Supplement to

Anti-leukemic effect of CDK9 inhibition in T-cell prolymphocytic leukemia

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Supplemental Tables

Please see seperate Excel files

Supplemental Figures

Figure S1.pdf

Figure S1. Transcriptomic profiling identifies deregulated molecular pathways in T-PLL

Comparative GEP of ten T-PLL vs five HD CD3+ T-cell samples yielded 674 differentially expressed genes (FC ≥2 or FC ≤-2, p≤0.05), which were subsequently subjected to the core analysis of IPA.

Figure S2. Gene expression profiling of T-PLL cells treated with LDC526

Genes down-regulated in T-PLL in response to LDC526 (10 µM) were analyzed in a GO enrichment analysis. A, fold enrichment of the 25 most significant (FDR <0.05) GO terms in the category biological process. B, Significantly (FDR <0.5) enriched molecular function GO terms.

Figure S3. RT-qPCR analysis of BCL2 expression in T-PLL cells cultured for 90 min in the absence (DMSO Control) or presence of LDC526 (10 µM)