Supplementary Information

Dynamic Protein Corona of Gold Nanoparticles with An Evolving Morphology

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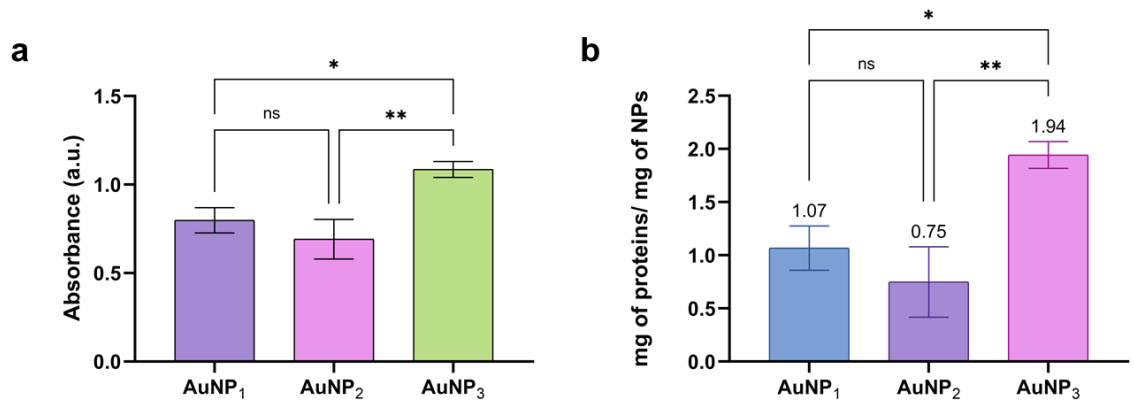
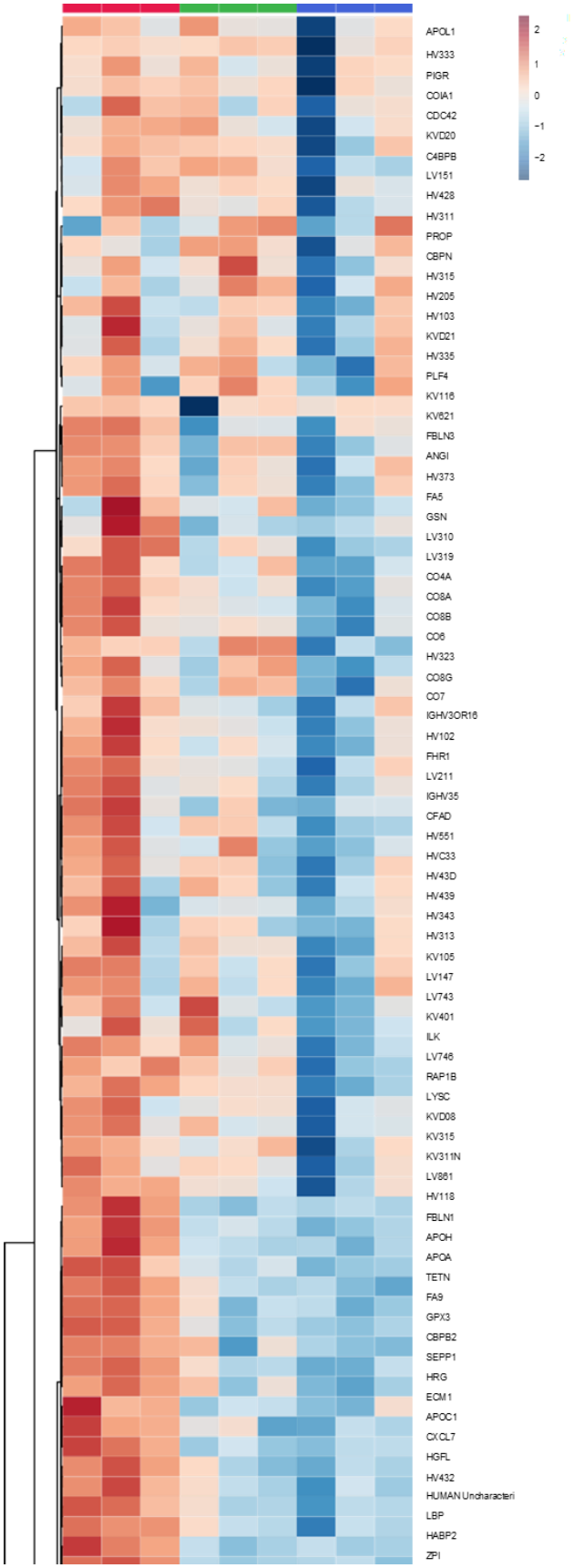


Figure S1. a) Adsorption measurement at 562 nm for different AuNP protein coronae. b) Total amount of proteins bound to different AuNPs (1 mg), determined from the BCA protein assay interpolating the BSA standard.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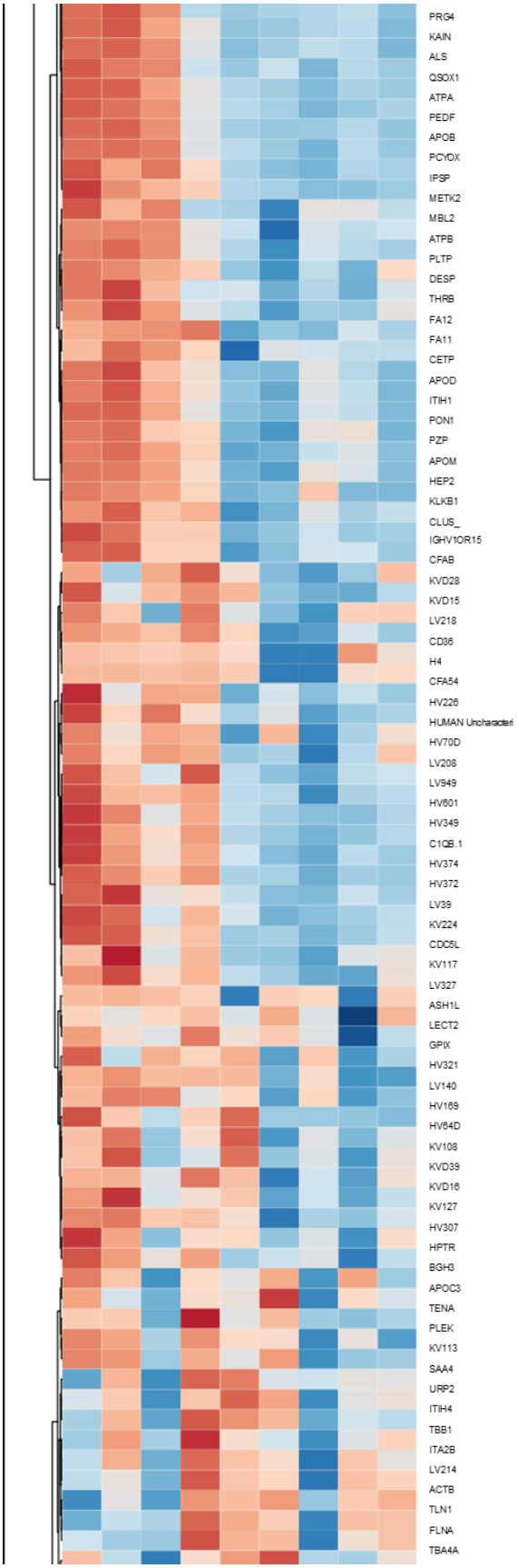
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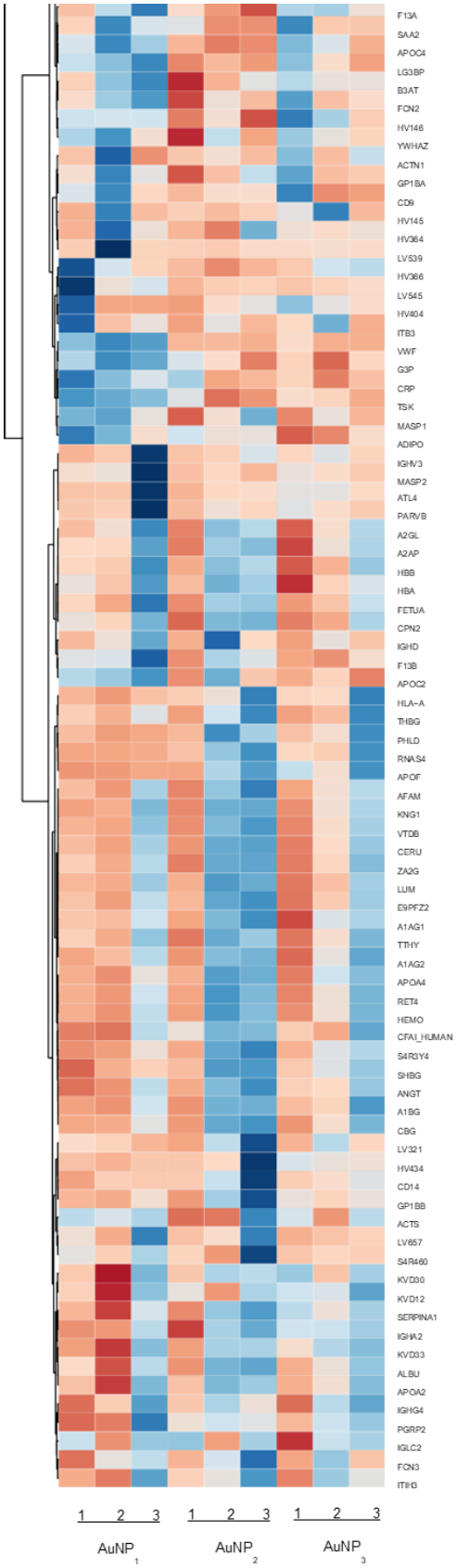

Figure S2. Hierarchical clustering heatmap for all 275 coronal proteins identified across the three AuNP groups.

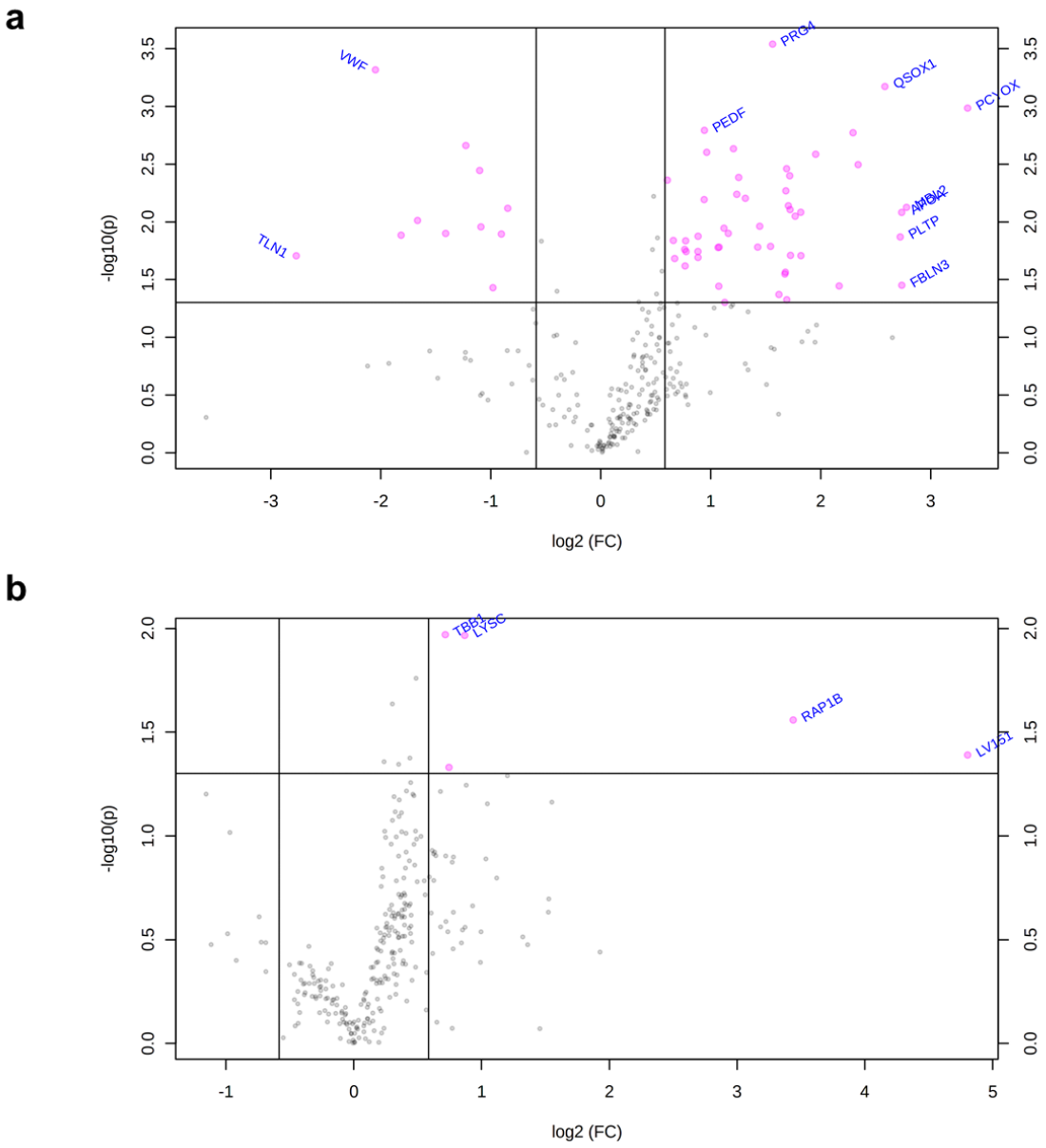

Figure S3. Volcano plot for the fold-change analysis (coronal proteins with a fold change cut-off below 0.5 and above 1.5, and with a *P*-value < 0.05) of a) $AuNP_1$ vs. $AuNP_2$ and b) $AuNP_2$ vs. $AuNP_3$.

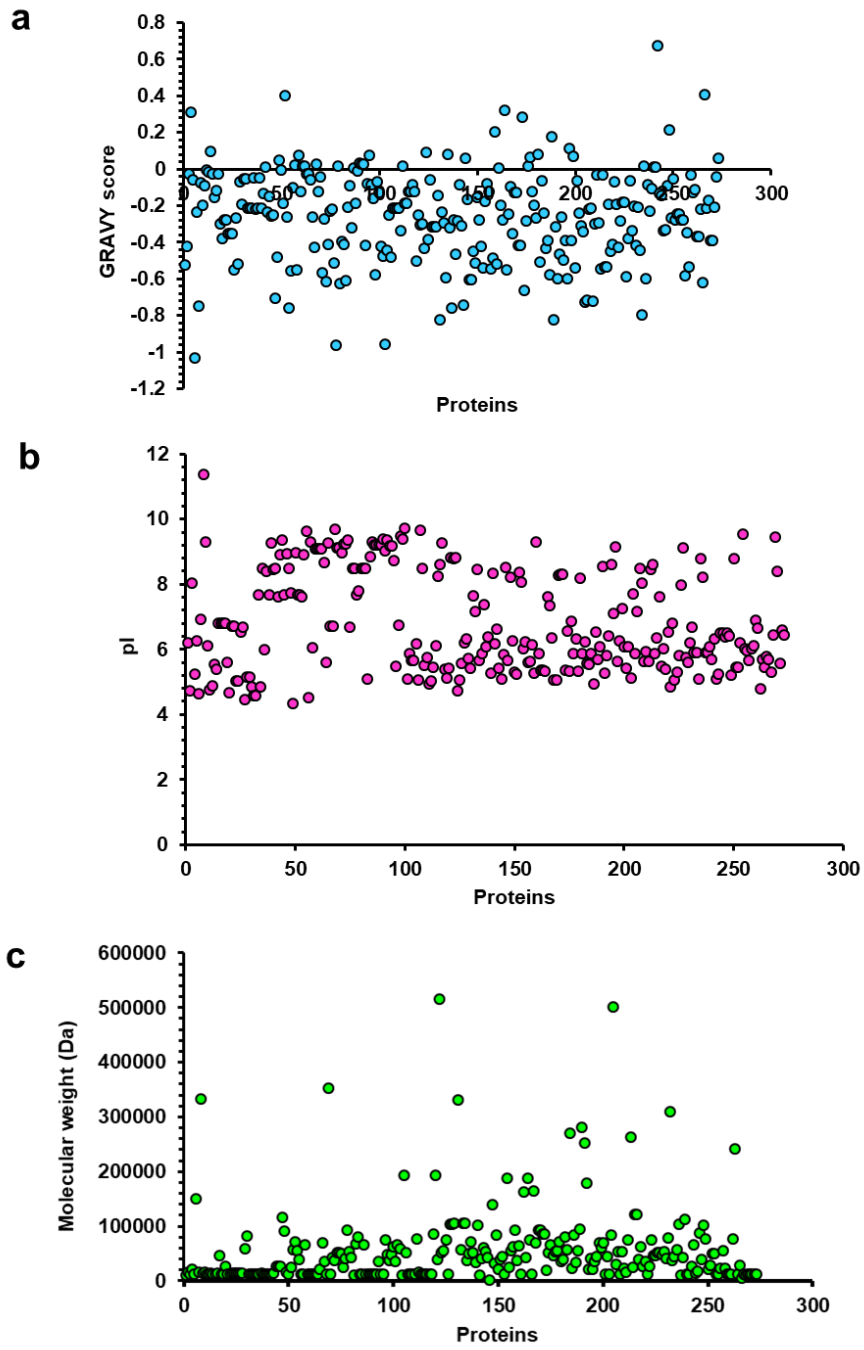

Figure S4. Coronal protein enrichment represented by a) grand average of hydropathy (GRAVY) index, b) isoelectric point (pI), and c) molecular weight for the common proteins identified across the AuNP series.

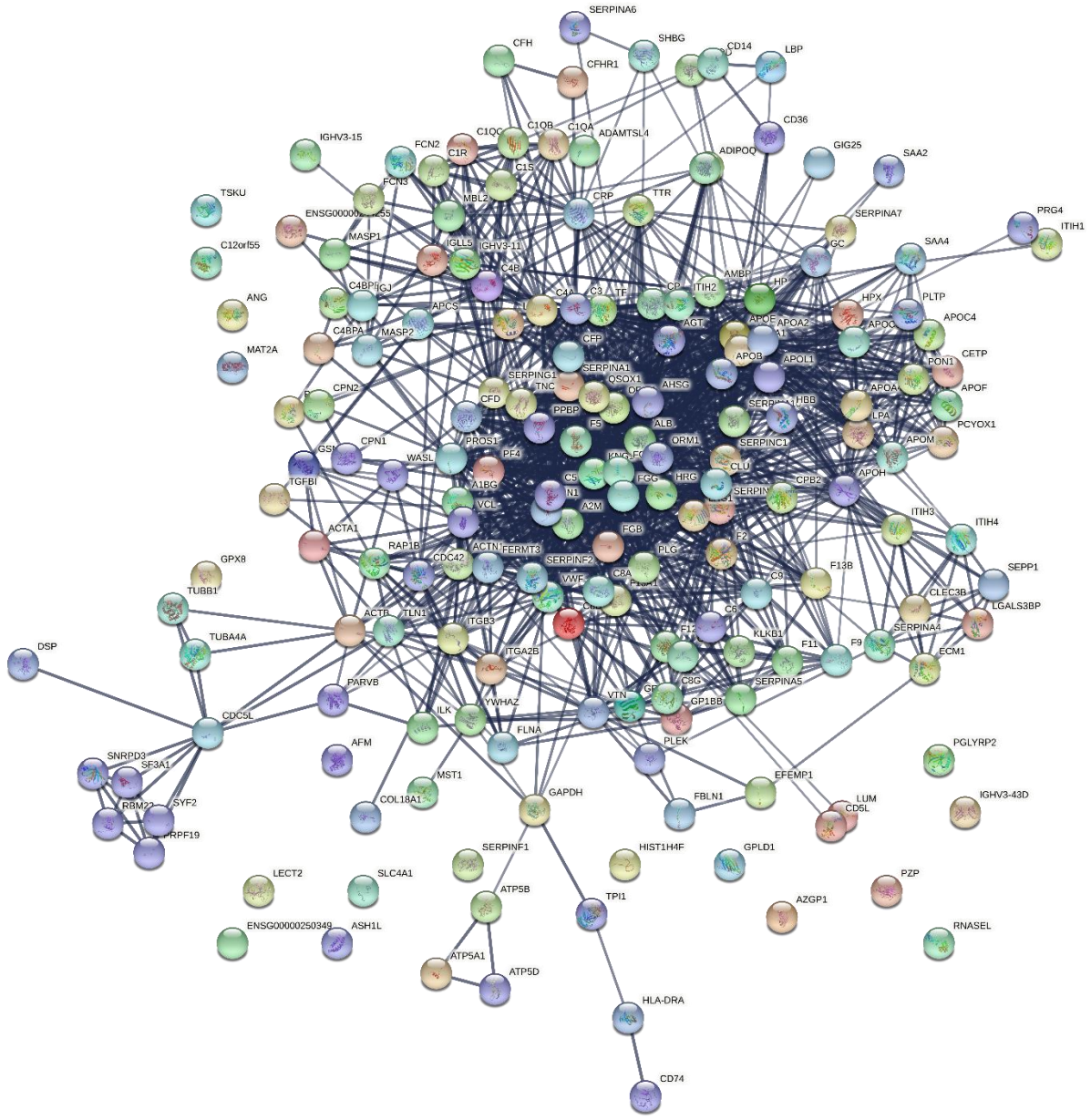

Figure S5. Compiled protein network for all 173 StringDB identified coronal proteins (out of 275, immunoglobulin sidechains excluded) across the three types of AuNPs.

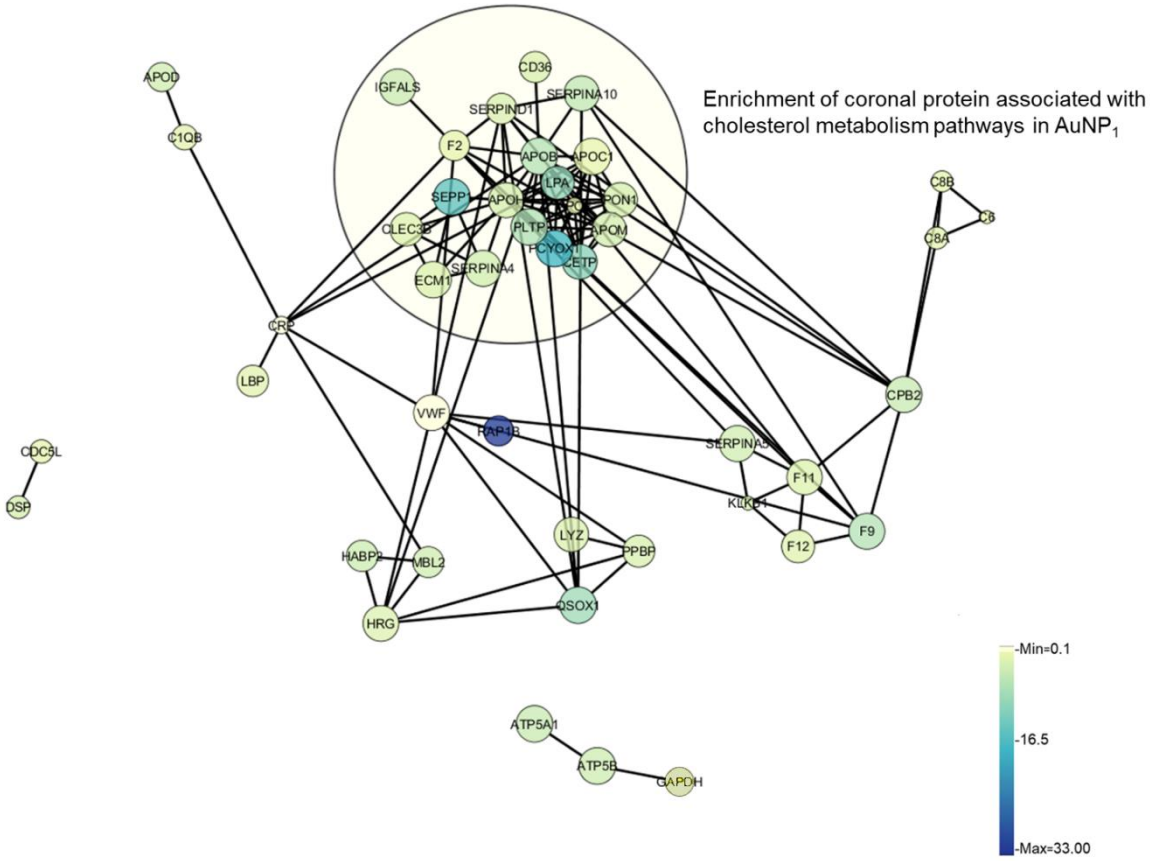

Figure S6. Protein interactive network generated in Cytoscape for the differentially associated coronal proteins on $AuNP_1$&$AuNP_3$. The relative fold change abundance ($AuNP_1$/$AuNP_3$) is indicated by the motif color and the size indicates the *p*-value for the relative fold change data. Cluster maker app from the cytoscape using Markov CLustering Algorithm (MCL) was used to highlight the enrichment of Apolipoproteins and other proteins involved in the cholesterol metabolism pathways in spiky $AuNP_1$.

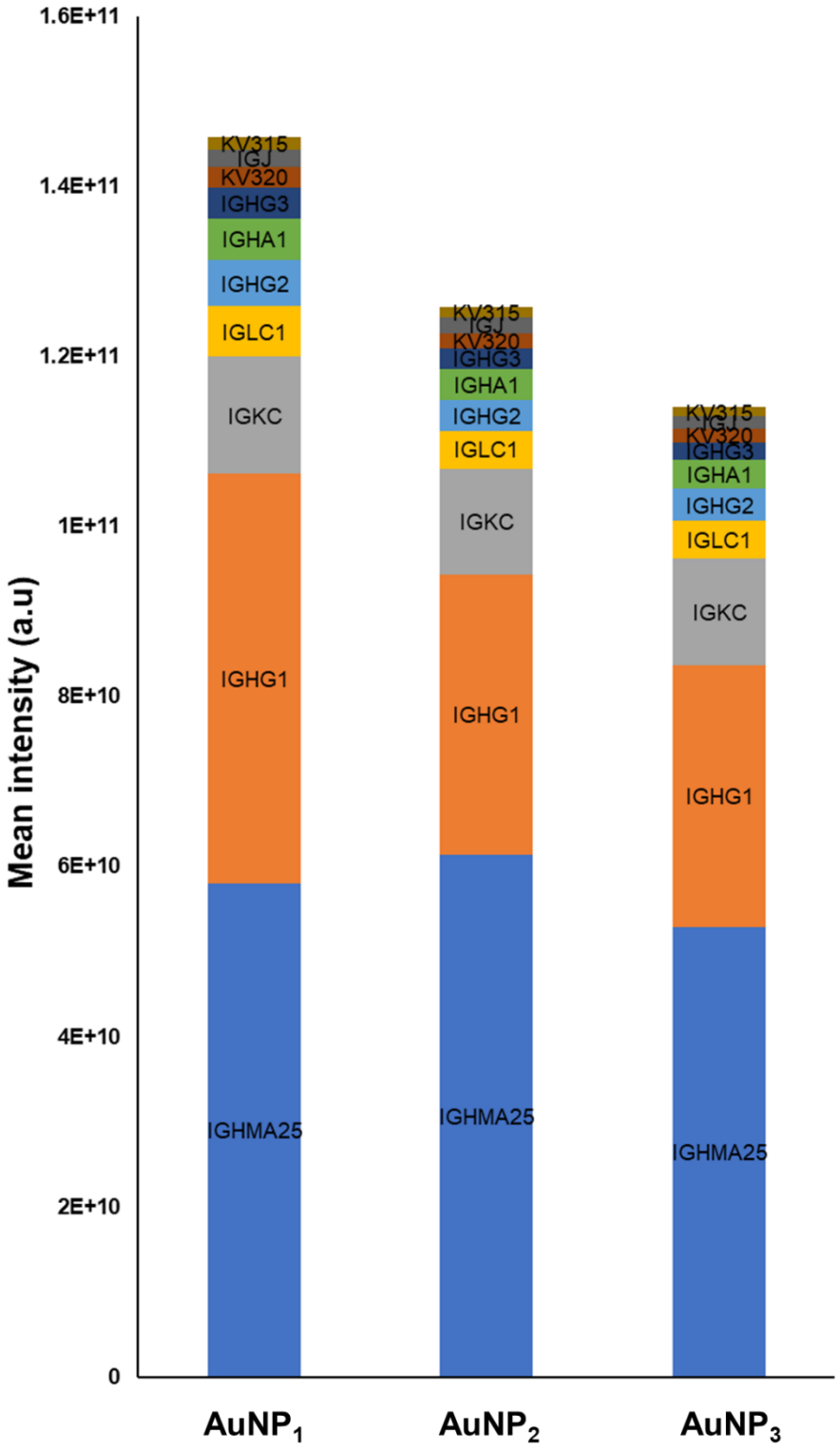

Figure S7. Mean intensity comparison of top-10 abundant immunoglobulin sidechains associated with the coronal proteins of the three types of AuNPs.