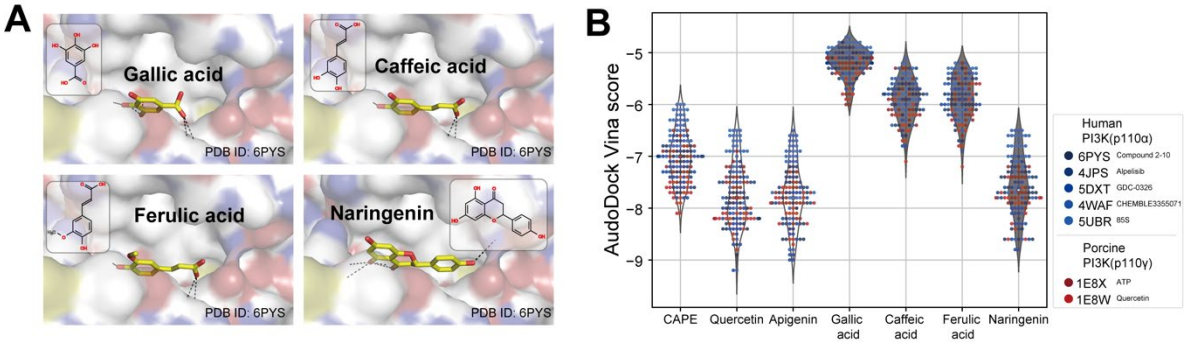

Figure S1. Distribution of binding scores. (**A**) The structural models of gallic acid, caffeic acid, ferulic acid, and naringenin on PI3K; (**B**) The distribution of binding scores for each compound against different structures of PI3K. The docking simulations were executed with multiple PI3K structures that were co-crystallized with different inhibitors. The protein data bank identifiers of the PI3Ks and the names of co-crystalized molecules are marked in the legend.