Fig. S7.

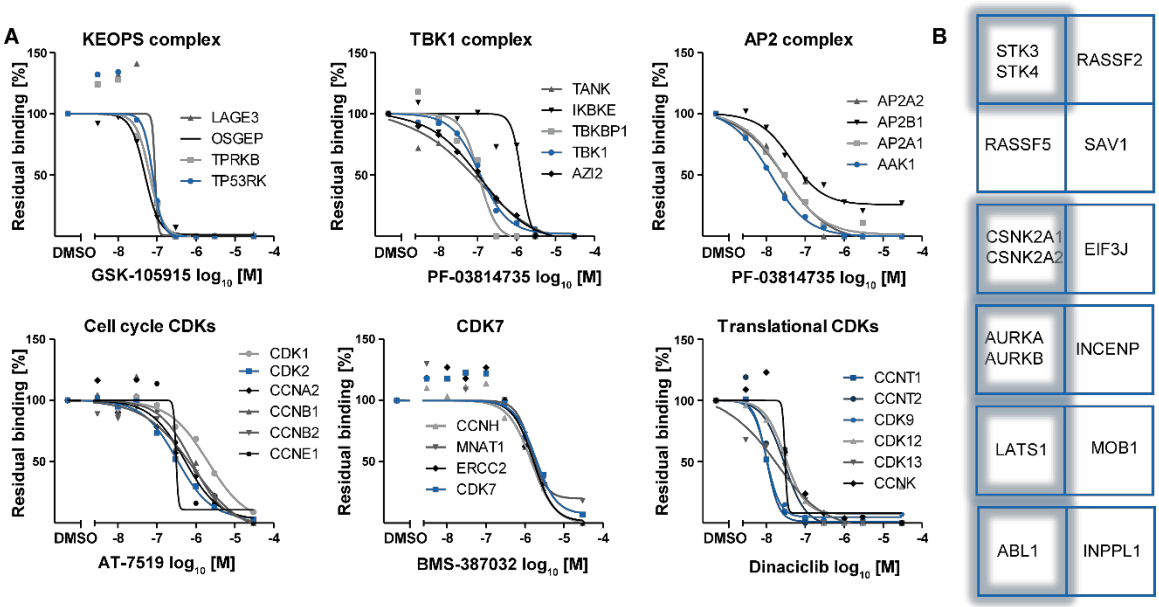

Fig. S7 | Kinobeads binding of protein complexes (A) Co-competed proteins forming KEOPS, TBK1, AP2 and CDK/Cyclin complexes are shown as examples. **(B)** Schematic representation of additional protein complexes identified in the Kinobeads pulldowns that showed similar curve characteristics (blue, direct Kinobead binder).

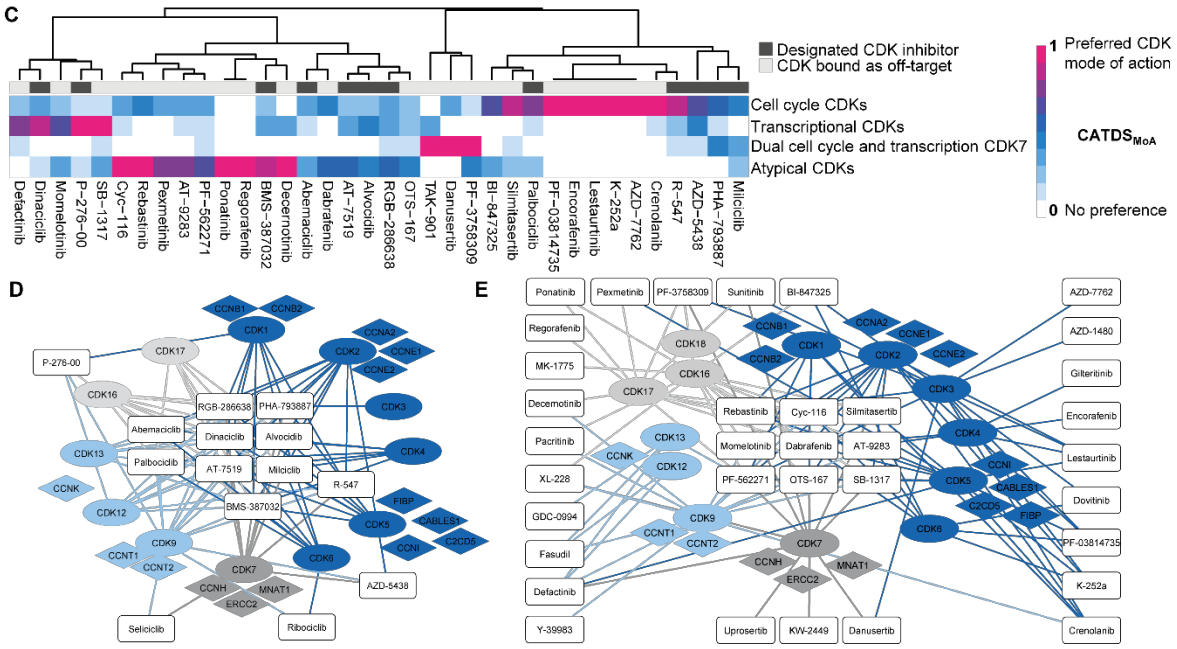

Fig. S7 continued | Kinobeads binding of protein complexes – CDKs. (C) Clustering of inhibitors targeting CDKs according to $CATDS_{MoA}$ (see Supplementary Text for details). Compounds either had no preference (white-light blue) or targeted the same biological process (pink; e.g., the cell cycle). Off-target CDK inhibitors (light grey bar) often inhibited one potential CDK mode-of-action. **(D)** Designated CDK inhibitors targeted all CDK/cyclins irrespective of the biological process a particular complex is involved in (cell cycle in dark blue, translation in light blue, dual cell cycle and transcription CDK7 in dark grey, atypical CDKs in light grey). **(E)** Conversely, off-target CDK inhibitors showed some preference for the cell cycle (dark blue), translation (light blue), dual cell cycle and transcription CDK7 (dark grey) or atypical CDKs (light grey).