



Supplementary Figure S1. Distribution of POLQ mRNA levels, expressed as \log_2 of the Transcript Count Per Million ($\log_2(\text{TPM} + 1)$), across the 1406 cell lines from the *Cancer Cell Line Encyclopaedia* (CCLE) (22Q2 dataset; mean \pm standard deviation) . The distribution of the cancer cell lines used in the CFAs shown in Figure 1B is highlighted in red.