Supplemental Materials

I. Supplemental Methods

a. Duplex Next Generation Sequencing

We selected 45 genes for targeted sequencing based on their recurrent alteration in myeloid malignancies (Supplemental Table 1).

Library Construction, quantification, and normalization

500ng genomic DNA was used as input for DNA fragmentation using a Covaris acoustic ultrasonicator, targeting 150 bp fragments. Library preparation was performed using the KAPA Biosystems (KAPA HyperPrep Kit with Library Amplification product KK8504) and IDT's duplex UMI adapters. The libraries were then paired with unique 8-base dual index sequences embedded within the p5 and p7 primers (IDT) during PCR. Enzymatic clean-ups were performed using Beckman Coulter AMPure XP beads. Libraries were quantified using the INvitrogen Quant-It broad range dsDNA quantification assay kit (Thermo Scientific) with a 1:200 PicoGreen dilution. Each library was normalized to 35ng/uL using Tris-HCl, 10 mM, pH 8.0.

Hybrid Selection, Cluster Amplification, and Sequencing

In solution hybrid selection was performed using IDT's XGen hybridization and wash kit, with creation of 12-plex pre-hybridization pools. Custom exome bait (TWIST bioscience) was added to the lyophilized pool prior to resuspension, followed by library normalization and hybridization performed using a Hamilton Starlet liquid handling platform and target capture on an Agilent Bravo automated platform. Post capture, a PCR was performed to

amplify the captured DNA. Cluster amplification using Exclusion Amplification cluster chemistry and HISeq amplification was performed according to manufacturer's protocol (Illumina) and using HiSeq X flowcells. Flowcells were sequenced on v2 Sequencing-by-Synthesis chemistry for HiSeq X flowcells. The flowcells were then analyzed using RTA v.2.7.3 or later. Each pool of whole genome libraries was run on paired 151 bp runs, reading the dual-indexed sequences to identify molecular indices and sequenced across the number of lanes needed to meet coverage for all libraries in the pool.

Variant calling

Reads were aligned with bwa-mem 0.7.15. Duplex consensus reads were called with fgbio 1.0 and realigned using bwa-mem. Consensus reads were required to have reads from both families αβ and βα, and consensus reads with Ns in excess of 5% of bases were discarded. Read one and two were soft-clipped from the 5′ end by 10 bases to reduce errors due to end repair. Single nucleotide and small insertion and deletion calling was performed with samtools-0.1.18 mpileup and Varscan 2.2.3. Variants were annotated to include information about cDNA and amino acid changes, sequence depth, number, and percentage of reads supporting the variant allele, population allele frequency in the Genome Aggregation Database (gnomAD). Variants were excluded if they had fewer than two total duplex-reassembled alternate reads at the position or fell outside of the target coordinates, caused synonymous changes, or were recurrent small insertions/deletions at low variant allele fraction adjacent to homopolymer repeat regions. Individual single nucleotide substitutions and small insertions or deletions were evaluated as candidate drivers of myeloid malignancies based on gene-specific characteristics, then curated

manually and classified as driver mutations based on genetic criteria and literature review. All interpretation of variants was blinded to clinical characteristics and thus agnostic to variables including age, sex, diagnosis, treatment status, and clinical outcomes; the genetic analysis was completed and locked prior to merging with any clinical data. The presence of sole persisting *DNMT3A* or *TET2* mutations was considered NGS-negative in post-diagnosis samples.

b. **BH3 profiling**

BH3 profiling was performed using the Eppendorf epMotion 5075l automated pipetting platform (Eppendorf, Enfield, CT, UA).[1] Bone marrow mononuclear cells were exposed to synthetic BH3 peptides after plasma membrane permeabilization with digitonin and sensitivity to BH3 peptides was measured by cytochrome c release using an iQue Screener Plus VBR flow cytometer, which uses Forecyt v8,2 software for acquisition, gating, and data export (Essen Bioscience/Sartorius, Ann Arbor, MI). Cytochrome c (Biolegend 983502) was stained overnight and the median fluorescence intensity (MFI) was calculated for each cell population. FMO served as a control well lacking the cytochrome c antibody. Cytochrome c release was calculated using the following formula:

$$Cyto\ c\ Release = 1 - \frac{MFI_{Sample} - MFI_{FMO}}{MFI_{Buffer\ alone} - MFI_{FMO}}$$

Values reported are the average of two technical duplicates for every treatment. DMSO and alamethicin were used as negative and positive controls, respectively. Cells were gated based on SSC, CD45 (BD 348805), CD33 (BD 340679), CD14 (BD 659450), CD11b (Biolegend 982608), and CD16 (Biolegend 980108) status. Individual flow plots

underwent hematopathology review. A minimum of 50 events per population per well was required to calculate cytochrome c release.

c. **Cell lines, viability and synergy evaluation**

AML cell lines (OCI-AML3 and OCI-AML2) were acquired from Dr. Benjamin Ebert's lab and authenticated by short tandem repeat analysis. Cell viability was measured using CellTiter Glo assay according to manufacturer's instructions (Promega). The effects of combining busulfan with venetoclax were calculated using the zero interaction potency model, where a positive delta score indicates percentage of cell inhibition, on the web-based synergyfinder application (http://synergyfinder.org).

References

1. Ryan J, Montero J, Rocco J, Letai A. iBH3: simple, fixable BH3 profiling to determine apoptotic priming in primary tissue by flow cytometry. Biol Chem 2016;397:671-8.

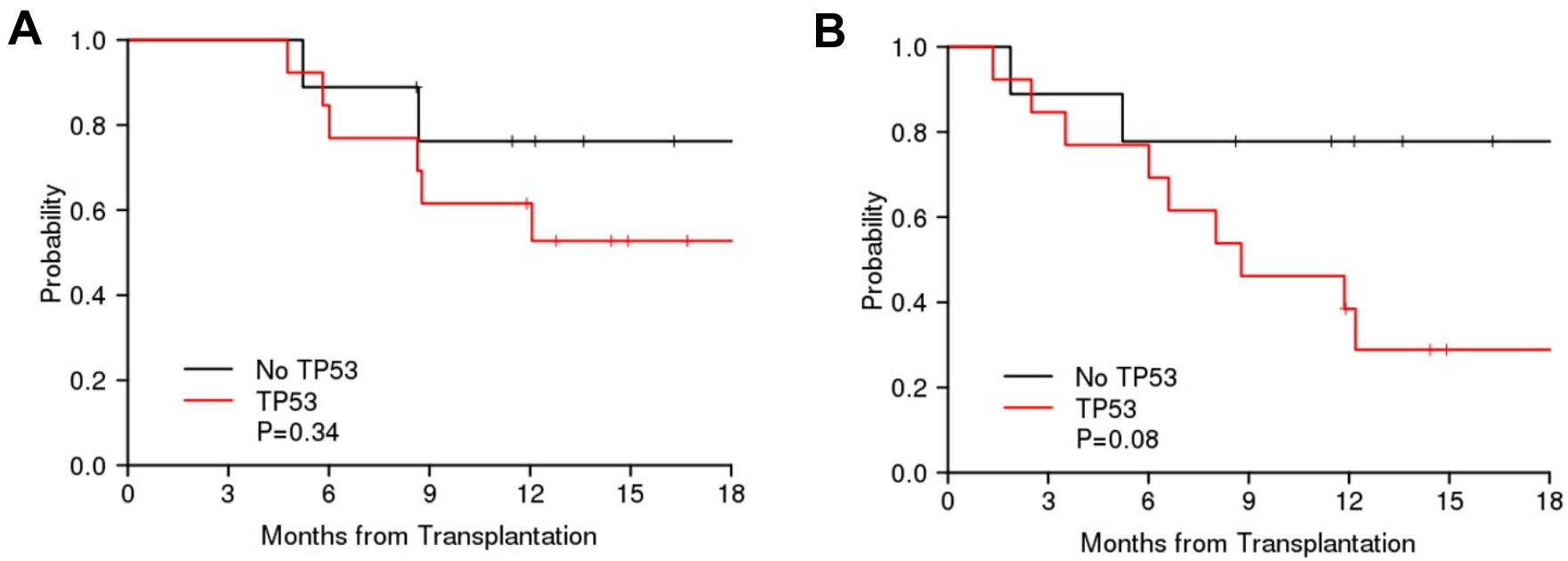
II. Supplemental Figure Legends and Figures

Supplemental Figure 1. Baseline *TP53* mutation status and outcome. Probability of **(A)** overall survival and **(B)** progression free survival based on baseline *TP53* wild type (black) versus *TP53* mutated (red) status shown here.

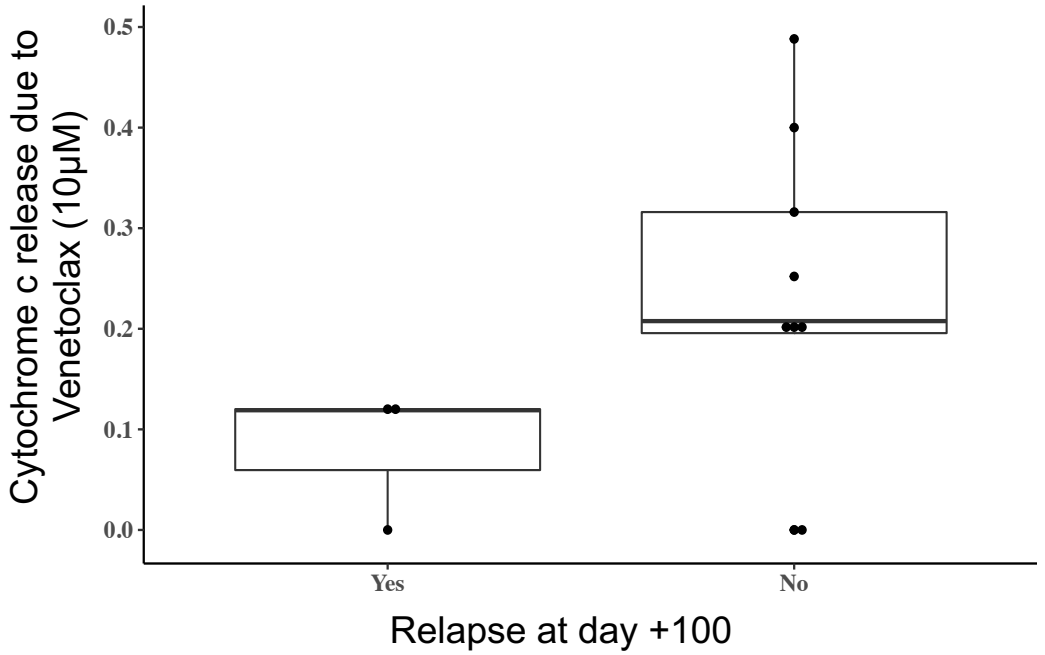
Supplemental Figure 2. BH3 profiling of monocyte population in screening marrow samples. Pre-transplant bone marrow samples from 12 patients treated at highest dose level (DL3) underwent BH3 profiling using venetoclax (10 μM) directly on mitochondria. Monocytes were gated using CD33+CD14+ immunophenotypic markers. At least 50 events/population per well were required for analysis. Cytochrome c release (to indicate mitochondrial apoptotic priming sensitivity) after venetoclax exposure and association to response status was explored.

Supplemental Figure 3. Effect of combination venetoclax and busulfan in AML cells. OCI-AML3 and OCI-AML2 cells were treated with busulfan and venetoclax treatment alone and in combination. Summary delta scores to quantify synergistic effects were calculated to average the overall interaction effect over all the dose pairs for a drug combination. Red and green indicate higher and lower delta score, respectively.

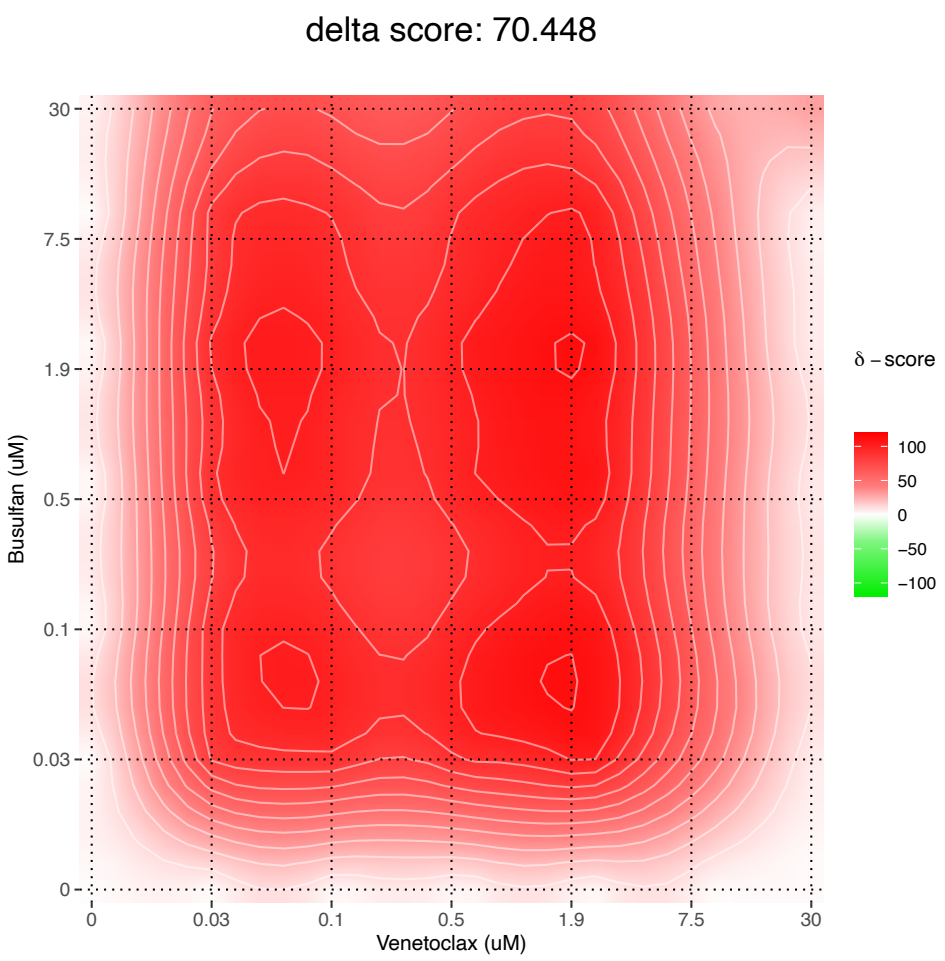
Supplemental Figure 1. Baseline *TP53* mutation status and outcome



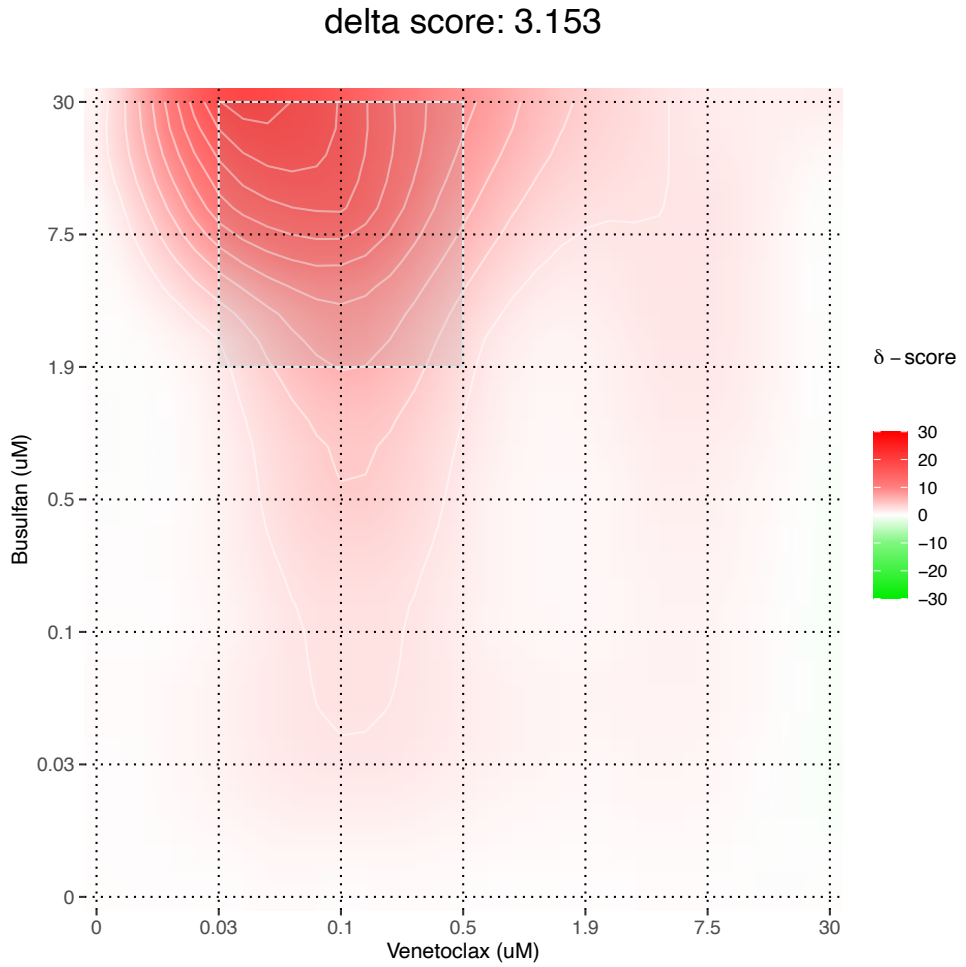
Supplemental Figure 2. BH3 profiling of monocyte population in screening marrow samples.



Supplemental Figure 3. Effect of combination venetoclax and busulfan in AML cells.



OCI-AML3



OCI-AML2

III. Supplemental Tables

Supplemental Table 1. Gene List.

ASXL1
ATM
BCOR
BCORL1
CBL
CEBPA
CREBBP
CSF3R
CUX1
DDX41
DNMT3A
EP300
ETV6
EZH2
FLT3
GATA2
GNB1
IDH1
IDH2
IKZF1
JAK2
KIT
KRAS
MYC
NF1
NFE2
NPM1
PPM1D
PRPF8
PTPN11
RAD21
RIT1
RUNX1
SETBP1
SF3B1

SH2B3
SMC1A
SMC3
SRSF2
STAG2
TERTpromoter
TET2
TP53
WT1
ZRSR2

Supplemental Table 2. Patient-Level Responses Detailed

DL	Patient	Disease	Pre-transplant	Day +100	+ 6 months	+12 months
1	1	MDS	Flow MRD n/a NGS pos	Flow MRD n/a NGS pos	Flow MRD n/a NGS pos	Relapse
	2	AML	Flow MRD pos NGS pos	Flow MRD neg NGS pos	Flow MRD neg NGS neg	Flow MRD neg NGS neg
	3	MDS	Flow MRD n/a NGS pos	Flow MRD n/a NGS pos	Flow MRD n/a NGS n/a	Deceased
2	4	MDS	Flow MRD n/a NGS pos	Flow MRD n/a NGS pos	Relapse	Deceased
	5	MDS	Flow MRD n/a NGS pos	Flow MRD n/a NGS neg	Flow MRD n/a NGS neg	Relapse
	6	CMML	Flow MRD n/a NGS pos	Flow MRD n/a NGS neg	Flow MRD n/a NGS neg	Flow MRD n/a NGS neg
3	7	AML	Flow MRD pos NGS pos	Flow MRD n/a NGS neg	Flow MRD neg NGS neg	Flow MRD neg NGS neg
	8	AML	Flow MRD n/a NGS pos	Flow MRD n/a NGS pos	Relapse	Deceased
	9	MDS	Flow MRD pos NGS pos	Relapse	Deceased	Deceased
	10	AML	Flow MRD pos NGS pos	Relapse	Deceased	Deceased
	11	MDS	Flow MRD pos NGS pos	Flow MRD neg NGS neg	Flow MRD neg NGS pos	Flow MRD pos NGS pos
	12	AML	Flow MRD neg NGS neg	Flow MRD neg NGS neg	Flow MRD n/a NGS neg	Flow MRD neg NGS n/a
	13	MDS	Flow MRD n/a NGS pos	Flow MRD n/a NGS neg	Flow MRD n/a NGS n/a	Flow MRD n/a NGS neg
	14	MDS	Flow MRD n/a NGS pos	Flow MRD neg NGS neg	Flow MRD n/a NGS n/a	Flow MRD neg NGS neg
	15	MDS/MPN	Flow MRD neg NGS neg	Flow MRD neg NGS neg	Flow MRD neg NGS neg	Flow MRD neg NGS neg
	16	AML	Flow MRD n/a NGS pos	Flow MRD neg NGS neg	Flow MRD n/a NGS n/a	Deceased
	17	MDS	Flow MRD neg NGS neg	Flow MRD neg NGS neg	Flow MRD neg NGS neg	Flow MRD neg NGS n/a
	18	MDS	Flow MRD pos NGS pos	Relapse	n/a	n/a
	19	MDS	Flow MRD pos NGS pos	Flow MRD neg NGS n/a	Flow MRD neg NGS pos	Flow MRD neg NGS n/a
	20	MDS	Flow MRD n/a NGS pos	Flow MRD neg NGS n/a	Flow MRD n/a NGS neg	Deceased
	21	MDS	Flow MRD neg NGS neg	Flow MRD pos NGS n/a	Flow MRD neg NGS neg	Flow MRD neg NGS n/a
	22	AML	Flow MRD neg NGS pos	Flow MRD neg NGS n/a	Flow MRD neg NGS n/a	Flow MRD neg NGS n/a

Supplemental Table 3: Individual Patient Pre/Post-Transplant Mutations

subject_id	gene	cdna	aa	result	Dx	Screening	Day +28	Day +100	Day +159	+6 months	Day +201	+1 year
1	CSF3R	c.C2326T	p.Q776X	stopgain	N	N	X	N	X	Y	Y	X
1	KRAS	c.C64A	p.Q22K	nonsynonymous SNV	N	N	X	N	X	N	Y	X
1	NF1	c.G958C	p.A320P	nonsynonymous SNV	N	N	X	N	X	Y	Y	X
1	TP53	c.G517A	p.V173M	nonsynonymous SNV	Y	Y	X	Y	X	Y	Y	X
2	ASXL1	c.2011_2018del	p.A671fs	frameshift deletion	Y	Y	X	Y	X	N	X	N
2	CREBBP	c.5545A>T	p.K1849*	nonsense	Y	N	X	N	X	N	X	N
2	CUX1	c.2616delA,c.2649delA	p.G872fs,p.G883fs	frameshift deletion	N	Y	X	N	X	N	X	N
2	CUX1	c.C2485T,c.C2518T	p.Q829X,p.Q840X	stopgain	N	Y	X	N	X	N	X	N
2	DNMT3A	c.A418T	p.K140X	stopgain	N	N	X	N	X	Y	X	N
2	DNMT3A	c.A2477C	p.K826T	nonsynonymous SNV	N	N	X	Y	X	Y	X	Y
2	DNMT3A	c.C1135T	p.R379C	nonsynonymous SNV	N	N	X	N	X	N	X	Y
2	EP300	c.4915delC	p.L1639fs	frameshift deletion	N	Y	X	N	X	N	X	N
2	IDH1	c.G395A	p.R132H	nonsynonymous SNV	Y	Y	X	indeterminate	X	N	X	N
2	RAD21	c.1636delG	p.G546fs	frameshift deletion	N	Y	X	N	X	N	X	N
2	RAD21	c.1455delA	p.P485fs	frameshift deletion	N	Y	X	N	X	N	X	N
2	SETBP1	c.G2602A	p.D868N	nonsynonymous SNV	Y	Y	X	Y	X	N	X	N
2	SH2B3	c.110delC	p.A37fs	frameshift deletion	N	Y	X	N	X	N	X	N
2	SRSF2	c.285_308del	p.95_103del	nonframeshift deletion	N	Y	X	Y	X	N	X	N
2	TET2	c.G3662T	p.C1221F	nonsynonymous SNV	N	Y	X	N	X	N	X	N
2	TET2	c.G3739T	p.E1247X	stopgain	N	Y	X	N	X	N	X	N
2	TET2	c.C5609A	p.S1870X	stopgain	N	N	X	Y	X	Y	X	Y
2	ZRSR2	c.1002delT	p.N334fs	frameshift deletion	N	Y	X	N	X	N	X	N
3	DNMT3A	c.T2261A	p.L754H	nonsynonymous SNV	N	Y	X	N	X	X	X	X
3	NFE2	c.783_786del	p.E261fs	frameshift deletion	N	Y	X	N	X	X	X	X
3	NFE2	c.G818T	p.R273L	nonsynonymous SNV	N	Y	X	N	X	X	X	X
3	TET2	c.A3910G	p.K1304E	nonsynonymous SNV	N	Y	X	indeterminate	X	X	X	X
3	TET2	c.C2872T	p.Q958X	stopgain	N	Y	X	N	X	X	X	X
3	TP53	c.455dupC	p.P152fs	frameshift insertion	Y	Y	X	Y	X	X	X	X
3	TP53	c.C844T	p.R282W	nonsynonymous SNV	Y	Y	X	Y	X	X	X	X
4	DNMT3A	c.1881delA	p.P627fs	frameshift deletion	N	Y	X	N	X	X	X	X
4	DNMT3A	c.C1584A	p.Y528X	stopgain	Y	Y	X	Y	X	X	X	X
4	GNB1	c.A266G	p.K89R	nonsynonymous SNV	N	Y	X	Y	X	X	X	X
4	IDH1	c.G395A	p.R132H	nonsynonymous SNV	N	Y	X	Y	X	X	X	X
4	PPM1D	c.G1426T	p.E476X	stopgain	N	Y	X	N	X	X	X	X
4	PPM1D	c.C1654T	p.R552X	stopgain	N	Y	X	N	X	X	X	X
4	SF3B1	c.A2294G	p.Y765C	nonsynonymous SNV	N	Y	X	N	X	X	X	X
4	TET2	c.T3819G	p.C1273W	nonsynonymous SNV	N	Y	X	N	X	X	X	X
4	TET2	c.C2905T	p.Q969X	stopgain	N	Y	X	indeterminate	X	X	X	X
4	TP53	c.C455T	p.P152L	nonsynonymous SNV	Y	Y	X	Y	X	X	X	X
4	TP53	c.C722T	p.S241F	nonsynonymous SNV	Y	Y	X	Y	X	X	X	X
5	DNMT3A	c.G2225T	p.R742L	nonsynonymous SNV	N	N	X	Y	X	Y	X	Y
5	IDH1	c.C394T	p.R132C	nonsynonymous SNV	N	N	X	N	X	N	X	Y
5	PPM1D	c.C1384T	p.Q462X	stopgain	N	Y	X	N	X	N	X	N
5	PPM1D	c.1528delC	p.Q510fs	frameshift deletion	N	N	X	N	X	N	X	indeterminate
5	SMC3	c.3239delG	p.G1080fs	frameshift deletion	N	Y	X	N	X	N	X	N
5	TP53	c.A659G	p.Y220C	nonsynonymous SNV	Y	Y	X	N	X	N	X	Y
6	ASXL1	c.2404G>T	p.E802*	nonsense	Y	Y	N	N	X	N	X	N
6	BCOR	c.4981C>T	p.R1627*	nonsense	N	Y	N	N	X	N	X	N
6	RUNX1	c.215_215insA	p.R72fs*	frameshift insertion	Y	Y	N	N	X	N	X	N
6	SETBP1	c.2603A>G	p.D868G	missense	Y	Y	N	N	X	N	X	N
7	FLT3	c.2503G>A	p.D835N	missense	Y	N	N	N	X	N	X	N
7	TP53	c.502delC	p.H168fs	frameshift deletion	N	Y	indeterminate	N	X	N	X	N
7	TP53	c.T584C	p.I195T	nonsynonymous SNV	Y	Y	indeterminate	N	X	N	X	N
7	TP53	c.A751T	p.I251F	nonsynonymous SNV	N	Y	N	N	X	N	X	N
7	TP53	c.C742T	p.R248W	nonsynonymous SNV	N	Y	N	N	X	N	X	N
7	TP53	c.502delG	p.Q167fs*3	frameshift deletion	Y	N	N	N	X	N	X	N
8	DNMT3A	c.G2120A	p.G707D	nonsynonymous SNV	X	Y	X	N	N	X	X	X
8	PPM1D	c.1363_1366del	p.E455fs	frameshift deletion	X	Y	X	N	N	X	X	X
8	PPM1D	c.A1603T	p.K535X	stopgain	X	Y	X	N	N	X	X	X
8	PPM1D	c.1445delT	p.L482fs	frameshift deletion	X	Y	X	N	N	X	X	X
8	PPM1D	c.1606delA	p.R536fs	frameshift deletion	X	Y	X	N	N	X	X	X
8	PPM1D	c.C1654T	p.R552X	stopgain	X	Y	X	N	N	X	X	X
8	PPM1D	c.1465delT	p.S489fs	frameshift deletion	N	Y	X	Y	indeterminate	X	X	X
8	TP53	c.G830C	p.C277S	nonsynonymous SNV	X	N	X	N	indeterminate	X	X	X
8	TP53	c.A623G	p.D208G	nonsynonymous SNV	X	Y	X	indeterminate	N	X	X	X
8	TP53	c.C817T	p.R273C	nonsynonymous SNV	X	Y	X	Y	Y	X	X	X
8	TP53	c.C844T	p.R282W	nonsynonymous SNV	X	Y	X	N	N	X	X	X
9	TP53	c.524-2A>G,c.920-2A>G,c.443-2A>G,c.803-2A>G,c.803-2A>G,c.803-2A>G)	c.524-2A>G	splicing	N	Y	Y	X	X	X	X	X
9	TP53	c.C574T	p.Q192X	stopgain	Y	Y	Y	X	X	X	X	X
10	KRAS	c.532_534del	p.178_178del	nonframeshift deletion	N	Y	Y	X	X	X	X	X
10	NF1	c.7265_7266del,c.7202_7203del	p.K2422fs,p.K2401fs	frameshift deletion	N	Y	N	X	X	X	X	X
11	DNMT3A	c.G1228A	p.A410T	nonsynonymous SNV	N	Y	X	N	X	N	X	N
11	TET2	c.G4108A	p.G1370R	nonsynonymous SNV	N	N	X	N	X	Y	X	Y
11	TET2	c.C4256G	p.P1419R	nonsynonymous SNV	N	Y	X	N	X	N	X	N
11	TP53	c.C844G	p.R282G	nonsynonymous SNV	Y	Y	X	N	X	Y	X	Y
11	U2AF1	c.475_475insTAT	p.Y158_E159insY	missense	Y	N	X	N	X	N	X	N
12	BCR-ABL	p190	.	.	Y	N	X	N	X	N	X	X
13	DNMT3A	c.1481-1G>T,c.1370-1G>T,c.1937-1G>T,c.1937-1G>T)	.	splicing	N	Y	Y	Y	X	X	X	N
13	DNMT3A	c.G2056T	p.D686Y	nonsynonymous SNV	N	Y	indeterminate	indeterminate	X	X	X	Y
13	DNMT3A	c.1314_1315insGGAC	p.M439fs	frameshift insertion	N	Y	indeterminate	N	X	X	X	N
13	TP53	c.G1045T	p.E349X	stopgain	Y	Y	N	N	X	X	X	N
13	TP53	c.G730A	p.G244S	nonsynonymous SNV	Y	Y	indeterminate	indeterminate	X	X	X	N
14	TP53	c.386+1G>A	.	splicing	N	Y	N	N	X	X	X	N
14	TP53	c.658-1G>C	.	splicing	N	Y	N	N	X	X	X	N
14	TP53	c.658-2A>C	.	splicing	N	Y	N	N	X	X	X	N
14	TP53	c.340_342del	p.114del_114del	nonframeshift deletion	N	Y	N	N	X	X	X	N
14	TP53	c.C843G	p.D281E	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.A857T	p.E286V	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.596_599del	p.G199fs	frameshift deletion	N	Y	N	N	X	X	X	N
14	TP53	c.T584C	p.I195T	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.T770C	p.L257P	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.C454A	p.P152T	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.C493T	p.Q165X	stopgain	N	Y	N	N	X	X	X	N
14	TP53	c.817_818insTGC	p.R273delinsLR	nonframeshift insertion	Y	Y	N	N	X	X	X	N
14	TP53	c.C844T	p.R282W	nonsynonymous SNV	N	Y	Y	N	X	X	X	N
14	TP53	c.A488G	p.Y163C	nonsynonymous SNV	N	Y	N	N	X	X	X	N
14	TP53	c.A659G	p.Y220C	nonsynonymous SNV	N	Y	N	N	X	X	X	N
15	DNMT3A	c.C2205A	p.Y735X	stopgain	N	Y	X	N	X	X	X	N
16	ATM	c.G7267A	p.E2423K	nonsynonymous SNV	N	Y	N	N	X	X	X	X
16	ATM	c.G7593A	p.M2531I	nonsynonymous SNV	N	Y	Y	Y	X	X	X	X
16	ATM	c.G7032A	p.W2344X	stopgain	N	Y	N	N	X	X	X	X
16	ATM	c.T4324G	p.Y1442D	nonsynonymous SNV	N	Y	N	N	X	X	X	X
16	DDX41	c.C1079T	p.T360I	nonsynonymous SNV	N	Y	Y	Y	X	X	X	X
16	PPM1D	c.C1434A	p.C478X	stopgain	N	Y	N	N	X	X	X	X
16	PPM1D	c.G1573T	p.E525X	stopgain	N	Y	N	N	X	X	X	X
16	PPM1D	c.1386delA	p.Q462fs	frameshift deletion	N	Y	N	N	X	X	X	X
16	PPM1D	c.1528delC	p.Q510fs	frameshift deletion	N	Y	N	N	X	X	X	X
16	PPM1D	c.C1654T	p.R552X	stopgain	N	Y	N	indeterminate	X	X	X	X
16	SF3B1	c.G1998C	p.K666N	nonsynonymous SNV	N	Y	N	N	X	X	X	X
16	SF3B1	c.G1998C	p.K666N	nonsynonymous SNV	Y	N	N	N	X	X	X	X
16	TP53	c.827_832del	p.276_278del	nonframeshift deletion	N	Y	N	N	X	X	X	X
16	TP53	c.T434C	p.L145P	nonsynonymous SNV	Y	Y	indeterminate	N	X	X	X	X
16	TP53	c.G743A	p.R248Q	nonsynonymous SNV	Y	Y	N	N	X	X	X	X
16	TP53	c.C380T	p.S127F	nonsynonymous SNV	N	Y	N	N	X	X	X	X
16	TP53	c.268_278del	p.S90fs	frameshift deletion	N	Y	N	N	X	X	X	X
17	DNMT3A	c.1642_1644del	p.548_548del	nonframeshift deletion	N	Y	N	N	X	N	X	X
17	PPM1D	c.C1654T	p.R552X	stopgain	N	Y	N	indeterminate	X	N	X	X
17	PPM1D	c.1716dupA	p.R572fs	frameshift insertion	N	Y	N	N	X	N	X	X
17	TET2	c.5501delA	p.Q1834fs	frameshift deletion	N	Y	N	N	X	N	X	X
17	TP53	c.C452G	p.P151R	nonsynonymous SNV	N	Y	indeterminate	N	X	N	X	X
18	BRCC3	c.806_830delCCAAGAATCTGTGCAGTCAGATGTCinsCAGATCTA	p.T269fs*	frameshift deletion	Y	N	N	X	X	X	X	X
18	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	N	Y	indeterminate	X	X	X	X	X
18	TET2	c.A3461G	p.N1154S	nonsynonymous SNV	N	Y	Y	X	X	X	X	X
18	TP53	c.A745G	p.R249G	nonsynonymous SNV	Y	Y	Y	X	X	X	X	X
19	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	Y	Y	indeterminate	X	X	Y	X	X
19	ASXL1	c.C1773G	p.Y591X	stopgain	N	Y	indeterminate	X	X	N	X	X

19	CUX1	c.4323_4330del,c.4290_4297del	p.E1441fs,p.E1430fs	frameshift deletion	N	Y	N	X	X	N	X	X
19	IDH1	c.G395A	p.R132H	nonsynonymous SNV	Y	Y	indeterminate	X	X	N	X	X
19	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	Y	Y	N	X	X	N	X	X
19	NF1	c.A5744G,c.A5807G	p.K1915R,p.K1936R	nonsynonymous SNV	N	Y	N	X	X	N	X	X
19	TET2	c.2641delA	p.R881fs	frameshift deletion	N	N	Y	X	X	Y	X	X
19	TET2	c.4777dupA	p.T1592fs	frameshift insertion	N	Y	N	X	X	N	X	X
19	TP53	c.T634G	p.F212V	nonsynonymous SNV	N	Y	N	X	X	N	X	X
19	U2AF1	c.470A>C	p.Q157P	missense	Y	N	N	X	X	N	X	X
20	DNMT3A	c.C2245T	p.R749C	nonsynonymous SNV	N	N	Y	X	X	Y	X	X
20	EZH2	c.475G>A	p.G159R	missense	Y	N	N	X	X	N	X	X
20	PPM1D	c.1312dupG	p.P437fs	frameshift insertion	N	Y	N	X	X	N	X	X
20	PPM1D	c.1529dupA	p.Q510fs	frameshift insertion	N	Y	N	X	X	N	X	X
20	PPM1D	c.C1711T	p.Q571X	stopgain	N	Y	N	X	X	N	X	X
20	TET2	c.3594+2T>C	.	splicing	N	Y	N	X	X	N	X	X
20	TP53	c.679_680insGGCT	p.S227fs	frameshift insertion	Y	Y	N	X	X	N	X	X
20	TP53	c.G646A	p.V216M	nonsynonymous SNV	N	Y	N	X	X	N	X	X
21	ASXL1	c.2421delT	p.V807fs	frameshift deletion	N	Y	N	X	X	N	X	X
21	ATM	c.T4324C	p.Y1442H	nonsynonymous SNV	N	Y	indeterminate	X	X	Y	X	X
21	DNMT3A	c.T884C	p.L295P	nonsynonymous SNV	Y	Y	indeterminate	X	X	N	X	X
21	DNMT3A	c.G2259A	p.W753X	stopgain	N	Y	N	X	X	N	X	X
21	TET2	c.T3755C	p.L1252P	nonsynonymous SNV	Y	Y	N	X	X	N	X	X
21	TP53	c.C388G	p.L130V	nonsynonymous SNV	N	Y	N	X	X	N	X	X
22	ASXL1	c.S689Afs*25	p.S689Afs*25	frameshift	Y	Y	X	X	X	X	X	X
22	RUNX1	c.335T>C	p.L112P	missense	Y	Y	X	X	X	X	X	X
22	SRSF2	c.284C>A	p.P95H	missense	Y	Y	X	X	X	X	X	X
22	TET2	c.4374_4375insG	p.E1459Gfs*19	frameshift insertion	Y	Y	X	X	X	X	X	X
22	TET2	c.4546C>T	p.R1516*	nonsense	Y	Y	X	X	X	X	X	X