

Supplementary Table 1: Optical Genome Mapping - Molecule Quality Parameter after Rare Variant Analysis

OGM Molecule Quality Data	AML diagnosis (0d)	Prior SCT (+155d)	Relapse (+225d)
Access Version	1.7	1.7	1.7
Solve Version	Solve3.7_10192021_74_1	Solve3.7_10192021_74_1	Solve3.7_10192021_74_1
RefAligner Version:	12463	12463	12463
NLV	7.176	11.275	10.315
PLV	2.745	2.61	2.732
bpp	493.72	491	486.07
res	2.608	2.589	2.582
sd	0.01303	0.01901	0.01854
sf	0.09035	0.1063	0.10524
sr	0.01696	0.01809	0.01693
Total number of molecules	4351058	9344283	9220623
Total length (Mbp)	1291978.923	2369060.204	2343890.409
Average length (kbp)	296.934	253.53	254.201
Molecule N50 (kbp)	313.427	257.705	257.703
Label density (/100kb)	16.06	15.337	15.319
Total number of aligned molecules	4180719	8686723	8665191
Fraction of aligned molecules	0.961	0.93	0.94
Total molecule align length (Mbp)	1114275.8	1937706.4	1929169.7
Total reference align length (Mbp)	1120158.3	1948007.2	1938732.3
Effective coverage of reference (X):	361.846	629.267	626.271
Average aligned length (kbp)	266527.3	223065.3	222634.4
Fraction aligned length	0.904	0.887	0.894
Average confidence	43.7	33.6	34.5
Deletions	811	857	983
Insertions	825	839	1026
Duplications	126	111	179
Inversion breakpoints	524	464	522
Interchr. translocation breakpoints:	32	10	32
Intrachr. translocation breakpoints:	15	8	19

Supplementary Table 2: Optical Genome Mapping - Rare Variant Pipeline – Rare and Confident Structural Variants

Time Point of Analysis (Day)	ChrA	ChrB	Reference Start	Reference End	Confidence	Type	Orientation	VAF	Size in bases	presence in % of controls	Overlap Genes	Putative Gene Fusion	Self molecule count	Result of OGM adapting ISCN
AML diagnosis (0d)	2	2	87083645	87097695	0.99	deletion	NA	0.28	4724	0	RMND5A;CD8B;ANAPC1P1	CD8B-ANAPC1P1	58	ogm[GRCh37]2p11.2(87083645_87097695)x1
AML diagnosis (0d)	3	3	111554983	111585361	0.99	deletion	NA	0.71	16189	0	PLCXD2;PHLDB2	PLCXD2-PHLDB2	122	ogm[GRCh37]3q13.2(111554983_111585361)x1
AML diagnosis (0d)	3	3	6997453	9689847	0.99	deletion	NA	0.4	2566875	0	GRM7;AK124857;LMCD1-AS1;U4atac;LMCD1;LINC00312;SSUH2;CAV3;OXTR;Mir_548;RAD18;SRGAP3;BC041457;SRGAP3-AS3;THUMP3;SETD5-AS1;SETD5;LHFPL4	-	78	ogm[GRCh37]3p26.1p25.3(6997453_9689847)x1
AML diagnosis (0d)	3	3	6997453	9689847	0.99	deletion	NA	0.4	2567122	0	GRM7;AK124857;LMCD1-AS1;U4atac;LMCD1;LINC00312;SSUH2;CAV3;OXTR;Mir_548;RAD18;SRGAP3;BC041457;SRGAP3-AS3;THUMP3;SETD5-AS1;SETD5;LHFPL4	-	80	ogm[GRCh37]3p26.1p25.3(6997453_9689847)x1
AML diagnosis (0d)	3	3	87218114	87594795	0.99	deletion	NA	0.19	134919	0	MIR4795;CHMP2B;POU1F1	-	29	ogm[GRCh37]3p11.2(87218114_87594795)x1
AML diagnosis (0d)	3	3	87449156	87754519	0.97	deletion	NA	0.21	281369	0	-	-	56	ogm[GRCh37]3p11.2(87449156_87754519)x1
AML diagnosis (0d)	3	3	9782366	12785919	0.99	deletion	NA	0.45	2962520	0	BRPF1;OGG1;CAMK1;AX748417;TADA3;TTLL3;RPU SD3;CIDEC;JAGN1;IL17RE;IL17RC;CRELD1;PRRT3;P RRT3-AS1;EMC3;AX747493;LOC401052;FW339974;FANCD 2;FANCD2OS;BRK1;VHL;IRAK2;TATDN2;LINC0085 2;GHRLOS;GHRL;SEC13;ATP2B2;MIR885;LINC00606 ;SLC6A11;SLC6A1;SLC6A1-AS1;HRH1;ATG7;AX748267;VGLL4;TAMM41;DQ583 118;SYN2;TIMP4;PPARG;TSEN2;C3orf83;MKRN2;RA F1;TMEM40	BRPF1-TMEM40	90	ogm[GRCh37]3p25.3p25.2(9782366_12785919)x1
AML diagnosis (0d)	4	4	40566455	40581577	0.99	deletion	NA	0.54	7105	0.6	RBM47	-	111	ogm[GRCh37]4p14(40566455_40581577)x1
AML diagnosis (0d)	7	7	62323427	62371140	0.99	deletion	NA	0.7	5976	0.6	-	-	64	ogm[GRCh37]7q11.21(62323427_62371140)x1
AML diagnosis (0d)	7	7	9901592	9914178	0.99	deletion	NA	0.45	5360	0	-	-	140	ogm[GRCh37]7p21.3(9901592_9914178)x1

AML diagnosis (0d)	8	8	70319014	70333359	0.99	deletion	NA	0.54	5338	0	-	-	144	ogm[GRCh37]8q13.2(70319014_70333359)x1
AML diagnosis (0d)	9	9	128496517	128507523	0.99	deletion	NA	0.71	5027	0	-	-	18	ogm[GRCh37]9q33.3(128496517_128507523)x1
AML diagnosis (0d)	9	9	128501229	128507163	0.99	deletion	NA	0.71	4380	0	-	-	144	ogm[GRCh37]9q33.3(128501229_128507163)x1
AML diagnosis (0d)	9	9	65843777	65858302	0.99	deletion	NA	0.41	11144	0.6	-	-	17	ogm[GRCh37]9q12(65843777_65858302)x1
AML diagnosis (0d)	9	9	95167003	95268123	0.99	deletion	NA	0.51	97459	0	CENPP;OMD;ASP;ECM2	-	124	ogm[GRCh37]9q22.31(95167003_95268123)x1
AML diagnosis (0d)	10	10	63429717	66057070	0.99	deletion	NA	0.41	2621700	0	C10orf107;ARID5B;MIR548AV;RTKN2;ZNF365;ADO;EGR2;NRBF2;JMJD1C;AX747628;MIR1296;JMJD1C-AS1;REEP3	-	77	ogm[GRCh37]10q21.2q21.3(63429717_66057070)x1
AML diagnosis (0d)	16	16	23932554	23944177	0.99	deletion	NA	0.64	8130	0.6	PRKCB	-	128	ogm[GRCh37]16p12.2(23932554_23944177)x1
AML diagnosis (0d)	20	20	44336706	44386740	0.99	deletion	NA	0.49	30726	0.6	WFDC13;SPINT4	-	112	ogm[GRCh37]20q13.12(44336706_44386740)x1
AML diagnosis (0d)	21	21	47038229	47058698	0.99	deletion	NA	0.33	6529	0	-	-	152	ogm[GRCh37]21q22.3(47038229_47058698)x1
AML diagnosis (0d)	1	1	103781820	103795767	0.99	insertion	NA	0.11	62347	0	-	-	18	ogm[GRCh37]ins(1;?)(p21.1;?)
AML diagnosis (0d)	1	1	225379891	225394366	0.99	insertion	NA	0.58	5969	0	DNAH14	-	227	ogm[GRCh37]ins(1;?)(q42.12;?)
AML diagnosis (0d)	2	2	234232954	234236530	0.99	insertion	NA	0.67	10670	0	SAG	-	175	ogm[GRCh37]ins(2;?)(q37.1;?)
AML diagnosis (0d)	3	3	139131709	139137532	0.99	insertion	NA	0.32	6047	0.6	-	-	110	ogm[GRCh37]ins(3;?)(q23;?)
AML diagnosis (0d)	5	5	33059463	33064516	0.99	insertion	NA	0.57	6440	0	-	-	182	ogm[GRCh37]ins(5;?)(p13.3;?)
AML diagnosis (0d)	6	6	124456554	124456554	0.99	insertion	NA	0.47	38227	0	NKAIN2	-	106	ogm[GRCh37]ins(6;?)(q22.31;?)
AML diagnosis (0d)	6	6	40586940	40591956	0.99	insertion	NA	0.5	6141	0	-	-	155	ogm[GRCh37]ins(6;?)(p21.1;?)
AML diagnosis (0d)	7	7	102314052	102331912	0.99	insertion	NA	0.5	96614	0	AK301666	-	61	ogm[GRCh37]ins(7;?)(q22.1;?)
AML diagnosis (0d)	10	10	1272968	1284604	0.99	insertion	NA	0.52	76622	0	ADARB2	-	73	ogm[GRCh37]ins(10;?)(p15.3;?)

AML diagnosis (0d)	10	10	18896114	18916103	0.99	insertion	NA	0.47	10120	0	NSUN6	-	153	ogm[GRCh37] ins(10;?)(p12.31;?)
AML diagnosis (0d)	10	10	47051136	47067228	0.99	insertion	NA	0.03	10653	0	-	-	16	ogm[GRCh37] ins(10;?)(q11.22;?)
AML diagnosis (0d)	11	11	4310787	4349873	0.99	insertion	NA	0.49	96419	0.6	-	-	76	ogm[GRCh37] ins(11;?)(p15.4;?)
AML diagnosis (0d)	11	11	60986963	60995766	0.99	insertion	NA	0.03	19188	0	PGA4	-	13	ogm[GRCh37] ins(11;?)(q12.2;?)
AML diagnosis (0d)	12	12	11541795	11550408	0.99	insertion	NA	0.37	79648	0	PRB2	-	165	ogm[GRCh37] ins(12;?)(p13.2;?)
AML diagnosis (0d)	13	13	113309756	113329149	0.99	insertion	NA	0.54	16412	0	C13orf35	-	85	ogm[GRCh37] ins(13;?)(q34;?)
AML diagnosis (0d)	19	19	53532751	53552487	0.99	insertion	NA	0.81	35054	0	ERVV-2	-	106	ogm[GRCh37] ins(19;?)(q13.41;?)
AML diagnosis (0d)	22	22	21845261	21864431	0.99	insertion	NA	0.08	24888	0.6	PI4KAP2	-	15	ogm[GRCh37] ins(22;?)(q11.21;?)
AML diagnosis (0d)	23	23	61787943	61878865	0.99	insertion	NA	0.2	8585	0	-	-	24	ogm[GRCh37] ins(23;?)(q11.1;?)
AML diagnosis (0d)	1	1	155349797	155349797	0.99	inversion	NA	0.11	-1	0	ASH1L	-	23	ogm[GRCh37] inv(1)(q22q22)
AML diagnosis (0d)	1	-1	155279255	-1	0.99	inversion_partial	NA	0.11	-1	-1	-	-	-1	ogm[GRCh37] inv(1)(q22q22)
AML diagnosis (0d)	3	3	5934692	6573492	0.98	inversion	NA	0.37	-1	0	AF279782	-	97	ogm[GRCh37] inv(3)(p26.1p26.1)
AML diagnosis (0d)	3	-1	5856855	-1	0.98	inversion_partial	NA	0.37	-1	-1	-	-	-1	ogm[GRCh37] inv(3)(p26.1p26.1)
AML diagnosis (0d)	5	5	115959912	115959912	0.74	inversion	NA	0.15	-1	0	-	-	97	ogm[GRCh37] inv(5)(q23.1q23.1)
AML diagnosis (0d)	5	-1	116077394	-1	0.74	inversion_partial	NA	0.15	-1	-1	-	-	-1	ogm[GRCh37] inv(5)(q23.1q23.1)
AML diagnosis (0d)	5	5	115959912	115959912	1	inversion	NA	0.15	-1	0	-	-	6	ogm[GRCh37] inv(5)(q23.1q23.1)
AML diagnosis (0d)	5	-1	116046316	-1	1	inversion_partial	NA	0.15	-1	-1	-	-	-1	ogm[GRCh37] inv(5)(q23.1q23.1)
AML diagnosis (0d)	10	10	66823948	70459974	1	inversion	NA	0.2	-1	0	CTNNA3;SnoU40;LRRTM3;H1650153;DNAJC12;U6;SI RT1;HERC4;MYPN;7SK;ATOH7;PBLD;HNRNPH3;R UFY2;DNA2;SLC25A16;TET1	-	76	ogm[GRCh37] inv(10)(q21.3q21.3)
AML diagnosis (0d)	10	-1	70684134	-1	1	inversion_partial	NA	0.2	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q21.3)
AML diagnosis (0d)	10	10	70699027	70736620	1	inversion	NA	0.2	-1	0	DDX50;DDX21	-	66	ogm[GRCh37] inv(10)(q22.1q22.1)
AML diagnosis (0d)	10	-1	70297175	-1	1	inversion_partial	NA	0.2	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q22.1q22.1)

AML diagnosis (0d)	23	23	148956827	148956827	0.96	inversion	NA	0.13	-1	0	-	-	15	ogm[GRCh37] inv(23)(q28q28)
AML diagnosis (0d)	23	-1	148659537	-1	0.96	inversion_partial	NA	0.13	-1	-1	-	-	-1	ogm[GRCh37] inv(23)(q28q28)
AML diagnosis (0d)	1	17	154534329	1280603	0.96	translocation_interchr	+/-	0.06	-1	0	YWHAE	-	11	ogm[GRCh37] t(1;17)(q21.3;p13.3)
AML diagnosis (0d)	1	11	155384865	3755020	0.87	translocation_interchr	+/+	0.1	-1	0	ASH1L;NUP98	ASH1L-NUP98	26	ogm[GRCh37] t(1;11)(q22;p15.4)
AML diagnosis (0d)	3	10	12842453	17364994	0.26	translocation_interchr	+/+	0.41	-1	0	CAND2;ST8SIA6	CAND2-ST8SIA6	92	ogm[GRCh37] t(3;10)(p25.2;p12.33)
AML diagnosis (0d)	3	10	16344791	72152951	1	translocation_interchr	+/+	0.45	-1	0	OXNAD1	-	117	ogm[GRCh37] t(3;10)(p25.1;q22.1)
AML diagnosis (0d)	3	10	170076915	18677477	1	translocation_interchr	+/+	0.23	-1	0	CACNB2	-	63	ogm[GRCh37] t(3;10)(q26.2;p12.32)
AML diagnosis (0d)	3	10	8383755	71718153	1	translocation_interchr	+/+	0.22	-1	0	LMCD1-AS1;COL13A1	LMCD1-AS1-COL13A1	40	ogm[GRCh37] t(3;10)(p26.1;q22.1)
AML diagnosis (0d)	3	10	86634401	63706716	1	translocation_interchr	+/+	0.44	-1	0	ARID5B	-	116	ogm[GRCh37] t(3;10)(p12.1;q21.2)
AML diagnosis (0d)	3	10	87218114	19452703	0.96	translocation_interchr	+/-	0.21	-1	0	-	-	38	ogm[GRCh37] t(3;10)(p11.2;p12.31)
AML diagnosis (0d)	3	10	87593525	42603355	0.19	translocation_interchr	+/+	0.22	-1	0	-	-	48	ogm[GRCh37] t(3;10)(p11.2;q11.21)
AML diagnosis (0d)	3	10	87594795	19216957	1	translocation_interchr	-/+	0.21	-1	0	-	-	47	ogm[GRCh37] t(3;10)(p11.2;p12.31)
AML diagnosis (0d)	3	10	9689847	72541265	0.99	translocation_interchr	+/+	0.17	-1	0	TBATA	-	36	ogm[GRCh37] t(3;10)(p25.3;q22.1)
AML diagnosis (0d)	3	10	9811091	17362391	0.89	translocation_interchr	+/+	0.24	-1	0	CAMK1	-	27	ogm[GRCh37] t(3;10)(p25.3;p12.33)
AML diagnosis (0d)	3	10	9811823	17362391	0.94	translocation_interchr	+/+	0.24	-1	0	-	-	56	ogm[GRCh37] t(3;10)(p25.3;p12.33)
AML diagnosis (0d)	3	10	9821683	17362391	0.72	translocation_interchr	+/+	0.24	-1	0	TADA3	-	10	ogm[GRCh37] t(3;10)(p25.3;p12.33)
AML diagnosis (0d)	3	10	9947565	62436894	0.86	translocation_interchr	+/+	0.21	-1	0	IL17RE	-	41	ogm[GRCh37] t(3;10)(p25.3;q21.2)
AML diagnosis (0d)	3	10	9954410	62436894	0.92	translocation_interchr	+/+	0.21	-1	0	IL17RE	-	40	ogm[GRCh37] t(3;10)(p25.3;q21.2)
AML diagnosis (0d)	5	10	132131355	75647791	1	translocation_interchr	+/+	0.46	-1	0	-	-	97	ogm[GRCh37] t(5;10)(q31.1;q22.2)
AML diagnosis (0d)	5	17	167564781	77536514	0.22	translocation_interchr	+/-	0.79	-1	0	TENM2	-	189	ogm[GRCh37] t(5;17)(q34;q25.3)
AML diagnosis (0d)	7	14	61676393	87129869	0.07	translocation_interchr	+/-	0.39	-1	0	-	-	103	ogm[GRCh37] t(7;14)(q11.1;q31.3)

AML diagnosis (0d)	11	17	111925791	16219538	0.99	translocation_interchr	-/+	0.09	-1	0	DLAT;PIGL	DLAT-PIGL	23	ogm[GRCh37] t(11;17)(q23.1;p11.2)
AML diagnosis (0d)	1	1	150764470	203733734	0.94	translocation_intrachr	+/+	0.09	-1	0	-	-	17	ogm[GRCh37] fus(1;1)(q21.3;q32.1)
AML diagnosis (0d)	3	3	19043437	85941272	1	translocation_intrachr	+/+	0.47	-1	0	CADM2	-	126	ogm[GRCh37] fus(3;3)(p24.3;p12.1)
AML diagnosis (0d)	3	3	5934692	87094899	0.52	translocation_intrachr	+/+	0.31	-1	0	-	-	86	ogm[GRCh37] fus(3;3)(p26.1;p12.1)
AML diagnosis (0d)	10	10	17362391	62436894	0.95	translocation_intrachr	+/+	0.22	-1	0	-	-	41	ogm[GRCh37] fus(10;10)(p12.33;q21.2)
AML diagnosis (0d)	6	6	115448373	115526974	-1	duplication	NA	0.36	78602	0	-	-	89	ogm[GRCh37] dup(6)(q22.1q22.1)
AML diagnosis (0d)	6	6	115449485	115556170	-1	duplication	NA	0.36	106686	0	-	-	64	ogm[GRCh37] dup(6)(q22.1q22.1)
AML diagnosis (0d)	7	7	143271389	143329948	-1	duplication	NA	0.34	58560	0.6	CTAGE15;DQ786304;FAM115C	CTAGE15-FAM115C	61	ogm[GRCh37] dup(7)(q35q35)
AML diagnosis (0d)	5	5	115956150	116046316	-1	duplication_inverted	NA	0.52	90167	0	Mir_633	-	43	ogm[GRCh37] dup(5)(q23.1q23.1)
AML diagnosis (0d)	5	5	115956150	116056399	-1	duplication_inverted	NA	0.52	100250	0	Mir_633	-	44	ogm[GRCh37] dup(5)(q23.1q23.1)
AML diagnosis (0d)	11	11	4143061	4331668	-1	duplication_inverted	NA	0.15	188608	0	RRM1;LOC100506082	-	46	ogm[GRCh37] dup(11)(p15.4p15.4)
AML diagnosis (0d)	23	23	148578211	148659537	-1	duplication_inverted	NA	0.12	81327	0	IDS;IDS2;LINC00893;CXorf40A	-	42	ogm[GRCh37] dup(23)(q28q28)
AML diagnosis (0d)	23	23	148679644	148737119	-1	duplication_inverted	NA	0.13	57476	0	TMEM185A	-	15	ogm[GRCh37] dup(23)(q28q28)
AML diagnosis (0d)	3	3	87449930	88537466	-1	duplication_split	NA	1	1087537	0	U6atac;HTR1F;CGGBP1;ZNF654;C3orf38	-	34	ogm[GRCh37] dup(3)(p11.2p11.1)
AML diagnosis (0d)	7	7	61533417	61902991	-1	duplication_split	NA	0.99	369575	0	-	-	6	ogm[GRCh37] dup(7)(q11.1q11.21)
Prior alloHSCT (+155d)	2	2	87083127	87097695	0.99	deletion	NA	0.74	4925	0	RMND5A;CD8B;ANAPC1P1	CD8B-ANAPC1P1	207	ogm[GRCh37] 2p11.2(87083127_87097695)x1
Prior alloHSCT (+155d)	2	2	87083566	87097774	0.99	deletion	NA	0.74	4934	0	RMND5A;CD8B;ANAPC1P1	CD8B-ANAPC1P1	134	ogm[GRCh37] 2p11.2(87083565_87097774)x1
Prior alloHSCT (+155d)	2	2	87083645	87097695	0.99	deletion	NA	0.74	4531	0	RMND5A;CD8B;ANAPC1P1	CD8B-ANAPC1P1	128	ogm[GRCh37] 2p11.2(87083645_87097695)x1
Prior alloHSCT (+155d)	3	3	111554983	111585361	0.99	deletion	NA	0.56	16119	0	PLCXD2;PHLDB2	PLCXD2-PHLDB2	280	ogm[GRCh37] 3q13.2(111554983_111585361)x1

Prior alloHSCT (+155d)	4	4	40566455	40581577	0.99	deletion	NA	0.51	7078	0.6	RBM47	-	282	ogm[GRCh37] 4p14(40566455_40581577)x1
Prior alloHSCT (+155d)	6	6	66238764	66266373	0.99	deletion	NA	0.89	2618	0	EYS	-	55	ogm[GRCh37] 6q12(66238764_66266373)x1
Prior alloHSCT (+155d)	7	7	62323427	62371140	0.99	deletion	NA	0.62	6054	0	-	-	64	ogm[GRCh37] 7q11.21(62323427_62371140)x1
Prior alloHSCT (+155d)	7	7	9901589	9914181	0.99	deletion	NA	0.52	5384	0	-	-	142	ogm[GRCh37] 7p21.3(9901588_9914181)x1
Prior alloHSCT (+155d)	7	7	9901592	9914178	0.99	deletion	NA	0.52	5344	0	-	-	255	ogm[GRCh37] 7p21.3(9901592_9914178)x1
Prior alloHSCT (+155d)	8	8	70319014	70333359	0.99	deletion	NA	0.48	5324	0.6	-	-	257	ogm[GRCh37] 8q13.2(70319014_70333359)x1
Prior alloHSCT (+155d)	9	9	46436460	46446136	0.99	deletion	NA	0.99	6079	0	-	-	91	ogm[GRCh37] 9p11.2(46436460_46446136)x1
Prior alloHSCT (+155d)	9	9	95167003	95268123	0.99	deletion	NA	0.5	97463	0	CENPP;OMD;ASPN;ECM2	-	184	ogm[GRCh37] 9q22.31(95167003_95268123)x1
Prior alloHSCT (+155d)	10	10	63429717	66057070	0.99	deletion	NA	0.1	2621676	0	C10orf107;ARID5B;MIR548AV;RTKN2;ZNF365;ADO;EGR2;NRBF2;JMJD1C;AX747628;MIR1296;JMJD1C-AS1;REEP3	-	37	ogm[GRCh37] 10q21.2q21.3(63429717_66057070)x1
Prior alloHSCT (+155d)	13	13	65341820	65357226	0.99	deletion	NA	0.47	3756	0	-	-	256	ogm[GRCh37] 13q21.31(65341820_65357226)x1
Prior alloHSCT (+155d)	16	16	23931090	23940422	0.99	deletion	NA	0.48	7787	0.6	PRKCB	-	196	ogm[GRCh37] 16p12.2(23931090_23940422)x1
Prior alloHSCT (+155d)	16	16	23932554	23944177	0.99	deletion	NA	0.48	8121	0.6	PRKCB	-	205	ogm[GRCh37] 16p12.2(23932554_23944177)x1
Prior alloHSCT (+155d)	20	20	44203215	44209690	0.99	deletion	NA	0.48	3180	0	WFDC8	-	286	ogm[GRCh37] 20q13.12(44203215_44209690)x1
Prior alloHSCT (+155d)	20	20	44336706	44386740	0.99	deletion	NA	0.51	30686	0.6	WFDC13;SPINT4	-	175	ogm[GRCh37] 20q13.12(44336706_44386740)x1
Prior alloHSCT (+155d)	21	21	34403641	36841365	0.99	deletion	NA	0.01	2420410	0	OLIG1;C21orf54;IFNAR2;IL10RB-AS1;IFNAR1;IFNGR2;TMEM50B;TMEM50B;DNAJC28;GART;SON;DONSON;CRYZL1;ITSN1;intersectin 1 long form;LINC00649;SLC5A3;MRPS6;LINC00310;KCNE2;	-	5	ogm[GRCh37] 21q22.11q22.12(34403641_36841365)x1

											SMIM11;BC049386;KCNE1;RCAN1;Mir_562;CLIC6;LIN000160;LOC100506385;RUNX1;AX746823;AX813477;RUNX1-IT1;LOC100506403			
Prior alloHSCT (+155d)	21	21	47038229	47058698	0.99	deletion	NA	0.62	6472	0	-	-	232	ogm[GRCh37]21q22.3(47038229_47058698)x1
Prior alloHSCT (+155d)	1	1	225388244	225394366	0.99	insertion	NA	0.48	6105	0	DNAH14	-	349	ogm[GRCh37]ins(1;?)(q42.12;?)
Prior alloHSCT (+155d)	2	2	136581892	136613712	0.99	insertion	NA	0.31	4539	0.6	LCT;MCM6	-	106	ogm[GRCh37]ins(2;?)(q21.3;?)
Prior alloHSCT (+155d)	2	2	234232954	234236530	0.99	insertion	NA	0.63	10696	0	SAG	-	259	ogm[GRCh37]ins(2;?)(q37.1;?)
Prior alloHSCT (+155d)	2	2	298743	310577	0.99	insertion	NA	0.62	3613	0.6	-	-	327	ogm[GRCh37]ins(2;?)(p25.3;?)
Prior alloHSCT (+155d)	3	3	139131709	139137532	0.99	insertion	NA	0.49	6084	0.6	-	-	321	ogm[GRCh37]ins(3;?)(q23;?)
Prior alloHSCT (+155d)	3	3	195820356	195840292	0.99	insertion	NA	0.46	4780	0.6	-	-	49	ogm[GRCh37]ins(3;?)(q29;?)
Prior alloHSCT (+155d)	3	3	195820356	195840886	0.99	insertion	NA	0.46	4098	0.6	-	-	190	ogm[GRCh37]ins(3;?)(q29;?)
Prior alloHSCT (+155d)	5	5	1837315	1872381	0.99	insertion	NA	0.61	4926	0.6	-	-	209	ogm[GRCh37]ins(5;?)(p15.33;?)
Prior alloHSCT (+155d)	5	5	33059463	33064516	0.99	insertion	NA	0.51	6508	0	-	-	342	ogm[GRCh37]ins(5;?)(p13.3;?)
Prior alloHSCT (+155d)	6	6	30435443	30440786	0.99	insertion	NA	0.48	4922	0	-	-	239	ogm[GRCh37]ins(6;?)(p21.33;?)
Prior alloHSCT (+155d)	6	6	31338429	31358385	0.99	insertion	NA	0.56	98043	0	-	-	103	ogm[GRCh37]ins(6;?)(p21.33;?)
Prior alloHSCT (+155d)	6	6	40586940	40591956	0.99	insertion	NA	0.49	6145	0	-	-	281	ogm[GRCh37]ins(6;?)(p21.1;?)
Prior alloHSCT (+155d)	7	7	102314052	102331912	0.99	insertion	NA	0.24	3815	0	AK301666	-	77	ogm[GRCh37]ins(7;?)(q22.1;?)
Prior alloHSCT (+155d)	8	8	12215199	12245552	0.99	insertion	NA	0.2	4043	0	ZNF705A;LOC649352	-	81	ogm[GRCh37]ins(8;?)(p23.1;?)
Prior alloHSCT (+155d)	10	10	1272968	1284604	0.99	insertion	NA	0.51	76648	0	ADARB2	-	89	ogm[GRCh37]ins(10;?)(p15.3;?)
Prior alloHSCT (+155d)	10	10	18896114	18916103	0.99	insertion	NA	0.49	10096	0	NSUN6	-	279	ogm[GRCh37]ins(10;?)(p12.31;?)
Prior alloHSCT (+155d)	13	13	113309756	113329149	0.99	insertion	NA	0.45	16496	0	C13orf35	-	174	ogm[GRCh37]ins(13;?)(q34;?)
Prior alloHSCT (+155d)	1	1	155349797	155349797	1	inversion	NA	0.04	-1	0.6	ASH1L	-	14	ogm[GRCh37]inv(1)(q22q22)

Prior alloHSCT (+155d)	1	-1	155279255	-1	1	inversion_partial	NA	0.04	-1	-1	-	-	-1	ogm[GRCh37] inv(1)(q22q22)
Prior alloHSCT (+155d)	3	3	5935872	6573492	0.99	inversion	NA	0.04	-1	0	AF279782	-	10	ogm[GRCh37] inv(3)(p26.1p26.1)
Prior alloHSCT (+155d)	3	-1	5856855	-1	0.99	inversion_partial	NA	0.04	-1	-1	-	-	-1	ogm[GRCh37] inv(3)(p26.1p26.1)
Prior alloHSCT (+155d)	5	5	115974899	115974899	0.9	inversion	NA	0.15	-1	0	-	-	27	ogm[GRCh37] inv(5)(q23.1q23.1)
Prior alloHSCT (+155d)	5	-1	116062655	-1	0.9	inversion_partial	NA	0.15	-1	-1	-	-	-1	ogm[GRCh37] inv(5)(q23.1q23.1)
Prior alloHSCT (+155d)	10	10	66823948	70478435	1	inversion	NA	0.08	-1	0	CTNNA3;SnoU40;LRRTM3;HI650153;DNAJC12;U6;SIRT1;HERC4;MYPN;7SK;ATOH7;PBLD;HNRNPH3;RUFY2;DNA2;SLC25A16;TET1	-	26	ogm[GRCh37] inv(10)(q21.3q21.3)
Prior alloHSCT (+155d)	10	-1	70700810	-1	1	inversion_partial	NA	0.08	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q21.3)
Prior alloHSCT (+155d)	10	10	70544201	70736620	1	inversion	NA	0.17	-1	0	CCAR1;STOX1;DDX50;DDX21	-	24	ogm[GRCh37] inv(10)(q21.3q22.1)
Prior alloHSCT (+155d)	10	-1	70297175	-1	1	inversion_partial	NA	0.17	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q22.1)
Prior alloHSCT (+155d)	1	11	155384865	3755020	0.69	translocation_interchr	+/+	0.05	-1	0	ASH1L;NUP98	ASH1L-NUP98	20	ogm[GRCh37] t(1;11)(q22;p15.4)
Prior alloHSCT (+155d)	3	10	16344791	72152951	0.99	translocation_interchr	+/+	0.13	-1	0	OXNAD1	-	23	ogm[GRCh37] t(3;10)(p25.1;q22.1)
Prior alloHSCT (+155d)	3	10	8383755	71718153	0.97	translocation_interchr	+/+	0.08	-1	0	LMCD1-AS1;COL13A1	LMCD1-AS1-COL13A1	26	ogm[GRCh37] t(3;10)(p26.1;q22.1)
Prior alloHSCT (+155d)	3	10	86013858	63895519	0.6	translocation_interchr	+/+	0.01	-1	0	CADM2	-	6	ogm[GRCh37] t(3;10)(p12.1;q21.2)
Prior alloHSCT (+155d)	3	10	86634401	63706716	0.99	translocation_interchr	+/+	0.08	-1	0	ARID5B	-	20	ogm[GRCh37] t(3;10)(p12.1;q21.2)
Prior alloHSCT (+155d)	5	10	132131355	75647791	0.98	translocation_interchr	+/+	0.09	-1	0	-	-	23	ogm[GRCh37] t(5;10)(q31.1;q22.2)
Prior alloHSCT (+155d)	7	17	154456988	27326038	0.2	translocation_interchr	+/+	0.26	-1	0	DPP6;SEZ6	DPP6-SEZ6	168	ogm[GRCh37] t(7;17)(q36.2;q11.2)
Prior alloHSCT (+155d)	3	3	5935872	87094899	0.5	translocation_intrachr	+/+	0.04	-1	0	-	-	13	ogm[GRCh37] fus(3;3)(p26.1;p12.1)
Prior alloHSCT (+155d)	3	3	7921134	15366443	0.92	translocation_intrachr	-/+	0.02	-1	0	SH3BP5	-	7	ogm[GRCh37] fus(3;3)(p26.1;p25.1)
Prior alloHSCT (+155d)	3	3	11711969	141424983	0.15	translocation_intrachr	-/+	0.02	-1	0	-	-	6	ogm[GRCh37] fus(3;3)(p25.3;q23)
Prior alloHSCT (+155d)	3	3	19043437	85941272	0.99	translocation_intrachr	+/+	0.09	-1	0	CADM2	-	30	ogm[GRCh37] fus(3;3)(p24.3;p12.1)

Prior alloHSCT (+155d)	6	6	115447157	115556170	-1	duplication	NA	0.06	109014	0	-	-	19	ogm[GRCh37] dup(6)(q22.1q22.1)
Prior alloHSCT (+155d)	6	6	124433875	124456554	-1	duplication	NA	0.46	22680	0	NKAIN2	-	61	ogm[GRCh37] dup(6)(q22.31q22.31)
Prior alloHSCT (+155d)	5	5	115956150	116056399	-1	duplication_inverted	NA	0.49	100250	0	Mir_633	-	86	ogm[GRCh37] dup(5)(q23.1q23.1)
Relapse (+225d)	1	1	182773347	182793139	0.99	deletion	NA	0.19	5368	0.6	NPL	-	242	ogm[GRCh37] 1q25.3(182773347_182793139)x1
Relapse (+225d)	1	1	73007503	73093313	0.99	deletion	NA	0.23	82366	0	-	-	77	ogm[GRCh37] 1p31.1(73007503_73093313)x1
Relapse (+225d)	3	3	111554983	111585361	0.99	deletion	NA	0.3	16165	0	PLCXD2;PHLDB2	PLCXD2- PHLDB2	218	ogm[GRCh37] 3q13.2(111554983_111585361)x1
Relapse (+225d)	3	3	18296458	18515116	0.97	deletion	NA	0.01	211886	0	LOC339862;SATB1	-	6	ogm[GRCh37] 3p24.3(18296457_18515116)x1
Relapse (+225d)	3	3	39760310	39781339	0.99	deletion	NA	0.36	17617	0	-	-	216	ogm[GRCh37] 3p22.1(39760310_39781339)x1
Relapse (+225d)	4	4	40566455	40581577	0.99	deletion	NA	0.29	7104	0.6	RBM47	-	202	ogm[GRCh37] 4p14(40566455_40581577)x1
Relapse (+225d)	5	5	21603512	21620550	0.99	deletion	NA	0.19	3283	0.6	BC038535	-	68	ogm[GRCh37] 5p14.3(21603511_21620549)x1
Relapse (+225d)	6	6	16563958	16575942	0.99	deletion	NA	0.29	5628	0	ATXN1	-	186	ogm[GRCh37] 6p22.3(16563958_16575941)x1
Relapse (+225d)	7	7	62323427	62371140	0.99	deletion	NA	0.4	6008	0	-	-	45	ogm[GRCh37] 7q11.21(62323427_62371140)x1
Relapse (+225d)	7	7	8881992	8897787	0.99	deletion	NA	0.27	6964	0	-	-	166	ogm[GRCh37] 7p21.3(8881992_8897787)x1
Relapse (+225d)	7	7	9901592	9914178	0.99	deletion	NA	0.25	5409	0	-	-	161	ogm[GRCh37] 7p21.3(9901592_9914178)x1
Relapse (+225d)	8	8	70319014	70333359	0.99	deletion	NA	0.24	5348	0.6	-	-	289	ogm[GRCh37] 8q13.2(70319014_70333359)x1
Relapse (+225d)	8	8	72213283	72218721	0.99	deletion	NA	0.43	3084	0	EYA1	-	243	ogm[GRCh37] 8q13.3(72213283_72218721)x1

Relapse (+225d)	9	9	67000179	67044327	0.99	deletion	NA	0.15	27700	0.6	LOC286297	-	12	ogm[GRCh37] 9q13(67000178_67044327)x1
Relapse (+225d)	9	9	95167003	95268123	0.99	deletion	NA	0.22	97409	0	CENPP;OMD;ASPN;ECM2	-	90	ogm[GRCh37] 9q22.31(95167003_95268123)x1
Relapse (+225d)	10	10	63429717	66057070	0.99	deletion	NA	0.37	2621687	0	C10orf107;ARID5B;MIR548AV;RTKN2;ZNF365;ADO;EGR2;NRBF2;JMJD1C;AX747628;MIR1296;JMJD1C-AS1;REEP3	-	203	ogm[GRCh37] 10q21.2q21.3(63429717_66057070)x1
Relapse (+225d)	10	10	65959767	66724105	0.99	deletion	NA	0.01	656533	0	ANXA2P3;DJ439558;DJ439576;DJ439561	-	5	ogm[GRCh37] 10q21.3(65959767_66724105)x1
Relapse (+225d)	11	11	21834510	21955750	0.99	deletion	NA	0.06	114015	0	-	-	7	ogm[GRCh37] 11p14.3(21834510_21955750)x1
Relapse (+225d)	16	16	23932554	23944177	0.99	deletion	NA	0.25	8141	0.6	PRKCB	-	166	ogm[GRCh37] 16p12.2(23932554_23944177)x1
Relapse (+225d)	16	16	23932554	23944177	0.99	deletion	NA	0.25	8150	0.6	PRKCB	-	158	ogm[GRCh37] 16p12.2(23932554_23944177)x1
Relapse (+225d)	16	16	4118206	4148313	0.99	deletion	NA	0.29	6848	0	ADCY9	-	193	ogm[GRCh37] 16p13.3(4118206_4148312)x1
Relapse (+225d)	18	18	7914268	8116237	0.99	deletion	NA	0.26	197730	0	PTPRM	-	100	ogm[GRCh37] 18p11.23(7914268_8116237)x1
Relapse (+225d)	20	20	44203215	44209690	0.99	deletion	NA	0.19	3185	0	WFDC8	-	131	ogm[GRCh37] 20q13.12(44203215_44209690)x1
Relapse (+225d)	20	20	44336706	44386740	0.99	deletion	NA	0.25	30747	0.6	WFDC13;SPINT4	-	85	ogm[GRCh37] 20q13.12(44336706_44386740)x1
Relapse (+225d)	21	21	47038229	47058698	0.99	deletion	NA	0.34	6482	0	-	-	195	ogm[GRCh37] 21q22.3(47038229_47058698)x1
Relapse (+225d)	23	23	113347567	113361950	0.99	deletion	NA	0.3	7225	0.6	-	-	232	ogm[GRCh37] 23q23(113347567_113361949)x1
Relapse (+225d)	1	1	225388244	225394366	0.99	insertion	NA	0.4	6220	0	DNAH14	-	415	ogm[GRCh37] ins(1;?)(q42.12;?)
Relapse (+225d)	1	1	23152779	23164560	0.99	insertion	NA	0.22	6186	0.6	EPHB2	-	119	ogm[GRCh37] ins(1;?)(p36.12;?)
Relapse (+225d)	2	2	234232954	234236530	0.99	insertion	NA	0.32	10610	0	SAG	-	275	ogm[GRCh37] ins(2;?)(q37.1;?)

Relapse (+225d)	3	3	139131709	139137532	0.99	insertion	NA	0.31	6061	0.6	-	-	341	ogm[GRCh37] ins(3;?)(q23;?)
Relapse (+225d)	3	3	195820356	195839697	0.99	insertion	NA	0.59	4531	0.6	-	-	300	ogm[GRCh37] ins(3;?)(q29;?)
Relapse (+225d)	3	3	195820356	195840292	0.99	insertion	NA	0.59	3967	0.6	-	-	33	ogm[GRCh37] ins(3;?)(q29;?)
Relapse (+225d)	4	4	120735721	120744497	0.99	insertion	NA	0.27	6100	0.6	-	-	237	ogm[GRCh37] ins(4;?)(q26;?)
Relapse (+225d)	5	5	1837283	1872413	0.99	insertion	NA	0.5	4935	0.6	-	-	171	ogm[GRCh37] ins(5;?)(p15.33;?)
Relapse (+225d)	5	5	33059463	33064516	0.99	insertion	NA	0.27	6463	0	-	-	253	ogm[GRCh37] ins(5;?)(p13.3;?)
Relapse (+225d)	5	5	527789	574944	0.99	insertion	NA	0.25	3354	0.6	MIR4456	-	51	ogm[GRCh37] ins(5;?)(p15.33;?)
Relapse (+225d)	6	6	30435443	30440786	0.99	insertion	NA	0.46	4841	0	-	-	151	ogm[GRCh37] ins(6;?)(p21.33;?)
Relapse (+225d)	6	6	31433503	31443800	0.99	insertion	NA	0.28	94426	0	HCP5;HCG26	-	89	ogm[GRCh37] ins(6;?)(p21.33;?)
Relapse (+225d)	6	6	40586940	40591956	0.99	insertion	NA	0.28	6148	0	-	-	260	ogm[GRCh37] ins(6;?)(p21.1;?)
Relapse (+225d)	8	8	7051958	7069891	0.99	insertion	NA	0.12	5875	0.6	-	-	26	ogm[GRCh37] ins(8;?)(p23.1;?)
Relapse (+225d)	10	10	1272968	1284604	0.99	insertion	NA	0.36	76579	0	ADARB2	-	83	ogm[GRCh37] ins(10;?)(p15.3;?)
Relapse (+225d)	10	10	18896114	18916103	0.99	insertion	NA	0.4	10060	0	NSUN6	-	293	ogm[GRCh37] ins(10;?)(p12.31;?)
Relapse (+225d)	11	11	43151429	43153757	0.99	insertion	NA	0.23	6190	0	-	-	122	ogm[GRCh37] ins(11;?)(p12;?)
Relapse (+225d)	13	13	113309756	113329149	0.99	insertion	NA	0.34	16528	0	C13orf35	-	136	ogm[GRCh37] ins(13;?)(q34;?)
Relapse (+225d)	13	13	90309287	90323108	0.99	insertion	NA	0.73	4385	0.6	-	-	187	ogm[GRCh37] ins(13;?)(q31.3;?)
Relapse (+225d)	1	1	155349797	155349797	1	inversion	NA	0.2	-1	0.6	ASH1L	-	26	ogm[GRCh37] inv(1)(q22q22)
Relapse (+225d)	1	-1	155278172	-1	1	inversion_partial	NA	0.2	-1	-1	-	-	-1	ogm[GRCh37] inv(1)(q22q22)
Relapse (+225d)	1	1	155349797	155349797	1	inversion	NA	0.2	-1	0.6	ASH1L	-	84	ogm[GRCh37] inv(1)(q22q22)
Relapse (+225d)	1	-1	155279255	-1	1	inversion_partial	NA	0.2	-1	-1	-	-	-1	ogm[GRCh37] inv(1)(q22q22)
Relapse (+225d)	3	3	16752942	17864305	1	inversion	NA	0.01	-1	0	PLCL2;TBC1D5;TRNA_Pseudo	-	5	ogm[GRCh37] inv(3)(p24.3p24.3)

Relapse (+225d)	3	-1	17946841	-1	1	inversion_partial	NA	0.01	-1	-1	-	-	-1	ogm[GRCh37] inv(3)(p24.3p24.3)
Relapse (+225d)	3	3	5935872	6573492	0.96	inversion	NA	0.14	-1	0	AF279782	-	35	ogm[GRCh37] inv(3)(p26.1p26.1)
Relapse (+225d)	3	-1	5856855	-1	0.96	inversion_partial	NA	0.14	-1	-1	-	-	-1	ogm[GRCh37] inv(3)(p26.1p26.1)
Relapse (+225d)	5	5	115945474	115956150	1	inversion	NA	0.21	-1	0	-	-	60	ogm[GRCh37] inv(5)(q23.1q23.1)
Relapse (+225d)	5	-1	116088873	-1	1	inversion_partial	NA	0.21	-1	-1	-	-	-1	ogm[GRCh37] inv(5)(q23.1q23.1)
Relapse (+225d)	5	5	115959912	115969748	1	inversion	NA	0.21	-1	0	-	-	7	ogm[GRCh37] inv(5)(q23.1q23.1)
Relapse (+225d)	5	-1	116077394	-1	1	inversion_partial	NA	0.21	-1	-1	-	-	-1	ogm[GRCh37] inv(5)(q23.1q23.1)
Relapse (+225d)	10	10	64177328	64462742	1	inversion	NA	0.07	-1	0	ZNF365	-	10	ogm[GRCh37] inv(10)(q21.2q21.2)
Relapse (+225d)	10	-1	64004769	-1	1	inversion_partial	NA	0.07	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.2q21.2)
Relapse (+225d)	10	10	66823948	70495589	0.99	inversion	NA	0.3	-1	0	CTNNA3;SnoU40;LRRTM3;HI650153;DNAJC12;U6;SI RT1;HERC4;MYPN;7SK;ATOH7;PBLD;HNRNPH3;R UFY2;DNA2;SLC25A16;TET1;CCAR1	-	153	ogm[GRCh37] inv(10)(q21.3q21.3)
Relapse (+225d)	10	-1	70700810	-1	0.99	inversion_partial	NA	0.3	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q21.3)
Relapse (+225d)	10	10	70495589	70736620	0.75	inversion	NA	0.19	-1	0	CCAR1;SNORD98;STOX1;DDX50;DDX21	-	104	ogm[GRCh37] inv(10)(q21.3q22.1)
Relapse (+225d)	10	-1	70297175	-1	0.75	inversion_partial	NA	0.19	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q22.1)
Relapse (+225d)	10	10	70597919	70740707	1	inversion	NA	0.19	-1	0	STOX1;DDX50;DDX21	-	7	ogm[GRCh37] inv(10)(q21.3q22.1)
Relapse (+225d)	10	-1	70436832	-1	1	inversion_partial	NA	0.19	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q21.3q22.1)
Relapse (+225d)	10	10	70880833	70892163	1	inversion	NA	0.02	-1	0	VPS26A	-	8	ogm[GRCh37] inv(10)(q22.1q22.1)
Relapse (+225d)	10	-1	70769692	-1	1	inversion_partial	NA	0.02	-1	-1	-	-	-1	ogm[GRCh37] inv(10)(q22.1q22.1)
Relapse (+225d)	1	11	155384865	3755020	0.27	translocation_interchr	-/-	0.16	-1	0	ASH1L;NUP98	ASH1L- NUP98	57	ogm[GRCh37] t(1;11)(q22;p15.4)
Relapse (+225d)	1	9	156684968	36297734	0.96	translocation_interchr	+/-	0.04	-1	0	-	-	8	ogm[GRCh37] t(1;9)(q23.1;p13.3)
Relapse (+225d)	3	10	10273471	71641510	0.38	translocation_interchr	+/+	0.02	-1	0	IRAK2;COL13A1	IRAK2- COL13A1	8	ogm[GRCh37] t(3;10)(p25.3;q22.1)
Relapse (+225d)	3	10	14768714	70495589	1	translocation_interchr	+/-	0.15	-1	0	C3orf20;CCAR1	C3orf20- CCAR1	43	ogm[GRCh37] t(3;10)(p25.1;q21.3)

Relapse (+225d)	3	10	15610571	64319172	0.96	translocation_interchr	+/+	0.02	-1	0	HACL1;ZNF365	HACL1-ZNF365	5	ogm[GRCh37] t(3;10)(p25.1;q21.2)
Relapse (+225d)	3	10	16344791	72152951	1	translocation_interchr	+/+	0.41	-1	0	OXNAD1	-	157	ogm[GRCh37] t(3;10)(p25.1;q22.1)
Relapse (+225d)	3	21	16778711	30261569	0.73	translocation_interchr	+/+	0.02	-1	0	-	-	5	ogm[GRCh37] t(3;21)(p24.3;q21.3)
Relapse (+225d)	3	10	17922015	64929786	0.68	translocation_interchr	-/+	0.01	-1	0	JMJD1C	-	5	ogm[GRCh37] t(3;10)(p24.3;q21.3)
Relapse (+225d)	3	10	17933829	64206980	0.97	translocation_interchr	+/+	0.02	-1	0	ZNF365	-	5	ogm[GRCh37] t(3;10)(p24.3;q21.2)
Relapse (+225d)	3	10	18210816	64882177	0.86	translocation_interchr	+/-	0.02	-1	0	LOC339862	-	8	ogm[GRCh37] t(3;10)(p24.3;q21.3)
Relapse (+225d)	3	21	18733184	42711338	0.33	translocation_interchr	+/+	0.03	-1	0	FAM3B	-	7	ogm[GRCh37] t(3;21)(p24.3;q22.3)
Relapse (+225d)	3	10	7650922	72512994	0.98	translocation_interchr	+/-	0.08	-1	0	GRM7;ADAMTS14	GRM7-ADAMTS14	22	ogm[GRCh37] t(3;10)(p26.1;q22.1)
Relapse (+225d)	3	10	8316163	64935875	0.75	translocation_interchr	+/+	0.02	-1	0	LMCD1-AS1;JMJD1C	LMCD1-AS1-JMJD1C	7	ogm[GRCh37] t(3;10)(p26.1;q21.3)
Relapse (+225d)	3	10	8383755	71718153	1	translocation_interchr	+/+	0.27	-1	0	LMCD1-AS1;COL13A1	LMCD1-AS1-COL13A1	126	ogm[GRCh37] t(3;10)(p26.1;q22.1)
Relapse (+225d)	3	10	86013858	63895519	0.97	translocation_interchr	+/+	0.14	-1	0	CADM2	-	63	ogm[GRCh37] t(3;10)(p12.1;q21.2)
Relapse (+225d)	3	10	86136385	71272364	1	translocation_interchr	+/+	0.17	-1	0	-	-	51	ogm[GRCh37] t(3;10)(p12.1;q22.1)
Relapse (+225d)	3	10	86634401	63706716	1	translocation_interchr	+/+	0.3	-1	0	ARID5B	-	126	ogm[GRCh37] t(3;10)(p12.1;q21.2)
Relapse (+225d)	3	10	9689847	72541265	0.98	translocation_interchr	+/+	0.28	-1	0	TBATA	-	103	ogm[GRCh37] t(3;10)(p25.3;q22.1)
Relapse (+225d)	5	10	132131355	75647791	1	translocation_interchr	+/+	0.25	-1	0	-	-	85	ogm[GRCh37] t(5;10)(q31.1;q22.2)
Relapse (+225d)	7	17	54524974	35512065	0.53	translocation_interchr	+/+	0.02	-1	0	ACACA	-	7	ogm[GRCh37] t(7;17)(p11.2;q12)
Relapse (+225d)	7	10	56030988	71551093	0.48	translocation_interchr	-/+	0.02	-1	0	-	-	6	ogm[GRCh37] t(7;10)(p11.2;q22.1)
Relapse (+225d)	10	21	72180437	34005936	0.81	translocation_interchr	+/+	0.06	-1	0	EIF4EBP2;SYNJ1	EIF4EBP2-SYNJ1	12	ogm[GRCh37] t(10;21)(q22.1;q22.11)
Relapse (+225d)	11	21	21948118	17221321	0.74	translocation_interchr	+/-	0.03	-1	0	USP25	-	6	ogm[GRCh37] t(11;21)(p14.3;q21.1)
Relapse (+225d)	3	3	11703830	141424983	0.99	translocation_intrachr	-/+	0.2	-1	0	-	-	82	ogm[GRCh37] fus(3;3)(p25.3;q23)

Relapse (+225d)	3	3	17664324	87820862	0.76	translocation_intrachr	+/+	0.01	-1	0	TBC1D5	-	5	ogm[GRCh37] fus(3;3)(p24.3;p11.2)
Relapse (+225d)	3	3	18334993	158408263	0.96	translocation_intrachr	-/+	0.02	-1	0	GFM1	-	14	ogm[GRCh37] fus(3;3)(p24.3;q25.32)
Relapse (+225d)	3	3	19043437	85941272	1	translocation_intrachr	+/+	0.36	-1	0	CADM2	-	131	ogm[GRCh37] fus(3;3)(p24.3;p12.1)
Relapse (+225d)	3	3	5935872	87094899	0.82	translocation_intrachr	+/+	0.17	-1	0	-	-	56	ogm[GRCh37] fus(3;3)(p26.1;p12.1)
Relapse (+225d)	3	3	5935872	87109137	0.76	translocation_intrachr	+/+	0.17	-1	0	-	-	56	ogm[GRCh37] fus(3;3)(p26.1;p12.1)
Relapse (+225d)	3	3	7921134	84406015	0.34	translocation_intrachr	+/+	0.06	-1	0	-	-	45	ogm[GRCh37] fus(3;3)(p26.1;p12.1)
Relapse (+225d)	3	3	7921824	15366443	0.85	translocation_intrachr	-/+	0.03	-1	0	SH3BP5	-	29	ogm[GRCh37] fus(3;3)(p26.1;p25.1)
Relapse (+225d)	3	3	8161284	18717679	0.71	translocation_intrachr	+/+	0.02	-1	0	-	-	7	ogm[GRCh37] fus(3;3)(p26.1;p24.3)
Relapse (+225d)	7	7	49327245	56028783	0.54	translocation_intrachr	+/-	0.02	-1	0	-	-	7	ogm[GRCh37] fus(7;7)(p12.2;p11.2)
Relapse (+225d)	21	21	24252871	42525873	0.24	translocation_intrachr	-/+	0.01	-1	0	-	-	5	ogm[GRCh37] fus(21;21)(q21.2;q22.2)
Relapse (+225d)	21	21	24495432	29856259	0.18	translocation_intrachr	-/+	0.03	-1	0	-	-	6	ogm[GRCh37] fus(21;21)(q21.2;q21.3)
Relapse (+225d)	6	6	115447157	115495071	-1	duplication	NA	0.93	47915	0	-	-	81	ogm[GRCh37] dup(6)(q22.1q22.1)
Relapse (+225d)	6	6	115449485	115556170	-1	duplication	NA	0.2	106686	0	-	-	79	ogm[GRCh37] dup(6)(q22.1q22.1)
Relapse (+225d)	6	6	31358385	31443800	-1	duplication	NA	0.52	85416	0	MICA;HCP5;HCG26	-	70	ogm[GRCh37] dup(6)(p21.33p21.33)
Relapse (+225d)	7	7	64992019	65031612	-1	duplication	NA	0.38	39594	0	-	-	88	ogm[GRCh37] dup(7)(q11.21q11.21)
Relapse (+225d)	5	5	115956150	116077394	-1	duplication_inverted	NA	0.33	121245	0	Mir_633	-	39	ogm[GRCh37] dup(5)(q23.1q23.1)
Relapse (+225d)	5	5	115956150	116088873	-1	duplication_inverted	NA	0.33	132724	0	Mir_633	-	74	ogm[GRCh37] dup(5)(q23.1q23.1)

Supplementary Table 3: Optical Genome Mapping - Rare Variant Pipeline Rare – Confident Copy Number Variants

Time point of analysis (Day)	Chr	Reference Start	Reference End	Size in bases	Type	fractional Copy Number	Copy Number	Confidence	VAF
AML diagnosis (0d)	1	246656863	249237532	2580670	gain	2.436	2	0.999999993	0.217879327
AML diagnosis (0d)	3	61829	6566166	6504338	loss	1.139	1	1	0.430326857
AML diagnosis (0d)	3	6997453	8342330	1344878	loss	1.401	1	1	0.299701917
AML diagnosis (0d)	3	8348572	9672818	1324247	loss	1.136	1	1	0.431986042
AML diagnosis (0d)	3	9680389	14839124	5158736	loss	1.460	1	1	0.269786568
AML diagnosis (0d)	3	14853297	16361890	1508594	loss	1.331	1	1	0.334635466
AML diagnosis (0d)	3	19043437	85935616	66892180	loss	1.116	1	1	0.442248822
AML diagnosis (0d)	3	87777096	88584653	807558	gain	2.458	2	0.999995058	0.229211347
AML diagnosis (0d)	3	89064454	90470323	1405870	loss	1.463	1	0.999998782	0.268466665
AML diagnosis (0d)	3	93508428	168821068	75312641	loss	1.564	2	1	0.218248752
AML diagnosis (0d)	5	132131355	180899715	48768361	loss	1.111	1	1	0.444318206
AML diagnosis (0d)	10	17448661	17962252	513592	gain	2.494	2	0.999999309	0.246993159
AML diagnosis (0d)	10	42408726	46418799	4010074	loss	1.131	1	1	0.434481743
AML diagnosis (0d)	10	48107282	49071953	964672	loss	1.020	1	1	0.490234346
AML diagnosis (0d)	10	49084367	51125780	2041414	loss	1.089	1	1	0.455680521
AML diagnosis (0d)	10	51398298	62428151	11029854	loss	1.096	1	1	0.452075057
AML diagnosis (0d)	10	66822698	70285006	3462309	loss	1.095	1	1	0.452400843
AML diagnosis (0d)	10	72462296	75699352	3237057	loss	1.096	1	1	0.452090902
AML diagnosis (0d)	11	125802530	130123237	4320708	gain	2.327	2	0.999976263	0.163386463
AML diagnosis (0d)	16	2263650	21369108	19105459	loss	1.674	2	0.999985365	0.163087363
AML diagnosis (0d)	16	22822268	32019651	9197384	loss	1.688	2	0.999980906	0.156072851
AML diagnosis (0d)	16	46438848	85148570	38709723	loss	1.679	2	0.999996089	0.160730158
Relapse (+225d)	1	155343758	158120830	2777073	gain	2.403	2	0.99999999	0.201653839
Relapse (+225d)	1	158125568	158955052	829485	gain	2.677	3	1	0.338344699
Relapse (+225d)	1	158956531	205916326	46959796	gain	2.496	2	1	0.248020756
Relapse (+225d)	1	205917505	234072600	28155096	gain	2.461	2	1	0.230680905
Relapse (+225d)	1	234074062	235161536	1087475	gain	2.650	3	1	0.325129032
Relapse (+225d)	1	235165389	245865547	10700159	gain	2.474	2	1	0.236758875
Relapse (+225d)	1	245871339	249237532	3366194	gain	2.617	3	1	0.308515864
Relapse (+225d)	3	61829	6647413	6585585	loss	1.532	2	1	0.233851276
Relapse (+225d)	3	8359889	9690592	1330704	loss	1.498	1	1	0.250796699
Relapse (+225d)	3	16384192	19041596	2657405	gain	2.443	2	1	0.221736922
Relapse (+225d)	3	19043437	61555309	42511873	loss	1.499	1	1	0.250595064
Relapse (+225d)	3	61559498	68436384	6876887	loss	1.441	1	1	0.279622487
Relapse (+225d)	3	68439578	85935616	17496039	loss	1.525	2	1	0.237250689
Relapse (+225d)	3	141393291	161042132	19648842	gain	2.391	2	0.999999685	0.195737799

Relapse (+225d)	3	161046813	197957467	36910655	gain	2.477	2	1	0.238472357
Relapse (+225d)	5	132065863	180899715	48833853	loss	1.494	1	1	0.252900709
Relapse (+225d)	10	517019	17962252	17445234	gain	2.451	2	1	0.225701756
Relapse (+225d)	10	17963081	39074032	21110952	gain	2.446	2	0.999999999	0.223194819
Relapse (+225d)	10	42907613	46418799	3511187	loss	1.472	1	1	0.264187944
Relapse (+225d)	10	48107282	48747765	640484	loss	1.409	1	1	0.295625551
Relapse (+225d)	10	49084367	51125780	2041414	loss	1.452	1	1	0.274092766
Relapse (+225d)	10	51398298	62428151	11029854	loss	1.497	1	1	0.251286239
Relapse (+225d)	10	62429156	63388827	959672	gain	2.472	2	0.999999997	0.235993032
Relapse (+225d)	10	63722712	65892309	2169598	gain	2.562	3	1	0.281143168
Relapse (+225d)	10	66791150	70285006	3493857	loss	1.532	2	1	0.233772502
Relapse (+225d)	10	72504636	75695386	3190751	loss	1.464	1	1	0.268229864
Relapse (+225d)	21	14755232	47282074	32526843	gain	2.446	2	1	0.223132469
Relapse (+225d)	22	16695297	17500113	804817	gain	2.996	3	1	0.498021235
Relapse (+225d)	22	17509712	18645711	1136000	gain	2.691	3	1	0.345268
Relapse (+225d)	22	18864171	20356873	1492703	gain	2.885	3	1	0.442335644
Relapse (+225d)	22	20625703	48840122	28214420	gain	2.816	3	1	0.408110605

Supplementary Table 4: Optical Genome Mapping - Rare Variant Pipeline – Confident Aneuploidy Calls

Time point	Chr	Aneuploidy type	Fraction of complete chromosome length	Confidence	Fractional Copy Number
AML diagnosis (0d)	3	loss	0,8204514067	1	1,114170659
AML diagnosis (0d)	16	loss	0,8778554944	0,9999999744	1,633344541
Relapse (+225d)	21	gain	0,936071812	1	2,444302749
Relapse (+225d)	22	gain	0,965232492	1	2,877173468