

Figure S1

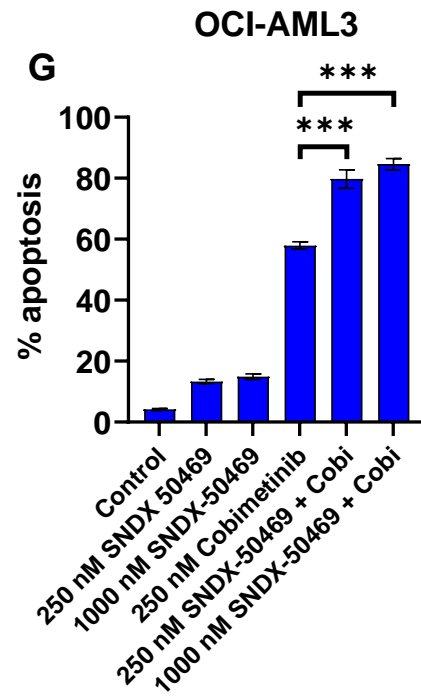
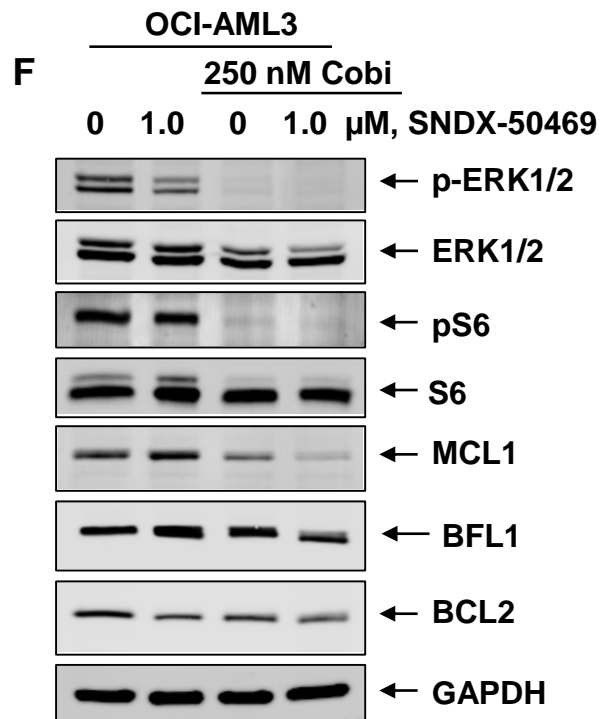


Figure S1

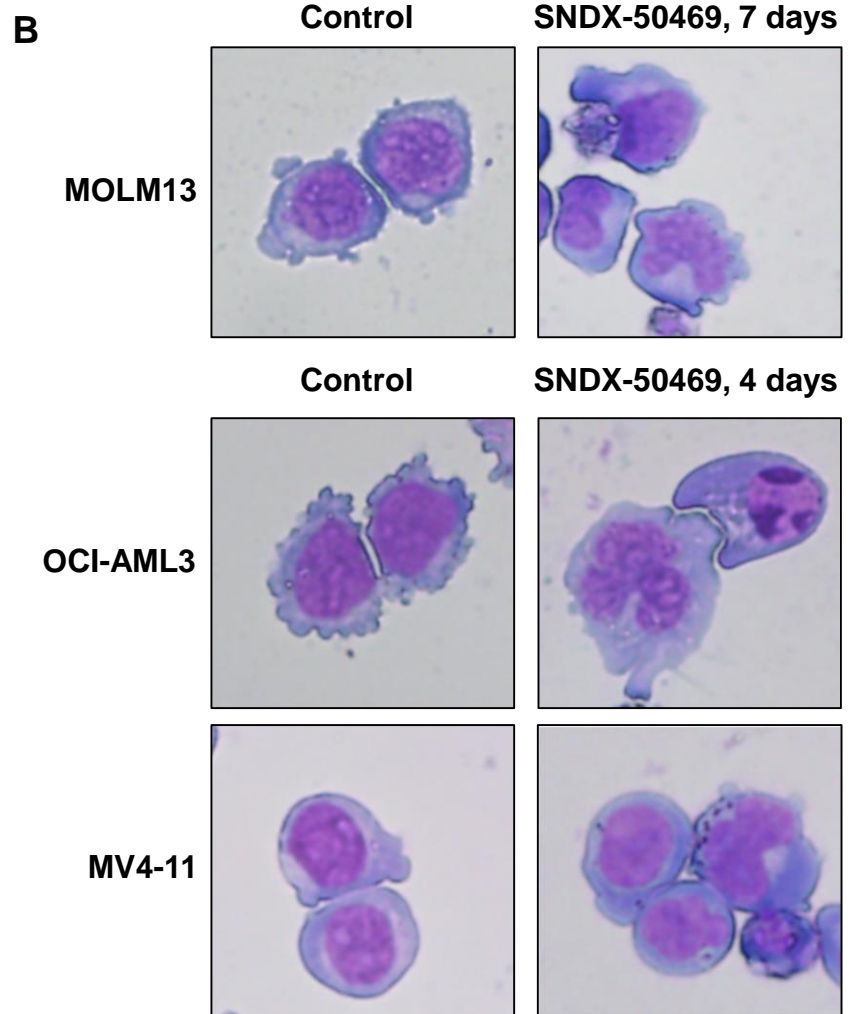
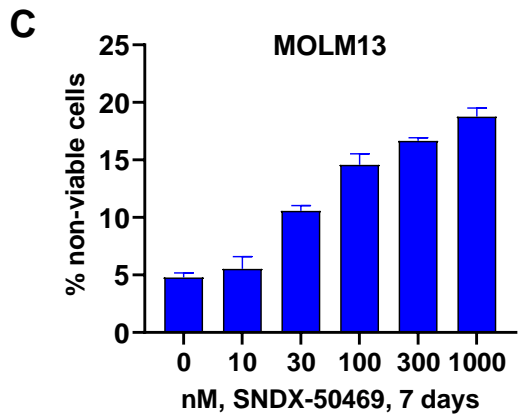
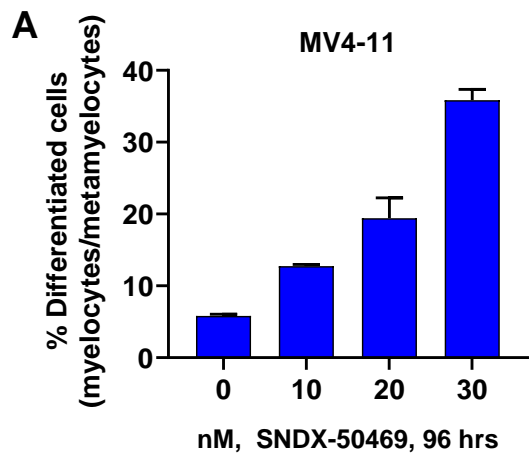


Figure S2

MOLM13

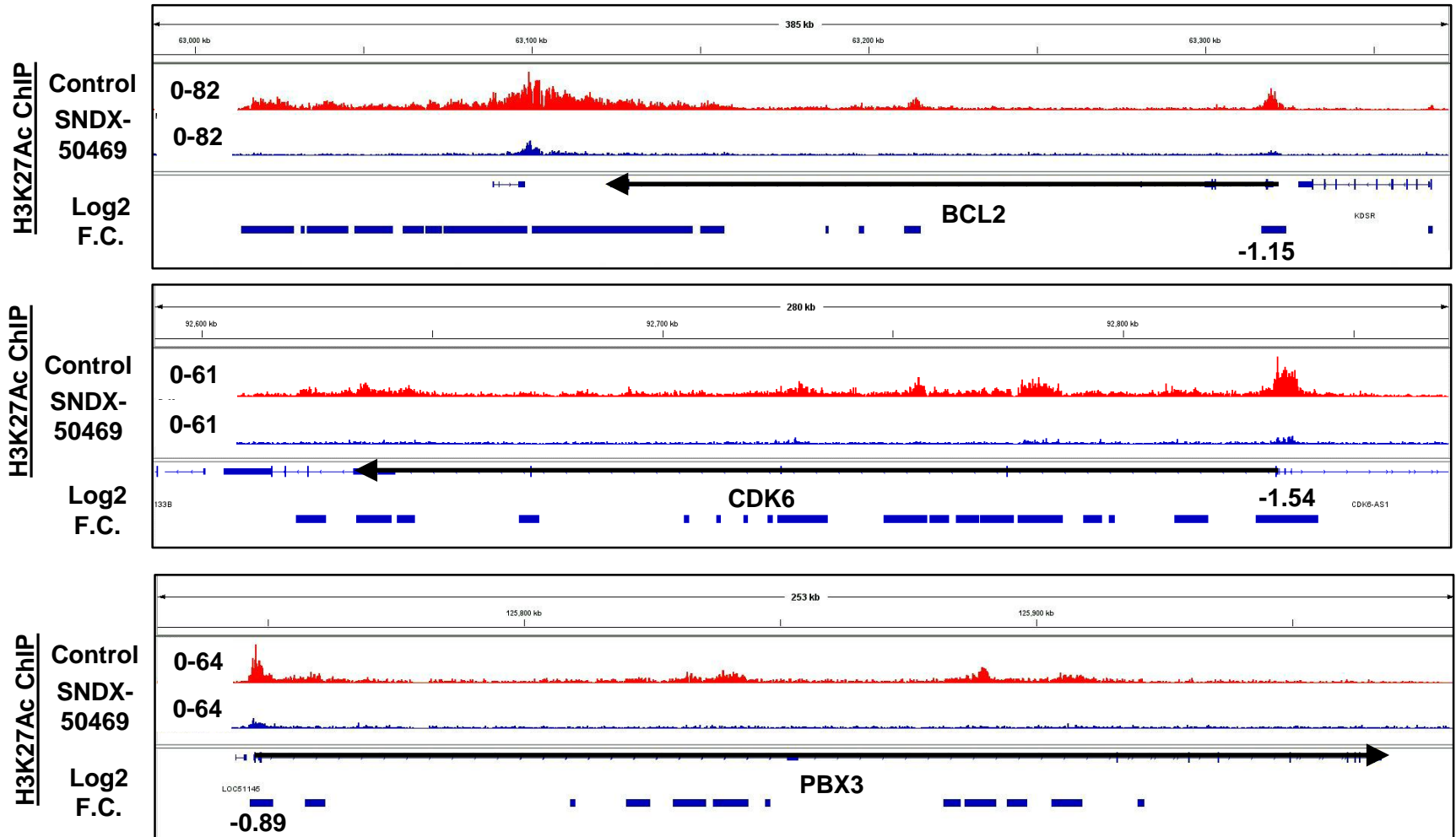


Figure S3

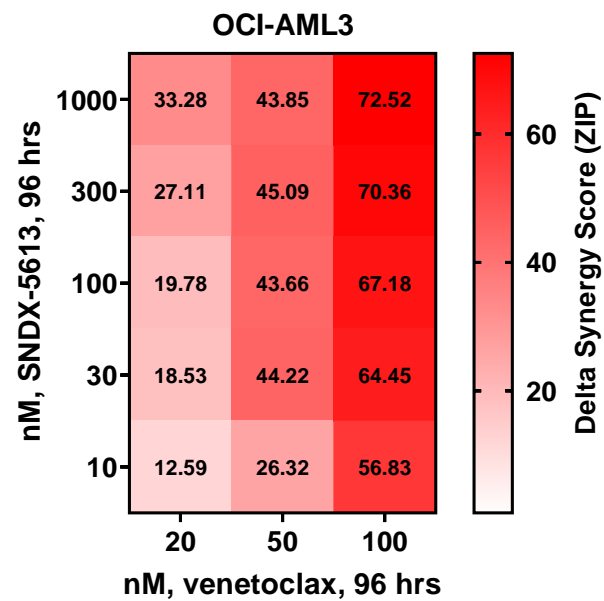
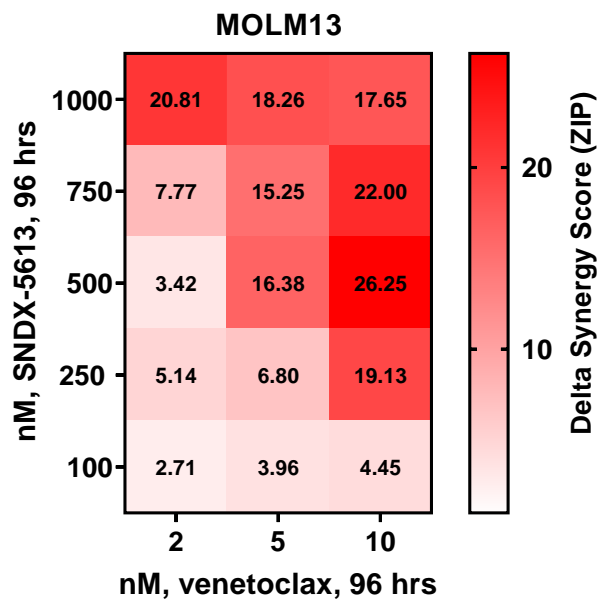
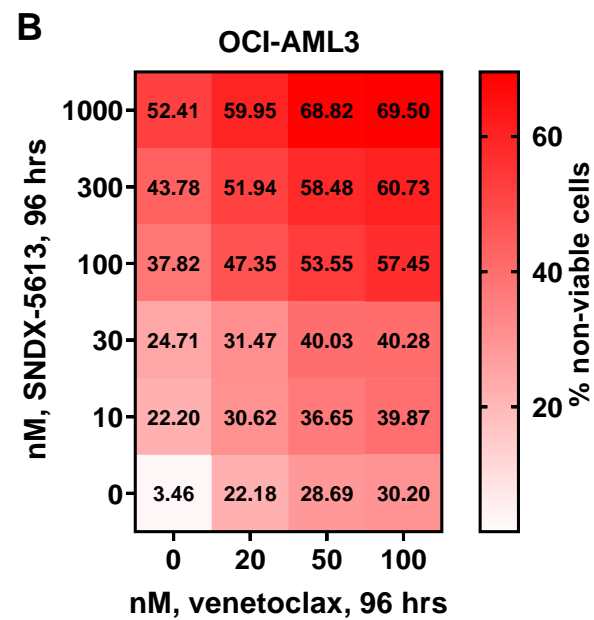
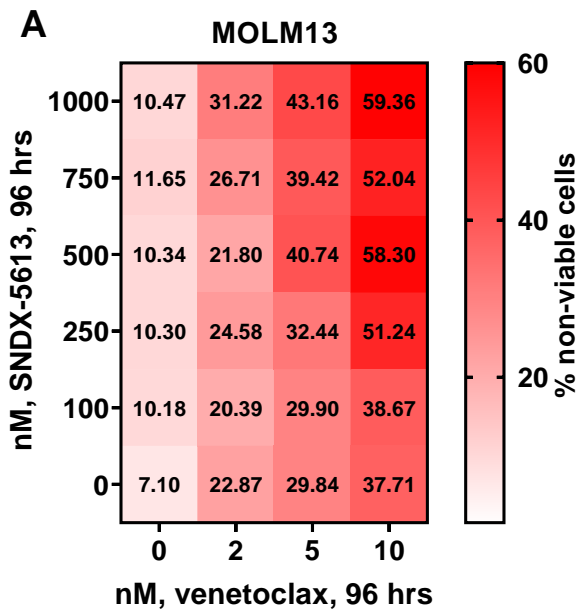


Figure S4

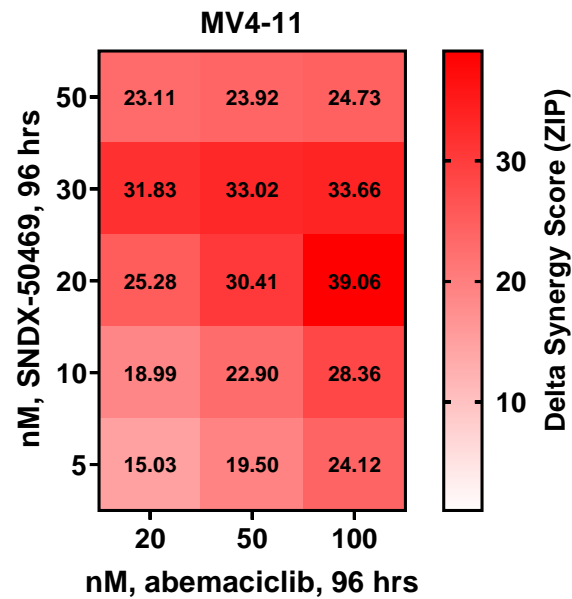
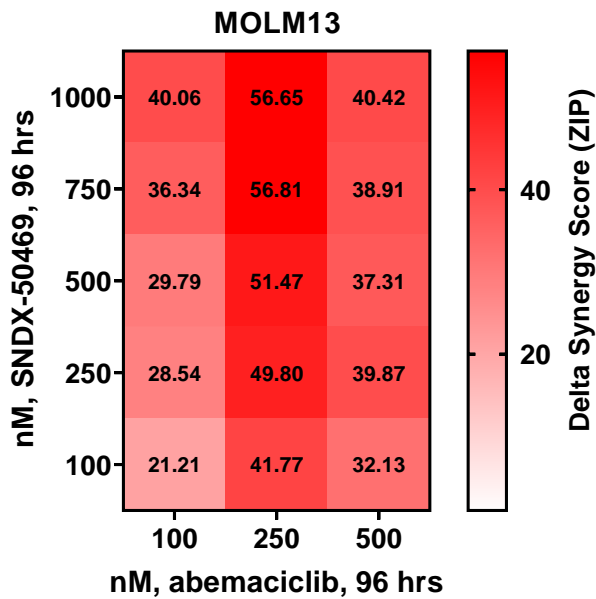
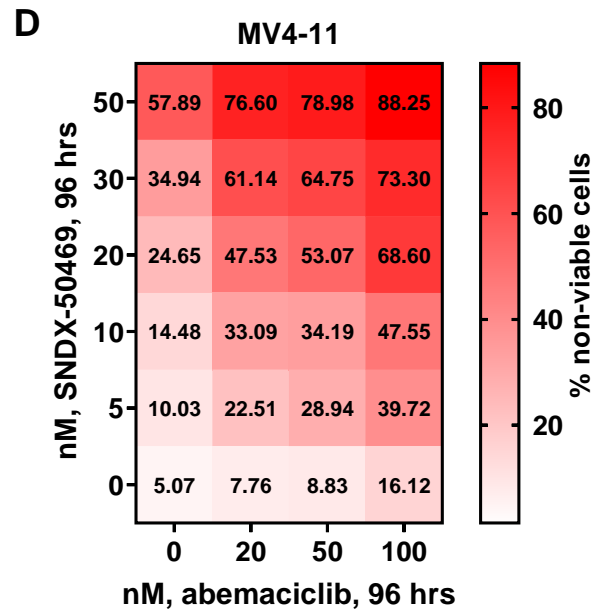
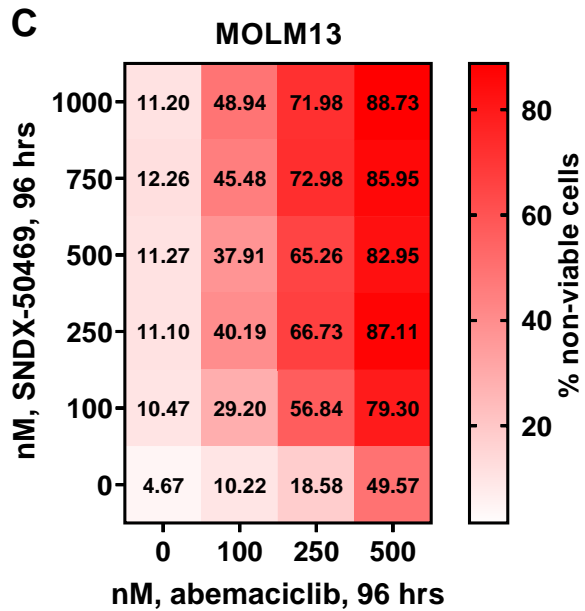


Figure S4

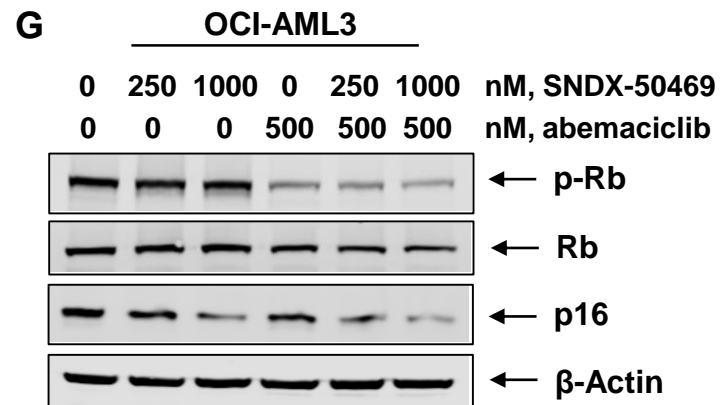
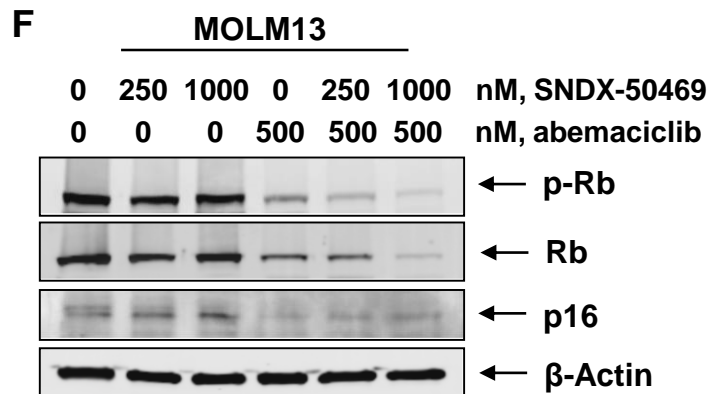
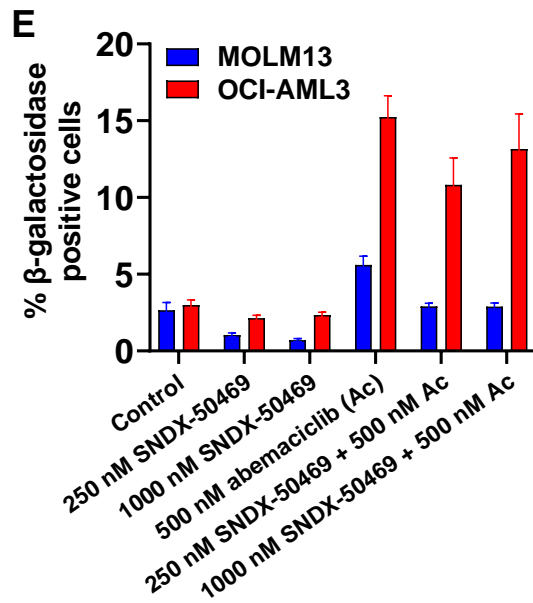


Figure S4

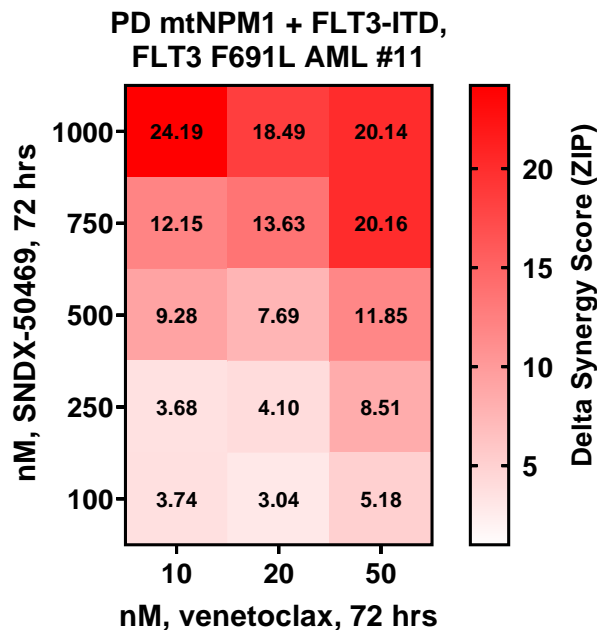
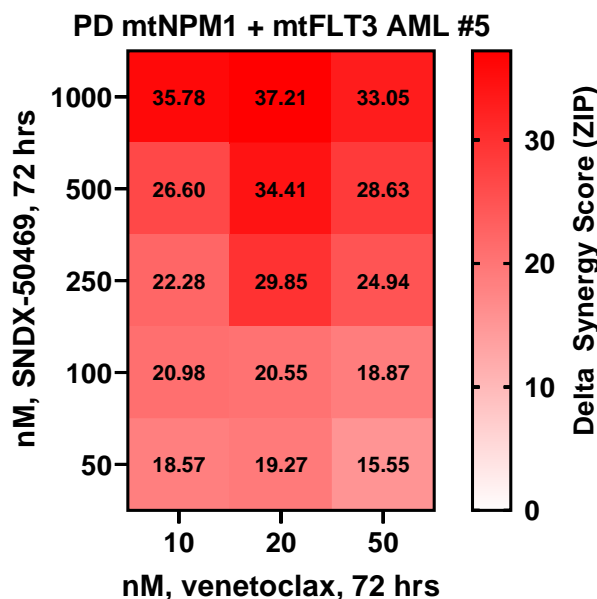
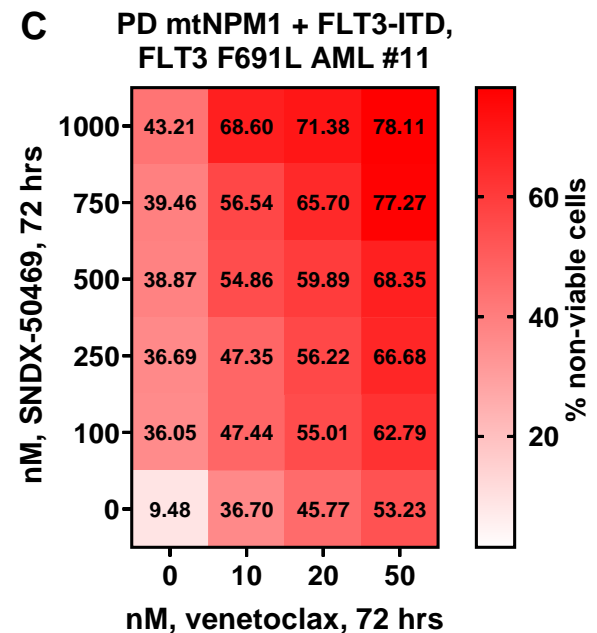
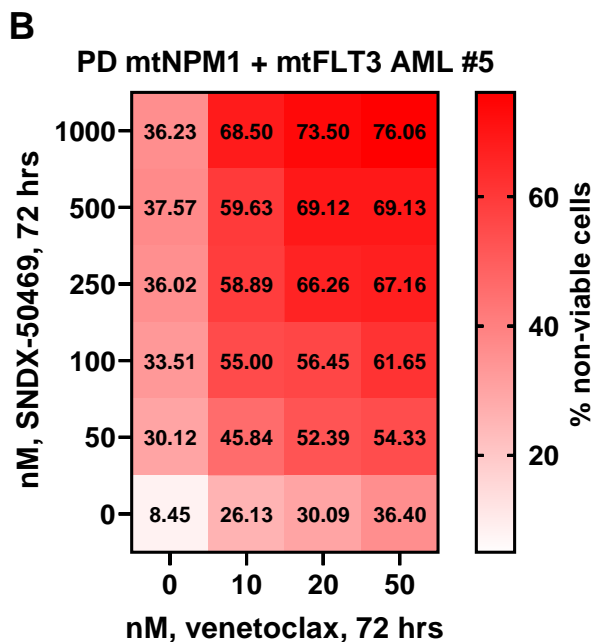
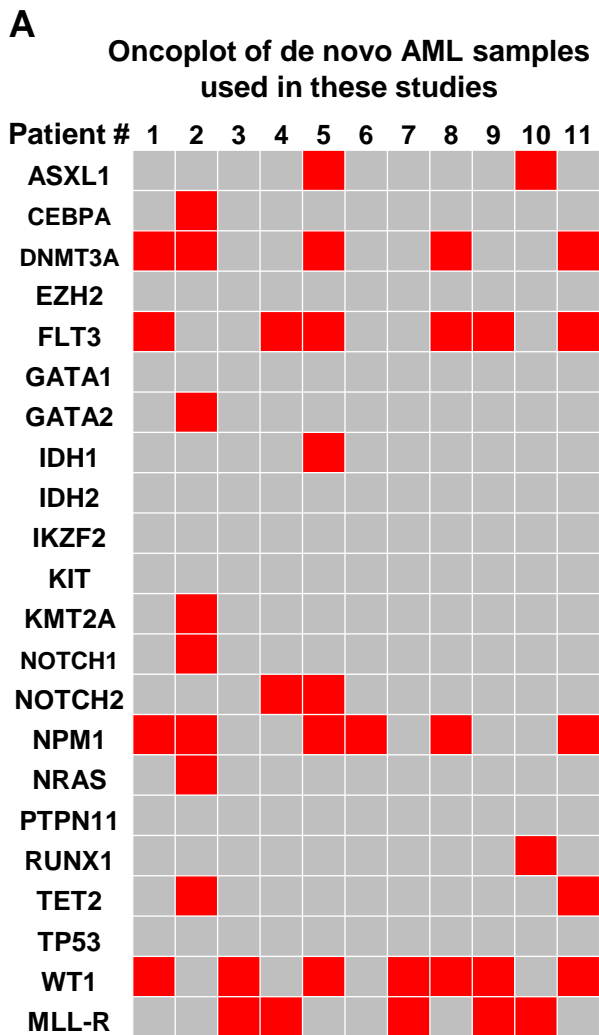


Figure S5

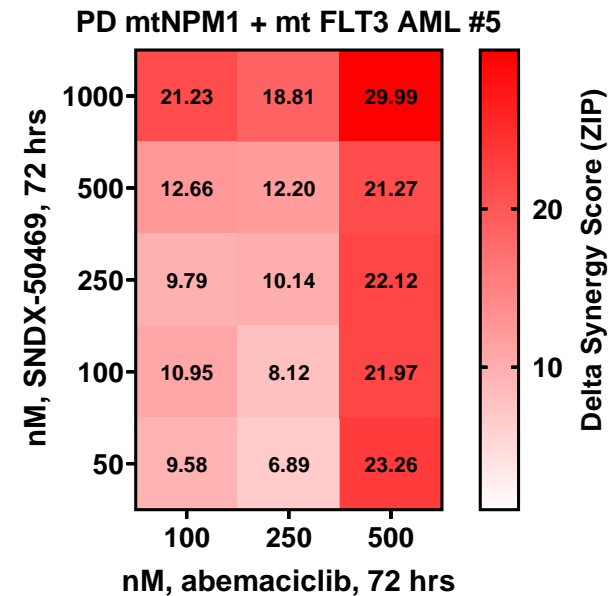
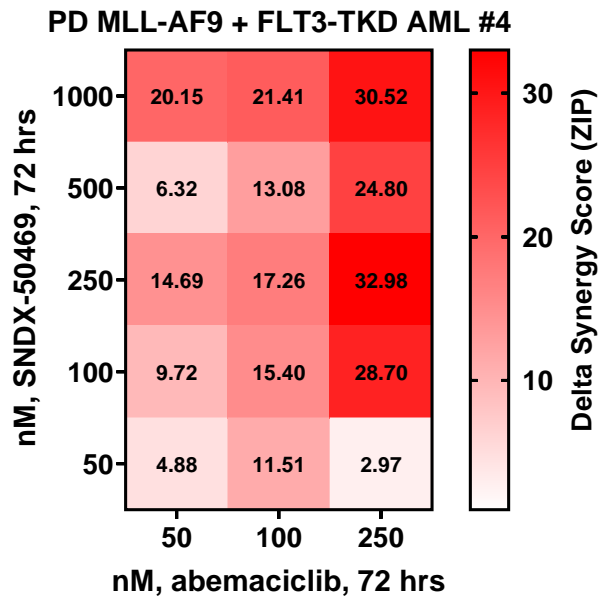
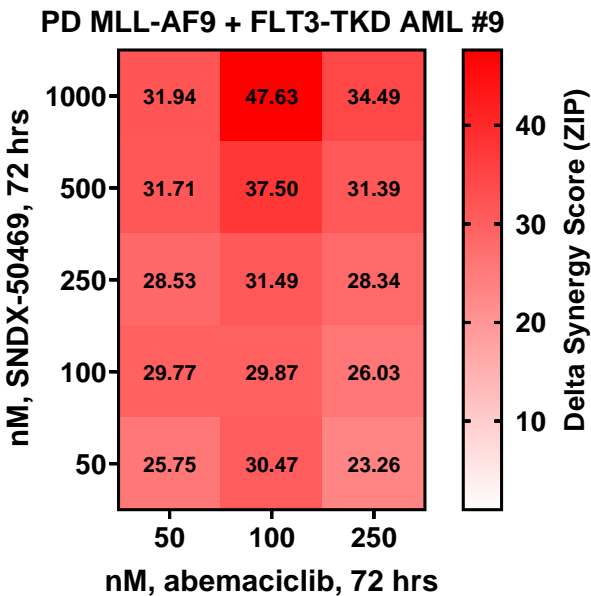
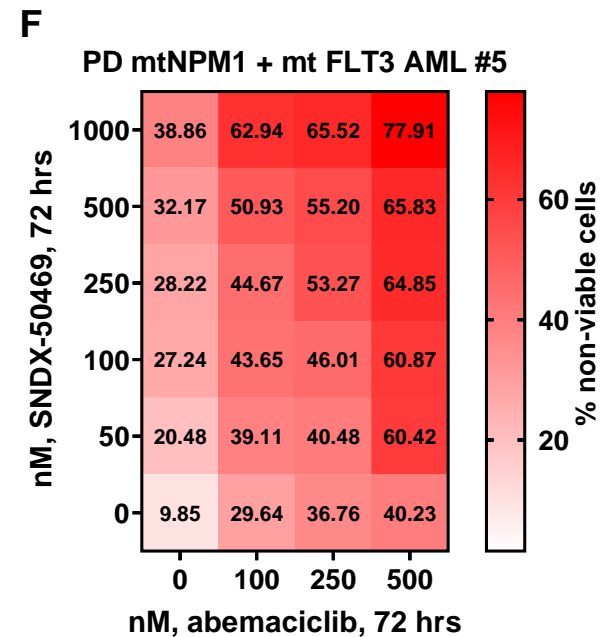
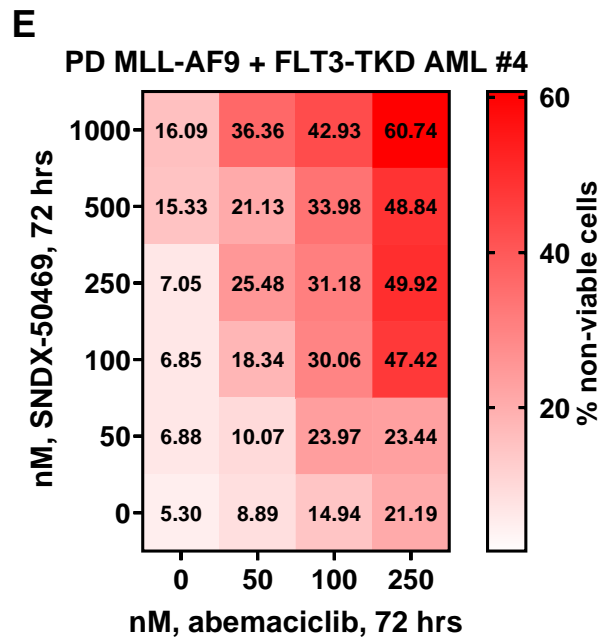
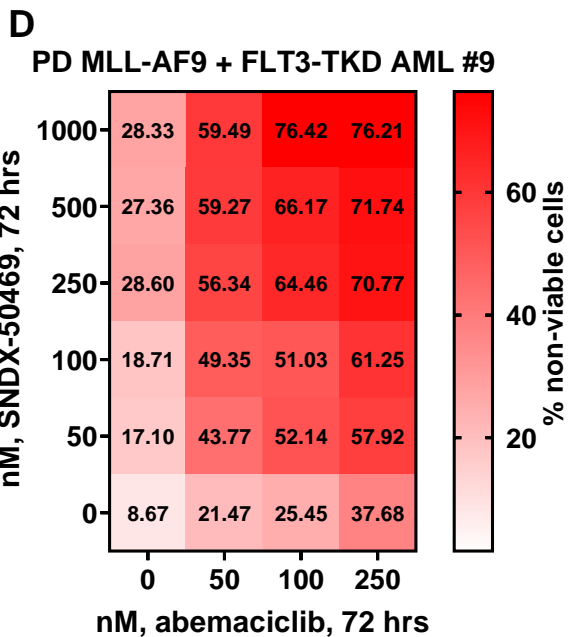


Figure S5

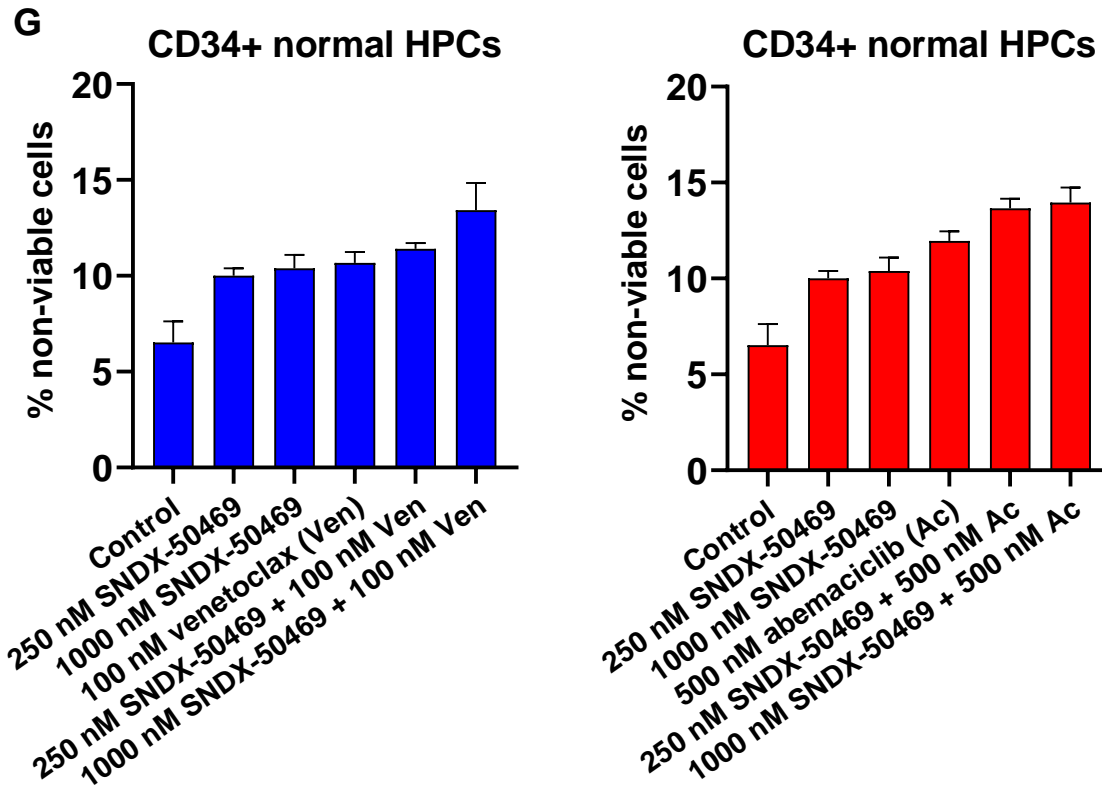


Figure S5

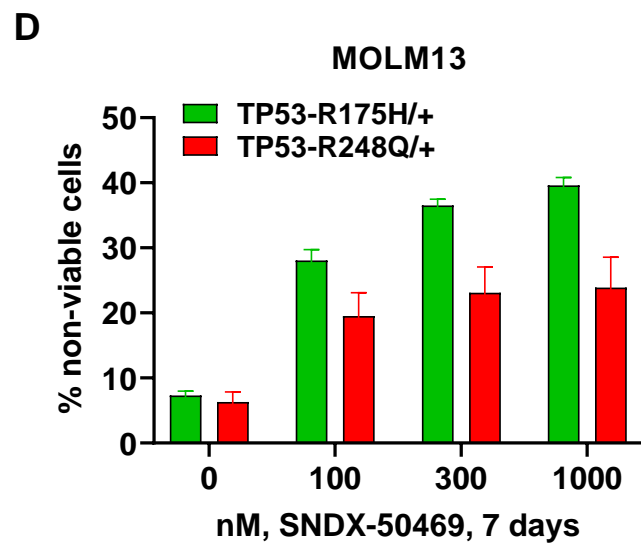
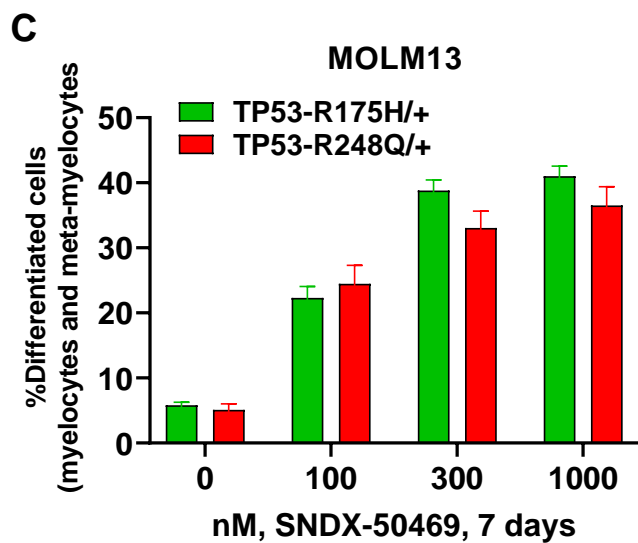
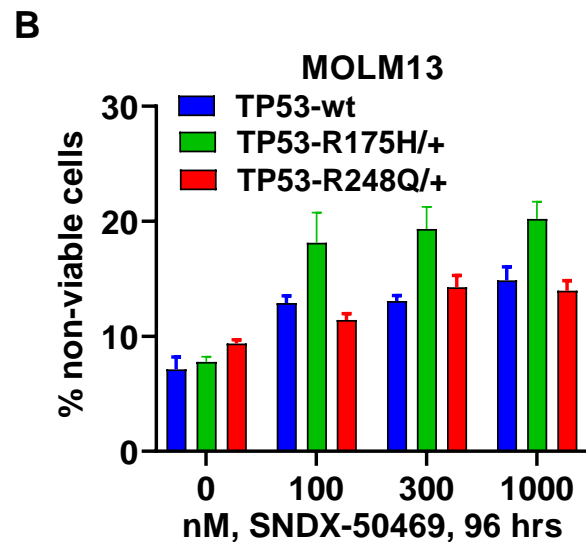
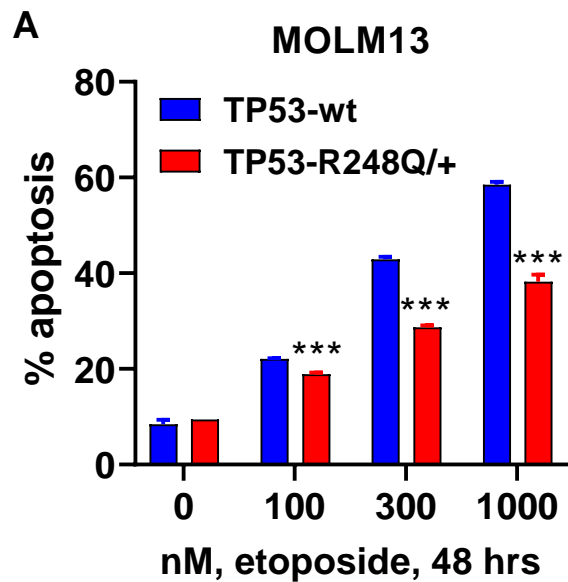


Figure S6

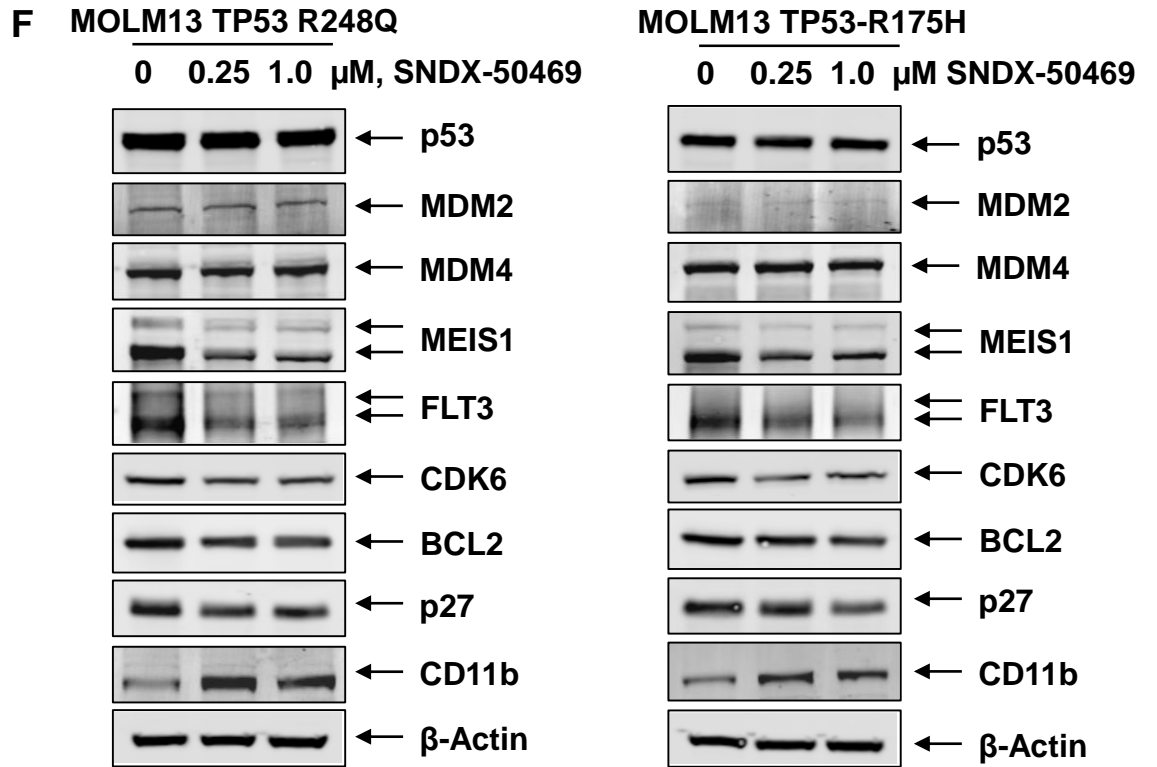
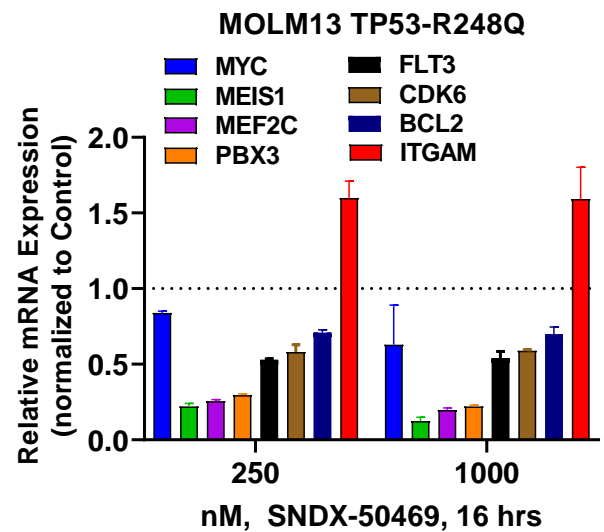
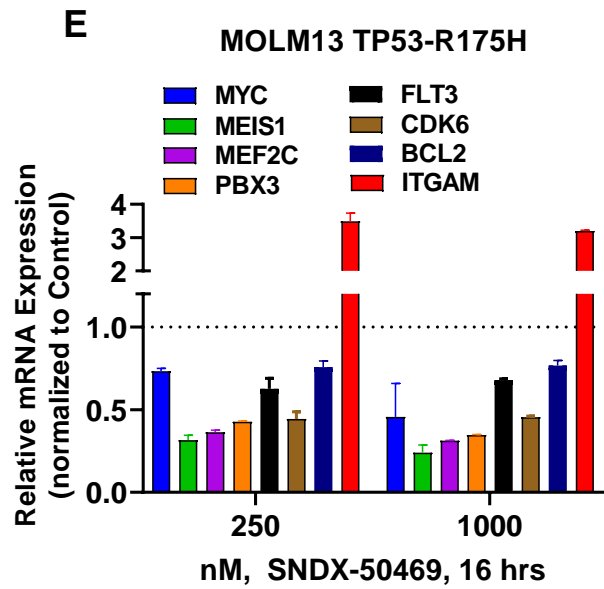


Figure S6

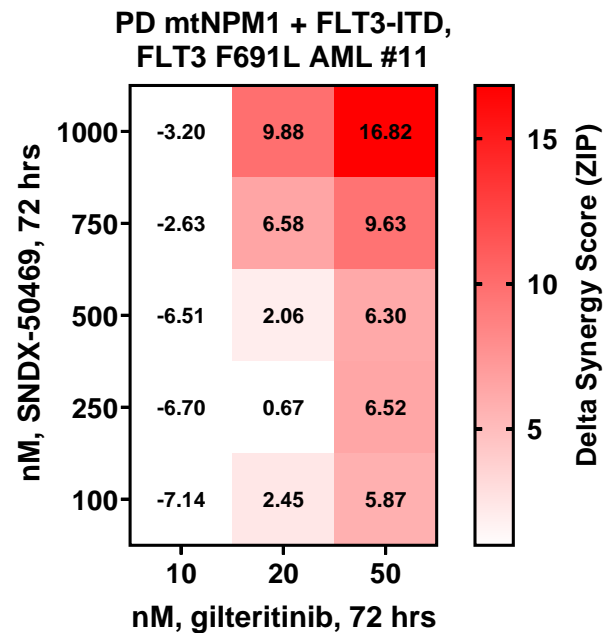
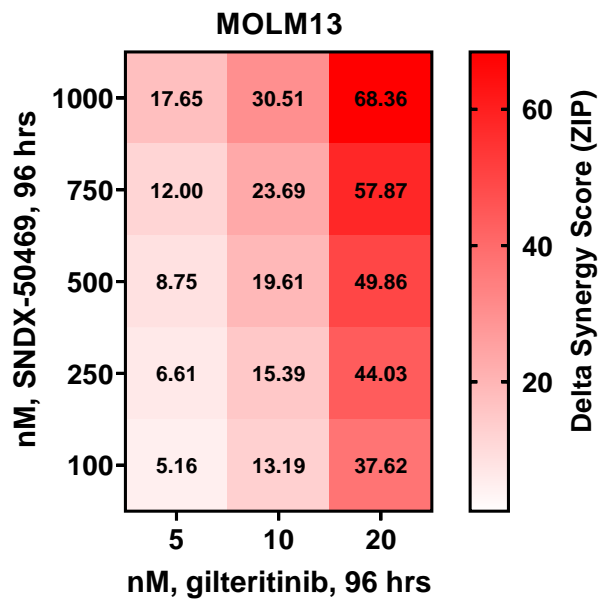
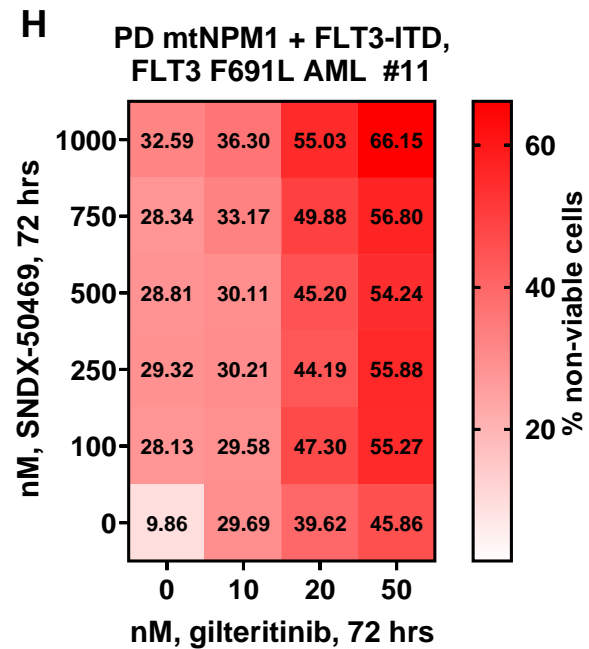
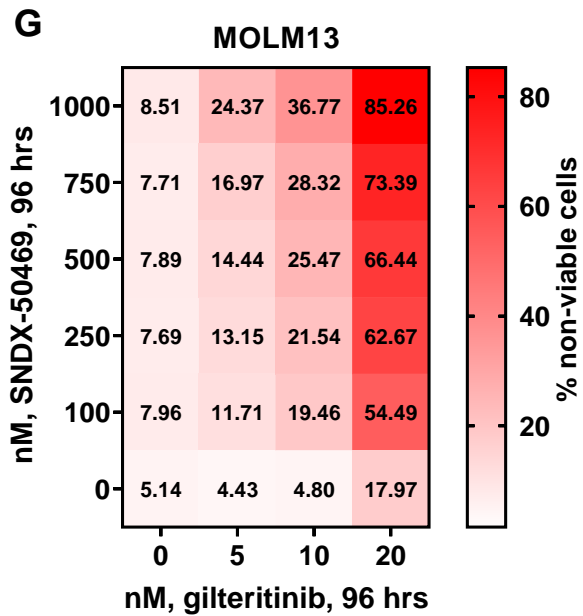


Figure S6

Co-mutations in AML#4 PDX

Gene	Protein Change	Variant Allele Freq (VAF)
FLT3	N676T	0.917355
KMT2C	C988F	0.363392
KMT2C	Y987H	0.18362
KMT2C	D348N	0.078125
KMT2C	V919L	0.073446
KMT2C	S990G	0.07
KMT2C	G315S	0.04148
KMT2C	R380L	0.041427
KMT2C	R284Q	0.035762
KMT2C	C391*	0.033722
KMT2C	P309S	0.031927
KMT2D	P2107T	0.521739
NOTCH2	G225R	0.395604
NOTCH2	C19W	0.448276
ARID1A	L1724R	0.448276
IRF8	*427Yext*24	0.540881
ABCA7	P1503L	0.539519
VPS13A	S734N	0.620079

Table S1

Table S2. In 190 patients with MLL1-r AML managed at M.D. Anderson Cancer Center (2012-2021), concurrent TP53 mutations were identified in 17 patients (~9%).

Patient Number	Cytogenetic Alteration (MLL rearrangement)	Nucleotide alteration in TP53	Protein alteration in TP53
1	t(9;11)(p22;q23)	c.659A>G	p.Y220C
2	t(9;11)(p22;q23)	c.542G>C	p.R181P
3	t(5;11)(p14;q23)	c.399_406del	p.M133fs*13
4	t(4;11)(q21;q23)	c.845_860delins31	p.R282_E287delinsPSVGS LPE EEE
5	t(4;11)(q21;q23)	c.845_846insAATATG	p.R282_R283ins
6	t(4;11)(q21;q23)	c.524G>A	p.R175H
7	t(4;11)(q21;q23)	c.817C>A	p.R273S
8	t(4;11)(q21;q23)	c.845G>C	p.R282P
9	t(4;11)(q21;q23)	c.488A>C	p.Y163S
10	t(4;11)(q21;q23)	c.818G>A	p.R273H
11	t(11;19)(q23;q13.3)	c.536A>G	p.H179R
12	t(11;18)(q23;q21.3)	c.139C>T	p.P47S
13	t(11;16)(q23;p13.3)	c.743G>A	p.R248Q
14	t(11;14)(q23;q32)	c.425dupC	p.V143fs
15	der(6)t(6;11)(q27;q23)	c.811G>T	p.E271*
16	der(4)t(4;11)(q21;q23)	c.845G>C	p.R282P
17	der(12)t(11;12)(q23;q22)	c.414dupC	p.K139fs

Co-mutations in AML# 5 PDX

Gene	Protein Change	Variant Allele Freq (VAF)
DNMT3A	R882H	0.487889
IDH1	R132H	0.484305
NPM1	W288Cfs*12	0.423358
FLT3	V194M	0.450135
WT1	H445Q	0.252137
KMT2C	R284Q	0.059818
KMT2C	P309S	0.138462
KMT2C	D348N	0.084453
KMT2C	C988F	0.217899
KMT2C	Y987H	0.270115
NOTCH2	C19W	0.416268
ZFH3	G3517D	0.5625
PCLO	S496P	0.079848
CCND3	L132F	0.463158
CD36	G217R	0.495017
ATM	F858L	0.489914
CIITA	S299F	0.446602
ZFH3	R3381_Q3387del	0.33119
NF1	V1453A	0.478814
STAT5A	P194L	0.477733
RNF213	S2334N	0.995122
SMARCA4	V720M	0.182266
ASXL1	G704R	0.498818
GNAS	R1023G	0.152589
ABCA7	A799E	0.4875