Supplementary Information

Exome Sequencing Identifies Somatic Mutations of DNA Methyltransferase

Gene *DNMT3A* in Acute Monocytic Leukemia
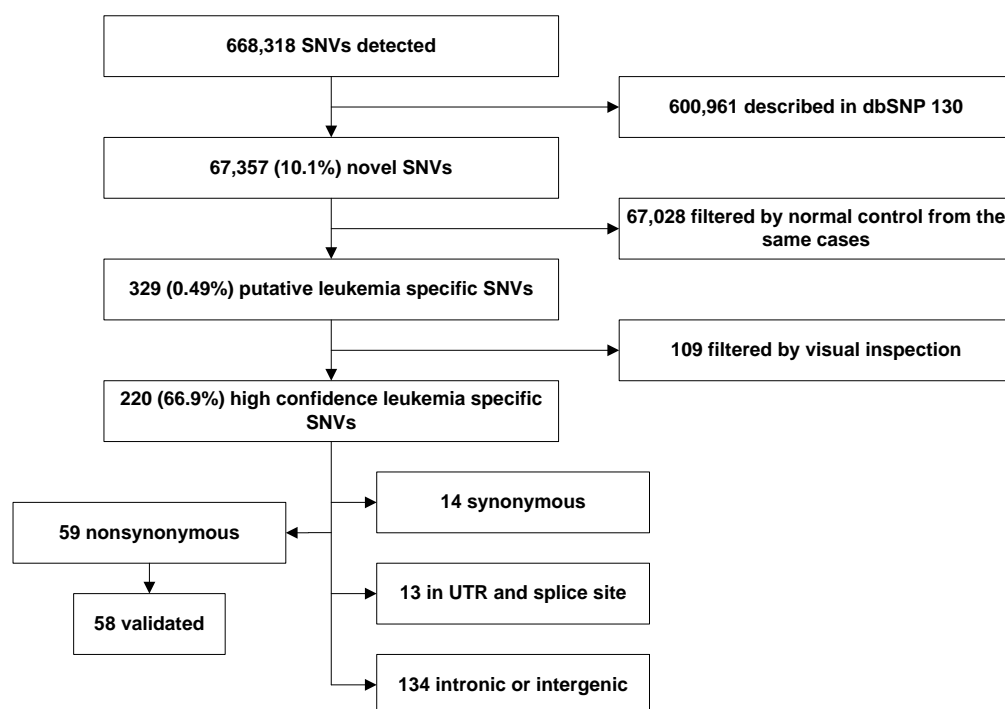
Xiao-Jing Yan*, Jie Xu*, Zhao-Hui Gu*, Chun-Ming Pan*, Gang Lu*, Yang Shen, Jing-Yi Shi, Yong-Mei Zhu, Lin Tang, Xiao-Wei Zhang, Wen-Xue Liang, Jian-Qing Mi, Huai-Dong Song, Ke-Qin Li, Zhu Chen, Sai-Juan Chen
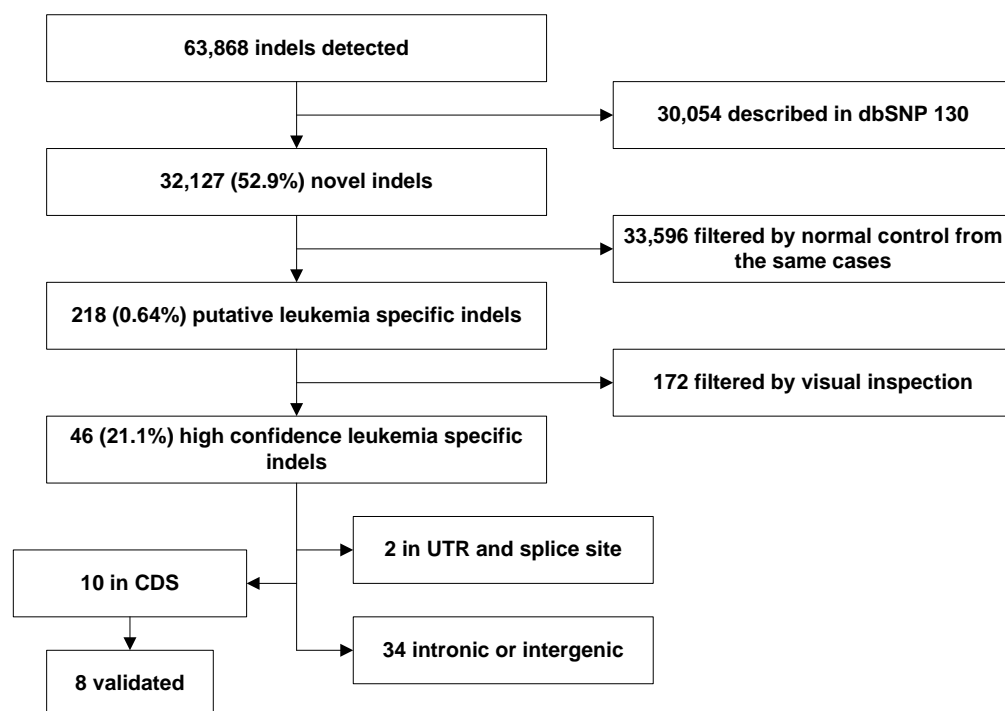
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Supplementary Figures

a.

668,318 SNVs detected

→ | 600,961 described in dbSNP 130 |

67,357 (10.1%) novel SNVs

→ | 67,028 filtered by normal control from the same cases |

329 (0.49%) putative leukemia specific SNVs

→ | 109 filtered by visual inspection |

220 (66.9%) high confidence leukemia specific SNVs

59 nonsynonymous	→	14 synonymous

58 validated

13 in UTR and splice site

134 intronic or intergenic

b.

63,868 indels detected

→ | 30,054 described in dbSNP 130 |

32,127 (52.9%) novel indels

→ | 33,596 filtered by normal control from the same cases |

218 (0.64%) putative leukemia specific indels

→ | 172 filtered by visual inspection |

46 (21.1%) high confidence leukemia specific indels

2 in UTR and splice site

10 in CDS

| 8 validated |
| --- |

34 intronic or intergenic

Supplementary Figure 1. Flow chart for identification of somatic point mutations (a) and small insertions and deletions (b) from database of nine initial sequencing patients. SNV denotes single-nucleotide variant, dbSNP single nucleotide polymorphism database, UTR untranslated regions, indels small insertions and deletions, and CDS coding sequence.
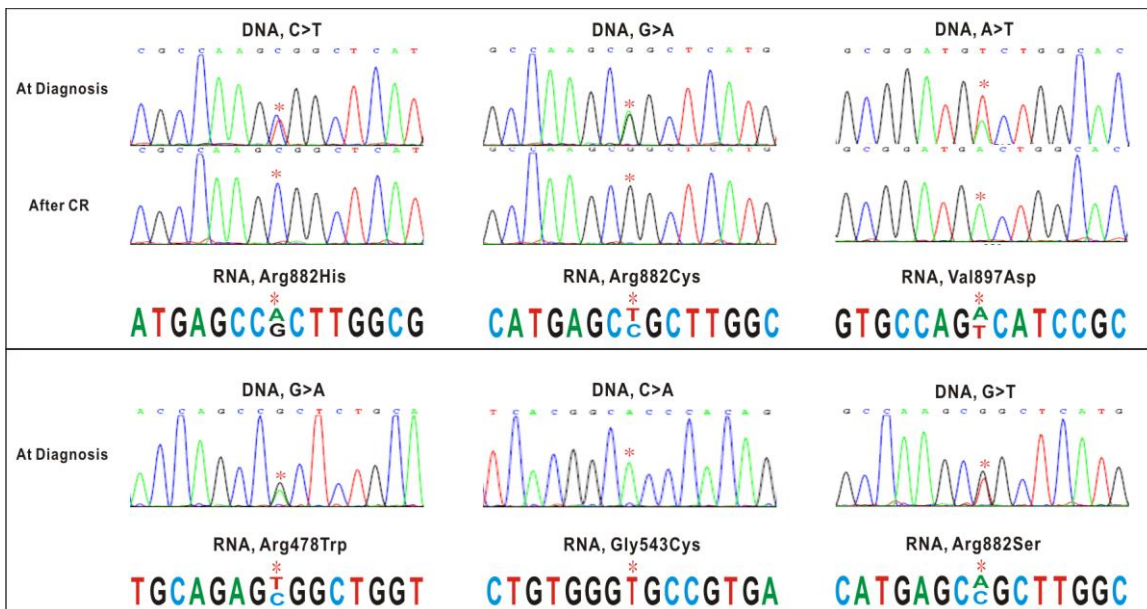
Supplementary Figure 2. Sequencing results of *DNMT3A* gene. Distinct mutations and amino acid replacements from the leukemia DNA samples and the paired cDNA collected (colorful letters) at diagnosis as well as the matched control samples collected during CR, were analyzed by Sanger sequencing.
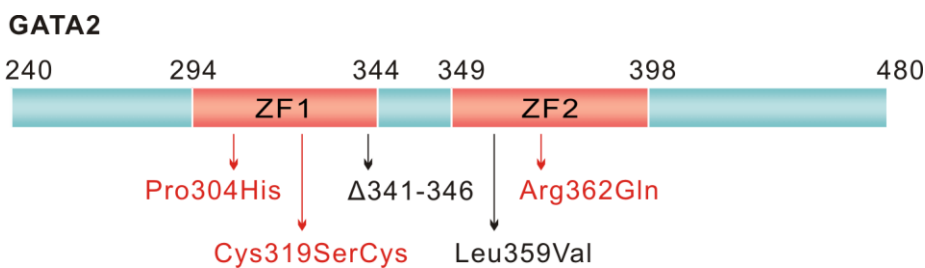
Supplementary Figure 3. Mutations of GATA2 in protein domains. GATA2 contains two zinc fingers (ZF1 and ZF2). The mutations in acute myelomonocytic blastic crisis of CML, which were previously reported by our lab, are labeled in black. Mutations newly found in this work are marked in red. These mutations are located in different sites of the two ZFs.
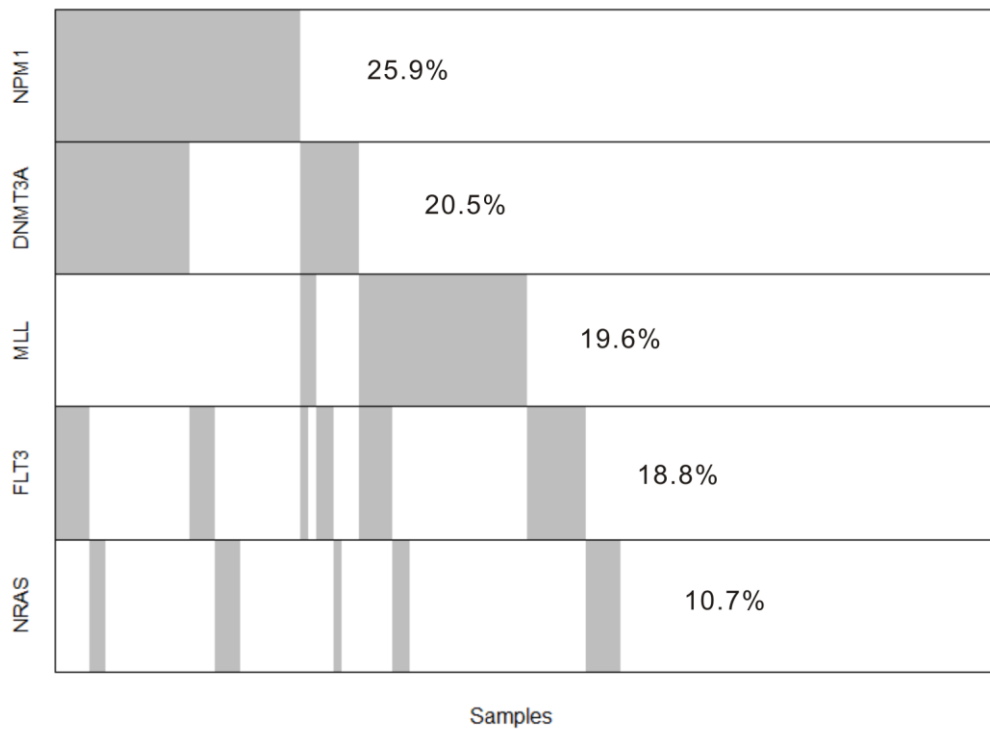
Supplementary Figure 4. Distribution and frequencies of *DNMT3A* mutations and other common mutations in 112 AML-M5 patients. Patients with and without genes mutations are indicated by gray filled and non-filled regions, respectively.

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hDNMT3A   438  DMWVEPEAAAYAPPPPAKKPRKSTAEKPKVKEIIDERTRERLVYEVRQKCRNIEDICISC
mDNMT3A   434  DMWVEPEAAAYAPPPPAKKPRKSTTEKPKVKEIIDERTRERLVYEVRQKCRNIEDICISC
chDNMT3A  403  EMWVEPEAAAYAPPPPAKKPRKSTTEKPKVKEIIDERTRERLVYEVRQKCRNIEDICISC
DrDNMT3A  380  EMW-EPEAASYTAPPPPAKKPRKNSVEKTKIKEIIDEGTRERLMLEVKQKCRNIEDICISC
hDNMT3B   380  RRRTADDSATSDYCPAPKRLKTNCYNNGKDRGDEDQ-SREQMASDVANNKSSLEDGCISC
hDNMT3L    10  ----EAEPSMDVILVGSSELSSSVSPGTG---------RDLIAYEVKANQRNIEDICICC
HhaI        1  ----------------------------------------MIEIKDKQLTGLRFIDLFA

hDNMT3A   498  GSLNVTLEHPLFVGGMCQNCKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRC
mDNMT3A   494  GSLNVTLEHPLFIGGMCQNCKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRC
chDNMT3A  463  GSLNVTLEHPLFIGGMCQNCKNCFLECAYQYDDDGYQSYCTICCGGREVLMCGNNNCCRC
DrDNMT3A  439  GSLNVTLEHPLFVGGAMCQSCKNSFLECAYQYDEDGYQSFCTICCGGRQVLMCGNNNCCRC
hDNMT3B   439  GRKNPVSFHPLFEGGLCQTCRDRFLELFYMYDDDGYQSYCTVCCEGRELLLCSNTSCCRC
hDNMT3L    57  GSLQVHTQHPLFEGGICAPCKDKFLDALFLYDDDGYQSYCSICCSGETLLICGNPDCTRC
HhaI       20  G-----------LGGFRLALESCGAECVYSNEWDKYAQEVYEMNFGE--KPEGDITQVNE

hDNMT3A   558  FCVECVDLLVGPGAAQAAIKEDPWNCYMCGHKGTYGLLRRREDWPSRLQMFFANNHDQEF
mDNM3TA   554  FCVECVDLLVGPGAAQAAIKEDPWNCYMCGHKGTYGLLRRREDWPSRLQMFFANNHDQEF
chDNMT3A  523  FCVECVDLLVGPGAAQAAIKEDPWNCYMCGHKGVYGLLRRREDWPSRLQMFFANNHDQEF
DrDNMT3A  499  YCVECVDLLVGPGTGCAQAAISEDPWNCYMCCSRSVFGLLRRDDWTSRLQLFFANNHDQDF
hDNMT3B   499  FCVECLEVLVGTGTAAEAKLQEPWSCYMCLPQRCHGVLRRRKDWNVRLQAFFTSDTGLEY
hDNMT3L   417  YCFECVDSLVGPGTSGKVHAMSNWVCYLCLPSSRSGLLQRRRKWRSQLKAFYDRESE---
HhaI       67  KTIPDHDILCAG-------------FPCQAFSISGKQKGFE--DSRGTLFFDIARIVRE

hDNMT3A   618  DPPKVYPPVPAEKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMVRH
mDNMT3A   614  DPPKVYPPVPAEKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMVRH
chDNMT3A  583  DPPKVYPPVPAEKRKPIRVLSLFDGIATGLLVLKDLGIQVDRYIASEVCEDSITVGMVRH
DrDNMT3A  559  EPPALYSPVAPEKRQPIRVLSLFDGIATGLLVLKDLGIQVDRYVASEVCEDSITVGMVRH
hDNMT3B   559  EAPKLYPAIPAARRRPIRVLSLFDGIATGYLVLKELGIKVGKYVASEVCEESIAVGTVKH
hDNMT3L   174  NPLEMFETVPVWRRQPVRVLSLFEDIKKELTSLGFLESGSD--------------------
HhaI      111  KKPKVVFMENVKNFASHDNGNTLEVVKN---TMNELDYSFHAKVLN-----AIDYGIPQK

hDNMT3A   678  QGKIMYVGDVRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRL
mDNMT3A   674  QGKIMYVGDVRSVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRL
chDNMT3A  643  QGKIMYVGDVRNVTQKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLYEGTGRLFFEFYRL
DrDNMT3A  619  FERITYVGDIRNITRKHIQEWGPFDLVIGGSPCNDLSIVNPARKGLFEGTGRLFFEFYRL
hDNMT3B   619  EGNIKYVNDVRNITKKNIEEWGPFDLVIGGSPCNDLSNVNPARKGLYEGTGRLFFEFYHL
hDNMT3L   215  PGQLKHVVDVTDTVRKDVEEWGPFDLVYGATPPLGHTCDRPP--------SWYLFQFHRL
HhaI      163  RERIYMICFRNDINIQNFQFPKPFELNT---FVKDLLLPDSE--------------VEHL

hDNMT3A   738  LHDARPKEGDDRPFFWLFENVVAMGVSDKRDISRFLESNPVMIDAKEVSAAHRARYFWGN
mDNMT3A   734  LHDARPKEGDDRPFFWLFENVVAMGVSDKRDISRFLESNPVMIDAKEVSAAHRARYFWGN
chDNMT3A  703  LHEARPKEGDDRPFFWLFENVVAMGVSDKRDISRFLESNPVMIDAKEVSAAHRARYFWGN
DrDNMT3A  679  LHEARPKEGDDRPFFWLFENVVAMGVSDKDISRFLECNPVMIDAKEVSAAHRARYFWGN
hDNMT3B   679  LNYSRPKEGDDRPFFWMFENVVAMKVGDKRDISRFLECNPVMIDAIKVSAAHRARYFWGN
hDNMT3L   267  LQYARPKPGSPRPFFWMFVDNLVLNKEDLDVASRFLEMEPVTIPDVHGGSLQNAVRVWSN
HhaI      206  VIDRKDLVMTNQEIEQTTPKTVRLGIVGKGGQGERIYS----TRGIAITLSAYGGGIFAK

hDNMT3A   798  LP-GMNRPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQGKDQHFPVFMNEKE
mDNMT3A   794  LP-GMNRPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQGKDQHFPVFMNEKE
chDNMT3A  763  LP-GMNRPLASTVNDKLELQECLEHGRIAKFSKVRTITTRSNSIKQGKDQHFPVFMNEKE
DrDNMT3A  739  LP-GMNRPLTAMVNDKLDLQDCLEHGRTAKFNKVRTITTRSNSIKQGKDQHYPVYMNNKE
hDNMT3B   739  LP-GMNRPVIASKNDKLELQDCLEYNRIAKLKKVQTITTKSNSIKQGKNQLFPVVMNGKE
hDNMT3L   327  IP-AIR------------------------------------------SSRHWALVSEE--
HhaI      262  TGG----------------------------------------------YLVNGKT

hDNMT3A   857  DILWCTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV----
mDNMT3A   853  DILWCTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV----
chDNMT3A  822  DILWCTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFACV----
DrDNMT3A  798  DILWCTEMERVFGFPVHYTDVSNMSRLARQRLLGRSWSVPVIRHLFAPLKEYFAC-----
hDNMT3B   798  DVLWCTELERIFGFPVHYTDVSNMGRGARQKLLGRSWSVPVIRHLFAPLKDYFACE----
hDNMT3L   343  -------------------ELSLIAQNKQSSKLAAKWPTKLVKNCFLPLREYFKYFSTEL
HhaI      272  RKLHPRECARVMGYPDSYKVHPSTSQAYKQ--FGNSVVINVLQYIAYNIGSSLNFKPY--
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Supplementary Figure 5. Alignment of DNMT3As among different species and with DNMT3B and DNMT3L. The mutation sites in DNMT3A are marked in red and indicated with arrow. All the four amino acids in DNMT3A mutated in AML-M5 are highly conserved among different species. The Gly543, Arg882 and Val897 are highly conserved between DNMT3A and DNMT3B. Arg882 in DNMT3A corresponds to Arg823 in DNMT3B, which has been found mutated in ICF (immunodeficiency, centromeric instability, facial anomalies) syndrome. h: Human, m: Mouse, ch: Chicken, Dr: Zebra fish (DANRE), HhaI: Bacterium (Haemophilus parahaemolyticus).
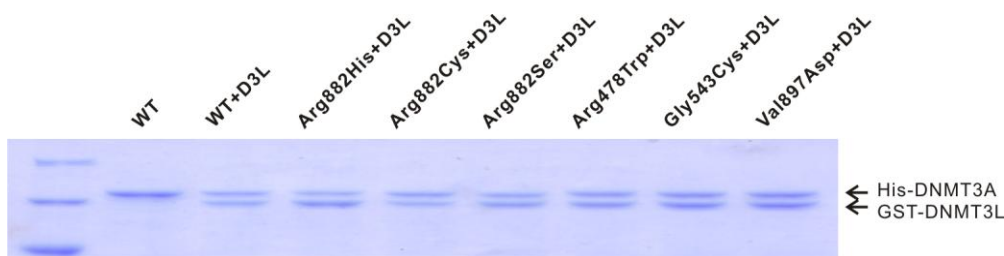
Supplementary Figure 6. Mutations in DNMT3A did not hamper the interaction of DNMT3A with DNMT3L. Recombinant DNMT3A or DNMT3A-DNMT3L (D3L) complex were purified from *E.coli*. The proteins used as enzymes (100 ng) were homogeneous which were monitored on 12% SDS-PAGE gel stained with Coomassie blue. WT: wild-type DNMT3A.
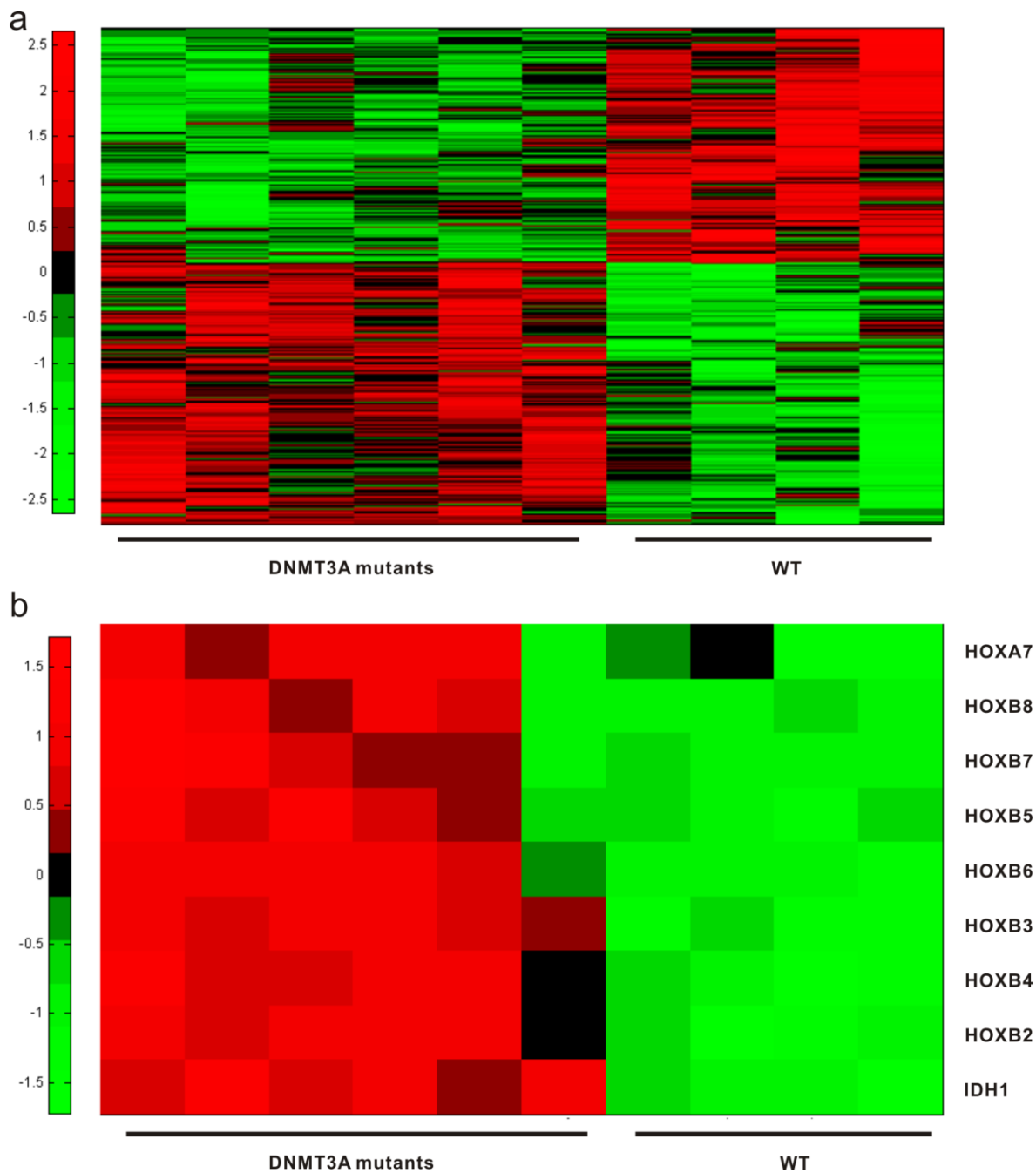
Supplementary Figure 7. Unsupervised hierarchical cluster of differently expressed genes. Six samples with *DNMT3A* mutations (mutants) and four cases with wild type (WT) *DNMT3A* were analyzed. Red color indicates relatively up-regulated genes, green label represents down-regulated genes, and the intermediate level is depicted as black color. (**a**) Cluster of 889 genes with significantly different expression levels between the two groups as described above. (**b**) *HOX* family and *IDH1* genes are picked up and clustered.
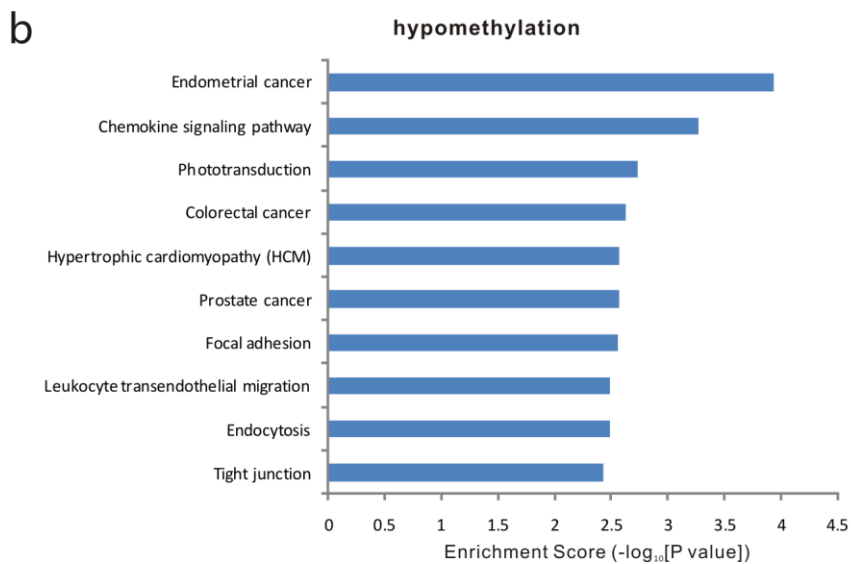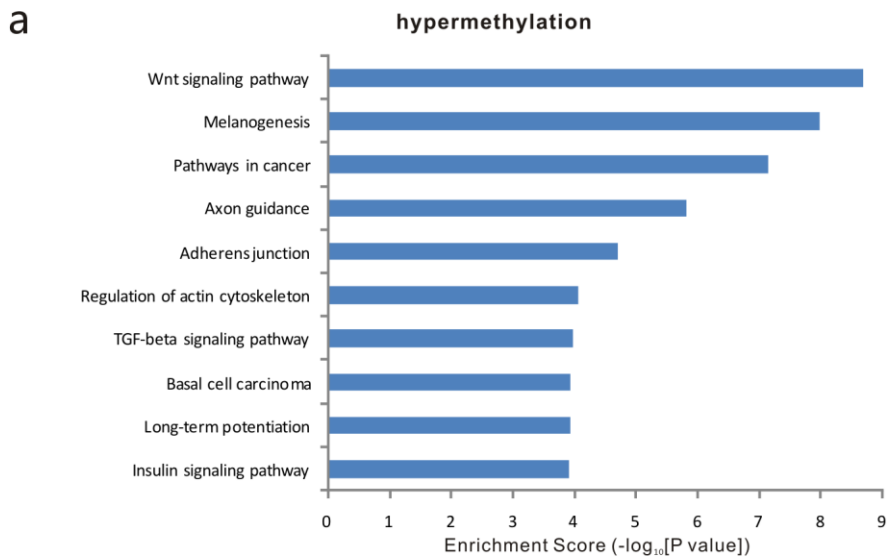
Supplementary Figure 8. Pathway analysis. Ten of the most significantly enriched pathways were plotted for genes of hypermethylation (**a**) or hypomethylation (**b**) in *DNMT3A* mutant patients as compared to those without the mutations. Enrichment Score reflects in an approximate way the proportion of genes involved in a pathway.
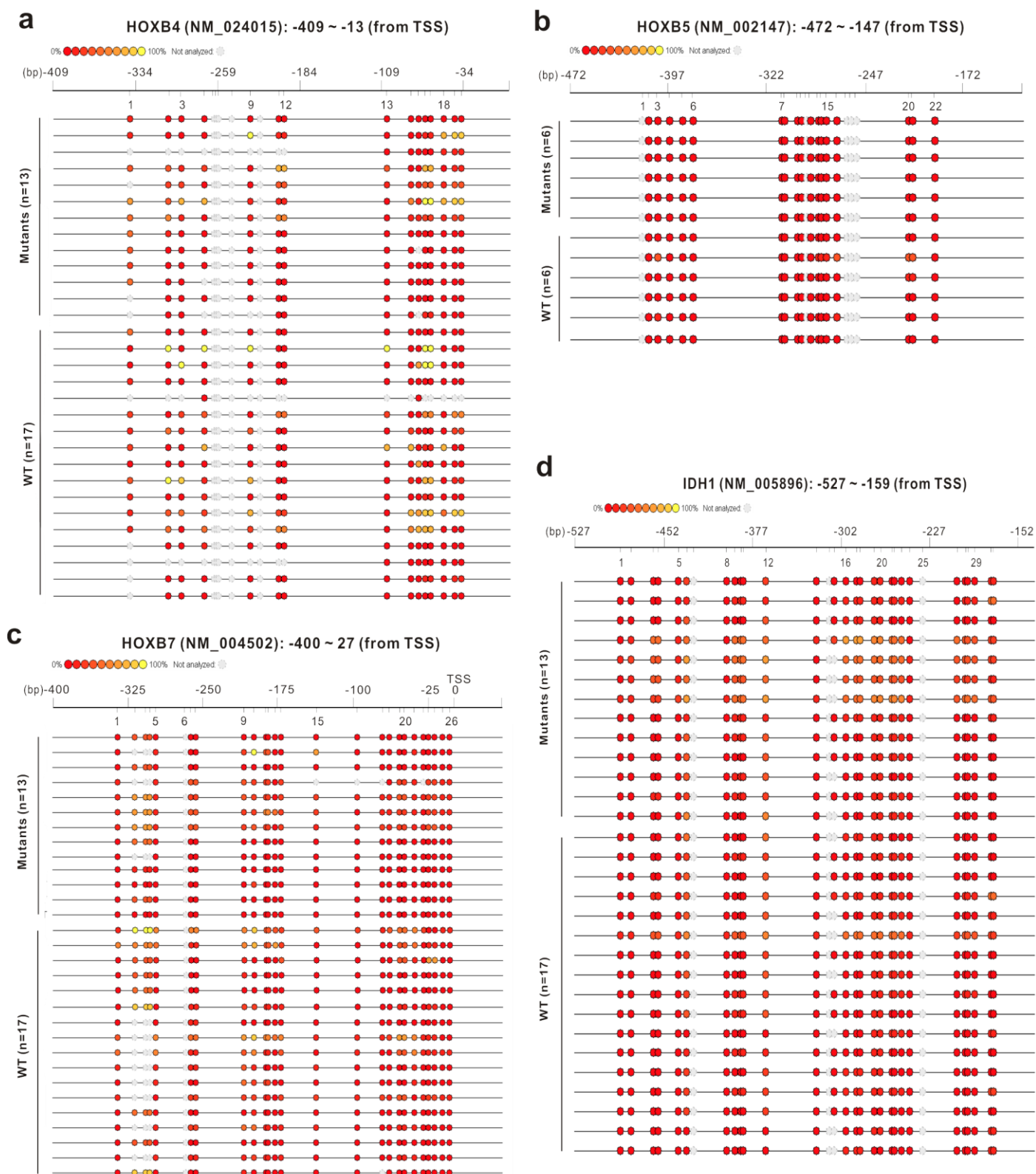
Supplementary Figure 9. Analysis of DNA methylation in AML-M5 patients. DNA methylation status in CpG islands adjacent to *HOXB4* (**a**), *HOXB5* (**b**), *HOXB7* (**c**) and *IDH1* (**d**) genes were analyzed respectively in AML-M5 samples.
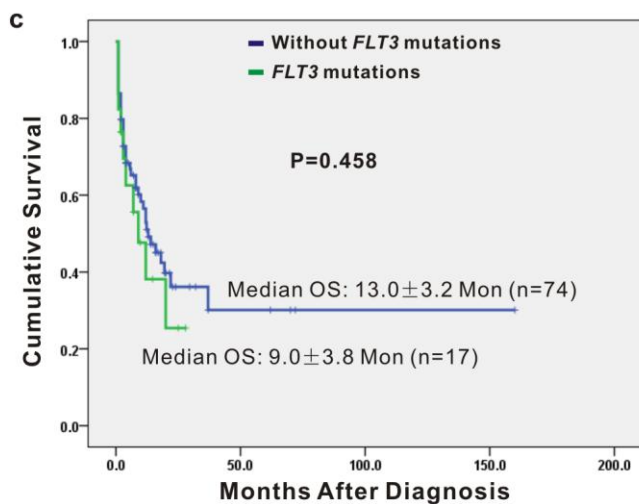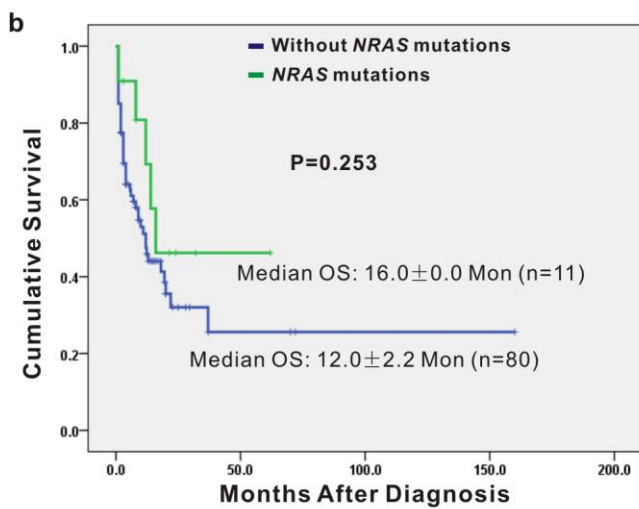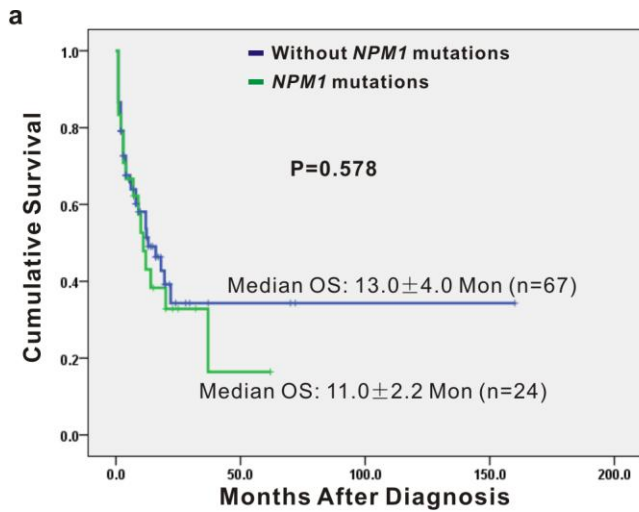
Supplementary Figure 10. Kaplan-Meier survival analysis according to genotype in the patients with AML-M5. No statistical differences of overall survival (OS) were observed between patients with or without mutations in *NPM1* (**a**), *NRAS* (**b**) or *FLT3* (**c**).
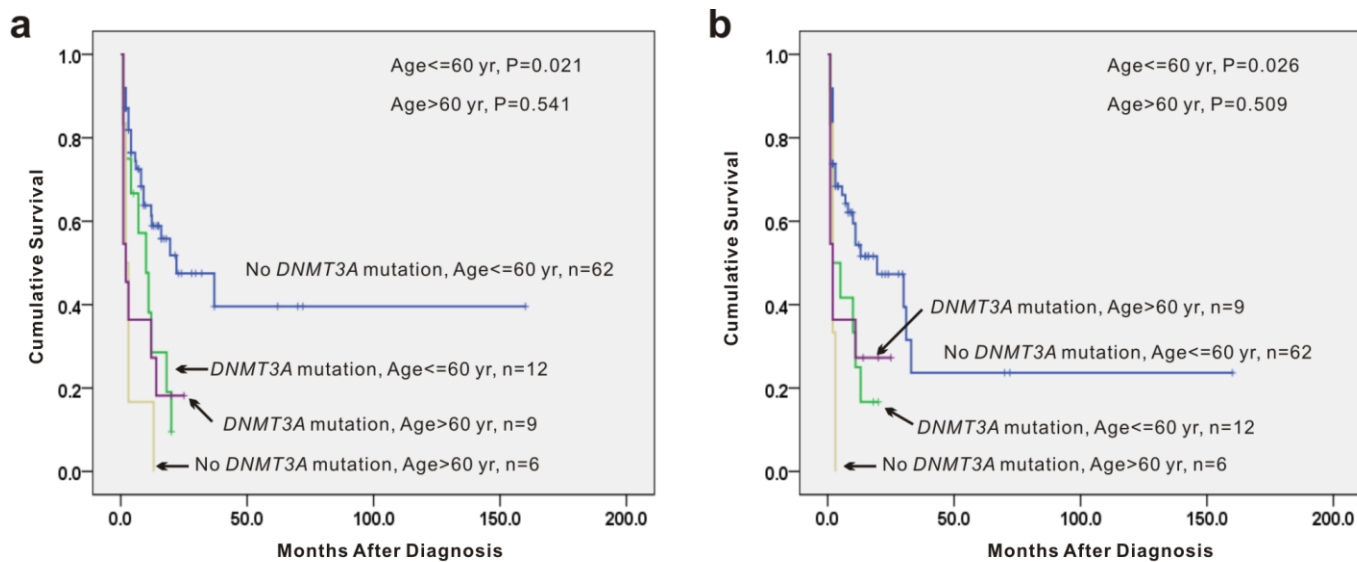
Supplementary Figure 11. Kaplan-Meier survival estimates according to *DNMT3A* mutations and ages. Data are shown for (**a**) OS and (**b**) time to treatment failure (TTF).

Supplementary Tables

Supplementary Table 1. Clinical characteristics of M5 patients in initial and expanded sequencing sets.									
Patient Number	Sex	Age	%BM Leukemia Cells at Diagnosis	White Cells Count ($\times 10^9$/L)	CR (0=no, 1=yes)	Death (0=no, 1=yes)	Relapse (0=no, 1=yes)	Months of OS (as of 08/10/10)	Months of EFS (as of 08/10/10)
In-1	F	58	90.8	55.4	1	0	0	22.8	21.7
In-2	M	30	74.5	86.0	1	0	1	21.5	10.3
In-3	M	61	94.9	1.1	1	0	0	20.0	18.5
In-4	M	29	90.4	1.2	1	0	0	14.7	13.4
In-5	M	53	84.4	2.9	1	0	0	9.0	8.4
In-6	F	54	89.0	24.9	1	0	0	12.3	7.4
In-7	M	30	89.6	60.0	1	0	0	9.8	4.6
In-8	F	16	86.5	26.7	1	0	0	29.6	26.8
In-9	M	48	94.0	152.8	1	0	0	160.1	159.4
Ex-1	M	40	87.2	50.1	1	1	1	19.5	8.7
Ex-2	F	28	95.1	376.8	0	1	0	5.7	0.0
Ex-3	M	25	96.6	71.6	1	1	1	12.3	6.4
Ex-4	M	75	44.0	66.4	1	0	0	19.6	17.1
Ex-5	M	55	95.2	80.6	0	1	0	18.1	0.0

Patient In-1 to In-9 had both bone marrow (BM) samples collected at the primary diagnosis and paired normal peripheral blood specimens obtained after chemotherapy-induced complete remission (CR), defined as initial sequencing set. Patient Ex-1 to Ex-5 had only bone marrow samples at the time of initial presentation, defined as expanded sequencing set. OS: overall survival. EFS: event free survival.

Supplementary Table 2. Sequencing depth and coverage of the nine paired initial sequencing samples.

Sample	Depth	Covered≥1X	≥2X	≥4X	≥8X	≥10X	≥15X	≥20X
BM1	74.07	97.86%	97.33%	96.55%	95.12%	94.37%	92.26%	89.73%
BM2	70.43	98.05%	97.54%	96.74%	95.21%	94.38%	92.00%	89.08%
BM3	69.47	97.90%	97.38%	96.60%	95.16%	94.40%	92.22%	89.51%
BM4	67.69	98.47%	98.13%	97.53%	96.11%	95.21%	92.33%	88.61%
BM5	106.75	98.69%	98.36%	97.84%	97.03%	96.67%	95.78%	94.82%
BM6	115.71	98.59%	98.28%	97.77%	96.98%	96.62%	95.75%	94.85%
BM7	100.16	98.52%	98.15%	97.52%	96.54%	96.09%	94.93%	93.64%
BM8	104.78	98.26%	97.79%	97.02%	95.79%	95.21%	93.72%	92.09%
BM9	159.57	98.77%	98.51%	98.12%	97.53%	97.28%	96.69%	96.14%
PB1	75.61	97.06%	96.08%	94.53%	91.61%	90.09%	86.23%	82.26%
PB2	73.23	98.15%	97.69%	96.96%	95.50%	94.68%	92.29%	89.34%
PB3	78.88	98.02%	97.48%	96.62%	94.89%	93.92%	91.13%	87.81%
PB4	73.42	98.25%	97.88%	97.34%	96.35%	95.80%	94.16%	91.96%
PB5	119.52	98.57%	98.20%	97.62%	96.71%	96.30%	95.25%	94.12%
PB6	118.06	98.31%	97.89%	97.23%	96.24%	95.79%	94.70%	93.58%
PB7	135.37	98.53%	98.13%	97.54%	96.65%	96.25%	95.29%	94.33%
PB8	138.35	98.42%	98.00%	97.38%	96.41%	95.97%	94.89%	93.76%
PB9	128.82	98.67%	98.32%	97.76%	96.90%	96.50%	95.55%	94.56%

Supplementary Table 3. Summary of somatic mutations in initial sequencing set.

Variant	SNVs (mutation number/Mb)	Indels[b] (mutation number/Mb)
All SNVs detected	220(0.25)	46(0.05)
Coding Region		10(0.05)
Missense	54(0.25)	-
Nonsense	5(0.02)	-
Synonymous	14(0.06)	-
Noncoding, transcribed		
5' UTR	3(0.30)	0(0)
3' UTR	6(0.19)	2(0.06)
Splice site[a]	4	0
Intronic	109(0.19)	24(0.04)
Intergenic	25(0.41)	10(0.16)

[a]Intronic mutations within 4 bp of exon/intron boundary. UTR: untranslated regions.

[b] Indels: small insertions and deletions.

Supplementary Table 4. Validated somatic mutations in the current work.

Annotated Gene	Mutation Type	Position	Allele Change	Amino Acid Change	RefSeq	PolyPhen Prediction	Gene Function	Sample Number
ADAM33	missense	chr20:3603311	C>T	p.S147N	NM_153202	probably damaging	metalloendopeptidase activity	In-5
ATP2A2	missense	chr12:109261491	A>G	p.K454R	NM_001135765	probably damaging	calcium-transporting ATPase activity	In-4
BCL11B	missense	chr14:98710294	C>T	p.G807Ser	NM_022898	benign	metal ion binding	In-2
BRWD3	missense	chrX:79934077	G>C	p.A121G	NM_153252	unknown	unknown	In-1
C10orf2	missense	chr10:102738655	A>G	p.Y233C	NM_021830	probably damaging	DNA helicase activity	In-4
C2orf24	missense	chr2:219747962	T>C	p.I125V	NM_015680	possibly damaging	unknown	In-4
CASQ1	nonsense	chr1:158429217	T>G	p.L94	NM_001231	damaging	calcium ion binding	In-2
CCND3	frameshift	chr6:42011723	*/+G	p.R271fs*23	NM_001760	damaging	protein kinase binding	In-2
CDH18	missense	chr5:19783000	G>T	p.H111N	NM_001167667	probably damaging	calcium ion binding	In-7
CEBPA	in-frame	chr19:38484247	*/+GCA	p.Q305>LQ	NM_004364	damaging	transcription factor activity	In-6
CHRNA4	missense	chr20:61451906	G>A	p.P434L	NM_000744	possibly damaging	acetylcholine receptor activity	In-9
COL7A1	missense	chr3:48607553	A>C	p.L15R	NM_000094	unknown	serine-type endopeptidase inhibitor activity	In-4
CP	missense	chr3:150422214	G>A	p.A19V	NM_000096	benign	copper ion binding	In-9
CPLX4	missense	chr18:55114924	A>G	p.C157R	NM_181654	probably damaging	syntaxin binding	In-2
CTCF	missense	chr16:66203450	C>A	p.P293T	NM_006565	probably damaging	transcription factor activity	In-1
DCAF8L1	missense	chrX:27908496	C>T	p.A293T	NM_001017930	benign	unknown	In-6
DCHS1	missense	chr11:6604029	G>C	p.H2175D	NM_003737	benign	calcium ion binding	In-1
DNMT3A	missense	chr2:25310701	A>T	p.V897D	NM_022552	probably damaging	methyltransferase activity	In-3
ELFN2	missense	chr22:36100262	C>T	p.R420H	NM_052906	probably damaging	receptor activity	In-2
EVPL	missense	chr17:71515389	T>C	p.Y1831C	NM_001988	probably damaging	structural molecule activity	In-1
EXOC4	missense	chr7:133273210	T>C	p.V685A	NM_021807	possibly damaging	protein complex binding	In-2
FBXO27	missense	chr19:44207934	C>T	p.R270H	NM_178820	probably damaging	glycoprotein binding	In-5
FBXO3	nonsense	chr11:33728710	C>A	p.E295	NM_012175	damaging	ubiquitin-protein ligase activity	In-6
FLT3	missense	chr13:27490641	T>A	p.D835V	NM_004119	probably damaging	phosphoinositide 3-kinase binding	In-4

Annotated Gene	Mutation Type	Position	Allele Change	Amino Acid Change	RefSeq	PolyPhen Prediction	Gene Function	Sample Number
GATA2	missense	chr3:129683410	C>T	p.R362Q	NM_032638	probably damaging	transcription factor activity	In-4
GATA2	in-frame	chr3:129685454	*/+AGG	p.C319>SC	NM_032638	damaging	transcription factor activity	In-6
HTR3C	missense	chr3:185260068	G>T	p.V291F	NM_130770	probably damaging	receptor activity	In-9
IFIH1	frameshift	chr2:162858376	*/+T	p.S273fs*4	NM_022168	damaging	helicase activity	In-8
KHK	missense	chr2:27175949	G>A	p.G271R	NM_006488	probably damaging	ketohexokinase activity	In-2
KIAA1217	missense	chr10:24767374	C>T	p.A189V	NM_001098500	benign	unknown	In-5
KIAA1244	missense	chr6:138697555	C>A	p.T1960N	NM_020340	unknown	ARF guanyl-nucleotide exchange factor activity	In-4
KIAA1244	missense	chr6:138699285	G>A	p.R2168K	NM_020340	unknown	ARF guanyl-nucleotide exchange factor activity	In-9
KIF2C	missense	chr1:44992066	T>G	p.S213A	NM_006845	possibly damaging	microtubule motor activity	In-3
KRT1	missense	chr12:51357124	T>G	p.N414H	NM_006121	benign	structural constituent of cytoskeleton	In-9
LAMA5	missense	chr20:60320649	G>A	p.A3160V	NM_005560	benign	structural molecule activity	In-5
LPL	missense	chr8:19853683	G>A	p.A125T	NM_000237	probably damaging	phospholipase activity	In-4
LRRC37A3	missense	chr17:60295063	A>T	p.M1011K	NM_199340	probably damaging	unknown	In-6
MIS12	missense	chr17:5333217	G>A	p.C104Y	NM_024039	probably damaging	protein binding	In-7
MLF1IP	frameshift	chr4:185855905	*/+TC	p.K345fs*17	NM_024629	damaging	protein binding	In-6
MRPL14	missense	chr6:44189722	G>C	p.P92A	NM_032111	probably damaging	structural constituent of ribosome	In-5
NDST3	missense	chr4:119381152	C>A	p.A715E	NM_004784	benign	sulfotransferase activity	In-2
NLRP4	missense	chr19:61061958	T>C	p.F463L	NM_134444	probably damaging	ATP binding	In-1
NLRP8	missense	chr19:61159052	G>A	p.V606I	NM_176811	benign	unknown	In-6
NOTCH4	missense	chr6:32278291	C>T	p.G1099R	NM_004557	benign	protein heterodimerization activity	In-4
NRAS	missense	chr1:115060271	C>T	p.G12S	NM_002524	probably damaging	GTPase activity	In-2
NRAS[a]	missense	chr1:115060270	C>T	p.G12D	NM_002524	probably damaging	GTPase activity	In-2
NSD1	missense	chr5:176627199	C>T	p.P1726L	NM_022455	probably damaging	histone methyltransferase activity	In-9
PBRM1	nonsense	chr3:52643665	G>A	p.Q400	NM_018165	damaging	Transcriptional activation and repression by chromatin binding	In-5

Annotated Gene	Mutation Type	Position	Allele Change	Amino Acid Change	RefSeq	PolyPhen Prediction	Gene Function	Sample Number
PCDHA8	missense	chr5:140201193	G>A	p.V35I	NM_031856	unknown	calcium ion binding	In-4
PCDHB10	missense	chr5:140552386	C>T	p.A26V	NM_018930	benign	calcium ion binding	In-8
PCMTD2	missense	chr20:62369700	G>A	p.R200H	NM_018257	probably damaging	protein-L-isoaspartate (D-aspartate) O-methyltransferase activity	In-4
PDLIM7	missense	chr5:176849207	C>T	p.R187H	NM_203352	benign	zinc ion binding	In-5
PIF1	missense	chr15:62897283	G>A	p.T530M	NM_025049	benign	ATP-dependent 5'-3' DNA/RNA helicase activity	In-4
PRICKLE3	missense	chrX:48922551	C>G	p.C186S	NM_006150	probably damaging	zinc ion binding	In-4
RANBP2	missense	chr2:108760116	A>G	p.K2866E	NM_006267	probably damaging	Ran GTPase binding	In-5
RUNX1	frameshift	chr21:35086708	*/+G	p.R319fs*136	NM_001001890	damaging	transcription factor activity	In-7
SLC24A3	missense	chr20:19612831	C>T	p.R305C	NM_020689	benign	calcium, potassium:sodium antiporter activity	In-9
SLC25A20	nonsense	chr3:48874982	G>A	p.R178	NM_000387	damaging	acyl carnitine transporter activity	In-3
SLC4A11	missense	chr20:3158413	T>A	p.K516M	NM_032034	probably damaging	boron transmembrane transporter activity	In-3
SORCS3	missense	chr10:107002617	C>G	p.T1067R	NM_014978	possibly damaging	neuropeptide receptor activity	In-4
STT3B	nonsense	chr3:31592892	G>A	p.W105	NM_178862	damaging	transferase activity	In-6
TCOF1	missense	chr5:149738661	G>T	p.V781L	NM_001008657	possibly damaging	transporter activity	In-3
TP53I11	missense	chr11:44916381	G>T	p.L28I	NM_006034	probably damaging	unknown	In-9
VIL1	missense	chr2:219002423	C>A	p.P247T	NM_007127	benign	actin binding	In-3
WDR11	missense	chr10:122656309	G>A	p.V1157M	NM_018117	benign	unknown	In-7
WT1	frameshift	chr11:32374521	*/+C	p.R369fs*15	NM_024424	damaging	transcription factor activity	In-4
WT1	in-frame	chr11:32370144	*/-AGAACT	p.K459_S461>T	NM_024424	damaging	transcription factor activity	In-8

[a]Only G12S mutation in *NRAS* was detected in initial sequencing, while both G12S and G12D were validated by Sanger sequencing. The primary exome sequencing data showed that both mutations existed and the G12D mutation was filtered due to low ratio of mutant in the sample and the two mutations were not in the same allele.

Supplementary Table 5. Mutation patterns in genes involved in at least two AML-M5 cases.

Annotated Gene	Mutation Type	Position	Allele Change	Amino Acid Change	RefSeq	Case Numbers With Mutations	Sample
ATP2A2	missense	chr12:109261491	A>G	p.K454R	NM_001135765	1	initial sequencing
	missense	chr12:109268521	G>T	p.V971L	NM_001135765	1	expanded sequencing
C10orf2	missense	chr10:102738655	A>G	p.Y233C	NM_021830	1	initial sequencing
	missense	chr10:102739451	A>G	p.Q435R	NM_021830	1	expanded sequencing
CCND3	frameshift	chr6:42011723	*/+G	p.R271fs*23	NM_001760	2	initial and expanded sequencing
DCAF8L1	missense	chrX:27908496	C>T	p.A293T	NM_001017930	1	initial sequencing
	missense	chrX:27907690	T>G	p.Q561H	NM_001017930	1	expanded sequencing
DNMT3A	missense	chr2:25310701	A>T	p.V897D	NM_022552	1	initial sequencing
	missense	chr2:25320953	C>A	p.G543C	NM_022552	1	expanded sequencing
EXOC4	missense	chr7:133273210	T>C	p.V685A	NM_021807	2	initial sequencing and validation
FLT3	missense	chr13:27490641	T>A	p.D835V	NM_004119	2	initial sequencing and validation
GATA2	missense	chr3:129683410	C>T	p.R362Q	NM_032638	2	initial sequencing and validation
	in-frame	chr3:129685454	*/+AGG	p.C319>SC	NM_032638	1	initial sequencing
KIAA1244	missense	chr6:138697555	C>A	p.T1960N	NM_020340	1	initial sequencing
	missense	chr6:138699285	G>A	p.R2168K	NM_020340	1	initial sequencing
LAMA5	missense	chr20:60320649	G>A	p.A3160V	NM_005560	1	initial sequencing
	missense	chr20:60337611	C>T	p.A1405T	NM_005560	1	expanded sequencing
PBRM1	nonsense	chr3:52643665	G>A	p.Q400	NM_018165	1	initial sequencing
	missense	chr3:52638005	T>C	p.N431S	NM_018165	1	expanded sequencing
TCOF1	missense	chr5:149738661	G>T	p.V781L	NM_001008657	2	initial sequencing and validation
WDR11	missense	chr10:122656309	G>A	p.V1157M	NM_018117	1	initial sequencing
	missense	chr10:122654904	G>A	p.A1093T	NM_018117	1	expanded sequencing
WT1	frameshift	chr11:32374521	*/+C	p.R369fs*15	NM_024424	2	initial sequencing and validation
	in-frame	chr11:32370144	*/-AGAACT	p.K459_S461>T	NM_024424	1	initial sequencing

Samples are from 9 of initial sequencing set, 5 of expanded sequencing set and 98 of M5 validation set. All these mutations were not detected in 509 of control validation set.

Supplementary Table 6. Mutations of genes already known with relatively high rate in AML-M5 samples.

Annotated Gene	Mutation Type	Mutations	Frequency (%)
MLL	translocation and PTD[a]	MLL-MLLT4, MLL-MLLT3, MLL-MLLT10, MLL-MLLT6, MLL-ELL, MLL-PTD	22/112 (19.6)
NPM1	frameshift	p.W288fs*11	29/112 (25.9)
NRAS	missense	p.G12S, p.G12D, p.G12V, p.G13D, p.Q61P, p.Q61R	12/112 (10.7)
FLT3	missense and ITD[b]	p.D835A, p.D835V, p.D835Y, FLT3-ITD	21/112 (18.8)

[a] **PTD: partial tandem duplication.** [b] **ITD: internal tandem duplication.**

Supplementary Table 7. Distribution of gene mutations in the AML-M5 patients.

Variable	WT	Mutations[a]	
		DNMT3A	MLL
NPM1 status			
Mutated (%)	13 (18.8)	16 (69.6)	0 (0.0)
Unmutated (%)	56 (81.2)	7 (30.4)	22 (100.0)
		P=0.000	
			P=0.000
FLT3 status			
Mutated (%)	10 (14.5)	7 (30.4)	5 (22.7)
Unmutated (%)	59 (85.5)	16 (69.6)	17 (77.3)
		P=0.120	
			P=0.738
NRAS status			
Mutated (%)	7 (10.1)	3 (13.0)	2 (9.1)
Unmutated (%)	62 (89.9)	20 (87.0)	20 (90.9)
		P=0.707	
			P=1.000

WT (Wild-type): the patients without DNMT3A or MLL mutations.

[a]**Two patients had both DNMT3A and MLL mutations and were grouped into two cohorts with mutations. MLL mutations including MLL translocation and MLL-PTD. The analysis was performed by Fisher's exact test. P Value was obtained by comparing two adjacent groups.**

Supplementary Table 8. MeDIP-chip analysis of DNA methylation in AML-M5.

	Hypermethylation	Hypomethylation
Genomic regions	2,246	1,602
Genes	1,946	1,291

Hypermethylation and hypomethylation: the status of DNA methylation in DNMT3A mutation samples compared to samples with wt DNMT3A. Detailed information was provided in methods.

Supplementary Table 9. MeDIP-chip pattern of DNA methylation in AML-M5.

SampleName	PeakID	PeakStart	PeakEnd	PeakScore	GeneName	Chromosome	Strand	PeakToTSS	Accession
D3A_WT	1381	63553766	63553915	2.13	A1BG	chr19	-	2837	NM_130786
D3A_WT	1069	76758044	76758529	2.86	AATK	chr17	-	-3819	NM_001080395
D3A_WT	842	8723587	8723843	2.38	ABAT	chr16	+	1642	NM_001127448
D3A_WT	2461	106727567	106727716	2.29	ABCA1	chr9	-	2616	NM_005502
D3A_WT	2522	139045598	139045832	2.71	ABCA2	chr9	-	-2520	NM_212533
D3A_WT	2522	139045598	139045832	2.71	ABCA2	chr9	-	-3154	NM_001606
D3A_WT	127	94656360	94657419	3.36	ABCD3	chr1	+	369	NM_002858
D3A_WT	1407	27195400	27195934	2.96	ABHD1	chr2	+	-4493	NM_032604
D3A_WT	2503	135139929	135140093	2.56	ABO	chr9	-	440	NM_020469
D3A_WT	1821	130080976	130081100	2.35	ACAD9	chr3	+	16	NM_014049
D3A_WT	13	1233219	1234854	2.63	ACAP3	chr1	-	-904	NM_030649
D3A_WT	175	178744378	178744603	2.3	ACBD6	chr1	-	-5845	NM_032360
D3A_WT	2260	100327650	100331691	3.28	ACHE	chr7	-	1807	NM_000665
D3A_WT	993	37328900	37329149	2.24	ACLY	chr17	-	-226	NM_198830
D3A_WT	2421	32374537	32375111	2.37	ACO1	chr9	+	224	NM_002197
D3A_WT	1830	142432391	142433930	4.03	ACPL2	chr3	+	-211	NM_001037172
D3A_WT	1757	49516500	49516644	2.93	ACR	chr22	+	-6945	NM_001097
D3A_WT	2580	70715787	70715936	3.21	ACRC	chrX	+	1263	NM_052957
D3A_WT	920	87687722	87688372	3.04	ACSF3	chr16	+	293	NM_001127214
D3A_WT	850	20498851	20499300	3.16	ACSM2B	chr16	-	-3879	NM_001105069
D3A_WT	2204	5536062	5536902	3.05	ACTB	chr7	-	276	NM_001101
D3A_WT	2203	5534955	5535109	2.05	ACTB	chr7	-	1726	NM_001101
D3A_WT	1074	77101096	77101550	3.13	ACTG1	chr17	-	-6901	NM_001614
D3A_WT	1840	180763734	180763973	2.42	ACTL6A	chr3	+	452	NM_004301
D3A_WT	659	68515255	68515599	2.81	ACTN1	chr14	-	409	NM_001130005
D3A_WT	211	234915722	234916890	2.7	ACTN2	chr1	+	-86	NM_001103
D3A_WT	1443	97646446	97647266	3.37	ACTR1B	chr2	-	137	NM_005735
D3A_WT	1455	114363510	114364369	2.83	ACTR3	chr2	+	-67	NM_005721
D3A_WT	1470	158193274	158193623	2.35	ACVR1C	chr2	-	197	NM_001111033
D3A_WT	2253	87401118	87401452	2.86	ADAM22	chr7	+	-352	NM_016351
D3A_WT	1985	5193175	5193894	3.11	ADAMTS16	chr5	+	92	NM_139056
D3A_WT	1643	45319259	45319838	2.51	ADARB1	chr21	+	628	NM_001160230
D3A_WT	1178	1858670	1858819	2.72	ADAT3	chr19	+	2328	NM_138422
D3A_WT	2287	140015748	140015980	2.16	ADCK2	chr7	+	-3557	NM_052853
D3A_WT	1312	45914651	45915296	4.23	ADCK4	chr19	-	-2155	NM_001142555
D3A_WT	1312	45914651	45915296	4.23	ADCK4	chr19	-	-343	NM_024876
D3A_WT	1987	7449779	7450793	3.47	ADCY2	chr5	+	944	NM_020546
D3A_WT	1405	25001729	25002473	3.83	ADCY3	chr2	-	-6542	NM_004036
D3A_WT	1818	124649607	124649766	2.29	ADCY5	chr3	-	396	NM_183357
D3A_WT	874	48874444	48874803	2.97	ADCY7	chr16	+	-4700	NM_001114
D3A_WT	1751	49259611	49260562	2.52	ADM2	chr22	+	-6791	NM_024866
D3A_WT	181	201363590	201364044	3.24	ADORA1	chr1	+	359	NM_001048230
D3A_WT	289	112828236	112829090	3.57	ADRA2A	chr10	+	1884	NM_000681

D3A_WT	426	66789844	66790873	3.08	ADRBK1	chr11	+	-122	NM_001619
D3A_WT	498	19484126	19484475	2.83	AEBP2	chr12	+	426	NM_001114176
D3A_WT	1925	88075233	88076260	2.7	AFF1	chr4	+	569	NM_001166693
D3A_WT	1558	32354504	32354968	2.71	AHCY	chr20	-	140	NM_000687
D3A_WT	2281	128652031	128652170	2.55	AHCYL2	chr7	+	1	NM_015328
D3A_WT	667	76993467	76994240	3.74	AHSA1	chr14	+	-272	NM_012111
D3A_WT	1674	19648837	19649478	2.33	AIFM3	chr22	+	-260	NM_001018060
D3A_WT	1674	19648837	19649478	2.33	AIFM3	chr22	+	-2289	NM_001146288
D3A_WT	2121	107066636	107066900	3.21	AIM1	chr6	+	346	NM_001624
D3A_WT	1637	44537922	44538571	3.16	AIRE	chr21	+	3545	NM_000658
D3A_WT	1023	52518651	52518795	2.02	AKAP1	chr17	+	1172	NM_003488
D3A_WT	2463	111850400	111850649	2.19	AKAP2	chr9	+	-272	NM_001004065
D3A_WT	100	39229729	39230493	4.03	AKIRIN1	chr1	+	609	NM_001136275
D3A_WT	2467	116200014	116200248	2.73	AKNA	chr9	-	-3625	NM_030767
D3A_WT	1344	55071648	55071812	2.78	AKT1S1	chr19	-	694	NM_001098633
D3A_WT	1344	55071648	55071812	2.78	AKT1S1	chr19	-	660	NM_032375
D3A_WT	1344	55071648	55071812	2.78	AKT1S1	chr19	-	726	NM_001098632
D3A_WT	214	242079375	242079635	2.03	AKT3	chr1	-	-6329	NM_181690
D3A_WT	269	97406219	97406353	3.29	ALDH18A1	chr10	-	271	NM_002860
D3A_WT	962	18027844	18028767	3.71	ALKBH5	chr17	+	714	NM_017758
D3A_WT	766	83161533	83162091	3.02	ALPK3	chr15	+	898	NM_020778
D3A_WT	824	2509786	2510605	4.25	AMDHD2	chr16	+	-168	NM_001145815
D3A_WT	134	109853828	109853982	2.06	AMIGO1	chr1	-	-46	NM_020703
D3A_WT	689	102456866	102457305	2.38	AMN	chr14	+	-1660	NM_030943
D3A_WT	374	10429030	10429349	2.88	AMPD3	chr11	+	390	NM_000480
D3A_WT	374	10429030	10429349	2.88	AMPD3	chr11	+	-4052	NM_001025389
D3A_WT	374	10429030	10429349	2.88	AMPD3	chr11	+	-4867	NM_001025390
D3A_WT	1903	24987850	24988194	2.42	ANAPC4	chr4	+	77	NM_013367
D3A_WT	450	101290878	101291012	2.76	ANGPTL5	chr11	-	1518	NM_178127
D3A_WT	578	131848624	131849271	2.03	ANKLE2	chr12	-	-423	NM_015114
D3A_WT	922	88083300	88083421	2.45	ANKRD11	chr16	-	1110	NM_013275
D3A_WT	976	24944638	24944796	2.38	ANKRD13B	chr17	+	65	NM_152345
D3A_WT	229	5971252	5972504	2.66	ANKRD16	chr10	-	-12	NM_001009941
D3A_WT	2447	94606122	94606866	2.7	ANKRD19	chr9	+	-5219	NR_026868
D3A_WT	1442	96892693	96892827	2.52	ANKRD39	chr2	-	-5277	NM_016466
D3A_WT	2022	132177418	132178291	2.97	ANKRD43	chr5	+	923	NM_175873
D3A_WT	1932	125853206	125853465	2.64	ANKRD50	chr4	-	2	NM_020337
D3A_WT	1427	71059897	71060051	2.31	ANKRD53	chr2	+	892	NM_001115116
D3A_WT	507	43896142	43896301	2.73	ANO6	chr12	+	185	NM_001142679
D3A_WT	507	43896142	43896301	2.73	ANO6	chr12	+	79	NM_001142680
D3A_WT	322	429570	431319	4.81	ANO9	chr11	-	1567	NM_001012302
D3A_WT	998	38256537	38256985	2.9	AOC3	chr17	+	35	NM_003734
D3A_WT	999	38258461	38258715	2.84	AOC3	chr17	+	1862	NM_003734
D3A_WT	330	915975	916993	3.41	AP2A2	chr11	+	644	NM_012305
D3A_WT	1911	40911241	40911882	2.91	APBB2	chr4	-	-169	NM_173075
D3A_WT	1169	1401058	1401207	2.62	APC2	chr19	+	-15	NM_005883
D3A_WT	57	10413064	10413508	3.57	APITD1	chr1	+	-100	NM_199295

D3A_WT	57	10413064	10413508	3.57	APITD1	chr1	+	541	NM_198544
D3A_WT	1425	68547801	68548273	2.83	APLF	chr2	+	-157	NM_173545
D3A_WT	1711	37685169	37685418	2.41	APOBEC3A	chr22	+	1821	NM_145699
D3A_WT	494	12768602	12769156	2.82	APOLD1	chr12	+	-1238	NM_001130415
D3A_WT	1804	57237435	57237679	3.05	APPL1	chr3	+	753	NM_012096
D3A_WT	919	87409331	87410274	4.31	APRT	chr16	-	-3959	NM_000485
D3A_WT	512	48652659	48652898	2.22	AQP6	chr12	+	-108	NM_001652
D3A_WT	1907	35922185	35922724	2.55	ARAP2	chr4	-	-80	NM_015230
D3A_WT	398	47158320	47159471	3.35	ARFGAP2	chr11	-	-3900	NM_032389
D3A_WT	1602	61809523	61810172	2.96	ARFRP1	chr20	-	-48	NM_003224
D3A_WT	2608	152846821	152847451	2.61	ARHGAP4	chrX	-	-2228	NM_001666
D3A_WT	1079	77422770	77423207	2.43	ARHGDIA	chr17	-	-461	NM_004309
D3A_WT	623	110567328	110567786	3.57	ARHGEF7	chr13	+	1933	NM_001113512
D3A_WT	80	26895435	26896386	2.82	ARID1A	chr1	+	802	NM_139135
D3A_WT	751	72620570	72620785	2.19	ARID3B	chr15	+	77	NM_006465
D3A_WT	1786	48930801	48931180	2.39	ARIH2	chr3	+	-294	NM_006321
D3A_WT	278	104464000	104464149	2.29	ARL3	chr10	-	106	NM_004311
D3A_WT	1805	69212003	69212241	2.91	ARL6IP5	chr3	+	-4657	NM_006407
D3A_WT	1502	231771440	231772306	2.77	ARMC9	chr2	+	288	NM_025139
D3A_WT	500	27377258	27377837	2.03	ARNTL2	chr12	+	293	NM_020183
D3A_WT	444	74740186	74740335	2.7	ARRB1	chr11	-	261	NM_020251
D3A_WT	942	4560489	4561104	2.43	ARRB2	chr17	+	259	NM_199004
D3A_WT	941	4553888	4554507	3.33	ARRB2	chr17	+	-6340	NM_199004
D3A_WT	1212	4860244	4860869	2.9	ARRDC5	chr19	-	-6677	NM_001080523
D3A_WT	1665	18383818	18384483	2.88	ARVCF	chr22	-	159	NM_001670
D3A_WT	2555	24940608	24941648	2.61	ARX	chrX	-	2858	NM_139058
D3A_WT	2328	17985617	17985966	2.93	ASAH1	chr8	-	996	NM_004315
D3A_WT	2328	17985617	17985966	2.93	ASAH1	chr8	-	368	NM_177924
D3A_WT	2119	101438480	101438829	2.67	ASCC3	chr6	-	-2709	NM_006828
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D3A_WT	2626	1528765	1529482	3.19	ASMTL	chrY	-	2721	NM_004192
D3A_WT	1349	55712758	55713407	4.13	ASPDH	chr19	-	-3323	NM_001024656
D3A_WT	1348	55707787	55707936	2.01	ASPDH	chr19	-	1898	NM_001024656
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D3A_WT	1348	55707787	55707936	2.01	ASPDH	chr19	-	1093	NM_001114598
D3A_WT	695	103621880	103622314	2.28	ASPG	chr14	+	297	NM_001080464
D3A_WT	2347	62789296	62789655	2.61	ASPH	chr8	-	278	NM_004318
D3A_WT	2468	119216773	119217688	3.95	ASTN2	chr9	-	-92	NM_014010
D3A_WT	2086	32203903	32204043	2.71	ATF6B	chr6	-	22	NM_004381
D3A_WT	1529	242224706	242226417	3.5	ATG4B	chr2	+	-138	NM_013325
D3A_WT	320	273711	274365	2.64	ATHL1	chr11	+	-5099	NM_025092
D3A_WT	488	6907745	6908170	2.84	ATN1	chr12	+	217	NM_001940
D3A_WT	1435	85834549	85834908	2.67	ATOH8	chr2	+	309	NM_032827
D3A_WT	1279	19635250	19635374	2.76	ATP13A1	chr19	-	191	NM_020410
D3A_WT	939	3814193	3814322	2.19	ATP2A3	chr17	-	228	NM_174955
D3A_WT	2611	153310101	153310875	3.43	ATP6AP1	chrX	+	317	NM_001183
D3A_WT	2278	128289946	128290816	2.27	ATP6V1F	chr7	+	248	NM_004231

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D3A_WT	1128	74930216	74931968	3.44	ATP9B	chr18	+	708	NM_198531
D3A_WT	428	66939607	66940077	2.2	ATPGD1	chr11	+	118	NM_001166222
D3A_WT	2268	105305294	105305447	2.04	ATXN7L1	chr7	-	-1103	NM_020725
D3A_WT	271	99437221	99437470	2.37	AVPI1	chr10	-	-340	NM_021732
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D3A_WT	108	44217503	44218150	3.48	B4GALT2	chr1	+	-943	NM_001005417
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D3A_WT	965	19206707	19207026	2.69	B9D1	chr17	-	-227	NM_015681
D3A_WT	1616	29592993	29594239	3.55	BACH1	chr21	+	-5814	NR_027655
D3A_WT	1616	29592993	29594239	3.55	BACH1	chr21	+	9	NM_206866
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D3A_WT	2117	91062816	91062957	2.38	BACH2	chr6	-	397	NM_021813
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D3A_WT	2105	57144904	57145846	3.63	BAG2	chr6	+	313	NM_004282
D3A_WT	2376	143542478	143543435	2.83	BAI1	chr8	+	578	NM_001702
D3A_WT	810	1323088	1323609	2.41	BAIAP3	chr16	+	-1315	NM_003933
D3A_WT	909	86542743	86543102	2.79	BANP	chr16	+	384	NM_017869
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D3A_WT	2452	95761163	95761387	2.29	BARX1	chr9	-	-3846	NM_021570
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D3A_WT	862	31027927	31028081	2.18	BCKDK	chr16	+	842	NM_005881
D3A_WT	1453	111596835	111597299	2.48	BCL2L11	chr2	+	2106	NM_138621
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D3A_WT	684	100110016	100110575	2.64	BEGAIN	chr14	-	-6135	NM_001159531
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D3A_WT	2104	56927609	56927948	3.79	BEND6	chr6	+	47	NM_152731
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D3A_WT	2586	102354336	102354775	2.02	BEX4	chrX	+	-2120	NM_001127688
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D3A_WT	1546	6696540	6697792	2.31	BMP2	chr20	+	422	NM_001200
D3A_WT	101	39729713	39729877	2.16	BMP8A	chr1	+	-109	NM_181809
D3A_WT	253	75163035	75163359	2.48	BMS1P4	chr10	-	-2919	NR_026592
D3A_WT	765	81744095	81744744	2.76	BNC1	chr15	-	53	NM_001717
D3A_WT	1815	114412584	114412713	2.05	BOC	chr3	+	-1416	NM_033254
D3A_WT	593	31783534	31783798	2.21	BRCA2	chr13	+	-3950	NM_000059
D3A_WT	2615	153952695	153952976	2.78	BRCC3	chrX	+	-68	NM_001018055
D3A_WT	2387	144845089	144846553	5.31	BREA2	chr8	+	-5451	NR_015445
D3A_WT	2388	144847099	144847827	2.85	BREA2	chr8	+	-3809	NR_015445
D3A_WT	2389	144850278	144850847	3.28	BREA2	chr8	+	-710	NR_015445
D3A_WT	707	104838135	104838389	2.86	BRF1	chr14	-	112	NM_001519
D3A_WT	423	65866199	65866328	2.53	BRMS1	chr11	-	2895	NM_001024957

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D3A_WT	1899	15314538	15314987	2.66	BST1	chr4	+	1092	NM_004334
D3A_WT	764	81526545	81526694	2.4	BTBD1	chr15	-	491	NM_025238
D3A_WT	545	106237158	106237792	4.09	BTBD11	chr12	+	1149	NM_001018072
D3A_WT	676	92868370	92868990	2.38	BTBD7	chr14	-	458	NM_001002860
D3A_WT	116	52294710	52295079	3.23	BTF3L4	chr1	+	450	NM_152265
D3A_WT	296	124898039	124898303	2.95	BUB3	chr10	+	-5578	NM_001007793
D3A_WT	1486	201385320	201385474	2.2	BZW1	chr2	+	506	NM_014670
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D3A_WT	291	115929228	115929362	2.42	C10orf118	chr10	-	-4941	NM_018017
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D3A_WT	305	134103304	134103738	2.82	C10orf91	chr10	+	-5182	NM_173541
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D3A_WT	455	110675174	110675600	2.65	C11orf92	chr11	-	362	NM_207429
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D3A_WT	542	102414677	102414825	2.67	C12orf42	chr12	-	-875	NM_198521
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D3A_WT	543	102875146	102875686	2.46	C12orf73	chr12	-	-293	NM_001135570
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D3A_WT	650	49170541	49171673	2.78	C14orf104	chr14	-	591	NM_001083908
D3A_WT	667	76993467	76994240	3.74	C14orf133	chr14	-	-196	NM_022067
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D3A_WT	663	76561989	76564437	3.5	C14orf4	chr14	-	1574	NM_024496
D3A_WT	788	550357	550906	2.96	C16orf11	chr16	+	209	NM_145270
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D3A_WT	791	631593	632329	3.41	C16orf13	chr16	-	-5613	NM_001040165
D3A_WT	790	623567	624646	2.56	C16orf13	chr16	-	2242	NM_001040165
D3A_WT	812	1483300	1483619	2.7	C16orf38	chr16	-	-4990	NM_001013658
D3A_WT	811	1338668	1339687	4.1	C16orf42	chr16	-	2697	NM_001001410
D3A_WT	852	21926934	21928491	3	C16orf52	chr16	+	756	NM_001164579
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D3A_WT	1119	50137943	50138222	2.41	C18orf54	chr18	+	-1086	NM_173529
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D3A_WT	1283	34898054	34898313	2.48	C19orf12	chr19	-	-380	NM_001031726
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D3A_WT	1292	40938496	40938840	2.53	C19orf55	chr19	+	-2215	NM_001039887
D3A_WT	1347	55674730	55675172	2.76	C19orf63	chr19	+	3404	NM_206538
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D3A_WT	1341	54883121	54883675	2.12	C19orf76	chr19	+	-355	NM_001101340
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D3A_WT	138	111308074	111308419	3.24	C1orf103	chr1	-	-157	NM_018372
D3A_WT	193	218930484	218930633	2.75	C1orf115	chr1	+	308	NM_024709
D3A_WT	149	149955637	149955776	2	C1orf230	chr1	+	-4930	NM_001144956
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D3A_WT	30	2507714	2508554	2.95	C1orf93	chr1	+	26	NM_152371
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D3A_WT	1554	30535428	30536376	2.86	C20orf112	chr20	-	-953	NM_080616
D3A_WT	1604	61963624	61964563	2.91	C20orf135	chr20	+	1084	NM_080622
D3A_WT	1598	61650934	61651164	2.84	C20orf195	chr20	+	-3767	NM_024059
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D3A_WT	1651	46426244	46426978	3.83	C21orf56	chr21	-	2190	NM_001142854
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D3A_WT	1654	46530979	46531154	2	C21orf57	chr21	+	372	NM_058181
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D3A_WT	1533	242462622	242464331	3.93	C2orf85	chr2	+	2918	NM_173821
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D3A_WT	1908	37134420	37134557	2.19	C4orf19	chr4	+	2542	NM_001104629
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D3A_WT	2087	32447234	32447413	2.36	C6orf10	chr6	-	311	NM_006781
D3A_WT	2074	13595123	13595477	2.5	C6orf114	chr6	-	-906	NM_033069
D3A_WT	2096	41148788	41149222	2.97	C6orf130	chr6	-	-839	NM_145063
D3A_WT	2084	30723232	30723501	2.73	C6orf136	chr6	+	572	NM_145029
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D3A_WT	2162	169934555	169935209	2.98	C6orf208	chr6	+	2789	NR_026780
D3A_WT	2175	882341	882485	2.48	C7orf20	chr7	+	-303	NM_015949
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D3A_WT	2228	44992585	44993144	4.34	C7orf40	chr7	-	-80	NR_003697
D3A_WT	2244	66023246	66024126	2.27	C7orf42	chr7	+	49	NM_017994
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D3A_WT	2400	145407968	145410181	2.93	C8orf30A	chr8	+	387	NM_016458
D3A_WT	2410	146248560	146249089	3.74	C8orf33	chr8	+	197	NM_023080
D3A_WT	2383	144526709	144527467	2.56	C8orf51	chr8	-	-4908	NR_026785
D3A_WT	2489	131122813	131123082	2.81	C9orf106	chr9	+	-168	NM_001012715
D3A_WT	2459	103288627	103289779	2.69	C9orf125	chr9	-	93	NM_032342
D3A_WT	2515	138497330	138497983	3.11	C9orf163	chr9	+	-111	NM_152571
D3A_WT	2527	139285198	139286747	3.6	C9orf167	chr9	+	-6128	NM_017723
D3A_WT	2441	88953196	88953737	2.88	C9orf170	chr9	+	88	NM_001001709
D3A_WT	2519	138858268	138859043	2.42	C9orf172	chr9	+	-32	NM_001080482
D3A_WT	2449	94898341	94899092	3.7	C9orf89	chr9	+	446	NM_032310
D3A_WT	1336	53840116	53840798	3.21	CA11	chr19	-	806	NM_001217
D3A_WT	1584	60418907	60423836	3.36	CABLES2	chr20	-	-5637	NM_031215
D3A_WT	558	119563036	119563960	2.57	CABP1	chr12	+	694	NM_001033677
D3A_WT	429	67054130	67054482	2.6	CABP2	chr11	-	-6831	NM_031204
D3A_WT	1692	28446275	28446701	2.99	CABP7	chr22	+	145	NM_182527
D3A_WT	1793	50514122	50515576	2.49	CACNA2D2	chr3	-	1047	NM_006030
D3A_WT	854	24174674	24174924	2.59	CACNG3	chr16	+	423	NM_006539
D3A_WT	226	5529511	5529661	2.22	CALML5	chr10	-	1947	NM_017422
D3A_WT	2247	71439627	71440046	2.45	CALN1	chr7	-	308	NM_001017440
D3A_WT	316	134998421	135003396	3.68	CALY	chr10	-	-443	NM_015722
D3A_WT	2226	44330350	44331204	2.97	CAMK2B	chr7	-	978	NM_172084
D3A_WT	1842	185461472	185461631	2.89	CAMK2N2	chr3	-	394	NM_033259

D3A_WT	50	6768081	6768434	2.07	CAMTA1	chr1	+	287	NM_015215
D3A_WT	620	110065856	110066290	2.54	CARKD	chr13	+	65	NM_018210
D3A_WT	367	3034810	3035344	3.71	CARS	chr11	-	170	NM_001751
D3A_WT	63	15723508	15724249	3.9	CASP9	chr1	-	-501	NM_032996
D3A_WT	421	65548639	65550588	2.47	CATSPER1	chr11	-	951	NM_053054
D3A_WT	78	26382834	26382956	2.1	CATSPER4	chr1	+	-6810	NM_198137
D3A_WT	882	65620382	65621227	2.05	CBFB	chr16	+	254	NM_022845
D3A_WT	1061	75433594	75433950	2.32	CBX4	chr17	-	-5964	NM_003655
D3A_WT	1059	75428265	75430641	2.58	CBX4	chr17	-	-1645	NM_003655
D3A_WT	1060	75431793	75432212	2.44	CBX4	chr17	-	-4194	NM_003655
D3A_WT	123	89230679	89231048	3.05	CCBL2	chr1	-	368	NM_001008661
D3A_WT	2014	114666831	114667213	2.65	CCDC112	chr5	-	-6665	NM_001040440
D3A_WT	2013	114662496	114662715	2.36	CCDC112	chr5	-	-2248	NM_001040440
D3A_WT	2014	114666831	114667213	2.65	CCDC112	chr5	-	-7136	NM_152549
D3A_WT	2013	114662496	114662715	2.36	CCDC112	chr5	-	-2719	NM_152549
D3A_WT	953	8590335	8591014	2.97	CCDC42	chr17	-	-1795	NM_001158261
D3A_WT	1822	130203485	130203919	2.83	CCDC48	chr3	+	541	NM_024768
D3A_WT	1849	192530002	192530544	2.92	CCDC50	chr3	+	706	NM_174908
D3A_WT	1087	77766403	77766662	2.52	CCDC57	chr17	-	-2554	NM_198082
D3A_WT	797	721772	722617	3.67	CCDC78	chr16	-	-5720	NM_001031737
D3A_WT	796	716441	716585	2.43	CCDC78	chr16	-	-39	NM_001031737
D3A_WT	408	63866574	63866743	2.35	CCDC88B	chr11	+	2393	NM_032251
D3A_WT	566	123023736	123024285	2.89	CCDC92	chr12	-	-894	NM_025140
D3A_WT	980	29635916	29636150	2.55	CCL11	chr17	+	-766	NM_002986
D3A_WT	982	31417089	31417218	2.63	CCL18	chr17	+	1398	NM_002988
D3A_WT	2423	34655289	34655876	2.93	CCL27	chr9	-	-2893	NM_006664
D3A_WT	2098	42017334	42017803	2.11	CCND3	chr6	-	-38	NM_001136125
D3A_WT	2443	89779441	89779790	2.38	CCRK	chr9	-	-128	NM_178432
D3A_WT	1001	39279981	39280230	2.12	CD300LG	chr17	+	64	NM_145273
D3A_WT	1473	160363002	160363253	3.1	CD302	chr2	-	-115	NM_014880
D3A_WT	1088	77870527	77870771	3.24	CD7	chr17	-	-1880	NM_006137
D3A_WT	1089	77871844	77873881	2.84	CD7	chr17	-	-4093	NM_006137
D3A_WT	2075	14226040	14226194	2.65	CD83	chr6	+	274	NM_004233
D3A_WT	1995	54504835	54504999	2.19	CDC20B	chr5	-	-157	NM_001145734
D3A_WT	2465	115077770	115078094	2.46	CDC26	chr9	-	-242	NM_139286
D3A_WT	1140	484962	485601	2.93	CDC34	chr19	+	2549	NM_004359
D3A_WT	1989	20028633	20028990	2.71	CDH18	chr5	-	-4701	NM_004934
D3A_WT	563	122323257	122323618	2.93	CDK2AP1	chr12	-	-797	NM_004642
D3A_WT	1952	184602786	184603045	2.28	CDKN2AIP	chr4	+	133	NM_017632
D3A_WT	1236	10541043	10541192	2.08	CDKN2D	chr19	-	-462	NM_079421
D3A_WT	1236	10541043	10541192	2.08	CDKN2D	chr19	-	-486	NM_001800
D3A_WT	853	22293056	22293405	2.73	CDR2	chr16	-	209	NM_001802
D3A_WT	1541	5048566	5049020	2.03	CDS2	chr20	+	-6688	NM_003818
D3A_WT	1826	134775285	134775714	3.01	CDV3	chr3	+	376	NM_017548
D3A_WT	1826	134775285	134775714	3.01	CDV3	chr3	+	-491	NM_001134423
D3A_WT	2071	4721009	4721635	2.89	CDYL	chr6	+	-356	NM_004824
D3A_WT	1659	16032200	16032516	2.16	CECR5	chr22	-	-6181	NM_017829

D3A_WT	1657	15980573	15982602	2.65	CECR6	chr22	-	670	NM_001163079
D3A_WT	1657	15980573	15982602	2.65	CECR6	chr22	-	626	NM_031890
D3A_WT	957	16197202	16197641	2.65	CENPV	chr17	-	116	NM_181716
D3A_WT	1466	130996901	130997066	2.63	CFC1	chr2	+	1678	NM_032545
D3A_WT	1466	130996901	130997066	2.63	CFC1B	chr2	+	1847	NM_001079530
D3A_WT	2563	47370977	47371126	2.81	CFP	chrX	-	3262	NM_001145252
D3A_WT	1407	27195400	27195934	2.96	CGREF1	chr2	-	-390	NM_001166239
D3A_WT	1407	27195400	27195934	2.96	CGREF1	chr2	-	-168	NM_001166240
D3A_WT	730	39032574	39033456	3.38	CHAC1	chr15	+	88	NM_024111
D3A_WT	1016	45898350	45899202	2.45	CHAD	chr17	-	2450	NM_001267
D3A_WT	1717	39964598	39964762	2.72	CHADL	chr22	-	2201	NM_138481
D3A_WT	44	6161697	6162061	2.46	CHD5	chr1	-	891	NM_015557
D3A_WT	1802	53855532	53855996	2.71	CHDH	chr3	-	-305	NM_018397
D3A_WT	468	125000591	125000735	2.38	CHEK1	chr11	+	418	NM_001114122
D3A_WT	468	125000591	125000735	2.38	CHEK1	chr11	+	-858	NM_001274
D3A_WT	139	111637336	111637586	2.44	CHIA	chr1	+	2401	NM_201653
D3A_WT	139	111637336	111637586	2.44	CHIA	chr1	+	2455	NM_021797
D3A_WT	1914	54625318	54625747	3.29	CHIC2	chr4	-	13	NM_012110
D3A_WT	1758	214957	215101	2.55	CHL1	chr3	+	1380	NM_006614
D3A_WT	2218	29201179	29201708	3.22	CHN2	chr7	+	798	NM_004067
D3A_WT	1494	220118366	220121700	4.54	CHPF	chr2	-	-3302	NM_024536
D3A_WT	1845	185580844	185581398	2.51	CHRD	chr3	+	567	NM_003741
D3A_WT	441	74119936	74120515	3.25	CHRDL2	chr11	-	-391	NM_015424
D3A_WT	721	28472430	28472924	2.89	CHRFAM7A	chr15	-	479	NM_139320
D3A_WT	396	46370218	46370462	2.65	CHRM4	chr11	-	-5657	NM_000741
D3A_WT	397	46371565	46371714	2.37	CHRM4	chr11	-	-6956	NM_000741
D3A_WT	394	46363428	46364647	5.25	CHRM4	chr11	-	646	NM_000741
D3A_WT	395	46368323	46368552	3.24	CHRM4	chr11	-	-3754	NM_000741
D3A_WT	1592	61465589	61466043	3.09	CHRNA4	chr20	-	-2677	NM_000744
D3A_WT	390	45644035	45644199	2.67	CHST1	chr11	-	-369	NM_003654
D3A_WT	2017	129268045	129268304	2.52	CHSY3	chr5	+	-247	NM_175856
D3A_WT	798	778442	779106	3.44	CHTF18	chr16	+	152	NM_022092
D3A_WT	799	780852	783152	2.87	CHTF18	chr16	+	3380	NM_022092
D3A_WT	274	101984444	101984605	2.35	CHUK	chr10	-	-5190	NM_001278
D3A_WT	1794	50624131	50624260	2.33	CISH	chr3	-	71	NM_145071
D3A_WT	2444	91115466	91116491	4.36	CKS2	chr9	+	46	NM_001827
D3A_WT	459	113152742	113152987	2.66	CLDN25	chr11	+	-2863	NM_001101389
D3A_WT	1662	17891250	17891594	2.49	CLDN5	chr22	-	1438	NM_001130861
D3A_WT	2284	138858977	138859625	2.72	CLEC2L	chr7	+	88	NM_001080511
D3A_WT	2521	139011284	139011730	3.2	CLIC3	chr9	-	-662	NM_004669
D3A_WT	1624	34963857	34964106	2.3	CLIC6	chr21	+	424	NM_053277
D3A_WT	2249	73341673	73342409	3.07	CLIP2	chr7	+	301	NM_032421
D3A_WT	2320	1698769	1698898	2.15	CLN8	chr8	+	-443	NM_018941
D3A_WT	1978	1397704	1398178	2.24	CLPTM1L	chr5	-	61	NM_030782
D3A_WT	110	47572282	47572631	2.57	CMPK1	chr1	+	401	NM_001136140
D3A_WT	1737	45071619	45072388	3.47	CN5H6.4	chr22	-	-782	NR_024009
D3A_WT	279	104668567	104669441	2.71	CNNM2	chr10	+	901	NM_199076

D3A_WT	2063	179854134	179854573	3.56	CNOT6	chr5	+	331	NM_015455
D3A_WT	1921	78959150	78961025	3.11	CNOT6L	chr4	-	-519	NM_144571
D3A_WT	1307	45424044	45425212	3.38	CNTD2	chr19	-	-191	NM_024877
D3A_WT	1759	2115450	2116398	3	CNTN4	chr3	+	-1322	NM_175607
D3A_WT	951	7775287	7776027	2.5	CNTROB	chr17	+	-540	NM_053051
D3A_WT	646	30413441	30414075	2.47	COCH	chr14	+	267	NM_001135058
D3A_WT	1646	45701182	45701306	2.48	COL18A1	chr21	+	1393	NM_130444
D3A_WT	1015	45631904	45632238	2.14	COL1A1	chr17	-	1928	NM_000088
D3A_WT	2052	177948885	177949129	2.31	COL23A1	chr5	-	1155	NM_173465
D3A_WT	619	109757367	109757511	2.82	COL4A1	chr13	-	58	NM_001845
D3A_WT	619	109757367	109757511	2.82	COL4A2	chr13	+	-192	NM_001846
D3A_WT	1650	46344903	46345422	2.67	COL6A2	chr21	+	2702	NM_001849
D3A_WT	2365	120146628	120146815	2.36	COLEC10	chr8	+	-1883	NM_006438
D3A_WT	1097	490590	491552	3.37	COLEC12	chr18	-	-342	NM_130386
D3A_WT	256	76665405	76665649	2.34	COMTD1	chr10	-	249	NM_144589
D3A_WT	255	76663729	76664347	3.05	COMTD1	chr10	-	1738	NM_144589
D3A_WT	1262	16998272	16998421	3.02	CPAMD8	chr19	-	279	NM_015692
D3A_WT	1851	195553919	195554758	3.35	CPN2	chr3	-	-988	NM_001080513
D3A_WT	923	88170101	88170560	2.67	CPNE7	chr16	+	654	NM_153636
D3A_WT	2402	145605638	145605867	2.31	CPSF1	chr8	-	-211	NM_013291
D3A_WT	2403	145609915	145611495	4.45	CPSF1	chr8	-	-5164	NM_013291
D3A_WT	404	60954055	60954419	2.65	CPSF7	chr11	-	-197	NM_001142565
D3A_WT	404	60954055	60954419	2.65	CPSF7	chr11	-	-278	NM_024811
D3A_WT	1754	49363271	49363720	2.55	CPT1B	chr22	-	249	NM_004377
D3A_WT	1754	49363271	49363720	2.55	CPT1B	chr22	-	467	NM_152245
D3A_WT	1754	49363271	49363720	2.55	CPT1B	chr22	-	-123	NM_001145137
D3A_WT	1341	54883121	54883675	2.12	CPT1C	chr19	+	-2814	NM_001136052
D3A_WT	1341	54883121	54883675	2.12	CPT1C	chr19	+	-2820	NM_152359
D3A_WT	756	76413965	76414119	2.31	CRABP1	chr15	+	-5678	NM_004378
D3A_WT	813	1604230	1605271	2.3	CRAMP1L	chr16	+	109	NM_020825
D3A_WT	2471	125158995	125159119	2.23	CRB2	chr9	+	789	NM_173689
D3A_WT	1220	6415665	6415804	2.03	CRB3	chr19	+	475	NM_174881
D3A_WT	2217	28415994	28416918	2.85	CREB5	chr7	+	-2212	NM_182898
D3A_WT	835	3870242	3870461	2.73	CREBBP	chr16	-	-229	NM_001079846
D3A_WT	239	35455741	35456087	2.36	CREM	chr10	+	108	NM_183013
D3A_WT	239	35455741	35456087	2.36	CREM	chr10	+	-479	NM_181571
D3A_WT	709	105007477	105007651	2.72	CRIP2	chr14	+	-4611	NM_001312
D3A_WT	2533	1290007	1290136	2.2	CRLF2	chrX	-	1456	NM_001012288
D3A_WT	2533	1290007	1290136	2.2	CRLF2	chrX	-	1459	NM_022148
D3A_WT	1542	5934609	5935158	2.33	CRLS1	chr20	+	145	NM_019095
D3A_WT	1542	5934609	5935158	2.33	CRLS1	chr20	+	-1014	NM_001127458
D3A_WT	771	88873875	88874737	3.51	CRTC3	chr15	+	105	NM_022769
D3A_WT	493	10767093	10767342	3.12	CSDA	chr12	-	3	NM_001145426
D3A_WT	2622	1345878	1346602	3.15	CSF2RA	chrY	+	-1452	NM_172246
D3A_WT	2534	1345633	1347217	3.06	CSF2RA	chrX	+	-1267	NM_172246
D3A_WT	752	72861701	72862456	2.21	CSK	chr15	+	601	NM_004383
D3A_WT	2321	4836671	4837285	2.67	CSMD1	chr8	-	2758	NM_033225

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D3A_WT	2637	24743538	24743992	2.2	CSPG4LYP2	chrY	-	-999	NR_002194
D3A_WT	1635	44020557	44020686	2.14	CSTB	chr21	-	66	NM_000100
D3A_WT	2613	153540106	153540950	2.16	CTAG2	chrX	-	-5493	NM_172377
D3A_WT	2613	153540106	153540950	2.16	CTAG2	chrX	-	-5492	NM_020994
D3A_WT	299	126839353	126840369	2.15	CTBP2	chr10	-	-247	NM_001083914
D3A_WT	298	126837626	126837902	2.17	CTBP2	chr10	-	1850	NM_001083914
D3A_WT	299	126839353	126840369	2.15	CTBP2	chr10	-	-768	NM_001329
D3A_WT	298	126837626	126837902	2.17	CTBP2	chr10	-	1329	NM_001329
D3A_WT	2137	132312950	132314009	3.73	CTGF	chr6	-	732	NM_001901
D3A_WT	916	87300544	87300673	2.46	CTU2	chr16	+	217	NM_001012759
D3A_WT	1228	7895330	7896211	2.38	CTXN1	chr19	-	1281	NM_206833
D3A_WT	2290	148026891	148027220	2.74	CUL1	chr7	+	190	NM_003592
D3A_WT	632	112911366	112912015	2.42	CUL4A	chr13	+	-241	NM_001008895
D3A_WT	632	112911366	112912015	2.42	CUL4A	chr13	+	604	NM_003589
D3A_WT	2264	101247637	101247786	2.7	CUX1	chr7	+	1700	NM_001913
D3A_WT	2264	101247637	101247786	2.7	CUX1	chr7	+	110	NM_181552
D3A_WT	2264	101247637	101247786	2.7	CUX1	chr7	+	1689	NM_181500
D3A_WT	243	44200072	44200491	3.18	CXCL12	chr10	-	267	NM_000609
D3A_WT	2589	103297680	103297934	2.35	CXorf39	chrX	+	-149	NM_207318
D3A_WT	2581	70898689	70898998	2.57	CXorf49	chrX	+	-1021	NM_001145140
D3A_WT	2581	70898689	70898998	2.57	CXorf49B	chrX	+	-1021	NM_001145139
D3A_WT	2107	84619835	84620264	3.25	CYB5R4	chr6	+	-6039	NM_016230
D3A_WT	2396	145221712	145223064	2.83	CYC1	chr8	+	441	NM_001916
D3A_WT	2397	145224590	145224864	2.26	CYC1	chr8	+	2780	NM_001916
D3A_WT	2381	144002172	144002521	2.83	CYP11B2	chr8	-	-6085	NM_000498
D3A_WT	740	49421417	49421541	2.21	CYP19A1	chr15	-	-3392	NM_000103
D3A_WT	1413	38157115	38157744	2.2	CYP1B1	chr2	-	-602	NM_000104
D3A_WT	1428	72228203	72228843	2.27	CYP26B1	chr2	-	-52	NM_019885
D3A_WT	1721	40855345	40855794	2.6	CYP2D6	chr22	-	1258	NM_001025161
D3A_WT	1957	187349740	187350122	3.28	CYP4V2	chr4	+	264	NM_207352
D3A_WT	1329	51856033	51856177	3.25	DACT3	chr19	-	130	NM_145056
D3A_WT	1788	49034806	49034950	2.87	DALRD3	chr3	-	-3857	NM_001009996
D3A_WT	1787	49030836	49031362	2.96	DALRD3	chr3	-	-78	NM_001009996
D3A_WT	1788	49034806	49034950	2.87	DALRD3	chr3	-	-1407	NM_018114
D3A_WT	1787	49030836	49031362	2.96	DALRD3	chr3	-	2372	NM_018114
D3A_WT	1471	159354102	159354264	2.04	DAPL1	chr2	+	-5891	NM_001017920
D3A_WT	2594	125127124	125128298	2.47	DCAF12L2	chrX	-	-96	NM_001013628
D3A_WT	1251	13926145	13926389	2.22	DCAF15	chr19	+	1949	NM_138353
D3A_WT	1811	100102540	100102774	2.51	DCBLD2	chr3	-	566	NM_080927
D3A_WT	2079	24468044	24468188	2.23	DCDC2	chr6	-	-1857	NM_016356
D3A_WT	1945	155632736	155632900	2.04	DCHS2	chr4	-	-491	NM_001142552
D3A_WT	1945	155632736	155632900	2.04	DCHS2	chr4	-	-438	NM_001142553
D3A_WT	820	2241296	2241615	2.36	DCI	chr16	-	149	NM_001919
D3A_WT	1801	53356789	53357140	2.13	DCP1A	chr3	-	-287	NM_018403
D3A_WT	122	85703043	85703662	2.34	DDAH1	chr1	-	125	NM_012137
D3A_WT	573	131201263	131201850	2.94	DDX51	chr12	-	-6723	NM_175066

D3A_WT	327	684680	685544	2.15	DEAF1	chr11	-	628	NM_021008
D3A_WT	166	159368853	159369406	2.75	DEDD	chr1	-	-249	NM_001039712
D3A_WT	166	159368853	159369406	2.75	DEDD	chr1	-	-27	NM_001039711
D3A_WT	928	88540864	88541123	2.52	DEF8	chr16	+	-1658	NM_017702
D3A_WT	928	88540864	88541123	2.52	DEF8	chr16	+	-1690	NM_207514
D3A_WT	1661	17489330	17490269	2.77	DGCR2	chr22	-	168	NM_005137
D3A_WT	1505	233927793	233928162	2.29	DGKD	chr2	+	86	NM_152879
D3A_WT	2282	137182383	137183308	2.76	DGKI	chr7	-	-696	NM_004717
D3A_WT	1867	956953	957701	2.61	DGKQ	chr4	-	17	NM_001347
D3A_WT	603	51276168	51276392	3.22	DHRS12	chr13	-	-45	NM_001031719
D3A_WT	603	51276168	51276392	3.22	DHRS12	chr13	-	14	NM_024705
D3A_WT	2543	2428847	2429753	2.85	DHRSX	chrX	-	-285	NM_145177
D3A_WT	561	121276763	121277086	2.47	DIABLO	chr12	-	1097	NM_138929
D3A_WT	514	49185067	49185206	2.14	DIP2B	chr12	+	102	NM_173602
D3A_WT	221	724832	725957	2.4	DIP2C	chr10	-	214	NM_014974
D3A_WT	222	732033	732583	2.61	DIP2C	chr10	-	-6700	NM_014974
D3A_WT	2446	92444788	92445037	2.62	DIRAS2	chr9	-	16	NM_017594
D3A_WT	1817	123996952	123997601	2.58	DIRC2	chr3	+	686	NM_032839
D3A_WT	2614	153644318	153644462	2.83	DKC1	chrX	+	166	NM_001363
D3A_WT	876	54782448	54783128	3.14	DKFZP434H168	chr16	-	3150	NR_026889
D3A_WT	418	65304952	65305782	2.48	DKFZp761E198	chr11	-	-969	NM_138368
D3A_WT	375	11986695	11987412	2.72	DKK3	chr11	-	152	NM_015881
D3A_WT	375	11986695	11987412	2.72	DKK3	chr11	-	-291	NM_001018057
D3A_WT	375	11986695	11987412	2.72	DKK3	chr11	-	440	NM_013253
D3A_WT	601	49601713	49602639	2.95	DLEU2	chr13	-	-4498	NR_002612
D3A_WT	947	7070974	7071398	2.41	DLG4	chr17	-	-7093	NM_001365
D3A_WT	2167	170440431	170441066	3.57	DLL1	chr6	-	874	NM_005618
D3A_WT	2412	967062	967481	2.33	DMRT3	chr9	+	308	NM_021240
D3A_WT	113	50659762	50660122	3.16	DMRTA2	chr1	-	1787	NM_032110
D3A_WT	1315	47040258	47040417	2.07	DMRTC2	chr19	+	-588	NM_001040283
D3A_WT	565	122812510	122813254	4.55	DNAH10	chr12	+	-112	NM_207437
D3A_WT	63	15723508	15724249	3.9	DNAJC16	chr1	+	-2060	NM_015291
D3A_WT	819	2223991	2227048	3.51	DNASE1L2	chr16	+	-949	NM_001374
D3A_WT	1500	230287846	230288090	2.65	DNER	chr2	-	-438	NM_139072
D3A_WT	1237	10689734	10690503	3.33	DNM2	chr19	+	364	NM_004945
D3A_WT	1636	44507104	44507458	2.78	DNMT3L	chr21	-	-754	NM_175867
D3A_WT	126	94116744	94117080	3.09	DNTTIP2	chr1	-	418	NM_014597
D3A_WT	2329	21832368	21833597	2.64	DOK2	chr8	-	-5831	NM_003974
D3A_WT	1572	52525466	52525645	2.16	DOK5	chr20	+	-117	NM_018431
D3A_WT	1887	3434761	3435088	3.13	DOK7	chr4	+	94	NM_173660
D3A_WT	1183	2116180	2116614	2.66	DOT1L	chr19	+	1250	NM_032482
D3A_WT	1182	2115078	2115300	2.12	DOT1L	chr19	+	42	NM_032482
D3A_WT	661	72429544	72429673	2.54	DPF3	chr14	-	954	NM_012074
D3A_WT	977	26322212	26322461	2.59	DPRXP4	chr17	+	-4142	NR_002221
D3A_WT	1287	35588537	35588916	2.78	DPY19L3	chr19	+	-144	NM_207325
D3A_WT	458	112851175	112851807	3.39	DRD2	chr11	-	-280	NM_016574
D3A_WT	2366	120936718	120937467	2.36	DSCC1	chr8	-	259	NM_024094

D3A_WT	1627	37562127	37562251	2.85	DSCR3	chr21	-	-486	NM_006052
D3A_WT	2131	116798912	116799061	2.23	DSE	chr6	+	184	NM_013352
D3A_WT	1560	34839692	34840146	3.47	DSN1	chr20	-	-4351	NM_024918
D3A_WT	1560	34839692	34840146	3.47	DSN1	chr20	-	-4275	NM_001145317
D3A_WT	2104	56927609	56927948	3.79	DST	chr6	-	-406	NM_001144769
D3A_WT	1549	17498615	17499059	3.13	DSTN	chr20	+	239	NM_006870
D3A_WT	735	43209482	43209706	2.52	DUOX1	chr15	+	111	NM_175940
D3A_WT	735	43209482	43209706	2.52	DUOXA1	chr15	-	-245	NM_144565
D3A_WT	1083	77616667	77616926	2.24	DUS1L	chr17	-	173	NM_022156
D3A_WT	163	158017209	158017858	2.66	DUSP23	chr1	+	151	NM_017823
D3A_WT	535	88271740	88271874	2.11	DUSP6	chr12	-	-1380	NM_022652
D3A_WT	340	1549665	1550512	2.2	DUSP8	chr11	-	-362	NM_004420
D3A_WT	2602	152561014	152562333	3.72	DUSP9	chrX	+	583	NM_001395
D3A_WT	14	1280314	1280886	3.27	DVL1	chr1	-	-6245	NM_004421
D3A_WT	688	101500745	101501014	2.43	DYNC1H1	chr14	+	262	NM_001376
D3A_WT	2353	86276895	86277449	2.39	E2F5	chr8	+	302	NM_001951
D3A_WT	818	2213768	2213927	2.29	E4F1	chr16	+	280	NM_004424
D3A_WT	300	131651909	131652759	2.47	EBF3	chr10	-	-253	NM_001005463
D3A_WT	1539	2621918	2622577	2.74	EBF4	chr20	+	724	NM_001110514
D3A_WT	1503	233059404	233060038	2.15	ECEL1	chr2	-	1055	NM_004826
D3A_WT	608	77391448	77391587	2.38	EDNRB	chr13	-	-550	NM_003991
D3A_WT	537	91847465	91847689	2.16	EEA1	chr12	-	-339	NM_003566
D3A_WT	1596	61598797	61599216	3.14	EEF1A2	chr20	-	1943	NM_001958
D3A_WT	2267	105010904	105011223	2.36	EFCAB10	chr7	-	-1851	NR_027068
D3A_WT	1164	1237099	1237318	2.38	EFNA2	chr19	+	41	NM_001405
D3A_WT	1163	1233695	1234219	2.78	EFNA2	chr19	+	-3210	NM_001405
D3A_WT	2576	67965558	67966202	3.47	EFNB1	chrX	+	316	NM_004429
D3A_WT	207	229624273	229624697	2.6	EGLN1	chr1	-	2928	NM_022051
D3A_WT	1313	45996802	45997247	3.22	EGLN2	chr19	+	-996	NM_053046
D3A_WT	1314	45999115	45999254	2.83	EGLN2	chr19	+	1164	NM_053046
D3A_WT	1313	45996802	45997247	3.22	EGLN2	chr19	+	137	NM_080732
D3A_WT	1314	45999115	45999254	2.83	EGLN2	chr19	+	2297	NM_080732
D3A_WT	2550	20069852	20070224	3.49	EIF1AX	chrX	-	-151	NM_001412
D3A_WT	1771	40326904	40327037	2.3	EIF1B	chr3	+	794	NM_005875
D3A_WT	1833	151746656	151747175	3.41	EIF2A	chr3	+	-348	NM_032025
D3A_WT	1438	88707376	88708355	2.75	EIF2AK3	chr2	-	244	NM_004836
D3A_WT	2374	141714649	141715505	3.91	EIF2C2	chr8	-	-249	NM_001164623
D3A_WT	1233	10091057	10091785	3.53	EIF3G	chr19	-	178	NM_003755
D3A_WT	2045	175989985	175990249	2.78	EIF4E1B	chr5	+	-171	NM_001099408
D3A_WT	1843	185515380	185516215	2.55	EIF4G1	chr3	+	748	NM_198241
D3A_WT	1843	185515380	185516215	2.55	EIF4G1	chr3	+	-5159	NM_004953
D3A_WT	1843	185515380	185516215	2.55	EIF4G1	chr3	+	133	NM_182917
D3A_WT	71	21375442	21376297	3.37	EIF4G3	chr1	-	58	NM_003760
D3A_WT	692	102869978	102871320	2.37	EIF5	chr14	+	-339	NM_183004
D3A_WT	692	102869978	102871320	2.37	EIF5	chr14	+	404	NM_001969
D3A_WT	1151	797605	797729	2.41	ELANE	chr19	+	-5623	NM_001972
D3A_WT	184	203867632	203868171	3.22	ELK4	chr1	-	722	NM_001973

D3A_WT	453	106968787	106968968	2.28	ELMOD1	chr11	+	1851	NM_001130037
D3A_WT	1434	85435254	85435608	3.01	ELMOD3	chr2	+	78	NM_001135023
D3A_WT	1254	14650057	14650410	2.93	EMR3	chr19	-	-3503	NM_032571
D3A_WT	1429	72998544	72999593	2.84	EMX1	chr2	+	957	NM_004097
D3A_WT	2002	73972594	73973336	2.58	ENC1	chr5	-	40	NM_003633
D3A_WT	943	4792983	4794220	2.65	ENO3	chr17	+	-1529	NM_053013
D3A_WT	1716	39817855	39818618	2.99	EP300	chr22	+	-323	NM_001429
D3A_WT	1418	46378101	46378942	3.5	EPAS1	chr2	+	477	NM_001430
D3A_WT	1498	222146356	222146805	2.3	EPHA4	chr2	-	-1326	NM_004438
D3A_WT	74	22762224	22763551	2.67	EPHA8	chr1	+	297	NM_020526
D3A_WT	125	92267948	92268202	2.13	EPHX4	chr1	+	-45	NM_173567
D3A_WT	2146	146098131	146098480	2.28	EPM2A	chr6	-	379	NM_001018041
D3A_WT	2394	145018297	145019341	2.88	EPPK1	chr8	-	603	NM_031308
D3A_WT	115	51757107	51757356	2.45	EPS15	chr1	-	352	NM_001981
D3A_WT	596	42464495	42464649	2.51	EPSTI1	chr13	-	-195	NM_001002264
D3A_WT	2000	65257860	65257994	2.19	ERBB2IP	chr5	+	-212	NM_001006600
D3A_WT	519	51950716	51951142	2.77	ESPL1	chr12	+	2580	NM_012291
D3A_WT	45	6401366	6401820	2.95	ESPN	chr1	+	-5841	NM_031475
D3A_WT	46	6407273	6407619	2.87	ESPN	chr1	+	12	NM_031475
D3A_WT	162	155374535	155375384	2.5	ETV3	chr1	-	-158	NM_005240
D3A_WT	162	155374535	155375384	2.5	ETV3	chr1	-	48	NM_001145312
D3A_WT	1000	38978575	38978724	2.16	ETV4	chr17	-	182	NM_001986
D3A_WT	1000	38978575	38978724	2.16	ETV4	chr17	-	639	NM_001079675
D3A_WT	1915	56414496	56414750	2.1	EXOC1	chr4	+	51	NM_178237
D3A_WT	1964	495892	496610	3.07	EXOC3	chr5	+	-82	NM_007277
D3A_WT	891	68843068	68843912	2.44	EXOSC6	chr16	-	-156	NM_058219
D3A_WT	387	44073876	44074330	2.39	EXT2	chr11	+	429	NM_000401
D3A_WT	2291	148211664	148212214	2.33	EZH2	chr7	-	408	NM_152998
D3A_WT	2005	76047642	76048116	3.35	F2R	chr5	+	256	NM_001992
D3A_WT	405	61353523	61353872	2.89	FADS2	chr11	+	1409	NM_004265
D3A_WT	760	78774287	78774416	2.54	FAM108C1	chr15	+	-355	NM_021214
D3A_WT	2168	170457762	170458116	2.45	FAM120B	chr6	+	171	NM_032448
D3A_WT	2574	63342159	63342510	2.5	FAM123B	chrX	-	15	NM_152424
D3A_WT	2476	128128849	128128998	2.43	FAM125B	chr9	+	-25	NM_033446
D3A_WT	1844	185536335	185536970	2.24	FAM131A	chr3	+	-4299	NM_144635
D3A_WT	2372	139575970	139576137	2.63	FAM135B	chr8	-	2194	NM_015912
D3A_WT	1389	277972	279119	3.4	FAM150B	chr2	-	-237	NM_001002919
D3A_WT	642	23686921	23687170	2.51	FAM158A	chr14	-	-6408	NM_016049
D3A_WT	1467	131567094	131567323	2.1	FAM168B	chr2	-	266	NM_001009993
D3A_WT	2003	74197515	74197849	2.47	FAM169A	chr5	-	689	NM_015566
D3A_WT	93	36560850	36561968	2.54	FAM176B	chr1	-	933	NM_018166
D3A_WT	1552	25984274	25984648	2.94	FAM182A	chr20	+	1212	NR_026713
D3A_WT	719	27650259	27650578	2.88	FAM189A1	chr15	-	-199	NM_015307
D3A_WT	1926	91267666	91268584	2.68	FAM190A	chr4	+	419	NM_001145065
D3A_WT	791	631593	632329	3.41	FAM195A	chr16	+	112	NM_138418
D3A_WT	790	623567	624646	2.56	FAM195A	chr16	+	-7743	NM_138418
D3A_WT	2628	9974079	9975173	3.08	FAM197Y2	chrY	-	-1749	NR_001553

D3A_WT	1743	47263856	47265009	3.32	FAM19A5	chr22	+	481	NM_001082967
D3A_WT	2170	286928	287062	2.62	FAM20C	chr7	+	-1056	NM_020223
D3A_WT	262	89104680	89105305	3	FAM22D	chr10	+	-2464	NM_001009610
D3A_WT	2434	67382092	67383101	3.39	FAM27B	chr9	-	1413	NR_027422
D3A_WT	971	21750112	21750666	3.02	FAM27L	chr17	+	893	NR_028336
D3A_WT	1852	195889724	195890183	2.48	FAM43A	chr3	+	2043	NM_153690
D3A_WT	2518	138726683	138727012	2.79	FAM69B	chr9	+	3	NM_152421
D3A_WT	1347	55674730	55675172	2.76	FAM71E1	chr19	-	-3136	NM_138411
D3A_WT	1367	60567221	60567370	2.04	FAM71E2	chr19	-	-863	NM_001145402
D3A_WT	2428	39887827	39887986	2.79	FAM74A1	chr9	+	-2293	NR_026803
D3A_WT	2498	133142234	133142458	2.62	FAM78A	chr9	-	-619	NM_033387
D3A_WT	2499	133147736	133147948	2.99	FAM78A	chr9	-	-6115	NM_033387
D3A_WT	722	28652334	28652533	2.34	FAM7A1	chr15	+	384	NR_026858
D3A_WT	722	28652334	28652533	2.34	FAM7A2	chr15	+	384	NR_027470
D3A_WT	963	18854420	18854571	2.23	FAM83G	chr17	-	-5710	NM_001039999
D3A_WT	2390	144894235	144894484	2.25	FAM83H	chr8	-	-6457	NM_198488
D3A_WT	2077	17708270	17709025	2.62	FAM8A1	chr6	+	151	NM_016255
D3A_WT	491	8269086	8269416	2.34	FAM90A1	chr12	-	2230	NM_018088
D3A_WT	377	13646362	13647217	2.35	FAR1	chr11	+	8	NM_032228
D3A_WT	615	97594117	97594297	2.37	FARP1	chr13	+	773	NM_005766
D3A_WT	1085	77649936	77650501	2.18	FASN	chr17	-	-823	NM_004104
D3A_WT	2037	167888832	167889961	2.88	FBLL1	chr5	+	237	NR_024356
D3A_WT	477	1573303	1573657	2.99	FBXL14	chr12	-	112	NM_152441
D3A_WT	2011	107745428	107745862	2.58	FBXL17	chr5	-	53	NM_001163315
D3A_WT	861	30844521	30844770	3	FBXL19	chr16	+	1249	NM_001099784
D3A_WT	988	34811533	34811757	2.47	FBXL20	chr17	-	-243	NM_032875
D3A_WT	1898	15265706	15266255	3.27	FBXL5	chr4	-	131	NM_012161
D3A_WT	229	5971252	5972504	2.66	FBXO18	chr10	+	-341	NM_178150
D3A_WT	229	5971252	5972504	2.66	FBXO18	chr10	+	-4476	NM_032807
D3A_WT	1301	44214834	44215063	2.4	FBXO27	chr19	-	90	NM_178820
D3A_WT	1425	68547801	68548273	2.83	FBXO48	chr2	-	-143	NM_001024680
D3A_WT	2520	138958325	138959045	2.99	FBXW5	chr9	-	309	NM_018998
D3A_WT	1942	153676024	153677778	3.28	FBXW7	chr4	-	-1279	NM_033632
D3A_WT	168	159741967	159742127	2.06	FCGR2A	chr1	+	219	NM_021642
D3A_WT	1441	96667644	96668123	3.55	FER1L5	chr2	+	-4417	NM_001113382
D3A_WT	1545	6051789	6051938	2.58	FERMT1	chr20	-	328	NM_017671
D3A_WT	467	124871220	124871769	2.83	FEZ1	chr11	-	-161	NM_005103
D3A_WT	617	101856447	101856895	2.7	FGF14	chr13	-	-4546	NM_175929
D3A_WT	432	69341034	69343301	2.56	FGF3	chr11	-	962	NM_005247
D3A_WT	1900	15551449	15551908	3.2	FGFBP1	chr4	-	-2609	NM_005130
D3A_WT	295	123347909	123348188	2.45	FGFR2	chr10	-	-4286	NM_001144916
D3A_WT	295	123347909	123348188	2.45	FGFR2	chr10	-	-1899	NM_001144915
D3A_WT	295	123347909	123348188	2.45	FGFR2	chr10	-	-86	NM_001144918
D3A_WT	295	123347909	123348188	2.45	FGFR2	chr10	-	-4577	NM_001144914
D3A_WT	1878	1758547	1759780	3.07	FGFR3	chr4	+	-5673	NM_022965
D3A_WT	1943	154076794	154078715	2.98	FHDC1	chr4	+	-5830	NM_033393
D3A_WT	96	38243365	38243532	2.09	FHL3	chr1	-	373	NM_004468

D3A_WT	884	65840033	65840781	2.35	FHOD1	chr16	-	-1481	NM_013241
D3A_WT	2497	132809059	132809284	2.12	FIBCD1	chr9	-	-4895	NM_001145106
D3A_WT	2497	132809059	132809284	2.12	FIBCD1	chr9	-	-5111	NM_032843
D3A_WT	385	35596799	35597113	2.73	FJX1	chr11	+	646	NM_014344
D3A_WT	2086	32203903	32204043	2.71	FKBPL	chr6	-	2072	NM_022110
D3A_WT	174	178430105	178430554	3.26	FLJ23867	chr1	+	-3437	NR_026900
D3A_WT	1675	19679570	19679994	2.99	FLJ39582	chr22	+	-6428	NR_027052
D3A_WT	1676	19680745	19681089	2.32	FLJ39582	chr22	+	-5293	NR_027052
D3A_WT	1325	50693125	50694289	2.67	FLJ40125	chr19	+	137	NM_001080401
D3A_WT	32	2977403	2977577	2.19	FLJ42875	chr1	-	-3341	NR_024371
D3A_WT	31	2974705	2975471	2.09	FLJ42875	chr1	-	-939	NR_024371
D3A_WT	2085	30820385	30820509	2.39	FLOT1	chr6	-	-2015	NM_005803
D3A_WT	668	85067961	85070155	3.65	FLRT2	chr14	+	2818	NM_013231
D3A_WT	828	2895211	2895570	2.68	FLYWCH1	chr16	+	-6590	NM_032296
D3A_WT	2340	43030610	43031259	2.27	FNTA	chr8	+	336	NM_001018677
D3A_WT	420	65423293	65424565	2.93	FOSL1	chr11	-	644	NM_005438
D3A_WT	2439	78825490	78825759	2.73	FOXB2	chr9	+	1234	NM_001013735
D3A_WT	2001	72779190	72779609	2.92	FOXD1	chr5	-	709	NM_004472
D3A_WT	2038	169464527	169466143	3.35	FOXI1	chr5	+	-159	NM_144769
D3A_WT	107	42573393	42574158	2.97	FOXJ3	chr1	-	-285	NM_014947
D3A_WT	595	40138184	40139215	3.58	FOXO1	chr13	-	35	NM_002015
D3A_WT	2127	108987744	108988668	3.03	FOXO3	chr6	+	488	NM_201559
D3A_WT	2127	108987744	108988668	3.03	FOXO3	chr6	+	-555	NM_001455
D3A_WT	2569	49013554	49013816	2.57	FOXP3	chrX	-	-5453	NM_001114377
D3A_WT	2068	1257600	1257834	2.49	FOXQ1	chr6	+	43	NM_033260
D3A_WT	1922	79197588	79198239	2.78	FRAS1	chr4	+	166	NM_025074
D3A_WT	651	51188912	51189146	2.9	FRMD6	chr14	+	704	NM_152330
D3A_WT	1075	77108726	77111395	3.48	FSCN2	chr17	+	49	NM_012418
D3A_WT	1205	4256123	4256755	2.74	FSD1	chr19	+	849	NM_024333
D3A_WT	1408	27469384	27469733	2.34	FTHL3P	chr2	-	389	NR_002201
D3A_WT	75	24067265	24067634	2.87	FUCA1	chr1	-	-3	NM_000147
D3A_WT	449	93917077	93918126	2.5	FUT4	chr11	+	937	NM_002033
D3A_WT	2522	139045598	139045832	2.71	FUT7	chr9	-	1398	NM_004479
D3A_WT	1290	40314827	40315751	4.57	FXYD1	chr19	+	-6942	NM_005031
D3A_WT	1291	40324498	40324667	2.58	FXYD1	chr19	+	2351	NM_005031
D3A_WT	1290	40314827	40315751	4.57	FXYD1	chr19	+	-6282	NM_021902
D3A_WT	1291	40324498	40324667	2.58	FXYD1	chr19	+	3011	NM_021902
D3A_WT	1291	40324498	40324667	2.58	FXYD7	chr19	+	-1411	NM_022006
D3A_WT	2254	90731832	90731991	2.06	FZD1	chr7	+	193	NM_003505
D3A_WT	187	207915309	207915963	2.99	G0S2	chr1	+	344	NM_015714
D3A_WT	1913	46729367	46729516	2.04	GABRB1	chr4	+	1390	NM_000812
D3A_WT	20	1940934	1941283	2.2	GABRD	chr1	+	481	NM_000815
D3A_WT	1479	171378378	171378602	2.7	GAD1	chr2	+	-2955	NM_000817
D3A_WT	669	87528750	87529811	3.96	GALC	chr14	-	380	NM_000153
D3A_WT	574	131253557	131253981	3.49	GALNT9	chr12	-	2757	NM_021808
D3A_WT	1373	61378135	61378650	2.79	GALP	chr19	+	-808	NM_033106
D3A_WT	382	22644949	22645299	2.02	GAS2	chr11	+	-1105	NM_177553

D3A_WT	382	22644949	22645299	2.02	GAS2	chr11	+	389	NM_001143830
D3A_WT	1691	28034208	28036852	3.56	GAS2L1	chr22	+	2534	NM_152236
D3A_WT	1585	60484755	60485289	2.65	GATA5	chr20	-	-601	NM_080473
D3A_WT	1274	19357458	19358007	3.63	GATAD2A	chr19	+	91	NM_017660
D3A_WT	1509	236746560	236746834	2.69	GBX2	chr2	-	-5306	NM_001485
D3A_WT	141	118278941	118279214	2.43	GDAP2	chr1	-	-5252	NM_017686
D3A_WT	228	5895042	5896477	3.01	GDI2	chr10	-	-241	NM_001115156
D3A_WT	1992	37875789	37876208	2.54	GDNF	chr5	-	-459	NM_000514
D3A_WT	1992	37875789	37876208	2.54	GDNF	chr5	-	-5343	NM_199234
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D3A_WT	1323	50266558	50267179	2.67	GEMIN7	chr19	+	-7489	NM_001007270
D3A_WT	1323	50266558	50267179	2.67	GEMIN7	chr19	+	-7501	NM_001007269
D3A_WT	1400	17798244	17798918	2.66	GEN1	chr2	+	-313	NM_001130009
D3A_WT	1400	17798244	17798918	2.66	GEN1	chr2	+	-76	NM_182625
D3A_WT	2074	13595123	13595477	2.5	GFOD1	chr6	-	466	NM_018988
D3A_WT	888	66310552	66310901	2.53	GFOD2	chr16	-	48	NM_030819
D3A_WT	2062	179712439	179713470	2.71	GFPT2	chr5	-	-33	NM_005110
D3A_WT	1540	3589577	3589706	2.18	GFRA4	chr20	-	2405	NM_145762
D3A_WT	983	31974104	31975563	2.13	GGNBP2	chr17	+	-83	NM_024835
D3A_WT	1504	233270212	233270366	2.8	GIGYF2	chr2	+	31	NM_001103148
D3A_WT	2296	149959943	149960272	2.36	GIMAP6	chr7	-	506	NM_024711
D3A_WT	976	24944638	24944796	2.38	GIT1	chr17	-	-3981	NM_014030
D3A_WT	2116	90654111	90654380	2.08	GJA10	chr6	+	-6663	NM_032602
D3A_WT	1004	40262982	40263116	2.72	GJC1	chr17	-	84	NM_005497
D3A_WT	1004	40262982	40263116	2.72	GJC1	chr17	-	656	NM_001080383
D3A_WT	2556	30581319	30581878	2.34	GK	chrX	+	202	NM_000167
D3A_WT	474	133706946	133707085	2.07	GLB1L2	chr11	+	38	NM_138342
D3A_WT	2208	7975079	7976099	2.44	GLCCI1	chr7	+	642	NM_138426
D3A_WT	740	49421417	49421541	2.21	GLDN	chr15	+	475	NM_181789
D3A_WT	528	56142497	56142748	2.08	GLI1	chr12	+	2422	NM_001167609
D3A_WT	528	56142497	56142748	2.08	GLI1	chr12	+	2438	NM_001160045
D3A_WT	2224	42242732	42242961	2.99	GLI3	chr7	-	297	NM_000168
D3A_WT	550	108802682	108803233	2.55	GLTP	chr12	-	-281	NM_016433
D3A_WT	840	4837595	4838144	2.72	GLYR1	chr16	-	-565	NM_032569
D3A_WT	1304	44524767	44525318	2.4	GMFG	chr19	-	-6476	NM_004877
D3A_WT	2198	2856397	2856982	3.15	GNA12	chr7	-	-6204	NM_007353
D3A_WT	1031	60482750	60483698	3.2	GNA13	chr17	-	158	NM_006572
D3A_WT	876	54782448	54783128	3.14	GNAO1	chr16	+	37	NM_020988
D3A_WT	1578	56850171	56850730	3.62	GNAS	chr20	+	2261	NM_016592
D3A_WT	1579	56899172	56899401	3.08	GNAS	chr20	+	-533	NM_001077489
D3A_WT	1579	56899172	56899401	3.08	GNAS	chr20	+	1712	NR_003259
D3A_WT	1579	56899172	56899401	3.08	GNAS	chr20	+	-877	NM_001077488
D3A_WT	1579	56899172	56899401	3.08	GNAS	chr20	+	-534	NM_080426
D3A_WT	17	1811327	1812553	3.44	GNB1	chr1	-	415	NM_002074
D3A_WT	811	1338668	1339687	4.1	GNPTG	chr16	+	-2755	NM_032520
D3A_WT	726	32663089	32663708	2.32	GOLGA8B	chr15	-	-335	NR_027410
D3A_WT	191	215870797	215870946	2.05	GPATCH2	chr1	-	161	NM_018040

D3A_WT	2595	132947621	132947760	2.88	GPC3	chrX	-	-351	NM_001164619
D3A_WT	587	26231588	26231942	3.4	GPR12	chr13	-	1157	NM_005288
D3A_WT	266	95316614	95316893	2.55	GPR120	chr10	+	342	NM_181745
D3A_WT	311	134751220	134751859	3.77	GPR123	chr10	+	141	NM_001083909
D3A_WT	2178	1058258	1058392	2.2	GPR146	chr7	+	-5341	NM_138445
D3A_WT	236	25503797	25505377	3.63	GPR158	chr10	+	292	NM_020752
D3A_WT	612	94052287	94052511	2.16	GPR180	chr13	+	295	NM_180989
D3A_WT	1519	241217400	241220145	3.94	GPR35	chr2	+	1305	NM_005301
D3A_WT	179	200358466	200359430	2.51	GPR37L1	chr1	+	297	NM_004767
D3A_WT	401	60377277	60377526	2.04	GPR44	chr11	-	2619	NM_004778
D3A_WT	671	90789629	90790073	2.53	GPR68	chr14	-	126	NM_003485
D3A_WT	129	100777387	100777631	2.08	GPR88	chr1	+	1194	NM_022049
D3A_WT	1739	45395556	45395975	3.22	GRAMD4	chr22	+	-5556	NM_015124
D3A_WT	1397	10003102	10003446	2.56	GRHL1	chr2	+	-5968	NM_198182
D3A_WT	95	37273130	37273389	3.11	GRIK3	chr1	-	-828	NM_000831
D3A_WT	1317	47264698	47265347	3.17	GRIK5	chr19	-	-3225	NM_002088
D3A_WT	2524	139152874	139153213	2.7	GRIN1	chr9	+	-386	NM_000832
D3A_WT	496	14025027	14025578	2.87	GRIN2B	chr12	-	-1013	NM_000834
D3A_WT	2460	103539818	103540057	2.03	GRIN3A	chr9	-	746	NM_133445
D3A_WT	1153	954170	954814	3.39	GRIN3B	chr19	+	3056	NM_138690
D3A_WT	1884	2937173	2937649	2.5	GRK4	chr4	+	2271	NM_001004057
D3A_WT	2275	126681324	126682143	2.51	GRM8	chr7	-	-2069	NM_001127323
D3A_WT	2276	126686696	126687075	2.21	GRM8	chr7	-	-7221	NM_001127323
D3A_WT	938	3573777	3574113	2.88	GSG2	chr17	+	0	NM_031965
D3A_WT	845	11916748	11917417	2.6	GSPT1	chr16	-	244	NM_002094
D3A_WT	845	11916748	11917417	2.6	GSPT1	chr16	-	938	NM_001130007
D3A_WT	666	76857490	76857634	2.31	GSTZ1	chr14	+	580	NM_145871
D3A_WT	666	76857490	76857634	2.31	GSTZ1	chr14	+	104	NM_001513
D3A_WT	588	27264814	27264958	2.16	GSX1	chr13	+	107	NM_145657
D3A_WT	1737	45071619	45072388	3.47	GTSE1	chr22	+	702	NM_016426
D3A_WT	106	42404608	42404732	2.27	GUCA2A	chr1	-	-1688	NM_033553
D3A_WT	452	106393913	106394447	2.55	GUCY1A2	chr11	-	201	NM_000855
D3A_WT	1947	156900467	156900616	2.98	GUCY1B3	chr4	+	966	NM_000857
D3A_WT	2240	65084538	65085077	3.16	GUSB	chr7	-	-71	NM_000181
D3A_WT	392	45901281	45901505	2.28	GYLTL1B	chr11	+	1622	NM_152312
D3A_WT	1141	492361	492875	2.96	GZMM	chr19	+	-2408	NM_005317
D3A_WT	1823	130522218	130523085	2.35	H1FX	chr3	-	-4841	NM_006026
D3A_WT	2588	103158387	103158719	2.42	H2BFWT	chrX	-	-3641	NM_001002916
D3A_WT	2587	103154018	103154196	2.48	H2BFWT	chrX	-	805	NM_001002916
D3A_WT	1051	71286749	71286978	2.25	H3F3B	chr17	-	592	NM_005324
D3A_WT	796	716441	716585	2.43	HAGHL	chr16	+	-753	NM_032304
D3A_WT	796	716441	716585	2.43	HAGHL	chr16	+	-445	NM_207112
D3A_WT	1272	19231572	19232936	2.63	HAPLN4	chr19	-	2342	NM_023002
D3A_WT	1273	19234273	19234422	2.09	HAPLN4	chr19	-	249	NM_023002
D3A_WT	1882	2213068	2214022	2.73	HAUS3	chr4	-	113	NM_024511
D3A_WT	780	149624	149783	2.51	HBM	chr16	+	-6269	NM_001003938
D3A_WT	832	3018824	3019889	3.89	HCFC1R1	chr16	-	-5068	NM_001002017

D3A_WT	1145	541227	541576	2.8	HCN2	chr19	+	509	NM_001194
D3A_WT	1764	13496736	13497085	3.37	HDAC11	chr3	+	67	NM_001136041
D3A_WT	1764	13496736	13497085	3.37	HDAC11	chr3	+	196	NM_024827
D3A_WT	509	46500070	46500324	2.62	HDAC7	chr12	-	-167	NM_001098416
D3A_WT	160	154987740	154988164	2.48	HDGF	chr1	-	912	NM_001126050
D3A_WT	160	154987740	154988164	2.48	HDGF	chr1	-	696	NM_001126051
D3A_WT	160	154987740	154988164	2.48	HDGF	chr1	-	215	NM_004494
D3A_WT	1528	241860424	241860588	2.31	HDLBP	chr2	-	468	NM_203346
D3A_WT	2174	733096	733420	2.78	HEATR2	chr7	+	395	NM_017802
D3A_WT	2143	138766948	138767303	2.2	HEBP2	chr6	+	97	NM_014320
D3A_WT	743	61917959	61918116	2.4	HERC1	chr15	-	-4837	NM_003922
D3A_WT	45	6401366	6401820	2.95	HES2	chr1	-	973	NM_019089
D3A_WT	46	6407273	6407619	2.87	HES2	chr1	-	-4880	NM_019089
D3A_WT	29	2458234	2458559	2.65	HES5	chr1	-	-6852	NM_001010926
D3A_WT	28	2450216	2451160	3.2	HES5	chr1	-	856	NM_001010926
D3A_WT	1515	238814355	238814829	2.44	HES6	chr2	-	-1172	NM_018645
D3A_WT	1514	238812886	238813300	2.48	HES6	chr2	-	327	NM_018645
D3A_WT	1091	77969561	77969910	2.62	HEXDC	chr17	+	195	NM_173620
D3A_WT	265	94441924	94442372	2.58	HHEX	chr10	+	2488	NM_002729
D3A_WT	128	100276794	100276938	2.21	HIAT1	chr1	+	490	NM_033055
D3A_WT	934	1900012	1901172	2.91	HIC1	chr17	+	-5761	NM_001098202
D3A_WT	934	1900012	1901172	2.91	HIC1	chr17	+	-4550	NM_006497
D3A_WT	1677	20100980	20101852	2.26	HIC2	chr22	+	-276	NM_015094
D3A_WT	2018	130528552	130528701	2.31	HINT1	chr5	-	307	NM_005340
D3A_WT	2018	130528552	130528701	2.31	HINT1	chr5	-	299	NR_024611
D3A_WT	562	121885802	121886845	4	HIP1R	chr12	+	332	NM_003959
D3A_WT	1309	45588269	45588607	3.12	HIPK4	chr19	-	-504	NM_144685
D3A_WT	246	70748709	70749238	2.6	HK1	chr10	+	3358	NM_033496
D3A_WT	246	70748709	70749238	2.6	HK1	chr10	+	365	NM_000188
D3A_WT	194	219119485	219120254	2.98	HLX	chr1	+	504	NM_021958
D3A_WT	1950	174491663	174491912	2.13	HMGB2	chr4	-	383	NM_002129
D3A_WT	1950	174491663	174491912	2.13	HMGB2	chr4	-	297	NM_001130688
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D3A_WT	1702	34107018	34107147	2.72	HMOX1	chr22	+	-4	NM_002133
D3A_WT	839	4466252	4467016	2.32	HMOX2	chr16	+	1915	NM_001127206
D3A_WT	839	4466252	4467016	2.32	HMOX2	chr16	+	293	NM_002134
D3A_WT	296	124898039	124898303	2.95	HMX2	chr10	+	544	NM_005519
D3A_WT	1564	42418534	42419060	3	HNF4A	chr20	+	943	NM_175914
D3A_WT	216	243093351	243093565	3.12	HNRNPU	chr1	-	992	NM_031844
D3A_WT	2339	42871290	42872440	3.63	HOOK3	chr8	+	676	NM_032410
D3A_WT	1009	43963505	43963723	2.5	HOXB1	chr17	-	-343	NM_002144
D3A_WT	1010	44053816	44054065	2.71	HOXB8	chr17	-	-6640	NM_024016
D3A_WT	1011	44058989	44059563	3.11	HOXB9	chr17	-	-442	NM_024017
D3A_WT	522	52631607	52631756	2.43	HOXC12	chr12	+	-3299	NM_173860
D3A_WT	523	52685248	52685517	2.26	HOXC8	chr12	+	-3774	NM_022658
D3A_WT	1482	176725109	176725354	3.09	HOXD4	chr2	+	873	NM_014621
D3A_WT	2330	22044094	22044228	2.16	HR	chr8	-	349	NM_018411

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D3A_WT	323	521954	523893	3.31	HRAS	chr11	-	2627	NM_001130442
D3A_WT	1582	60233613	60233862	3.32	HRH3	chr20	-	-5019	NM_007232
D3A_WT	815	1909542	1910081	2.33	HS3ST6	chr16	-	-1579	NM_001009606
D3A_WT	614	95541526	95541665	2.74	HS6ST3	chr13	+	502	NM_153456
D3A_WT	995	37960226	37960365	2.17	HSD17B1	chr17	+	2786	NM_000413
D3A_WT	899	80620371	80620525	2.41	HSD17B2	chr16	+	-5910	NM_002153
D3A_WT	293	118491602	118491849	2.72	HSPA12A	chr10	-	350	NM_025015
D3A_WT	1292	40938496	40938840	2.53	HSPB6	chr19	-	1102	NM_144617
D3A_WT	557	118101212	118101434	2.6	HSPB8	chr12	+	346	NM_014365
D3A_WT	1817	123996952	123997601	2.58	HSPBAP1	chr3	-	-1936	NM_024610
D3A_WT	2144	144371050	144371304	2.45	HYMAI	chr6	-	383	NR_002768
D3A_WT	1396	9532331	9532470	2.86	IAH1	chr2	+	280	NM_001039613
D3A_WT	1395	8740698	8741137	2.71	ID2	chr2	+	1354	NM_002166
D3A_WT	1249	13125321	13125445	2.9	IER2	chr19	+	3102	NM_004907
D3A_WT	2085	30820385	30820509	2.39	IER3	chr6	-	-141	NM_003897
D3A_WT	2488	130980618	130980782	2.22	IER5L	chr9	-	-339	NM_203434
D3A_WT	2487	130978841	130979672	2.4	IER5L	chr9	-	1105	NM_203434
D3A_WT	484	6534671	6535690	4.41	IFFO1	chr12	-	-6645	NM_080731
D3A_WT	484	6534671	6535690	4.41	IFFO1	chr12	-	310	NM_080730
D3A_WT	1622	33697557	33697821	2.4	IFNGR2	chr21	+	618	NM_005534
D3A_WT	813	1604230	1605271	2.3	IFT140	chr16	-	-2640	NM_014714
D3A_WT	1813	109428060	109428433	2.8	IFT57	chr3	-	-4139	NM_018010
D3A_WT	774	97008421	97009743	3.09	IGF1R	chr15	+	-1201	NM_000875
D3A_WT	775	97011310	97011941	2.66	IGF1R	chr15	+	1342	NM_000875
D3A_WT	2231	45927144	45927607	2.32	IGFBP3	chr7	-	21	NM_001013398
D3A_WT	1489	217265096	217265340	2.37	IGFBP5	chr2	-	3299	NM_000599
D3A_WT	164	158334760	158335006	3.13	IGSF8	chr1	-	149	NM_052868
D3A_WT	2338	42247594	42248258	2.34	IKBKB	chr8	+	-59	NM_001556
D3A_WT	582	20175316	20175730	2.75	IL17D	chr13	+	42	NM_138284
D3A_WT	1802	53855532	53855996	2.71	IL17RB	chr3	+	148	NM_018725
D3A_WT	76	24387457	24387592	2.19	IL28RA	chr1	-	-1186	NM_173064
D3A_WT	2021	131904246	131904565	2.74	IL5	chr5	-	2708	NM_000879
D3A_WT	1513	238776563	238777247	2.25	ILKAP	chr2	-	158	NM_030768
D3A_WT	1110	20255739	20256070	2.69	IMPACT	chr18	+	-4702	NM_018439
D3A_WT	2344	58068436	58068815	2.75	IMPAD1	chr8	-	356	NM_017813
D3A_WT	280	105026536	105027570	2.62	INA	chr10	+	144	NM_032727
D3A_WT	700	104223316	104223755	3.74	INF2	chr14	+	-3467	NM_032714
D3A_WT	700	104223316	104223755	3.74	INF2	chr14	+	-3452	NM_001031714
D3A_WT	1495	220143571	220144025	2.65	INHA	chr2	+	-1399	NM_002191
D3A_WT	436	71613720	71614061	2.46	INPPL1	chr11	+	361	NM_001567
D3A_WT	353	2141894	2142358	3.31	INS	chr11	-	-3111	NM_000207
D3A_WT	353	2141894	2142358	3.31	INS-IGF2	chr11	-	-3111	NM_001042376
D3A_WT	156	151966612	151967248	2.99	INTS3	chr1	+	-260	NM_023015
D3A_WT	848	19630091	19630220	2.21	IQCK	chr16	+	-5123	NM_153208
D3A_WT	2280	128366164	128366484	2.41	IRF5	chr7	+	1095	NM_001098630
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D3A_WT	2280	128366164	128366484	2.41	IRF5	chr7	+	-1683	NM_001098627
D3A_WT	907	84489878	84490332	2.33	IRF8	chr16	+	-169	NM_002163
D3A_WT	1319	48914477	48915236	4.18	IRGC	chr19	+	2803	NM_019612
D3A_WT	618	109234650	109237064	3.19	IRS2	chr13	-	1058	NM_003749
D3A_WT	2591	107865014	107866558	3.82	IRS4	chrX	-	477	NM_003604
D3A_WT	547	107482098	107482251	2	ISCU	chr12	+	1751	NM_213595
D3A_WT	1268	18406456	18407480	2.91	ISYNA1	chr19	-	2975	NM_016368
D3A_WT	1269	18408256	18408475	3.05	ISYNA1	chr19	-	1578	NM_016368
D3A_WT	1769	37468842	37469266	2.9	ITGA9	chr3	+	238	NM_002207
D3A_WT	1642	45177006	45177355	2.53	ITGB2	chr21	-	-3999	NM_001127491
D3A_WT	731	39575175	39575814	2.52	ITPKA	chr15	+	2081	NM_002220
D3A_WT	1312	45914651	45915296	4.23	ITPKC	chr19	+	126	NM_025194
D3A_WT	286	106088211	106088542	2.43	ITPRIP	chr10	-	-4723	NM_033397
D3A_WT	178	183557683	183558128	2.44	IVNS1ABP	chr1	-	-4821	NM_006469
D3A_WT	2216	28186258	28187416	3.08	JAZF1	chr7	-	125	NM_175061
D3A_WT	1349	55712758	55713407	4.13	JOSD2	chr19	-	-6925	NM_138334
D3A_WT	1348	55707787	55707936	2.01	JOSD2	chr19	-	-1704	NM_138334
D3A_WT	2351	75395244	75395879	3.35	JPH1	chr8	-	556	NM_020647
D3A_WT	640	23114758	23115287	3.63	JPH4	chr14	-	2827	NM_001146028
D3A_WT	639	22520500	22520954	2.33	JUB	chr14	-	-4455	NM_198086
D3A_WT	639	22520500	22520954	2.33	JUB	chr14	-	961	NM_032876
D3A_WT	2079	24468044	24468188	2.23	KAAG1	chr6	+	3007	NM_181337
D3A_WT	1337	54267289	54267628	3.2	KCNA7	chr19	-	552	NM_031886
D3A_WT	951	7775287	7776027	2.5	KCNAB3	chr17	-	-2179	NM_004732
D3A_WT	2350	73611614	73612128	2.65	KCNB2	chr8	+	-308	NM_004770
D3A_WT	379	17713102	17713546	2.55	KCNC1	chr11	+	-746	NM_001112741
D3A_WT	380	17714627	17715747	2.66	KCNC1	chr11	+	1117	NM_001112741
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D3A_WT	1569	49072758	49073197	2.69	KCNG1	chr20	-	105	NM_002237
D3A_WT	1135	75722559	75723019	2.39	KCNG2	chr18	+	-1866	NM_012283
D3A_WT	657	62582243	62583082	2.42	KCNH5	chr14	-	-954	NM_139318
D3A_WT	1901	20914955	20915209	2.31	KCNIP4	chr4	-	-455	NM_147183
D3A_WT	469	128223990	128224131	2.16	KCNJ1	chr11	-	-6487	NM_000220
D3A_WT	470	128265727	128266386	2.88	KCNJ5	chr11	+	-466	NM_000890
D3A_WT	257	79067024	79067948	2.61	KCNMA1	chr10	-	97	NM_001014797
D3A_WT	1266	17919735	17920194	2.69	KCNN1	chr19	+	-3146	NM_002248
D3A_WT	2012	113726146	113727186	2.95	KCNN2	chr5	+	752	NM_021614
D3A_WT	1320	48976586	48976730	2.76	KCNN4	chr19	-	591	NM_002250
D3A_WT	1321	48977981	48978445	2.46	KCNN4	chr19	-	-964	NM_002250
D3A_WT	1594	61574070	61574209	2.31	KCNQ2	chr20	-	298	NM_004518
D3A_WT	607	76357305	76358355	3.99	KCTD12	chr13	-	711	NM_138444
D3A_WT	2242	65731382	65731616	2.27	KCTD7	chr7	+	197	NM_001167961
D3A_WT	454	107874154	107874506	2.68	KDELC2	chr11	-	39	NM_153705
D3A_WT	560	120501670	120501899	2.95	KDM2B	chr12	-	1519	NM_032590
D3A_WT	560	120501670	120501899	2.95	KDM2B	chr12	-	963	NM_001005366
D3A_WT	950	7677692	7678316	2.71	KDM6B	chr17	+	-5955	NM_001080424
D3A_WT	1235	10474258	10475020	2.79	KEAP1	chr19	-	415	NM_203500

D3A_WT	1235	10474258	10475020	2.79	KEAP1	chr19	-	-158	NM_012289
D3A_WT	2371	136538985	136539433	2.37	KHDRBS3	chr8	+	312	NM_006558
D3A_WT	91	35795560	35796607	2.52	KIAA0319L	chr1	-	-459	NM_024874
D3A_WT	2200	4781521	4781970	2.53	KIAA0415	chr7	+	-44	NM_014855
D3A_WT	902	83618629	83618783	2.21	KIAA0513	chr16	+	-204	NM_014732
D3A_WT	1103	8707890	8708026	2.39	KIAA0802	chr18	+	590	NM_015210
D3A_WT	1986	5476235	5476584	2.96	KIAA0947	chr5	+	603	NM_015325
D3A_WT	758	77511688	77512507	3.15	KIAA1024	chr15	+	185	NM_015206
D3A_WT	2288	141048333	141048682	2.43	KIAA1147	chr7	-	-85	NM_001080392
D3A_WT	1441	96667644	96668123	3.55	KIAA1310	chr2	-	-41	NM_001115016
D3A_WT	450	101290878	101291012	2.76	KIAA1377	chr11	+	-10	NM_020802
D3A_WT	676	92868370	92868990	2.38	KIAA1409	chr14	+	-637	NM_020818
D3A_WT	1955	186361897	186362550	3.33	KIAA1430	chr4	-	-47	NM_020827
D3A_WT	495	13089098	13089242	2.79	KIAA1467	chr12	+	589	NM_020853
D3A_WT	89	32980215	32980465	2.18	KIAA1522	chr1	+	242	NM_020888
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D3A_WT	2283	138316882	138317507	3.6	KIAA1549	chr7	-	-590	NM_020910
D3A_WT	900	83102410	83102669	2.29	KIAA1609	chr16	-	-6750	NM_020947
D3A_WT	209	231530065	231530794	2.03	KIAA1804	chr1	+	293	NM_032435
D3A_WT	2399	145237592	145238931	2.98	KIAA1875	chr8	+	3645	NR_024207
D3A_WT	2398	145235287	145235736	2.21	KIAA1875	chr8	+	895	NR_024207
D3A_WT	2192	1575936	1576597	2.95	KIAA1908	chr7	+	32	NR_027328
D3A_WT	1816	114897998	114898469	3.14	KIAA2018	chr3	-	-50	NM_001009899
D3A_WT	1524	241408398	241408750	2.19	KIF1A	chr2	-	-277	NM_004321
D3A_WT	505	38122773	38123027	3.25	KIF21A	chr12	-	285	NM_017641
D3A_WT	696	103674137	103674989	2.84	KIF26A	chr14	+	-249	NM_015656
D3A_WT	1022	49255779	49256843	2.93	KIF2B	chr17	+	1074	NM_032559
D3A_WT	1782	47299349	47299528	2.26	KIF9	chr3	-	-97	NM_022342
D3A_WT	501	27824373	27824502	2.36	KLHDC5	chr12	+	-16	NM_020782
D3A_WT	1111	28613123	28613291	2.07	KLHL14	chr18	-	-6235	NM_020805
D3A_WT	2552	23953029	23953379	2.12	KLHL15	chrX	-	2020	NM_030624
D3A_WT	1782	47299349	47299528	2.26	KLHL18	chr3	+	105	NM_025010
D3A_WT	1673	19179937	19180387	3.72	KLHL22	chr22	-	-40	NM_032775
D3A_WT	1351	56277439	56277568	2.3	KLK14	chr19	-	1811	NM_022046
D3A_WT	1837	161765446	161765865	3.22	KPNA4	chr3	-	415	NM_002268
D3A_WT	1008	43082104	43082557	2.37	KPNB1	chr17	+	57	NM_002265
D3A_WT	499	25294721	25295548	3.12	KRAS	chr12	-	-13	NM_004985
D3A_WT	1236	10541043	10541192	2.08	KRI1	chr19	-	-3415	NM_023008
D3A_WT	518	51382523	51383397	2.62	KRT77	chr12	-	554	NM_175078
D3A_WT	1640	44824638	44824912	2.29	KRTAP10-5	chr21	-	134	NM_198694
D3A_WT	1563	41569941	41570169	2.8	L3MBTL	chr20	+	-6411	NM_015478
D3A_WT	1101	6404616	6405075	2.59	L3MBTL4	chr18	-	65	NM_173464
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D3A_WT	1102	7106942	7107196	2.22	LAMA1	chr18	-	744	NM_005559
D3A_WT	176	181259608	181260164	3.23	LAMC1	chr1	+	669	NM_002293
D3A_WT	1701	32645865	32646009	2.88	LARGE	chr22	-	479	NM_133642
D3A_WT	1933	129202274	129202918	2.89	LARP1B	chr4	+	644	NM_018078

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D3A_WT	147	149213597	149213733	2.11	LASS2	chr1	-	399	NM_181746
D3A_WT	513	48847169	48847550	2.05	LASS5	chr12	-	5	NM_147190
D3A_WT	197	223682682	223682841	2.38	LBR	chr1	-	381	NM_194442
D3A_WT	197	223682682	223682841	2.38	LBR	chr1	-	-354	NM_002296
D3A_WT	747	65907226	65907370	2.49	LBXCOR1	chr15	+	2304	NM_001031807
D3A_WT	87	32510846	32511295	3.37	LCK	chr1	+	-1228	NM_001042771
D3A_WT	2511	137549514	137549963	2.94	LCN1	chr9	+	-3368	NM_002297
D3A_WT	892	73705746	73705885	2.32	LDHD	chr16	-	2351	NM_194436
D3A_WT	1930	109308381	109309456	3.15	LEF1	chr4	-	643	NM_001130714
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D3A_WT	2089	33864401	33864755	2.91	LEMD2	chr6	-	-1881	NM_001143944
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D3A_WT	1361	59652220	59652944	3.2	LENG8	chr19	+	706	NM_052925
D3A_WT	1362	59668398	59668542	2.25	LENG9	chr19	-	-1764	NM_198988
D3A_WT	2337	38358825	38359587	2.18	LETM2	chr8	+	-3970	NM_144652
D3A_WT	1300	43998217	43998861	2.32	LGALS4	chr19	-	-2959	NM_006149
D3A_WT	1290	40314827	40315751	4.57	LGI4	chr19	-	2729	NM_139284
D3A_WT	1291	40324498	40324667	2.58	LGI4	chr19	-	-6564	NM_139284
D3A_WT	2470	124030603	124031355	2.35	LHX6	chr9	-	-139	NM_199160
D3A_WT	1693	28972447	28972601	2.62	LIF	chr22	-	272	NM_002309
D3A_WT	1993	38592180	38593243	2.94	LIFR	chr5	-	-206	NM_001127671
D3A_WT	1603	61834153	61834408	3.47	LIME1	chr20	+	-4141	NM_017806
D3A_WT	2303	156377963	156378113	2.82	LMBR1	chr7	-	625	NM_022458
D3A_WT	2256	97574145	97574314	2.51	LMTK2	chr7	+	97	NM_014916
D3A_WT	1335	53706373	53706887	2.62	LMTK3	chr19	-	1628	NM_001080434
D3A_WT	2477	128416172	128416341	3	LMX1B	chr9	+	-312	NM_002316
D3A_WT	2009	96297354	96297603	2.79	LNPEP	chr5	+	377	NM_005575
D3A_WT	1838	171167492	171167756	2.94	LOC100128164	chr3	-	-408	NR_027622
D3A_WT	1224	7448314	7450789	4.17	LOC100128573	chr19	-	-5304	NR_024491
D3A_WT	826	2746196	2746655	2.6	LOC100128788	chr16	-	-3823	NR_027275
D3A_WT	825	2731428	2731757	2.34	LOC100128788	chr16	-	3207	NR_027274
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D3A_WT	1780	47025513	47026641	2.14	LOC100129354	chr3	+	-1958	NR_024046
D3A_WT	1416	43307372	43307819	2.48	LOC100129726	chr2	+	-258	NR_027251
D3A_WT	575	131356384	131356633	2.32	LOC100130238	chr12	+	-5541	NR_024563
D3A_WT	1869	1190920	1191071	2.43	LOC100130872	chr4	-	1755	NR_024569
D3A_WT	151	150077298	150077737	2.87	LOC100132111	chr1	+	-51	NR_024237
D3A_WT	713	106007530	106007679	2.17	LOC100133469	chr14	+	-1895	NR_027457
D3A_WT	785	363906	365160	2.62	LOC100134368	chr16	+	-7708	NR_024453
D3A_WT	786	365901	368667	3.2	LOC100134368	chr16	+	-4957	NR_024453
D3A_WT	1754	49363271	49363720	2.55	LOC100144603	chr22	+	-4825	NR_021492
D3A_WT	806	1071702	1072132	2.88	LOC146336	chr16	-	-3185	NR_027242
D3A_WT	1663	17934365	17934514	2.08	LOC150185	chr22	-	-77	NR_024381
D3A_WT	1669	18567135	18567389	2.57	LOC150197	chr22	+	-6592	NR_026919
D3A_WT	2301	154425725	154426758	3.32	LOC202781	chr7	+	166	NR_028090
D3A_WT	334	1287386	1287735	2.74	LOC255512	chr11	+	47	NR_029409

D3A_WT	1966	531586	532049	3.12	LOC25845	chr5	-	-5737	NR_024158
D3A_WT	2513	138348222	138349655	3.14	LOC26102	chr9	-	-7338	NR_026964
D3A_WT	258	80497312	80498960	2.33	LOC283050	chr10	-	-925	NR_024429
D3A_WT	876	54782448	54783128	3.14	LOC283856	chr16	-	-281	NR_027078
D3A_WT	340	1549665	1550512	2.2	LOC338651	chr11	+	-458	NR_021489
D3A_WT	536	88627172	88627936	2.14	LOC338758	chr12	+	692	NR_028138
D3A_WT	1402	24197385	24197704	2.68	LOC375190	chr2	+	-2309	NM_001145710
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D3A_WT	1068	76746228	76747682	3.13	LOC388428	chr17	+	-6946	NR_027255
D3A_WT	38	3679125	3679479	2.26	LOC388588	chr1	+	91	NM_001163724
D3A_WT	2026	138758011	138758840	2.44	LOC389333	chr5	-	359	NM_001161546
D3A_WT	2233	56151146	56151565	2.32	LOC389493	chr7	-	229	NM_001145712
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D3A_WT	2348	65655193	65656116	2.23	LOC401463	chr8	-	-3280	NR_015374
D3A_WT	1037	63708604	63709028	2.49	LOC440461	chr17	+	2421	NR_027283
D3A_WT	1451	110062401	110063295	3.67	LOC440895	chr2	+	293	NR_027143
D3A_WT	1798	52544911	52546108	2.73	LOC440957	chr3	+	-151	NM_001124767
D3A_WT	400	50213819	50214489	2.89	LOC441601	chr11	-	45	NR_003034
D3A_WT	1930	109308381	109309456	3.15	LOC641518	chr4	+	-3806	NR_029373
D3A_WT	1930	109308381	109309456	3.15	LOC641518	chr4	+	789	NR_029374
D3A_WT	1050	71139822	71140041	2.63	LOC643008	chr17	+	-1177	NM_001162995
D3A_WT	1050	71139822	71140041	2.63	LOC643008	chr17	+	-4338	NR_028439
D3A_WT	453	106968787	106968968	2.28	LOC643923	chr11	+	1197	NR_028328
D3A_WT	1848	192063569	192063713	2.04	LOC647309	chr3	-	-482	NM_001146686
D3A_WT	155	151500128	151501367	2.56	LOR	chr1	+	1945	NM_000427
D3A_WT	1277	19600163	19600822	2.93	LPAR2	chr19	-	-453	NM_004720
D3A_WT	1278	19601748	19602112	2.33	LPAR2	chr19	-	-1891	NM_004720
D3A_WT	489	6996169	6996418	2.4	LPCAT3	chr12	-	-190	NM_005768
D3A_WT	598	46025626	46025855	2.27	LRCH1	chr13	+	444	NM_001164213
D3A_WT	1303	44502865	44503284	2.24	LRFN1	chr19	-	-5258	NM_020862
D3A_WT	1293	41122168	41123127	3.13	LRFN3	chr19	+	2786	NM_024509
D3A_WT	529	57599728	57600764	3.12	LRIG3	chr12	-	-652	NM_001136051
D3A_WT	529	57599728	57600764	3.12	LRIG3	chr12	-	283	NM_153377
D3A_WT	2363	105670838	105671077	2.32	LRP12	chr8	-	-561	NM_001135703
D3A_WT	2404	145723046	145723175	2.28	LRRC24	chr8	-	114	NM_001024678
D3A_WT	324	525648	526092	3.09	LRRC56	chr11	+	-1651	NM_198075
D3A_WT	323	521954	523893	3.31	LRRC56	chr11	+	-4598	NM_198075
D3A_WT	1511	238200720	238201052	2.72	LRRFIP1	chr2	+	-76	NM_001137550
D3A_WT	182	202920836	202920985	2.14	LRRN2	chr1	-	194	NM_006338
D3A_WT	182	202920836	202920985	2.14	LRRN2	chr1	-	310	NM_201630
D3A_WT	1544	5980792	5981011	3.98	LRRN4	chr20	-	1793	NM_152611
D3A_WT	1653	46472810	46473390	2.59	LSS	chr21	-	66	NM_002340
D3A_WT	1310	45794556	45794726	2.32	LTBP4	chr19	+	-4475	NM_001042545
D3A_WT	1311	45799040	45799608	2.59	LTBP4	chr19	+	208	NM_001042545
D3A_WT	1310	45794556	45794726	2.32	LTBP4	chr19	+	-339	NM_001042544
D3A_WT	2380	143853452	143855001	3.71	LYNX1	chr8	-	2415	NM_023946

D3A_WT	2380	143853452	143855001	3.71	LYNX1	chr8	-	1520	NM_177477
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D3A_WT	2378	143849378	143849597	2.69	LYNX1	chr8	-	-1239	NM_177458
D3A_WT	2379	143851354	143851798	2.37	LYNX1	chr8	-	-3328	NM_177458
D3A_WT	2380	143853452	143855001	3.71	LYNX1	chr8	-	-5978	NM_177458
D3A_WT	2380	143853452	143855001	3.71	LYNX1	chr8	-	2416	NM_177457
D3A_WT	1315	47040258	47040417	2.07	LYPD4	chr19	-	11	NM_173506
D3A_WT	2018	130528552	130528701	2.31	LYRM7	chr5	+	-5913	NM_181705
D3A_WT	1548	13923870	13924144	2.26	MACROD2	chr20	+	-138	NM_080676
D3A_WT	1139	442288	442612	2.4	MADCAM1	chr19	+	-5039	NM_130762
D3A_WT	896	78190449	78191468	2.5	MAF	chr16	-	1165	NM_005360
D3A_WT	2397	145224590	145224864	2.26	MAF1	chr8	+	-6565	NM_032272
D3A_WT	1562	38752335	38753704	3.89	MAFB	chr20	-	-1729	NM_005461
D3A_WT	2600	151037870	151039019	2.81	MAGEA5	chrX	-	-1344	NM_021049
D3A_WT	715	21442789	21443453	2.12	MAGEL2	chr15	-	965	NM_019066
D3A_WT	969	21127904	21128338	3.01	MAP2K3	chr17	+	-439	NM_145109
D3A_WT	969	21127904	21128338	3.01	MAP2K3	chr17	+	-7252	NM_002756
D3A_WT	1306	45389917	45390151	2.75	MAP3K10	chr19	+	544	NM_002446
D3A_WT	416	65142605	65142929	2.11	MAP3K11	chr11	-	-4471	NM_002419
D3A_WT	92	36394154	36395738	2.74	MAP7D1	chr1	+	557	NM_018067
D3A_WT	2060	179651468	179651918	2.26	MAPK9	chr5	-	-16	NM_139070
D3A_WT	1794	50624131	50624260	2.33	MAPKAPK3	chr3	+	-5409	NM_004635
D3A_WT	2129	114283083	114283217	2.64	MARCKS	chr6	+	-2069	NM_002356
D3A_WT	272	99463303	99463843	2.77	MARVELD1	chr10	+	103	NR_026753
D3A_WT	1201	3758639	3759322	3.78	MATK	chr19	-	-6170	NM_002378
D3A_WT	1174	1543152	1543306	2.33	MBD3	chr19	-	423	NM_003926
D3A_WT	1126	72973034	72974351	4.39	MBP	chr18	-	70	NM_001025101
D3A_WT	1107	13813373	13813592	2.93	MC5R	chr18	+	-2282	NM_005913
D3A_WT	626	112675083	112675217	2.13	MCF2L	chr13	+	-6505	NM_024979
D3A_WT	1714	39406776	39406905	2.46	MCHR1	chr22	+	1713	NM_005297
D3A_WT	1654	46530979	46531154	2	MCM3AP	chr21	-	-1402	NM_003906
D3A_WT	1653	46472810	46473390	2.59	MCM3APAS	chr21	+	-485	NR_002776
D3A_WT	2133	119297807	119298161	2.08	MCM9	chr6	-	18	NM_153255
D3A_WT	1423	63668848	63669197	2.35	MDH1	chr2	+	-603	NM_005917
D3A_WT	2115	90585964	90586123	2.05	MDN1	chr6	-	120	NM_014611
D3A_WT	85	29436762	29437211	2.43	MECR	chr1	-	-6945	NM_016011
D3A_WT	685	100358015	100358290	2.37	MEG3	chr14	+	-4063	NR_002766
D3A_WT	685	100358015	100358290	2.37	MEG3	chr14	+	-4045	NR_003531
D3A_WT	1718	40425797	40426061	2.57	MEI1	chr22	+	466	NM_152513
D3A_WT	761	79082450	79082904	2.97	MESDC1	chr15	+	2328	NM_022566
D3A_WT	769	88121103	88121447	3.11	MESP2	chr15	+	683	NM_001039958
D3A_WT	1098	2561372	2561731	2.62	METTL4	chr18	-	-62	NM_022840
D3A_WT	851	21514646	21514872	2.49	METTL9	chr16	+	-3597	NM_016025
D3A_WT	68	17185769	17187694	4.42	MFAP2	chr1	-	-6971	NM_002403
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D3A_WT	1949	171183838	171184786	3.63	MFAP3L	chr4	-	-308	NM_021647
D3A_WT	1053	72244201	72244435	2.1	MFSD11	chr17	+	-1059	NM_024311

D3A_WT	1862	672677	672896	2.39	MFSD7	chr4	-	187	NM_032219
D3A_WT	733	39739853	39740477	3.29	MGA	chr15	+	264	NM_001080541
D3A_WT	968	20348270	20348574	2.01	MGC102966	chr17	-	-19	NR_029393
D3A_WT	704	104353153	104353577	2.23	MGC23270	chr14	+	-5217	NR_024396
D3A_WT	2026	138758011	138758840	2.44	MGC29506	chr5	-	-4921	NM_016459
D3A_WT	2404	145723046	145723175	2.28	MGC70857	chr8	-	2156	NM_001001795
D3A_WT	195	220858172	220858326	2.03	MIA3	chr1	+	183	NM_198551
D3A_WT	1686	22566497	22567135	3.72	MIF	chr22	+	252	NM_002415
D3A_WT	1049	70779090	70779224	2.16	MIF4GD	chr17	-	-259	NM_020679
D3A_WT	1752	49274238	49274382	2.08	MIOX	chr22	+	2232	NM_017584
D3A_WT	1482	176725109	176725354	3.09	MIR10B	chr2	+	1955	NR_029609
D3A_WT	1586	60562679	60563333	2.5	MIR1-1	chr20	+	1049	NR_029780
D3A_WT	2401	145593628	145594177	2.98	MIR1234	chr8	-	2465	NR_031600
D3A_WT	1591	61273131	61273965	2.22	MIR124-3	chr20	+	-6748	NR_029670
D3A_WT	686	100418281	100418530	2.69	MIR127	chr14	+	-663	NR_029696
D3A_WT	1716	39817855	39818618	2.99	MIR1281	chr22	+	-226	NR_031694
D3A_WT	934	1900012	1901172	2.91	MIR132	chr17	-	-540	NR_029674
D3A_WT	686	100418281	100418530	2.69	MIR136	chr14	+	-2386	NR_029699
D3A_WT	1492	219867704	219868128	2.64	MIR153-1	chr2	-	-750	NR_029688
D3A_WT	2308	157066095	157066369	2.02	MIR153-2	chr7	-	-6357	NR_029689
D3A_WT	1177	1766486	1770324	4.16	MIR1909	chr19	-	-1168	NR_031730
D3A_WT	1788	49034806	49034950	2.87	MIR191	chr3	-	-1732	NR_029690
D3A_WT	1787	49030836	49031362	2.96	MIR191	chr3	-	2047	NR_029690
D3A_WT	1605	62047107	62047846	2.38	MIR1914	chr20	-	-4135	NR_031735
D3A_WT	846	14303558	14304388	2.74	MIR193B	chr16	+	-1351	NR_030177
D3A_WT	946	6859288	6859557	2.25	MIR195	chr17	-	2322	NR_029712
D3A_WT	291	115929228	115929362	2.42	MIR2110	chr10	-	-5367	NR_031747
D3A_WT	934	1900012	1901172	2.91	MIR212	chr17	-	-168	NR_029625
D3A_WT	2453	96885443	96885887	2.5	MIR23B	chr9	+	-1645	NR_029664
D3A_WT	2453	96885443	96885887	2.5	MIR24-1	chr9	+	-2458	NR_029496
D3A_WT	1770	37983234	37983758	3.27	MIR26A1	chr3	+	-2402	NR_029499
D3A_WT	2453	96885443	96885887	2.5	MIR27B	chr9	+	-1882	NR_029665
D3A_WT	2331	22158097	22158446	2.39	MIR320A	chr8	-	230	NR_029714
D3A_WT	947	7070974	7071398	2.41	MIR324	chr17	-	-3764	NR_029896
D3A_WT	443	74730517	74730666	2.18	MIR326	chr11	-	-6713	NR_029891
D3A_WT	883	65795095	65795844	3.3	MIR328	chr16	-	-1670	NR_029887
D3A_WT	54	9139822	9139966	2.49	MIR34A	chr1	-	-5471	NR_029610
D3A_WT	846	14303558	14304388	2.74	MIR365-1	chr16	+	-6669	NR_029854
D3A_WT	1788	49034806	49034950	2.87	MIR425	chr3	-	-2207	NR_029948
D3A_WT	1787	49030836	49031362	2.96	MIR425	chr3	-	1572	NR_029948
D3A_WT	686	100418281	100418530	2.69	MIR431	chr14	+	1309	NR_029965
D3A_WT	686	100418281	100418530	2.69	MIR432	chr14	+	-2167	NR_030173
D3A_WT	686	100418281	100418530	2.69	MIR433	chr14	+	430	NR_029966
D3A_WT	1995	54504835	54504999	2.19	MIR449A	chr5	-	-2710	NR_029960
D3A_WT	1995	54504835	54504999	2.19	MIR449B	chr5	-	-2590	NR_030387
D3A_WT	1995	54504835	54504999	2.19	MIR449C	chr5	-	-979	NR_031572
D3A_WT	946	6859288	6859557	2.25	MIR497	chr17	-	2643	NR_030178

D3A_WT	275	102719542	102719716	2.32	MIR608	chr10	+	-5102	NR_030339
D3A_WT	1053	72244201	72244435	2.1	MIR636	chr17	-	-93	NR_030366
D3A_WT	1237	10689734	10690503	3.33	MIR638	chr19	+	39	NR_030368
D3A_WT	1568	48630542	48630806	2.58	MIR645	chr20	+	-5055	NR_030375
D3A_WT	1605	62047107	62047846	2.38	MIR647	chr20	-	-2953	NR_030377
D3A_WT	158	153434174	153434309	2.43	MIR92B	chr1	+	2650	NR_030281
D3A_WT	767	87711984	87712932	2.5	MIR9-3	chr15	+	207	NR_029692
D3A_WT	2401	145593628	145594177	2.98	MIR939	chr8	-	-3649	NR_030635
D3A_WT	821	2257723	2258562	2.36	MIR940	chr16	+	-3606	NR_030636
D3A_WT	1806	69871241	69871575	2.78	MITF	chr3	+	86	NM_198159
D3A_WT	237	28074583	28075127	2.78	MKX	chr10	-	-71	NM_173576
D3A_WT	1954	185892205	185892334	2.16	MLF1IP	chr4	-	11	NM_024629
D3A_WT	600	48692282	48693126	2.06	MLNR	chr13	+	230	NM_001507
D3A_WT	1510	238062992	238063121	2.08	MLPH	chr2	+	2440	NM_001042467
D3A_WT	996	37972332	37973071	3.11	MLX	chr17	+	98	NM_198205
D3A_WT	109	45731326	45731654	2.4	MMACHC	chr1	+	-6952	NM_015506
D3A_WT	638	22376478	22376852	2.78	MMP14	chr14	+	1033	NM_004995
D3A_WT	1944	154485160	154486406	2.97	MND1	chr4	+	533	NM_032117
D3A_WT	2305	156495320	156496299	3.33	MNX1	chr7	-	-919	NM_001165255
D3A_WT	2305	156495320	156496299	3.33	MNX1	chr7	-	299	NM_005515
D3A_WT	2420	27519138	27519462	2.87	MOBKL2B	chr9	-	550	NM_024761
D3A_WT	2263	100631847	100632071	2.46	MOGAT3	chr7	-	-937	NM_178176
D3A_WT	1790	49942408	49942784	3.15	MON1A	chr3	-	-147	NM_001142501
D3A_WT	894	75785137	75785591	2.34	MON1B	chr16	+	3028	NM_014940
D3A_WT	1695	29695189	29695323	2.25	MORC2	chr22	-	-1069	NM_014941
D3A_WT	2258	100047940	100048674	2.98	MOSPD3	chr7	+	258	NM_023948
D3A_WT	2258	100047940	100048674	2.98	MOSPD3	chr7	+	319	NM_001040098
D3A_WT	2258	100047940	100048674	2.98	MOSPD3	chr7	+	647	NM_001040097
D3A_WT	949	7427431	7428065	2.59	MPDU1	chr17	+	60	NM_004870
D3A_WT	2212	24579727	24581101	3.57	MPP6	chr7	+	805	NM_016447
D3A_WT	1705	35744338	35744472	2.62	MPST	chr22	+	-1242	NM_021126
D3A_WT	369	3201824	3202373	2.89	MRGPRG	chr11	-	-5479	NM_001164377
D3A_WT	584	20649101	20649355	2.65	MRP63	chr13	+	857	NM_024026
D3A_WT	785	363906	365160	2.62	MRPL28	chr16	-	-3992	NM_006428
D3A_WT	786	365901	368667	3.2	MRPL28	chr16	-	-6743	NM_006428
D3A_WT	784	361431	362955	3.57	MRPL28	chr16	-	-1652	NM_006428
D3A_WT	94	36702163	36702492	3.08	MRPS15	chr1	-	300	NM_031280
D3A_WT	145	148534404	148534547	2.37	MRPS21	chr1	+	1583	NM_018997
D3A_WT	2349	72918204	72919359	3.57	MSC	chr8	-	504	NM_005098
D3A_WT	1419	47864093	47864655	3.22	MSH6	chr2	+	650	NM_000179
D3A_WT	989	35531962	35532123	2.09	MSL1	chr17	+	-273	NM_001012241
D3A_WT	798	778442	779106	3.44	MSLNL	chr16	-	-5847	NM_001025190
D3A_WT	2325	9949354	9950088	2.34	MSRA	chr8	+	482	NM_001135670
D3A_WT	234	23424155	23424716	2.22	MSRB2	chr10	+	3	NM_012228
D3A_WT	531	63958467	63959645	2.69	MSRB3	chr12	+	302	NM_198080
D3A_WT	1789	49699702	49699851	2.06	MST1	chr3	-	1424	NM_020998
D3A_WT	1889	4912837	4913088	2.47	MSX1	chr4	+	670	NM_002448

D3A_WT	1888	4909539	4910058	2.79	MSX1	chr4	+	-2494	NM_002448
D3A_WT	2093	37061536	37062580	3.03	MTCH1	chr6	-	-131	NM_014341
D3A_WT	2615	153952695	153952976	2.78	MTCP1	chrX	-	-94	NM_001018025
D3A_WT	2615	153952695	153952976	2.78	MTCP1NB	chrX	-	-94	NM_001018024
D3A_WT	1917	75242920	75243383	3.26	MTHFD2L	chr4	+	459	NM_001144978
D3A_WT	158	153434174	153434309	2.43	MUC1	chr1	-	-4917	NM_001044392
D3A_WT	1853	197023887	197024116	2.23	MUC4	chr3	-	-456	NM_138297
D3A_WT	1165	1305111	1306266	2.09	MUM1	chr19	+	-1634	NR_024247
D3A_WT	1165	1305111	1306266	2.09	MUM1	chr19	+	-287	NM_032853
D3A_WT	326	618385	618804	3.37	MUPCDH	chr11	-	-3587	NM_031264
D3A_WT	288	111975252	111977131	3.59	MXI1	chr10	+	440	NM_005962
D3A_WT	14	1280314	1280886	3.27	MXRA8	chr1	-	3178	NM_032348
D3A_WT	1356	59061487	59062860	3.54	MYADM	chr19	+	-775	NM_138373
D3A_WT	1356	59061487	59062860	3.54	MYADM	chr19	+	-2298	NM_001020821
D3A_WT	1356	59061487	59062860	3.54	MYADM	chr19	+	-2419	NM_001020818
D3A_WT	1356	59061487	59062860	3.54	MYADM	chr19	+	751	NM_001020820
D3A_WT	1412	33805666	33805920	2.48	MYADML	chr2	-	995	NR_003143
D3A_WT	399	47333975	47335020	3.79	MYBPC3	chr11	-	-3668	NM_000256
D3A_WT	1018	45940648	45940809	2.39	MYCBPAP	chr17	+	-15	NM_032133
D3A_WT	1399	16000164	16000691	2.34	MYCN	chr2	+	2294	NM_005378
D3A_WT	1399	16000164	16000691	2.34	MYCNOS	chr2	-	-1131	NR_026766
D3A_WT	431	68818120	68818249	2.05	MYEOV	chr11	+	-13	NM_138768
D3A_WT	1778	46886357	46886788	2.81	MYL3	chr3	-	-6595	NM_000258
D3A_WT	1559	34602616	34603661	2.9	MYL9	chr20	+	-172	NM_181526
D3A_WT	1485	191818278	191818557	2.36	MYO1B	chr2	+	66	NM_012223
D3A_WT	1485	191818278	191818557	2.36	MYO1B	chr2	+	-81	NM_001161819
D3A_WT	956	12509669	12510303	2.59	MYOCD	chr17	+	55	NM_153604
D3A_WT	2051	177472965	177473313	2.81	N4BP3	chr5	+	-22	NM_015111
D3A_WT	2362	102443834	102443958	2.31	NACAP1	chr8	+	-6400	NR_002182
D3A_WT	1248	13090027	13090466	2.52	NACC1	chr19	+	138	NM_052876
D3A_WT	1002	39437676	39438745	2.45	NAGS	chr17	+	653	NM_153006
D3A_WT	1327	51109411	51109625	2.73	NANOS2	chr19	-	358	NM_001029861
D3A_WT	533	74764430	74765397	3.52	NAP1L1	chr12	-	92	NM_004537
D3A_WT	1369	60686420	60686879	2.34	NAT14	chr19	+	-1756	NM_020378
D3A_WT	1370	60690828	60692293	3.42	NAT14	chr19	+	3155	NM_020378
D3A_WT	1880	2030086	2030335	2.63	NAT8L	chr4	+	-826	NM_178557
D3A_WT	1881	2031185	2031419	2.62	NAT8L	chr4	+	266	NM_178557
D3A_WT	1043	70283969	70284123	2.69	NAT9	chr17	-	19	NM_015654
D3A_WT	69	19843141	19843770	2.35	NBL1	chr1	+	61	NM_005380
D3A_WT	69	19843141	19843770	2.35	NBL1	chr1	+	1143	NM_182744
D3A_WT	2357	91066502	91066733	2.64	NBN	chr8	-	-542	NM_002485
D3A_WT	72	21639241	21639495	2.74	NBPF3	chr1	+	151	NM_032264
D3A_WT	91	35795560	35796607	2.52	NCDN	chr1	+	104	NM_014284
D3A_WT	1785	48698183	48698537	2.47	NCKIPSD	chr3	-	-22	NM_184231
D3A_WT	861	30844521	30844770	3	NCRNA00095	chr16	-	-2554	NR_024348
D3A_WT	2537	1474896	1475440	2.87	NCRNA00105	chrX	+	-4255	NR_026710
D3A_WT	1825	133923659	133923923	2.66	NCRNA00119	chr3	+	-84	NR_002811

D3A_WT	1381	63553766	63553915	2.13	NCRNA00181	chr19	+	-1307	NR_015380
D3A_WT	1098	2561372	2561731	2.62	NDC80	chr18	+	42	NM_006101
D3A_WT	1788	49034806	49034950	2.87	NDUFAF3	chr3	+	1967	NM_199074
D3A_WT	1787	49030836	49031362	2.96	NDUFAF3	chr3	+	-1812	NM_199074
D3A_WT	1788	49034806	49034950	2.87	NDUFAF3	chr3	+	1257	NM_199073
D3A_WT	1787	49030836	49031362	2.96	NDUFAF3	chr3	+	-2522	NM_199073
D3A_WT	1788	49034806	49034950	2.87	NDUFAF3	chr3	+	801	NM_199069
D3A_WT	1787	49030836	49031362	2.96	NDUFAF3	chr3	+	-2978	NM_199069
D3A_WT	66	16639978	16640137	2.14	NECAP2	chr1	+	304	NM_001145277
D3A_WT	541	95825099	95825854	2.97	NEDD1	chr12	+	102	NM_001135175
D3A_WT	541	95825099	95825854	2.97	NEDD1	chr12	+	345	NM_001135176
D3A_WT	1122	53862643	53863099	2.35	NEDD4L	chr18	+	255	NM_015277
D3A_WT	1122	53862643	53863099	2.35	NEDD4L	chr18	+	-2584	NM_001144964
D3A_WT	870	45734870	45735204	2.58	NETO2	chr16	-	372	NM_018092
D3A_WT	1484	182258033	182258194	2.4	NEUROD1	chr2	-	-4487	NM_002500
D3A_WT	1130	75262972	75263131	2.38	NFATC1	chr18	+	1738	NM_172387
D3A_WT	889	66671103	66671557	2.21	NFATC3	chr16	+	-5545	NM_173165
D3A_WT	643	23904926	23905175	2.1	NFATC4	chr14	+	-934	NM_001136022
D3A_WT	644	23906626	23907961	2.47	NFATC4	chr14	+	1309	NM_001136022
D3A_WT	643	23904926	23905175	2.1	NFATC4	chr14	+	-2015	NM_004554
D3A_WT	644	23906626	23907961	2.47	NFATC4	chr14	+	228	NM_004554
D3A_WT	2415	14303278	14304038	2.81	NFIB	chr9	-	287	NM_005596
D3A_WT	1245	12962783	12963252	3.21	NFIX	chr19	+	-4566	NM_002501
D3A_WT	1246	12968184	12969053	2.31	NFIX	chr19	+	1035	NM_002501
D3A_WT	2096	41148788	41149222	2.97	NFYA	chr6	+	321	NM_021705
D3A_WT	665	76806129	76807166	2.51	NGB	chr14	-	761	NM_021257
D3A_WT	594	38509768	38509927	2.29	NHLRC3	chr13	+	-607	NM_001017370
D3A_WT	788	550357	550906	2.96	NHLRC4	chr16	+	-6401	NM_176677
D3A_WT	789	551822	552101	2.36	NHLRC4	chr16	+	-5071	NM_176677
D3A_WT	2134	124166212	124166436	2.88	NKAIN2	chr6	+	-443	NM_001040214
D3A_WT	649	36120439	36121420	2.57	NKX2-8	chr14	-	608	NM_014360
D3A_WT	1896	13152650	13153504	2.64	NKX3-2	chr4	-	2135	NM_001189
D3A_WT	306	134450252	134450426	2.29	NKX6-2	chr10	-	-812	NM_177400
D3A_WT	981	30493024	30493188	2.28	NLE1	chr17	-	329	NM_018096
D3A_WT	1020	46598589	46599149	2.35	NME2	chr17	+	-10	NM_001018139
D3A_WT	1020	46598589	46599149	2.35	NME2	chr17	+	-212	NM_001018138
D3A_WT	1020	46598589	46599149	2.35	NME2	chr17	+	980	NM_001018137
D3A_WT	1020	46598589	46599149	2.35	NME2	chr17	+	232	NM_002512
D3A_WT	839	4466252	4467016	2.32	NMRAL1	chr16	-	-1737	NM_020677
D3A_WT	267	96111093	96111231	2.06	NOC3L	chr10	-	1511	NM_022451
D3A_WT	2219	30484897	30485349	2.7	NOD1	chr7	-	-205	NM_006092
D3A_WT	875	49284054	49284433	2.54	NOD2	chr16	+	-4307	NM_022162
D3A_WT	1884	2937173	2937649	2.5	NOP14	chr4	-	-2495	NM_003703
D3A_WT	1431	73283704	73284172	2.51	NOTO	chr2	+	1045	NM_001134462
D3A_WT	1609	62207436	62208509	2.61	NPBWR2	chr20	-	656	NM_005286
D3A_WT	1825	133923659	133923923	2.66	NPHP3	chr3	-	175	NM_153240
D3A_WT	41	5974251	5975899	3.03	NPHP4	chr1	-	43	NM_015102

D3A_WT	1346	55571615	55572074	2.11	NR1H2	chr19	+	348	NM_007121
D3A_WT	1765	14963752	14964191	2.15	NR2C2	chr3	+	-268	NM_003298
D3A_WT	2125	108596632	108597166	2.58	NR2E1	chr6	+	2992	NM_003269
D3A_WT	2474	126306329	126306902	3.02	NR5A1	chr9	-	2905	NM_004959
D3A_WT	2475	126310551	126310691	2.53	NR5A1	chr9	-	-1101	NM_004959
D3A_WT	2028	139401975	139402614	4.12	NRG2	chr5	-	769	NM_013981
D3A_WT	1487	206255234	206256370	2.16	NRP2	chr2	+	334	NM_201279
D3A_WT	2130	116528726	116528860	2.08	NT5DC1	chr6	+	102	NM_152729
D3A_WT	1798	52544911	52546108	2.73	NT5DC2	chr3	-	-1376	NM_022908
D3A_WT	1798	52544911	52546108	2.73	NT5DC2	chr3	-	-2676	NM_001134231
D3A_WT	959	17147420	17147854	2.58	NT5M	chr17	+	233	NM_020201
D3A_WT	955	8866402	8867441	3.63	NTN1	chr17	+	1338	NM_004822
D3A_WT	822	2457718	2457981	2.25	NTN3	chr16	+	-3651	NM_006181
D3A_WT	540	94708848	94709167	3.26	NTN4	chr12	-	-340	NM_021229
D3A_WT	2502	134027855	134028407	2.93	NTNG2	chr9	+	977	NM_032536
D3A_WT	81	27120979	27121193	2.76	NUDC	chr1	+	276	NM_006600
D3A_WT	706	104724079	104724634	2.9	NUDT14	chr14	-	-5651	NM_177533
D3A_WT	1763	13436554	13437003	3.59	NUP210	chr3	-	31	NM_024923
D3A_WT	1919	77292284	77292764	2.9	NUP54	chr4	-	-3845	NM_017426
D3A_WT	1048	70713713	70713944	2.35	NUP85	chr17	+	637	NM_024844
D3A_WT	933	828760	830440	2.28	NXN	chr17	-	160	NM_022463
D3A_WT	1184	2220450	2221995	3.12	OAZ1	chr19	+	703	NM_004152
D3A_WT	282	105667991	105668340	3.01	OBFC1	chr10	-	-130	NM_024928
D3A_WT	1495	220143571	220144025	2.65	OBSL1	chr2	-	457	NM_015311
D3A_WT	716	26023615	26024392	3.22	OCA2	chr15	-	-5950	NM_000275
D3A_WT	1589	60907212	60907831	2.7	OGFR	chr20	+	900	NM_007346
D3A_WT	2506	137101223	137101347	2.24	OLFM1	chr9	+	-5624	NM_014279
D3A_WT	2507	137107097	137108273	2.44	OLFM1	chr9	+	776	NM_014279
D3A_WT	2506	137101223	137101347	2.24	OLFM1	chr9	+	-5638	NM_006334
D3A_WT	2507	137107097	137108273	2.44	OLFM1	chr9	+	762	NM_006334
D3A_WT	2140	137855747	137856681	4	OLIG3	chr6	-	1010	NM_175747
D3A_WT	1121	53253630	53254073	2.51	ONECUT2	chr18	+	-63	NM_004852
D3A_WT	1176	1700186	1700939	3.21	ONECUT3	chr19	+	-4099	NM_001080488
D3A_WT	1257	15784996	15785432	2.48	OR10H1	chr19	-	-5278	NM_013940
D3A_WT	219	245988164	245988422	2.62	OR1C1	chr1	-	38	NM_012353
D3A_WT	2265	101860257	101861091	2.73	ORAI2	chr7	+	-326	NM_032831
D3A_WT	2111	88356351	88356496	2.07	ORC3L	chr6	+	-138	NM_181837
D3A_WT	1483	178766881	178767025	2.43	OSBPL6	chr2	+	-666	NM_032523
D3A_WT	1401	19421776	19422212	2.21	OSR1	chr2	-	-141	NM_145260
D3A_WT	1406	26559280	26559513	2.82	OTOF	chr2	-	-4982	NM_194323
D3A_WT	1045	70438724	70439068	2.59	OTOP3	chr17	+	-4595	NM_178233
D3A_WT	418	65304952	65305782	2.48	OVOL1	chr11	+	-5737	NM_004561
D3A_WT	2577	69395945	69396314	2.07	P2RY4	chrX	-	250	NM_002565
D3A_WT	2627	1622678	1622899	2.7	P2RY8	chrY	-	-6751	NM_178129
D3A_WT	252	74526061	74527485	2.94	P4HA1	chr10	-	-35	NM_001142596
D3A_WT	2361	101802701	101802925	2.9	PABPC1	chr8	-	678	NM_002568
D3A_WT	447	76862082	76863454	2.65	PAK1	chr11	-	-12	NM_002576

D3A_WT	727	38318680	38322230	4.74	PAK6	chr15	+	1129	NM_020168
D3A_WT	264	91394832	91394981	2.55	PANK1	chr10	-	-1279	NM_138316
D3A_WT	264	91394832	91394981	2.55	PANK1	chr10	-	289	NM_148977
D3A_WT	28	2450216	2451160	3.2	PANK4	chr1	-	-2793	NM_018216
D3A_WT	2285	139409325	139409469	2.37	PARP12	chr7	-	593	NM_022750
D3A_WT	376	12356011	12356235	2.88	PARVA	chr11	+	402	NM_018222
D3A_WT	1527	241737156	241737405	2.5	PASK	chr2	-	271	NM_015148
D3A_WT	383	31796131	31796480	2.55	PAX6	chr11	-	-6850	NM_000280
D3A_WT	383	31796131	31796480	2.55	PAX6	chr11	-	-220	NM_001127612
D3A_WT	1454	113752291	113752640	2.01	PAX8	chr2	-	503	NM_013951
D3A_WT	2301	154425725	154426758	3.32	PAXIP1	chr7	-	-626	NM_007349
D3A_WT	1426	70167920	70168155	2.05	PCBP1	chr2	+	-51	NM_006196
D3A_WT	2585	99551539	99552165	3.39	PCDH19	chrX	-	75	NM_020766
D3A_WT	2584	99548742	99549666	3.03	PCDH19	chrX	-	2723	NM_020766
D3A_WT	1906	30332534	30333398	3	PCDH7	chr4	+	1832	NM_032457
D3A_WT	2030	140221932	140222057	2.61	PCDHA11	chr5	+	-6020	NM_018902
D3A_WT	2029	140183036	140183465	3.1	PCDHA5	chr5	+	1706	NM_018908
D3A_WT	2029	140183036	140183465	3.1	PCDHA6	chr5	+	-4583	NM_031849
D3A_WT	2031	140779295	140779859	3.65	PCDHGA11	chr5	+	-1143	NM_032092
D3A_WT	2031	140779295	140779859	3.65	PCDHGB7	chr5	+	2112	NM_018927
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D3A_WT	986	34157422	34157977	2.6	PCGF2	chr17	-	385	NM_007144
D3A_WT	1863	689592	690156	2.51	PCGF3	chr4	+	302	NM_006315
D3A_WT	632	112911366	112912015	2.42	PCID2	chr13	-	-660	NM_001127202
D3A_WT	1541	5048566	5049020	2.03	PCNA	chr20	-	-146	NM_182649
D3A_WT	416	65142605	65142929	2.11	PCNXL3	chr11	+	2409	NM_032223
D3A_WT	1171	1442020	1442264	2.11	PCSK4	chr19	-	-735	NM_017573
D3A_WT	778	99847513	99848283	3.56	PCSK6	chr15	-	-188	NM_138319
D3A_WT	1531	242452407	242452761	2.59	PDCD1	chr2	-	-2853	NM_005018
D3A_WT	1532	242456092	242456541	2.2	PDCD1	chr2	-	-6585	NM_005018
D3A_WT	437	72030734	72031075	2.75	PDE2A	chr11	-	248	NM_001143839
D3A_WT	437	72030734	72031075	2.75	PDE2A	chr11	-	231	NR_026572
D3A_WT	1234	10423816	10424175	2.83	PDE4A	chr19	+	-637	NM_006202
D3A_WT	1998	59224815	59226066	2.58	PDE4D	chr5	-	-62	NM_001104631
D3A_WT	2007	76542067	76542841	3.28	PDE8B	chr5	+	-7	NM_001029851
D3A_WT	781	274235	276080	4.84	PDIA2	chr16	+	2039	NM_006849
D3A_WT	77	26310713	26311569	2.32	PDIK1L	chr1	+	287	NM_152835
D3A_WT	77	26310713	26311569	2.32	PDIK1L	chr1	+	899	NR_026685
D3A_WT	268	97040508	97040842	2.76	PDLIM1	chr10	-	96	NM_020992
D3A_WT	2050	176862491	176863530	3.14	PDLIM7	chr5	-	-5802	NM_203352
D3A_WT	881	65472430	65472779	2.65	PDP2	chr16	+	668	NM_020786
D3A_WT	1910	39654834	39656473	3.36	PDS5A	chr4	-	225	NM_015200
D3A_WT	1910	39654834	39656473	3.36	PDS5A	chr4	-	318	NM_001100399
D3A_WT	1808	73756184	73756503	2.14	PDZRN3	chr3	-	419	NM_015009
D3A_WT	652	55655379	55655613	3.52	PELI2	chr14	+	651	NM_021255
D3A_WT	942	4560489	4561104	2.43	PELP1	chr17	-	-6415	NM_014389
D3A_WT	941	4553888	4554507	3.33	PELP1	chr17	-	184	NM_014389

D3A_WT	2142	138470033	138470382	2.54	PERP	chr6	-	146	NM_022121
D3A_WT	392	45901281	45901505	2.28	PEX16	chr11	-	-5143	NM_057174
D3A_WT	1571	52258025	52258174	2.03	PFDN4	chr20	+	191	NM_002623
D3A_WT	230	6285030	6285269	2.34	PFKFB3	chr10	+	304	NM_004566
D3A_WT	1637	44537922	44538571	3.16	PFKL	chr21	+	-6111	NM_002626
D3A_WT	1637	44537922	44538571	3.16	PFKL	chr21	+	-6106	NR_024108
D3A_WT	224	3099725	3099879	2.5	PFKP	chr10	+	51	NM_002627
D3A_WT	943	4792983	4794220	2.65	PFN1	chr17	-	-1031	NM_005022
D3A_WT	2048	176763714	176764265	3.35	PFN3	chr5	-	-3746	NM_001029886
D3A_WT	1402	24197385	24197704	2.68	PFN4	chr2	-	2111	NM_199346
D3A_WT	1403	24199570	24199939	3.47	PFN4	chr2	-	-99	NM_199346
D3A_WT	220	247167098	247167547	3.61	PGBD2	chr1	+	258	NM_170725
D3A_WT	2360	97726608	97726952	2.86	PGCP	chr8	+	106	NM_016134
D3A_WT	440	73787153	73787491	2.54	PGM2L1	chr11	-	-172	NM_173582
D3A_WT	2161	169866542	169867058	2.93	PHF10	chr6	-	-769	NM_133325
D3A_WT	532	74711949	74712178	2.4	PHLDA1	chr12	-	-240	NM_007350
D3A_WT	366	2906692	2907769	2.44	PHLDA2	chr11	-	-4	NM_003311
D3A_WT	2519	138858268	138859043	2.42	PHPT1	chr9	+	-4421	NM_014172
D3A_WT	1499	229844159	229844493	2.66	PID1	chr2	-	-25	NM_001100818
D3A_WT	1854	197923579	197923824	3.22	PIGX	chr3	+	60	NM_017861
D3A_WT	1855	198180881	198181430	2.43	PIGZ	chr3	-	-1054	NM_025163
D3A_WT	2566	48659386	48661113	2.49	PIM2	chrX	-	1108	NM_006875
D3A_WT	1747	48738764	48739223	3	PIM3	chr22	+	-1153	NM_001001852
D3A_WT	945	6400816	6400950	2.04	PITPNM3	chr17	-	-282	NM_001165966
D3A_WT	749	70309168	70310104	3.47	PKM2	chr15	-	1102	NM_182471
D3A_WT	831	2970307	2970551	2.08	PKMYT1	chr16	-	46	NM_004203
D3A_WT	70	20339830	20340564	3.21	PLA2G2F	chr1	+	1788	NM_022819
D3A_WT	1333	53305561	53306005	2.63	PLA2G4C	chr19	-	138	NM_001159322
D3A_WT	1214	5518388	5518617	2.14	PLAC2	chr19	-	503	NR_027064
D3A_WT	2144	144371050	144371304	2.45	PLAGL1	chr6	-	57	NM_006718
D3A_WT	1409	28574917	28575467	2.91	PLB1	chr2	+	2707	NM_153021
D3A_WT	407	63775326	63776462	3.52	PLCB3	chr11	+	197	NM_000932
D3A_WT	2616	126960	127559	3.61	PLCXD1	chrY	+	-5731	NR_028057
D3A_WT	2617	134674	135079	2.3	PLCXD1	chrY	+	1886	NR_028057
D3A_WT	2617	134674	135079	2.3	PLCXD1	chrY	+	-3184	NM_018390
D3A_WT	1308	45546165	45546304	2.34	PLD3	chr19	+	63	NM_012268
D3A_WT	958	17049832	17050696	2.86	PLD6	chr17	-	107	NM_178836
D3A_WT	507	43896142	43896301	2.73	PLEKHA9	chr12	-	-165	NM_015899
D3A_WT	49	6472844	6473168	2.49	PLEKHG5	chr1	-	221	NM_001042664
D3A_WT	49	6472844	6473168	2.49	PLEKHG5	chr1	-	-4405	NM_001042665
D3A_WT	49	6472844	6473168	2.49	PLEKHG5	chr1	-	1341	NM_020631
D3A_WT	3	892017	892266	3.05	PLEKHN1	chr1	+	402	NM_001160184
D3A_WT	878	55875558	55875832	2.53	PLLP	chr16	-	390	NM_015993
D3A_WT	1820	128185591	128186575	2.49	PLXNA1	chr3	+	-4043	NM_032242
D3A_WT	186	206483565	206484014	2.78	PLXNA2	chr1	-	499	NM_025179
D3A_WT	2114	89912495	89912954	2.89	PM20D2	chr6	+	237	NM_001010853
D3A_WT	2603	152591486	152592235	2.37	PNCK	chrX	-	1150	NM_001039582

D3A_WT	2603	152591486	152592235	2.37	PNCK	chrX	-	77	NM_001135740
D3A_WT	2112	89847145	89848773	2.74	PNRC1	chr6	+	812	NM_006813
D3A_WT	1251	13926145	13926389	2.22	PODNL1	chr19	-	-1063	NM_001146255
D3A_WT	2553	24621609	24621738	2.21	POLA1	chrX	+	-303	NM_016937
D3A_WT	974	23708354	23708603	2.6	POLDIP2	chr17	-	252	NM_015584
D3A_WT	2331	22158097	22158446	2.39	POLR3D	chr8	+	-292	NM_001722
D3A_WT	666	76857490	76857634	2.31	POMT2	chr14	-	-584	NM_013382
D3A_WT	2120	105731898	105732656	2.41	POPDC3	chr6	-	2274	NM_022361
D3A_WT	2120	105731898	105732656	2.41	POPDC3	chr6	-	-1454	NR_024539
D3A_WT	170	165457686	165457835	2.4	POU2F1	chr1	+	994	NM_002697
D3A_WT	1449	104839522	104839671	2.68	POU3F3	chr2	+	1196	NM_006236
D3A_WT	609	78073723	78074272	2.5	POU4F1	chr13	-	1699	NM_006237
D3A_WT	610	78075335	78075689	2.65	POU4F1	chr13	-	184	NM_006237
D3A_WT	1941	147779555	147781214	3	POU4F2	chr4	+	890	NM_004575
D3A_WT	515	49874953	49875167	2.25	POU6F1	chr12	-	3157	NM_002702
D3A_WT	2221	38982141	38982385	2.34	POU6F2	chr7	+	-1870	NM_007252
D3A_WT	1996	54866349	54866478	2.16	PPAP2A	chr5	-	217	NM_176895
D3A_WT	2499	133147736	133147948	2.99	PPAPDC3	chr9	+	-7059	NM_032728
D3A_WT	1597	61622500	61623034	2.75	PPDPF	chr20	+	191	NM_024299
D3A_WT	2128	109868626	109869075	3.73	PPIL6	chr6	-	-310	NM_001111298
D3A_WT	1797	52248157	52248421	2.79	PPM1M	chr3	+	-6975	NM_144641
D3A_WT	534	78852661	78853225	2.42	PPP1R12A	chr12	-	423	NM_001143885
D3A_WT	534	78852661	78853225	2.42	PPP1R12A	chr12	-	166	NM_002480
D3A_WT	694	103382989	103384028	2.59	PPP1R13B	chr14	-	172	NM_015316
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D3A_WT	2150	150505921	150506760	2.73	PPP1R14C	chr6	+	460	NM_030949
D3A_WT	2324	9045594	9045734	2.82	PPP1R3B	chr8	-	-34	NM_024607
D3A_WT	2569	49013554	49013816	2.57	PPP1R3F	chrX	+	425	NM_033215
D3A_WT	1527	241737156	241737405	2.5	PPP1R7	chr2	+	-1294	NM_002712
D3A_WT	1014	45582206	45583456	3.18	PPP1R9B	chr17	-	45	NM_032595
D3A_WT	2336	30789339	30789864	2.76	PPP2CB	chr8	-	293	NM_001009552
D3A_WT	2620	219120	219689	3.25	PPP2R3B	chrY	-	3186	NM_199326
D3A_WT	189	210526226	210526385	2.72	PPP2R5A	chr1	+	804	NM_006243
D3A_WT	1928	102486185	102488658	2.73	PPP3CA	chr4	-	230	NM_001130692
D3A_WT	1807	73128499	73129417	2.88	PPP4R2	chr3	+	150	NM_174907
D3A_WT	1136	75811959	75814106	4	PQLC1	chr18	-	-391	NM_001146345
D3A_WT	472	129320344	129320693	2.88	PRDM10	chr11	-	2209	NM_199439
D3A_WT	32	2977403	2977577	2.19	PRDM16	chr1	+	1887	NM_199454
D3A_WT	31	2974705	2975471	2.09	PRDM16	chr1	+	-515	NM_199454
D3A_WT	62	13948894	13949650	2.13	PRDM2	chr1	+	810	NM_001007257
D3A_WT	1244	12778104	12778558	2.5	PRDX2	chr19	-	-4637	NM_005809
D3A_WT	1243	12776034	12776273	2.12	PRDX2	chr19	-	-2459	NM_005809
D3A_WT	1600	61675884	61676033	2.35	PRIC285	chr20	-	78	NM_001037335
D3A_WT	1599	61666363	61671502	3.72	PRIC285	chr20	-	619	NM_033405
D3A_WT	1600	61675884	61676033	2.35	PRIC285	chr20	-	-6407	NM_033405
D3A_WT	510	47700630	47700784	2.31	PRKAG1	chr12	-	-1848	NM_002733
D3A_WT	2174	733096	733420	2.78	PRKAR1B	chr7	-	246	NM_001164760

D3A_WT	2174	733096	733420	2.78	PRKAR1B	chr7	-	581	NM_001164759
D3A_WT	2269	106470491	106470827	2.22	PRKAR2B	chr7	+	-1754	NM_002736
D3A_WT	2270	106472380	106473250	3.03	PRKAR2B	chr7	+	402	NM_002736
D3A_WT	1033	61729317	61730137	2.87	PRKCA	chr17	+	340	NM_002737
D3A_WT	1357	59073899	59074445	2.88	PRKCG	chr19	+	-3106	NM_002739
D3A_WT	21	1972459	1972708	2.46	PRKCZ	chr1	+	815	NM_002744
D3A_WT	23	1995775	1995919	2.2	PRKCZ	chr1	+	902	NM_001033581
D3A_WT	22	1992263	1992602	2.82	PRKCZ	chr1	+	-2513	NM_001033581
D3A_WT	1340	54872756	54873109	2.62	PRMT1	chr19	+	625	NM_198318
D3A_WT	631	112855603	112855752	2.27	PROZ	chr13	+	-5291	NM_003891
D3A_WT	2465	115077770	115078094	2.46	PRPF4	chr9	+	138	NM_004697
D3A_WT	511	47975387	47975751	2.93	PRPH	chr12	+	394	NM_006262
D3A_WT	2156	166640663	166642040	3.88	PRR18	chr6	-	510	NM_175922
D3A_WT	2495	131467342	131468322	2.09	PRRX2	chr9	+	92	NM_016307
D3A_WT	1656	15462034	15462496	2.36	psiTPTE22	chr22	+	-535	NR_001591
D3A_WT	1581	60151957	60152601	2.4	PSMA7	chr20	-	-410	NM_002792
D3A_WT	2169	170703904	170704068	2.33	PSMB1	chr6	-	356	NM_002793
D3A_WT	986	34157422	34157977	2.6	PSMB3	chr17	+	-4828	NM_002795
D3A_WT	641	23675039	23675358	2.45	PSME1	chr14	+	-19	NM_006263
D3A_WT	642	23686921	23687170	2.51	PSME2	chr14	-	-1350	NM_002818
D3A_WT	2192	1575936	1576597	2.95	PSMG3	chr7	-	-72	NM_001134340
D3A_WT	2192	1575936	1576597	2.95	PSMG3	chr7	-	-111	NM_032302
D3A_WT	1219	6331269	6331393	2.01	PSPN	chr19	-	-4471	NM_004158
D3A_WT	59	11461769	11462633	3.58	PTCHD2	chr1	+	320	NM_020780
D3A_WT	235	23520792	23522017	2.37	PTF1A	chr10	+	-61	NM_178161
D3A_WT	745	63609886	63610125	2.64	PTPLAD1	chr15	+	126	NM_016395
D3A_WT	1924	87734411	87734580	2.05	PTPN13	chr4	+	4	NM_080684
D3A_WT	381	18768864	18770209	2.58	PTPN5	chr11	-	429	NM_032781
D3A_WT	85	29436762	29437211	2.43	PTPRU	chr1	+	1353	NM_133178
D3A_WT	2481	129517231	129517855	2.52	PTRH1	chr9	-	214	NM_001002913
D3A_WT	456	111602526	111602785	3.09	PTS	chr11	+	358	NM_000317
D3A_WT	2393	144983066	144983788	2.54	PUF60	chr8	-	98	NM_014281
D3A_WT	2393	144983066	144983788	2.54	PUF60	chr8	-	-243	NM_001136033
D3A_WT	13	1233219	1234854	2.63	PUSL1	chr1	+	180	NM_153339
D3A_WT	1704	35542664	35542943	2.3	PVALB	chr22	-	2660	NM_002854
D3A_WT	463	119104791	119105345	2.97	PVRL1	chr11	-	-423	NM_203285
D3A_WT	1814	112273446	112274164	3.66	PVRL3	chr3	+	251	NM_015480
D3A_WT	304	134059527	134059656	2.84	PWWP2B	chr10	+	-1100	NM_001098637
D3A_WT	1002	39437676	39438745	2.45	PYY	chr17	-	-847	NM_004160
D3A_WT	2512	138277193	138277852	2.05	QSOX2	chr9	-	-14	NM_181701
D3A_WT	787	416524	417666	2.77	RAB11FIP3	chr16	+	1427	NM_014700
D3A_WT	2286	139744671	139744950	2.36	RAB19	chr7	+	-5501	NM_001008749
D3A_WT	159	154290347	154290889	3.26	RAB25	chr1	+	-6971	NM_020387
D3A_WT	741	53369202	53369554	3.58	RAB27A	chr15	-	-85	NM_183235
D3A_WT	1042	70239866	70241710	3.47	RAB37	chr17	+	-4162	NM_001163990
D3A_WT	1042	70239866	70241710	3.47	RAB37	chr17	+	-3765	NM_001163989
D3A_WT	1267	18177774	18177994	2.3	RAB3A	chr19	-	-2010	NM_002866

D3A_WT	2578	69416294	69416653	2.89	RAB41	chrX	+	-2319	NM_001032726
D3A_WT	2549	13617364	13618314	3.11	RAB9A	chrX	+	578	NM_004251
D3A_WT	1082	77583742	77583981	2.11	RAC3	chr17	+	1041	NM_005052
D3A_WT	2462	109084699	109085437	2.08	RAD23B	chr9	+	-296	NM_002874
D3A_WT	961	17526333	17527190	2.17	RAI1	chr17	+	1250	NM_030665
D3A_WT	1557	32045088	32046205	2.63	RALY	chr20	+	254	NM_007367
D3A_WT	1666	18484698	18485527	2.43	RANBP1	chr22	+	89	NM_002882
D3A_WT	2039	170222202	170222351	2.22	RANBP17	chr5	+	677	NM_022897
D3A_WT	952	8134638	8134977	3.05	RANGRF	chr17	+	2094	NM_016492
D3A_WT	73	21850775	21851159	2.3	RAP1GAP	chr1	-	-32	NM_001145658
D3A_WT	1927	99401447	99401780	2.33	RAP1GDS1	chr4	+	64	NM_001100430
D3A_WT	2111	88356351	88356496	2.07	RARS2	chr6	-	31	NM_020320
D3A_WT	960	17339659	17340890	2.55	RASD1	chr17	-	158	NM_016084
D3A_WT	1703	34266119	34266779	2.98	RASD2	chr22	+	-848	NM_014310
D3A_WT	2059	179573274	179573519	3.39	RASGEF1C	chr5	-	-4660	NM_175062
D3A_WT	2058	179568565	179569399	2.7	RASGEF1C	chr5	-	-246	NM_175062
D3A_WT	2008	80291348	80291567	3.25	RASGRF2	chr5	+	-856	NM_006909
D3A_WT	1792	50349967	50350291	2.32	RASSF1	chr3	-	-230	NM_170713
D3A_WT	1792	50349967	50350291	2.32	RASSF1	chr3	-	3242	NM_170714
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D3A_WT	325	546111	546446	2.22	RASSF7	chr11	+	-5171	NM_003475
D3A_WT	325	546111	546446	2.22	RASSF7	chr11	+	-4692	NM_001143993
D3A_WT	2342	53789169	53789818	3.31	RB1CC1	chr8	-	86	NM_014781
D3A_WT	1575	55399977	55400141	2.66	RBM38	chr20	+	190	NM_017495
D3A_WT	1946	155922252	155922516	2.83	RBM46	chr4	+	508	NM_144979
D3A_WT	1474	161057771	161058030	2.84	RBMS1	chr2	-	664	NM_016836
D3A_WT	123	89230679	89231048	3.05	RBMXL1	chr1	-	368	NM_019610
D3A_WT	2593	114329929	114333498	4.62	RBMXL3	chrX	+	1495	NM_001145346
D3A_WT	2634	22106264	22106587	2.97	RBMY1A1	chrY	+	239	NM_005058
D3A_WT	2634	22106264	22106587	2.97	RBMY1B	chrY	+	239	NM_001006121
D3A_WT	2634	22106264	22106587	2.97	RBMY1D	chrY	+	233	NM_001006120
D3A_WT	490	7179067	7179598	2.81	RBP5	chr12	-	-6599	NM_031491
D3A_WT	1171	1442020	1442264	2.11	REEP6	chr19	+	-22	NM_138393
D3A_WT	26	2307369	2307712	2.55	RER1	chr1	+	-5533	NM_007033
D3A_WT	52	8406205	8406329	2.02	RERE	chr1	-	67	NM_001042682
D3A_WT	1434	85435254	85435608	3.01	RETSAT	chr2	-	-99	NM_017750
D3A_WT	2355	86760623	86762926	4.25	REXO1L1	chr8	-	746	NM_172239
D3A_WT	2354	86753872	86755639	5.73	REXO1L2P	chr8	-	402	NR_003594
D3A_WT	2355	86760623	86762926	4.25	REXO1L2P	chr8	-	-6617	NR_003594
D3A_WT	2355	86760623	86762926	4.25	REXO1L2P	chr8	-	220	NR_003594
D3A_WT	555	116939023	116939272	2.87	RFC5	chr12	+	257	NM_007370
D3A_WT	171	174442583	174443417	2.8	RFWD2	chr1	-	-7	NM_001001740
D3A_WT	1446	101456913	101457972	2.65	RFX8	chr2	-	155	NM_001145664
D3A_WT	773	91432867	91433720	2.27	RGMA	chr15	-	-537	NM_001166287
D3A_WT	773	91432867	91433720	2.27	RGMA	chr15	-	154	NM_020211
D3A_WT	794	662497	663146	3.17	RHBDL1	chr16	+	-3254	NM_003961
D3A_WT	425	66580802	66581566	2.67	RHOD	chr11	+	320	NM_014578

D3A_WT	793	651289	654618	3.95	RHOT2	chr16	+	-5180	NM_138769
D3A_WT	204	226938323	226938943	3.54	RHOU	chr1	+	1142	NM_021205
D3A_WT	319	198794	199743	4.08	RIC8A	chr11	+	739	NM_021932
D3A_WT	564	122583741	122583900	2.43	RILPL1	chr12	-	398	NM_178314
D3A_WT	1679	20234069	20234998	4.07	RIMBP3B	chr22	-	840	NM_001128635
D3A_WT	1679	20234069	20234998	4.07	RIMBP3C	chr22	-	1217	NM_001128633
D3A_WT	492	8742065	8742204	2.46	RIMKLB	chr12	+	350	NM_020734
D3A_WT	423	65866199	65866328	2.53	RIN1	chr11	-	-5687	NM_004292
D3A_WT	2107	84619835	84620264	3.25	RIPPLY2	chr6	+	346	NM_001009994
D3A_WT	1244	12778104	12778558	2.5	RNASEH2A	chr19	+	-96	NM_006397
D3A_WT	1243	12776034	12776273	2.12	RNASEH2A	chr19	+	-2274	NM_006397
D3A_WT	417	65244690	65244814	2.03	RNASEH2C	chr11	-	233	NM_032193
D3A_WT	946	6859288	6859557	2.25	RNASEK	chr17	+	2901	NM_001004333
D3A_WT	2159	167290701	167290845	2.01	RNASET2	chr6	-	-706	NM_003730
D3A_WT	1789	49699702	49699851	2.06	RNF123	chr3	+	-2217	NM_022064
D3A_WT	1147	617819	618148	2.04	RNF126	chr19	-	-3756	NM_194460
D3A_WT	977	26322212	26322461	2.59	RNF135	chr17	+	255	NM_032322
D3A_WT	1996	54866349	54866478	2.16	RNF138P1	chr5	-	-286	NR_001575
D3A_WT	2135	127629723	127630269	3.28	RNF146	chr6	+	284	NM_030963
D3A_WT	1938	142273161	142273300	2.2	RNF150	chr4	-	836	NM_020724
D3A_WT	916	87300544	87300673	2.46	RNF166	chr16	-	-307	NM_178841
D3A_WT	2339	42871290	42872440	3.63	RNF170	chr8	-	-842	NM_001160224
D3A_WT	642	23686921	23687170	2.51	RNF31	chr14	+	547	NM_017999
D3A_WT	2044	175894047	175894176	2.69	RNF44	chr5	-	2916	NM_014901
D3A_WT	553	115660021	115660485	2.51	RNFT2	chr12	+	-225	NM_032814
D3A_WT	821	2257723	2258562	2.36	RNPS1	chr16	-	-27	NM_080594
D3A_WT	821	2257723	2258562	2.36	RNPS1	chr16	-	-344	NM_006711
D3A_WT	159	154290347	154290889	3.26	ROBLD3	chr1	+	-522	NM_001145264
D3A_WT	151	150077298	150077737	2.87	RORC	chr1	-	-6545	NM_005060
D3A_WT	2326	10555152	10555297	2.09	RP1L1	chr8	-	-5197	NM_178857
D3A_WT	2220	33115429	33115693	2.32	RP9	chr7	-	-34	NM_203288
D3A_WT	931	205209	205458	2.82	RPH3AL	chr17	-	-2757	NM_006987
D3A_WT	1216	5638732	5638896	2.43	RPL36	chr19	+	-2457	NM_033643
D3A_WT	1216	5638732	5638896	2.43	RPL36	chr19	+	-2531	NM_015414
D3A_WT	2407	145994800	145995319	2.4	RPL8	chr8	-	-6526	NM_033301
D3A_WT	2407	145994800	145995319	2.4	RPL8	chr8	-	-6450	NM_000973
D3A_WT	1007	42411119	42411458	2.52	RPRML	chr17	-	325	NM_203400
D3A_WT	1168	1382757	1384504	3.58	RPS15	chr19	+	-5732	NM_001018
D3A_WT	2157	166960436	166960665	2.29	RPS6KA2	chr6	-	166	NM_021135
D3A_WT	798	778442	779106	3.44	RPUSD1	chr16	-	-390	NM_058192
D3A_WT	799	780852	783152	2.87	RPUSD1	chr16	-	-3618	NM_058192
D3A_WT	99	39097742	39097881	2.16	RRAGC	chr1	-	116	NM_022157
D3A_WT	371	4072206	4072463	2.42	RRM1	chr11	+	-165	NM_001033
D3A_WT	1017	45911157	45911386	2.09	RSAD1	chr17	+	83	NM_018346
D3A_WT	686	100418281	100418530	2.69	RTL1	chr14	-	2532	NM_001134888
D3A_WT	1325	50693125	50694289	2.67	RTN2	chr19	-	-1554	NM_206900
D3A_WT	1325	50693125	50694289	2.67	RTN2	chr19	-	-5393	NM_206901

D3A_WT	1325	50693125	50694289	2.67	RTN2	chr19	-	-1556	NM_005619
D3A_WT	1671	18635996	18636310	2.71	RTN4R	chr22	-	-337	NM_023004
D3A_WT	1827	135452107	135452246	2.41	RYK	chr3	-	100	NM_002958
D3A_WT	1215	5573466	5574815	3.12	SAFB	chr19	+	-23	NM_002967
D3A_WT	1215	5573466	5574815	3.12	SAFB2	chr19	-	-202	NM_014649
D3A_WT	1252	14061592	14062338	3.3	SAMD1	chr19	-	267	NM_138352
D3A_WT	1304	44524767	44525318	2.4	SAMD4B	chr19	+	95	NM_018028
D3A_WT	1727	42678960	42679389	2.13	SAMM50	chr22	+	-3419	NM_015380
D3A_WT	1463	128501272	128501686	2.77	SAP130	chr2	-	-140	NM_024545
D3A_WT	1366	60462119	60462493	2.27	SAPS1	chr19	-	-456	NM_014931
D3A_WT	249	71600089	71600413	2.52	SAR1A	chr10	-	40	NM_020150
D3A_WT	547	107482098	107482251	2	SART3	chr12	-	-2879	NM_014706
D3A_WT	1767	18441479	18442619	3.43	SATB1	chr3	-	-216	NM_002971
D3A_WT	1751	49259611	49260562	2.52	SBF1	chr22	-	244	NM_002972
D3A_WT	991	37228239	37228463	2.31	SC65	chr17	-	-6374	NM_006455
D3A_WT	754	72957598	72958074	3.06	SCAMP2	chr15	-	-5113	NM_005697
D3A_WT	1178	1858670	1858819	2.72	SCAMP4	chr19	+	2372	NM_079834
D3A_WT	2082	28663814	28664367	2.98	SCAND3	chr6	-	-999	NM_052923
D3A_WT	1783	47492365	47492529	2.47	SCAP	chr3	-	2	NM_012235
D3A_WT	2550	20069852	20070224	3.49	SCARNA9L	chrX	-	-5586	NR_023358
D3A_WT	218	244954229	244954558	2.81	SCCPDH	chr1	+	393	NM_016002
D3A_WT	2064	179954297	179954914	3.16	SCGB3A1	chr5	-	-3512	NM_052863
D3A_WT	1289	39780656	39780805	2.58	SCGBL	chr19	-	-3400	NM_001025591
D3A_WT	12	1209593	1210457	4.34	SCNN1D	chr1	+	2587	NM_002978
D3A_WT	12	1209593	1210457	4.34	SCNN1D	chr1	+	2674	NM_001130413
D3A_WT	1753	49310843	49311477	3.22	SCO2	chr22	-	-260	NM_005138
D3A_WT	1937	141484478	141484814	2.36	SCOC	chr4	+	582	NM_001153690
D3A_WT	1937	141484478	141484814	2.36	SCOC	chr4	+	600	NM_001153635
D3A_WT	2392	144975136	144977685	2.85	SCRIB	chr8	-	-6873	NM_015356
D3A_WT	326	618385	618804	3.37	SCT	chr11	-	-1421	NM_021920
D3A_WT	1723	42067840	42068802	2.53	SCUBE1	chr22	-	978	NM_173050
D3A_WT	1918	77130969	77131143	2.15	SDAD1	chr4	-	81	NM_018115
D3A_WT	10	1162629	1164255	2.21	SDF4	chr1	-	-6132	NM_016176
D3A_WT	404	60954055	60954419	2.65	SDHAF2	chr11	+	65	NM_017841
D3A_WT	1040	69152450	69152684	3.15	SDK2	chr17	-	-745	NM_001144952
D3A_WT	1123	54958335	54958579	2.02	SEC11C	chr18	+	353	NM_033280
D3A_WT	1694	29195958	29196107	2.75	SEC14L3	chr22	-	2002	NM_174975
D3A_WT	2515	138497330	138497983	3.11	SEC16A	chr9	-	-328	NM_014866
D3A_WT	1838	171167492	171167756	2.94	SEC62	chr3	+	351	NM_003262
D3A_WT	2124	108385531	108385680	3.38	SEC63	chr6	-	570	NM_007214
D3A_WT	2444	91115466	91116491	4.36	SECISBP2	chr9	+	-7253	NM_024077
D3A_WT	1548	13923870	13924144	2.26	SEL1L2	chr20	-	-4745	NM_025229
D3A_WT	1696	29833321	29833770	2.79	SELM	chr22	-	6	NM_080430
D3A_WT	1791	50272433	50273080	3.28	SEMA3B	chr3	+	-7287	NM_004636
D3A_WT	275	102719542	102719716	2.32	SEMA4G	chr10	+	-2646	NM_017893
D3A_WT	1209	4507236	4507655	2.87	SEMA6B	chr19	-	2058	NM_032108
D3A_WT	1847	186786549	186787306	2.65	SENP2	chr3	+	203	NM_021627

D3A_WT	1833	151746656	151747175	3.41	SERP1	chr3	-	203	NM_014445
D3A_WT	677	94055334	94056103	3.72	SERPINA12	chr14	-	-1784	NM_173850
D3A_WT	84	28458693	28459467	2.79	SESN2	chr1	+	488	NM_031459
D3A_WT	1781	47179907	47180771	3.35	SETD2	chr3	-	132	NM_014159
D3A_WT	2113	89883987	89884612	2.75	SFRS13B	chr6	-	220	NM_080743
D3A_WT	1619	32026416	32026550	2.3	SFRS15	chr21	-	-181	NM_001145444
D3A_WT	1053	72244201	72244435	2.1	SFRS2	chr17	-	689	NM_003016
D3A_WT	648	36052191	36052355	2.3	SFTA3	chr14	-	468	NM_001101341
D3A_WT	278	104464000	104464149	2.29	SFXN2	chr10	+	-213	NM_178858
D3A_WT	1430	73152404	73152943	2.58	SFXN5	chr2	-	-200	NM_144579
D3A_WT	1835	155321889	155322045	2.63	SGEF	chr3	+	129	NM_015595
D3A_WT	2139	134537805	134537949	2.34	SGK1	chr6	-	-150	NM_005627
D3A_WT	2139	134537805	134537949	2.34	SGK1	chr6	-	886	NM_001143678
D3A_WT	2139	134537805	134537949	2.34	SGK1	chr6	-	2826	NM_001143677
D3A_WT	245	52052546	52053126	2.48	SGMS1	chr10	-	907	NM_147156
D3A_WT	1929	108965400	108966029	2.43	SGMS2	chr4	+	545	NM_001136258
D3A_WT	1063	75809146	75809599	2.93	SGSH	chr17	-	-578	NM_000199
D3A_WT	1688	23532154	23532437	2.46	SGSM1	chr22	+	160	NM_001098498
D3A_WT	551	110328069	110328490	3.3	SH2B3	chr12	+	145	NM_005475
D3A_WT	261	82285666	82286005	2.15	SH2D4B	chr10	+	-4719	NM_001145719
D3A_WT	261	82285666	82286005	2.15	SH2D4B	chr10	+	-1802	NM_207372
D3A_WT	1766	15355191	15355920	2.62	SH3BP5	chr3	-	2350	NM_001018009
D3A_WT	1766	15355191	15355920	2.62	SH3BP5	chr3	-	-6447	NM_004844
D3A_WT	1755	49459528	49460154	2.08	SHANK3	chr22	+	-94	NM_001080420
D3A_WT	2399	145237592	145238931	2.98	SHARPIN	chr8	-	-7133	NM_030974
D3A_WT	2398	145235287	145235736	2.21	SHARPIN	chr8	-	-4383	NM_030974
D3A_WT	2424	38058043	38058187	2.35	SHB	chr9	-	1095	NM_003028
D3A_WT	2425	38063218	38063473	2.32	SHB	chr9	-	-4135	NM_003028
D3A_WT	1138	414832	415292	2.64	SHC2	chr19	-	-3066	NM_012435
D3A_WT	1784	48516589	48517048	2.63	SHISA5	chr3	-	-153	NM_016479
D3A_WT	2023	132189429	132189673	2.26	SHROOM1	chr5	-	350	NM_133456
D3A_WT	1834	151962468	151964108	2.79	SIAH2	chr3	-	665	NM_005067
D3A_WT	1633	43671296	43672013	2.51	SIK1	chr21	-	-224	NM_173354
D3A_WT	1626	36987882	36988431	2.76	SIM2	chr21	+	-5704	NM_005069
D3A_WT	654	60183710	60184174	3.2	SIX1	chr14	-	1966	NM_005982
D3A_WT	1417	45089642	45089776	2.67	SIX2	chr2	-	337	NM_016932
D3A_WT	584	20649101	20649355	2.65	SKA3	chr13	-	-487	NM_001166017
D3A_WT	1976	1164738	1165286	2.58	SLC12A7	chr5	-	160	NM_006598
D3A_WT	402	60475195	60476146	2.51	SLC15A3	chr11	-	163	NM_016582
D3A_WT	137	110740519	110740782	2.36	SLC16A4	chr1	-	-5491	NM_004696
D3A_WT	1710	36807010	36807254	2.67	SLC16A8	chr22	-	1984	NM_013356
D3A_WT	1590	61048617	61048789	2.03	SLC17A9	chr20	+	-5740	NM_022082
D3A_WT	384	35397495	35397724	3.42	SLC1A2	chr11	-	72	NM_004171
D3A_WT	1424	65069470	65070619	3.43	SLC1A4	chr2	+	85	NM_003038
D3A_WT	1424	65069470	65070619	3.43	SLC1A4	chr2	+	962	NM_001135581
D3A_WT	1256	14951359	14951913	2.69	SLC1A6	chr19	-	-6906	NM_005071
D3A_WT	1255	14943855	14944119	2.24	SLC1A6	chr19	-	743	NM_005071

D3A_WT	117	53384500	53384843	2.18	SLC1A7	chr1	-	-3794	NM_006671
D3A_WT	411	64077321	64077465	2.24	SLC22A11	chr11	+	-2280	NM_018484
D3A_WT	414	64108089	64108358	2.82	SLC22A12	chr11	+	-6634	NM_144585
D3A_WT	2154	160689442	160689791	2.47	SLC22A3	chr6	+	202	NM_021977
D3A_WT	2025	138743880	138744449	3.19	SLC23A1	chr5	-	2774	NM_152685
D3A_WT	1550	19140893	19142666	3.21	SLC24A3	chr20	+	490	NM_020689
D3A_WT	674	91859511	91860240	2.88	SLC24A4	chr14	+	1198	NM_153648
D3A_WT	674	91859511	91860240	2.88	SLC24A4	chr14	+	-79	NM_153647
D3A_WT	1077	77289622	77289761	2.46	SLC25A10	chr17	+	-84	NM_012140
D3A_WT	1078	77291991	77292370	3.94	SLC25A10	chr17	+	2405	NM_012140
D3A_WT	1220	6415665	6415804	2.03	SLC25A23	chr19	-	-4953	NM_024103
D3A_WT	130	108544289	108544563	2.9	SLC25A24	chr1	-	71	NM_013386
D3A_WT	1828	142143991	142144130	2.95	SLC25A36	chr3	+	709	NM_018155
D3A_WT	2334	23442446	23442675	2.92	SLC25A37	chr8	+	253	NM_016612
D3A_WT	2537	1474896	1475440	2.87	SLC25A6	chrX	-	-4129	NM_001636
D3A_WT	2536	1470798	1471512	3.16	SLC25A6	chrX	-	-116	NM_001636
D3A_WT	1063	75809146	75809599	2.93	SLC26A11	chr17	+	578	NM_001166349
D3A_WT	2035	149320567	149321532	3.31	SLC26A2	chr5	+	557	NM_000112
D3A_WT	1263	17442447	17442906	3.27	SLC27A1	chr19	+	377	NM_198580
D3A_WT	2484	130142660	130142909	3.07	SLC27A4	chr9	+	124	NM_005094
D3A_WT	424	65895689	65895838	2.22	SLC29A2	chr11	-	104	NM_001532
D3A_WT	1603	61834153	61834408	3.47	SLC2A4RG	chr20	+	-7374	NM_020062
D3A_WT	2480	129199508	129199963	2.18	SLC2A8	chr9	+	450	NM_014580
D3A_WT	192	218167960	218168514	3.39	SLC30A10	chr1	-	379	NM_018713
D3A_WT	2566	48659386	48661113	2.49	SLC35A2	chrX	-	-6070	NM_001042498
D3A_WT	2566	48659386	48661113	2.49	SLC35A2	chrX	-	-6372	NM_001032289
D3A_WT	2566	48659386	48661113	2.49	SLC35A2	chrX	-	-6388	NM_005660
D3A_WT	391	45782585	45782849	2.88	SLC35C1	chr11	+	519	NM_001145266
D3A_WT	391	45782585	45782849	2.88	SLC35C1	chr11	+	-499	NM_018389
D3A_WT	1259	16543955	16545202	2.67	SLC35E1	chr19	-	-385	NM_024881
D3A_WT	448	92570447	92570611	2.06	SLC36A4	chr11	-	214	NM_152313
D3A_WT	2286	139744671	139744950	2.36	SLC37A3	chr7	-	-30	NM_032295
D3A_WT	1070	76889128	76889507	2.5	SLC38A10	chr17	-	-5626	NM_001037984
D3A_WT	2403	145609915	145611495	4.45	SLC39A4	chr8	-	2020	NM_017767
D3A_WT	2403	145609915	145611495	4.45	SLC39A4	chr8	-	2376	NM_130849
D3A_WT	1991	34021436	34021993	2.68	SLC45A2	chr5	-	-1177	NM_016180
D3A_WT	863	31404461	31404780	2.1	SLC5A2	chr16	+	2681	NM_003041
D3A_WT	136	110494946	110495090	2.76	SLC6A17	chr1	+	364	NM_001010898
D3A_WT	890	66856168	66856297	2.39	SLC7A6	chr16	+	309	NM_003983
D3A_WT	1969	583933	584380	2.57	SLC9A3	chr5	-	-6607	NM_004174
D3A_WT	817	2016852	2017501	2.69	SLC9A3R2	chr16	+	288	NM_004785
D3A_WT	884	65840033	65840781	2.35	SLC9A5	chr16	+	52	NM_004594
D3A_WT	611	83351431	83351995	3.09	SLITRK1	chr13	-	2816	NM_052910
D3A_WT	283	105714690	105714825	2.92	SLK	chr10	+	-2702	NM_014720
D3A_WT	1939	146622420	146622549	2.31	SMAD1	chr4	+	84	NM_005900
D3A_WT	1939	146622420	146622549	2.31	SMAD1	chr4	+	-922	NM_001003688
D3A_WT	1116	43711158	43711502	2.97	SMAD2	chr18	-	183	NM_001135937

D3A_WT	1116	43711158	43711502	2.97	SMAD2	chr18	-	180	NM_001003652
D3A_WT	1116	43711158	43711502	2.97	SMAD2	chr18	-	-406	NM_005901
D3A_WT	746	64782739	64783008	2.27	SMAD6	chr15	+	-5110	NM_001142861
D3A_WT	746	64782739	64783008	2.27	SMAD6	chr15	+	1146	NM_005585
D3A_WT	2298	150604248	150605413	2.48	SMARCD3	chr7	-	-77	NM_001003802
D3A_WT	2298	150604248	150605413	2.48	SMARCD3	chr7	-	334	NM_003078
D3A_WT	2436	72063549	72063868	2.68	SMC5	chr9	+	11	NM_015110
D3A_WT	1400	17798244	17798918	2.66	SMC6	chr2	-	-4	NM_024624
D3A_WT	1712	38228351	38228500	2.01	SMCR7L	chr22	+	196	NM_019008
D3A_WT	672	91046457	91046901	2.66	SMEK1	chr14	-	-282	NM_032560
D3A_WT	2128	109868626	109869075	3.73	SMPD2	chr6	+	227	NM_003080
D3A_WT	1566	48032841	48033090	2.88	SNAI1	chr20	+	32	NM_005985
D3A_WT	2045	175989985	175990249	2.78	SNCB	chr5	-	46	NM_003085
D3A_WT	985	34014924	34015083	2.38	SNIP	chr17	-	706	NM_025248
D3A_WT	844	11669646	11670671	2.22	SNN	chr16	+	357	NM_003498
D3A_WT	2571	51826615	51829005	4.15	SNORA11D	chrX	-	-4501	NR_003711
D3A_WT	274	101984444	101984605	2.35	SNORA12	chr10	-	2525	NR_002954
D3A_WT	692	102869978	102871320	2.37	SNORA28	chr14	+	-3289	NR_002964
D3A_WT	2614	153644318	153644462	2.83	SNORA36A	chrX	+	-5606	NR_002969
D3A_WT	2006	76408843	76409312	2.53	SNORA47	chr5	-	3075	NR_003014
D3A_WT	2228	44992585	44993144	4.34	SNORA9	chr7	-	-1230	NR_002952
D3A_WT	1338	54280511	54280931	2.98	SNRNP70	chr19	+	445	NM_003089
D3A_WT	777	99652633	99652782	3.34	SNRPA1	chr15	-	276	NM_003090
D3A_WT	2367	121892183	121893104	3.08	SNTB1	chr8	-	847	NM_021021
D3A_WT	2109	86360200	86360429	2.36	SNX14	chr6	-	34	NM_020468
D3A_WT	1955	186361897	186362550	3.33	SNX25	chr4	+	-6054	NM_031953
D3A_WT	2126	108688723	108689067	3.16	SNX3	chr6	-	262	NM_152827
D3A_WT	419	65358514	65358768	2.46	SNX32	chr11	+	656	NM_152760
D3A_WT	2122	107918387	107919441	2.78	SOBP	chr6	+	905	NM_018013
D3A_WT	538	92487959	92488678	3.3	SOCS2	chr12	+	590	NM_003877
D3A_WT	539	92489830	92490089	2.39	SOCS2	chr12	+	2231	NM_003877
D3A_WT	1618	31954130	31954454	3.67	SOD1	chr21	+	487	NM_000454
D3A_WT	1902	24406673	24407110	2.55	SOD3	chr4	+	709	NM_003102
D3A_WT	2332	22464826	22464970	2.97	SORBS3	chr8	+	-297	NM_005775
D3A_WT	624	111770444	111770873	2.77	SOX1	chr13	+	745	NM_005986
D3A_WT	2343	55532850	55533502	2.92	SOX17	chr8	+	129	NM_022454
D3A_WT	1841	182913242	182913496	2.46	SOX2	chr3	+	954	NM_003106
D3A_WT	2597	139413794	139414573	2.59	SOX3	chrX	-	708	NM_005634
D3A_WT	2078	21703783	21704127	3.3	SOX4	chr6	+	2005	NM_003107
D3A_WT	2327	10628125	10628369	3.22	SOX7	chr8	-	-2815	NM_031439
D3A_WT	805	971920	972870	3.55	SOX8	chr16	+	587	NM_014587
D3A_WT	1038	67629381	67629535	2.25	SOX9	chr17	+	703	NM_000346
D3A_WT	521	52060172	52060395	2.66	SP1	chr12	+	38	NM_138473
D3A_WT	521	52060172	52060395	2.66	SP1	chr12	+	-411	NM_003109
D3A_WT	2210	20790761	20790910	2.56	SP8	chr7	-	2198	NM_182700
D3A_WT	2211	20791531	20792101	2.82	SP8	chr7	-	1217	NM_182700
D3A_WT	1481	174907650	174909892	2.72	SP9	chr2	+	705	NM_001145250

D3A_WT	979	28342328	28342472	2.49	SPACA3	chr17	+	-594	NM_173847
D3A_WT	191	215870797	215870946	2.05	SPATA17	chr1	+	-446	NM_138796
D3A_WT	66	16639978	16640137	2.14	SPATA21	chr1	-	-3551	NM_198546
D3A_WT	737	43482664	43483123	2.87	SPATA5L1	chr15	+	1083	NM_024063
D3A_WT	2103	44418385	44418514	2.14	SPATS1	chr6	+	75	NM_145026
D3A_WT	1106	12647880	12648299	2.05	SPIRE1	chr18	-	-177	NM_020148
D3A_WT	1106	12647880	12648299	2.05	SPIRE1	chr18	-	-1358	NM_001128627
D3A_WT	926	88422222	88422871	2.33	SPIRE2	chr16	+	139	NM_032451
D3A_WT	940	4351613	4351771	2.01	SPNS2	chr17	+	2815	NM_001124758
D3A_WT	55	9274971	9275721	2.56	SPSB1	chr1	+	-181	NM_025106
D3A_WT	56	9276296	9277120	2.96	SPSB1	chr1	+	1181	NM_025106
D3A_WT	814	1777229	1778648	3.23	SPSB3	chr16	-	-5356	NM_080861
D3A_WT	2100	43247124	43248052	2.85	SRF	chr6	+	691	NM_003131
D3A_WT	530	62524023	62524487	2.91	SRGAP1	chr12	+	-552	NM_020762
D3A_WT	1598	61650934	61651164	2.84	SRMS	chr20	-	-1748	NM_080823
D3A_WT	2604	152702234	152702358	2.07	SRPK3	chrX	+	2593	NM_014370
D3A_WT	2259	100310677	100311337	3.07	SRRT	chr7	+	371	NM_015908
D3A_WT	1538	581764	582192	2.74	SRXN1	chr20	-	-88	NM_080725
D3A_WT	1581	60151957	60152601	2.4	SS18L1	chr20	+	63	NM_198935
D3A_WT	1477	170363640	170363889	2.62	SSB	chr2	+	130	NM_003142
D3A_WT	1369	60686420	60686879	2.34	SSC5D	chr19	+	-5032	NM_001144950
D3A_WT	1370	60690828	60692293	3.42	SSC5D	chr19	+	-121	NM_001144950
D3A_WT	427	66824654	66825678	2.93	SSH3	chr11	+	-2328	NM_017857
D3A_WT	806	1071702	1072132	2.88	SSTR5	chr16	+	3136	NM_001053
D3A_WT	1715	39582849	39583398	3.28	ST13	chr22	-	-490	NM_003932
D3A_WT	1052	72092854	72094103	2.79	ST6GALNAC2	chr17	-	262	NM_006456
D3A_WT	2482	129701694	129701828	3.02	ST6GALNAC6	chr9	-	-69	NM_013443
D3A_WT	772	90736962	90739226	3.18	ST8SIA2	chr15	+	-49	NM_006011
D3A_WT	762	79403524	79403673	2.3	STARD5	chr15	-	-19	NM_181900
D3A_WT	1119	50137943	50138222	2.41	STARD6	chr18	-	-3141	NM_139171
D3A_WT	994	37793566	37793780	2.7	STAT3	chr17	-	366	NM_139276
D3A_WT	994	37793566	37793780	2.7	STAT3	chr17	-	258	NM_213662
D3A_WT	1459	119697153	119698202	2.15	STEAP3	chr2	+	-176	NM_182915
D3A_WT	1905	26471541	26472557	3.35	STIM2	chr4	+	588	NM_020860
D3A_WT	2040	171547496	171547645	2.37	STK10	chr5	-	381	NM_005990
D3A_WT	1160	1157623	1158348	2.73	STK11	chr19	+	1188	NM_000455
D3A_WT	1476	168811366	168812412	3.25	STK39	chr2	-	462	NM_013233
D3A_WT	1953	185063837	185065185	2.4	STOX2	chr4	+	1009	NM_020225
D3A_WT	794	662497	663146	3.17	STUB1	chr16	+	-7294	NM_005861
D3A_WT	1249	13125321	13125445	2.9	STX10	chr19	-	-3396	NM_003765
D3A_WT	568	129889280	129889529	2.84	STX2	chr12	-	360	NM_001980
D3A_WT	645	24589061	24589284	2.17	STXBP6	chr14	-	-237	NM_014178
D3A_WT	599	47472945	47473074	2.53	SUCLA2	chr13	-	454	NM_003850
D3A_WT	556	117298950	117299099	2.72	SUDS3	chr12	+	284	NM_022491
D3A_WT	858	28532476	28532895	2.51	SULT1A1	chr16	-	-4535	NM_177534
D3A_WT	858	28532476	28532895	2.51	SULT1A1	chr16	-	-3827	NM_177529
D3A_WT	1726	42589436	42590165	3.09	SULT4A1	chr22	-	-89	NM_014351

D3A_WT	1047	70690077	70690441	2.09	SUMO2	chr17	-	434	NM_001005849
D3A_WT	526	54676732	54676961	2.66	SUOX	chr12	+	-463	NM_001032387
D3A_WT	2464	113977093	113977337	2.21	SUSD1	chr9	-	162	NM_022486
D3A_WT	1687	22904057	22904192	2.14	SUSD2	chr22	+	-3319	NM_019601
D3A_WT	894	75785137	75785591	2.34	SYCE1L	chr16	+	-5485	NM_001129979
D3A_WT	2563	47370977	47371126	2.81	SYN1	chrX	-	-6851	NM_006950
D3A_WT	1760	12022298	12022432	3.15	SYN2	chr3	+	1504	NM_133625
D3A_WT	2110	86410106	86410656	2.96	SYNCRIP	chr6	-	-1022	NM_001159673
D3A_WT	2110	86410106	86410656	2.96	SYNCRIP	chr6	-	-619	NM_001159677
D3A_WT	2110	86410106	86410656	2.96	SYNCRIP	chr6	-	-1054	NM_001159674
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D3A_WT	133	109810749	109811290	2.63	SYPL2	chr1	+	397	NM_001040709
D3A_WT	1365	60389358	60389583	2.32	SYT5	chr19	-	-5938	NM_003180
D3A_WT	1877	1691498	1692457	2.29	TACC3	chr4	+	-1086	NM_006342
D3A_WT	248	70849404	70849970	3.05	TACR2	chr10	-	-3007	NM_001057
D3A_WT	206	227828051	227828293	2.43	TAF5L	chr1	-	245	NM_014409
D3A_WT	328	737657	737906	2.02	TALDO1	chr11	+	350	NM_006755
D3A_WT	556	117298950	117299099	2.72	TAOK3	chr12	-	-3891	NM_016281
D3A_WT	2088	33393371	33393816	2.51	TAPBP	chr6	-	-3451	NM_172209
D3A_WT	937	3518643	3519077	2.2	TAX1BP3	chr17	-	-138	NM_014604
D3A_WT	1344	55071648	55071812	2.78	TBC1D17	chr19	+	-763	NM_001168222
D3A_WT	822	2457718	2457981	2.25	TBC1D24	chr16	+	-7298	NM_020705
D3A_WT	823	2465432	2465661	2.4	TBC1D24	chr16	+	399	NM_020705
D3A_WT	606	74953781	74954400	3.26	TBC1D4	chr13	-	161	NM_014832
D3A_WT	2056	179267182	179267615	2.58	TBC1D9B	chr5	-	64	NM_015043
D3A_WT	1093	78302128	78302705	3.29	TBCD	chr17	+	-812	NM_005993
D3A_WT	2547	9393594	9394643	3.39	TBL1X	chrX	+	918	NM_005647
D3A_WT	2547	9393594	9394643	3.39	TBL1X	chrX	+	2784	NM_001139466
D3A_WT	1839	178404285	178404734	2.32	TBL1XR1	chr3	-	-6767	NM_024665
D3A_WT	2169	170703904	170704068	2.33	TBP	chr6	+	-1409	NM_003194
D3A_WT	2108	85530425	85530589	2.67	TBX18	chr6	-	111	NM_001080508
D3A_WT	1027	56829273	56829402	2.87	TBX2	chr17	+	-2701	NM_005994
D3A_WT	1028	56886895	56887064	2.55	TBX4	chr17	+	-1609	NM_018488
D3A_WT	673	91372244	91372698	2.31	TC2N	chr14	-	131	NM_152332
D3A_WT	1115	42812873	42813156	2.3	TCEB3B	chr18	-	2972	NM_016427
D3A_WT	1115	42812873	42813156	2.3	TCEB3C	chr18	-	-2567	NM_145653
D3A_WT	1115	42812873	42813156	2.3	TCEB3CL	chr18	-	-2803	NM_001100817
D3A_WT	301	133005668	133005803	2.09	TCERG1L	chr10	-	-5761	NM_174937
D3A_WT	290	114701819	114702283	2.23	TCF7L2	chr10	+	2053	NM_001146285
D3A_WT	430	67565389	67566568	3.67	TCIRG1	chr11	+	-1044	NM_006053
D3A_WT	430	67565389	67566568	3.67	TCIRG1	chr11	+	2920	NM_006019
D3A_WT	291	115929228	115929362	2.42	TDRD1	chr10	+	277	NM_198795
D3A_WT	605	59869508	59870057	2.81	TDRD3	chr13	+	355	NM_001146070
D3A_WT	605	59869508	59870057	2.81	TDRD3	chr13	+	1191	NM_030794
D3A_WT	173	177827581	177827923	3.05	TDRD5	chr1	+	105	NM_173533
D3A_WT	2456	99214454	99214593	2.19	TDRD7	chr9	+	401	NM_014290
D3A_WT	2091	35572124	35572560	2.46	TEAD3	chr6	-	497	NM_003214

D3A_WT	1440	94902882	94903116	2.16	TEKT4	chr2	+	2041	NM_144705
D3A_WT	812	1483300	1483619	2.7	TELO2	chr16	+	107	NM_016111
D3A_WT	109	45731326	45731654	2.4	TESK2	chr1	-	-2063	NM_007170
D3A_WT	827	2788650	2789080	2.36	TESSP1	chr16	+	379	NM_001135086
D3A_WT	2072	10527421	10527835	2.52	TFAP2A	chr6	-	-4172	NM_003220
D3A_WT	2072	10527421	10527835	2.52	TFAP2A	chr6	-	-7035	NM_001032280
D3A_WT	2072	10527421	10527835	2.52	TFAP2A	chr6	-	155	NM_001042425
D3A_WT	1574	54634668	54634917	2.6	TFAP2C	chr20	+	-2972	NM_003222
D3A_WT	634	113286568	113287529	3.15	TFDP1	chr13	+	45	NR_026580
D3A_WT	634	113286568	113287529	3.15	TFDP1	chr13	+	-8	NM_007111
D3A_WT	2568	48787783	48787961	3.08	TFE3	chrX	-	62	NM_006521
D3A_WT	1359	59318017	59318366	2.43	TFPT	chr19	-	-7324	NM_013342
D3A_WT	612	94052287	94052511	2.16	TGDS	chr13	-	-5887	NM_014305
D3A_WT	2457	100907443	100907587	2.62	TGFBR1	chr9	+	283	NM_001130916
D3A_WT	1529	242224706	242226417	3.5	THAP4	chr2	-	-163	NM_015963
D3A_WT	1137	330706	330836	2.26	THEG	chr19	-	-3762	NM_199202
D3A_WT	1845	185580844	185581398	2.51	THPO	chr3	-	-2495	NM_000460
D3A_WT	462	118798472	118798846	2.51	THY1	chr11	-	797	NM_006288
D3A_WT	1617	31853365	31853614	2.35	TIAM1	chr21	-	-328	NM_003253
D3A_WT	1189	2375088	2375922	2.56	TIMM13	chr19	-	3370	NM_012458
D3A_WT	2565	48643998	48644661	2.11	TIMM17B	chrX	-	-3959	NM_005834
D3A_WT	2435	70978603	70978882	2.27	TJP2	chr9	+	-166	NM_201629
D3A_WT	1193	2982055	2982175	2.38	TLE2	chr19	-	-1950	NM_003260
D3A_WT	1193	2982055	2982175	2.38	TLE2	chr19	-	-1503	NM_001144762
D3A_WT	748	68178273	68179421	2.22	TLE3	chr15	-	-1537	NM_020908
D3A_WT	2458	102274842	102276717	2.59	TMEFF1	chr9	+	242	NM_003692
D3A_WT	1043	70283969	70284123	2.69	TMEM104	chr17	+	-170	NM_017728
D3A_WT	1800	52906443	52906692	2.65	TMEM110	chr3	-	20	NM_198563
D3A_WT	506	42516090	42516319	2.85	TMEM117	chr12	+	-24	NM_032256
D3A_WT	710	105065125	105066779	2.79	TMEM121	chr14	+	1955	NM_025268
D3A_WT	1877	1691498	1692457	2.29	TMEM129	chr4	-	905	NM_001127266
D3A_WT	422	65816350	65817199	2.46	TMEM151A	chr11	+	826	NM_153266
D3A_WT	1775	45241862	45242812	3.51	TMEM158	chr3	-	481	NM_015444
D3A_WT	2592	109132400	109132778	2.53	TMEM164	chrX	+	-408	NM_032227
D3A_WT	2592	109132400	109132778	2.53	TMEM164	chrX	+	71	NM_017698
D3A_WT	2151	158877974	158878119	2.09	TMEM181	chr6	+	591	NM_020823
D3A_WT	1567	48203568	48204422	3.71	TMEM189	chr20	-	-253	NM_199129
D3A_WT	1567	48203568	48204422	3.71	TMEM189-UBE2V1	chr20	-	-253	NM_199203
D3A_WT	1494	220118366	220121700	4.54	TMEM198	chr2	+	3045	NM_001005209
D3A_WT	974	23708354	23708603	2.6	TMEM199	chr17	+	-335	NM_152464
D3A_WT	2437	73573341	73574495	2.77	TMEM2	chr9	-	-298	NM_001135820
D3A_WT	1100	5880626	5881170	2.29	TMEM200C	chr18	-	1205	NM_001080209
D3A_WT	466	123258953	123259229	2.14	TMEM225	chr11	-	2459	NM_001013743
D3A_WT	2274	123459928	123460867	3.1	TMEM229A	chr7	-	362	NM_001136002
D3A_WT	658	67051959	67052138	2.25	TMEM229B	chr14	-	-274	NM_182526
D3A_WT	655	60816980	60817434	3.09	TMEM30B	chr14	-	1076	NM_001017970
D3A_WT	1460	119905456	119905914	2.35	TMEM37	chr2	+	-230	NM_183240

D3A_WT	1260	16633010	16633249	2.68	TMEM38A	chr19	+	192	NM_024074
D3A_WT	2358	91727548	91727892	2.78	TMEM64	chr8	-	-411	NM_001146273
D3A_WT	327	684680	685544	2.15	TMEM80	chr11	+	-503	NM_174940
D3A_WT	64	15943509	15944123	3.01	TMEM82	chr1	+	2313	NM_001013641
D3A_WT	937	3518643	3519077	2.2	TMEM93	chr17	+	22	NM_031298
D3A_WT	1205	4256123	4256755	2.74	TMIGD2	chr19	-	-3011	NM_144615
D3A_WT	1706	35836454	35837198	2.47	TMPRSS6	chr22	-	-7187	NM_153609
D3A_WT	1547	7948087	7949074	2.94	TMX4	chr20	-	-187	NM_021156
D3A_WT	2141	138233454	138233933	2.29	TNFAIP3	chr6	+	3420	NM_006290
D3A_WT	48	6453355	6453690	2.86	TNFRSF25	chr1	-	-4680	NM_148970
D3A_WT	1601	61791100	61792019	3.38	TNFRSF6B	chr20	+	-5172	NM_032945
D3A_WT	1601	61791100	61792019	3.38	TNFRSF6B	chr20	+	-6905	NM_003823
D3A_WT	1221	6481642	6481776	2.48	TNFSF9	chr19	+	-300	NM_003811
D3A_WT	1883	2727582	2727716	2.17	TNIP2	chr4	-	-99	NM_001161527
D3A_WT	1883	2727582	2727716	2.17	TNIP2	chr4	-	252	NM_024309
D3A_WT	346	1818098	1819657	3.24	TNNI2	chr11	+	1583	NM_001145829
D3A_WT	346	1818098	1819657	3.24	TNNI2	chr11	+	2069	NM_003282
D3A_WT	346	1818098	1819657	3.24	TNNI2	chr11	+	870	NM_001145841
D3A_WT	347	1892427	1893662	3.37	TNNT3	chr11	+	-4330	NM_001042782
D3A_WT	149	149955637	149955776	2	TNRC4	chr1	-	208	NM_007185
D3A_WT	150	149960712	149960861	3.02	TNRC4	chr1	-	-4872	NM_007185
D3A_WT	334	1287386	1287735	2.74	TOLLIP	chr11	-	-145	NM_019009
D3A_WT	2359	96030480	96031327	3.46	TP53INP1	chr8	-	-112	NM_033285
D3A_WT	866	33113672	33113896	2.62	TP53TG3	chr16	+	1304	NM_016212
D3A_WT	866	33113672	33113896	2.62	TP53TG3B	chr16	+	2128	NM_001099687
D3A_WT	1604	61963624	61964563	2.91	TPD52L2	chr20	+	-2940	NM_199359
D3A_WT	37	3531845	3531969	2.11	TPRG1L	chr1	+	492	NM_182752
D3A_WT	951	7775287	7776027	2.5	TRAPPC1	chr17	-	385	NM_001166621
D3A_WT	951	7775287	7776027	2.5	TRAPPC1	chr17	-	335	NM_021210
D3A_WT	92	36394154	36395738	2.74	TRAPPC3	chr1	-	-7292	NM_014408
D3A_WT	2373	141536845	141536989	2.06	TRAPPC9	chr8	-	126	NM_001160372
D3A_WT	2373	141536845	141536989	2.06	TRAPPC9	chr8	-	943	NM_031466
D3A_WT	2369	126512566	126512695	2.05	TRIB1	chr8	+	886	NM_025195
D3A_WT	2368	126510679	126511218	3.75	TRIB1	chr8	+	-796	NM_025195
D3A_WT	1537	309907	310376	2.8	TRIB3	chr20	+	834	NM_021158
D3A_WT	140	114855027	114855654	2.68	TRIM33	chr1	-	-36	NM_033020
D3A_WT	2261	100516733	100517682	5.22	TRIM56	chr7	+	1702	NM_030961
D3A_WT	1768	32835070	32835314	2.02	TRIM71	chr3	+	679	NM_001039111
D3A_WT	1248	13090027	13090466	2.52	TRMT1	chr19	-	-1683	NM_001136035
D3A_WT	1248	13090027	13090466	2.52	TRMT1	chr19	-	-1783	NM_001142554
D3A_WT	1666	18484698	18485527	2.43	TRMT2A	chr22	-	-344	NM_022727
D3A_WT	1667	18490402	18490843	3.71	TRMT2A	chr22	-	-5854	NM_022727
D3A_WT	82	27193217	27193736	3.48	TRNP1	chr1	+	695	NM_001013642
D3A_WT	359	2406792	2407258	2.15	TRPM5	chr11	-	-6174	NM_014555
D3A_WT	2289	142298239	142298574	2.34	TRPV6	chr7	-	-4807	NM_018646
D3A_WT	597	44049405	44050254	3	TSC22D1	chr13	-	-1128	NM_183422
D3A_WT	2257	99918923	99919141	2.18	TSC22D4	chr7	-	-4194	NM_030935

D3A_WT	2375	143482371	143482500	2.01	TSNARE1	chr8	-	13	NM_145003
D3A_WT	260	82204451	82205081	2.82	TSPAN14	chr10	+	749	NM_001128309
D3A_WT	481	3056346	3056968	2.33	TSPAN9	chr12	+	-124	NM_001168320
D3A_WT	2628	9974079	9975173	3.08	TSPY3	chrY	+	-881	NM_001077697
D3A_WT	358	2378002	2378156	2.15	TSSC4	chr11	+	-2019	NM_005706
D3A_WT	1705	35744338	35744472	2.62	TST	chr22	-	1032	NM_003312
D3A_WT	457	112690646	112691071	3.03	TTC12	chr11	+	398	NM_017868
D3A_WT	2481	129517231	129517855	2.52	TTC16	chr9	+	-635	NM_144965
D3A_WT	8	1106165	1107205	3.67	TTLL10	chr1	+	1746	NM_153254
D3A_WT	2636	22997580	22997765	2.36	TTTY6	chrY	-	-678	NR_001527
D3A_WT	2636	22997580	22997765	2.36	TTTY6B	chrY	+	2545	NR_002175
D3A_WT	580	18654242	18654516	2.78	TUBA3C	chr13	-	-443	NM_006001
D3A_WT	927	88517157	88517301	2.71	TUBB3	chr16	+	-16	NM_006086
D3A_WT	1695	29695189	29695323	2.25	TUG1	chr22	+	-377	NR_002323
D3A_WT	2092	35594774	35595129	3.02	TULP1	chr6	-	-6326	NM_003322
D3A_WT	2419	25667969	25668188	2.12	TUSC1	chr9	-	778	NM_001004125
D3A_WT	1797	52248157	52248421	2.79	TWF2	chr3	-	-66	NM_007284
D3A_WT	1796	52246047	52246221	2.26	TWF2	chr3	-	2089	NM_007284
D3A_WT	116	52294710	52295079	3.23	TXNDC12	chr1	-	-1259	NM_015913
D3A_WT	142	144147945	144148515	3.38	TXNIP	chr1	+	-1588	NM_006472
D3A_WT	732	39638352	39638876	3.22	TYRO3	chr15	+	91	NM_006293
D3A_WT	169	160798146	160798430	2.37	UAP1	chr1	+	369	NM_003115
D3A_WT	1805	69212003	69212241	2.91	UBA3	chr3	-	92	NM_198195
D3A_WT	11	1198699	1198928	2.98	UBE2J2	chr1	-	284	NM_058167
D3A_WT	120	64441878	64442132	2.85	UBE2U	chr1	+	-72	NM_152489
D3A_WT	1013	44340796	44341210	2.22	UBE2Z	chr17	+	238	NM_023079
D3A_WT	840	4837595	4838144	2.72	UBN1	chr16	+	-43	NM_001079514
D3A_WT	840	4837595	4838144	2.72	UBN1	chr16	+	-4208	NM_016936
D3A_WT	2440	85512593	85512752	2.4	UBQLN1	chr9	-	316	NM_053067
D3A_WT	159	154290347	154290889	3.26	UBQLN4	chr1	-	-478	NM_020131
D3A_WT	2346	59486407	59486874	2.8	UBXN2B	chr8	+	264	NM_001077619
D3A_WT	2501	133403277	133403402	2.21	UCK1	chr9	-	-6856	NM_031432
D3A_WT	439	73371409	73371553	2.11	UCP2	chr11	-	56	NM_003355
D3A_WT	2260	100327650	100331691	3.28	UFSP1	chr7	-	-4395	NM_001015072
D3A_WT	1212	4860244	4860869	2.9	UHRF1	chr19	+	47	NM_001048201
D3A_WT	1212	4860244	4860869	2.9	UHRF1	chr19	+	-1009	NM_013282
D3A_WT	572	130945662	130946497	3.27	ULK1	chr12	+	848	NM_003565
D3A_WT	967	19711545	19711774	2.4	ULK2	chr17	-	172	NM_014683
D3A_WT	753	72923025	72923494	2.8	ULK3	chr15	-	-654	NM_001099436
D3A_WT	975	23903573	23903702	2.2	UNC119	chr17	-	136	NM_005148
D3A_WT	559	119632713	119633162	2.41	UNC119B	chr12	+	724	NM_001080533
D3A_WT	981	30493024	30493188	2.28	UNC45B	chr17	+	-5842	NM_173167
D3A_WT	250	72640384	72640918	3.5	UNC5B	chr10	+	-1652	NM_170744
D3A_WT	2182	1240008	1240847	2.44	UNCX	chr7	+	1248	NM_001080461
D3A_WT	2181	1237006	1237155	2.31	UNCX	chr7	+	-2099	NM_001080461
D3A_WT	1051	71286749	71286978	2.25	UNK	chr17	+	-5412	NM_001080419
D3A_WT	206	227828051	227828293	2.43	URB2	chr1	+	-431	NM_014777

D3A_WT	1096	148295	148755	3.16	USP14	chr18	+	43	NM_001037334
D3A_WT	118	55453465	55453604	2.1	USP24	chr1	-	93	NM_015306
D3A_WT	460	113251261	113251610	2.87	USP28	chr11	-	31	NM_020886
D3A_WT	1378	62322221	62322375	2.17	USP29	chr19	+	-1022	NM_020903
D3A_WT	1056	74348328	74349157	3.03	USP36	chr17	-	-178	NM_025090
D3A_WT	738	48503703	48504027	2.38	USP8	chr15	+	-5	NM_005154
D3A_WT	2633	13320559	13320811	2.22	USP9Y	chrY	+	-1868	NM_004654
D3A_WT	592	30089722	30090787	3.15	USPL1	chr13	+	425	NM_005800
D3A_WT	1849	192530002	192530544	2.92	UTS2D	chr3	-	746	NM_198152
D3A_WT	2638	57622880	57624486	2.57	VAMP7	chrY	+	343	NM_001145149
D3A_WT	1577	56393461	56393630	2.36	VAPB	chr20	+	-4105	NM_004738
D3A_WT	838	4361733	4361982	2.85	VASN	chr16	+	8	NM_138440
D3A_WT	1326	50701914	50702603	2.38	VASP	chr19	+	-269	NM_003370
D3A_WT	895	76380291	76380555	2.33	VAT1L	chr16	+	440	NM_020927
D3A_WT	254	75427699	75428538	2.78	VCL	chr10	+	241	NM_003373
D3A_WT	315	134898869	134899338	2.67	VENTX	chr10	+	-2294	NM_014468
D3A_WT	1024	53420941	53421295	2.69	VEZF1	chr17	-	-504	NM_007146
D3A_WT	2262	100592719	100593956	3.34	VGF	chr7	-	2235	NM_003378
D3A_WT	233	17310604	17311459	2.84	VIM	chr10	+	768	NM_003380
D3A_WT	2317	158630690	158630899	2.68	VIPR2	chr7	-	-384	NM_003382
D3A_WT	2599	150316291	150316808	2.28	VMA21	chrX	+	235	NM_001017980
D3A_WT	1684	22423282	22423428	2.34	VPREB3	chr22	-	3275	NM_013378
D3A_WT	403	60685424	60685563	2.33	VPS37C	chr11	-	-1	NM_017966
D3A_WT	678	96333669	96333893	2.54	VRK1	chr14	+	345	NM_003384
D3A_WT	238	28862023	28862569	3.1	WAC	chr10	+	864	NR_024557
D3A_WT	238	28862023	28862569	3.1	WAC	chr10	+	-133	NM_100486
D3A_WT	2246	70234524	70235778	3.04	WBSCR17	chr7	+	-573	NM_022479
D3A_WT	602	51056077	51056496	2.73	WDFY2	chr13	+	-198	NM_052950
D3A_WT	2564	48341079	48342198	2.85	WDR13	chrX	+	815	NM_017883
D3A_WT	2564	48341079	48342198	2.85	WDR13	chrX	+	471	NM_001166426
D3A_WT	791	631593	632329	3.41	WDR90	chr16	+	-7402	NM_145294
D3A_WT	792	638583	639530	3.12	WDR90	chr16	+	-307	NM_145294
D3A_WT	1472	159850839	159851669	2.69	WDSUB1	chr2	-	95	NM_001128213
D3A_WT	1472	159850839	159851669	2.69	WDSUB1	chr2	-	55	NM_152528
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D3A_WT	2288	141048333	141048682	2.43	WEE2	chr7	+	-6114	NM_001105558
D3A_WT	790	623567	624646	2.56	WFIKKN1	chr16	+	3094	NM_053284
D3A_WT	1890	6322109	6322661	2.21	WFS1	chr4	+	-92	NM_006005
D3A_WT	1879	1842991	1843755	2.47	WHSC1	chr4	+	453	NM_001042424
D3A_WT	2337	38358825	38359587	2.18	WHSC1L1	chr8	-	-259	NM_023034
D3A_WT	476	732514	733368	2.27	WNK1	chr12	+	456	NM_018979
D3A_WT	446	75598876	75599697	2.89	WNT11	chr11	-	-4064	NM_004626
D3A_WT	1803	55499271	55499422	2.28	WNT5A	chr3	-	-2975	NM_003392
D3A_WT	1491	219432091	219433042	3.04	WNT6	chr2	+	-223	NM_006522
D3A_WT	1734	44753627	44753766	2.36	WNT7B	chr22	-	-2024	NM_058238
D3A_WT	1735	44754307	44755369	3.38	WNT7B	chr22	-	-3166	NM_058238
D3A_WT	944	5913678	5914512	2.09	WSCD1	chr17	+	-562	NM_015253

D3A_WT	2153	160068667	160068923	2.46	WTAP	chr6	+	654	NM_004906
D3A_WT	2153	160068667	160068923	2.46	WTAP	chr6	+	186	NM_152857
D3A_WT	2548	9942640	9943464	2.37	WWC3	chrX	+	-742	NM_015691
D3A_WT	1227	7598927	7599091	2.45	XAB2	chr19	-	1430	NM_020196
D3A_WT	2572	52403552	52403861	2.49	XAGE2	chrX	-	115	NM_130777
D3A_WT	2572	52403552	52403861	2.49	XAGE2B	chrX	-	-965	NM_001079538
D3A_WT	1553	30019792	30020416	3.79	XKR7	chr20	+	639	NM_001011718
D3A_WT	1715	39582849	39583398	3.28	XPNPEP3	chr22	+	84	NM_022098
D3A_WT	2329	21832368	21833597	2.64	XPO7	chr8	+	-143	NM_015024
D3A_WT	422	65816350	65817199	2.46	YIF1A	chr11	-	-3560	NM_020470
D3A_WT	1297	43490975	43491694	2.48	YIF1B	chr19	-	1015	NM_033557
D3A_WT	1238	10900214	10900568	2.84	YIPF2	chr19	-	-34	NM_024029
D3A_WT	1276	19501841	19502090	2.47	YJEFN3	chr19	+	1246	NM_198537
D3A_WT	2225	44206929	44207358	2.75	YKT6	chr7	+	41	NM_006555
D3A_WT	860	30021695	30022035	2.5	YPEL3	chr16	-	-6843	NM_031477
D3A_WT	860	30021695	30022035	2.5	YPEL3	chr16	-	-6827	NM_001145524
D3A_WT	1411	30223757	30224096	3.41	YPEL5	chr2	+	673	NM_016061
D3A_WT	2551	21785236	21785385	2.39	YY2	chrX	+	787	NM_206923
D3A_WT	1444	97716457	97716706	2.58	ZAP70	chr2	+	-719	NM_207519
D3A_WT	593	31783534	31783798	2.21	ZAR1L	chr13	-	425	NM_001136571
D3A_WT	2543	2428847	2429753	2.85	ZBED1	chrX	-	-292	NM_004729
D3A_WT	1745	48629450	48630089	2.63	ZBED4	chr22	+	-3731	NM_014838
D3A_WT	2088	33393371	33393816	2.51	ZBTB22	chr6	-	104	NM_001145338
D3A_WT	2088	33393371	33393816	2.51	ZBTB22	chr6	-	-103	NM_005453
D3A_WT	2479	128662498	128662848	2.65	ZBTB34	chr9	+	-91	NM_001099270
D3A_WT	527	55683913	55684467	2.64	ZBTB39	chr12	-	2307	NM_014830
D3A_WT	157	153243008	153243152	2.53	ZBTB7B	chr1	+	1345	NM_015872
D3A_WT	88	32777940	32778294	3.07	ZBTB8A	chr1	+	759	NM_001040441
D3A_WT	915	87163875	87164699	2.91	ZC3H18	chr16	+	-2	NM_144604
D3A_WT	2582	73440599	73440848	2.98	ZCCHC13	chrX	+	-26	NM_203303
D3A_WT	1124	58340664	58340913	2.97	ZCCHC2	chr18	+	-849	NM_017742
D3A_WT	1536	226463	226612	2.53	ZCCHC3	chr20	+	334	NM_033089
D3A_WT	885	66007510	66007944	2.65	ZDHHC1	chr16	-	113	NM_013304
D3A_WT	1973	908447	909902	3.09	ZDHHC11	chr5	-	-5073	NM_024786
D3A_WT	1971	901837	901991	2.32	ZDHHC11	chr5	-	2187	NM_024786
D3A_WT	1972	906034	906388	2.32	ZDHHC11	chr5	-	-2110	NM_024786
D3A_WT	664	76678088	76679027	2	ZDHHC22	chr14	-	-670	NM_174976
D3A_WT	1682	22072743	22073000	2.47	ZDHHC8P	chr22	-	1928	NR_003950
D3A_WT	1468	144991219	144991755	2.13	ZEB2	chr2	-	2899	NM_014795
D3A_WT	2180	1166378	1166547	2.34	ZFAND2A	chr7	-	-81	NM_182491
D3A_WT	2094	37895121	37896295	3.04	ZFAND3	chr6	+	424	NM_021943
D3A_WT	2438	74169715	74170159	3.11	ZFAND5	chr9	-	46	NM_006007
D3A_WT	893	73740456	73740776	2.78	ZFP1	chr16	+	695	NM_153688
D3A_WT	1416	43307372	43307819	2.48	ZFP36L2	chr2	-	-346	NM_006887
D3A_WT	913	87046044	87048062	2.65	ZFPM1	chr16	+	-461	NM_153813
D3A_WT	2364	106400447	106401371	3.26	ZFPM2	chr8	+	587	NM_012082
D3A_WT	1602	61809523	61810172	2.96	ZGPAT	chr20	+	610	NM_001083113

D3A_WT	1602	61809523	61810172	2.96	ZGPAT	chr20	+	24	NM_181485
D3A_WT	1602	61809523	61810172	2.96	ZGPAT	chr20	+	13	NM_032527
D3A_WT	616	99420799	99421228	2.53	ZIC5	chr13	-	1166	NM_033132
D3A_WT	855	25176662	25177026	2.48	ZKSCAN2	chr16	-	-488	NM_001012981
D3A_WT	258	80497312	80498960	2.33	ZMIZ1	chr10	+	-661	NM_020338
D3A_WT	2227	44755084	44755303	3.52	ZMIZ2	chr7	+	-7118	NM_174929
D3A_WT	2227	44755084	44755303	3.52	ZMIZ2	chr7	+	139	NM_031449
D3A_WT	102	40489896	40490445	2.24	ZMPSTE24	chr1	+	-6149	NM_005857
D3A_WT	2579	70390283	70390749	2.57	ZMYM3	chrX	-	155	NM_201599
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D3A_WT	1279	19635250	19635374	2.76	ZNF101	chr19	+	-5350	NM_033204
D3A_WT	1280	19704642	19705292	2.83	ZNF14	chr19	-	-46	NM_021030
D3A_WT	1281	19711700	19711919	2.76	ZNF14	chr19	-	-6888	NM_021030
D3A_WT	1859	320549	321566	3.16	ZNF141	chr4	+	-538	NM_003441
D3A_WT	2409	146146814	146147065	2.44	ZNF16	chr8	-	139	NM_006958
D3A_WT	834	3390881	3391030	2.38	ZNF174	chr16	+	-235	NM_003450
D3A_WT	879	56587766	56590215	5.84	ZNF319	chr16	-	2273	NM_020807
D3A_WT	2081	26767963	26768422	2.52	ZNF322A	chr6	-	-250	NM_024639
D3A_WT	1386	63672483	63672834	3.38	ZNF324	chr19	+	2384	NM_014347
D3A_WT	1385	63655908	63657871	6.17	ZNF324B	chr19	+	2107	NM_207395
D3A_WT	1354	58732950	58733684	3.82	ZNF331	chr19	+	173	NM_001079906
D3A_WT	1355	58749250	58749989	2.72	ZNF331	chr19	+	-753	NM_001079907
D3A_WT	1555	31783568	31784017	2.42	ZNF341	chr20	+	324	NM_032819
D3A_WT	1294	42034304	42034766	2.43	ZNF345	chr19	+	1429	NM_003419
D3A_WT	2053	178219512	178219781	2.04	ZNF354B	chr5	+	87	NM_058230
D3A_WT	486	6668300	6668737	2.7	ZNF384	chr12	-	419	NM_001135734
D3A_WT	486	6668300	6668737	2.7	ZNF384	chr12	-	-432	NM_001039916
D3A_WT	486	6668300	6668737	2.7	ZNF384	chr12	-	412	NM_001039920
D3A_WT	486	6668300	6668737	2.7	ZNF384	chr12	-	270	NM_001039918
D3A_WT	1295	42260677	42260831	2.41	ZNF420	chr19	+	-467	NM_144689
D3A_WT	1241	12007015	12007174	2.31	ZNF433	chr19	-	431	NM_001080411
D3A_WT	834	3390881	3391030	2.38	ZNF434	chr16	-	71	NM_017810
D3A_WT	1386	63672483	63672834	3.38	ZNF446	chr19	+	-6948	NM_017908
D3A_WT	1387	63673700	63674319	3.37	ZNF446	chr19	+	-5597	NM_017908
D3A_WT	1388	63675170	63676119	4.15	ZNF446	chr19	+	-3962	NM_017908
D3A_WT	1239	11769811	11769950	2.39	ZNF491	chr19	+	-510	NM_152356
D3A_WT	1382	63571018	63571277	2.74	ZNF497	chr19	-	-5215	NM_198458
D3A_WT	1286	37528620	37528974	2.39	ZNF507	chr19	+	444	NM_014910
D3A_WT	1606	62068650	62069274	2.06	ZNF512B	chr20	-	2700	NM_020713
D3A_WT	2407	145994800	145995319	2.4	ZNF517	chr8	+	-5	NM_213605
D3A_WT	1895	10067633	10067887	2.28	ZNF518B	chr4	-	370	NM_053042
D3A_WT	1296	42731927	42732371	2.73	ZNF540	chr19	+	-1998	NM_152606
D3A_WT	1191	2852898	2853529	3.12	ZNF57	chr19	+	1318	NM_173480
D3A_WT	1317	47264698	47265347	3.17	ZNF574	chr19	+	-7107	NM_022752
D3A_WT	1374	61596618	61596997	3.09	ZNF582	chr19	-	-106	NM_144690
D3A_WT	1384	63611650	63612001	2.35	ZNF584	chr19	+	-49	NM_173548
D3A_WT	1856	42915	43094	3.07	ZNF595	chr4	+	-222	NM_182524

D3A_WT	816	1999641	1999970	2.98	ZNF598	chr16	-	-41	NM_178167
D3A_WT	1352	57531201	57531625	2.34	ZNF610	chr19	+	104	NM_001161427
D3A_WT	1772	40541312	40541976	3.24	ZNF621	chr3	+	265	NM_198484
D3A_WT	2386	144789617	144789761	2.43	ZNF623	chr8	+	174	NM_001082480
D3A_WT	566	123023736	123024285	2.89	ZNF664	chr12	+	388	NM_152437
D3A_WT	200	225814801	225815045	2.71	ZNF678	chr1	+	-2943	NM_178549
D3A_WT	199	225813296	225814025	4.4	ZNF678	chr1	+	-4206	NM_178549
D3A_WT	2408	146023987	146024121	2.43	ZNF7	chr8	+	348	NM_003416
D3A_WT	1684	22423282	22423428	2.34	ZNF70	chr22	-	-76	NM_021916
D3A_WT	1375	61798635	61799659	3.75	ZNF71	chr19	+	672	NM_021216
D3A_WT	770	88345684	88347108	3.05	ZNF710	chr15	+	641	NM_198526
D3A_WT	1856	42915	43094	3.07	ZNF718	chr4	+	-272	NM_001039127
D3A_WT	2295	148952554	148952703	2.42	ZNF767	chr7	-	186	NR_027788
D3A_WT	2455	98656325	98656459	2.34	ZNF782	chr9	-	-182	NM_001001662
D3A_WT	2293	148590124	148590263	2.28	ZNF783	chr7	+	-1	NR_015357
D3A_WT	1372	60825254	60825503	3.02	ZNF784	chr19	-	2375	NM_203374
D3A_WT	1940	147076736	147076985	2.35	ZNF827	chr4	-	2197	NM_178835
D3A_WT	2206	6621895	6622334	2.22	ZNF853	chr7	+	63	NM_017560
D3A_WT	1857	189930	190349	2.86	ZNF876P	chr4	+	-6249	NR_027481
D3A_WT	1858	196114	196873	2.66	ZNF876P	chr4	+	105	NR_027481
D3A_WT	1353	57565005	57565471	3.47	ZNF880	chr19	+	257	NM_001145434
D3A_WT	1379	63237031	63237865	3.12	ZSCAN1	chr19	+	203	NM_182572
D3A_WT	1999	60662380	60664643	2.64	ZSWIM6	chr5	+	-345	NM_020928
D3A_WT	459	113152742	113152987	2.66	ZW10	chr11	-	-3229	NM_004724
WT_D3A	3577	76751058	76751377	2.4	AATK	chr17	-	3250	NM_001080395
WT_D3A	3623	989922	990166	2.8	ABCA7	chr19	+	-1057	NM_019112
WT_D3A	3904	219792689	219793013	2.54	ABCB6	chr2	-	-935	NM_005689
WT_D3A	3905	219796707	219796851	2.22	ABCB6	chr2	-	-4863	NM_005689
WT_D3A	3903	219789759	219790035	2.69	ABCB6	chr2	-	2019	NM_005689
WT_D3A	4498	72789487	72789721	3	ABHD11	chr7	-	1522	NM_001145363
WT_D3A	4498	72789487	72789721	3	ABHD11	chr7	-	1516	NM_001145364
WT_D3A	3435	1032008	1032247	2.76	ABR	chr17	-	-2246	NM_021962
WT_D3A	3462	7066161	7067216	4.05	ACADVL	chr17	+	2812	NM_001033859
WT_D3A	2650	1240107	1240661	2.66	ACAP3	chr1	-	-7252	NM_030649
WT_D3A	2807	15175304	15175964	2.42	ACBD7	chr10	-	-4853	NM_001039844
WT_D3A	4544	150369968	150370197	2.69	ACCN3	chr7	+	-6455	NM_020322
WT_D3A	4545	150372943	150373697	2.45	ACCN3	chr7	+	-3217	NM_020322
WT_D3A	3913	220089070	220089604	2.91	ACCN4	chr2	+	2202	NM_182847
WT_D3A	3363	66253184	66253718	2.89	ACD	chr16	-	-1232	NM_022914
WT_D3A	3528	58910865	58911414	3.29	ACE	chr17	+	2974	NM_000789
WT_D3A	3528	58910865	58911414	3.29	ACE	chr17	+	-4769	NM_152830
WT_D3A	4392	24776908	24777048	2.06	ACOT13	chr6	+	1737	NM_018473
WT_D3A	4206	49523826	49524545	3.31	ACR	chr22	+	668	NM_001097
WT_D3A	2836	90708269	90708633	2.3	ACTA2	chr10	-	-5891	NM_001613
WT_D3A	3020	66065699	66067153	3.15	ACTN3	chr11	+	-4540	NM_001104
WT_D3A	3745	43824891	43825050	2.33	ACTN4	chr19	+	-5196	NM_004924
WT_D3A	3083	50592723	50593072	2.79	ACVRL1	chr12	+	518	NM_001077401

WT_D3A	3031	67171709	67172088	2.63	ACY3	chr11	-	2808	NM_080658
WT_D3A	4594	39291283	39291442	2.29	ADAM5P	chr8	+	24	NR_001448
WT_D3A	4746	135269210	135270101	2.94	ADAMTS13	chr9	+	-7285	NM_139027
WT_D3A	4747	135274139	135274678	4.21	ADAMTS13	chr9	+	-2532	NM_139027
WT_D3A	4746	135269210	135270101	2.94	ADAMTS13	chr9	+	376	NR_024514
WT_D3A	4382	178707839	178707999	2.02	ADAMTS2	chr5	-	-2984	NM_014244
WT_D3A	4749	135385527	135386046	2.72	ADAMTSL2	chr9	+	-1320	NM_001145320
WT_D3A	4748	135383302	135384346	3.15	ADAMTSL2	chr9	+	-3282	NM_001145320
WT_D3A	4749	135385527	135386046	2.72	ADAMTSL2	chr9	+	-4009	NM_014694
WT_D3A	4748	135383302	135384346	3.15	ADAMTSL2	chr9	+	-5971	NM_014694
WT_D3A	4448	963550	963719	2.28	ADAP1	chr7	-	-2819	NM_006869
WT_D3A	3387	74220239	74220468	2.25	ADAT1	chr16	-	-5698	NM_012091
WT_D3A	3175	23876962	23877521	2.61	ADCY4	chr14	-	-3537	NM_139247
WT_D3A	4205	49269628	49269957	2.64	ADM2	chr22	+	2915	NM_024866
WT_D3A	4204	49262421	49262580	2.5	ADM2	chr22	+	-4377	NM_024866
WT_D3A	3615	75965435	75965784	2.39	ADNP2	chr18	+	-2293	NM_014913
WT_D3A	3166	113151339	113151618	2.59	ADPRHL1	chr13	-	-20	NM_199162
WT_D3A	2714	36325463	36326422	2.94	ADPRHL2	chr1	+	-1097	NM_017825
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WT_D3A	4234	49729794	49730041	2.74	AMIGO3	chr3	-	2325	NM_198722
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WT_D3A	4848	152850992	152851261	3.23	ARD1A	chrX	-	2536	NM_003491
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WT_D3A	4170	38248548	38248872	2.6	ATF4	chr22	+	2196	NM_001675
WT_D3A	3074	6896039	6896793	2.46	ATN1	chr12	+	-7470	NM_001007026
WT_D3A	3230	23662682	23663426	2.32	ATP10A	chr15	-	-3612	NM_024490
WT_D3A	2765	158411232	158411877	3.06	ATP1A4	chr1	+	-2270	NM_001001734
WT_D3A	4839	152457182	152457326	2.74	ATP2B3	chrX	+	2481	NM_001001344
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WT_D3A	3284	349034	350383	3.52	AXIN1	chr16	-	-7243	NM_181050
WT_D3A	2986	62146207	62146356	2.81	B3GAT3	chr11	-	-257	NM_012200
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WT_D3A	2993	63812538	63813682	2.67	BAD	chr11	-	-4358	NM_004322
WT_D3A	4623	143539878	143540342	2.3	BAI1	chr8	+	-2268	NM_001702
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WT_D3A	4161	36840520	36840967	2.56	BAIAP2L2	chr22	-	-4121	NM_025045
WT_D3A	3019	66033138	66033372	2.2	BBS1	chr11	+	-1439	NM_024649
WT_D3A	3461	6867512	6868345	2.16	BCL6B	chr17	+	836	NM_181844
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WT_D3A	4651	145492129	145492273	2.26	BOP1	chr8	-	-6273	NM_015201
WT_D3A	4507	97745734	97746573	2.76	BRI3	chr7	+	-2761	NM_001159491
WT_D3A	3827	60480588	60480727	2.37	BRSK1	chr19	+	-6688	NM_032430
WT_D3A	2987	62237808	62238440	2.55	BSCL2	chr11	-	-6348	NM_001122955
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WT_D3A	2814	44799989	44800332	2.59	C10orf10	chr10	-	-5824	NM_007021
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WT_D3A	3186	75517016	75517843	3.07	C14orf179	chr14	+	-4419	NM_052873
WT_D3A	3211	104113228	104113762	2.51	C14orf180	chr14	+	-3605	NM_001008404
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WT_D3A	4180	43986144	43986463	2.16	C22orf9	chr22	-	708	NM_015264
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WT_D3A	3855	27283114	27283443	2.27	C2orf28	chr2	+	-5124	NM_080592
WT_D3A	3938	241485651	241485998	2.82	C2orf54	chr2	-	-1578	NM_001085437
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WT_D3A	3861	37313144	37313533	2.58	C2orf56	chr2	+	1061	NM_001083946
WT_D3A	3879	98589002	98589136	2.53	C2orf64	chr2	-	2318	NM_001008215
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WT_D3A	4289	1234884	1235058	2.59	C4orf42	chr4	+	795	NM_052861
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WT_D3A	4309	6047115	6048092	3.56	C4orf50	chr4	-	-6536	NM_207405
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WT_D3A	4364	157030871	157031616	3.3	C5orf52	chr5	+	105	NM_001145132
WT_D3A	4415	36410856	36411220	3.24	C6orf222	chr6	-	1602	NM_001010903
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WT_D3A	4533	134500910	134503757	4.83	C7orf49	chr7	-	3739	NM_024033
WT_D3A	4587	22515497	22515816	2.25	C8orf58	chr8	+	2590	NM_001013842
WT_D3A	4586	22514097	22514341	3.43	C8orf58	chr8	+	1153	NM_001013842
WT_D3A	4600	58354656	58354805	2.71	C8orf71	chr8	+	75	NR_026772
WT_D3A	4652	145546891	145547460	2.7	C8ORFK29	chr8	-	2138	NR_015428
WT_D3A	4760	137538611	137539152	3.03	C9orf116	chr9	-	-7299	NM_001048265
WT_D3A	4785	139001999	139002460	3.03	C9orf142	chr9	+	-4461	NM_183241
WT_D3A	4774	138490830	138491704	3.55	C9orf163	chr9	+	-6500	NM_152571
WT_D3A	4796	139258179	139259513	3.02	C9orf173	chr9	+	-6704	NM_001004353
WT_D3A	4700	124914330	124914709	3.41	C9orf45	chr9	-	3058	NR_026677
WT_D3A	4745	135235305	135235539	2.31	C9orf96	chr9	+	2318	NM_153710
WT_D3A	3028	66976021	66976470	2.04	CABP4	chr11	+	-3148	NM_145200
WT_D3A	3029	66978218	66979097	2.3	CABP4	chr11	+	-736	NM_145200
WT_D3A	3491	34603225	34605199	2.66	CACNB1	chr17	-	3215	NM_000723
WT_D3A	2848	105204622	105204781	2.79	CALHM2	chr10	-	-2549	NM_015916
WT_D3A	3249	66287309	66287463	2.67	CALML4	chr15	-	-1884	NM_001031733
WT_D3A	3694	16472937	16473285	2.47	CALR3	chr19	-	-5108	NM_145046
WT_D3A	4362	149646406	149646565	2.52	CAMK2A	chr5	-	3111	NM_171825
WT_D3A	4425	44229393	44230142	3.41	CAPN11	chr6	+	-4758	NM_007058
WT_D3A	2703	26387517	26388881	3.05	CATSPER4	chr1	+	-1506	NM_198137
WT_D3A	4207	8744325	8744651	2.81	CAV3	chr3	+	-6007	NM_033337
WT_D3A	3421	87529284	87532728	4.48	CBFA2T3	chr16	-	4103	NM_175931
WT_D3A	4065	43373064	43374091	2.82	CBS	chr21	-	-4468	NM_000071
WT_D3A	3892	130813714	130813975	2.37	CCDC115	chr2	-	2548	NM_032357
WT_D3A	4120	20316930	20317254	3.18	CCDC116	chr22	+	7	NM_152612

WT_D3A	3783	54585467	54585626	2.88	CCDC155	chr19	+	2229	NM_144688
WT_D3A	2762	158135792	158136614	2.32	CCDC19	chr1	-	327	NM_012337
WT_D3A	2668	3651468	3652527	2.35	CCDC27	chr1	+	-6827	NM_152492
WT_D3A	3505	38201259	38201908	2.92	CCDC56	chr17	-	2647	NM_001040431
WT_D3A	4247	113841398	113841557	2.14	CCDC80	chr3	-	1190	NM_199512
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WT_D3A	3754	46500663	46501087	3.14	CCDC97	chr19	+	-7058	NM_052848
WT_D3A	3486	31331843	31332493	3.06	CCL16	chr17	-	468	NM_004590
WT_D3A	3487	31552837	31552976	2.45	CCL3L1	chr17	-	-4637	NM_021006
WT_D3A	3487	31552837	31552976	2.45	CCL3L3	chr17	-	-4646	NM_001001437
WT_D3A	3034	69158084	69158728	3.35	CCND1	chr11	+	-6647	NM_053056
WT_D3A	4441	167449851	167450430	3.64	CCR6	chr6	+	-6090	NM_031409
WT_D3A	4220	45901226	45901375	2.35	CCR9	chr3	+	-1722	NM_031200
WT_D3A	4220	45901226	45901375	2.35	CCR9	chr3	+	-1754	NM_006641
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WT_D3A	3535	69969022	69969769	4.21	CD300A	chr17	+	-4721	NM_007261
WT_D3A	3530	59360386	59361120	2.49	CD79B	chr17	-	2683	NM_021602
WT_D3A	2927	2346623	2348042	3.6	CD81	chr11	+	-7790	NM_004356
WT_D3A	2928	2352509	2353343	4.02	CD81	chr11	+	-2196	NM_004356
WT_D3A	3065	6177615	6179099	3.46	CD9	chr12	+	-1458	NM_001769
WT_D3A	3071	6836178	6836325	2.16	CDCA3	chr12	-	-5534	NM_031299
WT_D3A	3007	64611521	64612565	3.32	CDCA5	chr11	-	-3852	NM_080668
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WT_D3A	3606	61570588	61570745	2.14	CDH7	chr18	+	2199	NM_033646
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WT_D3A	4547	150389870	150390094	2.13	CDK5	chr7	-	-3997	NM_001164410
WT_D3A	4546	150388770	150388905	2.31	CDK5	chr7	-	-2852	NM_001164410
WT_D3A	3171	22658147	22659526	2.57	CEBPE	chr14	-	-522	NM_001805
WT_D3A	3861	37313144	37313533	2.58	CEBPZ	chr2	-	-1094	NM_005760
WT_D3A	4106	16063444	16063626	2.19	CECR1	chr22	-	-2990	NM_177405
WT_D3A	4737	134921211	134921435	2.61	CEL	chr9	+	-5862	NM_001807
WT_D3A	4738	134928885	134929949	2.26	CEL	chr9	+	2232	NM_001807
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WT_D3A	3431	88258327	88258730	2.69	CHMP1A	chr16	-	-6898	NM_001083314
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WT_D3A	2988	62445823	62447262	3.23	CHRM1	chr11	-	-954	NM_000738
WT_D3A	3921	233113305	233113464	2.91	CHRNG	chr2	+	704	NM_005199
WT_D3A	2825	73396058	73396382	2.33	CHST3	chr10	+	2095	NM_004273
WT_D3A	3386	74126299	74127625	2.6	CHST5	chr16	-	-393	NM_024533
WT_D3A	4352	80564819	80564978	2.45	CKMT2	chr5	+	4	NM_001099736
WT_D3A	2687	16223943	16224372	2.75	CLCNKA	chr1	+	3085	NM_004070

WT_D3A	2689	16250487	16250636	2.15	CLCNKB	chr1	+	2691	NM_001165945
WT_D3A	2722	42976730	42976879	2.52	CLDN19	chr1	-	1708	NM_148960
WT_D3A	3317	3015407	3015861	2.34	CLDN6	chr16	-	-7445	NM_021195
WT_D3A	3316	3003840	3004169	2.48	CLDN9	chr16	+	1547	NM_020982
WT_D3A	3377	68764618	68765698	2.59	CLEC18C	chr16	+	-270	NM_173619
WT_D3A	3252	72688288	72689447	2.94	CLK3	chr15	+	1102	NM_003992
WT_D3A	3252	72688288	72689447	2.94	CLK3	chr15	+	-5520	NM_001130028
WT_D3A	3253	72691093	72691317	3.47	CLK3	chr15	+	-3182	NM_001130028
WT_D3A	3076	7172040	7172399	2.14	CLSTN3	chr12	+	-2014	NM_014718
WT_D3A	3390	80032623	80033077	3.53	CMIP	chr16	+	-3425	NM_198390
WT_D3A	3505	38201259	38201908	2.92	CNTD1	chr17	+	-2796	NM_173478
WT_D3A	3750	45429854	45430103	2.55	CNTD2	chr19	-	-5541	NM_024877
WT_D3A	3504	37967118	37967862	3.76	COASY	chr17	+	-127	NM_001042532
WT_D3A	2710	31944166	31945293	2.86	COL16A1	chr1	-	-2374	NM_001856
WT_D3A	4023	61390838	61392208	2.81	COL20A1	chr20	+	-3459	NM_020882
WT_D3A	3139	109752090	109753121	3.2	COL4A2	chr13	+	-5026	NM_001846
WT_D3A	3663	9978952	9979416	2.4	COL5A3	chr19	-	2963	NM_015719
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WT_D3A	3841	3622844	3623196	2.77	COLEC11	chr2	+	2509	NM_024027
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WT_D3A	3715	18896208	18896443	2.24	COPE	chr19	-	-5126	NM_199444
WT_D3A	3027	66969546	66969670	2.01	CORO1B	chr11	-	-2049	NM_020441
WT_D3A	3027	66969546	66969670	2.01	CORO1B	chr11	-	-1769	NM_001018070
WT_D3A	3403	84387324	84388246	2.81	COX4I1	chr16	+	-2911	NM_001861
WT_D3A	3403	84387324	84388246	2.81	COX4NB	chr16	-	2864	NM_006067
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WT_D3A	4532	129808104	129808428	3.71	CPA1	chr7	+	741	NM_001868
WT_D3A	4282	816470	816895	2.98	CPLX1	chr4	-	-6737	NM_006651
WT_D3A	4654	145602633	145602992	2.31	CPSF1	chr8	-	2729	NM_013291
WT_D3A	3790	54885216	54885795	2.65	CPT1C	chr19	+	-713	NM_152359
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WT_D3A	2775	205884942	205886209	2.8	CR1L	chr1	+	495	NM_175710
WT_D3A	4701	125152295	125154125	3.28	CRB2	chr9	+	-5058	NM_173689
WT_D3A	3655	6417737	6418200	3.01	CRB3	chr19	+	2709	NM_174881
WT_D3A	4201	48694082	48694341	2.4	CRELD2	chr22	+	-4075	NM_024324
WT_D3A	3397	83404214	83404378	2.5	CRISPLD2	chr16	+	-6791	NM_031476
WT_D3A	2691	17121831	17122585	2.69	CROCC	chr1	+	1177	NM_014675
WT_D3A	3897	208718727	208718871	2.42	CRYGB	chr2	-	323	NM_005210
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WT_D3A	3529	59311774	59311943	2.02	CSH2	chr17	-	-7037	NM_022645
WT_D3A	4866	26036506	26036700	2.18	CSPG4LYP1	chrY	+	-1839	NR_001554
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WT_D3A	3956	23536314	23536793	2.83	CST9	chr20	-	-1943	NM_001008693
WT_D3A	3994	54397342	54398681	3.89	CSTF1	chr20	+	-3102	NM_001033522
WT_D3A	3994	54397342	54398681	3.89	CSTF1	chr20	+	-2822	NM_001033521
WT_D3A	3994	54397342	54398681	3.89	CSTF1	chr20	+	-2969	NM_001324

WT_D3A	4832	134763613	134764272	2.46	CT45A4	chrX	-	459	NM_001017436
WT_D3A	4536	143085550	143085729	2.36	CTAGE6	chr7	-	137	NM_178561
WT_D3A	4289	1234884	1235058	2.59	CTBP1	chr4	-	-2063	NM_001328
WT_D3A	2864	126711508	126711832	2.45	CTBP2	chr10	-	-5227	NM_022802
WT_D3A	3096	56531740	56533211	4.37	CTDSP2	chr12	-	-5461	NM_005730
WT_D3A	3366	66522364	66522936	3.04	CTRL	chr16	-	616	NM_001907
WT_D3A	2896	1739000	1739769	3.26	CTSD	chr11	-	2414	NM_001909
WT_D3A	3659	7894030	7894494	3.09	CTXN1	chr19	-	2789	NM_206833
WT_D3A	4408	33491004	33491524	2.58	CUTA	chr6	-	2779	NM_001014433
WT_D3A	4829	70753166	70754335	2.53	CXCR3	chrX	-	1342	NM_001504
WT_D3A	3052	118270002	118270231	3.3	CXCR5	chr11	+	806	NM_032966
WT_D3A	3053	118271087	118272128	3.02	CXCR5	chr11	+	2297	NM_032966
WT_D3A	3603	46066277	46067196	3.58	CXXC1	chr18	-	1954	NM_014593
WT_D3A	3527	58870867	58872031	4.14	CYB561	chr17	-	490	NM_001017917
WT_D3A	3469	7694925	7695159	3.22	CYB5D1	chr17	+	-6746	NM_144607
WT_D3A	3414	87249897	87250046	3.17	CYBA	chr16	-	-5013	NM_000101
WT_D3A	3413	87245756	87245920	2.12	CYBA	chr16	-	-880	NM_000101
WT_D3A	3895	172082461	172083107	2.67	CYBRD1	chr2	+	-4327	NM_024843
WT_D3A	3548	72050080	72050743	2.73	CYGB	chr17	-	-5034	NM_134268
WT_D3A	4658	145665992	145666921	2.9	CYHR1	chr8	-	-5230	NM_138496
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WT_D3A	4696	123541999	123542343	2.53	DAB2IP	chr9	+	-2713	NM_138709
WT_D3A	4695	123368414	123368749	2.7	DAB2IP	chr9	+	-638	NM_032552
WT_D3A	2982	61206811	61206960	2.65	DAGLA	chr11	+	2400	NM_006133
WT_D3A	3644	3917883	3918132	2.26	DAPK3	chr19	-	2819	NM_001348
WT_D3A	4407	33395469	33397328	3.32	DAXX	chr6	-	2373	NM_001141970
WT_D3A	4324	41679361	41679680	2.54	DCAF4L1	chr4	+	1051	NM_001029955
WT_D3A	3585	77586612	77587191	2.41	DCXR	chr17	-	1961	NM_016286
WT_D3A	2981	60862236	60862407	2.3	DDB1	chr11	-	-5079	NM_001923
WT_D3A	2694	20863307	20864055	2.71	DDOST	chr1	-	-3057	NM_005216
WT_D3A	4398	30965672	30966291	2.45	DDR1	chr6	+	1538	NM_013994
WT_D3A	4162	37215329	37215463	2.7	DDX17	chr22	-	-915	NM_030881
WT_D3A	4374	176873876	176874010	2.2	DDX41	chr5	-	2630	NM_016222
WT_D3A	3115	131196408	131196672	2.58	DDX51	chr12	-	-1707	NM_175066
WT_D3A	4413	35367293	35367722	2.2	DEF6	chr6	+	-6065	NM_022047
WT_D3A	4576	6722678	6723312	3.74	DEFB1	chr8	-	-56	NM_005218
WT_D3A	4609	142201905	142202354	2.56	DENND3	chr8	+	-5772	NM_014957
WT_D3A	4116	18684585	18685044	2.18	DGCR6L	chr22	-	2794	NM_033257
WT_D3A	3924	233926606	233927065	2.8	DGKD	chr2	+	-1056	NM_152879
WT_D3A	2975	46341924	46342803	4.22	DGKZ	chr11	+	2643	NM_001105540
WT_D3A	3680	12659454	12659903	2.43	DHPS	chr19	-	-6001	NM_013407
WT_D3A	3382	70687882	70688409	2.5	DHX38	chr16	+	3030	NM_014003
WT_D3A	4597	42353363	42354437	3.96	DKK4	chr8	-	-69	NM_014420
WT_D3A	3782	54551964	54552738	3.01	DKKL1	chr19	+	-6502	NM_014419
WT_D3A	3462	7066161	7067216	4.05	DLG4	chr17	-	-5036	NM_001128827

WT_D3A	3462	7066161	7067216	4.05	DLG4	chr17	-	-2595	NM_001365
WT_D3A	2856	124311879	124312028	2.28	DMBT1	chr10	+	1783	NM_004406
WT_D3A	3734	40681779	40682131	2.46	DMKN	chr19	-	2698	NM_001035516
WT_D3A	3768	50973411	50973570	2.63	DMPK	chr19	-	2211	NM_001081563
WT_D3A	3767	50972321	50972785	2.42	DMPK	chr19	-	3148	NM_001081563
WT_D3A	4527	102770969	102771198	2.21	DNAJC2	chr7	-	1473	NM_001129887
WT_D3A	2991	63747212	63748069	2.43	DNAJC4	chr11	+	-6688	NM_005528
WT_D3A	4030	61991823	61992252	3.15	DNAJC5	chr20	+	-4924	NM_025219
WT_D3A	3320	3636874	3637013	2.77	DNASE1	chr16	+	-5997	NM_005223
WT_D3A	4855	153299717	153300063	2.39	DNASE1L1	chrX	-	-6269	NM_001009934
WT_D3A	3681	12856456	12856895	2.41	DNASE2	chr19	-	-3340	NM_001375
WT_D3A	3850	25332208	25332741	2.33	DNMT3A	chr2	-	-3790	NM_153759
WT_D3A	3908	219959390	219959724	2.7	DNPEP	chr2	-	1349	NM_012100
WT_D3A	3676	11236051	11238529	3.92	DOCK6	chr19	-	-3133	NM_020812
WT_D3A	4374	176873876	176874010	2.2	DOK3	chr5	-	-4479	NM_024872
WT_D3A	4374	176873876	176874010	2.2	DOK3	chr5	-	-3910	NM_001144876
WT_D3A	4304	3432266	3432695	2.4	DOK7	chr4	+	-2350	NM_173660
WT_D3A	4403	32045530	32045979	2.55	DOM3Z	chr6	-	2257	NM_005510
WT_D3A	3429	88208201	88208350	2.51	DPEP1	chr16	+	-6225	NM_004413
WT_D3A	3429	88208201	88208350	2.51	DPEP1	chr16	+	1059	NM_001128141
WT_D3A	4017	60942287	60942746	2.26	DPH3B	chr20	+	-4404	NM_080750
WT_D3A	3015	65439007	65439976	3.54	DRAP1	chr11	+	-3812	NM_006442
WT_D3A	3896	183645034	183645513	2.91	DUSP19	chr2	+	-6258	NM_001142314
WT_D3A	4591	33574336	33574820	3.54	DUSP26	chr8	-	2403	NM_024025
WT_D3A	4435	158988520	158988769	2.68	DYNLT1	chr6	-	-2916	NM_006519
WT_D3A	3749	45022643	45022787	2.1	DYRK1B	chr19	-	-6034	NM_006483
WT_D3A	4366	158457308	158458141	2.82	EBF1	chr5	-	1642	NM_024007
WT_D3A	4821	48258692	48259126	2.38	EBP	chrX	+	-6198	NM_006579
WT_D3A	3919	233064295	233064550	2.03	ECEL1	chr2	-	-3646	NM_004826
WT_D3A	3920	233065691	233066756	2.86	ECEL1	chr2	-	-5447	NM_004826
WT_D3A	3746	44020763	44020888	2.16	ECH1	chr19	-	-6488	NM_001398
WT_D3A	2720	41720098	41720367	2.54	EDN2	chr1	-	2699	NM_001956
WT_D3A	4213	19950205	19950629	4.11	EFHB	chr3	-	293	NM_144715
WT_D3A	4330	111050615	111050881	3.1	EGF	chr4	+	-2740	NM_001963
WT_D3A	4803	139626474	139626748	2.68	EHMT1	chr9	+	-6653	NM_024757
WT_D3A	4804	139629004	139629523	3.21	EHMT1	chr9	+	-4001	NM_024757
WT_D3A	3857	27452126	27453351	2.21	EIF2B4	chr2	-	-5910	NM_015636
WT_D3A	3857	27452126	27453351	2.21	EIF2B4	chr2	-	-6315	NM_172195
WT_D3A	4152	35260349	35260486	2.64	EIF3D	chr22	-	-5194	NM_003753
WT_D3A	2770	200247728	200248462	2.42	ELF3	chr1	+	1783	NM_004433
WT_D3A	2773	203874146	203875074	4.29	ELK4	chr1	-	-5987	NM_001973
WT_D3A	3246	41856921	41857370	2.66	ELL3	chr15	-	-351	NM_025165
WT_D3A	4499	73073898	73074537	3.02	ELN	chr7	+	-6145	NM_001081752
WT_D3A	4500	73075903	73076452	2.79	ELN	chr7	+	-4185	NM_001081752
WT_D3A	3975	39426422	39426971	3.16	EMILIN3	chr20	-	2216	NM_052846
WT_D3A	4707	129662855	129663281	2.77	ENG	chr9	-	-6200	NM_001114753
WT_D3A	3074	6896039	6896793	2.46	ENO2	chr12	+	2542	NM_001975

WT_D3A	3113	130995565	130995919	2.81	EP400	chr12	+	-4718	NM_015409
WT_D3A	4582	21964815	21965488	3.24	EPB49	chr8	+	-1875	NM_001114137
WT_D3A	4582	21964815	21965488	3.24	EPB49	chr8	+	-3122	NM_001114139
WT_D3A	4583	21970936	21972681	3.5	EPB49	chr8	+	3535	NM_001114139
WT_D3A	4582	21964815	21965488	3.24	EPB49	chr8	+	-6170	NM_001114135
WT_D3A	4583	21970936	21972681	3.5	EPB49	chr8	+	487	NM_001114135
WT_D3A	4582	21964815	21965488	3.24	EPB49	chr8	+	-7480	NM_001114138
WT_D3A	4583	21970936	21972681	3.5	EPB49	chr8	+	-823	NM_001114138
WT_D3A	4642	145021067	145021216	2.05	EPPK1	chr8	-	-1719	NM_031308
WT_D3A	2883	693433	693897	3.32	EPS8L2	chr11	+	-2454	NM_022772
WT_D3A	3658	7803952	7804211	2.52	EVI5L	chr19	+	2921	NM_145245
WT_D3A	3378	68844668	68846491	2.9	EXOSC6	chr16	-	-2245	NM_058219
WT_D3A	3379	68849230	68849563	2.14	EXOSC6	chr16	-	-6062	NM_058219
WT_D3A	3163	112823498	112823632	2.54	F10	chr13	+	-1548	NM_000504
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WT_D3A	4183	44086099	44086248	2.11	FAM118A	chr22	+	1725	NM_017911
WT_D3A	4183	44086099	44086248	2.11	FAM118A	chr22	+	2429	NM_001104595
WT_D3A	4796	139258179	139259513	3.02	FAM166A	chr9	-	3197	NM_001001710
WT_D3A	3189	93451828	93452162	2.54	FAM181A	chr14	+	-3015	NM_138344
WT_D3A	4196	47344314	47344638	2.45	FAM19A5	chr22	+	-6305	NM_015381
WT_D3A	4443	282523	284247	2.41	FAM20C	chr7	+	-4666	NM_020223
WT_D3A	2702	26013784	26013963	2.45	FAM54B	chr1	+	-5110	NM_001099625
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WT_D3A	2702	26013784	26013963	2.45	FAM54B	chr1	+	-6032	NM_001099626
WT_D3A	4841	152514852	152514981	2.31	FAM58A	chrX	-	2910	NM_152274
WT_D3A	4780	138723978	138724412	2.98	FAM69B	chr9	+	-2649	NM_152421
WT_D3A	3169	113656646	113656975	2.94	FAM70B	chr13	-	-4937	NM_182614
WT_D3A	4674	65233568	65234027	2.68	FAM74A4	chr9	-	409	NR_026802
WT_D3A	4670	39347664	39348498	2.67	FAM75A1	chr9	+	2383	NM_001085452
WT_D3A	4670	39347664	39348498	2.67	FAM75A2	chr9	+	2383	NM_001040065
WT_D3A	4732	133145950	133146283	2.96	FAM78A	chr9	-	-4389	NM_033387
WT_D3A	4605	124265956	124266300	3.28	FAM83A	chr8	+	2196	NM_207006
WT_D3A	4604	124262754	124262883	2.69	FAM83A	chr8	+	-1114	NM_207006
WT_D3A	3967	33349852	33350496	3.95	FAM83C	chr20	-	-6535	NM_178468
WT_D3A	3966	33345557	33345986	3.16	FAM83C	chr20	-	-2132	NM_178468
WT_D3A	3775	53809115	53809764	2.42	FAM83E	chr19	-	-933	NM_017708
WT_D3A	3263	87587456	87587744	2.35	FANCI	chr15	+	-597	NM_018193
WT_D3A	3587	77654264	77654413	2.21	FASN	chr17	-	-4943	NM_004104
WT_D3A	4686	96443044	96443488	3.17	FBP1	chr9	-	-914	NM_001127628
WT_D3A	4686	96443044	96443488	3.17	FBP1	chr9	-	-1522	NM_000507
WT_D3A	3346	30585529	30586658	3.9	FBRS	chr16	+	2815	NM_001105079
WT_D3A	2846	104166905	104167069	2.42	FBXL15	chr10	+	-2573	NM_024326
WT_D3A	3349	30845446	30845591	2.35	FBXL19	chr16	+	2122	NM_001099784
WT_D3A	4653	145557456	145557787	2.64	FBXL6	chr8	-	-4681	NM_024555
WT_D3A	4517	100018591	100020356	3.46	FBXO24	chr7	+	-5658	NM_012172
WT_D3A	4517	100018591	100020356	3.46	FBXO24	chr7	+	-2418	NM_033506
WT_D3A	4516	100016513	100016938	2.92	FBXO24	chr7	+	-5166	NM_033506

WT_D3A	3657	7674397	7674636	2.14	FCER2	chr19	-	-1484	NM_002002
WT_D3A	4360	141008842	141009586	2.9	FCHSD1	chr5	-	1956	NM_033449
WT_D3A	4759	136911680	136912559	3.64	FCN2	chr9	+	-359	NM_015837
WT_D3A	2761	158031760	158032407	3.57	FCRL6	chr1	+	-6713	NM_001004310
WT_D3A	2984	61309768	61310202	2.47	FEN1	chr11	+	-6740	NM_004111
WT_D3A	4682	94778813	94779052	2.72	FGD3	chr9	+	2394	NM_033086
WT_D3A	4681	94777205	94777484	2.36	FGD3	chr9	+	806	NM_033086
WT_D3A	4680	94751104	94751283	2.55	FGD3	chr9	+	1772	NM_001083536
WT_D3A	4323	15573535	15573779	3.18	FGFBP2	chr4	-	300	NM_031950
WT_D3A	4292	1761834	1762496	2.81	FGFR3	chr4	+	-2671	NM_022965
WT_D3A	4285	988573	988722	2.28	FGFRL1	chr4	+	-6962	NM_001004356
WT_D3A	4285	988573	988722	2.28	FGFRL1	chr4	+	-7112	NM_001004358
WT_D3A	2769	178432175	178432524	2.84	FLJ23867	chr1	+	-1417	NR_026900
WT_D3A	3691	16008149	16008298	2.23	FLJ25328	chr19	+	2701	NR_024335
WT_D3A	3690	15996166	15997325	3.36	FLJ25328	chr19	+	-7540	NR_024336
WT_D3A	2640	845694	845938	2.49	FLJ39609	chr1	-	-1136	NR_026874
WT_D3A	3765	50689743	50689987	2.59	FLJ40125	chr19	+	-3705	NM_001080401
WT_D3A	4806	139776926	139777050	2.46	FLJ40292	chr9	+	-306	NR_024341
WT_D3A	3310	2623649	2624263	3.26	FLJ42627	chr16	+	-5027	NR_024492
WT_D3A	3573	76620445	76622159	5.5	FLJ90757	chr17	-	1812	NR_026857
WT_D3A	2990	63622170	63622314	2.31	FLRT1	chr11	+	-5695	NM_013280
WT_D3A	3787	54671198	54671652	2.16	FLT3LG	chr19	+	2128	NM_001459
WT_D3A	2779	211100353	211101222	2.83	FLVCR1	chr1	+	2568	NM_014053
WT_D3A	3593	78264208	78264447	2.7	FN3KRP	chr17	+	-3543	NM_024619
WT_D3A	3594	78269526	78270046	3.11	FN3KRP	chr17	+	1916	NM_024619
WT_D3A	2712	33106167	33106586	2.48	FNDC5	chr1	-	2558	NM_153756
WT_D3A	4672	42708164	42709352	2.38	FOXD4L2	chr9	+	1529	NM_001099279
WT_D3A	4672	42708164	42709352	2.38	FOXD4L4	chr9	+	1529	NM_199244
WT_D3A	3177	28304431	28304557	2.41	FOXG1	chr14	+	-1543	NM_005249
WT_D3A	4473	4683886	4685326	3.35	FOXK1	chr7	+	-3849	NM_001037165
WT_D3A	4728	131976081	131976360	2.48	FREQ	chr9	+	1543	NM_014286
WT_D3A	3009	64903526	64903780	2.64	FRMD8	chr11	+	-6963	NM_031904
WT_D3A	3620	624630	624774	2.43	FSTL3	chr19	+	-2686	NM_005860
WT_D3A	3621	626135	626264	2.7	FSTL3	chr19	+	-1189	NM_005860
WT_D3A	4100	46398642	46398971	3.51	FTCD	chr21	-	1103	NM_206965
WT_D3A	4465	2245332	2245596	2.45	FTSJ2	chr7	-	2895	NM_013393
WT_D3A	3269	89209901	89210776	3.44	FURIN	chr15	+	-2550	NM_002569
WT_D3A	3731	40322197	40322351	2.53	FXYD1	chr19	+	43	NM_005031
WT_D3A	3731	40322197	40322351	2.53	FXYD1	chr19	+	703	NM_021902
WT_D3A	3731	40322197	40322351	2.53	FXYD7	chr19	+	-3719	NM_022006
WT_D3A	3641	3469465	3469604	2.02	FZR1	chr19	+	-4419	NM_001136197
WT_D3A	3543	71270371	71270525	2.17	GALK1	chr17	-	2427	NM_000154
WT_D3A	3417	87456188	87456437	2.44	GALNS	chr16	-	-5437	NM_000512
WT_D3A	3116	131261923	131262168	2.14	GALNT9	chr12	-	-5519	NM_021808
WT_D3A	4159	36549448	36549987	2.29	GALR3	chr22	+	383	NM_003614
WT_D3A	4008	60487731	60488080	2.56	GATA5	chr20	-	-3484	NM_080473
WT_D3A	4007	60481851	60482178	2.19	GATA5	chr20	-	2407	NM_080473

WT_D3A	4139	29012632	29012981	2.79	GATSL3	chr22	-	2810	NM_001037666
WT_D3A	4529	127009995	127010664	3.77	GCC1	chr7	-	2561	NM_024523
WT_D3A	3681	12856456	12856895	2.41	GCDH	chr19	+	-6298	NM_013976
WT_D3A	3238	38842841	38842970	2.54	GCHFR	chr15	+	-671	NM_005258
WT_D3A	4827	69561847	69562066	2.31	GDPD2	chrX	+	2241	NM_017711
WT_D3A	3509	40351311	40352012	2.61	GFAP	chr17	-	-3221	NM_002055
WT_D3A	3537	70775403	70776047	4.03	GGA3	chr17	-	-6453	NM_014001
WT_D3A	3447	4411094	4411234	2.28	GGT6	chr17	-	-539	NM_153338
WT_D3A	3529	59311774	59311943	2.02	GH2	chr17	-	1097	NM_022558
WT_D3A	4520	100122185	100123019	2.1	GIGYF1	chr7	-	2204	NM_022574
WT_D3A	3907	219824755	219825314	2.62	GLB1L	chr2	-	-6659	NM_024506
WT_D3A	3906	219816068	219816729	3.47	GLB1L	chr2	-	1977	NM_024506
WT_D3A	4711	130300587	130301021	2.27	GLE1	chr9	+	-5987	NM_001003722
WT_D3A	4667	36129133	36129302	2.76	GLIPR2	chr9	+	2476	NM_022343
WT_D3A	3722	19621224	19621678	2.28	GMIP	chr19	-	-5996	NM_016573
WT_D3A	3912	220065945	220066899	2.7	GMPPA	chr2	+	-5434	NM_013335
WT_D3A	3912	220065945	220066899	2.7	GMPPA	chr2	+	-5450	NM_205847
WT_D3A	4235	49739998	49740661	2.01	GMPPB	chr3	-	-3941	NM_013334
WT_D3A	3637	3046438	3046662	2.44	GNA11	chr19	+	1143	NM_002067
WT_D3A	2738	109887264	109888816	3.74	GNAI3	chr1	+	-4668	NM_006496
WT_D3A	4519	100103045	100103701	4.01	GNB2	chr7	+	-5925	NM_005273
WT_D3A	3289	793374	793723	2.82	GNG13	chr16	-	-2814	NM_016541
WT_D3A	3771	51832192	51832636	3.6	GNG8	chr19	-	-2635	NM_033258
WT_D3A	3292	1337068	1337287	3.04	GNPTG	chr16	+	-4755	NM_032520
WT_D3A	3122	131919584	131919829	2.17	GOLGA3	chr12	-	-4345	NM_005895
WT_D3A	4453	1090379	1091018	3.3	GPER	chr7	+	-3550	NM_001098201
WT_D3A	4453	1090379	1091018	3.3	GPER	chr7	+	-2270	NM_001505
WT_D3A	4631	144365976	144367095	3.37	GPIHBP1	chr8	+	93	NM_178172
WT_D3A	4822	48865423	48865575	2.08	GPKOW	chrX	-	1524	NM_015698
WT_D3A	4246	101806740	101807114	2.18	GPR128	chr3	+	-4195	NM_032787
WT_D3A	3220	104603522	104605041	3.23	GPR132	chr14	-	-1482	NM_013345
WT_D3A	2992	63805324	63805576	2.18	GPR137	chr11	+	-4456	NM_020155
WT_D3A	2993	63812538	63813682	2.67	GPR137	chr11	+	3204	NM_020155
WT_D3A	3534	69876065	69876789	3.17	GPR142	chr17	+	1188	NM_181790
WT_D3A	4452	1060458	1060692	2.26	GPR146	chr7	+	-3091	NM_138445
WT_D3A	3028	66976021	66976470	2.04	GPR152	chr11	-	531	NM_206997
WT_D3A	3029	66978218	66979097	2.3	GPR152	chr11	-	-1881	NM_206997
WT_D3A	2673	6246015	6246539	2.47	GPR153	chr1	-	-2655	NM_207370
WT_D3A	3886	128117547	128119296	3.16	GPR17	chr2	+	-1487	NM_005291
WT_D3A	3887	128122042	128122571	2.35	GPR17	chr2	+	2398	NM_005291
WT_D3A	4652	145546891	145547460	2.7	GPR172A	chr8	+	-5857	NM_024531
WT_D3A	3093	55675328	55676077	2.27	GPR182	chr12	+	1081	NM_007264
WT_D3A	4616	142439117	142444179	3.39	GPR20	chr8	-	4899	NM_005293
WT_D3A	2738	109887264	109888816	3.74	GPR61	chr1	+	4024	NM_031936
WT_D3A	3354	56260105	56261224	2.63	GPR97	chr16	+	1007	NM_170776
WT_D3A	3586	77606132	77607375	3.7	GPS1	chr17	+	3702	NM_004127
WT_D3A	3464	7161959	7162865	2.38	GPS2	chr17	-	-3030	NM_004489

WT_D3A	4768	138365620	138365859	2.81	GPSM1	chr9	+	-1590	NM_001145639
WT_D3A	4767	138336919	138337353	2.62	GPSM1	chr9	+	-4616	NM_001145638
WT_D3A	3476	18888563	18889592	2.42	GRAP	chr17	-	1984	NM_006613
WT_D3A	4645	145129215	145130159	2.64	GRINA	chr8	+	-6526	NM_001009184
WT_D3A	3168	113367737	113368851	3.57	GRK1	chr13	+	-1303	NM_002929
WT_D3A	4263	142979853	142980002	2.75	GRK7	chr3	+	195	NM_139209
WT_D3A	4636	144708537	144709101	3.09	GSDMD	chr8	+	-2800	NM_024736
WT_D3A	4636	144708537	144709101	3.09	GSDMD	chr8	+	2120	NM_001166237
WT_D3A	3335	27986524	27986651	2.3	GSG1L	chr16	-	-4256	NM_001109763
WT_D3A	4126	22683473	22683882	2.19	GSTTP1	chr22	-	-6419	NR_003081
WT_D3A	3703	17312179	17312743	3.47	GTPBP3	chr19	+	3106	NM_133644
WT_D3A	3702	17304260	17305039	3.53	GTPBP3	chr19	+	-4706	NM_133644
WT_D3A	3091	53154226	53154491	2.23	GTSF1	chr12	-	-705	NM_144594
WT_D3A	4423	42276448	42276575	3.28	GUCA1B	chr6	-	-5839	NM_002098
WT_D3A	2721	42384789	42385238	2.68	GUCA2B	chr1	+	-6665	NM_007102
WT_D3A	3130	50543969	50544713	3.3	GUCY1B2	chr13	-	-6047	NR_003923
WT_D3A	4264	150187746	150187910	2.05	GYG1	chr3	+	-4236	NM_004130
WT_D3A	2974	45893083	45893424	2.29	GYLTL1B	chr11	+	-6518	NM_152312
WT_D3A	4258	130745778	130746307	2.83	H1FOO	chr3	+	1296	NM_153833
WT_D3A	3803	56918333	56919287	2.53	HAS1	chr19	-	223	NM_001523
WT_D3A	4838	152387166	152387820	2.77	HAUS7	chrX	-	2304	NM_017518
WT_D3A	3697	17049534	17049698	2.52	HAUS8	chr19	-	-2273	NM_033417
WT_D3A	2896	1739000	1739769	3.26	HCCA2	chr11	-	2693	NM_053005
WT_D3A	3317	3015407	3015861	2.34	HCFC1R1	chr16	-	-1346	NM_001002017
WT_D3A	3933	239993517	239993772	2.66	HDAC4	chr2	-	-6064	NM_006037
WT_D3A	4483	35703167	35703421	2.88	HERPUD2	chr7	-	-1997	NM_022373
WT_D3A	2647	932075	932199	2.97	HES4	chr1	-	-6722	NM_001142467
WT_D3A	3510	40579499	40579748	2.66	HEXIM1	chr17	+	-843	NM_006460
WT_D3A	3523	45608144	45608493	2.23	HILS1	chr17	-	-3482	NR_024193
WT_D3A	3344	29920970	29921401	2.46	HIRIP3	chr16	-	-6297	NM_003609
WT_D3A	3343	29912021	29913145	3.01	HIRIP3	chr16	-	2305	NM_003609
WT_D3A	4394	26333485	26334029	3.25	HIST1H3E	chr6	+	396	NM_003532
WT_D3A	3624	1020208	1020746	3.57	HMHA1	chr19	+	2304	NM_012292
WT_D3A	3298	1670410	1671329	3.67	HN1L	chr16	+	2591	NM_144570
WT_D3A	3977	42465060	42466301	2.92	HNF4A	chr20	+	2343	NM_178849
WT_D3A	4482	27150946	27152226	3.79	HOXA5	chr7	-	-1774	NM_019102
WT_D3A	4482	27150946	27152226	3.79	HOXA6	chr7	-	2307	NM_024014
WT_D3A	3519	44026810	44028059	3.05	HOXB5	chr17	-	-1332	NM_002147
WT_D3A	3730	40225081	40225830	2.95	HPN	chr19	+	2206	NM_182983
WT_D3A	2880	529723	530097	2.56	HRAS	chr11	-	-4360	NM_001130442
WT_D3A	4666	35897022	35897571	2.91	HRCT1	chr9	+	1108	NM_001039792
WT_D3A	4369	175037229	175037978	2.85	HRH2	chr5	+	-3466	NM_022304
WT_D3A	4001	60231403	60232078	2.16	HRH3	chr20	-	-3022	NM_007232
WT_D3A	3849	20715922	20716586	2.32	HS1BP3	chr2	-	-1909	NM_022460
WT_D3A	3651	5627849	5627983	2.68	HSD11B1L	chr19	+	-4118	NM_198705
WT_D3A	3651	5627849	5627983	2.68	HSD11B1L	chr19	+	-4158	NM_198706
WT_D3A	3651	5627849	5627983	2.68	HSD11B1L	chr19	+	-4135	NM_198707

WT_D3A	3651	5627849	5627983	2.68	HSD11B1L	chr19	+	-4130	NM_198533
WT_D3A	4833	148489874	148490138	2.32	HSFX1	chrX	-	-5233	NM_016153
WT_D3A	4833	148489874	148490138	2.32	HSFX2	chrX	-	-5233	NM_001164415
WT_D3A	3692	16101068	16101292	2.27	HSH2D	chr19	+	-4657	NM_032855
WT_D3A	2852	118493708	118494627	3.88	HSPA12A	chr10	-	-2092	NM_025015
WT_D3A	3179	64077381	64079055	3.58	HSPA2	chr14	+	1280	NM_021979
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WT_D3A	3827	60480588	60480727	2.37	HSPBP1	chr19	-	2906	NM_012267
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WT_D3A	3068	6529673	6530792	3.83	IFFO1	chr12	-	-1697	NM_080731
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WT_D3A	3190	93664171	93664926	3.67	IFI27L2	chr14	-	1162	NM_032036
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WT_D3A	2916	2113527	2113661	2.28	IGF2AS	chr11	+	-4739	NR_028044
WT_D3A	2764	158181445	158181589	2.9	IGSF9	chr1	-	493	NM_020789
WT_D3A	4354	131423416	131423595	2.01	IL3	chr5	+	-740	NM_000588
WT_D3A	3892	130813714	130813975	2.37	IMP4	chr2	+	-3114	NM_033416
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WT_D3A	3710	18415155	18415379	3.07	ISYNA1	chr19	-	-5324	NM_016368
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WT_D3A	4245	52836959	52837183	2.36	ITIH4	chr3	-	2686	NM_001166449
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WT_D3A	3876	96355694	96357038	3.66	ITPRIPL1	chr2	+	705	NM_178495
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WT_D3A	3221	104708215	104710361	2.16	JAG2	chr14	-	-3082	NM_145159
WT_D3A	3240	39902906	39903675	3.77	JMJD7	chr15	+	-4284	NM_001114632
WT_D3A	3241	39904836	39906450	2.85	JMJD7	chr15	+	-1931	NM_001114632
WT_D3A	3242	39909434	39909668	2.61	JMJD7	chr15	+	1977	NM_001114632
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WT_D3A	3797	55703486	55703730	2.43	JOSD2	chr19	-	2549	NM_138334
WT_D3A	4628	143745331	143745981	2.33	JRK	chr8	-	2747	NM_001077527
WT_D3A	4528	119701790	119702529	2.06	KCND2	chr7	+	1202	NM_012281
WT_D3A	4368	169866153	169866680	2.79	KCNIP1	chr5	+	2791	NM_014592

WT_D3A	2969	17363816	17366380	3	KCNJ11	chr11	-	2356	NM_001166290
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WT_D3A	4761	137728325	137728469	2.14	KCNT1	chr9	+	-5454	NM_020822
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WT_D3A	4428	74029787	74030343	2.85	KHDC1	chr6	-	-437	NM_030568
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WT_D3A	2853	118757537	118757807	2.94	KIAA1598	chr10	-	-2594	NM_001127211
WT_D3A	3395	83096235	83096579	2.99	KIAA1609	chr16	-	-618	NM_020947
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WT_D3A	3409	86354041	86354277	2.21	KLHDC4	chr16	-	2884	NM_017566
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WT_D3A	2745	150998761	150998885	2.2	KPRP	chr1	+	1694	NM_001025231
WT_D3A	3772	52678069	52678608	2.84	KPTN	chr19	-	995	NM_007059
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WT_D3A	3088	51623449	51625104	2.45	KRT18	chr12	+	-4645	NM_199187
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WT_D3A	4004	60373624	60373788	2.23	LAMA5	chr20	-	2057	NM_005560
WT_D3A	3340	28902927	28903271	2.18	LAT	chr16	+	-548	NM_001014989
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WT_D3A	3368	66537878	66538037	2.41	LCAT	chr16	-	-2441	NM_000229
WT_D3A	3369	66538826	66539291	3.3	LCAT	chr16	-	-3542	NM_000229
WT_D3A	3367	66534088	66534227	2.11	LCAT	chr16	-	1359	NM_000229
WT_D3A	4781	138760307	138760436	2.65	LCN10	chr9	-	-3139	NM_001001712
WT_D3A	4783	138969123	138969377	2.27	LCN12	chr9	+	2662	NM_178536
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WT_D3A	4784	138996088	138997027	2.38	LCNL1	chr9	+	-708	NM_207510
WT_D3A	3893	136310852	136311176	2.39	LCT	chr2	-	206	NM_002299
WT_D3A	2834	88415327	88415791	2.94	LDB3	chr10	+	-2741	NM_001080116
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WT_D3A	3070	6804854	6805486	3.43	LEPREL2	chr12	+	-2662	NM_014262
WT_D3A	3566	74487790	74488169	2.16	LGALS3BP	chr17	-	-323	NM_005567
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WT_D3A	3890	128154913	128155276	2.18	LIMS2	chr2	-	-5860	NM_001161403
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WT_D3A	3886	128117547	128119296	3.16	LIMS2	chr2	-	3802	NR_027823
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WT_D3A	4010	60765541	60766270	2.87	LOC100127888	chr20	-	2513	NR_024470
WT_D3A	2656	2119774	2120013	2.1	LOC100128003	chr1	-	-5009	NR_024445
WT_D3A	2711	32602207	32602535	2.46	LOC100128071	chr1	-	-1940	NM_001167676
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WT_D3A	3118	131363914	131364138	3.1	LOC100130238	chr12	+	1977	NR_024563
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WT_D3A	3511	40687961	40688280	3.31	LOC100133991	chr17	+	-7220	NR_024435
WT_D3A	3952	2745617	2746066	3.01	LOC100288797	chr20	+	866	NM_001167670
WT_D3A	3291	1066907	1067226	2.56	LOC146336	chr16	-	1666	NR_027242
WT_D3A	2776	206061428	206062202	3.22	LOC148696	chr1	+	3469	NR_026817

WT_D3A	2793	245020126	245020380	2.3	LOC149134	chr1	+	712	NR_015422
WT_D3A	2794	245021536	245021675	2.99	LOC149134	chr1	+	2064	NR_015422
WT_D3A	3881	110579226	110579355	2.22	LOC151009	chr2	-	-2640	NR_027244
WT_D3A	4666	35897022	35897571	2.91	LOC158376	chr9	+	-2183	NR_024283
WT_D3A	4074	44054801	44055855	3.11	LOC284837	chr21	-	1548	NR_026961
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WT_D3A	4184	44860575	44860829	2.24	LOC400931	chr22	+	162	NR_027033
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WT_D3A	4123	21229226	21229601	2.51	LOC648691	chr22	+	-2342	NR_027426
WT_D3A	2736	103914666	103914800	2.66	LOC648740	chr1	+	1185	NR_024438
WT_D3A	2779	211100353	211101222	2.83	LQK1	chr1	-	-2684	NR_027286
WT_D3A	4517	100018591	100020356	3.46	LRCH4	chr7	-	2239	NM_002319
WT_D3A	3737	41121488	41121642	2.5	LRFN3	chr19	+	1704	NM_024509
WT_D3A	3023	66377980	66378219	2.28	LRFN4	chr11	+	-3352	NM_024036
WT_D3A	4131	24091527	24093606	2.81	LRP5L	chr22	-	-4042	NM_182492
WT_D3A	4789	139185918	139186857	2.98	LRRC26	chr9	-	-2075	NM_001013653
WT_D3A	4083	44701555	44701969	2.3	LRRC3	chr21	+	1942	NM_030891
WT_D3A	3584	77575827	77575961	2.68	LRRC45	chr17	+	1326	NM_144999
WT_D3A	2880	529723	530097	2.56	LRRC56	chr11	+	2389	NM_198075
WT_D3A	3063	1799981	1800435	2.59	LRTM2	chr12	+	515	NM_001163926
WT_D3A	3038	71470189	71470340	2.4	LRTOMT	chr11	+	924	NM_001145307
WT_D3A	3038	71470189	71470340	2.4	LRTOMT	chr11	+	1235	NM_001145308
WT_D3A	2901	1840526	1842048	3.45	LSP1	chr11	+	-7442	NM_001013255
WT_D3A	2900	1833626	1834255	2.76	LSP1	chr11	+	3165	NM_002339
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WT_D3A	2901	1840526	1842048	3.45	LSP1	chr11	+	-5191	NM_001013253
WT_D3A	3011	65083723	65085933	4.02	LTBP3	chr11	-	-2553	NM_021070
WT_D3A	4629	143830354	143830806	2.75	LYPD2	chr8	-	374	NM_205545
WT_D3A	4429	90405075	90405244	2.25	LYRM2	chr6	-	-222	NR_028495
WT_D3A	4429	90405075	90405244	2.25	LYRM2	chr6	-	36	NM_020466
WT_D3A	2843	102743018	102744149	2.18	LZTS2	chr10	+	-3371	NM_032429
WT_D3A	4465	2245332	2245596	2.45	MAD1L1	chr7	-	-6355	NM_003550
WT_D3A	2768	165224949	165225223	2.26	MAEL	chr1	+	-56	NM_032858
WT_D3A	4647	145226115	145227733	2.73	MAF1	chr8	+	-4368	NM_032272
WT_D3A	4635	144589269	144590008	2.95	MAFA	chr8	-	-5919	NM_201589
WT_D3A	4634	144586036	144586380	3.16	MAFA	chr8	-	-2489	NM_201589
WT_D3A	4457	1530111	1530375	2.22	MAFK	chr7	+	-6650	NM_002360
WT_D3A	4825	51943341	51943985	4.56	MAGED4	chrX	+	-1084	NM_001098800
WT_D3A	4825	51943341	51943985	4.56	MAGED4B	chrX	+	-995	NM_177535
WT_D3A	4786	139094774	139095233	2.54	MAN1B1	chr9	+	-6234	NM_016219

WT_D3A	3012	65141498	65141951	3.46	MAP3K11	chr11	-	-3428	NM_002419
WT_D3A	3090	52184756	52185790	2.74	MAP3K12	chr12	-	-5735	NM_006301
WT_D3A	4267	185028987	185029515	3.26	MAP6D1	chr3	-	-3164	NM_024871
WT_D3A	2973	45861405	45862330	3.84	MAPK8IP1	chr11	+	-1910	NM_005456
WT_D3A	3763	50439991	50440150	2.23	MARK4	chr19	+	-6611	NM_031417
WT_D3A	2707	30967060	30967379	2.57	MATN1	chr1	-	1800	NM_002379
WT_D3A	3341	29728578	29728817	2.56	MAZ	chr16	+	3342	NM_002383
WT_D3A	3603	46066277	46067196	3.58	MBD1	chr18	-	-4594	NM_015845
WT_D3A	3992	54257725	54257944	2.34	MC3R	chr20	+	640	NM_019888
WT_D3A	4424	43086305	43086969	2.92	MEA1	chr6	-	2959	NM_014623
WT_D3A	3100	115203321	115203509	2.05	MED13L	chr12	-	-4041	NM_015335
WT_D3A	3597	78627556	78627730	2.44	METRNL	chr17	+	-3212	NM_001004431
WT_D3A	3089	51933932	51934281	2.52	MFSD5	chr12	+	1960	NM_032889
WT_D3A	4169	38206816	38207465	2.83	MGAT3	chr22	+	-6034	NM_001098270
WT_D3A	3480	20352588	20353147	2.39	MGC102966	chr17	-	-4464	NR_029393
WT_D3A	3414	87249897	87250046	3.17	MGC23284	chr16	+	-7310	NR_024402
WT_D3A	2651	1543859	1544308	2.73	MIB2	chr1	+	3337	NM_080875
WT_D3A	2967	12266652	12267616	3.56	MICALCL	chr11	+	2112	NM_032867
WT_D3A	3537	70775403	70776047	4.03	MIF4GD	chr17	-	3173	NM_020679
WT_D3A	4480	7571857	7572323	2.08	MIOS	chr7	+	-1050	NM_019005
WT_D3A	4205	49269628	49269957	2.64	MIOX	chr22	+	-2286	NM_017584
WT_D3A	3204	100581418	100581647	3.47	MIR1185-1	chr14	+	2466	NR_031575
WT_D3A	3204	100581418	100581647	3.47	MIR1185-2	chr14	+	1245	NR_031571
WT_D3A	4654	145602633	145602992	2.31	MIR1234	chr8	-	-6445	NR_031600
WT_D3A	4402	32038368	32039410	2.9	MIR1236	chr6	-	-6193	NR_031601
WT_D3A	3575	76722051	76722385	2.39	MIR1250	chr17	-	-515	NR_031652
WT_D3A	3576	76723361	76723490	2.25	MIR1250	chr17	-	-1722	NR_031652
WT_D3A	4778	138682496	138682955	2.53	MIR126	chr9	+	-2149	NR_029695
WT_D3A	4114	18454060	18454886	2.4	MIR1306	chr22	+	893	NR_031706
WT_D3A	3040	72006988	72007632	2.78	MIR139	chr11	-	-3488	NR_029603
WT_D3A	3075	6933687	6936514	4.27	MIR141	chr12	+	-8420	NR_029682
WT_D3A	4531	129200191	129201141	3.37	MIR182	chr7	-	-3098	NR_029614
WT_D3A	4531	129200191	129201141	3.37	MIR183	chr7	-	1424	NR_029615
WT_D3A	4113	18396110	18397059	3.53	MIR185	chr22	+	-4077	NR_029706
WT_D3A	4031	62049017	62049366	2.69	MIR1914	chr20	-	-5850	NR_031735
WT_D3A	3484	26912160	26912304	2.42	MIR193A	chr17	+	1105	NR_029710
WT_D3A	3461	6867512	6868345	2.16	MIR195	chr17	-	-6184	NR_029712
WT_D3A	3460	6863195	6863828	2.98	MIR195	chr17	-	-1767	NR_029712
WT_D3A	3671	10795623	10795882	2.76	MIR199A1	chr19	-	-6580	NR_029586
WT_D3A	3670	10790617	10790786	2.32	MIR199A1	chr19	-	-1529	NR_029586
WT_D3A	3075	6933687	6936514	4.27	MIR200C	chr12	+	-8022	NR_029779
WT_D3A	3462	7066161	7067216	4.05	MIR324	chr17	-	734	NR_029896
WT_D3A	3360	65797420	65797665	2.44	MIR328	chr16	-	-3743	NR_029887
WT_D3A	3361	65799010	65799274	2.28	MIR328	chr16	-	-5343	NR_029887
WT_D3A	4449	1032415	1033297	2.42	MIR339	chr7	-	-3668	NR_029898
WT_D3A	3204	100581418	100581647	3.47	MIR381	chr14	+	-477	NR_029873
WT_D3A	4692	116007070	116007604	2.79	MIR455	chr9	+	-4197	NR_030255

WT_D3A	2916	2113527	2113661	2.28	MIR483	chr11	-	-1579	NR_030158
WT_D3A	4596	41641462	41642219	2.51	MIR486	chr8	-	-4657	NR_030161
WT_D3A	3204	100581418	100581647	3.47	MIR487A	chr14	+	-7003	NR_030162
WT_D3A	3204	100581418	100581647	3.47	MIR487B	chr14	+	-1012	NR_030267
WT_D3A	3203	100566632	100567348	2.33	MIR494	chr14	+	1267	NR_030174
WT_D3A	3203	100566632	100567348	2.33	MIR495	chr14	+	-2854	NR_030175
WT_D3A	3461	6867512	6868345	2.16	MIR497	chr17	-	-5863	NR_030178
WT_D3A	3460	6863195	6863828	2.98	MIR497	chr17	-	-1446	NR_030178
WT_D3A	3204	100581418	100581647	3.47	MIR539	chr14	+	-1878	NR_030256
WT_D3A	3203	100566632	100567348	2.33	MIR543	chr14	+	-1086	NR_030619
WT_D3A	2667	3473550	3473784	2.39	MIR551A	chr1	-	-6453	NR_030277
WT_D3A	4328	83898932	83900483	3.14	MIR575	chr4	-	-6100	NR_030301
WT_D3A	4478	5503911	5504145	2.78	MIR589	chr7	-	-1954	NR_030318
WT_D3A	4530	127502560	127502799	2.56	MIR593	chr7	+	-6469	NR_030324
WT_D3A	4563	158023886	158024155	2.27	MIR595	chr7	-	-5754	NR_030325
WT_D3A	4699	124913160	124913404	2.66	MIR600	chr9	-	461	NR_030331
WT_D3A	4700	124914330	124914709	3.41	MIR600	chr9	-	-776	NR_030331
WT_D3A	4703	125204854	125205078	2.28	MIR601	chr9	-	-263	NR_030332
WT_D3A	4810	139846412	139846651	3.11	MIR602	chr9	+	-6160	NR_030333
WT_D3A	2810	29879472	29879691	2.24	MIR604	chr10	-	-5549	NR_030335
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WT_D3A	3204	100581418	100581647	3.47	MIR655	chr14	+	-4107	NR_030391
WT_D3A	4553	150565444	150565868	2.29	MIR671	chr7	+	-783	NR_030407
WT_D3A	2758	155176874	155177018	2.11	MIR765	chr1	-	-4286	NR_030527
WT_D3A	3769	51216558	51217792	3.11	MIR769	chr19	+	3146	NR_030412
WT_D3A	3202	100388200	100388329	2.52	MIR770	chr14	+	-215	NR_030528
WT_D3A	3204	100581418	100581647	3.47	MIR889	chr14	+	-2458	NR_030595
WT_D3A	2753	153427091	153427240	2.12	MIR92B	chr1	+	-4426	NR_030281
WT_D3A	2752	153424796	153425155	2.56	MIR92B	chr1	+	-6616	NR_030281
WT_D3A	3806	59179500	59179635	2.51	MIR935	chr19	+	2195	NR_030632
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WT_D3A	4531	129200191	129201141	3.37	MIR96	chr7	-	1179	NR_029512
WT_D3A	3489	34116624	34117478	3.51	MLLT6	chr17	+	1653	NM_005937
WT_D3A	3504	37967118	37967862	3.76	MLX	chr17	+	-5113	NM_198205
WT_D3A	2835	88709455	88710034	3.71	MMRN2	chr10	-	-2339	NM_024756
WT_D3A	2730	46851425	46851744	2.56	MOBKL2C	chr1	-	1808	NM_145279
WT_D3A	2963	3210876	3211110	2.3	MRGPRE	chr11	-	-801	NM_001039165
WT_D3A	3517	43267847	43268401	2.47	MRPL10	chr17	-	-4222	NM_145255
WT_D3A	4347	1849548	1850027	3.2	MRPL36	chr5	-	3169	NM_032479
WT_D3A	4800	139561239	139561993	2.22	MRPL41	chr9	+	-4513	NM_032477
WT_D3A	2842	102733300	102734879	2.51	MRPL43	chr10	-	3173	NM_176792
WT_D3A	2843	102743018	102744149	2.18	MRPL43	chr10	-	-6321	NM_176792
WT_D3A	2717	36705076	36705613	2.59	MRPS15	chr1	-	-2717	NM_031280
WT_D3A	3299	1769444	1769588	2.1	MRPS34	chr16	-	-6375	NM_023936
WT_D3A	2985	62130341	62130555	2.47	MTA2	chr11	-	-4569	NM_004739

WT_D3A	3942	241696122	241696369	2.97	MTERFD2	chr2	-	-5825	NM_182501
WT_D3A	3941	241689473	241689862	2.39	MTERFD2	chr2	-	753	NM_182501
WT_D3A	3098	105903159	105903693	3.08	MTERFD3	chr12	-	1633	NM_025198
WT_D3A	2743	148172505	148173144	2.51	MTMR11	chr1	-	2066	NM_181873
WT_D3A	2743	148172505	148173144	2.51	MTMR11	chr1	-	2591	NM_001145862
WT_D3A	3526	53953334	53954061	2.66	MTMR4	chr17	-	-3447	NM_004687
WT_D3A	2753	153427091	153427240	2.12	MUC1	chr1	-	2159	NM_001044392
WT_D3A	4295	2230509	2230858	2.78	MXD4	chr4	-	2854	NM_006454
WT_D3A	3447	4411094	4411234	2.28	MYBBP1A	chr17	-	-5734	NM_001105538
WT_D3A	2977	47329134	47329383	2.57	MYBPC3	chr11	-	1571	NM_000256
WT_D3A	3848	16003370	16003797	2.57	MYCNOS	chr2	-	-4287	NR_026766
WT_D3A	4221	46877268	46878487	2.67	MYL3	chr3	-	2100	NM_000258
WT_D3A	3345	30290265	30292004	3.25	MYLPF	chr16	+	-2489	NM_013292
WT_D3A	3473	17952844	17954128	3.27	MYO15A	chr17	+	742	NM_016239
WT_D3A	3472	17951247	17951503	2.65	MYO15A	chr17	+	-1369	NM_016239
WT_D3A	3437	1347920	1348045	2.1	MYO1C	chr17	-	-6260	NM_033375
WT_D3A	3437	1347920	1348045	2.1	MYO1C	chr17	-	-5231	NM_001080779
WT_D3A	3697	17049534	17049698	2.52	MYO9B	chr19	+	2026	NM_004145
WT_D3A	3696	17041329	17042168	2.68	MYO9B	chr19	+	-5842	NM_004145
WT_D3A	2699	24309139	24309378	2.37	MYOM3	chr1	-	1994	NM_152372
WT_D3A	4709	129868646	129868995	2.74	NAIF1	chr9	-	600	NM_197956
WT_D3A	4329	89838483	89839104	2.66	NAP1L5	chr4	-	-747	NM_153757
WT_D3A	4638	144738769	144739108	2.25	NAPRT1	chr8	-	-7282	NM_145201
WT_D3A	2989	63459359	63459718	2.52	NAT11	chr11	+	-3479	NM_024771
WT_D3A	2970	19329177	19329411	2.48	NAV2	chr11	+	448	NM_001111018
WT_D3A	3639	3139587	3139836	2.73	NCLN	chr19	+	2837	NM_020170
WT_D3A	3638	3137868	3138317	2.96	NCLN	chr19	+	1218	NM_020170
WT_D3A	3349	30845446	30845591	2.35	NCRNA00095	chr16	-	-3427	NR_024348
WT_D3A	4812	1473000	1473424	3.62	NCRNA00105	chrX	+	-6211	NR_026710
WT_D3A	4813	1481528	1481947	2.7	NCRNA00105	chrX	+	2314	NR_026710
WT_D3A	4098	45670899	45671733	2.91	NCRNA00175	chr21	-	-1903	NR_027498
WT_D3A	4098	45670899	45671733	2.91	NCRNA00175	chr21	-	-1933	NR_028082
WT_D3A	4032	62131465	62131624	2.11	NCRNA00176	chr20	+	-4596	NR_027687
WT_D3A	4033	62134340	62134604	2.59	NCRNA00176	chr20	+	-1668	NR_027687
WT_D3A	4034	62136265	62136521	2.4	NCRNA00176	chr20	+	253	NR_027687
WT_D3A	2801	1188891	1189320	2.85	NCRNA00200	chr10	+	-6602	NR_015376
WT_D3A	4178	43345294	43346848	4.1	NCRNA00207	chr22	+	2188	NR_028411
WT_D3A	4232	49026420	49027254	3.25	NDUFAF3	chr3	+	-6784	NM_199073
WT_D3A	4232	49026420	49027254	3.25	NDUFAF3	chr3	+	-6074	NM_199074
WT_D3A	4232	49026420	49027254	3.25	NDUFAF3	chr3	+	-7240	NM_199069
WT_D3A	3046	77472589	77472834	2.61	NDUFC2	chr11	-	-3798	NM_004549
WT_D3A	2767	159428775	159429019	2.35	NDUFS2	chr1	+	-6831	NM_004550
WT_D3A	4347	1849548	1850027	3.2	NDUFS6	chr5	+	-4708	NM_004553
WT_D3A	3394	82556670	82557199	2.92	NECAB2	chr16	+	-2803	NM_019065
WT_D3A	3877	96538398	96539222	4.11	NEURL3	chr2	-	-1237	NR_026875
WT_D3A	3465	7171297	7171811	2.66	NEURL4	chr17	-	1808	NM_032442
WT_D3A	3492	35022504	35023171	3.12	NEUROD2	chr17	-	-5136	NM_006160

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WT_D3A	4022	61361632	61362271	2.74	NKAIN4	chr20	-	-5614	NM_152864
WT_D3A	4396	28335215	28335434	2.37	NKAPL	chr6	+	248	NM_001007531
WT_D3A	4339	1060477	1061026	2.6	NKD2	chr5	+	-1416	NM_033120
WT_D3A	4588	23595110	23595240	2.72	NKX3-1	chr8	-	1220	NM_006167
WT_D3A	4595	41626855	41628414	2.35	NKX6-3	chr8	-	-3599	NM_152568
WT_D3A	4828	70283859	70283993	2.66	NLGN3	chrX	+	2521	NM_001166660
WT_D3A	3970	35580035	35580769	2.41	NNAT	chr20	+	-2618	NM_181689
WT_D3A	2646	882242	883291	4.08	NOC2L	chr1	-	1776	NM_015658
WT_D3A	3115	131196408	131196672	2.58	NOC4L	chr12	+	1595	NM_024078
WT_D3A	2674	6538355	6538504	2.68	NOL9	chr1	-	-1261	NM_024654
WT_D3A	2845	103896631	103896970	2.73	NOLC1	chr10	+	-5122	NM_004741
WT_D3A	4370	175752460	175753829	3.43	NOP16	chr5	-	-4998	NM_016391
WT_D3A	4777	138557091	138557620	4.78	NOTCH1	chr9	-	2704	NM_017617
WT_D3A	3090	52184756	52185790	2.74	NPFF	chr12	-	2416	NM_003717
WT_D3A	3735	41031602	41032336	2.99	NPHS1	chr19	-	2766	NM_004646
WT_D3A	4581	21938433	21939357	4.57	NPM2	chr8	+	596	NM_182795
WT_D3A	3701	17221673	17222002	2.16	NR2F6	chr19	-	-4686	NM_005234
WT_D3A	4705	126308855	126309294	3.28	NR5A1	chr9	-	446	NM_004959
WT_D3A	4797	139321465	139323256	3.03	NRARP	chr9	-	-5836	NM_001004354
WT_D3A	3365	66473801	66475140	2.62	NRN1L	chr16	+	-1811	NM_198443
WT_D3A	3364	66472016	66472630	3.47	NRN1L	chr16	+	-3958	NM_198443
WT_D3A	4837	151743190	151744541	3.63	NSDHL	chrX	+	-6301	NM_015922
WT_D3A	2729	46579307	46581134	4.44	NSUN4	chr1	+	1244	NM_199044
WT_D3A	3328	15055366	15056411	2.72	NTAN1	chr16	-	1446	NM_173474
WT_D3A	2757	155090302	155090946	2.77	NTRK1	chr1	+	-6670	NM_001012331
WT_D3A	4011	60806166	60806485	3.2	NTSR1	chr20	+	-4308	NM_002531
WT_D3A	4012	60808744	60809883	2.56	NTSR1	chr20	+	-1320	NM_002531
WT_D3A	4013	60812364	60813598	2.81	NTSR1	chr20	+	2348	NM_002531
WT_D3A	3300	1771512	1771866	3.07	NUBP2	chr16	+	-1244	NM_012225
WT_D3A	3299	1769444	1769588	2.1	NUBP2	chr16	+	-3417	NM_012225
WT_D3A	3777	54090250	54090619	3.71	NUCB1	chr19	+	-5418	NM_006184
WT_D3A	4465	2245332	2245596	2.45	NUDT1	chr7	+	-2918	NM_198949
WT_D3A	4465	2245332	2245596	2.45	NUDT1	chr7	+	-3601	NM_198954
WT_D3A	4465	2245332	2245596	2.45	NUDT1	chr7	+	-2957	NM_198952
WT_D3A	3222	104716302	104716751	2.42	NUDT14	chr14	-	2179	NM_177533
WT_D3A	2991	63747212	63748069	2.43	NUDT22	chr11	+	-2673	NM_001128613
WT_D3A	3030	67155670	67158249	3.07	NUDT8	chr11	-	-2982	NM_181843
WT_D3A	3038	71470189	71470340	2.4	NUMA1	chr11	-	-1043	NM_006185
WT_D3A	3183	72995674	72995798	2.48	NUMB	chr14	-	-697	NM_001005745
WT_D3A	3753	45891981	45892744	3.25	NUMBL	chr19	-	-3966	NM_004756
WT_D3A	3336	28455807	28456826	3.39	NUPR1	chr16	-	1680	NM_012385
WT_D3A	3337	28457604	28458258	3.34	NUPR1	chr16	-	65	NM_012385
WT_D3A	3520	45005510	45006644	3.23	NXPH3	chr17	+	-2219	NM_007225
WT_D3A	3095	55889868	55890502	3.24	NXPH4	chr12	+	-6659	NM_007224
WT_D3A	3700	17191045	17191779	3.13	OCEL1	chr19	+	-6642	NM_024578
WT_D3A	3843	10510854	10511296	2.53	ODC1	chr2	-	-5171	NM_002539

WT_D3A	3618	430998	431349	2.22	ODF3L2	chr19	-	-5190	NM_182577
WT_D3A	4015	60901679	60901848	2.39	OGFR	chr20	+	-4858	NM_007346
WT_D3A	3044	76488936	76490191	2.69	OMP	chr11	+	-1970	NM_006189
WT_D3A	3766	50785877	50786656	2.37	OPA3	chr19	-	-6304	NM_001017989
WT_D3A	4646	145190631	145190898	2.22	OPLAH	chr8	-	-3192	NM_017570
WT_D3A	4852	153057626	153057845	2.49	OPN1LW	chrX	+	-5183	NM_020061
WT_D3A	2833	88406885	88407324	2.39	OPN4	chr10	+	2811	NM_033282
WT_D3A	4036	62176732	62177391	2.79	OPRL1	chr20	+	-4870	NM_000913
WT_D3A	4537	143457372	143457501	2.19	OR2A14	chr7	+	298	NM_001001659
WT_D3A	4524	101857229	101857478	2.33	ORAI2	chr7	+	-3647	NM_032831
WT_D3A	4002	60239614	60240068	2.41	OSBPL2	chr20	+	-7133	NM_144498
WT_D3A	3807	59301788	59303853	3.12	OSCAR	chr19	-	-6860	NM_133168
WT_D3A	3851	26556914	26557198	2.8	OTOF	chr2	-	-2642	NM_194323
WT_D3A	3852	26560266	26560937	2.77	OTOF	chr2	-	-6187	NM_194323
WT_D3A	3863	42847831	42848265	2.22	OXER1	chr2	-	-3143	NM_148962
WT_D3A	3583	77417853	77418407	2.89	P4HB	chr17	-	-6297	NM_000918
WT_D3A	4172	41671326	41671540	2.39	PACSIN2	chr22	-	1558	NM_007229
WT_D3A	2662	2446097	2446641	3.49	PANK4	chr1	-	1526	NM_018216
WT_D3A	3313	2960791	2962470	4.26	PAQR4	chr16	+	2288	NM_152341
WT_D3A	2756	154485663	154487312	3.82	PAQR6	chr1	-	-2071	NM_198406
WT_D3A	2756	154485663	154487312	3.82	PAQR6	chr1	-	-2020	NM_024897
WT_D3A	3363	66253184	66253718	2.89	PARD6A	chr16	+	1100	NM_016948
WT_D3A	3616	76109895	76110159	3.12	PARD6G	chr18	-	-3639	NM_032510
WT_D3A	4645	145129215	145130159	2.64	PARP10	chr8	-	2936	NM_032789
WT_D3A	4238	51946762	51946981	2.22	PARP3	chr3	+	-4529	NM_001003931
WT_D3A	4239	51953232	51953501	2.32	PARP3	chr3	+	1966	NM_001003931
WT_D3A	4177	42749520	42749949	3.16	PARVB	chr22	+	-1766	NM_013327
WT_D3A	3943	241741556	241741961	3.61	PASK	chr2	-	-4207	NM_015148
WT_D3A	2819	72316322	72316766	2.76	PCBD1	chr10	-	2003	NM_000281
WT_D3A	3132	57104859	57105123	2.72	PCDH17	chr13	+	1202	NM_001040429
WT_D3A	4359	140850855	140851224	2.89	PCDHGC5	chr5	+	2048	NM_018929
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WT_D3A	3656	7601442	7601701	3.19	PCP2	chr19	-	2999	NM_174895
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WT_D3A	3728	39582176	39582795	2.33	PDCD2L	chr19	+	-4657	NM_032346
WT_D3A	3580	77233402	77235024	3.2	PDE6G	chr17	-	-201	NM_002602
WT_D3A	4060	42944543	42945612	3.32	PDE9A	chr21	+	-1853	NM_001001569
WT_D3A	2838	97041688	97041847	2.24	PDLIM1	chr10	-	-996	NM_020992
WT_D3A	3309	2526112	2526682	2.34	PDPK1	chr16	+	-1573	NM_031268
WT_D3A	4072	43966234	43966658	2.39	PDXK	chr21	+	3041	NM_003681
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WT_D3A	3531	59814744	59815480	4.59	PECAM1	chr17	-	2631	NM_000442
WT_D3A	3448	4556188	4556719	3.9	PELP1	chr17	-	-2072	NM_014389
WT_D3A	2660	2338596	2338945	2.72	PEX10	chr1	-	-4900	NM_153818
WT_D3A	2974	45893083	45893424	2.29	PEX16	chr11	-	2997	NM_057174
WT_D3A	4266	181239744	181239888	2.34	PEX5L	chr3	-	-2605	NM_016559
WT_D3A	4081	44539209	44539543	3.19	PFKL	chr21	+	-4981	NM_002626

WT_D3A	4081	44539209	44539543	3.19	PFKL	chr21	+	-4976	NR_024108
WT_D3A	4373	176757306	176757455	2.24	PFN3	chr5	-	2863	NM_001029886
WT_D3A	4484	44070710	44071359	3.21	PGAM2	chr7	-	677	NM_000290
WT_D3A	3704	17477019	17477658	2.11	PGLS	chr19	+	-6093	NM_012088
WT_D3A	3769	51216558	51217792	3.11	PGLYRP1	chr19	-	988	NM_005091
WT_D3A	2713	33617574	33617826	2.68	PHC2	chr1	-	-3919	NM_198040
WT_D3A	3237	38424557	38424924	2.06	PHGR1	chr15	+	-5785	NM_001145643
WT_D3A	3039	71638581	71640200	3.09	PHOX2A	chr11	-	-6522	NM_005169
WT_D3A	4275	480007	481253	2.58	PIGG	chr4	+	-2358	NM_017733
WT_D3A	4664	35090951	35091305	2.1	PIGO	chr9	-	-4549	NM_152850
WT_D3A	4664	35090951	35091305	2.1	PIGO	chr9	-	-4582	NM_032634
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WT_D3A	2837	95711303	95711462	2.04	PIPSL	chr10	-	280	NR_002319
WT_D3A	4141	30353065	30354109	2.95	PISD	chr22	-	3223	NM_014338
WT_D3A	3315	2975776	2976547	3.01	PKMYT1	chr16	-	-5686	NM_004203
WT_D3A	3314	2971807	2972256	2.18	PKMYT1	chr16	-	-1556	NM_004203
WT_D3A	4713	130507327	130507771	2.54	PKN3	chr9	+	2927	NM_013355
WT_D3A	4712	130505455	130506594	2.6	PKN3	chr9	+	1402	NM_013355
WT_D3A	3244	40237811	40238190	2.09	PLA2G4F	chr15	-	-1898	NM_213600
WT_D3A	3450	4659906	4660460	3.48	PLD2	chr17	+	2806	NM_002663
WT_D3A	3449	4650801	4651570	2.3	PLD2	chr17	+	-6192	NM_002663
WT_D3A	3471	17047257	17047411	2.27	PLD6	chr17	-	3037	NM_178836
WT_D3A	4645	145129215	145130159	2.64	PLEC1	chr8	-	-6786	NM_000445
WT_D3A	4644	145117650	145118599	2.58	PLEC1	chr8	-	1561	NM_201378
WT_D3A	3776	54061851	54062875	2.52	PLEKHA4	chr19	-	1333	NM_020904
WT_D3A	2968	16993962	16994615	3.28	PLEKHA7	chr11	-	-1749	NM_175058
WT_D3A	4522	100652294	100652931	2.36	PLOD3	chr7	-	-4881	NM_001084
WT_D3A	4227	48442758	48443082	2.62	PLXNB1	chr3	-	2956	NM_002673
WT_D3A	3902	218838096	218839176	2.26	PNKD	chr2	+	-4722	NM_015488
WT_D3A	4800	139561239	139561993	2.22	PNPLA7	chr9	-	3191	NM_152286
WT_D3A	4801	139570276	139570615	2.83	PNPLA7	chr9	-	-5638	NM_152286
WT_D3A	3350	31014262	31014891	2.97	POL3S	chr16	-	-6945	NM_001039503
WT_D3A	3466	7321445	7322819	3.18	POLR2A	chr17	+	-6441	NM_000937
WT_D3A	4269	185557889	185558428	2.14	POLR2H	chr3	+	-5729	NM_006232
WT_D3A	4733	133153423	133154272	2.02	PPAPDC3	chr9	+	-1054	NM_032728
WT_D3A	4187	44921888	44923630	4.58	PPARA	chr22	+	-2403	NM_001001928
WT_D3A	4430	109874564	109875270	2.16	PPIL6	chr6	-	-6377	NM_001111298
WT_D3A	3025	66922729	66923348	3.34	PPP1CA	chr11	-	2914	NM_206873
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WT_D3A	3943	241741556	241741961	3.61	PPP1R7	chr2	+	3184	NM_002712
WT_D3A	2866	133593984	133594400	3.04	PPP2R2D	chr10	+	-3757	NM_018461
WT_D3A	3770	51544557	51544916	2.32	PPP5C	chr19	+	2603	NM_006247
WT_D3A	4123	21229226	21229601	2.51	PRAME	chr22	-	2283	NM_206953
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WT_D3A	3548	72050080	72050743	2.73	PRCD	chr17	+	2696	NM_001077620

WT_D3A	4054	42177909	42178152	2.7	PRDM15	chr21	-	-5370	NM_022115
WT_D3A	4054	42177909	42178152	2.7	PRDM15	chr21	-	-5379	NM_001040424
WT_D3A	4327	81330689	81331677	3.08	PRDM8	chr4	+	-6497	NM_001099403
WT_D3A	2994	63838586	63839335	2.66	PRDX5	chr11	+	-3184	NM_181652
WT_D3A	4556	151141394	151141933	3.48	PRKAG2	chr7	-	1227	NM_001040633
WT_D3A	3927	238140188	238140322	3.24	PRLH	chr2	+	300	NM_015893
WT_D3A	3326	11274458	11275102	3	PRM2	chr16	-	3058	NM_002762
WT_D3A	3326	11274458	11275102	3	PRM3	chr16	-	173	NM_021247
WT_D3A	3873	95306129	95307594	2.41	PROM2	chr2	+	2934	NM_144707
WT_D3A	3807	59301788	59303853	3.12	PRPF31	chr19	+	-7781	NM_015629
WT_D3A	3131	56627576	56628170	3.09	PRR20A	chr13	+	-4893	NM_198441
WT_D3A	3131	56627576	56628170	3.09	PRR20A	chr13	+	1678	NM_198441
WT_D3A	3131	56627576	56628170	3.09	PRR20B	chr13	+	1678	NM_001130404
WT_D3A	3131	56627576	56628170	3.09	PRR20B	chr13	+	-4893	NM_001130404
WT_D3A	3131	56627576	56628170	3.09	PRR20C	chr13	+	-4893	NM_001130405
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WT_D3A	3341	29728578	29728817	2.56	PRRT2	chr16	+	-2212	NM_145239
WT_D3A	2785	226070665	226072038	2.66	PRSS38	chr1	+	1311	NM_183062
WT_D3A	2846	104166905	104167069	2.42	PSD	chr10	-	1904	NM_002779
WT_D3A	3367	66534088	66534227	2.11	PSMB10	chr16	-	-5903	NM_002801
WT_D3A	4527	102770969	102771198	2.21	PSMC2	chr7	+	-4241	NM_002803
WT_D3A	3743	43550196	43550325	2.26	PSMD8	chr19	+	-6769	NM_002812
WT_D3A	3173	23690790	23691029	2.01	PSME2	chr14	-	-5214	NM_002818
WT_D3A	4727	131557274	131557423	2.59	PTGES	chr9	-	-2183	NM_004878
WT_D3A	3075	6933687	6936514	4.27	PTPN6	chr12	+	4406	NM_002831
WT_D3A	3823	60412555	60413019	2.36	PTPRH	chr19	-	-101	NM_001161440
WT_D3A	3112	130973450	130974124	2.29	PUS1	chr12	+	-5910	NM_001002020
WT_D3A	3112	130973450	130974124	2.29	PUS1	chr12	+	-5963	NM_001002019
WT_D3A	3112	130973450	130974124	2.29	PUS1	chr12	+	-5978	NM_025215
WT_D3A	2782	224175997	224176126	2.58	PYCR2	chr1	-	2527	NM_013328
WT_D3A	4640	144765619	144766563	2.87	PYCRL	chr8	-	-3184	NM_023078
WT_D3A	4233	49123149	49123878	2.89	QARS	chr3	-	-6338	NM_005051
WT_D3A	3976	42398845	42399419	2.72	R3HDML	chr20	+	93	NM_178491
WT_D3A	3928	238170865	238171024	2.34	RAB17	chr2	-	-6469	NM_022449
WT_D3A	3016	65786490	65786742	2.45	RAB1B	chr11	+	-6015	NM_030981
WT_D3A	3017	65790115	65791029	2.87	RAB1B	chr11	+	-2059	NM_030981
WT_D3A	3288	582216	582590	3.01	RAB40C	chr16	+	2224	NM_021168
WT_D3A	3584	77575827	77575961	2.68	RAC3	chr17	+	-6926	NM_005052
WT_D3A	4743	135018644	135019593	2.78	RALGDS	chr9	-	-4709	NM_001042368
WT_D3A	4744	135020422	135021069	2.34	RALGDS	chr9	-	-6336	NM_001042368

WT_D3A	4740	134988372	134988816	3	RALGDS	chr9	-	-2212	NM_006266
WT_D3A	4741	134992799	134993743	2.58	RALGDS	chr9	-	-6889	NM_006266
WT_D3A	4739	134984497	134985136	3.87	RALGDS	chr9	-	1566	NM_006266
WT_D3A	3666	10306729	10307555	3.07	RAVER1	chr19	-	-1828	NM_133452
WT_D3A	4865	22079194	22079363	2.17	RBMY1A1	chrY	+	-3367	NM_005058
WT_D3A	4865	22079194	22079363	2.17	RBMY1B	chrY	+	-3367	NM_001006121
WT_D3A	4865	22079194	22079363	2.17	RBMY1D	chrY	+	-3373	NM_001006120
WT_D3A	4865	22079194	22079363	2.17	RBMY1E	chrY	+	-3373	NM_001006118
WT_D3A	3076	7172040	7172399	2.14	RBP5	chr12	-	514	NM_031491
WT_D3A	4402	32038368	32039410	2.9	RDBP	chr6	-	-4046	NM_002904
WT_D3A	3663	9978952	9979416	2.4	RDH8	chr19	+	-5740	NM_015725
WT_D3A	3542	71181263	71181888	2.39	RECQL5	chr17	-	-6711	NM_001003715
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WT_D3A	4585	22061645	22062394	3.16	REEP4	chr8	-	-6626	NM_025232
WT_D3A	2659	2305728	2306109	3.39	RER1	chr1	+	-7155	NM_007033
WT_D3A	3630	1796967	1797226	2.62	REXO1	chr19	-	2356	NM_020695
WT_D3A	4746	135269210	135270101	2.94	REXO4	chr9	-	3330	NM_020385
WT_D3A	4747	135274139	135274678	4.21	REXO4	chr9	-	-1423	NM_020385
WT_D3A	3586	77606132	77607375	3.7	RFNG	chr17	-	-3814	NM_002917
WT_D3A	4137	28173308	28173759	2.54	RFPL1S	chr22	-	-5415	NR_002727
WT_D3A	4145	30932977	30933136	2.47	RFPL2	chr22	-	-2338	NM_001159545
WT_D3A	4145	30932977	30933136	2.47	RFPL2	chr22	-	-3592	NM_001098527
WT_D3A	4145	30932977	30933136	2.47	RFPL2	chr22	-	-4519	NM_001159546
WT_D3A	4148	31080587	31080821	2.56	RFPL3	chr22	+	-3149	NM_001098535
WT_D3A	4148	31080587	31080821	2.56	RFPL3	chr22	+	-167	NM_006604
WT_D3A	4125	22363757	22363883	2.41	RGL4	chr22	+	773	NM_153615
WT_D3A	4300	3278692	3279023	2.53	RGS12	chr4	+	-6814	NM_198229
WT_D3A	4301	3336450	3336999	3.1	RGS12	chr4	+	-4797	NM_198227
WT_D3A	4257	130729388	130729532	3	RHO	chr3	+	-711	NM_000539
WT_D3A	3175	23876962	23877521	2.61	RIPK3	chr14	-	1841	NM_006871
WT_D3A	4376	177483596	177485111	4.68	RMND5B	chr5	+	-6280	NM_022762
WT_D3A	3459	6854211	6854755	2.99	RNASEK	chr17	+	-2038	NM_001004333
WT_D3A	3506	38423924	38424068	2.54	RND2	chr17	+	-6787	NM_005440
WT_D3A	3453	4786989	4787448	3.06	RNF167	chr17	+	2844	NM_015528
WT_D3A	3452	4781575	4781949	2.49	RNF167	chr17	+	-2612	NM_015528
WT_D3A	3308	2261033	2261167	2.94	RNPS1	chr16	-	-3302	NM_006711
WT_D3A	3308	2261033	2261167	2.94	RNPS1	chr16	-	-2985	NM_080594
WT_D3A	4166	38039227	38040496	2.7	RNU86	chr22	-	2986	NR_000026
WT_D3A	3321	4793954	4794603	2.77	ROGDI	chr16	-	-1603	NM_024589
WT_D3A	2985	62130341	62130555	2.47	ROM1	chr11	+	-6340	NM_000327
WT_D3A	3491	34603225	34605199	2.66	RPL19	chr17	+	-5849	NM_000981
WT_D3A	4566	169534	169881	2.27	RPL23AP53	chr8	-	2611	NR_003572
WT_D3A	3828	60582136	60582295	2.37	RPL28	chr19	+	-6896	NM_001136135
WT_D3A	3829	60590644	60591583	2.94	RPL28	chr19	+	2002	NM_001136135
WT_D3A	4211	12855163	12855611	2.29	RPL32	chr3	-	2694	NM_001007073
WT_D3A	4211	12855163	12855611	2.29	RPL32	chr3	-	1562	NM_001007074
WT_D3A	3652	5635519	5635983	2.28	RPL36	chr19	+	-5594	NM_015414

WT_D3A	3653	5643538	5643667	2.83	RPL36	chr19	+	2257	NM_015414
WT_D3A	3652	5635519	5635983	2.28	RPL36	chr19	+	-5520	NM_033643
WT_D3A	3653	5643538	5643667	2.83	RPL36	chr19	+	2331	NM_033643
WT_D3A	3533	69708601	69708765	2.55	RPL38	chr17	+	-2706	NM_001035258
WT_D3A	4660	145986688	145986847	2.34	RPL8	chr8	-	1766	NM_033301
WT_D3A	4660	145986688	145986847	2.34	RPL8	chr8	-	1842	NM_000973
WT_D3A	2807	15175304	15175964	2.42	RPP38	chr10	+	-3553	NM_006414
WT_D3A	3516	42409000	42409864	2.93	RPRML	chr17	-	2181	NM_203400
WT_D3A	3788	54685978	54686142	2.49	RPS11	chr19	+	-5385	NM_001015
WT_D3A	3748	44615540	44615774	2.97	RPS16	chr19	-	2801	NM_001020
WT_D3A	2995	63876266	63877385	3.83	RPS6KA4	chr11	+	-6375	NM_003942
WT_D3A	3026	66947245	66947494	2.51	RPS6KB2	chr11	+	-5141	NM_003952
WT_D3A	3184	74456049	74456988	4.05	RPS6KL1	chr14	-	2380	NM_031464
WT_D3A	2966	6587500	6587664	2.18	RRP8	chr11	-	-6195	NM_015324
WT_D3A	4239	51953232	51953501	2.32	RRP9	chr3	-	-2404	NM_004704
WT_D3A	3765	50689743	50689987	2.59	RTN2	chr19	-	2288	NM_206900
WT_D3A	3765	50689743	50689987	2.59	RTN2	chr19	-	-1551	NM_206901
WT_D3A	3765	50689743	50689987	2.59	RTN2	chr19	-	2286	NM_005619
WT_D3A	4270	188900939	188901130	2.03	RTP2	chr3	-	2005	NM_001004312
WT_D3A	2700	25134581	25135422	2.64	RUNX3	chr1	-	-5644	NM_004350
WT_D3A	2701	25170235	25171062	3.71	RUNX3	chr1	-	-6560	NM_001031680
WT_D3A	2755	153561778	153561927	2.87	RUSC1	chr1	+	1011	NM_014328
WT_D3A	2755	153561778	153561927	2.87	RUSC1	chr1	+	1501	NM_001105205
WT_D3A	4256	129326023	129326546	3.38	RUVBL1	chr3	-	-923	NM_003707
WT_D3A	2748	151850348	151850817	3.75	S100A16	chr1	-	1556	NM_080388
WT_D3A	2746	151810674	151811311	4.28	S100A2	chr1	-	-6062	NM_005978
WT_D3A	4311	6745202	6746276	3.67	S100P	chr4	+	-727	NM_005980
WT_D3A	2735	101477373	101478212	4.02	S1PR1	chr1	+	2900	NM_001400
WT_D3A	2640	845694	845938	2.49	SAMD11	chr1	+	-5167	NM_152486
WT_D3A	3521	45567890	45568519	2.43	SAMD14	chr17	-	-6038	NM_174920
WT_D3A	3747	44526777	44527311	2.64	SAMD4B	chr19	+	2097	NM_018028
WT_D3A	4204	49262421	49262580	2.5	SBF1	chr22	-	-2170	NM_002972
WT_D3A	3626	1122890	1123139	2.59	SBNO2	chr19	-	2268	NM_014963
WT_D3A	3262	82968725	82969179	3.03	SCAND2	chr15	+	-6742	NR_003654
WT_D3A	4386	179953398	179953632	3.29	SCGB3A1	chr5	-	-2422	NM_052863
WT_D3A	4387	179957557	179957714	2.27	SCGB3A1	chr5	-	-6542	NM_052863
WT_D3A	3729	40206399	40207448	3.16	SCN1B	chr19	+	-6508	NM_001037
WT_D3A	3067	6354372	6355141	3.57	SCNN1A	chr12	-	-105	NM_001159576
WT_D3A	3067	6354372	6355141	3.57	SCNN1A	chr12	-	410	NM_001038
WT_D3A	3067	6354372	6355141	3.57	SCNN1A	chr12	-	2028	NM_001159575
WT_D3A	2649	1206601	1206740	2.04	SCNN1D	chr1	+	-768	NM_002978
WT_D3A	2649	1206601	1206740	2.04	SCNN1D	chr1	+	-681	NM_001130413
WT_D3A	4648	145386537	145386701	2.98	SCXA	chr8	+	-6885	NM_001008271
WT_D3A	4648	145386537	145386701	2.98	SCXB	chr8	+	-6885	NM_001080514
WT_D3A	3590	77890379	77890539	2.92	SECTM1	chr17	-	-5249	NM_003004
WT_D3A	3589	77887748	77888281	2.67	SECTM1	chr17	-	-2804	NM_003004
WT_D3A	4203	48975258	48975622	2.02	SELO	chr22	+	-6094	NM_031454

WT_D3A	4243	52459910	52460059	2.48	SEMA3G	chr3	-	-5901	NM_020163
WT_D3A	3646	4508706	4508953	2.44	SEMA6B	chr19	-	674	NM_032108
WT_D3A	3468	7400802	7401156	2.38	SENP3	chr17	+	-5063	NM_015670
WT_D3A	3302	1930901	1931445	2.34	SEPX1	chr16	-	2122	NM_016332
WT_D3A	2708	31653369	31653933	2.44	SERINC2	chr1	+	-4898	NM_178865
WT_D3A	3438	1595872	1596046	2.1	SERPINF2	chr17	+	3080	NM_001165921
WT_D3A	3438	1595872	1596046	2.1	SERPINF2	chr17	+	2890	NM_001165920
WT_D3A	2743	148172505	148173144	2.51	SF3B4	chr1	-	-6498	NM_005850
WT_D3A	4814	1673226	1673445	2.02	SFRS17A	chrX	+	2850	NM_005088
WT_D3A	3891	128173066	128173630	3.45	SFT2D3	chr2	+	-1718	NM_032740
WT_D3A	3522	45599782	45601224	2.59	SGCA	chr17	+	2139	NM_001135697
WT_D3A	3569	75805343	75806972	2.54	SGSH	chr17	-	2637	NM_000199
WT_D3A	3570	75810225	75810374	2.43	SGSH	chr17	-	-1505	NM_000199
WT_D3A	3633	2729664	2731813	2.91	SGTA	chr19	-	3616	NM_003021
WT_D3A	4297	2759684	2763103	4.71	SH3BP2	chr4	+	-3154	NM_001122681
WT_D3A	4862	504525	504729	2.12	SHOX	chrY	+	-451	NM_006883
WT_D3A	3050	116557809	116557958	2.39	SIDT2	chr11	+	2735	NM_001040455
WT_D3A	2877	402899	403143	2.31	SIGIRR	chr11	-	1978	NM_001135054
WT_D3A	3802	56653507	56654486	3.64	SIGLEC8	chr19	-	-476	NM_014442
WT_D3A	3013	65165976	65166435	2.95	SIPA1	chr11	+	2038	NM_153253
WT_D3A	3214	104283542	104283791	2.86	SIVA1	chr14	+	-6848	NM_021709
WT_D3A	3215	104292452	104292821	2.13	SIVA1	chr14	+	2122	NM_021709
WT_D3A	4341	1163142	1163591	2.98	SLC12A7	chr5	-	1806	NM_006598
WT_D3A	3785	54642192	54642531	2.18	SLC17A7	chr19	-	-5741	NM_020309
WT_D3A	4018	61047627	61047971	2.28	SLC17A9	chr20	+	-6644	NM_022082
WT_D3A	2997	64117306	64117845	3.63	SLC22A12	chr11	+	2718	NM_144585
WT_D3A	2952	2874608	2874952	2.75	SLC22A18	chr11	+	-2746	NM_183233
WT_D3A	2952	2874608	2874952	2.75	SLC22A18	chr11	+	-5307	NM_002555
WT_D3A	4357	138745812	138746356	2.4	SLC23A1	chr5	-	854	NM_152685
WT_D3A	3453	4786989	4787448	3.06	SLC25A11	chr17	-	-3011	NM_001165418
WT_D3A	3452	4781575	4781949	2.49	SLC25A11	chr17	-	2445	NM_001165418
WT_D3A	2884	783444	783893	3.41	SLC25A22	chr11	-	2553	NM_024698
WT_D3A	3655	6417737	6418200	3.01	SLC25A23	chr19	-	-7187	NM_024103
WT_D3A	4709	129868646	129868995	2.74	SLC25A25	chr9	+	-1479	NM_001006641
WT_D3A	2686	15927101	15928625	2.73	SLC25A34	chr1	+	-7532	NM_207348
WT_D3A	3716	19030835	19031284	2.89	SLC25A42	chr19	+	-4743	NM_178526
WT_D3A	3009	64903526	64903780	2.64	SLC25A45	chr11	-	3065	NM_182556
WT_D3A	4812	1473000	1473424	3.62	SLC25A6	chrX	-	-2173	NM_001636
WT_D3A	3569	75805343	75806972	2.54	SLC26A11	chr17	+	-2637	NM_001166349
WT_D3A	3570	75810225	75810374	2.43	SLC26A11	chr17	+	1505	NM_001166349
WT_D3A	4231	48654268	48654716	2.54	SLC26A6	chr3	-	-6562	NM_134426
WT_D3A	2749	152016633	152016912	2.18	SLC27A3	chr1	+	2381	NM_024330
WT_D3A	2820	72750250	72750664	2.33	SLC29A3	chr10	+	1442	NM_018344
WT_D3A	3463	7127238	7128112	3.67	SLC2A4	chr17	+	1898	NM_001042
WT_D3A	4320	9630933	9632077	2.48	SLC2A9	chr4	-	707	NM_020041
WT_D3A	4372	176744169	176744530	2.7	SLC34A1	chr5	+	312	NM_003052
WT_D3A	4794	139243386	139244110	2.87	SLC34A3	chr9	+	-1457	NM_080877

WT_D3A	3695	16547706	16547945	2.19	SLC35E1	chr19	-	-3632	NM_024881
WT_D3A	4249	127257938	127259797	2.62	SLC41A3	chr3	-	-559	NM_001008487
WT_D3A	4250	127262982	127263261	2.4	SLC41A3	chr3	-	-4813	NM_001008487
WT_D3A	4614	142311556	142311807	2.05	SLC45A4	chr8	-	-3826	NM_001080431
WT_D3A	4615	142312997	142314154	4.24	SLC45A4	chr8	-	-5720	NM_001080431
WT_D3A	3479	19560912	19561061	2.45	SLC47A2	chr17	-	-351	NM_152908
WT_D3A	4547	150389870	150390094	2.13	SLC4A2	chr7	+	2393	NM_003040
WT_D3A	4546	150388770	150388905	2.31	SLC4A2	chr7	+	1248	NM_003040
WT_D3A	4358	139718392	139718951	2.24	SLC4A9	chr5	+	-1299	NM_031467
WT_D3A	4209	10834513	10834652	2.67	SLC6A11	chr3	+	1666	NM_014229
WT_D3A	4343	1276046	1276711	2.57	SLC6A18	chr5	+	-2091	NM_182632
WT_D3A	4842	152602888	152603162	2.66	SLC6A8	chrX	+	-3920	NM_005629
WT_D3A	4843	152605013	152605542	2.41	SLC6A8	chrX	+	-1668	NM_005629
WT_D3A	4842	152602888	152603162	2.66	SLC6A8	chrX	+	-5134	NM_001142806
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WT_D3A	2725	44254297	44254436	2.24	SLC6A9	chr1	-	1218	NM_006934
WT_D3A	2726	44272443	44272771	2.57	SLC6A9	chr1	-	-2886	NM_001024845
WT_D3A	3371	66852553	66852885	2.87	SLC7A6	chr16	+	-3204	NM_003983
WT_D3A	3370	66851433	66851697	2.26	SLC7A6	chr16	+	-4358	NM_003983
WT_D3A	3305	2015921	2016170	2.64	SLC9A3R2	chr16	+	-843	NM_004785
WT_D3A	3474	18160117	18160481	3.14	SMCR8	chr17	+	981	NM_144775
WT_D3A	2792	244739211	244739335	2.54	SMYD3	chr1	-	-2006	NM_001167740
WT_D3A	3659	7894030	7894494	3.09	SNAPC2	chr19	+	2396	NR_030717
WT_D3A	3659	7894030	7894494	3.09	SNAPC2	chr19	+	3069	NM_003083
WT_D3A	2835	88709455	88710034	3.71	SNCG	chr10	+	1477	NM_003087
WT_D3A	3327	11671312	11671981	3.6	SNN	chr16	+	1845	NM_003498
WT_D3A	4825	51943341	51943985	4.56	SNORA11D	chrX	+	-6794	NR_003711
WT_D3A	4824	51824905	51825059	2.26	SNORA11D	chrX	-	-1673	NR_003711
WT_D3A	4824	51824905	51825059	2.26	SNORA11E	chrX	+	1800	NR_003712
WT_D3A	4859	153656517	153656876	2.72	SNORA56	chrX	+	230	NR_002984
WT_D3A	3974	36492961	36493408	2.76	SNORA71A	chr20	-	-3684	NR_002911
WT_D3A	3974	36492961	36493408	2.76	SNORA71B	chr20	-	-5792	NR_002910
WT_D3A	3974	36492961	36493408	2.76	SNORA71C	chr20	-	-1323	NR_003017
WT_D3A	3974	36492961	36493408	2.76	SNORA71D	chr20	-	2872	NR_003018
WT_D3A	4211	12855163	12855611	2.29	SNORA7A	chr3	-	1562	NR_002582
WT_D3A	3843	10510854	10511296	2.53	SNORA80B	chr2	-	-6649	NR_028374
WT_D3A	4662	33922208	33922447	2.56	SNORD121B	chr9	+	-1958	NR_003690
WT_D3A	4134	28060436	28060680	2.3	SNORD125	chr22	-	-1311	NR_003686
WT_D3A	4135	28061920	28062371	2.8	SNORD125	chr22	-	-2898	NR_003686
WT_D3A	4136	28063686	28063949	2.5	SNORD125	chr22	-	-4570	NR_003686
WT_D3A	4133	28057143	28057372	2.96	SNORD125	chr22	-	1990	NR_003686
WT_D3A	3788	54685978	54686142	2.49	SNORD32A	chr19	+	1026	NR_000021
WT_D3A	3788	54685978	54686142	2.49	SNORD33	chr19	+	375	NR_000020
WT_D3A	3788	54685978	54686142	2.49	SNORD34	chr19	+	85	NR_000019
WT_D3A	3788	54685978	54686142	2.49	SNORD35A	chr19	+	-183	NR_000018
WT_D3A	3788	54685978	54686142	2.49	SNORD35B	chr19	+	-6727	NR_001285
WT_D3A	4734	133343804	133344869	4.16	SNORD62A	chr9	+	-6536	NR_002914

WT_D3A	4734	133343804	133344869	4.16	SNORD62B	chr9	+	-6536	NR_003050
WT_D3A	4166	38039227	38040496	2.7	SNORD83A	chr22	-	1397	NR_000027
WT_D3A	4166	38039227	38040496	2.7	SNORD83B	chr22	-	1	NR_000028
WT_D3A	3014	65355692	65357161	2.98	SNX32	chr11	+	-1559	NM_152760
WT_D3A	4761	137728325	137728469	2.14	SOHLH1	chr9	-	2798	NM_001101677
WT_D3A	4762	137730495	137731665	2.79	SOHLH1	chr9	-	115	NM_001101677
WT_D3A	3287	519855	520204	2.47	SOLH	chr16	+	2173	NM_005632
WT_D3A	3862	39203585	39203749	2.24	SOS1	chr2	-	-2559	NM_005633
WT_D3A	4035	62157691	62157840	2.61	SOX18	chr20	-	-6342	NM_018419
WT_D3A	4412	34632285	34632539	2.43	SPDEF	chr6	-	-343	NM_012391
WT_D3A	3428	88096036	88096160	2.7	SPG7	chr16	+	-6207	NM_003119
WT_D3A	3775	53809115	53809764	2.42	SPHK2	chr19	+	-4920	NM_020126
WT_D3A	3796	55614028	55615478	2.89	SPIB	chr19	+	747	NM_003121
WT_D3A	3300	1771512	1771866	3.07	SPSB3	chr16	-	893	NM_080861
WT_D3A	3299	1769444	1769588	2.1	SPSB3	chr16	-	3066	NM_080861
WT_D3A	3022	66244878	66245712	2.83	SPTBN2	chr11	-	151	NM_006946
WT_D3A	3243	39972498	39973917	3.67	SPTBN5	chr15	-	360	NM_016642
WT_D3A	4521	100306904	100307343	3.03	SRRT	chr7	+	-3513	NM_015908
WT_D3A	4791	139199421	139199660	2.63	SSNA1	chr9	+	-3334	NM_003731
WT_D3A	4790	139197516	139197985	2.29	SSNA1	chr9	+	-5124	NM_003731
WT_D3A	4538	149106857	149107106	2.78	SSPO	chr7	+	2918	NM_198455
WT_D3A	4844	152708244	152708673	2.86	SSR4	chrX	+	-4829	NM_006280
WT_D3A	4155	35934718	35936437	3.13	SSTR3	chr22	-	2722	NM_001051
WT_D3A	3291	1066907	1067226	2.56	SSTR5	chr16	+	-1715	NM_001053
WT_D3A	4244	52498726	52499690	2.27	STAB1	chr3	+	-5187	NM_015136
WT_D3A	4592	38128368	38128942	3.14	STAR	chr8	-	-898	NM_000349
WT_D3A	3513	41430091	41430360	2.38	STH	chr17	+	-2227	NM_001007532
WT_D3A	2964	3833439	3833583	2.09	STIM1	chr11	+	3	NM_003156
WT_D3A	3906	219816068	219816729	3.47	STK16	chr2	+	-2046	NR_026909
WT_D3A	3906	219816068	219816729	3.47	STK16	chr2	+	-2037	NM_001008910
WT_D3A	4403	32045530	32045979	2.55	STK19	chr6	+	-1870	NM_032454
WT_D3A	4403	32045530	32045979	2.55	STK19	chr6	+	-1176	NR_026717
WT_D3A	3135	97970677	97971326	2.47	STK24	chr13	-	1341	NM_003576
WT_D3A	3136	97978554	97979004	2.53	STK24	chr13	-	-6437	NM_003576
WT_D3A	4664	35090951	35091305	2.1	STOML2	chr9	-	2026	NM_013442
WT_D3A	3584	77575827	77575961	2.68	STRA13	chr17	-	-1832	NM_144998
WT_D3A	3656	7601442	7601701	3.19	STXBP2	chr19	+	-6419	NM_006949
WT_D3A	3774	53748671	53749210	3.18	SULT2B1	chr19	+	1700	NM_177973
WT_D3A	3525	53790618	53790787	2.38	SUPT4H1	chr17	-	-6140	NM_003168
WT_D3A	4745	135235305	135235539	2.31	SURF4	chr9	-	-2631	NM_033161
WT_D3A	4408	33491004	33491524	2.58	SYNGAP1	chr6	+	-4560	NM_006772
WT_D3A	4167	38085837	38086801	2.62	SYNGR1	chr22	+	-3801	NM_145738
WT_D3A	3560	73673698	73674045	2.36	SYNGR2	chr17	+	-2394	NM_004710
WT_D3A	2826	75088424	75088685	2.42	SYNPO2L	chr10	-	-2716	NM_001114133
WT_D3A	4823	48948317	48948580	2.34	SYP	chrX	-	-4843	NM_003179
WT_D3A	2898	1803525	1805154	2.3	SYT8	chr11	+	-7910	NM_138567
WT_D3A	2899	1811724	1811948	2.74	SYT8	chr11	+	-413	NM_138567

WT_D3A	4435	158988520	158988769	2.68	SYTL3	chr6	+	-2389	NM_001009991
WT_D3A	2817	70845894	70846153	2.16	TACR2	chr10	-	657	NM_001057
WT_D3A	2966	6587500	6587664	2.18	TAF10	chr11	-	2439	NM_006284
WT_D3A	3051	116577957	116578216	2.31	TAGLN	chr11	+	2837	NM_003186
WT_D3A	2763	158165514	158165671	2.53	TAGLN2	chr1	-	-3684	NM_003564
WT_D3A	4407	33395469	33397328	3.32	TAPBP	chr6	-	-6256	NM_172209
WT_D3A	3090	52184756	52185790	2.74	TARBP2	chr12	+	3630	NM_134324
WT_D3A	2674	6538355	6538504	2.68	TAS1R1	chr1	+	409	NM_177540
WT_D3A	3345	30290265	30292004	3.25	TBC1D10B	chr16	-	-2111	NM_015527
WT_D3A	3025	66922729	66923348	3.34	TBC1D10C	chr11	+	-4949	NM_198517
WT_D3A	3791	55073257	55073411	2.25	TBC1D17	chr19	+	841	NM_001168222
WT_D3A	4384	179264493	179265047	3.33	TBC1D9B	chr5	-	2692	NM_015043
WT_D3A	2789	233592005	233592149	2.04	TBCE	chr1	+	-5273	NM_003193
WT_D3A	4112	18126046	18126185	2.11	TBX1	chr22	+	1890	NM_005992
WT_D3A	3642	3554274	3555123	3.17	TBXA2R	chr19	-	3133	NM_201636
WT_D3A	4035	62157691	62157840	2.61	TCEA2	chr20	+	-6688	NM_003195
WT_D3A	4035	62157691	62157840	2.61	TCEA2	chr20	+	-1117	NM_198723
WT_D3A	3602	42814370	42814639	3.03	TCEB3B	chr18	-	1482	NM_016427
WT_D3A	3602	42814370	42814639	3.03	TCEB3C	chr18	-	-4057	NM_145653
WT_D3A	3602	42814370	42814639	3.03	TCEB3CL	chr18	-	-4293	NM_001100817
WT_D3A	3433	88464320	88464679	2.16	TCF25	chr16	+	-2995	NM_014972
WT_D3A	3629	1609448	1610195	2.53	TCF3	chr19	-	-6495	NM_003200
WT_D3A	3033	67560218	67561942	4.83	TCIRG1	chr11	+	-1978	NM_006019
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WT_D3A	4039	32881645	32881808	2.2	TCP10L	chr21	-	-2010	NM_144659
WT_D3A	4038	32876268	32876700	2.41	TCP10L	chr21	-	3232	NM_144659
WT_D3A	4426	44379678	44380213	2.93	TCTE1	chr6	-	-6509	NM_182539
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WT_D3A	4414	35569834	35569988	2.38	TEAD3	chr6	-	2928	NM_003214
WT_D3A	2714	36325463	36326422	2.94	TEKT2	chr1	+	3680	NM_014466
WT_D3A	4665	35597681	35598150	2.32	TESK1	chr9	+	2635	NM_006285
WT_D3A	4058	42658727	42659146	3.44	TFF1	chr21	-	777	NM_003225
WT_D3A	4059	42661123	42661347	2.68	TFF1	chr21	-	-1522	NM_003225
WT_D3A	4518	100077506	100077955	2.3	TFR2	chr7	-	-621	NM_003227
WT_D3A	3185	75515821	75516344	2.67	TGFB3	chr14	-	1763	NM_003239
WT_D3A	3186	75517016	75517843	3.07	TGFB3	chr14	-	416	NM_003239
WT_D3A	3174	23806725	23806959	2.61	TGM1	chr14	-	-4586	NM_000359
WT_D3A	2917	2150923	2151247	3.45	TH	chr11	-	-1474	NM_000360
WT_D3A	3317	3015407	3015861	2.34	THOC6	chr16	+	1602	NM_001142350
WT_D3A	3633	2729664	2731813	2.91	THOP1	chr19	+	-5767	NM_003249
WT_D3A	4639	144746556	144746710	2.19	TIGD5	chr8	+	-4583	NM_032862
WT_D3A	4242	52238054	52238580	2.23	TLR9	chr3	-	-3098	NM_017442
WT_D3A	3557	73642588	73643342	2.9	TMC6	chr17	-	-2882	NM_007267
WT_D3A	3558	73644693	73646544	3.18	TMC6	chr17	-	-5535	NM_007267
WT_D3A	3557	73642588	73643342	2.9	TMC6	chr17	-	-6509	NM_001127198
WT_D3A	3556	73631863	73632042	2.39	TMC8	chr17	+	-6501	NM_152468
WT_D3A	3672	10806710	10806974	2.47	TMED1	chr19	-	1141	NM_006858

WT_D3A	4782	138808031	138808210	2.47	TMEM141	chr9	+	2523	NM_032928
WT_D3A	4459	1564493	1565057	3.36	TMEM184A	chr7	-	-2183	NM_001097620
WT_D3A	3828	60582136	60582295	2.37	TMEM190	chr19	+	2200	NM_139172
WT_D3A	3294	1525275	1528112	2.75	TMEM204	chr16	+	2462	NM_024600
WT_D3A	3854	27102350	27103174	2.48	TMEM214	chr2	+	-6515	NM_001083590
WT_D3A	2652	1843540	1843789	2.62	TMEM52	chr1	-	-3064	NM_178545
WT_D3A	3824	60429318	60429652	2.44	TMEM86B	chr19	-	2959	NM_173804
WT_D3A	3469	7694925	7695159	3.22	TMEM88	chr17	+	-4066	NM_203411
WT_D3A	4749	135385527	135386046	2.72	TMEM8C	chr9	-	-5897	NM_001080483
WT_D3A	4748	135383302	135384346	3.15	TMEM8C	chr9	-	-3935	NM_001080483
WT_D3A	3445	3512851	3513306	2.64	TMEM93	chr17	+	-5760	NM_031298
WT_D3A	3312	2829485	2830299	2.96	TMPRSS8	chr16	-	2861	NR_026864
WT_D3A	3868	84982179	84982348	2.03	TMSB10	chr2	+	-4010	NM_021103
WT_D3A	3207	102664449	102664768	2.75	TNFAIP2	chr14	+	2192	NM_006291
WT_D3A	3648	4592352	4592993	3.49	TNFAIP8L1	chr19	+	1644	NM_001167942
WT_D3A	3647	4591062	4591386	3.2	TNFAIP8L1	chr19	+	196	NM_001167942
WT_D3A	3648	4592352	4592993	3.49	TNFAIP8L1	chr19	+	2146	NM_152362
WT_D3A	3647	4591062	4591386	3.2	TNFAIP8L1	chr19	+	698	NM_152362
WT_D3A	3316	3003840	3004169	2.48	TNFRSF12A	chr16	+	-6309	NM_016639
WT_D3A	4171	40659166	40659795	2.9	TNFRSF13C	chr22	-	-6713	NM_052945
WT_D3A	2664	2483371	2483830	2.6	TNFRSF14	chr1	-	3013	NM_003820
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WT_D3A	2681	12110177	12110401	3.04	TNFRSF8	chr1	+	1745	NM_152942
WT_D3A	3467	7394430	7395654	3.7	TNFSF12	chr17	+	1944	NM_003809
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WT_D3A	3468	7400802	7401156	2.38	TNFSF13	chr17	+	-1353	NM_172088
WT_D3A	4273	197103863	197104582	3.77	TNK2	chr3	-	2607	NM_001010938
WT_D3A	4243	52459910	52460059	2.48	TNNC1	chr3	-	3113	NM_003280
WT_D3A	2899	1811724	1811948	2.74	TNNI2	chr11	+	-6171	NM_001145841
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WT_D3A	3899	217432462	217432586	2.66	TNP1	chr2	-	503	NM_003284
WT_D3A	3326	11274458	11275102	3	TNP2	chr16	-	-4119	NM_005425
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WT_D3A	3474	18160117	18160481	3.14	TOP3A	chr17	-	-1253	NM_004618
WT_D3A	3475	18162822	18162973	2.47	TOP3A	chr17	-	-3851	NM_004618
WT_D3A	4706	129540108	129540242	2.43	TOR2A	chr9	-	-2750	NM_001085347
WT_D3A	3058	128317011	128317560	2.64	TP53AIP1	chr11	-	747	NM_022112
WT_D3A	3072	6842780	6843734	2.62	TPI1	chr12	+	-3587	NM_001159287
WT_D3A	3073	6848488	6848717	2.56	TPI1	chr12	+	1758	NM_001159287
WT_D3A	3072	6842780	6843734	2.62	TPI1	chr12	+	-3696	NM_000365
WT_D3A	3073	6848488	6848717	2.56	TPI1	chr12	+	1649	NM_000365

WT_D3A	3072	6842780	6843734	2.62	TPI1	chr12	+	-4281	NR_027483
WT_D3A	3073	6848488	6848717	2.56	TPI1	chr12	+	1064	NR_027483
WT_D3A	3362	65990238	65990569	3.51	TPPP3	chr16	-	-5481	NM_015964
WT_D3A	3416	87444290	87444719	2.53	TRAPPC2L	chr16	+	-6502	NM_016209
WT_D3A	4265	161653396	161653523	2.72	TRIM59	chr3	-	-3139	NM_173084
WT_D3A	2994	63838586	63839335	2.66	TRMT112	chr11	-	2649	NM_016404
WT_D3A	2933	2401817	2402141	2.61	TRPM5	chr11	-	-1128	NM_014555
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WT_D3A	4735	134813754	134814404	2.65	TSC1	chr9	-	-4238	NM_001162427
WT_D3A	3306	2032041	2032210	2.42	TSC2	chr16	+	-5865	NM_001077183
WT_D3A	3307	2033152	2034181	2.6	TSC2	chr16	+	-4324	NM_001077183
WT_D3A	4620	143487146	143487619	2.44	TSNARE1	chr8	-	-4934	NM_145003
WT_D3A	4621	143488828	143489293	2.4	TSNARE1	chr8	-	-6612	NM_145003
WT_D3A	4619	143479967	143481526	3.76	TSNARE1	chr8	-	1702	NM_145003
WT_D3A	3579	77222115	77222649	3.5	TSPAN10	chr17	+	2629	NM_031945
WT_D3A	2832	82198050	82198381	2.04	TSPAN14	chr10	+	-5802	NM_001128309
WT_D3A	3865	54336155	54336504	2.79	TSPYL6	chr2	-	584	NM_001003937
WT_D3A	2711	32602207	32602535	2.46	TSSK3	chr1	+	1923	NM_052841
WT_D3A	3245	41005442	41005787	2.91	TTBK2	chr15	-	-5315	NM_173500
WT_D3A	2732	51580917	51581046	2.01	TTC39A	chr1	-	2392	NM_001144832
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WT_D3A	3907	219824755	219825314	2.62	TUBA4A	chr2	-	1848	NM_006000
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WT_D3A	4795	139256699	139256848	3.11	TUBB2C	chr9	+	1242	NM_006088
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WT_D3A	3599	12294359	12295608	3.1	TUBB6	chr18	+	-3273	NM_032525
WT_D3A	2875	134978429	134978683	2.27	TUBGCP2	chr10	-	-5922	NM_006659
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WT_D3A	3777	54090250	54090619	3.71	TULP2	chr19	-	3374	NM_003323
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WT_D3A	4236	50343474	50343693	2.85	TUSC2	chr3	-	-2911	NM_007275
WT_D3A	3436	1129840	1130574	2.68	TUSC5	chr17	+	501	NM_172367
WT_D3A	3382	70687882	70688409	2.5	TXNL4B	chr16	-	-3105	NM_017853
WT_D3A	3383	70690058	70690199	2.28	TXNL4B	chr16	-	-5088	NM_017853
WT_D3A	3382	70687882	70688409	2.5	TXNL4B	chr16	-	-2876	NM_001142317
WT_D3A	3383	70690058	70690199	2.28	TXNL4B	chr16	-	-4859	NM_001142317
WT_D3A	3382	70687882	70688409	2.5	TXNL4B	chr16	-	-2429	NM_001142318
WT_D3A	3383	70690058	70690199	2.28	TXNL4B	chr16	-	-4412	NM_001142318
WT_D3A	3239	39640158	39641402	2.9	TYRO3	chr15	+	2257	NM_006293
WT_D3A	4786	139094774	139095233	2.54	UAP1L1	chr9	+	3230	NM_207309
WT_D3A	2648	1195480	1196829	2.81	UBE2J2	chr1	-	2943	NM_058167

WT_D3A	4031	62049017	62049366	2.69	UCKL1AS	chr20	+	-5989	NR_027287
WT_D3A	4229	48578244	48578403	2.58	UCN2	chr3	-	-2118	NM_033199
WT_D3A	4230	48579315	48580977	2.64	UCN2	chr3	-	-3941	NM_033199
WT_D3A	4326	69577000	69577245	2.6	UGT2B15	chr4	-	-6143	NM_001076
WT_D3A	3254	72921950	72922274	2.86	ULK3	chr15	-	493	NM_001099436
WT_D3A	3545	71354017	71354166	2.33	UNC13D	chr17	-	-1698	NM_199242
WT_D3A	3546	71356002	71356656	3.42	UNC13D	chr17	-	-3936	NM_199242
WT_D3A	3879	98589002	98589136	2.53	UNC50	chr2	+	-2404	NM_014044
WT_D3A	4164	37486582	37487032	3	UNC84B	chr22	-	-4914	NM_015374
WT_D3A	4442	167627524	167627743	2.61	UNC93A	chr6	+	2841	NM_001143947
WT_D3A	2728	45245489	45245808	3	UROD	chr1	+	-4768	NM_000374
WT_D3A	3699	17184879	17185348	2.76	USE1	chr19	+	-2041	NM_018467
WT_D3A	3732	40453852	40454181	2.65	USF2	chr19	+	2281	NM_207291
WT_D3A	4819	46970264	46971708	3.23	USP11	chrX	+	-6271	NM_004651
WT_D3A	3047	77579624	77580063	2.01	USP35	chr11	+	2238	NM_020798
WT_D3A	3564	74351733	74352856	4.07	USP36	chr17	-	-3730	NM_025090
WT_D3A	4753	135845636	135845775	3.03	VAV2	chr9	-	1562	NM_003371
WT_D3A	4214	38010136	38010295	2.22	VILL	chr3	+	134	NM_015873
WT_D3A	4432	153116031	153116200	2.11	VIP	chr6	+	2490	NM_194435
WT_D3A	4565	158636953	158637087	2.18	VIPR2	chr7	-	-6610	NM_003382
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WT_D3A	3350	31014262	31014891	2.97	VKORC1	chr16	-	-799	NM_024006
WT_D3A	4655	145628310	145628935	2.9	VPS28	chr8	-	-3887	NM_016208
WT_D3A	4498	72789487	72789721	3	WBSCR26	chr7	+	2270	NR_026690
WT_D3A	4754	135997157	135997615	2.55	WDR5	chr9	+	2652	NM_052821
WT_D3A	3259	76383515	76383646	2.13	WDR61	chr15	-	-4585	NM_025234
WT_D3A	3978	43858863	43859212	2.47	WFDC3	chr20	-	-5083	NM_080614
WT_D3A	3656	7601442	7601701	3.19	XAB2	chr19	-	-1132	NM_020196
WT_D3A	2706	28157721	28157860	2.17	XKR8	chr1	+	-1300	NM_018053
WT_D3A	3760	48774388	48774705	2.88	XRCC1	chr19	-	-2976	NM_006297
WT_D3A	4120	20316930	20317254	3.18	YDJC	chr22	-	-2752	NM_001017964
WT_D3A	3674	10895716	10897465	3.14	YIPF2	chr19	-	3767	NM_024029
WT_D3A	4121	20423379	20423632	2.4	YPEL1	chr22	-	-3434	NM_013313
WT_D3A	4407	33395469	33397328	3.32	ZBTB22	chr6	-	-2701	NM_001145338
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WT_D3A	3466	7321445	7322819	3.18	ZBTB4	chr17	-	1536	NM_001128833
WT_D3A	4409	33523956	33524300	2.71	ZBTB9	chr6	+	-6205	NM_152735
WT_D3A	2718	37713539	37715513	3.8	ZC3H12A	chr1	+	1821	NM_025079
WT_D3A	4714	130524038	130524377	3.2	ZDHHC12	chr9	-	2022	NM_032799
WT_D3A	3020	66065699	66067153	3.15	ZDHHC24	chr11	-	3821	NM_207340
WT_D3A	4115	18493476	18494445	5.26	ZDHHC8	chr22	+	-5404	NM_013373
WT_D3A	4607	135777290	135777859	2.87	ZFAT	chr8	-	407	NM_001167583
WT_D3A	3412	87040342	87041261	3.79	ZFPM1	chr16	+	-6713	NM_153813
WT_D3A	3311	2819363	2819587	2.53	ZG16B	chr16	+	-698	NM_145252
WT_D3A	4396	28335215	28335434	2.37	ZKSCAN4	chr6	-	-7343	NM_019110
WT_D3A	4487	44760377	44760631	2.69	ZMIZ2	chr7	+	-1807	NM_174929
WT_D3A	4488	44762787	44763231	2.93	ZMIZ2	chr7	+	698	NM_174929

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WT_D3A	3762	49694502	49695976	2.84	ZNF180	chr19	-	1175	NM_013256
WT_D3A	3991	51631673	51633222	2.71	ZNF217	chr20	-	596	NM_006526
WT_D3A	3432	88311333	88312587	4	ZNF276	chr16	+	-2933	NM_152287
WT_D3A	3432	88311333	88312587	4	ZNF276	chr16	+	-3492	NM_001113525
WT_D3A	4660	145986688	145986847	2.34	ZNF34	chr8	-	-3238	NM_030580
WT_D3A	3835	63116791	63117253	2.24	ZNF417	chr19	-	2768	NM_152475
WT_D3A	3761	48819880	48820425	3.33	ZNF428	chr19	-	-4298	NM_182498
WT_D3A	4538	149106857	149107106	2.78	ZNF467	chr7	-	-5753	NM_207336
WT_D3A	2795	245558680	245559219	2.53	ZNF496	chr1	-	2719	NM_032752
WT_D3A	2796	245564402	245565435	2.85	ZNF496	chr1	-	-3250	NM_032752
WT_D3A	2828	76836430	76836583	2.34	ZNF503	chr10	-	-4987	NM_032772
WT_D3A	2873	134966536	134967510	3.06	ZNF511	chr10	+	-5389	NM_145806
WT_D3A	2874	134969361	134969695	2.31	ZNF511	chr10	+	-2884	NM_145806
WT_D3A	3635	2766624	2767761	3.35	ZNF554	chr19	+	-3679	NM_001102651
WT_D3A	3661	8795035	8795269	2.61	ZNF558	chr19	-	-587	NM_144693
WT_D3A	3738	42396048	42396361	2.94	ZNF585B	chr19	-	-2913	NM_152279
WT_D3A	4566	169534	169881	2.27	ZNF596	chr8	+	-2676	NM_001042416
WT_D3A	4566	169534	169881	2.27	ZNF596	chr8	+	-2492	NM_173539
WT_D3A	3304	1997726	1998365	3.6	ZNF598	chr16	-	1719	NM_178167
WT_D3A	2784	225815897	225816236	2.8	ZNF678	chr1	+	-1800	NM_178549
WT_D3A	4633	144438499	144438633	2.11	ZNF696	chr8	+	-6367	NM_030895
WT_D3A	4661	146016475	146017209	2.35	ZNF7	chr8	+	-6864	NM_003416
WT_D3A	4276	487172	487423	2.74	ZNF721	chr4	-	-3855	NM_133474
WT_D3A	4275	480007	481253	2.58	ZNF721	chr4	-	2812	NM_133474
WT_D3A	3595	78389990	78390157	2.37	ZNF750	chr17	-	1147	NM_024702
WT_D3A	3123	132119469	132119723	2.19	ZNF84	chr12	+	-4456	NM_001127372
WT_D3A	3123	132119469	132119723	2.19	ZNF84	chr12	+	-4354	NM_003428

D3A_WT: DNA hypermethylation in samples with DNMT3A mutations (D3A) compared to those without DNMT3A mutations (WT). WT_D3A: DNA hypermethylation in samples without DNMT3A mutations (WT) compared to those with DNMT3A mutations (D3A). Peak: DNA methylation enrichment region. PeakID: A serial number given by SQL software for each peak. PeakScore: The average -log10 (P-value) from probes within the peak. The scores reflect the probability of positive enrichment. (Cut off=2). GeneName: The gene which the peak overlaps its promoter region. PeakToTSS: The distance from the centre of the peak to the translation start site (TSS).

Supplementary Table 10. Multivariate analysis of clinical and molecular variables

Variables	CR		OS		TTF	
	P	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)
Age	NS	-	NS	-	NS	-
Gender	NS	-	NS	-	NS	-
WBC count	0.046	0.994 (0.988-1.000)	0.002	1.005 (1.002-1.007)	0.009	1.004 (1.001-1.007)
Monoblasts in BM	NS	-	NS	-	NS	-
DNMT3A mutations	0.047	0.349 (0.122-1.002)	0.009	2.169 (1.217-3.867)	0.019	2.018 (1.123-3.626)
MLL abnormalities	NS	-	NS	-	0.072	1.817 (0.948-3.480)
NPM1 mutations	NS	-	NS	-	NS	-
NRAS mutations	NS	-	NS	-	NS	-
FLT3 abnormalities	NS	-	NS	-	NS	-

NS: no significance.

Binary logistic regression was used for the multivariate analysis of CR rate. A Cox model was used to identify prognostic variables for OS and TTF. A limited backward selection procedure was used to exclude redundant or unnecessary variables. To provide quantitative information on the relevance of results, 95% confidence intervals (CI) of odds ratios (OR) was calculated.

Supplementary Table 11. Sequenom BS-MS analysis primers.

HOXB2_BS-MS_F	ATTTGGAAAAGAGGAAGGTTTTTTT
HOXB2_BS-MS_R	AAAACTCTCTCTATTAAACCCAAAACTC
HOXB4_BS-MS_F	GGGTTTTTGGAAGGTATAGAATGTT
HOXB4_BS-MS_R	CCCTCCTACTTACTATCAAATAAACAAAA
HOXB5_BS-MS_F	TGATTTTAAGAGGTAATTTATGTTTTATGG
HOXB5_BS-MS_R	TAAATAAAAAACCCAACCCCTACTC
HOXB7_BS-MS_F	TGGTTTGGTTTAATAAAGAATAGATTTG
HOXB7_BS-MS_R	AAAATCCAAATTTACACCAAAAAAA
IDH1_BS-MS_F	GATGGAGAATTTATGGTGTTATTTTT
IDH1_BS-MS_R	TTTTCCATCCTTTACATTAAACAAC
T7-promoter tag	CAGTAATACGACTCACTATAGGGAGA
Decamer linker	AGGAAGAGAG