

Exome sequencing identifies recurrent *BCOR* alterations and the absence of *KLF2*, *TNFAIP3* and *MYD88* mutations in splenic diffuse red pulp small B-cell lymphoma

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SUPPLEMENTAL DATA

Supplemental Figure 1 – Flowchart of the sequencing study

Supplemental Table 1 – Somatic mutations from whole-exome sequencing

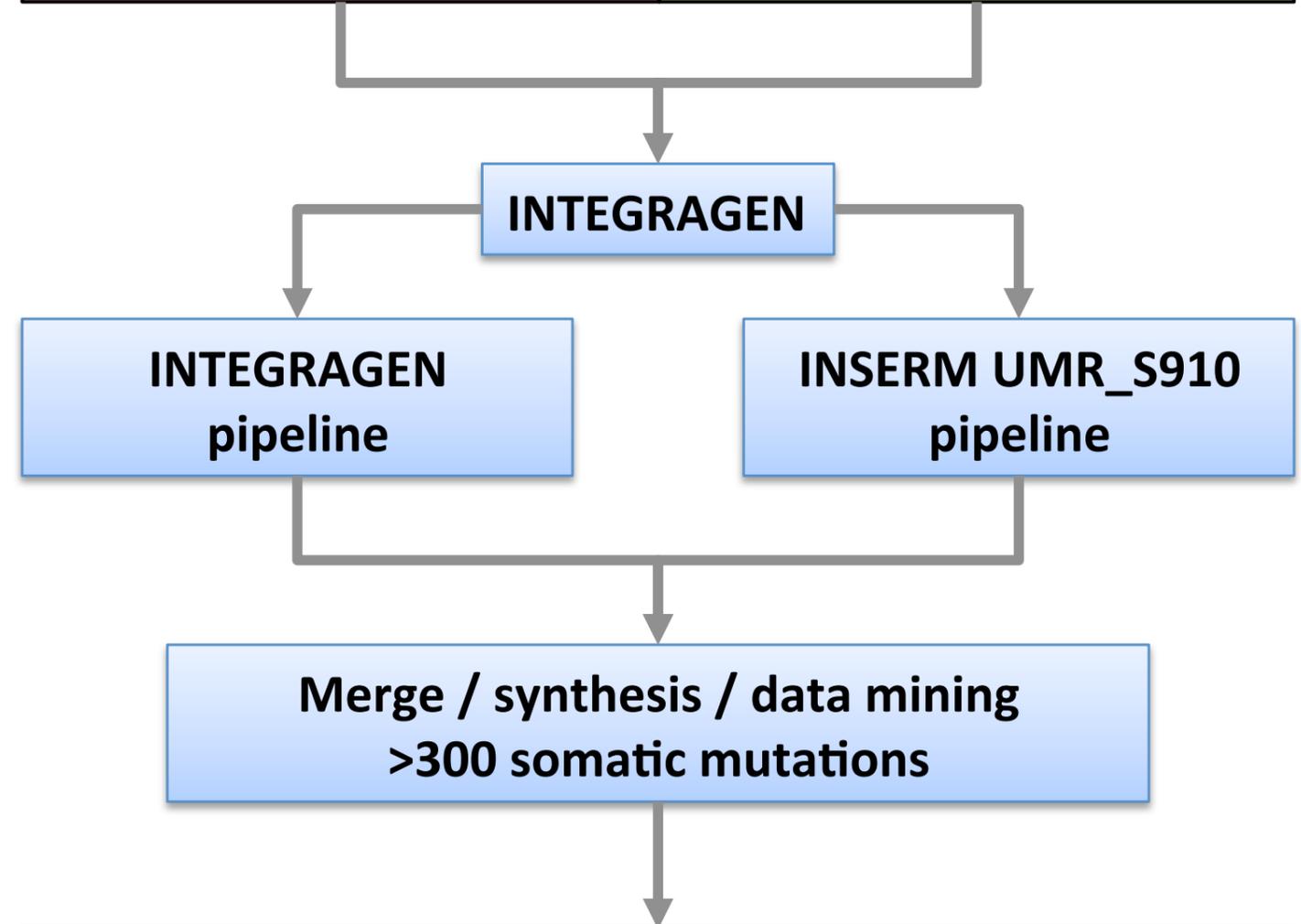
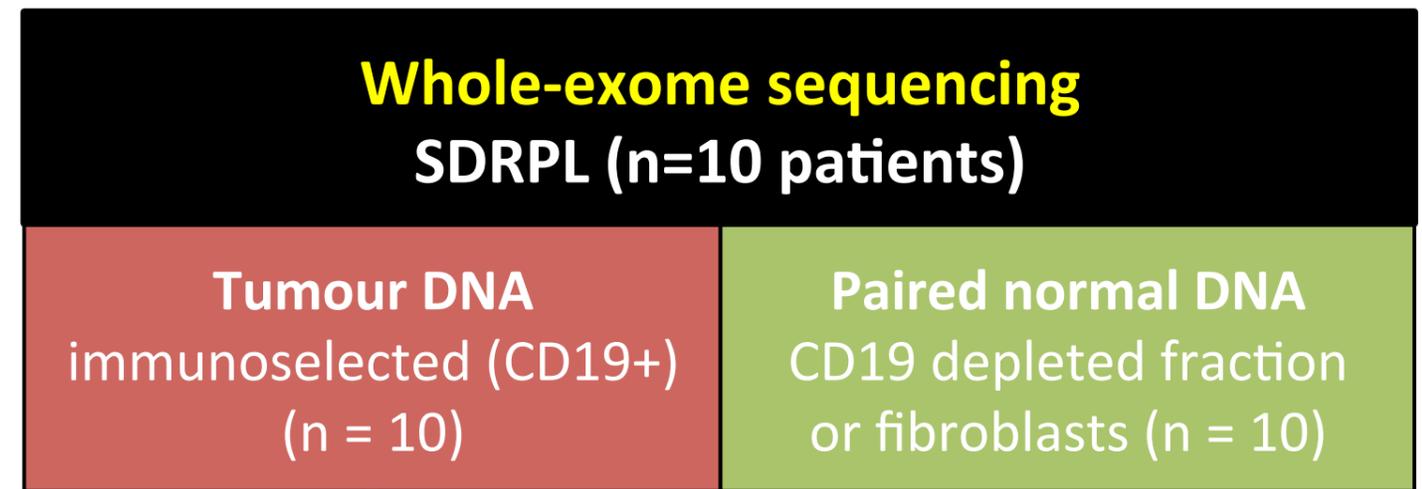
Supplemental Table 2 – List of the targeted-genes sequenced, exon positions and coverage

Supplemental Table 3 – Recurrently mutated genes from whole-exome and targeted sequencing.

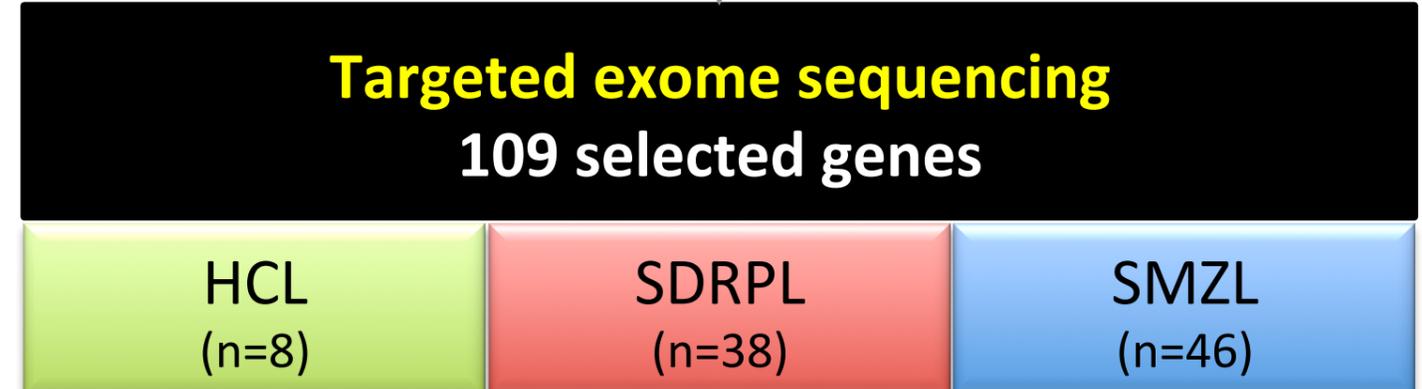
The orange coloured boxes indicate a case investigated by whole-exome sequencing. VL: villous lymphoma cell (SDRPL); MZ: marginal zone cell (SMZL); HC: hairy cell (HCL); PB: peripheral blood; B+: CD19+ immunoselected sample. Distribution of mutations between HCL, SDRPL and SMZL cases is shown in Figure 1.

WORKFLOW

Discovery cohort



Validation & comparison cohorts



WES sample	Gene name	Name detail	Chr	gDNA position	Localisation	CNV	Reference	Somatic mutation	Type mut	Effect	VAF	refseq	CDNA	Protein	dbSNP ref.	SIFT prediction	Polyphen-2 score prediction
9	ABCRC8	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	chr11	17,464,823	Exon 9		C	T	SNV	missense	0.110	NM_001287174	C1369G>A	p.Gly457Arg		Deleterious (score: 0.01)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
9	ADAM12	ADAM metalloproteinase domain 12	chr10	127,789,771	Exon 14		A	T	SNV	missense	0.481	NM_003474	C790G>A	p.Val264Met		Deleterious (score: 0.01)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
1	ADAMTS17	ADAM metalloproteinase with thrombospondin type 1 motif, 17	chr15	100,649,297	Exon 14		G	A	SNV	missense	0.183	NM_1339057	C1913C>T	p.Ser638Leu		Deleterious (score: 0.01)	benign with a score of 0.032 (sensitivity: 0.95; specificity: 0.82)
1	ADAMTS18	ADAM metalloproteinase with thrombospondin type 1 motif, 18	chr16	77,369,744	Exon 12		C	T	SNV	missense	0.552	NM_1993955	C1768G>A	p.Gly659Ser		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
15	ADAMTS8	ADAM metalloproteinase thrombospondin 8	chr11	130,275,559	Exon 8		T	S	SNV	missense	0.508	NM_007037	C2564G>A	p.Arg655Gln		Deleterious (score: 0)	probably damaging with a score of 0.987 (sensitivity: 0.73; specificity: 0.96)
1	ADAMTS11	ADAMTS-like 1	chr9	18,622,304	Exon 5		G	A	SNV	missense	0.224	NM_052866	C538G>A	p.Gly80Arg		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
12	AOC6	adenylate cyclase 6	chr12	49,165,328	Exon 18		G	A	SNV	missense	0.395	NM_020983	C3016C>T	p.Arg1006Trp		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
13	ADM2	adrenomedullin 2	chr22	50,921,279	Exon 2	+12	A	A	SNV	missense	0.522	NM_024866	C394G>A	p.Gly132Ser		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	AEBP2	AE binding protein 2	chr12	19,592,908	Exon 1		A	G	SNV	missense	0.304	NM_027540	C275A>G	p.Gln294Arg		Not scored	possibly damaging with a score of 0.895 (sensitivity: 0.82; specificity: 0.94)
15	ALIC	Albinocase	chr2	3,749,964	Exon 12		C	G	SNV	missense	0.451	NM_018436	C987C>G	p.Asn129Iys		Tolerated (score: 0.16)	possibly damaging with a score of 0.459 (sensitivity: 0.99; specificity: 0.80)
3	AMDH1	amidohydrolase domain containing 1	chr12	96,360,197	Exon 8		C	T	DEL	missense (1 D) Frameshift del.	0.480	NM_152435	C1104del	p.Arg369Met*34		Deleterious (score: 0.03)	possibly damaging with a score of 0.943 (sensitivity: 0.80; specificity: 0.95)
9	ANKK5	ankyrin repeat and sterile alpha motif domain containing 6	chr9	101,536,259	Exon 9		T	-	SNV	missense	0.351	NM_173551	C1212G>A	p.Arg457Gln		Deleterious (score: 0)	possibly damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
15	AOAH	Acylcoylol hydrolase	chr7	36,552,907	Exon 21		G	A	SNV	missense	0.430	NM_001637	C1679C>T	p.Pro650Leu		Deleterious (score: 0)	probably damaging with a score of 0.988 (sensitivity: 0.73; specificity: 0.96)
12	ARHGAP20	Rho GTPase activating protein 20	chr11	110,457,039	Exon 13		C	T	SNV	missense	0.220	NM_020809	C1316G>A	p.Arg439Gln		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
5	ARHGAP15	Rho guanine nucleotide exchange factor (GEF) 15	chr17	8,218,534	Exon 6		C	T	SNV	missense	0.323	NM_173728	C1199C>T	p.Pro401Leu		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.14; specificity: 0.99)
3	ARRG17	Rho guanine nucleotide exchange factor (GEF) 17	chr11	79,073,710	Exon 14		T	C	SNV	missense	0.361	NM_014786	C4927T>C	p.Ser164Pro		Deleterious (score: 0.03)	benign with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
8	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	chr14	197,065,198	Exon 19		C	T	SNV	missense	0.426	NM_018136	C6917G>A	p.Glu2973Iys		Tolerated (score: 0.79)	benign with a score of 0.328 (sensitivity: 0.90; specificity: 0.89)
3	ATG14	Atg14p	chr14	55,836,626	Exon 10		A	C	SNV	missense	0.171	NM_014924	C1190T>G	p.Val197Gly		?	benign with a score of 0.004 (sensitivity: 0.97; specificity: 0.59)
1	ATG16L2	ATG16 autophagy related 16-like 2 (S. cerevisiae)	chr11	72,533,561	Exon 6		C	T	SNV	missense	0.420	NM_033388	C683C>T	p.Ala228Val		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
9	ATM	ataxia telangiectasia mutated	chr11	108,163,473	Exon 30		G	G	SNV	missense	0.465	NM_1000051	C4564G>C	p.Gly1522Arg		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.16; specificity: 0.99)
3	ATP2B3	ATPase, Ca++ transporting, plasma membrane 3	chrX	152,845,563	Exon 20		C	T	SNV	missense	0.250	NM_001001344	C3470C>T	p.Pro1157Leu		Tolerated (score: 0.49)	probably damaging with a score of 0.974 (sensitivity: 0.74; specificity: 0.96)
12	ATP6V0M4	ATPase, H+ transporting, lysosomal V0 subunit a4	chr7	138,455,988	Exon 24		A	G	SNV	missense	0.655	NM_020622	C57C>T	p.Val21a		Tolerated (score: 1)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
9	ATP1AF2	ATP synthase mitochondrial F1 complex assembly factor 2	chr17	17,942,251	Exon 1		A	A	SNV	missense	0.260	NM_145691.3	C77C>T	p.Ser269Ile		Tolerated (score: 0.68)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
9	ATXN7L3	ataxin 7-like 3	chr17	42,274,988	Exon 2		G	A	SNV	missense	0.560	NM_020218	C162C>G	p.Arg54Glu		Tolerated (score: 0.55)	possibly damaging with a score of 0.951 (sensitivity: 0.79; specificity: 0.95)
9	BAB3	brain-specific angiogenesis inhibitor 3	chr6	70,064,135	Exon 27		A	A	SNV	missense	0.479	NM_001704	C4A1157Glu	p.Ala1157Glu		Deleterious (score: 0)	possibly damaging with a score of 0.651 (sensitivity: 0.87; specificity: 0.91)
1	BCAM	basal cell adhesion molecule (Lutheran blood group)	chr19	45,322,052	Exon 10		G	A	SNV	missense	0.341	NM_005581	C1249G>A	p.Arg417Asn		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
15	BCOR	BCO corepressor	chrX	39,921,391	Intron 9		C	A	SNV	intron+splice intron	0.417	NM_001123384	C4272+1G>T	p.?		?	benign with a score of 0.079 (sensitivity: 0.93; specificity: 0.85)
8	BCR	breakpoint cluster region	chr22	23,524,007	Exon 1		T	A	SNV	missense	0.429	NM_021574	C860T>A	p.His287Iys		Deleterious (score: 0.01)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
8	BCR	breakpoint cluster region	chr22	23,524,411	Exon 1		C	A	SNV	missense	0.375	NM_021574	C1264T>C	p.His227Iys		Tolerated (score: 0.72)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
3	BRIC3	baculoviral IAP repeat-containing 3 (IAP2)	chr11	102,201,942	Exon 7		G	G	SNV	missense (1 I) Frameshift ins.	0.330	NM_182962	C1295dup	p.Glu433Afs*5		Tolerated (score: 0.68)	benign with a score of 0.120 (sensitivity: 0.93; specificity: 0.86)
3	BRIC5	baculoviral IAP repeat-containing 5 (IAP4)	chr17	76,212,831	Exon 3		A	G	SNV	missense	0.474	NM_0011068	C353G>T	p.Lys126Arg		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
12	BMP4	bone morphogenetic protein 4	chr14	54,418,588	Exon 3		N	N	SNV	missense	0.417	NM_001202	C353G>T	p.Arg118Met		Tolerated (score: 0.1)	possibly damaging with a score of 0.568 (sensitivity: 0.88; specificity: 0.91)
9	BNIP1	BCL2 adenovirus E1B 19kD interacting protein like	chr1	151,016,100	Exon 7		G	A	SNV	missense	0.419	NM_138278	C748G>A	p.Val250Ile		Tolerated (score: 0.1)	possibly damaging with a score of 0.568 (sensitivity: 0.88; specificity: 0.91)
10	BRPA2	Bp1 fold containing family A, member 2	chr20	31,765,957	Exon 6		A	A	SNV	missense	0.267	NM_080574	C588A>C	p.Ser190Arg		Tolerated (score: 0.7)	probably damaging with a score of 0.985 (sensitivity: 0.74; specificity: 0.96)
12	BTF3	Basic transcription factor 3	chr5	72,798,747	Exon 4		T	C	SNV	missense	0.455	NM_001207	C190A>T	p.Val61Leu		Tolerated (score: 0.46)	possibly damaging with a score of 0.566 (sensitivity: 0.88; specificity: 0.91)
9	C6orf45	Chromosome 6 open reading frame 45	chr4	159,836,465	Exon 4		C	T	SNV	missense	0.502	NM_152543	C403G>A	p.Ala1315Thr		Deleterious (score: 0.04)	possibly damaging with a score of 0.948 (sensitivity: 0.79; specificity: 0.95)
13	C6orf38	Chromosome 6 open reading frame 38	chr6	127,901,428	Exon 3		T	A	SNV	3-UTR	0.436	NM_1786169	C1197A>A	p.?		?	possibly damaging with a score of 0.599 (sensitivity: 0.87; specificity: 0.91)
13	C6orf58	Chromosome 6 open reading frame 58	chr6	127,901,428	Exon 3		T	A	SNV	missense	0.450	NM_001201450	C407C>T	p.Arg235Ile*3		Deleterious (score: 0.03)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
12	C7orf76 (FUJ4280)	hypothetical LOC601388	chr7	96,115,626	Exon 3		C	T	SNV	missense	0.370	NM_001136112	C116G>A	p.Arg39Ser		Tolerated (score: 0.56)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
13	C8orf95	Caspase 5, apoptosis-related cysteine peptidase	chr11	104,879,687	Exon 2		-	T	SNV	nononsense	0.350	NM_001145411	C67dup	p.Gln277*		?	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
10	CCDC110	coiled-coil domain containing 110	chr4	186,379,562	Exon 5		A	A	SNV	nononsense	0.190	NM_001145411	C2179C>T	p.Gln277*		?	probably damaging with a score of 0.590 (sensitivity: 0.88; specificity: 0.91)
8	CCDC180	coiled-coil domain containing 180	chr9	100,092,968	Exon18		-	A	SNV	NS (6) nonframeshift ins.	0.190	NM_020893	C2332_2337dup	p.Glu779_Glu780dup		?	possibly damaging with a score of 0.580 (sensitivity: 0.88; specificity: 0.91)
8	CND3	cyclin D3	chr6	41,903,707	Exon 5		G	A	SNV	missense (2D) Frameshift del.	0.430	NM_10017360	C85C>T	p.Pro284Ser		Tolerated (score: 0.08)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
10	CND3	cyclin D3	chr6	41,903,684	Exon 5		GT	--	DEL	missense	0.210	NM_1001267434	C872_873del	p.His291Pro*32		?	possibly damaging with a score of 0.580 (sensitivity: 0.88; specificity: 0.91)
1	CD44	CD44 molecule (Indian blood group)	chr11	35,226,181	Exon 9		A	A	SNV	missense	0.404	NM_000610.3	C1276A>T	p.Thi426Ser		Tolerated (score: 0.26)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
9	CDCP1	CD4 domain combining protein 1	chr3	45,152,326	Exon 4		G	T	SNV	nononsense	0.434	NM_0202842	C663C>A	p.Cys421*		Tolerated (score: 0.45)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
15	CDH9	Cadherin 9	chr5	26,988,379	Exon 2		G	T	SNV	missense	0.568	NM_016279	C62C>A	p.Thi21Asn		?	benign with a score of 0.006 (sensitivity: 0.94; specificity: 0.83)
12	CDON	Cdon homolog (mouse)	chr11	125,893,374	5-UTR		T	T	SNV	5-UTR	0.250	NM_016932	C-3G>A	p.?		?	benign with a score of 0.002 (sensitivity: 0.99; specificity: 0.30)
3	CFTR	cystic fibrosis transmembrane conductance regulator (ATP-binding cassette subunit C)	chr7	117,232,223	Exon 14	-7q	C	C	SNV	missense	1.000	NM_000492	C2002C>T	p.Arg66Cys		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
5	CGN	cholinergic receptor, nicotinic, delta	chr1	151,508,807	Exon 19		G	T	SNV	missense	0.217	NM_020770	C3292G>T	p.Arg1089Iyr		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	CHRD	chondrin receptor, nuclear, delta	chr2	233,394,757	Exon 7		G	A	SNV	missense	0.397	NM_000751	p.Arg24His			Deleterious (score: 0.01)	probably damaging with a score of 0.994 (sensitivity: 0.69; specificity: 0.97)
15	CHST3	Chondroitin sulfotransferase 13	chr3	126,260,891	Exon 3		A	A	SNV	missense	0.482	NM_152889	C496G>A	p.Ala165Ile		Tolerated (score: 1)	benign with a score of 0.006 (sensitivity: 0.94; specificity: 0.83)
5	CNTF	chilery neurotrophic factor	chr11	58,391,693	Exon 2		A	G	SNV	missense	0.454	NM_1000614	C301A>G	p.Thi101Asn		Tolerated (score: 0.24)	benign with a score of 0.002 (sensitivity: 0.99; specificity: 0.30)
7	CNTNAP8	contactin associated protein-like 8	chr9	43,861,081	Exon 13		T	G	SNV	missense	0.286	NM_001201380	C1951T>G	p.Tyr652Arg		Tolerated (score: 1)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
5	CNTNAP5	contactin associated protein-like 5	chr2	125,232,398	Exon 7		A	T	SNV	missense	0.337	NM_130073	C1001A>T	p.Tyr333Phe		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
5	COL2A1	collagen, type XXV, alpha 1	chr1	86,488,533	Exon 16		C	T	SNV	missense	0.209	NM_152890	C2131G>A	p.Gly711Arg		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
15	COL5A1	Collagen type 5 alpha 1	chr9	137,712,052	Exon 58		G	A	SNV	missense	0.440	NM_000093	C4537G>A	p.Gly1513Ser		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1																	

9	EC04	enhancer of mRNA decapping 4	chr16	67 914 521	Exon 18	C	T	SNV	missense	0.548	NM_014329	C2159C>T	p.P6720L	rs113019470	Tolerated (score: 0.43)	probably damaging with a score of 0.939 (sensitivity: 0.70, specificity: 0.97)
9	EEF2	eukaryotic translation elongation factor 2	chr19	3 980 968	Exon 8	G	A	SNV	missense	0.412	NM_001961	C0211C>T	p.A634L		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
9	EEF3C	eukaryotic elongation factor, selenium-cysteine-tRNA-specific	chr3	127 872 535	Exon 1	C	G	SNV	missense	0.490	NM_1985197	C185C>G	p.A662G		Deleterious (score: 0)	benign with a score of 0.000 (sensitivity: 1.00, specificity: 0.00)
5	EFCAB5	EF-hand calcium binding domain 5	chr17	28 418 937	Exon 21	G	A	SNV	missense	0.130	NM_198529	C398G>A	p.A61329Gln		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
7	EHH1	EF-hand domain family, member A1	chr13	22 069 345	Exon 11	T	G	SNV	missense	0.459	NM_152726	C1155A>C	p.G16385Asp		Tolerated (score: 0.62)	benign with a score of 0.183 (sensitivity: 0.22, specificity: 0.87)
3	EGLAM	EGF-like, fibronectin type III and laminin G domains	chr5	38 464 023	Exon 6	C	C	SNV	missense	0.384	NM_286517	C2965T>C	p.Y7989His		Tolerated (score: 0.15)	benign with a score of 0.420 (sensitivity: 0.89, specificity: 0.90)
9	ELF4	ETfA-like factor 4 (ets domain transcription factor)	chrX	129 208 070	Exon 4	-	T	C	SNV	0.900	NM_1001127197	C294ddup	p.Leu997His*12		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
1	ENAM	enamelin	chr4	71 509 818	Exon 9	A	G	SNV	missense	0.443	NM_039189	C2675A>G	p.Y7692Asp		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
5	EPHA8	Eph receptor A8	chr3	96 533 611	Exon 3	C	C	SNV	missense	0.500	NM_001080448	C194dup	p.A851Cys*42		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
1	EPHA8	Eph receptor A8	chr1	22 902 833	Exon 1	C	T	SNV	missense	0.190	NM_020526.3	C283C>T	p.A495T		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.91, specificity: 0.88)
9	ERCC2	ELKS/RAB6-interacting/CST family member 2	chr3	56 173 623	Exon 6	G	T	SNV	missense	0.130	NM_015576	C1387C>A	p.G1646Gly		Deleterious (score: 0.03)	possibly damaging with a score of 0.843 (sensitivity: 0.83, specificity: 0.93)
15	ERN2	Endoplasmic reticulum to nucleus signaling 2	chr16	23 706 074	Exon 17	T	T	SNV	missense	0.545	NM_033266	C2219T>A	p.Leu740Gln		Deleterious (score: 0)	probably damaging with a score of 0.972 (sensitivity: 0.77, specificity: 0.96)
3	EZH1	enhancer of zeste homolog 1 (Drosophila)	chr17	40 854 585	Exon 21	A	T	SNV	missense	0.150	NM_001091	C2209T>A	p.Y737Asn		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
15	FAM151A	Family with sequence similarity 151, member A	chr1	55 081 691	Intron 3	A	T	SNV	Intron-splice intron	0.500	NM_176762	C415>T1>A	p.?		?	?
7	FAM160B2	Family with sequence similarity 160, member B2	chr8	21 933 920	Exon 3	T	T	SNV	missense	0.447	NM_022749	C197A>T	p.G1669Val		Tolerated (score: 0.19)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
3	FAP	fibroblast activation protein, alpha	chr21	42 720 541	Exon 6	G	T	SNV	missense	0.386	NM_206964	C508G>T	p.A4170Ser		Deleterious (score: 0.12)	benign with a score of 0.270 (sensitivity: 0.91, specificity: 0.88)
12	FAT1	FAT tumor suppressor homolog 1 (Drosophila)	chr2	163 072 487	Exon 10	G	A	SNV	missense	0.540	NM_004460	C787C>T	p.A4265Tyr	rs373219307	Deleterious (score: 0.01)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
13	FBX7	F-box and leucine-rich repeat protein 7	chr4	187 518 920	Exon 24	T	C	SNV	missense	0.338	NM_005245	C1284A>G	p.Asp4095Gly		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.04, specificity: 0.99)
8	FCRL6	Fc receptor-like 6	chr5	15 937 245	Exon 4	C	T	SNV	missense	0.282	NM_012304	C1246C>T	p.A4747Cys		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
15	FDCSP	Follicular dendritic cell secreted protein	chr1	159 779 320	Exon 5	G	A	SNV	missense	0.449	NM_001004310	C733G>A	p.G1624Lys		Tolerated (score: 0.23)	benign with a score of 0.101 (sensitivity: 0.93, specificity: 0.85)
15	FIG	Flagglin	chr4	71 099 896	Exon 4	A	A	SNV	missense	0.432	NM_152997	C230G>A	p.G1684Lys		Tolerated (score: 0.87)	benign with a score of 0.010 (sensitivity: 0.96, specificity: 0.77)
15	FMN2	formin 2	chr1	152 275 225	Exon 3	A	T	SNV	missense	0.393	NM_020016	C12137C>T	p.Ser4046Leu		Deleterious (score: 0)	possibly damaging with a score of 0.820 (sensitivity: 0.84, specificity: 0.93)
15	FOX2	Forkhead box B2	chr9	79 635 772	Exon 1	A	T	SNV	missense	0.397	NM_001013735	C1202C>A	p.Ala401Asp		Deleterious (score: 0.01)	benign with a score of 0.990 (sensitivity: 0.99, specificity: 0.94)
1	FOXL2	forkhead box L2	chr3	138 665 303	Exon 1	G	A	SNV	missense	0.508	NM_023067	C262T>C	p.Phe88Leu		Deleterious (score: 0.03)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
15	FRL	FRL-like	chr4	48 533 298	Exon 50	C	T	SNV	missense	0.475	NM_015030	C678A>G	p.Ser2200Gly		Tolerated (score: 0.64)	benign with a score of 0.002 (sensitivity: 0.99, specificity: 0.30)
10	FUCA1	fucosidase, alpha-L, tissue	chr1	24 175 323	Exon 6	T	T	SNV	missense	0.310	NM_000147	C976G>A	p.Val328Ile		Tolerated (score: 0.36)	benign with a score of 0.001 (sensitivity: 0.99, specificity: 0.15)
15	GGX3	Golgi-associated, gamma adaptin ear containing, ARF binding protein 3	chr17	73 238 912	Exon 7 (9)	T	C	SNV	synonymous+splice exon	0.368	NM_138619	C609A>G	p.-(G)G203(Gln)		?	?
3	GBA	glp junction protein, beta 4, 30 kDa	chr1	35 227 553	Exon 2	T	T	SNV	missense	0.150	NM_153212	C698C>T	p.Thr233Met		Deleterious (score: 0.03)	benign with a score of 0.069 (sensitivity: 0.94, specificity: 0.84)
1	GLDN	gliadin protein, beta 4, 30 kDa	chr15	51 693 885	Exon 9	G	A	SNV	missense	0.571	NM_181789	C1123G>A	p.Val375Ile		Tolerated (score: 0.28)	benign with a score of 0.248 (sensitivity: 0.91, specificity: 0.88)
1	GLP1R	glucagon-like peptide 1 receptor	chr6	39 046 739	Exon 9	G	T	SNV	missense	0.333	NM_002062	C891G>T	p.Trp297Cys		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
15	GLYR1	Glyoxylate reductase 1 homolog (Arabidopsis)	chr16	4 863 755	Exon 12	C	G	SNV	missense	0.452	NM_032569	C1102G>C	p.Val368Leu		Tolerated (score: 0.34)	benign with a score of 0.269 (sensitivity: 0.91, specificity: 0.88)
7	GNAT3	guanine nucleotide binding protein, alpha transducin 3	chr17	63 052 715	5-UTR	---	---	GC	NS (3) frameshift ins.	0.170	NM_006572	C-4_3insGGC	p.?		?	?
3	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	chr3	52 720 086	Exon 3	T	C	SNV	missense	0.406	NM_001102386	C295A>G	p.Arg99Gly		Tolerated (score: 0.51)	benign with a score of 0.000 (sensitivity: 1.00, specificity: 0.00)
5	GOLGB1	golgin B1, golgi integral membrane protein	chr3	121 417 221	Exon 13	G	G	SNV	missense	0.338	NM_200826	C-23T>G	p.?		Tolerated (score: 0.06)	probably damaging with a score of 0.986 (sensitivity: 0.74, specificity: 0.96)
15	GPATCH2	G patch domain containing 2	chr1	217 688 186	Exon 6	A	G	SNV	missense	0.397	NM_018040	C3121A>C	p.Ser388Pro		Deleterious (score: 0)	probably damaging with a score of 0.988 (sensitivity: 0.73, specificity: 0.96)
7	GPC6	glypican 6	chr13	94 680 043	Exon 4	C	T	SNV	missense	0.425	NM_1005708	C772C>T	p.A46258Tyr		Deleterious (score: 0.01)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
5	GPR115	G protein-coupled receptor 115	chr6	47 681 816	Exon 6	G	T	SNV	nononsense	0.259	NM_153838	C835G>T	p.Glu279*		Deleterious (score: 0)	benign with a score of 0.000 (sensitivity: 1.00, specificity: 0.00)
7	GPR158	G protein-coupled receptor 158	chr10	25 887 676	Exon 11	A	C	SNV	missense	0.410	NM_020752	C3121A>C	p.Thr1041Pro		?	?
5	GPR75 / ASB3	G protein-coupled receptor 75 / arylkyn repeat and SOCS box containing 3	chr2	53 921 038	Exon 18	A	G	SNV	missense	0.393	NM_001164165	C1466T>C	p.Ala820Pro		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
5	GPR98	G protein-coupled receptor 98	chr5	89 948 177	Exon 19	G	A	SNV	missense	0.282	NM_032119	C3431G>A	p.Arg1144Gln	rs199735008	Deleterious (score: 0)	probably damaging with a score of 0.000 (sensitivity: 1.00, specificity: 0.00)
3	GPX4	glutathione peroxidase 4 (phospholipid hydroperoxidase)	chr19	1 106 432	Exon 6	T	T	SNV	missense	0.308	NM_002085	C646C>T	p.Arg216Gly		Deleterious (score: 0.03)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
15	GRII2	Glutamate receptor, ionotropic, delta 2	chr4	94 411 888	Exon 12	G	A	SNV	missense	0.522	NM_001510	C1957G>A	p.Ala653Tyr		Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14, specificity: 0.99)
9	GRK5	G protein-coupled receptor kinase 5	chr10	121 207 743	Exon 13	G	A	SNV	missense	0.485	NM_000308	C1375G>A	p.Gly459Arg		Deleterious (score: 0)	benign with a score of 0.086 (sensitivity: 0.93, specificity: 0.85)
12	GTPBP2	GTP binding protein 2	chr6	43 589 199	3-UTR	CT	--	DEL	(2 D) 3-UTR	0.240	NM_019096	C*151_*152de p.?	p.?		?	?
5	GUCA1A	guanylate cyclase activator 1A (retina)	chr6	47 130 732	5-UTR	A	A	SNV	5-UTR	0.469	NM_000469	C-383G>A	p.?		?	?
7	HAGH	hydroxyacylglutathione hydrolase	chr16	1 867 207	Exon 7	C	G	SNV	missense	0.463	NM_1003326	C607G>C	p.Ala203Pro		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
12	HIST1H1D	histone cluster 1, H1d	chr6	26 234 828	Exon 1	C	T	SNV	missense	0.393	NM_000330	C334G>A	p.Ala117Tyr		Tolerated (score: 0.57)	possibly damaging with a score of 0.900 (sensitivity: 0.82, specificity: 0.94)
3	HIST1H2AD/HIST1H3D	histone cluster 1, H2ad	chr6	26 199 187	Exon 1	G	C	SNV	missense	0.517	NM_020065	C285C>G	p.Asp95Lys		Deleterious (score: 0)	probably damaging with a score of 0.992 (sensitivity: 0.70, specificity: 0.97)
7	HIST4A	histone cluster 4, H4	chr12	14 923 868	Exon 1	C	C	SNV	missense	0.403	NM_175054	C151A>G	p.Ile51Val		Deleterious (score: 0)	benign with a score of 0.061 (sensitivity: 0.94, specificity: 0.84)
15	HIST4A	histone cluster 4, H4	chr12	14 923 751	Exon 1	A	A	SNV	missense	0.320	NM_175054	C286G>T	p.Ala90Ser		Deleterious (score: 0)	benign with a score of 0.201 (sensitivity: 0.92, specificity: 0.88)
8	HK3	hexokinase 3 (white cell)	chr5	176 308 744	Exon 17	C	C	SNV	missense	0.395	NM_002215	NM_2342G>A	p.Arg781His		Tolerated (score: 0.2)	possibly damaging with a score of 0.801 (sensitivity: 0.84, specificity: 0.93)
9	HMCN1	hemicentin 1	chr1	185 969 291	Exon 26	C	T	SNV	missense	0.343	NM_039195	C3989C>T	p.Pro1330Leu		Deleterious (score: 0)	benign with a score of 0.070 (sensitivity: 0.94, specificity: 0.84)
13	HMMMR	Hyduronan-mediated motility receptor	chr5	162 911 228	Exon 16	G	A	SNV	missense	0.640	NM_001142556	C1993G>A	p.Arg647Asn		Tolerated (score: 0.23)	benign with a score of 0.004 (sensitivity: 0.97, specificity: 0.99)
15	HNRAS	V-Ha-ras Harvey rat sarcoma viral oncogene homolog	chr11	532 646	Exon 5	A	G	SNV	missense	0.516	NM_001130442	C560T>C	p.Val187Val		Tolerated (score: 0.4)	benign with a score of 0.001 (sensitivity: 0.99, specificity: 0.15)
15	hsa-mir-142		chr17	56 408 621		A	T	SNV		0.459					?	?
9	HSPD1	heat shock 60kDa protein 1 (Chaperonin)	chr2	198 362 094	Exon 3	T	C	SNV	missense	0.431	NM_002156	C197A>G	p.G1666Arg		Deleterious (score: 0)	probably damaging with a score of 0.993 (sensitivity: 0.70, specificity: 0.97)
5	HTR3B	5-hydroxytryptamine (serotonin) receptor 3B	chr11	113 780 176	Exon 2	T	C	SNV	missense+splice exon	0.220	NM_006028	C212T>C	p.Val714Asp		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
5	HIT5	interferon-induced protein with tetratricopeptide repeats 5	chr10	91 178 173	Exon 2	T	T	SNV	missense	0.230	NM_012420	C1217T>A	p.Val404Asp		Deleterious (score: 0)	possibly damaging with a score of 0.810 (sensitivity: 0.84, specificity: 0.93)
7	IHRTS	insulin-like growth factor 2 mRNA binding protein 2	chr3	188 407 168	Exon 6	T	G	SNV	missense	0.379	NM_1006548	C670A>C	p.Asn224His		Deleterious (score: 0.04)	benign with a score of 0.268 (sensitivity: 0.91, specificity: 0.88)
5	IGFBP2	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	chr8	42 178 326	Exon 16	C	G	SNV	missense	0.196	NM_001556	C1652C>G	p.Pro551Arg		Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
7	IKBKB	Intracellular A particle-promoted polypeptide	chr1	46 206 975	Exon 3	G	A	SNV	nononsense	0.394	NM_001145349	C323C>T	p.Gln108*		?	?
15	IPF	Integrin, alpha 8	chr10	15 617 557	Exon 24	A	T	SNV	missense	0.420	NM_003638	C2409T>A	p.His803Gln		Tolerated (score: 0.51)	benign with a score of 0.008 (sensitivity: 0.96, specificity: 0.61)
12	ITGA8	ITGA8	chr8	45 791 093	Exon 18	A	T	SNV	missense	0.230	NM_00109413	C4645G>A	p.Gly1549Ser		Tolerated (score: 0.08)	probably damaging with a score of 1.000 (sensitivity: 0.00, specificity: 1.00)
10	KAT5B / MYS13	Ki(Vsine) acetyltransferase 6A / MYST histone acetyltransferase (nucleocytoplasmic)	chr6	39 284 653	Exon 4	A	G	SNV	missense	0.279	NM_001135105	C566T>C	p.Met189Thr		Deleterious (score: 0.04)	possibly damaging with a score of 0.628 (sensitivity: 0.87, specificity: 0.91)
9	KCTD3	potassium channel tetramerisation domain containing 13	chr16	29 923 340	Exon 3	G	C	SNV	missense	0.290	NM_178863	C445C>G	p.Ileu149Val		Tolerated (score: 0.7)	benign with a score of 0.001 (sensitivity: 0.99, specificity: 0.15)
15	KDMA6A	Lysine-specific demethylase 6A	chrX	44 938 411	Exon 20	T	T	SNV	nononsense	0.630	NM_021140	C2939A>T	p.Lys987*		?	?
15	KHNVN	KH and NFN domain containing	chr14	24 901 627	Exon 3	A	G	SNV	missense	0.453	NM_015299	C1160A>G	p.Asp387Gly		Tolerated (score: 0.08)	possibly damaging with a score of 0.986

7	LRRCA4	leucine rich repeat containing 24	chr8	145 747 961	Exon 5	G	C	SNV	missense	0.385	NM_001024678	C1440C>G	p.His480Leu	Tolerated (score: 0.3)	benign with a score of 0.005 (sensitivity: 0.97; specificity: 0.74)
15	LRRCA0	leucine rich repeats containing 40	chr1	70 644 647	Exon 6	A	A	SNV	missense	0.486	NM_017768	C691C>T	p.Leu231Phe	Tolerated (score: 0.62)	possibly damaging with a score of 0.473 (sensitivity: 0.89; specificity: 0.90)
15	LRR101	leucine rich repeats and IQ motif containing 1	chr12	85 546 850	Exon 21	A	G	SNV	missense	0.303	NM_001079910	C448A>T	p.Asn1490Tyr	Not scored (score: 0.0)	benign with a score of 0.001 (sensitivity: 0.99; specificity: 0.15)
7	LYP1A2	lysophospholipase II	chr1	24 121 246	3-UTR	A	G	SNV	3-UTR	0.140	NM_007260	C24A>G	p.A	?	?
5	MAK	male germ cell-associated kinase	chr6	10 804 119	Exon 7	A	T	SNV	missense	0.407	NM_005906	C497G>A	p.A>G166His	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	MAIAT1	metastasis associated lung adenocarcinoma transcript 2	chr11	65 266 801	nRNA	G	A	SNV	substitution?	0.387	NR_020819	n.1578G>A	non-protein coding	?	?
7	MAKPL1L	metastasis associated lung adenocarcinoma transcript 1	chr11	55 518 998	5-UTR	A	A	SNV	substitution?	0.377	NM_002819	n.1569G>A	non-protein coding	?	?
9	MAPKAP5 (PRK4)	mitogen-activated protein kinase 1 interacting protein 1-like	chr14	55 538 998	5-UTR	C	T	SNV	5-UTR	0.400	NM_144578	C-128C>T	p.?	?	?
13	MCCR	mitogen-activated protein kinase-activated protein kinase 5	chr12	112 308 936	Exon 7	A	T	SNV	missense	0.376	NM_139078	C531A>T	p.Gln177His	Deleterious (score: 0)	probably damaging with a score of 0.981 (sensitivity: 0.75; specificity: 0.96)
7	ME8B	melanocortin 2 receptor (adrenocorticotrophic hormone)	chr18	13 885 385	Exon 2	T	T	SNV	missense	0.373	NM_000529	C136G>A	p.Val45Ile	Deleterious (score: 0)	benign with a score of 0.223 (sensitivity: 0.91; specificity: 0.88)
15	MEIK	mediator complex subunit 8	chr1	43 833 302	Exon 3	T	-	DEL	(1 D) frameshift del.	0.360	NM_052877	C142del	p.Ser484His*9	Tolerated (score: 1)	benign with a score of 0.001 (sensitivity: 0.99; specificity: 0.15)
5	MFLK	Maternal embryonic leucine zipper kinase	chr9	36 665 555	Exon 14	A	C	SNV	missense	0.462	NM_014791	C138A>C	p.Asn462Ile	Tolerated (score: 0.11)	benign with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
5	MFLP4	microfilin-associated protein 4	chr17	19 288 020	Exon 6	T	T	SNV	missense	0.221	NM_002404	C595G>A	p.Asp199Asn	Deleterious (score: 0)	probably damaging with a score of 0.993 (sensitivity: 0.74; specificity: 0.96)
15	MGA	MAX gene associated	chr15	42 028 541	Exon 13	A	G	SNV	missense	0.448	NM_001080541	C4079A>G	p.Asn1360Ser	?	?
8	MMMP8	matrix metalloproteinase 8 (neutrophil collagenase)	chr11	102 595 611	5-UTR	T	C	SNV	5-UTR	0.480	NM_002424	C-25A>G	p.?	?	?
5	MTR3A	metastasis associated 1 family, member 3	chr15	42 028 541	Exon 13	A	G	SNV	missense	0.439	NM_020744	C613A>T	p.Asn1360Ser	?	?
7	MTR14	myotubularin related protein 14	chr3	9 730 394	Exon 15	C	T	SNV	missense	0.482	NM_001077525	C1250C>T	p.Prp417Leu	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
9	MTROR	mechanistic target of rapamycin (serine/threonine kinase)	chr1	11 187 857	Exon 44	C	T	SNV	missense	0.571	NM_004958	C640G>A	p.Glu2014Iys	Tolerated (score: 0.07)	possibly damaging with a score of 0.959 (sensitivity: 0.78; specificity: 0.95)
3	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	chr8	128 750 945	Exon 2	C	T	SNV	missense	0.521	NM_002467	C482C>T	p.Ser616Leu	Deleterious (score: 0)	possibly damaging with a score of 0.840 (sensitivity: 0.84; specificity: 0.93)
3	MYO1H	myosin II	chr12	109 880 039	Exon 26	T	T	SNV	missense	0.281	NM_001101421	C2602C>T	p.Prp685Ser	?	?
10	NCKAP1	NCK-associated protein 1 (NAP125)	chr2	183 846 048	Exon 13	G	T	SNV	missense	0.311	NM_013436	C1283A>C	p.Tyr425Ser	Deleterious (score: 0)	benign with a score of 0.200 (sensitivity: 0.92; specificity: 0.88)
5	NCOA6	nuclear receptor coactivator 6	chr20	33 328 950	Exon 11	G	A	SNV	nonsense	0.320	NM_014071	C510C>T	p.Gln1704*	Tolerated (score: 0.29)	possibly damaging with a score of 0.875 (sensitivity: 0.83; specificity: 0.93)
1	NEB	nebulin	chr2	153 534 502	Exon 33	A	T	SNV	missense	0.481	NM_0004543	C345C>A	p.Ala1152Asp	?	?
3	NEFL	neurofilament, light polypeptide 68kDa	chr8	24 813 413	Exon1	G	A	SNV	missense	0.120	NM_006158	C617G>T	p.A>G206Leu	?	?
1	NFE213	nuclear factor (erythroid-derived 2)-like 3	chr7	26 225 179	Exon 4	AA	-	DEL	(2 D) frameshift del.	0.470	C5551_1552del p.Asp1851Tyrfs*4	C5551_1552del p.Asp1851Tyrfs*4	p.Ser2421Phe	?	?
9	NOTCH2	nipped 8 homolog (Drosophila)	chr5	37 022 469	Exon 29	GA	GA	DEL	(2 D) frameshift del.	0.440	NM_133433	C5551_1552del p.Asp1851Tyrfs*4	p.Ser2421Phe	?	?
12	NR1D1	nuclear receptor subfamily 1, group D, member 1	chr17	38 249 310	3-UTR	G	T	SNV	3-UTR	0.286	NM_020724	C1051G>A	p.Ala331Thr	Tolerated (score: 0.51)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	NR2F1	nuclear receptor subfamily 2, group F, member 1	chr5	92 929 327	Exon 3	G	A	SNV	missense	0.212	NM_000654	C1051G>A	p.Ala331Thr	?	?
7	NR4A3	nuclear receptor subfamily 4, group A, member 3	chr9	102 595 699	Exon 5	T	G	SNV	nonsense	0.366	NM_006981	C1217T>A	p.Leu406*	?	?
5	NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	chr1	115 258 747	Exon 2	C	A	SNV	missense	0.266	NM_005524	C35G>T	p.Gly22Ala	?	?
15	OC42	Oculocutaneous albinism II	chr15	28 259 989	Exon 9	C	T	SNV	missense	0.500	NM_000275	C977G>A	p.Ser326Asn	Tolerated (score: 0)	possibly damaging with a score of 0.718 (sensitivity: 0.86; specificity: 0.92)
9	OR10C1	olfactory receptor, family 10, subfamily C, member 1	chr6	29 408 027	Exon 1	C	A	SNV	missense	0.489	NM_013941	C235C>A	p.Leu73Met	Deleterious (score: 1)	benign with a score of 0.002 (sensitivity: 0.99; specificity: 0.30)
13	OR10R2	olfactory receptor, family 10, subfamily R, member 2	chr1	158 450 449	Exon 1	C	A	SNV	missense	0.420	NM_010004472	C782G>C	p.Leu73Met	Deleterious (score: 0)	possibly damaging with a score of 0.892 (sensitivity: 0.82; specificity: 0.94)
9	OR13A1	olfactory receptor, family 13, subfamily A, member 1	chr10	45 799 340	Exon 4	G	T	SNV	missense	0.237	NM_001004297	C531C>A	p.His177Gln	Deleterious (score: 0)	benign with a score of 0.372 (sensitivity: 0.90; specificity: 0.89)
1	OR14G6	olfactory receptor, family 14, subfamily G, member 6	chr1	248 512 380	Exon 1	A	A	SNV	missense	0.478	NM_001001918	C304G>A	p.Val10Meth	Tolerated (score: 0.08)	possibly damaging with a score of 0.930 (sensitivity: 0.81; specificity: 0.94)
1	OR113	olfactory receptor, family 2, subfamily L, member 13	chr1	248 262 866	Exon 3	A	A	SNV	missense	0.516	NM_175911	C189C>A	p.Ser63Met	Deleterious (score: 0)	probably damaging with a score of 0.964 (sensitivity: 0.78; specificity: 0.95)
10	OR5M11	olfactory receptor, family 5, subfamily M, member 11	chr11	56 310 243	Exon 1	C	T	SNV	missense	0.323	NM_001005245	C491G>A	p.A>G166His	?	?
3	OSBP1	oxysterol binding protein-like 3	chr7	24 911 634	Exon 3	G	G	SNV	missense	0.315	NM_145320	C151C>G	p.A>G166His	?	?
5	OSBP5	oxysterol binding protein-like 5	chr11	3 114 975	Intron 16	C	T	SNV	substitution intron-splice eir	0.496	NM_020896	C1809+1G>A	p.Prp651Asp	?	?
5	PAPPA2	pappalysin 2	chr1	176 563 976	Exon 3	C	A	SNV	missense	0.170	NM_020318	C1236C>A	p.Ser412Arg	Tolerated (score: 0.1)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
15	PARD3	Par3 partitioning defective 3 homolog (C. elegans)	chr10	34 408 641	Exon 24	A	A	SNV	missense	0.474	NM_019619	C3577G>T	p.Gly1193Trp	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
12	PARP2	poly (ADP-ribose) polymerase 2	chr14	20 825 945	Exon 16	C	T	SNV	nonsense	0.348	NM_001042418	C1741C>T	p.Gln581*	?	?
8	PAXA	paired box 4	chr7	127 220 921	3-UTR	G	T	SNV	3-UTR	0.342	NM_006193	C197C>A	p.?	?	?
9	PCHGA9	protocadherin gamma subfamily A, 9	chr5	140 782 712	Exon 1	T	T	SNV	missense	0.419	NM_018921	C193C>T	p.A>G65Cys	?	?
12	PDE8A	phosphodiesterase 8A	chr15	85 666 345	Exon 19	A	G	SNV	missense	0.140	NM_002605	C206G>A	p.Glu66Gly	Deleterious (score: 0.02)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
9	PDGFR	platelet derived growth factor D	chr11	103 870 840	Exon 2	G	A	SNV	missense	0.431	NM_025258	C268C>T	p.A>G90Trp	Deleterious (score: 0.02)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	PHK2	phosphoinositide 3-kinase, alpha 2 (liver)	chrX	18 919 618	Exon 27	A	A	SNV	missense	0.542	NM_000292	C3012G>T	p.A>G120Asp	Deleterious (score: 0.01)	benign with a score of 0.119 (sensitivity: 0.93; specificity: 0.86)
12	PK3CA	phosphoinositide-3-kinase, class 2, alpha polypeptide	chr11	17 118 692	Exon 26	G	A	SNV	missense	0.374	NM_000265	C428C>T	p.Prp4141Leu	Deleterious (score: 0.01)	probably damaging with a score of 0.972 (sensitivity: 0.77; specificity: 0.96)
12	PKL2	polc-like kinase 2	chr5	57 750 453	Exon 14	A	A	SNV	missense	0.439	NM_000362	C2015G>T	p.A>G672Leu	Deleterious (score: 0.02)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
12	PLD1	phosphatidylinositol 1, 2-oxoglutarate 5-dioxygenase 1	chr1	12 018 630	Exon 9	G	T	SNV	missense	0.358	NM_000302	C901G>T	p.Val901Ileu	Tolerated (score: 1)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
9	PLNM4	plein A4	chr7	131 888 142	Exon 11	C	T	SNV	LOH	1.000	NM_020911	C235G>A	p.Val173Met	Tolerated (score: 0.06)	probably damaging with a score of 0.983 (sensitivity: 0.74; specificity: 0.96)
13	POD2	polymerase (DNA directed), delta2, regulatory subunit 50kDa	chr7	44 154 986	Exon 10	A	E	SNV	missense	0.520	NM_001127218	C1017C>T	p.Prp386Leu	Deleterious (score: 0.03)	probably damaging with a score of 0.998 (sensitivity: 0.27; specificity: 0.99)
1	PON2	paraoxonase 2	chr7	95 033 877	Exon 2	C	A	SNV	missense	0.241	NM_001018161	C95G>T	p.A>G23Ile	Deleterious (score: 0.01)	possibly damaging with a score of 0.943 (sensitivity: 0.80; specificity: 0.95)
5	PPP2R3A	protein phosphatase 2 (formerly 2A), regulatory subunit B, alpha	chr3	135 742 005	Exon 1	C	T	SNV	missense	0.245	NM_181897	C94C>T	p.A>G23Trp	Deleterious (score: 0.01)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
13	PRH19	Protein rich 19	chr19	42 814 545	Exon 3	G	A	SNV	missense	0.950	NM_199285	C724C>G	p.Prp42Ala	Tolerated (score: 0.17)	benign with a score of 0.002 (sensitivity: 0.99; specificity: 0.30)
1	PRMD9	proresonin (prosome, macropan) 26S subunit, non-ATPase, 9	chr12	122 353 761	Intron 2	G	G	SNV	intron+splice intron	0.257	NM_001261400	C556+1G>A	p.?	?	?
5	RAT1	v-rat-1 murine leukemia viral oncogene homolog 1	chr3	12 645 688	Exon 7	G	A	SNV	missense	0.297	NM_002880	C781C>T	p.Prp261Ser	Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
5	RARGF2	Rap guanine nucleotide exchange factor (GEF) 2	chr4	160 262 962	Exon 14	A	G	SNV	missense	0.150	NM_014247	C2298G>C	p.Gln76His	Tolerated (score: 0.05)	benign with a score of 0.022 (sensitivity: 0.95; specificity: 0.80)
13	RBFX1	RNA binding protein, fox-1 homolog (C. elegans) 1	chr16	7 657 328	Exon 7	A	A	SNV	missense	0.200	NM_145891	C724G>A	p.Glu242Iys	?	?
12	RFTN1	raftlin, lipid raft linker 1	chr3	16 419 287	Exon 5	C	T	SNV	missense	0.415	NM_015150	C764G>A	p.Ser255Asn	Tolerated (score: 0.35)	benign with a score of 0.009 (sensitivity: 0.96; specificity: 0.77)
15	RFTN1	Raftlin, lipid raft linker 1	chr3	16 450 975	Exon 4	A	T	SNV	missense	0.344	NM_015150	C348T>A	p.Asp116Glu	Tolerated (score: 0.77)	benign with a score of 0.011 (sensitivity: 0.96; specificity: 0.78)
15	ROCK1	Rho-associated, coiled-coil containing protein kinase 1	chr18	18 535 004	Exon 31	A	G	SNV	missense+splice exon	0.357	NM_005406	C359T>C	p.Ile1198Trp	Deleterious (score: 0)	probably damaging with a score of 0.993 (sensitivity: 0.70; specificity: 0.97)
3	RPI1	retinoblastoma 1 (autosomal dominant)	chr8	55 534 143	Intron 2	T	C	SNV	intron+splice intron	0.292	NM_000629	C615+2T>C	p.?	?	?
9	RPH2	RNA polymerase II associated protein 2	chr1	92 798 990	Exon 9	C	T	SNV	missense	0.411	NM_024813	C1498C>G	p.His50Glu	Tolerated (score: 0.87)	probably damaging with a score of 0.997 (sensitivity: 0.41; specificity: 0.98)
12	RTP3	receptor (chemosensory) transporter protein 3	chr3	46 541 917	Exon 2	G	T	SNV	missense	0.375	NM_031440	C227G>T	p.Ser7Ile	Tolerated (score: 0.09)	probably damaging with a score of 0.990 (sensitivity: 0.72; specificity: 0.97)
1	SAAMD1	sterile alpha motif domain containing 9-like	chr7	92 762 824	Exon 5	T	T	SNV	missense	0.535	NM_152703	C2461G>A	p.Val82Ile	Tolerated (score: 0.58)	benign with a score of 0.001 (sensitivity: 0.99; specificity: 0.15)
12	SART3	squamous cell carcinoma antigen recognized by T cells 3	chr12	108 920 186	Exon 16	G	A	SNV	missense	0.370	NM_014706	C2460C>T	p.Ser687Phe	Deleterious (score: 0.02)	possibly damaging with a score of 0.472 (sensitivity: 0.89; specificity: 0.90)
9	SCN10A	sodium channel, voltage-gated, type X, alpha subunit	chr3	38 743 338	Exon 26	A	A	SNV	missense	0.546	NM_000654	C4649C>T	p.Ser150Cys	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
15	SCN2A	sodium channel, voltage-gated, type II, alpha subunit	chr2	166 188 076	Exon 14	A	A	SNV	missense	0.421	NM_001040142	C2386C>A	p.Leu756Met	Deleterious (score: 0)	probably damaging with a score of 0.987 (sensitivity: 0.73; specificity: 0.96)
15	SEC16A	SEC16 homolog A (S. cerevisiae)	chr9	139 370 441	Exon 14	A	A	SNV	missense	0.430	NM_014866	C1627G>T	p.Val549Phe	Deleterious (score: 0.02)	possibly damaging with a score of 0.834 (sensitivity: 0.84; specificity: 0.93)
1	SEC24B	SEC24 family, member B (S. cerevisiae)	chr4	110 441 542	Exon 12	C	C								

12	SLC35B1	solute carrier family 35, member B1	chr17	47 781 506	Exon 6	A	G	SNV	missense	0.329	NM_005837	C611T>C	p.Met204Thr	Deleterious (score: 0.01)	possibly damaging with a score of 0.885 (sensitivity: 0.82; specificity: 0.94)
1	SLC49A9	solute carrier family 4, sodium bicarbonate cotransporter, member 9	chr5	139 751 849	Exon 20	+	A	SNV	missense	0.231	NM_031467	C2693G>A	p.Asp688Gln	Tolerated (score: 0.05)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
7	SMM120 (Clorf52)	small integral membrane protein 20	chr4	25 915 975	Exon 1	-	ACCCGCCCTCAT	INS (14 1) frameshift ins.	missense	0.220	NM_001145432	C40_41ins14	p.Phe141Tyrfs*9	Deleterious (score: 0.05)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
9	SRAFG17	sperm associated antigen 17	chr1	118 579 467	Exon 24	C	A	SNV	missense	0.385	NM_206996	C339G>T	p.Gly1120Val	Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
12	SRSF51	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5-alpha-steroid delta 4-d	chr5	6 663 008	Exon 4	G	T	SNV	missense	0.409	NM_001047	C642G>T	p.Trp214Cys	Tolerated (score: 0.26)	benign with a score of 0.055 (sensitivity: 0.94; specificity: 0.84)
10	STAM	signal transducing adaptor molecule (SH3 domain and TRAM motif) 1	chr10	17 950 793	Exon 13	A	C	SNV	missense	0.323	NM_003473	C1238C>A	p.Pro4170Ile	Tolerated (score: 0.86)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.80)
1	STRADA	STE20-related kinase adaptor alpha	chr17	61 784 722	Exon 8	C	T	SNV	missense	0.500	NM_001003787.2	C638G>A	p.Gly213Asp	Tolerated (score: 0.44)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	SYK	spleen tyrosine kinase	chr9	99 636 993	Exon 9	A	G	SNV	missense	0.574	NM_001114167.1	C1043A>G	p.Tyr348Cys	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
10	TAF11	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 210	chr6	30 001 040	Exon 17	C	T	SNV	missense	0.287	NM_153809	C2359C>T	p.Arg787Trp	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.69; specificity: 0.97)
9	TAC2	TAG kinase 2	chr5	30 001 040	Exon 17	C	T	SNV	missense	0.544	NM_0004783	C2359C>T	p.Arg787Trp	Deleterious (score: 0.01)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
3	TAS2RH0	taste receptor, type 2, member 40	chr7	142 919 883	Exon 1	G	T	LOH	missense	1.000	NM_170882	C512G>T	p.Ser171Ile	Tolerated (score: 0.17)	benign with a score of 0.030 (sensitivity: 0.95; specificity: 0.82)
13	TBC1D108	TBC1 domain family, member 108	chr16	30 369 653	Exon 9	G	A	SNV	missense	0.770	NM_015527	C2039C>T	p.Pro680Leu	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
13	TBC1D19	TBC1 domain family, member 19	chr4	26 661 289	Exon 8	T	A	SNV	nonsense	0.590	NM_018317	C551T>A	p.Leu184*	Deleterious (score: 0)	probably damaging with a score of 0.968 (sensitivity: 0.77; specificity: 0.95)
15	TRK1	TANK-binding kinase 1	chr12	64 873 797	Exon 7	A	C	SNV	missense	0.352	NM_013254	C707A>C	p.Lys236Ile	Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
5	TCF7L2	transcription factor 7-like 2 (T-cell specific, HMG-box)	chr10	114 900 998	Exon 6	T	C	SNV	missense	0.120	NM_001146274	C608T>C	p.Leu203Pro	Tolerated (score: 0.11)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
1	TCHH	trichohyalin	chr1	152 082 585	Exon 3	CTCT	DEL	DEL	missense (4 D) frameshift del	0.280	NM_007113.2	C3105_3108del	p.Glu1036Asnfs*58	?	?
8	TEN1	transcobalamin (vitamin B12 binding protein, R binder family)	chr11	59 623 465	Exon 6	C	A	SNV	missense	0.359	NM_0010062	C814G>T	p.Val272Leu	Tolerated (score: 0.12)	benign with a score of 0.043 (sensitivity: 0.94; specificity: 0.83)
13	TD02	tryptophan 2,3-dioxygenase	chr4	158 835 493	Exon 8	G	A	SNV	missense	0.500	NM_005651	C745G>A	p.Glu249Iys	Deleterious (score: 0.05)	benign with a score of 0.036 (sensitivity: 0.94; specificity: 0.82)
5	TENM3 (ODZ3)	odt, odd O2/ten homolog 3 (Drosophila)	chr4	186 675 659	Exon 21	G	A	SNV	missense	0.469	NM_001080477	C419G>A	p.Arg1380Gln	Tolerated (score: 0.12)	probably damaging with a score of 0.995 (sensitivity: 0.68; specificity: 0.97)
12	TFR3	transforming growth factor, beta 3	chr14	76 425 610	Exon 7	T	C	SNV	missense	0.556	NM_003239	C1159A>G	p.Thr387Val	Tolerated (score: 0.32)	probably damaging with a score of 0.992 (sensitivity: 0.70; specificity: 0.97)
12	TRHA	thyroid hormone receptor, alpha (erythroid/leukemia viral (v-erb-a) oncogr	chr17	38 249 310	Exon 10	C	T	SNV	missense	0.286	NM_001190919	C1148C>T	p.Asp383Val	Tolerated (score: 0.17)	benign with a score of 0.035 (sensitivity: 0.94; specificity: 0.82)
13	TRP3	tight junction protein 3 (zona occludens 3)	chr19	3 733 793	Exon 6	C	T	SNV	missense	0.450	NM_014428	C817C>T	p.Arg273Trp	Deleterious (score: 0.01)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
15	TMEM196	transmembrane protein 196 ENSG00000179452	chr7	19 769 078	5-UTR	G	A	SNV	5-UTR	0.411	NM_152774	C148-17C>A	p.?	?	?
9	TMEM26	transmembrane protein 26	chr10	63 170 123	Exon 6	A	T	SNV	missense	0.110	NM_178505	C1064G>A	p.Arg355Gln	Tolerated (score: 0.38)	benign with a score of 0.003 (sensitivity: 0.98; specificity: 0.44)
10	TNFRSS5	transmembrane protease, serine 5	chr11	115 570 383	Exon 3	G	A	SNV	missense	0.427	NM_030770	C139C>T	p.Arg47Cys	Deleterious (score: 0)	probably damaging with a score of 0.994 (sensitivity: 0.69; specificity: 0.97)
10	TNFR18L2	tumor necrosis factor, alpha-induced protein 8-like 2 / sodium channel modifier	chr1	151 134 223	5-UTR	G	A	SNV	5-UTR	0.239	NM_024575	C2249T>C	p=	?	?
15	TNFK	TNFR2 and NCK interacting kinase	chr3	170 811 680	Exon 21	T	A	SNV	missense	0.513	NM_001161662	C258G>G	p.Asp853Gly	Tolerated (score: 0.38)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
13	TP311	tumor protein p53 inducible protein 11	chr4	44 956 544	Exon 4	A	C	SNV	INS (10 1) frameshift ins	0.290	NM_001076787	C452_461dup	p.Gly1558Phefs*2	?	?
5	TRAF3	TNF receptor-associated factor 3	chr14	103 338 301	Exon 4	A	G	SNV	missense	0.588	NM_145725	C293A>G	p.Asp98Gly	Deleterious (score: 0.01)	benign with a score of 0.027 (sensitivity: 0.95; specificity: 0.81)
5	TRIM14	tripartite motif-containing 14	chr9	100 843 377	3-UTR	G	A	SNV	3-UTR	0.217	NM_033220	C*28+6347C>T p.?	p.?	?	?
13	TRIM5	tripartite motif-containing 5	chr11	5 686 185	Exon 8	C	T	SNV	missense	0.438	NM_030304	C1336G>A	p.Ala447Ile	Tolerated (score: 0.06)	probably damaging with a score of 0.988 (sensitivity: 0.73; specificity: 0.96)
10	TSHR	thyroid stimulating hormone receptor	chr14	81 610 635	Exon 10	T	A	SNV	missense	0.308	NM_000369	C2233T>A	p.Ser745Trp	Tolerated (score: 0.46)	benign with a score of 0.13 (sensitivity: 0.96; specificity: 0.78)
1	TSEFAR	thrombospondin-type laminin G domain and EAR repeats	chr21	45 945 654	Exon 8	C	G	SNV	missense	0.403	NM_144991	C1218G>C	p.Trp40Cys	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
8	TTM2	Tweety homolog 2	chr17	72 240 168	Exon 6	C	A	SNV	missense	0.455	NM_032646	C784G>A	p.Ala262Trp	Tolerated (score: 0.19)	benign with a score of 0.009 (sensitivity: 0.96; specificity: 0.77)
3	TULP2	tubby like protein 2	chr19	49 399 684	Intron 4	C	A	SNV	Intron+splice intron	0.412	NM_003323	C211+3G>T	p.?	?	?
15	TNND08	Thioredoxin domain containing 8	chr9	113 096 602	Intron 1	T	A	SNV	Intron+splice intron	0.472	NM_001003936	C25_2A>T	p.?	?	?
3	UZA1	U2 small nuclear RNA auxiliary factor 1	chr21	44 524 456	Exon 2	G	A	SNV	missense	0.300	NM_001025203	C101C>T	p.Ser340Phe	Deleterious (score: 0)	probably damaging with a score of 1.000 (sensitivity: 0.00; specificity: 1.00)
10	USP29	ubiquitin specific peptidase 29	chr19	57 642 397	Exon 4	G	T	SNV	missense	0.333	NM_020903	C234G>T	p.Gly785Val	Deleterious (score: 0.04)	possibly damaging with a score of 0.761 (sensitivity: 0.85; specificity: 0.92)
1	WDR36	WD repeat domain 36	chr5	110 428 134	Exon 1	G	A	SNV	missense	0.634	NM_139281	C148G>A	p.Gly50Arg	Tolerated (score: 0.12)	benign with a score of 0.392 (sensitivity: 0.90; specificity: 0.90)
1	WDR37	WD repeat domain 37	chr10	1 151 191	Exon 11	T	G	SNV	missense	0.242	NM_014023	C1087T>G	p.Phe383Val	Deleterious (score: 0)	probably damaging with a score of 0.992 (sensitivity: 0.70; specificity: 0.97)
1	WDR93	WD repeat domain 93	chr15	90 280 856	Exon 15	G	A	SNV	missense	0.284	NM_020212	C1861G>A	p.Arg554His	Tolerated (score: 0.17)	possibly damaging with a score of 0.850 (sensitivity: 0.83; specificity: 0.93)
5	WFDC3	WAP four-disulfide core domain 3	chr20	44 404 239	Exon 6	G	A	SNV	missense	0.217	NM_080614	C496C>T	p.Arg166Ile	Tolerated (score: 0.07)	possibly damaging with a score of 0.811 (sensitivity: 0.84; specificity: 0.93)
9	WIS	wortless homolog (Drosophila) = GPR117	chr1	68 619 327	Exon 5	G	T	SNV	missense	0.563	NM_001002292	C670C>A	p.Gln224Iys	Deleterious (score: 0)	probably damaging with a score of 0.999 (sensitivity: 0.14; specificity: 0.99)
3	WNK1	WNK lysine deficient protein kinase 1	chr12	863 236	Exon 1	C	T	SNV	missense	0.400	NM_213655	C509C>T	p.Pro169Ser	Deleterious (score: 0.04)	probably damaging with a score of 0.13 (sensitivity: 0.96; specificity: 0.78)
12	VIP1	Vip1 domain family, member 1	chr1	54 332 580	Exon 8	T	C	SNV	missense	0.424	NM_018982	C499A>G	p.Ile167Val	Tolerated (score: 1)	benign with a score of 0.000 (sensitivity: 1.00; specificity: 0.00)
15	VIPM1	Vip motif containing 1	chr14	75 265 344	Exon 5	A	A	SNV	missense	0.485	NM_019589	C3344G>A	p.Arg115Gln	Tolerated (score: 0.14)	benign with a score of 0.440 (sensitivity: 0.89; specificity: 0.90)
3	ZAN	zinc finger protein 189	chr7	100 361 488	Exon 21	C	C	SNV	missense	0.346	NM_003386	C4046T>C	p.Met11349Thr	Deleterious (score: 0)	benign with a score of 0.451 (sensitivity: 0.99; specificity: 0.90)
15	ZNF536	Zinc finger protein 536	chr9	104 170 672	Exon 4	T	C	SNV	missense	0.409	NM_197977	C496T>C	p.Tyr168His	Deleterious (score: 0)	benign with a score of 0.065 (sensitivity: 0.94; specificity: 0.84)
15	ZNF610	Zinc finger protein 610	chr19	30 936 603	Exon 2	A	C	SNV	missense	0.543	NM_014717	C2134G>A	p.Glu721Iys	Deleterious (score: 0)	possibly damaging with a score of 0.953 (sensitivity: 0.79; specificity: 0.95)
15	ZNF746	Zinc finger protein 746	chr19	52 856 938	Exon 4	C	T	SNV	missense	0.636	NM_001161425	C67C>T	p.Arg23Cys	Tolerated (score: 0.05)	benign with a score of 0.204 (sensitivity: 0.92; specificity: 0.88)
3	ZNF790	Zinc finger protein 790	chr7	149 171 980	Exon 7	C	T	SNV	missense	0.571	NM_152557	C1424G>A	p.Cys475Tyr	Deleterious (score: 0.02)	benign with a score of 0.411 (sensitivity: 0.89; specificity: 0.90)
3	ZNHIT6	Zinc finger, HIT type 6	chr19	37 314 190	Exon 4	G	T	SNV	missense	0.395	NM_206894	C226C>A	p.Pro676Ile	Deleterious (score: 0)	benign with a score of 0.099 (sensitivity: 0.93; specificity: 0.85)
3	ZNHIT6	Zinc finger, HIT type 6	chr1	86 144 456	Exon 7	T	C	SNV	missense	0.457	NM_017953	C1097A>G	p.Asp386Gly	Deleterious (score: 0.02)	benign with a score of 0.007 (sensitivity: 0.96; specificity: 0.75)

Supplemental_Table_2

Ref Seq	Exon	chrom	start(-20 nt)	end(+20 nt)	intervalle (+/-20nt)	size (+/-20nt)	start	end	intervalle (strict)	size	details	transcript	coverage (%)
ADAMTSL1	exon1	chr9	18474210	18474313	chr9:18474210-18474313	104	18474230	18474293	chr9:18474230-18474293	64	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon2	chr9	18504806	18504974	chr9:18504806-18504974	169	18504826	18504954	chr9:18504826-18504954	129	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon3	chr9	18533224	18533310	chr9:18533224-18533310	87	18533244	18533290	chr9:18533244-18533290	47	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon4	chr9	18574007	18574284	chr9:18574007-18574284	278	18574027	18574264	chr9:18574027-18574264	238	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon5	chr9	18622220	18622387	chr9:18622220-18622387	168	18622240	18622367	chr9:18622240-18622367	128	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon6	chr9	18635920	18636035	chr9:18635920-18636035	116	18635940	18636015	chr9:18635940-18636015	76	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon7	chr9	18639231	18639429	chr9:18639231-18639429	199	18639251	18639409	chr9:18639251-18639409	159	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon8	chr9	18657616	18657768	chr9:18657616-18657768	153	18657636	18657748	chr9:18657636-18657748	113	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon9	chr9	18661912	18662091	chr9:18661912-18662091	180	18661932	18662071	chr9:18661932-18662071	140	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon10	chr9	18675834	18675925	chr9:18675834-18675925	92	18675854	18675905	chr9:18675854-18675905	52	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon11	chr9	18680289	18680534	chr9:18680289-18680534	246	18680309	18680514	chr9:18680309-18680514	206	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon12	chr9	18681789	18681977	chr9:18681789-18681977	189	18681809	18681957	chr9:18681809-18681957	149	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon13	chr9	18684693	18684822	chr9:18684693-18684822	130	18684713	18684802	chr9:18684713-18684802	90	refseq ADAMTSL1 isoform1 isoforrn	NM_001040272	100,00
ADAMTSL1	exon14	chr9	18706724	18707066	chr9:18706724-18707066	343	18706744	18707046	chr9:18706744-18707046	303	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon15	chr9	18721513	18721683	chr9:18721513-18721683	171	18721533	18721663	chr9:18721533-18721663	131	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon16	chr9	18753275	18753526	chr9:18753275-18753526	252	18753295	18753506	chr9:18753295-18753506	212	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon17	chr9	18770579	18770799	chr9:18770579-18770799	221	18770599	18770779	chr9:18770599-18770779	181	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon18	chr9	18775720	18775914	chr9:18775720-18775914	195	18775740	18775894	chr9:18775740-18775894	155	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon19	chr9	18776758	18777924	chr9:18776758-18777924	1167	18776778	18777904	chr9:18776778-18777904	1127	refseq ADAMTSL1 isoform2 :exon1	NM_001040272	100,00
ADAMTSL1	exon20	chr9	18795374	18795542	chr9:18795374-18795542	169	18795394	18795522	chr9:18795394-18795522	129	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon21	chr9	18817086	18817255	chr9:18817086-18817255	170	18817106	18817235	chr9:18817106-18817235	130	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon22	chr9	18826261	18826481	chr9:18826261-18826481	221	18826281	18826461	chr9:18826281-18826461	181	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon23	chr9	18829820	18829995	chr9:18829820-18829995	176	18829840	18829975	chr9:18829840-18829975	136	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon24	chr9	18887808	18888061	chr9:18887808-18888061	254	18887828	18888041	chr9:18887828-18888041	214	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon25	chr9	18889545	18889766	chr9:18889545-18889766	222	18889565	18889746	chr9:18889565-18889746	182	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon26	chr9	18892366	18892614	chr9:18892366-18892614	249	18892386	18892594	chr9:18892386-18892594	209	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon27	chr9	18905759	18905909	chr9:18905759-18905909	151	18905779	18905889	chr9:18905779-18905889	111	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon28	chr9	18906669	18906930	chr9:18906669-18906930	262	18906689	18906910	chr9:18906689-18906910	222	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADAMTSL1	exon29	chr9	18908419	18908656	chr9:18908419-18908656	148	18908439	18908546	chr9:18908439-18908546	108	refseq ADAMTSL1 isoform2 :exon2	NM_001040272	100,00
ADCV6	exon21	chr12	49162353	49162519	chr12:49162353-49162519	167	49162373	49162499	chr12:49162373-49162499	127	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon20	chr12	49162699	49162864	chr12:49162699-49162864	166	49162719	49162844	chr12:49162719-49162844	126	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon19	chr12	49164528	49164773	chr12:49164528-49164773	246	49164548	49164753	chr12:49164548-49164753	206	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon18	chr12	49165472	49165776	chr12:49165472-49165776	305	49165492	49165756	chr12:49165492-49165756	265	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon17	chr12	49166057	49166227	chr12:49166057-49166227	171	49166077	49166207	chr12:49166077-49166207	131	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon16	chr12	49166270	49166346	chr12:49166270-49166346	77	49166290	49166326	chr12:49166290-49166326	37	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon15	chr12	49167231	49167450	chr12:49167231-49167450	220	49167251	49167430	chr12:49167251-49167430	180	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon14	chr12	49167702	49167901	chr12:49167702-49167901	200	49167722	49167881	chr12:49167722-49167881	160	refseq ADCV6 isoform1 isoforrn	NM_015270	100,00
ADCV6	exon13	chr12	49168164	49168321	chr12:49168164-49168321	158	49168184	49168301	chr12:49168184-49168301	118	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon12	chr12	49168453	49168581	chr12:49168453-49168581	129	49168473	49168651	chr12:49168473-49168651	89	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon11	chr12	49168719	49168857	chr12:49168719-49168857	139	49168739	49168879	chr12:49168739-49168879	99	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon10	chr12	49169065	49169253	chr12:49169065-49169253	189	49169085	49169233	chr12:49169085-49169233	149	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon9	chr12	49169435	49169501	chr12:49169435-49169501	67	49169455	49169481	chr12:49169455-49169481	27	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon8	chr12	49169725	49169894	chr12:49169725-49169894	170	49169745	49169874	chr12:49169745-49169874	130	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon7	chr12	49169971	49170153	chr12:49169971-49170153	183	49169991	49170133	chr12:49169991-49170133	143	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon6	chr12	49170389	49170389	chr12:49170389-49170389	200	49170369	49170369	chr12:49170369-49170369	160	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon5	chr12	49170866	49171034	chr12:49170866-49171034	169	49170886	49171014	chr12:49170886-49171014	129	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon4	chr12	49171172	49171324	chr12:49171172-49171324	153	49171192	49171304	chr12:49171192-49171304	113	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon3	chr12	49171539	49171737	chr12:49171539-49171737	163	49171579	49171719	chr12:49171579-49171719	123	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon2	chr12	49171870	49172060	chr12:49171870-49172060	191	49171890	49172040	chr12:49171890-49172040	151	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
ADCV6	exon1	chr12	49172337	49172737	chr12:49172337-49172737	905	49172357	49172717	chr12:49172357-49172717	865	refseq ADCV6 isoform1 isoforrn	NM_015270, NM_020983	100,00
AEBP2	exon1	chr12	19592613	19593324	chr12:19592613-19593324	712	19592633	19593304	chr12:19592633-19593304	672	refseq AEBP2 isoform1 isoforrn	NM_01114176, NM_153207	29,46
AEBP2	exon1	chr12	19593618	19593681	chr12:19593618-19593681	64	19593638	19593664	chr12:19593638-19593664	24	refseq AEBP2 isoform3 :exon1 extn	NM_001267043	100,00
AEBP2	exon2	chr12	19615423	19615671	chr12:19615423-19615671	249	19615443	19615651	chr12:19615443-19615651	209	refseq AEBP2 isoform1 isoforrn	NM_01114176, NM_153207, NM_001	100,00
AEBP2	exon3	chr12	19626161	19626309	chr12:19626161-19626309	149	19626181	19626289	chr12:19626181-19626289	109	refseq AEBP2 isoform1 isoforrn	NM_01114176, NM_153207, NM_001	100,00
AEBP2	exon4	chr12	19646713	19646940	chr12:19646713-19646940	228	19646733	19646920	chr12:19646733-19646920	188	refseq AEBP2 isoform1 isoforrn	NM_01114176, NM_153207, NM_001	100,00
AEBP2	exon5	chr12	19653010	19653175	chr12:19653010-19653175	166	19653030	19653155	chr12:19653030-19653155	126	refseq AEBP2 isoform1 isoforrn	NM_001114176, NM_153207, NM_001	100,00
AEBP2	exon6	chr12	19665419	19665511</									

ARID1A	exon6	exon6	chr1	27087854	27087984	chr1:27087854-27087984	131	27087874	27087964	chr1:27087874-27087964	91	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon7	exon7	chr1	27088622	27088830	chr1:27088622-27088830	209	27088642	27088810	chr1:27088642-27088810	169	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon8	exon8	chr1	27089443	27089796	chr1:27089443-27089796	354	27089463	27089776	chr1:27089463-27089776	314	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon9	exon9	chr1	27092691	27092877	chr1:27092691-27092877	187	27092711	27092857	chr1:27092711-27092857	147	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon10	exon10	chr1	27092927	27093077	chr1:27092927-27093077	151	27092947	27093057	chr1:27092947-27093057	111	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon11	exon11	chr1	27094260	27094510	chr1:27094260-27094510	251	27094280	27094490	chr1:27094280-27094490	211	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon12	exon12	chr1	27097589	27097837	chr1:27097589-27097837	249	27097609	27097817	chr1:27097609-27097817	209	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon13	exon13	chr1	27098970	27099143	chr1:27098970-27099143	174	27098990	27099123	chr1:27098990-27099123	134	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon14	exon14	chr1	27099282	27099498	chr1:27099282-27099498	217	27099302	27099478	chr1:27099302-27099478	177	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon15	exon15	chr1	27099816	27100007	chr1:27099816-27100007	192	27099836	27099987	chr1:27099836-27099987	152	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon16	exon16	chr1	27100050	27100228	chr1:27100050-27100228	179	27100070	27100208	chr1:27100070-27100208	139	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon17	exon17	chr1	27100272	27100409	chr1:27100272-27100409	138	27100292	27100389	chr1:27100292-27100389	98	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon18	exon18	chr1	27100799	27101731	chr1:27100799-27101731	933	27100819	27101711	chr1:27100819-27101711	893	refseq	ARID1A(isoforme1 isoforme2):exon18	e NM_006015	100,00
ARID1A	exon19	exon19	chr1	27102047	27102218	chr1:27102047-27102218	172	27102067	27102198	chr1:27102067-27102198	132	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID1A	exon20	exon20	chr1	27105493	27107267	chr1:27105493-27107267	1775	27105513	27107247	chr1:27105513-27107247	1735	refseq	ARID1A(isoforme1 isoforme2)	NM_139135, NM_006015	100,00
ARID3A	exon1	chr19		929508	929916	chr19:929508-929916	409	929528	929896	chr19:929528-929896	369	refseq	ARID3A(isoforme1):exon1	exr NM_005224	91,87
ARID3A	exon2	chr19		932397	932762	chr19:932397-932762	366	932417	932742	chr19:932417-932742	326	refseq	ARID3A(isoforme1):exon2	exr NM_005224	100,00
ARID3A	exon3	chr19		960071	960184	chr19:960071-960184	114	960091	960164	chr19:960091-960164	74	refseq	ARID3A(isoforme1):exon3	exr NM_005224	100,00
ARID3A	exon4	chr19		964227	964451	chr19:964227-964451	225	964247	964431	chr19:964247-964431	185	refseq	ARID3A(isoforme1):exon4	exr NM_005224	100,00
ARID3A	exon5	chr19		964812	965100	chr19:964812-965100	289	964832	965080	chr19:964832-965080	249	refseq	ARID3A(isoforme1):exon5	exr NM_005224	100,00
ARID3A	exon6	chr19		966551	966888	chr19:966551-966888	338	966571	966868	chr19:966571-966868	298	refseq	ARID3A(isoforme1):exon6	exr NM_005224	100,00
ARID3A	exon7	chr19		968384	968523	chr19:968384-968523	140	968404	968503	chr19:968404-968503	100	refseq	ARID3A(isoforme1):exon7	exr NM_005224	100,00
ARID3A	exon8	chr19		971857	972085	chr19:971857-972085	229	971877	972065	chr19:971877-972065	189	refseq	ARID3A(isoforme1):exon8	exr NM_005224	100,00
ATP13A4	exon30	chr3		193120420	193120673	chr3:193120420-193120673	254	193120440	193120653	chr3:193120440-193120653	214	refseq	ATP13A4(isoforme1):exon30	NM_032279	100,00
ATP13A4	exon29	chr3		193125081	193125202	chr3:193125081-193125202	122	193125101	193125182	chr3:193125101-193125182	82	refseq	ATP13A4(isoforme1):exon29	NM_032279	100,00
ATP13A4	exon28	chr3		193128750	193128879	chr3:193128750-193128879	130	193128770	193128859	chr3:193128770-193128859	90	refseq	ATP13A4(isoforme1):exon28	NM_032279	100,00
ATP13A4	exon27	chr3		193129946	193130180	chr3:193129946-193130180	235	193129966	193130160	chr3:193129966-193130160	195	refseq	ATP13A4(isoforme1):exon27	NM_032279	100,00
ATP13A4	exon26	chr3		193132347	193132559	chr3:193132347-193132559	213	193132367	193132539	chr3:193132367-193132539	173	refseq	ATP13A4(isoforme1):exon26	NM_032279	100,00
ATP13A4	exon25	chr3		193151613	193151726	chr3:193151613-193151726	114	193151633	193151706	chr3:193151633-193151706	74	refseq	ATP13A4(isoforme1):exon25	NM_032279	100,00
ATP13A4	exon24	chr3		193153416	193153553	chr3:193153416-193153553	138	193153436	193153533	chr3:193153436-193153533	98	refseq	ATP13A4(isoforme1):exon24	NM_032279	100,00
ATP13A4	exon23	chr3		193156243	193156393	chr3:193156243-193156393	151	193156263	193156373	chr3:193156263-193156373	111	refseq	ATP13A4(isoforme1):exon23	NM_032279	100,00
ATP13A4	exon22	chr3		193156791	193156874	chr3:193156791-193156874	84	193156811	193156854	chr3:193156811-193156854	44	refseq	ATP13A4(isoforme1):exon22	NM_032279	100,00
ATP13A4	exon21	chr3		193158326	193158446	chr3:193158326-193158446	121	193158346	193158426	chr3:193158346-193158426	81	refseq	ATP13A4(isoforme1):exon21	NM_032279	100,00
ATP13A4	exon20	chr3		193159234	193159397	chr3:193159234-193159397	164	193159254	193159377	chr3:193159254-193159377	124	refseq	ATP13A4(isoforme1):exon20	NM_032279	100,00
ATP13A4	exon19	chr3		193160161	193160365	chr3:193160161-193160365	205	193160181	193160345	chr3:193160181-193160345	165	refseq	ATP13A4(isoforme1):exon19	NM_032279	100,00
ATP13A4	exon18	chr3		193165974	193166139	chr3:193165974-193166139	166	193165994	193166119	chr3:193165994-193166119	126	refseq	ATP13A4(isoforme1):exon18	NM_032279	100,00
ATP13A4	exon17	chr3		193171869	193172021	chr3:193171869-193172021	153	193171889	193172001	chr3:193171889-193172001	113	refseq	ATP13A4(isoforme1):exon17	NM_032279	100,00
ATP13A4	exon16	chr3		193174768	193174962	chr3:193174768-193174962	195	193174788	193174942	chr3:193174788-193174942	155	refseq	ATP13A4(isoforme1):exon16	NM_032279	100,00
ATP13A4	exon15	chr3		193175147	193175274	chr3:193175147-193175274	128	193175167	193175254	chr3:193175167-193175254	88	refseq	ATP13A4(isoforme1):exon15	NM_032279	100,00
ATP13A4	exon14	chr3		193176849	193177040	chr3:193176849-193177040	192	193176869	193177020	chr3:193176869-193177020	152	refseq	ATP13A4(isoforme1):exon14	NM_032279	100,00
ATP13A4	exon13	chr3		193180630	193180632	chr3:193180630-193180632	103	193180550	193180612	chr3:193180550-193180612	63	refseq	ATP13A4(isoforme1):exon13	NM_032279	100,00
ATP13A4	exon12	chr3		193182708	193182937	chr3:193182708-193182937	230	193182728	193182917	chr3:193182728-193182917	190	refseq	ATP13A4(isoforme1):exon12	NM_032279	100,00
ATP13A4	exon11	chr3		193183793	193183991	chr3:193183793-193183991	199	193183813	193183971	chr3:193183813-193183971	159	refseq	ATP13A4(isoforme1):exon11	NM_032279	100,00
ATP13A4	exon10	chr3		193185084	193185295	chr3:193185084-193185295	212	193185104	193185275	chr3:193185104-193185275	172	refseq	ATP13A4(isoforme1):exon10	NM_032279	100,00
ATP13A4	exon9	chr3		193188627	193188802	chr3:193188627-193188802	176	193188742	193188782	chr3:193188742-193188782	136	refseq	ATP13A4(isoforme1):exon9	e NM_032279	100,00
ATP13A4	exon8	chr3		193201704	193201814	chr3:193201704-193201814	111	193201724	193201794	chr3:193201724-193201794	71	refseq	ATP13A4(isoforme1):exon8	e NM_032279	100,00
ATP13A4	exon7	chr3		193207498	193207673	chr3:193207498-193207673	176	193207518	193207653	chr3:193207518-193207653	136	refseq	ATP13A4(isoforme1):exon7	e NM_032279	100,00
ATP13A4	exon6	chr3		193209097	193209207	chr3:193209097-193209207	111	193209117	193209187	chr3:193209117-193209187	71	refseq	ATP13A4(isoforme1):exon6	e NM_032279	100,00
ATP13A4	exon5	chr3		193210685	193210806	chr3:193210685-193210806	122	193210705	193210786	chr3:193210705-193210786	82	refseq	ATP13A4(isoforme1):exon5	e NM_032279	100,00
ATP13A4	exon4	chr3		193210858	193210969	chr3:193210858-193210969	112	193210878	193210949	chr3:193210878-193210949	72	refseq	ATP13A4(isoforme1):exon4	e NM_032279	100,00
ATP13A4	exon3	chr3		193220261	193220448	chr3:193220261-193220448	188	193220281	193220428	chr3:193220281-193220428	148	refseq	ATP13A4(isoforme1):exon3	e NM_032279	100,00
ATP13A4	exon2	chr3		193232466	193232680	chr3:193232466-193232680	215	193232486	193232660	chr3:193232486-193232660	175	refseq	ATP13A4(isoforme1):exon2	e NM_032279	100,00
ATP13A4	exon1	chr3		193272508	193272608	chr3:193272508-193272608	101	193272528	193272588	chr3:193272528-193272588	61	refseq	ATP13A4(isoforme1):exon1	e NM_032279	100,00
BCOR	exon14	exon1	chrX	39911341	39911673	chrX:39911341-39911673	333	39911361	39911653	chrX:39911361-39911653	293	refseq	BCOR(isoforme1 isoforme2)	is NM_001123383, NM_001123385, NM_001123388, NM_001123389	100,00
BCOR	exon13	exon1	chrX	39913118	39913315	chrX:39913118-39913315	198	39913138	39913295	chrX:39913138-39913295	158	refseq	BCOR(isoforme1 isoforme2)	is NM_001123383, NM_001123385, NM_001123388, NM_001123389	100,00
BCOR	exon12	exon1	chrX	39913488	39913606	chrX:39913488-39913606	119	39913508	39913586	chrX:39913508-39913586	79	refseq	BCOR(isoforme1 isoforme2)	is NM_001123383, NM_001123385, NM_001123388, NM_001123389	100,00
BCOR	exon11	exon1	chrX	39914600	39914786	chrX:39914600-39914786	187	39914620	39914766	chrX:39914620-39914766	147	refseq	BCOR(isoforme1 isoforme2)	is NM_001123383, NM_001123385, NM_001123388, NM_001123389	100,00
BCOR	exon10	exon1	chrX	39916387	39916594	chrX:39916387-39916594	208	39916407	39916574	chrX:39916407-39916574	168	refseq	BCOR(isoforme1 isoforme2)	is NM_001123383, NM_001123385, NM_001123388, NM_001123389	100,00
BCOR	exon9	exon9	chrX	39921371	39921666	chrX:39921371-39921666	296	3992139							

CREBBP	exon15 exon1	chr16	3817700	3817930	chr16:3817700-3817930	231	3817720	3817910	chr16:3817720-3817910	191	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon14 exon1	chr16	3819154	3819374	chr16:3819154-3819374	221	3819174	3819354	chr16:3819174-3819354	181	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon13 exon1	chr16	3820550	3821007	chr16:3820550-3821007	458	3820570	3820987	chr16:3820570-3820987	418	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon12 exon1	chr16	3823731	3823951	chr16:3823731-3823951	221	3823751	3823931	chr16:3823751-3823931	181	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon11 exon1	chr16	3824549	3824714	chr16:3824549-3824714	166	3824569	3824694	chr16:3824569-3824694	126	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon10 exon1	chr16	3827593	3827678	chr16:3827593-3827678	86	3827613	3827658	chr16:3827613-3827658	46	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon9 exon10	chr16	3827991	3828203	chr16:3827991-3828203	213	3828011	3828183	chr16:3828011-3828183	173	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon8 exon9	chr16	3828680	3828838	chr16:3828680-3828838	159	3828700	3828818	chr16:3828700-3828818	119	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon7 exon8	chr16	3830712	3830899	chr16:3830712-3830899	188	3830732	3830879	chr16:3830732-3830879	148	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon6 exon7	chr16	3831184	3831327	chr16:3831184-3831327	144	3831204	3831307	chr16:3831204-3831307	104	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon5 exon6	chr16	3832664	3832947	chr16:3832664-3832947	284	3832684	3832927	chr16:3832684-3832927	244	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon5	chr16	3841961	3842115	chr16:3841961-3842115	155	3841981	3842095	chr16:3841981-3842095	115	refseq CREBBP isoforme2:exon5 ex NM_004380		100,00
CREBBP	exon4 exon4	chr16	3843366	3843647	chr16:3843366-3843647	282	3843386	3843627	chr16:3843386-3843627	242	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon3 exon3	chr16	3860583	3860800	chr16:3860583-3860800	218	3860603	3860780	chr16:3860603-3860780	178	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CREBBP	exon2 exon2	chr16	3900277	3901030	chr16:3900277-3901030	754	3900297	3901010	chr16:3900297-3901010	714	refseq CREBBP isoforme1 isoforme2	NM_001079846, NM_004380	100,00
CUX2	exon1	chr12	111471961	111472064	chr12:111471961-111472064	104	111471981	111472044	chr12:111471981-111472044	64	refseq CUX2 isoforme1:exon1 exte NM_015267		100,00
CUX2	exon2	chr12	111651983	111652134	chr12:111651983-111652134	152	111652003	111652114	chr12:111652003-111652114	112	refseq CUX2 isoforme1:exon2 exte NM_015267		100,00
CUX2	exon3	chr12	111655673	111655761	chr12:111655673-111655761	89	111655693	111655741	chr12:111655693-111655741	49	refseq CUX2 isoforme1:exon3 exte NM_015267		100,00
CUX2	exon4	chr12	111701544	111701663	chr12:111701544-111701663	120	111701564	111701643	chr12:111701564-111701643	80	refseq CUX2 isoforme1:exon4 exte NM_015267		100,00
CUX2	exon5	chr12	111729201	111729376	chr12:111729201-111729376	176	111729221	111729356	chr12:111729221-111729356	136	refseq CUX2 isoforme1:exon5 exte NM_015267		100,00
CUX2	exon6	chr12	111731229	111731393	chr12:111731229-111731393	165	111731249	111731373	chr12:111731249-111731373	125	refseq CUX2 isoforme1:exon6 exte NM_015267		100,00
CUX2	exon7	chr12	111733116	111733233	chr12:111733116-111733233	118	111733136	111733213	chr12:111733136-111733213	78	refseq CUX2 isoforme1:exon7 exte NM_015267		100,00
CUX2	exon8	chr12	111734256	111734363	chr12:111734256-111734363	108	111734276	111734343	chr12:111734276-111734343	68	refseq CUX2 isoforme1:exon8 exte NM_015267		100,00
CUX2	exon9	chr12	111736324	111736413	chr12:111736324-111736413	90	111736344	111736393	chr12:111736344-111736393	50	refseq CUX2 isoforme1:exon9 exte NM_015267		100,00
CUX2	exon10	chr12	111741993	111742138	chr12:111741993-111742138	146	111742013	111742118	chr12:111742013-111742118	106	refseq CUX2 isoforme1:exon10 exte NM_015267		100,00
CUX2	exon11	chr12	111744704	111744936	chr12:111744704-111744936	233	111744724	111744916	chr12:111744724-111744916	193	refseq CUX2 isoforme1:exon11 exte NM_015267		100,00
CUX2	exon12	chr12	111744982	111745081	chr12:111744982-111745081	100	111745002	111745061	chr12:111745002-111745061	60	refseq CUX2 isoforme1:exon12 exte NM_015267		100,00
CUX2	exon13	chr12	111746068	111746157	chr12:111746068-111746157	90	111746088	111746137	chr12:111746088-111746137	50	refseq CUX2 isoforme1:exon13 exte NM_015267		100,00
CUX2	exon14	chr12	111746210	111746350	chr12:111746210-111746350	141	111746230	111746330	chr12:111746230-111746330	101	refseq CUX2 isoforme1:exon14 exte NM_015267		100,00
CUX2	exon15	chr12	111747824	111748506	chr12:111747824-111748506	683	111747844	111748486	chr12:111747844-111748486	643	refseq CUX2 isoforme1:exon15 exte NM_015267		100,00
CUX2	exon16	chr12	111749883	111750025	chr12:111749883-111750025	143	111749903	111750005	chr12:111749903-111750005	103	refseq CUX2 isoforme1:exon16 exte NM_015267		100,00
CUX2	exon17	chr12	111757795	111758599	chr12:111757795-111758599	805	111757815	111758579	chr12:111757815-111758579	765	refseq CUX2 isoforme1:exon17 exte NM_015267		100,00
CUX2	exon18	chr12	111760204	111760404	chr12:111760204-111760404	201	111760224	111760384	chr12:111760224-111760384	161	refseq CUX2 isoforme1:exon18 exte NM_015267		100,00
CUX2	exon19	chr12	111772224	111772534	chr12:111772224-111772534	311	111772244	111772514	chr12:111772244-111772514	271	refseq CUX2 isoforme1:exon19 exte NM_015267		100,00
CUX2	exon20	chr12	111776069	111776298	chr12:111776069-111776298	230	111776089	111776278	chr12:111776089-111776278	190	refseq CUX2 isoforme1:exon20 exte NM_015267		100,00
CUX2	exon21	chr12	111779563	111779877	chr12:111779563-111779877	315	111779583	111779857	chr12:111779583-111779857	275	refseq CUX2 isoforme1:exon21 exte NM_015267		100,00
CUX2	exon22	chr12	111785307	111786149	chr12:111785307-111786149	843	111785327	111786129	chr12:111785327-111786129	803	refseq CUX2 isoforme1:exon22 exte NM_015267		100,00
CXCR4	exon1	chr2	136872418	136873529	chr2:136872418-136873529	1112	136872438	136873509	chr2:136872438-136873509	1072	refseq CXCR4 isoforme2:exon1 exte NM_001008540		100,00
CXCR4	exon1	chr2	136875595	136875650	chr2:136875595-136875650	56	136875615	136875630	chr2:136875615-136875630	16	refseq CXCR4 isoforme1:exon1 exte NM_003467		100,00
DCDC1	exon7	chr11	31284589	31284640	chr11:31284589-31284640	52	31284609	31284620	chr11:31284609-31284620	12	refseq DCDC1 isoforme1:exon7 exte NM_181807		100,00
DCDC1	exon6	chr11	31287033	31287167	chr11:31287033-31287167	135	31287053	31287147	chr11:31287053-31287147	95	refseq DCDC1 isoforme1:exon6 exte NM_181807		100,00
DCDC1	exon5	chr11	31312173	31312419	chr11:31312173-31312419	247	31312193	31312399	chr11:31312193-31312399	207	refseq DCDC1 isoforme1:exon5 exte NM_181807		100,00
DCDC1	exon4	chr11	31327141	31327344	chr11:31327141-31327344	204	31327161	31327324	chr11:31327161-31327324	164	refseq DCDC1 isoforme1:exon4 exte NM_181807		100,00
DCDC1	exon3	chr11	31327758	31327955	chr11:31327758-31327955	198	31327778	31327935	chr11:31327778-31327935	158	refseq DCDC1 isoforme1:exon3 exte NM_181807		100,00
DCDC1	exon2	chr11	31329165	31329475	chr11:31329165-31329475	311	31329185	31329455	chr11:31329185-31329455	271	refseq DCDC1 isoforme1:exon2 exte NM_181807		100,00
DCDC1	exon1	chr11	31349643	31349847	chr11:31349643-31349847	205	31349663	31349827	chr11:31349663-31349827	165	refseq DCDC1 isoforme1:exon1 exte NM_181807		100,00
DGKI	exon22	chr7	137178508	137178602	chr7:137178508-137178602	95	137178528	137178582	chr7:137178528-137178582	55	refseq DGKI isoforme1:exon22 exte NM_004717		0,00
DGKI	exon1	chr7	137531187	137531628	chr7:137531187-137531628	442	137531207	137531608	chr7:137531207-137531608	402	refseq DGKI isoforme1:exon1 exte NM_004717		53,73
DGKI	exon34	chr7	137075945	137076102	chr7:137075945-137076102	158	137075965	137076082	chr7:137075965-137076082	118	refseq DGKI isoforme1:exon34 exte NM_004717		100,00
DGKI	exon33	chr7	137080323	137080463	chr7:137080323-137080463	141	137080343	137080443	chr7:137080343-137080443	101	refseq DGKI isoforme1:exon33 exte NM_004717		100,00
DGKI	exon32	chr7	137082102	137082179	chr7:137082102-137082179	78	137082122	137082159	chr7:137082122-137082159	38	refseq DGKI isoforme1:exon32 exte NM_004717		100,00
DGKI	exon31	chr7	137092600	137092761	chr7:137092600-137092761	162	137092620	137092741	chr7:137092620-137092741	122	refseq DGKI isoforme1:exon31 exte NM_004717		100,00
DGKI	exon30	chr7	137096895	137096973	chr7:137096895-137096973	79	137096915	137096953	chr7:137096915-137096953	39	refseq DGKI isoforme1:exon30 exte NM_004717		100,00
DGKI	exon29	chr7	137128802	137128868	chr7:137128802-137128868	67	137128822	137128848	chr7:137128822-137128848	27	refseq DGKI isoforme1:exon29 exte NM_004717		100,00
DGKI	exon28	chr7	137148214	137148377	chr7:137148214-137148377	164	137148234	137148357	chr7:137148234-137148357	124	refseq DGKI isoforme1:exon28 exte NM_004717		100,00
DGKI	exon27	chr7	137150633	137150801	chr7:137150633-137150801	169	137150653	137150781	chr7:137150653-137150781	129	refseq DGKI isoforme1:exon27 exte NM_004717		100,00
DGKI	exon26	chr7	137151627	137151678	chr7:137151627-137151678	52	137151647	137151658	chr7:137151647-137151658	12	refseq DGKI isoforme1:exon26 exte NM_004717		100,00
DGKI	exon25	chr7	137154275	137154385	chr7:137154275-137154385	111	137154295	137154365	chr7:137154295-137154365	71	refseq DGKI isoforme1:exon25 exte NM_004717		100,00
DGKI	exon24	chr7	137170099	137170184	chr7:137170099-137170184	86	137170119	137170164	chr7:137170119-137170164	46	refseq DGKI isoforme1:exon24 exte NM_004717		100,00
DGKI	exon23	chr7	137172335	137172455	chr7:137172335-137172455	121	137172355	137172435	chr7:137172355-137172435	81	refseq DGKI isoforme1:exon23 exte NM_004717		100,00
DGKI	exon21	chr7	137206591	137206732	chr7:137206591-137206732	142	137206611	137206712	chr7:137206611-137206712	102	refseq DGKI isoforme1:exon21 exte NM_004717		100,00
DGKI	exon20	chr7	137237334	137237394	chr7:137237334-137237394	241	137237114	137237314	chr7:137237114-137237314	201	refseq DGKI isoforme1:exon20 exte NM_004717		100,00
DGKI	exon19	chr7	137255900										

DNAH5	exon21	chr5	13882816	13882944	chr5:13882816-13882944	129	13882836	13882924	chr5:13882836-13882924	89	refseq DNAH5(isoforme1):exon21 e:NM_001369	100,00
DNAH5	exon20	chr5	13882992	13883223	chr5:13882992-13883223	232	13883012	13883203	chr5:13883012-13883203	192	refseq DNAH5(isoforme1):exon20 e:NM_001369	100,00
DNAH5	exon19	chr5	13885077	13885357	chr5:13885077-13885357	281	13885097	13885337	chr5:13885097-13885337	241	refseq DNAH5(isoforme1):exon19 e:NM_001369	100,00
DNAH5	exon18	chr5	13886052	13886258	chr5:13886052-13886258	207	13886072	13886238	chr5:13886072-13886238	167	refseq DNAH5(isoforme1):exon18 e:NM_001369	100,00
DNAH5	exon17	chr5	13891064	13891250	chr5:13891064-13891250	187	13891084	13891230	chr5:13891084-13891230	147	refseq DNAH5(isoforme1):exon17 e:NM_001369	100,00
DNAH5	exon16	chr5	13894738	13894950	chr5:13894738-13894950	213	13894758	13894930	chr5:13894758-13894930	173	refseq DNAH5(isoforme1):exon16 e:NM_001369	100,00
DNAH5	exon15	chr5	13900294	13900541	chr5:13900294-13900541	248	13900314	13900521	chr5:13900314-13900521	208	refseq DNAH5(isoforme1):exon15 e:NM_001369	100,00
DNAH5	exon14	chr5	13901340	13901702	chr5:13901340-13901702	363	13901360	13901682	chr5:13901360-13901682	323	refseq DNAH5(isoforme1):exon14 e:NM_001369	100,00
DNAH5	exon13	chr5	13902141	13902267	chr5:13902141-13902267	127	13902161	13902217	chr5:13902161-13902217	87	refseq DNAH5(isoforme1):exon13 e:NM_001369	100,00
DNAH5	exon12	chr5	13911474	13911622	chr5:13911474-13911622	149	13911494	13911602	chr5:13911494-13911602	109	refseq DNAH5(isoforme1):exon12 e:NM_001369	100,00
DNAH5	exon11	chr5	13913831	13914087	chr5:13913831-13914087	257	13913851	13914067	chr5:13913851-13914067	217	refseq DNAH5(isoforme1):exon11 e:NM_001369	100,00
DNAH5	exon10	chr5	13914608	13914771	chr5:13914608-13914771	164	13914628	13914751	chr5:13914628-13914751	124	refseq DNAH5(isoforme1):exon10 e:NM_001369	100,00
DNAH5	exon9	chr5	13916436	13916584	chr5:13916436-13916584	149	13916456	13916564	chr5:13916456-13916564	109	refseq DNAH5(isoforme1):exon9 e:NM_001369	100,00
DNAH5	exon8	chr5	13917231	13917385	chr5:13917231-13917385	155	13917251	13917365	chr5:13917251-13917365	115	refseq DNAH5(isoforme1):exon8 e:NM_001369	100,00
DNAH5	exon7	chr5	13919264	13919481	chr5:13919264-13919481	218	13919284	13919461	chr5:13919284-13919461	178	refseq DNAH5(isoforme1):exon7 e:NM_001369	100,00
DNAH5	exon6	chr5	13920568	13920746	chr5:13920568-13920746	179	13920588	13920726	chr5:13920588-13920726	139	refseq DNAH5(isoforme1):exon6 e:NM_001369	100,00
DNAH5	exon5	chr5	13922195	13922457	chr5:13922195-13922457	263	13922215	13922437	chr5:13922215-13922437	223	refseq DNAH5(isoforme1):exon5 e:NM_001369	100,00
DNAH5	exon4	chr5	13923368	13923569	chr5:13923368-13923569	202	13923388	13923549	chr5:13923388-13923549	162	refseq DNAH5(isoforme1):exon4 e:NM_001369	100,00
DNAH5	exon3	chr5	13928182	13928307	chr5:13928182-13928307	126	13928202	13928287	chr5:13928202-13928287	86	refseq DNAH5(isoforme1):exon3 e:NM_001369	100,00
DNAH5	exon2	chr5	13931198	13931373	chr5:13931198-13931373	176	13931218	13931353	chr5:13931218-13931353	136	refseq DNAH5(isoforme1):exon2 e:NM_001369	100,00
DNAH5	exon1	chr5	13944470	13944567	chr5:13944470-13944567	98	13944490	13944547	chr5:13944490-13944547	58	refseq DNAH5(isoforme1):exon1 e:NM_001369	100,00
DNAH7	exon65	chr2	196602624	196602871	chr2:196602624-196602871	248	196602644	196602851	chr2:196602644-196602851	208	refseq DNAH7(isoforme1):exon65 e:NM_018897	100,00
DNAH7	exon64	chr2	196605469	196605613	chr2:196605469-196605613	145	196605489	196605593	chr2:196605489-196605593	105	refseq DNAH7(isoforme1):exon64 e:NM_018897	100,00
DNAH7	exon63	chr2	196619040	196619258	chr2:196619040-196619258	219	196619060	196619238	chr2:196619060-196619238	179	refseq DNAH7(isoforme1):exon63 e:NM_018897	100,00
DNAH7	exon62	chr2	196620836	196621029	chr2:196620836-196621029	194	196620856	196621009	chr2:196620856-196621009	154	refseq DNAH7(isoforme1):exon62 e:NM_018897	100,00
DNAH7	exon61	chr2	196636363	196636634	chr2:196636363-196636634	272	196636383	196636614	chr2:196636383-196636614	232	refseq DNAH7(isoforme1):exon61 e:NM_018897	100,00
DNAH7	exon60	chr2	196640549	196640727	chr2:196640549-196640727	179	196640569	196640707	chr2:196640569-196640707	139	refseq DNAH7(isoforme1):exon60 e:NM_018897	100,00
DNAH7	exon59	chr2	196642503	196642729	chr2:196642503-196642729	227	196642523	196642709	chr2:196642523-196642709	187	refseq DNAH7(isoforme1):exon59 e:NM_018897	100,00
DNAH7	exon58	chr2	196651713	196651915	chr2:196651713-196651915	203	196651733	196651895	chr2:196651733-196651895	163	refseq DNAH7(isoforme1):exon58 e:NM_018897	100,00
DNAH7	exon57	chr2	196659041	196659282	chr2:196659041-196659282	242	196659061	196659262	chr2:196659061-196659262	202	refseq DNAH7(isoforme1):exon57 e:NM_018897	100,00
DNAH7	exon56	chr2	196661279	196661481	chr2:196661279-196661481	203	196661299	196661461	chr2:196661299-196661461	163	refseq DNAH7(isoforme1):exon56 e:NM_018897	100,00
DNAH7	exon55	chr2	196663999	196664216	chr2:196663999-196664216	218	196664019	196664196	chr2:196664019-196664196	178	refseq DNAH7(isoforme1):exon55 e:NM_018897	100,00
DNAH7	exon54	chr2	196671443	196671576	chr2:196671443-196671576	134	196671463	196671556	chr2:196671463-196671556	94	refseq DNAH7(isoforme1):exon54 e:NM_018897	100,00
DNAH7	exon53	chr2	196673385	196673620	chr2:196673385-196673620	236	196673405	196673600	chr2:196673405-196673600	196	refseq DNAH7(isoforme1):exon53 e:NM_018897	100,00
DNAH7	exon52	chr2	196674448	196674615	chr2:196674448-196674615	168	196674468	196674595	chr2:196674468-196674595	128	refseq DNAH7(isoforme1):exon52 e:NM_018897	100,00
DNAH7	exon51	chr2	196681331	196681707	chr2:196681331-196681707	377	196681351	196681687	chr2:196681351-196681687	337	refseq DNAH7(isoforme1):exon51 e:NM_018897	100,00
DNAH7	exon50	chr2	196682399	196682573	chr2:196682399-196682573	175	196682419	196682553	chr2:196682419-196682553	135	refseq DNAH7(isoforme1):exon50 e:NM_018897	100,00
DNAH7	exon49	chr2	196688958	196689189	chr2:196688958-196689189	232	196688978	196689169	chr2:196688978-196689169	192	refseq DNAH7(isoforme1):exon49 e:NM_018897	100,00
DNAH7	exon48	chr2	196698909	196699104	chr2:196698909-196699104	196	196698929	196699084	chr2:196698929-196699084	156	refseq DNAH7(isoforme1):exon48 e:NM_018897	100,00
DNAH7	exon47	chr2	196709705	196709909	chr2:196709705-196709909	205	196709725	196709889	chr2:196709725-196709889	165	refseq DNAH7(isoforme1):exon47 e:NM_018897	100,00
DNAH7	exon46	chr2	196718046	196718272	chr2:196718046-196718272	227	196718066	196718252	chr2:196718066-196718252	187	refseq DNAH7(isoforme1):exon46 e:NM_018897	100,00
DNAH7	exon45	chr2	196720514	196720735	chr2:196720514-196720735	222	196720534	196720715	chr2:196720534-196720715	182	refseq DNAH7(isoforme1):exon45 e:NM_018897	100,00
DNAH7	exon44	chr2	196722080	196722467	chr2:196722080-196722467	388	196722100	196722447	chr2:196722100-196722447	348	refseq DNAH7(isoforme1):exon44 e:NM_018897	100,00
DNAH7	exon43	chr2	196723177	196723548	chr2:196723177-196723548	372	196723197	196723528	chr2:196723197-196723528	332	refseq DNAH7(isoforme1):exon43 e:NM_018897	100,00
DNAH7	exon42	chr2	196726420	196726690	chr2:196726420-196726690	271	196726440	196726670	chr2:196726440-196726670	231	refseq DNAH7(isoforme1):exon42 e:NM_018897	100,00
DNAH7	exon41	chr2	196728852	196729765	chr2:196728852-196729765	914	196728872	196729745	chr2:196728872-196729745	874	refseq DNAH7(isoforme1):exon41 e:NM_018897	100,00
DNAH7	exon40	chr2	196736953	196737213	chr2:196736953-196737213	261	196736973	196737193	chr2:196736973-196737193	221	refseq DNAH7(isoforme1):exon40 e:NM_018897	100,00
DNAH7	exon39	chr2	196738271	196738438	chr2:196738271-196738438	168	196738291	196738418	chr2:196738291-196738418	128	refseq DNAH7(isoforme1):exon39 e:NM_018897	100,00
DNAH7	exon38	chr2	196740378	196740587	chr2:196740378-196740587	210	196740398	196740567	chr2:196740398-196740567	170	refseq DNAH7(isoforme1):exon38 e:NM_018897	100,00
DNAH7	exon37	chr2	196741247	196741443	chr2:196741247-196741443	197	196741267	196741423	chr2:196741267-196741423	157	refseq DNAH7(isoforme1):exon37 e:NM_018897	100,00
DNAH7	exon36	chr2	196746498	196746736	chr2:196746498-196746736	239	196746518	196746716	chr2:196746518-196746716	199	refseq DNAH7(isoforme1):exon36 e:NM_018897	100,00
DNAH7	exon35	chr2	196749288	196749553	chr2:196749288-196749553	266	196749308	196749533	chr2:196749308-196749533	226	refseq DNAH7(isoforme1):exon35 e:NM_018897	100,00
DNAH7	exon34	chr2	196750844	196751016	chr2:196750844-196751016	173	196750864	196750996	chr2:196750864-196750996	133	refseq DNAH7(isoforme1):exon34 e:NM_018897	100,00
DNAH7	exon33	chr2	196752961	196753178	chr2:196752961-196753178	218	196752981	196753158	chr2:196752981-196753158	178	refseq DNAH7(isoforme1):exon33 e:NM_018897	100,00
DNAH7	exon32	chr2	196753502	196753725	chr2:196753502-196753725	224	196753522	196753705	chr2:196753522-196753705	184	refseq DNAH7(isoforme1):exon32 e:NM_018897	100,00
DNAH7	exon31	chr2	196756358	196756548	chr2:196756358-196756548	191	196756378	196756528	chr2:196756378-196756528	151	refseq DNAH7(isoforme1):exon31 e:NM_018897	100,00
DNAH7	exon30	chr2	196759679	196759968	chr2:196759679-196759968	290	196759699	196759948	chr2:196759699-196759948	250	refseq DNAH7(isoforme1):exon30 e:NM_018897	100,00
DNAH7	exon29	chr2	196762370	196762509	chr2:196762370-196762509	140	196762390	196762489	chr2:196762390-196762489	100	refseq DNAH7(isoforme1):exon29 e:NM_018897	100,00
DNAH7	exon28	chr2	196764985	196765238	chr2:196764985-196765238	254	196765005	196765218	chr2:196765005-196765218	214	refseq DNAH7(isoforme1):exon28 e:NM_018897	100,00
DNAH7	exon27	chr2	196771362	196771530	chr2:196771362-196771530	169	196771382	196771510	chr2:196771382-196771510	129	refseq DNAH7(isoforme1):exon27 e:NM_018897	100,00
DNAH7	exon26	chr2	196771610	196771753	chr2:196771610-196771753	144	196771630	196771733	chr2:196771630-196771733	104	refseq DNAH7(isoforme1):exon26 e:NM_018897	100,00
DNAH7	exon25	chr2	196774730	196774939	chr2:196774730-196774939	210	196774750	196774919	chr2:196774750-196774919	170	refseq DNAH7(isoforme1):exon25 e:NM_018897	100,00
DNAH7	exon24	chr2	196786791	196786941	chr2:196786791-196786941	151	196786811	196786921	chr2:196786811-196786921	111	refseq DNAH7(isoforme1):exon24 e:NM_018897	100,00
DNAH7	exon23	chr2	196788298	196788551	chr2:196788298-196788551	254	196788318	196788318	chr2:19678			

DOCK6	exon41	chr19	11314736	11314791	chr19:11314736-11314791	56	11314756	11314771	chr19:11314756-11314771	16	refseq DOCK6 (isoform1):exon41 exNM_020812	100,00	
DOCK6	exon40	chr19	11314855	11315027	chr19:11314855-11315027	173	11314875	11315007	chr19:11314875-11315007	133	refseq DOCK6 (isoform1):exon40 exNM_020812	100,00	
DOCK6	exon39	chr19	11319341	11319525	chr19:11319341-11319525	185	11319361	11319505	chr19:11319361-11319505	145	refseq DOCK6 (isoform1):exon39 exNM_020812	100,00	
DOCK6	exon38	chr19	11319566	11319799	chr19:11319566-11319799	234	11319586	11319779	chr19:11319586-11319779	194	refseq DOCK6 (isoform1):exon38 exNM_020812	100,00	
DOCK6	exon37	chr19	11322431	11322572	chr19:11322431-11322572	142	11322451	11322552	chr19:11322451-11322552	102	refseq DOCK6 (isoform1):exon37 exNM_020812	100,00	
DOCK6	exon36	chr19	11322648	11322847	chr19:11322648-11322847	200	11322668	11322827	chr19:11322668-11322827	160	refseq DOCK6 (isoform1):exon36 exNM_020812	100,00	
DOCK6	exon35	chr19	11323831	11324024	chr19:11323831-11324024	194	11323851	11324004	chr19:11323851-11324004	154	refseq DOCK6 (isoform1):exon35 exNM_020812	100,00	
DOCK6	exon34	chr19	11324930	11325105	chr19:11324930-11325105	176	11324950	11325085	chr19:11324950-11325085	136	refseq DOCK6 (isoform1):exon34 exNM_020812	100,00	
DOCK6	exon33	chr19	11325208	11325345	chr19:11325208-11325345	138	11325228	11325325	chr19:11325228-11325325	98	refseq DOCK6 (isoform1):exon33 exNM_020812	100,00	
DOCK6	exon32	chr19	11326042	11326167	chr19:11326042-11326167	126	11326062	11326147	chr19:11326062-11326147	86	refseq DOCK6 (isoform1):exon32 exNM_020812	100,00	
DOCK6	exon31	chr19	11326456	11326623	chr19:11326456-11326623	168	11326476	11326603	chr19:11326476-11326603	128	refseq DOCK6 (isoform1):exon31 exNM_020812	100,00	
DOCK6	exon30	chr19	11327569	11327792	chr19:11327569-11327792	224	11327589	11327772	chr19:11327589-11327772	184	refseq DOCK6 (isoform1):exon30 exNM_020812	100,00	
DOCK6	exon29	chr19	11327886	11328087	chr19:11327886-11328087	202	11327906	11328067	chr19:11327906-11328067	162	refseq DOCK6 (isoform1):exon29 exNM_020812	100,00	
DOCK6	exon28	chr19	11332506	11332716	chr19:11332506-11332716	211	11332526	11332696	chr19:11332526-11332696	171	refseq DOCK6 (isoform1):exon28 exNM_020812	100,00	
DOCK6	exon27	chr19	11332764	11332944	chr19:11332764-11332944	181	11332784	11332924	chr19:11332784-11332924	141	refseq DOCK6 (isoform1):exon27 exNM_020812	100,00	
DOCK6	exon26	chr19	11333390	11333601	chr19:11333390-11333601	212	11333410	11333581	chr19:11333410-11333581	172	refseq DOCK6 (isoform1):exon26 exNM_020812	100,00	
DOCK6	exon25	chr19	11333648	11333802	chr19:11333648-11333802	155	11333668	11333782	chr19:11333668-11333782	115	refseq DOCK6 (isoform1):exon25 exNM_020812	100,00	
DOCK6	exon24	chr19	11337992	11338173	chr19:11337992-11338173	182	11338012	11338153	chr19:11338012-11338153	142	refseq DOCK6 (isoform1):exon24 exNM_020812	100,00	
DOCK6	exon23	chr19	11339595	11339731	chr19:11339595-11339731	137	11339615	11339711	chr19:11339615-11339711	97	refseq DOCK6 (isoform1):exon23 exNM_020812	100,00	
DOCK6	exon22	chr19	11343858	11344062	chr19:11343858-11344062	205	11343878	11344024	chr19:11343878-11344024	165	refseq DOCK6 (isoform1):exon22 exNM_020812	100,00	
DOCK6	exon21	chr19	11346253	11346455	chr19:11346253-11346455	203	11346273	11346335	chr19:11346273-11346335	163	refseq DOCK6 (isoform1):exon21 exNM_020812	100,00	
DOCK6	exon20	chr19	11347001	11347273	chr19:11347001-11347273	273	11347021	11347253	chr19:11347021-11347253	233	refseq DOCK6 (isoform1):exon20 exNM_020812	100,00	
DOCK6	exon19	chr19	11347448	11347575	chr19:11347448-11347575	128	11347468	11347555	chr19:11347468-11347555	88	refseq DOCK6 (isoform1):exon19 exNM_020812	100,00	
DOCK6	exon18	chr19	11348111	11348253	chr19:11348111-11348253	143	11348131	11348233	chr19:11348131-11348233	103	refseq DOCK6 (isoform1):exon18 exNM_020812	100,00	
DOCK6	exon17	chr19	11348296	11348475	chr19:11348296-11348475	180	11348316	11348455	chr19:11348316-11348455	140	refseq DOCK6 (isoform1):exon17 exNM_020812	100,00	
DOCK6	exon16	chr19	11348700	11348811	chr19:11348700-11348811	112	11348720	11348791	chr19:11348720-11348791	72	refseq DOCK6 (isoform1):exon16 exNM_020812	100,00	
DOCK6	exon15	chr19	11348842	11349000	chr19:11348842-11349000	159	11348862	11348980	chr19:11348862-11348980	119	refseq DOCK6 (isoform1):exon15 exNM_020812	100,00	
DOCK6	exon14	chr19	11352700	11352903	chr19:11352700-11352903	204	11352720	11352883	chr19:11352720-11352883	164	refseq DOCK6 (isoform1):exon14 exNM_020812	100,00	
DOCK6	exon13	chr19	11353714	11353848	chr19:11353714-11353848	135	11353734	11353828	chr19:11353734-11353828	95	refseq DOCK6 (isoform1):exon13 exNM_020812	100,00	
DOCK6	exon12	chr19	11353913	11354081	chr19:11353913-11354081	169	11353933	11354061	chr19:11353933-11354061	129	refseq DOCK6 (isoform1):exon12 exNM_020812	100,00	
DOCK6	exon11	chr19	11354212	11354406	chr19:11354212-11354406	195	11354232	11354386	chr19:11354232-11354386	155	refseq DOCK6 (isoform1):exon11 exNM_020812	100,00	
DOCK6	exon10	chr19	11354457	11354578	chr19:11354457-11354578	122	11354477	11354558	chr19:11354477-11354558	82	refseq DOCK6 (isoform1):exon10 exNM_020812	100,00	
DOCK6	exon9	chr19	11356218	11356408	chr19:11356218-11356408	191	11356238	11356388	chr19:11356238-11356388	151	refseq DOCK6 (isoform1):exon9 exNM_020812	100,00	
DOCK6	exon8	chr19	11356467	11356574	chr19:11356467-11356574	108	11356487	11356554	chr19:11356487-11356554	68	refseq DOCK6 (isoform1):exon8 exNM_020812	100,00	
DOCK6	exon7	chr19	11358721	11358847	chr19:11358721-11358847	127	11358741	11358827	chr19:11358741-11358827	87	refseq DOCK6 (isoform1):exon7 exNM_020812	100,00	
DOCK6	exon6	chr19	11361529	11361782	chr19:11361529-11361782	254	11361549	11361762	chr19:11361549-11361762	214	refseq DOCK6 (isoform1):exon6 exNM_020812	100,00	
DOCK6	exon5	chr19	11362774	11362944	chr19:11362774-11362944	171	11362794	11362924	chr19:11362794-11362924	131	refseq DOCK6 (isoform1):exon5 exNM_020812	100,00	
DOCK6	exon4	chr19	11363137	11363246	chr19:11363137-11363246	110	11363157	11363226	chr19:11363157-11363226	70	refseq DOCK6 (isoform1):exon4 exNM_020812	100,00	
DOCK6	exon3	chr19	11363438	11363654	chr19:11363438-11363654	217	11363458	11363634	chr19:11363458-11363634	177	refseq DOCK6 (isoform1):exon3 exNM_020812	100,00	
DOCK6	exon2	chr19	11364294	11364422	chr19:11364294-11364422	129	11364314	11364402	chr19:11364314-11364402	89	refseq DOCK6 (isoform1):exon2 exNM_020812	100,00	
DSP	exon1	exon1	chr6	7542128	7542338	chr6:7542128-7542338	211	7542148	7542318	chr6:7542148-7542318	171	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon2	exon2	chr6	7555930	7556073	chr6:7555930-7556073	144	7555950	7556053	chr6:7555950-7556053	104	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon3	exon3	chr6	7558328	7558517	chr6:7558328-7558517	190	7558348	7558497	chr6:7558348-7558497	150	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon4	exon4	chr6	7559438	7559653	chr6:7559438-7559653	216	7559458	7559633	chr6:7559458-7559633	176	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon5	exon5	chr6	7562864	7563033	chr6:7562864-7563033	170	7562884	7563013	chr6:7562884-7563013	136	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon6	exon6	chr6	7563948	7564039	chr6:7563948-7564039	92	7563968	7564019	chr6:7563968-7564019	52	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon7	exon7	chr6	7565571	7565773	chr6:7565571-7565773	203	7565591	7565753	chr6:7565591-7565753	163	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon8	exon8	chr6	7566589	7566734	chr6:7566589-7566734	146	7566609	7566714	chr6:7566609-7566714	106	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon9	exon9	chr6	7567566	7567702	chr6:7567566-7567702	137	7567586	7567682	chr6:7567586-7567682	97	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon10	exon10	chr6	7567993	7568159	chr6:7567993-7568159	167	7568013	7568139	chr6:7568013-7568139	127	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon11	exon11	chr6	7568649	7568842	chr6:7568649-7568842	194	7568669	7568822	chr6:7568669-7568822	154	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon12	exon12	chr6	7569398	7569593	chr6:7569398-7569593	196	7569418	7569573	chr6:7569418-7569573	156	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon13	exon13	chr6	7570649	7570816	chr6:7570649-7570816	168	7570669	7570796	chr6:7570669-7570796	128	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon14	exon14	chr6	7571595	7571837	chr6:7571595-7571837	243	7571615	7571817	chr6:7571615-7571817	203	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon15	exon15	chr6	7572054	7572321	chr6:7572054-7572321	268	7572074	7572301	chr6:7572074-7572301	228	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon16	exon16	chr6	7574298	7574505	chr6:7574298-7574505	208	7574318	7574485	chr6:7574318-7574485	168	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon17	exon17	chr6	7574869	7575048	chr6:7574869-7575048	180	7574889	7575028	chr6:7574889-7575028	140	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon18	exon18	chr6	7575507	7575741	chr6:7575507-7575741	235	7575527	7575721	chr6:7575527-7575721	195	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon19	exon19	chr6	7576506	7576709	chr6:7576506-7576709	204	7576526	7576689	chr6:7576526-7576689	164	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon20	exon20	chr6	7577171	7577295	chr6:7577171-7577295	125	7577191	7577253	chr6:7577191-7577253	85	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon21	exon21	chr6	7577991	7578139	chr6:7577991-7578139	149	7578011	7578119	chr6:7578011-7578119	109	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon22	exon22	chr6	7578676	7578815	chr6:7578676-7578815	140	7578696	7578795	chr6:7578696-7578795	100	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DSP	exon23	chr6	7579487	7581822	chr6:7579487-7581822	2336	7579507	7581802	chr6:7579507-7581802	2296	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00	
DSP	exon24	exon24	chr6	7582854	7586131	chr6:7582854-7586131	3278	7582874	7586111	chr6:7582874-7586111	3238	refseq DSP (isoform1 isoform2):exiNM_004415, NM_001008844	100,00
DTNB	exon17	exon17	chr2	25602167	25602212</								

EP300	exon26	chr22	41565486	41565640	chr22:41565486-41565640	155	41565506	41565620	chr22:41565506-41565620	115	refseq EP300 isoforme1 :exon26 extNM_001429	100,00
EP300	exon27	chr22	41566389	41566595	chr22:41566389-41566595	207	41566409	41566575	chr22:41566409-41566575	167	refseq EP300 isoforme1 :exon27 extNM_001429	100,00
EP300	exon28	chr22	41568482	41568687	chr22:41568482-41568687	206	41568502	41568667	chr22:41568502-41568667	166	refseq EP300 isoforme1 :exon28 extNM_001429	100,00
EP300	exon29	chr22	41569606	41569808	chr22:41569606-41569808	203	41569626	41569788	chr22:41569626-41569788	163	refseq EP300 isoforme1 :exon29 extNM_001429	100,00
EP300	exon30	chr22	41572230	41572552	chr22:41572230-41572552	323	41572250	41572532	chr22:41572250-41572532	283	refseq EP300 isoforme1 :exon30 extNM_001429	100,00
EP300	exon31	chr22	41572756	41574980	chr22:41572756-41574980	2225	41572776	41574960	chr22:41572776-41574960	2185	refseq EP300 isoforme1 :exon31 extNM_001429	100,00
EPHA8	exon1	chr1	22890108	22890242	chr1:22890108-22890242	135	22890128	22890222	chr1:22890128-22890222	95	refseq EPHA8 isoforme1 isoforme2 :NM_020526,NM_001006943	0,00
EPHA8	exon2	chr1	22895761	22895866	chr1:22895761-22895866	106	22895781	22895846	chr1:22895781-22895846	66	refseq EPHA8 isoforme1 isoforme2 :NM_020526,NM_001006943	100,00
EPHA8	exon3	chr1	22902689	22903393	chr1:22902689-22903393	705	22902709	22903373	chr1:22902709-22903373	665	refseq EPHA8 isoforme1 isoforme2 :NM_020526,NM_001006943	100,00
EPHA8	exon4	chr1	22912952	22913148	chr1:22912952-22913148	197	22912972	22913128	chr1:22912972-22913128	157	refseq EPHA8 isoforme1 isoforme2 :NM_020526,NM_001006943	100,00
EPHA8	exon5	chr1	22915343	22915892	chr1:22915343-22915892	550	22915363	22915872	chr1:22915363-22915872	510	refseq EPHA8 isoforme2 :exon5 extNM_001006943	100,00
EPHA8	exon6	chr1	22919798	22919963	chr1:22919798-22919963	166	22919818	22919943	chr1:22919818-22919943	126	refseq EPHA8 isoforme1 :exon6 extNM_020526	100,00
EPHA8	exon7	chr1	22919996	22920199	chr1:22919996-22920199	204	22920016	22920179	chr1:22920016-22920179	164	refseq EPHA8 isoforme1 :exon7 extNM_020526	100,00
EPHA8	exon8	chr1	22921702	22921836	chr1:22921702-22921836	135	22921722	22921816	chr1:22921722-22921816	95	refseq EPHA8 isoforme1 :exon8 extNM_020526	100,00
EPHA8	exon9	chr1	22922578	22922686	chr1:22922578-22922686	109	22922598	22922666	chr1:22922598-22922666	69	refseq EPHA8 isoforme1 :exon9 extNM_020526	100,00
EPHA8	exon10	chr1	22923784	22923989	chr1:22923784-22923989	206	22923804	22923969	chr1:22923804-22923969	166	refseq EPHA8 isoforme1 :exon10 extNM_020526	100,00
EPHA8	exon11	chr1	22924148	22924374	chr1:22924148-22924374	227	22924168	22924354	chr1:22924168-22924354	187	refseq EPHA8 isoforme1 :exon11 extNM_020526	100,00
EPHA8	exon12	chr1	22924623	22924725	chr1:22924623-22924725	103	22924643	22924705	chr1:22924643-22924705	63	refseq EPHA8 isoforme1 :exon12 extNM_020526	100,00
EPHA8	exon13	chr1	22925310	22925560	chr1:22925310-22925560	255	22925330	22925540	chr1:22925330-22925540	211	refseq EPHA8 isoforme1 :exon13 extNM_020526	100,00
EPHA8	exon14	chr1	22927133	22927323	chr1:22927133-22927323	191	22927153	22927303	chr1:22927153-22927303	151	refseq EPHA8 isoforme1 :exon14 extNM_020526	100,00
EPHA8	exon15	chr1	22927370	22927601	chr1:22927370-22927601	232	22927390	22927581	chr1:22927390-22927581	192	refseq EPHA8 isoforme1 :exon15 extNM_020526	100,00
EPHA8	exon16	chr1	22927772	22927986	chr1:22927772-22927986	215	22927792	22927966	chr1:22927792-22927966	175	refseq EPHA8 isoforme1 :exon16 extNM_020526	100,00
EPHA8	exon17	chr1	22928099	22928254	chr1:22928099-22928254	156	22928119	22928234	chr1:22928119-22928234	116	refseq EPHA8 isoforme1 :exon17 extNM_020526	100,00
FOXL2	exon1	chr3	13866443	13866584	chr3:13866443-13866584	1172	13866433	13866554	chr3:13866433-13866554	1132	refseq FOXL2 isoforme1 :exon1 extNM_023067	100,00
GNA13	exon3	chr17	63010354	63010967	chr17:63010354-63010967	614	63010374	63010947	chr17:63010374-63010947	574	refseq GNA13 isoforme1 isoforme2 :NM_001282425,NM_006572	100,00
GNA13	exon2	chr17	63014350	63014441	chr17:63014350-63014441	92	63014370	63014421	chr17:63014370-63014421	52	refseq GNA13 isoforme1 isoforme2 :NM_001282425,NM_006572	100,00
GNA13	exon2	chr17	63049599	63049866	chr17:63049599-63049866	268	63049619	63049846	chr17:63049619-63049846	228	refseq GNA13 isoforme2 :exon2 extNM_006572	100,00
GNA13	exon1	chr17	63052408	63052731	chr17:63052408-63052731	324	63052428	63052711	chr17:63052428-63052711	284	refseq GNA13 isoforme2 :exon1 extNM_006572	100,00
GPC6	exon1	chr13	93879689	93879889	chr13:93879689-93879889	201	93879709	93879869	chr13:93879709-93879869	161	refseq GPC6 isoforme1 :exon1 extNM_005708	100,00
GPC6	exon2	chr13	94197495	94197694	chr13:94197495-94197694	200	94197515	94197674	chr13:94197515-94197674	160	refseq GPC6 isoforme1 :exon2 extNM_005708	100,00
GPC6	exon3	chr13	94482386	94482818	chr13:94482386-94482818	433	94482406	94482798	chr13:94482406-94482798	393	refseq GPC6 isoforme1 :exon3 extNM_005708	100,00
GPC6	exon4	chr13	94679962	94680168	chr13:94679962-94680168	207	94679982	94680148	chr13:94679982-94680148	167	refseq GPC6 isoforme1 :exon4 extNM_005708	100,00
GPC6	exon5	chr13	94938582	94938753	chr13:94938582-94938753	172	94938602	94938733	chr13:94938602-94938733	132	refseq GPC6 isoforme1 :exon5 extNM_005708	100,00
GPC6	exon6	chr13	94958213	94958397	chr13:94958213-94958397	185	94958233	94958377	chr13:94958233-94958377	145	refseq GPC6 isoforme1 :exon6 extNM_005708	100,00
GPC6	exon7	chr13	95034647	95034824	chr13:95034647-95034824	178	95034667	95034804	chr13:95034667-95034804	138	refseq GPC6 isoforme1 :exon7 extNM_005708	100,00
GPC6	exon8	chr13	95050699	95050915	chr13:95050699-95050915	217	95050719	95050895	chr13:95050719-95050895	177	refseq GPC6 isoforme1 :exon8 extNM_005708	100,00
GPC6	exon9	chr13	95055248	95055491	chr13:95055248-95055491	244	95055268	95055471	chr13:95055268-95055471	204	refseq GPC6 isoforme1 :exon9 extNM_005708	100,00
GPR75	exon1	chr2	54080250	54081913	chr2:54080250-54081913	1664	54080270	54081893	chr2:54080270-54081893	1624	refseq GPR75 isoforme1 :exon1 extNM_006794	100,00
GPR98	exon1	chr5	89854692	89854754	chr5:89854692-89854754	63	89854712	89854734	chr5:89854712-89854734	23	refseq GPR98 isoforme1 :exon1 extNM_032119	100,00
GPR98	exon2	chr5	89910631	89910856	chr5:89910631-89910856	226	89910651	89910836	chr5:89910651-89910836	186	refseq GPR98 isoforme1 :exon2 extNM_032119	100,00
GPR98	exon3	chr5	89913600	89913790	chr5:89913600-89913790	191	89913620	89913770	chr5:89913620-89913770	151	refseq GPR98 isoforme1 :exon3 extNM_032119	100,00
GPR98	exon4	chr5	89914882	89915018	chr5:89914882-89915018	137	89914902	89914998	chr5:89914902-89914998	97	refseq GPR98 isoforme1 :exon4 extNM_032119	100,00
GPR98	exon5	chr5	89918393	89918538	chr5:89918393-89918538	146	89918413	89918518	chr5:89918413-89918518	106	refseq GPR98 isoforme1 :exon5 extNM_032119	100,00
GPR98	exon6	chr5	89920926	89921080	chr5:89920926-89921080	155	89920946	89921060	chr5:89920946-89921060	115	refseq GPR98 isoforme1 :exon6 extNM_032119	100,00
GPR98	exon7	chr5	89923007	89923613	chr5:89923007-89923613	607	89923027	89923593	chr5:89923027-89923593	567	refseq GPR98 isoforme1 :exon7 extNM_032119	100,00
GPR98	exon8	chr5	89924358	89924669	chr5:89924358-89924669	312	89924378	89924649	chr5:89924378-89924649	272	refseq GPR98 isoforme1 :exon8 extNM_032119	100,00
GPR98	exon9	chr5	89925006	89925376	chr5:89925006-89925376	371	89925026	89925356	chr5:89925026-89925356	331	refseq GPR98 isoforme1 :exon9 extNM_032119	100,00
GPR98	exon10	chr5	89930910	89931127	chr5:89930910-89931127	218	89930930	89931107	chr5:89930930-89931107	178	refseq GPR98 isoforme1 :exon10 extNM_032119	100,00
GPR98	exon11	chr5	89933521	89933785	chr5:89933521-89933785	265	89933541	89933765	chr5:89933541-89933765	225	refseq GPR98 isoforme1 :exon11 extNM_032119	100,00
GPR98	exon12	chr5	89938432	89938599	chr5:89938432-89938599	168	89938452	89938579	chr5:89938452-89938579	128	refseq GPR98 isoforme1 :exon12 extNM_032119	100,00
GPR98	exon13	chr5	89938652	89938878	chr5:89938652-89938878	227	89938672	89938858	chr5:89938672-89938858	187	refseq GPR98 isoforme1 :exon13 extNM_032119	100,00
GPR98	exon14	chr5	89939599	89939820	chr5:89939599-89939820	222	89939619	89939800	chr5:89939619-89939800	182	refseq GPR98 isoforme1 :exon14 extNM_032119	100,00
GPR98	exon15	chr5	89940502	89940706	chr5:89940502-89940706	205	89940522	89940686	chr5:89940522-89940686	165	refseq GPR98 isoforme1 :exon15 extNM_032119	100,00
GPR98	exon16	chr5	89941764	89941928	chr5:89941764-89941928	165	89941784	89941908	chr5:89941784-89941908	125	refseq GPR98 isoforme1 :exon16 extNM_032119	100,00
GPR98	exon17	chr5	89943294	89943601	chr5:89943294-89943601	308	89943314	89943581	chr5:89943314-89943581	268	refseq GPR98 isoforme1 :exon17 extNM_032119	100,00
GPR98	exon18	chr5	89947400	89947567	chr5:89947400-89947567	168	89947420	89947547	chr5:89947420-89947547	128	refseq GPR98 isoforme1 :exon18 extNM_032119	100,00
GPR98	exon19	chr5	89948142	89948400	chr5:89948142-89948400	259	89948162	89948380	chr5:89948162-89948380	219	refseq GPR98 isoforme1 :exon19 extNM_032119	100,00
GPR98	exon20	chr5	89949005	89949789	chr5:89949005-89949789	785	89949025	89949769	chr5:89949025-89949769	745	refseq GPR98 isoforme1 :exon20 extNM_032119	100,00
GPR98	exon21	chr5	89953701	89954115	chr5:89953701-89954115	415	89953721	89954095	chr5:89953721-89954095	375	refseq GPR98 isoforme1 :exon21 extNM_032119	100,00
GPR98	exon22	chr5	89968342	89968559	chr5:89968342-89968559	218	89968362	89968539	chr5:89968362-89968539	178	refseq GPR98 isoforme1 :exon22 extNM_032119	100,00
GPR98	exon23	chr5	89969850	89970071	chr5:89969850-89970071	222	89969870	89970051	chr5:89969870-89970051	182	refseq GPR98 isoforme1 :exon23 extNM_032119	100,00
GPR98	exon24	chr5	89971039	89971282	chr5:89971039-89971282	244	89971059	89971262	chr5:89971059-89971262	204	refseq GPR98 isoforme1 :exon24 extNM_032119	100,00
GPR98	exon25	chr5	89971876	89972046	chr5:89971876-89972046	171	89971896	89972026	chr5:89971896-89972026	131	refseq GPR98 isoforme1 :exon25 extNM_032119	100,00
GPR98	exon26	chr5	89975345	89975466	chr5:89975345-89975466	122	89975365	89975446	chr5:89975365-89975446	82	refseq GPR98 isoforme1 :exon26 extNM_032119	100,00
GPR98	exon27	chr5	89977111	89977291	chr5:89977111-89977291	181	89977131	89977271	chr5:89977131-89977271	141	refseq GPR98 isoforme1 :exon27 extNM_03211	

GRID2	exon3	chr4	94006125	94006450	chr4:94006125-94006450	326	94006145	94006430	chr4:94006145-94006430	286	refseq GRID2 isoforme2):exon3 exte	NM_001510	100,00
GRID2	exon3	exon4	chr4	94032124	chr4:94031878-94032124	247	94031898	94032104	chr4:94032104-94032104	207	refseq GRID2 isoforme2):exon3 exte	NM_001286838, NM_001510	100,00
GRID2	exon4	exon5	chr4	94128534	94128628	chr4:94128534-94128628	95	94128554	94128608	chr4:94128554-94128608	55	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon5	exon6	chr4	94137868	94138082	chr4:94137868-94138082	215	94137888	94138062	chr4:94137888-94138062	175	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon6	exon7	chr4	94145744	94145946	chr4:94145744-94145946	203	94145764	94145926	chr4:94145764-94145926	163	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon7	exon8	chr4	94159501	94159661	chr4:94159501-94159661	161	94159521	94159641	chr4:94159521-94159641	121	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon8	exon9	chr4	94316737	94316879	chr4:94316737-94316879	143	94316757	94316859	chr4:94316757-94316859	103	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon9	exon10	chr4	94343901	94344139	chr4:94343901-94344139	239	94343921	94344119	chr4:94343921-94344119	199	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon10	exon11	chr4	94376792	94377145	chr4:94376792-94377145	354	94376812	94377125	chr4:94376812-94377125	314	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon11	exon12	chr4	94411769	94411948	chr4:94411769-94411948	180	94411789	94411928	chr4:94411789-94411928	140	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon12	exon13	chr4	94436346	94436582	chr4:94436346-94436582	237	94436366	94436562	chr4:94436366-94436562	197	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon13	exon14	chr4	94547399	94547606	chr4:94547399-94547606	208	94547419	94547586	chr4:94547419-94547586	168	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon14	exon15	chr4	94690340	94690621	chr4:94690340-94690621	282	94690360	94690601	chr4:94690360-94690601	242	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRID2	exon15	exon16	chr4	94693206	94693669	chr4:94693206-94693669	464	94693226	94693649	chr4:94693226-94693649	424	refseq GRID2 isoforme1 isoforme2):NM_001286838, NM_001510	100,00
GRK5	exon1	chr10	120967409	120967501	chr10:120967409-120967501	93	120967429	120967481	chr10:120967429-120967481	53	refseq GRK5 isoforme1):exon1 exte	NM_005308	100,00
GRK5	exon2	chr10	121086007	121086143	chr10:121086007-121086143	137	121086027	121086123	chr10:121086027-121086123	97	refseq GRK5 isoforme1):exon2 exte	NM_005308	100,00
GRK5	exon3	chr10	121140306	121140459	chr10:121140306-121140459	154	121140326	121140439	chr10:121140326-121140439	114	refseq GRK5 isoforme1):exon3 exte	NM_005308	100,00
GRK5	exon4	chr10	121156186	121156304	chr10:121156186-121156304	119	121156206	121156286	chr10:121156206-121156286	79	refseq GRK5 isoforme1):exon4 exte	NM_005308	100,00
GRK5	exon5	chr10	121182657	121182798	chr10:121182657-121182798	142	121182677	121182778	chr10:121182677-121182778	102	refseq GRK5 isoforme1):exon5 exte	NM_005308	100,00
GRK5	exon6	chr10	121184484	121184617	chr10:121184484-121184617	134	121184504	121184597	chr10:121184504-121184597	94	refseq GRK5 isoforme1):exon6 exte	NM_005308	100,00
GRK5	exon7	chr10	121189866	121189970	chr10:121189866-121189970	105	121189886	121189950	chr10:121189886-121189950	65	refseq GRK5 isoforme1):exon7 exte	NM_005308	100,00
GRK5	exon8	chr10	121190878	121191059	chr10:121190878-121191059	182	121190898	121191039	chr10:121190898-121191039	142	refseq GRK5 isoforme1):exon8 exte	NM_005308	100,00
GRK5	exon9	chr10	121196142	121196373	chr10:121196142-121196373	232	121196162	121196353	chr10:121196162-121196353	192	refseq GRK5 isoforme1):exon9 exte	NM_005308	100,00
GRK5	exon10	chr10	121199222	121199300	chr10:121199222-121199300	79	121199242	121199280	chr10:121199242-121199280	39	refseq GRK5 isoforme1):exon10 exte	NM_005308	100,00
GRK5	exon11	chr10	121201490	121201620	chr10:121201490-121201620	131	121201510	121201600	chr10:121201510-121201600	91	refseq GRK5 isoforme1):exon11 exte	NM_005308	100,00
GRK5	exon12	chr10	121203035	121203284	chr10:121203035-121203284	250	121203055	121203264	chr10:121203055-121203264	210	refseq GRK5 isoforme1):exon12 exte	NM_005308	100,00
GRK5	exon13	chr10	121207614	121207792	chr10:121207614-121207792	179	121207634	121207772	chr10:121207634-121207772	139	refseq GRK5 isoforme1):exon13 exte	NM_005308	100,00
GRK5	exon14	chr10	121212162	121212340	chr10:121212162-121212340	179	121212182	121212320	chr10:121212182-121212320	139	refseq GRK5 isoforme1):exon14 exte	NM_005308	100,00
GRK5	exon15	chr10	121212636	121212808	chr10:121212636-121212808	173	121212656	121212788	chr10:121212656-121212788	133	refseq GRK5 isoforme1):exon15 exte	NM_005308	100,00
GRK5	exon16	chr10	121214460	121214599	chr10:121214460-121214599	140	121214480	121214579	chr10:121214480-121214579	100	refseq GRK5 isoforme1):exon16 exte	NM_005308	100,00
HIST1H1D	exon1	chr6	26234475	26235181	chr6:26234475-26235181	707	26234495	26235161	chr6:26234495-26235161	667	refseq HIST1H1D isoforme1):exon1	NM_005320	100,00
HIST1H2AD	exon1	chr6	26199058	26199491	chr6:26199058-26199491	434	26199078	26199471	chr6:26199078-26199471	394	refseq HIST1H2AD isoforme1):exon1	NM_021065	100,00
HIST1H2AG	exon1	chr6	27100830	27101263	chr6:27100830-27101263	434	27100850	27101243	chr6:27100850-27101243	394	refseq HIST1H2AG isoforme1):exon1	NM_021066	100,00
HIST1H2BK	exon1	chr6	27114176	27114597	chr6:27114176-27114597	422	27114196	27114577	chr6:27114196-27114577	382	refseq HIST1H2BK isoforme1):exon1	NM_080593	100,00
HIST4H4	exon1	chr12	14923686	14924038	chr12:14923686-14924038	353	14923706	14924018	chr12:14923706-14924018	313	refseq HIST4H4 isoforme1):exon1 e	NM_175054	100,00
HRAS	exon4	exon4	chr11	532615	532775	chr11:532615-532775	161	532635	532755	chr11:532635-532755	121	refseq HRAS isoforme1 isoforme3):NM_005343, NM_176795, NM_001131	100,00
HRAS	exon4	chr11	533275	533378	chr11:533275-533378	104	533295	533358	chr11:533295-533358	64	refseq HRAS isoforme2):exon4 exte	NM_176795	100,00
HRAS	exon3	exon3	chr11	533432	533632	chr11:533432-533632	201	533452	533612	chr11:533452-533612	161	refseq HRAS isoforme1 isoforme2 is:NM_005343, NM_176795, NM_001131	100,00
HRAS	exon2	exon2	chr11	533745	533964	chr11:533745-533964	220	533765	533944	chr11:533765-533944	180	refseq HRAS isoforme1 isoforme2 is:NM_005343, NM_176795, NM_001131	100,00
HRAS	exon1	exon1	chr11	534191	534342	chr11:534191-534342	152	534211	534322	chr11:534211-534322	112	refseq HRAS isoforme1 isoforme2 is:NM_005343, NM_176795, NM_001131	100,00
HSPD1	exon11	exon11	chr2	198351942	198351942	chr2:198351942-198351942	194	198351769	198351922	chr2:198351769-198351922	154	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon10	exon10	chr2	198352561	198352780	chr2:198352561-198352780	220	198352581	198352760	chr2:198352581-198352760	180	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon9	exon9	chr2	198353020	198353235	chr2:198353020-198353235	216	198353040	198353215	chr2:198353040-198353215	176	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon8	exon8	chr2	198353705	198353991	chr2:198353705-198353991	287	198353725	198353971	chr2:198353725-198353971	247	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon7	exon7	chr2	198354900	198355040	chr2:198354900-198355040	141	198354920	198355071	chr2:198354920-198355071	101	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon6	exon6	chr2	198358027	198358236	chr2:198358027-198358236	210	198358047	198358216	chr2:198358047-198358216	170	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon5	exon5	chr2	198358860	198358994	chr2:198358860-198358994	135	198358880	198358974	chr2:198358880-198358974	95	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon4	exon4	chr2	198359360	198359496	chr2:198359360-198359496	137	198359380	198359476	chr2:198359380-198359476	97	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon3	exon3	chr2	198359997	198360120	chr2:198359997-198360120	124	198360017	198360100	chr2:198360017-198360100	84	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon2	exon2	chr2	198361843	198362136	chr2:198361843-198362136	294	198361863	198362116	chr2:198361863-198362116	254	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
HSPD1	exon1	exon1	chr2	198363378	198363592	chr2:198363378-198363592	215	198363398	198363572	chr2:198363398-198363572	175	refseq HSPD1 isoforme1 isoforme2):NM_199440, NM_002156	100,00
IFIT5	exon1	chr10	91174535	91174580	chr10:91174535-91174580	46	91174555	91174560	chr10:91174555-91174560	6	refseq IFIT5 isoforme1):exon1 exte	NM_012420	100,00
IFIT5	exon2	chr10	91176941	91178425	chr10:91176941-91178425	1485	91176961	91178405	chr10:91176961-91178405	1445	refseq IFIT5 isoforme1):exon2 exte	NM_012420	100,00
IGF2BP2	exon16	exon16	chr3	185363298	185363431	chr3:185363298-185363431	134	185363318	185363411	chr3:185363318-185363411	94	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon15	exon15	chr3	185364792	185364946	chr3:185364792-185364946	155	185364812	185364926	chr3:185364812-185364926	115	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon14	exon14	chr3	185367170	185367342	chr3:185367170-185367342	173	185367190	185367322	chr3:185367190-185367322	133	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon13	exon13	chr3	185369861	185369976	chr3:185369861-185369976	116	185369881	185369956	chr3:185369881-185369956	76	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon12	exon12	chr3	185375210	185375053	chr3:185375210-185375053	158	185375073	185375190	chr3:185375073-185375190	118	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon11	exon11	chr3	185376108	185376217	chr3:185376108-185376217	110	185376128	185376197	chr3:185376128-185376197	70	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon10	exon10	chr3	185390308	185390477	chr3:185390308-185390477	170	185390328	185390457	chr3:185390328-185390457	130	refseq IGF2BP2 isoforme1 isoforme2):NM_006548, NM_001291873, NM_001510	100,00
IGF2BP2	exon9	exon9	chr3	185393063									

KIAA0368	exon3	chr9	114246244	114246561	chr9:114246244-114246561	318	114246264	114246541	chr9:114246264-114246541	278	refseq KIAA0368 isoform1 exon3 NM_001080398	11,15
KIAA0368	exon51	chr9	114124289	114124469	chr9:114124289-114124469	181	114124309	114124449	chr9:114124309-114124449	141	refseq KIAA0368 isoform1 exon51 NM_001080398	100,00
KIAA0368	exon50	chr9	114125847	114125959	chr9:114125847-114125959	113	114125867	114125939	chr9:114125867-114125939	73	refseq KIAA0368 isoform1 exon50 NM_001080398	100,00
KIAA0368	exon49	chr9	114128498	114128627	chr9:114128498-114128627	130	114128518	114128607	chr9:114128518-114128607	90	refseq KIAA0368 isoform1 exon49 NM_001080398	100,00
KIAA0368	exon48	chr9	114128781	114128927	chr9:114128781-114128927	147	114128801	114128907	chr9:114128801-114128907	107	refseq KIAA0368 isoform1 exon48 NM_001080398	100,00
KIAA0368	exon47	chr9	114131294	114131473	chr9:114131294-114131473	180	114131314	114131453	chr9:114131314-114131453	140	refseq KIAA0368 isoform1 exon47 NM_001080398	100,00
KIAA0368	exon46	chr9	114132694	114132927	chr9:114132694-114132927	234	114132714	114132907	chr9:114132714-114132907	194	refseq KIAA0368 isoform1 exon46 NM_001080398	100,00
KIAA0368	exon45	chr9	114132981	114133065	chr9:114132981-114133065	85	114133001	114133045	chr9:114133001-114133045	45	refseq KIAA0368 isoform1 exon45 NM_001080398	100,00
KIAA0368	exon44	chr9	114133880	114134129	chr9:114133880-114134129	250	114133900	114134109	chr9:114133900-114134109	210	refseq KIAA0368 isoform1 exon44 NM_001080398	100,00
KIAA0368	exon43	chr9	114134688	114134920	chr9:114134688-114134920	233	114134708	114134900	chr9:114134708-114134900	193	refseq KIAA0368 isoform1 exon43 NM_001080398	100,00
KIAA0368	exon42	chr9	114135429	114135536	chr9:114135429-114135536	108	114135449	114135516	chr9:114135449-114135516	68	refseq KIAA0368 isoform1 exon42 NM_001080398	100,00
KIAA0368	exon41	chr9	114135574	114135706	chr9:114135574-114135706	133	114135594	114135686	chr9:114135594-114135686	93	refseq KIAA0368 isoform1 exon41 NM_001080398	100,00
KIAA0368	exon40	chr9	114136231	114136338	chr9:114136231-114136338	108	114136251	114136318	chr9:114136251-114136318	68	refseq KIAA0368 isoform1 exon40 NM_001080398	100,00
KIAA0368	exon39	chr9	114137372	114137502	chr9:114137372-114137502	131	114137392	114137482	chr9:114137392-114137482	91	refseq KIAA0368 isoform1 exon39 NM_001080398	100,00
KIAA0368	exon38	chr9	114138735	114138841	chr9:114138735-114138841	107	114138755	114138821	chr9:114138755-114138821	67	refseq KIAA0368 isoform1 exon38 NM_001080398	100,00
KIAA0368	exon37	chr9	114140839	114141030	chr9:114140839-114141030	192	114140859	114141010	chr9:114140859-114141010	152	refseq KIAA0368 isoform1 exon37 NM_001080398	100,00
KIAA0368	exon36	chr9	114145470	114145632	chr9:114145470-114145632	163	114145490	114145612	chr9:114145490-114145612	123	refseq KIAA0368 isoform1 exon36 NM_001080398	100,00
KIAA0368	exon35	chr9	114146781	114146869	chr9:114146781-114146869	89	114146801	114146849	chr9:114146801-114146849	49	refseq KIAA0368 isoform1 exon35 NM_001080398	100,00
KIAA0368	exon34	chr9	114147596	114147742	chr9:114147596-114147742	147	114147616	114147722	chr9:114147616-114147722	107	refseq KIAA0368 isoform1 exon34 NM_001080398	100,00
KIAA0368	exon33	chr9	114148636	114148756	chr9:114148636-114148756	121	114148656	114148736	chr9:114148656-114148736	81	refseq KIAA0368 isoform1 exon33 NM_001080398	100,00
KIAA0368	exon32	chr9	114151815	114152023	chr9:114151815-114152023	209	114151835	114152003	chr9:114151835-114152003	169	refseq KIAA0368 isoform1 exon32 NM_001080398	100,00
KIAA0368	exon31	chr9	114152243	114152401	chr9:114152243-114152401	159	114152263	114152381	chr9:114152263-114152381	119	refseq KIAA0368 isoform1 exon31 NM_001080398	100,00
KIAA0368	exon30	chr9	114154015	114154124	chr9:114154015-114154124	110	114154035	114154104	chr9:114154035-114154104	70	refseq KIAA0368 isoform1 exon30 NM_001080398	100,00
KIAA0368	exon29	chr9	114155027	114155182	chr9:114155027-114155182	156	114155047	114155162	chr9:114155047-114155162	116	refseq KIAA0368 isoform1 exon29 NM_001080398	100,00
KIAA0368	exon28	chr9	114155939	114156034	chr9:114155939-114156034	96	114155959	114156014	chr9:114155959-114156014	56	refseq KIAA0368 isoform1 exon28 NM_001080398	100,00
KIAA0368	exon27	chr9	114156419	114156605	chr9:114156419-114156605	187	114156439	114156585	chr9:114156439-114156585	147	refseq KIAA0368 isoform1 exon27 NM_001080398	100,00
KIAA0368	exon26	chr9	114159289	114159453	chr9:114159289-114159453	165	114159309	114159433	chr9:114159309-114159433	125	refseq KIAA0368 isoform1 exon26 NM_001080398	100,00
KIAA0368	exon25	chr9	114170830	114170972	chr9:114170830-114170972	143	114170850	114170952	chr9:114170850-114170952	103	refseq KIAA0368 isoform1 exon25 NM_001080398	100,00
KIAA0368	exon24	chr9	114172300	114172513	chr9:114172300-114172513	214	114172320	114172493	chr9:114172320-114172493	174	refseq KIAA0368 isoform1 exon24 NM_001080398	100,00
KIAA0368	exon23	chr9	114173239	114173442	chr9:114173239-114173442	204	114173259	114173422	chr9:114173259-114173422	164	refseq KIAA0368 isoform1 exon23 NM_001080398	100,00
KIAA0368	exon22	chr9	114174273	114174448	chr9:114174273-114174448	176	114174293	114174428	chr9:114174293-114174428	136	refseq KIAA0368 isoform1 exon22 NM_001080398	100,00
KIAA0368	exon21	chr9	114176154	114176286	chr9:114176154-114176286	133	114176174	114176266	chr9:114176174-114176266	93	refseq KIAA0368 isoform1 exon21 NM_001080398	100,00
KIAA0368	exon20	chr9	114176688	114176951	chr9:114176688-114176951	264	114176708	114176931	chr9:114176708-114176931	224	refseq KIAA0368 isoform1 exon20 NM_001080398	100,00
KIAA0368	exon19	chr9	114178531	114178652	chr9:114178531-114178652	122	114178551	114178632	chr9:114178551-114178632	82	refseq KIAA0368 isoform1 exon19 NM_001080398	100,00
KIAA0368	exon18	chr9	114180142	114180306	chr9:114180142-114180306	165	114180162	114180286	chr9:114180162-114180286	125	refseq KIAA0368 isoform1 exon18 NM_001080398	100,00
KIAA0368	exon17	chr9	114182276	114182420	chr9:114182276-114182420	145	114182296	114182400	chr9:114182296-114182400	105	refseq KIAA0368 isoform1 exon17 NM_001080398	100,00
KIAA0368	exon16	chr9	114184180	114184343	chr9:114184180-114184343	164	114184200	114184323	chr9:114184200-114184323	124	refseq KIAA0368 isoform1 exon16 NM_001080398	100,00
KIAA0368	exon15	chr9	114184393	114184500	chr9:114184393-114184500	108	114184413	114184480	chr9:114184413-114184480	68	refseq KIAA0368 isoform1 exon15 NM_001080398	100,00
KIAA0368	exon14	chr9	114185458	114185548	chr9:114185458-114185548	91	114185478	114185528	chr9:114185478-114185528	51	refseq KIAA0368 isoform1 exon14 NM_001080398	100,00
KIAA0368	exon13	chr9	114187677	114187796	chr9:114187677-114187796	120	114187697	114187776	chr9:114187697-114187776	80	refseq KIAA0368 isoform1 exon13 NM_001080398	100,00
KIAA0368	exon12	chr9	114188002	114188128	chr9:114188002-114188128	127	114188022	114188108	chr9:114188022-114188108	87	refseq KIAA0368 isoform1 exon12 NM_001080398	100,00
KIAA0368	exon11	chr9	114190301	114190461	chr9:114190301-114190461	161	114190321	114190441	chr9:114190321-114190441	121	refseq KIAA0368 isoform1 exon11 NM_001080398	100,00
KIAA0368	exon10	chr9	114192806	114192928	chr9:114192806-114192928	123	114192826	114192908	chr9:114192826-114192908	83	refseq KIAA0368 isoform1 exon10 NM_001080398	100,00
KIAA0368	exon9	chr9	114195492	114195672	chr9:114195492-114195672	181	114195512	114195652	chr9:114195512-114195652	141	refseq KIAA0368 isoform1 exon9 NM_001080398	100,00
KIAA0368	exon8	chr9	114199199	114199408	chr9:114199199-114199408	210	114199219	114199388	chr9:114199219-114199388	170	refseq KIAA0368 isoform1 exon8 NM_001080398	100,00
KIAA0368	exon7	chr9	114202631	114202821	chr9:114202631-114202821	191	114202651	114202801	chr9:114202651-114202801	151	refseq KIAA0368 isoform1 exon7 NM_001080398	100,00
KIAA0368	exon6	chr9	114204565	114204724	chr9:114204565-114204724	160	114204585	114204704	chr9:114204585-114204704	120	refseq KIAA0368 isoform1 exon6 NM_001080398	100,00
KIAA0368	exon5	chr9	114206637	114206794	chr9:114206637-114206794	158	114206657	114206774	chr9:114206657-114206774	118	refseq KIAA0368 isoform1 exon5 NM_001080398	100,00
KIAA0368	exon4	chr9	114213684	114213855	chr9:114213684-114213855	172	114213704	114213835	chr9:114213704-114213835	132	refseq KIAA0368 isoform1 exon4 NM_001080398	100,00
KIAA0368	exon2	chr9	114246613	114246848	chr9:114246613-114246848	236	114246633	114246828	chr9:114246633-114246828	196	refseq KIAA0368 isoform1 exon2 NM_001080398	100,00
KIF26A	exon1	chr14	104605039	104605121	chr14:104605039-104605121	83	104605059	104605101	chr14:104605059-104605101	43	refseq KIF26A isoform1 exon1 NM_015656	100,00
KIF26A	exon2	chr14	104605359	104605645	chr14:104605359-104605645	287	104605379	104605625	chr14:104605379-104605625	247	refseq KIF26A isoform1 exon2 NM_015656	100,00
KIF26A	exon3	chr14	104618331	104618818	chr14:104618331-104618818	488	104618351	104618798	chr14:104618351-104618798	448	refseq KIF26A isoform1 exon3 NM_015656	100,00
KIF26A	exon4	chr14	104624071	104624299	chr14:104624071-104624299	229	104624091	104624279	chr14:104624091-104624279	189	refseq KIF26A isoform1 exon4 NM_015656	100,00
KIF26A	exon5	chr14	104633175	104633405	chr14:104633175-104633405	231	104633195	104633385	chr14:104633195-104633385	191	refseq KIF26A isoform1 exon5 NM_015656	100,00
KIF26A	exon6	chr14	104638039	104638292	chr14:104638039-104638292	254	104638059	104638272	chr14:104638059-104638272	214	refseq KIF26A isoform1 exon6 NM_015656	100,00
KIF26A	exon7	chr14	104638891	104639025	chr14:104638891-104639025	135	104638911	104639005	chr14:104638911-104639005	95	refseq KIF26A isoform1 exon7 NM_015656	100,00
KIF26A	exon8	chr14	104639293	104639596	chr14:104639293-104639596	304	104639313	104639576	chr14:104639313-104639576	264	refseq KIF26A isoform1 exon8 NM_015656	100,00
KIF26A	exon9	chr14	104639646	104639870	chr14:104639646-104639870	225	104639666	104639850	chr14:104639666-104639850	185	refseq KIF26A isoform1 exon9 NM_015656	100,00
KIF26A	exon10	chr14	104640022	104640225	chr14:104640022-104640225	204	104640042	104640205	chr14:104640042-104640205	164	refseq KIF26A isoform1 exon10 NM_015656	100,00
KIF26A	exon11	chr14	104640464	104640667	chr14:104640464-104640667	204	104640484	104640648	chr14:104640484-104640648			

MTA3	exon4 exon2 chr2	42836577	42836744	chr2:42836577-42836744	168	42836597	42836724	chr2:42836597-42836724	128	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon5 exon3 chr2	42867292	42867396	chr2:42867292-42867396	105	42867312	42867376	chr2:42867312-42867376	65	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon6 exon4 chr2	42871246	42871404	chr2:42871246-42871404	159	42871266	42871384	chr2:42871266-42871384	119	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon7 exon5 chr2	42883319	42883462	chr2:42883319-42883462	144	42883339	42883442	chr2:42883339-42883442	104	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon8 exon6 chr2	42886882	42887022	chr2:42886882-42887022	141	42886902	42887002	chr2:42886902-42887002	101	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon9 exon7 chr2	42909520	42909749	chr2:42909520-42909749	230	42909540	42909729	chr2:42909540-42909729	190	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon10 exon8 chr2	42922884	42922999	chr2:42922884-42922999	116	42922904	42922979	chr2:42922904-42922979	76	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon11 exon9 chr2	42924895	42924994	chr2:42924895-42924994	100	42924915	42924974	chr2:42924915-42924974	60	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	chr2	42931313	42931478	chr2:42931313-42931478	166	42931333	42931458	chr2:42931333-42931458	126	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon13 exon1 chr2	42935022	42935214	chr2:42935022-42935214	193	42935042	42935194	chr2:42935042-42935194	153	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon14 chr2	42935993	42936279	chr2:42935993-42936279	287	42936013	42936259	chr2:42936013-42936259	247	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon13 exon1 chr2	42946107	42946234	chr2:42946107-42946234	128	42946127	42946214	chr2:42946127-42946214	88	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon14 exon1 chr2	42950008	42950195	chr2:42950008-42950195	188	42950028	42950175	chr2:42950028-42950175	148	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTA3	exon15 exon1 chr2	42980493	42980559	chr2:42980493-42980559	67	42980513	42980539	chr2:42980513-42980539	27	refseq MTA3 isoforme1 isoforme2 is NM_020744, NM_001282756, NM_00:	100,00
MTOR	exon57 chr1	11167521	11167577	chr1:11167521-11167577	57	11167541	11167557	chr1:11167541-11167557	17	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon56 chr1	11168217	11168363	chr1:11168217-11168363	147	11168237	11168343	chr1:11168237-11168343	107	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon55 chr1	11169326	11169447	chr1:11169326-11169447	122	11169346	11169427	chr1:11169346-11169427	82	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon54 chr1	11169685	11169806	chr1:11169685-11169806	122	11169705	11169786	chr1:11169705-11169786	82	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon53 chr1	11172888	11172994	chr1:11172888-11172994	107	11172908	11172979	chr1:11172908-11172979	67	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon52 chr1	11174354	11174530	chr1:11174354-11174530	177	11174374	11174510	chr1:11174374-11174510	137	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon51 chr1	11174849	11174964	chr1:11174849-11174964	116	11174869	11174944	chr1:11174869-11174944	76	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon50 chr1	11175432	11175545	chr1:11175432-11175545	114	11175452	11175525	chr1:11175452-11175525	74	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon49 chr1	11177040	11177163	chr1:11177040-11177163	124	11177060	11177143	chr1:11177060-11177143	84	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon48 chr1	11181282	11181445	chr1:11181282-11181445	164	11181302	11181425	chr1:11181302-11181425	124	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon47 chr1	11182015	11182203	chr1:11182015-11182203	189	11182035	11182183	chr1:11182035-11182183	149	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon46 chr1	11184534	11184710	chr1:11184534-11184710	177	11184554	11184690	chr1:11184554-11184690	137	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon45 chr1	11186658	11186873	chr1:11186658-11186873	216	11186678	11186853	chr1:11186678-11186853	176	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon44 chr1	11187046	11187221	chr1:11187046-11187221	176	11187066	11187202	chr1:11187066-11187202	136	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon43 chr1	11187660	11187883	chr1:11187660-11187883	224	11187680	11187863	chr1:11187680-11187863	184	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon42 chr1	11188040	11188203	chr1:11188040-11188203	164	11188060	11188183	chr1:11188060-11188183	124	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon41 chr1	11188490	11188629	chr1:11188490-11188629	140	11188510	11188609	chr1:11188510-11188609	100	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon40 chr1	11188891	11189028	chr1:11188891-11189028	138	11188911	11189008	chr1:11188911-11189008	98	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon39 chr1	11189774	11189915	chr1:11189774-11189915	142	11189794	11189915	chr1:11189794-11189915	102	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon38 chr1	11190565	11190854	chr1:11190565-11190854	290	11190585	11190834	chr1:11190585-11190834	250	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon37 chr1	11193116	11193274	chr1:11193116-11193274	159	11193136	11193254	chr1:11193136-11193254	119	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon36 chr1	11194387	11194543	chr1:11194387-11194543	157	11194407	11194523	chr1:11194407-11194523	117	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon35 chr1	11199340	11199512	chr1:11199340-11199512	173	11199360	11199492	chr1:11199360-11199492	133	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon34 chr1	11199569	11199735	chr1:11199569-11199735	167	11199589	11199715	chr1:11199589-11199715	127	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon33 chr1	11204684	11204832	chr1:11204684-11204832	149	11204704	11204812	chr1:11204704-11204812	109	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon32 chr1	11205004	11205122	chr1:11205004-11205122	119	11205024	11205102	chr1:11205024-11205102	79	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon31 chr1	11206712	11206868	chr1:11206712-11206868	157	11206732	11206848	chr1:11206732-11206848	117	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon30 chr1	11210162	11210303	chr1:11210162-11210303	142	11210182	11210283	chr1:11210182-11210283	102	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon29 chr1	11217188	11217368	chr1:11217188-11217368	181	11217208	11217348	chr1:11217208-11217348	141	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon28 chr1	11227478	11227594	chr1:11227478-11227594	117	11227498	11227574	chr1:11227498-11227574	77	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon27 chr1	11259294	11259480	chr1:11259294-11259480	187	11259314	11259460	chr1:11259314-11259460	147	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon26 chr1	11259577	11259780	chr1:11259577-11259780	204	11259597	11259760	chr1:11259597-11259760	164	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon25 chr1	11264597	11264780	chr1:11264597-11264780	184	11264617	11264760	chr1:11264617-11264760	144	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon24 chr1	11269348	11269535	chr1:11269348-11269535	188	11269368	11269515	chr1:11269368-11269515	148	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon23 chr1	11270850	11270983	chr1:11270850-11270983	134	11270870	11270963	chr1:11270870-11270963	94	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon22 chr1	11272348	11272551	chr1:11272348-11272551	204	11272368	11272531	chr1:11272368-11272531	164	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon21 chr1	11272832	11272985	chr1:11272832-11272985	154	11272852	11272965	chr1:11272852-11272965	114	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon20 chr1	11273435	11273643	chr1:11273435-11273643	209	11273455	11273623	chr1:11273455-11273623	169	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon19 chr1	11276184	11276311	chr1:11276184-11276311	128	11276204	11276291	chr1:11276204-11276291	88	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon18 chr1	11288704	11288995	chr1:11288704-11288995	292	11288724	11288975	chr1:11288724-11288975	252	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon17 chr1	11290961	11291131	chr1:11290961-11291131	171	11290981	11291111	chr1:11290981-11291111	131	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon16 chr1	11291336	11291511	chr1:11291336-11291511	176	11291356	11291491	chr1:11291356-11291491	136	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon15 chr1	11292472	11292605	chr1:11292472-11292605	134	11292492	11292585	chr1:11292492-11292585	94	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon14 chr1	11293434	11293564	chr1:11293434-11293564	131	11293454	11293544	chr1:11293454-11293544	91	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon13 chr1	11294179	11294342	chr1:11294179-11294342	164	11294199	11294322	chr1:11294199-11294322	124	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon12 chr1	11297879	11298125	chr1:11297879-11298125	247	11297899	11298105	chr1:11297899-11298105	207	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon11 chr1	11298438	11298694	chr1:11298438-11298694	257	11298458	11298674	chr1:11298458-11298674	217	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon10 chr1	11300339	11300624	chr1:11300339-11300624	286	11300359	11300604	chr1:11300359-11300604	246	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon9 chr1	11301589	11301758	chr1:11301589-11301758	170	11301609	11301738	chr1:11301609-11301738	130	refseq MTOR isoforme1 isoforme2 is NM_004958, NM_001242539, NM_00:	100,00
MTOR	exon8 chr1	11303150	1130337								

NIPBL	exon16 exon1 chr5	37006438	37006710	chr5:37006438-37006710	273	37006458	37006690	chr5:37006458-37006690	233	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon17 exon1 chr5	37007404	37007596	chr5:37007404-37007596	193	37007424	37007576	chr5:37007424-37007576	153	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon18 exon1 chr5	37008089	37008210	chr5:37008089-37008210	122	37008109	37008190	chr5:37008109-37008190	82	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon19 exon1 chr5	37008704	37008845	chr5:37008704-37008845	142	37008724	37008825	chr5:37008724-37008825	102	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon20 exon2 chr5	37010168	37010347	chr5:37010168-37010347	180	37010188	37010327	chr5:37010188-37010327	140	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon21 exon2 chr5	37014764	37014887	chr5:37014764-37014887	124	37014784	37014867	chr5:37014784-37014867	84	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon22 exon2 chr5	37016119	37016292	chr5:37016119-37016292	174	37016139	37016272	chr5:37016139-37016272	134	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon23 exon2 chr5	37017100	37017284	chr5:37017100-37017284	185	37017120	37017264	chr5:37017120-37017264	145	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon24 exon2 chr5	37019392	37019522	chr5:37019392-37019522	131	37019412	37019502	chr5:37019412-37019502	91	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon25 exon2 chr5	37020540	37020795	chr5:37020540-37020795	256	37020560	37020775	chr5:37020560-37020775	216	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon26 exon2 chr5	37020856	37020999	chr5:37020856-37020999	144	37020876	37020979	chr5:37020876-37020979	104	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon27 exon2 chr5	37022132	37022271	chr5:37022132-37022271	140	37022152	37022251	chr5:37022152-37022251	100	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon28 exon2 chr5	37022325	37022512	chr5:37022325-37022512	188	37022345	37022492	chr5:37022345-37022492	148	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon29 exon2 chr5	37024666	37024841	chr5:37024666-37024841	176	37024686	37024821	chr5:37024686-37024821	136	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon30 exon3 chr5	37026310	37026449	chr5:37026310-37026449	140	37026330	37026429	chr5:37026330-37026429	100	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon31 exon3 chr5	37027440	37027534	chr5:37027440-37027534	95	37027460	37027514	chr5:37027460-37027514	55	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon32 exon3 chr5	37036460	37036609	chr5:37036460-37036609	150	37036480	37036589	chr5:37036480-37036589	110	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon33 exon3 chr5	37038683	37038860	chr5:37038683-37038860	178	37038703	37038840	chr5:37038703-37038840	138	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon34 exon3 chr5	37044428	37044609	chr5:37044428-37044609	182	37044448	37044589	chr5:37044448-37044589	142	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon35 exon3 chr5	37044717	37044851	chr5:37044717-37044851	135	37044737	37044831	chr5:37044737-37044831	95	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon36 exon3 chr5	37045524	37045719	chr5:37045524-37045719	196	37045544	37045699	chr5:37045544-37045699	156	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon37 exon3 chr5	37046190	37046321	chr5:37046190-37046321	132	37046210	37046301	chr5:37046210-37046301	92	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon38 exon3 chr5	37048583	37048797	chr5:37048583-37048797	215	37048603	37048777	chr5:37048603-37048777	175	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon39 exon3 chr5	37049192	37049423	chr5:37049192-37049423	232	37049212	37049403	chr5:37049212-37049403	192	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon40 exon4 chr5	37051860	37052008	chr5:37051860-37052008	149	37051880	37051988	chr5:37051880-37051988	109	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon41 exon4 chr5	37052447	37052688	chr5:37052447-37052688	242	37052467	37052668	chr5:37052467-37052668	202	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon42 exon4 chr5	37057267	37057454	chr5:37057267-37057454	188	37057287	37057434	chr5:37057287-37057434	148	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon43 exon4 chr5	37058972	37059287	chr5:37058972-37059287	316	37058992	37059267	chr5:37058992-37059267	276	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon44 exon4 chr5	37060925	37061140	chr5:37060925-37061140	216	37060945	37061120	chr5:37060945-37061120	176	refseq NIPBL isoforme1 isoforme2 :e:NM_133433, NM_015384	100,00
NIPBL	exon45 chr5	37063871	37064145	chr5:37063871-37064145	275	37063891	37064125	chr5:37063891-37064125	235	refseq NIPBL isoforme2 :exon45 ext:NM_015384	100,00
NIPBL	exon46 chr5	37064608	37065014	chr5:37064608-37065014	407	37064628	37064994	chr5:37064628-37064994	367	refseq NIPBL isoforme2 :exon46 ext:NM_133433	100,00
NOTCH1	exon34 chr9	139390502	139392030	chr9:139390502-139392030	1529	139390522	139392010	chr9:139390522-139392010	1489	refseq NOTCH1 isoforme1 :exon34 NM_017617	100,00
NOTCH1	exon33 chr9	139393330	139393468	chr9:139393330-139393468	139	139393350	139393448	chr9:139393350-139393448	99	refseq NOTCH1 isoforme1 :exon33 NM_017617	100,00
NOTCH1	exon32 chr9	139393543	139393731	chr9:139393543-139393731	189	139393563	139393711	chr9:139393563-139393711	149	refseq NOTCH1 isoforme1 :exon32 NM_017617	100,00
NOTCH1	exon31 chr9	139394983	139395319	chr9:139394983-139395319	337	139395003	139395299	chr9:139395003-139395299	297	refseq NOTCH1 isoforme1 :exon31 NM_017617	100,00
NOTCH1	exon30 chr9	139396179	139396385	chr9:139396179-139396385	207	139396199	139396365	chr9:139396199-139396365	167	refseq NOTCH1 isoforme1 :exon30 NM_017617	100,00
NOTCH1	exon29 chr9	139396432	139396650	chr9:139396432-139396650	129	139396452	139396640	chr9:139396452-139396640	89	refseq NOTCH1 isoforme1 :exon29 NM_017617	100,00
NOTCH1	exon28 chr9	139396703	139396960	chr9:139396703-139396960	258	139396723	139396940	chr9:139396723-139396940	218	refseq NOTCH1 isoforme1 :exon28 NM_017617	100,00
NOTCH1	exon27 chr9	139397613	139397802	chr9:139397613-139397802	190	139397633	139397782	chr9:139397633-139397782	150	refseq NOTCH1 isoforme1 :exon27 NM_017617	100,00
NOTCH1	exon26 chr9	139399104	139399576	chr9:139399104-139399576	473	139399124	139399556	chr9:139399124-139399556	433	refseq NOTCH1 isoforme1 :exon26 NM_017617	100,00
NOTCH1	exon25 chr9	139399741	139400353	chr9:139399741-139400353	613	139399761	139400333	chr9:139399761-139400333	573	refseq NOTCH1 isoforme1 :exon25 NM_017617	100,00
NOTCH1	exon24 chr9	139400958	139401111	chr9:139400958-139401111	154	139400978	139401091	chr9:139400978-139401091	114	refseq NOTCH1 isoforme1 :exon24 NM_017617	100,00
NOTCH1	exon23 chr9	139401147	139401445	chr9:139401147-139401445	299	139401167	139401425	chr9:139401167-139401425	259	refseq NOTCH1 isoforme1 :exon23 NM_017617	100,00
NOTCH1	exon22 chr9	139401736	139401909	chr9:139401736-139401909	174	139401756	139401889	chr9:139401756-139401889	134	refseq NOTCH1 isoforme1 :exon22 NM_017617	100,00
NOTCH1	exon21 chr9	139402386	139402611	chr9:139402386-139402611	226	139402406	139402591	chr9:139402406-139402591	186	refseq NOTCH1 isoforme1 :exon21 NM_017617	100,00
NOTCH1	exon20 chr9	139402663	139402857	chr9:139402663-139402857	195	139402683	139402837	chr9:139402683-139402837	155	refseq NOTCH1 isoforme1 :exon20 NM_017617	100,00
NOTCH1	exon19 chr9	139403301	139403543	chr9:139403301-139403543	243	139403321	139403523	chr9:139403321-139403523	203	refseq NOTCH1 isoforme1 :exon19 NM_017617	100,00
NOTCH1	exon18 chr9	139404164	139404433	chr9:139404164-139404433	270	139404184	139404413	chr9:139404184-139404413	230	refseq NOTCH1 isoforme1 :exon18 NM_017617	100,00
NOTCH1	exon17 chr9	139405084	139405277	chr9:139405084-139405277	194	139405104	139405257	chr9:139405104-139405257	154	refseq NOTCH1 isoforme1 :exon17 NM_017617	100,00
NOTCH1	exon16 chr9	139405583	139405743	chr9:139405583-139405743	161	139405603	139405723	chr9:139405603-139405723	121	refseq NOTCH1 isoforme1 :exon16 NM_017617	100,00
NOTCH1	exon15 chr9	139407452	139407606	chr9:139407452-139407606	155	139407472	139407586	chr9:139407472-139407586	115	refseq NOTCH1 isoforme1 :exon15 NM_017617	100,00
NOTCH1	exon14 chr9	139407823	139408009	chr9:139407823-139408009	187	139407843	139407989	chr9:139407843-139407989	147	refseq NOTCH1 isoforme1 :exon14 NM_017617	100,00
NOTCH1	exon13 chr9	139408941	139409174	chr9:139408941-139409174	234	139408961	139409154	chr9:139408961-139409154	194	refseq NOTCH1 isoforme1 :exon13 NM_017617	100,00
NOTCH1	exon12 chr9	139409721	139409872	chr9:139409721-139409872	152	139409741	139409852	chr9:139409741-139409852	112	refseq NOTCH1 isoforme1 :exon12 NM_017617	100,00
NOTCH1	exon11 chr9	139409914	139410188	chr9:139409914-139410188	275	139409934	139410168	chr9:139409934-139410168	235	refseq NOTCH1 isoforme1 :exon11 NM_017617	100,00
NOTCH1	exon10 chr9	139410412	139410566	chr9:139410412-139410566	155	139410432	139410546	chr9:139410432-139410546	115	refseq NOTCH1 isoforme1 :exon10 NM_017617	100,00
NOTCH1	exon9 chr9	139411703	139411857	chr9:139411703-139411857	155	139411723	139411837	chr9:139411723-139411837	115	refseq NOTCH1 isoforme1 :exon9 NM_017617	100,00
NOTCH1	exon8 chr9	139412183	139412409	chr9:139412183-139412409	227	139412203	139412389	chr9:139412203-139412389	187	refseq NOTCH1 isoforme1 :exon8 NM_017617	100,00
NOTCH1	exon7 chr9	139412568	139412764	chr9:139412568-139412764	197	139412588	139412744	chr9:139412588-139412744	157	refseq NOTCH1 isoforme1 :exon7 NM_017617	100,00
NOTCH1	exon6 chr9	139413022	139413296	chr9:139413022-139413296	275	139413042	139413276	chr9:139413042-139413276	235	refseq NOTCH1 isoforme1 :exon6 NM_017617	100,00
NOTCH1	exon5 chr9	139413874	139414037	chr9:139413874-139414037	164	139413894	139414017	chr9:139413894-139414017	124	refseq NOTCH1 isoforme1 :exon5 NM_017617	100,00
NOTCH1	exon4 chr9	139417281	139417660	chr9:139417281-139417660	380	139417301	139417640	chr9:139417301-139417640	340	refseq NOTCH1 isoforme1 :exon4 NM_017617	100,00
NOTCH1	exon3 chr9	139418148	139418451	chr9:139418148-139418451	304	139418168	139418431	chr9:139418168-139418431	264	refseq NOTCH1 isoforme1 :exon3 NM_017617	100,00
NOTCH1	exon2 chr9	139438455	139438574	chr9:139438455-139438574	120	139438475	139438554	chr9:139438475-139438554	80	refseq NOTCH1 isoforme1 :exon2 NM_017617	100,00
NOTCH1	exon1 chr9	139440157	139440258	chr9:139440157-139440258	102	139440177	139				

PDE8A	exon8 exon7 chr15	85634254	85634432	chr15:85634254-85634432	179	85634274	85634412	chr15:85634274-85634412	139	refseq PDE8A(isoforme1 isoforme3):NM_002605, NM_001243137	100,00
PDE8A	exon9 exon8 chr15	85641158	85641287	chr15:85641158-85641287	130	85641178	85641267	chr15:85641178-85641267	90	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon10 exon9 chr15	85643225	85643317	chr15:85643225-85643317	93	85643245	85643297	chr15:85643245-85643297	53	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon11 exon1 chr15	85643366	85643449	chr15:85643366-85643449	84	85643386	85643429	chr15:85643386-85643429	44	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon12 exon1 chr15	85652263	85652381	chr15:85652263-85652381	119	85652283	85652361	chr15:85652283-85652361	79	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon13 exon1 chr15	85656587	85656698	chr15:85656587-85656698	112	85656607	85656678	chr15:85656607-85656678	72	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon14 exon1 chr15	85657083	85657288	chr15:85657083-85657288	206	85657103	85657268	chr15:85657103-85657268	166	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon15 exon1 chr15	85658649	85658738	chr15:85658649-85658738	90	85658669	85658718	chr15:85658669-85658718	50	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon16 exon1 chr15	85659194	85659370	chr15:85659194-85659370	177	85659214	85659350	chr15:85659214-85659350	137	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon17 exon1 chr15	85660851	85661090	chr15:85660851-85661090	240	85660871	85661070	chr15:85660871-85661070	200	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon18 exon1 chr15	85664007	85664265	chr15:85664007-85664265	259	85664027	85664245	chr15:85664027-85664245	219	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon19 exon1 chr15	85666271	85666444	chr15:85666271-85666444	174	85666291	85666424	chr15:85666291-85666424	134	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon20 exon1 chr15	85669617	85669625	chr15:85669617-85669625	209	85669437	85669605	chr15:85669437-85669605	169	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon21 exon2 chr15	85679744	85679914	chr15:85679744-85679914	171	85679764	85679894	chr15:85679764-85679894	131	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PDE8A	exon22 exon2 chr15	85681007	85681154	chr15:85681007-85681154	148	85681027	85681134	chr15:85681027-85681134	108	refseq PDE8A(isoforme1 isoforme2 i:NM_002605, NM_173454, NM_00124:100,00	
PIK3C2A	exon32 chr11	17111264	17111487	chr11:17111264-17111487	224	17111284	17111467	chr11:17111284-17111467	184	refseq PIK3C2A(isoforme1):exon32 NM_002645	100,00
PIK3C2A	exon31 chr11	17112860	17113026	chr11:17112860-17113026	167	17112880	17113067	chr11:17112880-17113067	127	refseq PIK3C2A(isoforme1):exon31 NM_002645	100,00
PIK3C2A	exon30 chr11	17113073	17113223	chr11:17113073-17113223	151	17113093	17113203	chr11:17113093-17113203	111	refseq PIK3C2A(isoforme1):exon30 NM_002645	100,00
PIK3C2A	exon29 chr11	17113522	17113635	chr11:17113522-17113635	114	17113542	17113615	chr11:17113542-17113615	74	refseq PIK3C2A(isoforme1):exon29 NM_002645	100,00
PIK3C2A	exon28 chr11	17113685	17113843	chr11:17113685-17113843	159	17113707	17113823	chr11:17113707-17113823	119	refseq PIK3C2A(isoforme1):exon28 NM_002645	100,00
PIK3C2A	exon27 chr11	17115787	17115952	chr11:17115787-17115952	166	17115807	17115932	chr11:17115807-17115932	126	refseq PIK3C2A(isoforme1):exon27 NM_002645	100,00
PIK3C2A	exon26 chr11	17118583	17118831	chr11:17118583-17118831	249	17118603	17118811	chr11:17118603-17118811	209	refseq PIK3C2A(isoforme1):exon26 NM_002645	100,00
PIK3C2A	exon25 chr11	17121386	17121536	chr11:17121386-17121536	151	17121406	17121516	chr11:17121406-17121516	111	refseq PIK3C2A(isoforme1):exon25 NM_002645	100,00
PIK3C2A	exon24 chr11	17122804	17123001	chr11:17122804-17123001	198	17122824	17122981	chr11:17122824-17122981	158	refseq PIK3C2A(isoforme1):exon24 NM_002645	100,00
PIK3C2A	exon23 chr11	17124188	17124398	chr11:17124188-17124398	211	17124208	17124378	chr11:17124208-17124378	171	refseq PIK3C2A(isoforme1):exon23 NM_002645	100,00
PIK3C2A	exon22 chr11	17126695	17126872	chr11:17126695-17126872	178	17126715	17126852	chr11:17126715-17126852	138	refseq PIK3C2A(isoforme1):exon22 NM_002645	100,00
PIK3C2A	exon21 chr11	17131958	17132128	chr11:17131958-17132128	171	17131978	17132108	chr11:17131978-17132108	131	refseq PIK3C2A(isoforme1):exon21 NM_002645	100,00
PIK3C2A	exon20 chr11	17134100	17134233	chr11:17134100-17134233	134	17134120	17134213	chr11:17134120-17134213	94	refseq PIK3C2A(isoforme1):exon20 NM_002645	100,00
PIK3C2A	exon19 chr11	17135887	17136032	chr11:17135887-17136032	146	17135907	17136012	chr11:17135907-17136012	106	refseq PIK3C2A(isoforme1):exon19 NM_002645	100,00
PIK3C2A	exon18 chr11	17139017	17139238	chr11:17139017-17139238	222	17139037	17139218	chr11:17139037-17139218	182	refseq PIK3C2A(isoforme1):exon18 NM_002645	100,00
PIK3C2A	exon17 chr11	17140171	17140306	chr11:17140171-17140306	136	17140191	17140286	chr11:17140191-17140286	96	refseq PIK3C2A(isoforme1):exon17 NM_002645	100,00
PIK3C2A	exon16 chr11	17140746	17140880	chr11:17140746-17140880	135	17140766	17140860	chr11:17140766-17140860	95	refseq PIK3C2A(isoforme1):exon16 NM_002645	100,00
PIK3C2A	exon15 chr11	17141312	17141541	chr11:17141312-17141541	230	17141332	17141521	chr11:17141332-17141521	190	refseq PIK3C2A(isoforme1):exon15 NM_002645	100,00
PIK3C2A	exon14 chr11	17143714	17143900	chr11:17143714-17143900	187	17143734	17143880	chr11:17143734-17143880	147	refseq PIK3C2A(isoforme1):exon14 NM_002645	100,00
PIK3C2A	exon13 chr11	17144228	17144380	chr11:17144228-17144380	153	17144248	17144360	chr11:17144248-17144360	113	refseq PIK3C2A(isoforme1):exon13 NM_002645	100,00
PIK3C2A	exon12 chr11	17150826	17151034	chr11:17150826-17151034	209	17150846	17151014	chr11:17150846-17151014	169	refseq PIK3C2A(isoforme1):exon12 NM_002645	100,00
PIK3C2A	exon11 chr11	17153442	17153605	chr11:17153442-17153605	164	17153462	17153585	chr11:17153462-17153585	124	refseq PIK3C2A(isoforme1):exon11 NM_002645	100,00
PIK3C2A	exon10 chr11	17156345	17156596	chr11:17156345-17156596	252	17156365	17156576	chr11:17156365-17156576	212	refseq PIK3C2A(isoforme1):exon10 NM_002645	100,00
PIK3C2A	exon9 chr11	17156637	17156726	chr11:17156637-17156726	90	17156657	17156706	chr11:17156657-17156706	50	refseq PIK3C2A(isoforme1):exon9 NM_002645	100,00
PIK3C2A	exon8 chr11	17158008	17158192	chr11:17158008-17158192	185	17158028	17158172	chr11:17158028-17158172	145	refseq PIK3C2A(isoforme1):exon8 NM_002645	100,00
PIK3C2A	exon7 chr11	17167194	17167298	chr11:17167194-17167298	105	17167214	17167278	chr11:17167214-17167278	65	refseq PIK3C2A(isoforme1):exon7 NM_002645	100,00
PIK3C2A	exon6 chr11	17167389	17167509	chr11:17167389-17167509	121	17167409	17167489	chr11:17167409-17167489	81	refseq PIK3C2A(isoforme1):exon6 NM_002645	100,00
PIK3C2A	exon5 chr11	17169043	17169195	chr11:17169043-17169195	153	17169063	17169175	chr11:17169063-17169175	113	refseq PIK3C2A(isoforme1):exon5 NM_002645	100,00
PIK3C2A	exon4 chr11	17170193	17170354	chr11:17170193-17170354	162	17170213	17170334	chr11:17170213-17170334	122	refseq PIK3C2A(isoforme1):exon4 NM_002645	100,00
PIK3C2A	exon3 chr11	17172024	17172222	chr11:17172024-17172222	199	17172044	17172202	chr11:17172044-17172202	159	refseq PIK3C2A(isoforme1):exon3 NM_002645	100,00
PIK3C2A	exon2 chr11	17177052	17177196	chr11:17177052-17177196	145	17177072	17177176	chr11:17177072-17177176	105	refseq PIK3C2A(isoforme1):exon2 NM_002645	100,00
PK2	exon1 chr11	17190203	17191308	chr11:17190203-17191308	1106	17190223	17191288	chr11:17190223-17191288	1066	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon15 exon1 chr5	57750389	57750621	chr5:57750389-57750621	233	57750409	57750509	chr5:57750409-57750509	193	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon14 exon1 chr5	57750717	57750868	chr5:57750717-57750868	152	57750737	57750848	chr5:57750737-57750848	112	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon13 exon1 chr5	57751091	57751261	chr5:57751091-57751261	171	57751111	57751241	chr5:57751111-57751241	131	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon12 exon1 chr5	57751345	57751626	chr5:57751345-57751626	282	57751365	57751606	chr5:57751365-57751606	242	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon11 exon1 chr5	57751832	57752002	chr5:57751832-57752002	171	57751852	57751982	chr5:57751852-57751982	131	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon10 exon1 chr5	57752298	57752436	chr5:57752298-57752436	139	57752318	57752416	chr5:57752318-57752416	99	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon9 exon8 chr5	57752751	57752939	chr5:57752751-57752939	189	57752771	57752919	chr5:57752771-57752919	149	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon8 exon7 chr5	57752987	57753226	chr5:57752987-57753226	240	57753007	57753206	chr5:57753007-57753206	200	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon7 exon6 chr5	57753294	57753430	chr5:57753294-57753430	137	57753314	57753410	chr5:57753314-57753410	97	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon6 exon5 chr5	57753890	57754018	chr5:57753890-57754018	129	57753910	57753998	chr5:57753910-57753998	89	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon5 exon4 chr5	57754205	57754375	chr5:57754205-57754375	171	57754225	57754355	chr5:57754225-57754355	131	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon4 exon3 chr5	57754531	57754688	chr5:57754531-57754688	158	57754551	57754668	chr5:57754551-57754668	118	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon3 exon2 chr5	57754791	57754939	chr5:57754791-57754939	149	57754811	57754919	chr5:57754811-57754919	109	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
PK2	exon1 chr5	57755496	57755806	chr5:57755496-57755806	311	57755516	57755786	chr5:57755516-57755786	271	refseq PK2(isoforme1 isoforme2):NM_001252226, NM_006622	100,00
POLD2	exon11 exon1 chr7	44154363	44154564	chr7:44154363-44154564	202	44154383	44154544	chr7:44154383-44154544	162	refseq POLD2(isoforme1 isoforme2):NM_006230, NM_001127218, NM_00:100,00	
POLD2	exon10 exon9 chr7	44154873	44155015	chr7:44154873-44155015	143	44154893	44154995	chr7:44154893-44154995	103	refseq POLD2(isoforme1 isoforme2):NM_006230, NM_001127218, NM_00:100,00	
POLD2	exon9 exon8 chr7	44155344	44155512	chr7:44155344-44155512	169	44155364	44155492	chr7:44155364-44155492	129	refseq POLD2(isoforme1 isoforme2):NM_006230, NM_001127218, NM_00:100,00	
POLD2	ex										

TBC1D10B	exon3	chr16	30376405	30376553	chr16:30376405-30376553	149	30376425	30376533	chr16:30376425-30376533	109	refseq TBC1D10B isoforme1 exon3 NM_015527	100,00
TBC1D10B	exon2	chr16	30376795	30376935	chr16:30376795-30376935	141	30376815	30376915	chr16:30376815-30376915	101	refseq TBC1D10B isoforme1 exon2 NM_015527	100,00
TBC1D10B	exon1	chr16	30380528	30381524	chr16:30380528-30381524	997	30380548	30381504	chr16:30380548-30381504	957	refseq TBC1D10B isoforme1 exon1 NM_015527	100,00
TBC1D19	exon1	chr4	26585795	26585934	chr4:26585795-26585934	140	26585815	26585914	chr4:26585815-26585914	100	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon2	chr4	26614770	26614883	chr4:26614770-26614883	114	26614790	26614863	chr4:26614790-26614863	74	refseq TBC1D19 isoforme2 exon2 eNM_018317	100,00
TBC1D19	exon3	chr4	26616009	26616095	chr4:26616009-26616095	87	26616029	26616075	chr4:26616029-26616075	47	refseq TBC1D19 isoforme2 exon3 eNM_018317	100,00
TBC1D19	exon4	chr4	26622214	26622330	chr4:26622214-26622330	117	26622234	26622310	chr4:26622234-26622310	77	refseq TBC1D19 isoforme2 exon4 eNM_018317	100,00
TBC1D19	exon2	chr4	26638812	26638927	chr4:26638812-26638927	116	26638832	26638907	chr4:26638832-26638907	76	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon3	chr4	26640372	26640476	chr4:26640372-26640476	105	26640392	26640456	chr4:26640392-26640456	65	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon4	chr4	26641742	26641829	chr4:26641742-26641829	88	26641762	26641809	chr4:26641762-26641809	48	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon5	chr4	26661198	26661349	chr4:26661198-26661349	152	26661218	26661329	chr4:26661218-26661329	112	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon6	chr4	26667934	26668047	chr4:26667934-26668047	114	26667954	26668027	chr4:26667954-26668027	74	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon7	chr4	26673750	26673829	chr4:26673750-26673829	80	26673770	26673809	chr4:26673770-26673809	40	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon8	chr4	26675377	26675530	chr4:26675377-26675530	154	26675397	26675510	chr4:26675397-26675510	114	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon9	chr4	26685276	26685391	chr4:26685276-26685391	116	26685296	26685371	chr4:26685296-26685371	76	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon10	chr4	26689946	26690049	chr4:26689946-26690049	104	26689966	26690029	chr4:26689966-26690029	64	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon11	chr4	26719534	26719659	chr4:26719534-26719659	126	26719554	26719639	chr4:26719554-26719639	86	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon12	chr4	26721682	26721767	chr4:26721682-26721767	86	26721702	26721747	chr4:26721702-26721747	46	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon13	chr4	26737056	26737129	chr4:26737056-26737129	74	26737076	26737109	chr4:26737076-26737109	34	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon14	chr4	26741465	26741615	chr4:26741465-26741615	151	26741485	26741595	chr4:26741485-26741595	111	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon15	chr4	26744109	26744241	chr4:26744109-26744241	133	26744129	26744221	chr4:26744129-26744221	93	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon16	chr4	26750012	26750168	chr4:26750012-26750168	157	26750032	26750148	chr4:26750032-26750148	117	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon17	chr4	26755421	26755532	chr4:26755421-26755532	112	26755441	26755512	chr4:26755441-26755512	72	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D19	exon18	chr4	26756474	26756589	chr4:26756474-26756589	116	26756494	26756569	chr4:26756494-26756569	76	refseq TBC1D19 isoforme1 isoforme NM_001292054, NM_018317	100,00
TBC1D2	exon13	chr9	100961642	100961890	chr9:100961642-100961890	249	100961662	100961870	chr9:100961662-100961870	209	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421, NM_001267572	100,00
TBC1D2	exon12	chr9	100962514	100962676	chr9:100962514-100962676	163	100962534	100962656	chr9:100962534-100962656	123	refseq TBC1D2 isoforme1 isoforme4 NM_001267571, NM_001267572	100,00
TBC1D2	exon11	chr9	100963740	100963966	chr9:100963740-100963966	227	100963760	100963946	chr9:100963760-100963946	187	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421, NM_001267572	100,00
TBC1D2	exon10	chr9	100965549	100965710	chr9:100965549-100965710	162	100965569	100965690	chr9:100965569-100965690	122	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421, NM_001267572	100,00
TBC1D2	exon9	chr9	100970929	100971446	chr9:100970929-100971446	518	100970949	100971426	chr9:100970949-100971426	478	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421, NM_001267572	100,00
TBC1D2	exon8	chr9	100972917	100973145	chr9:100972917-100973145	229	100972937	100973125	chr9:100972937-100973125	189	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421, NM_001267572	100,00
TBC1D2	exon7	chr9	100975369	100975520	chr9:100975369-100975520	152	100975389	100975500	chr9:100975389-100975500	112	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon6	chr9	100983094	100983530	chr9:100983094-100983530	437	100983114	100983510	chr9:100983114-100983510	397	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon5	chr9	100991213	100991450	chr9:100991213-100991450	238	100991233	100991430	chr9:100991233-100991430	198	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon4	chr9	100995677	100995851	chr9:100995677-100995851	175	100995697	100995831	chr9:100995697-100995831	135	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon3	chr9	101006255	101006431	chr9:101006255-101006431	177	101006275	101006411	chr9:101006275-101006411	137	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon2	chr9	101014046	101014228	chr9:101014046-101014228	183	101014066	101014208	chr9:101014066-101014208	143	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBC1D2	exon1	chr9	101017434	101017843	chr9:101017434-101017843	410	101017454	101017823	chr9:101017454-101017823	370	refseq TBC1D2 isoforme1 isoforme2 NM_001267571, NM_018421	100,00
TBK1	exon1	chr12	64849630	64849757	chr12:64849630-64849757	128	64849650	64849737	chr12:64849650-64849737	88	refseq TBK1 isoforme1 exon1 exte NM_013254	100,00
TBK1	exon2	chr12	64853948	64854129	chr12:64853948-64854129	182	64853968	64854109	chr12:64853968-64854109	142	refseq TBK1 isoforme1 exon2 exte NM_013254	100,00
TBK1	exon3	chr12	64858093	64858263	chr12:64858093-64858263	171	64858113	64858243	chr12:64858113-64858243	131	refseq TBK1 isoforme1 exon3 exte NM_013254	100,00
TBK1	exon4	chr12	64860660	64860882	chr12:64860660-64860882	223	64860680	64860862	chr12:64860680-64860862	183	refseq TBK1 isoforme1 exon4 exte NM_013254	100,00
TBK1	exon5	chr12	64867989	64868190	chr12:64867989-64868190	202	64868009	64868170	chr12:64868009-64868170	162	refseq TBK1 isoforme1 exon5 exte NM_013254	100,00
TBK1	exon6	chr12	64873771	64873922	chr12:64873771-64873922	152	64873791	64873902	chr12:64873791-64873902	112	refseq TBK1 isoforme1 exon6 exte NM_013254	100,00
TBK1	exon7	chr12	64875601	64875821	chr12:64875601-64875821	221	64875621	64875801	chr12:64875621-64875801	181	refseq TBK1 isoforme1 exon7 exte NM_013254	100,00
TBK1	exon8	chr12	64878062	64878299	chr12:64878062-64878299	238	64878082	64878279	chr12:64878082-64878279	198	refseq TBK1 isoforme1 exon8 exte NM_013254	100,00
TBK1	exon9	chr12	64879214	64879313	chr12:64879214-64879313	100	64879234	64879293	chr12:64879234-64879293	60	refseq TBK1 isoforme1 exon9 exte NM_013254	100,00
TBK1	exon10	chr12	64879685	64879817	chr12:64879685-64879817	133	64879705	64879797	chr12:64879705-64879797	93	refseq TBK1 isoforme1 exon10 exte NM_013254	100,00
TBK1	exon11	chr12	64882246	64882388	chr12:64882246-64882388	143	64882266	64882368	chr12:64882266-64882368	103	refseq TBK1 isoforme1 exon11 exte NM_013254	100,00
TBK1	exon12	chr12	64883800	64883919	chr12:64883800-64883919	120	64883820	64883899	chr12:64883820-64883899	80	refseq TBK1 isoforme1 exon12 exte NM_013254	100,00
TBK1	exon13	chr12	64889242	64889404	chr12:64889242-64889404	163	64889262	64889384	chr12:64889262-64889384	123	refseq TBK1 isoforme1 exon13 exte NM_013254	100,00
TBK1	exon14	chr12	64889458	64889575	chr12:64889458-64889575	118	64889478	64889555	chr12:64889478-64889555	78	refseq TBK1 isoforme1 exon14 exte NM_013254	100,00
TBK1	exon15	chr12	64890126	64890206	chr12:64890126-64890206	81	64890146	64890186	chr12:64890146-64890186	41	refseq TBK1 isoforme1 exon15 exte NM_013254	100,00
TBK1	exon16	chr12	64890708	64890850	chr12:64890708-64890850	143	64890728	64890830	chr12:64890728-64890830	103	refseq TBK1 isoforme1 exon16 exte NM_013254	100,00
TBK1	exon17	chr12	64890922	64891059	chr12:64890922-64891059	138	64890942	64891039	chr12:64890942-64891039	98	refseq TBK1 isoforme1 exon17 exte NM_013254	100,00
TBK1	exon18	chr12	64891407	64891554	chr12:64891407-64891554	148	64891427	64891534	chr12:64891427-64891534	108	refseq TBK1 isoforme1 exon18 exte NM_013254	100,00
TBK1	exon19	chr12	64891727	64891839	chr12:64891727-64891839	113	64891747	64891819	chr12:64891747-64891819	73	refseq TBK1 isoforme1 exon19 exte NM_013254	100,00
TBK1	exon20	chr12	64895089	64895181	chr12:64895089-64895181	93	64895109	64895161	chr12:64895109-64895161	53	refseq TBK1 isoforme1 exon20 exte NM_013254	100,00
TCF7L2	exon1	chr10	114710724	114710951	chr10:114710724-114710951	230	114710751	114710704	chr10:114710751-114710704	190	refseq TCF7L2 isoforme1 isoforme2 INM_001146286, NM_001198525, NM_001198526, NM_001198527	100,00
TCF7L2	exon2	chr10	114710945	114711052	chr10:114710945-114711052	108	114710965	114711032	chr10:114710965-114711032	68	refseq TCF7L2 isoforme1 isoforme2 INM_001146286, NM_001198525, NM_001198526, NM_001198527	100,00
TCF7L2	exon3	chr10	114711221	114711386	chr10:114711221-114711386	166	114711241	114711366	chr10:114711241-114711366	126	refseq TCF7L2 isoforme1 isoforme2 INM_001146286, NM_001198525, NM_001198526, NM_001198527	100,00
TCF7L2	exon4	chr10	114724294	114724403	chr10:114724294-114724403	110	114724314	114724383	chr10:114724314-114724383	70	refseq TCF7L2 isoforme1 isoforme2 INM_001198531, NM_001146274	100,00
TCF7L2	exon4	chr10	114799763	114799905	chr10:114799763-114799905	143	114799783	114799885				

U2AF1	exon5 exon8 chr21	44513191	44513379	chr21:44513191-44513379	189	44513211	44513359	chr21:44513211-44513359	149	refseq U2AF1(isoforme1 isoforme2 i:NM_001025204, NM_006758, NM_00:	100,00
U2AF1	exon4 exon7 chr21	44514560	44514693	chr21:44514560-44514693	134	44514580	44514673	chr21:44514580-44514673	94	refseq U2AF1(isoforme1 isoforme2 i:NM_001025204, NM_006758, NM_00:	100,00
U2AF1	exon3 exon6 chr21	44514744	44514918	chr21:44514744-44514918	175	44514764	44514898	chr21:44514764-44514898	135	refseq U2AF1(isoforme1 isoforme2 i:NM_001025204, NM_006758, NM_00:	100,00
U2AF1	exon2 exon5 chr21	44515527	44515666	chr21:44515527-44515666	140	44515547	44515646	chr21:44515547-44515646	100	refseq U2AF1(isoforme1 isoforme2 i:NM_001025204, NM_006758, NM_00:	100,00
U2AF1	exon4 exon4 chr21	44515783	44515873	chr21:44515783-44515873	91	44515803	44515853	chr21:44515803-44515853	51	refseq U2AF1(isoforme2 isoforme3):NM_006758, NM_001025203	100,00
U2AF1	exon3 chr21	44520542	44520649	chr21:44520542-44520649	108	44520562	44520629	chr21:44520562-44520629	68	refseq U2AF1(isoforme2):exon3 extrNM_006758	100,00
U2AF1	exon3 chr21	44521455	44521562	chr21:44521455-44521562	108	44521475	44521542	chr21:44521475-44521542	68	refseq U2AF1(isoforme3):exon3 extrNM_001025203	100,00
U2AF1	exon2 exon2 chr21	44524404	44524532	chr21:44524404-44524532	129	44524424	44524512	chr21:44524424-44524512	89	refseq U2AF1(isoforme2 isoforme3):NM_006758, NM_001025203	100,00
USP29	exon1 chr19	57640023	57642832	chr19:57640023-57642832	2810	57640043	57642812	chr19:57640043-57642812	2770	refseq USP29(isoforme1):exon1 extrNM_020903	100,00
WNK1	exon1 exon1 chr12	862711	863510	chr12:862711-863510	800	862731	863490	chr12:862731-863490	760	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon2 exon2 chr12	922787	923000	chr12:922787-923000	214	922807	922980	chr12:922807-922980	174	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon3 exon3 chr12	936187	936448	chr12:936187-936448	262	936207	936428	chr12:936207-936428	222	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon4 exon4 chr12	939148	939346	chr12:939148-939346	199	939168	939326	chr12:939168-939326	159	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon5 exon5 chr12	966306	966435	chr12:966306-966435	130	966326	966415	chr12:966326-966415	90	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon6 exon6 chr12	968390	968650	chr12:968390-968650	261	968410	968630	chr12:968410-968630	221	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon7 exon7 chr12	970158	970529	chr12:970158-970529	372	970178	970509	chr12:970178-970509	332	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon8 exon8 chr12	971228	971456	chr12:971228-971456	229	971248	971436	chr12:971248-971436	189	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon9 chr12	974255	974550	chr12:974255-974550	296	974275	974530	chr12:974275-974530	256	refseq WNK1(isoforme3):exon9 extrNM_213655	100,00
WNK1	exon10 exon9 chr12	977011	978290	chr12:977011-978290	1280	977031	978270	chr12:977031-978270	1240	refseq WNK1(isoforme3 isoforme4):NM_213655, NM_001184985	100,00
WNK1	exon9 exon9 chr12	980410	980534	chr12:980410-980534	125	980430	980514	chr12:980430-980514	85	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon10 exon1 chr12	987357	987547	chr12:987357-987547	191	987377	987527	chr12:987377-987527	151	refseq WNK1(isoforme2 isoforme3 i:NM_018979, NM_213655, NM_00118:	100,00
WNK1	exon11 chr12	988718	989217	chr12:988718-989217	500	988738	989197	chr12:988738-989197	460	refseq WNK1(isoforme2):exon11 extrNM_018979	100,00
WNK1	exon12 exon1 chr12	989866	990185	chr12:989866-990185	320	989886	990165	chr12:989886-990165	280	refseq WNK1(isoforme2 isoforme4):NM_018979, NM_001184985	100,00
WNK1	exon11 exon1 chr12	990837	990975	chr12:990837-990975	139	990857	990955	chr12:990857-990955	99	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon12 exon1 chr12	991056	991259	chr12:991056-991259	204	991076	991239	chr12:991076-991239	164	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon13 exon1 chr12	992088	992245	chr12:992088-992245	158	992108	992225	chr12:992108-992225	118	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon14 exon1 chr12	992540	992754	chr12:992540-992754	215	992560	992734	chr12:992560-992734	175	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon15 exon1 chr12	992919	993017	chr12:992919-993017	99	992939	992997	chr12:992939-992997	59	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon16 exon1 chr12	993266	993429	chr12:993266-993429	164	993286	993409	chr12:993286-993409	124	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon17 exon1 chr12	993794	995270	chr12:993794-995270	1477	993814	995250	chr12:993814-995250	1437	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon18 exon2 chr12	996366	996490	chr12:996366-996490	125	996386	996470	chr12:996386-996470	85	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon19 exon2 chr12	998285	998409	chr12:998285-998409	125	998305	998389	chr12:998305-998389	85	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon22 exon2 chr12	999598	999699	chr12:999598-999699	102	999618	999679	chr12:999618-999679	62	refseq WNK1(isoforme2 isoforme3 i:NM_018979, NM_213655, NM_00118:	100,00
WNK1	exon21 exon2 chr12	1003707	1003821	chr12:1003707-1003821	115	1003727	1003801	chr12:1003727-1003801	75	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon22 exon2 chr12	1005216	1005918	chr12:1005216-1005918	703	1005236	1005898	chr12:1005236-1005898	663	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon23 exon2 chr12	1006624	1006867	chr12:1006624-1006867	244	1006644	1006847	chr12:1006644-1006847	204	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon24 exon2 chr12	1009621	1009856	chr12:1009621-1009856	236	1009641	1009836	chr12:1009641-1009836	196	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon25 exon2 chr12	1016992	1017220	chr12:1016992-1017220	229	1017012	1017200	chr12:1017012-1017200	189	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00
WNK1	exon26 exon2 chr12	1017620	1017978	chr12:1017620-1017978	359	1017640	1017958	chr12:1017640-1017958	319	refseq WNK1(isoforme1 isoforme2 i:NM_014823, NM_018979, NM_21365:	100,00

Supplemental_Table_3

Sample ID	Gene	gDNA	cDNA	LocalisatorType	CIGAR	Effect	Protein change	VAF	Comments
VL_243_Spleen_B+ #15	BCOR	ChrX(GRCh37):g.39921391C>A	NM_001123385.1(BCOR):c.4428+1G>T	Intron 10	Substitution	-	Splicing site p.?	0.42	heterozygote (female); same position than COSM521431
VL_201_PB	BCOR	ChrX(GRCh37):g.3993091A>T	NM_001123385.1(BCOR):c.3030T>A	Exon 5	Substitution	-	Nonsense p.Cys1010*	0.91	hemizygote (male)
VL_206_PB_+	BCOR	ChrX(GRCh37):g.39931762dup	NM_001123385.1(BCOR):c.2837dup	Exon 4	Duplication	1I	Frameshift p.Ala947Glyfs*2	0.12	hemizygote (male)
VL_208_PB_+	BCOR	ChrX(GRCh37):g.39916518_39916528del	NM_001123385.1(BCOR):c.4475_4485del	Exon 11	Deletion	11D	Frameshift p.His1492Argfs*8	0.40	hemizygote (male)
VL_208_PB_+	BCOR	ChrX(GRCh37):g.39911341-39937202	-	Exon 4	Copy number	-	Gain	-	gain chr.X (male)
VL_214_Spleen	BCOR	ChrX(GRCh37):g.39933583dup	NM_001123385.1(BCOR):c.1016dup	Exon 4	Duplication	1I	Frameshift p.Ser340Valfs*41	0.12	hemizygote (male)
VL_230_PB	BCOR	ChrX(GRCh37):g.39934211C>A	NM_001123385.1(BCOR):c.388G>T	Exon 4	Substitution	-	Nonsense p.Glu130*	0.57	hemizygote (male)
VL_232_PB_+ #08	BCOR	ChrX(GRCh37):g.39911341-39937202	-	-	Copy number	-	Loss	-	loss chr.X (female)
VL_234_PB	BCOR	ChrX(GRCh37):g.39911341-39937202	-	-	Copy number	-	Loss	-	loss chr.X (female)
VL_227_PB_+ #09	BCOR	ChrX(GRCh37):g.39911341-39937202	-	-	Copy number	-	Loss	-	loss chr.X (female)
VL_218_PB	BCOR	ChrX(GRCh37):g.39911341-39937202	-	-	Copy number	-	Loss	-	loss chr.X (female)
MZ_117_Spleen_B+	BCOR	ChrX(GRCh37):g.39911341_39913142del	NM_001123385.1(BCOR):c.4973_4974del	Exon 14	Deletion	2D	Frameshift p.Gln1658Argfs*13	0.46	heterozygote (female)
HC_301_Spleen	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.35	
HC_302_Spleen	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.10	
HC_303_PB	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.42	
HC_305_PB_+	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.48	
HC_306_PB_+	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.42	
HC_309_Spleen	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.40	
HC_310_PB_+	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.35	
HC_311_PB_+	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.29	
MZ_104_Spleen_B+	BRAP	Chr7(GRCh37):g.140453136A>T	NM_004333.4(BRAP):c.1799T>A	Exon 15	Substitution	-	Missense p.Val600Glu	0.26	
VL_203_PB_+	BRAP	Chr7(GRCh37):g.140481402C>G	NM_004333.4(BRAP):c.1406G>C	Exon 11	Substitution	-	Missense p.Gly469Ala	0.42	
HC_305_PB_+	KLF2	Chr19(GRCh37):g.16436489G>A	NM_016270.2(KLF2):c.538G>A	Exon 2	Substitution	-	Missense p.Gly180Ser	0.59	IGHV4-34; rs121913355 (pathogenic)
MZ_103_Spleen_B+	KLF2	Chr19(GRCh37):g.16436813C>T	NM_016270.2(KLF2):c.862C>T	Exon 2	Substitution	-	Missense p.His288Tyr	0.47	
MZ_104_Spleen_B+	KLF2	Chr19(GRCh37):g.16436287dup	NM_016270.2(KLF2):c.336dup	Exon 2	Duplication	1I	Frameshift p.Leu1138Serfs*15	0.26	
MZ_107_Spleen_B+	KLF2	Chr19(GRCh37):g.16436691_16436703del	NM_016270.2(KLF2):c.740_752del	Exon 2	Deletion	12D	Frameshift p.Ala247Glyfs*39	0.30	
MZ_107_Spleen_B+	KLF2	Chr19(GRCh37):g.16437747A>T	NM_016270.2(KLF2):c.973A>T	Exon 3	Substitution	-	Missense p.Lys325*	0.43	
MZ_110_Spleen_B+	KLF2	Chr19(GRCh37):g.16436772G>A	NM_016270.2(KLF2):c.821G>A	Exon 2	Substitution	-	Missense p.Cys274Tyr	0.42	
MZ_110_Spleen_B+	KLF2	Chr19(GRCh37):g.16436837C>T	NM_016270.2(KLF2):c.886C>T	Exon 2	Substitution	-	Missense p.His296Tyr	0.40	
MZ_113_Spleen_B+	KLF2	Chr19(GRCh37):g.16437685G>A	NM_016270.2(KLF2):c.911G>A	Exon 3	Substitution	-	Missense p.Cys304Tyr	0.47	
MZ_114_Spleen_B+	KLF2	Chr19(GRCh37):g.16436073T>G	NM_016270.2(KLF2):c.122T>G	Exon 2	Substitution	-	Missense p.Leu41Arg	0.49	
MZ_115_Spleen_B+	KLF2	Chr19(GRCh37):g.16436837C>T	NM_016270.2(KLF2):c.886C>T	Exon 2	Substitution	-	Missense p.His296Tyr	0.45	
MZ_117_Spleen_B+	KLF2	Chr19(GRCh37):g.16436432C>T	NM_016270.2(KLF2):c.481C>T	Exon 2	Substitution	-	Nonsense p.Arg161*	0.47	
MZ_123_Spleen	KLF2	Chr19(GRCh37):g.16436823C>T	NM_016270.2(KLF2):c.872C>T	Exon 2	Substitution	-	Missense p.Ala291Val	0.76	
MZ_127_Spleen	KLF2	Chr19(GRCh37):g.16436109_16436110insC	NM_016270.2(KLF2):c.158_159insC	Exon 2	Insertion	1I	Frameshift p.Asp540Glyfs*41	0.25	
MZ_129_Spleen	KLF2	Chr19(GRCh37):g.16437808A>T	NM_016270.2(KLF2):c.1034A>T	Exon 3	Substitution	-	Missense p.Asp345Val	0.38	
MZ_133_Spleen	KLF2	Chr19(GRCh37):g.16436156_16436157dup	NM_016270.2(KLF2):c.205_206dup	Exon 2	Duplication	2I	Frameshift p.Pro70Argfs*72	0.19	
MZ_133_Spleen	KLF2	Chr19(GRCh37):g.16436150A>T	NM_016270.2(KLF2):c.208G>T	Exon 2	Substitution	-	Missense p.Pro70Ser	0.28	
MZ_137_Spleen	KLF2	Chr19(GRCh37):g.16436026G>A	NM_016270.2(KLF2):c.76-1G>A	Intron 1	Substitution	-	Splicing site p.?	0.22	
MZ_137_Spleen	KLF2	Chr19(GRCh37):g.16436765C>T	NM_016270.2(KLF2):c.814C>T	Exon 2	Substitution	-	Missense p.His272Tyr	0.26	
MZ_137_Spleen	KLF2	Chr19(GRCh37):g.16436813C>T	NM_016270.2(KLF2):c.862C>T	Exon 2	Substitution	-	Missense p.His288Tyr	0.29	
MZ_148_Spleen_B+	KLF2	Chr19(GRCh37):g.16435804C>T	NM_016270.2(KLF2):c.70C>T	Exon 1	Substitution	-	Nonsense p.Gln24*	0.47	
VL_218_PB	KLF2	Chr19(GRCh37):g.1643662dup	NM_016270.2(KLF2):c.711dup	Exon 2	Duplication	1I	Frameshift p.Ala238Argfs*62	0.33	
VL_201_PB	MAP2K1	Chr15(GRCh37):g.66727463T>A	NM_002755.3(MAP2K1):c.179T>A	Exon 2	Substitution	-	Missense p.Val60Glu	0.30	IGHV3-23*01
VL_203_PB_+	MAP2K1	Chr15(GRCh37):g.66729100T>A	NM_002755.3(MAP2K1):c.308T>A	Exon 3	Substitution	-	Missense p.Ile103Asn	0.47	IGHV4-34*01
VL_208_PB_+	MAP2K1	Chr15(GRCh37):g.66729154G>C	NM_002755.3(MAP2K1):c.362G>C	Exon 3	Substitution	-	Missense p.Cys121Ser	0.48	IGHV1-3*01
MZ_102_Spleen_B+	MDM8	Chr3(GRCh37):g.38182641T>C	NM_002468.4(MDM8):c.794T>C	Exon 5	Substitution	-	Missense p.Leu265Pro	0.44	
MZ_114_Spleen_B+	MDM8	Chr3(GRCh37):g.38180153A>G	NM_001172567.1(MDM8):c.1A>G	Exon 1	Substitution	-	Start loss p.Het12*	0.47	
MZ_124_Spleen	MDM8	Chr3(GRCh37):g.38182025G>T	NM_001172567.1(MDM8):c.649G>T	Exon 3b	Substitution	-	Missense p.Val217Phe	0.37	
MZ_130_Spleen	MDM8	Chr3(GRCh37):g.38182025G>T	NM_001172567.1(MDM8):c.649G>T	Exon 3b	Substitution	-	Missense p.Val217Phe	0.33	
HC_310_PB_+	NOTCH1	Chr9(GRCh37):g.13940970G>A	NM_017617.3(NOTCH1):c.222T>C	Exon 14	Substitution	-	Missense p.Pro743Ser	0.50	
MZ_111_Spleen_B+	NOTCH1	Chr9(GRCh37):g.139409775C>T	NM_017617.3(NOTCH1):c.1981G>A	Exon 12	Substitution	-	Missense p.Gly661Ser	0.43	
MZ_119_Spleen_B+	NOTCH1	Chr9(GRCh37):g.139402516T>C	NM_017617.3(NOTCH1):c.3401A>G	Exon 21	Substitution	-	Missense p.Gln1134Arg	0.46	
MZ_128_Spleen	NOTCH1	Chr9(GRCh37):g.139412624G>A	NM_017617.3(NOTCH1):c.1220C>T	Exon 7	Substitution	-	Missense p.Pro407Leu	0.47	
MZ_134_Spleen	NOTCH1	Chr9(GRCh37):g.139409061C>T	NM_017617.3(NOTCH1):c.2108G>A	Exon 13	Substitution	-	Missense p.Arg703His	0.48	
VL_202_PB_+	NOTCH1	Chr9(GRCh37):g.139413972C>A	NM_017617.3(NOTCH1):c.788G>T	Exon 5	Substitution	-	Missense p.Gly263Val	0.38	
MZ_227_PB_+ #09	NOTCH2	Chr1(GRCh37):g.12045808G>A	NM_024408.2(NOTCH2):c.726C>T	Exon 34	Substitution	-	Missense p.Ser242Phe	0.47	
VL_227_PB_+ #09	NOTCH2	Chr1(GRCh37):g.12045808G>A	NM_024408.2(NOTCH2):c.725T>C	Exon 34	Substitution	-	Missense p.Ser2418Phe	0.48	
MZ_102_Spleen_B+	NOTCH2	Chr1(GRCh37):g.120478125A>C	NM_024408.2(NOTCH2):c.3625T>G	Exon 22	Substitution	-	Missense p.Phe1209Val	0.49	
MZ_108_Spleen_B+	NOTCH2	Chr1(GRCh37):g.120458255G>A	NM_024408.2(NOTCH2):c.7090C>T	Exon 34	Substitution	-	Nonsense p.Gln2364*	0.47	
MZ_109_Spleen_B+	NOTCH2	Chr1(GRCh37):g.120458147G>A	NM_024408.2(NOTCH2):c.7198C>T	Exon 34	Substitution	-	Nonsense p.Arg2400*	0.40	
MZ_114_Spleen_B+	NOTCH2	Chr1(GRCh37):g.120458466dup	NM_024408.2(NOTCH2):c.6879dup	Exon 34	Duplication	1I	Frameshift p.Ile2294Hisfs*19	0.36	
MZ_115_Spleen_B+	NOTCH2	Chr1(GRCh37):g.120458283del	NM_024408.2(NOTCH2):c.7062del	Exon 34	Deletion	1D	Frameshift p.Thr2355Leufs*3	0.58	
MZ_127_Spleen	NOTCH2	Chr1(GRCh37):g.120458430_120458435delinsAAAAAG	NM_024408.2(NOTCH2):c.6910_6915delinsCTTTTT	Exon 34	Deletion	6D/7I	Frameshift p.Ile2304Leufs*9	0.34	
MZ_134_Spleen	NOTCH2	Chr1(GRCh37):g.120458147G>A	NM_024408.2(NOTCH2):c.7198C>T	Exon 34	Substitution	-	Nonsense p.Arg2400*	0.44	
MZ_140_Spleen	NOTCH2	Chr1(GRCh37):g.120458895_120458896del	NM_024408.2(NOTCH2):c.6449_6450del	Exon 34	Deletion	2D	Frameshift p.Pro2150Argfs*2	0.15	
VL_215_PB	NOTCH2	Chr1(GRCh37):g.120458888del	NM_024408.2(NOTCH2):c.6457del	Exon 34	Deletion	1D	Frameshift p.Ser2153Profs*50	0.47	
VL_216_PB	NOTCH2	Chr1(GRCh37):g.120458102_120458121del	NM_024408.2(NOTCH2):c.7224_7243del	Exon 34	Deletion	19D	Frameshift p.Gln2409Aspfs*8	nd	
VL_236_PB	NOTCH2	Chr1(GRCh37):g.120458498_120458499insGTAT	NM_024408.2(NOTCH2):c.6846_6847insATAC	Exon 34	Insertion	4I	Frameshift p.Ala2293Ilefs*9	0.13	
MZ_114_Spleen_B+	SPEN	Chr1(GRCh37):g.16174594_16174595del	NM_015001.2(SPEN):c.32_33del	Exon 1	Deletion	2D	Frameshift p.Gly1161ufs*33	0.50	
MZ_145_Spleen	SPEN	Chr1(GRCh37):g.16261356del	NM_015001.2(SPEN):c.862del	Exon 11	Deletion	1D	Frameshift p.Pro2874Leufs*15	0.35	
MZ_145_Spleen	SPEN	Chr1(GRCh37):g.16256512del	NM_015001.2(SPEN):c.3777del	Exon 11	Deletion	1D	Frameshift p.Gly1260Valfs*17	0.36	
MZ_149_Spleen_B+	SPEN	Chr1(GRCh37):g.16256470C>A	NM_015001.2(SPEN):c.3735C>A	Exon 11	Substitution	-	Nonsense p.Tyr124*	0.50	
MZ_149_Spleen_B+	SPEN	Chr1(GRCh37):g.16262129A>G	NM_015001.2(SPEN):c.3934A>G	Exon 11	Substitution	-	Missense p.Arg3132Gly	0.51	
VL_229_PB	SPEN	Chr1(GRCh37):g.16256282C>T	NM_015001.2(SPEN):c.3793C>T	Exon 11	Substitution	-	Nonsense p.Arg1265*	0.28	
VL_233_PB	SPEN	Chr1(GRCh37):g.16237787A>G	NM_015001.2(SPEN):c.1234A>G	Exon 5	Substitution	-	Missense p.Ile412Val	0.52	
MZ_103_Spleen_B+	TNFAIP3	Chr6(GRCh37):g.138199621C>T	NM_001270507.1(TNFAIP3):c.1039G>T	Exon 7	Substitution	-	Nonsense p.Glu347*	0.24	
MZ_121_Spleen	TNFAIP3	Chr6(GRCh37):g.138199757del	NM_001270507.1(TNFAIP3):c.1175del	Exon 7	Deletion	1D	Frameshift p.Cys392Serfs*7	0.37	
MZ_129_Spleen	TNFAIP3	Chr6(GRCh37):g.138199950dup	NM_001270507.1(TNFAIP3):c.1368dup	Exon 7	Duplication	1I	Frameshift p.Pro457Alafs*16	0.28	
MZ_130_Spleen	TNFAIP3	Chr6(GRCh37):g.138199850C>G	NM_001270507.1(TNFAIP3):c.547C>G	Exon 4	Substitution	-	Missense p.Arg183Gly	0.46	
MZ_131_Spleen	TNFAIP3	Chr6(GRCh37):g.138199748C>T	NM_001270507.1(TNFAIP3):c.1166C>T	Exon 7	Substitution	-	Missense p.Thr389Met	0.47	
MZ_145_Spleen	TNFAIP3	Chr6(GRCh37):g.138198249del	NM_001270507.1(TNFAIP3):c.842del	Exon 6	Deletion	1D	Frameshift p.Gly381Glyfs*6	0.15	
MZ_145_Spleen	TNFAIP3	Chr6(GRCh37):g.138200325_138200326del	NM_001270507.1(TNFAIP3):c.1743_1744del	Exon 7	Deletion	2D	Frameshift p.Arg381Serfs*90	0.44	
MZ_148_Spleen_B+	TNFAIP3	Chr6(GRCh37):g.138198896_138198897del	NM_001270507.1(TNFAIP3):c.1314_1315del	Exon 7	Deletion	2D	Frameshift p.Arg439Glyfs*5	0.11	