Fig. S2.

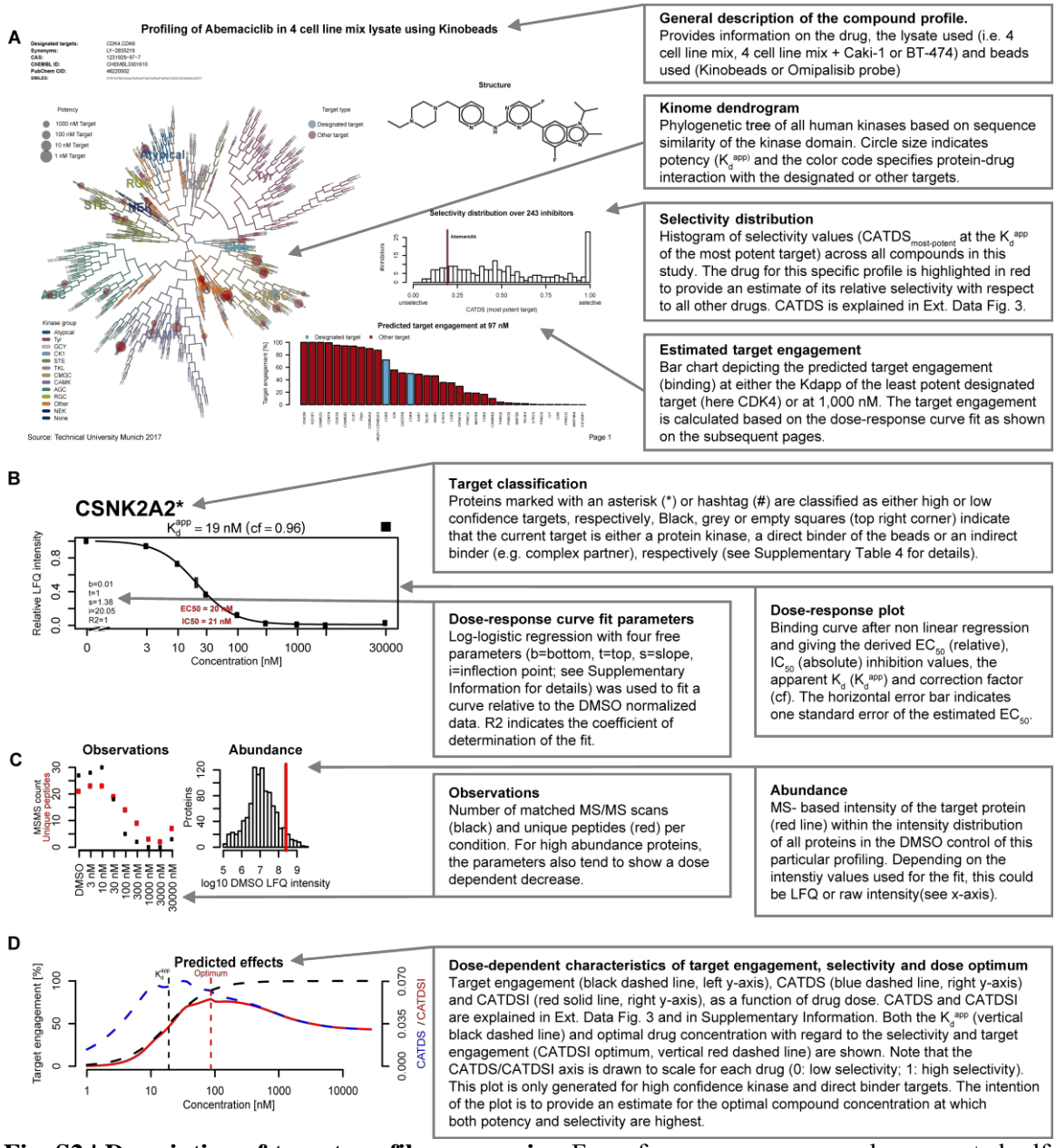

Fig. S2 | Description of target profile summaries. For reference purposes, we have created pdf files summarizing the target profiles of all 243 inhibitors used in a total of 281 experiments. **(A)** Page 1 highlights general information about the inhibitor. Each identified target kinase (blue for designated target, red for other targets) is highlighted on the phylogenetic tree of all human kinases. A histogram plot places the inhibitor on the distribution of selectivity of all drugs investigated in this study. The histogram at the bottom of panel (A) indicates the level of target engagement of the drug in the cell lysate at a defined concentration. **(B)** Beginning with the high confidence targets, the subsequent pages show all MS intensity-based dose-response profiles obtained for the compound including parameters for curve fitting and derived IC_{50}, EC_{50} and K_d^{app} values. **(C)** For each protein, further analytical evidence is provided (number of MS/MS scans, number of unique peptides) and how abundant the protein was within the experiment (LFQ or raw intensity in the DMSO control). **(D)** Target engagement, compound selectivity (CATDS) and predicted optimum

of compound selectivity and target engagement (CATDSI) as a function of applied compound dose. The optimum in the CATDSI curve indicates the drug concentration that represents the best compromise between selectivity and target engagement. Visualization information for proteins that do not show dose-dependent binding consists of **(B)** and **(C)** only. Links to all target summary files are provided in Table S2-3. The pdf files can also be retrieved from proteomeXchange and ProteomicsDB (see data availability).