LEE011 and ruxolitinib: a synergistic drug combination for natural killer/T-cell lymphoma (NKTCL)

SUPPLEMENTARY MATERIALS





Supplementary Figure 1: CDK4/6 siRNA KD inhibits growth in NKTCL cell lines. (A) Cell viability assay showed growth inhibition following dual KD of CDK4 and CDK6 compared to negative control #1 siRNA. In each experiment, duplicate values were averaged and cells that received CDK4/6 siRNA were normalised against those that received the control siRNA. Data is expressed as mean \pm SEM from three independent experiments (n = 3, * p<0.05, one-tailed student's *t*-test). **(B)** Western blot analysis of the KD efficiency of CDK4 and CDK6. Cells were harvested on Day 2 after transfection.

Supplementary Table 1: CI values for different combination concentrations of LEE011 and ruxolitinib for (A) NKYS, (B) NK-S1 and (C) KHYG

Α									
LEE011/uM		0.5			1			5	
Ruxolitinib/nM	25	200	500	25	200	500	25	200	500
Day 2	1.61	1.31	0.81	1.11	0.69	0.56	0.87	0.55	0.63
Day 3	0.73	0.90	1.12	1.03	0.82	0.92	0.79	0.61	0.76
В									
LEE011/uM		1			5		1	10	
Ruxolitinib/nM	25	200	500	25	200	500	25	200	500
Day 2	0.84	0.91	0.62	1.33	0.67	0.58	0.49	0.47	0.54
Day 3	1.35	0.74	0.98	0.99	0.87	0.99	0.99	0.88	0.94
С									
LEE011/uM		0.2			0.5			1	
Ruxolitinib/nM	5	25	200	5	25	200	5	25	200

Fraction inhibition at each condition was determined from the cell viability assay after averaging effects over three independent experiments. CI values of synergistic (CI < 1), additive effect (CI = 1) or antagonistic (CI > 1) relationship between two or more drugs.

0.71

175.27

0.57

1.11

0.33

0.13

0.66

167.32

0.34

0.26

0.20

0.03

Day 2

Day 3

4.39

29.35

0.93

2.44

0.51

0.33



Supplementary Figure 2: Basal phosphorylation of STAT3/5 proteins in NKYS, NK-S1 and KHYG cell lines. Cells were harvested two days after subculture. Phosphorylated STAT3/5 levels in each cell line were normalised with their respective total STAT3/5 levels to enable comparison between cell lines.

Supplementary	Table 2:	Primer	sequences	for a	quantitative	RT-PCR	analyses
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Gene	Direction	Sequence
CONDI	F	GCTCCTGGTGAACAAGCTCAA
CCNDI	R	TTGGAGAGGAAGTGTTCAATGAAA
P711	F	AGGAGTTTGCTGCTGCTCTC
EZH2	R	CCGAGAATTTGCTTCAGAGG
	F	GGCTGTGGGGCAAGGTCATCCCTGAG
GAPDH	R	GTCGCTGTTGAAGTCAGAGGAGACCACCTG

F and R stands for forward and reverse primers respectively.