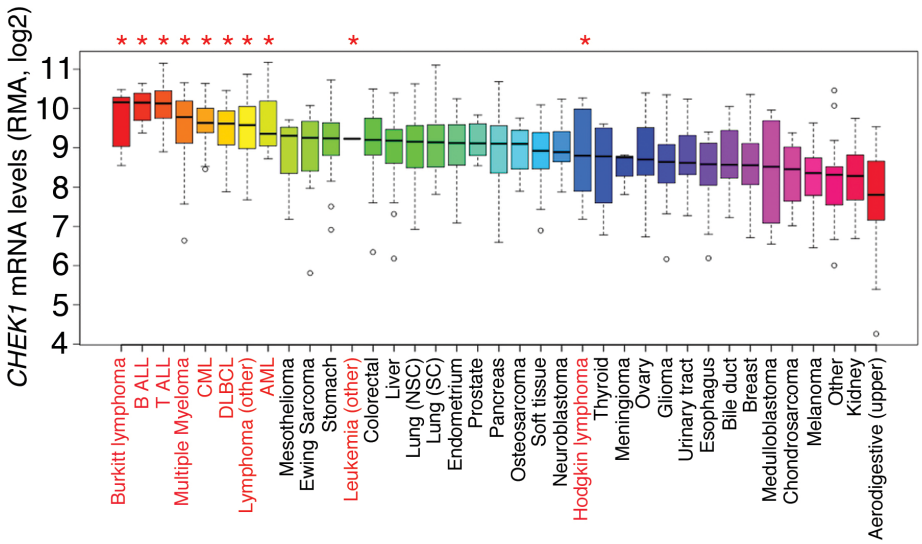

Fig. S1. *CHEK1* mRNA expression is highest in lymphomas and leukemias. The figure represents the expression levels of *CHK1* mRNA in a large variety of human cancer cell lines extracted from the Cancer Cell Line Encyclopedia (http://www.broadinstitute.org/ccle/home). Leukemias and lymphomas are marked in red, and with an asterisk on top of the panel. Expression is shown as RMA (Robust Multichip Average) on a log2 scale.

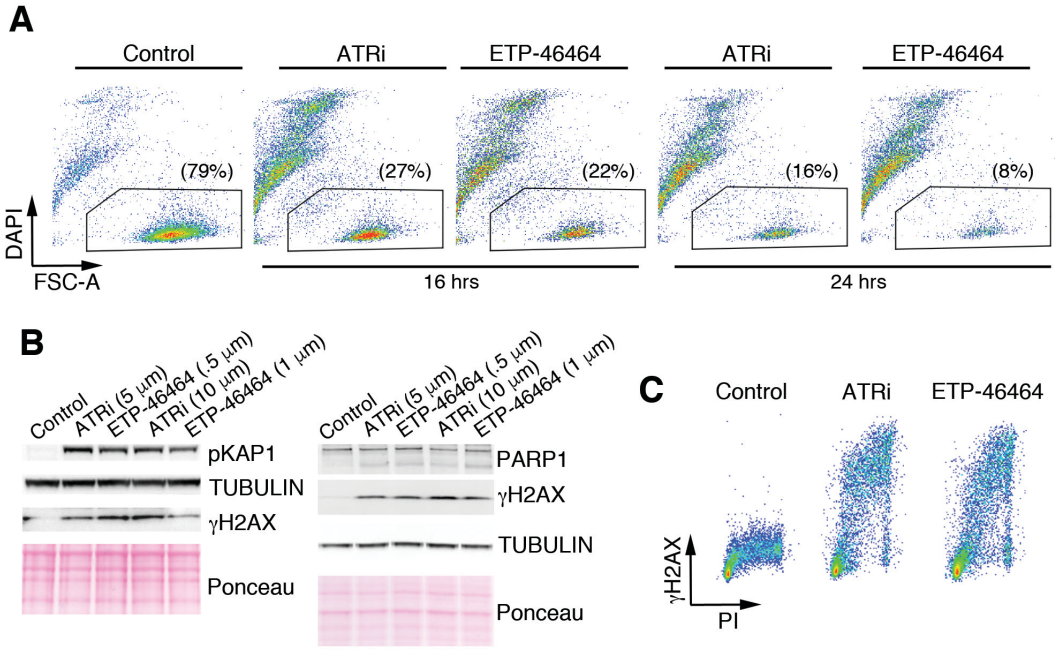

Fig. S2. Toxicity, replication stress, and DNA breakage induced by two distinct ATR inhibitors in AML^{MLL} cells. (**A**) FACS analysis showing the percentage of viable AML^{MLL} cells (identified by size and DAPI exclusion) either untreated or exposed to ATRi (10 μM) or to ETP-46464 (1 μM), an independent ATR inhibitor previously described by our group (Toledo *et al* Nat Struct Mol Biol 2011) for the indicated times. (**B**) Western blots showing markers of DNA breakage and cellular toxicity. The left Western blot shows KAP1 and γH2AX phosphorylation in AML^{MLL} cells exposed to ATRi or ETP-46464 at the indicated conditions. The right blot shows the accumulation of PARP1 cleavage (lower bands) products in cells with DNA damage indicated by γH2AX phosphorylation. (C) FACS analysis of DNA content (PI) and γH2AX phosphorylation in AML^{MLL} cells exposed to ATRi (10 μM, 6 hrs) or ETP-46464 (1 μM, 6 hrs), illustrating that the γH2AX signal detectable by Western blot is restricted to replicating cells.