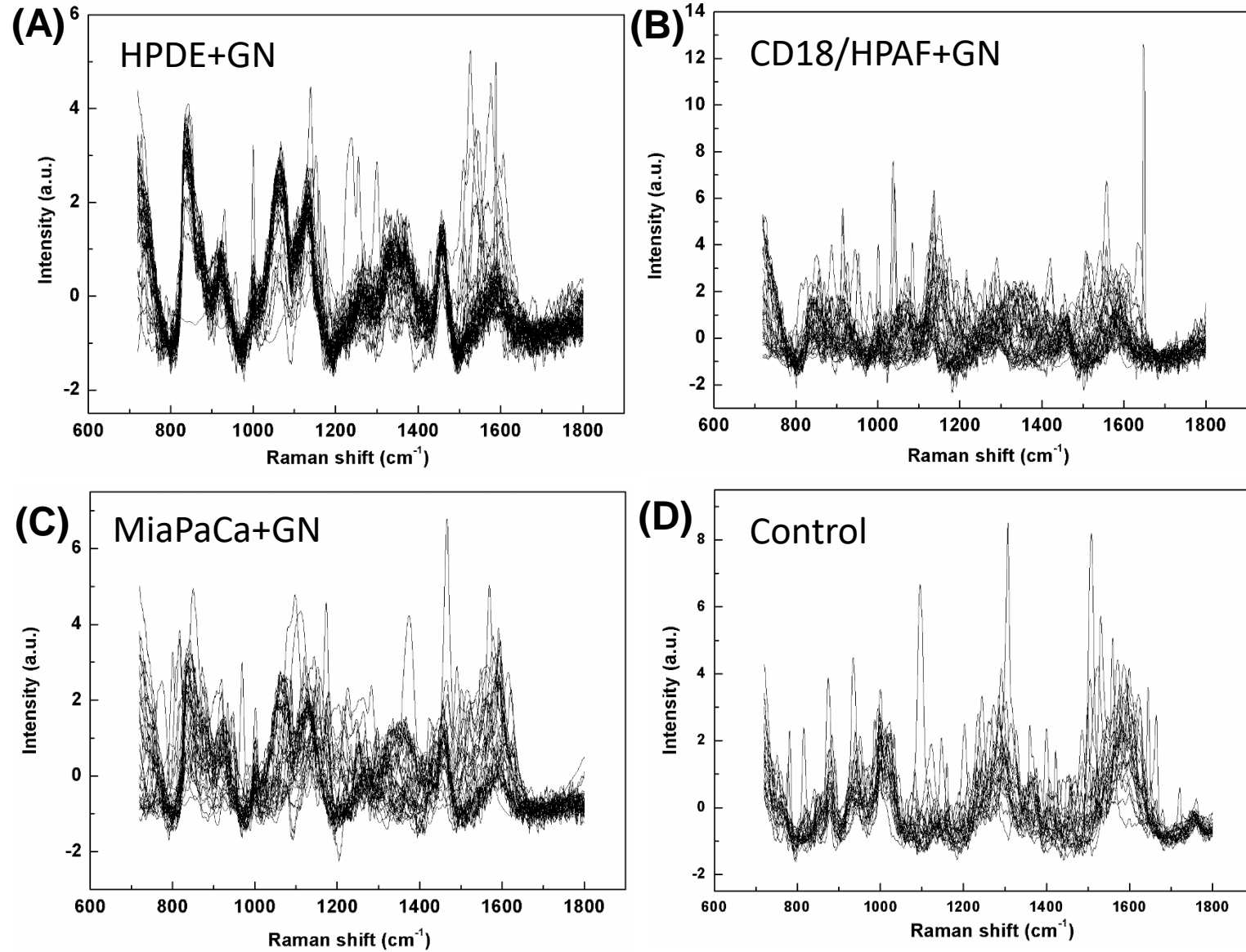
Supplemental Figure 1: NTA data for exosomes purified from (a) CD18/HPAF & (b) MiaPaCa pancreatic cancer cell lines and (c) HPDE pancreatic epithelial cell line. The y axis units are expressed $\times 10^8$ and the x-axis is particle size in nM.

SUPPLEMENTARY FIGURE 2



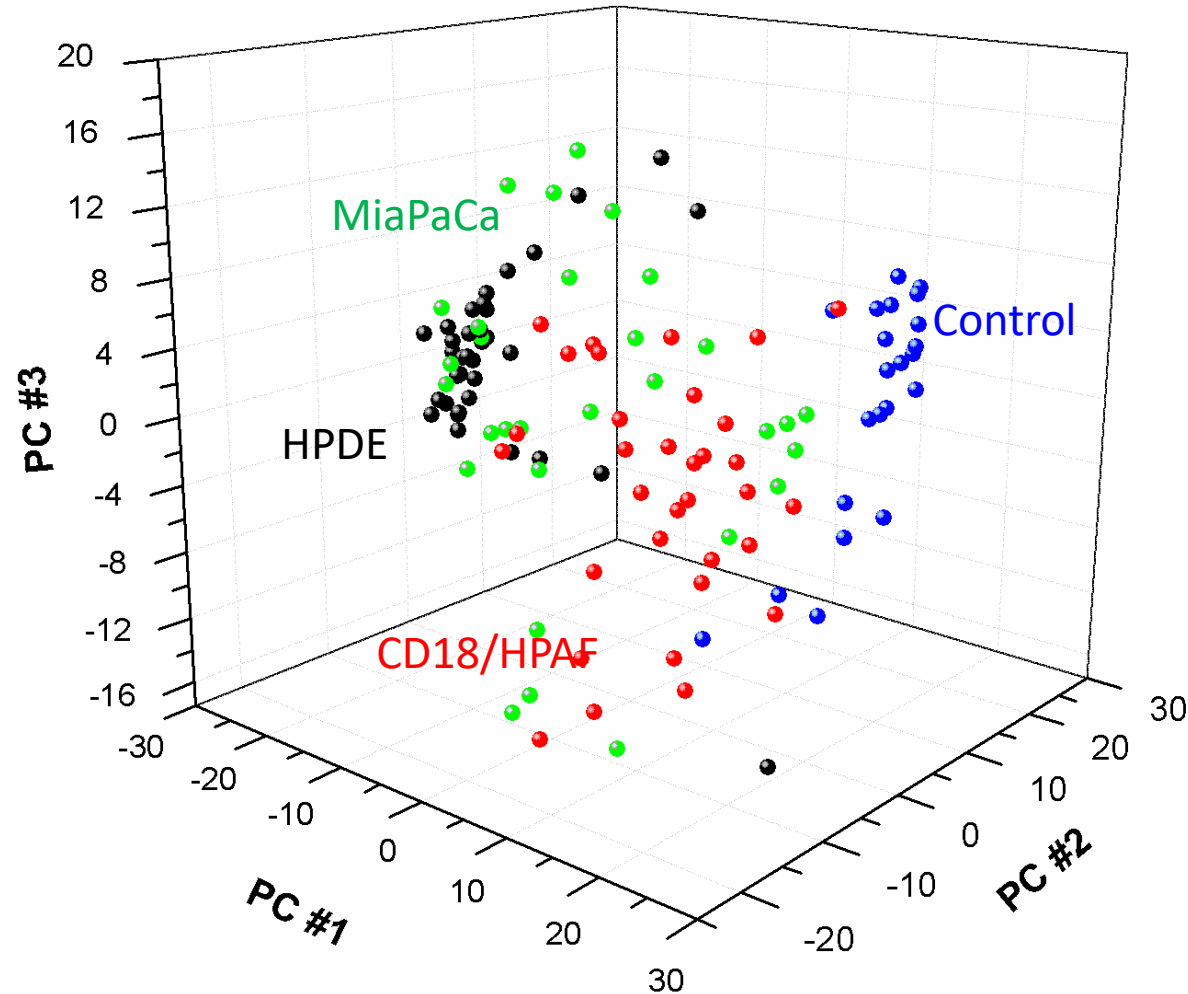
Supplemental Figure 2: Averaged SERS spectra for each sample type +/- standard deviation.

SUPPLEMENTARY FIGURE 3



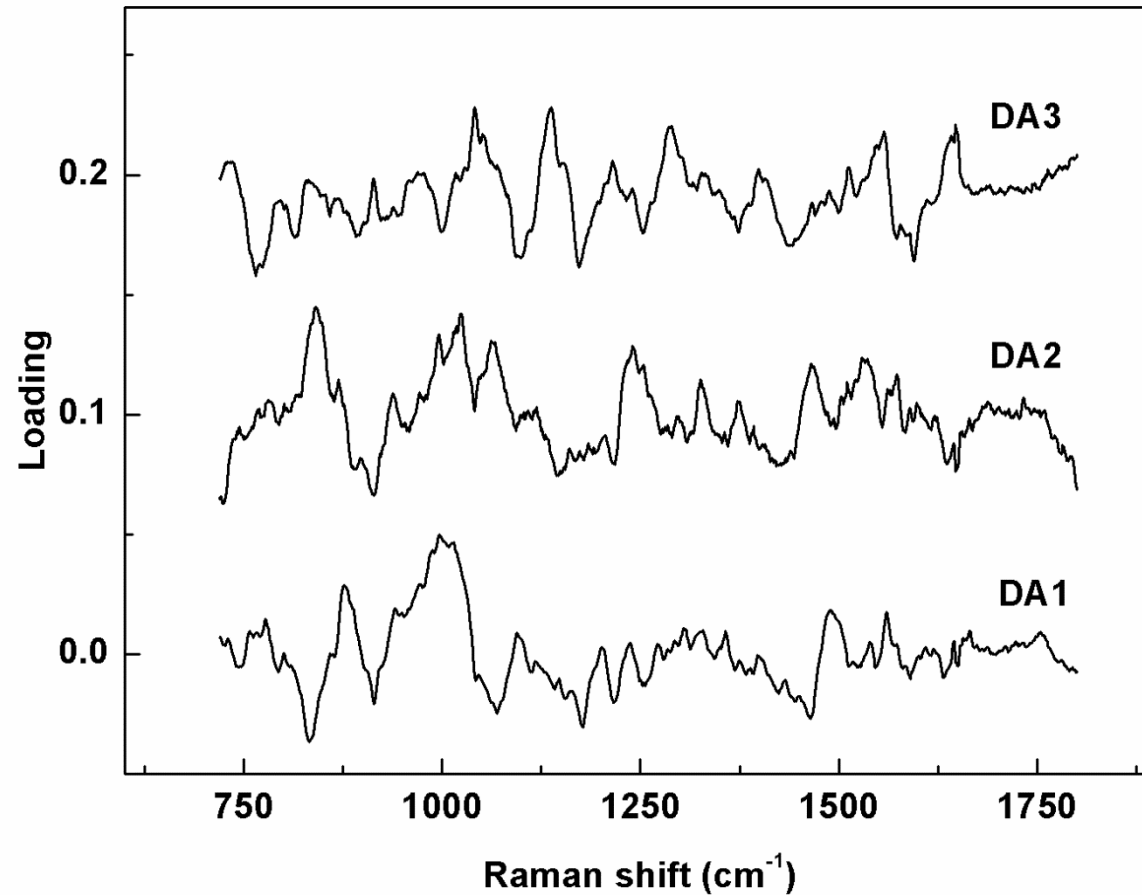
Supplemental Figure 3: (a)-(d) All of pre-processed SERS data for each sample population for use in PC-DFA.

SUPPLEMENTARY FIGURE 4



Supplemental Figure 4: 3D PCA plot showing exosome population clusters for first three PCs. PCA was used to reduce the number of variables considered from 1004 variables to 20 PCs which counted for 88.2% of the total variance. These 20 PCs were then utilized as the input independent variables for DFA.

SUPPLEMENTARY FIGURE 5



Supplementary Figure 5: Corresponding loading spectra for all three PC-DFA loadings to classify the three exosome groups and control group.