Supplementary Table 2. PCR primers used for examination of homozygou deletion

Chromosomal location	Gene	Exon	Primer sequence (Forward)	Primer sequence (Reverse)	Product size	Loction of genomic fragments amplified	
1p36	PRDM2/RIZ	ex2	CTGAAGACAAGTGAGCCAGA	TAGCATATAGAAGGCTCAGC	224bp	13972216	13972439
1p34	TIE1	ex9	ACCACAGCTGAGTTCGAGGT	TCTAGAGCCTACTCTGCTCA	170bp	43547676	43547845
2q22	LRP1B	ex1	GCGTGATGTAAGATCAGACG	TCAATGAGTCCAGCCAGTCA	163bp	142604908	142605070
		ex4	GCCAACAGCTGAATTGTCAG	GCACATGGTAGGTGCTCAAA	196bp	141728470	141728665
		ex8	GCACTGGCACTAGACCTAGT	ATGACTCATTGCAGCTCGAC	226bp	141535981	141536206
2q24	GALNT13	ex9	GCTTCAGTTGCTTCATCTCA	TGATGACATGACCAGTGCCA	173bp	154866104	154866276
2q24	KCNH7	ex1	GGCATGTGGCACCACAAAAT	GCCTCTTAAGTTGACAGAGC	176bp	163403083	163403258
	FIGN	ex2	GACATGGACTTGCATTCCTG	TCATGAGCAACTGCTTGCCA	385bp	164299555	164299939
	GRB14	ex2	GGTACATGTTCGCCTTAGCA	GGTCTGCTGACAACACAGAT	197bp	165184475	165184671
	COBLL1	ex2	ACTGATGTCTCTTCAGCTGC	CCACTGAGAGTTCAACGTCT	97bp	165308486	165308582
	SLC38A11	ex2	CTGTCCTATGTGCAACTTAC	TGCACAGTTGAAGTTGCAGA	262bp	165517418	165517679
	SCN3A	ex2	CATAGTAGAGTGGCTTACTG	TCCTGATACAGCTGTCCTTG	212bp	165751220	165751431
	SCN2A	ex2	GCAATCTCTCGATTCAGTGC	TGTAGCTCAATAACTTGGTC	154bp	165861800	165861953
	FAM130A2	ex2	GCTATAGCTCAGCTCATGTA	TGGATGGATTGACACTGTCC	265bp	166159687	166159951
	GALNT3	ex2	ATTGAGCCATGCCTGTAGGA	TAGGTGAGCCATTCTGACAT	180bp	166335445	166335624
	TTC21B	ex2	TTCAGAGCACCAGAATTCCT	CCTGAAGACTGGATCACTTC	149bp	166514382	166514530
	SCN1A	ex2	CATCTTCCGGTTCAGTGCCA	AGTGCTTACAGATCATGTAC	144bp	166623272	166623415
2q32	GULP1	ex2	CCATTACCTAGGTATCAGTA	TATCATACAGTTGCCATCAG	269bp	188956537	188956805
3p21	PBRM1	ex26	GATGCACCATAAGACCTTTC	TGAACAGGATGTAGCCACTC	112bp	52570943	52571054
3p14	FHIT	ex5	CAGAATGCATCTTGGTGAAC	CTGGTTAGGCTCAGAAGACT	334bp	60497576	6049790
4q31	MAML3	ex4	AGCAGCATCCAGTTGGACTT	GCTGATCAATGAGCATCTGC	159bp	140871112	140871270
5q11	PDE4D	ex LF-3	TTGTTGTAGGTCTTGGCCAGT	CACAGACAACATGGCAACAA	200bp	58516655	58516854
5q14	CETN3	ex2	AGCTGATGTACTGAAGATTC	CCTAACAGCTGCTGATTACA	120bp	89737218	89737337
	LOC153364	ex2	GCTCACTGTTATGCACATGC	TTGCAAGAGATCGCATGGCA	317bp	89792781	89793097
	POLR3G	ex2	GTGAGCAGTTCAACAGTCAG	AGGTATAAGCAGCACGTCCT	249bp	89816932	89817180
	LYSMD3	ex2	CCTGAATGTACGATGCATGC	CACTTGACTGAACTCCTGGA	145bp	89856808	89856952
	GPR98	ex2	GAGCCAGCAAATGTTACTGC	GGAGCACTCTATAAACCTGT	206bp	89946563	89946768
	ARRDC3	ex2	ACTCGCTACCTCATTCGAAG	ACAACTGCATAGTTTAGGTG	228bp	90708111	90708338
	C5orf21	ex2	CCTGATACCCTGGAAGGATT	CACCATGCAAGGATGTCACT	218bp	93414409	93414626
	FLJ25680	ex1	AGCACCAGTGTGCTTTCACC	AATCTGAGGAGGCCCAGAGT	123bp	93102043	93102165
	KIAA0825	ex2	GCTGCAGTCTATGGACTATC	TCCTGAAGAGTTGTCAGCAG	296bp	93943961	93944256
	BRCTD1	ex2	GGTGTAAGAGCTCTCATTTG	AACACTGCCAGAGCTCTGTA	255bp	94047925	94048149
	MCTP1	ex2	GGAATGTACCAGCTGGACAT	TAACTCAGGCAATCACGTGG	147bp	94378744	94378890
5q31	CTNNA1	ex4	TGATTTGATGAAGGCTGCTG	GCCAGTAGCAATCTTCCTGTG	223bp	138173627	138173849
6q24	UTRN	ex25	TTCCACAGCGTTAGCATGAG	CAAGCTCTTCTGGTGACTTG	309bp	144842480	144842788
7q35	CNTNAP2	ex4	CAAGCCCTACCATTGGATGA	GAAGGTAGTTTATTGTCAGAGA	366bp	146371827	146372192
8p23	CSMD1	ex4	TATAAGTGGCTCTCCATGGA	CTGACGATGCAGGTCAGGAT	211bp	3876882	3877092
8p21	HMBOX1	ex4	TCGGCGTACTGGAATGACTA	TGTATGACCTCTGACCCATG	344bp	28883554	28883897
8q21	WWP1	ex21	CAGTGGCTACAGTACTTCGA	TACCACCTTGACATCAGGAC	180bp	87533989	87534168
	FAM82B	ex5	TTACAGGCGTGAGCCACTGC	ACATCACTAAGGCAGATTGC	241bp	87566281	87566521
8q24	TG	ex43	CTGGAGACCATCATTGCTGA	ATGAGCAGATCGACCTCTAC	334bp	134177417	134177750
	SLA	ex1	GACTGGATATTCCTGTGCTG	TCCAAGCACAGGCATCTCCA	218bp	134184210	134184427
9p24	C9orf66	ex1	CTCAGACTTGCCTCAAAGGA	AGAATCTCGGTGCTCCTGGA	186bp	205242	205427
	DOCK8	ex3	CCAGAAAACTGGGTGAGAAC	GTTCAGATTGAAGGCATCTC	311bp	276413	276723
	KANK1	ex6	TTTCTTCTTGTGACCAATCG	AGCTGGCCTTGACAATGAAC	203bp	724705	724907
	DMRT1	ex2	TTTGAGCACCTACTGTCTGG	GTCATGAGGCACGGGTTACT	329bp	836756	837084
	DMRT3	ex2	TCCAGGAAGCCACTCTGATT	CCGTCTCCAAGTCGTTCTTC	247bp	979822	980068
	DMRT2	ex2	GCCATAGGTCTGCGTATATC	TCTGACTTGCCTCTGGTACA	347bp	1043444	1043790
9p23	PTPRD	ex B1	GGGCCTGTGTGGAATAGAAA	ATTGGGCATTGAAAAGCATC	171bp	10602327	10602497
		ex B7	GGTCTCAGGGTGGTGAACTT	GGACATGATCAAAAAGCGGTA	115bp	9564668	9564782
	TYRP1	ex4	CCCTCAGACACCGTTGATAT	GTCATCCGTGCAGATATCAC	226bp	12688309	12688534
	C9orf150	ex1	TAGTACCAGATGGGCAGTCA	GACTCCTCCGACACTAAGAT	2334bp	12765263	12765496
9p22	CER1	ex2	ATGCACTTGCCACTGAACTG	CAGCATGTAGGATGTGTCCA	118bp	14710126	14710243
	FREM1	ex2	TTGTCAGGAGTGATCAGCGA	CTTCAGGTCATCTCCTGACA	370bp	14858832	14859201
9p22	BNC2	ex1	CCGCTAAGAGGAGACCAAGA	TCATTTCTGAGGAAGTCTAG	110bp	16860591	16860700
	CNTLN	ex2	GATCTCACACAAGTGGTCAG	GGCATACCTGTACTTGGTGA	221bp	17133340	17133560
	SH3GL2	ex2	CCAAGCTAGATGATGACTTC	GTATTCTCAGAGACCAGTGG	147bp	17737098	17737244
9p21	ADAMTSL1	ex2	ATCCGAGAATCTGATTGCGC	TGCGTGAGCATTCACTCCAT	217bp	18494689	18494905
	SLC24A2	ex2	CTTAACTCATCCCAGGAGCA	AGGTACAGACAAAGCCACTG	201bp	19612231	19612431
	MLLT3	ex2	AATGTCAGGCGCAACGTTCA	TATGTTACTGTGCTCCGGAC	197bp	20610714	20610910
	hsa-mir491	ex1	ACCAGCAGAAGCCATCTTGA	AGGACCTGCAGGATATGACT	191bp	20706017	20706207
	KIAA1797	ex3	GTCAATCTGAACCATGAAGC	CAAGATTGCAATGTGAACTG	218bp	20684383	20684600
	PTPLAD2	ex2	TTCTCAGGTTGGCCAGTACA	AGTGGCCACAGAACTGGATT	150bp	21019342	21019491
	IFNB1	ex1	TAGTAGGCGACACTGTTCGT	CTGGAGCATCTCATAGATGG	284bp	21067614	21067897
	IFNW1	ex1	TGTGATCTGCCTCAGAACCA	TGCAGTTGCTGATGAAGTCC	281bp	21131220	21131500
	IFNA21	ex1	TCCATGAGATGATCCAGCAG	TGGAGTCCACATTCATCAGG	180bp	21156194	21156373
	IFNA4	ex1	CCTTGATACTCCTGGCACAA	CAGGATGGAGTCCTCATTCA	314bp	21177108	21177421
	IFNA14	ex2	ATGAGGACTTCATCCTGGCT	TGCACAGGTAAACACGATGC	325bp	21191434	21191758
	IFNA7	ex1	ACCTCAGGTAGCCTAGTGAT	CATGCTTCCAGGTCATTCAG	400bp	21191800	21192199
	IFNA10	ex1	CAGCAACTGAATGACCTGGA	ACTAGTGCCTGCACAGGTAT	401bp	21196357	21196757
	IFNA16	ex1	CCATGAGATGATCCAGCAGA	CTAGGTCATTCAGTTGCTGG	119bp	21206947	21207065
	IFNA17	ex1	CCTGAAGGACAGACATGACT	TGGAGTCCTCATTCATCAGG	263bp	21217755	21218017
	IFNA5	ex1	GACTCATCTGCTACTTGGGA	TCACAGTCAGGATAGAGTCC	148bp	21294826	21294973
	KLHL9	ex1	TCAGATTTGAGGTCCACAGC	CACCGAACTGTGAGTATTGC	319bp	21324754	21325072
	IFNA6	ex1	TCAGCTGCAAGTCAAGCTGC	CTGCTGAATCACCTCATGGA	218bp	21340629	21340846
	IFNA13	ex1	ATGAGCTGATCCAGCAGATC	AGTCATTCAGCTGCTGGTAG	114bp	21357652	21357765
	IFNA2	ex1	CAGTCTAGCAGCATCTGCAA	ATCTGTGCCAGGAGCATCAA	159bp	21375198	21375356
	IFNA8	ex1	TGATCTGCCTCAGACTCACA	AGCTGCTGGTCAAGTTCGAT	276bp	21399247	21399522
	IFNA1	ex1	AGAGTCACCCATCTCAGCAA	ATCTGCTGGATCAGCTCATG	274bp	21430493	21430766
	IFNE1	ex1	TCCATGAGATGCTTCAGCAG	TAAGCTCTTGCTTCATGTCG	360bp	21471093	21471452
	hsa-mir31	ex1	GCTGGCATAGCTGTTGAACT	ATACACGAAGGACTGGCATG	101bp	21502068	21502168
	MTAP	ex7	CTACCATACCTCAGATAGGG	GAGTCTACAGACATGCCTGA	97bp	21849369	21849465
	CDKN2A/p16	ex2	ACAAGCTTCCTTTCCGTCATGCCG	TGAGCTTTGGAAGCTCTCAG	421bp	21960851	21961271
	CDKN2A/p14ARF	ex1b	TCAGTAGCATCAGCACGAGG	TGCTCACCTCTGGTGCCAAAG	217bp	21984180	21984396
	CDKN2B/p15	ex2	TCTTTAAATGGCTCCACCTGCCTT	TCCCCGTTGGCAGCCTTCATCGAATTA	442bp	21995894	21996335
	DMRTA1	ex2	CCTAGAGTAGGTATCAGTCC	TCTGAAGTACAGTCTGCCAC	207bp	22441683	22441889
	ELAVL2	ex6	CCATGTACTGACCCTTGTAG	CCATAAGCCATATTGAGCAG	252bp	23683455	23683706
	TUSC1	ex1	GCTTTGTCTCAGAACCGATC	TATCCTCAGCTGAGTTGTGC	163bp	25668607	25668769
	C9orf82	ex2	TGGACCTGACTGTGTCATTG	ACATCAGGAAGCATCTTCTG	118bp	26877318	26877435
	PLAA	ex2	ATGTCCTAGGCTAAGTCAGG	AAGTGGCATTGGACTGTCCA	224bp	26925039	26925262
	IFT74	ex2	AGCCTTGTAGTGGTACACAG	GCAGTTGCCACTCGAATATT	271bp	26951814	26952084
	LRRC19	ex2	GCAACATGAAAGTCACAGGC	GTAGGTCAGATTTTCTTTGC	192bp	26989506	26989697
	TEK	ex2	CGAACCATGAAGATGCGTCA	ACATTCAGGTAGTGCATGCC	131bp	27148116	27148246
	C9orf11	ex2	CATTGCCTAATGTGCTACCT	GACACTTAAGTGAAACCAGG	192bp	27286545	27286736
	MOBKL2B	ex2	AGCTACAGGCTGTAAGACTG	CACAGATGGTGCCATAGATG	366bp	27445311	27445676
	IFNK	ex2	TTGCAGCCAGACTACCTAGA	ATGCTGTTAGTGGCATGAGC	251bp	27515886	27516136
	C9orf72	ex2	GAATGCAGTGATGTCGACTC	CTCCATCACTGAGAAGTACC	182bp	27556947	27557128
	LINGO2	ex2	AGTACCTCGGAAGTCCCAGA	TGCAGGCAGCTCATGATACA	245bp	28660234	28660478
9q21	PSAT1	ex2	TAAGTTGCATAATCGCTGGC	TGCCAACTCCTTTGTAGTCT	230bp	80105157	80105386
	TLE4	ex2	GATGCAGCGGCATTATGTCA	AACTTCAACTGCACTGGCAG	145bp	81379650	81379794
9q33	DBC1	ex3	GCAGATGATTGGAAGCTCCA	ATCGATGAACTGCTGAGTGG	300bp	121051111	121051410
10p11	PARD3	ex2	AGGAAGCGCCATATTGATCC	ATGGGCAGGAAGTTATCACG	365bp	35025424	35143757
		ex5	TCACGGACACCAAGAAGTCA	ATTGGCCTCCAGGTACTGAT	265bp	34677082	34798977
10p12	C10orf67	ex2	TAGCTCCAGATCACAAGAGC	CACTGGAATCAGTTTGAGTG	231bp	23662047	23662277
10p12	GPR158	ex4	CTTACCTACCTAAGAGGTGC	GTAGGCAGACATAGGCTTCT	122bp	25741132	25741253
11q14	DLG2	ex3	TTAACAGAAATAATCTGTCTCAGA	TTCAGCCAATTAAGTTCTACCACA	182bp	83639869	83640050
12p12	RERG	ex1	AACTCGCAAACGCAACCTGA	GTCACTTGCTTTCAGGCTAG	371bp	15265144	15265514
	PTPRO	ex2	ATGTCGTGACCATCTCCAGC	TGAGACGGCTATGAACGTAG	104bp	15593317	15593420
	EPS8	ex2	TGGCTACGGATCATCACCTA	AGCAAGCAGAGTTCATGGCT	262bp	15725242	15725503
	STRAP	ex2	CACTGAATAAGGATGCCACC	TGTATGGCAGCCAGTGAGTC	165bp	15927826	15927990
	DERA	ex2	AAGTGAATCACCCGGCAGTT	AGTCATGGACAGCTGCAATC	199bp	16001161	16001359
	MGST1	ex2	TTGACCTCACCCAGGTAATG	GCCAAACGATGGCATACTTC	264bp	16398458	16398721
	LMO3	ex2	TACTGGCATGAAGACTGCCT	CATCCAGTCATCACTGGTGT	150bp	16644819	16644968
	RERGL	ex2	CATGCTACCAATAGGGTCAC	CAGTCTGGCTTCAAGGTACT	199bp	18133508	18133706
	PIK3C2G	ex2	TTCTAGCCAAGTCAGTCTGG	CTTGATGCCAGGAGAGTTCA	206bp	18326378	18326583
	PLCZ1	ex2	AGTGCAGGTACCACATCTTG	TTCATGACCTGTAGAGCCGT	240bp	18781576	18781815
	CAPZA3	ex1	ATGACACTTAGCGTGCTGAG	CATCGATGCAGAGTGGTACA	199bp	18782470	18782668
	PLEKHA5	ex3	GTGCCAGAACATAGTTCCTC	GCTGAGGAGTAATCACAGCA	392bp	19176322	19176713
	AEBP2	ex2	GACAGCACAATTTCCAGTGG	GCTAGAGTTGAAGCAAGCCT	129bp	19506736	19506864
12p12	SOX5	ex2	GGTAGCCATGGTGACAAGCA	ACAAGTCTCTTGCGTCAGCA	148bp	23940030	23940177
	BCAT1	ex10	TGCTAGCACTCAGAGTCAGT	TTTGCTCAAGATGCGGCTTG	207bp	24874039	24874245
12p11	MLSTD1	ex2	ACGATGCTCTCACTGTCTGA	TGATGAGAATGGACTTGCCG	215bp	29314481	29314695
	ERGIC2	ex2	TAGAGACTTCAGCCAGTGGA	TTACAGCCAACAGAGTGGCA	184bp	29415571	29415754
	OVCH1	ex2	GTCTGCAGCTAAGTGCTATC	CATGGATGTCCAGTCACTGT	238bp	29540760	29540997
	TMTC1	ex2	TTGCCTTCTCAGTGAGACCA	CAGGTGTACATCAGCACAAG	354bp	29812180	29812533
12q12	ADAMTS20	ex3	CAGTTGATGGCTCTTAGTGA	CAATACTTCAGAGTCTGCAG	280bp	42212117	42212396
	PUS7L	ex2	TACACAGTGCCATTAGGCAG	TCGGATTACCAGCACTGCAA	294bp	42434499	42434792
	IRAK4	ex2	ATATGTGCGCTGCCTCAATG	CTGCCACATTAGACAGTACT	221bp	42448208	42448428
	TWF1	ex2	AGGATGCTACATGCTCCAGA	TGAGGAATCCAAGTTACCGT	332bp	42484426	42484757
	TMEM117	ex2	CTACGAACTGGGAGTTCTGA	GCCAGCTATTAGTCCTGTGA	272bp	42524699	42524970
	NELL2	ex2	CCCTACAGATTGACGTCTTA	AGTACTGTCATCCATGAGGC	214bp	43555166	43555379
	DBX2	ex2	ATTCTACTCGGCGTGCTGCG	CTGCTCACAATTGCTCAGTG	254bp	43715877	43716130
	PLEKHA9	ex3	ACTATCTGAGCAGTTGGCAG	AGGTCACAGCAGAGTCTTAG	349bp	43854387	43854735
	TMEM16F	ex2	TGGCATCGTCTGGTAGATCC	TGCTGACTTTCCAGTGATCC	259bp	43981863	43982121
13q14	RB1	ex27	ATGAGGATCTCAGGACCTTG	CAAGTGGCTTAGGAATCACC	176bp	47952205	47952380
	RCBTB2	ex2	CAGGACTGAGTCCATATGGA	TATCGGTGACCAATAGGTGC	139bp	47993953	47994091
	CYSLTR2	ex1	ATGTCACCAGCATCAGGAGT	CATGGTCTGCAGCTTAGCAA	161bp	48179397	48179557
	FNDC3A	ex2	CACTACTGGATACAACTCAGA	AACTCAGGGACTAGCACACT	363bp	48478344	48478706
13q14	TDRD3	ex13	GTGAATTCCAGGGCAGCTTA	CAGAGTTTGATCGTAGGTGC	146bp	60039544	60039689
	PCDH20	ex2	ATAGAGCATCCTGCTGTGGA	GTCACTGATGCCAATGGTGA	249bp	60885297	60885545
13q14	IPO5	ex15-16	GAGTAAGGTATGCAGCCTGT	AGTTAATGAGGGCAGCAGCT	255bp	97452946	97453200
	FARP1	ex2	TTGTGAGTGAACCGATGCCT	GTGTCATCCAGCATCTGGAT	318bp	97663329	97663646
	RNF113B	ex1	ACTACAAGGAGACTGGCTTC	AGATACAGTAGCGACCCTCT	120bp	97626780	97626899
	STK24	ex2	CTTATGTCCTGAACCTGCAG	CTGAGTCCGATTGTCAATGC	271bp	97969630	97969900
	SLC15A1	ex2	CAGAGGCTCTGAGTTTAGAC	CACTGGTTCCAGATGTACTG	203bp	98176990	98177192
	DOCK9	ex2	ATTGAGCCACTCGACTATGA	CACGTGGTTCTACGGATAGA	139bp	98405653	98405791
	GPR18	ex2	ATTACAAGGGGATGCCACAG	TGGTTCACAGAAAGCAGCAC	379bp	98706755	98707133
	EBI2	ex2	GTCTTCATCATTGGGCTCGT	ACACAAGGCATCTCCGATTC	192bp	98746089	98746280
17p12	HS3ST3A1	ex2	CAAGTTCTACCAGATGACCG	GCTTATACTTTATGACTGGG	316bp	13339969	13340284
17q11	TAOK1	ex2	TATGCCAACGTGACTTCATTC	GTCACTGACATCAAGCCACT	250bp	24802604	24802853
18p11	ARHGAP28	ex16	CATTGCTTGGATCCAGATGC	ACTGAGAATGCTGTAGGAAC	201bp	6902064	6902264
	LAMA1	ex2	TCACATGCCATAGATGGCAC	AGGGACTCCTTCTGTATACC	256bp	7069817	7070072
	PTPRM	ex2	GATGAGCCGTATAGCACATG	GCATCCATGGATCAGAAGTC	103bp	7764161	7764263
	RAB12	ex1	AGTTGCAGGTCATCATTATCG	AAAGACTCCCAGGCTCGAT	200bp	8599850	8600049
18p12	FHOD3	ex2	ACAGGCTCTTTCTCTTGCAG	GAAGGTCAAAGCCATGGTAG	232bp	32189480	32189711
18q21	MRO	ex4	CCAGGTCTCTTGGAAACTGA	ATAGGCCATGGTTCCCAAGT	136bp	46587087	46587222
	ME2	ex2	CGATGGACATGAAGGCCTAT	GTTCAGCATAAGTGGCTTGC	168bp	46676114	46676281
	ELAC1	ex2	GTCTATGGATGTGACATTCC	ATGCAACCATCAGGGCTGTT	259bp	46754775	46755033
	SMAD4	ex3	GCTTCAGAAATTGGAGACAT	CAATGCTCAGACAGGCATCA	107bp	46827366	46827472
	MEX3C	ex2	GCATATTGCCATGCGTACAG	AACTGCTAGGTCTTCTGAGC	316bp	46957217	46957532
19p13	KEAP1	ex2	ACCTTCAGCTACACCCTGGA	ATCCTGGTACTTGACCTGCA	111bp	10471449	10471559
19q13	MZF1	ex1	TACATCTGCCGGAAAGCATC	CTACGTCTCCCAGGATGCTC	424bp	63776302	63776725
	MGC2752	ex1	TAAAGCAGACGGCTCGCACT	GATCAGCACCTGCGCAGTAT	254bp	63778736	63778990
21q11	LIPI	ex2	TAAACTGTGCTGAGCCACTG	GCACACTCAAACTCACAGCA	258bp	14483243	14483500
	RBM11	ex3	GTGATTCCTCTATGCAGACA	ACAGTGCTGGGACATCTTGT	349bp	14518507	14518855
	STCH	ex2	CGGCTATTTGGCACAACAGT	TTGAATCTGCCAGCTCTACG	218bp	14675490	14675707
	SAMSN1	ex2	ACAGCCTTTGGATATTCCAG	GAATTATTCCGAAAACGATC	194bp	14815370	14815563
	NRIP1	ex4	CACTGTGGTCAGACTGCATT	TGTCAACGGCAGTACCTGAT	309bp	15262270	15262578
	USP25	ex2	CCAGATACTACAGCAAGCCT	CATGGACATCAGACTGCTGA	223bp	16057134	16057356
	C21orf34	ex2	CCTGAATGTAGGAGTCTGGA	TCCCAGGCTTACATGGCATA	384bp	16525131	16525514
	hsa-mir-99a	ex1	CGTAGATCCGATCTTGTGGT	AAGCCTGCCTTGTAAGACAG	217bp	16833296	16833512
	hsa-let-7c	ex1	CTTAGGTGTATGGCTGCCAT	GCCCAAATCAATGATCCAAG	266bp	16833940	16834205
	hsa-mir-125b-2	ex1	CCTGAGACCCTAACTTGTGA	GGTGGTAACTGCAGACAATC	113bp	16884446	16884558
	CXADR	ex2	GACATCGAGTGGCTGATATC	CAGATAGTTGCACAGACAGC	102bp	17841332	17841433
	BTG3	ex2	GGAGGTATATCTTACAGAGC	AACACCTGTAGGCATGGTCT	357bp	17903063	17903419
	C21orf91	ex2	AAGTGCAGGTGGCATCTCTA	AGCCTCTGGACTAGAGATTG	178bp	18090810	18090987
	CHODL	ex2	ACTTCCATGAACTGTCCAGC	TCAGACCACTGGTAGAGATC	238bp	18550748	18550985
	PRSS7	ex2	TGAGCCCCATTACTATGGAG	ATGCTGTGCCACTTTGCTTA	343bp	18691922	18692264
21q11	ADAMTS1	ex2	GACCAGTCGATGGCAGAATT	GTTCATCGTGGATGACCAAG	147bp	27136660	27136807
	ADAMTS5	ex2	CAGAGCAGTTCAGAAGAGTC	CTGCGCTCTGGAGAACATAT	249bp	27248988	27249236