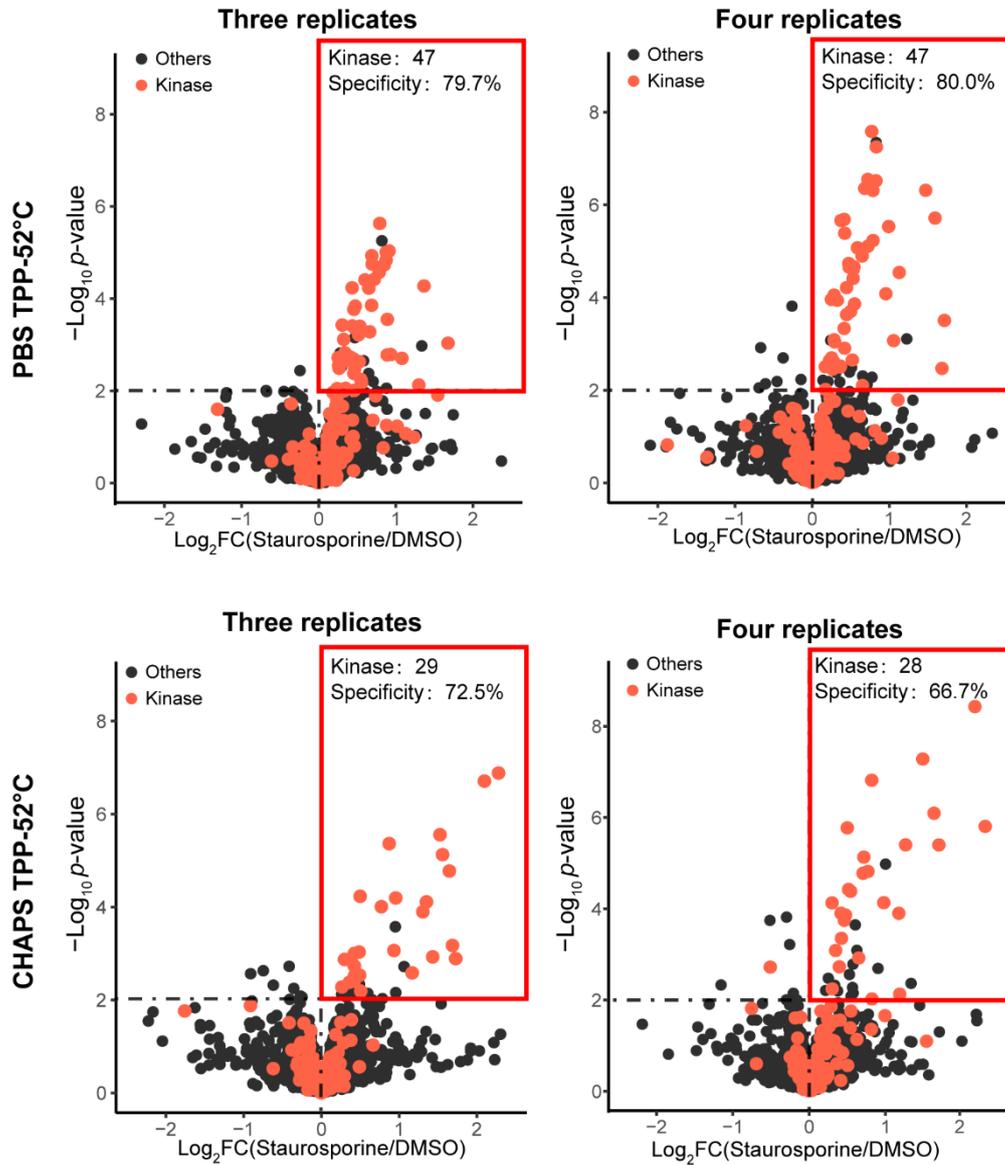
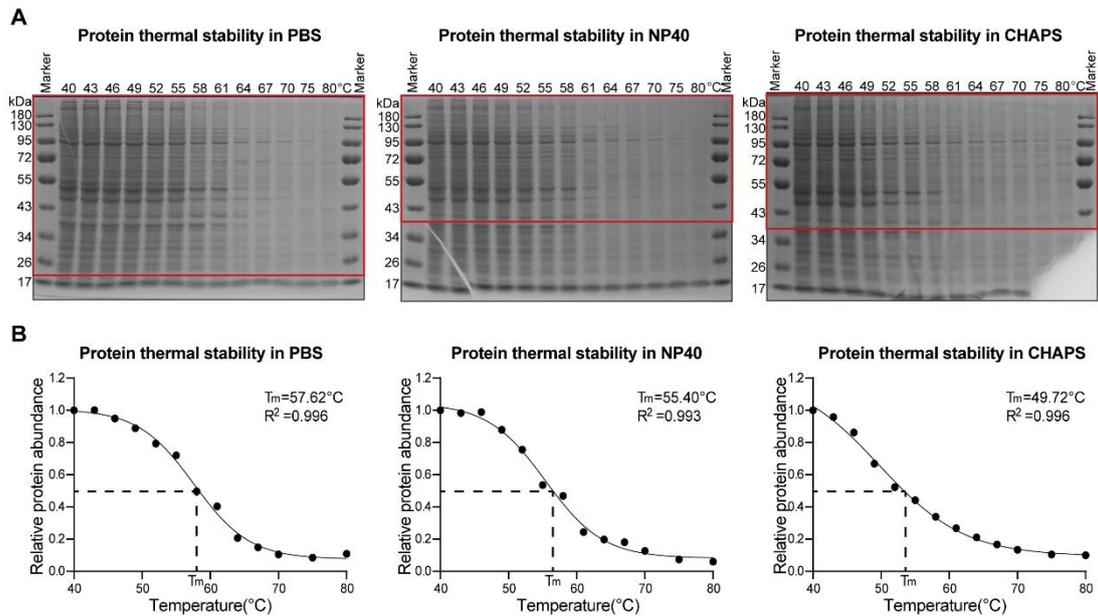


**Figure S1.** Melting temperature distributions of the kinase proteome and the whole proteome.



**Figure S2.** Comparing target identification performance of TPP between performing

three replicates and four replicates. **(A)** Volcano plot visualization of staurosporine kinase targets identified by PBS-TPP at 52 °C with three replicates (left) and with four replicates (right). **(B)** Volcano plot visualization of staurosporine kinase targets identified by CHAPS-TPP at 52 °C with three replicates (left) and with four replicates (right).



**Figure S3.** Comparing the thermal stabilities of the proteome in PBS, in PBS with 0.4% NP40, and in PBS with 1% CHAPS. **(A)** SDS-PAGE readout of proteins that were collected from the supernatants after heating. From left to right: in the context of PBS (**left**), in the context of PBS supplemented with 0.4% NP40 (**middle**), and in the context of PBS supplemented with 1% CHAPS (**right**). **(B)** Normalized protein quantification value according to the area denoted by the red frame in (A).  $T_m$  represents melting temperature;  $R^2$  refers to the Pearson correlation between the actual values and the fitted values of the four-parameter logistic curve. The  $T_m$  curves were fitted using Prism (version 8.0.2).