SUPPLEMENTARY APPENDIX

Ultrasensitive detection of acute myeloid leukemia minimal residual disease using single molecule molecular inversion probes

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SUPPLEMENTARY METHODS:

smMIP Design

A smMIP capture panel was designed against AML-relevant targets (**Table 2, Supplementary Table 2**) using the program MIPgen[1] with the following flags: -max_capture_size 162, -min_capture_size 152, -logistic_priority_score 0.5, -common_snps off, -arm_lengths 18:24,19:23,20:22,21:21, -starting_mip_overlap 1, -tag_sizes 4,4. Manual review of smMIPs with a logistic score of less than 0.6 was then performed, and smMIPs with near-zero logistic scores were manually redesigned. Based on recurrently mutated factors identified in published AML exome sequence data[2], this capture panel is predicted to identify cancer-assosciated mutations in ~80% of AML specimens. For this pilot work, dedicated smMIP probes were also designed to target identifying polymorphisms carried in cell lines[3] KMH2, RAJI, OCI-AML2, and L1236, as well as several other clinically relevant genes (*ABL1, ALK, JAK2, NT5C2,* and *ROS1*). All oligonucleotides were synthesized by Integrated DNA Technologies (Coralville, Iowa), using standard salt purification.

DNA extraction

DNA extraction from all specimens was performed using a QiAgen X-tractor with Reagent Pack DX (Germantown, MD).

smMIP capture protocol

smMIP pools were initially 5' phosphorylated using 1U T4 Polynucleotide Kinase (New England Biolabs, Ipswitch, Massachusetts) per 27 pmol probes in 1X T4 Ligase Buffer, by

incubating at 37°C for 45 minutes and 65° for 20 minutes. To perform smMIP capture, we combined 500ng genomic DNA, 20,000 smMIPs per genome (ie, 28.05 μmol), 2mM $MgCl_2$ (Thermo Fisher Scientific, Waltham, Massachusetts), 0.5mM NAD (NEB), 25mM KCl (Thermo Fisher Scientific), 0.01% triton-X 100 (Sigma-Aldrich, St. Louis, Missouri), 20mM Tris-HCl ph8.3 (Sigma-Aldrich), 320 pmols dNTPs (NEB), 1 U Q5 polymerase (NEB), and 1 U Ampiligase (Epicentre) in a total reaction volume of 25ul. Reactions were incubated for 95°C for 10 minutes, 60°C for 2.5 hours, then 8 cycles of 95°C for 1 minute, 60°C for 2.5 hours. Reactions were cooled on ice prior the addition of 5 U Exonuclease I (NEB) and 25 U Exonuclease III (NEB) in 1X Ampiligase buffer and incubation at 37°C for 45 minutes followed by 95°C for 2 minutes. PCR amplification and addition of index sequences was performed using 1X iProof High-Fidelity Master Mix with 23.75 pmol each oligonucleotide. PCR was carried out using an initial incubation of 98°C for 30 seconds, followed by 19 cycles of 98°C for 10 seconds, 60°C for 30 seconds, and 72°C for 30 seconds, and a final extension at 72°C for 2 minutes. After amplification, libraries were purified using 0.8X Agencourt AMPure XP (Beckman Coulter, Pasadena, California). Size selection for 280bp product was performed using a 3% agarose gel and Monarch Gel Purification Kit (NEB).

smMIP rebalancing

Initially, smMIP probes were pooled together at equimolar concentrations, capture performed using NA12878 genomic DNA, and sequenced to determine the relative abundance of reads from each probe. Probes were empirically rebalanced and repooled to achieve better performance uniformity, as well as to remove several probes with consistently poor performance.

Data analysis Pipeline

Reads were demultiplexed using bcl2fastq-v2.17 (Illumina). Fastq-mcf 1.04.676 was then used to remove regions from reads corresponding to the smMIP backbone and to remove reads less than 53 bp in length using parameters -l 53 -k 0 -q 0. Read pairs were then self-assembled using pear v0.9.5[4]. Read sequence identifiers were next renamed to contain a string corresponding to a concatenation of the 4 bp UMID at the 5' end of the assembled read and the 4 bp molecular tag at the 3' end of the assembled read. Reads were then mapped to hg37 using bwa mem v0.7.12[5] and samtools v1.1[6]. For performance reasons we split mapped reads first by chromosome and subsequently to files corresponding to individual smMIPs, based on their expected start and stop coordinates, and these files were independently processed.

For reads corresponding to each smMIP, UMIDs represented in only one sequence read were initially discarded. Remaining reads were grouped based on whether their UMID was contained in two, or more than two independent reads. Single nucleotide polymorphisms and indels were called on these read groups using the mpileup2snp and mpileup2indel commands of VarScan.v2.3.7 [7], respectively, using a "majority rule" approach. For UMID groups containing only two reads, variant calling was performed using the flags --min-coverage 2 --min-var-freq 1.0 --min-freq-for-hom 1.0 --strand-filter 0 --p-value 1 --output-vcf 1 in order to specify that 50% or more of the reads must contain a given variant in order to be called, whereas for UMID groups comprised of three or more reads parameters were set to --min-coverage 3 --min-var-freq 0.5 --min-freq-for-hom 0.5 --strand-filter 0 --p-value 1 --output-vcf 1 in order to specify that both reads must contain a given variant in order to be called.

Variant calls from each individual smMIP were then combined into a single file, including provisions to cumulatively add read counts in regions overlapped by multiple smMIPs. Variant files were annotated using ANNOVAR[8] (last accessed 2015-06-17).

In summary, the analysis pipeline expresses variant calls in terms of the number of unique smMIP capture events which are consistent with a given variant over the total number of smMIP capture events overlying that site.

Source code for the smMIP analysis pipeline is available from: ssh://git@bitbucket.org/uwlabmed/smmips_analysis.git

Error model

We produced a site- and mutation-specific error model in order to assess the significance of observed variation at each site in the smMIP panel. We sequenced DNA extracted from cell line NA12878 and bone marrow specimens from four healthy donors to serve as a baseline for measuring error rates. To determine the variant allele frequency threshold which defined heterozygous sites, we intersected variant calls for NA12878 from the smMIP assay with those from "platinum genome" datasets[9], and subsequently selected a minimum variant allele frequency threshold of 0.2 for defining heterozyogity. We therefore masked sites with variant allele frequency of 0.2 or greater, and considered all remaining variation to be errors. We empirically determined that our error distribution were best modeled as a β distribution. Thus, for each base position and each possible nucleotide substitution error, we fit a β distribution based on the mean fraction of capture events consistent with the error and the and standard deviation of this value across multiple samples. For sites and/or substitutions where no variation was detected in one or more of the baseline specimens, we assumed a fixed error rate of 1 in 15,000 consensus smMIP

reads, which can be considered a conservative threshold given the measured performance of the assay, and an appropriate β distribution was modeled. Subsequently, for each variant encountered experimentally, a site- and position-specific *p*-value was ascribed to each variant called using these pre-computed β distributions, and sites with $p>0.005$ were excluded as potential artifacts.

Comparison of conventional deep sequencing to smMIP capture

We utilized sequencing data from smMIP capture to compare error rate differences between conventional deep sequencing strategies and smMIP capture. To evaluate the effects of smMIP mediated error correction, standard smMIP analysis was implemented as above. To determine the error rate of conventional sequence analysis, the same sequence data were aligned to the human genome as above, with variant calling performed using VarScan's mpileup2snp and mpileup2indel functions with flags set to --min-reads2 2 --min-coverage 2 --min-var-freq 0.000000000001 --strand-filter 0 --p-value 1 for evaluating standard variant detection and --min-reads2 2 --min-coverage 2 --min-var-freq 0.000000000001 --strand-filter 0 --p-value 1 for ultrasensitive variant detection.

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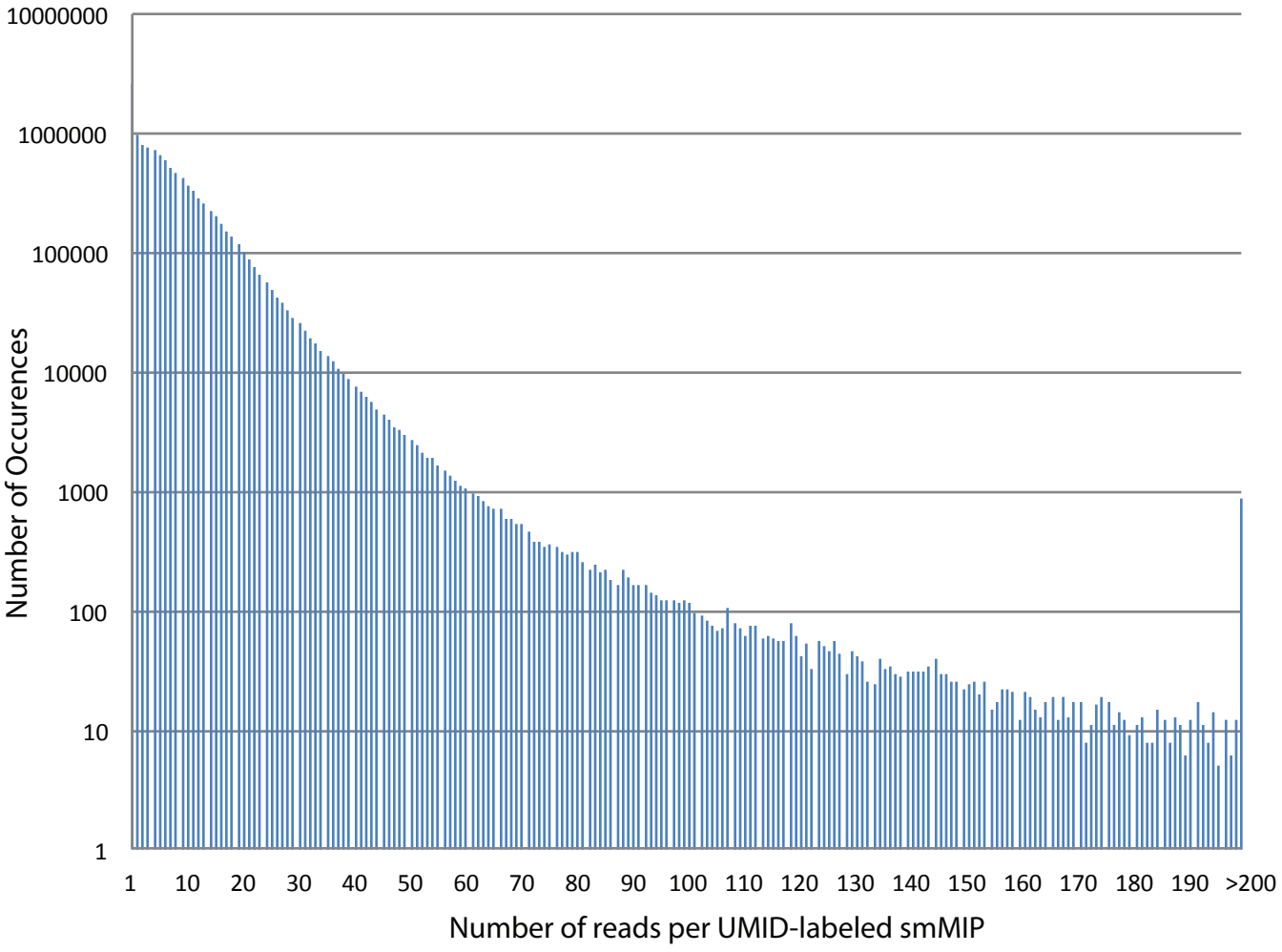

Figure S1. Distribution of reads across uniquely identifiable smMIP probes.

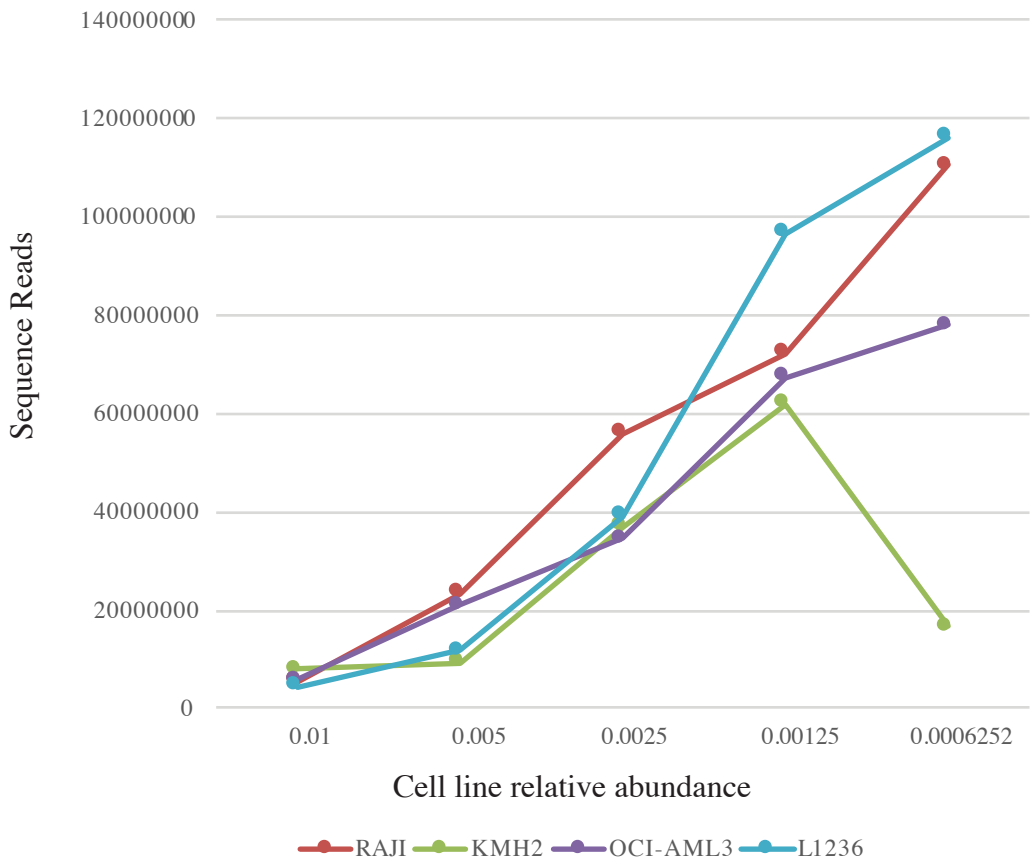

Figure S2. Total number of sequence reads required to detect mutations at different levels of relative abundance

Table S1. Additional patient testing results

Patient	Day from initial diagnosis	Days post transplant	Bone marrow blast percentage	White blood cell count (Thousand/µL)	Hemoglobin (g/dL)	Hematocrit (%)	Platelet count (Thousand/µL)	Cytogenetics	FISH	Chimerism
1	83	Not performed	Less than 1% blasts	N/A*	N/A	N/A	N/A	N/A	N/A	N/A
	196	Not performed	N/A	0.9 (27% monocytes, Absolute neutrophil count 100)	10	30	87	N/A	N/A	N/A
	329	Not performed	90% blasts by morphology	1.8 (Absolute neutrophil count 1.2)	9.6	26	34	N/A	N/A	N/A
	412	Not performed	N/A	4.1	9.4	28	65	N/A	N/A	N/A
	531	Not performed	esetimate 90% blasts	1	10	30 (MCV 87.6 fL, RDW 14%)	17	From day 430, ISCN Diagnosis: 48,XY,+8,+22[7]/46,XY[13]	From day 430, nuc ish(RUNX1T1x3,RUNX1x2)[37/200]	N/A
2	0	-97	2% blasts, diagnosed as negative with no significant morphologic evidence of residual acute monocytic leukemia	1.52	12	N/A	138	46,XY [28]	Prior testing, normal AML (5, 7, 8, 20q, MLL) and MDS (chr 5, 7, 8, 13q, 20q) FISH panel	N/A
	69	28	Blasts not increased	5.06	10.3	N/A	229	46,XY [1], 46,XX [19]	N/A	T cells 39% donor; NK cells 93% donor; no data for myeloid fraction
	125	84	Less than 5% blasts; no circulating blasts	4.59	9.3	26 (MCV 83 fL)	205	46,XX [20]	N/A	myeloid 100% donor; T cells 50% donor
	393	352	Blasts not increased	11.21	10.5	N/A	193	46,XX [20]	N/A	99% donor, 1% host
	397	356	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
	461	420	Less than 5% blasts; no circulating blasts	10.12 (1.52 eosinophils)	13.7	N/A	157	46,XX [20]	N/A	N/A
	579	538	Blasts not increased	17.01	16.1	N/A	232	N/A	N/A	T cells 71% donor; myeloid 100% donor
	746	705	"florid relapse, 80% blasts"	N/A	N/A	N/A	N/A	N/A	N/A	N/A
3	0	-115	N/A	1.0	8.7	24 (MCV 87 fL, RDW 14.3%)	32	46,XX [20]	Negative for deletion 7q/monosomy 7, t(8;21), t(9;22), MLL, t(15;17), inv(16)/t(16;16)	N/A
	94	-21	N/A	N/A	N/A	N/A	N/A	46,XX [20]	N/A	
	143	28	No blasts seen	5.29	9.3	N/A (RDW 20%)	331	46,XX [20]	N/A	N/A
	269	154	No blasts seen	2.36	9.7	30 (MCV 87 fL, RDW 15.4%)	32	N/A	N/A	100% donor
	346	231	No blasts seen	3.2	13.4	40 (MCV 108 fL, RDW 19.1%)	70	46,XX [20]	N/A	N/A
	437	322	No blasts seen	1.21	11.5	34 (MCV 114 fL, RDW 14.6%)	97	46,XX[20]	N/A	100% donor
	542	427	No blasts seen	2.35	11.5	34 (MCV 113 fL, RDW 18.1%)	38	N/A	N/A	N/A
	584	469	N/A	2.17	11.3	34 (MCV 117 fL, RDW 14.3%)	49	N/A	N/A	N/A
	599	484	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
4	269	-917	N/A	N/A	N/A	N/A	N/A	46,XY [20]	nuc ish(EGR1,D5S23)x2[199/200],(D7Z1,D7S486)x2[199/200],(D8Z2x2)[200/200],(D20S108x2)[200/200]	N/A
	1083	-103	Blasts not increased	2.67	10.8	32 (MCV 98 fL, RDW 13.7%)	56	46,XY [20]	Normal AML IFSH panel: absence of t(8;21), MLL, t(15;17), inversion or rearrangement CBFB	
	1214	28	Blasts not increased	6.92	11.8	35 (MCV 103 fL, RDW 18.9%)	186	46,XX [20]	N/A	N/A
	1556	370	Blasts not increased	6.88	14.4	35 (MCV 104 fL, RDW 14.6%)	282	46,XX [20]	N/A	N/A

* Not Available

Table S2. smMIP panel design

smMIP name	Chromosome	Extension Probe Start	Extension Probe Stop	Ligation Probe Start	Ligation Probe Stop	smMIP Sequence
SMC3/NM_005445_0053a	10	112341679	112341696	112341818	112341840	AATCAGGAACTTAACGAGACTCGNNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGGGCAAACGGGAAAA
SMC3/NM_005445_0053b	10	112341788	112341805	112341903	112341926	TATGAATTGTTAAACTCAGGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGACGAGCCCTGGAA
SMC3/NM_005445_0058b	10	112343723	112343745	112343616	112343634	TTCAAGCAGCTTCTGCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAGTGTTGGTGAAAGTTCTCAG
SMC3/NM_005445_0065a	10	112349733	112349752	112349591	112349613	CACATATGAGGATGCATTAACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCTTTCCTGTTGCTGCT
SMC3/NM_005445_0065b	10	112349768	112349789	112349667	112349686	TGCTTGCTGTTCTGCATTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACTCAGTGTAAACAGAGGTGA
SMC3/NM_005445_0087b	10	112362363	112362382	112362244	112362266	AACTTCTGGAATACTTCACTGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTTTGTGAGCCAGAACC
PTPN11/NM_080601_0128a	12	112891140	112891160	112891006	112891026	TTTCCCAGAGAGATGTCCATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACTTGCCGTCATTGCTCTCC
PTPN11/NM_080601_0128b	12	112891203	112891223	112891089	112891108	CAAAATCTCCAGGGTGGCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGCCAGACCCATTTTTCAAC
PTPN11/NM_002834_0148a	12	112942573	112942592	112942437	112942458	GACCACGCTGTTTAAGCTTACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTCTGAAGTTTTGGCAGGT
PPM1D/NM_003620_0190a	17	58725277	58725296	58725135	58725156	ATAGACGCAGAAAAGCATTTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCACAAATTCACCACTGA
PPM1D/NM_003620_0190b	17	58725383	58725403	58725247	58725267	AGCTCCACAAATCACCTGGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCATCTTGTGGTGGAATC
PPM1D/NM_003620_0198_SNP_aa	17	58740664	58740684	58740524	58740544	AGTCAGGGCTTTAGCGCAATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTTCTTTCAATTTCTTGG
PPM1D/NM_003620_0198_SNP_ab	17	58740767	58740787	58740636	58740656	TTTGGCCAGGAGTTGACATCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCAGGCTGAGCACCACTACT
TP53/NM_001276696_0162a	17	7576591	7576610	7576463	7576482	CATAGCTTAGCCTAGCCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTTCTATGACTTTGCCTG
TP53/NM_001276696_0162b	17	7576704	7576723	7576562	7576583	TGCTACTTGACTTACGATGGGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGGCTCCTGGTTGTAGCA
RUNX1/NM_001001890_0223b	21	36164565	36164585	36164681	36164701	GGCTTGGAACGGGCCTCCCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGAGGCGTTGGTGCAGGGC
RUNX1/NM_001754_0240a	21	36265281	36265301	36265167	36265187	GTACACACCTTCATAGATGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTTGCATTACTTTTATTTTC
TET2/NM_001127208_0314a	4	106196625	106196645	106196503	106196523	GGGTAAGGGTTCATGGGATTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATACAGATCCATCGGCTGAG
TET2/NM_001127208_0314b	4	106196709	106196729	106196593	106196613	TAGGAACCCAGATATGGGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCGGCTATTTCCAAACCTTG
EZH2/NM_004456_0343a	7	148514425	148514445	148514284	148514304	CCGATAAAAATGTTGTTAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAAATATTGAACCTCCTGAG
EZH2/NM_001203248_0349b	7	148523609	148523629	148523484	148523504	AAAGCAGCTTGGAGAGTGCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCAAAGCTTACACTCCTTTC
EZH2/NM_004456_0357a	7	148529737	148529758	148529879	148529898	AAAGGACAACCTTAAGCTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGTAGGGGAGACCAAGAATA
EZH2/NM_001203248_0359_SNP_aa	7	148543612	148543632	148543482	148543502	CATTTGTTTGGTTATTGGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGGAAACAGCGAAGGATAC
EZH2/NM_001203248_0359_SNP_ab	7	148543710	148543730	148543577	148543597	CTGACTTCTGTGAGCTCATTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNN
RAD21/NM_006265_0380b	8	117869745	117869765	117869604	117869624	CCTCCTATTAGAGTCTGAACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACAGTGCTATTTCTAATCTT
RAD21/NM_006265_0384b	8	117874224	117874244	117874093	117874113	TTCATGACTTTGATCAGCCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCCCTCTGATCCCTAGATA
RAD21/NM_006265_0385a	8	117875481	117875501	117875356	117875376	TCGGCCAGGTATTGTTAAACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGGTGAAAATGGCATTACGG
RAD21/NM_006265_0385b	8	117875537	117875557	117875412	117875432	GCCAAATACCTTCTTGCAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGACTATGAATGGCACGAA
RAD21/NM_006265_0387a	8	117878725	117878746	117878866	117878885	ACTCGAACACATGGGCTTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTCCAATGCCCCTACCTAAA
JAK2_p.V617F_0390a	9	5073794	5073814	5073654	5073674	GAATTGTTGTTTGACTGTTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCATTAGAAAGCCTGTAGTT
HNRNPK/NM_031262_0413a	9	86592689	86592709	86592559	86592579	TGAAGGTGGTTCATACTCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTTAGGTAAACGCCTGC
HNRNPK/NM_031262_0413b	9	86592719	86592739	86592602	86592622	CATTCTGCTTCAGAGCAAGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCGCTGCTTTCTTTGAAATGT
HNRNPK/NM_031262_0414b	9	86593220	86593240	86593118	86593138	CCCTAACACTGAAACCAATGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTTTCCAATAAGCCAAATG
STAG2/NM_006603_0483b	X	123179167	123179187	123179030	123179050	GAGGACCAGCCATGGTAAGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACTTGTGAGTCAGACAATCC
STAG2/NM_006603_0503a	X	123196698	123196718	123196800	123196820	ATCACTGAGCTTTTTGCCGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTTAACAGTGCTAATGGGC
STAG2/NM_006603_0522b	X	123215347	123215367	123215209	123215227	CTGTTTGGAAAGAAAGAAAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCAATGGCTTCTCTTGTTTT
STAG2/NM_006603_0531b	X	123224549	123224569	123224691	123224711	ATTCTCCTTGAAGCACGCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGGATAGCTTCATGAGTGT
STAG2/NM_001042750_0532b	X	123224821	123224841	123224697	123224717	ATGTTACCTGCGTGCTTCAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCAGACAATAAGGCACTCTC
TET2/NM_001127208_0295a	4	106162544	106162564	106162417	106162437	ACATCCACAAAGCTTAACCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGCTGCCACATTAGGACCTG
MTOR_KMH2_HAEMATOPOIETIC_ANI	1	11182236	11182256	11182105	11182125	CCCCACTGTGACACACTGCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCTGTGTTCTGAGCTGCTC
NRAS_p61_0002	1	115256463	115256480	115256591	115256614	GTAAGAATCCTGGGGGGTGTGGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAAATACACAGAGGAAG
NRAS_p.G12S_0003	1	115258661	115258680	115258791	115258812	GCAAGAACCTGTTGGAAACCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCCTCACCTCTATGGTG
NOTCH2_KMH2_HAEMATOPOIETIC_A	1	120506321	120506338	120506449	120506472	CAAGGATTCTCAAAGACCAAGGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGATTGCAGATGCAGGT
FAMSC/NM_199051_0007	1	190067249	190067267	190067116	190067138	TCAAGCACAACCCAAAATCTTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCGTCATAGACTCAAGC
FAMSC/NM_199051_0008	1	190067224	190067241	190067352	190067375	TGCTGAATCCTGGGATCCCTGAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCACCCTCACTA
FAMSC/NM_199051_0009	1	190067466	190067486	190067325	190067345	CAACTACTAGAGATCAGAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCGGAACCTGGGCTATATG
FAMSC/NM_199051_0010	1	190067419	190067437	190067553	190067575	GCGACTTCTCAGGTAGATGTGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTCAAAGTGCATGCTGT
FAMSC/NM_199051_0011	1	190067633	190067651	190067500	190067522	AGCATTTACTATGAACCTCTGGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGTTGGACCTACCCCTGC
FAMSC/NM_199051_0012	1	190067730	190067749	190067588	190067609	CTGGGGAACAAATGGAAGACATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGTGTTGGTCTGTTTATGTC
FAMSC/NM_199051_0013	1	190067699	190067716	190067832	190067855	GCTCTTCAAGGTGAGGAGCATCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTCTCAGAGTGGCTGC
FAMSC/NM_199051_0014	1	190067785	190067802	190067913	190067936	GGCATGGACTTCTATTCGTCTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAGAGAGACCCAAAATC
FAMSC/NM_199051_0015	1	190067866	190067883	190068004	190068027	GTGGACTCGGCGACTTCAGGCTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGGATCAAACCAGCTA
FAMSC/NM_199051_0005	1	190068102	190068119	190067968	190067991	TGGCTTTGAAACTGACCTGCAAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGACGCCTCTGCCTGC
FAMSC/NM_199051_0006	1	190068080	190068098	190068219	190068241	GCAGTAGAGAAAAGACTGGATGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTGTCTGGTGCGCATGT
FAMSC/NM_199051_0016	1	190068174	190068191	190068312	190068335	GTGTACTGCAGTAAACCGTAGCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGAGTGCGTCTCTTCTGA
FAMSC/NM_199051_0017	1	190129774	190129791	190129902	190129925	GTTCTCCAGTTGTTCATAACGGCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTACATTACCACAAATG
FAMSC/NM_199051_0018	1	190129990	190130007	190129856	190129879	AGGCGCAGAAAATTGTACACAAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTATGAAAAGGCTACC
FAMSC/NM_199051_0017	1	190130021	190130038	190129887	190129910	CTGGAGAACAGCATGAAACAACTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATTTTGACATTTTTCAG
FAMSC/NM_199051_0021	1	190195172	190195189	190195300	190195323	GCAGTTGCATTCTGGAAATTTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTCAATATTTAAAAGTGT
FAMSC/NM_199051_0022	1	190195278	190195296	190195412	190195434	CGTTCCTGAAGATAGTCTGGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCTTGAATGTCCATGGA
FAMSC/NM_199051_0020	1	190195452	190195469	190195318	190195341	TGCTGGTGTCACTGTGGTCCCAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCTTTGTTTGTTCTTC
FAMSC/NM_199051_0023	1	190203585	190203602	190203451	190203474	CTACAAGCCTGAATAGCAATTATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAAACACGGACTGGTCC
FAMSC/NM_199051_0024	1	190203527	190203544	190203655	190203678	GTCCTTTTGGTTCACTGTAGTTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTCTGAACCAGAACAGA
FAMSC/NM_199051_0025_SNP_a	1	190233946	190233964	190234075	190234097	GCTGATGTAGCGTCTCCAGAGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAAACAAACAATGGAAG
FAMSC/NM_199051_0026	1	190234036	190234054	190234170	190234192	GTGAGTGACTCCTCTCCTGCATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGGGTGCTGTCCCTGTC
FAMSC/NM_199051_0027	1	190234249	190234266	190234105	190234128	GAAGTGATTCCACCACCAATAGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTAGACCTTTCCACCTGC
FAMSC/NM_199051_0028	1	190250657	190250674	190250790	190250813	GCGGAAGAATTCAGGGGCAAGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACACAGGCACAAATAGG
FAMSC/NM_199051_0029	1	190250905	190250925	190250764	190250784	AAGACTTTTGGGACGTCGACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGATCGATAAAGAGGAAG
FAMSC/NM_199051_0030	1	190423902	190423919	190423758	190423781	TGAAGCAAAGGGAAAGCAATTACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTTCGGATCAGCATGC
FAMSC/NM_199051_0031	1	190423857	190423875	190423991	190424013	TTCAGCACCAGCTCTGCTTCGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGAAGGGTCCCTTATCAG
FAMSC/NM_199051_0032	1	190423892	190423910	190424021	190424043	GCTTCCACTGGGGATTTAGAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGCTTGTGGCATGCTGA
NTSC2_p.Q523_0034	10	104849561	104849579	104849428	104849450	GGAGGAGGAGGAGGAAGAATAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGATTTCAAAGACACTGAC
NTSC2_p.D407_0035	10	104850708	104850726	104850837	104850859	GCTGGAGTGCAGGGGTGTGATCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATGGAACTGATGTCTGGA
NTSC2_p.R359_0036	10	104852890	104852910	104853021	104853041	TCTTTTCCCTTGGCTCCCAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTTACAACTCTTGTCAGTCC
NTSC2_p.R238_0037	10	104857113	104857132	104856981	104857002	GGCCTAAAGAACTGTGAAGACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAAAACTGCCTTTGCTTC
SMC3/NM_005445_0038	10	112327479	112327497	112327608	112327630	TCCACCCCGTCATGGGCCGGTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGGGGAGGGGTCGCGT
SMC3/NM_005445_0039	10	112328650	112328667	112328778	112328801	GTTCTTGGTTTACTCGGTCATATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTTTTTTGTGGGGGTGG
SMC3/NM_005445_0042	10	112335032	112335051	112335162	112335183	GTGAGTGAGACTGCTTTAAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTTATAAATAAGTTATAAA
SMC3/NM_005445_0041	10	112335263	112335281	112335130	112335152	AGCCAACCGCTGTTCTGGACGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGATTGTGTCTTGTTCAC
SMC3/NM_005445_0043	10	112337310	112337327	112337176	112337199	AACACGAGGACCAGTACCTTCCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAAGTTTCAAAGTATG
SMC3/NM_005445_0045	10	112337510	112337529	112337640	112337661	GGATCAGTATTTCTTAGACAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCAAGGACTTTAAAATGAC
SMC3/NM_005445_0046	10	112337591	112337608	112337719	112337742	AGAGATGGGGTATTGCTGTGTTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGATCGATAAAGAGGAAG
SMC3/NM_005445_0048	10	112338421	112338441	112338290	112338310	TGGTTGATAGCATTAGGGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGATTGCTTCGAGAAAAAC
SMC3/NM_005445_0047	10	112338531	112338548	112338397	112338420	CAGCGCTTTCAAGGAGGTTCATCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACTCAAATCAATAAACC
SMC3/NM_005445_0049_SNP_a	10	112340743	112340763	112340612	112340632	TAGCTGTAGCCTCCGTTTAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGATGCTTTCTTCCTTTCG
SMC3/NM_005445_0050	10	112340703	112340720	112340831	112340854	GTGACAGAGTGGCTCCATGATGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTATTAAGAAGAAGTAGC
SMC3/NM_005445_0052	10	112341651	112341671	112341792	112341812	GACGAGCCCTGGAATATACCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTCCACCTCTCTCCCCATT
SMC3/NM_005445_0051	10	112341922	112341940	112341784	112341806	ATTCCAGGGCTCGTCTCATTTTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAAGTGTAATTATGGCC
SMC3/NM_005445_0054	10	112342211	112342228	112342339	112342362	CTAGTGGAGAAAAATCCAGACAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGCAGTTACTTTTGG
SMC3/NM_005445_0056	10	112343093	112343112	112343228	112343249	GCAGATTAAGCAGAGGACTAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTATTGTACTTCTAATTGC
SMC3/NM_005445_0057	10	112343204	112343221	112343332	112343355	GATGTGAATGTTCAGGTGAGTAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAGCTTAGTGCTGAAAG
SMC3/NM_005445_0060	10	112343902	112343919	112344040	112344063	GGACTCAAGTCTTTGATGATCAGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATTCTCCTTTCATCCC
SMC3/NM_005445_0061	10	112344142	112344159	112344008	112344031	CCACTTATCCCTTTCTTCTTTTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTACATTATACTGCTCC
SMC3/NM_005445_0062	10	112344170	112344188	112344037	112344059	GATCTAAAGACTTGAGTTCCTTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGATTTTTACAAAGCAGC
SMC3/NM_005445_0063	10	112349316	112349333	112349444	112349467	GATGAACTACAAAGTGAAAGAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATTAGTTTCATGAAATT
SMC3/NM_005445_0064	10	112349510	112349527	112349376	112349399	CTCGAGCTTTGACTTCATTAAGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACATAACAGCTAGTAACG
SMC3/NM_005445_0066	10	112350289	112350306	112350145	112350168	TGTAAGTTGTCAGAAATGAAAAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGTAGAAAGCTGGT
SMC3/NM_005445_0067	10	112350221	112350239	112350355	112350377	GCATTTTTAGAAGAGGGAATAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGAAAAGGAATAAACCAGC
SMC3/NM_005445_0068	10	112350842	112350859	112350698	112350721	TTTATTGGTACTCAGGGTCTCCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTAACTTGTTAAGAGGC
SMC3/NM_005445_0069	10	112350819	112350839	112350960	112350980	GCTAGTGCCCAGGCACTATACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCCTGGAGAGGTTACTTTT
SMC3/NM_005445_0070	10	112352933	112352952	112352791	112352812	CAACAGAGAGATCACAACACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCACGGGCCAGCTGGGTTGA
SMC3/NM_005445_0071	10	112353038	112353056	112352905	112352927	CCATGCTACGACAAATAAGAGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGCCCAGCCAGATTATATG
SMC3/NM_005445_0072	10	112356117	112356134	112356245	112356268	GCAGAAGAAGAACTAGGTGAACTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAGTTGTACAGACCTA
SMC3/NM_005445_0073	10	112356205	112356222	112356343	112356366	GTGGGGGAAGAACTGTGTTTTGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGAAGTCTCGACTTGA
SMC3/NM_005445_0074	10	112358003	112358020	112357859	112357882	GGAAAATTATCTCCAGGTTGTAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCTCTTCTCTTTTAGC
SMC3/NM_005445_0075	10	112358063	112358080	112357929	112357952	CTGGGTCTCGATCTGTTGCATTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCGATCTATAACCAAAG
SMC3/NM_005445_0076	10	112359498	112359516	112359365	112359387	GTAAGGTATTAGCCACTGTATTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAACTCAGTTGAGAAAGC
SMC3/NM_005445_0077	10	112359612	112359629	112359468	112359491	GTTCCCAGTTCTGCTTTCAATGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCTTTTCACAATAGCC
SMC3/NM_005445_0078	10	112360277	112360294	112360143	112360166	CATGTACATTTCACACACAGGAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTCCAAGCGTTTTCTC
SMC3/NM_005445_0080	10	112360869	112360886	112360735	112360758	CCATTAGTTTCAAATGTTATGACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCGATCGTGCCATAGTG
SMC3/NM_005445_0081	10	112360830	112360847	112360958	112360981	GTCCAAATAGGCAGAAGCATATGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACATCAGAACTTGAAGC
SMC3/NM_005445_0082	10	112361513	112361530	112361369	112361392	AAGATGGGGGGAAACAAAATTAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGTCATCTTTTCCAGT
SMC3/NM_005445_0084	10	112361709	112361727	112361576	112361598	GAAGTGATCCAAGTTCTCGAATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAACTATAAAGAGAAAAT
SMC3/NM_005445_0085	10	112361699	112361716	112361837	112361860	GCGTCAAGAAGAGTTAGATAGGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGAATACATATTTTCTC
SMC3/NM_005445_0086	10	112361813	112361830	112361951	112361974	GTAGTTAAAACATACACACAGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGAGCAGAAAGAAAAGTT
SMC3/NM_005445_0088	10	112362442	112362459	112362298	112362321	ACTGCCCTCCACATCTCCTTTCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGCTCTGAGGAAAATGG
SMC3/NM_005445_0089	10	112362532	112362552	112362673	112362693	GCCATTCAGAAATGTGACCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGGTGATTCTGCCCTTTAG
SMC3/NM_005445_0090	10	112362637	112362655	112362766	112362788	GTTTCAGTACAGTTTTGGTTTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACAGAAATCCTTGGTAG
SMC3/NM_005445_0092	10	112363013	112363030	112362879	112362902	GCAGATCTGAAAATTTAAAAAGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCATAGAATTTGTCAGC
SMC3/NM_005445_0091	10	112363117	112363134	112362983	112363006	AAGCAGTTCAGGCCTAAAAGTAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTCACTATTTAAGTAAC
SMC3/NM_005445_0093	10	112364070	112364087	112363936	112363959	TGTTAATTACATCAGTGTTTACATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAAACCAGTAGGTAGT
RET_p.804-806_0033	10	43615055	43615073	43614922	43614944	GTCAGGCAGCTTGGGTCTTCCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTGCCCAGGTAGCCAGGC
MLL_KMH2_HAEMATOPOIETIC_AND_	11	118360451	118360468	118360579	118360602	CCCACAAAGAAGAAGAAAGTCTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGTTGGGTGAAGGTAA

WT1/NM_001198551_0094	11	32410692	32410710	32410559	32410581	CAGTGTCCCAGGCAGCACAGTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGTCGGTGGCCAAGTTG
WT1/NM_001198551_0095	11	32410670	32410690	32410801	32410821	AAGTCATCACAAGGCACCCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGACCGGGCAAACTTTTTCTG
WT1/NM_001198551_0096	11	32413628	32413645	32413494	32413517	GTGCGTAAACTTTTCTTCACATTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTAGGGCCGAGGCTAGAC
WT1/NM_001198551_0097	11	32414305	32414323	32414172	32414194	TCATTGCTGGCAGCTGTGTTCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGAATATGTGTCTTCCCC
WT1/NM_001198551_0098	11	32417907	32417925	32417774	32417796	GTGCCCGCTGTCCAGTCTTGGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTCTGTGTCTCCCCCAAC
WT1/NM_001198551_0099	11	32417869	32417886	32418007	32418030	CGTAGGTCTTGAGGGAGAGTGAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGCACACATGAAGGGGC
WT1/NM_001198551_0100	11	32421600	32421617	32421466	32421489	GCACACAGACAGGCCCCAGCGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCTTTTTCCCTTCTTTG
WT1/NM_001198551_0101	11	32438139	32438159	32438008	32438028	GACAATGCGGAGATGGCAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGGGATCTGGGGGGCTTG
WT1/NM_001198551_0102	11	32439088	32439105	32439216	32439239	CTAGAGTTAGAAACACATAACCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTGTGGAAAGGCAATGG
WT1/NM_001198551_0103	11	32449596	32449613	32449462	32449485	CTCTGCGTCTGGGTCCTTGGGACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTCTGCAGGTGAGCAGC
WT1/NM_001198551_0104	11	32449675	32449693	32449542	32449564	CCACACCCCCACCGACAGCTGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTCGTGTCTCCCCCAAC
WT1/NM_001198551_0106	11	32450002	32450020	32450131	32450153	GCTGGCCGTCCGTCGAAGGTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGAAGGGGAGAAGGACT
WT1/NM_001198551_0105	11	32450209	32450227	32450076	32450098	GTTCCCCAACCACTCATCAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCACTGCCCCGTCTTGC
WT1/NM_001198551_0107	11	32452104	32452121	32451979	32451993	TCTCTCTCTCTCTCTGTGTCTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGCCCTGGGTCCCTGC
WT1/NM_024424_0114	11	32456307	32456325	32456164	32456186	CTAGGACACCCCCCTCTCCTACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCCGGCCAGGCCAGGATG
WT1/NM_024424_0115	11	32456403	32456420	32456269	32456292	CTACCTGCCCAGCTGCCTCGAGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCGCCTTCACTGTCCAC
PTPN11/NM_080601_0123	12	112884161	112884180	112884029	112884050	AAAAACAAGACACTGTCAGCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGGGTTACTTTTACTAGGC
PTPN11/NM_080601_0124	12	112884135	112884155	112884266	112884286	GCTTGGATAGCTTGCTGCCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAGTTGATGGCAGTTTTTG
PTPN11/NM_080601_0125	12	112888216	112888233	112888082	112888105	GAAAGGGAGGCAAGGGGACAAATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCATGTAATACTGGAC
PTPN11/NM_080601_0126	12	112888336	112888356	112888195	112888215	CAACTCAGCCAAAGTGGCAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGAGCAGCAGACTTTGTGG
PTPN11/NM_080601_0127	12	112890952	112890969	112891085	112891108	GCCAGAGCCACCCTGGAGATTTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAACCCATAGTAGAGCTA
PTPN11/NM_080601_0129	12	112891249	112891268	112891112	112891133	TCATCACCAGTGCGCACAGAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGTCTGTCTTCTTCTGTCAGC
PTPN11/NM_080601_0131	12	112892364	112892381	112892492	112892515	GATTGGAAAGCTCAAGCTTTCTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAGGAACTGAAATACGA
PTPN11/NM_080601_0132	12	112893820	112893837	112893686	112893709	GAAAACGGTGTTAATGCAAAAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTTATCTGTGGTCTCAGC
PTPN11/NM_080601_0133	12	112893790	112893807	112893918	112893941	GTGGAGGAGAAGTTGCTCTTGTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAGCAGAGTTCGAGAA
PTPN11/NM_080601_0135_SNP_a	12	112915563	112915582	112915431	112915452	AGAAGAAAAAGAGACCACGGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGGCTAGAAATGTATGGTC
PTPN11/NM_080601_0136	12	112915747	112915767	112915611	112915631	CACCTTAAAGTTACTTTCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGAACACCATCCGCCAAAAG
PTPN11/NM_080601_0137	12	112915727	112915745	112915861	112915883	GTATCAGACATGTCAGATTGGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCAAAACACGGTGAATG
PTPN11/NM_080601_0138	12	112919959	112919976	112919825	112919848	ATTCTGTGAACTCTGAAATAAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGTATAGTCATGAGCGGC
PTPN11/NM_080601_0139	12	112920054	112920072	112919921	112919943	CCTAACACGCATGACGCCATATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCCTGAATTCCTACACAC
PTPN11/NM_080601_0140	12	112924413	112924430	112924274	112924297	CCGTTCTCTCCGTATTCCCCTGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGTGCACCACGACCGGC
PTPN11/NM_080601_0142	12	112924490	112924507	112924356	112924379	ACCTCCTCCAGGAAGTCCAGCACGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAGGTAAAAGCAAGCCC
PTPN11/NM_002834_0143	12	112926315	112926332	112926181	112926204	ATGGGGGTTTCAGACTCAAAACCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCACCAGATGACCCAC
PTPN11/NM_002834_0144_SNP_a	12	112926781	112926798	112926914	112926937	CGATTTATCTATATGGCGGTCCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGGCTCTGCAGTTTCT
PTPN11/NM_002834_0145	12	112926865	112926883	112926994	112927016	GCTGGCATGCGGATTCTCATTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATGGTGCGGTCTCAGAGG
PTPN11/NM_002834_0146	12	112940039	112940056	112939905	112939928	ACATGTGAGGGACAATGGTTATTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACAGGGTGGCGTTGGAG
PTPN11/NM_002834_0147	12	112940149	112940166	112940015	112940038	TACAAGGCGGGAGAGGGCTCTGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGAAAGGCATGTGCTAC
KRAS_p.A146T_0117	12	25378664	25378682	25378531	25378553	AGACAGGTAAGTAACACTGAAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGAAGATGTACCTATGG
KRAS_p.A59T_0118	12	25380213	25380230	25380341	25380364	GGAATCCTGAGAAGGGAGAAACACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATACACAAAGAAAGCCC
KRAS_p.G12S_0119	12	25398291	25398308	25398157	25398180	CTGGTGCAGGACCATTCTTTGATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATAACTTGTGGTAGTTG
ERBB3_L1236_HAEMATOPOIETIC_ANI	12	56492347	56492365	56492214	56492236	CTTAGGATTTCCAAGTCCCAAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTGACCATAGCTCCAGAC
CDK4_L1236_HAEMATOPOIETIC_AND	12	58145487	58145504	58145353	58145376	GAGGAGGAGGTGGAGGAGGCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAATGGCTACCTCTCG
FLT3_p.I867S_0149	13	28589671	28589689	28589800	28589822	CAGGCTTTCGGGGGCCATCCATTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAGCAGAGGATGCAAAG
FLT3_p.G831E_0150	13	28592682	28592699	28592548	28592571	GGCTATTTTGTGTTGTGTCGTTATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACGTGCTTGTCACCCAC
FLT3_p.I687F_0151	13	28601332	28601352	28601463	28601483	GGAGGGCTTGGTTCTCTGCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAAGATCACCATAGCAACA
FLT3_p.D651G_0152	13	28602391	28602408	28602257	28602280	AGACTGTAGCTTGATGACAAAGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAGAAGAGGCACTCATG
FLT3_p.D651G_0153	13	28602369	28602389	28602500	28602520	CTCAGCTCAGAGTCAATCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNGGGTCATCATCTTGAGTTCTG
FLT3_p.Y572C_0154	13	28608330	28608348	28608197	28608219	GGTAAGAATGGAAATGTGCCAAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTAGGTATGAAAGCCAGC
FLT3_p.Y572C_0155	13	28608430	28608448	28608297	28608319	ACAGGTGACCGGCTCCTCAGATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTACAAAAAGGTAAAAGC
FLT3_p.S451F_0156	13	28610206	28610223	28610072	28610095	GAAGTGTTCAGACAAGTCTCCCAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGCCCAGCCAGTGAGC
IDH2_p.R172_0157	15	90631876	90631895	90631744	90631765	TCCTCGCCTAGCCATCCTCTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTGCAAAAACATCCCACGC
IDH2_p.R140_0158	15	90631843	90631860	90631971	90631994	GCTTGAACTCTGTGAGGACAGAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGGTGATGGGCTTGGT
PPM1D/NM_003620_0182	17	58677866	58677884	58677728	58677750	TCCACAGCAGCCCGCCGAATCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCAGCCGTCGGTTCGGG
PPM1D/NM_003620_0180	17	58677980	58678000	58677839	58677859	AACGATTTGAGTAACGTCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCCTCTCGGGCTGCCACCGC
PPM1D/NM_003620_0181	17	58678098	58678116	58677955	58677977	GGCCTTTCCCCGAGACTTCGCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCCGCCTCCCGCCCGC
PPM1D/NM_003620_0183	17	58678208	58678227	58678066	58678087	GCACACGGCGAAAAAGGCCACGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTGACAAGCGAGAAAGCC
PPM1D/NM_003620_0184	17	58678124	58678141	58678252	58678275	GTTCCCTGGCTTGTTTGGCGCCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGGAGCACTTGTGGGGT
PPM1D/NM_003620_0186	17	58700951	58700968	58701089	58701112	GAATCGAAGGACTTGGTGGGAGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGCATGAAGATGTATG
PPM1D/NM_003620_0187	17	58700985	58701002	58701123	58701146	CGTTTTCTCTTTCCTCTTTTGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCAGGGGTGGTTCTTGG
PPM1D/NM_003620_0189	17	58711389	58711406	58711255	58711278	GTCCATTGTGAGTGAGTCGAGGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTTTTATTTTGCCACC
PPM1D/NM_003620_0191	17	58725444	58725462	58725311	58725333	GGTCAAGAGTGTGGACACTTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTATTCAATCACATCTCAC
PPM1D/NM_003620_0192	17	58734063	58734080	58733924	58733947	GAACAAGGAGAAGGAAAGTAACTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACTTCTGGAGAGATGC
PPM1D/NM_003620_0193	17	58734159	58734178	58734027	58734048	CTAGTGTTATCTGCTCGGAGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAAGGAGTCATCACACAGG
PPM1D/NM_003620_0194	17	58734118	58734136	58734247	58734269	GTTCTTTGGTTAGCGTCACCTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGAACCTGACTGACAGC
PPM1D/NM_003620_0195	17	58740306	58740325	58740446	58740467	GAGGTTTCAGCTGAGATAGCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGTTCTGGGATAAATTTTT
PPM1D/NM_003620_0196	17	58740396	58740415	58740536	58740557	GCCCTGACTTTAAGGATACATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCATATACCTGCCCTGGTT
PPM1D/NM_003620_0197	17	58740627	58740644	58740483	58740506	GATCTTTGAGGGTATGACTACACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGACATCTTCAAATTTT
PPM1D/NM_003620_0199	17	58740663	58740683	58740794	58740814	CCCACAACCTCACAGCGAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCCAAGAAATTGAAAGAACCC
PPM1D/NM_003620_0200	17	58740765	58740782	58740903	58740926	GTGTTTGCTGAAATGCATCTGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGTAGTGGTGCTCAGC
PPM1D/NM_003620_0201	17	58740956	58740973	58740817	58740840	CGTCGCATGGTGAGTTTAACAGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAATTTAAAAAGCCCTC
TP53/NM_001126112_0159	17	7572881	7572900	7573011	7573032	GTAGGAGACAGAAGCAGGGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGGGGGTGGGAGGCTGT
TP53/NM_001126112_0161	17	7573969	7573986	7573835	7573858	ATTCTCATCCTGCCTTCATGGTCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGGAACTCAAGGATGC
TP53/NM_001126112_0160	17	7574077	7574094	7573943	7573966	AGGCTGGGAAGGAGCCAGGGGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCATCTTTAACTCAGG
TP53/NM_002176696_0163	17	7576718	7576735	7576584	7576607	TTCTATGACTTTGCCTGATACAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCTCAAAGACAATGGC
TP53/NM_002176695_0164_SNP_a	17	7576829	7576846	7576957	7576980	GTGAATCTGAGGCATAACTGCACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATAAGAGGTCCCAAGACT
TP53/NM_002176695_0165	17	7576981	7577001	7577112	7577132	CACAAACACGCACCTCAAAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGGTCTCCTCCACCGCTTC
TP53/NM_002176695_0166	17	7577084	7577103	7577224	7577245	AACCAGGCTCCATCTACTCCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGTGCGCCGGTCTCTCCC
TP53/NM_002176695_0167	17	7577601	7577620	7577469	7577490	CCACTTGCCACCCTGCACACTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTATCTCCTAGGTTGGCTC
TP53/NM_002176695_0168	17	7577645	7577663	7577512	7577534	GCCCATCCTCACCATCATCACACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACAGGTCTCCCCAAGGC
TP53/NM_002176695_0169	17	7578281	7578298	7578147	7578170	TTTGCAACTGGGGTCTCTGGGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTCTTAGGTCTGGCCC
TP53/NM_002176695_0170	17	7578355	7578372	7578221	7578244	GTGTGGAGTATTTGGATGACAGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGAGCAGCTGGGGCT
TP53/NM_002176695_0171	17	7578292	7578310	7578426	7578448	GTGCTGTGACTGCTTGTAGATGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGAGCAATCAGTGAGGAA
TP53/NM_002176695_0172	17	7578531	7578548	7578387	7578410	AGGCGCTGCCCCCACCATGAGCGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGCCCTCAACAAGATG
TP53/NM_002176695_0173	17	7578506	7578525	7578646	7578667	GTAAGCACCTCCTGCAACCCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCAGGTCTTGGCCAGTTGG
TP53/NM_002176695_0176	17	7579275	7579292	7579403	7579426	GATGACAGGGGCCAGGAGGGGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGTCTCATGGAAGCCA
TP53/NM_002176695_0175	17	7579442	7579460	7579309	7579331	CCAAGTCTGTGACTTGCACGGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCAGCAGCTCCTACACC
TP53/NM_002176695_0174	17	7579554	7579571	7579410	7579433	CTGCACCAGCCCCCCTCCTGGCCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAATGGATGATTTGATC
TP53/NM_002176695_0177	17	7579620	7579640	7579489	7579509	CCAGATGAAGCTCCCAGAATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGGGGCTGAGGACCTGGTC
TP53/NM_001126114_0178	17	7579808	7579826	7579675	7579697	AAGGACAAGGGTTGGGCTGGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTGGAAGGGCAGGCCCAC
TP53/NM_001126114_0179	17	7579802	7579821	7579932	7579953	GTCTGGCTGCTGCAAGAGGAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGTGGTGGGCCTGCCCTT
CEBPA/NM_004364_0208	19	33792312	33792329	33792173	33792196	AGGGAGTGGTTTGGGGTCGCCGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGCCGCGAACTGGACA
CEBPA/NM_004364_0212	19	33792260	33792279	33792400	33792421	GTTGCGCTGCTTGGCCTTGTCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCCTTGACCAAGGAGCT
IDH1_p.R132S_0218	2	209113083	209113102	209113213	209113234	GGTGCCATTTGGTGATTTCCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGCTTACTTGATCCCCA
DNMT3A_p.R882_0214	2	25457304	25457321	25457170	25457193	CCGCCACCTCTTCGCTCCGCTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCACCCTGCCCTCTCTGC
ALK_p.G1269_0215	2	29432723	29432740	29432589	29432612	CCACCTCAGCCCTCAAGAATGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTGCTGCCAGAAACTGC
ALK_p.F1174_0216	2	29443573	29443590	29443701	29443724	GCTGCAGAGCAGAGAGGGAGTGTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCGAGGGCGGGTCTCT
ALK_p.T1151_0217	2	29445171	29445190	29445301	29445322	GGAGGAGGAGGCTGTGAGCTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGGGAGTTGGGGTGAGGG
RUNX1/NM_001001890_0222	21	36164865	36164884	36164733	36164754	CCACGCGCTACCACACTACCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNNAGCGACCCGCGCCAGTTCCC
RUNX1/NM_001001890_0224	21	36164799	36164816	36164655	36164678	CTCGCCCTCCTACCACCTGTACTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCTACTCCCCGACGCC
RUNX1/NM_001001890_0225	21	36164799	36164816	36164932	36164955	GCGGAAGTGAGTAGGAGGTTGCGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGTCGGGGAGTAGGTG
RUNX1/NM_001001890_0226	21	36171703	36171720	36171559	36171582	ACACATTCTTTGCAGCTGAGCTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCAGTCCTACCAATACC
RUNX1/NM_001001890_0227	21	36171661	36171678	36171794	36171817	GTGGGGTGGGATTTAAAAAATGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGCGTTGCTGGGTGCA
RUNX1/NM_001122607_0228	21	36194050	36194069	36193918	36193939	CCCTCTCCCCAGCCAGGATAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGAATGCATTCGCGGCTCT
RUNX1/NM_001001890_0229	21	36206781	36206801	36206650	36206670	GCACCTGGGCCACCACCCACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTCAGCCCACACCACCCAGC
RUNX1/NM_001001890_0230	21	36206762	36206779	36206890	36206913	GCCGATGTCCTATTGTGGGGAGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACGAGGGTTGGGCGTGGG
RUNX1/NM_001001890_0232	21	36231861	36231879	36231728	36231750	CTGGTACACCCTCCAGGCTGGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAGGGAAAAGCTTCACTC
RUNX1/NM_001001890_0233	21	36231953	36231972	36231821	36231842	CAAACCCACCGCAAGTCGCCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAAGGGCTGGACAGCATAA
RUNX1/NM_001001890_0234	21	36252937	36252955	36252804	36252826	AAACACGTTTCATGGCAACAAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGATGAAAACTACTCGGC
RUNX1/NM_001001890_0235	21	36252901	36252919	36253035	36253057	GCAGACATCAGGGATGTTATACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTTCTTCATGGCTGCGG
RUNX1/NM_001001890_0238	21	36259103	36259121	36259237	36259259	TGGTCGGCCAGCACCTCCACCATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCGCCTGTCCTCCCACCA
RUNX1/NM_001001890_0237	21	36259278	36259298	36259147	36259167	CAACAAGACCCTGCCCATCGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGCCCTGGCCGGCAAGCTG
RUNX1/NM_001001890_0236	21	36259398	36259416	36259255	36259277	AGGAGCGGCGACCGCAGCATGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTGTGATGCGTATCCCC
RUNX1/NM_001001890_0239	21	36259517	36259534	36259373	36259396	TAGATGCCAGCACGAGCCGCCGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGCAGTAATAAAGGCCC
RUNX1/NM_001754_0241	21	36421217	36421234	36421083	36421106	TTGCTCAGCTTTGCCTGTAATGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGCCTTCAGAAGAGGG
U2AF1_p156_159_0242	21	44514873	44514892	44514741	44514762	GAGTGAGGAGTGGCCAGTGACGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGTGAGGAAGATGCGGAAAA
U2AF1_p34_0243	21	44524402	44524420	44524531	44524553	GCTGATTATTTTGCTGGGAAGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACATGAAAAAAGGCAAAC
RAF1_KMH2_HAEMATOPOIETIC_AND	3	12650282	12650300	12650411	12650433	CGTCTTCCGAGCCTACAACAAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTCCAGTCCACACACATA
PIK3CA_p.C420R_0245	3	178928019	178928038	178927887	178927908	CCCCAAAAGGAAAATTCAACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGATACTAGAGTGTCTGT
PIK3CA_p.Q546_0246	3	178936001	178936018	178936129	178936152	GCTAAAATGGAGATTCTCTGTTTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACAGACTAGCTAGAGAC
PIK3CA_p.N1044S_0247	3	178952182	178952200	178952049	178952071	TTGTTTCATGAAATACTCCAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGCAGTGTGGAATCCAG
TET2/NM_001127208_0258	4	106155065	106155084	106155200	106155221	TCCAGAATGGAAGCCCACTGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGCAGCCTTGTGGATGGC
TET2/NM_001127208_0259	4	106155305	106155322	106155161	106155184	GTTCTGTCTGGCAAATGGGAGGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCACACGACTATTCTGGC
TET2/NM_001127208_0260	4	106155258	106155275	106155391	106155414	GTTAGTGAACCTTCTCTCTCTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGCACTCTTTCAAAAG
TET2/NM_001127208_0261	4	106155346	106155363	106155474	106155497	CGGGGTAAGCCAAGAAAGAAATCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGGTATTCCAAGTGT
TET2/NM_001127208_0263	4	106155637	106155654	106155503	106155526	CGGAGACATTTGGTTGACTGCTTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCTCATTCAGAATCTG
TET2/NM_001127208_0264	4	106155599	106155616	106155727	106155750	GGTGCTACAGTTTCTGCCTCTTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAACACATAACTGCAGTG

TET2/NM_001127208_0265	4	106155677	106155697	106155808	106155828	TGTGTTTCCATTGCGGTGCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGACAAGAACATTGTATTAC
TET2/NM_001127208_0266	4	106155761	106155778	106155894	106155917	TCACCCATCGCATACCTCAGGGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACATGGTGAACTCCTGG
TET2/NM_001127208_0267	4	106155847	106155866	106155982	106156003	GCCTGTGATGCTGATGATGCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGCCATTAACAGTCAGGC
TET2/NM_001127208_0268	4	106156094	106156112	106155956	106155978	ACTCACCACTGCAGCTGGCTTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCTGCAGGAGATGGGC
TET2/NM_001127208_0270	4	106156278	106156297	106156136	106156157	CAGAATTCTTCACCAGACGCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGGTGGTGTGGTAGTGGCA
TET2/NM_001127208_0271	4	106156394	106156412	106156251	106156273	AGGAATCCTTAGTGAACACTGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGTAGTGGTGGTGTTCTT
TET2/NM_001127208_0272	4	106156474	106156492	106156341	106156363	CTTCTGAAGGAAGCTGAGGAACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATTAGGACTCTGGGAAGG
TET2/NM_001127208_0273	4	106156572	106156589	106156433	106156456	CCTCTATTTTCACTTCCCTTAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTCATTGTCCCTGCAGTC
TET2/NM_001127208_0274	4	106156529	106156546	106156657	106156680	GGTAGCAGTGGAGAGCTACAGGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGAAAGGCCTCAGAATA
TET2/NM_001127208_0275	4	106156617	106156636	106156752	106156773	TCTTGTGCCCCCAACACAGCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCAATGTCAGAACACCTCA
TET2/NM_001127208_0276	4	106156716	106156734	106156845	106156867	TGAGGCATCACTGCCATCAATTCNNNNCTTCAGCTTCCCGACGGTAGTGTNNNNGATTCTGAAGGGTCGAGAC
TET2/NM_001127208_0277	4	106156942	106156961	106156810	106156831	GGGATTCCGCTGGTGAAAACGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGTAAGCTTGCCTTGGAG
TET2/NM_001127208_0278	4	106157051	106157068	106156917	106156940	CCCCCAGGCATGTTGGAATTTCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGGTTTTGGAACTGGA
TET2/NM_001127208_0279	4	106157149	106157167	106157016	106157038	CTGTACCTTGGGACTGCCCTTGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAATCTGCTCTTTGTTG
TET2/NM_001127208_0280	4	106157116	106157133	106157244	106157267	CTCACACCTTTTGCAACATAAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGCAGTCACTGTGTGGC
TET2/NM_001127208_0281	4	106157222	106157240	106157361	106157383	GGAAATACTCCGAGACTTTTCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAGACTGAGCCATTTTC
TET2/NM_001127208_0282	4	106157446	106157463	106157307	106157330	TGTTGCTGGTTTTGAGGGAGATGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCACCATGAAAACATTC
TET2/NM_001127208_0283	4	106157547	106157566	106157415	106157436	AGTCTGGCCAAAGAATGATCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTCTGACTATAAGGGGAA
TET2/NM_001127208_0284	4	106157505	106157524	106157635	106157656	GAACAGACTACACATCCTGAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAAATGGGACTGGAGGAAG
TET2/NM_001127208_0285	4	106157741	106157758	106157597	106157620	CTAGGTGTGTATTTGTTGAACAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGTTCTTGAAAGCACC
TET2/NM_001127208_0286_SNP_a	4	106157703	106157720	106157836	106157859	CAACTTGCTCAGCAAAGGTACTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCAAATAATGTGATCCC
TET2/NM_001127208_0287	4	106157944	106157961	106157810	106157833	CAGCTTGTTGACCAGACATATCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACCTTAGAGCAGCATG
TET2/NM_001127208_0288	4	106157924	106157941	106158052	106158075	CCTGGATGCAAGCCACATGCCTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGAAGGACACTCAAA
TET2/NM_001127208_0289	4	106158170	106158187	106158026	106158049	CCACCTTAATTGGCCTGTGCATCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCCATGGTCTCAATGA
TET2/NM_001127208_0290	4	106158271	106158288	106158137	106158160	GCTGCACATTATCACAGCTTGCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGACTGGCCCTGACAT
TET2/NM_001127208_0291	4	106158357	106158376	106158220	106158241	GAGTAAGAGCCTTATGGTCAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGTGTCTTTCTGAAGAA
TET2/NM_001127208_0292	4	106158322	106158342	106158458	106158478	TGGATACACCTGTCAAGACTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATAGCCACACCCCAGCTTTA
TET2/NM_001127208_0294	4	106158517	106158535	106158656	106158678	GTCAAGTTACCGATGCTTGTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAATGTACTGAGACAC
TET2/NM_001127208_0296	4	106164089	106164106	106163955	106163978	CACAGAAACACACACACATACAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTTTATCAAGTCACAC
TET2/NM_001127208_0297	4	106164825	106164844	106164688	106164709	CCATCCCAAACACCCCCACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCGGGATTCCTTCCCACACC
TET2/NM_001127208_0298	4	106164795	106164813	106164934	106164956	GAGTAAGTGAAGCCCAGGGCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGAGGCTGCAGTGATTGTG
TET2/NM_001127208_0299	4	106164914	106164933	106165054	106165075	GCCTGTTTGGCAGTCATGCGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCGGTGTCCTTGAATGAA
TET2/NM_001127208_0300_SNP_a	4	106180873	106180890	106180729	106180752	CATTGCTATGGATAGCATTATATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGGATCTTGCTTCTGGC
TET2/NM_001127208_0301	4	106180803	106180820	106180931	106180954	GTTTACTTCCTGATGTATAATCGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCAGAAACCTGTGGTGC
TET2/NM_001127208_0303	4	106182898	106182915	106183026	106183049	GCAGCAATTGTAACAACTTACTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTATTCACTTTATACAG
TET2/NM_001127208_0302	4	106183045	106183062	106182911	106182934	GAGACTCCAGTTTCTCTTCCTGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTCATTAGTAACAAGT
TET2/NM_001127208_0304	4	106190863	106190883	106190732	106190752	TGTGTGTGAATGCGAAAGTAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTGTGCAAGTCTCTGTGGGC
TET2/NM_001127208_0305	4	106190924	106190941	106190785	106190808	CAGACCCAGACGGCACTCTGGTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTCAACAGCTGCTAAGC
TET2/NM_001127208_0306	4	106193679	106193698	106193814	106193835	GTGGATGAGTTTGGGAGTGTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGACCTGTAGTTGAGGCTG
TET2/NM_001127208_0307	4	106193769	106193787	106193898	106193920	GTCAGGATGTTAGCAGAGCCAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGATGAGCAGCTTCACG
TET2/NM_001127208_0308	4	106193873	106193893	106194014	106194034	AAAGTCAGCCCCATCACGTACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTACTGAGTTCTTTTCGGCG
TET2/NM_001127208_0309	4	106193964	106193981	106194092	106194115	GCATTTGTAGATAAATGTGTTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGAAAAGCTTTCCTCC
TET2/NM_001127208_0311	4	106196312	106196329	106196168	106196191	AAGAGAGAACAGAAACAGGTATCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCTGAGGGTGATGTGG
TET2/NM_001127208_0310	4	106196384	106196401	106196250	106196273	GTGGCTGCTTCTGTAGAGGCTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGACTAACTGGATTGGG
TET2/NM_001127208_0312	4	106196466	106196485	106196334	106196355	GAAGCAGAATAAGAGTTGACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCTGCAGCTTGAGATGAGG
TET2/NM_001127208_0313	4	106196442	106196459	106196575	106196598	CCTATCAGTGGACAACTGCTCCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGCCCTATGAACTTCT
TET2/NM_001127208_0315_SNP_a	4	106196770	106196790	106196629	106196649	TACCTATACAGATCCATCGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCTGAAACCATCTCCCTGC
TET2/NM_001127208_0316	4	106196851	106196868	106196717	106196740	AGATGTAAAACTCTGGCTATTTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGAAGTGGCCATCCATC
TET2/NM_001127208_0317_SNP_a	4	106196816	106196833	106196954	106196977	ATCCATAACTACAGTGCAGCTCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGTAGGGAAATTGCCT
TET2/NM_001127208_0318	4	106196930	106196950	106197066	106197086	TGCTTCCAGCTCTTAACCATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAACATCATTCACCTTCTCAC
TET2/NM_001127208_0319	4	106197164	106197183	106197032	106197053	CATTAGCTGTGTGGGAAAGCATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGAAGCCACACCCTGGAC
TET2/NM_001127208_0320	4	106197254	106197271	106197120	106197143	CCTGACCATTAGCATCACTTAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGAGTTGGAGCCACGGC
TET2/NM_001127208_0321	4	106197343	106197363	106197212	106197232	CAGAAAGCTCTGCTCGCTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAGATCCTGGTGGGGTGA
TET2/NM_001127208_0322	4	106197440	106197457	106197306	106197329	TCTTAAAGGGGTTGTGGCATGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCCTCTTTCTCACGGGC
TET2/NM_001127208_0323	4	106197544	106197564	106197403	106197423	GCTTCCCAAAGAGCCAAGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGCAGGTAAGTGGGCTCTGAA
TET2/NM_001127208_0324	4	106197504	106197524	106197635	106197655	GCCTTCACTCGGGTCACAGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAAAAAAGTGAAACGGGAGC
TET2/NM_001127208_0325	4	106197613	106197633	106197754	106197774	GCAGTGGGGAAAGGTCACAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACAGTAACTACATCTCCATA
KIT_p.D52N_0248	4	55561869	55561886	55561735	55561758	CGCGGACTATTAAGTCTGATTTTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGTTGGTGGCTTCTGC
KIT_p.Y503_F504insAY_0249	4	55592243	55592260	55592109	55592132	TGTGCTTGAATGCACTAGAATCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAGCCTAAACATCCCC
KIT_p.M541L_0250	4	55593436	55593454	55593565	55593587	TCCCTTTCTCCCCACAGAAACCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGTAGCTGGCATGATGTGC
KIT_p.P585P_0251	4	55593688	55593705	55593554	55593577	GGGGAGAAAGGGAAAAATAGATCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGCTCAGCCTGTTTCTGG
KIT_p.P585P_0252	4	55593731	55593749	55593598	55593620	CTCCTCAACAACCTTCCACTGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCCAAAAAGGTGACATGG
KIT_p.V654A_0253	4	55594134	55594153	55594264	55594285	TACTTGGAGCCTGCACCATTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCAGTTGTGCTTTTTGCT
KIT_p.T670I_0254	4	55595494	55595511	55595622	55595645	GAATCTTCTGCATTCAAAGGAGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTTTAGGGCCCACCCTG
KIT_p.S715del_0255	4	55597417	55597437	55597548	55597568	CCCAACCAAGGCCGACAAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGTAGAGCATGACCCATG
KIT_p.V825A_0256	4	55599246	55599265	55599376	55599397	GCTTGACAGTCCTGCAAAGGATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGACTTGGCAGCCAGAAAT
KIT_p.E839K_0257	4	55602732	55602750	55602599	55602621	GCTCAACAAAATTGAACAGAAGAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATCCCATAGGACCAGACG
ROS1_p.K2003_0326	6	117638453	117638470	117638319	117638342	CCTTCTTACTTATTTGCGTAAAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCATATCATCCAGCCTGT
ROS1_p.1982_0327	6	117639339	117639356	117639467	117639490	GCTCAGTGGGTTAATGGAGATTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCAGAGCTACCTCATC
ROS1_p.1951_0328	6	117641082	117641102	117641213	117641233	TTGTCTCCCCACCCTCCACATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTCCTTCATACACTTCTCC
BRAF_p.V600E_0330	7	140453229	140453248	140453097	140453118	GGTCCCATCAGTTTGAACAGTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGCTCTGATAGGAAAATG
BRAF_p.G469A_0331	7	140481473	140481491	140481340	140481362	GTGGTGACATTGTGACAAGTCATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAACACTTGGTAGACGGGAC
EZH2/NM_004456_0332	7	148504833	148504850	148504699	148504722	CCCCCCTCCTCTGAAACAGCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACATGTTGGATGGGTGG
EZH2/NM_004456_0333	7	148506122	148506139	148506250	148506273	GCAAAGAGACACACTGGTGTCAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAGCCCTTAGAGATCA
EZH2/NM_004456_0334	7	148506501	148506518	148506367	148506390	TGACGTGAGAATTGGAACTCCCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTATTCACTGGGCTGTGC
EZH2/NM_004456_0335	7	148507406	148507423	148507534	148507557	CTTTTGGATAAAGGTGATCAAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCCAGCTCTGAAACATA
EZH2/NM_004456_0336_SNP_a	7	148508697	148508714	148508825	148508848	ACACAATCACATCATCAAAAAAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAGGTTATCAGTGCTTT
EZH2/NM_004456_0337	7	148511137	148511154	148511003	148511026	GATTGTTTGTAGTTAGCTATTTAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAGTGTGACCCTGACC
EZH2/NM_004456_0338	7	148511107	148511126	148511237	148511258	GAGAGGTTTGGAGGTTCTTCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGGTCAGCGGCTCCACAA
EZH2/NM_004456_0339	7	148512111	148512128	148511977	148512000	TATTTGTTGCTTTGATGCAATTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCCTCTAACCATGTTT
EZH2/NM_004456_0340	7	148512213	148512231	148512080	148512102	CAACCCTGTGATCATCACGGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACTCCACAGGTAGTAGGG
EZH2/NM_004456_0341	7	148512572	148512589	148512700	148512723	GCTGCTTAACTGGATCTATCTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATGAGAGGAATGGAAAG
EZH2/NM_004456_0342	7	148513757	148513775	148513886	148513908	GTCACAGAGCCATGAGGACAGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTTCATGACAGACTCAC
EZH2/NM_004456_0344	7	148514368	148514386	148514502	148514524	GCACTGGTCAAGAAATGATTGGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAAGTGCCAATGAGGACT
EZH2/NM_004456_0345_SNP_a	7	148515070	148515087	148514926	148514949	TGGGTTTTACTGTTCTGTGAAAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATTAATGTGCTGGAATC
EZH2/NM_004456_0346	7	148515019	148515039	148515155	148515175	GTGGGGTCTTTATCCGCTCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCTCCCCCGTTTCAGTC
EZH2/NM_004456_0347	7	148515086	148515105	148515226	148515247	GTCAACATCAGGGCAAAGTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGTGGGGGTGCTGGGCCTG
EZH2/NM_004456_0348	7	148516654	148516671	148516782	148516805	GCAAAATAAATGAAACAAAGAATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTACCCTCTGCAATAATT
EZH2/NM_001203248_0350	7	148523750	148523768	148523612	148523634	GAGAGAGCAAAGCTTACACTCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATTTTGTTTCATGTTTAC
EZH2/NM_004456_0352	7	148524208	148524226	148524337	148524359	CGAGGTGGGCGGCTTTCTTTATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTACATACCATACAGGGC
EZH2/NM_004456_0351	7	148524409	148524428	148524277	148524298	CAATGTTTCCAGATAAGGGCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAGAGAAAATGAAAGATCA
EZH2/NM_004456_0353	7	148525921	148525938	148525787	148525810	CTGTGTAGCCATTACAGCTTTCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTGGTGAATGCCCTTGG
EZH2/NM_004456_0354	7	148525980	148525997	148525846	148525869	AGAAGAAAAGCAGAAGATCTGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTCTGACATTTGATGC
EZH2/NM_004456_0355	7	148526925	148526943	148526792	148526814	CCATATGCTCTTCTCTTGGAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAGGTGAAGATGAACATG
EZH2/NM_004456_0356	7	148527017	148527034	148526883	148526906	ATATGGGAGATGAAGTTTAGATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGACATGTACACATGAAA
EZH2/NM_004456_0358	7	148529923	148529940	148529789	148529812	ACACAAGTCATCCCATTAAAGACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAAATATTTGGGTAGGCA
EZH2/NM_001203248_0360	7	148543709	148543726	148543575	148543598	CCTGACTTCTGTGAGCTCATTGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTCTCCTTTCCTCTCC
EZH2/NM_004456_0361	7	148544354	148544371	148544220	148544243	TACAATTAAGGATAGGTTTTTTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATCTGAGAAGGGACCAG
EZH2/NM_004456_0362	7	148544306	148544325	148544436	148544457	CCAGCCTGAATATGATCACCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGTCTCAGTCGCATGTAC
EGFR_KMH2_HAEMATOPOIETIC_ANI	7	55273241	55273259	55273108	55273130	GAATGTGCTGTTGACACAGGTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTCAGCTGTGGAGCCC
RAD21/NM_006265_0363	8	117859716	117859735	117859851	117859872	GCGGCAGCTTGTTTTCTGTTCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTAGCTATAATGCTTCTAGC
RAD21/NM_006265_0364	8	117859804	117859821	117859942	117859965	CCAAAAAAGGGTAACTTAATCTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCAATAGCTTGCTGCT
RAD21/NM_006265_0365	8	117861153	117861170	117861281	117861304	GACCCCCAAAAAGCTGACAAAACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCATTTTCCTCTGAGAC
RAD21/NM_006265_0366	8	117862942	117862960	117862804	117862826	TTAGCAAAAACCTCCAACCAGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAAGAACCTCCAAATAT
RAD21/NM_006265_0367	8	117863013	117863030	117862879	117862902	AGAGAAGGAGAAAGAGAAGGAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTCTTATTTGTATTGC
RAD21/NM_006265_0369	8	117864362	117864379	117864228	117864251	CTCCACCACCACCTCAGGGAGTTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAACTGTATGACCTATG
RAD21/NM_006265_0370	8	117864907	117864925	117864764	117864786	TTTGTTCTGTTGGAATAGTTCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGCTTGTACCAGAAGACCT
RAD21/NM_006265_0371	8	117864879	117864896	117865007	117865030	CCACTGATTTCTATCTTCCAAAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCTCTCCTCCTTTCCT
RAD21/NM_006265_0372	8	117866437	117866456	117866567	117866588	ATTTCTTGGTGGGCGGTGCCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGATGCTCAAAATGTATATG
RAD21/NM_006265_0373	8	117866675	117866694	117866538	117866559	GTGGAAAGAGACAGGAGGAGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCAAGAGGAAGAGGAAGC
RAD21/NM_006265_0374	8	117866759	117866778	117866622	117866643	CAAGACAATTAGAGCCCAACTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCAGATCTTGTAGCTGTGTG
RAD21/NM_006265_0375	8	117868358	117868378	117868489	117868509	CAACGGGATCCACTGAATCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACCTTATGTTGTATGCTGT
RAD21/NM_006265_0376	8	117868586	117868605	117868454	117868475	CATGACTGATCAAACAACACTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTCCTCCCCATTTGTGGG
RAD21/NM_006265_0378	8	117868923	117868942	117869053	117869074	TGCCAAACCACAACAGCCAATCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTGCTCTGGCAACATCAC
RAD21/NM_006265_0379	8	117869605	117869622	117869471	117869494	TGATGGTTATTCCAGCATAAACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCTATTAGAGTCTGAAC
RAD21/NM_006265_0381	8	117869620	117869637	117869758	117869781	GCACTGTGATAAAAGAAAACTGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGGTTAGAAGTAGTAG
RAD21/NM_006265_0383	8	117870540	117870560	117870671	117870691	CTGAACTGCTGGGCCACATCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAACACAATATAACATTATAA
RAD21/NM_006265_0382	8	117870749	117870766	117870615	117870638	TGAGAGAAGAAGTTGGGAACATCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGAAATTGGGATTTGT
RAD21/NM_006265_0386	8	117875325	117875344	117875455	117875476	ACTCCCAGTAAGAGATGTCCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAAGTAAACAACAACAACA
RAD21/NM_006265_0388	8	117878841	117878859	117878970	117878992	GTTCTGGCTGGCTATGAAAACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCCACGCTGCTCTCTA
MYC_RAJI_HAEMATOPOIETIC_AND_I	8	128750634	128750652	128750501	128750523	AACGTTGAGGGGCATCGTCGCGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCCTCGCTGGGCGCCGGG
ABL1_p.255_0415_SNP_a	9	133738423	133738441	133738290	133738312	CCATCTCCCACTTGTCGTAGTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGGCAGTCCCAGCCTAC
ABL1_p.299_0416	9	133747467	133747485	133747596	133747618	CCTTGGTGAGTAAGCCCGGGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAAGCACTTCCTGAAAT
ABL1_p.317_0417	9	133748348	133748368	133748217	133748237	AGACAACGAGGACTTCAACACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGTACAGCAGCACCACGGC
ABL1_p.359_0418	9	133748337	133748355	133748466	133748488	GCGTGGAGCCGGGCAGCCTTTTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAGGTGAACGCCGTGGT
ABL1_p.S417Y_0419	9	133750391	133750411	133750260	133750280	CCAGGCAGTTTCGGGCAGCAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTTGTAGGCCAGGCTCTCGGG

ABL1_p.S417Y_0420		9	133750432	133750450	133750299	133750321	CAGGCCAAAATCAGCTACCTTCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAGCCCTTACCCCAGACG
ABL1_p.E459K_0421		9	133753791	133753808	133753919	133753942	GCTGCCCAGAGAAGGTCTATGAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCTTTCAGCATTTGG
ABL1_p.F486S_0422		9	133755576	133755593	133755442	133755465	CCACTGCCAACCTGGACAGATGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCTGCCCTTTCACCC
JAK2_L1236_HAEMATOPOIETIC_AND_		9	5078351	5078368	5078217	5078240	CAAGCCCCCAAAACAGATTTAAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTCTTCTCTGATAAGCAG
HNRNPK/NM_031263_0392		9	86584378	86584396	86584245	86584267	TAAGACTAGTGAAGAACTGAAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAAAATTCTAATTCGCAC
HNRNPK/NM_031263_0393		9	86584246	86584264	86584375	86584397	AAAGTGCGAATTAGAATTTTTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCAGTTCTTCACTAGTC
HNRNPK/NM_031262_0394		9	86585182	86585199	86585043	86585066	GTTTAGCTTTGTGTTAGCTTATACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGTCATGAGTCGGGAGC
HNRNPK/NM_031262_0395		9	86585161	86585180	86585296	86585317	ACTACCTGTATTTTCAAGGAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTCATCAATTTTGATCGA
HNRNPK/NM_031262_0396		9	86585749	86585766	86585615	86585638	ATACTACCAGGAACATTTTATCACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTAAATGAACTTACTGCTC
HNRNPK/NM_031262_0397		9	86585735	86585755	86585866	86585886	GTTGTAATTACTACCGGTACTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGATTTAAATAATGAGCAGT
HNRNPK/NM_031262_0399		9	86586165	86586182	86586293	86586316	ACATGAACCCGCATTGTATTTTGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACGAACAACTATGATAC
HNRNPK/NM_031262_0398		9	86586367	86586387	86586236	86586256	GATGAAACTGGGACTCTGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTGCCTATATATGTACCCTC
HNRNPK/NM_031262_0400		9	86586558	86586576	86586687	86586709	CACATATCAAATCAAAGTCTACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACACACTGGTAAATAAACCA
HNRNPK/NM_031262_0401		9	86586893	86586910	86586759	86586782	TTGTTGTTGATGGTTTTTTCTTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGATGATGAGCCCTCG
HNRNPK/NM_031262_0402		9	86586997	86587015	86586864	86586886	ACCACCTCCCCCTCCTCCCGGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCGTCGCGGACGCCCAGTG
HNRNPK/NM_031262_0403		9	86586952	86586969	86587080	86587103	GCTGTGCACGTCCTTTGATGGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGAGGCATTCTGTCAAA
HNRNPK/NM_031262_0404		9	86587006	86587025	86587146	86587167	GAGTCCTGCTTCATACCAATCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCGCGACGGTCATCAAACA
HNRNPK/NM_031262_0405		9	86587738	86587755	86587866	86587889	GCTTGATGGTGGTTTGAGTGTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAAAAAGTGTTCTGAAG
HNRNPK/NM_031262_0406		9	86587981	86588001	86587845	86587865	TTTTCCAGGAATGCTGTCCTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGTTTTTATATTGTGGGGG
HNRNPK/NM_031262_0407		9	86588169	86588187	86588298	86588320	CCTTTATAGTTGGTAGTCTGTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAAAGAATACGGCAGAATT
HNRNPK/NM_031262_0408		9	86588228	86588248	86588359	86588379	CCCCAATACACACTTATCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTGACCCCAATAATTCCTCC
HNRNPK/NM_031262_0409		9	86588915	86588932	86588781	86588804	GCCATTGAACCCCACTGAAGTATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACGCTAGACACTTAACC
HNRNPK/NM_031262_0410		9	86589505	86589522	86589371	86589394	AGGGGGGAATGTTTAAAGTATGTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATTTGTGGTGTTTGACAG
HNRNPK/NM_031262_0411		9	86590308	86590325	86590436	86590459	GCGTTCGTGGATGTTGGCATTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGGCAGGTAATAAAAT
HNRNPK/NM_031262_0412		9	86591999	86592018	86591867	86591888	TACTACACGAGCAGCTTCAGTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATTAATTTTAGGGAAAGGC
NPM1_ins		5	170837526	170837541	170837630	170837657	GATATCTGGCTGTCCTTTTTATAATGCANNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGNNNNNTTCCAGGCTATTCAAGA
STAG2/NM_006603_0476	X		123156444	123156463	123156574	123156595	GGGGAATGCATTAACTTCAGTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGACATTGAGGTGTTCCAG
STAG2/NM_006603_0477	X		123159800	123159817	123159666	123159689	CTGTGACAGAAAGATAAGAATTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGTGTGAGATCTTAGGA
STAG2/NM_006603_0478	X		123164763	123164780	123164901	123164924	GGTCATCACCAACAGAATGGAGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTCAAGGATAGTGATA
STAG2/NM_006603_0479	X		123164980	123164997	123164846	123164869	CCTCCTCCATTTCCACCTTTGCCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGAAGAACAACATAAATC
STAG2/NM_006603_0480	X		123171487	123171506	123171355	123171376	CTACAGCAGAGGGAAAAAAATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGAGCTGCTGATTTCAAAAT
STAG2/NM_006603_0481	X		123176475	123176492	123176341	123176364	AACTTCCAAGTAAGTCTCTAACACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCGAATTCTTCAGTCAT
STAG2/NM_006603_0482	X		123176571	123176588	123176437	123176460	CAGAGTTCTGCATATGTCTAAACANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCAGCCTAATGCTTAC
STAG2/NM_006603_0484	X		123179208	123179228	123179072	123179092	CGCCAATGAATTCACAAAAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAATACCGACCTGCCAGGGTG
STAG2/NM_006603_0485	X		123179328	123179346	123179185	123179207	CTTGTATGTCGAAATGCTCTGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGTCCTCTTAGTGGTCAC
STAG2/NM_006603_0488	X		123182929	123182948	123182797	123182818	GGAAGACAACCAAATGAACACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAAAAACTGTCACAACTTAC
STAG2/NM_006603_0489	X		123184136	123184153	123184002	123184025	GAAGGAAAAACGATGCATAATTAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGCATAGTCCAACCAAC
STAG2/NM_006603_0490	X		123184199	123184217	123184066	123184088	TCCAAATGCCAATCTCTTCAATGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGGTGCAGACAGCCACGC
STAG2/NM_006603_0491	X		123185057	123185076	123184925	123184946	GAGACAATGCATTAAAACTCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTACTAACCTTGAACCGACTG
STAG2/NM_006603_0492	X		123185157	123185175	123185024	123185046	CCAGTTTGGAATTAAGCTCTTTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACAATTCTATCCTAAGGAC
STAG2/NM_006603_0495	X		123189929	123189949	123190060	123190080	GCAGCTGGAGAATTTCTCTACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTAGAATTAGGACGTTACTA
STAG2/NM_006603_0496_SNP_a	X		123191797	123191814	123191663	123191686	GACAACAACAACAAAAAATTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGAAAAAAACCAATGTC
STAG2/NM_006603_0497	X		123191730	123191747	123191858	123191881	GTTCGAAAAATTTTGGAAAAGGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGATCCAGAGGAGGATG
STAG2/NM_006603_0499	X		123195172	123195192	123195041	123195061	AAGAGCAATGTGGTCTTAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTCCTCTCCACTAAGTGGC
STAG2/NM_006603_0498	X		123195224	123195242	123195091	123195113	CCCACATGCTATCCACAAGGTATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTACTTACAAAACTGTC
STAG2/NM_006603_0501	X		123195576	123195593	123195704	123195727	GGAAGAGGGACAGGAAAAAGGGTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGCTAACTCTTTCTGAC
STAG2/NM_006603_0500	X		123195758	123195775	123195624	123195647	GAGCACTCTCTTGCCTATCTGTTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAAAAGGAGAAATGGAG
STAG2/NM_006603_0502	X		123196882	123196899	123196748	123196771	TTCTCCTTTGCTGTAAGCACCTAANNNNCTTCAGCTTCCCGATACGGTAGTGTNNNNTTAGGGAAAAAAACTC
STAG2/NM_006603_0504	X		123197101	123197119	123196968	123196990	TCACCTTTTCTGCATCTACAGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACGCTATGATATAATGAAC
STAG2/NM_006603_0506	X		123197660	123197677	123197788	123197811	GCACTCTGTAATGAAGAGTTCACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGCCTTAGTTTTGATGA
STAG2/NM_006603_0507	X		123197740	123197758	123197874	123197896	CCGGCTTCTTGAAGATTTTCTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGCACACAGATACAGATG
STAG2/NM_006603_0508	X		123197931	123197950	123197789	123197810	GTGAACTCTTCATTACAGAGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTAGAGGGGCTCAACTGAC
STAG2/NM_006603_0509	X		123199741	123199758	123199607	123199630	CAAAACCACAAATGAACTTGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGATATGCATCATTTCTC
STAG2/NM_006603_0510	X		123199717	123199737	123199848	123199868	GCATGTTTGTGGGTATGTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATTTATAGGGTGAAGAACCT
STAG2/NM_006603_0513	X		123200158	123200176	123200287	123200309	GTTTGTGGTGGTTCAGTAGTGTTNNNNCTTCAGCTTCCCGATACGGTAGTGTNNNNGTCTTGTGACTTTTAAATT
STAG2/NM_006603_0514	X		123202357	123202374	123202485	123202508	GAATACTACTGTTAAGGAACAGGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAATGCTGAATTGTTTA
STAG2/NM_006603_0515	X		123202541	123202558	123202407	123202430	AAACGCAGCAAGTCCTCCTTGAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATTTATAAAGGTTGCT
STAG2/NM_006603_0517	X		123205185	123205203	123205052	123205074	GCTCTAACATGTCACGCCCTCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGATTTAATAAAAAGATGGC
STAG2/NM_006603_0518	X		123210161	123210179	123210290	123210312	CAGCTGCAGATATCTTCAAACAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTTTGGGACTTTTTCTCC
STAG2/NM_006603_0519	X		123210364	123210382	123210226	123210248	GCTGCAAGTAAATTTCTTCTCTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCATGCATAAAAACTAGCG
STAG2/NM_006603_0520	X		123211875	123211892	123211741	123211764	CTACTTGACAATAAGACAAATTTTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATAAGGGTCTTAGCACAC
STAG2/NM_006603_0521	X		123211846	123211863	123211974	123211997	GCAGTTGAAATTGGGCAAAGTGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTAAAACAAGGCAGATA
STAG2/NM_006603_0523	X		123215351	123215368	123215207	123215230	GCTGTTTGGAAAGAAAGAAAGCATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGGCAATGGCTTCTCTTG
STAG2/NM_006603_0524	X		123215305	123215323	123215444	123215466	GCCCTTTCATTTGGAATAACTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTTGCTCGACGTTTTGCTT
STAG2/NM_006603_0525	X		123217318	123217336	123217180	123217202	AGGAAATTCACTCACTACTTCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAATTTAAAGGTGGATGGC
STAG2/NM_006603_0526	X		123217433	123217453	123217297	123217317	TCTCCCCTTGCGGATTAGGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCCTTAAGAATCCCAAAATG
STAG2/NM_006603_0527	X		123220351	123220371	123220487	123220507	GCTAGCTGGTGGTGATGATGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACAGATTTCTGTATCAAAG
STAG2/NM_006603_0528	X		123220579	123220596	123220435	123220458	GCCACACATCCTCTCTTCGGAGTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACTTTCCGTTTTCCTG
STAG2/NM_006603_0529	X		123220540	123220558	123220669	123220691	CTGAATTGTCATTAAGGTTCACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGGTCAACAGTACGGAG
STAG2/NM_006603_0530	X		123224391	123224408	123224529	123224552	GAGCCCAAAAGATTACGGCCTGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTGACTAAACCTCGTCGT
STAG2/NM_006603_0534	X		123227962	123227979	123227828	123227851	CAAAGTCAAGATCTGAACTAATGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTGTCAAAATCCATTCC
STAG2/NM_006603_0535	X		123228065	123228082	123227931	123227954	AGATCCTCAATCCTCCCTTCTGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAAGTATTTCTCTACTC
STAG2/NM_006603_0536	X		123229202	123229219	123229330	123229353	GCAAAATCAGAAGTATAGGCAGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTATTTCCTTTTTCCTTT
STAG2/NM_006603_0537	X		123234397	123234414	123234525	123234548	GAAATTCTGTACAGATTTTTCTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTTTCTCCCCTCTCTCTC
PHF6/NM_032458_0538	X		133511618	133511635	133511751	133511774	AAAACCAGAAGGTGGCAGCGCACCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGTGGCATTCTAAAGGC
PHF6/NM_032458_0539	X		133511663	133511680	133511796	133511819	CGGCAGCAACAGAGACCTTGAAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAACAGAAAAAAGGGCCT
PHF6/NM_032458_0544	X		133527858	133527875	133527986	133528009	CATCATTTAGCCACGTTTCAGCCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTACTGCTCGTTTTCT
PHF6/NM_032458_0545	X		133547481	133547499	133547620	133547642	AAGGGCTGTCAGAAGATACCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGATTGGTCCATAAAAAG
PHF6/NM_032458_0546	X		133547574	133547591	133547702	133547725	CTGTTGGATTCTTACTTTTGTTGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTAAAAGAAAAGTCGC
PHF6/NM_032458_0548	X		133547909	133547926	133548037	133548060	GTTTGTTTTTCTTTGTTTCCCCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGCCATGTAGGGGAGGA
PHF6/NM_032458_0551	X		133548997	133549015	133549136	133549158	CGAGGAAAAAGAATGGTCTGTAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCTATAAGGATTCTGAA
PHF6/NM_032458_0552_SNP_a	X		133551149	133551169	133551280	133551300	GGAGTACAAGACAAAGCTAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCTGTTTTCTTGAAATACGG
PHF6/NM_032458_0555	X		133559250	133559268	133559379	133559401	TGGGATCTGTTGTCAGGATACAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGTGGAAATGATGAGAGAG
SMC1A/NM_006306_0423	X		53406979	53406999	53407110	53407130	GAAGGAGGAGGGAGAAAAAGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGACAGCTTAGGGATCCAGA
SMC1A/NM_006306_0424	X		53407603	53407620	53407469	53407492	CCAGGGCAGGAAAGGAAGGCTGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCAACTTCCAGGCCATCG
SMC1A/NM_006306_0425	X		53407712	53407730	53407579	53407601	CATCTCTCTCAAGGAGGAGTTCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCCTTCTGGTTGTGGCTGG
SMC1A/NM_006306_0426	X		53408011	53408028	53407877	53407900	CAGGTCGGGGTTGGGTTTCAGGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNACCTACTGGTTCCCTCCC
SMC1A/NM_006306_0427	X		53409131	53409151	53409272	53409292	GGGCTCTTCAGGGTTCTCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGCCCTAGGGGATCAGCCTTA
SMC1A/NM_006306_0428	X		53409356	53409373	53409217	53409240	CTCCTGGGAAACGCTTCCGGCCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTAGGCTTCCTGTCCC
SMC1A/NM_006306_0429	X		53409398	53409415	53409526	53409549	GATCTGTTCGAATGCCTGCTTGGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCTGGTTGGGTAAGGGG
SMC1A/NM_006306_0430	X		53409480	53409498	53409614	53409636	GCCCTGGCAAGAAGGACCTGCAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACAGATTCAAAACAAGC
SMC1A/NM_006306_0431	X		53410104	53410124	53409968	53409988	GATGAGGACAAGAGGCTAAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGCTGAATGAGCAGCAGAG
SMC1A/NM_006306_0432	X		53410181	53410200	53410049	53410070	GGCCATGGAAAAGCTGAAAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACATTGCTGGGCCTGGGGC
SMC1A/NM_006306_0433	X		53421807	53421824	53421673	53421696	TGAGGATCAACCACAGGGGTGTGGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCGTTGCCATTGCAGGG
SMC1A/NM_006306_0434	X		53421832	53421849	53421698	53421721	GGTGATCTGTGTGAGGATCTGAAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGGCCAGTCTGCTCCAC
SMC1A/NM_006306_0435	X		53423254	53423271	53423120	53423143	AGTATTGTGGCTGGTGGTGGGAGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGCCATTGAGACCAAGC
SMC1A/NM_006306_0436	X		53423362	53423381	53423230	53423251	GAACAGAAGCGCAGTGACCGTCGTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCAGGCCTGGGGTGGGAGGA
SMC1A/NM_006306_0437	X		53423352	53423371	53423492	53423513	GCTGAGCCATGGTCTCATCTATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTATCTACGTCCTCCCACC
SMC1A/NM_006306_0438	X		53423547	53423564	53423413	53423436	TCATGAGATGGAGGAGATTCGTAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGTCCTGTTCCCACTGC
SMC1A/NM_006306_0439	X		53426468	53426488	53426609	53426629	CCAACTGAATGCCCAAGCGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTCCAGTTATTAGTCTGTC
SMC1A/NM_006306_0440	X		53426678	53426697	53426541	53426562	GTGGGAGCAGACAGTGAAAAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGCTGATGAGATTATGAGTG
SMC1A/NM_006306_0441	X		53430538	53430557	53430406	53430427	GATGCTGTCATAGGCAAGGGTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAACATCCGGGAGTTTGAGG
SMC1A/NM_006306_0442	X		53430647	53430667	53430516	53430536	AGAAAAGGTGAAACGGCAGAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGACTGGGACTGGAAGCAGGA
SMC1A/NM_006306_0443	X		53430801	53430819	53430668	53430690	ATGCCAGCGTGTGTGTCAGGGCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCCAAGCTGGAGAGTGAGC
SMC1A/NM_006306_0444	X		53430880	53430900	53430749	53430769	CAAGAGGATCATTCAGAGCCGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGCCAATGCAGTCAAGGTA
SMC1A/NM_006306_0445	X		53431899	53431916	53432027	53432050	CCTGAGACTGCACCTGACGCAGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGTGGATGGCCTTTGG
SMC1A/NM_006306_0446	X		53432104	53432123	53431962	53431983	AGAACAGACCAAGACACGACATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCACCACCTTACCACCTAGC
SMC1A/NM_006306_0448	X		53432261	53432281	53432130	53432150	GCAGTGGGAGTCCTAAGCCTANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCTCTGGTGGGGCCAGTGAC
SMC1A/NM_006306_0447	X		53432316	53432336	53432185	53432205	AGAAGGAGCGCTTGACAGAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTGCTGTGTGTAGACAGTGGC
SMC1A/NM_006306_0449	X		53432250	53432269	53432385	53432406	TGAGCCTGTCCAGCTCCAGCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTTGGCCTTCAGGTCACTGGC
SMC1A/NM_006306_0450	X		53432532	53432549	53432393	53432416	TCCCTTGCCCAGGCTGGAGCTGGANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATGTGATTCGCTATGAGC
SMC1A/NM_006306_0451	X		53432607	53432624	53432473	53432496	GGCAATGCCCTTGTCTGTGACAACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGACTGAGCTTCTCCCCAC
SMC1A/NM_006306_0452	X		53432684	53432701	53432817	53432840	GCCCAAAACCTTGGTTACAGCAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAATCCCCAACAAGCCTCA
SMC1A/NM_006306_0453	X		53432924	53432944	53432788	53432808	GGATGCCATTATTGTGGACTCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTGAGCCAGCTTCCAAAAGC
SMC1A/NM_006306_0455	X		53435955	53435972	53436088	53436111	GCTGCTCCATCACCTGGTTCAGCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGTAAGTGCTCAGGAAATG
SMC1A/NM_006306_0454	X		53436159	53436176	53436025	53436048	AGCAGCGAAAGGCAGAGATAATGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTAGAGGGGGAGCTGAC
SMC1A/NM_006306_0456	X		53436233	53436250	53436094	53436117	ATAAGGAGCTGAACCAGGTGATGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAGTATTTTCTCACCAGC
SMC1A/NM_006306_0457	X		53436327	53436344	53436455	53436478	CATCAGGGGCTGCACGAGTTTACGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGGGGACAGATGCAGAGC
SMC1A/NM_006306_0458	X		53438805	53438824	53438668	53438689	AGGGATGATGGTCCACAGAAAAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGCCAGCAAGAGAGCAGC
SMC1A/NM_006306_0459	X		53438894	53438913	53438752	53438773	CGAGACCAGAAAGCTGACCAGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNATCCCTGGGCTGACATCTGC
SMC1A/NM_006306_0460	X		53438973	53438992	53438841	53438862	CCCTAACACAGGTGAAGAAATANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGAAGAGAGTCAGAGTCAGGG
SMC1A/NM_006306_0461	X		53439093	53439112	53438951	53438972	CAGAGATTTGACGTTGGAGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGAAGTCTCTGCAGAATGC
SMC1A/NM_006306_0462	X		53439175	53439192	53439041	53439064	GACATGGATGAGCTGGAGAAGGAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCAGAATTGAACCAGAAGC
SMC1A/NM_006306_0463	X		53439136	53439156	53439277	53439297	GGAGAGCTTGAGCCCCTGAGCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTGTGGGAGGTGTTCTCCTTGG
SMC1A/NM_006306_0464	X		53439803	53439820	53439941	53439964	GCTTCTTGTCCTTCTCGATCTCCTNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCGGCCTCTTGGTTTCCCA
SMC1A/NM_006306_0465	X		53440031	53440049	53439893	53439915	GAAGGAGAAGAAGAAGGAGCTGGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGCTCAGGTACAGCTGCAGC

SMC1A/NM_006306_0466	X	53440108	53440127	53439971	53439992	CTCAACAAGGAACTGGCCTCAANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTATCGATGCACCCCTGCCAC
SMC1A/NM_006306_0467	X	53440156	53440175	53440286	53440307	GCTTGTCATACTCCTGCGCCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAGCCAAGAGGTAGCTTGGCC
SMC1A/NM_006306_0468	X	53440265	53440285	53440406	53440426	CTTCCACTTCAGACCCCAGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCCTTCACCATTTCCTTCTTTC
SMC1A/NM_006306_0469	X	53441797	53441814	53441663	53441686	TTGGCTATCTGGTTTTTGCCAGACNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNTCTTCTGAGTACAAGATC
SMC1A/NM_006306_0470	X	53441704	53441721	53441832	53441855	GCATGAGTTGGCAAGGGTCAGGCCNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCACCTGGAAAACGAGGAA
SMC1A/NM_006306_0471	X	53441811	53441828	53441939	53441962	CACGGGCAAAGGTACGGTCCTCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAGAACCTCCTACAAGAC
SMC1A/NM_006306_0472	X	53442056	53442073	53441912	53441935	TTGTAGGTGGGTGAGGCTGGCCAGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNAAACCAGCAACCTGCGGG
SMC1A/NM_006306_0473	X	53441999	53442016	53442132	53442155	GACGAGGCAGTAGAGGGAAAGTCANNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNGGTTGGCAGCTGGCTTGC
SMC1A/NM_006306_0474	X	53449533	53449550	53449399	53449422	CGGCCCTGCGCACGTCCCGGCCTGNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCATGGGGTTCCTGAAACT
SMC1A/NM_006306_0475	X	53449580	53449599	53449448	53449469	CACCGCCATCATTGGACCCAATNNNNCTTCAGCTTCCCGATATCCGACGGTAGTGTNNNNCTCGGGCGTACGGCGCGGCC

Table S3. Quantitation of mutations in cell line dilution experiments

	RAJI			KMH2					OCI-AML3		L1236					
Measured % cell line	MYC:NM_002467 :exon2:c.G62C:p.S 21T & MYC:NM_002467 :exon2:c.G162C	TP53:NM_001126 115:exon3:c.T304 C:p.Y102H	TP53:NM_001126 115:exon2:c.G242 A:p.R81Q	MTOR:NM_00495 8:exon48:c.C6695 T:p.T2232I	EGFR:NM_00522 8:exon28:c.G3471 C:p.W1157C	NOTCH2:NM_001 200001:exon11:c.G 1759A:p.G587S	RAF1:NM_002880 :exon5:c.T436A:p. F146I	KMT2A:NM_0011 97104:exon12:c.A4 546T:p.T1516S	NRAS:NM_00252 4:exon3:c.A182T:p .Q61L	NPM1:NM_19918 5:exon10:c.772_77 3insTCTG	JAK2:NM_004972 :exon16:c.T2025G: p.C675W	ERBB3:NM_0019 82:exon22:c.A2663 G:p.Y888C	CDK4:NM_00007 5:exon2:c.G97C:p. A33P	Average	Standard Deviation	CV
0.0100000	0.001308356	0.005150916	0.006203331	0.01611829	0.017857143	0.010043042	0.011557572	0.007343722	0.010436588	0.002083333	0.020689655	0.010339734	0.007518797	0.00974234	0.00557926	0.57268196
0.0050000	0.000593522	0.002692273	0.003042473	0.007425455	0.006674757	0.004013761	0.004760368	0.003758833	0.005638064	0.003289474	0.005649718	0.003215434	0.003888723	0.0042033	0.00174876	0.41604431
0.0025000	0.000353899	0.001251924	0.001185352	0.002309913	0.005064573	0.002257336	0.002570263	0.002278356	0.00282516	0.001477105	0.003533569	0.000862813	0.00128522	0.00209658	0.00120507	0.57477951
0.0012500	3.70E-05	0.000576181	0.000855237	0.001604033	0.002554931	0.001005892	0.001030822	0.001051156	0.000900231	0.000979192	0.003514938	0.000475285	0.000797978	1.18E-03	0.0008827	0.74596425
0.0006250	3.43E-05	0.000558116	0.000770614	0.000899483	0.000825764	0.000771159	0.000762571	0.000331895	0.000924214	0	0.002150538	0.000367647	0.000874661	7.13E-04	0.00051526	0.72251585

Table S4. Quantitation of mutations in patient specimens

	Mutation (or NPM1NGS result)	Day from initial Diagnosis				
		83	**196**	**329**	**412**	**531**
Patient 1	NPM1NGS variant allele frequency	0.001	0	0.25	0.12	0.49
	NPM1:NM_199185:exon10:c.772_773insTCTG	Not Detected	Not Detected	0.31	0.15	0.55
	NRAS:NM_002524:exon2:c.G35A:p.G12D	0.001	Not Detected	0.25	0.11	0.5
	WT1:NM_000378:exon8:c.G1339A:p.D447N	Not Detected	Not Detected	0.23	0.14	0.72
	SMC1A:NM_006306:exon2:c.T198G:p.H66Q	0.002	0.006	0.53	0.26	0.99

	Mutation (or NPM1NGS result)	Day from initial Diagnosis							
		0	**69**	**125**	**393**	**397**	**461**	**579**	**746**
Patient 2	NPM1NGS variant allele frequency	0.05998	0.00041	0.00122	0.00149	0.00124	Not Detected	Not Detected	0.474
	NPM1:NM_199185:exon10:c.772_773insTCTG	0.058527376	0.000320376	0.001493358	0.001774308	0.001229875	Not Detected	Not Detected	0.614019117
	WT1:NM_001198551:c.134-57C>T	0.428050052	0.027350814	0.030102547	0.026605853	0.007879186	0.001394422	0.001300672	0.915941058
	TP53:NM_001126115:c.-112A>G	0.514041838	0.050551731	0.036071537	0.035118979	0.015493942	0.009309029	0.039795388	0.485174459
	TP53:NM_001126115:c.-107T>C	0.488877095	0.025558804	0.026826311	0.022991148	0.0069315	0.001168497	0.001300503	0.452075576
	TP53:NM_001126118:c.-182T>A	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	0.118644068	0.040236686
	TP53:NM_001126118:c.-185C>A	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	0.056497175	0.040236686
	WT1:NM_001198551.1:c.10+79C>T	0.314771198	0.004808909	0.002511805	0.002229965	0.00241955	0.00175312	0.002473717	0.136546185

	Mutation (or NPM1NGS result)	Day from initial Diagnosis								
		0	**94**	**143**	**269**	**346**	**437**	**542**	**584**	**599**
Patient 3	NPM1NGS variant allele frequency	0.000922	0.000077	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected
	NPM1:NM_199185:exon10:c.772_773insTCTG	0.001369394	0.000347705	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected
	WT1:NM_001198551:c.10+67T>C	0.033406917	0.032224889	0.000995644	Not Detected	0.001707456	0.00067659	0.004513043	0.001269036	Not Detected
	STAG2:NM_006603:exon16:c.T1616G:p.V539G	0.02950905	0.00094697	0.022482014	Not Detected	0.00204499	0.001409443	0.00425448	0.018535286	Not Detected
	RAD21:NM_006265:exon8:c.C839G:p.S280X	0.013621312	0.000200401	0.000421905	Not Detected	0.000470588	0.000386026	0.000531124	0.001582636	0.000842105
	PTPN11:NM_002834:exon4:c.T495A:p.S165S	0.013432836	0.009925558	0.016997167	0.009584665	0.021341463	0.002717391	0.000640369	0.005813953	0.008230453
	KRAS:NM_004985:exon2:c.G34A:p.G12S	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	4.61135E-05	0.00051595
	IDH1:NM_001282386:exon4:c.C394A:p.R132S	Not Detected	Not Detected	Not Detected	Not Detected	0.001100537	0.001453992	0.000937082	0.001924481	0.001413957