Supplementary Material

For Murdock, et al. Impact of diagnostic genetics on remission MRD and transplantation outcomes in older AML patients

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Supplemental Methods

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. *FLT3*-ITDs were called as previously described.[1] Variants were annotated to include information about cDNA and amino acid changes, sequence depth, number, and percentage of reads supporting the variant allele, and 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.

Data Sharing

All molecular data are contained in the manuscript and supplemental files.

Statistical Analysis

In order to build a baseline mutational prognostic model, we first performed univariable Cox regression analysis for each mutation with at least 10 cases using a bootstrap validation method with 10,000 resamples of size 295 with replacement.[2] The bootstrap method was used to adjust the model in order to decrease the impact of overfitting to the original dataset and reducing the influence of unusual or outlying values. Although the split-sample method is commonly used for validation, it greatly reduces the sample size for both the training and validation sets; if the process is repeated with a different split, different regression coefficients may be obtained from the validation set. This is a concern particularly when the sample size is not large.[2] The bootstrap validation method overcomes these drawbacks and obtains nearly unbiased estimates without sacrificing sample.[2] Using this method, mutations with p-values less than 0.05 were selected and classified into favorable, intermediate, and unfavorable group according to their hazard ratios. Variables with HRs of 1 to 1.5 received 0.5 points, those with HRs of 1.5 to 2 received 1 point, those with HRs of 2 to 2.5 received 1.5 points, and those with HRs ≥ 2.5 received 2 points (table S8). We then performed multivariable Cox model adjusting for other non-genetic risk factors using the same bootstrap method to build a final prognostic model for LFS. Center effect was tested using a frailty model and center was adjusted in every model (table S9). We also utilized the Akaike information index (AIC) for the assessment of model fit and C-index[3] for predictive ability of models. For NRM and relapse, multivariable competing risks regression analysis (i.e., Fine and Gray model) for NRM and relapse were performed. For those patients who have samples at remission, the association between baseline genetic and clinical characteristics and the likelihood of MRD positivity at remission (modeled as a binary outcome, all clear/DT or MRD positive) was assessed using univariable and multivariable logistic regression analysis. Factors with p-value less than 0.05 from univariable logistic analysis were included in the multivariable analysis. Prior to analysis, collinearity among characteristics was assessed using correlation analysis and unsupervised hierarchical clustering analysis. Prior use of hypomethylation agent was correlated with secondary AML and cytogenetic risk was correlated with mutational risk. Since collinearity makes it difficult to estimate regression coefficients while holding (highly correlated) variables constant, we performed multivariable analysis including each of these prognostic variables separately but adjusting for all other variables. All P-values were two-sided at a significance level of 0.05. All calculations were performed using SAS 9.3 (SAS Institute, Inc., Cary, NC) and R version 3.3.2.

1. Tsai HK, Brackett DG, Szeto D, et al. Targeted Informatics for Optimal Detection, Characterization, and Quantification of FLT3 Internal Tandem Duplications Across Multiple Next-Generation Sequencing Platforms. *J. Mol. Diagn.* 2020;22(9):1162–1178.

2. Efron and Tibshirani (1993). An Introduction to the Bootstrap, Chapman &Hall/CRC

3. Harrell FE (2001). Regression modeling strategies: with applications to linear models, logistic regression, and survival analysis. Springer

Table S1. Number of patients enrolled by center

Center	Number Enrolled
Dana-Farber Cancer Institute	104
Johns Hopkins University	58
Memorial Sloan Kettering Cancer Center	21
The Ohio State University	36
Roswell Park Comprehensive Cancer Center	48
The University of Pennsylvania	28

Table S2. Characteristics of patients with and without remission samples

Comparisons of distributions are by the Wilcoxon rank-sum test. Comparisons of categorical variables in 2 groups are by Fisher's exact test and comparisons of more than 2 groups are by Chi square.

	CR sample		No CR sample		P value
	N	%	N	%	
Full Cohort	**192**	**65**	**103**	**35**	NA
Recipient age, median (range)	66 (60-76)		66 (60-74)		0.53
Recipient sex					0.17
Female	82	43	35	37	
Male	110	57	68	66	
HCT-CI score					0.97
0	54	28	29	28	
1	52	27	29	28	
3+	76	40	44	43	
Missing	7	4	4	4	
Type of AML (clinically defined)					0.89
De novo	113	59	60	58	
Secondary	60	31	31	30	
Therapy-related	19	10	12	12	
Cytogenetics*					0.16
Normal	85	44	51	50	
Core binding factor	2	1	4	3	
Complex karyotype	31	16	10	10	
Other	74	39	38	37	
2017 ELN risk group					0.98
Favorable	35	18	18	18	
Intermediate	55	29	30	29	
Adverse	100	52	52	51	
Missing	3	2	2	2	
Initial therapy					0.87
Intensive induction	161	84	88	85	
Non-intensive induction	31	16	15	15	
Re-induction					0.9
Yes	58	30	32	31	
No	133	69	71	69	
Missing	1	0.5	2	2	
Pre-transplant consolidation					0.8
Yes	121	63	63	61	
No	71	37	40	39	
Remission quality					0.51
CR with hematologic recovery	147	77	78	76	
CRi	44	23	23	22	

Missing	1	0.5	2	2	
Donor type					0.008
Matched related	36	19	22	21	
Matched unrelated	106	55	68	66	
Mismatch related	2	1	0	0	
Mismatch unrelated	3	2	5	5	
Haploidentical	43	22	8	8	
Conditioning regimen					0.005
Myeloablative	11	6	17	16	
Reduced intensity	181	94	86	84	
Stem cell source					0.003
Peripheral blood	132	69	84	82	
Bone marrow	57	30	14	14	
Umbilical cord blood	3	1.5	5	5	
Molecular Risk					0.67
Favorable	65	34	30	29	
Intermediate	86	45	51	50	
Unfavorable	41	21	22	21	
Molecular Ontogeny					0.81
De Novo	86	45	49	48	
Secondary	83	43	44	43	
p53	23	12	10	10	
Overall Risk					0.76
Low	24	13	12	12	
Intermediate	79	41	37	36	
High	40	21	26	25	
Very High	49	26	28	27	

Table S3. Genes sequenced on diagnostic panel.

ACD	CSNK1A1	KDM6A	PHF6	SRSF2
ASXL1	CTC1	KDM6B	POT1	STAG2
ASXL2	CTCF	KIT	PPM1D	STAT3
ATM	CUX1	KRAS	PRPF8	STAT5B
ATR	DDX41	MBD4	PTPN11	SUZ12
ATRX	DKC1	MDM2	RAD21	TEN1
BAP1	DNMT3A	MLL-PTD	RING1	TERF1
BCOR	EED	MPL	RIT1	TERF2
BCORL1	EP300	MYC	RNF2	TERF2IP
BRAF	ETNK1	MYD88	RTEL1	TERT
BRCA1	ETV6	NAF1	RUNX1	TERC
BRCA2	EZH1	NF1	RYBP	TET2
BRCC3	EZH2	NFE2	SAMD9	TINF2
BRIP1	FLT3	NHP2	SAMD9L	TP53
CALR	GATA2	NOP10	SBDS	U2AF1
CBL	GNAS	NOTCH1	SETBP1	USP7
CDA	GNB1	NPM1	SETD2	WRAP53
CDKN2A	IDH1	NRAS	SF3B1	WT1
CDKN2B	IDH2	NSD2	SH2B3	ZBTB33
CEBPA	IKZF1	OBFC1	SKP1	ZNF318
CHEK2	JAK2	PARN	SMC1A	ZRSR2
CREBBP	KDM2B	PCGF1	SMC3	
CSF3R	KDM5A	PDS5B	SRCAP	

Table S4. Genes sequenced on remission panel

ASXL1	DDX41	KDM2B	RAD21	SRSF2
ASXL2	DKC1	KIT	RING1	STAG2
ATM	DNMT3A	KRAS	RIT1	STAT3
ATRX	EIF6	MDM2	RNF2	STAT5B
BCOR	EP300	MPL	RTEL1	TERT
BCORL1	ETNK1	MYC	RUNX1	TET2
BRAF	ETV6	NF1	SAMD9	TP53
BRCC3	EZH2	NOTCH1	SAMD9L	U2AF1
CALR	FLT3	NPM1	SBDS	USP7
CBL	GATA2	NRAS	SETBP1	WT1
CEBPA	GNAS	PCGF1	SETD2	ZBTB33
CREBBP	GNB1	PDS5B	SF3B1	ZRSR2
CSF3R	IDH1	PHF6	SH2B3	
CSNK1A1	IDH2	PPM1D	SKP1	
CTCF	IKZF1	PRPF8	SMC1A	
CUX1	JAK2	PTPN11	SMC3	

Table S5. Mutations detected at the time of diagnosis (and remission, if applicable)

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML174	chr20:31021625	-	TTG/	ASXL1	c.1624_1625insT	p.L542fs	frameshift insertion	0.426	857	No	.	.
OAML311	Chr20:31022271	A	T	ASXL1	c.A1756T	p.K586X	stopgain	0.070	627	No	.	.
OAML158	chr20:31022284	-	T	ASXL1	c.1770dupT	p.T590fs	frameshift insertion	0.397	1026	Yes	Yes	0.361
OAML074	chr20:31022286	-	A	ASXL1	c.1772dupA	p.Y591_Q59	stopgain	0.236	783	No	.	.
OAML057	chr20:31022288	C	G	ASXL1	c.C1773G	p.Y591X	stopgain	0.368	922	Yes	Yes	0.038
OAML068	Chr20:31022365	0	-	ASXL1	c.1850_1851del	p.I617fs	frameshift deletion	0.451	412	Yes	Yes	0.337
OAML290	Chr20:31022367	A	T	ASXL1	c.A1852T	p.K618X	stopgain	0.437	678	Yes	No	0.000
OAML001	chr20:31022402	0	-	ASXL1	c.1887_1909del	p.G629fs	frameshift deletion	0.139	2133	Yes	No	0.000
OAML144	chr20:31022402	0	-	ASXL1	c.1887_1909del	p.G629fs	frameshift deletion	0.278	710	Yes	Yes	0.000
OAML205	chr20:31022402	0	-	ASXL1	c.1887_1909del	p.G629fs	frameshift deletion	0.365	1029	No	.	.
OAML230	chr20:31022402	0	-	ASXL1	c.1887_1909del	p.G629fs	frameshift deletion	0.328	801	Yes	No	0.000
OAML293	Chr20:31022402	0	-	ASXL1	c.1887_1909del	p.G629fs	frameshift deletion	0.260	832	No	.	.
OAML054	chr20:31022414	0	-	ASXL1	c.1899_1900del	p.H633fs	frameshift deletion	0.269	958	No	.	.
OAML051	chr20:31022416	G	-	ASXL1	c.1901delG	p.R634fs	frameshift deletion	0.090	679	Yes	Yes	0.078
OAML099	chr20:31022416	G	-	ASXL1	c.1901delG	p.R634fs	frameshift deletion	0.113	1476	Yes	Yes	0.001
OAML168	chr20:31022416	G	-	ASXL1	c.1901delG	p.R634fs	frameshift deletion	0.094	608	No	.	.
OAML237	chr20:31022416	G	-	ASXL1	c.1901delG	p.R634fs	frameshift deletion	0.067	505	Yes	Yes	0.011
OAML256	chr20:31022416	G	-	ASXL1	c.1901delG	p.R634fs	frameshift deletion	0.066	651	Yes	Yes	0.004
OAML007	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.337	846	Yes	Yes	0.014
OAML024	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.276	994	No	.	.
OAML030	Chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.333	707	No	.	.
OAML035	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.263	732	Yes	Yes	0.146
OAML038	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.361	629	Yes	Yes	0.361
OAML064	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.076	841	Yes	No	0.000
OAML076	Chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.351	741	Yes	Yes	0.316
OAML076	Chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.351	741	Yes	Yes	0.316
OAML088	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.107	909	Yes	Yes	0.004
OAML110	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.147	739	No	.	.
OAML113	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.119	903	Yes	No	0.000
OAML121	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.441	1220	Yes	Yes	0.211
OAML122	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.294	1058	Yes	Yes	0.018
OAML127	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.369	906	Yes	Yes	0.430
OAML138	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.374	1188	Yes	Yes	0.323
OAML139	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.406	933	Yes	Yes	0.005
OAML142	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.384	954	No	.	.
OAML143	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.310	843	No	.	.
OAML160	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.292	1367	No	.	.
OAML178	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.308	710	No	.	.
OAML179	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.338	706	Yes	Yes	0.141
OAML191	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.380	744	No	.	.
OAML192	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.040	612	Yes	Yes	0.003
OAML226	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.137	507	No	.	.
OAML238	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.035	754	Yes	Yes	0.069
OAML253	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.364	864	Yes	Yes	0.365
OAML254	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.338	895	Yes	Yes	0.310
OAML271	chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.398	765	Yes	Yes	0.005
OAML313	Chr20:31022441	-	G	ASXL1	c.1927dupG	p.G642fs	frameshift insertion	0.149	921	No	.	.
OAML145	chr20:31022457	0	-	ASXL1	c.1942_1943del	p.G648fs	frameshift deletion	0.300	1101	Yes	Yes	0.032
OAML167	chr20:31022499	0	-	ASXL1	c.1984_1994del	p.G662fs	frameshift deletion	0.463	693	No	.	.
OAML065	chr20:31022643	G	T	ASXL1	c.G2128T	p.G710X	stopgain	0.049	1237	Yes	No	0.000
OAML274	chr20:31022768	-	G	ASXL1	c.2254dupG	p.V751fs	frameshift insertion	0.333	991	Yes	Yes	0.233
OAML301	Chr20:31022817	C	T	ASXL1	c.C2302T	p.Q768X	stopgain	0.205	1075	No	.	.
OAML063	Chr20:31022837	A	-	ASXL1	c.2322delA	p.R774fs	frameshift deletion	0.410	571	Yes	No	0.000
OAML207	chr20:31022853	C	T	ASXL1	c.C2338T	p.Q780X	stopgain	0.070	1023	No	.	.
OAML247	chr20:31022853	C	T	ASXL1	c.C2338T	p.Q780X	stopgain	0.355	1024	Yes	Yes	0.089
OAML055	chr20:31022916	G	T	ASXL1	c.G2401T	p.E801X	stopgain	0.186	853	Yes	Yes	0.165
OAML201	chr20:31022936	T	-	ASXL1	c.2421delT	p.V807fs	frameshift deletion	0.463	1230	No	.	.
OAML188	chr20:31022958	C	-	ASXL1	c.2443delC	p.L815fs	frameshift deletion	0.442	966	No	.	.
OAML322	Chr20:31023153	A	-	ASXL1	c.2638delA	p.T880fs	frameshift deletion	0.258	1225	No	.	.
OAML213	chr20:31023277	-	T	ASXL1	c.2763dupT	p.S921fs	frameshift insertion	0.802	614	No	.	.
OAML250	chr20:31023394	G	A	ASXL1	c.G2879A	p.W960X	stopgain	0.477	849	Yes	No	0.000
OAML238	chr20:31023408	C	T	ASXL1	c.C2893T	p.R965X	stopgain	0.401	918	Yes	Yes	0.027
OAML203	chr20:31023498	-	A	ASXL1	c.2984dupA	p.H995fs	frameshift insertion	0.350	960	No	.	.
OAML180	chr20:31024636	-	G	ASXL1	c.4122dupG	p.V1374fs	frameshift insertion	0.464	734	No	.	.
OAML190	Chr2:25966872	T	-	ASXL2	c.2334delA	p.P778fs	frameshift deletion	0.292	870	No	.	.
OAML309	Chr2:25967031	C	-	ASXL2	c.2175delG	p.K725fs	frameshift deletion	0.044	994	No	.	.
OAML098	chr2:25967233	-	C	ASXL2	c.1972dupG	p.A658fs	frameshift insertion	0.424	770	Yes	Yes	0.001
OAML118	chr2:25967233	-	C	ASXL2	c.1972dupG	p.A658fs	frameshift insertion	0.447	789	Yes	Yes	0.026
OAML005	chr2:25967279	-	A	ASXL2	c.1926dupT	p.P643fs	frameshift insertion	0.345	764	Yes	No	0.000
OAML217	chr2:25972652	-	GGG	ASXL2	c.1772_1773insT	p.R591fs	frameshift insertion	0.424	999	No	.	.
OAML222	chr2:25973115	T	-	ASXL2	c.1310delA	p.Q437fs	frameshift deletion	0.239	915	No	.	.
OAML025	chr2:25973179	C	A	ASXL2	c.G1246T	p.E416X	stopgain	0.424	1031	Yes	No	0.000
OAML274	chrX:39911489	-	C	BCOR	c.5140dupG	p.E1714fs	frameshift insertion	0.106	360	Yes	Yes	0.005
OAML054	chrX:39913252	T	-	BCOR	c.4863delA	p.P1621fs	frameshift deletion	0.522	452	No	.	.
OAML231	chrX:39913252	T	-	BCOR	c.4863delA	p.P1621fs	frameshift deletion	0.898	442	Yes	Yes	0.003

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML057	chrX:39913528	-	CGG	BCOR	c.4799_4800ins(	p.F1600fs	frameshift insertion	0.163	613	Yes	No	0.000
OAML258	chrX:39913528	-	A	BCOR	c.4799dupT	p.F1600fs	frameshift insertion	0.297	623	Yes	Yes	0.001
OAML199	chrX:39913588	T	C	BCOR	c.4640-2A>G		splicing	0.324	102	Yes	No	0.000
OAML274	chrX:39914723	G	A	BCOR	c.C4639T	p.R1547X	stopgain	0.064	376	Yes	Yes	0.006
OAML155	chrX:39914767	C	T	BCOR	c.4494-1G>A		splicing	0.904	500	Yes	Yes	0.003
OAML303	ChrX:39916415	-	AT	BCOR	c.4587_4588insA	p.G1530fs	frameshift insertion	0.668	310	No	.	.
OAML274	chrX:39916531	-	G	BCOR	c.4471_4472ins(	p.N1491fs	frameshift insertion	0.190	437	Yes	Yes	0.029
OAML025	chrX:39921391	C	T	BCOR	c.4326+1G>A		splicing	0.881	236	Yes	No	0.000
OAML280	chrX:39921391	C	T	BCOR	c.4326+1G>A		splicing	0.915	317	Yes	Yes	0.378
OAML153	chrX:39921457	T	A	BCOR	c.A4363T	p.R1455X	stopgain	0.932	395	Yes	Yes	0.655
OAML327	ChrX:39921997	A	C	BCOR	c.4071+2T>G		splicing	0.205	313	No	.	.
OAML046	chrX:39922123	-	A	BCOR	c.4048dupT	p.Y1350fs	frameshift insertion	0.287	859	Yes	No	0.000
OAML284	ChrX:39923086	G	-	BCOR	c.3622delC	p.Q1208fs	frameshift deletion	0.118	366	Yes	Yes	0.001
OAML117	chrX:39931848	-	GA	BCOR	c.2750_2751insT	p.T917fs	frameshift insertion	0.789	576	Yes	No	0.000
OAML064	chrX:39931993	0	-	BCOR	c.2605_2606del	p.Y869fs	frameshift deletion	0.079	1009	Yes	Yes	0.001
OAML023	chrX:39931996	G	-	BCOR	c.2603delC	p.T868fs	frameshift deletion	0.883	686	Yes	Yes	0.004
OAML285	ChrX:39932074	-	CTG/	BCOR	c.2524_2525ins(	p.V842fs	frameshift insertion	0.531	226	Yes	No	0.000
OAML064	chrX:39932171	G	A	BCOR	c.C2428T	p.R810X	stopgain	0.022	1035	Yes	No	0.000
OAML146	chrX:39932868	A	-	BCOR	c.1731delT	p.N577fs	frameshift deletion	0.401	1164	Yes	No	0.000
OAML139	chrX:39932984	G	A	BCOR	c.C1615T	p.Q539X	stopgain	0.087	588	Yes	No	0.000
OAML017	chrX:39933205	A	-	BCOR	c.1394delT	p.V465fs	frameshift deletion	0.614	399	Yes	Yes	0.671
OAML274	chrX:39933301	-	TGG(	BCOR	c.1297_1298ins(	p.T433fs	frameshift insertion	0.084	488	Yes	Yes	0.007
OAML238	chrX:39933505	-	TA	BCOR	c.1093_1094insT	p.S365fs	frameshift insertion	0.666	410	Yes	No	0.000
OAML309	ChrX:39933593	-	G	BCOR	c.1005dupC	p.S336fs	frameshift insertion	0.265	977	No	.	.
OAML166	chrX:39934027	C	T	BCOR	c.G572A	p.W191X	stopgain	0.829	368	No	.	.
OAML025	chrX:129148573	C	T	BCORL1	c.C1825T	p.R609X	stopgain	0.680	572	Yes	No	0.000
OAML263	chrX:129149098	C	T	BCORL1	c.C2350T	p.R784X	stopgain	0.132	509	Yes	No	0.000
OAML066	chrX:129155008	-	G	BCORL1	c.3491dupG	p.R1164fs	frameshift insertion	0.264	857	Yes	Yes	0.022
OAML219	chrX:129159072	C	T	BCORL1	c.C3796T	p.R1266X	stopgain	0.024	554	No	.	.
OAML263	chrX:129159150	C	T	BCORL1	c.C3874T	p.R1292X	stopgain	0.049	470	Yes	Yes	0.001
OAML117	chrX:129159171	C	T	BCORL1	c.C3895T	p.R1299X	stopgain	0.859	516	Yes	No	0.000
OAML255	chrX:129159270	C	T	BCORL1	c.C3994T	p.R1332X	stopgain	0.470	837	Yes	Yes	0.003
OAML258	chrX:129159270	C	T	BCORL1	c.C3994T	p.R1332X	stopgain	0.080	893	Yes	No	0.000
OAML285	ChrX:129162788	-	AG	BCORL1	c.4257_4258insA	p.K1419fs	frameshift insertion	0.614	69	Yes	No	0.000
OAML303	ChrX:129162837	G	A	BCORL1	c.4305+1G>A		splicing	0.588	160	No	.	.
OAML219	chrX:129171479	-	GCT(	BCORL1	c.4443_4444ins(	p.N1481fs	frameshift insertion	0.092	508	No	.	.
OAML003	chr7:140453136	A	T	BRAF	c.T1799A	p.V600E	nonsynonymous SNV	0.432	790	Yes	No	0.000
OAML329	Chr7:140453136	A	T	BRAF	c.T1799A	p.V600E	nonsynonymous SNV	0.063	382	No	.	.
OAML174	chr7:140453154	T	C	BRAF	c.A1781G	p.D594G	nonsynonymous SNV	0.507	713	No	.	.
OAML143	chrX:154299839	0	-	BRCC3	c.37_44del	p.H13fs	frameshift deletion	0.702	248	No	.	.
OAML263	chrX:154305490	C	T	BRCC3	c.C244T	p.R82X	stopgain	0.057	314	Yes	No	0.000
OAML020	chrX:154348273	G	A	BRCC3	c.728-1G>A		splicing	0.039	333	Yes	No	0.000
OAML119	chr19:13054571	-	A	CALR	c.1098_1099insA	p.L367fs*46	frameshift insertion	0.251	430	Yes	No	0.000
OAML169	chr19:13054571	-	A	CALR	c.1098_1099insA	p.L367fs*46	frameshift insertion	0.634	123	No	.	.
OAML243	chr11:119148546	G	C	CBL	c.G1087C	p.V363L	nonsynonymous SNV	0.095	728	Yes	Yes	0.012
OAML183	chr11:119148553	A	G	CBL	c.A1094G	p.Q365R	nonsynonymous SNV	0.438	626	No	.	.
OAML280	chr11:119148919	T	C	CBL	c.T1139C	p.L380P	nonsynonymous SNV	0.080	661	Yes	No	0.000
OAML226	chr11:119148931	G	A	CBL	c.G1151A	p.C384Y	nonsynonymous SNV	0.156	410	No	.	.
OAML080	Chr11:119148948	G	T	CBL	c.G1168T	p.D390Y	nonsynonymous SNV	0.138	549	Yes	No	0.000
OAML099	chr11:119148949	A	T	CBL	c.A1169T	p.D390V	nonsynonymous SNV	0.049	510	Yes	No	0.000
OAML072	Chr11:119148991	G	A	CBL	c.G1211A	p.C404Y	nonsynonymous SNV	0.717	152	Yes	Yes	0.187
OAML057	chr11:119149004	0	-	CBL	c.1224_1225del	p.W408fs	frameshift deletion	0.029	727	Yes	No	0.000
OAML058	chr19:33792257	C	G	CEBPA	c.G707C	p.G236A	nonsynonymous SNV	0.192	665	Yes	No	0.000
OAML162	chr19:33792371	A	T	CEBPA	c.T593A	p.L198fs*52	frameshift deletion	0.057	1148	Yes	No	0.000
OAML192	chr19:33792386	T	G	CEBPA	c.A935C	p.Q312P	nonsynonymous SNV	0.413	504	Yes	No	0.000
OAML183	chr19:33792403	-	CGC	CEBPA	c.917_918insGC	p.R306delins	nonframeshift insertion	0.486	627	No	.	.
OAML133	chr19:33792415	C	-	CEBPA	c.906delG	p.K302fs	frameshift deletion	0.122	1273	Yes	No	0.000
OAML267	chr19:33792419	-	GC	CEBPA	c.901_902insGC	p.D301fs	frameshift insertion	0.022	871	Yes	No	0.000
OAML021	chr19:33792420	C	T	CEBPA	c.G544A	p.D182*TTT	nonframeshift insertion	0.948	811	Yes	No	0.000
OAML078	chr19:33792440	0	-	CEBPA	c.879_881del	p.293_294de	nonframeshift deletion	0.477	757	Yes	Yes	0.420
OAML149	chr19:33792579	-	CG	CEBPA	c.741_742insCG	p.G248fs	frameshift insertion	0.433	348	Yes	No	0.000
OAML214	chr19:33792709	C	-	CEBPA	c.255delG	p.P85fs	frameshift deletion	0.468	139	No	.	.
OAML281	Chr19:33792709	C	-	CEBPA	c.612delG	p.P204fs	frameshift deletion	0.512	43	Yes	No	0.000
OAML109	chr19:33792825	-	GCG	CEBPA	c.495_496insCC	p.E166fs	frameshift insertion	0.046	237	No	.	.
OAML068	Chr19:33792884	-	G	CEBPA	c.436dupC	p.L146fs	frameshift insertion	0.311	45	Yes	No	0.000
OAML256	chr19:33792891	C	A	CEBPA	c.G430T	p.E144X	stopgain	0.042	354	Yes	No	0.000
OAML192	chr19:33793073	T	-	CEBPA	c.248delA	p.Q83fs	frameshift deletion	0.436	266	Yes	No	0.000
OAML162	chr19:33793075	G	-	CEBPA	c.204delC	p.F68fs	frameshift deletion	0.232	505	Yes	No	0.000
OAML194	chr19:33793099	-	T	CEBPA	c.221dupA	p.N74fs	frameshift insertion	0.135	222	Yes	No	0.000
OAML194	chr19:33793146	C	A	CEBPA	c.G175T	p.E59X	stopgain	0.075	254	Yes	No	0.000
OAML188	chr19:33793185	-	A	CEBPA	c.135_136insT	p.P46fs	frameshift insertion	0.050	384	No	.	.
OAML037	chr19:33793252	-	G	CEBPA	c.26dupC	p.P9fs	frameshift insertion	0.175	160	Yes	No	0.000
OAML183	chr19:33793252	-	G	CEBPA	c.68dupC	p.P23fs	frameshift insertion	0.442	317	No	.	.
OAML101	chr22:29083949	C	-	CHEK2	c.1367delG	p.R456fs	frameshift deletion	0.279	830	Yes	No	0.000
OAML017	chr22:29091856	A	-	CHEK2	c.900delT	p.T300fs	frameshift deletion	0.459	366	Yes	No	0.000

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML128	chr16:3779470	G	A	CREBBP	c.C5578T	p.Q1860X	stopgain	0.033	937	Yes	No	0.000
OAML314	Chr1:36932248	G	A	CSF3R	c.C2302T	p.Q768X	stopgain	0.200	30	No	.	.
OAML038	chr7:101758492	-	A	CUX1	c.599dupA	p.E200fs	frameshift insertion	0.026	348	Yes	Yes	0.096
OAML223	chr7:101840440	A	-	CUX1	c.1782delA	p.Q594fs	frameshift deletion	0.049	761	No	.	.
OAML181	chr7:101843371	C	T	CUX1	c.C2014T	p.R672X	stopgain	0.022	647	No	.	.
OAML174	chr7:101877454	C	T	CUX1	c.C3589T	p.Q1197X	stopgain	0.465	835	No	.	.
OAML125	chr7:101918631	-	T	CUX1	c.1563+1->T		splicing	0.503	1057	Yes	Yes	0.442
OAML008	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.022	901	Yes	No	0.000
OAML019	Chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.083	121	Yes	No	0.000
OAML065	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.060	1089	Yes	Yes	0.001
OAML110	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.369	783	No	.	.
OAML113	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.175	1114	Yes	No	0.000
OAML147	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.123	897	Yes	No	0.000
OAML157	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.109	1414	Yes	Yes	0.165
OAML181	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.181	807	No	.	.
OAML207	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.079	935	No	.	.
OAML216	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.079	953	No	.	.
OAML223	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.079	764	No	.	.
OAML226	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.144	597	No	.	.
OAML272	chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.157	925	Yes	No	0.000
OAML312	Chr5:176939370	C	T	DDX41	c.G1574A	p.R525H	nonsynonymous SNV	0.072	1452	No	.	.
OAML107	chr5:176940751	C	T	DDX41	c.G1033A	p.E345K	nonsynonymous SNV	0.498	819	No	.	.
OAML041	chr5:176940752	G	C	DDX41	c.C1032G	p.D344E	nonsynonymous SNV	0.095	599	Yes	No	0.000
OAML008	chr5:176940836	0	-	DDX41	c.947_948del	p.M316fs	frameshift deletion	0.483	706	Yes	Yes	0.469
OAML226	chr5:176940836	0	-	DDX41	c.947_948del	p.M316fs	frameshift deletion	0.525	446	No	.	.
OAML157	chr5:176940849	C	T	DDX41			splicing	0.027	1095	Yes	No	0.000
OAML002	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.457	791	Yes	Yes	0.383
OAML147	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.421	855	Yes	Yes	0.364
OAML181	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.441	862	No	.	.
OAML207	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.427	858	No	.	.
OAML216	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.427	859	No	.	.
OAML272	chr5:176942945	-	CAT(	DDX41	c.418_419insGA	p.D140_P14	stopgain	0.448	908	Yes	Yes	0.350
OAML065	chr5:176943186	0	-	DDX41	c.306_307del	p.K102fs	frameshift deletion	0.484	1085	Yes	Yes	0.453
OAML312	Chr5:176943288	C	T	DDX41	c.298+1G>A		splicing	0.516	1297	No	.	.
OAML019	Chr5:176943743	G	A	DDX41	c.C121T	p.Q41X	stopgain	0.569	102	Yes	Yes	0.469
OAML041	chr5:176943944	C	T	DDX41	c.G3A	p.M1I	nonsynonymous SNV	0.464	457	Yes	Yes	0.492
OAML084	chr5:176943944	C	T	DDX41	c.G3A	p.M1I	nonsynonymous SNV	0.516	758	Yes	Yes	0.459
OAML113	chr5:176943944	C	T	DDX41	c.G3A	p.M1I	nonsynonymous SNV	0.525	745	Yes	No	0.000
OAML223	chr5:176943944	C	T	DDX41	c.G3A	p.M1I	nonsynonymous SNV	0.486	546	No	.	.
OAML200	chr2:25457176	G	A	DNMT3A	c.C2711T	p.P904L	nonsynonymous SNV	0.025	482	Yes	Yes	0.116
OAML089	chr2:25457191	C	T	DNMT3A	c.G2696A	p.R899H	nonsynonymous SNV	0.267	862	Yes	Yes	0.016
OAML146	chr2:25457209	C	G	DNMT3A	c.G2678C	p.W893S	nonsynonymous SNV	0.380	1041	Yes	Yes	0.049
OAML140	chr2:25457232	C	A	DNMT3A	c.G2655T	p.R885S	nonsynonymous SNV	0.444	925	No	.	.
OAML010	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.353	730	Yes	Yes	0.189
OAML012	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.493	760	Yes	Yes	0.061
OAML018	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.454	1601	Yes	Yes	0.096
OAML025	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.471	835	Yes	Yes	0.392
OAML033	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.420	886	Yes	Yes	0.382
OAML034	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.311	640	No	.	.
OAML040	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.428	767	Yes	Yes	0.017
OAML049	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.487	#N/A	Yes	Yes	0.311
OAML128	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.357	1000	Yes	Yes	0.036
OAML133	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.413	1027	Yes	Yes	0.008
OAML136	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.439	772	Yes	Yes	0.441
OAML152	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.340	936	Yes	Yes	0.161
OAML155	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.456	1254	Yes	Yes	0.260
OAML185	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.413	574	No	.	.
OAML190	Chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.381	699	No	.	.
OAML204	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.270	751	Yes	Yes	0.223
OAML219	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.376	546	No	.	.
OAML234	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.429	860	Yes	Yes	0.145
OAML241	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.465	748	Yes	Yes	0.458
OAML250	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.499	691	Yes	Yes	0.004
OAML259	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.486	698	Yes	Yes	0.245
OAML260	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.457	792	Yes	Yes	0.355
OAML268	chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.423	714	Yes	Yes	0.074
OAML303	Chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.314	714	No	.	.
OAML325	Chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.380	513	No	.	.
OAML326	Chr2:25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.432	502	No	.	.
OAML044	chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.236	652	Yes	Yes	0.064
OAML048	chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.461	686	Yes	Yes	0.386
OAML123	chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.029	867	Yes	No	0.000
OAML172	chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.445	885	No	.	.
OAML186	chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.469	444	No	.	.
OAML301	Chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.201	672	No	.	.

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML316	Chr2:25457243	G	A	DNMT3A	c.C2644T	p.R882C	nonsynonymous SNV	0.367	949	Yes	No	0.000
OAML063	Chr2:25457252	T	C	DNMT3A	c.A2179G	p.N727D	nonsynonymous SNV	0.438	479	Yes	Yes	0.041
OAML153	chr2:25457252	T	C	DNMT3A	c.A2635G	p.N879D	nonsynonymous SNV	0.458	817	Yes	Yes	0.323
OAML250	chr2:25458661	T	C	DNMT3A	c.A2512G	p.N838D	nonsynonymous SNV	0.482	651	Yes	Yes	0.001
OAML087	chr2:25462005	0	-	DNMT3A	c.2391_2402del	p.797_801de	nonframeshift deletion	0.381	916	Yes	Yes	0.028
OAML091	chr2:25462068	A	G	DNMT3A	c.T2339C	p.I780T	nonsynonymous SNV	0.445	758	Yes	Yes	0.087
OAML249	chr2:25463181	C	T	DNMT3A	c.G2312A	p.R771Q	nonsynonymous SNV	0.460	765	Yes	Yes	0.417
OAML285	Chr2:25463195	0	-	DNMT3A	c.2297_2298del	p.K766fs	frameshift deletion	0.344	288	Yes	Yes	0.005
OAML081	chr2:25463214	G	-	DNMT3A	c.2279delC	p.A760fs	frameshift deletion	0.455	1306	Yes	Yes	0.021
OAML095	chr2:25463247	C	T	DNMT3A	c.G2246A	p.R749H	nonsynonymous SNV	0.154	726	Yes	Yes	0.114
OAML094	chr2:25463286	C	T	DNMT3A	c.G2207A	p.R736H	nonsynonymous SNV	0.291	1129	Yes	Yes	0.043
OAML046	chr2:25463291	G	-	DNMT3A	c.2202delC	p.F734fs	frameshift deletion	0.387	856	Yes	Yes	0.412
OAML287	Chr2:25463295	T	C	DNMT3A	c.A2198G	p.E733G	nonsynonymous SNV	0.022	503	Yes	Yes	0.021
OAML221	chr2:25463296	C	G	DNMT3A	c.G2197C	p.E733Q	nonsynonymous SNV	0.043	561	No	.	.
OAML059	chr2:25463297	0	-	DNMT3A	c.2194_2196del	p.732_732de	nonframeshift deletion	0.209	985	Yes	No	0.000
OAML009	chr2:25463300	G	C	DNMT3A	c.C2193G	p.F731L	nonsynonymous SNV	0.432	1080	Yes	Yes	0.004
OAML058	chr2:25463301	A	C	DNMT3A	c.T2192G	p.F731C	nonsynonymous SNV	0.195	850	Yes	Yes	0.032
OAML236	chr2:25463307	C	-	DNMT3A	c.2186delG	p.R729fs	frameshift deletion	0.107	754	Yes	Yes	0.001
OAML013	chr2:25463308	G	C	DNMT3A	c.C2185G	p.R729G	nonsynonymous SNV	0.240	25	Yes	No	0.000
OAML189	chr2:25463524	G	A	DNMT3A	c.C2158T	p.R720C	nonsynonymous SNV	0.812	837	Yes	No	0.000
OAML130	chr2:25463541	G	C	DNMT3A	c.C2141G	p.S714C	nonsynonymous SNV	0.443	1365	Yes	Yes	0.012
OAML170	chr2:25463541	G	C	DNMT3A	c.C2141G	p.S714C	nonsynonymous SNV	0.448	659	No	.	.
OAML313	Chr2:25463541	G	C	DNMT3A	c.C2141G	p.S714C	nonsynonymous SNV	0.201	885	No	.	.
OAML193	chr2:25463583	G	T	DNMT3A	c.C2099A	p.P700Q	nonsynonymous SNV	0.448	565	Yes	Yes	0.001
OAML110	chr2:25463589	C	T	DNMT3A	c.G2093A	p.W698X	stopgain	0.029	715	No	.	.
OAML235	chr2:25463589	C	T	DNMT3A	c.G2093A	p.W698X	stopgain	0.458	716	Yes	Yes	0.007
OAML073	Chr2:25464445	C	A	DNMT3A	c.G2068T	p.V690F	nonsynonymous SNV	0.424	294	Yes	Yes	0.005
OAML094	chr2:25466790	G	C	DNMT3A	c.C1913G	p.S638C	nonsynonymous SNV	0.288	972	Yes	No	0.000
OAML126	chr2:25466800	G	A	DNMT3A	c.C1903T	p.R635W	nonsynonymous SNV	0.027	887	Yes	Yes	0.059
OAML212	chr2:25466800	G	A	DNMT3A	c.C1903T	p.R635W	nonsynonymous SNV	0.350	765	No	.	.
OAML149	chr2:25466833	-	TTA	DNMT3A	c.1869_1870insT	p.P624delins	stopgain	0.452	829	Yes	No	0.000
OAML305	Chr2:25466852	C	T	DNMT3A	c.1396-1G>A		splicing	0.271	787	No	.	.
OAML256	chr2:25467023	C	T	DNMT3A	c.1395+1G>A		splicing	0.031	912	Yes	Yes	0.015
OAML269	chr2:25467133	C	-	DNMT3A	c.1742delG	p.W581X	stopgain	0.079	944	Yes	Yes	0.091
OAML273	chr2:25467137	G	T	DNMT3A	c.C1738A	p.P580T	nonsynonymous SNV	0.454	896	Yes	Yes	0.008
OAML095	chr2:25467190	C	A	DNMT3A	c.G1685T	p.C562F	nonsynonymous SNV	0.152	805	Yes	Yes	0.126
OAML281	Chr2:25467207	C	G	DNMT3A	c.G1668C	p.R556S	nonsynonymous SNV	0.412	434	Yes	Yes	0.008
OAML193	chr2:25467468	G	C	DNMT3A	c.C1608G	p.Y536X	stopgain	0.474	604	Yes	No	0.000
OAML218	chr2:25467497	G	A	DNMT3A	c.C1579T	p.Q527X	stopgain	0.386	738	No	.	.
OAML109	chr2:25467523	T	G	DNMT3A	c.1099-2A>C		splicing	0.333	942	No	.	.
OAML240	chr2:25468135	C	-	DNMT3A	c.1541delG	p.C514fs	frameshift deletion	0.404	730	Yes	Yes	0.236
OAML284	Chr2:25468892	C	A	DNMT3A	c.G1471T	p.E491X	stopgain	0.165	326	Yes	Yes	0.002
OAML223	chr2:25469525	G	A	DNMT3A	c.C1243T	p.Q415X	stopgain	0.071	574	No	.	.
OAML225	chr2:25469630	C	G	DNMT3A	c.G1138C	p.A380P	nonsynonymous SNV	0.076	630	No	.	.
OAML080	Chr2:25469974	C	-	DNMT3A	c.1068delG	p.Q356fs	frameshift deletion	0.387	1011	Yes	Yes	0.089
OAML056	chr2:25470464	G	T	DNMT3A	c.C1010A	p.S337X	stopgain	0.432	853	Yes	Yes	0.043
OAML140	chr2:25470494	C	T	DNMT3A	c.G980A	p.W327X	stopgain	0.462	1018	No	.	.
OAML255	chr2:25470497	C	T	DNMT3A	c.G977A	p.R326H	nonsynonymous SNV	0.447	1002	Yes	No	0.000
OAML282	Chr2:25470498	G	A	DNMT3A	c.C976T	p.R326C	nonsynonymous SNV	0.314	529	Yes	Yes	0.343
OAML130	chr2:25470516	G	A	DNMT3A	c.C958T	p.R320X	stopgain	0.423	1567	Yes	Yes	0.197
OAML016	chr2:25470557	C	T	DNMT3A	c.G917A	p.W306X	stopgain	0.328	988	Yes	No	0.000
OAML293	Chr2:25470590	A	G	DNMT3A	c.T884C	p.L295P	nonsynonymous SNV	0.957	936	No	.	.
OAML089	chr2:25471016	G	A	DNMT3A	c.C745T	p.Q249X	stopgain	0.238	555	Yes	No	0.000
OAML007	chr22:41545974	T	-	EP300	c.2589delT	p.V863fs	frameshift deletion	0.427	1048	Yes	Yes	0.003
OAML256	chr12:22811995	A	G	ETNK1	c.A731G	p.N244S	nonsynonymous SNV	0.024	663	Yes	Yes	0.016
OAML017	chr12:22811996	T	A	ETNK1	c.T732A	p.N244K	nonsynonymous SNV	0.335	511	Yes	Yes	0.307
OAML178	chr12:11992213	C	-	ETV6	c.303delC	p.D101fs	frameshift deletion	0.022	676	No	.	.
OAML305	Chr12:12022360	-	GG	ETV6	c.466_467insGG	p.N156fs	frameshift insertion	0.071	600	No	.	.
OAML027	chr12:12022362	0	-	ETV6	c.468_469del	p.N156fs	frameshift deletion	0.030	370	Yes	Yes	0.044
OAML178	chr12:12037406	A	G	ETV6	c.A1037G	p.Y346C	nonsynonymous SNV	0.030	564	No	.	.
OAML039	chr12:12038909	A	T	ETV6	c.A1202T	p.Y401F	nonsynonymous SNV	0.034	640	Yes	No	0.000
OAML157	chr7:148506443	C	T	EZH2	c.G2069A	p.R690H	nonsynonymous SNV	0.021	616	Yes	No	0.000
OAML057	chr7:148506477	C	T	EZH2	c.G2035A	p.V679M	nonsynonymous SNV	0.774	464	Yes	No	0.000
OAML121	chr7:148506477	C	T	EZH2	c.G2035A	p.V679M	nonsynonymous SNV	0.472	470	Yes	Yes	0.092
OAML277	chr7:148507446	A	G	EZH2	c.T2008C	p.F670L	nonsynonymous SNV	0.439	528	Yes	No	0.000
OAML136	chr7:148507448	C	G	EZH2	c.G2006C	p.S669T	nonsynonymous SNV	0.046	525	Yes	No	0.000
OAML120	chr7:148507449	T	C	EZH2	c.A2005G	p.S669G	nonsynonymous SNV	0.314	522	Yes	Yes	0.541
OAML130	chr7:148507464	-	AT	EZH2	c.1989_1990insA	p.D664fs	frameshift insertion	0.750	344	Yes	Yes	0.010
OAML207	chr7:148512087	G	-	EZH2	c.1591delC	p.P531fs	frameshift deletion	0.067	450	No	.	.
OAML077	Chr7:148512123	A	G	EZH2	c.T1555C	p.S519P	nonsynonymous SNV	0.478	345	Yes	Yes	0.464
OAML113	chr7:148514992	0	-	EZH2	c.1213_1217del	p.K405fs	frameshift deletion	0.139	642	Yes	No	0.000
OAML178	chr7:148523560	C	T	EZH2	c.892+1G>A		exonic;splicing	0.362	519	No	.	.
OAML065	chr7:148523666	-	G	EZH2	c.786dupC	p.N263fs	frameshift insertion	0.041	1075	Yes	No	0.000
OAML203	chr7:148525838	G	A	EZH2	c.C619T	p.R207X	stopgain	0.455	609	No	.	.
OAML287	Chr7:148526869	G	-	EZH2	c.435delC	p.F145fs	frameshift deletion	0.110	118	Yes	No	0.000

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML134	chr7:148543649	C	-	EZH2	c.159delG	p.T53fs	frameshift deletion	0.198	367	Yes	Yes	0.028
OAML224	chr13:28592622	G	T	FLT3	c.C2523A	p.N841K	nonsynonymous SNV	0.231	485	No	.	.
OAML077	Chr13:28592629	T	C	FLT3	c.A2516G	p.D839G	nonsynonymous SNV	0.117	657	Yes	No	0.000
OAML281	Chr13:28592640	A	T	FLT3	c.T2505A	p.D835E	nonsynonymous SNV	0.039	279	Yes	No	0.000
OAML224	chr13:28592641	T	A	FLT3	c.A2504T	p.D835V	nonsynonymous SNV	0.044	522	No	.	.
OAML022	chr13:28592642	C	A	FLT3	c.G2503T	p.D835Y	nonsynonymous SNV	0.108	953	Yes	Yes	0.002
OAML176	chr13:28592642	C	A	FLT3	c.G2503T	p.D835Y	nonsynonymous SNV	0.023	788	No	.	.
OAML179	chr13:28592642	C	G	FLT3	c.G2503C	p.D835H	nonsynonymous SNV	0.095	601	Yes	No	0.000
OAML185	chr13:28592642	C	A	FLT3	c.G2503T	p.D835Y	nonsynonymous SNV	0.449	506	No	.	.
OAML225	chr13:28592642	C	A	FLT3	c.G2503T	p.D835Y	nonsynonymous SNV	0.060	550	No	.	.
OAML236	chr13:28592642	C	T	FLT3	c.G2503A	p.D835N	nonsynonymous SNV	0.056	604	Yes	No	0.000
OAML308	Chr13:28592642	C	A	FLT3	c.G2503T	p.D835Y	nonsynonymous SNV	0.293	837	No	.	.
OAML259	chr13:28602329	G	A	FLT3	c.C2039T	p.A680V	nonsynonymous SNV	0.437	670	Yes	No	0.000
OAML056	chr13:28602340	G	T	FLT3	c.C2028A	p.N676K	nonsynonymous SNV	0.021	806	Yes	Yes	0.001
OAML057	chr13:28602340	G	C	FLT3	c.C2028G	p.N676K	nonsynonymous SNV	0.187	886	Yes	No	0.000
OAML281	Chr13:28608281	A	G	FLT3	c.T1775C	p.V592A	nonsynonymous SNV	0.063	111	Yes	No	0.000
OAML180	chr13:28608285	A	C	FLT3	c.T1771G	p.Y591D	nonsynonymous SNV	0.330	318	No	.	.
OAML080	Chr13:28608332	T	C	FLT3	c.A1724G	p.Q575R	nonsynonymous SNV	0.289	322	Yes	No	0.000
OAML176	chr13:28608341	T	C	FLT3	c.A1715G	p.Y572C	nonsynonymous SNV	0.053	359	No	.	.
OAML006	chr13	.	.	FLT3_ITD	c.1837+83_1837	not_exonic	ITD	0.001	.	Yes	No	0.000
OAML012	chr13	.	.	FLT3_ITD	c.1804_1805ins	p.L601_K602	ITD	0.403	.	Yes	No	0.000
OAML018	chr13	.	.	FLT3_ITD	c.1814_1815ins	p.F605_P60	ITD	0.112	.	Yes	Yes	0.003
OAML018	chr13	.	.	FLT3_ITD	c.1735_1839dup	p.579_613du	ITD	0.155	.	Yes	No	0.000
OAML020	chr13	.	.	FLT3_ITD	c.1775_1801dup	p.593_601du	ITD	0.031	.	Yes	No	0.000
OAML020	chr13	.	.	FLT3_ITD	c.1743_1793dup	p.582_598du	ITD	0.050	.	Yes	No	0.000
OAML022	chr13	.	.	FLT3_ITD	c.1787_1788ins	p.E596_Y59	ITD	0.044	.	Yes	No	0.000
OAML023	chr13	.	.	FLT3_ITD	c.1837_1837+1in	p.F612_G61	ITD	0.219	.	Yes	No	0.000
OAML028	chr13	.	.	FLT3_ITD	c.1747_1837+2d	p.582_583ins	ITD	0.337	.	Yes	No	0.000
OAML031	chr13	.	.	FLT3_ITD	c.1784_1837dup	p.596_613du	ITD	0.013	.	Yes	No	0.000
OAML037	chr13	.	.	FLT3_ITD	c.1770_1793dup	p.597_598ins	ITD	0.172	.	Yes	No	0.000
OAML048	chr13	.	.	FLT3_ITD	c.1771_1788dup	p.591_596du	ITD	0.012	.	Yes	No	0.000
OAML056	chr13	.	.	FLT3_ITD	c.1784_1785ins	p.R595_E59	ITD	0.042	.	Yes	No	0.000
OAML067	chr13	.	.	FLT3_ITD	c.1793_1794ins	p.E598_Y59	ITD	0.257	.	Yes	No	0.000
OAML073	chr13	.	.	FLT3_ITD	c.1748_1795dup	p.598_599ins	ITD	0.124	.	Yes	No	0.000
OAML085	chr13	.	.	FLT3_ITD	c.1786_1787ins	p.R595_E59	ITD	0.140	.	Yes	No	0.000
OAML085	chr13	.	.	FLT3_ITD	c.1742_1780dup	p.593_594ins	ITD	0.372	.	Yes	No	0.000
OAML087	chr13	.	.	FLT3_ITD	c.1756_1837+2d	p.585_586ins	ITD	0.031	.	Yes	No	0.000
OAML087	chr13	.	.	FLT3_ITD	c.1749_1838dup	p.584_613du	ITD	0.480	.	Yes	No	0.000
OAML091	chr13	.	.	FLT3_ITD	c.1781_1804dup	p.601_602ins	ITD	0.187	.	Yes	Yes	0.008
OAML093	chr13	.	.	FLT3_ITD	c.1777_1800dup	p.V592_D59	ITD	0.361	.	Yes	No	0.000
OAML097	chr13	.	.	FLT3_ITD	c.1772_1837dup	p.612_613ins	ITD	0.270	.	Yes	No	0.000
OAML115	chr13	.	.	FLT3_ITD	c.1792_1809dup	p.598_603du	ITD	0.453	.	No	.	.
OAML124	chr13	.	.	FLT3_ITD	c.1787_1804dup	p.597_602du	ITD	0.045	.	Yes	No	0.000
OAML141	chr13	.	.	FLT3_ITD	c.1747_1837+2d	p.582_583ins	ITD	0.032	.	No	.	.
OAML141	chr13	.	.	FLT3_ITD	c.1744_1803dup	p.582_601du	ITD	0.174	.	No	.	.
OAML141	chr13	.	.	FLT3_ITD	c.1781_1801dup	p.595_601du	ITD	0.426	.	No	.	.
OAML141	chr13	.	.	FLT3_ITD	c.1747_1837+2d	p.582_583ins	ITD	0.032	.	No	.	.
OAML141	chr13	.	.	FLT3_ITD	c.1744_1803dup	p.582_601du	ITD	0.174	.	No	.	.
OAML141	chr13	.	.	FLT3_ITD	c.1781_1801dup	p.595_601du	ITD	0.426	.	No	.	.
OAML152	chr13	.	.	FLT3_ITD	c.1834_1835ins	p.E611_F61	ITD	0.026	.	Yes	No	0.000
OAML152	chr13	.	.	FLT3_ITD	c.1787_1788ins	p.E596_Y59	ITD	0.067	.	Yes	No	0.000
OAML153	chr13	.	.	FLT3_ITD	c.1790_1791ins	p.Y597_E59	ITD	0.440	.	Yes	No	0.000
OAML159	chr13	.	.	FLT3_ITD	c.1828_1829ins	p.N609_L61	ITD	0.003	.	Yes	No	0.000
OAML159	chr13	.	.	FLT3_ITD	c.1837+3_1837+	not_exonic	ITD	0.010	.	Yes	No	0.000
OAML159	chr13	.	.	FLT3_ITD	c.1787_1788ins	p.E596_Y59	ITD	0.010	.	Yes	No	0.000
OAML159	chr13	.	.	FLT3_ITD	c.1837+88_1837	not_exonic	ITD	0.011	.	Yes	No	0.000
OAML159	chr13	.	.	FLT3_ITD	c.1812_1813ins	p.E604_F60	ITD	0.109	.	Yes	No	0.000
OAML164	chr13	.	.	FLT3_ITD	c.1766_1801dup	p.600_601ins	ITD	0.024	.	No	.	.
OAML166	chr13	.	.	FLT3_ITD	c.1770_1811dup	p.603_604ins	ITD	0.681	.	No	.	.
OAML170	chr13	.	.	FLT3_ITD	c.1837+4_1837+	not_exonic	ITD	0.185	.	No	.	.
OAML170	chr13	.	.	FLT3_ITD	c.1801_1802ins	p.D600_L601	ITD	0.717	.	No	.	.
OAML171	chr13	.	.	FLT3_ITD	c.1756_1836dup	p.S585_D58	ITD	0.388	.	No	.	.
OAML172	chr13	.	.	FLT3_ITD	c.1759_1824dup	p.587_608du	ITD	0.372	.	No	.	.
OAML177	chr13	.	.	FLT3_ITD	c.1786_1809dup	p.596_603du	ITD	0.009	.	No	.	.
OAML177	chr13	.	.	FLT3_ITD	c.1770_1811dup	p.603_604ins	ITD	0.292	.	No	.	.
OAML183	chr13	.	.	FLT3_ITD	c.1791_1871dup	p.598_624du	ITD	0.177	.	No	.	.
OAML184	chr13	.	.	FLT3_ITD	c.1772_1819dup	p.606_607ins	ITD	0.270	.	No	.	.
OAML187	chr13	.	.	FLT3_ITD	c.1837_1837+1in	p.F612_G61	ITD	0.015	.	No	.	.
OAML187	chr13	.	.	FLT3_ITD	c.1780_1806dup	p.594_602du	ITD	0.339	.	No	.	.
OAML189	chr13	.	.	FLT3_ITD	c.1714_1803dup	p.572_601du	ITD	0.098	.	Yes	No	0.000
OAML189	chr13	.	.	FLT3_ITD	c.1776_1790dup	p.593_597du	ITD	0.283	.	Yes	No	0.000
OAML191	chr13	.	.	FLT3_ITD	c.1789_1812dup	p.597_604du	ITD	0.436	.	No	.	.
OAML193	chr13	.	.	FLT3_ITD	c.1746_1781dup	p.583_594du	ITD	0.321	.	Yes	No	0.000
OAML197	chr13	.	.	FLT3_ITD	c.1743_1793dup	p.V581_T58	ITD	0.028	.	No	.	.
OAML202	chr13	.	.	FLT3_ITD	c.1798_1821dup	p.600_607du	ITD	0.019	.	No	.	.

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML202	chr13	.	.	FLT3_ITD	c.1837+4_1837+	not_exonic	ITD	0.031	.	No	.	.
OAML209	chr13	.	.	FLT3_ITD	c.1778_1825dup	p.594_609du	ITD	0.103	.	No	.	.
OAML211	chr13	.	.	FLT3_ITD	c.1747_1785dup	p.583_595du	ITD	0.374	.	No	.	.
OAML214	chr13	.	.	FLT3_ITD	c.1745_1789dup	p.596_597ins	ITD	0.399	.	No	.	.
OAML223	chr13	.	.	FLT3_ITD	c.1790_1791ins	p.Y597_E59	ITD	0.003	.	No	.	.
OAML224	chr13	.	.	FLT3_ITD	c.1733_1768dup	p.589_590ins	ITD	0.057	.	No	.	.
OAML233	chr13	.	.	FLT3_ITD	c.1797_1798insT	p.Y599_D60	ITD	0.326	.	Yes	Yes	0.036
OAML233	chr13	.	.	FLT3_ITD	c.1798_1830dup	p.600_610du	ITD	0.017	.	Yes	No	0.000
OAML233	chr13	.	.	FLT3_ITD	c.1770_1796dup	p.F590_Y591	ITD	0.032	.	Yes	No	0.000
OAML233	chr13	.	.	FLT3_ITD	c.1793_1794ins	p.Y597_E59	ITD	0.164	.	Yes	No	0.000
OAML234	chr13	.	.	FLT3_ITD	c.1734_1793dup	p.579_598du	ITD	0.025	.	Yes	No	0.000
OAML235	chr13	.	.	FLT3_ITD	c.1772_1786dup	p.595_596ins	ITD	0.384	.	Yes	No	0.000
OAML242	chr13	.	.	FLT3_ITD	c.1772_1786dup	p.595_596ins	ITD	0.006	.	Yes	No	0.000
OAML243	chr13	.	.	FLT3_ITD	c.1775_1795dup	p.598_599ins	ITD	0.005	.	Yes	Yes	0.001
OAML243	chr13	.	.	FLT3_ITD	c.1791_1835dup	p.598_612du	ITD	0.153	.	Yes	Yes	0.014
OAML243	chr13	.	.	FLT3_ITD	c.1784_1810dup	p.R595_E59	ITD	0.331	.	Yes	Yes	0.096
OAML245	chr13	.	.	FLT3_ITD	c.1820_1821ins	p.R607_E60	ITD	0.565	.	Yes	No	0.000
OAML255	chr13	.	.	FLT3_ITD	c.1757_1804dup	p.601_602ins	ITD	0.260	.	Yes	Yes	0.000
OAML260	chr13	.	.	FLT3_ITD	c.1772_1795dup	p.Y591_V59	ITD	0.363	.	Yes	No	0.000
OAML261	chr13	.	.	FLT3_ITD	c.1781_1801dup	p.595_601du	ITD	0.340	.	Yes	Yes	0.001
OAML262	chr13	.	.	FLT3_ITD	c.1800_1801ins	p.D600_L601	ITD	0.026	.	Yes	No	0.000
OAML262	chr13	.	.	FLT3_ITD	c.1824_1825ins	p.E608_N60	ITD	0.496	.	Yes	No	0.000
OAML268	chr13	.	.	FLT3_ITD	c.1778_1795dup	p.594_599du	ITD	0.119	.	Yes	No	0.000
OAML270	chr13	.	.	FLT3_ITD	c.1810_1811insT	p.W603_E60	ITD	0.382	.	Yes	Yes	0.153
OAML270	chr13	.	.	FLT3_ITD	c.1774_1794dup	p.Y591_V59	ITD	0.068	.	Yes	No	0.000
OAML273	chr13	.	.	FLT3_ITD	c.1776_1790dup	p.593_597du	ITD	0.075	.	Yes	No	0.000
OAML273	chr13	.	.	FLT3_ITD	c.1756_1794dup	p.S585_D58	ITD	0.501	.	Yes	No	0.000
OAML276	chr13	.	.	FLT3_ITD	c.1795_1837+2d	p.598_599ins	ITD	0.453	.	Yes	Yes	0.004
OAML278	chr13	.	.	FLT3_ITD	c.1837+2_1837+	not_exonic	ITD	0.488	.	Yes	Yes	0.001
OAML281	chr13	.	.	FLT3_ITD	c.1800_1801insT	p.D600_L601	ITD	0.121	.	Yes	No	0.000
OAML308	chr13	.	.	FLT3_ITD	c.1750_1800dup	p.584_600du	ITD	0.018	.	No	.	.
OAML308	chr13	.	.	FLT3_ITD	c.1770_1793dup	p.597_598ins	ITD	0.124	.	No	.	.
OAML321	chr13	.	.	FLT3_ITD	c.1776_1799dup	p.593_600du	ITD	0.011	.	No	.	.
OAML321	chr13	.	.	FLT3_ITD	c.1756_1797dup	p.586_599du	ITD	0.021	.	No	.	.
OAML326	chr13	.	.	FLT3_ITD	c.1815_1816ins	p.F605_P60	ITD	0.354	.	No	.	.
OAML267	chr3:128200139	0	-	GATA2	c.1161_1166del	p.387_389de	nonframeshift deletion	0.405	759	Yes	No	0.000
OAML173	chr3:128200699	-	CAG	GATA2	c.1105_1106ins	p.V369delins	nonframeshift insertion	0.327	530	No	.	.
OAML309	Chr3:128200729	A	G	GATA2	c.T1076C	p.L359S	nonsynonymous SNV	0.309	846	No	.	.
OAML192	chr3:128200744	G	A	GATA2	c.C1061T	p.T354M	nonsynonymous SNV	0.444	579	Yes	No	0.000
OAML078	chr3:128202731	C	T	GATA2	c.G989A	p.R330Q	nonsynonymous SNV	0.027	954	Yes	No	0.000
OAML267	chr3:128202731	C	A	GATA2	c.G989T	p.R330L	nonsynonymous SNV	0.461	1040	Yes	No	0.000
OAML021	chr3:128202758	A	G	GATA2	c.T962C	p.L321P	nonsynonymous SNV	0.427	1147	Yes	No	0.000
OAML183	chr3:128202761	C	T	GATA2	c.G959A	p.G320D	nonsynonymous SNV	0.205	819	No	.	.
OAML201	chr3:128202762	C	G	GATA2	c.G958C	p.G320R	nonsynonymous SNV	0.146	1087	No	.	.
OAML162	chr3:128202767	G	A	GATA2	c.C953T	p.A318V	nonsynonymous SNV	0.234	1112	Yes	No	0.000
OAML180	chr3:128202813	-	CCC	GATA2	c.906_907insGG	p.T303delins	nonframeshift insertion	0.101	698	No	.	.
OAML192	chr3:128202829	G	T	GATA2	c.C891A	p.N297K	nonsynonymous SNV	0.050	766	Yes	No	0.000
OAML274	chr3:128204604	0	-	GATA2	c.833_837del	p.F278fs	frameshift deletion	0.318	701	Yes	Yes	0.140
OAML198	chr3:128204841	-	C	GATA2	c.599dupG	p.G200fs	frameshift insertion	0.041	507	Yes	Yes	0.045
OAML073	Chr3:128205212	C	A	GATA2	c.230-1G>T		splicing	0.022	222	Yes	No	0.000
OAML216	chr1:1747229	T	C	GNB1	c.A169G	p.K57E	nonsynonymous SNV	0.052	749	No	.	.
OAML277	chr1:1747229	T	C	GNB1	c.A169G	p.K57E	nonsynonymous SNV	0.418	878	Yes	Yes	0.022
OAML010	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.315	520	Yes	Yes	0.001
OAML012	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.439	515	Yes	No	0.000
OAML016	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.317	555	Yes	No	0.000
OAML077	Chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.489	581	Yes	Yes	0.001
OAML080	Chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.074	582	Yes	No	0.000
OAML130	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.443	880	Yes	Yes	0.007
OAML214	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.410	613	No	.	.
OAML221	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.195	339	No	.	.
OAML252	chr2:209113112	C	T	IDH1	c.G395A	p.R132H	nonsynonymous SNV	0.442	556	Yes	No	0.000
OAML020	chr2:209113113	G	C	IDH1	c.C394G	p.R132G	nonsynonymous SNV	0.405	582	Yes	Yes	0.001
OAML027	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.059	387	Yes	Yes	0.011
OAML030	Chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.346	327	No	.	.
OAML033	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.456	680	Yes	Yes	0.350
OAML040	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.414	536	Yes	Yes	0.003
OAML051	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.383	723	Yes	No	0.000
OAML064	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.192	617	Yes	Yes	0.003
OAML088	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.105	523	Yes	No	0.000
OAML089	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.229	446	Yes	No	0.000
OAML095	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.036	494	Yes	No	0.000
OAML109	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.317	675	No	.	.
OAML136	chr2:209113113	G	C	IDH1	c.C394G	p.R132G	nonsynonymous SNV	0.457	593	Yes	Yes	0.349
OAML142	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.371	498	No	.	.
OAML146	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.372	568	Yes	Yes	0.002

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML155	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.450	716	Yes	No	0.000
OAML156	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.344	361	Yes	No	0.000
OAML175	chr2:209113113	G	T	IDH1	c.C394A	p.R132S	nonsynonymous SNV	0.312	426	No	.	.
OAML186	chr2:209113113	G	C	IDH1	c.C394G	p.R132G	nonsynonymous SNV	0.449	304	No	.	.
OAML201	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.467	610	No	.	.
OAML210	chr2:209113113	G	T	IDH1	c.C394A	p.R132S	nonsynonymous SNV	0.233	430	No	.	.
OAML218	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.384	438	No	.	.
OAML250	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.413	472	Yes	No	0.000
OAML256	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.388	533	Yes	Yes	0.017
OAML266	chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.410	520	Yes	Yes	0.001
OAML303	Chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.313	683	No	.	.
OAML305	Chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.282	642	No	.	.
OAML316	Chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.295	898	Yes	No	0.000
OAML327	Chr2:209113113	G	A	IDH1	c.C394T	p.R132C	nonsynonymous SNV	0.339	386	No	.	.
OAML139	chr15:90631837	C	A	IDH2	c.G516T	p.R172S	nonsynonymous SNV	0.328	913	Yes	No	0.000
OAML049	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.440	591	Yes	No	0.000
OAML053	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.452	923	Yes	No	0.000
OAML060	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.052	1048	Yes	No	0.000
OAML063	Chr15:90631838	C	T	IDH2	c.G359A	p.R120K	nonsynonymous SNV	0.452	334	Yes	No	0.000
OAML094	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.325	1355	Yes	No	0.000
OAML128	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.394	1115	Yes	No	0.000
OAML140	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.626	999	No	.	.
OAML149	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.483	1040	Yes	No	0.000
OAML178	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.297	740	No	.	.
OAML199	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.147	482	Yes	No	0.000
OAML204	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.114	862	Yes	Yes	0.186
OAML236	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.100	821	Yes	Yes	0.003
OAML240	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.423	1009	Yes	No	0.000
OAML247	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.296	899	Yes	No	0.000
OAML269	chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.051	906	Yes	Yes	0.105
OAML284	Chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.127	574	Yes	No	0.000
OAML293	Chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.466	874	No	.	.
OAML301	Chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.170	970	No	.	.
OAML313	Chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.175	950	No	.	.
OAML322	Chr15:90631838	C	T	IDH2	c.G515A	p.R172K	nonsynonymous SNV	0.247	1132	No	.	.
OAML006	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.151	819	Yes	No	0.000
OAML035	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.327	728	Yes	Yes	0.003
OAML056	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.457	972	Yes	No	0.000
OAML068	Chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.459	289	Yes	Yes	0.390
OAML087	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.461	1190	Yes	Yes	0.168
OAML091	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.405	951	Yes	Yes	0.044
OAML102	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.458	1038	No	.	.
OAML106	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.085	963	Yes	No	0.000
OAML107	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.039	830	No	.	.
OAML124	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.430	1017	Yes	No	0.000
OAML133	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.427	1154	Yes	Yes	0.005
OAML143	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.481	867	No	.	.
OAML145	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.242	1009	Yes	Yes	0.019
OAML169	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.452	602	No	.	.
OAML180	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.461	692	No	.	.
OAML184	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.453	669	No	.	.
OAML188	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.496	869	No	.	.
OAML190	Chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.353	754	No	.	.
OAML195	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.503	561	Yes	Yes	0.262
OAML202	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.405	252	No	.	.
OAML209	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.438	954	No	.	.
OAML230	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.373	785	Yes	No	0.000
OAML241	chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.391	895	Yes	Yes	0.001
OAML308	Chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.186	981	No	.	.
OAML321	Chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.462	940	No	.	.
OAML325	Chr15:90631934	C	T	IDH2	c.G419A	p.R140Q	nonsynonymous SNV	0.488	685	No	.	.
OAML231	chr15:90631935	G	A	IDH2	c.C418T	p.R140W	nonsynonymous SNV	0.462	937	Yes	Yes	0.003
OAML192	chr7:50367281	-	CG	IKZF1	c.88_89insCG	p.P30fs	frameshift insertion	0.046	541	Yes	No	0.000
OAML015	chr7:50444401	C	T	IKZF1	c.C331T	p.R111X	stopgain	0.084	622	Yes	No	0.000
OAML316	Chr7:50450274	-	T	IKZF1	c.197_198insT	p.S66fs	frameshift insertion	0.023	736	Yes	No	0.000
OAML106	chr7:50459492	T	-	IKZF1	c.394delT	p.S132fs	frameshift deletion	0.051	472	Yes	No	0.000
OAML138	chr9:5070035	0	-	JAK2	c.1624_1629del	p.542_543de	nonframeshift deletion	0.076	503	Yes	No	0.000
OAML030	Chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.288	132	No	.	.
OAML074	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.105	545	No	.	.
OAML136	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.947	527	Yes	Yes	0.496
OAML143	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.025	511	No	.	.
OAML239	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.534	354	Yes	No	0.000
OAML241	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.032	594	Yes	Yes	0.430
OAML251	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.399	544	Yes	Yes	0.009
OAML254	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.405	618	Yes	Yes	0.323

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML272	chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.115	479	Yes	No	0.000
OAML327	Chr9:5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.577	201	No	.	.
OAML251	chr9:5078360	A	G	JAK2	c.A2047G	p.R683G	nonsynonymous SNV	0.392	526	Yes	No	0.000
OAML328	Chr12:122018732	0	-	KDM2B	c.84_85del	p.T28fs	frameshift deletion	0.460	284	No	.	.
OAML073	Chr12:394759	C	A	KDM5A	c.G4936T	p.E1646X	stopgain	0.022	228	Yes	No	0.000
OAML073	Chr12:404813	C	A	KDM5A	c.G4381T	p.E1461X	stopgain	0.021	333	Yes	No	0.000
OAML044	chrX:44922973	C	T	KDM6A	c.C1699T	p.R567X	stopgain	0.056	588	Yes	No	0.000
OAML190	ChrX:44935941	G	C	KDM6A	c.2466-1G>C		splicing	0.132	167	No	.	.
OAML087	chrX:44942731	-	TA	KDM6A	c.3176_3177insT	p.T1059fs	frameshift insertion	0.064	817	Yes	No	0.000
OAML020	chrX:44949176	G	A	KDM6A	c.3499+1G>A		splicing	0.072	334	Yes	No	0.000
OAML222	chrX:44966736	-	GGG	KDM6A	c.3825_3826ins	p.H1275fs	frameshift insertion	0.516	278	No	.	.
OAML222	chr4:55599340	T	A	KIT	c.T2466A	p.N822K	nonsynonymous SNV	0.351	662	No	.	.
OAML005	chr12:25378561	G	A	KRAS	c.C437T	p.A146V	nonsynonymous SNV	0.043	588	Yes	No	0.000
OAML229	chr12:25378562	C	T	KRAS	c.G436A	p.A146T	nonsynonymous SNV	0.314	486	Yes	Yes	0.001
OAML116	chr12:25378648	T	C	KRAS	c.A350G	p.K117R	nonsynonymous SNV	0.531	842	Yes	Yes	0.069
OAML281	Chr12:25380282	G	C	KRAS	c.C176G	p.A59G	nonsynonymous SNV	0.115	270	Yes	No	0.000
OAML229	chr12:25380285	G	A	KRAS	c.C173T	p.T58I	nonsynonymous SNV	0.089	673	Yes	No	0.000
OAML005	chr12:25398281	C	T	KRAS	c.G38A	p.G13D	nonsynonymous SNV	0.034	645	Yes	No	0.000
OAML036	chr12:25398281	C	T	KRAS	c.G38A	p.G13D	nonsynonymous SNV	0.038	731	Yes	No	0.000
OAML179	chr12:25398281	C	T	KRAS	c.G38A	p.G13D	nonsynonymous SNV	0.093	486	Yes	No	0.000
OAML215	chr12:25398281	C	T	KRAS	c.G38A	p.G13D	nonsynonymous SNV	0.304	648	No	.	.
OAML234	chr12:25398281	C	T	KRAS	c.G38A	p.G13D	nonsynonymous SNV	0.056	656	Yes	No	0.000
OAML267	chr12:25398282	C	A	KRAS	c.G37T	p.G13C	nonsynonymous SNV	0.039	668	Yes	No	0.000
OAML005	chr12:25398284	C	A	KRAS	c.G35T	p.G12V	nonsynonymous SNV	0.028	635	Yes	No	0.000
OAML066	chr12:25398284	C	T	KRAS	c.G35A	p.G12D	nonsynonymous SNV	0.038	871	Yes	No	0.000
OAML108	chr12:25398284	C	T	KRAS	c.G35A	p.G12D	nonsynonymous SNV	0.024	783	No	.	.
OAML117	chr12:25398284	C	T	KRAS	c.G35A	p.G12D	nonsynonymous SNV	0.359	785	Yes	Yes	0.001
OAML197	chr12:25398284	C	G	KRAS	c.G35C	p.G12A	nonsynonymous SNV	0.116	778	No	.	.
OAML234	chr12:25398284	C	G	KRAS	c.G35C	p.G12A	nonsynonymous SNV	0.054	653	Yes	No	0.000
OAML242	chr12:25398284	C	A	KRAS	c.G35T	p.G12V	nonsynonymous SNV	0.353	627	Yes	No	0.000
OAML246	chr12:25398284	C	T	KRAS	c.G35A	p.G12D	nonsynonymous SNV	0.178	667	Yes	No	0.000
OAML280	chr12:25398284	C	A	KRAS	c.G35T	p.G12V	nonsynonymous SNV	0.048	670	Yes	No	0.000
OAML285	Chr12:25398284	C	T	KRAS	c.G35A	p.G12D	nonsynonymous SNV	0.268	164	Yes	No	0.000
OAML001	chr12:25398285	C	T	KRAS	c.G34A	p.G12S	nonsynonymous SNV	0.089	606	Yes	No	0.000
OAML007	chr12:25398285	C	T	KRAS	c.G34A	p.G12S	nonsynonymous SNV	0.026	725	Yes	No	0.000
OAML274	chr12:25398285	C	A	KRAS	c.G34T	p.G12C	nonsynonymous SNV	0.277	602	Yes	Yes	0.042
OAML023	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML044	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML049	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML087	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML119	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML124	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML139	chr11	.	.	MLL	PTD			.	.	Yes	No	0.000
OAML189	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML194	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML241	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML252	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML280	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML282	chr11	.	.	MLL	PTD			.	.	Yes	.	.
OAML184	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML188	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML190	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML201	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML202	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML228	#N/A	.	.	MLL	PTD			.	.	No	.	.
OAML143	chr1:43815009	G	T	MPL	c.G1544T	p.W515L	nonsynonymous SNV	0.116	727	No	.	.
OAML325	Chr1:43815009	G	T	MPL	c.G1544T	p.W515L	nonsynonymous SNV	0.037	485	No	.	.
OAML196	chr8:128750684	C	T	MYC	c.C221T	p.P74L	nonsynonymous SNV	0.411	718	Yes	No	0.000
OAML224	chr8:128750684	C	A	MYC	c.C221A	p.P74Q	nonsynonymous SNV	0.439	691	No	.	.
OAML234	chr8:128750684	C	A	MYC	c.C221A	p.P74Q	nonsynonymous SNV	0.343	1060	Yes	No	0.000
OAML090	chr17:29490349	T	-	NF1	c.434delT	p.L145fs	frameshift deletion	0.020	697	Yes	No	0.000
OAML046	chr17:29550586	G	A	NF1	c.1845+1G>A		splicing	0.343	286	Yes	No	0.000
OAML024	chr17:29553477	-	C	NF1	c.2027dupC	p.T676fs	frameshift insertion	0.413	854	No	.	.
OAML024	chr17:29553477	-	C	NF1	c.2027dupC	p.T676fs	frameshift insertion	0.413	854	No	.	.
OAML131	chr17:29553477	-	C	NF1	c.2027dupC	p.T676fs	frameshift insertion	0.302	537	Yes	Yes	0.126
OAML280	chr17:29553477	-	C	NF1	c.2027dupC	p.T676fs	frameshift insertion	0.475	721	Yes	Yes	0.317
OAML309	Chr17:29553477	-	C	NF1	c.2027dupC	p.T676fs	frameshift insertion	0.045	673	No	.	.
OAML018	chr17:29664534	-	GA	NF1	c.6513_6514ins	p.Y2171fs	frameshift insertion	0.029	747	Yes	Yes	0.004
OAML018	chr17:29667527	-	CCT	NF1	c.6863_6864ins	p.S2288fs	frameshift insertion	0.022	740	Yes	Yes	0.001
OAML130	chr17:29684326	C	T	NF1	c.C7846T	p.R2616X	stopgain	0.422	1169	Yes	Yes	0.012
OAML277	chr12:54686301	-	CA	NFE2	c.978_979insTG	p.T327_E32	stopgain	0.360	1126	Yes	No	0.000
OAML276	chr12:54686452	-	T	NFE2	c.827dupA	p.N276fs	frameshift insertion	0.420	744	Yes	No	0.000
OAML021	chr12:54686458	G	-	NFE2	c.822delC	p.G274fs	frameshift deletion	0.100	1215	Yes	No	0.000
OAML013	chr12:54686491	C	-	NFE2	c.789delG	p.Q263fs	frameshift deletion	0.250	24	Yes	No	0.000
OAML021	chr12:54686618	-	C	NFE2	c.661dupG	p.E221fs	frameshift insertion	0.156	1329	Yes	No	0.000

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML056	chr12:54688917	A	C	NFE2	c.114+2T>G		splicing	0.425	749	Yes	No	0.000
OAML006	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.096	271	Yes	No	0.000
OAML010	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.216	190	Yes	No	0.000
OAML012	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.332	215	Yes	No	0.000
OAML016	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.205	244	Yes	No	0.000
OAML020	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.251	177	Yes	No	0.000
OAML027	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.094	201	Yes	Yes	0.003
OAML031	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.287	167	Yes	No	0.000
OAML033	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.211	203	Yes	No	0.000
OAML037	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.223	154	Yes	No	0.000
OAML040	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.281	202	Yes	No	0.000
OAML048	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.243	140	Yes	No	0.000
OAML072	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.211	108	Yes	No	0.000
OAML073	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.191	104	Yes	No	0.000
OAML077	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.291	189	Yes	No	0.000
OAML080	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.159	182	Yes	No	0.000
OAML081	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.272	184	Yes	No	0.000
OAML083	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.213	197	Yes	No	0.000
OAML085	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.288	215	Yes	No	0.000
OAML091	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.259	160	Yes	Yes	0.003
OAML104	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.156	205	Yes	Yes	0.058
OAML141	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.335	187	No	.	.
OAML152	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.145	179	Yes	No	0.000
OAML159	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.316	252	Yes	No	0.000
OAML170	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.333	99	No	.	.
OAML171	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.315	159	No	.	.
OAML172	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.293	204	No	.	.
OAML173	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.245	147	No	.	.
OAML174	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.277	175	No	.	.
OAML175	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.110	200	No	.	.
OAML177	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.270	171	No	.	.
OAML179	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.276	160	Yes	No	0.000
OAML180	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.380	166	No	.	.
OAML185	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.308	117	No	.	.
OAML193	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.280	105	Yes	No	0.000
OAML209	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.335	182	No	.	.
OAML210	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.106	188	No	.	.
OAML214	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.329	152	No	.	.
OAML218	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.254	132	No	.	.
OAML224	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.289	97	No	.	.
OAML234	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.297	229	Yes	No	0.000
OAML245	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.258	207	Yes	No	0.000
OAML255	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.308	222	Yes	No	0.000
OAML259	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.209	185	Yes	No	0.000
OAML260	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.273	170	Yes	No	0.000
OAML261	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.259	196	Yes	No	0.000
OAML268	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.301	186	Yes	No	0.000
OAML273	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.329	228	Yes	No	0.000
OAML275	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.255	143	Yes	No	0.000
OAML276	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.364	173	Yes	Yes	0.001
OAML278	chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.343	138	Yes	No	0.000
OAML281	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.137	50	Yes	No	0.000
OAML308	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.313	396	No	.	.
OAML321	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.296	321	No	.	.
OAML326	Chr5:170837543	-	TCTC	NPM1	c.859_860insTCT	p.L287fs	frameshift insertion	0.187	91	No	.	.
OAML029	chr5:170837544	-	CTGC	NPM1	c.860_861insCTG	p.L287fs	frameshift insertion	0.259	227	Yes	No	0.000
OAML058	chr5:170837544	-	CTGC	NPM1	c.860_861insCTG	p.L287fs	frameshift insertion	0.085	231	Yes	No	0.000
OAML196	chr5:170837544	-	CTGC	NPM1	c.860_861insCTG	p.L287fs	frameshift insertion	0.219	119	Yes	No	0.000
OAML028	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.238	183	Yes	No	0.000
OAML056	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.319	184	Yes	No	0.000
OAML097	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.294	184	Yes	No	0.000
OAML108	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.322	182	No	.	.
OAML197	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.205	194	No	.	.
OAML221	chr5:170837545	-	TGCA	NPM1	c.861_862insTGC	p.L287fs	frameshift insertion	0.150	166	No	.	.
OAML211	chr5:170837551	-	AAAA	NPM1	c.867_868insAAA	p.Q289fs	frameshift insertion	0.225	191	No	.	.
OAML093	chr5:170837553	-	TTTC	NPM1	c.869_870insTTT	p.W290fs	frameshift insertion	0.046	151	Yes	No	0.000
OAML025	chr1:115252204	C	T	NRAS	c.G436A	p.A146T	nonsynonymous SNV	0.093	867	Yes	Yes	0.001
OAML215	chr1:115256528	T	A	NRAS	c.A183T	p.Q61H	nonsynonymous SNV	0.062	812	No	.	.
OAML309	Chr1:115256528	T	A	NRAS	c.A183T	p.Q61H	nonsynonymous SNV	0.211	882	No	.	.
OAML029	chr1:115256529	T	C	NRAS	c.A182G	p.Q61R	nonsynonymous SNV	0.298	852	Yes	No	0.000
OAML117	chr1:115256529	T	C	NRAS	c.A182G	p.Q61R	nonsynonymous SNV	0.021	926	Yes	No	0.000
OAML188	chr1:115256529	T	G	NRAS	c.A182C	p.Q61P	nonsynonymous SNV	0.299	740	No	.	.
OAML217	chr1:115256529	T	C	NRAS	c.A182G	p.Q61R	nonsynonymous SNV	0.432	829	No	.	.
OAML219	chr1:115256529	T	A	NRAS	c.A182T	p.Q61L	nonsynonymous SNV	0.170	531	No	.	.
OAML304	Chr1:115256529	T	C	NRAS	c.A182G	p.Q61R	nonsynonymous SNV	0.484	759	No	.	.

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML102	chr1:115256530	G	T	NRAS	c.C181A	p.Q61K	nonsynonymous SNV	0.460	897	No	.	.
OAML081	chr1:115256536	C	T	NRAS	c.G175A	p.A59T	nonsynonymous SNV	0.090	957	Yes	No	0.000
OAML001	chr1:115258744	C	T	NRAS	c.G38A	p.G13D	nonsynonymous SNV	0.314	1552	Yes	Yes	0.003
OAML007	chr1:115258744	C	T	NRAS	c.G38A	p.G13D	nonsynonymous SNV	0.211	831	Yes	No	0.000
OAML055	chr1:115258744	C	T	NRAS	c.G38A	p.G13D	nonsynonymous SNV	0.027	669	Yes	No	0.000
OAML173	chr1:115258744	C	T	NRAS	c.G38A	p.G13D	nonsynonymous SNV	0.045	642	No	.	.
OAML267	chr1:115258744	C	A	NRAS	c.G38T	p.G13V	nonsynonymous SNV	0.148	638	Yes	No	0.000
OAML267	chr1:115258744	C	A	NRAS	c.G38T	p.G13V	nonsynonymous SNV	0.148	638	Yes	No	0.000
OAML025	chr1:115258745	C	G	NRAS	c.G37C	p.G13R	nonsynonymous SNV	0.211	969	Yes	No	0.000
OAML188	chr1:115258745	C	G	NRAS	c.G37C	p.G13R	nonsynonymous SNV	0.032	729	No	.	.
OAML267	chr1:115258745	C	G	NRAS	c.G37C	p.G13R	nonsynonymous SNV	0.033	843	Yes	No	0.000
OAML023	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.173	989	Yes	No	0.000
OAML033	chr1:115258747	C	A	NRAS	c.G35T	p.G12V	nonsynonymous SNV	0.033	960	Yes	No	0.000
OAML052	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.084	798	Yes	No	0.000
OAML054	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.270	790	No	.	.
OAML056	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.133	853	Yes	No	0.000
OAML066	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.103	1059	Yes	Yes	0.001
OAML096	chr1:115258747	C	G	NRAS	c.G35C	p.G12A	nonsynonymous SNV	0.042	731	No	.	.
OAML096	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.267	955	No	.	.
OAML108	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.147	983	No	.	.
OAML125	chr1:115258747	C	G	NRAS	c.G35C	p.G12A	nonsynonymous SNV	0.406	795	Yes	Yes	0.036
OAML127	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.406	807	Yes	Yes	0.393
OAML140	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.023	791	No	.	.
OAML144	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.224	662	Yes	No	0.000
OAML188	chr1:115258747	C	G	NRAS	c.G35C	p.G12A	nonsynonymous SNV	0.071	741	No	.	.
OAML196	chr1:115258747	C	A	NRAS	c.G35T	p.G12V	nonsynonymous SNV	0.024	546	Yes	No	0.000
OAML253	chr1:115258747	C	A	NRAS	c.G35T	p.G12V	nonsynonymous SNV	0.023	772	Yes	No	0.000
OAML264	chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.074	673	Yes	Yes	0.017
OAML309	Chr1:115258747	C	T	NRAS	c.G35A	p.G12D	nonsynonymous SNV	0.048	807	No	.	.
OAML010	chr1:115258748	C	T	NRAS	c.G34A	p.G12S	nonsynonymous SNV	0.224	700	Yes	No	0.000
OAML025	chr1:115258748	C	A	NRAS	c.G34T	p.G12C	nonsynonymous SNV	0.094	990	Yes	No	0.000
OAML077	Chr1:115258748	C	A	NRAS	c.G34T	p.G12C	nonsynonymous SNV	0.285	666	Yes	No	0.000
OAML129	chr1:115258748	C	T	NRAS	c.G34A	p.G12S	nonsynonymous SNV	0.074	812	Yes	No	0.000
OAML273	chr1:115258748	C	T	NRAS	c.G34A	p.G12S	nonsynonymous SNV	0.027	786	Yes	No	0.000
OAML288	Chr1:115258748	C	T	NRAS	c.G34A	p.G12S	nonsynonymous SNV	0.045	311	Yes	No	0.000
OAML293	Chr1:115258748	C	G	NRAS	c.G34C	p.G12R	nonsynonymous SNV	0.420	617	No	.	.
OAML223	chr13:33344887	C	-	PDS5B	c.4160delC	p.P1387fs	frameshift deletion	0.047	264	No	.	.
OAML084	chrX:133511668	-	A	PHF6	c.22dupA	p.Q7fs	frameshift insertion	0.024	209	Yes	No	0.000
OAML186	chrX:133511668	-	A	PHF6	c.22dupA	p.Q7fs	frameshift insertion	0.793	145	No	.	.
OAML207	chrX:133511716	-	A	PHF6	c.70dupA	p.N23fs	frameshift insertion	0.026	265	No	.	.
OAML144	chrX:133511720	-	C	PHF6	c.73_74insC	p.D25fs	frameshift insertion	0.738	221	Yes	Yes	0.011
OAML213	chrX:133527949	C	T	PHF6	c.C385T	p.R129X	stopgain	0.879	181	No	.	.
OAML237	chrX:133527984	T	C	PHF6	c.418+2T>C		splicing	0.092	164	Yes	No	0.000
OAML060	chrX:133547549	-	GAA(	PHF6	c.447_448insGA	p.H149fs	frameshift insertion	0.083	278	Yes	No	0.000
OAML025	chrX:133547940	C	T	PHF6	c.C673T	p.R225X	stopgain	0.893	421	Yes	Yes	0.001
OAML290	ChrX:133547982	C	T	PHF6	c.C715T	p.H239Y	nonsynonymous SNV	0.465	271	Yes	No	0.000
OAML113	chrX:133547992	G	A	PHF6	c.G725A	p.C242Y	nonsynonymous SNV	0.229	410	Yes	No	0.000
OAML303	ChrX:133549101	A	T	PHF6	c.A785T	p.D262V	nonsynonymous SNV	0.639	144	No	.	.
OAML312	ChrX:133549146	G	C	PHF6	c.G830C	p.R277T	nonsynonymous SNV	0.040	348	No	.	.
OAML168	chrX:133551197	A	G	PHF6	c.835-2A>G		splicing	0.465	480	No	.	.
OAML202	chrX:133551236	G	A	PHF6	c.G872A	p.G291E	nonsynonymous SNV	0.880	125	No	.	.
OAML274	chrX:133551254	G	A	PHF6	c.G890A	p.C297Y	nonsynonymous SNV	0.033	243	Yes	Yes	0.005
OAML269	chrX:133551258	T	-	PHF6	c.894delT	p.V298fs	frameshift deletion	0.050	662	Yes	No	0.000
OAML190	ChrX:133551267	C	G	PHF6	c.C903G	p.Y301X	stopgain	0.167	192	No	.	.
OAML167	chrX:133551296	C	G	PHF6	c.C932G	p.A311G	nonsynonymous SNV	0.915	201	No	.	.
OAML146	chrX:133551305	T	C	PHF6	c.T941C	p.I314T	nonsynonymous SNV	0.426	465	Yes	No	0.000
OAML266	chrX:133551319	C	T	PHF6	c.C955T	p.R319X	stopgain	0.491	383	Yes	No	0.000
OAML142	chrX:133551328	T	C	PHF6	c.T964C	p.Y322H	nonsynonymous SNV	0.759	212	No	.	.
OAML312	ChrX:133559289	G	T	PHF6	c.G1027T	p.E343X	stopgain	0.101	277	No	.	.
OAML111	chr17:58740438	A	-	PPM1D	c.1343delA	p.N448fs	frameshift deletion	0.449	789	Yes	Yes	0.021
OAML026	chr17:58740546	T	G	PPM1D	c.T1451G	p.L484X	stopgain	0.115	1091	Yes	Yes	0.032
OAML264	chr17:58740572	0	-	PPM1D	c.1477_1487del	p.S493fs	frameshift deletion	0.370	775	Yes	Yes	0.004
OAML195	chr17:58740623	C	-	PPM1D	c.1528delC	p.Q510fs	frameshift deletion	0.452	533	Yes	Yes	0.304
OAML166	chr17:1563289	C	T	PRPF8	c.G4792A	p.D1598N	nonsynonymous SNV	0.428	587	No	.	.
OAML211	chr12:112888156	A	G	PTPN11	c.A172G	p.N58D	nonsynonymous SNV	0.021	711	No	.	.
OAML254	chr12:112888156	A	T	PTPN11	c.A172T	p.N58Y	nonsynonymous SNV	0.114	660	Yes	No	0.000
OAML029	chr12:112888163	G	T	PTPN11	c.G179T	p.G60V	nonsynonymous SNV	0.081	627	Yes	No	0.000
OAML108	chr12:112888163	G	C	PTPN11	c.G179C	p.G60A	nonsynonymous SNV	0.062	761	No	.	.
OAML158	chr12:112888165	G	C	PTPN11	c.G181C	p.D61H	nonsynonymous SNV	0.035	878	Yes	Yes	0.076
OAML303	Chr12:112888165	G	T	PTPN11	c.G181T	p.D61Y	nonsynonymous SNV	0.302	559	No	.	.
OAML261	chr12:112888166	A	T	PTPN11	c.A182T	p.D61V	nonsynonymous SNV	0.022	580	Yes	No	0.000
OAML282	Chr12:112888166	A	T	PTPN11	c.A182T	p.D61V	nonsynonymous SNV	0.174	196	Yes	No	0.000
OAML170	chr12:112888195	T	A	PTPN11	c.T211A	p.F71I	nonsynonymous SNV	0.431	452	No	.	.
OAML080	Chr12:112888199	C	T	PTPN11	c.C215T	p.A72V	nonsynonymous SNV	0.021	576	Yes	Yes	0.001
OAML081	chr12:112888199	C	T	PTPN11	c.C215T	p.A72V	nonsynonymous SNV	0.091	837	Yes	Yes	0.001

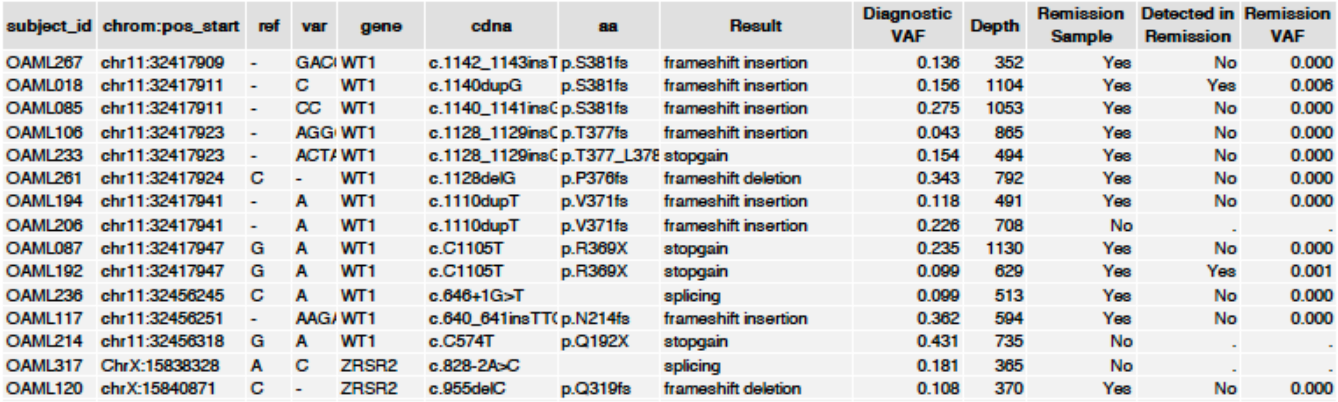
subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML109	chr12:112888199	C	T	PTPN11	c.C215T	p.A72V	nonsynonymous SNV	0.282	804	No	.	.
OAML254	chr12:112888199	C	T	PTPN11	c.C215T	p.A72V	nonsynonymous SNV	0.104	761	Yes	Yes	0.001
OAML083	chr12:112888202	C	T	PTPN11	c.C218T	p.T73I	nonsynonymous SNV	0.042	929	Yes	No	0.000
OAML158	chr12:112888202	C	T	PTPN11	c.C218T	p.T73I	nonsynonymous SNV	0.224	958	Yes	Yes	0.211
OAML258	chr12:112888202	C	T	PTPN11	c.C218T	p.T73I	nonsynonymous SNV	0.072	740	Yes	No	0.000
OAML179	chr12:112888210	G	A	PTPN11	c.G226A	p.E76K	nonsynonymous SNV	0.025	552	Yes	No	0.000
OAML285	Chr12:112888210	G	C	PTPN11	c.G226C	p.E76Q	nonsynonymous SNV	0.070	214	Yes	No	0.000
OAML081	chr12:112888211	A	G	PTPN11	c.A227G	p.E76G	nonsynonymous SNV	0.211	830	Yes	No	0.000
OAML254	chr12:112888211	A	T	PTPN11	c.A227T	p.E76V	nonsynonymous SNV	0.138	752	Yes	No	0.000
OAML261	chr12:112888301	A	C	PTPN11	c.A317C	p.D106A	nonsynonymous SNV	0.338	429	Yes	No	0.000
OAML057	chr12:112910785	G	A	PTPN11	c.G794A	p.R265Q	nonsynonymous SNV	0.049	708	Yes	No	0.000
OAML255	chr12:112915523	A	G	PTPN11	c.A922G	p.N308D	nonsynonymous SNV	0.398	719	Yes	Yes	0.001
OAML083	chr12:112915524	A	C	PTPN11	c.A923C	p.N308T	nonsynonymous SNV	0.077	815	Yes	No	0.000
OAML245	chr12:112926248	G	A	PTPN11	c.G1381A	p.A461T	nonsynonymous SNV	0.030	810	Yes	No	0.000
OAML277	chr12:112926884	T	G	PTPN11	c.T1504G	p.S502A	nonsynonymous SNV	0.035	927	Yes	No	0.000
OAML016	chr12:112926888	G	A	PTPN11	c.G1508A	p.G503E	nonsynonymous SNV	0.247	930	Yes	No	0.000
OAML122	chr12:112926888	G	C	PTPN11	c.G1508C	p.G503A	nonsynonymous SNV	0.301	940	Yes	Yes	0.004
OAML100	chr12:112926909	A	T	PTPN11	c.A1529T	p.Q510L	nonsynonymous SNV	0.032	883	No	.	.
OAML222	chr8:117859816	G	A	RAD21	c.C1819T	p.Q607X	stopgain	0.335	669	No	.	.
OAML197	chr8:117861253	C	-	RAD21	c.1636delG	p.G546fs	frameshift deletion	0.438	657	No	.	.
OAML276	chr8:117862901	0	-	RAD21	c.1575_1576del	p.K525fs	frameshift deletion	0.479	568	Yes	Yes	0.005
OAML141	chr8:117868464	T	-	RAD21	c.878delA	p.Q293fs	frameshift deletion	0.485	507	No	.	.
OAML223	chr8:117868527	0	-	RAD21	c.815delT	p.M272fs	frameshift deletion	0.230	160	No	.	.
OAML263	chr8:117868892	-	TTTC	RAD21	c.806_807insGA	p.N269fs	frameshift insertion	0.302	701	Yes	Yes	0.001
OAML224	chr1:155874261	C	G	RIT1	c.G270C	p.M90I	nonsynonymous SNV	0.078	629	No	.	.
OAML193	chr1:155874286	A	C	RIT1	c.T245G	p.F82C	nonsynonymous SNV	0.054	591	Yes	No	0.000
OAML100	chr1:155874289	T	G	RIT1	c.A242C	p.E81A	nonsynonymous SNV	0.180	886	No	.	.
OAML176	chr20:62321155	A	-	RTEL1	c.2078delA	p.Q693fs	frameshift deletion	0.477	968	No	.	.
OAML240	chr21:36164504	-	C	RUNX1	c.1370dupG	p.G457fs	frameshift insertion	0.091	419	Yes	No	0.000
OAML236	chr21:36164523	-	CG	RUNX1	c.1351_1352insC	p.D451fs	frameshift insertion	0.112	338	Yes	No	0.000
OAML168	chr21:36164702	-	G	RUNX1	c.1172dupC	p.A391fs	frameshift insertion	0.478	633	No	.	.
OAML007	chr21:36164745	-	A	RUNX1	c.1129dupT	p.Y377fs	frameshift insertion	0.412	679	Yes	Yes	0.005
OAML142	chr21:36164771	0	-	RUNX1	c.1097_1104del	p.I366fs	frameshift deletion	0.304	749	No	.	.
OAML191	chr21:36164790	-	TCTA	RUNX1	c.1084_1085insA	p.S362_G36	stopgain	0.330	590	No	.	.
OAML133	chr21:36164804	-	G	RUNX1	c.1070dupC	p.P357fs	frameshift insertion	0.193	1083	Yes	No	0.000
OAML057	chr21:36164810	G	T	RUNX1	c.C1065A	p.Y355X	stopgain	0.799	724	Yes	No	0.000
OAML202	chr21:36164838	-	G	RUNX1	c.1036dupC	p.R346fs	frameshift insertion	0.474	192	No	.	.
OAML166	chr21:36164859	-	GCG	RUNX1	c.1015_1016insC	p.L339fs	frameshift insertion	0.140	498	No	.	.
OAML263	chr21:36164865	0	-	RUNX1	c.1007_1010del	p.F336fs	frameshift deletion	0.219	525	Yes	No	0.000
OAML290	Chr21:36164895	-	GGT	RUNX1	c.979_980insCG	p.L327fs	frameshift insertion	0.313	305	Yes	No	0.000
OAML120	chr21:36164898	-	CGG	RUNX1	c.976_977insCC	p.D326fs	frameshift insertion	0.062	503	Yes	Yes	0.039
OAML285	Chr21:36171600	-	A	RUNX1	c.964dupT	p.S322fs	frameshift insertion	0.304	240	Yes	No	0.000
OAML240	chr21:36171612	-	A	RUNX1	c.952dupT	p.S318fs	frameshift insertion	0.291	848	Yes	No	0.000
OAML303	Chr21:36171612	-	A	RUNX1	c.952dupT	p.S318fs	frameshift insertion	0.342	695	No	.	.
OAML325	Chr21:36171634	-	CATC	RUNX1	c.930_931insGC	p.T311_T312	stopgain	0.285	463	No	.	.
OAML198	chr21:36171635	-	A	RUNX1	c.929dupT	p.M310fs	frameshift insertion	0.121	495	Yes	Yes	0.043
OAML054	chr21:36171709	G	A	RUNX1	c.C856T	p.Q286X	stopgain	0.326	876	No	.	.
OAML015	chr21:36171729	C	T	RUNX1	c.G836A	p.W279X	stopgain	0.410	539	Yes	Yes	0.004
OAML219	chr21:36206704	0	-	RUNX1	RUNX1(NM_001754:exon7:r.s		splicing	0.591	208	No	.	.
OAML309	Chr21:36206706	C	A	RUNX1	c.805+1G>T		splicing	0.300	327	No	.	.
OAML280	chr21:36206773	-	T	RUNX1	c.738_739insA	p.P247fs	frameshift insertion	0.418	521	Yes	Yes	0.151
OAML099	chr21:36206778	0	-	RUNX1	c.721_734del	p.H241fs	frameshift deletion	0.463	1198	Yes	Yes	0.002
OAML076	Chr21:36206845	C	A	RUNX1	c.G667T	p.E223X	stopgain	0.351	478	Yes	Yes	0.322
OAML076	Chr21:36206845	C	A	RUNX1	c.G667T	p.E223X	stopgain	0.351	478	Yes	Yes	0.322
OAML113	chr21:36206874	T	-	RUNX1	c.638delA	p.Q213fs	frameshift deletion	0.123	554	Yes	No	0.000
OAML258	chr21:36206890	0	-	RUNX1	c.621_622del	p.R207fs	frameshift deletion	0.285	404	Yes	Yes	0.001
OAML123	chr21:36206893	G	A	RUNX1	c.C619T	p.R207W	nonsynonymous SNV	0.056	444	Yes	Yes	0.008
OAML190	Chr21:36231770	-	T	RUNX1	c.613+1->A		splicing	0.504	421	No	.	.
OAML243	chr21:36231773	C	T	RUNX1	c.G611A	p.R204Q	nonsynonymous SNV	0.860	728	Yes	Yes	0.406
OAML025	chr21:36231774	G	A	RUNX1	c.C610T	p.R204X	stopgain	0.101	849	Yes	No	0.000
OAML213	chr21:36231774	G	A	RUNX1	c.C610T	p.R204X	stopgain	0.833	722	No	.	.
OAML274	chr21:36231782	C	T	RUNX1	c.G602A	p.R201Q	nonsynonymous SNV	0.357	749	Yes	Yes	0.192
OAML053	chr21:36231785	G	A	RUNX1	c.C599T	p.P200L	nonsynonymous SNV	0.463	708	Yes	No	0.000
OAML151	chr21:36231790	A	-	RUNX1	c.594delT	p.D198fs	frameshift deletion	0.050	744	Yes	No	0.000
OAML238	chr21:36231791	T	C	RUNX1	c.A593G	p.D198G	nonsynonymous SNV	0.734	730	Yes	No	0.000
OAML251	chr21:36231791	T	C	RUNX1	c.A593G	p.D198G	nonsynonymous SNV	0.424	707	Yes	No	0.000
OAML001	chr21:36231792	C	T	RUNX1	c.G592A	p.D198N	nonsynonymous SNV	0.504	572	Yes	No	0.000
OAML139	chr21:36231792	C	A	RUNX1	c.G592T	p.D198Y	nonsynonymous SNV	0.079	768	Yes	No	0.000
OAML017	chr21:36231813	T	A	RUNX1	c.A571T	p.R191X	stopgain	0.331	523	Yes	Yes	0.300
OAML120	chr21:36231822	T	C	RUNX1	c.A562G	p.T188A	nonsynonymous SNV	0.022	859	Yes	No	0.000
OAML135	chr21:36231831	G	A	RUNX1	c.C553T	p.Q185X	stopgain	0.182	379	No	.	.
OAML124	chr21:36252856	-	T	RUNX1	c.505dupA	p.R169fs	frameshift insertion	0.191	839	Yes	No	0.000
OAML237	chr21:36252856	-	T	RUNX1	c.505dupA	p.R169fs	frameshift insertion	0.024	635	Yes	No	0.000
OAML130	chr21:36252865	C	A	RUNX1	c.G497T	p.R166L	nonsynonymous SNV	0.496	1163	Yes	Yes	0.019
OAML151	chr21:36252865	C	T	RUNX1	c.G497A	p.R166Q	nonsynonymous SNV	0.355	888	Yes	Yes	0.001

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML182	chr21:36252865	C	T	RUNX1	c.G497A	p.R166Q	nonsynonymous SNV	0.970	436	No	.	.
OAML099	chr21:36252867	-	C	RUNX1	c.494dupG	p.G165fs	frameshift insertion	0.208	530	Yes	No	0.000
OAML051	chr21:36252869	C	G	RUNX1	c.G493C	p.G165R	nonsynonymous SNV	0.034	649	Yes	No	0.000
OAML106	chr21:36252877	C	T	RUNX1	c.G485A	p.R162K	nonsynonymous SNV	0.167	562	Yes	No	0.000
OAML205	chr21:36252878	T	C	RUNX1	c.A484G	p.R162G	nonsynonymous SNV	0.449	902	No	.	.
OAML117	chr21:36252902	G	A	RUNX1	c.C460T	p.Q154X	stopgain	0.404	1071	Yes	No	0.000
OAML205	chr21:36252916	-	CGG	RUNX1	c.445_446insGC	p.A149_A15	stopgain	0.212	849	No	.	.
OAML212	chr21:36252916	-	CGG	RUNX1	c.445_446insGC	p.A149_A15	stopgain	0.176	793	No	.	.
OAML258	chr21:36252916	G	T	RUNX1	c.C446A	p.A149E	nonsynonymous SNV	0.100	944	Yes	No	0.000
OAML044	chr21:36252938	-	CCG	RUNX1	c.423_424insAG	p.A142fs	frameshift insertion	0.195	671	Yes	No	0.000
OAML263	chr21:36252939	-	TTT	RUNX1	c.422_423insCA	p.S141delins	nonframeshift insertion	0.243	722	Yes	No	0.000
OAML258	chr21:36252940	G	C	RUNX1	c.C422G	p.S141W	nonsynonymous SNV	0.178	905	Yes	Yes	0.001
OAML017	chr21:36252952	T	C	RUNX1	c.A410G	p.D137G	nonsynonymous SNV	0.303	650	Yes	Yes	0.305
OAML155	chr21:36252958	C	T	RUNX1	c.G404A	p.G135D	nonsynonymous SNV	0.449	1251	Yes	No	0.000
OAML203	chr21:36252965	0	-	RUNX1	c.396_397del	p.V132fs	frameshift deletion	0.311	830	No	.	.
OAML015	chr21:36252987	T	-	RUNX1	c.375delA	p.P125fs	frameshift deletion	0.035	603	Yes	Yes	0.001
OAML124	chr21:36252998	C	-	RUNX1	c.364delG	p.G122fs	frameshift deletion	0.054	962	Yes	No	0.000
OAML151	chr21:36253000	A	G	RUNX1	c.T362C	p.L121P	nonsynonymous SNV	0.230	936	Yes	Yes	0.001
OAML237	chr21:36253009	A	T	RUNX1	c.T353A	p.V118E	nonsynonymous SNV	0.426	625	Yes	Yes	0.002
OAML076	Chr21:36259139	C	A	RUNX1	c.351+1G>T		splicing	0.037	514	Yes	Yes	0.012
OAML076	Chr21:36259139	C	A	RUNX1	c.351+1G>T		splicing	0.037	514	Yes	Yes	0.012
OAML206	chr21:36259139	C	T	RUNX1	c.351+1G>A		splicing	0.449	621	No	.	.
OAML167	chr21:36259172	G	A	RUNX1	c.C319T	p.R107C	nonsynonymous SNV	0.924	486	No	.	.
OAML153	chr21:36259175	A	G	RUNX1	c.T316C	p.W106R	nonsynonymous SNV	0.813	459	Yes	Yes	0.460
OAML253	chr21:36259195	C	T	RUNX1	c.G296A	p.C99Y	nonsynonymous SNV	0.444	870	Yes	Yes	0.376
OAML212	chr21:36259198	A	-	RUNX1	c.293delT	p.L98fs	frameshift deletion	0.360	766	No	.	.
OAML147	chr21:36421143	-	GCG	RUNX1	c.53_54insTCGC	p.M18fs	frameshift insertion	0.076	383	Yes	No	0.000
OAML024	chr18:42531907	G	A	SETBP1	c.G2602A	p.D868N	nonsynonymous SNV	0.331	378	No	.	.
OAML182	chr18:42531907	G	A	SETBP1	c.G2602A	p.D868N	nonsynonymous SNV	0.405	178	No	.	.
OAML073	Chr3:47125247	A	T	SETD2	c.T6023A	p.L2008X	stopgain	0.065	276	Yes	No	0.000
OAML073	Chr3:47155365	C	G	SETD2	c.4715+1G>C		splicing	0.042	193	Yes	No	0.000
OAML114	chr2:198266494	T	C	SF3B1	c.A2342G	p.D781G	nonsynonymous SNV	0.118	646	Yes	Yes	0.009
OAML122	chr2:198266611	C	T	SF3B1	c.G2225A	p.G742D	nonsynonymous SNV	0.336	685	Yes	Yes	0.022
OAML017	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.341	478	Yes	Yes	0.288
OAML059	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.226	855	Yes	No	0.000
OAML092	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.082	526	No	.	.
OAML151	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.405	723	Yes	Yes	0.001
OAML219	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.301	472	No	.	.
OAML258	chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.347	736	Yes	Yes	0.028
OAML311	Chr2:198266834	T	C	SF3B1	c.A2098G	p.K700E	nonsynonymous SNV	0.069	568	No	.	.
OAML243	chr2:198267359	C	A	SF3B1	c.G1998T	p.K666N	nonsynonymous SNV	0.442	789	Yes	Yes	0.317
OAML115	chr2:198267360	T	A	SF3B1	c.A1997T	p.K666M	nonsynonymous SNV	0.477	755	No	.	.
OAML314	Chr2:198267484	G	A	SF3B1	c.C1873T	p.R625C	nonsynonymous SNV	0.524	21	No	.	.
OAML186	chrX:53438710	C	T	SMC1A	c.1188+1G>A		splicing	0.719	185	No	.	.
OAML241	chrX:53438710	C	T	SMC1A	c.1188+1G>A		splicing	0.024	383	Yes	No	0.000
OAML166	chr10:112340660	A	T	SMC3	c.430-2A>T		splicing	0.395	365	No	.	.
OAML106	chr10:112340661	G	C	SMC3	c.430-1G>C		splicing	0.060	348	Yes	No	0.000
OAML231	chr17:74732935	0	-	SRSF2	c.285_308del	p.95_103del	nonframeshift deletion	0.430	454	Yes	No	0.000
OAML012	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.471	474	Yes	No	0.000
OAML015	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.400	474	Yes	Yes	0.077
OAML024	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.467	730	No	.	.
OAML038	chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.410	424	Yes	Yes	0.360
OAML051	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.446	576	Yes	Yes	0.362
OAML063	Chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.467	164	Yes	No	0.000
OAML068	Chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.510	153	Yes	Yes	0.421
OAML074	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.239	490	No	.	.
OAML076	Chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.480	321	Yes	Yes	0.319
OAML076	Chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.480	321	Yes	Yes	0.319
OAML077	Chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.454	436	Yes	No	0.000
OAML088	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.171	522	Yes	Yes	0.224
OAML095	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.054	466	Yes	Yes	0.002
OAML098	chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.444	475	Yes	No	0.000
OAML099	chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.474	1145	Yes	Yes	0.045
OAML102	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.456	579	No	.	.
OAML107	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.037	461	No	.	.
OAML124	chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.461	640	Yes	No	0.000
OAML127	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.479	457	Yes	Yes	0.423
OAML132	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.347	619	Yes	Yes	0.062
OAML133	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.420	710	Yes	No	0.000
OAML142	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.434	627	No	.	.
OAML143	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.508	437	No	.	.
OAML145	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.316	583	Yes	Yes	0.025
OAML147	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.078	424	Yes	No	0.000
OAML156	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.358	369	Yes	Yes	0.012
OAML158	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.468	737	Yes	Yes	0.349

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML167	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.501	399	No	.	.
OAML173	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.524	380	No	.	.
OAML175	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.263	338	No	.	.
OAML179	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.427	379	Yes	Yes	0.142
OAML180	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.439	378	No	.	.
OAML182	chr17:74732959	-	GGC	SRSF2	c.283_284insGC	p.P95delinsR	nonframeshift insertion	0.601	630	No	.	.
OAML188	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.500	494	No	.	.
OAML195	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.430	309	Yes	Yes	0.017
OAML201	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.430	558	No	.	.
OAML203	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.348	443	No	.	.
OAML205	chr17:74732959	-	GGC	SRSF2	c.283_284insGC	p.P95delinsR	nonframeshift insertion	0.575	690	No	.	.
OAML210	chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.214	374	No	.	.
OAML212	chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.322	480	No	.	.
OAML237	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.353	455	Yes	No	0.000
OAML238	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.433	476	Yes	Yes	0.119
OAML253	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.417	638	Yes	Yes	0.398
OAML266	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.446	480	Yes	No	0.000
OAML274	chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.368	496	Yes	Yes	0.176
OAML305	Chr17:74732959	G	T	SRSF2	c.C284A	p.P95H	nonsynonymous SNV	0.281	609	No	.	.
OAML316	Chr17:74732959	G	A	SRSF2	c.C284T	p.P95L	nonsynonymous SNV	0.312	857	Yes	No	0.000
OAML325	Chr17:74732959	G	C	SRSF2	c.C284G	p.P95R	nonsynonymous SNV	0.497	431	No	.	.
OAML213	chr17:74732960	G	C	SRSF2	c.C283G	p.P95A	nonsynonymous SNV	0.447	461	No	.	.
OAML103	chr17:74733073	A	T	SRSF2	c.T170A	p.F57Y	nonsynonymous SNV	0.453	561	Yes	Yes	0.143
OAML147	chr17:74733073	A	T	SRSF2	c.T170A	p.F57Y	nonsynonymous SNV	0.027	518	Yes	No	0.000
OAML145	chrX:123164932	T	-	STAG2	c.245delT	p.M82fs	frameshift deletion	0.024	370	Yes	Yes	0.001
OAML277	chrX:123171392	-	G	STAG2	c.305dupG	p.W102fs	frameshift insertion	0.841	296	Yes	No	0.000
OAML253	chrX:123171416	C	T	STAG2	c.C328T	p.R110X	stopgain	0.730	215	Yes	Yes	0.769
OAML266	chrX:123171416	C	T	STAG2	c.C328T	p.R110X	stopgain	0.465	393	Yes	Yes	0.001
OAML194	chrX:123171455	C	T	STAG2	c.C367T	p.Q123X	stopgain	0.410	178	Yes	No	0.000
OAML035	chrX:123179024	0	-	STAG2	c.473_474del	p.D158fs	frameshift deletion	0.522	228	Yes	Yes	0.002
OAML213	chrX:123179028	T	-	STAG2	c.477delT	p.Y159fs	frameshift deletion	0.058	293	No	.	.
OAML191	chrX:123179054	G	A	STAG2	c.G503A	p.W168X	stopgain	0.849	252	No	.	.
OAML124	chrX:123179115	T	G	STAG2	c.T564G	p.Y188X	stopgain	0.901	364	Yes	No	0.000
OAML068	ChrX:123179197	C	T	STAG2	c.C646T	p.R216X	stopgain	0.829	76	Yes	No	0.000
OAML274	chrX:123179197	C	T	STAG2	c.C646T	p.R216X	stopgain	0.729	277	Yes	Yes	0.246
OAML110	chrX:123179201	-	T	STAG2	c.651dupT	p.H217fs	frameshift insertion	0.092	119	No	.	.
OAML200	chrX:123181311	C	T	STAG2	c.C775T	p.R259X	stopgain	0.290	252	Yes	No	0.000
OAML256	chrX:123181311	C	T	STAG2	c.C775T	p.R259X	stopgain	0.286	503	Yes	Yes	0.005
OAML241	chrX:123182922	-	AT	STAG2	c.887_888insAT	p.R296fs	frameshift insertion	0.780	240	Yes	No	0.000
OAML144	chrX:123182927	C	-	STAG2	c.892delC	p.R298fs	frameshift deletion	0.347	121	Yes	No	0.000
OAML224	chrX:123190037	C	G	STAG2	c.C1256G	p.S419X	stopgain	0.908	184	No	.	.
OAML305	ChrX:123191804	-	T	STAG2	c.1394dupT	p.V465fs	frameshift insertion	0.262	316	No	.	.
OAML038	chrX:123195627	0	-	STAG2	c.1541_1544del	p.T514fs	frameshift deletion	0.247	77	Yes	No	0.000
OAML188	chrX:123196822	0	-	STAG2	c.1709_1712del	p.A570fs	frameshift deletion	0.905	262	No	.	.
OAML076	ChrX:123197782	-	A	STAG2	c.1907dupA	p.Y636_H63	stopgain	0.860	179	Yes	Yes	0.677
OAML076	ChrX:123197782	-	A	STAG2	c.1907dupA	p.Y636_H63	stopgain	0.860	179	Yes	Yes	0.677
OAML271	chrX:123197803	-	AGT	STAG2	c.1927_1928insA	p.E643fs	frameshift insertion	0.358	432	Yes	No	0.000
OAML230	chrX:123199793	-	T	STAG2	c.2094dupT	p.H698fs	frameshift insertion	0.142	162	Yes	No	0.000
OAML132	chrX:123200026	0	-	STAG2	c.2098_2104del	p.A700fs	frameshift deletion	0.174	116	Yes	Yes	0.019
OAML054	chrX:123202507	G	A	STAG2	c.2358+1G>A		splicing	0.560	175	No	.	.
OAML041	chrX:123210181	G	A	STAG2	c.2534-1G>A		splicing	0.141	156	Yes	No	0.000
OAML185	chrX:123210307	A	T	STAG2	c.A2659T	p.K887X	stopgain	0.464	274	No	.	.
OAML253	chrX:123211852	-	TCC	STAG2	c.2719_2720insT	p.T907fs	frameshift insertion	0.035	201	Yes	No	0.000
OAML088	chrX:123211879	-	CTA	STAG2	c.2746_2747insC	p.A916fs	frameshift insertion	0.021	241	Yes	No	0.000
OAML250	chrX:123215264	A	-	STAG2	c.2810delA	p.N937fs	frameshift deletion	0.878	262	Yes	No	0.000
OAML252	chrX:123217380	C	T	STAG2	c.C3034T	p.R1012X	stopgain	0.917	229	Yes	Yes	0.036
OAML203	chrX:123220476	C	T	STAG2	c.C3133T	p.R1045X	stopgain	0.346	676	No	.	.
OAML037	chr17:40359673	C	A	STAT5B	c.G1980T	p.L660F	nonsynonymous SNV	0.030	495	Yes	No	0.000
OAML106	chr17:40359729	T	G	STAT5B	c.A1924C	p.N642H	nonsynonymous SNV	0.055	587	Yes	No	0.000
OAML168	chr17:40359729	T	G	STAT5B	c.A1924C	p.N642H	nonsynonymous SNV	0.471	522	No	.	.
OAML325	Chr17:40359729	T	G	STAT5B	c.A1924C	p.N642H	nonsynonymous SNV	0.454	280	No	.	.
OAML048	chr17:30322782	G	A	SUZ12	c.1794+1G>A		splicing	0.289	363	Yes	No	0.000
OAML189	chr3:169482460	G	A	TERC			ncRNA_exonic	0.484	630	Yes	Yes	.
OAML047	chr3:169482812	T	C	TERC			ncRNA_exonic	0.507	751	Yes	Yes	.
OAML153	chr5:1280287	G	C	TERT	c.C1936G	p.R646G	nonsynonymous SNV	0.514	661	Yes	Yes	0.468
OAML153	chr5:1280288	G	C	TERT	c.C1935G	p.F645L	nonsynonymous SNV	0.511	663	Yes	Yes	0.469
OAML173	chr5:1282548	T	C	TERT	c.A1765G	p.I589V	nonsynonymous SNV	0.555	409	No	.	.
OAML103	chr4:106155511	C	T	TET2	c.C412T	p.Q138X	stopgain	0.465	959	Yes	Yes	0.024
OAML197	chr4:106155920	T	-	TET2	c.821delT	p.I274fs	frameshift deletion	0.460	1382	No	.	.
OAML171	chr4:106156042	T	-	TET2	c.943delT	p.S315fs	frameshift deletion	0.460	859	No	.	.
OAML259	chr4:106156091	T	-	TET2	c.992delT	p.I331fs	frameshift deletion	0.835	694	Yes	Yes	0.415
OAML263	chr4:106156158	0	-	TET2	c.1059_1060del	p.C353fs	frameshift deletion	0.304	898	Yes	No	0.000
OAML148	chr4:106156160	C	-	TET2	c.1061delC	p.S354X	stopgain	0.158	1113	Yes	Yes	0.070
OAML159	chr4:106156253	C	G	TET2	c.C1154G	p.S385X	stopgain	0.930	759	Yes	Yes	0.001
OAML219	chr4:106156360	G	-	TET2	c.1261delG	p.E421fs	frameshift deletion	0.247	665	No	.	.

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML273	chr4:106156413	-	A	TET2	c.1315dupA	p.P438fs	frameshift insertion	0.021	899	Yes	No	0.000
OAML046	chr4:106156540	0	-	TET2	c.1441_1442del	p.Q481fs	frameshift deletion	0.273	963	Yes	Yes	0.012
OAML121	chr4:106156700	G	-	TET2	c.1601delG	p.R534fs	frameshift deletion	0.483	1154	Yes	Yes	0.399
OAML079	chr4:106156729	C	T	TET2	c.C1630T	p.R544X	stopgain	0.026	800	Yes	Yes	0.033
OAML028	chr4:106156758	-	C	TET2	c.1660dupC	p.V553fs	frameshift insertion	0.423	1223	Yes	Yes	0.020
OAML119	chr4:106156894	-	A	TET2	c.1796dupA	p.Q599fs	frameshift insertion	0.905	761	Yes	Yes	0.672
OAML273	chr4:106156896	0	-	TET2	c.1797_1801del	p.Q599fs	frameshift deletion	0.037	871	Yes	No	0.000
OAML097	chr4:106156915	0	-	TET2	c.1816_1817del	p.T606fs	frameshift deletion	0.407	919	Yes	Yes	0.044
OAML031	chr4:106156941	G	-	TET2	c.1842delG	p.G614fs	frameshift deletion	0.369	889	Yes	Yes	0.004
OAML015	chr4:106157001	C	A	TET2	c.C1902A	p.Y634X	stopgain	0.393	888	Yes	Yes	0.062
OAML213	chr4:106157008	G	T	TET2	c.G1909T	p.E637X	stopgain	0.438	975	No	.	.
OAML148	chr4:106157074	C	T	TET2	c.C1975T	p.Q659X	stopgain	0.144	1053	Yes	Yes	0.064
OAML177	chr4:106157352	0	-	TET2	c.2253_2256del	p.K751fs	frameshift deletion	0.391	613	No	.	.
OAML031	chr4:106157371	C	T	TET2	c.C2272T	p.Q758X	stopgain	0.462	805	Yes	Yes	0.367
OAML120	chr4:106157375	C	-	TET2	c.2276delC	p.T759fs	frameshift deletion	0.023	1062	Yes	No	0.000
OAML038	chr4:106157384	-	C	TET2	c.2286dupC	p.H762fs	frameshift insertion	0.164	935	Yes	No	0.000
OAML118	chr4:106157446	G	-	TET2	c.2347delG	p.E783fs	frameshift deletion	0.431	764	Yes	Yes	0.223
OAML012	chr4:106157527	C	T	TET2	c.C2428T	p.Q810X	stopgain	0.480	830	Yes	Yes	0.012
OAML290	Chr4:106157542	A	T	TET2	c.A2443T	p.R815X	stopgain	0.454	295	Yes	No	0.000
OAML081	chr4:106157617	-	TAG	TET2	c.2518_2519insT	p.L840fs	frameshift insertion	0.218	968	Yes	No	0.000
OAML285	Chr4:106157677	C	-	TET2	c.2578delC	p.Q860fs	frameshift deletion	0.331	260	Yes	No	0.000
OAML013	chr4:106157755	C	T	TET2	c.C2656T	p.Q886X	stopgain	0.286	21	Yes	No	0.000
OAML121	chr4:106157887	G	-	TET2	c.2788delG	p.V930fs	frameshift deletion	0.466	1160	Yes	Yes	0.396
OAML273	chr4:106157983	C	T	TET2	c.C2884T	p.Q962X	stopgain	0.447	804	Yes	Yes	0.008
OAML253	chr4:106157998	C	T	TET2	c.C2899T	p.Q967X	stopgain	0.365	877	Yes	Yes	0.328
OAML255	chr4:106158065	C	-	TET2	c.2966delC	p.P989fs	frameshift deletion	0.026	916	Yes	No	0.000
OAML177	chr4:106158187	C	T	TET2	c.C3088T	p.Q1030X	stopgain	0.447	710	No	.	.
OAML025	chr4:106158252	-	A	TET2	c.3154dupA	p.Q1051fs	frameshift insertion	0.465	1142	Yes	Yes	0.441
OAML076	Chr4:106158301	C	T	TET2	c.C3202T	p.Q1068X	stopgain	0.440	539	Yes	Yes	0.308
OAML076	Chr4:106158301	C	T	TET2	c.C3202T	p.Q1068X	stopgain	0.440	539	Yes	Yes	0.308
OAML141	chr4:106158503	G	A	TET2	c.G3404A	p.C1135Y	nonsynonymous SNV	0.516	452	No	.	.
OAML151	chr4:106158503	G	A	TET2	c.G3404A	p.C1135Y	nonsynonymous SNV	0.399	753	Yes	No	0.000
OAML179	chr4:106162495	G	C	TET2	c.3410-1G>C		splicing	0.461	256	Yes	Yes	0.106
OAML081	chr4:106162535	A	C	TET2	c.A3449C	p.H1150P	nonsynonymous SNV	0.333	761	Yes	Yes	0.016
OAML116	chr4:106162587	G	A	TET2	c.3500+1G>A		splicing	0.595	630	Yes	Yes	0.384
OAML079	chr4:106163998	C	T	TET2	c.C3508T	p.Q1170X	stopgain	0.133	467	Yes	Yes	0.005
OAML015	chr4:106164061	C	T	TET2	c.C3571T	p.Q1191X	stopgain	0.372	578	Yes	Yes	0.035
OAML275	chr4:106164085	G	A	TET2	c.3594+1G>A		splicing	0.460	454	Yes	Yes	0.257
OAML329	Chr4:106164763	T	C	TET2	c.T3631C	p.C1211R	nonsynonymous SNV	0.464	336	No	.	.
OAML290	Chr4:106164861	0	-	TET2	c.3729_3730del	p.K1243fs	frameshift deletion	0.422	237	Yes	No	0.000
OAML213	chr4:106164913	C	T	TET2	c.C3781T	p.R1261C	nonsynonymous SNV	0.028	534	No	.	.
OAML028	chr4:106164916	C	T	TET2	c.C3784T	p.R1262W	nonsynonymous SNV	0.427	592	Yes	Yes	0.015
OAML275	chr4:106180774	0	-	TET2	c.3804_3814del	p.E1268fs	frameshift deletion	0.320	577	Yes	Yes	0.011
OAML173	chr4:106180778	G	T	TET2	c.G3806T	p.R1269I	nonsynonymous SNV	0.464	617	No	.	.
OAML103	chr4:106180783	T	G	TET2	c.T3811G	p.C1271G	nonsynonymous SNV	0.435	883	Yes	Yes	0.172
OAML174	chr4:106180790	G	C	TET2	c.G3818C	p.C1273S	nonsynonymous SNV	0.977	835	No	.	.
OAML038	chr4:106180792	C	T	TET2	c.C3820T	p.Q1274X	stopgain	0.207	932	Yes	No	0.000
OAML329	Chr4:106180899	T	G	TET2	c.T3927G	p.F1309L	nonsynonymous SNV	0.453	450	No	.	.
OAML060	chr4:106180904	T	C	TET2	c.T3932C	p.L1311P	nonsynonymous SNV	0.113	855	Yes	Yes	0.041
OAML001	chr4:106180925	A	C	TET2	c.A3953C	p.E1318A	nonsynonymous SNV	0.458	295	Yes	Yes	0.529
OAML249	chr4:106182902	0	-	TET2	c.3955_3973del	p.E1319fs	frameshift deletion	0.655	231	Yes	Yes	0.116
OAML317	Chr4:106182968	0	-	TET2	c.4007_4008del	p.T1336fs	frameshift deletion	0.170	651	No	.	.
OAML179	chr4:106190766	G	T	TET2	c.4045-1G>T		splicing	0.429	464	Yes	Yes	0.106
OAML168	chr4:106190795	G	T	TET2	c.G4073T	p.C1358F	nonsynonymous SNV	0.948	676	No	.	.
OAML001	chr4:106190822	C	G	TET2	c.C4100G	p.P1367R	nonsynonymous SNV	0.458	708	Yes	Yes	0.432
OAML173	chr4:106190882	A	G	TET2	c.A4160G	p.N1387S	nonsynonymous SNV	0.058	604	No	.	.
OAML171	chr4:106190887	C	T	TET2	c.C4165T	p.Q1389X	stopgain	0.442	568	No	.	.
OAML097	chr4:106190896	A	C	TET2	c.A4174C	p.S1392R	nonsynonymous SNV	0.471	624	Yes	Yes	0.001
OAML118	chr4:106190900	C	T	TET2	c.C4178T	p.T1393I	nonsynonymous SNV	0.450	585	Yes	Yes	0.266
OAML116	chr4:106193779	A	T	TET2	c.A4241T	p.Q1414L	nonsynonymous SNV	0.348	940	Yes	Yes	0.435
OAML182	chr4:106193785	A	-	TET2	c.4247delA	p.H1416fs	frameshift deletion	0.328	305	No	.	.
OAML278	chr4:106193833	-	G	TET2	c.4296dupG	p.V1432fs	frameshift insertion	0.949	508	Yes	Yes	0.247
OAML138	chr4:106193892	C	T	TET2	c.C4354T	p.R1452X	stopgain	0.023	875	Yes	No	0.000
OAML191	chr4:106193931	C	T	TET2	c.C4393T	p.R1465X	stopgain	0.464	528	No	.	.
OAML221	chr4:106193931	C	T	TET2	c.C4393T	p.R1465X	stopgain	0.198	489	No	.	.
OAML243	chr4:106193931	C	T	TET2	c.C4393T	p.R1465X	stopgain	0.474	761	Yes	Yes	0.445
OAML060	chr4:106194057	C	-	TET2	c.4519delC	p.Q1507fs	frameshift deletion	0.067	464	Yes	Yes	0.008
OAML211	chr4:106196349	0	-	TET2	c.4682_4683del	p.S1561fs	frameshift deletion	0.455	1049	No	.	.
OAML191	chr4:106196753	T	-	TET2	c.5086delT	p.Y1696fs	frameshift deletion	0.390	1049	No	.	.
OAML254	chr4:106196907	0	-	TET2	c.5240_5253del	p.P1747fs	frameshift deletion	0.391	877	Yes	Yes	0.070
OAML238	chr4:106197038	-	C	TET2	c.5372dupC	p.S1791fs	frameshift insertion	0.396	1001	Yes	Yes	0.095
OAML074	chr4:106197273	G	T	TET2	c.G5606T	p.G1869V	nonsynonymous SNV	0.233	935	No	.	.
OAML173	chr4:106197285	T	C	TET2	c.T5618C	p.I1873T	nonsynonymous SNV	0.480	759	No	.	.
OAML227	chr4:106197285	T	C	TET2	c.T5618C	p.I1873T	nonsynonymous SNV	0.452	644	No	.	.
OAML282	Chr4:106197285	T	C	TET2	c.T5618C	p.I1873T	nonsynonymous SNV	0.241	398	Yes	Yes	0.007

subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML322	Chr4:106197285	T	C	TET2	c.T5618C	p.I1873T	nonsynonymous SNV	0.242	1041	No	.	.
OAML100	chr4:106197317	A	-	TET2	c.5650delA	p.T1884fs	frameshift deletion	0.249	1046	No	.	.
OAML138	chr4:106197348	C	A	TET2	c.C5681A	p.P1894H	nonsynonymous SNV	0.466	1137	Yes	Yes	0.214
OAML266	chr4:106197552	C	T	TET2	c.C5885T	p.P1962L	nonsynonymous SNV	0.503	753	Yes	Yes	0.464
OAML220	chr17:7576541	G	A	TP53	c.C560T	p.S187L	nonsynonymous SNV	0.488	252	No	.	.
OAML240	chr17:7577049	0	-	TP53	c.861_889del	p.E287fs	frameshift deletion	0.022	815	Yes	No	0.000
OAML212	chr17:7577087	G	A	TP53	c.C851T	p.T284I	nonsynonymous SNV	0.476	777	No	.	.
OAML036	chr17:7577114	C	A	TP53	c.G824T	p.C275F	nonsynonymous SNV	0.203	645	Yes	Yes	0.049
OAML239	chr17:7577114	C	T	TP53	c.G824A	p.C275Y	nonsynonymous SNV	0.433	367	Yes	Yes	0.262
OAML132	chr17:7577120	C	T	TP53	c.G818A	p.R273H	nonsynonymous SNV	0.761	860	Yes	Yes	0.764
OAML171	chr17:7577120	C	T	TP53	c.G818A	p.R273H	nonsynonymous SNV	0.473	778	No	.	.
OAML283	Chr17:7577120	C	T	TP53	c.G818A	p.R273H	nonsynonymous SNV	0.211	190	Yes	Yes	0.004
OAML288	Chr17:7577120	C	T	TP53	c.G818A	p.R273H	nonsynonymous SNV	0.301	219	Yes	Yes	0.003
OAML137	chr17:7577144	A	G	TP53	c.T794C	p.L265P	nonsynonymous SNV	0.811	555	Yes	Yes	0.131
OAML317	Chr17:7577511	A	G	TP53	c.T770C	p.L257P	nonsynonymous SNV	0.037	833	No	.	.
OAML317	Chr17:7577520	A	T	TP53	c.T761A	p.I254N	nonsynonymous SNV	0.065	784	No	.	.
OAML090	chr17:7577556	C	T	TP53	c.G725A	p.C242Y	nonsynonymous SNV	0.300	534	Yes	No	0.000
OAML064	chr17:7577559	G	A	TP53	c.C722T	p.S241F	nonsynonymous SNV	0.377	576	Yes	Yes	0.039
OAML126	chr17:7577559	G	T	TP53	c.C722A	p.S241Y	nonsynonymous SNV	0.410	486	Yes	No	0.000
OAML242	chr17:7577563	T	C	TP53	c.A718G	p.S240G	nonsynonymous SNV	0.784	342	Yes	Yes	0.231
OAML134	chr17:7577566	-	A	TP53	c.714dupT	p.N239_S24(	stopgain	0.474	591	Yes	Yes	0.188
OAML207	chr17:7577568	C	A	TP53	c.G713T	p.C238F	nonsynonymous SNV	0.028	614	No	.	.
OAML062	chr17:7577580	T	C	TP53	c.A701G	p.Y234C	nonsynonymous SNV	0.421	496	Yes	Yes	0.002
OAML066	chr17:7577580	T	C	TP53	c.A701G	p.Y234C	nonsynonymous SNV	0.825	718	Yes	Yes	0.020
OAML009	chr17:7577587	T	A	TP53	c.A694T	p.I232F	nonsynonymous SNV	0.734	488	Yes	Yes	0.002
OAML052	chr17:7578190	T	C	TP53	c.A659G	p.Y220C	nonsynonymous SNV	0.410	603	Yes	Yes	0.036
OAML287	Chr17:7578211	C	A	TP53	c.G638T	p.R213L	nonsynonymous SNV	0.168	435	Yes	Yes	0.001
OAML164	chr17:7578263	G	A	TP53	c.C586T	p.R196X	stopgain	0.312	413	No	.	.
OAML013	chr17:7578382	G	C	TP53	c.C548G	p.S183X	stopgain	0.333	18	Yes	Yes	0.834
OAML052	chr17:7578406	C	T	TP53	c.G524A	p.R175H	nonsynonymous SNV	0.417	743	Yes	Yes	0.038
OAML100	chr17:7578428	G	-	TP53	c.502delC	p.H168fs	frameshift deletion	0.381	766	No	.	.
OAML317	Chr17:7578443	A	G	TP53	c.T487C	p.Y163H	nonsynonymous SNV	0.102	1006	No	.	.
OAML317	Chr17:7578460	A	C	TP53	c.T470G	p.V157G	nonsynonymous SNV	0.139	917	No	.	.
OAML239	chr17:7578465	0	-	TP53	c.461_465del	p.G154fs	frameshift deletion	0.343	344	Yes	No	0.000
OAML047	chr17:7578478	G	T	TP53	c.C452A	p.P151H	nonsynonymous SNV	0.237	812	Yes	Yes	0.021
OAML109	chr17:7578479	G	C	TP53	c.C451G	p.P151A	nonsynonymous SNV	0.055	1000	No	.	.
OAML041	chr17:7578508	C	T	TP53	c.G422A	p.C141Y	nonsynonymous SNV	0.122	517	Yes	No	0.000
OAML136	chr17:7578532	A	G	TP53	c.T398C	p.M133T	nonsynonymous SNV	0.063	718	Yes	No	0.000
OAML092	chr17:7578535	T	C	TP53	c.A395G	p.K132R	nonsynonymous SNV	0.064	701	No	.	.
OAML069	Chr17:7578553	T	G	TP53	c.A377C	p.Y126S	nonsynonymous SNV	0.927	68	Yes	Yes	0.095
OAML064	chr17:7578555	C	T	TP53	c.259-1G>A		splicing	0.049	567	Yes	Yes	0.135
OAML131	chr17:7578556	T	C	TP53	c.259-2A>G		splicing	0.858	507	Yes	Yes	0.263
OAML054	chr17:7579358	C	T	TP53	c.G329A	p.R110H	nonsynonymous SNV	0.463	583	No	.	.
OAML030	Chr21:44514777	T	G	U2AF1	c.A470C	p.Q157P	nonsynonymous SNV	0.421	394	No	.	.
OAML169	chr21:44514777	T	G	U2AF1	c.A470C	p.Q157P	nonsynonymous SNV	0.452	578	No	.	.
OAML178	chr21:44514777	T	G	U2AF1	c.A470C	p.Q157P	nonsynonymous SNV	0.337	680	No	.	.
OAML247	chr21:44514777	T	G	U2AF1	c.A470C	p.Q157P	nonsynonymous SNV	0.326	899	Yes	No	0.000
OAML264	chr21:44514777	T	C	U2AF1	c.A470G	p.Q157R	nonsynonymous SNV	0.355	726	Yes	Yes	0.019
OAML322	Chr21:44514777	T	G	U2AF1	c.A470C	p.Q157P	nonsynonymous SNV	0.265	1040	No	.	.
OAML023	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.417	612	Yes	Yes	0.343
OAML039	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.121	587	Yes	Yes	0.133
OAML042	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.291	539	Yes	Yes	0.001
OAML054	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.304	483	No	.	.
OAML067	Chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.486	107	Yes	Yes	0.017
OAML117	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.380	637	Yes	Yes	0.022
OAML153	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.492	463	Yes	Yes	0.315
OAML176	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.432	472	No	.	.
OAML204	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.234	410	Yes	Yes	0.199
OAML228	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.455	288	No	.	.
OAML249	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.434	465	Yes	Yes	0.439
OAML251	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.439	529	Yes	Yes	0.061
OAML264	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.346	480	Yes	Yes	0.027
OAML271	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.449	534	Yes	No	0.000
OAML280	chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.435	545	Yes	Yes	0.185
OAML285	Chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.293	99	Yes	No	0.000
OAML313	Chr21:44524456	G	A	U2AF1	c.C101T	p.S34F	nonsynonymous SNV	0.225	546	No	.	.
OAML211	chr11:32413556	T	C	WT1	c.A1394G	p.H465R	nonsynonymous SNV	0.026	643	No	.	.
OAML235	chr11:32413560	C	T	WT1	c.G1390A	p.D464N	nonsynonymous SNV	0.468	502	Yes	No	0.000
OAML183	chr11:32413584	A	C	WT1	c.T1366G	p.C456G	nonsynonymous SNV	0.092	492	No	.	.
OAML183	chr11:32414250	C	G	WT1	c.G1301C	p.R434P	nonsynonymous SNV	0.340	592	No	.	.
OAML058	chr11:32417907	-	CCG.	WT1	c.1144_1145insT	p.A382fs	frameshift insertion	0.199	956	Yes	No	0.000
OAML061	chr11:32417907	-	C	WT1	c.1144dupG	p.A382fs	frameshift insertion	0.020	486	Yes	Yes	0.003
OAML245	chr11:32417907	G	-	WT1	c.1145delC	p.A382fs	frameshift deletion	0.481	898	Yes	No	0.000
OAML093	chr11:32417909	-	GAC(	WT1	c.1142_1143insT	p.S381fs	frameshift insertion	0.246	1276	Yes	No	0.000
OAML262	chr11:32417909	-	GAC(	WT1	c.1142_1143insC	p.S381fs	frameshift insertion	0.306	788	Yes	No	0.000



subject_id	chrom:pos_start	ref	var	gene	cdna	aa	Result	Diagnostic VAF	Depth	Remission Sample	Detected in Remission	Remission VAF
OAML267	chr11:32417909	-	GAC	WT1	c.1142_1143insT	p.S381fs	frameshift insertion	0.136	352	Yes	No	0.000
OAML018	chr11:32417911	-	C	WT1	c.1140dupG	p.S381fs	frameshift insertion	0.156	1104	Yes	Yes	0.006
OAML085	chr11:32417911	-	CC	WT1	c.1140_1141ins	p.S381fs	frameshift insertion	0.275	1053	Yes	No	0.000
OAML106	chr11:32417923	-	AGG	WT1	c.1128_1129ins	p.T377fs	frameshift insertion	0.043	865	Yes	No	0.000
OAML233	chr11:32417923	-	ACT	WT1	c.1128_1129ins	p.T377_L378	stopgain	0.154	494	Yes	No	0.000
OAML261	chr11:32417924	C	-	WT1	c.1128delG	p.P376fs	frameshift deletion	0.343	792	Yes	No	0.000
OAML194	chr11:32417941	-	A	WT1	c.1110dupT	p.V371fs	frameshift insertion	0.118	491	Yes	No	0.000
OAML206	chr11:32417941	-	A	WT1	c.1110dupT	p.V371fs	frameshift insertion	0.226	708	No	.	.
OAML087	chr11:32417947	G	A	WT1	c.C1105T	p.R369X	stopgain	0.235	1130	Yes	No	0.000
OAML192	chr11:32417947	G	A	WT1	c.C1105T	p.R369X	stopgain	0.099	629	Yes	Yes	0.001
OAML236	chr11:32456245	C	A	WT1	c.646+1G>T		splicing	0.099	513	Yes	No	0.000
OAML117	chr11:32456251	-	AAG	WT1	c.640_641insTT	p.N214fs	frameshift insertion	0.362	594	Yes	No	0.000
OAML214	chr11:32456318	G	A	WT1	c.C574T	p.Q192X	stopgain	0.431	735	No	.	.
OAML317	ChrX:15838328	A	C	ZRSR2	c.828-2A>C		splicing	0.181	365	No	.	.
OAML120	chrX:15840871	C	-	ZRSR2	c.955delC	p.Q319fs	frameshift deletion	0.108	370	Yes	No	0.000

Table S6. Univariable molecular associations with outcomes

	LFS			Relapse			NRM		
	HR	95% CI	P value	sHR	95% CI	P value	sHR	95% CI	P value
NPM1+, *FLT3*-ITD-	0.56	0.37-0.81	0.002	0.56	0.31-0.91	0.02	0.75	0.38-1.33	0.29
DNMT3A	0.73	0.51-1.02	0.056	0.68	0.44-1.04	0.068	0.94	0.55-1.53	0.78
DDX41	0.55	0.25-0.95	0.036	0.23	0-0.68	0.008	1.36	0.46-2.55	0.44
TP53	3.36	2.32-5.23	<0.001	5.6	3.52-9.17	<0.001	0.28	0-0.73	0.002
JAK2	2.66	1.88-4.08	<0.001	1.62	0.6-3.25	0.276	2.23	0.58-5.6	0.18
FLT3-ITD+, *NPM1*-	2.22	1.49-3.41	<0.001	2.28	1.18-3.88	0.012	1.07	0.38-2.25	0.86
KRAS	2.00	1.36-2.95	0.004	1.3	0.54-2.61	0.546	2.25	1.07-4.17	0.034

HR: hazard ratio from Cox proportional hazards model; sHR: subdistribution hazard ratio from Fine and Gray model.

Table S7. Univariable non-genetic associations with leukemia-free survival

	HR	95% CI	P value
Age ≥ 65 at transplant	1.3	0.96-1.77	0.09
Adverse cytogenetics, not monosomal	1.7	1.1-2.6	0.013
Adverse, monosomal	4.4	2.9-6.8	<0.001
sAML	1.77	1.31-2.38	0.0002
Prior HMA	1.68	1.12-2.51	0.012
Non-intensive induction	1.56	1.09-2.24	0.016
Consolidation prior to transplant	0.7	0.52-0.94	0.016
CRi	1.83	1.32-2.54	0.0003
WBC < 2k at transplant	1.67	1.18-2.35	0.0034
HCT-CI ≥ 3	1.8	1.3-2.7	0.002

Table S8. Score assigned based on hazard ratio

For each variable in the final model for LFS, scores were assigned based on the hazard ratio for death or relapse. Details are in the supplemental methods.

HR	Score
1.00 - 1.50	0.5
1.51 - 2.00	1
2.01 - 2.50	1.5
>2.5	2

Table S9. Cox frailty model for LFS incorporating both clinical and genetic factors

Five variables retained significance in a multivariable Cox model for LFS. The score assigned for each variable level is reported in the final column of the table. Additional details are in the supplemental methods.

		HR	95% CI	Score Assigned
Cytogenetics	Favorable/Intermediate	Ref		0
	Adverse, not monosomal	1.56	0.93-2.59	1
	Adverse, monosomal	2.32	1.37-3.97	1.5
HCT-CI	0-2	Ref		0
	≥ 3	1.39	1.01-1.95	0.5
CR	CR	Ref		0
	CRi	1.49	1.05-2.16	0.5
sAML	No	Ref		0
	Yes	1.54	1.12-2.14	1
Molecular risk	Favorable	Ref		0
	Intermediate	1.31	0.88-2.00	0.5
	High	2.90	1.85-4.64	2

Table S10. Non-genetic associations with relapse and NRM

Shown are the associations with relapse and NRM for the four variables other than molecular risk that are included in the final model.

Variable		Relapse			NRM		
		sHR	95% CI	P value	sHR	95% CI	P-value
Cytogenetics	Favorable/Intermediate	Ref					
	Adverse, not monosomal	1.54	0.87-2.73	0.13	1.24	0.65-2.37	0.52
	Adverse, monosomal	4.37	2.65-7.21	<0.0001	0.87	0.37-2.04	0.75
HCT-CI	0-2	Ref			Ref		
	≥ 3	0.98	0.67 – 1.44	0.93	2.38	1.50-3.78	0.0002
CR	CR	Ref			Ref		
	CRi	1.95	1.30 – 2.90	0.0011	1.04	0.60-1.78	0.89
sAML	No	Ref			Ref		
	Yes	1.58	1.07 – 2.33	0.0207	1.46	0.91-2.33	0.11

sHR: subdistribution hazard ratio from Fine and Gray model.

Table S11. Assignment of prognostic groups based on score

Shown are the hazard ratios for death or relapse based on total scores for all 5 variables in the model, with corresponding prognostic groups labeled in the final column.

Sum score	HR	95% CI	Prognostic Group
0	Ref		Low
0.5	2.88	1.33-8.46	Int
1	3.39	1.5-9.96	
1.5	6.23	2.58-19.92	High
2	4.16	1.83-12.51	
2.5	8.70	3.86-26.19	Very High
3	10.07	3.32-38.93	
3.5	21.84	9.21-74.02	
4	21.98	9.92-65.78	

Table S12. LFS, OS, Relapse, NRM for baseline prognostic groups

Shown are the hazard ratios (HR) for leukemia-free survival (LFS), and overall survival (OS) from Cox proportional hazards models and subdistribution hazard ratios (sHR) for non-relapse mortality (NRM) and relapse from Fine and Gray models for the four tiers of overall risk in the final model.

	N	LFS			OS			NRM			Relapse		
		HR	95% CI	p-value	HR	95% CI	p-value	HR	95% CI	p-value	HR	95% CI	p-value
Low	35	Ref			Ref			Ref			Ref		
Int	113	3.7	1.8-11.3	0.0004	3.6	1.7-10.9	0.0006	11.5	2.7-80.8	0.02	1.7	0.8-6.4	0.17
High	71	5.6	2.6-17.7	<0.0001	5.4	2.5-16.8	<0.0001	15.7	3.6-110.2	0.0095	2.3	1.0-8.5	0.037
V high	74	13.4	6.3-42.2	<0.0001	12.7	5.9-40.3	<0.0001	12.5	2.9-87.7	0.018	6.4	3.0-22.9	<0.0001

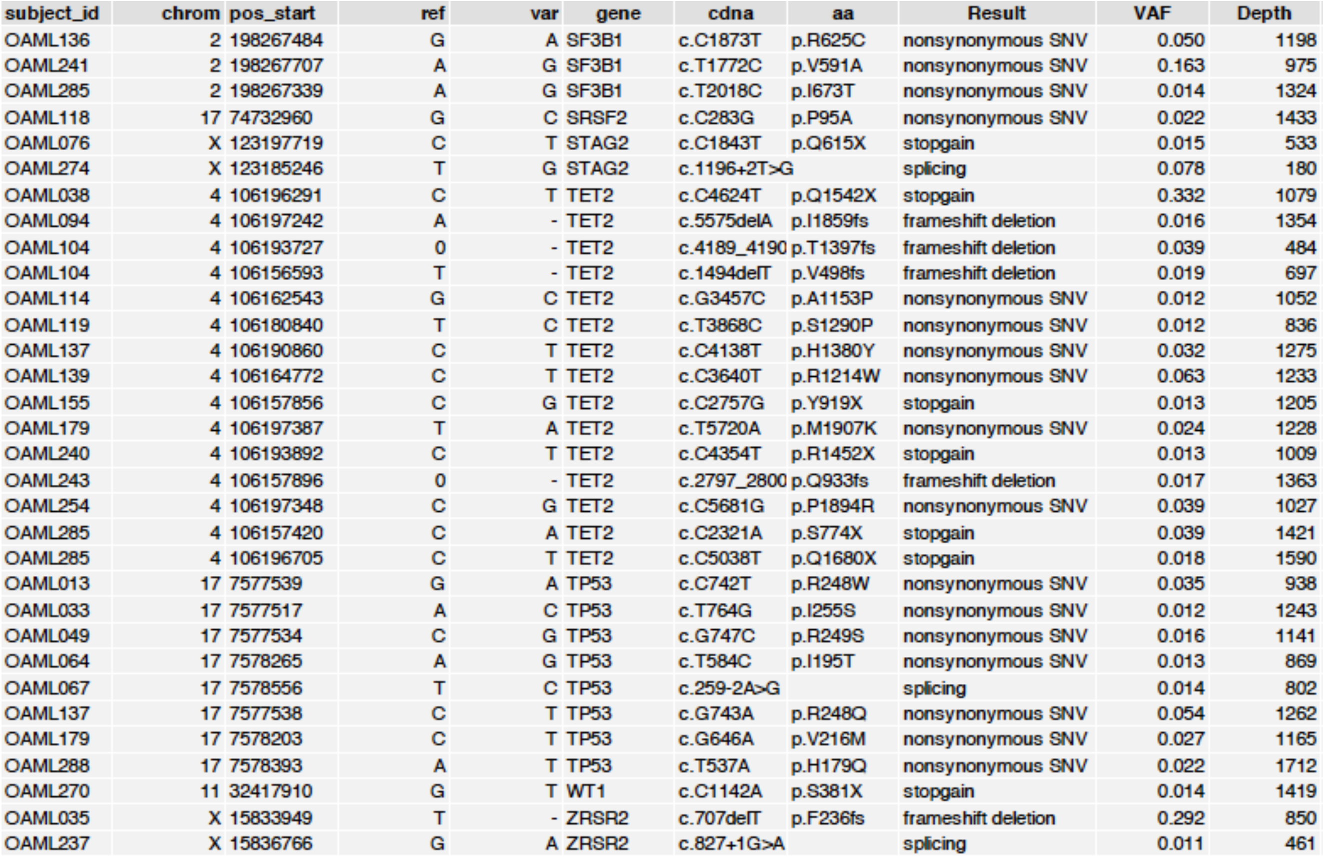
Table S13. Outcomes 3 years after transplant

Shown are the 3-year rates of leukemia-free survival (LFS), overall survival (OS), non-relapse mortality (NRM), and relapse for the four tiers of overall risk in the final model. The Kaplan-Meier method was used to estimate LFS and OS and log-rank test was used for group comparison of LFS and OS. Cumulative incidence (CI) of NRM and relapse were estimated in the competing risks framework treating each event as a competing event. Gray test was used for group comparison of CI (cumulative incidence) of NRM and relapse.

	N	LFS (95% CI)	OS (95% CI)	CI NRM (95% CI)	CI Relapse (95% CI)
Low	35	86% (69, 94)	86% (69, 94)	2.9% (0.2, 13)	11% (3.5, 24)
Intermediate	113	54% (44, 63)	58% (48, 67)	20% (13, 28)	26% (18, 35)
High	71	35% (23, 47)	35% (23, 47)	32% (21, 43)	33% (22, 45)
Very high	74	9% (4, 17)	9% (4, 17)	26% (16, 36)	65% (53, 75)
p-value		<0.0001	<0.0001	0.006	<0.0001

Table S14. Treatment-Emergent Mutations

subject_id	chrom	pos_start	ref	var	gene	cdna	aa	Result	VAF	Depth
OAML007	20	31023777	C	T	ASXL1	c.C3262T	p.Q1088X	stopgain	0.093	1606
OAML254	20	31023360	0	-	ASXL1	c.2845_2846	p.G949fs	frameshift deletion	0.011	1203
OAML285	20	31024395	C	T	ASXL1	c.C3880T	p.Q1294X	stopgain	0.013	1663
OAML121	X	154348290	G	-	BRCC3	c.744delG	p.L248fs	frameshift deletion	0.070	472
OAML238	X	154348273	G	A	BRCC3	c.728-1G>A		splicing	0.039	330
OAML254	X	154299812	C	T	BRCC3	c.C10T	p.Q4X	stopgain	0.043	536
OAML036	11	119148949	A	T	CBL	c.A1169T	p.D390V	nonsynonymous SNV	0.020	565
OAML243	11	119149248	G	A	CBL	c.G1256A	p.C419Y	nonsynonymous SNV	0.066	1161
OAML051	7	101882758	C	T	CUX1	c.C3781T	p.R1261X	stopgain	0.011	1329
OAML076	7	101891808	G	-	CUX1	c.4004delG	p.G1335fs	frameshift deletion	0.019	1266
OAML003	2	25468133	G	A	DNMT3A	c.C1543T	p.Q515X	stopgain	0.023	778
OAML005	2	25457242	C	T	DNMT3A	c.G2645A	p.R882H	nonsynonymous SNV	0.043	1305
OAML005	2	25471019	G	A	DNMT3A	c.C742T	p.Q248X	stopgain	0.013	1373
OAML057	2	25462017	T	C	DNMT3A	c.A2390G	p.N797S	nonsynonymous SNV	0.041	1427
OAML063	2	25457252	T	C	DNMT3A	c.A2635G	p.N879D	nonsynonymous SNV	0.041	710
OAML072	2	25466800	G	A	DNMT3A	c.C1903T	p.R635W	nonsynonymous SNV	0.018	1011
OAML094	2	25458644	G	-	DNMT3A	c.2529delC	p.G843fs	frameshift deletion	0.122	1140
OAML098	2	25462086	T	C	DNMT3A	c.1867-2A>G		splicing	0.012	677
OAML117	2	25469072	C	-	DNMT3A	c.1386delG	p.A462fs	frameshift deletion	0.014	1124
OAML124	2	25463510	G	T	DNMT3A	c.C2172A	p.Y724X	stopgain	0.013	915
OAML126	2	25463562	C	T	DNMT3A	c.G2120A	p.G707D	nonsynonymous SNV	0.023	914
OAML137	2	25469139	C	T	DNMT3A	c.G1319A	p.W440X	stopgain	0.039	1402
OAML138	2	25464535	A	G	DNMT3A	c.T1978C	p.Y660H	nonsynonymous SNV	0.046	1135
OAML146	2	25463289	T	C	DNMT3A	c.A2204G	p.Y735C	nonsynonymous SNV	0.011	1236
OAML151	2	25463182	G	A	DNMT3A	c.C2311T	p.R771X	stopgain	0.148	772
OAML151	2	25461998	C	A	DNMT3A	c.1952+1G>T		splicing	0.024	765
OAML151	2	25463548	C	T	DNMT3A	c.G2134A	p.D712N	nonsynonymous SNV	0.010	973
OAML194	2	25466773	C	T	DNMT3A	c.G1930A	p.A644T	nonsynonymous SNV	0.011	831
OAML235	2	25458637	G	A	DNMT3A	c.C2536T	p.Q846X	stopgain	0.027	1196
OAML242	2	25463596	G	A	DNMT3A	c.C2086T	p.Q696X	stopgain	0.096	781
OAML250	2	25463240	G	T	DNMT3A	c.C2253A	p.F751L	nonsynonymous SNV	0.014	880
OAML273	2	25470002	A	T	DNMT3A	c.T1040A	p.L347Q	nonsynonymous SNV	0.010	882
OAML285	2	25462007	A	-	DNMT3A	c.2400delT	p.G800fs	frameshift deletion	0.060	1344
OAML001	22	41526008	G	A	EP300	c.1282+1G>A		splicing	0.019	216
OAML263	7	148508719	C	G	EZH2	c.G1945C	p.E649Q	nonsynonymous SNV	0.011	616
OAML025	9	5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.414	674
OAML068	9	5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.397	708
OAML116	9	5073770	G	T	JAK2	c.G1849T	p.V617F	nonsynonymous SNV	0.020	872
OAML179	12	122012473	G	A	KDM2B	c.C283T	p.R95X	stopgain	0.010	1269
OAML116	1	43815009	G	T	MPL	c.G1544T	p.W515L	nonsynonymous SNV	0.020	1282
OAML265	17	29562641	C	T	NF1	c.C3721T	p.R1241X	stopgain	0.057	1149
OAML270	1	115258744	C	T	NRAS	c.G38A	p.G13D	nonsynonymous SNV	0.019	1405
OAML001	X	133527983	G	A	PHF6	c.418+1G>A		splicing	0.327	205
OAML268	X	133551278	G	A	PHF6	c.G914A	p.C305Y	nonsynonymous SNV	0.103	1094
OAML268	X	133551319	C	T	PHF6	c.C955T	p.R319X	stopgain	0.016	740
OAML268	X	133527636	C	T	PHF6	c.C346T	p.R116X	stopgain	0.015	954
OAML268	X	133551203	G	A	PHF6	c.G839A	p.C280Y	nonsynonymous SNV	0.014	871
OAML269	X	133551305	T	C	PHF6	c.T941C	p.I314T	nonsynonymous SNV	0.030	1059
OAML269	X	133549137	G	A	PHF6	c.G821A	p.R274Q	nonsynonymous SNV	0.030	1140
OAML007	17	58740498	C	G	PPM1D	c.C1403G	p.S468X	stopgain	0.019	1048
OAML021	17	58740432	C	A	PPM1D	c.C1337A	p.S446X	stopgain	0.017	1213
OAML042	17	58740737	A	T	PPM1D	c.A1642T	p.K548X	stopgain	0.055	904
OAML047	17	58740749	C	T	PPM1D	c.C1654T	p.R552X	stopgain	0.015	1208
OAML064	17	58740749	C	T	PPM1D	c.C1654T	p.R552X	stopgain	0.158	843
OAML064	17	58740710	G	T	PPM1D	c.G1615T	p.E539X	stopgain	0.021	780
OAML095	17	58740432	C	G	PPM1D	c.C1337G	p.S446X	stopgain	0.048	1192
OAML095	17	58740375	G	A	PPM1D	c.G1280A	p.W427X	stopgain	0.011	1039
OAML229	17	58740543	C	-	PPM1D	c.1448delC	p.T483fs	frameshift deletion	0.020	984
OAML236	17	58740707	-	C	PPM1D	c.1612_1613	p.L538fs	frameshift insertion	0.091	1018
OAML259	17	58740809	C	T	PPM1D	c.C1714T	p.R572X	stopgain	0.016	1088
OAML288	17	58740518	G	T	PPM1D	c.G1423T	p.E475X	stopgain	0.101	1598
OAML013	12	112924357	G	A	PTPN11	c.G1303A	p.V435M	nonsynonymous SNV	0.415	978
OAML099	12	112910775	C	T	PTPN11	c.C784T	p.L262F	nonsynonymous SNV	0.017	931
OAML155	12	112888172	A	G	PTPN11	c.A188G	p.Y63C	nonsynonymous SNV	0.020	1033
OAML231	12	112926270	C	T	PTPN11	c.C1403T	p.T468M	nonsynonymous SNV	0.066	1138
OAML235	8	117868978	-	A	RAD21	c.720dupT	p.I241fs	frameshift insertion	0.024	1009
OAML076	21	36206763	-	T	RUNX1	c.748_749ins	p.R250fs	frameshift insertion	0.012	1368
OAML038	18	42531907	G	A	SETBP1	c.G2602A	p.D868N	nonsynonymous SNV	0.254	993



subject_id	chrom	pos_start	ref	var	gene	cdna	aa	Result	VAF	Depth
OAML136	2	198267484	G	A	SF3B1	c.C1873T	p.R625C	nonsynonymous SNV	0.050	1198
OAML241	2	198267707	A	G	SF3B1	c.T1772C	p.V591A	nonsynonymous SNV	0.163	975
OAML285	2	198267339	A	G	SF3B1	c.T2018C	p.I673T	nonsynonymous SNV	0.014	1324
OAML118	17	74732960	G	C	SRSF2	c.C283G	p.P95A	nonsynonymous SNV	0.022	1433
OAML076	X	123197719	C	T	STAG2	c.C1843T	p.Q615X	stopgain	0.015	533
OAML274	X	123185246	T	G	STAG2	c.1196+2T>G		splicing	0.078	180
OAML038	4	106196291	C	T	TET2	c.C4624T	p.Q1542X	stopgain	0.332	1079
OAML094	4	106197242	A	-	TET2	c.5575delA	p.I1859fs	frameshift deletion	0.016	1354
OAML104	4	106193727	0	-	TET2	c.4189_4190	p.T1397fs	frameshift deletion	0.039	484
OAML104	4	106156593	T	-	TET2	c.1494delT	p.V498fs	frameshift deletion	0.019	697
OAML114	4	106162543	G	C	TET2	c.G3457C	p.A1153P	nonsynonymous SNV	0.012	1052
OAML119	4	106180840	T	C	TET2	c.T3868C	p.S1290P	nonsynonymous SNV	0.012	836
OAML137	4	106190860	C	T	TET2	c.C4138T	p.H1380Y	nonsynonymous SNV	0.032	1275
OAML139	4	106164772	C	T	TET2	c.C3640T	p.R1214W	nonsynonymous SNV	0.063	1233
OAML155	4	106157856	C	G	TET2	c.C2757G	p.Y919X	stopgain	0.013	1205
OAML179	4	106197387	T	A	TET2	c.T5720A	p.M1907K	nonsynonymous SNV	0.024	1228
OAML240	4	106193892	C	T	TET2	c.C4354T	p.R1452X	stopgain	0.013	1009
OAML243	4	106157896	0	-	TET2	c.2797_2800	p.Q933fs	frameshift deletion	0.017	1363
OAML254	4	106197348	C	G	TET2	c.C5681G	p.P1894R	nonsynonymous SNV	0.039	1027
OAML285	4	106157420	C	A	TET2	c.C2321A	p.S774X	stopgain	0.039	1421
OAML285	4	106196705	C	T	TET2	c.C5038T	p.Q1680X	stopgain	0.018	1590
OAML013	17	7577539	G	A	TP53	c.C742T	p.R248W	nonsynonymous SNV	0.035	938
OAML033	17	7577517	A	C	TP53	c.T764G	p.I255S	nonsynonymous SNV	0.012	1243
OAML049	17	7577534	C	G	TP53	c.G747C	p.R249S	nonsynonymous SNV	0.016	1141
OAML064	17	7578265	A	G	TP53	c.T584C	p.I195T	nonsynonymous SNV	0.013	869
OAML067	17	7578556	T	C	TP53	c.259-2A>G		splicing	0.014	802
OAML137	17	7577538	C	T	TP53	c.G743A	p.R248Q	nonsynonymous SNV	0.054	1262
OAML179	17	7578203	C	T	TP53	c.G646A	p.V216M	nonsynonymous SNV	0.027	1165
OAML288	17	7578393	A	T	TP53	c.T537A	p.H179Q	nonsynonymous SNV	0.022	1712
OAML270	11	32417910	G	T	WT1	c.C1142A	p.S381X	stopgain	0.014	1419
OAML035	X	15833949	T	-	ZRSR2	c.707delT	p.F236fs	frameshift deletion	0.292	850
OAML237	X	15836766	G	A	ZRSR2	c.827+1G>A		splicing	0.011	461

Table S15. Likelihood of mutation persistence by gene mutated at AML diagnosis.

Shown are all genes mutated at the time of AML diagnosis in at least 5 individuals with available remission samples. Significant associations (P<0.05) are highlighted in gray. Note that *DDX41* mutations shown here include only putative somatic mutations.

Gene	N, persisting	N, diagnosis	%	OR for persistence	95% CI	P value
ASXL1	30	38	79	3.5	1.6-7.7	0.0016
BCOR	23	13	57	1.5	0.66-3.4	0.40
BCORL1	3	8	38	0.67	0.18-2.6	0.73
CBL	6	2	33	0.6	0.1-2.4	0.69
CEBPA	1	16	6	0.07	0.006-0.43	0.0006
DDX41	2	9	22	0.3	0.06-1.4	0.18
DNMT3A	55	66	83	6.6	3.4-12.7	<0.0001
EZH2	5	12	42	0.81	0.29-2.3	0.78
FLT3-ITD	11	58	19	0.24	0.12-0.46	<0.0001
FLT3-TKD	2	10	20	0.29	0.06-1.1	0.11
GATA2	2	10	20	0.29	0.06-1.1	0.11
IDH1	12	24	50	1.1	0.5-2.6	0.84
IDH2	16	28	57	1.6	0.7-3.3	0.33
JAK2	4	8	50	1.1	0.3-3.8	>0.99
KRAS	4	21	19	0.25	0.09-0.76	0.013
NF1	5	7	71	2.8	0.6-14.1	0.27
NPM1	4	43	9	0.1	0.04-0.28	<0.0001
NRAS	6	28	21	0.30	0.13-0.73	0.0064
PHF6	3	11	27	0.4	0.12-1.4	0.23
PTPN11	7	23	30	0.49	0.19-1.2	0.14
RUNX1	24	53	45	0.94	0.54-1.7	0.89
SF3B1	6	7	86	6.7	1.1-77.6	0.057
SRSF2	20	32	63	2.0	0.94-4.0	0.072
STAG2	10	24	42	0.81	0.37-1.8	0.68
TET2	47	61	77	4.2	2.3-7.8	<0.0001
TP53	20	26	77	3.8	1.5-9.1	0.0036
U2AF1	12	15	80	4.6	1.4-15.2	0.016
WT1	3	17	18	0.23	0.07-0.79	0.024

Table S16. Comparison of molecular and flow-cytometry based MRD assessments.

87 patients in the remission cohort had data available from clinical evaluation of MRD by flow cytometry. This table shows the results of a comparison between these assessments ("Flow MRD") and results of remission sample sequencing ("molecular MRD").

	Flow MRD+	Flow MRD-
Molecular MRD+	21	32
Molecular MRD-	5	29

Table S17. Univariable and multivariable associations with MRD positivity

		Univariable Logistic			Multivariable Logistic		
		OR	95% CI	P value	OR	95% CI	P value
sAML	Y vs N	1.9	1.0-3.7	0.05	1.0	0.4-2.2	0.98
CRi	Y vs N	4.5	1.9-10.8	0.0006	3.7	1.5-9.1	0.0048
Prior HMA	Y vs N	3.4	1.2-9.6	0.023	1.4	0.4-5.2	0.63
Intensive induction	Y vs N	3.0	1.2-7.8	0.021	1.1	0.4-3.2	0.91
Any consolidation	Y vs N	0.5	0.3-1.0	0.052	0.7	0.4-1.6	0.44
Cytogenetic risk	Int vs Low	2.5	1.0-6.3	0.048	1.8	0.7-4.8	0.2
	High vs Low	6.4	1.4-28.9	0.016	5.7	1.2-26.6	0.027
Molecular ontogeny	Secondary vs De Novo	8.0	3.9-16.4	<0.0001	7.9	3.6-17.0	<0.0001
	P53 vs De Novo	8.4	2.6-27.0	0.0003	7.7	2.3-26.0	0.001

Figure S1. Post-transplant outcomes of the full cohort.

Shown are overall survival and leukemia-free survival (A), as well as cumulative incidence of relapse and cumulative incidence of non-relapse mortality (B) for full cohort.

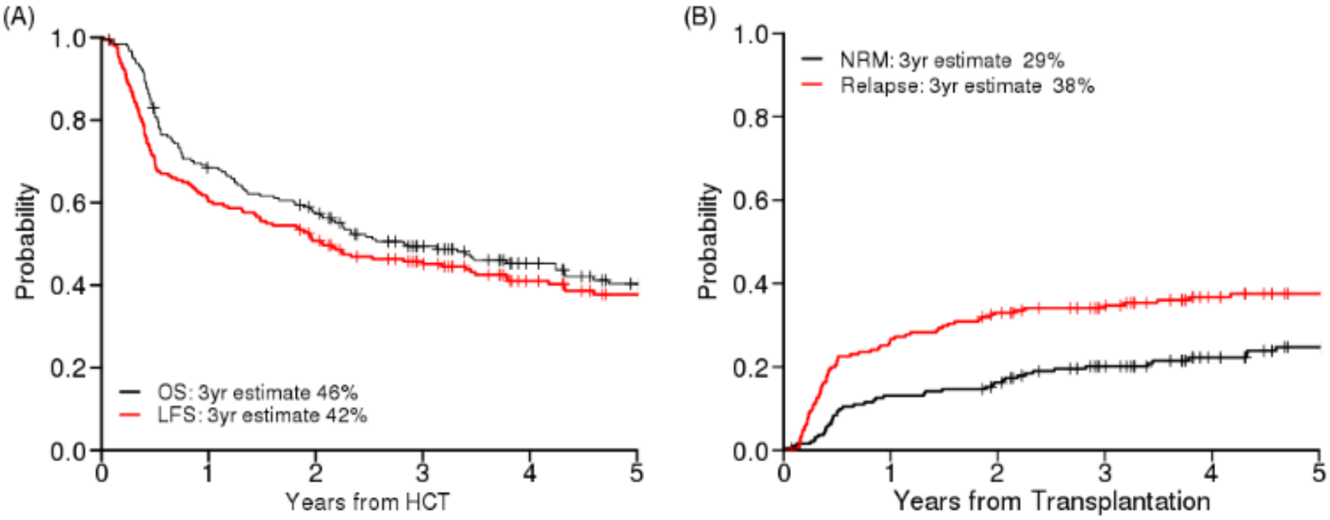


Figure S2. Outcomes by molecular risk group.

Shown are outcomes for patients with unfavorable genetics (*TP53* mutation, *JAK2* mutation, or *FLT3*-ITD without an *NPM1* mutation), favorable genetics (absence of unfavorable mutation plus either *NPM1* mutation without *FLT3-ITD*, *DDX41* mutation, or *DNMT3A* mutation), and intermediate genetics (all others).

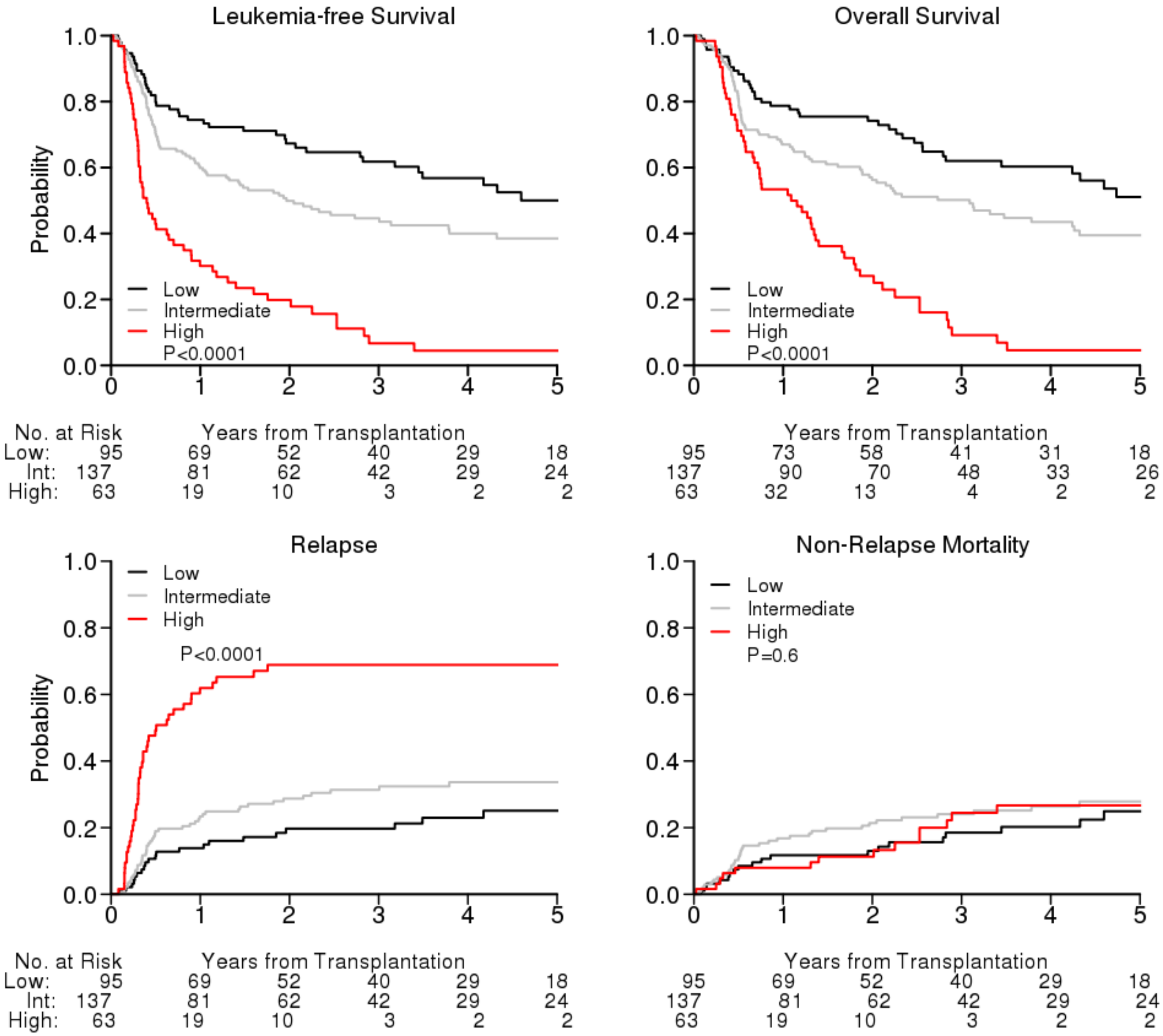


Figure S3. Likelihood of mutation persistence by gene using ELN definition of MRD

This figure shows the results of Fisher’s exact test for clearance or persistence of mutations in each gene, plotting the odds of clearance on the x axis and significance, expressed as the negative log of the uncorrected P value, on the y axis. Mutations that are more likely to persist at remission appear towards the left, and those that are more likely to clear appear towards the right. Panel B shows the variant allele frequency (VAF) of remission mutations. Median VAF is denoted by a black dashed line, and the range is indicated by the red violin plot for each gene. This analysis is limited to the 326 persistent mutations with VAF ≥ 0.001, consistent with ELN guidelines for molecular MRD in AML.

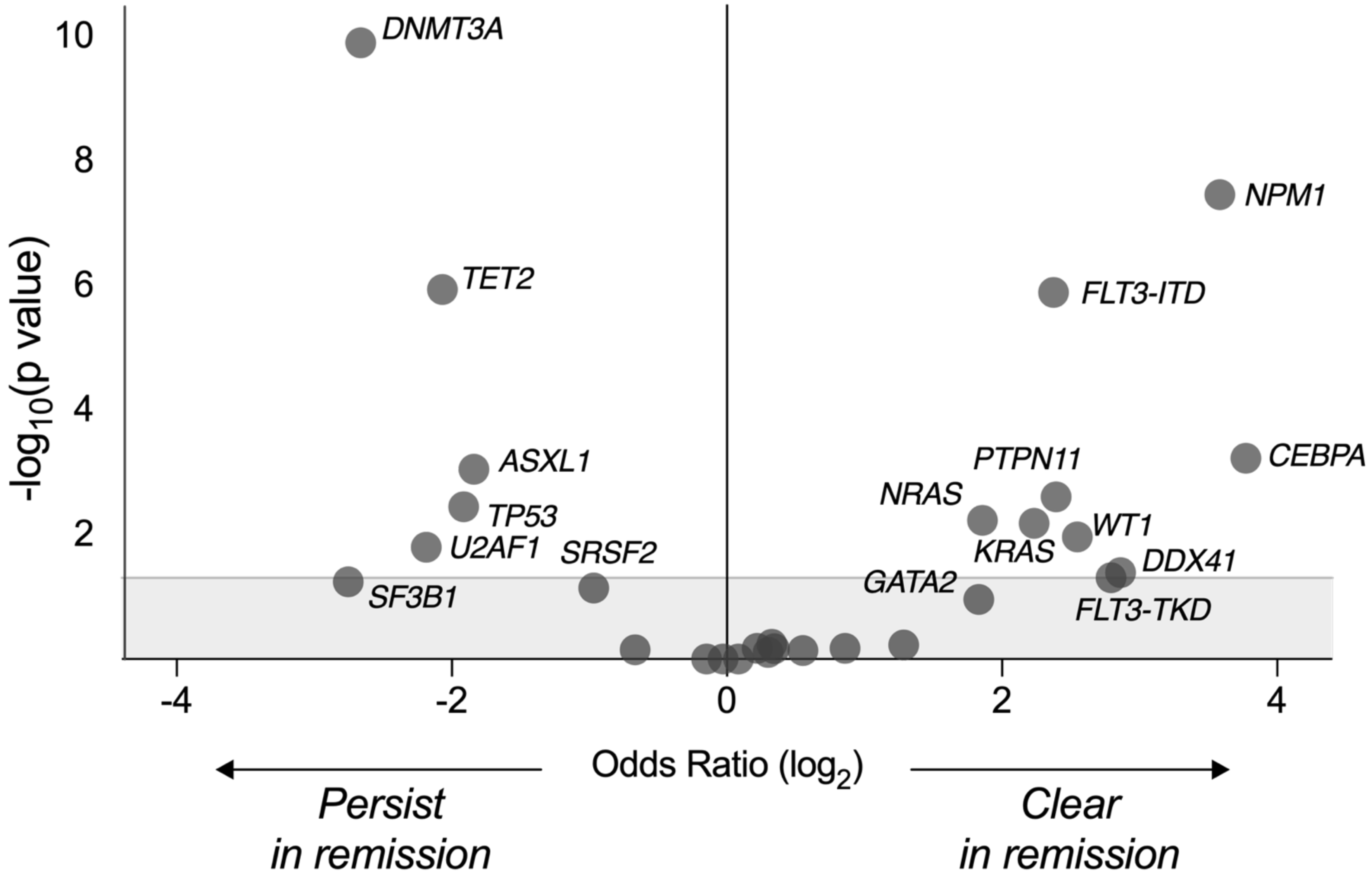


Figure S4. Clonal abundance of persistent mutations

Shown is the maximum variant allele fraction (VAF) for each patient with molecular residual disease (detectable diagnostic mutations in genes other than *DNMT3A* or *TET2*). Patients are grouped by the molecular ontogeny of their leukemia. *TP53* ontogeny includes all patients with *TP53* mutations at the time of diagnosis; secondary ontogeny includes all patients with mutations in *SRSF2, SF3B1, U2AF1, ZRSR2, ASXL1, BCOR, BCORL1, EZH2,* or *STAG2* at the time of diagnosis; pan-AML/*de novo* ontogeny includes all other patients. The median VAF of persistent mutations for patients with *TP53* ontogeny was 0.113, for those with secondary-type ontogeny was 0.042, and for those with pan-AML/*de novo* ontogeny was 0.021. Unadjusted P-values are from the Wilcoxon rank-sum test.

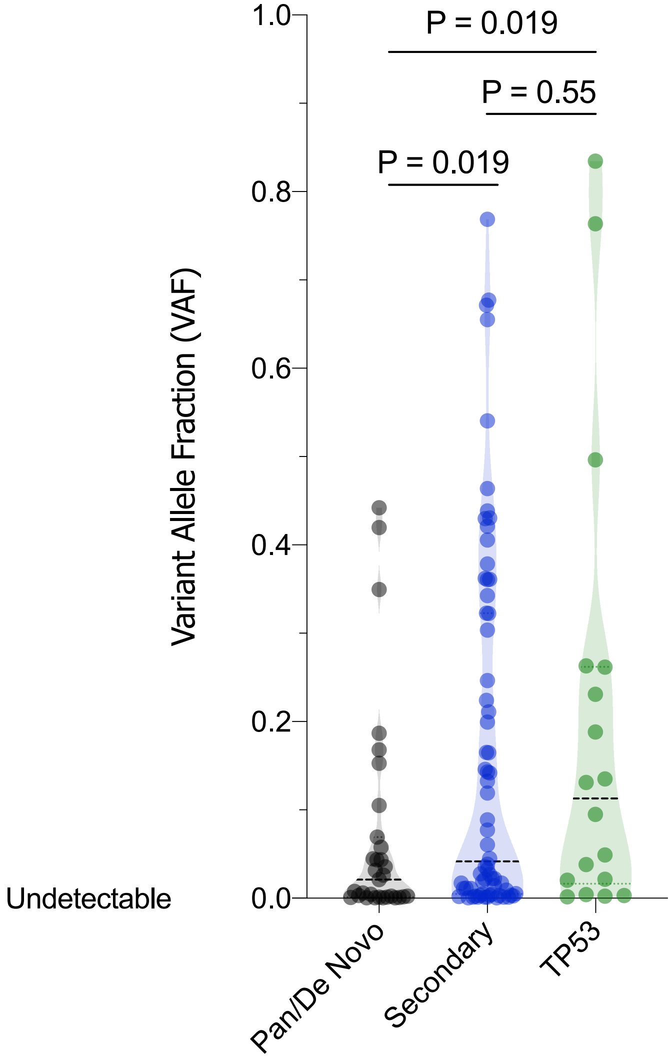


Figure S5. Leukemia-free survival by MRD status using ELN definition.

This figure shows unadjusted LFS for all remission cohort patients (N = 192) according to MRD status defined by ELN criteria (at least one mutation VAF ≥ 0.001).

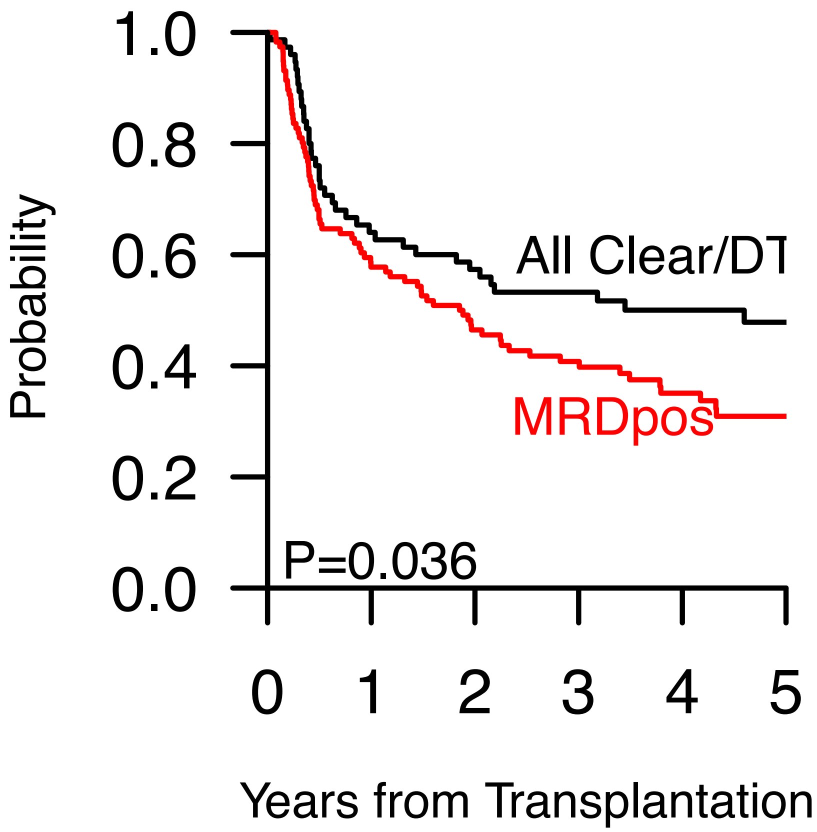


Figure S6. Incidence of relapse using DTA as MRD-negative equivalent.

In our study, we defined remissions with only persistent *DNMT3A* or *TET2* mutations (“DT”) as equivalent to an MRD-negative remission. Previous studies of MRD in AML have also included sole remission mutations in *ASXL1* (with/without *DNMT3A* or *TET2*, but without other mutations) in this definition. In this cohort, 6 patients classified as MRD positive using a DT only definition would have been reclassified as MRD-negative using a DTA definition. This figure shows the rates of relapse using the DT definition (left), as in the text, or DTA definition (right).