

Supplemental Table S7. sgRNA target sites and sequences

gene_name	sequence	crispr_pam	crispr_gc	chromosome	chr_direction	chr_start	chr_stop	exon	transcript_id	direction	crispr_start	crispr_stop
ACTL6A	GCGGATAAAA	CGG	50	chr3	(+)	179570136	179570158	[exon3, exor	NM_004301	(+)	7257	7279
ACTL6A	ACCACCATAC	AGG	45	chr3	(-)	179570076	179570098	[exon3]	NM_004301	(+)	7197	7219
ACTL6A	GCGGTGTTCC	TGG	55	chr3	(+)	179570189	179570211	[exon3, exor	NM_004301	(+)	7310	7332
ACTL6A	GGATCCTAT	TGG	50	chr3	(+)	179569853	179569875	[exon2]	NM_004301	(+)	6974	6996
ACTL6B	AGACTTGAC	AGG	47,37	chr7	(+)	100655058	100655080	exon4	NM_016188	(-)	11956	11978
ACTL6B	AGGTGGAT	CGG	57,89	chr7	(+)	100655078	100655100	exon4	NM_016188	(-)	11976	11998
ACTL6B	GTACATGTCG	TGG	57,89	chr7	(-)	100655426	100655448	exon3	NM_016188	(-)	12324	12346
AEBP2	ATACATGTAT	AGG	45	chr12	(+)	19462691	19462713	[exon2, exor	NM_001114	(+)	23018	23040
AEBP2	CCAGTCAAA	AGG	40	chr12	(+)	19473297	19473319	[exon3, exor	NM_001114	(+)	33624	33646
AEBP2	GGATGTGAT	GGG	50	chr12	(-)	19462663	19462685	[exon2, exor	NM_001114	(+)	22990	23012
AEBP2	TGCTGGAGT	TGG	60	chr12	(-)	19462548	19462570	[exon2, exor	NM_001114	(+)	22875	22897
AFF1	CCTGCTTCG	AGG	47,37	chr4	(+)	87046187	87046209	exon2, exon3	NM_001313	(+)	39187	39209
AFF1	TAGTCGAAT	TGG	36,84	chr4	(+)	87046718	87046740	exon3, exon4	NM_001313	(+)	39718	39740
AFF1	GAGTGTGAC	AGG	42,11	chr4	(-)	87046766	87046788	exon3, exon4	NM_001313	(+)	39766	39788
AFF1	CTTGAGGG	GGG	47,37	chr4	(-)	87046264	87046286	exon2, exon3	NM_001313	(+)	39264	39286
AFF4	TGCGTATGA	AGG	47,37	chr5	(-)	132937142	132937164	exon2	NM_014423	(-)	61764	61786
AFF4	TTGATGGC	AGG	42,11	chr5	(+)	132937071	132937093	exon2	NM_014423	(-)	61693	61715
AFF4	CAGTCTCAG	AGG	52,63	chr5	(-)	132934688	132934710	exon3	NM_014423	(-)	59310	59332
AFF4	GCAGCATAT	CGG	57,89	chr5	(+)	132937162	132937184	exon2	NM_014423	(-)	61784	61806
AICDA	ATGTGGCCG	GGG	55	chr12	(-)	8605342	8605364	[exon3]	NM_020661	(-)	3177	3199
AICDA	TCGTCCGTA	TGG	60	chr12	(-)	8605438	8605460	[exon3]	NM_020661	(-)	3273	3295
AICDA	ACCTGTGCT	AGG	50	chr12	(-)	8606916	8606938	[exon2]	NM_020661	(-)	4751	4773
AICDA	ACTTCTCCG	AGG	50	chr12	(+)	8606990	8607012	[exon2]	NM_020661	(-)	4825	4847
AIRE	GTGGTTGGT	GGG	52,63	chr21	(+)	44290809	44290831				0	0
AIRE	ACCGGGTTT	GGG	47,37	chr21	(+)	44290859	44290881				0	0
AIRE	GACTACAAC	TGG	57,89	chr21	(+)	44286674	44286696	exon2	NM_000383	(+)	837	859
AIRE	AAGAGACG	GGG	57,89	chr21	(-)	44291061	44291083				0	0
AKAP1	GACTCTGAT	TGG	52,63	chr17	(-)	57105762	57105784	exon3, exon3	NM_001242	(+)	20571	20593
AKAP1	GGTGTTAGC	AGG	52,63	chr17	(-)	57105784	57105806	exon3, exon3	NM_001242	(+)	20593	20615
AKAP1	TGCTCGCAA	TGG	47,37	chr17	(-)	57105805	57105827	exon3, exon3	NM_001242	(+)	20614	20636
AKAP1	GTGGACAGT	AGG	47,37	chr17	(-)	57105693	57105715	exon3, exon3	NM_001242	(+)	20502	20524
ARID1A	GAGAACTC	CGG	55	chr1	(+)	26696703	26696725	[exon1, exor	NM_006015	(+)	673	695
ARID1A	AAGAACTCG	GGG	55	chr1	(+)	26696704	26696726	[exon1, exor	NM_006015	(+)	674	696
ARID1A	CGGACCTGA	GGG	55	chr1	(+)	26696696	26696718	[exon1, exor	NM_006015	(+)	666	688
ARID1A	CGTTCCTGT	AGG	55	chr1	(-)	26696700	26696722	[exon1, exor	NM_006015	(+)	670	692
ARID1B	CGCCAACTG	TGG	50	chr6	(-)	156778127	156778149	[exon1, exor	NM_017515	(+)	198	220
ARID1B	CGGTTTTCA	GGG	45	chr6	(-)	156778121	156778143	[exon1, exor	NM_017515	(+)	192	214
ARID1B	ACGGTTTTT	CGG	40	chr6	(-)	156778122	156778144	[exon1, exor	NM_017515	(+)	193	215
ARID1B	AACCACTAT	TGG	40	chr6	(+)	156778125	156778147	[exon1, exor	NM_017515	(+)	196	218
ARID2	GAATCTTCT	AGG	35	chr12	(-)	45811421	45811443	[exon4]	NM_152641	(+)	81585	81607
ARID2	GCAGCGTTA	GGG	45	chr12	(-)	45731265	45731287	[exon3]	NM_152641	(+)	1429	1451
ARID2	ACCAGAGTC	CGG	45	chr12	(+)	45730105	45730127	[exon2]	NM_152641	(+)	269	291
ARID2	ATTGCACCA	TGG	45	chr12	(-)	45811491	45811513	[exon4]	NM_152641	(+)	81655	81677
ARID4A	TCGGTACTT	CGG	52,63	chr14	(-)	58301614	58301636	exon3, exon3	NM_023001	(+)	3111	3133
ARID4A	GCAAGTTGA	TGG	47,37	chr14	(+)	58306080	58306102	exon5, exon5	NM_023001	(+)	7577	7599
ARID4A	GTACATCTG	TGG	36,84	chr14	(-)	58304966	58304988	exon4, exon4	NM_023001	(+)	6463	6485
ARID4A	GTACCGAGG	AGG	57,89	chr14	(+)	58301630	58301652	exon3, exon3	NM_023001	(+)	3127	3149
ARID4B	GTGCCACT	AGG	52,63	chr1	(+)	235260718	235260740	exon3, exon3	NM_001206	(-)	93824	93846
ARID4B	CGATCTTCA	AGG	52,63	chr1	(-)	235252755	235252777	exon6, exon6	NM_001206	(-)	85861	85883
ARID4B	AGTGCCAAA	TGG	52,63	chr1	(+)	235246467	235246489	exon7, exon7	NM_001206	(-)	79573	79595
ARID4B	GTTCCAGAT	GGG	42,11	chr1	(-)	235257192	235257192	exon4, exon4	NM_001206	(-)	90276	90298
ASH1L	TTTCTCGAT	AGG	47,37	chr1	(+)	155521354	155521376	exon2	NM_018489	(-)	186094	186116
ASH1L	CGAGAAAG	TGG	42,11	chr1	(-)	155521338	155521360	exon2	NM_018489	(-)	186078	186100
ASH1L	GACCAATGT	TGG	52,63	chr1	(+)	155521424	155521446	exon2	NM_018489	(-)	186164	186186
ASH1L	GGATTGGGT	AGG	52,63	chr1	(-)	155521470	155521492	exon2	NM_018489	(-)	186210	186232
ASH2L	CGGATGTTT	GGG	47,37	chr8	(-)	38110787	38110809	exon5, exon4	NM_001261	(+)	4995	5017
ASH2L	GCAAACTGT	CGG	42,11	chr8	(+)	38106382	38106404	exon2	NM_004674	(+)	890	912
ASH2L	GTGGGAAT	CGG	42,11	chr8	(+)	38110435	38110457	exon4, exon3	NM_001261	(+)	4643	4665
ASH2L	GCCTACCTC	CGG	57,89	chr8	(-)	38107086	38107108	exon3, exon3	NM_001261	(+)	1294	1316
ASXL1	TAGCATTTA	GGG	52,63	chr20	(-)	32369024	32369046	exon3, exon3	NM_015338	(+)	10681	10703
ASXL1	GTGAAAAGC	AGG	52,63	chr20	(-)	32369094	32369116	exon3, exon3	NM_015338	(+)	10751	10773
ASXL1	CTACATTCCA	AGG	36,84	chr20	(+)	32369049	32369071	exon3, exon3	NM_015338	(+)	10706	10728
ASXL1	GTATGAACC	TGG	47,37	chr20	(+)	32372227	32372249				0	0
ASXL2	CATACAGTT	AGG	42,11	chr2	(-)	25806246	25806268	exon3	NM_018263	(-)	66863	66885
ASXL2	ATGCTTCACT	AGG	42,11	chr2	(-)	25806284	25806306	exon3	NM_018263	(-)	66901	66923
ASXL2	ATTGCATTCT	AGG	42,11	chr2	(+)	25806305	25806327	exon3	NM_018263	(-)	66922	66944
ASXL2	CTTCAAGTT	AGG	42,11	chr2	(-)	25845496	25845518	exon2	NM_018263	(-)	106113	106135
ASXL3	GTGAAGCAT	AGG	42,11	chr18	(-)	33644911	33644933	exon3	NM_030632	(+)	66335	66357
ASXL3	AATCCAACG	GGG	52,63	chr18	(-)	33646262	33646284	exon4	NM_030632	(+)	67686	67708
ASXL3	TTCACTATA	GGG	36,84	chr18	(+)	33644929	33644951	exon3	NM_030632	(+)	66353	66375
ASXL3	GGATGGTAC	AGG	52,63	chr18	(+)	33646304	33646326	exon4	NM_030632	(+)	67728	67750
ATAD2	AGGAAGTTC	CGG	42,11	chr8	(-)	123380639	123380661	exon2	NM_014109	(-)	60789	60811
ATAD2	ATAACGGAG	TGG	42,11	chr8	(-)	123380544	123380566	exon2	NM_014109	(-)	60694	60716
ATAD2	TCCAGTGA	TGG	52,63	chr8	(-)	123396264	123396286	exon1	NM_014109	(-)	76414	76436
ATAD2	GAAGTCACT	AGG	57,89	chr8	(+)	123396274	123396296	exon1	NM_014109	(-)	76424	76446
ATAD2B	ACGAAGTAC	AGG	52,63	chr2	(-)	23895847	23895869	exon2, exon2	NM_001242	(-)	147184	147206
ATAD2B	GATGAAATG	CGG	52,63	chr2	(+)	23926654	23926676	exon1, exon1	NM_001242	(-)	177991	178013
ATAD2B	TTCAAGATG	AGG	47,37	chr2	(+)	23895906	23895928	exon2, exon2	NM_001242	(-)	147243	147265
ATAD2B	CTTCTCGGG	TGG	57,89	chr2	(-)	23926718	23926740	exon1, exon1	NM_001242	(-)	178055	178077
ATAT1	TGATGCTAT	CGG	42,11	chr6	(-)	30627649	30627671	exon3, exon3	NM_001318	(+)	808	830
ATAT1	TGATCGTGA	AGG	42,11	chr6	(+)	30628034	30628056	exon5, exon5	NM_001318	(+)	1193	1215
ATAT1	AACAGCGCG	CGG	57,89	chr6	(-)	30626895	30626917	exon1, exon1	NM_001318	(+)	54	76
ATAT1	CATGAGTCT	TGG	57,89	chr6	(+)	30628089	30628111	exon5, exon5	NM_001318	(+)	1248	1270
ATF7IP	GCAACTTGA	AGG	45	chr12	(+)	14423987	14424009	[exon2, exor	NM_181352	(+)	58356	58378
ATF7IP	GGCAGTTTA	TGG	50	chr12	(-)	14424270	14424292	[exon2, exor	NM_181352	(+)	58639	58661

ATF7IP	GTTATATTA1AGG	35	chr12	(-)	14424246	14424268	[exon2, exor [NM_181352 (+)	58615	58637
ATF7IP	TTTGACCC/ TGG	50	chr12	(+)	14424071	14424093	[exon2, exor [NM_181352 (+)	58440	58462
ATM	AATAACGTC/ AGG	36,84	chr11	(-)	108289750	108289772	exon29 NM_000051 (+)	66919	66941
ATM	ATCAGTGC/ AGG	36,84	chr11	(-)	108289002	108289024	exon28 NM_000051 (+)	66171	66193
ATM	TGACTGGCA TGG	42,11	chr11	(-)	108287666	108287688	exon27 NM_000051 (+)	64835	64857
ATM	TTCACTGCT/ TGG	47,37	chr11	(-)	108289627	108289649	exon29 NM_000051 (+)	66796	66818
ATR	GGATCATAA CGG	42,11	chr3	(-)	142563075	142563097	exon4 NM_001184 (-)	113841	113863
ATR	GAATCAAG AGG	42,11	chr3	(+)	142566200	142566222	exon3 NM_001184 (-)	116966	116988
ATR	TTGTGTAAC/ GGG	36,84	chr3	(+)	142563040	142563062	exon4 NM_001184 (-)	113806	113828
ATR	AGTGGAAAG/ AGG	57,89	chr3	(-)	142566132	142566154	exon3 NM_001184 (-)	116898	116920
ATRX	TCGTGACGA TGG	52,63	chrX	(+)	77697591	77697613	exon4, exon4 NM_000489, (-)	192714	192736
ATRX	TGATTCAATC/ AGG	42,11	chrX	(+)	77717139	77717161	exon2, exon2 NM_000489, (-)	212262	212284
ATRX	TGGAAGTAA TGG	36,84	chrX	(-)	77698591	77698613	exon3, exon3 NM_000489, (-)	193714	193736
ATRX	ATTCCTTGA AGG	42,11	chrX	(+)	77717179	77717201	exon2, exon2 NM_000489, (-)	212302	212324
AURKB	GCGCAGAG/ AGG	52,63	chr17	(-)	8207186	8207208	exon5, exon5 NM_001284 (-)	2456	2478
AURKB	ATTCTAGAG/ CGG	52,63	chr17	(-)	8206808	8206830	exon6, exon6 NM_001284 (-)	2078	2100
AURKB	TTTGAGATT/ GGG	52,63	chr17	(-)	8207323	8207345	exon5, exon5 NM_001284 (-)	2593	2615
AURKB	TTGGAAACG CGG	47,37	chr17	(-)	8207289	8207311	exon5, exon5 NM_001284 (-)	2559	2581
BAP1	TCAAATGGA CGG	50	chr3	(-)	52408558	52408580	[exon4] [NM_004656 (-)	7555	7577
BAP1	CACGGACGT AGG	55	chr3	(+)	52408516	52408538	[exon4] [NM_004656 (-)	7513	7535
BAP1	CGACCTTCA/ AGG	50	chr3	(-)	52409555	52409577	[exon3] [NM_004656 (-)	8552	8574
BAP1	CGCATGAAG GGG	50	chr3	(-)	52407971	52407993	[exon5] [NM_004656 (-)	6968	6990
BAZ1A	TTCACTGTA/ GGG	47,37	chr14	(+)	34862127	34862149	exon3, exon3 NM_013448, (-)	109397	109419
BAZ1A	AACGGCTTT/ CGG	52,63	chr14	(+)	34874579	34874601	exon2, exon2 NM_013448, (-)	121849	121871
BAZ1A	GCCTCTGA1/ AGG	52,63	chr14	(+)	34862236	34862258	exon3, exon3 NM_013448, (-)	109506	109528
BAZ1A	TGAGTGGC/ TGG	57,89	chr14	(+)	34874494	34874516	exon2, exon2 NM_013448, (-)	121764	121786
BAZ1B	GTTAGTAGA TGG	42,11	chr7	(-)	73508371	73508393	exon3 NM_032408 (-)	67974	67996
BAZ1B	ACAAGCTT/ AGG	47,37	chr7	(+)	73508433	73508455	exon3 NM_032408 (-)	68036	68058
BAZ1B	ATTTGGACG TGG	42,11	chr7	(-)	73510793	73510815	exon2 NM_032408 (-)	70396	70418
BAZ2A	GGGGGACA/ CGG	57,89	chr12	(-)	56615376	56615398	exon3, exon3 NM_013449, (-)	19781	19803
BAZ2A	GTATTTGCC/ GGG	57,89	chr12	(+)	56615387	56615409	exon3, exon3 NM_013449, (-)	19792	19814
BAZ2A	GTAGTCCA/ AGG	52,63	chr12	(+)	56615465	56615487	exon3, exon3 NM_013449, (-)	19870	19892
BAZ2A	TGGGAGACC/ AGG	52,63	chr12	(+)	56617419	56617441	exon2, exon2 NM_013449, (-)	21824	21846
BAZ2B	GAATCATGA GGG	50	chr2	(+)	159448298	159448320	exon5, exon5 NM_013450, (-)	129320	129342
BAZ2B	GTCTACATT/ GGG	50	chr2	(-)	159453692	159453714	exon4, exon4 NM_013450, (-)	134714	134736
BAZ2B	ACTGATGCT/ AGG	45	chr2	(-)	159448367	159448389	exon5, exon5 NM_013450, (-)	129389	129411
BAZ2B	AGGCACTCG AGG	60	chr2	(+)	159453742	159453764	exon4, exon4 NM_013450, (-)	134764	134786
BMI1	AACGTGTAT NGG	40			0	0	Not available	0	0
BMI1	ACAAATAGG NGG	35			0	0	Not available	0	0
BMI1	GTGGTCTGG NGG	50			0	0	Not available	0	0
BMI1	TGAACCTGG NGG	35			0	0	Not available	0	0
BOP1	CCGATTGG CGG	52,63	chr8	(-)	144276244	144276266	exon3 NM_015201 (-)	14199	14221
BOP1	ACTGTGGCC/ GGG	57,89	chr8	(+)	144289128	144289150	exon2 NM_015201 (-)	27083	27105
BOP1	TGTCACTGC/ AGG	52,63	chr8	(+)	144289196	144289218	exon2 NM_015201 (-)	27151	27173
BOP1	GGATGATGA/ AGG	57,89	chr8	(-)	144289166	144289188	exon2 NM_015201 (-)	27121	27143
BPTF	GTACGATGA AGG	60	chr17	(+)	67826099	67826121	exon1, exon1 NM_004459, (+)	436	458
BPTF	ATCGTACCC/ CGG	40	chr17	(-)	67826083	67826105	exon1, exon1 NM_004459, (+)	420	442
BRD1	TGACCTACG/ AGG	52,63	chr22	(-)	49824204	49824226	exon2, exon2 NM_001304 (-)	50927	50949
BRD1	AGGTCAGCG GGG	57,89	chr22	(+)	49824221	49824243	exon2, exon2 NM_001304 (-)	50944	50966
BRD1	TACTCCAGG/ GGG	57,89	chr22	(+)	49823938	49823960	exon2, exon2 NM_001304 (-)	50661	50683
BRD1	CGCTTAGTT/ AGG	42,11	chr22	(+)	49824046	49824068	exon2, exon2 NM_001304 (-)	50769	50791
BRD2	ATCAGTTCCG/ CGG	47,37	chr6	(+)	32974710	32974732	exon3, exon2 NM_005104, (+)	3823	3845
BRD2	TGTAACCTG/ GGG	47,37	chr6	(-)	32974637	32974659	exon3, exon2 NM_005104, (+)	3750	3772
BRD2	CCTACACA/ AGG	47,37	chr6	(+)	32974675	32974697	exon3, exon2 NM_005104, (+)	3788	3810
BRD2	AAAGCCCTC/ AGG	42,11	chr6	(-)	32974539	32974561	exon3, exon2 NM_005104, (+)	3652	3674
BRD3	ATTTGATTG/ TGG	52,63	chr9	(+)	134053276	134053298	exon2 NM_007371 (-)	22953	22975
BRD3	GAGTGCAAC/ AGG	47,37	chr9	(-)	134052347	134052369	exon3 NM_007371 (-)	22024	22046
BRD3	CATTAGCAC/ TGG	36,84	chr9	(+)	134051686	134051708	exon4 NM_007371 (-)	21363	21385
BRD3	GCAGTACAT/ TGG	47,37	chr9	(-)	134053339	134053361	exon2 NM_007371 (-)	23016	23038
BRD4	TTCACTGTA/ AGG	52,63	chr19	(+)	15272822	15272844	exon2, exon2 NM_058243, (-)	25787	25809
BRD4	GATTTCTCA/ GGG	47,37	chr19	(+)	15273060	15273082	exon2, exon2 NM_058243, (-)	26025	26047
BRD4	ACTGCAAT/ TGG	47,37	chr19	(-)	15272892	15272914	exon2, exon2 NM_058243, (-)	25857	25879
BRD4	GAATGCTCA/ AGG	42,11	chr19	(-)	15268946	15268968	exon3, exon3 NM_058243, (-)	21911	21933
BRD7	GTGGGACAA AGG	52,63	chr16	(-)	50368726	50368748	exon1, exon1 NM_013263, (-)	49709	49731
BRD7	GGAGGCAAC/ AGG	47,37	chr16	(+)	50354831	50354853	exon3, exon3 NM_013263, (-)	35814	35836
BRD7	GATCGTTTT/ AGG	36,84	chr16	(+)	50368185	50368207	exon2, exon2 NM_013263, (-)	49168	49190
BRD7	GAAGTCACC/ GGG	52,63	chr16	(-)	50368229	50368251	exon2, exon2 NM_013263, (-)	49212	49234
BRD8	CTCTAAAG/ GGG	47,37	chr5	(+)	138171378	138171400	exon4, exon4 NM_139199, (-)	14495	14517
BRD8	CCGAGGTTT TGG	63,16	chr5	(-)	138169311	138169333	exon8, exon8 NM_139199, (-)	12428	12450
BRD8	GGAGCTGAC TGG	52,63	chr5	(-)	138169239	138169261	exon8, exon8 NM_139199, (-)	12356	12378
BRD8	AGCTTCTCT/ TGG	57,89	chr5	(+)	138177613	138177635	exon2, exon2 NM_139199, (-)	20730	20752
BRD9	GCCTCTAAA/ AGG	52,63	chr5	(-)	891807	891829	exon2 NM_023924 (-)	28073	28095
BRD9	CGACTTTGA/ AGG	52,63	chr5	(-)	891209	891231	exon3, exon3 NM_001009 (-)	27475	27497
BRD9	GTCCAGGAT TGG	52,63	chr5	(-)	889112	889134	exon5, exon5 NM_001317 (-)	25378	25400
BRDT	TCTCCCTTGA GGG	52,63	chr1	(+)	91976379	91976401	exon5, exon5 NM_001242 (+)	24228	24250
BRDT	TTGGGCGC/ TGG	52,63	chr1	(-)	91976416	91976438	exon5, exon5 NM_001242 (+)	24265	24287
BRDT	ATGGCCCTT/ TGG	52,63	chr1	(+)	91962901	91962923	exon2, exon2 NM_207189, (+)	10750	10772
BRDT	AGAGCAAGT AGG	47,37	chr1	(+)	91968223	91968245	exon4, exon4 NM_001242 (+)	16072	16094
BRPF1	GCCTAGTCG/ TGG	57,89	chr3	(-)	9734173	9734195	exon2, exon2 NM_004634, (+)	2445	2467
BRPF1	CTCCGCAAG/ GGG	47,37	chr3	(+)	9734312	9734334	exon2, exon2 NM_004634, (+)	2584	2606
BRPF1	GTGCATAGC CGG	52,63	chr3	(-)	9734398	9734420	exon2, exon2 NM_004634, (+)	2670	2692
BRPF1	TGTCGTGGT AGG	47,37	chr3	(-)	9734263	9734285	exon2, exon2 NM_004634, (+)	2535	2557
BRPF3	GTCTACCTCC GGG	57,89	chr6	(-)	36200432	36200454	exon2 NM_015695 (+)	3660	3682
BRPF3	GAGTCCACC/ GGG	57,89	chr6	(-)	36200671	36200693	exon2 NM_015695 (+)	3899	3921
BRPF3	CACCGAATG/ AGG	42,11	chr6	(+)	36200535	36200557	exon2 NM_015695 (+)	3763	3785
BRPF3	GTCCAAGAA AGG	52,63	chr6	(+)	36200589	36200611	exon2 NM_015695 (+)	3817	3839
BRWD1	CCAGCGCAT/ TGG	63,16	chr21	(-)	39298513	39298535	exon5, exon5 NM_033656, (-)	2077	2099

BRWD1	GTTGCCGAA GGG	52,63	chr21	(-)	39312876	39312898	exon4, exon4	NM_033656, (-)	16440	16462
BRWD1	CCTTATCGCC CGG	57,89	chr21	(-)	39313267	39313289	exon2, exon2	NM_033656, (-)	16831	16853
BRWD1	CAGATTTGGC AGG	31,58	chr21	(+)	39298536	39298558	exon5, exon5	NM_033656, (-)	2100	2122
BRWD3	GATTCCGCG GGG	57,89	chrX	(-)	80808574	80808596	exon4	NM_153252 (-)	139087	139109
BRWD3	AGCTGTATT AGG	47,37	chrX	(-)	80809282	80809304	exon2	NM_153252 (-)	139795	139817
BRWD3	CCTAAATC AGG	42,11	chrX	(+)	80793657	80793679	exon5	NM_153252 (-)	124170	124192
BRWD3	GCTTTTGC AGG	52,63	chrX	(-)	80791901	80791923	exon6	NM_153252 (-)	122414	122436
C14orf169	GCGAAGTTGG	55	chr14	(+)	73491146	73491168	exon1	NM_024644 (+)	213	235
C14orf169	GATTCTCCG AGG	55	chr14	(-)	73491192	73491214	exon1	NM_024644 (+)	259	281
C14orf169	TCGTATCTTC AGG	50	chr14	(-)	73491115	73491137	exon1	NM_024644 (+)	182	204
C14orf169	GCGAAGCT AGG	60	chr14	(+)	73491196	73491218	exon1	NM_024644 (+)	263	285
CARM1	AACATCTG GGG	47,37	chr19	(+)	10908056	10908078	exon3	NM_199141 (+)	36480	36502
CARM1	GCAGTCCTT GGG	52,63	chr19	(+)	10905015	10905037	exon2	NM_199141 (+)	33439	33461
CARM1	TGAAGGACT CGG	57,89	chr19	(-)	10905003	10905025	exon2	NM_199141 (+)	33427	33449
CARM1	TGGGTGTG AGG	57,89	chr19	(-)	10905051	10905073	exon2	NM_199141 (+)	33475	33497
CBX1	CTCGACCGT GGG	57,89	chr17	(-)	48076904	48076926	exon2, exon2	NM_006807, (-)	6853	6875
CBX1	CAGAACTCG CGG	47,37	chr17	(+)	48076115	48076137	exon3, exon3	NM_006807, (-)	6064	6086
CBX1	CTTTGCTCG AGG	52,63	chr17	(-)	48075061	48075083	exon4, exon4	NM_006807, (-)	5010	5032
CBX1	ACATGAGAC AGG	31,58	chr17	(-)	48076075	48076097	exon3, exon3	NM_006807, (-)	6024	6046
CBX2	CAGATAACG AGG	57,89	chr17	(+)	79779362	79779384	exon3, exon3	NM_032647, (+)	1185	1207
CBX2	GAGGTGCAC AGG	57,89	chr17	(+)	79781709	79781731	exon4, exon4	NM_032647, (+)	3532	3554
CBX2	AGCTGGAGT TGG	52,63	chr17	(+)	79778388	79778410	exon2, exon2	NM_032647, (+)	211	233
CBX2	GACATGGCA TGG	57,89	chr17	(-)	79781751	79781773	exon4, exon4	NM_032647, (+)	3574	3596
CBX3	AGAAACGCT TGG	31,58	chr7	(-)	26208433	26208455	exon4, exon4	NM_007276, (+)	6730	6752
CBX3	CTAGATCGA TGG	47,37	chr7	(+)	26206449	26206471	exon3, exon3	NM_007276, (+)	4746	4768
CBX3	TTTTCCACGA AGG	31,58	chr7	(-)	26206422	26206444	exon3, exon3	NM_007276, (+)	4719	4741
CBX3	TTTCTAACT TGG	31,58	chr7	(+)	26208451	26208473	exon4, exon4	NM_007276, (+)	6748	6770
CBX4	ATATAACAC AGG	47,37	chr17	(-)	79837880	79837902	exon3	NM_003655 (-)	4725	4747
CBX4	GACATTGGA AGG	57,89	chr17	(+)	79835366	79835388	exon5	NM_003655 (-)	2211	2233
CBX4	CTGATGGGA AGG	47,37	chr17	(-)	79835674	79835696	exon4	NM_003655 (-)	2519	2541
CBX4	CTTGGCACG AGG	57,89	chr17	(+)	79835324	79835346	exon5	NM_003655 (-)	2169	2191
CBX5	CAGAGCAAT GGG	47,37	chr12	(-)	54246193	54246215	exon4, exon4	NM_012117, (-)	15248	15270
CBX5	GCGCGTGGT TGG	57,89	chr12	(-)	54257545	54257567	exon2, exon2	NM_012117, (-)	26600	26622
CBX5	GGGTGAAA GGG	36,84	chr12	(-)	54252118	54252140	exon3, exon3	NM_012117, (-)	21173	21195
CBX5	AGAACTGTC TGG	57,89	chr12	(+)	54257615	54257637	exon2, exon2	NM_012117, (-)	26670	26692
CBX6	CGAATCCA CGG	47,37	chr22	(-)	38872131	38872153	exon1, exon1	NM_001303, (-)	10705	10727
CBX6	CGAGTCCAG CGG	57,89	chr22	(+)	38871718	38871740	exon3, exon3	NM_001303, (-)	10292	10314
CBX6	GCATCGAGT TGG	52,63	chr22	(-)	38871919	38871941	exon2, exon2	NM_001303, (-)	10493	10515
CBX6	AATGCACAT AGG	47,37	chr22	(+)	38867159	38867181	exon5	NM_014292 (-)	5733	5755
CBX7	TCTTCTATA CGG	52,63	chr22	(+)	39138668	39138690	exon4	NM_175709 (-)	7895	7917
CBX7	AGAGAGGTC CGG	52,63	chr22	(-)	39138648	39138670	exon4	NM_175709 (-)	7875	7897
CBX7	AAGTCGAGT TGG	42,11	chr22	(-)	39149806	39149828	exon2	NM_175709 (-)	19033	19055
CBX8	GTTCGGAAG GGG	52,63	chr17	(-)	79795504	79795526	exon5	NM_020649 (-)	1128	1150
CBX8	GTACAGCAC AGG	57,89	chr17	(-)	79796293	79796315	exon3	NM_020649 (-)	1917	1939
CBX8	GGCTTGGGT GGG	57,89	chr17	(+)	79796076	79796098	exon4	NM_020649 (-)	1700	1722
CCDC101	ACGCAGCTT AGG	52,63	chr16	(-)	28585654	28585676			0	0
CCDC101	ACATCCAGA CGG	47,37	chr16	(+)	28584947	28584969			0	0
CCDC101	CGCGGAAAT TGG	52,63	chr16	(+)	28589127	28589149			0	0
CCDC101	TGCGCGTCT CGG	52,63	chr16	(+)	28590106	28590128			0	0
CDYL	AAAGCCGGT TGG	52,63	chr6	(+)	4892240	4892262	exon2, exon2	NM_001143, (+)	2249	2271
CDYL	TAACGGGGC AGG	52,63	chr6	(-)	4892114	4892136	exon2, exon2	NM_001143, (+)	2123	2145
CDYL	AATCACGAG AGG	47,37	chr6	(-)	4891969	4891991	exon2	NM_004824 (+)	115524	115546
CDYL	CGTTAAGAG TGG	57,89	chr6	(+)	4892132	4892154	exon2, exon2	NM_001143, (+)	2141	2163
CDYL2	GAGTATCTT AGG	42,11	chr16	(-)	80685062	80685084	exon2	NM_152342 (-)	81284	81306
CDYL2	GCAAGGGG CGG	57,89	chr16	(-)	80684836	80684858	exon2	NM_152342 (-)	81058	81080
CDYL2	TAAACTCTC AGG	42,11	chr16	(+)	80685000	80685022	exon2	NM_152342 (-)	81222	81244
CDYL2	GGGACAGTT GGG	52,63	chr16	(+)	80684883	80684905	exon2	NM_152342 (-)	81105	81127
CECR2	TCACCGAGA AGG	52,63	chr22	(+)	17504913	17504935	exon7, exon7	NM_001290, (+)	144965	144987
CECR2	CCGACTCTG TGG	57,89	chr22	(+)	17497535	17497557	exon3	NM_001290, (+)	128170	128192
CECR2	ATCTCCACC AGG	57,89	chr22	(-)	17497506	17497528	exon3	NM_001290, (+)	128141	128163
CECR2	CACGTATCT CGG	47,37	chr22	(-)	17477598	17477620	exon2	NM_001290, (+)	108233	108255
CHAF1A	CTGATCGTCI CGG	47,37	chr19	(-)	4408948	4408970	exon3	NM_005483 (+)	6286	6308
CHAF1A	TCAGGCGCT CGG	57,89	chr19	(-)	4408904	4408926	exon3	NM_005483 (+)	6242	6264
CHAF1A	CCGAAACTT GGG	52,63	chr19	(+)	4409064	4409086	exon3	NM_005483 (+)	6402	6424
CHAF1A	GTCCAAAAG CGG	47,37	chr19	(-)	4408996	4409018	exon3	NM_005483 (+)	6334	6356
CHAF1B	ACGCACAAG TGG	52,63	chr21	(-)	36387668	36387690	exon3	NM_005441 (+)	2278	2300
CHAF1B	GCAGATCGC AGG	47,37	chr21	(+)	36391597	36391619	exon4	NM_005441 (+)	6207	6229
CHAF1B	TCCACGATG TGG	47,37	chr21	(-)	36387619	36387641	exon3	NM_005441 (+)	2229	2251
CHAF1B	TGTGCGTTT GGG	42,11	chr21	(+)	36387684	36387706	exon3	NM_005441 (+)	2294	2316
CHD1	CATCAAGCCI CGG	36,84	chr5	(-)	98903802	98903824	exon3	NM_001270 (-)	48599	48621
CHD1	ACCCAGAAT TGG	47,37	chr5	(+)	98905076	98905098	exon2	NM_001270 (-)	49873	49895
CHD1	ATCGGAATC AGG	42,11	chr5	(+)	98902938	98902960	exon4	NM_001270 (-)	47735	47757
CHD1	GCAAAACCA TGG	47,37	chr5	(-)	98904904	98904926	exon2	NM_001270 (-)	49701	49723
CHD1L	CATTCTGAC TGG	47,37	chr1	(-)	147252669	147252691	exon2	NM_004284 (+)	10029	10051
CHD1L	TCACTACGC TGG	52,63	chr1	(+)	147252627	147252649	exon2	NM_004284 (+)	9987	10009
CHD1L	GTCCGCTGC AGG	47,37	chr1	(-)	147255830	147255852	exon4, exon4	NM_024568, (+)	13190	13212
CHD1L	GATCAGGCT AGG	47,37	chr1	(-)	147264493	147264515	exon7, exon7	NM_024568, (+)	21853	21875
CHD2	GGCATGGTT CGG	52,63	chr15	(-)	92927288	92927310	exon4, exon4	NM_001271, (+)	26968	26990
CHD2	TGAACCCGA AGG	47,37	chr15	(-)	92924329	92924351	exon3, exon3	NM_001271, (+)	24009	24031
CHD2	AGCTATCCG AGG	42,11	chr15	(-)	92924518	92924540	exon3, exon3	NM_001271, (+)	24198	24220
CHD2	CAGTCAGTC AGG	52,63	chr15	(+)	92924360	92924382	exon3, exon3	NM_001271, (+)	24040	24062
CHD3	CAGTGAATA CGG	47,37	chr17	(+)	7890633	7890655	exon3, exon3	NM_005852, (+)	5829	5851
CHD3	GTTCTGAGO CGG	47,37	chr17	(+)	7890590	7890612	exon3, exon3	NM_005852, (+)	5786	5808
CHD3	GACAAAGCG GGG	52,63	chr17	(+)	7890699	7890721	exon3, exon3	NM_005852, (+)	5895	5917
CHD3	TTGCGTTTT TGG	47,37	chr17	(-)	7889747	7889769	exon2, exon2	NM_005852, (+)	4943	4965
CHD4	ATGCTCTAT AGG	57,89	chr12	(-)	6602150	6602172	exon4	NM_001273 (-)	32069	32091
CHD4	CGCTTGCTC AGG	47,37	chr12	(+)	6602389	6602411	exon3, exon2	NM_001273, (-)	32308	32330

CHD4	GAGGGCAGTGG	57,89	chr12	(-)	6602060	6602082	exon4, exon3	NM_001273, (-)	31979	32001
CHD4	GAAGAGCAAGG	52,63	chr12	(-)	6601998	6602020	exon4, exon3	NM_001273, (-)	31917	31939
CHD5	CGCCGAGGAAGG	57,89	chr1	(-)	6179957	6179979	exon1	NM_015557 (-)	78171	78193
CHD5	CTTCGATGAATGG	42,11	chr1	(-)	6168230	6168252	exon2	NM_015557 (-)	66444	66466
CHD5	TGAGCTATCGAGG	36,84	chr1	(-)	6159482	6159504	exon3	NM_015557 (-)	57696	57718
CHD5	TGGGTTTCTAGG	42,11	chr1	(+)	6168197	6168219	exon2	NM_015557 (-)	66411	66433
CHD6	GGACCTGTAAGG	47,37	chr20	(-)	41533405	41533427	exon3	NM_032221 (-)	131303	131325
CHD6	GACATCCCAATGG	47,37	chr20	(-)	41533354	41533376	exon3	NM_032221 (-)	131252	131274
CHD6	TTCGGTTTCTTGG	47,37	chr20	(+)	41533230	41533252	exon3	NM_032221 (-)	131128	131150
CHD6	TAGTCACTGAGG	52,63	chr20	(-)	41533426	41533448	exon3	NM_032221 (-)	131324	131346
CHD7	TGCTGACCCATGG	42,11	chr8	(-)	60741529	60741551	exon1, exon2	NM_0013161 (+)	62765	62787
CHD7	GAATGATGAGGG	52,63	chr8	(+)	60741695	60741717	exon1, exon2	NM_0013161 (+)	62931	62953
CHD7	CAGCAAATGAGG	47,37	chr8	(+)	60741547	60741569	exon1, exon2	NM_0013161 (+)	62783	62805
CHD7	AGTGAAGGTCGG	52,63	chr8	(+)	60741484	60741506	exon1, exon2	NM_0013161 (+)	62720	62742
CHD8	TGGATAGTTAGG	42,11	chr14	(+)	21429157	21429179	exon2, exon3	NM_0011701 (-)	43964	43986
CHD8	TGAATCGAAATGG	47,37	chr14	(-)	21429311	21429333	exon2, exon3	NM_0011701 (-)	44118	44140
CHD8	GGACATCGGAGG	57,89	chr14	(-)	21429256	21429278	exon2, exon3	NM_0011701 (-)	44063	44085
CHD8	GTACAGCAGGGG	47,37	chr14	(-)	21429025	21429047	exon2, exon3	NM_0011701 (-)	43832	43854
CHD9	TCAACTAGTCTGG	42,11	chr16	(-)	53156177	53156199	exon2, exon1	NM_025134, (+)	252	274
CHD9	TATCAGATGTGG	42,11	chr16	(+)	53156442	53156464	exon2, exon1	NM_025134, (+)	517	539
CHD9	ACAAACCATTTGG	42,11	chr16	(-)	53156410	53156432	exon2, exon1	NM_025134, (+)	485	507
CHD9	GTGTTGGGACGG	47,37	chr16	(-)	53156251	53156273	exon2, exon1	NM_025134, (+)	326	348
CHAC1	GTCTGGGTCGG	55	chr8	(+)	140511512	140511534	[exon1]	[NM_017444 (+)]	215	237
CHAC1	TATTCCTACA TGG	50	chr8	(+)	140514396	140514418	[exon2]	[NM_017444 (+)]	3099	3121
CHAC1	CTTCATGATCGGG	55	chr8	(-)	140511564	140511586	[exon1]	[NM_017444 (+)]	267	289
CHAC1	CATCATGAATAGG	60	chr8	(+)	140511577	140511599	[exon1]	[NM_017444 (+)]	280	302
CLOCK	CTAGTGAAATGG	42,11	chr4	(-)	55476011	55476033	exon8, exon7	NM_0012671 (-)	48111	48133
CLOCK	TCTGTGTAATGG	42,11	chr4	(-)	55478866	55478888	exon7, exon6	NM_0012671 (-)	50966	50988
CLOCK	TTTGGTGGGAGG	47,37	chr4	(-)	55479653	55479675	exon6, exon5	NM_0012671 (-)	51753	51775
CLOCK	GCTCATTTTACGG	36,84	chr4	(+)	55482753	55482775	exon5, exon4	NM_0012671 (-)	54853	54875
CREBBP	AGCGGCTCTAGG	52,63	chr16	(-)	3850841	3850863	exon2, exon2	NM_004380, (-)	125787	125809
CREBBP	GCTGTCAATCGG	52,63	chr16	(+)	3879836	3879858	exon1, exon1	NM_004380, (-)	154782	154804
CREBBP	GATGAGCTGAGG	47,37	chr16	(-)	3850949	3850971	exon2, exon2	NM_004380, (-)	125895	125917
CREBBP	CTGTCCGAGAGG	57,89	chr16	(-)	3850865	3850887	exon2, exon2	NM_004380, (-)	125811	125833
CSTL1	CCTACTTATAAGG	42,11	chr20	(+)	23440443	23440465	exon2	NM_138283 (+)	759	781
CSTL1	GTCTGTGCTTAGG	52,63	chr20	(-)	23440419	23440441	exon2	NM_138283 (+)	735	757
CSTL1	CGTGTCAATCTGG	47,37	chr20	(-)	23443980	23444002	exon3	NM_138283 (+)	4296	4318
CSTL1	GAGCTGGGAATAGG	36,84	chr20	(-)	23444805	23444827	exon4	NM_138283 (+)	5121	5143
CTCF	AGTTTCGGGATGG	50	chr16	(-)	67610855	67610877	[exon3]	[NM_006565 (+)]	48449	48471
CTCF	GTAGCAACAAGG	50	chr16	(-)	67611193	67611215	[exon3]	[NM_006565 (+)]	48787	48809
CTCF	TACCCAGAAAGGG	55	chr16	(+)	67610951	67610973	[exon3]	[NM_006565 (+)]	48545	48567
CTCF	ACTTACCAGTAGG	60	chr16	(+)	67610902	67610924	[exon3]	[NM_006565 (+)]	48496	48518
CXXC1	CGATAGCGAGGG	47,37	chr18	(+)	50286227	50286249	exon4, exon4	NM_014593, (-)	3885	3907
CXXC1	GCTATCGGCCGG	52,63	chr18	(-)	50286211	50286233	exon4, exon4	NM_014593, (-)	3869	3891
CXXC1	CTACTGCTATCGG	52,63	chr18	(-)	50286759	50286781	exon2, exon2	NM_014593, (-)	4417	4439
CXXC1	GGACAGCAAGGG	52,63	chr18	(-)	50286795	50286817	exon2, exon2	NM_014593, (-)	4453	4475
DAXX	ATTCGAGGTCGG	45	chr6	(-)	33322892	33322914	[exon1]	[NM_001141 (-)]	4335	4357
DAXX	CACGTGTGCTAGG	55	chr6	(+)	33321492	33321514	[exon3, exor]	[NM_00135C (-)]	2935	2957
DAXX	TCTATGTGGTCGG	55	chr6	(-)	33321163	33321185	[exon3, exor]	[NM_00135C (-)]	2606	2628
DAXX	CGGCAAGAAATGG	50	chr6	(-)	33321742	33321764	[exon2, exor]	[NM_00135C (-)]	3185	3207
DIDO1	GACCACTATTAGG	57,89	chr20	(-)	62911498	62911520	exon3, exon3	NM_001193, (-)	6501	6523
DIDO1	CAAAGGCGAAGG	57,89	chr20	(-)	62911582	62911604	exon3, exon3	NM_001193, (-)	6585	6607
DIDO1	AGCGCTTCTCGG	52,63	chr20	(-)	62911242	62911264	exon3, exon3	NM_001193, (-)	6245	6267
DIDO1	GGAAACCATAGG	47,37	chr20	(-)	62911520	62911542	exon3, exon3	NM_001193, (-)	6523	6545
DMAP1	CGGGACATTGGG	52,63	chr1	(+)	44213775	44213797	exon2, exon2	NM_0010341 (+)	323	345
DMAP1	AGAACTATTGGG	47,37	chr1	(-)	44214817	44214839	exon4, exon4	NM_0010341 (+)	1365	1387
DMAP1	CGGTACAGTTGG	57,89	chr1	(+)	44214745	44214767	exon4, exon4	NM_0010341 (+)	1293	1315
DMAP1	ACTGACTTTTAGG	52,63	chr1	(+)	44214376	44214398	exon3, exon3	NM_0010341 (+)	924	946
DNMT1	ACGGTGTCTCGG	47,37	chr19	(-)	10180492	10180514	exon4, exon4	NM_001318, (-)	47149	47171
DNMT1	TGAAGCCCCGGG	57,89	chr19	(-)	10180428	10180450	exon4, exon4	NM_001318, (-)	47085	47107
DNMT1	AGCATGAGCAGG	57,89	chr19	(+)	10180501	10180523	exon4, exon4	NM_001318, (-)	47158	47180
DNMT3A	CTCGTCATCCNGG	60			0	0	Not available	0	0	0
DNMT3A	GAGATCACCGGG	60			0	0	Not available	0	0	0
DNMT3A	GGAAGCGCNGG	60			0	0	Not available	0	0	0
DNMT3A	CCATTGGGNGG	50			0	0	Not available	0	0	0
DNMT3B	AGAGTCGCGCGG	52,63	chr20	(-)	32781354	32781376	exon3, exon3	NM_175848, (+)	1503	1525
DNMT3B	AGACTCGATGGG	52,63	chr20	(+)	32780377	32780399	exon2, exon2	NM_175848, (+)	526	548
DNMT3B	TGCGGATAGGGG	57,89	chr20	(-)	32780428	32780450	exon2, exon2	NM_175848, (+)	577	599
DNMT3B	AAGCTCGCGGGG	57,89	chr20	(+)	32781363	32781385	exon3, exon3	NM_175848, (+)	1512	1534
DNMT3L	CGTCATCGTCTAGG	52,63	chr21	(+)	44259510	44259532	exon5, exon5	NM_013369, (-)	13172	13194
DNMT3L	AGCATGGACGGG	47,37	chr21	(-)	44261198	44261220	exon2, exon2	NM_013369, (-)	14860	14882
DNMT3L	ATGCTACTGTGGG	47,37	chr21	(-)	44258672	44258694	exon6, exon6	NM_013369, (-)	12334	12356
DNMT3L	CTCTCAAGCTCGG	52,63	chr21	(-)	44261165	44261187	exon2, exon2	NM_013369, (-)	14827	14849
DOT1L	CGTAGTTGTGGG	47,37	chr19	(-)	2191110	2191132	exon5	NM_032482 (+)	26962	26984
DOT1L	CCGGATCTTGGG	63,16	chr19	(+)	2185873	2185895	exon3	NM_032482 (+)	21725	21747
DOT1L	GATATGGCGTGG	57,89	chr19	(-)	2191055	2191077	exon5	NM_032482 (+)	26907	26929
DOT1L	GTTTCAGCTTGGG	57,89	chr19	(-)	2191022	2191044	exon5	NM_032482 (+)	26874	26896
DPF1	GGGTACGTCGGG	47,37	chr19	(+)	38222434	38222456	exon3, exon3	NM_0012891 (-)	11429	11451
DPF1	GTTTCCGCAATGG	57,89	chr19	(-)	38218623	38218645	exon5, exon5	NM_0012891 (-)	7618	7640
DPF1	TCTACTGTGTTGGG	52,63	chr19	(-)	38218978	38219000	exon4, exon4	NM_0012891 (-)	7973	7995
DPF1	CCCGTGTTCGGG	57,89	chr19	(-)	38222409	38222431	exon3, exon3	NM_0012891 (-)	11404	11426
DPF2	GAAAGTCGTGGG	52,63	chr11	(-)	65341031	65341053	exon3	NM_006268 (+)	7278	7300
DPF2	GTAGGAGTATAGG	57,89	chr11	(-)	65340972	65340994	exon3	NM_006268 (+)	7219	7241
DPF2	ACAATTGCTCTGGG	47,37	chr11	(-)	65340489	65340511	exon2	NM_006268 (+)	6736	6758
DPF2	CTTTGTAGTATAGG	52,63	chr11	(-)	65340385	65340407	exon2	NM_006268 (+)	6632	6654
DPF3	GCTCGGGGATAGG	63,16	chr14	(-)	72771871	72771893	exon2, exon3	NM_0012801 (-)	110829	110851
DPF3	ACAGCCGTGCGG	47,37	chr14	(+)	72771832	72771854	exon2, exon3	NM_0012801 (-)	110790	110812

DPF3	CGCAGTTCCTTGG	47,37	chr14	(+)	72753284	72753306	exon3, exon4	NM_001280! (-)	92242	92264
DPF3	GGTATGATCG GGG	52,63	chr14	(+)	72753342	72753364	exon3, exon4	NM_001280! (-)	92300	92322
DPY30	GTGAGACCG AGG	52,63	chr2	(+)	32039292	32039314	exon3	NM_032574 (-)	15390	15412
DPY30	GAAGATCGA TGG	36,84	chr2	(-)	32024176	32024198			0	0
DPY30	GCTAGAAAT TGG	36,84	chr2	(+)	32024230	32024252	exon5	NM_032574 (-)	328	350
DPY30	CCATGATCAITGG	42,11	chr2	(-)	32024092	32024114			0	0
EED	GGCGTGTTC AGG	47,37	chr11	(-)	86250338	86250360	exon2, exon2	NM_003797, (+)	5955	5977
EED	GACGCTGTC TGG	42,11	chr11	(+)	86250299	86250321	exon2, exon2	NM_003797, (+)	5916	5938
EED	TTCTCGTCTC TGG	52,63	chr11	(-)	86245320	86245342	exon1, exon1	NM_003797, (+)	937	959
EED	ACAAACACG TGG	47,37	chr11	(+)	86250350	86250372	exon2, exon2	NM_003797, (+)	5967	5989
EHMT1	TAACCTCGGA GGG	42,11	chr9	(+)	137716803	137716825	exon3, exon3	NM_024757, (+)	97812	97834
EHMT1	CGGATACATCGG	31,58	chr9	(+)	137716909	137716931	exon3, exon3	NM_024757, (+)	97918	97940
EHMT1	CAAAGTCGT TGG	57,89	chr9	(-)	137716861	137716883	exon3, exon3	NM_024757, (+)	97870	97892
EHMT1	ACACCTATG AGG	57,89	chr9	(+)	137716628	137716650	exon3, exon3	NM_024757, (+)	97637	97659
EHMT2	ATGAGTGGT AGG	52,63	chr6	(+)	31896668	31896690	exon2, exon3	NM_001289, (-)	16909	16931
EHMT2	GGCAGGGT TGG	52,63	chr6	(+)	31896779	31896801	exon2, exon3	NM_001289, (-)	17020	17042
EHMT2	CTGAGAATC GGG	47,37	chr6	(-)	31896634	31896656	exon2, exon3	NM_001289, (-)	16875	16897
EHMT2	ATTGACATC AGG	57,89	chr6	(+)	31896444	31896466	exon3, exon4	NM_001289, (-)	16685	16707
ELP3	CGGATAGCT TGG	57,89	chr8	(-)	28110370	28110392	exon6, exon5	NM_001284, (+)	17304	17326
ELP3	CGGTGCTCT TGG	57,89	chr8	(-)	28097286	28097308	exon2, exon2	NM_001284, (-)	4220	4242
ELP3	CAGCAATGA CGG	47,37	chr8	(-)	28099873	28099895	exon3, exon3	NM_001284, (+)	6807	6829
ELP3	ATAGCCAAT TGG	47,37	chr8	(-)	28107951	28107973	exon5, exon4	NM_001284, (+)	14885	14907
ELP4	GTAGTGTGG GGG	57,89	chr11	(+)	31509807	31509829	exon1, exon1	NM_001288, (+)	79	101
ELP4	GCAACGTCA AGG	52,63	chr11	(+)	31509855	31509877	exon1, exon1	NM_001288, (+)	127	149
ELP4	TGTCAATGG TGG	42,11	chr11	(+)	31539723	31539745	exon3, exon3	NM_001288, (+)	29995	30017
ELP4	GGACAGCTG CGG	52,63	chr11	(+)	31509959	31509981	exon1, exon1	NM_001288, (+)	231	253
EP300	TAGTTCCTT TGG	42,11	chr22	(+)	41117356	41117378	exon2	NM_001429, (+)	24747	24769
EP300	AGTTTAGGC AGG	57,89	chr22	(-)	41093035	41093057	exon1	NM_001429, (+)	426	448
EP300	CGCGCTTAA CGG	52,63	chr22	(+)	41093046	41093068	exon1	NM_001429, (+)	437	459
EP300	GAATTGGGA TGG	42,11	chr22	(+)	41117246	41117268	exon2	NM_001429, (+)	24637	24659
EP400	GGTGATGTT CGG	55	chr12	(-)	131960822	131960844	exon2	NM_015409, (+)	10903	10925
EP400	GAACATCAC TGG	60	chr12	(+)	131960835	131960857	exon2	NM_015409, (+)	10916	10938
EP400	GTATTTGAT TGG	40	chr12	(-)	131960772	131960794	exon2	NM_015409, (+)	10853	10875
EP400	AGCTGATGC GGG	55	chr12	(-)	131960638	131960660	exon2	NM_015409, (+)	10719	10741
EPC1	TATGGTTAT AGG	47,37	chr10	(-)	32305850	32305872	exon2, exon2	NM_001282, (-)	38135	38157
EPC1	GCGGGCTAT AGG	57,89	chr10	(-)	32305895	32305917	exon2, exon2	NM_001282, (-)	38180	38202
EPC1	GACCACTGC CGG	47,37	chr10	(+)	32293597	32293619	exon3, exon3	NM_001282, (-)	25882	25904
EPC1	CGCTTCTCT TGG	42,11	chr10	(+)	32293058	32293080	exon4, exon4	NM_001282, (-)	25343	25365
EPC2	GTAAACTCT CGG	52,63	chr2	(+)	148645022	148645044	exon1	NM_015630, (+)	32	54
EPC2	GAGACGCAC AGG	52,63	chr2	(-)	148645093	148645115	exon1	NM_015630, (+)	103	125
EPC2	ACGACTCGG CGG	52,63	chr2	(+)	148645103	148645125	exon1	NM_015630, (+)	113	135
ERCC5	GATCTTCCCT CGG	55	chr13	(-)	102846322	102846344	exon1	NM_000123, (+)	482	504
ERCC5	AGCGCTGGA TGG	60	chr13	(+)	102846326	102846348	exon1	NM_000123, (+)	486	508
EZH1	TGCGACTTC CGG	42,11	chr17	(-)	42728849	42728871	exon3	NM_001991, (-)	28575	28597
EZH1	ATATGTTGG CGG	36,84	chr17	(+)	42724381	42724403	exon5	NM_001991, (-)	24107	24129
EZH1	ACAGGCTTC AGG	42,11	chr17	(+)	42727660	42727682	exon4	NM_001991, (-)	27386	27408
EZH1	AGTGATACA GGG	36,84	chr17	(+)	42728903	42728925	exon3	NM_001991, (-)	28629	28651
EZH2	TGCGACTGA AGG	52,63	chr7	(-)	148847206	148847228	exon2, exon2	NM_001203, (-)	39835	39857
EZH2	ACACGCTTC TGG	52,63	chr7	(+)	148847243	148847265	exon2, exon2	NM_001203, (-)	39872	39894
EZH2	CGGAAATCT TGG	36,84	chr7	(-)	148846536	148846558	exon3, exon3	NM_001203, (-)	39165	39187
EZH2	TTATGATGG GGG	36,84	chr7	(-)	148829734	148829756	exon5, exon5	NM_001203, (-)	22363	22385
FBXL19	TTCCGGGCAC AGG	57,89	chr16	(+)	30930231	30930253	exon7, exon7	NM_001282, (+)	5657	5679
FBXL19	GGTATGAAAG GGG	52,63	chr16	(+)	30924736	30924758	exon1	NM_001099, (+)	162	184
FBXL19	ATGCAGATA CGG	52,63	chr16	(-)	30930535	30930557	exon7, exon7	NM_001282, (+)	5961	5983
FBXL19	CCCCGAACCT CGG	52,63	chr16	(-)	30925862	30925884	exon2	NM_001099, (+)	1288	1310
FBXO17	AAGATGAGG GGG	50	chr19	(+)	38949988	38950010	exon2, exon2	NM_024907, (-)	8588	8610
FBXO17	GAAGATGAC AGG	55	chr19	(+)	38949987	38950009	exon2, exon2	NM_024907, (-)	8587	8609
FBXO17	CCCCAGCAA AGG	60	chr19	(-)	38950052	38950074	exon2, exon2	NM_024907, (-)	8652	8674
FBXO17	CCTTGCTCT AGG	60	chr19	(+)	38950055	38950077	exon2, exon2	NM_024907, (-)	8655	8677
FBXO44	AGGATCTCT AGG	52,63	chr1	(+)	11658321	11658343	exon3, exon4	NM_033182, (+)	3947	3969
FBXO44	TGGTACTTG TGG	52,63	chr1	(-)	11658749	11658771	exon5, exon6	NM_033182, (+)	4375	4397
FBXO44	CAGTGATGA AGG	57,89	chr1	(-)	11655988	11656010	exon2, exon3	NM_033182, (+)	1614	1636
FBXO44	ATGTGAATG TGG	47,37	chr1	(+)	11658291	11658313	exon3, exon4	NM_033182, (+)	3917	3939
FBXW9	TTTTGGCGG GGG	52,63	chr19	(+)	12696456	12696478	exon1	NM_032301, (-)	7541	7563
FBXW9	GCTCGAGAT TGG	57,89	chr19	(-)	12696299	12696321	exon1	NM_032301, (-)	7384	7406
FBXW9	CTCACTACG TGG	57,89	chr19	(+)	12696354	12696376	exon1	NM_032301, (-)	7439	7461
FBXW9	TCGTGCTG TGG	52,63	chr19	(-)	12696222	12696244	exon1	NM_032301, (-)	7307	7329
FKBP1A	TCCCTTAGCT GGG	50	chr20	(-)	1372075	1372097	exon3	NM_001199, (-)	3099	3121
FKBP1A	GTTTATGCT AGG	50	chr20	(-)	1375523	1375545	exon3, exon3	NM_054014, (-)	6547	6569
FKBP1A	TAAGGAAAT GGG	30	chr20	(-)	1372052	1372074			0	0
FKBP1A	GTGATCCGA AGG	60	chr20	(-)	1375501	1375523	exon3, exon3	NM_054014, (-)	6525	6547
FKBP2	GTCCCATCA GGG	52,63	chr11	(+)	64242512	64242534	exon2, exon2	NM_004470, (+)	397	419
FKBP2	CAAAAGGAA GGG	47,37	chr11	(+)	64242468	64242490	exon2, exon2	NM_004470, (+)	353	375
FKBP2	TGGACAGTA CGG	52,63	chr11	(-)	64242405	64242427	exon2, exon2	NM_004470, (+)	290	312
FKBP2	GAAGACAAA GGG	52,63	chr11	(-)	64243239	64243261	exon3, exon3	NM_004470, (+)	1124	1146
FKBP5	GTTCATTTC AGG	42,11	chr6	(+)	35620145	35620167	exon4, exon4	NM_004117, (-)	39589	39611
FKBP5	GCCGAGCCA TGG	47,37	chr6	(+)	35620178	35620200	exon4, exon4	NM_004117, (-)	39622	39644
FKBP5	GGTGAGGA TGG	57,89	chr6	(-)	35637115	35637137	exon3, exon3	NM_004117, (-)	56559	56581
FKBP5	TCATCAAGG GGG	47,37	chr6	(-)	35620246	35620268	exon4, exon4	NM_004117, (-)	39690	39712
FMR1	GTCAGATTG AGG	57,89	chrX	(+)	147925574	147925596	exon3, exon3	NM_001185, (+)	13624	13646
FMR1	GCACATCCA TGG	47,37	chrX	(-)	147928766	147928788	exon5, exon5	NM_001185, (+)	16816	16838
FMR1	TTAGCTAAC AGG	47,37	chrX	(-)	147928349	147928371	exon4, exon4	NM_001185, (+)	16399	16421
FMR1	AGCTAAAGT AGG	36,84	chrX	(+)	147928366	147928388	exon4, exon4	NM_001185, (+)	16416	16438
FXR2	GGTAGCCGC AGG	63,16	chr17	(+)	7605694	7605716	exon3	NM_004860, (-)	14465	14487
FXR2	TCCTTATTAT AGG	36,84	chr17	(+)	7605670	7605692	exon3	NM_004860, (-)	14441	14463
FXR2	TTATTCTCG AGG	36,84	chr17	(-)	7604056	7604078	exon4	NM_004860, (-)	12827	12849
FXR2	TAACCTGCC AGG	57,89	chr17	(+)	7603830	7603852	exon5	NM_004860, (-)	12601	12623

G2E3	TGATAACTTGGG	31,58	chr14	(-)	30592371	30592393	exon5, exon4	NM_017769, (+)	33249	33271
G2E3	CGAAGTTATG	36,84	chr14	(+)	30592383	30592405	exon5, exon4	NM_017769, (+)	33261	33283
G2E3	GATGACTGT CGG	31,58	chr14	(+)	30586741	30586763	exon3	NM_017769 (+)	27619	27641
G2E3	TGCTGTGTT TGG	36,84	chr14	(+)	30592326	30592348	exon5, exon4	NM_017769, (+)	33204	33226
GADD45A	GGCACACA CGG	52,63	chr1	(-)	67686353	67686375	exon2, exon3	NM_001199, (+)	1177	1199
GADD45A	AGTCAGCGC CGG	57,89	chr1	(+)	67686074	67686096	exon2, exon2	NM_001199, (+)	898	920
GADD45A	AAGTCGCTA GGG	42,11	chr1	(+)	67687723	67687745	exon3, exon4	NM_001199, (+)	2547	2569
GADD45A	GTGGAAC TG	57,89	chr1	(-)	67687887	67687909			0	0
GADD45B	CATCAACATC CGG	57,89	chr19	(+)	2477140	2477162	exon3	NM_015675 (+)	1016	1038
GADD45B	GATGTCGTT AGG	52,63	chr19	(-)	2477121	2477143	exon3	NM_015675 (+)	997	1019
GADD45B	GAGCGTGA GGG	52,63	chr19	(-)	2477091	2477113	exon3	NM_015675 (+)	967	989
GADD45B	CCTCCTCGTC AGG	57,89	chr19	(-)	2477053	2477075	exon3	NM_015675 (+)	929	951
GATAD2A	CTCGTTTCTG CGG	50	chr19	(-)	19465363	19465385	[exon2, exor	[NM_01766C (+)	24	46
GATAD2A	TCGGAGAGC AGG	55	chr19	(-)	19492337	19492359	[exon3, exor	[NM_01766C (+)	26998	27020
GATAD2A	GTCAGAAAC CGG	50	chr19	(+)	19465374	19465396	[exon2, exor	[NM_01766C (+)	35	57
GATAD2A	TTCTGAGTG CGG	55	chr19	(-)	19494333	19494355	[exon5, exor	[NM_01766C (+)	28994	29016
GATAD2B	GCAAGACGA GGG	45	chr1	(-)	153828241	153828263	[exon2]	[NM_020695 (-)	23515	23537
GATAD2B	CGTCTAGCA AGG	50	chr1	(+)	153828016	153828038	[exon2]	[NM_020695 (-)	23290	23312
GATAD2B	GGAGTTAGT TGG	60	chr1	(+)	153819709	153819731	[exon3]	[NM_020695 (-)	14983	15005
GATAD2B	ACATGAGTT AGG	45	chr1	(-)	153828146	153828168	[exon2]	[NM_020695 (-)	23420	23442
GLYR1	GAATCGACG AGG	42,11	chr16	(-)	4832170	4832192	exon5, exon5	NM_032569, (-)	28968	28990
GLYR1	CGCAAACTT AGG	52,63	chr16	(-)	4832115	4832137	exon5, exon5	NM_032569, (-)	28913	28935
GLYR1	CGACAGCAT TGG	57,89	chr16	(+)	4832809	4832831	exon4, exon4	NM_032569, (-)	29607	29629
GLYR1	ATGCTGTGC AGG	47,37	chr16	(-)	4832795	4832817	exon4, exon4	NM_032569, (-)	29593	29615
GTF2B	CCACAAAA TGG	47,37	chr1	(+)	88887312	88887334	exon2	NM_001514 (-)	34675	34697
GTF2B	TGAGAATCT TGG	47,37	chr1	(+)	88864027	88864049	exon3	NM_001514 (-)	11390	11412
GTF2B	GATATGATC TGG	36,84	chr1	(-)	88887272	88887294	exon2	NM_001514 (-)	34635	34657
GTF2B	GCAATTCTA CGG	36,84	chr1	(-)	88860233	88860255	exon4	NM_001514 (-)	7596	7618
GTF2F1	CGACGTATT TGG	42,11	chr19	(+)	6392870	6392892	exon2	NM_002096 (-)	13302	13324
GTF2F1	GAAGTACGC AGG	57,89	chr19	(-)	6389502	6389524	exon4	NM_002096 (-)	9934	9956
GTF2F1	CGTAGCAAA CGG	42,11	chr19	(+)	6391911	6391933	exon3	NM_002096 (-)	12343	12365
GTF2H1	TAGTTGTGT AGG	52,63	chr11	(-)	18335803	18335825	exon3, exon4	NM_005316, (+)	13535	13557
GTF2H1	TTCTTCTGG TGG	31,58	chr11	(-)	18335755	18335777	exon3, exon4	NM_005316, (+)	13487	13509
GTF2H1	TTTCACTGCT TGG	42,11	chr11	(-)	18335838	18335860	exon3, exon4	NM_005316, (+)	13570	13592
GTF2H1	GGATGGAGT TGG	57,89	chr11	(+)	18333134	18333156	exon2, exon3	NM_005316, (+)	10866	10888
GTF3C4	CACCGATA CCG	57,89	chr9	(-)	132670768	132670790	exon1	NM_012204 (+)	734	756
GTF3C4	CATTCGCCCT CGG	57,89	chr9	(+)	132670735	132670757	exon1	NM_012204 (+)	701	723
GTF3C4	TGCCGTGG TGG	57,89	chr9	(-)	132670895	132670917	exon1	NM_012204 (+)	861	883
GTF3C4	TTGAGGAGA CGG	47,37	chr9	(-)	132670932	132670954	exon1	NM_012204 (+)	898	920
H2AFZ	GACTGGTCG AGG	47,37	chr4	(+)	99949338	99949360	exon3	NM_002106 (-)	1252	1274
H2AFZ	TTGCGATGA GGG	57,89	chr4	(+)	99949362	99949384	exon3	NM_002106 (-)	1276	1298
H2AFZ	GACGACCAG TGG	57,89	chr4	(-)	99949326	99949348	exon3	NM_002106 (-)	1240	1262
H2AFZ	GGTAAGGCT CGG	52,63	chr4	(-)	99949712	99949734	exon2	NM_002106 (-)	1626	1648
H3F3A	CTTTACCAC NGG	50			0	0	Not available		0	0
H3F3A	TTTACCACG NGG	50			0	0	Not available		0	0
H3F3A	TTTGCGAAT NGG	40			0	0	Not available		0	0
H3F3A	AAGATGCGC NGG	60			0	0	Not available		0	0
HAT1	CAACACGGA AGG	42,11	chr2	(-)	171952938	171952960	exon4	NM_003642 (+)	30514	30536
HAT1	GTATGAAGT TGG	42,11	chr2	(-)	171965440	171965462	exon5	NM_003642 (+)	43016	43038
HAT1	AACTGCTAG TGG	36,84	chr2	(+)	171965858	171965880	exon6	NM_003642 (+)	43434	43456
HAT1	GAGTATACG TGG	42,11	chr2	(+)	171946755	171946777	exon3	NM_003642 (+)	24331	24353
HCFC1	CGAACTGCA CGG	52,63	chrX	(-)	153970648	153970670	exon1	NM_005334 (-)	23092	23114
HCFC1	GCCTATGGC CGG	57,89	chrX	(-)	153964648	153964670	exon2	NM_005334 (-)	17092	17114
HCFC1	GAGCTCATC CGG	52,63	chrX	(-)	153970692	153970714	exon1	NM_005334 (-)	23136	23158
HDAC1	ACTCCGACA CGG	47,37	chr1	(-)	32316739	32316761	exon3	NM_004964 (+)	24633	24655
HDAC1	GCAGCAAA CCG	36,84	chr1	(-)	32302676	32302698	exon2	NM_004964 (+)	10570	10592
HDAC1	AGTAGTAAC CGG	36,84	chr1	(-)	32292190	32292212	exon1	NM_004964 (+)	84	106
HDAC1	CTATGGTCT TGG	42,11	chr1	(+)	32302703	32302725	exon2	NM_004964 (+)	10597	10619
HDAC10	GACCGCGCT AGG	57,89	chr22	(-)	50251005	50251027	exon1, exon1	NM_032019, (-)	5822	5844
HDAC10	GTAGATGGC CGG	52,63	chr22	(+)	50250436	50250458	exon3, exon3	NM_032019, (-)	5253	5275
HDAC10	AGAGTATGT GGG	47,37	chr22	(-)	50250498	50250520	exon3, exon3	NM_032019, (-)	5315	5337
HDAC10	TCACGGGAG GGG	47,37	chr22	(-)	50250077	50250099	exon4, exon4	NM_032019, (-)	4894	4916
HDAC11	ACGATTGGC TGG	57,89	chr3	(-)	13481277	13481299	exon2	NM_024827 (+)	1063	1085
HDAC11	GCCTACAA TGG	52,63	chr3	(+)	13481309	13481331	exon2	NM_024827 (+)	1095	1117
HDAC11	GCCCATTTT AGG	57,89	chr3	(-)	13481350	13481372	exon2, exon2	NM_0011361 (+)	1136	1158
HDAC11	TGGCACATG GGG	57,89	chr3	(-)	13481257	13481279	exon2	NM_024827 (+)	1043	1065
HDAC2	TCCAACATC CGG	40	chr6	(+)	113946050	113946072	exon9	NM_001527 (-)	9895	9917
HDAC2	CGGAAACTG CGG	50	chr6	(-)	113939097	113939119			0	0
HDAC2	CTAACTGGC GGG	40	chr6	(+)	113940500	113940522			0	0
HDAC2	GAAACTTAG GGG	40	chr6	(-)	113939535	113939557			0	0
HDAC3	TATTTCTACG GGG	52,63	chr5	(-)	141636750	141636772	exon1	NM_003883 (-)	15875	15897
HDAC3	AGTCAATGT TGG	47,37	chr5	(+)	141634887	141634909	exon3	NM_003883 (-)	14012	14034
HDAC3	GGTGAAGCT TGG	47,37	chr5	(+)	141634846	141634868	exon3	NM_003883 (-)	13971	13993
HDAC3	CATAGCCTG CGG	52,63	chr5	(-)	141636567	141636589	exon2	NM_003883 (-)	15692	15714
HDAC4	GCAGGATTC TGG	57,89	chr2	(+)	239236619	239236641	exon3	NM_006037 (-)	188452	188474
HDAC4	GCCTCTGGA AGG	57,89	chr2	(+)	239189886	239189908	exon4	NM_006037 (-)	141719	141741
HDAC4	GCAGTGAG AGG	57,89	chr2	(+)	239189994	239190016	exon4	NM_006037 (-)	141827	141849
HDAC4	CAGCTCTG TGG	63,16	chr2	(+)	239176522	239176544	exon5	NM_006037 (-)	128355	128377
HDAC5	AGTCCGCG AGG	63,16	chr17	(+)	44110754	44110776	exon3, exon3	NM_005474, (-)	34002	34024
HDAC5	AACAGCATG AGG	52,63	chr17	(-)	44093608	44093630	exon4, exon4	NM_005474, (-)	16856	16878
HDAC5	GTTTCTGGA AGG	47,37	chr17	(+)	44093628	44093650	exon4, exon4	NM_005474, (-)	16876	16898
HDAC5	AGAGCCATG GGG	57,89	chr17	(-)	44093789	44093811	exon4, exon4	NM_005474, (-)	17037	17059
HDAC6	CCGCTCTATC CGG	52,63	chrX	(+)	48802900	48802922	exon3	NM_006044 (+)	821	843
HDAC6	ACCTAATCG GGG	52,63	chrX	(+)	48802974	48802996	exon3	NM_006044 (+)	895	917
HDAC6	GAAAGGAC AGG	57,89	chrX	(-)	48805498	48805520	exon5	NM_006044 (+)	3419	3441
HDAC7	CGTGGTCAA CGG	52,63	chr12	(-)	47798181	47798203	exon5, exon5	NM_001098, (-)	15471	15493
HDAC7	GGGATGGA GGG	47,37	chr12	(+)	47798131	47798153	exon5, exon5	NM_001098, (-)	15421	15443

HDAC7	TTCGCTTGCT TGG	47,37	chr12	(+)	47798562	47798584	exon4, exon4 NM_001098 (-)	15852	15874
HDAC7	AAAAGCTGC CGG	47,37	chr12	(+)	47797444	47797466	exon6, exon6 NM_001098 (-)	14734	14756
HDAC8	CATCCGGAC TGG	45	chrX	(-)	72568759	72568781	exon3, exon3 NM_018486 (-)	1178	1200
HDAC8	GTAGCAATT AGG	45	chrX	(-)	72567907	72567929	exon4, exon4 NM_018486 (-)	326	348
HDAC8	CATTCCGTC A GGG	45	chrX	(+)	72567936	72567958	exon4, exon4 NM_018486 (-)	355	377
HDAC8	TGGGACTA CGG	35	chrX	(+)	72572694	72572716	exon1, exon1 NM_001166 (-)	5113	5135
HDAC9	GAACCTGAC AGG	57,89	chr7	(+)	18585477	18585499	exon3, exon2 NM_178423 (+)	76201	76223
HDAC9	CCATCTCAC AGG	47,37	chr7	(+)	18585317	18585339	exon3, exon2 NM_178423 (+)	89572	89594
HDAC9	CCGTGAGAA AGG	52,63	chr7	(+)	18585381	18585403	exon3, exon2 NM_178423 (+)	76105	76127
HDAC9	ACGAAAGAC TGG	42,11	chr7	(+)	18591578	18591600	exon5, exon4 NM_178423 (+)	82302	82324
HDGF	AGCCGGAAC GGG	57,89	chr1	(+)	156745013	156745035	exon3, exon3 NM_001126 (-)	2907	2929
HDGF	CTTCCCTTAC AGG	52,63	chr1	(-)	156745100	156745122	exon3, exon3 NM_001126 (-)	2994	3016
HDGF	CTCGTAAGG TGG	52,63	chr1	(+)	156745110	156745132	exon3, exon3 NM_001126 (-)	3004	3026
HDGFL1	GGAAATCGA CGG	52,63	chr6	(+)	22569815	22569837	exon1 NM_138574 (+)	367	389
HDGFL1	GTTCCTGTA AGG	57,89	chr6	(+)	22569743	22569765	exon1 NM_138574 (+)	295	317
HDGFL1	TTGTACGGG GGG	52,63	chr6	(-)	22569732	22569754	exon1 NM_138574 (+)	284	306
HDGFL1	GGCATGCCC CGG	52,63	chr6	(+)	22569588	22569610	exon1 NM_138574 (+)	140	162
HDGFRP2	AGTACGGG A AGG	52,63	chr19	(+)	4475495	4475517	exon3, exon3 NM_001001 (+)	3300	3322
HDGFRP2	TTAGCGAAC GGG	52,63	chr19	(-)	4472369	4472391	exon1, exon1 NM_001001 (+)	174	196
HDGFRP2	TCGTAGGGG GGG	57,89	chr19	(-)	4475458	4475480	exon3, exon3 NM_001001 (+)	3263	3285
HDGFRP2	TTGGTGTTC GGG	42,11	chr19	(+)	4472378	4472400	exon1, exon1 NM_001001 (+)	183	205
HDGFRP3	ATAGGATAC AGG	36,84	chr15	(+)	83164023	83164045	exon2 NM_016073 (-)	25972	25994
HDGFRP3	TACTGCAGA AGG	47,37	chr15	(-)	83157504	83157526	exon4 NM_016073 (-)	19453	19475
HDGFRP3	GGAAAGTCA AGG	42,11	chr15	(-)	83157964	83157986	exon3 NM_016073 (-)	19913	19935
HDGFRP3	CAGAGCTCT GGG	47,37	chr15	(-)	83157539	83157561	exon4 NM_016073 (-)	19488	19510
HELLS	CGTCGTTTT AGG	57,89	chr10	(-)	94590434	94590456	exon12, exon NM_001289 (+)	44668	44690
HELLS	ACGACTACT AGG	42,11	chr10	(-)	94588283	94588305	exon11, exon NM_001289 (+)	42517	42539
HELLS	GACCATTAC GGG	52,63	chr10	(-)	94574082	94574104	exon8, exon8 NM_001289 (+)	28316	28338
HELLS	TACCCGGCC AGG	57,89	chr10	(+)	94546423	94546445	exon2, exon2 NM_001289 (+)	657	679
HIF1AN	GGAAGCTAT TGG	47,37	chr10	(-)	100536048	100536070	exon1 NM_017902 (+)	165	187
HIF1AN	CTTTAAGCCC GGG	52,63	chr10	(+)	100536572	100536594	exon2 NM_017902 (+)	689	711
HIF1AN	TTTGTGTCA AGG	52,63	chr10	(-)	100536414	100536436	exon2 NM_017902 (+)	531	553
HIF1AN	TCAATAAGC GGG	52,63	chr10	(-)	100536106	100536128	exon1 NM_017902 (+)	223	245
HIRA	TTGCGAACT GGG	57,89	chr22	(+)	19410728	19410750	exon2 NM_003325 (-)	80028	80050
HIRA	TCTATCCTC AGG	42,11	chr22	(-)	19405788	19405810	exon5 NM_003325 (-)	75088	75110
HIRA	CTTACCACCTG CGG	57,89	chr22	(+)	19405841	19405863	exon5 NM_003325 (-)	75141	75163
HIRA	TGTTGTGCGG TGG	52,63	chr22	(-)	19407241	19407263	exon4 NM_003325 (-)	76541	76563
HIST1H1B	GGCGGCTCA GGG	55	chr6	(+)	27867317	27867339	[exon1] [NM_005322 (-)]	526	548
HIST1H1B	GAAATCCCC AGG	50	chr6	(-)	27867460	27867482	[exon1] [NM_005322 (-)]	669	691
HIST1H1B	TTTAGCGGG TGG	60	chr6	(+)	27867140	27867162	[exon1] [NM_005322 (-)]	349	371
HIST1H1B	TGGTGATCA GGG	50	chr6	(+)	27867385	27867407	[exon1] [NM_005322 (-)]	594	616
HIST1H1C	AACTCCGCT A AGG	50	chr6	(+)	26056258	26056280	[exon1] [NM_005315 (-)]	519	541
HIST1H1C	TCCGCCGCC TGG	55	chr6	(+)	26056054	26056076	[exon1] [NM_005315 (-)]	315	337
HIST1H1C	GGCGGCCTT GGG	55	chr6	(+)	26056354	26056376	[exon1] [NM_005315 (-)]	615	637
HIST1H1C	GGCTGCTCT TGG	50	chr6	(-)	26056230	26056252	[exon1] [NM_005315 (-)]	491	513
HIST1H3B	CTCGTACTA A CGG	45	chr6	(-)	26032034	26032056	[exon1] [NM_003537 (-)]	446	468
HIST1H3B	GAAGATCGC TGG	45	chr6	(+)	26031811	26031833	[exon1] [NM_003537 (-)]	223	245
HIST1H3B	ACTCGGTCG CGG	50	chr6	(+)	26031880	26031902	[exon1] [NM_003537 (-)]	292	314
HIST1H3B	AGTCGACCG CGG	50	chr6	(-)	26031869	26031891	[exon1] [NM_003537 (-)]	281	303
HLTF	TTTGGACTA GGG	42,11	chr3	(-)	149084686	149084708	exon2, exon2 NM_139048 (-)	54560	54582
HLTF	GTCTGCAAG TGG	42,11	chr3	(+)	149084863	149084885	exon2, exon2 NM_139048 (-)	54737	54759
HLTF	CATCTGGAG TGG	47,37	chr3	(+)	149084771	149084793	exon2, exon2 NM_139048 (-)	54645	54667
HLTF	AGGTGCTTT TGG	47,37	chr3	(-)	149075906	149075928	exon3, exon3 NM_139048 (-)	45780	45802
HNF1A	GATGTTGTG AGG	55	chr12	(-)	120988868	120988890	[exon2, exon NM_000545 (+)]	10301	10323
HNF1A	TGAGGTTCT AGG	50	chr12	(-)	120979023	120979045	[exon1, exon NM_000545 (+)]	456	478
HNF1A	AGCAGACA CGG	55	chr12	(+)	120988877	120988899	[exon2, exon NM_000545 (+)]	10310	10332
HNF1A	TAAACTGAG CGG	50	chr12	(+)	120978777	120978799	[exon1, exon NM_000545 (+)]	210	232
HR	TCTCAGATC GGG	52,63	chr8	(+)	22129096	22129118	exon2, exon2 NM_005144 (-)	14678	14700
HR	CTCGAGATG GGG	57,89	chr8	(-)	22129054	22129076	exon2, exon2 NM_005144 (-)	14636	14658
HR	AGTACGCCG GGG	57,89	chr8	(-)	22129142	22129164	exon2, exon2 NM_005144 (-)	14724	14746
HR	CACTATGCTC GGG	52,63	chr8	(+)	22128789	22128811	exon2, exon2 NM_005144 (-)	14371	14393
HSPBAP1	ATCGTATCTC AGG	47,37	chr3	(+)	122777751	122777773	exon2, exon2 NM_024610 (-)	37755	37777
HSPBAP1	AGCCGCAAO TGG	57,89	chr3	(+)	122793636	122793658	exon1, exon1 NM_024610 (-)	53640	53662
HSPBAP1	AGCAGATAA GGG	36,84	chr3	(-)	122777740	122777762	exon2, exon2 NM_024610 (-)	37744	37766
HSPBAP1	CACCTGAAG TGG	47,37	chr3	(-)	122768821	122768843	exon3, exon3 NM_024610 (-)	28825	28847
IDH1	GCATGACGA AGG	45	chr2	(+)	208248382	208248404	[exon4, exon NM_005896 (-)]	12156	12178
IDH1	ACGAAATAT CGG	45	chr2	(-)	208248464	208248486	[exon4, exon NM_005896 (-)]	12238	12260
IDH1	ATGTAGATC AGG	40	chr2	(+)	208251432	208251454	[exon3, exon NM_005896 (-)]	15206	15228
IDH1	CTATCACTCC AGG	45	chr2	(-)	208248537	208248559	[exon4, exon NM_005896 (-)]	12311	12333
IDH2	GAAGGTGATC AGG	55	chr15	(-)	90088393	90088415	[exon5, exon NM_001285 (-)]	4414	4436
IDH2	ACTATCCGG GGG	55	chr15	(-)	90088687	90088709	[exon4, exon NM_001285 (-)]	4708	4730
IDH2	CGCCACCTTC CGG	50	chr15	(+)	90091619	90091641	[exon2] [NM_002168 (-)]	7640	7662
IDH2	ACCATACTG TGG	45	chr15	(-)	90087475	90087497	[exon6, exon NM_001285 (-)]	3496	3518
ING1	TTGAACGTC CGG	57,89	chr13	(+)	110715603	110715625	exon1 NM_005537 (+)	592	614
ING1	CGTTCCGCA AGG	57,89	chr13	(-)	110715462	110715484	exon1, exon1 NM_005537 (+)	26	48
ING1	AAATCGCGC CGG	47,37	chr13	(+)	110715720	110715742	exon1 NM_005537 (+)	709	731
ING1	TGCGGAACG AGG	57,89	chr13	(+)	110715476	110715498	exon1, exon1 NM_005537 (+)	40	62
ING2	TGCTCGAAT CGG	42,11	chr4	(+)	183510429	183510451	exon2, exon2 NM_001291 (+)	5380	5402
ING2	AAGGTAGTC AGG	52,63	chr4	(-)	183505269	183505291	exon1 NM_001564 (+)	220	242
ING2	GCAGCAGCA CGG	57,89	chr4	(+)	183505210	183505232	exon1 NM_001564 (+)	161	183
ING2	ACGTTCTCT GGG	52,63	chr4	(-)	183505310	183505332	exon1 NM_001564 (+)	261	283
ING3	TCTCGCGCA1 CGG	52,63	chr7	(-)	120951195	120951217	exon2, exon2 NM_198267 (+)	433	455
ING3	AATGCGCGA AGG	57,89	chr7	(+)	120951207	120951229	exon2, exon2 NM_198267 (+)	445	467
ING3	GTGTGACCT TGG	36,84	chr7	(+)	120950899	120950921	exon1, exon1 NM_198267 (+)	137	159
ING3	GAAAAATAA GGG	36,84	chr7	(+)	120953356	120953378	exon3, exon3 NM_198267 (+)	2594	2616
ING4	CCGTTTTGA AGG	52,63	chr12	(-)	6652990	6653012	exon4, exon3 NM_001127 (-)	2453	2475
ING4	GCTGCTCGT AGG	63,16	chr12	(-)	6652722	6652744	exon5, exon4 NM_001127 (-)	2185	2207

ING4	GGCACTACTTGG	42,11 chr12	(+)	6653347	6653369	exon3, exon2 NM_001127(-)	2810	2832
ING4	GGACAAACA TGG	57,89 chr12	(-)	6653026	6653048	exon4, exon3 NM_001127(-)	2489	2511
ING5	GATCTGCTT AGG	57,89 chr2	(-)	241711409	241711431	exon4 NM_032329 (+)	9369	9391
ING5	GAAGTTCTT AGG	47,37 chr2	(-)	241704668	241704690	exon2 NM_032329 (+)	2628	2650
ING5	ATAGTGCTC CGG	42,11 chr2	(-)	241702073	241702095	exon1 NM_032329 (+)	33	55
ING5	GAACGCCTA AGG	57,89 chr2	(+)	241709313	241709335	exon3 NM_032329 (+)	7273	7295
INO80	GTCCGAGAA CGG	47,37 chr15	(+)	41096202	41096224	exon2 NM_017553 (-)	117322	117344
INO80	AATCCATTATGG	42,11 chr15	(-)	41095875	41095897	exon3 NM_017553 (-)	116995	117017
INO80	TCTCCAAGTA AGG	36,84 chr15	(+)	41096232	41096254	exon2 NM_017553 (-)	117352	117374
INO80	GGATCCCTTA AGG	36,84 chr15	(-)	41095852	41095874	exon3 NM_017553 (-)	116972	116994
INTS12	TGCTTCGATG CGG	42,11 chr4	(-)	105699883	105699905	exon3, exon2 NM_020395, (-)	17256	17278
INTS12	CTTTTGAGA TGG	42,11 chr4	(+)	105699850	105699872	exon3, exon2 NM_020395, (-)	17223	17245
INTS12	CAAGGTCTT AGG	47,37 chr4	(-)	105695551	105695573	exon4, exon3 NM_020395, (-)	12924	12946
INTS12	TTCTCCAATC TGG	36,84 chr4	(+)	105693431	105693453	exon5, exon4 NM_020395, (-)	10804	10826
IWS1	GAATCCCGT TGG	47,37 chr2	(+)	127523752	127523774	exon2 NM_017969 (-)	42946	42968
IWS1	CAACACTCCG TGG	52,63 chr2	(-)	127523698	127523720	exon2 NM_017969 (-)	42892	42914
IWS1	CAACGGGAAT CGG	57,89 chr2	(-)	127523740	127523762	exon2 NM_017969 (-)	42934	42956
IWS1	ATGGACTCG CGG	36,84 chr2	(-)	127526186	127526208	exon1 NM_017969 (-)	45380	45402
JADE1	GCACAACA CCG	42,11 chr4	(-)	128846432	128846454	exon4, exon4 NM_001287 (+)	36810	36832
JADE1	TCATCCGGG AGG	57,89 chr4	(-)	128846418	128846440	exon4, exon4 NM_001287 (+)	36796	36818
JADE1	GCAGGAGCT GGG	57,89 chr4	(-)	128842986	128843008	exon3, exon3 NM_001287 (+)	33364	33386
JADE1	GATGACACG GGG	42,11 chr4	(-)	128849017	128849039	exon5, exon5 NM_001287 (+)	39395	39417
JADE2	AGACCCATG GGG	57,89 chr5	(+)	134552132	134552154	exon4, exon4 NM_015288, (+)	27758	27780
JADE2	GGCTTCTTT GGG	47,37 chr5	(-)	134538054	134538076	exon3, exon3 NM_015288, (+)	13680	13702
JADE2	CAGTTTGGA CGG	42,11 chr5	(-)	134538007	134538029	exon3, exon3 NM_015288, (+)	13633	13655
JADE2	GCCAGGATG CGG	47,37 chr5	(-)	134552109	134552131	exon4, exon4 NM_015288, (+)	27735	27757
JADE3	AGTGAATAT CGG	47,37 chrX	(-)	47024760	47024782	exon5, exon5 NM_001077 (+)	112328	112350
JADE3	TCCATGATG AGG	42,11 chrX	(-)	47024806	47024828	exon5, exon5 NM_001077 (+)	112374	112396
JADE3	GATTATAGC AGG	36,84 chrX	(+)	47024724	47024746	exon5, exon5 NM_001077 (+)	112292	112314
JADE3	CTGTGGAAC TGG	57,89 chrX	(-)	46998244	46998266	exon4, exon4 NM_001077 (+)	85812	85834
JARID2	ATCGGTCGG CGG	57,89 chr6	(+)	15487514	15487536	exon6, exon6 NM_001267 (+)	241540	241562
JARID2	GATTCGTG GGG	47,37 chr6	(+)	15374131	15374153	exon2 NM_004973 (+)	128157	128179
JARID2	ATCGCTGTG CGG	47,37 chr6	(-)	15487379	15487401	exon6, exon6 NM_001267 (+)	241405	241427
JARID2	ACTAACATC AGG	42,11 chr6	(-)	15410308	15410330	exon3 NM_004973 (+)	164334	164356
JMJD1C	TTGGCATTAT AGG	47,37 chr10	(-)	63215586	63215608	exon5, exon5 NM_001282 (-)	48366	48388
JMJD1C	ATCCGTCAC GGG	42,11 chr10	(-)	63215331	63215353	exon6, exon6 NM_001282 (-)	48111	48133
JMJD1C	ATTCATAAC GGG	36,84 chr10	(+)	63217213	63217235	exon4, exon5 NM_001282 (-)	49993	50015
JMJD1C	ACAGAATGT TGG	42,11 chr10	(-)	63215663	63215685	exon5, exon5 NM_001282 (-)	48443	48465
JMJD6	TTGCGCATT CGG	42,11 chr17	(+)	76725757	76725779	exon2, exon2 NM_001081 (-)	7315	7337
JMJD6	GGACTCTGG AGG	57,89 chr17	(-)	76725709	76725731	exon2, exon2 NM_001081 (-)	7267	7289
JMJD6	AGCTCTCGT CGG	47,37 chr17	(+)	76726373	76726395	exon1, exon1 NM_001081 (-)	7931	7953
JMJD6	GGATGCGCT TGG	52,63 chr17	(+)	76726448	76726470	exon1, exon1 NM_001081 (-)	8006	8028
JMJD8	GACAGTTTG TGG	55 chr16	(-)	683735	683757	exon4 NM_001005 (-)	2069	2091
JMJD8	ACAGGTTGC GGG	50 chr16	(-)	683734	683756	exon4 NM_001005 (-)	2068	2090
JMJD8	GGCTTCGTT TGG	60 chr16	(-)	683724	683746	exon4 NM_001005 (-)	2058	2080
JMJD8	TTTGTGGTA TGG	45 chr16	(+)	683686	683708	exon4 NM_001005 (-)	2020	2042
KANS11	ACACCATATC TGG	42,11 chr17	(-)	46172077	46172099	exon2, exon2 NM_015443, (-)	142162	142184
KANS11	GGAGTCTTT GGG	42,11 chr17	(-)	46171843	46171865	exon2, exon2 NM_015443, (-)	141928	141950
KANS11	GAACCCGA GGG	57,89 chr17	(-)	46171767	46171789	exon2, exon2 NM_015443, (-)	141852	141874
KANS11	CGTTATTTT GGG	52,63 chr17	(+)	46172032	46172054	exon2, exon2 NM_015443, (-)	142117	142139
KAT2A	TTCTCAAGCT CGG	52,63 chr17	(+)	42120991	42121013	exon1 NM_021078 (-)	7881	7903
KAT2A	TTTCCAGCCA AGG	36,84 chr17	(+)	42120797	42120819	exon2 NM_021078 (-)	7687	7709
KAT2A	GACTTGCGO TGG	57,89 chr17	(+)	42121023	42121045	exon1 NM_021078 (-)	7913	7935
KAT2A	TGAGAAGCT CGG	52,63 chr17	(-)	42120974	42120996	exon1 NM_021078 (-)	7864	7886
KAT2B	GCGCTTTCTT CGG	57,89 chr3	(-)	20040696	20040718	exon1 NM_003884 (+)	665	687
KAT2B	GACAATTAT CGG	42,11 chr3	(-)	20072397	20072419	exon2 NM_003884 (+)	32366	32388
KAT2B	TTCTCCAGTT CGG	52,63 chr3	(-)	20040733	20040755	exon1 NM_003884 (+)	702	724
KAT2B	GAGGAGTCT TGG	36,84 chr3	(+)	20072336	20072358	exon2 NM_003884 (+)	32305	32327
KAT5	GTCTTCAAC CGG	57,89 chr11	(-)	65712772	65712794	exon3, exon2 NM_006388, (+)	771	793
KAT5	GATCCAGTT AGG	47,37 chr11	(+)	65712974	65712996	exon4, exon3 NM_006388, (+)	973	995
KAT5	GCCAAGACC CGG	57,89 chr11	(+)	65712996	65713018	exon4, exon3 NM_006388, (+)	995	1017
KAT5	GATTGGCAA TGG	57,89 chr11	(-)	65713364	65713386	exon5, exon4 NM_006388, (+)	1363	1385
KAT6A	GAATAGCAC CGG	47,37 chr8	(-)	42048720	42048742	exon2, exon2 NM_006766, (-)	106672	106694
KAT6A	CTGATAAAG GGG	52,63 chr8	(-)	42048652	42048674	exon2, exon2 NM_006766, (-)	106604	106626
KAT6A	AACAGCGTC AGG	47,37 chr8	(-)	42048885	42048907	exon2, exon2 NM_006766, (-)	106837	106859
KAT6A	GACTATTGC AGG	47,37 chr8	(+)	42048736	42048758	exon2, exon2 NM_006766, (-)	106688	106710
KAT6B	TAACTAGTG GGG	47,37 chr10	(-)	74843085	74843107	exon3, exon3 NM_012330, (+)	16673	16695
KAT6B	GTTGTCTGG AGG	47,37 chr10	(-)	74843063	74843085	exon3, exon3 NM_012330, (+)	16651	16673
KAT6B	ATGCGGTCA GGG	52,63 chr10	(+)	74842958	74842980	exon3, exon3 NM_012330, (+)	16546	16568
KAT6B	GTTTATTCCA CGG	31,58 chr10	(-)	74843163	74843185	exon3, exon3 NM_012330, (+)	16751	16773
KAT7	GATGAACGA AGG	52,63 chr17	(-)	49796863	49796885	exon3, exon3 NM_001199 (+)	8245	8267
KAT7	TACCCGCCTC TGG	57,89 chr17	(+)	49798348	49798370	exon4, exon4 NM_001199 (+)	9730	9752
KAT7	CTGACTACG TGG	52,63 chr17	(-)	49796807	49796829	exon3, exon3 NM_001199 (+)	8189	8211
KAT7	CTCGAGATC CGG	36,84 chr17	(-)	49791923	49791945	exon2, exon2 NM_001199 (+)	3305	3327
KAT8	ACGAGTGGC CGG	47,37 chr16	(+)	31120354	31120376	exon3, exon3 NM_182958, (+)	2691	2713
KAT8	GTCTCGAGT AGG	57,89 chr16	(+)	31120205	31120227	exon2, exon2 NM_182958, (+)	2542	2564
KAT8	TGGGAGAAA CGG	52,63 chr16	(+)	31117851	31117873	exon1, exon1 NM_182958, (+)	188	210
KDM1A	GAATAGCAG GGG	55 chr1	(+)	23019895	23019917	exon1, exon1 NM_015013, (+)	448	470
KDM1A	GGAATAGCA GGG	55 chr1	(+)	23019894	23019916	exon1, exon1 NM_015013, (+)	447	469
KDM1A	TGGAATAGC AGG	55 chr1	(+)	23019893	23019915	exon1, exon1 NM_015013, (+)	446	468
KDM1A	CTGCTATTCC GGG	45 chr1	(-)	23019881	23019903	exon1, exon1 NM_015013, (+)	434	456
KDM1B	AAAATGGCT TGG	52,63 chr6	(+)	18162843	18162865	exon5 NM_153042 (+)	7456	7478
KDM1B	GCCATGAAA AGG	52,63 chr6	(-)	18166334	18166356	exon6 NM_153042 (+)	10947	10969
KDM1B	TACCGGAGC AGG	57,89 chr6	(-)	18159955	18159977	exon3 NM_153042 (+)	4568	4590
KDM1B	ATGTGAAAA CGG	47,37 chr6	(+)	18161395	18161417	exon4 NM_153042 (+)	6008	6030
KDM2A	GTACTATAG AGG	42,11 chr11	(-)	67243050	67243072	exon13, exor NM_012308, (+)	3016	3038
KDM2A	CGTCTGGCT CGG	57,89 chr11	(-)	67245300	67245322	exon14, exor NM_012308, (+)	5266	5288

KDM2A	CTCCACGGT AGG	52,63	chr11	(+)	67245262	67245284	exon14, exor NM_012308, (+)	5228	5250
KDM2A	TAAATTCCTC AGG	52,63	chr11	(+)	67245191	67245213	exon14, exor NM_012308, (+)	5157	5179
KDM2B	TGCTATCGC CGG	57,89	chr12	(+)	121578921	121578943	exon2, exon2 NM_032590, (-)	149826	149848
KDM2B	CCACGCGATA AGG	57,89	chr12	(-)	121578910	121578932	exon2, exon2 NM_032590, (-)	149815	149837
KDM2B	TCTCGTAGT TGG	42,11	chr12	(+)	121549552	121549574	exon5, exon5 NM_032590, (-)	120457	120479
KDM2B	ACGTCTCGG AGG	47,37	chr12	(+)	121574561	121574583	exon4, exon4 NM_032590, (-)	145466	145488
KDM3A	CAGATCCCTT CGG	47,37	chr2	(-)	86442208	86442230	exon2, exon2 NM_018433, (+)	748	770
KDM3A	TTTCTGAAC TGG	31,58	chr2	(+)	86449931	86449953	exon3, exon3 NM_018433, (+)	8471	8493
KDM3A	GGTGTGGG TGG	57,89	chr2	(-)	86442187	86442209	exon2, exon2 NM_018433, (+)	727	749
KDM3A	TGCTCACGC TGG	57,89	chr2	(+)	86442052	86442074	exon2, exon2 NM_018433, (+)	592	614
KDM3B	GTATCGTG AGG	52,63	chr5	(+)	138372740	138372762	exon2 NM_016604, (+)	20145	20167
KDM3B	AGACTCGAA AGG	57,89	chr5	(-)	138372796	138372818	exon2 NM_016604, (+)	20201	20223
KDM3B	TACTCCCTT TGG	36,84	chr5	(+)	138375098	138375120	exon3 NM_016604, (+)	22503	22525
KDM3B	TAACCTGAA GGG	47,37	chr5	(+)	138372697	138372719	exon2 NM_016604, (+)	20102	20124
KDM4A	TTCAAACTCA GGG	36,84	chr1	(-)	43660306	43660328	exon4 NM_014663, (+)	10181	10203
KDM4A	TATCGCTATT CGG	36,84	chr1	(-)	43655743	43655765	exon3 NM_014663, (+)	5618	5640
KDM4A	CCATTCAACA GGG	52,63	chr1	(+)	43655661	43655683	exon3 NM_014663, (+)	5536	5558
KDM4A	TTGAATCCC CGG	47,37	chr1	(+)	43653276	43653298	exon2 NM_014663, (+)	3151	3173
KDM4B	ATGTCATCA TGG	47,37	chr19	(-)	5039860	5039882	exon4 NM_015015, (+)	70748	70770
KDM4B	GTATGATGA TGG	47,37	chr19	(+)	5039871	5039893	exon4 NM_015015, (+)	70759	70781
KDM4B	GGATATTGT AGG	42,11	chr19	(-)	5039937	5039959	exon4 NM_015015, (+)	70825	70847
KDM4B	CTGGCCCTA AGG	57,89	chr19	(+)	5032983	5033005	exon3 NM_015015, (+)	63871	63893
KDM4C	CTTTGCAAG GGG	57,89	chr9	(-)	6793110	6793132	exon2, exon2 NM_015061, (+)	35470	35492
KDM4C	GGCCACCTC GGG	57,89	chr9	(-)	6792978	6793000	exon2 NM_001146, (+)	72116	72138
KDM4C	CGATGACTG AGG	47,37	chr9	(+)	6805732	6805754	exon3, exon3 NM_015061, (+)	48092	48114
KDM4C	GAAGGTCAT TGG	36,84	chr9	(-)	6793023	6793045	exon2, exon2 NM_015061, (+)	35383	35405
KDM4D	GCGATACTC TGG	63,16	chr11	(-)	94997656	94997678	exon3 NM_018039, (+)	23976	23998
KDM4D	GATATTATC TGG	31,58	chr11	(-)	94997548	94997570	exon3 NM_018039, (+)	23868	23890
KDM4D	TCTTCGAAA TGG	42,11	chr11	(-)	94997709	94997731	exon3 NM_018039, (+)	24029	24051
KDM4D	ATTTGGATT TGG	47,37	chr11	(-)	94997395	94997417	exon3 NM_018039, (+)	23715	23737
KDM4E	TGCCAAGGT AGG	52,63	chr11	(+)	95025692	95025714	exon1 NM_001161, (+)	435	457
KDM4E	TCCCAAGGC TGG	57,89	chr11	(+)	95025666	95025688	exon1 NM_001161, (+)	409	431
KDM4E	GATGGTATG GGG	47,37	chr11	(-)	95025580	95025602	exon1 NM_001161, (+)	323	345
KDM4E	CCGGTAAT TGG	47,37	chr11	(+)	95025936	95025958	exon1 NM_001161, (+)	679	701
KDM5A	TCAGCTTTAT CGG	52,63	chr12	(-)	388972	388994	exon1 NM_001042, (-)	108916	108938
KDM5A	CTCCCAACTC CGG	57,89	chr12	(+)	389011	389033	exon1 NM_001042, (-)	108955	108977
KDM5A	CGGCCGAAT CGG	52,63	chr12	(+)	388933	388955	exon1 NM_001042, (-)	108877	108899
KDM5B	ATGCCAGTC GGG	57,89	chr1	(+)	202808124	202808146	exon1, exon1 NM_006618, (-)	82940	82962
KDM5B	ACTCCCACTA TGG	42,11	chr1	(+)	202774681	202774703	exon3, exon3 NM_006618, (-)	49497	49519
KDM5B	TGAAAAATTC AGG	36,84	chr1	(-)	202774643	202774665	exon3, exon3 NM_006618, (-)	49459	49481
KDM5B	TCCTTGGA GGG	42,11	chr1	(+)	202808152	202808174	exon1, exon1 NM_006618, (-)	82968	82990
KDM5C	TTCGTAGTG AGG	57,89	chrX	(+)	53217844	53217866	exon2, exon4 NM_001146, (-)	26524	26546
KDM5C	ATGCCCGAT GGG	52,63	chrX	(+)	53224762	53224784	exon1, exon1 NM_001146, (-)	33442	33464
KDM5C	TGGTGGA TGG	57,89	chrX	(+)	53217883	53217905	exon2, exon4 NM_001146, (-)	26563	26585
KDM5C	CACACGTCC AGG	36,84	chrX	(-)	53217247	53217269	exon3, exon5 NM_001146, (-)	25927	25949
KDM5D	GATTTACTCC AGG	52,63	chrY	(-)	19743177	19743199	exon3, exon3 NM_001146, (-)	37763	37785
KDM5D	CACACACCC AGG	47,37	chrY	(-)	19739632	19739654	exon5, exon6 NM_001146, (-)	34218	34240
KDM5D	GATGCCAGA TGG	52,63	chrY	(+)	19744406	19744428	exon2, exon2 NM_001146, (-)	38992	39014
KDM5D	GCTGAATTC TGG	57,89	chrY	(-)	19744449	19744471	exon2, exon2 NM_001146, (-)	39035	39057
KDM6A	GAAATCTCAT AGG	42,11	chrX	(-)	44873927	44873949	exon2, exon2 NM_001291, (-)	753	775
KDM6A	GATTTCATG AGG	47,37	chrX	(+)	44873944	44873966	exon2, exon2 NM_001291, (+)	770	792
KDM6A	TTCTCATCA CGG	52,63	chrX	(-)	44873595	44873617	exon1, exon1 NM_001291, (+)	421	443
KDM6A	ACTGTAAAC TGG	36,84	chrX	(-)	44974679	44974701	exon4, exon4 NM_001291, (+)	101505	101527
KDM6B	CGAGTCAGA AGG	52,63	chr17	(+)	7846192	7846214	exon6 NM_001080, (+)	6276	6298
KDM6B	GAACACTG GGG	47,37	chr17	(-)	7845915	7845937	exon5 NM_001080, (+)	5999	6021
KDM6B	AGCAAAACA AGG	36,84	chr17	(+)	7845948	7845970	exon5 NM_001080, (+)	6032	6054
KDM6B	GATTCAGC GGG	52,63	chr17	(-)	7846094	7846116	exon6 NM_001080, (+)	6178	6200
KDM7A	AGTGCAGATA TGG	47,37	chr7	(-)	140176755	140176777	exon1 NM_030647, (-)	92010	92032
KDM7A	TATCGCACT CGG	42,11	chr7	(+)	140176769	140176791	exon1 NM_030647, (-)	92024	92046
KDM7A	GGTTCCAAA TGG	52,63	chr7	(-)	140133584	140133606	exon3 NM_030647, (-)	48839	48861
KDM7A	CACAGTTGG AGG	47,37	chr7	(+)	140139129	140139151	exon2 NM_030647, (-)	54384	54406
KDM8	ACGTAGACA CGG	52,63	chr16	(+)	27210380	27210402	exon2, exon2 NM_001145, (+)	6895	6917
KDM8	GGTCTCTT AGG	52,63	chr16	(-)	27210198	27210220	exon2, exon2 NM_001145, (+)	6713	6735
KDM8	GGTGATCTT GGG	57,89	chr16	(+)	27210330	27210352	exon2, exon2 NM_001145, (+)	6845	6867
KIAA2026	GAGACCTC AGG	60	chr9	(+)	6007539	6007561	exon1 NM_001017, (-)	88532	88554
KIAA2026	CTGACCTAC GGG	55	chr9	(-)	6007543	6007565	exon1 NM_001017, (-)	88536	88558
KIAA2026	GCTGACCTA GGG	60	chr9	(-)	6007544	6007566	exon1 NM_001017, (-)	88537	88559
KIAA2026	GAGATGGA CGG	55	chr9	(-)	6007591	6007613	exon1 NM_001017, (-)	88584	88606
KMT2A	TCATCGCTCT AGG	55	chr11	(+)	118436795	118436817	exon1, exon1 NM_001197, (+)	306	328
KMT2A	TGACGAGA CGG	55	chr11	(-)	118436775	118436797	exon1, exon1 NM_001197, (+)	286	308
KMT2A	CATCGTCTCT GGG	55	chr11	(+)	118436796	118436818	exon1, exon1 NM_001197, (+)	307	329
KMT2A	CGATGAGA AGG	55	chr11	(-)	118436778	118436800	exon1, exon1 NM_001197, (+)	289	311
KMT2B	CAGAGCTAG CGG	55	chr19	(-)	35718137	35718159	exon1 NM_014727, (+)	119	141
KMT2C	GCGATCTGT CGG	52,63	chr7	(-)	152330641	152330663	exon3 NM_170606, (-)	195717	195739
KMT2C	GACACAGAT TGG	52,63	chr7	(+)	152330652	152330674	exon3 NM_170606, (-)	195728	195750
KMT2C	CGAGTTTTC AGG	52,63	chr7	(+)	152358652	152358674	exon2 NM_170606, (-)	223728	223750
KMT2C	CAAAGAACA AGG	36,84	chr7	(-)	152330713	152330735	exon3 NM_170606, (-)	195789	195811
KMT2D	AGTTGCCAT CGG	47,37	chr12	(-)	49054649	49054671	exon3 NM_003482, (-)	35675	35697
KMT2D	AATCTGTGA TGG	42,11	chr12	(+)	49054574	49054596	exon3 NM_003482, (-)	35600	35622
KMT2D	CAGAGACCT GGG	57,89	chr12	(+)	49054949	49054971	exon2 NM_003482, (-)	35975	35997
KMT2E	GAGCATAGT GGG	47,37	chr7	(+)	105040955	105040977	exon3, exon2 NM_182931, (+)	26766	26788
KMT2E	GTATGGTA AGG	36,84	chr7	(+)	105063502	105063524	exon5, exon4 NM_182931, (+)	49313	49335
KMT2E	GAGGACGAC TGG	47,37	chr7	(-)	105063353	105063375	exon5, exon4 NM_182931, (+)	49164	49186
KMT2E	TACCACAGG CGG	52,63	chr7	(-)	105062172	105062194	exon4, exon3 NM_182931, (+)	47983	48005
L3MBTL1	CGGGCTTAT CGG	47,37	chr20	(-)	43514637	43514659	exon1, exon4 NM_015478, (+)	6958	6980
L3MBTL1	GACCGAATA GGG	52,63	chr20	(+)	43514715	43514737	exon1, exon4 NM_015478, (+)	7036	7058
L3MBTL1	TACGGGTCC CGG	57,89	chr20	(-)	43514576	43514598	exon1 NM_015478, (+)	141	163

L3MBTL1	GTATAAGCC CGG	47,37	chr20	(+)	43514649	43514671	exon1, exon4	NM_015478, (+)	6970	6992
L3MBTL2	CGGAGTTAT GGG	47,37	chr22	(+)	41209771	41209793	exon2	NM_031488 (+)	4463	4485
L3MBTL2	GTGTGGTAT GGG	52,63	chr22	(+)	41213906	41213928	exon3	NM_031488 (+)	8598	8620
L3MBTL2	TTCACTTGAC AGG	47,37	chr22	(-)	41209808	41209830	exon2	NM_031488 (+)	4500	4522
L3MBTL2	CTGTAACCTA TGG	42,11	chr22	(-)	41214004	41214026	exon3	NM_031488 (+)	8696	8718
L3MBTL3	AGTGCCGGC AGG	60	chr6	(+)	130057473	130057495	exon9, exon8	NM_032438, (+)	38891	38913
L3MBTL3	GGATTCCGGC AGG	50	chr6	(+)	130055233	130055255	exon8, exon7	NM_032438, (+)	36651	36673
L3MBTL3	CTCTTGACCA AGG	50	chr6	(-)	130042713	130042735	exon3, exon3	NM_032438, (+)	24131	24153
L3MBTL3	TGGGATGCC AGG	50	chr6	(+)	130051265	130051287	exon6, exon5	NM_032438, (+)	32683	32705
L3MBTL4	CATTGATCCC CGG	50	chr18	(-)	6244510	6244532	exon6	NM_173464 (-)	289805	289827
L3MBTL4	AGATCGATC TGG	50	chr18	(+)	6311563	6311585	exon3	NM_173464 (-)	356858	356880
L3MBTL4	ACATGAAC T AGG	45	chr18	(-)	6243294	6243316	exon7	NM_173464 (-)	288589	288611
L3MBTL4	GTCCGCCAC AGG	60	chr18	(+)	6239787	6239809	exon9	NM_173464 (-)	285082	285104
LBR	GATCGGCG TGG	57,89	chr1	(+)	225422153	225422175	exon3, exon3	NM_194442, (-)	20652	20674
LBR	CTTCTTAAT TGG	52,63	chr1	(+)	225422118	225422140	exon3, exon3	NM_194442, (-)	20617	20639
LBR	CCATCGGCA TGG	47,37	chr1	(+)	225424050	225424072	exon2, exon2	NM_194442, (-)	22549	22571
LBR	GCCGATGGT AGG	52,63	chr1	(-)	225424035	225424057	exon2, exon2	NM_194442, (-)	22534	22556
Mar-05	ATCCACCCAC AGG	52,63	chr10	(-)	92311233	92311255	exon2	NM_017824 (+)	20071	20093
Mar-05	GTGCAGAGC GGG	42,11	chr10	(+)	92311201	92311223	exon2	NM_017824 (+)	20039	20061
Mar-05	AGATCCAAAG TGG	42,11	chr10	(-)	92340675	92340697	exon3	NM_017824 (+)	49513	49535
Mar-05	GCTGCAGCA CGG	52,63	chr10	(+)	92340732	92340754	exon3	NM_017824 (+)	49570	49592
MBD1	CGCGAAGTC AGG	52,63	chr18	(-)	50279919	50279941	exon2, exon2	NM_015847, (-)	8451	8473
MBD1	AACCTGAC TGG	52,63	chr18	(+)	50276924	50276946	exon4, exon4	NM_015847, (-)	5456	5478
MBD1	ACCTCTTCG AGG	47,37	chr18	(-)	50277115	50277137	exon3, exon3	NM_015847, (-)	5647	5669
MBD1	GTTGAGCTG GGG	52,63	chr18	(-)	50277154	50277176	exon3, exon3	NM_015847, (-)	5686	5708
MBD2	GGTTCTGCC GGG	55	chr18	(+)	54202913	54202935	exon3	NM_015832 (-)	234	256
MBD2	AATAACAAT GGG	40	chr18	(+)	54202868	54202890			0	0
MBD2	GAGGAAGT TGG	45	chr18	(-)	54224054	54224076	exon1, exon1	NM_015832, (-)	72454	72476
MBD2	CCTCAGTGC GGG	55	chr18	(-)	54205107	54205129	exon2, exon2	NM_015832, (-)	53507	53529
MBD3	TGGTTGGTA CGG	42,11	chr19	(+)	1584595	1584617	exon3, exon3	NM_001281 (-)	7925	7947
MBD3	TTCATGACAT CGG	52,63	chr19	(+)	1585111	1585133	exon2, exon2	NM_001281 (-)	8441	8463
MBD3	CAGCAATGT AGG	52,63	chr19	(+)	1582664	1582686	exon4, exon4	NM_001281 (-)	5991	6016
MBD3	TCGCTCTTG GGG	52,63	chr19	(+)	1584571	1584593	exon3, exon3	NM_001281 (-)	7901	7923
MBD4	TCTTAAAGG GGG	42,11	chr3	(+)	129433952	129433974	exon5, exon5	NM_001276 (-)	3009	3031
MBD4	GCGATGGGT GGG	52,63	chr3	(+)	129437846	129437868	exon2, exon2	NM_001276 (-)	6903	6925
MBD4	ACGAGATTA AGG	42,11	chr3	(+)	129433918	129433940	exon5, exon5	NM_001276 (-)	2975	2997
MBD4	TGCCGTAAG TGG	52,63	chr3	(-)	129437789	129437811	exon2, exon2	NM_001276 (-)	6846	6868
MBD5	GGACAGAA TGG	50	chr2	(+)	148468568	148468590	exon9	NM_018328 (+)	447558	447580
MBD5	CAGCGTCGT TGG	50	chr2	(+)	148458834	148458856	exon6	NM_018328 (+)	437824	437846
MBD5	GTCTACCCCC GGG	55	chr2	(+)	148468532	148468554	exon9	NM_018328 (+)	447522	447544
MBD5	GAGAACGCA AGG	45	chr2	(+)	148463774	148463796	exon8	NM_018328 (+)	442764	442786
MBTD1	GCGGCTAGC AGG	52,63	chr17	(+)	51218980	51219002	exon5	NM_017643 (-)	41556	41578
MBTD1	CGGTTATGA AGG	47,37	chr17	(-)	51225131	51225153	exon3	NM_017643 (-)	47707	47729
MBTD1	TTGATAATC AGG	36,84	chr17	(+)	51225055	51225077	exon3	NM_017643 (-)	47631	47653
MBTD1	TTACTCGTCA AGG	42,11	chr17	(-)	51220353	51220375	exon4	NM_017643 (-)	42929	42951
MECOM	TATCCGGCG TGG	52,63	chr3	(+)	169131435	169131457	exon4, exon3	NM_004991, (-)	47937	47959
MECOM	GTAGTTGCA GGG	52,63	chr3	(-)	169131497	169131519	exon4, exon4	NM_004991, (-)	47999	48021
MECOM	GCCTCAACA TGG	47,37	chr3	(+)	169143770	169143792	exon3, exon3	NM_004991, (-)	60272	60294
MECOM	CTCAAGTAC TGG	36,84	chr3	(-)	169143744	169143766	exon3, exon3	NM_004991, (-)	60246	60268
MECP2	GATGATGG TGG	63,16	chrX	(+)	154032320	154032342	exon3, exon2	NM_004992, (-)	2086	2108
MECP2	GGTCATCAT CGG	52,63	chrX	(+)	154032292	154032314	exon3, exon2	NM_004992, (-)	2058	2080
MECP2	GGACACGG AGG	52,63	chrX	(-)	154032251	154032273	exon3, exon4	NM_004992, (-)	2017	2039
MECP2	CATCATACT CGG	47,37	chrX	(+)	154032220	154032242	exon3, exon4	NM_004992, (-)	1986	2008
MEN1	AGAGGGCG AGG	57,89	chr11	(+)	64809842	64809864	exon3, exon2	NM_130804, (-)	6329	6351
MEN1	AGAAGGTCT TGG	47,37	chr11	(-)	64809732	64809754	exon3, exon2	NM_130804, (-)	6219	6241
MEN1	GTCCCTCTAT GGG	52,63	chr11	(-)	64809779	64809801	exon3, exon2	NM_130804, (-)	6266	6288
MEN1	GTGAGCTCG AGG	63,16	chr11	(+)	64809925	64809947	exon3, exon2	NM_130804, (-)	6412	6434
MINA	GATGAAGTT GGG	42,11	chr3	(-)	97967509	97967531	exon2, exon2	NM_001042 (-)	25693	25715
MINA	CATAGTATG GGG	52,63	chr3	(+)	97967362	97967384	exon2, exon2	NM_001042 (-)	25546	25568
MINA	GGTCATCTC AGG	47,37	chr3	(+)	97967383	97967405	exon2, exon2	NM_001042 (-)	25567	25589
MINA	CTCTTCCATA CGG	47,37	chr3	(+)	97967299	97967321	exon2, exon2	NM_001042 (-)	25483	25505
MLLT10	AACGTTAGA GGG	47,37	chr10	(-)	21556731	21556753	exon4, exon4	NM_001195 (+)	22560	22582
MLLT10	GGCATTGTT TGG	47,37	chr10	(+)	21538841	21538863	exon3, exon2	NM_004641, (+)	4670	4692
MLLT10	TGCCCGTCG CGG	52,63	chr10	(-)	21534756	21534778	exon2, exon1	NM_004641, (+)	585	607
MLLT10	CGAGGTGCT AGG	52,63	chr10	(+)	21534680	21534702	exon2, exon1	NM_004641, (+)	509	531
MLLT6	CACGTTGGC CGG	52,63	chr17	(-)	38707796	38707818	exon4	NM_005937 (+)	2177	2199
MLLT6	CTGTTACAT AGG	52,63	chr17	(+)	38709175	38709197	exon5	NM_005937 (+)	3556	3578
MLLT6	TGGCATCGT CGG	57,89	chr17	(+)	38706957	38706979	exon2	NM_005937 (+)	1338	1360
MLLT6	CTGCGTATG GGG	57,89	chr17	(+)	38705656	38705678	exon1	NM_005937 (+)	37	59
MORF4L1	TTAGGCTTCC CGG	57,89	chr15	(-)	78873024	78873046	exon1, exon1	NM_006791, (+)	244	266
MORF4L1	TTTTCTCCG GGG	52,63	chr15	(-)	78891521	78891543	exon5, exon7	NM_001265 (+)	18741	18763
MORF4L1	CAAAGATTT TGG	42,11	chr15	(-)	78884981	78885003	exon4	NM_206839 (+)	12201	12223
MORF4L1	CTCTTCAGC AGG	47,37	chr15	(-)	78885027	78885049	exon4	NM_206839 (+)	12247	12269
MPHOSPH8	ATCTCGGAC GGG	52,63	chr13	(+)	19633938	19633960	exon1	NM_017520 (+)	291	313
MPHOSPH8	GATAATGAC AGG	57,89	chr13	(+)	19633857	19633879	exon1	NM_017520 (+)	210	232
MPHOSPH8	AAGTTCTTT TGG	31,58	chr13	(+)	19642119	19642141	exon2	NM_017520 (+)	8472	8494
MPHOSPH8	ACAGTCCTCC CGG	52,63	chr13	(-)	19642176	19642198	exon2	NM_017520 (+)	8529	8551
MSH6	GGAACTTC AGG	52,63	chr2	(+)	47791015	47791037	exon2	NM_000179 (+)	7934	7956
MSH6	GCATCAAAA AGG	47,37	chr2	(-)	47799139	47799161	exon4, exon3	NM_001281 (+)	16058	16080
MSH6	GGGTGGTTC AGG	52,63	chr2	(-)	47790985	47791007	exon2	NM_000179 (+)	7904	7926
MSH6	CGCCTAGAT AGG	52,63	chr2	(-)	47798680	47798702	exon2, exon4	NM_001281 (+)	15599	15621
MSL3	CTGTAATCT CGG	31,58	chrX	(-)	11760444	11760466	exon3, exon3	NM_078628, (+)	2286	2308
MSL3	TTTAAGACA AGG	42,11	chrX	(-)	11760874	11760896	exon4, exon4	NM_078628, (+)	2716	2738
MSL3	CATCTTTTC AGG	42,11	chrX	(-)	11760900	11760922	exon4, exon4	NM_078628, (+)	2742	2764
MSL3	CTGTGGCA TGG	42,11	chrX	(-)	11763907	11763929	exon8, exon7	NM_078628, (+)	5749	5771
MTA1	ATACCTGAT AGG	47,37	chr14	(+)	105438706	105438728	exon2, exon2	NM_004689, (+)	18858	18880
MTA1	AGTCTGCTA CGG	52,63	chr14	(+)	105449366	105449388	exon4, exon4	NM_004689, (+)	29518	29540

MTA1	TAAAGCACC/ CGG	57,89	chr14	(+)	105450112	105450134	exon5, exon5	NM_004689, (+)	30264	30286
MTA1	TCCGACCCCTC/ CGG	52,63	chr14	(-)	105420040	105420062	exon1, exon1	NM_004689, (+)	192	214
MTA2	TACTAGAAA/ CGG	47,37	chr11	(+)	62600196	62600218	exon3	NM_004739 (-)	6994	7016
MTA2	GTTCCCGGT/ TGG	57,89	chr11	(+)	62598568	62598590	exon4	NM_004739 (-)	5366	5388
MTA2	AGATATCTT/ TGG	42,11	chr11	(-)	62598335	62598357	exon5	NM_004739 (-)	5133	5155
MTA2	TCAATCCGT/ AGG	47,37	chr11	(+)	62600635	62600657	exon2	NM_004739 (-)	7433	7455
MTA3	GCAACCCAT/ AGG	42,11	chr2	(+)	42570464	42570486	exon2	NM_020744 (+)	1948	1970
MTA3	TGCGAGCAT/ TGG	42,11	chr2	(-)	42579165	42579187	exon3	NM_020744 (+)	10649	10671
MTA3	GGATCCAAA/ CGG	47,37	chr2	(+)	42656246	42656268	exon7, exon7	NM_001282 (+)	161678	161700
MTF2	ACAGCTTGG/ GGG	47,37	chr1	(-)	93110296	93110318	exon2, exon2	NM_001164 (+)	31062	31084
MTF2	TATGACCTG/ AGG	47,37	chr1	(-)	93115550	93115572	exon4, exon4	NM_001164 (+)	36316	36338
MTF2	GACGTAAAG/ TGG	52,63	chr1	(-)	93110260	93110282	exon2, exon2	NM_001164 (+)	31026	31048
MTF2	GCAGACATT/ TGG	42,11	chr1	(+)	93115523	93115545	exon4, exon4	NM_001164 (+)	36289	36311
MUM1	GCCGATGGC/ TGG	50	chr19	(+)	1356418	1356440	exon2	NM_032853 (+)	1442	1464
MUM1	GACGACACG/ GGG	55	chr19	(+)	1360630	1360652	exon5	NM_032853 (+)	5654	5676
MUM1	TGCAAAAGT/ GGG	45	chr19	(+)	1360435	1360457	exon5	NM_032853 (+)	5459	5481
MUM1	TTTTGTTGA/ GGG	45	chr19	(-)	1357016	1357038	exon3	NM_032853 (+)	2040	2062
NAP1L1	GGTCTGGTA/ AGG	47,37	chr12	(-)	76067383	76067405	exon4, exon4	NM_004537, (-)	18385	18407
NAP1L1	ACTCGTCTT/ AGG	42,11	chr12	(+)	76060253	76060275	exon5, exon5	NM_004537, (-)	11255	11277
NAP1L1	TCTGTGCAC/ AGG	36,84	chr12	(+)	76060215	76060237	exon5, exon5	NM_004537, (-)	11217	11239
NAP1L1	ACCATCAAG/ GGG	36,84	chr12	(+)	76067403	76067425	exon4, exon4	NM_004537, (-)	18405	18427
NAP1L2	ACGGTGAAC/ GGG	52,63	chrX	(-)	73214289	73214311	exon1	NM_021963 (-)	1989	2011
NAP1L2	CTTGGAGAC/ CGG	52,63	chrX	(-)	73214350	73214372	exon1	NM_021963 (-)	2050	2072
NAP1L2	GACCGTCCA/ CGG	47,37	chrX	(-)	73214215	73214237	exon1	NM_021963 (-)	1915	1937
NAP1L3	TAGCTCGAC/ GGG	42,11	chrX	(-)	93673214	93673236	exon1	NM_004538 (-)	2289	2311
NAP1L3	CGAGCTAGC/ CGG	57,89	chrX	(+)	93673230	93673252	exon1	NM_004538 (-)	2305	2327
NAP1L3	GCCGCTTGT/ AGG	42,11	chrX	(-)	93673068	93673090	exon1	NM_004538 (-)	2143	2165
NAP1L3	CACGAAATT/ GGG	42,11	chrX	(+)	93673014	93673036	exon1	NM_004538 (-)	2089	2111
NCOA1	GTATTGCAC/ CGG	50	chr2	(+)	24693273	24693295	exon8, exon8	NM_003743, (+)	108797	108819
NCOA1	TTTCGTGCT/ AGG	50	chr2	(-)	24691498	24691520	exon7, exon7	NM_003743, (+)	107022	107044
NCOA1	GTCTACAGC/ GGG	50	chr2	(+)	24683062	24683084	exon6, exon6	NM_003743, (+)	98586	98608
NCOA1	CTAACCCAG/ AGG	45	chr2	(+)	24658712	24658734	exon3, exon3	NM_003743, (+)	74236	74258
NCOA3	AAAGCCGAT/ AGG	36,84	chr20	(+)	47625413	47625435	exon5, exon5	NM_006534, (+)	123557	123579
NCOA3	CGTCTCGAT/ AGG	47,37	chr20	(-)	47627016	47627038	exon6, exon6	NM_006534, (+)	125160	125182
NCOA3	TTTCGTGAA/ TGG	47,37	chr20	(-)	47622275	47622297	exon3, exon3	NM_006534, (+)	120419	120441
NCOA3	CCATGTGAT/ AGG	52,63	chr20	(+)	47622308	47622330	exon3, exon3	NM_006534, (+)	120452	120474
NCOR1	CGGTGTTC/ AGG	57,89	chr17	(+)	16158794	16158816	exon5, exon5	NM_001190 (-)	128701	128723
NCOR1	GTATACTGG/ AGG	47,37	chr17	(+)	16194487	16194509	exon1, exon1	NM_001190 (-)	164394	164416
NCOR1	TGGTTGCCC/ AGG	52,63	chr17	(+)	16165105	16165127	exon4, exon2	NM_001190 (-)	135012	135034
NCOR1	GGAAGAGTT/ TGG	36,84	chr17	(-)	16165041	16165063	exon4, exon2	NM_001190 (-)	134948	134970
NCOR2	TGGTCACGG/ GGG	55	chr12	(+)	124426739	124426761	exon13, exor	NM_001206 (-)	102329	102351
NCOR2	GCTTATGGC/ AGG	60	chr12	(-)	124426686	124426708	exon13, exor	NM_001206 (-)	102276	102298
NSD1	ATGCAGTTA/ TGG	42,11	chr5	(+)	177135245	177135267	exon2	NM_022455 (+)	1414	1436
NSD1	TGTAGGACC/ AGG	57,89	chr5	(-)	177135447	177135469	exon2	NM_022455 (+)	1616	1638
NSD1	ACTGCGGAG/ TGG	52,63	chr5	(+)	177135316	177135338	exon2	NM_022455 (+)	1485	1507
NSD1	TGCATAGTA/ TGG	36,84	chr5	(-)	177135227	177135249	exon2	NM_022455 (+)	1396	1418
ORC1	GTGCAGTTT/ AGG	52,40	chr1	(+)	52402143	52402165	exon2, exon2	NM_001190 (-)	29315	29337
ORC1	GCCTGTAAC/ GGG	47,37	chr1	(-)	52397776	52397798	exon4, exon4	NM_001190 (-)	24948	24970
ORC1	CGAGCACGT/ AGG	52,63	chr1	(+)	52397833	52397855	exon4, exon4	NM_001190 (-)	25005	25027
ORC1	ACCGAGATT/ TGG	47,37	chr1	(-)	52401436	52401458	exon3, exon3	NM_001190 (-)	28608	28630
PADI1	CAGTGAGGT/ CGG	52,63	chr1	(-)	17223665	17223687	exon3	NM_013358 (+)	18540	18562
PADI1	CATCAGTGT/ CGG	57,89	chr1	(-)	17222395	17222417	exon2	NM_013358 (+)	17270	17292
PADI1	TGCAGACAT/ TGG	47,37	chr1	(+)	17222416	17222438	exon2	NM_013358 (+)	17291	17313
PADI1	ATTTCCCTT/ AGG	42,11	chr1	(+)	17224369	17224391	exon4	NM_013358 (+)	19244	19266
PADI2	GTAGACATC/ AGG	57,89	chr1	(+)	17119282	17119304	exon1	NM_007365 (-)	52522	52544
PADI2	AACCTTCAG/ CGG	52,63	chr1	(-)	17105018	17105040	exon2	NM_007365 (-)	38258	38280
PADI3	GATTGCGAC/ GGG	52,63	chr1	(+)	17265670	17265692	exon4	NM_016233 (+)	16573	16595
PADI3	CGCGACTTT/ TGG	52,63	chr1	(+)	17259698	17259720	exon2	NM_016233 (+)	10601	10623
PADI3	GAGATGTAC/ AGG	52,63	chr1	(-)	17259621	17259643	exon2	NM_016233 (+)	10524	10546
PADI3	GCTGTGTTT/ TGG	52,63	chr1	(-)	17259733	17259755	exon2	NM_016233 (+)	10636	10658
PADI4	GTTGGTCGTG/ CGG	57,89	chr1	(+)	17331018	17331040	exon2	NM_012387 (+)	22824	22846
PADI4	GCCTTGACT/ GGG	52,63	chr1	(-)	17333964	17333986	exon3	NM_012387 (+)	25770	25792
PADI4	AGCTCTACT/ GGG	52,63	chr1	(+)	17333984	17334006	exon3	NM_012387 (+)	25790	25812
PADI4	GGTGACCTT/ TGG	52,63	chr1	(+)	17331101	17331123	exon2	NM_012387 (+)	22907	22929
PADI6	ATCTTCACTG/ GGG	52,63	chr1	(-)	17373177	17373199	exon2	NM_207421 (+)	982	1004
PADI6	CTTGATCGA/ CGG	52,63	chr1	(+)	17373107	17373129	exon2	NM_207421 (+)	912	934
PADI6	GATGATACT/ TGG	47,37	chr1	(-)	17372268	17372290	exon1	NM_207421 (+)	73	95
PADI6	GTGAAGCAC/ GGG	52,63	chr1	(-)	17373063	17373085	exon2	NM_207421 (+)	868	890
PAF1	GGTGATGAA/ AGG	57,89	chr19	(+)	39390089	39390111	exon2, exon3	NM_001256 (-)	4460	4482
PAF1	TGAGATGCA/ AGG	57,89	chr19	(+)	39389673	39389695	exon3, exon4	NM_001256 (-)	4044	4066
PAF1	TACTCTGTCT/ TGG	47,37	chr19	(+)	39389336	39389358	exon5, exon6	NM_001256 (-)	3707	3729
PAF1	GGCTATTGC/ CGG	47,37	chr19	(+)	39390124	39390146	exon2, exon3	NM_001256 (-)	4495	4517
PARP1	AAGTACGTG/ TGG	52,63	chr1	(-)	226392213	226392235	exon3	NM_001618 (-)	31523	31545
PARP1	ACCTGACG/ GGG	57,89	chr1	(-)	226402281	226402303	exon2	NM_001618 (-)	41591	41613
PARP1	GGGACTTTT/ GGG	42,11	chr1	(+)	226402354	226402376	exon2	NM_001618 (-)	41664	41686
PARP1	GCACGTACT/ TGG	52,63	chr1	(+)	226392226	226392248	exon3	NM_001618 (-)	31536	31558
PARP2	TCTACGAGT/ GGG	42,11	chr14	(-)	20344986	20345008	exon2, exon2	NM_005484, (+)	1373	1395
PARP2	CCAGAGTGT/ GGG	57,89	chr14	(+)	20345438	20345460	exon3, exon3	NM_005484, (+)	1825	1847
PARP2	GTAAAGGCG/ TGG	47,37	chr14	(+)	20345413	20345435	exon3, exon3	NM_005484, (+)	1800	1822
PARP2	GGAGTCGA/ TGG	47,37	chr14	(+)	20345020	20345042	exon2, exon2	NM_005484, (+)	1407	1429
PAXIP1	GAGGTCAAC/ GGG	52,63	chr7	(-)	155002865	155002887	exon1	NM_007349 (-)	59176	59198
PAXIP1	GGGCTTTGG/ GGG	47,37	chr7	(-)	154983282	154983304	exon5	NM_007349 (-)	39593	39615
PAXIP1	ACGGACAGA/ AGG	52,63	chr7	(+)	154993747	154993769	exon3	NM_007349 (-)	50058	50080
PAXIP1	GTGATTCTG/ TGG	47,37	chr7	(-)	154993738	154993760	exon3	NM_007349 (-)	50049	50071
PBRM1	TAATACCATC/ AGG	36,84	chr3	(-)	52678552	52678574	exon3	NM_018313 (-)	133201	133223
PBRM1	GGCCTGGTG/ TGG	57,89	chr3	(+)	52679621	52679643	exon2	NM_018313 (-)	134270	134292
PBRM1	GGATGGTA/ TGG	36,84	chr3	(+)	52678564	52678586	exon3	NM_018313 (-)	133213	133235

PBRM1	CACCAGGCC AGG	63,16	chr3	(-)	52679607	52679629	exon2	NM_018313	(-)	134256	134278
PCGF1	CGATGACCC AGG	57,89	chr2	(+)	74506771	74506793	exon3	NM_032673	(-)	1729	1751
PCGF1	TTGCGATCG CGG	57,89	chr2	(-)	74507621	74507643	exon1	NM_032673	(-)	2579	2601
PCGF1	GCAGGACAT TGG	47,37	chr2	(-)	74506750	74506772	exon3	NM_032673	(-)	1708	1730
PCGF1	TGTACAAGA CGG	52,63	chr2	(-)	74507582	74507604	exon1	NM_032673	(-)	2540	2562
PCGF2	CATCGACGC TGG	57,89	chr17	(-)	38740306	38740328	exon3	NM_007144	(-)	6410	6432
PCGF2	ACGTGCAGG CGG	47,37	chr17	(-)	38739603	38739625	exon4	NM_007144	(-)	5707	5729
PCGF2	AACCTGCAT TGG	57,89	chr17	(-)	38739653	38739675	exon4	NM_007144	(-)	5757	5779
PCGF2	TTGTCTACA GGG	42,11	chr17	(-)	38739208	38739230	exon5	NM_007144	(-)	5312	5334
PCGF5	GATCAAGCC CGG	47,37	chr10	(+)	91222946	91222968	exon2, exon2	NM_001256	(+)	2345	2367
PCGF5	ATACCTTTA AGG	31,58	chr10	(-)	91222921	91222943	exon2, exon2	NM_001256	(+)	2320	2342
PCGF5	ATTATATTTA TGG	31,58	chr10	(+)	91248527	91248549	exon4, exon4	NM_001256	(+)	27926	27948
PCGF5	TGAACCTGG TGG	52,63	chr10	(-)	91240531	91240553	exon3, exon3	NM_001256	(+)	19930	19952
PCGF6	CACCTCTCG GGG	55	chr10	(-)	103350738	103350760	exon1, exon1	NM_032154	(-)	47943	47965
PCGF6	ACATGAGTC AGG	45	chr10	(-)	103350746	103350768	exon1, exon1	NM_032154	(-)	47951	47973
PCGF6	GAGTCACTT TGG	55	chr10	(-)	103350742	103350764	exon1, exon1	NM_032154	(-)	47947	47969
PCMT1	GATTGTGGA TGG	47,37	chr6	(-)	149749928	149749950	exon1, exon1	NM_005389	(+)	234	256
PCMT1	TCGCTAAGC AGG	57,89	chr6	(-)	149749880	149749902	exon1, exon1	NM_005389	(+)	186	208
PCMT1	TACATTTTGC CGG	36,84	chr6	(-)	149771214	149771236	exon2, exon2	NM_005389	(+)	21520	21542
PHC1	CAATGGGAC GGG	47,37	chr12	(+)	8917713	8917735	exon2	NM_004426	(+)	2994	3016
PHC1	AAGTGACAT GGG	36,84	chr12	(-)	8917748	8917770	exon2	NM_004426	(+)	3029	3051
PHC1	TAGCACAGA TGG	47,37	chr12	(-)	8921671	8921693	exon5	NM_004426	(+)	6952	6974
PHC1	CACAATTGCI AGG	57,89	chr12	(+)	8920987	8921009	exon4	NM_004426	(+)	6268	6290
PHC2	ACTTATAGG CGG	42,11	chr1	(+)	33331391	33331413	exon11, exor	NM_198040	(-)	7769	7791
PHC2	ACCCCTCGAT AGG	47,37	chr1	(+)	33334122	33334144	exon9, exon2	NM_198040	(-)	10500	10522
PHC2	CGAAGGGTT AGG	52,63	chr1	(-)	33334107	33334129	exon9, exon2	NM_198040	(-)	10485	10507
PHC2	AGCTCACACI GGG	42,11	chr1	(+)	33331420	33331442	exon11, exor	NM_198040	(-)	7798	7820
PHC3	AGACCATTCT AGG	47,37	chr3	(-)	170171410	170171432	exon4, exon4	NM_024947	(-)	83831	83853
PHC3	ATGGATACTI GGG	42,11	chr3	(-)	170178894	170178916	exon2, exon2	NM_024947	(-)	91315	91337
PHC3	TAAGGACCA TGG	42,11	chr3	(-)	170178913	170178935	exon2	NM_024947	(-)	91334	91356
PHC3	CAGCATCAAI GGG	47,37	chr3	(+)	170172623	170172645	exon3, exon3	NM_024947	(-)	85044	85066
PHF1	ACTGCGAAT TGG	42,11	chr6	(-)	33412537	33412559	exon3, exon3	NM_024165	(+)	1542	1564
PHF1	GTCAAGATG TGG	57,89	chr6	(+)	33412364	33412386	exon2, exon2	NM_024165	(+)	1369	1391
PHF1	ACTGATGGG GGG	47,37	chr6	(+)	33412387	33412409	exon2, exon2	NM_024165	(+)	1392	1414
PHF1	TGCTCTGGT TGG	52,63	chr6	(+)	33412729	33412751	exon4, exon4	NM_024165	(+)	1734	1756
PHF10	GCGACGAGI AGG	52,63	chr6	(-)	169717877	169717899	exon4, exon4	NM_018288	(-)	13972	13994
PHF10	CCCATTCCGC TGG	57,89	chr6	(+)	169721053	169721075	exon2, exon2	NM_018288	(-)	17148	17170
PHF10	TAATGACAT AGG	31,58	chr6	(+)	169717844	169717866	exon4, exon4	NM_018288	(-)	13939	13961
PHF10	TGGGTGTGA AGG	47,37	chr6	(-)	169718798	169718820	exon3, exon3	NM_018288	(-)	14893	14915
PHF11	TCATAAAAG TGG	47,37	chr13	(+)	49518032	49518054	exon4, exon4	NM_001040	(+)	20977	20999
PHF11	TTCAGGACT AGG	42,11	chr13	(+)	49513067	49513089	exon3, exon3	NM_001040	(+)	16012	16034
PHF11	CATTATATTC GGG	26,32	chr13	(-)	49506684	49506706	exon2, exon2	NM_001040	(+)	9629	9651
PHF11	TCTCTGATTC AGG	36,84	chr13	(-)	49506708	49506730	exon2, exon2	NM_001040	(+)	9653	9675
PHF12	GGGTACGAC AGG	47,37	chr12	(-)	28950908	28950930	exon1, exon1	NM_020889	(-)	45656	45678
PHF12	AATGGACTG TGG	42,11	chr17	(-)	28924247	28924269	exon4, exon4	NM_020889	(-)	18995	19017
PHF12	CGGTGACAC AGG	57,89	chr17	(+)	28927010	28927032	exon3, exon3	NM_020889	(-)	21758	21780
PHF12	CAAGTCGTA TGG	52,63	chr17	(+)	28950919	28950941	exon1, exon1	NM_020889	(-)	45667	45689
PHF13	TTGGCTCGC AGG	57,89	chr1	(-)	6619944	6619966	exon3	NM_153812	(+)	6249	6271
PHF13	TACCATTGA(GGG	57,89	chr1	(+)	6619850	6619872	exon3	NM_153812	(+)	6155	6177
PHF13	TGGCTACAT AGG	52,63	chr1	(+)	6616834	6616856	exon2	NM_153812	(+)	3139	3161
PHF13	TACCAGCAG GGG	52,63	chr1	(-)	6619829	6619851	exon3	NM_153812	(+)	6134	6156
PHF14	TCCAGCAGA AGG	55	chr7	(-)	10974867	10974889	exon2	NM_014660	(+)	996	1018
PHF14	CCGTTTGGC TGG	60	chr7	(+)	10974866	10974888	exon2	NM_014660	(+)	995	1017
PHF14	TGGATCGCA AGG	60	chr7	(+)	10974835	10974857	exon2	NM_014660	(+)	964	986
PHF14	GAGGAGGC TGG	60	chr7	(+)	10974851	10974873	exon2	NM_014660	(+)	980	1002
PHF19	TTGATGCC(NGG	45			0		Not available			0	0
PHF19	GTTGTTCTC NGG	50			0		Not available			0	0
PHF19	TCCACCGGC NGG	60			0		Not available			0	0
PHF2	TGAAGCGC(GGG	52,63	chr9	(-)	93576809	93576831	exon1	NM_005392	(+)	183	205
PHF2	AAGCGGACC CGG	57,89	chr9	(+)	93636419	93636441	exon3	NM_005392	(+)	59793	59815
PHF2	GACGTCAAG TGG	63,16	chr9	(+)	93636458	93636480	exon3	NM_005392	(+)	59832	59854
PHF2	TGAGTGAC CGG	57,89	chr9	(-)	93645647	93645669	exon4	NM_005392	(+)	69021	69043
PHF20	AAGCATCCA AGG	47,37	chr20	(+)	35801529	35801551	exon2	NM_016436	(+)	29529	29551
PHF20	GAAGACATT AGG	47,37	chr20	(+)	35842589	35842611	exon3	NM_016436	(+)	70589	70611
PHF20	GGAACCATC TGG	42,11	chr20	(+)	35842638	35842660	exon3	NM_016436	(+)	70638	70660
PHF20	TTCTCTAAAC AGG	36,84	chr20	(-)	35842676	35842698	exon3	NM_016436	(+)	70676	70698
PHF20L1	GTGATTCCA(GGG	52,63	chr8	(-)	132777841	132777863	exon2, exon2	NM_001277	(+)	2484	2506
PHF20L1	GGAGTCATC TGG	42,11	chr8	(+)	132794475	132794497	exon3, exon3	NM_001277	(+)	19118	19140
PHF20L1	CTTAGTGCT(GGG	47,37	chr8	(-)	132794525	132794547	exon3, exon3	NM_001277	(+)	19168	19190
PHF20L1	GATGACTCC TGG	52,63	chr8	(-)	132794461	132794483	exon3, exon3	NM_001277	(+)	19104	19126
PHF21A	ACTGGTTGC AGG	42,11	chr11	(-)	46079142	46079164	exon4, exon4	NM_001101	(-)	149824	149846
PHF21A	GGCTGTATT CGG	42,11	chr11	(+)	45979893	45979915	exon6, exon6	NM_001101	(-)	50575	50597
PHF21A	GGAGTTGCA AGG	52,63	chr11	(-)	46084195	46084217	exon3, exon3	NM_001101	(-)	154877	154899
PHF21A	CTCACTCAA TGG	42,11	chr11	(+)	46076760	46076782	exon5, exon5	NM_001101	(-)	147442	147464
PHF21B	ATCGCCTCA AGG	57,89	chr22	(-)	44896058	44896080	exon6, exon7	NM_001242	(-)	14896	14918
PHF21B	GATCACTGC CGG	57,89	chr22	(-)	44920457	44920479	exon3, exon4	NM_001242	(-)	39295	39317
PHF21B	CGGTGGCCT GGG	57,89	chr22	(+)	44916537	44916559	exon4, exon5	NM_001242	(-)	35375	35397
PHF21B	TCAAGAAGC AGG	52,63	chr22	(-)	45008578	45008600	exon2, exon3	NM_001242	(-)	127416	127438
PHF23	GAAACGGCC AGG	47,37	chr17	(-)	7237447	7237469	exon3, exon3	NM_024297	(-)	2420	2442
PHF23	GACCGAAAG GGG	47,37	chr17	(-)	7236361	7236383	exon4, exon4	NM_024297	(-)	1334	1356
PHF23	TTTCGTTCT AGG	47,37	chr17	(+)	7236376	7236398	exon4, exon4	NM_024297	(-)	1349	1371
PHF23	CAAGCAAGG GGG	52,63	chr17	(+)	7236542	7236564	exon4, exon4	NM_024297	(-)	1515	1537
PHF3	TGGTGCTGC TGG	52,63	chr6	(-)	63684162	63684184	exon3, exon5	NM_015153	(+)	47682	47704
PHF3	AGCGATAAG AGG	47,37	chr6	(+)	63646699	63646721	exon1, exon2	NM_015153	(+)	10219	10241
PHF3	CCAGGTTGG AGG	47,37	chr6	(-)	63646608	63646630	exon1, exon2	NM_015153	(+)	10128	10150
PHF5A	TGCAGCAGA GGG	52,63	chr22	(+)	41460355	41460377				0	0
PHF5A	CATATGCGC GGG	57,89	chr22	(+)	41467554	41467576	exon3	NM_032758	(-)	7838	7860

PHF5A	GTAACATATG GGG	36,84	chr22	(-)	41467523	41467545	exon3	NM_032758	(-)	7807	7829
PHF5A	CTCCCCAGAT TGG	47,37	chr22	(+)	41460453	41460475	exon4	NM_032758	(-)	737	759
PHF6	ATACGAGAG AGG	42,11	chrX	(+)	134393603	134393625	exon4, exon4	NM_032458, (+)		20292	20314
PHF6	CCTACAAGAI TGG	47,37	chrX	(+)	134377648	134377670	exon2, exon2	NM_032458, (+)		4337	4359
PHF6	TATGGTGCG TGG	57,89	chrX	(-)	134377725	134377747	exon2, exon2	NM_032458, (+)		4414	4436
PHF7	TATCTAGTA/ AGG	42,11	chr3	(+)	52419837	52419859	exon4, exon5	NM_001278: (+)		9277	9299
PHF7	TGGCTATGCG TGG	52,63	chr3	(+)	52414501	52414523	exon3, exon4	NM_001278: (+)		3941	3963
PHF7	AGACTAGGA AGG	52,63	chr3	(+)	52414007	52414029	exon2, exon3	NM_001278: (+)		3447	3469
PHF7	TGGGGATCC GGG	42,11	chr3	(+)	52414521	52414543	exon3, exon4	NM_001278: (+)		3961	3983
PHF8	CACGGTCAG TGG	47,37	chrX	(+)	54017776	54017798	exon5, exon5	NM_001184: (-)		81097	81119
PHF8	CAGGTTCGT GGG	52,63	chrX	(+)	54042762	54042784	exon2	NM_001184: (-)		106083	106105
PHF8	AAAACGCCG AGG	47,37	chrX	(-)	54022341	54022363	exon4, exon4	NM_001184: (-)		85662	85684
PHF8	GGAGCTCTC GGG	57,89	chrX	(+)	54022278	54022300	exon4, exon4	NM_001184: (-)		85599	85621
PHIP	TGCAAGCAI AGG	47,37	chr6	(-)	79060552	79060574	exon6	NM_017934	(-)	126134	126156
PHIP	CTGCAAATA AGG	42,11	chr6	(-)	79060760	79060782	exon5	NM_017934	(-)	126342	126364
PHIP	ATCGCCCG TGG	63,16	chr6	(-)	79077877	79077899	exon2	NM_017934	(-)	143459	143481
PHIP	CATATTTGCA AGG	36,84	chr6	(+)	79060772	79060794	exon5	NM_017934	(-)	126354	126376
PHRF1	TCCGAGGAT CGG	52,63	chr11	(+)	587261	587283	exon4, exon4	NM_001286: (+)		10816	10838
PHRF1	TCTCAACGC AGG	47,37	chr11	(+)	587377	587399	exon4, exon4	NM_001286: (+)		10932	10954
PHRF1	AAGTAATGG CGG	42,11	chr11	(-)	587411	587433	exon4, exon4	NM_001286: (+)		10966	10988
PHRF1	GACGACAGT TGG	63,16	chr11	(+)	581997	582019	exon3, exon3	NM_001286: (+)		5552	5574
POLE3	TCAATGGGG TGG	55	chr9	(+)	113409625	113409647	[exon4, exor	[NM_017443	(-)	2387	2409
POLE3	GATCACCAG AGG	50	chr9	(-)	113410230	113410252	[exon2, exor	[NM_017443	(-)	2992	3014
POLE3	GATCCTGGT TGG	55	chr9	(+)	113410240	113410262	[exon2, exor	[NM_017443	(-)	3002	3024
POLE3	CGGTGTCAG AGG	55	chr9	(-)	113410110	113410132	[exon3, exor	[NM_017443	(-)	2872	2894
POLR2B	CGCTCTCTC AGG	52,63	chr4	(+)	56990838	56990860	exon3, exon4	NM_000938, (+)		12199	12221
POLR2B	TGCTTCTGC GGG	47,37	chr4	(-)	56986387	56986409	exon2, exon3	NM_000938, (+)		7748	7770
POLR2B	CAAGCCTTT AGG	42,11	chr4	(-)	56990750	56990772	exon3, exon4	NM_000938, (+)		12111	12133
POLR2B	ATCTTCCAA TGG	47,37	chr4	(+)	56994435	56994457	exon4, exon3	NM_000938, (+)		15796	15818
PPARGC1A	ATCTGTCAG AGG	42,11	chr4	(+)	23831644	23831666	exon3	NM_013261	(-)	39624	39646
PPARGC1A	TGAAGTACA TGG	42,11	chr4	(-)	23884847	23884869	exon2	NM_013261	(-)	92827	92849
PPARGC1A	GCAATCCGT GGG	52,63	chr4	(+)	23831667	23831689	exon3	NM_013261	(-)	39647	39669
PPARGC1A	GCTTCTCGG TGG	52,63	chr4	(-)	23884815	23884837	exon2	NM_013261	(-)	92795	92817
PRDM1	ATTGTGAGC AGG	52,63	chr6	(-)	106099519	106099541	exon2, exon4	NM_182907, (+)		13200	13222
PRDM1	AACCTGGCT CGG	57,89	chr6	(+)	106099402	106099424	exon2, exon4	NM_182907, (+)		13083	13105
PRDM1	CATTAAAGC TGG	36,84	chr6	(-)	106099323	106099345	exon2, exon4	NM_182907, (+)		13004	13026
PRDM1	AATACCACA TGG	36,84	chr6	(-)	106099467	106099489	exon2, exon4	NM_182907, (+)		13148	13170
PRDM10	GGACCCATC TGG	57,89	chr11	(+)	129947314	129947336	exon1, exon5	NM_199438, (-)		47609	47631
PRDM10	GCCTCAGTG CGG	57,89	chr11	(-)	129944964	129944986	exon2, exon6	NM_199438, (-)		45259	45281
PRDM10	CTGTCTATG GGG	47,37	chr11	(+)	129944886	129944908	exon2, exon6	NM_199438, (-)		45181	45203
PRDM10	TGTAGATGG TGG	57,89	chr11	(-)	129947304	129947326	exon1, exon5	NM_199438, (-)		47599	47621
PRDM11	GGAAGCTTT AGG	52,63	chr11	(-)	45182309	45182331	exon3, exon3	NM_001256: (+)		34967	34989
PRDM11	ATTTCATCAC TGG	42,11	chr11	(-)	45182874	45182896	exon4, exon4	NM_001256: (+)		35532	35554
PRDM11	GAGGTGGT TGG	52,63	chr11	(+)	45182989	45183011	exon4, exon4	NM_001256: (+)		35647	35669
PRDM11	CCATACTCT TGG	57,89	chr11	(-)	45181854	45181876	exon2, exon2	NM_001256: (+)		34512	34534
PRDM12	TCCCGCCTTG TGG	63,16	chr9	(-)	130666695	130666717	exon2	NM_021619	(+)	2102	2124
PRDM12	GATGTCGGA CGG	52,63	chr9	(-)	130664727	130664749	exon1	NM_021619	(+)	134	156
PRDM12	ATCAAGGCG GGG	57,89	chr9	(+)	130666706	130666728	exon2	NM_021619	(+)	2113	2135
PRDM12	ACGTCTTGG AGG	52,63	chr9	(-)	130666681	130666703	exon2	NM_021619	(+)	2088	2110
PRDM13	GCTATTGCA AGG	52,63	chr6	(+)	99608846	99608868	exon2	NM_021620	(+)	2073	2095
PRDM13	GATGTCGAA AGG	57,89	chr6	(-)	99609251	99609273	exon3	NM_021620	(+)	2478	2500
PRDM13	CAAGTACCT GGG	57,89	chr6	(+)	99607136	99607158	exon1	NM_021620	(+)	363	385
PRDM13	TGGAGTGG/ CGG	42,11	chr6	(+)	99608790	99608812	exon2	NM_021620	(+)	2017	2039
PRDM14	ACGTGGGG/ CGG	57,89	chr8	(+)	70069541	70069563	exon2	NM_024504	(-)	17891	17913
PRDM14	TACCAGGGC AGG	52,63	chr8	(+)	70069577	70069599	exon2	NM_024504	(-)	17927	17949
PRDM14	AGGTTGGAA CGG	52,63	chr8	(+)	70069705	70069727	exon2	NM_024504	(-)	18055	18077
PRDM15	GTTTGTACT CGG	50	chr21	(+)	41879053	41879075	exon2	NM_022115	(-)	78060	78082
PRDM15	TTTGTATAC CGG	50	chr21	(-)	41879079	41879101	exon2	NM_022115	(-)	78086	78108
PRDM15	TGGCGATCG CGG	55	chr21	(-)	41879049	41879071	exon2	NM_022115	(-)	78056	78078
PRDM15	CGAATGTAA CGG	35	chr21	(+)	41879089	41879111	exon2	NM_022115	(-)	78096	78118
PRDM16	ATGTAGACA CGG	57,89	chr1	(-)	3186286	3186308	exon2, exon2	NM_022114, (+)		117109	117131
PRDM16	AGCTCGAAG CGG	57,89	chr1	(-)	3186322	3186344	exon2, exon2	NM_022114, (+)		117145	117167
PRDM16	GGGCGAAAC CGG	57,89	chr1	(+)	3186445	3186467	exon2, exon2	NM_022114, (+)		117268	117290
PRDM16	TAATATGTA GGG	36,84	chr1	(+)	3186144	3186166	exon2, exon2	NM_022114, (+)		116967	116989
PRDM2	GCCGCTTCT TGG	57,89	chr1	(-)	13778549	13778571	exon8, exon3	NM_012231, (+)		73695	73717
PRDM2	ATGATGAGT GGG	42,11	chr1	(+)	13778652	13778674	exon8, exon3	NM_012231, (+)		73798	73820
PRDM2	ATTAGAAGC AGG	47,37	chr1	(+)	13778560	13778582	exon8, exon3	NM_012231, (+)		73706	73728
PRDM2	GGCTTCTCT AGG	47,37	chr1	(-)	13778420	13778442	exon8, exon3	NM_012231, (+)		73566	73588
PRDM4	TAATGCTAC GGG	36,84	chr12	(-)	107754024	107754046	exon4	NM_012406	(-)	21159	21181
PRDM4	TTAGGGTGC AGG	47,37	chr12	(+)	107752158	107752180	exon5	NM_012406	(-)	19293	19315
PRDM4	GGTTTGGAA AGG	52,63	chr12	(+)	107754086	107754108	exon4	NM_012406	(-)	21221	21243
PRDM4	AATAACTGC GGG	47,37	chr12	(+)	107753942	107753964	exon4	NM_012406	(-)	21077	21099
PRDM5	TTTTGGATG CGG	47,37	chr4	(-)	120853487	120853509	exon3, exon3	NM_018699, (-)		161575	161597
PRDM5	CTGGCTTCG AGG	52,63	chr4	(-)	120853456	120853478	exon3, exon3	NM_018699, (-)		161544	161566
PRDM5	GAAAGATTG TGG	47,37	chr4	(-)	120907532	120907554	exon2, exon2	NM_018699, (-)		215620	215642
PRDM5	GACTTCAGG CGG	52,63	chr4	(+)	120922568	120922590	exon1, exon1	NM_018699, (-)		230656	230678
PRDM6	GGTAGGCTC AGG	60	chr5	(-)	123090050	123090072	exon2	NM_001136: (+)		905	927
PRDM6	GGCTGGGTC AGG	60	chr5	(-)	123090046	123090068	exon2	NM_001136: (+)		901	923
PRDM6	CAGCAACTC AGG	60	chr5	(+)	123090084	123090106	exon2	NM_001136: (+)		939	961
PRDM7	TTCTGTAAT AGG	47,37	chr16	(+)	90061957	90061979	exon7	NM_001098: (-)		5392	5414
PRDM7	CCTAGGTGT CGG	47,37	chr16	(+)	90074923	90074945	exon3	NM_001098: (-)		18358	18380
PRDM7	TAGCCAGGA TGG	47,37	chr16	(+)	90061921	90061943	exon7	NM_001098: (-)		5378	5380
PRDM7	TCTCCTCTGA AGG	57,89	chr16	(+)	90066880	90066902	exon4	NM_001098: (-)		10315	10337
PRDM8	AACTAGTAA TGG	42,11	chr4	(-)	80201432	80201454	exon9, exon3	NM_020226, (+)		3930	3952
PRDM8	GGTCCAATC AGG	57,89	chr4	(+)	80201343	80201365	exon9, exon3	NM_020226, (+)		3841	3863
PRDM8	GAACAGTAC CGG	36,84	chr4	(+)	80200277	80200299	exon8, exon2	NM_020226, (+)		2775	2797
PRDM8	GTCGCAGGT TGG	57,89	chr4	(-)	80200160	80200182	exon8, exon2	NM_020226, (+)		2658	2680

PRDM9	CTCGCTATAC AGG	40	chr5	(+)	23509546	23509568	exon3, exon3	NM_020227, (+)	1892	1914
PRDM9	ACTCTTAAGC AGG	50	chr5	(-)	23517886	23517908	exon5, exon5	NM_020227, (+)	10232	10254
PRDM9	TCCACTCTTA AGG	50	chr5	(-)	23517889	23517911	exon5, exon5	NM_020227, (+)	10235	10257
PRKAA1	CGGCACCTTC AGG	63,16	chr5	(-)	40798063	40798085	exon1, exon1	NM_206907, (-)	38685	38707
PRKAA1	ATTCGGAGC AGG	52,63	chr5	(-)	40777505	40777527	exon2, exon2	NM_206907, (-)	18127	18149
PRKAA1	TACATTCTGC GGG	52,63	chr5	(-)	40798089	40798111	exon1, exon1	NM_206907, (-)	38711	38733
PRKAA1	CCCGTCGTG CGG	57,89	chr5	(+)	40798130	40798152	exon1, exon1	NM_206907, (-)	38752	38774
PRKAA2	AAGATCGGA GGG	52,63	chr1	(+)	56645421	56645443	exon1	NM_006252, (+)	105	127
PRKAA2	ACTACATCTC CGG	42,11	chr1	(+)	56691465	56691487	exon3	NM_006252, (+)	46149	46171
PRKAA2	AATCTGCTG TGG	52,63	chr1	(-)	56692374	56692396	exon4	NM_006252, (+)	47058	47080
PRKAA2	GTAATCGGA AGG	36,84	chr1	(+)	56691431	56691453	exon3	NM_006252, (+)	46115	46137
PRKCD	TCGAACGTC AGG	52,63	chr3	(-)	53179618	53179640	exon4, exon4	NM_006254, (+)	18412	18434
PRKCD	GTTCGATGO AGG	47,37	chr3	(+)	53179635	53179657	exon4, exon4	NM_006254, (+)	18429	18451
PRKCD	ATTGTTCTTC CGG	47,37	chr3	(-)	53179736	53179758	exon4, exon4	NM_006254, (+)	18530	18552
PRKCD	TTGAAGGCG CGG	57,89	chr3	(-)	53178429	53178451	exon3, exon3	NM_006254, (+)	17223	17245
PRMT1	ACATGGAGT AGG	47,37	chr19	(-)	49681936	49681958	exon4, exon3	NM_001536, (+)	4785	4807
PRMT1	CAGGTGCCG TGG	52,63	chr19	(-)	49681953	49681975	exon4, exon3	NM_001536, (+)	4802	4824
PRMT1	CCGGCACCTC AGG	63,16	chr19	(+)	49681966	49681988	exon4, exon3	NM_001536, (+)	4815	4837
PRMT1	GATGTCATG GGG	52,63	chr19	(-)	49680520	49680542	exon3, exon2	NM_001536, (+)	3369	3391
PRMT2	ACATTCCGG GGG	47,37	chr21	(+)	46644394	46644416	exon5, exon4	NM_206962, (+)	8800	8822
PRMT2	GAAGAGTAC TGG	52,63	chr21	(+)	46644459	46644481	exon5, exon4	NM_206962, (+)	8865	8887
PRMT2	GGTATTTAG TGG	42,11	chr21	(-)	46648484	46648506	exon6, exon5	NM_206962, (+)	12890	12912
PRMT2	GACAAACCA TGG	47,37	chr21	(+)	46644343	46644365	exon5, exon4	NM_206962, (+)	8749	8771
PRMT3	ACTGTCTGCT TGG	57,89	chr11	(+)	20395909	20395931	exon6, exon5	NM_005788, (+)	8380	8402
PRMT3	GTACCCCTTC TGG	52,63	chr11	(+)	20395832	20395854	exon6, exon5	NM_005788, (+)	8303	8325
PRMT3	GTCACTACT CGG	36,84	chr11	(+)	20397625	20397647	exon7, exon6	NM_005788, (+)	10096	10118
PRMT3	TATGAGAAG CGG	42,11	chr11	(-)	20395823	20395845	exon6, exon5	NM_005788, (+)	8294	8316
PRMT5	CTTCCATCCG GGG	52,63	chr14	(-)	22928569	22928591	exon2, exon2	NM_001282, (-)	8059	8081
PRMT5	GAACCTGCT CGG	52,63	chr14	(-)	22928535	22928557	exon2, exon2	NM_001282, (-)	8025	8047
PRMT5	AGTTCATAG AGG	42,11	chr14	(+)	22924922	22924944	exon4, exon7	NM_001282, (-)	4412	4434
PRMT5	CTATTTCCGG AGG	47,37	chr14	(+)	22929283	22929305	exon1, exon1	NM_001282, (-)	8773	8795
PRMT6	CGAGTGCTA CGG	57,89	chr1	(+)	107056859	107056881	exon1	NM_018137, (+)	215	237
PRMT6	AGGCAAGAC TGG	57,89	chr1	(+)	107056961	107056983	exon1	NM_018137, (+)	317	339
PRMT6	AGTTCCGAA CGG	52,63	chr1	(-)	107056925	107056947	exon1	NM_018137, (+)	281	303
PRMT6	AGTAGCACT TGG	47,37	chr1	(-)	107056847	107056869	exon1	NM_018137, (+)	203	225
PRMT7	GTTTGACAC GGG	47,37	chr16	(+)	68337502	68337524	exon7, exon5	NM_019023, (+)	26389	26411
PRMT7	CTCGATGGC CGG	52,63	chr16	(-)	68324810	68324832	exon5, exon5	NM_019023, (+)	13697	13719
PRMT7	AGTGCCAAT AGG	52,63	chr16	(-)	68324747	68324769	exon5, exon5	NM_019023, (+)	13634	13656
PRMT7	CATTCCACCG AGG	57,89	chr16	(+)	68329147	68329169	exon6, exon4	NM_019023, (+)	18034	18056
PRMT8	GGATCCACG AGG	52,63	chr12	(-)	3576930	3576952	exon7, exon7	NM_001256, (+)	85733	85755
PRMT8	TAAATAGG TGG	47,37	chr12	(-)	3583141	3583163	exon8, exon8	NM_001256, (+)	91944	91966
PRMT8	AGTCGTTGC AGG	52,63	chr12	(-)	3583114	3583136	exon8, exon8	NM_001256, (+)	91917	91939
PRMT8	GTCGAAGTA AGG	36,84	chr12	(-)	3540742	3540764	exon2, exon2	NM_001256, (+)	49545	49567
PSIP1	GGTGGCTTT AGG	52,63	chr9	(+)	15506603	15506625	exon3, exon3	NM_033222, (-)	35960	35982
PSIP1	AGATGAAAC TGG	42,11	chr9	(-)	15510126	15510148	exon2, exon2	NM_033222, (-)	39483	39505
PSIP1	ATGACTCGC TGG	42,11	chr9	(-)	15510166	15510188	exon2, exon2	NM_033222, (-)	39523	39545
PSIP1	GCTGGCTTT CGG	47,37	chr9	(+)	15486833	15486855	exon5, exon5	NM_033222, (-)	16190	16212
PWWP2B	CTTCGAAGT GGG	52,63	chr10	(-)	132404845	132404867	exon2, exon2	NM_138499, (+)	7648	7670
PWWP2B	TCCCCTGTCA TGG	63,16	chr10	(+)	132404678	132404700	exon2, exon2	NM_138499, (+)	7481	7503
PWWP2B	TGACAGGGC TGG	57,89	chr10	(-)	132404665	132404687	exon2, exon2	NM_138499, (+)	7468	7490
PWWP2B	GATGCAGAC GGG	57,89	chr10	(+)	132404720	132404742	exon2, exon2	NM_138499, (+)	7523	7545
PYGO1	TGACGAAGC AGG	42,11	chr15	(+)	55547022	55547044	exon3	NM_015617, (-)	8136	8158
PYGO1	GGATAACCA TGG	52,63	chr15	(+)	55546996	55547018	exon3	NM_015617, (-)	8110	8132
PYGO1	TGGTCAGAG TGG	47,37	chr15	(+)	55547089	55547111	exon3	NM_015617, (-)	8203	8225
PYGO1	GATAGTGG AGG	52,63	chr15	(-)	55548968	55548990	exon2	NM_015617, (-)	10082	10104
PYGO2	GGTGATCCA GGG	57,89	chr1	(+)	154959786	154959808	exon3	NM_138300, (-)	2761	2783
PYGO2	GCTCCGAAG AGG	47,37	chr1	(+)	154959749	154959771	exon3	NM_138300, (-)	2724	2746
PYGO2	GTTCGAGCC TGG	63,16	chr1	(-)	154959713	154959735	exon3	NM_138300, (-)	2688	2710
RAG2	TCGCTGCAC TGG	36593781	chr11	(-)	36593781	36593803	exon3, exon3	NM_001243, (-)	1839	1861
RAG2	CCAGCCACTT AGG	52,63	chr11	(-)	36593924	36593946	exon3, exon3	NM_001243, (-)	1982	2004
RAG2	CATCAATAC AGG	36,84	chr11	(-)	36593882	36593904	exon3, exon3	NM_001243, (-)	1940	1962
RAG2	GGTTATGCT TGG	42,11	chr11	(+)	36594009	36594031	exon3, exon3	NM_001243, (-)	2067	2089
RAI1	TAGGCGTGA AGG	52,63	chr17	(-)	17793007	17793029	exon3	NM_030665, (+)	111535	111557
RAI1	CATCAGCCT AGG	42,11	chr17	(+)	17793019	17793041	exon3	NM_030665, (+)	111547	111569
RAI1	CTGCGGGTT TGG	47,37	chr17	(-)	17793088	17793110	exon3	NM_030665, (+)	111616	111638
RAI1	CCTTACCCGA TGG	57,89	chr17	(+)	17793111	17793133	exon3	NM_030665, (+)	111639	111661
RBBP4	CGCATGATA GGG	47,37	chr1	(-)	32668314	32668336	exon4, exon4	NM_005610, (+)	16957	16979
RBBP4	TTCTTCCACT AGG	57,89	chr1	(-)	32651917	32651939	exon2, exon2	NM_005610, (+)	770	792
RBBP4	GGAAAGAACC AGG	47,37	chr1	(+)	32651933	32651955	exon2, exon2	NM_005610, (+)	786	808
RBBP4	CAAACTGAG GGG	36,84	chr1	(-)	32657520	32657542	exon3, exon3	NM_005610, (+)	6163	6185
RBBP5	GTCAATTGA AGG	52,63	chr1	(-)	205101604	205101626	exon6, exon6	NM_005057, (-)	15463	15485
RBBP5	TGACTCCGA TGG	42,11	chr1	(-)	205103910	205103932	exon5, exon5	NM_005057, (-)	17769	17791
RBBP5	GGCATCTTT GGG	47,37	chr1	(-)	205103889	205103911	exon5, exon5	NM_005057, (-)	17748	17770
RBBP5	TTTCAGGCG AGG	52,63	chr1	(-)	205105078	205105100	exon4, exon4	NM_005057, (-)	18937	18959
RBBP7	TACACCGTT TGG	36,84	chrX	(-)	16869137	16869159	exon2, exon2	NM_001198, (-)	24486	24508
RBBP7	ACCCTTGTC GGG	47,37	chrX	(+)	16862956	16862978	exon3, exon3	NM_001198, (-)	18305	18327
RBBP7	GGCCAGATC TGG	57,89	chrX	(-)	16869093	16869115	exon2, exon2	NM_001198, (-)	24442	24464
RBBP7	GCCTTCATT GGG	57,89	chrX	(-)	16863059	16863081	exon3, exon3	NM_001198, (-)	18408	18430
RING1	TAAGATCTA AGG	47,37	chr6	(+)	33209999	33210021	exon4	NM_002931, (+)	1491	1513
RING1	ATTGTACAC CGG	52,63	chr6	(+)	33209764	33209786	exon3	NM_002931, (+)	1256	1278
RING1	GATAAGCAC GGG	47,37	chr6	(-)	33210031	33210053	exon4	NM_002931, (+)	1523	1545
RING1	CCACGTTTTG GGG	52,63	chr6	(-)	33208842	33208864	exon2	NM_002931, (+)	334	356
RNF17	GGTCTTCTT GGG	52,63	chr13	(+)	24764238	24764260	exon1, exon1	NM_001184, (+)	76	98
RNF17	CAACGCTAC TGG	52,63	chr13	(+)	24774837	24774859	exon3, exon3	NM_001184, (+)	10675	10697
RNF17	ACTGCTGAT TGG	42,11	chr13	(+)	24778326	24778348	exon4, exon4	NM_001184, (+)	14164	14186
RNF17	ACAATCAGG TGG	31,58	chr13	(-)	24767341	24767363	exon2, exon2	NM_001184, (+)	3179	3201
RNF2	ACTAGTTTTT AGG	42,11	chr1	(-)	185093074	185093096	exon4	NM_007212, (+)	47656	47678

RNF2	AATTCACGTG1AGG	36,84	chr1	(-)	185091615	185091637	exon3	NM_007212 (+)	46197	46219
RNF2	ATCATCACAT TGG	42,11	chr1	(+)	185091717	185091739	exon3	NM_007212 (+)	46299	46321
RNF2	GTCTGGGCTT TGG	47,37	chr1	(-)	185093099	185093121	exon4	NM_007212 (+)	47681	47703
RNF20	TCGGTTGAC AGG	36,84	chr9	(-)	101540336	101540358	exon3	NM_019592 (+)	6488	6510
RNF20	AAACGTTAT1 GGG	42,11	chr9	(+)	101540517	101540539	exon4	NM_019592 (+)	6669	6691
RNF20	GTTCGGTT1 AGG	52,63	chr9	(-)	101540570	101540592	exon4	NM_019592 (+)	6722	6744
RNF20	GTGGAAACA AGG	36,84	chr9	(+)	101535517	101535539	exon2	NM_019592 (+)	1669	1691
RNF217	ACCAGACGA GGG	52,63	chr6	(-)	125057950	125057972	exon5, exon3	NM_152553, (+)	95406	95428
RNF217	GGGCCAGCC GGG	57,89	chr6	(+)	125058051	125058073	exon5, exon3	NM_152553, (+)	95507	95529
RNF217	GCATGAAGC AGG	47,37	chr6	(+)	125057995	125058017	exon5, exon3	NM_152553, (+)	95451	95473
RNF217	GCTTGGTGC CGG	47,37	chr6	(-)	125045339	125045361	exon4, exon2	NM_152553, (+)	82795	82817
RNF40	ATCGAGCCC AGG	52,63	chr16	(+)	30762642	30762664	exon2, exon2	NM_001286, (+)	1031	1053
RNF40	GCGATTGAC TGG	52,63	chr16	(-)	30763251	30763273	exon3, exon3	NM_001286, (+)	1640	1662
RNF40	AGCACTCAG1 GGG	47,37	chr16	(-)	30762595	30762617	exon2, exon2	NM_001286, (+)	984	1006
RNF40	CCGAGAACG TGG	47,37	chr16	(+)	30763204	30763226	exon3, exon3	NM_001286, (+)	1593	1615
RPA3	TGTACACA1 TGG	52,63	chr7	(+)	7637901	7637923	exon7	NM_002947 (-)	1339	1361
RPA3	GATGAATTG CGG	42,11	chr7	(+)	7640356	7640378	exon5	NM_002947 (-)	3794	3816
RPA3	ACAAGCCTG1 GGG	52,63	chr7	(-)	7640332	7640354	exon5	NM_002947 (-)	3770	3792
RPA3	GATGGCTAT TGG	31,58	chr7	(+)	7637870	7637892	exon7	NM_002947 (-)	1308	1330
RPH3A	TGGACCGCC AGG	47,37	chr12	(+)	112865422	112865444	exon5, exon6	NM_014954, (+)	73679	73701
RPH3A	GTGAACCGC TGG	52,63	chr12	(+)	112865466	112865488	exon5, exon6	NM_014954, (+)	73723	73745
RPH3A	GTGGGATGT CGG	52,63	chr12	(+)	112828353	112828375	exon3, exon3	NM_014954, (+)	36610	36632
RPH3A	ACAGTCTCT1 AGG	42,11	chr12	(-)	112865515	112865537	exon5, exon6	NM_014954, (+)	73772	73794
RPS6KA5	GCGACTGCC NGG	55	chr14		90868121	91060648	Not available: NM_004755.2, NM_1823:		0	0
RPS6KA5	GCAAGTCGT1 NGG	60	chr14		90868121	91060648	Not available: NM_004755.2, NM_1823:		0	0
RPS6KA5	CATTAGGCA1 NGG	45	chr14		90868121	91060648	Not available: NM_004755.2, NM_1823:		0	0
RPS6KA5	AAGGACAG1 NGG	50	chr14		90868121	91060648	Not available: NM_004755.2, NM_1823:		0	0
RSF1	GGAGCAGAC1 TGG	63,16	chr11	(+)	77820631	77820653	exon1	NM_016578 (-)	154403	154425
RSF1	GTTTAAACG1 GGG	47,37	chr11	(-)	77747095	77747117	exon3	NM_016578 (-)	80867	80889
RSF1	AACTCAGGC CGG	52,63	chr11	(+)	77820590	77820612	exon1	NM_016578 (-)	154362	154384
RSF1	ATCTGTTACT GGG	42,11	chr11	(-)	77764615	77764637	exon2	NM_016578 (-)	98387	98409
RTF1	AGACGTCTC1 AGG	60	chr15	(-)	41438394	41438416	[exon2]	[NM_015138 (+)]	21291	21313
RTF1	GGACCACCA1 CGG	50	chr15	(+)	41417228	41417250	[exon1]	[NM_015138 (+)]	125	147
RTF1	CGTGATCGA AGG	60	chr15	(+)	41417262	41417284	[exon1]	[NM_015138 (+)]	159	181
RTF1	GGCAAAGCC AGG	60	chr15	(+)	41438341	41438363	[exon2]	[NM_015138 (+)]	21238	21260
SATB1	GCAATGCCA1 TGG	47,37	chr3	(+)	18416944	18416966	exon3, exon3	NM_002971, (-)	69304	69326
SATB1	GCCCATTGA1 AGG	42,11	chr3	(-)	18417013	18417035	exon3, exon3	NM_002971, (-)	69373	69395
SATB1	GGGAGTGCC CGG	47,37	chr3	(-)	18420787	18420809	exon2, exon2	NM_002971, (-)	73147	73169
SATB1	ATTTGAACG1 GGG	42,11	chr3	(-)	18420938	18420960	exon2, exon2	NM_002971, (-)	73298	73320
SCMH1	ATCTTGAAC1 AGG	42,11	chr1	(+)	41143081	41143103	exon6, exon6	NM_012236, (-)	115883	115905
SCMH1	TTACATCGC GGG	52,63	chr1	(+)	41075412	41075434	exon9, exon1	NM_012236, (-)	48214	48236
SCMH1	GGGTAAACC GGG	47,37	chr1	(-)	41075323	41075345	exon9, exon1	NM_012236, (-)	48125	48147
SCMH1	CTGTCTTGG1 GGG	47,37	chr1	(-)	41075354	41075376	exon9, exon1	NM_012236, (-)	48156	48178
SCML2	GCTACGGT1 TGG	36,84	chrX	(-)	18323987	18324009	exon5	NM_006089 (-)	84675	84697
SCML2	ATACTGAAG GGG	47,37	chrX	(+)	18324015	18324037	exon5	NM_006089 (-)	84703	84725
SCML2	AGGTTACGG TGG	52,63	chrX	(-)	18323960	18323982	exon5	NM_006089 (-)	84648	84670
SCML2	CCCAGACA1 GGG	52,63	chrX	(-)	18323899	18323921	exon5	NM_006089 (-)	84587	84609
SCML4	CCTCTTGCA AGG	57,89	chr6	(+)	107720863	107720885	exon5, exon6	NM_001286, (-)	18707	18729
SCML4	TTTCTGAAG1 AGG	47,37	chr6	(+)	107707870	107707892	exon6, exon7	NM_001286, (-)	5714	5736
SCML4	CATCTGGCG GGG	57,89	chr6	(+)	107707982	107708004	exon6, exon7	NM_001286, (-)	5826	5848
SCML4	GCCTCACCT GGG	52,63	chr6	(-)	107720900	107720922	exon5, exon6	NM_001286, (-)	18744	18766
SETD1A	TATGTGCCG1 AGG	47,37	chr16	(+)	30961356	30961378	exon4	NM_014712 (+)	4063	4085
SETD1A	TAGCGGTAC AGG	52,63	chr16	(-)	30958834	30958856	exon2	NM_014712 (+)	1541	1563
SETD1A	CAAGGCTGA CGG	47,37	chr16	(+)	30961316	30961338	exon4	NM_014712 (+)	4023	4045
SETD1A	TAGTTCCGC1 CGG	57,89	chr16	(-)	30958768	30958790	exon2	NM_014712 (+)	1475	1497
SETD1B	CTTCGACA1 CGG	52,63	chr12	(-)	121805129	121805151	exon2	NM_015048 (+)	398	420
SETD1B	GGAAATTGT GGG	47,37	chr12	(+)	121805138	121805160	exon2	NM_015048 (+)	407	429
SETD1B	GATTGACCC1 AGG	52,63	chr12	(+)	121804842	121804864	exon1	NM_015048 (+)	111	133
SETD1B	ATAAACTGT1 GGG	42,11	chr12	(+)	121804871	121804893	exon1	NM_015048 (+)	140	162
SETD2	GGAGTCGAC AGG	52,63	chr3	(+)	47124295	47124317	exon3	NM_014159 (-)	107888	107910
SETD2	TCTAGTCGA1 AGG	42,11	chr3	(-)	47124463	47124485	exon3	NM_014159 (-)	108056	108078
SETD2	ATCAAAGGA AGG	36,84	chr3	(-)	47124493	47124515	exon3	NM_014159 (-)	108086	108108
SETD2	TCGTAGAAA CGG	47,37	chr3	(+)	47163875	47163897	exon1	NM_014159 (-)	147468	147490
SETD3	GTATGTGCA TGG	52,63	chr14	(-)	99463513	99463535	exon3, exon3	NM_199123, (-)	65768	65790
SETD3	TGAAAATGC AGG	47,37	chr14	(-)	99461254	99461276	exon4, exon4	NM_199123, (-)	63509	63531
SETD3	TACAGCAAC AGG	47,37	chr14	(-)	99465736	99465758	exon2, exon2	NM_199123, (-)	67991	68013
SETD3	GAGGCCCAT AGG	42,11	chr14	(+)	99461277	99461299	exon4, exon4	NM_199123, (-)	63532	63554
SETD4	GCTTCGAAT1 TGG	52,63	chr21	(+)	36048331	36048353	exon6, exon5	NM_001286, (-)	4648	4670
SETD4	CAGTGATT1 GGG	42,11	chr21	(-)	36048322	36048344	exon6, exon5	NM_001286, (-)	4639	4661
SETD4	GGAAAGAA1 CGG	47,37	chr21	(+)	36045853	36045875	exon7, exon6	NM_001286, (-)	2170	2192
SETD4	ACAGGGCAC GGG	57,89	chr21	(+)	36045886	36045908	exon7, exon6	NM_001286, (-)	2203	2225
SETD5	GTACCTACCT TGG	52,63	chr3	(+)	9434421	9434443	exon5	NM_001080, (+)	36722	36744
SETD5	TAGACTTCA1 AGG	52,63	chr3	(+)	9434848	9434870	exon6, exon7	NM_001080, (+)	37149	37171
SETD5	ATGAGCATT1 GGG	47,37	chr3	(+)	9428939	9428961	exon3	NM_001080, (+)	31240	31262
SETD5	GACTAGCCT1 GGG	52,63	chr3	(-)	9433845	9433867	exon4	NM_001080, (+)	36146	36168
SETD6	AAAGTAGGC AGG	60	chr16	(-)	58516277	58516299	exon3, exon4	NM_001160, (+)	799	821
SETD6	CACCACGAA1 CGG	55	chr16	(-)	58516017	58516039	exon2, exon3	NM_001160, (+)	539	561
SETD7	GACGATGAC CGG	57,89	chr4	(-)	139547019	139547041	exon2, exon2	NM_030648, (-)	14441	14463
SETD7	CACGGAGAA GGG	52,63	chr4	(-)	139546944	139546966	exon2, exon2	NM_030648, (-)	14366	14388
SETD7	CATCCACATA AGG	47,37	chr4	(+)	139533341	139533363	exon3, exon3	NM_030648, (-)	763	785
SETD7	GGATAGCG1 TGG	57,89	chr4	(-)	139556113	139556135	exon1, exon1	NM_030648, (-)	23535	23557
SETD8	GCATTGTTC1 AGG	52,63	chr12	(-)	123390664	123390686			0	0
SETD8	ACTGAGTTC GGG	42,11	chr12	(-)	123390702	123390724			0	0
SETD8	GAAATGCTG CGG	52,63	chr12	(+)	123395053	123395075			0	0
SETD8	AAGATCAAA AGG	47,37	chr12	(+)	123395100	123395122			0	0
SETDB1	CCGGTATTG1 TGG	57,89	chr1	(-)	150930008	150930030	exon3, exon3	NM_001243, (+)	3670	3692
SETDB1	ACTTCGGCA1 AGG	42,11	chr1	(+)	150927831	150927853	exon2, exon2	NM_001243, (+)	1493	1515

SETDB1	ATACCGGGA AGG	52,63	chr1	(+)	150930024	150930046	exon3, exon3	NM_001243	(+)	3686	3708
SETDB1	CAAACCAAA AGG	57,89	chr1	(-)	150927723	150927745	exon2, exon2	NM_001243	(+)	1385	1407
SETDB2	GGAGTTTTT AGG	36,84	chr13	(-)	49467915	49467937	exon6, exon5	NM_031915	(+)	23623	23645
SETDB2	TCCTATGCCT AGG	52,63	chr13	(+)	49467865	49467887	exon6, exon5	NM_031915	(+)	23573	23595
SETDB2	TGGATGGAC TGG	47,37	chr13	(+)	49460124	49460146	exon3, exon3	NM_031915	(+)	15832	15854
SETDB2	CATTCTACT TGG	36,84	chr13	(-)	49461104	49461126	exon4, exon4	NM_031915	(+)	16812	16834
SETMAR	CAAAGACGA GGG	57,89	chr3	(+)	4303387	4303409	exon1, exon1	NM_006515	(+)	84	106
SETMAR	CATCATAGT CGG	42,11	chr3	(-)	4313011	4313033	exon2, exon2	NM_006515	(+)	9708	9730
SETMAR	CCGGGAAAC GGG	47,37	chr3	(-)	4312940	4312962	exon2, exon2	NM_006515	(+)	9637	9659
SETMAR	GTGGGATCA AGG	52,63	chr3	(-)	4312922	4312944	exon2, exon2	NM_006515	(+)	9619	9641
SFMBT1	GGTCCACAG GGG	57,89	chr3	(-)	52954329	52954351	exon3	NM_016329	(-)	50763	50785
SFMBT1	GTGGACACA TGG	47,37	chr3	(-)	52943571	52943593	exon4	NM_016329	(-)	40005	40027
SFMBT1	TACCTCTTCC CGG	47,37	chr3	(+)	52954386	52954408	exon3	NM_016329	(-)	50820	50842
SFMBT1	TTGCTCCTTC TGG	52,63	chr3	(-)	52943460	52943482	exon4	NM_016329	(-)	39894	39916
SFMBT2	GACTACGTC CGG	52,63	chr10	(+)	7367713	7367735	exon4, exon4	NM_001029	(-)	209090	209112
SFMBT2	GAACAACCC GGG	57,89	chr10	(-)	7367808	7367830	exon4, exon4	NM_001029	(-)	209185	209207
SFMBT2	CCACGATCA GGG	52,63	chr10	(-)	7367782	7367804	exon4, exon4	NM_001029	(-)	209159	209181
SFMBT2	TTCTGCGCT GGG	52,63	chr10	(-)	7367749	7367771	exon4, exon4	NM_001029	(-)	209126	209148
SHPRH	GCTTCATTG AGG	36,84	chr6	(-)	145955241	145955263	exon2, exon2	NM_173082	(-)	70433	70455
SHPRH	GAAACGTGC GGG	57,89	chr6	(-)	145955286	145955308	exon2, exon2	NM_173082	(-)	70478	70500
SHPRH	TGGCTCACAC AGG	42,11	chr6	(-)	145955107	145955129	exon2, exon2	NM_173082	(-)	70299	70321
SHPRH	AGAGGTATC AGG	52,63	chr6	(+)	145955173	145955195	exon2, exon2	NM_173082	(-)	70365	70387
SIN3A	GCTATGAAC CGG	42,11	chr15	(+)	75422764	75422786	exon3, exon3	NM_001145	(-)	53386	53408
SIN3A	TGCGTATCI AGG	42,11	chr15	(-)	75414281	75414303	exon4, exon4	NM_001145	(-)	44903	44925
SIN3A	TTTGGATGA CGG	47,37	chr15	(-)	75430342	75430364	exon2, exon2	NM_001145	(-)	60964	60986
SIN3B	AAGCGTTGA AGG	36,84	chr19	(-)	16831551	16831573	exon3, exon3	NM_015260	(+)	2165	2187
SIN3B	GATCTTACC AGG	52,63	chr19	(-)	16829807	16829829	exon2, exon2	NM_015260	(+)	421	443
SIN3B	GAGACACGT AGG	52,63	chr19	(-)	16831504	16831526	exon3, exon3	NM_015260	(+)	2118	2140
SIN3B	GATCTCCAG AGG	57,89	chr19	(-)	16829852	16829874	exon2, exon2	NM_015260	(+)	466	488
SIRT1	TCGTACAAG NGG	55			0	0	Not available			0	0
SIRT1	TACAAGTTG NGG	60			0	0	Not available			0	0
SIRT1	GTCTTCGTC NGG	45			0	0	Not available			0	0
SIRT2	TAGGTTGTC TGG	52,63	chr19	(+)	38889909	38889931	exon6, exon5	NM_012237	(-)	11355	11377
SIRT2	GCGCATGAA TGG	52,63	chr19	(+)	38889129	38889151	exon8, exon7	NM_012237	(-)	10575	10597
SIRT2	AGCGTTCCG CGG	52,63	chr19	(+)	38893414	38893436	exon4, exon3	NM_012237	(-)	14860	14882
SIRT3	CGTTGGGCT GGG	52,63	chr11	(+)	233067	233089	exon3, exon3	NM_012239	(-)	18038	18060
SIRT3	TCTACACGC GGG	47,37	chr11	(-)	232993	233015	exon3, exon3	NM_012239	(-)	17964	17986
SIRT3	ATGAGCTTC AGG	42,11	chr11	(+)	230515	230537	exon4, exon4	NM_012239	(-)	15486	15508
SIRT3	GGTACGGG/ TGG	57,89	chr11	(+)	233163	233185	exon3, exon3	NM_012239	(-)	18134	18156
SIRT4	GTCTGGTAT TGG	57,89	chr12	(-)	120303758	120303780	exon2	NM_012240	(+)	1438	1460
SIRT4	CGTGCTCGA GGG	57,89	chr12	(+)	120303629	120303651	exon2	NM_012240	(+)	1309	1331
SIRT4	TACTGGGCG AGG	52,63	chr12	(+)	120303874	120303896	exon2	NM_012240	(+)	1554	1576
SIRT4	GAGACTCCT GGG	47,37	chr12	(+)	120303726	120303748	exon2	NM_012240	(+)	1406	1428
SIRT5	GTGCAGCTC GGG	52,63	chr6	(-)	13591835	13591857	exon4, exon3	NM_001242	(+)	17209	17231
SIRT5	AACTTGGCC AGG	47,37	chr6	(-)	13584200	13584222	exon3, exon3	NM_031244	(+)	9574	9596
SIRT5	TCAATCGACI TGG	42,11	chr6	(-)	13584122	13584144	exon3, exon3	NM_031244	(+)	9496	9518
SIRT5	AGTGGTAGA CGG	52,63	chr6	(-)	13591707	13591729	exon5, exon5	NM_031244	(+)	17081	17103
SIRT6	ATGTCGGTG GGG	52,63	chr19	(-)	4182517	4182539	exon1, exon1	NM_016539	(-)	8409	8431
SIRT6	AAAGGTGGI GGG	47,37	chr19	(+)	4179223	4179245	exon3, exon3	NM_016539	(-)	5115	5137
SIRT6	GGTCTGGCA TGG	57,89	chr19	(-)	4180834	4180856	exon2, exon2	NM_016539	(-)	6726	6748
SIRT6	CTTCTGGTC TGG	57,89	chr19	(-)	4179135	4179157	exon3, exon3	NM_016539	(-)	5027	5049
SIRT7	CGACCAAGT CGG	47,37	chr17	(+)	81917641	81917663	exon3	NM_016538	(-)	5703	5725
SIRT7	CAGCGTCTA CGG	52,63	chr17	(-)	81915658	81915680	exon4	NM_016538	(-)	3720	3742
SIRT7	AAATACTTG AGG	36,84	chr17	(-)	81917631	81917653	exon3	NM_016538	(-)	5693	5715
SIRT7	GTGTGGACA AGG	52,63	chr17	(-)	81915623	81915645	exon4	NM_016538	(-)	3685	3707
SMARCA1	TTCAAAITCTC CGG	42,11	chrX	(+)	129516471	129516493	exon3, exon3	NM_003069	(-)	69971	69993
SMARCA1	GTGGGAGAT AGG	47,37	chrX	(+)	129516406	129516428	exon3, exon3	NM_003069	(-)	69906	69928
SMARCA1	TAAAGCGCC AGG	36,84	chrX	(-)	129518390	129518412	exon2, exon2	NM_003069	(-)	71890	71912
SMARCA2	CATCGAAGA AGG	47,37	chr9	(+)	2161688	2161710	exon28, exor	NM_139045	(+)	4009	4031
SMARCA2	GGATTGCTA CGG	31,58	chr9	(+)	2182145	2182167	exon30, exor	NM_139045	(+)	24466	24488
SMARCA2	GATAGCCGG TGG	57,89	chr9	(+)	2159883	2159905	exon2, exon2	NM_001289	(+)	1432	1454
SMARCA2	GGTGACAGT AGG	57,89	chr9	(-)	2161815	2161837	exon28, exor	NM_139045	(+)	4136	4158
SMARCA4	CCGCGCTAC AGG	55	chr19	(+)	10985312	10985334	exon2, exon3	NM_001128	(+)	24391	24413
SMARCA4	TTCTCATGCA GGG	45	chr19	(-)	10985273	10985295	exon2, exon3	NM_001128	(+)	24352	24374
SMARCA4	ATCTGGTGC AGG	50	chr19	(-)	10984344	10984366	exon1, exon2	NM_001128	(+)	23423	23445
SMARCA4	ATGGAGTCC GGG	45	chr19	(+)	10985276	10985298	exon2, exon3	NM_001128	(+)	24355	24377
SMARCA5	ATATTGTAT TGG	36,84	chr4	(+)	143517358	143517380	exon2	NM_003601	(+)	3896	3918
SMARCA5	TTTTTTATTO TGG	47,37	chr4	(-)	143521540	143521562	exon3	NM_003601	(+)	8078	8100
SMARCA5	GTGGGAGTC AGG	52,63	chr4	(-)	143521498	143521520	exon3	NM_003601	(+)	8036	8058
SMARCB1	AACTACTCC AGG	50	chr22	(+)	23791762	23791784	[exon2, exor	[NM_001007	(+)	4832	4854
SMARCB1	GACGGCGAC CGG	50	chr22	(+)	23787233	23787255	[exon1, exor	[NM_001007	(+)	303	325
SMARCB1	CCACTTCGA AGG	50	chr22	(-)	23793593	23793615	[exon3, exor	[NM_001007	(+)	6663	6685
SMARCB1	ATGGCGCTG CGG	55	chr22	(+)	23787179	23787201	[exon1, exor	[NM_001007	(+)	249	271
SMARCC1	CCTAGCTGTI AGG	50	chr3	(-)	47781695	47781717	exon1	NM_003074	(-)	195808	195830
SMARCC1	GCTGTTTAT TGG	50	chr3	(-)	47781691	47781713	exon1	NM_003074	(-)	195804	195826
SMARCC1	CCTTCGTCG AGG	50	chr3	(+)	47781695	47781717	exon1	NM_003074	(-)	195808	195830
SMARCC1	TCGATAAAC CGG	50	chr3	(+)	47781702	47781724	exon1	NM_003074	(-)	195815	195837
SMARCC2	AGTTTCGACA TGG	57,89	chr12	(-)	56189372	56189394	exon1, exon1	NM_001130	(-)	27521	27543
SMARCC2	ACTGTACAA AGG	47,37	chr12	(+)	56187252	56187274	exon2, exon2	NM_001130	(-)	25401	25423
SMARCC2	ATCACGCAT TGG	52,63	chr12	(-)	56185065	56185087	exon4, exon4	NM_001130	(-)	23214	23236
SMARCC2	GGCCTGCTA TGG	57,89	chr12	(+)	56189411	56189433	exon1, exon1	NM_001130	(-)	27560	27582
SMARCD1	GGACTGATC GGG	57,89	chr12	(-)	50086258	50086280	exon2, exon2	NM_003076	(+)	1059	1081
SMARCD1	AGGCAGCCG AGG	57,89	chr12	(+)	50086178	50086200	exon2, exon2	NM_003076	(+)	979	1001
SMARCD1	TGGACCTGC AGG	57,89	chr12	(-)	50086296	50086318	exon2, exon2	NM_003076	(+)	1097	1119
SMARCD1	GATTTTGA TGG	57,89	chr12	(-)	50086316	50086338	exon2, exon2	NM_003076	(+)	1117	1139
SMARCD2	TCGGAATGG TGG	50	chr17	(+)	63837494	63837516	[exon2] [NM_001098	(-)	5414	5436	
SMARCD2	CGGAATGGG GGG	50	chr17	(+)	63837495	63837517	[exon2] [NM_001098	(-)	5415	5437	

SMARCD2	TTTTCGGAA`TGG	40	chr17	(+)	63837491	63837513 [exon2]	[NM_00109E (-)	5411	5433
SMARCD2	ACAAGCAGG TGG	50	chr17	(+)	63837480	63837502 [exon2]	[NM_00109E (-)	5400	5422
SMARCD3	ATCAAACCA1 CGG	42,11	chr7	(-)	151242757	151242779 exon5, exon5	NM_003078, (-)	3785	3807
SMARCD3	TGGACCTCT1 AGG	47,37	chr7	(-)	151242787	151242809 exon5, exon5	NM_003078, (-)	3815	3837
SMARCD3	GTCCATGTA/ CGG	57,89	chr7	(+)	151242805	151242827 exon5, exon5	NM_003078, (-)	3833	3855
SMARCD3	CTGACAAAA AGG	47,37	chr7	(-)	151243659	151243681 exon4, exon4	NM_003078, (-)	4687	4709
SMARCE1	TTTTGGAATI AGG	36,84	chr17	(+)	40637546	40637568 exon5	NM_003079 (-)	9819	9841
SMARCE1	GGCGCTTATI GGG	57,89	chr17	(+)	40637521	40637543 exon5	NM_003079 (-)	9794	9816
SMARCE1	TTGTAGGCG TGG	47,37	chr17	(+)	40642501	40642523 exon4	NM_003079 (-)	14774	14796
SMARCE1	ATCTCGCCTA AGG	42,11	chr17	(-)	40642491	40642513 exon4	NM_003079 (-)	14764	14786
SMNDC1	GTGTTATGA AGG	42,11	chr10	(-)	110297706	110297728 exon4	NM_005871 (-)	4667	4689
SMNDC1	ACCGTGCA/ TGG	52,63	chr10	(-)	110297663	110297685 exon4	NM_005871 (-)	4624	4646
SMNDC1	GAAGCTGCA TGG	42,11	chr10	(-)	110303508	110303530 exon2	NM_005871 (-)	10469	10491
SMNDC1	TTCCTTCTTC AGG	42,11	chr10	(+)	110297607	110297629 exon4	NM_005871 (-)	4568	4590
SMYD1	GTTCGGCCA` GGG	47,37	chr2	(+)	88084447	88084469 exon2	NM_198274 (+)	16668	16690
SMYD1	TGGCCGAAC TGG	42,11	chr2	(-)	88084433	88084455 exon2	NM_198274 (+)	16654	16676
SMYD1	TGAGCGGGT TGG	57,89	chr2	(+)	88067969	88067991 exon1	NM_198274 (+)	190	212
SMYD2	GTTAGTCTT/ GGG	47,37	chr1	(-)	214314828	214314850 exon3	NM_020197 (+)	33607	33629
SMYD2	GACCGTGAG AGG	63,16	chr1	(-)	214281367	214281389 exon1	NM_020197 (+)	146	168
SMYD2	TGGTGAAGC TGG	52,63	chr1	(-)	214281404	214281426 exon1	NM_020197 (+)	183	205
SMYD3	CACTACAGT/ CGG	47,37	chr1	(+)	246355042	246355064 exon2, exon2	NM_022743, (-)	605703	605725
SMYD3	AACTCTGCC/ CGG	47,37	chr1	(+)	246335379	246335401 exon3, exon3	NM_022743, (-)	586040	586062
SMYD3	AAGCTTGGC CGG	52,63	chr1	(-)	246335448	246335470 exon3, exon3	NM_022743, (-)	586109	586131
SMYD3	ATCTGGGTT AGG	42,11	chr1	(+)	246335414	246335436 exon3, exon3	NM_022743, (-)	586075	586097
SMYD4	TTGTGACCTC GGG	47,37	chr17	(+)	1827916	1827938 exon2	NM_052928 (-)	48382	48404
SMYD4	ACTGTGTCA` CGG	52,63	chr17	(-)	1804655	1804677 exon4	NM_052928 (-)	25121	25143
SMYD4	TTACTGTGTC CGG	47,37	chr17	(-)	1812054	1812076 exon3	NM_052928 (-)	32520	32542
SMYD4	ACATTCAAG AGG	42,11	chr17	(-)	1804685	1804707 exon4	NM_052928 (-)	25151	25173
SMYD5	GCTCACGAA CGG	57,89	chr2	(-)	73214331	73214353 exon1	NM_006062 (+)	94	116
SMYD5	CATCTTCGTA TGG	57,89	chr2	(+)	73218905	73218927 exon2	NM_006062 (+)	4668	4690
SMYD5	GACGTGTTT GGG	57,89	chr2	(+)	73214285	73214307 exon1	NM_006062 (+)	48	70
SMYD5	TGTACTGCAI CGG	47,37	chr2	(+)	73220665	73220687 exon4	NM_006062 (+)	6428	6450
SND1	AGGTTGATC AGG	57,89	chr7	(-)	127686664	127686686 exon2	NM_014390 (+)	34517	34539
SND1	CGCCACACA/ AGG	57,89	chr7	(+)	127686726	127686748 exon2	NM_014390 (+)	34579	34601
SND1	TTTCGAAGG TGG	47,37	chr7	(-)	127694840	127694862 exon3	NM_014390 (+)	42693	42715
SND1	GATAGAAAA AGG	42,11	chr7	(+)	127694893	127694915 exon3	NM_014390 (+)	42746	42768
SP100	TTGTGATGA CGG	42,11	chr2	(-)	230443063	230443085 exon4, exon3	NM_001206: (+)	26908	26930
SP100	AAGACCAGG AGG	47,37	chr2	(+)	230442948	230442970 exon4, exon3	NM_001206: (+)	26793	26815
SP100	TGCAAAATCG` AGG	52,63	chr2	(-)	230417640	230417662 exon2, exon2	NM_003113, (+)	1485	1507
SP100	TCTTCTTCAC AGG	36,84	chr2	(-)	230446836	230446858 exon6, exon5	NM_001206: (+)	30681	30703
SP110	GGTTAAAGT TGG	47,37	chr2	(+)	230215034	230215056 exon4, exon3	NM_0011851 (-)	46109	46131
SP110	CCAGATTGG AGG	47,37	chr2	(+)	230214977	230214999 exon4, exon3	NM_0011851 (-)	46052	46074
SP110	TTGTGCACC/ AGG	47,37	chr2	(+)	230215066	230215088 exon4, exon3	NM_0011851 (-)	46141	46163
SP110	GTCTAGGAG AGG	52,63	chr2	(+)	230216811	230216833 exon3, exon2	NM_0011851 (-)	47886	47908
SP140	CGTAGAGGC AGG	57,89	chr2	(+)	230237104	230237126 exon2, exon2	NM_007237, (+)	11375	11397
SP140	TTAAATCAG/ AGG	36,84	chr2	(-)	230238332	230238354 exon3, exon3	NM_007237, (+)	12603	12625
SP140L	TTGTGATGA CGG	47,37	chr2	(-)	230357931	230357953 exon3, exon2	NM_138402, (+)	30752	30774
SP140L	TTTGGAAAGC AGG	47,37	chr2	(+)	230359056	230359078 exon4, exon3	NM_138402, (+)	31877	31899
SP140L	GGAAGACCA AGG	47,37	chr2	(+)	230357814	230357836 exon3, exon2	NM_138402, (+)	30635	30657
SRCAP	GGTTGTCTC AGG	57,89	chr16	(+)	30704064	30704086 exon4	NM_006662 (+)	4924	4946
SRCAP	CCATGCCCA/ AGG	47,37	chr16	(+)	30704285	30704307 exon4	NM_006662 (+)	5145	5167
SRCAP	GATAAGCTG GGG	52,63	chr16	(-)	30704217	30704239 exon4	NM_006662 (+)	5077	5099
SSRP1	GTTCAACGA/ AGG	47,37	chr11	(-)	57335082	57335104 exon2	NM_003146 (-)	9098	9120
SSRP1	GGCCATGTC TGG	47,37	chr11	(-)	57334476	57334498 exon3	NM_003146 (-)	8492	8514
SSRP1	TCGACTGAG AGG	57,89	chr11	(-)	57334618	57334640 exon3	NM_003146 (-)	8634	8656
SSRP1	TGCCTTGAC AGG	52,63	chr11	(-)	57333480	57333502 exon4	NM_003146 (-)	7496	7518
STK31	ACTGTCTGA/ AGG	52,63	chr7	(+)	23717522	23717544 exon4, exon4	NM_032944, (+)	7356	7378
STK31	CTAGAAAAC AGG	47,37	chr7	(-)	23729157	23729179 exon6, exon6	NM_032944, (+)	18991	19013
STK31	GCCAAAAAG GGG	26,32	chr7	(+)	23729184	23729206 exon6, exon6	NM_032944, (+)	19018	19040
STK31	CTGGTGAGC` TGG	47,37	chr7	(+)	23729094	23729116 exon6, exon6	NM_032944, (+)	18928	18950
SUPT16H	CGTATTAGC AGG	47,37	chr14	(+)	21371881	21371903 exon3	NM_007192 (-)	20410	20432
SUPT16H	GATGCCATT/ GGG	42,11	chr14	(-)	21373381	21373403 exon2	NM_007192 (-)	21910	21932
SUPT16H	AGAGACTGT CGG	42,11	chr14	(-)	21383862	21383884 exon1	NM_007192 (-)	32391	32413
SUPT16H	AAACAGATT/ GGG	36,84	chr14	(-)	21371926	21371948 exon3	NM_007192 (-)	20455	20477
SUV39H1	GGTTCCTCT AGG	47,37	chrX	(-)	48698978	48699000 exon2, exon2	NM_001282: (+)	2246	2268
SUV39H1	GATATCCAC/ AGG	47,37	chrX	(-)	48700105	48700127 exon3, exon3	NM_001282: (+)	3373	3395
SUV39H1	ACTCGACTTC AGG	36,84	chrX	(-)	48698999	48699021 exon2, exon2	NM_001282: (+)	2267	2289
SUV39H2	AACGAATAC TGG	42,11	chr10	(+)	14897185	14897207 exon2, exon2	NM_024670, (+)	18403	18425
SUV39H2	GGGCACTTC AGG	47,37	chr10	(-)	14896906	14896928 exon3, exon3	NM_001193: (+)	18124	18146
SUV39H2	AATCACGTA` TGG	31,58	chr10	(+)	14899592	14899614 exon4, exon4	NM_001193: (+)	20810	20832
SUV39H2	GTATCAAGT/ AGG	42,11	chr10	(-)	14881511	14881533 exon2, exon2	NM_001193: (+)	2729	2751
SUV420H1	TTCTTGGGC AGG	52,63	chr11	(+)	68185861	68185883		0	0
SUV420H1	AATCAAAAT` GGG	31,58	chr11	(-)	68189969	68189991		0	0
SUV420H1	TGATGACCT/ TGG	47,37	chr11	(-)	68185827	68185849		0	0
SUV420H1	AATGGTAAC AGG	42,11	chr11	(-)	68185904	68185926		0	0
SUV420H2	ACTGTGCGA TGG	57,89	chr19	(+)	55341966	55341988		0	0
SUV420H2	TTCTCGTGCT CGG	52,63	chr19	(-)	55341944	55341966		0	0
SUV420H2	CGCTACTCCA CGG	57,89	chr19	(+)	55342802	55342824		0	0
SUV420H2	AAGTTTCCA/ AGG	57,89	chr19	(-)	55342245	55342267		0	0
SUZ12	ACCGGTGAA TGG	50	chr17	(+)	31937453	31937475 exon1	NM_015355 (+)	429	451
SUZ12	GCCTGGACG CGG	55	chr17	(-)	31937466	31937488 exon1	NM_015355 (+)	442	464
SUZ12	GCCGAAAAAT AGG	60	chr17	(+)	31937465	31937487 exon1	NM_015355 (+)	441	463
SUZ12	TCCATTTTCG CGG	45	chr17	(-)	31937454	31937476 exon1	NM_015355 (+)	430	452
TAF1	CGAAGATAC GGG	52,63	chrX	(+)	71368122	71368144 exon3, exon3	NM_0012861 (+)	1884	1906
TAF1	AGCGACGAA AGG	57,89	chrX	(+)	71366390	71366412 exon1, exon1	NM_0012861 (+)	152	174
TAF1	GGCGGCCCA GGG	52,63	chrX	(+)	71366411	71366433 exon1, exon1	NM_0012861 (+)	173	195
TAF1	TGCGCAACA` GGG	52,63	chrX	(+)	71366442	71366464 exon1, exon1	NM_0012861 (+)	204	226

TAF1L	TTTCGGCAAI CGG	47,37	chr9	(-)	32635435	32635457	exon1	NM_153809 (-)	5982	6004
TAF1L	GGATACCCG GGG	42,11	chr9	(+)	32635459	32635481	exon1	NM_153809 (-)	6006	6028
TAF1L	CATGT CAGAI AGG	57,89	chr9	(-)	32635501	32635523	exon1	NM_153809 (-)	6048	6070
TAF1L	CCACCCCTCA AGG	47,37	chr9	(+)	32635283	32635305	exon1	NM_153809 (-)	5830	5852
TAF3	TGACGGAAT AGG	52,63	chr10	(-)	7824423	7824445	exon2	NM_031923 (+)	5920	5942
TAF3	CATCCAAAAT CGG	42,11	chr10	(-)	7824322	7824344	exon2	NM_031923 (+)	5819	5841
TAF3	GTAGACTAA TGG	52,63	chr10	(-)	7824361	7824383	exon2	NM_031923 (+)	5858	5880
TAF3	GTCTGTGTT TGG	57,89	chr10	(+)	7818730	7818752	exon1	NM_031923 (+)	227	249
TCEA1	TCGCAAGCAI AGG	47,37	chr8	(-)	53999996	54000018	exon3, exon2	NM_006756, (-)	33443	33465
TCEA1	AACTGACAT TGG	36,84	chr8	(+)	54000027	54000049	exon3, exon2	NM_006756, (-)	33474	33496
TCEA1	CTGTCTTGC AGG	42,11	chr8	(+)	53993689	53993711	exon4, exon3	NM_006756, (-)	27136	27158
TCEA1	GGTCCGCTT TGG	57,89	chr8	(-)	54022089	54022111	exon1, exon1	NM_006756, (-)	55536	55558
TCF19	ACAAGTACG AGG	47,37	chr6	(+)	31161574	31161596	exon3, exon3	NM_007109, (+)	3051	3073
TCF19	TGCTTCCAAC AGG	57,89	chr6	(+)	31159479	31159501	exon2, exon2	NM_007109, (+)	956	978
TCF19	AATAATGTG AGG	42,11	chr6	(+)	31161458	31161480	exon3, exon3	NM_007109, (+)	2935	2957
TCF19	GAAACATGAA AGG	42,11	chr6	(-)	31161549	31161571	exon3, exon3	NM_007109, (+)	3026	3048
TCF20	GTATCTGCT AGG	52,63	chr22	(+)	42215276	42215298	exon1, exon2	NM_181492, (-)	55264	55286
TCF20	AGAAGAGTT AGG	52,63	chr22	(-)	42215203	42215225	exon1, exon2	NM_181492, (-)	55191	55213
TCF20	GGCAATCAG GGG	52,63	chr22	(-)	42214905	42214927	exon1, exon2	NM_181492, (-)	54893	54915
TCF20	TGAAACCTT TGG	47,37	chr22	(+)	42215059	42215081	exon1, exon2	NM_181492, (-)	55047	55069
TDG	CCTGTTGAG TGG	31,58	chr12	(+)	103979899	103979921	exon3	NM_003211 (+)	14085	14107
TDG	GATTGAAGC GGG	31,58	chr12	(-)	103980036	103980058	exon3	NM_003211 (+)	14222	14244
TDG	GATGGCTGA TGG	47,37	chr12	(+)	103976969	103976991	exon2	NM_003211 (+)	11155	11177
TDG	TTGGGTTCC TGG	47,37	chr12	(-)	103979872	103979894	exon3	NM_003211 (+)	14058	14080
TDRD1	TCAAACCCG/ CGG	47,37	chr10	(+)	114188090	114188112	exon2	NM_198795 (+)	8821	8843
TDRD1	GAATTACTTT TGG	36,84	chr10	(-)	114190975	114190997	exon3	NM_198795 (+)	11706	11728
TDRD1	GGACTTCTT TGG	36,84	chr10	(-)	114187940	114187962	exon2	NM_198795 (+)	8671	8693
TDRD1	CAACAATAI AGG	31,58	chr10	(+)	114188050	114188072	exon2	NM_198795 (+)	8781	8803
TDRD10	GATCATATC/ TGG	52,63	chr1	(-)	154521436	154521458	exon6, exon6	NM_182499, (+)	19218	19240
TDRD10	GAGGGTTG/ AGG	47,37	chr1	(-)	154520318	154520340	exon5, exon5	NM_182499, (+)	18100	18122
TDRD10	ACAGTTTAT/ GGG	36,84	chr1	(-)	154507259	154507281	exon3, exon3	NM_182499, (+)	5041	5063
TDRD10	TGTATGTTG TGG	42,11	chr1	(+)	154508448	154508470	exon4, exon4	NM_182499, (+)	6230	6252
TDRD12	TAAACGATT/ CGG	31,58	chr19	(-)	32742784	32742806	exon4	NM_001110I (+)	23012	23034
TDRD12	CGCTGTGTA/ TGG	42,11	chr19	(-)	32731813	32731835	exon2	NM_001110I (+)	12041	12063
TDRD12	TGTTCTTGG/ AGG	47,37	chr19	(-)	32738951	32738973	exon3	NM_001110I (+)	19179	19201
TDRD12	AAACCCCTTA/ AGG	36,84	chr19	(+)	32731857	32731879	exon2	NM_001110I (+)	12085	12107
TDRD3	CTGCGATTAI TGG	47,37	chr13	(+)	60460470	60460492	exon4, exon4	NM_030794, (+)	64014	64036
TDRD3	CACATTGTAI AGG	47,37	chr13	(-)	60444712	60444734	exon3	NM_001146I (+)	47420	47442
TDRD3	TCGCAATGT/ AGG	52,63	chr13	(+)	60460415	60460437	exon4	NM_001146I (+)	63123	63145
TDRD3	GACTCTAAC/ TGG	47,37	chr13	(+)	60467314	60467336	exon5, exon5	NM_030794, (+)	70858	70880
TDRD5	TCACATCCG/ GGG	47,37	chr1	(+)	179635825	179635847	exon9, exon9	NM_001199I (+)	44213	44235
TDRD5	CGGGACATC AGG	52,63	chr1	(+)	179639901	179639923	exon10, exor	NM_001199I (+)	48289	48311
TDRD5	GGGAAGTGC GGG	52,63	chr1	(-)	179635759	179635781	exon9, exon9	NM_001199I (+)	44147	44169
TDRD5	GCGCTGTTA TGG	42,11	chr1	(+)	179639839	179639861	exon10, exor	NM_001199I (+)	48227	48249
TDRD6	ATCGGGATG AGG	63,16	chr6	(-)	46688184	46688206	exon1, exon1	NM_001168I (+)	310	332
TDRD6	AATTTGCCCT GGG	52,63	chr6	(+)	46688489	46688511	exon1, exon1	NM_001168I (+)	615	637
TDRD6	ACAAAAGCO AGG	57,89	chr6	(-)	46688347	46688369	exon1, exon1	NM_001168I (+)	473	495
TDRD6	ATGTGATCC TGG	57,89	chr6	(+)	46688205	46688227	exon1, exon1	NM_001168I (+)	331	353
TDRD7	GTAGCATTAI AGG	63,16	chr9	(+)	97428529	97428551	exon2	NM_014290 (+)	16510	16532
TDRD7	TGGATCCCI AGG	52,63	chr9	(+)	97428577	97428599	exon2	NM_014290 (+)	16558	16580
TDRD7	GGAGAGTAI TGG	47,37	chr9	(+)	97428550	97428572	exon2	NM_014290 (+)	16531	16553
TDRD7	CTCGTCAAA/ AGG	42,11	chr9	(+)	97430988	97431010	exon3, exon2	NM_014290, (+)	18969	18991
TDRD9	CCAGTCTTT TGG	57,89	chr14	(-)	103928526	103928548	exon1	NM_153046 (+)	47	69
TDRD9	ATCAAGGAC/ CGG	47,37	chr14	(+)	103928537	103928559	exon1	NM_153046 (+)	58	80
TDRD9	ACTCTACTTC TGG	47,37	chr14	(-)	103955673	103955695	exon2	NM_153046 (+)	27194	27216
TDRD9	CGGCAAGAC TGG	57,89	chr14	(+)	103928557	103928579	exon1	NM_153046 (+)	78	100
TDKHH	TCGGATTGA AGG	47,37	chr1	(-)	151780098	151780120	exon4, exon4	NM_001083I (-)	8534	8556
TDKHH	TATCCTATAC GGG	42,11	chr1	(-)	151782908	151782930	exon2, exon2	NM_001083I (-)	11344	11366
TDKHH	GATATAGGC TGG	42,11	chr1	(+)	151782927	151782949	exon2, exon2	NM_001083I (-)	11363	11385
TDKHH	GTTTAATATI CGG	36,84	chr1	(+)	151781483	151781505	exon3, exon3	NM_001083I (-)	9919	9941
TET1	GGTCGTAGC AGG	47,37	chr10	(+)	68572698	68572720	exon2	NM_030625 (+)	12339	12361
TET1	TACGAAGCA AGG	47,37	chr10	(+)	68572655	68572677	exon2	NM_030625 (+)	12296	12318
TET1	CGCCATTGT/ AGG	47,37	chr10	(-)	68572631	68572653	exon2	NM_030625 (+)	12272	12294
TET1	CAACTACGA/ GGG	42,11	chr10	(+)	68572414	68572436	exon2	NM_030625 (+)	12055	12077
TET2	CAGGACTCAI TGG	47,37	chr4	(-)	105234149	105234171	exon3, exon3	NM_001127I (+)	88275	88297
TET2	TGGAGAAAC GGG	42,11	chr4	(+)	105234299	105234321	exon3, exon3	NM_001127I (+)	88425	88447
TET2	GACTTTACA/ AGG	31,58	chr4	(+)	105234171	105234193	exon3, exon3	NM_001127I (+)	88297	88319
TET3	CGAAAAGGC/ GGG	57,89	chr2	(-)	74046507	74046529	exon3	NM_001287I (+)	60104	60126
TET3	CTTGAGTCC/ TGG	57,89	chr2	(-)	74046335	74046357	exon3	NM_001287I (+)	59932	59954
TET3	TTTCATACCA GGG	57,89	chr2	(-)	74046699	74046721	exon3	NM_001287I (+)	60296	60318
TET3	ACGACTCAT/ AGG	52,63	chr2	(-)	74046585	74046607	exon3	NM_001287I (+)	60182	60204
TP53BP1	AACGAGGAC GGG	47,37	chr15	(-)	43492036	43492058	exon3, exon3	NM_001141I (-)	84823	84845
TP53BP1	CAGGTTCTAI TGG	42,11	chr15	(-)	43492351	43492373	exon2, exon2	NM_001141I (-)	85138	85160
TP53BP1	GAATCCAAC/ AGG	47,37	chr15	(+)	43492432	43492454	exon2, exon2	NM_001141I (-)	85219	85241
TP53BP1	TGTGCGTCTI AGG	52,63	chr15	(+)	43492301	43492323	exon2, exon2	NM_001141I (-)	85088	85110
TRIM24	AGCGCTGGC AGG	60	chr7	(-)	138460767	138460789	exon1, exon1	NM_003852, (+)	434	456
TRIM24	ACACGGCGC AGG	60	chr7	(-)	138460701	138460723	exon1, exon1	NM_003852, (+)	368	390
TRIM24	AGTGTCACAI GGG	55	chr7	(-)	138460691	138460713	exon1, exon1	NM_003852, (+)	358	380
TRIM24	AAGTGTCAC/ CGG	50	chr7	(-)	138460692	138460714	exon1, exon1	NM_003852, (+)	359	381
TRIM28	GAAGCACTG CGG	52,63	chr19	(-)	58545437	58545459	exon2	NM_005762 (+)	969	991
TRIM28	TCGGCCTGT/ AGG	63,16	chr19	(+)	58545013	58545035	exon1	NM_005762 (+)	545	567
TRIM28	CTACAGGCC/ GGG	57,89	chr19	(-)	58545001	58545023	exon1	NM_005762 (+)	533	555
TRIM28	GTGCTTCTCC TGG	47,37	chr19	(+)	58545453	58545475	exon2	NM_005762 (+)	985	1007
TRIM33	CTGCAAGCTI CGG	55	chr1	(+)	114510678	114510700	exon1, exon1	NM_015906, (-)	117902	117924
TRIM33	TTCACTCTCTI TGG	60	chr1	(-)	114510821	114510843	exon1, exon1	NM_015906, (-)	118045	118067
TRIM33	ATGGCGGA/ CGG	55	chr1	(-)	114511054	114511076	exon1, exon1	NM_015906, (-)	118278	118300
TRIM66	AGCGATTGC AGG	52,63	chr11	(+)	8649827	8649849	exon3	NM_014818 (-)	37791	37813

TRIM66	ACAATACAA CGG	36,84	chr11	(+)	8648511	8648533	exon4	NM_014818 (-)	36475	36497
TRIM66	GTATTGTCC AGG	42,11	chr11	(-)	8648495	8648517	exon4	NM_014818 (-)	36459	36481
TRIM66	GGAAGGTG TGG	52,63	chr11	(-)	8648019	8648041	exon5	NM_014818 (-)	35983	36005
UBE2A	TCCGTCGCA TGG	47,37	chrX	(+)	119574937	119574959	exon2, exon2	NM_181762, (+)	471	493
UBE2A	GTGTGGAAC CGG	52,63	chrX	(+)	119574959	119574981	exon2, exon2	NM_001282: (+)	493	515
UBE2A	CGGGTACAG TGG	42,11	chrX	(+)	119583259	119583281			0	0
UBE2A	GAGACAAAT TGG	36,84	chrX	(-)	119581554	119581576	exon4, exon4	NM_001282: (+)	7088	7110
UBE2B	TTGGACTCC AGG	47,37	chr5	(-)	134388356	134388378	exon5	NM_003337 (+)	17181	17203
UBE2B	TTACAAGAG GGG	52,63	chr5	(+)	134374384	134374406	exon2	NM_003337 (+)	3209	3231
UBE2B	TTGGCTGGA CGG	47,37	chr5	(-)	134390240	134390262	exon6	NM_003337 (+)	19065	19087
UBE2B	TTCTCAAAATGG	42,11	chr5	(-)	134376670	134376692	exon3	NM_003337 (+)	5495	5517
UBE2E1	GAATACACC CGG	47,37	chr3	(-)	23887629	23887651	exon3, exon4	NM_182666, (+)	77187	77209
UBE2E1	GAAGTGAGC AGG	42,11	chr3	(-)	23889219	23889241	exon4, exon5	NM_182666, (+)	78777	78799
UBE2E1	AATGGAGAT GGG	36,84	chr3	(+)	23887596	23887618	exon3, exon4	NM_182666, (+)	77154	77176
UBE2E1	TTCATAGATC TGG	36,84	chr3	(-)	23887575	23887597	exon3, exon4	NM_182666, (+)	77133	77155
UBE2I	ACCCGAATG GGG	52,63	chr16	(+)	1320198	1320220	exon5, exon5	NM_003345, (+)	10572	10594
UBE2I	GCACGATGA TGG	47,37	chr16	(+)	1314327	1314349	exon3, exon3	NM_003345, (+)	4701	4723
UBE2I	GTGCTGTGC AGG	52,63	chr16	(+)	1320226	1320248	exon5, exon5	NM_003345, (+)	10600	10622
UBE2I	TGCGCATTG AGG	52,63	chr16	(+)	1314353	1314375	exon3, exon3	NM_003345, (+)	4727	4749
UBR7	ATCGTTGGT AGG	52,63	chr14	(+)	93207367	93207367	exon1	NM_175748 (+)	290	312
UBR7	GTGAAGACT AGG	52,63	chr14	(+)	93214960	93214982	exon5	NM_175748 (+)	7905	7927
UBR7	GTGGGCTTA TGG	52,63	chr14	(+)	93215256	93215278	exon6	NM_175748 (+)	8201	8223
UBR7	ACGCACTGG TGG	47,37	chr14	(-)	93214932	93214954	exon5	NM_175748 (+)	7877	7899
UHRF1	CCATACCTC AGG	52,63	chr19	(+)	4929233	4929255	exon3, exon2	NM_001290 (+)	18867	18889
UHRF1	ATCCAGGTT CGG	57,89	chr19	(+)	4910892	4910914	exon2, exon1	NM_001290 (+)	526	548
UHRF1	TCACAGCAAG CGG	57,89	chr19	(+)	4929378	4929400	exon3, exon2	NM_001290 (+)	19012	19034
UHRF1	ATGTGGGAT GGG	47,37	chr19	(+)	4929444	4929466	exon3, exon2	NM_001290 (+)	19078	19100
UHRF2	CGTGCCCGT TGG	52,63	chr9	(+)	6421104	6421126	exon2	NM_152896 (+)	7954	7976
UHRF2	GCACGTCTT TGG	57,89	chr9	(-)	6413510	6413532	exon1	NM_152896 (+)	360	382
UHRF2	GTCTCAATC TGG	57,89	chr9	(-)	6413522	6413544	exon1	NM_152896 (+)	372	394
UHRF2	TGATTGGAA CGG	52,63	chr9	(-)	6421065	6421087	exon2	NM_152896 (+)	7915	7937
USP22	CTGCTCGTA TGG	52,63	chr17	(+)	21021204	21021226	exon3	NM_015276 (-)	21612	21634
USP22	GCATATTCAC AGG	52,63	chr17	(-)	21028560	21028582	exon2	NM_015276 (-)	28968	28990
USP22	CATGGAAAT AGG	42,11	chr17	(-)	21021140	21021162	exon3	NM_015276 (-)	21548	21570
USP22	CCACAGCAAT TGG	57,89	chr17	(+)	21042695	21042717	exon1	NM_015276 (-)	43103	43125
USP27X	GTGAGATGT CGG	52,63	chrX	(+)	49880678	49880700	exon1	NM_001145 (+)	812	834
USP27X	AGCTTTACG AGG	36,84	chrX	(+)	49880521	49880543	exon1	NM_001145 (+)	655	677
USP27X	AATCTCTCA TGG	47,37	chrX	(-)	49880598	49880620	exon1	NM_001145 (+)	732	754
USP27X	AGGTTGGGAGG	47,37	chrX	(-)	49880433	49880455	exon1	NM_001145 (+)	567	589
USP51	GTCTTCGAG AGG	57,89	chrX	(-)	55488777	55488799	exon2	NM_201286 (-)	4162	4184
USP51	CTCCACGTCA CGG	52,63	chrX	(+)	55488716	55488738	exon2	NM_201286 (-)	4101	4123
USP51	GCAAAGAAATGG	42,11	chrX	(+)	55488912	55488934	exon2	NM_201286 (-)	4297	4319
USP51	CGCGGCTCA TGG	63,16	chrX	(+)	55488740	55488762	exon2	NM_201286 (-)	4125	4147
UTY	AAATCTTGC AGG	45	chrY	(+)	13359779	13359801	exon12, exor	NM_001258: (-)	111401	111423
UTY	CCTTGGCTCC GGG	55	chrY	(+)	13411055	13411077	exon6, exon6	NM_001258: (-)	162677	162699
UTY	GTCTGTTAG AGG	55	chrY	(-)	13479542	13479564	exon1, exon1	NM_001258: (-)	231164	231186
UTY	CGCTGTTGC AGG	60	chrY	(-)	13479611	13479633	exon1, exon1	NM_001258: (-)	231233	231255
WDR5	ATCTGACGA CGG	52,63	chr9	(-)	134141956	134141978	exon4, exon5	NM_052821, (+)	5869	5891
WDR5	GTGAACCTT TGG	36,84	chr9	(-)	134140718	134140740	exon2, exon3	NM_052821, (+)	4631	4653
WDR5	AAATTTGGG GGG	47,37	chr9	(+)	134141528	134141550	exon3, exon4	NM_052821, (+)	5441	5463
WDR5	CATCTGAGG AGG	47,37	chr9	(-)	134141984	134142006	exon4, exon5	NM_052821, (+)	5897	5919
WDR82	TAAGGTGTT CGG	47,37	chr3	(-)	52278298	52278320	exon1	NM_025222 (-)	23877	23899
WDR82	CTGCATGAG AGG	42,11	chr3	(+)	52270748	52270770	exon2	NM_025222 (-)	16327	16349
WDR82	TGCTTCGATT CGG	52,63	chr3	(-)	52278264	52278286	exon1	NM_025222 (-)	23843	23865
WDR82	CGTGCTCTA AGG	57,89	chr3	(-)	52278205	52278227	exon1	NM_025222 (-)	23784	23806
WHSC1	CTTACTTCC TGG	47,37	chr4	(+)	1900898	1900920	exon2, exon4	NM_133335, (+)	8117	8139
WHSC1	GAAATCTCC CGG	57,89	chr4	(+)	1900730	1900752	exon2, exon4	NM_133335, (+)	7949	7971
WHSC1	CAGCTTGTC AGG	52,63	chr4	(-)	1900869	1900891	exon2, exon4	NM_133335, (+)	8088	8110
WHSC1	GGGGTCATC CGG	47,37	chr4	(+)	1900832	1900854	exon2, exon4	NM_133335, (+)	8051	8073
WHSC1L1	GGATACCCA AGG	47,37	chr8	(+)	38347951	38347973	exon2, exon2	NM_023034, (-)	31535	31557
WHSC1L1	GAAGATCTT GGG	42,11	chr8	(+)	38347973	38347995	exon2, exon2	NM_023034, (-)	31557	31579
WHSC1L1	TATCTAATC TGG	47,37	chr8	(-)	38347876	38347898	exon2, exon2	NM_023034, (-)	31460	31482
WHSC1L1	TTGGCGGAC AGG	47,37	chr8	(+)	38348092	38348114	exon2, exon2	NM_023034, (-)	31676	31698
YY1	ACCATCGAG GGG	55	chr14	(+)	100239347	100239369	[exon1]	[NM_003403 (+)]	583	605
YY1	GACCATCGA TGG	60	chr14	(+)	100239346	100239368	[exon1]	[NM_003403 (+)]	582	604
YY1	GGAGACCAT TGG	60	chr14	(+)	100239343	100239365	[exon1]	[NM_003403 (+)]	579	601
ZCWPW1	TTGTAGCCCA AGG	52,63	chr7	(-)	100419797	100419819	exon4, exon4	NM_001258 (-)	18926	18948
ZCWPW1	GGGACTTCT TGG	47,37	chr7	(+)	100419126	100419148	exon5, exon5	NM_001258 (-)	18255	18277
ZCWPW1	AGTTAGGGC AGG	42,11	chr7	(+)	100419806	100419828	exon4, exon4	NM_001258 (-)	18935	18957
ZCWPW1	GGTGGGGCG TGG	52,63	chr7	(+)	100419847	100419869	exon4, exon4	NM_001258 (-)	18976	18998
ZCWPW2	GGCATCCCC TGG	50	chr3	(+)	28435205	28435227	exon4	NM_001040 (+)	86057	86079
ZCWPW2	TTTGCCCTG GGG	40	chr3	(+)	28435124	28435146	exon4	NM_001040 (+)	85976	85998
ZCWPW2	AGGTTGATC TGG	40	chr3	(+)	28413220	28413242	exon3	NM_001040 (+)	64072	64094
ZCWPW2	TTGCTGCACI AGG	45	chr3	(+)	28492151	28492173	exon6	NM_001040 (+)	143003	143025
ZGPAT	AGAGACCGT AGG	47,37	chr20	(+)	63708883	63708905	exon2, exon2	NM_001195 (+)	1442	1464
ZGPAT	TTTCGGGGA AGG	57,89	chr20	(+)	63708823	63708845	exon2, exon2	NM_001195 (+)	1382	1404
ZGPAT	GGTACTCAG CGG	52,63	chr20	(-)	63708796	63708818	exon2, exon2	NM_001195 (+)	1355	1377
ZGPAT	CAGCCTGCT AGG	57,89	chr20	(-)	63708661	63708683	exon2, exon2	NM_001195 (+)	1220	1242
ZMYND11	CTGGTTCCG TGG	42,11	chr10	(-)	180074	180096	exon2, exon1	NM_006624, (+)	81	103
ZMYND11	GCTGACGGC GGG	57,89	chr10	(-)	209916	209938	exon3, exon2	NM_006624, (+)	29923	29945
ZMYND11	ATTCATTGT AGG	47,37	chr10	(+)	236888	236910	exon5, exon4	NM_006624, (+)	56895	56917
ZMYND11	ACTCTAACAC AGG	52,63	chr10	(+)	209974	209996	exon3, exon2	NM_006624, (+)	29981	30003
ZMYND8	GTTGATGTT TGG	52,63	chr20	(-)	47298868	47298890	exon4, exon4	NM_012408, (-)	89655	89677
ZMYND8	TTGATGTGT TGG	57,89	chr20	(+)	47310115	47310137	exon3, exon3	NM_012408, (-)	100902	100924
ZMYND8	GACTGACAT GGG	52,63	chr20	(-)	47298753	47298775	exon4, exon4	NM_012408, (-)	89540	89562