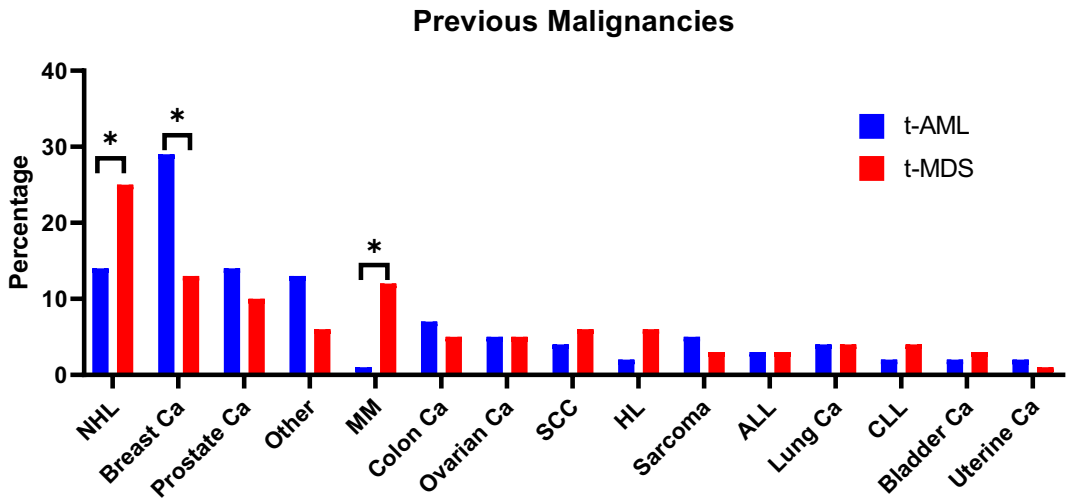
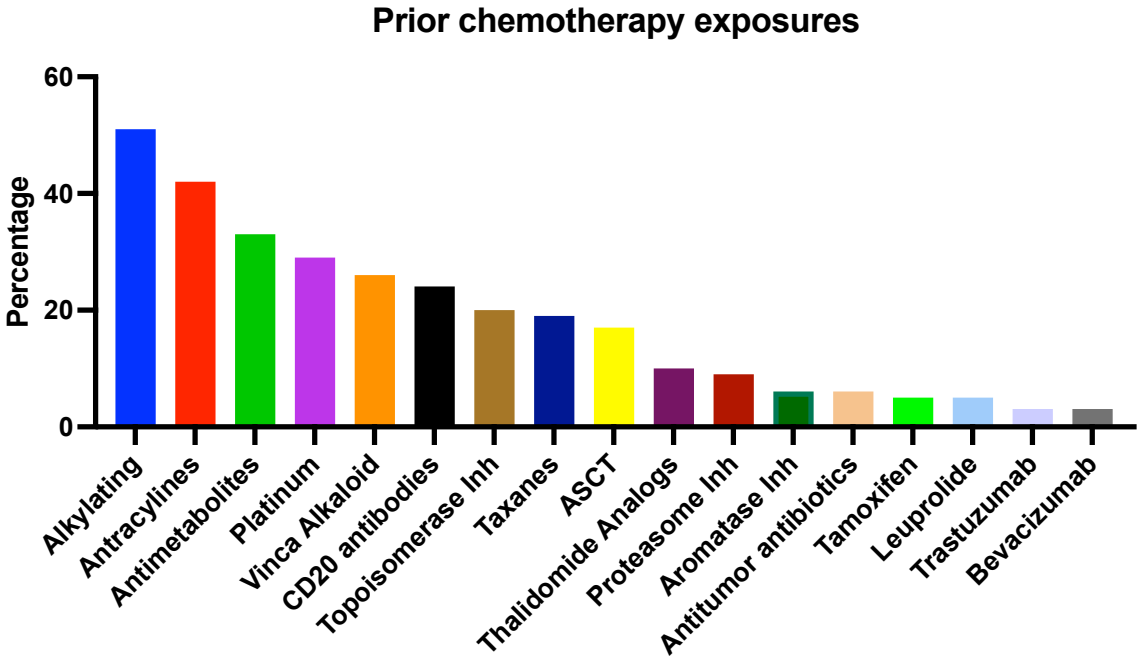
A



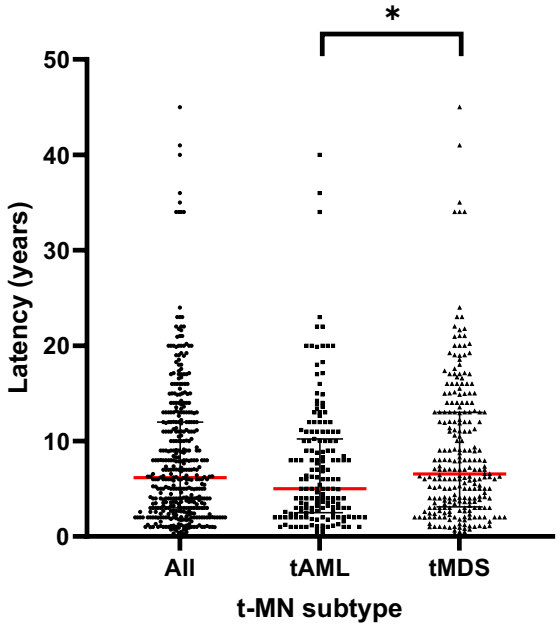
B



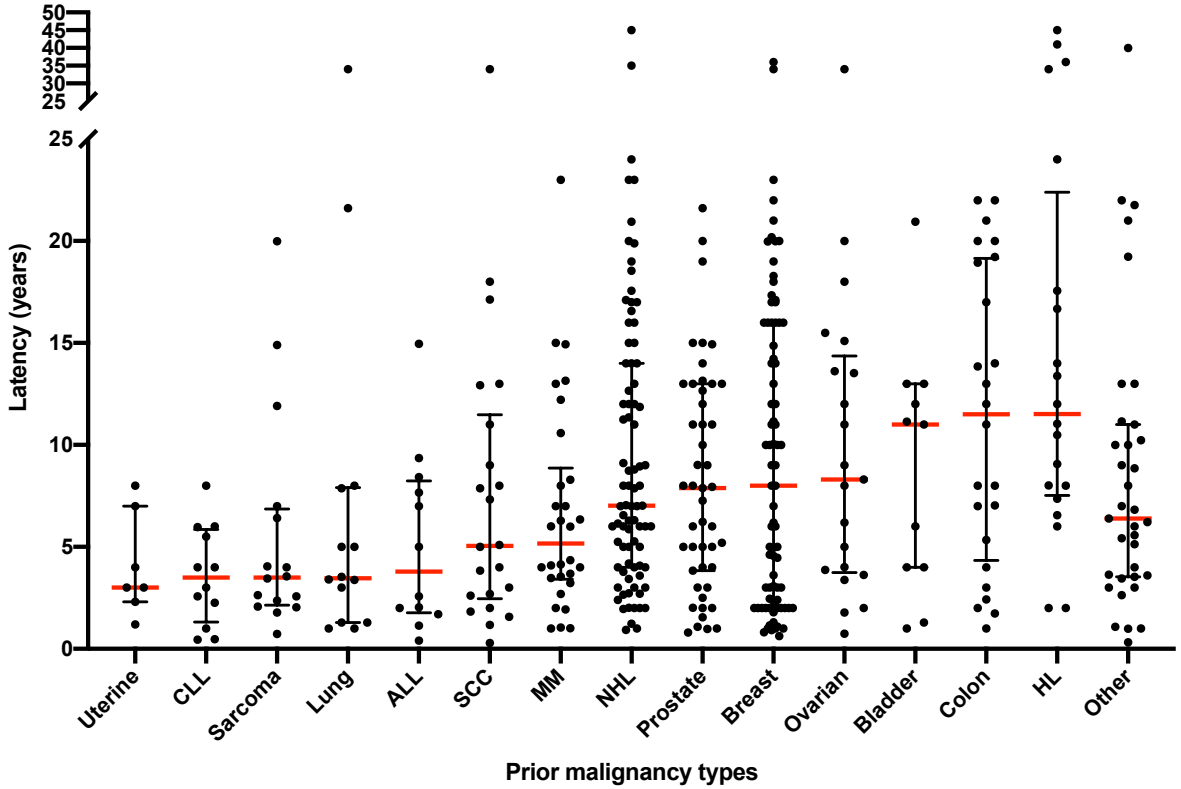
Supplementary Figure S1. Detailed information on primary cancers and exposures in 416 t-MN patients. (**A**) Frequency of primary cancers (**B**) Frequency of prior exposures.

Abbreviations: t-AML: therapy-related acute myeloid leukemia, t-MDS: therapy-related myelodysplastic syndrome, NHL: non-Hodgkin lymphoma, Ca: cancer, SCC: squamous cell carcinoma, HL: Hodgkin lymphoma, ALL: acute lymphocytic leukemia, Lung Ca: lung carcinoma, CLL: chronic lymphocytic leukemia, Bladder Ca: bladder carcinoma, Uterine Ca: uterine carcinoma, ASCT: autologous stem cell transplant. (*) P value <0.01 between t-AML vs. t-MDS.

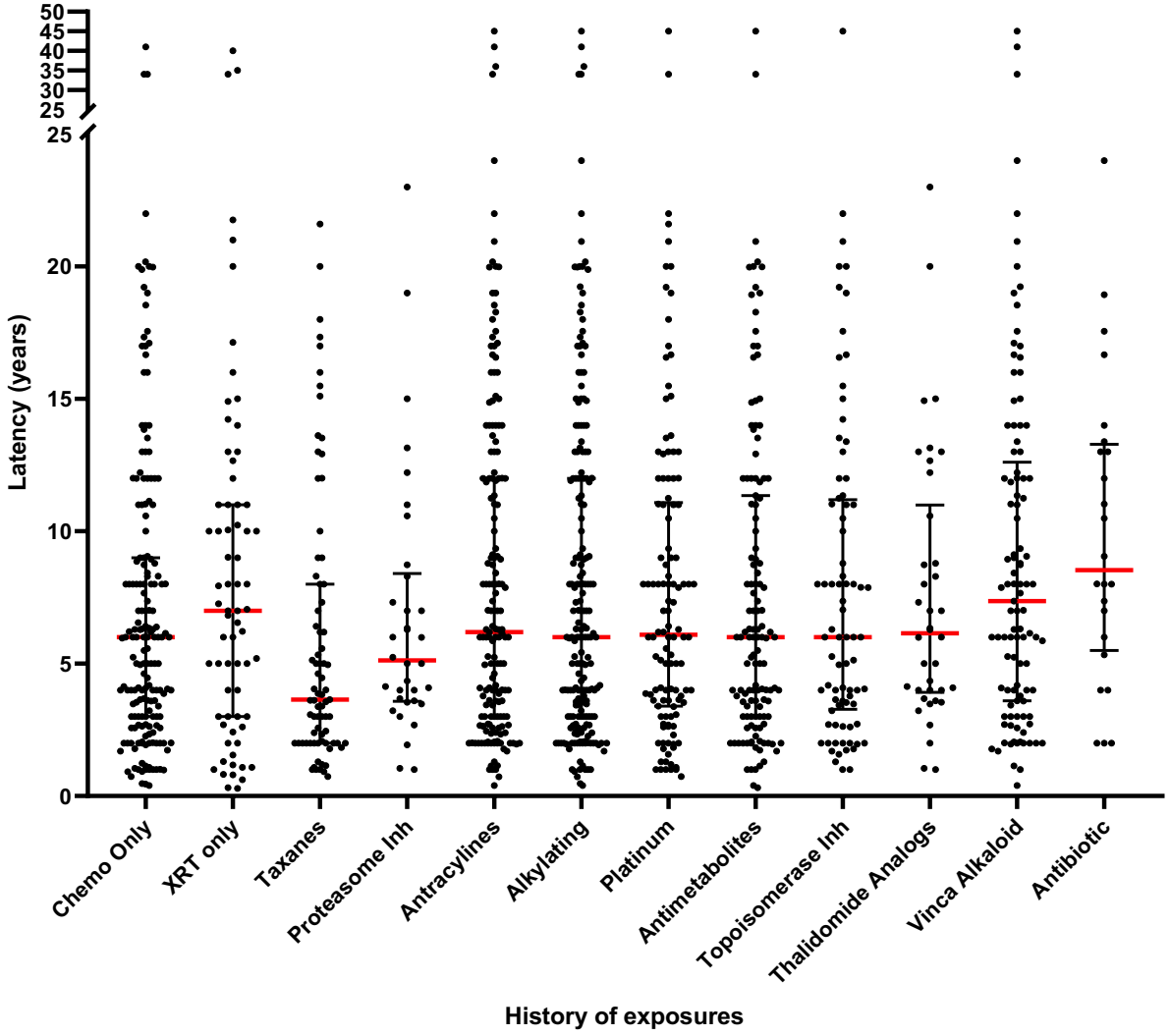
A


*
50
40
30
20
10
0
Latency (years)
All
tAML
tMDS
t-MN subtype

B

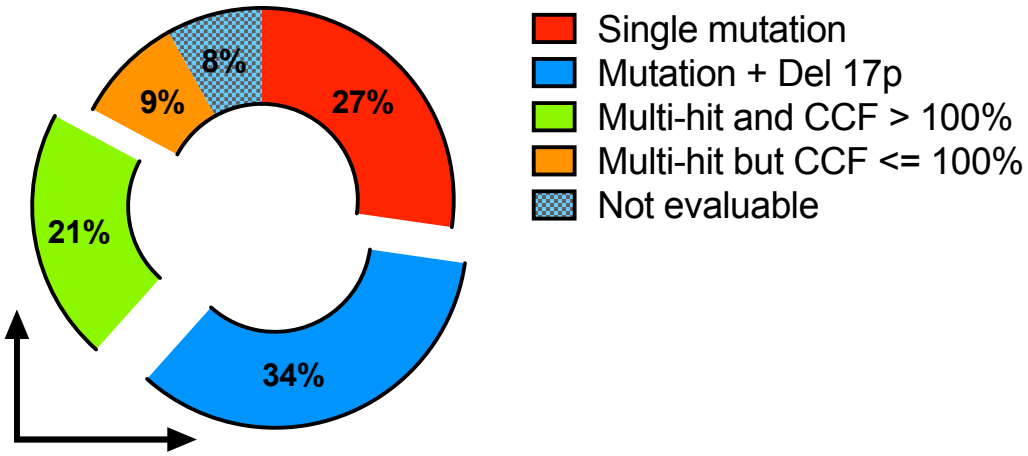

50
45
40
35
30
25
25
20
15
10
5
0
Latency (years)
Uterine
CLL
Sarcoma
Lung
ALL
SCC
MM
NHL
Prostate
Breast
Ovarian
Bladder
Colon
HL
Other
Prior malignancy types

C

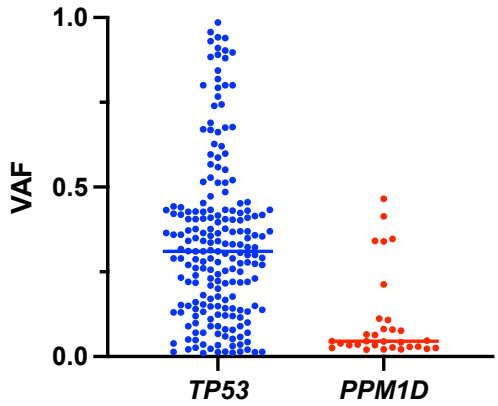


Supplementary Figure S2. Latency to t-MN development. (**A**) In all patients and based on t-AML or t-MDS subtype, (**B**) Latency from the diagnosis of initial primary cancer. (**C**) Latency from the initial exposure. The red lines indicate median. The bottom whiskers and the top whiskers indicate first and third quartiles, respectively. The red line indicates median. The error bar indicates interquartile range. * P <0.05

Abbreviations: CLL: chronic lymphocytic leukemia, ALL: acute lymphocytic leukemia, MM: Multiple myeloma, NHL: non-Hodgkin lymphoma, HL: Hodgkin lymphoma, XRT: radiation.

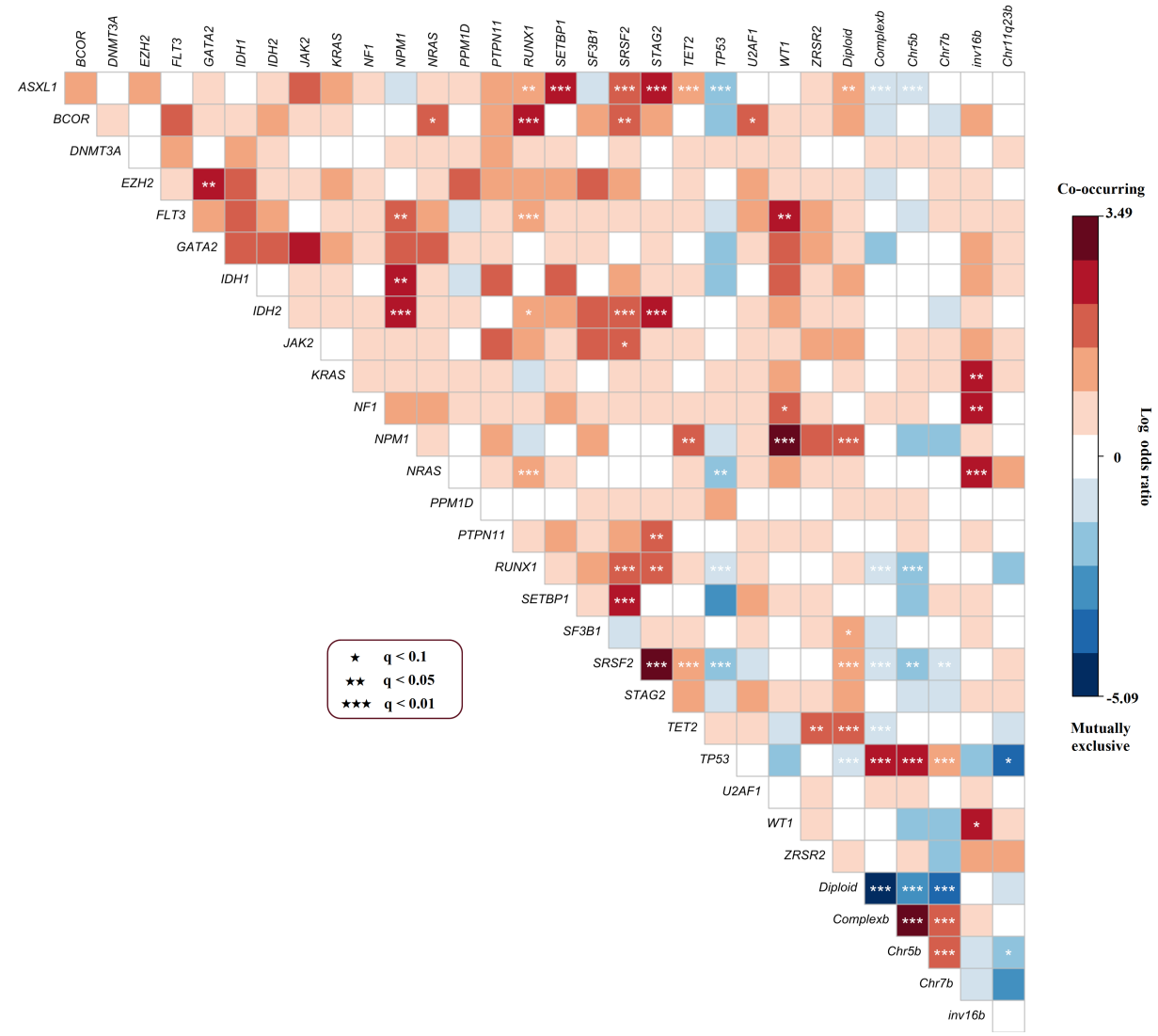


Supplementary Figure S3. **Allelic status of *TP53* mutations**. Allelic status of *TP53* mutations were inferred based on the cooccurrence of deletion 17p and cancer cell fraction (CCF) of the mutations calculated from variant allele frequency (VAF). Co-occurrence of *TP53* mutations with deletion 17p or multi-hit *TP53* mutations with total CCF exceeding 100% were considered as likely bi-allelic involvement.

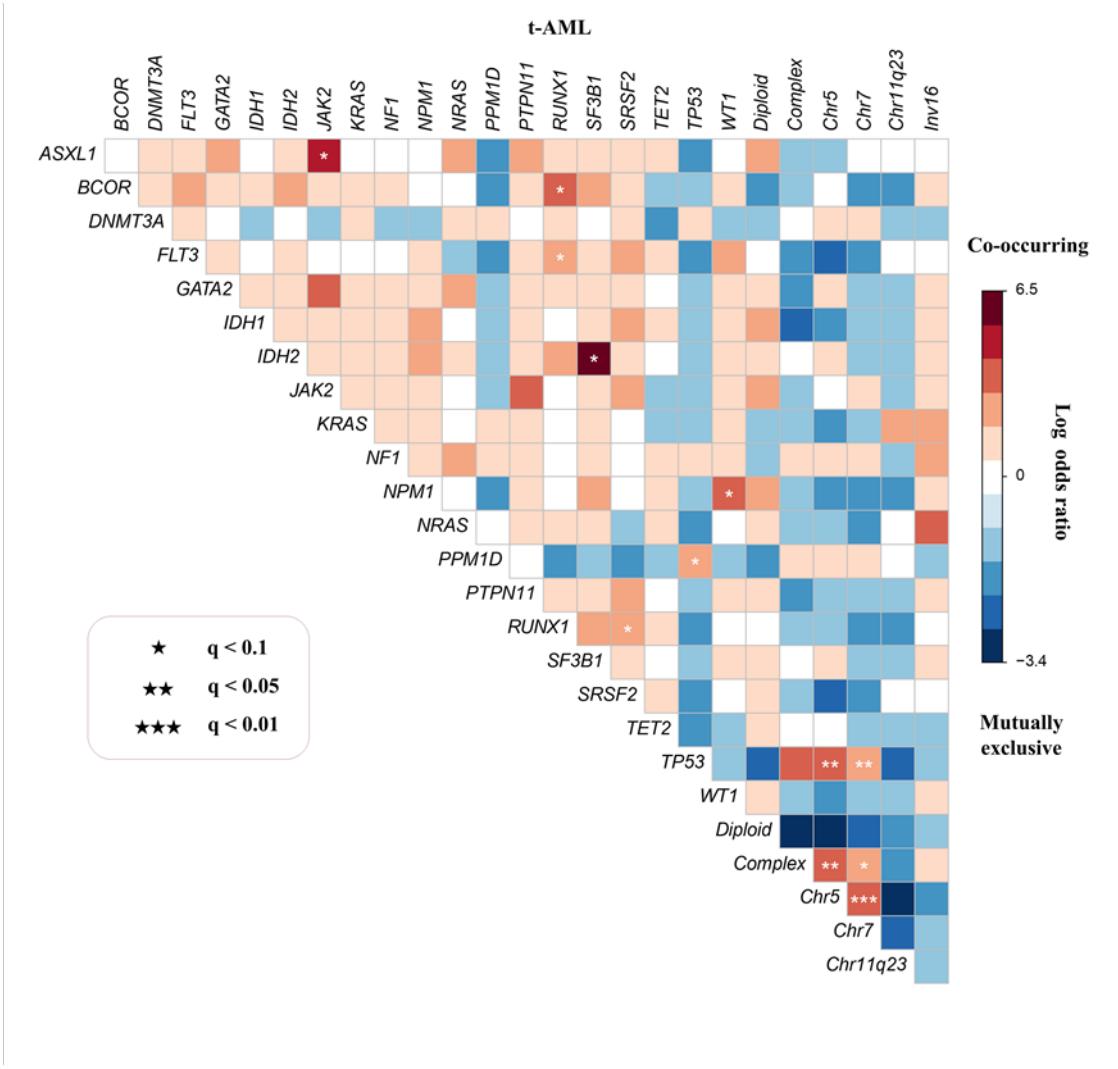


Supplementary Figure S4. The variant allele frequency (VAF) of *TP53* and *PPM1D* mutations. The line indicates median (*TP53* median VAF 0.31, *PPM1D* median VAF 0.045)

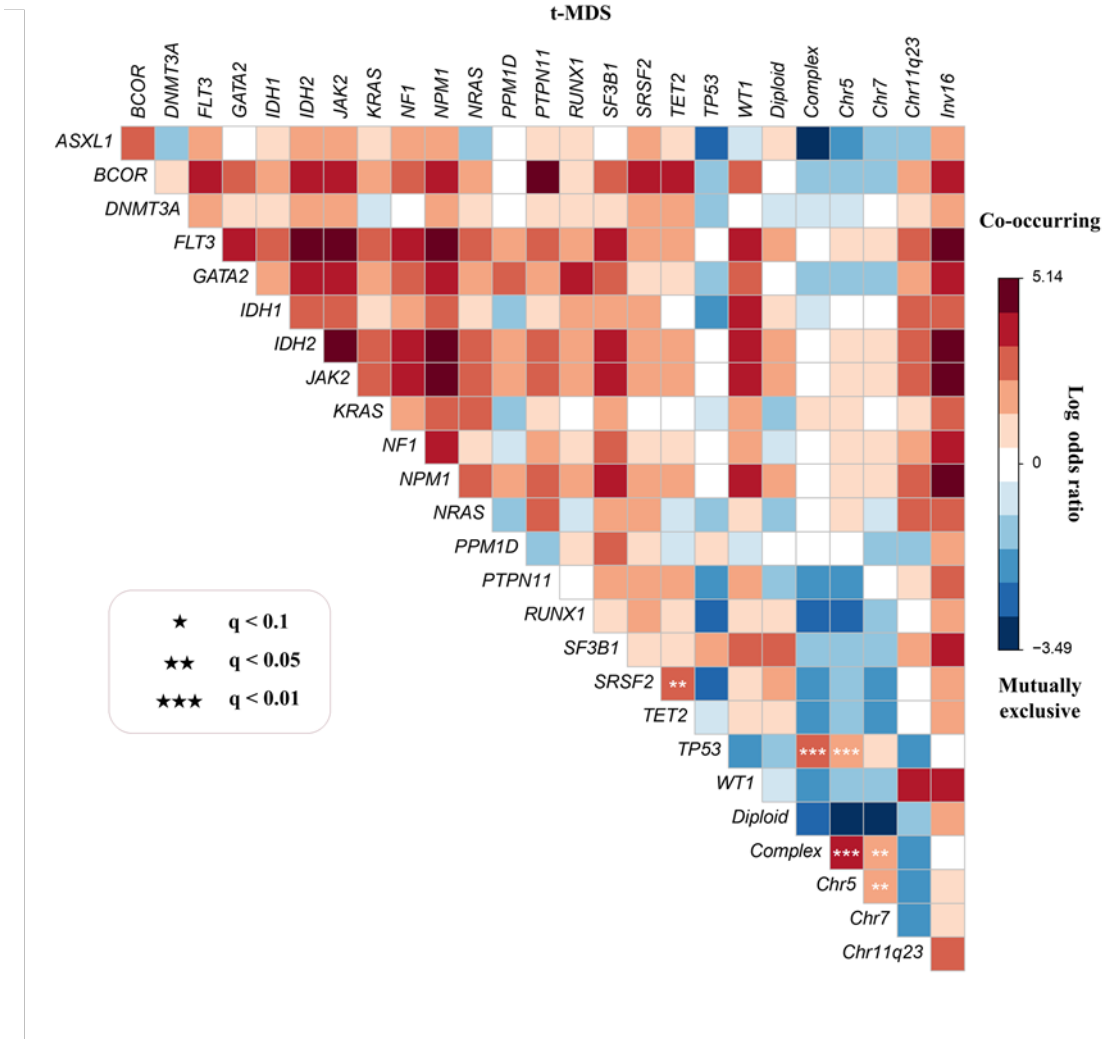
A


BCOR
DNMT3A
EZH2
FLT3
GATA2
IDH1
IDH2
JAK2
KRAS
NF1
NPM1
NRAS
PPM1D
PTPN11
RUNX1
SETBP1
SF3B1
SRSF2
STAG2
TET2
TP53
U2AF1
WT1
ZRSR2
Diploid
Complexb
Chr5b
Chr7b
inv16b
Chr11q23b
ASXL1
★ q < 0.1
★★ q < 0.05
★★★ q < 0.01
Co-occurring
3.49
0
-5.09
Mutually exclusive
Log odds ratio

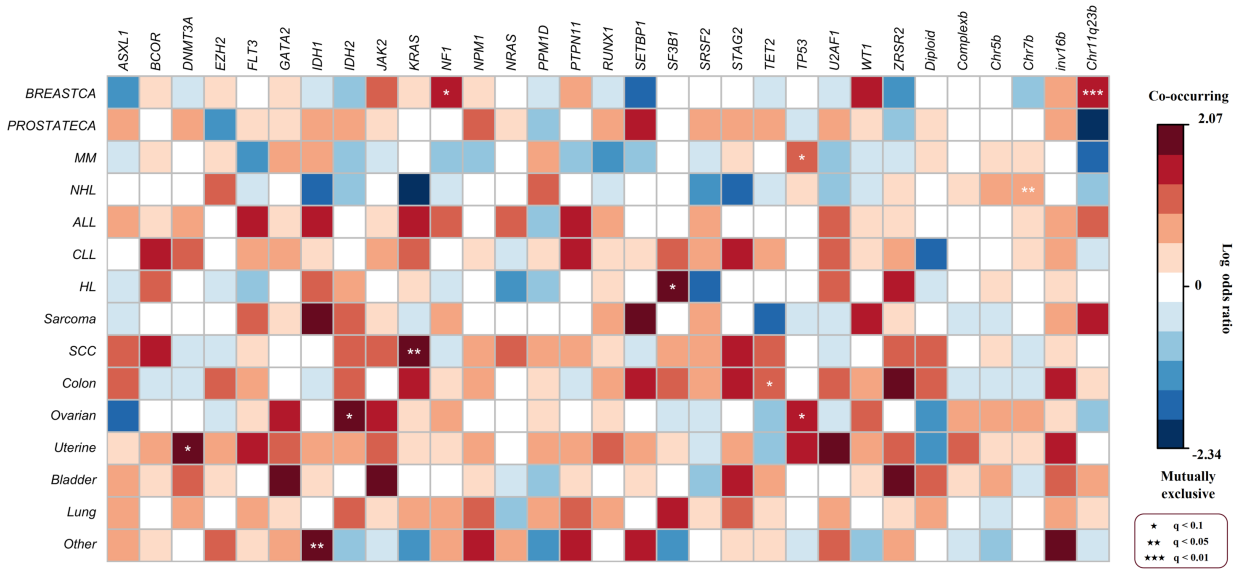
B


t-AML
BCOR
DNMT3A
FLT3
GATA2
IDH1
IDH2
JAK2
KRAS
NF1
NPM1
NRAS
PPM1D
PTPN11
RUNX1
SF3B1
SRSF2
TET2
TP53
WT1
Diploid
Complex
Chr5
Chr7
Chr11q23
Inv16
ASXL1
★ q < 0.1
★★ q < 0.05
★★★ q < 0.01
Co-occurring
6.5
0
−3.4
Log odds ratio
Mutually exclusive

C

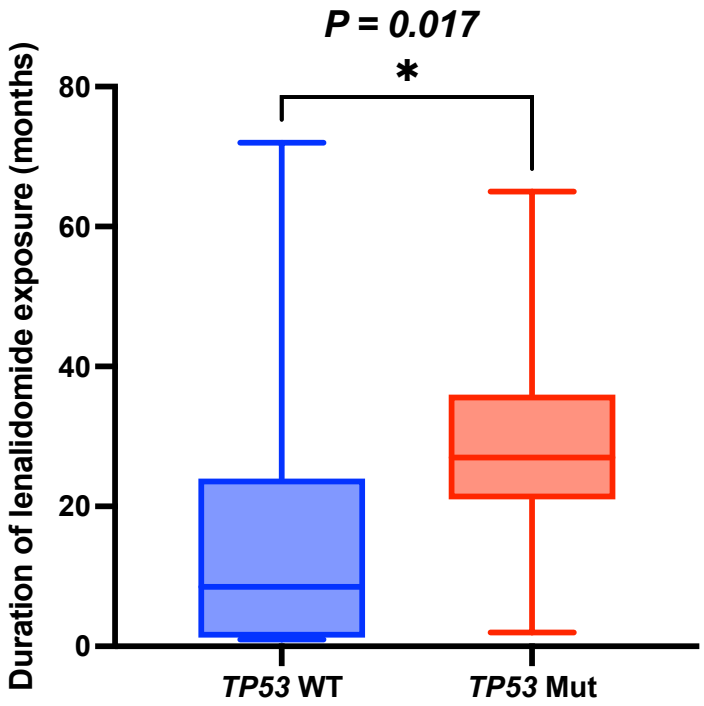


Supplementary Figure S5. Pair-wise analysis of mutation co-occurrence and mutual exclusivity among (**A**) 416 t-MN patients, (**B**) 167 t-AML, and (**C**) 249 t-MDS patients. Clonal relationship between two mutations are shown as log odds ratio. Red color indicates co-occurrence and blue color indicates mutual exclusivity. Statistical significance is described with q value (false discovery rate).



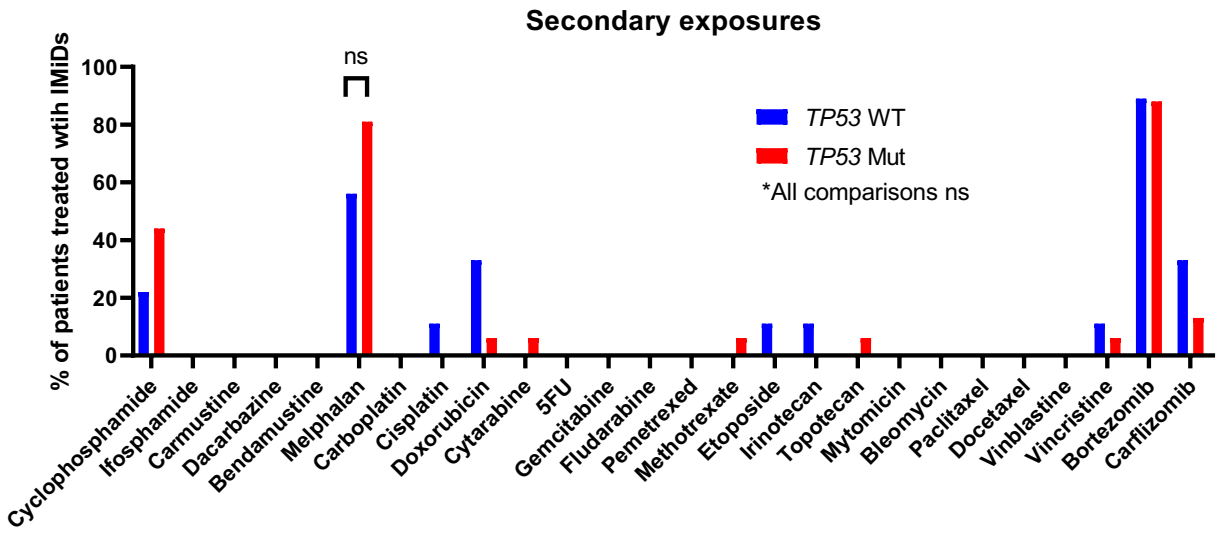
Supplementary Figure S6. Correlation between gene mutations and primary malignancies. Association is shown as log odds ratio. Red color indicates positive correlation and blue color indicates negative correlation. Statistical significance is shown with q value (false discovery rate).

BREASTCA: breast cancer, PROSTATECA: prostate cancer, MM: multiple myeloma, NHL: non-Hodgkin's lymphoma, ALL: acute lymphoblastic leukemia, CLL: chronic lymphocytic leukemia, HL: Hodgkin's lymphoma, SCC: squamous cell carcinoma of head and neck including esophagus.

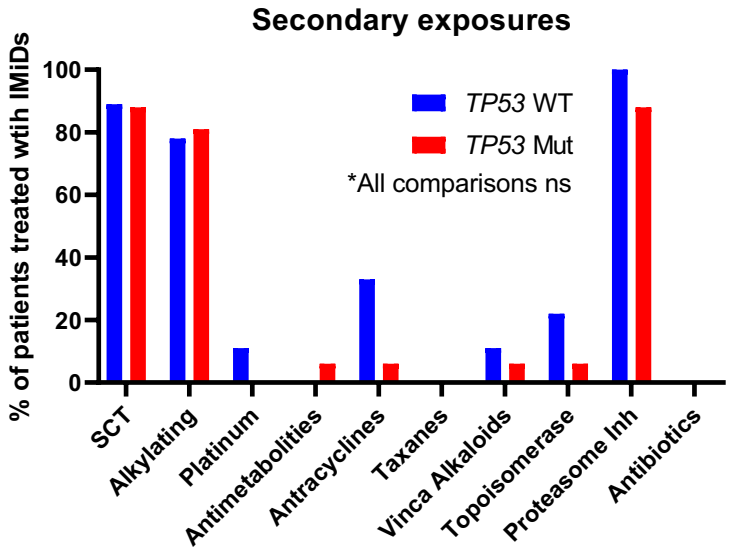


Supplementary Figure S7. Duration of exposure to lenalidomide is associated with *TP53* mutation status in t-MN. t-MN patients with *TP53* mutations had significantly longer duration of exposure to lenalidomide (median 27 months vs. 8.5 months, P = 0.017, Mann-Whitney test).

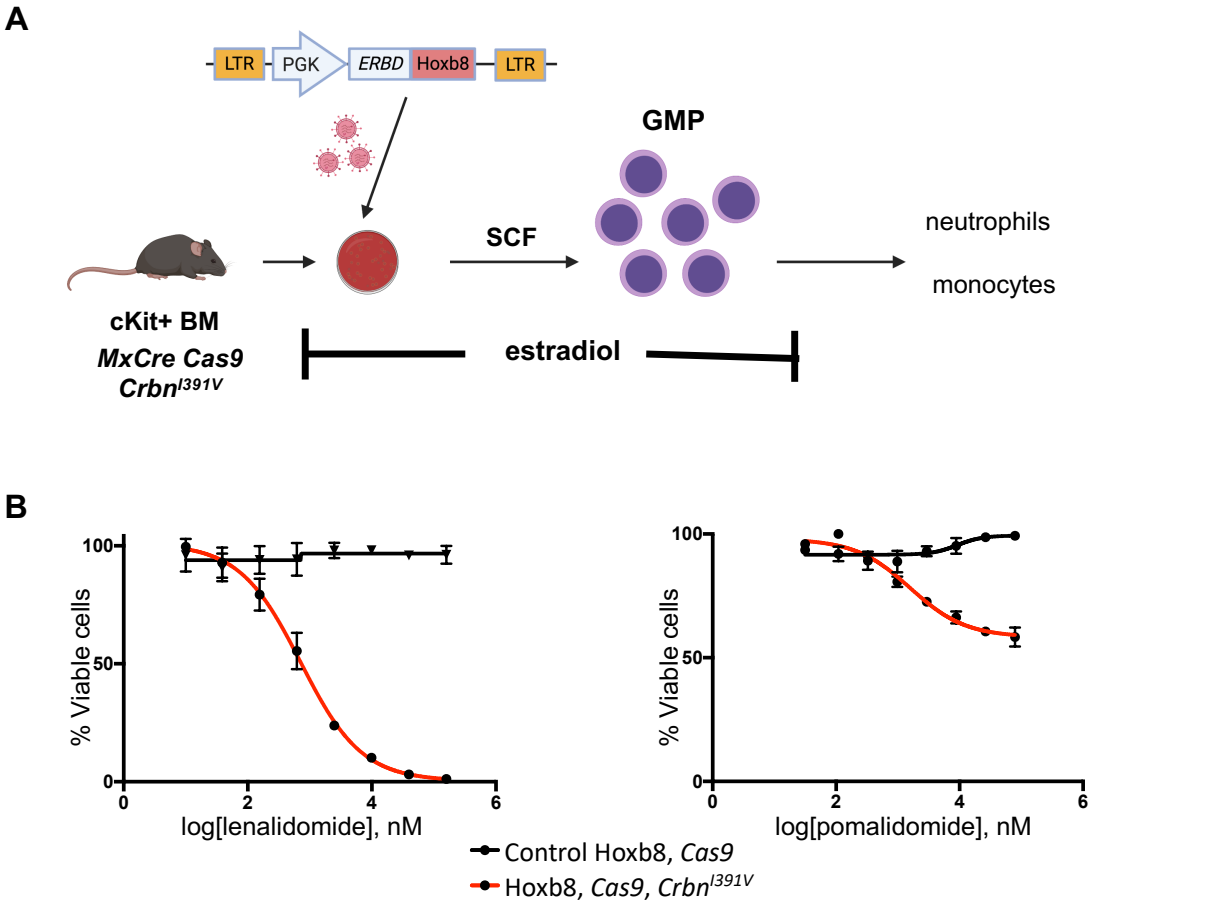
A



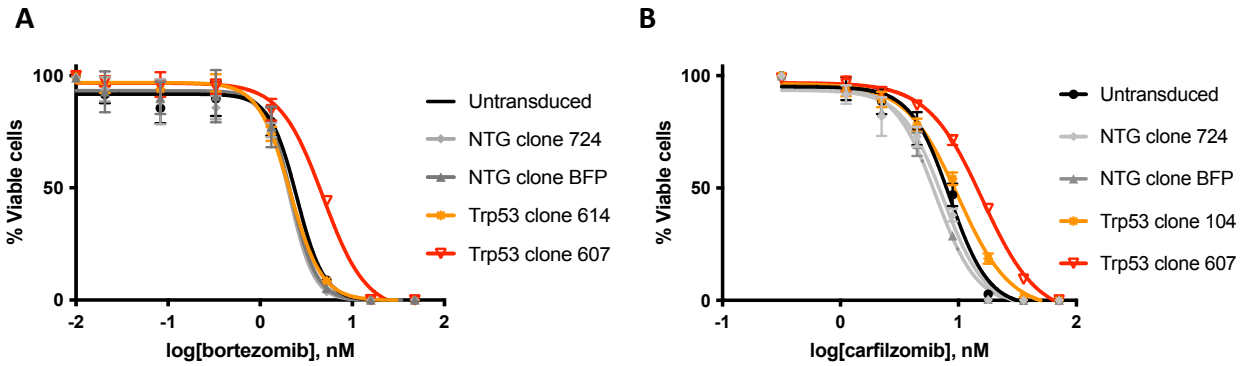
B



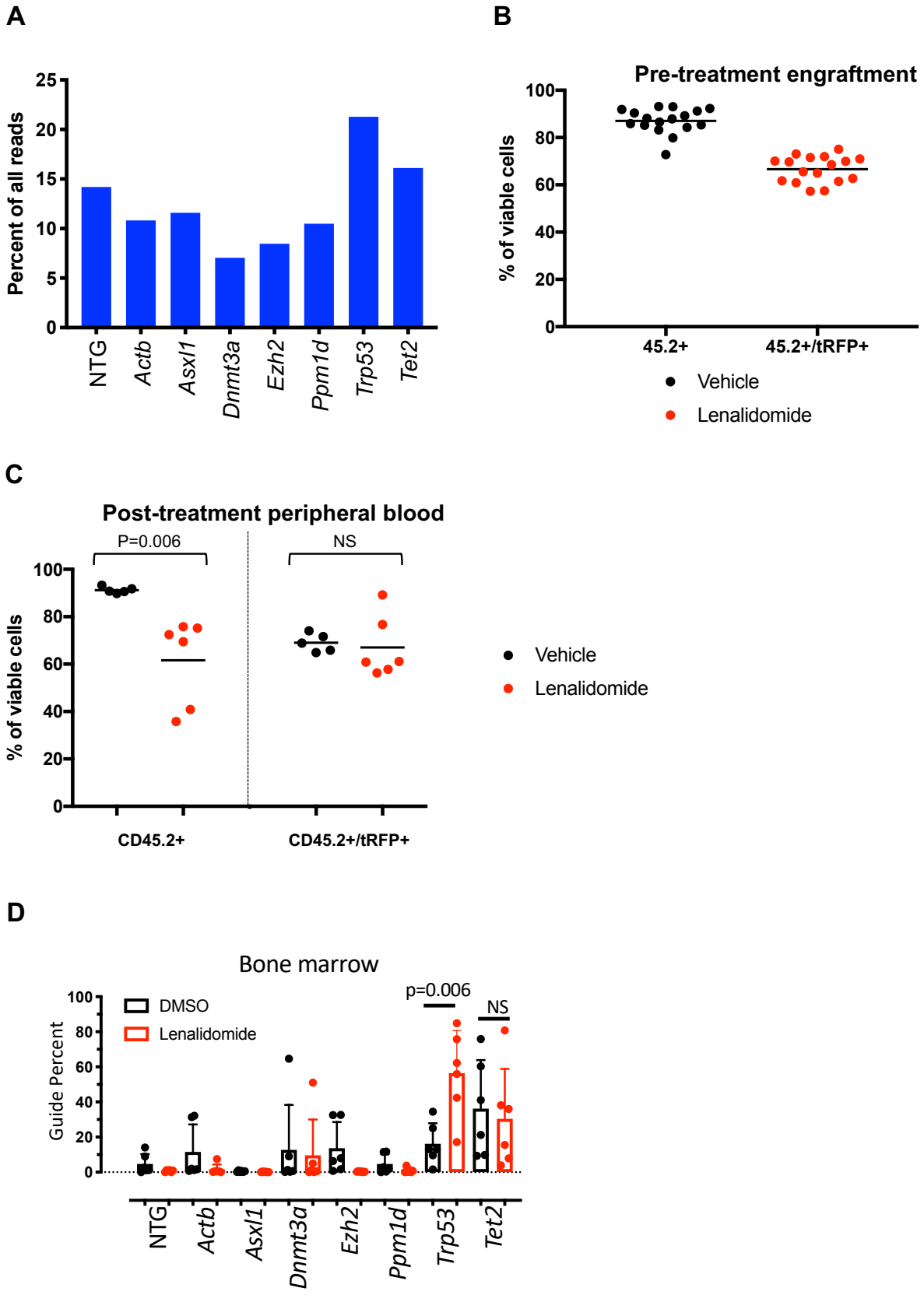
Supplementary Figure S8. Secondary exposures in multiple myeloma (MM) patients treated with thalidomide analogs and developed t-MNs. There were no statistical difference in secondary exposures between patients developed t-MNs with *TP53* mutations and without the mutations. (**A**) is by actual drugs. (**B**) is by drug class.


A
LTR
PGK
ERBD
Hoxb8
LTR
GMP
SCF
neutrophils
monocytes
cKit+ BM
MxCre Cas9
Crbn^I391V
estradiol
B
% Viable cells
log[lenalidomide], nM
log[pomalidomide], nM
Control Hoxb8, Cas9
Hoxb8, Cas9, Crbn^I391V
C
Control cells (BFP+)
Test cells (tRFP+)
MIX
90 : 10
Comparisons
1 NTG - BFP Actb
2 NTG - BFP Trp53
Drug / Vehicle
day 6
day 12
Flow assessment of relative proportions of different fluors
D
Actb
Trp53
% tRFP+ cells
Days in culture
DMSO
1000nM Lenalidomide
2500nM Lenalidomide
1000nM Pomalidomide
2500nM Pomalidomide
10000nM Pomalidomide

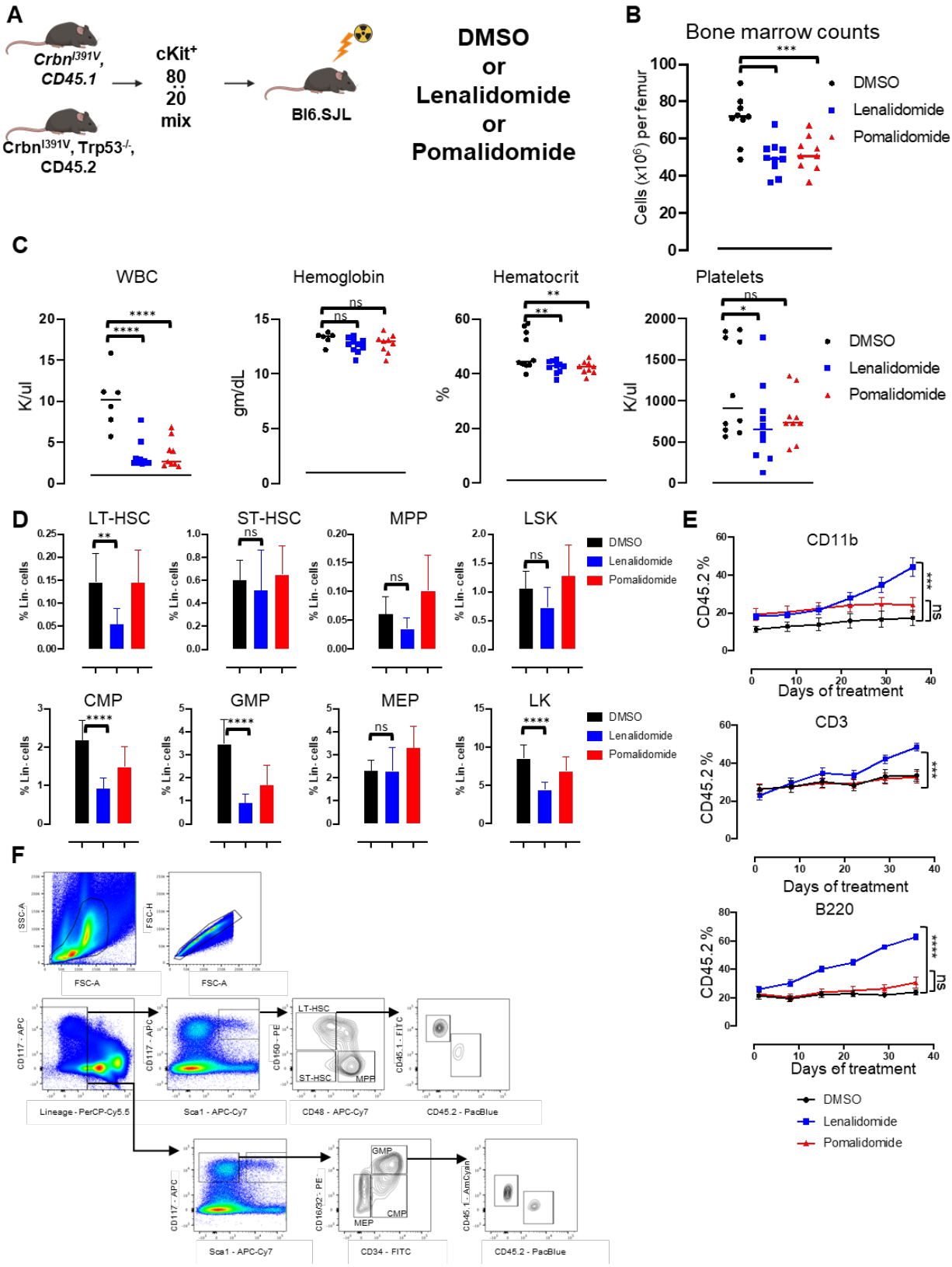
Supplementary Figure S9. (A) Schematic for generation of Hoxb8 lines. **(B)** Hoxb8 lines were generated from the CRBN^{I391V} and wild type Bl6 mice and treated with serial dilutions of lenalidomide or pomalidomide for 72 hours and cell density measured using CellTiter-Glo. Data are normalized to the vehicle (DMSO) control and shown as the mean +/- standard deviation (SD) (n = 3 replicates). Curves represent the logistic regression. **(C)** Schematic for long term competition experiments with Hoxb8 lines. **(D)** Hoxb8 cells were transduced with a non-targeting control (NTG) or sgRNAs targeting Trp53 or a cutting control guide targeting intronic sequence within the β-actin gene (*Actb*). Cells were mixed at a 90:10 ratio (NTG:*Trp53* or *Actb*) and treated with vehicle (DMSO) or increasing concentrations of lenalidomide and pomalidomide. A small aliquot of cells was subjected to analysis with fluorescence assisted cell sorting at the indicated times. Shown is the mean +/- SD (n = 3 replicates).



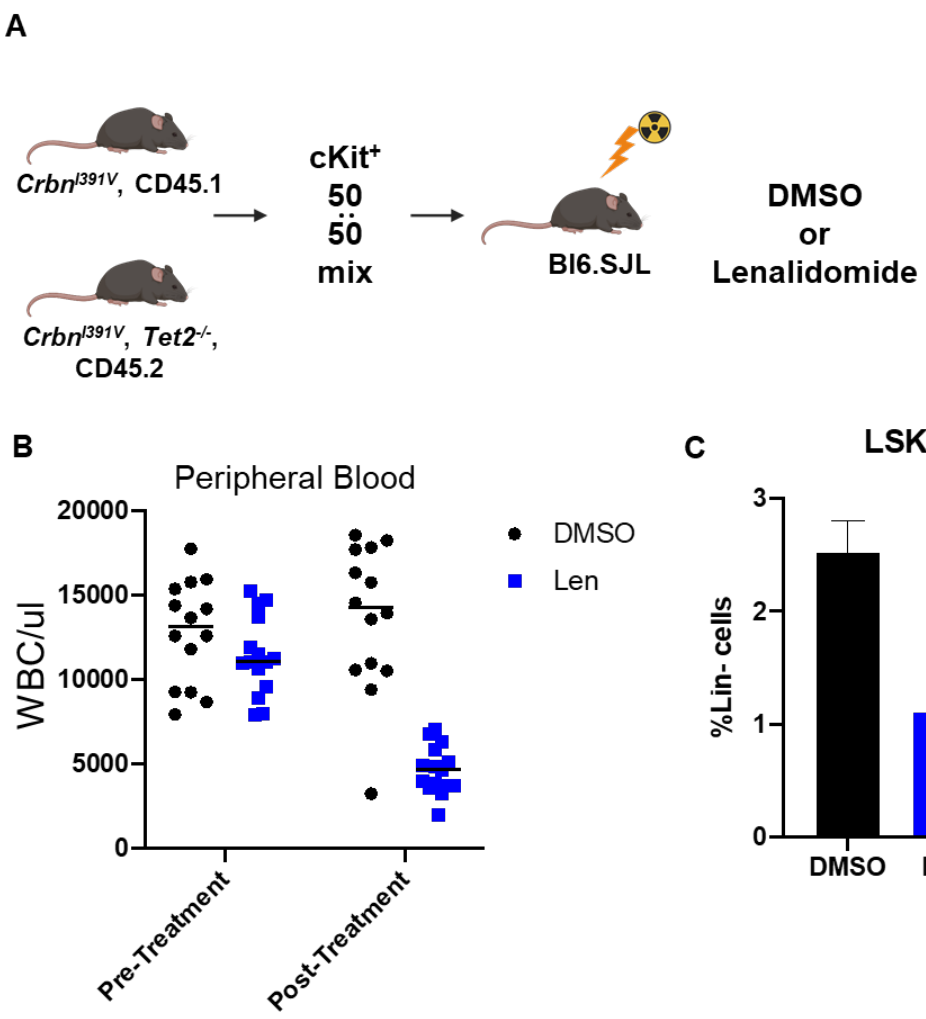
Supplementary Figure S10. Hoxb8 cells were transduced with a non-targeting control (NTG) or sgRNAs targeting Trp53 and were treated with serial dilutions of (A) bortezomib or (B) carfilzomib for 72 hours and cell density measured using CellTiter-Glo. Data are normalized to the vehicle (DMSO) control and shown as the mean +/- standard deviation (SD) (n = 3 replicates). Curves represent the logistic regression.


A
Percent of all reads
25
20
15
10
5
0
NTG
Actb
Asxl1
Dnmt3a
Ezh2
Ppm1d
Trp53
Tet2
B
Pre-treatment engraftment
% of viable cells
100
80
60
40
20
0
45.2+
45.2+/tRFP+
Vehicle
Lenalidomide
C
Post-treatment peripheral blood
P=0.006
NS
% of viable cells
100
80
60
40
20
0
CD45.2+
CD45.2+/tRFP+
Vehicle
Lenalidomide
D
Bone marrow
DMSO
Lenalidomide
p=0.006
NS
Guide Percent
100
80
60
40
20
0
NTG
Actb
Asxl1
Dnmt3a
Ezh2
Ppm1d
Trp53
Tet2

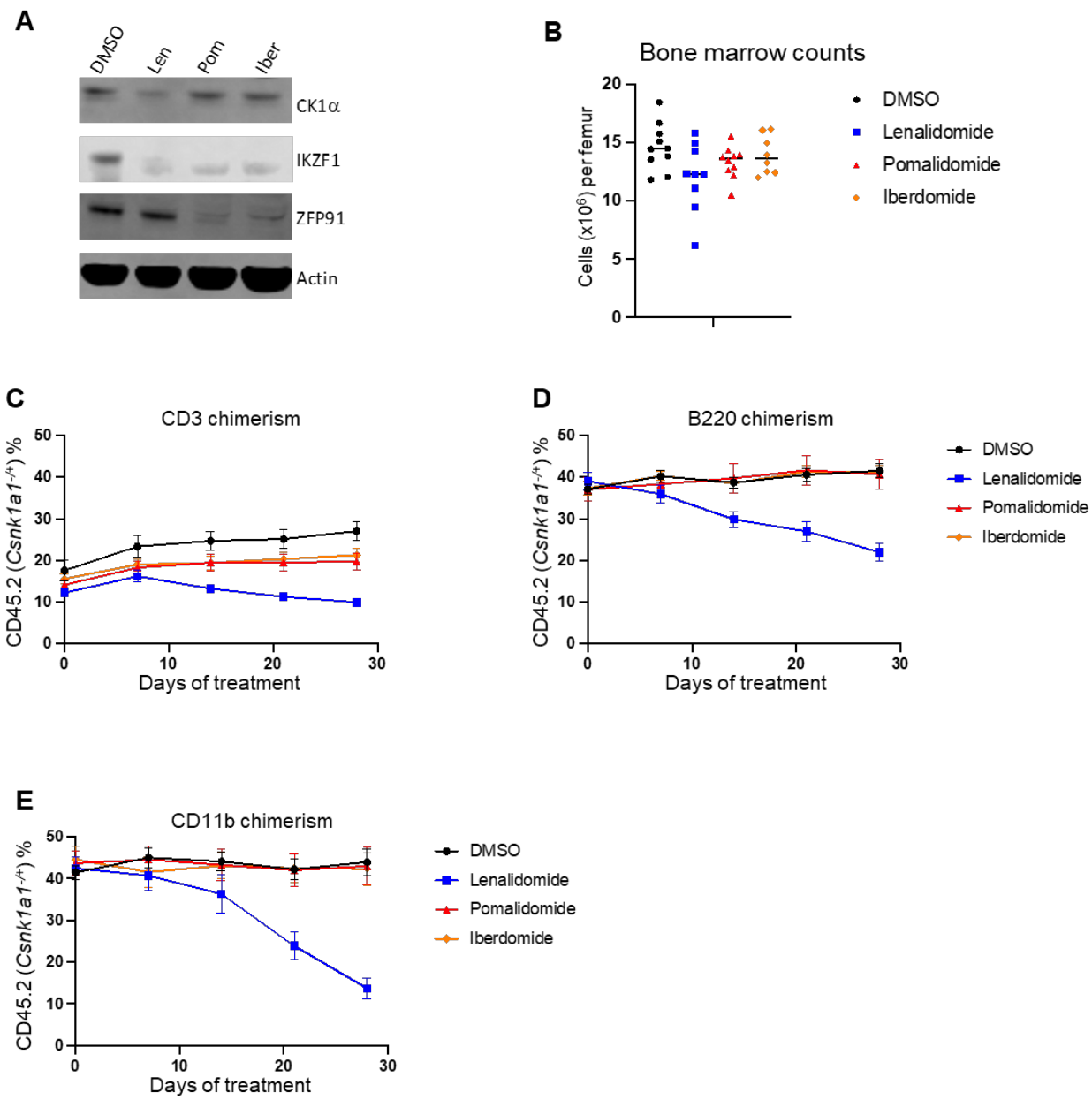
Supplementary Figure S11. Lineage^{lo}, Sca1+, cKit+ (LSK) cells were lentivirally transduced with individual guides, pooled at equal ratios and then transplanted into lethally irradiated Bl6.SJL recipient mice. (**A**) Remaining pooled cells were grown in culture for 48 hours at which time the guide frequency was determined using next generation sequencing. NTG1: non-targeting guide. *Actb*: cutting guide targeting intronic sequence within *β-actin* gene. (**B**) Following hematopoietic reconstitution 8 weeks post-transplant, mice were bled and the CD45.2 donor chimerism and transduction efficiency (CD45.2, tRFP+ percent) was determined. (**C**) Mice were treated with vehicle (DMSO) or lenalidomide 50mg/kg BID for 35 days and then bled and the CD45.2 donor chimerism and transduction efficiency (CD45.2, tRFP+ percent) was determined. Shown is the mean. P-values are from unpaired two-sided T-tests. **(D)** Whole bone marrow was harvested from mice following treatment with vehicle or lenalidomide and sgRNA sequence was amplified and quantitated using NGS. The frequency of each sgRNA sequence for each mouse is plotted. Shown is the mean +/- SD (n = 6 mice per group). P-values are from unpaired single-sided T-tests.


A
Crbn^I391V, CD45.1
Crbn^I391V, Trp53^-/-, CD45.2
cKit+ 80 20 mix
Bl6.SJL
DMSO or Lenalidomide or Pomalidomide
B
Bone marrow counts
Cells (x10^6) per femur
DMSO
Lenalidomide
Pomalidomide
C
WBC
Hemoglobin
Hematocrit
Platelets
K/ul
gm/dL
%
D
LT-HSC
ST-HSC
MPP
LSK
CMP
GMP
MEP
LK
% Lin- cells
E
CD11b
CD3
B220
CD45.2 %
Days of treatment
F
SSC-A
FSC-A
FSC-H
CD117 - APC
Lineage - PerCP-Cy5.5
Sca1 - APC-Cy7
CD150 - PE
CD48 - APC-Cy7
CD45.1 - FITC
CD45.2 - PacBlue
CD16/32 - PE
CD34 - FITC

Supplementary Figure S12. (A) Schematic for the Trp53 competitive transplant experiment. Following hematopoietic reconstitution, chimeric transplants containing 20% *Trp53*$^{-/-}$, *Crbn*^{I391V} (mutant, CD45.2) and 80% *Crbn*^{I391V} (WT, CD45.1) were treated with vehicle (DMSO), lenalidomide 50mg/kg BID, or pomalidomide 20mg/kg BID. **(B)** Bone marrow cellularity per femur following Trp53 competitive transplant and treatment. **(C)** Peripheral blood parameters were measured on the hemavet following completion of treatment course. **(D)** Total number of cells within each bone marrow compartment plotted as percent of Lineage^{lo} viable cells. Lineage^{lo}, Sca1^{+}, cKit^{+} (LSK), long term hematopoietic stem cells (LT-HSC: LSK, CD150^{+}, CD48^{-}), short term-HSC (ST-HSC: LSK, CD150^{-}, CD48^{-}), multipotent progenitor (MPP: LSK, CD150^{-}, CD48^{+}), common myeloid progenitor (CMP: LK, CD16/32^{-}, CD34^{+}), granulocyte-monocyte progenitor (GMP: LK, CD16/32^{+}, CD34^{+}), megakaryocyte-erythroid progenitor (MEP: LK, CD16/32^{-}, CD34^{-}). (**E**) Chimerism was measured within each of the three primary peripheral white blood cell lineages at the times noted. Shown is the mean +/- SEM. * = $p<0.05$; ** = $p<0.01$, *** = $p<0.001$, **** = $p<0.0001$, ns = not significant. P-values are from one-way ANOVA. **(F)** Representative fluorescence assisted cell sorting gating schema for bone marrow HSC and progenitor analyses.


A
Crbn^I391V, CD45.1
Crbn^I391V, Tet2^-/-, CD45.2
cKit+
50
50
mix
BI6.SJL
DMSO
or
Lenalidomide
B
Peripheral Blood
WBC/ul
20000
15000
10000
5000
0
DMSO
Len
Pre-Treatment
Post-Treatment
C
LSK
%Lin- cells
3
2
1
0
DMSO
Len
D
LSK
%CD45.2
100
80
60
40
20
0
DMSO
Len

Supplementary Figure S13. (A) Schematic for the *Tet2* competitive transplant experiment. **(B)** Peripheral blood leukocyte counts measured using fluorescence assisted cell sorting before and after treatment with lenalidomide 50mg/kg BID. **(C)** Bone marrow Lineage^{lo}, Sca1^{+}, cKit^{+} (LSK) cells as a percent of all viable Lineage^{lo} cells. **(D)** *Tet2* mutant (CD45.2) chimerism within the LSK gate. Shown is the mean +/- SEM.



Supplementary Figure S14. (A) Western blot of KG-1 cells following overnight treatment with the indicated drug or vehicle at 10uM. DMSO = dimethyl sulfoxide; Len = lenalidomide; Pom = pomalidomide; Iber = iberdomide. Following *Csnk1a1* competitive transplant and treatment experiment. **(B)** Bone marrow cellularity per femur. Chimerism was measured within each of the three primary peripheral white blood cell lineages, CD3 T-cells **(C)**, B220 B-cells **(D)**, and CD11b myeloid cells **(E)** at the times noted. Shown is the mean +/- SEM.

Supplementary Table S1. Clinical characteristics of 1,021 patients with MDS and AML without prior exposures.

	Total	AML (%)	MDS (%)
N	1021	611 (60)	410 (40)
Median Age [Range]	67 [18-94]	64 [18-94]	70 [19-93]
Male	622 (61)	323 (53)	299 (73)
Hgb [Range]	9.2 [2.9-17.3]	9.0 [2.9-15.2]	9.7 [5.2-17.3]
WBC [Range]	4.3 [0-341.4]	5.5 [0.0-341.4]	3.9 [0.5-185.1]
ANC [Range]	2.4 [0-112.9]	3.0 [0-103.7]	2.27[0.01-112.9]
PLT [Range]	64 [0-1069]	49 [0-1069]	98 [5-695]
ELN Risk			
Favorable		134 (22)	NA
Intermediate		198 (33)	NA
Adverse		274 (45)	NA
IPSS-R Risk			
Very Low		NA	25 (6)
Low		NA	111 (27)
Intermediate		NA	112 (27)
High		NA	74 (18)
Very High		NA	88 (22)
Cytogenetics			
Diploid	503 (49)	275 (45)	228 (56)
Complex	192 (19)	113 (18)	79 (19)
-5/del 5q	126 (12)	76 (12)	50 (12)
-7/del7-	99 (10)	67 (11)	32 (8)
Inv 16/t(16;16)	23 (2)	23 (4)	0 (0)
11q23	26 (3)	18 (3)	8 (2)
t(15;17)	31 (3)	31 (5)	0 (0)
t(8;21)	19 (2)	19 (3)	0 (0)
-Y	30 (3)	18 (3)	12 (3)
del(11)	14 (3)	6 (4)	8 (3)
del(20q)	57 (6)	20 (3)	37 (9)

del(12)	37 (4)	22 (4)	15 (4)
Trisomy 8	97 (9)	53 (9)	44 (11)
Inv3q/t(3;3)	8 (1)	6 (1)	2 (0.5)

Supplementary Table 2. Genes targeted by 81 gene panel and 300 gene panel. Genes covered by both panels are highlighted in red.

81 gene Agilent SureSelect XTHS panel

ANKRD26	*CBLB*	*EED*	*GFI1*	*JAK1*	*NF1*	*PTEN*	*SH2B3*	*SUZ12*
ASXL1	*CBLC*	*ELANE*	*GNAS*	*JAK2*	*NOTCH1*	*PTPN11*	*SMC1A*	*TERC*
ASXL2	*CEBPA*	*ETNK1*	*HNRNPK*	*JAK3*	*NPM1*	*RAD21*	*SMC3*	*TERT*
BCOR	*CREBBP*	*ETV6*	*HRAS*	*KDM6A*	*NRAS*	*RARA*	*SRSF2*	*TET2*
BCORL1	*CRLF2*	*EZH2*	*IDH1*	*KIT*	*PAX5*	*RUNX1*	*STAG1*	*TP53*
BRAF	*CSF3R*	*FBXW7*	*IDH2*	*KTM2A*	*PHF6*	*SETBP1*	*STAG2*	*U2AF1*
BRINP3	*CUX1*	*FLT3*	*IKZF1*	*KRAS*	*PIGA*	*SF1*	*STAT3*	*U2AF2*
CALR	*DDX41*	*GATA1*	*IL2RG*	*MAP2K1*	*PML*	*SF3A1*	*STAT5A*	*WT1*
CBL	*DNMT3A*	*GATA2*	*IL7R*	*MPL*	*PRPF40B*	*SF3B1*	*STAT5B*	*ZRSR2*

300 gene Agilent SureSelect XT panel

ABCC9	BTK	CTLA4	FANCA	HIST1H2AD	LAMB4	NBN	PLCG2	SF3B1	TLR2
ABL1	BTLA	CTNNA1	FANCB	HIST1H2BE	LEF1	NCOR1	POT1	SFRS1	TLR9
ACD	C22orf194	CUL5	FANCC	HIST1H2BF	LRP1B	NCOR2	PPM1D	SFRS7	TNFAIP3
ACTG1	CALR	CUX1	FANCD2	HIST1H3D	LTB	NF1	POU2AF1	SGK1	TNFRSF14
AKT1	CARD11	CYLD	FANCE	HIST1H4D	LUC7L2	NFE2	PRDM1	SH2B3	TNKS
ANKRD11	CBL	DAXX	FANCG	HNRNPK	LYN	NFKB1	PRKCB	SHH	TOX
ANKRD26	CBLB	DCLRE1C	FANCI	HRAS	MALT1	NFKB2	PTEN	SMAD2	TP53
ARID1A	CCND1	DDX3X	FANCL	ICOS	MAP2K1	NFKBIA	PTPN1	SMC1A	TRAF3
ARID1B	CCND3	DDX41	FAS	ID3	MAPK1	NFKBIE	PTPN11	SMC3	TRAF6
ARID2	CD200	DIS3	FAT1	IDH1	MAX	NOTCH1	RAD21	SMC5	TYK2
ARID5B	CD274	DKC1	FAT3	IDH2	MDM2	NOTCH2	RAD51C	SNX7	TYK3
ARPP21	CD58	DLC1	FBXW7	IKBKA	MED12	NPM1	RAG1	SOCS1	U2AF1
ASXL1	CD79A	DNM2	FGFR3	IKZF1	MEF2B	NR3C2	RAG2	SOX5	U2AF2
ATF7IP	CD79B	DNMT1	FLI1	IKZF2	MEF2C	NRAS	RASA2	SP140	UBR5
ATM	CDK4	DNMT3A	FLT3	IKZF3	MGA	NSD2	RB1	SPEN	USP29
ATRX	CDKN2A	DNMT3B	FNDC3A	IL7R	miR125a	NT5C2	REL	SPIB	VPREB1
B2M	CDKN2B	EBF1	FOXP1	IRAK1	miR-142	PAG1	RELA	SRSF2	WHSC1
BCL10	CDKN2C	ECT2L	FYN	IRAK4	mIR155	PALB2	RELB	STAG1	WHSC1L1
BCL2	CEBPA	EED	G6PC3	IRF1	mIR15a	PAX5	RELN	STAG2	WT1
BCL6	CEBPE	EGR1	GAB2	IRF4	mIR16-1	PDCD1	RHOA	STAT1	XPO1
BCL7A	CHD2	EGR2	GATA1	IRF7	MIR17HG	PDCD1LG2	RIPK1	STAT3	ZAP70
BCOR	CHK2	ELANE	GATA2	ITPKB	mIR21	PDGFRB	ROBO1	SUZ12	ZMYM2
BCR	CIITA	EP300	GATA3	JAK1	mir34b	PEG3	ROR1	SYK	ZMYM3
BIRC3	CNOT3	EPHA7	GCET2	JAK2	mir34c	PHF6	RPL10	TBL1XR1	ZRSR2
BLK	CREBBP	EPOR	GFI1B	JAK3	MLL	PHIP	RPL5	TCF3	
BMI1	CRLF2	ERG	GNA13	JARID2	MLL2	PIGA	RTEL1	TERC	
BRAF	CSF2RA	ETNK1	GNAS	KDM4C	MLL3	PIK3CA	RUNX1	TERT	
BRCA1	CSF3R	ETV6	GNB1	KDM6A	MPL	PIK3CB	RUNX2	TET1	
BRCA2	CTBP1	EZH2	GPRC5A	KIT	MS4A1	PIK3CG	SAMHD1	TET2	
BRIP1	CTBP2	FAM46C	HAX1	KLHL6	MYB	PIK3R1	SETBP1	TGDS	
BTG1	CTCF	FAM5C	HIST1H1E	KRAS	MYD88	PLA2G2D	SETD2	TINF2 (TIN2)	

Supplementary Table S3. Sequences of 8 sgRNA

Guide	Sequence
NTG	GACGGAGGCTAAGCGTCGCAA
***Actb*.g0**	AGGTTGCTCTGACAACCACA
***Asxl1*.g3**	GGCAGTGGGGCCATCGATGA
***Tet2*.g1**	AATACTATCCTAGTTCCGAC
***Dnmt3a*.g1**	AATGAAGAGTGGGTGCTCCA
***Ezh2*.g2**	AGAGTACATTATAGGCACCG
***Ppm1d*.g1**	TGGCTTAAGTCGAAGTAGCG
***Trp53*.g3**	GAAGTCACAGCACATGACGG

Supplementary Table S4 Multivariable logistic regression analysis for each gene mutation against prior exposures.

Gene	Exposures	Odds Ratio	Lower 95% CI	Higher 95% CI	P value
TP53	Thalidomide analogs	3.136274807	1.592845192	6.175251503	0.00094415
	Platinum	1.590410732	0.9401736	2.690360904	0.083638249
	Taxanes	1.643444244	0.929247368	2.906555429	0.0876882
	Topoisomerase Inh	0.486786683	0.261689608	0.905505103	0.02300099
	Vinca Alkaloid	1.755328275	1.053295525	2.925273373	0.030832734
PPM1D	Platinum	3	1.317265665	6.832334768	0.008892515
TET2	Alkylating	0.394583502	0.226466221	0.687502707	0.001028518
	Platinum	0.555409168	0.292838422	1.053411441	0.071760577
IDH2	Alkylating	0.247792978	0.050937838	0.979726915	0.046512203
	Antimetabolites	2.433825817	0.774212665	7.321009215	0.123980192
	Anthracyclines	3.51233392	0.899425615	12.56429188	0.069634342
	Vinca Alkaloid	0.066630236	0.000494715	0.669835086	0.01801596
ASXL1	Antimetabolites	0.572308332	0.288064676	1.137025307	0.111085555
	Thalidomide analogs	0.322763494	0.075187762	1.385548261	0.128190241
EZH2	Vinca Alkaloid	3.44281042	1.130913755	10.48085545	0.029513529
BCOR	Platinum	0.237500001	0.030071329	1.875748505	0.172752852
RUNX1	Thalidomide analogs	0.325791858	0.076324914	1.390638119	0.129871014
STAG2	Anthracyclines	0.282103493	0.060834577	1.308176772	0.105929973
	Platinum	0.230159889	0.029280198	1.809194563	0.162599224
SRSF2	SCT	0.187538713	0.024370528	1.44316812	0.107918192
	Taxanes	0.446255852	0.167582049	1.188339005	0.106385935
	Topoisomerase Inh	0.129573295	0.017102406	0.981688685	0.047945491
	XRT	1.687274821	0.836887055	3.401768862	0.143678864
U2AF1	SCT	0.262753608	0.034026165	2.02901084	0.200006082
	Taxanes	0.241453277	0.031301843	1.862500071	0.172781245
SF3B1	Platinum	0.260079176	0.051762135	1.306769468	0.102023847
	SCT	0.237299775	0.02804762	2.007699158	0.186754025
	Topoisomerase Inh	3.604242472	0.970209284	13.38944495	0.055518494
Splicing	Platinum	0.593825312	0.308196604	1.144167379	0.119354547
	SCT	0.283984432	0.108035316	0.746488842	0.010683206
	Taxanes	0.405792998	0.184962465	0.890277695	0.024456043
	Vinca Alkaloid	0.535545449	0.279540786	1.026000293	0.05975693
NPM1	Alkylating	0.035203766	0.000273475	0.272812489	0.000124387
	Platinum	3.048932395	0.896642627	9.794107071	0.072644886
	Taxanes	0.087721491	0.000660126	0.805530678	0.027916799
NRAS	Topoisomerase Inh	0.197555329	0.044106567	0.884859338	0.034017515
	Vinca Alkaloid	2.063986213	0.903640464	4.714307577	0.085518193
KRAS	Platinum	2.096671139	0.778365082	5.647773733	0.143092471

	Taxanes	0.159367553	0.020152777	1.260273817	0.081735065
	XRT	3.52742523	1.140775885	10.90725087	0.028622948
NRAS.KRAS	Alkylating	0.481097878	0.198674493	1.164996898	0.104906588
	Thalidomide analogs	2.636324228	0.800649698	8.680706994	0.110867753
	SCT	0.397161609	0.123976206	1.272319488	0.120060685
	Vinca Alkaloid	2.788701636	1.079049692	7.207135009	0.034258906
	XRT	1.636067252	0.834651588	3.206986115	0.151679493
FLT3	Antimetabolites	2.048207187	0.843384605	4.974186933	0.113258678
	SCT	0.204737039	0.026881037	1.559361524	0.125749673
PTPN11	Antimetabolites	0.319393149	0.066092409	1.543475034	0.155617519
	Thalidomide analogs	6.347848578	0.789838322	51.01699985	0.0821961
	SCT	0.077643363	0.004996584	1.206522706	0.06787527
	XRT	0.183435235	0.046663411	0.72108928	0.015176287
NF1	Alkylating	0.400199172	0.135524794	1.181771787	0.097387221
	Taxanes	2.857425843	0.997888304	8.182160685	0.050462128
SETBP1	Alkylating	0.239615278	0.037213586	1.542863425	0.132685019
	Anthracyclines	5.623735582	0.875021098	36.14358782	0.068862693
	Platinum	0.174618891	0.020951809	1.455328119	0.106718303
	XRT	4.096452134	0.847901652	19.79111616	0.079317366
Diploid	Alkylating	0.523395484	0.305370849	0.897082459	0.01852111
	Platinum	0.439956	0.235021873	0.823588373	0.01026821
	SCT	0.328447629	0.121743419	0.886108226	0.027895317
	XRT	0.68475348	0.409184418	1.145907095	0.149436285
11q23	Alkylating	3.561349505	1.103275562	11.49595871	0.033641212
	Antimetabolites	0.468847712	0.182078331	1.207272579	0.116499312
	Anthracyclines	2.519421704	0.820464187	7.736456784	0.106470506
	SCT	0.085986417	0.010232517	0.722565544	0.023873129
	Topoisomerase Inh	3.176083864	1.154003178	8.741317965	0.025269262
	Vinca Alkaloid	0.223614215	0.070470818	0.709560621	0.011011338
Del 5q/-5	Antibiotic	1.940353545	0.800973144	4.700497026	0.142006573
	Anthracyclines	1.457598342	0.934968831	2.272367653	0.096281107
	Thalidomide analogs	1.95294113	0.993890319	3.837424498	0.052115139
	Platinum	1.664277156	1.002337628	2.763358745	0.048954324
	Topoisomerase Inh	0.431658238	0.226062423	0.82423621	0.010906377
Del 7q/-7	Antibiotic	2.068503677	0.847173656	5.05056718	0.110528223
	Thalidomide analogs	2.850109171	1.453545192	5.588489669	0.002299077
	Platinum	1.946944977	1.170879367	3.237391359	0.010228482
	Topoisomerase Inh	0.62551881	0.333440261	1.173444921	0.143831022
	Vinca Alkaloid	2.171020328	1.296114636	3.636506472	0.003224481
Del 17p/-17	Thalidomide analogs	3.715819023	1.274888858	10.83020761	0.016175692
	Platinum	2.811829805	1.541025313	5.130601546	0.000753478

	SCT	0.356194867	0.129311137	0.981158985	0.045851667
Del 20q	Antibiotic	3.896935474	1.440681634	10.54091739	0.007381563
	Topoisomerase Inh	1.803520862	0.844682351	3.850781888	0.127553928
-Y	Antibiotic	4.842999147	0.913607836	25.67254768	0.063769553
	Anthracyclines	0.146183327	0.030582715	0.698746501	0.015993523
Inv3q.t.3.x.	Antimetabolites	0.348113528	0.11852286	1.022444349	0.054910162
	Anthracyclines	2.800168516	1.07606755	7.286664965	0.034840175
	Platinum	2.656524855	1.041647126	6.774966427	0.040816876
	SCT	2.245452424	0.846161686	5.958738943	0.104270262
Trisomy 8	Thalidomide analogs	0.289141625	0.077612067	1.077189192	0.064435208
	SCT	2.911924763	1.073164947	7.901213927	0.035851243
	Topoisomerase Inh	0.395030424	0.152654369	1.022237602	0.055540299
Trisomy 21	Anthracyclines	0.232854654	0.072376999	0.749150849	0.014509647
	Taxanes	2.309277917	0.991085266	5.380732295	0.0524751
	Vinca Alkaloid	4.071166991	1.12108283	14.7842784	0.032870004
Complex	Platinum	1.880747126	1.225698868	2.885871763	0.003833219

Supplementary Table S5. The list of high-confidence somatic mutations detected in t-MN patients by the 300 gene panel sequencing.

Sample ID	Gene	AA change or nucleotide change	VAF
1004981-7	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.458484
1004981-7	*TET2*	TET2:uc011cez.2:exon11:c.A5774G:p.H1925R	0.493078
1005468-11	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.493317
1005468-11	*NPM1*	NPM1:uc003mbi.3:exon11:c.859_860insTCTG:p.L287fs	0.2816
1005468-11	*TET2*	TET2:uc011cez.2:exon11:c.A5774G:p.H1925R	0.471475
1005468-11	*TET2*	TET2:uc011cez.2:exon11:c.5344_5345del:p.H1782fs	0.3533
1005468-4	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.448957
1005468-4	*TET2*	TET2:uc011cez.2:exon11:c.A5774G:p.H1925R	0.467811
1013908-4	*NF1*	NF1:uc002hgg.3:exon42:c.G6208T:p.E2070X	0.598361
1013908-4	*TET2*	TET2:uc011cez.2:exon10:c.G4345T:p.E1449X	0.135093
1019548-3	*NRAS*	NRAS:uc009wgu.3:exon3:c.A183T:p.Q61H	0.154273
1019548-3	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35T:p.G12V	0.076433
1019548-3	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.519187
1032799-1	*TP53*	TP53:uc002gii.2:exon4:c.G334T:p.E112X	0.416537
1032799-1	*TP53*	TP53:uc002gio.3:exon2:c.81_82insCGCGCC:p.M28delinsRAM	0.3005
1039307-1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2270delA:p.Q757fs	0.3114
1039307-1	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35C:p.G12A	0.097297
1039307-1	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.583_584insAA:p.I195fs	0.2483
1039307-1	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.314031
1039307-1	*STAG2*	STAG2:uc004eud.3:exon15:c.1394dupT:p.V465fs	0.2201
1039307-1	*STAG2*	STAG2:uc004eud.3:exon5:c.220delC:p.H74fs	0.1111
152539-1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.G4232A:p.W1411X	0.089077
323458-5	*KRAS*	KRAS:uc001rgq.1:exon3:c.C173T:p.T58I	0.060109
334470-13	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.135106
334470-8	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.153017
336040-3	*PPM1D*	p.N574fs	0.0354
336040-3	*TP53*	TP53:uc002gii.2:exon1:c.C46G:p.R16G	0.530103
338884-11	*RUNX1*	chr21:36252852:A-G, splicing	0.995862
338884-11	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.284_307del:p.95_103del	0.3955
338884-11	*TET2*	TET2:uc011cez.2:exon6:c.3779_3780insTCTGGCTGACAAACTCTAC TCGGAGCTTACCGAGACGCTGAGGAAATACGGCACGCTCACCAA TCGCCGGTGTGCCTTG:p.S1260fs	0.3034
338884-8	*RUNX1*	chr21:36252852:A-G, splicing	0.742515
349858-4	*IDH2*	IDH2:uc002box.3:exon4:c.G419A:p.R140Q	0.263889
349858-4	*NPM1*	NPM1:uc003mbi.3:exon11:c.861_862insTGCA:p.L287fs	0.1635
349858-4	*SF3B1*	SF3B1:uc002uue.3:exon14:c.G1998T:p.K666N	0.295238
352429-1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1927dupG:p.G642fs	0.0573
352429-1	*TET2*	TET2:uc011cez.2:exon3:c.1505_1506del:p.Q502fs	0.0544
352429-1	*TP53*	TP53:uc002gio.3:exon2:c.C9G:p.C3W	0.118393

504987-3	*ETV6*	ETV6:uc001qzz.3:exon5:c.T536A:p.L179X	0.184422
529042-1	*DNMT3A*	chr2:25470459:C-T, splicing	0.313869
529042-1	*TP53*	TP53:uc002gig.1:exon3:c.A358G:p.K120E	0.332046
529042-1	*TP53*	TP53:uc002gii.2:exon7:c.662delA:p.H221fs	0.3008
641158-2	*TET2*	TET2:uc011cez.2:exon3:c.2310_2316del:p.Q770fs	0.0776
641158-4	*TET2*	TET2:uc011cez.2:exon3:c.2310_2316del:p.Q770fs	0.0853
658064-4	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.315718
658064-4	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284T:p.P95L	0.368039
670527-1	*TP53*	TP53:uc002gii.2:exon2:c.C100G:p.H34D	0.226218
670527-1	*TP53*	TP53:uc002gio.3:exon2:c.C56A:p.P19H	0.205128
670527-1	*TP53*	TP53:uc002gig.1:exon3:c.97delT:p.S33fs	0.0703
672259-5	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1927dupG:p.G642fs	0.1441
672259-5	*KRAS*	KRAS:uc001rgq.1:exon2:c.G35A:p.G12D	0.222467
755527-1	*TET2*	TET2:uc011cez.2:exon3:c.2310_2316del:p.Q770fs	0.0984
755527-2	*DNMT3A*	DNMT3A:uc002rgd.4:exon10:c.1238dupG:p.G413fs	0.0622
755527-2	*TET2*	TET2:uc011cez.2:exon3:c.2310_2316del:p.Q770fs	0.0965
770771-1	*DNMT3A*	DNMT3A:uc002rgd.4:exon10:c.1238dupG:p.G413fs	0.2538
775168-6	*DNMT3A*	DNMT3A:uc002rgd.4:exon23:c.C2644T:p.R882C	0.47654
775168-6	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.409326
775168-6	*TET2*	TET2:uc011cez.2:exon3:c.C1834T:p.Q612X	0.481915
775168-6	*TET2*	TET2:uc011cez.2:exon11:c.5682_5685del:p.I1894fs	0.3808
839168-5	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284G:p.P95R	0.303398
839168-5	*STAG2*	STAG2:uc004eud.3:exon27:c.2763_2764del:p.L921fs	0.3096
848193-3	*PPM1D*	p.E475fs	0.0284
848193-3	*TP53*	TP53:uc002gio.3:exon2:c.C17T:p.A6V	0.147826
848193-3	*TP53*	TP53:uc002gii.2:exon5:c.T466A:p.S156T	0.415758
865122-7	*EZH2*	EZH2:uc011kui.2:exon2:c.62dupC:p.S21fs	0.1619
865122-7	*GATA2*	GATA2:uc003ekm.3:exon4:c.813_814insTG:p.G272fs	0.0512
865122-7	*IKZF1*	IKZF1:uc003tow.4:exon6:c.658dupA:p.H219fs	0.0598
865122-7	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.C1714T:p.R572X	0.042
865122-7	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.C422A:p.S141X	0.07957
865961-3	*DNMT3A*	DNMT3A:uc002rgd.4:exon18:c.T2114C:p.I705T	0.087379
865961-6	*DNMT3A*	DNMT3A:uc002rgd.4:exon18:c.T2114C:p.I705T	0.189338
865961-6	*PPM1D*	p.Q520fs	0.0765
865961-6	*TP53*	TP53:uc002gii.2:exon3:c.287_289del:p.96_97del	0.2765
883956-5	*DNMT3A*	DNMT3A:uc002rgd.4:exon23:c.C2644T:p.R882C	0.345714
883956-5	*RUNX1*	chr21:36231876:C-T, splicing	0.397089
885798-5	*TP53*	TP53:uc002gii.2:exon4:c.C340T:p.R114C	0.372315
885798-5	*TP53*	chr17:7577156:C-T	0.318966
888746-6	*TP53*	17:7578370:C-T	0.365169
888746-6	*TP53*	17:7579311:C-T	0.3187

889584-4	*TP53*	TP53:uc002gii.2:exon4:c.G334T:p.E112X	0.375
889584-4	*TP53*	TP53:uc002gio.3:exon2:c.81_82insCGCGCC:p.M28delinsRAM	0.2621
889588-6	*PPM1D*	p.G463fs	0.1119
889588-6	*TP53*	TP53:uc002gii.2:exon2:c.175_177del:p.59_59del	0.2975
889588-6	*TP53*	TP53:uc002gii.2:exon3:c.246delC:p.S82fs	0.295
890350-5	*PPM1D*	p.V464fs	0.0654
890350-5	*SF3B1*	SF3B1:uc002uue.3:exon14:c.C1986G:p.H662Q	0.176678
890350-5	*TP53*	TP53:uc002gii.2:exon3:c.C265T:p.R89W	0.095238
895306-5	*TP53*	chr17:7578370:C-T	0.060284
895306-5	*TP53*	TP53:uc002gii.2:exon1:c.A59G:p.H20R	0.070968
896109-6	*TET2*	TET2:uc011cez.2:exon3:c.C2935T:p.Q979X	0.431302
896109-6	*TP53*	TP53:uc002gii.2:exon3:c.G253T:p.G85C	0.666667
896109-6	*ZRSR2*	ZRSR2:uc004cxg.4:exon2:c.C106T:p.R36X	0.12037
898783-8	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.C3202T:p.R1068X	0.478723
898783-8	*JAK2*	JAK2:uc003ziw.3:exon14:c.G1849T:p.V617F	0.370518
898783-8	*PTPN11*	PTPN11:uc001ttx.3:exon13:c.C1472T:p.P491L	0.408
898783-8	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.450549
900169-3	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.C3202T:p.R1068X	0.39886
900169-3	*JAK2*	JAK2:uc003ziw.3:exon14:c.G1849T:p.V617F	0.406667
900169-3	*PTPN11*	PTPN11:uc001ttx.3:exon13:c.C1472T:p.P491L	0.35518
900169-3	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.5
902226-2	*TP53*	TP53:uc002gii.2:exon2:c.A182C:p.Y61S	0.888889
905254-5	*RUNX1*	RUNX1:uc002yur.1:exon2:c.218delG:p.S73fs	0.1988
917999-5	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1888_1910del:p.H630fs	0.1401
920712-5	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.C2077T:p.R693X	0.171765
928586-5	*TP53*	TP53:uc002gii.2:exon2:c.125delT:p.L42fs	0.3543
935979-5	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.C1714T:p.R572X	0.0447
940374-6	*WT1*	WT1:uc001mtn.2:exon1:c.239_240insTGCT:p.L80fs	0.3871
941257-5	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.A1540T:p.K514X	0.0814
941257-5	*PPM1D*	p.N448fs	0.007
941257-5	*PPM1D*	p.T483fs	0.0231
941257-5	*TP53*	TP53:uc002gii.2:exon3:c.G236A:p.C79Y	0.174342
944298-3	*NF1*	NF1:uc002hgg.3:exon49:c.7213delA:p.I2405fs	0.3977
944298-3	*TP53*	TP53:uc002gio.3:exon2:c.T2A:p.M1K	0.910761
945086-5	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.138482
946415-5	*DNMT3A*	DNMT3A:uc002rgd.4:exon7:c.710delA:p.Q237fs	0.11
950354-3	*TP53*	TP53:uc002gii.2:exon2:c.125delT:p.L42fs	0.2961
952938-3	*TP53*	TP53:uc002gii.2:exon1:c.C46G:p.R16G	0.806985
952938-6	*TP53*	TP53:uc002gii.2:exon1:c.C46G:p.R16G	0.985507
955470-4	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1927dupG:p.G642fs	0.1304
955470-4	*SETBP1*	SETBP1:uc010dni.3:exon4:c.G2608A:p.G870S	0.113561

955470-4	*U2AF1*	U2AF1:uc002zda.1:exon6:c.A470C:p.Q157P	0.288204
955470-8	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1927dupG:p.G642fs	0.1858
955470-8	*CUX1*	CUX1:uc003uyx.4:exon11:c.834dupG:p.Q278fs	0.1008
955470-8	*SETBP1*	SETBP1:uc010dni.3:exon4:c.G2608A:p.G870S	0.084337
955470-8	*U2AF1*	U2AF1:uc002zda.1:exon6:c.A470C:p.Q157P	0.434783
965417-5	*TP53*	TP53:uc002gig.1:exon3:c.G158A:p.W53X	0.357309
965857-7	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.C1547G:p.S516X	0.0391
965857-7	*PPM1D*	p.R429fs	0.0402
965857-7	*TP53*	chr17:7579311:C-T	0.11828
966645-8	*TP53*	TP53:uc002gio.3:exon2:c.G77A:p.R26H	0.522989
966645-8	*U2AF1*	U2AF1:uc002zda.1:exon6:c.G467A:p.R156H	0.431373
968257-1	*PTPN11*	PTPN11:uc001ttx.3:exon13:c.G1508C:p.G503A	0.137255
973131-3	*TP53*	TP53:uc002gii.2:exon2:c.G169A:p.V57M	0.349866
973131-3	*TP53*	TP53:uc002gii.2:exon4:c.379delG:p.E127fs	0.3777
973680-3	*DNMT3A*	DNMT3A:uc002rgd.4:exon11:c.1315_1316del:p.M439fs	0.3345
973680-3	*KRAS*	KRAS:uc001rgq.1:exon4:c.A351C:p.K117N	0.861171
973680-3	*PPM1D*	p.N477fs	0.2132
974690-1	*PPM1D*	p.E540fs	0.0269
974690-1	*TP53*	TP53:uc002gii.2:exon2:c.A182G:p.Y61C	0.145394
974690-1	*TP53*	TP53:uc002gii.2:exon2:c.T181C:p.Y61H	0.134066
977695-1	*TP53*	TP53:uc002gio.3:exon2:c.G42A:p.W14X	0.804511
978451-7	*KRAS*	KRAS:uc001rgq.1:exon2:c.G35A:p.G12D	0.407328
988575-1	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.445545
992670-1	*GNAS*	GNAS:uc002xzw.3:exon1:c.2009_2012del:p.D670fs	0.105
993055-3	*BCOR*	BCOR:uc004dep.4:exon12:c.C4537T:p.R1513X	0.062069
993112-2	*TP53*	TP53:uc002gio.3:exon2:c.G42A:p.W14X	0.885714
993291-1	*TP53*	TP53:uc002gii.2:exon3:c.A224G:p.Y75C	0.126806
993291-1	*TP53*	TP53:uc002gii.2:exon3:c.T223C:p.Y75H	0.105519
994371-1	*TP53*	TP53:uc002gii.2:exon1:c.74_77del:p.D25fs	0.2692
995045-8	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1927dupG:p.G642fs	0.1373
995045-8	*EZH2*	EZH2:uc011kui.2:exon5:c.467_473del:p.K156fs	0.2361
995045-8	*PPM1D*	p.Q520fs	0.0254
995393-2	*NF1*	NF1:uc002hgg.3:exon50:c.C7348T:p.R2450X	0.084795
995393-2	*NRAS*	NRAS:uc009wgu.3:exon2:c.G34T:p.G12C	0.133477
995393-6	*NF1*	NF1:uc002hgg.3:exon50:c.C7348T:p.R2450X	0.117506
995393-6	*NF1*	NF1:uc002hgg.3:exon47:c.6926_6927insAG:p.S2309fs	0.2376
995393-6	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.056383
995393-6	*NRAS*	NRAS:uc009wgu.3:exon2:c.G34T:p.G12C	0.199787
999001-1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2270delA:p.Q757fs	0.3197
999001-1	*PPM1D*	p.G554fs	0.0335
999001-1	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.583_584insAA:p.I195fs	0.3129

999001-1	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.326255
999001-1	*STAG2*	STAG2:uc004eud.3:exon15:c.1394dupT:p.V465fs	0.3
AL1000A1406M9	*DNMT3A*	DNMT3A:uc002rgd.3:exon21:c.2426delT:p.V809fs	0.0725
AL1000A1406M9	*TP53*	TP53:uc002gii.1:exon4:c.G418A:p.V140M	0.443038
AL1007A1413M5	*NRAS*	NRAS:uc009wgu.3:exon3:c.A183T:p.Q61H	0.408163
AL1007A1413M5	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.G1618T:p.E540X	0.465
AL1017A1423M2	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.525_526insT:p.L175fs	0.2105
AL1017A1423M2	*ZRSR2*	ZRSR2:uc004cxg.4:exon8:c.733delC:p.P245fs	0.2
AL1029A1435M3	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.A1603T:p.K535X	0.0795
AL1029A1435M3	*TP53*	TP53:uc002gii.1:exon2:c.A187T:p.I63F	0.146667
AL1029A1435M3	*TP53*	TP53:uc002gii.1:exon1:c.G131A:p.C44Y	0.162162
AL1057A5172M2	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.G2645A:p.R882H	0.279412
AL1094A1628M4	*EZH2*	uc011kuh.2:exon18:c.1906-2A>G)	0.293542
AL1094A1628M4	*PPM1D*	p.N448fs	0.0208
AL1094A1628M4	*TP53*	TP53:uc002gii.1:exon3:c.A340C:p.M114L	0.343465
AL1103A1637M2	*PPM1D*	p.N448fs	0.0215
AL1104A1638M9	*PPM1D*	p.R429fs	0.3394
AL1104A1638M9	*TET2*	TET2:uc011cez.2:exon3:c.800delC:p.T267fs	0.1314
AL1133A1669M0	*TP53*	TP53:uc002gii.1:exon2:c.174_175insC:p.P58fs	0.2217
AL1139A1675M9	*CBL*	CBL:uc001pwe.3:exon4:c.A679T:p.T227S	0.066019
AL1139A1675M9	*STAG2*	STAG2:uc004eud.3:exon12:c.1047_1048del:p.349_350del	0.2787
AL1139A1675M9	*TET2*	TET2:uc011cez.2:exon3:c.C1826G:p.S609X	0.08548
AL1156A1694M0	*SF3B1*	SF3B1:uc002uue.3:exon14:c.A1997C:p.K666T	0.388298
AL1157A1695M7	*BCOR*	BCOR, splicing, uc004deo.4:exon12:c.4585+1G>A	0.423831
AL1157A1695M7	*FLT3*	FLT3:uc010tdn.2:exon14:c.1800_1801insCTACGTTGATTTCAGAGAA TATGAATATGA:p.D600delinsDYVDFREYEYD	0.0868
AL1157A1695M7	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.423_424insA:p.S141fs	0.1608
AL1165A1705M8	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1404
AL1165A1705M8	*CEBPA*	CEBPA:uc002nun.3:exon1:c.384_385insC:p.P128fs	0.0889
AL1165A1705M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon10:c.1239_1240insG:p.G413fs	0.1661
AL1165A1705M8	*EZH2*	EZH2:uc011kui.2:exon8:c.787_788insC:p.N263fs	0.1671
AL1165A1705M8	*EZH2*	EZH2:uc011kui.2:exon10:c.1105_1106insC:p.T369fs	0.2139
AL1165A1705M8	*PPM1D*	p.G544fs	0.3416
AL1165A1705M8	*RUNX1*	RUNX1:uc010gmv.3:exon9:c.1390_1391insC:p.T464fs	0.1212
AL1165A1705M8	*RUNX1*	RUNX1:uc010gmv.3:exon9:c.1037_1038insC:p.R346fs	0.2158
AL1165A1705M8	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.602_603insC:p.R201fs	0.1141
AL1165A1705M8	*SH2B3*	SH2B3:uc001tse.3:exon7:c.1261_1262insG:p.R421fs	0.2044
AL1165A1705M8	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C283G:p.P95A	0.09009
AL1165A1705M8	*TET2*	TET2:uc011cez.2:exon3:c.1722_1723insC:p.V574fs	0.2096
AL1165A1705M8	*TET2*	TET2:uc011cez.2:exon3:c.2348_2349insC:p.H783fs	0.1991
AL1218A1766M1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1521
AL1218A1766M1	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.G2645A:p.R882H	0.385986

AL1218A1766M1	*NRAS*	NRAS:uc009wgu.3:exon2:c.G38A:p.G13D	0.252376
AL1218A1766M1	*RUNX1*	RUNX1:uc010gmv.3:exon8:c.C958T:p.R320X	0.375948
AL1496A2114M0	*PPM1D*	p.Q510fs	0.0468
AL1496A2114M0	*PPM1D*	p.N448fs	0.04
AL1539A2169M1	*PPM1D*	p.D488fs	0.0293
AL1539A2169M1	*PPM1D*	p.N448fs	0.0273
AL1539A2169M1	*PPM1D*	p.E476fs	0.0255
AL1539A2169M1	*TP53*	TP53:uc002gii.1:exon4:c.G418A:p.V140M	0.0837
AL1539A2169M1	*TP53*	TP53:uc002gii.1:exon1:c.C132A:p.C44X	0.092593
AL1632A2299M7	*NF1*	NF1:uc002hgg.3:exon54:c.C7909T:p.R2637X	0.097242
AL1632A2299M7	*PPM1D*	p.K480fs	0.0334
AL1632A2299M7	*TP53*	TP53:uc002gii.1:exon2:c.C241T:p.R81X	0.132605
AL1654A2332M0	*NF1*	NF1:uc002hgh.3:exon8:c.G801A:p.W267X	0.616511
AL1718A2420M6	*PPM1D*	p.V464fs	0.0458
AL1718A2420M6	*PPM1D*	p.Q510fs	0.0276
AL1718A2420M6	*TP53*	TP53:uc002gii.1:exon4:c.G443A:p.R148K	0.425721
AL1737A2447M5	*KIT*	KIT:uc010igr.3:exon17:c.A2447T:p.D816V	0.455032
AL1737A2447M5	*NPM1*	NPM1:uc003mbi.3:exon11:c.859_860insTCTG:p.L287fs	0.1667
AL1737A2447M5	*WT1*	WT1:uc001mtm.2:exon6:c.455_456insTGTACGGT:p.S152fs	0.311
AL1816A3323M4	*DNMT3A*	DNMT3A:uc002rgd.3:exon14:c.1604_1605insACGACGACGACGGCTACCAGT:p.S535delinsYDDDGYQS	0.1022
AL1816A3323M4	*TP53*	TP53:uc002gig.1:exon4:c.A394G:p.K132E	0.294707
AL1947A4439M6	*DNMT3A*		0.2196
AL1947A4439M6	*IDH1*	IDH1:uc002vcu.3:exon4:c.C394T:p.R132C	0.099675
AL2061A3607M3	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.3055_3056del:p.1019_1019del	0.148
AL2158A4397M9	*U2AF1*	U2AF1:uc002zda.1:exon2:c.C101A:p.S34Y	0.138408
AL2213A5649M5	*PTPN11*	PTPN11:uc001ttx.3:exon13:c.C1472T:p.P491L	0.094595
AL2285A5866M9	*DNMT3A*	uc002rgd.3:exon19:c.2173+2T>C	0.828986
AL2285A5866M9	*ETV6*	ETV6:uc001qzz.3:exon6:c.1146delC:p.N382fs	0.2345
AL2285A5866M9	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284T:p.P95L	0.442155
AL2285A5866M9	*TET2*	TET2:uc011cez.2:exon3:c.2978_2979insT:p.S993fs	0.2179
AL2481A5022M5	*PPM1D*	p.Q510fs	0.0211
AL2481A5022M5	*PPM1D*	p.Q510fs	0.0289
AL2510A5446M9	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1475
AL2510A5446M9	*BCOR*	BCOR:uc004dep.4:exon13:c.4709_4710del:p.1570_1570del	0.681
AL2510A5446M9	*PTPN11*	PTPN11:uc001ttx.3:exon13:c.C1472T:p.P491L	0.449568
AL2510A5446M9	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284T:p.P95L	0.485887
AL2510A5446M9	*STAG2;STAG2*	STAG2:uc004eud.3:exon16:c.1418_1419insA:p.L473fs	0.3189
AL2510A5446M9	*TET2*	TET2:uc011cez.2:exon3:c.742_743insA:p.E248fs	0.2775
AL2547A6289M9	*DNMT3A*	DNMT3A:uc002rgd.3:exon14:c.G1627T:p.G543C	0.057332
AL2621A6897M6	*TP53*	TP53:uc002gii.1:exon1:c.G42A:p.W14X	0.428571
AL2621A6897M6	*TP53*	TP53:uc010vug.2:exon5:c.G556A:p.V186I	0.415179

AL2709A6501M7	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.G2645A:p.R882H	0.057915
AL2709A6501M7	*PPM1D*	p.T483fs	0.0451
AL2709A6501M7	*TP53*	TP53:uc002gii.1:exon2:c.G250A:p.V84M	0.83642
AL2724A6516M9	*FLT3*	FLT3:uc010tdn.2:exon14:c.1836_1837insCAGAGAATATGAATATGATCTCAAATGGGAGTTTCCAAGAGAAAATTTAGAGTT:p.F612delinsFREYEYDLKWEFPRENLEF	0.1697
AL2735A6530M7	*PPM1D*	p.F534fs	0.3471
AL2736A6531M4	*NRAS*	NRAS:uc009wgu.3:exon3:c.C181A:p.Q61K	0.261456
AL2743A6541M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon19:c.2316delT:p.F772fs	0.1083
AL2743A6541M8	*PPM1D*	p.S541fs	0.0638
AL2826A6672M2	*TET2*	TET2:uc011cez.2:exon6:c.C3828A:p.Y1276X	0.180617
AL2826A6672M2	*TP53*	TP53:uc002gii.1:exon2:c.A218G:p.Y73C	0.223118
AL2826A6672M2	*U2AF1*	U2AF1:uc002zda.1:exon6:c.A470C:p.Q157P	0.117296
AL2829A6675M3	*WT1*	WT1:uc001mtm.2:exon6:c.C455A:p.S152X	0.147497
AL2830A6676M0	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1199
AL2831A6677M7	*FLT3*	FLT3:uc010tdn.2:exon14:c.1779_1780insAGCCCCCGGGGAAGTTGA:p.D593delinsEAPGEVD	0.2245
AL2831A6677M7	*KDM6A*	KDM6A:uc011mkz.2:exon18:c.C2128T:p.R710X	0.721212
AL2831A6677M7	*RAD21*	RAD21:uc003yod.3:exon13:c.G1657T:p.E553X	0.412017
AL2831A6677M7	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.C610T:p.R204X	0.306667
AL2831A6677M7	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.495_496insGG:p.G165fs	0.2066
AL2831A6677M7	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.335766
AL2832A6678M4	*PPM1D*	p.N448fs	0.0227
AL2832A6678M4	*TP53*	TP53:uc002gii.1:exon2:c.T185A:p.L62H	0.419729
AL2905A6801M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.132222
AL2905A6801M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon7:c.C852A:p.Y284X	0.133178
AL2905A6801M8	*PPM1D*	p.N448fs	0.025
AL2905A6801M8	*TP53*	TP53:uc002gii.1:exon1:c.G71C:p.R24P	0.158205
AL2905A6801M8	*TP53*	TP53:uc002gii.1:exon1:c.59delC:p.P20fs	0.1581
AL2905A6849M2	*DNMT3A*	DNMT3A:uc002rgd.3:exon7:c.C852A:p.Y284X	0.406977
AL2905A6849M2	*TP53*	TP53:uc002gii.1:exon1:c.G71C:p.R24P	0.452713
AL2905A6849M2	*TP53*	TP53:uc002gii.1:exon1:c.59delC:p.P20fs	0.3114
AL2937A6858M3	*TP53*	TP53:uc002gii.1:exon3:c.C346T:p.R116W	0.051447
AL2938A6859M0	*SH2B3*	SH2B3:uc001tse.3:exon7:c.1261_1262insG:p.R421fs	0.479167
AL2938A6859M0	*TP53*	TP53:uc002gii.1:exon4:c.G415A:p.E139K	0.403877
AL2947A6868M0	*PPM1D*	p.E459fs	0.4134
AL2950A6871M9	*BCOR*	BCOR:uc004dep.4:exon7:c.3410_3411del:p.1137_1137del	0.415
AL2950A6871M9	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.G2645A:p.R882H	0.303303
AL2950A6871M9	*FLT3*	FLT3:uc010tdn.2:exon14:c.1796_1797insGGGTACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTACGTTGATTTCAGAGAATATGAAT:p.Y599delinsWVQVTGSSDNEYFYVDFREYEY	0.1057
AL2950A6871M9	*RUNX1*	RUNX1:uc010gmv.3:exon8:c.903delC:p.P301fs	0.3369
AL2950A6871M9	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284A:p.P95H	0.25
AL2957A6880M3	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.A2734T:p.K912X	0.242826

AL2957A6880M3	*FLT3*	FLT3:uc001urw.3:exon20:c.2508_2510del:p.836_837del	0.0663
AL2957A6880M3	*TET2*	TET2:uc011cez.2:exon3:c.2320_2335del:p.774_779del	0.4067
AL2957A6880M3	*TET2*	TET2:uc011cez.2:exon3:c.2415delT:p.C805fs	0.1366
AL2957A6880M3	*ZRSR2*	ZRSR2:uc004cxg.4:exon2:c.C94T:p.Q32X	0.498077
AL2959A6882M7	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.C1773G:p.Y591X	0.466192
AL2959A6882M7	*NF1*	NF1:uc002hgg.3:exon46:c.6853_6854insA:p.Y2285_N2286delinsX	0.1368
AL2966A6889M5	*FLT3*	exon15:c.1837>ATCTCAAATGGGAGTTTCCAAGAGAAAATTTAGAGTTTG)	0.1186
AL2966A6889M5	*NPM1*	NPM1:uc003mbi.3:exon11:c.860_861insCTGC:p.L287fs	0.1828
AL2966A6889M5	*WT1*	WT1:uc001mtm.2:exon6:c.422_423insC:p.R141fs	0.236
AL2971A6909M1	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2384delC:p.S795fs	0.0546
AL2971A6909M1	*JAK2*	JAK2:uc003ziw.3:exon14:c.G1849T:p.V617F	0.294043
AL3097A7164M2	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1386
AL3097A7164M2	*GATA2*	GATA2:uc003ekm.3:exon6:c.T1075G:p.L359V	0.351548
AL3097A7164M2	*JAK2*	JAK2:uc003ziw.3:exon14:c.G1849T:p.V617F	0.42953
AL641A743M9	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.072917
AL641A743M9	*WT1*	WT1:uc001mtm.2:exon6:c.456_457insCGGTC:p.S152fs	0.2045
AL658A777M8	*BCOR*	BCOR:uc004deq.4:exon4:c.613_614insAC:p.P205fs	0.1009
AL658A777M8	*IDH2*	IDH2:uc002box.3:exon4:c.G419A:p.R140Q	0.5
AL658A777M8	*PHF6*	PHF6:uc004exk.3:exon9:c.C903G:p.Y301X	0.15
AL658A777M8	*RUNX1*	RUNX1:uc010gmv.3:exon9:c.1252_1277del:p.418_426del	0.0845
AL658A777M8	*SF3B1*	SF3B1:uc002uue.3:exon15:c.A2098G:p.K700E	0.229167
AL691A843M7	*PPM1D*	PPM1D:uc002iyt.2:exon6:c.1527delC:p.D509fs	0.1081
AL698A857M3	*TP53*	TP53:uc002gii.1:exon1:c.T130A:p.C44S	0.743902
AL749A960M6	*TET2*	TET2:uc011cez.2:exon9:c.4147_4177del:p.1383_1393del	0.2256
AL749A960M6	*TET2*	TET2:uc011cez.2:exon3:c.1671_1672del:p.557_558del	0.3367
AL762A5244M5	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2852_2853insTCTTCAC:p.D951fs	0.2951
AL762A5244M5	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.441111
AL762A5244M5	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.386412
AL762A5244M5	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.493_494insAGGGGT:p.G165delinsRGG	0.3092
AL762A5521M9	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2852_2853insTCTTCAC:p.D951fs	0.3016
AL762A5521M9	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.483787
AL762A5521M9	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.74197
AL762A5521M9	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.493_494insAGGGGT:p.G165delinsRGG	0.3248
AL762A6961M4	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2852_2853insTCTTCAC:p.D951fs	0.3108
AL762A6961M4	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.513774
AL762A6961M4	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.740107
AL762A6961M4	*RUNX1*	RUNX1:uc010gmw.1:exon5:c.493_494insAGGGGT:p.G165delinsRGG	0.3018
AL762A986M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.352941
AL770A1002M9	*EZH2*	EZH2:uc011kui.2:exon8:c.G863A:p.R288Q	0.237288
AL781A1024M0	*KRAS*	KRAS:uc001rgq.1:exon4:c.A351C:p.K117N	0.095238
AL792A1046M1	*TP53*	TP53:uc002gii.1:exon1:c.C132A:p.C44X	0.625767

AL832A1180M1	*TET2*	TET2:uc011cez.2:exon3:c.C1858T:p.Q620X\	0.896552
AL852A1221M0	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.470588
AL852A1221M0	*NRAS*	NRAS:uc009wgu.3:exon2:c.G38T:p.G13V	0.088235
AL852A1221M0	*PTPN11*	PTPN11:uc001ttx.3:exon3:c.G179T:p.G60V	0.148148
AL852A1221M0	*SETBP1*	SETBP1:uc010dni.3:exon4:c.G2602T:p.D868Y	0.401515
AL876A1276M3	*TP53*	TP53:uc002gii.1:exon2:c.T188C:p.I63T	0.142857
AL876A4637M1	*TP53*	TP53:uc002gii.1:exon2:c.T188C:p.I63T	0.593482
AL885A1285M3	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.2263delG:p.G755fs	0.1989
AL885A1285M3	*IDH1*	IDH1:uc002vcu.3:exon4:c.G395A:p.R132H	0.470588
AL885A1285M3	*RUNX1*	RUNX1:uc010gmw.1:exon6:c.567_568insA:p.Y189_H190delinsX	0.2235
AL885A1285M3	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.284_285insGCC:p.P95delinsRP	0.2566
AL909A1309M3	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.1333
AL909A1309M3	*NRAS*	NRAS:uc009wgu.3:exon2:c.G35A:p.G12D	0.333333
AL909A1309M3	*TET2*	TET2:uc011cez.2:exon3:c.C1654T:p.Q552X	0.450292
AL909A1309M3	*TET2*	TET2:uc011cez.2:exon3:c.C2809T:p.Q937X	0.428571
AL927A1333M5	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.C2077T:p.R693X	0.389937
AL927A1333M5	*CBL*	CBL:uc001pwe.3:exon8:c.T1111C:p.Y371H	0.382979
AL927A1333M5	*CBL*	CBL:uc001pwe.3:exon9:c.C1257G:p.C419W	0.487179
AL927A1333M5	*EZH2*	EZH2:uc011kui.2:exon7:c.716_717insC:p.E239fs	0.1458
AL927A1333M5	*U2AF1*	U2AF1:uc002zda.1:exon6:c.A470C:p.Q157P	0.433333
AL955A1361M1	*ZRSR2*	uc004cxg.4:exon9:c.827+1G>T	0.0625
AL962A1368M0	*ASXL1*	ASXL1:uc021wbw.1:exon13:c.1926_1927insG:p.G642fs	0.178
AL962A1368M0	*CBL*	CBL:uc001pwe.3:exon8:c.T1111C:p.Y371H	0.122449
AL962A1368M0	*EZH2*	EZH2:uc011kuh.2:exon16:c.1848delG:p.G616fs	0.3298
AL962A1368M0	*SETBP1*	SETBP1:uc010dni.3:exon4:c.G2608A:p.G870S	0.494565
AL962A1368M0	*SRSF2*	SRSF2:uc010wtg.2:exon1:c.C284T:p.P95L	0.513158
AL965A1371M8	*DNMT3A*	DNMT3A:uc002rgd.3:exon23:c.C2644T:p.R882C	0.313725
AL974A5715M6	*KIT*	KIT:uc010igr.3:exon17:c.A2447T:p.D816V	0.186638
AL980A1386M0	*GATA2*	GATA2:uc003ekm.3:exon4:c.T756G:p.Y252X	0.162264
AL980A1386M0	*NRAS*	NRAS:uc009wgu.3:exon2:c.G38A:p.G13D	0.163043
AL980A5945M5	*FLT3*	FLT3:uc010tdn.2:exon14:c.1801_1802insGAAAGCCAGCTACAGATGGTACAGGTGACCGGCTCCTCAGATAATGAGTACTTCTACGTTGATTTCAGAGAATATGAATATGAT:p.L601delinsESQLQMVQVTGSSDNEYFYVDFREYEYDL	0.2667
AL980A5945M5	*GATA2*	GATA2:uc003ekm.3:exon4:c.T756G:p.Y252X	0.220377
AL980A5945M5	*NPM1*	NPM1:uc003mbi.3:exon11:c.861_862insTGCT:p.L287fs	0.201
AL997A1403M3	*RUNX1*	RUNX1:uc010gmw.1:exon4:c.273_274insGGCGAGCTGGTGCG:p.R91fs	0.2308
AL997A1403M3	*WT1*	WT1:uc001mtm.2:exon8:c.C697T:p.R233W	0.084746
BM-15-2015	*KRAS*	KRAS:uc001rgq.1:exon2:c.G35C:p.G12A	0.102804
BM-15-2015	*NRAS*	NRAS:uc009wgu.3:exon2:c.G37C:p.G13R	0.170996
BM-15-2015	*TP53*	TP53:uc002gig.1:exon3:c.C321A:p.Y107X	0.971564