SUPPLEMENTARY INFORMATION

RECURRENT MUTATIONS IN THE *U2AF1* SPLICING FACTOR IN MYELODYSPLASTIC SYNDROMES

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SUPPLEMENTARY NOTE

Clinical history of index case (UPN 266395). The patient was a 65 year old male of European ancestry who presented with anemia and thrombocytopenia (white blood cell count 5,900/mcl, hemoglobin 9.6 g/dl, platelet count 53,000/mcl). A bone marrow biopsy and aspirate showed 60% cellularity with trilineage hematopoiesis, without excess blasts or overt dysplasia. His marrow was felt to be abnormal, but not diagnostic of a myelodysplastic or myeloproliferative disorder. Cytogenetics showed a 46, XY karyotype. He was initially treated with recombinant erythropoietin without improvement, and two months later was referred for evaluation with the following blood counts: white blood cell count 40,300/mcl, hemoglobin 9.4 g/dl, platelet count 33,000/mcl. A bone marrow biopsy and aspirate were repeated (including specimens obtained for tissue banking after obtaining informed consent with specific language authorizing whole genome sequencing which was approved by the Washington University Human Research Protection Office), and showed a 100% cellular marrow, with trilineage dysplasia and 7% blasts, interpreted as MDS/RAEB-1. Cytogenetics again showed a normal male karyotype. His IPSS score was 1.5 (Intermediate-2). At that time, erythropoietin was continued and hydroxyurea was added (1500 mg daily).

One month later, the patient presented with increased fatigue, blurred vision, and dyspnea and was found to have a white blood cell count of 147,000/mcl, hemoglobin 8.9 g/dl, platelet count 36,000/mcl, with 27% circulating blasts. A bone marrow biopsy and aspirate were repeated (including specimens obtained for tissue banking after obtaining informed consent with specific language authorizing whole genome sequencing which was approved by the Washington University Human Research Protection Office). The bone marrow biopsy showed >90% cellularity, with 60% blasts with irregular nuclear contours (NBE positive, largely myeloperoxidase negative). Flow cytometry demonstrated coexpression of CD13 and CD33, with variable expression of CD64 and CD117, most consistent with AML M5b (AML with monocytic differentiation). He received emergency leukopheresis and began 5-azacytidine (160 mg subcutaneously, days 1-7 of 28), for a total of 6 cycles.

Seven months later, the patient developed mental status changes and was found to have leukemic relapse in the central nervous system. He received supportive care until his death 322 days after initial presentation, and 246 days after evolution to sAML.

The patient had a prior history of coronary artery disease, hyperlipidemia, and recurrent pneumonia. There was no significant family history of cancer.

RESULTS

Genome coverage. Individual reads were aligned to the reference genome (NCBI build 36) and only unique reads (deduplicated reads) were used to determine haploid coverage of the genome for the normal and sAML samples (38.23x and 39.12x, respectively, **Supplementary Table 1**). We obtained at least 32x haploid coverage for all autosomal chromosomes in the normal genome and ~half this coverage for chromosomes X and Y, as expected (**Supplementary Fig. 2**). At least 99.42% of the consensus coding DNA sequence (CCDS) was covered by at least 1 read in both genomes (**Supplementary Table 1**). We identified all the heterozygous and homozygous SNPs present in the normal and sAML genomes using the Affymetrix SNP 6.0 arrays and determined diploid coverage for each genome based on the number of these SNPs that were identified using the WGS data, as previously described[1]. Using this approach, we achieved 98.91% and 99.31% diploid coverage of the normal and sAML genomes, respectively (**Supplementary Table 1**).

Detection and validation of somatic single nucleotide variants and insertions/deletions. 1281 potential somatic single nucleotide variants (SNVs) and 8801 indels were identified in the

sAML genome after filtering out low quality data and variants present in the matched normal genome and previously identified SNPs. These variant calls were prioritized into non-overlapping tiers for downstream validation, as previously described[1]. 1233 SNV predictions were tested using the custom capture approach, of which 507 validated (**Supplementary Table 2**). This represents an overall validation rate of 507/1233 (41%) and 16/38 (42%) for tier 1 high confidence (HC). 16 indel predictions were validated (none in Tier 1). 505 of the 507 SNVs (99.6 %) were present in the MDS genome, and 2 were new in the sAML genome (sAML-specific) (**Supplementary Table 2**).

***Copy number alterations and loss of heterozygosity*.** Using WGS data, we identified 42 putative amplifications. None of these calls were supported by LOH analysis and there were no instances of copy number neutral LOH (**Supplementary Fig. 2**). 4 putative copy number alterations were detected using the Affymetrix SNP 6.0 array data (SNPa). Deep sequencing after solid phase capture of the called sites in the normal, MDS, and sAML samples did not support any of the copy number predictions. Therefore, no confirmed structural variants were detected in this genome.

Luciferase-β-galactosidase double-reporter assay. Transient co-expression of the pTN24 double-reporter plasmid and the wild-type or S34F mutant *U2AF1* cDNA, with or without the Tra2α splicing enhancer or hnRNPG splicing inhibitor, was performed in 293T cells in 3 independent experiments, with one representative example shown in **Fig. 3a**. Each experiment had 6 replicate data values for each combination of conditions. A significant increase in splicing (as detected by an increase in the luciferase/β-galactosidase ratio) occurred with expression of the mutant *U2AF1* compared to wild-type *U2AF1* when co-expressed with pTN24 in 3 experiments ($P \leq 0.004$). Co-expression of the Tra2α splicing enhancer or hnRNPG splicing inhibitor resulted in increased and decreased splicing of the pTN24 reporter plasmid, as expected, that was independent of wild-type or mutant *U2AF1* expression. Experiments were analyzed independently. Transient co-expression of a control plasmid (vector) or the mutant *U2AF1* with or without a siRNA targeting the endogenous *U2AF1* was performed in 3 independent experiments, with one representative example shown in **Fig. 3b**. Each experiment had 6 replicate data values for each combination of conditions. A significant increase in splicing (as detected by an increase in the luciferase/β-galactosidase ratio) occurred in all 3 experiments when comparing the vector and *U2AF1* mutant cDNAs, independent of knockdown of *U2AF1* ($P \leq 0.04$).

Alternative splicing of FMR1. The *FMR1* gene*,* fragile X mental retardation 1, contains several alternative cryptic 3' splice acceptor sites in exon 15[2]. We performed RT-PCR using primers that flanked the cryptic splice sites and measured the relative abundance of splice acceptor site usage, as previously described[2]. We used RNA extracted from 7 unfractionated bone marrow samples harvested from MDS patients with a *U2AF1* mutation and 5 samples from MDS patients without a *U2AF1* mutation. Two independent experiments were performed using cDNA obtained from these samples and results are shown in **Supplementary Fig. 3a**. The splicing ratio is defined as the ratio of mRNAs resulting from the use of an alternative 3' cryptic splice acceptor site located within exon 15 (resulting in 124 or 85 base pair amplicons) compared to the normal splice acceptor site (160 base pair amplicon). There was an increased utilization of a cryptic 3' splice acceptor site in MDS samples harboring a *U2AF1* mutation compared to MDS samples without *U2AF1* mutations ($p<0.03$ for both independent experiments, $p=0.0001$ for pooled data).

Next, we validated this result by creating a *FMR1* minigene splicing reporter construct using the same genomic locus interrogated in the clinical samples. Each experiment was repeated with four biologic replicates. The *FMR1* minigene was transiently transfected into 293T cells with a control plasmid (pcDNA3.1-YFP), wild-type *U2AF1* cDNA, or mutant (S34F)

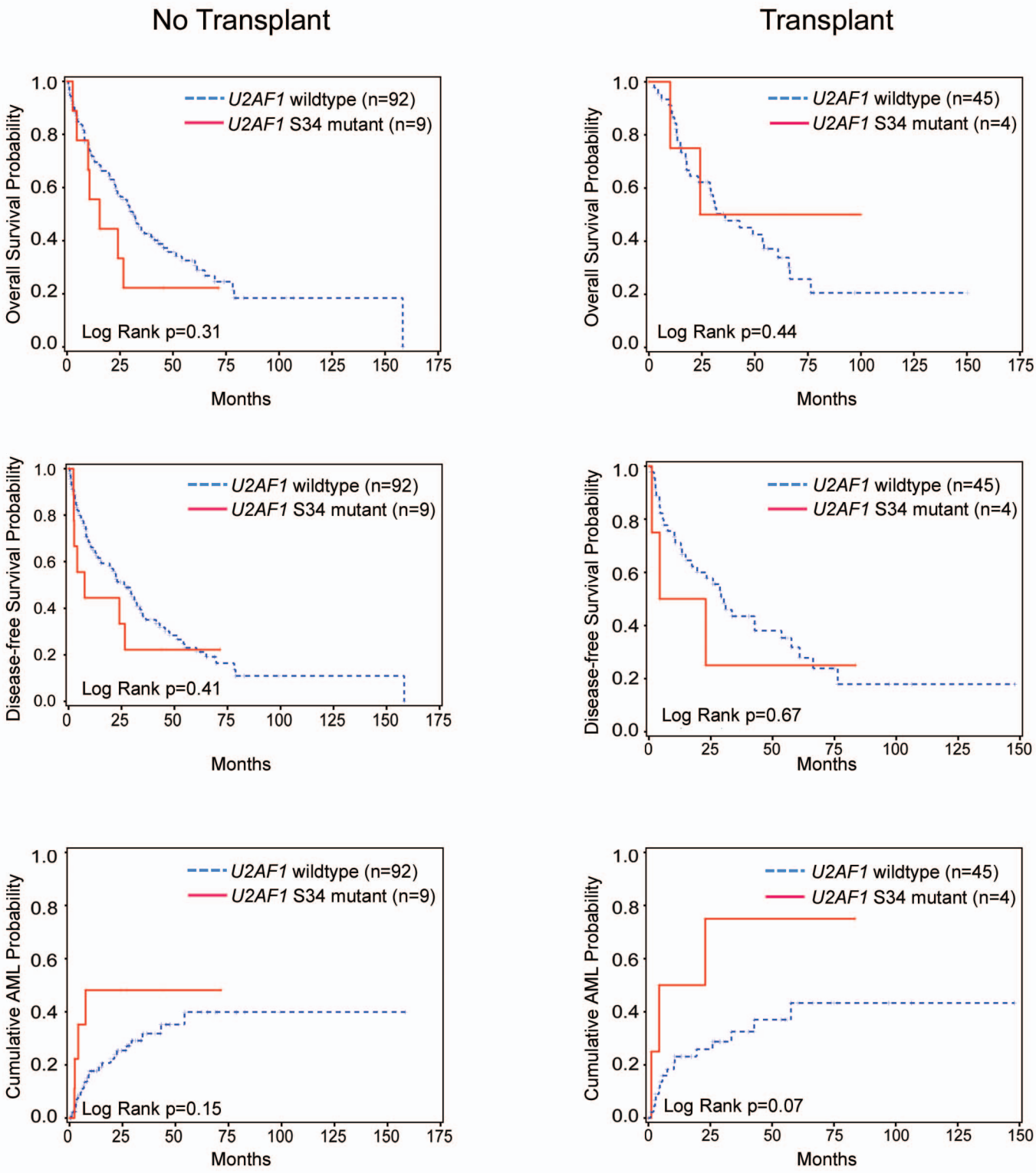
U2AF1 cDNA in the presence of a control siRNA or siRNA targeting the endogenous *U2AF1*. RNA was harvested 48 hours later and a reverse transcriptase (RT) reaction was performed to create cDNA. Expression of the S34F mutant *U2AF1* resulted in an increase in cryptic 3' splice acceptor usage compared to control or wild-type *U2AF1*, independent of endogenous *U2AF1* levels (P<0.04) (**Supplementary Fig. 3b**).

RT-PCR of U2AF1. Quantitative RT-PCR of *U2AF1* revealed no difference in the expression levels between mutant and wild-type MDS samples (p=0.73, **Supplementary Fig. 4a, left panel**). A dominant RT-PCR product was identified for both wild-type and mutant *U2AF1,* consistent with isoform "a" expression (**Supplementary Fig. 4a, right panel**). Cloning and sequencing of RT-PCR products obtained from *U2AF1* mutant MDS samples UPN 300813 and UPN 571656 revealed isoform "a" by Sanger sequencing (data not shown) and next-generation sequencing (**Fig. 1c**).

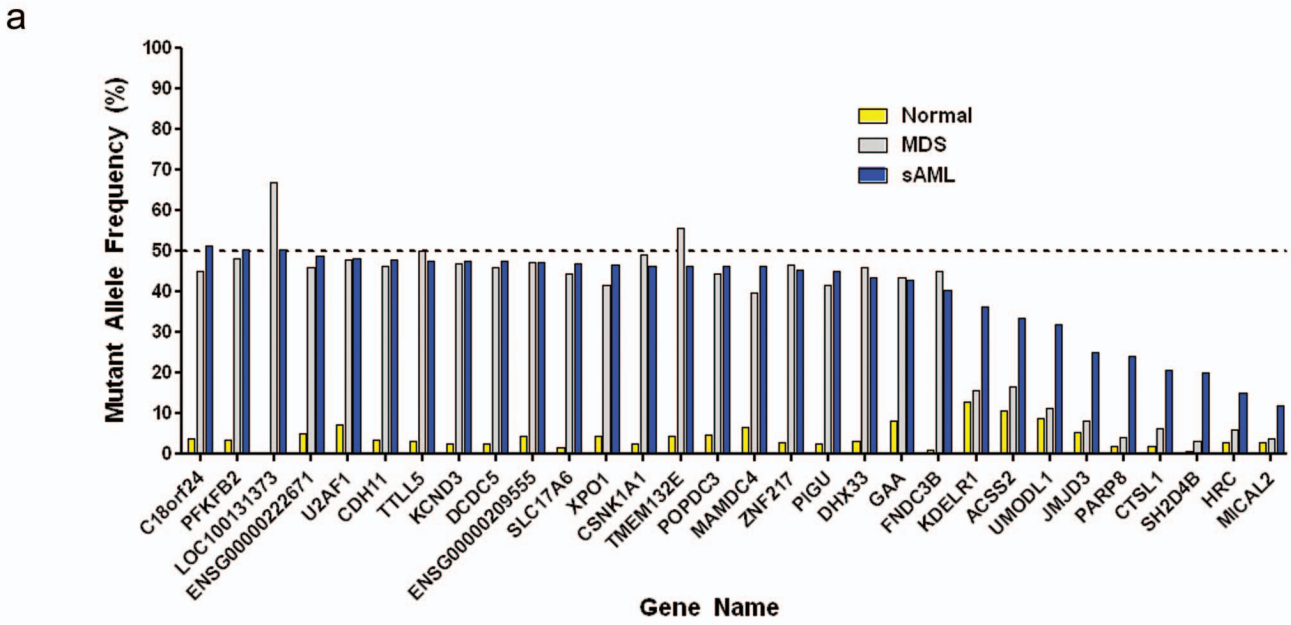
***Gene expression profiling*.** We compared the expression level of the 30 genes containing tier 1 mutations in our index sAML sample (UPN 266395) with the expression in 43 *de novo* AML samples for which exon array data was available (T. Ley, unpublished data). 28 genes had at least 3 probesets on the array. For these 28 genes, at least one probeset was called present in 27 genes in the sAML case (**Supplementary Table 9**). All 27 genes were also expressed in >50% of the *de novo* AML cases and the one gene not expressed in the sAML case (*POPDC3*) had only 1/13 probes expressed in ~50% of AML cases (**Supplementary Table 9**). 27 of the 30 mutated genes had probesets in the mutated exon. 14 of these were expressed in sAML (and in *de novo* AML) and 13 were not (vs. 11 absent in >50% of *de novo* AML cases). Overall, the expression pattern of the 28 genes with tier 1 mutations analyzed by microarray was highly similar in the sAML and *de novo* AML samples.

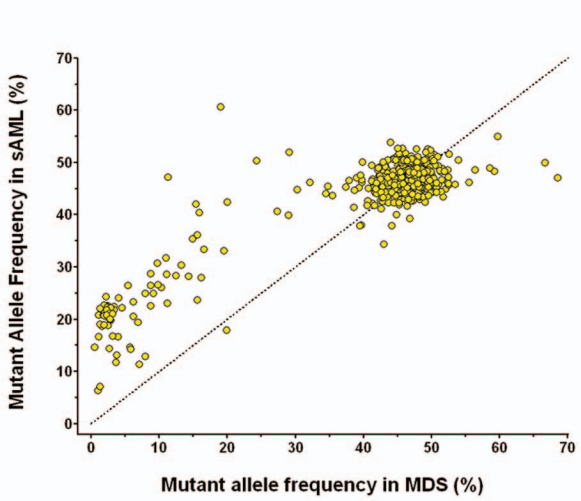
Affymetrix U133plus2 gene expression array data was available for 15 MDS and 4 control samples, as previously described[3]. RNA was extracted from CD34+ purified bone marrow cells for all samples. Array data was generated from the same batch analysis for the 19 samples and 6 of the 15 MDS samples had *U2AF1* mutations. First, we performed unsupervised hierarchical clustering using 19 arrays (4 control, 6 *U2AF1* mutant MDS samples, and 9 *U2AF1* wild-type MDS samples) and observed that clustering of samples was independent of disease or mutation status. When we restricted our clustering analysis to the 4 control and 6 *U2AF1* mutant samples, using 37,552 probesets that remained after removing probesets absent in all samples and using Ward's, UPGMA, or WPGMA clustering algorithms with Euclidean distance, we observed segregation of the mutant samples (**Supplementary Fig. 4b, left panel**). To identify the most significantly differentially expressed genes between control and *U2AF1* mutant MDS samples from the list of 37,552 probesets, we used the Significance Analysis of Microarray (SAM)[4] and Gene Set Enrichment Analysis (GSEA)[5] supervised algorithms. While we found no significant gene sets using GSEA, we did identify 50 probesets that were up-regulated and 351 probesets that were down-regulated in *U2AF1* mutant samples compared to controls with a false discovery rate (FDR) <0.005 (**Supplementary Table 6**). *U2AF1* mutant and control samples segregated by hierarchical clustering when we used 401 SAM defined probesets, as expected (**Supplementary Fig. 4b, right panel**). We analyzed up- and down-regulated genes to identify common pathways based on functional annotation categories (including gene ontology) using DAVID[6]. Nine annotation clusters were identified by DAVID using the 351 down-regulated probesets (300 with unique gene symbols) in *U2AF1* mutant samples that had an enrichment score >2. Three of the 9 clusters contained "mRNA splicing/processing" genes (enrichment score = 2.46) and two clusters with "RRM"(RNA recognition motif) genes (enrichment scores = 3-4.3) involved in splicing (**Supplementary Fig. 4c, Supplementary Table 6**). When genes that segregated control samples from *U2AF1* wild-type MDS samples were analyzed in DAVID, "splicing" and "RRM" categories were not

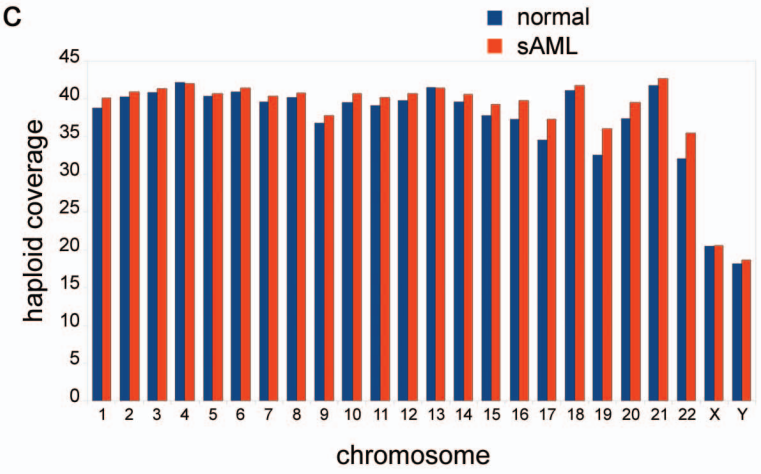
enriched, suggesting that down-regulation of splicing and RRM genes is not common to all MDS samples, but instead is associated with *U2AF1* mutations. Collectively, these results suggest that a regulatory feedback loop may exist for mRNA splicing genes when *U2AF1* is mutated.

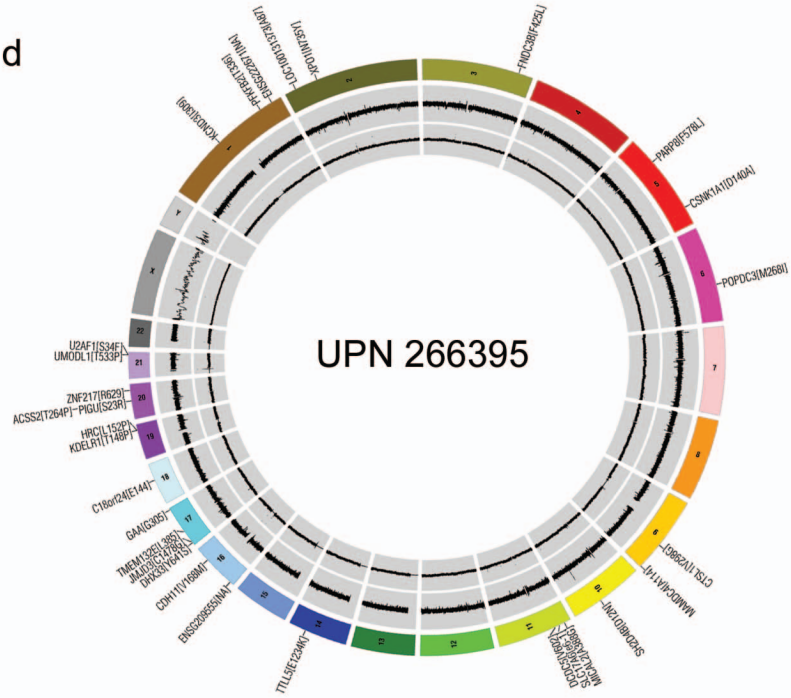


Supplementary Figure 1. Survival analysis in transplanted vs. non-transplanted patients.
(left column) Overall, event-free survival, and probability of progression to sAML was not significantly different in U2AF1 wildtype vs. mutant MDS patients who did not undergo stem cell transplantation. (right) Overall, event-free survival, and probability of progression to sAML was not significantly different in U2AF1 wildtype vs. mutant MDS patients who did undergo stem cell transplantation.

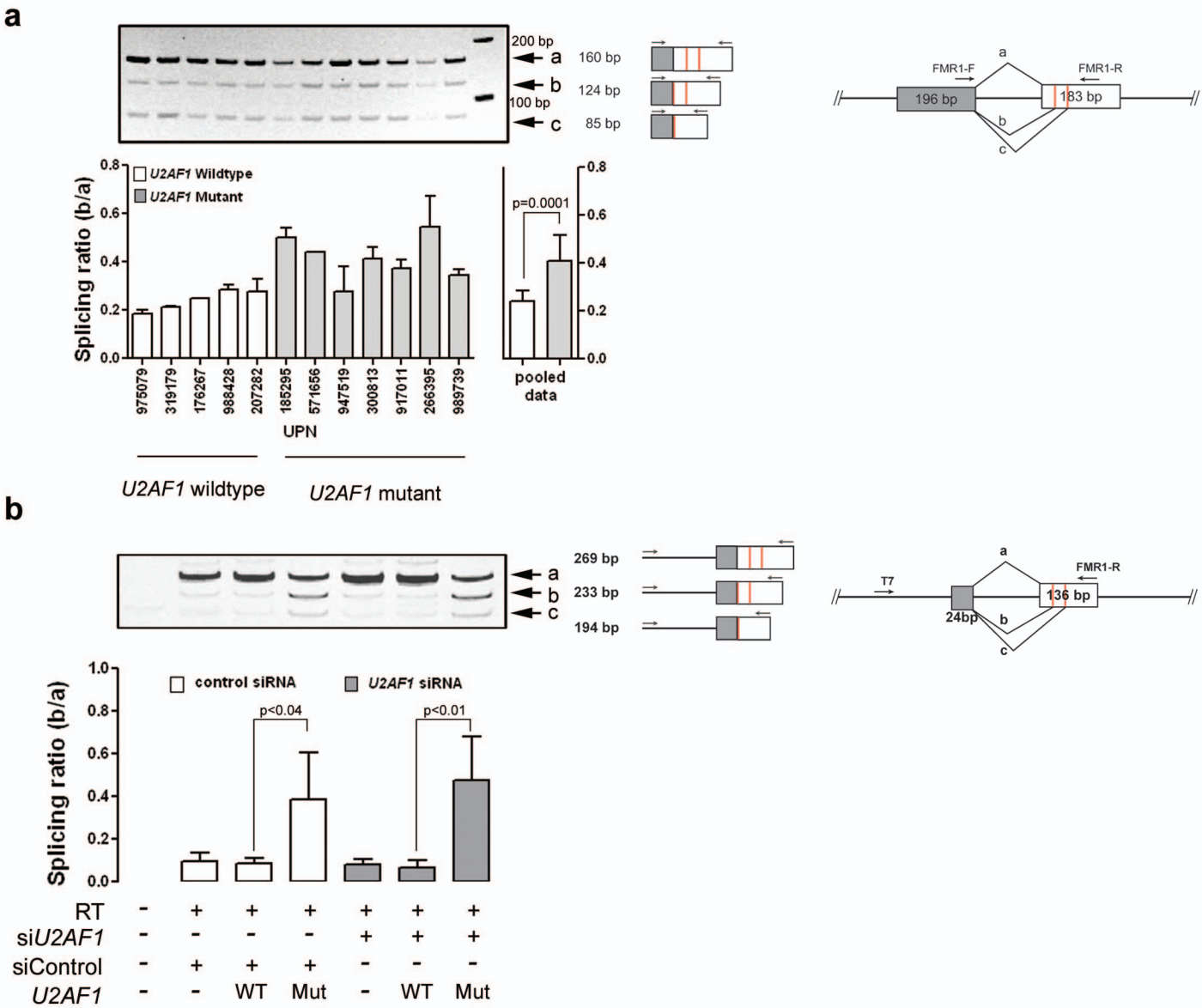






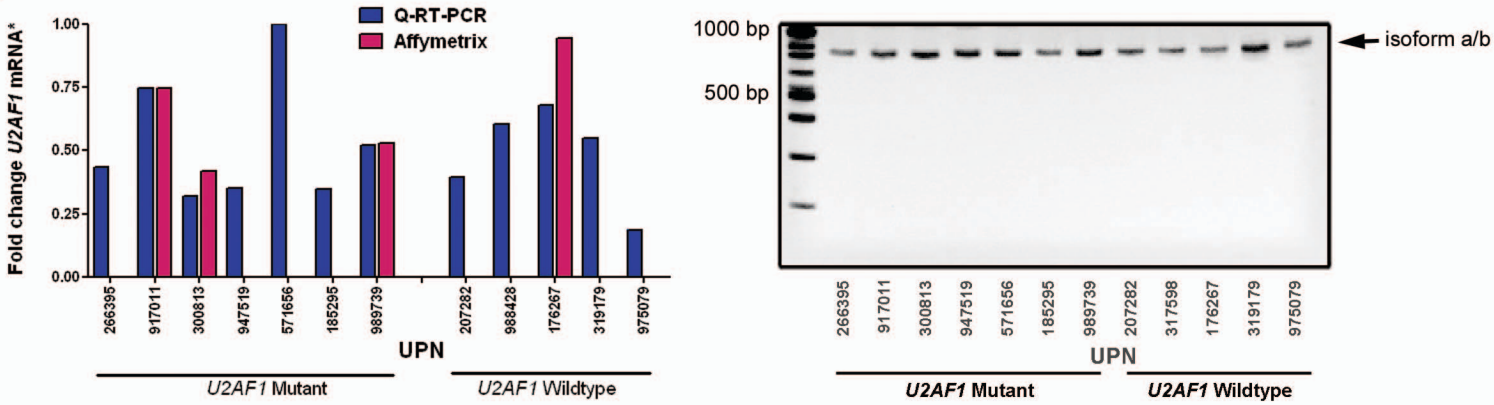


Supplementary Figure 2. Genomic architecture of UPN266395 index MDS patient. (a) Mutant allele frequencies of tier 1 SNVs from capture/deep sequencing of normal (skin), MDS, and sAML samples are shown. (b) Mutant allele frequencies of 507 validated somatic tier 1-3 SNVs from capture/deep sequencing are shown for the MDS vs. sAML samples. A single dominant clone was present in MDS and persisted at the sAML stage. Only 2 SNVs were acquired or enriched between MDS and sAML. (c) Sequence coverage from WGS was uniform across chromosomes and between normal (skin) and sAML samples. (d) Circos plot summarizing somatic changes identified by WGS in index case. Outer ring: validated tier 1 SNVs; middle ring: heterozygosity of sAML sample (no loss of heterozygosity detected); inner ring: copy number of sAML sample (no copy number alterations detected). SNV, single nucleotide variant. UPN, unique patient number.



Supplementary Figure 3. U2AF1 S34F mutation induces splicing alterations in FMR1. (a) The relative ratios of alternatively spliced products was measured following RT-PCR of RNA extracted from unpurified bone marrow cells from patients with (n=7) and without (n=5) U2AF1 mutations. A cartoon of FMR1 exons14 and 15 that are interrogated by the assay and the possible splice products are indicated (labeled a, b, or c). A representative PCR gel image is shown and the ratio of the middle band (amplicon b, utilizing the 3' cryptic splice acceptor site) relative to the fully spliced upper band (amplicon a) is shown for each condition. The ratio of splice products was measured by densitometry and plotted in the bar graph with the p-value listed. Patient samples with U2AF1 mutations had increased usage of a cryptic 3' splice acceptor site in exon 15 of FMR1 relative to nonmutant patient samples (left panel, error bars represent two independent experiments) (wildtype vs. mutant splicing ratio, p<0.03 for both independent experiments in the left panel, p=0.0001 for pooled data in the right panel). (b) The FMR1 minigene (generated using primers shown in panel a) was transiently transfected into 293T cells with a control plasmid (pcDNA3.1-YFP), wild-type U2AF1 cDNA, or mutant (S34F) U2AF1 cDNA in the presence of a control siRNA or siRNA targeting endogenous U2AF1. RNA was harvested 48 hours later and a reverse transcriptase reaction was performed to create cDNA. PCR using the indicated primers resulted in a fully spliced 269 base pair amplicon or smaller amplicons (233 or 194 basepairs) that skip the first splice acceptor site. A representative PCR gel image is shown and the ratio of the middle band (cryptic 3' splice acceptor site = amplicon b) relative to the fully spliced upper band (amplicon a) is shown for each condition. Expression of S34F mutant U2AF1 resulted in an increase in cryptic 3' splice acceptor usage compared to control or wild-type U2AF1, independent of endogenous U2AF1 levels (n=4, P<0.04).

a



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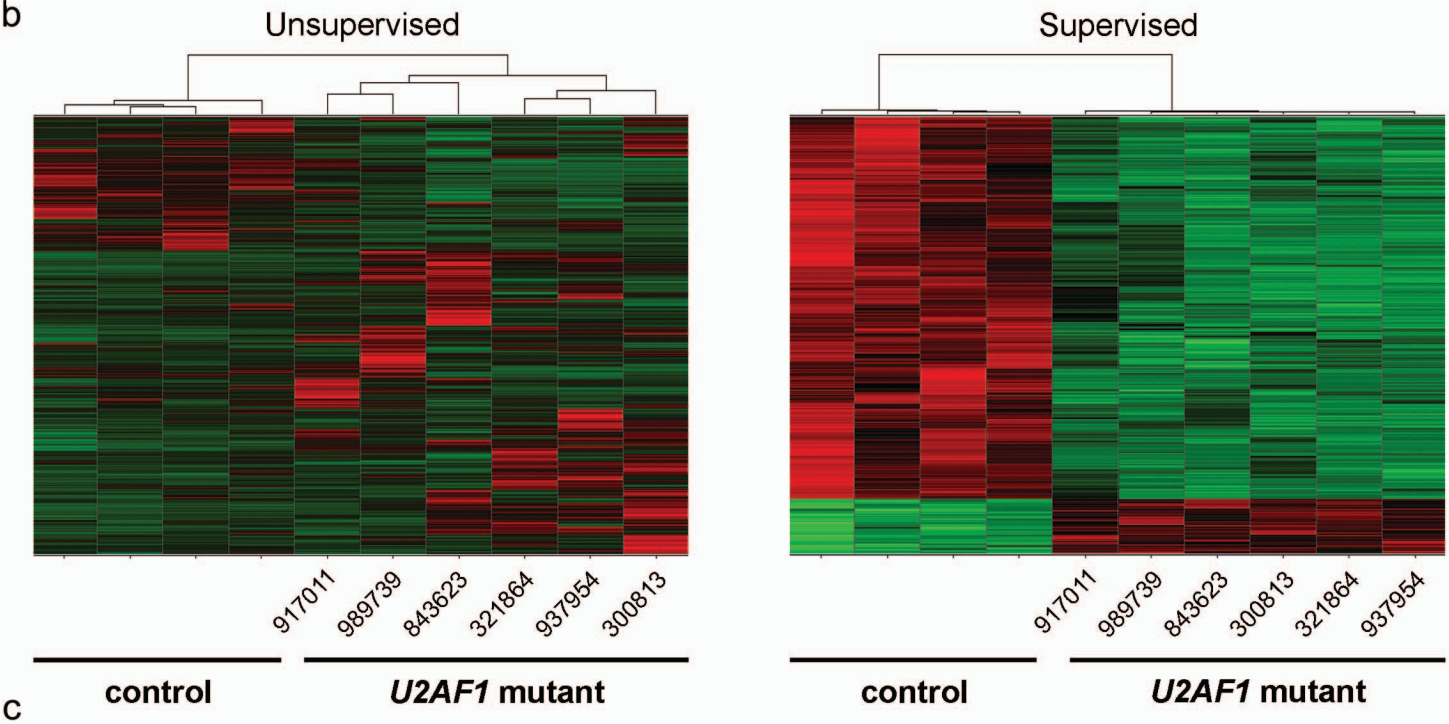

c

Annotation Cluster 1	Enrichment Score: 7.715				
Category	Term	# genes	% total genes	Fold Enrichment	Benjamini p-value
GOTERM_CC_FAT	GO:0031974:membrane-enclosed lumen	67	22.33	2.09	8.89E-07
GOTERM_CC_FAT	GO:0070013:intracellular organelle lumen	64	21.33	2.08	1.41E-06
GOTERM_CC_FAT	GO:0043233:organelle lumen	64	21.33	2.03	2.29E-06
GOTERM_CC_FAT	GO:0031981:nuclear lumen	52	17.33	2.07	3.73E-05
Annotation Cluster 2	**Enrichment Score: 4.311**				
Category	Term	# genes	% total genes	Fold Enrichment	Benjamini p-value
SMART	SM00360:RRM	14	4.67	4.18	3.33E-03
INTERPRO	IPR000504:RNA recognition motif, RNP-1	14	4.67	3.92	3.70E-02
INTERPRO	IPR012677:Nucleotide-binding, alpha-beta plait	14	4.67	3.88	2.05E-02

Supplementary Figure 4. U2AF1 quantitative RT-PCR and global expression profiling. (a, left panel) qRT-PCR of U2AF1 (exons 2-3 of isoform A) mRNA was performed using RNA extracted from unpurified bone marrow cells from patients with (n=7) and without (n=5) U2AF1 mutations. Affymetrix U133plus2 array data were available for 4 of the patients and are plotted for comparison. There was no significant difference in the expression of U2AF1 in mutant vs. wild-type MDS patient samples (p=0.73). (a, right panel) RT-PCR was performed using RNA extracted from unpurified bone marrow cells from patients with (n=7) and without (n=5) U2AF1 mutations. Primers were designed to detect all 3 isoforms of U2AF1. Full-length isoform a was detected in all samples, independent of mutation status. (b, left panel) Unsupervised hierarchical clustering results using Ward's method and 37,552 probesets from Affymetrix U133plus2 arrays (probesets were excluded only if absent in all samples being compared). RNA was obtained from CD34+ purified bone marrow cells from 4 normal healthy controls and 6 MDS samples with a U2AF1 mutation. (b, right panel) Supervised hierarchical clustering using Ward's method and 401 probesets identified by Significance Analysis of Microarrays (SAM), comparing control and U2AF1 mutant MDS samples with a false discovery rate (FDR) < 0.005. (c) Nine gene ontology annotation clusters were identified by DAVID using 351 probesets (300 gene symbols) that were down-regulated in U2AF1 mutant compared to control samples (identified by SAM) and had an enrichment score > 2 in DAVID. The top 2 clusters are shown. RNA recognition motif (RRM) gene categories were down-regulated in the U2AF1 samples compared to control samples. UPN, unique patient number. * relative to GAPDH mRNA expression.

Supplementary Table 1. Sequence metrics.

Parameter	Normal Genome	MDS Tumor Genome	sAML Tumor Genome
Whole Genome Sequence			
lanes	8	ND	12
sequence production (Gbp)	134.91	ND	132.24
aligned (Gbp)	122.80	ND	124.37
deduplicated (Gbp)	114.50	ND	116.32
haploid coverage	38.23	ND	39.12
bases with >=1x coverage (%)	92.97	ND	93.00
bases with >10x coverage (%)	91.87	ND	92.49
bases with >20x coverage (%)	86.23	ND	89.12
CCDS bases with >=1x coverage (%)	99.42	ND	99.67
CCDS bases with >=10x coverage (%)	92.24	ND	97.21
CCDS bases with >=20x coverage (%)	73.61	ND	88.52
Het SNPs (Affy)	226,603	ND	224,808
Hom SNPs (Affy)	166,483	ND	167,609
Diploid coverage Het SNPs (%)	98.91	ND	99.31
Diploid coverage Hom SNPs (%)	99.55	ND	99.17
Capture Validation			
target bases with >=1x coverage (%)	93.06	93.78	94.86
target bases with >10x coverage (%)	87.16	88.53	91.34
target bases with >20x coverage (%)	84.22	86.15	89.84

CCDS, consensus coding DNA sequence; ND, not done.

Het SNPs, single nucleotide polymorphic sites genotyped as heterozygous using Affymetric 6.0 SNP array and both wildtype and variant alleles detected in whole genome sequence data

Hom SNPs, single nucleotide polymorphic sites genotyped as homozygous using Affymetric 6.0 SNP array and only variant allele detected in whole genome sequence data

Supplementary Table 2. Validated Tier 1-3 SNVs in the MDS and sAML genomes.

Chr	Start	Ref Allele	Var Allele	Gene Name	Tier	Mutation	Ref Reads in Normal	Var Reads in Normal	Var Freq in Normal	Ref Reads in MDS	Var Reads in MDS	Var Freq in MDS	Copy number adjusted Var Freq in MDS	Var Type MDS	Somatic P-value	Ref Reads in AML	Var Reads in AML	Var Freq in AML	Copy number adjusted Var Freq in AML	Var Type AML	Somatic P-value	Mutation Cluster
1	19,065,087	G	A	TAS1R2	3	5_prime_flanking_region	559	16	2.78	82	79	49.07	49.07	Somatic	0.000	241	236	49.48	49.48	Somatic	0.000	1
1	19,575,544	G	A	CAPZB	3	intronic	240	14	5.51	90	70	43.75	43.75	Somatic	0.000	220	186	45.81	45.81	Somatic	0.000	1
1	35,025,125	A	G	GJA4	2	5_prime_flanking_region	891	11	1.22	383	318	45.36	45.36	Somatic	0.000	437	345	44.12	44.12	Somatic	0.000	1
1	43,382,798	G	A	FAM183A	3	5_prime_untranslated_region	1361	56	3.95	559	480	46.20	46.20	Somatic	0.000	406	341	45.65	45.65	Somatic	0.000	1
1	53,979,456	C	T	GLIS1	3	5_prime_flanking_region	219	28	11.34	231	203	46.77	46.77	Somatic	0.000	201	180	47.24	47.24	Somatic	0.000	1
1	54,441,310	C	T	MRPL37	2	intronic	691	34	4.69	274	259	48.59	48.59	Somatic	0.000	286	254	47.04	47.04	Somatic	0.000	1
1	60,329,124	A	G	C1orf87	2	5_prime_flanking_region	664	25	3.63	679	571	45.68	45.68	Somatic	0.000	394	355	47.40	47.40	Somatic	0.000	1
1	61,483,596	C	T	NFIA	3	intronic	134	10	6.94	127	120	48.58	48.58	Somatic	0.000	203	171	45.72	45.72	Somatic	0.000	1
1	63,400,074	G	T	ENSG00000210785	2	3_prime_flanking_region	792	27	3.30	942	938	49.89	49.89	Somatic	0.000	470	422	47.31	47.31	Somatic	0.000	1
1	66,393,703	C	T	PDE4B	3	intronic	638	27	4.06	591	451	43.28	43.28	Somatic	0.000	306	273	47.15	47.15	Somatic	0.000	1
1	84,880,057	A	C	C1orf180	3	5_prime_flanking_region	366	15	3.94	930	61	6.16	6.16	Somatic	0.201	599	183	23.40	23.40	Somatic	0.000	0
1	91,923,288	C	T	TGFBR3	3	intronic	603	27	4.29	488	507	50.95	50.95	Somatic	0.000	329	321	49.38	49.38	Somatic	0.000	1
1	97,037,795	T	C	PTBP2	3	intronic	269	8	2.89	568	529	48.22	48.22	Somatic	0.000	296	259	46.67	46.67	Somatic	0.000	1
1	106,376,327	C	G	LOC126987	3	3_prime_flanking_region	242	9	3.59	279	280	50.09	50.09	Somatic	0.000	325	293	47.41	47.41	Somatic	0.000	1
1	111,623,853	C	T	CHIA	2	5_prime_flanking_region	1328	27	1.99	897	735	45.04	45.04	Somatic	0.000	567	416	42.32	42.32	Somatic	0.000	1
1	112,325,945	G	T	KCND3	1	silent	708	17	2.34	278	245	46.85	46.85	Somatic	0.000	298	268	47.35	47.35	Somatic	0.000	1
1	146,213,819	A	T	LOC100132219	3	5_prime_flanking_region	801	40	4.76	206	173	45.65	45.65	Somatic	0.000	332	286	46.28	46.28	Somatic	0.000	1
1	157,603,769	G	T	OR10J1	3	intronic	616	31	4.79	462	372	44.60	44.60	Somatic	0.000	278	243	46.64	46.64	Somatic	0.000	1
1	163,243,072	C	T	ENSG00000201270	3	5_prime_flanking_region	595	18	2.94	654	556	45.95	45.95	Somatic	0.000	310	249	44.54	44.54	Somatic	0.000	1
1	165,197,653	G	A	ILDR2	3	intronic	1699	61	3.47	475	437	47.92	47.92	Somatic	0.000	469	423	47.42	47.42	Somatic	0.000	1
1	165,827,772	C	T	CREG1	3	5_prime_flanking_region	238	13	5.18	218	165	43.08	43.08	Somatic	0.000	311	254	44.96	44.96	Somatic	0.000	1
1	174,944,913	C	T	PAPPA2	3	intronic	946	1	0.11	1713	47	2.67	2.67	Somatic	0.000	514	136	20.92	20.92	Somatic	0.000	2
1	175,516,166	C	A	FAM5B	3	splice_region	679	27	3.82	680	565	45.38	45.38	Somatic	0.000	329	311	48.59	48.59	Somatic	0.000	1
1	205,309,412	C	G	PFKFB2	1	silent	593	21	3.42	447	414	48.08	48.08	Somatic	0.000	331	332	50.08	50.08	Somatic	0.000	1
1	206,921,075	G	A	ENSG00000217293	3	3_prime_flanking_region	396	11	2.70	275	256	48.21	48.21	Somatic	0.000	389	293	42.96	42.96	Somatic	0.000	1
1	215,059,819	C	T	ESRRG	3	intronic	321	8	2.43	306	271	46.97	46.97	Somatic	0.000	417	311	42.72	42.72	Somatic	0.000	1
1	215,500,402	A	T	ENSG00000201753	2	3_prime_flanking_region	830	23	2.70	933	745	44.40	44.40	Somatic	0.000	428	371	46.43	46.43	Somatic	0.000	1
1	225,042,030	C	T	ITPKB	3	5_prime_flanking_region	422	19	4.31	197	181	47.88	47.88	Somatic	0.000	215	193	47.30	47.30	Somatic	0.000	1
1	229,096,537	T	C	ENSG00000222671	1	rna	406	20	4.69	172	146	45.91	45.91	Somatic	0.000	231	219	48.67	48.67	Somatic	0.000	1
1	232,624,711	A	C	TARBP1	3	intronic	444	21	4.52	964	122	11.23	11.23	Somatic	0.048	287	257	47.24	47.24	Somatic	0.000	0
1	242,682,289	T	G	ADSS	2	5_prime_flanking_region	110	0	0.00	372	7	1.85	1.85	Somatic	0.165	460	133	22.43	22.43	Somatic	0.000	2
1	244,630,678	C	T	SMYD3	2	intronic	292	10	3.31	299	198	39.84	39.84	Somatic	0.000	302	303	50.08	50.08	Somatic	0.000	1
1	246,007,658	G	A	OR1C1	3	5_prime_flanking_region	434	8	1.81	579	510	46.83	46.83	Somatic	0.000	369	286	43.66	43.66	Somatic	0.000	1
2	863,187	C	T	LOC391343	3	3_prime_flanking_region	379	21	5.25	106	46	30.26	30.26	Somatic	0.000	310	252	44.84	44.84	Somatic	0.000	0
2	12,407,391	G	A	0	3	0	1171	40	3.30	634	556	46.72	46.72	Somatic	0.000	403	394	49.44	49.44	Somatic	0.000	1
2	20,289,990	C	T	LOC100131373	1	silent	20	0	0.00	8	16	66.67	66.67	Somatic	0.000	92	92	50.00	50.00	Somatic	0.000	0
2	35,703,943	G	A	0	3	0	682	24	3.40	511	518	50.34	50.34	Somatic	0.000	344	293	46.00	46.00	Somatic	0.000	1
2	35,720,616	T	C	0	3	0	501	24	4.57	608	526	46.38	46.38	Somatic	0.000	427	368	46.29	46.29	Somatic	0.000	1
2	39,902,719	T	C	THUMPD2	3	5_prime_flanking_region	340	7	2.02	538	477	47.00	47.00	Somatic	0.000	189	169	47.21	47.21	Somatic	0.000	1
2	61,569,230	T	A	XPO1	1	missense	386	17	4.22	206	145	41.31	41.31	Somatic	0.000	373	322	46.33	46.33	Somatic	0.000	1
2	69,027,275	A	G	GKN2	3	intronic	519	3	0.57	1093	51	4.46	4.46	Somatic	0.000	545	156	22.25	22.25	Somatic	0.000	2
2	77,345,681	G	T	LRRTM4	3	intronic	540	25	4.42	1135	1029	47.55	47.55	Somatic	0.000	399	352	46.87	46.87	Somatic	0.000	1
2	80,591,943	A	G	CTNNA2	3	intronic	548	18	3.18	547	453	45.30	45.30	Somatic	0.000	392	309	44.08	44.08	Somatic	0.000	1
2	89,010,893	C	T	ENSG00000219044	3	5_prime_flanking_region	198	4	1.98	226	200	46.95	46.95	Somatic	0.000	274	228	45.42	45.42	Somatic	0.000	1
2	98,221,020	T	A	VWA3B	3	intronic	736	52	6.60	442	407	47.94	47.94	Somatic	0.000	283	263	48.17	48.17	Somatic	0.000	1
2	123,201,256	G	A	0	3	0	126	2	1.56	158	116	42.34	42.34	Somatic	0.000	194	167	46.26	46.26	Somatic	0.000	1
2	125,241,196	C	T	CNTNAP5	2	intronic	683	75	9.89	925	708	43.36	43.36	Somatic	0.000	303	289	48.82	48.82	Somatic	0.000	1
2	126,115,254	G	T	0	3	0	537	11	2.01	690	544	44.08	44.08	Somatic	0.000	265	232	46.68	46.68	Somatic	0.000	1
2	129,312,063	T	C	0	3	0	222	3	1.33	165	124	42.91	42.91	Somatic	0.000	227	119	34.39	34.39	Somatic	0.000	0
2	132,910,452	A	C	GPR39	3	intronic	335	1	0.30	398	383	49.04	49.04	Somatic	0.000	361	266	42.42	42.42	Somatic	0.000	1
2	138,312,675	C	T	0	3	0	917	14	1.50	557	438	44.02	44.02	Somatic	0.000	444	360	44.78	44.78	Somatic	0.000	1
2	148,169,122	C	G	0	3	0	776	39	4.79	384	367	48.87	48.87	Somatic	0.000	371	365	49.59	49.59	Somatic	0.000	1
2	148,826,888	C	G	MBD5	3	intronic	403	31	7.14	332	320	49.08	49.08	Somatic	0.000	233	239	50.64	50.64	Somatic	0.000	1
2	151,024,156	A	T	RND3	3	3_prime_flanking_region	517	10	1.90	500	442	46.92	46.92	Somatic	0.000	252	254	50.20	50.20	Somatic	0.000	1
2	163,476,519	G	T	0	3	0	609	14	2.25	474	360	43.17	43.17	Somatic	0.000	412	403	49.45	49.45	Somatic	0.000	1
2	164,335,975	T	C	FIGN	3	5_prime_flanking_region	598	22	3.55	555	470	45.85	45.85	Somatic	0.000	395	325	45.14	45.14	Somatic	0.000	1
2	165,485,434	G	A	SLC38A11	3	intronic	876	27	2.99	965	915	48.67	48.67	Somatic	0.000	369	361	49.45	49.45	Somatic	0.000	1
2	173,997,180	T	A	LOC100130171	3	3_prime_flanking_region	28	0	0.00	20	29	59.18	59.18	Somatic	0.000	78	73	48.34	48.34	Somatic	0.000	0
2	176,980,601	G	A	ENSG00000221304	2	5_prime_flanking_region	537	23	4.11	416	316	43.17	43.17	Somatic	0.000	251	219	46.60	46.60	Somatic	0.000	1
2	177,423,844	A	C	LOC100131991	3	5_prime_flanking_region	663	6	0.90	1615	18	1.10	1.10	Somatic	0.048	748	150	16.70	16.70	Somatic	0.000	0
2	184,200,811	G	A	LOC644877	3	5_prime_flanking_region	393	10	2.48	542	476	46.76	46.76	Somatic	0.000	309	247	44.42	44.42	Somatic	0.000	1
2	193,919,617	T	C	0	3	0	92	5	5.15	235	129	35.44	35.44	Somatic	0.000	228	177	43.70	43.70	Somatic	0.000	0
2	194,557,414	C	T	ENSG00000222759	2	5_prime_flanking_region	394	8	1.99	335	338	50.22	50.22	Somatic	0.000	393	351	47.18	47.18	Somatic	0.000	1
2	195,682,545	C	T	0	3	0	416	11	2.58	665	516	43.69	43.69	Somatic	0.000	416	338	44.83	44.83	Somatic	0.000	1
2	196,945,824	C	G	HECW2	2	intronic	290	12	3.97	267	230	46.28	46.28	Somatic	0.000	266	213	44.47	44.47	Somatic	0.000	1
2	201,394,089	G	A	BZW1	3	intronic	455	29	5.99	333	293	46.81	46.81	Somatic	0.000	401	378	48.52	48.52	Somatic	0.000	1
2	210,037,049	G	T	MAP2	2	intronic	246	11	4.28	402	353	46.75	46.75	Somatic	0.000	279	228	44.97	44.97	Somatic	0.000	1
2	210,201,325	G	A	MAP2	3	intronic	347	5	1.42	405	372	47.88	47.88	Somatic	0.000	337	299	47.01	47.01	Somatic	0.000	1
2	212,992,222	G	A	ERBB4	3	intronic	245	12	4.67	408	355	46.53	46.53	Somatic	0.000	380	356	48.37	48.37	Somatic	0.000	1
2	215,954,173	A	C	FN1	3	intronic	448	14	3.03	391	340	46.51	46.51	Somatic	0.000	413	366	46.98	46.98	Somatic	0.000	1
2	224,668,756	C	A	0	2	0	855	2	0.23	1976	50	2.47	2.47	Somatic	0.000	565	165	22.60	22.60	Somatic	0.000	2
2	230,165,735	G	T	DNER	3	intronic	1620	66	3.91	499	431	46.34	46.34	Somatic	0.000	463	401	46.41	46.41	Somatic	0.000	1
2	236,501,607	G	A	AGAP1	3	intronic	512	6	1.16	265	192	42.01	42.01	Somatic	0.000	257	224	46.57	46.57	Somatic	0.000	1
2	236,719,796	G	A	LOC100128572	3	5_prime_flanking_region	357	15	4.03	61	61	50.00	50.00	Somatic	0.000	307	274	47.16	47.16	Somatic	0.000	1
3	2,659,195	T	G	CNTN4	3	intronic	890	34	3.68	580	485	45.54	45.54	Somatic	0.000	333	339	50.45	50.45	Somatic	0.000	1
3	10,616,558	G	A	ATP2B2	3	intronic	602	41	6.38	271	258	48.77	48.77	Somatic	0.000	185	155	45.59	45.59	Somatic	0.000	1

3	13,411,614	G	A	NUP210		3	intronic		193	6	3.02	65	61	48.41	48.41	Somatic	0.000	161	136	45.79	45.79	Somatic	0.000	1
3	21,855,819	A	C	ENSG00000221384		3	3_prime_flanking_region		405	53	11.57	791	197	19.94	19.94	Somatic	0.000	303	223	42.40	42.40	Somatic	0.000	0
3	26,376,984	G	A		0	3		0	269	9	3.24	302	283	48.38	48.38	Somatic	0.000	163	132	44.75	44.75	Somatic	0.000	1
3	26,998,497	G	A		0	3		0	692	37	5.08	983	698	41.52	41.52	Somatic	0.000	411	347	45.78	45.78	Somatic	0.000	1
3	40,732,099	G	T	LOC729505		2	5_prime_flanking_region		683	26	3.67	626	616	49.60	49.60	Somatic	0.000	458	376	45.08	45.08	Somatic	0.000	1
3	45,981,158	T	G	FYCO1		3	intronic		345	17	4.70	326	31	8.68	8.68	Somatic	0.324	377	136	26.51	26.51	Somatic	0.000	0
3	47,603,402	G	T	SMARCC1		3	3_prime_untranslated_region		564	70	11.04	275	42	13.25	13.25	Somatic	0.533	404	176	30.34	30.34	Somatic	0.000	0
3	53,603,765	T	G	CACNA1D		3	intronic		821	89	9.78	1229	297	19.46	19.46	Somatic	0.000	411	204	33.17	33.17	Somatic	0.000	0
3	75,444,179	C	T	ENSG00000179799		3	3_prime_flanking_region		1238	2	0.16	1384	31	2.19	2.19	Somatic	0.000	598	163	21.42	21.42	Somatic	0.000	2
3	75,472,731	A	C	LOC728135		3	3_prime_flanking_region		322	12	3.59	226	186	45.15	45.15	Somatic	0.000	187	164	46.72	46.72	Somatic	0.000	1
3	76,099,526	G	A	ROBO2		3	intronic		277	5	1.77	476	225	32.10	32.10	Somatic	0.000	230	198	46.26	46.26	Somatic	0.000	0
3	76,586,575	C	T	ROBO2		3	intronic		233	2	0.85	354	144	28.92	28.92	Somatic	0.000	293	195	39.96	39.96	Somatic	0.000	0
3	80,602,658	G	A		0	3		0	126	3	2.33	171	147	46.23	46.23	Somatic	0.000	243	234	49.06	49.06	Somatic	0.000	1
3	81,055,536	G	A		0	3		0	490	35	6.67	686	616	47.31	47.31	Somatic	0.000	429	366	46.04	46.04	Somatic	0.000	1
3	85,219,286	T	G	CADM2		3	intronic		159	15	8.62	261	169	39.30	39.30	Somatic	0.000	286	236	45.21	45.21	Somatic	0.000	1
3	86,451,526	T	C	ENSG00000222934		3	5_prime_flanking_region		25	3	10.71	39	55	58.51	58.51	Somatic	0.000	51	49	49.00	49.00	Somatic	0.000	0
3	99,901,474	T	G	ST3GAL6		2	5_prime_flanking_region		36	5	12.20	81	19	19.00	19.00	Somatic	0.285	55	85	60.71	60.71	Somatic	0.001	0
3	100,667,116	C	T		0	3		0	819	2	0.24	2861	55	1.89	1.89	Somatic	0.000	614	181	22.77	22.77	Somatic	0.000	2
3	111,192,335	T	C		0	3		0	338	7	2.03	438	411	48.41	48.41	Somatic	0.000	302	247	44.99	44.99	Somatic	0.000	1
3	111,431,333	C	T		0	3		0	153	1	0.65	287	213	42.60	42.60	Somatic	0.000	258	181	41.23	41.23	Somatic	0.000	1
3	115,134,962	G	T	GRAMD1C		3	intronic		141	2	1.40	252	200	44.25	44.25	Somatic	0.000	236	188	44.34	44.34	Somatic	0.000	1
3	115,150,252	C	G	ZDHHC23		2	intronic		296	7	2.31	480	393	45.02	45.02	Somatic	0.000	271	236	46.55	46.55	Somatic	0.000	1
3	133,430,465	T	G	LOC729677		3	3_prime_flanking_region		1116	22	1.93	1852	136	6.84	6.84	Somatic	0.000	614	148	19.42	19.42	Somatic	0.000	0
3	133,441,990	C	A	LOC729677		3	3_prime_flanking_region		542	37	6.39	721	670	48.17	48.17	Somatic	0.000	450	412	47.80	47.80	Somatic	0.000	1
3	134,386,054	A	T	TMEM108		3	intronic		134	8	5.63	147	128	46.55	46.55	Somatic	0.000	233	185	44.26	44.26	Somatic	0.000	1
3	136,219,503	A	G	EPHB1		3	intronic		1277	59	4.42	1050	100	8.70	8.70	Somatic	0.004	342	100	22.62	22.62	Somatic	0.000	0
3	136,463,072	C	T	EPHB1		3	3_prime_flanking_region		332	8	2.35	245	187	43.29	43.29	Somatic	0.000	177	151	46.04	46.04	Somatic	0.000	1
3	158,727,296	T	A	C3orf55		3	5_prime_flanking_region		545	25	4.39	313	272	46.50	46.50	Somatic	0.000	256	205	44.47	44.47	Somatic	0.000	1
3	163,509,409	G	C		0	3		0	315	7	2.17	549	459	45.54	45.54	Somatic	0.000	381	349	47.81	47.81	Somatic	0.000	1
3	166,201,621	C	T	SI		3	intronic		89	3	3.26	152	122	44.53	44.53	Somatic	0.000	109	83	43.23	43.23	Somatic	0.000	1
3	170,819,805	C	T	MDS1		3	intronic		687	20	2.83	683	638	48.30	48.30	Somatic	0.000	312	250	44.48	44.48	Somatic	0.000	1
3	173,529,456	C	A	FNDC3B		1	missense		262	2	0.76	439	356	44.78	44.78	Somatic	0.000	219	146	40.00	40.00	Somatic	0.000	0
3	177,936,424	A	T	ENSG00000208490		3	5_prime_flanking_region		614	30	4.66	602	426	41.44	41.44	Somatic	0.000	460	380	45.24	45.24	Somatic	0.000	1
3	188,400,850	C	A	RTP1		3	3_prime_untranslated_region		341	5	1.45	405	383	48.60	48.60	Somatic	0.000	278	215	43.61	43.61	Somatic	0.000	1
4	2,261,310	G	A	ZFYVE28		2	intronic		131	11	7.75	37	26	41.27	41.27	Somatic	0.000	283	249	46.80	46.80	Somatic	0.000	1
4	7,365,576	T	A	SORCS2		3	intronic		1048	8	0.76	270	3	1.10	1.10	Somatic	0.401	446	117	20.78	20.78	Somatic	0.000	2
4	7,395,182	A	T	SORCS2		3	intronic		148	3	1.99	113	97	46.19	46.19	Somatic	0.000	121	130	51.79	51.79	Somatic	0.000	1
4	16,550,472	C	T	LDB2		3	5_prime_flanking_region		241	14	5.49	252	214	45.92	45.92	Somatic	0.000	229	213	48.19	48.19	Somatic	0.000	1
4	18,139,490	C	T	ENSG00000209956		3	3_prime_flanking_region		392	25	6.00	687	531	43.60	43.60	Somatic	0.000	305	224	42.34	42.34	Somatic	0.000	1
4	22,362,173	A	G	GBA3		3	intronic		1156	44	3.67	896	834	48.21	48.21	Somatic	0.000	371	366	49.66	49.66	Somatic	0.000	1
4	29,185,860	G	A		0	3		0	304	11	3.49	536	498	48.16	48.16	Somatic	0.000	344	313	47.64	47.64	Somatic	0.000	1
4	29,629,786	G	A		0	3		0	397	3	0.75	378	266	41.30	41.30	Somatic	0.000	273	199	42.16	42.16	Somatic	0.000	1
4	31,623,175	A	G	LOC100133713		3	5_prime_flanking_region		246	15	5.75	264	253	48.94	48.94	Somatic	0.000	316	315	49.92	49.92	Somatic	0.000	1
4	32,768,631	G	A		0	3		0	398	15	3.63	653	505	43.61	43.61	Somatic	0.000	307	268	46.61	46.61	Somatic	0.000	1
4	36,443,632	T	A		0	3		0	374	16	4.10	365	341	48.30	48.30	Somatic	0.000	382	293	43.41	43.41	Somatic	0.000	1
4	43,458,657	C	T		0	3		0	104	3	2.80	138	88	38.94	38.94	Somatic	0.000	209	186	47.09	47.09	Somatic	0.000	1
4	44,155,349	C	T	KCTD8		3	5_prime_flanking_region		1221	18	1.45	614	514	45.57	45.57	Somatic	0.000	437	365	45.51	45.51	Somatic	0.000	1
4	63,541,472	C	A		0	3		0	268	1	0.37	410	315	43.45	43.45	Somatic	0.000	287	221	43.50	43.50	Somatic	0.000	1
4	77,073,409	T	C	NAAA		3	intronic		79	2	2.47	57	55	49.11	49.11	Somatic	0.000	188	147	43.88	43.88	Somatic	0.000	1
4	86,518,791	A	C		0	2		0	805	62	7.15	574	503	46.70	46.70	Somatic	0.000	410	346	45.77	45.77	Somatic	0.000	1
4	110,783,030	T	G	CCDC109B		2	intronic		784	63	7.44	1497	250	14.31	14.31	Somatic	0.000	512	201	28.19	28.19	Somatic	0.000	0
4	112,604,557	G	A		0	3		0	193	7	3.50	418	416	49.88	49.88	Somatic	0.000	263	226	46.22	46.22	Somatic	0.000	1
4	118,188,338	A	G	TRAM1L1		3	3_prime_flanking_region		551	32	5.49	392	397	50.32	50.32	Somatic	0.000	297	263	46.96	46.96	Somatic	0.000	1
4	125,746,802	G	A		0	3		0	372	9	2.36	677	499	42.43	42.43	Somatic	0.000	295	220	42.72	42.72	Somatic	0.000	1
4	126,682,546	A	T	FAT4		3	3_prime_flanking_region		561	15	2.60	506	477	48.52	48.52	Somatic	0.000	424	431	50.41	50.41	Somatic	0.000	1
4	128,277,343	C	T		0	3		0	637	24	3.63	843	699	45.33	45.33	Somatic	0.000	360	347	49.08	49.08	Somatic	0.000	1
4	132,318,397	C	T		0	3		0	273	10	3.53	410	324	44.14	44.14	Somatic	0.000	336	205	37.89	37.89	Somatic	0.000	0
4	136,046,582	T	A	LOC646272		3	5_prime_flanking_region		585	12	2.01	456	243	34.76	34.76	Somatic	0.000	281	234	45.44	45.44	Somatic	0.000	0
4	136,492,542	G	A	ENSG00000207188		3	5_prime_flanking_region		62	2	3.13	182	130	41.67	41.67	Somatic	0.000	183	145	44.21	44.21	Somatic	0.000	1
4	137,716,185	C	T		0	2		0	400	14	3.38	269	229	45.98	45.98	Somatic	0.000	293	273	48.23	48.23	Somatic	0.000	1
4	139,423,585	T	A	SLC7A11		2	5_prime_flanking_region		46	1	2.13	57	61	51.69	51.69	Somatic	0.000	39	30	43.48	43.48	Somatic	0.000	1
4	145,369,376	C	T		0	3		0	473	21	4.25	375	302	44.61	44.61	Somatic	0.000	252	213	45.81	45.81	Somatic	0.000	1
4	146,313,010	T	C	OTUD4		3	intronic		335	15	4.29	387	429	52.57	52.57	Somatic	0.000	306	326	51.58	51.58	Somatic	0.000	1
4	155,766,017	C	T	FGA		3	5_prime_flanking_region		693	13	1.84	661	581	46.78	46.78	Somatic	0.000	433	395	47.71	47.71	Somatic	0.000	1
4	161,787,610	C	T		0	3		0	830	36	4.16	742	574	43.62	43.62	Somatic	0.000	458	402	46.74	46.74	Somatic	0.000	1
4	171,548,377	A	G		0	3		0	444	19	4.10	409	400	49.44	49.44	Somatic	0.000	393	359	47.74	47.74	Somatic	0.000	1
4	176,093,925	C	T	ADAM29		3	intronic		401	15	3.61	577	444	43.49	43.49	Somatic	0.000	300	268	47.18	47.18	Somatic	0.000	1
4	182,035,355	T	C		0	3		0	333	8	2.35	436	325	42.71	42.71	Somatic	0.000	354	263	42.63	42.63	Somatic	0.000	1
4	182,931,532	C	T	LOC728191		3	3_prime_flanking_region		542	22	3.90	1257	1076	46.12	46.12	Somatic	0.000	446	364	44.94	44.94	Somatic	0.000	1
4	187,888,928	A	C	FAT1		3	5_prime_flanking_region		399	18	4.32	311	39	11.14	11.14	Somatic	0.034	613	184	23.09	23.09	Somatic	0.000	0
4	189,659,093	G	A		0	2		0	494	22	4.26	221	233	51.32	51.32	Somatic	0.000	344	320	48.19	48.19	Somatic	0.000	1
5	2,764,759	C	A	C5orf38		3	5_prime_flanking_region		245	6	2.39	232	198	46.05	46.05	Somatic	0.000	185	145	43.94	43.94	Somatic	0.000	1
5	3,143,761	G	A		0	3		0	379	10	2.57	159	235	59.64	59.64	Somatic	0.000	102	125	55.07	55.07	Somatic	0.000	0
5	6,867,720	G	A	ENSG00000200243		3	3_prime_flanking_region		675	17	2.46	618	516	45.50	45.50	Somatic	0.000	336	322	48.94	48.94	Somatic	0.000	1
5	7,536,758	C	T	ADCY2		2	intronic		1132	25	2.16	587	536	47.73	47.73	Somatic	0.000	303	258	45.99	45.99	Somatic	0.000	1
5	8,137,295	C	T		0	3		0	713	23	3.13	459	414	47.42	47.42	Somatic	0.000	196	162	45.25	45.25	Somatic	0.000	1
5	24,473,965	T	C	CDH10		3	3_prime_flanking_region		299	0	0.00	803	23	2.78	2.78	Somatic	0.001	518	148	22.22	22.22	Somatic	0.000	2
5	41,377,755	G	A	PLCXD3		3	intronic		699	20	2.78	1125	1049	48.25	48.25	Somatic	0.000	472	459	49.30	49.30	Somatic	0.000	1
5	50,152,869	C	G	PARP8		1	missense		785	14	1.75	1414	59	4.01	4.01	Somatic	0.016	635	201	24.04	24.04	Somatic	0.000	2
5	50,184,608	C	T	PARP8		3	3_prime_flanking_region		857	42	4.67	747	596	44.38	44.38	Somatic	0.000	399	293	42.34	42.34	Somatic	0.000	1

5	51,503,256	G	A		0	2		0	571	25	4.19	523	486	48.17	48.17	Somatic	0.000	358	330	47.97	47.97	Somatic	0.000	1
5	68,314,881	T	A	ENSG00000222762		3	5_prime_flanking_region		328	16	4.65	679	591	46.54	46.54	Somatic	0.000	300	285	48.72	48.72	Somatic	0.000	1
5	71,888,102	G	A	ZNF366		2	5_prime_flanking_region		549	16	2.83	444	345	43.73	43.73	Somatic	0.000	301	254	45.77	45.77	Somatic	0.000	1
5	89,673,080	A	T		0	3		0	302	18	5.63	341	327	48.95	48.95	Somatic	0.000	258	234	47.56	47.56	Somatic	0.000	1
5	92,816,744	G	A		0	3		0	499	17	3.29	423	349	45.21	45.21	Somatic	0.000	382	338	46.94	46.94	Somatic	0.000	1
5	96,065,480	A	G	CAST		2	intronic		278	5	1.77	255	251	49.60	49.60	Somatic	0.000	320	325	50.39	50.39	Somatic	0.000	1
5	100,118,060	T	C	ENSG00000207269		3	3_prime_flanking_region		504	17	3.26	343	326	48.73	48.73	Somatic	0.000	346	311	47.34	47.34	Somatic	0.000	1
5	113,227,599	C	T		0	3		0	624	28	4.29	663	547	45.21	45.21	Somatic	0.000	322	306	48.73	48.73	Somatic	0.000	1
5	117,884,100	G	A		0	3		0	782	0	0.00	1820	51	2.73	2.73	Somatic	0.000	714	194	21.37	21.37	Somatic	0.000	2
5	123,015,301	C	T	ENSG00000208978		3	5_prime_flanking_region		815	26	3.09	821	687	45.56	45.56	Somatic	0.000	406	335	45.21	45.21	Somatic	0.000	1
5	123,877,689	C	T		0	2		0	313	12	3.69	172	122	41.50	41.50	Somatic	0.000	280	234	45.53	45.53	Somatic	0.000	1
5	132,897,276	C	T	FSTL4		3	intronic		595	16	2.62	922	804	46.58	46.58	Somatic	0.000	433	360	45.40	45.40	Somatic	0.000	1
5	140,439,825	T	C	PCDHB2		3	5_prime_flanking_region		349	13	3.59	250	186	42.66	42.66	Somatic	0.000	384	359	48.32	48.32	Somatic	0.000	1
5	140,469,201	G	T	PCDHB5		3	5_prime_flanking_region		1075	33	2.98	195	146	42.82	42.82	Somatic	0.000	383	345	47.39	47.39	Somatic	0.000	1
5	147,696,652	G	A	SPINK9		3	intronic		530	18	3.28	665	573	46.28	46.28	Somatic	0.000	342	353	50.79	50.79	Somatic	0.000	1
5	148,880,083	T	G	CSNK1A1		1	missense		531	13	2.39	473	450	48.75	48.75	Somatic	0.000	379	326	46.24	46.24	Somatic	0.000	1
5	149,525,443	T	C	PDGFRB		3	5_prime_flanking_region		262	4	1.50	172	7	3.91	3.91	Somatic	0.168	529	106	16.69	16.69	Somatic	0.000	0
5	160,513,086	G	A		0	3		0	327	17	4.94	238	183	43.47	43.47	Somatic	0.000	295	251	45.97	45.97	Somatic	0.000	1
5	162,193,041	C	A	ENSG00000208481		3	3_prime_flanking_region		452	5	1.09	433	333	43.47	43.47	Somatic	0.000	325	250	43.48	43.48	Somatic	0.000	1
5	164,071,958	G	A		0	3		0	576	18	3.03	581	494	45.95	45.95	Somatic	0.000	417	415	49.88	49.88	Somatic	0.000	1
5	165,820,268	C	A		0	3		0	790	37	4.47	768	743	49.17	49.17	Somatic	0.000	456	454	49.89	49.89	Somatic	0.000	1
5	166,002,175	C	A		0	2		0	561	17	2.94	586	460	43.98	43.98	Somatic	0.000	372	328	46.86	46.86	Somatic	0.000	1
6	900,039	T	C	LOC730397		3	5_prime_flanking_region		304	12	3.80	399	400	50.06	50.06	Somatic	0.000	347	276	44.30	44.30	Somatic	0.000	1
6	5,996,224	G	A	NRN1		3	5_prime_flanking_region		606	15	2.42	517	562	52.09	52.09	Somatic	0.000	360	294	44.95	44.95	Somatic	0.000	1
6	6,260,424	C	T	F13A1		3	intronic		483	12	2.42	404	344	45.99	45.99	Somatic	0.000	411	402	49.45	49.45	Somatic	0.000	1
6	9,584,137	C	T		0	2		0	1427	97	6.36	962	905	48.47	48.47	Somatic	0.000	503	470	48.30	48.30	Somatic	0.000	1
6	12,118,719	G	T	HIVEP1		2	5_prime_flanking_region		246	6	2.38	261	208	44.35	44.35	Somatic	0.000	307	287	48.32	48.32	Somatic	0.000	1
6	23,624,936	C	T		0	3		0	163	6	3.55	224	220	49.55	49.55	Somatic	0.000	260	216	45.38	45.38	Somatic	0.000	1
6	33,967,359	C	G	LOC100132252		3	3_prime_flanking_region		268	15	5.30	89	94	51.37	51.37	Somatic	0.000	336	269	44.46	44.46	Somatic	0.000	1
6	44,532,555	C	T	LOC100128935		2	5_prime_flanking_region		483	26	5.11	392	336	46.15	46.15	Somatic	0.000	224	227	50.33	50.33	Somatic	0.000	1
6	45,133,962	A	C	SUPT3H		3	intronic		492	21	4.09	783	649	45.32	45.32	Somatic	0.000	339	274	44.70	44.70	Somatic	0.000	1
6	51,440,235	T	C	ENSG00000212532		3	3_prime_flanking_region		396	14	3.41	349	277	44.25	44.25	Somatic	0.000	253	201	44.27	44.27	Somatic	0.000	1
6	54,067,267	T	G	C6orf142		3	intronic		287	19	6.21	253	215	45.94	45.94	Somatic	0.000	266	225	45.82	45.82	Somatic	0.000	1
6	77,277,763	C	T	LOC643281		3	3_prime_flanking_region		175	10	5.41	278	276	49.82	49.82	Somatic	0.000	290	230	44.23	44.23	Somatic	0.000	1
6	85,673,094	G	A		0	3		0	621	7	1.11	566	546	49.10	49.10	Somatic	0.000	226	210	48.17	48.17	Somatic	0.000	1
6	89,065,419	C	T	ENSG00000220267		3	5_prime_flanking_region		980	46	4.48	928	868	48.33	48.33	Somatic	0.000	448	432	49.09	49.09	Somatic	0.000	1
6	91,891,502	G	T		0	2		0	786	31	3.79	644	494	43.41	43.41	Somatic	0.000	367	338	47.94	47.94	Somatic	0.000	1
6	95,400,882	C	T		0	3		0	632	0	0.00	864	14	1.59	1.59	Somatic	0.000	499	115	18.73	18.73	Somatic	0.000	2
6	105,713,110	C	A	POPDC3		1	missense		174	8	4.40	175	138	44.09	44.09	Somatic	0.000	246	211	46.17	46.17	Somatic	0.000	1
6	113,767,508	C	T		0	3		0	821	5	0.61	745	615	45.22	45.22	Somatic	0.000	362	266	42.36	42.36	Somatic	0.000	1
6	125,900,869	G	A		0	3		0	400	3	0.74	341	254	42.69	42.69	Somatic	0.000	344	263	43.33	43.33	Somatic	0.000	1
6	133,329,889	T	C	ENSG00000213122		3	3_prime_flanking_region		244	8	3.17	447	370	45.29	45.29	Somatic	0.000	262	208	44.26	44.26	Somatic	0.000	1
6	134,376,650	C	G	SLC2A12		3	intronic		325	10	2.99	522	379	42.06	42.06	Somatic	0.000	264	250	48.64	48.64	Somatic	0.000	1
6	135,937,118	C	T	ENSG00000213112		3	3_prime_flanking_region		383	8	2.05	413	364	46.85	46.85	Somatic	0.000	346	292	45.77	45.77	Somatic	0.000	1
6	137,632,989	G	A		0	3		0	677	32	4.51	363	305	45.66	45.66	Somatic	0.000	220	246	52.79	52.79	Somatic	0.000	1
6	138,308,151	T	C	ENSG00000219463		3	5_prime_flanking_region		1695	93	5.20	1166	1159	49.85	49.85	Somatic	0.000	404	436	51.90	51.90	Somatic	0.000	1
6	146,176,900	G	T	FBXO30		2	intronic		415	8	1.89	492	391	44.28	44.28	Somatic	0.000	378	325	46.23	46.23	Somatic	0.000	1
6	150,184,625	C	T	LRP11		2	intronic		389	8	2.02	320	271	45.85	45.85	Somatic	0.000	316	309	49.44	49.44	Somatic	0.000	1
6	162,878,522	C	T	PARK2		3	intronic		690	17	2.40	561	488	46.52	46.52	Somatic	0.000	384	322	45.61	45.61	Somatic	0.000	1
6	166,045,320	A	G	PDE10A		3	5_prime_flanking_region		171	8	4.47	79	60	43.17	43.17	Somatic	0.000	344	334	49.26	49.26	Somatic	0.000	1
7	14,766,804	G	A	DGKB		3	intronic		311	3	0.96	435	376	46.36	46.36	Somatic	0.000	398	285	41.73	41.73	Somatic	0.000	1
7	19,322,718	C	T		0	3		0	325	16	4.69	236	195	45.24	45.24	Somatic	0.000	243	197	44.77	44.77	Somatic	0.000	1
7	23,245,489	G	A	GPNMB		2	5_prime_flanking_region		1053	56	5.05	409	367	47.29	47.29	Somatic	0.000	249	249	50.00	50.00	Somatic	0.000	1
7	40,891,373	G	A	C7orf10		3	3_prime_flanking_region		374	15	3.86	405	346	46.07	46.07	Somatic	0.000	342	327	48.88	48.88	Somatic	0.000	1
7	41,710,975	T	C	INHBA		2	5_prime_flanking_region		633	48	7.05	375	318	45.89	45.89	Somatic	0.000	287	309	51.85	51.85	Somatic	0.000	1
7	42,368,306	C	T		0	3		0	866	27	3.02	604	436	41.92	41.92	Somatic	0.000	385	303	44.04	44.04	Somatic	0.000	1
7	44,255,955	C	T	CAMK2B		2	intronic		305	0	0.00	200	5	2.44	2.44	Somatic	0.040	460	118	20.42	20.42	Somatic	0.000	2
7	49,636,687	C	T		0	3		0	830	30	3.49	1210	1124	48.16	48.16	Somatic	0.000	395	304	43.49	43.49	Somatic	0.000	1
7	50,762,444	A	G	GRB10		3	intronic		608	2	0.33	709	17	2.34	2.34	Somatic	0.001	482	124	20.46	20.46	Somatic	0.000	2
7	51,944,112	C	A		0	3		0	710	0	0.00	789	45	5.40	5.40	Somatic	0.000	433	156	26.49	26.49	Somatic	0.000	0
7	67,497,348	G	A		0	3		0	680	17	2.44	515	483	48.40	48.40	Somatic	0.000	380	354	48.23	48.23	Somatic	0.000	1
7	91,954,454	T	C	PEX1		3	3_prime_untranslated_region		116	2	1.69	293	322	52.36	52.36	Somatic	0.000	170	161	48.64	48.64	Somatic	0.000	1
7	104,632,275	C	A	SRPK2		3	intronic		949	50	5.01	723	643	47.07	47.07	Somatic	0.000	313	280	47.22	47.22	Somatic	0.000	1
7	112,616,563	T	G		0	3		0	579	13	2.20	505	580	53.46	53.46	Somatic	0.000	353	298	45.78	45.78	Somatic	0.000	1
7	113,764,441	G	A	ENSG00000218695		2	5_prime_flanking_region		191	7	3.54	237	156	39.69	39.69	Somatic	0.000	283	248	46.70	46.70	Somatic	0.000	1
7	117,410,969	A	G		0	3		0	353	9	2.49	186	189	50.40	50.40	Somatic	0.000	286	303	51.44	51.44	Somatic	0.000	1
7	119,505,592	A	T		0	3		0	336	15	4.27	296	262	46.95	46.95	Somatic	0.000	151	128	45.88	45.88	Somatic	0.000	1
7	121,622,431	C	T	RPL31P37		3	5_prime_flanking_region		540	6	1.10	509	63	11.01	11.01	Somatic	0.000	274	110	28.65	28.65	Somatic	0.000	0
7	121,918,102	T	C	CADPS2		3	intronic		63	0	0.00	442	11	2.43	2.43	Somatic	0.185	199	55	21.65	21.65	Somatic	0.000	2
7	122,805,962	C	A		0	3		0	533	7	1.30	859	11	1.26	1.26	Somatic	0.665	534	151	22.04	22.04	Somatic	0.003	2
7	125,918,641	C	T	GRM8		2	intronic		255	12	4.49	233	214	47.87	47.87	Somatic	0.000	294	286	49.31	49.31	Somatic	0.000	1
7	126,071,188	T	C	GRM8		3	intronic		1063	68	6.01	942	797	45.83	45.83	Somatic	0.000	443	407	47.88	47.88	Somatic	0.000	1
7	145,918,106	C	T	CNTNAP2		3	intronic		1029	95	8.45	801	614	43.39	43.39	Somatic	0.000	379	309	44.91	44.91	Somatic	0.000	1
7	152,588,820	T	A		0	3		0	1246	40	3.11	961	806	45.61	45.61	Somatic	0.000	424	373	46.80	46.80	Somatic	0.000	1
7	157,961,948	G	T	PTPRN2		2	intronic		364	10	2.67	99	93	48.44	48.44	Somatic	0.000	381	339	47.08	47.08	Somatic	0.000	1
8	2,557,154	G	A		0	3		0	817	43	5.00	367	310	45.79	45.79	Somatic	0.000	331	322	49.31	49.31	Somatic	0.000	1
8	4,037,718	G	A	CSMD1		3	intronic		594	16	2.62	538	593	52.43	52.43	Somatic	0.000	447	376	45.69	45.69	Somatic	0.000	1
8	10,585,716	C	A	C8orf74		3	intronic		261	9	3.33	84	63	42.86	42.86	Somatic	0.000	172	148	46.25	46.25	Somatic	0.000	1
8	12,961,660	G	A	DLC1		2	3_prime_flanking_region		758	59	7.22	295	298	50.25	50.25	Somatic	0.000	335	292	46.57	46.57	Somatic	0.000	1
8	25,752,625	G	A	EBF2		3	3_prime_flanking_region		1428	32	2.19	653	533	44.94	44.94	Somatic	0.000	372	314	45.77	45.77	Somatic	0.000	1

8	36,228,367	G	A	ENSG00000210631		3	5_prime_flanking_region		451	20	4.25	704	599	45.97	45.97	Somatic	0.000	296	244	45.19	45.19	Somatic	0.000	1
8	39,742,880	T	A	ADAM2		3	intronic		210	11	4.98	404	287	41.53	41.53	Somatic	0.000	284	204	41.80	41.80	Somatic	0.000	1
8	52,586,888	C	T	PXDNL		3	intronic		1045	33	3.06	530	504	48.74	48.74	Somatic	0.000	400	377	48.52	48.52	Somatic	0.000	1
8	66,534,946	A	T		0	2		0	905	44	4.64	590	493	45.52	45.52	Somatic	0.000	461	403	46.64	46.64	Somatic	0.000	1
8	68,491,540	A	G	CPA6		3	3_prime_flanking_region		61	2	3.17	118	116	49.57	49.57	Somatic	0.000	225	215	48.86	48.86	Somatic	0.000	1
8	70,103,300	G	A	LOC100129096		2	intronic		143	1	0.69	254	203	44.42	44.42	Somatic	0.000	315	281	47.15	47.15	Somatic	0.000	1
8	75,925,059	T	C	PI15		3	3_prime_untranslated_region		440	16	3.51	391	388	49.81	49.81	Somatic	0.000	321	344	51.73	51.73	Somatic	0.000	1
8	77,914,894	C	G	ZFHX4		2	intronic		506	16	3.07	801	781	49.37	49.37	Somatic	0.000	258	286	52.57	52.57	Somatic	0.000	1
8	84,408,136	G	A		0	3		0	634	45	6.63	758	690	47.65	47.65	Somatic	0.000	459	428	48.25	48.25	Somatic	0.000	1
8	85,565,386	G	A	RALYL		3	intronic		618	34	5.21	414	382	47.99	47.99	Somatic	0.000	184	179	49.31	49.31	Somatic	0.000	1
8	86,568,817	T	G	CA2		3	intronic		202	18	8.18	192	196	50.52	50.52	Somatic	0.000	267	262	49.53	49.53	Somatic	0.000	1
8	87,836,982	T	A	CNGB3		3	5_prime_flanking_region		424	13	2.97	319	190	37.33	37.33	Somatic	0.000	287	238	45.33	45.33	Somatic	0.000	1
8	88,641,249	C	T		0	3		0	641	13	1.99	753	711	48.57	48.57	Somatic	0.000	330	272	45.18	45.18	Somatic	0.000	1
8	90,190,284	C	T		0	3		0	308	6	1.91	326	252	43.60	43.60	Somatic	0.000	281	241	46.17	46.17	Somatic	0.000	1
8	93,512,629	G	A		0	3		0	537	11	2.01	231	218	48.55	48.55	Somatic	0.000	353	311	46.84	46.84	Somatic	0.000	1
8	94,755,932	G	A	FAM92A1		3	5_prime_flanking_region		356	6	1.66	416	387	48.19	48.19	Somatic	0.000	427	335	43.96	43.96	Somatic	0.000	1
8	111,759,719	C	G		0	3		0	368	5	1.34	436	457	51.18	51.18	Somatic	0.000	320	301	48.47	48.47	Somatic	0.000	1
8	115,838,142	G	A		0	3		0	315	16	4.83	432	316	42.25	42.25	Somatic	0.000	330	298	47.45	47.45	Somatic	0.000	1
8	128,300,749	C	T		0	2		0	1013	18	1.75	873	773	46.96	46.96	Somatic	0.000	422	347	45.12	45.12	Somatic	0.000	1
8	129,958,522	A	G		0	2		0	437	20	4.38	416	356	46.11	46.11	Somatic	0.000	411	400	49.32	49.32	Somatic	0.000	1
8	131,851,617	C	T	ADCY8		3	3_prime_flanking_region		1767	45	2.48	1215	1061	46.62	46.62	Somatic	0.000	465	418	47.34	47.34	Somatic	0.000	1
8	139,813,942	G	A	COL22A1		3	intronic		1021	50	4.67	352	348	49.71	49.71	Somatic	0.000	310	299	49.10	49.10	Somatic	0.000	1
8	142,815,582	G	A		0	3		0	140	4	2.78	62	57	47.90	47.90	Somatic	0.000	245	256	51.10	51.10	Somatic	0.000	1
8	143,778,000	A	C	LY6K		2	5_prime_flanking_region		219	31	12.40	100	32	24.24	24.24	Somatic	0.296	310	314	50.32	50.32	Somatic	0.000	0
9	7,463,965	A	G	LOC158345		3	3_prime_flanking_region		876	40	4.37	815	743	47.69	47.69	Somatic	0.000	412	366	47.04	47.04	Somatic	0.000	1
9	9,091,885	C	T	PTPRD		3	intronic		59	0	0.00	78	72	48.00	48.00	Somatic	0.000	158	126	44.37	44.37	Somatic	0.000	1
9	24,383,946	T	C		0	3		0	403	31	7.14	439	368	45.60	45.60	Somatic	0.000	268	268	50.00	50.00	Somatic	0.000	1
9	25,082,867	C	T	ENSG00000222693		3	5_prime_flanking_region		283	15	5.03	439	392	47.17	47.17	Somatic	0.000	318	282	47.00	47.00	Somatic	0.000	1
9	26,311,659	C	T		0	3		0	712	20	2.73	527	407	43.58	43.58	Somatic	0.000	348	280	44.59	44.59	Somatic	0.000	1
9	28,033,354	A	G	LINGO2		3	intronic		1342	56	4.01	793	709	47.20	47.20	Somatic	0.000	395	303	43.41	43.41	Somatic	0.000	1
9	30,430,017	C	A		0	2		0	318	12	3.64	602	528	46.73	46.73	Somatic	0.000	339	220	39.36	39.36	Somatic	0.000	0
9	30,927,679	C	T	ENSG00000214020		2	3_prime_flanking_region		370	10	2.63	361	308	46.04	46.04	Somatic	0.000	296	261	46.86	46.86	Somatic	0.000	1
9	32,208,802	T	C		0	3		0	182	6	3.19	363	299	45.17	45.17	Somatic	0.000	322	290	47.39	47.39	Somatic	0.000	1
9	35,669,773	G	A	CA9		3	intronic		603	16	2.58	57	56	49.56	49.56	Somatic	0.000	184	173	48.46	48.46	Somatic	0.000	1
9	36,409,304	T	A	RNF38		3	5_prime_flanking_region		601	8	1.31	443	279	38.64	38.64	Somatic	0.000	385	311	44.68	44.68	Somatic	0.000	1
9	67,834,918	C	T	ENSG00000219957		3	5_prime_flanking_region		369	6	1.60	327	279	46.04	46.04	Somatic	0.000	240	226	48.50	48.50	Somatic	0.000	1
9	89,535,224	T	G	CTSL1		1	missense		378	6	1.56	303	20	6.19	6.19	Somatic	0.170	487	126	20.55	20.55	Somatic	0.000	0
9	90,908,623	G	A	SHC3		2	intronic		1897	92	4.63	1469	1258	46.13	46.13	Somatic	0.000	414	390	48.51	48.51	Somatic	0.000	1
9	97,330,168	C	T	PTCH1		3	5_prime_flanking_region		787	22	2.72	351	288	45.07	45.07	Somatic	0.000	315	264	45.60	45.60	Somatic	0.000	1
9	100,197,933	C	T	GABBR2		3	intronic		406	5	1.22	127	89	41.20	41.20	Somatic	0.000	207	180	46.51	46.51	Somatic	0.000	1
9	100,343,785	A	G	GABBR2		3	intronic		1249	25	1.96	748	734	49.53	49.53	Somatic	0.000	476	449	48.54	48.54	Somatic	0.000	1
9	105,224,758	G	A		0	3		0	359	13	3.49	450	336	42.75	42.75	Somatic	0.000	342	284	45.37	45.37	Somatic	0.000	1
9	109,348,264	G	C	ENSG00000216493		3	5_prime_flanking_region		780	11	1.39	326	301	48.01	48.01	Somatic	0.000	383	339	46.95	46.95	Somatic	0.000	1
9	122,056,927	G	A	MIRN147		3	5_prime_flanking_region		794	48	5.70	464	400	46.30	46.30	Somatic	0.000	314	277	46.87	46.87	Somatic	0.000	1
9	122,561,326	T	C	FBXW2		3	3_prime_untranslated_region		393	12	2.96	316	271	46.17	46.17	Somatic	0.000	310	318	50.64	50.64	Somatic	0.000	1
9	131,535,363	A	T	PRRX2		3	3_prime_flanking_region		136	10	6.85	31	27	46.55	46.55	Somatic	0.000	192	176	47.83	47.83	Somatic	0.000	1
9	133,745,510	T	A	MED27		3	intronic		313	9	2.80	226	197	46.57	46.57	Somatic	0.000	330	249	43.01	43.01	Somatic	0.000	1
9	136,875,556	G	A	COL5A1		3	3_prime_untranslated_region		468	13	2.70	64	39	37.86	37.86	Somatic	0.000	199	174	46.65	46.65	Somatic	0.000	1
9	138,867,831	C	T	MAMDC4		1	silent		15	1	6.25	38	25	39.68	39.68	Somatic	0.012	217	186	46.15	46.15	Somatic	0.001	1
10	3,603,767	C	T	LOC100134102		3	5_prime_flanking_region		415	15	3.49	289	212	42.32	42.32	Somatic	0.000	302	273	47.48	47.48	Somatic	0.000	1
10	4,156,953	T	G	LOC731787		3	3_prime_flanking_region		494	12	2.37	1854	63	3.29	3.29	Somatic	0.475	411	119	22.45	22.45	Somatic	0.000	2
10	11,030,362	C	T		0	3		0	998	37	3.57	675	641	48.71	48.71	Somatic	0.000	335	257	43.41	43.41	Somatic	0.000	1
10	11,670,740	C	A	USP6NL		3	intronic		249	6	2.35	368	252	40.65	40.65	Somatic	0.000	251	187	42.69	42.69	Somatic	0.000	1
10	12,214,774	C	T	SEC61A2		3	intronic		525	17	3.14	311	281	47.47	47.47	Somatic	0.000	316	290	47.85	47.85	Somatic	0.000	1
10	14,654,478	A	C	FAM107B		3	intronic		473	9	1.87	1121	869	43.67	43.67	Somatic	0.000	386	324	45.63	45.63	Somatic	0.000	1
10	19,373,250	T	G	LOC100130846		3	5_prime_flanking_region		326	15	4.40	265	217	45.02	45.02	Somatic	0.000	268	237	46.93	46.93	Somatic	0.000	1
10	21,300,024	C	A	NEBL		2	intronic		186	6	3.13	564	454	44.60	44.60	Somatic	0.000	289	243	45.68	45.68	Somatic	0.000	1
10	34,032,764	G	A		0	3		0	658	18	2.66	727	617	45.91	45.91	Somatic	0.000	447	412	47.96	47.96	Somatic	0.000	1
10	45,273,565	G	A	MARCH8		3	3_prime_untranslated_region		558	3	0.53	706	9	1.26	1.26	Somatic	0.323	500	118	19.09	19.09	Somatic	0.000	2
10	46,461,650	G	A	PPYR1		2	5_prime_flanking_region		443	4	0.89	1284	13	1.00	1.00	Somatic	0.536	902	61	6.33	6.33	Somatic	0.000	0
10	48,121,263	G	A	ENSG00000221361		3	5_prime_flanking_region		717	32	4.27	307	215	41.19	41.19	Somatic	0.000	305	299	49.50	49.50	Somatic	0.000	1
10	58,815,611	G	A		0	3		0	243	3	1.22	371	289	43.79	43.79	Somatic	0.000	323	289	47.22	47.22	Somatic	0.000	1
10	59,817,876	G	C	TFAM		3	intronic		198	0	0.00	316	8	2.47	2.47	Somatic	0.021	404	94	18.88	18.88	Somatic	0.000	2
10	65,639,660	C	T	LOC100129267		3	5_prime_flanking_region		509	22	4.14	665	596	47.26	47.26	Somatic	0.000	453	399	46.83	46.83	Somatic	0.000	1
10	82,288,101	G	A	SH2D4B		1	missense		183	1	0.54	445	13	2.84	2.84	Somatic	0.056	416	103	19.85	19.85	Somatic	0.000	2
10	91,891,008	T	G	ENSG00000222451		2	3_prime_flanking_region		377	16	4.07	491	56	10.24	10.24	Somatic	0.111	397	140	26.07	26.07	Somatic	0.000	0
10	100,872,010	T	C	HPSE2		3	intronic		43	0	0.00	180	4	2.17	2.17	Somatic	0.423	149	48	24.37	24.37	Somatic	0.000	2
10	106,996,776	C	A	SORCS3		3	intronic		502	14	2.71	390	343	46.79	46.79	Somatic	0.000	388	367	48.61	48.61	Somatic	0.000	1
10	118,418,794	A	G	C10orf82		3	intronic		296	15	4.82	185	180	49.32	49.32	Somatic	0.000	225	195	46.43	46.43	Somatic	0.000	1
10	121,026,998	A	C	GRK5		3	intronic		638	55	7.94	451	85	15.86	15.86	Somatic	0.008	247	168	40.48	40.48	Somatic	0.000	0
10	122,679,947	C	T	BRWD2		3	3_prime_flanking_region		526	14	2.59	534	455	46.01	46.01	Somatic	0.000	424	369	46.53	46.53	Somatic	0.000	1
10	131,344,480	G	A	MGMT		3	intronic		917	22	2.34	294	264	47.31	47.31	Somatic	0.000	287	294	50.60	50.60	Somatic	0.000	1
10	132,932,645	C	T	TCERG1L		3	intronic		431	15	3.36	201	170	45.82	45.82	Somatic	0.000	243	196	44.65	44.65	Somatic	0.000	1
10	133,590,997	C	G	PPP2R2D		3	5_prime_flanking_region		678	38	5.31	344	370	51.82	51.82	Somatic	0.000	293	274	48.32	48.32	Somatic	0.000	1
11	9,492,873	A	G	ZNF143		3	intronic		1415	23	1.60	986	32	3.14	3.14	Somatic	0.281	616	124	16.76	16.76	Somatic	0.000	0
11	12,198,538	C	G	MICAL2		1	missense		578	15	2.53	507	19	3.61	3.61	Somatic	0.416	474	63	11.73	11.73	Somatic	0.006	0
11	12,297,694	T	G	MICALCL		2	intronic		468	36	7.14	648	119	15.51	15.51	Somatic	0.003	316	98	23.67	23.67	Somatic	0.000	0
11	22,340,860	G	T	SLC17A6		1	splice_site		741	11	1.46	556	443	44.34	44.34	Somatic	0.000	386	337	46.61	46.61	Somatic	0.000	1
11	24,275,763	C	T		0	3		0	342	11	3.12	405	312	43.51	43.51	Somatic	0.000	282	241	46.08	46.08	Somatic	0.000	1
11	27,187,819	C	G		0	2		0	1307	66	4.81	597	491	45.13	45.13	Somatic	0.000	375	286	43.27	43.27	Somatic	0.000	1

11	30,881,639	A	G	DCDC5		1	silent		400	9	2.20	643	545	45.88	45.88	Somatic	0.000	357	320	47.27	47.27	Somatic	0.000	1
11	65,523,582	C	G	EIF1AD		3	intronic		1168	28	2.34	273	230	45.73	45.73	Somatic	0.000	371	376	50.33	50.33	Somatic	0.000	1
11	70,869,608	G	A	NADSYN1		3	intronic		205	12	5.53	104	114	52.29	52.29	Somatic	0.000	278	239	46.23	46.23	Somatic	0.000	1
11	88,164,936	A	T	GRM5		3	intronic		334	11	3.19	412	363	46.84	46.84	Somatic	0.000	246	235	48.86	48.86	Somatic	0.000	1
11	96,540,220	G	A		0	3		0	750	0	0.00	1293	25	1.90	1.90	Somatic	0.000	567	133	19.00	19.00	Somatic	0.000	2
11	118,994,585	G	T	ENSG00000199217		3	5_prime_flanking_region		464	6	1.28	107	70	39.55	39.55	Somatic	0.000	316	287	47.60	47.60	Somatic	0.000	1
11	124,600,145	C	T	PKNOX2		2	intronic		1980	71	3.46	380	334	46.78	46.78	Somatic	0.000	287	259	47.44	47.44	Somatic	0.000	1
12	7,610,680	C	T	LOC100134191		2	3_prime_flanking_region		941	26	2.69	706	562	44.32	44.32	Somatic	0.000	246	253	50.70	50.70	Somatic	0.000	1
12	10,740,491	A	G	STYK1		3	5_prime_flanking_region		947	35	3.56	610	477	43.88	43.88	Somatic	0.000	315	367	53.81	53.81	Somatic	0.000	1
12	40,159,842	G	C	PDZRN4		3	intronic		864	29	3.25	491	446	47.60	47.60	Somatic	0.000	386	359	48.19	48.19	Somatic	0.000	1
12	56,424,837	C	T	TSPAN31		2	5_prime_flanking_region		320	14	4.19	105	102	49.28	49.28	Somatic	0.000	208	170	44.97	44.97	Somatic	0.000	1
12	71,706,640	T	C		0	3		0	395	16	3.89	663	563	45.92	45.92	Somatic	0.000	365	314	46.24	46.24	Somatic	0.000	1
12	71,787,601	T	A		0	3		0	804	5	0.62	1106	27	2.38	2.38	Somatic	0.001	646	186	22.36	22.36	Somatic	0.000	2
12	76,730,664	C	G	NAV3		3	5_prime_flanking_region		277	10	3.48	334	300	47.32	47.32	Somatic	0.000	339	307	47.52	47.52	Somatic	0.000	1
12	97,164,212	C	A		0	3		0	780	8	1.02	861	863	50.06	50.06	Somatic	0.000	436	448	50.68	50.68	Somatic	0.000	1
12	99,688,821	T	C	ANO4		2	5_prime_flanking_region		210	8	3.67	353	367	50.97	50.97	Somatic	0.000	265	224	45.81	45.81	Somatic	0.000	1
12	105,956,296	G	A	CRY1		2	intronic		1387	65	4.48	797	748	48.41	48.41	Somatic	0.000	472	450	48.81	48.81	Somatic	0.000	1
12	106,519,449	C	T	BTBD11		3	intronic		485	16	3.19	363	348	48.95	48.95	Somatic	0.000	276	281	50.45	50.45	Somatic	0.000	1
12	113,287,422	C	T	TBX5		3	intronic		409	2	0.49	284	195	40.71	40.71	Somatic	0.000	249	204	45.03	45.03	Somatic	0.000	1
12	117,961,498	C	A	KIAA1853		2	intronic		2340	75	3.11	744	609	45.01	45.01	Somatic	0.000	327	321	49.54	49.54	Somatic	0.000	1
12	128,573,952	C	T	TMEM132D		2	intronic		426	13	2.96	343	313	47.71	47.71	Somatic	0.000	394	355	47.40	47.40	Somatic	0.000	1
13	30,843,489	T	G	B3GALTL		3	3_prime_flanking_region		441	20	4.34	568	35	5.80	5.80	Somatic	0.760	651	109	14.34	14.34	Somatic	0.000	0
13	33,827,688	G	A		0	3		0	1310	74	5.35	593	534	47.38	47.38	Somatic	0.000	317	264	45.44	45.44	Somatic	0.000	1
13	35,857,458	T	G	SPG20		3	5_prime_flanking_region		265	8	2.93	237	261	52.41	52.41	Somatic	0.000	269	241	47.25	47.25	Somatic	0.000	1
13	37,251,407	C	A	TRPC4		3	intronic		496	10	1.98	725	616	45.94	45.94	Somatic	0.000	351	286	44.90	44.90	Somatic	0.000	1
13	54,761,858	G	A		0	2		0	530	10	1.85	1050	899	46.13	46.13	Somatic	0.000	380	385	50.33	50.33	Somatic	0.000	1
13	55,648,661	C	T	ENSG00000219006		3	5_prime_flanking_region		316	6	1.86	706	563	44.37	44.37	Somatic	0.000	418	375	47.29	47.29	Somatic	0.000	1
13	57,494,427	G	C	ENSG00000202422		3	3_prime_flanking_region		305	0	0.00	823	15	1.79	1.79	Somatic	0.009	556	146	20.80	20.80	Somatic	0.000	2
13	59,327,359	C	T	DIAPH3		3	intronic		361	24	6.23	424	367	46.40	46.40	Somatic	0.000	374	309	45.24	45.24	Somatic	0.000	1
13	60,197,987	T	A		0	3		0	499	24	4.59	433	431	49.88	49.88	Somatic	0.000	354	329	48.17	48.17	Somatic	0.000	1
13	60,264,538	A	G	ENSG00000206854		3	3_prime_flanking_region		371	11	2.88	773	733	48.67	48.67	Somatic	0.000	305	275	47.41	47.41	Somatic	0.000	1
13	84,248,715	G	A		0	3		0	604	35	5.48	667	538	44.65	44.65	Somatic	0.000	332	294	46.96	46.96	Somatic	0.000	1
13	103,366,966	C	A		0	3		0	152	8	5.00	155	143	47.99	47.99	Somatic	0.000	157	150	48.86	48.86	Somatic	0.000	1
13	105,042,162	A	G		0	2		0	161	1	0.62	196	160	44.94	44.94	Somatic	0.000	214	219	50.58	50.58	Somatic	0.000	1
13	105,714,967	G	T		0	3		0	496	8	1.59	486	437	47.35	47.35	Somatic	0.000	396	348	46.77	46.77	Somatic	0.000	1
13	107,212,497	G	T	FAM155A		3	intronic		518	1	0.19	667	19	2.77	2.77	Somatic	0.000	532	133	20.00	20.00	Somatic	0.000	2
13	108,489,194	G	T	MYO16		3	intronic		221	8	3.49	147	146	49.83	49.83	Somatic	0.000	118	130	52.42	52.42	Somatic	0.000	1
14	25,375,341	T	G	ENSG00000212270		2	5_prime_flanking_region		614	24	3.76	1044	112	9.69	9.69	Somatic	0.023	418	186	30.79	30.79	Somatic	0.000	0
14	27,583,816	G	A		0	3		0	92	0	0.00	203	133	39.58	39.58	Somatic	0.000	130	80	38.10	38.10	Somatic	0.000	0
14	27,583,817	C	A		0	3		0	90	0	0.00	204	133	39.47	39.47	Somatic	0.000	131	80	37.91	37.91	Somatic	0.000	0
14	31,875,476	C	G	AKAP6		3	intronic		748	21	2.73	924	777	45.68	45.68	Somatic	0.000	469	437	48.23	48.23	Somatic	0.000	1
14	32,863,416	T	C	NPAS3		2	intronic		547	16	2.84	671	616	47.86	47.86	Somatic	0.000	348	318	47.75	47.75	Somatic	0.000	1
14	42,520,196	A	T		0	3		0	240	12	4.76	233	194	45.43	45.43	Somatic	0.000	232	212	47.75	47.75	Somatic	0.000	1
14	43,259,343	C	A		0	3		0	298	10	3.25	331	242	42.23	42.23	Somatic	0.000	261	252	49.12	49.12	Somatic	0.000	1
14	43,940,576	A	T	LOC729165		3	3_prime_flanking_region		96	5	4.95	103	70	40.46	40.46	Somatic	0.000	173	124	41.75	41.75	Somatic	0.000	1
14	45,179,799	G	A		0	2		0	497	11	2.17	490	362	42.49	42.49	Somatic	0.000	295	257	46.56	46.56	Somatic	0.000	1
14	47,634,587	C	G		0	2		0	992	32	3.13	1125	899	44.42	44.42	Somatic	0.000	379	389	50.65	50.65	Somatic	0.000	1
14	49,219,295	A	T	POLE2		3	intronic		102	1	0.97	85	88	50.87	50.87	Somatic	0.000	179	187	51.09	51.09	Somatic	0.000	1
14	69,096,682	A	C	LOC100130174		2	3_prime_flanking_region		443	85	16.10	311	117	27.34	27.34	Somatic	0.000	314	215	40.64	40.64	Somatic	0.000	0
14	69,239,804	G	A	KIAA0247		3	intronic		567	37	6.13	402	325	44.70	44.70	Somatic	0.000	352	273	43.68	43.68	Somatic	0.000	1
14	75,418,958	G	A	TTLL5		1	missense		303	9	2.88	258	256	49.81	49.81	Somatic	0.000	289	261	47.45	47.45	Somatic	0.000	1
14	80,669,474	G	A	TSHR		2	intronic		542	28	4.91	408	330	44.72	44.72	Somatic	0.000	375	313	45.49	45.49	Somatic	0.000	1
14	86,938,324	C	T		0	3		0	255	0	0.00	583	20	3.32	3.32	Somatic	0.001	432	121	21.88	21.88	Somatic	0.000	2
14	91,505,353	G	A	FBLN5		2	5_prime_flanking_region		349	25	6.68	561	56	9.08	9.08	Somatic	0.544	409	136	24.95	24.95	Somatic	0.000	0
14	95,369,238	C	T	LOC730125		3	5_prime_flanking_region		493	7	1.40	626	522	45.47	45.47	Somatic	0.000	407	358	46.80	46.80	Somatic	0.000	1
14	98,438,420	A	T		0	3		0	1424	59	3.98	491	450	47.82	47.82	Somatic	0.000	361	363	50.14	50.14	Somatic	0.000	1
14	100,771,639	C	G		0	2		0	242	3	1.22	60	57	48.72	48.72	Somatic	0.000	110	111	50.23	50.23	Somatic	0.000	1
14	103,846,656	T	A	LOC100131034		2	3_prime_flanking_region		180	1	0.55	68	67	49.63	49.63	Somatic	0.000	340	297	46.62	46.62	Somatic	0.000	1
15	18,435,184	C	T	VSIG7		3	5_prime_flanking_region		289	16	5.25	217	114	34.44	34.44	Somatic	0.000	284	224	44.09	44.09	Somatic	0.000	0
15	25,956,026	G	A	OCA2		3	intronic		982	27	2.68	338	279	45.22	45.22	Somatic	0.000	349	375	51.80	51.80	Somatic	0.000	1
15	27,762,153	G	A	ENSG00000212769		3	5_prime_flanking_region		123	4	3.15	71	69	49.29	49.29	Somatic	0.000	243	227	48.30	48.30	Somatic	0.000	1
15	31,122,283	A	T	FMN1		3	intronic		91	3	3.19	104	9	7.96	7.96	Somatic	0.026	256	38	12.93	12.93	Somatic	0.001	0
15	35,751,548	T	C		0	2		0	607	9	1.46	639	543	45.94	45.94	Somatic	0.000	388	360	48.13	48.13	Somatic	0.000	1
15	35,928,644	G	A		0	3		0	830	18	2.12	1006	914	47.60	47.60	Somatic	0.000	399	379	48.71	48.71	Somatic	0.000	1
15	40,101,234	C	T	PLA2G4E		3	intronic		223	11	4.70	83	72	46.45	46.45	Somatic	0.000	153	136	47.06	47.06	Somatic	0.000	1
15	47,739,162	C	T	C15orf33		3	5_prime_flanking_region		833	4	0.48	1244	25	1.97	1.97	Somatic	0.002	503	135	21.16	21.16	Somatic	0.000	2
15	50,336,360	C	A	MYO5C		3	intronic		187	1	0.53	215	163	43.12	43.12	Somatic	0.000	285	227	44.34	44.34	Somatic	0.000	1
15	58,766,926	G	C	RORA		3	intronic		267	7	2.55	309	361	53.88	53.88	Somatic	0.000	292	298	50.51	50.51	Somatic	0.000	0
15	68,465,810	A	C		0	2		0	365	0	0.00	312	6	1.89	1.89	Somatic	0.009	502	136	21.32	21.32	Somatic	0.000	2
15	73,354,279	G	C	LOC730036		3	5_prime_flanking_region		776	4	0.51	542	134	19.82	19.82	Somatic	0.000	833	182	17.93	17.93	Somatic	0.000	0
15	84,663,238	C	T	AGBL1		3	intronic		704	37	4.99	511	501	49.51	49.51	Somatic	0.000	347	269	43.67	43.67	Somatic	0.000	1
15	85,748,727	C	A		0	3		0	855	26	2.95	1790	1517	45.87	45.87	Somatic	0.000	421	359	46.03	46.03	Somatic	0.000	1
15	99,605,527	T	C	CHSY1		3	intronic		386	17	4.22	339	348	50.66	50.66	Somatic	0.000	479	396	45.26	45.26	Somatic	0.000	1
16	4,409,599	C	T	CORO7		3	5_prime_flanking_region		579	2	0.34	224	3	1.32	1.32	Somatic	1.000	538	41	7.08	7.08	Somatic	0.003	0
16	6,155,641	C	G	A2BP1		3	intronic		881	28	3.08	775	677	46.63	46.63	Somatic	0.000	469	415	46.95	46.95	Somatic	0.000	1
16	7,716,860	C	T	ENSG00000209555		1	rna		397	17	4.11	487	430	46.89	46.89	Somatic	0.000	377	335	47.05	47.05	Somatic	0.000	1
16	8,850,511	T	C	LOC100132944		3	5_prime_untranslated_region		368	12	3.16	991	75	7.04	7.04	Somatic	0.006	317	41	11.45	11.45	Somatic	0.000	0
16	9,302,727	C	T		0	3		0	1114	25	2.19	846	782	48.03	48.03	Somatic	0.000	472	452	48.92	48.92	Somatic	0.000	1
16	10,149,701	A	G	GRIN2A		3	intronic		579	29	4.77	354	310	46.69	46.69	Somatic	0.000	211	190	47.38	47.38	Somatic	0.000	1
16	14,074,440	A	T	MKL2		3	intronic		145	8	5.23	269	246	47.77	47.77	Somatic	0.000	211	234	52.58	52.58	Somatic	0.000	1

16	26,024,776	G	A	HS3ST4		3	intronic		942	20	2.08	567	538	48.69	48.69	Somatic	0.000	331	291	46.78	46.78	Somatic	0.000	1
16	26,732,330	G	T		0	2		0	2087	1	0.05	3254	72	2.16	2.16	Somatic	0.000	773	225	22.55	22.55	Somatic	0.000	2
16	50,030,298	C	T		0	3		0	509	19	3.60	423	331	43.90	43.90	Somatic	0.000	388	333	46.19	46.19	Somatic	0.000	1
16	50,680,429	C	T	LOC388276		3	5_prime_flanking_region		368	15	3.92	295	298	50.25	50.25	Somatic	0.000	284	251	46.92	46.92	Somatic	0.000	1
16	51,518,521	T	A	LOC390730		3	5_prime_flanking_region		416	11	2.58	223	190	46.00	46.00	Somatic	0.000	232	184	44.23	44.23	Somatic	0.000	1
16	57,441,427	T	G		0	3		0	251	17	6.34	218	31	12.45	12.45	Somatic	0.005	341	135	28.36	28.36	Somatic	0.000	0
16	57,599,867	C	T		0	3		0	281	4	1.40	247	215	46.54	46.54	Somatic	0.000	282	247	46.69	46.69	Somatic	0.000	1
16	59,855,653	G	C		0	3		0	455	0	0.00	927	27	2.83	2.83	Somatic	0.000	454	130	22.26	22.26	Somatic	0.000	2
16	63,589,987	C	T	CDH11		1	missense		1112	39	3.39	806	689	46.09	46.09	Somatic	0.000	364	333	47.78	47.78	Somatic	0.000	1
16	74,512,157	C	T		0	2		0	434	7	1.59	366	318	46.49	46.49	Somatic	0.000	337	325	49.09	49.09	Somatic	0.000	1
16	77,161,670	G	A	WWOX		3	intronic		160	3	1.84	156	115	42.44	42.44	Somatic	0.000	201	177	46.83	46.83	Somatic	0.000	1
16	77,367,408	G	A	WWOX		3	intronic		811	40	4.70	637	514	44.66	44.66	Somatic	0.000	404	347	46.21	46.21	Somatic	0.000	1
16	78,207,037	C	A	MAF		3	5_prime_flanking_region		996	36	3.49	546	483	46.94	46.94	Somatic	0.000	405	425	51.20	51.20	Somatic	0.000	1
16	81,204,189	C	T	CDH13		2	5_prime_flanking_region		855	36	4.04	593	510	46.24	46.24	Somatic	0.000	425	399	48.42	48.42	Somatic	0.000	1
16	81,731,917	C	T	CDH13		3	intronic		1040	2	0.19	1218	23	1.85	1.85	Somatic	0.000	519	136	20.76	20.76	Somatic	0.000	2
16	82,624,963	C	T	SLC38A8		3	intronic		1027	24	2.28	170	160	48.48	48.48	Somatic	0.000	344	327	48.73	48.73	Somatic	0.000	1
17	4,480,344	C	T	ENSG00000222429		3	5_prime_flanking_region		376	21	5.29	114	99	46.48	46.48	Somatic	0.000	255	234	47.85	47.85	Somatic	0.000	1
17	5,288,451	T	G	DHX33		1	missense		604	18	2.89	187	158	45.80	45.80	Somatic	0.000	254	193	43.18	43.18	Somatic	0.000	1
17	7,533,418	A	G	WRAP53		2	intronic		519	24	4.42	125	91	42.13	42.13	Somatic	0.000	248	201	44.77	44.77	Somatic	0.000	1
17	7,696,343	T	G	JMJD3		1	missense		114	6	5.00	70	6	7.89	7.89	Somatic	0.135	289	96	24.94	24.94	Somatic	0.005	0
17	21,950,614	C	T	ENSG00000209244		2	5_prime_flanking_region		85	3	3.41	44	42	48.84	48.84	Somatic	0.000	73	62	45.93	45.93	Somatic	0.000	1
17	24,186,705	T	C	C17orf63		3	intronic		406	15	3.56	136	144	51.43	51.43	Somatic	0.000	329	289	46.76	46.76	Somatic	0.000	1
17	25,735,564	A	C	CPD		3	intronic		108	21	16.28	234	96	29.09	29.09	Somatic	0.025	211	228	51.94	51.94	Somatic	0.000	0
17	26,580,889	G	C	NF1		3	intronic		477	10	2.05	540	458	45.89	45.89	Somatic	0.000	233	238	50.53	50.53	Somatic	0.000	1
17	28,127,819	C	T	MYO1D		3	intronic		324	17	4.99	243	180	42.55	42.55	Somatic	0.000	277	221	44.38	44.38	Somatic	0.000	1
17	29,981,226	C	T	TMEM132E		1	silent		1815	79	4.17	275	343	55.50	55.50	Somatic	0.000	289	248	46.18	46.18	Somatic	0.000	0
17	35,007,340	T	C	STARD3		2	5_prime_flanking_region		681	29	4.08	97	80	45.20	45.20	Somatic	0.000	159	115	41.97	41.97	Somatic	0.000	1
17	36,096,311	T	C	SMARCE1		2	5_prime_flanking_region		128	1	0.78	196	174	47.03	47.03	Somatic	0.000	253	232	47.84	47.84	Somatic	0.000	1
17	48,968,272	G	A	ENSG00000221534		3	5_prime_flanking_region		329	2	0.60	384	241	38.56	38.56	Somatic	0.000	249	176	41.41	41.41	Somatic	0.000	1
17	49,442,081	C	T		0	2		0	576	20	3.36	394	342	46.47	46.47	Somatic	0.000	326	241	42.50	42.50	Somatic	0.000	1
17	50,661,710	T	C	HLF		3	5_prime_flanking_region		1225	58	4.52	647	485	42.84	42.84	Somatic	0.000	486	487	50.05	50.05	Somatic	0.000	1
17	59,597,932	C	G	TEX2		3	intronic		322	5	1.53	441	12	2.65	2.65	Somatic	0.195	380	64	14.41	14.41	Somatic	0.000	0
17	67,860,759	A	C	ENSG00000211264		3	3_prime_flanking_region		286	4	1.38	185	190	50.67	50.67	Somatic	0.000	291	232	44.36	44.36	Somatic	0.000	1
17	75,696,250	G	A	GAA		1	silent		23	2	8.00	17	13	43.33	43.33	Somatic	0.016	85	63	42.57	42.57	Somatic	0.001	1
18	2,228,633	C	T	LOC100131655		2	intronic		1078	46	4.09	1107	952	46.24	46.24	Somatic	0.000	344	333	49.19	49.19	Somatic	0.000	1
18	5,155,122	G	A	ENSG00000215368		3	5_prime_flanking_region		957	30	3.04	597	492	45.18	45.18	Somatic	0.000	400	338	45.80	45.80	Somatic	0.000	1
18	11,368,929	G	A		0	3		0	359	17	4.52	443	408	47.94	47.94	Somatic	0.000	318	245	43.52	43.52	Somatic	0.000	1
18	18,624,758	T	C		0	2		0	1300	41	3.06	866	768	47.00	47.00	Somatic	0.000	440	402	47.74	47.74	Somatic	0.000	1
18	26,038,883	G	A		0	3		0	443	0	0.00	736	17	2.26	2.26	Somatic	0.000	524	146	21.79	21.79	Somatic	0.000	2
18	29,585,389	T	G	ASXL3		3	3_prime_flanking_region		162	6	3.57	120	116	49.15	49.15	Somatic	0.000	186	201	51.94	51.94	Somatic	0.000	1
18	29,798,038	G	A	NOL4		3	intronic		543	21	3.72	860	644	42.82	42.82	Somatic	0.000	441	337	43.32	43.32	Somatic	0.000	1
18	30,590,076	A	G	DTNA		2	intronic		432	14	3.14	407	314	43.55	43.55	Somatic	0.000	323	329	50.46	50.46	Somatic	0.000	1
18	36,013,083	C	T		0	3		0	303	11	3.50	426	307	41.88	41.88	Somatic	0.000	279	238	46.03	46.03	Somatic	0.000	1
18	36,630,355	T	G		0	3		0	175	9	4.89	207	186	47.33	47.33	Somatic	0.000	183	174	48.74	48.74	Somatic	0.000	1
18	46,165,704	G	A	C18orf24		1	silent		327	12	3.54	298	242	44.81	44.81	Somatic	0.000	302	315	51.05	51.05	Somatic	0.000	1
18	47,449,416	C	T		0	2		0	431	6	1.37	496	445	47.29	47.29	Somatic	0.000	434	323	42.67	42.67	Somatic	0.000	1
18	51,514,701	A	G		0	3		0	540	20	3.57	391	381	49.35	49.35	Somatic	0.000	371	347	48.33	48.33	Somatic	0.000	1
18	52,121,185	G	A		0	3		0	393	12	2.96	392	396	50.25	50.25	Somatic	0.000	246	250	50.40	50.40	Somatic	0.000	1
18	52,654,678	A	C	WDR7		3	intronic		533	12	2.20	1205	115	8.71	8.71	Somatic	0.000	393	159	28.80	28.80	Somatic	0.000	0
18	62,821,154	G	T		0	3		0	283	11	3.74	477	424	47.06	47.06	Somatic	0.000	310	319	50.72	50.72	Somatic	0.000	1
18	63,165,104	T	C		0	3		0	412	1	0.24	1155	33	2.78	2.78	Somatic	0.000	688	185	21.19	21.19	Somatic	0.000	2
18	64,146,279	G	T		0	3		0	348	13	3.60	447	360	44.61	44.61	Somatic	0.000	314	257	45.01	45.01	Somatic	0.000	1
18	64,226,339	T	G		0	3		0	422	41	8.86	925	162	14.90	14.90	Somatic	0.798	394	216	35.41	35.41	Somatic	0.005	0
18	67,103,868	C	T		0	3		0	226	12	5.04	256	251	49.51	49.51	Somatic	0.000	262	232	46.96	46.96	Somatic	0.000	1
18	67,787,857	G	A		0	3		0	142	5	3.40	165	127	43.49	43.49	Somatic	0.000	194	173	47.14	47.14	Somatic	0.000	1
18	69,657,558	A	G		0	3		0	771	52	6.32	682	675	49.74	49.74	Somatic	0.000	372	324	46.55	46.55	Somatic	0.000	1
18	70,624,608	A	G	ZNF407		2	intronic		258	4	1.53	494	472	48.86	48.86	Somatic	0.000	327	311	48.75	48.75	Somatic	0.000	1
18	74,833,430	C	T	SALL3		3	5_prime_flanking_region		94	5	5.05	17	37	68.52	68.52	Somatic	0.000	242	215	47.05	47.05	Somatic	0.000	0
19	16,885,826	C	T	CPAMD8		3	intronic		524	11	2.06	146	150	50.68	50.68	Somatic	0.000	293	250	46.04	46.04	Somatic	0.000	1
19	18,513,222	G	A	FKBP8		3	intronic		396	23	5.49	88	72	45.00	45.00	Somatic	0.000	204	228	52.78	52.78	Somatic	0.000	1
19	19,045,292	G	A	SLC25A42		3	intronic		1127	38	3.26	119	94	44.13	44.13	Somatic	0.000	391	312	44.38	44.38	Somatic	0.000	1
19	20,320,043	C	T	ZNF826		3	3_prime_flanking_region		75	4	5.06	58	64	52.46	52.46	Somatic	0.000	86	73	45.91	45.91	Somatic	0.000	1
19	39,677,436	C	T	WTIP		3	intronic		270	10	3.57	147	107	42.13	42.13	Somatic	0.000	232	223	49.01	49.01	Somatic	0.000	1
19	48,741,326	C	T	XRCC1		3	intronic		1207	60	4.74	248	178	41.78	41.78	Somatic	0.000	358	293	45.01	45.01	Somatic	0.000	1
19	49,554,552	C	G	ZFP112		3	5_prime_flanking_region		278	4	1.42	327	262	44.48	44.48	Somatic	0.000	217	183	45.75	45.75	Somatic	0.000	1
19	53,579,461	T	G	KDELR1		1	missense		1035	149	12.58	184	34	15.60	15.60	Somatic	0.079	375	212	36.12	36.12	Somatic	0.000	0
19	54,349,852	A	G	HRC		1	missense		404	11	2.65	335	20	5.63	5.63	Somatic	0.396	330	57	14.73	14.73	Somatic	0.000	0
19	56,489,635	G	A	IGLON5		3	5_prime_flanking_region		354	16	4.32	177	153	46.36	46.36	Somatic	0.000	263	267	50.38	50.38	Somatic	0.000	1
19	61,964,333	C	G	ZIM2		2	3_prime_flanking_region		1141	36	3.06	765	672	46.76	46.76	Somatic	0.000	304	285	48.39	48.39	Somatic	0.000	1
20	2,498,536	G	A	TMC2		3	intronic		320	9	2.74	175	156	47.13	47.13	Somatic	0.000	251	197	43.97	43.97	Somatic	0.000	1
20	3,953,163	T	C	RNF24		3	5_prime_flanking_region		239	4	1.65	192	1	0.52	0.52	Reference	1.000	251	43	14.63	14.63	Somatic	0.000	0
20	10,400,224	T	G	C20orf94		3	intronic		405	19	4.48	834	90	9.74	9.74	Somatic	0.505	457	166	26.65	26.65	Somatic	0.000	0
20	24,021,637	C	T		0	3		0	936	28	2.90	372	295	44.23	44.23	Somatic	0.000	435	395	47.59	47.59	Somatic	0.000	1
20	32,728,482	A	C	PIGU		1	missense		212	5	2.30	62	44	41.51	41.51	Somatic	0.000	113	92	44.88	44.88	Somatic	0.000	1
20	32,965,857	A	C	ACSS2		1	missense		804	94	10.47	672	133	16.52	16.52	Somatic	0.828	305	153	33.41	33.41	Somatic	0.000	0
20	39,133,828	A	G	TOP1		3	intronic		670	53	7.33	825	734	47.08	47.08	Somatic	0.000	394	358	47.61	47.61	Somatic	0.000	1
20	40,082,860	C	T	ENSG00000220309		3	5_prime_flanking_region		1120	28	2.44	499	418	45.58	45.58	Somatic	0.000	382	341	47.16	47.16	Somatic	0.000	1
20	51,626,823	T	C	ZNF217		1	silent		552	15	2.65	209	181	46.41	46.41	Somatic	0.000	312	256	45.07	45.07	Somatic	0.000	1
20	53,344,924	C	T		0	3		0	370	32	7.96	453	423	48.29	48.29	Somatic	0.000	280	231	45.21	45.21	Somatic	0.000	1
20	61,146,741	C	T	C20orf51		2	intronic		379	10	2.57	228	243	51.59	51.59	Somatic	0.000	278	266	48.90	48.90	Somatic	0.000	1

21	26,646,726	G	A		0	3		0	215	0	0.00	385	9	2.28	2.28	Somatic	0.018	522	137	20.79	20.79	Somatic	0.000	2
21	30,459,290	C	T	CLDN8		3	3_prime_flanking_region		370	16	4.15	921	766	45.41	45.41	Somatic	0.000	354	330	48.25	48.25	Somatic	0.000	1
21	41,416,902	G	A	BACE2		3	5_prime_flanking_region		1038	32	2.99	664	560	45.75	45.75	Somatic	0.000	399	339	45.93	45.93	Somatic	0.000	1
21	42,402,818	A	C	UMODL1		1	missense		84	8	8.70	65	8	10.96	10.96	Somatic	0.577	161	75	31.78	31.78	Somatic	0.000	0
21	43,397,525	G	A	U2AF1		1	missense		404	30	6.91	91	83	47.70	47.70	Somatic	0.000	343	317	48.03	48.03	Somatic	0.000	1
21	46,252,211	C	T	COL6A1		2	3_prime_flanking_region		92	1	1.08	89	67	42.95	42.95	Somatic	0.000	213	170	44.39	44.39	Somatic	0.000	1
21	46,301,845	G	T	COL6A2		2	5_prime_flanking_region		46	0	0.00	11	2	15.38	15.38	Reference	0.041	251	182	42.03	42.03	Somatic	0.000	0
22	18,187,764	C	T	GNB1L		3	intronic		387	7	1.78	104	92	46.94	46.94	Somatic	0.000	223	211	48.62	48.62	Somatic	0.000	1
22	19,294,334	C	G	ENSG00000220150		3	5_prime_flanking_region		265	25	8.62	128	119	48.18	48.18	Somatic	0.000	360	298	45.29	45.29	Somatic	0.000	1
22	20,866,781	G	A	IGLV11-55		3	5_prime_flanking_region		328	21	6.02	185	239	56.37	56.37	Somatic	0.000	165	156	48.60	48.60	Somatic	0.000	0
22	36,194,879	A	C	ELFN2		3	5_prime_flanking_region		735	74	9.15	291	56	16.14	16.14	Somatic	0.000	502	195	27.98	27.98	Somatic	0.000	0
22	38,089,713	C	T	SYNGR1		3	intronic		954	46	4.60	97	89	47.85	47.85	Somatic	0.000	145	139	48.94	48.94	Somatic	0.000	1
22	46,395,195	C	T	FLJ46257		3	3_prime_flanking_region		378	10	2.58	137	111	44.76	44.76	Somatic	0.000	302	308	50.49	50.49	Somatic	0.000	1
22	46,512,620	A	G		0	3		0	471	11	2.28	526	17	3.13	3.13	Somatic	0.421	431	115	21.06	21.06	Somatic	0.000	2
X	3,387,861	G	A		0	3		0	375	0	0.00	362	21	5.48	2.74	Somatic	0.000	167	112	40.14	20.07	Somatic	0.000	2
X	29,779,410	G	A	IL1RAPL1		2	intronic		121	6	4.72	21	384	94.81	47.41	Somatic	0.000	19	292	93.89	46.95	Somatic	0.000	1
X	32,777,396	C	T	DMD		3	intronic		414	38	8.41	31	496	94.12	47.06	Somatic	0.000	21	292	93.29	46.65	Somatic	0.000	1
X	34,705,765	A	G		0	3		0	217	29	11.79	7	287	97.62	48.81	Somatic	0.000	12	311	96.28	48.14	Somatic	0.000	1
X	39,157,340	A	G		0	3		0	283	22	7.21	22	391	94.67	47.34	Somatic	0.000	22	413	94.94	47.47	Somatic	0.000	1
X	52,897,186	C	T	FAM156B		3	5_prime_flanking_region		226	11	4.64	18	368	95.34	47.67	Somatic	0.000	14	282	95.27	47.64	Somatic	0.000	1
X	104,353,541	G	C	IL1RAPL2		3	intronic		141	21	12.96	24	327	93.16	46.58	Somatic	0.000	19	424	95.71	47.86	Somatic	0.000	1
X	111,088,560	G	A	TRPC5		3	intronic		253	11	4.17	39	584	93.74	46.87	Somatic	0.000	15	321	95.54	47.77	Somatic	0.000	1
X	116,699,743	C	A		0	3		0	219	25	10.25	34	461	93.13	46.57	Somatic	0.000	11	396	97.30	48.65	Somatic	0.000	1
X	118,033,017	G	A	LONRF3		3	intronic		473	37	7.25	18	437	96.04	48.02	Somatic	0.000	16	351	95.64	47.82	Somatic	0.000	1
X	132,324,635	C	T	GPC4		3	intronic		642	64	9.07	61	841	93.24	46.62	Somatic	0.000	21	412	95.15	47.58	Somatic	0.000	1
X	142,016,065	C	T	ENSG00000202473		3	3_prime_flanking_region		59	6	9.23	10	139	93.29	46.64	Somatic	0.000	8	164	95.35	47.67	Somatic	0.000	1
X	151,265,229	C	T	GABRA3		3	intronic		621	28	4.31	50	711	93.43	46.71	Somatic	0.000	14	376	96.41	48.21	Somatic	0.000	1
Y	9,231,939	G	A	TTTY20		2	intronic		115	8	6.50	6	96	94.12	47.06	Somatic	0.000	17	226	93.00	46.50	Somatic	0.000	1
Y	15,681,536	T	C		0	3		0	359	9	2.45	512	41	7.41	3.71	Somatic	0.015	308	110	26.32	13.16	Somatic	0.000	0
Y	22,378,497	C	T	ENSG00000217635		3	5_prime_flanking_region		217	24	9.96	9	209	95.87	47.94	Somatic	0.000	17	196	92.02	46.01	Somatic	0.000	1
Y	22,830,969	C	T	RBMY1J		3	5_prime_flanking_region		158	11	6.51	12	215	94.71	47.36	Somatic	0.000	13	321	96.11	48.05	Somatic	0.000	1

Supplementary Table 3. Annotated Tier 1 Mutations in the MDS and sAML genomes.

Chromosome	Position*	Reference allele	Variant allele	Gene symbol	Transcript ID	Strand	Mutation type	Mutated in MDS	Mutated in sAML	Zygosity	Coding position	Amino acid change
1	112,325,945	G	T	KCND3	NM_004980	-1	synonymous	Y	Y	Het	c.927	I309
1	205,309,412	C	G	PFKFB2	NM_006212	1	synonymous	Y	Y	Het	c.1008	T336
1	229,096,537	T	C	ENSG00000222671	ENST00000410739	1	non-coding RNA	Y	Y	Het	NA	NA
2	20,289,990	C	T	LOC100131373	XM_001720891	1	synonymous	Y	Y	Het	c.261	A87
2	61,569,230	T	A	XPO1	NM_003400	-1	missense	Y	Y	Het	c.2203	N735Y
3	173,529,456	C	A	FNDC3B	NM_022763	1	missense	Y	Y	Het	c.1275	F425L
5	50,152,869	C	G	PARP8	NM_024615	1	missense	Y	Y	Het	c.1734	F578L
5	148,880,083	T	G	CSNK1A1	NM_001025105	-1	missense	Y	Y	Het	c.419	D140A
6	105,713,110	C	A	POPDC3	NM_022361	-1	missense	Y	Y	Het	c.804	M268I
9	89,535,224	T	G	CTSL1	NM_001912	1	missense	Y	Y	Het	c.893	V298G
9	138,867,831	C	T	MAMDC4	NM_206920	1	synonymous	Y	Y	Het	c.342	A114
10	82,288,101	G	A	SH2D4B	NM_207372	1	missense	Y	Y	Het	c.34	D12N
11	12,198,538	C	G	MICAL2	NM_014632	1	missense	Y	Y	Het	c.1163	A388G
11	22,340,860	G	T	SLC17A6	NM_020346	1	splice_site	Y	Y	Het	c.662-1	e6-1
11	30,881,639	A	G	DCDC5	ENST00000406071	-1	synonymous	Y	Y	Het	c.1806	V602
14	75,418,958	G	A	TTLL5	NM_015072	1	missense	Y	Y	Het	c.3700	E1234K
16	7,716,860	C	T	ENSG00000209555	ENST00000386820	-1	non-coding RNA	Y	Y	Het	NA	NA
16	63,589,987	C	T	CDH11	NM_001797	-1	missense	Y	Y	Het	c.502	V168M
17	5,288,451	T	G	DHX33	NM_020162	-1	missense	Y	Y	Het	c.1922	Y641S
17	7,696,343	T	G	JMJD3	NM_001080424	1	missense	Y	Y	Het	c.4432	C1478G
17	29,981,226	C	T	TMEM132E	NM_207313	1	synonymous	Y	Y	Het	c.1155	L385
17	75,696,250	G	A	GAA	NM_000152	1	synonymous	Y	Y	Het	c.915	G305
18	46,165,704	G	A	C18orf24	NM_001039535	1	synonymous	Y	Y	Het	c.432	E144
19	53,579,461	T	G	KDELR1	NM_006801	-1	missense	Y	Y	Het	c.442	T148P
19	54,349,852	A	G	HRC	NM_002152	-1	missense	Y	Y	Het	c.455	L152P
20	32,728,482	A	C	PIGU	NM_080476	-1	missense	Y	Y	Het	c.69	S23R
20	32,965,857	A	C	ACSS2	NM_018677	1	missense	Y	Y	Het	c.790	T264P
20	51,626,823	T	C	ZNF217	NM_006526	-1	synonymous	Y	Y	Het	c.1887	R629
21	42,402,818	A	C	UMODL1	NM_173568	1	missense	Y	Y	Het	c.1597	T533P
21	43,397,525	G	A	U2AF1	NM_001025203	-1	missense	Y	Y	Het	c.101	S34F

*build 36

Supplementary Table 4. U2AF1 Somatic Mutations in MDS.

UPN	gene name	chromosome	start	stop	reference allele	variant allele	transcript	strand	mutation type	coding position	amino acid change	SIFT	SIFT score	PolyPhen2	PolyPhen2 score
02-86	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
185295	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
266395	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
300813	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
321864	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
463763	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
571656	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
843623	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
917011	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
947519*	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
989739	U2AF1	21	43397525	43397525	G	A	NM_001025203	-1	missense	c.101	p.S34F	damaging	0	probably damaging	1
137250	U2AF1	21	43397525	43397525	G	T	NM_001025203	-1	missense	c.101	p.S34Y	damaging	0	probably damaging	1
937954	U2AF1	21	43397525	43397525	G	T	NM_001025203	-1	missense	c.101	p.S34Y	damaging	0	probably damaging	1
947519*	U2AF1	21	43387846	43387846	T	C	NM_001025203	-1	missense	c.470	p.Q157R	damaging	0	probably damaging	0.999

UPN, unique patient number
* same UPN

Supplementary Table 5. Characteristics of MDS patients with *U2AF1* Mutations

UPN	Gender	Age at diagnosis	FAB	Karyotype	%BM Blast	IPSS	Therapy after MDS banking (months)	AML Progression?	OS (months)	EFS (months)
266395[a]	M	65	RAEB	46,XY[20]	7	1	azacytidine (6)	yes	11	2
137250	F	54	RAEB	46,XX[20]	19	2	standard induction, allogeneic SCT	yes	100	1
185295	M	50	RA	46,XY,del(20)(q11.2q13.3)[7]/46,XY,[13]	0	0.5	PTK/ZK (<1), azacytidine (2), allogeneic SCT	no	97	83
300813	F	42	RA	46,XX[20]	2	0	none	no	71	71
321864	F	63	RAEB	46,XX+8[20]	12	2.5	standard induction	no	3	3
571656	M	71	RAEB	46,XY,del(20)(q11.2q13.3)[12]/46XY[8]	4	0.5	standard induction	yes	10	8
843623	M	60	RAEB	46,XY,del(20)(q11.3)[2]/46,XY[18]	6	1	none	yes	5	2
917011	M	79	RA	46,XY,del(20)(q11.2)[12]/ 46,XY[8]	0	0.5	lenalidomide (3)	no	27	25
937954	M	51	RAEB	47,XY,+8[1]/47,idem,del(16)(q12.1)[13]/48,idem,+Y,del(16)(q11.1)[5]/46,XY[1]	12	2.5	azacytidine (3)	no	24	24
947519	M	59	RAEB	46,XY,1-5dims[10]/46,XY[12]	7	1.5	decitabine (3), allogeneic SCT, standard induction, salvage chemotherapy	yes	24	23
02-86	M	53	RAEB-T	92<4n>,XXYY,del(4)(q33)x2,del(5)(q13),add(11) (q23)x2[cp8]/46,XY[12]	21	3	decitabine (2)	yes	10	4
463763	M	54	RA	47,XY,+Y[6]/46,XY[14]	0	0.5	none	no	46	44
989739	M	71	RAEB	46,XY,del(7)(q21)[11]/47,XY,+8[5]/46,XY[4]	18	3	decitabine (8)	yes	15	4

UPN, unique patient number; OS, overall survival; EFS, event-free survival; PTK/ZK (Vatalanib), VEGF inhibitor.

[a]index case

Supplementary Table 6. Dysregulated genes in *U2AF1* mutant MDS samples

Affymetrix Probe ID	Gene Symbol	Fold Change mutant vs. control	q-value (%)	local FDR (%)	Annotation Cluster 1 Enrichment Score: 7.715				Annotation Cluster 2 Enrichment Score: 4.311			Annotation Cluster 3 Enrichment Score: 3.556			Annotation Cluster 4 Enrichment Score: 3.011			Annotation Cluster 5 Enrichment Score: 2.998			Annotation Cluster 6 Enrichment Score: 2.458						Annotation Cluster 7 Enrichment Score: 2.436			Annotation Cluster 8 Enrichment Score: 2.420				Annotation Cluster 9 Enrichment Score: 2.224		
					GO:0031974	GO:0070013	GO:0043233	GO:0031981	SM00360	IPR000504	IPR012677	GO:0006886	GO:0070727	GO:0034613	GO:0015031	GO:0045184	GO:0008104	Uniprot domain	Uniprot domain	Uniprot domain	Swiss-Prot feature	GO:0008380	GO:0006397	Swiss-Prot feature	GO:0016071	GO:0006396	GO:0042981	GO:0043067	GO:0010941	GO:0019866	GO:0005743	GO:0005740	GO:0031966	GO:0043065	GO:0043068	GO:0010942
					membrane-enclosed	intracellular organelle lumen	organelle lumen	nuclear lumen	RRM	RNA recognition motif, RNP-1	Nucleotide binding, alpha-beta plait	Intracellular protein transport	cellular macromolecule localization	cellular protein localization	protein transport	establishment of protein localization	protein localization	RRM 2	RRM 1	RRM 3	mrna splicing	RNA splicing	mRNA processing	mrna processing	mRNA metabolic process	RNA processing	regulation of apoptosis	regulation of programmed cell death	regulation of cell death	organelle inner membrane	mitochondrial inner membrane	mitochondrial envelope	mitochondrial membrane	positive regulation of apoptosis	positive regulation of programmed cell death	positive regulation of cell death
Upregulated in U2AF1 mutant vs. controls (50 probesets)					**(1=gene in cluster, 0=gene not in cluster)**																															
221740_x_at	LOC10050616	3.05	0.000	0.898	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241402_at	TSEN54	3.04	0.000	0.968	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227815_at	---	2.11	0.000	1.117	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213391_at	DPY19L4	3.31	0.000	1.187	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226217_at	SLC30A7	1.70	0.000	1.207	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219406_at	C1orf50*	1.88	0.000	1.210	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235104_at	ERAP2	5.94	0.000	1.182	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
239943_x_at	---	2.22	0.000	1.172	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
243113_at	---	7.07	0.000	1.170	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209358_at	TAF11	1.91	0.000	1.165	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
242916_at	CEP110	2.78	0.000	1.118	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229303_at	---	3.09	0.236	1.092	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222111_at	---	2.92	0.236	1.084	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234192_s_at	GKAP1	2.34	0.236	1.064	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226600_at	TMTC3	3.53	0.236	1.055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234733_s_at	FANCM	3.29	0.236	1.052	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201807_at	VPS26A	1.66	0.236	1.015	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235493_at	---	2.91	0.236	1.014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1558919_a_at	---	3.12	0.236	1.001	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212754_s_at	MON2	3.07	0.236	0.921	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234701_at	ANKRD11	2.81	0.236	0.920	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241242_at	---	3.91	0.236	0.890	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
62212_at	C1orf50*	2.12	0.346	0.785	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211063_s_at	NCK1	1.52	0.346	0.750	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210114_at	INVS	2.19	0.346	0.748	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222447_at	METTL9	1.89	0.346	0.712	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241472_at	---	3.80	0.346	0.688	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1553103_at	NFX1	3.15	0.346	0.669	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
236007_at	AKAP10	3.81	0.346	0.631	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215182_x_at	---	3.66	0.346	0.594	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228963_at	---	2.82	0.346	0.560	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
240239_at	ZNF566	3.92	0.346	0.554	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231919_at	DBT	2.89	0.346	0.508	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230379_x_at	C2orf56	2.69	0.455	0.480	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234491_s_at	SAV1	2.68	0.455	0.457	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227002_at	FAM78A	2.83	0.455	0.440	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229431_at	RFXAP	2.30	0.455	0.431	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
239007_at	ZNF616	7.13	0.455	0.405	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226338_at	TMEM55A	1.85	0.455	0.389	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224873_s_at	MRPS25	2.18	0.455	0.383	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210554_s_at	CTBP2	1.48	0.455	0.363	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235620_x_at	ZMYM5	4.46	0.455	0.352	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235893_at	---	3.51	0.455	0.345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227665_at	---	2.28	0.455	0.345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241905_at	PIK3C2A	2.31	0.455	0.345	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217627_at	ZNF573	4.83	0.455	0.343	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
244818_at	ZNF780B	3.27	0.455	0.324	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
240765_at	---	3.27	0.455	0.315	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228913_at	LOC10019093	3.25	0.455	0.297	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218965_s_at	TUT1	2.12	0.455	0.291	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Downregulated in U2AF1 mutant vs. controls (351 probesets)																																				
201104_x_at	NBPF	0.63	0.000	0.283	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222479_s_at	DYNC1LI1	0.58	0.000	0.289	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200659_s_at	PHB*	0.43	0.000	0.321	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0
201377_at	UBAP2L	0.38	0.000	0.322	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
236388_at	STRN*	0.31	0.000	0.323	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1553369_at	FAM129C*	0.10	0.000	0.325	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208948_s_at	STAU1*	0.41	0.000	0.328	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212488_at	COL5A1*	0.10	0.000	0.328	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221021_s_at	CTNNBL1	0.24	0.000	0.327	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
210450_at	IGHV5-78	0.06	0.000	0.325	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213720_s_at	SMARCA4*	0.47	0.000	0.323	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217736_s_at	EIF2AK1	0.40	0.000	0.323	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201075_s_at	SMARCC1	0.43	0.000	0.322	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226987_at	RBM15B	0.42	0.000	0.321	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
226037_s_at	TAF9B	0.38	0.000	0.320	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
226849_at	DENND1A	0.27	0.000	0.317	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
239964_at	TCL6	0.10	0.000	0.314	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210011_s_at	EWSR1	0.40	0.000	0.311	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222885_at	EMCN	0.16	0.000	0.297	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225468_at	PATL1	0.44	0.000	0.297	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201609_x_at	ICMT	0.29	0.000	0.293	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1559618_at	LOC10012944	0.10	0.000	0.289	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230983_at	FAM129C*	0.10	0.000	0.282	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220068_at	VPREB3	0.04	0.000	0.281	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207320_x_at	STAU1*	0.50	0.000	0.278	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202059_s_at	KPNA1	0.40	0.000	0.273	1	1	1	1	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212489_at	COL5A1*	0.07	0.000	0.269	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202784_s_at	NNT	0.58	0.000	0.265	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
200913_at	PPM1G	0.31	0.000	0.264	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223211_at	HACL1	0.33	0.000	0.262	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208931_s_at	ILF3	0.33	0.000	0.258	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200850_s_at	AHCYL1	0.48	0.000	0.250	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217787_s_at	GALNT2	0.17	0.000	0.246	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231935_at	ARPP21*	0.04	0.000	0.236	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227530_at	AKAP12*	0.04	0.000	0.235	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209208_at	MPDU1	0.11	0.000	0.228	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201180_s_at	GNAI3	0.45	0.000	0.181	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218402_s_at	HPS4	0.19	0.000	0.181	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214359_s_at	HSP90AB1*	0.25	0.000	0.181	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
237297_at	FAM53B	0.18	0.000	0.175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212214_at	OPA1	0.45	0.000	0.157	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
200065_s_at	ARF1	0.25	0.000	0.140	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209174_s_at	QRICH1	0.42	0.000	0.138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201678_s_at	C3orf37*	0.22	0.000	0.134	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
241813_at	MBD1	0.36	0.000	0.128	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212206_s_at	H2AFV	0.22	0.000	0.120	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224578_at	RCC2	0.54	0.000	0.116	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226985_at	FGD5	0.21	0.000	0.097	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227336_at	DTX1	0.12	0.000	0.087	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219485_s_at	PSMD10	0.50	0.000	0.085	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216379_x_at	CD24*	0.11	0.000	0.085	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
219718_at	FGGY	0.30	0.000	0.084	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208643_s_at	XRCC5	0.50	0.000	0.082	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
216080_s_at	FADS3*	0.18	0.000	0.074	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223239_at	C14orf129	0.43	0.000	0.062	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224609_at	SLC44A2*	0.13	0.000	0.055	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210337_s_at	ACLY*	0.36	0.000	0.048	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1553998_at	DMRTC1	0.31	0.000	0.045	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201133_s_at	PJA2	0.46	0.000	0.010	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
244280_at	---	0.08	0.000	0.007	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225601_at	HMGB3	0.26	0.000	0.006	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218480_at	AGBL5	0.22	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218949_s_at	QRSL1	0.35	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204753_s_at	HLF	0.15	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207628_s_at	WBSCR22	0.35	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211276_at	TCEAL2	0.11	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212312_at	BCL2L1	0.50	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	1	1	1	1	1
222569_at	UGGT1	0.58	0.000	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234998_at	RAB11A	0.42	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209211_at	KLF5	0.37	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217821_s_at	WBP11	0.42	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
207431_s_at	DEGS1	0.23	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206788_s_at	CBFB	0.44	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200918_s_at	SRPR	0.36	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226556_at	MAP3K13	0.16	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200052_s_at	ILF2	0.41	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223302_s_at	ZNF655	0.40	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206621_s_at	EIF4H	0.34	0.000	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208842_s_at	GORASP2*	0.54	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
243524_at	---	0.34	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225935_at	CUX1	0.51	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

203066_at	CHST15	0.15	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219758_at	TTC26*	0.25	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200049_at	MYST2	0.31	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211934_x_at	GANAB	0.27	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208843_s_at	GORASP2*	0.57	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1554592_a_at	SLC1A6*	0.15	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208821_at	SNRPB	0.24	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
202164_s_at	CNOT8*	0.38	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229323_at	LOC387723	0.18	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212165_at	TMEM183A	0.53	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224582_s_at	NUCKS1	0.28	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200694_s_at	DDX24	0.45	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201361_at	TMEM109	0.26	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217726_at	COPZ1*	0.32	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200957_s_at	SSRP1	0.37	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208836_at	ATP1B3	0.42	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204441_s_at	POLA2	0.23	0.000	0.000	1	1	1	1	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209771_x_at	CD24*	0.13	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
202492_at	ATG9A	0.36	0.000	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212485_at	GPATCH8	0.61	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
65591_at	WDR48*	0.43	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200675_at	CD81	0.16	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225232_at	MTMR12	0.43	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214885_at	MYST1	0.48	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210298_x_at	FHL1	0.35	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210338_s_at	HSPA8	0.39	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210759_s_at	PSMA1	0.39	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225366_at	PGM2	0.40	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224060_s_at	DPH5*	0.41	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1570420_at	STXBP2	0.19	0.000	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1553709_a_at	PRPF38A	0.43	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
222157_s_at	WDR48*	0.34	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220607_x_at	TH1L	0.38	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222030_at	SIVA1	0.42	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
239886_at	---	0.48	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204152_s_at	MFNG	0.24	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201529_s_at	RPA1	0.38	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208793_x_at	SMARCA4*	0.24	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204305_at	MIPEP	0.40	0.000	0.000	1	1	1	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216237_s_at	MCM5*	0.29	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208631_s_at	HADHA	0.32	0.000	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
201970_s_at	NASP	0.45	0.000	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216483_s_at	C19orf10	0.30	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214500_at	H2AFY	0.27	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203462_x_at	EIF3B*	0.36	0.000	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1563849_at	SH2D4B	0.08	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1554593_s_at	SLC1A6*	0.28	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219126_at	PHF10	0.35	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207891_s_at	HAUS7	0.18	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201908_at	DVL3	0.48	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226053_at	MAP2K7	0.31	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209852_x_at	PSME3	0.35	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
1555833_a_at	IRGQ*	0.27	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200776_s_at	BZW1	0.31	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219939_s_at	CSDE1	0.54	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
225738_at	RAPGEF1*	0.28	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
266_s_at	CD24*	0.10	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
232213_at	PELI1	0.37	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221558_s_at	LEF1	0.14	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211271_x_at	PTBP1*	0.40	0.000	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
1559221_at	---	0.17	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227529_s_at	AKAP12*	0.03	0.000	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200072_s_at	HNRNPM	0.41	0.000	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
201898_s_at	UBE2A	0.32	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226320_at	THOC4	0.30	0.000	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
200932_s_at	DCTN2	0.40	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209103_s_at	UFD1L	0.28	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226046_at	MAPK8	0.35	0.000	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
201632_at	EIF2B1	0.47	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208611_s_at	SPTAN1	0.38	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201388_at	PSMD3	0.22	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201127_s_at	ACLY*	0.58	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208714_at	NDUFV1	0.22	0.000	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
206492_at	FHIT	0.20	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210567_s_at	SKP2	0.33	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
1569353_at	CP110	0.29	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230734_x_at	STRN*	0.47	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200713_s_at	MAPRE1	0.49	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
233168_s_at	SELO	0.33	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
231777_at	CSNK2B	0.22	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220744_s_at	IFT122	0.22	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230233_at	---	0.34	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234926_s_at	C20orf43*	0.33	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203885_at	RAB21	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227633_at	RHEB	0.19	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201237_at	CAPZA2	0.44	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206484_s_at	XPNPEP2*	0.08	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1559048_at	BAHCC1	0.28	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201834_at	PRKAB1	0.43	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210976_s_at	PFKM	0.26	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218756_s_at	DHRS11	0.33	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215707_s_at	PRNP	0.39	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
226389_s_at	RAPGEF1*	0.41	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201192_s_at	PITPNA	0.47	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214437_s_at	SHMT2	0.39	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
210131_x_at	SDHC*	0.45	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
201476_s_at	RRM1	0.36	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201747_s_at	SAFB	0.20	0.319	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213822_s_at	UBE3B	0.29	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209323_at	PRKRIR	0.51	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
230150_at	BCAP29	0.45	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201720_s_at	LAPTM5*	0.20	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203382_s_at	APOE	0.24	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
203325_s_at	COL5A1*	0.08	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
234304_s_at	IPO11	0.28	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207000_s_at	PPP3CC	0.37	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
210786_s_at	FLI1	0.55	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1568611_at	---	0.08	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207883_s_at	TFR2	0.24	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
243659_at	---	0.22	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
220477_s_at	C20orf30	0.48	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226440_at	DUSP22	0.50	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210978_s_at	TAGLN2	0.28	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204545_at	PEX6	0.12	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217872_at	PIH1D1	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211501_s_at	EIF3B*	0.31	0.319	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201671_x_at	USP14	0.46	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212114_at	ATXN7L3B	0.45	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207511_s_at	C2orf24	0.38	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202189_x_at	PTBP1*	0.49	0.319	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
202580_x_at	FOXM1	0.27	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201173_x_at	NUDC	0.56	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
227808_at	DNAJC15	0.45	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211596_s_at	LRIG1	0.07	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200640_at	YWHAZ	0.32	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
212194_s_at	TM9SF4	0.54	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208713_at	HNRNPUL1	0.44	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0
201629_s_at	ACP1	0.43	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225198_at	VAPA	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212041_at	ATP6V0D1	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212161_at	AP2A2	0.38	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217142_at	---	0.35	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202004_x_at	SDHC*	0.32	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
224753_at	CDCA5	0.18	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226044_at	TDP1	0.41	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211714_x_at	TUBB	0.23	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
201801_s_at	SLC29A1	0.37	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204178_s_at	RBM14	0.45	0.319	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
212219_at	PSME4	0.52	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217540_at	FAM55C	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
64488_at	IRGQ*	0.30	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209052_s_at	WHSC1	0.28	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201416_at	SOX4	0.37	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
222466_s_at	MRPL42	0.41	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201246_s_at	OTUB1	0.15	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218080_x_at	FAF1	0.46	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
201379_s_at	TPD52L2	0.35	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202103_at	BRD4	0.40	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

209154_at	TAX1BP3	0.46	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210983_s_at	MCM7	0.13	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201393_s_at	IGF2R	0.28	0.319	0.000	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
208302_at	HMHB1	0.12	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201773_at	ADNP	0.68	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
1554510_s_at	GHITM	0.51	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216306_x_at	PTBP1*	0.35	0.319	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
225175_s_at	SLC44A2*	0.17	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201677_at	C3orf37*	0.10	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208688_x_at	EIF3B*	0.40	0.319	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206918_s_at	CPNE1	0.30	0.319	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208680_at	PRDX1	0.32	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
200866_s_at	PSAP	0.22	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203435_s_at	MME	0.01	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200064_at	HSP90AB1*	0.46	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
206474_at	CDK17	0.31	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204775_at	CHAF1B	0.29	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201903_at	UQCRC1	0.19	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
205512_s_at	AIFM1	0.37	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	1	0	1	1	1
212751_at	UBE2N	0.57	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200611_s_at	WDR1*	0.42	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
242361_at	IMMT	0.47	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
238777_x_at	ATMIN	0.26	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201118_at	PGD	0.37	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
242705_x_at	LRPAP1	0.26	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
202356_s_at	GTF2F1	0.50	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0
201755_at	MCM5*	0.22	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203248_at	ZNF24	0.27	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218122_s_at	SENP2	0.38	0.319	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212291_at	HIPK1	0.37	0.319	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
224640_at	SPPL3	0.50	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
230752_at	---	0.35	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221548_s_at	ILKAP	0.50	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226295_at	ITFG2	0.32	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212101_at	KPNA6	0.41	0.319	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215631_s_at	BRMS1	0.37	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201275_at	FDPS	0.60	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
205049_s_at	CD79A	0.06	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225833_at	DAGLB	0.30	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
207677_s_at	NCF4	0.33	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217806_s_at	POLDIP2	0.43	0.319	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
226118_at	CENPO	0.54	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223020_at	CLPTM1L	0.32	0.319	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
205996_s_at	AK2	0.38	0.319	0.000	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
207829_s_at	BNIP1*	0.34	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
225012_at	HDLBP	0.49	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216910_at	XPNPEP2*	0.13	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212532_s_at	LSM12	0.28	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218496_at	RNASEH1	0.61	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209197_at	SYT11	0.41	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203771_s_at	BLVRA	0.44	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209316_s_at	HBS1L*	0.36	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229022_at	ZFX	0.37	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218206_x_at	SCAND1*	0.23	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
204333_s_at	AGA	0.46	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
221727_at	SUB1	0.34	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
210418_s_at	IDH3B	0.47	0.380	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208828_at	POLE3	0.40	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208940_at	SEPHS1	0.29	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211270_x_at	PTBP1*	0.57	0.380	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
206591_at	RAG1	0.05	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0
201175_at	TMX2	0.42	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215236_s_at	PICALM	0.42	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
228094_at	AMICA1	0.23	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217789_at	SNX6	0.58	0.380	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
229864_at	C3orf75	0.39	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203411_s_at	LMNA	0.20	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
37226_at	BNIP1*	0.33	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
202162_s_at	CNOT8*	0.41	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
204257_at	FADS3*	0.34	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200811_at	CIRBP	0.20	0.380	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219633_at	TTPAL	0.42	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223001_at	OSTC	0.49	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201120_s_at	PGRMC1	0.43	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201052_s_at	PSMF1	0.31	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201853_s_at	CDC25B	0.36	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200792_at	XRCC6	0.53	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
235203_at	---	0.35	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1560018_at	ARPP21*	0.06	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
211090_s_at	PRPF4B	0.63	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
200693_at	YWHAQ	0.47	0.380	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
244876_at	---	0.08	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212045_at	GLG1	0.41	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200658_s_at	PHB*	0.31	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	0	0	0
235542_at	TET3	0.52	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218381_s_at	U2AF2	0.43	0.380	0.000	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
215794_x_at	GLUD2	0.49	0.380	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212563_at	BOP1	0.29	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
218355_at	KIF4A	0.38	0.380	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
215117_at	RAG2	0.07	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
203546_at	IPO13	0.43	0.380	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
219816_s_at	RBM23	0.48	0.380	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0
224196_x_at	DPH5*	0.47	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
217737_x_at	C20orf43*	0.38	0.380	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
222386_s_at	COPZ1*	0.40	0.455	0.000	0	0	0	0	0	0	0	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200051_at	SART1	0.29	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	1	1	1
211574_s_at	CD46	0.37	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225174_at	DNAJC10	0.68	0.455	0.000	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
208761_s_at	SUMO1	0.52	0.455	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
212085_at	SLC25A6	0.37	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
227974_at	---	0.43	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
200894_s_at	FKBP4	0.34	0.455	0.000	1	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1555427_s_at	SYNCRIP	0.56	0.455	0.000	1	1	1	1	1	1	1	0	0	0	0	0	0	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0	0
232652_x_at	SCAND1*	0.27	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	1	1	1
233999_s_at	TTC26*	0.21	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
205521_at	EXOG	0.56	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
210935_s_at	WDR1*	0.34	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209870_s_at	APBA2	0.33	0.455	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216903_s_at	CBARA1	0.53	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225784_s_at	ZC4H2	0.35	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
214153_at	ELOVL5	0.36	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
225830_at	PDZD8	0.28	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
223504_at	DNAJC27	0.53	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224913_s_at	TIMM50	0.38	0.455	0.000	1	1	1	1	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0
201721_s_at	LAPTM5*	0.27	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
224600_at	CGGBP1	0.50	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
218391_at	SNF8	0.39	0.455	0.000	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213787_s_at	EBP	0.31	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
201895_at	ARAF	0.53	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
209314_s_at	HBS1L*	0.33	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
216032_s_at	ERGIC3	0.34	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
213079_at	TSR2	0.30	0.455	0.000	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Total number of unique gene symbols in each group					67	64	64	52	14	14	14	19	20	19	28	28	30	8	8	6	12	14	15	12	15	17	27	27	27	15	14	16	15	17	17	17
Fold Enrichment					2.09	2.08	2.03	2.07	4.18	3.92	3.88	2.77	2.64	2.52	2.00	1.99	1.86	5.10	5.10	7.72	3.72	2.69	2.55	2.99	2.21	1.70	1.83	1.81	1.81	2.64	2.65	2.21	2.20	2.16	2.14	2.13
Benjamini p-value					8.89E-07	1.41E-06	2.29E-06	3.73E-05	3.33E-03	3.70E-02	2.05E-02	6.85E-02	6.64E-02	1.37E-01	1.36E-01	1.38E-01	2.13E-01	6.20E-01	6.20E-01	3.96E-01	2.00E-02	2.52E-01	2.49E-01	7.27E-02	4.04E-01	6.53E-01	3.13E-01	2.97E-01	2.95E-01	4.73E-02	5.28E-02	9.57E-02	1.21E-01	3.62E-01	3.64E-01	3.66E-01

*denotes gene represented by multiple probe sets
blue shading highlights genes that are within the indicated cluster.

Supplementary Table 7. Clinical Characteristics of MDS replication cohort.

UPN	Gender	Age @ Diagnosis	%BM Blast	FAB	Cytogenetics	[-5, del(5q)] (0=no/1=yes)	[-20, del(20q)] (0=no/1=yes)	[-7, del(7q)] (0=no/1=yes)	[+8] (0=no/1=yes)	IPSS	Disease Status (0 alive/ 1 dead)	Days from Dx to Death or Last Follow-up	Evolution to AML (0=no/1=yes)	Days from Dx to AML or last Follow-up	DNMT3A status (0=wt/1=mut)	U2AF1 status (0=wt/1=mut)
100901	M	70	4	RA	46,XY,del(3)(q21)[16]/46,XY[4]	0	0	0	0	0.5	1	1835	0	1654	0	0
105327	F	54	1	RA	46,XX[20]	0	0	0	0	0.0	1	1647	0	1646	0	0
112848	M	62	5	RAEB	46,XY,del(5)(q13q33)[18]/46,XY[1]/45,XY,-5[1]	1	0	0	0	0.5	1	2116	0	2033	0	0
116960	F	55	2	RA	46,XX,t(11;13)(q23;q14)[14]/47,idem,+21[2]/46,XX[3]/46,XX,inv(14)(q11.1q32)[1]	0	0	0	0	1.0	0	2362	0	2246	0	0
123363	M	64	0	RA	46,XY[19]/46,XY,del(20)(q11.2q13.1)[1]	0	0	0	0	0.0	0	2421	0	2402	0	0
124124	F	66	18	RAEB	46,XX[20]	0	0	0	0	2.0	1	998	1	891	0	0
127804	M	63	2	RA	46,XY[20]	0	0	0	0	0.5	1	2375	0	2368	0	0
131153	M	78	8	RAEB	44,XY,dup(3)(p21p25),-5,-6,del(12)(q15q22),psu dic(15;14)(p13;q32),add(17)(p11.2),add(19)(q13.3),?t(22;22)(q12;13),+mar[20]	1	0	0	0	2.0	1	621	0	619	0	0
137250	F	54	19	RAEB	46,XX[20]	0	0	0	0	2.0	0	3037	1	38	0	1
137313	F	77	0	RA	47,XX,+8[6]/46,XX[14]	0	0	0	1	1.0	1	320	0	144	0	0
137404	F	70	0	RAR	46,XX,add(1)(p13),del(1)(q23),add(3)(p13),del(5)(q13q33),add(8)(p11.2),add(9)(q22),add(10)(q22),add(11)(p14),-12,del(17)(q21),+mar[17]/46,XX[3]	1	0	0	0	1.0	1	674	0	663	0	0
173005	M	77	10	RAEB	45,XY,der(3;5)(q10;p10),-18,-20,+2mar[12]/46,idem,+21[5]/46,XY[3]	0	1	0	0	2.0	1	800	0	71	0	0
176267	M	56	7	RAEB	43-47,XY,del(5)(q13q33),der(7)t(7;11)(q11.2;q21),-9,-12,der(16)t(12;16)(q10;q22),add(16)(q23),+mar1,+mar2[cp12]/44-46,XY,del(5)(q13q33),der(7)t(7;11)(q11.2;q21),t(12;16)(q10;q22)[cp8]	1	0	0	0	2.0	1	137	1	93	1	0
177356	F	76	2	RA	46,XX[20]	0	0	0	0	0.0	0	1304	0	747	0	0
182896	M	75	0	RA	46,XY,add(4)(p16),t(4;20)(q25;p13),del(5)(q15q31)[13]/46,idem,del(6)(q?25)[1]/47,XY,+8[6]	1	0	0	1	1.0	1	1205	1	1047	0	0
184368	F	49	0	RA	46,XX[20]	0	0	0	0	0.0	0	2013	0	81	0	0
184874	F	56	2	RAR	47,XX,+8[10]/46,XX[10]	0	0	0	1	0.5	1	2020	0	2020	0	0
185295	M	50	0	RA	46,XY,del(20)(q11.2q13.3)[7]/46,XY[13]	0	1	0	0	0.5	0	2939	0	2538	0	1
189012	M	54	3	RA	46,XY,del(5)(q15q33)[16]/46,XY,del(5)(q12q33), del(7)(q21q32)[1]/46,XY[3]	1	0	0	0	0.5	0	1250	0	1230	0	0
189474	M	61	4	RAEB	46,XY[3]	0	0	0	0	0.5	0	1336	0	907	0	0
194328	M	52	1	RA	46,XY[20]	0	0	0	0	0.0	0	1702	0	809	0	0
197795	M	50	17	RAEB	46,XY[20]	0	0	0	0	1.5	1	1064	0	457	0	0
199019	F	60	0	RA	45-49,XX,+1,add(3)(p11),del(5)(q13q33),del(10)(q24q26),add(18)(q21),+19,-20,+21,+1-2mar[cp20]	1	1	0	0	1.5	1	1491	1	1020	0	0
201641	M	62	14	RAEB	44~45,XY,del(3)(q12),add(5)(q35),del(5)(q12q33),del(7)(q22),-12,der(17)t(7;17)(q22p13)[15]/46,XY[5]	1	0	1	0	3.0	1	220	0	199	0	0
207282	M	76	11	RAEB	46,XY[20]	0	0	0	0	2.0	1	251	1	122	1	0
222841	F	46	17	RAEB	60<3n>,XX,-X,add(1)(q44),ins(1)(p36)add(1)(q12),-5,del(5)(q11.2q33),+6,-7,add(7)(p22),-10,-11,del(12)(q13),add(12)(p13),-13,-14,hsr(14)(p11.1),-16,-16,-18,der(19;21)(q10;q10),+21,-22,+mar[5]/46,XX[15]	1	0	1	0	2.5	1	528	0	528	0	0
266395	M	65	7	RAEB	46,XY[20]	0	0	0	0	1.0	1	321	1	75	0	1
288033	F	31	13	RAEB	46,XX[20]	0	0	0	0	2.0	1	367	1	28	0	0
298273	M	27	18	RAEB-T	46,XY[20]	0	0	0	0	2.0	1	540	1	131	0	0
300813	F	42	2	RA	46,XX[20]	0	0	0	0	0.0	0	2172	0	2172	0	1
312519	F	71	0	RA	46,XX[20]	0	0	0	0	0.5	1	1026	0	436	0	0
313175	M	74	5	RAEB	46,XY[20]	0	0	0	0	0.0	0	961	0	702	0	0
315529	M	56	12	RAEB	46,XY,add(7)(q32),r(8)(p21q24.3),add(11)(p15),t(12;13)(q24.2;q13),-17,r(19)(p13.3q13.4),-20,add(20)(q13.1),-21,+3mar[18]/46,idem,del(5)(q22q34)[1]/46,XY[1]	0	1	0	0	3.0	1	147	0	147	0	0
317598	M	86	11	RAEB	46,XY[20]	0	0	0	0	2.0	1	30	0	30	1	0
319179	F	74	6	RAEB	46,XX[20]	0	0	0	0	0.5	1	483	1	482	1	0
321864	F	63	12	RAEB	47,XX,+8[20]	0	0	0	1	2.5	1	80	0	80	0	1
322997	M	65	0	RA	46,XY[20]	0	0	0	0	0.5	1	249	0	186	0	0
335224	M	65	3	RA	45,XY,del(5)(q22q33),hsr(11)(p15),der(17;22)(q10;q10)[17]/45,XY,idem,hsr(11)(p15)(q23)[3]	1	0	0	0	1.5	1	202	1	104	0	0
335875	F	46	2	RA	46,XX[20]	0	0	0	0	0.0	0	1387	0	1229	0	0
337081	M	67	10	RAEB	46,XY[20]	0	0	0	0	0.5	1	1108	0	31	0	0
342760	F	77	12	RAEB	46,XX[20]	0	0	0	0	1.5	1	1447	0	1447	0	0
343306	F	62	15	RAEB	40~45,XX,-4,-5,add(10)(p15),add(15)(p11.2),-17,+add(19)(p13.3),add(21)(p11.2),-22,+mar[cp3]/46,XX[10]--only 13 analyzed	1	0	0	0	3.0	1	686	0	683	0	0
346313	M	62	6	RAEB	46,XY[20]	0	0	0	0	1.0	1	965	1	787	0	0
350460	M	30	4	RA	46,XY[17]	0	0	0	0	0.5	1	905	0	904	0	0
362699	F	73	2	RA	46,XX[18]/47,XX,+4[1]/47,XX,+9[1]	0	0	0	0	0.5	1	307	0	127	0	0
369682	M	59	ND	RA	45,XY,der(5)t(3;5)(q21;q13)[9]/46,idem,+8[6]/46,idem,+mar[1]/46,XY[4]	0	0	0	1	UK	1	94	1	91	0	0
372440	M	59	2	RA	46,XY[20]	0	0	0	0	0.0	0	1891	0	1894	0	0
379929	F	39	3	RA	46,XX[20]	0	0	0	0	0.5	1	290	1	224	1	0
391828	M	50	3	RA	46,XY,inv(3)(q21q26.2)[6]/46,XY[14]	0	0	0	0	1.0	1	1852	0	1852	0	0
392543	M	74	13	RAEB	55-57,XY,+1,+2,+6,der(7)t(7;11)(p22;q13),+9,-10,+11,+13,+14,add(14)(p11.2),add(17)(p11.2),-18,+21,add(21)(p11.2),+22,+1-2r,+1-3mar[cp7]/46,XY[13]	0	0	0	0	2.5	1	599	1	589	0	0
395621	F	35	6	RAEB	46,XX, der(15)t(1;15)(q10;q10)[15]/46,XX[5]	0	0	0	0	1.0	1	541	1	140	0	0
411330	M	83	2	RA	45,X,-Y[3]/46,XY[17]	0	0	0	0	0.0	1	18	0	18	0	0
421452	F	33	10	RAEB	46,XX[20]	0	0	0	0	1.0	0	2016	1	90	0	0
429531	F	38	0	RA	46,XX,del(5)(q12q33)[18]/46,XX[2]	1	0	0	0	0.5	0	2951	0	2577	0	0
430998	M	56	0	RA	47,XY,+14[5],46,XY,i(14)(q10)[5]/46,XY[10]	0	0	0	0	0.5	0	1067	0	706	0	0
431137	M	55	7	RAEB	46,XY,add(3)(q25),del(3)(p13),del(5)(q15q31),-6,+8,add(12)(p11.2),add(15)(p11.1),-18,+22[cp4]/44,sl,-8,-20,-22,+mar[cp5]/44,sl1,-del(3),-7,+2mar[cp5]/43,sl1,add(X)(q28),-add(12p),+12,-mar[cp6]	1	1	1	1	2.0	1	181	0	181	0	0
431586	M	68	6	RAEB	87,XY,+X,+1,+1,+2,+2,+3,+3,+4,+4,+5,+5,+6,+7,+7,+8,+8,+9,+9,+10,+10,+11,+11,+12,+12,+13,+13,+14,+14,+15,+16,+16,+17,+17,+18,+18,+19,+19,+20,+20,+21,+21,+22,+22[3]/46,XY[22]	0	0	0	1	1.5	1	337	1	275	0	0
447189	M	76	0	RA	46,XY[20]	0	0	0	0	0.5	0	1795	0	1436	0	0
455113	F	68	2	RA	46,XY[20]	0	0	0	0	0.0	0	2244	0	1982	0	0
455194	M	62	2	RA	47,XY,+8[19]/46,XY[1]	0	0	0	1	0.5	0	1529	0	1302	0	0
457721	M	63	22	RAEB-T	46,XY[20]	0	0	0	0	2.5	1	398	1	173	1	0
461282	M	65	6	RAEB	46,XY,-17,del(20)(q11.2),r[5]/46,idem,del(5)(q31q33)[10]/46,idem,del(5)(q13q33)[3]/46,idem,-X,add(X)(q22),der(12)t(12;?)(p11.2;?)del(12)(q22)[2]	1	1	0	0	2.0	1	2009	1	1751	0	0
461321	F	78	6	RAEB	46,XX[18]	0	0	0	0	0.5	0	981	1	178	0	0
462596	M	78	0	RA	46,XY[20]	0	0	0	0	0.5	1	395	0	177	0	0
463763	M	54	0	RA	47,XY,+Y[6]/46,XY[14]	0	0	0	0	0.5	0	1385	0	1332	0	1
485523	M	62	11	RAEB	46,XY[20]	0	0	0	0	2.0	0	814	0	804	0	0
497942	M	38	0	RA	46,XY,der(1;22)(q10;q10)[4]/46,XY[16]	0	0	0	0	1.0	1	4626	0	4553	0	0
511734	M	69	4	RAEB-T	46,XY[20]	0	0	0	0	0.0	1	353	0	353	0	0
518747	F	47	6	RAEB	46,XX[11]	0	0	0	0	1.0	0	844	0	816	0	0
530722	M	69	13	RAEB	46,XY[20]	0	0	0	0	2.0	1	311	1	24	0	0
530724	F	67	11	RAEB	Failed	0	0	0	0	UK	1	32	0	12	0	0
537426	F	57	2	RA	45,XX,-7[20]	0	0	1	0	1.5	0	1908	0	1833	0	0
538267	F	49	12	RAEB	42~88,XX,-X,t(3;17)(q21;q21),del(5)(q15q33),-10,t(2;18)(q11.2;q11.2),-12,-13,t(17;20)(q21;11.2)add(17)(p11.2),dic(19;21)(p13q22),+r,+mar[cp18]/46,XX[2]	1	0	0	0	3.0	1	407	0	407	0	0
543465	M	75	11	RAEB	46,XY[20]	0	0	0	0	2.0	0	3080	1	160	0	0
547403	M	61	16	RAEB	46,X,-Y,+14[2]/45,X,-Y[2]/45,XY,-20[1]	0	0	0	0	2.5	1	132	0	132	0	0
554562	M	80	0	RA	46,XY,del(20)(q11.2q13.3)[8]/46,XY,+8[3]/46,XY[9]	0	1	0	1	0.5	1	1256	1	1314	0	0
557468	M	76	18	RAEB	46,XY[20]	0	0	0	0	2.0	1	712	1	217	0	0
558896	M	73	15	RAEB	47~50,XY,t(2;19)(p16;p13),del(5)(q12q33),-11,-18,-20,+r,+2~6mar[4]/41~50,sl,+5,del(5)(q12q33),[8]/47~50,sdl1,+r[8]	1	1	0	0	3.0	1	57	0	57	0	0
571656	M	71	4	RAEB	46,del(20)(q11.2q13.3)[12]/46,XY[8]	0	1	0	0	0.5	1	303	1	231	0	1
574490	M	57	1	RA	46,XY[20]	0	0	0	0	0.0	1	874	0	874	0	0
577164	M	87	17	RAEB	43-46,XY,-3,-5,-7,+8,-12,-13,add(17)(p11.2),add(21)(p11.2),-22,+2-4mar[cp20]	1	0	1	1	3.0	1	78	0	78	0	0
597501	F	52	3	RAR	46,XX[20]	0	0	0	0	0.0	1	2321	0	1938	0	0
608870	M	42	0	RA	46,XY[20]	0	0	0	0	0.0	0	2311	0	2279	0	0
610184	F	45	0	RA	42,XX,add(1)(p36.3),del(5)(q13q33),-13,dic(16;21)(p13.3;q11.2),add(17)(p13),-18,-22[20]	1	0	0	0	1.0	1	589	1	314	0	0
611835	F	56	1	RA	46,XX, inv(17)(p11.2q23)?c[20]	0	0	0	0	1.0	0	2533	0	2516	0	0
625765	F	61	1	RA	46,XX[20]	0	0	0	0	0.5	0	1316	0	21	0	0
631698	M	64	0	RA	47,XY,+8[13]/46,XY[7]	0	0	0	1	1.0	1	491	1	422	0	0
641987	F	83	3	RAEB	46,XY, del(5)q,-7,-13,-19, +11, [10]/46,XX[10]	1	0	1	0	1.5	1	460	0	132	0	0

643607	F	79	3	RA	46,XX[20]	0	0	0	0	0.0	1	897	0	14	0	0
657314	F	28	4	RAEB	45,XX,-7[5]	0	0	1	0	1.5	0	1704	0	1681	0	0
667720	F	66	10	RAEB	46,XX[20]	0	0	0	0	1.0	1	724	1	644	0	0
672525	F	73	5	RAEB	46,XX[20]	0	0	0	0	1.0	1	2395	0	2247	0	0
684211	F	62	1	RAR	46, XX,del(5)(q13q33),del(20)(q11.2)[cp5]	1	1	0	0	0.5	1	325	1	231	0	0
690100	M	66	15	RAEB	43-45,XY,del(5q)(q22q35),der(16)t(16,17)(q22;q21),-17,add(17)(p11.2),-18, dic(18;21)(p11.1;q22), der(22)t(1;22)(p13;p11.2),+0-2mar[cp19]/47,XY,+12[1]	1	0	0	0	3.0	1	331	1	324	1	0
693881	F	78	11	RAEB	44,XX,-3,del(5)(q13q33),-7,add(9)(q22),add(13)(p11.2),-18,add(18)(p11.2),-20,+2mar[18]/46,XX[2]	1	1	1	0	3.0	1	383	0	369	0	0
696026	M	48	0	RA	47,XY,+8[2]/47,idem,add(3)(q21)[6]/47,add(3)(q21),del(12)(p11.2p13)[12]	0	0	0	1	1.5	0	4566	0	4498	0	0
697296	M	71	3	RA	46,XY[20]	0	0	0	0	0.5	1	1385	0	87	0	0
698840	F	77	13	RAEB	46,XX,del(5)(q13q233)[1]/42~47,sl,dic(15;20)(p11.2;q13.3),add(22)(p11.1)[cp3]/44~47,sl,der(3)t(3;15)(p11.2;q11.1),der(14;22)(q10;q10),+0-5mar[cp6]/82~87,slx2,-3,del(4)(q?27)x2,-7,add(12)(p11.2)x2,der(15;21)(q10;q10),der(15;22)(q10;q10),-17,-17,+19,-21,add(21)(p11.2),-22,-22,+0-5mar[cp9]/46,XX[1]	0	0	1	0	3.0	1	253	0	7	0	0
703653	F	20	0	RA	46,XX[20]	0	0	0	0	0.5	0	2257	0	2092	0	0
705782	M	34	5	RAEB	46, XY, t(3;5)(q21;q31)[13]/46,idem,?add(12)(q24.3)[5]/46,XY, ?add(12)(q24.3)[2]	0	0	0	0	2.0	0	1711	0	1703	0	0
717045	F	48	2	RA	46,XX,del(5)(q13q33)[20]	1	0	0	0	0.5	1	393	0	393	0	0
732776	F	47	8	RAEB	46,XX[20]	0	0	0	0	1.0	0	2255	0	11	0	0
736895	M	54	2	RA	43~49,XY,-4,-5,-7,add(12)(p11.2),-20,-21,+1~6mar[cp7]	1	1	1	0	1.5	1	38	0	26	0	0
747967	M	41	2	RA	46,XY,+1,der(1;15)(q10;q10)[8]/46,XY,+1,der(1;7)(q10;p10)[4]46,XY[8]	0	0	0	0	1.0	0	1940	0	1899	0	0
753222	M	79	0	RA	60-61,XXY,add(3)(p21),del(5)(q13q33),add(6)(q25),-7,-8,-9,add(14)(p11.2),-16,-17,+19,add(19)(q13.4)x2,-22[cp2]/46,XY[68]	1	0	1	0	1.5	1	123	0	123	0	0
783437	M	63	8	RAEB	46,XX[20]	0	0	0	0	1.0	1	1095	1	594	0	0
785104	F	44	2	RA	46,XX[20]	0	0	0	0	0.0	0	1317	0	1172	0	0
791334	F	66	3	RA	46,XX[20]	0	0	0	0	0.5	1	923	0	923	0	0
804059	M	69	9	RAEB	47,XY,+8[20]	0	0	0	1	1.5	1	878	1	287	0	0
809605	M	75	14	RAEB	46,XY[12]	0	0	0	0	2.0	0	849	0	849	0	0
817019	F	65	3	RA	46,XX,idel(20)(q11.2)[9]/46,XX[11]	0	1	0	0	0.0	0	1172	0	861	0	0
827584	M	62	8	RAEB	47,XY,+8[15]/46,XY[5]	0	0	0	1	1.0	0	1710	0	1703	0	0
843623	M	60	6	RAEB	46,XY,del(20)(q11.2q13.3)[2]/46,XY[18]	0	1	0	0	1.0	1	139	1	71	0	1
845446	M	73	13	RAEB	47,XY,+8,del(12)(p11.2p13)[18]/47,idem,del(3)(q21)[2]	0	0	0	1	3.0	1	251	0	251	0	0
846155	M	64	0	RA	46,XY[20]	0	0	0	0	0.5	0	1023	0	1026	0	0
854400	M	63	0	RA	46,XY,Yqh+[20]	0	0	0	0	0.0	1	945	0	923	0	0
855934	M	62	26	RAEB-T	46,XY[20]	0	0	0	0	2.5	1	453	0	453	0	0
857645	M	60	ND	RA	46,XY[20]	0	0	0	0	UK	1	860	1	821	0	0
859640	F	64	3	RA	46,XX[20]	0	0	0	0	0.0	1	609	1	252	0	0
861691	M	62	13	RAEB	45,XY,-7[15]/46,XY[5]	0	0	1	0	3.0	0	3144	0	118	0	0
875301	F	62	14	RAEB	46,XX[20]	0	0	0	0	1.5	1	463	1	81	0	0
879047	F	74	17	RAEB	46,XX,del(11)(q21q24)[13]/46,XX[7]	0	0	0	0	2.5	1	980	0	980	0	0
882525	M	57	7	RAEB	41~49, XY, +X, +X, del(5q)(q22q35), del(7)(q22), +8, -12, add(12)(p12), -13, -18, +1~4mar[cp20]	1	0	1	1	2.0	1	148	1	88	0	0
889352	M	72	14	RAEB	39~44,XY,del(4)(q31)[14],der(5)t(5;?)(q21;?)[17],del(6)(q21)[19],-7[19],add(12)(p13)[18],-18[18][cp19]	0	0	1	0	3.0	1	42	0	42	0	0
911999	M	36	4	RA	46,XY[20]	0	0	0	0	0.0	0	3250	0	3232	0	0
912290	M	59	1	RA	46,XY[20]	0	0	0	0	0.5	1	696	0	696	0	0
917011	M	79	0	RA	46,XY,del(20)(q11.2)[12]/46,XY[8]	0	1	0	0	0.5	1	809	0	769	1	1
936943	M	43	ND	RAEB	failed.	0	0	0	0	UK	1	1300	0	1289	0	0
937954	M	51	12	RAEB	47,XY,+8[1]/47,idem,del(16)(q12.1)[13]/48,idem,+Y,del(16)(q11.1)[5]/46,XY[1]	0	0	0	1	2.5	1	729	0	131	0	1
943264	M	65	11	RAEB	46,XY[20]	0	0	0	0	1.5	0	891	0	848	0	0
944541	M	54	20	RAEB	45,XY,-7[19]/46,XY[1]	0	0	1	0	3.0	1	1630	0	1630	0	0
947519	M	59	7	RAEB	46,XY,1-5dims[10]/46,XY[12]	0	0	0	0	1.5	1	734	1	699	0	1
949197	F	60	2	RA	failed	0	0	0	0	UK	1	108	0	89	0	0
958595	F	82	4	RA	46,XX,del(11)(q23)[20]	0	0	0	0	1.0	1	975	0	975	1	0
973424	M	56	3	RA	46,XY[20]	0	0	0	0	0.0	0	1228	0	1027	0	0
975079	M	62	0	RA	46,XY[20]	0	0	0	0	0.0	1	1563	0	1563	1	0
983677	F	60	8	RAEB	46,XX,del(5)(q21q35)[4]/69,XX,+X,+1,+1,+2,+del(5)(q21q35),+5,+6,+8,+9,+9,+10,+11,+11,+13,+13,+14,+16,+16,+19,+19,+20,+21,-22,+mar1,+mar2[7]/46,XX[9]	1	0	0	1	2.0	1	85	1	44	0	0
987089	F	64	3	RAEB	56-58,XX,+X,+del(3)(p12),del(5)(q13q33),+6,+8,+der(8)add(8q22),+10,+11,+13,+14,-17,+19,+21,+mar[cp20]	1	0	0	1	2.0	1	762	1	678	0	0
988428	M	70	2	RAR	47,XY,-9,+2mar[1]/46,XY[19]	0	0	0	0	0.5	1	1975	0	1891	1	0
989739	M	71	18	RAEB	46,XY,del(7)(q21)[11]/47,XY,+8[5]/46,XY[4]	0	0	1	1	3.0	1	468	1	125	1	1
994096	M	72	3	RA	46,XY,del(5)(q14q34),+8,del(11)(q21q23)[19]/46,idem,del(17)(q24)[1]	1	0	0	1	1.0	1	1307	0	1178	0	0
999103	F	66	6	RAEB	46,XX,del(5)(q15q13)[20]	1	0	0	0	1.0	1	4813	0	2839	0	0
01-13	F	41	12	RAEB	46,XX,inv(3)(q21q26)[13]/46,idem,t(14;17)(q13;p13)[1]	0	0	0	0	2.0	1	1649	1	1301	0	0
02-21	M	57	3	RA	46,XY,t(3;12)(q27;p13)[20]	0	0	0	0	1.0	1	709	0	709	0	0
02-28	M	60	1	RA	46,XY,t(5;15)(p10;q10)[2]/46,XY[18]	0	0	0	0	1.0	1	76	0	76	0	0
02-30	M	72	2	RA	46-48,XY,add(5)(q11.2),-?oradd(7)(q11.2),add(8)(p22),del(13)(q21),add(16)(q?22),del(22)(q12),+1-3mar[cp19]/46,XY[1]	0	0	1	0	1.5	1	239	1	205	0	0
02-75	F	46	10	RAEB	46,XX[20]	0	0	0	0	0.5	0	3247	0	3014	0	0
02-77	M	67	28	RAEB-T	46,XY[20]	0	0	0	0	2.0	1	1863	1	1662	0	0
02-86	M	53	21	RAEB-T	92<4n>,XXYY,del(4)(q33)x2,del(5)(q13),add(11)(q23)x2[cp8]/46,XY[12]	1	0	0	0	3.0	1	308	1	133	0	1
02-99	M	66	16	RAEB	46,XY,del(2)(q33),del(5)(q15q33),-7,+del(11)(q2?3)[cp6]	1	0	1	0	3.0	1	945	0	933	0	0

Supplementary Table 8. Primers used for U2AF1 sequencing.

Ensembl TranscriptID	Chromosome	Exon#	Exon Start	Exon Stop	Primer 1 Sequence*	Primer 2 Sequence	Ensembl ExonIDs
gDNA primers: targets U2AF1 hotspot only							
ENST00000398137	21	2	43397494	43397581	tgtactactcAAACAAACCTGGTAAACGTCG	acatgatgagAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	acgactacagAAACAAACCTGGTAAACGTCG	tgctgatgtcAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	cgtagactagAAACAAACCTGGTAAACGTCG	gcatctgatcAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tacgagtatgAAACAAACCTGGTAAACGTCG	atgctcatacAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tactctcgtgAAACAAACCTGGTAAACGTCG	atgagagcacAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tagagacgagAAACAAACCTGGTAAACGTCG	atctctgctcAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tcgtcgctcgAAACAAACCTGGTAAACGTCG	agcagcgagcAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	acatacgcgtAAACAAACCTGGTAAACGTCG	tgtatgcgcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	acgcgactatAAACAAACCTGGTAAACGTCG	tgcgctgataAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	actactatgtAAACAAACCTGGTAAACGTCG	tgatgatacaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	actgtacagtAAACAAACCTGGTAAACGTCG	tgacatgtcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	agactatactAAACAAACCTGGTAAACGTCG	tctgatatgaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	agcgtcgtctAAACAAACCTGGTAAACGTCG	tcgcagcagaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	agtacgctatAAACAAACCTGGTAAACGTCG	tcatgcgataAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	atagagtactAAACAAACCTGGTAAACGTCG	tatctcatgaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	cacgctacgtAAACAAACCTGGTAAACGTCG	gtgcgatgcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	cagtagacgtAAACAAACCTGGTAAACGTCG	gtcatctgcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	cgacgtgactAAACAAACCTGGTAAACGTCG	gctgcactgaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tacacacactAAACAAACCTGGTAAACGTCG	atgtgtgtgaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tacacgtgatAAACAAACCTGGTAAACGTCG	atgtgcactaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tacagatcgtAAACAAACCTGGTAAACGTCG	atgtctagcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tacgctgtctAAACAAACCTGGTAAACGTCG	atgcgacagaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tagtgtagatAAACAAACCTGGTAAACGTCG	atcacatctaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tcgatcacgtAAACAAACCTGGTAAACGTCG	agctagtgcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tcgcactagtAAACAAACCTGGTAAACGTCG	agcgtgatcaAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
cDNA primers: targets U2AF1 hotspot only							
ENST00000398137	21	1-4	43393632	43400757	acgagtgcgtGGAGTATCTGGCCTCCATCTTC	tgctcacgcaGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	acgctcgacaGGAGTATCTGGCCTCCATCTTC	tgcgagctgtGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	agacgcactcGGAGTATCTGGCCTCCATCTTC	tctgcgtgagGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	agcactgtagGGAGTATCTGGCCTCCATCTTC	tcgtgacatcGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	atcagacacgGGAGTATCTGGCCTCCATCTTC	tagtctgtgcGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	atatcgcgagGGAGTATCTGGCCTCCATCTTC	tatagcgctcGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	cgtgtctctaGGAGTATCTGGCCTCCATCTTC	gcacagagatGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	ctcgcgtgtcGGAGTATCTGGCCTCCATCTTC	gagcgcacagGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
ENST00000398137	21	1-4	43393632	43400757	tagtatcagcGGAGTATCTGGCCTCCATCTTC	atcatagtcgGTCAGCAGACTGGGAAGAGTTT	ENSE00001582950, ENSE00001531800, ENSE00001531797, ENSE00001531794
3730 recurrent screening primers: targets all U2AF1 coding exons							
ENST00000398137	21	9	43386136	43386428	tgtaaaacgacggccagtTGAGAGAGTGGGTGTGGTTCTG	caggaaacagctatgaccCCCTTATGAACTGGTTTGGTCAAT	ENSE00001138177
ENST00000398137	21	9	43386136	43386428	tgtaaaacgacggccagtGAGAGTGGGTGTGGTTCTGTGC	caggaaacagctatgaccTCTTTCACGATCTCTCGACCG	ENSE00001138177
ENST00000398137	21	8	43387650	43387742	tgtaaaacgacggccagtTAACCGTTGGTTTAATGGACAGCC	caggaaacagctatgaccGAGGGTTGTGAGGGGAGAAAGAAG	ENSE00001268168
ENST00000398137	21	7	43387834	43387967	tgtaaaacgacggccagtTAACCGTTGGTTTAATGGACAGCC	caggaaacagctatgaccGAGGGTTGTGAGGGGAGAAAGAAG	ENSE00001050518
ENST00000398137	21	7	43387834	43387967	tgtaaaacgacggccagtAAAGTCTTATTAAAGCGTGGATGGC	caggaaacagctatgaccCATACTGACGGCAGCAGGC	ENSE00001050518
ENST00000398137	21	6	43388617	43388715	tgtaaaacgacggccagtGTTGATCTTCTGTATCTGTTTGGAAGG	caggaaacagctatgaccCACTGTCTCGCTTTCGCCTG	ENSE00001050529
ENST00000398137	21	5	43388873	43388922	tgtaaaacgacggccagtCGTGTGTGTTACTGTAGCAGTTTGAG	caggaaacagctatgaccACCTCCTGAAGGGAGACCACAG	ENSE00001531791
ENST00000398137	21	4	43393632	43393698	tgtaaaacgacggccagtGAATCTCAACTGAAGCACTTGCC	caggaaacagctatgaccCCTTGCCACCTCTAGTGAAACG	ENSE00001531794
ENST00000398137	21	3	43394545	43394611	tgtaaaacgacggccagtGCCATTTGCAAACAAATTGTCTCT	caggaaacagctatgaccCAGCAGCTCAGAAGCCAACAT	ENSE00001531797
ENST00000398137	21	2	43397494	43397581	tgtaaaacgacggccagtTGAACACAAATGGAAAATACAACTACG	caggaaacagctatgaccTTCAAAATTGGAGCATGTCGTC	ENSE00001531800
ENST00000398137	21	2	43397494	43397581	tgtaaaacgacggccagtAAACAAACCTGGTAAACGTCG	caggaaacagctatgaccAATTTGATAGTGTATGTCATGCTGCTG	ENSE00001531800
ENST00000398137	21	1	43400630	43400757	tgtaaaacgacggccagtAGAGCGTCGTCGCGTCCG	caggaaacagctatgaccCCACCGCCTCAACCACCC	ENSE00001582950

***lower case, bar code; upper case,*U2AF1 sequence**

Supplementary Table 9. Expression of Tier 1 mutated genes in sAML sample.

							Present Probes					Present Probes in Mutant Exon			
Chromosome	Position*	Gene name	Transcript ID	Exons	Mutant Exon	Total Probes	in UPN 266395	in > 50% of AML samples	in > 75% of AML samples	in > 90% of AML samples	Probes in Mutant Exon	in UPN 266395	in > 50% of AML samples	in > 75% of AML samples	in > 90% of AML samples
1	112325945	KCND3	NM_004980	8	2	20	3	2	2	1	3	0	0	0	0
1	205309412	PFKFB2	NM_006212	15	11	29	2	15	9	4	1	0	1	0	0
1	229096537	ENSG00000222671	ENST00000410739	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
2	20289990	LOC100131373	XM_001720891	1	1	3	1	3	1	1	1	1	1	0	0
2	61569230	XPO1	NM_003400	25	18	38	31	33	33	33	1	1	1	1	1
3	173529456	FNDC3B	NM_022763	25	11	43	41	43	43	42	2	2	2	2	2
5	50152869	PARP8	NM_024615	26	16	31	28	30	29	27	1	1	1	1	1
5	148880083	CSNK1A1	NM_001025105	11	4	26	24	25	24	24	1	1	1	1	1
6	105713110	POPDC3	NM_022361	4	4	13	0	1	0	0	3	0	0	0	0
9	89535224	CTSL1	NM_001912	8	7	20	9	11	5	5	1	1	1	1	1
9	138867831	MAMDC4	NM_206920	27	4	49	12	13	11	9	1	0	0	0	0
9	139117274	MAN1B1	ENST00000371587	9	9	45	17	21	17	15	8	5	6	5	5
10	82288101	SH2D4B	NM_207372	7	1	17	4	6	4	1	1	0	0	0	0
11	22340860	SLC17A6	NM_020346	12	splice_site	15	2	2	2	0	NA	NA	NA	NA	NA
11	30881639	DCDC5	ENST00000406071	15	12	54	3	3	3	2	2	0	0	0	0
14	75418958	TTLL5	NM_015072	32	30	50	41	45	44	40	2	2	2	2	2
16	7716860	ENSG00000209555	ENST00000386820	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
16	63589987	CDH11	NM_001797	13	4	28	5	8	4	4	2	0	0	0	0
17	5288451	DHX33	NM_020162	12	12	17	6	13	11	7	1	0	0	0	0
17	7696343	JMJD3	NM_001080424	22	19	44	19	27	22	21	1	0	0	0	0
17	29981226	TMEM132E	NM_207313	10	6	13	4	3	2	2	1	0	0	0	0
17	75696250	GAA	NM_000152	20	5	27	5	6	4	2	1	0	0	0	0
18	46165704	C18orf24	NM_001039535	7	5	14	3	6	2	2	1	0	1	0	0
19	53579461	KDELR1	NM_006801	5	4	12	7	8	8	6	2	1	2	2	1
19	54349852	HRC	NM_002152	6	1	16	1	3	3	2	9	1	2	2	2
20	32728482	PIGU	NM_080476	12	1	18	16	16	15	12	1	1	1	1	0
20	32965857	ACSS2	NM_018677	18	7	28	18	16	11	7	2	1	1	1	0
20	51626823	ZNF217	NM_006526	5	3	15	15	15	15	12	5	5	5	5	5
21	42402818	UMODL1	NM_173568	22	10	28	4	5	4	4	1	0	0	0	0
21	43397525	U2AF1	NM_001025203	8	2	22	18	22	22	20	1	1	1	1	1

*using NCBI Build 36. NA, not available.

Supplementary References

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