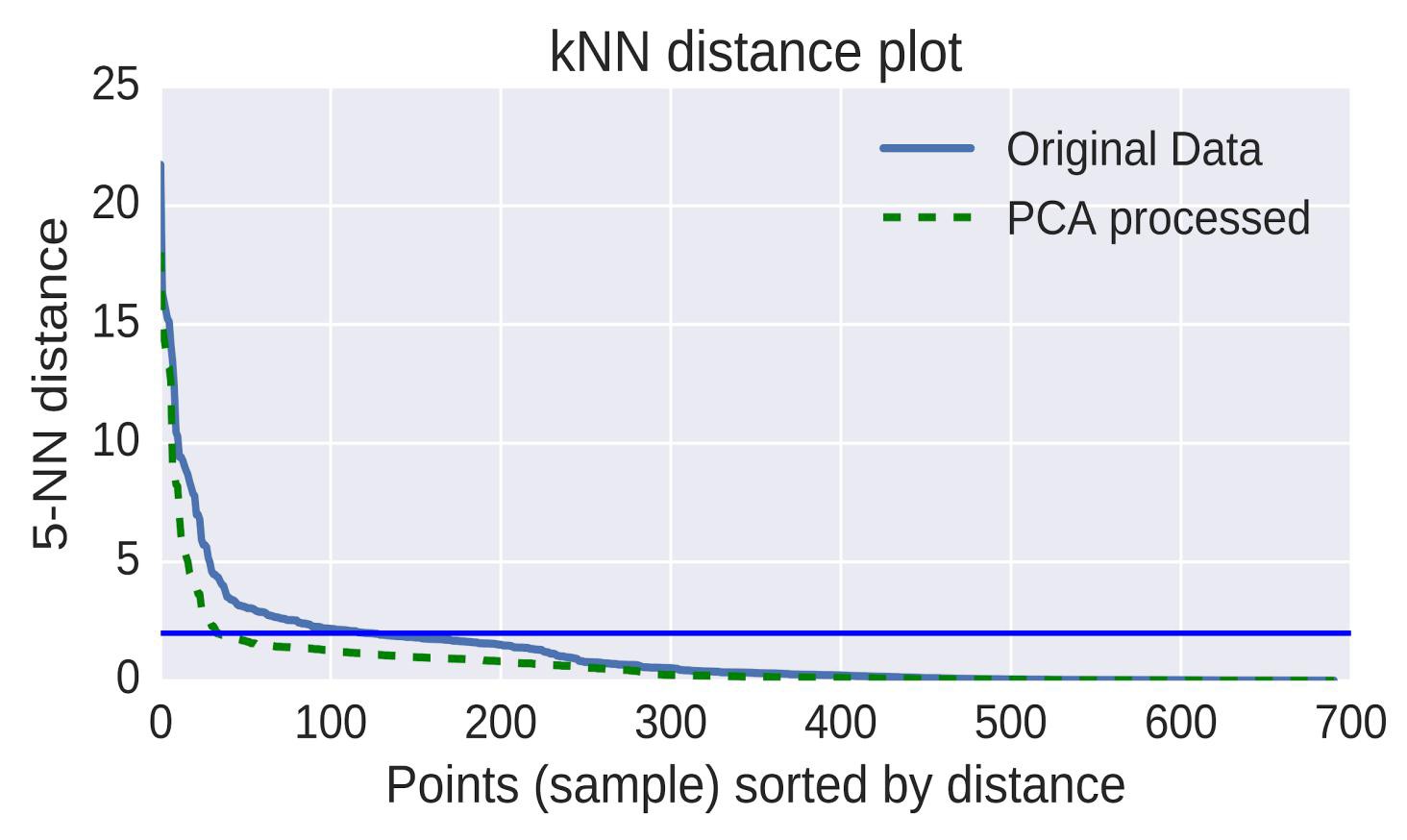
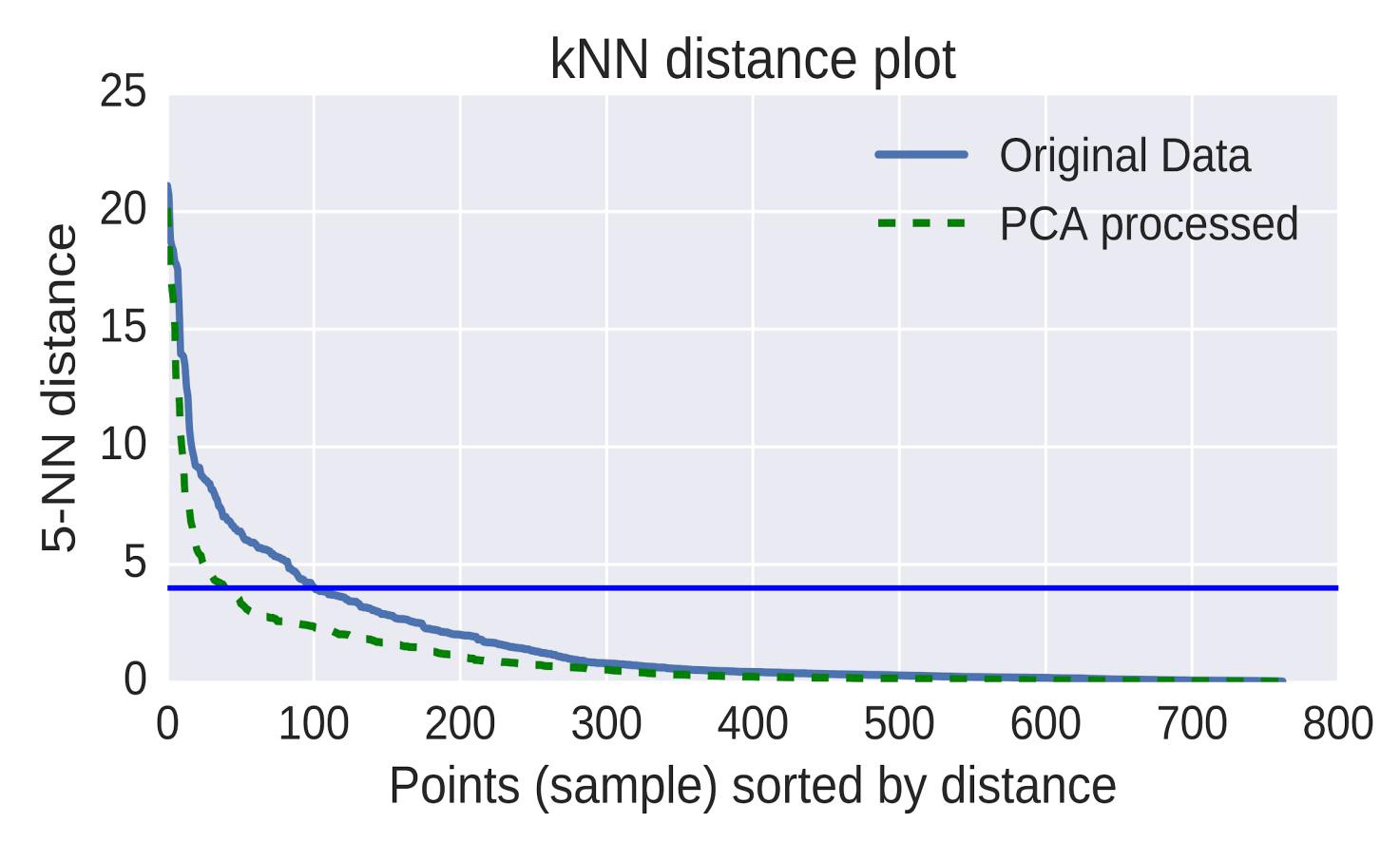
**Supporting Material**

***In vitro* and *in silico* determination of the interaction of artemisinin with human serum albumin.**

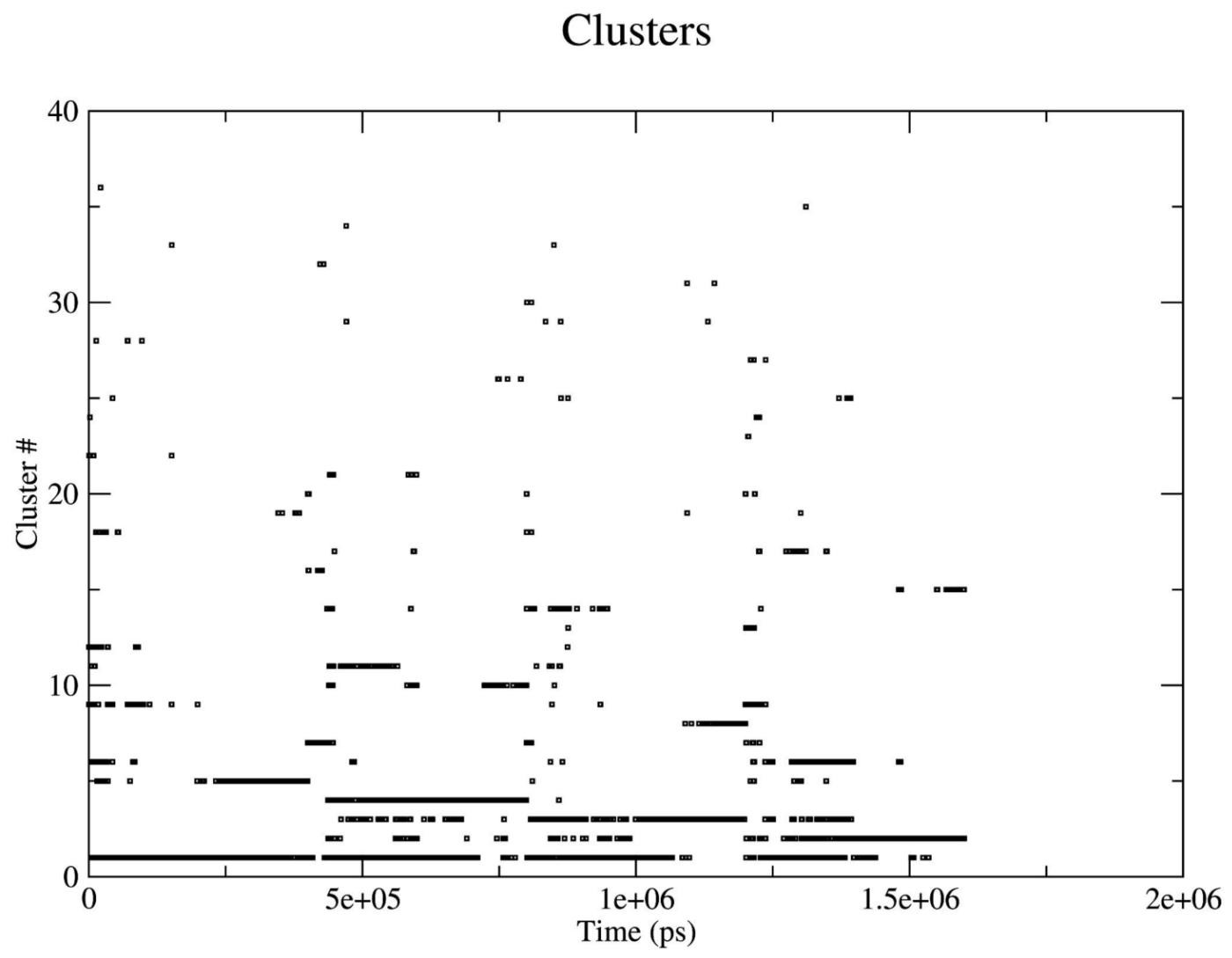
*S. Ginosyan, H. Grabski, S. Tiratsuyan*



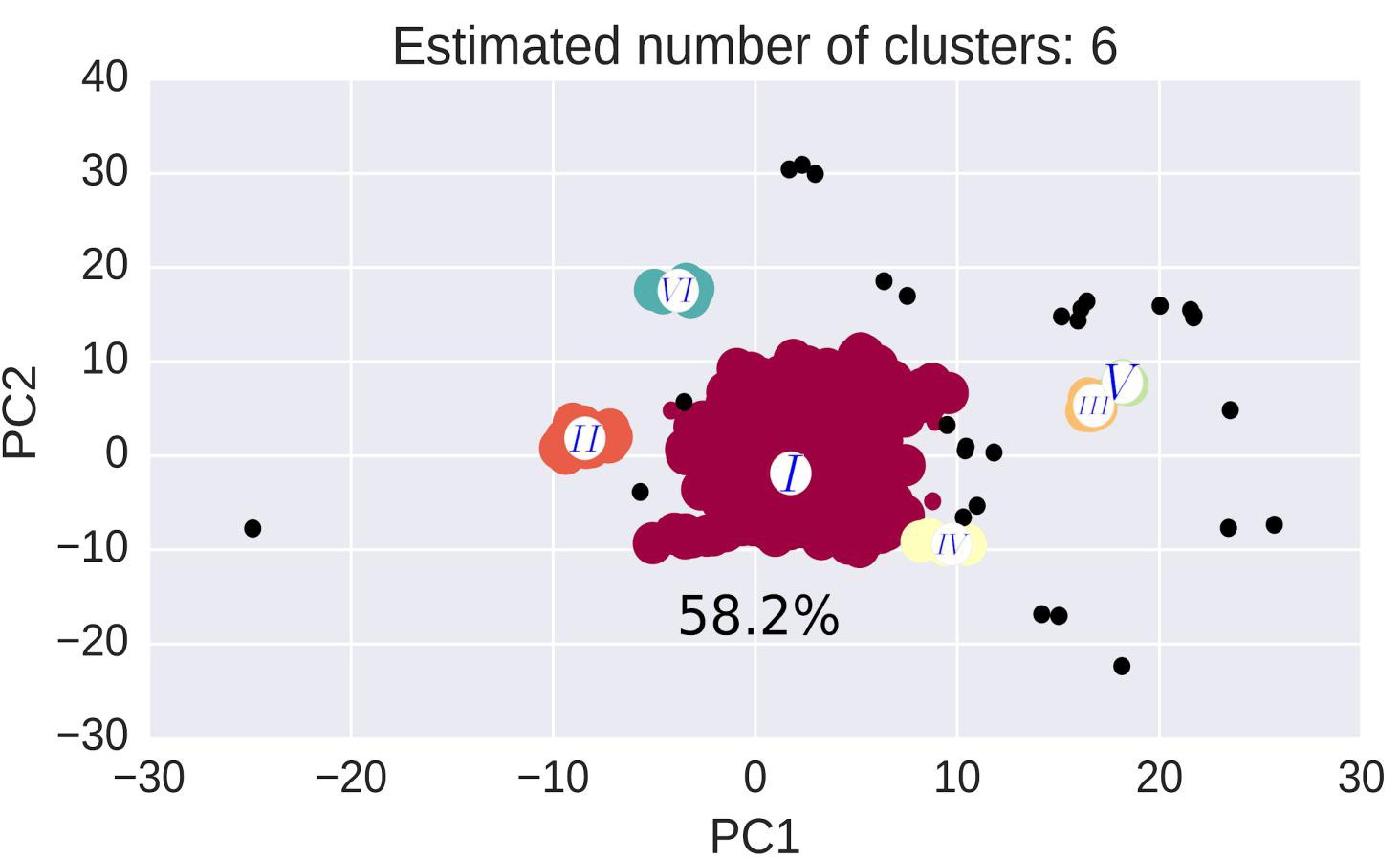
**Figure S1.** k-Nearest Neighbor distance plot of the center of mass coordinates from the results of multiple docking runs of ART.



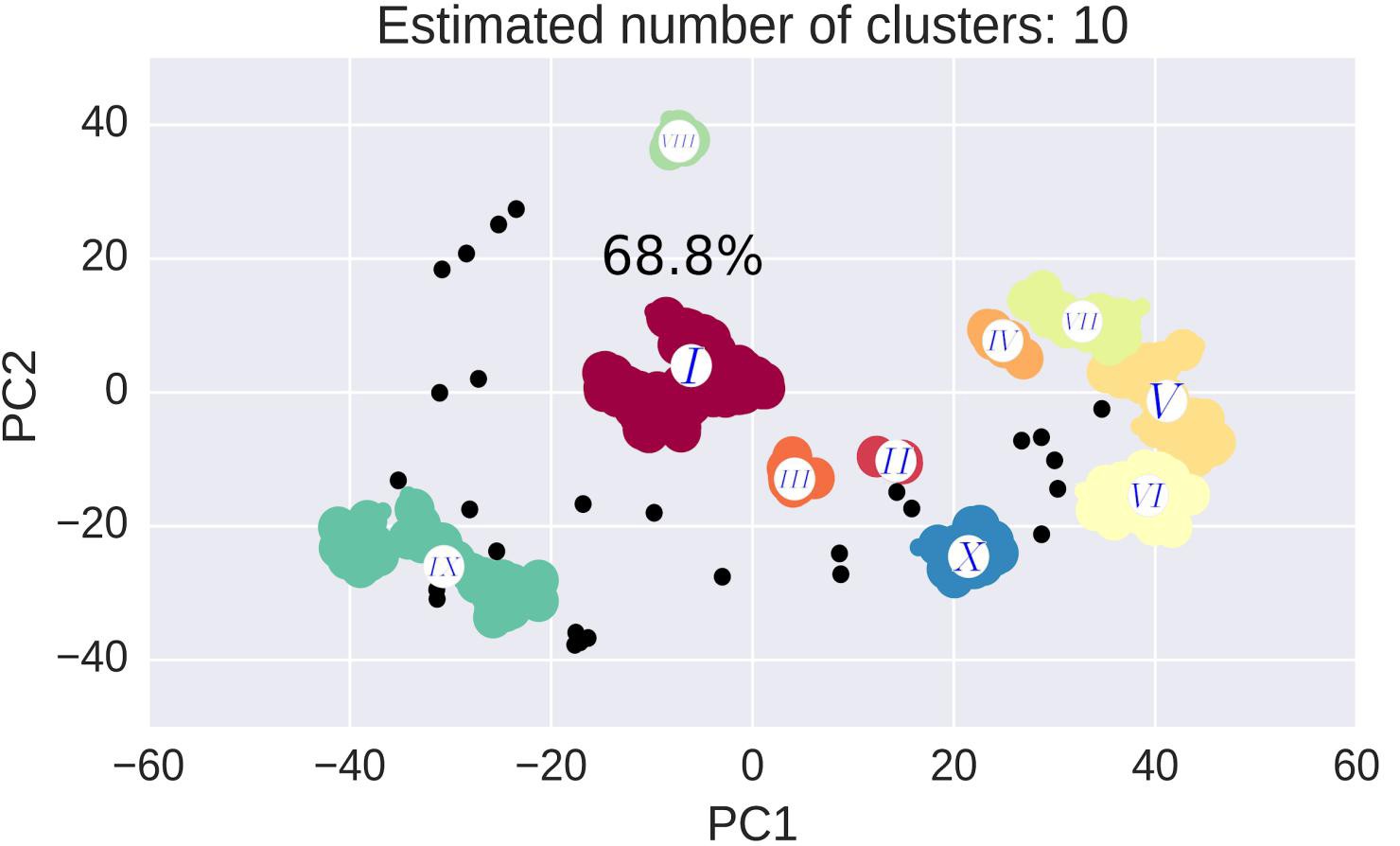
**Figure S2**. k-Nearest Neighbor distance plot of the center of mass coordinates from the results of multiple docking runs of DEXA.



**Figure S3.** Distribution of HSA conformations over time.



**Figure S4.** Cluster analysis of the COM data from the docking results of ART with HSA using the DBSCAN algorithm. Roman numerals denote clusters, where the 1st cluster contains 58.2% of docking conformations.



**Figure S5.** Cluster analysis of the COM data from the docking results of DEXA with HSA using the DBSCAN algorithm. Roman numerals denote clusters, where the 1st cluster contains 68.8% of docking conformations.