Supplementary Table S4. High frequency mutations unique to each Gp3 or Gp4 tumor focus. For each focus of tumor, somatic mutations found in only one focus of tumor (Gp3 or Gp4, as indicated) are shown with the cancer cell fraction (CCF) for the mutant allele. To avoid misclassifying a shared mutation or undercovered germline SNP, mutations were considered exclusive if the other foci were covered at a power to conclude the mutation was not present (as described in Methods). Also shown is the reference and alternative allele depth for the matched benign control.

Case	**Focus**	**Genomic Coordinates**	**Classification**	**Gene Symbol**	**Effect**	**Description**	**Normal coverage (freq.)**	**Tumor coverage (freq.)**	**Tumor CCF**
10-01	Gp3	g.chr2:219129752G>A	Missense Mutation	AAMP	p.A408V	angio-associated, migrat	17 (0.00)	31 (0.26)	0.69
10-01	Gp3	g.chr7:48563944C>G	Missense Mutation	ABCA13	p.L4718V	ATP-binding cassette, s	75 (0.00)	31 (0.16)	0.43
10-01	Gp3	g.chr11:62287806C>A	Missense Mutation	AHNAK	p.V4695L	AHNAK nucleoprotein	23 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chr11:62292480G>A	Missense Mutation	AHNAK	p.P3137S	AHNAK nucleoprotein	44 (0.00)	45 (0.16)	0.41
10-01	Gp3	g.chr6:151674085C>T	Missense Mutation	AKAP12	p.A1520V	A kinase (PRKA) ancho	54 (0.00)	51 (0.16)	0.42
10-01	Gp3	g.chr2:202617894G>A	Missense Mutation	ALS2	p.S571F	amyotrophic lateral scle	36 (0.00)	34 (0.15)	0.39
10-01	Gp3	g.chr11:10503646C>T	Silent	AMPD3	p.L164L	adenosine monophosph	32 (0.00)	29 (0.17)	0.46
10-01	Gp3	g.chr10:61833212G>A	Missense Mutation	ANK3	p.S2476F	ankyrin 3, node of Ranv	34 (0.00)	28 (0.21)	0.57
10-01	Gp3	g.chr20:56798114G>A	Silent	ANKRD60	p.P185P	ankyrin repeat domain 6	24 (0.00)	32 (0.19)	0.50
10-01	Gp3	g.chr20:47628543C>A	Missense Mutation	ARFGEF2	p.N1280K	ADP-ribosylation factor	23 (0.00)	30 (0.20)	0.53
10-01	Gp3	g.chr19:42407881G>A	Missense Mutation	ARHGEF1	p.R636H	Rho guanine nucleotide	27 (0.00)	51 (0.20)	0.52
10-01	Gp3	g.chr2:239353312C>A	Nonsense Mutation	ASB1	p.S174*	ankyrin repeat and SOC	23 (0.00)	29 (0.17)	0.46
10-01	Gp3	g.chr7:105254421C>A	Missense Mutation	ATXN7L1	p.S787I	ataxin 7-like 1	26 (0.00)	22 (0.27)	0.73
10-01	Gp3	g.chr12:668573G>A	Nonsense Mutation	B4GALNT3	p.W958*	beta-1,4-N-acetyl-galact	27 (0.00)	40 (0.15)	0.40
10-01	Gp3	g.chr11:27679871C>A	Nonsense Mutation	BDNF	p.E81*	brain-derived neurotrop	24 (0.00)	41 (0.15)	0.39
10-01	Gp3	g.chr12:27234157C>A	Missense Mutation	C12orf71	p.G254C	chromosome 12 open re	15 (0.00)	17 (0.35)	0.94
10-01	Gp3	g.chr8:86389428C>A	Nonsense Mutation	CA2	p.S196*	carbonic anhydrase II	25 (0.00)	48 (0.17)	0.44
10-01	Gp3	g.chr3:85440808C>T	Intron	CADM2		cell adhesion molecule	32 (0.03)	26 (0.19)	0.51
10-01	Gp3	g.chr3:85517111C>T	Intron	CADM2		cell adhesion molecule	53 (0.00)	53 (0.17)	0.45
10-01	Gp3	g.chr3:85567132G>A	Intron	CADM2		cell adhesion molecule	28 (0.00)	27 (0.26)	0.69
10-01	Gp3	g.chr2:179770062G>A	Missense Mutation	CCDC141	p.S420F	coiled-coil domain cont	52 (0.02)	31 (0.16)	0.43
10-01	Gp3	g.chr4:77969527C>T	Missense Mutation	CCNI	p.E327K	cyclin I	64 (0.00)	61 (0.15)	0.39
10-01	Gp3	g.chr11:125859609G>A	Missense Mutation	CDON	p.S899F	cell adhesion associated	39 (0.00)	29 (0.17)	0.46
10-01	Gp3	g.chr13:25459486G>T	Missense Mutation	CENPJ	p.F1135L	centromere protein J	50 (0.00)	41 (0.15)	0.39
10-01	Gp3	g.chr12:10215739C>T	Silent	CLEC9A	p.H135H	C-type lectin domain fa	21 (0.00)	23 (0.22)	0.58

10-01	Gp3	g.chr6:25087146C>T	RNA	CMAHP		cytidine monophospho-	26 (0.00)	42 (0.14)	0.38
10-01	Gp3	g.chr2:208994346G>A	Missense Mutation	CRYGC	p.P24L	crystallin, gamma C	60 (0.00)	65 (0.18)	0.49
10-01	Gp3	g.chr15:75982110C>T	Silent	CSPG4	p.L432L	chondroitin sulfate prot	21 (0.00)	25 (0.20)	0.53
10-01	Gp3	g.chr19:41707182T>G	Missense Mutation	CYP2S1	p.M294R	cytochrome P450, famil	20 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chr9:124434229G>A	Intron	DAB2IP		DAB2 interacting protei	41 (0.00)	46 (0.15)	0.41
10-01	Gp3	g.chr9:124434852C>T	Intron	DAB2IP		DAB2 interacting protei	21 (0.00)	29 (0.17)	0.46
10-01	Gp3	g.chr9:37861161G>A	Missense Mutation	DCAF10	p.E446K	DDB1 and CUL4 associ	33 (0.00)	39 (0.15)	0.41
10-01	Gp3	g.chr6:24301992G>T	Missense Mutation	DCDC2	p.L170I	doublecortin domain co	38 (0.00)	38 (0.16)	0.42
10-01	Gp3	g.chr12:31253965C>T	Silent	DDX11	p.H651H	DEAD/H (Asp-Glu-Ala	28 (0.00)	37 (0.22)	0.58
10-01	Gp3	g.chr2:169952153C>T	Missense Mutation	DHRS9	p.T279I	dehydrogenase/reductas	35 (0.03)	24 (0.21)	0.56
10-01	Gp3	g.chr6:83839085C>A	Missense Mutation	DOPEY1	p.N733K	dopey family member 1	36 (0.00)	33 (0.15)	0.40
10-01	Gp3	g.chr3:128753063C>A	Missense Mutation	EFCC1	p.A447D	EF-hand and coiled-coil	20 (0.00)	35 (0.14)	0.38
10-01	Gp3	g.chr19:39127542C>G	Missense Mutation	EIF3K	p.I126M	eukaryotic translation in	22 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chrX:154130404C>A	Nonsense Mutation	F8	p.G2013*	coagulation factor VIII,	30 (0.00)	21 (0.24)	0.40
10-01	Gp3	g.chr4:187540380G>A	Missense Mutation	FAT1	p.R2454W	FAT atypical cadherin 1	70 (0.00)	54 (0.35)	0.94
10-01	Gp3	g.chr5:127645706G>A	Silent	FBN2	p.Y1723Y	fibrillin 2	25 (0.00)	42 (0.14)	0.38
10-01	Gp3	g.chrX:131216410C>T	Missense Mutation	FRMD7	p.G296S	FERM domain containi	36 (0.00)	35 (0.34)	0.57
10-01	Gp3	g.chr3:179119060C>G	Missense Mutation	GNB4	p.D322H	guanine nucleotide bind	55 (0.00)	41 (0.15)	0.39
10-01	Gp3	g.chr7:126544062C>A	Missense Mutation	GRM8	p.A328S	glutamate receptor, met	24 (0.00)	24 (0.21)	0.56
10-01	Gp3	g.chr8:130774931G>T	Missense Mutation	GSDMC	p.T206N	gasdermin C	32 (0.00)	47 (0.13)	0.41
10-01	Gp3	g.chr11:93796813G>A	Silent	HEPHL1	p.V185V	hephaestin-like 1	38 (0.00)	35 (0.14)	0.38
10-01	Gp3	g.chr19:46832533G>A	Missense Mutation	HIF3A	p.A504T	hypoxia inducible facto	28 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chr10:71144612C>T	Missense Mutation	HK1	p.P594S	hexokinase 1	19 (0.00)	25 (0.20)	0.53
10-01	Gp3	g.chr22:35789481C>T	Missense Mutation	HMOX1	p.P253S	heme oxygenase (decyc	39 (0.00)	27 (0.19)	0.49
10-01	Gp3	g.chr1:23637462C>T	Missense Mutation	HNRNPR	p.D466N	heterogeneous nuclear r	24 (0.00)	27 (0.22)	0.59
10-01	Gp3	g.chr2:231973508G>A	Missense Mutation	HTR2B	p.A390V	5-hydroxytryptamine (s	46 (0.00)	31 (0.16)	0.43
10-01	Gp3	g.chr6:52884123G>T	Silent	ICK	p.L131L	intestinal cell (MAK-lik	29 (0.00)	23 (0.22)	0.58
10-01	Gp3	g.chr6:52884126G>A	Silent	ICK	p.N130N	intestinal cell (MAK-lik	30 (0.00)	22 (0.23)	0.61
10-01	Gp3	g.chr15:65622724C>G	Missense Mutation	IGDCC3	p.V589L	immunoglobulin superf	22 (0.00)	20 (0.25)	0.67
10-01	Gp3	g.chr4:143308334C>T	Intron	INPP4B		inositol polyphosphate-	48 (0.02)	47 (0.15)	0.40
10-01	Gp3	g.chr4:143751676G>A	Intron	INPP4B		inositol polyphosphate-	29 (0.00)	26 (0.27)	0.72
10-01	Gp3	g.chr2:201369552G>A	Silent	KCTD18	p.I97I	potassium channel tetra	27 (0.00)	34 (0.18)	0.47
10-01	Gp3	g.chr4:123192317G>A	Silent	KIAA1109	p.K2546K	KIAA1109	23 (0.00)	17 (0.29)	0.78
10-01	Gp3	g.chrX:69516908G>A	Missense Mutation	KIF4A	p.G99E	kinesin family member	19 (0.00)	19 (0.26)	0.44
10-01	Gp3	g.chr19:51506432G>A	Missense Mutation	KLK9	p.R230C	kallikrein-related peptid	15 (0.00)	38 (0.16)	0.42
10-01	Gp3	g.chr13:76382060G>A	Nonsense Mutation	LMO7	p.W314*	LIM domain 7	62 (0.00)	46 (0.20)	0.52

10-01	Gp3	g.chr7:77770299G>A	Intron	MAGI2		membrane associated gu	19 (0.00)	31 (0.19)	0.52
10-01	Gp3	g.chr7:77773950C>T	Intron	MAGI2		membrane associated gu	24 (0.00)	36 (0.17)	0.44
10-01	Gp3	g.chr7:77991803G>A	Intron	MAGI2		membrane associated gu	73 (0.00)	48 (0.17)	0.44
10-01	Gp3	g.chr7:78554059C>A	Intron	MAGI2		membrane associated gu	18 (0.00)	30 (0.17)	0.44
10-01	Gp3	g.chr7:78750926C>T	Intron	MAGI2		membrane associated gu	39 (0.00)	22 (0.41)	1.09
10-01	Gp3	g.chr7:78956693G>A	Intron	MAGI2		membrane associated gu	48 (0.00)	63 (0.16)	0.42
10-01	Gp3	g.chr1:38261466C>A	Nonsense Mutation	MANEAL	p.S203*	mannosidase, endo-alph	26 (0.00)	20 (0.25)	0.67
10-01	Gp3	g.chr8:99019726G>A	Silent	MATN2	p.L490L	matrilin 2	33 (0.00)	40 (0.15)	0.40
10-01	Gp3	g.chr8:67789741G>A	Missense Mutation	MCMDC2	p.R148K	minichromosome maint	26 (0.00)	32 (0.19)	0.50
10-01	Gp3	g.chr6:90499573C>A	Missense Mutation	MDN1	p.G386C	MDN1, midasin homolo	36 (0.00)	43 (0.16)	0.43
10-01	Gp3	g.chr17:74771205C>T	Missense Mutation	MFSD11	p.P334L	major facilitator superfa	24 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chr7:141722104C>T	Silent	MGAM	p.D249D	maltase-glucoamylase (	35 (0.00)	33 (0.15)	0.40
10-01	Gp3	g.chr7:141791841G>A	Missense Mutation	MGAM	p.M2313I	maltase-glucoamylase (	73 (0.00)	22 (0.27)	0.73
10-01	Gp3	g.chr14:39716740G>A	Missense Mutation	MIA2	p.G321E	melanoma inhibitory act	44 (0.00)	37 (0.19)	0.50
10-01	Gp3	g.chr19:9057790C>A	Nonsense Mutation	MUC16	p.E9886*	mucin 16, cell surface a	21 (0.00)	19 (0.26)	0.70
10-01	Gp3	g.chr17:10450857T>C	Missense Mutation	MYH2	p.T95A	myosin, heavy chain 2,	34 (0.00)	34 (0.24)	0.63
10-01	Gp3	g.chr17:15965088C>T	Silent	NCOR1	p.V1836V	nuclear receptor corepre	83 (0.00)	34 (0.21)	0.55
10-01	Gp3	g.chr2:152467370G>A	Missense Mutation	NEB	p.T3939I	nebulin	42 (0.00)	45 (0.16)	0.41
10-01	Gp3	g.chr19:56307548C>T	Missense Mutation	NLRP11	p.S747N	NLR family, pyrin doma	19 (0.00)	17 (0.29)	0.78
10-01	Gp3	g.chr16:14975421C>T	Missense Mutation	NOMO1	p.S969F	NODAL modulator 1	25 (0.00)	23 (0.22)	0.72
10-01	Gp3	g.chr4:164271621C>A	Missense Mutation	NPY5R	p.L66I	neuropeptide Y receptor	79 (0.00)	49 (0.14)	0.38
10-01	Gp3	g.chr2:50692672G>A	Missense Mutation	NRXN1	p.S1131L	neurexin 1	38 (0.00)	32 (0.22)	0.58
10-01	Gp3	g.chr11:6912839G>A	Missense Mutation	OR2D2	p.A298V	olfactory receptor, famil	18 (0.00)	21 (0.24)	0.63
10-01	Gp3	g.chr11:59271873C>T	Silent	OR4D11	p.F275F	olfactory receptor, famil	20 (0.00)	35 (0.14)	0.38
10-01	Gp3	g.chr11:5424628C>A	Missense Mutation	OR51J1	p.H268N	olfactory receptor, famil	30 (0.00)	33 (0.15)	0.40
10-01	Gp3	g.chr11:5410999C>G	Missense Mutation	OR51M1	p.S124C	olfactory receptor, famil	31 (0.00)	34 (0.21)	0.55
10-01	Gp3	g.chr11:55606372G>A	Missense Mutation	OR5D16	p.V49M	olfactory receptor, famil	41 (0.00)	34 (0.15)	0.39
10-01	Gp3	g.chr5:140773089G>A	Missense Mutation	PCDHGA8	p.D237N	protocadherin gamma su	35 (0.00)	34 (0.15)	0.39
10-01	Gp3	g.chr16:70180102C>T	Missense Mutation	PDPR	p.P645S	pyruvate dehydrogenase	26 (0.00)	33 (0.27)	0.73
10-01	Gp3	g.chr17:7139154C>G	Missense Mutation	PHF23	p.D205H	PHD finger protein 23	40 (0.00)	44 (0.18)	0.48
10-01	Gp3	g.chr18:60444107T>C	Intron	PHLPP1		PH domain and leucine	26 (0.00)	30 (0.17)	0.44
10-01	Gp3	g.chr18:60587111G>T	Intron	PHLPP1		PH domain and leucine	54 (0.00)	28 (0.21)	0.57
10-01	Gp3	g.chr22:21087278G>A	Silent	PI4KA	p.A1423A	phosphatidylinositol 4-k	15 (0.00)	23 (0.22)	0.58
10-01	Gp3	g.chr7:75140394C>A	RNA	PMS2P3		postmeiotic segregation	49 (0.00)	40 (0.15)	0.40
10-01	Gp3	g.chr7:75145492G>A	RNA	PMS2P3		postmeiotic segregation	17 (0.00)	23 (0.26)	0.70
10-01	Gp3	g.chr14:39649838G>A	Missense Mutation	PNN	p.E309K	pinin, desmosome assoc	28 (0.00)	26 (0.19)	0.51

10-01	Gp3	g.chr2:113309556G>A	Missense Mutation	POLR1B	p.A267T	polymerase (RNA) I pol	31 (0.00)	42 (0.17)	0.44
10-01	Gp3	g.chr14:30102078G>A	Silent	PRKD1	p.Y463Y	protein kinase D1	18 (0.00)	21 (0.24)	0.63
10-01	Gp3	g.chr4:148559718G>T	Missense Mutation	PRMT10	p.H835N		79 (0.00)	36 (0.17)	0.44
10-01	Gp3	g.chr2:95953154G>A	Missense Mutation	PROM2	p.C729Y	prominin 2	23 (0.00)	36 (0.17)	0.44
10-01	Gp3	g.chr9:79325065C>T	Missense Mutation	PRUNE2	p.E709K	prune homolog 2 (Drosc	19 (0.00)	33 (0.24)	0.65
10-01	Gp3	g.chr7:77265569G>A	Intron	PTPN12		protein tyrosine phospha	42 (0.00)	38 (0.16)	0.42
10-01	Gp3	g.chr20:34241079G>A	Silent	RBM12	p.N722N	RNA binding motif prot	18 (0.00)	32 (0.19)	0.50
10-01	Gp3	g.chr17:73658855C>A	Missense Mutation	RECQL5	p.A159S	RecQ protein-like 5	27 (0.00)	30 (0.17)	0.44
10-01	Gp3	g.chr6:72968794G>A	Silent	RIMS1	p.Q1011Q	regulating synaptic mem	51 (0.00)	30 (0.17)	0.44
10-01	Gp3	g.chr1:148939806T>G	lincRNA	RP11-14N7.2			19 (0.00)	22 (0.27)	0.73
10-01	Gp3	g.chr3:139128513T>A	RNA	RP11-319G6.1			28 (0.00)	18 (0.28)	0.49
10-01	Gp3	g.chr3:98030912C>T	lincRNA	RP11-325B23.2			29 (0.00)	28 (0.21)	0.57
10-01	Gp3	g.chr3:38616857G>A	Silent	SCN5A	p.Y1198Y	sodium channel, voltage	28 (0.00)	28 (0.18)	0.48
10-01	Gp3	g.chr6:25811660C>T	Missense Mutation	SLC17A1	p.G382R	solute carrier family 17	50 (0.00)	32 (0.16)	0.42
10-01	Gp3	g.chr1:153751848C>T	Silent	SLC27A3	p.L720L	solute carrier family 27	27 (0.00)	49 (0.14)	0.38
10-01	Gp3	g.chr10:73121930G>A	Silent	SLC29A3	p.E331E	solute carrier family 29	20 (0.00)	29 (0.21)	0.55
10-01	Gp3	g.chr4:20620478G>A	Missense Mutation	SLIT2	p.R1479Q	slit homolog 2 (Drosoph	24 (0.00)	41 (0.15)	0.39
10-01	Gp3	g.chr17:1715350G>A	Missense Mutation	SMYD4	p.S65L	SET and MYND domai	38 (0.00)	33 (0.18)	0.48
10-01	Gp3	g.chr8:121551190C>A	Missense Mutation	SNTB1	p.C515F	syntrophin, beta 1 (dystr	43 (0.00)	26 (0.19)	0.51
10-01	Gp3	g.chr2:228884208C>T	Silent	SPHKAP	p.Q454Q	SPHK1 interactor, AKA	18 (0.00)	21 (0.24)	0.63
10-01	Gp3	g.chr12:64502809C>G	Missense Mutation	SRGAP1	p.F637L	SLIT-ROBO Rho GTPa	30 (0.00)	37 (0.19)	0.50
10-01	Gp3	g.chr4:98633884G>A	Missense Mutation	STPG2	p.S429F	sperm-tail PG-rich repea	100 (0.00)	73 (0.15)	0.40
10-01	Gp3	g.chr13:48563103G>A	Silent	SUCLA2	p.V95V	succinate-CoA ligase, A	16 (0.00)	31 (0.16)	0.43
10-01	Gp3	g.chr1:33160499C>T	Silent	SYNC	p.R400R	syncoilin, intermediate f	65 (0.00)	64 (0.16)	0.42
10-01	Gp3	g.chr1:155838187G>A	Missense Mutation	SYT11	p.V156I	synaptotagmin XI	24 (0.00)	44 (0.16)	0.42
10-01	Gp3	g.chr9:32631119G>T	Missense Mutation	TAF1L	p.Q1487K	TAF1 RNA polymerase	27 (0.00)	24 (0.21)	0.56
10-01	Gp3	g.chr11:33087388G>A	Missense Mutation	TCP11L1	p.D329N	t-complex 11, testis-spe	38 (0.00)	40 (0.15)	0.40
10-01	Gp3	g.chr12:106712238G>A	Missense Mutation	TCP11L2	p.R137K	t-complex 11, testis-spe	40 (0.00)	30 (0.17)	0.44
10-01	Gp3	g.chr3:52257115G>T	Silent	TLR9	p.G559G	toll-like receptor 9	17 (0.00)	16 (0.44)	1.17
10-01	Gp3	g.chrX:101770040G>A	Silent	TMSB15A	p.L18L	thymosin beta 15a	53 (0.00)	25 (0.36)	0.60
10-01	Gp3	g.chr17:38652276G>T	Silent	TNS4	p.T134T	tensin 4	34 (0.00)	37 (0.22)	0.58
10-01	Gp3	g.chr5:180627015C>A	Nonsense Mutation	TRIM7	p.E229*	tripartite motif containi	16 (0.00)	22 (0.23)	0.61
10-01	Gp3	g.chr4:70359441G>A	Silent	UGT2B4	p.L280L	UDP glucuronosyltransf	43 (0.00)	38 (0.34)	0.91
10-01	Gp3	g.chr19:17722601C>T	Missense Mutation	UNC13A	p.G1541E	unc-13 homolog A (C. e	39 (0.00)	51 (0.16)	0.42
10-01	Gp3	g.chr3:14212086C>T	Intron	XPC		xeroderma pigmentosum	40 (0.00)	34 (0.15)	0.39
10-01	Gp3	g.chr10:27412584C>G	Missense Mutation	YME1L1	p.A332P	YME1-like 1 ATPase	52 (0.00)	40 (0.15)	0.40

10-01	Gp3	g.chr11:130131111G>A	Nonsense Mutation	ZBTB44	p.Q220*	zinc finger and BTB do	40 (0.00)	25 (0.20)	0.53
10-01	Gp3	g.chr19:58353193G>A	Missense Mutation	ZNF587B	p.C384Y	zinc finger protein 587B	27 (0.00)	29 (0.17)	0.46
10-01	Gp3	g.chr19:22498518T>C	Silent	ZNF729	p.L767L	zinc finger protein 729	54 (0.00)	46 (0.15)	0.41
10-01	Gp3	g.chr19:22498520G>C	Missense Mutation	ZNF729	p.L767F	zinc finger protein 729	49 (0.00)	41 (0.15)	0.39
10-01	Gp3	g.chr19:57956683C>G	Missense Mutation	ZNF749	p.P723A	zinc finger protein 749	46 (0.00)	56 (0.14)	0.38
10-01	Gp3	g.chr19:52658952C>T	Missense Mutation	ZNF836	p.G662R	zinc finger protein 836	27 (0.00)	31 (0.16)	0.43
10-01	Gp3	g.chr6:28359350G>A	Silent	ZSCAN12	p.C239C	zinc finger and SCAN d	56 (0.02)	48 (0.23)	0.61
10-01	Gp4	g.chr17:67085605C>A	Splice Site	ABCA6		ATP-binding cassette, s	43 (0.00)	23 (0.22)	0.58
10-01	Gp4	g.chr16:20486750C>G	Missense Mutation	ACSM2A	p.Q321E	acyl-CoA synthetase me	28 (0.00)	49 (0.16)	0.44
10-01	Gp4	g.chr11:72421435G>A	Silent	ARAP1	p.L471L	ArfGAP with RhoGAP	16 (0.00)	26 (0.23)	0.62
10-01	Gp4	g.chr2:23985151C>T	Missense Mutation	ATAD2B	p.V1108I	ATPase family, AAA d	72 (0.01)	48 (0.17)	0.44
10-01	Gp4	g.chr16:84495671G>A	Silent	ATP2C2	p.Q915Q	ATPase, Ca++ transport	45 (0.02)	49 (0.20)	0.39
10-01	Gp4	g.chr3:133185762G>A	Missense Mutation	BFSP2	p.V328I	beaded filament structur	43 (0.00)	35 (0.17)	0.46
10-01	Gp4	g.chr14:36334957G>A	Silent	BRMS1L	p.V239V	breast cancer metastasis	30 (0.00)	26 (0.19)	0.51
10-01	Gp4	g.chr15:76430172G>T	Missense Mutation	C15orf27	p.V55F	chromosome 15 open re	50 (0.00)	85 (0.18)	0.47
10-01	Gp4	g.chr12:22680775G>A	Missense Mutation	C2CD5	p.H77Y	C2 calcium-dependent d	32 (0.00)	21 (0.24)	0.63
10-01	Gp4	g.chr9:35679189G>A	Silent	CA9	p.E305E	carbonic anhydrase IX	31 (0.00)	50 (0.16)	0.43
10-01	Gp4	g.chr3:85392375C>T	Intron	CADM2		cell adhesion molecule	57 (0.02)	35 (0.14)	0.38
10-01	Gp4	g.chr1:200827183C>T	Missense Mutation	CAMSAP2	p.A1478V	calmodulin regulated sp	28 (0.00)	35 (0.14)	0.38
10-01	Gp4	g.chr3:39374844G>A	Missense Mutation	CCR8	p.C341Y	chemokine (C-C motif)	21 (0.00)	29 (0.24)	0.64
10-01	Gp4	g.chr14:23523425C>G	Silent	CDH24	p.L299L	cadherin 24, type 2	25 (0.00)	40 (0.20)	0.53
10-01	Gp4	g.chr15:93492293C>A	Missense Mutation	CHD2	p.H497N	chromodomain helicase	44 (0.00)	36 (0.17)	0.44
10-01	Gp4	g.chr11:99827700G>A	Missense Mutation	CNTN5	p.R279K	contactin 5	29 (0.00)	32 (0.16)	0.42
10-01	Gp4	g.chr2:219677060C>A	Silent	CYP27A1	p.R188R	cytochrome P450, famil	25 (0.00)	36 (0.17)	0.44
10-01	Gp4	g.chr9:124409624G>T	Intron	DAB2IP		DAB2 interacting protei	50 (0.00)	60 (0.17)	0.44
10-01	Gp4	g.chr11:30928254G>A	Missense Mutation	DCDC1	p.P1313S	doublecortin domain co	18 (0.00)	33 (0.15)	0.40
10-01	Gp4	g.chr5:134109534G>A	Missense Mutation	DDX46	p.S199N	DEAD (Asp-Glu-Ala-A	24 (0.00)	35 (0.14)	0.38
10-01	Gp4	g.chr11:9182280G>A	Missense Mutation	DENND5A	p.H806Y	DENN/MADD domain	19 (0.00)	32 (0.16)	0.42
10-01	Gp4	g.chr10:124376751G>A	Nonsense Mutation	DMBT1	p.W1493*	deleted in malignant bra	48 (0.00)	26 (0.19)	0.51
10-01	Gp4	g.chr1:6696274C>A	Silent	DNAJC11	p.V519V	DnaJ (Hsp40) homolog,	21 (0.00)	20 (0.25)	0.67
10-01	Gp4	g.chr3:19921235C>A	Missense Mutation	EFHB	p.W667L	EF-hand domain family,	51 (0.00)	31 (0.16)	0.43
10-01	Gp4	g.chr1:11129671T>C	Silent	EXOSC10	p.P811P	exosome component 10	57 (0.02)	49 (0.14)	0.38
10-01	Gp4	g.chr5:150897262C>A	Missense Mutation	FAT2	p.W3794C	FAT atypical cadherin 2	21 (0.00)	24 (0.21)	0.56
10-01	Gp4	g.chr5:56542276G>C	Missense Mutation	GPBP1	p.G217R	GC-rich promoter bindi	73 (0.00)	83 (0.17)	0.45
10-01	Gp4	g.chr2:203676499C>A	Missense Mutation	ICA1L	p.D294Y	islet cell autoantigen 1,	72 (0.00)	42 (0.14)	0.38

10-01	Gp4	g.chr14:107211399C>G	RNA	IGHV3-73		immunoglobulin heavy	30 (0.00)	49 (0.14)	0.38
10-01	Gp4	g.chr2:191231564G>A	Missense Mutation	INPP1	p.D137N	inositol polyphosphate-	15 (0.00)	33 (0.18)	0.48
10-01	Gp4	g.chr4:143566427G>T	Intron	INPP4B		inositol polyphosphate-	30 (0.00)	34 (0.15)	0.39
10-01	Gp4	g.chr1:196311308G>T	Missense Mutation	KCNT2	p.S485Y	potassium channel, subf	24 (0.00)	27 (0.22)	0.59
10-01	Gp4	g.chr1:44169995G>A	Missense Mutation	KDM4A	p.R1050Q	lysine (K)-specific dem	26 (0.00)	43 (0.16)	0.43
10-01	Gp4	g.chr11:93458851C>T	Missense Mutation	KIAA1731	p.T298I	KIAA1731	82 (0.00)	48 (0.17)	0.44
10-01	Gp4	g.chr4:1816171C>G	Missense Mutation	LETM1	p.V734L	leucine zipper-EF-hand	16 (0.00)	36 (0.17)	0.44
10-01	Gp4	g.chr21:45876913C>A	Missense Mutation	LRRC3	p.P129H	leucine rich repeat cont	16 (0.00)	24 (0.21)	0.56
10-01	Gp4	g.chr21:45876914C>A	Silent	LRRC3	p.P129P	leucine rich repeat cont	16 (0.00)	24 (0.21)	0.56
10-01	Gp4	g.chr7:78497872A>T	Intron	MAGI2		membrane associated g	42 (0.00)	48 (0.23)	0.61
10-01	Gp4	g.chr17:61766201G>A	Silent	MAP3K3	p.R273R	mitogen-activated prote	20 (0.00)	30 (0.20)	0.53
10-01	Gp4	g.chr7:99693416C>T	Missense Mutation	MCM7	p.D526N	minichromosome maint	36 (0.00)	35 (0.20)	0.53
10-01	Gp4	g.chr5:41051137C>A	Missense Mutation	MROH2B	p.R429L	maestro heat-like repeat	20 (0.00)	34 (0.15)	0.39
10-01	Gp4	g.chr19:9064952G>A	Silent	MUC16	p.D7498D	mucin 16, cell surface a	16 (0.00)	36 (0.17)	0.44
10-01	Gp4	g.chr17:8404250G>A	Missense Mutation	MYH10	p.A1182V	myosin, heavy chain 10,	70 (0.01)	50 (0.16)	0.43
10-01	Gp4	g.chr2:152534129C>A	Missense Mutation	NEB	p.D1242Y	nebulin	36 (0.00)	29 (0.17)	0.46
10-01	Gp4	g.chr12:80733036G>A	Missense Mutation	OTOGL	p.G1660E	otogelin-like	25 (0.00)	31 (0.29)	0.77
10-01	Gp4	g.chr12:3921397G>A	Silent	PARP11	p.S303S	poly (ADP-ribose) poly	45 (0.00)	21 (0.24)	0.49
10-01	Gp4	g.chr2:198953617C>T	Silent	PLCL1	p.L917L	phospholipase C-like 1	63 (0.02)	62 (0.16)	0.43
10-01	Gp4	g.chr9:8499758G>A	Silent	PTPRD	p.P737P	protein tyrosine phosph	65 (0.00)	46 (0.15)	0.41
10-01	Gp4	g.chr1:213434967A>G	Missense Mutation	RPS6KC1	p.E981G	ribosomal protein S6 ki	17 (0.00)	32 (0.28)	0.75
10-01	Gp4	g.chr2:166245851C>T	Silent	SCN2A	p.P1845P	sodium channel, voltage	46 (0.02)	50 (0.16)	0.43
10-01	Gp4	g.chr3:72828045C>G	Intron	SHQ1		SHQ1, H/ACA ribonucl	113 (0.00)	105 (0.27)	0.71
10-01	Gp4	g.chr14:21469391C>T	Missense Mutation	SLC39A2	p.L195F	solute carrier family 39	27 (0.00)	24 (0.25)	0.67
10-01	Gp4	g.chr2:92092832T>A	RNA	SLC9B1P2		solute carrier family 9,	23 (0.00)	16 (0.31)	0.83
10-01	Gp4	g.chr6:170871052G>A	Silent	TBP	p.Q76Q	TATA box binding prot	15 (0.00)	26 (0.31)	0.82
10-01	Gp4	g.chr4:83839228G>A	Silent	THAP9	p.Q621Q	THAP domain containi	43 (0.00)	44 (0.16)	0.42
10-01	Gp4	g.chr15:63089448G>A	Silent	TLN2	p.L2027L	talin 2	47 (0.00)	34 (0.15)	0.39
10-01	Gp4	g.chr12:94976260C>T	Missense Mutation	TMCC3	p.G45R	transmembrane and coil	23 (0.00)	31 (0.16)	0.43
10-01	Gp4	g.chr11:57077146G>A	Silent	TNKS1BP1	p.S1013S	tankyrase 1 binding pro	16 (0.00)	34 (0.15)	0.39
10-01	Gp4	g.chr7:138252255G>A	Silent	TRIM24	p.Q520Q	tripartite motif containi	44 (0.00)	31 (0.16)	0.43
10-01	Gp4	g.chr3:142731145G>T	Nonsense Mutation	U2SURP	p.E58*	U2 snRNP-associated S	36 (0.00)	30 (0.20)	0.53
10-01	Gp4	g.chr2:234545421G>A	Missense Mutation	UGT1A10	p.D85N	UDP glucuronosyltrans	27 (0.00)	29 (0.17)	0.46
10-01	Gp4	g.chr8:35608225C>T	Silent	UNC5D	p.A618A	unc-5 homolog D (C. el	29 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr10:52569802G>A	Splice Site	A1CF	p.I495I	APOBEC1 complement	61 (0.00)	28 (0.18)	0.48

11-01	Gp3	g.chr12:9229495G>A	Missense Mutation	A2M	p.S1130L	alpha-2-macroglobulin	67 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr12:9002786C>T	Missense Mutation	A2ML1	p.S717L	alpha-2-macroglobulin-l	95 (0.01)	93 (0.30)	0.80
11-01	Gp3	g.chr12:9013893G>A	Splice Site	A2ML1	p.G1168R	alpha-2-macroglobulin-l	43 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr3:151474835C>A	Missense Mutation	AADACL2	p.P220H	arylacetamide deacetyla	22 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr1:12779548G>T	Silent	AADACL3	p.P23P	arylacetamide deacetyla	86 (0.00)	86 (0.15)	0.40
11-01	Gp3	g.chr8:117954909G>T	Missense Mutation	AARD	p.S146I	alanine and arginine ric	18 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr17:41102732G>C	Missense Mutation	AARSD1	p.L373V	alanyl-tRNA synthetase	15 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr7:121721622C>A	Missense Mutation	AASS	p.V738L	aminoadipate-semialdeh	44 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr9:107584912C>T	Missense Mutation	ABCA1	p.G898D	ATP-binding cassette, s	21 (0.00)	35 (0.86)	2.29
11-01	Gp3	g.chr9:107591368C>T	Nonsense Mutation	ABCA1	p.W648*	ATP-binding cassette, s	38 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr9:107593207T>C	Splice Site	ABCA1	p.I631V	ATP-binding cassette, s	96 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr17:67150020G>T	Missense Mutation	ABCA10	p.A1306E	ATP-binding cassette, s	103 (0.00)	73 (0.18)	0.47
11-01	Gp3	g.chr7:48314706G>A	Missense Mutation	ABCA13	p.A1815T	ATP-binding cassette, s	64 (0.00)	41 (0.29)	0.78
11-01	Gp3	g.chr7:48391861C>T	Missense Mutation	ABCA13	p.R3489W	ATP-binding cassette, s	35 (0.00)	28 (0.43)	1.14
11-01	Gp3	g.chr7:48431615G>A	Missense Mutation	ABCA13	p.G3918S	ATP-binding cassette, s	50 (0.00)	53 (0.25)	0.65
11-01	Gp3	g.chr1:94473189C>T	Splice Site	ABCA4		ATP-binding cassette, s	56 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr1:94514499C>T	Missense Mutation	ABCA4	p.E890K	ATP-binding cassette, s	32 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr1:94526129C>G	Missense Mutation	ABCA4	p.M708I	ATP-binding cassette, s	49 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr1:94526275C>T	Missense Mutation	ABCA4	p.V660M	ATP-binding cassette, s	20 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr17:67012498G>C	Missense Mutation	ABCA9	p.R979G	ATP-binding cassette, s	36 (0.00)	34 (0.26)	0.71
11-01	Gp3	g.chr2:169788957G>C	Missense Mutation	ABCB11	p.A1048G	ATP-binding cassette, s	127 (0.00)	82 (0.33)	0.88
11-01	Gp3	g.chr2:169824975C>A	Silent	ABCB11	p.A679A	ATP-binding cassette, s	101 (0.01)	56 (0.20)	0.52
11-01	Gp3	g.chr2:169836388C>A	Missense Mutation	ABCB11	p.E395D	ATP-binding cassette, s	50 (0.00)	30 (0.37)	0.98
11-01	Gp3	g.chr7:87038599C>T	Missense Mutation	ABCB4	p.E1012K	ATP-binding cassette, s	82 (0.00)	53 (0.21)	0.55
11-01	Gp3	g.chr7:87049342G>A	Missense Mutation	ABCB4	p.S789L	ATP-binding cassette, s	64 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr16:16205319G>A	Missense Mutation	ABCC1	p.V987M	ATP-binding cassette, s	29 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr16:48227838C>T	Silent	ABCC11	p.T820T	ATP-binding cassette, s	69 (0.00)	56 (0.25)	0.67
11-01	Gp3	g.chr10:101560189G>A	Missense Mutation	ABCC2	p.G360R	ATP-binding cassette, s	180 (0.01)	84 (0.30)	0.79
11-01	Gp3	g.chr10:101571347C>A	Missense Mutation	ABCC2	p.A652D	ATP-binding cassette, s	35 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr13:95714961A>C	Silent	ABCC4	p.P1121P	ATP-binding cassette, s	71 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr12:40012847G>C	Missense Mutation	ABCD2	p.Q191E	ATP-binding cassette, s	34 (0.00)	33 (0.48)	1.29
11-01	Gp3	g.chr12:40013182C>T	Missense Mutation	ABCD2	p.G79E	ATP-binding cassette, s	41 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr1:94980739C>T	Missense Mutation	ABCD3	p.S628F	ATP-binding cassette, s	47 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr14:74766260C>T	Silent	ABCD4	p.L92L	ATP-binding cassette, s	107 (0.00)	109 (0.23)	0.61
11-01	Gp3	g.chr21:43646003G>A	Missense Mutation	ABCG1	p.G89R	ATP-binding cassette, s	51 (0.00)	40 (0.35)	0.93

11-01	Gp3	g.chr2:44051449C>G	Missense Mutation	ABCG5	p.E172Q	ATP-binding cassette, s	36 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr3:100489651G>T	Silent	ABI3BP	p.T848T	ABI family, member 3 (	63 (0.00)	59 (0.24)	0.63
11-01	Gp3	g.chr9:133729574C>T	Missense Mutation	ABL1	p.A68V	ABL proto-oncogene 1,	81 (0.00)	42 (0.52)	1.40
11-01	Gp3	g.chr9:133748254C>T	Silent	ABL1	p.C305C	ABL proto-oncogene 1,	26 (0.00)	44 (0.45)	1.21
11-01	Gp3	g.chr5:148617026G>T	Nonsense Mutation	ABLIM3	p.E302*	actin binding LIM prote	59 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr17:995070G>A	Silent	ABR	p.A122A	active BCR-related	22 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr3:127395393C>T	Silent	ABTB1	p.A165A	ankyrin repeat and BTB	37 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr16:20843514C>T	Nonsense Mutation	AC004381.6	p.Q399*		52 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr16:20856404G>A	Silent	AC004381.6	p.Q655Q		58 (0.02)	38 (0.18)	0.49
11-01	Gp3	g.chr17:28903207G>T	RNA	AC006050.2			18 (0.00)	12 (0.67)	1.78
11-01	Gp3	g.chr2:58688722C>A	lincRNA	AC007092.1			57 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr7:131626093G>T	lincRNA	AC009518.4			47 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr2:130792397C>A	RNA	AC018865.8			39 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr17:20418790C>A	RNA	AC025627.9			31 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr17:37778528G>A	lincRNA	AC087491.2			28 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr17:20628258G>A	RNA	AC126365.1			30 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr12:73184273C>T	RNA	AC131213.1			79 (0.00)	33 (0.30)	0.81
11-01	Gp3	g.chr3:38168065G>T	Missense Mutation	ACAA1	p.S251R	acetyl-CoA acyltransfer	59 (0.00)	71 (0.15)	0.41
11-01	Gp3	g.chr3:38168079C>T	Missense Mutation	ACAA1	p.G247S	acetyl-CoA acyltransfer	68 (0.00)	66 (0.20)	0.53
11-01	Gp3	g.chr17:35549152G>T	Missense Mutation	ACACA	p.P1395Q	acetyl-CoA carboxylase	71 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr17:35634885C>G	Missense Mutation	ACACA	p.M171I	acetyl-CoA carboxylase	27 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr12:109577473G>C	Missense Mutation	ACACB	p.R88P	acetyl-CoA carboxylase	22 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr12:109625961C>G	Missense Mutation	ACACB	p.A713G	acetyl-CoA carboxylase	20 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr12:109685423C>T	Silent	ACACB	p.L1862L	acetyl-CoA carboxylase	28 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr12:112130610C>T	Nonsense Mutation	ACAD10	p.R33*	acyl-CoA dehydrogenas	52 (0.00)	42 (0.21)	0.57
11-01	Gp3	g.chr3:128622975G>A	Splice Site	ACAD9	p.Q343Q	acyl-CoA dehydrogenas	42 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr11:108018112C>T	Silent	ACAT1	p.L427L	acetyl-CoA acetyltransf	108 (0.00)	81 (0.21)	0.56
11-01	Gp3	g.chr1:226340079G>A	Silent	ACBD3	p.S444S	acyl-CoA binding doma	45 (0.00)	51 (0.29)	0.78
11-01	Gp3	g.chr11:44098890C>A	Silent	ACCS	p.G206G	1-aminocyclopropane-1	15 (0.00)	24 (0.67)	1.78
11-01	Gp3	g.chr7:100490940C>T	Missense Mutation	ACHE	p.R305Q	acetylcholinesterase (Yt	21 (0.00)	30 (0.40)	1.07
11-01	Gp3	g.chr14:23550970G>T	Missense Mutation	ACIN1	p.S229Y	apoptotic chromatin con	27 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr15:78485903C>T	Missense Mutation	ACSBG1	p.C203Y	acyl-CoA synthetase bu	53 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr5:131290040C>G	Missense Mutation	ACSL6	p.D661H	acyl-CoA synthetase lo	17 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr16:20563477C>G	Missense Mutation	ACSM2B	p.V295L	acyl-CoA synthetase m	68 (0.00)	31 (0.42)	1.12
11-01	Gp3	g.chr12:81647289A>G	Missense Mutation	ACSS3	p.E612G	acyl-CoA synthetase sh	93 (0.00)	51 (0.18)	0.47

11-01	Gp3	g.chr12:81647302G>A	Silent	ACSS3	p.L616L	acyl-CoA synthetase sh	95 (0.00)	57 (0.28)	0.75
11-01	Gp3	g.chr1:229567370C>A	Missense Mutation	ACTA1	p.R337L	actin, alpha 1, skeletal	42 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr9:111625115C>A	Missense Mutation	ACTL7A	p.D171E	actin-like 7A	36 (0.00)	43 (0.28)	0.74
11-01	Gp3	g.chr2:158397621G>A	Silent	ACVR1C	p.A402A	activin A receptor, type	59 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr12:52309079G>C	Missense Mutation	ACVRL1	p.E107D	activin A receptor type	28 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr15:43641242G>T	Splice Site	ADAL	p.L257L	adenosine deaminase-lik	75 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr15:58889803C>T	Silent	ADAM10	p.Q730Q	ADAM metallopeptidas	43 (0.00)	28 (0.57)	1.52
11-01	Gp3	g.chr2:207437900G>A	Missense Mutation	ADAM23	p.C573Y	ADAM metallopeptidas	64 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr4:175897208G>T	Nonsense Mutation	ADAM29	p.E178*	ADAM metallopeptidas	40 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr1:120437752C>T	Missense Mutation	ADAM30	p.G403E	ADAM metallopeptidas	50 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr21:28209987C>G	Missense Mutation	ADAMTS1	p.D939H	ADAM metallopeptidas	36 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr21:28212679C>A	Silent	ADAMTS1	p.P527P	ADAM metallopeptidas	71 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr19:8651471C>A	Nonsense Mutation	ADAMTS10	p.G792*	ADAM metallopeptidas	31 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr5:33561165G>A	Silent	ADAMTS12	p.P1364P	ADAM metallopeptidas	24 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr5:33576274G>A	Missense Mutation	ADAMTS12	p.T1286I	ADAM metallopeptidas	108 (0.00)	34 (0.32)	0.86
11-01	Gp3	g.chr9:136305526C>A	Silent	ADAMTS13	p.T616T	ADAM metallopeptidas	45 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr5:5182189C>T	Silent	ADAMTS16	p.Y178Y	ADAM metallopeptidas	122 (0.00)	60 (0.33)	0.89
11-01	Gp3	g.chr15:100871145T>A	Missense Mutation	ADAMTS17	p.S189C	ADAM metallopeptidas	51 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr5:178541139G>T	Missense Mutation	ADAMTS2	p.T1122N	ADAM metallopeptidas	63 (0.00)	29 (0.38)	1.01
11-01	Gp3	g.chr12:43792951C>A	Missense Mutation	ADAMTS20	p.C1457F	ADAM metallopeptidas	131 (0.00)	112 (0.17)	0.45
11-01	Gp3	g.chr12:43793021C>A	Missense Mutation	ADAMTS20	p.G1434C	ADAM metallopeptidas	50 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr21:28327142C>G	Missense Mutation	ADAMTS5	p.G385R	ADAM metallopeptidas	19 (0.00)	13 (0.62)	1.64
11-01	Gp3	g.chr3:64601011C>A	Nonsense Mutation	ADAMTS9	p.G1059*	ADAM metallopeptidas	117 (0.00)	69 (0.55)	1.47
11-01	Gp3	g.chr9:18906904G>T	Nonsense Mutation	ADAMTSL1	p.E1726*	ADAMTS-like 1	68 (0.00)	26 (0.58)	0.91
11-01	Gp3	g.chr15:84659967G>A	Splice Site	ADAMTSL3		ADAMTS-like 3	61 (0.00)	42 (0.48)	1.27
11-01	Gp3	g.chr7:944753G>C	Missense Mutation	ADAP1	p.R149G	ArfGAP with dual PH d	26 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr21:46596513G>A	Silent	ADARB1	p.L299L	adenosine deaminase, R	41 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr14:24788334G>A	Missense Mutation	ADCY4	p.H976Y	adenylate cyclase 4	138 (0.00)	74 (0.18)	0.47
11-01	Gp3	g.chr16:4165059G>A	Silent	ADCY9	p.L129L	adenylate cyclase 9	21 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr7:31132320C>T	Silent	ADCYAP1R1	p.D339D	adenylate cyclase activa	66 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr6:147045434C>A	Silent	ADGB	p.T736T	androglobin	102 (0.00)	65 (0.29)	0.78
11-01	Gp3	g.chr6:147045438G>A	Missense Mutation	ADGB	p.A738T	androglobin	102 (0.00)	65 (0.34)	0.90
11-01	Gp3	g.chr4:100232714G>A	Silent	ADH1B	p.L310L	alcohol dehydrogenase	79 (0.00)	123 (0.17)	0.46
11-01	Gp3	g.chr8:67357642G>A	Silent	ADHFE1	p.L181L	alcohol dehydrogenase,	58 (0.00)	55 (0.20)	0.67
11-01	Gp3	g.chr20:49511043G>A	Missense Mutation	ADNP	p.R70W	activity-dependent neur	30 (0.00)	20 (0.50)	1.33

11-01	Gp3	g.chr15:73044897G>C	Missense Mutation	ADPGK	p.L426V	ADP-dependent glucoki	143 (0.00)	64 (0.16)	0.42
11-01	Gp3	g.chr13:114107713C>T	Missense Mutation	ADPRHL1	p.G14S	ADP-ribosylhydrolase l	67 (0.00)	110 (0.16)	0.44
11-01	Gp3	g.chr8:26722006G>A	Missense Mutation	ADRA1A	p.P161S	adrenoceptor alpha 1A	31 (0.00)	19 (0.32)	0.47
11-01	Gp3	g.chr22:26081173C>G	Missense Mutation	ADRBK2	p.H262D	adrenergic, beta, recepto	16 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr22:26105884C>T	Missense Mutation	ADRBK2	p.H450Y	adrenergic, beta, recepto	84 (0.00)	38 (0.32)	0.84
11-01	Gp3	g.chr5:148691697C>A	Missense Mutation	AFAP1L1	p.P317Q	actin filament associate	27 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr4:74308145G>A	Splice Site	AFP	p.K205K	alpha-fetoprotein	60 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr2:236792067G>A	Missense Mutation	AGAP1	p.V377M	ArfGAP with GTPase d	99 (0.00)	80 (0.19)	0.50
11-01	Gp3	g.chr2:236817491G>T	Missense Mutation	AGAP1	p.S422I	ArfGAP with GTPase d	36 (0.00)	25 (0.40)	1.07
11-01	Gp3	g.chr15:86814893C>A	Silent	AGBL1	p.G631G	ATP/GTP binding prote	32 (0.00)	24 (0.67)	1.78
11-01	Gp3	g.chr1:100336046G>T	Missense Mutation	AGL	p.R252I	amylo-alpha-1, 6-glucos	79 (0.00)	65 (0.17)	0.45
11-01	Gp3	g.chr1:36437779G>T	Missense Mutation	AGO3	p.S156I	argonaute RISC catalyti	41 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr1:36439108C>T	Silent	AGO3	p.I218I	argonaute RISC catalyti	82 (0.01)	53 (0.17)	0.45
11-01	Gp3	g.chr1:36288544C>A	Missense Mutation	AGO4	p.N89K	argonaute RISC catalyti	44 (0.00)	67 (0.34)	0.92
11-01	Gp3	g.chr2:178402887C>T	Silent	AGPS	p.D647D	alkylglycerone phospha	133 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr1:247006031T>A	Missense Mutation	AHCTF1	p.K2226N	AT hook containing tra	34 (0.00)	22 (0.82)	1.72
11-01	Gp3	g.chr1:247070986G>A	Silent	AHCTF1	p.L246L	AT hook containing tra	76 (0.00)	63 (0.21)	0.43
11-01	Gp3	g.chr6:135639750C>G	Silent	AHI1	p.L1111L	Abelson helper integrati	46 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr11:62290902C>A	Nonsense Mutation	AHNAK	p.E3663*	AHNAK nucleoprotein	45 (0.00)	36 (0.58)	1.56
11-01	Gp3	g.chr11:62293939G>C	Silent	AHNAK	p.G2650G	AHNAK nucleoprotein	27 (0.00)	22 (0.64)	1.70
11-01	Gp3	g.chr11:62294344C>T	Missense Mutation	AHNAK	p.M2515I	AHNAK nucleoprotein	60 (0.00)	62 (0.27)	0.73
11-01	Gp3	g.chr11:62295229G>T	Silent	AHNAK	p.I2220I	AHNAK nucleoprotein	49 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr11:62296129G>T	Silent	AHNAK	p.P1920P	AHNAK nucleoprotein	79 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr11:62297875C>T	Silent	AHNAK	p.K1338K	AHNAK nucleoprotein	52 (0.00)	39 (0.41)	1.09
11-01	Gp3	g.chr14:105406005C>G	Missense Mutation	AHNAK2	p.E259D	AHNAK nucleoprotein	99 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr16:31539826G>A	Silent	AHSP	p.V41V	alpha hemoglobin stabil	50 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr6:143457981G>A	Missense Mutation	AIG1	p.A51T	androgen-induced 1	102 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr6:107016364C>A	Missense Mutation	AIM1	p.Q1699K	absent in melanoma 1	69 (0.00)	65 (0.35)	0.55
11-01	Gp3	g.chr1:33480137G>T	Missense Mutation	AK2	p.P162T	adenylate kinase 2	82 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr6:109965836G>A	Missense Mutation	AK9	p.P272L	adenylate kinase 9	73 (0.00)	23 (0.61)	0.94
11-01	Gp3	g.chr13:42875157G>T	Nonsense Mutation	AKAP11	p.E759*	A kinase (PRKA) ancho	106 (0.00)	45 (0.20)	0.53
11-01	Gp3	g.chr13:42877060C>A	Nonsense Mutation	AKAP11	p.S1393*	A kinase (PRKA) ancho	29 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr6:151671437G>A	Silent	AKAP12	p.K637K	A kinase (PRKA) ancho	62 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr6:151674176C>A	Silent	AKAP12	p.V1550V	A kinase (PRKA) ancho	55 (0.00)	43 (0.33)	0.87
11-01	Gp3	g.chr14:33242896G>A	Missense Mutation	AKAP6	p.E1129K	A kinase (PRKA) ancho	61 (0.00)	66 (0.61)	1.62

11-01	Gp3	g.chr14:33242955G>A	Silent	AKAP6	p.L1148L	A kinase (PRKA) ancho	77 (0.00)	69 (0.51)	1.35
11-01	Gp3	g.chr14:33293299G>C	Missense Mutation	AKAP6	p.V2094L	A kinase (PRKA) ancho	56 (0.02)	40 (0.20)	0.53
11-01	Gp3	g.chr7:91630770G>A	Silent	AKAP9	p.K513K	A kinase (PRKA) ancho	75 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr7:91631002G>A	Missense Mutation	AKAP9	p.A591T	A kinase (PRKA) ancho	57 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr7:91714132G>A	Splice Site	AKAP9		A kinase (PRKA) ancho	89 (0.01)	56 (0.14)	0.38
11-01	Gp3	g.chr7:91724416C>T	Missense Mutation	AKAP9	p.L3220F	A kinase (PRKA) ancho	80 (0.00)	121 (0.19)	0.51
11-01	Gp3	g.chr7:134134482T>C	Missense Mutation	AKR1B1	p.D140G	aldo-keto reductase fam	88 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr1:243736254C>G	Missense Mutation	AKT3	p.G265R	v-akt murine thymoma	54 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr10:82012803C>A	Silent	AL359195.1	p.T107T		53 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr10:97402833G>A	Silent	ALDH18A1	p.I73I	aldehyde dehydrogenas	48 (0.02)	24 (0.25)	0.67
11-01	Gp3	g.chr9:75520921G>A	Silent	ALDH1A1	p.A462A	aldehyde dehydrogenas	26 (0.00)	26 (0.35)	1.13
11-01	Gp3	g.chr14:74538138T>C	Missense Mutation	ALDH6A1	p.T164A	aldehyde dehydrogenas	35 (0.00)	31 (0.45)	1.20
11-01	Gp3	g.chr5:125912859C>T	Missense Mutation	ALDH7A1	p.V188I	aldehyde dehydrogenas	22 (0.00)	21 (0.38)	1.02
11-01	Gp3	g.chr1:165638613C>A	Missense Mutation	ALDH9A1	p.Q335H	aldehyde dehydrogenas	15 (0.00)	24 (0.46)	1.22
11-01	Gp3	g.chr1:95448682C>A	Missense Mutation	ALG14	p.A201S	ALG14, UDP-N-acetyl	111 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr3:183963328G>A	Silent	ALG3	p.A84A	ALG3, alpha-1,3- mann	65 (0.02)	28 (0.36)	0.95
11-01	Gp3	g.chr14:78140431C>T	Silent	ALKBH1	p.G298G	alkB, alkylation repair h	21 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr11:43941526C>T	Missense Mutation	ALKBH3	p.T276I	alkB, alkylation repair h	81 (0.00)	65 (0.29)	0.78
11-01	Gp3	g.chr7:102100144G>A	Silent	ALKBH4	p.I76I	alkB, alkylation repair h	16 (0.00)	20 (0.55)	1.47
11-01	Gp3	g.chr2:73677141C>T	Missense Mutation	ALMS1	p.H1162Y	Alstrom syndrome 1	152 (0.00)	41 (0.37)	0.55
11-01	Gp3	g.chr4:113351967C>G	Missense Mutation	ALPK1	p.Q422E	alpha-kinase 1	58 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr18:56246073C>G	Missense Mutation	ALPK2	p.Q645H	alpha-kinase 2	93 (0.00)	56 (0.55)	1.48
11-01	Gp3	g.chr12:85677437C>T	Missense Mutation	ALX1	p.S105F	ALX homeobox 1	107 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chrX:63413023G>T	Silent	AMER1	p.G48G	APC membrane recruit	40 (0.00)	57 (0.39)	0.64
11-01	Gp3	g.chr11:118081424C>A	Nonsense Mutation	AMICA1	p.E68*	adhesion molecule, inte	65 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr11:94592721C>T	Missense Mutation	AMOTL1	p.P659L	angiomotin like 1	55 (0.02)	15 (0.53)	1.42
11-01	Gp3	g.chr7:38457528G>A	Missense Mutation	AMPH	p.P432L	amphiphysin	43 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr4:145916696C>G	Missense Mutation	ANAPC10	p.K129N	anaphase promoting co	48 (0.00)	42 (0.57)	1.52
11-01	Gp3	g.chr8:108334166C>G	Missense Mutation	ANGPT1	p.D56H	angiopoietin 1	25 (0.00)	49 (0.20)	0.54
11-01	Gp3	g.chr4:114275778G>C	Missense Mutation	ANK2	p.D1969H	ankyrin 2, neuronal	31 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr4:114276620C>A	Silent	ANK2	p.T2249T	ankyrin 2, neuronal	53 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr10:61830227C>A	Missense Mutation	ANK3	p.G3471V	ankyrin 3, node of Ranv	18 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr10:61846574G>A	Silent	ANK3	p.V1203V	ankyrin 3, node of Ranv	19 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr17:54535258G>T	Missense Mutation	ANKFN1	p.R495M	ankyrin-repeat and fibro	72 (0.00)	51 (0.20)	0.52
11-01	Gp3	g.chr17:4077203C>A	Splice Site	ANKFY1		ankyrin repeat and FYV	37 (0.00)	16 (0.38)	1.00

11-01	Gp3	g.chr17:4087205G>A	Splice Site	ANKFY1	p.A567V	ankyrin repeat and FYV	44 (0.00)	32 (0.47)	1.25
11-01	Gp3	g.chr5:14758622C>T	Silent	ANKH	p.L133L	ANKH inorganic pyrop	22 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr5:139819747G>A	Missense Mutation	ANKHD1	p.V221I	ankyrin repeat and KH	37 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr7:91957144G>A	Missense Mutation	ANKIB1	p.M239I	ankyrin repeat and IBR	83 (0.01)	22 (0.41)	1.09
11-01	Gp3	g.chr2:241420505G>A	Silent	ANKMY1	p.F778F	ankyrin repeat and MY	43 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr13:111532342C>A	Missense Mutation	ANKRD10	p.C302F	ankyrin repeat domain 1	33 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr4:73944582C>T	Silent	ANKRD17	p.S2395S	ankyrin repeat domain 1	38 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr4:73957712G>A	Missense Mutation	ANKRD17	p.P1878L	ankyrin repeat domain 1	134 (0.00)	82 (0.20)	0.52
11-01	Gp3	g.chr9:33548461G>A	Missense Mutation	ANKRD18B	p.G497S	ankyrin repeat domain 1	191 (0.00)	90 (0.31)	0.83
11-01	Gp3	g.chr9:95649967C>A	RNA	ANKRD19P		ankyrin repeat domain 1	79 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr2:95522916G>A	RNA	ANKRD20A8P		ankyrin repeat domain 2	19 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr10:27366395C>A	Nonsense Mutation	ANKRD26	p.E317*	ankyrin repeat domain 2	53 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr3:15762574C>T	Missense Mutation	ANKRD28	p.D252N	ankyrin repeat domain 2	76 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr10:37422914G>A	Missense Mutation	ANKRD30A	p.D174N	ankyrin repeat domain 3	62 (0.02)	41 (0.61)	1.63
11-01	Gp3	g.chr10:37430847G>T	Missense Mutation	ANKRD30A	p.C285F	ankyrin repeat domain 3	37 (0.00)	27 (0.56)	1.48
11-01	Gp3	g.chr10:37505182C>T	Silent	ANKRD30A	p.H925H	ankyrin repeat domain 3	52 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr18:14752910G>A	Missense Mutation	ANKRD30B	p.V137M	ankyrin repeat domain 3	85 (0.01)	65 (0.32)	0.86
11-01	Gp3	g.chr2:96652614G>T	Missense Mutation	ANKRD36C	p.P124Q	ankyrin repeat domain 3	176 (0.01)	111 (0.19)	0.50
11-01	Gp3	g.chr7:6075998A>T	Missense Mutation	ANKRD61	p.D413V	ankyrin repeat domain 6	36 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr7:36435884G>A	Missense Mutation	ANLN	p.E10K	anillin, actin binding pr	46 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr7:36492185C>T	Silent	ANLN	p.C1117C	anillin, actin binding pr	82 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr12:101381422C>T	Silent	ANO4	p.A201A	anoctamin 4	99 (0.00)	112 (0.13)	0.46
11-01	Gp3	g.chr12:101491636G>C	Missense Mutation	ANO4	p.S605T	anoctamin 4	61 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr2:242138766C>A	Nonsense Mutation	ANO7	p.Y169*	anoctamin 7	33 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr19:17442144C>A	Missense Mutation	ANO8	p.M221I	anoctamin 8	28 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr17:41001368G>A	Silent	AOC2	p.E618E	amine oxidase, copper	42 (0.00)	37 (0.57)	1.51
11-01	Gp3	g.chr21:33954568C>G	Missense Mutation	AP000275.65	p.W275S		48 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr22:23825318G>A	lincRNA	AP000345.1			119 (0.00)	65 (0.46)	1.23
11-01	Gp3	g.chr11:71117522C>T	RNA	AP002387.1			40 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr18:15325744G>A	RNA	AP005901.1			73 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr22:29735047G>T	Missense Mutation	AP1B1	p.L692M	adaptor-related protein	87 (0.00)	44 (0.30)	0.47
11-01	Gp3	g.chr16:71768576C>G	Missense Mutation	AP1G1	p.S768T	adaptor-related protein	77 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr11:1006572C>A	Missense Mutation	AP2A2	p.L751I	adaptor-related protein	26 (0.00)	56 (0.20)	0.52
11-01	Gp3	g.chr11:970298C>T	Missense Mutation	AP2A2	p.T89M	adaptor-related protein	64 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr5:77334982C>T	Silent	AP3B1	p.K849K	adaptor-related protein	59 (0.00)	32 (0.25)	0.67

11-01	Gp3	g.chr15:83345228C>T	Silent	AP3B2	p.L518L	adaptor-related protein	93 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr14:31535496G>A	Missense Mutation	AP4S1	p.E32K	adaptor-related protein	93 (0.00)	89 (0.16)	0.42
11-01	Gp3	g.chr12:99056471C>G	Missense Mutation	APAF1	p.P281R	apoptotic peptidase acti	50 (0.00)	28 (0.18)	0.61
11-01	Gp3	g.chr9:72071282G>A	Silent	APBA1	p.L557L	amyloid beta (A4) precu	156 (0.01)	82 (0.15)	0.39
11-01	Gp3	g.chr18:10471917C>A	Silent	APCDD1	p.L211L	adenomatosis polyposis	74 (0.00)	101 (0.18)	0.48
11-01	Gp3	g.chr11:43345013C>T	Silent	API5	p.L193L	apoptosis inhibitor 5	58 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr11:43363986G>A	Missense Mutation	API5	p.R499K	apoptosis inhibitor 5	75 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr2:68729963C>T	Missense Mutation	APLF	p.S90F	aprataxin and PNKP lik	64 (0.00)	63 (0.19)	0.51
11-01	Gp3	g.chr19:36369506G>A	Missense Mutation	APLP1	p.A534T	amyloid beta (A4) precu	64 (0.00)	41 (0.32)	0.85
11-01	Gp3	g.chr20:24944611G>A	Silent	APMAP	p.L363L	adipocyte plasma memb	40 (0.00)	28 (0.57)	1.52
11-01	Gp3	g.chr2:21231247G>T	Silent	APOB	p.S2831S	apolipoprotein B	56 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr2:21252572G>A	Missense Mutation	APOB	p.P519L	apolipoprotein B	48 (0.00)	54 (0.35)	0.94
11-01	Gp3	g.chr2:21260832G>A	Silent	APOB	p.L179L	apolipoprotein B	64 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr22:36661852C>G	Missense Mutation	APOL1	p.P324A	apolipoprotein L, 1	58 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr5:115339048C>A	Missense Mutation	AQPEP	p.L670I		23 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr15:35210465C>A	Nonsense Mutation	AQR	p.G446*	aquarius intron-binding	15 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr11:72412808T>A	Missense Mutation	ARAP1	p.M730L	ArfGAP with RhoGAP	30 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr14:75136830C>T	Splice Site	AREL1		apoptosis resistant E3 ul	42 (0.00)	39 (0.28)	0.75
11-01	Gp3	g.chr20:61907886G>A	Missense Mutation	ARFGAP1	p.M75I	ADP-ribosylation factor	30 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr10:32150363C>A	Missense Mutation	ARHGAP12	p.S303I	Rho GTPase activating	34 (0.00)	34 (0.38)	1.02
11-01	Gp3	g.chr2:144525682C>A	Missense Mutation	ARHGAP15	p.Q457K	Rho GTPase activating	91 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr16:24964266G>A	Missense Mutation	ARHGAP17	p.P317L	Rho GTPase activating	54 (0.00)	73 (0.37)	0.99
11-01	Gp3	g.chr10:99019270C>A	Silent	ARHGAP19	p.L243L	Rho GTPase activating	27 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr10:24873973G>A	Missense Mutation	ARHGAP21	p.P1749S	Rho GTPase activating	32 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr10:24874007C>G	Missense Mutation	ARHGAP21	p.M1737I	Rho GTPase activating	49 (0.00)	41 (0.24)	0.65
11-01	Gp3	g.chr10:24886925G>C	Missense Mutation	ARHGAP21	p.T1049S	Rho GTPase activating	40 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr10:24908879G>T	Missense Mutation	ARHGAP21	p.Q649K	Rho GTPase activating	58 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr10:49654506C>G	Missense Mutation	ARHGAP22	p.R681S	Rho GTPase activating	88 (0.00)	80 (0.16)	0.43
11-01	Gp3	g.chr10:49667812C>T	Missense Mutation	ARHGAP22	p.G198R	Rho GTPase activating	50 (0.00)	41 (0.39)	1.04
11-01	Gp3	g.chr2:69049732G>A	Missense Mutation	ARHGAP25	p.M447I	Rho GTPase activating	16 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr11:128855912G>A	Silent	ARHGAP32	p.P141P	Rho GTPase activating	20 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr19:47424258G>C	Missense Mutation	ARHGAP35	p.D776H	Rho GTPase activating	104 (0.00)	52 (0.52)	1.38
11-01	Gp3	g.chr12:15097764C>A	Missense Mutation	ARHGDIB	p.D118Y	Rho GDP dissociation i	48 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr8:1905221C>T	Missense Mutation	ARHGEF10	p.S1276L	Rho guanine nucleotide	27 (0.00)	20 (0.50)	0.75
11-01	Gp3	g.chr1:156906608C>A	Splice Site	ARHGEF11	p.G1544C	Rho guanine nucleotide	37 (0.00)	27 (0.33)	0.89

11-01	Gp3	g.chr11:120348002C>T	Missense Mutation	ARHGEF12	p.S1147L	Rho guanine nucleotide	37 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr3:153870716C>A	Missense Mutation	ARHGEF26	p.S494R	Rho guanine nucleotide	65 (0.00)	45 (0.33)	0.89
11-01	Gp3	g.chr3:56779401G>A	Silent	ARHGEF3	p.V205V	Rho guanine nucleotide	77 (0.01)	64 (0.62)	1.67
11-01	Gp3	g.chr3:56785099G>A	Silent	ARHGEF3	p.P170P	Rho guanine nucleotide	86 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr2:39193149G>A	Silent	ARHGEF33	p.E782E	Rho guanine nucleotide	31 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr13:111938533C>A	Missense Mutation	ARHGEF7	p.P507T	Rho guanine nucleotide	89 (0.01)	39 (0.21)	0.55
11-01	Gp3	g.chr1:27087965G>C	Splice Site	ARID1A		AT rich interactive dom	82 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr1:27107137G>A	Missense Mutation	ARID1A	p.E2033K	AT rich interactive dom	48 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr6:157405822C>T	Silent	ARID1B	p.L688L	AT rich interactive dom	44 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr14:58838653G>A	Missense Mutation	ARID4A	p.M1240I	AT rich interactive dom	32 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr10:63810695G>A	Missense Mutation	ARID5B	p.R261K	AT rich interactive dom	102 (0.00)	56 (0.30)	0.81
11-01	Gp3	g.chr10:63845477G>A	Missense Mutation	ARID5B	p.E406K	AT rich interactive dom	53 (0.00)	35 (0.43)	1.14
11-01	Gp3	g.chr2:232079553G>T	Missense Mutation	ARMC9	p.V63F	armadillo repeat contain	64 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr15:80743288G>T	Silent	ARNT2	p.V33V	aryl-hydrocarbon recept	63 (0.00)	30 (0.30)	0.80
11-01	Gp3	g.chr11:13378628G>T	Missense Mutation	ARNTL	p.R69M	aryl hydrocarbon recept	55 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr15:52844162G>A	Missense Mutation	ARPP19	p.P103L	cAMP-regulated phosph	82 (0.00)	42 (0.26)	0.70
11-01	Gp3	g.chr19:4896863G>A	Silent	ARRDC5	p.H107H	arrestin domain containi	116 (0.00)	95 (0.15)	0.39
11-01	Gp3	g.chrX:2924658C>G	Missense Mutation	ARSH	p.T2R	arylsulfatase family, me	20 (0.00)	20 (0.70)	1.17
11-01	Gp3	g.chr5:149676924C>T	Silent	ARSI	p.G521G	arylsulfatase family, me	49 (0.00)	46 (0.33)	0.87
11-01	Gp3	g.chr10:52005053G>A	Nonsense Mutation	ASAH2	p.Q97*	N-acylsphingosine amid	105 (0.00)	28 (0.39)	1.05
11-01	Gp3	g.chr3:57312405C>A	Splice Site	ASB14	p.K477N	ankyrin repeat and SOC	21 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chrX:15270506G>A	Silent	ASB9	p.D101D	ankyrin repeat and SOC	26 (0.00)	20 (0.60)	1.00
11-01	Gp3	g.chr1:155408159C>A	Missense Mutation	ASH1L	p.Q1929H	ash1 (absent, small, or h	47 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr1:155448884G>T	Nonsense Mutation	ASH1L	p.Y1259*	ash1 (absent, small, or h	109 (0.00)	76 (0.17)	0.46
11-01	Gp3	g.chr7:65546919G>A	Missense Mutation	ASL	p.G48S	argininosuccinate lyase	21 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr2:70187951C>G	Missense Mutation	ASPRV1	p.Q290H	aspartic peptidase, retro	70 (0.00)	18 (0.28)	0.42
11-01	Gp3	g.chr1:176934366G>C	Missense Mutation	ASTN1	p.P511A	astrotactin 1	55 (0.00)	21 (0.48)	1.27
11-01	Gp3	g.chr9:119567953G>A	Missense Mutation	ASTN2	p.T734I	astrotactin 2	45 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr9:119738421C>A	Missense Mutation	ASTN2	p.G524W	astrotactin 2	31 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr20:31019194C>A	Missense Mutation	ASXL1	p.N263K	additional sex combs lik	87 (0.00)	52 (0.50)	1.33
11-01	Gp3	g.chr2:25965296G>A	Nonsense Mutation	ASXL2	p.Q1304*	additional sex combs lik	34 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr2:25965396C>A	Missense Mutation	ASXL2	p.Q1270H	additional sex combs lik	98 (0.00)	79 (0.22)	0.57
11-01	Gp3	g.chr2:25967087C>A	Missense Mutation	ASXL2	p.G707W	additional sex combs lik	38 (0.00)	27 (0.74)	1.98
11-01	Gp3	g.chr2:25967114C>G	Missense Mutation	ASXL2	p.G698R	additional sex combs lik	41 (0.00)	25 (0.72)	1.92
11-01	Gp3	g.chr8:124384876C>A	Splice Site	ATAD2		ATPase family, AAA d	46 (0.00)	28 (0.29)	0.76

11-01	Gp3	g.chr5:81354358G>A	Silent	ATG10	p.K51K	autophagy related 10	42 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr11:64662515C>T	Missense Mutation	ATG2A	p.R1916H	autophagy related 2A	15 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr2:242608085C>T	Silent	ATG4B	p.D314D	autophagy related 4B, c	32 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr11:108151732C>T	Missense Mutation	ATM	p.A1138V	ATM serine/threonine k	37 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr11:108158382C>T	Missense Mutation	ATM	p.T1350M	ATM serine/threonine k	95 (0.00)	59 (0.29)	0.77
11-01	Gp3	g.chr11:108214071T>C	Silent	ATM	p.S2797S	ATM serine/threonine k	49 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr15:25925043G>C	Silent	ATP10A	p.P1315P	ATPase, class V, type 1	27 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr15:25936921C>T	Missense Mutation	ATP10A	p.V1036I	ATPase, class V, type 1	33 (0.00)	25 (0.64)	1.71
11-01	Gp3	g.chr4:47593348G>A	Missense Mutation	ATP10D	p.E1411K	ATPase, class V, type 1	99 (0.01)	57 (0.28)	0.75
11-01	Gp3	g.chr13:113487180G>A	Missense Mutation	ATP11A	p.E468K	ATPase, class VI, type 1	111 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr13:113514675C>A	Silent	ATP11A	p.L934L	ATPase, class VI, type 1	43 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr13:113514688G>A	Missense Mutation	ATP11A	p.V939I	ATPase, class VI, type 1	43 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chrX:138856974G>C	Silent	ATP11C	p.L700L	ATPase, class VI, type 1	60 (0.00)	35 (0.37)	0.62
11-01	Gp3	g.chr13:25264560G>A	Missense Mutation	ATP12A	p.G211R	ATPase, H+/K+ transpo	64 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr13:25266575G>C	Silent	ATP12A	p.L359L	ATPase, H+/K+ transpo	55 (0.00)	41 (0.27)	0.72
11-01	Gp3	g.chr3:192992921G>A	Silent	ATP13A5	p.N1189N	ATPase type 13A5	37 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr3:193068980G>T	Missense Mutation	ATP13A5	p.P206Q	ATPase type 13A5	17 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chr1:116941664G>T	Silent	ATP1A1	p.L802L	ATPase, Na+/K+ transp	84 (0.00)	58 (0.24)	0.64
11-01	Gp3	g.chr1:169100690C>T	Missense Mutation	ATP1B1	p.T270I	ATPase, Na+/K+ transp	71 (0.01)	34 (0.32)	0.86
11-01	Gp3	g.chr16:28898805C>A	Silent	ATP2A1	p.T230T	ATPase, Ca++ transport	31 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr12:90049629C>T	Missense Mutation	ATP2B1	p.S12N	ATPase, Ca++ transport	45 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr1:203669339C>T	Silent	ATP2B4	p.L219L	ATPase, Ca++ transport	78 (0.00)	82 (0.20)	0.52
11-01	Gp3	g.chr16:84482178G>A	Missense Mutation	ATP2C2	p.E515K	ATPase, Ca++ transport	38 (0.00)	23 (0.30)	0.64
11-01	Gp3	g.chr16:84494322C>G	Missense Mutation	ATP2C2	p.T828S	ATPase, Ca++ transport	75 (0.00)	39 (0.18)	0.38
11-01	Gp3	g.chr17:40639346C>G	Silent	ATP6V0A1	p.T335T	ATPase, H+ transportin	21 (0.00)	20 (0.40)	1.07
11-01	Gp3	g.chr12:124209209G>A	Silent	ATP6V0A2	p.L101L	ATPase, H+ transportin	174 (0.00)	173 (0.19)	0.51
11-01	Gp3	g.chr7:138424325C>T	Missense Mutation	ATP6V0A4	p.G511E	ATPase, H+ transportin	27 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr8:20075734C>A	Nonsense Mutation	ATP6V1B2	p.S446*	ATPase, H+ transportin	80 (0.00)	29 (0.55)	0.82
11-01	Gp3	g.chr2:46739318G>A	Missense Mutation	ATP6V1E2	p.A178V	ATPase, H+ transportin	118 (0.00)	99 (0.22)	0.59
11-01	Gp3	g.chrX:77227181G>T	Nonsense Mutation	ATP7A	p.E15*	ATPase, Cu++ transport	34 (0.00)	29 (0.48)	0.80
11-01	Gp3	g.chrX:77268522C>A	Silent	ATP7A	p.A773A	ATPase, Cu++ transport	39 (0.00)	31 (0.29)	0.48
11-01	Gp3	g.chr18:55322617C>A	Nonsense Mutation	ATP8B1	p.E914*	ATPase, aminophospho	74 (0.00)	67 (0.18)	0.48
11-01	Gp3	g.chr18:55351296G>C	Missense Mutation	ATP8B1	p.C534W	ATPase, aminophospho	99 (0.00)	85 (0.15)	0.41
11-01	Gp3	g.chr18:55364917C>A	Missense Mutation	ATP8B1	p.D211Y	ATPase, aminophospho	22 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr1:154304134G>A	Missense Mutation	ATP8B2	p.E173K	ATPase, aminophospho	66 (0.00)	75 (0.17)	0.46

11-01	Gp3	g.chr20:50292744G>A	Missense Mutation	ATP9A	p.T268I	ATPase, class II, type 9	27 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr3:142281400C>G	Missense Mutation	ATR	p.E282Q	ATR serine/threonine ki	60 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr3:48491495G>C	Silent	ATRIP	p.G100G	ATR interacting protein	107 (0.00)	39 (0.46)	1.23
11-01	Gp3	g.chr20:3556524G>A	Missense Mutation	ATRN	p.A715T	attractin	56 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr20:3575147C>T	Missense Mutation	ATRN	p.A1115V	attractin	68 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:111948269G>A	Missense Mutation	ATXN2	p.A454V	ataxin 2	83 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr14:92549520C>T	Missense Mutation	ATXN3	p.M186I	ataxin 3	59 (0.00)	37 (0.38)	1.01
11-01	Gp3	g.chr3:63982114C>A	Silent	ATXN7	p.T872T	ataxin 7	34 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr1:110033616C>T	Silent	ATXN7L2	p.S477S	ataxin 7-like 2	57 (0.00)	59 (0.20)	0.54
11-01	Gp3	g.chr17:42271728C>T	Missense Mutation	ATXN7L3	p.S323N	ataxin 7-like 3	39 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr17:42273448C>A	Missense Mutation	ATXN7L3	p.Q166H	ataxin 7-like 3	28 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr9:93983144C>T	Silent	AUH	p.Q262Q	AU RNA binding protei	40 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chr1:26162102C>A	Missense Mutation	AUNIP	p.E152D	aurora kinase A and nin	34 (0.03)	29 (0.21)	0.55
11-01	Gp3	g.chr19:57743588C>A	Missense Mutation	AURKC	p.L98I	aurora kinase C	37 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr19:57743589T>C	Missense Mutation	AURKC	p.L98P	aurora kinase C	36 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr7:69900767G>C	Splice Site	AUTS2	p.K230N	autism susceptibility car	45 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr7:70227988C>A	Missense Mutation	AUTS2	p.P292H	autism susceptibility car	47 (0.00)	85 (0.21)	0.56
11-01	Gp3	g.chr17:63537606C>G	Missense Mutation	AXIN2	p.K342N	axin 2	54 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr17:79176168G>C	Silent	AZI1	p.G220G		22 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr1:235647728G>A	Silent	B3GALNT2	p.I155I	beta-1,3-N-acetylgalact	47 (0.00)	50 (0.24)	0.64
11-01	Gp3	g.chr2:62449741C>A	Nonsense Mutation	B3GNT2	p.S129*	UDP-GlcNAc:betaGal b	58 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr6:70071273C>T	Nonsense Mutation	BAI3	p.Q1370*	brain-specific angiogen	90 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr17:79077767G>T	Missense Mutation	BAIAP2	p.D172Y	BAI1-associated protein	15 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr14:35245657T>A	Missense Mutation	BAZ1A	p.R767S	bromodomain adjacent t	56 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr7:72856630C>G	Missense Mutation	BAZ1B	p.V1450L	bromodomain adjacent t	75 (0.00)	85 (0.16)	0.44
11-01	Gp3	g.chr12:56998533G>A	Silent	BAZ2A	p.D933D	bromodomain adjacent t	17 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr2:160289802C>T	Missense Mutation	BAZ2B	p.A456T	bromodomain adjacent t	148 (0.00)	84 (0.19)	0.51
11-01	Gp3	g.chr4:123664326A>T	Missense Mutation	BBS12	p.I427L	Bardet-Biedl syndrome	82 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr16:56519572G>C	Missense Mutation	BBS2	p.N663K	Bardet-Biedl syndrome	55 (0.00)	19 (0.53)	1.40
11-01	Gp3	g.chr19:45317413C>T	Silent	BCAM	p.P263P	basal cell adhesion mol	22 (0.00)	29 (0.38)	1.01
11-01	Gp3	g.chr1:156621482G>A	Splice Site	BCAN		brevican	44 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr20:52601849G>A	Silent	BCAS1	p.L373L	breast carcinoma amplif	63 (0.00)	58 (0.33)	0.87
11-01	Gp3	g.chr19:41920012C>A	Missense Mutation	BCKDHA	p.A145D	branched chain keto aci	24 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr15:52402134G>A	Missense Mutation	BCL2L10	p.T199I	BCL2-like 10 (apoptosi	40 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr12:122492782C>A	Missense Mutation	BCL7A	p.Q171K	B-cell CLL/lymphoma	69 (0.00)	41 (0.29)	0.78

11-01	Gp3	g.chr1:147091188G>T	Missense Mutation	BCL9	p.M409I	B-cell CLL/lymphoma	76 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr6:136599333G>A	Missense Mutation	BCLAF1	p.P229L	BCL2-associated transc	87 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr16:81320964C>A	Missense Mutation	BCMO1	p.A456E		49 (0.00)	33 (0.21)	0.45
11-01	Gp3	g.chr11:112064333G>A	Missense Mutation	BCO2	p.E39K	beta-carotene oxygenas	66 (0.00)	53 (0.23)	0.60
11-01	Gp3	g.chrX:39934064G>A	Missense Mutation	BCOR	p.L179F	BCL6 corepressor	35 (0.00)	43 (0.26)	0.43
11-01	Gp3	g.chrX:129148115G>C	Missense Mutation	BCORL1	p.S456T	BCL6 corepressor-like	18 (0.00)	21 (0.29)	0.48
11-01	Gp3	g.chr10:13534804C>T	Missense Mutation	BEND7	p.R163K	BEN domain containing	60 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr12:70048943T>A	Missense Mutation	BEST3	p.D584V	bestrophin 3	36 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr12:70048984G>A	Silent	BEST3	p.S570S	bestrophin 3	48 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr12:70049108G>A	Missense Mutation	BEST3	p.S529F	bestrophin 3	67 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr12:70049321C>T	Missense Mutation	BEST3	p.G458E	bestrophin 3	53 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr12:26277501G>A	Missense Mutation	BHLHE41	p.S26F	basic helix-loop-helix fa	49 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr12:32481316G>T	Missense Mutation	BICD1	p.V643L	bicaudal D homolog 1 (	41 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:32491864C>T	Silent	BICD1	p.I905I	bicaudal D homolog 1 (	28 (0.00)	30 (0.80)	2.13
11-01	Gp3	g.chr11:102195535C>A	Missense Mutation	BIRC3	p.L99I	baculoviral IAP repeat c	41 (0.00)	40 (0.38)	1.00
11-01	Gp3	g.chr2:32631617C>A	Missense Mutation	BIRC6	p.S490Y	baculoviral IAP repeat c	52 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr2:32664611C>T	Missense Mutation	BIRC6	p.H1223Y	baculoviral IAP repeat c	53 (0.00)	59 (0.32)	0.86
11-01	Gp3	g.chr15:91267832G>A	Intron	BLM		Bloom syndrome, RecQ	164 (0.00)	107 (0.21)	0.57
11-01	Gp3	g.chr15:91272857G>A	Intron	BLM		Bloom syndrome, RecQ	46 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr15:91286958G>T	Intron	BLM		Bloom syndrome, RecQ	40 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr15:91306494G>A	Intron	BLM		Bloom syndrome, RecQ	72 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr15:91318061G>A	Intron	BLM		Bloom syndrome, RecQ	44 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr15:91329939G>T	Intron	BLM		Bloom syndrome, RecQ	25 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr4:79832378G>T	Nonsense Mutation	BMP2K	p.E893*	BMP2 inducible kinase	94 (0.01)	42 (0.14)	0.38
11-01	Gp3	g.chr6:7880504C>A	Nonsense Mutation	BMP6	p.Y490*	bone morphogenetic pr	129 (0.00)	61 (0.21)	0.57
11-01	Gp3	g.chr10:43287184G>A	Nonsense Mutation	BMS1	p.W249*	BMS1 ribosome biogen	75 (0.00)	55 (0.31)	0.82
11-01	Gp3	g.chr15:59971887C>A	Missense Mutation	BNIP2	p.G67C	BCL2/adenovirus E1B	169 (0.01)	32 (0.38)	1.00
11-01	Gp3	g.chr4:13590374C>T	Missense Mutation	BOD1L1	p.G2751D	biorientation of chromo	51 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr13:73321171C>G	Missense Mutation	BORA	p.F468L	bora, aurora kinase A ac	35 (0.00)	36 (0.39)	1.04
11-01	Gp3	g.chr20:31873953C>T	Missense Mutation	BPIFB1	p.P25L	BPI fold containing fam	35 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr20:31644440C>A	Missense Mutation	BPIFB3	p.L73M	BPI fold containing fam	48 (0.00)	62 (0.19)	0.52
11-01	Gp3	g.chr17:65850301C>T	Missense Mutation	BPTF	p.H287Y	bromodomain PHD fing	137 (0.01)	114 (0.17)	0.44
11-01	Gp3	g.chr17:65862691C>T	Silent	BPTF	p.L516L	bromodomain PHD fing	59 (0.00)	21 (0.38)	1.02
11-01	Gp3	g.chr17:65909222C>T	Missense Mutation	BPTF	p.P1741L	bromodomain PHD fing	156 (0.01)	110 (0.20)	0.53
11-01	Gp3	g.chr17:41199105G>C	Intron	BRCA1		breast cancer 1, early on	53 (0.00)	49 (0.27)	0.71

11-01	Gp3	g.chr17:41200643C>T	Intron	BRCA1		breast cancer 1, early on	43 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr17:41211556C>A	Intron	BRCA1		breast cancer 1, early on	110 (0.00)	65 (0.40)	1.07
11-01	Gp3	g.chr17:41220070A>G	Intron	BRCA1		breast cancer 1, early on	64 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr17:41221268G>A	Intron	BRCA1		breast cancer 1, early on	47 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr17:41223037C>A	Missense Mutation	BRCA1	p.V1632L	breast cancer 1, early on	41 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr17:41227535C>A	Intron	BRCA1		breast cancer 1, early on	100 (0.00)	33 (0.30)	0.81
11-01	Gp3	g.chr17:41266636G>C	Intron	BRCA1		breast cancer 1, early on	98 (0.00)	46 (0.26)	0.70
11-01	Gp3	g.chr13:32917888G>A	Intron	BRCA2		breast cancer 2, early on	56 (0.00)	30 (0.40)	1.07
11-01	Gp3	g.chr13:32918357C>T	Intron	BRCA2		breast cancer 2, early on	42 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr13:32935957G>A	Intron	BRCA2		breast cancer 2, early on	69 (0.00)	74 (0.55)	1.48
11-01	Gp3	g.chr13:32957610C>A	Intron	BRCA2		breast cancer 2, early on	114 (0.00)	46 (0.26)	0.70
11-01	Gp3	g.chr13:32960288C>A	Intron	BRCA2		breast cancer 2, early on	52 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr13:32968178G>A	Intron	BRCA2		breast cancer 2, early on	49 (0.00)	17 (0.65)	1.73
11-01	Gp3	g.chr13:32970886C>A	Intron	BRCA2		breast cancer 2, early on	66 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr5:137485483C>G	Missense Mutation	BRD8	p.E1042Q	bromodomain containin	19 (0.00)	15 (0.73)	1.96
11-01	Gp3	g.chr5:878528C>G	Missense Mutation	BRD9	p.E405Q	bromodomain containin	39 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr10:93713541G>A	Missense Mutation	BTAF1	p.M204I	BTAF1 RNA polymeras	157 (0.00)	92 (0.16)	0.43
11-01	Gp3	g.chr6:26505207G>A	Missense Mutation	BTN1A1	p.C161Y	butyrophilin, subfamily	52 (0.00)	50 (0.18)	0.48
11-01	Gp3	g.chr2:111408192G>C	Missense Mutation	BUB1	p.P712A	BUB1 mitotic checkpoi	36 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr10:124457767C>T	Missense Mutation	C10orf120	p.V164I	chromosome 10 open re	44 (0.02)	30 (0.20)	0.53
11-01	Gp3	g.chr10:96954331C>G	Missense Mutation	C10orf129	p.T30S		34 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr10:50531129C>G	Missense Mutation	C10orf71	p.P180R	chromosome 10 open re	69 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr10:50532222C>T	Silent	C10orf71	p.L544L	chromosome 10 open re	106 (0.01)	38 (0.26)	0.70
11-01	Gp3	g.chr10:103773778C>A	Missense Mutation	C10orf76	p.V225L	chromosome 10 open re	66 (0.00)	84 (0.15)	0.41
11-01	Gp3	g.chr10:103773783T>A	Splice Site	C10orf76		chromosome 10 open re	66 (0.00)	85 (0.14)	0.38
11-01	Gp3	g.chr10:128192949G>A	Missense Mutation	C10orf90	p.P227S	chromosome 10 open re	45 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr11:111795050G>A	Splice Site	C11orf52	p.W11*	chromosome 11 open re	98 (0.00)	71 (0.18)	0.49
11-01	Gp3	g.chr11:122774959G>T	Missense Mutation	C11orf63	p.S224I	chromosome 11 open re	55 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr11:122828070G>T	Splice Site	C11orf63		chromosome 11 open re	61 (0.00)	73 (0.18)	0.47
11-01	Gp3	g.chr11:66581374G>A	Silent	C11orf80	p.L141L	chromosome 11 open re	56 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr12:53699994C>T	Missense Mutation	C12orf10	p.R56C	chromosome 12 open re	23 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr12:48888640C>A	Missense Mutation	C12orf54	p.S101Y	chromosome 12 open re	61 (0.00)	29 (0.48)	1.29
11-01	Gp3	g.chr14:23467931C>G	Missense Mutation	C14orf93	p.R101T	chromosome 14 open re	29 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr16:49433162C>A	Missense Mutation	C16orf78	p.F257L	chromosome 16 open re	41 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr17:34190562G>C	Splice Site	C17orf66	p.A190G		24 (0.00)	28 (0.32)	0.86

11-01	Gp3	g.chr17:16344368C>T	RNA	C17orf76-AS1			100 (0.00)	105 (0.20)	0.53
11-01	Gp3	g.chr19:51301693C>G	Missense Mutation	C19orf48	p.E5Q	chromosome 19 open re	39 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr1:162344163G>A	Missense Mutation	C1orf111	p.T154I	chromosome 1 open rea	96 (0.00)	75 (0.25)	0.68
11-01	Gp3	g.chr1:75038319G>A	Silent	C1orf173	p.C1025C		28 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr1:75038964C>T	Silent	C1orf173	p.R810R		30 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr1:75072479C>A	Missense Mutation	C1orf173	p.R432M		127 (0.00)	66 (0.20)	0.53
11-01	Gp3	g.chr1:186388145G>T	Silent	C1orf27	p.V434V	chromosome 1 open rea	22 (0.00)	34 (0.50)	1.33
11-01	Gp3	g.chr1:43263855G>A	Missense Mutation	C1orf50	p.A223T	chromosome 1 open rea	144 (0.00)	90 (0.36)	0.95
11-01	Gp3	g.chr1:150255808C>G	Missense Mutation	C1orf51	p.P44R		49 (0.00)	35 (0.26)	0.69
11-01	Gp3	g.chr1:150257044A>T	Missense Mutation	C1orf51	p.M187L		23 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr1:152692379C>T	Nonsense Mutation	C1orf68	p.Q128*	chromosome 1 open rea	113 (0.00)	50 (0.36)	0.96
11-01	Gp3	g.chr1:156263818G>A	Silent	C1orf85	p.A263A	chromosome 1 open rea	34 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr1:60463415G>A	Missense Mutation	C1orf87	p.P449L	chromosome 1 open rea	41 (0.00)	58 (0.24)	0.64
11-01	Gp3	g.chr1:60521014G>T	Silent	C1orf87	p.P68P	chromosome 1 open rea	106 (0.00)	62 (0.45)	1.20
11-01	Gp3	g.chr5:34043091G>A	Missense Mutation	C1QTNF3	p.T47I	C1q and tumor necrosis	97 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr13:24895659C>T	Missense Mutation	C1QTNF9	p.T252I	C1q and tumor necrosis	72 (0.01)	40 (0.30)	0.80
11-01	Gp3	g.chr13:24895880G>A	Missense Mutation	C1QTNF9	p.G326R	C1q and tumor necrosis	100 (0.00)	71 (0.17)	0.45
11-01	Gp3	g.chr20:20079443G>C	Missense Mutation	C20orf26	p.V282L		41 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr20:20180469C>A	Silent	C20orf26	p.R619R		80 (0.00)	94 (0.32)	0.85
11-01	Gp3	g.chr20:20180521C>T	Missense Mutation	C20orf26	p.P636L		65 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr22:19839384T>A	Missense Mutation	C22orf29	p.D134V	chromosome 22 open re	125 (0.00)	141 (0.16)	0.42
11-01	Gp3	g.chr11:73748635C>A	Missense Mutation	C2CD3	p.Q1923H	C2 calcium-dependent d	55 (0.00)	58 (0.16)	0.41
11-01	Gp3	g.chr12:22637656C>G	Missense Mutation	C2CD5	p.G509R	C2 calcium-dependent d	55 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr12:22678633C>T	Missense Mutation	C2CD5	p.R119H	C2 calcium-dependent d	79 (0.00)	72 (0.29)	0.78
11-01	Gp3	g.chr2:27800169C>T	Nonsense Mutation	C2orf16	p.R244*	chromosome 2 open rea	90 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr2:24260619C>T	Silent	C2orf44	p.L582L	chromosome 2 open rea	128 (0.00)	70 (0.33)	0.88
11-01	Gp3	g.chr2:29295037G>T	Silent	C2orf71	p.G697G	chromosome 2 open rea	37 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr19:6685152G>A	Silent	C3	p.T1272T	complement component	24 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr3:118866290C>T	Silent	C3orf30	p.I418I	chromosome 3 open rea	94 (0.00)	61 (0.15)	0.39
11-01	Gp3	g.chr3:118870080G>A	Missense Mutation	C3orf30	p.E518K	chromosome 3 open rea	105 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr4:113507733T>C	Missense Mutation	C4orf21	p.S1262G		57 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr4:128949890C>T	Silent	C4orf29	p.R320R	chromosome 4 open rea	92 (0.00)	93 (0.15)	0.40
11-01	Gp3	g.chr4:130023885G>T	Missense Mutation	C4orf33	p.R40S	chromosome 4 open rea	65 (0.00)	53 (0.19)	0.50
11-01	Gp3	g.chr19:47823691G>A	Silent	C5AR1	p.T219T	complement component	26 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr5:134782433C>A	Missense Mutation	C5orf20	p.Q122H		46 (0.00)	32 (0.16)	0.42

11-01	Gp3	g.chr5:31545778C>G	Missense Mutation	C5orf22	p.Q340E	chromosome 5 open rea	59 (0.00)	52 (0.52)	1.38
11-01	Gp3	g.chr5:37138892C>T	Missense Mutation	C5orf42	p.D2854N	chromosome 5 open rea	124 (0.01)	99 (0.20)	0.54
11-01	Gp3	g.chr5:37198918C>T	Silent	C5orf42	p.K1186K	chromosome 5 open rea	26 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr5:7832034C>A	Missense Mutation	C5orf49	p.A123S	chromosome 5 open rea	43 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr5:7832083C>A	Missense Mutation	C5orf49	p.Q106H	chromosome 5 open rea	50 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr5:171217852G>T	Missense Mutation	C5orf50	p.R93S		64 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr6:88074817G>T	Missense Mutation	C6orf163	p.E231D	chromosome 6 open rea	69 (0.01)	17 (0.47)	0.74
11-01	Gp3	g.chr6:36294411G>A	Silent	C6orf222	p.H304H	chromosome 6 open rea	138 (0.00)	79 (0.38)	1.01
11-01	Gp3	g.chr7:25175953G>T	Missense Mutation	C7orf31	p.L471I	chromosome 7 open rea	85 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr7:50136123G>T	Nonsense Mutation	C7orf72	p.G148*	chromosome 7 open rea	30 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr8:96281289G>A	Silent	C8orf37	p.N43N	chromosome 8 open rea	67 (0.00)	174 (0.15)	0.50
11-01	Gp3	g.chr9:35045344C>G	Missense Mutation	C9orf131	p.H906Q	chromosome 9 open rea	122 (0.00)	56 (0.23)	0.62
11-01	Gp3	g.chr9:97522087G>T	Missense Mutation	C9orf3	p.A8S	chromosome 9 open rea	64 (0.00)	68 (0.21)	0.55
11-01	Gp3	g.chr9:97522648C>A	Missense Mutation	C9orf3	p.P195T	chromosome 9 open rea	62 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr9:77614646C>A	Splice Site	C9orf41	p.R244I	chromosome 9 open rea	31 (0.00)	24 (0.46)	1.50
11-01	Gp3	g.chr9:132591818G>A	Missense Mutation	C9orf78	p.A182V	chromosome 9 open rea	95 (0.01)	136 (0.31)	0.82
11-01	Gp3	g.chr9:136256541C>A	Missense Mutation	C9orf96	p.D184E		28 (0.00)	45 (0.49)	1.30
11-01	Gp3	g.chr17:49710938G>A	Missense Mutation	CA10	p.P288L	carbonic anhydrase X	31 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr8:86389481C>G	Missense Mutation	CA2	p.P214A	carbonic anhydrase II	24 (0.00)	19 (0.26)	0.88
11-01	Gp3	g.chr13:49951120G>T	Missense Mutation	CAB39L	p.Q87K	calcium binding protein	56 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr1:65129497C>G	Missense Mutation	CACHD1	p.L640V	cache domain containin	82 (0.00)	43 (0.44)	1.18
11-01	Gp3	g.chr1:65147723C>T	Nonsense Mutation	CACHD1	p.R1123*	cache domain containin	62 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr19:13345815C>A	Missense Mutation	CACNA1A	p.E1723D	calcium channel, voltag	77 (0.00)	68 (0.28)	0.75
11-01	Gp3	g.chr19:13423522C>A	Silent	CACNA1A	p.R543R	calcium channel, voltag	45 (0.00)	37 (0.46)	1.23
11-01	Gp3	g.chr12:2566832C>A	Missense Mutation	CACNA1C	p.F239L	calcium channel, voltag	115 (0.00)	104 (0.20)	0.54
11-01	Gp3	g.chr12:2695009G>A	Missense Mutation	CACNA1C	p.M823I	calcium channel, voltag	138 (0.01)	71 (0.21)	0.56
11-01	Gp3	g.chr12:2786274G>A	Missense Mutation	CACNA1C	p.V1663I	calcium channel, voltag	58 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr1:181707532G>A	Silent	CACNA1E	p.T1194T	calcium channel, voltag	226 (0.00)	115 (0.15)	0.39
11-01	Gp3	g.chr22:40061917G>A	Missense Mutation	CACNA1I	p.G1337D	calcium channel, voltag	40 (0.00)	37 (0.51)	1.37
11-01	Gp3	g.chr1:201028422G>A	Silent	CACNA1S	p.Y1140Y	calcium channel, voltag	35 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr3:54798295G>A	Missense Mutation	CACNA2D3	p.E433K	calcium channel, voltag	132 (0.00)	71 (0.24)	0.64
11-01	Gp3	g.chr17:37334308G>A	Nonsense Mutation	CACNB1	p.R359*	calcium channel, voltag	55 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr3:85013798A>G	Intron	CADM2		cell adhesion molecule	62 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr3:85014855C>T	Intron	CADM2		cell adhesion molecule	25 (0.00)	49 (0.22)	0.60
11-01	Gp3	g.chr3:85042350G>A	Intron	CADM2		cell adhesion molecule	145 (0.00)	72 (0.24)	0.63

11-01	Gp3	g.chr3:85054210C>T	Intron	CADM2	cell adhesion molecule	92 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr3:85066449G>C	Intron	CADM2	cell adhesion molecule	45 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr3:85080966C>T	Intron	CADM2	cell adhesion molecule	43 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr3:85088255C>T	Intron	CADM2	cell adhesion molecule	47 (0.02)	22 (0.23)	0.61
11-01	Gp3	g.chr3:85103725G>A	Intron	CADM2	cell adhesion molecule	134 (0.00)	84 (0.14)	0.38
11-01	Gp3	g.chr3:85113305C>A	Intron	CADM2	cell adhesion molecule	105 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr3:85150208C>A	Intron	CADM2	cell adhesion molecule	28 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr3:85191354C>A	Intron	CADM2	cell adhesion molecule	55 (0.02)	16 (0.31)	0.83
11-01	Gp3	g.chr3:85226015G>C	Intron	CADM2	cell adhesion molecule	29 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr3:85259479T>C	Intron	CADM2	cell adhesion molecule	32 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr3:85265277C>G	Intron	CADM2	cell adhesion molecule	84 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr3:85315550G>C	Intron	CADM2	cell adhesion molecule	17 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chr3:85330075G>A	Intron	CADM2	cell adhesion molecule	17 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr3:85335082G>C	Intron	CADM2	cell adhesion molecule	24 (0.00)	15 (0.73)	1.96
11-01	Gp3	g.chr3:85348878C>A	Intron	CADM2	cell adhesion molecule	53 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr3:85384408C>A	Intron	CADM2	cell adhesion molecule	56 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr3:85404159C>A	Intron	CADM2	cell adhesion molecule	47 (0.02)	32 (0.19)	0.50
11-01	Gp3	g.chr3:85410685G>A	Intron	CADM2	cell adhesion molecule	128 (0.00)	68 (0.19)	0.51
11-01	Gp3	g.chr3:85410793C>A	Intron	CADM2	cell adhesion molecule	86 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr3:85427824C>G	Intron	CADM2	cell adhesion molecule	68 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr3:85431047C>T	Intron	CADM2	cell adhesion molecule	22 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr3:85438934C>T	Intron	CADM2	cell adhesion molecule	27 (0.00)	21 (0.52)	1.40
11-01	Gp3	g.chr3:85458721C>A	Intron	CADM2	cell adhesion molecule	56 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr3:85471020C>T	Intron	CADM2	cell adhesion molecule	75 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr3:85472283G>A	Intron	CADM2	cell adhesion molecule	17 (0.00)	28 (0.39)	1.05
11-01	Gp3	g.chr3:85479222G>T	Intron	CADM2	cell adhesion molecule	70 (0.00)	40 (0.23)	0.60
11-01	Gp3	g.chr3:85544011G>T	Intron	CADM2	cell adhesion molecule	46 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr3:85560293C>T	Intron	CADM2	cell adhesion molecule	182 (0.01)	100 (0.16)	0.43
11-01	Gp3	g.chr3:85560294C>T	Intron	CADM2	cell adhesion molecule	181 (0.01)	100 (0.16)	0.43
11-01	Gp3	g.chr3:85576462G>A	Intron	CADM2	cell adhesion molecule	101 (0.00)	94 (0.20)	0.54
11-01	Gp3	g.chr3:85578402G>T	Intron	CADM2	cell adhesion molecule	97 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr3:85599362C>T	Intron	CADM2	cell adhesion molecule	34 (0.00)	27 (0.59)	1.58
11-01	Gp3	g.chr3:85603670G>A	Intron	CADM2	cell adhesion molecule	79 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr3:85632073T>A	Intron	CADM2	cell adhesion molecule	60 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr3:85662163G>A	Intron	CADM2	cell adhesion molecule	80 (0.00)	22 (0.23)	0.61

11-01	Gp3	g.chr3:85670914C>T	Intron	CADM2		cell adhesion molecule	71 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr3:85691169C>A	Intron	CADM2		cell adhesion molecule	33 (0.00)	30 (0.80)	2.13
11-01	Gp3	g.chr3:85707077G>A	Intron	CADM2		cell adhesion molecule	80 (0.00)	74 (0.15)	0.40
11-01	Gp3	g.chr3:85712593G>C	Intron	CADM2		cell adhesion molecule	153 (0.00)	120 (0.17)	0.47
11-01	Gp3	g.chr3:85719172G>T	Intron	CADM2		cell adhesion molecule	57 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr3:85763900G>A	Intron	CADM2		cell adhesion molecule	170 (0.00)	83 (0.16)	0.42
11-01	Gp3	g.chr3:85783504C>A	Intron	CADM2		cell adhesion molecule	103 (0.00)	58 (0.16)	0.41
11-01	Gp3	g.chr3:85795786C>A	Intron	CADM2		cell adhesion molecule	53 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr3:85795787T>C	Intron	CADM2		cell adhesion molecule	51 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr3:85822175G>A	Intron	CADM2		cell adhesion molecule	64 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr3:85856295G>A	Intron	CADM2		cell adhesion molecule	62 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr3:85865567C>A	Intron	CADM2		cell adhesion molecule	33 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr3:85866808C>G	Intron	CADM2		cell adhesion molecule	49 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr3:85882167G>A	Intron	CADM2		cell adhesion molecule	22 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr3:85886807G>C	Intron	CADM2		cell adhesion molecule	75 (0.00)	81 (0.19)	0.49
11-01	Gp3	g.chr3:85891463G>T	Intron	CADM2		cell adhesion molecule	37 (0.03)	18 (0.56)	1.48
11-01	Gp3	g.chr3:85962812G>C	Intron	CADM2		cell adhesion molecule	62 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr3:85988147G>T	Intron	CADM2		cell adhesion molecule	73 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr3:86001206T>C	Intron	CADM2		cell adhesion molecule	36 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr3:86001964A>T	Intron	CADM2		cell adhesion molecule	27 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr3:86002012C>T	Intron	CADM2		cell adhesion molecule	38 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr3:86003651G>A	Intron	CADM2		cell adhesion molecule	45 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr3:86023106C>T	Intron	CADM2		cell adhesion molecule	268 (0.00)	225 (0.17)	0.46
11-01	Gp3	g.chr3:86032441G>A	Intron	CADM2		cell adhesion molecule	49 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr3:86034091C>T	Intron	CADM2		cell adhesion molecule	25 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr3:86049421G>A	Intron	CADM2		cell adhesion molecule	32 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr3:86055457C>G	Intron	CADM2		cell adhesion molecule	44 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr3:86062669C>T	Intron	CADM2		cell adhesion molecule	49 (0.02)	29 (0.69)	1.84
11-01	Gp3	g.chr3:86078640T>C	Intron	CADM2		cell adhesion molecule	114 (0.00)	46 (0.24)	0.64
11-01	Gp3	g.chr3:86098964C>A	Intron	CADM2		cell adhesion molecule	24 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr3:62543174C>A	Silent	CADPS	p.T553T	Ca++-dependent secreti	63 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr7:121960340C>T	Missense Mutation	CADPS2	p.S1216N	Ca++-dependent secreti	158 (0.01)	84 (0.18)	0.48
11-01	Gp3	g.chr3:9804885G>C	Silent	CAMK1	p.P76P	calcium/calmodulin-dep	67 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr3:49898923C>G	Silent	CAMKV	p.L130L	CaM kinase-like vesicle	24 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr9:138714176C>A	Missense Mutation	CAMSAP1	p.M777I	calmodulin regulated sp	39 (0.00)	47 (0.19)	0.51

11-01	Gp3	g.chr1:200818328G>A	Missense Mutation	CAMSAP2	p.E811K	calmodulin regulated sp	55 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr1:7804968C>G	Missense Mutation	CAMTA1	p.P1419R	calmodulin binding tran	52 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr3:12859348C>A	Missense Mutation	CAND2	p.P973T	cullin-associated and ne	22 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr2:30964811C>A	Missense Mutation	CAPN13	p.G500V	calpain 13	50 (0.00)	36 (0.22)	0.59
11-01	Gp3	g.chr2:30993292C>T	Silent	CAPN13	p.V137V	calpain 13	133 (0.00)	99 (0.16)	0.43
11-01	Gp3	g.chr11:34101245G>C	Missense Mutation	CAPRIN1	p.Q253H	cell cycle associated pro	79 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr12:18891266G>T	Missense Mutation	CAPZA3	p.A22S	capping protein (actin fi	69 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr1:19683205G>A	Missense Mutation	CAPZB	p.S197F	capping protein (actin fi	115 (0.01)	46 (0.22)	0.58
11-01	Gp3	g.chr19:48741784C>A	Missense Mutation	CARD8	p.S22I	caspase recruitment don	70 (0.00)	55 (0.20)	0.53
11-01	Gp3	g.chr16:8949158C>T	Missense Mutation	CARHSP1	p.E103K	calcium regulated heat s	32 (0.00)	36 (0.25)	0.67
11-01	Gp3	g.chr13:111353839G>A	Silent	CARS2	p.V113V	cysteinyl-tRNA synthet	59 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr6:90576085G>A	RNA	CASP8AP2		caspase 8 associated pro	47 (0.00)	19 (0.32)	0.50
11-01	Gp3	g.chr20:32212589G>T	Missense Mutation	CBFA2T2	p.D238Y	core-binding factor, run	139 (0.00)	63 (0.21)	0.55
11-01	Gp3	g.chr14:24897022G>A	Silent	CBLN3	p.F146F	cerebellin 3 precursor	136 (0.00)	64 (0.19)	0.50
11-01	Gp3	g.chr1:52821452C>T	Missense Mutation	CC2D1B	p.A713T	coiled-coil and C2 dom	46 (0.00)	62 (0.19)	0.52
11-01	Gp3	g.chr4:15482411G>A	Silent	CC2D2A	p.K69K	coiled-coil and C2 dom	54 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr2:219886626C>T	Silent	CCDC108	p.G1002G	coiled-coil domain cont	147 (0.01)	204 (0.15)	0.39
11-01	Gp3	g.chr2:219888771T>C	Missense Mutation	CCDC108	p.Y854C	coiled-coil domain cont	37 (0.03)	57 (0.18)	0.47
11-01	Gp3	g.chr2:179912075C>T	Missense Mutation	CCDC141	p.G54D	coiled-coil domain cont	164 (0.00)	142 (0.20)	0.53
11-01	Gp3	g.chr4:77283435C>A	Nonsense Mutation	CCDC158	p.E622*	coiled-coil domain cont	93 (0.00)	33 (0.36)	0.97
11-01	Gp3	g.chr4:77283446G>A	Missense Mutation	CCDC158	p.A618V	coiled-coil domain cont	86 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr6:109616795C>T	RNA	CCDC162P		coiled-coil domain cont	58 (0.00)	30 (0.30)	0.47
11-01	Gp3	g.chr6:151859277C>T	Missense Mutation	CCDC170	p.S95L	coiled-coil domain cont	59 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr6:151917524C>T	Missense Mutation	CCDC170	p.R508W	coiled-coil domain cont	53 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr1:93683421G>T	Nonsense Mutation	CCDC18	p.E652*	coiled-coil domain cont	31 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr9:100111493G>A	Silent	CCDC180	p.E969E	coiled-coil domain cont	39 (0.00)	47 (0.53)	1.42
11-01	Gp3	g.chr1:169390896C>T	Missense Mutation	CCDC181	p.R258K	coiled-coil domain cont	114 (0.00)	84 (0.20)	0.54
11-01	Gp3	g.chr1:43110474G>A	Missense Mutation	CCDC30	p.G629E	coiled-coil domain cont	217 (0.00)	146 (0.20)	0.53
11-01	Gp3	g.chr12:94772600C>A	Missense Mutation	CCDC41	p.L256F		66 (0.00)	36 (0.25)	0.85
11-01	Gp3	g.chr12:94794724G>C	Missense Mutation	CCDC41	p.L151V		19 (0.00)	32 (0.38)	1.28
11-01	Gp3	g.chr13:52440042C>A	Silent	CCDC70	p.A176A	coiled-coil domain cont	41 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr3:49201437C>G	Missense Mutation	CCDC71	p.D69H	coiled-coil domain cont	30 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr16:66803994G>C	Missense Mutation	CCDC79	p.S497R	coiled-coil domain cont	160 (0.01)	126 (0.15)	0.40
11-01	Gp3	g.chr2:55529039G>A	Silent	CCDC88A	p.G1519G	coiled-coil domain cont	113 (0.00)	92 (0.15)	0.41
11-01	Gp3	g.chr5:68470230C>G	Missense Mutation	CCNB1	p.F233L	cyclin B1	73 (0.00)	31 (0.19)	0.52

11-01	Gp3	g.chr6:41908172G>T	Missense Mutation	CCND3	p.T117K	cyclin D3	39 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr4:78081971T>C	Missense Mutation	CCNG2	p.V125A	cyclin G2	43 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr5:86695296C>A	Nonsense Mutation	CCNH	p.E189*	cyclin H	90 (0.00)	56 (0.54)	1.43
11-01	Gp3	g.chr10:97817676C>T	Missense Mutation	CCNJ	p.S277F	cyclin J	40 (0.00)	55 (0.24)	0.63
11-01	Gp3	g.chr3:156868139C>A	Missense Mutation	CCNL1	p.V236L	cyclin L1	45 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr1:1328795G>T	Missense Mutation	CCNL2	p.H214N	cyclin L2	50 (0.00)	42 (0.33)	0.89
11-01	Gp3	g.chr10:35855074C>T	Silent	CCNY	p.P290P	cyclin Y	65 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr12:69987338C>A	Silent	CCT2	p.V309V	chaperonin containing T	46 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr7:64526798A>T	RNA	CCT6P3		chaperonin containing T	22 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr22:17071952G>A	Silent	CCT8L2	p.L497L	chaperonin containing T	99 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr6:74533297C>T	Silent	CD109	p.H1426H	CD109 molecule	50 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr12:7639147G>T	Silent	CD163	p.G802G	CD163 molecule	40 (0.00)	24 (0.67)	1.78
11-01	Gp3	g.chr12:7640154G>T	Silent	CD163	p.A617A	CD163 molecule	68 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr18:67540475G>A	Silent	CD226	p.T245T	CD226 molecule	26 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr6:47577011C>T	Silent	CD2AP	p.C595C	CD2-associated protein	146 (0.00)	91 (0.16)	0.44
11-01	Gp3	g.chr19:51729121C>T	Silent	CD33	p.L161L	CD33 molecule	52 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr17:7484231C>A	Missense Mutation	CD68	p.Q260K	CD68 molecule	69 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr17:7484356G>T	Missense Mutation	CD68	p.Q301H	CD68 molecule	59 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr2:87017597G>T	Missense Mutation	CD8A	p.T86N	CD8a molecule	23 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr2:87042746C>A	Missense Mutation	CD8B	p.W209L	CD8b molecule	88 (0.01)	47 (0.32)	0.85
11-01	Gp3	g.chr2:107107362C>G	RNA	CD8BP		CD8b molecule pseudog	54 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr19:14516575C>T	Silent	CD97	p.L549L	CD97 molecule	26 (0.00)	64 (0.19)	0.50
11-01	Gp3	g.chr19:14517719C>A	Silent	CD97	p.L718L	CD97 molecule	55 (0.00)	73 (0.15)	0.40
11-01	Gp3	g.chr19:14517733C>G	Missense Mutation	CD97	p.S723C	CD97 molecule	69 (0.00)	97 (0.14)	0.38
11-01	Gp3	g.chr13:49842138C>A	Missense Mutation	CDADC1	p.P315T	cytidine and dCMP dea	25 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chr1:100964793C>A	Missense Mutation	CDC14A	p.A577E	cell division cycle 14A	21 (0.00)	30 (0.40)	1.07
11-01	Gp3	g.chr5:137661531C>T	Missense Mutation	CDC25C	p.M144I	cell division cycle 25C	16 (0.00)	13 (0.62)	1.64
11-01	Gp3	g.chr19:10502250C>T	Missense Mutation	CDC37	p.D372N	cell division cycle 37	31 (0.00)	35 (0.31)	0.84
11-01	Gp3	g.chr1:227300073C>G	Missense Mutation	CDC42BPA	p.K647N	CDC42 binding protein	83 (0.00)	51 (0.37)	0.99
11-01	Gp3	g.chr17:38450702C>T	Missense Mutation	CDC6	p.P344S	cell division cycle 6	68 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr14:105478219G>A	Silent	CDCA4	p.D16D	cell division cycle assoc	26 (0.00)	34 (0.44)	1.18
11-01	Gp3	g.chr5:24487817C>A	Missense Mutation	CDH10	p.K774N	cadherin 10, type 2 (T2-	44 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr5:24488007C>T	Missense Mutation	CDH10	p.R711Q	cadherin 10, type 2 (T2-	43 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr16:64981886C>A	Nonsense Mutation	CDH11	p.E671*	cadherin 11, type 2, OB-	93 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr16:64981895C>A	Missense Mutation	CDH11	p.G668C	cadherin 11, type 2, OB-	63 (0.00)	33 (0.33)	0.89

11-01	Gp3	g.chr18:64239402G>A	Missense Mutation	CDH19	p.P14S	cadherin 19, type 2	59 (0.00)	36 (0.33)	0.89
11-01	Gp3	g.chr10:73330590C>T	Missense Mutation	CDH23	p.A228V	cadherin-related 23	101 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr10:73376961G>A	Splice Site	CDH23		cadherin-related 23	57 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr10:73548736G>T	Missense Mutation	CDH23	p.D1959Y	cadherin-related 23	60 (0.00)	41 (0.37)	0.98
11-01	Gp3	g.chr10:73574956C>T	Missense Mutation	CDH23	p.T3334I	cadherin-related 23	25 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr18:63477053G>A	Silent	CDH7	p.K108K	cadherin 7, type 2	80 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr5:26881394C>A	Nonsense Mutation	CDH9	p.E741*	cadherin 9, type 2 (T1-c	107 (0.00)	80 (0.24)	0.63
11-01	Gp3	g.chr10:85970759C>A	Silent	CDHR1	p.L441L	cadherin-related family	102 (0.00)	131 (0.26)	0.69
11-01	Gp3	g.chr7:105645115G>A	Missense Mutation	CDHR3	p.C345Y	cadherin-related family	67 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr7:105660890C>T	Silent	CDHR3	p.L575L	cadherin-related family	128 (0.00)	65 (0.32)	0.86
11-01	Gp3	g.chr7:105662666C>T	Silent	CDHR3	p.T616T	cadherin-related family	164 (0.00)	58 (0.21)	0.55
11-01	Gp3	g.chr16:4563763G>A	Missense Mutation	CDIP1	p.H24Y	cell death-inducing p53	29 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr17:37676248G>A	Silent	CDK12	p.L1001L	cyclin-dependent kinase	40 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr7:40134267C>A	Missense Mutation	CDK13	p.D1409E	cyclin-dependent kinase	38 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr11:67274950C>A	Missense Mutation	CDK2AP2	p.A67S	cyclin-dependent kinase	24 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr6:21201372G>A	Missense Mutation	CDKAL1	p.G472E	CDK5 regulatory subun	94 (0.00)	53 (0.30)	0.81
11-01	Gp3	g.chr14:50811772G>A	Missense Mutation	CDKL1	p.P100S	cyclin-dependent kinase	36 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr4:184368044C>T	Nonsense Mutation	CDKN2AIP	p.Q403*	CDKN2A interacting pr	81 (0.01)	78 (0.17)	0.44
11-01	Gp3	g.chr5:115146982G>T	Nonsense Mutation	CDO1	p.C93*	cysteine dioxygenase ty	37 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr11:125885243C>T	Missense Mutation	CDON	p.G364E	cell adhesion associated	64 (0.00)	60 (0.30)	0.80
11-01	Gp3	g.chr5:149562343C>A	Missense Mutation	CDX1	p.T153N	caudal type homeobox 1	58 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr19:45026846C>A	RNA	CEACAM20		carcinoembryonic antig	20 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr19:42219776C>A	Nonsense Mutation	CEACAM5	p.S304*	carcinoembryonic antig	38 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr19:42231188C>G	Silent	CEACAM5	p.A686A	carcinoembryonic antig	78 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr19:42231220G>A	Missense Mutation	CEACAM5	p.G697E	carcinoembryonic antig	65 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr2:27016091C>G	Missense Mutation	CENPA	p.P123A	centromere protein A	55 (0.00)	39 (0.26)	0.68
11-01	Gp3	g.chrX:100387178G>T	Splice Site	CENPI		centromere protein I	53 (0.02)	33 (0.33)	0.56
11-01	Gp3	g.chr13:25486967C>T	Missense Mutation	CENPJ	p.S66N	centromere protein J	49 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr16:81050930G>T	Splice Site	CENPN		centromere protein N	38 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr17:63848034C>T	Missense Mutation	CEP112	p.R761K	centrosomal protein 112	46 (0.00)	22 (0.41)	1.09
11-01	Gp3	g.chr15:49044593C>A	Missense Mutation	CEP152	p.G1140V	centrosomal protein 152	71 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr15:49054746C>T	Missense Mutation	CEP152	p.D802N	centrosomal protein 152	47 (0.02)	26 (0.50)	1.33
11-01	Gp3	g.chr1:243329226T>C	Missense Mutation	CEP170	p.E679G	centrosomal protein 170	196 (0.00)	179 (0.22)	0.58
11-01	Gp3	g.chr14:105361091C>T	Silent	CEP170B	p.L1487L	centrosomal protein 170	17 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr18:13059218G>T	Missense Mutation	CEP192	p.W1465C	centrosomal protein 192	112 (0.00)	55 (0.42)	1.12

11-01	Gp3	g.chr18:13068230T>A	Missense Mutation	CEP192	p.D1584E	centrosomal protein 192	63 (0.00)	46 (0.37)	0.99
11-01	Gp3	g.chr18:13124664C>A	Missense Mutation	CEP192	p.F2503L	centrosomal protein 192	39 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr20:34095916G>T	Missense Mutation	CEP250	p.W2268L	centrosomal protein 250	128 (0.00)	76 (0.25)	0.67
11-01	Gp3	g.chr1:180064687G>T	Missense Mutation	CEP350	p.Q2847H	centrosomal protein 350	54 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr1:180064723C>A	Silent	CEP350	p.L2859L	centrosomal protein 350	57 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr1:26581800C>A	Missense Mutation	CEP85	p.S116Y	centrosomal protein 85k	59 (0.02)	32 (0.31)	0.83
11-01	Gp3	g.chr1:26581801T>A	Silent	CEP85	p.S116S	centrosomal protein 85k	59 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr3:101451367G>A	Silent	CEP97	p.Q199Q	centrosomal protein 97k	28 (0.00)	17 (0.59)	1.57
11-01	Gp3	g.chr3:101477067G>C	Missense Mutation	CEP97	p.M480I	centrosomal protein 97k	27 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr22:47116799C>T	Splice Site	CERK	p.V86I	ceramide kinase	57 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr1:196796101G>T	Silent	CFHR1	p.R132R	complement factor H-re	123 (0.00)	118 (0.15)	0.41
11-01	Gp3	g.chr4:110670441T>A	Missense Mutation	CFI	p.S369C	complement factor I	115 (0.01)	129 (0.30)	0.81
11-01	Gp3	g.chr7:117171127A>G	Missense Mutation	CFTR	p.M150V	cystic fibrosis transmem	57 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr15:57835915C>A	Missense Mutation	CGNL1	p.L1105I	cingulin-like 1	59 (0.00)	65 (0.17)	0.45
11-01	Gp3	g.chr2:27324720C>T	Missense Mutation	CGREF1	p.D127N	cell growth regulator wi	35 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr14:55005096C>T	Missense Mutation	CGRRF1	p.L332F	cell growth regulator wi	24 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr7:132659989G>A	Silent	CHCHD3	p.T103T	coiled-coil-helix-coiled-	52 (0.00)	54 (0.20)	0.54
11-01	Gp3	g.chr3:14157944C>T	Missense Mutation	CHCHD4	p.D35N	coiled-coil-helix-coiled-	59 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr5:98205314G>C	Intron	CHD1		chromodomain helicase	145 (0.00)	96 (0.18)	0.47
11-01	Gp3	g.chr5:98226816C>A	Intron	CHD1		chromodomain helicase	18 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr1:146763196G>A	Missense Mutation	CHD1L	p.V785I	chromodomain helicase	32 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr15:93467644G>A	Silent	CHD2	p.E52E	chromodomain helicase	37 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr15:93510722C>T	Missense Mutation	CHD2	p.A723V	chromodomain helicase	62 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr15:93522437G>A	Missense Mutation	CHD2	p.V934I	chromodomain helicase	38 (0.03)	27 (0.52)	1.38
11-01	Gp3	g.chr12:6707165C>G	Missense Mutation	CHD4	p.R593P	chromodomain helicase	126 (0.00)	74 (0.20)	0.54
11-01	Gp3	g.chr1:6175375A>G	Intron	CHD5		chromodomain helicase	21 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chr1:6186354C>G	Intron	CHD5		chromodomain helicase	32 (0.03)	68 (0.15)	0.39
11-01	Gp3	g.chr1:6186390C>G	Intron	CHD5		chromodomain helicase	31 (0.00)	59 (0.17)	0.45
11-01	Gp3	g.chr1:6235733C>A	Intron	CHD5		chromodomain helicase	69 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr20:40102131C>A	Missense Mutation	CHD6	p.R832L	chromodomain helicase	29 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr8:61734614C>T	Missense Mutation	CHD7	p.S956L	chromodomain helicase	59 (0.02)	30 (0.23)	0.62
11-01	Gp3	g.chr8:61764639G>C	Silent	CHD7	p.L1909L	chromodomain helicase	84 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr8:61765656C>G	Missense Mutation	CHD7	p.F2124L	chromodomain helicase	129 (0.00)	48 (0.35)	0.94
11-01	Gp3	g.chr14:21860964C>T	Missense Mutation	CHD8	p.R2158H	chromodomain helicase	55 (0.02)	47 (0.19)	0.51
11-01	Gp3	g.chr14:21884039G>A	Nonsense Mutation	CHD8	p.R582*	chromodomain helicase	54 (0.00)	40 (0.75)	2.00

11-01	Gp3	g.chr1:111777579C>A	Missense Mutation	CHI3L2	p.S127Y	chitinase 3-like 2	31 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr1:203192776C>A	Missense Mutation	CHIT1	p.M109I	chitinase 1 (chitotriosid	51 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr1:241797990G>C	Missense Mutation	CHML	p.T360S	choroideremia-like (Ra	61 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr2:86734627G>A	Silent	CHMP3	p.D166D	charged multivesicular	201 (0.00)	200 (0.23)	0.63
11-01	Gp3	g.chr2:86737506C>T	Missense Mutation	CHMP3	p.R128K	charged multivesicular	60 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr9:33270684C>T	Silent	CHMP5	p.T95T	charged multivesicular	60 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chrX:109937439C>A	Nonsense Mutation	CHRDL1	p.G244*	chordin-like 1	34 (0.00)	34 (0.24)	0.39
11-01	Gp3	g.chr15:34355527C>G	Nonsense Mutation	CHRM5	p.Y203*	cholinergic receptor, m	212 (0.00)	152 (0.14)	0.39
11-01	Gp3	g.chr2:175624242G>T	Missense Mutation	CHRNA1	p.L55M	cholinergic receptor, nic	45 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr15:78885499C>A	Missense Mutation	CHRNA3	p.R475L	cholinergic receptor, nic	27 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr20:61982280G>A	Silent	CHRNA4	p.C161C	cholinergic receptor, nic	28 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr4:40351257G>A	Missense Mutation	CHRNA9	p.V242I	cholinergic receptor, nic	46 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr4:40351271C>A	Silent	CHRNA9	p.I246I	cholinergic receptor, nic	47 (0.00)	38 (0.29)	0.77
11-01	Gp3	g.chr17:7350464C>G	Missense Mutation	CHRNB1	p.S80R	cholinergic receptor, nic	15 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr2:233404511G>T	Splice Site	CHRNG	p.L18L	cholinergic receptor, nic	18 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr2:233407749C>G	Silent	CHRNG	p.L254L	cholinergic receptor, nic	117 (0.00)	87 (0.16)	0.43
11-01	Gp3	g.chr11:45671739C>A	Missense Mutation	CHST1	p.E245D	carbohydrate (keratan s	20 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr3:142840889C>A	Missense Mutation	CHST2	p.Q411K	carbohydrate (N-acetylg	29 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr18:24497140C>T	Missense Mutation	CHST9	p.A139T	carbohydrate (N-acetylg	84 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr12:120295413C>T	Missense Mutation	CIT	p.E110K	citron rho-interacting se	161 (0.00)	130 (0.18)	0.47
11-01	Gp3	g.chr2:113513937G>A	Silent	CKAP2L	p.P337P	cytoskeleton associated	62 (0.00)	48 (0.27)	0.72
11-01	Gp3	g.chr2:122283460C>A	Silent	CLASP1	p.V169V	cytoplasmic linker asso	38 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr2:122286312C>A	Missense Mutation	CLASP1	p.V107L	cytoplasmic linker asso	84 (0.00)	66 (0.26)	0.69
11-01	Gp3	g.chr3:33661229G>A	Splice Site	CLASP2	p.H396Y	cytoplasmic linker asso	28 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr19:40225108A>G	Missense Mutation	CLC	p.F40L	Charcot-Leyden crystal	37 (0.00)	25 (0.72)	1.92
11-01	Gp3	g.chr1:86904648C>T	Silent	CLCA2	p.F354F	chloride channel access	54 (0.00)	41 (0.37)	0.98
11-01	Gp3	g.chr1:87038398C>A	Missense Mutation	CLCA4	p.L488I	chloride channel access	56 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:170628237G>A	Missense Mutation	CLCN3	p.V657I	chloride channel, voltag	70 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr1:11886239C>A	Silent	CLCN6	p.I225I	chloride channel, voltag	34 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr3:190026195C>T	Nonsense Mutation	CLDN1	p.W169*	claudin 1	16 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr13:96212430C>A	Missense Mutation	CLDN10	p.L89M	claudin 10	42 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr16:11071124C>T	Silent	CLEC16A	p.H257H	C-type lectin domain fa	30 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr7:139226835C>G	Missense Mutation	CLEC2L	p.H167Q	C-type lectin domain fa	31 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr12:8278257C>A	Missense Mutation	CLEC4A	p.F61L	C-type lectin domain fa	45 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr12:122826206C>T	Silent	CLIP1	p.L515L	CAP-GLY domain cont	67 (0.00)	33 (0.21)	0.57

11-01	Gp3	g.chr7:73814719C>T	Missense Mutation	CLIP2	p.S967L	CAP-GLY domain cont	67 (0.00)	122 (0.15)	0.39
11-01	Gp3	g.chr14:95677128C>A	Missense Mutation	CLMN	p.V233L	calmin (calponin-like, tr	45 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr11:57428845C>A	Silent	CLP1	p.A341A	cleavage and polyadeny	36 (0.00)	34 (0.38)	1.02
11-01	Gp3	g.chr15:65445948C>A	Missense Mutation	CLPX	p.L547F	caseinolytic mitochondr	84 (0.00)	69 (0.14)	0.39
11-01	Gp3	g.chr1:36203009C>A	Missense Mutation	CLSPN	p.M1226I	claspin	72 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr17:57760456G>A	Splice Site	CLTC	p.D1292N	clathrin, heavy chain (H	98 (0.00)	88 (0.16)	0.42
11-01	Gp3	g.chr22:19175514C>G	Silent	CLTCL1	p.L1471L	clathrin, heavy chain-lik	37 (0.00)	22 (0.41)	1.09
11-01	Gp3	g.chr22:19183825G>C	Missense Mutation	CLTCL1	p.H1381Q	clathrin, heavy chain-lik	90 (0.00)	65 (0.29)	0.78
11-01	Gp3	g.chr18:618053G>C	Missense Mutation	CLUL1	p.S43T	clusterin-like 1 (retinal)	92 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr6:25093936G>T	RNA	CMAHP		cytidine monophospho-	102 (0.00)	36 (0.31)	0.81
11-01	Gp3	g.chr2:7001437C>T	Silent	CMPK2	p.Q290Q	cytidine monophosphat	36 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr14:23847651C>T	Missense Mutation	CMTM5	p.L74F	CKLF-like MARVEL tr	22 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr6:37446206G>C	Missense Mutation	CMTR1	p.K725N	cap methyltransferase 1	97 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr5:79048582C>A	Nonsense Mutation	CMYA5	p.S3692*	cardiomyopathy associa	100 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chrX:150912804C>G	Missense Mutation	CNGA2	p.T610S	cyclic nucleotide gated	55 (0.00)	32 (0.28)	0.47
11-01	Gp3	g.chr2:99012317G>A	Silent	CNGA3	p.E232E	cyclic nucleotide gated	116 (0.00)	90 (0.21)	0.56
11-01	Gp3	g.chr16:57953128G>A	Missense Mutation	CNGB1	p.P611L	cyclic nucleotide gated	44 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr8:87588130C>T	Missense Mutation	CNGB3	p.G778R	cyclic nucleotide gated	102 (0.00)	91 (0.16)	0.55
11-01	Gp3	g.chr8:87638241G>T	Missense Mutation	CNGB3	p.F516L	cyclic nucleotide gated	42 (0.00)	45 (0.20)	0.67
11-01	Gp3	g.chrX:21444682G>T	Silent	CNKSR2	p.L44L	connector enhancer of k	24 (0.00)	16 (0.38)	0.62
11-01	Gp3	g.chr1:95367284G>A	Nonsense Mutation	CNN3	p.Q148*	calponin 3, acidic	22 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr10:101120600C>A	Silent	CNNM1	p.R576R	cyclin and CBS domain	101 (0.00)	56 (0.20)	0.52
11-01	Gp3	g.chr10:101122009C>A	Nonsense Mutation	CNNM1	p.Y628*	cyclin and CBS domain	88 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr2:97463272G>A	Silent	CNNM4	p.R523R	cyclin and CBS domain	25 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr5:154242887G>A	Missense Mutation	CNOT8	p.A17T	CCR4-NOT transcriptio	114 (0.00)	77 (0.22)	0.59
11-01	Gp3	g.chr1:205034367G>T	Missense Mutation	CNTN2	p.G558W	contactin 2 (axonal)	15 (0.00)	11 (0.73)	1.94
11-01	Gp3	g.chr3:74316479C>T	Missense Mutation	CNTN3	p.V919M	contactin 3 (plasmacyto	86 (0.01)	58 (0.17)	0.46
11-01	Gp3	g.chr3:74334540C>A	Missense Mutation	CNTN3	p.A874S	contactin 3 (plasmacyto	103 (0.00)	57 (0.19)	0.51
11-01	Gp3	g.chr3:2861217C>A	Silent	CNTN4	p.R136R	contactin 4	72 (0.00)	45 (0.27)	0.71
11-01	Gp3	g.chr3:3078963G>A	Silent	CNTN4	p.G681G	contactin 4	92 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr7:146818174G>C	Silent	CNTNAP2	p.R286R	contactin associated pro	74 (0.00)	58 (0.33)	0.87
11-01	Gp3	g.chr7:147336208G>A	Silent	CNTNAP2	p.V636V	contactin associated pro	110 (0.00)	44 (0.20)	0.55
11-01	Gp3	g.chr9:43737500C>T	Missense Mutation	CNTNAP3B	p.R124C	contactin associated pro	180 (0.01)	210 (0.16)	0.42
11-01	Gp3	g.chr2:124999946G>A	Silent	CNTNAP5	p.Q119Q	contactin associated pro	97 (0.01)	55 (0.16)	0.44
11-01	Gp3	g.chr2:124999961C>A	Missense Mutation	CNTNAP5	p.D124E	contactin associated pro	41 (0.00)	17 (0.53)	1.41

11-01	Gp3	g.chr9:123921226G>A	Missense Mutation	CNTRL	p.A1620T	centriolin	89 (0.00)	56 (0.39)	1.05
11-01	Gp3	g.chr17:7840021C>A	Silent	CNTROB	p.T238T	centrobin, centrosomal	163 (0.00)	77 (0.17)	0.45
11-01	Gp3	g.chr7:51095855G>A	Nonsense Mutation	COBL	p.Q980*	cordon-bleu WH2 repea	45 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr7:51096199C>A	Missense Mutation	COBL	p.S865I	cordon-bleu WH2 repea	31 (0.00)	17 (0.82)	2.20
11-01	Gp3	g.chr7:51098596C>T	Missense Mutation	COBL	p.A473T	cordon-bleu WH2 repea	65 (0.00)	41 (0.24)	0.65
11-01	Gp3	g.chr2:165578661G>A	Missense Mutation	COBLL1	p.P307L	cordon-bleu WH2 repea	24 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr1:230814681T>C	Missense Mutation	COG2	p.F350S	component of oligomeri	64 (0.00)	26 (0.27)	0.56
11-01	Gp3	g.chr1:230827230G>A	Missense Mutation	COG2	p.V679I	component of oligomeri	99 (0.00)	36 (0.25)	0.52
11-01	Gp3	g.chr16:70531264C>A	Missense Mutation	COG4	p.K447N	component of oligomeri	111 (0.00)	127 (0.36)	0.97
11-01	Gp3	g.chr13:40301647G>C	Missense Mutation	COG6	p.L596F	component of oligomeri	77 (0.00)	76 (0.17)	0.46
11-01	Gp3	g.chr9:101831985C>G	Missense Mutation	COL15A1	p.S1328R	collagen, type XV, alph	56 (0.00)	28 (0.71)	1.90
11-01	Gp3	g.chr10:105833004C>T	Splice Site	COL17A1		collagen, type XVII, alp	126 (0.00)	84 (0.19)	0.51
11-01	Gp3	g.chr6:55922502T>A	Missense Mutation	COL21A1	p.S943C	collagen, type XXI, alp	23 (0.00)	18 (0.50)	1.33
11-01	Gp3	g.chr1:86340349C>T	Missense Mutation	COL24A1	p.G1041R	collagen, type XXIV, al	32 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr1:86437030C>A	Missense Mutation	COL24A1	p.G804V	collagen, type XXIV, al	17 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr4:109820327C>A	Nonsense Mutation	COL25A1	p.G282*	collagen, type XXV, alp	33 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr9:116931134C>T	Silent	COL27A1	p.P433P	collagen, type XXVII, a	95 (0.00)	155 (0.19)	0.52
11-01	Gp3	g.chr9:116956683G>A	Splice Site	COL27A1		collagen, type XXVII, a	47 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr9:117002507C>A	Missense Mutation	COL27A1	p.P912Q	collagen, type XXVII, a	26 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr9:117072877G>C	Missense Mutation	COL27A1	p.D1829H	collagen, type XXVII, a	97 (0.00)	52 (0.21)	0.56
11-01	Gp3	g.chr7:7421216C>T	Missense Mutation	COL28A1	p.G722S	collagen, type XXVIII,	70 (0.00)	60 (0.20)	0.53
11-01	Gp3	g.chr12:48387801G>A	Silent	COL2A1	p.G282G	collagen, type II, alpha	80 (0.00)	55 (0.22)	0.58
11-01	Gp3	g.chr2:228131774C>T	Missense Mutation	COL4A3	p.P492S	collagen, type IV, alpha	26 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr2:227895216G>A	Missense Mutation	COL4A4	p.P1306S	collagen, type IV, alpha	22 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr2:227924185C>A	Missense Mutation	COL4A4	p.R773S	collagen, type IV, alpha	63 (0.00)	29 (0.41)	1.10
11-01	Gp3	g.chr2:227953503C>A	Nonsense Mutation	COL4A4	p.G497*	collagen, type IV, alpha	21 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr9:137619165C>T	Silent	COL5A1	p.Y236Y	collagen, type V, alpha	61 (0.02)	59 (0.15)	0.41
11-01	Gp3	g.chr19:10087929C>G	Silent	COL5A3	p.G1088G	collagen, type V, alpha	38 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr2:238274467G>A	Silent	COL6A3	p.D1904D	collagen, type VI, alpha	21 (0.00)	35 (0.40)	1.07
11-01	Gp3	g.chr3:130292975G>T	Missense Mutation	COL6A6	p.E1051D	collagen, type VI, alpha	110 (0.00)	62 (0.39)	1.03
11-01	Gp3	g.chr3:130345357G>A	Missense Mutation	COL6A6	p.G1636E	collagen, type VI, alpha	80 (0.00)	86 (0.48)	1.27
11-01	Gp3	g.chr1:183938450C>G	Missense Mutation	COLGALT2	p.W262S	collagen beta(1-O)galac	73 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr3:15507887G>T	Missense Mutation	COLQ	p.Q259K	collagen-like tail subuni	63 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr11:36300113G>T	Silent	COMMD9	p.S35S	COMM domain contain	68 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr1:160262331G>A	Missense Mutation	COPA	p.T968I	coatomer protein compl	44 (0.00)	28 (0.21)	0.57

11-01	Gp3	g.chr1:160278907G>A	Silent	COPA	p.D401D	coatomer protein compl	21 (0.00)	46 (0.46)	1.22
11-01	Gp3	g.chr11:14501150C>A	Missense Mutation	COPB1	p.K441N	coatomer protein compl	74 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr3:139077930G>T	Missense Mutation	COPB2	p.F798L	coatomer protein compl	75 (0.01)	23 (0.22)	0.58
11-01	Gp3	g.chr3:128976576C>A	Missense Mutation	COPG1	p.D248E	coatomer protein compl	224 (0.00)	97 (0.20)	0.52
11-01	Gp3	g.chr7:99688883G>A	Silent	COPS6	p.Q224Q	COP9 signalosome subu	70 (0.00)	38 (0.29)	0.77
11-01	Gp3	g.chr12:109041269T>A	Missense Mutation	CORO1C	p.L445F	coronin, actin binding p	39 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr16:85834879C>A	Missense Mutation	COX4I1	p.A23D	cytochrome c oxidase su	54 (0.00)	10 (0.60)	1.27
11-01	Gp3	g.chr16:85839458C>A	Missense Mutation	COX4I1	p.Q121K	cytochrome c oxidase su	21 (0.00)	16 (0.38)	0.79
11-01	Gp3	g.chr7:129951900C>T	Missense Mutation	CPA4	p.A339V	carboxypeptidase A4	38 (0.00)	48 (0.31)	0.83
11-01	Gp3	g.chr7:129962438C>T	Silent	CPA4	p.N396N	carboxypeptidase A4	97 (0.00)	58 (0.16)	0.41
11-01	Gp3	g.chr17:28782378C>T	Missense Mutation	CPD	p.T1076I	carboxypeptidase D	77 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr4:166414409C>T	Silent	CPE	p.H400H	carboxypeptidase E	63 (0.02)	42 (0.19)	0.51
11-01	Gp3	g.chr5:173317310C>T	Nonsense Mutation	CPEB4	p.Q192*	cytoplasmic polyadenyla	94 (0.00)	60 (0.23)	0.62
11-01	Gp3	g.chr7:120764427C>T	Nonsense Mutation	CPED1	p.Q321*	cadherin-like and PC-es	59 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr3:131283194C>A	Splice Site	CPNE4		copine IV	24 (0.00)	13 (0.62)	1.64
11-01	Gp3	g.chr3:9768853G>A	Missense Mutation	CPNE9	p.E487K	copine family member I	104 (0.00)	59 (0.25)	0.68
11-01	Gp3	g.chr2:207833941G>T	Silent	CPO	p.G302G	carboxypeptidase O	88 (0.00)	58 (0.17)	0.46
11-01	Gp3	g.chr8:97847274G>A	Silent	CPQ	p.K169K	carboxypeptidase Q	45 (0.00)	73 (0.15)	0.50
11-01	Gp3	g.chr1:207758101C>T	Missense Mutation	CR1	p.P1804S	complement component	74 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr1:207641919C>T	Missense Mutation	CR2	p.H165Y	complement component	66 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr16:1709991C>T	Silent	CRAMP1L	p.P780P	Crm, cramped-like (Dro	18 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr1:197297729C>T	Missense Mutation	CRB1	p.A83V	crumbs family member	35 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr1:197446835C>G	Silent	CRB1	p.G1237G	crumbs family member	41 (0.00)	21 (0.52)	1.40
11-01	Gp3	g.chr2:208434980C>G	Nonsense Mutation	CREB1	p.S147*	cAMP responsive eleme	86 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr16:3830801G>A	Silent	CREBBP	p.S585S	CREB binding protein	35 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr7:30706898C>A	Silent	CRHR2	p.G87G	corticotropin releasing h	24 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr6:49704148G>A	Silent	CRISP3	p.L62L	cysteine-rich secretory p	64 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr17:29119518G>A	Missense Mutation	CRLF3	p.S300L	cytokine receptor-like fa	78 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr3:97596740G>A	Silent	CRYBG3	p.K286K	beta-gamma crystallin d	17 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr2:209007394C>T	Missense Mutation	CRYGB	p.G166S	crystallin, gamma B	43 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr2:209010671G>A	Nonsense Mutation	CRYGB	p.Q27*	crystallin, gamma B	37 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr13:20978847C>A	Missense Mutation	CRYL1	p.G258V	crystallin, lambda 1	91 (0.00)	47 (0.23)	0.62
11-01	Gp3	g.chr1:110466301C>G	Nonsense Mutation	CSF1	p.S353*	colony stimulating facto	90 (0.00)	70 (0.16)	0.42
11-01	Gp3	g.chr22:37334401C>G	Missense Mutation	CSF2RB	p.L851V	colony stimulating facto	45 (0.00)	84 (0.15)	0.41
11-01	Gp3	g.chr10:43659488G>A	Silent	CSGALNACT	p.E385E	chondroitin sulfate N-ac	67 (0.00)	52 (0.23)	0.62

11-01	Gp3	g.chr8:2818715G>T	Missense Mutation	CSMD1	p.P3218Q	CUB and Sushi multiple	69 (0.00)	18 (0.28)	0.41
11-01	Gp3	g.chr1:34003114G>T	Missense Mutation	CSMD2	p.P3243T	CUB and Sushi multiple	31 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr1:34090173G>A	Silent	CSMD2	p.L730L	CUB and Sushi multiple	20 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr8:113332153G>A	Missense Mutation	CSMD3	p.T2408M	CUB and Sushi multiple	68 (0.01)	17 (0.47)	1.25
11-01	Gp3	g.chr8:113518976G>A	Silent	CSMD3	p.D1613D	CUB and Sushi multiple	71 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr4:70810573C>T	Silent	CSN1S1	p.F136F	casein alpha s1	144 (0.00)	117 (0.32)	0.84
11-01	Gp3	g.chr12:51458038G>A	Missense Mutation	CSRNP2	p.L375F	cysteine-serine-rich nuc	53 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr2:166532891G>A	Missense Mutation	CSRNP3	p.D192N	cysteine-serine-rich nuc	188 (0.00)	96 (0.27)	0.72
11-01	Gp3	g.chr3:122060367G>T	Nonsense Mutation	CSTA	p.G84*	cystatin A (stefin A)	40 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr20:54970777G>A	Splice Site	CSTF1	p.G57R	cleavage stimulation fac	71 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr20:54974152G>C	Missense Mutation	CSTF1	p.D259H	cleavage stimulation fac	47 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr5:134678987G>A	Missense Mutation	CTC-349C3.1	p.S90N		73 (0.00)	39 (0.33)	0.89
11-01	Gp3	g.chr19:22869250T>A	RNA	CTC-457E21.9			32 (0.00)	54 (0.24)	0.64
11-01	Gp3	g.chr15:81962787C>A	lincRNA	CTD-2034I4.2			15 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr1:227598522G>A	lincRNA	CTD-2090I13.1			25 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr19:50562849C>T	RNA	CTD-2126E3.1			44 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr17:37214269C>A	RNA	CTD-2206N4.4			42 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr19:51671119C>T	RNA	CTD-3187F8.14			33 (0.00)	35 (0.74)	1.98
11-01	Gp3	g.chr19:51671126C>T	RNA	CTD-3187F8.14			30 (0.00)	34 (0.71)	1.88
11-01	Gp3	g.chr18:46238063G>A	Missense Mutation	CTIF	p.R194Q	CBP80/20-dependent tra	127 (0.01)	110 (0.15)	0.41
11-01	Gp3	g.chr2:204735548C>T	Nonsense Mutation	CTLA4	p.Q117*	cytotoxic T-lymphocyte	86 (0.01)	78 (0.22)	0.58
11-01	Gp3	g.chr20:36365783G>A	Missense Mutation	CTNNBL1	p.E75K	catenin, beta like 1	29 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr11:57569469C>G	Silent	CTNND1	p.L407L	catenin (cadherin-associ	82 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr5:11732381G>A	Missense Mutation	CTNND2	p.A14V	catenin (cadherin-associ	63 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr17:3561388G>A	Silent	CTNS	p.V257V	cystinosin, lysosomal cy	18 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr1:41471750C>T	Missense Mutation	CTPS1	p.T427M	CTP synthase 1	20 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chrX:16685675C>A	Missense Mutation	CTPS2	p.D420Y	CTP synthase 2	21 (0.00)	25 (0.92)	1.53
11-01	Gp3	g.chr16:67964635G>T	Silent	CTRL	p.V104V	chymotrypsin-like	18 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr11:88033767G>T	Missense Mutation	CTSC	p.H230N	cathepsin C	49 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr9:90401753G>A	RNA	CTSL3P		cathepsin L family mem	43 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr9:90401773C>G	RNA	CTSL3P		cathepsin L family mem	45 (0.00)	35 (0.26)	0.69
11-01	Gp3	g.chr1:112999793G>C	Missense Mutation	CTTNBP2NL	p.S560T	CTTNBP2 N-terminal li	101 (0.00)	66 (0.21)	0.57
11-01	Gp3	g.chr10:16989269G>A	Silent	CUBN	p.V1769V	cubilin (intrinsic factor-	34 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr10:17164841C>G	Missense Mutation	CUBN	p.L182F	cubilin (intrinsic factor-	30 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr10:104184105G>A	Silent	CUEDC2	p.I109I	CUE domain containing	52 (0.00)	76 (0.14)	0.39

11-01	Gp3	g.chr7:148489836G>A	Missense Mutation	CUL1	p.A609T	cullin 1	20 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr13:113909419C>G	Missense Mutation	CUL4A	p.Q671E	cullin 4A	18 (0.00)	17 (0.41)	1.10
11-01	Gp3	g.chr6:43018062G>A	Silent	CUL7	p.D436D	cullin 7	15 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr6:43167034G>A	Silent	CUL9	p.E1027E	cullin 9	155 (0.01)	117 (0.19)	0.50
11-01	Gp3	g.chr10:101993052C>T	Missense Mutation	CWF19L1	p.D232N	CWF19-like 1, cell cycl	53 (0.02)	32 (0.50)	1.33
11-01	Gp3	g.chr4:49019310C>A	Silent	CWH43	p.R384R	cell wall biogenesis 43 (	61 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr3:39307715C>A	Missense Mutation	CX3CR1	p.G96C	chemokine (C-X3-C mo	34 (0.00)	25 (0.44)	1.17
11-01	Gp3	g.chrX:45013232C>A	Missense Mutation	CXorf36	p.G295V	chromosome X open rea	52 (0.00)	22 (0.27)	0.45
11-01	Gp3	g.chr11:7690541G>T	Missense Mutation	CYB5R2	p.Q95K	cytochrome b5 reductas	32 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr11:7690542G>T	Silent	CYB5R2	p.P94P	cytochrome b5 reductas	32 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr6:84644355G>T	Missense Mutation	CYB5R4	p.V286F	cytochrome b5 reductas	90 (0.00)	49 (0.24)	0.65
11-01	Gp3	g.chr15:22939178C>T	Missense Mutation	CYFIP1	p.L302F	cytoplasmic FMR1 inte	41 (0.00)	24 (0.42)	1.11
11-01	Gp3	g.chr5:156760428G>T	Nonsense Mutation	CYFIP2	p.E761*	cytoplasmic FMR1 inte	46 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr5:156768127C>A	Missense Mutation	CYFIP2	p.P853T	cytoplasmic FMR1 inte	25 (0.00)	36 (0.22)	0.59
11-01	Gp3	g.chr16:50815165G>A	Silent	CYLD	p.E506E	cylindromatosis (turban	76 (0.00)	58 (0.19)	0.51
11-01	Gp3	g.chr15:74659804G>T	Silent	CYP11A1	p.S41S	cytochrome P450, famil	22 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr15:51514629G>A	Missense Mutation	CYP19A1	p.S182L	cytochrome P450, famil	88 (0.00)	46 (0.33)	0.87
11-01	Gp3	g.chr2:204131355C>G	Missense Mutation	CYP20A1	p.T184R	cytochrome P450, famil	100 (0.00)	125 (0.17)	0.45
11-01	Gp3	g.chr2:72360239G>A	Silent	CYP26B1	p.Y162Y	cytochrome P450, famil	17 (0.00)	22 (0.36)	0.55
11-01	Gp3	g.chr19:41597700G>A	Missense Mutation	CYP2A13	p.E240K	cytochrome P450, famil	87 (0.00)	86 (0.19)	0.50
11-01	Gp3	g.chr19:41384694T>A	Missense Mutation	CYP2A7	p.I268F	cytochrome P450, famil	26 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr19:41497274C>T	Missense Mutation	CYP2B6	p.R22C	cytochrome P450, famil	90 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr10:96698447C>T	Missense Mutation	CYP2C9	p.S3F	cytochrome P450, famil	161 (0.00)	89 (0.20)	0.54
11-01	Gp3	g.chr10:96698472C>T	Silent	CYP2C9	p.L11L	cytochrome P450, famil	148 (0.00)	79 (0.25)	0.68
11-01	Gp3	g.chr1:60359411G>T	Missense Mutation	CYP2J2	p.P474Q	cytochrome P450, famil	98 (0.00)	72 (0.22)	0.59
11-01	Gp3	g.chr7:99359716G>T	Missense Mutation	CYP3A4	p.L401I	cytochrome P450, famil	61 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr7:99359833C>A	Nonsense Mutation	CYP3A4	p.E362*	cytochrome P450, famil	45 (0.02)	23 (0.39)	1.04
11-01	Gp3	g.chr7:99375696C>T	Missense Mutation	CYP3A4	p.C58Y	cytochrome P450, famil	67 (0.01)	51 (0.24)	0.63
11-01	Gp3	g.chr7:99247735G>A	Silent	CYP3A5	p.V458V	cytochrome P450, famil	108 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr7:99306836C>A	Missense Mutation	CYP3A7	p.V359L	cytochrome P450, famil	44 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr4:5018692C>T	Splice Site	CYTL1		cytokine-like 1	67 (0.00)	60 (0.33)	0.89
11-01	Gp3	g.chr6:39835308C>T	Silent	DAAM2	p.L151L	dishevelled associated a	164 (0.00)	92 (0.17)	0.46
11-01	Gp3	g.chr1:57602244C>A	Missense Mutation	DAB1	p.G93V	Dab, reelin signal transd	35 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr5:39377119C>A	Missense Mutation	DAB2	p.L590F	Dab, mitogen-responsiv	75 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr9:124338691C>T	Intron	DAB2IP		DAB2 interacting protei	197 (0.00)	150 (0.15)	0.41

11-01	Gp3	g.chr9:124341496G>T	Intron	DAB2IP		DAB2 interacting protei	144 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr9:124368924G>A	Intron	DAB2IP		DAB2 interacting protei	43 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr9:124380271C>T	Intron	DAB2IP		DAB2 interacting protei	83 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr9:124381391C>A	Intron	DAB2IP		DAB2 interacting protei	191 (0.01)	128 (0.30)	0.81
11-01	Gp3	g.chr9:124382316C>G	Intron	DAB2IP		DAB2 interacting protei	46 (0.00)	37 (0.76)	2.02
11-01	Gp3	g.chr9:124390321G>A	Intron	DAB2IP		DAB2 interacting protei	36 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr9:124395612C>A	Intron	DAB2IP		DAB2 interacting protei	42 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr9:124405956C>T	Intron	DAB2IP		DAB2 interacting protei	59 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr9:124413239C>T	Intron	DAB2IP		DAB2 interacting protei	99 (0.00)	94 (0.28)	0.74
11-01	Gp3	g.chr9:124422620G>T	Intron	DAB2IP		DAB2 interacting protei	52 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr9:124432161G>T	Intron	DAB2IP		DAB2 interacting protei	84 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr9:124440786G>A	Intron	DAB2IP		DAB2 interacting protei	90 (0.00)	104 (0.26)	0.69
11-01	Gp3	g.chr9:124441780G>A	Intron	DAB2IP		DAB2 interacting protei	68 (0.00)	61 (0.26)	0.70
11-01	Gp3	g.chr9:124454033G>T	Intron	DAB2IP		DAB2 interacting protei	40 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr9:124456526C>T	Intron	DAB2IP		DAB2 interacting protei	57 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr9:124475337G>T	Intron	DAB2IP		DAB2 interacting protei	51 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr9:124475365C>T	Intron	DAB2IP		DAB2 interacting protei	41 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr9:124478145G>A	Intron	DAB2IP		DAB2 interacting protei	68 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr9:124479041C>G	Intron	DAB2IP		DAB2 interacting protei	33 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr9:124499317G>A	Intron	DAB2IP		DAB2 interacting protei	36 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr9:124501467C>T	Intron	DAB2IP		DAB2 interacting protei	83 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr9:124509314G>A	Intron	DAB2IP		DAB2 interacting protei	60 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr9:124509326G>C	Intron	DAB2IP		DAB2 interacting protei	58 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr9:124510250G>C	Intron	DAB2IP		DAB2 interacting protei	148 (0.01)	67 (0.15)	0.40
11-01	Gp3	g.chr9:124521760C>T	Intron	DAB2IP		DAB2 interacting protei	50 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr9:124540184G>A	Intron	DAB2IP		DAB2 interacting protei	259 (0.00)	236 (0.15)	0.40
11-01	Gp3	g.chr1:173794378C>A	Missense Mutation	DARS2	p.P4H	aspartyl-tRNA syntheta	53 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr1:173826789C>A	Silent	DARS2	p.P628P	aspartyl-tRNA syntheta	46 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr17:42825720C>T	Missense Mutation	DBF4B	p.S359F	DBF4 zinc finger B	48 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr5:176894328G>T	Silent	DBN1	p.T161T	drebrin 1	16 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr1:100672026G>A	Missense Mutation	DBT	p.T395I	dihydrolipoamide branc	76 (0.00)	62 (0.15)	0.39
11-01	Gp3	g.chr8:104453792C>A	Missense Mutation	DCAF13	p.S551Y	DDB1 and CUL4 associ	55 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr19:14071165C>G	Silent	DCAF15	p.V531V	DDB1 and CUL4 associ	22 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr14:73425428T>C	Missense Mutation	DCAF4	p.F298S	DDB1 and CUL4 associ	25 (0.00)	34 (0.35)	0.94
11-01	Gp3	g.chr8:88885570C>A	Missense Mutation	DCAF4L2	p.L210F	DDB1 and CUL4 associ	27 (0.00)	25 (0.20)	0.67

11-01	Gp3	g.chr3:98568381G>A	Silent	DCBLD2	p.I165I	discoidin, CUB and LC	117 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr11:6652320G>A	Silent	DCHS1	p.S1298S	dachsous cadherin-relat	25 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr4:155254155G>T	Missense Mutation	DCHS2	p.L570M	dachsous cadherin-relat	70 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr4:155256214G>A	Missense Mutation	DCHS2	p.T341I	dachsous cadherin-relat	55 (0.00)	50 (0.24)	0.64
11-01	Gp3	g.chr10:115601320C>A	Splice Site	DCLRE1A		DNA cross-link repair 1	43 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr12:91539999C>T	Missense Mutation	DCN	p.V306I	decorin	38 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr13:95117913G>C	Missense Mutation	DCT	p.F279L	dopachrome tautomeras	18 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr11:108577527C>T	Nonsense Mutation	DDX10	p.Q429*	DEAD (Asp-Glu-Ala-A	53 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr12:31255454C>A	Missense Mutation	DDX11	p.L789I	DEAD/H (Asp-Glu-Ala	70 (0.00)	46 (0.52)	1.39
11-01	Gp3	g.chr16:70363866C>A	Silent	DDX19B	p.T306T	DEAD (Asp-Glu-Ala-A	42 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr1:112303197C>A	Missense Mutation	DDX20	p.Q223K	DEAD (Asp-Glu-Ala-A	60 (0.02)	56 (0.18)	0.48
11-01	Gp3	g.chr10:70728752A>C	Missense Mutation	DDX21	p.T371P	DEAD (Asp-Glu-Ala-A	25 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chrX:134714066G>T	Nonsense Mutation	DDX26B	p.E788*	DEAD/H (Asp-Glu-Ala	45 (0.00)	15 (0.40)	0.67
11-01	Gp3	g.chr16:68056263G>T	Silent	DDX28	p.S281S	DEAD (Asp-Glu-Ala-A	46 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr5:55075872G>A	Missense Mutation	DDX4	p.G159R	DEAD (Asp-Glu-Ala-A	62 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr5:134120216G>A	Missense Mutation	DDX46	p.G443R	DEAD (Asp-Glu-Ala-A	98 (0.00)	122 (0.17)	0.46
11-01	Gp3	g.chr10:70666761G>A	Missense Mutation	DDX50	p.E128K	DEAD (Asp-Glu-Ala-A	34 (0.03)	23 (0.39)	1.04
11-01	Gp3	g.chr10:70706381G>A	Missense Mutation	DDX50	p.D737N	DEAD (Asp-Glu-Ala-A	65 (0.00)	48 (0.35)	0.94
11-01	Gp3	g.chrX:23019372G>C	Missense Mutation	DDX53	p.D400H	DEAD (Asp-Glu-Ala-A	47 (0.00)	12 (0.67)	1.11
11-01	Gp3	g.chr4:169195233C>T	Splice Site	DDX60	p.R769Q	DEAD (Asp-Glu-Ala-A	18 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr1:161093938C>A	Missense Mutation	DEDD	p.R105S	death effector domain c	20 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr6:35280141G>T	Silent	DEF6	p.L162L	differentially expressed	22 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr6:35280153G>T	Silent	DEF6	p.L166L	differentially expressed	24 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:140302030C>A	Missense Mutation	DENND2A	p.K56N	DENN/MADD domain	49 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr1:153903016T>A	Splice Site	DENND4B	p.I1448I	DENN/MADD domain	62 (0.02)	31 (0.32)	0.86
11-01	Gp3	g.chr9:19300313C>A	Missense Mutation	DENND4C	p.A432D	DENN/MADD domain	32 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr12:31555468C>T	Missense Mutation	DENND5B	p.M971I	DENN/MADD domain	92 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr12:31568306G>A	Silent	DENND5B	p.D849D	DENN/MADD domain	21 (0.00)	14 (0.79)	2.10
11-01	Gp3	g.chr12:123247426G>A	Missense Mutation	DENR	p.R54K	density-regulated protei	22 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr8:120940804G>T	Missense Mutation	DEPTOR	p.G96V	DEP domain containing	48 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr1:244849944C>T	Missense Mutation	DESI2	p.H30Y	desumoylating isopepti	57 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr12:56330808C>T	Silent	DGKA	p.T24T	diacylglycerol kinase, al	53 (0.00)	56 (0.25)	0.67
11-01	Gp3	g.chr7:14217750C>G	Missense Mutation	DGKB	p.V718L	diacylglycerol kinase, b	76 (0.00)	92 (0.24)	0.64
11-01	Gp3	g.chr11:46400006G>C	Splice Site	DGKZ		diacylglycerol kinase, z	48 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr1:55340858C>T	Missense Mutation	DHCR24	p.E174K	24-dehydrocholesterol r	29 (0.00)	29 (0.21)	0.55

11-01	Gp3	g.chr14:24766019G>C	Missense Mutation	DHRS1	p.S73R	dehydrogenase/reductas	46 (0.00)	59 (0.22)	0.59
11-01	Gp3	g.chr17:9680562G>T	Silent	DHRS7C	p.I173I	dehydrogenase/reductas	42 (0.00)	65 (0.28)	0.74
11-01	Gp3	g.chr17:9683329C>A	Silent	DHRS7C	p.L97L	dehydrogenase/reductas	29 (0.00)	54 (0.26)	0.69
11-01	Gp3	g.chr2:169939948C>T	Silent	DHRS9	p.L141L	dehydrogenase/reductas	44 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr10:12123535C>T	Silent	DHTKD1	p.I73I	dehydrogenase E1 and t	60 (0.00)	50 (0.24)	0.64
11-01	Gp3	g.chr10:12139862C>T	Missense Mutation	DHTKD1	p.A513V	dehydrogenase E1 and t	33 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr19:47858437G>T	Nonsense Mutation	DHX34	p.E283*	DEAH (Asp-Glu-Ala-H	30 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr20:37597835G>A	Missense Mutation	DHX35	p.R51K	DEAH (Asp-Glu-Ala-H	62 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr17:41582079G>T	Missense Mutation	DHX8	p.W538C	DEAH (Asp-Glu-Ala-H	61 (0.00)	28 (0.39)	1.05
11-01	Gp3	g.chr1:210010291C>A	Missense Mutation	DIEXF	p.S266Y	digestive organ expansi	61 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr12:51090857C>G	Silent	DIP2B	p.S649S	DIP2 disco-interacting	71 (0.00)	59 (0.15)	0.41
11-01	Gp3	g.chr12:51127925C>T	Missense Mutation	DIP2B	p.S1330L	DIP2 disco-interacting	61 (0.00)	59 (0.27)	0.72
11-01	Gp3	g.chr10:408515C>A	Silent	DIP2C	p.L903L	DIP2 disco-interacting	43 (0.00)	21 (0.52)	1.40
11-01	Gp3	g.chr19:2717707C>A	Missense Mutation	DIRAS1	p.R33L	DIRAS family, GTP-bir	18 (0.00)	36 (0.19)	0.64
11-01	Gp3	g.chr2:189599393C>G	Missense Mutation	DIRC1	p.R85S	disrupted in renal carcin	40 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr3:122598218C>A	Missense Mutation	DIRC2	p.S477Y	disrupted in renal carcin	23 (0.00)	17 (0.41)	1.10
11-01	Gp3	g.chr1:223178570C>G	Nonsense Mutation	DISP1	p.Y1277*	dispatched homolog 1 (	94 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chrX:153993728C>A	Missense Mutation	DKC1	p.H32N	dyskeratosis congenita	122 (0.00)	26 (0.50)	0.83
11-01	Gp3	g.chr3:38126801G>C	Missense Mutation	DLEC1	p.G433A	deleted in lung and esop	81 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chrX:69720395C>A	Silent	DLG3	p.A772A	discs, large homolog 3 (	16 (0.00)	26 (0.23)	0.38
11-01	Gp3	g.chrX:69720401C>A	Missense Mutation	DLG3	p.F774L	discs, large homolog 3 (	16 (0.00)	26 (0.73)	1.22
11-01	Gp3	g.chr17:7096417C>A	Silent	DLG4	p.R568R	discs, large homolog 4 (	177 (0.00)	158 (0.15)	0.41
11-01	Gp3	g.chr17:7122168T>C	Start Codon SNP	DLG4	p.M1V	discs, large homolog 4 (	50 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr10:79569407G>A	Silent	DLG5	p.H1515H	discs, large homolog 5 (	103 (0.00)	67 (0.37)	1.00
11-01	Gp3	g.chr6:170597853C>A	Missense Mutation	DLL1	p.A126S	delta-like 1 (Drosophila	26 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr10:124399664C>A	Missense Mutation	DMBT1	p.Q2222K	deleted in malignant bra	92 (0.00)	92 (0.18)	0.49
11-01	Gp3	g.chr22:38962647C>T	Missense Mutation	DMC1	p.G64E	DNA meiotic recombina	47 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chrX:31227700G>C	Missense Mutation	DMD	p.R3160G	dystrophin	24 (0.00)	43 (0.35)	0.58
11-01	Gp3	g.chrX:32407728G>A	Missense Mutation	DMD	p.R1470C	dystrophin	35 (0.00)	35 (0.23)	0.38
11-01	Gp3	g.chr19:36001275C>T	Missense Mutation	DMKN	p.E19K	dermokine	37 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr5:118469514G>A	Missense Mutation	DMXL1	p.R632K	Dmx-like 1	68 (0.00)	36 (0.25)	0.67
11-01	Gp3	g.chr5:118485228C>A	Missense Mutation	DMXL1	p.H1236N	Dmx-like 1	78 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr5:118485528C>T	Missense Mutation	DMXL1	p.L1336F	Dmx-like 1	55 (0.00)	51 (0.16)	0.42
11-01	Gp3	g.chr12:124298369T>C	Silent	DNAH10	p.I1112I	dynein, axonemal, heav	84 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr12:124358188C>A	Silent	DNAH10	p.T2505T	dynein, axonemal, heav	23 (0.00)	23 (0.83)	2.20

11-01	Gp3	g.chr12:124364340C>G	Missense Mutation	DNAH10	p.L2758V	dynein, axonemal, heav	169 (0.00)	78 (0.31)	0.82
11-01	Gp3	g.chr7:21695529G>A	Missense Mutation	DNAH11	p.R1675K	dynein, axonemal, heav	117 (0.00)	92 (0.15)	0.41
11-01	Gp3	g.chr1:225506331C>T	Missense Mutation	DNAH14	p.A2350V	dynein, axonemal, heav	64 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr17:76475696C>G	Missense Mutation	DNAH17	p.A2586P	dynein, axonemal, heav	59 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr17:7695593G>A	Silent	DNAH2	p.V2359V	dynein, axonemal, heav	22 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr16:20963789C>A	Missense Mutation	DNAH3	p.K3718N	dynein, axonemal, heav	43 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr5:13776583C>T	Nonsense Mutation	DNAH5	p.W3113*	dynein, axonemal, heav	56 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr5:13845029C>A	Missense Mutation	DNAH5	p.G1730W	dynein, axonemal, heav	63 (0.00)	50 (0.18)	0.48
11-01	Gp3	g.chr2:196636586G>A	Missense Mutation	DNAH7	p.S3744L	dynein, axonemal, heav	131 (0.00)	103 (0.32)	0.85
11-01	Gp3	g.chr2:196664151C>A	Missense Mutation	DNAH7	p.A3408S	dynein, axonemal, heav	31 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr2:196728985C>A	Missense Mutation	DNAH7	p.C2465F	dynein, axonemal, heav	45 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr2:196765016C>A	Missense Mutation	DNAH7	p.G1513V	dynein, axonemal, heav	106 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr6:38749040C>T	Missense Mutation	DNAH8	p.S500F	dynein, axonemal, heav	84 (0.01)	44 (0.45)	1.21
11-01	Gp3	g.chr17:11806083G>T	Missense Mutation	DNAH9	p.E3818D	dynein, axonemal, heav	48 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr9:34485212C>A	Missense Mutation	DNAI1	p.P52T	dynein, axonemal, inter	99 (0.00)	146 (0.23)	0.60
11-01	Gp3	g.chr16:46990969C>T	Missense Mutation	DNAJA2	p.G404E	DnaJ (Hsp40) homolog,	165 (0.00)	109 (0.17)	0.46
11-01	Gp3	g.chr16:46998611T>A	Missense Mutation	DNAJA2	p.Q229L	DnaJ (Hsp40) homolog,	123 (0.00)	95 (0.19)	0.51
11-01	Gp3	g.chr16:4484519G>C	Splice Site	DNAJA3		DnaJ (Hsp40) homolog,	152 (0.00)	99 (0.25)	0.67
11-01	Gp3	g.chr19:14626916C>T	Missense Mutation	DNAJB1	p.D287N	DnaJ (Hsp40) homolog,	56 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr19:14626955G>A	Missense Mutation	DNAJB1	p.P274S	DnaJ (Hsp40) homolog,	59 (0.00)	60 (0.18)	0.49
11-01	Gp3	g.chr1:6705160C>A	Silent	DNAJC11	p.L307L	DnaJ (Hsp40) homolog,	54 (0.00)	63 (0.17)	0.47
11-01	Gp3	g.chr1:6714023C>T	Missense Mutation	DNAJC11	p.S152N	DnaJ (Hsp40) homolog,	85 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr1:6714046C>T	Silent	DNAJC11	p.E144E	DnaJ (Hsp40) homolog,	66 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr3:132218618C>T	Missense Mutation	DNAJC13	p.T1461I	DnaJ (Hsp40) homolog,	56 (0.00)	83 (0.42)	1.12
11-01	Gp3	g.chr1:15888765A>G	Missense Mutation	DNAJC16	p.Q428R	DnaJ (Hsp40) homolog,	61 (0.00)	17 (0.41)	1.10
11-01	Gp3	g.chr5:34945012G>A	Missense Mutation	DNAJC21	p.V342M	DnaJ (Hsp40) homolog,	282 (0.00)	155 (0.14)	0.38
11-01	Gp3	g.chr12:49745186C>T	Silent	DNAJC22	p.N309N	DnaJ (Hsp40) homolog,	40 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr2:25170513C>T	Missense Mutation	DNAJC27	p.R265Q	DnaJ (Hsp40) homolog,	66 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr1:65849886C>A	Missense Mutation	DNAJC6	p.A226E	DnaJ (Hsp40) homolog,	47 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr17:40134275G>A	Missense Mutation	DNAJC7	p.P410L	DnaJ (Hsp40) homolog,	28 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr1:84867762G>A	Splice Site	DNASE2B		deoxyribonuclease II be	93 (0.00)	73 (0.33)	0.88
11-01	Gp3	g.chr11:6567813G>A	Missense Mutation	DNHD1	p.E1882K	dynein heavy chain dom	32 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr11:6591267C>T	Nonsense Mutation	DNHD1	p.Q4298*	dynein heavy chain dom	51 (0.00)	28 (0.50)	1.33
11-01	Gp3	g.chr1:172001610C>A	Missense Mutation	DNM3	p.L220I	dynamin 3	204 (0.00)	88 (0.39)	1.03
11-01	Gp3	g.chr10:101657967C>T	Silent	DNMBP	p.L932L	dynamin binding protei	57 (0.00)	50 (0.22)	0.59

11-01	Gp3	g.chr10:101715472C>A	Missense Mutation	DNMBP	p.D587Y	dynamin binding protei	63 (0.00)	55 (0.16)	0.44
11-01	Gp3	g.chr19:10270737G>A	Missense Mutation	DNMT1	p.T333M	DNA (cytosine-5-)-metl	27 (0.00)	19 (0.79)	2.11
11-01	Gp3	g.chr2:25463207G>A	Silent	DNMT3A	p.G539G	DNA (cytosine-5-)-metl	74 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr20:44430086C>A	Missense Mutation	DNTTIP1	p.L163I	deoxynucleotidyltransfe	64 (0.00)	53 (0.21)	0.55
11-01	Gp3	g.chr16:30020398C>G	Missense Mutation	DOC2A	p.R149T	double C2-like domains	42 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr10:128798511C>T	Silent	DOCK1	p.L309L	dedicator of cytokinesis	63 (0.00)	60 (0.17)	0.44
11-01	Gp3	g.chrX:117742300C>A	Nonsense Mutation	DOCK11	p.S953*	dedicator of cytokinesis	21 (0.00)	19 (0.42)	0.70
11-01	Gp3	g.chr3:51183992G>C	Silent	DOCK3	p.L253L	dedicator of cytokinesis	84 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chr3:51315161C>A	Nonsense Mutation	DOCK3	p.C933*	dedicator of cytokinesis	34 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr7:111644172G>A	Nonsense Mutation	DOCK4	p.R18*	dedicator of cytokinesis	36 (0.00)	15 (0.80)	2.13
11-01	Gp3	g.chr9:131708059C>T	Silent	DOLK	p.G508G	dolichol kinase	59 (0.02)	55 (0.15)	0.39
11-01	Gp3	g.chr9:131708498G>A	Missense Mutation	DOLK	p.A362V	dolichol kinase	121 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr6:83841908C>G	Missense Mutation	DOPEY1	p.T877R	dopey family member 1	72 (0.00)	62 (0.26)	0.69
11-01	Gp3	g.chr6:83865763C>T	Missense Mutation	DOPEY1	p.A2182V	dopey family member 1	39 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr6:83866998A>G	Silent	DOPEY1	p.Q2234Q	dopey family member 1	43 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr21:37642428G>A	Missense Mutation	DOPEY2	p.E1869K	dopey family member 2	156 (0.00)	105 (0.14)	0.38
11-01	Gp3	g.chr11:118967933G>A	Silent	DPAGT1	p.N360N	dolichyl-phosphate (UD	107 (0.00)	107 (0.21)	0.55
11-01	Gp3	g.chr11:118971377C>A	Missense Mutation	DPAGT1	p.K153N	dolichyl-phosphate (UD	33 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr16:89704074C>T	Silent	DPEP1	p.A296A	dipeptidase 1 (renal)	39 (0.03)	19 (0.26)	0.70
11-01	Gp3	g.chr16:68025758G>A	Silent	DPEP2	p.H215H	dipeptidase 2	39 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr3:109028157C>A	Nonsense Mutation	DPPA2	p.E68*	developmental pluripote	45 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr1:98058829C>T	Missense Mutation	DPYD	p.R358H	dihydropyrimidine dehy	96 (0.00)	77 (0.22)	0.59
11-01	Gp3	g.chr8:26435782G>A	Silent	DPYSL2	p.Q4Q	dihydropyrimidinase-lik	46 (0.00)	40 (0.53)	0.78
11-01	Gp3	g.chr8:26501061C>T	Silent	DPYSL2	p.P306P	dihydropyrimidinase-lik	23 (0.00)	12 (0.50)	0.75
11-01	Gp3	g.chr2:26644211C>A	Missense Mutation	DRC1	p.A100D	dynein regulatory comp	44 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr2:26653657G>A	Missense Mutation	DRC1	p.A228T	dynein regulatory comp	90 (0.00)	53 (0.19)	0.50
11-01	Gp3	g.chr4:9784956G>A	Missense Mutation	DRD5	p.D435N	dopamine receptor D5	50 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr5:31526740C>A	Silent	DROSHA	p.P100P	drosha, ribonuclease typ	19 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr18:28711715G>C	Missense Mutation	DSC1	p.Q777E	desmocollin 1	44 (0.00)	65 (0.20)	0.53
11-01	Gp3	g.chr18:28736067G>A	Missense Mutation	DSC1	p.A137V	desmocollin 1	44 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr18:28737474T>G	Missense Mutation	DSC1	p.I71L	desmocollin 1	28 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr11:117340684G>A	Missense Mutation	DSCAML1	p.P1049L	Down syndrome cell adl	43 (0.02)	21 (0.24)	0.63
11-01	Gp3	g.chr11:117403108G>T	Missense Mutation	DSCAML1	p.A274E	Down syndrome cell adl	20 (0.05)	19 (0.53)	1.40
11-01	Gp3	g.chr6:7571645G>C	Missense Mutation	DSP	p.M577I	desmoplakin	88 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr6:7583061G>T	Nonsense Mutation	DSP	p.E1856*	desmoplakin	67 (0.01)	71 (0.25)	0.68

11-01	Gp3	g.chr6:56422189T>C	Silent	DST	p.E4645E	dystonin	18 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr6:56464922G>A	Missense Mutation	DST	p.A3669V	dystonin	74 (0.00)	40 (0.45)	1.20
11-01	Gp3	g.chr6:56468411G>A	Missense Mutation	DST	p.S3420F	dystonin	158 (0.00)	109 (0.28)	0.76
11-01	Gp3	g.chr12:58001386G>A	Missense Mutation	DTX3	p.G247D	deltex 3, E3 ubiquitin li	51 (0.00)	57 (0.19)	0.51
11-01	Gp3	g.chr11:58959625C>T	Nonsense Mutation	DTX4	p.Q426*	deltex 4, E3 ubiquitin li	79 (0.00)	58 (0.29)	0.78
11-01	Gp3	g.chr15:45400349C>A	Silent	DUOX2	p.L490L	dual oxidase 2	38 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr1:161723007G>A	Missense Mutation	DUSP12	p.V273I	dual specificity phospha	31 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr6:348108C>A	Missense Mutation	DUSP22	p.A90D	dual specificity phospha	49 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr14:102469137C>T	Missense Mutation	DYNC1H1	p.T1573I	dynein, cytoplasmic 1, h	52 (0.00)	50 (0.20)	0.53
11-01	Gp3	g.chr14:102493587G>A	Missense Mutation	DYNC1H1	p.V2950I	dynein, cytoplasmic 1, h	128 (0.01)	40 (0.15)	0.40
11-01	Gp3	g.chr14:102507948C>A	Silent	DYNC1H1	p.I3993I	dynein, cytoplasmic 1, h	24 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr7:95616462C>G	Missense Mutation	DYNC1I1	p.L297V	dynein, cytoplasmic 1, i	98 (0.00)	67 (0.36)	0.96
11-01	Gp3	g.chr7:95665064G>A	Splice Site	DYNC1I1	p.S472N	dynein, cytoplasmic 1, i	87 (0.00)	64 (0.19)	0.50
11-01	Gp3	g.chr11:103004414G>T	Missense Mutation	DYNC2H1	p.W695L	dynein, cytoplasmic 2, h	121 (0.00)	49 (0.33)	0.87
11-01	Gp3	g.chr1:206822002C>T	Silent	DYRK3	p.L487L	dual-specificity tyrosine	131 (0.00)	59 (0.15)	0.41
11-01	Gp3	g.chr13:96274690G>T	Missense Mutation	DZIP1	p.N339K	DAZ interacting zinc fir	113 (0.00)	144 (0.18)	0.48
11-01	Gp3	g.chr12:77449762C>A	Missense Mutation	E2F7	p.W81L	E2F transcription factor	37 (0.03)	56 (0.32)	0.86
11-01	Gp3	g.chr10:131646681G>A	Missense Mutation	EBF3	p.P368L	early B-cell factor 3	24 (0.00)	25 (0.52)	1.39
11-01	Gp3	g.chr1:43632895C>T	Silent	EBNA1BP2	p.E183E	EBNA1 binding protein	71 (0.00)	58 (0.17)	0.46
11-01	Gp3	g.chr3:172520714C>T	Missense Mutation	ECT2	p.H653Y	epithelial cell transform	50 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr6:139164224C>G	Missense Mutation	ECT2L	p.H151D	epithelial cell transform	28 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr6:139164240C>T	Missense Mutation	ECT2L	p.T156I	epithelial cell transform	31 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr1:236645568G>A	Splice Site	EDARADD	p.E79E	EDAR-associated death	53 (0.00)	32 (0.28)	0.53
11-01	Gp3	g.chr15:74963984C>A	Missense Mutation	EDC3	p.G99V	enhancer of mRNA deca	40 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr20:33714069G>C	Nonsense Mutation	EDEM2	p.Y318*	ER degradation enhance	54 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr5:83402480C>T	Nonsense Mutation	EDIL3	p.W213*	EGF-like repeats and dis	42 (0.00)	34 (0.38)	1.02
11-01	Gp3	g.chr12:93173007C>A	Missense Mutation	EEA1	p.D1180Y	early endosome antigen	38 (0.03)	33 (0.58)	1.54
11-01	Gp3	g.chr13:32527498C>G	RNA	EEF1DP3		eukaryotic translation el	44 (0.02)	47 (0.17)	0.45
11-01	Gp3	g.chr11:62338459G>C	Missense Mutation	EEF1G	p.T167S	eukaryotic translation el	163 (0.00)	99 (0.16)	0.43
11-01	Gp3	g.chr19:3982406C>T	Missense Mutation	EEF2	p.G210D	eukaryotic translation el	27 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr22:44063077C>G	Missense Mutation	EFCAB6	p.K630N	EF-hand calcium bindin	117 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr3:19921152C>A	Missense Mutation	EFHB	p.D695Y	EF-hand domain family,	29 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr3:19921185T>C	Missense Mutation	EFHB	p.I684V	EF-hand domain family,	29 (0.00)	15 (0.67)	1.78
11-01	Gp3	g.chr1:15752440C>T	Nonsense Mutation	EFHD2	p.Q128*	EF-hand domain family,	37 (0.00)	29 (0.34)	0.92
11-01	Gp3	g.chr1:155057672G>A	Silent	EFNA3	p.G73G	ephrin-A3	37 (0.00)	49 (0.14)	0.38

11-01	Gp3	g.chr8:132980611C>A	Silent	EFR3A	p.R309R	EFR3 homolog A (S. ce	154 (0.01)	89 (0.17)	0.45
11-01	Gp3	g.chr14:23829031G>T	Missense Mutation	EFS	p.A219D	embryonal Fyn-associat	24 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr17:42959076G>A	Silent	EFTUD2	p.D169D	elongation factor Tu GT	37 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr4:110890220C>G	Missense Mutation	EGF	p.P515A	epidermal growth factor	108 (0.00)	61 (0.28)	0.74
11-01	Gp3	g.chrX:13651103G>A	Splice Site	EGFL6		EGF-like-domain, multi	77 (0.00)	42 (0.40)	0.67
11-01	Gp3	g.chr5:38427253G>A	Silent	EGFLAM	p.L651L	EGF-like, fibronectin ty	50 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr2:62934395C>A	Silent	EHBP1	p.S23S	EH domain binding prot	80 (0.00)	37 (0.27)	0.72
11-01	Gp3	g.chr2:62934407C>A	Silent	EHBP1	p.L27L	EH domain binding prot	61 (0.00)	28 (0.36)	0.95
11-01	Gp3	g.chr9:140622973C>T	Missense Mutation	EHMT1	p.S272L	euchromatic histone-lys	42 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr19:40023077C>T	Silent	EID2B	p.V122V	EP300 interacting inhibi	17 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr15:40259908C>A	Missense Mutation	EIF2AK4	p.Q461K	eukaryotic translation in	54 (0.00)	56 (0.34)	0.90
11-01	Gp3	g.chr15:40293216C>T	Missense Mutation	EIF2AK4	p.H984Y	eukaryotic translation in	114 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr14:67843258T>A	Missense Mutation	EIF2S1	p.Y142N	eukaryotic translation in	31 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr20:32693214G>A	Silent	EIF2S2	p.D51D	eukaryotic translation in	21 (0.00)	33 (0.58)	1.54
11-01	Gp3	g.chr12:10659637G>T	Missense Mutation	EIF2S3L	p.R379I		80 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr10:120825038G>A	Missense Mutation	EIF3A	p.T332I	eukaryotic translation in	30 (0.00)	23 (0.39)	1.04
11-01	Gp3	g.chr7:2400484G>T	Missense Mutation	EIF3B	p.K213N	eukaryotic translation in	48 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr16:28734799G>A	Missense Mutation	EIF3C	p.E323K	eukaryotic translation in	180 (0.01)	55 (0.15)	0.39
11-01	Gp3	g.chr8:117668163G>A	Silent	EIF3H	p.V227V	eukaryotic translation in	48 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr15:44846829G>A	Missense Mutation	EIF3J	p.E125K	eukaryotic translation in	55 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr3:184039368C>T	Silent	EIF4G1	p.S245S	eukaryotic translation in	36 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr3:184043688C>T	Silent	EIF4G1	p.I970I	eukaryotic translation in	47 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr11:10820590C>A	Missense Mutation	EIF4G2	p.W869C	eukaryotic translation in	74 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr11:10820591C>A	Missense Mutation	EIF4G2	p.W869L	eukaryotic translation in	72 (0.00)	44 (0.20)	0.55
11-01	Gp3	g.chr7:73609092G>T	Missense Mutation	EIF4H	p.G164V	eukaryotic translation in	56 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr13:41507662G>A	Nonsense Mutation	ELF1	p.Q587*	E74-like factor 1 (ets do	91 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr5:95242361G>C	Missense Mutation	ELL2	p.Q203E	elongation factor, RNA	107 (0.00)	101 (0.23)	0.61
11-01	Gp3	g.chr7:37253022G>A	Missense Mutation	ELMO1	p.A291V	engulfment and cell mot	16 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr7:73474292G>A	Silent	ELN	p.L497L	elastin	22 (0.00)	40 (0.28)	0.73
11-01	Gp3	g.chr10:103988958C>T	Silent	ELOVL3	p.F254F	ELOVL fatty acid elong	56 (0.00)	69 (0.20)	0.54
11-01	Gp3	g.chr14:89093181C>T	Splice Site	EML5		echinoderm microtubule	50 (0.00)	31 (0.39)	1.03
11-01	Gp3	g.chr14:89153569C>A	Nonsense Mutation	EML5	p.G949*	echinoderm microtubule	58 (0.00)	29 (0.48)	1.29
11-01	Gp3	g.chr2:55056593G>A	Missense Mutation	EML6	p.E276K	echinoderm microtubule	44 (0.00)	27 (0.41)	1.09
11-01	Gp3	g.chr2:55143971G>A	Missense Mutation	EML6	p.D1192N	echinoderm microtubule	50 (0.00)	23 (0.74)	1.97
11-01	Gp3	g.chr2:55189679C>A	Silent	EML6	p.T1663T	echinoderm microtubule	29 (0.00)	22 (0.32)	0.85

11-01	Gp3	g.chr1:225706957C>A	Nonsense Mutation	ENAH	p.E268*	enabled homolog (Dros	127 (0.01)	111 (0.30)	0.79
11-01	Gp3	g.chr4:71508264C>A	Missense Mutation	ENAM	p.P374Q	enamelin	65 (0.00)	31 (0.39)	1.03
11-01	Gp3	g.chr5:73930813C>A	Missense Mutation	ENC1	p.D427Y	ectodermal-neural corte	121 (0.00)	81 (0.16)	0.43
11-01	Gp3	g.chr5:73930863C>T	Missense Mutation	ENC1	p.R410H	ectodermal-neural corte	76 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr9:130605455G>A	Missense Mutation	ENG	p.T46I	endoglin	37 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr9:130605511T>A	Silent	ENG	p.T27T	endoglin	32 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr12:7028861C>A	Missense Mutation	ENO2	p.P148T	enolase 2 (gamma, neur	32 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr6:46129364C>A	Missense Mutation	ENPP5	p.C378F	ectonucleotide pyrophos	65 (0.00)	36 (0.44)	1.19
11-01	Gp3	g.chr14:74440651C>A	Missense Mutation	ENTPD5	p.C272F	ectonucleoside triphosp	19 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr22:41569667A>T	Missense Mutation	EP300	p.N1553I	E1A binding protein p3	40 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr22:41569703G>T	Missense Mutation	EP300	p.R1565M	E1A binding protein p3	55 (0.02)	53 (0.17)	0.45
11-01	Gp3	g.chr22:41569744G>A	Missense Mutation	EP300	p.D1579N	E1A binding protein p3	54 (0.00)	76 (0.14)	0.39
11-01	Gp3	g.chr12:132474647C>A	Missense Mutation	EP400	p.Q850K	E1A binding protein p4	132 (0.00)	89 (0.22)	0.60
11-01	Gp3	g.chr1:29424320C>A	Splice Site	EPB41	p.P729H	erythrocyte membrane p	33 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr20:34765969C>T	Silent	EPB41L1	p.D146D	erythrocyte membrane p	53 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr20:34800270C>T	Missense Mutation	EPB41L1	p.T719I	erythrocyte membrane p	57 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr18:5407734G>A	Splice Site	EPB41L3	p.S708L	erythrocyte membrane p	25 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr15:43503612A>T	Splice Site	EPB42		erythrocyte membrane p	28 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr10:32575769G>A	Splice Site	EPC1	p.P415L	enhancer of polycomb h	34 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr18:43497747C>T	Missense Mutation	EPG5	p.G1046R	ectopic P-granules auto	89 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chr3:89499503C>G	Missense Mutation	EPHA3	p.I891M	EPH receptor A3	73 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr2:222294743G>T	Silent	EPHA4	p.V875V	EPH receptor A4	59 (0.00)	53 (0.25)	0.65
11-01	Gp3	g.chr3:96962983T>A	Missense Mutation	EPHA6	p.H486Q	EPH receptor A6	120 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr6:94068009C>A	Missense Mutation	EPHA7	p.R318M	EPH receptor A7	79 (0.00)	46 (0.39)	0.62
11-01	Gp3	g.chr1:92511122G>A	Nonsense Mutation	EPHX4	p.W170*	epoxide hydrolase 4	94 (0.00)	52 (0.29)	0.77
11-01	Gp3	g.chr17:48614050G>T	Missense Mutation	EPN3	p.D45Y	epsin 3	23 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr1:220153478G>A	Silent	EPRS	p.D1220D	glutamyl-prolyl-tRNA s	86 (0.00)	102 (0.22)	0.58
11-01	Gp3	g.chr2:26590072C>A	Missense Mutation	EPT1	p.F98L	ethanolaminephosphotr	75 (0.00)	88 (0.19)	0.52
11-01	Gp3	g.chr17:56276960C>A	Missense Mutation	EPX	p.L448M	eosinophil peroxidase	62 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr17:27184975G>A	Missense Mutation	ERAL1	p.G170S	Era-like 12S mitochond	73 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr5:96228073G>T	Silent	ERAP2	p.T347T	endoplasmic reticulum	49 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr17:37883113C>T	Missense Mutation	ERBB2	p.R1006C	v-erb-b2 avian erythrob	46 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr12:56489522T>C	Missense Mutation	ERBB3	p.F663L	v-erb-b2 avian erythrob	61 (0.00)	104 (0.16)	0.44
11-01	Gp3	g.chr2:212288940C>T	Missense Mutation	ERBB4	p.G936R	v-erb-b2 avian erythrob	28 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr16:14020486C>A	Missense Mutation	ERCC4	p.R153S	excision repair cross-co	47 (0.00)	64 (0.16)	0.42

11-01	Gp3	g.chr10:50724167C>A	Missense Mutation	ERCC6-PGBD	p.V800F	ERCC6-PGBD3 readthr	36 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr21:39764199C>T	Intron	ERG		v-ets avian erythroblast	43 (0.00)	51 (0.16)	0.42
11-01	Gp3	g.chr21:39764703C>A	Intron	ERG		v-ets avian erythroblast	52 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr21:39786077T>A	Intron	ERG		v-ets avian erythroblast	84 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr21:39786981C>A	Intron	ERG		v-ets avian erythroblast	94 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr21:39791180G>A	Intron	ERG		v-ets avian erythroblast	60 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr21:39795958C>T	Intron	ERG		v-ets avian erythroblast	58 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr21:39809690T>A	Intron	ERG		v-ets avian erythroblast	104 (0.00)	92 (0.21)	0.55
11-01	Gp3	g.chr21:39828788C>A	Intron	ERG		v-ets avian erythroblast	53 (0.00)	50 (0.28)	0.75
11-01	Gp3	g.chr21:39837524G>C	Intron	ERG		v-ets avian erythroblast	15 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr21:39846893C>A	Intron	ERG		v-ets avian erythroblast	83 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr21:39850483C>G	Intron	ERG		v-ets avian erythroblast	75 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr21:39895293C>T	Intron	ERG		v-ets avian erythroblast	41 (0.00)	14 (0.71)	0.81
11-01	Gp3	g.chr21:39983506G>A	Intron	ERG		v-ets avian erythroblast	98 (0.00)	94 (0.44)	0.50
11-01	Gp3	g.chr21:39997450C>A	Intron	ERG		v-ets avian erythroblast	72 (0.00)	14 (0.57)	0.65
11-01	Gp3	g.chr21:40014991A>T	Intron	ERG		v-ets avian erythroblast	117 (0.00)	37 (0.35)	0.40
11-01	Gp3	g.chr21:40019201C>G	Intron	ERG		v-ets avian erythroblast	71 (0.00)	18 (0.33)	0.38
11-01	Gp3	g.chr1:44687268G>A	Nonsense Mutation	ERI3	p.R326*	ERI1 exoribonuclease f	30 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr7:64453300C>T	Silent	ERV3-1	p.T35T	endogenous retrovirus g	64 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr6:11104920C>A	Silent	ERVFRD-1	p.R208R	endogenous retrovirus g	60 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr3:138187699C>G	Silent	ESYT3	p.A470A	extended synaptotagmin	114 (0.00)	69 (0.14)	0.39
11-01	Gp3	g.chr3:138189862G>A	Silent	ESYT3	p.V578V	extended synaptotagmin	55 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr1:93160923G>T	Missense Mutation	EVI5	p.L329I	ecotropic viral integrati	78 (0.00)	87 (0.20)	0.52
11-01	Gp3	g.chr17:74004276C>A	Missense Mutation	EVPL	p.E1670D	envoplakin	28 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr22:29692283G>A	Missense Mutation	EWSR1	p.G412R	EWS RNA-binding prot	56 (0.00)	51 (0.43)	0.69
11-01	Gp3	g.chr15:41482158C>G	Missense Mutation	EXD1	p.A345P	exonuclease 3'-5' domai	39 (0.00)	71 (0.15)	0.41
11-01	Gp3	g.chr15:41482279C>G	Silent	EXD1	p.L304L	exonuclease 3'-5' domai	34 (0.03)	29 (0.31)	0.83
11-01	Gp3	g.chr6:486749G>A	Silent	EXOC2	p.L899L	exocyst complex compo	80 (0.00)	63 (0.32)	0.85
11-01	Gp3	g.chr7:133689666G>A	Splice Site	EXOC4	p.V784I	exocyst complex compo	36 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr7:133749271C>A	Missense Mutation	EXOC4	p.T972N	exocyst complex compo	83 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr14:57676467G>C	Missense Mutation	EXOC5	p.Q586E	exocyst complex compo	72 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr2:72945249C>T	Missense Mutation	EXOC6B	p.E218K	exocyst complex compo	72 (0.00)	57 (0.26)	0.40
11-01	Gp3	g.chr1:231471790G>A	Missense Mutation	EXOC8	p.H564Y	exocyst complex compo	49 (0.00)	37 (0.24)	0.50
11-01	Gp3	g.chr3:38542937G>T	Silent	EXOG	p.G85G	endo/exonuclease (5'-3')	26 (0.00)	41 (0.24)	0.65
11-01	Gp3	g.chr10:99197027G>A	Silent	EXOSC1	p.S134S	exosome component 1	25 (0.00)	13 (0.38)	1.03

11-01	Gp3	g.chr1:11129788C>A	Splice Site	EXOSC10		exosome component 10	40 (0.00)	61 (0.38)	1.01
11-01	Gp3	g.chr9:37783940C>T	Missense Mutation	EXOSC3	p.A149T	exosome component 3	105 (0.00)	47 (0.26)	0.39
11-01	Gp3	g.chr3:45038655C>T	Missense Mutation	EXOSC7	p.R111W	exosome component 7	37 (0.00)	64 (0.50)	1.33
11-01	Gp3	g.chr11:108382224C>A	Missense Mutation	EXPH5	p.R1337M	exophilin 5	57 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr11:108383794G>T	Missense Mutation	EXPH5	p.Q814K	exophilin 5	61 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr11:44193165G>C	Missense Mutation	EXT2	p.R393P	exostosin glycosyltransf	47 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr11:44219484C>T	Missense Mutation	EXT2	p.R471W	exostosin glycosyltransf	36 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr11:44219504C>T	Silent	EXT2	p.S477S	exostosin glycosyltransf	47 (0.00)	49 (0.20)	0.54
11-01	Gp3	g.chr1:101342383G>A	Silent	EXTL2	p.T157T	exostosin-like glycosylt	96 (0.00)	45 (0.27)	0.71
11-01	Gp3	g.chr1:28319954C>A	Silent	EYA3	p.R420R	EYA transcriptional coa	24 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr6:66205171G>T	Missense Mutation	EYS	p.L45I	eyes shut homolog (Dro	115 (0.00)	71 (0.14)	0.38
11-01	Gp3	g.chr7:148512620G>C	Missense Mutation	EZH2	p.C508W	enhancer of zeste 2 poly	54 (0.00)	59 (0.17)	0.45
11-01	Gp3	g.chr5:76029110C>A	Missense Mutation	F2R	p.L354I	coagulation factor II (th	59 (0.00)	48 (0.25)	0.67
11-01	Gp3	g.chr5:75914401G>A	Missense Mutation	F2RL2	p.P22L	coagulation factor II (th	65 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr2:88425713C>A	Missense Mutation	FABP1	p.M74I	fatty acid binding protei	92 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr5:159656588G>A	Silent	FABP6	p.E8E	fatty acid binding protei	95 (0.00)	79 (0.19)	0.51
11-01	Gp3	g.chr8:82373740C>A	Nonsense Mutation	FABP9	p.G7*	fatty acid binding protei	47 (0.02)	24 (0.29)	0.97
11-01	Gp3	g.chr6:170627546T>A	Nonsense Mutation	FAM120B	p.C356*	family with sequence si	92 (0.00)	87 (0.18)	0.49
11-01	Gp3	g.chrX:54117822G>A	Missense Mutation	FAM120C	p.R784C	family with sequence si	19 (0.00)	41 (0.51)	0.85
11-01	Gp3	g.chr13:51854790G>C	Missense Mutation	FAM124A	p.A347P	family with sequence si	32 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr13:51854803C>G	Missense Mutation	FAM124A	p.P351R	family with sequence si	40 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr2:201862207G>A	Missense Mutation	FAM126B	p.P196L	family with sequence si	17 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr1:184859260G>A	Missense Mutation	FAM129A	p.H139Y	family with sequence si	113 (0.00)	67 (0.21)	0.56
11-01	Gp3	g.chr2:220043714G>T	Missense Mutation	FAM134A	p.D118Y	family with sequence si	59 (0.00)	30 (0.37)	0.98
11-01	Gp3	g.chr5:16475174C>A	Silent	FAM134B	p.T249T	family with sequence si	40 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr17:40738798C>T	Silent	FAM134C	p.K163K	family with sequence si	60 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr4:89653185G>A	Silent	FAM13A	p.D937D	family with sequence si	55 (0.00)	38 (0.42)	1.12
11-01	Gp3	g.chr10:61083806G>A	Missense Mutation	FAM13C	p.H129Y	family with sequence si	55 (0.00)	52 (0.33)	0.87
11-01	Gp3	g.chr4:187088396C>A	Missense Mutation	FAM149A	p.T452K	family with sequence si	49 (0.00)	28 (0.29)	0.76
11-01	Gp3	g.chr13:108518248C>A	Nonsense Mutation	FAM155A	p.E233*	family with sequence si	19 (0.00)	27 (0.78)	2.07
11-01	Gp3	g.chr10:116602841G>A	Silent	FAM160B1	p.L224L	family with sequence si	114 (0.01)	60 (0.18)	0.49
11-01	Gp3	g.chr8:21956798G>A	Missense Mutation	FAM160B2	p.V360I	family with sequence si	28 (0.00)	25 (0.72)	1.07
11-01	Gp3	g.chr2:62065707C>A	Missense Mutation	FAM161A	p.A573S	family with sequence si	24 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr1:179783273C>A	Silent	FAM163A	p.G151G	family with sequence si	85 (0.00)	92 (0.14)	0.38
11-01	Gp3	g.chr10:15255020G>C	Missense Mutation	FAM171A1	p.A856G	family with sequence si	118 (0.00)	62 (0.16)	0.43

11-01	Gp3	g.chr6:119345170C>A	Missense Mutation	FAM184A	p.C203F	family with sequence si	60 (0.00)	21 (0.43)	0.66
11-01	Gp3	g.chr10:128936223G>A	Missense Mutation	FAM196A	p.P440S	family with sequence si	85 (0.00)	28 (0.36)	0.95
11-01	Gp3	g.chr10:128974605C>T	Missense Mutation	FAM196A	p.E19K	family with sequence si	29 (0.00)	70 (0.53)	1.41
11-01	Gp3	g.chr4:159052012A>T	Silent	FAM198B	p.V426V	family with sequence si	23 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr3:68587949G>A	Missense Mutation	FAM19A1	p.C101Y	family with sequence si	103 (0.00)	82 (0.18)	0.49
11-01	Gp3	g.chr9:34726829G>A	Silent	FAM205A	p.S136S	family with sequence si	36 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr9:34835782C>A	RNA	FAM205B		family with sequence si	117 (0.00)	71 (0.25)	0.68
11-01	Gp3	g.chr10:5799546G>A	Missense Mutation	FAM208B	p.G2266R	family with sequence si	96 (0.00)	79 (0.23)	0.61
11-01	Gp3	g.chr18:13671970C>A	Missense Mutation	FAM210A	p.G159V	family with sequence si	88 (0.00)	54 (0.19)	0.49
11-01	Gp3	g.chr3:49841925C>T	Silent	FAM212A	p.P123P	family with sequence si	32 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr20:58519289C>G	Silent	FAM217B	p.L97L	family with sequence si	61 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr2:24406211G>C	Missense Mutation	FAM228A	p.E74Q	family with sequence si	75 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr6:116833356C>T	Missense Mutation	FAM26E	p.T166I	family with sequence si	43 (0.00)	19 (0.84)	1.31
11-01	Gp3	g.chr7:121011355C>T	Splice Site	FAM3C	p.V91I	family with sequence si	27 (0.00)	11 (0.82)	2.18
11-01	Gp3	g.chr6:24875943C>G	Missense Mutation	FAM65B	p.S26T	family with sequence si	88 (0.00)	66 (0.21)	0.57
11-01	Gp3	g.chr20:49209612G>A	Silent	FAM65C	p.V774V	family with sequence si	83 (0.00)	59 (0.20)	0.54
11-01	Gp3	g.chr8:11986063C>T	RNA	FAM66D		family with sequence si	154 (0.01)	38 (0.32)	0.47
11-01	Gp3	g.chr1:93309107G>T	Missense Mutation	FAM69A	p.L374I	family with sequence si	84 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr18:72113869T>C	Missense Mutation	FAM69C	p.E283G	family with sequence si	37 (0.00)	23 (0.39)	1.04
11-01	Gp3	g.chr6:54805935G>A	Silent	FAM83B	p.E722E	family with sequence si	52 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr20:33874555C>T	Missense Mutation	FAM83C	p.G676D	family with sequence si	44 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr20:33874600C>T	Missense Mutation	FAM83C	p.R661H	family with sequence si	20 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr20:37580315C>G	Missense Mutation	FAM83D	p.H334D	family with sequence si	123 (0.00)	92 (0.17)	0.46
11-01	Gp3	g.chr11:67564291G>A	RNA	FAM86C2P		family with sequence si	75 (0.00)	74 (0.16)	0.43
11-01	Gp3	g.chr3:75476963C>G	RNA	FAM86DP		family with sequence si	57 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr12:8376747C>A	Missense Mutation	FAM90A1	p.C63F	family with sequence si	93 (0.00)	80 (0.16)	0.43
11-01	Gp3	g.chr9:35078600A>T	Splice Site	FANCG		Fanconi anemia, comple	29 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr9:35078627C>A	Missense Mutation	FANCG	p.Q94H	Fanconi anemia, comple	27 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr15:89849279G>T	Nonsense Mutation	FANCI	p.E1131*	Fanconi anemia, comple	65 (0.00)	48 (0.25)	0.67
11-01	Gp3	g.chr10:127685183G>A	Missense Mutation	FANK1	p.G149R	fibronectin type III and	100 (0.00)	54 (0.22)	0.59
11-01	Gp3	g.chr2:163031454G>A	Missense Mutation	FAP	p.S631L	fibroblast activation pro	57 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr2:242380806C>T	Missense Mutation	FARP2	p.P416S	FERM, RhoGEF and pl	29 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr5:7867160T>A	Missense Mutation	FASTKD3	p.H346L	FAST kinase domains 3	56 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr4:187524720C>T	Missense Mutation	FAT1	p.E3654K	FAT atypical cadherin 1	77 (0.00)	56 (0.18)	0.48
11-01	Gp3	g.chr4:187532632G>T	Missense Mutation	FAT1	p.A3254E	FAT atypical cadherin 1	122 (0.00)	36 (0.17)	0.44

11-01	Gp3	g.chr4:187538347G>T	Missense Mutation	FAT1	p.P2963T	FAT atypical cadherin 1	86 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr4:187627754G>T	Silent	FAT1	p.G1076G	FAT atypical cadherin 1	59 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr11:92088031C>G	Nonsense Mutation	FAT3	p.S768*	FAT atypical cadherin 3	208 (0.00)	95 (0.24)	0.65
11-01	Gp3	g.chr11:92523109G>A	Splice Site	FAT3	p.V1296I	FAT atypical cadherin 3	66 (0.00)	51 (0.18)	0.47
11-01	Gp3	g.chr11:92568145C>T	Silent	FAT3	p.V3177V	FAT atypical cadherin 3	69 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr4:126329650G>A	Missense Mutation	FAT4	p.G1874E	FAT atypical cadherin 4	45 (0.00)	62 (0.16)	0.43
11-01	Gp3	g.chr4:126336801C>T	Missense Mutation	FAT4	p.T2228I	FAT atypical cadherin 4	47 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr4:126373542C>A	Missense Mutation	FAT4	p.L3791I	FAT atypical cadherin 4	59 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr6:99771429C>T	Silent	FAXC	p.T238T	failed axon connections	44 (0.00)	11 (0.45)	0.71
11-01	Gp3	g.chr17:73922445C>A	Missense Mutation	FBF1	p.D206Y	Fas (TNFRSF6) binding	40 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr15:48703488C>T	Missense Mutation	FBN1	p.S2772N	fibrillin 1	124 (0.00)	91 (0.15)	0.41
11-01	Gp3	g.chr15:48704809C>T	Missense Mutation	FBN1	p.R2728K	fibrillin 1	42 (0.00)	23 (0.57)	1.51
11-01	Gp3	g.chr15:48704920C>T	Missense Mutation	FBN1	p.G2691D	fibrillin 1	79 (0.00)	44 (0.57)	1.52
11-01	Gp3	g.chr15:48707842C>T	Missense Mutation	FBN1	p.D2648N	fibrillin 1	48 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr15:48734035C>T	Missense Mutation	FBN1	p.E2016K	fibrillin 1	120 (0.00)	118 (0.32)	0.86
11-01	Gp3	g.chr5:127624945C>T	Splice Site	FBN2		fibrillin 2	50 (0.00)	56 (0.20)	0.52
11-01	Gp3	g.chr5:127648481C>T	Missense Mutation	FBN2	p.R1575H	fibrillin 2	145 (0.00)	100 (0.21)	0.56
11-01	Gp3	g.chr19:9922296G>A	Missense Mutation	FBXL12	p.P62S	F-box and leucine-rich r	19 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr3:33415133C>T	Silent	FBXL2	p.G173G	F-box and leucine-rich r	38 (0.00)	18 (0.50)	1.33
11-01	Gp3	g.chr3:33415166G>T	Silent	FBXL2	p.L184L	F-box and leucine-rich r	32 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr12:117612508G>T	Nonsense Mutation	FBXO21	p.C229*	F-box protein 21	39 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr7:100198173G>T	Missense Mutation	FBXO24	p.C465F	F-box protein 24	17 (0.00)	26 (0.46)	1.23
11-01	Gp3	g.chr6:146125831G>A	Missense Mutation	FBXO30	p.P571S	F-box protein 30	72 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr6:146126284G>A	Missense Mutation	FBXO30	p.L420F	F-box protein 30	76 (0.00)	48 (0.25)	0.67
11-01	Gp3	g.chr6:146126308C>A	Nonsense Mutation	FBXO30	p.E412*	F-box protein 30	81 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr6:146127381G>A	Missense Mutation	FBXO30	p.P54L	F-box protein 30	123 (0.00)	89 (0.15)	0.39
11-01	Gp3	g.chr1:16632321G>A	Missense Mutation	FBXO42	p.P115L	F-box protein 42	45 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr6:153296361C>A	Nonsense Mutation	FBXO5	p.E167*	F-box protein 5	46 (0.00)	39 (0.33)	0.89
11-01	Gp3	g.chr22:32894131C>T	Splice Site	FBXO7	p.L395L	F-box protein 7	53 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr6:52957272A>T	Missense Mutation	FBXO9	p.R233S	F-box protein 9	85 (0.01)	34 (0.18)	0.47
11-01	Gp3	g.chr17:18668054G>A	Splice Site	FBXW10		F-box and WD repeat d	59 (0.02)	33 (0.42)	1.13
11-01	Gp3	g.chr17:18673325G>T	Missense Mutation	FBXW10	p.G645W	F-box and WD repeat d	66 (0.00)	28 (0.29)	0.76
11-01	Gp3	g.chr1:161512880C>T	Silent	FCGR3A	p.V229V	Fc fragment of IgG, low	85 (0.01)	46 (0.35)	0.93
11-01	Gp3	g.chr19:17887068C>A	Missense Mutation	FCHO1	p.R399S	FCH domain only 1	50 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr1:157736746C>T	Missense Mutation	FCRL2	p.R393K	Fc receptor-like 2	36 (0.00)	54 (0.33)	0.89

11-01	Gp3	g.chr1:161680656C>A	Silent	FCRLA	p.V79V	Fc receptor-like A	66 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr18:55221632G>T	Missense Mutation	FECH	p.P313T	ferrochelatase	194 (0.00)	73 (0.15)	0.40
11-01	Gp3	g.chr2:97361570C>A	RNA	FER1L5		fer-1-like family membe	29 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr2:97370094G>A	RNA	FER1L5		fer-1-like family membe	99 (0.01)	59 (0.15)	0.41
11-01	Gp3	g.chr8:124987502G>A	Silent	FER1L6	p.L213L	fer-1-like family membe	109 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr8:124993043C>G	Missense Mutation	FER1L6	p.P468A	fer-1-like family membe	65 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr8:125047531G>A	Missense Mutation	FER1L6	p.R767Q	fer-1-like family membe	58 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr3:186370296C>T	Missense Mutation	FETUB	p.S277F	fetuin B	66 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr11:125318455C>G	Missense Mutation	FEZ1	p.A369P	fasciculation and elonga	27 (0.00)	15 (0.53)	1.42
11-01	Gp3	g.chr2:36805951G>C	Missense Mutation	FEZ2	p.A231G	fasciculation and elonga	65 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr2:36805993G>T	Nonsense Mutation	FEZ2	p.S217*	fasciculation and elonga	64 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr4:155507801C>T	Silent	FGA	p.E260E	fibrinogen alpha chain	151 (0.00)	81 (0.15)	0.40
11-01	Gp3	g.chr4:155510029C>T	Missense Mutation	FGA	p.E94K	fibrinogen alpha chain	71 (0.00)	75 (0.17)	0.46
11-01	Gp3	g.chr12:32764179G>A	Missense Mutation	FGD4	p.A546T	FYVE, RhoGEF and PH	84 (0.00)	53 (0.23)	0.60
11-01	Gp3	g.chr3:14922096A>T	Missense Mutation	FGD5	p.R892S	FYVE, RhoGEF and PH	37 (0.03)	17 (0.53)	1.41
11-01	Gp3	g.chr4:123813528C>A	Missense Mutation	FGF2	p.L149I	fibroblast growth factor	39 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr15:49716709G>A	Missense Mutation	FGF7	p.R72Q	fibroblast growth factor	41 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr4:155528065G>A	Silent	FGG	p.F307F	fibrinogen gamma chain	63 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr8:17739581C>A	Missense Mutation	FGL1	p.E57D	fibrinogen-like 1	44 (0.00)	22 (0.27)	0.41
11-01	Gp3	g.chr1:15692399G>T	Nonsense Mutation	FHAD1	p.E1020*	forkhead-associated (FH	39 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr16:67271636C>A	Silent	FHOD1	p.L226L	formin homology 2 dom	83 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr18:34156508G>A	Splice Site	FHOD3	p.K202K	formin homology 2 dom	36 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr11:27016667G>A	Silent	FIBIN	p.G198G	fin bud initiation factor	60 (0.02)	33 (0.27)	0.73
11-01	Gp3	g.chr2:164466811C>T	Missense Mutation	FIGN	p.A511T	fidgetin	37 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr2:164467783G>T	Missense Mutation	FIGN	p.P187T	fidgetin	89 (0.00)	68 (0.16)	0.43
11-01	Gp3	g.chr7:50514217T>C	Missense Mutation	FIGNL1	p.R257G	fidgetin-like 1	78 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr6:76023092G>A	Missense Mutation	FILIP1	p.T819M	filamin A interacting pr	124 (0.01)	105 (0.21)	0.56
11-01	Gp3	g.chr6:76023689T>A	Missense Mutation	FILIP1	p.E620V	filamin A interacting pr	120 (0.00)	111 (0.43)	1.15
11-01	Gp3	g.chr9:115936836C>T	Missense Mutation	FKBP15	p.A751T	FK506 binding protein 1	103 (0.00)	68 (0.18)	0.47
11-01	Gp3	g.chr9:115945138G>T	Missense Mutation	FKBP15	p.Q608K	FK506 binding protein 1	81 (0.01)	83 (0.63)	1.67
11-01	Gp3	g.chr12:2907894G>A	Missense Mutation	FKBP4	p.G139E	FK506 binding protein 4	58 (0.00)	40 (0.28)	0.73
11-01	Gp3	g.chr7:72744243G>A	Missense Mutation	FKBP6	p.G119E	FK506 binding protein 6	63 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr7:33014262G>A	Silent	FKBP9	p.V85V	FK506 binding protein 9	60 (0.00)	51 (0.20)	0.52
11-01	Gp3	g.chr7:55750402C>A	RNA	FKBP9L			205 (0.00)	134 (0.21)	0.56
11-01	Gp3	g.chr9:108366630T>C	Silent	FKTN	p.T168T	fukutin	33 (0.00)	35 (0.26)	0.69

11-01	Gp3	g.chr1:152324090G>A	Missense Mutation	FLG2	p.H2058Y	filaggrin family membe	74 (0.00)	79 (0.29)	0.78
11-01	Gp3	g.chr1:152325869G>A	Missense Mutation	FLG2	p.H1465Y	filaggrin family membe	34 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr17:18149723C>T	Silent	FLII	p.K1035K	flightless I homolog (Dr	28 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr7:128493049C>A	Missense Mutation	FLNC	p.Q2058K	filamin C, gamma	20 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr17:27209696C>T	Silent	FLOT2	p.V120V	flotillin 2	41 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr13:28963952C>A	Missense Mutation	FLT1	p.K650N	fms-related tyrosine kin	68 (0.00)	44 (0.45)	1.21
11-01	Gp3	g.chr13:28601234G>A	Missense Mutation	FLT3	p.P733L	fms-related tyrosine kin	48 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr1:146685000G>A	Missense Mutation	FMO5	p.A121V	flavin containing monoc	51 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr2:216285423G>T	Silent	FN1	p.R550R	fibronectin 1	53 (0.00)	54 (0.22)	0.59
11-01	Gp3	g.chr2:216288983C>A	Missense Mutation	FN1	p.G368C	fibronectin 1	77 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr17:80684374G>T	Missense Mutation	FN3KRP	p.D163Y	fructosamine 3 kinase re	70 (0.01)	54 (0.20)	0.54
11-01	Gp3	g.chr1:94000452G>T	Missense Mutation	FNBP1L	p.G326V	formin binding protein 1	43 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr1:109261570C>A	Missense Mutation	FNDC7	p.T166K	fibronectin type III dom	96 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr17:33456448G>T	Missense Mutation	FNDC8	p.W198L	fibronectin type III dom	104 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr17:33456514C>T	Missense Mutation	FNDC8	p.T220I	fibronectin type III dom	75 (0.00)	42 (0.21)	0.57
11-01	Gp3	g.chr9:20720380C>T	Splice Site	FOCAD	p.T45I	focadhesin	42 (0.00)	23 (0.26)	0.43
11-01	Gp3	g.chr9:20946722G>C	Missense Mutation	FOCAD	p.C1193S	focadhesin	42 (0.00)	20 (0.40)	0.65
11-01	Gp3	g.chr9:20990351C>A	Missense Mutation	FOCAD	p.P1745Q	focadhesin	24 (0.00)	15 (0.33)	0.54
11-01	Gp3	g.chr11:49207337G>A	Missense Mutation	FOLH1	p.P237L	folate hydrolase (prostat	85 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr11:94039713T>A	Missense Mutation	FOLR4	p.L58H	folate receptor 4, delta (	77 (0.00)	96 (0.16)	0.42
11-01	Gp3	g.chr14:75747586G>A	Missense Mutation	FOS	p.R201Q	FBJ murine osteosarcon	61 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr16:86612614C>T	Silent	FOXL1	p.N95N	forkhead box L1	38 (0.00)	56 (0.27)	0.57
11-01	Gp3	g.chr14:89817129C>T	Nonsense Mutation	FOXN3	p.W189*	forkhead box N3	72 (0.00)	101 (0.16)	0.42
11-01	Gp3	g.chr7:114174761G>A	Splice Site	FOXP2	p.Q86Q	forkhead box P2	42 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr4:79207678C>T	Missense Mutation	FRAS1	p.R507C	Fraser extracellular mat	68 (0.00)	60 (0.17)	0.44
11-01	Gp3	g.chr4:79258838A>G	Silent	FRAS1	p.P763P	Fraser extracellular mat	95 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr4:79410210G>A	Silent	FRAS1	p.R2978R	Fraser extracellular mat	56 (0.00)	45 (0.49)	1.30
11-01	Gp3	g.chr4:79461864C>A	Missense Mutation	FRAS1	p.D3875E	Fraser extracellular mat	81 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr9:14805106C>A	Missense Mutation	FREM1	p.V1107L	FRAS1 related extracell	50 (0.00)	29 (0.34)	0.54
11-01	Gp3	g.chr4:144619135C>T	Silent	FREM3	p.G898G	FRAS1 related extracell	80 (0.00)	45 (0.20)	0.53
11-01	Gp3	g.chr10:13789767C>A	Missense Mutation	FRMD4A	p.A173S	FERM domain containi	47 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr3:69221044G>A	Missense Mutation	FRMD4B	p.H1025Y	FERM domain containi	53 (0.00)	59 (0.22)	0.59
11-01	Gp3	g.chr15:44166607G>T	Missense Mutation	FRMD5	p.H397N	FERM domain containi	51 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr10:49386184G>A	Missense Mutation	FRMPD2	p.S934F	FERM and PDZ domair	44 (0.02)	17 (0.53)	1.41
11-01	Gp3	g.chrX:12734578C>T	Missense Mutation	FRMPD4	p.P667L	FERM and PDZ domair	94 (0.00)	39 (0.33)	0.56

11-01	Gp3	g.chr13:32605992C>A	Silent	FRY	p.S20S	furry homolog (Drosoph	21 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr13:32753033G>A	Missense Mutation	FRY	p.V912I	furry homolog (Drosoph	103 (0.00)	54 (0.22)	0.59
11-01	Gp3	g.chr13:32808724G>A	Silent	FRY	p.E1847E	furry homolog (Drosoph	80 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr13:32811634C>T	Missense Mutation	FRY	p.R1977W	furry homolog (Drosoph	89 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr13:32811969C>T	Silent	FRY	p.L2088L	furry homolog (Drosoph	33 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr9:108270952C>A	Missense Mutation	FSD1L	p.A65D	fibronectin type III and	41 (0.00)	27 (0.41)	1.09
11-01	Gp3	g.chr2:186657419C>A	Missense Mutation	FSIP2	p.H1852Q	fibrous sheath interactin	28 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr2:186661467G>C	Missense Mutation	FSIP2	p.V3202L	fibrous sheath interactin	109 (0.00)	54 (0.20)	0.54
11-01	Gp3	g.chr2:186669767C>T	Missense Mutation	FSIP2	p.S5245L	fibrous sheath interactin	78 (0.00)	49 (0.27)	0.71
11-01	Gp3	g.chr5:132535055G>C	Missense Mutation	FSTL4	p.A754G	follistatin-like 4	33 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr17:61897718G>T	Missense Mutation	FTSJ3	p.P718H	FtsJ homolog 3 (E. coli)	63 (0.00)	44 (0.32)	0.85
11-01	Gp3	g.chr1:78430418C>A	Missense Mutation	FUBP1	p.M250I	far upstream element (F	70 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr2:84518188G>T	RNA	FUNDC2P2		FUN14 domain containi	83 (0.00)	41 (0.27)	0.41
11-01	Gp3	g.chr10:135169297C>A	Nonsense Mutation	FUOM	p.E70*	fucose mutarotase	82 (0.00)	51 (0.22)	0.58
11-01	Gp3	g.chr19:49206333G>A	Silent	FUT2	p.E40E	fucosyltransferase 2 (se	42 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr17:7497631C>T	Silent	FXR2	p.Q315Q	fragile X mental retarda	52 (0.02)	40 (0.17)	0.47
11-01	Gp3	g.chr5:39201934C>A	Nonsense Mutation	FYB	p.G377*	FYN binding protein	100 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr7:90895452G>T	Missense Mutation	FZD1	p.W419C	frizzled class receptor 1	19 (0.00)	49 (0.22)	0.60
11-01	Gp3	g.chr8:28360564C>T	Missense Mutation	FZD3	p.P12S	frizzled class receptor 3	88 (0.00)	30 (0.30)	0.45
11-01	Gp3	g.chr11:86663436C>G	Missense Mutation	FZD4	p.C121S	frizzled class receptor 4	76 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr4:144381635G>A	Missense Mutation	GAB1	p.D630N	GRB2-associated bindin	114 (0.01)	59 (0.27)	0.72
11-01	Gp3	g.chr11:77938042C>T	Missense Mutation	GAB2	p.A226T	GRB2-associated bindin	29 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr9:101235575C>A	Missense Mutation	GABBR2	p.W284C	gamma-aminobutyric ac	35 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr9:101235579C>G	Missense Mutation	GABBR2	p.G283A	gamma-aminobutyric ac	35 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr1:151090641G>A	Missense Mutation	GABPB2	p.G419E	GA binding protein tran	68 (0.00)	62 (0.19)	0.52
11-01	Gp3	g.chr5:161292730G>A	Missense Mutation	GABRA1	p.R64H	gamma-aminobutyric ac	33 (0.00)	12 (0.75)	2.00
11-01	Gp3	g.chr5:160721162G>A	Missense Mutation	GABRB2	p.R489W	gamma-aminobutyric ac	38 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chrX:151131090G>A	Missense Mutation	GABRE	p.S123F	gamma-aminobutyric ac	29 (0.00)	12 (0.50)	0.83
11-01	Gp3	g.chr6:89910911C>T	Missense Mutation	GABRR1	p.D83N	gamma-aminobutyric ac	151 (0.00)	25 (0.28)	0.44
11-01	Gp3	g.chr6:89978911C>A	Nonsense Mutation	GABRR2	p.E111*	gamma-aminobutyric ac	71 (0.00)	39 (0.54)	0.85
11-01	Gp3	g.chr10:26505798C>A	Silent	GAD2	p.S20S	glutamate decarboxylas	17 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr14:88407804C>T	Missense Mutation	GALC	p.R590K	galactosylceramidase	105 (0.00)	75 (0.28)	0.75
11-01	Gp3	g.chr2:38908501G>T	Missense Mutation	GALM	p.G142V	galactose mutarotase (al	64 (0.00)	52 (0.42)	1.13
11-01	Gp3	g.chr18:33267136G>C	Silent	GALNT1	p.R282R	polypeptide N-acetylgal	32 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr5:153677564G>A	Missense Mutation	GALNT10	p.R109Q	polypeptide N-acetylgal	82 (0.00)	75 (0.16)	0.43

11-01	Gp3	g.chr9:101606469G>A	Missense Mutation	GALNT12	p.C479Y	polypeptide N-acetylgal	29 (0.00)	25 (0.64)	1.71
11-01	Gp3	g.chr2:155158086C>T	Silent	GALNT13	p.F380F	polypeptide N-acetylgal	96 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr12:51757937C>T	Silent	GALNT6	p.K339K	polypeptide N-acetylgal	21 (0.00)	23 (0.39)	1.04
11-01	Gp3	g.chr16:81388072G>A	Silent	GAN	p.T115T	gigaxonin	93 (0.00)	40 (0.23)	0.48
11-01	Gp3	g.chr16:81388228G>C	Silent	GAN	p.T167T	gigaxonin	34 (0.00)	16 (0.31)	0.66
11-01	Gp3	g.chr3:115439685G>A	Missense Mutation	GAP43	p.E261K	growth associated protei	94 (0.00)	75 (0.24)	0.64
11-01	Gp3	g.chr9:128088819A>G	Silent	GAPVD1	p.G640G	GTPase activating prote	58 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr18:29890186G>A	Silent	GAREM	p.Y121Y	GRB2 associated, regul	87 (0.00)	53 (0.36)	0.96
11-01	Gp3	g.chr21:34889371A>G	Missense Mutation	GART	p.F678L	phosphoribosylglycina	73 (0.00)	36 (0.25)	0.67
11-01	Gp3	g.chr7:99821598G>A	Silent	GATS	p.G106G	GATS, stromal antigen	75 (0.00)	95 (0.15)	0.39
11-01	Gp3	g.chr4:22749459G>A	RNA	GBA3		glucosidase, beta, acid 3	77 (0.00)	33 (0.52)	1.37
11-01	Gp3	g.chr1:155186219T>G	RNA	GBAP1		glucosidase, beta, acid p	35 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr1:155188682G>T	RNA	GBAP1		glucosidase, beta, acid p	24 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr10:104117924C>T	Silent	GBF1	p.T256T	golgi brefeldin A resista	149 (0.00)	134 (0.17)	0.46
11-01	Gp3	g.chr1:89661045G>A	Missense Mutation	GBP4	p.H100Y	guanylate binding protei	36 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr1:89727943C>G	Missense Mutation	GBP5	p.W536S	guanylate binding protei	36 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr7:150846136C>T	Missense Mutation	GBX1	p.G211D	gastrulation brain home	240 (0.00)	247 (0.18)	0.48
11-01	Gp3	g.chr2:109087433C>T	Nonsense Mutation	GCC2	p.Q550*	GRIP and coiled-coil d	73 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr2:109103012C>A	Missense Mutation	GCC2	p.H1280N	GRIP and coiled-coil d	73 (0.00)	75 (0.20)	0.53
11-01	Gp3	g.chr6:53370683G>A	Missense Mutation	GCLC	p.S403F	glutamate-cysteine ligas	70 (0.00)	41 (0.27)	0.72
11-01	Gp3	g.chr12:120611566C>A	Missense Mutation	GCN1L1	p.M419I	GCN1 general control o	53 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr9:79117881C>G	Missense Mutation	GCNT1	p.A195G	glucosaminyl (N-acetyl)	94 (0.00)	74 (0.19)	0.62
11-01	Gp3	g.chr5:74325521C>T	Silent	GCNT4	p.Q114Q	glucosaminyl (N-acetyl)	45 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr12:7848241G>A	Silent	GDF3	p.V28V	growth differentiation f	31 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr20:34022523C>A	Missense Mutation	GDF5	p.E230D	growth differentiation f	40 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr10:5842620G>T	Missense Mutation	GDI2	p.H32N	GDP dissociation inhibi	121 (0.00)	72 (0.22)	0.59
11-01	Gp3	g.chr5:37815859G>T	Missense Mutation	GDNF	p.A177E	glial cell derived neurot	112 (0.00)	45 (0.38)	1.01
11-01	Gp3	g.chr8:95262647C>G	Missense Mutation	GEM	p.S261T	GTP binding protein ov	88 (0.00)	66 (0.12)	0.40
11-01	Gp3	g.chr5:154271151C>T	Silent	GEMIN5	p.R1304R	gem (nuclear organelle)	28 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr5:154271152C>T	Missense Mutation	GEMIN5	p.R1304K	gem (nuclear organelle)	29 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr5:154316621C>T	Silent	GEMIN5	p.E97E	gem (nuclear organelle)	55 (0.00)	44 (0.30)	0.79
11-01	Gp3	g.chr3:158363992C>G	Silent	GFM1	p.S91S	G elongation factor, mit	19 (0.00)	21 (0.67)	1.78
11-01	Gp3	g.chr6:55198590G>A	Missense Mutation	GFRAL	p.G55D	GDNF family receptor	121 (0.00)	166 (0.23)	0.61
11-01	Gp3	g.chr22:22989308C>T	Silent	GGTLC2	p.N87N	gamma-glutamyltransfe	60 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr17:40344277C>T	Missense Mutation	GHDC	p.A291T	GH3 domain containing	20 (0.00)	35 (0.14)	0.38

11-01	Gp3	g.chr11:59604702G>A	Silent	GIF	p.L272L	gastric intrinsic factor (	52 (0.00)	34 (0.41)	1.10
11-01	Gp3	g.chr2:233659483C>T	Silent	GIGYF2	p.P430P	GRB10 interacting GYF	97 (0.00)	73 (0.26)	0.69
11-01	Gp3	g.chr2:233704566C>G	Missense Mutation	GIGYF2	p.S919C	GRB10 interacting GYF	22 (0.00)	22 (0.59)	1.58
11-01	Gp3	g.chr2:233709157G>T	Missense Mutation	GIGYF2	p.D1054Y	GRB10 interacting GYF	18 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr7:150389647G>A	Silent	GIMAP2	p.L91L	GTPase, IMAP family	30 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr7:150270139G>A	Silent	GIMAP4	p.A327A	GTPase, IMAP family	28 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr7:150439822C>T	Nonsense Mutation	GIMAP5	p.Q199*	GTPase, IMAP family	37 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr7:150439983G>A	Silent	GIMAP5	p.Q252Q	GTPase, IMAP family	40 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr16:58438480C>A	Silent	GINS3	p.A166A	GINS complex subunit	16 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr15:35045322C>T	Missense Mutation	GJD2	p.R108H	gap junction protein, del	57 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chrX:30709267C>G	Missense Mutation	GK	p.T122S	glycerol kinase	18 (0.00)	19 (0.63)	1.05
11-01	Gp3	g.chr15:69548650C>A	Missense Mutation	GLCE	p.H105N	glucuronic acid epimera	101 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr9:6604587C>T	Splice Site	GLDC		glycine dehydrogenase (	83 (0.00)	37 (0.38)	0.60
11-01	Gp3	g.chr9:131285912G>T	Silent	GLE1	p.V228V	GLE1 RNA export med	47 (0.00)	34 (0.41)	1.10
11-01	Gp3	g.chr7:42063136G>A	Silent	GLI3	p.V476V	GLI family zinc finger	22 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr7:42262826C>T	Silent	GLI3	p.T9T	GLI family zinc finger	23 (0.00)	17 (0.41)	1.10
11-01	Gp3	g.chr12:75875711C>A	Missense Mutation	GLIPR1	p.P91Q	GLI pathogenesis-relate	71 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr4:175710056C>T	Missense Mutation	GLRA3	p.R37Q	glycine receptor, alpha	37 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr10:131943513C>T	Missense Mutation	GLRX3	p.P44L	glutaredoxin 3	48 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr12:129360498G>A	Silent	GLT1D1	p.K36K	glycosyltransferase 1 do	40 (0.03)	35 (0.77)	2.06
11-01	Gp3	g.chr12:104383226G>A	Missense Mutation	GLT8D2	p.P337L	glycosyltransferase 8 do	50 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr11:58723441G>T	Nonsense Mutation	GLYATL1	p.E284*	glycine-N-acyltransfera	20 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr3:179137194C>T	Missense Mutation	GNB4	p.D66N	guanine nucleotide bind	63 (0.00)	33 (0.36)	0.97
11-01	Gp3	g.chr9:36233988C>A	Missense Mutation	GNE	p.G194V	glucosamine (UDP-N-a	77 (0.01)	27 (0.41)	0.62
11-01	Gp3	g.chr3:52723211T>A	Nonsense Mutation	GNL3	p.L177*	guanine nucleotide bind	39 (0.00)	69 (0.19)	0.50
11-01	Gp3	g.chr12:102155359C>T	Missense Mutation	GNPTAB	p.M966I	N-acetylglucosamine-1-	49 (0.00)	50 (0.28)	0.75
11-01	Gp3	g.chr12:102179940G>A	Silent	GNPTAB	p.L141L	N-acetylglucosamine-1-	27 (0.00)	33 (0.33)	0.89
11-01	Gp3	g.chr9:131019933G>A	Missense Mutation	GOLGA2	p.R862W	golgin A2	69 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr12:133381339C>A	Missense Mutation	GOLGA3	p.E520D	golgin A3	26 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr3:37365621G>A	Silent	GOLGA4	p.Q770Q	golgin A4	31 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr3:37366433C>A	Nonsense Mutation	GOLGA4	p.S1041*	golgin A4	59 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr3:121414107C>A	Missense Mutation	GOLGB1	p.D1755Y	golgin B1	53 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr3:121416230T>C	Missense Mutation	GOLGB1	p.E1047G	golgin B1	60 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr17:28849325C>T	Missense Mutation	GOSR1	p.R226W	golgi SNAP receptor co	28 (0.00)	22 (0.55)	1.45
11-01	Gp3	g.chr17:4835967C>A	Missense Mutation	GP1BA	p.S23Y	glycoprotein Ib (platelet	63 (0.00)	41 (0.22)	0.59

11-01	Gp3	g.chr17:4835968C>A	Silent	GP1BA	p.S23S	glycoprotein Ib (platelet	63 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr10:113920612G>T	Silent	GPAM	p.S503S	glycerol-3-phosphate ac	35 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr6:24456803G>A	Silent	GPLD1	p.G357G	glycosylphosphatidylinc	109 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr4:176556076G>A	Missense Mutation	GPM6A	p.R273W	glycoprotein M6A	53 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chrX:135405376G>T	Missense Mutation	GPR112	p.E170D	G protein-coupled recep	27 (0.00)	18 (0.28)	0.46
11-01	Gp3	g.chrX:135427820A>G	Missense Mutation	GPR112	p.N652S	G protein-coupled recep	46 (0.00)	34 (0.26)	0.44
11-01	Gp3	g.chrX:135429941G>A	Missense Mutation	GPR112	p.S1359N	G protein-coupled recep	34 (0.00)	20 (0.25)	0.42
11-01	Gp3	g.chrX:135430843C>T	Missense Mutation	GPR112	p.P1660S	G protein-coupled recep	28 (0.00)	24 (0.42)	0.69
11-01	Gp3	g.chr2:26534912C>G	Missense Mutation	GPR113	p.D493H	G protein-coupled recep	27 (0.00)	12 (0.75)	2.00
11-01	Gp3	g.chr6:142711446C>T	Missense Mutation	GPR126	p.P425L	G protein-coupled recep	57 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr3:100373865G>A	Silent	GPR128	p.P227P	G protein-coupled recep	59 (0.02)	36 (0.56)	1.48
11-01	Gp3	g.chr3:100413790C>T	Missense Mutation	GPR128	p.P485L	G protein-coupled recep	68 (0.00)	58 (0.17)	0.46
11-01	Gp3	g.chr12:131593347C>A	Missense Mutation	GPR133	p.H342N	G protein-coupled recep	24 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr1:236341927G>T	Missense Mutation	GPR137B	p.L226F	G protein-coupled recep	73 (0.00)	22 (0.41)	0.78
11-01	Gp3	g.chr1:236341928G>T	Nonsense Mutation	GPR137B	p.E227*	G protein-coupled recep	73 (0.00)	22 (0.41)	0.78
11-01	Gp3	g.chr5:145895263C>A	Missense Mutation	GPR151	p.M138I	G protein-coupled recep	44 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr1:6314735C>G	Missense Mutation	GPR153	p.E77D	G protein-coupled recep	18 (0.00)	19 (0.58)	1.54
11-01	Gp3	g.chr12:57389174C>A	Missense Mutation	GPR182	p.L61M	G protein-coupled recep	26 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr12:57389224C>A	Silent	GPR182	p.V77V	G protein-coupled recep	25 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr12:57390068C>T	Missense Mutation	GPR182	p.H359Y	G protein-coupled recep	18 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr16:57685144C>T	Missense Mutation	GPR56	p.R33C	G protein-coupled recep	17 (0.00)	20 (0.70)	1.87
11-01	Gp3	g.chr2:53956635G>A	Missense Mutation	GPR75-ASB3	p.S143F	GPR75-ASB3 readthrou	125 (0.00)	97 (0.14)	0.38
11-01	Gp3	g.chr5:89933661C>A	Silent	GPR98	p.G712G	G protein-coupled recep	37 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr5:89990235G>C	Missense Mutation	GPR98	p.L2554F	G protein-coupled recep	65 (0.00)	25 (0.48)	1.28
11-01	Gp3	g.chr5:176025465G>T	Missense Mutation	GPRIN1	p.D457E	G protein regulated indu	17 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chr16:46940848C>G	Missense Mutation	GPT2	p.D179E	glutamic pyruvate transa	28 (0.00)	15 (0.60)	1.60
11-01	Gp3	g.chr1:53072361C>T	Silent	GPX7	p.S48S	glutathione peroxidase	63 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr11:123480981T>C	Silent	GRAMD1B	p.H475H	GRAM domain containi	29 (0.00)	17 (0.53)	1.41
11-01	Gp3	g.chr5:125816397C>T	Silent	GRAMD3	p.L245L	GRAM domain containi	53 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr22:47069680C>G	Missense Mutation	GRAMD4	p.F451L	GRAM domain containi	24 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr7:50660672G>T	Missense Mutation	GRB10	p.H588N	growth factor receptor-b	25 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr7:50663163G>C	Missense Mutation	GRB10	p.Q537E	growth factor receptor-b	111 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr2:11752668G>A	Silent	GREB1	p.L1018L	growth regulation by est	83 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr5:153054134C>A	Nonsense Mutation	GRIA1	p.Y268*	glutamate receptor, iono	54 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr4:158256933C>A	Missense Mutation	GRIA2	p.F459L	glutamate receptor, iono	67 (0.00)	34 (0.24)	0.63

11-01	Gp3	g.chr10:87484283C>A	Missense Mutation	GRID1	p.D562Y	glutamate receptor, iono	79 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:94693326G>T	Missense Mutation	GRID2	p.D901Y	glutamate receptor, iono	81 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr11:120732718C>A	Silent	GRIK4	p.I265I	glutamate receptor, iono	154 (0.00)	65 (0.34)	0.90
11-01	Gp3	g.chr11:120732736C>A	Missense Mutation	GRIK4	p.F271L	glutamate receptor, iono	212 (0.00)	92 (0.34)	0.90
11-01	Gp3	g.chr12:13906452G>A	Missense Mutation	GRIN2B	p.P270L	glutamate receptor, iono	39 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr12:66788031G>T	Missense Mutation	GRIP1	p.P644T	glutamate receptor inter	76 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr3:14567038C>G	RNA	GRIP2		glutamate receptor inter	58 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr1:182152111G>T	lincRNA	GS1-122H1.2			23 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr7:76982959C>G	Splice Site	GSAP		gamma-secretase activa	206 (0.00)	82 (0.16)	0.42
11-01	Gp3	g.chr7:77011907C>T	Silent	GSAP	p.L170L	gamma-secretase activa	23 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr16:85697065C>A	Missense Mutation	GSE1	p.P830Q	Gse1 coiled-coil protein	23 (0.00)	23 (0.74)	1.56
11-01	Gp3	g.chr20:33533871G>A	Missense Mutation	GSS	p.P54S	glutathione synthetase	46 (0.00)	71 (0.15)	0.41
11-01	Gp3	g.chr4:106639143G>A	Missense Mutation	GSTCD	p.E125K	glutathione S-transferas	47 (0.00)	38 (0.24)	0.63
11-01	Gp3	g.chr7:142961658C>A	Missense Mutation	GSTK1	p.L58M	glutathione S-transferas	138 (0.00)	88 (0.18)	0.48
11-01	Gp3	g.chr7:142965229C>T	Missense Mutation	GSTK1	p.H195Y	glutathione S-transferas	256 (0.00)	247 (0.15)	0.41
11-01	Gp3	g.chr1:110217380G>A	Silent	GSTM2	p.K193K	glutathione S-transferas	38 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr10:106037784C>T	Silent	GSTO2	p.Y92Y	glutathione S-transferas	21 (0.00)	19 (0.68)	1.82
11-01	Gp3	g.chr10:106039188C>A	Missense Mutation	GSTO2	p.L143M	glutathione S-transferas	97 (0.00)	112 (0.16)	0.43
11-01	Gp3	g.chr10:106059025G>A	Missense Mutation	GSTO2	p.D239N	glutathione S-transferas	41 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr1:89352997A>G	Missense Mutation	GTF2B	p.V24A	general transcription fac	73 (0.00)	33 (0.33)	0.89
11-01	Gp3	g.chr12:124144743G>A	Silent	GTF2H3	p.V296V	general transcription fac	94 (0.00)	63 (0.29)	0.76
11-01	Gp3	g.chr9:135554540T>C	Missense Mutation	GTF3C4	p.F512L	general transcription fac	45 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr7:89983832T>C	Silent	GTPBP10	p.I96I	GTP-binding protein 10	35 (0.00)	54 (0.26)	0.69
11-01	Gp3	g.chr7:90012375C>A	Missense Mutation	GTPBP10	p.Q295K	GTP-binding protein 10	113 (0.00)	73 (0.32)	0.84
11-01	Gp3	g.chr6:43592675G>A	Missense Mutation	GTPBP2	p.S277L	GTP binding protein 2	26 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr11:106681181C>T	Missense Mutation	GUCY1A2	p.M431I	guanylate cyclase 1, sol	56 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr7:65429388G>A	Silent	GUSB	p.L571L	glucuronidase, beta	85 (0.00)	89 (0.19)	0.51
11-01	Gp3	g.chr11:6737984G>A	RNA	GVINP1		GTPase, very large inte	115 (0.01)	77 (0.16)	0.42
11-01	Gp3	g.chr20:23345114G>A	Missense Mutation	GZF1	p.D32N	GDNF-inducible zinc fi	52 (0.00)	49 (0.20)	0.54
11-01	Gp3	g.chr20:23350824G>C	Missense Mutation	GZF1	p.E628Q	GDNF-inducible zinc fi	98 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr5:54327195C>A	Missense Mutation	GZMK	p.Q123K	granzyme K (granzyme	27 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr2:26415187C>T	Silent	HADHA	p.K664K	hydroxyacyl-CoA dehy	44 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr19:35775870C>T	Silent	HAMP	p.D60D	hepcidin antimicrobial p	44 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr5:82937482C>A	Nonsense Mutation	HAPLN1	p.G300*	hyaluronan and proteog	95 (0.00)	40 (0.42)	1.13
11-01	Gp3	g.chr5:140073524C>A	Missense Mutation	HARS2	p.T63N	histidyl-tRNA synthetas	69 (0.00)	39 (0.26)	0.68

11-01	Gp3	g.chr15:42853598C>A	Missense Mutation	HAUS2	p.H129Q	HAUS augmin-like com	17 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr9:19058309C>A	Missense Mutation	HAUS6	p.G819V	HAUS augmin-like com	31 (0.00)	16 (0.56)	0.89
11-01	Gp3	g.chr1:154247680C>A	Missense Mutation	HAX1	p.Q203K	HCLS1 associated prote	34 (0.00)	29 (0.59)	1.56
11-01	Gp3	g.chr6:135308816C>T	Silent	HBS1L	p.T399T	HBS1-like translational	94 (0.00)	60 (0.35)	0.93
11-01	Gp3	g.chr12:123187249G>A	Silent	HCAR2	p.L194L	hydroxycarboxylic acid	68 (0.00)	37 (0.32)	0.86
11-01	Gp3	g.chr12:123187253A>G	Missense Mutation	HCAR2	p.F193S	hydroxycarboxylic acid	66 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr20:30659476T>A	Missense Mutation	HCK	p.M4K	HCK proto-oncogene, S	38 (0.00)	26 (0.42)	1.13
11-01	Gp3	g.chr20:30659477G>A	Missense Mutation	HCK	p.M4I	HCK proto-oncogene, S	38 (0.00)	25 (0.44)	1.17
11-01	Gp3	g.chr3:121366234C>T	Missense Mutation	HCLS1	p.E74K	hematopoietic cell-speci	18 (0.00)	37 (0.73)	1.95
11-01	Gp3	g.chr5:141009680G>A	Silent	HDAC3	p.P98P	histone deacetylase 3	102 (0.00)	91 (0.25)	0.67
11-01	Gp3	g.chr7:18554373G>A	Intron	HDAC9		histone deacetylase 9	40 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr7:18570751C>A	Intron	HDAC9		histone deacetylase 9	26 (0.00)	46 (0.74)	1.97
11-01	Gp3	g.chr7:18572923C>T	Intron	HDAC9		histone deacetylase 9	90 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr7:18578758G>A	Intron	HDAC9		histone deacetylase 9	23 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr7:18580880C>T	Intron	HDAC9		histone deacetylase 9	33 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr7:18585801G>C	Intron	HDAC9		histone deacetylase 9	25 (0.00)	27 (0.59)	1.58
11-01	Gp3	g.chr7:18593276G>A	Intron	HDAC9		histone deacetylase 9	25 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr7:18603392G>T	Intron	HDAC9		histone deacetylase 9	39 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr7:18606135C>A	Intron	HDAC9		histone deacetylase 9	49 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr7:18610344C>T	Intron	HDAC9		histone deacetylase 9	69 (0.00)	78 (0.19)	0.51
11-01	Gp3	g.chr7:18610370C>T	Intron	HDAC9		histone deacetylase 9	46 (0.00)	65 (0.23)	0.62
11-01	Gp3	g.chr7:18638822G>C	Intron	HDAC9		histone deacetylase 9	34 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr7:18650386G>A	Intron	HDAC9		histone deacetylase 9	90 (0.00)	62 (0.16)	0.43
11-01	Gp3	g.chr7:18656880C>T	Intron	HDAC9		histone deacetylase 9	251 (0.00)	124 (0.30)	0.80
11-01	Gp3	g.chr7:18703110G>A	Intron	HDAC9		histone deacetylase 9	87 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr7:18703321G>C	Intron	HDAC9		histone deacetylase 9	111 (0.00)	98 (0.14)	0.38
11-01	Gp3	g.chr7:18703910G>A	Intron	HDAC9		histone deacetylase 9	40 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:18726067C>G	Intron	HDAC9		histone deacetylase 9	70 (0.00)	51 (0.18)	0.47
11-01	Gp3	g.chr7:18743577C>T	Intron	HDAC9		histone deacetylase 9	59 (0.00)	69 (0.30)	0.81
11-01	Gp3	g.chr7:18744844C>T	Intron	HDAC9		histone deacetylase 9	159 (0.01)	126 (0.16)	0.42
11-01	Gp3	g.chr7:18747538G>T	Intron	HDAC9		histone deacetylase 9	55 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr7:18748306G>T	Intron	HDAC9		histone deacetylase 9	206 (0.00)	127 (0.27)	0.71
11-01	Gp3	g.chr7:18765431G>C	Intron	HDAC9		histone deacetylase 9	55 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr7:18781915A>T	Intron	HDAC9		histone deacetylase 9	49 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr7:18782854C>A	Intron	HDAC9		histone deacetylase 9	32 (0.00)	30 (0.40)	1.07

11-01	Gp3	g.chr7:18795762C>A	Intron	HDAC9		histone deacetylase 9	104 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr7:18827796C>A	Intron	HDAC9		histone deacetylase 9	26 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr7:18868301G>T	Intron	HDAC9		histone deacetylase 9	22 (0.00)	33 (0.30)	0.81
11-01	Gp3	g.chr7:18881170G>C	Intron	HDAC9		histone deacetylase 9	59 (0.00)	45 (0.29)	0.77
11-01	Gp3	g.chr7:18884275G>A	Intron	HDAC9		histone deacetylase 9	80 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr7:18888154G>A	Intron	HDAC9		histone deacetylase 9	30 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr7:18893714G>T	Intron	HDAC9		histone deacetylase 9	16 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr7:18898987C>T	Intron	HDAC9		histone deacetylase 9	65 (0.00)	42 (0.33)	0.89
11-01	Gp3	g.chr7:18905831G>C	Intron	HDAC9		histone deacetylase 9	97 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr7:18932937C>G	Intron	HDAC9		histone deacetylase 9	98 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr7:18934013G>A	Intron	HDAC9		histone deacetylase 9	70 (0.00)	46 (0.39)	1.04
11-01	Gp3	g.chr7:18934787C>T	Intron	HDAC9		histone deacetylase 9	97 (0.00)	62 (0.19)	0.52
11-01	Gp3	g.chr7:18940332G>C	Intron	HDAC9		histone deacetylase 9	24 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr7:18950407T>A	Intron	HDAC9		histone deacetylase 9	43 (0.00)	35 (0.31)	0.84
11-01	Gp3	g.chr7:18956016G>T	Intron	HDAC9		histone deacetylase 9	65 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr7:18957458C>T	Intron	HDAC9		histone deacetylase 9	45 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr7:18963182C>G	Intron	HDAC9		histone deacetylase 9	103 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr7:18964894C>G	Intron	HDAC9		histone deacetylase 9	78 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr7:18978399C>A	Intron	HDAC9		histone deacetylase 9	24 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr7:18988866A>G	Intron	HDAC9		histone deacetylase 9	143 (0.00)	96 (0.26)	0.69
11-01	Gp3	g.chr7:18995697C>T	Intron	HDAC9		histone deacetylase 9	59 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr7:19016278G>A	Intron	HDAC9		histone deacetylase 9	52 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr7:19021421C>T	Intron	HDAC9		histone deacetylase 9	27 (0.00)	40 (0.45)	1.20
11-01	Gp3	g.chr1:236736065C>T	Missense Mutation	HEATR1	p.G1175S	HEAT repeat containing	70 (0.00)	72 (0.22)	0.42
11-01	Gp3	g.chr1:236736113C>G	Missense Mutation	HEATR1	p.E1159Q	HEAT repeat containing	49 (0.00)	59 (0.24)	0.45
11-01	Gp3	g.chr1:236746439G>C	Missense Mutation	HEATR1	p.L767V	HEAT repeat containing	92 (0.00)	88 (0.20)	0.39
11-01	Gp3	g.chr1:236759283G>A	Missense Mutation	HEATR1	p.S269F	HEAT repeat containing	82 (0.00)	46 (0.28)	0.54
11-01	Gp3	g.chr14:73974895C>A	Missense Mutation	HEATR4	p.K608N	HEAT repeat containing	62 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr2:37232852G>A	Missense Mutation	HEATR5B	p.H1610Y	HEAT repeat containing	44 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr14:31583232G>C	Missense Mutation	HECTD1	p.L1903V	HECT domain containir	39 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr14:31598182G>A	Silent	HECTD1	p.G1465G	HECT domain containir	74 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr10:93272106G>C	Missense Mutation	HECTD2	p.G766R	HECT domain containir	74 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr1:45475086C>T	Missense Mutation	HECTD3	p.G315D	HECT domain containir	73 (0.00)	66 (0.21)	0.57
11-01	Gp3	g.chr1:45475672C>T	Missense Mutation	HECTD3	p.V249I	HECT domain containir	56 (0.00)	42 (0.26)	0.70
11-01	Gp3	g.chr12:112600244G>C	Missense Mutation	HECTD4	p.L4256V	HECT domain containir	60 (0.00)	19 (0.26)	0.70

11-01	Gp3	g.chr12:112681213G>A	Silent	HECTD4	p.V1488V	HECT domain containir	17 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr7:43519220G>A	Silent	HECW1	p.V1003V	HECT, C2 and WW dor	25 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr2:197183986G>A	Missense Mutation	HECW2	p.A187V	HECT, C2 and WW dor	28 (0.00)	24 (0.71)	1.89
11-01	Gp3	g.chr3:124729347G>A	Silent	HEG1	p.D1003D	heart development prote	61 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr3:124731563C>G	Missense Mutation	HEG1	p.V954L	heart development prote	115 (0.00)	155 (0.20)	0.53
11-01	Gp3	g.chr17:65105537G>A	Missense Mutation	HELZ	p.P1395L	helicase with zinc fingei	89 (0.00)	76 (0.17)	0.46
11-01	Gp3	g.chr15:63908067G>A	Missense Mutation	HERC1	p.P4665L	HECT and RLD domair	28 (0.00)	24 (0.50)	1.33
11-01	Gp3	g.chr15:63920958T>A	Missense Mutation	HERC1	p.Q4341H	HECT and RLD domair	110 (0.01)	76 (0.30)	0.81
11-01	Gp3	g.chr15:63930724C>A	Silent	HERC1	p.L3993L	HECT and RLD domair	190 (0.00)	190 (0.14)	0.38
11-01	Gp3	g.chr15:63967142T>C	Silent	HERC1	p.E2415E	HECT and RLD domair	101 (0.00)	76 (0.37)	0.98
11-01	Gp3	g.chr15:63988469G>C	Missense Mutation	HERC1	p.L1659V	HECT and RLD domair	54 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr15:64039190C>G	Missense Mutation	HERC1	p.G816A	HECT and RLD domair	57 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr15:28483329C>T	Silent	HERC2	p.L1261L	HECT and RLD domair	249 (0.00)	146 (0.27)	0.73
11-01	Gp3	g.chr15:28491088G>A	Silent	HERC2	p.N1172N	HECT and RLD domair	64 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr15:28513758G>A	Missense Mutation	HERC2	p.P484L	HECT and RLD domair	17 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr15:28902482G>T	RNA	HERC2P9		hect domain and RLD 2	47 (0.00)	30 (0.30)	0.80
11-01	Gp3	g.chr4:89574166G>A	Missense Mutation	HERC3	p.A204T	HECT and RLD domair	43 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr16:56976099G>T	Missense Mutation	HERPUD1	p.D321Y	homocysteine-inducible	93 (0.00)	122 (0.22)	0.59
11-01	Gp3	g.chr3:57232934C>T	Silent	HESX1	p.G68G	HESX homeobox 1	69 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr5:74016278C>A	Missense Mutation	HEXB	p.F481L	hexosaminidase B (beta	47 (0.00)	55 (0.20)	0.53
11-01	Gp3	g.chr17:80382306C>T	Missense Mutation	HEXDC	p.L41F	hexosaminidase (glycos	69 (0.00)	48 (0.25)	0.67
11-01	Gp3	g.chr3:120365852G>C	Missense Mutation	HGD	p.L173V	homogentisate 1,2-dioxy	73 (0.00)	53 (0.28)	0.75
11-01	Gp3	g.chr7:81335719C>T	Nonsense Mutation	HGF	p.W547*	hepatocyte growth facto	38 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr7:81339465G>A	Silent	HGF	p.Y513Y	hepatocyte growth facto	20 (0.00)	19 (0.68)	1.82
11-01	Gp3	g.chr8:43033323C>T	Silent	HGSNAT	p.L320L	heparan-alpha-glucosan	166 (0.01)	126 (0.18)	0.49
11-01	Gp3	g.chr1:210560862G>A	Nonsense Mutation	HHAT	p.W70*	hedgehog acyltransferas	57 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr4:145655924G>T	Missense Mutation	HHIP	p.V598L	hedgehog interacting pr	40 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr1:222705411C>T	Nonsense Mutation	HHIPL2	p.W540*	HHIP-like 2	18 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr14:62205006C>G	Nonsense Mutation	HIF1A	p.S485*	hypoxia inducible factoı	29 (0.00)	35 (0.43)	1.14
11-01	Gp3	g.chr11:119003405C>T	Silent	HINFP	p.T263T	histone H4 transcription	23 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr22:19349352C>A	Silent	HIRA	p.L626L	histone cell cycle regula	61 (0.00)	51 (0.24)	0.63
11-01	Gp3	g.chr6:26033526C>T	Missense Mutation	HIST1H2AB	p.D91N	histone cluster 1, H2ab	63 (0.00)	80 (0.19)	0.50
11-01	Gp3	g.chr6:26046002C>A	Missense Mutation	HIST1H3C	p.P122T	histone cluster 1, H3c	31 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr6:27778141G>T	Missense Mutation	HIST1H3H	p.C97F	histone cluster 1, H3h	23 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr6:143092384C>A	Missense Mutation	HIVEP2	p.Q1164H	human immunodeficien	164 (0.00)	84 (0.18)	0.48

11-01	Gp3	g.chr10:70992584C>T	Silent	HKDC1	p.V97V	hexokinase domain cont	145 (0.00)	87 (0.22)	0.58
11-01	Gp3	g.chr21:38309024C>T	Missense Mutation	HLCS	p.G241R	holocarboxylase synthet	52 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr3:129017248G>A	Missense Mutation	HMCES	p.D169N	5-hydroxymethylcytosir	78 (0.01)	37 (0.22)	0.58
11-01	Gp3	g.chr1:186055386A>G	Missense Mutation	HMCN1	p.S2965G	hemicentin 1	61 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr1:186059988C>A	Missense Mutation	HMCN1	p.P3276T	hemicentin 1	28 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr1:24128986G>T	Missense Mutation	HMGCL	p.S315R	3-hydroxymethyl-3-met	31 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr6:55360335G>A	Missense Mutation	HMGCLL1	p.P226L	3-hydroxymethyl-3-met	32 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr5:149431569C>T	Silent	HMGXB3	p.Y1231Y	HMG box domain conta	35 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr22:35783031C>T	Silent	HMOX1	p.F166F	heme oxygenase (decyc	22 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr5:177633888G>A	Silent	HNRNPAB	p.G178G	heterogeneous nuclear r	20 (0.00)	22 (0.64)	1.70
11-01	Gp3	g.chr2:38812866G>A	Missense Mutation	HNRNPLL	p.P156S	heterogeneous nuclear r	34 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr14:23745541G>T	Missense Mutation	HOMEZ	p.A299D	homeobox and leucine z	66 (0.00)	53 (0.38)	1.01
11-01	Gp3	g.chr14:23746049G>A	Missense Mutation	HOMEZ	p.R130W	homeobox and leucine z	47 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr19:12874391C>G	Missense Mutation	HOOK2	p.S652T	hook microtubule-tether	99 (0.00)	77 (0.22)	0.59
11-01	Gp3	g.chr7:27238953G>A	Silent	HOXA13	p.G248G	homeobox A13	21 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr17:46690779G>A	Missense Mutation	HOXB8	p.R173C	homeobox B8	41 (0.00)	72 (0.15)	0.41
11-01	Gp3	g.chr12:54350240C>G	Missense Mutation	HOXC12	p.L247V	homeobox C12	101 (0.00)	82 (0.15)	0.39
11-01	Gp3	g.chr16:72110415C>A	Missense Mutation	HPR	p.P161H	haptoglobin-related prot	58 (0.00)	40 (0.45)	1.20
11-01	Gp3	g.chr16:72110562C>A	Missense Mutation	HPR	p.P210H	haptoglobin-related prot	67 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr16:72110906G>A	Missense Mutation	HPR	p.V325M	haptoglobin-related prot	96 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr10:100202920G>A	Silent	HPS1	p.L26L	Hermansky-Pudlak sync	22 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr5:175111023G>T	Missense Mutation	HRH2	p.D263Y	histamine receptor H2	31 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr2:20838308C>T	Missense Mutation	HS1BP3	p.E171K	HCLS1 binding protein	21 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr2:20838346C>T	Missense Mutation	HS1BP3	p.S158N	HCLS1 binding protein	33 (0.00)	29 (0.45)	1.20
11-01	Gp3	g.chr2:20840851C>G	Missense Mutation	HS1BP3	p.K96N	HCLS1 binding protein	88 (0.00)	134 (0.15)	0.40
11-01	Gp3	g.chr16:26147093A>T	Missense Mutation	HS3ST4	p.T299S	heparan sulfate (glucosa	35 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr16:67470770G>A	Missense Mutation	HSD11B2	p.R361H	hydroxysteroid (11-beta	24 (0.00)	97 (0.29)	0.77
11-01	Gp3	g.chr16:84163943T>A	Missense Mutation	HSDL1	p.Q105L	hydroxysteroid dehydro	73 (0.00)	23 (0.35)	0.74
11-01	Gp3	g.chr16:67202957C>A	Missense Mutation	HSF4	p.Q403K	heat shock transcription	41 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr4:190395893G>A	RNA	HSP90AA4P		heat shock protein 90kD	162 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr4:190395894A>G	RNA	HSP90AA4P		heat shock protein 90kD	161 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr6:44219757C>T	Missense Mutation	HSP90AB1	p.A495V	heat shock protein 90kD	97 (0.00)	136 (0.26)	0.69
11-01	Gp3	g.chr12:104340684C>G	Missense Mutation	HSP90B1	p.L743V	heat shock protein 90kD	53 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr14:65008910G>A	Missense Mutation	HSPA2	p.G448D	heat shock 70kDa protei	30 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr9:128001325C>T	Silent	HSPA5	p.R297R	heat shock 70kDa protei	40 (0.00)	44 (0.20)	0.55

11-01	Gp3	g.chr13:47466607G>A	Silent	HTR2A	p.I177I	5-hydroxytryptamine (s	163 (0.00)	89 (0.17)	0.45
11-01	Gp3	g.chrX:114141732G>A	Silent	HTR2C	p.R377R	5-hydroxytryptamine (s	67 (0.00)	44 (0.23)	0.38
11-01	Gp3	g.chr4:3208313C>A	Missense Mutation	HTT	p.Q1937K	huntingtin	36 (0.00)	26 (0.58)	1.54
11-01	Gp3	g.chr4:3211581C>A	Missense Mutation	HTT	p.Q2107K	huntingtin	131 (0.00)	51 (0.16)	0.42
11-01	Gp3	g.chr4:3237112C>A	Missense Mutation	HTT	p.A2853E	huntingtin	27 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr4:3237906C>A	Nonsense Mutation	HTT	p.S2939*	huntingtin	86 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chrX:53569469C>T	Missense Mutation	HUWE1	p.R3804Q	HECT, UBA and WWE	22 (0.00)	20 (0.35)	0.58
11-01	Gp3	g.chrX:53569486C>T	Silent	HUWE1	p.Q3798Q	HECT, UBA and WWE	20 (0.00)	17 (0.35)	0.59
11-01	Gp3	g.chrX:53585653C>T	Missense Mutation	HUWE1	p.G2708D	HECT, UBA and WWE	40 (0.00)	12 (0.42)	0.69
11-01	Gp3	g.chr7:123508870C>G	Silent	HYAL4	p.T181T	hyaluronoglucosaminid	46 (0.00)	44 (0.30)	0.79
11-01	Gp3	g.chr15:78825824C>A	Missense Mutation	HYKK	p.R312S	hydroxylysine kinase	59 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr11:125770022C>A	Silent	HYLS1	p.S253S	hydrolethalus syndrome	74 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr6:82927854C>A	Splice Site	IBTK	p.V417L	inhibitor of Bruton agan	36 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr2:203644321C>A	Missense Mutation	ICA1L	p.D462Y	islet cell autoantigen 1,	72 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr2:203653633G>T	Missense Mutation	ICA1L	p.S388Y	islet cell autoantigen 1,	25 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr6:52876892G>A	Missense Mutation	ICK	p.S429F	intestinal cell (MAK-lik	39 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr15:90630754C>T	Nonsense Mutation	IDH2	p.W135*	isocitrate dehydrogenas	53 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr10:1088687G>T	Missense Mutation	IDI1	p.T141K	isopentenyl-diphosphat	24 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr10:91178007G>C	Missense Mutation	IFIT5	p.G351R	interferon-induced prot	38 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr9:21367522C>A	Missense Mutation	IFNA13	p.C163F	interferon, alpha 13	72 (0.01)	14 (0.71)	1.16
11-01	Gp3	g.chr9:21481134C>A	Missense Mutation	IFNE	p.S187I	interferon, epsilon	201 (0.00)	139 (0.27)	0.43
11-01	Gp3	g.chr6:137527280G>A	Silent	IFNGR1	p.C122C	interferon gamma recep	86 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr3:129185759G>T	Missense Mutation	IFT122	p.R197I	intraflagellar transport 1	53 (0.00)	37 (0.51)	1.37
11-01	Gp3	g.chr3:129233239C>A	Missense Mutation	IFT122	p.L999I	intraflagellar transport 1	18 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr20:42247607G>A	Missense Mutation	IFT52	p.G214S	intraflagellar transport 5	45 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr20:42271264G>A	Splice Site	IFT52	p.Q422Q	intraflagellar transport 5	43 (0.00)	48 (0.23)	0.61
11-01	Gp3	g.chr3:107925528T>A	Missense Mutation	IFT57	p.N201Y	intraflagellar transport 5	52 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr3:185375078A>G	Missense Mutation	IGF2BP2	p.I461T	insulin-like growth fact	35 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr6:160484536G>A	Missense Mutation	IGF2R	p.E1254K	insulin-like growth fact	61 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr17:38610251C>T	Silent	IGFBP4	p.H193H	insulin-like growth fact	45 (0.00)	71 (0.20)	0.53
11-01	Gp3	g.chr19:46627402C>A	Missense Mutation	IGFL3	p.G31C	IGF-like family membe	64 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr19:46627552G>T	Missense Mutation	IGFL3	p.L18I	IGF-like family membe	50 (0.00)	30 (0.33)	0.89
11-01	Gp3	g.chr1:201169501C>A	Missense Mutation	IGFN1	p.Q199K	immunoglobulin-like an	24 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr14:106091465C>A	RNA	IGHG4		immunoglobulin heavy	19 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr11:68705728G>A	Missense Mutation	IGHMBP2	p.C897Y	immunoglobulin mu bin	27 (0.00)	24 (0.38)	1.00

11-01	Gp3	g.chr15:22448537C>A	RNA	IGHV1OR15-1		immunoglobulin heavy	46 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr14:106926273G>A	RNA	IGHV3-43		immunoglobulin heavy	54 (0.00)	37 (0.54)	1.44
11-01	Gp3	g.chr2:89417305C>A	RNA	IGKV1-17		immunoglobulin kappa	93 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr2:90192965C>A	RNA	IGKV1D-13		immunoglobulin kappa	65 (0.00)	40 (0.28)	0.73
11-01	Gp3	g.chr2:89459317C>A	RNA	IGKV6-21		immunoglobulin kappa	52 (0.00)	66 (0.17)	0.44
11-01	Gp3	g.chr22:22764343G>C	RNA	IGLV1-40		immunoglobulin lambd	70 (0.00)	52 (0.21)	0.56
11-01	Gp3	g.chrX:130412616C>A	Missense Mutation	IGSF1	p.K611N	immunoglobulin superfa	25 (0.00)	15 (0.47)	0.78
11-01	Gp3	g.chr3:151163182G>A	Silent	IGSF10	p.H1529H	immunoglobulin superfa	64 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr3:151164485G>T	Missense Mutation	IGSF10	p.A1095D	immunoglobulin superfa	26 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr11:18738428T>C	Missense Mutation	IGSF22	p.K365E	immunoglobulin superfa	68 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr11:18741429G>A	Missense Mutation	IGSF22	p.A177V	immunoglobulin superfa	108 (0.00)	83 (0.24)	0.64
11-01	Gp3	g.chr5:140037180G>T	Missense Mutation	IK	p.K281N	IK cytokine, down-regu	146 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr9:111653606C>A	Missense Mutation	IKBKAP	p.G1013C	inhibitor of kappa light	63 (0.00)	71 (0.20)	0.53
11-01	Gp3	g.chr9:111668667C>G	Missense Mutation	IKBKAP	p.S520T	inhibitor of kappa light	36 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:56428465G>C	Missense Mutation	IKZF4	p.G325R	IKAROS family zinc fir	58 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr5:158745788G>A	Silent	IL12B	p.L271L	interleukin 12B	97 (0.01)	36 (0.17)	0.44
11-01	Gp3	g.chr1:67833543G>C	Missense Mutation	IL12RB2	p.E432Q	interleukin 12 receptor,	195 (0.00)	129 (0.17)	0.45
11-01	Gp3	g.chr15:81601120C>T	Missense Mutation	IL16	p.T1326I	interleukin 16	61 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr13:21295985C>T	Silent	IL17D	p.C167C	interleukin 17D	16 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr3:9965629G>T	Missense Mutation	IL17RC	p.E300D	interleukin 17 receptor	21 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr3:57130498G>A	Missense Mutation	IL17RD	p.L715F	interleukin 17 receptor	107 (0.00)	95 (0.18)	0.48
11-01	Gp3	g.chr3:57132109G>A	Missense Mutation	IL17RD	p.S541F	interleukin 17 receptor	24 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr3:9950957G>A	Nonsense Mutation	IL17RE	p.W264*	interleukin 17 receptor	40 (0.03)	24 (0.21)	0.56
11-01	Gp3	g.chr2:113591039C>A	Missense Mutation	IL1B	p.M71I	interleukin 1, beta	46 (0.00)	31 (0.45)	1.20
11-01	Gp3	g.chr3:190326927G>A	Missense Mutation	IL1RAP	p.G165E	interleukin 1 receptor ac	16 (0.00)	17 (0.53)	1.41
11-01	Gp3	g.chr3:190341152G>T	Silent	IL1RAP	p.V241V	interleukin 1 receptor ac	25 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr2:102851377G>T	Nonsense Mutation	IL1RL2	p.E440*	interleukin 1 receptor-li	65 (0.02)	26 (0.35)	0.92
11-01	Gp3	g.chr6:137322745G>A	Missense Mutation	IL20RA	p.L538F	interleukin 20 receptor,	103 (0.00)	51 (0.31)	0.84
11-01	Gp3	g.chr4:123536976G>T	Nonsense Mutation	IL21	p.S74*	interleukin 21	38 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr12:56733768C>G	Silent	IL23A	p.L150L	interleukin 23, alpha su	27 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr19:14153267G>A	Silent	IL27RA	p.L179L	interleukin 27 receptor,	49 (0.00)	30 (0.47)	1.24
11-01	Gp3	g.chr5:131398045G>A	Missense Mutation	IL3	p.R82K	interleukin 3	149 (0.01)	75 (0.25)	0.68
11-01	Gp3	g.chr5:55204208C>A	Silent	IL31RA	p.I490I	interleukin 31 receptor	62 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr5:55212936G>A	Silent	IL31RA	p.K761K	interleukin 31 receptor	71 (0.00)	25 (0.44)	1.17
11-01	Gp3	g.chr5:55237352G>A	Missense Mutation	IL6ST	p.P772L	interleukin 6 signal tran	38 (0.00)	29 (0.24)	0.64

11-01	Gp3	g.chr7:128034653G>A	Splice Site	IMPDH1	p.S427S	IMP (inosine 5'-monoph	44 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr6:76731869G>A	Silent	IMPG1	p.L210L	interphotoreceptor matri	56 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr1:62594604G>A	Missense Mutation	INADL	p.R1753H	InaD-like (Drosophila)	127 (0.00)	93 (0.17)	0.46
11-01	Gp3	g.chr11:61912726C>A	Missense Mutation	INCENP	p.Q601K	inner centromere protei	52 (0.02)	74 (0.18)	0.47
11-01	Gp3	g.chr7:41729275C>T	Missense Mutation	INHBA	p.M418I	inhibin, beta A	66 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr15:41319799G>C	Missense Mutation	INO80	p.P1015A	INO80 complex subunit	36 (0.00)	24 (0.42)	1.11
11-01	Gp3	g.chr2:206872033G>C	Missense Mutation	INO80D	p.D631E	INO80 complex subunit	53 (0.00)	41 (0.44)	1.17
11-01	Gp3	g.chr2:99152594G>T	Missense Mutation	INPP4A	p.M130I	inositol polyphosphate-	29 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr4:142950446G>T	Intron	INPP4B		inositol polyphosphate-	50 (0.00)	20 (0.40)	1.07
11-01	Gp3	g.chr4:142956004G>T	Intron	INPP4B		inositol polyphosphate-	61 (0.02)	39 (0.18)	0.48
11-01	Gp3	g.chr4:142961873C>T	Intron	INPP4B		inositol polyphosphate-	52 (0.00)	61 (0.18)	0.48
11-01	Gp3	g.chr4:142965031G>A	Intron	INPP4B		inositol polyphosphate-	87 (0.00)	87 (0.22)	0.58
11-01	Gp3	g.chr4:142983390G>T	Intron	INPP4B		inositol polyphosphate-	259 (0.00)	226 (0.26)	0.70
11-01	Gp3	g.chr4:142997217G>T	Intron	INPP4B		inositol polyphosphate-	46 (0.00)	54 (0.22)	0.59
11-01	Gp3	g.chr4:143006417G>C	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr4:143006453C>T	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr4:143021486C>A	Intron	INPP4B		inositol polyphosphate-	84 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr4:143029161G>C	Intron	INPP4B		inositol polyphosphate-	67 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr4:143031801C>T	Intron	INPP4B		inositol polyphosphate-	60 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr4:143031810C>T	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr4:143043362C>A	Missense Mutation	INPP4B	p.G685V	inositol polyphosphate-	54 (0.00)	10 (0.60)	1.60
11-01	Gp3	g.chr4:143044720G>A	Intron	INPP4B		inositol polyphosphate-	42 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr4:143047819C>T	Intron	INPP4B		inositol polyphosphate-	59 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr4:143053592A>T	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr4:143057588C>T	Intron	INPP4B		inositol polyphosphate-	71 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr4:143067854G>T	Intron	INPP4B		inositol polyphosphate-	106 (0.00)	43 (0.28)	0.74
11-01	Gp3	g.chr4:143101044G>A	Intron	INPP4B		inositol polyphosphate-	255 (0.00)	150 (0.15)	0.39
11-01	Gp3	g.chr4:143105372A>G	Intron	INPP4B		inositol polyphosphate-	40 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr4:143117806G>T	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chr4:143121580C>T	Intron	INPP4B		inositol polyphosphate-	83 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr4:143160185G>A	Intron	INPP4B		inositol polyphosphate-	87 (0.01)	52 (0.15)	0.41
11-01	Gp3	g.chr4:143160212C>G	Intron	INPP4B		inositol polyphosphate-	57 (0.02)	41 (0.17)	0.46
11-01	Gp3	g.chr4:143169166G>T	Intron	INPP4B		inositol polyphosphate-	52 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr4:143174439G>A	Intron	INPP4B		inositol polyphosphate-	82 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr4:143184415C>A	Intron	INPP4B		inositol polyphosphate-	70 (0.00)	25 (0.20)	0.53

11-01	Gp3	g.chr4:143185249G>A	Intron	INPP4B	inositol polyphosphate-4	81 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr4:143204706C>T	Intron	INPP4B	inositol polyphosphate-4	36 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr4:143206519C>G	Intron	INPP4B	inositol polyphosphate-4	36 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr4:143236596C>T	Intron	INPP4B	inositol polyphosphate-4	75 (0.01)	50 (0.22)	0.59
11-01	Gp3	g.chr4:143269979G>T	Intron	INPP4B	inositol polyphosphate-4	38 (0.00)	35 (0.26)	0.69
11-01	Gp3	g.chr4:143269990C>T	Intron	INPP4B	inositol polyphosphate-4	40 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr4:143276581T>A	Intron	INPP4B	inositol polyphosphate-4	34 (0.00)	22 (0.55)	1.45
11-01	Gp3	g.chr4:143289115G>C	Intron	INPP4B	inositol polyphosphate-4	51 (0.00)	35 (0.37)	0.99
11-01	Gp3	g.chr4:143319192G>A	Intron	INPP4B	inositol polyphosphate-4	53 (0.00)	37 (0.27)	0.72
11-01	Gp3	g.chr4:143323254C>A	Intron	INPP4B	inositol polyphosphate-4	99 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr4:143324268G>A	Intron	INPP4B	inositol polyphosphate-4	53 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr4:143327970G>A	Intron	INPP4B	inositol polyphosphate-4	62 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr4:143328971A>G	Intron	INPP4B	inositol polyphosphate-4	92 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr4:143332643C>T	Intron	INPP4B	inositol polyphosphate-4	107 (0.01)	78 (0.18)	0.48
11-01	Gp3	g.chr4:143370256T>C	Intron	INPP4B	inositol polyphosphate-4	83 (0.01)	85 (0.16)	0.44
11-01	Gp3	g.chr4:143387319G>A	Intron	INPP4B	inositol polyphosphate-4	87 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr4:143424065A>G	Intron	INPP4B	inositol polyphosphate-4	42 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr4:143426572G>A	Intron	INPP4B	inositol polyphosphate-4	49 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr4:143429289G>A	Intron	INPP4B	inositol polyphosphate-4	63 (0.00)	68 (0.15)	0.39
11-01	Gp3	g.chr4:143438888C>T	Intron	INPP4B	inositol polyphosphate-4	111 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr4:143458252C>T	Intron	INPP4B	inositol polyphosphate-4	88 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr4:143465613C>G	Intron	INPP4B	inositol polyphosphate-4	37 (0.00)	33 (0.64)	1.70
11-01	Gp3	g.chr4:143470430C>G	Intron	INPP4B	inositol polyphosphate-4	44 (0.02)	10 (0.50)	1.33
11-01	Gp3	g.chr4:143475809T>A	Intron	INPP4B	inositol polyphosphate-4	112 (0.01)	64 (0.27)	0.71
11-01	Gp3	g.chr4:143481307C>A	Intron	INPP4B	inositol polyphosphate-4	36 (0.00)	26 (0.65)	1.74
11-01	Gp3	g.chr4:143487073G>A	Intron	INPP4B	inositol polyphosphate-4	70 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr4:143487871C>A	Intron	INPP4B	inositol polyphosphate-4	103 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr4:143492128G>T	Intron	INPP4B	inositol polyphosphate-4	45 (0.00)	46 (0.28)	0.75
11-01	Gp3	g.chr4:143498451C>A	Intron	INPP4B	inositol polyphosphate-4	39 (0.03)	15 (0.47)	1.24
11-01	Gp3	g.chr4:143504762G>T	Intron	INPP4B	inositol polyphosphate-4	51 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr4:143511240G>A	Intron	INPP4B	inositol polyphosphate-4	283 (0.00)	288 (0.18)	0.48
11-01	Gp3	g.chr4:143520126G>A	Intron	INPP4B	inositol polyphosphate-4	32 (0.00)	62 (0.27)	0.73
11-01	Gp3	g.chr4:143544647G>T	Intron	INPP4B	inositol polyphosphate-4	29 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:143577577C>T	Intron	INPP4B	inositol polyphosphate-4	42 (0.00)	24 (0.54)	1.44
11-01	Gp3	g.chr4:143578173C>G	Intron	INPP4B	inositol polyphosphate-4	27 (0.00)	29 (0.21)	0.55

11-01	Gp3	g.chr4:143588413C>T	Intron	INPP4B		inositol polyphosphate-	41 (0.00)	45 (0.31)	0.83
11-01	Gp3	g.chr4:143602706G>A	Intron	INPP4B		inositol polyphosphate-	47 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr4:143617513G>A	Intron	INPP4B		inositol polyphosphate-	56 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr4:143653369G>A	Intron	INPP4B		inositol polyphosphate-	29 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr4:143664070G>A	Intron	INPP4B		inositol polyphosphate-	30 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr4:143675191G>A	Intron	INPP4B		inositol polyphosphate-	37 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr4:143689289G>A	Intron	INPP4B		inositol polyphosphate-	108 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr4:143698258C>A	Intron	INPP4B		inositol polyphosphate-	106 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr4:143700731G>A	Intron	INPP4B		inositol polyphosphate-	117 (0.00)	97 (0.14)	0.38
11-01	Gp3	g.chr4:143715379G>A	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	18 (0.56)	1.48
11-01	Gp3	g.chr4:143719631C>A	Intron	INPP4B		inositol polyphosphate-	17 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr4:143744298C>T	Intron	INPP4B		inositol polyphosphate-	92 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr4:143745379G>A	Intron	INPP4B		inositol polyphosphate-	55 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr4:143746908G>A	Intron	INPP4B		inositol polyphosphate-	180 (0.00)	110 (0.15)	0.41
11-01	Gp3	g.chr4:143750320T>C	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	25 (0.64)	1.71
11-01	Gp3	g.chr4:143765787G>T	Intron	INPP4B		inositol polyphosphate-	106 (0.00)	85 (0.20)	0.53
11-01	Gp3	g.chr1:38353933G>A	Missense Mutation	INPP5B	p.P294L	inositol polyphosphate-	29 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr1:38353983C>G	Missense Mutation	INPP5B	p.Q277H	inositol polyphosphate-	28 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr17:60002426G>A	Silent	INTS2	p.L110L	integrator complex subu	134 (0.00)	76 (0.28)	0.74
11-01	Gp3	g.chr1:153745729G>A	Missense Mutation	INTS3	p.G1038S	integrator complex subu	95 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr7:65173473C>A	RNA	INTS4L2		integrator complex subu	34 (0.03)	39 (0.18)	0.48
11-01	Gp3	g.chr4:128637517G>T	Missense Mutation	INTU	p.V919F	inturned planar cell pola	28 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr13:98637686G>A	Missense Mutation	IPO5	p.M61I	importin 5	76 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr13:98637699C>A	Missense Mutation	IPO5	p.L66I	importin 5	81 (0.00)	41 (0.32)	0.85
11-01	Gp3	g.chr12:30802127C>T	Missense Mutation	IPO8	p.A533T	importin 8	89 (0.01)	63 (0.14)	0.38
11-01	Gp3	g.chr2:237246950C>A	Missense Mutation	IQCA1	p.V678L	IQ motif containing wit	117 (0.00)	46 (0.22)	0.58
11-01	Gp3	g.chr2:237272521C>A	Nonsense Mutation	IQCA1	p.E591*	IQ motif containing wit	76 (0.00)	76 (0.32)	0.84
11-01	Gp3	g.chr2:237272526C>A	Missense Mutation	IQCA1	p.C589F	IQ motif containing wit	74 (0.00)	74 (0.31)	0.83
11-01	Gp3	g.chr12:113633544C>A	Nonsense Mutation	IQCD	p.E294*	IQ motif containing D	39 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr3:159604056C>T	Silent	IQCJ-SCHIP1	p.D273D	IQCJ-SCHIP1 readthrou	50 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr16:19741781G>A	Missense Mutation	IQCK	p.E71K	IQ motif containing K	31 (0.00)	42 (0.29)	0.76
11-01	Gp3	g.chr15:91019945G>A	Silent	IQGAP1	p.L945L	IQ motif containing GT	97 (0.00)	53 (0.32)	0.86
11-01	Gp3	g.chr1:156505014C>T	Missense Mutation	IQGAP3	p.V1150I	IQ motif containing GT	166 (0.00)	142 (0.20)	0.54
11-01	Gp3	g.chr3:10251293C>A	Missense Mutation	IRAK2	p.H149N	interleukin-1 receptor-a	23 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr4:185309945C>T	Silent	IRF2	p.S339S	interferon regulatory fac	51 (0.00)	14 (0.36)	0.95

11-01	Gp3	g.chr16:47196555C>A	Missense Mutation	ITFG1	p.A492S	integrin alpha FG-GAP	51 (0.00)	43 (0.28)	0.74
11-01	Gp3	g.chr5:52160873C>T	Silent	ITGA1	p.V151V	integrin, alpha 1	79 (0.01)	55 (0.20)	0.53
11-01	Gp3	g.chr1:145530383G>A	Missense Mutation	ITGA10	p.E200K	integrin, alpha 10	70 (0.00)	79 (0.18)	0.47
11-01	Gp3	g.chr1:145535883C>T	Missense Mutation	ITGA10	p.R691C	integrin, alpha 10	58 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr17:48154801G>A	Missense Mutation	ITGA3	p.R710Q	integrin, alpha 3 (antige	37 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr17:48155574G>A	Silent	ITGA3	p.S741S	integrin, alpha 3 (antige	69 (0.00)	62 (0.35)	0.95
11-01	Gp3	g.chr2:173339739C>A	Missense Mutation	ITGA6	p.Q357K	integrin, alpha 6	24 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr10:15714677C>T	Missense Mutation	ITGA8	p.A250T	integrin, alpha 8	55 (0.00)	33 (0.36)	0.97
11-01	Gp3	g.chr17:3620025C>T	Missense Mutation	ITGAE	p.G1134D	integrin, alpha E (antige	183 (0.00)	89 (0.24)	0.63
11-01	Gp3	g.chr16:31288342G>A	Silent	ITGAM	p.V395V	integrin, alpha M (comp	21 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr2:187532428G>A	Silent	ITGAV	p.P786P	integrin, alpha V	98 (0.01)	31 (0.26)	0.69
11-01	Gp3	g.chr7:20438579G>A	Missense Mutation	ITGB8	p.G415S	integrin, beta 8	27 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr3:52833884C>G	Missense Mutation	ITIH3	p.P341R	inter-alpha-trypsin inhib	63 (0.02)	49 (0.14)	0.38
11-01	Gp3	g.chr10:7621720G>C	Missense Mutation	ITIH5	p.I472M	inter-alpha-trypsin inhib	28 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr12:26752200G>C	Missense Mutation	ITPR2	p.Q1294E	inositol 1,4,5-trisphosph	66 (0.00)	46 (0.26)	0.70
11-01	Gp3	g.chr21:35134278T>A	Missense Mutation	ITSN1	p.L259Q	intersectin 1 (SH3 doma	76 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr2:24484463G>A	Missense Mutation	ITSN2	p.T835I	intersectin 2	48 (0.00)	75 (0.16)	0.43
11-01	Gp3	g.chr6:150715381C>T	Missense Mutation	IYD	p.A226V	iodotyrosine deiodinase	78 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr1:65344806G>A	Silent	JAK1	p.L77L	Janus kinase 1	50 (0.00)	47 (0.36)	0.96
11-01	Gp3	g.chr10:133961531G>A	Missense Mutation	JAKMIP3	p.E609K	Janus kinase and microt	21 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr7:27872454C>G	Missense Mutation	JAZF1	p.V233L	JAZF zinc finger 1	74 (0.00)	39 (0.31)	0.82
11-01	Gp3	g.chr15:42136678G>A	Missense Mutation	JMJD7-PLA2G	p.V528I	JMJD7-PLA2G4B readt	148 (0.00)	145 (0.15)	0.40
11-01	Gp3	g.chr3:124196149C>A	Missense Mutation	KALRN	p.L1385I	kalirin, RhoGEF kinase	52 (0.02)	31 (0.23)	0.60
11-01	Gp3	g.chr3:124398380G>C	Missense Mutation	KALRN	p.V82L	kalirin, RhoGEF kinase	36 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr9:732573G>A	Missense Mutation	KANK1	p.M1067I	KN motif and ankyrin re	139 (0.00)	62 (0.26)	0.41
11-01	Gp3	g.chr12:49065666C>T	Missense Mutation	KANSL2	p.D209N	KAT8 regulatory NSL c	196 (0.00)	104 (0.17)	0.46
11-01	Gp3	g.chr2:97270020G>T	Missense Mutation	KANSL3	p.L706M	KAT8 regulatory NSL c	30 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr10:76602934T>A	Missense Mutation	KAT6B	p.W107R	K(lysine) acetyltransfera	62 (0.00)	71 (0.31)	0.83
11-01	Gp3	g.chr13:41705491G>T	Missense Mutation	KBTBD6	p.A386D	kelch repeat and BTB (I	79 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr3:67054609C>T	Silent	KBTBD8	p.N406N	kelch repeat and BTB (I	66 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr11:30032321G>A	Silent	KCNA4	p.D635D	potassium voltage-gated	62 (0.00)	35 (0.49)	1.30
11-01	Gp3	g.chr19:49573971G>A	Silent	KCNA7	p.N240N	potassium voltage-gated	48 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr1:6145265G>A	Splice Site	KCNAB2	p.A95T	potassium voltage-gated	37 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr20:47990765G>A	Silent	KCNB1	p.S444S	potassium voltage-gated	29 (0.00)	30 (0.43)	1.16
11-01	Gp3	g.chr20:47991481G>A	Silent	KCNB1	p.L206L	potassium voltage-gated	43 (0.00)	29 (0.31)	0.83

11-01	Gp3	g.chr8:73849231C>A	Silent	KCNB2	p.I547I	potassium voltage-gated	80 (0.00)	50 (0.12)	0.40
11-01	Gp3	g.chr8:73849540G>A	Silent	KCNB2	p.P650P	potassium voltage-gated	42 (0.00)	33 (0.15)	0.50
11-01	Gp3	g.chr8:73849570T>A	Silent	KCNB2	p.P660P	potassium voltage-gated	61 (0.02)	29 (0.28)	0.92
11-01	Gp3	g.chr17:40315246C>A	Splice Site	KCNH4	p.G862W	potassium voltage-gated	27 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr17:40327651G>T	Silent	KCNH4	p.I311I	potassium voltage-gated	30 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr14:63174643C>T	Silent	KCNH5	p.E850E	potassium voltage-gated	45 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr2:163228368C>T	Missense Mutation	KCNH7	p.V1188I	potassium voltage-gated	75 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr2:163250985A>G	Missense Mutation	KCNH7	p.L875P	potassium voltage-gated	26 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr6:18197404C>A	Silent	KDM1B	p.I230I	lysine (K)-specific deme	42 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr5:137727178A>G	Silent	KDM3B	p.E619E	lysine (K)-specific deme	99 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr5:137762882G>T	Nonsense Mutation	KDM3B	p.E1503*	lysine (K)-specific deme	74 (0.00)	74 (0.30)	0.79
11-01	Gp3	g.chr11:94731574C>T	Silent	KDM4D	p.D346D	lysine (K)-specific deme	36 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr1:202698199G>A	Missense Mutation	KDM5B	p.R1534C	lysine (K)-specific deme	50 (0.02)	45 (0.33)	0.89
11-01	Gp3	g.chr1:202731917G>A	Silent	KDM5B	p.S276S	lysine (K)-specific deme	123 (0.00)	104 (0.18)	0.49
11-01	Gp3	g.chr17:7754457G>T	Missense Mutation	KDM6B	p.Q1264H	lysine (K)-specific deme	33 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr18:61011667G>T	Silent	KDSR	p.G223G	3-ketodihydrosphingosi	104 (0.00)	112 (0.21)	0.57
11-01	Gp3	g.chr19:6420461G>A	Silent	KHSRP	p.Y149Y	KH-type splicing regula	24 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr17:26948453C>T	Missense Mutation	KIAA0100	p.G1675R	KIAA0100	60 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr17:26962288G>T	Missense Mutation	KIAA0100	p.L773M	KIAA0100	89 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr19:34818457T>A	Missense Mutation	KIAA0355	p.S279R	KIAA0355	34 (0.00)	32 (0.34)	0.92
11-01	Gp3	g.chr17:6493272G>A	Silent	KIAA0753	p.A871A	KIAA0753	27 (0.00)	12 (0.67)	1.78
11-01	Gp3	g.chr17:6511743G>A	Missense Mutation	KIAA0753	p.T585I	KIAA0753	97 (0.00)	63 (0.19)	0.51
11-01	Gp3	g.chr5:5461121G>A	Silent	KIAA0947	p.S558S		60 (0.00)	70 (0.37)	0.99
11-01	Gp3	g.chr1:92642888C>T	Missense Mutation	KIAA1107	p.T275I	KIAA1107	83 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr1:92646248C>A	Missense Mutation	KIAA1107	p.A565E	KIAA1107	34 (0.00)	34 (0.32)	0.86
11-01	Gp3	g.chr4:123170680G>A	Silent	KIAA1109	p.K1851K	KIAA1109	66 (0.00)	55 (0.18)	0.48
11-01	Gp3	g.chr7:141366198G>A	Nonsense Mutation	KIAA1147	p.Q237*	KIAA1147	26 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chrX:118215397G>A	Silent	KIAA1210	p.L1675L	KIAA1210	86 (0.00)	52 (0.29)	0.48
11-01	Gp3	g.chr4:37432311G>T	Nonsense Mutation	KIAA1239	p.E159*		43 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr3:128690239C>A	Missense Mutation	KIAA1257	p.Q241H	KIAA1257	126 (0.00)	99 (0.15)	0.40
11-01	Gp3	g.chr3:113737644C>A	Silent	KIAA1407	p.G348G	KIAA1407	45 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr3:113761588G>T	Missense Mutation	KIAA1407	p.P126Q	KIAA1407	48 (0.00)	15 (0.67)	1.78
11-01	Gp3	g.chr9:5769254C>A	Missense Mutation	KIAA1432	p.T1141N		98 (0.00)	40 (0.35)	0.55
11-01	Gp3	g.chr7:138583765G>A	Silent	KIAA1549	p.N1261N	KIAA1549	90 (0.00)	93 (0.17)	0.46
11-01	Gp3	g.chr7:138603909C>T	Missense Mutation	KIAA1549	p.D155N	KIAA1549	99 (0.00)	72 (0.19)	0.52

11-01	Gp3	g.chr11:33565594G>A	Missense Mutation	KIAA1549L	p.V532M	KIAA1549-like	204 (0.00)	149 (0.15)	0.39
11-01	Gp3	g.chr11:33589661A>T	Missense Mutation	KIAA1549L	p.N1076I	KIAA1549-like	23 (0.00)	9 (0.67)	1.78
11-01	Gp3	g.chr12:32135977C>A	Silent	KIAA1551	p.L696L	KIAA1551	42 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr12:32145377C>T	Missense Mutation	KIAA1551	p.P1718S	KIAA1551	73 (0.00)	71 (0.15)	0.41
11-01	Gp3	g.chr6:111587126C>T	Missense Mutation	KIAA1919	p.H121Y	KIAA1919	43 (0.00)	30 (0.33)	0.52
11-01	Gp3	g.chrX:73960813C>T	Silent	KIAA2022	p.Q1193Q	KIAA2022	29 (0.00)	18 (0.39)	0.65
11-01	Gp3	g.chr1:200586947G>C	Nonsense Mutation	KIF14	p.S302*	kinesin family member	102 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr20:16409611C>T	Silent	KIF16B	p.T487T	kinesin family member	63 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr1:21031139C>A	Missense Mutation	KIF17	p.M308I	kinesin family member	23 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr17:43004387G>A	Missense Mutation	KIF18B	p.T779I	kinesin family member	23 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr1:10356996A>T	Missense Mutation	KIF1B	p.N635Y	kinesin family member	43 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr12:39688279C>T	Missense Mutation	KIF21A	p.D1658N	kinesin family member	83 (0.00)	78 (0.22)	0.58
11-01	Gp3	g.chr1:200965348C>A	Missense Mutation	KIF21B	p.E751D	kinesin family member	96 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr1:200969562G>T	Missense Mutation	KIF21B	p.D547E	kinesin family member	36 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr16:29814107G>T	Missense Mutation	KIF22	p.S365I	kinesin family member	57 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr9:34257363C>T	Missense Mutation	KIF24	p.E748K	kinesin family member	142 (0.01)	50 (0.16)	0.43
11-01	Gp3	g.chr1:245809504C>G	Nonsense Mutation	KIF26B	p.S727*	kinesin family member	42 (0.00)	26 (0.65)	1.74
11-01	Gp3	g.chr1:45216132C>A	Missense Mutation	KIF2C	p.T112N	kinesin family member	150 (0.00)	72 (0.15)	0.41
11-01	Gp3	g.chr1:45220448G>C	Missense Mutation	KIF2C	p.W230C	kinesin family member	147 (0.00)	99 (0.14)	0.38
11-01	Gp3	g.chr1:45226316G>T	Missense Mutation	KIF2C	p.S542I	kinesin family member	33 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr5:132046737G>T	Nonsense Mutation	KIF3A	p.S381*	kinesin family member	75 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr5:132062179C>T	Missense Mutation	KIF3A	p.A98T	kinesin family member	94 (0.00)	73 (0.44)	1.17
11-01	Gp3	g.chr5:154395472G>T	Nonsense Mutation	KIF4B	p.E685*	kinesin family member	184 (0.00)	88 (0.16)	0.42
11-01	Gp3	g.chr12:57958721G>A	Missense Mutation	KIF5A	p.V156M	kinesin family member	32 (0.00)	22 (0.41)	1.09
11-01	Gp3	g.chr12:57963357G>C	Missense Mutation	KIF5A	p.E336D	kinesin family member	77 (0.00)	108 (0.18)	0.47
11-01	Gp3	g.chr12:57972035G>T	Missense Mutation	KIF5A	p.E816D	kinesin family member	62 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr6:39512344T>G	Missense Mutation	KIF6	p.R471S	kinesin family member	57 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr19:55284899G>A	Missense Mutation	KIR2DL1	p.R62K	killer cell immunoglobu	15 (0.00)	13 (0.62)	1.64
11-01	Gp3	g.chr19:55340886C>T	Silent	KIR3DL1	p.F357F	killer cell immunoglobu	85 (0.01)	46 (0.26)	0.70
11-01	Gp3	g.chr1:158058186G>A	Missense Mutation	KIRREL	p.C127Y	kin of IRRE like (Droso	46 (0.00)	61 (0.46)	1.22
11-01	Gp3	g.chr19:36350494C>T	Missense Mutation	KIRREL2	p.P212S	kin of IRRE like 2 (Dro	45 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr2:10188283C>A	Silent	KLF11	p.T273T	Kruppel-like factor 11	43 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr4:38691488C>T	Missense Mutation	KLF3	p.A228V	Kruppel-like factor 3 (b	116 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr10:3826273C>A	Intron	KLF6		Kruppel-like factor 6	20 (0.00)	22 (0.50)	1.33
11-01	Gp3	g.chr16:87782400G>A	Nonsense Mutation	KLHDC4	p.Q129*	kelch domain containin	99 (0.00)	23 (0.26)	0.70

11-01	Gp3	g.chr1:205308854G>T	Missense Mutation	KLHDC8A	p.D153E	kelch domain containing	17 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr3:49211718C>G	Silent	KLHDC8B	p.P141P	kelch domain containing	23 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr18:30257157C>G	Silent	KLHL14	p.V575V	kelch-like family memb	67 (0.01)	38 (0.21)	0.56
11-01	Gp3	g.chr4:166232672C>T	Missense Mutation	KLHL2	p.P436S	kelch-like family memb	86 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr2:170591945G>A	Missense Mutation	KLHL23	p.G141R	kelch-like family memb	23 (0.00)	28 (0.29)	0.76
11-01	Gp3	g.chr2:170592626G>A	Missense Mutation	KLHL23	p.G368S	kelch-like family memb	90 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr4:39083752G>C	Missense Mutation	KLHL5	p.L276F	kelch-like family memb	54 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr3:183217491C>T	Missense Mutation	KLHL6	p.R345H	kelch-like family memb	47 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr3:183226234G>A	Silent	KLHL6	p.C174C	kelch-like family memb	60 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr19:51559900C>T	Missense Mutation	KLK13	p.E260K	kallikrein-related peptid	54 (0.00)	55 (0.24)	0.63
11-01	Gp3	g.chr19:51559937G>A	Silent	KLK13	p.V247V	kallikrein-related peptid	50 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr7:151845353G>A	Silent	KMT2C	p.L4553L	lysine (K)-specific meth	34 (0.00)	50 (0.20)	0.53
11-01	Gp3	g.chr7:151856094C>T	Missense Mutation	KMT2C	p.G3842R	lysine (K)-specific meth	37 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr7:151884347C>T	Splice Site	KMT2C	p.D1670N	lysine (K)-specific meth	33 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr12:49434175G>A	Missense Mutation	KMT2D	p.R2460C	lysine (K)-specific meth	23 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr3:186459877G>A	Silent	KNG1	p.Q564Q	kininogen 1	80 (0.00)	61 (0.18)	0.48
11-01	Gp3	g.chr17:66038449G>T	Missense Mutation	KPNA2	p.W184L	karyopherin alpha 2 (R	111 (0.01)	74 (0.22)	0.58
11-01	Gp3	g.chr1:32635597G>A	Silent	KPNA6	p.E453E	karyopherin alpha 6 (im	54 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr17:45738531G>A	Missense Mutation	KPNB1	p.C83Y	karyopherin (importin)	27 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr12:25380198G>T	Missense Mutation	KRAS	p.T87N	Kirsten rat sarcoma vira	24 (0.00)	31 (0.55)	1.46
11-01	Gp3	g.chr12:25398232C>A	Silent	KRAS	p.V29V	Kirsten rat sarcoma vira	36 (0.03)	37 (0.24)	0.65
11-01	Gp3	g.chr17:8272813C>A	Missense Mutation	KRBA2	p.S291I	KRAB-A domain contai	44 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr17:38976883C>T	Silent	KRT10	p.E249E	keratin 10	64 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr17:39741296G>A	Missense Mutation	KRT14	p.T180I	keratin 14	51 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr12:95228286G>A	RNA	KRT19P2		keratin 19 pseudogene 2	77 (0.00)	42 (0.14)	0.49
11-01	Gp3	g.chr17:38956024G>T	Missense Mutation	KRT28	p.A41D	keratin 28	19 (0.00)	11 (0.82)	2.18
11-01	Gp3	g.chr12:53187908C>T	Missense Mutation	KRT3	p.D285N	keratin 3	20 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr12:52632550C>T	Silent	KRT7	p.L228L	keratin 7	43 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:52635334G>T	Missense Mutation	KRT7	p.D258Y	keratin 7	53 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr12:52946598G>A	Silent	KRT71	p.A88A	keratin 71	26 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr12:52946670C>T	Silent	KRT71	p.G64G	keratin 71	28 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr12:52967153G>A	Missense Mutation	KRT74	p.R137C	keratin 74	17 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr12:53169381C>T	Silent	KRT76	p.R202R	keratin 76	31 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr12:52574300C>T	Silent	KRT80	p.E221E	keratin 80	42 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr12:52799673C>T	Missense Mutation	KRT82	p.R130H	keratin 82	66 (0.02)	44 (0.30)	0.79

11-01	Gp3	g.chr21:46011416C>T	Missense Mutation	KRTAP10-6	p.C317Y	keratin associated protei	22 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr21:31933428C>G	Missense Mutation	KRTAP19-7	p.G61R	keratin associated protei	94 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr21:31709889C>A	Missense Mutation	KRTAP27-1	p.R33I	keratin associated protei	82 (0.00)	74 (0.32)	0.86
11-01	Gp3	g.chr17:25934955G>T	Silent	KSR1	p.R555R	kinase suppressor of ras	40 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr12:117968754C>A	Silent	KSR2	p.S598S	kinase suppressor of ras	57 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr3:134322856C>A	Silent	KY	p.R517R	kyphoscoliosis peptidas	52 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr6:130392196G>A	Missense Mutation	L3MBTL3	p.V390I	l(3)mbt-like 3 (Drosoph	95 (0.00)	84 (0.15)	0.41
11-01	Gp3	g.chr13:44464290C>T	Nonsense Mutation	LACC1	p.Q392*	laccase (multicopper ox	56 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr18:6973091G>C	Missense Mutation	LAMA1	p.L2247V	laminin, alpha 1	88 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr18:6978322G>A	Silent	LAMA1	p.S2021S	laminin, alpha 1	50 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr18:7037710C>A	Missense Mutation	LAMA1	p.S535I	laminin, alpha 1	44 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr18:7080338G>A	Silent	LAMA1	p.P60P	laminin, alpha 1	89 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr6:129813598C>T	Silent	LAMA2	p.A2738A	laminin, alpha 2	147 (0.00)	55 (0.22)	0.58
11-01	Gp3	g.chr18:21484044C>A	Missense Mutation	LAMA3	p.L2156M	laminin, alpha 3	70 (0.01)	41 (0.29)	0.78
11-01	Gp3	g.chr7:107577700C>T	Missense Mutation	LAMB1	p.E1262K	laminin, beta 1	63 (0.02)	25 (0.60)	1.60
11-01	Gp3	g.chr7:107580528C>A	Missense Mutation	LAMB1	p.V1223L	laminin, beta 1	50 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr7:107594199C>T	Splice Site	LAMB1	p.G952D	laminin, beta 1	67 (0.00)	42 (0.21)	0.57
11-01	Gp3	g.chr3:49167389C>A	Missense Mutation	LAMB2	p.A430S	laminin, beta 2 (laminin	57 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr1:209805930G>A	Nonsense Mutation	LAMB3	p.Q274*	laminin, beta 3	47 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr1:209811935C>G	Missense Mutation	LAMB3	p.R81P	laminin, beta 3	27 (0.00)	44 (0.20)	0.55
11-01	Gp3	g.chr9:133963151G>A	Missense Mutation	LAMC3	p.R1475H	laminin, gamma 3	34 (0.00)	40 (0.40)	1.07
11-01	Gp3	g.chrX:119581775C>A	Missense Mutation	LAMP2	p.G221V	lysosomal-associated m	21 (0.00)	18 (0.44)	0.74
11-01	Gp3	g.chr22:33780227G>T	Missense Mutation	LARGE	p.T319N	like-glycosyltransferase	51 (0.00)	49 (0.24)	0.65
11-01	Gp3	g.chr5:145524042G>T	Missense Mutation	LARS	p.L550M	leucyl-tRNA synthetase	37 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr3:45533051C>A	Missense Mutation	LARS2	p.Q428K	leucyl-tRNA synthetase	52 (0.00)	46 (0.33)	0.87
11-01	Gp3	g.chr6:150004617G>A	Silent	LATS1	p.T536T	large tumor suppressor	85 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr11:111428306T>C	Silent	LAYN	p.I241I	layilin	270 (0.00)	91 (0.15)	0.41
11-01	Gp3	g.chr2:30546402G>T	Nonstop Mutation	LBH	p.*49Y	limb bud and heart deve	151 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chr6:80197235A>C	Missense Mutation	LCA5	p.I527S	Leber congenital amaur	68 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr21:40778134C>T	Missense Mutation	LCA5L	p.E563K	Leber congenital amaur	39 (0.00)	12 (0.58)	0.66
11-01	Gp3	g.chr4:17847472C>A	Missense Mutation	LCORL	p.A277S	ligand dependent nuclea	79 (0.00)	45 (0.33)	0.89
11-01	Gp3	g.chr11:18425354G>C	Missense Mutation	LDHA	p.E236Q	lactate dehydrogenase A	33 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr12:21796927A>T	Silent	LDHB	p.I121I	lactate dehydrogenase B	36 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr12:21797026G>T	Silent	LDHB	p.A88A	lactate dehydrogenase B	25 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr19:11230832C>A	Missense Mutation	LDLR	p.S637Y	low density lipoprotein	27 (0.00)	18 (0.33)	0.89

11-01	Gp3	g.chr19:11240277C>T	Silent	LDLR	p.P826P	low density lipoprotein	64 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr11:63283134G>T	Missense Mutation	LGALS12	p.Q272H	lectin, galactoside-bindi	19 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr19:35616200G>A	Missense Mutation	LGI4	p.A504V	leucine-rich repeat LGI	16 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr12:71977707C>A	Silent	LGR5	p.V639V	leucine-rich repeat conta	57 (0.00)	24 (0.62)	1.67
11-01	Gp3	g.chr2:48936161C>A	Splice Site	LHCGR	p.L202L	luteinizing hormone/chc	71 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr17:33310124C>A	Missense Mutation	LIG3	p.Q34K	ligase III, DNA, ATP-d	42 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr19:55106171G>A	Missense Mutation	LILRA1	p.V38M	leukocyte immunoglobu	64 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr19:54845216G>A	Missense Mutation	LILRA4	p.P426S	leukocyte immunoglobu	50 (0.02)	42 (0.14)	0.38
11-01	Gp3	g.chr19:54783780C>T	Missense Mutation	LILRB2	p.R74Q	leukocyte immunoglobu	77 (0.00)	64 (0.28)	0.75
11-01	Gp3	g.chr12:50571267C>A	Missense Mutation	LIMA1	p.E621D	LIM domain and actin b	50 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr12:50616135C>A	Missense Mutation	LIMA1	p.R100I	LIM domain and actin b	19 (0.05)	14 (0.36)	0.95
11-01	Gp3	g.chr4:41526432G>A	Silent	LIMCH1	p.L58L	LIM and calponin homo	35 (0.00)	56 (0.16)	0.43
11-01	Gp3	g.chr4:41648780T>A	Missense Mutation	LIMCH1	p.V353D	LIM and calponin homo	72 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr7:73530281G>A	Missense Mutation	LIMK1	p.M550I	LIM domain kinase 1	37 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr2:128396970C>G	Silent	LIMS2	p.V152V	LIM and senescent cell	93 (0.00)	115 (0.21)	0.56
11-01	Gp3	g.chr18:1363061C>A	lincRNA	LINC00470		long intergenic non-prot	47 (0.02)	22 (0.50)	1.33
11-01	Gp3	g.chr3:108897260A>T	lincRNA	LINC00488		long intergenic non-prot	16 (0.00)	10 (0.70)	1.87
11-01	Gp3	g.chr3:108897261C>T	lincRNA	LINC00488		long intergenic non-prot	16 (0.00)	10 (0.70)	1.87
11-01	Gp3	g.chr6:10430289G>A	lincRNA	LINC00518		long intergenic non-prot	50 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr6:10430302G>A	lincRNA	LINC00518		long intergenic non-prot	49 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr7:47805840T>A	RNA	LINC00525		long intergenic non-prot	22 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr13:21894838C>A	lincRNA	LINC00539		long intergenic non-prot	16 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr21:35335554C>G	RNA	LINC00649		long intergenic non-prot	21 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr3:106825105C>A	lincRNA	LINC00882		long intergenic non-prot	85 (0.00)	71 (0.21)	0.56
11-01	Gp3	g.chr3:106825649C>T	lincRNA	LINC00882		long intergenic non-prot	61 (0.00)	33 (0.30)	0.81
11-01	Gp3	g.chr3:195392946T>C	lincRNA	LINC00969		long intergenic non-prot	55 (0.02)	33 (0.18)	0.48
11-01	Gp3	g.chr15:77906638G>A	Silent	LINGO1	p.G537G	leucine rich repeat and I	39 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr15:77907737G>T	Nonsense Mutation	LINGO1	p.S171*	leucine rich repeat and I	57 (0.00)	90 (0.17)	0.44
11-01	Gp3	g.chr10:90484356G>T	Missense Mutation	LIPK	p.G19V	lipase, family member K	37 (0.00)	18 (0.39)	0.53
11-01	Gp3	g.chr10:90528622C>T	Silent	LIPN	p.I203I	lipase, family member N	69 (0.00)	22 (0.41)	0.56
11-01	Gp3	g.chr10:90537820G>A	Missense Mutation	LIPN	p.A340T	lipase, family member N	68 (0.00)	38 (0.29)	0.40
11-01	Gp3	g.chr1:145498775C>T	Silent	LIX1L	p.C337C	Lix1 homolog (chicken)	83 (0.00)	72 (0.15)	0.41
11-01	Gp3	g.chr22:37361505T>C	RNA	LL22NC01-81G9.3			75 (0.01)	42 (0.29)	0.76
11-01	Gp3	g.chr15:75116803G>A	Missense Mutation	LMAN1L	p.G479S	lectin, mannose-binding	90 (0.00)	69 (0.25)	0.66
11-01	Gp3	g.chr12:49494202G>T	Missense Mutation	LMBR1L	p.S403R	limb development meml	193 (0.00)	140 (0.22)	0.59

11-01	Gp3	g.chr16:1004514G>A	Silent	LMF1	p.L116L	lipase maturation factor	73 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr3:197748464G>A	Missense Mutation	LMLN	p.E542K	leishmanolysin-like (me	52 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr13:76393627G>A	Silent	LMO7	p.K488K	LIM domain 7	29 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr18:44102127G>C	Missense Mutation	LOXHD1	p.S563R	lipoxygenase homology	21 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr18:44125286C>G	Missense Mutation	LOXHD1	p.D94H	lipoxygenase homology	23 (0.00)	14 (0.79)	2.10
11-01	Gp3	g.chr15:74241853G>A	Silent	LOXL1	p.V552V	lysyl oxidase-like 1	31 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr6:160905166G>C	RNA	LPAL2		lipoprotein, Lp(a)-like 2	47 (0.00)	33 (0.42)	1.13
11-01	Gp3	g.chr1:82436153G>C	Missense Mutation	LPHN2	p.L959F	latrophilin 2	71 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr1:82456601G>A	Silent	LPHN2	p.P1384P	latrophilin 2	49 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr18:2931284C>T	Missense Mutation	LPIN2	p.G476S	lipin 2	27 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr1:99772002C>G	Missense Mutation	LPPR4	p.I576M		50 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:155665568G>A	Silent	LRAT	p.A30A	lecithin retinol acyltrans	23 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr4:151849757C>G	Missense Mutation	LRBA	p.D154H	LPS-responsive vesicle	32 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr7:133812142C>T	Missense Mutation	LRGUK	p.L8F	leucine-rich repeats and	63 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr10:85994071C>T	Missense Mutation	LRIT1	p.G218D	leucine-rich repeat, imm	19 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr8:105509727C>A	Missense Mutation	LRP12	p.R351S	low density lipoprotein	25 (0.00)	29 (0.52)	1.38
11-01	Gp3	g.chr2:141283899C>A	Nonsense Mutation	LRP1B	p.E2595*	low density lipoprotein	53 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr2:170101314C>A	Missense Mutation	LRP2	p.A970S	low density lipoprotein	23 (0.00)	21 (0.48)	1.27
11-01	Gp3	g.chr12:12315272C>A	Missense Mutation	LRP6	p.V712L	low density lipoprotein	91 (0.00)	91 (0.27)	0.73
11-01	Gp3	g.chr1:53727740C>T	Splice Site	LRP8	p.E191E	low density lipoprotein	23 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr14:24532540G>A	Missense Mutation	LRRC16B	p.S926N	leucine rich repeat conta	20 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr17:62859116G>A	Missense Mutation	LRRC37A3	p.A1025V	leucine rich repeat conta	88 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr17:62864646C>T	Missense Mutation	LRRC37A3	p.G996E	leucine rich repeat conta	69 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr7:127668792G>T	Silent	LRRC4	p.I634I	leucine rich repeat conta	79 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr17:17900940C>G	Missense Mutation	LRRC48	p.H331D	leucine rich repeat conta	43 (0.00)	55 (0.18)	0.48
11-01	Gp3	g.chr17:17919414G>T	Missense Mutation	LRRC48	p.G455W	leucine rich repeat conta	85 (0.00)	96 (0.16)	0.42
11-01	Gp3	g.chr15:71302202C>T	Silent	LRRC49	p.A194A	leucine rich repeat conta	82 (0.01)	34 (0.15)	0.39
11-01	Gp3	g.chr15:42836299G>A	Silent	LRRC57	p.T234T	leucine rich repeat conta	94 (0.00)	68 (0.22)	0.59
11-01	Gp3	g.chr1:90399220C>A	Nonsense Mutation	LRRC8D	p.S198*	leucine rich repeat conta	27 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr1:90399848T>C	Silent	LRRC8D	p.S407S	leucine rich repeat conta	50 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr8:86041607C>T	Missense Mutation	LRRCC1	p.A540V	leucine rich repeat and c	79 (0.00)	22 (0.32)	1.06
11-01	Gp3	g.chr12:85450933C>T	Nonsense Mutation	LRRIQ1	p.R788*	leucine-rich repeats and	90 (0.00)	42 (0.33)	0.89
11-01	Gp3	g.chr12:40728846G>T	Missense Mutation	LRRK2	p.L1945F	leucine-rich repeat kinas	56 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr3:3887642C>T	Silent	LRRN1	p.I439I	leucine rich repeat neur	56 (0.00)	55 (0.31)	0.82
11-01	Gp3	g.chr3:194365345G>A	Missense Mutation	LSG1	p.A585V	large 60S subunit nuclea	43 (0.00)	17 (0.41)	1.10

11-01	Gp3	g.chr12:21175799C>A	Missense Mutation	LST3	p.S166Y		143 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr12:96416006C>A	Silent	LTA4H	p.V168V	leukotriene A4 hydrolas	26 (0.00)	25 (0.48)	1.63
11-01	Gp3	g.chr2:33518241C>A	Missense Mutation	LTBP1	p.L664M	latent transforming grow	23 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr6:144178561G>A	Silent	LTV1	p.E173E	LTV1 ribosome biogene	34 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr6:144184359G>T	Missense Mutation	LTV1	p.R418L	LTV1 ribosome biogene	106 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr12:91502700C>G	Missense Mutation	LUM	p.Q19H	lumican	19 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr2:160667085G>T	Missense Mutation	LY75-CD302	p.Q1551K	LY75-CD302 readthrou	61 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr2:160746763G>T	Missense Mutation	LY75-CD302	p.L255M	LY75-CD302 readthrou	64 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr2:160755242C>A	Missense Mutation	LY75-CD302	p.K141N	LY75-CD302 readthrou	96 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr2:99860539G>A	Missense Mutation	LYG2	p.A148V	lysozyme G-like 2	82 (0.01)	58 (0.16)	0.41
11-01	Gp3	g.chr1:235866056G>A	Silent	LYST	p.I3455I	lysosomal trafficking re	38 (0.00)	23 (0.48)	0.91
11-01	Gp3	g.chr1:235950552G>T	Missense Mutation	LYST	p.Q1604K	lysosomal trafficking re	93 (0.00)	60 (0.28)	0.54
11-01	Gp3	g.chr1:235973079C>A	Nonsense Mutation	LYST	p.E347*	lysosomal trafficking re	82 (0.00)	35 (0.23)	0.43
11-01	Gp3	g.chr1:9994861C>T	Missense Mutation	LZIC	p.A99T	leucine zipper and CTN	123 (0.00)	66 (0.27)	0.73
11-01	Gp3	g.chr10:102763365C>T	Silent	LZTS2	p.T170T	leucine zipper, putative	40 (0.00)	40 (0.25)	0.67
11-01	Gp3	g.chr7:20199255C>A	Silent	MACC1	p.V243V	metastasis associated in	75 (0.00)	61 (0.25)	0.66
11-01	Gp3	g.chr1:39765893G>A	Silent	MACF1	p.E836E	microtubule-actin crossl	27 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr1:39788680G>A	Splice Site	MACF1	p.E1417E	microtubule-actin crossl	24 (0.00)	39 (0.31)	0.82
11-01	Gp3	g.chr1:39800239G>A	Missense Mutation	MACF1	p.S2665N	microtubule-actin crossl	37 (0.00)	16 (0.62)	1.67
11-01	Gp3	g.chr1:39806281G>A	Silent	MACF1	p.L3446L	microtubule-actin crossl	40 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr1:39893242G>A	Missense Mutation	MACF1	p.G5483S	microtubule-actin crossl	98 (0.00)	55 (0.35)	0.92
11-01	Gp3	g.chr1:39906797G>A	Splice Site	MACF1	p.E6089E	microtubule-actin crossl	40 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr1:39913818G>A	Silent	MACF1	p.K6593K	microtubule-actin crossl	41 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr11:47312298G>C	Missense Mutation	MADD	p.A1098P	MAP-kinase activating	36 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr11:47330905G>T	Missense Mutation	MADD	p.E1335D	MAP-kinase activating	25 (0.00)	10 (0.60)	1.60
11-01	Gp3	g.chr11:47350629C>A	Silent	MADD	p.L1624L	MAP-kinase activating	74 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr16:79632746C>A	Missense Mutation	MAF	p.V352L	v-maf avian musculoap	17 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chrX:151935277G>C	Missense Mutation	MAGEA3	p.P297R	melanoma antigen famil	34 (0.00)	24 (0.33)	0.56
11-01	Gp3	g.chrX:140994279T>A	Missense Mutation	MAGEC1	p.S363R	melanoma antigen famil	70 (0.00)	30 (0.27)	0.44
11-01	Gp3	g.chr3:184428919G>T	Missense Mutation	MAGEF1	p.H231N	melanoma antigen famil	31 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr3:65350542C>A	Silent	MAGI1	p.G1025G	membrane associated gu	17 (0.00)	15 (0.73)	1.96
11-01	Gp3	g.chr3:65479297C>A	Missense Mutation	MAGI1	p.R147L	membrane associated gu	22 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr7:77667353C>A	Intron	MAGI2		membrane associated gu	86 (0.00)	98 (0.26)	0.68
11-01	Gp3	g.chr7:77667354C>A	Intron	MAGI2		membrane associated gu	86 (0.00)	95 (0.26)	0.70
11-01	Gp3	g.chr7:77674923G>C	Intron	MAGI2		membrane associated gu	101 (0.00)	109 (0.22)	0.59

11-01	Gp3	g.chr7:77679026G>A	Intron	MAGI2		membrane associated gu	62 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr7:77680166G>C	Intron	MAGI2		membrane associated gu	63 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr7:77687132G>A	Intron	MAGI2		membrane associated gu	76 (0.00)	72 (0.22)	0.59
11-01	Gp3	g.chr7:77696136G>A	Intron	MAGI2		membrane associated gu	111 (0.01)	105 (0.32)	0.86
11-01	Gp3	g.chr7:77708353G>T	Missense Mutation	MAGI2	p.T1206K	membrane associated gu	32 (0.00)	26 (0.58)	1.54
11-01	Gp3	g.chr7:77713709C>A	Intron	MAGI2		membrane associated gu	96 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr7:77724893C>T	Intron	MAGI2		membrane associated gu	45 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr7:77753744G>T	Intron	MAGI2		membrane associated gu	51 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr7:77753989T>C	Intron	MAGI2		membrane associated gu	55 (0.00)	22 (0.41)	1.09
11-01	Gp3	g.chr7:77762382G>A	Intron	MAGI2		membrane associated gu	77 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr7:77769784G>A	Intron	MAGI2		membrane associated gu	21 (0.00)	17 (0.65)	1.73
11-01	Gp3	g.chr7:77777094C>T	Intron	MAGI2		membrane associated gu	68 (0.00)	48 (0.23)	0.61
11-01	Gp3	g.chr7:77781013G>T	Intron	MAGI2		membrane associated gu	74 (0.01)	48 (0.31)	0.83
11-01	Gp3	g.chr7:77781096C>A	Intron	MAGI2		membrane associated gu	76 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr7:77781102C>T	Intron	MAGI2		membrane associated gu	75 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr7:77797834C>G	Intron	MAGI2		membrane associated gu	48 (0.00)	22 (0.55)	1.45
11-01	Gp3	g.chr7:77798485C>A	Intron	MAGI2		membrane associated gu	37 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr7:77803733G>A	Intron	MAGI2		membrane associated gu	46 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr7:77806660G>T	Intron	MAGI2		membrane associated gu	41 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr7:77808344C>A	Intron	MAGI2		membrane associated gu	67 (0.00)	64 (0.17)	0.46
11-01	Gp3	g.chr7:77810868A>G	Intron	MAGI2		membrane associated gu	51 (0.02)	35 (0.57)	1.52
11-01	Gp3	g.chr7:77816945G>A	Intron	MAGI2		membrane associated gu	72 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr7:77818554C>A	Intron	MAGI2		membrane associated gu	61 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:77839885C>A	Intron	MAGI2		membrane associated gu	85 (0.00)	44 (0.43)	1.15
11-01	Gp3	g.chr7:77858873G>A	Intron	MAGI2		membrane associated gu	33 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr7:77885297G>C	Silent	MAGI2	p.P670P	membrane associated gu	20 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr7:77896561C>T	Intron	MAGI2		membrane associated gu	38 (0.00)	42 (0.48)	1.27
11-01	Gp3	g.chr7:77906183G>A	Intron	MAGI2		membrane associated gu	17 (0.00)	19 (0.74)	1.96
11-01	Gp3	g.chr7:77907022C>T	Intron	MAGI2		membrane associated gu	55 (0.02)	30 (0.27)	0.71
11-01	Gp3	g.chr7:77909135C>T	Intron	MAGI2		membrane associated gu	62 (0.02)	63 (0.43)	1.14
11-01	Gp3	g.chr7:77916572C>T	Intron	MAGI2		membrane associated gu	88 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr7:77939110G>A	Intron	MAGI2		membrane associated gu	85 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr7:77980926C>T	Intron	MAGI2		membrane associated gu	49 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr7:78011569G>A	Intron	MAGI2		membrane associated gu	29 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr7:78014742G>A	Intron	MAGI2		membrane associated gu	55 (0.00)	29 (0.59)	1.56

11-01	Gp3	g.chr7:78018102G>T	Intron	MAGI2	membrane associated gu	40 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr7:78021807G>T	Intron	MAGI2	membrane associated gu	21 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr7:78043988C>T	Intron	MAGI2	membrane associated gu	65 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr7:78047085C>A	Intron	MAGI2	membrane associated gu	65 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr7:78059319C>T	Intron	MAGI2	membrane associated gu	48 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr7:78064406G>A	Intron	MAGI2	membrane associated gu	33 (0.00)	18 (0.50)	1.33
11-01	Gp3	g.chr7:78066884C>A	Intron	MAGI2	membrane associated gu	20 (0.00)	25 (0.68)	1.81
11-01	Gp3	g.chr7:78073820G>C	Intron	MAGI2	membrane associated gu	21 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr7:78078430G>A	Intron	MAGI2	membrane associated gu	50 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr7:78095224C>G	Intron	MAGI2	membrane associated gu	34 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr7:78117050G>T	Intron	MAGI2	membrane associated gu	124 (0.00)	90 (0.18)	0.47
11-01	Gp3	g.chr7:78122111C>A	Intron	MAGI2	membrane associated gu	50 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr7:78127422C>G	Intron	MAGI2	membrane associated gu	38 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr7:78134910C>A	Intron	MAGI2	membrane associated gu	22 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr7:78141470G>C	Intron	MAGI2	membrane associated gu	38 (0.03)	21 (0.33)	0.89
11-01	Gp3	g.chr7:78143934C>A	Intron	MAGI2	membrane associated gu	71 (0.00)	100 (0.16)	0.43
11-01	Gp3	g.chr7:78155504G>A	Intron	MAGI2	membrane associated gu	25 (0.00)	16 (0.56)	1.50
11-01	Gp3	g.chr7:78178956G>T	Intron	MAGI2	membrane associated gu	29 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr7:78198248G>C	Intron	MAGI2	membrane associated gu	61 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr7:78200714G>T	Intron	MAGI2	membrane associated gu	25 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr7:78204209G>A	Intron	MAGI2	membrane associated gu	56 (0.02)	47 (0.23)	0.62
11-01	Gp3	g.chr7:78227790G>A	Intron	MAGI2	membrane associated gu	159 (0.00)	91 (0.19)	0.50
11-01	Gp3	g.chr7:78237470G>A	Intron	MAGI2	membrane associated gu	70 (0.00)	59 (0.29)	0.77
11-01	Gp3	g.chr7:78243228C>T	Intron	MAGI2	membrane associated gu	22 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr7:78260792C>T	Intron	MAGI2	membrane associated gu	32 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr7:78261105C>T	Intron	MAGI2	membrane associated gu	68 (0.00)	48 (0.27)	0.72
11-01	Gp3	g.chr7:78263808G>T	Intron	MAGI2	membrane associated gu	110 (0.01)	82 (0.17)	0.46
11-01	Gp3	g.chr7:78288429C>G	Intron	MAGI2	membrane associated gu	44 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr7:78307697G>A	Intron	MAGI2	membrane associated gu	48 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr7:78310016C>G	Intron	MAGI2	membrane associated gu	35 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr7:78328786G>T	Intron	MAGI2	membrane associated gu	29 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr7:78343930C>A	Intron	MAGI2	membrane associated gu	107 (0.01)	69 (0.29)	0.77
11-01	Gp3	g.chr7:78345337G>T	Intron	MAGI2	membrane associated gu	75 (0.00)	50 (0.22)	0.59
11-01	Gp3	g.chr7:78353868G>A	Intron	MAGI2	membrane associated gu	116 (0.00)	96 (0.27)	0.72
11-01	Gp3	g.chr7:78364012C>A	Intron	MAGI2	membrane associated gu	117 (0.00)	63 (0.35)	0.93

11-01	Gp3	g.chr7:78381258C>G	Intron	MAGI2	membrane associated gu	29 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr7:78385646C>A	Intron	MAGI2	membrane associated gu	57 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr7:78398758T>A	Intron	MAGI2	membrane associated gu	83 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr7:78404136G>A	Intron	MAGI2	membrane associated gu	49 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr7:78406920C>A	Intron	MAGI2	membrane associated gu	104 (0.01)	80 (0.23)	0.60
11-01	Gp3	g.chr7:78411627T>A	Intron	MAGI2	membrane associated gu	38 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr7:78418330G>A	Intron	MAGI2	membrane associated gu	80 (0.00)	51 (0.35)	0.94
11-01	Gp3	g.chr7:78427851G>T	Intron	MAGI2	membrane associated gu	41 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr7:78446463T>A	Intron	MAGI2	membrane associated gu	42 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr7:78466496C>T	Intron	MAGI2	membrane associated gu	42 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr7:78473946C>G	Intron	MAGI2	membrane associated gu	35 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr7:78479687A>T	Intron	MAGI2	membrane associated gu	23 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr7:78515013T>A	Intron	MAGI2	membrane associated gu	51 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr7:78528328G>A	Intron	MAGI2	membrane associated gu	39 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr7:78579254C>A	Intron	MAGI2	membrane associated gu	38 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr7:78585475T>A	Intron	MAGI2	membrane associated gu	61 (0.00)	48 (0.27)	0.72
11-01	Gp3	g.chr7:78599931A>T	Intron	MAGI2	membrane associated gu	24 (0.00)	16 (0.56)	1.50
11-01	Gp3	g.chr7:78606695C>A	Intron	MAGI2	membrane associated gu	40 (0.03)	49 (0.51)	1.36
11-01	Gp3	g.chr7:78612904C>T	Intron	MAGI2	membrane associated gu	58 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr7:78641772G>A	Intron	MAGI2	membrane associated gu	34 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr7:78699512G>T	Intron	MAGI2	membrane associated gu	20 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr7:78725410G>A	Intron	MAGI2	membrane associated gu	76 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr7:78726901C>A	Intron	MAGI2	membrane associated gu	81 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr7:78738252G>C	Intron	MAGI2	membrane associated gu	72 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr7:78748117C>A	Intron	MAGI2	membrane associated gu	107 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr7:78754049G>A	Intron	MAGI2	membrane associated gu	109 (0.00)	115 (0.21)	0.56
11-01	Gp3	g.chr7:78765768G>C	Intron	MAGI2	membrane associated gu	78 (0.00)	38 (0.42)	1.12
11-01	Gp3	g.chr7:78766286G>A	Intron	MAGI2	membrane associated gu	36 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr7:78767068C>G	Intron	MAGI2	membrane associated gu	73 (0.00)	53 (0.21)	0.55
11-01	Gp3	g.chr7:78772133C>T	Intron	MAGI2	membrane associated gu	60 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr7:78773800C>T	Intron	MAGI2	membrane associated gu	19 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr7:78784736G>A	Intron	MAGI2	membrane associated gu	68 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr7:78798819G>A	Intron	MAGI2	membrane associated gu	39 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr7:78817911C>A	Intron	MAGI2	membrane associated gu	66 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr7:78829362C>A	Intron	MAGI2	membrane associated gu	54 (0.00)	26 (0.19)	0.51

11-01	Gp3	g.chr7:78833089G>T	Intron	MAGI2		membrane associated gu	51 (0.02)	14 (0.36)	0.95
11-01	Gp3	g.chr7:78846880C>A	Intron	MAGI2		membrane associated gu	40 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr7:78848063G>C	Intron	MAGI2		membrane associated gu	41 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr7:78908293C>T	Intron	MAGI2		membrane associated gu	106 (0.00)	71 (0.17)	0.45
11-01	Gp3	g.chr7:78919867T>A	Intron	MAGI2		membrane associated gu	41 (0.02)	29 (0.28)	0.74
11-01	Gp3	g.chr7:78929156G>T	Intron	MAGI2		membrane associated gu	63 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr7:78929514G>A	Intron	MAGI2		membrane associated gu	60 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr7:78930685C>T	Intron	MAGI2		membrane associated gu	36 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr7:78940756G>A	Intron	MAGI2		membrane associated gu	117 (0.00)	130 (0.16)	0.43
11-01	Gp3	g.chr7:78941199C>G	Intron	MAGI2		membrane associated gu	62 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr7:78982776C>A	Intron	MAGI2		membrane associated gu	71 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr7:78983850G>T	Intron	MAGI2		membrane associated gu	88 (0.00)	58 (0.21)	0.55
11-01	Gp3	g.chr7:78992992C>T	Intron	MAGI2		membrane associated gu	45 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr7:79023756G>A	Intron	MAGI2		membrane associated gu	68 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr7:79028770G>T	Intron	MAGI2		membrane associated gu	47 (0.02)	42 (0.26)	0.70
11-01	Gp3	g.chr7:79042782C>T	Intron	MAGI2		membrane associated gu	73 (0.00)	51 (0.41)	1.10
11-01	Gp3	g.chr7:79044579G>C	Intron	MAGI2		membrane associated gu	103 (0.00)	75 (0.31)	0.82
11-01	Gp3	g.chr7:79057185C>G	Intron	MAGI2		membrane associated gu	56 (0.00)	44 (0.25)	0.67
11-01	Gp3	g.chr18:56377300C>T	Silent	MALT1	p.I307I	mucosa associated lymp	32 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr9:72785532C>T	Missense Mutation	MAMDC2	p.H546Y	MAM domain containin	27 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr11:95825854G>A	Silent	MAML2	p.A447A	mastermind-like 2 (Dros	71 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr1:118039497G>T	Missense Mutation	MAN1A2	p.G466V	mannosidase, alpha, cla	72 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr12:27916189G>A	Missense Mutation	MANSC4	p.P169S	MANSC domain contai	158 (0.01)	131 (0.15)	0.39
11-01	Gp3	g.chr15:43818556C>T	Nonsense Mutation	MAP1A	p.Q1867*	microtubule-associated	67 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr1:242161885G>A	Missense Mutation	MAP1LC3C	p.P51L	microtubule-associated	23 (0.00)	40 (0.38)	1.00
11-01	Gp3	g.chr2:210561422C>A	Missense Mutation	MAP2	p.A1446D	microtubule-associated	42 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr17:67532295G>A	Silent	MAP2K6	p.E307E	mitogen-activated prote	22 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr5:56178236C>A	Missense Mutation	MAP3K1	p.T1070K	mitogen-activated prote	30 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr5:56178257C>A	Nonsense Mutation	MAP3K1	p.S1077*	mitogen-activated prote	33 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr17:61767726C>A	Missense Mutation	MAP3K3	p.A385D	mitogen-activated prote	70 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr6:161508945G>A	Missense Mutation	MAP3K4	p.V928M	mitogen-activated prote	73 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr6:161530934C>T	Missense Mutation	MAP3K4	p.R1462C	mitogen-activated prote	106 (0.00)	40 (0.23)	0.60
11-01	Gp3	g.chr6:136990504G>A	Missense Mutation	MAP3K5	p.T428I	mitogen-activated prote	111 (0.00)	71 (0.31)	0.83
11-01	Gp3	g.chr19:39108509G>C	Missense Mutation	MAP4K1	p.F9L	mitogen-activated prote	18 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chr11:75298305C>A	Missense Mutation	MAP6	p.K747N	microtubule-associated	100 (0.00)	81 (0.23)	0.63

11-01	Gp3	g.chr15:52342279G>A	Missense Mutation	MAPK6	p.M215I	mitogen-activated protei	30 (0.00)	40 (0.50)	1.33
11-01	Gp3	g.chr5:179665334G>A	Missense Mutation	MAPK9	p.S292L	mitogen-activated protei	53 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr15:42105901C>G	Missense Mutation	MAPKBP1	p.P301R	mitogen-activated protei	84 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr17:60799902C>T	Missense Mutation	MARCH10	p.D721N	membrane-associated ri	25 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr5:10417406G>A	Missense Mutation	MARCH6	p.V725M	membrane-associated ri	100 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr2:119748200G>T	Nonsense Mutation	MARCO	p.G367*	macrophage receptor wi	46 (0.02)	18 (0.44)	1.19
11-01	Gp3	g.chr2:198571445C>A	Nonsense Mutation	MARS2	p.S439*	methionyl-tRNA synthe	33 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr3:186971069C>A	Missense Mutation	MASP1	p.C147F	mannan-binding lectin s	32 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr3:187003676G>A	Silent	MASP1	p.I32I	mannan-binding lectin s	43 (0.00)	20 (0.55)	1.47
11-01	Gp3	g.chr1:11087672C>A	Missense Mutation	MASP2	p.R444L	mannan-binding lectin s	23 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr19:18234060C>A	Missense Mutation	MAST3	p.L116I	microtubule associated s	15 (0.00)	28 (0.39)	1.05
11-01	Gp3	g.chr19:18255992G>C	Missense Mutation	MAST3	p.V969L	microtubule associated s	58 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr2:149226434C>A	Missense Mutation	MBD5	p.P308T	methyl-CpG binding do	22 (0.00)	29 (0.34)	0.92
11-01	Gp3	g.chr6:20118704C>G	Missense Mutation	MBOAT1	p.W325C	membrane bound O-acy	46 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr18:74728936C>A	Missense Mutation	MBP	p.R10M	myelin basic protein	32 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr18:58038622G>A	Missense Mutation	MC4R	p.P321S	melanocortin 4 receptor	33 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr18:58038863A>T	Missense Mutation	MC4R	p.N240K	melanocortin 4 receptor	38 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chrX:138684645G>T	Missense Mutation	MCF2	p.Q662K	MCF.2 cell line derived	27 (0.00)	14 (0.36)	0.60
11-01	Gp3	g.chr3:127334746C>T	Silent	MCM2	p.D490D	minichromosome maint	25 (0.00)	16 (0.69)	1.83
11-01	Gp3	g.chr21:47679006C>T	Splice Site	MCM3AP		minichromosome maint	29 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr21:47703692C>A	Missense Mutation	MCM3AP	p.G427V	minichromosome maint	57 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr21:47703693C>A	Missense Mutation	MCM3AP	p.G427W	minichromosome maint	58 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr21:47704095G>T	Missense Mutation	MCM3AP	p.S369Y	minichromosome maint	72 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr8:48880043C>G	Missense Mutation	MCM4	p.T391R	minichromosome maint	97 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr2:136630370C>G	Missense Mutation	MCM6	p.E51Q	minichromosome maint	102 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr12:69222704C>T	Missense Mutation	MDM2	p.S195L	MDM2 proto-oncogene,	95 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr6:90500056G>A	Missense Mutation	MDN1	p.S307F	MDN1, midasin homolo	76 (0.00)	41 (0.54)	0.85
11-01	Gp3	g.chr6:83949350C>A	Missense Mutation	ME1	p.A274S	malic enzyme 1, NADP	52 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr18:48473428C>A	Nonsense Mutation	ME2	p.Y543*	malic enzyme 2, NAD(+	15 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr11:86159283C>A	Silent	ME3	p.L382L	malic enzyme 3, NADP	49 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr1:37967588C>T	Missense Mutation	MEAF6	p.G117E	MYST/Esa1-associated	56 (0.00)	68 (0.26)	0.71
11-01	Gp3	g.chr3:150883718G>C	Missense Mutation	MED12L	p.E481D	mediator complex subur	80 (0.00)	42 (0.40)	1.08
11-01	Gp3	g.chr3:151101985G>C	Missense Mutation	MED12L	p.M1600I	mediator complex subur	51 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr17:60039045G>A	Silent	MED13	p.T1720T	mediator complex subur	119 (0.00)	80 (0.16)	0.43
11-01	Gp3	g.chr17:60108887G>C	Missense Mutation	MED13	p.H309Q	mediator complex subur	60 (0.00)	45 (0.16)	0.41

11-01	Gp3	g.chr19:39883103G>A	Splice Site	MED29		mediator complex subur	19 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr17:17394714C>T	Nonsense Mutation	MED9	p.Q116*	mediator complex subur	52 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr15:100252768C>T	Missense Mutation	MEF2A	p.P429L	myocyte enhancer facto	43 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr5:126776434G>T	Missense Mutation	MEGF10	p.C746F	multiple EGF-like-doma	87 (0.00)	68 (0.15)	0.39
11-01	Gp3	g.chr2:66796193G>T	Nonsense Mutation	MEIS1	p.G376*	Meis homeobox 1	122 (0.01)	65 (0.29)	0.78
11-01	Gp3	g.chr19:47918062G>T	Missense Mutation	MEIS3	p.P153H	Meis homeobox 3	31 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr6:46777180C>T	Silent	MEP1A	p.L96L	meprin A, alpha (PABA	25 (0.04)	12 (0.50)	1.33
11-01	Gp3	g.chr4:88766656C>T	Silent	MEPE	p.S212S	matrix extracellular pho	50 (0.00)	21 (0.62)	1.65
11-01	Gp3	g.chr2:112765988G>A	Silent	MERTK	p.E632E	MER proto-oncogene, t	33 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr15:81274485G>A	Silent	MESDC2	p.H84H	mesoderm development	24 (0.00)	18 (0.78)	2.07
11-01	Gp3	g.chr7:130144882C>A	Missense Mutation	MEST	p.F331L	mesoderm specific trans	76 (0.00)	55 (0.22)	0.58
11-01	Gp3	g.chr4:99978961T>C	Missense Mutation	METAP1	p.I330T	methionyl aminopeptida	23 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr12:95905757G>C	Missense Mutation	METAP2	p.E351Q	methionyl aminopeptida	24 (0.00)	21 (0.38)	1.30
11-01	Gp3	g.chr6:110636581T>C	Missense Mutation	METTL24	p.Q174R	methyltransferase like 2	27 (0.00)	23 (0.30)	0.47
11-01	Gp3	g.chr12:82796837G>A	Missense Mutation	METTL25	p.E403K	methyltransferase like 2	48 (0.00)	28 (0.46)	1.24
11-01	Gp3	g.chr17:60522242G>A	Missense Mutation	METTL2A	p.G285D	methyltransferase like 2	50 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr17:60525092G>C	Missense Mutation	METTL2A	p.R316T	methyltransferase like 2	165 (0.00)	69 (0.17)	0.46
11-01	Gp3	g.chr7:128141012C>A	Missense Mutation	METTL2B	p.F324L	methyltransferase like 2	148 (0.00)	93 (0.19)	0.52
11-01	Gp3	g.chr14:21967704G>T	Missense Mutation	METTL3	p.Q462K	methyltransferase like 3	69 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr15:44106856G>A	Nonsense Mutation	MFAP1	p.Q154*	microfibrillar-associatec	37 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr4:170913264C>A	Missense Mutation	MFAP3L	p.M165I	microfibrillar-associatec	32 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr12:8804282G>A	Missense Mutation	MFAP5	p.L75F	microfibrillar associated	56 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr2:228212100G>A	Splice Site	MFF	p.R200K	mitochondrial fission fa	75 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr1:12057430C>T	Missense Mutation	MFN2	p.P184L	mitofusin 2	43 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr1:12065958C>T	Silent	MFN2	p.S562S	mitofusin 2	91 (0.00)	59 (0.15)	0.41
11-01	Gp3	g.chr1:40430904G>T	Silent	MFSD2A	p.L125L	major facilitator superfa	54 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr15:41988355G>T	Nonsense Mutation	MGA	p.E383*	MGA, MAX dimerizati	167 (0.00)	177 (0.14)	0.38
11-01	Gp3	g.chr15:42003201C>A	Nonsense Mutation	MGA	p.S913*	MGA, MAX dimerizati	120 (0.00)	53 (0.21)	0.55
11-01	Gp3	g.chr15:42040978C>T	Missense Mutation	MGA	p.R1786W	MGA, MAX dimerizati	87 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr15:42041335G>T	Missense Mutation	MGA	p.A1844S	MGA, MAX dimerizati	90 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr15:42041359C>A	Missense Mutation	MGA	p.P1852T	MGA, MAX dimerizati	75 (0.00)	53 (0.34)	0.91
11-01	Gp3	g.chr15:42041819C>G	Missense Mutation	MGA	p.A2005G	MGA, MAX dimerizati	113 (0.00)	105 (0.45)	1.19
11-01	Gp3	g.chr7:141752219C>T	Silent	MGAM	p.N977N	maltase-glucoamylase (a	62 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr7:141756670C>A	Silent	MGAM	p.T1207T	maltase-glucoamylase (a	100 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr14:50088575C>T	Missense Mutation	MGAT2	p.P197S	mannosyl (alpha-1,6-)-g	45 (0.00)	47 (0.15)	0.40

11-01	Gp3	g.chr14:39716420C>T	Silent	MIA2	p.V214V	melanoma inhibitory ac	92 (0.00)	89 (0.18)	0.48
11-01	Gp3	g.chr11:12371424G>A	Nonsense Mutation	MICALCL	p.W590*	MICAL C-terminal like	47 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr1:67411919G>C	Missense Mutation	MIER1	p.E41Q	mesoderm induction ear	54 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr17:4789775C>T	Missense Mutation	MINK1	p.T268I	misshapen-like kinase 1	80 (0.00)	84 (0.23)	0.60
11-01	Gp3	g.chr13:24443477G>C	Silent	MIPEP	p.S299S	mitochondrial intermedi	74 (0.00)	56 (0.32)	0.86
11-01	Gp3	g.chr13:24443483C>G	Silent	MIPEP	p.G297G	mitochondrial intermedi	89 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr6:52013794C>A	lincRNA	MIR133BHG			58 (0.00)	34 (0.41)	1.10
11-01	Gp3	g.chr11:62338436C>T	Splice Site	MIR3654		microRNA 3654	144 (0.00)	88 (0.24)	0.64
11-01	Gp3	g.chr19:54194141C>T	RNA	MIR520A		microRNA 520a	107 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr3:168269712C>T	RNA	MIR551B		microRNA 551b	24 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr17:5392666C>A	Missense Mutation	MIS12	p.L162I	MIS12 kinetochore com	97 (0.00)	103 (0.31)	0.83
11-01	Gp3	g.chr14:45693434C>G	Missense Mutation	MIS18BP1	p.A786P	MIS18 binding protein	48 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr10:129904227C>A	Missense Mutation	MKI67	p.E1959D	marker of proliferation	43 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr10:129904719G>C	Missense Mutation	MKI67	p.I1795M	marker of proliferation	38 (0.00)	40 (0.25)	0.67
11-01	Gp3	g.chr20:10393924G>A	Missense Mutation	MKKS	p.S80F	McKusick-Kaufman sy	70 (0.00)	51 (0.20)	0.52
11-01	Gp3	g.chr16:14345755C>T	Missense Mutation	MKL2	p.P764S	MKL/myocardin-like 2	51 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr16:14345814C>G	Missense Mutation	MKL2	p.N783K	MKL/myocardin-like 2	46 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr3:37061895C>T	Nonsense Mutation	MLH1	p.Q86*	mutL homolog 1	55 (0.00)	47 (0.23)	0.62
11-01	Gp3	g.chr3:37089121C>A	Missense Mutation	MLH1	p.L374M	mutL homolog 1	38 (0.00)	33 (0.52)	1.37
11-01	Gp3	g.chr14:75514630C>T	Missense Mutation	MLH3	p.A577T	mutL homolog 3	75 (0.00)	42 (0.26)	0.70
11-01	Gp3	g.chr1:233518169C>T	Silent	MLK4	p.I941I		51 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr16:74716628C>G	Missense Mutation	MLKL	p.E293Q	mixed lineage kinase do	35 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr16:74729196C>A	Splice Site	MLKL	p.D154Y	mixed lineage kinase do	42 (0.00)	34 (0.38)	1.02
11-01	Gp3	g.chr4:146567269G>C	Missense Mutation	MMAA	p.E232Q	methylmalonic aciduria	121 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr11:102667893C>A	Splice Site	MMP1	p.R117S	matrix metallopeptidase	41 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr11:102643737C>T	Splice Site	MMP10	p.G356E	matrix metallopeptidase	20 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr11:102742630G>A	RNA	MMP12		matrix metallopeptidase	28 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr11:102742631G>A	RNA	MMP12		matrix metallopeptidase	31 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr11:102824965G>T	Missense Mutation	MMP13	p.A186D	matrix metallopeptidase	36 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr11:102495929G>A	Missense Mutation	MMP20	p.A41V	matrix metallopeptidase	43 (0.00)	41 (0.29)	0.78
11-01	Gp3	g.chr6:97677083C>A	Missense Mutation	MMS22L	p.A576S	MMS22-like, DNA rep	44 (0.00)	13 (0.38)	0.60
11-01	Gp3	g.chr6:97677093C>A	Missense Mutation	MMS22L	p.K572N	MMS22-like, DNA rep	50 (0.00)	20 (0.55)	0.85
11-01	Gp3	g.chr18:33778689C>A	Missense Mutation	MOCOS	p.T90N	molybdenum cofactor s	33 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr20:49576643G>T	Missense Mutation	MOCS3	p.V422L	molybdenum cofactor s	18 (0.00)	11 (0.73)	1.94
11-01	Gp3	g.chr2:74690433C>T	Silent	MOGS	p.E220E	mannosyl-oligosacchari	62 (0.02)	28 (0.36)	0.54

11-01	Gp3	g.chr16:77228430C>A	Nonsense Mutation	MON1B	p.S116*	MON1 secretory traffic	19 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr9:124931986C>G	Silent	MORN5	p.G86G	MORN repeat containin	90 (0.00)	80 (0.16)	0.43
11-01	Gp3	g.chr9:13140078G>A	Missense Mutation	MPDZ	p.A1304V	multiple PDZ domain p	167 (0.00)	89 (0.48)	0.76
11-01	Gp3	g.chr11:58978599G>A	Silent	MPEG1	p.S580S	macrophage expressed 1	18 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr16:133062G>C	Silent	MPG	p.R109R	N-methylpurine-DNA g	37 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr12:123645802C>A	Nonsense Mutation	MPHOSPH9	p.E1088*	M-phase phosphoprotei	80 (0.00)	53 (0.19)	0.50
11-01	Gp3	g.chr12:123687393G>A	Missense Mutation	MPHOSPH9	p.S520F	M-phase phosphoprotei	43 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr2:27535933C>T	Missense Mutation	MPV17	p.G27R	MpV17 mitochondrial i	28 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr4:6642607C>T	Silent	MRFAP1	p.I6I	Morf4 family associated	34 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr11:18956171C>A	Missense Mutation	MRGPRX1	p.C54F	MAS-related GPR, men	49 (0.02)	34 (0.18)	0.47
11-01	Gp3	g.chr11:18195292C>G	Missense Mutation	MRGPRX4	p.F163L	MAS-related GPR, men	69 (0.00)	55 (0.31)	0.82
11-01	Gp3	g.chr5:41055906C>T	Missense Mutation	MROH2B	p.S324N	maestro heat-like repeat	89 (0.00)	39 (0.41)	1.09
11-01	Gp3	g.chr8:142505493C>T	RNA	MROH5		maestro heat-like repeat	31 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr1:55158122C>T	Silent	MROH7	p.L913L	maestro heat-like repeat	38 (0.00)	29 (0.72)	1.93
11-01	Gp3	g.chr20:35742391A>G	Splice Site	MROH8		maestro heat-like repeat	63 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr8:55060038C>T	Missense Mutation	MRPL15	p.A217V	mitochondrial ribosoma	24 (0.00)	46 (0.15)	0.51
11-01	Gp3	g.chr11:59573975C>A	Missense Mutation	MRPL16	p.D201Y	mitochondrial ribosoma	51 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr6:42176037C>A	Missense Mutation	MRPS10	p.S199I	mitochondrial ribosoma	57 (0.00)	84 (0.35)	0.92
11-01	Gp3	g.chr6:42176053C>A	Nonsense Mutation	MRPS10	p.E194*	mitochondrial ribosoma	50 (0.02)	70 (0.14)	0.38
11-01	Gp3	g.chr19:39423003C>G	Missense Mutation	MRPS12	p.T27S	mitochondrial ribosoma	28 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr3:15094121C>A	Missense Mutation	MRPS25	p.R87S	mitochondrial ribosoma	59 (0.00)	37 (0.41)	1.08
11-01	Gp3	g.chr17:73258946C>T	Nonsense Mutation	MRPS7	p.Q113*	mitochondrial ribosoma	32 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr9:125033266G>A	Silent	MRRF	p.K32K	mitochondrial ribosome	265 (0.00)	190 (0.23)	0.62
11-01	Gp3	g.chr1:19583972G>A	Missense Mutation	MRTO4	p.V100M	mRNA turnover 4 homo	144 (0.01)	86 (0.16)	0.43
11-01	Gp3	g.chr11:10648112C>A	Missense Mutation	MRVI1	p.A257S	murine retrovirus integr	46 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr11:60231788G>T	Missense Mutation	MS4A1	p.A103S	membrane-spanning 4-d	54 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr11:124637460A>C	Missense Mutation	MSANTD2	p.I431S	Myb/SANT-like DNA-	17 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr2:47643563G>A	Silent	MSH2	p.E357E	mutS homolog 2	37 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr5:80150109G>A	Missense Mutation	MSH3	p.A992T	mutS homolog 3	78 (0.00)	49 (0.47)	1.25
11-01	Gp3	g.chr3:135871387C>T	Silent	MSL2	p.Q112Q	male-specific lethal 2 h	43 (0.00)	28 (0.61)	1.62
11-01	Gp3	g.chr10:75184896G>A	Missense Mutation	MSS51	p.L375F	MSS51 mitochondrial tr	78 (0.00)	46 (0.24)	0.64
11-01	Gp3	g.chr2:190922014C>G	Silent	MSTN	p.A366A	myostatin	52 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr16:56670818G>A	RNA	MT1JP		metallothionein 1J, pseu	101 (0.01)	125 (0.17)	0.45
11-01	Gp3	g.chr16:56667316G>A	Splice Site	MT1M	p.K31K	metallothionein 1M	52 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr2:42909604G>A	Missense Mutation	MTA3	p.V256I	metastasis associated 1	67 (0.00)	90 (0.27)	0.71

11-01	Gp3	g.chr1:38280964C>G	Missense Mutation	MTF1	p.E702D	metal-regulatory transcr	57 (0.02)	189 (0.76)	2.02
11-01	Gp3	g.chr1:38304382C>T	Missense Mutation	MTF1	p.E232K	metal-regulatory transcr	31 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr20:60768617C>T	Silent	MTG2	p.G47G	mitochondrial ribosome	34 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr6:151247409G>T	Nonsense Mutation	MTHFD1L	p.G412*	methylenetetrahydrofola	41 (0.00)	22 (0.50)	1.33
11-01	Gp3	g.chr2:74438403G>A	Missense Mutation	MTHFD2	p.V250I	methylenetetrahydrofola	105 (0.00)	35 (0.26)	0.39
11-01	Gp3	g.chr2:55481875C>A	Nonsense Mutation	MTIF2	p.E140*	mitochondrial translatio	38 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr15:31239475G>A	Missense Mutation	MTMR10	p.A469V	myotubularin related pr	68 (0.00)	46 (0.28)	0.75
11-01	Gp3	g.chr1:149906117C>A	Missense Mutation	MTMR11	p.S145I	myotubularin related pr	31 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr3:9714399C>A	Silent	MTMR14	p.A236A	myotubularin related pr	37 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr1:11188096C>T	Missense Mutation	MTOR	p.E2000K	mechanistic target of ra	139 (0.00)	50 (0.22)	0.59
11-01	Gp3	g.chr10:30615506G>C	Missense Mutation	MTPAP	p.A280G	mitochondrial poly(A) p	52 (0.00)	79 (0.23)	0.61
11-01	Gp3	g.chr10:30625844G>T	Missense Mutation	MTPAP	p.P223Q	mitochondrial poly(A) p	98 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr1:236966919G>A	Missense Mutation	MTR	p.D76N	5-methyltetrahydrofolat	59 (0.00)	26 (0.27)	0.51
11-01	Gp3	g.chr13:41834950G>A	Nonsense Mutation	MTRF1	p.Q32*	mitochondrial translatio	59 (0.00)	73 (0.16)	0.44
11-01	Gp3	g.chr5:7886756G>A	Silent	MTRR	p.A362A	5-methyltetrahydrofolat	75 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr7:100648276G>A	Missense Mutation	MUC12	p.G4954D	mucin 12, cell surface a	44 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr7:100648457G>T	Missense Mutation	MUC12	p.M5014I	mucin 12, cell surface a	84 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr3:124641127A>G	Missense Mutation	MUC13	p.S220P	mucin 13, cell surface a	94 (0.00)	79 (0.19)	0.51
11-01	Gp3	g.chr19:8999431C>T	Missense Mutation	MUC16	p.G13582S	mucin 16, cell surface a	251 (0.00)	44 (0.27)	0.73
11-01	Gp3	g.chr19:9047542C>A	Missense Mutation	MUC16	p.R11363S	mucin 16, cell surface a	163 (0.00)	63 (0.27)	0.72
11-01	Gp3	g.chr19:9047912G>A	Missense Mutation	MUC16	p.A11240V	mucin 16, cell surface a	31 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr19:9048635G>A	Missense Mutation	MUC16	p.T10999I	mucin 16, cell surface a	96 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr19:9050139C>T	Missense Mutation	MUC16	p.V10498I	mucin 16, cell surface a	89 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr19:9059156G>A	Silent	MUC16	p.N9430N	mucin 16, cell surface a	105 (0.00)	49 (0.33)	0.87
11-01	Gp3	g.chr19:9059399G>A	Silent	MUC16	p.T9349T	mucin 16, cell surface a	172 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr19:9065814G>A	Missense Mutation	MUC16	p.P7211L	mucin 16, cell surface a	73 (0.00)	52 (0.21)	0.56
11-01	Gp3	g.chr19:9066659G>A	Silent	MUC16	p.S6929S	mucin 16, cell surface a	165 (0.00)	93 (0.17)	0.46
11-01	Gp3	g.chr19:9068139C>A	Missense Mutation	MUC16	p.G6436V	mucin 16, cell surface a	112 (0.00)	105 (0.23)	0.61
11-01	Gp3	g.chr19:9068630C>T	Silent	MUC16	p.V6272V	mucin 16, cell surface a	65 (0.00)	71 (0.24)	0.64
11-01	Gp3	g.chr19:9073240G>A	Missense Mutation	MUC16	p.P4736S	mucin 16, cell surface a	179 (0.01)	129 (0.15)	0.39
11-01	Gp3	g.chr19:9077241G>A	Missense Mutation	MUC16	p.T3402I	mucin 16, cell surface a	162 (0.00)	100 (0.21)	0.56
11-01	Gp3	g.chr19:9084156T>A	Silent	MUC16	p.G2553G	mucin 16, cell surface a	120 (0.01)	100 (0.15)	0.40
11-01	Gp3	g.chr19:9084680C>A	Missense Mutation	MUC16	p.A2379S	mucin 16, cell surface a	72 (0.00)	38 (0.37)	0.98
11-01	Gp3	g.chr19:9085128C>A	Missense Mutation	MUC16	p.L2229F	mucin 16, cell surface a	63 (0.00)	36 (0.50)	1.33
11-01	Gp3	g.chr19:9086063C>T	Missense Mutation	MUC16	p.G1918R	mucin 16, cell surface a	146 (0.00)	59 (0.17)	0.45

11-01	Gp3	g.chr19:9086065G>C	Missense Mutation	MUC16	p.P1917R	mucin 16, cell surface a	144 (0.00)	58 (0.16)	0.41
11-01	Gp3	g.chr19:9088078G>A	Missense Mutation	MUC16	p.T1246I	mucin 16, cell surface a	114 (0.00)	76 (0.22)	0.60
11-01	Gp3	g.chr19:9088858G>T	Nonsense Mutation	MUC16	p.S986*	mucin 16, cell surface a	172 (0.01)	46 (0.46)	1.22
11-01	Gp3	g.chr7:100674448C>T	Nonsense Mutation	MUC17	p.Q44*	mucin 17, cell surface a	69 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr7:100675194C>A	Missense Mutation	MUC17	p.T166N	mucin 17, cell surface a	42 (0.00)	34 (0.53)	1.41
11-01	Gp3	g.chr7:100679669T>C	Missense Mutation	MUC17	p.S1658P	mucin 17, cell surface a	76 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr7:100679676G>A	Missense Mutation	MUC17	p.S1660N	mucin 17, cell surface a	75 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr7:100679856C>T	Missense Mutation	MUC17	p.P1720L	mucin 17, cell surface a	189 (0.00)	107 (0.19)	0.50
11-01	Gp3	g.chr11:1092417C>G	Missense Mutation	MUC2	p.S1412R	mucin 2, oligomeric mu	17 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr11:1265777C>T	Missense Mutation	MUC5B	p.T2556I	mucin 5B, oligomeric m	153 (0.00)	56 (0.18)	0.48
11-01	Gp3	g.chr11:1267898C>T	Missense Mutation	MUC5B	p.S3263F	mucin 5B, oligomeric m	104 (0.00)	100 (0.36)	0.96
11-01	Gp3	g.chr9:113530242G>A	Missense Mutation	MUSK	p.A355T	muscle, skeletal, recept	81 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr9:113562694G>A	Missense Mutation	MUSK	p.S679N	muscle, skeletal, recept	103 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr6:49416594G>C	Missense Mutation	MUT	p.A460G	methylmalonyl CoA mu	74 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr10:112038940G>A	Missense Mutation	MXI1	p.R147Q	MAX interactor 1, dime	75 (0.00)	62 (0.60)	1.59
11-01	Gp3	g.chrX:3241466G>A	Missense Mutation	MXRA5	p.P754S	matrix-remodelling asso	36 (0.00)	26 (0.42)	0.71
11-01	Gp3	g.chr17:4442839G>A	Silent	MYBBP1A	p.V1286V	MYB binding protein (	44 (0.00)	28 (0.29)	0.76
11-01	Gp3	g.chr8:67488365C>T	Silent	MYBL1	p.K449K	v-myb avian myeloblast	55 (0.00)	18 (0.28)	0.92
11-01	Gp3	g.chr20:42343854C>A	Missense Mutation	MYBL2	p.F635L	v-myb avian myeloblast	90 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr13:77672819G>A	Missense Mutation	MYCBP2	p.P2786S	MYC binding protein 2,	67 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr13:77739493G>A	Missense Mutation	MYCBP2	p.S2087L	MYC binding protein 2,	20 (0.00)	23 (0.43)	1.16
11-01	Gp3	g.chr13:77785394C>T	Silent	MYCBP2	p.V1070V	MYC binding protein 2,	27 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr13:77786180C>G	Missense Mutation	MYCBP2	p.G1020A	MYC binding protein 2,	51 (0.00)	36 (0.22)	0.59
11-01	Gp3	g.chr1:40363420C>G	Missense Mutation	MYCL	p.R270T	v-myc avian myelocyto	35 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr17:10404651C>G	Missense Mutation	MYH1	p.E1172Q	myosin, heavy chain 1,	88 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr17:10231375C>T	Nonsense Mutation	MYH13	p.W833*	myosin, heavy chain 13,	61 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr17:10258017C>A	Nonsense Mutation	MYH13	p.E329*	myosin, heavy chain 13,	50 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr17:10258048T>A	Silent	MYH13	p.G318G	myosin, heavy chain 13,	38 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr3:108163626T>C	Missense Mutation	MYH15	p.E859G	myosin, heavy chain 15	51 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr3:108163630C>T	Missense Mutation	MYH15	p.G858R	myosin, heavy chain 15	48 (0.00)	32 (0.31)	0.83
11-01	Gp3	g.chr17:10450920C>T	Missense Mutation	MYH2	p.D74N	myosin, heavy chain 2,	44 (0.00)	46 (0.28)	0.75
11-01	Gp3	g.chr17:10450928G>T	Missense Mutation	MYH2	p.T71K	myosin, heavy chain 2,	44 (0.02)	44 (0.23)	0.61
11-01	Gp3	g.chr17:10451041C>A	Missense Mutation	MYH2	p.G66V	myosin, heavy chain 2,	57 (0.00)	11 (0.73)	1.94
11-01	Gp3	g.chr17:10536005C>A	Nonsense Mutation	MYH3	p.E1582*	myosin, heavy chain 3,	93 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr17:10558361C>A	Missense Mutation	MYH3	p.M7I	myosin, heavy chain 3,	72 (0.00)	34 (0.21)	0.55

11-01	Gp3	g.chr17:10348564G>T	Missense Mutation	MYH4	p.A1762D	myosin, heavy chain 4, s	110 (0.00)	50 (0.24)	0.64
11-01	Gp3	g.chr17:10358013C>A	Missense Mutation	MYH4	p.E850D	myosin, heavy chain 4, s	129 (0.00)	86 (0.16)	0.43
11-01	Gp3	g.chr17:10367997C>A	Splice Site	MYH4		myosin, heavy chain 4, s	53 (0.00)	56 (0.16)	0.43
11-01	Gp3	g.chr14:23884417C>G	Missense Mutation	MYH7	p.M1782I	myosin, heavy chain 7,	40 (0.00)	41 (0.29)	0.78
11-01	Gp3	g.chr20:33568414C>T	Missense Mutation	MYH7B	p.P168S	myosin, heavy chain 7B	86 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr20:33568515C>G	Missense Mutation	MYH7B	p.N201K	myosin, heavy chain 7B	15 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr17:10310068C>T	Missense Mutation	MYH8	p.G704S	myosin, heavy chain 8, s	76 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr22:36714311G>A	Missense Mutation	MYH9	p.L390F	myosin, heavy chain 9,	51 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr16:46755077G>A	Missense Mutation	MYLK3	p.T307I	myosin light chain kinas	57 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr3:169492117G>C	Missense Mutation	MYNN	p.E12Q	myoneurin	64 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr17:27421767C>A	Silent	MYO18A	p.L1537L	myosin XVIIIA	50 (0.00)	33 (0.48)	1.29
11-01	Gp3	g.chr2:192225382T>A	Silent	MYO1B	p.V196V	myosin IB	168 (0.00)	59 (0.24)	0.63
11-01	Gp3	g.chr17:1381424G>A	Missense Mutation	MYO1C	p.T418M	myosin IC	19 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr15:59515276C>T	Missense Mutation	MYO1E	p.A298T	myosin IE	68 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr15:59553664C>A	Missense Mutation	MYO1E	p.Q64H	myosin IE	71 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr12:109838964G>A	Missense Mutation	MYO1H	p.E197K	myosin IH	65 (0.00)	57 (0.21)	0.56
11-01	Gp3	g.chr2:171240280G>A	Missense Mutation	MYO3B	p.A416T	myosin IIIB	51 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr2:171264249C>T	Missense Mutation	MYO3B	p.L849F	myosin IIIB	153 (0.01)	113 (0.24)	0.64
11-01	Gp3	g.chr2:171509509G>A	Missense Mutation	MYO3B	p.D1302N	myosin IIIB	34 (0.00)	63 (0.44)	1.19
11-01	Gp3	g.chr18:47566666C>A	Missense Mutation	MYO5B	p.D53Y	myosin VB	70 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr15:52517714C>G	Missense Mutation	MYO5C	p.E1075Q	myosin VC	38 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr2:128341711G>C	Missense Mutation	MYO7B	p.C453S	myosin VIIB	83 (0.00)	71 (0.24)	0.64
11-01	Gp3	g.chr19:17256288G>T	Missense Mutation	MYO9B	p.G308C	myosin IXB	42 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr18:3126880G>T	Missense Mutation	MYOM1	p.P937H	myomesin 1	52 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr18:3135560C>G	Missense Mutation	MYOM1	p.V732L	myomesin 1	42 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr11:61545950G>A	Missense Mutation	MYRF	p.V668M	myelin regulatory factor	51 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr11:61548617C>A	Silent	MYRF	p.T860T	myelin regulatory factor	45 (0.02)	31 (0.19)	0.52
11-01	Gp3	g.chr20:62838947G>T	Splice Site	MYT1	p.G133V	myelin transcription fac	35 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr20:62848635G>A	Splice Site	MYT1		myelin transcription fac	49 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr2:1891298C>T	Silent	MYT1L	p.K866K	myelin transcription fac	129 (0.00)	100 (0.20)	0.53
11-01	Gp3	g.chr15:57921976C>T	Missense Mutation	MYZAP	p.A201V	myocardial zonula adhe	41 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr16:48580077G>T	Missense Mutation	N4BP1	p.Q772K	NEDD4 binding protein	105 (0.00)	109 (0.18)	0.49
11-01	Gp3	g.chr4:40121835C>T	Nonsense Mutation	N4BP2	p.Q702*	NEDD4 binding protein	39 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr13:41897299G>A	Silent	NAA16	p.L170L	N(alpha)-acetyltransfera	60 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr12:112481511C>A	Missense Mutation	NAA25	p.R723L	N(alpha)-acetyltransfera	83 (0.00)	52 (0.19)	0.51

11-01	Gp3	g.chr12:56620177C>T	Missense Mutation	NABP2	p.T137I	nucleic acid binding pro	62 (0.00)	61 (0.30)	0.79
11-01	Gp3	g.chr11:71184393G>A	Missense Mutation	NADSYN1	p.E177K	NAD synthetase 1	40 (0.03)	32 (0.22)	0.58
11-01	Gp3	g.chr22:42463190C>A	Missense Mutation	NAGA	p.Q143H	N-acetylgalactosaminid	38 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr13:101997663C>G	Silent	NALCN	p.L251L	sodium leak channel, no	69 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr9:100840508C>T	Missense Mutation	NANS	p.S161L	N-acetylneuraminic aci	73 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr11:34163869G>A	Silent	NAT10	p.G953G	N-acetyltransferase 10 (	35 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr11:20066795C>A	Silent	NAV2	p.R1097R	neuron navigator 2	105 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr11:20117292G>A	Silent	NAV2	p.G1933G	neuron navigator 2	133 (0.00)	95 (0.32)	0.84
11-01	Gp3	g.chr11:20125247C>A	Missense Mutation	NAV2	p.N2143K	neuron navigator 2	34 (0.00)	42 (0.29)	0.76
11-01	Gp3	g.chr2:15506719G>T	Missense Mutation	NBAS	p.L1268M	neuroblastoma amplifie	61 (0.02)	20 (0.25)	0.67
11-01	Gp3	g.chr2:203980755G>T	Missense Mutation	NBEAL1	p.D823Y	neurobeachin-like 1	38 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr2:203980758C>A	Missense Mutation	NBEAL1	p.L824M	neurobeachin-like 1	39 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr2:204000460T>A	Missense Mutation	NBEAL1	p.W1263R	neurobeachin-like 1	181 (0.00)	123 (0.15)	0.39
11-01	Gp3	g.chr2:204009533C>G	Missense Mutation	NBEAL1	p.P1658A	neurobeachin-like 1	36 (0.00)	30 (0.33)	0.89
11-01	Gp3	g.chr1:16913617C>A	Missense Mutation	NBPF1	p.V236F	neuroblastoma breakpoi	69 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr1:146401702C>T	Silent	NBPF12	p.V270V	neuroblastoma breakpoi	76 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr1:148756484C>A	Missense Mutation	NBPF16	p.Q605K		152 (0.00)	89 (0.16)	0.42
11-01	Gp3	g.chr12:6626131T>C	Silent	NCAPD2	p.D375D	non-SMC condensin I c	93 (0.01)	75 (0.31)	0.82
11-01	Gp3	g.chr4:17814734G>C	Missense Mutation	NCAPG	p.Q170H	non-SMC condensin I c	19 (0.00)	18 (0.61)	1.63
11-01	Gp3	g.chr4:17816613G>A	Missense Mutation	NCAPG	p.A228T	non-SMC condensin I c	38 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr7:158451093C>G	Missense Mutation	NCAPG2	p.R666P	non-SMC condensin II	21 (0.00)	32 (0.47)	1.25
11-01	Gp3	g.chr2:97020047G>A	Missense Mutation	NCAPH	p.D366N	non-SMC condensin I c	79 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr3:196663904C>G	Missense Mutation	NCBP2	p.G80A	nuclear cap binding pro	49 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr12:54925573C>A	Silent	NCKAP1L	p.L915L	NCK-associated protein	23 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr2:133541922G>T	Missense Mutation	NCKAP5	p.A821D	NCK-associated protein	294 (0.00)	164 (0.21)	0.57
11-01	Gp3	g.chr2:24980983C>A	Missense Mutation	NCOA1	p.S1341R	nuclear receptor coactiv	36 (0.00)	27 (0.70)	1.88
11-01	Gp3	g.chr8:71036216C>T	Missense Mutation	NCOA2	p.G1399D	nuclear receptor coactiv	28 (0.00)	36 (0.14)	0.46
11-01	Gp3	g.chr8:71060655G>C	Missense Mutation	NCOA2	p.Q820E	nuclear receptor coactiv	54 (0.00)	42 (0.21)	0.71
11-01	Gp3	g.chr8:71068923C>G	Missense Mutation	NCOA2	p.M559I	nuclear receptor coactiv	205 (0.00)	151 (0.13)	0.44
11-01	Gp3	g.chr20:46271050C>T	Silent	NCOA3	p.H1058H	nuclear receptor coactiv	24 (0.00)	29 (0.38)	1.01
11-01	Gp3	g.chr20:44695693C>A	Splice Site	NCOA5		nuclear receptor coactiv	67 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr17:16022753C>T	Missense Mutation	NCOR1	p.M633I	nuclear receptor corepre	18 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr20:26094530G>C	RNA	NCOR1P1		nuclear receptor corepre	129 (0.00)	51 (0.22)	0.58
11-01	Gp3	g.chr12:124904514C>T	Missense Mutation	NCOR2	p.G491S	nuclear receptor corepre	33 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr17:8351938G>A	Missense Mutation	NDEL1	p.E154K	nudE neurodevelopmen	37 (0.00)	27 (0.19)	0.49

11-01	Gp3	g.chr5:141511424C>A	Missense Mutation	NDFIP1	p.P39T	Nedd4 family interacting	22 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr4:121957733C>A	Missense Mutation	NDNF	p.A465S	neuron-derived neurotro	54 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr8:134274403G>A	Silent	NDRG1	p.T71T	N-myc downstream regu	22 (0.00)	18 (0.61)	1.63
11-01	Gp3	g.chr10:75567689C>T	Missense Mutation	NDST2	p.S153N	N-deacetylase/N-sulfotr	43 (0.00)	52 (0.15)	0.41
11-01	Gp3	g.chr9:32572895G>A	Missense Mutation	NDUFB6	p.S55F	NADH dehydrogenase (	92 (0.00)	32 (0.28)	0.46
11-01	Gp3	g.chr11:67376968C>A	Silent	NDUFV1	p.T124T	NADH dehydrogenase (	25 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr2:152342351C>A	Nonsense Mutation	NEB	p.E8501*	nebulin	103 (0.00)	37 (0.38)	1.01
11-01	Gp3	g.chr2:152359394C>G	Missense Mutation	NEB	p.L7947F	nebulin	65 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr2:152363516C>A	Missense Mutation	NEB	p.Q7821H	nebulin	15 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr2:152382562G>A	Silent	NEB	p.V7357V	nebulin	160 (0.00)	78 (0.22)	0.58
11-01	Gp3	g.chr2:152398039C>A	Missense Mutation	NEB	p.K6868N	nebulin	111 (0.00)	74 (0.28)	0.76
11-01	Gp3	g.chr2:152404162C>T	Missense Mutation	NEB	p.E6750K	nebulin	125 (0.00)	40 (0.35)	0.93
11-01	Gp3	g.chr2:152541424T>A	Missense Mutation	NEB	p.Q901H	nebulin	25 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr3:27326389G>A	Missense Mutation	NEK10	p.S618F	NIMA-related kinase 1(	59 (0.00)	45 (0.38)	1.01
11-01	Gp3	g.chr1:211846988C>T	Missense Mutation	NEK2	p.S131N	NIMA-related kinase 2	45 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr17:27068184C>A	Silent	NEK8	p.V607V	NIMA-related kinase 8	73 (0.00)	41 (0.29)	0.78
11-01	Gp3	g.chr12:44913817C>T	Missense Mutation	NELL2	p.G791S	NEL-like 2 (chicken)	40 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr12:45004650C>T	Silent	NELL2	p.G516G	NEL-like 2 (chicken)	86 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr12:45105148T>C	Silent	NELL2	p.S372S	NEL-like 2 (chicken)	17 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr15:73468803G>A	Missense Mutation	NEO1	p.V359I	neogenin 1	21 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr17:7221232C>A	Silent	NEURL4	p.P1360P	neuralized E3 ubiquitin	42 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr1:204931257C>G	Missense Mutation	NFASC	p.S237C	neurofascin	56 (0.00)	20 (0.50)	1.33
11-01	Gp3	g.chr20:50133392C>A	Silent	NFATC2	p.R421R	nuclear factor of activat	45 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr19:36387840G>A	Silent	NFKBID	p.L43L	nuclear factor of kappa l	21 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr4:47900814G>A	Missense Mutation	NFXL1	p.A350V	nuclear transcription fac	75 (0.00)	88 (0.24)	0.64
11-01	Gp3	g.chr12:104522241A>T	Missense Mutation	NFYB	p.Y21N	nuclear transcription fac	43 (0.00)	51 (0.16)	0.42
11-01	Gp3	g.chr1:115828974G>A	Missense Mutation	NGF	p.T148I	nerve growth factor (bet	74 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr3:25778939T>A	Missense Mutation	NGLY1	p.N255Y	N-glycanase 1	48 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr15:90814824C>A	Missense Mutation	NGRN	p.P227H	neugrin, neurite outgrow	90 (0.00)	74 (0.22)	0.58
11-01	Gp3	g.chr1:236205462C>A	Missense Mutation	NID1	p.D295Y	nidogen 1	16 (0.00)	18 (0.28)	0.53
11-01	Gp3	g.chr2:201759986G>C	Splice Site	NIF3L1		NIF3 NGG1 interacting	18 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr5:43280264C>A	Silent	NIM1	p.I248I		76 (0.00)	44 (0.30)	0.79
11-01	Gp3	g.chr14:51208373G>A	Missense Mutation	NIN	p.T1792I	ninein (GSK3B interacti	45 (0.02)	55 (0.84)	2.23
11-01	Gp3	g.chr14:51224859C>A	Missense Mutation	NIN	p.Q963H	ninein (GSK3B interacti	83 (0.01)	92 (0.29)	0.78
11-01	Gp3	g.chr14:51230655G>A	Nonsense Mutation	NIN	p.Q555*	ninein (GSK3B interacti	30 (0.00)	36 (0.19)	0.52

11-01	Gp3	g.chr3:52526114C>A	Missense Mutation	NISCH	p.S1377R	nischarin	24 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr12:10588569C>T	Missense Mutation	NKG2-E	p.G6E		36 (0.00)	50 (0.22)	0.59
11-01	Gp3	g.chrX:118724476G>A	Silent	NKRF	p.S304S	NFKB repressing factor	27 (0.00)	29 (0.28)	0.46
11-01	Gp3	g.chr3:42687447G>A	Missense Mutation	NKTR	p.E1457K	natural killer cell trigge	55 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr17:33463187C>T	Splice Site	NLE1		notchless homolog 1 (D	120 (0.00)	91 (0.29)	0.76
11-01	Gp3	g.chr3:173998751G>A	Silent	NLGN1	p.R710R	neuroligin 1	56 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr2:32460564C>A	Silent	NLRC4	p.L896L	NLR family, CARD do	37 (0.00)	40 (0.30)	0.80
11-01	Gp3	g.chr16:57060439C>T	Silent	NLRC5	p.A528A	NLR family, CARD do	89 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr16:57095565C>T	Missense Mutation	NLRC5	p.A1369V	NLR family, CARD do	15 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr19:56552397G>A	Missense Mutation	NLRP5	p.E966K	NLR family, pyrin dom	69 (0.00)	61 (0.46)	1.22
11-01	Gp3	g.chr19:56569710G>T	Missense Mutation	NLRP5	p.S1135I	NLR family, pyrin dom	43 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr19:56241249C>A	Missense Mutation	NLRP9	p.A648S	NLR family, pyrin dom	59 (0.02)	33 (0.24)	0.65
11-01	Gp3	g.chr5:137451432G>C	Missense Mutation	NME5	p.L193V	NME/NM23 family me	38 (0.00)	33 (0.55)	1.45
11-01	Gp3	g.chr17:43181098G>A	Missense Mutation	NMT1	p.D396N	N-myristoyltransferase	82 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr2:232389810G>T	Missense Mutation	NMUR1	p.H409N	neuromedin U receptor	18 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr5:43587459G>A	RNA	NNT-AS1		NNT antisense RNA 1	35 (0.00)	37 (0.32)	0.86
11-01	Gp3	g.chr7:30492478G>A	Silent	NOD1	p.D185D	nucleotide-binding olig	16 (0.00)	37 (0.32)	0.86
11-01	Gp3	g.chr2:10712249C>T	Missense Mutation	NOL10	p.R672H	nucleolar protein 10	113 (0.00)	45 (0.40)	1.07
11-01	Gp3	g.chr2:10712278C>T	Silent	NOL10	p.L662L	nucleolar protein 10	79 (0.00)	29 (0.31)	0.83
11-01	Gp3	g.chr9:33464082G>A	Nonsense Mutation	NOL6	p.Q953*	nucleolar protein 6 (RN	116 (0.00)	57 (0.23)	0.61
11-01	Gp3	g.chr9:95062258G>A	Silent	NOL8	p.V1034V	nucleolar protein 8	82 (0.00)	68 (0.51)	1.37
11-01	Gp3	g.chr9:95086417G>A	Silent	NOL8	p.R9R	nucleolar protein 8	28 (0.00)	64 (0.39)	1.04
11-01	Gp3	g.chr12:117681231C>A	Missense Mutation	NOS1	p.D979Y	nitric oxide synthase 1 (	62 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr1:120462232G>A	Silent	NOTCH2	p.G1828G	notch 2	21 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr1:120539898G>A	Missense Mutation	NOTCH2	p.T158I	notch 2	52 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr19:46443277C>T	Silent	NOVA2	p.Q441Q	neuro-oncological ventr	22 (0.00)	72 (0.18)	0.48
11-01	Gp3	g.chr11:89177365T>C	Missense Mutation	NOX4	p.N129D	NADPH oxidase 4	58 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr15:24922060G>A	Missense Mutation	NPAP1	p.G349D	nuclear pore associated	46 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr11:66192299G>A	Missense Mutation	NPAS4	p.M646I	neuronal PAS domain p	55 (0.00)	23 (0.57)	1.51
11-01	Gp3	g.chr18:21123440C>A	Nonsense Mutation	NPC1	p.E742*	Niemann-Pick disease, t	145 (0.00)	65 (0.26)	0.70
11-01	Gp3	g.chr4:72994572C>A	Silent	NPFFR2	p.A88A	neuropeptide FF recept	18 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr18:11619753G>C	RNA	NPIPB1P		nuclear pore complex in	64 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr18:11625558G>C	RNA	NPIPB1P		nuclear pore complex in	106 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr17:79534516G>C	Missense Mutation	NPLOC4	p.S498C	nuclear protein localizat	79 (0.00)	55 (0.18)	0.48
11-01	Gp3	g.chr7:34698162C>A	Nonsense Mutation	NPSR1	p.Y46*	neuropeptide S receptor	32 (0.00)	11 (0.55)	1.45

11-01	Gp3	g.chr4:156136234C>T	Silent	NPY2R	p.V381V	neuropeptide Y receptor	20 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr16:69747024C>G	Missense Mutation	NQO1	p.K104N	NAD(P)H dehydrogena:	92 (0.00)	80 (0.15)	0.40
11-01	Gp3	g.chr16:69752154T>A	Nonsense Mutation	NQO1	p.K59*	NAD(P)H dehydrogena:	45 (0.00)	28 (0.29)	0.76
11-01	Gp3	g.chrX:30322813G>C	Silent	NR0B1	p.T432T	nuclear receptor subfam	48 (0.00)	43 (0.23)	0.39
11-01	Gp3	g.chr11:47283131G>A	Missense Mutation	NR1H3	p.E248K	nuclear receptor subfam	32 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr3:119531648C>A	Missense Mutation	NR1I2	p.S251Y	nuclear receptor subfam	29 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr12:95416032G>T	Missense Mutation	NR2C1	p.N595K	nuclear receptor subfam	17 (0.00)	10 (0.50)	1.70
11-01	Gp3	g.chr15:96880759C>A	Missense Mutation	NR2F2	p.R385S	nuclear receptor subfam	69 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr10:115393896T>G	Missense Mutation	NRAP	p.K501T	nebulin-related anchorir	48 (0.00)	64 (0.28)	0.75
11-01	Gp3	g.chr5:111071185A>G	Missense Mutation	NREP	p.F8S	neuronal regeneration re	80 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr7:129297211C>T	Missense Mutation	NRF1	p.T7I	nuclear respiratory facto	19 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr2:206617671C>G	Missense Mutation	NRP2	p.S672R	neuropilin 2	57 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr2:50723126T>A	Missense Mutation	NRXN1	p.D1036V	neurexin 1	125 (0.00)	74 (0.35)	0.94
11-01	Gp3	g.chr2:50850490C>T	Missense Mutation	NRXN1	p.A399T	neurexin 1	133 (0.00)	104 (0.17)	0.46
11-01	Gp3	g.chr5:176710891C>T	Missense Mutation	NSD1	p.T2038I	nuclear receptor binding	99 (0.00)	55 (0.16)	0.44
11-01	Gp3	g.chr17:44828925G>A	Silent	NSF	p.G700G	N-ethylmaleimide-sensi	69 (0.00)	56 (0.18)	0.48
11-01	Gp3	g.chr8:59499055C>T	Missense Mutation	NSMAF	p.C803Y	neutral sphingomyelinas	37 (0.00)	29 (0.17)	0.58
11-01	Gp3	g.chr10:104850509C>A	Missense Mutation	NT5C2	p.M436I	5'-nucleotidase, cytosoli	28 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr17:39987139C>A	Missense Mutation	NT5C3B	p.W73C	5'-nucleotidase, cytosoli	61 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr1:233092110G>A	Missense Mutation	NTPCR	p.G72E	nucleoside-triphosphata:	35 (0.00)	33 (0.18)	0.38
11-01	Gp3	g.chr9:87570348G>A	Silent	NTRK2	p.R680R	neurotrophic tyrosine ki	24 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr12:106464663C>A	Missense Mutation	NUAK1	p.V241L	NUAK family, SNF1-lil	32 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr13:48619932C>T	Silent	NUDT15	p.L164L	nudix (nucleoside dipho	43 (0.02)	26 (0.42)	1.13
11-01	Gp3	g.chr10:12209716G>T	Silent	NUDT5	p.P215P	nudix (nucleoside dipho	106 (0.00)	68 (0.15)	0.39
11-01	Gp3	g.chr16:77769832C>T	Silent	NUDT7	p.L99L	nudix (nucleoside dipho	57 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr14:73751025G>A	Missense Mutation	NUMB	p.S238F	numb homolog (Drosop	110 (0.00)	78 (0.17)	0.44
11-01	Gp3	g.chr6:17637632G>A	Missense Mutation	NUP153	p.A739V	nucleoporin 153kDa	70 (0.01)	88 (0.32)	0.85
11-01	Gp3	g.chr6:17640220G>A	Missense Mutation	NUP153	p.P599L	nucleoporin 153kDa	28 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr11:47840927C>A	Splice Site	NUP160	p.R454I	nucleoporin 160kDa	102 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr7:135307609G>A	Missense Mutation	NUP205	p.S1472N	nucleoporin 205kDa	28 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr7:135327961C>T	Missense Mutation	NUP205	p.P1805L	nucleoporin 205kDa	70 (0.00)	35 (0.26)	0.69
11-01	Gp3	g.chr1:154061998G>A	Missense Mutation	NUP210L	p.R754C	nucleoporin 210kDa-lik	54 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr9:134072980G>A	Missense Mutation	NUP214	p.G1367S	nucleoporin 214kDa	50 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chrX:106397368C>G	Missense Mutation	NUP62CL	p.Q101H	nucleoporin 62kDa C-te	49 (0.00)	49 (0.27)	0.44
11-01	Gp3	g.chr11:3720557G>A	Missense Mutation	NUP98	p.T1255I	nucleoporin 98kDa	77 (0.00)	49 (0.31)	0.82

11-01	Gp3	g.chrX:101821737G>A	RNA	NXF4		nuclear RNA export fac	36 (0.00)	22 (0.27)	0.45
11-01	Gp3	g.chr1:228432111G>T	Missense Mutation	OBSCN	p.W1199L	obscurin, cytoskeletal ca	79 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr1:228434246G>T	Missense Mutation	OBSCN	p.A1351S	obscurin, cytoskeletal ca	90 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr1:228509488C>A	Missense Mutation	OBSCN	p.H5939Q	obscurin, cytoskeletal ca	45 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr4:71063863G>A	Missense Mutation	ODAM	p.G122S	odontogenic, ameloblast	47 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr9:131231556C>T	Missense Mutation	ODF2	p.S110L	outer dense fiber of sper	77 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr7:44715749G>A	Splice Site	OGDH		oxoglutarate (alpha-ketc	19 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr11:7530823C>T	Missense Mutation	OLFML1	p.R205W	olfactomedin-like 1	67 (0.00)	82 (0.15)	0.39
11-01	Gp3	g.chr1:114522157C>T	Missense Mutation	OLFML3	p.L7F	olfactomedin-like 3	47 (0.00)	36 (0.22)	0.59
11-01	Gp3	g.chr1:114523915C>T	Nonsense Mutation	OLFML3	p.R249*	olfactomedin-like 3	32 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr6:74078948G>A	Silent	OOEP	p.H62H	oocyte expressed protein	62 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chrX:67283979G>A	Silent	OPHN1	p.S625S	oligophrenin 1	37 (0.00)	21 (0.33)	0.56
11-01	Gp3	g.chrX:67413765C>A	Missense Mutation	OPHN1	p.V390F	oligophrenin 1	20 (0.00)	14 (0.50)	0.83
11-01	Gp3	g.chr10:13178833G>A	Silent	OPTN	p.T567T	optineurin	49 (0.00)	10 (0.80)	2.13
11-01	Gp3	g.chr11:6891892C>A	Missense Mutation	OR10A2	p.P303T	olfactory receptor, famil	19 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr14:22038856G>A	Missense Mutation	OR10G3	p.T7I	olfactory receptor, famil	28 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr11:123900387G>C	Missense Mutation	OR10G8	p.A20P	olfactory receptor, famil	45 (0.02)	32 (0.34)	0.92
11-01	Gp3	g.chr11:123900946C>G	Missense Mutation	OR10G8	p.A206G	olfactory receptor, famil	55 (0.00)	31 (0.77)	2.06
11-01	Gp3	g.chr19:15904960G>T	Missense Mutation	OR10H5	p.M34I	olfactory receptor, famil	48 (0.02)	28 (0.43)	1.14
11-01	Gp3	g.chr1:159409910C>T	Missense Mutation	OR10J1	p.T121I	olfactory receptor, famil	39 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr14:19377774G>T	Missense Mutation	OR11H12	p.A61S	olfactory receptor, famil	144 (0.00)	54 (0.17)	0.44
11-01	Gp3	g.chr10:45798917G>A	Silent	OR13A1	p.A318A	olfactory receptor, famil	70 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr9:107367442G>T	Missense Mutation	OR13C2	p.S156Y	olfactory receptor, famil	50 (0.00)	41 (0.32)	0.85
11-01	Gp3	g.chr9:107380165C>A	Missense Mutation	OR13C9	p.M107I	olfactory receptor, famil	138 (0.00)	95 (0.26)	0.70
11-01	Gp3	g.chr1:248512448C>T	Silent	OR14C36	p.V124V	olfactory receptor, famil	48 (0.00)	30 (0.23)	0.49
11-01	Gp3	g.chr17:3300829C>T	Silent	OR1E1	p.L292L	olfactory receptor, famil	51 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr9:125273799C>T	Missense Mutation	OR1J2	p.T240I	olfactory receptor, famil	47 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr7:99474257C>G	Missense Mutation	OR2AE1	p.V134L	olfactory receptor, famil	66 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr11:6806593G>A	Missense Mutation	OR2AG1	p.G109S	olfactory receptor, famil	55 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr7:143657511G>A	Missense Mutation	OR2F1	p.V150I	olfactory receptor, famil	46 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr9:114090114C>G	Silent	OR2K2	p.V200V	olfactory receptor, famil	45 (0.02)	40 (0.42)	1.13
11-01	Gp3	g.chr1:248202418G>C	Missense Mutation	OR2L2	p.M283I	olfactory receptor, famil	40 (0.00)	26 (0.31)	0.65
11-01	Gp3	g.chr1:248186039C>G	Missense Mutation	OR2L5	p.L264V	olfactory receptor, famil	60 (0.00)	64 (0.22)	0.46
11-01	Gp3	g.chr5:180582488G>A	Missense Mutation	OR2V2	p.M182I	olfactory receptor, famil	77 (0.00)	59 (0.24)	0.63
11-01	Gp3	g.chr17:3194976G>T	Missense Mutation	OR3A1	p.Q301K	olfactory receptor, famil	81 (0.00)	54 (0.17)	0.44

11-01	Gp3	g.chr11:51412047C>T	Missense Mutation	OR4A5	p.A117T	olfactory receptor, famil	54 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr11:50003738A>G	Silent	OR4C12	p.Y100Y	olfactory receptor, famil	131 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr11:123810725C>T	Silent	OR4D5	p.L134L	olfactory receptor, famil	39 (0.00)	40 (0.35)	0.93
11-01	Gp3	g.chr15:102359080G>T	Missense Mutation	OR4F15	p.G231C	olfactory receptor, famil	81 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr14:20502258G>C	Silent	OR4K13	p.V220V	olfactory receptor, famil	55 (0.00)	24 (0.46)	1.22
11-01	Gp3	g.chr14:20444103G>C	Missense Mutation	OR4K15	p.M142I	olfactory receptor, famil	33 (0.00)	38 (0.50)	1.33
11-01	Gp3	g.chr14:20248542C>T	Missense Mutation	OR4M1	p.R21W	olfactory receptor, famil	56 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr14:20248842G>A	Missense Mutation	OR4M1	p.D121N	olfactory receptor, famil	86 (0.00)	79 (0.20)	0.54
11-01	Gp3	g.chr11:4976408G>T	Missense Mutation	OR51A2	p.S179Y	olfactory receptor, famil	48 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr11:5373439G>A	Silent	OR51B6	p.K234K	olfactory receptor, famil	40 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr11:4842809G>C	Missense Mutation	OR51F2	p.C65S	olfactory receptor, famil	140 (0.01)	150 (0.17)	0.44
11-01	Gp3	g.chr11:4843533C>T	Silent	OR51F2	p.Y306Y	olfactory receptor, famil	32 (0.00)	53 (0.25)	0.65
11-01	Gp3	g.chr11:4843587G>A	Silent	OR51F2	p.K324K	olfactory receptor, famil	29 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr11:5475624C>G	Silent	OR51I2	p.A302A	olfactory receptor, famil	90 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr11:5411194C>T	Missense Mutation	OR51M1	p.S189L	olfactory receptor, famil	60 (0.00)	22 (0.59)	1.58
11-01	Gp3	g.chr11:5443536C>T	Missense Mutation	OR51Q1	p.L36F	olfactory receptor, famil	30 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr11:5878701C>T	Missense Mutation	OR52E8	p.G78S	olfactory receptor, famil	148 (0.00)	94 (0.21)	0.57
11-01	Gp3	g.chr11:4615953G>A	Missense Mutation	OR52I1	p.V229I	olfactory receptor, famil	206 (0.00)	153 (0.16)	0.42
11-01	Gp3	g.chr11:4825601C>A	Missense Mutation	OR52R1	p.A4S	olfactory receptor, famil	57 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr11:5968864C>T	Silent	OR56A3	p.I96I	olfactory receptor, famil	61 (0.00)	80 (0.17)	0.47
11-01	Gp3	g.chr3:97806113T>C	Missense Mutation	OR5AC2	p.F33L	olfactory receptor, famil	73 (0.01)	64 (0.19)	0.50
11-01	Gp3	g.chr11:58126529G>A	Missense Mutation	OR5B17	p.T5I	olfactory receptor, famil	32 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr3:98216621G>A	Missense Mutation	OR5K2	p.A33T	olfactory receptor, famil	148 (0.01)	64 (0.22)	0.58
11-01	Gp3	g.chr11:56230787C>T	Missense Mutation	OR5M9	p.A31T	olfactory receptor, famil	47 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr11:56230814G>A	Nonsense Mutation	OR5M9	p.Q22*	olfactory receptor, famil	33 (0.00)	23 (0.39)	1.04
11-01	Gp3	g.chr11:55681354G>A	Silent	OR5W2	p.F235F	olfactory receptor, famil	56 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr12:55688902C>A	Missense Mutation	OR6C6	p.G39W	olfactory receptor, famil	16 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr14:23103244G>A	Missense Mutation	OR6J1	p.P158L	olfactory receptor, famil	45 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr1:158747006G>A	Silent	OR6N2	p.L140L	olfactory receptor, famil	76 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr14:21109275G>A	Silent	OR6S1	p.C192C	olfactory receptor, famil	34 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr7:142750079C>T	Silent	OR6V1	p.I214I	olfactory receptor, famil	143 (0.00)	88 (0.17)	0.45
11-01	Gp3	g.chr7:142760352G>A	RNA	OR6W1P		olfactory receptor, famil	48 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr19:14910043C>T	Silent	OR7C1	p.G302G	olfactory receptor, famil	42 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr11:124440109C>T	Missense Mutation	OR8A1	p.L49F	olfactory receptor, famil	36 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr11:124412651C>A	Silent	OR8B12	p.L300L	olfactory receptor, famil	33 (0.00)	18 (0.33)	0.89

11-01	Gp3	g.chr11:124310170C>T	Missense Mutation	OR8B8	p.G271D	olfactory receptor, famil	45 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr11:124310500G>A	Missense Mutation	OR8B8	p.A161V	olfactory receptor, famil	61 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr11:124120953T>A	RNA	OR8G1		olfactory receptor, famil	111 (0.00)	65 (0.28)	0.74
11-01	Gp3	g.chr11:55890374C>A	Missense Mutation	OR8H3	p.H176N	olfactory receptor, famil	54 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr11:56086095C>A	Missense Mutation	OR8K3	p.L105I	olfactory receptor, famil	60 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr12:48919467C>G	Missense Mutation	OR8S1	p.S18C	olfactory receptor, famil	49 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr11:56143408C>T	Silent	OR8U1	p.C103C	olfactory receptor, famil	139 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr12:55523599C>G	Missense Mutation	OR9K2	p.A16G	olfactory receptor, famil	71 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr2:201785027T>A	Missense Mutation	ORC2	p.N462Y	origin recognition comp	30 (0.00)	31 (0.42)	1.12
11-01	Gp3	g.chr2:201822820G>A	Silent	ORC2	p.D9D	origin recognition comp	23 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr16:46725021C>A	Missense Mutation	ORC6	p.P62T	origin recognition comp	48 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr11:59349024G>A	Missense Mutation	OSBP	p.T561I	oxysterol binding protei	31 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr11:59349028C>G	Splice Site	OSBP		oxysterol binding protei	17 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr3:125279339C>G	Missense Mutation	OSBPL11	p.D347H	oxysterol binding protei	30 (0.00)	28 (0.39)	1.05
11-01	Gp3	g.chr18:21750351C>G	Silent	OSBPL1A	p.T786T	oxysterol binding protei	97 (0.01)	48 (0.17)	0.44
11-01	Gp3	g.chr7:24843989C>A	Nonsense Mutation	OSBPL3	p.E838*	oxysterol binding protei	104 (0.00)	113 (0.18)	0.47
11-01	Gp3	g.chr7:24882020C>G	Missense Mutation	OSBPL3	p.D427H	oxysterol binding protei	37 (0.00)	35 (0.34)	0.91
11-01	Gp3	g.chr2:179197461G>A	Missense Mutation	OSBPL6	p.E156K	oxysterol binding protei	42 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr14:20916149G>A	Missense Mutation	OSGEP	p.T236I	O-sialoglycoprotein end	78 (0.00)	33 (0.42)	1.13
11-01	Gp3	g.chr8:90937598G>A	Silent	OSGIN2	p.E496E	oxidative stress induced	117 (0.01)	107 (0.21)	0.69
11-01	Gp3	g.chr6:159262696C>A	RNA	OSTCP1		oligosaccharyltransferas	33 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr16:21689926G>A	Splice Site	OTOA	p.D31N	otoancorin	45 (0.00)	56 (0.25)	0.67
11-01	Gp3	g.chr16:21716536G>T	Missense Mutation	OTOA	p.A343S	otoancorin	48 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr12:80747224G>T	Missense Mutation	OTOGL	p.V1822L	otogelin-like	63 (0.00)	45 (0.20)	0.53
11-01	Gp3	g.chr20:16729070C>A	Missense Mutation	OTOR	p.F8L	otoraplin	195 (0.00)	125 (0.15)	0.41
11-01	Gp3	g.chr4:146058825C>A	Missense Mutation	OTUD4	p.L1034F	OTU deubiquitinase 4	117 (0.00)	58 (0.22)	0.60
11-01	Gp3	g.chr4:146065514C>T	Missense Mutation	OTUD4	p.D499N	OTU deubiquitinase 4	124 (0.01)	42 (0.17)	0.44
11-01	Gp3	g.chr4:146083793C>A	Splice Site	OTUD4	p.Q165H	OTU deubiquitinase 4	19 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr14:57507914G>A	RNA	OTX2-AS1		OTX2 antisense RNA 1	80 (0.01)	59 (0.31)	0.81
11-01	Gp3	g.chr12:29644126C>A	Splice Site	OVCH1		ovochymase 1	51 (0.00)	30 (0.37)	0.98
11-01	Gp3	g.chr1:111957416C>A	Silent	OVGP1	p.V569V	oviductal glycoprotein 1	24 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr5:41840601C>A	Missense Mutation	OXCT1	p.R228S	3-oxoacid CoA transfera	67 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr3:25833080G>C	Missense Mutation	OXSM	p.G190A	3-oxoacyl-ACP synthas	71 (0.00)	46 (0.24)	0.64
11-01	Gp3	g.chr3:38278418G>A	Missense Mutation	OXSR1	p.S347N	oxidative stress responsi	201 (0.00)	127 (0.16)	0.42
11-01	Gp3	g.chr3:38278449C>A	Silent	OXSR1	p.L357L	oxidative stress responsi	183 (0.00)	123 (0.16)	0.43

11-01	Gp3	g.chr12:121570878G>C	Silent	P2RX7	p.V35V	purinergic receptor P2X	79 (0.00)	45 (0.29)	0.77
11-01	Gp3	g.chr12:121622149G>C	Silent	P2RX7	p.L444L	purinergic receptor P2X	60 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr3:49039020C>T	Silent	P4HTM	p.L196L	prolyl 4-hydroxylase, tr	27 (0.00)	24 (0.54)	1.44
11-01	Gp3	g.chr12:56500780C>T	Missense Mutation	PA2G4	p.A75V	proliferation-associated	31 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr8:101730445C>A	Missense Mutation	PABPC1	p.W86L	poly(A) binding protein	40 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr11:66001701C>A	Missense Mutation	PACS1	p.P698T	phosphofurin acidic clus	57 (0.00)	73 (0.23)	0.62
11-01	Gp3	g.chr11:47201128G>C	Missense Mutation	PACSIN3	p.Q205E	protein kinase C and cas	34 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr1:17548940C>A	Missense Mutation	PADI1	p.A83D	peptidyl arginine deimi	99 (0.00)	55 (0.35)	0.92
11-01	Gp3	g.chr1:17681042C>A	Silent	PADI4	p.G390G	peptidyl arginine deimi	44 (0.02)	17 (0.47)	1.25
11-01	Gp3	g.chrX:55247880C>T	Missense Mutation	PAGE5	p.P42L	P antigen family, memb	18 (0.00)	23 (0.26)	0.43
11-01	Gp3	g.chr4:169433328G>A	Missense Mutation	PALLD	p.E225K	palladin, cytoskeletal as	91 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr4:169630213C>A	Missense Mutation	PALLD	p.F512L	palladin, cytoskeletal as	69 (0.00)	30 (0.60)	1.60
11-01	Gp3	g.chr9:112899172G>A	Missense Mutation	PALM2-AKA	p.E450K	PALM2-AKAP2 readth	74 (0.01)	42 (0.24)	0.63
11-01	Gp3	g.chr12:56718365C>A	Splice Site	PAN2	p.Q576H	PAN2 poly(A) specific	50 (0.00)	68 (0.24)	0.63
11-01	Gp3	g.chr11:93911705C>T	Silent	PANX1	p.D164D	pannexin 1	47 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr11:124489539G>A	Missense Mutation	PANX3	p.R296Q	pannexin 3	47 (0.00)	38 (0.76)	2.04
11-01	Gp3	g.chr2:61007904G>A	Nonsense Mutation	PAPOLG	p.W299*	poly(A) polymerase gan	93 (0.00)	78 (0.24)	0.65
11-01	Gp3	g.chr1:176668247G>T	Missense Mutation	PAPPA2	p.V920L	pappalysin 2	102 (0.00)	51 (0.22)	0.58
11-01	Gp3	g.chr15:69682044C>A	Missense Mutation	PAQR5	p.T146N	progestin and adipoQ re	29 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr10:34666954G>T	Missense Mutation	PARD3	p.L494I	par-3 family cell polarit	83 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr12:3939135T>C	Missense Mutation	PARP11	p.E23G	poly (ADP-ribose) poly	70 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr3:122419680T>A	Missense Mutation	PARP14	p.F760Y	poly (ADP-ribose) poly	63 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr15:72552956G>A	Missense Mutation	PARP6	p.R207C	poly (ADP-ribose) poly	89 (0.01)	102 (0.23)	0.60
11-01	Gp3	g.chr3:122274497C>T	Missense Mutation	PARP9	p.C209Y	poly (ADP-ribose) poly	30 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr11:12495499G>T	Missense Mutation	PARVA	p.R129L	parvin, alpha	32 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr2:242065820G>A	Missense Mutation	PASK	p.A837V	PAS domain containing	28 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr11:125616249G>A	Missense Mutation	PATE1	p.R17K	prostate and testis expre	32 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr2:223086025C>G	Missense Mutation	PAX3	p.G291R	paired box 3	167 (0.00)	70 (0.17)	0.46
11-01	Gp3	g.chr21:47333867C>A	Silent	PCBP3	p.S169S	poly(rC) binding protei	28 (0.00)	57 (0.21)	0.56
11-01	Gp3	g.chr3:51992976C>T	Splice Site	PCBP4		poly(rC) binding protei	35 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr13:100953746C>T	Silent	PCCA	p.G366G	propionyl CoA carboxy	54 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr10:55570354C>T	Missense Mutation	PCDH15	p.V1489M	protocadherin-related 1	64 (0.00)	47 (0.28)	0.74
11-01	Gp3	g.chr5:140166721C>T	Silent	PCDHA1	p.D282D	protocadherin alpha 1	66 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr5:140167076T>C	Missense Mutation	PCDHA1	p.F401L	protocadherin alpha 1	46 (0.00)	65 (0.17)	0.45
11-01	Gp3	g.chr5:140167078C>T	Silent	PCDHA1	p.F401F	protocadherin alpha 1	46 (0.00)	65 (0.20)	0.53

11-01	Gp3	g.chr5:140236058C>A	Missense Mutation	PCDHA10	p.P142H	protocadherin alpha 10	58 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr5:140250862C>T	Missense Mutation	PCDHA11	p.T725M	protocadherin alpha 11	23 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr5:140257295G>A	Silent	PCDHA12	p.G746G	protocadherin alpha 12	35 (0.00)	47 (0.23)	0.62
11-01	Gp3	g.chr5:140262082G>A	Missense Mutation	PCDHA13	p.V77I	protocadherin alpha 13	115 (0.00)	59 (0.29)	0.77
11-01	Gp3	g.chr5:140221424G>A	Missense Mutation	PCDHA8	p.S173N	protocadherin alpha 8	25 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr5:140580774C>A	Missense Mutation	PCDHB11	p.T476K	protocadherin beta 11	18 (0.00)	63 (0.89)	2.37
11-01	Gp3	g.chr5:140589224G>A	Missense Mutation	PCDHB12	p.V249M	protocadherin beta 12	19 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr5:140480606G>A	Missense Mutation	PCDHB3	p.D125N	protocadherin beta 3	119 (0.00)	44 (0.20)	0.55
11-01	Gp3	g.chr5:140515474C>A	Missense Mutation	PCDHB5	p.P153H	protocadherin beta 5	81 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr5:140531224C>A	Missense Mutation	PCDHB6	p.N462K	protocadherin beta 6	22 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr5:140885008C>A	Missense Mutation	PCDHGA12	p.D844E	protocadherin gamma su	87 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr5:140724944C>G	Missense Mutation	PCDHGA3	p.N448K	protocadherin gamma su	36 (0.00)	39 (0.62)	1.64
11-01	Gp3	g.chr5:140725588C>A	Missense Mutation	PCDHGA3	p.A663D	protocadherin gamma su	15 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr5:140735293G>A	Missense Mutation	PCDHGA4	p.G176S	protocadherin gamma su	64 (0.02)	27 (0.22)	0.59
11-01	Gp3	g.chr5:140764086G>C	Silent	PCDHGA7	p.P540P	protocadherin gamma su	42 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr5:140752278G>A	Missense Mutation	PCDHGB3	p.E773K	protocadherin gamma su	48 (0.02)	19 (0.37)	0.98
11-01	Gp3	g.chr5:140866367C>A	Missense Mutation	PCDHGC4	p.P543T	protocadherin gamma su	72 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr11:82876652T>A	Missense Mutation	PCF11	p.L238H	PCF11 cleavage and pol	119 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr17:36894833C>A	Missense Mutation	PCGF2	p.K147N	polycomb group ring fir	26 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr7:82582498T>C	Missense Mutation	PCLO	p.T2591A	piccolo presynaptic cyto	91 (0.01)	38 (0.24)	0.63
11-01	Gp3	g.chr7:82595686G>A	Missense Mutation	PCLO	p.P1140S	piccolo presynaptic cyto	183 (0.00)	69 (0.17)	0.46
11-01	Gp3	g.chr7:82785092C>A	Missense Mutation	PCLO	p.V289L	piccolo presynaptic cyto	58 (0.00)	49 (0.24)	0.65
11-01	Gp3	g.chr8:17810531G>T	Missense Mutation	PCM1	p.R375M	pericentriolar material 1	45 (0.00)	14 (0.43)	0.64
11-01	Gp3	g.chr6:150094279C>A	Missense Mutation	PCMT1	p.Q114K	protein-L-isoaspartate (D	42 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr14:60591309C>A	Missense Mutation	PCNXL4	p.P807Q	pecanex-like 4 (Drosoph	149 (0.00)	59 (0.34)	0.90
11-01	Gp3	g.chr1:161254226C>A	Silent	PCP4L1	p.G54G	Purkinje cell protein 4 li	52 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr5:95730615C>T	Missense Mutation	PCSK1	p.V613I	proprotein convertase su	132 (0.00)	98 (0.17)	0.46
11-01	Gp3	g.chr5:95746652C>T	Silent	PCSK1	p.S307S	proprotein convertase su	26 (0.00)	24 (0.62)	1.67
11-01	Gp3	g.chr20:17417373C>T	Missense Mutation	PCSK2	p.P244S	proprotein convertase su	68 (0.00)	56 (0.21)	0.57
11-01	Gp3	g.chr9:78686696G>T	Missense Mutation	PCSK5	p.S259I	proprotein convertase su	100 (0.01)	50 (0.12)	0.39
11-01	Gp3	g.chr9:78925616G>T	Missense Mutation	PCSK5	p.G1218C	proprotein convertase su	37 (0.00)	28 (0.29)	0.94
11-01	Gp3	g.chr9:78947464C>T	Silent	PCSK5	p.C1535C	proprotein convertase su	40 (0.00)	47 (0.36)	1.18
11-01	Gp3	g.chr12:54966415G>A	Missense Mutation	PDE1B	p.D168N	phosphodiesterase 1B, c	246 (0.00)	121 (0.21)	0.57
11-01	Gp3	g.chr12:54970365C>T	Missense Mutation	PDE1B	p.R422C	phosphodiesterase 1B, c	15 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr11:14808054G>T	Silent	PDE3B	p.L367L	phosphodiesterase 3B, c	120 (0.00)	38 (0.16)	0.42

11-01	Gp3	g.chr11:14889171C>A	Silent	PDE3B	p.S951S	phosphodiesterase 3B, c	19 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr1:66384404C>T	Missense Mutation	PDE4B	p.S56F	phosphodiesterase 4B, c	23 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr1:144918838G>C	Missense Mutation	PDE4DIP	p.L587V	phosphodiesterase 4D ir	75 (0.00)	54 (0.19)	0.49
11-01	Gp3	g.chr5:149274832A>G	Missense Mutation	PDE6A	p.S548P	phosphodiesterase 6A, c	34 (0.03)	35 (0.14)	0.38
11-01	Gp3	g.chr10:95400236G>T	Missense Mutation	PDE6C	p.R553S	phosphodiesterase 6C, c	44 (0.00)	29 (0.34)	0.92
11-01	Gp3	g.chr15:85661014C>T	Missense Mutation	PDE8A	p.H560Y	phosphodiesterase 8A	53 (0.00)	70 (0.19)	0.50
11-01	Gp3	g.chr21:44108103C>A	Splice Site	PDE9A	p.R73S	phosphodiesterase 9A	21 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr7:540877C>A	Silent	PDGFA	p.V152V	platelet-derived growth	71 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr5:149497194G>T	Missense Mutation	PDGFRB	p.P1042T	platelet-derived growth	21 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr3:122865032G>A	Silent	PDIA5	p.K356K	protein disulfide isomer	80 (0.00)	56 (0.16)	0.43
11-01	Gp3	g.chr13:33344486G>A	Silent	PDS5B	p.P1284P	PDS5, regulator of cohe	96 (0.00)	98 (0.15)	0.41
11-01	Gp3	g.chr10:27013023G>A	Missense Mutation	PDSS1	p.A268T	prenyl (decaprenyl) dipl	81 (0.00)	64 (0.22)	0.58
11-01	Gp3	g.chr16:70065868C>T	RNA	PDXDC2P		pyridoxal-dependent de	40 (0.00)	57 (0.56)	1.50
11-01	Gp3	g.chr21:45168938C>T	Silent	PDXK	p.I147I	pyridoxal (pyridoxine, v	21 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr20:1961185G>T	Silent	PDYN	p.P183P	prodynorphin	59 (0.00)	51 (0.25)	0.68
11-01	Gp3	g.chr20:1961186G>T	Missense Mutation	PDYN	p.P183H	prodynorphin	60 (0.00)	52 (0.25)	0.67
11-01	Gp3	g.chr10:119042887G>C	Nonsense Mutation	PDZD8	p.Y1119*	PDZ domain containing	56 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr1:145748375C>T	Missense Mutation	PDZK1	p.T83I	PDZ domain containing	27 (0.00)	9 (0.56)	1.48
11-01	Gp3	g.chr1:145931877C>T	RNA	PDZK1P1		PDZ domain containing	142 (0.00)	30 (0.53)	1.42
11-01	Gp3	g.chr15:77473505C>T	Missense Mutation	PEAK1	p.S255N	pseudopodium-enriched	65 (0.00)	42 (0.21)	0.57
11-01	Gp3	g.chr2:64322385A>G	Silent	PELI1	p.N236N	pellino E3 ubiquitin pro	41 (0.00)	17 (0.41)	1.10
11-01	Gp3	g.chr11:66239924G>A	Missense Mutation	PELI3	p.D123N	pellino E3 ubiquitin pro	23 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr17:17412827C>A	Missense Mutation	PEMT	p.V130L	phosphatidylethanolami	26 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr8:57354154G>A	Silent	PENK	p.L161L	proenkephalin	48 (0.00)	24 (0.38)	1.25
11-01	Gp3	g.chr8:57354299C>A	Missense Mutation	PENK	p.K112N	proenkephalin	63 (0.00)	39 (0.13)	0.43
11-01	Gp3	g.chr17:8049957G>T	Missense Mutation	PER1	p.S621Y	period circadian clock 1	33 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr22:30974829G>T	Silent	PES1	p.R421R	pescadillo ribosomal bi	63 (0.00)	27 (0.26)	0.41
11-01	Gp3	g.chr1:145517388C>A	Splice Site	PEX11B	p.L58I	peroxisomal biogenesis	37 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr17:33904507C>G	Missense Mutation	PEX12	p.R77T	peroxisomal biogenesis	118 (0.00)	69 (0.16)	0.43
11-01	Gp3	g.chr12:7355232C>A	Missense Mutation	PEX5	p.Q260K	peroxisomal biogenesis	67 (0.00)	72 (0.18)	0.48
11-01	Gp3	g.chr17:8168914C>T	Silent	PFAS	p.I834I	phosphoribosylformylgl	32 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr3:48587606G>A	Silent	PFKFB4	p.T53T	6-phosphofructo-2-kina	24 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr6:28254916G>A	Missense Mutation	PGBD1	p.V205M	piggyBac transposable	71 (0.00)	45 (0.40)	1.07
11-01	Gp3	g.chr6:49754785C>A	Missense Mutation	PGK2	p.R39M	phosphoglycerate kinas	19 (0.00)	14 (0.57)	1.52
11-01	Gp3	g.chr19:15586684G>A	Missense Mutation	PGLYRP2	p.S266F	peptidoglycan recogniti	21 (0.00)	27 (0.19)	0.49

11-01	Gp3	g.chr1:153303279G>C	Nonsense Mutation	PGLYRP4	p.Y362*	peptidoglycan recogniti	60 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr1:153312954C>T	Missense Mutation	PGLYRP4	p.G243R	peptidoglycan recogniti	24 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr1:153314209G>C	Missense Mutation	PGLYRP4	p.I173M	peptidoglycan recogniti	18 (0.00)	12 (0.92)	2.44
11-01	Gp3	g.chr1:28793042G>A	Missense Mutation	PHACTR4	p.A206T	phosphatase and actin re	42 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr17:27251171C>A	Silent	PHF12	p.L157L	PHD finger protein 12	21 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr4:129770157C>T	Missense Mutation	PHF17	p.L107F		28 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr9:123636944G>A	Silent	PHF19	p.L26L	PHD finger protein 19	53 (0.02)	107 (0.26)	0.70
11-01	Gp3	g.chr8:133829268G>A	Missense Mutation	PHF20L1	p.G440E	PHD finger protein 20-l	54 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr6:64404483G>A	Missense Mutation	PHF3	p.G837S	PHD finger protein 3	73 (0.00)	46 (0.28)	0.75
11-01	Gp3	g.chr1:120266061C>T	Missense Mutation	PHGDH	p.A118V	phosphoglycerate dehyd	38 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr1:120286612C>A	Missense Mutation	PHGDH	p.S517R	phosphoglycerate dehyd	58 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr16:30768239C>A	Missense Mutation	PHKG2	p.H348N	phosphorylase kinase, g	22 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr3:111630546C>A	Missense Mutation	PHLDB2	p.S23Y	pleckstrin homology-lik	26 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr18:60396694C>T	Intron	PHLPP1		PH domain and leucine	35 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr18:60401233C>T	Intron	PHLPP1		PH domain and leucine	74 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr18:60412703T>A	Intron	PHLPP1		PH domain and leucine	56 (0.02)	32 (0.53)	1.42
11-01	Gp3	g.chr18:60426563C>T	Intron	PHLPP1		PH domain and leucine	51 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr18:60434413G>A	Intron	PHLPP1		PH domain and leucine	35 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr18:60440727C>A	Intron	PHLPP1		PH domain and leucine	61 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr18:60446952G>A	Intron	PHLPP1		PH domain and leucine	45 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr18:60467946G>T	Intron	PHLPP1		PH domain and leucine	42 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr18:60470171G>A	Intron	PHLPP1		PH domain and leucine	151 (0.00)	94 (0.15)	0.40
11-01	Gp3	g.chr18:60475104G>C	Intron	PHLPP1		PH domain and leucine	72 (0.00)	51 (0.22)	0.58
11-01	Gp3	g.chr18:60483041T>A	Intron	PHLPP1		PH domain and leucine	24 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr18:60490220C>A	Intron	PHLPP1		PH domain and leucine	23 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr18:60496229C>G	Intron	PHLPP1		PH domain and leucine	32 (0.00)	36 (0.33)	0.89
11-01	Gp3	g.chr18:60518435G>T	Intron	PHLPP1		PH domain and leucine	113 (0.00)	112 (0.20)	0.52
11-01	Gp3	g.chr18:60523459G>A	Intron	PHLPP1		PH domain and leucine	73 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr18:60532872G>T	Intron	PHLPP1		PH domain and leucine	81 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr18:60550776C>A	Intron	PHLPP1		PH domain and leucine	77 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr18:60551286C>T	Intron	PHLPP1		PH domain and leucine	18 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr18:60551293C>G	Intron	PHLPP1		PH domain and leucine	19 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr18:60553488G>A	Intron	PHLPP1		PH domain and leucine	133 (0.01)	60 (0.22)	0.58
11-01	Gp3	g.chr18:60586844C>A	Intron	PHLPP1		PH domain and leucine	83 (0.00)	61 (0.21)	0.57
11-01	Gp3	g.chr18:60593869G>C	Intron	PHLPP1		PH domain and leucine	106 (0.00)	75 (0.59)	1.56

11-01	Gp3	g.chr18:60601773C>T	Intron	PHLPP1		PH domain and leucine	67 (0.00)	69 (0.14)	0.39
11-01	Gp3	g.chr18:60605833C>A	Intron	PHLPP1		PH domain and leucine	16 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr18:60612387G>A	Silent	PHLPP1	p.G1069G	PH domain and leucine	35 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr18:60634170C>T	Intron	PHLPP1		PH domain and leucine	199 (0.00)	109 (0.23)	0.61
11-01	Gp3	g.chr16:71697863C>T	Intron	PHLPP2		PH domain and leucine	47 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr16:71703586G>A	Intron	PHLPP2		PH domain and leucine	59 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr16:71703608C>A	Intron	PHLPP2		PH domain and leucine	54 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr16:71724583G>A	Nonsense Mutation	PHLPP2	p.R150*	PH domain and leucine	60 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr16:71736628C>A	Silent	PHLPP2	p.L97L	PH domain and leucine	37 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr7:77551987G>A	Silent	PHTF2	p.E299E	putative homeodomain t	83 (0.00)	46 (0.22)	0.58
11-01	Gp3	g.chr7:77552010C>A	Nonsense Mutation	PHTF2	p.S307*	putative homeodomain t	86 (0.01)	43 (0.23)	0.62
11-01	Gp3	g.chr4:25254085G>A	Silent	PI4K2B	p.K137K	phosphatidylinositol 4-k	56 (0.00)	21 (0.48)	1.27
11-01	Gp3	g.chr22:21153471C>T	Silent	PI4KA	p.L638L	phosphatidylinositol 4-k	36 (0.00)	39 (0.21)	0.55
11-01	Gp3	g.chr1:151271436C>A	Missense Mutation	PI4KB	p.Q606H	phosphatidylinositol 4-k	45 (0.02)	33 (0.27)	0.73
11-01	Gp3	g.chr22:38461035G>T	Missense Mutation	PICK1	p.L60F	protein interacting with	33 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr22:38471075C>T	Missense Mutation	PICK1	p.P395L	protein interacting with	18 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr1:172411172C>G	Silent	PIGC	p.L197L	phosphatidylinositol gly	34 (0.00)	50 (0.22)	0.59
11-01	Gp3	g.chr17:34892981G>T	Missense Mutation	PIGW	p.V11F	phosphatidylinositol gly	36 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr3:196460660G>C	Missense Mutation	PIGX	p.V181L	phosphatidylinositol gly	63 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr1:9784385G>A	Missense Mutation	PIK3CD	p.G924R	phosphatidylinositol-4,5	23 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr5:67569301G>T	Nonsense Mutation	PIK3R1	p.E140*	phosphoinositide-3-kina	77 (0.00)	38 (0.39)	1.05
11-01	Gp3	g.chr2:209200096C>T	Silent	PIKFYVE	p.A1403A	phosphoinositide kinase	148 (0.01)	132 (0.42)	1.11
11-01	Gp3	g.chr17:36935699G>A	Silent	PIP4K2B	p.Y197Y	phosphatidylinositol-5-p	80 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr9:71532592G>A	Silent	PIP5K1B	p.Q300Q	phosphatidylinositol-4-p	42 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr22:32058206C>A	De novo Start OutOf	PISD		phosphatidylserine deca	23 (0.00)	28 (0.25)	0.40
11-01	Gp3	g.chr17:1456298C>T	Splice Site	PITPNA	p.S66N	phosphatidylinositol tra	78 (0.01)	44 (0.32)	0.85
11-01	Gp3	g.chr10:3181119G>A	Missense Mutation	PITRM1	p.A965V	pitrilysin metallopeptida	84 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr7:47897397G>A	Nonsense Mutation	PKD1L1	p.Q1466*	polycystic kidney diseas	24 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr5:137226219C>T	Silent	PKD2L2	p.T27T	polycystic kidney diseas	74 (0.00)	73 (0.22)	0.58
11-01	Gp3	g.chr2:42284415C>A	Missense Mutation	PKDCC	p.P426Q	protein kinase domain c	36 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr22:46653797G>A	Missense Mutation	PKDREJ	p.P1808L	polycystin (PKD) family	204 (0.00)	198 (0.18)	0.47
11-01	Gp3	g.chr6:51889437C>T	Missense Mutation	PKHD1	p.G1724E	polycystic kidney and h	175 (0.01)	79 (0.38)	1.01
11-01	Gp3	g.chr6:51889754G>A	Silent	PKHD1	p.I1618I	polycystic kidney and h	67 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr8:110456985C>A	Silent	PKHD1L1	p.I1629I	polycystic kidney and h	236 (0.00)	121 (0.15)	0.40
11-01	Gp3	g.chr8:110461618C>T	Missense Mutation	PKHD1L1	p.P2026L	polycystic kidney and h	72 (0.00)	60 (0.15)	0.40

11-01	Gp3	g.chr8:110523074G>C	Missense Mutation	PKHD1L1	p.V3822L	polycystic kidney and h	90 (0.00)	64 (0.20)	0.54
11-01	Gp3	g.chr8:110523107A>G	Missense Mutation	PKHD1L1	p.T3833A	polycystic kidney and h	75 (0.00)	49 (0.27)	0.71
11-01	Gp3	g.chr15:72502732G>T	Missense Mutation	PKM	p.L112I	pyruvate kinase, muscle	93 (0.00)	98 (0.14)	0.38
11-01	Gp3	g.chr1:89250495G>A	Missense Mutation	PKN2	p.D387N	protein kinase N2	29 (0.00)	19 (0.53)	1.40
11-01	Gp3	g.chr12:33003840C>A	Missense Mutation	PKP2	p.R413L	plakophilin 2	92 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr3:119334902C>A	Silent	PLA1A	p.V63V	phospholipase A1 meml	19 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr16:14766496G>T	Missense Mutation	PLA2G10	p.L156I	phospholipase A2, grou	23 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr15:42373730C>G	Missense Mutation	PLA2G4D	p.A302P	phospholipase A2, grou	75 (0.01)	56 (0.14)	0.38
11-01	Gp3	g.chr15:42285004G>A	Silent	PLA2G4E	p.S467S	phospholipase A2, grou	23 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr8:57080709G>A	Silent	PLAG1	p.D40D	pleiomorphic adenoma g	33 (0.00)	16 (0.38)	1.25
11-01	Gp3	g.chr8:57080825C>G	Missense Mutation	PLAG1	p.A2P	pleiomorphic adenoma g	50 (0.00)	21 (0.29)	0.96
11-01	Gp3	g.chr6:144263008G>A	Silent	PLAGL1	p.S315S	pleiomorphic adenoma g	149 (0.00)	109 (0.21)	0.56
11-01	Gp3	g.chr20:30784717C>A	Missense Mutation	PLAGL2	p.Q343H	pleiomorphic adenoma g	43 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr19:44153107G>C	Missense Mutation	PLAUR	p.L315V	plasminogen activator, u	52 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr15:40582818C>T	Missense Mutation	PLCB2	p.G1057S	phospholipase C, beta 2	87 (0.00)	76 (0.25)	0.67
11-01	Gp3	g.chr3:155200357G>A	Missense Mutation	PLCH1	p.S1161F	phospholipase C, eta 1	20 (0.00)	17 (0.71)	1.88
11-01	Gp3	g.chr2:198949132C>T	Silent	PLCL1	p.R297R	phospholipase C-like 1	91 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr2:198949152G>A	Missense Mutation	PLCL1	p.C304Y	phospholipase C-like 1	89 (0.00)	54 (0.19)	0.49
11-01	Gp3	g.chr2:198949952G>T	Missense Mutation	PLCL1	p.D571Y	phospholipase C-like 1	43 (0.00)	31 (0.32)	0.86
11-01	Gp3	g.chr5:41382023C>A	Missense Mutation	PLCXD3	p.K239N	phosphatidylinositol-spe	43 (0.02)	24 (0.33)	0.89
11-01	Gp3	g.chr2:179365841G>A	Missense Mutation	PLEKHA3	p.R238Q	pleckstrin homology do	73 (0.00)	12 (0.42)	1.11
11-01	Gp3	g.chr1:204210941G>A	Splice Site	PLEKHA6	p.P745L	pleckstrin homology do	60 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr12:6428028C>G	Missense Mutation	PLEKHG6	p.P465A	pleckstrin homology do	23 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr12:6428261C>A	Missense Mutation	PLEKHG6	p.T504N	pleckstrin homology do	21 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr2:208725924C>G	Silent	PLEKHM3	p.V671V	pleckstrin homology do	58 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr19:4512931C>T	Silent	PLIN4	p.V333V	perilipin 4	35 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr5:57750785T>A	Nonsense Mutation	PLK2	p.K607*	polo-like kinase 2	118 (0.00)	117 (0.21)	0.55
11-01	Gp3	g.chr4:128812302C>A	Missense Mutation	PLK4	p.S588Y	polo-like kinase 4	23 (0.00)	16 (0.56)	1.50
11-01	Gp3	g.chr4:155461937C>T	Splice Site	PLRG1	p.K279K	pleiotropic regulator 1	73 (0.00)	34 (0.26)	0.71
11-01	Gp3	g.chr17:37296061C>A	Missense Mutation	PLXDC1	p.G34V	plexin domain containin	24 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr17:37296062C>G	Missense Mutation	PLXDC1	p.G34R	plexin domain containin	24 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr3:126751304C>A	Missense Mutation	PLXNA1	p.T1769K	plexin A1	41 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr7:131866155C>T	Silent	PLXNA4	p.T1159T	plexin A4	70 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr3:48464182G>A	Silent	PLXNB1	p.L428L	plexin B1	21 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr3:48464299G>A	Missense Mutation	PLXNB1	p.R389W	plexin B1	26 (0.00)	27 (0.48)	1.28

11-01	Gp3	g.chr1:205811861C>G	Missense Mutation	PM20D1	p.M282I	peptidase M20 domain	33 (0.00)	42 (0.38)	1.02
11-01	Gp3	g.chr7:6760378G>T	RNA	PMS2CL		PMS2 C-terminal like p	34 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr6:99848489C>T	Missense Mutation	PNISR	p.R782Q	PNN-interacting serine/	184 (0.00)	95 (0.31)	0.47
11-01	Gp3	g.chr6:160240034C>T	Silent	PNLDC1	p.V438V	poly(A)-specific ribonu	35 (0.00)	28 (0.36)	0.95
11-01	Gp3	g.chr19:46974230G>A	Silent	PNMAL1	p.I21I	paraneoplastic Ma antig	33 (0.00)	35 (0.34)	0.91
11-01	Gp3	g.chr14:39650483C>T	Silent	PNN	p.L524L	pinin, desmosome assoc	87 (0.00)	86 (0.19)	0.50
11-01	Gp3	g.chr9:140438006C>A	Missense Mutation	PNPLA7	p.K103N	patatin-like phospholipa	15 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr3:127379902C>G	Missense Mutation	PODXL2	p.T344R	podocalyxin-like 2	76 (0.00)	60 (0.17)	0.44
11-01	Gp3	g.chr3:119190176C>G	Missense Mutation	POGLUT1	p.T66S	protein O-glucosyltrans	69 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr1:151377999G>A	Missense Mutation	POGZ	p.P1162L	pogo transposable elem	48 (0.02)	47 (0.15)	0.40
11-01	Gp3	g.chr1:151378074G>A	Missense Mutation	POGZ	p.A1137V	pogo transposable elem	44 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr12:133202878G>C	Missense Mutation	POLE	p.T2119R	polymerase (DNA direc	24 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr14:50140843G>T	Missense Mutation	POLE2	p.Q139K	polymerase (DNA direc	63 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr6:43572393C>T	Missense Mutation	POLH	p.P309L	polymerase (DNA direc	82 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr6:43581422C>T	Missense Mutation	POLH	p.L424F	polymerase (DNA direc	98 (0.00)	80 (0.21)	0.57
11-01	Gp3	g.chr10:103345146G>C	Missense Mutation	POLL	p.S167C	polymerase (DNA direc	21 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr2:113326388C>G	Silent	POLR1B	p.L605L	polymerase (RNA) I pol	61 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr17:7415476G>T	Splice Site	POLR2A		polymerase (RNA) II (	18 (0.00)	10 (0.50)	1.33
11-01	Gp3	g.chr16:57503972C>A	Missense Mutation	POLR2C	p.A180E	polymerase (RNA) II (	33 (0.00)	25 (0.36)	0.96
11-01	Gp3	g.chr11:62532878G>T	Splice Site	POLR2G		polymerase (RNA) II (	51 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr10:79737276A>G	Missense Mutation	POLR3A	p.I1378T	polymerase (RNA) III (	109 (0.00)	62 (0.15)	0.39
11-01	Gp3	g.chr10:79785514T>A	Missense Mutation	POLR3A	p.T62S	polymerase (RNA) III (	35 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr1:145608408C>T	Missense Mutation	POLR3C	p.M133I	polymerase (RNA) III (	121 (0.01)	85 (0.16)	0.44
11-01	Gp3	g.chr1:145457292G>A	Missense Mutation	POLR3GL	p.P134S	polymerase (RNA) III (	16 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr18:14533145G>A	Missense Mutation	POTEC	p.L324F	POTE ankyrin domain f	66 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr1:167334738G>A	Silent	POU2F1	p.Q43Q	POU class 2 homeobox	46 (0.00)	41 (0.34)	0.91
11-01	Gp3	g.chr1:167370776C>T	Missense Mutation	POU2F1	p.T502M	POU class 2 homeobox	26 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr22:46614288G>C	Missense Mutation	PPARA	p.M166I	peroxisome proliferator-	157 (0.00)	110 (0.15)	0.39
11-01	Gp3	g.chr12:81747019C>A	Missense Mutation	PPFIA2	p.D625Y	protein tyrosine phosph	210 (0.00)	198 (0.16)	0.42
11-01	Gp3	g.chr12:82147793G>T	Silent	PPFIA2	p.R70R	protein tyrosine phosph	43 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr19:49641646G>A	Missense Mutation	PPFIA3	p.A680T	protein tyrosine phosph	20 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr12:27835572C>A	Missense Mutation	PPFIBP1	p.P728H	PTPRF interacting prot	60 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr12:42792759C>A	Missense Mutation	PPHLN1	p.S171Y	periphilin 1	23 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:42792760T>A	Silent	PPHLN1	p.S171S	periphilin 1	23 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr7:44839030G>A	Missense Mutation	PPIA	p.G47D	peptidylprolyl isomeras	68 (0.00)	61 (0.33)	0.87

11-01	Gp3	g.chr5:102495032G>T	Splice Site	PPIP5K2	p.K640N	diphosphoinositol penta	43 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr12:63226000G>A	Missense Mutation	PPM1H	p.T102I	protein phosphatase, Mg	27 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr4:89199653A>G	Missense Mutation	PPM1K	p.L28P	protein phosphatase, Mg	41 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr1:202385984G>A	Missense Mutation	PPP1R12B	p.D121N	protein phosphatase 1, r	52 (0.02)	52 (0.15)	0.41
11-01	Gp3	g.chr17:37790236G>A	Silent	PPP1R1B	p.L114L	protein phosphatase 1, r	77 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr11:111631661C>A	Missense Mutation	PPP2R1B	p.V141L	protein phosphatase 2, r	25 (0.00)	30 (0.33)	0.89
11-01	Gp3	g.chr14:102359423C>T	Missense Mutation	PPP2R5C	p.S259F	protein phosphatase 2, r	42 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr14:63920434C>G	Missense Mutation	PPP2R5E	p.E109D	protein phosphatase 2, r	26 (0.00)	33 (0.45)	1.21
11-01	Gp3	g.chr10:75198161G>A	Missense Mutation	PPP3CB	p.P472S	protein phosphatase 3, c	86 (0.00)	44 (0.23)	0.61
11-01	Gp3	g.chr8:22368632C>T	Missense Mutation	PPP3CC	p.A173V	protein phosphatase 3, c	142 (0.00)	48 (0.27)	0.40
11-01	Gp3	g.chr9:127933448G>A	Silent	PPP6C	p.D29D	protein phosphatase 6, c	49 (0.00)	46 (0.30)	0.81
11-01	Gp3	g.chr19:55757044T>A	Missense Mutation	PPP6R1	p.Y77F	protein phosphatase 6, r	15 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr11:68343428C>G	Missense Mutation	PPP6R3	p.L256V	protein phosphatase 6, r	42 (0.00)	56 (0.39)	1.05
11-01	Gp3	g.chr11:68343437G>A	Missense Mutation	PPP6R3	p.E259K	protein phosphatase 6, r	46 (0.02)	69 (0.49)	1.31
11-01	Gp3	g.chr10:103909687C>T	Silent	PPRC1	p.S1632S	peroxisome proliferator-	76 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr5:64867676G>A	Missense Mutation	PPWD1	p.G178R	peptidylprolyl isomerase	58 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr22:22890747C>T	Silent	PRAME	p.Q424Q	preferentially expressed	74 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr1:12854277C>T	Silent	PRAMEF1	p.L167L	PRAME family member	305 (0.00)	151 (0.15)	0.41
11-01	Gp3	g.chr1:12854487C>T	Silent	PRAMEF1	p.L237L	PRAME family member	281 (0.00)	132 (0.17)	0.46
11-01	Gp3	g.chr1:12887512G>A	Silent	PRAMEF11	p.L115L	PRAME family member	115 (0.00)	93 (0.38)	1.00
11-01	Gp3	g.chr1:12837389G>T	Missense Mutation	PRAMEF12	p.A367S	PRAME family member	87 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr1:12837411G>T	Missense Mutation	PRAMEF12	p.R374L	PRAME family member	91 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr1:13475086G>T	Missense Mutation	PRAMEF18	p.A348D	PRAME family member	37 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr1:13475107C>T	Missense Mutation	PRAMEF18	p.R341Q	PRAME family member	27 (0.00)	17 (0.53)	1.41
11-01	Gp3	g.chr15:91524785C>A	Missense Mutation	PRC1	p.D206Y	protein regulator of cyto	71 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr6:106553788G>A	Missense Mutation	PRDM1	p.G549S	PR domain containing 1	36 (0.00)	13 (0.46)	0.72
11-01	Gp3	g.chr11:129780402C>A	Silent	PRDM10	p.L1044L	PR domain containing 1	50 (0.00)	33 (0.24)	0.65
11-01	Gp3	g.chr8:70970875C>T	Splice Site	PRDM14	p.K462K	PR domain containing 1	60 (0.00)	55 (0.13)	0.42
11-01	Gp3	g.chr8:70970914G>T	Silent	PRDM14	p.I449I	PR domain containing 1	68 (0.00)	69 (0.19)	0.63
11-01	Gp3	g.chr21:43277385C>A	Missense Mutation	PRDM15	p.G99V	PR domain containing 1	41 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr16:90126855G>A	Missense Mutation	PRDM7	p.S376L	PR domain containing 7	30 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr2:27354881G>A	Silent	PREB	p.L332L	prolactin regulatory eler	51 (0.02)	50 (0.18)	0.48
11-01	Gp3	g.chr2:27354883G>A	Missense Mutation	PREB	p.L332F	prolactin regulatory eler	51 (0.00)	50 (0.18)	0.48
11-01	Gp3	g.chr1:203452858C>A	Missense Mutation	PRELP	p.H182Q	proline/arginine-rich enc	60 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr1:203453022C>A	Missense Mutation	PRELP	p.P237Q	proline/arginine-rich enc	105 (0.01)	75 (0.19)	0.50

11-01	Gp3	g.chr1:186278068C>T	Missense Mutation	PRG4	p.L1073F	proteoglycan 4	114 (0.00)	62 (0.32)	0.86
11-01	Gp3	g.chr12:42858962G>T	Missense Mutation	PRICKLE1	p.P292T	prickle homolog 1 (Dros	27 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr12:120117776G>A	Missense Mutation	PRKAB1	p.M69I	protein kinase, AMP-ac	40 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr12:120117802T>C	Missense Mutation	PRKAB1	p.I78T	protein kinase, AMP-ac	38 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr17:66519037G>T	Silent	PRKAR1A	p.T106T	protein kinase, cAMP-d	37 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr3:53217572G>A	Silent	PRKCD	p.L254L	protein kinase C, delta	25 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr3:53223978G>A	Silent	PRKCD	p.L611L	protein kinase C, delta	91 (0.00)	68 (0.15)	0.39
11-01	Gp3	g.chr2:46237822G>T	Splice Site	PRKCE		protein kinase C, epsilo	46 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr14:61924356C>G	Missense Mutation	PRKCH	p.H413D	protein kinase C, eta	45 (0.00)	33 (0.82)	2.18
11-01	Gp3	g.chr10:6506277C>T	Silent	PRKCQ	p.A481A	protein kinase C, theta	232 (0.00)	174 (0.15)	0.40
11-01	Gp3	g.chr2:179314986C>T	Missense Mutation	PRKRA	p.G73D	protein kinase, interfero	92 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr7:102040085T>C	Missense Mutation	PRKRIP1	p.M42T	PRKR interacting protei	34 (0.00)	40 (0.42)	1.13
11-01	Gp3	g.chrX:3573255G>A	Silent	PRKX	p.I178I	protein kinase, X-linked	42 (0.00)	40 (0.30)	0.50
11-01	Gp3	g.chr6:22294726C>A	Missense Mutation	PRL	p.C39F	prolactin	20 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr4:148594930G>T	Missense Mutation	PRMT10	p.A145E		43 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr16:68379688C>A	Nonsense Mutation	PRMT7	p.Y346*	protein arginine methylt	30 (0.00)	26 (0.35)	0.92
11-01	Gp3	g.chr4:16035014C>T	Missense Mutation	PROM1	p.G132E	prominin 1	97 (0.00)	47 (0.28)	0.74
11-01	Gp3	g.chr1:150325375C>T	Missense Mutation	PRPF3	p.R658C	pre-mRNA processing f	36 (0.00)	58 (0.17)	0.46
11-01	Gp3	g.chr1:109238328C>A	Missense Mutation	PRPF38B	p.T94K	pre-mRNA processing f	44 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr12:50025684G>A	Missense Mutation	PRPF40B	p.M90I	PRP40 pre-mRNA proc	60 (0.00)	86 (0.33)	0.87
11-01	Gp3	g.chr12:50036776C>T	Missense Mutation	PRPF40B	p.H728Y	PRP40 pre-mRNA proc	18 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr6:4032916G>C	Missense Mutation	PRPF4B	p.G389R	pre-mRNA processing f	67 (0.00)	85 (0.34)	0.91
11-01	Gp3	g.chr6:4032980C>A	Missense Mutation	PRPF4B	p.S410Y	pre-mRNA processing f	58 (0.00)	72 (0.28)	0.74
11-01	Gp3	g.chr17:1556844G>A	Missense Mutation	PRPF8	p.R2121W	pre-mRNA processing f	49 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr17:1562797G>A	Silent	PRPF8	p.I1664I	pre-mRNA processing f	85 (0.00)	101 (0.15)	0.40
11-01	Gp3	g.chr17:1585160C>A	Missense Mutation	PRPF8	p.V203L	pre-mRNA processing f	33 (0.00)	23 (0.39)	1.04
11-01	Gp3	g.chr7:18067306T>A	Nonsense Mutation	PRPS1L1	p.K34*	phosphoribosyl pyropho	219 (0.00)	141 (0.23)	0.61
11-01	Gp3	g.chr17:18781017G>T	Silent	PRPSAP2	p.V82V	phosphoribosyl pyropho	22 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr19:50118234G>A	Silent	PRR12	p.R1664R	proline rich 12	28 (0.00)	35 (0.49)	1.30
11-01	Gp3	g.chr22:32081672C>T	Silent	PRR14L	p.R2099R	proline rich 14-like	66 (0.00)	36 (0.28)	0.44
11-01	Gp3	g.chr22:32134537C>T	Missense Mutation	PRR14L	p.A104T	proline rich 14-like	24 (0.00)	23 (0.70)	1.11
11-01	Gp3	g.chr9:134360087G>T	Missense Mutation	PRRC2B	p.Q1131H	proline-rich coiled-coil	82 (0.00)	64 (0.17)	0.46
11-01	Gp3	g.chr1:171511289C>T	Missense Mutation	PRRC2C	p.P1560S	proline-rich coiled-coil	102 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr1:171546708G>A	Missense Mutation	PRRC2C	p.S2362N	proline-rich coiled-coil	153 (0.01)	211 (0.16)	0.42
11-01	Gp3	g.chr7:142457361T>C	Missense Mutation	PRSS1	p.F9S	protease, serine, 1 (tryps	80 (0.00)	31 (0.16)	0.43

11-01	Gp3	g.chr6:84234030C>A	Nonsense Mutation	PRSS35	p.Y290*	protease, serine, 35	34 (0.00)	10 (0.50)	1.33
11-01	Gp3	g.chr7:141537702C>A	Missense Mutation	PRSS37	p.V130F	protease, serine, 37	62 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr16:58314455G>A	Silent	PRSS54	p.F287F	protease, serine, 54	27 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr10:25160939C>A	Silent	PRTFDC1	p.T131T	phosphoribosyl transfera	45 (0.00)	66 (0.26)	0.69
11-01	Gp3	g.chr15:55964725C>A	Silent	PRTG	p.L653L	protogenin	56 (0.00)	74 (0.15)	0.40
11-01	Gp3	g.chr15:55974675C>T	Missense Mutation	PRTG	p.G188E	protogenin	50 (0.02)	28 (0.32)	0.86
11-01	Gp3	g.chr10:73578818C>T	Silent	PSAP	p.V467V	prosaposin	49 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr5:139217259C>G	Missense Mutation	PSD2	p.A572G	pleckstrin and Sec7 dom	54 (0.00)	50 (0.28)	0.75
11-01	Gp3	g.chr5:139221949C>T	Silent	PSD2	p.L736L	pleckstrin and Sec7 dom	17 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr14:73678531G>A	Missense Mutation	PSEN1	p.S245N	presenilin 1	43 (0.00)	40 (0.28)	0.73
11-01	Gp3	g.chr1:227068358G>A	Silent	PSEN2	p.G4G	presenilin 2	175 (0.00)	61 (0.15)	0.39
11-01	Gp3	g.chr1:227081758G>C	Missense Mutation	PSEN2	p.G408R	presenilin 2	25 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr19:43579555C>G	Silent	PSG2	p.R220R	pregnancy specific beta-	247 (0.00)	203 (0.15)	0.39
11-01	Gp3	g.chr19:43242967G>A	Silent	PSG3	p.T113T	pregnancy specific beta-	68 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr19:43689077G>C	Missense Mutation	PSG5	p.T96S	pregnancy specific beta-	71 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr19:43411315G>A	Silent	PSG6	p.L240L	pregnancy specific beta-	77 (0.00)	63 (0.17)	0.47
11-01	Gp3	g.chr19:43262204C>T	Missense Mutation	PSG8	p.R220Q	pregnancy specific beta-	187 (0.01)	113 (0.19)	0.52
11-01	Gp3	g.chr14:90736646C>A	Missense Mutation	PSMC1	p.L380M	proteasome (prosome, m	28 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr3:184021785G>A	Silent	PSMD2	p.E458E	proteasome (prosome, m	65 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr3:184022152G>A	Silent	PSMD2	p.V504V	proteasome (prosome, m	59 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr9:123580283G>A	Silent	PSMD5	p.I472I	proteasome (prosome, m	44 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr2:54115127C>A	Splice Site	PSME4		proteasome (prosome, m	31 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr2:54115128T>A	Splice Site	PSME4		proteasome (prosome, m	31 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr2:54127089C>G	Missense Mutation	PSME4	p.Q1117H	proteasome (prosome, m	53 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr20:1108081C>T	Nonsense Mutation	PSMF1	p.Q99*	proteasome (prosome, m	110 (0.00)	45 (0.29)	0.77
11-01	Gp3	g.chr20:1145057C>T	Missense Mutation	PSMF1	p.P234L	proteasome (prosome, m	105 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr9:72333308C>A	Missense Mutation	PTAR1	p.A387S	protein prenyltransferase	17 (0.00)	17 (0.53)	1.41
11-01	Gp3	g.chr10:27688110C>A	Missense Mutation	PTCHD3	p.D473Y	patched domain contain	25 (0.00)	21 (0.57)	1.52
11-01	Gp3	g.chr6:47846092C>G	Missense Mutation	PTCHD4	p.E830Q	patched domain contain	54 (0.02)	33 (0.55)	1.45
11-01	Gp3	g.chr8:97345688C>A	Missense Mutation	PTDSS1	p.S439Y	phosphatidylserine synth	31 (0.00)	39 (0.36)	1.20
11-01	Gp3	g.chr10:89646386C>A	Intron	PTEN		phosphatase and tensin h	123 (0.00)	22 (0.59)	0.81
11-01	Gp3	g.chr10:89647711G>A	Intron	PTEN		phosphatase and tensin h	166 (0.00)	28 (0.29)	0.39
11-01	Gp3	g.chr10:89695984C>G	Intron	PTEN		phosphatase and tensin h	179 (0.01)	12 (0.58)	0.80
11-01	Gp3	g.chr10:89698360G>C	Intron	PTEN		phosphatase and tensin h	155 (0.00)	27 (0.63)	0.86
11-01	Gp3	g.chr5:40692300C>A	Silent	PTGER4	p.T429T	prostaglandin E receptor	27 (0.00)	26 (0.31)	0.82

11-01	Gp3	g.chr2:209353823G>T	Missense Mutation	PTH2R	p.G388V	parathyroid hormone 2 r	19 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr1:32377301C>T	Missense Mutation	PTP4A2	p.G106R	protein tyrosine phospha	33 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr9:96866587C>A	Missense Mutation	PTPDC1	p.H742N	protein tyrosine phospha	44 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr7:77170376C>A	Intron	PTPN12		protein tyrosine phospha	72 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr7:77174591C>A	Intron	PTPN12		protein tyrosine phospha	51 (0.00)	50 (0.36)	0.96
11-01	Gp3	g.chr7:77176791G>A	Intron	PTPN12		protein tyrosine phospha	58 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr7:77180656G>A	Intron	PTPN12		protein tyrosine phospha	37 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr7:77186727C>T	Intron	PTPN12		protein tyrosine phospha	124 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr7:77186744C>A	Intron	PTPN12		protein tyrosine phospha	70 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr7:77193778G>A	Intron	PTPN12		protein tyrosine phospha	28 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr7:77206847C>A	Intron	PTPN12		protein tyrosine phospha	90 (0.00)	40 (0.38)	1.00
11-01	Gp3	g.chr7:77247479G>C	Intron	PTPN12		protein tyrosine phospha	57 (0.00)	39 (0.26)	0.68
11-01	Gp3	g.chr7:77260319G>A	Intron	PTPN12		protein tyrosine phospha	57 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr4:87622897C>A	Silent	PTPN13	p.R380R	protein tyrosine phospha	59 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr4:87694111G>C	Splice Site	PTPN13	p.L1788L	protein tyrosine phospha	21 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr4:87731062C>A	Nonsense Mutation	PTPN13	p.C2413*	protein tyrosine phospha	97 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr1:214588019C>T	Missense Mutation	PTPN14	p.R132Q	protein tyrosine phospha	57 (0.00)	41 (0.41)	1.11
11-01	Gp3	g.chr14:88951505C>A	Splice Site	PTPN21		protein tyrosine phospha	44 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr1:114380392C>A	Missense Mutation	PTPN22	p.G544C	protein tyrosine phospha	36 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr11:18755173C>A	Missense Mutation	PTPN5	p.S313I	protein tyrosine phospha	24 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr12:7064613G>A	Missense Mutation	PTPN6	p.D238N	protein tyrosine phospha	52 (0.00)	63 (0.19)	0.51
11-01	Gp3	g.chr15:75763077C>A	Missense Mutation	PTPN9	p.G435C	protein tyrosine phospha	105 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr20:3003453C>G	Missense Mutation	PTPRA	p.Q474E	protein tyrosine phospha	28 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr10:129854475C>G	Missense Mutation	PTPRE	p.P170R	protein tyrosine phospha	29 (0.00)	46 (0.35)	0.93
11-01	Gp3	g.chr3:62142789C>T	Missense Mutation	PTPRG	p.A244V	protein tyrosine phospha	91 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr11:48157787C>T	Silent	PTPRJ	p.I604I	protein tyrosine phospha	39 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr12:71286584G>A	Missense Mutation	PTPRR	p.H78Y	protein tyrosine phospha	95 (0.00)	34 (0.44)	1.18
11-01	Gp3	g.chr19:5208258C>A	Missense Mutation	PTPRS	p.V1878F	protein tyrosine phospha	22 (0.00)	34 (0.24)	0.63
11-01	Gp3	g.chr20:40710634G>A	Missense Mutation	PTPRT	p.T1387I	protein tyrosine phospha	36 (0.00)	39 (0.44)	1.16
11-01	Gp3	g.chr11:112103898C>G	Missense Mutation	PTS	p.Q86E	6-pyruvoyltetrahydropte	71 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr5:159849828C>A	Missense Mutation	PTTG1	p.N68K	pituitary tumor-transfor	101 (0.00)	85 (0.16)	0.44
11-01	Gp3	g.chr11:125764109C>A	Missense Mutation	PUS3	p.E339D	pseudouridylate synthas	42 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr7:105148776G>T	Missense Mutation	PUS7	p.P62T	pseudouridylate synthas	53 (0.00)	69 (0.22)	0.58
11-01	Gp3	g.chr19:45153134G>A	Missense Mutation	PVR	p.V161M	poliovirus receptor	36 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr6:36359607G>T	Missense Mutation	PXT1	p.F115L	peroxisomal, testis speci	41 (0.00)	12 (0.50)	1.33

11-01	Gp3	g.chr3:49136553G>A	Missense Mutation	QARS	p.P583L	glutaminyl-tRNA synth	41 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr3:49094974G>T	Missense Mutation	QRICH1	p.S220Y	glutamine-rich 1	21 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr11:32956112C>A	Missense Mutation	QSER1	p.S974Y	glutamine and serine ric	71 (0.00)	45 (0.24)	0.65
11-01	Gp3	g.chr7:140111735G>T	Missense Mutation	RAB19	p.R88L	RAB19, member RAS c	21 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr11:87882999G>A	Silent	RAB38	p.D109D	RAB38, member RAS c	34 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr1:52403066G>A	Missense Mutation	RAB3B	p.R83W	RAB3B, member RAS	21 (0.00)	29 (0.52)	1.38
11-01	Gp3	g.chr17:5241354C>T	Missense Mutation	RABEP1	p.P190L	rabaptin, RAB GTPase	39 (0.00)	29 (0.34)	0.92
11-01	Gp3	g.chr9:125760961C>T	Silent	RABGAP1	p.V430V	RAB GTPase activating	82 (0.00)	108 (0.21)	0.57
11-01	Gp3	g.chr2:114398999C>T	Missense Mutation	RABL2A	p.S159L	RAB, member of RAS	325 (0.00)	120 (0.21)	0.56
11-01	Gp3	g.chr5:131925424C>T	Silent	RAD50	p.I449I	RAD50 homolog (S. ce	38 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr1:46725765T>A	Missense Mutation	RAD54L	p.L134H	RAD54-like (S. cerevisi	33 (0.00)	59 (0.47)	1.27
11-01	Gp3	g.chr1:46733164T>A	Missense Mutation	RAD54L	p.Y309N	RAD54-like (S. cerevisi	50 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr1:46738149G>A	Missense Mutation	RAD54L	p.R394Q	RAD54-like (S. cerevisi	86 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr3:51667591A>G	Splice Site	RAD54L2		RAD54-like 2 (S. cerevi	24 (0.04)	33 (0.24)	0.65
11-01	Gp3	g.chr3:51673458G>C	Silent	RAD54L2	p.L628L	RAD54-like 2 (S. cerevi	24 (0.00)	28 (0.54)	1.43
11-01	Gp3	g.chr3:51679084T>A	Missense Mutation	RAD54L2	p.V832E	RAD54-like 2 (S. cerevi	60 (0.00)	71 (0.14)	0.38
11-01	Gp3	g.chr12:110943421G>A	Splice Site	RAD9B		RAD9 homolog B (S. p	24 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr2:121036352G>A	Missense Mutation	RALB	p.E38K	v-ral simian leukemia vi	55 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr18:9517187G>C	Missense Mutation	RALBP1	p.A197P	ralA binding protein 1	35 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr18:9533721G>T	Missense Mutation	RALBP1	p.S533I	ralA binding protein 1	61 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr20:20563755C>T	Silent	RALGAPA2	p.V882V	Ral GTPase activating p	97 (0.00)	35 (0.40)	1.07
11-01	Gp3	g.chr20:37191325G>A	Missense Mutation	RALGAPB	p.E1224K	Ral GTPase activating p	31 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr9:129961315T>C	Missense Mutation	RALGPS1	p.F406S	Ral GEF with PH doma	15 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr1:178852651C>A	Missense Mutation	RALGPS2	p.S296Y	Ral GEF with PH doma	42 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr20:32659995G>C	Missense Mutation	RALY	p.E39Q	RALY heterogeneous n	40 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr8:85799931G>A	Missense Mutation	RALYL	p.E260K	RALY RNA binding pr	136 (0.00)	77 (0.13)	0.43
11-01	Gp3	g.chr7:45222905C>A	Missense Mutation	RAMP3	p.P114H	receptor (G protein-cou	45 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr22:20109945G>C	Splice Site	RANBP1		RAN binding protein 1	25 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr6:13639938C>A	Missense Mutation	RANBP9	p.R461L	RAN binding protein 9	69 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr1:21938240C>T	Missense Mutation	RAP1GAP	p.G228S	RAP1 GTPase activatin	38 (0.00)	41 (0.27)	0.72
11-01	Gp3	g.chr17:2901516T>C	Splice Site	RAP1GAP2	p.L349P	RAP1 GTPase activatin	66 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr9:134465363T>A	Missense Mutation	RAPGEF1	p.Y757F	Rap guanine nucleotide	27 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr4:160251103G>A	Missense Mutation	RAPGEF2	p.V254M	Rap guanine nucleotide	55 (0.00)	22 (0.55)	1.45
11-01	Gp3	g.chr2:173885381T>A	Missense Mutation	RAPGEF4	p.F731I	Rap guanine nucleotide	93 (0.00)	93 (0.16)	0.43
11-01	Gp3	g.chr7:22190104G>A	Missense Mutation	RAPGEF5	p.P299L	Rap guanine nucleotide	118 (0.00)	39 (0.18)	0.48

11-01	Gp3	g.chr17:38348926C>T	Silent	RAPGEFL1	p.F424F	Rap guanine nucleotide	205 (0.00)	100 (0.33)	0.88
11-01	Gp3	g.chr3:25638016G>T	Missense Mutation	RARB	p.S419I	retinoic acid receptor, b	111 (0.00)	71 (0.31)	0.83
11-01	Gp3	g.chr3:158415579G>A	Missense Mutation	RARRES1	p.P258L	retinoic acid receptor re	32 (0.00)	20 (0.55)	1.47
11-01	Gp3	g.chr6:88227897G>C	Missense Mutation	RARS2	p.H501D	arginyl-tRNA synthetas	115 (0.00)	48 (0.29)	0.46
11-01	Gp3	g.chr22:35947596C>T	Silent	RASD2	p.F106F	RASD family, member	20 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr4:82363478C>G	Silent	RASGEF1B	p.V327V	RasGEF domain family,	43 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr5:80419472T>A	Missense Mutation	RASGRF2	p.S828T	Ras protein-specific gua	41 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr13:48982669A>G	Intron	RB1		retinoblastoma 1	65 (0.00)	36 (0.36)	0.96
11-01	Gp3	g.chr13:48982954C>T	Intron	RB1		retinoblastoma 1	15 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr13:49003114G>A	Intron	RB1		retinoblastoma 1	53 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr13:49009323G>A	Intron	RB1		retinoblastoma 1	41 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr13:49026878C>T	Intron	RB1		retinoblastoma 1	39 (0.00)	34 (0.26)	0.71
11-01	Gp3	g.chr13:49028641G>A	Intron	RB1		retinoblastoma 1	88 (0.00)	68 (0.16)	0.43
11-01	Gp3	g.chr8:53540715C>A	Missense Mutation	RB1CC1	p.D1505Y	RB1-inducible coiled-cc	16 (0.00)	14 (0.50)	1.67
11-01	Gp3	g.chr20:18470621G>A	Silent	RBBP9	p.R116R	retinoblastoma binding	24 (0.00)	26 (0.54)	1.44
11-01	Gp3	g.chr16:7568190G>T	Missense Mutation	RBFOX1	p.Q59H	RNA binding protein, fc	82 (0.00)	98 (0.14)	0.38
11-01	Gp3	g.chr7:127977191C>G	Missense Mutation	RBM28	p.A203P	RNA binding motif prot	24 (0.00)	11 (0.64)	1.70
11-01	Gp3	g.chr7:155567697G>T	Missense Mutation	RBM33	p.D1159Y	RNA binding motif prot	50 (0.00)	55 (0.18)	0.48
11-01	Gp3	g.chr4:155720400G>A	Silent	RBM46	p.P362P	RNA binding motif prot	52 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr12:7280952G>T	Missense Mutation	RBP5	p.Q46K	retinol binding protein 5	24 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr4:26422283C>A	Silent	RBPJ	p.L143L	recombination signal bi	29 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr1:173921211G>A	Silent	RC3H1	p.P812P	ring finger and CCCH-t	26 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr1:173939703C>A	Missense Mutation	RC3H1	p.R425I	ring finger and CCCH-t	39 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr9:125622331G>A	Silent	RC3H2	p.L572L	ring finger and CCCH-t	105 (0.01)	112 (0.28)	0.74
11-01	Gp3	g.chr9:125622370C>A	Missense Mutation	RC3H2	p.A559S	ring finger and CCCH-t	71 (0.00)	73 (0.15)	0.40
11-01	Gp3	g.chr13:49070381G>A	Silent	RCBTB2	p.I487I	regulator of chromosom	32 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr13:49070390C>A	Missense Mutation	RCBTB2	p.K484N	regulator of chromosom	29 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr11:63682198C>G	Missense Mutation	RCOR2	p.V137L	REST corepressor 2	98 (0.01)	67 (0.39)	1.03
11-01	Gp3	g.chr2:18736733C>A	Missense Mutation	RDH14	p.L245F	retinol dehydrogenase 1	75 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr7:103197536C>T	Missense Mutation	RELN	p.M1895I	reelin	24 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr7:103214648C>T	Missense Mutation	RELN	p.A1468T	reelin	69 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr4:57797423C>T	Missense Mutation	REST	p.P800L	RE1-silencing transcript	92 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr1:151315845G>C	Silent	RFX5	p.A277A	regulatory factor X, 5 (i	44 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr15:56387853G>A	Silent	RFX7	p.G594G	regulatory factor X, 7	155 (0.00)	86 (0.20)	0.53
11-01	Gp3	g.chr19:19308988G>A	Missense Mutation	RFXANK	p.D171N	regulatory factor X-asso	25 (0.00)	29 (0.34)	0.92

11-01	Gp3	g.chr13:42041015C>A	Missense Mutation	RGCC	p.P98T	regulator of cell cycle	80 (0.01)	91 (0.15)	0.41
11-01	Gp3	g.chr2:108476215C>T	Missense Mutation	RGPD4	p.H558Y	RANBP2-like and GRII	82 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr10:86014161C>A	Missense Mutation	RGR	p.L202I	retinal G protein couple	77 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:3318590C>T	Silent	RGS12	p.I231I	regulator of G-protein si	80 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr1:163042289G>T	Splice Site	RGS4	p.R50I	regulator of G-protein si	76 (0.00)	70 (0.20)	0.53
11-01	Gp3	g.chr1:163044236C>T	Silent	RGS4	p.F168F	regulator of G-protein si	101 (0.00)	91 (0.46)	1.23
11-01	Gp3	g.chr16:109806C>T	Missense Mutation	RHBDF1	p.A581T	rhomboid 5 homolog 1 (	27 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr16:110440G>T	Missense Mutation	RHBDF1	p.P552H	rhomboid 5 homolog 1 (	22 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr15:90020037G>T	Missense Mutation	RHCG	p.F420L	Rh family, C glycoprote	36 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr2:20647562C>A	Silent	RHOB	p.I112I	ras homolog family mer	15 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr14:63749897C>T	Missense Mutation	RHOJ	p.P154L	ras homolog family mer	73 (0.00)	57 (0.18)	0.47
11-01	Gp3	g.chr17:30538135C>A	Splice Site	RHOT1	p.F612L	ras homolog family mer	120 (0.00)	67 (0.34)	0.92
11-01	Gp3	g.chr1:228879131G>C	Missense Mutation	RHOU	p.E141Q	ras homolog family mer	99 (0.00)	93 (0.16)	0.43
11-01	Gp3	g.chr22:45818184G>C	Missense Mutation	RIBC2	p.E118Q	RIB43A domain with cc	115 (0.00)	67 (0.21)	0.56
11-01	Gp3	g.chr22:45818253G>C	Missense Mutation	RIBC2	p.V141L	RIB43A domain with cc	152 (0.00)	100 (0.16)	0.43
11-01	Gp3	g.chr12:130927013G>A	Missense Mutation	RIMBP2	p.T278I	RIMS binding protein 2	28 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr22:21742765G>T	Missense Mutation	RIMBP3B	p.V1540L	RIMS binding protein 3	64 (0.02)	26 (0.23)	0.62
11-01	Gp3	g.chr6:73023229G>A	Silent	RIMS1	p.Q1328Q	regulating synaptic men	34 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr7:105190920G>A	Silent	RINT1	p.T440T	RAD50 interactor 1	76 (0.00)	70 (0.14)	0.38
11-01	Gp3	g.chr6:3083435C>A	Nonsense Mutation	RIPK1	p.Y192*	receptor (TNFRSF)-inte	78 (0.01)	45 (0.18)	0.47
11-01	Gp3	g.chr14:24807744C>A	Missense Mutation	RIPK3	p.Q167H	receptor-interacting seri	30 (0.00)	10 (0.60)	1.60
11-01	Gp3	g.chr1:40703828C>A	Missense Mutation	RLF	p.H1152N	rearranged L-myc fusio	40 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr1:40705706C>T	Nonsense Mutation	RLF	p.Q1778*	rearranged L-myc fusio	19 (0.00)	44 (0.48)	1.27
11-01	Gp3	g.chr15:41029891C>G	Missense Mutation	RMDN3	p.A387P	regulator of microtubule	29 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr14:21052184G>T	Missense Mutation	RNASE11	p.S150R	ribonuclease, RNase A	59 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr14:21250221G>A	Silent	RNASE6	p.Q121Q	ribonuclease, RNase A	78 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr3:49740131G>T	Silent	RNF123	p.L565L	ring finger protein 123	151 (0.00)	131 (0.18)	0.49
11-01	Gp3	g.chr5:179393906G>C	Missense Mutation	RNF130	p.N350K	ring finger protein 130	65 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr6:127608673G>A	Silent	RNF146	p.Q304Q	ring finger protein 146	85 (0.00)	20 (0.30)	0.47
11-01	Gp3	g.chr11:74546969C>A	Silent	RNF169	p.R441R	ring finger protein 169	25 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr13:25352485G>A	Missense Mutation	RNF17	p.G124S	ring finger protein 17	40 (0.00)	64 (0.27)	0.71
11-01	Gp3	g.chr8:101300201C>T	Missense Mutation	RNF19A	p.G68S	ring finger protein 19A,	97 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr17:78318709G>C	Missense Mutation	RNF213	p.G2241R	ring finger protein 213	42 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr17:78319754C>A	Nonsense Mutation	RNF213	p.S2589*	ring finger protein 213	18 (0.00)	13 (0.69)	1.85
11-01	Gp3	g.chr17:78321522G>A	Silent	RNF213	p.V3178V	ring finger protein 213	44 (0.00)	31 (0.19)	0.52

11-01	Gp3	g.chr17:78321687G>A	Silent	RNF213	p.Q3233Q	ring finger protein 213	34 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr17:78343330C>A	Silent	RNF213	p.R4111R	ring finger protein 213	50 (0.00)	43 (0.30)	0.81
11-01	Gp3	g.chr17:78360091G>C	Missense Mutation	RNF213	p.D4910H	ring finger protein 213	103 (0.00)	59 (0.32)	0.86
11-01	Gp3	g.chr7:5780768G>C	Missense Mutation	RNF216	p.H294D	ring finger protein 216	22 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr7:5781384C>T	Silent	RNF216	p.L88L	ring finger protein 216	109 (0.00)	72 (0.24)	0.63
11-01	Gp3	g.chr12:121858429C>A	Nonsense Mutation	RNF34	p.S259*	ring finger protein 34, E	53 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr17:56438228G>C	Silent	RNF43	p.A255A	ring finger protein 43	19 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr11:498017G>C	Missense Mutation	RNH1	p.L361V	ribonuclease/angiogenin	21 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr3:78685113C>G	Silent	ROBO1	p.G1061G	roundabout, axon guidar	137 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr1:151801912G>T	Silent	RORC	p.T21T	RAR-related orphan rec	21 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr8:55534130G>A	Missense Mutation	RP1	p.D202N	retinitis pigmentosa 1 (a	29 (0.00)	38 (0.29)	0.97
11-01	Gp3	g.chr8:55539440G>T	Missense Mutation	RP1	p.G1000C	retinitis pigmentosa 1 (a	117 (0.01)	93 (0.16)	0.54
11-01	Gp3	g.chr8:55541789G>A	Missense Mutation	RP1	p.V1783I	retinitis pigmentosa 1 (a	41 (0.00)	39 (0.18)	0.60
11-01	Gp3	g.chr6:85140387G>A	lincRNA	RP1-90L14.1			62 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr6:85140425C>T	lincRNA	RP1-90L14.1			49 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr15:72905283C>A	lincRNA	RP11-1006G14.2			20 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr12:57689283G>A	Nonsense Mutation	RP11-123K3.4	p.Q28*		127 (0.00)	111 (0.26)	0.70
11-01	Gp3	g.chr17:45128035G>A	RNA	RP11-156P1.3			91 (0.00)	41 (0.24)	0.65
11-01	Gp3	g.chr19:23445102G>T	RNA	RP11-15H20.6			68 (0.00)	35 (0.31)	0.84
11-01	Gp3	g.chr3:149768893G>A	RNA	RP11-167H9.4			27 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr13:47033250C>T	lincRNA	RP11-189B4.6			89 (0.00)	34 (0.53)	1.41
11-01	Gp3	g.chr7:128109067G>A	RNA	RP11-212P7.3			76 (0.00)	30 (0.43)	1.16
11-01	Gp3	g.chr3:101713471G>A	lincRNA	RP11-221J22.1			38 (0.00)	31 (0.35)	0.95
11-01	Gp3	g.chr3:70300929G>C	RNA	RP11-231I13.2			58 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chrX:115828035G>A	lincRNA	RP11-232D9.3			24 (0.00)	19 (0.42)	0.70
11-01	Gp3	g.chr15:76072686A>G	RNA	RP11-24M17.5			25 (0.00)	21 (0.62)	1.65
11-01	Gp3	g.chr15:76073158G>T	RNA	RP11-24M17.5			38 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr15:76074731G>A	RNA	RP11-24M17.5			99 (0.00)	64 (0.17)	0.46
11-01	Gp3	g.chr16:74382979C>T	RNA	RP11-252A24.2			74 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr7:128220161C>A	RNA	RP11-274B21.1			24 (0.00)	15 (0.60)	1.60
11-01	Gp3	g.chr13:24860997G>T	Missense Mutation	RP11-307N16.	p.C737F		50 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr13:24871578C>T	Silent	RP11-307N16.	p.S974S		59 (0.02)	24 (0.21)	0.56
11-01	Gp3	g.chr9:105966994C>G	lincRNA	RP11-341A22.2			43 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr10:28725848G>A	lincRNA	RP11-351M16.3			86 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr16:22574786T>A	RNA	RP11-368J21.3			64 (0.00)	31 (0.42)	1.12

11-01	Gp3	g.chr9:84547797C>A	lincRNA	RP11-383M4.6			22 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr12:20095272G>A	lincRNA	RP11-405A12.2			32 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr1:83920447C>G	lincRNA	RP11-413G15.1			108 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr2:96191452G>A	lincRNA	RP11-440D17.3			16 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr14:24518610G>A	RNA	RP11-468E2.9			16 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr10:52388587G>A	RNA	RP11-50E11.3			48 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr17:60374210G>T	RNA	RP11-51L5.5			21 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr17:42000158G>T	RNA	RP11-527L4.5			213 (0.00)	90 (0.17)	0.44
11-01	Gp3	g.chr17:42000167G>T	RNA	RP11-527L4.5			216 (0.00)	92 (0.15)	0.41
11-01	Gp3	g.chr12:31265976C>A	RNA	RP11-551L14.1			47 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr6:75115397C>T	lincRNA	RP11-554D15.1			17 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr1:162351759C>A	Missense Mutation	RP11-565P22.	p.S132Y		24 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr4:159199306G>A	RNA	RP11-597D13.7			21 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr5:89538131G>C	RNA	RP11-61G23.1			16 (0.00)	21 (0.38)	1.02
11-01	Gp3	g.chr12:104309589G>A	RNA	RP11-642P15.1			81 (0.00)	45 (0.42)	1.13
11-01	Gp3	g.chr12:104309661G>A	RNA	RP11-642P15.1			71 (0.01)	43 (0.49)	1.30
11-01	Gp3	g.chr12:90313412G>T	lincRNA	RP11-654D12.2			52 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr11:82516608G>T	lincRNA	RP11-718B12.2			37 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr11:82517018G>C	lincRNA	RP11-718B12.2			52 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr3:128634309G>T	Missense Mutation	RP11-723O4.6	p.S473Y		55 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr4:171278500A>G	lincRNA	RP11-789C1.2			18 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr17:43627078C>T	lincRNA	RP11-798G7.6			302 (0.00)	114 (0.18)	0.49
11-01	Gp3	g.chr14:21388065C>A	lincRNA	RP11-84C10.3			96 (0.00)	79 (0.27)	0.71
11-01	Gp3	g.chr10:27535744G>A	lincRNA	RP11-85G18.6			52 (0.00)	80 (0.19)	0.50
11-01	Gp3	g.chr10:27539647C>A	lincRNA	RP11-85G18.6			122 (0.00)	47 (0.23)	0.62
11-01	Gp3	g.chr1:19213006C>G	Splice Site	RP13-279N23.2			21 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr1:87104673C>T	RNA	RP4-651E10.4			24 (0.00)	22 (0.45)	1.21
11-01	Gp3	g.chr20:21142502G>T	RNA	RP4-777D9.2			48 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr20:21142632G>T	RNA	RP4-777D9.2			50 (0.00)	75 (0.16)	0.43
11-01	Gp3	g.chr20:22381239C>G	lincRNA	RP5-1004I9.1			33 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr16:72762501C>T	RNA	RP5-991G20.1			21 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr14:47120455C>T	Missense Mutation	RPL10L	p.R162H	ribosomal protein L10-l	78 (0.00)	77 (0.18)	0.48
11-01	Gp3	g.chr17:41150800G>T	Silent	RPL27	p.V11V	ribosomal protein L27	55 (0.00)	60 (0.15)	0.40
11-01	Gp3	g.chr15:71089232G>A	RNA	RPL29P30		ribosomal protein L29 p	47 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr3:197678079C>A	Missense Mutation	RPL35A	p.Q21K	ribosomal protein L35a	50 (0.00)	41 (0.17)	0.46

11-01	Gp3	g.chr3:197678083G>A	Missense Mutation	RPL35A	p.R22K	ribosomal protein L35a	52 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr3:134070786G>A	RNA	RPL39P5		ribosomal protein L39 p	27 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr6:4996615T>A	Missense Mutation	RPP40	p.Y177F	ribonuclease P/MRP 40	62 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr20:36718262G>C	Silent	RPRD1B	p.L322L	regulation of nuclear pr	114 (0.00)	110 (0.15)	0.41
11-01	Gp3	g.chr1:150443068G>T	Silent	RPRD2	p.G548G	regulation of nuclear pr	71 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr1:150443342G>C	Missense Mutation	RPRD2	p.A640P	regulation of nuclear pr	55 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr1:150444380G>A	Missense Mutation	RPRD2	p.G986S	regulation of nuclear pr	191 (0.00)	110 (0.23)	0.61
11-01	Gp3	g.chr1:150444520G>A	Silent	RPRD2	p.K1032K	regulation of nuclear pr	138 (0.00)	134 (0.29)	0.78
11-01	Gp3	g.chr14:91444717C>A	Missense Mutation	RPS6KA5	p.R109S	ribosomal protein S6 ki	103 (0.00)	107 (0.18)	0.47
11-01	Gp3	g.chr1:152127922G>C	Missense Mutation	RPTN	p.D551E	repetin	191 (0.00)	133 (0.14)	0.38
11-01	Gp3	g.chr1:152129238A>T	Missense Mutation	RPTN	p.F113I	repetin	142 (0.01)	74 (0.20)	0.54
11-01	Gp3	g.chr1:152129243C>T	Missense Mutation	RPTN	p.C111Y	repetin	139 (0.01)	73 (0.21)	0.55
11-01	Gp3	g.chr17:78857678G>T	Missense Mutation	RPTOR	p.R583M	regulatory associated pr	18 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr1:39311722C>T	Missense Mutation	RRAGC	p.E313K	Ras-related GTP bindin	43 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr11:4142932C>T	Silent	RRM1	p.A325A	ribonucleotide reductas	56 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr2:10267028C>A	Missense Mutation	RRM2	p.T199K	ribonucleotide reductas	44 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr10:99160176C>A	Silent	RRP12	p.L85L	ribosomal RNA process	37 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr8:109001311G>A	Nonsense Mutation	RSPO2	p.R86*	R-spondin 2	27 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr10:16806412C>A	Missense Mutation	RSU1	p.Q86H	Ras suppressor protein	93 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr3:187416420C>G	Missense Mutation	RTP2	p.E182Q	receptor (chemosensory	56 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr18:67697314C>A	Missense Mutation	RTTN	p.M1893I	rotatin	45 (0.00)	57 (0.44)	1.17
11-01	Gp3	g.chr18:67733080G>A	Nonsense Mutation	RTTN	p.Q1578*	rotatin	48 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr18:67741222C>A	Missense Mutation	RTTN	p.D1525Y	rotatin	30 (0.00)	34 (0.41)	1.10
11-01	Gp3	g.chr10:70136620C>G	Missense Mutation	RUFY2	p.E439Q	RUN and FYVE domai	30 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr4:71588327C>T	Missense Mutation	RUFY3	p.P13S	RUN and FYVE domai	96 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr8:93027024G>A	Missense Mutation	RUNX1T1	p.P84L	runt-related transcriptio	17 (0.00)	25 (0.24)	0.80
11-01	Gp3	g.chr9:35560097G>T	Nonsense Mutation	RUSC2	p.E1154*	RUN and SH3 domain c	104 (0.01)	97 (0.29)	0.77
11-01	Gp3	g.chr3:127816246G>T	Missense Mutation	RUVBL1	p.H245N	RuvB-like AAA ATPas	15 (0.00)	10 (0.90)	2.40
11-01	Gp3	g.chr3:72431459G>A	Intron	RYBP		RING1 and YY1 bindin	56 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr3:72433016C>T	Intron	RYBP		RING1 and YY1 bindin	41 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr3:72435351C>G	Intron	RYBP		RING1 and YY1 bindin	46 (0.00)	53 (0.15)	0.40
11-01	Gp3	g.chr3:72448187G>T	Intron	RYBP		RING1 and YY1 bindin	54 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr3:72452244C>T	Intron	RYBP		RING1 and YY1 bindin	74 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr3:72489335C>G	Intron	RYBP		RING1 and YY1 bindin	59 (0.00)	32 (0.44)	1.17
11-01	Gp3	g.chr19:39013898G>T	Missense Mutation	RYR1	p.E3463D	ryanodine receptor 1 (sk	28 (0.00)	44 (0.50)	1.33

11-01	Gp3	g.chr19:39051877G>T	Missense Mutation	RYR1	p.R4136L	ryanodine receptor 1 (sk	25 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr1:237789064G>A	Silent	RYR2	p.K2042K	ryanodine receptor 2 (ca	34 (0.00)	21 (0.52)	0.99
11-01	Gp3	g.chr1:237813372G>A	Missense Mutation	RYR2	p.E2570K	ryanodine receptor 2 (ca	113 (0.00)	42 (0.24)	0.45
11-01	Gp3	g.chr15:33840353G>A	Missense Mutation	RYR3	p.G255R	ryanodine receptor 3	23 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr15:34032126G>A	Missense Mutation	RYR3	p.A2584T	ryanodine receptor 3	92 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr15:34077877G>C	Missense Mutation	RYR3	p.D3095H	ryanodine receptor 3	40 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr4:6698677G>A	Missense Mutation	S100P	p.D66N	S100 calcium binding p	144 (0.00)	61 (0.31)	0.83
11-01	Gp3	g.chr1:101704878C>G	Missense Mutation	S1PR1	p.T113S	sphingosine-1-phosphat	47 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr13:23905396C>T	Missense Mutation	SACS	p.V4207I	sacsin molecular chaper	41 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr19:47653627G>A	Missense Mutation	SAE1	p.D127N	SUMO1 activating enzy	23 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr16:51173422G>T	Nonsense Mutation	SALL1	p.S904*	spalt-like transcription f	22 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr14:77843865C>A	Missense Mutation	SAMD15	p.A35D	sterile alpha motif doma	27 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr22:44379873G>T	Missense Mutation	SAMM50	p.Q356H	SAMM50 sorting and as	67 (0.00)	88 (0.38)	1.00
11-01	Gp3	g.chr17:26715552G>A	Silent	SARM1	p.V605V	sterile alpha and TIR m	82 (0.00)	61 (0.57)	1.53
11-01	Gp3	g.chr3:18436271G>A	Missense Mutation	SATB1	p.R297W	SATB homeobox 1	67 (0.00)	45 (0.36)	0.95
11-01	Gp3	g.chr14:51101994C>T	Missense Mutation	SAV1	p.M353I	salvador family WW do	79 (0.00)	63 (0.22)	0.59
11-01	Gp3	g.chr6:39073255C>A	Nonsense Mutation	SAYSD1	p.E169*	SAYSVFN motif domai	64 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr11:9990036G>T	Silent	SBF2	p.S484S	SET binding factor 2	51 (0.02)	29 (0.21)	0.55
11-01	Gp3	g.chr12:123829964G>C	Missense Mutation	SBNO1	p.R131G	strawberry notch homol	55 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr8:73993441C>A	Silent	SBSPON	p.P74P	somatomedin B and thr	53 (0.00)	45 (0.13)	0.44
11-01	Gp3	g.chr11:121174176C>A	Missense Mutation	SC5D	p.A31D	sterol-C5-desaturase	82 (0.00)	47 (0.17)	0.45
11-01	Gp3	g.chr21:33068904G>C	Missense Mutation	SCAF4	p.P313A	SR-related CTD-associa	15 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr6:155154360G>A	Missense Mutation	SCAF8	p.G1216D	SR-related CTD-associa	28 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr15:76673884C>A	Silent	SCAPER	p.L1180L	S-phase cyclin A-associ	42 (0.00)	24 (0.25)	0.67
11-01	Gp3	g.chr10:102107961C>G	Missense Mutation	SCD	p.D56E	stearoyl-CoA desaturase	95 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr3:38888612G>A	Missense Mutation	SCN11A	p.A1650V	sodium channel, voltage	67 (0.00)	33 (0.27)	0.73
11-01	Gp3	g.chr2:166848742C>A	Missense Mutation	SCN1A	p.M1653I	sodium channel, voltage	66 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr2:166894463G>T	Silent	SCN1A	p.I895I	sodium channel, voltage	125 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr2:166172242G>A	Missense Mutation	SCN2A	p.E549K	sodium channel, voltage	71 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr2:165984240G>C	Missense Mutation	SCN3A	p.S1098R	sodium channel, voltage	27 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr17:62020336G>C	Missense Mutation	SCN4A	p.L1380V	sodium channel, voltage	57 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr3:38601881G>A	Silent	SCN5A	p.I1333I	sodium channel, voltage	29 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr2:167304195C>A	Missense Mutation	SCN7A	p.M438I	sodium channel, voltage	102 (0.00)	42 (0.31)	0.83
11-01	Gp3	g.chr12:52156446C>T	Nonsense Mutation	SCN8A	p.R844*	sodium channel, voltage	36 (0.00)	47 (0.15)	0.40
11-01	Gp3	g.chr12:52162891C>T	Silent	SCN8A	p.H1048H	sodium channel, voltage	55 (0.00)	49 (0.47)	1.25

11-01	Gp3	g.chr2:167108293C>A	Nonsense Mutation	SCN9A	p.E1141*	sodium channel, voltage	127 (0.01)	51 (0.33)	0.89
11-01	Gp3	g.chr16:23364346C>A	Missense Mutation	SCNN1B	p.A179E	sodium channel, non-vo	45 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr16:23366642G>A	Missense Mutation	SCNN1B	p.C203Y	sodium channel, non-vo	20 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr16:23223396A>G	Silent	SCNN1G	p.K406K	sodium channel, non-vo	39 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr17:10590153G>A	Missense Mutation	SCO1	p.S221F	SCO1 cytochrome c oxi	81 (0.00)	75 (0.33)	0.89
11-01	Gp3	g.chr7:29980416G>A	Silent	SCRN1	p.Y207Y	secernin 1	37 (0.03)	33 (0.18)	0.48
11-01	Gp3	g.chr17:45916900A>T	Missense Mutation	SCRN2	p.S156T	secernin 2	76 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr6:35205680G>T	Splice Site	SCUBE3	p.E238D	signal peptide, CUB do	59 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr6:35208959G>T	Missense Mutation	SCUBE3	p.G371C	signal peptide, CUB do	260 (0.00)	248 (0.18)	0.48
11-01	Gp3	g.chr6:35214033G>T	Missense Mutation	SCUBE3	p.A935S	signal peptide, CUB do	109 (0.00)	88 (0.24)	0.64
11-01	Gp3	g.chr12:100717403C>G	Missense Mutation	SCYL2	p.T499R	SCY1-like 2 (S. cerevisi	17 (0.00)	49 (0.14)	0.49
11-01	Gp3	g.chr1:169824012G>T	Missense Mutation	SCYL3	p.S523Y	SCY1-like 3 (S. cerevisi	22 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr1:161310383G>A	Splice Site	SDHC		succinate dehydrogenas	38 (0.00)	28 (0.50)	1.33
11-01	Gp3	g.chr16:5046970C>T	Missense Mutation	SEC14L5	p.L299F	SEC14-like 5 (S. cerevis	16 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr9:139357927G>A	Silent	SEC16A	p.C1367C	SEC16 homolog A (S. c	38 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr9:139372015G>T	Missense Mutation	SEC16A	p.A18D	SEC16 homolog A (S. c	23 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr1:177899766C>A	Nonsense Mutation	SEC16B	p.E1009*	SEC16 homolog B (S. c	23 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr10:121663649G>A	Missense Mutation	SEC23IP	p.V321I	SEC23 interacting prote	90 (0.00)	50 (0.40)	1.07
11-01	Gp3	g.chr10:121689133C>A	Nonsense Mutation	SEC23IP	p.Y776*	SEC23 interacting prote	23 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr5:134002579G>A	Missense Mutation	SEC24A	p.G211E	SEC24 family member	48 (0.02)	40 (0.20)	0.53
11-01	Gp3	g.chr4:119718894C>G	Missense Mutation	SEC24D	p.A329P	SEC24 family member	133 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr4:83748542G>C	Missense Mutation	SEC31A	p.P1091A	SEC31 homolog A (S. c	58 (0.00)	56 (0.20)	0.52
11-01	Gp3	g.chr10:12204250G>A	Silent	SEC61A2	p.R402R	Sec61 alpha 2 subunit	93 (0.00)	72 (0.35)	0.93
11-01	Gp3	g.chr4:25849096C>T	Missense Mutation	SEL1L3	p.D185N	sel-1 suppressor of lin-1	21 (0.00)	13 (0.62)	1.64
11-01	Gp3	g.chr1:151339276G>A	Missense Mutation	SELENBP1	p.H196Y	selenium binding protei	52 (0.00)	39 (0.38)	1.03
11-01	Gp3	g.chr12:109017984G>T	Missense Mutation	SELPLG	p.P50T	selectin P ligand	35 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr7:83610695C>T	Missense Mutation	SEMA3A	p.D532N	sema domain, immunog	17 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr7:84636138C>G	Missense Mutation	SEMA3D	p.G630R	sema domain, immunog	57 (0.00)	48 (0.31)	0.83
11-01	Gp3	g.chr3:52472946G>A	Missense Mutation	SEMA3G	p.S500F	sema domain, immunog	98 (0.01)	117 (0.23)	0.62
11-01	Gp3	g.chr1:156142714C>T	Missense Mutation	SEMA4A	p.S411F	sema domain, immunog	56 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr2:74902715C>G	Missense Mutation	SEMA4F	p.A479G	sema domain, immunog	67 (0.01)	52 (0.27)	0.41
11-01	Gp3	g.chr3:185324164C>T	Missense Mutation	SENP2	p.R166C	SUMO1/sentrin/SMT3	105 (0.00)	70 (0.19)	0.50
11-01	Gp3	g.chr3:185327061G>T	Missense Mutation	SENP2	p.K215N	SUMO1/sentrin/SMT3	18 (0.00)	15 (0.53)	1.42
11-01	Gp3	g.chr15:72432326A>G	Missense Mutation	SENP8	p.H121R	SUMO/sentrin specific	61 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr5:132097188C>A	Missense Mutation	SEPT8	p.M306I	septin 8	44 (0.00)	31 (0.19)	0.52

11-01	Gp3	g.chr22:42969989C>T	Silent	SERHL2	p.S291S	serine hydrolase-like 2	113 (0.00)	127 (0.25)	0.67
11-01	Gp3	g.chr6:122768351G>A	Missense Mutation	SERINC1	p.P304S	serine incorporator 1	57 (0.00)	23 (0.43)	0.67
11-01	Gp3	g.chr20:43129879A>G	Missense Mutation	SERINC3	p.I373T	serine incorporator 3	70 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr14:94780864G>A	Missense Mutation	SERPINA6	p.S41L	serpin peptidase inhibito	104 (0.00)	59 (0.19)	0.50
11-01	Gp3	g.chr6:2838164C>T	Missense Mutation	SERPINB1	p.E126K	serpin peptidase inhibito	74 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr6:2892071C>T	Missense Mutation	SERPINB9	p.S240N	serpin peptidase inhibito	45 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr17:1657640G>A	Missense Mutation	SERPINF2	p.V430M	serpin peptidase inhibito	20 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr18:42281770G>A	Silent	SETBP1	p.E153E	SET binding protein 1	84 (0.00)	97 (0.42)	1.13
11-01	Gp3	g.chr18:42530116G>A	Missense Mutation	SETBP1	p.G271R	SET binding protein 1	16 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr4:140441505G>A	Missense Mutation	SETD7	p.L230F	SET domain containing	44 (0.00)	62 (0.15)	0.39
11-01	Gp3	g.chr9:135145074C>A	Missense Mutation	SETX	p.L2405F	senataxin	60 (0.00)	36 (0.61)	1.63
11-01	Gp3	g.chr22:26747101C>A	Missense Mutation	SEZ6L	p.Q831K	seizure related 6 homolo	36 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr22:26747102A>T	Missense Mutation	SEZ6L	p.Q831L	seizure related 6 homolo	36 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr11:64536718C>A	Silent	SF1	p.G226G	splicing factor 1	82 (0.00)	29 (0.45)	1.20
11-01	Gp3	g.chr11:64536741G>A	Missense Mutation	SF1	p.R219W	splicing factor 1	74 (0.00)	25 (0.48)	1.28
11-01	Gp3	g.chr11:65828175G>A	Silent	SF3B2	p.L567L	splicing factor 3b, subun	57 (0.00)	76 (0.32)	0.84
11-01	Gp3	g.chr16:70601377G>A	Missense Mutation	SF3B3	p.G964R	splicing factor 3b, subun	64 (0.00)	55 (0.25)	0.68
11-01	Gp3	g.chr10:81373703G>T	Missense Mutation	SFTPA1	p.S209I	surfactant protein A1	95 (0.00)	86 (0.29)	0.78
11-01	Gp3	g.chr10:81317314G>A	Missense Mutation	SFTPA2	p.T133I	surfactant protein A2	75 (0.01)	53 (0.83)	2.21
11-01	Gp3	g.chr10:81701235C>T	Missense Mutation	SFTPD	p.G196S	surfactant protein D	59 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr5:174940487C>A	Silent	SFXN1	p.P206P	sideroflexin 1	24 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr1:67137668G>A	Missense Mutation	SGIP1	p.E184K	SH3-domain GRB2-like	15 (0.00)	18 (0.72)	1.93
11-01	Gp3	g.chr1:67139016C>T	Silent	SGIP1	p.L205L	SH3-domain GRB2-like	211 (0.00)	154 (0.15)	0.40
11-01	Gp3	g.chr1:67147987C>T	Missense Mutation	SGIP1	p.P417L	SH3-domain GRB2-like	113 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr6:134491566G>A	Missense Mutation	SGK1	p.P379L	serum/glucocorticoid re	26 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr8:8233893C>G	Missense Mutation	SGK223	p.D676H		58 (0.00)	44 (0.32)	0.47
11-01	Gp3	g.chr2:201436492C>T	Missense Mutation	SGOL2	p.L475F	shugoshin-like 2 (S. pon	162 (0.00)	174 (0.24)	0.63
11-01	Gp3	g.chr14:64153166C>T	Missense Mutation	SGPP1	p.G328E	sphingosine-1-phosphat	47 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr5:171785849C>T	Missense Mutation	SH3PXD2B	p.G199S	SH3 and PX domains 2	25 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr5:148418000G>A	Silent	SH3TC2	p.L280L	SH3 domain and tetratri	122 (0.01)	68 (0.24)	0.63
11-01	Gp3	g.chr9:91652989G>T	Silent	SHC3	p.T525T	SHC (Src homology 2 d	28 (0.00)	28 (0.64)	1.71
11-01	Gp3	g.chr7:155604814C>A	Start Codon SNP	SHH	p.M1I	sonic hedgehog	44 (0.00)	36 (0.28)	0.74
11-01	Gp3	g.chr19:41084066C>A	Silent	SHKBP1	p.V89V	SH3KBP1 binding prote	104 (0.00)	30 (0.53)	1.42
11-01	Gp3	g.chr19:41086809G>A	Missense Mutation	SHKBP1	p.A271T	SH3KBP1 binding prote	16 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr17:18232191C>G	Missense Mutation	SHMT1	p.R442T	serine hydroxymethyltra	43 (0.00)	45 (0.16)	0.41

11-01	Gp3	g.chr3:72810776C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	58 (0.00)	44 (0.34)	0.91
11-01	Gp3	g.chr3:72811090A>G	Intron	SHQ1		SHQ1, H/ACA ribonucl	23 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chr3:72817109C>G	Intron	SHQ1		SHQ1, H/ACA ribonucl	71 (0.00)	52 (0.42)	1.13
11-01	Gp3	g.chr3:72818847C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	49 (0.00)	34 (0.53)	1.41
11-01	Gp3	g.chr3:72828443G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	115 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr3:72832249C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	130 (0.00)	81 (0.22)	0.59
11-01	Gp3	g.chr3:72832695C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	38 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr3:72850305C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	38 (0.00)	21 (0.38)	1.02
11-01	Gp3	g.chr3:72857648C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	64 (0.00)	50 (0.18)	0.48
11-01	Gp3	g.chr3:72858723C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	39 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr3:72859283G>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	74 (0.00)	35 (0.26)	0.69
11-01	Gp3	g.chr3:72860361C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	103 (0.00)	46 (0.24)	0.64
11-01	Gp3	g.chr3:72866034C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	83 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr3:72871776G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	55 (0.00)	54 (0.19)	0.49
11-01	Gp3	g.chr3:72874293C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	46 (0.02)	48 (0.25)	0.67
11-01	Gp3	g.chr3:72878247G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	53 (0.02)	50 (0.22)	0.59
11-01	Gp3	g.chr3:72878543G>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	67 (0.00)	86 (0.20)	0.53
11-01	Gp3	g.chr3:72887174G>C	Intron	SHQ1		SHQ1, H/ACA ribonucl	61 (0.00)	68 (0.26)	0.71
11-01	Gp3	g.chr4:77660203G>A	Missense Mutation	SHROOM3	p.G293S	shroom family member	16 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr3:164709985G>T	Silent	SI	p.R1655R	sucrase-isomaltase (alph	44 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr21:38115852C>A	Missense Mutation	SIM2	p.P388Q	single-minded family bH	35 (0.00)	30 (0.63)	1.69
11-01	Gp3	g.chr15:75705350C>A	Missense Mutation	SIN3A	p.Q170H	SIN3 transcription regul	38 (0.03)	36 (0.28)	0.74
11-01	Gp3	g.chr14:72128132G>A	Missense Mutation	SIPA1L1	p.V735I	signal-induced prolifera	32 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr14:72190434C>T	Missense Mutation	SIPA1L1	p.L1427F	signal-induced prolifera	52 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr14:72190523G>A	Silent	SIPA1L1	p.Q1456Q	signal-induced prolifera	68 (0.00)	79 (0.49)	1.32
11-01	Gp3	g.chr14:72202073G>T	Missense Mutation	SIPA1L1	p.E1696D	signal-induced prolifera	119 (0.00)	56 (0.27)	0.71
11-01	Gp3	g.chr20:1629808C>T	Missense Mutation	SIRPG	p.S107N	signal-regulatory protei	63 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr19:39384478G>A	Silent	SIRT2	p.A31A	sirtuin 2	21 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr1:160465980G>T	Silent	SLAMF6	p.R85R	SLAM family member (	57 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr16:56926026G>A	Silent	SLC12A3	p.G800G	solute carrier family 12	46 (0.00)	48 (0.23)	0.61
11-01	Gp3	g.chr20:44663639G>T	Missense Mutation	SLC12A5	p.E35D	solute carrier family 12	30 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr15:34551102C>T	Missense Mutation	SLC12A6	p.R152H	solute carrier family 12	15 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr17:26822771C>T	Silent	SLC13A2	p.T469T	solute carrier family 13	84 (0.00)	57 (0.21)	0.56
11-01	Gp3	g.chr13:99368170G>T	Missense Mutation	SLC15A1	p.Q229K	solute carrier family 15	61 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chrX:73744551C>T	Silent	SLC16A2	p.F311F	solute carrier family 16,	26 (0.00)	24 (0.46)	0.76

11-01	Gp3	g.chr17:62950350G>A	RNA	SLC16A6P1		SLC16A6 pseudogene 1	41 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr19:49934036C>A	Missense Mutation	SLC17A7	p.A475S	solute carrier family 17	33 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr12:100813706G>A	Silent	SLC17A8	p.E513E	solute carrier family 17	45 (0.00)	37 (0.24)	0.83
11-01	Gp3	g.chr10:119003695C>A	Missense Mutation	SLC18A2	p.A112D	solute carrier family 18	70 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr1:169437466G>T	Missense Mutation	SLC19A2	p.S416R	solute carrier family 19	38 (0.00)	39 (0.26)	0.68
11-01	Gp3	g.chr11:35339051C>T	Start Codon SNP	SLC1A2	p.M1I	solute carrier family 1 (	84 (0.00)	38 (0.29)	0.77
11-01	Gp3	g.chr11:2937971G>A	Splice Site	SLC22A18		solute carrier family 22,	19 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr6:160664675C>T	Missense Mutation	SLC22A2	p.R403H	solute carrier family 22	27 (0.00)	23 (0.35)	0.93
11-01	Gp3	g.chr5:131670540G>T	Missense Mutation	SLC22A4	p.L392F	solute carrier family 22	138 (0.00)	67 (0.31)	0.84
11-01	Gp3	g.chr20:4913102G>A	Splice Site	SLC23A2	p.P36L	solute carrier family 23	24 (0.04)	25 (0.32)	0.85
11-01	Gp3	g.chr15:65916816C>A	Missense Mutation	SLC24A1	p.T133K	solute carrier family 24	73 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr15:65918221G>A	Silent	SLC24A1	p.K601K	solute carrier family 24	129 (0.00)	72 (0.19)	0.52
11-01	Gp3	g.chr2:172648079G>A	Silent	SLC25A12	p.L489L	solute carrier family 25	57 (0.02)	47 (0.15)	0.40
11-01	Gp3	g.chr7:95818905T>C	Missense Mutation	SLC25A13	p.Y279C	solute carrier family 25	86 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr22:18066185G>T	Missense Mutation	SLC25A18	p.M98I	solute carrier family 25	44 (0.00)	51 (0.33)	0.89
11-01	Gp3	g.chr22:18066190G>T	Missense Mutation	SLC25A18	p.R100L	solute carrier family 25	44 (0.00)	51 (0.33)	0.89
11-01	Gp3	g.chr12:98993839C>G	Missense Mutation	SLC25A3	p.P251A	solute carrier family 25	33 (0.00)	30 (0.23)	0.79
11-01	Gp3	g.chr12:98995188C>A	Missense Mutation	SLC25A3	p.T324N	solute carrier family 25	28 (0.00)	15 (0.47)	1.59
11-01	Gp3	g.chr3:39431045C>A	Silent	SLC25A38	p.L43L	solute carrier family 25,	32 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr19:6432215C>A	Splice Site	SLC25A41	p.V70L	solute carrier family 25,	19 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr7:103018201C>A	Missense Mutation	SLC26A5	p.D611Y	solute carrier family 26	30 (0.00)	23 (0.70)	1.86
11-01	Gp3	g.chr7:103061885G>A	Missense Mutation	SLC26A5	p.P26L	solute carrier family 26	38 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr3:48667359C>T	Missense Mutation	SLC26A6	p.G456D	solute carrier family 26	43 (0.00)	60 (0.18)	0.49
11-01	Gp3	g.chr8:92330496C>T	Missense Mutation	SLC26A7	p.P177L	solute carrier family 26	27 (0.00)	33 (0.18)	0.61
11-01	Gp3	g.chr8:92352780G>C	Splice Site	SLC26A7		solute carrier family 26	32 (0.00)	24 (0.29)	0.97
11-01	Gp3	g.chr6:35919238G>A	Silent	SLC26A8	p.L757L	solute carrier family 26	34 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr1:153752394C>T	Silent	SLC27A3	p.Y784Y	solute carrier family 27	16 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr12:7973921C>G	Splice Site	SLC2A14	p.V289L	solute carrier family 2 (	48 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr9:136343416G>A	Missense Mutation	SLC2A6	p.P72L	solute carrier family 2 (	25 (0.00)	34 (0.26)	0.71
11-01	Gp3	g.chr9:116021143G>A	Splice Site	SLC31A1		solute carrier family 31	52 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr4:25665858C>A	Missense Mutation	SLC34A2	p.F95L	solute carrier family 34	124 (0.00)	70 (0.27)	0.72
11-01	Gp3	g.chr1:100476969C>T	Nonsense Mutation	SLC35A3	p.Q172*	solute carrier family 35	25 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr3:112299708C>G	Missense Mutation	SLC35A5	p.I248M	solute carrier family 35,	39 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr7:133994231C>A	Splice Site	SLC35B4	p.R26R	solute carrier family 35	29 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr3:136573697C>G	Missense Mutation	SLC35G2	p.P132R	solute carrier family 35,	52 (0.00)	14 (0.43)	1.14

11-01	Gp3	g.chr7:140035248G>A	Silent	SLC37A3	p.L483L	solute carrier family 37,	102 (0.00)	75 (0.15)	0.39
11-01	Gp3	g.chr12:46622995C>G	Missense Mutation	SLC38A1	p.M85I	solute carrier family 38,	50 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr12:46764380C>A	Missense Mutation	SLC38A2	p.V77L	solute carrier family 38,	112 (0.00)	120 (0.17)	0.44
11-01	Gp3	g.chr3:50256437G>A	RNA	SLC38A3		solute carrier family 38,	41 (0.00)	44 (0.20)	0.55
11-01	Gp3	g.chr12:47172308G>C	Silent	SLC38A4	p.P323P	solute carrier family 38,	62 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr5:54922379G>A	Silent	SLC38A9	p.F480F	solute carrier family 38,	109 (0.00)	73 (0.19)	0.51
11-01	Gp3	g.chr2:196571361C>T	Missense Mutation	SLC39A10	p.S413F	solute carrier family 39	36 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr8:22273657C>T	Silent	SLC39A14	p.A337A	solute carrier family 39	22 (0.00)	16 (0.56)	0.84
11-01	Gp3	g.chr14:21469282C>T	Silent	SLC39A2	p.P158P	solute carrier family 39	40 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr3:125741762G>A	Silent	SLC41A3	p.V204V	solute carrier family 41,	37 (0.00)	26 (0.62)	1.64
11-01	Gp3	g.chr5:33954530C>A	Missense Mutation	SLC45A2	p.S323I	solute carrier family 45,	20 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr17:19458620G>A	Silent	SLC47A1	p.V190V	solute carrier family 47	50 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr2:162730483G>T	Nonsense Mutation	SLC4A10	p.E306*	solute carrier family 4, s	134 (0.00)	81 (0.22)	0.59
11-01	Gp3	g.chr4:72338501G>A	Missense Mutation	SLC4A4	p.A573T	solute carrier family 4 (s	87 (0.00)	96 (0.42)	1.11
11-01	Gp3	g.chr16:24919380C>T	Silent	SLC5A11	p.I454I	solute carrier family 5 (s	75 (0.00)	71 (0.23)	0.60
11-01	Gp3	g.chr11:26718750G>T	Missense Mutation	SLC5A12	p.P334Q	solute carrier family 5 (s	128 (0.00)	83 (0.16)	0.42
11-01	Gp3	g.chr11:26743236C>A	Missense Mutation	SLC5A12	p.W9L	solute carrier family 5 (s	101 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr2:27427747C>A	Missense Mutation	SLC5A6	p.G263C	solute carrier family 5 (s	33 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr19:49797171T>A	Missense Mutation	SLC6A16	p.S511C	solute carrier family 6, r	180 (0.00)	85 (0.21)	0.56
11-01	Gp3	g.chr19:49812618G>A	Silent	SLC6A16	p.F309F	solute carrier family 6, r	25 (0.00)	69 (0.22)	0.58
11-01	Gp3	g.chr1:110734731C>G	Silent	SLC6A17	p.A334A	solute carrier family 6 (n	25 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr3:45804495T>G	Missense Mutation	SLC6A20	p.D458A	solute carrier family 6 (p	71 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr11:20648352C>A	Missense Mutation	SLC6A5	p.F453L	solute carrier family 6 (n	49 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr1:44468052G>A	Silent	SLC6A9	p.L234L	solute carrier family 6 (n	49 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr8:87242398C>A	Missense Mutation	SLC7A13	p.G37C	solute carrier family 7 (a	67 (0.01)	61 (0.15)	0.49
11-01	Gp3	g.chr14:23243213C>T	Missense Mutation	SLC7A7	p.G453D	solute carrier family 7 (a	50 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr14:23244715G>T	Missense Mutation	SLC7A7	p.P345T	solute carrier family 7 (a	54 (0.02)	34 (0.24)	0.63
11-01	Gp3	g.chr14:23282476G>A	Silent	SLC7A7	p.C44C	solute carrier family 7 (a	77 (0.00)	97 (0.19)	0.49
11-01	Gp3	g.chr14:23596512C>G	Missense Mutation	SLC7A8	p.V277L	solute carrier family 7 (a	41 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr19:33334858C>T	Splice Site	SLC7A9		solute carrier family 7 (a	23 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr14:70633465G>A	Missense Mutation	SLC8A3	p.R559W	solute carrier family 8 (s	20 (0.00)	9 (0.56)	1.48
11-01	Gp3	g.chr12:113748055G>T	Missense Mutation	SLC8B1	p.P414H	solute carrier family 8 (s	17 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr1:27429801G>T	Silent	SLC9A1	p.G496G	solute carrier family 9, s	32 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr1:27440435C>A	Missense Mutation	SLC9A1	p.S232I	solute carrier family 9, s	18 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr5:476469C>A	Nonsense Mutation	SLC9A3	p.E639*	solute carrier family 9, s	18 (0.00)	42 (0.14)	0.38

11-01	Gp3	g.chr2:103130615C>T	Silent	SLC9A4	p.S542S	solute carrier family 9, s	38 (0.00)	41 (0.32)	0.85
11-01	Gp3	g.chr4:103964510T>A	Silent	SLC9B2	p.G306G	solute carrier family 9, s	58 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr1:173493956C>T	Missense Mutation	SLC9C2	p.G826S	solute carrier family 9, r	46 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr12:21422669C>A	Missense Mutation	SLCO1A2	p.R477I	solute carrier organic an	36 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr12:21358916C>A	Silent	SLCO1B1	p.I482I	solute carrier organic an	82 (0.00)	45 (0.18)	0.47
11-01	Gp3	g.chr12:21358924G>A	Missense Mutation	SLCO1B1	p.C485Y	solute carrier organic an	77 (0.00)	43 (0.26)	0.68
11-01	Gp3	g.chr11:74913947G>T	Splice Site	SLCO2B1	p.G334*	solute carrier organic an	38 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr15:92690336C>G	Missense Mutation	SLCO3A1	p.I545M	solute carrier organic an	34 (0.00)	44 (0.27)	0.73
11-01	Gp3	g.chr5:101599462G>A	Silent	SLCO4C1	p.I275I	solute carrier organic an	155 (0.01)	111 (0.20)	0.53
11-01	Gp3	g.chr8:70744100G>A	Missense Mutation	SLCO5A1	p.A270V	solute carrier organic an	25 (0.00)	22 (0.27)	0.91
11-01	Gp3	g.chr10:98806550G>A	Silent	SLIT1	p.L572L	slit homolog 1 (Drosoph	46 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr4:20270494C>T	Silent	SLIT2	p.L129L	slit homolog 2 (Drosoph	60 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr5:168244429C>A	Silent	SLIT3	p.L223L	slit homolog 3 (Drosoph	28 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chrX:144904520C>A	Missense Mutation	SLITRK2	p.L193I	SLIT and NTRK-like fa	51 (0.02)	27 (0.37)	0.62
11-01	Gp3	g.chr3:164907847C>T	Missense Mutation	SLITRK3	p.D258N	SLIT and NTRK-like fa	53 (0.00)	40 (0.25)	0.67
11-01	Gp3	g.chr15:59181664C>A	Missense Mutation	SLTM	p.R723S	SAFB-like, transcriptio	79 (0.00)	44 (0.30)	0.79
11-01	Gp3	g.chr5:159830391G>A	Silent	SLU7	p.S554S	SLU7 splicing factor ho	132 (0.00)	128 (0.23)	0.62
11-01	Gp3	g.chr5:159842297G>C	Nonsense Mutation	SLU7	p.S2*	SLU7 splicing factor ho	39 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr15:67462938C>T	Silent	SMAD3	p.N174N	SMAD family member	47 (0.00)	27 (0.30)	0.79
11-01	Gp3	g.chr15:67479777G>A	Missense Mutation	SMAD3	p.A318T	SMAD family member	88 (0.00)	56 (0.25)	0.67
11-01	Gp3	g.chr18:48567677G>A	Intron	SMAD4		SMAD family member	54 (0.00)	68 (0.25)	0.67
11-01	Gp3	g.chr18:48567763C>T	Intron	SMAD4		SMAD family member	35 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr18:48568520G>A	Intron	SMAD4		SMAD family member	55 (0.00)	32 (0.47)	1.25
11-01	Gp3	g.chr18:48579460C>T	Intron	SMAD4		SMAD family member	52 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr18:48586223G>A	Intron	SMAD4		SMAD family member	50 (0.02)	21 (0.43)	1.14
11-01	Gp3	g.chr18:48587850C>G	Intron	SMAD4		SMAD family member	82 (0.00)	76 (0.17)	0.46
11-01	Gp3	g.chr5:135510322G>A	Splice Site	SMAD5		SMAD family member	39 (0.00)	26 (0.54)	1.44
11-01	Gp3	g.chr6:71567723G>A	Missense Mutation	SMAP1	p.G354S	small ArfGAP 1	23 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr1:40882500G>T	Missense Mutation	SMAP2	p.S219I	small ArfGAP2	38 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr9:2039602G>C	Missense Mutation	SMARCA2	p.M164I	SWI/SNF related, matri	60 (0.00)	12 (0.50)	0.79
11-01	Gp3	g.chr19:11121100G>T	Missense Mutation	SMARCA4	p.A723S	SWI/SNF related, matri	101 (0.00)	53 (0.21)	0.55
11-01	Gp3	g.chr19:11132594G>T	Missense Mutation	SMARCA4	p.S937I	SWI/SNF related, matri	27 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr4:95191922G>A	Missense Mutation	SMARCAD1	p.A79T	SWI/SNF-related, matri	50 (0.00)	37 (0.30)	0.79
11-01	Gp3	g.chr2:217293433C>A	Missense Mutation	SMARCAL1	p.P421Q	SWI/SNF related, matri	39 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr3:47814324C>A	Missense Mutation	SMARCC1	p.A100S	SWI/SNF related, matri	49 (0.02)	36 (0.25)	0.67

11-01	Gp3	g.chr18:2738517G>A	Silent	SMCHD1	p.V1133V	structural maintenance	22 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr18:2772321C>T	Missense Mutation	SMCHD1	p.S1709L	structural maintenance	39 (0.00)	48 (0.38)	1.00
11-01	Gp3	g.chr18:2784536A>T	Missense Mutation	SMCHD1	p.K1879I	structural maintenance	75 (0.00)	51 (0.18)	0.47
11-01	Gp3	g.chr18:2784607G>T	Missense Mutation	SMCHD1	p.G1903W	structural maintenance	53 (0.00)	41 (0.22)	0.59
11-01	Gp3	g.chr16:18860691G>A	Missense Mutation	SMG1	p.P1824L	SMG1 phosphatidylinos	92 (0.00)	92 (0.20)	0.52
11-01	Gp3	g.chr16:18893627C>T	Missense Mutation	SMG1	p.D385N	SMG1 phosphatidylinos	172 (0.01)	169 (0.17)	0.46
11-01	Gp3	g.chr2:130911430C>T	Missense Mutation	SMPD4	p.A619T	sphingomyelin phospho	34 (0.00)	46 (0.24)	0.64
11-01	Gp3	g.chr2:130912753G>T	Missense Mutation	SMPD4	p.L496M	sphingomyelin phospho	45 (0.00)	65 (0.22)	0.57
11-01	Gp3	g.chr16:88747586G>C	Missense Mutation	SNAI3	p.H205D	snail family zinc finger	25 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr20:10329870C>G	RNA	SNAP25-AS1		SNAP25 antisense RNA	22 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr1:227968246G>A	Missense Mutation	SNAP47	p.G423R	synaptosomal-associate	16 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr9:15459848C>T	Missense Mutation	SNAPC3	p.P407L	small nuclear RNA acti	100 (0.00)	50 (0.64)	1.01
11-01	Gp3	g.chr15:25328809C>T	RNA	SNHG14		small nucleolar RNA ho	55 (0.00)	34 (0.71)	1.88
11-01	Gp3	g.chr15:25429512T>A	RNA	SNHG14		small nucleolar RNA ho	95 (0.00)	76 (0.18)	0.49
11-01	Gp3	g.chr15:25429513C>A	RNA	SNHG14		small nucleolar RNA ho	97 (0.00)	73 (0.19)	0.51
11-01	Gp3	g.chr1:38005984C>T	Missense Mutation	SNIP1	p.E234K	Smad nuclear interactin	56 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr1:38006005C>A	Nonsense Mutation	SNIP1	p.E227*	Smad nuclear interactin	52 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr15:25492563C>T	RNA	SNORD115-42		small nucleolar RNA, C	63 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr3:43389720C>A	Missense Mutation	SNRK	p.Q657K	SNF related kinase	25 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr2:96940882G>A	Silent	SNRNP200	p.D2093D	small nuclear ribonucle	75 (0.00)	39 (0.26)	0.68
11-01	Gp3	g.chr2:96942847C>G	Missense Mutation	SNRNP200	p.E2022Q	small nuclear ribonucle	44 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr16:69333551C>T	Silent	SNTB2	p.T468T	syntrophin, beta 2 (dyst	29 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr17:46196394C>T	Nonsense Mutation	SNX11	p.Q129*	sorting nexin 11	92 (0.00)	111 (0.16)	0.43
11-01	Gp3	g.chr16:29370676G>T	RNA	SNX29P2		sorting nexin 29 pseudo	65 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr16:29437256C>A	lincRNA	SNX29P2		sorting nexin 29 pseudo	18 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr1:179310326C>T	Missense Mutation	SOAT1	p.L221F	sterol O-acyltransferase	103 (0.00)	62 (0.15)	0.39
11-01	Gp3	g.chr18:67992276C>G	Silent	SOCS6	p.S124S	suppressor of cytokine s	26 (0.00)	26 (0.54)	1.44
11-01	Gp3	g.chr6:160103551C>A	Nonsense Mutation	SOD2	p.E169*	superoxide dismutase 2,	50 (0.00)	57 (0.19)	0.51
11-01	Gp3	g.chr21:34924738G>T	Missense Mutation	SON	p.M1067I	SON DNA binding prot	41 (0.00)	25 (0.32)	0.85
11-01	Gp3	g.chr10:108412140C>T	Splice Site	SORCS1	p.E825E	sortilin-related VPS10 d	50 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr10:106602567G>C	Silent	SORCS3	p.T215T	sortilin-related VPS10 d	25 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr11:121444948A>T	Splice Site	SORL1		sortilin-related receptor,	33 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr11:121461774C>A	Nonsense Mutation	SORL1	p.C336*	sortilin-related receptor,	69 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr1:109856981G>T	Missense Mutation	SORT1	p.L795M	sortilin 1	58 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr14:50671052G>A	Silent	SOS2	p.L55L	son of sevenless homolo	30 (0.00)	46 (0.17)	0.46

11-01	Gp3	g.chr1:204091074G>C	Silent	SOX13	p.V274V	SRY (sex determining r	37 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr12:23818492C>G	Missense Mutation	SOX5	p.G263R	SRY (sex determining r	126 (0.00)	71 (0.24)	0.64
11-01	Gp3	g.chr11:16208421G>C	Missense Mutation	SOX6	p.L206V	SRY (sex determining r	129 (0.00)	59 (0.37)	0.99
11-01	Gp3	g.chr1:118584556G>A	Missense Mutation	SPAG17	p.A975V	sperm associated antige	109 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr17:26905693G>T	Silent	SPAG5	p.L1065L	sperm associated antige	71 (0.00)	33 (0.21)	0.57
11-01	Gp3	g.chr17:49071194G>T	Missense Mutation	SPAG9	p.Q763K	sperm associated antige	46 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr17:49075848G>A	Missense Mutation	SPAG9	p.L585F	sperm associated antige	69 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr5:151047047G>A	Missense Mutation	SPARC	p.T189I	secreted protein, acidic,	26 (0.00)	13 (0.54)	1.44
11-01	Gp3	g.chr4:88414882G>A	Missense Mutation	SPARCL1	p.A232V	SPARC-like 1 (hevin)	47 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr17:48632670C>T	Silent	SPATA20	p.N745N	spermatogenesis associa	28 (0.00)	50 (0.40)	1.07
11-01	Gp3	g.chr9:40701757C>A	Missense Mutation	SPATA31A3	p.H79Q	SPATA31 subfamily A,	61 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr9:65506462C>A	Missense Mutation	SPATA31A7	p.L366F	SPATA31 subfamily A,	152 (0.00)	28 (0.43)	1.14
11-01	Gp3	g.chr9:84607970C>A	Missense Mutation	SPATA31D1	p.S862Y	SPATA31 subfamily D,	80 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr9:84609615G>A	Silent	SPATA31D1	p.R1410R	SPATA31 subfamily D,	102 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr9:84530553C>T	RNA	SPATA31D5P		SPATA31 subfamily D,	107 (0.00)	126 (0.15)	0.40
11-01	Gp3	g.chr9:84531501G>A	RNA	SPATA31D5P		SPATA31 subfamily D,	56 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr9:84531761C>A	RNA	SPATA31D5P		SPATA31 subfamily D,	62 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr9:90501738G>A	Missense Mutation	SPATA31E1	p.G779D	SPATA31 subfamily E,	120 (0.01)	54 (0.19)	0.49
11-01	Gp3	g.chr9:90501757G>A	Silent	SPATA31E1	p.V785V	SPATA31 subfamily E,	117 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr2:169730191C>T	Missense Mutation	SPC25	p.E152K	SPC25, NDC80 kinetoc	18 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr17:8660607G>A	Missense Mutation	SPDYE4	p.H105Y	speedy/RINGO cell cyc	48 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr22:24730458G>A	Missense Mutation	SPECC1L	p.G826E	sperm antigen with calp	71 (0.00)	45 (0.71)	1.90
11-01	Gp3	g.chr5:35753823C>T	Missense Mutation	SPEF2	p.T1138I	sperm flagellar 2	48 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr5:35793286C>G	Missense Mutation	SPEF2	p.T1522R	sperm flagellar 2	26 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr5:35793290C>G	Silent	SPEF2	p.V1523V	sperm flagellar 2	27 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr5:35807354C>G	Splice Site	SPEF2	p.P1788R	sperm flagellar 2	73 (0.00)	33 (0.42)	1.13
11-01	Gp3	g.chr1:16199523C>T	Missense Mutation	SPEN	p.S99F	spen family transcriptio	18 (0.00)	23 (0.65)	1.74
11-01	Gp3	g.chr1:16261746G>A	Missense Mutation	SPEN	p.G3004E	spen family transcriptio	27 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr2:228881492G>A	Missense Mutation	SPHKAP	p.P1360S	SPHK1 interactor, AKA	25 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr9:91090080C>A	Nonsense Mutation	SPIN1	p.S226*	spindlin 1	29 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr5:147496007G>A	Missense Mutation	SPINK5	p.G697D	serine peptidase inhibit	34 (0.00)	26 (0.42)	1.13
11-01	Gp3	g.chr5:147496025C>G	Missense Mutation	SPINK5	p.T703S	serine peptidase inhibit	38 (0.00)	24 (0.46)	1.22
11-01	Gp3	g.chr20:55906926G>C	Missense Mutation	SPO11	p.D57H	SPO11 meiotic protein	38 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr17:47701627G>A	Intron	SPOP		speckle-type POZ protei	55 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr17:47706019C>A	Intron	SPOP		speckle-type POZ protei	49 (0.00)	27 (0.19)	0.49

11-01	Gp3	g.chr17:47711492T>A	Intron	SPOP		speckle-type POZ protei	31 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr17:47720198G>A	Intron	SPOP		speckle-type POZ protei	67 (0.00)	55 (0.29)	0.78
11-01	Gp3	g.chr17:47729786G>C	Intron	SPOP		speckle-type POZ protei	33 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr17:47731607C>G	Intron	SPOP		speckle-type POZ protei	51 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr17:47735971G>C	Intron	SPOP		speckle-type POZ protei	63 (0.02)	50 (0.34)	0.91
11-01	Gp3	g.chr17:47739021C>T	Intron	SPOP		speckle-type POZ protei	80 (0.00)	63 (0.22)	0.59
11-01	Gp3	g.chr17:47749601C>T	Intron	SPOP		speckle-type POZ protei	48 (0.00)	58 (0.21)	0.55
11-01	Gp3	g.chr15:38643514G>A	Silent	SPRED1	p.E328E	sprouty-related, EVH1	69 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr15:38643590G>A	Missense Mutation	SPRED1	p.D354N	sprouty-related, EVH1	100 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr1:153012802C>G	Missense Mutation	SPRR2D	p.Q7H	small proline-rich protei	54 (0.00)	20 (0.50)	1.33
11-01	Gp3	g.chr1:158647576G>C	Silent	SPTA1	p.L287L	spectrin, alpha, erythroc	31 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr1:158650450C>T	Missense Mutation	SPTA1	p.E201K	spectrin, alpha, erythroc	37 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr9:131383491C>T	Missense Mutation	SPTAN1	p.R1925C	spectrin, alpha, non-eryt	49 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr2:54872518G>A	Silent	SPTBN1	p.L1474L	spectrin, beta, non-eryth	18 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr2:54882305G>A	Missense Mutation	SPTBN1	p.G1974E	spectrin, beta, non-eryth	26 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr11:66458772G>A	Nonsense Mutation	SPTBN2	p.Q1850*	spectrin, beta, non-eryth	47 (0.00)	62 (0.18)	0.47
11-01	Gp3	g.chr19:41077930G>A	Nonsense Mutation	SPTBN4	p.W2442*	spectrin, beta, non-eryth	81 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr15:42144849G>T	Missense Mutation	SPTBN5	p.Q3478K	spectrin, beta, non-eryth	71 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr15:42165759C>T	Silent	SPTBN5	p.R1646R	spectrin, beta, non-eryth	31 (0.00)	36 (0.33)	0.89
11-01	Gp3	g.chr15:45968449G>C	Missense Mutation	SQRDL	p.D269H	sulfide quinone reductas	76 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr22:42266957G>A	Missense Mutation	SREBF2	p.G262D	sterol regulatory elemen	89 (0.00)	59 (0.24)	0.63
11-01	Gp3	g.chr1:144014117C>T	RNA	SRGAP2B		SLIT-ROBO Rho GTPa	34 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr11:126137484C>G	Missense Mutation	SRPR	p.G81R	signal recognition partic	32 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr3:133534479G>A	Silent	SRPRB	p.V152V	signal recognition partic	22 (0.00)	15 (0.87)	2.31
11-01	Gp3	g.chrX:99924277G>A	Silent	SRPX2	p.V376V	sushi-repeat containing	33 (0.00)	36 (0.25)	0.42
11-01	Gp3	g.chr17:2224681G>C	Missense Mutation	SRR	p.A161P	serine racemase	82 (0.00)	72 (0.24)	0.63
11-01	Gp3	g.chr1:24993367G>A	Missense Mutation	SRRM1	p.A564T	serine/arginine repetitiv	38 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr17:56082798G>A	Missense Mutation	SRSF1	p.P239L	serine/arginine-rich spli	46 (0.02)	51 (0.33)	0.89
11-01	Gp3	g.chr2:170665054G>T	Missense Mutation	SSB	p.R206I	Sjogren syndrome antig	67 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr19:56011269G>C	Missense Mutation	SSC5D	p.G598R	scavenger receptor cyst	37 (0.00)	53 (0.19)	0.50
11-01	Gp3	g.chr19:56011370G>A	Nonsense Mutation	SSC5D	p.W631*	scavenger receptor cyst	30 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr17:27957960C>T	Missense Mutation	SSH2	p.V1391M	slingshot protein phosp	43 (0.02)	25 (0.40)	1.07
11-01	Gp3	g.chr17:27975232G>A	Nonsense Mutation	SSH2	p.R426*	slingshot protein phosp	52 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr7:149493510C>T	RNA	SSPO		SCO-spondin	115 (0.00)	171 (0.16)	0.44
11-01	Gp3	g.chrX:48123243C>T	Silent	SSX1	p.D119D	synovial sarcoma, X bre	56 (0.02)	32 (0.38)	0.62

11-01	Gp3	g.chr1:44303978C>A	Missense Mutation	ST3GAL3	p.F99L	ST3 beta-galactoside al	64 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr11:8720484C>A	Missense Mutation	ST5	p.R492L	suppression of tumorige	90 (0.00)	48 (0.19)	0.50
11-01	Gp3	g.chr11:8751632G>A	Missense Mutation	ST5	p.P402L	suppression of tumorige	92 (0.00)	70 (0.16)	0.42
11-01	Gp3	g.chr11:8752074G>A	Missense Mutation	ST5	p.R255W	suppression of tumorige	22 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr2:107459912C>T	Silent	ST6GAL2	p.K174K	ST6 beta-galactosamide	28 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr9:130658583G>T	Missense Mutation	ST6GALNAC	p.P19T	ST6 (alpha-N-acetyl-ne	19 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr7:116771961G>A	Silent	ST7	p.E196E	suppression of tumorige	52 (0.00)	27 (0.59)	1.58
11-01	Gp3	g.chr15:93007574G>A	Missense Mutation	ST8SIA2	p.A363T	ST8 alpha-N-acetyl-neu	60 (0.02)	39 (0.33)	0.89
11-01	Gp3	g.chr3:136141326C>T	Missense Mutation	STAG1	p.D655N	stromal antigen 1	131 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr7:99786463C>T	Missense Mutation	STAG3	p.P180L	stromal antigen 3	20 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr7:99797859G>A	Splice Site	STAG3	p.G560S	stromal antigen 3	31 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr7:38256671C>A	Missense Mutation	STARD3NL	p.L143I	STARD3 N-terminal lik	124 (0.00)	98 (0.28)	0.73
11-01	Gp3	g.chr15:42977889G>A	Silent	STARD9	p.G1371G	StAR-related lipid trans	92 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr2:191905858G>A	Missense Mutation	STAT4	p.T423I	signal transducer and ac	69 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr2:120005539G>C	Silent	STEAP3	p.L259L	STEAP family member	37 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr7:87908787C>A	Missense Mutation	STEAP4	p.V436F	STEAP family member	47 (0.00)	34 (0.29)	0.78
11-01	Gp3	g.chr4:26959288C>A	Missense Mutation	STIM2	p.H113N	stromal interaction mole	24 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr2:220473879G>C	Missense Mutation	STK11IP	p.D624H	serine/threonine kinase	31 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr2:242438722G>T	Missense Mutation	STK25	p.P179T	serine/threonine kinase	25 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr7:23751900G>A	Missense Mutation	STK31	p.A49T	serine/threonine kinase	40 (0.00)	22 (0.41)	1.09
11-01	Gp3	g.chr2:219540778C>G	Missense Mutation	STK36	p.T154R	serine/threonine kinase	73 (0.00)	45 (0.22)	0.59
11-01	Gp3	g.chr6:36463687G>T	Silent	STK38	p.A424A	serine/threonine kinase	153 (0.00)	81 (0.15)	0.40
11-01	Gp3	g.chr1:36809024G>A	Missense Mutation	STK40	p.P344S	serine/threonine kinase	32 (0.00)	18 (0.44)	1.19
11-01	Gp3	g.chr9:124111602C>A	Splice Site	STOM		stomatin	28 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr2:48808017C>T	Missense Mutation	STON1	p.S82F	stonin 1	42 (0.00)	18 (0.50)	1.33
11-01	Gp3	g.chr14:81743659G>C	Missense Mutation	STON2	p.P666A	stonin 2	29 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr2:202343101G>A	Missense Mutation	STRADB	p.G283S	STE20-related kinase ac	69 (0.00)	16 (0.38)	1.00
11-01	Gp3	g.chr7:129094038A>T	Missense Mutation	STRIP2	p.S196C	striatin interacting prote	24 (0.00)	20 (0.35)	0.93
11-01	Gp3	g.chr14:31404368C>G	Splice Site	STRN3		striatin, calmodulin bin	86 (0.00)	64 (0.22)	0.58
11-01	Gp3	g.chr11:125484218G>A	Splice Site	STT3A		STT3A, subunit of the	208 (0.00)	179 (0.26)	0.69
11-01	Gp3	g.chr20:57243177C>A	Silent	STX16-NPEP	p.I129I	STX16-NPEPL1 readth	39 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr3:93733920G>T	Missense Mutation	STX19	p.A65E	syntaxin 19	30 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr6:132792621C>A	Missense Mutation	STX7	p.R123I	syntaxin 7	77 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr19:48387043C>T	Splice Site	SULT2A1		sulfotransferase family,	22 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr7:56136314C>T	Silent	SUMF2	p.V69V	sulfatase modifying fact	27 (0.00)	23 (0.22)	0.58

11-01	Gp3	g.chr6:44921155C>G	Splice Site	SUPT3H		suppressor of Ty 3 hom	96 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr17:27008316C>T	Silent	SUPT6H	p.Y464Y	suppressor of Ty 6 hom	30 (0.00)	20 (0.50)	1.33
11-01	Gp3	g.chr10:70945784G>A	Missense Mutation	SUPV3L1	p.E105K	suppressor of var1, 3-lik	83 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr9:136199150G>T	Missense Mutation	SURF6	p.A214E	surfeit 6	34 (0.00)	70 (0.17)	0.46
11-01	Gp3	g.chr9:114860943C>T	Splice Site	SUSD1		sushi domain containing	28 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr22:24583547C>T	Missense Mutation	SUSD2	p.H634Y	sushi domain containing	33 (0.00)	75 (0.19)	0.50
11-01	Gp3	g.chr5:75490887G>T	Missense Mutation	SV2C	p.G242C	synaptic vesicle glycopr	121 (0.01)	117 (0.15)	0.39
11-01	Gp3	g.chr5:75594750C>A	Missense Mutation	SV2C	p.T545K	synaptic vesicle glycopr	54 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr5:75597330C>T	Missense Mutation	SV2C	p.L654F	synaptic vesicle glycopr	82 (0.01)	55 (0.18)	0.48
11-01	Gp3	g.chr9:113168874G>T	Nonsense Mutation	SVEP1	p.C2979*	sushi, von Willebrand fa	32 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr9:113169077C>G	Missense Mutation	SVEP1	p.G2912R	sushi, von Willebrand fa	96 (0.00)	42 (0.40)	1.08
11-01	Gp3	g.chr9:113171134C>A	Missense Mutation	SVEP1	p.R2226L	sushi, von Willebrand fa	39 (0.00)	25 (0.56)	1.49
11-01	Gp3	g.chr6:10955415C>T	Missense Mutation	SYCP2L	p.S674F	synaptonemal complex	70 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr3:12112913G>A	RNA	SYN2		synapsin II	34 (0.00)	39 (0.38)	1.03
11-01	Gp3	g.chr1:33160576G>T	Missense Mutation	SYNC	p.L375M	syncoilin, intermediate	62 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr6:152621896G>A	Silent	SYNE1	p.H5854H	spectrin repeat containir	41 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr14:64540793C>T	Missense Mutation	SYNE2	p.T3635I	spectrin repeat containir	76 (0.00)	55 (0.22)	0.58
11-01	Gp3	g.chr14:95932427G>T	Silent	SYNE3	p.A156A	spectrin repeat containir	35 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr21:34011378G>A	Missense Mutation	SYNJ1	p.S1291F	synaptojanin 1	32 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr21:34029338C>T	Missense Mutation	SYNJ1	p.A891T	synaptojanin 1	50 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr15:99671257C>G	Missense Mutation	SYNM	p.L612V	synemin, intermediate fi	63 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr15:99673001C>T	Missense Mutation	SYNM	p.A881V	synemin, intermediate fi	71 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr12:79693296G>A	Missense Mutation	SYT1	p.E259K	synaptotagmin I	156 (0.01)	70 (0.14)	0.38
11-01	Gp3	g.chr16:19234398C>T	Missense Mutation	SYT17	p.S267L	synaptotagmin XVII	40 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr18:40850408G>A	Silent	SYT4	p.V392V	synaptotagmin IV	82 (0.00)	58 (0.45)	1.20
11-01	Gp3	g.chr18:40854059G>C	Missense Mutation	SYT4	p.P112R	synaptotagmin IV	74 (0.00)	61 (0.33)	0.87
11-01	Gp3	g.chr11:85411607G>A	Silent	SYTL2	p.N769N	synaptotagmin-like 2	19 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chrX:99955986C>T	Missense Mutation	SYTL4	p.R149K	synaptotagmin-like 4	19 (0.00)	19 (0.32)	0.53
11-01	Gp3	g.chr1:43903151C>T	Nonsense Mutation	SZT2	p.R2031*	seizure threshold 2 hom	61 (0.00)	47 (0.30)	0.79
11-01	Gp3	g.chr6:132938814C>A	Silent	TAAR2	p.G132G	trace amine associated r	43 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr6:132910018T>A	Missense Mutation	TAAR5	p.I270L	trace amine associated r	52 (0.02)	58 (0.17)	0.46
11-01	Gp3	g.chr6:132891849G>A	Missense Mutation	TAAR6	p.R130K	trace amine associated r	90 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr6:149691182C>A	Silent	TAB2	p.R17R	TGF-beta activated kina	60 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr10:123843441G>T	Nonsense Mutation	TACC2	p.G476*	transforming, acidic coil	66 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr10:123843447A>T	Nonsense Mutation	TACC2	p.K478*	transforming, acidic coil	66 (0.02)	48 (0.23)	0.61

11-01	Gp3	g.chr10:123843936G>A	Missense Mutation	TACC2	p.A641T	transforming, acidic coil	28 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr10:123844578G>A	Missense Mutation	TACC2	p.G855R	transforming, acidic coil	163 (0.00)	80 (0.20)	0.53
11-01	Gp3	g.chr10:123970420G>A	Silent	TACC2	p.E238E	transforming, acidic coil	148 (0.00)	55 (0.25)	0.68
11-01	Gp3	g.chr10:123976295G>T	Missense Mutation	TACC2	p.D578Y	transforming, acidic coil	99 (0.01)	76 (0.41)	1.09
11-01	Gp3	g.chr10:8006910G>A	Silent	TAF3	p.L479L	TAF3 RNA polymerase	67 (0.00)	41 (0.20)	0.52
11-01	Gp3	g.chr18:23969894G>T	Missense Mutation	TAF4B	p.C836F	TAF4b RNA polymeras	88 (0.01)	58 (0.26)	0.69
11-01	Gp3	g.chr11:760138G>A	Missense Mutation	TALDO1	p.D116N	transaldolase 1	64 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chr3:11858677C>T	Missense Mutation	TAMM41	p.G233S	TAM41, mitochondrial	84 (0.00)	47 (0.19)	0.51
11-01	Gp3	g.chr2:160087198C>A	Missense Mutation	TANC1	p.T1754K	tetratricopeptide repeat,	64 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr2:160087263G>T	Nonsense Mutation	TANC1	p.G1776*	tetratricopeptide repeat,	73 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr17:61489029C>A	Missense Mutation	TANC2	p.F1175L	tetratricopeptide repeat,	54 (0.00)	66 (0.18)	0.48
11-01	Gp3	g.chr16:68943221C>A	Silent	TANGO6	p.G636G	transport and golgi orga	81 (0.00)	68 (0.15)	0.39
11-01	Gp3	g.chr16:29990328C>A	Missense Mutation	TAOK2	p.A129E	TAO kinase 2	124 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr1:6639076C>T	Missense Mutation	TAS1R1	p.S653L	taste receptor, type 1, m	46 (0.00)	75 (0.15)	0.39
11-01	Gp3	g.chr12:10978124A>G	Missense Mutation	TAS2R10	p.C249R	taste receptor, type 2, m	78 (0.00)	54 (0.20)	0.54
11-01	Gp3	g.chr7:141478496G>T	Missense Mutation	TAS2R4	p.V70F	taste receptor, type 2, m	68 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr8:125506111G>T	Missense Mutation	TATDN1	p.H252N	TatD DNase domain co	61 (0.02)	38 (0.16)	0.42
11-01	Gp3	g.chr8:125535177C>T	Splice Site	TATDN1		TatD DNase domain co	67 (0.00)	36 (0.17)	0.44
11-01	Gp3	g.chr10:96269894G>A	Silent	TBC1D12	p.L549L	TBC1 domain family, n	48 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr12:72314522C>T	Silent	TBC1D15	p.T537T	TBC1 domain family, n	65 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr12:65268936G>C	Missense Mutation	TBC1D30	p.V552L	TBC1 domain family, n	85 (0.00)	80 (0.28)	0.73
11-01	Gp3	g.chr6:121427190C>G	Missense Mutation	TBC1D32	p.M1148I	TBC1 domain family, n	63 (0.00)	29 (0.52)	0.80
11-01	Gp3	g.chr6:121600267C>A	Splice Site	TBC1D32	p.S578I	TBC1 domain family, n	53 (0.00)	36 (0.44)	0.69
11-01	Gp3	g.chr17:34590452C>A	Start Codon SNP	TBC1D3C	p.M1I	TBC1 domain family, n	160 (0.01)	76 (0.24)	0.63
11-01	Gp3	g.chr2:101656644C>T	Missense Mutation	TBC1D8	p.R344K	TBC1 domain family, n	39 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr3:186272730G>C	Missense Mutation	TBCCD1	p.H239D	TBCC domain containi	39 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr17:80724152T>C	Missense Mutation	TBCD	p.Y115H	tubulin folding cofactor	79 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr11:67402720C>A	Missense Mutation	TBX10	p.G8C	T-box 10	34 (0.00)	62 (0.18)	0.47
11-01	Gp3	g.chr1:168262423C>A	Missense Mutation	TBX19	p.H170Q	T-box 19	21 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr1:168274295C>A	Missense Mutation	TBX19	p.N259K	T-box 19	66 (0.02)	28 (0.21)	0.57
11-01	Gp3	g.chr12:114837349C>T	Missense Mutation	TBX5	p.D111N	T-box 5	109 (0.00)	47 (0.32)	0.85
11-01	Gp3	g.chr7:139706946T>A	Missense Mutation	TBXAS1	p.I397N	thromboxane A syntha	85 (0.00)	38 (0.34)	0.91
11-01	Gp3	g.chrX:102508766C>T	Missense Mutation	TCEAL8	p.G48R	transcription elongation	49 (0.00)	21 (0.24)	0.40
11-01	Gp3	g.chr1:24078283G>A	Missense Mutation	TCEB3	p.M396I	transcription elongation	63 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr1:24080655C>T	Nonsense Mutation	TCEB3	p.Q535*	transcription elongation	85 (0.00)	75 (0.24)	0.64

11-01	Gp3	g.chr15:57545504C>A	Silent	TCF12	p.I435I	transcription factor 12	37 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr15:57555353C>A	Silent	TCF12	p.I542I	transcription factor 12	37 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr15:57555365C>A	Missense Mutation	TCF12	p.N546K	transcription factor 12	38 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr22:42607146T>A	Missense Mutation	TCF20	p.K1389M	transcription factor 20 (	19 (0.00)	16 (0.50)	1.33
11-01	Gp3	g.chr22:42607396G>T	Missense Mutation	TCF20	p.Q1306K	transcription factor 20 (	20 (0.00)	24 (0.75)	2.00
11-01	Gp3	g.chr22:31013451C>A	Missense Mutation	TCN2	p.L355M	transcobalamin II	23 (0.00)	27 (0.26)	0.41
11-01	Gp3	g.chr6:167790057G>T	Silent	TCP10	p.R185R	t-complex 10	30 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr12:124158178C>A	Missense Mutation	TCTN2	p.T95K	tectonic family member	46 (0.00)	52 (0.17)	0.46
11-01	Gp3	g.chr10:97453126G>A	Missense Mutation	TCTN3	p.L122F	tectonic family member	59 (0.00)	50 (0.18)	0.48
11-01	Gp3	g.chr10:115958986G>A	Missense Mutation	TDRD1	p.E147K	tudor domain containing	55 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr10:115978214C>T	Missense Mutation	TDRD1	p.P789S	tudor domain containing	30 (0.00)	31 (0.23)	0.60
11-01	Gp3	g.chr10:115980446G>A	Missense Mutation	TDRD1	p.E872K	tudor domain containing	62 (0.00)	61 (0.15)	0.39
11-01	Gp3	g.chr19:33233717G>T	Missense Mutation	TDRD12	p.Q117H	tudor domain containing	84 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr2:21360974G>A	Missense Mutation	TDRD15	p.R212K	tudor domain containing	96 (0.00)	42 (0.40)	1.08
11-01	Gp3	g.chr2:21364413C>A	Silent	TDRD15	p.A1358A	tudor domain containing	21 (0.00)	21 (0.43)	1.14
11-01	Gp3	g.chr13:61084813G>A	Silent	TDRD3	p.L262L	tudor domain containing	171 (0.00)	87 (0.17)	0.46
11-01	Gp3	g.chr1:179603605G>A	Silent	TDRD5	p.K380K	tudor domain containing	41 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr11:121060480C>T	Silent	TECTA	p.D2086D	tectorin alpha	31 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr10:114053799G>T	Missense Mutation	TECTB	p.Q217H	tectorin beta	43 (0.00)	49 (0.14)	0.38
11-01	Gp3	g.chr17:73987556C>T	Silent	TEN1	p.L34L	TEN1 CST complex su	125 (0.01)	55 (0.36)	0.97
11-01	Gp3	g.chr17:73987578G>A	Missense Mutation	TEN1	p.V42I	TEN1 CST complex su	130 (0.00)	55 (0.18)	0.48
11-01	Gp3	g.chrX:123775822C>T	Missense Mutation	TENM1	p.M632I	teneurin transmembrane	24 (0.00)	27 (0.81)	1.36
11-01	Gp3	g.chr5:167673981G>A	Missense Mutation	TENM2	p.G1774S	teneurin transmembrane	73 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr11:78380490C>A	Silent	TENM4	p.V2300V	teneurin transmembrane	79 (0.00)	62 (0.21)	0.56
11-01	Gp3	g.chr14:20837923C>T	Missense Mutation	TEP1	p.G2337R	telomerase-associated p	37 (0.00)	20 (0.30)	0.80
11-01	Gp3	g.chr16:75690408G>T	Missense Mutation	TERF2IP	p.D367Y	telomeric repeat binding	66 (0.00)	66 (0.17)	0.44
11-01	Gp3	g.chr1:45821011G>A	Silent	TESK2	p.H168H	testis-specific kinase 2	18 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr12:55359851G>T	Missense Mutation	TESPA1	p.N144K	thymocyte expressed, p	56 (0.00)	51 (0.18)	0.47
11-01	Gp3	g.chr10:70450739C>A	Missense Mutation	TET1	p.A1860D	tet methylcytosine diox	46 (0.02)	26 (0.19)	0.51
11-01	Gp3	g.chr4:106158268G>T	Nonsense Mutation	TET2	p.E1057*	tet methylcytosine diox	39 (0.00)	35 (0.43)	1.14
11-01	Gp3	g.chr2:74326583C>T	Nonsense Mutation	TET3	p.R1015*	tet methylcytosine diox	21 (0.00)	28 (0.25)	0.38
11-01	Gp3	g.chr17:56663355G>A	Silent	TEX14	p.S965S	testis expressed 14	91 (0.00)	71 (0.21)	0.56
11-01	Gp3	g.chr17:62290419C>A	Missense Mutation	TEX2	p.G387W	testis expressed 2	68 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr17:62291341G>T	Silent	TEX2	p.P79P	testis expressed 2	171 (0.00)	92 (0.14)	0.38
11-01	Gp3	g.chr22:37387576C>T	Missense Mutation	TEX33	p.E231K	testis expressed 33	94 (0.00)	81 (0.16)	0.43

11-01	Gp3	g.chr3:133476628G>T	Missense Mutation	TF	p.D296Y	transferrin	28 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr3:133485235C>A	Missense Mutation	TF	p.P482T	transferrin	26 (0.00)	29 (0.41)	1.10
11-01	Gp3	g.chr6:50683011C>T	Silent	TFAP2D	p.F74F	transcription factor AP-	51 (0.00)	37 (0.24)	0.65
11-01	Gp3	g.chr16:4312368G>T	Missense Mutation	TFAP4	p.T104N	transcription factor AP-	36 (0.03)	56 (0.32)	0.86
11-01	Gp3	g.chr16:4312394G>A	Silent	TFAP4	p.Y95Y	transcription factor AP-	35 (0.03)	43 (0.47)	1.24
11-01	Gp3	g.chr6:155578979G>A	Silent	TFB1M	p.Y344Y	transcription factor B1,	49 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr21:43771054C>A	Missense Mutation	TFF2	p.D5Y	trefoil factor 2	15 (0.00)	10 (0.50)	1.33
11-01	Gp3	g.chr22:26892072C>A	Missense Mutation	TFIP11	p.A606S	tuftelin interacting prote	219 (0.00)	152 (0.17)	0.46
11-01	Gp3	g.chr2:188332652G>A	Silent	TFPI	p.H212H	tissue factor pathway in	20 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr19:54610415G>C	Missense Mutation	TFPT	p.S235C	TCF3 (E2A) fusion part	18 (0.00)	19 (0.47)	1.26
11-01	Gp3	g.chr3:195782058C>T	Missense Mutation	TFRC	p.V598M	transferrin receptor	96 (0.00)	94 (0.28)	0.74
11-01	Gp3	g.chr8:133899496G>T	Nonsense Mutation	TG	p.E627*	thyroglobulin	57 (0.00)	69 (0.43)	1.16
11-01	Gp3	g.chr8:133925456G>A	Missense Mutation	TG	p.E1442K	thyroglobulin	16 (0.00)	12 (0.58)	1.56
11-01	Gp3	g.chr8:134030071C>T	Missense Mutation	TG	p.S2204F	thyroglobulin	24 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr3:30713279G>A	Missense Mutation	TGFBR2	p.E202K	transforming growth fac	61 (0.00)	37 (0.27)	0.72
11-01	Gp3	g.chr3:30713295G>A	Missense Mutation	TGFBR2	p.R207Q	transforming growth fac	59 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr20:35207193C>A	Missense Mutation	TGIF2-C20orf	p.L6I	TGIF2-C20orf24 readth	36 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr20:36760789G>A	Silent	TGM2	p.L577L	transglutaminase 2	36 (0.00)	34 (0.41)	1.10
11-01	Gp3	g.chr20:36766732G>A	Silent	TGM2	p.A466A	transglutaminase 2	36 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr20:2291737A>T	Missense Mutation	TGM3	p.T168S	transglutaminase 3	51 (0.00)	11 (0.45)	1.21
11-01	Gp3	g.chr15:43568686C>A	Missense Mutation	TGM7	p.K700N	transglutaminase 7	81 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr8:56699292G>C	Missense Mutation	TGS1	p.A279P	trimethylguanosine synt	86 (0.00)	40 (0.20)	0.67
11-01	Gp3	g.chr8:56711632C>A	Missense Mutation	TGS1	p.P568T	trimethylguanosine synt	44 (0.00)	18 (0.28)	0.93
11-01	Gp3	g.chr11:2189381C>T	Silent	TH	p.E203E	tyrosine hydroxylase	23 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr2:43801682G>A	Missense Mutation	THADA	p.H508Y	thyroid adenoma associ	70 (0.00)	41 (0.15)	0.39
11-01	Gp3	g.chr16:67877055G>A	Missense Mutation	THAP11	p.E200K	THAP domain containir	19 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr2:242572729G>A	Silent	THAP4	p.A281A	THAP domain containir	25 (0.00)	49 (0.37)	0.98
11-01	Gp3	g.chr4:83829077C>A	Silent	THAP9	p.S240S	THAP domain containir	49 (0.00)	65 (0.28)	0.74
11-01	Gp3	g.chr15:39881440G>A	Missense Mutation	THBS1	p.G604E	thrombospondin 1	110 (0.00)	56 (0.21)	0.57
11-01	Gp3	g.chr15:39885634C>G	Missense Mutation	THBS1	p.T1011S	thrombospondin 1	74 (0.00)	55 (0.25)	0.68
11-01	Gp3	g.chr5:79378234G>A	Missense Mutation	THBS4	p.R806Q	thrombospondin 4	19 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chrX:122866867C>A	Silent	THOC2	p.A2A	THO complex 2	22 (0.00)	31 (0.39)	0.65
11-01	Gp3	g.chr19:2794854T>C	Missense Mutation	THOP1	p.F108L	thimet oligopeptidase 1	45 (0.00)	45 (0.13)	0.44
11-01	Gp3	g.chr17:38244615G>A	Missense Mutation	THRA	p.V282I	thyroid hormone recept	50 (0.00)	52 (0.33)	0.87
11-01	Gp3	g.chr1:36759517C>A	Missense Mutation	THRAP3	p.P699H	thyroid hormone recept	44 (0.00)	37 (0.22)	0.58

11-01	Gp3	g.chr1:36766490G>A	Silent	THRAP3	p.K769K	thyroid hormone recept	69 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr3:24164392C>A	Nonsense Mutation	THRB	p.E472*	thyroid hormone recept	93 (0.00)	54 (0.26)	0.69
11-01	Gp3	g.chr3:24185104C>G	Missense Mutation	THRB	p.G224A	thyroid hormone recept	66 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr21:32595896C>A	Missense Mutation	TIAM1	p.W607C	T-cell lymphoma invasi	84 (0.00)	75 (0.15)	0.39
11-01	Gp3	g.chr6:155486506C>A	Missense Mutation	TIAM2	p.A87D	T-cell lymphoma invasi	32 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr1:43772563G>C	Silent	TIE1	p.L179L	tyrosine kinase with im	34 (0.00)	22 (0.36)	0.97
11-01	Gp3	g.chr4:153691553C>T	Missense Mutation	TIGD4	p.E202K	tigger transposable elem	62 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr5:149374924G>T	Missense Mutation	TIGD6	p.L330I	tigger transposable elem	46 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr5:149375756G>T	Silent	TIGD6	p.T52T	tigger transposable elem	53 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr12:56822406C>A	Missense Mutation	TIMELESS	p.E445D	timeless circadian clock	15 (0.00)	15 (0.33)	0.89
11-01	Gp3	g.chr19:39976402G>T	Silent	TIMM50	p.T149T	translocase of inner mit	44 (0.00)	28 (0.25)	0.67
11-01	Gp3	g.chr15:30011091G>T	Silent	TJP1	p.P1009P	tight junction protein 1	79 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr9:71869158C>T	Silent	TJP2	p.S1147S	tight junction protein 2	67 (0.00)	60 (0.23)	0.62
11-01	Gp3	g.chr19:3730685G>A	Silent	TJP3	p.V207V	tight junction protein 3	24 (0.00)	49 (0.20)	0.54
11-01	Gp3	g.chrX:153555936G>A	Splice Site	TKTL1		transketolase-like 1	37 (0.00)	22 (0.32)	0.53
11-01	Gp3	g.chr9:84208125G>T	Missense Mutation	TLE1	p.L466I	transducin-like enhance	16 (0.00)	30 (0.27)	0.87
11-01	Gp3	g.chr10:98146799C>A	Missense Mutation	TLL2	p.C588F	tolloid-like 2	36 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr4:187004848G>A	Missense Mutation	TLR3	p.E393K	toll-like receptor 3	99 (0.00)	48 (0.25)	0.67
11-01	Gp3	g.chr1:223283850C>T	Missense Mutation	TLR5	p.E842K	toll-like receptor 5	33 (0.00)	28 (0.46)	1.24
11-01	Gp3	g.chr3:52256399G>A	Missense Mutation	TLR9	p.A798V	toll-like receptor 9	37 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr8:38852890C>A	Missense Mutation	TM2D2	p.D88Y	TM2 domain containing	25 (0.00)	38 (0.26)	0.39
11-01	Gp3	g.chr14:24662386C>T	Missense Mutation	TM9SF1	p.M354I	transmembrane 9 superf	47 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr16:19027802C>A	Silent	TMC7	p.L114L	transmembrane channel-	47 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr16:19033117G>A	Splice Site	TMC7	p.M209I	transmembrane channel-	48 (0.00)	46 (0.17)	0.46
11-01	Gp3	g.chr1:20097919G>A	Missense Mutation	TMCO4	p.A79V	transmembrane and coil	54 (0.00)	105 (0.14)	0.38
11-01	Gp3	g.chr2:193049181C>G	Missense Mutation	TMEFF2	p.G104A	transmembrane protein	46 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr17:7339800C>T	Missense Mutation	TMEM102	p.P168S	transmembrane protein	20 (0.00)	31 (0.29)	0.77
11-01	Gp3	g.chr17:41365186T>A	Missense Mutation	TMEM106A	p.F42L	transmembrane protein	37 (0.00)	25 (0.40)	1.07
11-01	Gp3	g.chr11:102272781G>A	Missense Mutation	TMEM123	p.T105I	transmembrane protein	122 (0.00)	164 (0.35)	0.93
11-01	Gp3	g.chr4:4247979G>A	Silent	TMEM128	p.T63T	transmembrane protein	35 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr2:98375490G>A	Nonsense Mutation	TMEM131	p.R1745*	transmembrane protein	137 (0.00)	41 (0.56)	1.50
11-01	Gp3	g.chr12:126128684G>A	Silent	TMEM132B	p.T495T	transmembrane protein	59 (0.00)	26 (0.27)	0.72
11-01	Gp3	g.chr11:87017012C>T	Missense Mutation	TMEM135	p.H245Y	transmembrane protein	45 (0.00)	68 (0.37)	0.98
11-01	Gp3	g.chr19:48836684G>A	Missense Mutation	TMEM143	p.S391F	transmembrane protein	16 (0.00)	27 (0.33)	0.89
11-01	Gp3	g.chr10:104230656C>A	Silent	TMEM180	p.L162L	transmembrane protein	15 (0.00)	14 (0.36)	0.95

11-01	Gp3	g.chr12:72094736G>A	Silent	TMEM19	p.L324L	transmembrane protein	117 (0.00)	28 (0.21)	0.57
11-01	Gp3	g.chr4:166021870G>A	Missense Mutation	TMEM192	p.H117Y	transmembrane protein	27 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr9:74345767G>T	Missense Mutation	TMEM2	p.Q543K	transmembrane protein	60 (0.00)	50 (0.12)	0.39
11-01	Gp3	g.chr19:11453535C>A	Missense Mutation	TMEM205	p.G176W	transmembrane protein	51 (0.00)	48 (0.23)	0.61
11-01	Gp3	g.chr7:129841795G>T	Silent	TMEM209	p.T156T	transmembrane protein	35 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr7:129841811C>T	Missense Mutation	TMEM209	p.S151N	transmembrane protein	39 (0.00)	26 (0.31)	0.82
11-01	Gp3	g.chr3:171571529C>T	Silent	TMEM212	p.Y144Y	transmembrane protein	75 (0.00)	37 (0.32)	0.86
11-01	Gp3	g.chr7:138487671C>T	Missense Mutation	TMEM213	p.R37W	transmembrane protein	31 (0.00)	32 (0.22)	0.58
11-01	Gp3	g.chr7:138487710G>A	Missense Mutation	TMEM213	p.A50T	transmembrane protein	34 (0.00)	38 (0.21)	0.56
11-01	Gp3	g.chr14:93652640G>T	Missense Mutation	TMEM251	p.R7L	transmembrane protein	107 (0.00)	60 (0.23)	0.62
11-01	Gp3	g.chr14:93652886G>A	Missense Mutation	TMEM251	p.C89Y	transmembrane protein	36 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr14:57070547C>A	Missense Mutation	TMEM260	p.S120Y	transmembrane protein	105 (0.00)	110 (0.15)	0.41
11-01	Gp3	g.chr9:108467918G>A	Nonsense Mutation	TMEM38B	p.W51*	transmembrane protein	59 (0.00)	59 (0.19)	0.50
11-01	Gp3	g.chr9:108468032C>A	Silent	TMEM38B	p.I89I	transmembrane protein	58 (0.00)	42 (0.40)	1.08
11-01	Gp3	g.chr12:64202533G>T	Silent	TMEM5	p.P331P	transmembrane protein	48 (0.00)	50 (0.34)	0.91
11-01	Gp3	g.chr6:44107455C>T	Silent	TMEM63B	p.A187A	transmembrane protein	44 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr17:48356637G>C	Missense Mutation	TMEM92	p.D150H	transmembrane protein	53 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr17:38991022G>A	Missense Mutation	TMEM99	p.C85Y	transmembrane protein	33 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr17:28651890C>T	Missense Mutation	TMIGD1	p.C195Y	transmembrane and imn	66 (0.02)	37 (0.16)	0.43
11-01	Gp3	g.chr4:68688095G>A	Missense Mutation	TMPRSS11D	p.T406I	transmembrane protease	165 (0.00)	122 (0.16)	0.42
11-01	Gp3	g.chr12:51237657C>T	Nonsense Mutation	TMPRSS12	p.Q74*	transmembrane (C-term	42 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr21:42868254G>A	Intron	TMPRSS2		transmembrane protease	100 (0.00)	48 (0.77)	0.88
11-01	Gp3	g.chr21:42871568C>T	Intron	TMPRSS2		transmembrane protease	123 (0.00)	87 (0.16)	0.43
11-01	Gp3	g.chr21:42878424C>T	Intron	TMPRSS2		transmembrane protease	50 (0.00)	70 (0.19)	0.50
11-01	Gp3	g.chr11:117975428C>A	Silent	TMPRSS4	p.S111S	transmembrane protease	29 (0.00)	23 (0.48)	1.28
11-01	Gp3	g.chr12:29670490G>A	Missense Mutation	TMTC1	p.A742V	transmembrane and tetr	145 (0.01)	95 (0.21)	0.56
11-01	Gp3	g.chr13:101264750C>T	Missense Mutation	TMTC4	p.A526T	transmembrane and tetr	17 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr6:138192394G>A	Silent	TNFAIP3	p.L10L	tumor necrosis factor, al	68 (0.00)	24 (0.42)	1.11
11-01	Gp3	g.chr5:118728942G>A	Missense Mutation	TNFAIP8	p.V155I	tumor necrosis factor, al	101 (0.00)	56 (0.43)	1.14
11-01	Gp3	g.chr8:22972217G>T	Missense Mutation	TNFRSF10C	p.G72C	tumor necrosis factor re	37 (0.00)	15 (0.33)	0.50
11-01	Gp3	g.chr1:175066560C>T	Silent	TNN	p.D532D	tenascin N	53 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr7:128619098C>T	Missense Mutation	TNPO3	p.R601H	transportin 3	171 (0.00)	132 (0.14)	0.38
11-01	Gp3	g.chr1:175375532C>T	Missense Mutation	TNR	p.D107N	tenascin R	71 (0.00)	45 (0.36)	0.95
11-01	Gp3	g.chr7:5396677C>A	Silent	TNRC18	p.L1688L	trinucleotide repeat cont	115 (0.00)	87 (0.17)	0.46
11-01	Gp3	g.chr16:24816434C>T	Missense Mutation	TNRC6A	p.L1362F	trinucleotide repeat cont	76 (0.00)	29 (0.24)	0.64

11-01	Gp3	g.chr22:40657846G>T	Silent	TNRC6B	p.V78V	trinucleotide repeat cont	51 (0.00)	28 (0.57)	1.52
11-01	Gp3	g.chr7:47436421C>T	Missense Mutation	TNS3	p.E334K	tensin 3	63 (0.00)	35 (0.23)	0.61
11-01	Gp3	g.chr17:53014475C>A	Silent	TOM1L1	p.T307T	target of myb1 (chicken	49 (0.00)	13 (0.38)	1.03
11-01	Gp3	g.chr7:22852795C>A	Missense Mutation	TOMM7	p.G100V	translocase of outer mit	41 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr7:22852796C>A	Missense Mutation	TOMM7	p.G100W	translocase of outer mit	41 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr8:145656493G>A	Silent	TONSL	p.H1259H	tonsoku-like, DNA repa	26 (0.00)	49 (0.22)	0.60
11-01	Gp3	g.chr17:38546259G>A	Silent	TOP2A	p.D1475D	topoisomerase (DNA) II	44 (0.02)	31 (0.19)	0.52
11-01	Gp3	g.chr17:38557196C>T	Missense Mutation	TOP2A	p.G857D	topoisomerase (DNA) II	112 (0.00)	82 (0.35)	0.94
11-01	Gp3	g.chr17:38564311C>A	Missense Mutation	TOP2A	p.V470F	topoisomerase (DNA) II	81 (0.00)	75 (0.21)	0.57
11-01	Gp3	g.chr3:25665186G>A	Silent	TOP2B	p.F844F	topoisomerase (DNA) II	49 (0.00)	33 (0.33)	0.89
11-01	Gp3	g.chr16:52473745G>A	Missense Mutation	TOX3	p.L375F	TOX high mobility grou	54 (0.00)	51 (0.22)	0.58
11-01	Gp3	g.chr1:223983888C>A	Missense Mutation	TP53BP2	p.A785S	tumor protein p53 bindi	99 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr8:80950439C>G	Missense Mutation	TPD52	p.G156A	tumor protein D52	50 (0.00)	35 (0.23)	0.76
11-01	Gp3	g.chr6:125541243G>A	Silent	TPD52L1	p.P13P	tumor protein D52-like	49 (0.00)	10 (0.90)	1.40
11-01	Gp3	g.chr12:72372805C>A	Nonsense Mutation	TPH2	p.Y293*	tryptophan hydroxylase	115 (0.00)	74 (0.27)	0.72
11-01	Gp3	g.chr9:35684487C>T	Missense Mutation	TPM2	p.E234K	tropomyosin 2 (beta)	46 (0.02)	40 (0.20)	0.53
11-01	Gp3	g.chr1:154143175C>T	Missense Mutation	TPM3	p.E219K	tropomyosin 3	62 (0.02)	59 (0.20)	0.54
11-01	Gp3	g.chr1:186313629C>T	Missense Mutation	TPR	p.A1099T	translocated promoter re	95 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr1:186316571T>C	Silent	TPR	p.E932E	translocated promoter re	21 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr21:10934045G>T	Missense Mutation	TPTE	p.T311N	transmembrane phospha	61 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chr7:23547075G>A	Missense Mutation	TRA2A	p.T202I	transformer 2 alpha hom	238 (0.00)	168 (0.23)	0.62
11-01	Gp3	g.chr2:85066338C>A	Missense Mutation	TRABD2A	p.G260V	TraB domain containing	70 (0.00)	51 (0.25)	0.39
11-01	Gp3	g.chr12:112589810G>C	Missense Mutation	TRAFD1	p.Q495H	TRAF-type zinc finger	141 (0.00)	119 (0.14)	0.38
11-01	Gp3	g.chr14:22975639G>T	RNA	TRAJ35		T cell receptor alpha joi	72 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr2:202251118A>G	Missense Mutation	TRAK2	p.F596L	trafficking protein, kine	80 (0.00)	57 (0.25)	0.65
11-01	Gp3	g.chr3:36897423T>A	Nonsense Mutation	TRANK1	p.R670*	tetratricopeptide repeat	137 (0.01)	99 (0.21)	0.57
11-01	Gp3	g.chr3:36940729A>G	Missense Mutation	TRANK1	p.S58P	tetratricopeptide repeat	27 (0.00)	29 (0.24)	0.64
11-01	Gp3	g.chr16:3736135C>A	Silent	TRAP1	p.V111V	TNF receptor-associated	32 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr5:64960341G>C	Missense Mutation	TRAPPC13	p.G386A	trafficking protein partic	42 (0.00)	45 (0.16)	0.41
11-01	Gp3	g.chr5:64960374C>G	Missense Mutation	TRAPPC13	p.T397R	trafficking protein partic	39 (0.00)	55 (0.15)	0.39
11-01	Gp3	g.chr14:22521196C>T	RNA	TRAV21		T cell receptor alpha var	56 (0.00)	27 (0.19)	0.49
11-01	Gp3	g.chr14:22217488T>C	RNA	TRAV5		T cell receptor alpha var	94 (0.00)	112 (0.18)	0.48
11-01	Gp3	g.chr14:22600924C>G	RNA	TRAV8-7		T cell receptor alpha var	40 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:142176437G>A	RNA	TRBV7-4		T cell receptor beta vari	42 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr7:142239999G>A	RNA	TRBV9		T cell receptor beta vari	25 (0.00)	30 (0.23)	0.62

11-01	Gp3	g.chr6:42224499C>T	Silent	TRERF1	p.L849L	transcriptional regulatin	40 (0.00)	36 (0.19)	0.52
11-01	Gp3	g.chr6:42237286C>A	Missense Mutation	TRERF1	p.G15C	transcriptional regulatin	39 (0.00)	26 (0.38)	1.03
11-01	Gp3	g.chr7:38301802G>T	RNA	TRGC1		T cell receptor gamma c	96 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr7:38389026C>T	RNA	TRGV5		T cell receptor gamma v	30 (0.00)	40 (0.20)	0.53
11-01	Gp3	g.chr7:38389422G>A	RNA	TRGV5		T cell receptor gamma v	20 (0.00)	14 (0.43)	1.14
11-01	Gp3	g.chr12:73056946C>A	Missense Mutation	TRHDE	p.Q1016K	thyrotropin-releasing ho	44 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr4:154236996G>T	Missense Mutation	TRIM2	p.D516Y	tripartite motif containin	74 (0.00)	96 (0.28)	0.75
11-01	Gp3	g.chr7:138200033G>A	Missense Mutation	TRIM24	p.C187Y	tripartite motif containin	84 (0.00)	43 (0.26)	0.68
11-01	Gp3	g.chr5:180651279G>A	Missense Mutation	TRIM41	p.D94N	tripartite motif containin	23 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr3:140401365C>A	Missense Mutation	TRIM42	p.P135T	tripartite motif containin	43 (0.02)	26 (0.19)	0.51
11-01	Gp3	g.chr2:96260124C>T	Missense Mutation	TRIM43	p.S118F	tripartite motif containin	97 (0.00)	54 (0.15)	0.40
11-01	Gp3	g.chr1:155149431G>A	Silent	TRIM46	p.K231K	tripartite motif containin	36 (0.00)	55 (0.44)	1.16
11-01	Gp3	g.chr11:49080591G>A	Missense Mutation	TRIM64C	p.P25L	tripartite motif containin	52 (0.00)	47 (0.28)	0.74
11-01	Gp3	g.chr11:49080595C>A	Missense Mutation	TRIM64C	p.D24Y	tripartite motif containin	51 (0.00)	45 (0.20)	0.53
11-01	Gp3	g.chr1:231333194C>G	Missense Mutation	TRIM67	p.N374K	tripartite motif containin	84 (0.00)	42 (0.26)	0.54
11-01	Gp3	g.chr14:51561129C>T	Missense Mutation	TRIM9	p.E177K	tripartite motif containin	17 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr22:38121535C>T	Missense Mutation	TRIOBP	p.T991I	TRIO and F-actin bindin	16 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr19:6750547G>C	Missense Mutation	TRIP10	p.E464D	thyroid hormone recepto	57 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr1:40307450C>T	Missense Mutation	TRIT1	p.G457E	tRNA isopentenyltransfe	93 (0.01)	48 (0.27)	0.72
11-01	Gp3	g.chr1:40318449C>A	Nonsense Mutation	TRIT1	p.E172*	tRNA isopentenyltransfe	109 (0.00)	109 (0.21)	0.56
11-01	Gp3	g.chr1:40318542C>A	Nonsense Mutation	TRIT1	p.E141*	tRNA isopentenyltransfe	39 (0.00)	24 (0.29)	0.78
11-01	Gp3	g.chr4:8453732G>A	Missense Mutation	TRMT44	p.V334M	tRNA methyltransferase	121 (0.00)	46 (0.28)	0.75
11-01	Gp3	g.chr4:8453736C>A	Missense Mutation	TRMT44	p.A335D	tRNA methyltransferase	117 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr4:8477716G>C	Missense Mutation	TRMT44	p.K754N	tRNA methyltransferase	42 (0.00)	43 (0.21)	0.56
11-01	Gp3	g.chr22:46751425G>T	Missense Mutation	TRMU	p.A320S	tRNA 5-methylaminome	22 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr22:46751479G>A	Missense Mutation	TRMU	p.A338T	tRNA 5-methylaminome	22 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chrX:111155672C>A	Missense Mutation	TRPC5	p.K249N	transient receptor potent	35 (0.00)	13 (0.38)	0.64
11-01	Gp3	g.chr15:31355454C>G	Missense Mutation	TRPM1	p.G278R	transient receptor potent	25 (0.00)	21 (0.33)	0.89
11-01	Gp3	g.chr2:234878452G>T	Splice Site	TRPM8		transient receptor potent	158 (0.00)	95 (0.16)	0.42
11-01	Gp3	g.chr17:16325932G>A	Silent	TRPV2	p.T118T	transient receptor potent	26 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:98555646C>T	Missense Mutation	TRRAP	p.L2066F	transformation/transcrip	16 (0.00)	10 (0.50)	1.33
11-01	Gp3	g.chr10:116735008G>C	Missense Mutation	TRUB1	p.C307S	TruB pseudouridine (psi	81 (0.01)	29 (0.17)	0.46
11-01	Gp3	g.chr10:116735009C>T	Silent	TRUB1	p.C307C	TruB pseudouridine (psi	81 (0.01)	27 (0.19)	0.49
11-01	Gp3	g.chr13:45147717C>T	Missense Mutation	TSC22D1	p.V832I	TSC22 domain family, m	68 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr13:45148119G>C	Missense Mutation	TSC22D1	p.P698A	TSC22 domain family, m	34 (0.00)	55 (0.33)	0.87

11-01	Gp3	g.chr3:12531464G>C	Missense Mutation	TSEN2	p.E55D	TSEN2 tRNA splicing e	56 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr18:72999894G>T	Silent	TSHZ1	p.V844V	teashirt zinc finger hom	31 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr20:51871901G>A	Missense Mutation	TSHZ2	p.R635H	teashirt zinc finger hom	85 (0.00)	64 (0.20)	0.54
11-01	Gp3	g.chr19:31767912G>T	Silent	TSHZ3	p.P929P	teashirt zinc finger hom	17 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr8:143427199G>A	Missense Mutation	TSNARE1	p.P48L	t-SNARE domain conta	51 (0.00)	67 (0.15)	0.40
11-01	Gp3	g.chr1:231700468C>A	Missense Mutation	TSNAX	p.F230L	translin-associated facto	65 (0.00)	49 (0.18)	0.38
11-01	Gp3	g.chr19:11408928G>T	Silent	TSPAN16	p.L60L	tetraspanin 16	69 (0.00)	41 (0.17)	0.46
11-01	Gp3	g.chr11:113230165G>T	Missense Mutation	TTC12	p.Q509H	tetratricopeptide repeat	36 (0.00)	28 (0.18)	0.48
11-01	Gp3	g.chr11:43469568C>T	Silent	TTC17	p.Y894Y	tetratricopeptide repeat	36 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr10:75037019C>T	Silent	TTC18	p.L372L		60 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr10:75108268C>A	Nonsense Mutation	TTC18	p.E88*		39 (0.00)	22 (0.27)	0.73
11-01	Gp3	g.chr3:39170288G>A	Silent	TTC21A	p.T594T	tetratricopeptide repeat	74 (0.00)	29 (0.72)	1.93
11-01	Gp3	g.chr2:32891782C>T	Missense Mutation	TTC27	p.L296F	tetratricopeptide repeat	53 (0.00)	51 (0.18)	0.47
11-01	Gp3	g.chr20:36641323G>T	Missense Mutation	TTI1	p.S299Y	TELO2 interacting prot	59 (0.00)	42 (0.19)	0.51
11-01	Gp3	g.chr9:124751733C>T	Missense Mutation	TTLL11	p.R427H	tubulin tyrosine ligase-li	58 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr3:9868851C>T	Missense Mutation	TTLL3	p.L137F	tubulin tyrosine ligase-li	81 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr20:30513882C>A	Missense Mutation	TTLL9	p.H246N	tubulin tyrosine ligase-li	24 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr2:179393000C>T	Splice Site	TTN		titin	129 (0.00)	73 (0.23)	0.62
11-01	Gp3	g.chr2:179397441G>T	Missense Mutation	TTN	p.P34634Q	titin	120 (0.00)	80 (0.19)	0.50
11-01	Gp3	g.chr2:179408789C>A	Missense Mutation	TTN	p.A32028S	titin	158 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr2:179410280G>C	Missense Mutation	TTN	p.R31853G	titin	191 (0.00)	115 (0.18)	0.49
11-01	Gp3	g.chr2:179410337C>T	Missense Mutation	TTN	p.D31834N	titin	180 (0.00)	99 (0.27)	0.73
11-01	Gp3	g.chr2:179421724C>T	Missense Mutation	TTN	p.S29386N	titin	72 (0.00)	59 (0.49)	1.31
11-01	Gp3	g.chr2:179421774G>A	Silent	TTN	p.G29369G	titin	86 (0.00)	56 (0.21)	0.57
11-01	Gp3	g.chr2:179429286C>T	Nonsense Mutation	TTN	p.W27191*	titin	27 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr2:179431042G>A	Missense Mutation	TTN	p.A26606V	titin	98 (0.00)	40 (0.23)	0.60
11-01	Gp3	g.chr2:179434101G>T	Missense Mutation	TTN	p.S25586R	titin	74 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr2:179437223C>T	Missense Mutation	TTN	p.D24546N	titin	56 (0.00)	44 (0.18)	0.48
11-01	Gp3	g.chr2:179454097G>A	Silent	TTN	p.D20785D	titin	139 (0.00)	59 (0.24)	0.63
11-01	Gp3	g.chr2:179454585C>A	Missense Mutation	TTN	p.V20623F	titin	85 (0.00)	68 (0.25)	0.67
11-01	Gp3	g.chr2:179455290C>T	Missense Mutation	TTN	p.A20388T	titin	99 (0.00)	78 (0.18)	0.48
11-01	Gp3	g.chr2:179463965C>A	Missense Mutation	TTN	p.G18852V	titin	93 (0.01)	30 (0.47)	1.24
11-01	Gp3	g.chr2:179477636C>A	Silent	TTN	p.G16604G	titin	27 (0.00)	20 (0.65)	1.73
11-01	Gp3	g.chr2:179483129C>A	Nonsense Mutation	TTN	p.G15686*	titin	107 (0.00)	43 (0.23)	0.62
11-01	Gp3	g.chr2:179514964C>T	Silent	TTN	p.E13248E	titin	64 (0.00)	41 (0.37)	0.98

11-01	Gp3	g.chr2:179528587G>A	Missense Mutation	TTN	p.P12136L	titin	126 (0.00)	64 (0.16)	0.42
11-01	Gp3	g.chr2:179536995C>T	Splice Site	TTN		titin	55 (0.00)	17 (0.65)	1.73
11-01	Gp3	g.chr2:179567187C>T	Missense Mutation	TTN	p.D10143N	titin	173 (0.00)	122 (0.20)	0.52
11-01	Gp3	g.chr2:179577094G>T	Nonsense Mutation	TTN	p.Y9185*	titin	118 (0.00)	44 (0.36)	0.97
11-01	Gp3	g.chr2:179577120C>T	Missense Mutation	TTN	p.E9177K	titin	95 (0.00)	50 (0.44)	1.17
11-01	Gp3	g.chr2:179582320T>A	Silent	TTN	p.I8427I	titin	108 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr2:179584283G>T	Missense Mutation	TTN	p.S7979Y	titin	90 (0.00)	71 (0.20)	0.53
11-01	Gp3	g.chr2:179592321G>T	Missense Mutation	TTN	p.L6662I	titin	61 (0.00)	27 (0.44)	1.19
11-01	Gp3	g.chr2:179621192C>G	Missense Mutation	TTN	p.V3671L	titin	57 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr8:63978576C>G	Missense Mutation	TTPA	p.V147L	tocopherol (alpha) trans	42 (0.00)	38 (0.13)	0.44
11-01	Gp3	g.chr17:72249305C>A	Missense Mutation	TTYH2	p.Q449K	tweety family member 2	78 (0.00)	105 (0.14)	0.38
11-01	Gp3	g.chr12:49578885G>A	Missense Mutation	TUBA1A	p.R422C	tubulin, alpha 1a	95 (0.00)	67 (0.28)	0.76
11-01	Gp3	g.chr12:49521888G>C	Silent	TUBA1B	p.A403A	tubulin, alpha 1b	141 (0.00)	73 (0.16)	0.44
11-01	Gp3	g.chr2:132238223C>A	Nonsense Mutation	TUBA3D	p.Y319*	tubulin, alpha 3d	40 (0.00)	58 (0.26)	0.69
11-01	Gp3	g.chr16:90161061G>A	RNA	TUBB8P7		tubulin, beta 8 class VII	25 (0.00)	30 (0.20)	0.53
11-01	Gp3	g.chr16:90162422C>A	RNA	TUBB8P7		tubulin, beta 8 class VII	155 (0.01)	98 (0.18)	0.49
11-01	Gp3	g.chr15:22861870C>A	Silent	TUBGCP5	p.S630S	tubulin, gamma comple	66 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr16:28854441T>C	Missense Mutation	TUFM	p.K408R	Tu translation elongatio	59 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr12:3043654G>A	Missense Mutation	TULP3	p.G284D	tubby like protein 3	66 (0.00)	56 (0.32)	0.86
11-01	Gp3	g.chr16:10868841G>A	Missense Mutation	TVP23A	p.L68F	trans-golgi network vesi	152 (0.00)	130 (0.18)	0.47
11-01	Gp3	g.chr17:18694276G>T	Missense Mutation	TVP23B	p.G55W	trans-golgi network vesi	60 (0.02)	45 (0.27)	0.71
11-01	Gp3	g.chrX:16838352G>T	Missense Mutation	TXLNG	p.A158S	taxilin gamma	61 (0.00)	25 (0.44)	0.73
11-01	Gp3	g.chr16:11829962C>T	Missense Mutation	TXNDC11	p.V128I	thioredoxin domain con	46 (0.00)	77 (0.16)	0.42
11-01	Gp3	g.chr18:669126C>T	Missense Mutation	TYMS	p.T87I	thymidylate synthetase	45 (0.00)	39 (0.18)	0.48
11-01	Gp3	g.chr18:669168C>T	Missense Mutation	TYMS	p.P101L	thymidylate synthetase	35 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr7:72081728C>G	RNA	TYW1B		tRNA-yW synthesizing	172 (0.00)	142 (0.15)	0.39
11-01	Gp3	g.chr9:139974584C>A	Silent	UAP1L1	p.R390R	UDP-N-acetylglucosam	56 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr3:69112141G>A	Missense Mutation	UBA3	p.P229S	ubiquitin-like modifier	31 (0.00)	38 (0.55)	1.47
11-01	Gp3	g.chr4:68905068G>A	RNA	UBA6-AS1		UBA6 antisense RNA 1	52 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr11:118244337C>T	Silent	UBE4A	p.Y358Y	ubiquitination factor E4	39 (0.03)	27 (0.30)	0.79
11-01	Gp3	g.chr11:118247293G>T	Missense Mutation	UBE4A	p.L492F	ubiquitination factor E4	95 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr1:10221341C>G	Silent	UBE4B	p.P936P	ubiquitination factor E4	27 (0.00)	30 (0.30)	0.80
11-01	Gp3	g.chr6:42561936C>A	Missense Mutation	UBR2	p.T142K	ubiquitin protein ligase	27 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr2:170806483C>A	Silent	UBR3	p.R1151R	ubiquitin protein ligase	114 (0.00)	53 (0.53)	1.41
11-01	Gp3	g.chr1:19499499G>A	Missense Mutation	UBR4	p.A1127V	ubiquitin protein ligase	36 (0.00)	12 (0.42)	1.11

11-01	Gp3	g.chr1:19510363G>A	Missense Mutation	UBR4	p.A709V	ubiquitin protein ligase	39 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr17:42285132T>C	Missense Mutation	UBTF	p.K654E	upstream binding transc	56 (0.00)	46 (0.22)	0.58
11-01	Gp3	g.chr17:42285133A>T	Silent	UBTF	p.R653R	upstream binding transc	56 (0.00)	46 (0.22)	0.58
11-01	Gp3	g.chr17:42285134C>T	Missense Mutation	UBTF	p.R653H	upstream binding transc	57 (0.02)	46 (0.22)	0.58
11-01	Gp3	g.chr1:20517444G>A	Silent	UBXN10	p.V130V	UBX domain protein 10	65 (0.02)	49 (0.14)	0.38
11-01	Gp3	g.chr1:20517756C>G	Silent	UBXN10	p.T234T	UBX domain protein 10	42 (0.00)	10 (0.60)	1.60
11-01	Gp3	g.chr2:24222599G>T	Silent	UBXN2A	p.P214P	UBX domain protein 2	31 (0.00)	15 (0.40)	1.07
11-01	Gp3	g.chr4:141484599G>A	Silent	UCP1	p.P133P	uncoupling protein 1 (m	49 (0.00)	28 (0.75)	2.00
11-01	Gp3	g.chr4:69433776C>T	Missense Mutation	UGT2B17	p.E143K	UDP glucuronosyltrans	62 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr4:69434054C>T	Missense Mutation	UGT2B17	p.G50D	UDP glucuronosyltrans	67 (0.00)	40 (0.55)	1.47
11-01	Gp3	g.chr4:70146359T>A	Silent	UGT2B28	p.V47V	UDP glucuronosyltrans	87 (0.01)	52 (0.25)	0.67
11-01	Gp3	g.chr6:34802564G>A	Missense Mutation	UHRF1BP1	p.D199N	UHRF1 binding protein	48 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr6:34826888G>A	Missense Mutation	UHRF1BP1	p.D919N	UHRF1 binding protein	21 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr6:34826898C>A	Nonsense Mutation	UHRF1BP1	p.S922*	UHRF1 binding protein	21 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr12:100452105C>A	Missense Mutation	UHRF1BP1L	p.V984F	UHRF1 binding protein	48 (0.00)	29 (0.21)	0.70
11-01	Gp3	g.chr9:35259002G>A	Missense Mutation	UNC13B	p.E161K	unc-13 homolog B (C. e	37 (0.00)	27 (0.37)	0.99
11-01	Gp3	g.chr9:35380510G>C	Missense Mutation	UNC13B	p.D668H	unc-13 homolog B (C. e	26 (0.00)	32 (0.25)	0.67
11-01	Gp3	g.chr15:54919105C>A	Silent	UNC13C	p.R2147R	unc-13 homolog C (C. e	104 (0.00)	53 (0.17)	0.45
11-01	Gp3	g.chr14:94044201C>T	Missense Mutation	UNC79	p.S565F	unc-79 homolog (C. ele	83 (0.00)	41 (0.34)	0.91
11-01	Gp3	g.chr2:210685141C>T	Missense Mutation	UNC80	p.P690L	unc-80 homolog (C. ele	52 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr19:18960999C>T	Missense Mutation	UPF1	p.L193F	UPF1 regulator of nons	48 (0.00)	32 (0.28)	0.75
11-01	Gp3	g.chr10:11994221C>A	Nonsense Mutation	UPF2	p.E960*	UPF2 regulator of nons	38 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr10:12070919G>A	Missense Mutation	UPF2	p.P324S	UPF2 regulator of nons	71 (0.00)	48 (0.21)	0.56
11-01	Gp3	g.chr10:12070989C>A	Missense Mutation	UPF2	p.E300D	UPF2 regulator of nons	47 (0.00)	48 (0.15)	0.39
11-01	Gp3	g.chr1:229771150G>A	Missense Mutation	URB2	p.G264R	URB2 ribosome biogen	48 (0.00)	33 (0.33)	0.69
11-01	Gp3	g.chr7:43908593G>C	Missense Mutation	URGCP-MRPS	p.P109A	URGCP-MRPS24 readt	19 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr1:161011620G>A	Missense Mutation	USF1	p.A98V	upstream transcription f	55 (0.00)	47 (0.21)	0.57
11-01	Gp3	g.chr17:72915736G>C	Missense Mutation	USH1G	p.L399V	Usher syndrome 1G (au	16 (0.00)	37 (0.16)	0.43
11-01	Gp3	g.chr1:215844562C>G	Missense Mutation	USH2A	p.E4629Q	Usher syndrome 2A (au	65 (0.00)	27 (0.26)	0.69
11-01	Gp3	g.chr1:215956210T>A	Silent	USH2A	p.G3485G	Usher syndrome 2A (au	18 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr4:76708269C>A	Missense Mutation	USO1	p.Q306K	USO1 vesicle transport	120 (0.00)	106 (0.20)	0.53
11-01	Gp3	g.chr4:76721611G>A	Silent	USO1	p.E566E	USO1 vesicle transport	86 (0.00)	53 (0.23)	0.60
11-01	Gp3	g.chr8:11996222G>A	Silent	USP17L2	p.H16H	ubiquitin specific peptid	204 (0.00)	37 (0.27)	0.40
11-01	Gp3	g.chr3:49147919C>A	Missense Mutation	USP19	p.A1271S	ubiquitin specific peptid	41 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr9:132620800G>T	Missense Mutation	USP20	p.A85S	ubiquitin specific peptid	21 (0.00)	18 (0.28)	0.74

11-01	Gp3	g.chr1:55619577G>A	Missense Mutation	USP24	p.S609L	ubiquitin specific peptid	22 (0.00)	14 (0.36)	0.95
11-01	Gp3	g.chr1:78187821G>C	Missense Mutation	USP33	p.L484V	ubiquitin specific peptid	34 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr1:78191382C>T	Missense Mutation	USP33	p.V401I	ubiquitin specific peptid	32 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr2:61441439G>A	Missense Mutation	USP34	p.P2813L	ubiquitin specific peptid	66 (0.02)	34 (0.29)	0.78
11-01	Gp3	g.chr2:61492630C>A	Missense Mutation	USP34	p.V1894F	ubiquitin specific peptid	48 (0.00)	45 (0.29)	0.77
11-01	Gp3	g.chr2:234436104C>G	Missense Mutation	USP40	p.L557F	ubiquitin specific peptid	67 (0.00)	42 (0.38)	1.02
11-01	Gp3	g.chr2:234449338C>T	Silent	USP40	p.K379K	ubiquitin specific peptid	26 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr4:53494172C>A	Missense Mutation	USP46	p.K92N	ubiquitin specific peptid	66 (0.00)	43 (0.35)	0.93
11-01	Gp3	g.chr12:6968641G>C	Missense Mutation	USP5	p.D356H	ubiquitin specific peptid	29 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr4:120214304C>G	Missense Mutation	USP53	p.H1054D	ubiquitin specific peptid	31 (0.00)	23 (0.30)	0.81
11-01	Gp3	g.chr17:5066244C>T	Missense Mutation	USP6	p.A994V	ubiquitin specific peptid	83 (0.00)	44 (0.39)	1.03
11-01	Gp3	g.chr17:5074021G>C	Missense Mutation	USP6	p.E1255D	ubiquitin specific peptid	70 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr17:5074050C>A	Missense Mutation	USP6	p.A1265D	ubiquitin specific peptid	169 (0.00)	67 (0.24)	0.64
11-01	Gp3	g.chr10:11504608C>T	Silent	USP6NL	p.Q773Q	USP6 N-terminal like	141 (0.00)	38 (0.26)	0.70
11-01	Gp3	g.chr10:11505444C>A	Missense Mutation	USP6NL	p.A495S	USP6 N-terminal like	114 (0.00)	49 (0.20)	0.54
11-01	Gp3	g.chr15:50773847C>G	Missense Mutation	USP8	p.A386G	ubiquitin specific peptid	29 (0.00)	20 (0.25)	0.67
11-01	Gp3	g.chr15:50774164G>A	Missense Mutation	USP8	p.E492K	ubiquitin specific peptid	70 (0.00)	55 (0.20)	0.53
11-01	Gp3	g.chrX:41012200G>A	Splice Site	USP9X		ubiquitin specific peptid	59 (0.00)	27 (0.26)	0.43
11-01	Gp3	g.chrX:129055247G>A	Silent	UTP14A	p.E344E	UTP14, U3 small nucle	50 (0.00)	28 (0.29)	0.48
11-01	Gp3	g.chr12:101755780G>T	Missense Mutation	UTP20	p.G1911V	UTP20, small subunit (	74 (0.00)	61 (0.16)	0.44
11-01	Gp3	g.chr6:144835834C>A	Missense Mutation	UTRN	p.R1708S	utrophin	85 (0.00)	89 (0.15)	0.39
11-01	Gp3	g.chr19:46029246G>A	Missense Mutation	VASP	p.E364K	vasodilator-stimulated p	87 (0.00)	84 (0.17)	0.44
11-01	Gp3	g.chrX:154456683G>A	Missense Mutation	VBP1	p.M101I	von Hippel-Lindau bind	99 (0.00)	64 (0.38)	0.62
11-01	Gp3	g.chrX:154464649G>T	Splice Site	VBP1		von Hippel-Lindau bind	49 (0.00)	32 (0.28)	0.47
11-01	Gp3	g.chr5:82850843G>A	Missense Mutation	VCAN	p.D500N	versican	94 (0.00)	98 (0.16)	0.44
11-01	Gp3	g.chr9:35057508G>A	Missense Mutation	VCP	p.P727L	valosin containing prote	73 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr8:67547289G>A	Missense Mutation	VCPIP1	p.P1039L	valosin containing prote	121 (0.00)	53 (0.13)	0.44
11-01	Gp3	g.chr8:67577395C>T	Missense Mutation	VCPIP1	p.G600E	valosin containing prote	50 (0.00)	37 (0.30)	0.99
11-01	Gp3	g.chr17:56052207G>T	Missense Mutation	VEZF1	p.T398N	vascular endothelial zin	29 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr3:10188290C>T	Nonsense Mutation	VHL	p.Q145*	von Hippel-Lindau tum	69 (0.01)	108 (0.15)	0.40
11-01	Gp3	g.chr10:17276742G>A	Silent	VIM	p.Q311Q	vimentin	45 (0.00)	45 (0.36)	0.95
11-01	Gp3	g.chr6:153077282G>A	Missense Mutation	VIP	p.E117K	vasoactive intestinal pe	26 (0.00)	14 (0.50)	1.33
11-01	Gp3	g.chr3:51456135G>A	Silent	VPRBP	p.S695S	Vpr (HIV-1) binding pr	90 (0.00)	61 (0.18)	0.48
11-01	Gp3	g.chr9:79931155G>A	Missense Mutation	VPS13A	p.V1566I	vacuolar protein sorting	60 (0.00)	56 (0.12)	0.41
11-01	Gp3	g.chr8:100568860T>A	Missense Mutation	VPS13B	p.L1668H	vacuolar protein sorting	75 (0.00)	29 (0.21)	0.55

11-01	Gp3	g.chr8:100791009G>A	Missense Mutation	VPS13B	p.R2535Q	vacuolar protein sorting	119 (0.00)	46 (0.37)	0.99
11-01	Gp3	g.chr8:100830964C>G	Missense Mutation	VPS13B	p.I2848M	vacuolar protein sorting	36 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr8:100831088C>A	Missense Mutation	VPS13B	p.L2890I	vacuolar protein sorting	34 (0.00)	19 (0.37)	0.98
11-01	Gp3	g.chr15:62201307C>G	Silent	VPS13C	p.V2954V	vacuolar protein sorting	44 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr15:62211649C>T	Splice Site	VPS13C		vacuolar protein sorting	34 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr1:12331100A>T	Silent	VPS13D	p.R674R	vacuolar protein sorting	23 (0.00)	18 (0.33)	0.89
11-01	Gp3	g.chr1:12371651G>A	Missense Mutation	VPS13D	p.R2264Q	vacuolar protein sorting	123 (0.00)	66 (0.15)	0.40
11-01	Gp3	g.chr1:12405459C>T	Silent	VPS13D	p.L2972L	vacuolar protein sorting	84 (0.00)	51 (0.24)	0.63
11-01	Gp3	g.chr20:2845225G>T	Missense Mutation	VPS16	p.K617N	vacuolar protein sorting	180 (0.00)	100 (0.28)	0.75
11-01	Gp3	g.chr8:17143872G>T	Missense Mutation	VPS37A	p.R377I	vacuolar protein sorting	36 (0.00)	22 (0.32)	0.47
11-01	Gp3	g.chr16:69356582C>T	Silent	VPS4A	p.L397L	vacuolar protein sorting	15 (0.00)	12 (0.67)	1.78
11-01	Gp3	g.chr14:97321569G>T	Missense Mutation	VRK1	p.L195F	vaccinia related kinase	31 (0.00)	33 (0.18)	0.48
11-01	Gp3	g.chr19:50482398G>T	Missense Mutation	VRK3	p.L460M	vaccinia related kinase	45 (0.00)	30 (0.23)	0.62
11-01	Gp3	g.chrX:107301365G>A	Silent	VSIG1	p.V49V	V-set and immunoglobu	51 (0.00)	17 (0.35)	0.59
11-01	Gp3	g.chr12:118509249C>A	Silent	VSIG10	p.V415V	V-set and immunoglobu	64 (0.00)	28 (0.32)	0.86
11-01	Gp3	g.chr12:118520063C>A	Missense Mutation	VSIG10	p.G178V	V-set and immunoglobu	61 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr1:159828016G>T	Silent	VSIG8	p.R98R	V-set and immunoglobu	31 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr1:20680399G>T	Silent	VWA5B1	p.P1102P	von Willebrand factor A	16 (0.00)	26 (0.19)	0.51
11-01	Gp3	g.chr7:12409540G>T	Missense Mutation	VWDE	p.P798T	von Willebrand factor D	25 (0.00)	13 (0.46)	1.23
11-01	Gp3	g.chr7:12410064C>A	Missense Mutation	VWDE	p.C623F	von Willebrand factor D	44 (0.00)	49 (0.18)	0.49
11-01	Gp3	g.chr7:12410108G>A	Silent	VWDE	p.D608D	von Willebrand factor D	67 (0.00)	71 (0.18)	0.49
11-01	Gp3	g.chr7:12423194G>T	Missense Mutation	VWDE	p.S170Y	von Willebrand factor D	35 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr12:6128410G>A	Missense Mutation	VWF	p.R1392W	von Willebrand factor	22 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr12:6131119G>A	Silent	VWF	p.A1207A	von Willebrand factor	76 (0.00)	67 (0.24)	0.64
11-01	Gp3	g.chr12:6219591G>T	Missense Mutation	VWF	p.L161M	von Willebrand factor	92 (0.00)	41 (0.24)	0.65
11-01	Gp3	g.chr10:88211741C>T	Missense Mutation	WAPAL	p.V1033I	wings apart-like homol	31 (0.00)	14 (0.36)	0.49
11-01	Gp3	g.chr1:119683189G>A	Missense Mutation	WARS2	p.P27S	tryptophanyl tRNA synt	41 (0.00)	30 (0.17)	0.44
11-01	Gp3	g.chr2:74687364C>T	Silent	WBP1	p.F156F	WW domain binding pr	22 (0.00)	18 (0.50)	0.76
11-01	Gp3	g.chr18:30093567C>G	RNA	WBP11P1		WW domain binding pr	138 (0.00)	116 (0.15)	0.39
11-01	Gp3	g.chr4:85638132C>A	Missense Mutation	WDFY3	p.G2598C	WD repeat and FYVE d	147 (0.00)	74 (0.23)	0.61
11-01	Gp3	g.chr4:85752650G>T	Missense Mutation	WDFY3	p.L229M	WD repeat and FYVE d	83 (0.00)	48 (0.17)	0.44
11-01	Gp3	g.chr17:9515659C>G	Missense Mutation	WDR16	p.I296M	WD repeat domain 16	35 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:177071001C>T	Silent	WDR17	p.C647C	WD repeat domain 17	79 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr4:39233564G>A	Silent	WDR19	p.L710L	WD repeat domain 19	51 (0.00)	68 (0.29)	0.78
11-01	Gp3	g.chr14:102675474G>A	Missense Mutation	WDR20	p.D323N	WD repeat domain 20	82 (0.00)	31 (0.26)	0.69

11-01	Gp3	g.chr1:118475976G>A	Missense Mutation	WDR3	p.A12T	WD repeat domain 3	63 (0.02)	50 (0.36)	0.96
11-01	Gp3	g.chr17:80574448C>T	Missense Mutation	WDR45B	p.G294S	WD repeat domain 45B	16 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr9:137019614G>C	Missense Mutation	WDR5	p.V220L	WD repeat domain 5	72 (0.00)	88 (0.23)	0.61
11-01	Gp3	g.chr3:113049154G>A	Missense Mutation	WDR52	p.S1326L		58 (0.00)	54 (0.20)	0.54
11-01	Gp3	g.chr3:113146109C>T	Missense Mutation	WDR52	p.E60K		17 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr19:36550872G>A	Missense Mutation	WDR62	p.C91Y	WD repeat domain 62	32 (0.00)	52 (0.42)	1.13
11-01	Gp3	g.chr19:36584967C>G	Missense Mutation	WDR62	p.H790D	WD repeat domain 62	81 (0.01)	34 (0.15)	0.39
11-01	Gp3	g.chr1:85563273G>T	Missense Mutation	WDR63	p.A429S	WD repeat domain 63	30 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr1:241815852G>A	Silent	WDR64	p.L22L	WD repeat domain 64	126 (0.00)	53 (0.23)	0.60
11-01	Gp3	g.chr1:43689735G>T	Nonsense Mutation	WDR65	p.E909*		77 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr12:122399973G>A	Missense Mutation	WDR66	p.M799I	WD repeat domain 66	75 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr18:54444098C>A	Missense Mutation	WDR7	p.F978L	WD repeat domain 7	74 (0.00)	61 (0.39)	1.05
11-01	Gp3	g.chr18:54483360G>A	Missense Mutation	WDR7	p.D1097N	WD repeat domain 7	41 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr15:53957885C>T	Missense Mutation	WDR72	p.V626I	WD repeat domain 72	21 (0.00)	38 (0.16)	0.42
11-01	Gp3	g.chr1:67292626G>T	Missense Mutation	WDR78	p.P739Q	WD repeat domain 78	53 (0.02)	94 (0.33)	0.88
11-01	Gp3	g.chr19:38380134C>G	Missense Mutation	WDR87	p.A1354P	WD repeat domain 87	87 (0.00)	25 (0.64)	1.71
11-01	Gp3	g.chr19:38385359G>A	Silent	WDR87	p.Y289Y	WD repeat domain 87	44 (0.02)	29 (0.31)	0.83
11-01	Gp3	g.chr19:33647312C>G	Missense Mutation	WDR88	p.F287L	WD repeat domain 88	42 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr15:90272952C>G	Missense Mutation	WDR93	p.H388D	WD repeat domain 93	54 (0.00)	49 (0.16)	0.44
11-01	Gp3	g.chr4:6303230C>T	Missense Mutation	WFS1	p.L570F	Wolfram syndrome 1 (w	20 (0.00)	45 (0.20)	0.53
11-01	Gp3	g.chr17:38420851C>T	Silent	WIPF2	p.S141S	WAS/WASL interacting	77 (0.00)	57 (0.16)	0.42
11-01	Gp3	g.chr17:66426166G>A	Silent	WIPI1	p.S312S	WD repeat domain, pho	32 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr12:1005618C>G	Missense Mutation	WNK1	p.L1989V	WNK lysine deficient p	52 (0.02)	37 (0.30)	0.79
11-01	Gp3	g.chr12:995182G>A	Missense Mutation	WNK1	p.V1738I	WNK lysine deficient p	126 (0.00)	54 (0.19)	0.49
11-01	Gp3	g.chr2:219735790G>T	Missense Mutation	WNT6	p.C41F	wingless-type MMTV i	28 (0.00)	34 (0.15)	0.39
11-01	Gp3	g.chr17:25628959G>A	Silent	WSB1	p.P31P	WD repeat and SOCS b	53 (0.00)	49 (0.27)	0.71
11-01	Gp3	g.chr17:6014212C>A	Missense Mutation	WSCD1	p.F377L	WSC domain containing	65 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr16:69905713C>G	Missense Mutation	WWP2	p.H194Q	WW domain containing	27 (0.00)	36 (0.36)	0.96
11-01	Gp3	g.chr2:31572597C>G	Missense Mutation	XDH	p.S975T	xanthine dehydrogenase	90 (0.00)	62 (0.16)	0.43
11-01	Gp3	g.chr2:31572961C>T	Silent	XDH	p.G920G	xanthine dehydrogenase	81 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chr2:31572971C>T	Missense Mutation	XDH	p.G917E	xanthine dehydrogenase	77 (0.01)	38 (0.18)	0.49
11-01	Gp3	g.chr3:39230720C>T	Missense Mutation	XIRP1	p.V73M	xin actin-binding repeat	19 (0.00)	35 (0.20)	0.53
11-01	Gp3	g.chrX:73064680G>C	lincRNA	XIST		X inactive specific trans	31 (0.00)	19 (0.32)	0.53
11-01	Gp3	g.chrX:73066014G>A	lincRNA	XIST		X inactive specific trans	37 (0.00)	30 (0.23)	0.39
11-01	Gp3	g.chrX:100183023C>T	Missense Mutation	XKRX	p.D91N	XK, Kell blood group c	24 (0.00)	12 (0.42)	0.69

11-01	Gp3	g.chr3:14197916C>T	Missense Mutation	XPC	p.R651Q	xeroderma pigmentosun	80 (0.00)	51 (0.16)	0.42
11-01	Gp3	g.chr3:14214864C>T	Intron	XPC		xeroderma pigmentosun	85 (0.00)	75 (0.15)	0.39
11-01	Gp3	g.chr6:43499282G>A	Silent	XPO5	p.D825D	exportin 5	68 (0.01)	35 (0.14)	0.38
11-01	Gp3	g.chr16:28118864G>A	Missense Mutation	XPO6	p.P826S	exportin 6	69 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr8:21840249G>T	Missense Mutation	XPO7	p.M401I	exportin 7	67 (0.01)	28 (0.50)	0.75
11-01	Gp3	g.chr2:217069111G>A	Missense Mutation	XRCC5	p.D726N	X-ray repair complemer	61 (0.00)	23 (0.26)	0.70
11-01	Gp3	g.chr3:142145625G>T	Missense Mutation	XRN1	p.P123T	5'-3' exoribonuclease 1	58 (0.00)	50 (0.16)	0.43
11-01	Gp3	g.chr11:74570305A>G	Silent	XRRA1	p.P348P	X-ray radiation resistan	41 (0.00)	28 (0.54)	1.43
11-01	Gp3	g.chr1:33245738G>A	Missense Mutation	YARS	p.P428S	tyrosyl-tRNA synthetas	53 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr12:10856704G>C	Missense Mutation	YBX3	p.A275G	Y box binding protein 3	34 (0.00)	35 (0.14)	0.38
11-01	Gp3	g.chr14:75290958G>A	Splice Site	YLPM1		YLP motif containing 1	57 (0.00)	63 (0.17)	0.47
11-01	Gp3	g.chr1:155629480C>T	Missense Mutation	YY1AP1	p.D730N	YY1 associated protein	38 (0.00)	68 (0.24)	0.63
11-01	Gp3	g.chr1:155638432C>T	Missense Mutation	YY1AP1	p.D278N	YY1 associated protein	84 (0.00)	69 (0.16)	0.43
11-01	Gp3	g.chrX:21875451C>T	Silent	YY2	p.H283H	YY2 transcription facto	79 (0.00)	38 (0.24)	0.39
11-01	Gp3	g.chr7:100350479G>A	RNA	ZAN		zonadhesin (gene/pseud	86 (0.01)	28 (0.29)	0.76
11-01	Gp3	g.chr7:100350487C>T	RNA	ZAN		zonadhesin (gene/pseud	90 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr7:100350623C>T	RNA	ZAN		zonadhesin (gene/pseud	138 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr7:100385500C>T	RNA	ZAN		zonadhesin (gene/pseud	15 (0.07)	24 (0.29)	0.78
11-01	Gp3	g.chr1:244217175T>G	Missense Mutation	ZBTB18	p.C33W	zinc finger and BTB do	59 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr6:109803106T>A	Missense Mutation	ZBTB24	p.I42F	zinc finger and BTB do	51 (0.00)	18 (0.56)	0.86
11-01	Gp3	g.chr6:109803107T>A	Missense Mutation	ZBTB24	p.L41F	zinc finger and BTB do	51 (0.00)	18 (0.56)	0.86
11-01	Gp3	g.chr19:36205531G>A	Start Codon SNP	ZBTB32	p.M1I	zinc finger and BTB do	62 (0.02)	43 (0.19)	0.50
11-01	Gp3	g.chr19:36205548G>A	Missense Mutation	ZBTB32	p.R7K	zinc finger and BTB do	59 (0.00)	43 (0.19)	0.50
11-01	Gp3	g.chr9:129642044C>A	Nonsense Mutation	ZBTB34	p.C122*	zinc finger and BTB do	142 (0.01)	190 (0.22)	0.59
11-01	Gp3	g.chr1:173854915G>A	Missense Mutation	ZBTB37	p.D389N	zinc finger and BTB do	71 (0.00)	56 (0.14)	0.38
11-01	Gp3	g.chr1:22838327C>A	Missense Mutation	ZBTB40	p.Q721K	zinc finger and BTB do	49 (0.00)	17 (0.35)	0.94
11-01	Gp3	g.chr9:129594868G>A	Missense Mutation	ZBTB43	p.R27H	zinc finger and BTB do	58 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr6:144207284C>A	Missense Mutation	ZC2HC1B	p.S69Y	zinc finger, C2HC-type	41 (0.02)	39 (0.21)	0.55
11-01	Gp3	g.chr14:75538298C>A	Missense Mutation	ZC2HC1C	p.P341Q	zinc finger, C2HC-type	41 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr1:37941253G>T	Silent	ZC3H12A	p.V52V	zinc finger CCCH-type	19 (0.00)	35 (0.37)	0.99
11-01	Gp3	g.chrX:64722464C>T	Missense Mutation	ZC3H12B	p.P629L	zinc finger CCCH-type	43 (0.00)	32 (0.41)	0.68
11-01	Gp3	g.chr11:110036067G>T	Missense Mutation	ZC3H12C	p.D754Y	zinc finger CCCH-type	53 (0.00)	30 (0.53)	1.42
11-01	Gp3	g.chr6:149780766G>A	Missense Mutation	ZC3H12D	p.A165V	zinc finger CCCH-type	19 (0.00)	35 (0.37)	0.99
11-01	Gp3	g.chr14:89075613C>T	Missense Mutation	ZC3H14	p.A619V	zinc finger CCCH-type	29 (0.00)	24 (0.38)	1.00
11-01	Gp3	g.chr16:88688781C>T	Missense Mutation	ZC3H18	p.A551V	zinc finger CCCH-type	15 (0.00)	28 (0.18)	0.48

11-01	Gp3	g.chr8:144620691G>C	Silent	ZC3H3	p.P282P	zinc finger CCCH-type	29 (0.00)	33 (0.30)	0.81
11-01	Gp3	g.chr19:47588356C>G	Missense Mutation	ZC3H4	p.G355A	zinc finger CCCH-type	27 (0.00)	24 (0.67)	1.78
11-01	Gp3	g.chr2:113090034C>A	Missense Mutation	ZC3H6	p.T1180N	zinc finger CCCH-type	151 (0.00)	129 (0.23)	0.62
11-01	Gp3	g.chr8:17067949C>T	Nonsense Mutation	ZDHHC2	p.Q304*	zinc finger, DHHC-type	123 (0.00)	27 (0.30)	0.44
11-01	Gp3	g.chr3:113672575G>A	Missense Mutation	ZDHHC23	p.E64K	zinc finger, DHHC-type	62 (0.02)	20 (0.35)	0.93
11-01	Gp3	g.chr11:57466832G>A	Missense Mutation	ZDHHC5	p.A642T	zinc finger, DHHC-type	76 (0.00)	43 (0.40)	1.05
11-01	Gp3	g.chr2:145156482G>A	Missense Mutation	ZEB2	p.L758F	zinc finger E-box bindir	157 (0.00)	151 (0.43)	1.15
11-01	Gp3	g.chr2:145157056G>A	Silent	ZEB2	p.V566V	zinc finger E-box bindir	85 (0.00)	56 (0.18)	0.48
11-01	Gp3	g.chr6:38029552G>A	Splice Site	ZFAND3		zinc finger, AN1-type d	43 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr10:46111926C>T	Silent	ZFAND4	p.E714E	zinc finger, AN1-type d	50 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr12:72030810C>A	Silent	ZFC3H1	p.V585V	zinc finger, C3H1-type	59 (0.00)	48 (0.54)	1.44
11-01	Gp3	g.chr16:72821108C>A	Missense Mutation	ZFHX3	p.K3689N	zinc finger homeobox 3	67 (0.00)	54 (0.22)	0.59
11-01	Gp3	g.chr16:72829442G>T	Nonsense Mutation	ZFHX3	p.S2380*	zinc finger homeobox 3	51 (0.00)	31 (0.35)	0.95
11-01	Gp3	g.chr16:72829483C>T	Silent	ZFHX3	p.E2366E	zinc finger homeobox 3	105 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr16:72845849G>A	Silent	ZFHX3	p.L1206L	zinc finger homeobox 3	85 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr8:77616460C>A	Missense Mutation	ZFHX4	p.S46Y	zinc finger homeobox 4	55 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr8:77763698G>T	Missense Mutation	ZFHX4	p.G1514V	zinc finger homeobox 4	125 (0.00)	121 (0.17)	0.44
11-01	Gp3	g.chr8:77764307C>G	Missense Mutation	ZFHX4	p.A1717G	zinc finger homeobox 4	71 (0.00)	56 (0.77)	2.05
11-01	Gp3	g.chr19:36831906A>G	Silent	ZFP14	p.H274H	ZFP14 zinc finger prote	58 (0.00)	54 (0.26)	0.69
11-01	Gp3	g.chr11:58381770C>A	Silent	ZFP91	p.L352L	ZFP91 zinc finger prote	133 (0.00)	126 (0.14)	0.38
11-01	Gp3	g.chr8:106813343G>T	Missense Mutation	ZFPM2	p.D345Y	zinc finger protein, FOC	178 (0.00)	104 (0.28)	0.74
11-01	Gp3	g.chr5:32400212G>A	Missense Mutation	ZFR	p.P538L	zinc finger RNA bindin	72 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chrX:24229394C>T	Silent	ZFX	p.D773D	zinc finger protein, X-li	34 (0.00)	32 (0.56)	0.94
11-01	Gp3	g.chr14:73448496C>T	Splice Site	ZFYVE1		zinc finger, FYVE dom	66 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr14:73490835C>T	Missense Mutation	ZFYVE1	p.E128K	zinc finger, FYVE dom	42 (0.00)	34 (0.18)	0.47
11-01	Gp3	g.chr14:73490857C>G	Silent	ZFYVE1	p.V120V	zinc finger, FYVE dom	34 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr14:73490940G>A	Nonsense Mutation	ZFYVE1	p.Q93*	zinc finger, FYVE dom	68 (0.00)	42 (0.24)	0.63
11-01	Gp3	g.chr14:68268932G>T	Missense Mutation	ZFYVE26	p.F501L	zinc finger, FYVE dom	21 (0.00)	42 (0.14)	0.38
11-01	Gp3	g.chr1:52734147G>A	Missense Mutation	ZFYVE9	p.R823K	zinc finger, FYVE dom	34 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr1:52734234C>T	Missense Mutation	ZFYVE9	p.S852F	zinc finger, FYVE dom	40 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr8:124266526G>C	Missense Mutation	ZHX1	p.T554S	zinc fingers and homeo	64 (0.00)	52 (0.19)	0.51
11-01	Gp3	g.chr8:123965725G>A	Missense Mutation	ZHX2	p.D659N	zinc fingers and homeo	52 (0.00)	29 (0.28)	0.74
11-01	Gp3	g.chr20:39831429C>A	Nonsense Mutation	ZHX3	p.E710*	zinc fingers and homeo	61 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr20:39831430C>G	Silent	ZHX3	p.L709L	zinc fingers and homeo	60 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr3:147131308C>A	Silent	ZIC1	p.L438L	Zic family member 1	72 (0.00)	49 (0.16)	0.44

11-01	Gp3	g.chr16:25258127C>A	Nonsense Mutation	ZKSCAN2	p.E464*	zinc finger with KRAB	55 (0.00)	54 (0.48)	1.28
11-01	Gp3	g.chr3:44598952G>T	Missense Mutation	ZKSCAN7	p.G138V	zinc finger with KRAB	37 (0.00)	40 (0.17)	0.47
11-01	Gp3	g.chr1:40733511C>T	Silent	ZMPSTE24	p.F108F	zinc metallopeptidase S	113 (0.00)	117 (0.31)	0.82
11-01	Gp3	g.chr1:35579310A>G	Missense Mutation	ZMYM1	p.T627A	zinc finger, MYM-type	37 (0.00)	34 (0.21)	0.55
11-01	Gp3	g.chr13:20611050G>A	Splice Site	ZMYM2		zinc finger, MYM-type	16 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr20:45875140G>A	Silent	ZMYND8	p.N607N	zinc finger, MYND-typ	31 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr19:58131910C>G	Missense Mutation	ZNF134	p.F141L	zinc finger protein 134	19 (0.00)	22 (0.23)	0.61
11-01	Gp3	g.chr19:19825225C>T	Silent	ZNF14	p.Q25Q	zinc finger protein 14	72 (0.00)	35 (0.17)	0.46
11-01	Gp3	g.chr4:337681G>A	Silent	ZNF141	p.R38R	zinc finger protein 141	128 (0.00)	59 (0.44)	1.18
11-01	Gp3	g.chr2:219508755C>A	Silent	ZNF142	p.V828V	zinc finger protein 142	30 (0.00)	44 (0.27)	0.73
11-01	Gp3	g.chr2:219508989C>A	Missense Mutation	ZNF142	p.L750F	zinc finger protein 142	46 (0.00)	17 (0.47)	1.25
11-01	Gp3	g.chr2:219509561G>A	Silent	ZNF142	p.L560L	zinc finger protein 142	58 (0.00)	44 (0.16)	0.42
11-01	Gp3	g.chr3:124952685C>A	Silent	ZNF148	p.L295L	zinc finger protein 148	40 (0.00)	16 (0.44)	1.17
11-01	Gp3	g.chr8:146156272C>A	Missense Mutation	ZNF16	p.C634F	zinc finger protein 16	48 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr19:53572995C>T	Silent	ZNF160	p.K264K	zinc finger protein 160	41 (0.00)	12 (0.50)	1.33
11-01	Gp3	g.chr9:97062180G>T	Missense Mutation	ZNF169	p.G114C	zinc finger protein 169	37 (0.00)	38 (0.18)	0.49
11-01	Gp3	g.chr16:71509675C>T	Missense Mutation	ZNF19	p.E217K	zinc finger protein 19	58 (0.02)	22 (0.64)	1.70
11-01	Gp3	g.chr3:44673992G>T	Missense Mutation	ZNF197	p.V224L	zinc finger protein 197	53 (0.00)	38 (0.42)	1.12
11-01	Gp3	g.chr19:58152111A>G	Missense Mutation	ZNF211	p.E151G	zinc finger protein 211	17 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr19:58152134G>A	Missense Mutation	ZNF211	p.V159M	zinc finger protein 211	17 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr11:7022012A>G	Missense Mutation	ZNF214	p.V301A	zinc finger protein 214	87 (0.01)	42 (0.17)	0.44
11-01	Gp3	g.chr11:6953646G>A	Missense Mutation	ZNF215	p.R48H	zinc finger protein 215	25 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr19:44571170G>T	Nonsense Mutation	ZNF223	p.E507*	zinc finger protein 223	38 (0.00)	37 (0.19)	0.50
11-01	Gp3	g.chr19:44612258G>A	Missense Mutation	ZNF224	p.E649K	zinc finger protein 224	55 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr19:44622693G>A	Missense Mutation	ZNF225	p.M67I	zinc finger protein 225	71 (0.00)	21 (0.29)	0.76
11-01	Gp3	g.chr17:5009793C>A	Nonsense Mutation	ZNF232	p.E221*	zinc finger protein 232	25 (0.00)	40 (0.40)	1.07
11-01	Gp3	g.chr17:5012756G>T	Missense Mutation	ZNF232	p.P144H	zinc finger protein 232	115 (0.00)	51 (0.20)	0.52
11-01	Gp3	g.chr19:44792117C>G	Missense Mutation	ZNF235	p.E491Q	zinc finger protein 235	21 (0.00)	16 (0.31)	0.83
11-01	Gp3	g.chr10:44052373G>A	Silent	ZNF239	p.S385S	zinc finger protein 239	46 (0.00)	39 (0.15)	0.41
11-01	Gp3	g.chr16:89799811G>A	Missense Mutation	ZNF276	p.R424H	zinc finger protein 276	109 (0.01)	92 (0.18)	0.49
11-01	Gp3	g.chr22:22869292C>T	Silent	ZNF280A	p.Q221Q	zinc finger protein 280A	56 (0.00)	30 (0.27)	0.71
11-01	Gp3	g.chrX:129349905A>G	Silent	ZNF280C	p.H566H	zinc finger protein 280C	74 (0.00)	104 (0.38)	0.64
11-01	Gp3	g.chr1:200376360G>A	Missense Mutation	ZNF281	p.T825M	zinc finger protein 281	72 (0.01)	23 (0.35)	0.93
11-01	Gp3	g.chr6:43305709C>A	Missense Mutation	ZNF318	p.E2009D	zinc finger protein 318	52 (0.00)	41 (0.27)	0.72
11-01	Gp3	g.chr19:58639475C>A	Missense Mutation	ZNF329	p.D466Y	zinc finger protein 329	19 (0.00)	28 (0.18)	0.48

11-01	Gp3	g.chr19:58639734G>A	Silent	ZNF329	p.S379S	zinc finger protein 329	21 (0.00)	10 (0.70)	1.87
11-01	Gp3	g.chr19:58640814T>A	Silent	ZNF329	p.V19V	zinc finger protein 329	94 (0.00)	115 (0.21)	0.56
11-01	Gp3	g.chr20:44578487G>A	Silent	ZNF335	p.T1207T	zinc finger protein 335	32 (0.00)	37 (0.22)	0.58
11-01	Gp3	g.chr20:44592442C>T	Silent	ZNF335	p.E430E	zinc finger protein 335	72 (0.00)	85 (0.18)	0.47
11-01	Gp3	g.chr10:43088660G>A	Missense Mutation	ZNF33B	p.P580S	zinc finger protein 33B	38 (0.00)	19 (0.26)	0.70
11-01	Gp3	g.chr5:178139643G>A	Silent	ZNF354A	p.C412C	zinc finger protein 354A	45 (0.00)	8 (0.62)	1.67
11-01	Gp3	g.chr5:178140571G>C	Nonsense Mutation	ZNF354A	p.S103*	zinc finger protein 354A	27 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr10:43019155C>T	RNA	ZNF37BP		zinc finger protein 37B,	45 (0.00)	31 (0.39)	1.03
11-01	Gp3	g.chr2:180634229C>A	Splice Site	ZNF385B		zinc finger protein 385B	38 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr3:21792394C>T	Missense Mutation	ZNF385D	p.M5I	zinc finger protein 385D	54 (0.00)	50 (0.20)	0.53
11-01	Gp3	g.chr18:72343595C>T	Missense Mutation	ZNF407	p.S207F	zinc finger protein 407	211 (0.00)	166 (0.21)	0.56
11-01	Gp3	g.chr19:9639620C>T	Silent	ZNF426	p.K329K	zinc finger protein 426	17 (0.00)	35 (0.29)	0.76
11-01	Gp3	g.chr19:21366341C>G	Missense Mutation	ZNF431	p.S412C	zinc finger protein 431	28 (0.00)	20 (0.45)	1.20
11-01	Gp3	g.chr19:21366517C>A	Missense Mutation	ZNF431	p.L471I	zinc finger protein 431	23 (0.00)	27 (0.48)	1.28
11-01	Gp3	g.chr19:12129080C>A	Missense Mutation	ZNF433	p.V14L	zinc finger protein 433	28 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr10:31134018G>A	Missense Mutation	ZNF438	p.R787W	zinc finger protein 438	30 (0.00)	19 (0.53)	1.40
11-01	Gp3	g.chr10:31134132C>G	Missense Mutation	ZNF438	p.G749R	zinc finger protein 438	34 (0.00)	9 (0.56)	1.48
11-01	Gp3	g.chr19:37149263G>C	Missense Mutation	ZNF461	p.P25R	zinc finger protein 461	116 (0.00)	95 (0.29)	0.79
11-01	Gp3	g.chr19:57088944C>G	Missense Mutation	ZNF470	p.L383V	zinc finger protein 470	90 (0.00)	33 (0.15)	0.40
11-01	Gp3	g.chr19:11917692C>T	Silent	ZNF491	p.F308F	zinc finger protein 491	23 (0.00)	18 (0.39)	1.04
11-01	Gp3	g.chr19:22836802G>A	Missense Mutation	ZNF492	p.V39I	zinc finger protein 492	59 (0.00)	22 (0.32)	0.85
11-01	Gp3	g.chr9:99521949G>T	Missense Mutation	ZNF510	p.T388K	zinc finger protein 510	115 (0.00)	60 (0.17)	0.44
11-01	Gp3	g.chr4:10447024T>C	Missense Mutation	ZNF518B	p.N310S	zinc finger protein 518B	81 (0.00)	23 (0.22)	0.58
11-01	Gp3	g.chr4:10447849G>A	Missense Mutation	ZNF518B	p.P35L	zinc finger protein 518B	180 (0.01)	90 (0.24)	0.65
11-01	Gp3	g.chr19:42728595C>A	Missense Mutation	ZNF526	p.Q14K	zinc finger protein 526	19 (0.00)	23 (0.43)	1.16
11-01	Gp3	g.chr19:57888677G>A	Silent	ZNF547	p.E111E	zinc finger protein 547	40 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr19:58042464G>A	Silent	ZNF549	p.V20V	zinc finger protein 549	33 (0.00)	19 (0.42)	1.12
11-01	Gp3	g.chr19:8922196C>A	Nonsense Mutation	ZNF558	p.E324*	zinc finger protein 558	44 (0.00)	19 (0.32)	0.84
11-01	Gp3	g.chr19:37488178C>A	Missense Mutation	ZNF568	p.H465N	zinc finger protein 568	70 (0.00)	24 (0.33)	0.89
11-01	Gp3	g.chr19:37975011C>G	Missense Mutation	ZNF570	p.Q163E	zinc finger protein 570	176 (0.00)	181 (0.18)	0.47
11-01	Gp3	g.chr19:53014121C>A	Missense Mutation	ZNF578	p.H163N	zinc finger protein 578	103 (0.00)	120 (0.48)	1.29
11-01	Gp3	g.chr17:5085912T>A	Missense Mutation	ZNF594	p.K547I	zinc finger protein 594	93 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr19:35250239G>T	Nonsense Mutation	ZNF599	p.Y489*	zinc finger protein 599	29 (0.00)	25 (0.20)	0.53
11-01	Gp3	g.chr19:58489761G>A	Missense Mutation	ZNF606	p.R763C	zinc finger protein 606	48 (0.00)	25 (0.24)	0.64
11-01	Gp3	g.chr15:64967927C>T	Silent	ZNF609	p.P958P	zinc finger protein 609	53 (0.00)	73 (0.30)	0.80

11-01	Gp3	g.chr19:53210013C>T	Missense Mutation	ZNF611	p.G99R	zinc finger protein 611	143 (0.00)	71 (0.20)	0.53
11-01	Gp3	g.chr19:52443528G>A	Missense Mutation	ZNF613	p.A28T	zinc finger protein 613	45 (0.00)	40 (0.15)	0.40
11-01	Gp3	g.chr9:116795008G>A	Splice Site	ZNF618	p.E390K	zinc finger protein 618	103 (0.01)	36 (0.19)	0.52
11-01	Gp3	g.chr3:40558247G>A	Missense Mutation	ZNF620	p.G274S	zinc finger protein 620	28 (0.00)	31 (0.35)	0.95
11-01	Gp3	g.chr19:20807811C>G	Missense Mutation	ZNF626	p.G291A	zinc finger protein 626	82 (0.00)	46 (0.15)	0.41
11-01	Gp3	g.chr17:47395033C>A	Missense Mutation	ZNF652	p.V19L	zinc finger protein 652	22 (0.00)	43 (0.16)	0.43
11-01	Gp3	g.chr3:88189985C>A	Missense Mutation	ZNF654	p.L509I	zinc finger protein 654	43 (0.00)	30 (0.30)	0.80
11-01	Gp3	g.chr9:40774125C>A	Missense Mutation	ZNF658	p.D384Y	zinc finger protein 658	128 (0.00)	163 (0.19)	0.51
11-01	Gp3	g.chr3:42950294C>A	Missense Mutation	ZNF662	p.P75Q	zinc finger protein 662	82 (0.00)	48 (0.31)	0.83
11-01	Gp3	g.chr1:247265351G>A	Missense Mutation	ZNF669	p.S109F	zinc finger protein 669	54 (0.00)	38 (0.21)	0.44
11-01	Gp3	g.chr19:53740505C>T	Missense Mutation	ZNF677	p.C492Y	zinc finger protein 677	27 (0.00)	21 (0.24)	0.63
11-01	Gp3	g.chr19:53747003C>T	Missense Mutation	ZNF677	p.E55K	zinc finger protein 677	55 (0.00)	25 (0.28)	0.75
11-01	Gp3	g.chr19:20117036G>A	Silent	ZNF682	p.Y425Y	zinc finger protein 682	18 (0.00)	18 (0.28)	0.74
11-01	Gp3	g.chr1:247163257G>C	Missense Mutation	ZNF695	p.I41M	zinc finger protein 695	57 (0.00)	15 (0.33)	0.70
11-01	Gp3	g.chr19:9407226C>T	Missense Mutation	ZNF699	p.G285E	zinc finger protein 699	70 (0.00)	39 (0.23)	0.62
11-01	Gp3	g.chr19:12058046G>A	Nonsense Mutation	ZNF700	p.W38*	zinc finger protein 700	69 (0.00)	26 (0.23)	0.62
11-01	Gp3	g.chr19:12059243G>A	Missense Mutation	ZNF700	p.G135D	zinc finger protein 700	97 (0.01)	74 (0.24)	0.65
11-01	Gp3	g.chr8:81555339C>G	Missense Mutation	ZNF704	p.G353A	zinc finger protein 704	17 (0.00)	31 (0.29)	0.97
11-01	Gp3	g.chr19:23159109C>T	Missense Mutation	ZNF728	p.E344K	zinc finger protein 728	19 (0.00)	26 (0.54)	1.44
11-01	Gp3	g.chr6:35258148C>A	Missense Mutation	ZNF76	p.H180N	zinc finger protein 76	102 (0.00)	70 (0.23)	0.61
11-01	Gp3	g.chr19:53958558G>A	RNA	ZNF761		zinc finger protein 761	142 (0.00)	77 (0.14)	0.38
11-01	Gp3	g.chr19:52794368C>T	Missense Mutation	ZNF766	p.H442Y	zinc finger protein 766	74 (0.00)	63 (0.14)	0.38
11-01	Gp3	g.chr19:2934646C>A	Missense Mutation	ZNF77	p.G160V	zinc finger protein 77	49 (0.00)	76 (0.21)	0.56
11-01	Gp3	g.chr19:40541408G>A	Missense Mutation	ZNF780B	p.A305V	zinc finger protein 780B	62 (0.00)	15 (0.47)	1.24
11-01	Gp3	g.chr9:130197465C>T	Missense Mutation	ZNF79	p.P68S	zinc finger protein 79	42 (0.00)	42 (0.17)	0.44
11-01	Gp3	g.chr19:58806238C>A	Missense Mutation	ZNF8	p.S355Y	zinc finger protein 8	55 (0.00)	27 (0.22)	0.59
11-01	Gp3	g.chr19:53056552C>A	Missense Mutation	ZNF808	p.P128H	zinc finger protein 808	200 (0.00)	205 (0.26)	0.70
11-01	Gp3	g.chr19:53994910C>G	Missense Mutation	ZNF813	p.T475R	zinc finger protein 813	41 (0.00)	31 (0.26)	0.69
11-01	Gp3	g.chr19:58386094G>C	Missense Mutation	ZNF814	p.H222D	zinc finger protein 814	54 (0.00)	31 (0.19)	0.52
11-01	Gp3	g.chr19:11833700C>A	Nonsense Mutation	ZNF823	p.E217*	zinc finger protein 823	93 (0.00)	47 (0.26)	0.68
11-01	Gp3	g.chr19:11833745C>A	Missense Mutation	ZNF823	p.V202F	zinc finger protein 823	66 (0.00)	32 (0.38)	1.00
11-01	Gp3	g.chr19:20607666G>T	RNA	ZNF826P		zinc finger protein 826,	50 (0.00)	29 (0.21)	0.55
11-01	Gp3	g.chr19:37405911C>T	Missense Mutation	ZNF829	p.E18K	zinc finger protein 829	28 (0.04)	18 (0.33)	0.89
11-01	Gp3	g.chr7:149544896C>T	Missense Mutation	ZNF862	p.P105L	zinc finger protein 862	71 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr19:52877648G>A	Missense Mutation	ZNF880	p.G79D	zinc finger protein 880	69 (0.01)	29 (0.52)	1.38

11-01	Gp3	g.chr19:20215064G>A	Missense Mutation	ZNF90	p.R7K	zinc finger protein 90	43 (0.00)	11 (0.55)	1.45
11-01	Gp3	g.chr19:20229204G>T	Nonsense Mutation	ZNF90	p.G281*	zinc finger protein 90	74 (0.01)	80 (0.45)	1.20
11-01	Gp3	g.chr16:21222846C>A	Missense Mutation	ZP2	p.G8V	zona pellucida glycopro	18 (0.00)	24 (0.21)	0.56
11-01	Gp3	g.chr7:76062873G>A	Missense Mutation	ZP3	p.V208M	zona pellucida glycopro	26 (0.00)	17 (0.29)	0.78
11-01	Gp3	g.chr7:76062947C>G	Silent	ZP3	p.T232T	zona pellucida glycopro	29 (0.00)	22 (0.77)	2.06
11-01	Gp3	g.chr6:28365808C>T	Silent	ZSCAN12	p.E125E	zinc finger and SCAN d	109 (0.00)	46 (0.20)	0.52
11-01	Gp3	g.chr7:99655333C>T	Missense Mutation	ZSCAN21	p.P138S	zinc finger and SCAN d	52 (0.00)	32 (0.19)	0.50
11-01	Gp3	g.chr6:28403261C>A	Nonsense Mutation	ZSCAN23	p.E178*	zinc finger and SCAN d	63 (0.00)	31 (0.16)	0.43
11-01	Gp3	g.chr19:58189825C>T	Missense Mutation	ZSCAN4	p.S285F	zinc finger and SCAN d	67 (0.00)	43 (0.26)	0.68
11-01	Gp3	g.chr2:187694526G>T	Silent	ZSWIM2	p.G341G	zinc finger, SWIM-type	44 (0.00)	32 (0.16)	0.42
11-01	Gp3	g.chr1:45553766G>A	Missense Mutation	ZSWIM5	p.H247Y	zinc finger, SWIM-type	42 (0.00)	63 (0.16)	0.42
11-01	Gp3	g.chr6:116987961C>T	Missense Mutation	ZUFSP	p.S132N	zinc finger with UFM1-	78 (0.01)	21 (0.52)	0.81
11-01	Gp3	g.chr11:113614565G>T	Silent	ZW10	p.A490A	zw10 kinetochore protei	61 (0.00)	29 (0.17)	0.46
11-01	Gp3	g.chr1:53279323G>A	Missense Mutation	ZYG11B	p.G604E	zyg-11 family member I	42 (0.00)	36 (0.25)	0.67
11-01	Gp3	g.chr17:3984700C>A	Missense Mutation	ZZEF1	p.M933I	zinc finger, ZZ-type wit	78 (0.01)	41 (0.44)	1.17
11-01	Gp3	g.chr17:4007959G>A	Missense Mutation	ZZEF1	p.A514V	zinc finger, ZZ-type wit	32 (0.00)	34 (0.24)	0.63
11-01	Gp4	g.chr13:95839106C>A	Missense Mutation	ABCC4	p.S465I	ATP-binding cassette, s	15 (0.00)	35 (0.14)	0.38
11-01	Gp4	g.chr12:109629418G>A	Splice Site	ACACB	p.S715S	acetyl-CoA carboxylase	19 (0.00)	39 (0.13)	0.46
11-01	Gp4	g.chr1:26669305G>T	Silent	AIM1L	p.L174L	absent in melanoma 1-li	17 (0.00)	34 (0.15)	0.39
11-01	Gp4	g.chr15:83346037C>T	Missense Mutation	AP3B2	p.D461N	adaptor-related protein c	55 (0.00)	65 (0.15)	0.41
11-01	Gp4	g.chr19:36362848G>T	Missense Mutation	APLP1	p.D254Y	amyloid beta (A4) precu	20 (0.00)	49 (0.16)	0.44
11-01	Gp4	g.chr22:39441146C>T	Silent	APOBEC3F	p.Y124Y	apolipoprotein B mRNA	24 (0.00)	35 (0.14)	0.38
11-01	Gp4	g.chr5:148997780C>T	Missense Mutation	ARHGEF37	p.R234W	Rho guanine nucleotide	23 (0.00)	55 (0.15)	0.39
11-01	Gp4	g.chr1:150807109G>A	Silent	ARNT	p.I236I	aryl hydrocarbon recept	26 (0.00)	23 (0.26)	0.70
11-01	Gp4	g.chr12:32481295A>C	Missense Mutation	BICD1	p.I636L	bicaudal D homolog 1 (	50 (0.00)	86 (0.33)	0.87
11-01	Gp4	g.chr3:53806865C>G	Silent	CACNA1D	p.L1335L	calcium channel, voltag	34 (0.00)	36 (0.17)	0.44
11-01	Gp4	g.chr16:83712004G>A	Silent	CDH13	p.V539V	cadherin 13	40 (0.00)	40 (0.15)	0.40
11-01	Gp4	g.chr16:66413370C>T	Missense Mutation	CDH5	p.R44C	cadherin 5, type 2 (vasc	39 (0.00)	49 (0.24)	0.65
11-01	Gp4	g.chr3:74411045C>A	Nonsense Mutation	CNTN3	p.E454*	contactin 3 (plasmacyto	29 (0.00)	42 (0.14)	0.38
11-01	Gp4	g.chr1:34002670G>A	Silent	CSMD2	p.D3277D	CUB and Sushi multiple	19 (0.00)	27 (0.19)	0.49
11-01	Gp4	g.chr10:53457519C>T	Silent	CSTF2T	p.E597E	cleavage stimulation fac	17 (0.00)	21 (0.24)	0.63
11-01	Gp4	g.chr18:1768925G>T	lincRNA	CTD-2015H3.2			17 (0.00)	21 (0.24)	0.63
11-01	Gp4	g.chr19:15739436G>A	RNA	CYP4F8		cytochrome P450, famil	20 (0.00)	37 (0.16)	0.43
11-01	Gp4	g.chr6:39856524G>A	Silent	DAAM2	p.K710K	dishevelled associated a	22 (0.00)	34 (0.15)	0.39
11-01	Gp4	g.chr8:88885877G>A	Missense Mutation	DCAF4L2	p.T108M	DDB1 and CUL4 associ	96 (0.01)	140 (0.20)	0.72

11-01	Gp4	g.chr3:52404493G>A	Splice Site	DNAH1	p.G2087S	dynein, axonemal, heav	28 (0.00)	39 (0.21)	0.55
11-01	Gp4	g.chr6:38702324G>A	Missense Mutation	DNAH8	p.D12N	dynein, axonemal, heav	16 (0.00)	27 (0.19)	0.49
11-01	Gp4	g.chr17:41852181G>C	Missense Mutation	DUSP3	p.T84R	dual specificity phospha	21 (0.00)	30 (0.17)	0.44
11-01	Gp4	g.chr16:23711912C>T	Silent	ERN2	p.Q439Q	endoplasmic reticulum t	30 (0.00)	31 (0.16)	0.43
11-01	Gp4	g.chr11:108384306C>T	Missense Mutation	EXPH5	p.S643N	exophilin 5	21 (0.00)	27 (0.19)	0.49
11-01	Gp4	g.chr19:8181642C>T	Missense Mutation	FBN3	p.G1210S	fibrillin 3	27 (0.04)	23 (0.26)	0.70
11-01	Gp4	g.chr20:6075611G>A	Missense Mutation	FERMT1	p.L372F	fermitin family member	17 (0.00)	28 (0.21)	0.57
11-01	Gp4	g.chr7:121942866C>T	Silent	FEZF1	p.G352G	FEZ family zinc finger	16 (0.00)	19 (0.37)	0.98
11-01	Gp4	g.chr15:44211694G>A	Missense Mutation	FRMD5	p.P98S	FERM domain containi	27 (0.00)	43 (0.23)	0.62
11-01	Gp4	g.chr13:99907461C>T	Silent	GPR18	p.L222L	G protein-coupled recep	20 (0.00)	26 (0.23)	0.62
11-01	Gp4	g.chr13:99907462A>T	Missense Mutation	GPR18	p.L222Q	G protein-coupled recep	19 (0.00)	26 (0.23)	0.62
11-01	Gp4	g.chr13:99907463G>T	Missense Mutation	GPR18	p.L222M	G protein-coupled recep	19 (0.00)	26 (0.23)	0.62
11-01	Gp4	g.chr1:110201702A>T	Silent	GSTM4	p.P179P	glutathione S-transferas	90 (0.00)	38 (0.18)	0.49
11-01	Gp4	g.chr7:18555990G>A	Intron	HDAC9		histone deacetylase 9	30 (0.03)	41 (0.15)	0.39
11-01	Gp4	g.chr12:112669383G>A	Missense Mutation	HECTD4	p.S1899F	HECT domain containi	40 (0.00)	91 (0.11)	0.40
11-01	Gp4	g.chr6:52906014G>A	Silent	ICK	p.I7I	intestinal cell (MAK-lik	31 (0.00)	32 (0.16)	0.42
11-01	Gp4	g.chr3:185410538G>C	Missense Mutation	IGF2BP2	p.T118R	insulin-like growth fact	28 (0.00)	37 (0.19)	0.50
11-01	Gp4	g.chr17:39458232G>A	Missense Mutation	KRTAP29-1	p.T291I	keratin associated protei	40 (0.00)	48 (0.15)	0.39
11-01	Gp4	g.chr6:129687459C>G	Missense Mutation	LAMA2	p.P1605A	laminin, alpha 2	44 (0.00)	51 (0.16)	0.42
11-01	Gp4	g.chr19:54849792G>A	Missense Mutation	LILRA4	p.S77F	leukocyte immunoglobu	51 (0.00)	35 (0.14)	0.38
11-01	Gp4	g.chr10:72136265C>A	Missense Mutation	LRRC20	p.V9L	leucine rich repeat conta	22 (0.00)	35 (0.14)	0.38
11-01	Gp4	g.chr17:17891346C>T	Silent	LRRC48	p.S126S	leucine rich repeat conta	18 (0.00)	17 (0.76)	0.91
11-01	Gp4	g.chr1:39901387G>A	Missense Mutation	MACF1	p.R5877H	microtubule-actin crossl	66 (0.00)	84 (0.18)	0.48
11-01	Gp4	g.chr7:78062752G>T	Intron	MAGI2		membrane associated gu	22 (0.00)	33 (0.15)	0.40
11-01	Gp4	g.chr7:78535825C>A	Intron	MAGI2		membrane associated gu	40 (0.00)	38 (0.16)	0.42
11-01	Gp4	g.chr7:78765854G>T	Intron	MAGI2		membrane associated gu	51 (0.02)	62 (0.47)	1.25
11-01	Gp4	g.chr9:72724707C>T	Silent	MAMDC2	p.T164T	MAM domain containin	110 (0.01)	101 (0.24)	0.84
11-01	Gp4	g.chr5:71491739G>T	Missense Mutation	MAP1B	p.D853Y	microtubule-associated	143 (0.01)	146 (0.32)	0.84
11-01	Gp4	g.chr15:90321352C>A	Silent	MESP2	p.P327P	mesoderm posterior bas	16 (0.00)	29 (0.17)	0.46
11-01	Gp4	g.chr16:14354909C>T	Missense Mutation	MKL2	p.P920S	MKL/myocardin-like 2	39 (0.03)	63 (0.14)	0.38
11-01	Gp4	g.chr19:9060673C>T	Missense Mutation	MUC16	p.A8925T	mucin 16, cell surface a	33 (0.00)	37 (0.16)	0.43
11-01	Gp4	g.chr1:24424468C>T	Silent	MYOM3	p.V230V	myomesin 3	29 (0.00)	31 (0.16)	0.43
11-01	Gp4	g.chr4:120072127G>A	Silent	MYOZ2	p.K59K	myozenin 2	17 (0.00)	23 (0.26)	0.70
11-01	Gp4	g.chr1:198231738G>T	Missense Mutation	NEK7	p.D78Y	NIMA-related kinase 7	47 (0.00)	35 (0.20)	0.53
11-01	Gp4	g.chr7:139726085G>A	Silent	PARP12	p.H564H	poly (ADP-ribose) poly	25 (0.00)	35 (0.14)	0.38

11-01	Gp4	g.chr6:137193355C>A	Missense Mutation	PEX7	p.S256Y	peroxisomal biogenesis	85 (0.00)	54 (0.22)	0.59
11-01	Gp4	g.chr18:10784822G>A	Missense Mutation	PIEZO2	p.L818F	piezo-type mechanosens	24 (0.00)	49 (0.18)	0.49
11-01	Gp4	g.chr10:3185635T>A	Missense Mutation	PITRM1	p.N864I	pitrilysin metallopeptid	19 (0.00)	30 (0.20)	0.53
11-01	Gp4	g.chr3:17052154C>T	Missense Mutation	PLCL2	p.S313L	phospholipase C-like 2	56 (0.00)	83 (0.14)	0.39
11-01	Gp4	g.chr1:12012679G>C	Splice Site	PLOD1		procollagen-lysine, 2-ox	26 (0.00)	23 (0.22)	0.58
11-01	Gp4	g.chr1:40557836C>G	Missense Mutation	PPT1	p.E81D	palmitoyl-protein thioes	42 (0.00)	37 (0.16)	0.43
11-01	Gp4	g.chr4:148591837C>A	Silent	PRMT10	p.V267V		29 (0.00)	35 (0.20)	0.53
11-01	Gp4	g.chr10:89692079G>T	Intron	PTEN		phosphatase and tensin	116 (0.00)	11 (0.55)	0.59
11-01	Gp4	g.chr22:36205898G>A	Missense Mutation	RBFOX2	p.L131F	RNA binding protein, f	30 (0.00)	48 (0.19)	0.50
11-01	Gp4	g.chr22:24036099G>T	Missense Mutation	RGL4	p.D148Y	ral guanine nucleotide d	22 (0.00)	35 (0.14)	0.38
11-01	Gp4	g.chr19:49502617G>A	Silent	RUVBL2	p.R18R	RuvB-like AAA ATPas	23 (0.00)	43 (0.19)	0.50
11-01	Gp4	g.chr7:45767903C>A	RNA	SEPT7P2		septin 7 pseudogene 2	32 (0.00)	36 (0.22)	0.59
11-01	Gp4	g.chr4:128688375G>A	Splice Site	SLC25A31	p.K211K	solute carrier family 25	26 (0.00)	37 (0.16)	0.43
11-01	Gp4	g.chr16:24895379G>T	Silent	SLC5A11	p.L197L	solute carrier family 5 (	27 (0.00)	50 (0.16)	0.43
11-01	Gp4	g.chr2:220466001C>T	Missense Mutation	STK11IP	p.P36S	serine/threonine kinase	20 (0.00)	28 (0.18)	0.48
11-01	Gp4	g.chrX:9673141T>A	Missense Mutation	TBL1X	p.F357Y	transducin (beta)-like 1	19 (0.00)	34 (0.29)	0.49
11-01	Gp4	g.chr1:155170314G>A	Missense Mutation	THBS3	p.P546S	thrombospondin 3	22 (0.00)	29 (0.24)	0.64
11-01	Gp4	g.chr14:24661933A>T	Missense Mutation	TM9SF1	p.D505E	transmembrane 9 superf	37 (0.00)	34 (0.15)	0.39
11-01	Gp4	g.chr17:3446767C>T	Splice Site	TRPV3		transient receptor potent	45 (0.00)	71 (0.21)	0.56
11-01	Gp4	g.chr11:5529969C>A	Missense Mutation	UBQLN3	p.G274C	ubiquilin 3	49 (0.00)	31 (0.16)	0.43
11-01	Gp4	g.chr3:183474459G>C	Missense Mutation	YEATS2	p.A512P	YEATS domain contain	63 (0.00)	74 (0.18)	0.47
11-01	Gp4	g.chr18:74587550G>A	Missense Mutation	ZNF236	p.C255Y	zinc finger protein 236	18 (0.00)	27 (0.19)	0.49
11-01	Gp4	g.chr19:21558102C>A	Missense Mutation	ZNF738	p.D53E	zinc finger protein 738	19 (0.00)	51 (0.16)	0.42
11-02	Gp3	g.chr9:107547909C>G	Missense Mutation	ABCA1	p.G2138A	ATP-binding cassette, s	25 (0.00)	36 (0.19)	0.52
11-02	Gp3	g.chr9:107549241C>T	Missense Mutation	ABCA1	p.G2074D	ATP-binding cassette, s	23 (0.00)	21 (0.29)	0.76
11-02	Gp3	g.chr16:2373655C>A	Missense Mutation	ABCA3	p.R161I	ATP-binding cassette, s	73 (0.00)	40 (0.25)	0.67
11-02	Gp3	g.chr3:15176037G>T	RNA	AC090954.1			101 (0.00)	42 (0.19)	0.51
11-02	Gp3	g.chr12:112153761G>A	Silent	ACAD10	p.E329E	acyl-CoA dehydrogenas	69 (0.01)	91 (0.22)	0.59
11-02	Gp3	g.chr4:8394119G>T	Missense Mutation	ACOX3	p.T414N	acyl-CoA oxidase 3, pri	25 (0.00)	57 (0.18)	0.47
11-02	Gp3	g.chr3:179294061C>G	Missense Mutation	ACTL6A	p.T178S	actin-like 6A	26 (0.00)	24 (0.21)	0.56
11-02	Gp3	g.chr4:100235236G>A	Silent	ADH1B	p.V190V	alcohol dehydrogenase	23 (0.00)	31 (0.16)	0.43
11-02	Gp3	g.chr2:100194797G>A	Silent	AFF3	p.F970F	AF4/FMR2 family, me	41 (0.00)	45 (0.18)	0.47
11-02	Gp3	g.chr11:62295179G>A	Missense Mutation	AHNAK	p.P2237L	AHNAK nucleoprotein	35 (0.00)	58 (0.31)	0.83
11-02	Gp3	g.chr18:14183647G>A	RNA	ANKRD20A5P		ankyrin repeat domain 2	76 (0.00)	52 (0.21)	0.56
11-02	Gp3	g.chr12:99223032G>T	Missense Mutation	ANKS1B	p.Q996K	ankyrin repeat and steril	35 (0.00)	23 (0.22)	0.58

11-02	Gp3	g.chr16:71807237G>A	Nonsense Mutation	AP1G1	p.Q119*	adaptor-related protein c	18 (0.00)	43 (0.28)	0.74
11-02	Gp3	g.chr20:47648602C>A	Missense Mutation	ARFGEF2	p.L1694I	ADP-ribosylation factor	53 (0.00)	48 (0.17)	0.44
11-02	Gp3	g.chr10:99003832G>T	Missense Mutation	ARHGAP19	p.P360T	Rho GTPase activating	21 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr14:32561810G>A	Silent	ARHGAP5	p.L645L	Rho GTPase activating	47 (0.00)	39 (0.15)	0.41
11-02	Gp3	g.chr12:46231417C>T	Silent	ARID2	p.L419L	AT rich interactive dom	43 (0.02)	28 (0.18)	0.48
11-02	Gp3	g.chr1:197061161C>A	Missense Mutation	ASPM	p.R3107L	asp (abnormal spindle)	22 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr1:197061162G>A	Nonsense Mutation	ASPM	p.R3107*	asp (abnormal spindle)	22 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr9:133346888C>A	Missense Mutation	ASS1	p.L195M	argininosuccinate synth	18 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr3:11340199C>T	Silent	ATG7	p.L10L	autophagy related 7	38 (0.00)	57 (0.16)	0.42
11-02	Gp3	g.chr13:113512162C>T	Missense Mutation	ATP11A	p.H817Y	ATPase, class VI, type	32 (0.00)	31 (0.19)	0.52
11-02	Gp3	g.chr3:194151847C>T	Missense Mutation	ATP13A3	p.D844N	ATPase type 13A3	37 (0.00)	29 (0.21)	0.55
11-02	Gp3	g.chr1:160091037C>A	Missense Mutation	ATP1A2	p.S58Y	ATPase, Na+/K+ transp	57 (0.00)	49 (0.14)	0.38
11-02	Gp3	g.chr8:104078555C>T	Silent	ATP6V1C1	p.G311G	ATPase, H+ transportin	39 (0.00)	39 (0.15)	0.41
11-02	Gp3	g.chr16:31122010C>A	Splice Site	BCKDK	p.P215H	branched chain ketoacid	21 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr17:41202363T>C	Intron	BRCA1		breast cancer 1, early on	32 (0.00)	31 (0.16)	0.43
11-02	Gp3	g.chr17:41242830C>G	Intron	BRCA1		breast cancer 1, early on	25 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr11:82645323C>A	Silent	C11orf82	p.G981G		42 (0.00)	25 (0.20)	0.53
11-02	Gp3	g.chr15:40628976G>A	Missense Mutation	C15orf52	p.L305F	chromosome 15 open re	18 (0.00)	31 (0.16)	0.43
11-02	Gp3	g.chr9:117400911G>A	Missense Mutation	C9orf91	p.E252K	chromosome 9 open rea	24 (0.00)	63 (0.16)	0.42
11-02	Gp3	g.chr3:50471752C>T	Missense Mutation	CACNA2D2	p.A133T	calcium channel, voltag	30 (0.00)	56 (0.14)	0.38
11-02	Gp3	g.chr3:85064050G>A	Intron	CADM2		cell adhesion molecule	54 (0.00)	63 (0.25)	0.68
11-02	Gp3	g.chr3:85201524C>T	Intron	CADM2		cell adhesion molecule	69 (0.00)	24 (0.21)	0.56
11-02	Gp3	g.chr3:85201583G>A	Intron	CADM2		cell adhesion molecule	49 (0.00)	21 (0.29)	0.76
11-02	Gp3	g.chr3:85434353G>A	Intron	CADM2		cell adhesion molecule	24 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr3:86026961G>T	Intron	CADM2		cell adhesion molecule	40 (0.00)	30 (0.17)	0.44
11-02	Gp3	g.chr7:134635213C>A	Nonsense Mutation	CALD1	p.S628*	caldesmon 1	39 (0.00)	31 (0.16)	0.43
11-02	Gp3	g.chr17:38324611C>A	Missense Mutation	CASC3	p.P636T	cancer susceptibility car	17 (0.00)	25 (0.24)	0.64
11-02	Gp3	g.chr2:132289275G>A	Missense Mutation	CCDC74A	p.D195N	coiled-coil domain cont	19 (0.00)	35 (0.14)	0.38
11-02	Gp3	g.chr16:68712172C>A	Missense Mutation	CDH3	p.L128M	cadherin 3, type 1, P-ca	29 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr8:61761617G>A	Missense Mutation	CHD7	p.D1770N	chromodomain helicase	113 (0.00)	86 (0.17)	0.47
11-02	Gp3	g.chr14:21868443C>T	Missense Mutation	CHD8	p.G1532R	chromodomain helicase	62 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr15:20489547C>T	RNA	CHEK2P2		checkpoint kinase 2 pse	83 (0.00)	69 (0.14)	0.39
11-02	Gp3	g.chr12:10051545C>A	Missense Mutation	CLEC2A	p.W147C	C-type lectin domain fa	25 (0.00)	23 (0.22)	0.58
11-02	Gp3	g.chr12:8618095C>T	Missense Mutation	CLEC6A	p.P80L	C-type lectin domain fa	27 (0.00)	34 (0.18)	0.47
11-02	Gp3	g.chr14:92627592T>A	Splice Site	CPSF2		cleavage and polyadeny	40 (0.00)	44 (0.25)	0.67

11-02	Gp3	g.chr11:61178521C>T	Missense Mutation	CPSF7	p.R428K	cleavage and polyadeny	17 (0.00)	11 (0.45)	1.21
11-02	Gp3	g.chr7:29135764G>A	Missense Mutation	CPVL	p.L120F	carboxypeptidase, vitell	30 (0.00)	64 (0.34)	0.92
11-02	Gp3	g.chr7:143882664G>T	Missense Mutation	CTAGE4	p.G690C	CTAGE family, membe	40 (0.00)	25 (0.36)	0.96
11-02	Gp3	g.chr6:132030116G>A	Missense Mutation	CTAGE9	p.S681F	CTAGE family, membe	34 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr6:132030126G>A	Missense Mutation	CTAGE9	p.P678S	CTAGE family, membe	33 (0.00)	35 (0.23)	0.61
11-02	Gp3	g.chr19:7521218C>A	Silent	CTD-2207O23	p.S473S		32 (0.00)	41 (0.20)	0.52
11-02	Gp3	g.chr10:96827346C>A	Nonsense Mutation	CYP2C8	p.G91*	cytochrome P450, famil	39 (0.00)	24 (0.25)	0.67
11-02	Gp3	g.chr9:124411628C>G	Intron	DAB2IP		DAB2 interacting protei	19 (0.00)	56 (0.18)	0.48
11-02	Gp3	g.chr9:124473685G>A	Intron	DAB2IP		DAB2 interacting protei	20 (0.00)	29 (0.21)	0.55
11-02	Gp3	g.chr11:6654767G>A	Silent	DCHS1	p.D777D	dachsous cadherin-relat	15 (0.00)	32 (0.19)	0.50
11-02	Gp3	g.chr11:6654818G>A	Silent	DCHS1	p.I760I	dachsous cadherin-relat	15 (0.00)	29 (0.17)	0.46
11-02	Gp3	g.chr2:118583888G>A	Missense Mutation	DDX18	p.G522E	DEAD (Asp-Glu-Ala-A	29 (0.00)	26 (0.19)	0.51
11-02	Gp3	g.chr20:37632550G>A	Splice Site	DHX35	p.K337K	DEAH (Asp-Glu-Ala-H	27 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr16:72142714G>A	Missense Mutation	DHX38	p.V1091M	DEAH (Asp-Glu-Ala-H	15 (0.00)	24 (0.21)	0.56
11-02	Gp3	g.chr7:107557806G>A	Missense Mutation	DLD	p.G379S	dihydrolipoamide dehy	26 (0.00)	29 (0.28)	0.74
11-02	Gp3	g.chr18:3567547C>A	Silent	DLGAP1	p.G666G	discs, large (Drosophila	32 (0.00)	21 (0.24)	0.63
11-02	Gp3	g.chr9:34997062G>A	Missense Mutation	DNAJB5	p.G285S	DnaJ (Hsp40) homolog,	21 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr2:207558036C>T	Missense Mutation	DYTN	p.M281I	dystrotelin	26 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr11:85975301G>A	Missense Mutation	EED	p.S241N	embryonic ectoderm de	43 (0.00)	56 (0.16)	0.43
11-02	Gp3	g.chr8:132997280C>A	Silent	EFR3A	p.V614V	EFR3 homolog A (S. ce	42 (0.00)	31 (0.16)	0.43
11-02	Gp3	g.chr3:150280354A>G	Missense Mutation	EIF2A	p.K42E	eukaryotic translation in	33 (0.00)	13 (0.38)	1.03
11-02	Gp3	g.chr7:37382280C>A	Silent	ELMO1	p.A5A	engulfment and cell mo	37 (0.00)	39 (0.23)	0.62
11-02	Gp3	g.chr21:39761098G>A	Intron	ERG		v-ets avian erythroblast	34 (0.00)	47 (0.30)	0.79
11-02	Gp3	g.chr21:39797584G>A	Intron	ERG		v-ets avian erythroblast	22 (0.00)	43 (0.35)	0.93
11-02	Gp3	g.chr21:39847761C>T	Intron	ERG		v-ets avian erythroblast	23 (0.00)	28 (0.21)	0.57
11-02	Gp3	g.chr21:39861648G>A	Intron	ERG		v-ets avian erythroblast	50 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr1:169499024G>A	Silent	F5	p.P1747P	coagulation factor V (pr	48 (0.00)	47 (0.15)	0.40
11-02	Gp3	g.chr15:80467408C>T	Silent	FAH	p.D296D	fumarylacetoacetate hy	30 (0.00)	38 (0.16)	0.42
11-02	Gp3	g.chr15:102496011G>A	lincRNA	FAM138E		family with sequence si	49 (0.00)	31 (0.29)	0.77
11-02	Gp3	g.chr1:78267141G>A	Nonsense Mutation	FAM73A	p.W107*	family with sequence si	57 (0.00)	28 (0.32)	0.86
11-02	Gp3	g.chr4:187541415C>A	Missense Mutation	FAT1	p.D2109Y	FAT atypical cadherin 1	34 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr17:18673336G>A	Missense Mutation	FBXW10	p.M648I	F-box and WD repeat d	59 (0.00)	42 (0.19)	0.51
11-02	Gp3	g.chr16:67271994C>A	Silent	FHOD1	p.L195L	formin homology 2 dom	25 (0.00)	34 (0.18)	0.47
11-02	Gp3	g.chr17:80684378G>T	Missense Mutation	FN3KRP	p.W164L	fructosamine 3 kinase r	17 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr17:80684773G>T	Missense Mutation	FN3KRP	p.W219L	fructosamine 3 kinase r	26 (0.00)	46 (0.15)	0.41

11-02	Gp3	g.chr9:132740816G>A	Silent	FNBP1	p.S91S	formin binding protein 1	43 (0.00)	31 (0.23)	0.60
11-02	Gp3	g.chr4:159780261G>T	Missense Mutation	FNIP2	p.A304S	folliculin interacting pr	16 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr9:20944665C>A	Silent	FOCAD	p.L1149L	focadhesin	45 (0.00)	37 (0.16)	0.43
11-02	Gp3	g.chr3:197497070G>A	Missense Mutation	FYTTD1	p.R84K	forty-two-three domain	16 (0.00)	31 (0.23)	0.60
11-02	Gp3	g.chr9:74817504G>T	Missense Mutation	GDA	p.G77V	guanine deaminase	64 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr3:150917079C>A	Missense Mutation	GPR171	p.S32I	G protein-coupled recep	17 (0.00)	17 (0.41)	1.10
11-02	Gp3	g.chr17:36484929G>A	Missense Mutation	GPR179	p.A1508V	G protein-coupled recep	17 (0.00)	27 (0.22)	0.59
11-02	Gp3	g.chr2:11738007T>A	Missense Mutation	GREB1	p.N685K	growth regulation by es	31 (0.00)	45 (0.16)	0.41
11-02	Gp3	g.chrX:122561882G>A	Silent	GRIA3	p.L656L	glutamate receptor, ion	44 (0.00)	26 (0.23)	0.38
11-02	Gp3	g.chr5:21459846G>T	RNA	GUSBP1		glucuronidase, beta pse	18 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr7:18562979G>A	Intron	HDAC9		histone deacetylase 9	77 (0.00)	44 (0.16)	0.42
11-02	Gp3	g.chr7:18829212C>T	Intron	HDAC9		histone deacetylase 9	39 (0.00)	37 (0.19)	0.50
11-02	Gp3	g.chr7:18870232A>T	Intron	HDAC9		histone deacetylase 9	35 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr11:63327562G>A	Missense Mutation	HRASLS2	p.P38L	HRAS-like suppressor 2	20 (0.00)	31 (0.26)	0.69
11-02	Gp3	g.chr5:118835205G>A	Missense Mutation	HSD17B4	p.G371E	hydroxysteroid (17-beta	48 (0.00)	30 (0.20)	0.53
11-02	Gp3	g.chr8:39785371G>A	Silent	IDO1	p.Q293Q	indoleamine 2,3-dioxyg	54 (0.00)	68 (0.16)	0.43
11-02	Gp3	g.chr10:91144424G>A	Missense Mutation	IFIT1B	p.E452K	interferon-induced prote	47 (0.00)	32 (0.19)	0.50
11-02	Gp3	g.chr14:106236007G>A	RNA	IGHG3		immunoglobulin heavy	34 (0.00)	63 (0.14)	0.38
11-02	Gp3	g.chr2:89278504G>T	RNA	IGKV3-7		immunoglobulin kappa	51 (0.02)	62 (0.16)	0.43
11-02	Gp3	g.chr5:55195961G>A	Splice Site	IL31RA		interleukin 31 receptor	34 (0.00)	28 (0.18)	0.48
11-02	Gp3	g.chr4:142984490A>T	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	37 (0.16)	0.43
11-02	Gp3	g.chr4:143105810C>T	Intron	INPP4B		inositol polyphosphate-	96 (0.00)	60 (0.17)	0.44
11-02	Gp3	g.chr4:143350126G>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr4:143476258T>A	Intron	INPP4B		inositol polyphosphate-	60 (0.00)	77 (0.16)	0.42
11-02	Gp3	g.chr4:143645053C>T	Intron	INPP4B		inositol polyphosphate-	74 (0.00)	49 (0.24)	0.65
11-02	Gp3	g.chr4:143707350G>A	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr4:143750196G>A	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	47 (0.15)	0.40
11-02	Gp3	g.chr3:197665627C>T	Missense Mutation	IQCG	p.G103R	IQ motif containing G	72 (0.00)	40 (0.15)	0.40
11-02	Gp3	g.chr17:3626649C>G	Missense Mutation	ITGAE	p.C1057S	integrin, alpha E (antige	31 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr21:35183527G>T	Splice Site	ITSN1		intersectin 1 (SH3 doma	24 (0.00)	43 (0.19)	0.50
11-02	Gp3	g.chr1:111144668C>T	Missense Mutation	KCNA2	p.G340D	potassium voltage-gated	45 (0.00)	32 (0.34)	0.92
11-02	Gp3	g.chr7:150649858G>A	Silent	KCNH2	p.S404S	potassium voltage-gated	18 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr6:39163723C>T	Missense Mutation	KCNK5	p.G76E	potassium channel, subf	30 (0.00)	48 (0.15)	0.39
11-02	Gp3	g.chr19:18100549C>A	Missense Mutation	KCNN1	p.L399I	potassium intermediate/	59 (0.00)	38 (0.24)	0.63
11-02	Gp3	g.chr5:113740304C>A	Missense Mutation	KCNN2	p.T251N	potassium intermediate/	49 (0.00)	18 (0.33)	0.89

11-02	Gp3	g.chr19:10597371T>A	Missense Mutation	KEAP1	p.E611V	kelch-like ECH-associat	19 (0.00)	35 (0.17)	0.46
11-02	Gp3	g.chr9:5747316G>T	Missense Mutation	KIAA1432	p.Q421H		25 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr1:200965334T>A	Missense Mutation	KIF21B	p.K756M	kinesin family member	42 (0.00)	53 (0.15)	0.40
11-02	Gp3	g.chr8:145694113C>T	Missense Mutation	KIFC2	p.R337W	kinesin family member	29 (0.00)	72 (0.19)	0.52
11-02	Gp3	g.chr19:55263121G>A	Missense Mutation	KIR2DL3	p.V246I	killer cell immunoglobu	65 (0.00)	84 (0.14)	0.38
11-02	Gp3	g.chr12:49446756C>T	Missense Mutation	KMT2D	p.A352T	lysine (K)-specific meth	27 (0.00)	34 (0.18)	0.47
11-02	Gp3	g.chr17:38928013C>T	Nonsense Mutation	KRT26	p.W118*	keratin 26	26 (0.00)	22 (0.23)	0.61
11-02	Gp3	g.chr17:39551546C>T	Missense Mutation	KRT31	p.R276K	keratin 31	20 (0.00)	30 (0.23)	0.62
11-02	Gp3	g.chr11:18421069G>A	Missense Mutation	LDHA	p.R73K	lactate dehydrogenase A	28 (0.00)	26 (0.23)	0.62
11-02	Gp3	g.chr19:54662181G>A	Missense Mutation	LENG1	p.R51W	leukocyte receptor clust	30 (0.00)	35 (0.14)	0.38
11-02	Gp3	g.chr8:29961891G>A	Silent	LEPROTL1	p.V56V	leptin receptor overlapp	25 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr1:152629142C>T	lincRNA	LINC00302		long intergenic non-prot	56 (0.00)	36 (0.17)	0.44
11-02	Gp3	g.chr5:176778242G>A	Missense Mutation	LMAN2	p.L83F	lectin, mannose-binding	21 (0.00)	46 (0.15)	0.41
11-02	Gp3	g.chr2:74777459G>A	Silent	LOXL3	p.D110D	lysyl oxidase-like 3	24 (0.00)	31 (0.19)	0.52
11-02	Gp3	g.chr1:82456442G>A	Silent	LPHN2	p.R1331R	latrophilin 2	15 (0.00)	21 (0.38)	1.02
11-02	Gp3	g.chr2:11922535C>T	Missense Mutation	LPIN1	p.A83V	lipin 1	30 (0.00)	33 (0.21)	0.57
11-02	Gp3	g.chr14:42356592C>A	Missense Mutation	LRFN5	p.S255Y	leucine rich repeat and f	33 (0.00)	40 (0.17)	0.47
11-02	Gp3	g.chr1:90179101G>A	Silent	LRRC8C	p.L324L	leucine rich repeat conta	47 (0.00)	36 (0.22)	0.59
11-02	Gp3	g.chr2:33505147C>T	Nonsense Mutation	LTBP1	p.Q633*	latent transforming gro	27 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr7:20199560C>A	Nonsense Mutation	MACC1	p.E142*	metastasis associated in	22 (0.00)	21 (0.24)	0.63
11-02	Gp3	g.chr7:78023711G>A	Intron	MAGI2		membrane associated gu	20 (0.00)	18 (0.28)	0.74
11-02	Gp3	g.chr7:78095328C>T	Intron	MAGI2		membrane associated gu	38 (0.00)	24 (0.21)	0.56
11-02	Gp3	g.chr7:78121589G>A	Intron	MAGI2		membrane associated gu	25 (0.00)	13 (0.46)	1.23
11-02	Gp3	g.chr7:78272269G>T	Intron	MAGI2		membrane associated gu	64 (0.00)	59 (0.15)	0.41
11-02	Gp3	g.chr7:78400587A>T	Intron	MAGI2		membrane associated gu	43 (0.00)	36 (0.17)	0.44
11-02	Gp3	g.chr7:78543236C>T	Intron	MAGI2		membrane associated gu	58 (0.02)	69 (0.16)	0.43
11-02	Gp3	g.chr7:79041039T>A	Intron	MAGI2		membrane associated gu	53 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr7:79068478C>T	Intron	MAGI2		membrane associated gu	228 (0.00)	213 (0.19)	0.51
11-02	Gp3	g.chr15:43816562G>A	Missense Mutation	MAP1A	p.S1202N	microtubule-associated	18 (0.00)	26 (0.23)	0.62
11-02	Gp3	g.chr6:84056051G>T	Silent	ME1	p.A147A	malic enzyme 1, NADP	32 (0.00)	35 (0.14)	0.38
11-02	Gp3	g.chr1:40432278G>A	Silent	MFSD2A	p.K240K	major facilitator superfa	25 (0.00)	43 (0.16)	0.43
11-02	Gp3	g.chr22:18379546G>A	Missense Mutation	MICAL3	p.R384W	microtubule associated	44 (0.00)	51 (0.18)	0.47
11-02	Gp3	g.chr6:168312017C>T	Missense Mutation	MLLT4	p.H629Y	myeloid/lymphoid or mi	42 (0.00)	59 (0.15)	0.41
11-02	Gp3	g.chr20:49576537G>A	Silent	MOCS3	p.L386L	molybdenum cofactor s	28 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr8:142470106G>A	RNA	MROH5		maestro heat-like repeat	17 (0.00)	44 (0.16)	0.42

11-02	Gp3	g.chr20:35742515G>T	Missense Mutation	MROH8	p.L857I	maestro heat-like repeat	18 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr20:35783475G>T	Silent	MROH8	p.L355L	maestro heat-like repeat	30 (0.00)	29 (0.17)	0.46
11-02	Gp3	g.chr3:15091402C>A	Missense Mutation	MRPS25	p.V124L	mitochondrial ribosoma	21 (0.00)	22 (0.27)	0.73
11-02	Gp3	g.chr11:60476230C>A	Missense Mutation	MS4A8	p.D170E	membrane-spanning 4-d	18 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr19:8996394C>A	Missense Mutation	MUC16	p.E13726D	mucin 16, cell surface a	39 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr19:9028308G>A	Silent	MUC16	p.L12162L	mucin 16, cell surface a	46 (0.00)	68 (0.15)	0.39
11-02	Gp3	g.chr19:9046853G>A	Missense Mutation	MUC16	p.P11593L	mucin 16, cell surface a	40 (0.00)	49 (0.14)	0.38
11-02	Gp3	g.chr19:9065652G>T	Missense Mutation	MUC16	p.A7265D	mucin 16, cell surface a	27 (0.00)	39 (0.18)	0.48
11-02	Gp3	g.chr19:9076570C>T	Missense Mutation	MUC16	p.D3626N	mucin 16, cell surface a	21 (0.00)	31 (0.19)	0.52
11-02	Gp3	g.chr6:153043034C>T	Silent	MYCT1	p.H118H	myc target 1	39 (0.00)	28 (0.18)	0.48
11-02	Gp3	g.chr17:10265687C>A	Missense Mutation	MYH13	p.W113L	myosin, heavy chain 13,	71 (0.01)	42 (0.31)	0.83
11-02	Gp3	g.chr12:56553842G>A	Missense Mutation	MYL6	p.E87K	myosin, light chain 6, al	21 (0.00)	23 (0.26)	0.70
11-02	Gp3	g.chr7:105909003C>A	Missense Mutation	NAMPT	p.G217V	nicotinamide phosphoril	66 (0.00)	54 (0.15)	0.40
11-02	Gp3	g.chr1:148251892C>T	Missense Mutation	NBPF20	p.V4617I	neuroblastoma breakpoi	139 (0.01)	85 (0.15)	0.41
11-02	Gp3	g.chr6:126176366T>A	Missense Mutation	NCOA7	p.L84Q	nuclear receptor coactiv	23 (0.00)	22 (0.23)	0.61
11-02	Gp3	g.chr18:70451069C>A	Missense Mutation	NETO1	p.D238Y	neuropilin (NRP) and to	72 (0.00)	52 (0.15)	0.41
11-02	Gp3	g.chr8:63492200G>A	Missense Mutation	NKAIN3	p.G53R	Na+/K+ transporting A	42 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr10:96121516C>T	Silent	NOC3L	p.K41K	nucleolar complex asso	37 (0.00)	25 (0.20)	0.53
11-02	Gp3	g.chr2:50692676C>A	Missense Mutation	NRXN1	p.D1130Y	neurexin 1	19 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr5:102894792G>A	Missense Mutation	NUDT12	p.T177I	nudix (nucleoside dipho	39 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr19:17338655C>T	Silent	OCEL1	p.Y153Y	occludin/ELL domain c	19 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr16:56500879G>A	Splice Site	OGFOD1	p.Q219Q	2-oxoglutarate and iron-	25 (0.00)	32 (0.22)	0.58
11-02	Gp3	g.chr9:125437502C>G	Missense Mutation	OR1L3	p.L32V	olfactory receptor, famil	29 (0.00)	33 (0.15)	0.40
11-02	Gp3	g.chr11:4842738C>T	Silent	OR51F2	p.I41I	olfactory receptor, famil	77 (0.01)	119 (0.16)	0.43
11-02	Gp3	g.chr11:56143248G>A	Missense Mutation	OR8U1	p.R50K	olfactory receptor, famil	73 (0.00)	48 (0.15)	0.39
11-02	Gp3	g.chr12:80732975C>T	Missense Mutation	OTOGL	p.L1640F	otogelin-like	49 (0.00)	48 (0.31)	0.83
11-02	Gp3	g.chr12:47629953C>T	Silent	PCED1B	p.V369V	PC-esterase domain con	42 (0.02)	34 (0.18)	0.47
11-02	Gp3	g.chr18:60505218G>A	Intron	PHLPP1		PH domain and leucine	27 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr18:60580385C>A	Intron	PHLPP1		PH domain and leucine	15 (0.00)	12 (0.42)	1.11
11-02	Gp3	g.chr18:60606903T>C	Intron	PHLPP1		PH domain and leucine	57 (0.00)	32 (0.19)	0.50
11-02	Gp3	g.chr1:204438288C>T	Missense Mutation	PIK3C2B	p.G215R	phosphatidylinositol-4-	16 (0.00)	21 (0.33)	0.89
11-02	Gp3	g.chr1:204438350A>T	Nonsense Mutation	PIK3C2B	p.L194*	phosphatidylinositol-4-	16 (0.00)	25 (0.24)	0.64
11-02	Gp3	g.chr11:7660963G>A	Splice Site	PPFIBP2	p.D270N	PTPRF interacting prot	88 (0.00)	107 (0.16)	0.42
11-02	Gp3	g.chr11:7660994C>A	Missense Mutation	PPFIBP2	p.P280H	PTPRF interacting prot	74 (0.00)	89 (0.16)	0.42
11-02	Gp3	g.chr14:60749752C>T	Missense Mutation	PPM1A	p.H111Y	protein phosphatase, M	27 (0.00)	20 (0.30)	0.80

11-02	Gp3	g.chr21:43248594C>A	Missense Mutation	PRDM15	p.A525S	PR domain containing 1	16 (0.00)	50 (0.16)	0.43
11-02	Gp3	g.chr14:61924348C>G	Missense Mutation	PRKCH	p.A410G	protein kinase C, eta	42 (0.00)	46 (0.24)	0.64
11-02	Gp3	g.chr14:61924365C>T	Missense Mutation	PRKCH	p.L416F	protein kinase C, eta	45 (0.00)	46 (0.22)	0.58
11-02	Gp3	g.chr1:151006333G>A	Missense Mutation	PRUNE	p.A329T	prune exopolyphosphata	29 (0.00)	46 (0.17)	0.46
11-02	Gp3	g.chr6:47847475G>A	Nonsense Mutation	PTCHD4	p.Q369*	patched domain contain	45 (0.02)	43 (0.16)	0.43
11-02	Gp3	g.chr4:87643569G>A	Missense Mutation	PTPN13	p.M530I	protein tyrosine phospha	49 (0.00)	39 (0.18)	0.48
11-02	Gp3	g.chr15:75766088G>A	Missense Mutation	PTPN9	p.R384C	protein tyrosine phospha	32 (0.00)	63 (0.14)	0.38
11-02	Gp3	g.chr12:110960177C>A	Missense Mutation	RAD9B	p.S293R	RAD9 homolog B (S. p	30 (0.00)	12 (0.50)	1.33
11-02	Gp3	g.chr2:109382915G>A	Missense Mutation	RANBP2	p.A1974T	RAN binding protein 2	102 (0.00)	161 (0.17)	0.46
11-02	Gp3	g.chr12:53609467C>G	Missense Mutation	RARG	p.G99A	retinoic acid receptor, g	29 (0.00)	31 (0.19)	0.52
11-02	Gp3	g.chr21:15599412C>A	Nonsense Mutation	RBM11	p.S215*	RNA binding motif prot	28 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr5:145641127G>T	Nonsense Mutation	RBM27	p.E650*	RNA binding motif prot	17 (0.00)	23 (0.22)	0.58
11-02	Gp3	g.chr13:34404969G>A	Missense Mutation	RFC3	p.M229I	replication factor C (acti	16 (0.00)	14 (0.36)	0.95
11-02	Gp3	g.chr2:107041629T>C	Missense Mutation	RGPD3	p.N932D	RANBP2-like and GRII	37 (0.00)	22 (0.23)	0.61
11-02	Gp3	g.chr6:73110228G>T	Missense Mutation	RIMS1	p.D158Y	regulating synaptic mem	64 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr2:86831259C>A	Nonsense Mutation	RNF103	p.E589*	ring finger protein 103	61 (0.00)	43 (0.16)	0.43
11-02	Gp3	g.chr17:41321096C>T	lincRNA	RP11-242D8.1			51 (0.02)	39 (0.15)	0.41
11-02	Gp3	g.chr11:71883557C>T	RNA	RP11-807H22.7			46 (0.02)	61 (0.15)	0.39
11-02	Gp3	g.chr11:71628760G>A	Missense Mutation	RP11-849H4.2	p.P84S		25 (0.00)	28 (0.18)	0.48
11-02	Gp3	g.chr1:152128561A>G	Silent	RPTN	p.G338G	repetin	23 (0.00)	26 (0.38)	1.03
11-02	Gp3	g.chr2:7035982C>A	Missense Mutation	RSAD2	p.A332D	radical S-adenosyl meth	32 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr2:120219539C>A	Missense Mutation	SCTR	p.C225F	secretin receptor	22 (0.00)	58 (0.16)	0.41
11-02	Gp3	g.chr1:169847850C>T	Silent	SCYL3	p.L92L	SCY1-like 3 (S. cerevisi	73 (0.00)	50 (0.18)	0.48
11-02	Gp3	g.chr2:192701129C>G	Missense Mutation	SDPR	p.E266D	serum deprivation respo	63 (0.00)	54 (0.30)	0.79
11-02	Gp3	g.chr11:57367608C>T	Missense Mutation	SERPING1	p.T108I	serpin peptidase inhibitc	33 (0.00)	35 (0.14)	0.38
11-02	Gp3	g.chr19:38643504G>A	Silent	SIPA1L3	p.L1186L	signal-induced prolifera	18 (0.00)	45 (0.16)	0.41
11-02	Gp3	g.chr6:133093327C>A	Missense Mutation	SLC18B1	p.E368D	solute carrier family 18,	25 (0.00)	21 (0.43)	1.14
11-02	Gp3	g.chr11:107677576C>T	Silent	SLC35F2	p.V147V	solute carrier family 35,	20 (0.00)	30 (0.20)	0.53
11-02	Gp3	g.chr3:136573439G>A	Missense Mutation	SLC35G2	p.G46E	solute carrier family 35,	73 (0.00)	83 (0.23)	0.61
11-02	Gp3	g.chr17:19458552G>A	Missense Mutation	SLC47A1	p.G168R	solute carrier family 47	31 (0.00)	42 (0.14)	0.38
11-02	Gp3	g.chr2:46986732G>A	Missense Mutation	SOCS5	p.G355R	suppressor of cytokine s	22 (0.00)	42 (0.14)	0.38
11-02	Gp3	g.chr10:107012537C>T	Missense Mutation	SORCS3	p.T1037I	sortilin-related VPS10 d	26 (0.00)	42 (0.14)	0.38
11-02	Gp3	g.chr4:52928427G>A	Silent	SPATA18	p.R117R	spermatogenesis associa	28 (0.00)	23 (0.22)	0.58
11-02	Gp3	g.chr9:90500141C>T	Nonsense Mutation	SPATA31E1	p.Q247*	SPATA31 subfamily E,	15 (0.00)	28 (0.29)	0.76
11-02	Gp3	g.chr5:35654817G>A	Missense Mutation	SPEF2	p.E323K	sperm flagellar 2	45 (0.00)	34 (0.15)	0.39

11-02	Gp3	g.chr3:113169348G>T	Missense Mutation	SPICE1	p.Q720K	spindle and centriole ass	51 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr12:119588882C>T	Silent	SRRM4	p.S379S	serine/arginine repetitiv	35 (0.00)	36 (0.17)	0.44
11-02	Gp3	g.chr7:89791253G>A	Nonsense Mutation	STEAP1	p.W208*	six transmembrane epit	33 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr2:169023845C>A	Missense Mutation	STK39	p.D132Y	serine threonine kinase	23 (0.00)	26 (0.19)	0.51
11-02	Gp3	g.chr13:37614715G>T	Missense Mutation	SUPT20H	p.Q171K	suppressor of Ty 20 ho	33 (0.00)	26 (0.23)	0.62
11-02	Gp3	g.chr10:29813467G>T	Missense Mutation	SVIL	p.D840E	supervillin	25 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr19:46355615G>A	Missense Mutation	SYMPK	p.S85L	symplekin	54 (0.00)	43 (0.16)	0.43
11-02	Gp3	g.chr1:155838178G>A	Missense Mutation	SYT11	p.E153K	synaptotagmin XI	22 (0.00)	23 (0.22)	0.58
11-02	Gp3	g.chr11:763433C>T	Missense Mutation	TALDO1	p.T184I	transaldolase 1	18 (0.00)	38 (0.26)	0.70
11-02	Gp3	g.chr5:167643909C>A	Silent	TENM2	p.S1166S	teneurin transmembrane	29 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr5:1278807G>A	Silent	TERT	p.A745A	telomerase reverse trans	28 (0.00)	42 (0.26)	0.70
11-02	Gp3	g.chr1:36060043G>A	Silent	TFAP2E	p.P365P	transcription factor AP-	39 (0.00)	43 (0.16)	0.43
11-02	Gp3	g.chr5:135389730C>T	Missense Mutation	TGFBI	p.R409W	transforming growth fac	33 (0.00)	31 (0.23)	0.60
11-02	Gp3	g.chr17:4675274C>T	Silent	TM4SF5	p.L19L	transmembrane 4 L six	31 (0.00)	32 (0.16)	0.42
11-02	Gp3	g.chr3:129547172C>T	Missense Mutation	TMCC1	p.G17D	transmembrane and coil	26 (0.00)	25 (0.24)	0.64
11-02	Gp3	g.chr19:36038273C>T	Missense Mutation	TMEM147	p.A200V	transmembrane protein	20 (0.00)	32 (0.19)	0.50
11-02	Gp3	g.chr3:170912422C>T	Silent	TNIK	p.L103L	TRAF2 and NCK intera	32 (0.00)	29 (0.17)	0.46
11-02	Gp3	g.chr14:21961036C>G	Missense Mutation	TOX4	p.R421G	TOX high mobility grou	29 (0.00)	35 (0.14)	0.38
11-02	Gp3	g.chr1:154164397G>T	Missense Mutation	TPM3	p.A33E	tropomyosin 3	20 (0.00)	33 (0.18)	0.48
11-02	Gp3	g.chr7:142124183C>T	RNA	TRBV6-8		T cell receptor beta vari	46 (0.00)	88 (0.16)	0.42
11-02	Gp3	g.chr21:45815402C>T	Missense Mutation	TRPM2	p.R634C	transient receptor potent	23 (0.00)	31 (0.19)	0.52
11-02	Gp3	g.chr9:73254084C>T	Silent	TRPM3	p.L491L	transient receptor potent	41 (0.00)	34 (0.15)	0.39
11-02	Gp3	g.chr2:179413004G>A	Missense Mutation	TTN	p.P31117S	titin	80 (0.00)	56 (0.21)	0.57
11-02	Gp3	g.chr7:19738184C>A	Nonsense Mutation	TWISTNB	p.E258*	TWIST neighbor	44 (0.00)	44 (0.18)	0.48
11-02	Gp3	g.chr3:49848060G>T	Missense Mutation	UBA7	p.L453I	ubiquitin-like modifier	50 (0.00)	44 (0.16)	0.42
11-02	Gp3	g.chr12:125396449G>A	Silent	UBC	p.L243L	ubiquitin C	35 (0.00)	23 (0.22)	0.58
11-02	Gp3	g.chr1:202304786C>T	Missense Mutation	UBE2T	p.D33N	ubiquitin-conjugating en	28 (0.00)	36 (0.17)	0.44
11-02	Gp3	g.chr2:210818859C>T	Missense Mutation	UNC80	p.P2370L	unc-80 homolog (C. ele	20 (0.00)	36 (0.19)	0.52
11-02	Gp3	g.chr2:219350433C>A	Missense Mutation	USP37	p.G470C	ubiquitin specific peptid	30 (0.00)	42 (0.14)	0.38
11-02	Gp3	g.chr4:53494169C>T	Silent	USP46	p.K93K	ubiquitin specific peptid	65 (0.00)	34 (0.18)	0.47
11-02	Gp3	g.chr2:106721279C>T	Silent	UXS1	p.G298G	UDP-glucuronate decar	30 (0.00)	23 (0.35)	0.93
11-02	Gp3	g.chr1:109525368G>A	Missense Mutation	WDR47	p.T711I	WD repeat domain 47	32 (0.00)	41 (0.15)	0.39
11-02	Gp3	g.chr3:39229640C>A	Nonsense Mutation	XIRP1	p.E433*	xin actin-binding repeat	36 (0.00)	55 (0.18)	0.48
11-02	Gp3	g.chr16:17221564C>T	Missense Mutation	XYLT1	p.A728T	xylosyltransferase I	30 (0.00)	30 (0.17)	0.44
11-02	Gp3	g.chr7:100350511C>T	RNA	ZAN		zonadhesin (gene/pseud	60 (0.00)	77 (0.21)	0.55

11-02	Gp3	g.chr7:100352996C>T	RNA	ZAN		zonadhesin (gene/pseud	32 (0.00)	60 (0.15)	0.40
11-02	Gp3	g.chr19:44501329G>A	Silent	ZNF155	p.K451K	zinc finger protein 155	35 (0.00)	35 (0.17)	0.46
11-02	Gp3	g.chr19:58153218G>A	Missense Mutation	ZNF211	p.C520Y	zinc finger protein 211	38 (0.00)	36 (0.17)	0.44
11-02	Gp3	g.chr16:71483677G>C	Missense Mutation	ZNF23	p.S84C	zinc finger protein 23	39 (0.00)	29 (0.21)	0.55
11-02	Gp3	g.chr5:176468189G>A	Missense Mutation	ZNF346	p.A80T	zinc finger protein 346	34 (0.00)	34 (0.18)	0.47
11-02	Gp3	g.chr8:28217174G>T	Silent	ZNF395	p.P136P	zinc finger protein 395	15 (0.00)	20 (0.25)	0.67
11-02	Gp3	g.chr19:37618915G>A	Missense Mutation	ZNF420	p.G341E	zinc finger protein 420	35 (0.00)	27 (0.19)	0.49
11-02	Gp3	g.chr2:95818989C>A	Nonsense Mutation	ZNF514	p.E4*	zinc finger protein 514	26 (0.00)	30 (0.27)	0.71
11-02	Gp3	g.chr19:38103622C>A	Missense Mutation	ZNF540	p.Q481K	zinc finger protein 540	21 (0.00)	18 (0.28)	0.74
11-02	Gp3	g.chr19:58059092G>A	Nonsense Mutation	ZNF550	p.Q133*	zinc finger protein 550	19 (0.00)	25 (0.20)	0.53
11-02	Gp3	g.chr19:7083237A>G	Missense Mutation	ZNF557	p.T259A	zinc finger protein 557	21 (0.00)	22 (0.23)	0.61
11-02	Gp3	g.chr19:37975279G>A	Missense Mutation	ZNF570	p.G252E	zinc finger protein 570	59 (0.02)	28 (0.18)	0.48
11-02	Gp3	g.chr8:144733362C>T	Silent	ZNF623	p.F440F	zinc finger protein 623	41 (0.00)	43 (0.16)	0.43
11-02	Gp3	g.chr1:247151464C>T	Missense Mutation	ZNF695	p.C118Y	zinc finger protein 695	64 (0.00)	45 (0.33)	0.89
11-02	Gp3	g.chr8:7215966G>T	Silent	ZNF705G	p.V145V	zinc finger protein 705C	71 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 1	g.chr21:43645879C>T	Silent	ABCG1	p.D47D	ATP-binding cassette, s	23 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr3:100494114G>A	Missense Mutation	ABI3BP	p.P756S	ABI family, member 3 (	34 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr2:62373941A>G	RNA	AC018462.2			58 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 1	g.chr17:61560475G>A	Nonsense Mutation	ACE	p.W476*	angiotensin I converting	21 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 1	g.chr14:23548758T>A	Nonsense Mutation	ACIN1	p.K654*	apoptotic chromatin con	26 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 1	g.chr1:55074779C>A	Silent	ACOT11	p.T593T	acyl-CoA thioesterase 1	20 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr7:17373675C>G	Missense Mutation	AHR	p.T282S	aryl hydrocarbon recept	78 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr2:202359356G>T	Missense Mutation	ALS2CR11	p.H570N	amyotrophic lateral scle	26 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr7:36698791G>A	Missense Mutation	AOAH	p.H124Y	acyloxyacyl hydrolase (	27 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr22:39413877G>A	Nonsense Mutation	APOBEC3C	p.W94*	apolipoprotein B mRNA	18 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr12:14577708C>T	Missense Mutation	ATF7IP	p.R287C	activating transcription	58 (0.00)	53 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr17:40659636C>T	Silent	ATP6V0A1	p.D708D	ATPase, H+ transportin	39 (0.00)	63 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr13:52548503C>T	Missense Mutation	ATP7B	p.V285I	ATPase, Cu++ transport	55 (0.02)	56 (0.23)	0.62
11-02	Gp4 Focus 1	g.chr7:72957881G>A	Nonsense Mutation	BCL7B	p.Q88*	B-cell CLL/lymphoma	31 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr10:43280998C>T	Missense Mutation	BMS1	p.P82L	BMS1 ribosome biogen	65 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr17:41203989C>G	Intron	BRCA1		breast cancer 1, early on	20 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 1	g.chrX:154348368G>A	Silent	BRCC3	p.L274L	BRCA1/BRCA2-contai	22 (0.00)	23 (0.48)	0.80
11-02	Gp4 Focus 1	g.chr11:76253396C>A	Silent	C11orf30	p.T807T	chromosome 11 open re	47 (0.02)	46 (0.20)	0.52
11-02	Gp4 Focus 1	g.chr11:66581326G>A	Splice Site	C11orf80		chromosome 11 open re	32 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr17:42750786C>T	Missense Mutation	C17orf104	p.A837V	chromosome 17 open re	54 (0.00)	22 (0.23)	0.61

11-02	Gp4 Focus 1	g.chr20:20056148C>T	Missense Mutation	C20orf26	p.T152I		80 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr20:20079325G>A	Missense Mutation	C20orf26	p.M242I		59 (0.00)	90 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr20:20144848G>T	Missense Mutation	C20orf26	p.C394F		21 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr4:113540481T>G	Silent	C4orf21	p.A239A		37 (0.03)	38 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr3:53835144C>T	Silent	CACNA1D	p.S1685S	calcium channel, voltag	39 (0.00)	71 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr3:85030486G>T	Intron	CADM2		cell adhesion molecule	33 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr3:85592347C>T	Intron	CADM2		cell adhesion molecule	40 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr3:85785742C>A	Intron	CADM2		cell adhesion molecule	58 (0.02)	37 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr3:86114081C>T	Intron	CADM2		cell adhesion molecule	34 (0.00)	53 (0.17)	0.45
11-02	Gp4 Focus 1	g.chr6:7378997G>A	Silent	CAGE1	p.N180N	cancer antigen 1	54 (0.00)	29 (0.31)	0.45
11-02	Gp4 Focus 1	g.chr19:15164317C>T	Missense Mutation	CASP14	p.R18C	caspase 14, apoptosis-re	32 (0.00)	52 (0.21)	0.56
11-02	Gp4 Focus 1	g.chr3:112068651C>T	Missense Mutation	CD200	p.R263W	CD200 molecule	34 (0.03)	30 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr2:87042805G>A	Silent	CD8B	p.P189P	CD8b molecule	30 (0.00)	45 (0.18)	0.47
11-02	Gp4 Focus 1	g.chr15:49044589G>A	Silent	CEP152	p.H1141H	centrosomal protein 152	66 (0.00)	54 (0.28)	0.74
11-02	Gp4 Focus 1	g.chr17:57771202T>A	Missense Mutation	CLTC	p.Y1673N	clathrin, heavy chain (H	35 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr22:19178915C>A	Silent	CLTCL1	p.L1408L	clathrin, heavy chain-lik	22 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr4:47939447C>T	Nonsense Mutation	CNGA1	p.W424*	cyclic nucleotide gated	28 (0.00)	37 (0.30)	0.79
11-02	Gp4 Focus 1	g.chr3:74334553C>T	Silent	CNTN3	p.L869L	contactin 3 (plasmacyto	80 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr6:75890671C>A	Missense Mutation	COL12A1	p.E716D	collagen, type XII, alph	36 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 1	g.chr7:7420316C>A	Missense Mutation	COL28A1	p.G766V	collagen, type XXVIII,	24 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr2:238006362T>C	Missense Mutation	COPS8	p.Y203H	COP9 signalosome sub	32 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr8:3000122G>A	Missense Mutation	CSMD1	p.H2037Y	CUB and Sushi multipl	37 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr2:204736181C>A	Missense Mutation	CTLA4	p.L180I	cytotoxic T-lymphocyte	18 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr20:36488691C>T	Silent	CTNNBL1	p.H329H	catenin, beta like 1	31 (0.00)	58 (0.16)	0.41
11-02	Gp4 Focus 1	g.chr9:124350015G>A	Intron	DAB2IP		DAB2 interacting protei	24 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 1	g.chr9:124351438G>A	Intron	DAB2IP		DAB2 interacting protei	24 (0.00)	44 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr9:124454745T>A	Intron	DAB2IP		DAB2 interacting protei	62 (0.00)	41 (0.32)	0.85
11-02	Gp4 Focus 1	g.chr8:11851525C>T	Silent	DEFB134	p.Q55Q	defensin, beta 134	23 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr11:9167340G>A	Silent	DENND5A	p.I960I	DENN/MADD domain	57 (0.00)	88 (0.17)	0.45
11-02	Gp4 Focus 1	g.chr8:1626449C>T	Silent	DLGAP2	p.F706F	discs, large (Drosophila	19 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr3:52434390G>A	Silent	DNAH1	p.E4242E	dynein, axonemal, heav	48 (0.00)	58 (0.21)	0.55
11-02	Gp4 Focus 1	g.chr5:13793793G>A	Silent	DNAH5	p.F2685F	dynein, axonemal, heav	21 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr19:10260618C>T	Silent	DNMT1	p.K748K	DNA (cytosine-5-)-met	28 (0.00)	43 (0.26)	0.68
11-02	Gp4 Focus 1	g.chr6:83828683G>A	Missense Mutation	DOPEY1	p.R286Q	dopey family member 1	57 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 1	g.chr2:109539864G>A	Silent	EDAR	p.V134V	ectodysplasin A recepto	30 (0.00)	26 (0.19)	0.51

11-02	Gp4 Focus 1	g.chr2:31484573G>T	Missense Mutation	EHD3	p.R358S	EH-domain containing	17 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr21:39759873C>T	Intron	ERG		v-ets avian erythroblast	16 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 1	g.chr21:39828512C>G	Intron	ERG		v-ets avian erythroblast	34 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr8:139144969C>A	Missense Mutation	FAM135B	p.R1363L	family with sequence si	24 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr3:68466517G>T	Missense Mutation	FAM19A1	p.C69F	family with sequence si	39 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 1	g.chr1:179019498C>T	Silent	FAM20B	p.D154D	family with sequence si	18 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr10:88782077C>T	Missense Mutation	FAM25A	p.A27V	family with sequence si	25 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr16:67576736G>A	Missense Mutation	FAM65A	p.E697K	family with sequence si	19 (0.00)	49 (0.20)	0.54
11-02	Gp4 Focus 1	g.chr3:75480010C>T	RNA	FAM86DP		family with sequence si	37 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 1	g.chr12:50047588C>A	Missense Mutation	FMNL3	p.V330F	formin-like 3	63 (0.00)	120 (0.15)	0.40
11-02	Gp4 Focus 1	g.chrX:49110956G>A	Intron	FOXP3		forkhead box P3	22 (0.00)	20 (0.30)	0.50
11-02	Gp4 Focus 1	g.chr1:155187141C>A	RNA	GBAP1		glucosidase, beta, acid p	20 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 1	g.chr11:134163074G>T	Missense Mutation	GLB1L3	p.D283Y	galactosidase, beta 1-lik	24 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 1	g.chr7:86394782G>A	Silent	GRM3	p.E107E	glutamate receptor, met	49 (0.00)	49 (0.16)	0.44
11-02	Gp4 Focus 1	g.chr6:52761661C>A	Missense Mutation	GSTA3	p.R204S	glutathione S-transferas	16 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr7:18539193C>T	Intron	HDAC9		histone deacetylase 9	27 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 1	g.chr7:18743873G>T	Intron	HDAC9		histone deacetylase 9	67 (0.00)	48 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr7:18796465G>A	Intron	HDAC9		histone deacetylase 9	84 (0.00)	84 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr12:66704368C>T	Missense Mutation	HELB	p.H554Y	helicase (DNA) B	27 (0.00)	54 (0.20)	0.54
11-02	Gp4 Focus 1	g.chr17:65124801C>T	Missense Mutation	HELZ	p.G1118E	helicase with zinc finge	55 (0.02)	35 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr15:63946451C>A	Missense Mutation	HERC1	p.W3386L	HECT and RLD domai	16 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 1	g.chrX:131762852G>T	Missense Mutation	HS6ST2	p.S446Y	heparan sulfate 6-O-sul	28 (0.00)	25 (0.36)	0.60
11-02	Gp4 Focus 1	g.chr5:63256374G>A	Silent	HTR1A	p.S391S	5-hydroxytryptamine (s	22 (0.00)	37 (0.30)	0.79
11-02	Gp4 Focus 1	g.chr3:50340004G>A	Silent	HYAL1	p.I128I	hyaluronoglucosaminid	39 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr14:106235827C>G	RNA	IGHG3		immunoglobulin heavy	18 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr4:142955703C>G	Intron	INPP4B		inositol polyphosphate-	27 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr4:142956213C>T	Intron	INPP4B		inositol polyphosphate-	45 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr4:143067699C>T	Intron	INPP4B		inositol polyphosphate-	135 (0.00)	86 (0.17)	0.47
11-02	Gp4 Focus 1	g.chr4:143275368C>A	Intron	INPP4B		inositol polyphosphate-	63 (0.00)	62 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr4:143410918G>A	Intron	INPP4B		inositol polyphosphate-	41 (0.00)	41 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr4:143723310C>G	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr19:7170717G>A	Silent	INSR	p.L438L	insulin receptor	45 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr20:13260484G>A	Silent	ISM1	p.R194R	isthmin 1, angiogenesis	30 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 1	g.chr12:26731671G>A	Silent	ITPR2	p.S1535S	inositol 1,4,5-trisphosph	50 (0.00)	63 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr10:64968225C>G	Missense Mutation	JMJD1C	p.M1068I	jumonji domain contain	21 (0.00)	32 (0.16)	0.42

11-02	Gp4 Focus 1	g.chr17:45747113G>A	Missense Mutation	KPNB1	p.V287I	karyopherin (importin)	27 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr12:53164961C>A	Nonsense Mutation	KRT76	p.G436*	keratin 76	19 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr1:183209311C>T	Missense Mutation	LAMC2	p.T1069M	laminin, gamma 2	24 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr19:54783777G>C	Missense Mutation	LILRB2	p.P75R	leukocyte immunoglobu	28 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr22:31668537G>A	Missense Mutation	LIMK2	p.D469N	LIM domain kinase 2	18 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 1	g.chr4:83867604G>A	Silent	LIN54	p.T325T	lin-54 DREAM MuvB c	48 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr1:211591173C>G	RNA	LINC00467		long intergenic non-prot	31 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 1	g.chr4:54344843G>A	Missense Mutation	LNX1	p.L518F	ligand of numb-protein	18 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr2:99900919C>T	Silent	LYG1	p.L174L	lysozyme G-like 1	15 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr7:77686192C>G	Intron	MAGI2		membrane associated gu	58 (0.00)	43 (0.23)	0.62
11-02	Gp4 Focus 1	g.chr7:77789007G>A	Intron	MAGI2		membrane associated gu	67 (0.00)	69 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr7:77845738C>T	Intron	MAGI2		membrane associated gu	63 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr7:77862753G>A	Intron	MAGI2		membrane associated gu	34 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 1	g.chr7:77871589G>A	Intron	MAGI2		membrane associated gu	62 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr7:77991375T>G	Intron	MAGI2		membrane associated gu	25 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 1	g.chrX:43590528G>A	Missense Mutation	MAOA	p.R229Q	monoamine oxidase A	17 (0.00)	26 (0.23)	0.38
11-02	Gp4 Focus 1	g.chr1:232941108A>T	Silent	MAP10	p.R113R	microtubule-associated	19 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 1	g.chr2:27246242G>T	Missense Mutation	MAPRE3	p.C55F	microtubule-associated	21 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 1	g.chr5:112384889C>T	Silent	MCC	p.V852V	mutated in colorectal ca	17 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 1	g.chr14:47687273C>G	Missense Mutation	MDGA2	p.E113D	MAM domain containin	38 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 1	g.chr7:116415163G>A	Missense Mutation	MET	p.R1104K	MET proto-oncogene, r	26 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr11:12315287C>T	Silent	MICALCL	p.L103L	MICAL C-terminal like	24 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr10:129904320C>A	Silent	MKI67	p.L1928L	marker of proliferation	21 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 1	g.chr6:168289995C>A	Missense Mutation	MLLT4	p.P333Q	myeloid/lymphoid or mi	52 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr6:42176624G>C	Missense Mutation	MRPS10	p.P165R	mitochondrial ribosoma	37 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr2:190926977C>A	Nonsense Mutation	MSTN	p.E116*	myostatin	67 (0.00)	55 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr1:155160769G>A	Missense Mutation	MUC1	p.S253F	mucin 1, cell surface as	35 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 1	g.chr19:9017374G>A	Silent	MUC16	p.T12650T	mucin 16, cell surface a	41 (0.00)	47 (0.21)	0.57
11-02	Gp4 Focus 1	g.chrX:3248695C>A	Missense Mutation	MXRA5	p.S103I	matrix-remodelling asso	28 (0.00)	28 (0.25)	0.42
11-02	Gp4 Focus 1	g.chr17:10247281G>A	Missense Mutation	MYH13	p.A577V	myosin, heavy chain 13,	34 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr1:148753402C>G	Silent	NBPF16	p.G473G		33 (0.00)	37 (0.19)	0.50
11-02	Gp4 Focus 1	g.chr2:152410459C>A	Missense Mutation	NEB	p.K6503N	nebulin	117 (0.00)	92 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr1:179533840G>A	Silent	NPHS2	p.I121I	nephrosis 2, idiopathic,	25 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr18:11619712C>T	RNA	NPIPB1P		nuclear pore complex in	42 (0.02)	32 (0.19)	0.50
11-02	Gp4 Focus 1	g.chr14:90782992C>T	Missense Mutation	NRDE2	p.D113N	NRDE-2, necessary for	67 (0.01)	74 (0.24)	0.65

11-02	Gp4 Focus 1	g.chr10:74884001G>A	Missense Mutation	NUDT13	p.E130K	nudix (nucleoside dipho	31 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 1	g.chr12:69115726G>A	Missense Mutation	NUP107	p.D444N	nucleoporin 107kDa	32 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 1	g.chr8:103573071C>A	Missense Mutation	ODF1	p.P238T	outer dense fiber of sper	18 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr9:131262402C>T	Silent	ODF2	p.S781S	outer dense fiber of sper	26 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr9:137990310C>T	Missense Mutation	OLFM1	p.S185F	olfactomedin 1	28 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr17:3119514C>T	Silent	OR1A1	p.Y200Y	olfactory receptor, famil	27 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr5:180167047G>T	Missense Mutation	OR2Y1	p.F4L	olfactory receptor, famil	40 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 1	g.chr2:179248852G>T	Missense Mutation	OSBPL6	p.E679D	oxysterol binding protei	29 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 1	g.chr12:29649170G>A	Silent	OVCH1	p.S75S	ovochymase 1	53 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr3:16336429G>T	Silent	OXNAD1	p.L119L	oxidoreductase NAD-bi	33 (0.00)	45 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr1:233386551G>A	Missense Mutation	PCNXL2	p.S719F	pecanex-like 2 (Drosop	29 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 1	g.chr12:54969820G>A	Missense Mutation	PDE1B	p.D397N	phosphodiesterase 1B, c	17 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 1	g.chr16:70016514C>A	RNA	PDXDC2P		pyridoxal-dependent de	36 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr5:139682637C>T	Missense Mutation	PFDN1	p.E8K	prefoldin subunit 1	47 (0.00)	68 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr3:111632200G>A	Missense Mutation	PHLDB2	p.C43Y	pleckstrin homology-lik	71 (0.00)	70 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr18:60392303G>A	Intron	PHLPP1		PH domain and leucine	45 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr10:99410734C>A	Missense Mutation	PI4K2A	p.P158T	phosphatidylinositol 4-k	27 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 1	g.chr7:47847872G>A	Silent	PKD1L1	p.D2600D	polycystic kidney diseas	19 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr8:48866366C>T	Splice Site	PRKDC		protein kinase, DNA-ac	40 (0.00)	54 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr9:80919829G>A	Missense Mutation	PSAT1	p.V124I	phosphoserine aminotra	26 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr4:87610284G>A	Missense Mutation	PTPN13	p.A163T	protein tyrosine phospha	80 (0.00)	83 (0.14)	0.39
11-02	Gp4 Focus 1	g.chr17:29848234C>T	Missense Mutation	RAB11FIP4	p.S205F	RAB11 family interacti	15 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 1	g.chr20:20493370G>T	Missense Mutation	RALGAPA2	p.T1548N	Ral GTPase activating p	47 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr2:33749101G>A	Silent	RASGRP3	p.K224K	RAS guanyl releasing p	49 (0.00)	54 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr16:24581289C>T	Missense Mutation	RBBP6	p.S1093F	retinoblastoma binding	18 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 1	g.chr12:130892351G>A	Missense Mutation	RIMBP2	p.R949C	RIMS binding protein 2	29 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr20:19951526C>G	Missense Mutation	RIN2	p.T243R	Ras and Rab interactor	55 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 1	g.chr12:49258603C>G	Missense Mutation	RND1	p.E57D	Rho family GTPase 1	16 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr2:11375994A>C	Missense Mutation	ROCK2	p.V186G	Rho-associated, coiled-	92 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr9:94488909C>T	Missense Mutation	ROR2	p.A434T	receptor tyrosine kinase	26 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr12:130521351G>A	lincRNA	RP11-474D1.3			37 (0.00)	42 (0.24)	0.63
11-02	Gp4 Focus 1	g.chr14:62014499G>C	Nonstop Mutation	RP11-47I22.4	p.*105S		25 (0.00)	64 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr9:91262386C>T	lincRNA	RP13-60M5.2			25 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr22:42973163C>A	RNA	RRP7B		ribosomal RNA process	20 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr1:237433839G>A	Missense Mutation	RYR2	p.E31K	ryanodine receptor 2 (ca	41 (0.00)	34 (0.18)	0.47

11-02	Gp4 Focus 1	g.chr1:109779137C>T	Silent	SARS	p.I408I	seryl-tRNA synthetase	39 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr11:92881964G>A	Silent	SLC36A4	p.F283F	solute carrier family 36	40 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr2:103324751C>T	Missense Mutation	SLC9A2	p.P748S	solute carrier family 9, s	26 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 1	g.chr21:34922313C>G	Nonsense Mutation	SON	p.S259*	SON DNA binding prot	31 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 1	g.chr17:47693677G>C	Intron	SPOP		speckle-type POZ protei	24 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 1	g.chr1:158644160C>T	Missense Mutation	SPTA1	p.V437M	spectrin, alpha, erythroc	24 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 1	g.chr1:24976542C>T	Silent	SRRM1	p.S162S	serine/arginine repetitiv	57 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr15:42982000G>C	Missense Mutation	STARD9	p.A2742P	StAR-related lipid trans	23 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 1	g.chr9:113231257C>A	Silent	SVEP1	p.T1018T	sushi, von Willebrand fa	25 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 1	g.chr20:60582632G>A	Missense Mutation	TAF4	p.P649S	TAF4 RNA polymerase	25 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr15:78309013C>T	Silent	TBC1D2B	p.K550K	TBC1 domain family, m	29 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 1	g.chr5:133481963C>A	Missense Mutation	TCF7	p.P375Q	transcription factor 7 (T	17 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 1	g.chr10:115985900C>T	Missense Mutation	TDRD1	p.P1034S	tudor domain containing	23 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr12:117494688C>T	Silent	TESC	p.K44K	tescalcin	18 (0.00)	51 (0.16)	0.42
11-02	Gp4 Focus 1	g.chr14:24730920G>T	Silent	TGM1	p.I163I	transglutaminase 1	52 (0.00)	82 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr4:153692066T>A	Missense Mutation	TIGD4	p.N31Y	tigger transposable elem	64 (0.00)	55 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr16:84516239T>A	Missense Mutation	TLDC1	p.M346L	TBC/LysM-associated c	19 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 1	g.chr20:2591130G>A	Silent	TMC2	p.L493L	transmembrane channel-	26 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 1	g.chr9:32544248G>A	Missense Mutation	TOPORS	p.T92I	topoisomerase I binding	42 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr3:36899298C>T	Missense Mutation	TRANK1	p.D45N	tetratricopeptide repeat a	23 (0.00)	75 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr6:42196305C>T	Silent	TRERF1	p.E1127E	transcriptional regulatin	19 (0.00)	47 (0.17)	0.45
11-02	Gp4 Focus 1	g.chr7:72430569G>A	Missense Mutation	TRIM74	p.H237Y	tripartite motif containin	16 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 1	g.chr10:75051504C>T	Silent	TTC18	p.L177L		30 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr2:179396504C>A	Silent	TTN	p.L34946L	titin	19 (0.00)	36 (0.25)	0.67
11-02	Gp4 Focus 1	g.chr2:179424827C>A	Missense Mutation	TTN	p.D28678Y	titin	35 (0.00)	46 (0.15)	0.41
11-02	Gp4 Focus 1	g.chr2:179438809G>A	Missense Mutation	TTN	p.A24017V	titin	51 (0.00)	58 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr2:179580233G>A	Silent	TTN	p.S8636S	titin	28 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr2:179638312C>A	Missense Mutation	TTN	p.V2491L	titin	24 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 1	g.chr13:96536912G>A	Missense Mutation	UGGT2	p.P1021S	UDP-glucose glycoprote	29 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 1	g.chr19:17722620C>T	Missense Mutation	UNC13A	p.E1535K	unc-13 homolog A (C. e	23 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr2:210642248G>A	Missense Mutation	UNC80	p.V189M	unc-80 homolog (C. eleg	36 (0.00)	56 (0.14)	0.38
11-02	Gp4 Focus 1	g.chr11:17542914C>T	Missense Mutation	USH1C	p.R355K	Usher syndrome 1C (au	45 (0.00)	79 (0.19)	0.51
11-02	Gp4 Focus 1	g.chr16:23079601G>T	Missense Mutation	USP31	p.H1275Q	ubiquitin specific peptid	56 (0.00)	74 (0.16)	0.43
11-02	Gp4 Focus 1	g.chr10:75280686G>A	Missense Mutation	USP54	p.A821V	ubiquitin specific peptid	24 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr7:123329143G>A	Missense Mutation	WASL	p.A470V	Wiskott-Aldrich syndro	33 (0.00)	27 (0.33)	0.89

11-02	Gp4 Focus 1	g.chr4:6302782C>G	Silent	WFS1	p.P420P	Wolfram syndrome 1 (w	30 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 1	g.chr10:27405204C>T	Missense Mutation	YME1L1	p.S597N	YME1-like 1 ATPase	34 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr3:28566036G>A	Missense Mutation	ZCWPW2	p.E310K	zinc finger, CW type wi	45 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 1	g.chr8:135596155G>A	Missense Mutation	ZFAT	p.T936I	zinc finger and AT hook	33 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 1	g.chrX:24228965C>A	Missense Mutation	ZFX	p.S630R	zinc finger protein, X-li	19 (0.00)	12 (0.42)	0.69
11-02	Gp4 Focus 1	g.chr15:56970932G>A	Silent	ZNF280D	p.Y351Y	zinc finger protein 280D	36 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 1	g.chr14:74376100T>A	Missense Mutation	ZNF410	p.S251T	zinc finger protein 410	15 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 1	g.chr19:57839364C>T	Silent	ZNF543	p.L178L	zinc finger protein 543	25 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 1	g.chr7:149318673T>A	RNA	ZNF767			17 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 1	g.chr7:149557613G>A	Missense Mutation	ZNF862	p.R455K	zinc finger protein 862	20 (0.00)	32 (0.31)	0.83
11-02	Gp4 Focus 1	g.chr10:75557813G>A	Missense Mutation	ZSWIM8	p.V1308I	zinc finger, SWIM-type	41 (0.02)	35 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr10:52603852G>A	Missense Mutation	A1CF	p.P44S	APOBEC1 complement	38 (0.00)	15 (0.33)	1.14
11-02	Gp4 Focus 2	g.chr12:9242999G>T	Missense Mutation	A2M	p.A850E	alpha-2-macroglobulin	63 (0.02)	73 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr12:9268437C>T	Silent	A2M	p.K3K	alpha-2-macroglobulin	39 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr12:9001485G>A	Missense Mutation	A2ML1	p.G668D	alpha-2-macroglobulin-l	26 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr12:53701422G>A	Missense Mutation	AAAS	p.L498F	achalasia, adrenocortica	32 (0.00)	12 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr12:53702550C>T	Missense Mutation	AAAS	p.G349E	achalasia, adrenocortica	52 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:125587239G>T	Silent	AACS	p.R195R	acetoacetyl-CoA synthe	131 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr5:178208048G>T	RNA	AACSP1		acetoacetyl-CoA synthe	26 (0.00)	28 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr17:35376342G>A	Silent	AATF	p.L479L	apoptosis antagonizing t	37 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr9:107556725G>A	Nonsense Mutation	ABCA1	p.R1817*	ATP-binding cassette, s	68 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr17:67149460C>A	Silent	ABCA10	p.G1374G	ATP-binding cassette, s	19 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr7:48287910G>T	Missense Mutation	ABCA13	p.W578C	ATP-binding cassette, s	62 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr7:48390297G>A	Missense Mutation	ABCA13	p.G3421D	ATP-binding cassette, s	43 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr7:48634306G>A	Splice Site	ABCA13	p.D4881N	ATP-binding cassette, s	44 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr16:2373669G>A	Silent	ABCA3	p.F156F	ATP-binding cassette, s	70 (0.00)	18 (0.67)	2.13
11-02	Gp4 Focus 2	g.chr1:94528783C>T	Missense Mutation	ABCA4	p.A549T	ATP-binding cassette, s	42 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:1046289C>T	Silent	ABCA7	p.G364G	ATP-binding cassette, s	18 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr17:66873690C>G	Missense Mutation	ABCA8	p.R1390T	ATP-binding cassette, s	32 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr1:229676409G>A	Missense Mutation	ABCB10	p.H383Y	ATP-binding cassette, s	44 (0.00)	33 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr7:150730897G>A	Missense Mutation	ABCB8	p.A101T	ATP-binding cassette, s	17 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr16:16225750C>T	Silent	ABCC1	p.F1308F	ATP-binding cassette, s	24 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr3:183700654G>A	Nonsense Mutation	ABCC5	p.R245*	ATP-binding cassette, s	83 (0.00)	56 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr3:183707156C>T	Missense Mutation	ABCC5	p.A49T	ATP-binding cassette, s	75 (0.00)	62 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr16:16295867C>A	Silent	ABCC6	p.V389V	ATP-binding cassette, s	21 (0.00)	31 (0.16)	0.43

11-02	Gp4 Focus 2	g.chr12:21968812G>A	Missense Mutation	ABCC9	p.P1303L	ATP-binding cassette, s	24 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr14:74766254G>A	Silent	ABCD4	p.S94S	ATP-binding cassette, s	41 (0.02)	17 (0.94)	2.51
11-02	Gp4 Focus 2	g.chr7:150923413C>T	Silent	ABCF2	p.E44E	ATP-binding cassette, s	50 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:119030937G>A	Splice Site	ABCG4	p.V480M	ATP-binding cassette, s	16 (0.00)	32 (0.41)	1.08
11-02	Gp4 Focus 2	g.chr1:179078022G>A	Nonsense Mutation	ABL2	p.Q794*	ABL proto-oncogene 2,	24 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr1:179078412T>C	Missense Mutation	ABL2	p.T664A	ABL proto-oncogene 2,	51 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr5:148632387G>A	Missense Mutation	ABLIM3	p.R642K	actin binding LIM prote	89 (0.00)	70 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr17:1003973C>T	Silent	ABR	p.V83V	active BCR-related	41 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr19:35898950G>A	lincRNA	AC002511.1			22 (0.00)	106 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr16:20856031C>T	Silent	AC004381.6	p.G600G		43 (0.00)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr2:137302049G>A	RNA	AC010146.2			21 (0.00)	23 (0.39)	1.27
11-02	Gp4 Focus 2	g.chr19:52096143C>G	Missense Mutation	AC018755.1	p.A179P		20 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr2:27930863C>T	Missense Mutation	AC074091.13	p.G57E		40 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr2:42119219C>T	lincRNA	AC104654.1			62 (0.00)	46 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr17:35536345G>A	Silent	ACACA	p.S1608S	acetyl-CoA carboxylase	30 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr12:109690936C>T	Silent	ACACB	p.I2006I	acetyl-CoA carboxylase	68 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:76199278G>T	Missense Mutation	ACADM	p.G151W	acyl-CoA dehydrogenas	67 (0.01)	53 (0.17)	0.55
11-02	Gp4 Focus 2	g.chr11:108017059G>A	Missense Mutation	ACAT1	p.G379E	acetyl-CoA acetyltransf	20 (0.00)	30 (0.50)	1.33
11-02	Gp4 Focus 2	g.chrX:15609867C>T	Silent	ACE2	p.V184V	angiotensin I converting	65 (0.00)	12 (0.67)	1.11
11-02	Gp4 Focus 2	g.chr5:80640738G>T	Missense Mutation	ACOT12	p.T299K	acyl-CoA thioesterase 1	20 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr5:80640745G>A	Missense Mutation	ACOT12	p.L297F	acyl-CoA thioesterase 1	21 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chrX:108921282C>T	Missense Mutation	ACSL4	p.E289K	acyl-CoA synthetase lo	38 (0.00)	23 (0.65)	1.45
11-02	Gp4 Focus 2	g.chr10:114169389G>A	Silent	ACSL5	p.L219L	acyl-CoA synthetase lo	74 (0.00)	45 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr15:35085674C>T	Missense Mutation	ACTC1	p.G76S	actin, alpha, cardiac mu	16 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr11:66322620C>T	RNA	ACTN3		actinin, alpha 3 (gene/ps	36 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr11:66322686G>A	RNA	ACTN3		actinin, alpha 3 (gene/ps	36 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr2:98277087G>A	Missense Mutation	ACTR1B	p.R46W	ARP1 actin-related prot	33 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr12:52379070C>A	Silent	ACVR1B	p.V306V	activin A receptor, type	23 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr10:127782564C>T	Missense Mutation	ADAM12	p.A382T	ADAM metallopeptidas	43 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr8:39007387G>A	Splice Site	ADAM32		ADAM metallopeptidas	41 (0.00)	31 (0.32)	1.04
11-02	Gp4 Focus 2	g.chr20:3655323C>T	Missense Mutation	ADAM33	p.S143N	ADAM metallopeptidas	15 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr5:33637704G>A	Silent	ADAMTS12	p.H622H	ADAM metallopeptidas	39 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr5:33881274G>A	Nonsense Mutation	ADAMTS12	p.Q147*	ADAM metallopeptidas	26 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr11:130343350C>T	Silent	ADAMTS15	p.S829S	ADAM metallopeptidas	24 (0.00)	39 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr9:18681872A>G	Silent	ADAMTSL1	p.G468G	ADAMTS-like 1	57 (0.00)	33 (0.24)	0.79

11-02	Gp4 Focus 2	g.chr1:150526041G>A	Missense Mutation	ADAMTSL4	p.E192K	ADAMTS-like 4	24 (0.00)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr1:154575071G>A	Missense Mutation	ADAR	p.P16L	adenosine deaminase, R	25 (0.00)	21 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr16:75637023G>A	Silent	ADAT1	p.L446L	adenosine deaminase, tR	69 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:33549690C>T	Silent	ADC	p.L81L		15 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr7:45632412C>T	Missense Mutation	ADCY1	p.R7W	adenylate cyclase 1 (bra	30 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr7:45743303G>A	Silent	ADCY1	p.E892E	adenylate cyclase 1 (bra	26 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr1:167815389G>A	Silent	ADCY10	p.P850P	adenylate cyclase 10 (so	64 (0.00)	49 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr1:167825636G>A	Silent	ADCY10	p.A646A	adenylate cyclase 10 (so	95 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr16:50346800G>A	Splice Site	ADCY7		adenylate cyclase 7	19 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr16:4016199G>A	Silent	ADCY9	p.Y1213Y	adenylate cyclase 9	43 (0.00)	27 (0.26)	0.83
11-02	Gp4 Focus 2	g.chr10:111893340G>A	Silent	ADD3	p.L695L	adducin 3 (gamma)	51 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr6:146978046G>A	Missense Mutation	ADGB	p.C181Y	androglobin	90 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr6:147109689G>A	Missense Mutation	ADGB	p.G1494R	androglobin	18 (0.00)	47 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr8:67359513G>A	Missense Mutation	ADHFE1	p.G189R	alcohol dehydrogenase,	21 (0.00)	24 (0.21)	0.70
11-02	Gp4 Focus 2	g.chr17:10614457G>A	Missense Mutation	ADPRM	p.C342Y	ADP-ribose/CDP-alcoho	46 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr14:22935321G>A	RNA	AE000661.37			22 (0.00)	15 (0.53)	0.78
11-02	Gp4 Focus 2	g.chr4:7840283G>A	Nonsense Mutation	AFAP1	p.Q232*	actin filament associated	44 (0.00)	27 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr5:148680716C>T	Missense Mutation	AFAP1L1	p.R84W	actin filament associated	25 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr5:148680717G>T	Missense Mutation	AFAP1L1	p.R84L	actin filament associated	25 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:88026819C>T	Silent	AFF1	p.D434D	AF4/FMR2 family, men	38 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chrX:148048511G>A	Missense Mutation	AFF2	p.M1035I	AF4/FMR2 family, men	40 (0.00)	33 (0.52)	1.24
11-02	Gp4 Focus 2	g.chrX:148048557C>T	Silent	AFF2	p.L1051L	AF4/FMR2 family, men	45 (0.00)	37 (0.32)	0.78
11-02	Gp4 Focus 2	g.chr2:100623274C>T	Silent	AFF3	p.P231P	AF4/FMR2 family, men	15 (0.00)	30 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr12:58126632C>T	Silent	AGAP2	p.Q560Q	ArfGAP with GTPase d	89 (0.00)	98 (0.20)	0.54
11-02	Gp4 Focus 2	g.chr10:51464877C>T	Missense Mutation	AGAP7	p.G527R		85 (0.00)	89 (0.18)	0.62
11-02	Gp4 Focus 2	g.chr2:27277641G>A	Missense Mutation	AGBL5	p.S232N	ATP/GTP binding prote	74 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr2:27278650C>T	Missense Mutation	AGBL5	p.H337Y	ATP/GTP binding prote	39 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr2:27278977G>A	Missense Mutation	AGBL5	p.G446R	ATP/GTP binding prote	44 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr2:27278978G>A	Missense Mutation	AGBL5	p.G446E	ATP/GTP binding prote	44 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr7:100146444G>A	Splice Site	AGFG2		ArfGAP with FG repeat	35 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr1:15904180C>T	Splice Site	AGMAT	p.Q300Q	agmatine ureohydrolase	15 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr21:45391294G>A	Silent	AGPAT3	p.L230L	1-acylglycerol-3-phosph	30 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr21:45391320C>G	Missense Mutation	AGPAT3	p.S239C	1-acylglycerol-3-phosph	30 (0.00)	35 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr1:27878234C>T	Silent	AHDC1	p.L131L	AT hook, DNA binding	18 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr11:62299695C>T	Missense Mutation	AHNAK	p.D732N	AHNAK nucleoprotein	74 (0.00)	29 (0.76)	2.02

11-02	Gp4 Focus 2	g.chr6:143458032C>T	Nonsense Mutation	AIG1	p.R68*	androgen-induced 1	26 (0.00)	59 (0.20)	0.54
11-02	Gp4 Focus 2	g.chr9:135742312G>A	Silent	AK8	p.P66P	adenylate kinase 8	65 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr17:55183608G>C	Missense Mutation	AKAP1	p.E261D	A kinase (PRKA) ancho	36 (0.00)	52 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr13:42874193G>A	Silent	AKAP11	p.V437V	A kinase (PRKA) ancho	115 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr6:151671080G>A	Silent	AKAP12	p.K518K	A kinase (PRKA) ancho	76 (0.00)	51 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr6:151671324G>A	Missense Mutation	AKAP12	p.G600R	A kinase (PRKA) ancho	26 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr6:151671960C>A	Missense Mutation	AKAP12	p.P812T	A kinase (PRKA) ancho	16 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr15:86064707G>A	Missense Mutation	AKAP13	p.D28N	A kinase (PRKA) ancho	122 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr15:86236651C>T	Silent	AKAP13	p.P1815P	A kinase (PRKA) ancho	75 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr15:86261244G>A	Missense Mutation	AKAP13	p.G1956D	A kinase (PRKA) ancho	16 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chrX:49957830G>A	Nonsense Mutation	AKAP4	p.Q503*	A kinase (PRKA) ancho	29 (0.00)	20 (0.75)	1.25
11-02	Gp4 Focus 2	g.chr14:33014554C>T	Missense Mutation	AKAP6	p.P232L	A kinase (PRKA) ancho	35 (0.00)	10 (0.50)	1.59
11-02	Gp4 Focus 2	g.chr1:109380197G>C	Missense Mutation	AKNAD1	p.S504C	AKNA domain containi	51 (0.00)	25 (0.28)	0.59
11-02	Gp4 Focus 2	g.chr7:134222339C>T	Missense Mutation	AKR1B10	p.P223S	aldo-keto reductase fam	81 (0.00)	35 (0.54)	1.45
11-02	Gp4 Focus 2	g.chr7:134223018G>A	Missense Mutation	AKR1B10	p.E272K	aldo-keto reductase fam	43 (0.00)	33 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr10:5248246G>A	Silent	AKR1C4	p.E152E	aldo-keto reductase fam	37 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr10:5204933G>A	Silent	AKR1CL1	p.G48G	aldo-keto reductase fam	18 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr10:82013150T>A	Missense Mutation	AL359195.1	p.L223Q		125 (0.00)	60 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr9:116151267G>A	Silent	ALAD	p.F307F	aminolevulinate dehydr	24 (0.00)	17 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr3:52246391G>A	Missense Mutation	ALAS1	p.A573T	aminolevulinate, delta-,	133 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:52246414C>T	Silent	ALAS1	p.P580P	aminolevulinate, delta-,	128 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr10:97373840G>A	Nonsense Mutation	ALDH18A1	p.Q562*	aldehyde dehydrogenas	141 (0.00)	26 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr12:105420419G>A	Silent	ALDH1L2	p.L874L	aldehyde dehydrogenas	80 (0.00)	30 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr6:24532405G>A	Splice Site	ALDH5A1	p.G440S	aldehyde dehydrogenas	18 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr12:34175670C>T	Nonsense Mutation	ALG10	p.Q46*	ALG10, alpha-1,2-gluc	72 (0.00)	47 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr13:52593231G>A	Missense Mutation	ALG11	p.G76E	ALG11, alpha-1,2-man	27 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr9:101980475G>A	Missense Mutation	ALG2	p.P331L	ALG2, alpha-1,3/1,6-ma	17 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr17:4535299G>T	Missense Mutation	ALOX15	p.P565Q	arachidonate 15-lipoxyg	21 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr17:4535314G>A	Missense Mutation	ALOX15	p.T560M	arachidonate 15-lipoxyg	21 (0.00)	30 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr4:113553055G>A	Nonsense Mutation	ALPK1	p.W784*	alpha-kinase 1	26 (0.00)	36 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr18:56203756C>T	Silent	ALPK2	p.E1221E	alpha-kinase 2	27 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr18:56247511G>A	Missense Mutation	ALPK2	p.S166F	alpha-kinase 2	30 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:202352505G>C	Missense Mutation	ALS2CR11	p.H1765D	amyotrophic lateral scle	61 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr11:46439499C>T	Missense Mutation	AMBRA1	p.G937D	autophagy/beclin-1 regu	32 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr11:46439580G>A	Missense Mutation	AMBRA1	p.P910L	autophagy/beclin-1 regu	23 (0.00)	14 (0.43)	1.14

11-02	Gp4 Focus 2	g.chr11:46563529G>A	Missense Mutation	AMBRA1	p.P590S	autophagy/beclin-1 regu	51 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr1:110051092G>A	Missense Mutation	AMIGO1	p.A148V	adhesion molecule with	63 (0.00)	20 (0.30)	0.63
11-02	Gp4 Focus 2	g.chr1:110172901C>T	Missense Mutation	AMPD2	p.A731V	adenosine monophosph	15 (0.00)	18 (0.50)	1.04
11-02	Gp4 Focus 2	g.chr19:10203301C>T	Silent	ANGPTL6	p.R459R	angiopoietin-like 6	16 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr4:114276396G>A	Missense Mutation	ANK2	p.E2175K	ankyrin 2, neuronal	53 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr10:61828490G>T	Missense Mutation	ANK3	p.T4050K	ankyrin 3, node of Ranv	69 (0.00)	27 (0.48)	1.53
11-02	Gp4 Focus 2	g.chr10:61835537G>A	Missense Mutation	ANK3	p.S1701L	ankyrin 3, node of Ranv	38 (0.00)	18 (0.33)	1.06
11-02	Gp4 Focus 2	g.chr5:139908840T>C	Silent	ANKHD1	p.A2103A	ankyrin repeat and KH	156 (0.00)	51 (0.31)	0.84
11-02	Gp4 Focus 2	g.chr12:133304659C>T	Nonsense Mutation	ANKLE2	p.W213*	ankyrin repeat and LEM	30 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr18:9257478T>A	Missense Mutation	ANKRD12	p.L1405I	ankyrin repeat domain 1	44 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr12:110461909G>A	Missense Mutation	ANKRD13A	p.E265K	ankyrin repeat domain 1	86 (0.00)	66 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr12:110474073C>T	Missense Mutation	ANKRD13A	p.S506L	ankyrin repeat domain 1	26 (0.00)	71 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr18:21218832G>A	Missense Mutation	ANKRD29	p.S104F	ankyrin repeat domain 2	33 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr18:14763706C>T	Missense Mutation	ANKRD30B	p.P281L	ankyrin repeat domain 3	38 (0.00)	57 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr2:132905780G>A	Missense Mutation	ANKRD30BL	p.P234L	ankyrin repeat domain 3	148 (0.00)	63 (0.30)	0.97
11-02	Gp4 Focus 2	g.chr5:79854638G>A	Missense Mutation	ANKRD34B	p.P401S	ankyrin repeat domain 3	18 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:145562313G>A	Silent	ANKRD35	p.Q667Q	ankyrin repeat domain 3	41 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr2:197878295G>A	Nonsense Mutation	ANKRD44	p.Q597*	ankyrin repeat domain 4	17 (0.00)	27 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr12:56639375C>T	Silent	ANKRD52	p.V730V	ankyrin repeat domain 5	40 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr3:149508622C>A	Missense Mutation	ANKUB1	p.W60C	ankyrin repeat and ubiq	29 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:220098476G>A	Missense Mutation	ANKZF1	p.A287T	ankyrin repeat and zinc	37 (0.00)	72 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr11:26677997C>T	Missense Mutation	ANO3	p.A911V	anoctamin 3	85 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr11:22257740G>A	Missense Mutation	ANO5	p.G227D	anoctamin 5	79 (0.00)	44 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr15:90340813G>A	Missense Mutation	ANPEP	p.P717L	alanyl (membrane) ami	22 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr10:47663357G>A	Silent	ANTXRL	p.R104R	anthrax toxin receptor-li	63 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr10:47681713C>A	Missense Mutation	ANTXRL	p.P384Q	anthrax toxin receptor-li	42 (0.00)	39 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr5:150496725C>A	Missense Mutation	ANXA6	p.G512V	annexin A6	23 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr5:150502506C>T	Missense Mutation	ANXA6	p.R402Q	annexin A6	33 (0.00)	48 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:150967088C>T	Silent	ANXA9	p.I296I	annexin A9	71 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr7:150558050C>A	Missense Mutation	AOC1	p.T670K	amine oxidase, copper c	23 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr17:40996887G>A	Missense Mutation	AOC2	p.A82T	amine oxidase, copper c	29 (0.00)	27 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr11:125366566G>A	Silent	AP000708.1	p.E150E		36 (0.00)	76 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr11:64942967C>T	RNA	AP003068.18			20 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr21:11181022C>T	lincRNA	AP003900.6			108 (0.00)	47 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr14:24032982G>A	Missense Mutation	AP1G2	p.S392F	adaptor-related protein	17 (0.00)	16 (0.31)	0.46

11-02	Gp4 Focus 2	g.chr5:77311260G>A	Silent	AP3B1	p.V986V	adaptor-related protein	32 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr12:99043339G>T	Missense Mutation	APAF1	p.A135S	apoptotic peptidase acti	33 (0.00)	52 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr9:72130963G>A	Silent	APBA1	p.T388T	amyloid beta (A4) precu	16 (0.00)	16 (0.38)	1.21
11-02	Gp4 Focus 2	g.chr9:72130983G>A	Missense Mutation	APBA1	p.R382C	amyloid beta (A4) precu	17 (0.00)	21 (0.24)	0.77
11-02	Gp4 Focus 2	g.chr5:112175765G>A	Missense Mutation	APC	p.A1492T	adenomatous polyposis	34 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr11:43345126G>A	Silent	API5	p.S230S	apoptosis inhibitor 5	86 (0.00)	120 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr1:10493933G>A	Missense Mutation	APITD1-COR	p.C29Y	APITD1-CORT readthr	91 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr19:36363386C>A	Splice Site	APLP1	p.V284V	amyloid beta (A4) precu	26 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr11:129979474G>A	Missense Mutation	APLP2	p.E86K	amyloid beta (A4) precu	24 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr2:21225608G>A	Missense Mutation	APOB	p.S4229F	apolipoprotein B	38 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr2:21237399G>A	Missense Mutation	APOB	p.L1255F	apolipoprotein B	21 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr2:21247907G>A	Silent	APOB	p.R778R	apolipoprotein B	27 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr22:36122884G>A	Missense Mutation	APOL5	p.A257T	apolipoprotein L, 5	64 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr9:33442880G>C	Missense Mutation	AQP3	p.H154Q	aquaporin 3 (Gill blood	43 (0.00)	41 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr20:47606206C>T	Silent	ARFGEF2	p.C933C	ADP-ribosylation factor	35 (0.03)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr2:143913191G>A	Missense Mutation	ARHGAP15	p.M44I	Rho GTPase activating	51 (0.00)	19 (0.32)	1.03
11-02	Gp4 Focus 2	g.chr16:24942661G>A	Silent	ARHGAP17	p.G653G	Rho GTPase activating	36 (0.00)	66 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr10:24874012C>G	Missense Mutation	ARHGAP21	p.V1736L	Rho GTPase activating	43 (0.00)	11 (0.82)	2.74
11-02	Gp4 Focus 2	g.chr10:49654512C>A	Missense Mutation	ARHGAP22	p.L679F	Rho GTPase activating	41 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr10:49654513A>C	Missense Mutation	ARHGAP22	p.L679W	Rho GTPase activating	42 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr4:86863355G>A	Silent	ARHGAP24	p.L176L	Rho GTPase activating	25 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr11:128851348G>A	Silent	ARHGAP32	p.F218F	Rho GTPase activating	55 (0.00)	36 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr19:47422027G>A	Missense Mutation	ARHGAP35	p.G32E	Rho GTPase activating	22 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr19:47423471C>T	Silent	ARHGAP35	p.S513S	Rho GTPase activating	115 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr19:47423819T>A	Missense Mutation	ARHGAP35	p.D629E	Rho GTPase activating	83 (0.00)	80 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr17:12812227T>C	Missense Mutation	ARHGAP44	p.L71S	Rho GTPase activating	39 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr14:32561177C>A	Missense Mutation	ARHGAP5	p.F434L	Rho GTPase activating	56 (0.00)	25 (0.20)	0.64
11-02	Gp4 Focus 2	g.chr8:1814752C>T	Silent	ARHGEF10	p.N202N	Rho guanine nucleotide	27 (0.00)	45 (0.18)	0.61
11-02	Gp4 Focus 2	g.chr1:17958906G>A	Missense Mutation	ARHGEF10L	p.E520K	Rho guanine nucleotide	54 (0.00)	46 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr11:120319897G>A	Missense Mutation	ARHGEF12	p.R606K	Rho guanine nucleotide	48 (0.00)	84 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr1:155924736G>A	Silent	ARHGEF2	p.P580P	Rho/Rac guanine nucle	34 (0.00)	32 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr4:106576795C>T	Silent	ARHGEF38	p.D383D	Rho guanine nucleotide	51 (0.02)	31 (0.65)	1.72
11-02	Gp4 Focus 2	g.chr9:35664399G>A	Silent	ARHGEF39	p.A108A	Rho guanine nucleotide	76 (0.00)	67 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr7:144059783G>A	Silent	ARHGEF5	p.Q7Q	Rho guanine nucleotide	55 (0.00)	56 (0.23)	0.62
11-02	Gp4 Focus 2	g.chrX:135761812C>T	Missense Mutation	ARHGEF6	p.S571N	Rac/Cdc42 guanine nuc	44 (0.00)	16 (0.44)	1.05

11-02	Gp4 Focus 2	g.chr1:27100200G>A	Silent	ARID1A	p.Q1332Q	AT rich interactive dom	26 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr6:157517318C>T	Silent	ARID1B	p.P1294P	AT rich interactive dom	49 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr10:63851682C>T	Silent	ARID5B	p.P820P	AT rich interactive dom	58 (0.00)	16 (0.50)	1.58
11-02	Gp4 Focus 2	g.chr11:30358308G>A	Missense Mutation	ARL14EP	p.G250E	ADP-ribosylation factor	47 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:104436664G>A	Missense Mutation	ARL3	p.A179V	ADP-ribosylation factor	60 (0.00)	16 (0.69)	1.83
11-02	Gp4 Focus 2	g.chr11:13393712G>A	Splice Site	ARNTL		aryl hydrocarbon recept	48 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr7:98951580G>T	Silent	ARPC1A	p.T183T	actin related protein 2/3	25 (0.00)	105 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:98951605G>A	Missense Mutation	ARPC1A	p.G192R	actin related protein 2/3	27 (0.00)	95 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr3:35833915C>T	Silent	ARPP21	p.L692L	cAMP-regulated phosph	26 (0.00)	27 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr19:18121440C>T	Missense Mutation	ARRDC2	p.P358S	arrestin domain containi	20 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr19:4891474C>T	Missense Mutation	ARRDC5	p.V205I	arrestin domain containi	20 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr4:114899922C>T	Silent	ARSJ	p.K23K	arylsulfatase family, me	28 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr8:131130453C>T	Missense Mutation	ASAP1	p.A612T	ArfGAP with SH3 dom	30 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr2:239353226C>T	Silent	ASB1	p.H145H	ankyrin repeat and SOC	22 (0.00)	16 (0.88)	2.33
11-02	Gp4 Focus 2	g.chrX:15307645C>A	Silent	ASB11	p.V212V	ankyrin repeat and SOC	69 (0.00)	23 (0.30)	0.51
11-02	Gp4 Focus 2	g.chrX:15307752C>T	Missense Mutation	ASB11	p.E177K	ankyrin repeat and SOC	33 (0.00)	11 (0.64)	1.06
11-02	Gp4 Focus 2	g.chr3:57314442C>T	Missense Mutation	ASB14	p.G259R	ankyrin repeat and SOC	27 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr7:123267265G>A	Missense Mutation	ASB15	p.G267R	ankyrin repeat and SOC	24 (0.00)	30 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr1:155311727C>A	Splice Site	ASH1L	p.S2820S	ash1 (absent, small, or h	21 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:220396616G>A	Missense Mutation	ASIC4	p.R367K	acid-sensing (proton-gat	41 (0.00)	20 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr2:220396620G>A	Silent	ASIC4	p.E368E	acid-sensing (proton-gat	42 (0.00)	22 (0.73)	1.94
11-02	Gp4 Focus 2	g.chr8:62438550G>A	Missense Mutation	ASPH	p.T629M	aspartate beta-hydroxyl	48 (0.00)	10 (0.80)	2.70
11-02	Gp4 Focus 2	g.chr8:62438557G>A	Nonsense Mutation	ASPH	p.Q627*	aspartate beta-hydroxyl	50 (0.00)	10 (0.50)	1.69
11-02	Gp4 Focus 2	g.chr20:31024141G>A	Missense Mutation	ASXL1	p.S1209N	additional sex combs lik	15 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr2:25965352C>A	Missense Mutation	ASXL2	p.S1285I	additional sex combs lik	85 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr2:25966253T>A	Nonsense Mutation	ASXL2	p.K985*	additional sex combs lik	59 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr18:31325413G>A	Silent	ASXL3	p.Q1867Q	additional sex combs lik	97 (0.00)	108 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr2:24033352G>A	Missense Mutation	ATAD2B	p.T763I	ATPase family, AAA d	54 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr2:24046218G>A	Missense Mutation	ATAD2B	p.P681S	ATPase family, AAA d	149 (0.00)	48 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:212791491G>A	Missense Mutation	ATF3	p.R88K	activating transcription	92 (0.00)	87 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr1:212791545A>T	Missense Mutation	ATF3	p.K106M	activating transcription	110 (0.00)	130 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr22:39918530C>T	Silent	ATF4	p.L327L	activating transcription	17 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr12:14577960G>A	Missense Mutation	ATF7IP	p.V371I	activating transcription	19 (0.00)	32 (0.41)	1.08
11-02	Gp4 Focus 2	g.chr2:234172683G>A	Missense Mutation	ATG16L1	p.D121N	autophagy related 16-lik	62 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr14:96756882C>T	Missense Mutation	ATG2B	p.R1916Q	autophagy related 2B	43 (0.00)	11 (0.73)	1.94

11-02	Gp4 Focus 2	g.chr3:11399930G>A	Silent	ATG7	p.G441G	autophagy related 7	46 (0.02)	42 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr14:51054659G>A	Missense Mutation	ATL1	p.D49N	atlastin GTPase 1	128 (0.00)	57 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr4:94751049G>A	Silent	ATOH1	p.Q324Q	atonal homolog 1 (Dros	33 (0.00)	25 (0.20)	0.91
11-02	Gp4 Focus 2	g.chr15:25925382G>A	Missense Mutation	ATP10A	p.S1251F	ATPase, class V, type 1	24 (0.00)	59 (0.61)	2.25
11-02	Gp4 Focus 2	g.chr15:25932949C>T	Silent	ATP10A	p.V1064V	ATPase, class V, type 1	62 (0.00)	29 (0.21)	0.76
11-02	Gp4 Focus 2	g.chr15:25940259C>T	Missense Mutation	ATP10A	p.C932Y	ATPase, class V, type 1	17 (0.00)	41 (0.17)	0.63
11-02	Gp4 Focus 2	g.chr5:160067493G>A	Silent	ATP10B	p.I325I	ATPase, class V, type 1	46 (0.00)	32 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr5:160067498G>A	Missense Mutation	ATP10B	p.L324F	ATPase, class V, type 1	50 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr4:47574900C>T	Silent	ATP10D	p.A1084A	ATPase, class V, type 1	105 (0.00)	67 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr13:113473686C>T	Silent	ATP11A	p.T213T	ATPase, class VI, type 1	56 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr13:113526074C>T	Missense Mutation	ATP11A	p.T1006M	ATPase, class VI, type 1	37 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr13:25262583C>T	Silent	ATP12A	p.L119L	ATPase, H+/K+ transpo	109 (0.00)	37 (0.49)	1.30
11-02	Gp4 Focus 2	g.chr1:17314964C>T	Missense Mutation	ATP13A2	p.C872Y	ATPase type 13A2	18 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr1:116931599G>A	Missense Mutation	ATP1A1	p.E238K	ATPase, Na+/K+ transp	36 (0.00)	33 (0.21)	0.44
11-02	Gp4 Focus 2	g.chr1:160156114C>T	Silent	ATP1A4	p.V1006V	ATPase, Na+/K+ transp	27 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chrX:119509392G>A	Missense Mutation	ATP1B4	p.G243E	ATPase, Na+/K+ transp	29 (0.00)	10 (0.60)	1.34
11-02	Gp4 Focus 2	g.chr17:3839738G>A	Silent	ATP2A3	p.L783L	ATPase, Ca++ transport	15 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:203678448G>A	Missense Mutation	ATP2B4	p.G526D	ATPase, Ca++ transport	20 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr18:43666355G>T	Missense Mutation	ATP5A1	p.Q428K	ATP synthase, H+ trans	39 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr12:57032950G>A	Missense Mutation	ATP5B	p.H477Y	ATP synthase, H+ trans	68 (0.01)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:41939442G>A	Splice Site	ATP5SL	p.L145F	ATP5S-like	47 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr5:81614028G>A	Missense Mutation	ATP6AP1L	p.R195Q	ATPase, H+ transportin	20 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr17:40673109C>T	Missense Mutation	ATP6V0A1	p.H830Y	ATPase, H+ transportin	64 (0.00)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr8:20067946G>A	Missense Mutation	ATP6V1B2	p.M127I	ATPase, H+ transportin	30 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr8:20074759C>T	Missense Mutation	ATP6V1B2	p.S397L	ATPase, H+ transportin	124 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr18:55322513G>A	Silent	ATP8B1	p.C948C	ATPase, aminophospho	95 (0.00)	63 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr3:142242872G>C	Nonsense Mutation	ATR	p.S1372*	ATR serine/threonine ki	84 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr3:142268516C>T	Splice Site	ATR		ATR serine/threonine ki	33 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr20:3543979C>T	Silent	ATRN	p.C585C	attractin	70 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr10:116889297G>A	Splice Site	ATRNL1	p.G277S	attractin-like 1	21 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr12:111893913G>A	Nonsense Mutation	ATXN2	p.Q957*	ataxin 2	61 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr1:110034200G>A	Missense Mutation	ATXN7L2	p.R672Q	ataxin 7-like 2	21 (0.00)	22 (0.36)	0.76
11-02	Gp4 Focus 2	g.chr7:32598596G>A	Missense Mutation	AVL9	p.M245I	AVL9 homolog (S. cere	34 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:32612981C>T	Silent	AVL9	p.A507A	AVL9 homolog (S. cere	38 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr16:396491G>A	Missense Mutation	AXIN1	p.P179S	axin 1	36 (0.00)	31 (0.19)	0.62

11-02	Gp4 Focus 2	g.chr8:103841576C>A	Missense Mutation	AZIN1	p.D387Y	antizyme inhibitor 1	144 (0.00)	28 (0.32)	1.10
11-02	Gp4 Focus 2	g.chr8:103841655C>A	Missense Mutation	AZIN1	p.E360D	antizyme inhibitor 1	132 (0.00)	35 (0.43)	1.47
11-02	Gp4 Focus 2	g.chr1:235647758G>A	Silent	B3GALNT2	p.V145V	beta-1,3-N-acetylgalact	53 (0.00)	31 (0.39)	1.03
11-02	Gp4 Focus 2	g.chr21:41033194C>T	Silent	B3GALT5	p.V236V	UDP-Gal:betaGlcNAc	15 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr11:66114330G>A	Silent	B3GNT1	p.D229D	UDP-GlcNAc:betaGal	19 (0.00)	9 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr2:62449667G>A	Silent	B3GNT2	p.S104S	UDP-GlcNAc:betaGal	55 (0.00)	36 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr9:104125201G>A	Missense Mutation	BAAT	p.L256F	bile acid CoA:amino aci	54 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr11:117163836C>G	Missense Mutation	BACE1	p.W258C	beta-site APP-cleaving	53 (0.00)	18 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr21:11098798G>C	RNA	BAGE2		B melanoma antigen far	18 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr6:69684670G>A	Missense Mutation	BAI3	p.C514Y	brain-specific angiogen	61 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr6:69944973G>A	Missense Mutation	BAI3	p.G886D	brain-specific angiogen	48 (0.00)	19 (0.58)	1.54
11-02	Gp4 Focus 2	g.chr6:69944982G>A	Missense Mutation	BAI3	p.C889Y	brain-specific angiogen	50 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr10:28971092G>A	Missense Mutation	BAMBI	p.R182K	BMP and activin memb	42 (0.00)	14 (0.50)	1.67
11-02	Gp4 Focus 2	g.chr10:28971177G>A	Silent	BAMBI	p.K210K	BMP and activin memb	48 (0.00)	28 (0.43)	1.43
11-02	Gp4 Focus 2	g.chr16:88068928G>A	Splice Site	BANP		BTG3 associated nuclea	17 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr16:88068969G>A	Missense Mutation	BANP	p.G403E	BTG3 associated nuclea	17 (0.00)	19 (0.58)	1.54
11-02	Gp4 Focus 2	g.chr2:160287535G>A	Missense Mutation	BAZ2B	p.S678F	bromodomain adjacent t	30 (0.00)	15 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr2:160304816G>A	Missense Mutation	BAZ2B	p.H147Y	bromodomain adjacent t	81 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr2:160310275G>A	Silent	BAZ2B	p.N61N	bromodomain adjacent t	31 (0.00)	30 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr20:52644957G>A	Nonsense Mutation	BCAS1	p.Q233*	breast carcinoma amplif	96 (0.00)	75 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr17:59115400G>A	Missense Mutation	BCAS3	p.S653N	breast carcinoma amplif	18 (0.00)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr2:60687570C>T	Missense Mutation	BCL11A	p.R792Q	B-cell CLL/lymphoma	89 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr20:30309566C>T	Silent	BCL2L1	p.V152V	BCL2-like 1	96 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr20:30309609C>T	Missense Mutation	BCL2L1	p.G138D	BCL2-like 1	97 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr7:72957901G>A	Missense Mutation	BCL7B	p.S81F	B-cell CLL/lymphoma	24 (0.00)	48 (0.92)	3.96
11-02	Gp4 Focus 2	g.chr7:72957941G>A	Nonsense Mutation	BCL7B	p.R68*	B-cell CLL/lymphoma	28 (0.00)	46 (0.91)	3.94
11-02	Gp4 Focus 2	g.chr16:14758797G>A	Silent	BFAR	p.L218L	bifunctional apoptosis r	20 (0.05)	24 (0.92)	2.44
11-02	Gp4 Focus 2	g.chrX:102004037C>T	Silent	BHLHB9	p.A38A	basic helix-loop-helix d	43 (0.00)	24 (0.58)	1.30
11-02	Gp4 Focus 2	g.chr3:5024631G>A	Missense Mutation	BHLHE40	p.D165N	basic helix-loop-helix fa	212 (0.00)	66 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr10:60566869G>A	Missense Mutation	BICC1	p.R776K	BicC family RNA bindi	40 (0.00)	30 (0.17)	0.53
11-02	Gp4 Focus 2	g.chr12:32490723G>A	Missense Mutation	BICD1	p.R848Q	bicaudal D homolog 1 (	27 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr9:95480231C>A	Splice Site	BICD2		bicaudal D homolog 2 (	36 (0.00)	44 (0.39)	1.03
11-02	Gp4 Focus 2	g.chr2:32602748C>T	Missense Mutation	BIRC6	p.L140F	baculoviral IAP repeat c	102 (0.00)	47 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr2:32707621C>A	Nonsense Mutation	BIRC6	p.S2556*	baculoviral IAP repeat c	108 (0.00)	61 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr2:32724768G>A	Missense Mutation	BIRC6	p.D2875N	baculoviral IAP repeat c	85 (0.00)	51 (0.31)	0.84

11-02	Gp4 Focus 2	g.chr15:91286883G>A	Intron	BLM		Bloom syndrome, RecQ	28 (0.00)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr15:91304345C>T	Missense Mutation	BLM	p.T581I	Bloom syndrome, RecQ	28 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr15:91312735C>T	Missense Mutation	BLM	p.P825L	Bloom syndrome, RecQ	54 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr15:91321124C>T	Intron	BLM		Bloom syndrome, RecQ	81 (0.01)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr15:91329297G>A	Intron	BLM		Bloom syndrome, RecQ	24 (0.00)	19 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr15:91330546A>G	Intron	BLM		Bloom syndrome, RecQ	20 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr15:91331342T>A	Intron	BLM		Bloom syndrome, RecQ	64 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr15:91332889C>T	Intron	BLM		Bloom syndrome, RecQ	62 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr15:91339401G>A	Intron	BLM		Bloom syndrome, RecQ	34 (0.03)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr8:22037273C>T	Missense Mutation	BMP1	p.P298S	bone morphogenetic prc	15 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr8:22054840G>A	Missense Mutation	BMP1	p.E672K	bone morphogenetic prc	38 (0.03)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr7:34125618G>A	Silent	BMPER	p.K553K	BMP binding endotheli	40 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr4:96036838C>T	Silent	BMPR1B	p.D83D	bone morphogenetic prc	53 (0.02)	11 (0.45)	2.07
11-02	Gp4 Focus 2	g.chr2:203242233C>A	Silent	BMPR2	p.P12P	bone morphogenetic prc	38 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr4:13616127T>C	Silent	BOD1L1	p.E289E	biorientation of chromo	91 (0.00)	16 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr13:73321107G>A	Nonsense Mutation	BORA	p.W447*	bora, aurora kinase A ac	45 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr6:3137670G>A	Missense Mutation	BPHL	p.A186T	biphenyl hydrolase-like	21 (0.00)	17 (0.94)	1.80
11-02	Gp4 Focus 2	g.chr7:140434455C>A	Missense Mutation	BRAF	p.C748F	B-Raf proto-oncogene,	63 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr17:41204517G>A	Intron	BRCA1		breast cancer 1, early on	26 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr17:41205419C>T	Intron	BRCA1		breast cancer 1, early on	46 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr17:41206235C>T	Intron	BRCA1		breast cancer 1, early on	51 (0.00)	41 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr17:41211669G>A	Intron	BRCA1		breast cancer 1, early on	119 (0.00)	59 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr17:41261356C>A	Intron	BRCA1		breast cancer 1, early on	35 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr17:41276526C>T	Intron	BRCA1		breast cancer 1, early on	69 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr13:32913238C>T	Silent	BRCA2	p.T1582T	breast cancer 2, early on	116 (0.00)	49 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr13:32928661G>A	Intron	BRCA2		breast cancer 2, early on	221 (0.00)	114 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr13:32934992C>G	Intron	BRCA2		breast cancer 2, early on	56 (0.00)	49 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr13:32955577C>T	Intron	BRCA2		breast cancer 2, early on	94 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr13:32955581G>C	Intron	BRCA2		breast cancer 2, early on	116 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr13:32955729G>A	Intron	BRCA2		breast cancer 2, early on	66 (0.00)	54 (0.31)	0.84
11-02	Gp4 Focus 2	g.chr13:32957813C>G	Intron	BRCA2		breast cancer 2, early on	191 (0.00)	60 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr13:32959265T>A	Intron	BRCA2		breast cancer 2, early on	33 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr13:32970688C>T	Intron	BRCA2		breast cancer 2, early on	34 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr22:50187924G>A	Missense Mutation	BRD1	p.P706L	bromodomain containin	25 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr19:15375539G>A	Silent	BRD4	p.T296T	bromodomain containin	31 (0.00)	14 (0.50)	1.33

11-02	Gp4 Focus 2	g.chr1:190067716C>T	Missense Mutation	BRINP3	p.G578D	bone morphogenetic pr	67 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr14:93712538G>T	Missense Mutation	BTBD7	p.P739H	BTB (POZ) domain con	53 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr3:15686557G>A	Missense Mutation	BTD	p.M400I	biotinidase	78 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr3:15686650G>A	Silent	BTD	p.E431E	biotinidase	86 (0.00)	55 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr7:99015184G>A	Missense Mutation	BUD31	p.C88Y	BUD31 homolog (S. ce	24 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr2:201680428G>A	Missense Mutation	BZW1	p.D94N	basic leucine zipper and	42 (0.00)	23 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr10:98742517C>A	Missense Mutation	C10orf12	p.A457E	chromosome 10 open re	40 (0.00)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr10:96954330A>C	Missense Mutation	C10orf129	p.T30P		30 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr10:128193058G>A	Silent	C10orf90	p.D190D	chromosome 10 open re	35 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr11:122774696G>A	Silent	C11orf63	p.K136K	chromosome 11 open re	153 (0.01)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr14:91639667G>A	Missense Mutation	C14orf159	p.C159Y	chromosome 14 open re	42 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr14:77294717G>A	Missense Mutation	C14orf166B	p.V58M		44 (0.00)	49 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr15:81429068G>A	Missense Mutation	C15orf26	p.R124K	chromosome 15 open re	26 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr15:81440782A>T	Missense Mutation	C15orf26	p.R272W	chromosome 15 open re	41 (0.00)	24 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr15:76467968C>T	Nonsense Mutation	C15orf27	p.Q241*	chromosome 15 open re	33 (0.00)	50 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr15:76468010C>T	Nonsense Mutation	C15orf27	p.Q255*	chromosome 15 open re	25 (0.00)	47 (0.40)	1.08
11-02	Gp4 Focus 2	g.chr15:83677389G>A	Missense Mutation	C15orf40	p.P93S	chromosome 15 open re	37 (0.00)	75 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr16:81094830G>A	Missense Mutation	C16orf46	p.P375L	chromosome 16 open re	30 (0.00)	13 (0.85)	2.26
11-02	Gp4 Focus 2	g.chr16:5106130G>A	Silent	C16orf89	p.A229A	chromosome 16 open re	16 (0.00)	17 (0.41)	1.31
11-02	Gp4 Focus 2	g.chr17:7329134G>A	Missense Mutation	C17orf74	p.V43M	chromosome 17 open re	57 (0.00)	81 (0.53)	0.39
11-02	Gp4 Focus 2	g.chr1:162825045G>A	Missense Mutation	C1orf110	p.P140L	chromosome 1 open rea	38 (0.00)	34 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr1:169821967G>A	Missense Mutation	C1orf112	p.E801K	chromosome 1 open rea	27 (0.00)	62 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:154184802G>A	Missense Mutation	C1orf43	p.A187V	chromosome 1 open rea	45 (0.00)	28 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr1:43240459A>C	Missense Mutation	C1orf50	p.I112L	chromosome 1 open rea	26 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr1:150255948G>A	Missense Mutation	C1orf51	p.G91R		52 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr1:150255972G>A	Missense Mutation	C1orf51	p.D99N		44 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr12:7187919C>T	Missense Mutation	C1R	p.G627R	complement component	31 (0.00)	58 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr20:56730598G>A	Silent	C20orf85	p.P75P	chromosome 20 open re	33 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr11:73785627C>T	Missense Mutation	C2CD3	p.G1541E	C2 calcium-dependent d	21 (0.00)	25 (0.56)	1.49
11-02	Gp4 Focus 2	g.chr12:22659733C>T	Silent	C2CD5	p.L353L	C2 calcium-dependent d	42 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr2:20990039T>C	Missense Mutation	C2orf43	p.K92E	chromosome 2 open rea	65 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr2:219232229C>T	Silent	C2orf62	p.F303F		15 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr2:29296826G>A	Missense Mutation	C2orf71	p.S101F	chromosome 2 open rea	52 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr2:61390285G>A	Missense Mutation	C2orf74	p.R110K	chromosome 2 open rea	50 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:74040957G>A	Missense Mutation	C2orf78	p.D151N	chromosome 2 open rea	41 (0.00)	25 (0.24)	0.64

11-02	Gp4 Focus 2	g.chr3:63805244G>A	Missense Mutation	C3orf49	p.G33S	chromosome 3 open rea	77 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr4:113468528G>T	Silent	C4orf21	p.P1837P		56 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr4:120221552C>T	Missense Mutation	C4orf3	p.D47N	chromosome 4 open rea	90 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr5:37201778C>T	Missense Mutation	C5orf42	p.S1141N	chromosome 5 open rea	74 (0.00)	45 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr6:71298392G>A	Missense Mutation	C6orf57	p.D98N	chromosome 6 open rea	37 (0.00)	36 (0.31)	0.81
11-02	Gp4 Focus 2	g.chr5:40955556C>T	Silent	C7	p.G387G	complement component	37 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:40314158C>T	Missense Mutation	C7orf10	p.T215I		95 (0.00)	42 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr7:25218798C>T	Missense Mutation	C7orf31	p.D44N	chromosome 7 open rea	37 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr7:25218834G>A	Missense Mutation	C7orf31	p.P32S	chromosome 7 open rea	38 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr7:139102412G>T	Missense Mutation	C7orf55-LUC7	p.S313I	C7orf55-LUC7L2 readtl	32 (0.00)	43 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr8:67425811G>A	Missense Mutation	C8orf46	p.S106N	chromosome 8 open rea	22 (0.00)	37 (0.86)	2.92
11-02	Gp4 Focus 2	g.chr9:131591033C>T	Silent	C9orf114	p.A63A	chromosome 9 open rea	37 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr9:35045543C>A	Missense Mutation	C9orf131	p.H973N	chromosome 9 open rea	58 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:112969692C>A	Missense Mutation	C9orf152	p.Q56H	chromosome 9 open rea	36 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr9:100675734G>A	Missense Mutation	C9orf156	p.H120Y	chromosome 9 open rea	63 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:135374847G>T	Silent	C9orf171	p.V128V	chromosome 9 open rea	23 (0.00)	45 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr9:136251423G>A	Missense Mutation	C9orf96	p.R81Q		16 (0.00)	35 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr15:63638858G>A	Silent	CA12	p.L53L	carbonic anhydrase XII	19 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr8:86163129C>T	Silent	CA13	p.S66S	carbonic anhydrase XIII	39 (0.00)	84 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr13:49906103C>T	Missense Mutation	CAB39L	p.E272K	calcium binding protein	111 (0.00)	56 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr13:49906160C>T	Missense Mutation	CAB39L	p.E253K	calcium binding protein	132 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr22:24460559C>T	Missense Mutation	CABIN1	p.T599I	calcineurin binding prot	30 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr22:24481018C>T	Silent	CABIN1	p.Y1009Y	calcineurin binding prot	34 (0.00)	21 (0.62)	1.65
11-02	Gp4 Focus 2	g.chr9:140952675G>A	Missense Mutation	CACNA1B	p.M1427I	calcium channel, voltag	25 (0.00)	23 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr1:181548355A>T	Missense Mutation	CACNA1E	p.N255I	calcium channel, voltag	71 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr1:181620530C>G	Missense Mutation	CACNA1E	p.I336M	calcium channel, voltag	32 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr16:1255243G>A	Missense Mutation	CACNA1H	p.D861N	calcium channel, voltag	18 (0.00)	12 (0.50)	1.60
11-02	Gp4 Focus 2	g.chr1:201052384G>A	Silent	CACNA1S	p.V433V	calcium channel, voltag	17 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr3:54871248G>A	Silent	CACNA2D3	p.Q487Q	calcium channel, voltag	85 (0.01)	47 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr2:152698482G>C	Missense Mutation	CACNB4	p.L366V	calcium channel, voltag	49 (0.00)	38 (0.18)	0.60
11-02	Gp4 Focus 2	g.chr2:27454914G>A	Missense Mutation	CAD	p.V760M	carbamoyl-phosphate sy	23 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr3:85029779G>A	Intron	CADM2		cell adhesion molecule	46 (0.02)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:85041162A>T	Intron	CADM2		cell adhesion molecule	36 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr3:85057829C>T	Intron	CADM2		cell adhesion molecule	15 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:85087388G>A	Intron	CADM2		cell adhesion molecule	79 (0.00)	15 (0.33)	0.89

11-02	Gp4 Focus 2	g.chr3:85091943G>A	Intron	CADM2	cell adhesion molecule	85 (0.00)	45 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr3:85138125C>T	Intron	CADM2	cell adhesion molecule	27 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:85157100A>G	Intron	CADM2	cell adhesion molecule	31 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr3:85167665C>G	Intron	CADM2	cell adhesion molecule	17 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:85200292T>A	Intron	CADM2	cell adhesion molecule	58 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr3:85200320T>A	Intron	CADM2	cell adhesion molecule	57 (0.00)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr3:85208527G>A	Intron	CADM2	cell adhesion molecule	73 (0.00)	47 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr3:85210758G>A	Intron	CADM2	cell adhesion molecule	51 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr3:85218402C>A	Intron	CADM2	cell adhesion molecule	25 (0.00)	51 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr3:85221908G>A	Intron	CADM2	cell adhesion molecule	81 (0.00)	86 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr3:85280678G>A	Intron	CADM2	cell adhesion molecule	38 (0.00)	31 (0.35)	0.95
11-02	Gp4 Focus 2	g.chr3:85303162C>T	Intron	CADM2	cell adhesion molecule	97 (0.01)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr3:85322566G>A	Intron	CADM2	cell adhesion molecule	71 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr3:85405513G>A	Intron	CADM2	cell adhesion molecule	46 (0.00)	51 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr3:85479320G>A	Intron	CADM2	cell adhesion molecule	58 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr3:85502142G>A	Intron	CADM2	cell adhesion molecule	69 (0.00)	25 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr3:85576403C>T	Intron	CADM2	cell adhesion molecule	45 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr3:85621587C>T	Intron	CADM2	cell adhesion molecule	85 (0.00)	71 (0.61)	1.62
11-02	Gp4 Focus 2	g.chr3:85637900G>A	Intron	CADM2	cell adhesion molecule	48 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr3:85654758C>T	Intron	CADM2	cell adhesion molecule	119 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr3:85683290G>A	Intron	CADM2	cell adhesion molecule	65 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr3:85703576G>A	Intron	CADM2	cell adhesion molecule	48 (0.00)	59 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:85711782C>T	Intron	CADM2	cell adhesion molecule	87 (0.01)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr3:85734331G>T	Intron	CADM2	cell adhesion molecule	20 (0.00)	28 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr3:85742225T>C	Intron	CADM2	cell adhesion molecule	19 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr3:85757172G>A	Intron	CADM2	cell adhesion molecule	16 (0.00)	12 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr3:85759254C>A	Intron	CADM2	cell adhesion molecule	106 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr3:85768810G>A	Intron	CADM2	cell adhesion molecule	55 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr3:85781658G>A	Intron	CADM2	cell adhesion molecule	30 (0.00)	29 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr3:85844614C>T	Intron	CADM2	cell adhesion molecule	67 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr3:85855322G>A	Intron	CADM2	cell adhesion molecule	42 (0.00)	44 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr3:85857528G>A	Intron	CADM2	cell adhesion molecule	28 (0.00)	38 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr3:85857563C>T	Intron	CADM2	cell adhesion molecule	36 (0.00)	38 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr3:85912686C>T	Intron	CADM2	cell adhesion molecule	77 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr3:85914133C>T	Intron	CADM2	cell adhesion molecule	42 (0.00)	46 (0.17)	0.46

11-02	Gp4 Focus 2	g.chr3:85939355G>A	Intron	CADM2		cell adhesion molecule	53 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr3:85939404G>A	Intron	CADM2		cell adhesion molecule	56 (0.00)	35 (0.31)	0.84
11-02	Gp4 Focus 2	g.chr3:85939741G>A	Intron	CADM2		cell adhesion molecule	44 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr3:86018187C>T	Intron	CADM2		cell adhesion molecule	148 (0.00)	63 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr3:86023459G>A	Intron	CADM2		cell adhesion molecule	114 (0.00)	37 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr3:86071047G>A	Intron	CADM2		cell adhesion molecule	56 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr3:86075386G>A	Intron	CADM2		cell adhesion molecule	45 (0.00)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr3:62751612G>A	Silent	CADPS	p.F163F	Ca++-dependent secreti	39 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr17:46928453G>A	Silent	CALCOCO2	p.E206E	calcium binding and coi	72 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:105209545G>A	Missense Mutation	CALHM2	p.R52W	calcium homeostasis mo	19 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr10:12802986G>A	Silent	CAMK1D	p.K113K	calcium/calmodulin-dep	23 (0.00)	22 (0.41)	1.37
11-02	Gp4 Focus 2	g.chr4:114436259G>A	Missense Mutation	CAMK2D	p.T262I	calcium/calmodulin-dep	47 (0.00)	43 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr3:48266134C>A	Silent	CAMP	p.A120A	cathelicidin antimicrobi	15 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr9:138715028G>A	Silent	CAMSAP1	p.I493I	calmodulin regulated sp	39 (0.00)	55 (0.25)	0.68
11-02	Gp4 Focus 2	g.chr1:200825218C>G	Missense Mutation	CAMSAP2	p.T1326R	calmodulin regulated sp	38 (0.00)	52 (0.19)	0.51
11-02	Gp4 Focus 2	g.chrX:110494194C>A	Missense Mutation	CAPN6	p.R370L	calpain 6	37 (0.00)	33 (0.21)	0.47
11-02	Gp4 Focus 2	g.chr16:55600747G>T	Missense Mutation	CAPNS2	p.G27C	calpain, small subunit 2	35 (0.00)	46 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr16:55601307G>A	Silent	CAPNS2	p.L213L	calpain, small subunit 2	119 (0.00)	72 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr11:34097943C>T	Missense Mutation	CAPRIN1	p.P176L	cell cycle associated pro	71 (0.00)	55 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr11:34098185C>A	Silent	CAPRIN1	p.T228T	cell cycle associated pro	54 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr7:116544351G>A	Missense Mutation	CAPZA2	p.E114K	capping protein (actin fi	69 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr1:19683233C>A	Missense Mutation	CAPZB	p.G188C	capping protein (actin fi	81 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:48715074G>A	Silent	CARD8	p.L503L	caspase recruitment don	39 (0.00)	39 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr11:67191016C>T	Silent	CARNS1	p.D476D	carnosine synthase 1	30 (0.00)	27 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr13:111298411T>A	Missense Mutation	CARS2	p.K407M	cysteinyl-tRNA synthet	19 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr13:111335444C>T	Silent	CARS2	p.K203K	cysteinyl-tRNA synthet	22 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr15:40914194C>T	Missense Mutation	CASC5	p.H604Y	cancer susceptibility car	63 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr15:40943712C>A	Missense Mutation	CASC5	p.Q2112K	cancer susceptibility car	15 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr20:32217675G>A	Missense Mutation	CBFA2T2	p.V395I	core-binding factor, run	15 (0.00)	32 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr10:70506960G>A	Silent	CCAR1	p.L187L	cell division cycle and a	31 (0.00)	38 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr8:22475225G>A	Silent	CCAR2	p.E669E	cell cycle and apoptosis	38 (0.00)	81 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr18:66564492G>A	Missense Mutation	CCDC102B	p.D364N	coiled-coil domain cont	102 (0.00)	57 (0.12)	0.39
11-02	Gp4 Focus 2	g.chr2:55764661G>A	Missense Mutation	CCDC104	p.E194K		47 (0.00)	35 (0.49)	1.30
11-02	Gp4 Focus 2	g.chr7:31682549T>C	Missense Mutation	CCDC129	p.M430T	coiled-coil domain cont	69 (0.00)	101 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr3:42754685G>A	Silent	CCDC13	p.A614A	coiled-coil domain cont	17 (0.00)	14 (0.64)	1.71

11-02	Gp4 Focus 2	g.chr16:57764854G>A	Silent	CCDC135	p.E801E		22 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr3:123667787G>A	Missense Mutation	CCDC14	p.P189L	coiled-coil domain conta	35 (0.00)	41 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr2:179718186G>A	Missense Mutation	CCDC141	p.L1076F	coiled-coil domain conta	37 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr2:179718201G>A	Nonsense Mutation	CCDC141	p.Q1071*	coiled-coil domain conta	36 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr11:124829840G>A	Missense Mutation	CCDC15	p.G153R	coiled-coil domain conta	62 (0.00)	36 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:197521538C>T	Missense Mutation	CCDC150	p.R120W	coiled-coil domain conta	64 (0.00)	45 (0.51)	1.36
11-02	Gp4 Focus 2	g.chr6:151894582G>A	Missense Mutation	CCDC170	p.E350K	coiled-coil domain conta	22 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr9:15724949C>A	Missense Mutation	CCDC171	p.S556Y	coiled-coil domain conta	28 (0.00)	71 (0.79)	2.57
11-02	Gp4 Focus 2	g.chr1:3669145C>T	Nonsense Mutation	CCDC27	p.Q34*	coiled-coil domain conta	28 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr15:74536359T>A	Missense Mutation	CCDC33	p.S19T	coiled-coil domain conta	30 (0.00)	56 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr17:78032777G>A	Missense Mutation	CCDC40	p.E480K	coiled-coil domain conta	18 (0.00)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr10:61552866G>A	Missense Mutation	CCDC6	p.P412S	coiled-coil domain conta	28 (0.00)	16 (0.44)	1.39
11-02	Gp4 Focus 2	g.chr12:119926600G>A	Nonsense Mutation	CCDC60	p.W162*	coiled-coil domain conta	32 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr12:119937952G>A	Silent	CCDC60	p.E209E	coiled-coil domain conta	27 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr12:111317878G>A	Missense Mutation	CCDC63	p.A180T	coiled-coil domain conta	56 (0.00)	39 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr12:120436381G>A	Silent	CCDC64	p.E162E	coiled-coil domain conta	33 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr3:56647749G>A	Missense Mutation	CCDC66	p.E513K	coiled-coil domain conta	76 (0.00)	80 (0.34)	0.90
11-02	Gp4 Focus 2	g.chr11:93088691G>A	Missense Mutation	CCDC67	p.D62N	coiled-coil domain conta	143 (0.00)	43 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr2:56570027C>T	Silent	CCDC85A	p.S418S	coiled-coil domain conta	51 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr14:91745601G>A	Silent	CCDC88C	p.S1583S	coiled-coil domain conta	33 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr14:91810002C>A	Splice Site	CCDC88C		coiled-coil domain conta	33 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr4:7043691C>T	Silent	CCDC96	p.K325K	coiled-coil domain conta	36 (0.00)	49 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr5:68467123G>A	Missense Mutation	CCNB1	p.M130I	cyclin B1	39 (0.00)	15 (0.53)	1.77
11-02	Gp4 Focus 2	g.chr4:77969397G>C	Missense Mutation	CCNI	p.P370R	cyclin I	28 (0.00)	20 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:39373957G>A	Silent	CCR8	p.L45L	chemokine (C-C motif)	22 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr12:69987312G>A	Missense Mutation	CCT2	p.E301K	chaperonin containing T	25 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr1:156287267C>A	Missense Mutation	CCT3	p.Q277H	chaperonin containing T	85 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr17:33288405G>A	Missense Mutation	CCT6B	p.A3V	chaperonin containing T	22 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr22:17072550C>T	Silent	CCT8L2	p.G297G	chaperonin containing T	87 (0.00)	42 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr1:117568381C>T	Silent	CD101	p.V893V	CD101 molecule	40 (0.00)	76 (0.20)	0.41
11-02	Gp4 Focus 2	g.chr12:7559290G>C	Missense Mutation	CD163L1	p.L319V	CD163 molecule-like 1	23 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:158226046C>T	Missense Mutation	CD1A	p.A193V	CD1a molecule	27 (0.00)	51 (0.65)	1.73
11-02	Gp4 Focus 2	g.chr1:158299350C>A	Missense Mutation	CD1B	p.K232N	CD1b molecule	24 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:112063843G>A	Silent	CD200	p.L43L	CD200 molecule	25 (0.00)	46 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr3:112068664G>A	Missense Mutation	CD200	p.R267Q	CD200 molecule	33 (0.00)	23 (0.74)	1.97

11-02	Gp4 Focus 2	g.chr19:7808041C>T	Missense Mutation	CD209	p.D367N	CD209 molecule	36 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:160811415G>A	Missense Mutation	CD244	p.S113F	CD244 molecule, natur	23 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr11:66082812C>T	Missense Mutation	CD248	p.A563T	CD248 molecule, endos	21 (0.00)	29 (0.59)	1.56
11-02	Gp4 Focus 2	g.chr1:208062037C>A	Missense Mutation	CD34	p.G321V	CD34 molecule	107 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr11:35201954G>A	Splice Site	CD44	p.A123T	CD44 molecule (Indian	37 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr1:207966907T>G	Missense Mutation	CD46	p.S391A	CD46 molecule, comple	29 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr1:157805895G>A	Missense Mutation	CD5L	p.R36W	CD5 molecule-like	25 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr11:44626618C>A	Silent	CD82	p.S49S	CD82 molecule	15 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr2:87013056G>A	Missense Mutation	CD8A	p.A232V	CD8a molecule	27 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr2:87085534G>A	Missense Mutation	CD8B	p.H17Y	CD8b molecule	26 (0.00)	39 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr19:14507156G>A	Missense Mutation	CD97	p.V117M	CD97 molecule	31 (0.00)	36 (0.31)	0.81
11-02	Gp4 Focus 2	g.chr9:4685039G>A	Missense Mutation	CDC37L1	p.A99T	cell division cycle 37-li	44 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr6:110532007G>A	Splice Site	CDC40		cell division cycle 40	17 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:227235682G>A	Silent	CDC42BPA	p.H978H	CDC42 binding protein	21 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr14:103438377C>T	Missense Mutation	CDC42BPB	p.R588H	CDC42 binding protein	27 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr6:44390476G>A	Missense Mutation	CDC5L	p.R445Q	cell division cycle 5-lik	59 (0.00)	62 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr8:25364867G>A	Silent	CDCA2	p.R895R	cell division cycle assoc	82 (0.00)	31 (0.35)	0.95
11-02	Gp4 Focus 2	g.chr2:174229693G>A	Silent	CDCA7	p.R211R	cell division cycle assoc	33 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr16:68857342G>A	Silent	CDH1	p.E659E	cadherin 1, type 1, E-ca	47 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:68857394C>A	Missense Mutation	CDH1	p.Q677K	cadherin 1, type 1, E-ca	27 (0.00)	60 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr16:68857463C>T	Missense Mutation	CDH1	p.P700S	cadherin 1, type 1, E-ca	35 (0.00)	52 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr10:73406351G>A	Missense Mutation	CDH23	p.G481R	cadherin-related 23	29 (0.00)	60 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr10:73472452G>A	Missense Mutation	CDH23	p.G1089D	cadherin-related 23	19 (0.00)	36 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:1636391C>T	Silent	CDK11A	p.E460E	cyclin-dependent kinase	29 (0.00)	26 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:90613515G>A	Missense Mutation	CDK14	p.G334R	cyclin-dependent kinase	20 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr20:31984582C>T	Missense Mutation	CDK5RAP1	p.G97R	CDK5 regulatory subun	74 (0.01)	41 (0.54)	1.43
11-02	Gp4 Focus 2	g.chr9:123210402C>T	Silent	CDK5RAP2	p.E932E	CDK5 regulatory subun	49 (0.00)	70 (0.56)	1.16
11-02	Gp4 Focus 2	g.chr9:123298750C>T	Missense Mutation	CDK5RAP2	p.E188K	CDK5 regulatory subun	18 (0.00)	13 (0.46)	0.96
11-02	Gp4 Focus 2	g.chr9:123301319C>T	Splice Site	CDK5RAP2	p.K169K	CDK5 regulatory subun	89 (0.00)	14 (0.64)	1.34
11-02	Gp4 Focus 2	g.chr9:21970358G>A	Intron	CDKN2A		cyclin-dependent kinase	23 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr5:115151983C>T	Missense Mutation	CDO1	p.E38K	cysteine dioxygenase ty	49 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr11:125880400G>A	Missense Mutation	CDON	p.S463L	cell adhesion associated	50 (0.00)	42 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr19:45182170G>A	Silent	CEACAM19	p.S207S	carcinoembryonic antig	37 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr19:42213813C>T	Silent	CEACAM5	p.P93P	carcinoembryonic antig	47 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr19:42223994G>A	Silent	CEACAM5	p.R545R	carcinoembryonic antig	17 (0.00)	22 (0.64)	1.70

11-02	Gp4 Focus 2	g.chr19:42190909T>G	Missense Mutation	CEACAM7	p.Y103S	carcinoembryonic antig	18 (0.00)	49 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr22:17983882C>G	Missense Mutation	CECR2	p.S72C	cat eye syndrome chrom	29 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr1:214818935G>A	Missense Mutation	CENPF	p.E2008K	centromere protein F, 3	22 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chrX:100364530G>A	Missense Mutation	CENPI	p.V145I	centromere protein I	68 (0.01)	18 (0.50)	1.11
11-02	Gp4 Focus 2	g.chr11:117258040G>C	Missense Mutation	CEP164	p.E616Q	centrosomal protein 164	45 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr18:13056610C>G	Missense Mutation	CEP192	p.L1341V	centrosomal protein 192	73 (0.00)	19 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr1:180031471G>A	Silent	CEP350	p.E1793E	centrosomal protein 350	67 (0.01)	53 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr7:130042634G>A	Silent	CEP41	p.I143I	centrosomal protein 41k	17 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr10:95278693G>A	Silent	CEP55	p.L351L	centrosomal protein 55k	57 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr6:109480498C>T	Silent	CEP57L1	p.I283I	centrosomal protein 57k	44 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr1:26581722C>T	Missense Mutation	CEP85	p.P90L	centrosomal protein 85k	71 (0.00)	60 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr6:118786620G>A	Missense Mutation	CEP85L	p.T789I	centrosomal protein 85k	42 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr3:101476748A>T	Missense Mutation	CEP97	p.D374V	centrosomal protein 97k	23 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr2:202025265C>T	Missense Mutation	CFLAR	p.H302Y	CASP8 and FADD-like	58 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr17:48543071C>T	Missense Mutation	CHAD	p.R312Q	chondroadherin	19 (0.00)	63 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr17:48543180C>T	Missense Mutation	CHAD	p.E276K	chondroadherin	47 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr19:4409022G>A	Missense Mutation	CHAF1A	p.E76K	chromatin assembly fac	55 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr13:115089763C>T	Missense Mutation	CHAMP1	p.T149I	chromosome alignment	50 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr5:98215964G>A	Intron	CHD1		chromodomain helicase	216 (0.00)	45 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr5:98259868G>A	Intron	CHD1		chromodomain helicase	24 (0.00)	54 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr1:146724340C>G	Missense Mutation	CHD1L	p.Q64E	chromodomain helicase	104 (0.00)	44 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr15:93518140G>A	Missense Mutation	CHD2	p.R846Q	chromodomain helicase	47 (0.00)	15 (0.40)	1.32
11-02	Gp4 Focus 2	g.chr12:6701112G>A	Silent	CHD4	p.N1017N	chromodomain helicase	25 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr12:6709443C>G	Missense Mutation	CHD4	p.M391I	chromodomain helicase	21 (0.00)	17 (0.76)	2.04
11-02	Gp4 Focus 2	g.chr1:6167543G>A	Intron	CHD5		chromodomain helicase	24 (0.00)	41 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr1:6168283G>A	Intron	CHD5		chromodomain helicase	21 (0.00)	47 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr1:6168331G>A	Intron	CHD5		chromodomain helicase	18 (0.00)	31 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr1:6168408G>A	Intron	CHD5		chromodomain helicase	24 (0.00)	51 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr1:6168921G>A	Intron	CHD5		chromodomain helicase	16 (0.00)	47 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr1:6210692G>A	Intron	CHD5		chromodomain helicase	31 (0.00)	51 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr1:6210764G>A	Intron	CHD5		chromodomain helicase	29 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr1:6235968G>A	Intron	CHD5		chromodomain helicase	79 (0.00)	97 (0.25)	0.66
11-02	Gp4 Focus 2	g.chr1:6235969G>A	Intron	CHD5		chromodomain helicase	79 (0.00)	98 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr8:61736563G>A	Silent	CHD7	p.K1122K	chromodomain helicase	30 (0.00)	15 (0.40)	1.35
11-02	Gp4 Focus 2	g.chr8:61766011G>A	Missense Mutation	CHD7	p.E2243K	chromodomain helicase	44 (0.00)	38 (0.24)	0.80

11-02	Gp4 Focus 2	g.chr8:61766043G>A	Silent	CHD7	p.E2253E	chromodomain helicase	33 (0.00)	39 (0.18)	0.61
11-02	Gp4 Focus 2	g.chr8:61773585G>A	Silent	CHD7	p.G2577G	chromodomain helicase	145 (0.00)	25 (0.20)	0.68
11-02	Gp4 Focus 2	g.chr14:21873383G>A	Missense Mutation	CHD8	p.P1098S	chromodomain helicase	85 (0.00)	24 (0.33)	0.49
11-02	Gp4 Focus 2	g.chr16:53358056C>A	Missense Mutation	CHD9	p.A2632E	chromodomain helicase	78 (0.00)	32 (0.41)	1.08
11-02	Gp4 Focus 2	g.chr20:5904588C>T	Nonsense Mutation	CHGB	p.Q600*	chromogranin B (secret	40 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr1:111826761C>A	RNA	CHIAP2		chitinase, acidic pseudo	69 (0.00)	19 (0.26)	0.55
11-02	Gp4 Focus 2	g.chr19:59063026C>A	Missense Mutation	CHMP2A	p.R220L	charged multivesicular b	56 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr19:59065532C>T	Silent	CHMP2A	p.R16R	charged multivesicular b	32 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr8:23114001C>T	Missense Mutation	CHMP7	p.A229V	charged multivesicular b	35 (0.00)	26 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:184102345G>A	Silent	CHRD	p.G487G	chordin	15 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr17:4805349G>A	Silent	CHRNE	p.A126A	cholinergic receptor, nic	17 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr2:101010137C>G	Missense Mutation	CHST10	p.R214T	carbohydrate sulfotransf	52 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr1:153610832C>G	Missense Mutation	CHTOP	p.Q43E	chromatin target of PRM	80 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr16:57466433G>A	Missense Mutation	CIAPIN1	p.T199I	cytokine induced apopto	31 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:42799035C>T	Silent	CIC	p.L2413L	capicua transcriptional r	33 (0.00)	26 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr16:11000748G>A	Missense Mutation	CIITA	p.D467N	class II, major histocom	17 (0.00)	17 (0.29)	0.94
11-02	Gp4 Focus 2	g.chr12:120135825G>A	Silent	CIT	p.F1886F	citron rho-interacting se	36 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr12:120139702C>T	Missense Mutation	CIT	p.G1789E	citron rho-interacting se	32 (0.00)	21 (0.52)	1.40
11-02	Gp4 Focus 2	g.chr11:46776507C>T	Missense Mutation	CKAP5	p.M1600I	cytoskeleton associated	33 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr1:86904659G>A	Missense Mutation	CLCA2	p.G358E	chloride channel access	37 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:86919226T>A	Missense Mutation	CLCA2	p.V777E	chloride channel access	68 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr7:143018521C>A	Missense Mutation	CLCN1	p.T166N	chloride channel, voltag	15 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr3:184069853C>A	Missense Mutation	CLCN2	p.C744F	chloride channel, voltag	22 (0.00)	44 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr4:170634366G>A	Silent	CLCN3	p.V762V	chloride channel, voltag	42 (0.00)	18 (0.39)	1.33
11-02	Gp4 Focus 2	g.chr1:11883773G>A	Missense Mutation	CLCN6	p.A155T	chloride channel, voltag	17 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:16352609G>A	Missense Mutation	CLCNKA	p.G122E	chloride channel, voltag	41 (0.00)	78 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr3:190026069C>T	Silent	CLDN1	p.V211V	claudin 1	15 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:137749924G>A	Missense Mutation	CLDN18	p.G243R	claudin 18	93 (0.00)	40 (0.72)	1.93
11-02	Gp4 Focus 2	g.chr16:78056549G>A	Missense Mutation	CLEC3A	p.C18Y	C-type lectin domain fa	27 (0.00)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:8289444G>A	Missense Mutation	CLEC4A	p.E171K	C-type lectin domain fa	59 (0.00)	46 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr12:122839746C>A	Silent	CLIP1	p.L373L	CAP-GLY domain cont	36 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:155237827G>A	Silent	CLK2	p.I214I	CDC-like kinase 2	28 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr13:77569344G>A	Missense Mutation	CLN5	p.G156E	ceroid-lipofuscinosis, ne	51 (0.00)	32 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr11:72114062G>A	Missense Mutation	CLPB	p.H164Y	ClpB caseinolytic peptid	20 (0.00)	27 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr3:150690365G>A	Missense Mutation	CLRN1	p.A44V	clarin 1	36 (0.00)	17 (0.41)	1.10

11-02	Gp4 Focus 2	g.chr1:36202555G>T	Missense Mutation	CLSPN	p.P1290H	claspin	50 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr1:36212584A>T	Missense Mutation	CLSPN	p.N879K	claspin	39 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr8:27462583C>T	Silent	CLU	p.L229L	clusterin	31 (0.00)	47 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr5:10290704G>A	Silent	CMBL	p.P57P	carboxymethylenebuten	51 (0.00)	24 (0.83)	2.22
11-02	Gp4 Focus 2	g.chr5:79028117G>A	Missense Mutation	CMYA5	p.V1177I	cardiomyopathy associa	82 (0.00)	42 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr20:34582998C>T	Silent	CNBD2	p.A298A	cyclic nucleotide bindin	44 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr18:72185788A>T	Nonsense Mutation	CNDP2	p.K375*	CNDP dipeptidase 2 (m	23 (0.00)	36 (0.17)	0.53
11-02	Gp4 Focus 2	g.chr2:99013236G>A	Missense Mutation	CNGA3	p.V539I	cyclic nucleotide gated	50 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr2:99013271C>A	Nonsense Mutation	CNGA3	p.Y550*	cyclic nucleotide gated	64 (0.00)	31 (0.39)	1.03
11-02	Gp4 Focus 2	g.chr8:87591463C>T	Missense Mutation	CNGB3	p.G600E	cyclic nucleotide gated	52 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr1:95363363G>A	Missense Mutation	CNN3	p.H309Y	calponin 3, acidic	129 (0.00)	17 (0.65)	1.73
11-02	Gp4 Focus 2	g.chr10:104679760G>A	Missense Mutation	CNNM2	p.C508Y	cyclin and CBS domain	24 (0.00)	24 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr16:58559176G>A	Missense Mutation	CNOT1	p.H2231Y	CCR4-NOT transcriptio	27 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr3:32815077G>A	Missense Mutation	CNOT10	p.A737T	CCR4-NOT transcriptio	39 (0.03)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr2:220039815G>A	Silent	CNPPD1	p.S92S	cyclin Pas1/PHO80 dom	48 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr7:99720146G>A	Silent	CNPY4	p.R96R	canopy FGF signaling r	17 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:99720523G>A	Silent	CNPY4	p.K153K	canopy FGF signaling r	15 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr11:58391862G>A	Nonsense Mutation	CNTF	p.W157*	ciliary neurotrophic fact	28 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr12:41419092G>A	Silent	CNTN1	p.G888G	contactin 1	95 (0.00)	41 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr11:100179147C>T	Missense Mutation	CNTN5	p.L893F	contactin 5	15 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr3:1363341C>T	Missense Mutation	CNTN6	p.P257S	contactin 6	89 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr7:147259253G>A	Missense Mutation	CNTNAP2	p.A601T	contactin associated pro	18 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr9:123880785C>T	Silent	CNTRL	p.A539A	centriolin	56 (0.00)	33 (0.36)	0.76
11-02	Gp4 Focus 2	g.chr7:51097145C>T	Missense Mutation	COBL	p.D550N	cordon-bleu WH2 repea	19 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr2:165557110G>A	Missense Mutation	COBLL1	p.S500L	cordon-bleu WH2 repea	28 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr14:31355260G>C	Missense Mutation	COCH	p.A295P	cochlin	45 (0.00)	34 (0.21)	0.65
11-02	Gp4 Focus 2	g.chr14:31355397C>T	Silent	COCH	p.F340F	cochlin	56 (0.02)	61 (0.36)	1.15
11-02	Gp4 Focus 2	g.chr6:75861861C>T	Missense Mutation	COL12A1	p.G1274D	collagen, type XII, alpha	72 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr10:71700774C>T	Missense Mutation	COL13A1	p.P626S	collagen, type XIII, alph	24 (0.00)	37 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr9:101810105G>A	Missense Mutation	COL15A1	p.G906D	collagen, type XV, alph	29 (0.00)	21 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr10:105813716G>A	Missense Mutation	COL17A1	p.P599L	collagen, type XVII, alp	21 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr6:70850847G>A	Splice Site	COL19A1	p.G483E	collagen, type XIX, alph	57 (0.00)	20 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr7:94057609C>T	Silent	COL1A2	p.Y1177Y	collagen, type I, alpha 2	52 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr8:139793206G>A	Silent	COL22A1	p.P538P	collagen, type XXII, alp	22 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr8:139793224C>T	Splice Site	COL22A1		collagen, type XXII, alp	20 (0.00)	34 (0.18)	0.47

11-02	Gp4 Focus 2	g.chr1:86554904G>A	Nonsense Mutation	COL24A1	p.Q554*	collagen, type XXIV, al	22 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:86578258C>T	Missense Mutation	COL24A1	p.G531S	collagen, type XXIV, al	64 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr12:48369176G>A	Silent	COL2A1	p.R1270R	collagen, type II, alpha	27 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr12:48393805G>A	Silent	COL2A1	p.L63L	collagen, type II, alpha	21 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr2:189871107G>A	Missense Mutation	COL3A1	p.G1044S	collagen, type III, alpha	28 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr13:111082892G>A	Splice Site	COL4A2	p.G196R	collagen, type IV, alpha	80 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr2:227945229C>T	Missense Mutation	COL4A4	p.G578E	collagen, type IV, alpha	56 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chrX:107403817G>A	Silent	COL4A6	p.Y1467Y	collagen, type IV, alpha	41 (0.00)	35 (0.20)	0.45
11-02	Gp4 Focus 2	g.chr2:189927911G>A	Missense Mutation	COL5A2	p.P619L	collagen, type V, alpha	66 (0.00)	29 (0.69)	1.84
11-02	Gp4 Focus 2	g.chr3:130159322C>T	Missense Mutation	COL6A5	p.T2047I	collagen, type VI, alpha	85 (0.01)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr3:130293069C>T	Missense Mutation	COL6A6	p.L1083F	collagen, type VI, alpha	104 (0.01)	28 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr1:183942750C>T	Splice Site	COLGALT2	p.K209K	collagen beta(1-O)galac	44 (0.02)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr1:160262276G>A	Silent	COPA	p.N986N	coatomer protein compl	44 (0.00)	54 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr3:128993779G>A	Silent	COPG1	p.K785K	coatomer protein compl	40 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr2:237998539G>A	Missense Mutation	COPS8	p.G78E	COP9 signalosome subu	20 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr4:47655620C>T	Missense Mutation	CORIN	p.R598K	corin, serine peptidase	90 (0.00)	24 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:101483788G>A	Silent	COX15	p.A225A	cytochrome c oxidase as	26 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr2:98263847C>T	Missense Mutation	COX5B	p.T73I	cytochrome c oxidase su	93 (0.00)	60 (0.32)	0.84
11-02	Gp4 Focus 2	g.chrX:77160720G>A	Missense Mutation	COX7B	p.V69I	cytochrome c oxidase su	80 (0.00)	19 (0.32)	0.53
11-02	Gp4 Focus 2	g.chr4:46737152G>A	Nonsense Mutation	COX7B2	p.Q20*	cytochrome c oxidase su	25 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr7:129950772G>C	Silent	CPA4	p.L313L	carboxypeptidase A4	29 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:207823041G>A	Missense Mutation	CPO	p.G95D	carboxypeptidase O	43 (0.00)	39 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr2:207823069C>T	Silent	CPO	p.D104D	carboxypeptidase O	56 (0.00)	38 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr11:68542790C>A	Silent	CPT1A	p.P523P	carnitine palmitoyltrans	59 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr7:29135767C>A	Nonsense Mutation	CPVL	p.G119*	carboxypeptidase, vitell	28 (0.00)	27 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr10:125521632C>A	Silent	CPXM2	p.V511V	carboxypeptidase X (M	17 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr1:207785077C>T	Silent	CR1	p.D2117D	complement component	92 (0.00)	55 (0.65)	1.75
11-02	Gp4 Focus 2	g.chr1:207647166C>A	Missense Mutation	CR2	p.Q726K	complement component	17 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr1:207647168G>A	Silent	CR2	p.Q726Q	complement component	17 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr16:1715107C>T	Missense Mutation	CRAMP1L	p.S907F	Crm, cramped-like (Dro	130 (0.00)	23 (0.30)	0.97
11-02	Gp4 Focus 2	g.chr1:197404142G>A	Missense Mutation	CRB1	p.R938K	crumbs family member	43 (0.00)	17 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr1:197411375C>A	Missense Mutation	CRB1	p.Q1208K	crumbs family member	28 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr7:137590518G>A	Missense Mutation	CREB3L2	p.P282L	cAMP responsive eleme	25 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr19:4164512C>T	Silent	CREB3L3	p.L197L	cAMP responsive eleme	25 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr19:4164523C>T	Silent	CREB3L3	p.S200S	cAMP responsive eleme	25 (0.00)	29 (0.17)	0.46

11-02	Gp4 Focus 2	g.chr1:153941524C>T	Missense Mutation	CREB3L4	p.P98L	cAMP responsive eleme	58 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:3807815G>A	Missense Mutation	CREBBP	p.R1202C	CREB binding protein	22 (0.00)	31 (0.55)	1.75
11-02	Gp4 Focus 2	g.chr16:3817760C>G	Missense Mutation	CREBBP	p.A1071P	CREB binding protein	53 (0.00)	21 (0.43)	1.37
11-02	Gp4 Focus 2	g.chr2:36706751G>A	Missense Mutation	CRIM1	p.G429D	cysteine rich transmemb	16 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr8:75928901G>A	Missense Mutation	CRISPLD1	p.D277N	cysteine-rich secretory p	186 (0.00)	60 (0.32)	1.07
11-02	Gp4 Focus 2	g.chr16:84872250C>T	Missense Mutation	CRISPLD2	p.A50V	cysteine-rich secretory p	23 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr16:84888369G>A	Missense Mutation	CRISPLD2	p.G215S	cysteine-rich secretory p	25 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr20:20028433G>A	Missense Mutation	CRNKL1	p.R200W	crooked neck pre-mRN	45 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr1:17264146C>T	Silent	CROCC	p.L402L	ciliary rootlet coiled-coi	29 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr15:91169162G>A	Missense Mutation	CRTC3	p.V302M	CREB regulated transcr	73 (0.00)	72 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr12:107415900G>A	Missense Mutation	CRY1	p.R77C	cryptochrome circadian	25 (0.00)	46 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr1:36933545G>A	Missense Mutation	CSF3R	p.S581F	colony stimulating facto	16 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr10:43678942G>A	Silent	CSGALNACT	p.T527T	chondroitin sulfate N-ac	79 (0.01)	47 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr8:3046426C>T	Missense Mutation	CSMD1	p.E1837K	CUB and Sushi multiple	15 (0.00)	24 (0.25)	0.85
11-02	Gp4 Focus 2	g.chr1:34191111G>A	Missense Mutation	CSMD2	p.T845I	CUB and Sushi multiple	23 (0.00)	15 (0.73)	1.96
11-02	Gp4 Focus 2	g.chr8:113812470C>T	Silent	CSMD3	p.V631V	CUB and Sushi multiple	32 (0.00)	12 (0.42)	1.43
11-02	Gp4 Focus 2	g.chr4:70823502G>A	Silent	CSN2	p.I55I	casein beta	32 (0.00)	103 (0.45)	1.19
11-02	Gp4 Focus 2	g.chr11:11374112G>A	Silent	CSNK2A3	p.G185G	casein kinase 2, alpha 3	45 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr15:75979623C>T	Silent	CSPG4	p.Q1261Q	chondroitin sulfate prote	21 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr8:68107638A>G	Missense Mutation	CSPP1	p.D1159G	centrosome and spindle	42 (0.00)	87 (0.25)	0.85
11-02	Gp4 Focus 2	g.chr20:23472439G>A	Silent	CST8	p.V45V	cystatin 8 (cystatin-relat	32 (0.00)	30 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr20:23472493G>A	Silent	CST8	p.K63K	cystatin 8 (cystatin-relat	27 (0.00)	33 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr10:53457956C>T	Missense Mutation	CSTF2T	p.G452S	cleavage stimulation fac	27 (0.00)	44 (0.18)	0.62
11-02	Gp4 Focus 2	g.chr10:53457973C>T	Missense Mutation	CSTF2T	p.R446K	cleavage stimulation fac	27 (0.00)	41 (0.20)	0.67
11-02	Gp4 Focus 2	g.chr10:53458477C>T	Missense Mutation	CSTF2T	p.G278D	cleavage stimulation fac	25 (0.00)	39 (0.18)	0.62
11-02	Gp4 Focus 2	g.chr17:34292169G>A	RNA	CTB-186H2.2			32 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr19:18142570G>A	RNA	CTB-52I2.4			37 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr5:134678969G>T	Missense Mutation	CTC-349C3.1	p.G84V		35 (0.00)	33 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr17:8132516G>T	Nonsense Mutation	CTC1	p.C1055*	CTS telomere maintena	95 (0.00)	14 (0.86)	0.64
11-02	Gp4 Focus 2	g.chr11:66281891C>T	Silent	CTD-3074O7.	p.D95D		26 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr11:66281943G>A	Missense Mutation	CTD-3074O7.	p.V113M		26 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr11:66291266G>A	Silent	CTD-3074O7.	p.R378R		16 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr18:46287799C>T	Silent	CTIF	p.N370N	CBP80/20-dependent tra	16 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr10:68940116G>A	Missense Mutation	CTNNA3	p.R336C	catenin (cadherin-associ	70 (0.00)	31 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr10:68979422C>T	Missense Mutation	CTNNA3	p.M262I	catenin (cadherin-associ	77 (0.01)	30 (0.17)	0.44

11-02	Gp4 Focus 2	g.chr20:36407688G>A	Missense Mutation	CTNNBL1	p.E141K	catenin, beta like 1	36 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr1:41475217G>A	Silent	CTPS1	p.G549G	CTP synthase 1	30 (0.00)	42 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr11:10796753G>A	Splice Site	CTR9		CTR9, Paf1/RNA polyn	45 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr20:44522703G>A	Missense Mutation	CTSA	p.V275M	cathepsin A	43 (0.00)	62 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr1:150724435G>C	Missense Mutation	CTSS	p.A150G	cathepsin S	41 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr7:117368229G>A	Silent	CTTNBP2	p.A1323A	cortactin binding protei	43 (0.00)	45 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr6:43152349C>T	Missense Mutation	CUL9	p.P101S	cullin 9	26 (0.00)	52 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr6:43156317G>T	Missense Mutation	CUL9	p.A682S	cullin 9	16 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr6:43182841C>T	Missense Mutation	CUL9	p.P1877S	cullin 9	43 (0.00)	24 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr12:111729262C>T	Silent	CUX2	p.D114D	cut-like homeobox 2	17 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr17:36966734G>A	Missense Mutation	CWC25	p.H205Y	CWC25 spliceosome-as	39 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr5:64079801G>T	Nonsense Mutation	CWC27	p.G131*	CWC27 spliceosome-as	35 (0.00)	36 (0.17)	0.55
11-02	Gp4 Focus 2	g.chr11:107224439G>A	Silent	CWF19L2	p.D632D	CWF19-like 2, cell cycl	24 (0.00)	23 (0.48)	1.28
11-02	Gp4 Focus 2	g.chrX:149100932C>T	Missense Mutation	CXorf40B	p.E103K	chromosome X open rea	15 (0.00)	12 (0.50)	0.83
11-02	Gp4 Focus 2	g.chr11:7690878C>T	Missense Mutation	CYB5R2	p.G79D	cytochrome b5 reductas	48 (0.00)	44 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr5:156766215C>G	Missense Mutation	CYFIP2	p.L820V	cytoplasmic FMR1 inte	63 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr5:156788484G>A	Missense Mutation	CYFIP2	p.E947K	cytoplasmic FMR1 inte	50 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:41350556G>A	Missense Mutation	CYP2A6	p.A428V	cytochrome P450, famil	68 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr19:41626307G>A	Silent	CYP2F1	p.Q130Q	cytochrome P450, famil	40 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr19:41626351G>A	Missense Mutation	CYP2F1	p.R145Q	cytochrome P450, famil	35 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr7:6204606G>A	Missense Mutation	CYTH3	p.T390M	cytohesin 3	32 (0.00)	18 (0.28)	0.99
11-02	Gp4 Focus 2	g.chr5:39394394G>A	Missense Mutation	DAB2	p.T10I	Dab, mitogen-responsiv	71 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr9:124338203G>A	Intron	DAB2IP		DAB2 interacting protei	27 (0.00)	12 (0.67)	1.39
11-02	Gp4 Focus 2	g.chr9:124347725C>T	Intron	DAB2IP		DAB2 interacting protei	29 (0.00)	19 (0.26)	0.55
11-02	Gp4 Focus 2	g.chr9:124356975G>A	Intron	DAB2IP		DAB2 interacting protei	32 (0.00)	33 (0.24)	0.51
11-02	Gp4 Focus 2	g.chr9:124362970G>A	Intron	DAB2IP		DAB2 interacting protei	104 (0.00)	21 (0.24)	0.50
11-02	Gp4 Focus 2	g.chr9:124374100G>A	Intron	DAB2IP		DAB2 interacting protei	33 (0.00)	24 (0.21)	0.43
11-02	Gp4 Focus 2	g.chr9:124376296G>A	Intron	DAB2IP		DAB2 interacting protei	59 (0.00)	26 (0.38)	0.80
11-02	Gp4 Focus 2	g.chr9:124377804A>G	Intron	DAB2IP		DAB2 interacting protei	51 (0.00)	41 (0.20)	0.41
11-02	Gp4 Focus 2	g.chr9:124381414G>A	Intron	DAB2IP		DAB2 interacting protei	111 (0.00)	82 (0.33)	0.69
11-02	Gp4 Focus 2	g.chr9:124391745C>T	Intron	DAB2IP		DAB2 interacting protei	47 (0.02)	25 (0.40)	0.83
11-02	Gp4 Focus 2	g.chr9:124400283C>A	Intron	DAB2IP		DAB2 interacting protei	52 (0.00)	21 (0.29)	0.60
11-02	Gp4 Focus 2	g.chr9:124401286G>A	Intron	DAB2IP		DAB2 interacting protei	35 (0.00)	31 (0.29)	0.61
11-02	Gp4 Focus 2	g.chr9:124409272G>A	Intron	DAB2IP		DAB2 interacting protei	63 (0.00)	22 (0.23)	0.47
11-02	Gp4 Focus 2	g.chr9:124419669C>T	Intron	DAB2IP		DAB2 interacting protei	60 (0.00)	21 (0.24)	0.50

11-02	Gp4 Focus 2	g.chr9:124425358G>C	Intron	DAB2IP		DAB2 interacting protei	68 (0.00)	61 (0.23)	0.48
11-02	Gp4 Focus 2	g.chr9:124434305C>T	Intron	DAB2IP		DAB2 interacting protei	22 (0.00)	33 (0.39)	0.82
11-02	Gp4 Focus 2	g.chr9:124436280G>A	Intron	DAB2IP		DAB2 interacting protei	22 (0.00)	30 (0.27)	0.56
11-02	Gp4 Focus 2	g.chr9:124436998C>A	Intron	DAB2IP		DAB2 interacting protei	30 (0.00)	23 (0.22)	0.45
11-02	Gp4 Focus 2	g.chr9:124445855G>A	Intron	DAB2IP		DAB2 interacting protei	39 (0.00)	44 (0.61)	1.28
11-02	Gp4 Focus 2	g.chr9:124453355G>A	Intron	DAB2IP		DAB2 interacting protei	34 (0.00)	20 (0.45)	0.94
11-02	Gp4 Focus 2	g.chr9:124472571G>A	Intron	DAB2IP		DAB2 interacting protei	17 (0.00)	39 (0.41)	0.86
11-02	Gp4 Focus 2	g.chr9:124481973C>T	Intron	DAB2IP		DAB2 interacting protei	34 (0.03)	43 (0.37)	0.78
11-02	Gp4 Focus 2	g.chr9:124484396G>A	Intron	DAB2IP		DAB2 interacting protei	52 (0.00)	27 (0.22)	0.46
11-02	Gp4 Focus 2	g.chr9:124489445C>T	Intron	DAB2IP		DAB2 interacting protei	62 (0.00)	26 (0.81)	1.69
11-02	Gp4 Focus 2	g.chr9:124496740G>A	Intron	DAB2IP		DAB2 interacting protei	31 (0.00)	36 (0.22)	0.46
11-02	Gp4 Focus 2	g.chr6:168694852C>A	Missense Mutation	DACT2	p.K252N	dishevelled-binding anta	24 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr6:168708956C>A	Missense Mutation	DACT2	p.S494I	dishevelled-binding anta	15 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr15:64218145C>T	Silent	DAPK2	p.E269E	death-associated protein	82 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr1:159175928G>A	Silent	DARC	p.K233K		26 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr1:159176240G>A	Silent	DARC	p.*337*		35 (0.00)	65 (0.92)	2.46
11-02	Gp4 Focus 2	g.chr1:173810084G>A	Silent	DARS2	p.V367V	aspartyl-tRNA syntheta	29 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr17:42800290G>A	Missense Mutation	DBF4B	p.G42D	DBF4 zinc finger B	30 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr8:104438325G>A	Silent	DCAF13	p.G292G	DDB1 and CUL4 associ	87 (0.00)	38 (0.32)	1.08
11-02	Gp4 Focus 2	g.chr14:69521357G>A	Silent	DCAF5	p.T682T	DDB1 and CUL4 associ	38 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr14:69522212C>T	Silent	DCAF5	p.G397G	DDB1 and CUL4 associ	24 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr17:61662575G>A	Silent	DCAF7	p.V47V	DDB1 and CUL4 associ	18 (0.00)	33 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr18:50592476G>T	Missense Mutation	DCC	p.V56L	DCC netrin 1 receptor	48 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr11:31128378G>A	Nonsense Mutation	DCDC1	p.Q573*	doublecortin domain co	69 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr11:6645109G>A	Missense Mutation	DCHS1	p.P2600S	dachsous cadherin-relat	48 (0.00)	33 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr11:6652927C>T	Missense Mutation	DCHS1	p.V1199I	dachsous cadherin-relat	24 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr4:155298497C>T	Missense Mutation	DCHS2	p.D112N	dachsous cadherin-relat	22 (0.00)	29 (0.59)	1.56
11-02	Gp4 Focus 2	g.chr1:114450746C>G	Silent	DCLRE1B	p.S157S	DNA cross-link repair 1	54 (0.00)	14 (0.43)	0.90
11-02	Gp4 Focus 2	g.chr1:155007129G>A	Splice Site	DCST1	p.G63D	DC-STAMP domain co	34 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr11:61081878G>A	Silent	DDB1	p.N497N	damage-specific DNA b	57 (0.00)	50 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr11:61099161G>A	Missense Mutation	DDB1	p.H22Y	damage-specific DNA b	27 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr8:38091962G>A	Missense Mutation	DDHD2	p.V91I	DDHD domain containi	100 (0.00)	36 (0.25)	0.81
11-02	Gp4 Focus 2	g.chr1:20979134G>A	Missense Mutation	DDOST	p.H384Y	dolichyl-diphosphoolig	34 (0.03)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr1:20979153G>A	Silent	DDOST	p.Y377Y	dolichyl-diphosphoolig	36 (0.00)	19 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr10:70723195G>A	Silent	DDX21	p.L252L	DEAD (Asp-Glu-Ala-A	35 (0.00)	74 (0.64)	1.69

11-02	Gp4 Focus 2	g.chr20:47855812G>A	Missense Mutation	DDX27	p.A643T	DEAD (Asp-Glu-Ala-A	19 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr20:47858438G>A	Missense Mutation	DDX27	p.A667T	DEAD (Asp-Glu-Ala-A	39 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr20:47860219G>A	Missense Mutation	DDX27	p.G784E	DEAD (Asp-Glu-Ala-A	51 (0.02)	42 (0.40)	1.08
11-02	Gp4 Focus 2	g.chr9:135522266C>T	Missense Mutation	DDX31	p.V488I	DEAD (Asp-Glu-Ala-A	41 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr17:61885210G>A	Missense Mutation	DDX42	p.D325N	DEAD (Asp-Glu-Ala-A	51 (0.00)	15 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr17:61889308C>T	Missense Mutation	DDX42	p.T472I	DEAD (Asp-Glu-Ala-A	81 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr12:12978984G>A	Silent	DDX47	p.K362K	DEAD (Asp-Glu-Ala-A	18 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr12:124102388C>T	Missense Mutation	DDX55	p.S378L	DEAD (Asp-Glu-Ala-A	16 (0.00)	40 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr9:118138994G>A	Splice Site	DEC1	p.V5I	deleted in esophageal ca	53 (0.00)	18 (0.28)	0.58
11-02	Gp4 Focus 2	g.chr6:35278334G>C	Missense Mutation	DEF6	p.M112I	differentially expressed	80 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr20:210288C>T	Missense Mutation	DEFB129	p.T143I	defensin, beta 129	42 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr9:126520005C>T	Silent	DENND1A	p.A93A	DENN/MADD domain	25 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr7:140302059T>A	Nonsense Mutation	DENND2A	p.K47*	DENN/MADD domain	23 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:115151333G>A	Nonsense Mutation	DENND2C	p.Q454*	DENN/MADD domain	57 (0.00)	21 (0.29)	0.60
11-02	Gp4 Focus 2	g.chr15:65960315C>T	Missense Mutation	DENND4A	p.R1601K	DENN/MADD domain	39 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr22:32198751C>T	Silent	DEPDC5	p.I336I	DEP domain containing	22 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr22:32302437C>T	Missense Mutation	DEPDC5	p.T1580M	DEP domain containing	21 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr22:20073958G>A	Missense Mutation	DGCR8	p.D158N	DGCR8 microprocessor	59 (0.02)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr2:169938385G>T	Missense Mutation	DHRS9	p.K98N	dehydrogenase/reductas	30 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr5:54603384C>T	Silent	DHX29	p.K6K	DEAH (Asp-Glu-Ala-H	34 (0.00)	19 (0.32)	1.05
11-02	Gp4 Focus 2	g.chr20:37621054G>A	Missense Mutation	DHX35	p.G190S	DEAH (Asp-Glu-Ala-H	72 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr2:39029968C>A	Silent	DHX57	p.V1302V	DEAH (Asp-Glu-Ala-A	63 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr17:41577344C>T	Silent	DHX8	p.S473S	DEAH (Asp-Glu-Ala-H	100 (0.00)	46 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr5:140953174G>A	Missense Mutation	DIAPH1	p.P748L	diaphanous-related forn	16 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:210012431G>A	Missense Mutation	DIEXF	p.E414K	digestive organ expansi	81 (0.01)	40 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr12:51108330C>T	Silent	DIP2B	p.C934C	DIP2 disco-interacting	30 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr1:68512763G>A	Missense Mutation	DIRAS3	p.T73I	DIRAS family, GTP-bi	44 (0.00)	24 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr3:122545834A>G	Missense Mutation	DIRC2	p.N209D	disrupted in renal carcin	55 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr13:73349381C>T	Missense Mutation	DIS3	p.D289N	DIS3 exosome endoribo	43 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr13:73349395C>T	Missense Mutation	DIS3	p.G284D	DIS3 exosome endoribo	43 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr2:232995410C>G	Missense Mutation	DIS3L2	p.S228C	DIS3 like 3'-5' exoribon	29 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr3:38158485G>A	Missense Mutation	DLEC1	p.S1400N	deleted in lung and esop	35 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr14:75360096G>A	Missense Mutation	DLST	p.G214E	dihydrolipoamide S-suc	35 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr10:124390744G>A	Missense Mutation	DMBT1	p.G1969D	deleted in malignant bra	58 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr10:124402681C>T	Missense Mutation	DMBT1	p.L2337F	deleted in malignant bra	21 (0.00)	31 (0.16)	0.43

11-02	Gp4 Focus 2	g.chr7:86822559C>T	Nonsense Mutation	DMTF1	p.Q514*	cyclin D binding myb-li	87 (0.00)	20 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr15:51772264C>T	Missense Mutation	DMXL2	p.A2213T	Dmx-like 2	114 (0.00)	36 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr15:51791707C>T	Silent	DMXL2	p.L1238L	Dmx-like 2	54 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr16:84203534G>C	Missense Mutation	DNAAF1	p.G367A	dynein, axonemal, asse	35 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr12:124330680G>A	Silent	DNAH10	p.R1813R	dynein, axonemal, heav	33 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr12:124364270C>T	Silent	DNAH10	p.F2734F	dynein, axonemal, heav	80 (0.00)	63 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr12:124401172G>T	Missense Mutation	DNAH10	p.D3513Y	dynein, axonemal, heav	37 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:21657395G>C	Splice Site	DNAH11	p.G1418G	dynein, axonemal, heav	26 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:225512031G>A	Silent	DNAH14	p.L2455L	dynein, axonemal, heav	44 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr1:225580109G>A	Missense Mutation	DNAH14	p.V3373I	dynein, axonemal, heav	38 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr16:20944638G>A	Silent	DNAH3	p.D4063D	dynein, axonemal, heav	36 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr16:20946732C>T	Missense Mutation	DNAH3	p.V3979I	dynein, axonemal, heav	30 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr5:13862686C>G	Missense Mutation	DNAH5	p.L1589F	dynein, axonemal, heav	36 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr5:13867915C>A	Missense Mutation	DNAH5	p.D1341Y	dynein, axonemal, heav	42 (0.00)	42 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr2:84851625C>T	Silent	DNAH6	p.L1412L	dynein, axonemal, heav	78 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr17:11865210G>A	Missense Mutation	DNAH9	p.M4214I	dynein, axonemal, heav	42 (0.00)	36 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr16:4496885A>T	Splice Site	DNAJA3		DnaJ (Hsp40) homolog,	23 (0.00)	16 (0.31)	1.00
11-02	Gp4 Focus 2	g.chr3:186299275T>C	Missense Mutation	DNAJB11	p.V191A	DnaJ (Hsp40) homolog,	63 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr2:183593648G>A	Missense Mutation	DNAJC10	p.G187D	DnaJ (Hsp40) homolog,	42 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:15888740G>A	Missense Mutation	DNAJC16	p.V420M	DnaJ (Hsp40) homolog,	26 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr1:15892453C>T	Silent	DNAJC16	p.A546A	DnaJ (Hsp40) homolog,	96 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr5:34945042G>A	Missense Mutation	DNAJC21	p.E352K	DnaJ (Hsp40) homolog,	148 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr13:96443131G>A	Missense Mutation	DNAJC3	p.M403I	DnaJ (Hsp40) homolog,	35 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr1:84864291C>T	Missense Mutation	DNASE2B	p.A15V	deoxyribonuclease II be	56 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr11:6532621C>T	Missense Mutation	DNHD1	p.H452Y	dynein heavy chain dom	82 (0.00)	43 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr15:84958382C>T	RNA	DNM1P51		DNM1 pseudogene 51	31 (0.00)	33 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr10:101639678G>A	Missense Mutation	DNMBP	p.P1480S	dynamin binding protei	42 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr19:10270697G>A	Silent	DNMT1	p.S346S	DNA (cytosine-5-)-met	21 (0.00)	37 (0.43)	1.15
11-02	Gp4 Focus 2	g.chr3:51393891C>T	Silent	DOCK3	p.I1490I	dedicator of cytokinesis	59 (0.00)	48 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:111430587G>A	Missense Mutation	DOCK4	p.L1081F	dedicator of cytokinesis	64 (0.00)	30 (0.83)	2.22
11-02	Gp4 Focus 2	g.chr8:25174610C>T	Missense Mutation	DOCK5	p.T469M	dedicator of cytokinesis	65 (0.00)	47 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:449847G>A	Missense Mutation	DOCK8	p.V1861I	dedicator of cytokinesis	67 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr20:53227021G>A	Missense Mutation	DOK5	p.E232K	docking protein 5	29 (0.00)	30 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr21:37642341G>A	Missense Mutation	DOPEY2	p.G1840R	dopey family member 2	98 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr16:68012408G>A	Missense Mutation	DPEP3	p.S204L	dipeptidase 3	37 (0.03)	51 (0.25)	0.68

11-02	Gp4 Focus 2	g.chr7:154172098G>A	Missense Mutation	DPP6	p.D145N	dipeptidyl-peptidase 6	23 (0.00)	25 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr7:154645512G>A	Silent	DPP6	p.T563T	dipeptidyl-peptidase 6	23 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr7:34981457G>A	Missense Mutation	DPY19L1	p.L464F	dpy-19-like 1 (C. elegan	49 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr19:32923641C>T	Missense Mutation	DPY19L3	p.S86L	dpy-19-like 3 (C. elegan	33 (0.00)	31 (0.35)	0.95
11-02	Gp4 Focus 2	g.chr19:32959644C>T	Missense Mutation	DPY19L3	p.P541L	dpy-19-like 3 (C. elegan	60 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr8:26509931G>A	Silent	DPYSL2	p.K480K	dihydropyrimidinase-lik	22 (0.00)	26 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr2:26647241G>A	Silent	DRC1	p.L153L	dynein regulatory comp	37 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr5:174868988G>A	Missense Mutation	DRD1	p.S372F	dopamine receptor D1	24 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chrX:100486627C>A	De novo Start InFran	DRP2		dystrophin related prote	19 (0.00)	14 (0.36)	0.80
11-02	Gp4 Focus 2	g.chr18:28650802G>A	Silent	DSC2	p.L714L	desmocollin 2	72 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr11:117391931G>A	Missense Mutation	DSCAML1	p.A436V	Down syndrome cell adl	29 (0.00)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr11:117651256C>T	Missense Mutation	DSCAML1	p.E166K	Down syndrome cell adl	36 (0.00)	37 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr6:116752219G>A	Missense Mutation	DSE	p.G258E	dermatan sulfate epimer	22 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr18:29122565C>T	Missense Mutation	DSG2	p.T695M	desmoglein 2	34 (0.00)	60 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr18:29055917C>A	Nonsense Mutation	DSG3	p.C898*	desmoglein 3	40 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr6:7579772G>A	Missense Mutation	DSP	p.E1117K	desmoplakin	52 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr6:7581069G>C	Missense Mutation	DSP	p.R1549T	desmoplakin	113 (0.00)	27 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr4:88535003G>A	Missense Mutation	DSPP	p.E397K	dentin sialophosphoprot	32 (0.00)	17 (0.82)	2.20
11-02	Gp4 Focus 2	g.chr6:56473419G>A	Nonsense Mutation	DST	p.Q1792*	dystonin	121 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr15:45455732C>T	Silent	DUOX1	p.I1417I	dual oxidase 1	27 (0.00)	35 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr12:12640110C>A	Missense Mutation	DUSP16	p.Q181H	dual specificity phospha	21 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr12:12653603C>T	Silent	DUSP16	p.E127E	dual specificity phospha	34 (0.00)	30 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:159752037C>A	Missense Mutation	DUSP23	p.A121D	dual specificity phospha	19 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr12:89743232C>G	Silent	DUSP6	p.S315S	dual specificity phospha	82 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr10:82122763G>A	Missense Mutation	DYDC2	p.M82I	DPY30 domain containi	16 (0.00)	20 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr18:46956642G>A	Silent	DYM	p.F41F	dymeclin	61 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr14:102477094C>T	Silent	DYNC1H1	p.V2141V	dynein, cytoplasmic 1, h	23 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr3:108392989G>A	Missense Mutation	DZIP3	p.C885Y	DAZ interacting zinc fir	57 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr16:67228797G>A	Missense Mutation	E2F4	p.R241H	E2F transcription factor	50 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:77419591G>A	Missense Mutation	E2F7	p.T771I	E2F transcription factor	24 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr12:77419621G>A	Missense Mutation	E2F7	p.S761F	E2F transcription factor	24 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr16:23546271G>A	Missense Mutation	EARS2	p.A299V	glutamyl-tRNA syntheta	16 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr16:23555888G>A	Silent	EARS2	p.P144P	glutamyl-tRNA syntheta	15 (0.00)	41 (0.46)	1.24
11-02	Gp4 Focus 2	g.chr16:67917511G>A	Missense Mutation	EDC4	p.C1297Y	enhancer of mRNA deca	76 (0.00)	99 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr4:148407166G>A	Missense Mutation	EDNRA	p.M111I	endothelin receptor type	105 (0.00)	17 (0.35)	0.94

11-02	Gp4 Focus 2	g.chr13:78477460C>T	Missense Mutation	EDNRB	p.G301E	endothelin receptor type	148 (0.01)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr3:127965713C>T	Silent	EEFSEC	p.I117I	eukaryotic elongation fa	51 (0.00)	84 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr14:90420987G>A	Silent	EFCAB11	p.A6A	EF-hand calcium bindin	15 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:168530246G>A	RNA	EGFEM1P		EGF-like and EMI dom	46 (0.00)	41 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr5:38448414G>A	Missense Mutation	EGFLAM	p.A826T	EGF-like, fibronectin ty	73 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr10:64573942G>A	Silent	EGR2	p.C152C	early growth response 2	16 (0.00)	37 (0.19)	0.60
11-02	Gp4 Focus 2	g.chr11:65350884C>T	Missense Mutation	EHBP1L1	p.S914F	EH domain binding prot	26 (0.00)	13 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr2:88870545G>A	Silent	EIF2AK3	p.F944F	eukaryotic translation in	97 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr1:45340432C>T	Missense Mutation	EIF2B3	p.V374I	eukaryotic translation in	37 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:45340474G>A	Missense Mutation	EIF2B3	p.P360S	eukaryotic translation in	31 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr2:27591320C>T	Missense Mutation	EIF2B4	p.R170Q	eukaryotic translation in	29 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr11:8017509C>T	Silent	EIF3F	p.T338T	eukaryotic translation in	221 (0.00)	29 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr17:78111219C>A	Nonsense Mutation	EIF4A3	p.E317*	eukaryotic translation in	18 (0.00)	45 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr11:10820603G>T	Missense Mutation	EIF4G2	p.A865D	eukaryotic translation in	88 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr1:21268299G>A	Missense Mutation	EIF4G3	p.P400S	eukaryotic translation in	36 (0.00)	29 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr20:33867431G>A	Silent	EIF6	p.F222F	eukaryotic translation in	41 (0.00)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr13:41508028T>A	Nonsense Mutation	ELF1	p.K465*	E74-like factor 1 (ets do	41 (0.00)	53 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr13:41517991G>A	Silent	ELF1	p.N200N	E74-like factor 1 (ets do	32 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr12:96617396C>T	Nonsense Mutation	ELK3	p.Q18*	ELK3, ETS-domain pro	35 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr7:36895173C>T	Missense Mutation	ELMO1	p.V723I	engulfment and cell mot	56 (0.00)	42 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr11:107524948G>A	Splice Site	ELMOD1	p.G227E	ELMO/CED-12 domain	44 (0.00)	81 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr7:73474307C>G	Silent	ELN	p.G502G	elastin	23 (0.00)	31 (0.19)	0.84
11-02	Gp4 Focus 2	g.chr1:43829629C>A	Missense Mutation	ELOVL1	p.Q266H	ELOVL fatty acid elong	22 (0.00)	19 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr1:43829630T>A	Missense Mutation	ELOVL1	p.Q266L	ELOVL fatty acid elong	23 (0.00)	19 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr1:19563646C>T	Silent	EMC1	p.L433L	ER membrane protein c	32 (0.00)	51 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr16:1825083G>A	Silent	EME2	p.E173E	essential meiotic structu	63 (0.00)	14 (0.36)	1.14
11-02	Gp4 Focus 2	g.chr11:62375688C>T	Silent	EML3	p.K397K	echinoderm microtubule	79 (0.01)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr2:55143955C>A	Silent	EML6	p.I1186I	echinoderm microtubule	35 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr5:73931828G>A	Silent	ENC1	p.C88C	ectodermal-neural corte	56 (0.00)	59 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr13:43872615C>T	Nonsense Mutation	ENOX1	p.W438*	ecto-NOX disulfide-thic	52 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr3:69056908C>G	Missense Mutation	EOGT	p.E126Q	EGF domain-specific O	79 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr6:131190919G>C	Silent	EPB41L2	p.A727A	erythrocyte membrane p	60 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr6:131206331C>T	Missense Mutation	EPB41L2	p.G580R	erythrocyte membrane p	96 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr5:111598199G>A	Missense Mutation	EPB41L4A	p.P212S	erythrocyte membrane p	81 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr15:43498731G>C	Missense Mutation	EPB42	p.A472G	erythrocyte membrane p	17 (0.00)	28 (0.32)	0.86

11-02	Gp4 Focus 2	g.chr18:43438659G>A	Silent	EPG5	p.C2366C	ectopic P-granules auto	37 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr18:43447616C>T	Missense Mutation	EPG5	p.S2108N	ectopic P-granules auto	116 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr3:89498519C>T	Nonsense Mutation	EPHA3	p.Q831*	EPH receptor A3	31 (0.00)	52 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr3:89521653C>T	Silent	EPHA3	p.I910I	EPH receptor A3	34 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:134920352G>A	Missense Mutation	EPHB1	p.G723S	EPH receptor B1	62 (0.00)	60 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr7:100417850G>T	Missense Mutation	EPHB4	p.H293N	EPH receptor B4	35 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr8:27361242G>A	Missense Mutation	EPHX2	p.R37H	epoxide hydrolase 2, cy	19 (0.00)	9 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr12:56478809G>A	Missense Mutation	ERBB3	p.V89M	v-erb-b2 avian erythrob	41 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr12:56478895C>T	Silent	ERBB3	p.I117I	v-erb-b2 avian erythrob	49 (0.00)	49 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr3:56468779G>A	Missense Mutation	ERC2	p.T86I	ELKS/RAB6-interactin	15 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr2:128018918C>A	Missense Mutation	ERCC3	p.M650I	excision repair cross-co	19 (0.00)	18 (0.33)	1.08
11-02	Gp4 Focus 2	g.chr21:39768537G>A	Intron	ERG		v-ets avian erythroblast	56 (0.02)	27 (0.93)	2.47
11-02	Gp4 Focus 2	g.chr21:39778469G>A	Intron	ERG		v-ets avian erythroblast	58 (0.00)	55 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr21:39787607G>A	Intron	ERG		v-ets avian erythroblast	30 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr21:39788074G>A	Intron	ERG		v-ets avian erythroblast	30 (0.00)	29 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr21:39791003G>A	Intron	ERG		v-ets avian erythroblast	87 (0.01)	75 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr21:39797844G>A	Intron	ERG		v-ets avian erythroblast	61 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr21:39813360G>A	Intron	ERG		v-ets avian erythroblast	60 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr21:39845235C>T	Intron	ERG		v-ets avian erythroblast	55 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr21:39856649G>A	Intron	ERG		v-ets avian erythroblast	114 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr21:39867360G>A	Intron	ERG		v-ets avian erythroblast	20 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr21:39891928T>C	Intron	ERG		v-ets avian erythroblast	29 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr21:39891932G>C	Intron	ERG		v-ets avian erythroblast	29 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr21:39961039C>G	Intron	ERG		v-ets avian erythroblast	32 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr21:39963831G>A	Intron	ERG		v-ets avian erythroblast	61 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr21:39983403C>G	Intron	ERG		v-ets avian erythroblast	34 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr21:39988555G>A	Intron	ERG		v-ets avian erythroblast	41 (0.00)	39 (0.95)	2.53
11-02	Gp4 Focus 2	g.chr21:39998135G>A	Intron	ERG		v-ets avian erythroblast	76 (0.00)	25 (0.56)	1.49
11-02	Gp4 Focus 2	g.chr21:40010537G>T	Intron	ERG		v-ets avian erythroblast	34 (0.00)	14 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr21:40012277G>A	Intron	ERG		v-ets avian erythroblast	22 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr20:34143994G>A	Silent	ERGIC3	p.Q277Q	ERGIC and golgi 3	17 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr8:37601924C>T	Silent	ERLIN2	p.V96V	ER lipid raft associated	97 (0.01)	25 (0.60)	1.94
11-02	Gp4 Focus 2	g.chr1:43300765G>A	Missense Mutation	ERMAP	p.V164I	erythroblast membrane-	15 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr9:5798923C>T	Missense Mutation	ERMP1	p.G718E	endoplasmic reticulum	40 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr12:112460322G>T	Missense Mutation	ERP29	p.A117S	endoplasmic reticulum	25 (0.00)	33 (0.42)	1.13

11-02	Gp4 Focus 2	g.chr6:11105051G>A	Nonsense Mutation	ERVFRD-1	p.Q165*	endogenous retrovirus g	135 (0.00)	42 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:53680207G>A	Silent	ESPL1	p.L1229L	extra spindle pole bodie	57 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr12:53680352G>A	Missense Mutation	ESPL1	p.G1278S	extra spindle pole bodie	49 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr16:68264213G>A	Silent	ESRP2	p.P690P	epithelial splicing regula	38 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr16:68264849G>A	Missense Mutation	ESRP2	p.S598L	epithelial splicing regula	17 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr14:76966370C>G	Silent	ESRRB	p.G487G	estrogen-related recepto	19 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr12:56524601G>A	Silent	ESYT1	p.L153L	extended synaptotagmin	22 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr4:109677646G>A	Missense Mutation	ETNPPL	p.S73F	ethanolamine-phosphate	40 (0.03)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr21:40190438C>A	Missense Mutation	ETS2	p.P227T	v-ets avian erythroblasto	67 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr7:13971242C>T	Silent	ETV1	p.Q229Q	ets variant 1	53 (0.00)	54 (0.19)	0.66
11-02	Gp4 Focus 2	g.chr7:13971292G>A	Missense Mutation	ETV1	p.R213C	ets variant 1	55 (0.00)	52 (0.27)	0.96
11-02	Gp4 Focus 2	g.chr4:5735156G>T	Missense Mutation	EVC	p.K232N	Ellis van Creveld syndro	96 (0.01)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr22:29694858G>A	Missense Mutation	EWSR1	p.R523Q	EWS RNA-binding prot	22 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr15:41507990G>A	Nonsense Mutation	EXD1	p.Q144*	exonuclease 3'-5' domai	53 (0.00)	51 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr1:242016714C>T	Silent	EXO1	p.V112V	exonuclease 1	45 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:242021915C>T	Silent	EXO1	p.Y217Y	exonuclease 1	35 (0.00)	48 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr1:40980716C>T	Missense Mutation	EXO5	p.P167L	exonuclease 5	52 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr4:56759920G>A	Missense Mutation	EXOC1	p.V643I	exocyst complex compo	20 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr6:564648G>A	Missense Mutation	EXOC2	p.L522F	exocyst complex compo	44 (0.00)	21 (0.33)	0.64
11-02	Gp4 Focus 2	g.chr5:462278C>T	Silent	EXOC3	p.S503S	exocyst complex compo	22 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:231471489G>T	Missense Mutation	EXOC8	p.P664Q	exocyst complex compo	128 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr9:133570899G>A	Missense Mutation	EXOSC2	p.G48E	exosome component 2	47 (0.00)	35 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr1:26357727G>A	Silent	EXTL1	p.Q402Q	exostosin-like glycosylt	25 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr8:28573675C>T	Silent	EXTL3	p.S33S	exostosin-like glycosylt	15 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr8:28595046G>A	Missense Mutation	EXTL3	p.E763K	exostosin-like glycosylt	41 (0.00)	72 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr8:72184079G>A	Nonsense Mutation	EYA1	p.R294*	EYA transcriptional coa	72 (0.00)	23 (0.35)	1.17
11-02	Gp4 Focus 2	g.chr20:45633599C>T	Silent	EYA2	p.L58L	EYA transcriptional coa	34 (0.00)	45 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr17:40876387G>A	Missense Mutation	EZH1	p.S31L	enhancer of zeste 1 poly	63 (0.02)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr13:113803291C>T	Missense Mutation	F10	p.S306L	coagulation factor X	16 (0.00)	91 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr11:46744790G>A	Missense Mutation	F2	p.G126D	coagulation factor II (th	21 (0.00)	52 (0.44)	1.18
11-02	Gp4 Focus 2	g.chr1:169510423G>A	Missense Mutation	F5	p.T1302I	coagulation factor V (pr	46 (0.00)	125 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr2:96679541C>T	RNA	FAHD2CP		fumarylacetoacetate hyd	22 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:207078369C>G	Missense Mutation	FAIM3	p.A390P	Fas apoptotic inhibitory	24 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr5:14601228G>A	Silent	FAM105A	p.L73L	family with sequence si	21 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr22:45728582C>T	Nonsense Mutation	FAM118A	p.Q310*	family with sequence si	25 (0.00)	49 (0.24)	0.65

11-02	Gp4 Focus 2	g.chr6:170626982C>T	Silent	FAM120B	p.L168L	family with sequence si	56 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chrX:133930217C>T	Missense Mutation	FAM122B	p.E7K	family with sequence si	34 (0.00)	23 (0.65)	1.39
11-02	Gp4 Focus 2	g.chr2:225266318C>T	Silent	FAM124B	p.K56K	family with sequence si	15 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:184764146G>A	Nonsense Mutation	FAM129A	p.Q918*	family with sequence si	38 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr9:130279135C>T	Splice Site	FAM129B		family with sequence si	43 (0.00)	25 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr2:220044475C>T	Missense Mutation	FAM134A	p.H137Y	family with sequence si	73 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr10:61083814G>T	Missense Mutation	FAM13C	p.T126K	family with sequence si	54 (0.00)	80 (0.17)	0.55
11-02	Gp4 Focus 2	g.chr1:55077407G>A	Missense Mutation	FAM151A	p.T271M	family with sequence si	37 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr14:74413009G>A	Silent	FAM161B	p.V181V	family with sequence si	23 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:15255796G>A	Silent	FAM171A1	p.V597V	family with sequence si	35 (0.00)	39 (0.13)	0.43
11-02	Gp4 Focus 2	g.chr14:45433517G>A	Silent	FAM179B	p.R631R	family with sequence si	46 (0.00)	16 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr7:135433276G>A	Missense Mutation	FAM180A	p.S18F	family with sequence si	58 (0.00)	55 (0.76)	2.04
11-02	Gp4 Focus 2	g.chr7:102427914C>T	Missense Mutation	FAM185A	p.T355I	family with sequence si	227 (0.00)	44 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr4:2695461C>T	Silent	FAM193A	p.H715H	family with sequence si	16 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr5:176952110C>A	Nonsense Mutation	FAM193B	p.E458*	family with sequence si	25 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr5:176952111C>A	Missense Mutation	FAM193B	p.L457F	family with sequence si	25 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr5:176952130G>A	Missense Mutation	FAM193B	p.P451L	family with sequence si	26 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr9:34835152C>T	RNA	FAM205B		family with sequence si	31 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr3:49841922G>A	Silent	FAM212A	p.Q122Q	family with sequence si	15 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:46272856G>T	Missense Mutation	FAM21C	p.V760L	family with sequence si	21 (0.00)	38 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr1:809349G>A	lincRNA	FAM41C		family with sequence si	55 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr15:59146727G>A	Missense Mutation	FAM63B	p.G595E	family with sequence si	42 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:67576474C>T	Silent	FAM65A	p.V609V	family with sequence si	98 (0.00)	76 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr16:67576512C>T	Missense Mutation	FAM65A	p.P622L	family with sequence si	58 (0.00)	57 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr7:128366904G>A	Missense Mutation	FAM71F1	p.E177K	family with sequence si	98 (0.00)	37 (0.57)	1.51
11-02	Gp4 Focus 2	g.chr8:94713567G>A	Missense Mutation	FAM92A1	p.A48T	family with sequence si	111 (0.00)	34 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr2:33817240G>A	Silent	FAM98A	p.L82L	family with sequence si	110 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr15:31229403G>A	Missense Mutation	FAN1	p.E1000K	FANCD2/FANCI-assoc	46 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr3:10081514T>C	Missense Mutation	FANCD2	p.V227A	Fanconi anemia, comple	48 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr3:10115047G>A	Splice Site	FANCD2		Fanconi anemia, comple	39 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr14:45605440G>T	Missense Mutation	FANCM	p.C69F	Fanconi anemia, comple	28 (0.00)	18 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:172634935C>G	Missense Mutation	FASLG	p.H209D	Fas ligand (TNF superfa	55 (0.00)	67 (0.63)	1.67
11-02	Gp4 Focus 2	g.chr2:207655383G>A	Silent	FASTKD2	p.L662L	FAST kinase domains 2	229 (0.00)	43 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr4:187510201G>A	Missense Mutation	FAT1	p.P4438S	FAT atypical cadherin 1	139 (0.00)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr4:187554856G>A	Silent	FAT1	p.T1435T	FAT atypical cadherin 1	28 (0.00)	31 (0.58)	1.55

11-02	Gp4 Focus 2	g.chr4:187627891G>A	Missense Mutation	FAT1	p.P1031S	FAT atypical cadherin 1	31 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:187628126G>A	Silent	FAT1	p.H952H	FAT atypical cadherin 1	54 (0.00)	37 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr4:187628138C>G	Missense Mutation	FAT1	p.W948C	FAT atypical cadherin 1	55 (0.00)	41 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr5:150889588C>T	Missense Mutation	FAT2	p.G4018E	FAT atypical cadherin 2	50 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr11:92088454G>A	Missense Mutation	FAT3	p.G909E	FAT atypical cadherin 3	76 (0.00)	34 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr11:92088538G>A	Missense Mutation	FAT3	p.G937D	FAT atypical cadherin 3	35 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr11:92533867C>A	Missense Mutation	FAT3	p.P2413H	FAT atypical cadherin 3	44 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr11:92538390C>T	Silent	FAT3	p.L2840L	FAT atypical cadherin 3	36 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr4:126336855G>A	Missense Mutation	FAT4	p.S2246N	FAT atypical cadherin 4	29 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:73929151G>A	Missense Mutation	FBF1	p.P17L	Fas (TNFRSF6) binding	24 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr15:48704915C>T	Missense Mutation	FBN1	p.G2693S	fibrillin 1	60 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr15:48808445G>A	Missense Mutation	FBN1	p.P421L	fibrillin 1	31 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr5:127855028C>T	Missense Mutation	FBN2	p.R189H	fibrillin 2	39 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr5:107559896G>A	Missense Mutation	FBXL17	p.H116Y	F-box and leucine-rich r	18 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr5:15928498G>A	Silent	FBXL7	p.Q209Q	F-box and leucine-rich r	41 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr9:37537799G>A	Silent	FBXO10	p.L243L	F-box protein 10	36 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr7:100187605G>A	Silent	FBXO24	p.K15K	F-box protein 24	18 (0.00)	43 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr19:39521707C>G	Silent	FBXO27	p.L178L	F-box protein 27	38 (0.00)	133 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr6:146126242G>A	Silent	FBXO30	p.L434L	F-box protein 30	77 (0.00)	24 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr14:55818462G>A	Missense Mutation	FBXO34	p.E452K	F-box protein 34	71 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr5:41929969C>T	Missense Mutation	FBXO4	p.S199F	F-box protein 4	108 (0.00)	25 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr3:121341453T>C	Missense Mutation	FBXO40	p.S393P	F-box protein 40	32 (0.00)	22 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr8:101153462G>A	Silent	FBXO43	p.S340S	F-box protein 43	17 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr1:207133025G>T	Splice Site	FCAMR	p.T524T	Fc receptor, IgA, IgM, h	34 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:161483712C>T	Missense Mutation	FCGR2A	p.A257V	Fc fragment of IgG, low	30 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr1:161518350C>T	Nonsense Mutation	FCGR3A	p.W60*	Fc fragment of IgG, low	58 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr1:157504465G>A	Silent	FCRL5	p.Y540Y	Fc receptor-like 5	36 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr11:61563223G>T	Silent	FEN1	p.L130L	flap structure-specific en	40 (0.00)	41 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr2:97366073C>G	RNA	FER1L5		fer-1-like family membe	51 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr8:125058023C>T	Missense Mutation	FER1L6	p.L869F	fer-1-like family membe	83 (0.00)	18 (0.39)	1.33
11-02	Gp4 Focus 2	g.chr11:125351502G>A	Silent	FEZ1	p.Y113Y	fasciculation and elonga	76 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr4:155507531C>T	Silent	FGA	p.G350G	fibrinogen alpha chain	27 (0.00)	35 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:155490821G>A	Missense Mutation	FGB	p.V153M	fibrinogen beta chain	47 (0.00)	20 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:14862411C>T	Silent	FGD5	p.S611S	FYVE, RhoGEF and PH	34 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr3:14964560G>A	Missense Mutation	FGD5	p.C1272Y	FYVE, RhoGEF and PH	58 (0.00)	34 (0.24)	0.63

11-02	Gp4 Focus 2	g.chr3:14974637G>T	Splice Site	FGD5		FYVE, RhoGEF and PH	29 (0.00)	45 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr4:153884213T>C	Silent	FHDC1	p.S320S	FH2 domain containing	36 (0.00)	32 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr3:60522631G>A	Missense Mutation	FHIT	p.S22F	fragile histidine triad	26 (0.00)	20 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr16:67272811A>T	Missense Mutation	FHOD1	p.I123N	formin homology 2 dom	32 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr6:76024753G>A	Silent	FILIP1	p.S265S	filamin A interacting pro	55 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr3:99568062G>A	Missense Mutation	FILIP1L	p.R820C	filamin A interacting pro	68 (0.00)	25 (0.28)	0.54
11-02	Gp4 Focus 2	g.chr17:39969470G>A	Missense Mutation	FKBP10	p.G62R	FK506 binding protein 1	77 (0.00)	13 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr6:63921737C>T	Silent	FKBP1C	p.I92I	FK506 binding protein 1	22 (0.00)	53 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr6:35554828C>T	Missense Mutation	FKBP5	p.G275R	FK506 binding protein 5	53 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:55752938C>A	RNA	FKBP9L			39 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr3:58108836C>T	Missense Mutation	FLNB	p.P1048L	filamin B, beta	41 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr3:58120467G>A	Missense Mutation	FLNB	p.A1578T	filamin B, beta	20 (0.00)	26 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr14:86089691C>T	Silent	FLRT2	p.S611S	fibronectin leucine rich	24 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr14:76045760G>A	Missense Mutation	FLVCR2	p.G149S	feline leukemia virus su	35 (0.00)	16 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr15:33192233C>T	Missense Mutation	FMN1	p.A1201T	formin 1	75 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr2:153417469C>T	Silent	FMNL2	p.I172I	formin-like 2	23 (0.00)	26 (0.35)	1.13
11-02	Gp4 Focus 2	g.chr2:216235118G>A	Missense Mutation	FN1	p.T2251I	fibronectin 1	33 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr2:216241351G>A	Silent	FN1	p.T1919T	fibronectin 1	15 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr17:80684388C>T	Silent	FN3KRP	p.F167F	fructosamine 3 kinase re	18 (0.00)	20 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr1:94016559G>A	Silent	FNBP1L	p.E569E	formin binding protein 1	71 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:109275931G>T	Silent	FNDC7	p.L639L	fibronectin type III dom	47 (0.00)	39 (0.44)	0.91
11-02	Gp4 Focus 2	g.chr5:131008561C>T	Missense Mutation	FNIP1	p.G481S	folliculin interacting pro	41 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr9:20976511G>A	Missense Mutation	FOCAD	p.A1409T	focadhesin	57 (0.00)	16 (0.31)	1.02
11-02	Gp4 Focus 2	g.chr17:80545130C>T	Missense Mutation	FOXK2	p.H590Y	forkhead box K2	17 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chrX:70321577C>A	Missense Mutation	FOXO4	p.F499L	forkhead box O4	16 (0.00)	11 (0.45)	0.76
11-02	Gp4 Focus 2	g.chr4:79188586G>A	Splice Site	FRAS1	p.R327R	Fraser extracellular matr	37 (0.00)	31 (0.39)	1.03
11-02	Gp4 Focus 2	g.chr4:79254464C>A	Missense Mutation	FRAS1	p.P726T	Fraser extracellular matr	23 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr4:79300969G>A	Missense Mutation	FRAS1	p.V1128I	Fraser extracellular matr	131 (0.01)	67 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr4:144618406G>A	Silent	FREM3	p.L1141L	FRAS1 related extracell	70 (0.00)	33 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:49430371G>A	Silent	FRMPD2	p.G480G	FERM and PDZ domain	63 (0.02)	51 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr10:49431234C>T	Silent	FRMPD2	p.K416K	FERM and PDZ domain	31 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr10:49440183G>A	Silent	FRMPD2	p.T381T	FERM and PDZ domain	32 (0.00)	16 (0.69)	1.83
11-02	Gp4 Focus 2	g.chr6:41744673G>A	Missense Mutation	FRS3	p.P18L	fibroblast growth factor	29 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr13:32653073C>T	Missense Mutation	FRY	p.P58L	furry homolog (Drosoph	89 (0.00)	23 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr13:32752547G>A	Silent	FRY	p.Q885Q	furry homolog (Drosoph	53 (0.00)	36 (0.17)	0.44

11-02	Gp4 Focus 2	g.chr13:32841337C>T	Silent	FRY	p.P2659P	furry homolog (Drosop	16 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr2:186604094G>A	Missense Mutation	FSIP2	p.A41T	fibrous sheath interactin	35 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr2:186656437C>T	Missense Mutation	FSIP2	p.S1525L	fibrous sheath interactin	75 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr2:186678711C>T	Missense Mutation	FSIP2	p.T6756I	fibrous sheath interactin	88 (0.01)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr5:52781782C>T	Splice Site	FST	p.S318S	follistatin	118 (0.00)	54 (0.19)	0.61
11-02	Gp4 Focus 2	g.chr3:120122155C>A	Missense Mutation	FSTL1	p.D210Y	follistatin-like 1	28 (0.00)	22 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr17:61902261G>A	Missense Mutation	FTSJ3	p.T247I	FtsJ homolog 3 (E. coli)	22 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:78414953G>A	Missense Mutation	FUBP1	p.P605S	far upstream element (F	18 (0.00)	17 (0.71)	2.30
11-02	Gp4 Focus 2	g.chr6:143825309G>A	Missense Mutation	FUCA2	p.L165F	fucosidase, alpha-L- 2,	64 (0.02)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr19:49254032G>A	Silent	FUT1	p.C169C	fucosyltransferase 1 (ga	30 (0.00)	58 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr5:39153612G>A	Silent	FYB	p.H410H	FYN binding protein	167 (0.00)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:46008706C>G	Missense Mutation	FYCO1	p.G707A	FYVE and coiled-coil d	28 (0.00)	67 (0.28)	0.76
11-02	Gp4 Focus 2	g.chr4:76570740C>T	Silent	G3BP2	p.V441V	GTPase activating prote	53 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:41056058G>A	Splice Site	G6PC		glucose-6-phosphatase,	18 (0.00)	18 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr4:144390183G>A	Splice Site	GAB1		GRB2-associated bindi	79 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr5:161116287G>A	Missense Mutation	GABRA6	p.M158I	gamma-aminobutyric ac	33 (0.00)	39 (0.26)	0.68
11-02	Gp4 Focus 2	g.chrX:151123842G>T	Missense Mutation	GABRE	p.H379N	gamma-aminobutyric ac	31 (0.00)	14 (0.43)	0.71
11-02	Gp4 Focus 2	g.chrX:151124015G>A	Missense Mutation	GABRE	p.T321I	gamma-aminobutyric ac	29 (0.00)	39 (0.64)	1.07
11-02	Gp4 Focus 2	g.chr15:27772753C>T	Missense Mutation	GABRG3	p.T347I	gamma-aminobutyric ac	37 (0.00)	19 (0.37)	1.36
11-02	Gp4 Focus 2	g.chr6:89888630C>G	Missense Mutation	GABRR1	p.R433S	gamma-aminobutyric ac	29 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr6:89890148G>A	Missense Mutation	GABRR1	p.R337C	gamma-aminobutyric ac	23 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr2:171702097C>G	Missense Mutation	GAD1	p.A278G	glutamate decarboxylas	33 (0.00)	40 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr7:99757718C>T	Missense Mutation	GAL3ST4	p.A432T	galactose-3-O-sulfotran	32 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr15:49584655C>T	Silent	GALK2	p.N296N	galactokinase 2	50 (0.00)	49 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr15:49584656C>T	Missense Mutation	GALK2	p.P297S	galactokinase 2	50 (0.00)	49 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr5:153760135C>T	Silent	GALNT10	p.Y294Y	polypeptide N-acetylgal	27 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr14:69814598G>A	Nonsense Mutation	GALNT16	p.W473*	polypeptide N-acetylgal	31 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr12:4835955C>T	Silent	GALNT8	p.L157L	polypeptide N-acetylgal	41 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr11:62393557G>C	Missense Mutation	GANAB	p.A924G	glucosidase, alpha; neut	58 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr15:42631866G>A	Splice Site	GANC		glucosidase, alpha; neut	27 (0.00)	36 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr9:128065034G>A	Missense Mutation	GAPVD1	p.V320I	GTPase activating prote	61 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr9:128094221G>A	Silent	GAPVD1	p.K709K	GTPase activating prote	22 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr9:130104587C>T	Nonsense Mutation	GARNL3	p.Q409*	GTPase activating Rap/	45 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr15:45668807C>T	Missense Mutation	GATM	p.E94K	glycine amidinotransfer	61 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr7:56062612G>A	Missense Mutation	GBAS	p.D176N	glioblastoma amplified	97 (0.00)	40 (0.57)	1.53

11-02	Gp4 Focus 2	g.chr3:81539601C>T	Missense Mutation	GBE1	p.S689N	glucan (1,4-alpha-), brai	137 (0.00)	80 (0.15)	0.79
11-02	Gp4 Focus 2	g.chr10:104136161C>T	Missense Mutation	GBF1	p.A1339V	golgi brefeldin A resista	23 (0.00)	22 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr10:104140440C>T	Nonsense Mutation	GBF1	p.Q1723*	golgi brefeldin A resista	30 (0.00)	41 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr10:104140967G>A	Missense Mutation	GBF1	p.G1752S	golgi brefeldin A resista	23 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr22:38212648G>C	Missense Mutation	GCAT	p.V421L	glycine C-acetyltransfer	15 (0.00)	42 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr19:13008604G>A	Silent	GCDH	p.G390G	glutaryl-CoA dehydroge	24 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr7:44190573C>T	Silent	GCK	p.R155R	glucokinase (hexokinas	17 (0.00)	39 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:120576601C>A	Silent	GCN1L1	p.L2018L	GCN1 general control o	72 (0.00)	76 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr9:74828852G>A	Missense Mutation	GDA	p.D175N	guanine deaminase	30 (0.00)	22 (0.27)	0.88
11-02	Gp4 Focus 2	g.chr20:42891868A>T	Splice Site	GDAP1L1		ganglioside induced diff	74 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr20:42891962C>T	Missense Mutation	GDAP1L1	p.L214F	ganglioside induced diff	58 (0.02)	46 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr1:118455191G>A	Missense Mutation	GDAP2	p.S144F	ganglioside induced diff	21 (0.00)	14 (0.36)	0.75
11-02	Gp4 Focus 2	g.chr20:34022598G>C	Missense Mutation	GDF5OS	p.Q214H	growth differentiation fa	39 (0.00)	41 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr5:132197740C>T	Silent	GDF9	p.V302V	growth differentiation fa	45 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr17:650815G>A	Silent	GEMIN4	p.D156D	gem (nuclear organelle)	89 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:650828G>A	Missense Mutation	GEMIN4	p.T152I	gem (nuclear organelle)	88 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr5:154278017G>A	Silent	GEMIN5	p.L1110L	gem (nuclear organelle)	61 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr19:45593436A>T	Missense Mutation	GEMIN7	p.S22C	gem (nuclear organelle)	47 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr17:42990674C>T	Missense Mutation	GFAP	p.S248N	glial fibrillary acidic prc	20 (0.00)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr17:42990690C>T	Missense Mutation	GFAP	p.E243K	glial fibrillary acidic prc	20 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr3:158376742G>A	Missense Mutation	GFM1	p.R372H	G elongation factor, mit	34 (0.03)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr16:23481457G>A	Missense Mutation	GGA2	p.R494W	golgi-associated, gamma	26 (0.00)	25 (0.84)	2.24
11-02	Gp4 Focus 2	g.chr17:34935774G>A	Silent	GGNBP2	p.Q315Q	gametogenetin binding	103 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:40342271C>T	Missense Mutation	GHDC	p.A436T	GH3 domain containing	27 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr10:85903802G>A	Missense Mutation	GHITM	p.G94E	growth hormone inducil	88 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr10:85904696G>T	Missense Mutation	GHITM	p.G136V	growth hormone inducil	32 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr17:17965242G>A	Silent	GID4	p.K264K	GID complex subunit 4	20 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr2:233613793G>A	Splice Site	GIGYF2		GRB10 interacting GYF	28 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr2:233655476G>T	Missense Mutation	GIGYF2	p.D255Y	GRB10 interacting GYF	98 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr2:233655869G>A	Missense Mutation	GIGYF2	p.R355K	GRB10 interacting GYF	57 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr12:110418806C>T	Silent	GIT2	p.Q223Q	G protein-coupled recep	131 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr6:90604208G>A	Silent	GJA10	p.L7L	gap junction protein, alp	141 (0.01)	65 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr2:69173568T>A	Nonsense Mutation	GKN2	p.K114*	gastrokine 2	32 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr9:6604765G>A	Missense Mutation	GLDC	p.T294I	glycine dehydrogenase (	26 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr15:51693845G>A	Silent	GLDN	p.T361T	gliomedin	19 (0.00)	22 (0.36)	0.97

11-02	Gp4 Focus 2	g.chr2:121742058C>T	Silent	GLI2	p.I565I	GLI family zinc finger 2	66 (0.00)	36 (0.75)	2.39
11-02	Gp4 Focus 2	g.chr9:36147818C>T	Missense Mutation	GLIPR2	p.H17Y	GLI pathogenesis-relate	71 (0.00)	151 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr17:9739756G>A	Missense Mutation	GLP2R	p.V116I	glucagon-like peptide 2	40 (0.00)	38 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr17:9792832G>A	Missense Mutation	GLP2R	p.R491Q	glucagon-like peptide 2	19 (0.00)	39 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr12:129467576G>A	Missense Mutation	GLT1D1	p.V328M	glycosyltransferase 1 do	22 (0.00)	85 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr3:52729314C>G	Missense Mutation	GLT8D1	p.G273R	glycosyltransferase 8 do	104 (0.00)	49 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr16:4873831G>A	Silent	GLYR1	p.T205T	glyoxylate reductase 1 h	93 (0.00)	68 (0.18)	0.56
11-02	Gp4 Focus 2	g.chr19:19745436C>T	Missense Mutation	GMIP	p.G655E	GEM interacting protei	57 (0.00)	44 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr20:57484257G>A	Missense Mutation	GNAS	p.V177M	GNAS complex locus	34 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr15:52439692C>T	Missense Mutation	GNB5	p.C153Y	guanine nucleotide bind	31 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr12:102158229G>A	Silent	GNPTAB	p.T822T	N-acetylglucosamine-1-	68 (0.00)	23 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr3:37367019G>A	Silent	GOLGA4	p.A1236A	golgin A4	40 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr14:93282739G>A	Silent	GOLGA5	p.Q488Q	golgin A5	49 (0.00)	60 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr15:34673692G>A	Missense Mutation	GOLGA8A	p.H578Y	golgin A8 family, mem	72 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr15:34673725G>A	Missense Mutation	GOLGA8A	p.P567S	golgin A8 family, mem	28 (0.00)	55 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr15:23261918C>T	Missense Mutation	GOLGA8I	p.R344W	golgin A8 family, mem	29 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr15:23610245C>T	Silent	GOLGA8S	p.F614F	golgin A8 family, mem	41 (0.00)	57 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr1:170521382G>A	Missense Mutation	GORAB	p.E322K	golgin, RAB6-interactin	53 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:101163301G>A	Missense Mutation	GOT1	p.T295I	glutamic-oxaloacetic tra	20 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr16:58756106G>A	Missense Mutation	GOT2	p.A108V	glutamic-oxaloacetic tra	22 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr13:45578491C>T	Missense Mutation	GPALPP1	p.S47L	GPALPP motifs contain	73 (0.00)	47 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr19:33608898C>T	Silent	GPATCH1	p.F788F	G patch domain contain	18 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr14:76639960G>A	Missense Mutation	GPATCH2L	p.V326I	G patch domain contain	42 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr14:76642986G>A	Silent	GPATCH2L	p.L335L	G patch domain contain	60 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr17:42478700G>A	Silent	GPATCH8	p.L249L	G patch domain contain	75 (0.00)	44 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr6:24454242C>T	Splice Site	GPLD1		glycosylphosphatidylin	62 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:27215543G>A	Missense Mutation	GPN2	p.S162F	GPN-loop GTPase 2	64 (0.02)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr6:46977834C>T	Missense Mutation	GPR110	p.S446N	G protein-coupled recep	37 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chrX:135405517G>A	Silent	GPR112	p.K217K	G protein-coupled recep	48 (0.00)	41 (0.32)	0.53
11-02	Gp4 Focus 2	g.chr4:22390071G>A	Nonsense Mutation	GPR125	p.Q1075*	G protein-coupled recep	26 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr3:100373877C>T	Silent	GPR128	p.C231C	G protein-coupled recep	59 (0.00)	23 (0.39)	0.76
11-02	Gp4 Focus 2	g.chr7:37780395G>A	Missense Mutation	GPR141	p.A134T	G protein-coupled recep	29 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:37780643A>T	Silent	GPR141	p.L216L	G protein-coupled recep	57 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:175324639G>A	Missense Mutation	GPR155	p.P580S	G protein-coupled recep	17 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr15:40099372C>A	Missense Mutation	GPR176	p.G87V	G protein-coupled recep	45 (0.00)	20 (0.50)	1.33

11-02	Gp4 Focus 2	g.chr13:99907407C>T	Silent	GPR18	p.Q240Q	G protein-coupled recep	20 (0.00)	35 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr9:125797575G>T	Missense Mutation	GPR21	p.A244S	G protein-coupled recep	27 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:107115373G>A	Missense Mutation	GPR22	p.V290I	G protein-coupled recep	37 (0.00)	26 (0.58)	1.54
11-02	Gp4 Focus 2	g.chr1:27720855G>C	Missense Mutation	GPR3	p.G185R	G protein-coupled recep	25 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chrX:150348333G>A	Missense Mutation	GPR50	p.G93D	G protein-coupled recep	32 (0.00)	17 (0.71)	1.18
11-02	Gp4 Focus 2	g.chr11:94113895G>A	Missense Mutation	GPR83	p.P189L	G protein-coupled recep	21 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr5:89943369G>A	Missense Mutation	GPR98	p.R1026K	G protein-coupled recep	86 (0.00)	66 (0.35)	1.40
11-02	Gp4 Focus 2	g.chr5:89975390G>A	Missense Mutation	GPR98	p.G1823E	G protein-coupled recep	59 (0.00)	51 (0.20)	0.79
11-02	Gp4 Focus 2	g.chr5:89975444G>A	Missense Mutation	GPR98	p.R1841H	G protein-coupled recep	55 (0.02)	54 (0.35)	1.41
11-02	Gp4 Focus 2	g.chr5:89990418C>T	Silent	GPR98	p.G2615G	G protein-coupled recep	66 (0.00)	73 (0.21)	0.82
11-02	Gp4 Focus 2	g.chr5:90052357A>T	Silent	GPR98	p.P3889P	G protein-coupled recep	81 (0.01)	28 (0.32)	1.29
11-02	Gp4 Focus 2	g.chr5:90073826G>A	Missense Mutation	GPR98	p.R4211Q	G protein-coupled recep	117 (0.00)	45 (0.53)	2.14
11-02	Gp4 Focus 2	g.chr5:90086768G>A	Missense Mutation	GPR98	p.G4708R	G protein-coupled recep	119 (0.00)	45 (0.24)	0.98
11-02	Gp4 Focus 2	g.chrX:101912606G>A	Silent	GPRASP1	p.L1255L	G protein-coupled recep	32 (0.00)	18 (0.44)	0.99
11-02	Gp4 Focus 2	g.chr12:13065440C>T	Silent	GPRC5A	p.Y347Y	G protein-coupled recep	49 (0.00)	16 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr12:13102994C>T	Missense Mutation	GPRC5D	p.A109T	G protein-coupled recep	24 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr9:37426582C>T	Missense Mutation	GRHPR	p.A112V	glyoxylate reductase/hy	16 (0.00)	26 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr10:87487708G>A	Silent	GRID1	p.G479G	glutamate receptor, iono	64 (0.00)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr10:87615822C>T	Nonsense Mutation	GRID1	p.W359*	glutamate receptor, iono	34 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr16:9857891G>A	Silent	GRIN2A	p.N1170N	glutamate receptor, iono	16 (0.00)	32 (0.47)	1.50
11-02	Gp4 Focus 2	g.chr9:104385633G>A	Missense Mutation	GRIN3A	p.L861F	glutamate receptor, iono	41 (0.00)	15 (0.73)	1.96
11-02	Gp4 Focus 2	g.chr9:104449352G>A	Missense Mutation	GRIN3A	p.T277I	glutamate receptor, iono	93 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr3:7348208G>T	Missense Mutation	GRM7	p.R301I	glutamate receptor, met	99 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr8:130762713G>A	Silent	GSDMC	p.L349L	gasdermin C	43 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr16:85697046G>A	Missense Mutation	GSE1	p.E824K	Gse1 coiled-coil protein	24 (0.00)	10 (0.90)	2.40
11-02	Gp4 Focus 2	g.chr16:85699607G>A	Silent	GSE1	p.L928L	Gse1 coiled-coil protein	30 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr20:33517270C>T	Missense Mutation	GSS	p.R412Q	glutathione synthetase	84 (0.00)	73 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr6:52616394G>T	Missense Mutation	GSTA2	p.S176Y	glutathione S-transferas	16 (0.00)	41 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:110231688G>A	Missense Mutation	GSTM1	p.G66R	glutathione S-transferas	26 (0.00)	27 (0.56)	1.16
11-02	Gp4 Focus 2	g.chr3:120469535G>A	Missense Mutation	GTF2E1	p.E46K	general transcription fac	75 (0.00)	45 (0.78)	2.07
11-02	Gp4 Focus 2	g.chr3:120469744G>A	Silent	GTF2E1	p.E115E	general transcription fac	77 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr3:120489720C>T	Silent	GTF2E1	p.N198N	general transcription fac	171 (0.01)	30 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:120495292G>A	Missense Mutation	GTF2E1	p.A225T	general transcription fac	38 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr7:72657816G>A	RNA	GTF2IRD2P1		GTF2I repeat domain c	28 (0.00)	32 (0.22)	0.95
11-02	Gp4 Focus 2	g.chr7:72657890G>A	RNA	GTF2IRD2P1		GTF2I repeat domain c	34 (0.00)	28 (0.32)	1.39

11-02	Gp4 Focus 2	g.chr16:27476714G>A	Missense Mutation	GTF3C1	p.A1741V	general transcription fac	52 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr2:27556635G>A	Missense Mutation	GTF3C2	p.T540I	general transcription fac	52 (0.02)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr2:27560394C>T	Missense Mutation	GTF3C2	p.A328T	general transcription fac	31 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr2:27560418G>A	Nonsense Mutation	GTF3C2	p.Q320*	general transcription fac	32 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr9:135553764G>A	Nonsense Mutation	GTF3C4	p.W253*	general transcription fac	51 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr7:89976068A>G	Missense Mutation	GTPBP10	p.S5G	GTP-binding protein 10	64 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr3:108635060G>A	Splice Site	GUCA1C	p.A119V	guanylate cyclase activa	24 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr11:106558385G>A	Silent	GUCY1A2	p.L718L	guanylate cyclase 1, solu	20 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr11:106810282C>T	Silent	GUCY1A2	p.K370K	guanylate cyclase 1, solu	58 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr11:106810669G>A	Silent	GUCY1A2	p.H241H	guanylate cyclase 1, solu	61 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr11:106810680G>A	Missense Mutation	GUCY1A2	p.H238Y	guanylate cyclase 1, solu	60 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr2:189452626G>A	Missense Mutation	GULP1	p.G265R	GULP, engulfment adap	129 (0.00)	55 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr5:21491618G>A	RNA	GUSBP1		glucuronidase, beta pseu	81 (0.00)	74 (0.24)	1.28
11-02	Gp4 Focus 2	g.chr12:21727087A>T	Missense Mutation	GYS2	p.H223Q	glycogen synthase 2 (liv	40 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr20:23345291C>T	Missense Mutation	GZF1	p.L91F	GDNF-inducible zinc fi	27 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr10:71849877G>A	Silent	H2AFY2	p.P78P	H2A histone family, me	73 (0.00)	46 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr12:31944913C>T	Missense Mutation	H3F3C	p.R63Q	H3 histone, family 3C	20 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr10:115335714C>T	Silent	HABP2	p.T94T	hyaluronan binding prot	25 (0.00)	31 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr6:105219079G>A	Nonsense Mutation	HACE1	p.Q734*	HECT domain and anky	17 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr3:15642674C>G	Missense Mutation	HACL1	p.G37R	2-hydroxyacyl-CoA lyas	15 (0.00)	18 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr17:39881166C>T	Silent	HAP1	p.E601E	huntingtin-associated pr	43 (0.00)	56 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr15:89424920G>A	Missense Mutation	HAPLN3	p.P116L	hyaluronan and proteogl	17 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr5:140076557C>A	Missense Mutation	HARS2	p.Q286K	histidyl-tRNA synthetas	148 (0.00)	71 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr11:5289744C>T	Silent	HBE1	p.K133K	hemoglobin, epsilon 1	129 (0.00)	26 (0.35)	0.92
11-02	Gp4 Focus 2	g.chr5:139715483C>T	Silent	HBEGF	p.L176L	heparin-binding EGF-lik	25 (0.00)	51 (0.25)	0.68
11-02	Gp4 Focus 2	g.chr12:123200237C>T	Missense Mutation	HCAR3	p.G350S	hydroxycarboxylic acid	16 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr7:18563066G>A	Intron	HDAC9		histone deacetylase 9	61 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr7:18585987G>A	Intron	HDAC9		histone deacetylase 9	61 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr7:18617939A>G	Intron	HDAC9		histone deacetylase 9	31 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr7:18636660G>A	Intron	HDAC9		histone deacetylase 9	31 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr7:18636706G>T	Intron	HDAC9		histone deacetylase 9	27 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr7:18638620G>A	Intron	HDAC9		histone deacetylase 9	35 (0.00)	12 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr7:18645290C>T	Intron	HDAC9		histone deacetylase 9	82 (0.01)	51 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr7:18675833C>A	Intron	HDAC9		histone deacetylase 9	85 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:18681963C>T	Intron	HDAC9		histone deacetylase 9	51 (0.00)	25 (0.36)	0.96

11-02	Gp4 Focus 2	g.chr7:18694597G>A	Intron	HDAC9		histone deacetylase 9	98 (0.00)	53 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr7:18706049G>A	Missense Mutation	HDAC9	p.A481T	histone deacetylase 9	34 (0.03)	28 (0.46)	1.24
11-02	Gp4 Focus 2	g.chr7:18734077G>A	Intron	HDAC9		histone deacetylase 9	36 (0.00)	20 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr7:18738303G>A	Intron	HDAC9		histone deacetylase 9	75 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr7:18748867T>C	Intron	HDAC9		histone deacetylase 9	17 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:18761585G>A	Intron	HDAC9		histone deacetylase 9	40 (0.00)	56 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr7:18764559G>A	Intron	HDAC9		histone deacetylase 9	87 (0.00)	90 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr7:18795580C>T	Intron	HDAC9		histone deacetylase 9	85 (0.01)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr7:18808118C>T	Intron	HDAC9		histone deacetylase 9	89 (0.00)	69 (0.14)	0.39
11-02	Gp4 Focus 2	g.chr7:18843954G>A	Intron	HDAC9		histone deacetylase 9	121 (0.01)	67 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr7:18860928G>A	Intron	HDAC9		histone deacetylase 9	42 (0.00)	38 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr7:18866253G>A	Intron	HDAC9		histone deacetylase 9	20 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr7:18869884G>A	Intron	HDAC9		histone deacetylase 9	81 (0.01)	38 (0.71)	1.89
11-02	Gp4 Focus 2	g.chr7:18906148C>T	Intron	HDAC9		histone deacetylase 9	25 (0.00)	27 (0.59)	1.58
11-02	Gp4 Focus 2	g.chr7:18926847C>T	Intron	HDAC9		histone deacetylase 9	60 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr7:18942061G>A	Intron	HDAC9		histone deacetylase 9	21 (0.00)	33 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr7:18953278G>A	Intron	HDAC9		histone deacetylase 9	20 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr7:18957141G>A	Intron	HDAC9		histone deacetylase 9	33 (0.00)	34 (0.62)	1.65
11-02	Gp4 Focus 2	g.chr7:18957918C>T	Intron	HDAC9		histone deacetylase 9	38 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr7:18977806A>G	Intron	HDAC9		histone deacetylase 9	33 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr7:18989002C>T	Intron	HDAC9		histone deacetylase 9	132 (0.00)	33 (0.61)	1.62
11-02	Gp4 Focus 2	g.chr7:19024372T>A	Intron	HDAC9		histone deacetylase 9	164 (0.00)	24 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr7:19024373T>A	Intron	HDAC9		histone deacetylase 9	166 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr15:50534686C>A	Missense Mutation	HDC	p.C587F	histidine decarboxylase	79 (0.00)	71 (0.23)	0.60
11-02	Gp4 Focus 2	g.chrX:6995283G>A	Missense Mutation	HDHD1	p.S120F	haloacid dehalogenase-l	21 (0.00)	18 (0.50)	1.02
11-02	Gp4 Focus 2	g.chr1:236718617G>A	Nonsense Mutation	HEATR1	p.Q1968*	HEAT repeat containing	101 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:236746403G>A	Nonsense Mutation	HEATR1	p.Q779*	HEAT repeat containing	33 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr14:73974907C>T	Silent	HEATR4	p.L604L	HEAT repeat containing	46 (0.00)	34 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr14:31828151C>T	Silent	HEATR5A	p.L728L	HEAT repeat containing	69 (0.01)	22 (0.36)	1.16
11-02	Gp4 Focus 2	g.chr14:31856346C>T	Nonsense Mutation	HEATR5A	p.W390*	HEAT repeat containing	117 (0.00)	22 (0.36)	1.16
11-02	Gp4 Focus 2	g.chr2:37234348C>T	Missense Mutation	HEATR5B	p.S1541N	HEAT repeat containing	28 (0.00)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr14:31638572G>A	Missense Mutation	HECTD1	p.L479F	HECT domain containir	41 (0.00)	53 (0.15)	0.48
11-02	Gp4 Focus 2	g.chr12:112650299G>A	Nonsense Mutation	HECTD4	p.Q2395*	HECT domain containir	97 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:112657247C>T	Missense Mutation	HECTD4	p.M2193I	HECT domain containir	19 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr7:43436489G>A	Splice Site	HECW1		HECT, C2 and WW dor	17 (0.00)	23 (0.22)	0.58

11-02	Gp4 Focus 2	g.chr3:124731964G>A	Missense Mutation	HEG1	p.T820I	heart development prote	15 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr3:124732096G>C	Missense Mutation	HEG1	p.A776G	heart development prote	15 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:65074632G>A	Silent	HELZ	p.F1855F	helicase with zinc finge	61 (0.00)	98 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr11:124794654C>A	Missense Mutation	HEPACAM	p.G133W	hepatic and glial cell ad	26 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr11:93806497G>A	Missense Mutation	HEPHL1	p.G466S	hephaestin-like 1	63 (0.00)	42 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr15:63932440C>T	Missense Mutation	HERC1	p.E3938K	HECT and RLD domai	177 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr15:63935700C>T	Missense Mutation	HERC1	p.G3745E	HECT and RLD domai	46 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr15:63952043G>T	Silent	HERC1	p.R3106R	HECT and RLD domai	34 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr15:63958335C>A	Missense Mutation	HERC1	p.A2780S	HECT and RLD domai	23 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr15:63958633G>A	Missense Mutation	HERC1	p.P2749S	HECT and RLD domai	70 (0.00)	49 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr15:28437200C>T	Silent	HERC2	p.V2786V	HECT and RLD domai	75 (0.00)	45 (0.33)	1.23
11-02	Gp4 Focus 2	g.chr15:28437240C>T	Missense Mutation	HERC2	p.S2773N	HECT and RLD domai	70 (0.01)	42 (0.21)	0.79
11-02	Gp4 Focus 2	g.chr15:28492023C>G	Missense Mutation	HERC2	p.G1086R	HECT and RLD domai	37 (0.00)	36 (0.17)	0.61
11-02	Gp4 Focus 2	g.chr15:23318677A>T	RNA	HERC2P2		hect domain and RLD 2	156 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr16:56976114G>A	Missense Mutation	HERPUD1	p.D326N	homocysteine-inducible	77 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:35733890C>T	Silent	HERPUD2	p.P17P	HERPUD family memb	46 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr5:74014147G>A	Missense Mutation	HEXB	p.G401R	hexosaminidase B (beta	74 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr1:40098340G>A	Missense Mutation	HEYL	p.A43V	hes-related family bHL	60 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr3:120365157C>T	Silent	HGD	p.E202E	homogentisate 1,2-diox	36 (0.00)	46 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr1:222717457G>A	Silent	HHIPL2	p.L132L	HHIP-like 2	70 (0.00)	72 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:75174446C>T	Missense Mutation	HIP1	p.R816Q	huntingtin interacting p	76 (0.00)	18 (0.50)	2.16
11-02	Gp4 Focus 2	g.chr12:123338624C>T	Silent	HIP1R	p.S204S	huntingtin interacting p	49 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:114483505G>A	Missense Mutation	HIPK1	p.S167N	homeodomain interactin	19 (0.00)	35 (0.37)	0.78
11-02	Gp4 Focus 2	g.chr1:114483965C>T	Silent	HIPK1	p.N320N	homeodomain interactin	55 (0.00)	25 (0.24)	0.50
11-02	Gp4 Focus 2	g.chr11:33374860C>T	Missense Mutation	HIPK3	p.P1111S	homeodomain interactin	75 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr22:19348799C>T	Silent	HIRA	p.K682K	histone cell cycle regula	17 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr22:19371192C>T	Missense Mutation	HIRA	p.D456N	histone cell cycle regula	16 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr16:30005704C>T	Silent	HIRIP3	p.K254K	HIRA interacting protei	72 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:30005709C>T	Missense Mutation	HIRIP3	p.E253K	HIRA interacting protei	70 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr6:25727229C>T	Silent	HIST1H2BA	p.R31R	histone cluster 1, H2ba	68 (0.00)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr6:26216813G>A	Missense Mutation	HIST1H2BG	p.T20I	histone cluster 1, H2bg	78 (0.00)	34 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr6:26273449G>A	Silent	HIST1H2BI	p.A82A	histone cluster 1, H2bi	70 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr6:143074637G>A	Silent	HIVEP2	p.N2316N	human immunodeficien	22 (0.00)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr6:143081323G>A	Silent	HIVEP2	p.S2034S	human immunodeficien	29 (0.00)	43 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr6:143081344C>T	Missense Mutation	HIVEP2	p.M2027I	human immunodeficien	25 (0.00)	40 (0.53)	1.40

11-02	Gp4 Focus 2	g.chr1:42045683G>A	Missense Mutation	HIVEP3	p.P1596S	human immunodeficien	58 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr2:75081445G>A	Missense Mutation	HK2	p.R2H	hexokinase 2	83 (0.00)	17 (0.71)	1.88
11-02	Gp4 Focus 2	g.chr1:186024700C>T	Silent	HMCN1	p.H2346H	hemicentin 1	42 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr1:186045701G>A	Nonsense Mutation	HMCN1	p.W2811*	hemicentin 1	41 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr1:186045709G>A	Missense Mutation	HMCN1	p.D2814N	hemicentin 1	23 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr1:186120356G>A	Missense Mutation	HMCN1	p.S4878N	hemicentin 1	41 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr5:74643123G>A	Missense Mutation	HMGCR	p.G182D	3-hydroxy-3-methylglut	70 (0.00)	21 (0.52)	1.40
11-02	Gp4 Focus 2	g.chr1:120302567C>T	Missense Mutation	HMGCS2	p.S202N	3-hydroxy-3-methylglut	19 (0.00)	21 (0.29)	0.60
11-02	Gp4 Focus 2	g.chr15:45847851G>A	RNA	HMGN2P46		high mobility group nuc	25 (0.00)	36 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr5:149398148G>A	Missense Mutation	HMGXB3	p.R310Q	HMG box domain conta	31 (0.00)	32 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr5:149425088G>A	Silent	HMGXB3	p.T930T	HMG box domain conta	38 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr7:26233311C>T	Missense Mutation	HNRNPA2B1	p.G242D	heterogeneous nuclear r	34 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr5:179047977G>A	Missense Mutation	HNRNPH1	p.P105S	heterogeneous nuclear r	94 (0.01)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr10:70101416G>C	Missense Mutation	HNRNPH3	p.G284R	heterogeneous nuclear r	72 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr19:8527415G>A	Missense Mutation	HNRNPM	p.G96S	heterogeneous nuclear r	32 (0.00)	69 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr19:41812358C>T	Missense Mutation	HNRNPUL1	p.A820V	heterogeneous nuclear r	65 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr10:99359914G>A	Missense Mutation	HOGA1	p.A232T	4-hydroxy-2-oxoglutara	27 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr8:42829294G>A	Silent	HOOK3	p.E426E	hook microtubule-tether	85 (0.01)	61 (0.26)	0.85
11-02	Gp4 Focus 2	g.chr7:27222631G>A	Silent	HOXA11	p.R242R	homeobox A11	34 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr12:54447841C>T	Silent	HOXC4	p.F45F	homeobox C4	35 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:176959240G>A	Missense Mutation	HOXD13	p.V272I	homeobox D13	81 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr2:176996144G>A	Missense Mutation	HOXD8	p.R42K	homeobox D8	143 (0.00)	56 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr16:72110891G>A	Missense Mutation	HPR	p.D320N	haptoglobin-related prot	63 (0.00)	50 (0.30)	0.80
11-02	Gp4 Focus 2	g.chrX:133632459G>A	Silent	HPRT1	p.K175K	hypoxanthine phosphori	34 (0.00)	26 (0.23)	0.49
11-02	Gp4 Focus 2	g.chr10:100202959G>A	Silent	HPS1	p.V13V	Hermansky-Pudlak sync	17 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr3:148877856G>T	Missense Mutation	HPS3	p.Q467H	Hermansky-Pudlak sync	71 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr22:26868906C>T	Splice Site	HPS4		Hermansky-Pudlak sync	15 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr11:6458767C>T	Silent	HPX	p.Q202Q	hemopexin	26 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:152193200C>T	Missense Mutation	HRNR	p.G302E	hornerin	22 (0.00)	59 (0.31)	0.81
11-02	Gp4 Focus 2	g.chr16:22926547C>T	Silent	HS3ST2	p.H256H	heparan sulfate (glucosa	40 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chrX:131762925G>A	Missense Mutation	HS6ST2	p.P422S	heparan sulfate 6-O-sulf	32 (0.00)	38 (0.42)	0.89
11-02	Gp4 Focus 2	g.chr1:120057104G>A	Missense Mutation	HSD3B1	p.V320I	hydroxy-delta-5-steroid	50 (0.00)	13 (0.38)	0.80
11-02	Gp4 Focus 2	g.chr6:122733883G>A	Missense Mutation	HSF2	p.D102N	heat shock transcription	72 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr19:16259678T>A	Missense Mutation	HSH2D	p.S40T	hematopoietic SH2 dom	39 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr14:102568358C>A	Nonsense Mutation	HSP90AA1	p.G74*	heat shock protein 90kD	58 (0.00)	20 (0.45)	1.20

11-02	Gp4 Focus 2	g.chr14:102568360G>A	Missense Mutation	HSP90AA1	p.S73F	heat shock protein 90kD	58 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr14:65008773G>C	Missense Mutation	HSPA2	p.L402F	heat shock 70kDa protei	18 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr2:231988419C>T	Silent	HTR2B	p.Q20Q	5-hydroxytryptamine (s	58 (0.00)	32 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr7:154876110C>A	Silent	HTR5A	p.S329S	5-hydroxytryptamine (s	39 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr10:92508638G>A	Missense Mutation	HTR7	p.A418V	5-hydroxytryptamine (s	41 (0.00)	42 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr10:92508807G>A	Missense Mutation	HTR7	p.P362S	5-hydroxytryptamine (s	45 (0.00)	56 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:74758810G>A	Silent	HTRA2	p.L342L	HtrA serine peptidase 2	73 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr8:38832598C>A	Missense Mutation	HTRA4	p.A172E	HtrA serine peptidase 4	61 (0.00)	58 (0.38)	1.23
11-02	Gp4 Focus 2	g.chr3:50332918G>A	Missense Mutation	HYAL3	p.S39L	hyaluronoglucosaminid	41 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr16:70989278C>T	Splice Site	HYDIN	p.A2106T	HYDIN, axonemal cent	20 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr9:94984926G>A	Silent	IARS	p.L1194L	isoleucyl-tRNA syntheta	42 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:209104611G>A	Nonsense Mutation	IDH1	p.Q323*	isocitrate dehydrogenas	28 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr8:39775707G>T	Missense Mutation	IDO1	p.G95V	indoleamine 2,3-dioxyg	43 (0.00)	25 (0.24)	0.78
11-02	Gp4 Focus 2	g.chrX:148582517G>A	Missense Mutation	IDS	p.P157L	iduronate 2-sulfatase	20 (0.00)	18 (0.56)	1.34
11-02	Gp4 Focus 2	g.chr10:91143389C>G	Missense Mutation	IFIT1B	p.H107D	interferon-induced prote	23 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr10:91143813C>T	Missense Mutation	IFIT1B	p.S248F	interferon-induced prote	96 (0.00)	44 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr16:1607942A>G	Missense Mutation	IFT140	p.I798T	intraflagellar transport 1	15 (0.00)	18 (0.33)	1.06
11-02	Gp4 Focus 2	g.chr2:27688727C>T	Missense Mutation	IFT172	p.R572Q	intraflagellar transport 1	30 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr2:27700471C>T	Nonsense Mutation	IFT172	p.W392*	intraflagellar transport 1	19 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr3:185407200G>A	Missense Mutation	IGF2BP2	p.A207V	insulin-like growth fact	21 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr6:160511049G>A	Missense Mutation	IGF2R	p.G2190E	insulin-like growth fact	30 (0.00)	32 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr6:160511068G>A	Silent	IGF2R	p.V2196V	insulin-like growth fact	31 (0.00)	26 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr11:68696741G>C	Missense Mutation	IGHMBP2	p.S384T	immunoglobulin mu bin	18 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr15:22473037G>A	RNA	IGHV4OR15-8		immunoglobulin heavy	19 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr2:89339984G>A	RNA	IGKV1-12		immunoglobulin kappa	63 (0.00)	68 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr2:89246990C>T	RNA	IGKV1-5		immunoglobulin kappa	40 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr2:89278465G>A	RNA	IGKV3-7		immunoglobulin kappa	69 (0.00)	30 (0.67)	1.78
11-02	Gp4 Focus 2	g.chrX:130409690G>A	Silent	IGSF1	p.P973P	immunoglobulin superf	20 (0.00)	32 (0.47)	1.00
11-02	Gp4 Focus 2	g.chr3:151161480G>A	Missense Mutation	IGSF10	p.T1752I	immunoglobulin superf	29 (0.00)	12 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr3:151161577G>A	Nonsense Mutation	IGSF10	p.Q1720*	immunoglobulin superf	24 (0.00)	22 (0.73)	1.94
11-02	Gp4 Focus 2	g.chr3:151163660G>A	Missense Mutation	IGSF10	p.T1370I	immunoglobulin superf	100 (0.00)	70 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr3:151163790C>T	Missense Mutation	IGSF10	p.A1327T	immunoglobulin superf	135 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr1:159900041C>T	Missense Mutation	IGSF9	p.E668K	immunoglobulin superf	45 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:159904602G>A	Silent	IGSF9	p.V228V	immunoglobulin superf	27 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr5:140031333C>A	Missense Mutation	IK	p.L40I	IK cytokine, down-regu	20 (0.00)	40 (0.35)	0.93

11-02	Gp4 Focus 2	g.chr5:140037171C>T	Silent	IK	p.V278V	IK cytokine, down-regu	120 (0.00)	49 (0.20)	0.54
11-02	Gp4 Focus 2	g.chr8:42163944G>A	Silent	IKBKB	p.Q187Q	inhibitor of kappa light	21 (0.00)	23 (0.26)	0.84
11-02	Gp4 Focus 2	g.chr8:42163945T>A	Missense Mutation	IKBKB	p.Y188N	inhibitor of kappa light	21 (0.00)	23 (0.26)	0.84
11-02	Gp4 Focus 2	g.chr1:206945642C>T	Missense Mutation	IL10	p.A47T	interleukin 10	34 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr15:81593846C>T	Missense Mutation	IL16	p.T1104I	interleukin 16	32 (0.00)	27 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr2:102851433C>T	Silent	IL1RL2	p.G458G	interleukin 1 receptor-li	36 (0.03)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr19:14153309C>A	Silent	IL27RA	p.I193I	interleukin 27 receptor,	26 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr5:55248168C>G	Missense Mutation	IL6ST	p.E488Q	interleukin 6 signal tran	21 (0.00)	14 (0.64)	2.13
11-02	Gp4 Focus 2	g.chr19:10782115G>A	Silent	ILF3	p.K105K	interleukin enhancer bin	17 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr2:239090733C>T	Missense Mutation	ILKAP	p.R270K	integrin-linked kinase-a	63 (0.00)	30 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr2:86408431C>A	Missense Mutation	IMMT	p.G37V	inner membrane protein	99 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr18:22028108G>A	Silent	IMPACT	p.G240G	impact RWD domain pr	40 (0.00)	52 (0.35)	0.92
11-02	Gp4 Focus 2	g.chr1:62503719G>A	Missense Mutation	INADL	p.E1344K	InaD-like (Drosophila)	107 (0.00)	75 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr1:62594600G>A	Missense Mutation	INADL	p.G1752R	InaD-like (Drosophila)	84 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr2:206869744G>A	Missense Mutation	INO80D	p.T811I	INO80 complex subunit	64 (0.00)	130 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr2:206872165C>T	Splice Site	INO80D	p.R587R	INO80 complex subunit	52 (0.00)	122 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr2:191224916C>T	Nonsense Mutation	INPP1	p.Q30*	inositol polyphosphate-	48 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr2:99169292G>A	Missense Mutation	INPP4A	p.V408I	inositol polyphosphate-	39 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr4:142950004C>T	Missense Mutation	INPP4B	p.M902I	inositol polyphosphate-	40 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr4:142953555C>T	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:142961437C>T	Intron	INPP4B		inositol polyphosphate-	40 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:142965437C>G	Intron	INPP4B		inositol polyphosphate-	22 (0.00)	24 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr4:142969601C>T	Intron	INPP4B		inositol polyphosphate-	97 (0.01)	16 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr4:143007000C>T	Intron	INPP4B		inositol polyphosphate-	60 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr4:143012948G>A	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	34 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr4:143019945G>A	Intron	INPP4B		inositol polyphosphate-	30 (0.00)	37 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr4:143057876G>C	Intron	INPP4B		inositol polyphosphate-	63 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:143059844T>C	Intron	INPP4B		inositol polyphosphate-	118 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr4:143069117G>A	Intron	INPP4B		inositol polyphosphate-	119 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr4:143072416C>T	Intron	INPP4B		inositol polyphosphate-	72 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:143075816G>A	Intron	INPP4B		inositol polyphosphate-	23 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr4:143086183G>A	Intron	INPP4B		inositol polyphosphate-	59 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:143106229C>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr4:143124134C>T	Intron	INPP4B		inositol polyphosphate-	113 (0.00)	37 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr4:143187183G>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	34 (0.21)	0.55

11-02	Gp4 Focus 2	g.chr4:143226613C>T	Silent	INPP4B	p.L167L	inositol polyphosphate-	121 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr4:143239509G>A	Intron	INPP4B		inositol polyphosphate-	37 (0.00)	41 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr4:143239542G>A	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	40 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr4:143241383C>A	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr4:143257674C>T	Intron	INPP4B		inositol polyphosphate-	30 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr4:143260035A>C	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:143266727C>T	Intron	INPP4B		inositol polyphosphate-	39 (0.00)	51 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:143269487G>A	Intron	INPP4B		inositol polyphosphate-	82 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr4:143289135C>T	Intron	INPP4B		inositol polyphosphate-	60 (0.02)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr4:143290275G>A	Intron	INPP4B		inositol polyphosphate-	55 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr4:143293712A>G	Intron	INPP4B		inositol polyphosphate-	180 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr4:143293768C>A	Intron	INPP4B		inositol polyphosphate-	187 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr4:143299687C>G	Intron	INPP4B		inositol polyphosphate-	91 (0.00)	27 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr4:143309946G>T	Intron	INPP4B		inositol polyphosphate-	139 (0.01)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr4:143336473G>A	Intron	INPP4B		inositol polyphosphate-	15 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr4:143339927A>G	Intron	INPP4B		inositol polyphosphate-	55 (0.00)	53 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr4:143353955G>A	Intron	INPP4B		inositol polyphosphate-	17 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:143419437G>A	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr4:143452060G>A	Intron	INPP4B		inositol polyphosphate-	110 (0.00)	61 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr4:143458296G>A	Intron	INPP4B		inositol polyphosphate-	77 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr4:143462545G>A	Intron	INPP4B		inositol polyphosphate-	98 (0.00)	27 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr4:143469322G>A	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr4:143476595G>A	Intron	INPP4B		inositol polyphosphate-	66 (0.00)	54 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr4:143494383C>G	Intron	INPP4B		inositol polyphosphate-	57 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr4:143507547C>A	Intron	INPP4B		inositol polyphosphate-	135 (0.00)	70 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr4:143507587G>T	Intron	INPP4B		inositol polyphosphate-	126 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr4:143520092G>A	Intron	INPP4B		inositol polyphosphate-	20 (0.00)	9 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr4:143535347C>T	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	53 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr4:143550383G>A	Intron	INPP4B		inositol polyphosphate-	49 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr4:143583756C>T	Intron	INPP4B		inositol polyphosphate-	39 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr4:143591824G>A	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	22 (0.73)	1.94
11-02	Gp4 Focus 2	g.chr4:143604324C>T	Intron	INPP4B		inositol polyphosphate-	94 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr4:143620046G>A	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr4:143620219C>T	Intron	INPP4B		inositol polyphosphate-	182 (0.01)	51 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr4:143634178G>A	Intron	INPP4B		inositol polyphosphate-	53 (0.00)	27 (0.26)	0.69

11-02	Gp4 Focus 2	g.chr4:143639335G>A	Intron	INPP4B		inositol polyphosphate-4	150 (0.01)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr4:143654870G>A	Intron	INPP4B		inositol polyphosphate-4	45 (0.00)	23 (0.61)	1.62
11-02	Gp4 Focus 2	g.chr4:143692716C>T	Intron	INPP4B		inositol polyphosphate-4	30 (0.00)	14 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr4:143717703C>T	Intron	INPP4B		inositol polyphosphate-4	103 (0.00)	37 (0.68)	1.80
11-02	Gp4 Focus 2	g.chr4:143726808T>C	Intron	INPP4B		inositol polyphosphate-4	24 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr4:143728569G>A	Intron	INPP4B		inositol polyphosphate-4	45 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:143732519G>A	Intron	INPP4B		inositol polyphosphate-4	18 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr4:143741113C>T	Intron	INPP4B		inositol polyphosphate-4	71 (0.00)	54 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr4:143747606G>A	Intron	INPP4B		inositol polyphosphate-4	40 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr17:1401413C>T	Silent	INPP5K	p.E260E	inositol polyphosphate-5	21 (0.00)	53 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr17:1413070C>T	Silent	INPP5K	p.G95G	inositol polyphosphate-5	74 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr17:1413089G>A	Missense Mutation	INPP5K	p.S89F	inositol polyphosphate-5	73 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr11:77672059A>C	Missense Mutation	INTS4	p.I199M	integrator complex subu	76 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr11:77672078G>A	Missense Mutation	INTS4	p.A193V	integrator complex subu	77 (0.01)	23 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr7:64662999G>A	RNA	INTS4L1		integrator complex subu	32 (0.00)	31 (0.35)	1.53
11-02	Gp4 Focus 2	g.chr3:49765570G>A	Missense Mutation	IP6K1	p.S253L	inositol hexakisphospha	30 (0.00)	47 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr1:44423714C>T	Missense Mutation	IPO13	p.H536Y	importin 13	21 (0.00)	27 (0.70)	1.88
11-02	Gp4 Focus 2	g.chr13:98654723G>A	Missense Mutation	IPO5	p.D371N	importin 5	32 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr2:237240091G>A	Nonsense Mutation	IQCA1	p.Q762*	IQ motif containing witl	77 (0.01)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:237240118C>T	Missense Mutation	IQCA1	p.V753M	IQ motif containing witl	80 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr3:121489380G>A	Missense Mutation	IQCB1	p.L537F	IQ motif containing B1	74 (0.00)	58 (0.53)	1.43
11-02	Gp4 Focus 2	g.chr15:67713874G>A	Missense Mutation	IQCH	p.D822N	IQ motif containing H	36 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr15:91030778G>A	Silent	IQGAP1	p.L1404L	IQ motif containing GT	63 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr5:75991412G>A	Missense Mutation	IQGAP2	p.R1376K	IQ motif containing GT	34 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr3:10264387G>A	Missense Mutation	IRAK2	p.V361I	interleukin-1 receptor-as	17 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr6:401510C>T	Missense Mutation	IRF4	p.H278Y	interferon regulatory fac	18 (0.00)	12 (0.75)	1.43
11-02	Gp4 Focus 2	g.chr2:227660524C>T	Silent	IRS1	p.R977R	insulin receptor substrat	41 (0.00)	48 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:156694016C>T	Missense Mutation	ISG20L2	p.R291Q	interferon stimulated ex	40 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr14:77950766G>A	Missense Mutation	ISM2	p.T176M	isthmin 2	21 (0.00)	38 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr3:128852953C>T	Missense Mutation	ISY1	p.G211R	ISY1 splicing factor hor	29 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr16:47196526G>A	Silent	ITFG1	p.N501N	integrin alpha FG-GAP	96 (0.00)	50 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr16:304665G>T	Missense Mutation	ITFG3	p.D85Y	integrin alpha FG-GAP	46 (0.00)	68 (0.21)	0.66
11-02	Gp4 Focus 2	g.chr5:52344268G>A	Missense Mutation	ITGA2	p.D155N	integrin, alpha 2 (CD49	116 (0.00)	65 (0.12)	0.41
11-02	Gp4 Focus 2	g.chr2:173330375C>T	Silent	ITGA6	p.I97I	integrin, alpha 6	29 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr17:3638153G>A	Silent	ITGAE	p.A871A	integrin, alpha E (antige	44 (0.00)	13 (0.38)	1.03

11-02	Gp4 Focus 2	g.chr17:3643131G>T	Silent	ITGAE	p.V830V	integrin, alpha E (antige	19 (0.00)	26 (0.35)	0.92
11-02	Gp4 Focus 2	g.chr17:3653660C>A	Missense Mutation	ITGAE	p.Q670H	integrin, alpha E (antige	25 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:33208872G>A	Silent	ITGB1	p.G470G	integrin, beta 1 (fibrone	72 (0.00)	16 (0.44)	1.46
11-02	Gp4 Focus 2	g.chr2:161029087G>A	Missense Mutation	ITGB6	p.T263I	integrin, beta 6	15 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr12:53589413G>A	Silent	ITGB7	p.Y356Y	integrin, beta 7	25 (0.00)	24 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr7:20420388G>A	Silent	ITGB8	p.K245K	integrin, beta 8	78 (0.00)	18 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr3:4725141C>T	Missense Mutation	ITPR1	p.T1063M	inositol 1,4,5-trisphosph	106 (0.00)	70 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr12:26869148T>A	Missense Mutation	ITPR2	p.M185L	inositol 1,4,5-trisphosph	39 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr12:26869149C>A	Missense Mutation	ITPR2	p.L184F	inositol 1,4,5-trisphosph	39 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr20:10625595G>A	Missense Mutation	JAG1	p.H754Y	jagged 1	19 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr19:17945699C>T	Missense Mutation	JAK3	p.G721S	Janus kinase 3	19 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr19:17949123G>A	Silent	JAK3	p.Y506Y	Janus kinase 3	25 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr16:733072G>T	Missense Mutation	JMJD8	p.P199T	jumonji domain contain	26 (0.00)	30 (0.30)	0.96
11-02	Gp4 Focus 2	g.chr22:39095813G>A	Silent	JOSD1	p.F60F	Josephin domain contai	82 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr3:124160822G>A	Missense Mutation	KALRN	p.V1075M	kalirin, RhoGEF kinase	38 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr9:713136G>A	Silent	KANK1	p.L790L	KN motif and ankyrin r	51 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr12:49061475C>T	Splice Site	KANSL2		KAT8 regulatory NSL c	29 (0.00)	73 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:97271081G>A	Missense Mutation	KANSL3	p.P637S	KAT8 regulatory NSL c	38 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr2:97278074G>A	Missense Mutation	KANSL3	p.P344L	KAT8 regulatory NSL c	99 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr17:40271583C>T	Missense Mutation	KAT2A	p.V285M	K(lysine) acetyltransfera	47 (0.00)	47 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr11:65482121G>A	Silent	KAT5	p.P249P	K(lysine) acetyltransfera	56 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr8:41791615C>T	Missense Mutation	KAT6A	p.E1375K	K(lysine) acetyltransfera	15 (0.00)	11 (0.55)	1.76
11-02	Gp4 Focus 2	g.chr17:47899083G>A	Silent	KAT7	p.E439E	K(lysine) acetyltransfera	15 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr12:5021828C>T	Silent	KCNA1	p.L428L	potassium voltage-gated	111 (0.00)	31 (0.68)	1.81
11-02	Gp4 Focus 2	g.chr1:111146798G>A	Missense Mutation	KCNA2	p.H203Y	potassium voltage-gated	29 (0.00)	35 (0.51)	1.07
11-02	Gp4 Focus 2	g.chr1:111215744T>A	Missense Mutation	KCNA3	p.N563I	potassium voltage-gated	15 (0.00)	22 (0.23)	0.47
11-02	Gp4 Focus 2	g.chr1:110766145G>A	Missense Mutation	KCNC4	p.R413Q	potassium voltage-gated	39 (0.00)	15 (0.67)	1.39
11-02	Gp4 Focus 2	g.chr7:120386073G>A	Silent	KCND2	p.L569L	potassium voltage-gated	23 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:211192208C>A	Nonsense Mutation	KCNH1	p.E317*	potassium voltage-gated	42 (0.02)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:163256771G>A	Missense Mutation	KCNH7	p.L779F	potassium voltage-gated	29 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr3:19575208G>A	Missense Mutation	KCNH8	p.A981T	potassium voltage-gated	76 (0.00)	43 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr2:18112486C>T	Missense Mutation	KCNS3	p.R71W	potassium voltage-gated	46 (0.00)	47 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr8:36663894G>A	Nonsense Mutation	KCNU1	p.W192*	potassium channel, subf	51 (0.00)	12 (0.42)	1.35
11-02	Gp4 Focus 2	g.chr8:36694344G>A	Missense Mutation	KCNU1	p.D467N	potassium channel, subf	114 (0.01)	64 (0.12)	0.40
11-02	Gp4 Focus 2	g.chr8:110984767C>A	Silent	KCNV1	p.L237L	potassium channel, subf	21 (0.00)	19 (0.32)	1.08

11-02	Gp4 Focus 2	g.chr18:24081158C>T	Silent	KCTD1	p.L14L	potassium channel tetra	69 (0.01)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr12:109907378C>T	Silent	KCTD10	p.Q53Q	potassium channel tetra	20 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr6:36454913C>T	Silent	KCTD20	p.A407A	potassium channel tetra	92 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr11:108345643G>A	Missense Mutation	KDELC2	p.R479C	KDEL (Lys-Asp-Glu-L	28 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr22:38877456G>A	Silent	KDELR3	p.L197L	KDEL (Lys-Asp-Glu-L	60 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr1:44156556C>A	Nonsense Mutation	KDM4A	p.S693*	lysine (K)-specific dem	91 (0.01)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chrX:53228310C>T	Missense Mutation	KDM5C	p.E698K	lysine (K)-specific dem	19 (0.00)	23 (0.43)	0.72
11-02	Gp4 Focus 2	g.chr4:55974057G>A	Missense Mutation	KDR	p.P420L	kinase insert domain rec	36 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr18:61011691G>A	Silent	KDSR	p.Y215Y	3-ketodihydrosphingosi	71 (0.01)	25 (0.24)	0.77
11-02	Gp4 Focus 2	g.chr18:61011701G>A	Missense Mutation	KDSR	p.T212I	3-ketodihydrosphingosi	72 (0.00)	25 (0.20)	0.64
11-02	Gp4 Focus 2	g.chr8:136619234C>T	Nonsense Mutation	KHDRBS3	p.Q282*	KH domain containing,	29 (0.00)	23 (0.61)	1.62
11-02	Gp4 Focus 2	g.chr17:26959250G>A	Silent	KIAA0100	p.S1271S	KIAA0100	47 (0.00)	50 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr17:26962168G>A	Missense Mutation	KIAA0100	p.R813W	KIAA0100	41 (0.00)	66 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr4:6863127G>A	Missense Mutation	KIAA0232	p.E340K	KIAA0232	64 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr14:70175644G>A	Missense Mutation	KIAA0247	p.G237R	KIAA0247	33 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr6:24576733C>T	Missense Mutation	KIAA0319	p.A533T	KIAA0319	66 (0.00)	55 (0.25)	0.68
11-02	Gp4 Focus 2	g.chr6:127768680T>A	Missense Mutation	KIAA0408	p.N262Y	KIAA0408	88 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr16:27640054C>T	Silent	KIAA0556	p.V71V	KIAA0556	70 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr14:58895117G>A	Silent	KIAA0586	p.P57P	KIAA0586	63 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr14:58949331G>A	Silent	KIAA0586	p.E1068E	KIAA0586	104 (0.00)	69 (0.14)	0.39
11-02	Gp4 Focus 2	g.chr16:67210836G>A	Silent	KIAA0895L	p.L432L	KIAA0895-like	38 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr1:155885749C>T	Silent	KIAA0907	p.L520L	KIAA0907	38 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr1:92634463G>A	Nonsense Mutation	KIAA1107	p.W57*	KIAA1107	74 (0.00)	36 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr4:123185467G>A	Missense Mutation	KIAA1109	p.S2401N	KIAA1109	43 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr10:24809167G>A	Missense Mutation	KIAA1217	p.V448I	KIAA1217	22 (0.00)	16 (0.44)	1.46
11-02	Gp4 Focus 2	g.chr6:138576606G>T	Missense Mutation	KIAA1244	p.L268F	KIAA1244	105 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr6:138576607G>T	Missense Mutation	KIAA1244	p.G269W	KIAA1244	105 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr6:138601151C>T	Nonsense Mutation	KIAA1244	p.Q771*	KIAA1244	29 (0.00)	39 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr6:138649199C>G	Missense Mutation	KIAA1244	p.N1681K	KIAA1244	51 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr9:5747414C>T	Missense Mutation	KIAA1432	p.P454L		28 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:33233684G>A	Missense Mutation	KIAA1522	p.G84D	KIAA1522	48 (0.00)	33 (0.39)	1.05
11-02	Gp4 Focus 2	g.chr7:138555953G>A	Missense Mutation	KIAA1549	p.R1501C	KIAA1549	20 (0.00)	97 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr7:138579136C>T	Silent	KIAA1549	p.K1328K	KIAA1549	47 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:138583735G>C	Missense Mutation	KIAA1549	p.I1271M	KIAA1549	55 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr11:33564636G>A	Silent	KIAA1549L	p.Q212Q	KIAA1549-like	29 (0.00)	52 (0.38)	1.03

11-02	Gp4 Focus 2	g.chr11:33565623C>T	Silent	KIAA1549L	p.N541N	KIAA1549-like	121 (0.00)	33 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr1:180885981G>A	Missense Mutation	KIAA1614	p.V248M	KIAA1614	60 (0.02)	30 (0.63)	1.69
11-02	Gp4 Focus 2	g.chr11:93439971G>A	Missense Mutation	KIAA1731	p.S66N	KIAA1731	26 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr11:93454533G>A	Silent	KIAA1731	p.E115E	KIAA1731	108 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr9:115336796G>A	Missense Mutation	KIAA1958	p.D146N	KIAA1958	29 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr9:115337400C>T	Missense Mutation	KIAA1958	p.P347L	KIAA1958	90 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr9:115421596G>A	Silent	KIAA1958	p.K466K	KIAA1958	17 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr3:113388970G>A	Nonsense Mutation	KIAA2018	p.Q53*	KIAA2018	25 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr3:44852383G>A	Missense Mutation	KIF15	p.V673I	kinesin family member	40 (0.00)	10 (0.80)	2.13
11-02	Gp4 Focus 2	g.chr5:137517189C>T	Nonsense Mutation	KIF20A	p.Q82*	kinesin family member	85 (0.00)	55 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr10:91498746C>T	Missense Mutation	KIF20B	p.R1230C	kinesin family member	45 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr15:69728087G>A	Missense Mutation	KIF23	p.A417T	kinesin family member	18 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr9:34255917G>A	Missense Mutation	KIF24	p.L1230F	kinesin family member	85 (0.00)	27 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr9:34255972T>C	Silent	KIF24	p.G1211G	kinesin family member	75 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr9:34256713G>A	Silent	KIF24	p.A964A	kinesin family member	23 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:45218877G>T	Missense Mutation	KIF2C	p.E171D	kinesin family member	15 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr2:149818609A>G	Missense Mutation	KIF5C	p.M365V	kinesin family member	90 (0.00)	79 (0.13)	0.41
11-02	Gp4 Focus 2	g.chr2:149818610T>A	Missense Mutation	KIF5C	p.M365K	kinesin family member	94 (0.00)	78 (0.12)	0.38
11-02	Gp4 Focus 2	g.chr2:149835452A>G	Missense Mutation	KIF5C	p.Q437R	kinesin family member	48 (0.00)	19 (0.47)	1.54
11-02	Gp4 Focus 2	g.chr15:90189250G>A	Missense Mutation	KIF7	p.T599I	kinesin family member	24 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr13:33635129G>A	Nonsense Mutation	KL	p.W638*	klotho	26 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr13:33635466G>T	Missense Mutation	KL	p.E750D	klotho	39 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr4:39408614T>C	Silent	KLB	p.I15I	klotho beta	32 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr9:110249416C>T	Missense Mutation	KLF4	p.R386Q	Kruppel-like factor 4 (g	34 (0.00)	26 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr14:50241368G>A	Missense Mutation	KLHDC2	p.G108E	kelch domain containing	67 (0.00)	37 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr3:47385356C>G	Missense Mutation	KLHL18	p.C550W	kelch-like family memb	40 (0.00)	74 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr19:51381702G>A	Missense Mutation	KLK2	p.G225S	kallikrein-related peptid	42 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr19:51412582C>T	Missense Mutation	KLK4	p.M50I	kallikrein-related peptid	15 (0.00)	16 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr12:10530822G>A	Silent	KLRK1	p.L148L	killer cell lectin-like rec	20 (0.00)	29 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr19:36211330C>T	Silent	KMT2B	p.L361L	lysine (K)-specific meth	29 (0.00)	40 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr7:151845774G>A	Missense Mutation	KMT2C	p.T4413I	lysine (K)-specific meth	27 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr7:151845776C>A	Missense Mutation	KMT2C	p.L4412F	lysine (K)-specific meth	27 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr12:49421053G>A	Missense Mutation	KMT2D	p.S4899F	lysine (K)-specific meth	31 (0.00)	49 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr12:49422670C>T	Missense Mutation	KMT2D	p.E4775K	lysine (K)-specific meth	109 (0.00)	96 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr12:49424498G>A	Silent	KMT2D	p.L4575L	lysine (K)-specific meth	25 (0.00)	37 (0.27)	0.72

11-02	Gp4 Focus 2	g.chr12:49432321G>A	Missense Mutation	KMT2D	p.P2940S	lysine (K)-specific meth	34 (0.00)	49 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr16:19722715C>A	Missense Mutation	KNOP1	p.M322I	lysine-rich nucleolar pr	29 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr15:40679376G>A	Missense Mutation	KNSTRN	p.D152N	kinetochore-localized a	38 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr13:50296181G>A	Silent	KPNA3	p.I212I	karyopherin alpha 3 (im	23 (0.00)	15 (0.87)	2.31
11-02	Gp4 Focus 2	g.chr7:98779571G>A	Silent	KPNA7	p.L418L	karyopherin alpha 7 (im	33 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr17:45755536C>T	Missense Mutation	KPNB1	p.S598F	karyopherin (importin)	91 (0.00)	49 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr1:152732615A>T	Missense Mutation	KPRP	p.Y184F	keratinocyte proline-ric	39 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr17:39659350C>T	Splice Site	KRT13	p.E246K	keratin 13	42 (0.00)	27 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr17:39767334C>T	Nonsense Mutation	KRT16	p.W307*	keratin 16	23 (0.00)	37 (0.62)	1.66
11-02	Gp4 Focus 2	g.chr17:39680100G>A	Silent	KRT19	p.L366L	keratin 19	17 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr17:38859623C>T	Missense Mutation	KRT24	p.S108N	keratin 24	151 (0.00)	96 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr17:38911208C>T	Missense Mutation	KRT25	p.D106N	keratin 25	45 (0.00)	30 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr17:39553609C>T	Silent	KRT31	p.Q61Q	keratin 31	21 (0.00)	69 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr17:39521090C>T	Silent	KRT33B	p.R346R	keratin 33B	42 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr12:52881732C>T	Silent	KRT6A	p.V489V	keratin 6A	30 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr21:46057760C>T	Silent	KRTAP10-10	p.C142C	keratin associated protei	18 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr21:46057771G>T	Missense Mutation	KRTAP10-10	p.C146F	keratin associated protei	20 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr21:31869323C>T	Missense Mutation	KRTAP19-4	p.G36S	keratin associated protei	42 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr21:31933526C>T	Missense Mutation	KRTAP19-7	p.G28E	keratin associated protei	55 (0.00)	54 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr17:39389229G>A	Missense Mutation	KRTAP9-3	p.C159Y	keratin associated protei	45 (0.00)	46 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr17:39394416G>A	Missense Mutation	KRTAP9-8	p.C38Y	keratin associated protei	17 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr3:134322831G>A	Nonsense Mutation	KY	p.Q526*	kyphoscoliosis peptidas	62 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:23286520C>T	Missense Mutation	LACTBL1	p.D78N	lactamase, beta-like 1	21 (0.00)	23 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr1:201355710G>A	Missense Mutation	LAD1	p.A260V	ladinin 1	19 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr18:6982540G>C	Missense Mutation	LAMA1	p.S1949C	laminin, alpha 1	68 (0.00)	44 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr18:21437823C>A	Silent	LAMA3	p.I1384I	laminin, alpha 3	35 (0.00)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr7:107746267C>T	Missense Mutation	LAMB4	p.G289R	laminin, beta 4	43 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr13:113965154C>T	Silent	LAMP1	p.Y178Y	lysosomal-associated m	48 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr13:113974687C>T	Missense Mutation	LAMP1	p.P260S	lysosomal-associated m	65 (0.00)	52 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr3:45517960G>A	Splice Site	LARS2	p.V287I	leucyl-tRNA synthetase	99 (0.01)	70 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr3:45537804G>A	Missense Mutation	LARS2	p.D521N	leucyl-tRNA synthetase	56 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr1:225592172C>T	Missense Mutation	LBR	p.G541S	lamin B receptor	49 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr1:32740036G>A	Splice Site	LCK		LCK proto-oncogene, S	22 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr16:25176030C>G	Missense Mutation	LCMT1	p.N227K	leucine carboxyl methyl	91 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr13:46733010G>A	Missense Mutation	LCP1	p.T60I	lymphocyte cytosolic pr	130 (0.00)	30 (0.20)	0.53

11-02	Gp4 Focus 2	g.chr13:46733114G>A	Silent	LCP1	p.G25G	lymphocyte cytosolic pr	97 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr15:66850067G>A	Silent	LCTL	p.D305D	lactase-like	25 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr4:16900041G>A	Missense Mutation	LDB2	p.P23L	LIM domain binding 2	31 (0.00)	19 (0.74)	1.96
11-02	Gp4 Focus 2	g.chr19:54969692G>T	Missense Mutation	LENG8	p.M744I	leukocyte receptor clust	24 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr7:127892090T>C	Missense Mutation	LEP	p.C7R	leptin	31 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr3:189690731G>A	Missense Mutation	LEPREL1	p.S544F	leprecan-like 1	22 (0.00)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr19:39292965G>A	Missense Mutation	LGALS4	p.T217I	lectin, galactoside-bindi	32 (0.00)	16 (0.81)	2.17
11-02	Gp4 Focus 2	g.chrX:111914548G>A	Missense Mutation	LHFPL1	p.S24F	lipoma HMGIC fusion	23 (0.00)	51 (0.92)	2.05
11-02	Gp4 Focus 2	g.chr1:197896870A>G	Missense Mutation	LHX9	p.K295E	LIM homeobox 9	57 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr5:38482170G>A	Missense Mutation	LIFR	p.P941S	leukemia inhibitory fact	79 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr17:33313065G>A	Silent	LIG3	p.L202L	ligase III, DNA, ATP-d	43 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr19:54782294C>T	Missense Mutation	LILRB2	p.G360R	leukocyte immunoglobu	16 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr12:50575707G>A	Silent	LIMA1	p.S419S	LIM domain and actin b	27 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr22:31674305G>A	Missense Mutation	LIMK2	p.D599N	LIM domain kinase 2	54 (0.02)	31 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr19:52208410C>T	RNA	LINC00085			52 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr21:30566586G>A	RNA	LINC00189		long intergenic non-prot	45 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr21:30660364G>T	RNA	LINC00189		long intergenic non-prot	35 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr14:94468149G>A	RNA	LINC00521		long intergenic non-prot	23 (0.00)	25 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr20:11791057G>A	lincRNA	LINC00687		long intergenic non-prot	31 (0.00)	67 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr6:40312272C>T	lincRNA	LINC00951		long intergenic non-prot	19 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:151773636G>A	Silent	LINGO4	p.N515N	leucine rich repeat and I	19 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr10:90438215A>C	Missense Mutation	LIPF	p.Y325S	lipase, gastric	33 (0.00)	18 (0.94)	2.52
11-02	Gp4 Focus 2	g.chr2:97399309C>T	Missense Mutation	LMAN2L	p.V152M	lectin, mannose-binding	42 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr13:76393601G>T	Nonsense Mutation	LMO7	p.E480*	LIM domain 7	34 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr13:76430677C>T	Missense Mutation	LMO7	p.P1333L	LIM domain 7	65 (0.00)	48 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr3:69168118C>T	Missense Mutation	LMOD3	p.S463N	leiomodin 3 (fetal)	108 (0.01)	50 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:97820173C>T	Missense Mutation	LMTK2	p.P378S	lemur tyrosine kinase 2	32 (0.00)	25 (0.56)	1.49
11-02	Gp4 Focus 2	g.chr19:49012157C>T	Missense Mutation	LMTK3	p.A170T	lemur tyrosine kinase 3	25 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr3:100148576G>A	Start Codon SNP	LNP1	p.M1I	leukemia NUP98 fusion	69 (0.00)	17 (0.53)	1.03
11-02	Gp4 Focus 2	g.chr13:28136659C>T	Missense Mutation	LNX2	p.G372E	ligand of numb-protein	64 (0.00)	64 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr2:74762776G>C	Missense Mutation	LOXL3	p.T452S	lysyl oxidase-like 3	16 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:188202472G>A	Missense Mutation	LPP	p.E96K	LIM domain containing	153 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr4:151520192G>A	Missense Mutation	LRBA	p.P2005S	LPS-responsive vesicle	60 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr3:197574745G>A	Silent	LRCH3	p.L461L	leucine-rich repeats and	19 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr3:66434656G>A	Silent	LRIG1	p.I610I	leucine-rich repeats and	34 (0.00)	82 (0.30)	0.81

11-02	Gp4 Focus 2	g.chr3:66460632G>A	Missense Mutation	LRIG1	p.H286Y	leucine-rich repeats and	34 (0.00)	62 (0.40)	1.08
11-02	Gp4 Focus 2	g.chr2:141027856C>T	Missense Mutation	LRP1B	p.G4401D	low density lipoprotein	33 (0.00)	46 (0.20)	0.64
11-02	Gp4 Focus 2	g.chr2:141201997C>T	Missense Mutation	LRP1B	p.G3399D	low density lipoprotein	59 (0.00)	25 (0.20)	0.65
11-02	Gp4 Focus 2	g.chr2:170059440G>A	Missense Mutation	LRP2	p.H2679Y	low density lipoprotein	21 (0.00)	89 (0.72)	1.92
11-02	Gp4 Focus 2	g.chr11:46900739G>A	Missense Mutation	LRP4	p.T981I	low density lipoprotein	21 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr6:53706994G>A	Missense Mutation	LRRC1	p.M82I	leucine rich repeat conta	44 (0.00)	56 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr7:102574454C>T	Missense Mutation	LRRC17	p.H32Y	leucine rich repeat conta	15 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr10:134161860G>A	Splice Site	LRRC27	p.R309K	leucine rich repeat conta	51 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr18:7231442C>T	Silent	LRRC30	p.C102C	leucine rich repeat conta	21 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr17:44626869C>A	Missense Mutation	LRRC37A2	p.S1455Y	leucine rich repeat conta	100 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:62855678C>T	Missense Mutation	LRRC37A3	p.S1529N	leucine rich repeat conta	55 (0.00)	55 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr17:62856953C>T	Missense Mutation	LRRC37A3	p.G1104E	leucine rich repeat conta	93 (0.00)	55 (0.58)	1.55
11-02	Gp4 Focus 2	g.chr7:127670635G>A	Missense Mutation	LRRC4	p.P20L	leucine rich repeat conta	16 (0.00)	55 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr17:45912754C>T	Silent	LRRC46	p.I87I	leucine rich repeat conta	24 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr11:40137133C>T	Missense Mutation	LRRC4C	p.G237D	leucine rich repeat conta	49 (0.00)	23 (0.26)	1.41
11-02	Gp4 Focus 2	g.chr1:165532981G>A	Missense Mutation	LRRC52	p.A288T	leucine rich repeat conta	25 (0.00)	26 (0.35)	0.92
11-02	Gp4 Focus 2	g.chr15:42839586G>A	Missense Mutation	LRRC57	p.A122V	leucine rich repeat conta	28 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr17:48460581G>A	Missense Mutation	LRRC59	p.S231F	leucine rich repeat conta	15 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr1:156902274G>T	Missense Mutation	LRRC71	p.M500I	leucine rich repeat conta	19 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr7:16572163C>T	Missense Mutation	LRRC72	p.A45V	leucine rich repeat conta	38 (0.00)	12 (0.75)	2.68
11-02	Gp4 Focus 2	g.chr1:90178389C>T	Missense Mutation	LRRC8C	p.S87F	leucine rich repeat conta	32 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr19:7965691G>A	Missense Mutation	LRRC8E	p.E762K	leucine rich repeat conta	29 (0.00)	37 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr3:169540724G>A	Missense Mutation	LRRIQ4	p.G339R	leucine-rich repeats and	30 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr12:40626184C>T	Splice Site	LRRK2	p.Q116*	leucine-rich repeat kinas	21 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr12:40734095G>A	Splice Site	LRRK2		leucine-rich repeat kinas	55 (0.00)	42 (0.60)	1.59
11-02	Gp4 Focus 2	g.chr12:40734253C>T	Missense Mutation	LRRK2	p.P2036S	leucine-rich repeat kinas	23 (0.00)	44 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:194373563C>T	Silent	LSG1	p.Q356Q	large 60S subunit nuclea	64 (0.00)	56 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr3:46480885C>T	Missense Mutation	LTF	p.E602K	lactotransferrin	29 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr3:46485031C>A	Missense Mutation	LTF	p.R517I	lactotransferrin	49 (0.00)	65 (0.22)	0.57
11-02	Gp4 Focus 2	g.chr2:160755227C>T	Silent	LY75-CD302	p.E146E	LY75-CD302 readthrou	39 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr4:4276142C>T	Missense Mutation	LYAR	p.E262K	Ly1 antibody reactive	59 (0.00)	40 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr19:42342237C>T	Missense Mutation	LYPD4	p.A104T	LY6/PLAUR domain c	28 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr1:235878550G>A	Silent	LYST	p.H3245H	lysosomal trafficking re	36 (0.00)	15 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr3:45869964G>A	Silent	LZTFL1	p.L248L	leucine zipper transcript	27 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr10:102763496C>T	Missense Mutation	LZTS2	p.S214L	leucine zipper, putative	25 (0.00)	50 (0.18)	0.48

11-02	Gp4 Focus 2	g.chr1:39781189C>T	Missense Mutation	MACF1	p.T1097I	microtubule-actin crossl	50 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr1:39853929G>A	Missense Mutation	MACF1	p.D5144N	microtubule-actin crossl	20 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr11:47297476G>A	Missense Mutation	MADD	p.G229E	MAP-kinase activating	78 (0.01)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr11:47331155C>T	Silent	MADD	p.L1384L	MAP-kinase activating	58 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chrX:55479329G>A	Silent	MAGEH1	p.L174L	melanoma antigen famil	38 (0.00)	96 (0.81)	1.35
11-02	Gp4 Focus 2	g.chr7:77659387C>T	Intron	MAGI2		membrane associated gu	39 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr7:77662239G>A	Intron	MAGI2		membrane associated gu	63 (0.00)	33 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:77664732G>A	Intron	MAGI2		membrane associated gu	32 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr7:77679926C>T	Intron	MAGI2		membrane associated gu	69 (0.00)	49 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr7:77710148C>T	Intron	MAGI2		membrane associated gu	122 (0.01)	47 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr7:77711151G>A	Intron	MAGI2		membrane associated gu	125 (0.00)	29 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr7:77740080C>A	Intron	MAGI2		membrane associated gu	81 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr7:77756618G>A	Nonsense Mutation	MAGI2	p.Q1107*	membrane associated gu	50 (0.00)	57 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr7:77756634G>A	Silent	MAGI2	p.P1101P	membrane associated gu	51 (0.00)	50 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr7:77759752G>A	Intron	MAGI2		membrane associated gu	58 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr7:77761191C>T	Intron	MAGI2		membrane associated gu	35 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr7:77761797C>T	Intron	MAGI2		membrane associated gu	49 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr7:77762233G>A	Missense Mutation	MAGI2	p.P1059L	membrane associated gu	49 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr7:77781778G>A	Intron	MAGI2		membrane associated gu	28 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr7:77810868A>G	Intron	MAGI2		membrane associated gu	37 (0.00)	26 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr7:77818261C>T	Intron	MAGI2		membrane associated gu	77 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr7:77826891G>A	Intron	MAGI2		membrane associated gu	21 (0.00)	31 (0.39)	1.03
11-02	Gp4 Focus 2	g.chr7:77862459G>A	Intron	MAGI2		membrane associated gu	30 (0.00)	57 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr7:77931358G>T	Intron	MAGI2		membrane associated gu	36 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr7:77936921G>A	Intron	MAGI2		membrane associated gu	167 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr7:77983515G>A	Intron	MAGI2		membrane associated gu	89 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr7:77983529G>A	Intron	MAGI2		membrane associated gu	65 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr7:77991799G>A	Intron	MAGI2		membrane associated gu	57 (0.00)	68 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:78022566A>G	Intron	MAGI2		membrane associated gu	64 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr7:78041978C>T	Intron	MAGI2		membrane associated gu	176 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr7:78057979C>T	Intron	MAGI2		membrane associated gu	91 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr7:78057985C>T	Intron	MAGI2		membrane associated gu	92 (0.00)	43 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr7:78060448G>A	Intron	MAGI2		membrane associated gu	56 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr7:78064456G>A	Intron	MAGI2		membrane associated gu	48 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:78096014G>A	Intron	MAGI2		membrane associated gu	56 (0.00)	37 (0.22)	0.58

11-02	Gp4 Focus 2	g.chr7:78096736G>A	Intron	MAGI2	membrane associated gu	90 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr7:78165839G>A	Intron	MAGI2	membrane associated gu	63 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr7:78170942G>A	Intron	MAGI2	membrane associated gu	38 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr7:78172029G>A	Intron	MAGI2	membrane associated gu	40 (0.00)	37 (0.89)	2.38
11-02	Gp4 Focus 2	g.chr7:78179294G>A	Intron	MAGI2	membrane associated gu	22 (0.00)	32 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr7:78183857C>A	Intron	MAGI2	membrane associated gu	118 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr7:78190525G>A	Intron	MAGI2	membrane associated gu	100 (0.00)	60 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr7:78191087G>C	Intron	MAGI2	membrane associated gu	62 (0.00)	60 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr7:78191151G>A	Intron	MAGI2	membrane associated gu	94 (0.00)	82 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:78191194G>A	Intron	MAGI2	membrane associated gu	95 (0.00)	59 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr7:78198185G>A	Intron	MAGI2	membrane associated gu	50 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr7:78225218C>T	Intron	MAGI2	membrane associated gu	21 (0.00)	16 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr7:78233604G>A	Intron	MAGI2	membrane associated gu	45 (0.02)	33 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr7:78244351C>A	Intron	MAGI2	membrane associated gu	24 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr7:78248209G>A	Intron	MAGI2	membrane associated gu	88 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr7:78251676C>T	Intron	MAGI2	membrane associated gu	24 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:78258688C>T	Intron	MAGI2	membrane associated gu	85 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:78288927T>A	Intron	MAGI2	membrane associated gu	57 (0.00)	22 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr7:78300850G>A	Intron	MAGI2	membrane associated gu	47 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr7:78353749G>A	Intron	MAGI2	membrane associated gu	92 (0.01)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr7:78368809C>T	Intron	MAGI2	membrane associated gu	37 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr7:78381185C>T	Intron	MAGI2	membrane associated gu	38 (0.00)	21 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr7:78381309C>A	Intron	MAGI2	membrane associated gu	22 (0.00)	12 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr7:78391100G>T	Intron	MAGI2	membrane associated gu	94 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr7:78392084C>T	Intron	MAGI2	membrane associated gu	51 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr7:78411598G>A	Intron	MAGI2	membrane associated gu	35 (0.03)	25 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr7:78422433C>T	Intron	MAGI2	membrane associated gu	41 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:78455889G>A	Intron	MAGI2	membrane associated gu	66 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:78478887G>A	Intron	MAGI2	membrane associated gu	71 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr7:78515265G>A	Intron	MAGI2	membrane associated gu	27 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr7:78532146G>A	Intron	MAGI2	membrane associated gu	81 (0.00)	42 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr7:78554449C>T	Intron	MAGI2	membrane associated gu	31 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:78569948G>A	Intron	MAGI2	membrane associated gu	72 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr7:78582583C>A	Intron	MAGI2	membrane associated gu	92 (0.01)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr7:78609785C>A	Intron	MAGI2	membrane associated gu	35 (0.00)	25 (0.36)	0.96

11-02	Gp4 Focus 2	g.chr7:78636452C>T	Silent	MAGI2	p.E124E	membrane associated gu	61 (0.00)	26 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr7:78647924G>A	Intron	MAGI2		membrane associated gu	29 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr7:78703070C>T	Intron	MAGI2		membrane associated gu	75 (0.00)	52 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr7:78730788T>C	Intron	MAGI2		membrane associated gu	21 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr7:78739388A>G	Intron	MAGI2		membrane associated gu	22 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr7:78779305T>A	Intron	MAGI2		membrane associated gu	51 (0.02)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:78812350G>A	Intron	MAGI2		membrane associated gu	84 (0.00)	54 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr7:78814239G>A	Intron	MAGI2		membrane associated gu	48 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr7:78825299G>A	Intron	MAGI2		membrane associated gu	51 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr7:78826376T>C	Intron	MAGI2		membrane associated gu	83 (0.01)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr7:78872959G>A	Intron	MAGI2		membrane associated gu	30 (0.00)	42 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr7:78872961G>A	Intron	MAGI2		membrane associated gu	30 (0.00)	41 (0.49)	1.30
11-02	Gp4 Focus 2	g.chr7:78876079C>A	Intron	MAGI2		membrane associated gu	47 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr7:78881852G>A	Intron	MAGI2		membrane associated gu	31 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr7:78898170C>T	Intron	MAGI2		membrane associated gu	112 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr7:78908113C>A	Intron	MAGI2		membrane associated gu	90 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr7:78908137G>A	Intron	MAGI2		membrane associated gu	77 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr7:78928653G>A	Intron	MAGI2		membrane associated gu	57 (0.00)	83 (0.31)	0.84
11-02	Gp4 Focus 2	g.chr7:78928771C>A	Intron	MAGI2		membrane associated gu	31 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr7:78945206G>A	Intron	MAGI2		membrane associated gu	55 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr7:78953278G>A	Intron	MAGI2		membrane associated gu	112 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr7:78983205G>A	Intron	MAGI2		membrane associated gu	16 (0.00)	30 (0.57)	1.51
11-02	Gp4 Focus 2	g.chr7:78983247G>A	Intron	MAGI2		membrane associated gu	18 (0.00)	37 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr7:78986616C>T	Intron	MAGI2		membrane associated gu	92 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr7:78995328C>T	Intron	MAGI2		membrane associated gu	42 (0.02)	96 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr7:79001283G>A	Intron	MAGI2		membrane associated gu	130 (0.00)	30 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr7:79068696C>T	Intron	MAGI2		membrane associated gu	88 (0.00)	36 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr1:114214393G>A	Silent	MAGI3	p.R951R	membrane associated gu	48 (0.00)	13 (0.54)	1.13
11-02	Gp4 Focus 2	g.chr1:114214416G>A	Missense Mutation	MAGI3	p.R959K	membrane associated gu	50 (0.00)	13 (0.38)	0.80
11-02	Gp4 Focus 2	g.chr5:179195877G>A	Silent	MAML1	p.V586V	mastermind-like 1 (Dros	46 (0.00)	100 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr11:95724708G>A	Silent	MAML2	p.L773L	mastermind-like 2 (Dros	45 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr4:140640856G>A	Missense Mutation	MAML3	p.A1013V	mastermind-like 3 (Dros	16 (0.00)	26 (0.27)	1.23
11-02	Gp4 Focus 2	g.chr4:140641140G>A	Silent	MAML3	p.S918S	mastermind-like 3 (Dros	60 (0.00)	33 (0.18)	0.83
11-02	Gp4 Focus 2	g.chr4:140810539G>A	Missense Mutation	MAML3	p.A684V	mastermind-like 3 (Dros	75 (0.00)	79 (0.30)	1.39
11-02	Gp4 Focus 2	g.chr4:140811340G>A	Missense Mutation	MAML3	p.S417F	mastermind-like 3 (Dros	29 (0.00)	42 (0.14)	0.65

11-02	Gp4 Focus 2	g.chr4:140811782G>A	Nonsense Mutation	MAML3	p.Q270*	mastermind-like 3 (Dros	69 (0.00)	34 (0.24)	1.08
11-02	Gp4 Focus 2	g.chr1:26090424C>T	Silent	MAN1C1	p.N369N	mannosidase, alpha, cla	42 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr19:12760181G>A	Missense Mutation	MAN2B1	p.P777S	mannosidase, alpha, cla	17 (0.00)	69 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr15:75649155C>T	Missense Mutation	MAN2C1	p.G780D	mannosidase, alpha, cla	24 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr15:43804404C>T	Silent	MAP1A	p.N85N	microtubule-associated	81 (0.00)	53 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr5:56152496G>A	Missense Mutation	MAP3K1	p.M184I	mitogen-activated protei	17 (0.00)	19 (0.37)	1.22
11-02	Gp4 Focus 2	g.chr12:53879178C>T	Missense Mutation	MAP3K12	p.M301I	mitogen-activated protei	30 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr6:161469746G>A	Missense Mutation	MAP3K4	p.A148T	mitogen-activated protei	69 (0.00)	30 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr6:161469750C>G	Missense Mutation	MAP3K4	p.A149G	mitogen-activated protei	54 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:39570549G>A	Missense Mutation	MAP4K3	p.S97F	mitogen-activated protei	18 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr2:102446053C>T	Missense Mutation	MAP4K4	p.L169F	mitogen-activated protei	93 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:102482940G>A	Missense Mutation	MAP4K4	p.R589K	mitogen-activated protei	62 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr2:102482952G>A	Missense Mutation	MAP4K4	p.G593D	mitogen-activated protei	67 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:206904984G>A	Splice Site	MAPKAPK2		mitogen-activated protei	39 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr12:112326794C>T	Silent	MAPKAPK5	p.L402L	mitogen-activated protei	22 (0.00)	14 (0.79)	2.10
11-02	Gp4 Focus 2	g.chr18:32706917G>A	Missense Mutation	MAPRE2	p.A163T	microtubule-associated	54 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr2:27245095C>T	Silent	MAPRE3	p.V3V	microtubule-associated	34 (0.00)	29 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr1:220955220G>A	Missense Mutation	MARC2	p.D329N	mitochondrial amidoxin	99 (0.01)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr5:16067814G>T	Missense Mutation	MARCH11	p.D325E	membrane-associated ri	32 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr11:63667370G>A	Missense Mutation	MARK2	p.D153N	MAP/microtubule affini	59 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr14:103934477G>A	Silent	MARK3	p.Q406Q	MAP/microtubule affini	19 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr2:198570992C>T	Missense Mutation	MARS2	p.T288I	methionyl-tRNA synthe	24 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:46488938C>T	Missense Mutation	MAST2	p.P507S	microtubule associated	91 (0.01)	71 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr5:66458434G>A	Splice Site	MAST4		microtubule associated	69 (0.00)	19 (0.47)	1.57
11-02	Gp4 Focus 2	g.chr5:138658535G>A	Missense Mutation	MATR3	p.G676E	matrin 3	60 (0.00)	60 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr14:65543362C>A	Silent	MAX	p.A105A	MYC associated factor	34 (0.00)	45 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr3:129156679C>T	Silent	MBD4	p.Q73Q	methyl-CpG binding do	43 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr6:20109936G>A	Silent	MBOAT1	p.L418L	membrane bound O-acy	33 (0.00)	39 (0.36)	1.39
11-02	Gp4 Focus 2	g.chr6:52141919G>A	Missense Mutation	MCM3	p.R371W	minichromosome maint	47 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr14:47687327C>T	Silent	MDGA2	p.L95L	MAM domain containin	26 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr6:90385272C>T	Silent	MDN1	p.R4224R	MDN1, midasin homol	52 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr6:90394600G>A	Missense Mutation	MDN1	p.L3942F	MDN1, midasin homol	17 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr6:90396712C>T	Missense Mutation	MDN1	p.M3827I	MDN1, midasin homol	72 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr18:48466723T>C	Silent	ME2	p.N518N	malic enzyme 2, NAD(	15 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr17:37571299G>A	Silent	MED1	p.F493F	mediator complex subu	22 (0.00)	49 (0.27)	0.71

11-02	Gp4 Focus 2	g.chr3:150840745C>T	Missense Mutation	MED12L	p.S127F	mediator complex subur	50 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr3:150883682C>T	Silent	MED12L	p.H469H	mediator complex subur	65 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr16:3293285C>T	Silent	MEFV	p.V554V	Mediterranean fever	33 (0.00)	21 (0.29)	0.91
11-02	Gp4 Focus 2	g.chr16:3293656G>A	Missense Mutation	MEFV	p.L431F	Mediterranean fever	38 (0.00)	17 (0.82)	2.63
11-02	Gp4 Focus 2	g.chr16:3306453G>A	Silent	MEFV	p.I45I	Mediterranean fever	25 (0.00)	22 (0.32)	1.02
11-02	Gp4 Focus 2	g.chr22:42101541C>T	Missense Mutation	MEI1	p.T111I	meiosis inhibitor 1	117 (0.00)	53 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr11:64571878C>T	Missense Mutation	MEN1	p.M532I	multiple endocrine neop	72 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr18:29793207C>T	Missense Mutation	MEP1B	p.L422F	meprin A, beta	48 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:112758777G>A	Splice Site	MERTK		MER proto-oncogene, t	68 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr7:130143815C>T	Missense Mutation	MEST	p.P290S	mesoderm specific trans	45 (0.00)	32 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr12:95868079A>G	Missense Mutation	METAP2	p.K42E	methionyl aminopeptida	24 (0.00)	44 (0.66)	1.76
11-02	Gp4 Focus 2	g.chr1:170135666C>G	Missense Mutation	METTL11B	p.D118E	methyltransferase like 1	73 (0.00)	142 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr14:21464950G>A	Silent	METTL17	p.L424L	methyltransferase like 1	24 (0.00)	20 (0.40)	0.59
11-02	Gp4 Focus 2	g.chr12:56075785G>A	Missense Mutation	METTL7B	p.A83T	methyltransferase like 7	23 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:179076711G>T	Missense Mutation	MFN1	p.C111F	mitofusin 1	18 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:40431202G>A	Silent	MFSD2A	p.R179R	major facilitator superfa	28 (0.00)	39 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr15:42041005C>T	Missense Mutation	MGA	p.P1795S	MGA, MAX dimerizati	56 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr15:42052605C>T	Missense Mutation	MGA	p.R2426W	MGA, MAX dimerizati	27 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr7:141740608C>A	Silent	MGAM	p.I820I	maltase-glucoamylase (	40 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr7:141782004C>T	Silent	MGAM	p.P2055P	maltase-glucoamylase (	15 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr7:141795419C>T	Silent	MGAM	p.L2505L	maltase-glucoamylase (	37 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr3:127411068G>T	Silent	MGLL	p.A269A	monoglyceride lipase	15 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr22:18387461G>A	Silent	MICAL3	p.L137L	microtubule associated	88 (0.00)	42 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr22:18387503G>A	Missense Mutation	MICAL3	p.R123C	microtubule associated	67 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr13:24453446G>A	Missense Mutation	MIPEP	p.A167V	mitochondrial intermedi	39 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr14:37777600T>A	Missense Mutation	MIPOL1	p.I204K	mirror-image polydacty	19 (0.00)	13 (0.46)	1.47
11-02	Gp4 Focus 2	g.chr3:163889267C>T	RNA	MIR1263		microRNA 1263	26 (0.00)	26 (0.85)	2.26
11-02	Gp4 Focus 2	g.chrX:63005967C>T	RNA	MIR1468		microRNA 1468	45 (0.00)	22 (0.45)	0.76
11-02	Gp4 Focus 2	g.chr10:129910560G>C	Silent	MKI67	p.A602A	marker of proliferation	16 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr10:129913820G>A	Silent	MKI67	p.T284T	marker of proliferation	23 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:14234481G>A	Silent	MKL2	p.A6A	MKL/myocardin-like 2	19 (0.00)	18 (0.44)	1.42
11-02	Gp4 Focus 2	g.chr1:47027230G>A	Missense Mutation	MKNK1	p.L350F	MAP kinase interacting	23 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr22:50523217G>A	Silent	MLC1	p.L39L	megalencephalic leukoe	20 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr16:74725218C>T	Missense Mutation	MLKL	p.V227M	mixed lineage kinase do	97 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr19:6230611C>T	Silent	MLLT1	p.E130E	myeloid/lymphoid or mi	51 (0.00)	22 (0.27)	0.73

11-02	Gp4 Focus 2	g.chr1:151039766G>A	Silent	MLLT11	p.L22L	myeloid/lymphoid or mi	38 (0.00)	68 (0.72)	1.92
11-02	Gp4 Focus 2	g.chr6:168344088C>T	Missense Mutation	MLLT4	p.R1051C	myeloid/lymphoid or mi	26 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr16:83940661G>A	Missense Mutation	MLYCD	p.V200I	malonyl-CoA decarboxy	72 (0.00)	19 (0.58)	1.54
11-02	Gp4 Focus 2	g.chr16:83940693G>A	Silent	MLYCD	p.Q210Q	malonyl-CoA decarboxy	65 (0.00)	24 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr1:45973107G>A	Missense Mutation	MMACHC	p.S54N	methylmalonic aciduria	31 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr12:56231137C>A	Missense Mutation	MMP19	p.D381Y	matrix metallopeptidase	15 (0.00)	49 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr16:55539291G>A	Silent	MMP2	p.L564L	matrix metallopeptidase	57 (0.00)	52 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr22:28146974C>T	Missense Mutation	MN1	p.V1298M	meningioma (disrupted	15 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr20:49576586G>T	Missense Mutation	MOCS3	p.G403W	molybdenum cofactor sy	29 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr14:102732230G>A	Silent	MOK	p.L48L	MOK protein kinase	51 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr16:77229564G>A	Silent	MON1B	p.E367E	MON1 secretory traffick	25 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr12:62954549G>A	Missense Mutation	MON2	p.V1207I	MON2 homolog (S. cere	38 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr22:31338227C>T	Missense Mutation	MORC2	p.R153Q	MORC family CW-type	84 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr22:50563963C>A	Missense Mutation	MOV10L1	p.P571Q	Mov10 RISC complex R	35 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr9:13106985G>A	Silent	MPDZ	p.V2035V	multiple PDZ domain pr	40 (0.00)	27 (0.22)	0.72
11-02	Gp4 Focus 2	g.chr9:13222341T>C	Missense Mutation	MPDZ	p.K213R	multiple PDZ domain pr	138 (0.00)	37 (0.14)	0.44
11-02	Gp4 Focus 2	g.chr2:71375227G>T	Missense Mutation	MPHOSPH10	p.E552D	M-phase phosphoprotein	29 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr1:43805233G>A	Missense Mutation	MPL	p.S228N	MPL proto-oncogene, th	16 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr17:56352964G>T	Missense Mutation	MPO	p.P435H	myeloperoxidase	16 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chrX:154014670G>A	Silent	MPP1	p.F162F	membrane protein, palm	60 (0.00)	64 (0.27)	0.44
11-02	Gp4 Focus 2	g.chr7:24689243G>A	Missense Mutation	MPP6	p.A95T	membrane protein, palm	92 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr10:28491141C>T	Missense Mutation	MPP7	p.E33K	membrane protein, palm	48 (0.00)	10 (0.50)	1.67
11-02	Gp4 Focus 2	g.chr17:17075037G>A	Silent	MPRIP	p.T723T	myosin phosphatase Rho	76 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:181021483C>T	Silent	MR1	p.N239N	major histocompatibility	49 (0.00)	31 (0.84)	2.24
11-02	Gp4 Focus 2	g.chr10:18138627G>A	Missense Mutation	MRC1	p.G395S	mannose receptor, C typ	38 (0.03)	25 (0.40)	1.34
11-02	Gp4 Focus 2	g.chr10:17875703G>A	Missense Mutation	MRC1L1	p.D223N		38 (0.00)	20 (0.30)	1.00
11-02	Gp4 Focus 2	g.chr17:60749511C>T	Missense Mutation	MRC2	p.P487S	mannose receptor, C typ	37 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr11:94201043T>C	Missense Mutation	MRE11A	p.E345G	MRE11 meiotic recomb	73 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr1:55174688G>A	Splice Site	MROH7	p.G1223G	maestro heat-like repeat	23 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr1:55174702G>A	Missense Mutation	MROH7	p.C1228Y	maestro heat-like repeat	23 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr11:6703553C>T	Silent	MRPL17	p.L108L	mitochondrial ribosoma	96 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr21:35497753C>T	Missense Mutation	MRPS6	p.A53V	mitochondrial ribosoma	243 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr9:125075659G>A	Silent	MRRF	p.E235E	mitochondrial ribosome	28 (0.00)	21 (0.24)	0.50
11-02	Gp4 Focus 2	g.chr11:10597988G>A	Missense Mutation	MRVI1	p.S877F	murine retrovirus integra	73 (0.00)	87 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr11:10625976C>A	Silent	MRVI1	p.L573L	murine retrovirus integra	70 (0.00)	22 (0.23)	0.61

11-02	Gp4 Focus 2	g.chr11:10631287C>T	Missense Mutation	MRVI1	p.S520N	murine retrovirus integr	22 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr11:60235857G>A	Silent	MS4A1	p.E270E	membrane-spanning 4-d	31 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr10:75184911G>A	Missense Mutation	MSS51	p.P370S	MSS51 mitochondrial tr	41 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr10:75184930G>A	Silent	MSS51	p.D363D	MSS51 mitochondrial tr	42 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:56667727G>A	Silent	MT1M	p.T53T	metallothionein 1M	76 (0.00)	64 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr8:121463249C>T	Missense Mutation	MTBP	p.S69L	MDM2 binding protein	22 (0.00)	19 (0.32)	1.08
11-02	Gp4 Focus 2	g.chr15:65319329G>A	Missense Mutation	MTFMT	p.P87S	mitochondrial methiony	50 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr2:55476566C>T	Missense Mutation	MTIF2	p.G316S	mitochondrial translatio	56 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chrX:149895727G>A	Silent	MTMR1	p.V123V	myotubularin related pro	34 (0.00)	31 (0.23)	0.38
11-02	Gp4 Focus 2	g.chr1:149905823G>A	Silent	MTMR11	p.Y160Y	myotubularin related pro	78 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr3:9730655G>A	Missense Mutation	MTMR14	p.S441N	myotubularin related pro	35 (0.00)	60 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr8:17157389G>A	Silent	MTMR7	p.A655A	myotubularin related pro	35 (0.00)	32 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr6:74176006G>A	Missense Mutation	MTO1	p.G98S	mitochondrial tRNA tra	56 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr7:135614743C>G	Silent	MTPN	p.V96V	myotrophin	45 (0.00)	41 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr13:41791319G>A	Silent	MTRF1	p.L424L	mitochondrial translatio	64 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr5:79286470G>A	Missense Mutation	MTX3	p.S33F	metaxin 3	76 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr7:100635274C>T	Missense Mutation	MUC12	p.T620I	mucin 12, cell surface as	59 (0.02)	51 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr7:100643524C>T	Missense Mutation	MUC12	p.P3370L	mucin 12, cell surface as	465 (0.00)	178 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr19:8971738G>A	Missense Mutation	MUC16	p.T14285I	mucin 16, cell surface as	35 (0.00)	9 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr19:9018186G>A	Silent	MUC16	p.F12584F	mucin 16, cell surface as	17 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr19:9024840C>T	Missense Mutation	MUC16	p.S12341N	mucin 16, cell surface as	71 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr19:9047270G>A	Missense Mutation	MUC16	p.P11454L	mucin 16, cell surface as	49 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr19:9048201C>T	Missense Mutation	MUC16	p.V11144I	mucin 16, cell surface as	46 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr19:9060539C>T	Silent	MUC16	p.V8969V	mucin 16, cell surface as	26 (0.00)	129 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr19:9062536G>A	Silent	MUC16	p.L8304L	mucin 16, cell surface as	20 (0.00)	59 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr19:9064750C>T	Missense Mutation	MUC16	p.V7566M	mucin 16, cell surface as	88 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr19:9070141C>A	Nonsense Mutation	MUC16	p.E5769*	mucin 16, cell surface as	60 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr19:9073518G>A	Missense Mutation	MUC16	p.A4643V	mucin 16, cell surface as	37 (0.00)	18 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr19:9075970C>T	Missense Mutation	MUC16	p.G3826R	mucin 16, cell surface as	78 (0.00)	135 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr19:9077378C>T	Silent	MUC16	p.G3356G	mucin 16, cell surface as	24 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr19:9083895G>A	Silent	MUC16	p.F2640F	mucin 16, cell surface as	24 (0.00)	40 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:9088600G>A	Missense Mutation	MUC16	p.T1072I	mucin 16, cell surface as	43 (0.02)	50 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr19:9090696G>A	Silent	MUC16	p.T373T	mucin 16, cell surface as	15 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr7:100680987C>T	Missense Mutation	MUC17	p.P2097L	mucin 17, cell surface as	31 (0.00)	13 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr3:195487827G>A	Silent	MUC4	p.L690L	mucin 4, cell surface ass	16 (0.00)	12 (0.67)	1.78

11-02	Gp4 Focus 2	g.chr11:1264091G>T	Missense Mutation	MUC5B	p.R1994L	mucin 5B, oligomeric m	70 (0.00)	51 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr19:1360162C>A	Missense Mutation	MUM1	p.P82H	melanoma associated an	17 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr11:65632541G>A	Silent	MUS81	p.G442G	MUS81 structure-specif	83 (0.00)	31 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr9:113547156C>A	Silent	MUSK	p.S482S	muscle, skeletal, recept	86 (0.00)	44 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr16:29859118C>T	Silent	MVP	p.T830T	major vault protein	35 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr6:135511482G>A	Missense Mutation	MYB	p.G175E	v-myb avian myeloblast	29 (0.00)	22 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr8:128753058A>G	Missense Mutation	MYC	p.K407E	v-myc avian myelocyto	68 (0.00)	33 (0.45)	1.56
11-02	Gp4 Focus 2	g.chr13:77641995G>A	Missense Mutation	MYCBP2	p.T4021I	MYC binding protein 2,	75 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr15:48443727A>G	Missense Mutation	MYEF2	p.F417L	myelin expression facto	264 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr15:48446046G>A	Missense Mutation	MYEF2	p.P344S	myelin expression facto	27 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr16:15826475C>T	Silent	MYH11	p.Q1199Q	myosin, heavy chain 11,	24 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr17:10235503C>G	Silent	MYH13	p.G737G	myosin, heavy chain 13,	47 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr3:108147371G>A	Silent	MYH15	p.L1244L	myosin, heavy chain 15	74 (0.00)	44 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:108175686C>T	Missense Mutation	MYH15	p.G709S	myosin, heavy chain 15	33 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:10442603G>A	Silent	MYH2	p.R445R	myosin, heavy chain 2,	66 (0.00)	73 (0.25)	0.66
11-02	Gp4 Focus 2	g.chr17:10537014G>A	Missense Mutation	MYH3	p.T1514I	myosin, heavy chain 3,	25 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr17:10541369C>T	Silent	MYH3	p.S1240S	myosin, heavy chain 3,	38 (0.00)	55 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:10541370G>T	Nonsense Mutation	MYH3	p.S1240*	myosin, heavy chain 3,	38 (0.00)	56 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:10541401C>T	Missense Mutation	MYH3	p.D1230N	myosin, heavy chain 3,	36 (0.00)	50 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:10350372C>T	Silent	MYH4	p.E1709E	myosin, heavy chain 4,	62 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr17:10359219C>T	Splice Site	MYH4		myosin, heavy chain 4,	48 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr14:23868190G>A	Silent	MYH6	p.D546D	myosin, heavy chain 6,	15 (0.00)	13 (0.38)	0.56
11-02	Gp4 Focus 2	g.chr22:36716396A>G	Missense Mutation	MYH9	p.L294S	myosin, heavy chain 9,	18 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr3:123451767A>T	Missense Mutation	MYLK	p.C498S	myosin light chain kina	21 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr6:2679543C>T	Missense Mutation	MYLK4	p.M286I	myosin light chain kina	85 (0.00)	45 (0.20)	0.38
11-02	Gp4 Focus 2	g.chr6:2679599C>T	Missense Mutation	MYLK4	p.E268K	myosin light chain kina	90 (0.00)	22 (0.23)	0.43
11-02	Gp4 Focus 2	g.chr6:2679615C>T	Silent	MYLK4	p.V262V	myosin light chain kina	58 (0.00)	19 (0.26)	0.50
11-02	Gp4 Focus 2	g.chr5:16675200G>A	Silent	MYO10	p.L1576L	myosin X	16 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr5:16754955G>A	Silent	MYO10	p.I637I	myosin X	51 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr5:16766253G>A	Missense Mutation	MYO10	p.A372V	myosin X	66 (0.00)	39 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr17:18069778C>T	Silent	MYO15A	p.L561L	myosin XVA	29 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr17:34857067G>A	Missense Mutation	MYO19	p.P697S	myosin XIX	21 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr12:57441087C>G	Splice Site	MYO1A	p.A144P	myosin IA	34 (0.00)	17 (0.71)	1.88
11-02	Gp4 Focus 2	g.chr19:8618256G>A	Missense Mutation	MYO1F	p.S131F	myosin IF	17 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr12:109876370G>A	Missense Mutation	MYO1H	p.A731T	myosin IH	27 (0.00)	17 (0.71)	1.88

11-02	Gp4 Focus 2	g.chr12:109882089G>A	Splice Site	MYO1H		myosin IH	136 (0.00)	55 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr17:12649298C>A	Missense Mutation	MYOCD	p.P345H	myocardin	72 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr4:120072061C>A	Missense Mutation	MYOZ2	p.S37R	myozenin 2	17 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:1926331C>T	Missense Mutation	MYT1L	p.G404R	myelin transcription fac	26 (0.00)	13 (0.38)	1.25
11-02	Gp4 Focus 2	g.chr3:175184861C>A	Silent	NAALADL2	p.I474I	N-acetylated alpha-link	121 (0.00)	37 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr11:71166216G>A	Splice Site	NADSYN1	p.C49Y	NAD synthetase 1	35 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr17:40695054G>A	Missense Mutation	NAGLU	p.E344K	N-acetylglucosaminidas	37 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr17:80422162G>A	Splice Site	NARF		nuclear prelamin A reco	26 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:46073091A>G	Missense Mutation	NASP	p.T170A	nuclear autoantigenic sp	23 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr11:34153684T>A	Missense Mutation	NAT10	p.N511K	N-acetyltransferase 10 (	104 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr1:201687882G>A	Splice Site	NAV1	p.G422S	neuron navigator 1	52 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:201763609G>A	Missense Mutation	NAV1	p.D1097N	neuron navigator 1	41 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr11:20070467C>T	Missense Mutation	NAV2	p.P1302S	neuron navigator 2	21 (0.00)	41 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr12:78225277G>T	Missense Mutation	NAV3	p.Q12H	neuron navigator 3	88 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr12:78513277G>A	Missense Mutation	NAV3	p.A1101T	neuron navigator 3	96 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr13:35733379C>A	Missense Mutation	NBEA	p.T1024N	neurobeachin	155 (0.00)	43 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr13:36242649G>A	Missense Mutation	NBEA	p.D2912N	neurobeachin	82 (0.00)	43 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr2:204078348T>A	Missense Mutation	NBEAL1	p.I2652N	neurobeachin-like 1	27 (0.00)	27 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr1:16892246C>T	Silent	NBPF1	p.L982L	neuroblastoma breakpoi	153 (0.00)	59 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr11:113076362G>A	Missense Mutation	NCAM1	p.G37D	neural cell adhesion mo	150 (0.01)	76 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr12:6637133G>A	Splice Site	NCAPD2		non-SMC condensin I c	60 (0.00)	35 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr12:6637175G>A	Missense Mutation	NCAPD2	p.V1021I	non-SMC condensin I c	53 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr7:158443563G>T	Silent	NCAPG2	p.I1012I	non-SMC condensin II	69 (0.00)	52 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:183534883G>A	Missense Mutation	NCF2	p.A319V	neutrophil cytosolic fact	20 (0.00)	22 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr2:24929742C>T	Missense Mutation	NCOA1	p.S468F	nuclear receptor coactiv	84 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr2:24929808G>A	Missense Mutation	NCOA1	p.R490K	nuclear receptor coactiv	56 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr20:44691228G>A	Missense Mutation	NCOA5	p.P484L	nuclear receptor coactiv	26 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr20:33334692G>T	Missense Mutation	NCOA6	p.Q945K	nuclear receptor coactiv	52 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr12:124915216C>T	Missense Mutation	NCOR2	p.E334K	nuclear receptor corepre	17 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr16:15758708T>A	Missense Mutation	NDE1	p.Y25N	nudE neurodevelopmen	15 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr7:140402703C>T	Nonsense Mutation	NDUFB2	p.Q19*	NADH dehydrogenase (	39 (0.00)	42 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:206994871G>A	Missense Mutation	NDUFS1	p.A550V	NADH dehydrogenase (	84 (0.01)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:67377091G>A	Silent	NDUFV1	p.E165E	NADH dehydrogenase (	44 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:152362040G>A	Silent	NEB	p.D7898D	nebulin	146 (0.01)	24 (0.71)	2.30
11-02	Gp4 Focus 2	g.chr2:152424832G>A	Nonsense Mutation	NEB	p.Q5912*	nebulin	16 (0.00)	21 (0.48)	1.55

11-02	Gp4 Focus 2	g.chr2:152477454G>A	Silent	NEB	p.A3513A	nebulin	79 (0.00)	34 (0.35)	1.15
11-02	Gp4 Focus 2	g.chr2:152507241G>A	Silent	NEB	p.S2358S	nebulin	119 (0.00)	72 (0.25)	0.81
11-02	Gp4 Focus 2	g.chr8:24775269C>T	Missense Mutation	NEFM	p.P634L	neurofilament, medium	37 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr17:27068157C>T	Silent	NEK8	p.R598R	NIMA-related kinase 8	44 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr10:5494420C>T	Silent	NET1	p.L101L	neuroepithelial cell tran	30 (0.03)	18 (0.78)	2.60
11-02	Gp4 Focus 2	g.chr1:204985517G>A	Silent	NFASC	p.L1191L	neurofascin	52 (0.00)	35 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr16:69687152C>T	Nonsense Mutation	NFAT5	p.Q182*	nuclear factor of activat	31 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr12:54686940C>T	Missense Mutation	NFE2	p.G114S	nuclear factor, erythroid	20 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr9:14125733C>A	Nonsense Mutation	NFIB	p.E320*	nuclear factor I/B	67 (0.00)	30 (0.27)	0.87
11-02	Gp4 Focus 2	g.chr9:14125743C>T	Missense Mutation	NFIB	p.M316I	nuclear factor I/B	62 (0.00)	30 (0.37)	1.19
11-02	Gp4 Focus 2	g.chr4:103459079G>A	Missense Mutation	NFKB1	p.S75N	nuclear factor of kappa	112 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr4:103514711G>A	Missense Mutation	NFKB1	p.G399E	nuclear factor of kappa	81 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr4:103514717C>T	Missense Mutation	NFKB1	p.T401I	nuclear factor of kappa	37 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr10:104157285G>A	Splice Site	NFKB2	p.E168E	nuclear factor of kappa	76 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr10:104157790C>G	Silent	NFKB2	p.G238G	nuclear factor of kappa	68 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr19:39395720C>A	Missense Mutation	NFKBIB	p.A82D	nuclear factor of kappa	67 (0.00)	12 (0.83)	2.22
11-02	Gp4 Focus 2	g.chr6:44227963G>A	Silent	NFKBIE	p.G418G	nuclear factor of kappa	17 (0.00)	47 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr11:129758672C>T	Missense Mutation	NFRKB	p.V52I	nuclear factor related to	22 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr20:34278410G>A	Silent	NFS1	p.S162S	NFS1 cysteine desulfur	23 (0.00)	36 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr4:47887934T>A	Missense Mutation	NFXL1	p.E542D	nuclear transcription fac	126 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr2:233757684C>T	Missense Mutation	NGEF	p.A264T	neuronal guanine nucle	22 (0.00)	40 (0.75)	2.00
11-02	Gp4 Focus 2	g.chr3:25781120C>T	Missense Mutation	NGLY1	p.E235K	N-glycanase 1	41 (0.00)	35 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr5:37059099G>A	Missense Mutation	NIPBL	p.R2506H	Nipped-B homolog (Dr	24 (0.00)	60 (0.28)	0.76
11-02	Gp4 Focus 2	g.chr6:28227597G>A	Missense Mutation	NKAPL	p.E150K	NFKB activating protei	44 (0.00)	70 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr16:50667185C>T	Silent	NKD1	p.A302A	naked cuticle homolog 1	21 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr17:40175861G>A	Missense Mutation	NKIRAS2	p.A120T	NFKB inhibitor interact	32 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr3:42678683C>T	Missense Mutation	NKTR	p.S496L	natural killer cell trigge	58 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr3:42678695G>T	Missense Mutation	NKTR	p.W500L	natural killer cell trigge	58 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr3:42678698C>T	Missense Mutation	NKTR	p.S501F	natural killer cell trigge	57 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr3:173997181C>A	Missense Mutation	NLGN1	p.Q464K	neuroligin 1	48 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr3:173998576C>T	Missense Mutation	NLGN1	p.T652I	neuroligin 1	46 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr17:26370319G>A	Silent	NLK	p.P140P	nemo-like kinase	72 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr16:57100503G>A	Silent	NLRC5	p.E1433E	NLR family, CARD do	16 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr17:5433981C>G	Missense Mutation	NLRP1	p.G1114R	NLR family, pyrin dom	56 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr17:5462433G>A	Missense Mutation	NLRP1	p.T528I	NLR family, pyrin dom	31 (0.00)	26 (0.42)	1.13

11-02	Gp4 Focus 2	g.chr19:54313706C>T	Missense Mutation	NLRP12	p.V403I	NLR family, pyrin dom	65 (0.02)	30 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr19:56423897C>A	Missense Mutation	NLRP13	p.W429L	NLR family, pyrin dom	35 (0.00)	30 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr11:7063968G>A	Nonsense Mutation	NLRP14	p.W237*	NLR family, pyrin dom	61 (0.00)	52 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr19:55493572G>A	Missense Mutation	NLRP2	p.R169Q	NLR family, pyrin dom	45 (0.00)	198 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr10:15161400T>A	Missense Mutation	NMT2	p.E371V	N-myristoyltransferase	45 (0.00)	38 (0.84)	2.82
11-02	Gp4 Focus 2	g.chr2:10811711G>A	Missense Mutation	NOL10	p.P145S	nucleolar protein 10	36 (0.00)	21 (0.62)	1.65
11-02	Gp4 Focus 2	g.chr9:95076758G>A	Missense Mutation	NOL8	p.L717F	nucleolar protein 8	146 (0.01)	34 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr9:95081575G>T	Missense Mutation	NOL8	p.N115K	nucleolar protein 8	21 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr10:103920074C>T	Missense Mutation	NOLC1	p.A358V	nucleolar and coiled-bo	47 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr16:14969039C>T	Missense Mutation	NOMO1	p.T734I	NODAL modulator 1	96 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr16:18542861C>A	Silent	NOMO2	p.V488V	NODAL modulator 2	48 (0.00)	13 (0.92)	2.46
11-02	Gp4 Focus 2	g.chr16:18555027C>T	Missense Mutation	NOMO2	p.G216D	NODAL modulator 2	27 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr16:16367889G>A	Silent	NOMO3	p.E771E	NODAL modulator 3	91 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr12:6669280G>A	Silent	NOP2	p.I587I	NOP2 nucleolar protein	20 (0.00)	24 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr12:117660643C>T	Silent	NOS1	p.L1318L	nitric oxide synthase 1 (	26 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr12:117681124G>A	Silent	NOS1	p.A1014A	nitric oxide synthase 1 (	22 (0.00)	35 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr12:117723988G>A	Missense Mutation	NOS1	p.T404I	nitric oxide synthase 1 (	17 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr17:26084353G>A	Silent	NOS2	p.I1127I	nitric oxide synthase 2, i	31 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:89135609G>A	Missense Mutation	NOX4	p.S244L	NADPH oxidase 4	54 (0.00)	15 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr11:108031948C>T	Missense Mutation	NPAT	p.A1289T	nuclear protein, ataxia-t	70 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr17:45662983G>A	Missense Mutation	NPEPPS	p.V256I	aminopeptidase puromy	127 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr17:45681352C>T	Silent	NPEPPS	p.G604G	aminopeptidase puromy	98 (0.00)	28 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr3:132407595A>T	Nonsense Mutation	NPHP3	p.Y1008*	nephronophthisis 3 (ado	123 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr3:132407598C>T	Silent	NPHP3	p.L1007L	nephronophthisis 3 (ado	119 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr19:36321827G>A	Silent	NPHS1	p.F1171F	nephrosis 1, congenital,	30 (0.00)	33 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr17:79564334C>T	Nonsense Mutation	NPLOC4	p.W310*	nuclear protein localizat	28 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr17:79564342C>T	Splice Site	NPLOC4	p.V308I	nuclear protein localizat	28 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr9:35792984C>T	Silent	NPR2	p.G193G	natriuretic peptide recep	19 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr15:73884326C>T	Missense Mutation	NPTN	p.A198T	neuroplastin	44 (0.00)	65 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr15:73889560C>T	Missense Mutation	NPTN	p.G81D	neuroplastin	15 (0.00)	41 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr16:69747007G>A	Missense Mutation	NQO1	p.T110I	NAD(P)H dehydrogena	59 (0.00)	76 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr19:50881479G>A	Silent	NR1H2	p.E85E	nuclear receptor subfam	62 (0.00)	44 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr11:47283484G>T	Missense Mutation	NR1H3	p.E301D	nuclear receptor subfam	56 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr14:90769367G>T	Missense Mutation	NRDE2	p.L370M	NRDE-2, necessary for	84 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chrX:105153784C>G	Silent	NRK	p.L717L	Nik related kinase	24 (0.00)	23 (0.26)	0.58

11-02	Gp4 Focus 2	g.chr2:206628431G>A	Missense Mutation	NRP2	p.S693N	neuropilin 2	27 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr2:50758545C>T	Missense Mutation	NRXN1	p.G763R	neurexin 1	25 (0.00)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr2:50765519C>T	Missense Mutation	NRXN1	p.C712Y	neurexin 1	178 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr14:80328019G>A	Silent	NRXN3	p.E966E	neurexin 3	51 (0.00)	51 (0.49)	1.31
11-02	Gp4 Focus 2	g.chr5:176694637G>A	Missense Mutation	NSD1	p.G1741R	nuclear receptor binding	64 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr7:75044486C>A	RNA	NSUN5P1		NOP2/Sun domain fami	37 (0.00)	30 (0.47)	2.02
11-02	Gp4 Focus 2	g.chr12:104182632C>T	Missense Mutation	NT5DC3	p.G362D	5'-nucleotidase domain	101 (0.00)	43 (0.40)	1.05
11-02	Gp4 Focus 2	g.chr12:96076591C>T	Missense Mutation	NTN4	p.D468N	netrin 4	18 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr9:87635180G>A	Silent	NTRK2	p.R728R	neurotrophic tyrosine ki	26 (0.00)	12 (0.42)	1.34
11-02	Gp4 Focus 2	g.chr12:106466615C>T	Missense Mutation	NUAK1	p.D196N	NUAK family, SNF1-li	29 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:205274382C>G	Missense Mutation	NUAK2	p.K256N	NUAK family, SNF1-li	20 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr10:74890509G>A	Missense Mutation	NUDT13	p.D303N	nudix (nucleoside dipho	34 (0.00)	22 (0.77)	2.06
11-02	Gp4 Focus 2	g.chr10:12215801C>T	Missense Mutation	NUDT5	p.D101N	nudix (nucleoside dipho	20 (0.00)	28 (0.18)	0.60
11-02	Gp4 Focus 2	g.chr11:71724189G>A	Silent	NUMA1	p.L1454L	nuclear mitotic apparatu	70 (0.00)	46 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr12:69115705C>T	Nonsense Mutation	NUP107	p.Q437*	nucleoporin 107kDa	35 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr6:17626364G>A	Silent	NUP153	p.F1192F	nucleoporin 153kDa	25 (0.00)	23 (0.22)	0.84
11-02	Gp4 Focus 2	g.chr6:17675891G>A	Nonsense Mutation	NUP153	p.Q149*	nucleoporin 153kDa	103 (0.00)	25 (0.40)	1.55
11-02	Gp4 Focus 2	g.chr6:17675907G>A	Silent	NUP153	p.S143S	nucleoporin 153kDa	109 (0.00)	27 (0.30)	1.15
11-02	Gp4 Focus 2	g.chr6:17675929A>G	Missense Mutation	NUP153	p.L136P	nucleoporin 153kDa	110 (0.00)	25 (0.24)	0.93
11-02	Gp4 Focus 2	g.chr9:131768593G>A	Silent	NUP188	p.P1673P	nucleoporin 188kDa	17 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr7:135272405C>T	Missense Mutation	NUP205	p.S434L	nucleoporin 205kDa	58 (0.00)	45 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr1:153984805G>A	Silent	NUP210L	p.D1565D	nucleoporin 210kDa-lik	41 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr19:50412824G>A	Missense Mutation	NUP62	p.L81F	nucleoporin 62kDa	16 (0.00)	35 (0.57)	1.52
11-02	Gp4 Focus 2	g.chrX:106418357G>A	Missense Mutation	NUP62CL	p.S7L	nucleoporin 62kDa C-te	70 (0.00)	52 (0.19)	0.43
11-02	Gp4 Focus 2	g.chr17:73230854G>A	Missense Mutation	NUP85	p.D535N	nucleoporin 85kDa	22 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr16:56864440G>A	Splice Site	NUP93	p.D310N	nucleoporin 93kDa	81 (0.00)	58 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr13:25895207C>A	Missense Mutation	NUPL1	p.D297E	nucleoporin like 1	68 (0.00)	23 (0.57)	1.51
11-02	Gp4 Focus 2	g.chr15:34646911C>A	Missense Mutation	NUTM1	p.S447Y	NUT midline carcinoma	30 (0.00)	56 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr10:89118070C>T	Silent	NUTM2D	p.D16D	NUT family member 2	23 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr11:62560116G>C	Silent	NXF1	p.L606L	nuclear RNA export fac	49 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:113445566G>A	Silent	OAS2	p.L571L	2'-5'-oligoadenylate syn	48 (0.00)	37 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr12:113388699G>A	Missense Mutation	OAS3	p.E526K	2'-5'-oligoadenylate syn	35 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr12:113400543G>T	Missense Mutation	OAS3	p.W640C	2'-5'-oligoadenylate syn	63 (0.00)	64 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr1:228432250C>T	Silent	OBSCN	p.V1245V	obscurin, cytoskeletal c	20 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr1:228456235C>T	Silent	OBSCN	p.P1806P	obscurin, cytoskeletal c	28 (0.00)	20 (0.40)	1.07

11-02	Gp4 Focus 2	g.chr1:228486398C>T	Missense Mutation	OBSCN	p.S4397L	obscurin, cytoskeletal ca	32 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chrX:128692824C>T	Missense Mutation	OCRL	p.R190C	oculocerebrorenal syndr	19 (0.00)	12 (0.50)	1.06
11-02	Gp4 Focus 2	g.chrX:128695198T>C	Silent	OCRL	p.F289F	oculocerebrorenal syndr	20 (0.00)	28 (0.68)	1.44
11-02	Gp4 Focus 2	g.chr10:74671513C>T	Missense Mutation	OIT3	p.H236Y	oncoprotein induced tra	56 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr9:138011925C>T	Silent	OLFM1	p.D426D	olfactomedin 1	37 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr1:102269966G>C	Missense Mutation	OLFM3	p.T422S	olfactomedin 3	51 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr13:53616225A>G	Missense Mutation	OLFM4	p.S180G	olfactomedin 4	31 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr13:53624517G>A	Missense Mutation	OLFM4	p.D382N	olfactomedin 4	64 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:114524270G>A	Missense Mutation	OLFML3	p.R367H	olfactomedin-like 3	19 (0.00)	24 (0.33)	0.70
11-02	Gp4 Focus 2	g.chr3:193380743C>T	Missense Mutation	OPA1	p.P830S	optic atrophy 1 (autoson	55 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chrX:153416182C>G	Missense Mutation	OPN1LW	p.T56S	opsin 1 (cone pigments)	17 (0.00)	11 (0.64)	1.06
11-02	Gp4 Focus 2	g.chr6:47776081C>G	Missense Mutation	OPN5	p.C316W	opsin 5	82 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr1:158435839T>A	Missense Mutation	OR10K1	p.V163E	olfactory receptor, famil	34 (0.00)	31 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr11:57971265G>A	Missense Mutation	OR1S2	p.T130I	olfactory receptor, famil	88 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr12:55968784G>A	Missense Mutation	OR2AP1	p.V196I	olfactory receptor, famil	47 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr11:74800742C>T	Missense Mutation	OR2AT4	p.C6Y	olfactory receptor, famil	37 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr6:27925710C>T	Missense Mutation	OR2B6	p.A231V	olfactory receptor, famil	118 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr6:27925795C>T	Silent	OR2B6	p.Y259Y	olfactory receptor, famil	39 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr7:143657503C>T	Missense Mutation	OR2F1	p.T147I	olfactory receptor, famil	27 (0.00)	34 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr1:248685767G>A	Missense Mutation	OR2G6	p.V274I	olfactory receptor, famil	42 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr1:248616173C>T	Silent	OR2T2	p.P25P	olfactory receptor, famil	111 (0.00)	32 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr1:248637071G>A	Silent	OR2T3	p.L140L	olfactory receptor, famil	52 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr1:248525410G>A	Silent	OR2T4	p.L176L	olfactory receptor, famil	50 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr5:180166819C>T	Silent	OR2Y1	p.Q80Q	olfactory receptor, famil	16 (0.00)	23 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr17:3195121G>A	Silent	OR3A1	p.A252A	olfactory receptor, famil	74 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr17:3195136G>A	Silent	OR3A1	p.H247H	olfactory receptor, famil	67 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr17:3195427C>T	Silent	OR3A1	p.A150A	olfactory receptor, famil	17 (0.00)	47 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr17:56247586T>A	Silent	OR4D2	p.T190T	olfactory receptor, famil	24 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr15:102346093C>T	Silent	OR4F6	p.S57S	olfactory receptor, famil	45 (0.00)	75 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr15:102346198C>T	Silent	OR4F6	p.I92I	olfactory receptor, famil	61 (0.00)	27 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr14:20585714G>A	Missense Mutation	OR4K17	p.S50N	olfactory receptor, famil	77 (0.00)	32 (0.44)	0.64
11-02	Gp4 Focus 2	g.chr11:4967754C>T	Missense Mutation	OR51A4	p.D193N	olfactory receptor, famil	64 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr11:4929313T>A	Missense Mutation	OR51A7	p.N238K	olfactory receptor, famil	48 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:5364106C>T	Missense Mutation	OR51B5	p.V217M	olfactory receptor, famil	75 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr11:5410691C>T	Silent	OR51M1	p.S21S	olfactory receptor, famil	200 (0.01)	18 (0.33)	0.89

11-02	Gp4 Focus 2	g.chr11:4615851G>A	Missense Mutation	OR52I1	p.D195N	olfactory receptor, famil	168 (0.01)	98 (0.22)	0.60
11-02	Gp4 Focus 2	g.chr11:6007404G>A	Missense Mutation	OR52L1	p.L253F	olfactory receptor, famil	27 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr11:5968813C>G	Silent	OR56A3	p.L79L	olfactory receptor, famil	32 (0.00)	58 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr11:55579011G>A	Silent	OR5L1	p.L23L	olfactory receptor, famil	16 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr11:56380440G>A	Missense Mutation	OR5M1	p.A180V	olfactory receptor, famil	52 (0.02)	30 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr11:7847281A>G	Missense Mutation	OR5P3	p.V80A	olfactory receptor, famil	26 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr11:56185234G>T	Missense Mutation	OR5R1	p.H159N	olfactory receptor, famil	34 (0.00)	40 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr11:56185487G>A	Silent	OR5R1	p.S74S	olfactory receptor, famil	17 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr12:55945190C>T	Silent	OR6C4	p.F60F	olfactory receptor, famil	55 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:55863289C>T	Missense Mutation	OR6C70	p.V212I	olfactory receptor, famil	40 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr11:123814474C>T	Silent	OR6T1	p.Q24Q	olfactory receptor, famil	44 (0.00)	73 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr11:123624723G>A	Silent	OR6X1	p.G168G	olfactory receptor, famil	22 (0.00)	45 (0.51)	1.36
11-02	Gp4 Focus 2	g.chr19:9362138G>A	Missense Mutation	OR7E24	p.R140Q	olfactory receptor, famil	35 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr11:124120684G>A	RNA	OR8G1		olfactory receptor, famil	80 (0.00)	33 (0.61)	1.62
11-02	Gp4 Focus 2	g.chr11:56468248C>T	Silent	OR9G1	p.L129L	olfactory receptor, famil	55 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr11:56511240C>T	Missense Mutation	OR9G4	p.M16I	olfactory receptor, famil	35 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr12:58112175G>A	Missense Mutation	OS9	p.E429K	osteosarcoma amplified	16 (0.00)	61 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:24870402C>T	Silent	OSBPL3	p.Q623Q	oxysterol binding protei	85 (0.00)	36 (0.81)	2.15
11-02	Gp4 Focus 2	g.chr7:24874187G>A	Missense Mutation	OSBPL3	p.T555M	oxysterol binding protei	27 (0.00)	35 (0.31)	0.84
11-02	Gp4 Focus 2	g.chr5:38924630G>A	Silent	OSMR	p.G659G	oncostatin M receptor	54 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr8:99961735C>T	Silent	OSR2	p.Y185Y	odd-skipped related tran	43 (0.00)	10 (0.90)	2.40
11-02	Gp4 Focus 2	g.chr6:159263138G>A	RNA	OSTCP1		oligosaccharyltransferas	56 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr16:21737853C>T	Silent	OTOA	p.Y630Y	otoancorin	29 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr1:149920888G>C	Missense Mutation	OTUD7B	p.D407E	OTU deubiquitinase 7B	38 (0.00)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr12:29597141A>T	Missense Mutation	OVCH1	p.V985D	ovochymase 1	72 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr12:29597148C>T	Missense Mutation	OVCH1	p.E983K	ovochymase 1	62 (0.02)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr5:131546035G>A	Silent	P4HA2	p.V217V	prolyl 4-hydroxylase, al	34 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr17:79804877G>A	Silent	P4HB	p.D223D	prolyl 4-hydroxylase, b	31 (0.00)	61 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr1:17708676C>T	RNA	PADI6		peptidyl arginine deimi	17 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr12:103237545C>G	Missense Mutation	PAH	p.E355Q	phenylalanine hydroxyl	20 (0.00)	16 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr9:112898583C>A	Silent	PALM2-AKAI	p.P253P	PALM2-AKAP2 readth	30 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr1:100154547G>A	Missense Mutation	PALMD	p.R244K	palmdelphin	57 (0.00)	29 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr7:4899770G>A	Missense Mutation	PAPOLB	p.P557S	poly(A) polymerase bet	26 (0.00)	19 (0.26)	0.94
11-02	Gp4 Focus 2	g.chr2:60995679C>G	Missense Mutation	PAPOLG	p.H107Q	poly(A) polymerase gan	29 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:176709195C>T	Silent	PAPPA2	p.T1338T	pappalysin 2	88 (0.00)	22 (0.27)	0.73

11-02	Gp4 Focus 2	g.chr16:14576514G>A	Missense Mutation	PARN	p.H551Y	poly(A)-specific ribonu	156 (0.00)	50 (0.36)	1.15
11-02	Gp4 Focus 2	g.chr7:139724537C>T	Nonsense Mutation	PARP12	p.W643*	poly (ADP-ribose) poly	23 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr3:122419776G>A	Missense Mutation	PARP14	p.C792Y	poly (ADP-ribose) poly	60 (0.00)	36 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr14:20825837G>A	Missense Mutation	PARP2	p.G532R	poly (ADP-ribose) poly	74 (0.00)	16 (0.50)	0.73
11-02	Gp4 Focus 2	g.chr13:25030552G>A	Missense Mutation	PARP4	p.S830F	poly (ADP-ribose) poly	69 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:37020732C>T	Missense Mutation	PAX5	p.R38H	paired box 5	35 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr3:52649381G>A	Missense Mutation	PBRM1	p.P652L	polybromo 1	40 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr3:52649426C>T	Missense Mutation	PBRM1	p.R637K	polybromo 1	37 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr1:154923964C>T	Missense Mutation	PBXIP1	p.E76K	pre-B-cell leukemia hon	28 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr4:134071365G>A	Missense Mutation	PCDH10	p.V24I	protocadherin 10	17 (0.00)	18 (0.33)	1.52
11-02	Gp4 Focus 2	g.chr4:134072821G>T	Missense Mutation	PCDH10	p.G509V	protocadherin 10	36 (0.00)	30 (0.17)	0.76
11-02	Gp4 Focus 2	g.chr4:138451329G>A	Silent	PCDH18	p.I418I	protocadherin 18	68 (0.00)	22 (0.55)	2.49
11-02	Gp4 Focus 2	g.chr13:61985781G>A	Silent	PCDH20	p.L817L	protocadherin 20	29 (0.00)	24 (0.33)	1.72
11-02	Gp4 Focus 2	g.chr5:140186827C>T	Missense Mutation	PCDHA4	p.L19F	protocadherin alpha 4	24 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr5:140208503C>G	Missense Mutation	PCDHA6	p.A276G	protocadherin alpha 6	31 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr5:140230345G>A	Silent	PCDHA9	p.R755R	protocadherin alpha 9	25 (0.00)	23 (0.57)	1.51
11-02	Gp4 Focus 2	g.chr5:140594357C>T	Missense Mutation	PCDHB13	p.P221L	protocadherin beta 13	36 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr5:140474536G>A	Silent	PCDHB2	p.L54L	protocadherin beta 2	30 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr5:140501756C>T	Missense Mutation	PCDHB4	p.A59V	protocadherin beta 4	20 (0.00)	36 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr5:140501785G>A	Missense Mutation	PCDHB4	p.D69N	protocadherin beta 4	25 (0.00)	40 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr5:140802291G>A	Silent	PCDHGA11	p.G499G	protocadherin gamma s	32 (0.00)	63 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr5:140736263C>T	Missense Mutation	PCDHGA4	p.A499V	protocadherin gamma s	30 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr5:140769629G>A	Silent	PCDHGB4	p.Q726Q	protocadherin gamma s	60 (0.00)	39 (0.56)	1.50
11-02	Gp4 Focus 2	g.chr5:140855953C>T	Silent	PCDHGC3	p.D90D	protocadherin gamma s	31 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr5:140869099G>A	Missense Mutation	PCDHGC5	p.A98T	protocadherin gamma s	21 (0.00)	41 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr20:2816916C>T	Missense Mutation	PCED1A	p.G296R	PC-esterase domain con	22 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr11:82879527G>A	Missense Mutation	PCF11	p.R717Q	PCF11 cleavage and pol	53 (0.00)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:82879864G>A	Silent	PCF11	p.G829G	PCF11 cleavage and pol	18 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr11:82893040G>A	Missense Mutation	PCF11	p.G1438R	PCF11 cleavage and pol	49 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr10:93011189G>A	Missense Mutation	PCGF5	p.V156I	polycomb group ring fir	59 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr7:82579202G>A	Nonsense Mutation	PCLO	p.Q3568*	piccolo presynaptic cyt	118 (0.00)	29 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr7:82784432G>A	Missense Mutation	PCLO	p.P509S	piccolo presynaptic cyt	53 (0.00)	90 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr7:82784550A>G	Silent	PCLO	p.P469P	piccolo presynaptic cyt	37 (0.00)	48 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr8:17869274G>A	Missense Mutation	PCM1	p.D1809N	pericentriolar material 1	108 (0.00)	85 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr8:52733222G>A	Missense Mutation	PCMTD1	p.L255F	protein-L-isoaspartate (	153 (0.00)	21 (0.24)	0.80

11-02	Gp4 Focus 2	g.chr21:47783511G>A	Silent	PCNT	p.E757E	pericentrin	36 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr14:71445326G>A	Missense Mutation	PCNX	p.A758T	pecanex homolog (Dros	56 (0.02)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr14:71524343G>A	Missense Mutation	PCNX	p.C1585Y	pecanex homolog (Dros	77 (0.00)	47 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr14:60591075C>T	Missense Mutation	PCNXL4	p.T729I	pecanex-like 4 (Drosop	100 (0.01)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr9:78853915T>A	Nonsense Mutation	PCSK5	p.C969*	proprotein convertase s	26 (0.00)	27 (0.37)	1.19
11-02	Gp4 Focus 2	g.chr9:78942924G>A	Splice Site	PCSK5		proprotein convertase s	64 (0.00)	47 (0.34)	1.10
11-02	Gp4 Focus 2	g.chr1:55524172G>A	Splice Site	PCSK9	p.G452D	proprotein convertase s	26 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr2:70486596G>A	Missense Mutation	PCYOX1	p.G73S	prenylcysteine oxidase	121 (0.00)	96 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr5:148747743C>T	Silent	PCYOX1L	p.V337V	prenylcysteine oxidase	115 (0.00)	47 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr10:105166400C>T	Silent	PDCD11	p.C241C	programmed cell death	40 (0.00)	23 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr10:105199579A>G	Missense Mutation	PDCD11	p.N1368D	programmed cell death	24 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr15:65421478C>T	Missense Mutation	PDCD7	p.V301I	programmed cell death	106 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr11:14852369G>A	Missense Mutation	PDE3B	p.A594T	phosphodiesterase 3B, c	30 (0.03)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr5:59284514C>T	Missense Mutation	PDE4D	p.E25K	phosphodiesterase 4D, c	112 (0.00)	15 (0.33)	1.11
11-02	Gp4 Focus 2	g.chr1:144917636G>A	Splice Site	PDE4DIP	p.R627W	phosphodiesterase 4D in	94 (0.00)	45 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr10:95386583G>A	Nonsense Mutation	PDE6C	p.W342*	phosphodiesterase 6C, c	25 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr5:76621410G>A	Nonsense Mutation	PDE8B	p.W149*	phosphodiesterase 8B	70 (0.00)	69 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr11:103780429G>A	Missense Mutation	PDGFD	p.P369L	platelet derived growth	38 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr5:149497220G>A	Missense Mutation	PDGFRB	p.A1033V	platelet-derived growth	22 (0.00)	47 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr4:96761487C>T	Silent	PDHA2	p.Y62Y	pyruvate dehydrogenase	22 (0.00)	17 (0.29)	1.34
11-02	Gp4 Focus 2	g.chr2:10929899G>A	Silent	PDIA6	p.N324N	protein disulfide isomer	26 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr16:66918259A>C	Missense Mutation	PDP2	p.R24S	pyruvate dehyrogenase	79 (0.00)	18 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr16:70176460C>A	Silent	PDPR	p.L492L	pyruvate dehydrogenase	97 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr4:39851209C>T	Missense Mutation	PDS5A	p.M1050I	PDS5, regulator of cohe	69 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr16:15102652C>T	Missense Mutation	PDXDC1	p.P199L	pyridoxal-dependent de	67 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr16:70016623C>T	RNA	PDXDC2P		pyridoxal-dependent de	84 (0.00)	38 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr16:70044667C>T	RNA	PDXDC2P		pyridoxal-dependent de	28 (0.00)	36 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr17:17480264G>A	Silent	PEMT	p.T21T	phosphatidylethanolami	29 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr2:239161614G>A	Missense Mutation	PER2	p.A1017V	period circadian clock 2	57 (0.02)	67 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr2:239165579C>T	Silent	PER2	p.K683K	period circadian clock 2	38 (0.00)	56 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:92119140G>A	Missense Mutation	PEX1	p.P1118L	peroxisomal biogenesis	24 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:179519699G>A	Silent	PEX5L	p.L600L	peroxisomal biogenesis	53 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr6:42932537G>C	Missense Mutation	PEX6	p.L933V	peroxisomal biogenesis	33 (0.00)	55 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr6:42933429C>T	Missense Mutation	PEX6	p.V821M	peroxisomal biogenesis	64 (0.00)	63 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr6:42933501G>A	Missense Mutation	PEX6	p.P797S	peroxisomal biogenesis	19 (0.00)	21 (0.52)	1.40

11-02	Gp4 Focus 2	g.chr5:139682644C>T	Silent	PFDN1	p.V5V	prefoldin subunit 1	43 (0.00)	45 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr1:161071864G>A	Missense Mutation	PFDN2	p.P88S	prefoldin subunit 2	27 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:53691849C>T	Silent	PFDN5	p.D56D	prefoldin subunit 5	108 (0.01)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr10:3150956G>A	Missense Mutation	PFKP	p.G312R	phosphofructokinase, pl	27 (0.00)	28 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr6:28270023C>T	Missense Mutation	PGBD1	p.H798Y	piggyBac transposable e	59 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr1:64095177G>A	Missense Mutation	PGM1	p.G110S	phosphoglucomutase 1	29 (0.00)	17 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr15:99512852G>A	Missense Mutation	PGPEP1L	p.A4V	pyroglutamyl-peptidase	15 (0.00)	40 (0.28)	0.91
11-02	Gp4 Focus 2	g.chr3:169846696G>A	Missense Mutation	PHC3	p.P522S	polyhomeotic homolog	85 (0.00)	91 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr17:27239702G>C	Silent	PHF12	p.P629P	PHD finger protein 12	23 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr17:27240985C>T	Missense Mutation	PHF12	p.G402E	PHD finger protein 12	22 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr4:129783000G>A	Missense Mutation	PHF17	p.E375K		23 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr9:123625018G>A	Silent	PHF19	p.C326C	PHD finger protein 19	34 (0.00)	26 (0.19)	0.40
11-02	Gp4 Focus 2	g.chr9:96425193C>A	Missense Mutation	PHF2	p.T568K	PHD finger protein 2	50 (0.00)	49 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr8:133816278G>A	Splice Site	PHF20L1		PHD finger protein 20-l	45 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr6:64395639C>T	Silent	PHF3	p.P672P	PHD finger protein 3	100 (0.00)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr1:120286517G>A	Missense Mutation	PHGDH	p.A486T	phosphoglycerate dehyd	44 (0.00)	34 (0.21)	0.43
11-02	Gp4 Focus 2	g.chr11:118498721G>T	Missense Mutation	PHLDB1	p.K394N	pleckstrin homology-lik	23 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr11:118498796C>T	Silent	PHLDB1	p.S419S	pleckstrin homology-lik	20 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr3:111632233C>T	Missense Mutation	PHLDB2	p.S54F	pleckstrin homology-lik	73 (0.00)	39 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr18:60395931G>A	Intron	PHLPP1		PH domain and leucine	21 (0.00)	36 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr18:60407262G>A	Intron	PHLPP1		PH domain and leucine	107 (0.00)	71 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr18:60409082G>A	Intron	PHLPP1		PH domain and leucine	199 (0.00)	95 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr18:60454726C>A	Intron	PHLPP1		PH domain and leucine	26 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr18:60458006G>T	Intron	PHLPP1		PH domain and leucine	63 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr18:60460680G>A	Intron	PHLPP1		PH domain and leucine	124 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr18:60463719G>T	Intron	PHLPP1		PH domain and leucine	40 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr18:60464817G>A	Intron	PHLPP1		PH domain and leucine	78 (0.00)	57 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr18:60468007G>A	Intron	PHLPP1		PH domain and leucine	69 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr18:60476670A>C	Intron	PHLPP1		PH domain and leucine	24 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr18:60491651C>T	Intron	PHLPP1		PH domain and leucine	35 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr18:60509221G>A	Intron	PHLPP1		PH domain and leucine	126 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr18:60512282G>A	Intron	PHLPP1		PH domain and leucine	54 (0.00)	19 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr18:60549021C>A	Intron	PHLPP1		PH domain and leucine	21 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr18:60549022G>A	Intron	PHLPP1		PH domain and leucine	21 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr18:60549044G>A	Intron	PHLPP1		PH domain and leucine	23 (0.00)	11 (0.45)	1.21

11-02	Gp4 Focus 2	g.chr18:60550596G>A	Intron	PHLPP1		PH domain and leucine	62 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr18:60551011C>T	Intron	PHLPP1		PH domain and leucine	76 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr18:60553540G>T	Intron	PHLPP1		PH domain and leucine	139 (0.00)	43 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr18:60555230G>A	Intron	PHLPP1		PH domain and leucine	35 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr18:60561708G>A	Intron	PHLPP1		PH domain and leucine	21 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr18:60571819G>T	Intron	PHLPP1		PH domain and leucine	137 (0.01)	34 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr18:60594171C>T	Intron	PHLPP1		PH domain and leucine	81 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr18:60628277C>T	Intron	PHLPP1		PH domain and leucine	18 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr18:60629442C>T	Intron	PHLPP1		PH domain and leucine	45 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr18:60644055G>A	Intron	PHLPP1		PH domain and leucine	78 (0.00)	12 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr18:60645295C>T	Intron	PHLPP1		PH domain and leucine	17 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr16:71687421C>T	Intron	PHLPP2		PH domain and leucine	50 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr16:71687894C>T	Intron	PHLPP2		PH domain and leucine	23 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr16:71704135G>A	Intron	PHLPP2		PH domain and leucine	57 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr16:71704669G>A	Intron	PHLPP2		PH domain and leucine	45 (0.00)	46 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr16:71709892G>A	Intron	PHLPP2		PH domain and leucine	85 (0.01)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr16:71743611C>T	Intron	PHLPP2		PH domain and leucine	17 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr16:71743615C>T	Intron	PHLPP2		PH domain and leucine	19 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr11:601610C>A	Missense Mutation	PHRF1	p.P354Q	PHD and ring finger do	34 (0.00)	46 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr22:21159355G>A	Missense Mutation	PI4KA	p.R423W	phosphatidylinositol 4-k	25 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr1:151271353G>A	Missense Mutation	PI4KB	p.A634V	phosphatidylinositol 4-k	48 (0.00)	69 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr16:88783613G>A	Missense Mutation	PIEZO1	p.P2160S	piezo-type mechanosens	26 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr18:10784879G>A	Silent	PIEZO2	p.L799L	piezo-type mechanosens	25 (0.00)	27 (0.78)	2.07
11-02	Gp4 Focus 2	g.chr9:35093426G>A	Missense Mutation	PIGO	p.P311S	phosphatidylinositol gly	21 (0.00)	74 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr19:49954062G>A	Missense Mutation	PIH1D1	p.S45L	PIH1 domain containing	30 (0.00)	29 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr12:18499771G>A	Splice Site	PIK3C2G		phosphatidylinositol-4-p	98 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr3:178942597A>G	Missense Mutation	PIK3CA	p.K802E	phosphatidylinositol-4,5	79 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr7:106508912G>A	Silent	PIK3CG	p.E302E	phosphatidylinositol-4,5	16 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr7:106523482G>A	Missense Mutation	PIK3CG	p.M878I	phosphatidylinositol-4,5	116 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr5:67569285G>A	Silent	PIK3R1	p.K134K	phosphoinositide-3-kina	85 (0.00)	28 (0.18)	0.59
11-02	Gp4 Focus 2	g.chr5:67569306G>A	Silent	PIK3R1	p.K141K	phosphoinositide-3-kina	70 (0.01)	14 (0.36)	1.18
11-02	Gp4 Focus 2	g.chr3:130437260G>A	Silent	PIK3R4	p.D700D	phosphoinositide-3-kina	23 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr10:22830743C>T	Silent	PIP4K2A	p.K342K	phosphatidylinositol-5-p	40 (0.00)	28 (0.61)	2.03
11-02	Gp4 Focus 2	g.chr12:57989720G>T	Missense Mutation	PIP4K2C	p.R140L	phosphatidylinositol-5-p	20 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:1438536C>T	Silent	PITPNA	p.L195L	phosphatidylinositol tra	102 (0.00)	25 (0.20)	0.53

11-02	Gp4 Focus 2	g.chr17:65528987G>A	Missense Mutation	PITPNC1	p.E40K	phosphatidylinositol tra	16 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr11:67269868C>G	Missense Mutation	PITPNM1	p.V104L	phosphatidylinositol tra	24 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr12:123497202C>T	Missense Mutation	PITPNM2	p.V125M	phosphatidylinositol tra	84 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr17:6387557G>A	Silent	PITPNM3	p.I110I	PITPNM family membe	39 (0.00)	58 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr10:3200253C>A	Missense Mutation	PITRM1	p.R410I	pitrilysin metallopeptida	92 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr10:3209142C>T	Silent	PITRM1	p.T84T	pitrilysin metallopeptida	81 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr16:81197350C>T	RNA	PKD1L2		polycystic kidney diseas	20 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr16:72020068G>A	RNA	PKD1L3		polycystic kidney diseas	23 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr22:46657204G>A	Silent	PKDREJ	p.D672D	polycystin (PKD) family	78 (0.00)	62 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr22:46657796C>A	Missense Mutation	PKDREJ	p.R475I	polycystin (PKD) family	42 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr15:72502151G>A	Missense Mutation	PKM	p.T143M	pyruvate kinase, muscle	68 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr19:14568857G>T	Missense Mutation	PKN1	p.V394L	protein kinase N1	63 (0.00)	65 (0.25)	0.66
11-02	Gp4 Focus 2	g.chr2:159499090C>T	Silent	PKP4	p.N596N	plakophilin 4	47 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr2:159535099G>A	Missense Mutation	PKP4	p.S1088N	plakophilin 4	19 (0.00)	12 (0.83)	2.22
11-02	Gp4 Focus 2	g.chr22:31532688C>A	Missense Mutation	PLA2G3	p.D433Y	phospholipase A2, grou	56 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr1:186901980C>A	Nonsense Mutation	PLA2G4A	p.S215*	phospholipase A2, grou	25 (0.00)	38 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr2:160879371C>T	Splice Site	PLA2R1		phospholipase A2 recep	43 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr8:42037832C>A	Nonsense Mutation	PLAT	p.E295*	plasminogen activator, t	70 (0.00)	49 (0.31)	0.99
11-02	Gp4 Focus 2	g.chr10:75675029C>A	Missense Mutation	PLAU	p.Q331K	plasminogen activator, u	19 (0.00)	26 (0.35)	0.92
11-02	Gp4 Focus 2	g.chr2:219495421G>A	Missense Mutation	PLCD4	p.E390K	phospholipase C, delta 4	48 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr20:39798103G>A	Missense Mutation	PLCG1	p.D863N	phospholipase C, gamm	40 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr3:155314037C>A	Missense Mutation	PLCH1	p.K58N	phospholipase C, eta 1	45 (0.00)	9 (0.56)	1.48
11-02	Gp4 Focus 2	g.chr6:151054915C>T	Missense Mutation	PLEKHG1	p.T33I	pleckstrin homology do	49 (0.00)	56 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr14:68029593G>T	Silent	PLEKHH1	p.L415L	pleckstrin homology do	22 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr17:62793434G>A	RNA	PLEKHM1P		pleckstrin homology do	27 (0.00)	29 (0.38)	1.01
11-02	Gp4 Focus 2	g.chr15:65140929C>T	Silent	PLEKHO2	p.V50V	pleckstrin homology do	36 (0.03)	41 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr6:161134043G>A	Missense Mutation	PLG	p.E145K	plasminogen	52 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr6:161152149C>T	Silent	PLG	p.D441D	plasminogen	78 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:19126238G>A	Missense Mutation	PLIN2	p.L34F	perilipin 2	20 (0.00)	19 (0.26)	0.86
11-02	Gp4 Focus 2	g.chr1:45271019C>T	Missense Mutation	PLK3	p.L573F	polo-like kinase 3	65 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:128812764G>A	Missense Mutation	PLK4	p.G595S	polo-like kinase 4	75 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chrX:114879374G>A	Nonsense Mutation	PLS3	p.W406*	plastin 3	22 (0.00)	14 (0.79)	1.75
11-02	Gp4 Focus 2	g.chr15:74326821G>A	Missense Mutation	PML	p.E554K	promyelocytic leukemia	20 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:102949466C>T	Missense Mutation	PMPCB	p.A306V	peptidase (mitochondria	40 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr10:118385619C>T	RNA	PNLIPRP2		pancreatic lipase-related	45 (0.00)	19 (0.84)	2.25

11-02	Gp4 Focus 2	g.chr10:118389531G>A	RNA	PNLIPRP2		pancreatic lipase-related	64 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr14:39650607G>A	Missense Mutation	PNN	p.R565Q	pinin, desmosome assoc	19 (0.00)	22 (0.41)	1.30
11-02	Gp4 Focus 2	g.chr7:108154658C>T	Missense Mutation	PNPLA8	p.C279Y	patatin-like phospholipa	98 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr7:131195838G>A	Missense Mutation	PODXL	p.A152V	podocalyxin-like	53 (0.00)	25 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr1:151377796C>T	Missense Mutation	POGZ	p.V1230I	pogo transposable elem	41 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:151377853G>A	Nonsense Mutation	POGZ	p.Q1211*	pogo transposable elem	20 (0.00)	24 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr11:65048595G>A	Missense Mutation	POLA2	p.E293K	polymerase (DNA direc	51 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr12:133233764C>T	Silent	POLE	p.Q1180Q	polymerase (DNA direc	16 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr17:62492784G>A	Silent	POLG2	p.P101P	polymerase (DNA direc	37 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr3:121179021G>A	Missense Mutation	POLQ	p.S2343F	polymerase (DNA direc	54 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr3:121258368G>A	Silent	POLQ	p.F181F	polymerase (DNA direc	21 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:86310218C>T	Silent	POLR1A	p.L268L	polymerase (RNA) I pol	30 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr2:86315744G>A	Silent	POLR1A	p.I225I	polymerase (RNA) I pol	41 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr2:113331330C>T	Silent	POLR1B	p.Y765Y	polymerase (RNA) I pol	55 (0.00)	64 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr9:37495216C>T	Missense Mutation	POLR1E	p.L200F	polymerase (RNA) I pol	20 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr1:145608446C>A	Missense Mutation	POLR3C	p.V121F	polymerase (RNA) III (	86 (0.00)	63 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr1:145608542G>A	Missense Mutation	POLR3C	p.P89S	polymerase (RNA) III (	76 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr8:22105413G>A	Missense Mutation	POLR3D	p.D85N	polymerase (RNA) III (	15 (0.00)	39 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr13:38158133G>A	Silent	POSTN	p.L406L	periostin, osteoblast spe	15 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr14:19553698C>T	Silent	POTEG	p.L94L	POTE ankyrin domain f	15 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr1:167384962C>T	Missense Mutation	POU2F1	p.A728V	POU class 2 homeobox	19 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr8:128429015T>C	Missense Mutation	POU5F1B	p.S302P	POU class 5 homeobox	68 (0.00)	13 (0.62)	2.11
11-02	Gp4 Focus 2	g.chr10:71966054C>T	Missense Mutation	PPA1	p.C254Y	pyrophosphatase (inorga	50 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr22:46627932G>A	Missense Mutation	PPARA	p.A319T	peroxisome proliferator-	37 (0.00)	36 (0.31)	0.81
11-02	Gp4 Focus 2	g.chr11:70118333G>C	Missense Mutation	PPFIA1	p.G19R	protein tyrosine phospha	35 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr11:7672116G>A	Missense Mutation	PPFIBP2	p.V580M	PTPRF interacting prote	23 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr16:4937162C>T	Missense Mutation	PPL	p.E861K	periplakin	55 (0.00)	41 (0.22)	0.70
11-02	Gp4 Focus 2	g.chr16:4941860T>A	Silent	PPL	p.T640T	periplakin	16 (0.00)	23 (0.26)	0.83
11-02	Gp4 Focus 2	g.chr2:44428429G>A	Missense Mutation	PPM1B	p.G31R	protein phosphatase, Mg	109 (0.00)	60 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr2:44428467T>C	Silent	PPM1B	p.V43V	protein phosphatase, Mg	71 (0.00)	46 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr17:57057699C>A	Nonsense Mutation	PPM1E	p.C525*	protein phosphatase, Mg	20 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:80199447G>A	Missense Mutation	PPP1R12A	p.A642V	protein phosphatase 1, r	127 (0.00)	26 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr19:49376856G>A	Silent	PPP1R15A	p.E122E	protein phosphatase 1, r	33 (0.00)	25 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr19:49377777G>A	Silent	PPP1R15A	p.L429L	protein phosphatase 1, r	47 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:48686899G>T	Nonsense Mutation	PPP1R21	p.E128*	protein phosphatase 1, r	27 (0.00)	14 (0.43)	1.14

11-02	Gp4 Focus 2	g.chr7:94898663G>T	Missense Mutation	PPP1R9A	p.A990S	protein phosphatase 1, r	65 (0.02)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr11:111622948C>T	Missense Mutation	PPP2R1B	p.E380K	protein phosphatase 2, r	55 (0.00)	48 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr6:42974996C>T	Silent	PPP2R5D	p.D195D	protein phosphatase 2, r	98 (0.00)	45 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr11:68341626G>A	Missense Mutation	PPP6R3	p.A233T	protein phosphatase 6, r	62 (0.00)	51 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr10:103899718G>A	Missense Mutation	PPRC1	p.G485R	peroxisome proliferator-	25 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr1:40557790G>A	Nonsense Mutation	PPT1	p.Q97*	palmitoyl-protein thioes	67 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr1:13695891G>A	Silent	PRAMEF19	p.D289D	PRAME family membe	33 (0.00)	118 (0.49)	1.31
11-02	Gp4 Focus 2	g.chr1:13001314C>T	Silent	PRAMEF6	p.G123G	PRAME family membe	63 (0.00)	41 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr4:121774689C>T	Missense Mutation	PRDM5	p.G62R	PR domain containing 5	71 (0.00)	68 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr1:173450484C>T	Missense Mutation	PRDX6	p.H39Y	peroxiredoxin 6	58 (0.00)	27 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr8:69031732G>A	Missense Mutation	PREX2	p.E1163K	phosphatidylinositol-3,4	61 (0.00)	30 (0.17)	0.56
11-02	Gp4 Focus 2	g.chr1:186277330G>A	Missense Mutation	PRG4	p.A827T	proteoglycan 4	124 (0.00)	73 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr3:64132672G>A	Silent	PRICKLE2	p.I554I	prickle homolog 2 (Dro	23 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr3:64138955G>A	Silent	PRICKLE2	p.G286G	prickle homolog 2 (Dro	40 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr4:185580533G>A	Missense Mutation	PRIMPOL	p.G74R	primase and polymerase	39 (0.00)	19 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr5:40765261C>T	Missense Mutation	PRKAA1	p.D301N	protein kinase, AMP-ac	80 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr1:84668378G>A	Missense Mutation	PRKACB	p.A266T	protein kinase, cAMP-d	40 (0.00)	31 (0.55)	1.46
11-02	Gp4 Focus 2	g.chr1:84668384G>A	Missense Mutation	PRKACB	p.D268N	protein kinase, cAMP-d	40 (0.00)	31 (0.55)	1.46
11-02	Gp4 Focus 2	g.chr17:64800101G>A	Silent	PRKCA	p.G655G	protein kinase C, alpha	20 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr14:61995914G>A	Missense Mutation	PRKCH	p.D519N	protein kinase C, eta	40 (0.00)	53 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr3:169991115C>G	Missense Mutation	PRKCI	p.D211E	protein kinase C, iota	23 (0.00)	21 (0.76)	2.03
11-02	Gp4 Focus 2	g.chr2:37543468C>T	Missense Mutation	PRKD3	p.G67D	protein kinase D3	80 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr11:20414508G>A	Silent	PRMT3	p.L121L	protein arginine methylt	40 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr13:39585534G>A	Nonsense Mutation	PROSER1	p.Q935*	proline and serine rich 1	53 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr13:39588360G>A	Silent	PROSER1	p.P343P	proline and serine rich 1	43 (0.00)	44 (0.43)	1.15
11-02	Gp4 Focus 2	g.chr13:39588362G>A	Missense Mutation	PROSER1	p.P343S	proline and serine rich 1	43 (0.00)	44 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr10:13647711G>A	Silent	PRPF18	p.R110R	pre-mRNA processing f	148 (0.00)	50 (0.20)	0.67
11-02	Gp4 Focus 2	g.chr1:150297505G>A	Silent	PRPF3	p.L35L	pre-mRNA processing f	47 (0.02)	43 (0.40)	1.05
11-02	Gp4 Focus 2	g.chr1:150315863G>A	Missense Mutation	PRPF3	p.R454K	pre-mRNA processing f	16 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr12:50037897G>A	Silent	PRPF40B	p.T867T	PRP40 pre-mRNA proc	26 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr17:1577807G>A	Silent	PRPF8	p.D1076D	pre-mRNA processing f	37 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr17:1578913C>T	Splice Site	PRPF8		pre-mRNA processing f	57 (0.00)	14 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr6:42689559G>A	Missense Mutation	PRPH2	p.R172W	peripherin 2 (retinal deg	75 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr22:32111707G>A	Silent	PRR14L	p.T706T	proline rich 14-like	60 (0.00)	50 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr12:10999870T>C	Missense Mutation	PRR4	p.D66G	proline rich 4 (lacrimal)	26 (0.00)	67 (0.30)	0.80

11-02	Gp4 Focus 2	g.chr5:139217251G>A	Silent	PSD2	p.L569L	pleckstrin and Sec7 don	17 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr8:18413773G>A	Silent	PSD3	p.V958V	pleckstrin and Sec7 don	53 (0.00)	46 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr19:43702223G>A	Missense Mutation	PSG4	p.A212V	pregnancy specific beta-	131 (0.00)	31 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr19:43689226G>A	Silent	PSG5	p.S46S	pregnancy specific beta-	33 (0.00)	55 (0.71)	1.89
11-02	Gp4 Focus 2	g.chr17:4700776C>T	Missense Mutation	PSMB6	p.H72Y	proteasome (prosome, n	48 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr11:47445615C>T	Silent	PSMC3	p.L191L	proteasome (prosome, n	23 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr2:231949755G>A	Missense Mutation	PSMD1	p.G582E	proteasome (prosome, n	95 (0.00)	30 (0.73)	1.96
11-02	Gp4 Focus 2	g.chr3:184021185G>A	Missense Mutation	PSMD2	p.A383T	proteasome (prosome, n	26 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr17:38146426C>T	Silent	PSMD3	p.H319H	proteasome (prosome, n	25 (0.00)	15 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr1:28477329G>C	Missense Mutation	PTAFR	p.I68M	platelet-activating facto	22 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr9:115060164G>A	Silent	PTBP3	p.I25I	polypyrimidine tract bin	56 (0.00)	25 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr2:86333424G>A	Silent	PTCD3	p.Q18Q	pentatricopeptide repeat	27 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr10:89646899G>A	Intron	PTEN		phosphatase and tensin	143 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr10:89676442C>T	Intron	PTEN		phosphatase and tensin	73 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr10:89681333G>A	Intron	PTEN		phosphatase and tensin	28 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr10:89681825G>A	Intron	PTEN		phosphatase and tensin	48 (0.00)	25 (0.72)	1.92
11-02	Gp4 Focus 2	g.chr10:89706751G>A	Intron	PTEN		phosphatase and tensin	163 (0.00)	102 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr10:89721162G>A	Intron	PTEN		phosphatase and tensin	65 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr10:89723489A>G	Intron	PTEN		phosphatase and tensin	64 (0.00)	75 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr17:41122347C>T	Missense Mutation	PTGES3L	p.V136I	prostaglandin E synthas	103 (0.00)	74 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr7:77175389C>T	Intron	PTPN12		protein tyrosine phospha	18 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr7:77177981G>A	Intron	PTPN12		protein tyrosine phospha	81 (0.00)	37 (0.49)	1.30
11-02	Gp4 Focus 2	g.chr7:77200029G>A	Intron	PTPN12		protein tyrosine phospha	86 (0.00)	55 (0.51)	1.36
11-02	Gp4 Focus 2	g.chr7:77214346G>A	Intron	PTPN12		protein tyrosine phospha	35 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr7:77217668G>A	Intron	PTPN12		protein tyrosine phospha	46 (0.00)	43 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr7:77244925G>A	Intron	PTPN12		protein tyrosine phospha	32 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr4:87653847G>A	Missense Mutation	PTPN13	p.D596N	protein tyrosine phospha	110 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr4:87703402A>T	Missense Mutation	PTPN13	p.D2009V	protein tyrosine phospha	64 (0.02)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr18:12817232C>T	Missense Mutation	PTPN2	p.G181R	protein tyrosine phospha	30 (0.00)	40 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr2:120709635G>A	Silent	PTPN4	p.Q581Q	protein tyrosine phospha	29 (0.00)	24 (0.42)	1.33
11-02	Gp4 Focus 2	g.chr12:70946701G>A	Missense Mutation	PTPRB	p.A1660V	protein tyrosine phospha	106 (0.00)	37 (0.59)	1.59
11-02	Gp4 Focus 2	g.chr9:8341129C>T	Missense Mutation	PTPRD	p.G1696E	protein tyrosine phospha	48 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr9:8518145C>T	Missense Mutation	PTPRD	p.A416T	protein tyrosine phospha	57 (0.02)	20 (0.55)	1.47
11-02	Gp4 Focus 2	g.chr1:44084320G>A	Nonsense Mutation	PTPRF	p.W1455*	protein tyrosine phospha	21 (0.00)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr6:128294971G>A	Splice Site	PTPRK	p.P1330L	protein tyrosine phospha	16 (0.00)	32 (0.16)	0.42

11-02	Gp4 Focus 2	g.chr6:128718768C>T	Missense Mutation	PTPRK	p.E56K	protein tyrosine phospha	91 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr18:8113582C>T	Missense Mutation	PTPRM	p.A652V	protein tyrosine phospha	47 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr12:15679197G>A	Splice Site	PTPRO		protein tyrosine phospha	35 (0.00)	38 (0.63)	1.68
11-02	Gp4 Focus 2	g.chr12:15742450G>A	Missense Mutation	PTPRO	p.D1158N	protein tyrosine phospha	64 (0.00)	77 (0.32)	0.87
11-02	Gp4 Focus 2	g.chr12:71033048C>A	Missense Mutation	PTPRR	p.M518I	protein tyrosine phospha	69 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr8:144898944C>T	Missense Mutation	PUF60	p.D476N	poly-U binding splicing	19 (0.00)	32 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr5:139494511G>A	Missense Mutation	PURA	p.V249M	purine-rich element bin	42 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr7:105108800G>A	Silent	PUS7	p.D503D	pseudouridylate synthas	128 (0.00)	91 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr5:159520808G>A	Silent	PWWP2A	p.N283N	PWWP domain containi	131 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr2:1652070C>T	Missense Mutation	PXDN	p.R1161Q	peroxidasin homolog (D	58 (0.00)	51 (0.16)	0.51
11-02	Gp4 Focus 2	g.chr20:25255237G>A	Missense Mutation	PYGB	p.A180T	phosphorylase, glycoge	22 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr12:9349652G>A	Missense Mutation	PZP	p.L275F	pregnancy-zone protein	46 (0.02)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr6:163991727C>T	Splice Site	QKI	p.A337A	QKI, KH domain contai	222 (0.00)	102 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr1:180153105C>T	Silent	QSOX1	p.L269L	quiescin Q6 sulfhydryl	36 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr10:99969408G>A	Missense Mutation	R3HCC1L	p.G513S	R3H domain and coiled-	53 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr8:37732359C>G	Missense Mutation	RAB11FIP1	p.R432S	RAB11 family interacti	50 (0.00)	19 (0.47)	1.53
11-02	Gp4 Focus 2	g.chr8:37732650G>A	Silent	RAB11FIP1	p.I335I	RAB11 family interacti	28 (0.00)	19 (0.32)	1.02
11-02	Gp4 Focus 2	g.chr17:29858684G>A	Silent	RAB11FIP4	p.Q616Q	RAB11 family interacti	19 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:238485939G>A	Silent	RAB17	p.N5N	RAB17, member RAS c	25 (0.00)	26 (0.85)	2.26
11-02	Gp4 Focus 2	g.chr19:11448022G>A	Silent	RAB3D	p.N18N	RAB3D, member RAS	51 (0.00)	30 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr11:61665813C>T	Silent	RAB3IL1	p.E362E	RAB3A interacting prot	26 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr9:125758380G>A	Silent	RABGAP1	p.K328K	RAB GTPase activating	43 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr9:125835830G>A	Splice Site	RABGAP1		RAB GTPase activating	145 (0.00)	40 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr1:174945263C>T	Nonsense Mutation	RABGAP1L	p.Q184*	RAB GTPase activating	38 (0.00)	34 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr1:174952030G>A	Silent	RABGAP1L	p.L250L	RAB GTPase activating	24 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr3:51667766C>T	Silent	RAD54L2	p.A333A	RAD54-like 2 (S. cerevi	40 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr17:17697507G>A	Silent	RAI1	p.K415K	retinoic acid induced 1	18 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr5:34811131G>A	Silent	RAI14	p.P155P	retinoic acid induced 14	97 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr14:36159046G>A	Silent	RALGAPA1	p.A810A	Ral GTPase activating p	27 (0.00)	15 (0.40)	1.27
11-02	Gp4 Focus 2	g.chr20:20621434C>T	Missense Mutation	RALGAPA2	p.C154Y	Ral GTPase activating p	48 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr20:37177331G>A	Splice Site	RALGAPB		Ral GTPase activating p	56 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:135983518C>T	Missense Mutation	RALGDS	p.E352K	ral guanine nucleotide d	15 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr9:129931005C>T	Missense Mutation	RALGPS1	p.R266C	Ral GEF with PH doma	27 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr17:40914412G>A	Missense Mutation	RAMP2	p.C73Y	receptor (G protein-cou	25 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr2:109380869G>A	Missense Mutation	RANBP2	p.A1292T	RAN binding protein 2	20 (0.00)	15 (0.40)	1.07

11-02	Gp4 Focus 2	g.chr2:109380890G>A	Missense Mutation	RANBP2	p.E1299K	RAN binding protein 2	23 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr4:160260329G>A	Missense Mutation	RAPGEF2	p.S625N	Rap guanine nucleotide	54 (0.00)	50 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr2:204304663G>A	Silent	RAPH1	p.L1084L	Ras association (RalGD	18 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr5:167937667G>T	Missense Mutation	RARS	p.K476N	arginyl-tRNA synthetas	15 (0.00)	13 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr1:178433454G>A	Silent	RASAL2	p.E1098E	RAS protein activator li	21 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr19:15567374G>C	Silent	RASAL3	p.A505A	RAS protein activator li	17 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr22:35947944C>T	Silent	RASD2	p.V222V	RASD family, member	19 (0.00)	34 (0.44)	1.18
11-02	Gp4 Focus 2	g.chr15:79296430G>A	Silent	RASGRF1	p.F721F	Ras protein-specific gua	25 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr5:80497194C>T	Silent	RASGRF2	p.L947L	Ras protein-specific gua	69 (0.00)	20 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr2:33745660C>T	Missense Mutation	RASGRP3	p.L93F	RAS guanyl releasing p	117 (0.00)	26 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr4:53731836A>G	Missense Mutation	RASL11B	p.K204R	RAS-like, family 11, m	84 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr13:48906957G>A	Intron	RB1		retinoblastoma 1	112 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr13:48906970G>A	Intron	RB1		retinoblastoma 1	108 (0.00)	55 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr13:48920182G>A	Intron	RB1		retinoblastoma 1	30 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr13:48940260T>C	Intron	RB1		retinoblastoma 1	74 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr13:48944347G>A	Intron	RB1		retinoblastoma 1	57 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr13:48945127G>A	Intron	RB1		retinoblastoma 1	67 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr13:49011786C>T	Intron	RB1		retinoblastoma 1	30 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr13:49011796C>T	Intron	RB1		retinoblastoma 1	32 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr13:49019423C>G	Intron	RB1		retinoblastoma 1	94 (0.00)	36 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr13:49021822G>A	Intron	RB1		retinoblastoma 1	45 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr13:49032700G>A	Intron	RB1		retinoblastoma 1	78 (0.00)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr7:5097349G>T	Missense Mutation	RBAK-RBAK	p.K59N	RBAK-RBAKDN readt	71 (0.00)	18 (0.28)	0.99
11-02	Gp4 Focus 2	g.chr1:205070740G>A	Missense Mutation	RBBP5	p.A207V	retinoblastoma binding	31 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr18:77802150C>T	Silent	RBFA	p.S169S	ribosome binding factor	19 (0.00)	35 (0.26)	0.82
11-02	Gp4 Focus 2	g.chr22:36155987C>T	Missense Mutation	RBFOX2	p.V353I	RNA binding protein, f	29 (0.00)	21 (0.81)	2.16
11-02	Gp4 Focus 2	g.chr20:34242913G>C	Nonsense Mutation	RBM12	p.S111*	RNA binding motif prot	104 (0.00)	40 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr5:145631391C>G	Missense Mutation	RBM27	p.S466C	RNA binding motif prot	120 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:238733009G>A	Missense Mutation	RBM44	p.G800E	RNA binding motif prot	53 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr4:155719364G>A	Missense Mutation	RBM46	p.G185S	RNA binding motif prot	50 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:17748788C>A	Splice Site	RCC2		regulator of chromosom	26 (0.00)	42 (0.52)	1.40
11-02	Gp4 Focus 2	g.chr15:91503680G>A	Missense Mutation	RCCD1	p.D299N	RCC1 domain containin	24 (0.00)	30 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:4844682G>T	Splice Site	RCL1		RNA terminal phosphat	33 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr14:103188668G>A	Missense Mutation	RCOR1	p.G445D	REST corepressor 1	145 (0.00)	42 (0.55)	1.46
11-02	Gp4 Focus 2	g.chr17:9808156G>A	Silent	RCVRN	p.N114N	recoverin	20 (0.00)	26 (0.19)	0.51

11-02	Gp4 Focus 2	g.chr14:24642597C>A	Missense Mutation	REC8	p.P147T	REC8 meiotic recombin	22 (0.00)	21 (0.43)	0.63
11-02	Gp4 Focus 2	g.chr19:45537769T>C	Missense Mutation	RELB	p.L446P	v-rel avian reticuloendo	21 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr7:103143605C>A	Missense Mutation	RELN	p.G2783C	reelin	29 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:103143606G>A	Silent	RELN	p.F2782F	reelin	30 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr7:103301840C>T	Missense Mutation	RELN	p.R475K	reelin	33 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr4:57797744C>G	Missense Mutation	REST	p.P907R	RE1-silencing transcript	31 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr6:111694221C>T	Silent	REV3L	p.R1779R	REV3-like, polymerase	82 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr3:16535263G>A	Silent	RFTN1	p.Y38Y	raftlin, lipid raft linker 1	106 (0.01)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:198436905G>A	Missense Mutation	RFTN2	p.H445Y	raftlin family member 2	35 (0.00)	34 (0.44)	1.18
11-02	Gp4 Focus 2	g.chr6:117248301C>G	Missense Mutation	RFX6	p.P666R	regulatory factor X, 6	96 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr15:56386709C>T	Missense Mutation	RFX7	p.G976S	regulatory factor X, 7	112 (0.00)	45 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr15:56386724C>T	Missense Mutation	RFX7	p.G971R	regulatory factor X, 7	115 (0.00)	38 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr10:86008732G>T	Silent	RGR	p.V101V	retinal G protein couple	20 (0.00)	66 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr8:54764561T>A	Nonsense Mutation	RGS20	p.Y34*	regulator of G-protein si	41 (0.00)	22 (0.23)	0.77
11-02	Gp4 Focus 2	g.chr1:182443674C>A	Nonsense Mutation	RGSL1	p.C476*	regulator of G-protein si	18 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr12:2997280C>T	Silent	RHNO1	p.S110S	RAD9-HUS1-RAD1 int	21 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr12:2997452T>C	Missense Mutation	RHNO1	p.C168R	RAD9-HUS1-RAD1 int	37 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr10:62631992G>A	Silent	RHOBTB1	p.Y624Y	Rho-related BTB domai	33 (0.00)	19 (0.32)	1.00
11-02	Gp4 Focus 2	g.chr5:95119514G>A	Silent	RHOBTB3	p.Q490Q	Rho-related BTB domai	48 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr1:113245192A>G	Missense Mutation	RHOC	p.M134T	ras homolog family mer	43 (0.00)	41 (0.22)	0.46
11-02	Gp4 Focus 2	g.chr12:107219519T>C	Missense Mutation	RIC8B	p.F253L	RIC8 guanine nucleotid	23 (0.00)	13 (0.62)	1.64
11-02	Gp4 Focus 2	g.chr12:107279688G>A	Silent	RIC8B	p.E526E	RIC8 guanine nucleotid	27 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr12:8926285G>A	Missense Mutation	RIMKLB	p.E356K	ribosomal modification	27 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr6:72947580G>A	Missense Mutation	RIMS1	p.V638I	regulating synaptic men	33 (0.00)	41 (0.59)	1.56
11-02	Gp4 Focus 2	g.chr14:93022143G>A	Missense Mutation	RIN3	p.G31D	Ras and Rab interactor	20 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr8:87498813C>T	Missense Mutation	RMDN1	p.S132N	regulator of microtubule	68 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr1:182551299G>A	Missense Mutation	RNASEL	p.S554F	ribonuclease L (2',5'-oli	39 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr2:86849829C>T	Missense Mutation	RNF103	p.G61R	ring finger protein 103	114 (0.00)	55 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr15:59323874C>T	Missense Mutation	RNF111	p.H285Y	ring finger protein 111	43 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr6:127608343G>A	Silent	RNF146	p.E194E	ring finger protein 146	37 (0.00)	71 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr4:141888948G>A	Silent	RNF150	p.T188T	ring finger protein 150	36 (0.00)	67 (0.22)	1.02
11-02	Gp4 Focus 2	g.chr9:104307056G>A	Silent	RNF20	p.L212L	ring finger protein 20, E	61 (0.02)	52 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr9:104309484C>T	Silent	RNF20	p.I320I	ring finger protein 20, E	47 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr17:78328297G>T	Nonsense Mutation	RNF213	p.E3644*	ring finger protein 213	21 (0.00)	30 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr13:79190767G>A	Missense Mutation	RNF219	p.P377S	ring finger protein 219	48 (0.00)	40 (0.38)	1.00

11-02	Gp4 Focus 2	g.chr1:45101221G>A	Silent	RNF220	p.R318R	ring finger protein 220	30 (0.00)	34 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr2:219530710G>T	Missense Mutation	RNF25	p.H168N	ring finger protein 25	26 (0.00)	20 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr17:56437552G>A	Missense Mutation	RNF43	p.H304Y	ring finger protein 43	20 (0.00)	41 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr3:78685081G>A	Missense Mutation	ROBO1	p.P1072L	roundabout, axon guida	58 (0.00)	65 (0.11)	0.56
11-02	Gp4 Focus 2	g.chr3:78685082G>A	Missense Mutation	ROBO1	p.P1072S	roundabout, axon guida	58 (0.00)	65 (0.11)	0.56
11-02	Gp4 Focus 2	g.chr3:78987858C>T	Missense Mutation	ROBO1	p.R131H	roundabout, axon guida	52 (0.00)	35 (0.29)	1.50
11-02	Gp4 Focus 2	g.chr3:77530311G>A	Missense Mutation	ROBO2	p.C203Y	roundabout, axon guida	31 (0.00)	46 (0.15)	0.80
11-02	Gp4 Focus 2	g.chr9:94493213G>A	Silent	ROR2	p.L388L	receptor tyrosine kinase	19 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr15:72901180G>A	lincRNA	RP11-1006G14.2			24 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr12:57689233C>T	Silent	RP11-123K3.4	p.Q44Q		81 (0.01)	27 (0.70)	1.88
11-02	Gp4 Focus 2	g.chr12:57689286C>T	Missense Mutation	RP11-123K3.4	p.E27K		91 (0.00)	44 (0.95)	2.55
11-02	Gp4 Focus 2	g.chr5:177059465C>T	RNA	RP11-1277A3.2			45 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr17:45131896C>A	RNA	RP11-156P1.3			16 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr17:45131915G>A	RNA	RP11-156P1.3			17 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr17:58050956C>T	lincRNA	RP11-178C3.2			35 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr10:28725880G>A	lincRNA	RP11-351M16.3			46 (0.00)	18 (0.33)	1.12
11-02	Gp4 Focus 2	g.chr17:15501940G>C	Missense Mutation	RP11-385D13.	p.C797W		31 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr14:39819370C>A	Missense Mutation	RP11-407N17.	p.P1308T		49 (0.00)	16 (0.44)	1.39
11-02	Gp4 Focus 2	g.chr13:19761269G>A	Missense Mutation	RP11-408E5.4	p.E15K		31 (0.00)	13 (0.54)	1.85
11-02	Gp4 Focus 2	g.chr5:989895G>A	RNA	RP11-43F13.3			42 (0.00)	51 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:193721433C>T	lincRNA	RP11-699L21.1			20 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr12:56215786T>A	Splice Site	RP11-762I7.5	p.E324D		45 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr17:43626732C>T	lincRNA	RP11-798G7.6			83 (0.00)	42 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr20:21143618G>A	RNA	RP4-777D9.2			35 (0.00)	42 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr1:149398931G>A	RNA	RP5-998N21.10			45 (0.00)	35 (0.51)	1.37
11-02	Gp4 Focus 2	g.chr15:41827061T>A	Missense Mutation	RPAP1	p.Q205L	RNA polymerase II ass	18 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr14:21793131C>T	Missense Mutation	RPGRIP1	p.A706V	retinitis pigmentosa GT	44 (0.00)	12 (0.50)	0.73
11-02	Gp4 Focus 2	g.chr1:24022374G>A	Silent	RPL11	p.E161E	ribosomal protein L11	62 (0.00)	57 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr3:12881006G>A	Silent	RPL32	p.G40G	ribosomal protein L32	43 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr10:15145809G>A	Missense Mutation	RPP38	p.E166K	ribonuclease P/MRP 38	27 (0.00)	20 (0.45)	1.51
11-02	Gp4 Focus 2	g.chr17:78727884G>A	Silent	RPTOR	p.L243L	regulatory associated pr	45 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr9:19050133G>A	Missense Mutation	RRAGA	p.C159Y	Ras-related GTP bindin	19 (0.00)	30 (0.23)	0.76
11-02	Gp4 Focus 2	g.chr9:19050487C>T	Missense Mutation	RRAGA	p.S277L	Ras-related GTP bindin	45 (0.00)	23 (0.52)	1.70
11-02	Gp4 Focus 2	g.chr20:17622562G>A	Silent	RRBP1	p.A255A	ribosome binding protei	31 (0.00)	22 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr10:99118340C>T	Missense Mutation	RRP12	p.D1249N	ribosomal RNA process	60 (0.00)	119 (0.20)	0.54

11-02	Gp4 Focus 2	g.chr1:114310886G>A	Missense Mutation	RSBN1	p.T595M	round spermatid basic p	44 (0.00)	23 (0.43)	0.91
11-02	Gp4 Focus 2	g.chr7:77402564G>A	Missense Mutation	RSBN1L	p.G576R	round spermatid basic p	87 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr7:5967973G>A	Silent	RSPH10B	p.V762V	radial spoke head 10 ho	89 (0.00)	40 (0.72)	2.60
11-02	Gp4 Focus 2	g.chr2:74654604C>T	Missense Mutation	RTKN	p.R351Q	rhotekin	51 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:55253055G>T	Missense Mutation	RTN4	p.P727Q	reticulon 4	49 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr2:55254517G>A	Missense Mutation	RTN4	p.P240S	reticulon 4	20 (0.00)	21 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr3:187416518G>A	Missense Mutation	RTP2	p.P149L	receptor (chemosensory	15 (0.00)	23 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr3:46542010C>A	Missense Mutation	RTP3	p.T107K	receptor (chemosensory	21 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr18:67692085C>T	Splice Site	RTTN		rotatin	27 (0.00)	33 (0.27)	0.87
11-02	Gp4 Focus 2	g.chr21:36206846G>A	Silent	RUNX1	p.S195S	runt-related transcriptio	20 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr3:72457893G>A	Intron	RYBP		RING1 and YY1 bindin	69 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr3:72483805G>A	Intron	RYBP		RING1 and YY1 bindin	132 (0.00)	23 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr19:39034054G>A	Silent	RYR1	p.V3919V	ryanodine receptor 1 (sk	20 (0.00)	32 (0.81)	2.17
11-02	Gp4 Focus 2	g.chr1:237817674G>A	Missense Mutation	RYR2	p.R2642K	ryanodine receptor 2 (ca	35 (0.00)	15 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr1:237817676A>C	Missense Mutation	RYR2	p.K2643Q	ryanodine receptor 2 (ca	35 (0.00)	15 (0.73)	1.96
11-02	Gp4 Focus 2	g.chr1:237817677A>C	Missense Mutation	RYR2	p.K2643T	ryanodine receptor 2 (ca	35 (0.00)	14 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr1:237817678G>T	Missense Mutation	RYR2	p.K2643N	ryanodine receptor 2 (ca	36 (0.00)	14 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr15:33872261G>A	Silent	RYR3	p.Q451Q	ryanodine receptor 3	58 (0.00)	59 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr15:33961617G>A	Silent	RYR3	p.E1894E	ryanodine receptor 3	108 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr15:34064280C>T	Silent	RYR3	p.Y2992Y	ryanodine receptor 3	15 (0.00)	24 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr15:34113528G>A	Missense Mutation	RYR3	p.G3625S	ryanodine receptor 3	24 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr15:34117816G>A	Silent	RYR3	p.L3695L	ryanodine receptor 3	75 (0.01)	79 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr1:153431423G>A	Missense Mutation	S100A7	p.R23C	S100 calcium binding p	22 (0.00)	17 (0.71)	1.88
11-02	Gp4 Focus 2	g.chr13:23905233G>A	Missense Mutation	SACS	p.T4261I	sacsin molecular chaper	45 (0.00)	14 (0.93)	2.48
11-02	Gp4 Focus 2	g.chr2:128773983C>A	Missense Mutation	SAP130	p.A163S	Sin3A-associated protei	43 (0.00)	17 (0.29)	0.95
11-02	Gp4 Focus 2	g.chr2:200246464C>T	Missense Mutation	SATB2	p.M142I	SATB homeobox 2	50 (0.00)	35 (0.37)	0.99
11-02	Gp4 Focus 2	g.chr12:123834862G>A	Nonsense Mutation	SBNO1	p.Q43*	strawberry notch homol	31 (0.00)	54 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr12:123834975C>T	Missense Mutation	SBNO1	p.G5E	strawberry notch homol	45 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr8:73993354C>T	Silent	SBSPON	p.Q103Q	somatomedin B and thr	36 (0.00)	23 (0.22)	0.73
11-02	Gp4 Focus 2	g.chr6:155148329C>T	Missense Mutation	SCAF8	p.P699S	SR-related CTD-associa	123 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr15:76696968C>T	Missense Mutation	SCAPER	p.V1122M	S-phase cyclin A-associ	44 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr4:77095374G>A	Missense Mutation	SCARB2	p.S163L	scavenger receptor class	100 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr15:32983961G>A	Silent	SCG5	p.R180R	secretogranin V (7B2 pr	22 (0.00)	27 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr1:41494282G>A	Missense Mutation	SCMH1	p.P611S	sex comb on midleg ho	21 (0.00)	48 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr1:41512224G>A	Silent	SCMH1	p.N441N	sex comb on midleg ho	32 (0.00)	16 (0.44)	1.17

11-02	Gp4 Focus 2	g.chrX:17768332G>A	Missense Mutation	SCML1	p.G208R	sex comb on midleg-lik	20 (0.00)	15 (0.53)	0.89
11-02	Gp4 Focus 2	g.chr2:165986532G>A	Missense Mutation	SCN3A	p.T947I	sodium channel, voltage	167 (0.00)	23 (0.43)	1.16
11-02	Gp4 Focus 2	g.chr12:52096605C>T	Silent	SCN8A	p.N347N	sodium channel, voltage	48 (0.00)	43 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr12:52096641C>T	Silent	SCN8A	p.A359A	sodium channel, voltage	27 (0.00)	40 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr12:6458142C>T	Silent	SCNN1A	p.Q532Q	sodium channel, non-vo	28 (0.00)	47 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr16:23364149G>A	Silent	SCNN1B	p.K113K	sodium channel, non-vo	31 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr20:18794913G>T	Missense Mutation	SCP2D1	p.D152Y	SCP2 sterol-binding dor	15 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr11:9077376G>A	Nonsense Mutation	SCUBE2	p.R391*	signal peptide, CUB dor	76 (0.00)	25 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr4:76878792C>A	Missense Mutation	SDAD1	p.V550F	SDA1 domain containin	129 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr7:3998593G>A	Missense Mutation	SDK1	p.S394N	sidekick cell adhesion m	37 (0.00)	27 (0.48)	1.72
11-02	Gp4 Focus 2	g.chr9:139354541G>A	Nonsense Mutation	SEC16A	p.Q1498*	SEC16 homolog A (S. c	19 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr9:139366513C>T	Silent	SEC16A	p.A1028A	SEC16 homolog A (S. c	17 (0.00)	28 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr10:75519823G>A	Missense Mutation	SEC24C	p.G177S	SEC24 family member	15 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:119745890C>A	Missense Mutation	SEC24D	p.A45S	SEC24 family member	94 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr9:91964734G>A	Silent	SECISBP2	p.E594E	SECIS binding protein	26 (0.00)	27 (0.19)	0.60
11-02	Gp4 Focus 2	g.chr14:81952684C>T	Missense Mutation	SEL1L	p.E583K	sel-1 suppressor of lin-1	203 (0.00)	92 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr4:25836881C>T	Silent	SEL1L3	p.K266K	sel-1 suppressor of lin-1	73 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:169698692C>T	Missense Mutation	SELE	p.G280R	selectin E	40 (0.00)	47 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr1:169564016C>T	Missense Mutation	SELP	p.C734Y	selectin P (granule mem	43 (0.00)	11 (0.82)	2.18
11-02	Gp4 Focus 2	g.chr9:92017831C>T	Silent	SEMA4D	p.A69A	sema domain, immunog	18 (0.00)	29 (0.17)	0.56
11-02	Gp4 Focus 2	g.chr10:102740355G>A	Missense Mutation	SEMA4G	p.A458T	sema domain, immunog	17 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:151107685C>T	Missense Mutation	SEMA6C	p.V512I	sema domain, transmem	21 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr15:48057118G>A	Missense Mutation	SEMA6D	p.G431E	sema domain, transmem	20 (0.00)	49 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr15:48063797C>T	Nonsense Mutation	SEMA6D	p.Q1013*	sema domain, transmem	36 (0.03)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:185304253C>T	Missense Mutation	SENP2	p.R18W	SUMO1/sentrin/SMT3	30 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr2:242283166G>A	Splice Site	SEPT2		septin 2	62 (0.00)	43 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr17:56602441C>A	Missense Mutation	SEPT4	p.E220D	septin 4	69 (0.00)	32 (0.50)	1.33
11-02	Gp4 Focus 2	g.chrX:118759343C>T	Splice Site	SEPT6		septin 6	32 (0.00)	34 (0.21)	0.46
11-02	Gp4 Focus 2	g.chr5:132097212G>A	Silent	SEPT8	p.Y298Y	septin 8	19 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:48284375G>A	Missense Mutation	SEPW1	p.G40E	selenoprotein W, 1	27 (0.00)	14 (0.64)	1.71
11-02	Gp4 Focus 2	g.chr14:94914748G>A	Missense Mutation	SERPINA11	p.L122F	serpin peptidase inhibit	44 (0.00)	63 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr18:61233905A>G	Silent	SERPINB12	p.E313E	serpin peptidase inhibit	93 (0.00)	27 (0.26)	0.83
11-02	Gp4 Focus 2	g.chr18:61233934C>T	Missense Mutation	SERPINB12	p.T323I	serpin peptidase inhibit	87 (0.01)	37 (0.41)	1.30
11-02	Gp4 Focus 2	g.chr18:61650824G>A	Missense Mutation	SERPINB8	p.E146K	serpin peptidase inhibit	30 (0.00)	29 (0.52)	1.66
11-02	Gp4 Focus 2	g.chr2:224866479G>A	Missense Mutation	SERPINE2	p.P47S	serpin peptidase inhibit	52 (0.00)	24 (0.25)	0.67

11-02	Gp4 Focus 2	g.chr21:37418085C>A	Missense Mutation	SETD4	p.R174I	SET domain containing	84 (0.00)	48 (0.40)	1.06
11-02	Gp4 Focus 2	g.chr3:9483349G>A	Missense Mutation	SETD5	p.D295N	SET domain containing	66 (0.00)	76 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr3:9490288G>A	Missense Mutation	SETD5	p.D774N	SET domain containing	95 (0.00)	25 (0.84)	2.24
11-02	Gp4 Focus 2	g.chr17:27284412G>A	Silent	SEZ6	p.R816R	seizure related 6 homol	55 (0.00)	23 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr17:27306712C>T	Missense Mutation	SEZ6	p.G282S	seizure related 6 homol	27 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr22:26690391G>A	Splice Site	SEZ6L	p.Q323Q	seizure related 6 homol	16 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr22:30741112G>A	Missense Mutation	SF3A1	p.A154V	splicing factor 3a, subu	18 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr11:65830985G>A	Missense Mutation	SF3B2	p.E717K	splicing factor 3b, subu	86 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr12:132210016C>T	Nonsense Mutation	SFSWAP	p.Q225*	splicing factor, suppress	22 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr12:132210038C>T	Missense Mutation	SFSWAP	p.A232V	splicing factor, suppress	20 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr10:102794464C>T	Missense Mutation	SFXN3	p.P5S	sideroflexin 3	114 (0.00)	31 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr6:134493353G>A	Missense Mutation	SGK1	p.S255F	serum/glucocorticoid re	25 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr2:201436345G>A	Missense Mutation	SGOL2	p.G426R	shugoshin-like 2 (S. po	99 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:111884969C>T	Silent	SH2B3	p.L323L	SH2B adaptor protein 3	46 (0.00)	34 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr12:111885157G>A	Missense Mutation	SH2B3	p.D349N	SH2B adaptor protein 3	22 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr19:6754998C>T	Silent	SH2D3A	p.Q275Q	SH2 domain containing	27 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr8:19190612G>A	Missense Mutation	SH2D4A	p.A65T	SH2 domain containing	15 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr4:152095913C>A	Silent	SH3D19	p.V201V	SH3 domain containing	63 (0.02)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr5:171773145C>T	Missense Mutation	SH3PXD2B	p.V395I	SH3 and PX domains 2	23 (0.00)	29 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr4:170038696C>T	Silent	SH3RF1	p.Q585Q	SH3 domain containing	76 (0.00)	36 (0.19)	0.66
11-02	Gp4 Focus 2	g.chr4:170077629G>A	Missense Mutation	SH3RF1	p.P199S	SH3 domain containing	136 (0.00)	45 (0.16)	0.53
11-02	Gp4 Focus 2	g.chr5:148386538G>A	Missense Mutation	SH3TC2	p.S1187F	SH3 domain and tetratri	17 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr5:148386558G>A	Silent	SH3TC2	p.D1180D	SH3 domain and tetratri	16 (0.00)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr5:148407915C>T	Silent	SH3TC2	p.Q453Q	SH3 domain and tetratri	56 (0.00)	31 (0.35)	0.95
11-02	Gp4 Focus 2	g.chr17:18238894G>A	Missense Mutation	SHMT1	p.P304S	serine hydroxymethyltr	64 (0.00)	52 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr10:112724328C>T	Missense Mutation	SHOC2	p.T71M	soc-2 suppressor of clea	39 (0.00)	59 (0.25)	0.68
11-02	Gp4 Focus 2	g.chr17:3526745G>A	Missense Mutation	SHPK	p.H179Y	sedoheptulokinase	28 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:72802708C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	67 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr3:72823993C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	56 (0.00)	54 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr3:72842413C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	29 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr3:72859928C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	91 (0.00)	22 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:72861424T>C	Intron	SHQ1		SHQ1, H/ACA ribonucl	186 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr3:72871584G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	65 (0.00)	49 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr3:72875175C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	42 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr3:72878627C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	38 (0.00)	12 (0.58)	1.56

11-02	Gp4 Focus 2	g.chr3:72880811G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	211 (0.00)	46 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr3:72886427G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	44 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr3:72895662C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	36 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr5:132159573C>T	Missense Mutation	SHROOM1	p.G594R	shroom family member	18 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr4:77670216C>T	Missense Mutation	SHROOM3	p.P1267L	shroom family member	85 (0.00)	21 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr4:77691985G>A	Silent	SHROOM3	p.S1852S	shroom family member	23 (0.00)	32 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr11:124530539C>T	Silent	SIAE	p.Q130Q	sialic acid acetylesteras	53 (0.02)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr11:117063874C>A	Missense Mutation	SIDT2	p.A704D	SID1 transmembrane fa	36 (0.00)	48 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr19:51914589G>A	Missense Mutation	SIGLEC10	p.P477S	sialic acid binding Ig-lik	28 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr5:175740810C>T	Silent	SIMC1	p.N183N	SUMO-interacting moti	28 (0.00)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr5:175740821C>T	Missense Mutation	SIMC1	p.S187F	SUMO-interacting moti	28 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr15:75715144G>A	Silent	SIN3A	p.S70S	SIN3 transcription regul	21 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr1:232581482C>T	Missense Mutation	SIPA1L2	p.S1049N	signal-induced prolifera	48 (0.00)	87 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr6:13599387G>A	Splice Site	SIRT5	p.V247V	sirtuin 5	19 (0.00)	33 (0.15)	0.59
11-02	Gp4 Focus 2	g.chr13:78320946C>T	Missense Mutation	SLAIN1	p.P120L	SLAIN motif family, m	16 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr4:48384828G>A	Missense Mutation	SLAIN2	p.R369Q	SLAIN motif family, m	55 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr1:160719697C>T	Missense Mutation	SLAMF7	p.H155Y	SLAM family member	41 (0.00)	60 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:159799727G>A	Missense Mutation	SLAMF8	p.A38T	SLAM family member	63 (0.00)	75 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:159799748G>A	Missense Mutation	SLAMF8	p.V45I	SLAM family member	62 (0.00)	74 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr4:87744924C>T	Missense Mutation	SLC10A6	p.G351S	solute carrier family 10	45 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr2:219249975C>T	Missense Mutation	SLC11A1	p.L127F	solute carrier family 11	29 (0.00)	56 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr2:219249977C>T	Silent	SLC11A1	p.L127L	solute carrier family 11	30 (0.00)	54 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr16:67985173G>A	Silent	SLC12A4	p.D389D	solute carrier family 12	17 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr20:44676101C>T	Missense Mutation	SLC12A5	p.S599F	solute carrier family 12	28 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr15:34546570G>A	Missense Mutation	SLC12A6	p.S366F	solute carrier family 12	34 (0.00)	51 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr15:34546598C>T	Missense Mutation	SLC12A6	p.A357T	solute carrier family 12	35 (0.00)	44 (0.20)	0.55
11-02	Gp4 Focus 2	g.chr7:135387599G>A	Silent	SLC13A4	p.H208H	solute carrier family 13	15 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:121648195G>A	Splice Site	SLC15A2	p.R518K	solute carrier family 15	28 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr10:91192990C>T	Missense Mutation	SLC16A12	p.R461K	solute carrier family 16,	43 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr6:25850814G>A	Missense Mutation	SLC17A3	p.A289V	solute carrier family 17	36 (0.00)	15 (0.80)	2.13
11-02	Gp4 Focus 2	g.chr8:20022565C>A	Silent	SLC18A1	p.V304V	solute carrier family 18	15 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr6:133097533G>A	Silent	SLC18B1	p.F277F	solute carrier family 18,	32 (0.00)	39 (0.36)	0.96
11-02	Gp4 Focus 2	g.chr6:133100511G>A	Silent	SLC18B1	p.L231L	solute carrier family 18,	16 (0.00)	33 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:4573949C>T	Silent	SLC1A1	p.I270I	solute carrier family 1 (	80 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr9:4585519G>A	Silent	SLC1A1	p.K512K	solute carrier family 1 (	26 (0.00)	21 (0.81)	2.16

11-02	Gp4 Focus 2	g.chr5:36686270G>A	Missense Mutation	SLC1A3	p.G510S	solute carrier family 1 (	83 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr2:113405315G>A	Splice Site	SLC20A1	p.K187K	solute carrier family 20	100 (0.00)	12 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr11:63065107A>T	Silent	SLC22A10	p.I246I	solute carrier family 22,	53 (0.00)	17 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr6:3416009T>A	Silent	SLC22A23	p.L245L	solute carrier family 22,	71 (0.00)	12 (0.83)	1.59
11-02	Gp4 Focus 2	g.chr15:65943220C>T	Silent	SLC24A1	p.Y911Y	solute carrier family 24	18 (0.00)	85 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr15:48426504C>A	Silent	SLC24A5	p.G117G	solute carrier family 24	77 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr2:172644153G>A	Missense Mutation	SLC25A12	p.S588F	solute carrier family 25	84 (0.00)	47 (0.66)	1.76
11-02	Gp4 Focus 2	g.chr6:46637902G>A	Silent	SLC25A27	p.L245L	solute carrier family 25,	21 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr14:100795944G>A	Missense Mutation	SLC25A47	p.E297K	solute carrier family 25,	20 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr5:135215670G>A	Missense Mutation	SLC25A48	p.G222D	solute carrier family 25,	29 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr12:58016900G>A	Missense Mutation	SLC26A10	p.D345N	solute carrier family 26,	15 (0.00)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr1:205904837G>A	Missense Mutation	SLC26A9	p.R38C	solute carrier family 26	23 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr15:85438274G>A	Silent	SLC28A1	p.L127L	solute carrier family 28	15 (0.00)	14 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr12:8074021G>A	Silent	SLC2A3	p.T493T	solute carrier family 2 (	122 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr12:8078497C>T	Silent	SLC2A3	p.E303E	solute carrier family 2 (	151 (0.00)	27 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr5:176824946C>T	Missense Mutation	SLC34A1	p.P527S	solute carrier family 34	20 (0.00)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr5:176825006C>T	Missense Mutation	SLC34A1	p.P547S	solute carrier family 34	21 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr4:25671408G>A	Missense Mutation	SLC34A2	p.D259N	solute carrier family 34	35 (0.00)	45 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr9:99106199C>T	Missense Mutation	SLC35D2	p.G224E	solute carrier family 35	145 (0.00)	59 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr5:150701702G>A	Missense Mutation	SLC36A2	p.A362V	solute carrier family 36	33 (0.00)	52 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr5:150668001G>A	Silent	SLC36A3	p.T145T	solute carrier family 36,	25 (0.00)	24 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr2:165772431C>T	Missense Mutation	SLC38A11	p.V168I	solute carrier family 38,	27 (0.00)	23 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr5:54922437A>G	Missense Mutation	SLC38A9	p.L461P	solute carrier family 38,	98 (0.00)	34 (0.18)	0.59
11-02	Gp4 Focus 2	g.chr18:33702193G>A	Missense Mutation	SLC39A6	p.P394L	solute carrier family 39	82 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr18:33703559G>A	Missense Mutation	SLC39A6	p.P347S	solute carrier family 39	116 (0.00)	77 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr11:62651959G>A	Missense Mutation	SLC3A2	p.V280M	solute carrier family 3 (	30 (0.00)	55 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:190428380C>T	Silent	SLC40A1	p.E444E	solute carrier family 40	33 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:205760742G>A	Silent	SLC41A1	p.D487D	solute carrier family 41	17 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr8:142221615G>A	Missense Mutation	SLC45A4	p.P775S	solute carrier family 45,	49 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr8:142231719G>A	Silent	SLC45A4	p.G78G	solute carrier family 45,	18 (0.00)	41 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr2:162730490G>A	Missense Mutation	SLC4A10	p.G308E	solute carrier family 4,	72 (0.00)	50 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr2:162735649G>A	Silent	SLC4A10	p.L319L	solute carrier family 4,	24 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr4:72319263C>T	Silent	SLC4A4	p.A458A	solute carrier family 4 (	64 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr12:51888798G>T	Missense Mutation	SLC4A8	p.V947L	solute carrier family 4,	39 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr17:4937369G>A	Silent	SLC52A1	p.L139L	solute carrier family 52	20 (0.00)	14 (0.71)	1.90

11-02	Gp4 Focus 2	g.chr17:18863885C>T	Nonsense Mutation	SLC5A10	p.Q125*	solute carrier family 5 (s	34 (0.00)	54 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr17:18863902C>T	Silent	SLC5A10	p.G130G	solute carrier family 5 (s	33 (0.00)	51 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr12:101555779C>T	Missense Mutation	SLC5A8	p.V535M	solute carrier family 5 (s	22 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr19:49797102G>A	Missense Mutation	SLC6A16	p.H534Y	solute carrier family 6, r	83 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr19:49797112G>A	Silent	SLC6A16	p.F530F	solute carrier family 6, r	84 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr17:28548782C>T	Silent	SLC6A4	p.A65A	solute carrier family 6 (r	17 (0.00)	32 (0.41)	1.08
11-02	Gp4 Focus 2	g.chr3:14489139C>T	Silent	SLC6A6	p.Y138Y	solute carrier family 6 (r	80 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr16:68309072C>T	Missense Mutation	SLC7A6	p.A148V	solute carrier family 7 (a	41 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr16:68328643C>T	Missense Mutation	SLC7A6	p.P353L	solute carrier family 7 (a	41 (0.02)	60 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr12:113758238C>T	Missense Mutation	SLC8B1	p.A198T	solute carrier family 8 (s	44 (0.00)	36 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr3:143212577G>A	Silent	SLC9A9	p.N411N	solute carrier family 9, s	62 (0.00)	18 (0.72)	1.93
11-02	Gp4 Focus 2	g.chr20:61299474C>T	Silent	SLCO4A1	p.F583F	solute carrier organic an	88 (0.01)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr17:33585892G>A	Silent	SLFN5	p.E61E	schlafen family member	33 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr5:168175361C>T	Missense Mutation	SLIT3	p.S739N	slit homolog 3 (Drosoph	16 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chrX:144904539C>T	Missense Mutation	SLITRK2	p.A199V	SLIT and NTRK-like fa	21 (0.00)	12 (0.50)	1.20
11-02	Gp4 Focus 2	g.chr3:164907002G>A	Silent	SLITRK3	p.F539F	SLIT and NTRK-like fa	27 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr13:86369794G>C	Missense Mutation	SLITRK6	p.H284D	SLIT and NTRK-like fa	16 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr10:105770621C>T	Silent	SLK	p.L944L	STE20-like kinase	16 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr9:2058440A>G	Silent	SMARCA2	p.E499E	SWI/SNF related, matri	41 (0.00)	20 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr9:2096659G>T	Silent	SMARCA2	p.V962V	SWI/SNF related, matri	29 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr17:61914290G>A	Missense Mutation	SMARCD2	p.P187S	SWI/SNF related, matri	74 (0.00)	67 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr18:2703863G>A	Silent	SMCHD1	p.K607K	structural maintenance c	89 (0.01)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr16:18826862T>A	Missense Mutation	SMG1	p.T3472S	SMG1 phosphatidylinos	88 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr17:2202277G>A	Silent	SMG6	p.N590N	SMG6 nonsense mediat	51 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr22:31485737C>T	Missense Mutation	SMTN	p.P175L	smoothelin	17 (0.00)	15 (0.53)	1.42
11-02	Gp4 Focus 2	g.chr17:62543816T>A	Missense Mutation	SMURF2	p.K658I	SMAD specific E3 ubiq	35 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr2:88390582G>A	Missense Mutation	SMYD1	p.G194S	SET and MYND domai	27 (0.00)	20 (0.80)	2.13
11-02	Gp4 Focus 2	g.chr6:84291985C>T	Missense Mutation	SNAP91	p.G702E	synaptosomal-associate	64 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr19:7986350G>A	Missense Mutation	SNAPC2	p.E76K	small nuclear RNA acti	16 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr7:127484428G>A	Missense Mutation	SND1	p.V432M	staphylococcal nuclease	27 (0.00)	41 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr17:47014458C>T	Silent	SNF8	p.L91L	SNF8, ESCRT-II compl	42 (0.00)	24 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr15:25422050C>T	RNA	SNHG14		small nucleolar RNA ho	46 (0.00)	34 (0.47)	1.73
11-02	Gp4 Focus 2	g.chr15:25423974G>A	RNA	SNHG14		small nucleolar RNA ho	24 (0.00)	28 (0.39)	1.45
11-02	Gp4 Focus 2	g.chr15:25436593G>A	RNA	SNHG14		small nucleolar RNA ho	20 (0.00)	24 (0.29)	1.08
11-02	Gp4 Focus 2	g.chr15:25481304G>A	RNA	SNHG14		small nucleolar RNA ho	46 (0.00)	34 (0.76)	2.82

11-02	Gp4 Focus 2	g.chr2:96953260T>G	Missense Mutation	SNRNP200	p.K1134T	small nuclear ribonucle	50 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr2:96970560G>A	Missense Mutation	SNRNP200	p.T31I	small nuclear ribonucle	20 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:49589702G>A	Missense Mutation	SNRNP70	p.A11T	small nuclear ribonucle	77 (0.00)	55 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr8:51449338C>T	Missense Mutation	SNTG1	p.S217F	syntrophin, gamma 1	19 (0.00)	25 (0.32)	1.08
11-02	Gp4 Focus 2	g.chr17:46198800G>A	Missense Mutation	SNX11	p.R248K	sorting nexin 11	16 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr11:130748419G>A	Silent	SNX19	p.I959I	sorting nexin 19	28 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr16:29370697A>T	RNA	SNX29P2		sorting nexin 29 pseudo	21 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr16:29370717G>T	RNA	SNX29P2		sorting nexin 29 pseudo	20 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr9:115580049G>A	Nonsense Mutation	SNX30	p.W138*	sorting nexin family me	39 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr10:97096742G>A	Missense Mutation	SORBS1	p.H1059Y	sorbin and SH3 domain	17 (0.00)	41 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr4:186598439T>A	Silent	SORBS2	p.L68L	sorbin and SH3 domain	226 (0.00)	43 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr1:109888416C>T	Missense Mutation	SORT1	p.G307D	sortilin 1	128 (0.00)	41 (0.22)	0.46
11-02	Gp4 Focus 2	g.chr1:109888424G>A	Silent	SORT1	p.Y304Y	sortilin 1	125 (0.00)	41 (0.22)	0.46
11-02	Gp4 Focus 2	g.chr2:39262634G>A	Missense Mutation	SOS1	p.A291V	son of sevenless homolo	34 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr5:157065477T>C	Silent	SOX30	p.S547S	SRY (sex determining r	31 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr2:231037654C>T	Missense Mutation	SP110	p.E538K	SP110 nuclear body pro	39 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr2:174819720G>A	Missense Mutation	SP3	p.T507I	Sp3 transcription factor	52 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:118509308G>A	Silent	SPAG17	p.A2152A	sperm associated antige	61 (0.00)	56 (0.20)	0.41
11-02	Gp4 Focus 2	g.chr1:118629585G>A	Missense Mutation	SPAG17	p.P469L	sperm associated antige	44 (0.00)	17 (0.29)	0.61
11-02	Gp4 Focus 2	g.chr17:49054496C>T	Missense Mutation	SPAG9	p.V1152I	sperm associated antige	107 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr4:52927016G>A	Missense Mutation	SPATA18	p.A88T	spermatogenesis associa	17 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr9:43625419G>T	Missense Mutation	SPATA31A6	p.Q1090K	SPATA31 subfamily A,	45 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr9:90534223G>A	RNA	SPATA31C1		SPATA31 subfamily C,	30 (0.00)	37 (0.14)	0.44
11-02	Gp4 Focus 2	g.chr9:90501864C>T	Missense Mutation	SPATA31E1	p.S821F	SPATA31 subfamily E,	29 (0.00)	16 (0.88)	2.82
11-02	Gp4 Focus 2	g.chr17:20108116G>A	Missense Mutation	SPECC1	p.E171K	sperm antigen with calp	58 (0.00)	58 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr17:20108455G>A	Missense Mutation	SPECC1	p.V284I	sperm antigen with calp	68 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr22:24718854G>A	Missense Mutation	SPECC1L	p.D636N	sperm antigen with calp	41 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr1:16258253G>A	Missense Mutation	SPEN	p.V1840I	spen family transcriptio	39 (0.00)	43 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr1:16264028G>A	Missense Mutation	SPEN	p.S3466N	spen family transcriptio	25 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr15:65273277G>A	Silent	SPG21	p.P50P	spastic paraplegia 21 (a	30 (0.00)	47 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:228883158G>A	Silent	SPHKAP	p.L804L	SPHK1 interactor, AKA	37 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:47681490C>T	Intron	SPOP		speckle-type POZ protei	86 (0.00)	12 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr17:47687069G>A	Intron	SPOP		speckle-type POZ protei	52 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr17:47693875C>T	Intron	SPOP		speckle-type POZ protei	43 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr17:47716133C>T	Intron	SPOP		speckle-type POZ protei	104 (0.00)	35 (0.26)	0.69

11-02	Gp4 Focus 2	g.chr17:47716459C>G	Intron	SPOP		speckle-type POZ protei	129 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:153066192G>A	Silent	SPRR2E	p.C12C	small proline-rich protei	26 (0.00)	61 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:131345033G>A	Missense Mutation	SPTAN1	p.D571N	spectrin, alpha, non-eryt	57 (0.00)	36 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr19:41008340C>T	Nonsense Mutation	SPTBN4	p.Q377*	spectrin, beta, non-eryth	19 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr15:42166539C>G	Missense Mutation	SPTBN5	p.S1547T	spectrin, beta, non-eryth	23 (0.00)	41 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr15:42175674C>T	Missense Mutation	SPTBN5	p.V511I	spectrin, beta, non-eryth	43 (0.00)	38 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr15:42185104G>T	Missense Mutation	SPTBN5	p.F124L	spectrin, beta, non-eryth	19 (0.00)	38 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr9:94797146G>A	Missense Mutation	SPTLC1	p.A425V	serine palmitoyltransfer	68 (0.00)	48 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr8:126015658C>T	Missense Mutation	SQLE	p.L178F	squalene epoxidase	73 (0.00)	18 (0.50)	1.71
11-02	Gp4 Focus 2	g.chr5:179249997A>G	Missense Mutation	SQSTM1	p.E82G	sequestosome 1	23 (0.00)	38 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr16:30731638G>A	Silent	SRCAP	p.K991K	Snf2-related CREBBP a	37 (0.00)	35 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr16:30735138G>A	Missense Mutation	SRCAP	p.V1465I	Snf2-related CREBBP a	31 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr17:2224720G>A	Splice Site	SRR		serine racemase	57 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr1:24972490C>T	Nonsense Mutation	SRRM1	p.Q13*	serine/arginine repetitiv	52 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr1:24976528G>A	Missense Mutation	SRRM1	p.E158K	serine/arginine repetitiv	53 (0.02)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr1:24987244C>T	Silent	SRRM1	p.S450S	serine/arginine repetitiv	59 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr1:24993337C>T	Missense Mutation	SRRM1	p.P554S	serine/arginine repetitiv	26 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr16:2817008C>T	Missense Mutation	SRRM2	p.P2160L	serine/arginine repetitiv	19 (0.00)	19 (0.37)	1.18
11-02	Gp4 Focus 2	g.chr6:36566634G>A	Missense Mutation	SRSF3	p.C72Y	serine/arginine-rich spli	65 (0.00)	9 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr2:170657528C>A	Missense Mutation	SSB	p.Q20K	Sjogren syndrome antig	70 (0.00)	16 (0.69)	1.83
11-02	Gp4 Focus 2	g.chr8:53071510C>T	Missense Mutation	ST18	p.C585Y	suppression of tumorige	15 (0.00)	21 (0.29)	0.96
11-02	Gp4 Focus 2	g.chr8:53092798C>T	Missense Mutation	ST18	p.R54K	suppression of tumorige	30 (0.00)	17 (0.35)	1.19
11-02	Gp4 Focus 2	g.chr11:8751599G>T	Nonsense Mutation	ST5	p.S413*	suppression of tumorige	50 (0.00)	104 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr3:186760886G>A	Missense Mutation	ST6GAL1	p.G132D	ST6 beta-galactosamide	16 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr15:93007420C>T	Silent	ST8SIA2	p.Y311Y	ST8 alpha-N-acetyl-neu	35 (0.00)	27 (0.74)	2.44
11-02	Gp4 Focus 2	g.chr7:99795421G>A	Silent	STAG3	p.K362K	stromal antigen 3	37 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr7:99802925C>T	Silent	STAG3	p.Y1052Y	stromal antigen 3	23 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr13:33685012G>A	Silent	STARD13	p.N880N	StAR-related lipid trans	20 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr15:42980385G>A	Missense Mutation	STARD9	p.M2203I	StAR-related lipid trans	60 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr15:42981285G>A	Silent	STARD9	p.K2503K	StAR-related lipid trans	30 (0.00)	16 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr2:191839659C>T	Splice Site	STAT1		signal transducer and ac	34 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr5:171583759C>T	Missense Mutation	STK10	p.A64T	serine/threonine kinase	43 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr2:168931725C>G	Missense Mutation	STK39	p.G369A	serine threonine kinase	56 (0.00)	13 (0.69)	1.85
11-02	Gp4 Focus 2	g.chr17:61784684G>A	Missense Mutation	STRADA	p.R197W	STE20-related kinase ac	25 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr2:202342431G>A	Missense Mutation	STRADB	p.G213E	STE20-related kinase ac	36 (0.00)	10 (0.50)	1.33

11-02	Gp4 Focus 2	g.chr7:129094011C>T	Missense Mutation	STRIP2	p.R187W	striatin interacting prote	26 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr7:129096355G>A	Missense Mutation	STRIP2	p.A304T	striatin interacting prote	16 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr7:129096357T>A	Silent	STRIP2	p.A304A	striatin interacting prote	16 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr7:129096358G>A	Missense Mutation	STRIP2	p.E305K	striatin interacting prote	16 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr16:732188G>A	Silent	STUB1	p.L231L	STIP1 homology and U	36 (0.00)	45 (0.44)	1.42
11-02	Gp4 Focus 2	g.chr1:28128296T>A	Silent	STX12	p.I132I	syntaxin 12	23 (0.00)	11 (0.73)	1.94
11-02	Gp4 Focus 2	g.chr11:59558002G>A	Silent	STX3	p.K100K	syntaxin 3	32 (0.00)	42 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr11:62594850C>T	Missense Mutation	STX5	p.S106N	syntaxin 5	88 (0.00)	23 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr17:53237206G>A	Silent	STXBP4	p.L510L	syntaxin binding protei	93 (0.00)	37 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr7:56141878G>A	Nonsense Mutation	SUMF2	p.W117*	sulfatase modifying fact	44 (0.00)	42 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr7:48033968C>T	Missense Mutation	SUN3	p.E269K	Sad1 and UNC84 domai	45 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr14:21820851G>A	Missense Mutation	SUPT16H	p.P1042L	suppressor of Ty 16 ho	91 (0.00)	50 (0.38)	0.56
11-02	Gp4 Focus 2	g.chr13:37591426G>C	Missense Mutation	SUPT20H	p.P650A	suppressor of Ty 20 ho	115 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr17:27017150C>T	Silent	SUPT6H	p.S1131S	suppressor of Ty 6 hom	48 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr3:33194548C>G	Missense Mutation	SUSD5	p.V526L	sushi domain containing	65 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr9:113170378G>A	Missense Mutation	SVEP1	p.P2478L	sushi, von Willebrand f	22 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:113194761G>A	Silent	SVEP1	p.G1715G	sushi, von Willebrand f	69 (0.01)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr9:113233669G>A	Silent	SVEP1	p.G968G	sushi, von Willebrand f	56 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr11:22848775G>A	Missense Mutation	SVIP	p.P66L	small VCP/p97-interacti	19 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr1:185130049G>A	Missense Mutation	SWT1	p.G26S	SWT1 RNA endoribonu	39 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr8:110587168C>T	Silent	SYBU	p.S652S	syntabulin (syntaxin-int	42 (0.00)	41 (0.22)	0.75
11-02	Gp4 Focus 2	g.chr8:110587201C>T	Silent	SYBU	p.L641L	syntabulin (syntaxin-int	38 (0.00)	45 (0.22)	0.76
11-02	Gp4 Focus 2	g.chr8:110592175G>A	Missense Mutation	SYBU	p.P195L	syntabulin (syntaxin-int	48 (0.00)	48 (0.40)	1.35
11-02	Gp4 Focus 2	g.chr9:93641140G>T	Missense Mutation	SYK	p.A496S	spleen tyrosine kinase	64 (0.00)	35 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr1:33160483C>T	Missense Mutation	SYNC	p.E406K	syncoilin, intermediate	149 (0.00)	55 (0.49)	1.31
11-02	Gp4 Focus 2	g.chr6:152522958C>T	Splice Site	SYNE1		spectrin repeat containi	22 (0.00)	32 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr6:152719773G>A	Missense Mutation	SYNE1	p.A2444V	spectrin repeat containi	63 (0.02)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr6:152720852C>T	Missense Mutation	SYNE1	p.G2379D	spectrin repeat containi	96 (0.00)	31 (0.84)	2.24
11-02	Gp4 Focus 2	g.chr14:64491721C>T	Silent	SYNE2	p.L1978L	spectrin repeat containi	28 (0.00)	37 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr14:64518648C>T	Nonsense Mutation	SYNE2	p.Q2706*	spectrin repeat containi	59 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr14:95912365G>A	Missense Mutation	SYNE3	p.L505F	spectrin repeat containi	32 (0.00)	60 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr21:34018813G>A	Missense Mutation	SYNJ1	p.P1085L	synaptojanin 1	29 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr6:158513996G>A	Missense Mutation	SYNJ2	p.D1202N	synaptojanin 2	20 (0.00)	45 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:119951193G>A	Silent	SYNPO2	p.A421A	synaptopodin 2	43 (0.00)	30 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr14:62547665G>A	Silent	SYT16	p.V369V	synaptotagmin XVI	15 (0.00)	27 (0.70)	1.88

11-02	Gp4 Focus 2	g.chr14:62567230G>C	Silent	SYT16	p.V581V	synaptotagmin XVI	45 (0.00)	48 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:55687131G>A	Silent	SYT5	p.T162T	synaptotagmin V	20 (0.00)	32 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr19:55687144C>T	Missense Mutation	SYT5	p.R158K	synaptotagmin V	21 (0.00)	37 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr1:43902995G>A	Splice Site	SZT2		seizure threshold 2 hom	25 (0.00)	15 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr8:38678075G>A	Missense Mutation	TACC1	p.S438N	transforming, acidic coil	52 (0.00)	51 (0.14)	0.44
11-02	Gp4 Focus 2	g.chr8:38704220C>T	Silent	TACC1	p.A744A	transforming, acidic coil	45 (0.00)	14 (0.57)	1.85
11-02	Gp4 Focus 2	g.chr10:123988921G>A	Missense Mutation	TACC2	p.V731I	transforming, acidic coil	106 (0.00)	16 (0.94)	2.50
11-02	Gp4 Focus 2	g.chr4:104510942C>T	Missense Mutation	TACR3	p.R432K	tachykinin receptor 3	63 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr1:166833146G>A	Missense Mutation	TADA1	p.S82F	transcriptional adaptor 1	30 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr4:7056067G>A	Silent	TADA2B	p.T183T	transcriptional adaptor 2	38 (0.00)	45 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr4:7056130C>A	Silent	TADA2B	p.A204A	transcriptional adaptor 2	48 (0.00)	34 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr4:7056185G>A	Missense Mutation	TADA2B	p.A223T	transcriptional adaptor 2	70 (0.01)	38 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr16:84215651G>A	Silent	TAF1C	p.V245V	TATA box binding prot	26 (0.00)	35 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr9:32630658A>G	Silent	TAF1L	p.A1640A	TAF1 RNA polymerase	38 (0.00)	34 (0.26)	0.71
11-02	Gp4 Focus 2	g.chr1:229738475G>A	Nonsense Mutation	TAF5L	p.Q147*	TAF5-like RNA polyme	48 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr7:99710482G>A	Silent	TAF6	p.G208G	TAF6 RNA polymerase	32 (0.00)	35 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr2:160031540C>T	Missense Mutation	TANC1	p.A527V	tetratricopeptide repeat,	69 (0.00)	42 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:160087281G>A	Missense Mutation	TANC1	p.A1782T	tetratricopeptide repeat,	52 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr17:61492907G>A	Missense Mutation	TANC2	p.A1263T	tetratricopeptide repeat,	77 (0.00)	41 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr16:68934358C>T	Missense Mutation	TANGO6	p.P467S	transport and golgi orga	24 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr2:162036200C>T	Silent	TANK	p.L9L	TRAF family member-a	55 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:29994970C>A	Silent	TAOK2	p.I469I	TAO kinase 2	33 (0.00)	46 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr16:30002165G>A	Missense Mutation	TAOK2	p.E836K	TAO kinase 2	15 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr12:118675954C>T	Missense Mutation	TAOK3	p.E121K	TAO kinase 3	35 (0.00)	26 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:150459987C>T	Missense Mutation	TARS2	p.H21Y	threonyl-tRNA syntheta	38 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr1:150463978G>A	Silent	TARS2	p.Q207Q	threonyl-tRNA syntheta	43 (0.00)	51 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:6631014G>A	Missense Mutation	TAS1R1	p.M79I	taste receptor, type 1, m	26 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr1:6631017G>A	Silent	TAS1R1	p.R80R	taste receptor, type 1, m	26 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr1:6631072G>A	Missense Mutation	TAS1R1	p.G99R	taste receptor, type 1, m	24 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr1:6639231C>T	Missense Mutation	TAS1R1	p.P705S	taste receptor, type 1, m	16 (0.00)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr7:141478894C>T	Silent	TAS2R4	p.S202S	taste receptor, type 2, m	72 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:212988363T>C	Silent	TATDN3	p.N209N	TatD DNase domain co	49 (0.00)	24 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr22:30688373G>T	Silent	TBC1D10A	p.T513T	TBC1 domain family, m	24 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr22:30691770C>T	Silent	TBC1D10A	p.R167R	TBC1 domain family, m	19 (0.00)	20 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr4:6925596C>A	Silent	TBC1D14	p.S160S	TBC1 domain family, m	23 (0.00)	34 (0.21)	0.55

11-02	Gp4 Focus 2	g.chr15:78346454C>T	Missense Mutation	TBC1D2B	p.D146N	TBC1 domain family, m	143 (0.01)	101 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr12:65269520G>A	Silent	TBC1D30	p.R746R	TBC1 domain family, m	45 (0.00)	28 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr17:60344566G>A	RNA	TBC1D3P2		TBC1 domain family, m	26 (0.00)	19 (0.68)	1.82
11-02	Gp4 Focus 2	g.chr17:60348238C>T	RNA	TBC1D3P2		TBC1 domain family, m	29 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr13:75876522C>A	Missense Mutation	TBC1D4	p.R923L	TBC1 domain family, m	25 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chrX:106093273C>T	Missense Mutation	TBC1D8B	p.A619V	TBC1 domain family, m	16 (0.00)	18 (0.44)	0.99
11-02	Gp4 Focus 2	g.chr4:141549485G>A	Silent	TBC1D9	p.L927L	TBC1 domain family, m	57 (0.00)	16 (0.38)	1.71
11-02	Gp4 Focus 2	g.chr3:186272863G>A	Silent	TBCCD1	p.T194T	TBCC domain containin	28 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr1:235582858G>A	Missense Mutation	TBCE	p.V148I	tubulin folding cofactor	43 (0.02)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr14:55895536C>T	Silent	TBPL2	p.Q315Q	TATA box binding prot	70 (0.00)	32 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr14:55903548C>T	Silent	TBPL2	p.Q113Q	TATA box binding prot	33 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr16:30099918C>T	Missense Mutation	TBX6	p.A263T	T-box 6	20 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr16:30100033G>C	Missense Mutation	TBX6	p.T250R	T-box 6	22 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr7:139661915C>T	Silent	TBXAS1	p.L339L	thromboxane A synthas	19 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chrX:102586530G>A	Missense Mutation	TCEAL7	p.D67N	transcription elongation	20 (0.00)	12 (0.75)	1.67
11-02	Gp4 Focus 2	g.chr5:145834688A>G	Silent	TCERG1	p.P43P	transcription elongation	21 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:27375699C>T	Silent	TCF23	p.S203S	transcription factor 23	41 (0.00)	33 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr18:53131314G>A	Missense Mutation	TCF4	p.P67L	transcription factor 4	72 (0.00)	125 (0.22)	0.60
11-02	Gp4 Focus 2	g.chr1:152081849C>T	Missense Mutation	TCHH	p.E1282K	trichohyalin	30 (0.00)	29 (0.34)	0.92
11-02	Gp4 Focus 2	g.chr14:96178615G>T	Missense Mutation	TCL1A	p.P80H	T-cell leukemia/lympho	21 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr11:59633872C>T	Silent	TCN1	p.E24E	transcobalamin I (vitam	35 (0.00)	58 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr5:149758821C>T	Silent	TCOF1	p.N836N	Treacher Collins-France	17 (0.00)	45 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr6:160200980C>T	Missense Mutation	TCP1	p.G413S	t-complex 1	43 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr13:61084872G>A	Missense Mutation	TDRD3	p.G282E	tudor domain containin	87 (0.00)	40 (0.12)	0.65
11-02	Gp4 Focus 2	g.chr6:46660258G>A	Missense Mutation	TDRD6	p.E1465K	tudor domain containin	28 (0.00)	16 (0.62)	1.67
11-02	Gp4 Focus 2	g.chr14:102900876C>T	Silent	TECPR2	p.H574H	tectonin beta-propeller r	15 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr4:65175566G>A	Missense Mutation	TECRL	p.T212I	trans-2,3-enoyl-CoA rec	39 (0.00)	13 (0.62)	3.52
11-02	Gp4 Focus 2	g.chr16:10729657G>A	Missense Mutation	TEKT5	p.P402L	tektin 5	16 (0.00)	31 (0.23)	0.72
11-02	Gp4 Focus 2	g.chr5:167631400G>A	Missense Mutation	TENM2	p.E968K	teneurin transmembrane	25 (0.00)	40 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr5:167642275G>A	Missense Mutation	TENM2	p.R1120K	teneurin transmembrane	60 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr5:167645248G>A	Missense Mutation	TENM2	p.G1212E	teneurin transmembrane	39 (0.03)	36 (0.31)	0.81
11-02	Gp4 Focus 2	g.chr5:167645947G>T	Missense Mutation	TENM2	p.G1445V	teneurin transmembrane	114 (0.00)	60 (0.28)	0.76
11-02	Gp4 Focus 2	g.chr5:167655003G>A	Silent	TENM2	p.A1557A	teneurin transmembrane	134 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr4:183522146C>T	Missense Mutation	TENM3	p.A194V	teneurin transmembrane	77 (0.00)	21 (0.48)	1.27
11-02	Gp4 Focus 2	g.chr4:183714938C>A	Silent	TENM3	p.I2371I	teneurin transmembrane	115 (0.00)	19 (0.58)	1.54

11-02	Gp4 Focus 2	g.chr11:78380008G>T	Missense Mutation	TENM4	p.S2461Y	teneurin transmembrane	51 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr14:20845778C>T	Silent	TEP1	p.R1844R	telomerase-associated p	27 (0.00)	16 (0.38)	0.55
11-02	Gp4 Focus 2	g.chr14:20869175C>T	Missense Mutation	TEP1	p.G398E	telomerase-associated p	95 (0.00)	39 (0.31)	0.45
11-02	Gp4 Focus 2	g.chr8:73958227G>A	Missense Mutation	TERF1	p.R392K	telomeric repeat binding	16 (0.00)	13 (0.62)	2.08
11-02	Gp4 Focus 2	g.chr8:73958263C>A	Missense Mutation	TERF1	p.S404Y	telomeric repeat binding	15 (0.00)	15 (0.53)	1.80
11-02	Gp4 Focus 2	g.chr12:117513086G>A	Missense Mutation	TESC	p.P40S	tescalcin	42 (0.00)	39 (0.44)	1.16
11-02	Gp4 Focus 2	g.chr10:70332861G>A	Missense Mutation	TET1	p.A256T	tet methylcytosine diox	16 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr10:70332878C>T	Silent	TET1	p.T261T	tet methylcytosine diox	18 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:51718582T>A	Missense Mutation	TEX264	p.Y138N	testis expressed 264	22 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr5:135390416C>T	Missense Mutation	TGFBI	p.P426S	transforming growth fac	158 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr3:30713661C>T	Missense Mutation	TGFBR2	p.A329V	transforming growth fac	77 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:30733031G>A	Silent	TGFBR2	p.S548S	transforming growth fac	23 (0.00)	70 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr1:92200488G>A	Missense Mutation	TGFBR3	p.S138L	transforming growth fac	101 (0.00)	23 (0.65)	1.74
11-02	Gp4 Focus 2	g.chr15:43568667C>T	Missense Mutation	TGM7	p.A707T	transglutaminase 7	35 (0.00)	48 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr2:242573374G>A	Silent	THAP4	p.S66S	THAP domain containi	28 (0.00)	53 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr15:39877720C>T	Missense Mutation	THBS1	p.S359F	thrombospondin 1	29 (0.03)	49 (0.22)	0.60
11-02	Gp4 Focus 2	g.chr5:79368152G>A	Missense Mutation	THBS4	p.R500Q	thrombospondin 4	40 (0.00)	54 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr6:128134035G>A	Missense Mutation	THEMIS	p.S505F	thymocyte selection ass	50 (0.00)	26 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr22:29907184C>T	Silent	THOC5	p.L633L	THO complex 5	67 (0.01)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr16:3077045G>T	Nonsense Mutation	THOC6	p.G224*	THO complex 6 homol	18 (0.00)	32 (0.28)	0.90
11-02	Gp4 Focus 2	g.chr1:36752262G>A	Missense Mutation	THRAP3	p.R144K	thyroid hormone recept	38 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr3:24169142T>C	Missense Mutation	THRB	p.N346S	thyroid hormone recept	54 (0.00)	27 (0.30)	0.79
11-02	Gp4 Focus 2	g.chr3:24184992C>T	Splice Site	THRB	p.L261L	thyroid hormone recept	65 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr7:11632921G>A	Missense Mutation	THSD7A	p.P411S	thrombospondin, type I,	105 (0.00)	41 (0.41)	1.48
11-02	Gp4 Focus 2	g.chr2:138000089G>A	Missense Mutation	THSD7B	p.C738Y	thrombospondin, type I,	21 (0.00)	10 (0.70)	2.28
11-02	Gp4 Focus 2	g.chr2:138434111A>T	Missense Mutation	THSD7B	p.H1586L	thrombospondin, type I,	57 (0.00)	40 (0.15)	0.49
11-02	Gp4 Focus 2	g.chr16:20748485C>T	Missense Mutation	THUMPD1	p.R260K	THUMP domain contai	115 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr3:9426277G>A	Missense Mutation	THUMPD3	p.A477T	THUMP domain contai	100 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr21:32638963G>A	Missense Mutation	TIAM1	p.T109I	T-cell lymphoma invasi	20 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr15:90167181C>T	Missense Mutation	TICRR	p.H1214Y	TOPBP1-interacting ch	97 (0.00)	28 (0.54)	1.43
11-02	Gp4 Focus 2	g.chr11:65124017G>A	Nonsense Mutation	TIGD3	p.W246*	tigger transposable elem	33 (0.00)	43 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr17:902125G>A	Silent	TIMM22	p.L115L	translocase of inner mit	26 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr17:902792G>A	Missense Mutation	TIMM22	p.G159D	translocase of inner mit	49 (0.00)	63 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr22:33254092G>A	Silent	TIMP3	p.L135L	TIMP metallopeptidase	33 (0.00)	54 (0.20)	0.54
11-02	Gp4 Focus 2	g.chr3:12195190G>A	Missense Mutation	TIMP4	p.P167L	TIMP metallopeptidase	27 (0.00)	19 (0.26)	0.70

11-02	Gp4 Focus 2	g.chr6:54212223C>T	Silent	TINAG	p.S269S	tubulointerstitial nephrit	48 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr6:54254639G>A	Silent	TINAG	p.R449R	tubulointerstitial nephrit	27 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr17:60637436G>A	Silent	TLK2	p.K260K	tousled-like kinase 2	30 (0.00)	31 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr9:35717709G>T	Silent	TLN1	p.A690A	talin 1	17 (0.00)	28 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr4:187004890C>A	Missense Mutation	TLR3	p.H407N	toll-like receptor 3	126 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chrX:12906459C>T	Silent	TLR7	p.S944S	toll-like receptor 7	46 (0.00)	22 (0.32)	0.53
11-02	Gp4 Focus 2	g.chr12:27127089C>A	Nonsense Mutation	TM7SF3	p.G508*	transmembrane 7 superf	69 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr12:27149747G>A	Missense Mutation	TM7SF3	p.P149L	transmembrane 7 superf	27 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr4:164436609C>T	Silent	TMA16	p.G128G	translation machinery as	41 (0.00)	67 (0.31)	1.07
11-02	Gp4 Focus 2	g.chr16:19485519G>A	Missense Mutation	TMC5	p.V619M	transmembrane channel-	39 (0.00)	49 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr16:19058453C>T	Missense Mutation	TMC7	p.P541L	transmembrane channel-	72 (0.01)	73 (0.16)	0.44
11-02	Gp4 Focus 2	g.chr16:19063042G>A	Missense Mutation	TMC7	p.R592K	transmembrane channel-	66 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr3:129373845G>A	Missense Mutation	TMCC1	p.A214V	transmembrane and coil	110 (0.00)	53 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr5:177022389G>A	Missense Mutation	TMED9	p.S227N	transmembrane emp24	26 (0.00)	36 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr12:129822286G>A	Silent	TMEM132D	p.L398L	transmembrane protein	34 (0.00)	43 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr7:129825032C>T	Splice Site	TMEM209	p.E317E	transmembrane protein	23 (0.00)	46 (0.59)	1.57
11-02	Gp4 Focus 2	g.chr2:27262629C>T	Missense Mutation	TMEM214	p.L516F	transmembrane protein	41 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr2:27262667G>A	Silent	TMEM214	p.A528A	transmembrane protein	39 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr11:123753889G>A	Silent	TMEM225	p.L212L	transmembrane protein	28 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr11:61558006C>T	Silent	TMEM258	p.V19V	transmembrane protein	26 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr19:16791238C>T	Silent	TMEM38A	p.L104L	transmembrane protein	31 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr3:44905741C>T	Missense Mutation	TMEM42	p.S82F	transmembrane protein	61 (0.02)	32 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr6:44106232C>T	Silent	TMEM63B	p.L129L	transmembrane protein	26 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr8:29923613A>G	Silent	TMEM66	p.Y295Y		31 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr8:29923622G>A	Silent	TMEM66	p.Y292Y		30 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr8:128960221G>A	Silent	TMEM75	p.D20D	transmembrane protein	132 (0.00)	30 (0.33)	1.14
11-02	Gp4 Focus 2	g.chr1:156255099C>T	Missense Mutation	TMEM79	p.P28S	transmembrane protein	19 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr1:205053336G>A	Missense Mutation	TMEM81	p.A38V	transmembrane protein	30 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr9:100286501C>T	Missense Mutation	TMOD1	p.R11C	tropomodulin 1	75 (0.00)	26 (0.65)	1.74
11-02	Gp4 Focus 2	g.chr9:100308569G>A	Missense Mutation	TMOD1	p.A75T	tropomodulin 1	44 (0.00)	17 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr15:52075002C>T	Missense Mutation	TMOD2	p.R237C	tropomodulin 2 (neuron	55 (0.02)	30 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr15:52186054C>T	Missense Mutation	TMOD3	p.P180L	tropomodulin 3 (ubiquit	39 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:151146920G>A	Missense Mutation	TMOD4	p.A76V	tropomodulin 4 (muscle	66 (0.00)	53 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr1:151146971G>A	Missense Mutation	TMOD4	p.P59L	tropomodulin 4 (muscle	38 (0.00)	57 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr4:68699101T>A	Splice Site	TMPRSS11D		transmembrane protease	62 (0.00)	47 (0.28)	0.74

11-02	Gp4 Focus 2	g.chr11:117785182C>A	Nonsense Mutation	TMPRSS13	p.E202*	transmembrane protease	41 (0.00)	62 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr21:42859288G>A	Intron	TMPRSS2		transmembrane protease	54 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr21:42859301C>A	Intron	TMPRSS2		transmembrane protease	74 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr21:42877825C>T	Intron	TMPRSS2		transmembrane protease	140 (0.01)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr22:37466551G>A	Missense Mutation	TMPRSS6	p.T605I	transmembrane protease	16 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr19:2410284C>T	Silent	TMPRSS9	p.A348A	transmembrane protease	31 (0.00)	36 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr9:117803253C>T	Missense Mutation	TNC	p.E1605K	tenascin C	57 (0.00)	18 (0.44)	0.93
11-02	Gp4 Focus 2	g.chr6:138200281C>T	Missense Mutation	TNFAIP3	p.P567S	tumor necrosis factor, al	40 (0.00)	35 (0.46)	1.22
11-02	Gp4 Focus 2	g.chr1:173010768C>T	Silent	TNFSF18	p.Q113Q	tumor necrosis factor (li	72 (0.00)	34 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr3:170906507G>A	Missense Mutation	TNIK	p.A208V	TRAF2 and NCK intera	46 (0.00)	44 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr5:150422456C>T	Splice Site	TNIP1		TNFAIP3 interacting pr	89 (0.00)	144 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr8:9413801C>T	Missense Mutation	TNKS	p.P118S	tankyrase, TRF1-interac	70 (0.00)	31 (0.35)	0.95
11-02	Gp4 Focus 2	g.chr8:9437713G>A	Missense Mutation	TNKS	p.A3T	tankyrase, TRF1-interac	76 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr8:9437738G>A	Missense Mutation	TNKS	p.G11E	tankyrase, TRF1-interac	74 (0.00)	37 (0.24)	0.65
11-02	Gp4 Focus 2	g.chr11:57075961C>T	Silent	TNKS1BP1	p.E1408E	tankyrase 1 binding prot	107 (0.00)	56 (0.70)	1.86
11-02	Gp4 Focus 2	g.chr1:175116141C>T	Silent	TNN	p.G1278G	tenascin N	30 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr1:74957806G>C	Missense Mutation	TNNI3K	p.S736T	TNNI3 interacting kinas	33 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr1:175375497G>A	Silent	TNR	p.I118I	tenascin R	29 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:175375513G>A	Missense Mutation	TNR	p.T113I	tenascin R	28 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr1:175375517C>A	Missense Mutation	TNR	p.V112F	tenascin R	27 (0.00)	12 (0.42)	1.11
11-02	Gp4 Focus 2	g.chr16:24802808C>T	Nonsense Mutation	TNRC6A	p.Q949*	trinucleotide repeat cont	33 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr16:24804831C>T	Silent	TNRC6A	p.A1071A	trinucleotide repeat cont	62 (0.00)	28 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr22:40704605G>T	Nonsense Mutation	TNRC6B	p.E600*	trinucleotide repeat cont	49 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr17:76045569G>A	Silent	TNRC6C	p.G142G	trinucleotide repeat cont	49 (0.02)	16 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr17:76045674G>A	Silent	TNRC6C	p.Q177Q	trinucleotide repeat cont	36 (0.00)	14 (0.79)	2.10
11-02	Gp4 Focus 2	g.chr7:47467955C>T	Missense Mutation	TNS3	p.G115E	tensin 3	34 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr20:43580534C>T	Missense Mutation	TOMM34	p.E164K	translocase of outer mit	31 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr1:161198840C>T	Silent	TOMM40L	p.H294H	translocase of outer mit	32 (0.00)	26 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr8:144406268C>T	Silent	TOP1MT	p.R189R	topoisomerase (DNA) I,	32 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr3:25639942C>T	Silent	TOP2B	p.Q1574Q	topoisomerase (DNA) I	134 (0.00)	41 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr3:133356756G>A	Silent	TOPBP1	p.S828S	topoisomerase (DNA) I	141 (0.00)	42 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr1:179886604C>T	Nonsense Mutation	TOR1AIP1	p.Q328*	torsin A interacting prot	258 (0.00)	34 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr1:179886625A>G	Missense Mutation	TOR1AIP1	p.R335G	torsin A interacting prot	255 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr16:52484455G>T	Missense Mutation	TOX3	p.Q138K	TOX high mobility grou	31 (0.00)	38 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:24303783C>T	Silent	TP53I3	p.Q175Q	tumor protein p53 induc	158 (0.00)	21 (0.24)	0.63

11-02	Gp4 Focus 2	g.chr12:113722424G>A	Missense Mutation	TPCN1	p.E393K	two pore segment chann	33 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr6:125578259C>T	Silent	TPD52L1	p.F147F	tumor protein D52-like	31 (0.00)	39 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr12:72366298G>T	Splice Site	TPH2		tryptophan hydroxylase	66 (0.00)	99 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr11:6638023G>A	Missense Mutation	TPP1	p.A252V	tripeptidyl peptidase I	20 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr13:103279443C>T	Missense Mutation	TPP2	p.A289V	tripeptidyl peptidase II	93 (0.00)	58 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr13:103279456C>T	Silent	TPP2	p.S293S	tripeptidyl peptidase II	94 (0.00)	53 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr3:188925229G>A	Missense Mutation	TPRG1	p.G19E	tumor protein p63 regul	40 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr3:189028287C>T	Missense Mutation	TPRG1	p.P198S	tumor protein p63 regul	20 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr13:45964656G>A	RNA	TPT1-AS1		TPT1 antisense RNA 1	37 (0.03)	33 (0.42)	1.13
11-02	Gp4 Focus 2	g.chr20:30380615G>A	Missense Mutation	TPX2	p.M497I	TPX2, microtubule-assc	55 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr2:85069126G>A	Silent	TRABD2A	p.I225I	TraB domain containing	23 (0.00)	31 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr17:27076257G>A	Missense Mutation	TRAF4	p.E359K	TNF receptor-associate	40 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr17:27076301C>A	Silent	TRAF4	p.A373A	TNF receptor-associate	36 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr12:112589656G>A	Missense Mutation	TRAFD1	p.G444E	TRAF-type zinc finger	43 (0.00)	30 (0.27)	0.71
11-02	Gp4 Focus 2	g.chr3:36873711G>T	Missense Mutation	TRANK1	p.L1861I	tetratricopeptide repeat	52 (0.00)	11 (0.73)	1.94
11-02	Gp4 Focus 2	g.chr3:36875047G>A	Silent	TRANK1	p.T1415T	tetratricopeptide repeat	31 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr14:22434157G>A	RNA	TRAV12-3		T cell receptor alpha va	27 (0.00)	18 (0.44)	0.65
11-02	Gp4 Focus 2	g.chr14:22434193G>A	RNA	TRAV12-3		T cell receptor alpha va	20 (0.00)	13 (0.46)	0.68
11-02	Gp4 Focus 2	g.chr14:22521050C>T	RNA	TRAV21		T cell receptor alpha va	51 (0.00)	14 (0.50)	0.73
11-02	Gp4 Focus 2	g.chr7:142498811G>A	RNA	TRBC2		T cell receptor beta cons	25 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr7:142197691C>A	lincRNA	TRBV11-2		T cell receptor beta vari	36 (0.00)	18 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr9:33629545G>A	RNA	TRBV21OR9-2		T cell receptor beta vari	17 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr14:22564652G>A	RNA	TRDV1		T cell receptor delta var	230 (0.00)	19 (0.37)	0.54
11-02	Gp4 Focus 2	g.chr6:42224714G>A	Silent	TRERF1	p.D821D	transcriptional regulatin	19 (0.00)	25 (0.28)	0.75
11-02	Gp4 Focus 2	g.chr7:38305246G>A	RNA	TRGC1		T cell receptor gamma c	149 (0.00)	41 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr17:18638478G>A	Nonsense Mutation	TRIM16L	p.W251*	tripartite motif containi	45 (0.00)	26 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr1:228596932G>A	Missense Mutation	TRIM17	p.T275I	tripartite motif containi	19 (0.00)	30 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr11:6472258G>A	Silent	TRIM3	p.P578P	tripartite motif containi	32 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr9:119460545A>T	Missense Mutation	TRIM32	p.K175M	tripartite motif containi	36 (0.00)	29 (0.31)	0.65
11-02	Gp4 Focus 2	g.chr5:180651378G>A	Missense Mutation	TRIM41	p.E127K	tripartite motif containi	22 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr11:35685285G>A	Missense Mutation	TRIM44	p.G209D	tripartite motif containi	121 (0.00)	18 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:155148497G>A	Silent	TRIM46	p.L153L	tripartite motif containi	53 (0.00)	53 (0.25)	0.65
11-02	Gp4 Focus 2	g.chr7:72738755C>A	Nonsense Mutation	TRIM50	p.E11*	tripartite motif containi	16 (0.00)	36 (0.14)	0.60
11-02	Gp4 Focus 2	g.chr7:100730631C>T	Missense Mutation	TRIM56	p.A13V	tripartite motif containi	30 (0.00)	42 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr11:8641059G>C	Missense Mutation	TRIM66	p.I1110M	tripartite motif containi	15 (0.00)	18 (0.28)	0.74

11-02	Gp4 Focus 2	g.chr11:8671396G>A	Silent	TRIM66	p.I16I	tripartite motif containir	42 (0.00)	18 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:104414987G>A	Missense Mutation	TRIM8	p.G273R	tripartite motif containir	27 (0.00)	54 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr2:230679858G>A	Missense Mutation	TRIP12	p.S218F	thyroid hormone recepto	75 (0.01)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr19:13226154G>A	Missense Mutation	TRMT1	p.R194C	tRNA methyltransferase	26 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr2:29092467C>T	Missense Mutation	TRMT61B	p.G226E	tRNA methyltransferase	163 (0.00)	21 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr12:49722991G>A	Silent	TROAP	p.R356R	trophinin associated pro	64 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr8:72975788G>A	Missense Mutation	TRPA1	p.P191S	transient receptor potent	23 (0.00)	26 (0.46)	1.56
11-02	Gp4 Focus 2	g.chr4:122828602G>A	Missense Mutation	TRPC3	p.P638L	transient receptor potent	95 (0.00)	19 (0.32)	0.84
11-02	Gp4 Focus 2	g.chr11:101374793C>T	Missense Mutation	TRPC6	p.E303K	transient receptor potent	24 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr15:31358283G>A	Silent	TRPM1	p.N262N	transient receptor potent	22 (0.00)	25 (0.72)	1.92
11-02	Gp4 Focus 2	g.chr9:77353401G>A	Silent	TRPM6	p.L1900L	transient receptor potent	30 (0.00)	14 (0.36)	1.15
11-02	Gp4 Focus 2	g.chr7:142573326G>A	Silent	TRPV6	p.Y339Y	transient receptor potent	42 (0.00)	65 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr7:142573329C>T	Silent	TRPV6	p.L338L	transient receptor potent	25 (0.00)	66 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr13:45010762C>T	Start Codon SNP	TSC22D1	p.M1I	TSC22 domain family, ı	176 (0.00)	66 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr13:45149714C>T	Missense Mutation	TSC22D1	p.G166E	TSC22 domain family, ı	30 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr17:73519744G>A	Splice Site	TSEN54	p.R438R	TSEN54 tRNA splicing	22 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr12:58180005C>T	Silent	TSFM	p.L97L	Ts translation elongatio	29 (0.00)	23 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr1:115576721A>T	Missense Mutation	TSHB	p.Y97F	thyroid stimulating horn	94 (0.00)	11 (0.55)	1.14
11-02	Gp4 Focus 2	g.chr19:11408922C>T	Silent	TSPAN16	p.G58G	tetraspanin 16	34 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr11:44948263C>T	Silent	TSPAN18	p.Y218Y	tetraspanin 18	38 (0.00)	17 (0.94)	2.51
11-02	Gp4 Focus 2	g.chr7:128806629G>T	Missense Mutation	TSPAN33	p.C157F	tetraspanin 33	64 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr17:2235560C>T	Missense Mutation	TSR1	p.A467T	TSR1, 20S rRNA accun	50 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr17:2235566C>T	Missense Mutation	TSR1	p.E465K	TSR1, 20S rRNA accun	47 (0.00)	19 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr17:2236302C>T	Missense Mutation	TSR1	p.E420K	TSR1, 20S rRNA accun	74 (0.00)	24 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr17:2236311C>T	Missense Mutation	TSR1	p.D417N	TSR1, 20S rRNA accun	72 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr15:43086925C>T	Silent	TTBK2	p.K264K	tau tubulin kinase 2	26 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr5:34840816G>T	Missense Mutation	TTC23L	p.D14Y	tetratricopeptide repeat (	155 (0.00)	107 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:32897407G>A	Missense Mutation	TTC27	p.M336I	tetratricopeptide repeat (	42 (0.00)	43 (0.35)	0.93
11-02	Gp4 Focus 2	g.chr2:178416795C>T	Missense Mutation	TTC30B	p.G233S	tetratricopeptide repeat (	64 (0.00)	32 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr5:94861333G>A	Silent	TTC37	p.S393S	tetratricopeptide repeat (	88 (0.00)	62 (0.66)	1.76
11-02	Gp4 Focus 2	g.chr14:71134411C>T	Silent	TTC9	p.D179D	tetratricopeptide repeat (	92 (0.01)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr1:117617555C>G	Missense Mutation	TTF2	p.H117D	transcription terminatio	31 (0.00)	15 (0.33)	0.70
11-02	Gp4 Focus 2	g.chr20:36640417G>A	Missense Mutation	TTI1	p.T601I	TELO2 interacting prot	83 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr20:36641891G>A	Nonsense Mutation	TTI1	p.Q110*	TELO2 interacting prot	57 (0.00)	13 (0.46)	1.23
11-02	Gp4 Focus 2	g.chr22:43464591C>A	Missense Mutation	TTLL1	p.V110F	tubulin tyrosine ligase-li	24 (0.00)	30 (0.20)	0.53

11-02	Gp4 Focus 2	g.chr6:167755081G>A	Missense Mutation	TTLL2	p.A565T	tubulin tyrosine ligase-li	22 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr14:76149971G>A	Missense Mutation	TTLL5	p.E115K	tubulin tyrosine ligase-li	69 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr14:76259418G>A	Missense Mutation	TTLL5	p.S1064N	tubulin tyrosine ligase-li	74 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr2:179396658G>T	Nonsense Mutation	TTN	p.S34895*	titin	15 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr2:179397366G>A	Missense Mutation	TTN	p.S34659F	titin	111 (0.00)	45 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr2:179403771G>A	Missense Mutation	TTN	p.P32964L	titin	61 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr2:179429322G>A	Silent	TTN	p.A27179A	titin	27 (0.00)	38 (0.18)	0.49
11-02	Gp4 Focus 2	g.chr2:179434585G>A	Missense Mutation	TTN	p.S25425F	titin	61 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:179439690G>A	Silent	TTN	p.V23723V	titin	43 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr2:179462359G>A	Silent	TTN	p.I19150I	titin	61 (0.00)	13 (0.77)	2.05
11-02	Gp4 Focus 2	g.chr2:179529450G>A	Nonsense Mutation	TTN	p.Q12045*	titin	64 (0.00)	29 (0.48)	1.29
11-02	Gp4 Focus 2	g.chr2:179529649G>A	Silent	TTN	p.P12016P	titin	45 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr2:179544132G>A	Missense Mutation	TTN	p.P11226S	titin	97 (0.01)	32 (0.78)	2.08
11-02	Gp4 Focus 2	g.chr2:179598351T>A	Missense Mutation	TTN	p.L5255F	titin	141 (0.00)	25 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr2:179605561G>A	Silent	TTN	p.C4133C	titin	130 (0.01)	85 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr2:179664331G>A	Missense Mutation	TTN	p.P266L	titin	27 (0.00)	41 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr11:8118952G>A	Missense Mutation	TUB	p.D289N	tubby bipartite transcrip	23 (0.00)	28 (0.71)	1.90
11-02	Gp4 Focus 2	g.chr12:49522569C>T	Silent	TUBA1B	p.Q176Q	tubulin, alpha 1b	30 (0.00)	41 (0.20)	0.52
11-02	Gp4 Focus 2	g.chr12:49522581G>A	Silent	TUBA1B	p.Y172Y	tubulin, alpha 1b	33 (0.00)	47 (0.17)	0.45
11-02	Gp4 Focus 2	g.chr12:49666119C>T	Silent	TUBA1C	p.L153L	tubulin, alpha 1c	16 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr12:49666823G>A	Nonsense Mutation	TUBA1C	p.W388*	tubulin, alpha 1c	74 (0.00)	22 (0.36)	0.97
11-02	Gp4 Focus 2	g.chr2:132238049G>T	Silent	TUBA3D	p.P261P	tubulin, alpha 3d	36 (0.00)	21 (0.29)	0.92
11-02	Gp4 Focus 2	g.chr20:57599118C>A	Missense Mutation	TUBB1	p.F212L	tubulin, beta 1 class VI	69 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr16:90161729C>T	RNA	TUBB8P7		tubulin, beta 8 class VII	24 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr22:31369004G>A	RNA	TUG1		taurine up-regulated 1 (	85 (0.00)	56 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr12:3042656G>A	Missense Mutation	TULP3	p.D257N	tubby like protein 3	33 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr12:3043631C>T	Silent	TULP3	p.T276T	tubby like protein 3	20 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr7:19738143C>T	Nonsense Mutation	TWISTNB	p.W271*	TWIST neighbor	42 (0.00)	53 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr9:12695757G>A	Missense Mutation	TYRP1	p.E210K	tyrosinase-related protei	46 (0.00)	29 (0.21)	0.67
11-02	Gp4 Focus 2	g.chr4:68514860C>T	Missense Mutation	UBA6	p.A392T	ubiquitin-like modifier	64 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr9:138847147C>T	Missense Mutation	UBAC1	p.D85N	UBA domain containing	39 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr1:154227784C>T	Missense Mutation	UBAP2L	p.T689I	ubiquitin associated pro	41 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr19:59068460G>A	Silent	UBE2M	p.L58L	ubiquitin-conjugating e	21 (0.00)	29 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr17:74394607G>T	Silent	UBE2O	p.G614G	ubiquitin-conjugating e	26 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr15:76168580G>A	Missense Mutation	UBE2Q2	p.R214K	ubiquitin-conjugating e	62 (0.00)	58 (0.33)	0.87

11-02	Gp4 Focus 2	g.chr17:46990269C>T	Missense Mutation	UBE2Z	p.P155L	ubiquitin-conjugating er	40 (0.00)	49 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr16:23569581G>A	Silent	UBFD1	p.Q112Q	ubiquitin family domain	28 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr7:138969274G>T	Missense Mutation	UBN2	p.R1208I	ubinuclein 2	35 (0.00)	31 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr6:42630006G>A	Missense Mutation	UBR2	p.C1176Y	ubiquitin protein ligase	18 (0.00)	20 (0.65)	1.73
11-02	Gp4 Focus 2	g.chr1:19440206G>A	Missense Mutation	UBR4	p.S3815F	ubiquitin protein ligase	50 (0.00)	62 (0.18)	0.47
11-02	Gp4 Focus 2	g.chr1:19440230C>T	Missense Mutation	UBR4	p.C3807Y	ubiquitin protein ligase	56 (0.00)	64 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr1:19467886T>A	Missense Mutation	UBR4	p.M2815L	ubiquitin protein ligase	17 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr1:19478832G>A	Missense Mutation	UBR4	p.T2324I	ubiquitin protein ligase	62 (0.00)	22 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr1:19491361C>T	Silent	UBR4	p.Q1481Q	ubiquitin protein ligase	30 (0.00)	33 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr1:19511610G>T	Missense Mutation	UBR4	p.R641S	ubiquitin protein ligase	41 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr1:19511644C>T	Silent	UBR4	p.Q629Q	ubiquitin protein ligase	40 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr8:103297785G>A	Missense Mutation	UBR5	p.P1808S	ubiquitin protein ligase	50 (0.00)	19 (0.53)	1.40
11-02	Gp4 Focus 2	g.chr8:103307862G>A	Splice Site	UBR5		ubiquitin protein ligase	64 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr10:99327838G>A	Missense Mutation	UBTD1	p.A80T	ubiquitin domain contai	21 (0.00)	49 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr5:171639034G>A	Missense Mutation	UBTD2	p.R169C	ubiquitin domain contai	67 (0.01)	43 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr9:134401363G>A	Splice Site	UCK1	p.T202I	uridine-cytidine kinase	25 (0.00)	33 (0.27)	0.73
11-02	Gp4 Focus 2	g.chr11:73687963G>A	Missense Mutation	UCP2	p.A146V	uncoupling protein 2 (m	20 (0.00)	40 (0.68)	1.80
11-02	Gp4 Focus 2	g.chr1:161126778C>A	Missense Mutation	UFC1	p.F54L	ubiquitin-fold modifier	33 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr2:234676937G>A	Missense Mutation	UGT1A6	p.V385I	UDP glucuronosyltrans	21 (0.00)	40 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr12:100478296G>A	Missense Mutation	UHRF1BP1L	p.P416S	UHRF1 binding protein	46 (0.00)	82 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr5:176370393G>A	Missense Mutation	UIMC1	p.P514S	ubiquitin interaction mo	68 (0.00)	40 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr21:43541228C>T	Silent	UMODL1	p.D907D	uromodulin-like 1	38 (0.00)	43 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr9:35243322C>T	Silent	UNC13B	p.Y143Y	unc-13 homolog B (C. e	96 (0.00)	66 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:35399209G>A	Silent	UNC13B	p.L1293L	unc-13 homolog B (C. e	30 (0.00)	18 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr15:54306980G>A	Missense Mutation	UNC13C	p.S627N	unc-13 homolog C (C. e	52 (0.00)	44 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr17:73831004C>T	Silent	UNC13D	p.V663V	unc-13 homolog D (C.	35 (0.00)	49 (0.31)	0.82
11-02	Gp4 Focus 2	g.chr14:94100969G>A	Missense Mutation	UNC79	p.S1763N	unc-79 homolog (C. ele	52 (0.00)	77 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr2:210678443C>T	Nonsense Mutation	UNC80	p.R360*	unc-80 homolog (C. ele	51 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr2:210782666C>A	Missense Mutation	UNC80	p.A1661E	unc-80 homolog (C. ele	16 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr19:18974285C>A	Nonsense Mutation	UPF1	p.S880*	UPF1 regulator of nons	19 (0.00)	98 (0.28)	0.73
11-02	Gp4 Focus 2	g.chr10:11997364G>A	Missense Mutation	UPF2	p.S906F	UPF2 regulator of nons	34 (0.00)	11 (0.45)	1.52
11-02	Gp4 Focus 2	g.chr7:48139385G>A	Splice Site	UPP1		uridine phosphorylase 1	40 (0.00)	31 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr2:158974411G>A	Missense Mutation	UPP2	p.D139N	uridine phosphorylase 2	68 (0.00)	39 (0.15)	0.41
11-02	Gp4 Focus 2	g.chr2:158991377G>A	Missense Mutation	UPP2	p.R310K	uridine phosphorylase 2	51 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr2:158991399C>T	Silent	UPP2	p.D317D	uridine phosphorylase 2	51 (0.00)	34 (0.26)	0.71

11-02	Gp4 Focus 2	g.chr21:33745974C>T	Silent	URB1	p.V286V	URB1 ribosome biogen	37 (0.00)	41 (0.66)	1.76
11-02	Gp4 Focus 2	g.chr1:229772088G>A	Missense Mutation	URB2	p.M576I	URB2 ribosome biogen	35 (0.00)	74 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr1:229787071T>A	Splice Site	URB2		URB2 ribosome biogen	24 (0.00)	15 (0.47)	1.24
11-02	Gp4 Focus 2	g.chr1:215847811C>T	Missense Mutation	USH2A	p.R4481K	Usher syndrome 2A (au	33 (0.00)	19 (0.47)	1.26
11-02	Gp4 Focus 2	g.chr1:62914196C>T	Missense Mutation	USP1	p.S494L	ubiquitin specific peptid	24 (0.00)	22 (0.32)	0.85
11-02	Gp4 Focus 2	g.chr16:84773939C>T	Silent	USP10	p.L39L	ubiquitin specific peptid	77 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:84778297T>C	Silent	USP10	p.T70T	ubiquitin specific peptid	152 (0.00)	17 (0.35)	0.94
11-02	Gp4 Focus 2	g.chr11:119229502C>T	Silent	USP2	p.R406R	ubiquitin specific peptid	20 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:161135217G>A	Missense Mutation	USP21	p.E560K	ubiquitin specific peptid	17 (0.00)	10 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr1:55613367G>A	Silent	USP24	p.G691G	ubiquitin specific peptid	50 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr11:113670056G>A	Missense Mutation	USP28	p.P1047L	ubiquitin specific peptid	40 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr12:109519824G>A	Splice Site	USP30	p.K258K	ubiquitin specific peptid	45 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr16:23096953A>G	Silent	USP31	p.T551T	ubiquitin specific peptid	76 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr17:58288845C>T	Missense Mutation	USP32	p.S737N	ubiquitin specific peptid	31 (0.00)	42 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr2:61441451C>T	Missense Mutation	USP34	p.C2809Y	ubiquitin specific peptid	66 (0.00)	50 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr2:61575125C>A	Missense Mutation	USP34	p.C722F	ubiquitin specific peptid	16 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr4:53468111G>A	Silent	USP46	p.L278L	ubiquitin specific peptid	54 (0.00)	72 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr11:11969656G>A	Missense Mutation	USP47	p.D1106N	ubiquitin specific peptid	90 (0.01)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr12:6971709G>A	Silent	USP5	p.V583V	ubiquitin specific peptid	37 (0.00)	16 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr10:75276980C>G	Silent	USP54	p.L1068L	ubiquitin specific peptid	61 (0.00)	18 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:11505240C>T	Missense Mutation	USP6NL	p.A563T	USP6 N-terminal like	30 (0.00)	36 (0.19)	0.65
11-02	Gp4 Focus 2	g.chrX:41057873C>T	Silent	USP9X	p.V1491V	ubiquitin specific peptid	21 (0.00)	21 (0.52)	0.87
11-02	Gp4 Focus 2	g.chr13:31233114C>T	Missense Mutation	USPL1	p.T967I	ubiquitin specific peptid	22 (0.00)	35 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr13:52604415C>A	Missense Mutation	UTP14C	p.P492Q	UTP14, U3 small nucle	188 (0.01)	103 (0.17)	0.47
11-02	Gp4 Focus 2	g.chr4:71555794G>A	Missense Mutation	UTP3	p.G467D	UTP3, small subunit (S	135 (0.00)	60 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr6:144814583G>C	Silent	UTRN	p.L1528L	utrophin	42 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr6:144820435G>A	Missense Mutation	UTRN	p.A1546T	utrophin	51 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr11:75851803C>A	Missense Mutation	UVRAG	p.S110R	UV radiation resistance	56 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr11:75852420C>A	Missense Mutation	UVRAG	p.S316Y	UV radiation resistance	55 (0.00)	34 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr2:106717565C>T	Silent	UXS1	p.V311V	UDP-glucuronate decar	19 (0.00)	14 (0.43)	1.14
11-02	Gp4 Focus 2	g.chr16:70765435G>A	Missense Mutation	VAC14	p.R542W	Vac14 homolog (S. cere	42 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr1:213146187G>A	Missense Mutation	VASH2	p.E255K	vasohibin 2	18 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr1:213146197G>A	Missense Mutation	VASH2	p.S258N	vasohibin 2	20 (0.00)	11 (0.64)	1.70
11-02	Gp4 Focus 2	g.chr1:101198024G>T	Nonsense Mutation	VCAM1	p.E526*	vascular cell adhesion	51 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr1:101198225G>A	Missense Mutation	VCAM1	p.E593K	vascular cell adhesion	38 (0.00)	41 (0.29)	0.78

11-02	Gp4 Focus 2	g.chr9:35057491G>A	Nonsense Mutation	VCP	p.R733*	valosin containing prote	27 (0.00)	39 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr9:35068274C>G	Missense Mutation	VCP	p.D35H	valosin containing prote	56 (0.00)	55 (0.33)	0.87
11-02	Gp4 Focus 2	g.chr9:35068312C>A	Missense Mutation	VCP	p.R22L	valosin containing prote	64 (0.00)	63 (0.52)	1.40
11-02	Gp4 Focus 2	g.chr9:35068314G>A	Silent	VCP	p.N21N	valosin containing prote	64 (0.00)	64 (0.52)	1.38
11-02	Gp4 Focus 2	g.chr8:67576857G>A	Silent	VCPIP1	p.I779I	valosin containing prote	77 (0.01)	38 (0.26)	0.89
11-02	Gp4 Focus 2	g.chr19:57966931G>A	Silent	VN1R1	p.T308T	vomeronasal 1 receptor	32 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr3:51452215C>A	Missense Mutation	VPRBP	p.D785Y	Vpr (HIV-1) binding pr	56 (0.00)	32 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr1:12368665G>A	Missense Mutation	VPS13D	p.R2206K	vacuolar protein sorting	27 (0.00)	82 (0.26)	0.68
11-02	Gp4 Focus 2	g.chr1:12368669G>A	Silent	VPS13D	p.L2207L	vacuolar protein sorting	26 (0.00)	77 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr1:12405486C>A	Missense Mutation	VPS13D	p.Q2981K	vacuolar protein sorting	72 (0.00)	23 (0.52)	1.39
11-02	Gp4 Focus 2	g.chr1:12568974G>A	Missense Mutation	VPS13D	p.V4355I	vacuolar protein sorting	59 (0.00)	36 (0.19)	0.52
11-02	Gp4 Focus 2	g.chr20:2841704C>T	Missense Mutation	VPS16	p.T240I	vacuolar protein sorting	61 (0.00)	40 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr17:40925850G>A	Silent	VPS25	p.V51V	vacuolar protein sorting	26 (0.00)	10 (0.70)	1.87
11-02	Gp4 Focus 2	g.chr12:122745942G>A	Missense Mutation	VPS33A	p.R117C	vacuolar protein sorting	85 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr15:91549642G>A	Missense Mutation	VPS33B	p.S271F	vacuolar protein sorting	29 (0.00)	21 (0.24)	0.78
11-02	Gp4 Focus 2	g.chr1:151150503G>A	Silent	VPS72	p.P227P	vacuolar protein sorting	52 (0.00)	26 (0.27)	0.72
11-02	Gp4 Focus 2	g.chr10:116014694G>A	Missense Mutation	VWA2	p.V50M	von Willebrand factor A	15 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr2:215440449G>A	Missense Mutation	VWC2L	p.V192M	von Willebrand factor C	65 (0.00)	32 (0.44)	1.17
11-02	Gp4 Focus 2	g.chr2:215440523C>A	Nonsense Mutation	VWC2L	p.C216*	von Willebrand factor C	60 (0.00)	17 (0.53)	1.41
11-02	Gp4 Focus 2	g.chr1:119619134G>A	Nonsense Mutation	WARS2	p.Q63*	tryptophanyl tRNA synt	44 (0.00)	26 (0.23)	0.48
11-02	Gp4 Focus 2	g.chr6:110423330G>A	Missense Mutation	WASF1	p.P328L	WAS protein family, m	92 (0.00)	101 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr7:123332706G>A	Missense Mutation	WASL	p.P348S	Wiskott-Aldrich syndro	21 (0.00)	87 (0.29)	0.77
11-02	Gp4 Focus 2	g.chr13:41639401G>T	Missense Mutation	WBP4	p.L80F	WW domain binding pr	28 (0.00)	26 (0.19)	0.51
11-02	Gp4 Focus 2	g.chr7:71036328G>A	Missense Mutation	WBSCR17	p.G341S	Williams-Beuren syndr	35 (0.00)	18 (0.28)	1.20
11-02	Gp4 Focus 2	g.chr4:85661554G>A	Nonsense Mutation	WDFY3	p.Q2084*	WD repeat and FYVE d	24 (0.00)	11 (0.45)	1.21
11-02	Gp4 Focus 2	g.chr10:122643329G>T	Nonsense Mutation	WDR11	p.E593*	WD repeat domain 11	42 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr1:118492672C>A	Silent	WDR3	p.V555V	WD repeat domain 3	227 (0.00)	24 (0.29)	0.61
11-02	Gp4 Focus 2	g.chr9:116094187C>T	Splice Site	WDR31	p.G39D	WD repeat domain 31	68 (0.00)	31 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr9:116094284G>A	Nonsense Mutation	WDR31	p.Q7*	WD repeat domain 31	82 (0.00)	28 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:128467302C>T	Missense Mutation	WDR33	p.R1146Q	WD repeat domain 33	50 (0.00)	22 (0.27)	0.88
11-02	Gp4 Focus 2	g.chr21:44270192C>T	Silent	WDR4	p.K402K	WD repeat domain 4	38 (0.00)	41 (0.34)	0.91
11-02	Gp4 Focus 2	g.chr5:76736707G>A	Silent	WDR41	p.T271T	WD repeat domain 41	21 (0.00)	17 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr1:109524445C>G	Missense Mutation	WDR47	p.A771P	WD repeat domain 47	53 (0.00)	44 (0.25)	0.52
11-02	Gp4 Focus 2	g.chr1:109544925G>C	Missense Mutation	WDR47	p.Q453E	WD repeat domain 47	72 (0.00)	33 (0.18)	0.38
11-02	Gp4 Focus 2	g.chr3:113063522G>A	Missense Mutation	WDR52	p.H1035Y		26 (0.00)	27 (0.26)	0.69

11-02	Gp4 Focus 2	g.chr7:158663846G>A	Missense Mutation	WDR60	p.G28D	WD repeat domain 60	37 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr1:43689744G>A	Missense Mutation	WDR65	p.E912K		32 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr18:54426129G>A	Silent	WDR7	p.K931K	WD repeat domain 7	43 (0.00)	18 (0.61)	1.63
11-02	Gp4 Focus 2	g.chr11:62603254G>A	Silent	WDR74	p.P86P	WD repeat domain 74	43 (0.00)	31 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr8:38205600C>T	Silent	WHSC1L1	p.Q30Q	Wolf-Hirschhorn syndrc	17 (0.00)	14 (0.57)	1.85
11-02	Gp4 Focus 2	g.chr1:68624889G>A	Missense Mutation	WLS	p.R141C	wntless Wnt ligand secr	68 (0.00)	22 (0.41)	1.09
11-02	Gp4 Focus 2	g.chr12:988949C>T	Missense Mutation	WNK1	p.P862S	WNK lysine deficient p	97 (0.00)	109 (0.75)	2.01
11-02	Gp4 Focus 2	g.chr17:40940171T>A	Silent	WNK4	p.R629R	WNK lysine deficient p	47 (0.00)	14 (0.36)	0.95
11-02	Gp4 Focus 2	g.chr3:55504215C>T	Missense Mutation	WNT5A	p.V350M	wingless-type MMTV i	76 (0.00)	19 (0.42)	1.12
11-02	Gp4 Focus 2	g.chr1:3552582C>T	Missense Mutation	WRAP73	p.D177N	WD repeat containing, a	15 (0.00)	18 (0.67)	1.78
11-02	Gp4 Focus 2	g.chr17:25636220C>T	Missense Mutation	WSB1	p.A269V	WD repeat and SOCS b	113 (0.00)	20 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr4:184166601G>A	Missense Mutation	WWC2	p.G212E	WW and C2 domain co	40 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr4:184203996C>T	Silent	WWC2	p.N940N	WW and C2 domain co	84 (0.00)	36 (0.22)	0.59
11-02	Gp4 Focus 2	g.chrX:10090744C>T	Silent	WWC3	p.A572A	WWC family member 3	21 (0.00)	29 (0.24)	0.49
11-02	Gp4 Focus 2	g.chr16:69833191G>A	Silent	WWP2	p.G111G	WW domain containing	15 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr3:39229568C>T	Missense Mutation	XIRP1	p.E457K	xin actin-binding repeat	31 (0.00)	19 (0.74)	1.96
11-02	Gp4 Focus 2	g.chr1:28293695C>T	Missense Mutation	XKR8	p.S391L	XK, Kell blood group c	17 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr3:14200265G>A	Missense Mutation	XPC	p.A373V	xeroderma pigmentosun	22 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr3:14219095G>A	Intron	XPC		xeroderma pigmentosun	135 (0.00)	69 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr13:21395922C>T	Missense Mutation	XPO4	p.S365N	exportin 4	26 (0.00)	13 (0.38)	1.32
11-02	Gp4 Focus 2	g.chr6:43491658G>A	Missense Mutation	XPO5	p.T1188M	exportin 5	47 (0.00)	84 (0.37)	0.98
11-02	Gp4 Focus 2	g.chr6:43492257G>A	Silent	XPO5	p.D1143D	exportin 5	48 (0.00)	61 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr20:21349130G>A	Missense Mutation	XRN2	p.G829D	5'-3' exoribonuclease 2	38 (0.00)	14 (0.57)	1.52
11-02	Gp4 Focus 2	g.chr11:74632390G>A	Silent	XRRA1	p.F167F	X-ray radiation resistanc	53 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr3:194877276C>G	Silent	XXYLT1	p.L229L	xyloside xylosyltransfer	37 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr3:38415952G>A	Splice Site	XYLB		xylulokinase homolog (	17 (0.00)	32 (0.47)	1.25
11-02	Gp4 Focus 2	g.chr16:17221526G>A	Silent	XYLT1	p.S740S	xylosyltransferase I	29 (0.00)	35 (0.83)	2.21
11-02	Gp4 Focus 2	g.chr1:33272090C>T	Missense Mutation	YARS	p.G168E	tyrosyl-tRNA synthetas	30 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr6:43480020G>A	Missense Mutation	YIPF3	p.P319L	Yip1 domain family, m	38 (0.00)	57 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr6:43480021G>A	Missense Mutation	YIPF3	p.P319S	Yip1 domain family, m	38 (0.00)	57 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr14:75248748C>A	Missense Mutation	YLPM1	p.P668T	YLP motif containing 1	81 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr22:22064957C>T	Missense Mutation	YPEL1	p.C26Y	yippee-like 1 (Drosophi	60 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr1:29069986G>A	Missense Mutation	YTHDF2	p.D402N	YTH domain family, m	25 (0.00)	26 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr20:43530386C>T	Missense Mutation	YWHAB	p.T71I	tyrosine 3-monooxygen	82 (0.00)	35 (0.14)	0.38
11-02	Gp4 Focus 2	g.chr7:75959101G>A	Silent	YWHAG	p.Y179Y	tyrosine 3-monooxygen	22 (0.00)	39 (0.18)	0.78

11-02	Gp4 Focus 2	g.chr14:100728672G>A	Silent	YY1	p.V237V	YY1 transcription facto	27 (0.00)	41 (0.32)	0.85
11-02	Gp4 Focus 2	g.chrX:21875541C>A	Nonsense Mutation	YY2	p.C313*	YY2 transcription facto	53 (0.00)	30 (0.27)	0.44
11-02	Gp4 Focus 2	g.chr7:100350318C>T	RNA	ZAN		zonadhesin (gene/pseud	49 (0.00)	37 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr7:100361499G>A	RNA	ZAN		zonadhesin (gene/pseud	17 (0.00)	27 (0.48)	1.28
11-02	Gp4 Focus 2	g.chr7:100364704G>T	RNA	ZAN		zonadhesin (gene/pseud	21 (0.00)	21 (0.38)	1.02
11-02	Gp4 Focus 2	g.chr7:150027663G>A	Missense Mutation	ZBED6CL	p.C57Y	ZBED6 C-terminal like	23 (0.00)	28 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr8:81412314G>A	Missense Mutation	ZBTB10	p.G520S	zinc finger and BTB do	37 (0.00)	50 (0.14)	0.47
11-02	Gp4 Focus 2	g.chr3:101384243C>T	Silent	ZBTB11	p.L396L	zinc finger and BTB do	52 (0.00)	33 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr6:151687837G>A	Missense Mutation	ZBTB2	p.P122S	zinc finger and BTB do	20 (0.00)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr3:114069212C>A	Silent	ZBTB20	p.G498G	zinc finger and BTB do	18 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr11:62520913G>A	Missense Mutation	ZBTB3	p.A125V	zinc finger and BTB do	92 (0.00)	48 (0.19)	0.50
11-02	Gp4 Focus 2	g.chr12:57398612G>A	Silent	ZBTB39	p.C30C	zinc finger and BTB do	51 (0.00)	78 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr1:22816852C>T	Silent	ZBTB40	p.F137F	zinc finger and BTB do	43 (0.00)	29 (0.21)	0.55
11-02	Gp4 Focus 2	g.chrX:64709274G>A	Missense Mutation	ZC3H12B	p.S198N	zinc finger CCCH-type	54 (0.00)	37 (0.24)	0.41
11-02	Gp4 Focus 2	g.chr13:46616338G>A	Silent	ZC3H13	p.P100P	zinc finger CCCH-type	18 (0.00)	16 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr2:113069485G>A	Missense Mutation	ZC3H6	p.V240M	zinc finger CCCH-type	99 (0.00)	18 (0.50)	1.33
11-02	Gp4 Focus 2	g.chrX:117959554C>G	Missense Mutation	ZCCHC12	p.A116G	zinc finger, CCHC dom	28 (0.00)	19 (0.32)	0.70
11-02	Gp4 Focus 2	g.chr18:60242154G>A	Missense Mutation	ZCCHC2	p.S947N	zinc finger, CCHC dom	101 (0.00)	33 (0.21)	0.57
11-02	Gp4 Focus 2	g.chr9:37126846G>A	Missense Mutation	ZCCHC7	p.V173M	zinc finger, CCHC dom	79 (0.00)	56 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr12:122958402T>A	Missense Mutation	ZCCHC8	p.K351M	zinc finger, CCHC dom	25 (0.00)	30 (0.23)	0.62
11-02	Gp4 Focus 2	g.chr7:100013690C>T	Missense Mutation	ZCWPW1	p.G100E	zinc finger, CW type wi	21 (0.00)	27 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr10:99212651G>A	Splice Site	ZDHHC16		zinc finger, DHHC-type	78 (0.00)	55 (0.25)	0.68
11-02	Gp4 Focus 2	g.chr12:77222233C>T	Silent	ZDHHC17	p.F368F	zinc finger, DHHC-type	59 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr14:77600091G>A	Silent	ZDHHC22	p.L243L	zinc finger, DHHC-type	39 (0.00)	46 (0.41)	1.10
11-02	Gp4 Focus 2	g.chr22:20126767G>A	Missense Mutation	ZDHHC8	p.G52D	zinc finger, DHHC-type	20 (0.00)	11 (0.55)	1.45
11-02	Gp4 Focus 2	g.chr2:145161539C>A	Missense Mutation	ZEB2	p.A251S	zinc finger E-box bindir	56 (0.00)	28 (0.21)	0.70
11-02	Gp4 Focus 2	g.chr2:220072720C>T	Missense Mutation	ZFAND2B	p.H132Y	zinc finger, AN1-type d	31 (0.00)	37 (0.43)	1.15
11-02	Gp4 Focus 2	g.chr12:72036258C>T	Missense Mutation	ZFC3H1	p.E529K	zinc finger, C3H1-type	40 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr12:72057187T>A	Silent	ZFC3H1	p.G68G	zinc finger, C3H1-type	17 (0.00)	18 (0.39)	1.04
11-02	Gp4 Focus 2	g.chr16:72831570C>T	Missense Mutation	ZFHX3	p.A1671T	zinc finger homeobox 3	24 (0.00)	29 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr8:77767203C>T	Silent	ZFHX4	p.A2682A	zinc finger homeobox 4	25 (0.00)	17 (0.29)	0.99
11-02	Gp4 Focus 2	g.chr8:106811146G>A	Missense Mutation	ZFPM2	p.A312T	zinc finger protein, FOC	83 (0.00)	50 (0.46)	1.57
11-02	Gp4 Focus 2	g.chr14:68244848G>A	Silent	ZFYVE26	p.L1598L	zinc finger, FYVE doma	118 (0.00)	29 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr20:39831800G>A	Missense Mutation	ZHX3	p.T586I	zinc fingers and homeol	20 (0.00)	32 (0.16)	0.42
11-02	Gp4 Focus 2	g.chr8:40532348G>A	Missense Mutation	ZMAT4	p.A151V	zinc finger, matrin-type	28 (0.00)	22 (0.41)	1.32

11-02	Gp4 Focus 2	g.chr1:35884096G>A	Silent	ZMYM4	p.V1454V	zinc finger, MYM-type	33 (0.00)	24 (0.21)	0.56
11-02	Gp4 Focus 2	g.chr17:11886711A>T	Missense Mutation	ZNF18	p.H255Q	zinc finger protein 18	37 (0.00)	30 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr3:44670988G>A	Silent	ZNF197	p.V114V	zinc finger protein 197	26 (0.00)	24 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr16:3273905C>T	Missense Mutation	ZNF200	p.R392Q	zinc finger protein 200	56 (0.00)	55 (0.56)	1.80
11-02	Gp4 Focus 2	g.chr11:123597360C>G	Missense Mutation	ZNF202	p.G431A	zinc finger protein 202	40 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr20:52198570G>A	Silent	ZNF217	p.L266L	zinc finger protein 217	58 (0.00)	28 (0.29)	0.76
11-02	Gp4 Focus 2	g.chr19:44469123G>A	Missense Mutation	ZNF221	p.V35M	zinc finger protein 221	134 (0.00)	43 (0.28)	0.74
11-02	Gp4 Focus 2	g.chr19:44471326G>A	Missense Mutation	ZNF221	p.G558R	zinc finger protein 221	36 (0.00)	29 (0.31)	0.83
11-02	Gp4 Focus 2	g.chr19:44564681G>A	Missense Mutation	ZNF223	p.R140K	zinc finger protein 223	29 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr19:44564926C>T	Missense Mutation	ZNF223	p.T166I	zinc finger protein 223	20 (0.00)	29 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr19:44611602G>A	Missense Mutation	ZNF224	p.C430Y	zinc finger protein 224	20 (0.00)	13 (0.38)	1.03
11-02	Gp4 Focus 2	g.chr17:5012276C>T	Silent	ZNF232	p.Q190Q	zinc finger protein 232	40 (0.00)	24 (0.38)	1.00
11-02	Gp4 Focus 2	g.chr19:44803038G>A	Missense Mutation	ZNF235	p.P54L	zinc finger protein 235	31 (0.00)	27 (0.19)	0.49
11-02	Gp4 Focus 2	g.chr18:74593413G>A	Silent	ZNF236	p.E452E	zinc finger protein 236	50 (0.00)	21 (0.24)	0.76
11-02	Gp4 Focus 2	g.chr18:74639088G>A	Missense Mutation	ZNF236	p.V1373I	zinc finger protein 236	74 (0.00)	24 (0.38)	1.20
11-02	Gp4 Focus 2	g.chr19:22255621C>T	Missense Mutation	ZNF257	p.T5I	zinc finger protein 257	62 (0.00)	32 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr11:116650494G>A	Silent	ZNF259	p.Y413Y		32 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr19:44590944G>A	Missense Mutation	ZNF284	p.S438N	zinc finger protein 284	51 (0.00)	80 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:57869201C>T	Missense Mutation	ZNF304	p.S655F	zinc finger protein 304	67 (0.00)	34 (0.21)	0.55
11-02	Gp4 Focus 2	g.chr6:43322830C>T	Missense Mutation	ZNF318	p.A748T	zinc finger protein 318	30 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr4:142154891G>A	Silent	ZNF330	p.R237R	zinc finger protein 330	72 (0.00)	52 (0.19)	0.88
11-02	Gp4 Focus 2	g.chr4:142154919G>A	Missense Mutation	ZNF330	p.A247T	zinc finger protein 330	72 (0.00)	52 (0.21)	0.97
11-02	Gp4 Focus 2	g.chr19:54080166C>T	Missense Mutation	ZNF331	p.P118S	zinc finger protein 331	23 (0.00)	34 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr19:54080268A>G	Missense Mutation	ZNF331	p.I152V	zinc finger protein 331	43 (0.00)	31 (0.65)	1.72
11-02	Gp4 Focus 2	g.chr20:32354826G>A	Missense Mutation	ZNF341	p.M457I	zinc finger protein 341	22 (0.00)	19 (0.26)	0.70
11-02	Gp4 Focus 2	g.chr5:178154088G>A	Silent	ZNF354A	p.T24T	zinc finger protein 354A	31 (0.00)	31 (0.16)	0.43
11-02	Gp4 Focus 2	g.chr1:33747312C>T	Silent	ZNF362	p.L270L	zinc finger protein 362	20 (0.00)	15 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr2:180311360G>A	Missense Mutation	ZNF385B	p.P270S	zinc finger protein 385B	36 (0.00)	12 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr18:72344329G>A	Missense Mutation	ZNF407	p.G452S	zinc finger protein 407	134 (0.00)	68 (0.25)	0.80
11-02	Gp4 Focus 2	g.chr18:72344721G>A	Silent	ZNF407	p.Q582Q	zinc finger protein 407	140 (0.00)	79 (0.37)	1.18
11-02	Gp4 Focus 2	g.chr18:72345995C>A	Missense Mutation	ZNF407	p.S1007Y	zinc finger protein 407	72 (0.00)	73 (0.25)	0.79
11-02	Gp4 Focus 2	g.chr19:9645917C>T	Missense Mutation	ZNF426	p.E22K	zinc finger protein 426	90 (0.00)	54 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr10:31138775C>T	Missense Mutation	ZNF438	p.A187T	zinc finger protein 438	41 (0.00)	26 (0.19)	0.64
11-02	Gp4 Focus 2	g.chr10:31138810G>T	Missense Mutation	ZNF438	p.P175Q	zinc finger protein 438	36 (0.00)	45 (0.18)	0.60
11-02	Gp4 Focus 2	g.chr19:11977038G>A	Missense Mutation	ZNF439	p.D23N	zinc finger protein 439	52 (0.00)	34 (0.18)	0.47

11-02	Gp4 Focus 2	g.chr9:109688408G>T	Missense Mutation	ZNF462	p.D739Y	zinc finger protein 462	50 (0.02)	36 (0.22)	0.59
11-02	Gp4 Focus 2	g.chr5:121488693G>A	Silent	ZNF474	p.R336R	zinc finger protein 474	40 (0.03)	29 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr9:114304274C>T	Silent	ZNF483	p.T353T	zinc finger protein 483	30 (0.00)	33 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr2:27600773G>A	Missense Mutation	ZNF513	p.P422L	zinc finger protein 513	19 (0.00)	20 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr2:27600975G>A	Missense Mutation	ZNF513	p.P355S	zinc finger protein 513	15 (0.00)	40 (0.30)	0.80
11-02	Gp4 Focus 2	g.chr18:74092081C>T	Silent	ZNF516	p.R663R	zinc finger protein 516	16 (0.00)	14 (0.36)	1.14
11-02	Gp4 Focus 2	g.chr4:10447907C>T	Missense Mutation	ZNF518B	p.G16R	zinc finger protein 518B	104 (0.01)	54 (0.15)	0.40
11-02	Gp4 Focus 2	g.chr19:58774050G>A	Missense Mutation	ZNF544	p.C693Y	zinc finger protein 544	74 (0.00)	95 (0.15)	0.39
11-02	Gp4 Focus 2	g.chr19:42582774G>A	Missense Mutation	ZNF574	p.E6K	zinc finger protein 574	63 (0.00)	73 (0.26)	0.69
11-02	Gp4 Focus 2	g.chr19:42583287G>A	Missense Mutation	ZNF574	p.V177M	zinc finger protein 574	15 (0.00)	32 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr19:52376126C>T	Missense Mutation	ZNF577	p.E373K	zinc finger protein 577	45 (0.00)	15 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr19:52447744C>T	Missense Mutation	ZNF613	p.P203L	zinc finger protein 613	24 (0.00)	39 (0.18)	0.48
11-02	Gp4 Focus 2	g.chr19:52447907G>A	Silent	ZNF613	p.E257E	zinc finger protein 613	36 (0.00)	23 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr19:52505456G>A	Silent	ZNF615	p.L32L	zinc finger protein 615	94 (0.00)	45 (0.16)	0.41
11-02	Gp4 Focus 2	g.chr9:116811542C>T	Nonsense Mutation	ZNF618	p.Q654*	zinc finger protein 618	19 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr3:40529291C>T	Silent	ZNF619	p.C470C	zinc finger protein 619	21 (0.00)	25 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr8:144733328G>A	Missense Mutation	ZNF623	p.R429K	zinc finger protein 623	45 (0.00)	20 (0.45)	1.20
11-02	Gp4 Focus 2	g.chr2:71650818C>T	Missense Mutation	ZNF638	p.P1392S	zinc finger protein 638	48 (0.00)	13 (0.54)	1.44
11-02	Gp4 Focus 2	g.chr16:31089865G>A	Silent	ZNF646	p.G740G	zinc finger protein 646	15 (0.00)	43 (0.30)	0.81
11-02	Gp4 Focus 2	g.chr16:31090709G>T	Missense Mutation	ZNF646	p.A1022S	zinc finger protein 646	15 (0.00)	25 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr1:151259920G>A	Missense Mutation	ZNF687	p.V385M	zinc finger protein 687	19 (0.00)	15 (0.40)	1.07
11-02	Gp4 Focus 2	g.chr19:12015698G>A	Silent	ZNF69	p.K162K	zinc finger protein 69	43 (0.00)	20 (0.60)	1.60
11-02	Gp4 Focus 2	g.chr19:2934250C>T	Missense Mutation	ZNF77	p.G292E	zinc finger protein 77	30 (0.00)	10 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr9:99607218C>T	Silent	ZNF782	p.L32L	zinc finger protein 782	34 (0.00)	28 (0.79)	2.10
11-02	Gp4 Focus 2	g.chr7:148963471C>T	Missense Mutation	ZNF783	p.P24S	zinc finger family meml	15 (0.00)	24 (0.29)	0.78
11-02	Gp4 Focus 2	g.chr9:130207431C>G	Missense Mutation	ZNF79	p.C484W	zinc finger protein 79	38 (0.00)	35 (0.17)	0.46
11-02	Gp4 Focus 2	g.chr19:58797122C>T	Nonsense Mutation	ZNF8	p.Q36*	zinc finger protein 8	49 (0.02)	30 (0.17)	0.44
11-02	Gp4 Focus 2	g.chr19:53058172G>A	Nonsense Mutation	ZNF808	p.W668*	zinc finger protein 808	50 (0.00)	27 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr19:11776987C>T	lincRNA	ZNF833P		zinc finger protein 833,	60 (0.00)	35 (0.20)	0.53
11-02	Gp4 Focus 2	g.chr20:47887048G>A	Missense Mutation	ZNFX1	p.T434I	zinc finger, NFX1-type	56 (0.00)	40 (0.23)	0.60
11-02	Gp4 Focus 2	g.chr3:102196320C>T	Missense Mutation	ZPLD1	p.A369V	zona pellucida-like dom	73 (0.00)	67 (0.24)	0.64
11-02	Gp4 Focus 2	g.chr16:3141547G>A	Missense Mutation	ZSCAN10	p.P206S	zinc finger and SCAN d	18 (0.00)	53 (0.49)	1.57
11-02	Gp4 Focus 2	g.chr15:85147168G>A	Missense Mutation	ZSCAN2	p.A4T	zinc finger and SCAN d	18 (0.00)	37 (0.32)	0.86
11-02	Gp4 Focus 2	g.chr7:99654653G>A	Missense Mutation	ZSCAN21	p.M8I	zinc finger and SCAN d	25 (0.00)	24 (0.58)	1.56
11-02	Gp4 Focus 2	g.chr15:43656193G>A	Missense Mutation	ZSCAN29	p.S537F	zinc finger and SCAN d	57 (0.00)	55 (0.15)	0.39

11-02	Gp4 Focus 2	g.chr15:43661189C>T	Missense Mutation	ZSCAN29	p.R152K	zinc finger and SCAN d	74 (0.00)	21 (0.33)	0.89
11-02	Gp4 Focus 2	g.chr20:44505851A>G	Silent	ZSWIM3	p.P218P	zinc finger, SWIM-type	18 (0.00)	18 (0.44)	1.19
11-02	Gp4 Focus 2	g.chr1:45484486C>T	Silent	ZSWIM5	p.K1066K	zinc finger, SWIM-type	20 (0.00)	22 (0.23)	0.61
11-02	Gp4 Focus 2	g.chr1:45486362C>T	Missense Mutation	ZSWIM5	p.A850T	zinc finger, SWIM-type	68 (0.00)	34 (0.24)	0.63
11-02	Gp4 Focus 2	g.chr1:45508891C>T	Splice Site	ZSWIM5	p.E537K	zinc finger, SWIM-type	57 (0.00)	36 (0.25)	0.67
11-02	Gp4 Focus 2	g.chr10:75548564G>A	Silent	ZSWIM8	p.E115E	zinc finger, SWIM-type	19 (0.00)	43 (0.44)	1.18
11-02	Gp4 Focus 2	g.chr10:75560478G>A	Missense Mutation	ZSWIM8	p.D1698N	zinc finger, SWIM-type	48 (0.00)	14 (0.50)	1.33
11-02	Gp4 Focus 2	g.chr10:58118598C>T	Silent	ZWINT	p.Q197Q	ZW10 interacting kinet	30 (0.00)	69 (0.22)	0.58
11-02	Gp4 Focus 2	g.chr17:3969771C>T	Missense Mutation	ZZEF1	p.E1407K	zinc finger, ZZ-type wit	113 (0.01)	27 (0.33)	0.89
11-03	Gp3	g.chr12:125587321C>T	Silent	AACS	p.L223L	acetoacetyl-CoA synthe	132 (0.00)	128 (0.23)	0.60
11-03	Gp3	g.chr3:151535345C>T	Silent	AADAC	p.I110I	arylacetamide deacetyla	27 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr17:41113260G>T	Missense Mutation	AARSD1	p.L94M	alanyl-tRNA synthetase	63 (0.00)	113 (0.16)	0.42
11-03	Gp3	g.chr9:107576423G>T	Missense Mutation	ABCA1	p.P1293T	ATP-binding cassette, s	16 (0.00)	25 (0.48)	1.28
11-03	Gp3	g.chr7:48375020C>A	Splice Site	ABCA13	p.A3334D	ATP-binding cassette, s	19 (0.00)	20 (0.35)	0.93
11-03	Gp3	g.chr1:94502310C>G	Missense Mutation	ABCA4	p.G1283A	ATP-binding cassette, s	31 (0.00)	103 (0.15)	0.39
11-03	Gp3	g.chr2:169792804G>T	Missense Mutation	ABCB11	p.T917K	ATP-binding cassette, s	41 (0.00)	46 (0.17)	0.46
11-03	Gp3	g.chr16:48204022G>T	Missense Mutation	ABCC11	p.N1295K	ATP-binding cassette, s	32 (0.00)	52 (0.19)	0.51
11-03	Gp3	g.chr16:48139075G>T	Missense Mutation	ABCC12	p.S883Y	ATP-binding cassette, s	31 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr12:22069875A>T	Missense Mutation	ABCC9	p.V190D	ATP-binding cassette, s	47 (0.00)	25 (0.32)	0.85
11-03	Gp3	g.chr3:111710380C>A	Missense Mutation	ABHD10	p.H245N	abhydrolase domain con	22 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr9:74485050C>T	Missense Mutation	ABHD17B	p.R199Q	abhydrolase domain con	17 (0.00)	26 (0.46)	1.23
11-03	Gp3	g.chr10:116225491G>A	Silent	ABLIM1	p.T469T	actin binding LIM prote	25 (0.00)	46 (0.15)	0.41
11-03	Gp3	g.chr3:15175899C>A	RNA	AC090954.1			216 (0.00)	146 (0.21)	0.55
11-03	Gp3	g.chr2:239141006C>A	RNA	AC096574.4			31 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr2:208687173C>T	lincRNA	AC096772.6			26 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr17:35487078C>G	Missense Mutation	ACACA	p.G1879R	acetyl-CoA carboxylase	37 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr17:35487087G>C	Missense Mutation	ACACA	p.H1876D	acetyl-CoA carboxylase	39 (0.00)	36 (0.19)	0.52
11-03	Gp3	g.chr17:35609859T>A	Nonsense Mutation	ACACA	p.R607*	acetyl-CoA carboxylase	58 (0.00)	64 (0.28)	0.75
11-03	Gp3	g.chr15:89401416G>A	Missense Mutation	ACAN	p.G1867D	aggrecan	30 (0.00)	22 (0.32)	0.85
11-03	Gp3	g.chr11:44080222G>T	Missense Mutation	ACCSL	p.A533S	1-aminocyclopropane-1	17 (0.00)	34 (0.24)	0.63
11-03	Gp3	g.chr16:89178533C>T	Missense Mutation	ACSF3	p.R21W	acyl-CoA synthetase fa	50 (0.02)	39 (0.28)	0.75
11-03	Gp3	g.chr4:185681649G>T	Silent	ACSL1	p.G548G	acyl-CoA synthetase lo	116 (0.00)	68 (0.16)	0.43
11-03	Gp3	g.chr20:24988446G>A	Silent	ACSS1	p.I674I	acyl-CoA synthetase sh	27 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr1:236924429G>A	Missense Mutation	ACTN2	p.A828T	actinin, alpha 2	18 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr11:67410231C>T	Missense Mutation	ACY3	p.M187I	aspartoacylase (aminoc	18 (0.00)	32 (0.38)	1.00

11-03	Gp3	g.chr10:127737878C>T	Missense Mutation	ADAM12	p.D624N	ADAM metallopeptidas	64 (0.02)	43 (0.16)	0.43
11-03	Gp3	g.chr2:207424774G>C	Missense Mutation	ADAM23	p.Q367H	ADAM metallopeptidas	19 (0.00)	15 (0.40)	1.07
11-03	Gp3	g.chr8:39111939G>A	Missense Mutation	ADAM32	p.D637N	ADAM metallopeptidas	19 (0.00)	45 (0.18)	0.47
11-03	Gp3	g.chr3:64640269G>T	Missense Mutation	ADAMTS9	p.H397N	ADAM metallopeptidas	73 (0.00)	45 (0.20)	0.53
11-03	Gp3	g.chr7:45724621G>A	Missense Mutation	ADCY1	p.C676Y	adenylate cyclase 1 (bra	65 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr12:49167329G>A	Silent	ADCY6	p.I848I	adenylate cyclase 6	30 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr8:132002753G>A	Silent	ADCY8	p.N332N	adenylate cyclase 8 (bra	43 (0.00)	43 (0.19)	0.50
11-03	Gp3	g.chr8:67361144C>A	Missense Mutation	ADHFE1	p.P225T	alcohol dehydrogenase,	55 (0.00)	50 (0.22)	0.59
11-03	Gp3	g.chr4:87968029C>G	Missense Mutation	AFF1	p.F107L	AF4/FMR2 family, men	36 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr2:100185376G>A	Splice Site	AFF3	p.P974S	AF4/FMR2 family, men	21 (0.00)	20 (0.30)	0.80
11-03	Gp3	g.chr2:100209939G>T	Silent	AFF3	p.A728A	AF4/FMR2 family, men	15 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr4:74364911C>T	Missense Mutation	AFM	p.A457V	afamin	29 (0.00)	63 (0.14)	0.38
11-03	Gp3	g.chr4:84511383G>A	Missense Mutation	AGPAT9	p.V226I	1-acylglycerol-3-phosph	24 (0.00)	25 (0.24)	0.64
11-03	Gp3	g.chr1:65691794C>A	Silent	AK4	p.I202I	adenylate kinase 4	28 (0.00)	23 (0.35)	0.93
11-03	Gp3	g.chr10:5204913G>A	Missense Mutation	AKR1CL1	p.A55V	aldo-keto reductase fam	23 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr10:4872962G>A	Silent	AKR1E2	p.E45E	aldo-keto reductase fam	32 (0.00)	39 (0.21)	0.55
11-03	Gp3	g.chr16:53532348G>A	Missense Mutation	AKTIP	p.A68V	AKT interacting protein	45 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr17:19554983G>T	Missense Mutation	ALDH3A2	p.D93Y	aldehyde dehydrogenas	28 (0.00)	49 (0.18)	0.49
11-03	Gp3	g.chr2:29449941C>T	Splice Site	ALK		anaplastic lymphoma re	58 (0.00)	42 (0.21)	0.57
11-03	Gp3	g.chr2:73676993G>C	Missense Mutation	ALMS1	p.E1112D	Alstrom syndrome 1	23 (0.04)	42 (0.19)	0.51
11-03	Gp3	g.chr4:113353699C>A	Missense Mutation	ALPK1	p.T999K	alpha-kinase 1	68 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr18:56247690G>A	Silent	ALPK2	p.C106C	alpha-kinase 2	36 (0.00)	52 (0.31)	0.82
11-03	Gp3	g.chr7:91972443C>A	Missense Mutation	ANKIB1	p.A298D	ankyrin repeat and IBR	73 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr12:133331575G>A	Missense Mutation	ANKLE2	p.A109V	ankyrin repeat and LEM	53 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr12:110457078C>T	Missense Mutation	ANKRD13A	p.L227F	ankyrin repeat domain 1	62 (0.00)	60 (0.25)	0.67
11-03	Gp3	g.chr4:73964232G>T	Missense Mutation	ANKRD17	p.P1527T	ankyrin repeat domain 1	35 (0.00)	28 (0.21)	0.57
11-03	Gp3	g.chr2:97911323G>A	Missense Mutation	ANKRD36	p.E1667K	ankyrin repeat domain 3	100 (0.00)	67 (0.45)	1.19
11-03	Gp3	g.chr7:36450211C>T	Silent	ANLN	p.H395H	anillin, actin binding pr	33 (0.00)	31 (0.26)	0.69
11-03	Gp3	g.chr12:5941748C>G	Missense Mutation	ANO2	p.G216R	anoctamin 2, calcium ac	17 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr19:16338436C>T	Missense Mutation	AP1M1	p.R251C	adaptor-related protein	22 (0.00)	24 (0.29)	1.03
11-03	Gp3	g.chr19:47342802C>A	Missense Mutation	AP2S1	p.A63S	adaptor-related protein	50 (0.00)	40 (0.15)	0.53
11-03	Gp3	g.chr10:75893807T>A	Silent	AP3M1	p.I187I	adaptor-related protein	54 (0.00)	78 (0.19)	0.51
11-03	Gp3	g.chr12:99053051C>A	Missense Mutation	APAF1	p.Q214K	apoptotic peptidase acti	58 (0.00)	51 (0.16)	0.42
11-03	Gp3	g.chr3:49719327C>T	Silent	APEH	p.P510P	acylaminoacyl-peptide	36 (0.00)	22 (0.36)	0.97
11-03	Gp3	g.chr1:156563674G>A	Splice Site	APOA1BP	p.G222E	apolipoprotein A-I bindi	43 (0.00)	24 (0.38)	0.71

11-03	Gp3	g.chr6:131904595G>A	Missense Mutation	ARG1	p.E256K	arginase 1	37 (0.00)	27 (0.33)	0.54
11-03	Gp3	g.chr15:30951048G>A	Splice Site	ARHGAP11B		Rho GTPase activating	19 (0.00)	30 (0.23)	0.62
11-03	Gp3	g.chr16:24979672C>T	Splice Site	ARHGAP17	p.R154K	Rho GTPase activating	26 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr11:128868237T>A	Missense Mutation	ARHGAP32	p.H28L	Rho GTPase activating	87 (0.01)	45 (0.18)	0.47
11-03	Gp3	g.chr3:153972549G>A	Silent	ARHGEF26	p.K803K	Rho guanine nucleotide	58 (0.02)	70 (0.14)	0.38
11-03	Gp3	g.chr1:27094361G>T	Missense Mutation	ARID1A	p.W1023C	AT rich interactive dom	42 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr6:157150454C>T	Missense Mutation	ARID1B	p.P546S	AT rich interactive dom	33 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr15:72874415G>T	Splice Site	ARIH1		ariadne RBR E3 ubiquit	51 (0.02)	26 (0.23)	0.62
11-03	Gp3	g.chr4:57389985C>A	Silent	ARL9	p.P105P	ADP-ribosylation factor	26 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr12:110873963C>T	Silent	ARPC3	p.L142L	actin related protein 2/3	35 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr8:62465670C>A	Nonsense Mutation	ASPH	p.E516*	aspartate beta-hydroxyl	48 (0.02)	24 (0.21)	0.56
11-03	Gp3	g.chr20:30954250G>A	Missense Mutation	ASXL1	p.E41K	additional sex combs lik	41 (0.00)	70 (0.14)	0.38
11-03	Gp3	g.chr20:31020753G>C	Missense Mutation	ASXL1	p.W350C	additional sex combs lik	27 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr11:46679138C>A	Missense Mutation	ATG13	p.P142T	autophagy related 13	22 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr15:25932922G>A	Silent	ATP10A	p.L1073L	ATPase, class V, type 1	42 (0.02)	43 (0.30)	0.81
11-03	Gp3	g.chr15:25947134C>A	Missense Mutation	ATP10A	p.V897F	ATPase, class V, type 1	21 (0.00)	14 (0.43)	1.14
11-03	Gp3	g.chr4:42583750C>T	Splice Site	ATP8A1		ATPase, aminophospho	60 (0.00)	39 (0.18)	0.48
11-03	Gp3	g.chr20:50307358C>A	Splice Site	ATP9A	p.D215Y	ATPase, class II, type 9	22 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr18:77037157G>C	Missense Mutation	ATP9B	p.E458Q	ATPase, class II, type 9	29 (0.00)	46 (0.17)	0.46
11-03	Gp3	g.chr10:117059655G>A	Missense Mutation	ATRNL1	p.D843N	attractin-like 1	28 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr21:11038839C>T	RNA	BAGE2		B melanoma antigen fa	35 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr20:52570037A>G	Silent	BCAS1	p.N538N	breast carcinoma amplif	36 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr12:12240146G>A	Splice Site	BCL2L14		BCL2-like 14 (apoptosi	20 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr1:147095774G>C	Missense Mutation	BCL9	p.G1099R	B-cell CLL/lymphoma	75 (0.00)	52 (0.38)	1.03
11-03	Gp3	g.chr20:17475429C>A	Missense Mutation	BFSP1	p.D430Y	beaded filament structur	79 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr20:17475435G>A	Missense Mutation	BFSP1	p.P428S	beaded filament structur	85 (0.01)	35 (0.20)	0.53
11-03	Gp3	g.chr15:91348569T>C	Intron	BLM		Bloom syndrome, RecQ	42 (0.02)	76 (0.21)	0.56
11-03	Gp3	g.chr8:22054929C>T	Silent	BMP1	p.F701F	bone morphogenetic pro	25 (0.00)	35 (0.54)	0.72
11-03	Gp3	g.chrX:50659312C>A	Missense Mutation	BMP15	p.P295H	bone morphogenetic pro	30 (0.00)	13 (0.38)	0.64
11-03	Gp3	g.chr4:79832083G>T	Missense Mutation	BMP2K	p.E794D	BMP2 inducible kinase	77 (0.00)	60 (0.18)	0.49
11-03	Gp3	g.chr9:16436700G>C	Missense Mutation	BNC2	p.H498D	basonuclin 2	48 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr8:26265814G>T	Missense Mutation	BNIP3L	p.G138V	BCL2/adenovirus E1B	30 (0.00)	25 (0.32)	0.43
11-03	Gp3	g.chr4:13604882G>C	Silent	BOD1L1	p.S1214S	biorientation of chromos	70 (0.00)	43 (0.21)	0.56
11-03	Gp3	g.chr17:65909253G>T	Missense Mutation	BPTF	p.L1751F	bromodomain PHD fing	93 (0.00)	80 (0.16)	0.43
11-03	Gp3	g.chr17:41232169G>A	Intron	BRCA1		breast cancer 1, early on	28 (0.00)	32 (0.22)	0.58

11-03	Gp3	g.chr17:41276867G>A	Intron	BRCA1		breast cancer 1, early on	19 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr1:190068061C>A	Missense Mutation	BRINP3	p.C463F	bone morphogenetic pr	15 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr6:26444532G>T	Splice Site	BTN3A3	p.A103S	butyrophilin, subfamily	41 (0.00)	44 (0.16)	0.42
11-03	Gp3	g.chr10:71391587C>T	Missense Mutation	C10orf35	p.P30S	chromosome 10 open re	32 (0.03)	28 (0.18)	0.48
11-03	Gp3	g.chr10:50531797C>G	Missense Mutation	C10orf71	p.Q403E	chromosome 10 open re	77 (0.00)	85 (0.33)	0.64
11-03	Gp3	g.chr11:66581366C>G	Missense Mutation	C11orf80	p.L139V	chromosome 11 open re	27 (0.00)	47 (0.15)	0.40
11-03	Gp3	g.chr12:110488874C>T	Silent	C12orf76	p.E79E	chromosome 12 open re	52 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr14:23727835C>A	Silent	C14orf164	p.A102A		25 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr17:42744547G>A	Missense Mutation	C17orf104	p.G423E	chromosome 17 open re	56 (0.02)	35 (0.20)	0.53
11-03	Gp3	g.chr18:21104127C>A	Missense Mutation	C18orf8	p.P284Q	chromosome 18 open re	53 (0.02)	25 (0.20)	0.53
11-03	Gp3	g.chr2:70387817C>A	Missense Mutation	C2orf42	p.G486C	chromosome 2 open rea	64 (0.00)	42 (0.17)	0.44
11-03	Gp3	g.chr5:40947862C>T	Silent	C7	p.Y299Y	complement component	38 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr9:97563235C>T	Silent	C9orf3	p.L439L	chromosome 9 open rea	24 (0.00)	25 (0.32)	0.85
11-03	Gp3	g.chr3:54905625G>T	Silent	CACNA2D3	p.V562V	calcium channel, voltag	44 (0.00)	38 (0.24)	0.63
11-03	Gp3	g.chr3:85010092C>A	Intron	CADM2		cell adhesion molecule	62 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr3:85022780C>A	Intron	CADM2		cell adhesion molecule	17 (0.00)	27 (0.33)	0.49
11-03	Gp3	g.chr3:85493055C>T	Intron	CADM2		cell adhesion molecule	49 (0.00)	46 (0.28)	0.42
11-03	Gp3	g.chr3:85680350C>A	Intron	CADM2		cell adhesion molecule	47 (0.00)	21 (0.76)	1.13
11-03	Gp3	g.chr3:85752673C>G	Intron	CADM2		cell adhesion molecule	28 (0.00)	18 (0.56)	0.82
11-03	Gp3	g.chr3:86040213C>T	Intron	CADM2		cell adhesion molecule	25 (0.00)	25 (0.32)	0.47
11-03	Gp3	g.chr3:86063464C>T	Intron	CADM2		cell adhesion molecule	40 (0.00)	23 (0.26)	0.39
11-03	Gp3	g.chr7:122111479G>T	Silent	CADPS2	p.T709T	Ca++-dependent secreti	35 (0.00)	24 (0.29)	0.78
11-03	Gp3	g.chr6:7374231G>A	Missense Mutation	CAGE1	p.S274F	cancer antigen 1	35 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr17:46919190C>G	Missense Mutation	CALCOCO2	p.H41D	calcium binding and coi	36 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr1:230903441G>A	Missense Mutation	CAPN9	p.G231S	calpain 9	89 (0.01)	57 (0.28)	0.75
11-03	Gp3	g.chr2:202068456G>C	Missense Mutation	CASP10	p.E230Q	caspase 10, apoptosis-re	15 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr20:32224476G>A	Missense Mutation	CBFA2T2	p.G420D	core-binding factor, run	28 (0.00)	55 (0.20)	0.53
11-03	Gp3	g.chr17:42978449G>A	Missense Mutation	CCDC103	p.R28Q	coiled-coil domain cont	15 (0.00)	20 (0.30)	0.80
11-03	Gp3	g.chr6:151894414G>A	Missense Mutation	CCDC170	p.E294K	coiled-coil domain cont	40 (0.03)	30 (0.40)	1.07
11-03	Gp3	g.chr19:30308411C>A	Missense Mutation	CCNE1	p.P142Q	cyclin E1	36 (0.03)	32 (0.22)	0.58
11-03	Gp3	g.chr14:99959079C>A	Missense Mutation	CCNK	p.P22Q	cyclin K	29 (0.00)	29 (0.28)	0.74
11-03	Gp3	g.chr10:35841983G>A	Missense Mutation	CCNY	p.D206N	cyclin Y	31 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr15:55652131G>A	Missense Mutation	CCPG1	p.P614S	cell cycle progression 1	52 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr3:46415177G>T	Nonsense Mutation	CCR5	p.E262*	chemokine (C-C motif)	101 (0.00)	54 (0.17)	0.44
11-03	Gp3	g.chr1:229462521C>T	Silent	CCSAP	p.K200K	centriole, cilia and spin	17 (0.00)	16 (0.44)	1.17

11-03	Gp3	g.chr21:30432971G>T	Missense Mutation	CCT8	p.P487H	chaperonin containing T	48 (0.00)	24 (0.25)	0.67
11-03	Gp3	g.chr1:100964625C>T	Missense Mutation	CDC14A	p.S521F	cell division cycle 14A	44 (0.00)	21 (0.38)	1.02
11-03	Gp3	g.chr16:68845622G>A	Missense Mutation	CDH1	p.D290N	cadherin 1, type 1, E-ca	33 (0.00)	49 (0.53)	1.41
11-03	Gp3	g.chr16:68856084C>T	Missense Mutation	CDH1	p.T631I	cadherin 1, type 1, E-ca	57 (0.00)	55 (0.15)	0.39
11-03	Gp3	g.chr5:19721472G>A	Silent	CDH18	p.S209S	cadherin 18, type 2	61 (0.00)	51 (0.25)	0.68
11-03	Gp3	g.chr10:73330613G>A	Missense Mutation	CDH23	p.D236N	cadherin-related 23	65 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr2:202688429G>A	Silent	CDK15	p.G195G	cyclin-dependent kinase	19 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr17:15496717C>A	Missense Mutation	CDRT1	p.C647F	CMT1A duplicated regi	31 (0.00)	89 (0.19)	0.51
11-03	Gp3	g.chr20:5165575G>A	Missense Mutation	CDS2	p.R248Q	CDP-diacylglycerol syn	50 (0.00)	54 (0.15)	0.40
11-03	Gp3	g.chr19:51984800C>A	Missense Mutation	CEACAM18	p.P185Q	carcinoembryonic antig	27 (0.00)	28 (0.29)	0.76
11-03	Gp3	g.chr19:42219780C>A	Missense Mutation	CEACAM5	p.D305E	carcinoembryonic antig	18 (0.00)	35 (0.37)	0.99
11-03	Gp3	g.chr22:18028342C>T	Missense Mutation	CECR2	p.P958L	cat eye syndrome chrom	15 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr1:214830542G>A	Missense Mutation	CENPF	p.E2918K	centromere protein F, 3	48 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr15:49030885C>T	Missense Mutation	CEP152	p.G1565E	centrosomal protein 152	19 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr11:117258017G>A	Missense Mutation	CEP164	p.R608K	centrosomal protein 164	40 (0.00)	38 (0.29)	0.77
11-03	Gp3	g.chr18:13073100T>A	Missense Mutation	CEP192	p.F1844L	centrosomal protein 192	32 (0.03)	29 (0.17)	0.46
11-03	Gp3	g.chr18:13087166G>C	Missense Mutation	CEP192	p.A1923P	centrosomal protein 192	17 (0.00)	28 (0.29)	0.76
11-03	Gp3	g.chr19:33409182C>G	Missense Mutation	CEP89	p.L444F	centrosomal protein 89k	44 (0.00)	29 (0.24)	0.64
11-03	Gp3	g.chr17:62525531C>A	Missense Mutation	CEP95	p.Q478K	centrosomal protein 95k	45 (0.00)	40 (0.40)	1.07
11-03	Gp3	g.chr10:90966441G>T	Missense Mutation	CH25H	p.F203L	cholesterol 25-hydroxyl	46 (0.00)	16 (0.56)	0.42
11-03	Gp3	g.chr1:6176971C>A	Intron	CHD5		chromodomain helicase	34 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr1:6186797C>A	Nonsense Mutation	CHD5	p.E1305*	chromodomain helicase	17 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr20:40050674C>T	Missense Mutation	CHD6	p.R1534H	chromodomain helicase	19 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr16:53357980G>A	Missense Mutation	CHD9	p.V2607M	chromodomain helicase	42 (0.00)	32 (0.59)	1.58
11-03	Gp3	g.chr16:53358003G>A	Silent	CHD9	p.R2614R	chromodomain helicase	46 (0.00)	35 (0.54)	1.45
11-03	Gp3	g.chr1:203188407C>G	Silent	CHIT1	p.V322V	chitinase 1 (chitotriosid	18 (0.00)	17 (0.59)	1.57
11-03	Gp3	g.chr3:369945G>A	Missense Mutation	CHL1	p.G98E	cell adhesion molecule l	52 (0.00)	46 (0.20)	0.52
11-03	Gp3	g.chr3:33648117C>A	Missense Mutation	CLASP2	p.D555Y	cytoplasmic linker assoc	37 (0.00)	41 (0.32)	0.85
11-03	Gp3	g.chr3:190106156C>T	Missense Mutation	CLDN16	p.A83V	claudin 16	40 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr3:190122587C>T	Missense Mutation	CLDN16	p.A155V	claudin 16	33 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr1:36202600C>A	Missense Mutation	CLSPN	p.S1275I	claspin	41 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr3:140275406G>A	Missense Mutation	CLSTN2	p.G576R	calsyntenin 2	43 (0.00)	30 (0.33)	0.89
11-03	Gp3	g.chr22:19222226G>A	Silent	CLTCL1	p.L325L	clathrin, heavy chain-lik	71 (0.00)	77 (0.14)	0.38
11-03	Gp3	g.chr6:25093923G>T	RNA	CMAHP		cytidine monophospho-	53 (0.00)	23 (0.30)	0.81
11-03	Gp3	g.chrX:150912578C>G	Missense Mutation	CNGA2	p.R535G	cyclic nucleotide gated	20 (0.00)	12 (0.42)	0.69

11-03	Gp3	g.chr19:11658639G>A	Missense Mutation	CNN1	p.V90M	calponin 1, basic, smoot	17 (0.00)	40 (0.33)	1.09
11-03	Gp3	g.chr8:17089998G>A	Missense Mutation	CNOT7	p.P223S	CCR4-NOT transcriptio	33 (0.00)	17 (0.29)	0.39
11-03	Gp3	g.chr7:147926844C>G	Silent	CNTNAP2	p.T1118T	contactin associated pro	49 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr9:39175963G>A	Missense Mutation	CNTNAP3	p.P352S	contactin associated pro	37 (0.03)	32 (0.22)	0.58
11-03	Gp3	g.chr9:43737419C>T	Nonsense Mutation	CNTNAP3B	p.Q97*	contactin associated pro	46 (0.00)	33 (0.30)	0.81
11-03	Gp3	g.chr9:123888093C>G	Missense Mutation	CNTRL	p.A635G	centriolin	79 (0.00)	38 (0.16)	0.42
11-03	Gp3	g.chr1:103471414G>T	Missense Mutation	COL11A1	p.P609T	collagen, type XI, alpha	15 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr1:86375632C>G	Splice Site	COL24A1		collagen, type XXIV, al	36 (0.00)	24 (0.46)	1.22
11-03	Gp3	g.chr9:116931208C>T	Missense Mutation	COL27A1	p.A458V	collagen, type XXVII, a	97 (0.00)	65 (0.18)	0.49
11-03	Gp3	g.chr13:111088659C>T	Missense Mutation	COL4A2	p.T257I	collagen, type IV, alpha	20 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chrX:107403853C>A	Missense Mutation	COL4A6	p.M1455I	collagen, type IV, alpha	17 (0.00)	21 (0.24)	0.40
11-03	Gp3	g.chr2:238249748G>A	Missense Mutation	COL6A3	p.P2604L	collagen, type VI, alpha	74 (0.00)	56 (0.27)	0.71
11-03	Gp3	g.chr3:148917582A>G	Missense Mutation	CP	p.L473P	ceruloplasmin (ferroxid	19 (0.00)	30 (0.30)	0.80
11-03	Gp3	g.chr1:207718722G>A	Missense Mutation	CR1	p.G769E	complement component	99 (0.01)	40 (0.25)	0.41
11-03	Gp3	g.chr1:207718724C>A	Missense Mutation	CR1	p.Q770K	complement component	100 (0.00)	41 (0.24)	0.40
11-03	Gp3	g.chr1:207718748C>A	Missense Mutation	CR1	p.P778T	complement component	88 (0.00)	41 (0.24)	0.40
11-03	Gp3	g.chr20:20020291C>T	Missense Mutation	CRNKL1	p.E503K	crooked neck pre-mRN	18 (0.00)	31 (0.29)	0.77
11-03	Gp3	g.chr1:34082573G>T	Silent	CSMD2	p.G856G	CUB and Sushi multipl	28 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr15:64592601G>T	Nonsense Mutation	CSNK1G1	p.S33*	casein kinase 1, gamma	56 (0.00)	70 (0.17)	0.46
11-03	Gp3	g.chr20:18142648C>T	Silent	CSRP2BP	p.T288T	CSRP2 binding protein	46 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr20:18167932C>T	Silent	CSRP2BP	p.T725T	CSRP2 binding protein	69 (0.00)	42 (0.19)	0.51
11-03	Gp3	g.chr18:46238028C>A	Missense Mutation	CTIF	p.H182Q	CBP80/20-dependent tr	89 (0.00)	44 (0.18)	0.48
11-03	Gp3	g.chrX:16685647G>A	Missense Mutation	CTPS2	p.P429L	CTP synthase 2	16 (0.00)	161 (0.25)	0.42
11-03	Gp3	g.chr11:88027470G>A	Missense Mutation	CTSC	p.H366Y	cathepsin C	39 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr10:104183330C>T	Splice Site	CUEDC2		CUE domain containing	70 (0.00)	48 (0.17)	0.44
11-03	Gp3	g.chr7:148481082A>G	Missense Mutation	CUL1	p.N404S	cullin 1	20 (0.00)	35 (0.23)	0.61
11-03	Gp3	g.chr6:43160931G>A	Silent	CUL9	p.Q791Q	cullin 9	85 (0.00)	85 (0.16)	0.44
11-03	Gp3	g.chr6:43172580C>G	Missense Mutation	CUL9	p.S1478R	cullin 9	35 (0.00)	22 (0.64)	1.70
11-03	Gp3	g.chr19:15996780C>A	Nonsense Mutation	CYP4F2	p.E357*	cytochrome P450, famil	73 (0.00)	44 (0.16)	0.42
11-03	Gp3	g.chr8:59409351C>A	Missense Mutation	CYP7A1	p.E240D	cytochrome P450, famil	19 (0.00)	26 (0.35)	0.92
11-03	Gp3	g.chr6:39835356G>A	Missense Mutation	DAAM2	p.A167T	dishevelled associated a	38 (0.00)	32 (0.41)	1.08
11-03	Gp3	g.chr9:124396222G>A	Intron	DAB2IP		DAB2 interacting protei	19 (0.00)	16 (0.44)	1.17
11-03	Gp3	g.chr9:124396271C>A	Intron	DAB2IP		DAB2 interacting protei	21 (0.00)	16 (0.44)	1.17
11-03	Gp3	g.chr9:124471241G>A	Intron	DAB2IP		DAB2 interacting protei	31 (0.03)	21 (0.24)	0.63
11-03	Gp3	g.chr9:124510058C>A	Intron	DAB2IP		DAB2 interacting protei	51 (0.02)	78 (0.22)	0.58

11-03	Gp3	g.chr3:98518245C>A	Nonsense Mutation	DCBLD2	p.E767*	discoidin, CUB and LC	73 (0.01)	42 (0.19)	0.51
11-03	Gp3	g.chr11:125780267C>A	Nonsense Mutation	DDX25	p.C172*	DEAD (Asp-Glu-Ala-A	56 (0.00)	30 (0.27)	0.71
11-03	Gp3	g.chr11:125781347C>A	Missense Mutation	DDX25	p.T255N	DEAD (Asp-Glu-Ala-A	22 (0.00)	47 (0.15)	0.40
11-03	Gp3	g.chr5:176943332G>A	Silent	DDX41	p.V85V	DEAD (Asp-Glu-Ala-A	54 (0.00)	28 (0.43)	1.14
11-03	Gp3	g.chr20:29978235C>G	Missense Mutation	DEFB119	p.V18L	defensin, beta 119	51 (0.00)	61 (0.20)	0.52
11-03	Gp3	g.chr1:197564340G>A	Missense Mutation	DENND1B	p.P349S	DENN/MADD domain	88 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr9:19300213A>G	Missense Mutation	DENND4C	p.N399D	DENN/MADD domain	21 (0.00)	16 (0.38)	1.00
11-03	Gp3	g.chr12:31576601C>A	Silent	DENND5B	p.S800S	DENN/MADD domain	55 (0.02)	31 (0.16)	0.43
11-03	Gp3	g.chr10:12131185G>A	Silent	DHTKD1	p.Q306Q	dehydrogenase E1 and t	29 (0.00)	27 (0.26)	0.69
11-03	Gp3	g.chr4:24531230G>A	Missense Mutation	DHX15	p.P755L	DEAH (Asp-Glu-Ala-H	20 (0.00)	31 (0.32)	0.86
11-03	Gp3	g.chr1:182853896C>A	Missense Mutation	DHX9	p.Q1137K	DEAH (Asp-Glu-Ala-H	46 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr5:140951572C>T	Nonsense Mutation	DIAPH1	p.W798*	diaphanous-related for	46 (0.00)	54 (0.15)	0.40
11-03	Gp3	g.chr21:47959793C>T	Missense Mutation	DIP2A	p.S638L	DIP2 disco-interacting	46 (0.00)	36 (0.31)	0.81
11-03	Gp3	g.chr10:327151G>A	Silent	DIP2C	p.S1469S	DIP2 disco-interacting	23 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr4:107845774C>T	Missense Mutation	DKK2	p.G153S	dickkopf WNT signalin	22 (0.00)	13 (0.46)	1.23
11-03	Gp3	g.chr6:43420746T>A	Nonsense Mutation	DLK2	p.K90*	delta-like 2 homolog (D	65 (0.00)	53 (0.23)	0.60
11-03	Gp3	g.chr5:118469387T>C	Silent	DMXL1	p.L590L	Dmx-like 1	24 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr12:124270391C>A	Missense Mutation	DNAH10	p.N382K	dynein, axonemal, heav	15 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr17:7696430G>A	Missense Mutation	DNAH2	p.M2492I	dynein, axonemal, heav	85 (0.01)	14 (0.36)	0.45
11-03	Gp3	g.chr5:13753483G>C	Missense Mutation	DNAH5	p.N3577K	dynein, axonemal, heav	33 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr17:11784611C>A	Missense Mutation	DNAH9	p.Q3563K	dynein, axonemal, heav	50 (0.00)	21 (0.33)	0.89
11-03	Gp3	g.chr4:100851688G>A	Missense Mutation	DNAJB14	p.P75L	DnaJ (Hsp40) homolog,	54 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr7:157178310G>T	Missense Mutation	DNAJB6	p.K232N	DnaJ (Hsp40) homolog,	33 (0.00)	57 (0.32)	0.84
11-03	Gp3	g.chr12:49743437C>T	Missense Mutation	DNAJC22	p.A261V	DnaJ (Hsp40) homolog,	40 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr20:31395664C>G	Missense Mutation	DNMT3B	p.I839M	DNA (cytosine-5-)-met	35 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr10:128795093C>A	Missense Mutation	DOCK1	p.F185L	dedicator of cytokinesis	76 (0.00)	31 (0.26)	0.69
11-03	Gp3	g.chr10:128851012T>C	Missense Mutation	DOCK1	p.Y736H	dedicator of cytokinesis	77 (0.00)	82 (0.15)	0.39
11-03	Gp3	g.chr2:225661090C>T	Silent	DOCK10	p.R1627R	dedicator of cytokinesis	51 (0.00)	36 (0.19)	0.52
11-03	Gp3	g.chr5:169412892G>T	Nonsense Mutation	DOCK2	p.G479*	dedicator of cytokinesis	17 (0.00)	27 (0.30)	0.79
11-03	Gp3	g.chr3:51297638C>A	Silent	DOCK3	p.R746R	dedicator of cytokinesis	46 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr7:111629173C>T	Missense Mutation	DOCK4	p.E121K	dedicator of cytokinesis	55 (0.00)	41 (0.17)	0.46
11-03	Gp3	g.chr7:111629174A>T	Missense Mutation	DOCK4	p.N120K	dedicator of cytokinesis	55 (0.00)	42 (0.17)	0.44
11-03	Gp3	g.chr13:99537971C>T	Missense Mutation	DOCK9	p.E751K	dedicator of cytokinesis	65 (0.00)	29 (0.38)	1.01
11-03	Gp3	g.chr18:29126520G>A	Silent	DSG2	p.L1057L	desmoglein 2	40 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr18:28968847G>A	Missense Mutation	DSG4	p.R128Q	desmoglein 4	55 (0.00)	47 (0.30)	0.79

11-03	Gp3	g.chr6:7584936G>T	Nonsense Mutation	DSP	p.E2481*	desmoplakin	22 (0.00)	18 (0.33)	0.89
11-03	Gp3	g.chr7:76112300C>A	Missense Mutation	DTX2	p.N248K	deltex 2, E3 ubiquitin li	37 (0.00)	29 (0.21)	0.55
11-03	Gp3	g.chr1:221879599C>T	Missense Mutation	DUSP10	p.D341N	dual specificity phospha	93 (0.00)	43 (0.19)	0.50
11-03	Gp3	g.chr17:35872602G>T	Silent	DUSP14	p.V76V	dual specificity phospha	22 (0.00)	20 (0.25)	0.67
11-03	Gp3	g.chr3:108363240G>A	Silent	DZIP3	p.K457K	DAZ interacting zinc fir	47 (0.00)	37 (0.22)	0.58
11-03	Gp3	g.chr16:22284998G>T	Nonsense Mutation	EEF2K	p.E606*	eukaryotic elongation fa	41 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr17:78111277C>A	Missense Mutation	EIF4A3	p.M297I	eukaryotic translation in	32 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr3:184049091G>A	Missense Mutation	EIF4G1	p.G1313E	eukaryotic translation in	54 (0.00)	36 (0.19)	0.52
11-03	Gp3	g.chr19:48517459C>T	Silent	ELSPBP1	p.T34T	epididymal sperm bindi	28 (0.00)	19 (0.37)	1.30
11-03	Gp3	g.chr11:62375768C>T	Splice Site	EML3	p.D371N	echinoderm microtubul	74 (0.00)	63 (0.17)	0.47
11-03	Gp3	g.chr11:62375769C>T	Splice Site	EML3		echinoderm microtubul	74 (0.00)	63 (0.16)	0.42
11-03	Gp3	g.chr14:89087233C>T	Missense Mutation	EML5	p.R1747H	echinoderm microtubul	44 (0.00)	56 (0.14)	0.38
11-03	Gp3	g.chr14:89148295G>T	Silent	EML5	p.T1021T	echinoderm microtubul	72 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr19:6986347G>T	RNA	EMR4P		egf-like module contain	90 (0.00)	58 (0.12)	0.46
11-03	Gp3	g.chr17:77073766C>G	Missense Mutation	ENGASE	p.T79S	endo-beta-N-acetylgluc	43 (0.00)	14 (0.43)	1.14
11-03	Gp3	g.chr22:40161390C>A	Missense Mutation	ENTHD1	p.D353Y	ENTH domain containi	19 (0.00)	30 (0.23)	0.62
11-03	Gp3	g.chr10:101445560C>A	Missense Mutation	ENTPD7	p.A187D	ectonucleoside triphosp	32 (0.00)	25 (0.24)	0.64
11-03	Gp3	g.chr3:89390154A>C	Silent	EPHA3	p.S301S	EPH receptor A3	33 (0.00)	48 (0.15)	0.39
11-03	Gp3	g.chr17:19215416G>A	Missense Mutation	EPN2	p.E311K	epsin 2	97 (0.01)	102 (0.18)	0.47
11-03	Gp3	g.chr17:19215426G>A	Missense Mutation	EPN2	p.R314K	epsin 2	75 (0.00)	93 (0.19)	0.52
11-03	Gp3	g.chr5:96118857C>T	Missense Mutation	ERAP1	p.R728Q	endoplasmic reticulum	30 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr21:39807279T>C	Intron	ERG		v-ets avian erythroblast	16 (0.00)	26 (0.31)	0.53
11-03	Gp3	g.chr21:39811696C>G	Intron	ERG		v-ets avian erythroblast	41 (0.00)	39 (0.23)	0.40
11-03	Gp3	g.chr21:39907195G>A	Intron	ERG		v-ets avian erythroblast	32 (0.00)	25 (0.28)	0.48
11-03	Gp3	g.chr21:39919274G>A	Intron	ERG		v-ets avian erythroblast	15 (0.00)	55 (0.38)	0.66
11-03	Gp3	g.chr21:39921764C>A	Intron	ERG		v-ets avian erythroblast	20 (0.00)	28 (0.32)	0.55
11-03	Gp3	g.chr12:56527655C>T	Missense Mutation	ESYT1	p.P491S	extended synaptotagmin	24 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr4:5578040C>G	Missense Mutation	EVC2	p.E1067Q	Ellis van Creveld syndr	26 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr6:488997G>A	Missense Mutation	EXOC2	p.S888F	exocyst complex compo	45 (0.00)	44 (0.25)	0.67
11-03	Gp3	g.chr14:57714346C>T	Missense Mutation	EXOC5	p.D38N	exocyst complex compo	24 (0.00)	13 (0.38)	1.03
11-03	Gp3	g.chr9:133578479C>T	Missense Mutation	EXOSC2	p.R238W	exosome component 2	30 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr17:18430079G>A	Silent	FAM106A	p.L13L	family with sequence si	107 (0.00)	45 (0.16)	0.41
11-03	Gp3	g.chr9:96326625G>T	Missense Mutation	FAM120A	p.V1054L	family with sequence si	33 (0.00)	20 (0.35)	0.93
11-03	Gp3	g.chr10:15256055C>A	Missense Mutation	FAM171A1	p.S511I	family with sequence si	33 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr10:15258105G>A	Silent	FAM171A1	p.P292P	family with sequence si	56 (0.00)	34 (0.29)	0.78

11-03	Gp3	g.chr5:93294562C>A	Missense Mutation	FAM172A	p.G163W	family with sequence si	28 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr12:49994241G>T	Silent	FAM186B	p.T394T	family with sequence si	15 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr4:2695496C>G	Missense Mutation	FAM193A	p.T727R	family with sequence si	20 (0.00)	29 (0.28)	0.74
11-03	Gp3	g.chr1:179023672G>T	Missense Mutation	FAM20B	p.G158V	family with sequence si	30 (0.00)	35 (0.17)	0.46
11-03	Gp3	g.chr1:93309390C>A	Silent	FAM69A	p.V279V	family with sequence si	30 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr2:33813501C>A	Missense Mutation	FAM98A	p.E141D	family with sequence si	51 (0.02)	42 (0.14)	0.38
11-03	Gp3	g.chr16:89877450G>A	Silent	FANCA	p.L105L	Fanconi anemia, comple	57 (0.00)	39 (0.23)	0.62
11-03	Gp3	g.chr15:89801996C>A	Missense Mutation	FANCI	p.A49D	Fanconi anemia, comple	31 (0.00)	53 (0.15)	0.40
11-03	Gp3	g.chr15:89826395G>A	Missense Mutation	FANCI	p.A538T	Fanconi anemia, comple	69 (0.01)	103 (0.44)	1.17
11-03	Gp3	g.chr14:45642361G>T	Missense Mutation	FANCM	p.C729F	Fanconi anemia, comple	26 (0.00)	15 (0.33)	0.89
11-03	Gp3	g.chr4:187524878G>C	Missense Mutation	FAT1	p.A3601G	FAT atypical cadherin 1	39 (0.00)	39 (0.15)	0.41
11-03	Gp3	g.chr5:150923229C>T	Missense Mutation	FAT2	p.E2487K	FAT atypical cadherin 2	28 (0.00)	26 (0.23)	0.46
11-03	Gp3	g.chr11:92577145C>A	Missense Mutation	FAT3	p.R3388S	FAT atypical cadherin 3	27 (0.00)	34 (0.24)	0.63
11-03	Gp3	g.chr11:92622393G>T	Missense Mutation	FAT3	p.V4214F	FAT atypical cadherin 3	20 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr19:40424283C>T	Nonsense Mutation	FCGBP	p.W640*	Fc fragment of IgG bind	26 (0.04)	28 (0.25)	0.67
11-03	Gp3	g.chr11:72560855G>A	Missense Mutation	FCHSD2	p.P327L	FCH and double SH3 d	81 (0.01)	80 (0.15)	0.40
11-03	Gp3	g.chr1:155289606G>T	Missense Mutation	FDPS	p.G316W	farnesyl diphosphate sy	51 (0.00)	26 (0.35)	0.92
11-03	Gp3	g.chr20:6077627C>T	Silent	FERMT1	p.E337E	fermitin family member	23 (0.04)	39 (0.54)	1.44
11-03	Gp3	g.chr15:91430476C>A	Missense Mutation	FES	p.H182N	FES proto-oncogene, ty	29 (0.00)	26 (0.31)	0.82
11-03	Gp3	g.chr12:32786607G>A	Missense Mutation	FGD4	p.R741K	FYVE, RhoGEF and P	25 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr10:123353286C>T	Missense Mutation	FGFR2	p.A16T	fibroblast growth factor	109 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr1:152285455C>A	Missense Mutation	FLG	p.R636M	filaggrin	44 (0.00)	38 (0.24)	0.44
11-03	Gp3	g.chr14:86088880G>A	Missense Mutation	FLRT2	p.G341D	fibronectin leucine rich	55 (0.02)	49 (0.37)	0.98
11-03	Gp3	g.chr5:180043921C>G	Missense Mutation	FLT4	p.M1025I	fms-related tyrosine kin	15 (0.00)	12 (0.42)	1.11
11-03	Gp3	g.chr2:153482020C>T	Missense Mutation	FMNL2	p.P11S	formin-like 2	68 (0.00)	25 (0.40)	1.07
11-03	Gp3	g.chr1:171303826C>T	Silent	FMO4	p.I368I	flavin containing mono	43 (0.00)	43 (0.16)	0.43
11-03	Gp3	g.chr6:159667938T>A	Missense Mutation	FNDC1	p.F1543I	fibronectin type III dom	18 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr12:2981335C>A	Missense Mutation	FOXM1	p.G194V	forkhead box M1	52 (0.00)	47 (0.15)	0.40
11-03	Gp3	g.chr13:41134782C>A	Missense Mutation	FOXO1	p.E282D	forkhead box O1	36 (0.00)	33 (0.24)	0.65
11-03	Gp3	g.chr19:52249646C>A	Missense Mutation	FPR1	p.R201I	formyl peptide receptor	25 (0.00)	33 (0.30)	0.81
11-03	Gp3	g.chr9:14808036C>A	Missense Mutation	FREM1	p.G997V	FRAS1 related extracell	53 (0.00)	40 (0.28)	0.73
11-03	Gp3	g.chrX:153774314C>T	Silent	G6PD	p.E49E	glucose-6-phosphate de	15 (0.00)	12 (0.50)	0.83
11-03	Gp3	g.chr3:30875725G>A	Silent	GADL1	p.L318L	glutamate decarboxylas	29 (0.00)	46 (0.24)	0.64
11-03	Gp3	g.chr4:844840C>T	Missense Mutation	GAK	p.E1181K	cyclin G associated kina	34 (0.00)	32 (0.38)	1.00
11-03	Gp3	g.chr22:30951569G>A	Nonsense Mutation	GAL3ST1	p.R215*	galactose-3-O-sulfotran	21 (0.00)	27 (0.19)	0.49

11-03	Gp3	g.chr11:62407142C>T	Missense Mutation	GANAB	p.D34N	glucosidase, alpha; neut	32 (0.00)	44 (0.32)	0.85
11-03	Gp3	g.chr16:90099257G>A	Silent	GAS8	p.K140K	growth arrest-specific 8	21 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr19:19616154C>T	Splice Site	GATAD2A	p.G592G	GATA zinc finger dom	36 (0.00)	31 (0.29)	0.77
11-03	Gp3	g.chr1:155187132C>T	RNA	GBAP1		glucosidase, beta, acid	31 (0.00)	17 (0.41)	1.10
11-03	Gp3	g.chr3:141901888C>T	Missense Mutation	GK5	p.A274T	glycerol kinase 5 (putati	39 (0.03)	36 (0.17)	0.44
11-03	Gp3	g.chr17:679118C>T	Silent	GLOD4	p.R101R	glyoxalase domain cont	37 (0.03)	57 (0.16)	0.42
11-03	Gp3	g.chrX:102974051G>A	Silent	GLRA4	p.G289G	glycine receptor, alpha	23 (0.00)	21 (0.24)	0.40
11-03	Gp3	g.chr6:1961118C>T	Missense Mutation	GMDS	p.G143D	GDP-mannose 4,6-dehy	24 (0.00)	30 (0.27)	0.71
11-03	Gp3	g.chr10:101162451G>T	Silent	GOT1	p.R330R	glutamic-oxaloacetic tra	44 (0.00)	57 (0.25)	0.65
11-03	Gp3	g.chr17:4836268C>A	Silent	GP1BA	p.V123V	glycoprotein Ib (platelet	35 (0.00)	18 (0.33)	0.42
11-03	Gp3	g.chr4:22439902C>T	Silent	GPR125	p.V354V	G protein-coupled recep	19 (0.00)	12 (0.42)	1.11
11-03	Gp3	g.chr6:142691912G>T	Nonsense Mutation	GPR126	p.E351*	G protein-coupled recep	50 (0.00)	62 (0.15)	0.39
11-03	Gp3	g.chr7:37780214G>C	Missense Mutation	GPR141	p.L73F	G protein-coupled recep	17 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chrX:19027894C>T	Silent	GPR64	p.L421L	G protein-coupled recep	18 (0.00)	15 (0.33)	0.56
11-03	Gp3	g.chrX:19027896G>T	Missense Mutation	GPR64	p.L421M	G protein-coupled recep	18 (0.00)	14 (0.36)	0.60
11-03	Gp3	g.chr5:89949151G>T	Missense Mutation	GPR98	p.A1254S	G protein-coupled recep	97 (0.01)	55 (0.35)	0.92
11-03	Gp3	g.chr5:89990371G>A	Missense Mutation	GPR98	p.E2600K	G protein-coupled recep	54 (0.00)	45 (0.47)	1.24
11-03	Gp3	g.chr17:7216981G>A	Silent	GPS2	p.F180F	G protein pathway supp	54 (0.00)	11 (0.55)	0.69
11-03	Gp3	g.chr12:66788053T>A	Silent	GRIP1	p.S636S	glutamate receptor inter	38 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr6:146719966C>T	Silent	GRM1	p.I597I	glutamate receptor, met	36 (0.00)	54 (0.17)	0.44
11-03	Gp3	g.chr7:86394614C>T	Silent	GRM3	p.G51G	glutamate receptor, met	22 (0.00)	28 (0.21)	0.57
11-03	Gp3	g.chrX:16142232G>T	Silent	GRPR	p.L52L	gastrin-releasing peptid	43 (0.02)	30 (0.63)	1.06
11-03	Gp3	g.chr8:30541638C>A	Missense Mutation	GSR	p.G374W	glutathione reductase	45 (0.00)	15 (0.53)	0.71
11-03	Gp3	g.chr1:110257761G>A	Missense Mutation	GSTM5	p.V115M	glutathione S-transferas	42 (0.00)	39 (0.26)	0.68
11-03	Gp3	g.chr12:124144713G>A	Splice Site	GTF2H3	p.E286E	general transcription fac	50 (0.00)	46 (0.15)	0.41
11-03	Gp3	g.chr11:76414516G>A	RNA	GUCY2EP		guanylate cyclase 2E, p	36 (0.03)	33 (0.21)	0.57
11-03	Gp3	g.chr7:65441189C>T	Splice Site	GUSB	p.G242E	glucuronidase, beta	15 (0.00)	22 (0.23)	0.79
11-03	Gp3	g.chr4:144801602G>A	Missense Mutation	GYPE	p.S33F	glycophorin E (MNS bl	125 (0.00)	61 (0.15)	0.39
11-03	Gp3	g.chr12:21728860A>T	Missense Mutation	GYS2	p.H145Q	glycogen synthase 2 (liv	23 (0.00)	42 (0.24)	0.63
11-03	Gp3	g.chr2:172822404G>T	Missense Mutation	HAT1	p.D196Y	histone acetyltransferas	28 (0.00)	30 (0.27)	0.71
11-03	Gp3	g.chr7:18702262C>A	Intron	HDAC9		histone deacetylase 9	47 (0.00)	41 (0.20)	0.52
11-03	Gp3	g.chr7:18820512T>A	Intron	HDAC9		histone deacetylase 9	42 (0.00)	16 (0.44)	1.17
11-03	Gp3	g.chr7:18865206A>G	Intron	HDAC9		histone deacetylase 9	31 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr7:18868859G>T	Intron	HDAC9		histone deacetylase 9	17 (0.00)	30 (0.33)	0.89
11-03	Gp3	g.chr7:18905211C>T	Intron	HDAC9		histone deacetylase 9	53 (0.00)	51 (0.20)	0.52

11-03	Gp3	g.chr7:18957525G>T	Intron	HDAC9		histone deacetylase 9	16 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr7:19033452G>A	Intron	HDAC9		histone deacetylase 9	79 (0.00)	44 (0.34)	0.91
11-03	Gp3	g.chr2:242178111C>T	Missense Mutation	HDLBP	p.R901Q	high density lipoprotein	42 (0.02)	33 (0.24)	0.65
11-03	Gp3	g.chr1:236719140G>A	Silent	HEATR1	p.L1872L	HEAT repeat containing	53 (0.02)	34 (0.21)	0.55
11-03	Gp3	g.chr1:236719168G>A	Silent	HEATR1	p.S1862S	HEAT repeat containing	41 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr12:112677821G>A	Missense Mutation	HECTD4	p.L1511F	HECT domain containi	47 (0.02)	44 (0.39)	1.03
11-03	Gp3	g.chr17:65146062G>T	Missense Mutation	HELZ	p.A799D	helicase with zinc finge	33 (0.00)	54 (0.22)	0.59
11-03	Gp3	g.chr9:100693459C>A	Missense Mutation	HEMGN	p.R73L	hemogen	49 (0.02)	67 (0.21)	0.56
11-03	Gp3	g.chr15:63967147G>A	Missense Mutation	HERC1	p.H2414Y	HECT and RLD domai	51 (0.00)	104 (0.16)	0.44
11-03	Gp3	g.chr15:64048745G>T	Missense Mutation	HERC1	p.T475K	HECT and RLD domai	16 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr15:20618532C>A	RNA	HERC2P3		hect domain and RLD 2	20 (0.00)	42 (0.33)	0.89
11-03	Gp3	g.chr4:89317188G>A	Missense Mutation	HERC6	p.G261R	HECT and RLD domai	15 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr7:35674992C>G	Missense Mutation	HERPUD2	p.A232P	HERPUD family memb	41 (0.00)	49 (0.18)	0.49
11-03	Gp3	g.chr8:43014188G>T	Splice Site	HGSNAT		heparan-alpha-glucosa	69 (0.01)	43 (0.16)	0.43
11-03	Gp3	g.chr9:99735141C>T	Missense Mutation	HIATL2	p.M66I	hippocampus abundant	57 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr14:62187117G>A	Missense Mutation	HIF1A	p.R19Q	hypoxia inducible facto	20 (0.00)	21 (0.43)	1.14
11-03	Gp3	g.chr7:75192347C>A	Silent	HIP1	p.L304L	huntingtin interacting pr	37 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr6:27114939C>T	Missense Mutation	HIST1H2AH	p.A11V	histone cluster 1, H2ah	34 (0.03)	33 (0.21)	0.57
11-03	Gp3	g.chr6:12161772C>T	Silent	HIVEP1	p.D2196D	human immunodeficien	47 (0.00)	26 (0.31)	0.82
11-03	Gp3	g.chr6:143091630C>T	Missense Mutation	HIVEP2	p.G1416S	human immunodeficien	50 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr6:143095304C>A	Missense Mutation	HIVEP2	p.C191F	human immunodeficien	25 (0.00)	39 (0.23)	0.62
11-03	Gp3	g.chr21:38308775G>A	Missense Mutation	HLCS	p.R324C	holocarboxylase synthet	41 (0.00)	33 (0.48)	1.29
11-03	Gp3	g.chr16:4556988G>A	Missense Mutation	HMOX2	p.G60D	heme oxygenase (decyc	114 (0.01)	149 (0.15)	0.41
11-03	Gp3	g.chr17:73132267G>A	Missense Mutation	HN1	p.P86L	hematological and neur	25 (0.00)	43 (0.16)	0.43
11-03	Gp3	g.chr8:76476216C>T	Missense Mutation	HNF4G	p.P408L	hepatocyte nuclear facto	16 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr5:179043149G>T	Silent	HNRNPH1	p.G426G	heterogeneous nuclear r	28 (0.00)	64 (0.17)	0.46
11-03	Gp3	g.chr19:41807570G>A	Missense Mutation	HNRNPUL1	p.G550R	heterogeneous nuclear r	67 (0.01)	34 (0.29)	0.78
11-03	Gp3	g.chr1:152187913C>A	Missense Mutation	HRNR	p.Q2064H	hornerin	70 (0.00)	22 (0.41)	0.76
11-03	Gp3	g.chr17:14248897C>T	Silent	HS3ST3B1	p.R369R	heparan sulfate (glucosa	47 (0.00)	52 (0.35)	0.92
11-03	Gp3	g.chr1:162762515G>A	Silent	HSD17B7	p.A34A	hydroxysteroid (17-beta	36 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr10:38654460G>A	RNA	HSD17B7P2		hydroxysteroid (17-beta	68 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr4:128725170C>A	Missense Mutation	HSPA4L	p.Q305K	heat shock 70kDa protei	29 (0.00)	21 (0.33)	0.89
11-03	Gp3	g.chr11:113860424T>C	Missense Mutation	HTR3A	p.L459P	5-hydroxytryptamine (s	16 (0.00)	17 (0.35)	0.94
11-03	Gp3	g.chr10:124268264G>A	Silent	HTRA1	p.E366E	HtrA serine peptidase 1	41 (0.02)	38 (0.37)	0.98
11-03	Gp3	g.chr4:3214302C>T	Silent	HTT	p.L2214L	huntingtin	72 (0.00)	35 (0.14)	0.38

11-03	Gp3	g.chr11:118926028C>A	Silent	HYOU1	p.T96T	hypoxia up-regulated 1	27 (0.00)	19 (0.37)	0.98
11-03	Gp3	g.chr9:95040554G>A	Nonsense Mutation	IARS	p.R254*	isoleucyl-tRNA syntheta	65 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr1:220284255C>A	Silent	IARS2	p.I413I	isoleucyl-tRNA syntheta	19 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr19:10385665G>T	Missense Mutation	ICAM1	p.D98Y	intercellular adhesion m	27 (0.00)	53 (0.17)	0.57
11-03	Gp3	g.chr15:78454047C>T	Silent	IDH3A	p.T138T	isocitrate dehydrogenas	33 (0.00)	42 (0.36)	0.95
11-03	Gp3	g.chr8:39785524C>T	Silent	IDO1	p.S344S	indoleamine 2,3-dioxyg	24 (0.00)	34 (0.44)	1.18
11-03	Gp3	g.chr17:41165648G>T	Silent	IFI35	p.G179G	interferon-induced prote	22 (0.00)	26 (0.42)	1.13
11-03	Gp3	g.chr12:102796292C>A	Missense Mutation	IGF1	p.R136M	insulin-like growth fact	19 (0.00)	34 (0.35)	0.94
11-03	Gp3	g.chr12:102869459G>A	Missense Mutation	IGF1	p.A45V	insulin-like growth fact	46 (0.00)	34 (0.21)	0.55
11-03	Gp3	g.chr12:102869491C>T	Silent	IGF1	p.P34P	insulin-like growth fact	29 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr14:106109941C>T	RNA	IGHG2		immunoglobulin heavy	16 (0.00)	30 (0.43)	1.16
11-03	Gp3	g.chr14:106586176G>A	RNA	IGHV3-13		immunoglobulin heavy	71 (0.00)	35 (0.17)	0.46
11-03	Gp3	g.chr14:107013124G>A	RNA	IGHV3-49		immunoglobulin heavy	58 (0.00)	41 (0.17)	0.46
11-03	Gp3	g.chr2:89399430T>A	RNA	IGKV1-16		immunoglobulin kappa	25 (0.00)	25 (0.20)	0.40
11-03	Gp3	g.chr22:22764540G>A	RNA	IGLV1-40		immunoglobulin lambd	26 (0.00)	33 (0.21)	0.57
11-03	Gp3	g.chr22:23214078G>A	RNA	IGLV4-3		immunoglobulin lambd	23 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr1:206651620C>T	Silent	IKBKE	p.V310V	inhibitor of kappa light	29 (0.00)	41 (0.24)	0.40
11-03	Gp3	g.chr3:136699331C>T	Missense Mutation	IL20RB	p.P38S	interleukin 20 receptor	38 (0.00)	48 (0.29)	0.78
11-03	Gp3	g.chr7:22768374C>A	Missense Mutation	IL6	p.N91K	interleukin 6	50 (0.00)	46 (0.22)	0.58
11-03	Gp3	g.chr1:153640102T>A	Missense Mutation	ILF2	p.Y108F	interleukin enhancer bin	101 (0.01)	133 (0.27)	0.51
11-03	Gp3	g.chr19:10799921C>A	Missense Mutation	ILF3	p.S873Y	interleukin enhancer bin	48 (0.00)	37 (0.14)	0.45
11-03	Gp3	g.chr7:128038643C>T	Missense Mutation	IMPDH1	p.C210Y	IMP (inosine 5'-monopl	27 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr3:100949935C>A	Silent	IMPG2	p.V1096V	interphotoreceptor matri	29 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr4:142974222A>T	Intron	INPP4B		inositol polyphosphate-	76 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr4:142996512C>T	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr4:143204099A>G	Intron	INPP4B		inositol polyphosphate-	54 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr4:143211042C>T	Intron	INPP4B		inositol polyphosphate-	24 (0.00)	38 (0.16)	0.42
11-03	Gp3	g.chr4:143233037C>A	Intron	INPP4B		inositol polyphosphate-	20 (0.00)	41 (0.46)	1.24
11-03	Gp3	g.chr4:143234988C>A	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	34 (0.26)	0.71
11-03	Gp3	g.chr4:143257329C>A	Intron	INPP4B		inositol polyphosphate-	23 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr4:143275514G>A	Intron	INPP4B		inositol polyphosphate-	27 (0.00)	36 (0.17)	0.44
11-03	Gp3	g.chr4:143285941C>G	Intron	INPP4B		inositol polyphosphate-	50 (0.00)	23 (0.30)	0.81
11-03	Gp3	g.chr4:143296588G>T	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr4:143322263C>A	Intron	INPP4B		inositol polyphosphate-	53 (0.00)	52 (0.17)	0.46
11-03	Gp3	g.chr4:143332678A>T	Intron	INPP4B		inositol polyphosphate-	46 (0.00)	43 (0.16)	0.43

11-03	Gp3	g.chr4:143402953G>T	Intron	INPP4B		inositol polyphosphate-4	43 (0.00)	54 (0.15)	0.40
11-03	Gp3	g.chr4:143511232G>A	Intron	INPP4B		inositol polyphosphate-4	88 (0.00)	56 (0.20)	0.52
11-03	Gp3	g.chr4:143527454C>T	Intron	INPP4B		inositol polyphosphate-4	24 (0.00)	35 (0.20)	0.53
11-03	Gp3	g.chr4:143544206G>A	Intron	INPP4B		inositol polyphosphate-4	35 (0.00)	26 (0.42)	1.13
11-03	Gp3	g.chr4:143582359C>A	Intron	INPP4B		inositol polyphosphate-4	59 (0.00)	27 (0.48)	1.28
11-03	Gp3	g.chr4:143582360T>A	Intron	INPP4B		inositol polyphosphate-4	57 (0.00)	28 (0.43)	1.14
11-03	Gp3	g.chr4:143587928C>T	Intron	INPP4B		inositol polyphosphate-4	26 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr4:143645624C>T	Intron	INPP4B		inositol polyphosphate-4	30 (0.00)	38 (0.37)	0.98
11-03	Gp3	g.chr4:143673948C>A	Intron	INPP4B		inositol polyphosphate-4	38 (0.00)	29 (0.21)	0.55
11-03	Gp3	g.chr4:143688963G>A	Intron	INPP4B		inositol polyphosphate-4	46 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr4:143735143G>A	Intron	INPP4B		inositol polyphosphate-4	78 (0.00)	53 (0.28)	0.75
11-03	Gp3	g.chr4:143753248G>A	Intron	INPP4B		inositol polyphosphate-4	69 (0.00)	51 (0.16)	0.42
11-03	Gp3	g.chr4:143765852C>T	Intron	INPP4B		inositol polyphosphate-4	56 (0.00)	61 (0.26)	0.70
11-03	Gp3	g.chr17:60002380C>T	Missense Mutation	INTS2	p.S125N	integrator complex subu	99 (0.00)	48 (0.23)	0.61
11-03	Gp3	g.chr11:77649811C>A	Missense Mutation	INTS4	p.G351C	integrator complex subu	39 (0.00)	43 (0.16)	0.43
11-03	Gp3	g.chr11:9466685G>A	Missense Mutation	IPO7	p.A1021T	importin 7	26 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr1:156505021C>T	Silent	IQGAP3	p.V1147V	IQ motif containing GT	71 (0.00)	46 (0.24)	0.45
11-03	Gp3	g.chr3:10280486C>A	Missense Mutation	IRAK2	p.L510I	interleukin-1 receptor-a	19 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr16:71949619G>T	Nonsense Mutation	IST1	p.E26*	increased sodium tolera	37 (0.00)	34 (0.26)	0.71
11-03	Gp3	g.chr3:128813884G>A	Missense Mutation	ISY1-RAB43	p.T327I	ISY1-RAB43 readthrou	16 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr5:52344287G>T	Missense Mutation	ITGA2	p.S161I	integrin, alpha 2 (CD49	45 (0.00)	27 (0.41)	1.09
11-03	Gp3	g.chr16:30531250C>A	Missense Mutation	ITGAL	p.L1101M	integrin, alpha L (antige	56 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr3:4669545C>G	Missense Mutation	ITPR1	p.L88V	inositol 1,4,5-trisphosph	65 (0.00)	39 (0.59)	1.04
11-03	Gp3	g.chr4:6051560G>A	Missense Mutation	JAKMIP1	p.L650F	janus kinase and microt	121 (0.01)	82 (0.22)	0.59
11-03	Gp3	g.chr6:15501467G>A	Missense Mutation	JARID2	p.G759R	jumonji, AT rich interac	56 (0.00)	42 (0.40)	1.08
11-03	Gp3	g.chr10:64975313G>A	Splice Site	JMJD1C	p.H274H	jumonji domain contain	20 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr1:6142328C>A	Missense Mutation	KCNAB2	p.A92D	potassium voltage-gated	26 (0.00)	15 (0.33)	0.89
11-03	Gp3	g.chr17:7828458G>A	Silent	KCNAB3	p.D194D	potassium voltage-gated	37 (0.03)	57 (0.44)	0.55
11-03	Gp3	g.chr14:63174581C>A	Missense Mutation	KCNH5	p.S871I	potassium voltage-gated	35 (0.00)	21 (0.33)	0.89
11-03	Gp3	g.chr11:77884887G>A	Silent	KCTD21	p.I238I	potassium channel tetra	21 (0.00)	43 (0.21)	0.56
11-03	Gp3	g.chr1:23381623C>G	Missense Mutation	KDM1A	p.F284L	lysine (K)-specific dem	17 (0.00)	42 (0.31)	0.83
11-03	Gp3	g.chr9:2829790G>T	Missense Mutation	KIAA0020	p.T279K	KIAA0020	31 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr1:155887340A>T	Missense Mutation	KIAA0907	p.F464I	KIAA0907	17 (0.00)	25 (0.24)	0.64
11-03	Gp3	g.chr6:84895095G>C	Silent	KIAA1009	p.A491A		72 (0.00)	17 (0.29)	0.38
11-03	Gp3	g.chr5:175774676C>G	Missense Mutation	KIAA1191	p.G282A	KIAA1191	22 (0.00)	48 (0.15)	0.39

11-03	Gp3	g.chr15:81181900A>T	Silent	KIAA1199	p.P351P		19 (0.00)	22 (0.45)	1.21
11-03	Gp3	g.chr10:70768648G>T	Missense Mutation	KIAA1279	p.G281C	KIAA1279	41 (0.02)	26 (0.31)	0.82
11-03	Gp3	g.chr18:34802045G>A	Missense Mutation	KIAA1328	p.R526H	KIAA1328	36 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr1:33234264G>A	Silent	KIAA1522	p.T99T	KIAA1522	43 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr1:180885981G>A	Missense Mutation	KIAA1614	p.V248M	KIAA1614	72 (0.00)	37 (0.22)	0.58
11-03	Gp3	g.chr22:25566876G>A	Silent	KIAA1671	p.T1540T	KIAA1671	27 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr9:5922328G>A	Missense Mutation	KIAA2026	p.P1223L	KIAA2026	48 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr6:17764842C>T	Silent	KIF13A	p.S1639S	kinesin family member	27 (0.00)	44 (0.18)	0.48
11-03	Gp3	g.chr1:10394623C>A	Silent	KIF1B	p.I990I	kinesin family member	56 (0.00)	27 (0.19)	0.63
11-03	Gp3	g.chr1:10407826C>A	Missense Mutation	KIF1B	p.P1269T	kinesin family member	20 (0.00)	15 (0.67)	2.27
11-03	Gp3	g.chr1:10434420G>T	Nonsense Mutation	KIF1B	p.E1665*	kinesin family member	79 (0.00)	113 (0.19)	0.63
11-03	Gp3	g.chr13:33635004C>T	Silent	KL	p.S596S	klotho	50 (0.00)	25 (0.36)	0.41
11-03	Gp3	g.chr10:3825048A>T	Intron	KLF6		Kruppel-like factor 6	99 (0.00)	45 (0.16)	0.41
11-03	Gp3	g.chr17:39998197C>T	Missense Mutation	KLHL10	p.P106L	kelch-like family memb	39 (0.00)	34 (0.24)	0.63
11-03	Gp3	g.chr19:51518726C>T	Missense Mutation	KLK10	p.V209I	kallikrein-related peptid	15 (0.00)	51 (0.31)	1.11
11-03	Gp3	g.chr11:118343281C>T	Silent	KMT2A	p.S469S	lysine (K)-specific meth	16 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr12:49420638C>T	Silent	KMT2D	p.E5037E	lysine (K)-specific meth	36 (0.00)	21 (0.33)	0.89
11-03	Gp3	g.chr7:104752545G>T	Nonsense Mutation	KMT2E	p.E1448*	lysine (K)-specific meth	69 (0.00)	61 (0.16)	0.44
11-03	Gp3	g.chr7:98771378C>T	Missense Mutation	KPNA7	p.D502N	karyopherin alpha 7 (im	48 (0.02)	37 (0.16)	0.43
11-03	Gp3	g.chr12:52941666G>A	Missense Mutation	KRT71	p.S360L	keratin 71	52 (0.00)	17 (0.53)	0.43
11-03	Gp3	g.chr12:117968797G>A	Missense Mutation	KSR2	p.T584M	kinase suppressor of ras	28 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr19:54868215G>C	Silent	LAIR1	p.S156S	leukocyte-associated im	16 (0.00)	11 (0.45)	1.21
11-03	Gp3	g.chr7:107626705C>A	Missense Mutation	LAMB1	p.G176V	laminin, beta 1	41 (0.00)	41 (0.27)	0.72
11-03	Gp3	g.chr7:107745061G>T	Missense Mutation	LAMB4	p.H292N	laminin, beta 4	83 (0.00)	66 (0.15)	0.40
11-03	Gp3	g.chr1:183085751T>A	Nonsense Mutation	LAMC1	p.C456*	laminin, gamma 1 (form	26 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr4:129019426C>T	Silent	LARP1B	p.L252L	La ribonucleoprotein do	24 (0.00)	24 (0.29)	0.78
11-03	Gp3	g.chr16:25176017C>G	Missense Mutation	LCMT1	p.A223G	leucine carboxyl methyl	93 (0.01)	67 (0.19)	0.52
11-03	Gp3	g.chr19:40197949A>T	Missense Mutation	LGALS14	p.E104V	lectin, galactoside-bindi	35 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr17:25975930C>A	Nonsense Mutation	LGALS9	p.Y298*	lectin, galactoside-bindi	28 (0.00)	24 (0.25)	0.67
11-03	Gp3	g.chr1:202269980G>T	Silent	LGR6	p.G263G	leucine-rich repeat conta	89 (0.01)	38 (0.16)	0.42
11-03	Gp3	g.chr4:83905425C>G	Missense Mutation	LIN54	p.R191S	lin-54 DREAM MuvB c	17 (0.00)	22 (0.41)	1.09
11-03	Gp3	g.chr22:47857547T>C	Silent	LL22NC03-75	p.R51R		50 (0.02)	34 (0.15)	0.39
11-03	Gp3	g.chr17:18145232G>A	Missense Mutation	LLGL1	p.R934H	lethal giant larvae homo	39 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr3:100174762C>T	Missense Mutation	LNP1	p.P177S	leukemia NUP98 fusion	30 (0.00)	27 (0.63)	1.68
11-03	Gp3	g.chr5:96320838T>C	Silent	LNPEP	p.C305C	leucyl/cystinyl aminope	25 (0.00)	36 (0.17)	0.44

11-03	Gp3	g.chr9:113704191G>T	Silent	LPAR1	p.A101A	lysophosphatidic acid re	26 (0.00)	20 (0.35)	0.93
11-03	Gp3	g.chr16:55562423T>C	Missense Mutation	LPCAT2	p.F149S	lysophosphatidylcholine	101 (0.00)	55 (0.22)	0.58
11-03	Gp3	g.chr2:11959611G>A	Splice Site	LPIN1	p.E496K	lipin 1	57 (0.00)	47 (0.21)	0.57
11-03	Gp3	g.chr2:11959698T>A	Missense Mutation	LPIN1	p.Y525N	lipin 1	53 (0.00)	65 (0.15)	0.41
11-03	Gp3	g.chr8:105503697A>T	Missense Mutation	LRP12	p.M595K	low density lipoprotein	34 (0.00)	60 (0.15)	0.40
11-03	Gp3	g.chr2:141055383G>A	Nonsense Mutation	LRP1B	p.Q4321*	low density lipoprotein	43 (0.00)	132 (0.54)	1.43
11-03	Gp3	g.chr2:141116486G>A	Missense Mutation	LRP1B	p.H3721Y	low density lipoprotein	53 (0.00)	31 (0.29)	0.77
11-03	Gp3	g.chr12:7015658C>A	Missense Mutation	LRRC23	p.P108T	leucine rich repeat conta	16 (0.00)	102 (0.34)	0.92
11-03	Gp3	g.chr9:114371360T>A	RNA	LRRC37A5P		leucine rich repeat conta	46 (0.00)	45 (0.24)	0.65
11-03	Gp3	g.chr2:160755259C>G	Missense Mutation	LY75-CD302	p.A136P	LY75-CD302 readthrou	35 (0.00)	13 (0.62)	0.84
11-03	Gp3	g.chr1:39927653C>A	Missense Mutation	MACF1	p.H7107N	microtubule-actin crossl	59 (0.02)	58 (0.22)	0.60
11-03	Gp3	g.chr11:47307122G>A	Silent	MADD	p.G844G	MAP-kinase activating	45 (0.00)	26 (0.23)	0.62
11-03	Gp3	g.chrX:151092955G>A	Silent	MAGEA4	p.L273L	melanoma antigen famil	21 (0.00)	49 (0.24)	0.41
11-03	Gp3	g.chr7:77671238G>T	Intron	MAGI2		membrane associated gu	84 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr7:77855907G>A	Intron	MAGI2		membrane associated gu	57 (0.00)	27 (0.26)	0.69
11-03	Gp3	g.chr7:77889673G>A	Intron	MAGI2		membrane associated gu	44 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr7:77925411G>A	Intron	MAGI2		membrane associated gu	24 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr7:77930848T>A	Intron	MAGI2		membrane associated gu	52 (0.00)	47 (0.19)	0.51
11-03	Gp3	g.chr7:77960442C>A	Intron	MAGI2		membrane associated gu	20 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr7:77984851C>A	Intron	MAGI2		membrane associated gu	50 (0.00)	46 (0.15)	0.41
11-03	Gp3	g.chr7:78039374G>T	Intron	MAGI2		membrane associated gu	48 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr7:78062938C>T	Intron	MAGI2		membrane associated gu	33 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr7:78068937G>A	Intron	MAGI2		membrane associated gu	25 (0.00)	34 (0.26)	0.71
11-03	Gp3	g.chr7:78177739A>G	Intron	MAGI2		membrane associated gu	24 (0.00)	53 (0.17)	0.45
11-03	Gp3	g.chr7:78240792C>A	Intron	MAGI2		membrane associated gu	90 (0.00)	67 (0.24)	0.64
11-03	Gp3	g.chr7:78598643C>G	Intron	MAGI2		membrane associated gu	23 (0.00)	41 (0.20)	0.52
11-03	Gp3	g.chr7:78614029C>T	Intron	MAGI2		membrane associated gu	27 (0.00)	36 (0.28)	0.74
11-03	Gp3	g.chr7:78632328G>C	Intron	MAGI2		membrane associated gu	27 (0.00)	26 (0.19)	0.51
11-03	Gp3	g.chr7:78832158C>G	Intron	MAGI2		membrane associated gu	23 (0.00)	14 (0.43)	1.14
11-03	Gp3	g.chr7:78940208C>G	Intron	MAGI2		membrane associated gu	51 (0.00)	31 (0.23)	0.60
11-03	Gp3	g.chr7:78951214C>T	Intron	MAGI2		membrane associated gu	38 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr7:78976874C>T	Intron	MAGI2		membrane associated gu	55 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr7:79044488G>C	Intron	MAGI2		membrane associated gu	33 (0.00)	35 (0.37)	0.99
11-03	Gp3	g.chr5:71495089G>A	Silent	MAP1B	p.V1969V	microtubule-associated	26 (0.00)	18 (0.39)	1.04
11-03	Gp3	g.chr2:210518034G>A	Missense Mutation	MAP2	p.G47E	microtubule-associated	20 (0.00)	14 (0.36)	0.95

11-03	Gp3	g.chr17:43345070G>A	RNA	MAP3K14-AS1		MAP3K14 antisense RN	122 (0.00)	64 (0.19)	0.50
11-03	Gp3	g.chr1:85498409T>C	Silent	MCOLN3	p.E234E	mucolipin 3	78 (0.01)	53 (0.28)	0.46
11-03	Gp3	g.chr17:37596676C>A	Missense Mutation	MED1	p.C121F	mediator complex subur	41 (0.00)	46 (0.22)	0.58
11-03	Gp3	g.chr3:151067850G>A	Missense Mutation	MED12L	p.E717K	mediator complex subur	17 (0.06)	52 (0.17)	0.46
11-03	Gp3	g.chr22:20921090C>A	Missense Mutation	MED15	p.P343T	mediator complex subur	55 (0.00)	50 (0.18)	0.48
11-03	Gp3	g.chr15:100252655C>A	Missense Mutation	MEF2A	p.S391R	myocyte enhancer facto	31 (0.00)	17 (0.35)	0.94
11-03	Gp3	g.chr5:88047697C>G	Missense Mutation	MEF2C	p.R187P	myocyte enhancer facto	96 (0.00)	74 (0.20)	0.54
11-03	Gp3	g.chr1:156452415C>A	Silent	MEF2D	p.R24R	myocyte enhancer facto	38 (0.00)	40 (0.20)	0.53
11-03	Gp3	g.chr2:112754930C>T	Missense Mutation	MERTK	p.P494L	MER proto-oncogene, t	45 (0.00)	29 (0.24)	0.64
11-03	Gp3	g.chr7:116380975C>A	Missense Mutation	MET	p.P533T	MET proto-oncogene, r	46 (0.02)	37 (0.32)	0.86
11-03	Gp3	g.chr1:170135783C>T	Silent	METTL11B	p.N157N	methyltransferase like 1	103 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr12:31814999G>T	Nonsense Mutation	METTL20	p.G38*	methyltransferase like 2	26 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr18:2554824C>T	Missense Mutation	METTL4	p.D225N	methyltransferase like 4	38 (0.00)	13 (0.54)	1.44
11-03	Gp3	g.chr17:8701456G>T	Nonsense Mutation	MFSD6L	p.S328*	major facilitator superfa	19 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr15:42021542G>A	Missense Mutation	MGA	p.A1280T	MGA, MAX dimerizati	48 (0.00)	41 (0.32)	0.61
11-03	Gp3	g.chr7:141731570G>A	Missense Mutation	MGAM	p.V521I	maltase-glucoamylase (	42 (0.02)	52 (0.42)	0.65
11-03	Gp3	g.chr7:141734634T>A	Missense Mutation	MGAM	p.I651N	maltase-glucoamylase (	32 (0.00)	17 (0.29)	0.45
11-03	Gp3	g.chr10:103558758C>A	Silent	MGEA5	p.A550A	meningioma expressed	19 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr16:14334189T>A	Silent	MKL2	p.I309I	MKL/myocardin-like 2	22 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr1:233489677G>A	Missense Mutation	MLK4	p.E371K		29 (0.00)	42 (0.38)	1.02
11-03	Gp3	g.chr6:168276110G>A	Missense Mutation	MLLT4	p.R225Q	myeloid/lymphoid or mi	109 (0.01)	134 (0.16)	0.42
11-03	Gp3	g.chr1:158813860C>T	Missense Mutation	MNDA	p.P173L	myeloid cell nuclear dif	44 (0.00)	85 (0.14)	0.38
11-03	Gp3	g.chr5:52397259C>G	Missense Mutation	MOCS2	p.V103L	molybdenum cofactor sy	58 (0.00)	30 (0.30)	0.80
11-03	Gp3	g.chr22:31333815C>T	Silent	MORC2	p.K452K	MORC family CW-type	50 (0.00)	23 (0.39)	1.04
11-03	Gp3	g.chr22:31336790G>T	Missense Mutation	MORC2	p.R287S	MORC family CW-type	17 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr9:13190278C>A	Missense Mutation	MPDZ	p.E663D	multiple PDZ domain p	60 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr11:18195323G>A	Missense Mutation	MRGPRX4	p.E174K	MAS-related GPR, mem	32 (0.00)	20 (0.25)	0.67
11-03	Gp3	g.chr5:71533896C>A	Missense Mutation	MRPS27	p.R114M	mitochondrial ribosoma	50 (0.00)	30 (0.30)	0.80
11-03	Gp3	g.chr5:71533897T>A	Missense Mutation	MRPS27	p.R114W	mitochondrial ribosoma	49 (0.00)	31 (0.23)	0.60
11-03	Gp3	g.chr2:42909679G>T	Nonsense Mutation	MTA3	p.E281*	metastasis associated 1	27 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr6:151209016G>A	Missense Mutation	MTHFD1L	p.G227R	methylenetetrahydrofola	27 (0.00)	52 (0.44)	1.18
11-03	Gp3	g.chr2:74438397G>A	Missense Mutation	MTHFD2	p.D248N	methylenetetrahydrofola	64 (0.00)	40 (0.15)	0.40
11-03	Gp3	g.chr2:55464449G>T	Silent	MTIF2	p.T662T	mitochondrial translatio	48 (0.00)	24 (0.38)	1.00
11-03	Gp3	g.chr1:149904180C>A	Missense Mutation	MTMR11	p.G271V	myotubularin related pr	35 (0.00)	53 (0.25)	0.65
11-03	Gp3	g.chr1:237001875C>A	Silent	MTR	p.V497V	5-methyltetrahydrofolat	31 (0.00)	41 (0.17)	0.46

11-03	Gp3	g.chr7:100636680C>A	Missense Mutation	MUC12	p.H1089N	mucin 12, cell surface a	79 (0.01)	131 (0.16)	0.43
11-03	Gp3	g.chr19:9033240G>A	Missense Mutation	MUC16	p.A12129V	mucin 16, cell surface a	22 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr19:9049788G>A	Missense Mutation	MUC16	p.P10615S	mucin 16, cell surface a	83 (0.00)	34 (0.24)	0.63
11-03	Gp3	g.chr19:9071033G>T	Silent	MUC16	p.I5471I	mucin 16, cell surface a	45 (0.00)	52 (0.15)	0.41
11-03	Gp3	g.chr19:9072566C>T	Silent	MUC16	p.L4960L	mucin 16, cell surface a	91 (0.00)	51 (0.25)	0.68
11-03	Gp3	g.chr19:9076571T>A	Missense Mutation	MUC16	p.L3625F	mucin 16, cell surface a	16 (0.00)	21 (0.38)	1.02
11-03	Gp3	g.chr11:1093667C>T	Missense Mutation	MUC2	p.T1829I	mucin 2, oligomeric mu	26 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr3:195484146T>C	Missense Mutation	MUC4	p.I778V	mucin 4, cell surface as	31 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr17:10416024C>T	Missense Mutation	MYH1	p.D328N	myosin, heavy chain 1,	44 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr17:8452049G>A	Missense Mutation	MYH10	p.P316S	myosin, heavy chain 10,	37 (0.00)	29 (0.31)	0.39
11-03	Gp3	g.chr17:10442542C>A	Missense Mutation	MYH2	p.A466S	myosin, heavy chain 2,	32 (0.00)	45 (0.36)	0.95
11-03	Gp3	g.chr5:16694657C>A	Missense Mutation	MYO10	p.R1208L	myosin X	55 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr5:16694659G>A	Silent	MYO10	p.F1207F	myosin X	51 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr12:57430556C>A	Splice Site	MYO1A	p.K758N	myosin IA	64 (0.00)	44 (0.18)	0.48
11-03	Gp3	g.chr17:31075962G>A	Silent	MYO1D	p.G422G	myosin ID	50 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr15:59510108G>A	Silent	MYO1E	p.V363V	myosin IE	69 (0.01)	41 (0.20)	0.52
11-03	Gp3	g.chr10:26446335G>T	Missense Mutation	MYO3A	p.D964Y	myosin IIIA	32 (0.00)	22 (0.50)	1.33
11-03	Gp3	g.chr1:24421939G>A	Silent	MYOM3	p.I261I	myomesin 3	40 (0.00)	45 (0.18)	0.47
11-03	Gp3	g.chr5:137222942G>A	Silent	MYOT	p.R340R	myotilin	17 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr4:120107209C>A	Missense Mutation	MYOZ2	p.P217T	myozenin 2	16 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr4:40154422G>C	Missense Mutation	N4BP2	p.K1722N	NEDD4 binding protein	31 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr13:101733918G>A	Missense Mutation	NALCN	p.S1282L	sodium leak channel, no	40 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr18:10549028C>T	Nonsense Mutation	NAPG	p.Q244*	N-ethylmaleimide-sensi	127 (0.00)	67 (0.24)	0.64
11-03	Gp3	g.chr11:34137418A>T	Nonsense Mutation	NAT10	p.R182*	N-acetyltransferase 10 (	16 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr11:34155929G>C	Missense Mutation	NAT10	p.A600P	N-acetyltransferase 10 (	34 (0.00)	30 (0.27)	0.71
11-03	Gp3	g.chr8:90967591T>A	Silent	NBN	p.I439I	nibrin	55 (0.00)	60 (0.17)	0.44
11-03	Gp3	g.chr1:146420165G>A	Missense Mutation	NBPF12	p.R973H	neuroblastoma breakpoi	52 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr17:41342736C>T	Missense Mutation	NBR1	p.P269L	neighbor of BRCA1 ger	56 (0.00)	41 (0.27)	0.72
11-03	Gp3	g.chr11:134054836G>A	Missense Mutation	NCAPD3	p.A766V	non-SMC condensin II	61 (0.00)	186 (0.15)	0.39
11-03	Gp3	g.chr7:158457323C>A	Missense Mutation	NCAPG2	p.E533D	non-SMC condensin II	17 (0.00)	15 (0.33)	0.89
11-03	Gp3	g.chr1:183536120C>T	Missense Mutation	NCF2	p.G287R	neutrophil cytosolic fact	23 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr2:133486484G>A	Missense Mutation	NCKAP5	p.P1829S	NCK-associated protein	59 (0.00)	22 (0.41)	0.71
11-03	Gp3	g.chr2:24985619C>T	Missense Mutation	NCOA1	p.L1377F	nuclear receptor coactiv	114 (0.00)	52 (0.19)	0.51
11-03	Gp3	g.chr20:46279896G>A	Silent	NCOA3	p.Q1274Q	nuclear receptor coactiv	41 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr20:33329366C>T	Missense Mutation	NCOA6	p.S1565N	nuclear receptor coactiv	41 (0.00)	39 (0.18)	0.48

11-03	Gp3	g.chr4:121957543G>A	Missense Mutation	NDNF	p.T528I	neuron-derived neurotro	23 (0.00)	49 (0.14)	0.38
11-03	Gp3	g.chr2:152374934G>A	Silent	NEB	p.Y7566Y	nebulin	37 (0.00)	45 (0.40)	1.07
11-03	Gp3	g.chr2:152417188C>G	Missense Mutation	NEB	p.R6411T	nebulin	21 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr2:152500433C>T	Missense Mutation	NEB	p.V2619I	nebulin	51 (0.00)	81 (0.25)	0.66
11-03	Gp3	g.chr2:152522786C>A	Missense Mutation	NEB	p.G1617C	nebulin	25 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr6:11190573C>A	Missense Mutation	NEDD9	p.S510I	neural precursor cell ex	18 (0.00)	29 (0.28)	0.74
11-03	Gp3	g.chr20:57566421G>T	Missense Mutation	NELFCD	p.A355S	negative elongation fact	28 (0.00)	26 (0.19)	0.51
11-03	Gp3	g.chr12:55421124G>A	Missense Mutation	NEUROD4	p.G301S	neuronal differentiation	47 (0.00)	68 (0.44)	1.18
11-03	Gp3	g.chr11:129751393G>A	Silent	NFRKB	p.S443S	nuclear factor related to	53 (0.00)	26 (0.27)	0.72
11-03	Gp3	g.chr5:177580540C>T	Missense Mutation	NHP2	p.R61Q	NHP2 ribonucleoprotei	38 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr5:177580560C>T	Splice Site	NHP2	p.A54A	NHP2 ribonucleoprotei	33 (0.00)	31 (0.23)	0.60
11-03	Gp3	g.chr15:23006629G>A	Silent	NIPA2	p.L225L	non imprinted in Prader	28 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chrX:118723769G>C	Nonsense Mutation	NKRF	p.S540*	NFKB repressing factor	46 (0.00)	20 (0.30)	0.50
11-03	Gp3	g.chr5:65105928G>T	Silent	NLN	p.S593S	neurolysin (metallopepti	60 (0.00)	45 (0.18)	0.47
11-03	Gp3	g.chr19:56320746C>T	Silent	NLRP11	p.L410L	NLR family, pyrin dom	44 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr11:7067942G>A	Missense Mutation	NLRP14	p.V668M	NLR family, pyrin dom	37 (0.03)	67 (0.27)	0.53
11-03	Gp3	g.chr19:56370090G>A	Missense Mutation	NLRP4	p.R444H	NLR family, pyrin dom	45 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr19:56481953G>C	Missense Mutation	NLRP8	p.G809R	NLR family, pyrin dom	29 (0.00)	54 (0.19)	0.49
11-03	Gp3	g.chr2:152132015G>A	Missense Mutation	NMI	p.T206M	N-myc (and STAT) inte	21 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr10:96098424C>A	Missense Mutation	NOC3L	p.D678Y	nucleolar complex asso	25 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr17:65734029A>T	Silent	NOL11	p.L490L	nucleolar protein 11	21 (0.00)	19 (0.26)	0.70
11-03	Gp3	g.chr18:31463302G>A	Silent	NOL4	p.D258D	nucleolar protein 4	30 (0.00)	49 (0.33)	0.87
11-03	Gp3	g.chr16:18549864C>A	Missense Mutation	NOMO2	p.D402Y	NODAL modulator 2	134 (0.01)	181 (0.34)	0.90
11-03	Gp3	g.chr16:16367672G>A	Silent	NOMO3	p.E727E	NODAL modulator 3	67 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr1:5993286G>A	Missense Mutation	NPHP4	p.P408L	nephronophthisis 4	59 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr5:32783023G>A	Missense Mutation	NPR3	p.E439K	natriuretic peptide recep	61 (0.02)	65 (0.15)	0.41
11-03	Gp3	g.chr4:156135843G>T	Missense Mutation	NPY2R	p.S251I	neuropeptide Y receptor	42 (0.00)	42 (0.19)	0.51
11-03	Gp3	g.chr21:16337172C>T	Silent	NRIP1	p.T1114T	nuclear receptor interact	24 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr21:16340330G>T	Missense Mutation	NRIP1	p.Q62K	nuclear receptor interact	33 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr20:61391376C>A	Silent	NTSR1	p.L338L	neurotensin receptor 1 (	44 (0.02)	46 (0.20)	0.52
11-03	Gp3	g.chr8:110257617G>C	Missense Mutation	NUDCD1	p.L465V	NudC domain containin	36 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr10:74882040G>A	Missense Mutation	NUDT13	p.G111S	nudix (nucleoside dipho	43 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr14:73749117G>A	Missense Mutation	NUMB	p.P349L	numb homolog (Drosop	28 (0.00)	29 (0.28)	0.74
11-03	Gp3	g.chr11:47858456G>A	Nonsense Mutation	NUP160	p.R309*	nucleoporin 160kDa	38 (0.00)	27 (0.37)	0.99
11-03	Gp3	g.chr7:135323416G>A	Missense Mutation	NUP205	p.D1793N	nucleoporin 205kDa	43 (0.02)	33 (0.27)	0.73

11-03	Gp3	g.chr1:153984778G>T	Silent	NUP210L	p.L1574L	nucleoporin 210kDa-lik	34 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr9:134073762C>T	Silent	NUP214	p.G1627G	nucleoporin 214kDa	18 (0.00)	24 (0.62)	1.67
11-03	Gp3	g.chr13:25905590G>A	Silent	NUPL1	p.Q431Q	nucleoporin like 1	43 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr8:103564079C>A	Missense Mutation	ODF1	p.H42N	outer dense fiber of sper	50 (0.00)	71 (0.17)	0.45
11-03	Gp3	g.chr15:76019516C>T	Missense Mutation	ODF3L1	p.L154F	outer dense fiber of sper	15 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr17:29622241G>A	Missense Mutation	OMG	p.S370L	oligodendrocyte myelin	25 (0.00)	39 (0.31)	0.82
11-03	Gp3	g.chr11:59712804C>A	Nonsense Mutation	OOSP1	p.C122*	oocyte secreted protein	22 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr11:6890994C>T	Silent	OR10A2	p.F3F	olfactory receptor, famil	57 (0.00)	53 (0.47)	0.93
11-03	Gp3	g.chr11:6866928C>T	Silent	OR10A5	p.N5N	olfactory receptor, famil	61 (0.00)	48 (0.23)	0.45
11-03	Gp3	g.chr11:55735310G>A	Silent	OR10AG1	p.G210G	olfactory receptor, famil	16 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr11:123909377C>T	Missense Mutation	OR10G7	p.C111Y	olfactory receptor, famil	52 (0.02)	57 (0.30)	0.80
11-03	Gp3	g.chr11:123909459C>T	Missense Mutation	OR10G7	p.V84M	olfactory receptor, famil	64 (0.00)	70 (0.33)	0.88
11-03	Gp3	g.chr11:123909460C>T	Silent	OR10G7	p.L83L	olfactory receptor, famil	64 (0.00)	69 (0.33)	0.89
11-03	Gp3	g.chr1:247886671C>T	Silent	OR14A2	p.K225K	olfactory receptor, famil	40 (0.03)	40 (0.30)	0.80
11-03	Gp3	g.chr1:248202412C>A	Silent	OR2L2	p.T281T	olfactory receptor, famil	16 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr1:248637363G>A	Missense Mutation	OR2T3	p.G238S	olfactory receptor, famil	93 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr1:248550938G>A	Missense Mutation	OR2T6	p.R10K	olfactory receptor, famil	43 (0.00)	40 (0.15)	0.40
11-03	Gp3	g.chr5:180166337C>A	Missense Mutation	OR2Y1	p.G241V	olfactory receptor, famil	27 (0.00)	51 (0.16)	0.42
11-03	Gp3	g.chr15:102346189C>G	Missense Mutation	OR4F6	p.H89Q	olfactory receptor, famil	43 (0.02)	35 (0.23)	0.61
11-03	Gp3	g.chr14:20444078G>A	Missense Mutation	OR4K15	p.S134N	olfactory receptor, famil	16 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr11:6150455G>A	Missense Mutation	OR56B3P	p.V206M	olfactory receptor, famil	44 (0.00)	51 (0.22)	0.43
11-03	Gp3	g.chr11:59189485G>A	Silent	OR5A2	p.H314H	olfactory receptor, famil	51 (0.00)	36 (0.17)	0.44
11-03	Gp3	g.chr11:59190360G>A	Nonsense Mutation	OR5A2	p.Q23*	olfactory receptor, famil	34 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr11:56258452C>A	Missense Mutation	OR5M8	p.G132V	olfactory receptor, famil	40 (0.00)	29 (0.38)	1.01
11-03	Gp3	g.chr11:55681605C>A	Nonsense Mutation	OR5W2	p.G152*	olfactory receptor, famil	39 (0.03)	34 (0.26)	0.71
11-03	Gp3	g.chr11:124253169C>A	Missense Mutation	OR8B2	p.R24L	olfactory receptor, famil	42 (0.00)	69 (0.20)	0.54
11-03	Gp3	g.chr11:124135691G>T	Silent	OR8G5	p.L323L	olfactory receptor, famil	97 (0.00)	62 (0.19)	0.52
11-03	Gp3	g.chr3:125295097G>A	Missense Mutation	OSBPL11	p.S201F	oxysterol binding protei	33 (0.00)	51 (0.20)	0.52
11-03	Gp3	g.chr4:146059565G>A	Missense Mutation	OTUD4	p.P788S	OTU deubiquitinase 4	40 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chrX:48792117G>A	Silent	OTUD5	p.S259S	OTU deubiquitinase 5	68 (0.01)	30 (0.30)	0.50
11-03	Gp3	g.chr1:111965573G>T	Missense Mutation	OVGP1	p.S195Y	oviductal glycoprotein 1	94 (0.00)	61 (0.23)	0.61
11-03	Gp3	g.chr22:21399255C>T	RNA	P2RX6P		purinergic receptor P2X	35 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr11:74015429C>T	Missense Mutation	P4HA3	p.E77K	prolyl 4-hydroxylase, al	21 (0.00)	30 (0.23)	0.62
11-03	Gp3	g.chr11:65984171G>A	Silent	PACS1	p.L301L	phosphofurin acidic clus	35 (0.00)	50 (0.18)	0.48
11-03	Gp3	g.chr1:17682566C>T	Silent	PADI4	p.L467L	peptidyl arginine deimir	30 (0.00)	43 (0.19)	0.50

11-03	Gp3	g.chr15:40557170G>T	Missense Mutation	PAK6	p.V62L	p21 protein (Cdc42/Rac	88 (0.00)	32 (0.31)	0.83
11-03	Gp3	g.chr4:169433372C>A	Silent	PALLD	p.A239A	palladin, cytoskeletal as	38 (0.00)	31 (0.29)	0.77
11-03	Gp3	g.chr12:56726691G>A	Missense Mutation	PAN2	p.S63F	PAN2 poly(A) specific	36 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr1:176738867C>T	Missense Mutation	PAPPA2	p.T1483I	pappalysin 2	28 (0.00)	20 (0.35)	0.93
11-03	Gp3	g.chr15:72552957C>A	Silent	PARP6	p.G206G	poly (ADP-ribose) poly	38 (0.00)	80 (0.36)	0.97
11-03	Gp3	g.chr5:49962966G>A	Missense Mutation	PARP8	p.D13N	poly (ADP-ribose) poly	36 (0.00)	56 (0.14)	0.38
11-03	Gp3	g.chr5:140262752G>A	Missense Mutation	PCDHA13	p.G300E	protocadherin alpha 13	34 (0.03)	32 (0.22)	0.58
11-03	Gp3	g.chr5:140562251G>A	Silent	PCDHB16	p.T39T	protocadherin beta 16	24 (0.00)	20 (0.25)	0.67
11-03	Gp3	g.chr5:140614370G>A	RNA	PCDHB18		protocadherin beta 18 ps	25 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr5:140811976G>A	Silent	PCDHGA12	p.L550L	protocadherin gamma su	53 (0.00)	95 (0.31)	0.81
11-03	Gp3	g.chr5:140724605C>A	Silent	PCDHGA3	p.V335V	protocadherin gamma su	86 (0.01)	36 (0.19)	0.52
11-03	Gp3	g.chr5:140798462G>A	Missense Mutation	PCDHGB7	p.E346K	protocadherin gamma su	65 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr11:82880870C>A	Missense Mutation	PCF11	p.P1165T	PCF11 cleavage and pol	87 (0.00)	52 (0.21)	0.56
11-03	Gp3	g.chr7:82544726C>A	Missense Mutation	PCLO	p.K4192N	piccolo presynaptic cyt	42 (0.00)	30 (0.30)	0.80
11-03	Gp3	g.chr7:82579217C>A	Missense Mutation	PCLO	p.G3563C	piccolo presynaptic cyt	44 (0.00)	95 (0.18)	0.48
11-03	Gp3	g.chr20:5096145G>A	Missense Mutation	PCNA	p.T219I	proliferating cell nuclea	24 (0.00)	38 (0.50)	1.33
11-03	Gp3	g.chr9:78973833C>A	Missense Mutation	PCSK5	p.Q1860K	proprotein convertase su	33 (0.00)	52 (0.27)	0.72
11-03	Gp3	g.chr1:144916632C>G	Missense Mutation	PDE4DIP	p.E712Q	phosphodiesterase 4D i	72 (0.00)	62 (0.32)	0.86
11-03	Gp3	g.chr15:85666404G>A	Missense Mutation	PDE8A	p.A689T	phosphodiesterase 8A	33 (0.00)	44 (0.16)	0.42
11-03	Gp3	g.chr2:10928872G>A	Silent	PDIA6	p.L369L	protein disulfide isomer	65 (0.02)	43 (0.16)	0.43
11-03	Gp3	g.chr8:94935757C>T	Silent	PDP1	p.N490N	pyruvate dehyrogenase	53 (0.00)	47 (0.19)	0.51
11-03	Gp3	g.chr10:119043301G>T	Missense Mutation	PDZD8	p.D981E	PDZ domain containing	62 (0.02)	79 (0.27)	0.71
11-03	Gp3	g.chr3:73440226G>A	Silent	PDZRN3	p.G149G	PDZ domain containing	20 (0.00)	38 (0.21)	0.56
11-03	Gp3	g.chr8:77896012C>A	Missense Mutation	PEX2	p.V135F	peroxisomal biogenesis	50 (0.00)	21 (0.38)	1.02
11-03	Gp3	g.chr1:28818225G>C	Missense Mutation	PHACTR4	p.V658L	phosphatase and actin re	57 (0.00)	99 (0.13)	0.43
11-03	Gp3	g.chr20:34451282C>A	Silent	PHF20	p.P256P	PHD finger protein 20	16 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr18:60435567G>C	Intron	PHLPP1		PH domain and leucine	56 (0.00)	68 (0.15)	0.39
11-03	Gp3	g.chr18:60465854G>A	Intron	PHLPP1		PH domain and leucine	24 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr18:60480157G>A	Intron	PHLPP1		PH domain and leucine	38 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr18:60518201G>C	Intron	PHLPP1		PH domain and leucine	48 (0.00)	34 (0.26)	0.71
11-03	Gp3	g.chr18:60555302C>A	Intron	PHLPP1		PH domain and leucine	25 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr18:60642717C>A	Missense Mutation	PHLPP1	p.F1281L	PH domain and leucine	100 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr16:71703908G>C	Intron	PHLPP2		PH domain and leucine	69 (0.00)	37 (0.19)	0.50
11-03	Gp3	g.chr10:13325785G>T	Silent	PHYH	p.R245R	phytanoyl-CoA 2-hydro	69 (0.01)	111 (0.17)	0.46
11-03	Gp3	g.chr8:75756330G>T	Nonsense Mutation	PI15	p.G130*	peptidase inhibitor 15	15 (0.00)	26 (0.27)	0.72

11-03	Gp3	g.chr22:20383929C>T	RNA	PI4KAP1		phosphatidylinositol 4-k	25 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr1:145585379C>T	Silent	PIAS3	p.T548T	protein inhibitor of activ	109 (0.00)	61 (0.28)	0.74
11-03	Gp3	g.chr10:98469327C>A	Nonsense Mutation	PIK3AP1	p.E143*	phosphoinositide-3-kina	70 (0.00)	18 (0.56)	1.48
11-03	Gp3	g.chr7:106513276C>A	Missense Mutation	PIK3CG	p.A727D	phosphatidylinositol-4,5	18 (0.00)	26 (0.19)	0.51
11-03	Gp3	g.chr16:71985570C>T	RNA	PKD1L3		polycystic kidney diseas	37 (0.00)	25 (0.24)	0.64
11-03	Gp3	g.chr6:51768438G>T	Missense Mutation	PKHD1	p.T2318K	polycystic kidney and h	33 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr9:26928186G>T	Silent	PLAA	p.I159I	phospholipase A2-activa	27 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr10:95931065G>A	Missense Mutation	PLCE1	p.E541K	phospholipase C, epsilo	47 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr3:155199516G>A	Silent	PLCH1	p.G1441G	phospholipase C, eta 1	46 (0.00)	30 (0.23)	0.62
11-03	Gp3	g.chr19:39915383A>T	Missense Mutation	PLEKHG2	p.I1204L	pleckstrin homology do	59 (0.00)	43 (0.19)	0.50
11-03	Gp3	g.chr10:20436783C>A	Missense Mutation	PLXDC2	p.F245L	plexin domain containin	15 (0.00)	22 (0.55)	1.45
11-03	Gp3	g.chr7:6045662A>T	Splice Site	PMS2	p.S8R	PMS2 postmeiotic segre	21 (0.00)	36 (0.36)	0.96
11-03	Gp3	g.chr7:75144083G>T	RNA	PMS2P3		postmeiotic segregation	28 (0.00)	61 (0.36)	0.96
11-03	Gp3	g.chr10:118220804T>C	Splice Site	PNLIPRP3		pancreatic lipase-related	26 (0.00)	12 (0.42)	1.11
11-03	Gp3	g.chr14:74179977G>A	Silent	PNMA1	p.V122V	paraneoplastic Ma antig	58 (0.00)	31 (0.16)	0.43
11-03	Gp3	g.chr1:166818273C>T	Missense Mutation	POGK	p.R153C	pogo transposable elem	64 (0.00)	34 (0.41)	1.10
11-03	Gp3	g.chr6:43581681G>C	Missense Mutation	POLH	p.S510T	polymerase (DNA direc	42 (0.00)	31 (0.39)	1.03
11-03	Gp3	g.chr18:51807139G>A	Missense Mutation	POLI	p.C118Y	polymerase (DNA direc	38 (0.00)	20 (0.50)	1.33
11-03	Gp3	g.chr7:72400590C>T	Missense Mutation	POM121	p.P141S	POM121 transmembran	28 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr7:72418966C>T	Missense Mutation	POM121	p.P986L	POM121 transmembran	43 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr18:14537880G>A	Missense Mutation	POTEC	p.H244Y	POTE ankyrin domain f	71 (0.00)	46 (0.22)	0.58
11-03	Gp3	g.chr22:16287591C>A	Missense Mutation	POTEH	p.G99C	POTE ankyrin domain f	40 (0.00)	78 (0.22)	0.58
11-03	Gp3	g.chr3:87311278C>T	Missense Mutation	POU1F1	p.A183T	POU class 1 homeobox	30 (0.00)	25 (0.32)	0.47
11-03	Gp3	g.chr1:167341207G>T	Missense Mutation	POU2F1	p.Q101H	POU class 2 homeobox	95 (0.00)	60 (0.20)	0.53
11-03	Gp3	g.chr11:7586931C>A	Missense Mutation	PPFIBP2	p.A71E	PTPRF interacting prote	29 (0.00)	31 (0.19)	0.38
11-03	Gp3	g.chr1:12921136C>T	Silent	PRAMEF2	p.D309D	PRAME family membe	209 (0.00)	115 (0.17)	0.44
11-03	Gp3	g.chr1:12921256C>A	Silent	PRAMEF2	p.A349A	PRAME family membe	123 (0.00)	48 (0.27)	0.72
11-03	Gp3	g.chr1:14105424C>T	Silent	PRDM2	p.H378H	PR domain containing 2	55 (0.00)	36 (0.25)	0.67
11-03	Gp3	g.chr7:645868C>T	Missense Mutation	PRKAR1B	p.G171R	protein kinase, cAMP-d	17 (0.00)	37 (0.22)	0.58
11-03	Gp3	g.chr3:53220345T>C	Missense Mutation	PRKCD	p.F417L	protein kinase C, delta	19 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr11:76063069C>A	Missense Mutation	PRKRIR	p.M375I	protein-kinase, interfero	59 (0.00)	41 (0.17)	0.46
11-03	Gp3	g.chr6:4032932G>A	Missense Mutation	PRPF4B	p.S394N	pre-mRNA processing f	20 (0.05)	31 (0.23)	0.60
11-03	Gp3	g.chr9:80921258C>T	Silent	PSAT1	p.L142L	phosphoserine aminotra	36 (0.00)	44 (0.16)	0.42
11-03	Gp3	g.chr9:80932698G>A	Missense Mutation	PSAT1	p.D283N	phosphoserine aminotra	49 (0.00)	80 (0.29)	0.77
11-03	Gp3	g.chr19:43262246C>G	Missense Mutation	PSG8	p.G206A	pregnancy specific beta-	75 (0.00)	55 (0.35)	0.92

11-03	Gp3	g.chr17:38142896G>A	Silent	PSMD3	p.L160L	proteasome (prosome, n	60 (0.00)	51 (0.31)	0.84
11-03	Gp3	g.chr1:151237972G>A	Missense Mutation	PSMD4	p.D181N	proteasome (prosome, n	86 (0.00)	82 (0.15)	0.39
11-03	Gp3	g.chr1:151237976C>A	Missense Mutation	PSMD4	p.A182D	proteasome (prosome, n	85 (0.00)	88 (0.19)	0.52
11-03	Gp3	g.chr13:20279922C>T	Missense Mutation	PSPC1	p.M422I	paraspeckle component	42 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr9:98218592C>T	Missense Mutation	PTCH1	p.G1091D	patched 1	82 (0.01)	27 (0.26)	0.69
11-03	Gp3	g.chr6:47846647G>A	Missense Mutation	PTCHD4	p.P645S	patched domain contain	114 (0.00)	91 (0.19)	0.50
11-03	Gp3	g.chr7:77201779T>G	Intron	PTPN12		protein tyrosine phospha	40 (0.00)	61 (0.15)	0.39
11-03	Gp3	g.chr7:77217925C>T	Intron	PTPN12		protein tyrosine phospha	15 (0.00)	12 (0.50)	1.33
11-03	Gp3	g.chr9:112172695C>T	Splice Site	PTPN3	p.E438E	protein tyrosine phospha	36 (0.00)	11 (0.45)	1.21
11-03	Gp3	g.chr12:70953253G>T	Missense Mutation	PTPRB	p.N1440K	protein tyrosine phospha	80 (0.00)	35 (0.20)	0.53
11-03	Gp3	g.chr6:128294867C>T	Missense Mutation	PTPRK	p.V1365M	protein tyrosine phospha	44 (0.02)	19 (0.42)	0.68
11-03	Gp3	g.chr18:7888132G>A	Silent	PTPRM	p.G75G	protein tyrosine phospha	19 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr18:7888307G>A	Missense Mutation	PTPRM	p.G134R	protein tyrosine phospha	19 (0.00)	34 (0.21)	0.55
11-03	Gp3	g.chr4:37962465C>A	Missense Mutation	PTTG2	p.A137E	pituitary tumor-transfor	72 (0.00)	40 (0.17)	0.47
11-03	Gp3	g.chr8:144898851C>T	Missense Mutation	PUF60	p.E507K	poly-U binding splicing	38 (0.00)	56 (0.16)	0.43
11-03	Gp3	g.chr20:25260907G>A	Nonsense Mutation	PYGB	p.W366*	phosphorylase, glycoge	32 (0.00)	35 (0.29)	0.76
11-03	Gp3	g.chr15:55838549C>A	Missense Mutation	PYGO1	p.R311I	pygopus family PHD fir	19 (0.00)	41 (0.17)	0.46
11-03	Gp3	g.chr11:73429857C>G	Missense Mutation	RAB6A	p.A88P	RAB6A, member RAS	34 (0.00)	34 (0.21)	0.55
11-03	Gp3	g.chr2:130738055C>T	Silent	RAB6C	p.L123L	RAB6C, member RAS	115 (0.00)	35 (0.26)	0.45
11-03	Gp3	g.chr9:125835915G>A	Missense Mutation	RABGAP1	p.D690N	RAB GTPase activating	64 (0.00)	38 (0.24)	0.63
11-03	Gp3	g.chr9:134514093C>T	Missense Mutation	RAPGEF1	p.V194M	Rap guanine nucleotide	48 (0.00)	31 (0.42)	1.12
11-03	Gp3	g.chr4:82380560C>A	Missense Mutation	RASGEF1B	p.D35Y	RasGEF domain family,	20 (0.00)	35 (0.20)	0.53
11-03	Gp3	g.chr13:48967204G>T	Intron	RB1		retinoblastoma 1	44 (0.02)	58 (0.19)	0.51
11-03	Gp3	g.chr7:155493615G>C	Missense Mutation	RBM33	p.R279T	RNA binding motif prot	35 (0.00)	43 (0.30)	0.81
11-03	Gp3	g.chr3:50131275G>A	Silent	RBM5	p.L102L	RNA binding motif prot	72 (0.00)	60 (0.17)	0.44
11-03	Gp3	g.chr11:32119955C>T	Missense Mutation	RCN1	p.R170C	reticulocalbin 1, EF-han	82 (0.00)	57 (0.18)	0.47
11-03	Gp3	g.chr11:63680184G>T	Missense Mutation	RCOR2	p.R331S	REST corepressor 2	27 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr19:10129542G>A	Missense Mutation	RDH8	p.R153Q	retinol dehydrogenase 8	21 (0.00)	30 (0.17)	0.56
11-03	Gp3	g.chr17:73654381G>A	Silent	RECQL5	p.L382L	RecQ protein-like 5	88 (0.00)	92 (0.32)	0.84
11-03	Gp3	g.chr9:136279846G>A	Nonsense Mutation	REXO4	p.R171*	REX4, RNA exonucleas	51 (0.02)	42 (0.14)	0.38
11-03	Gp3	g.chr4:39314377C>T	Missense Mutation	RFC1	p.D460N	replication factor C (act	34 (0.00)	67 (0.21)	0.56
11-03	Gp3	g.chr4:39314478G>A	Missense Mutation	RFC1	p.A426V	replication factor C (act	39 (0.00)	49 (0.14)	0.38
11-03	Gp3	g.chr7:73657557G>A	Nonsense Mutation	RFC2	p.Q152*	replication factor C (act	37 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr2:108487699G>T	Missense Mutation	RGPD4	p.R1080M	RANBP2-like and GRII	143 (0.01)	103 (0.26)	0.70
11-03	Gp3	g.chr1:42880190G>A	Missense Mutation	RIMKLA	p.G241S	ribosomal modification	36 (0.00)	34 (0.15)	0.39

11-03	Gp3	g.chr19:39359780C>G	Missense Mutation	RINL	p.W555C	Ras and Rab interactor-	25 (0.00)	21 (0.29)	0.96
11-03	Gp3	g.chr15:89755084C>T	Missense Mutation	RLBP1	p.E192K	retinaldehyde binding p	16 (0.00)	23 (0.30)	0.81
11-03	Gp3	g.chr13:25352498C>A	Nonsense Mutation	RNF17	p.S128*	ring finger protein 17	25 (0.04)	33 (0.24)	0.65
11-03	Gp3	g.chr12:121855600C>T	Silent	RNF34	p.S173S	ring finger protein 34, E	83 (0.00)	105 (0.19)	0.64
11-03	Gp3	g.chr5:177059544C>G	RNA	RP11-1277A3.2			52 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr3:192874144C>T	lincRNA	RP11-143P4.2			43 (0.02)	23 (0.48)	1.28
11-03	Gp3	g.chr17:15519008C>A	Missense Mutation	RP11-385D13.	p.L517F		55 (0.00)	88 (0.15)	0.39
11-03	Gp3	g.chr10:46914639G>A	lincRNA	RP11-38L15.8			44 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr14:24629603C>T	Missense Mutation	RP11-468E2.4	p.A526V		65 (0.00)	66 (0.18)	0.48
11-03	Gp3	g.chr12:122701132C>A	Splice Site	RP11-512M8.5			35 (0.00)	60 (0.18)	0.49
11-03	Gp3	g.chr15:90814419G>A	Splice Site	RP11-697E2.6			23 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr10:27537724C>A	lincRNA	RP11-85G18.6			24 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr18:47016876G>A	Missense Mutation	RPL17-C18orf	p.A88V	RPL17-C18orf32 readth	15 (0.00)	26 (0.19)	0.51
11-03	Gp3	g.chr22:39713635C>A	Splice Site	RPL3		ribosomal protein L3	20 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr3:12880915G>A	Missense Mutation	RPL32	p.P71S	ribosomal protein L32	50 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr3:129116244C>T	RNA	RPL32P3		ribosomal protein L32 p	107 (0.00)	130 (0.20)	0.53
11-03	Gp3	g.chr1:152129151C>T	Missense Mutation	RPTN	p.G142R	repetin	75 (0.00)	58 (0.41)	0.77
11-03	Gp3	g.chr11:4144576C>T	Silent	RRM1	p.L428L	ribonucleotide reductas	45 (0.02)	73 (0.21)	0.55
11-03	Gp3	g.chr1:114310957G>A	Silent	RSBN1	p.R571R	round spermatid basic p	19 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr16:11933740C>T	Missense Mutation	RSL1D1	p.D320N	ribosomal L1 domain c	61 (0.00)	36 (0.22)	0.59
11-03	Gp3	g.chr10:70115110C>T	Splice Site	RUFY2	p.Q533Q	RUN and FYVE domai	36 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr3:72448859C>T	Intron	RYBP		RING1 and YY1 bindin	46 (0.00)	21 (0.48)	0.62
11-03	Gp3	g.chr15:33858887C>A	Silent	RYR3	p.L385L	ryanodine receptor 3	41 (0.00)	29 (0.21)	0.55
11-03	Gp3	g.chr11:18111006T>C	Missense Mutation	SAAL1	p.D214G	serum amyloid A-like 1	26 (0.00)	28 (0.21)	0.57
11-03	Gp3	g.chr13:23932487G>T	Silent	SACS	p.V197V	sacsin molecular chaper	21 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chrX:134988653C>T	Missense Mutation	SAGE1	p.P227S	sarcoma antigen 1	23 (0.00)	13 (0.38)	0.64
11-03	Gp3	g.chr15:77021017C>A	Missense Mutation	SCAPER	p.R695M	S-phase cyclin A-associ	69 (0.00)	35 (0.26)	0.69
11-03	Gp3	g.chr2:224463115G>A	Missense Mutation	SCG2	p.R296W	secretogranin II	37 (0.03)	26 (0.27)	0.72
11-03	Gp3	g.chr15:32976830T>A	Missense Mutation	SCG5	p.L150H	secretogranin V (7B2 pr	74 (0.00)	64 (0.16)	0.42
11-03	Gp3	g.chr3:38951626G>A	Silent	SCN11A	p.N344N	sodium channel, voltage	25 (0.00)	30 (0.27)	0.43
11-03	Gp3	g.chr2:166848835G>T	Silent	SCN1A	p.I1622I	sodium channel, voltage	49 (0.00)	41 (0.22)	0.59
11-03	Gp3	g.chr7:4051771T>G	Missense Mutation	SDK1	p.I775R	sidekick cell adhesion m	31 (0.00)	37 (0.14)	0.45
11-03	Gp3	g.chr7:4247757G>A	Silent	SDK1	p.Q1727Q	sidekick cell adhesion m	55 (0.02)	28 (0.18)	0.60
11-03	Gp3	g.chr7:4259793G>T	Silent	SDK1	p.L1844L	sidekick cell adhesion m	17 (0.00)	12 (0.42)	1.40
11-03	Gp3	g.chr12:113875740C>A	Silent	SDSL	p.A282A	serine dehydratase-like	28 (0.00)	32 (0.22)	0.58

11-03	Gp3	g.chr18:12984167T>A	Missense Mutation	SEH1L	p.L350I	SEH1-like (S. cerevisia	44 (0.00)	49 (0.18)	0.49
11-03	Gp3	g.chr14:81972452G>T	Missense Mutation	SEL1L	p.D158E	sel-1 suppressor of lin-1	39 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr7:82996951C>T	Missense Mutation	SEMA3E	p.R760H	sema domain, immunog	26 (0.00)	26 (0.46)	1.23
11-03	Gp3	g.chr11:94917663C>T	Missense Mutation	SESN3	p.M147I	sestrin 3	28 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr4:140441448G>A	Nonsense Mutation	SETD7	p.R249*	SET domain containing	44 (0.00)	28 (0.36)	0.95
11-03	Gp3	g.chr16:70566490C>T	Missense Mutation	SF3B3	p.P227S	splicing factor 3b, subur	24 (0.00)	55 (0.16)	0.44
11-03	Gp3	g.chr10:102794560C>A	Missense Mutation	SFXN3	p.L37M	sideroflexin 3	45 (0.00)	44 (0.27)	0.73
11-03	Gp3	g.chr20:42213501G>A	Missense Mutation	SGK2	p.A317T	serum/glucocorticoid re	55 (0.00)	72 (0.44)	1.19
11-03	Gp3	g.chr6:80383471C>G	Silent	SH3BGRL2	p.G62G	SH3 domain binding glu	35 (0.00)	46 (0.46)	1.22
11-03	Gp3	g.chr5:148406495G>A	Missense Mutation	SH3TC2	p.H927Y	SH3 domain and tetratri	74 (0.01)	56 (0.36)	0.71
11-03	Gp3	g.chr15:49135608C>T	Missense Mutation	SHC4	p.G494E	SHC (Src homology 2 d	43 (0.00)	33 (0.48)	1.29
11-03	Gp3	g.chr13:26620904G>A	Missense Mutation	SHISA2	p.T212I	shisa family member 2	30 (0.00)	13 (0.46)	1.23
11-03	Gp3	g.chr6:146231623G>A	Silent	SHPRH	p.T1492T	SNF2 histone linker PH	50 (0.02)	21 (0.24)	0.63
11-03	Gp3	g.chr19:51770751G>A	Missense Mutation	SIGLECL1	p.V179I	SIGLEC family like 1	53 (0.02)	25 (0.28)	0.75
11-03	Gp3	g.chr15:75668125T>A	Missense Mutation	SIN3A	p.N1158Y	SIN3 transcription regul	93 (0.00)	61 (0.16)	0.44
11-03	Gp3	g.chr15:75705331C>T	Missense Mutation	SIN3A	p.D177N	SIN3 transcription regul	30 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr14:72152079G>A	Splice Site	SIPA1L1	p.R1035R	signal-induced prolifera	41 (0.00)	39 (0.23)	0.62
11-03	Gp3	g.chr5:131729375C>T	Silent	SLC22A5	p.Y486Y	solute carrier family 22	45 (0.00)	30 (0.27)	0.71
11-03	Gp3	g.chr20:19664832G>A	Missense Mutation	SLC24A3	p.R305H	solute carrier family 24	22 (0.00)	38 (0.26)	0.70
11-03	Gp3	g.chr7:95750636G>A	Missense Mutation	SLC25A13	p.P632L	solute carrier family 25	40 (0.00)	32 (0.25)	0.67
11-03	Gp3	g.chr1:108681704C>T	Missense Mutation	SLC25A24	p.V390M	solute carrier family 25	24 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr12:98992321A>T	Missense Mutation	SLC25A3	p.T162S	solute carrier family 25	16 (0.00)	30 (0.20)	0.53
11-03	Gp3	g.chr3:39435918C>T	Missense Mutation	SLC25A38	p.L215F	solute carrier family 25,	19 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr7:103033473G>A	Missense Mutation	SLC26A5	p.L338F	solute carrier family 26	54 (0.00)	39 (0.15)	0.41
11-03	Gp3	g.chr15:50497455G>A	Silent	SLC27A2	p.R54R	solute carrier family 27	20 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr15:45556945G>A	Silent	SLC28A2	p.Q227Q	solute carrier family 28	18 (0.00)	27 (0.33)	0.89
11-03	Gp3	g.chr3:170715847G>T	Missense Mutation	SLC2A2	p.L474M	solute carrier family 2 (f	115 (0.00)	13 (0.38)	1.03
11-03	Gp3	g.chr12:8075487G>A	Missense Mutation	SLC2A3	p.A401V	solute carrier family 2 (f	121 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr6:118635407G>T	Missense Mutation	SLC35F1	p.V407L	solute carrier family 35,	30 (0.00)	22 (0.41)	0.66
11-03	Gp3	g.chr3:136574276G>A	Missense Mutation	SLC35G2	p.C325Y	solute carrier family 35,	122 (0.01)	50 (0.16)	0.43
11-03	Gp3	g.chr5:33963963G>T	Missense Mutation	SLC45A2	p.P241T	solute carrier family 45,	44 (0.00)	19 (0.32)	0.84
11-03	Gp3	g.chr16:24922656G>A	Missense Mutation	SLC5A11	p.M610I	solute carrier family 5 (s	28 (0.00)	65 (0.17)	0.45
11-03	Gp3	g.chr12:85279290C>A	Missense Mutation	SLC6A15	p.L59F	solute carrier family 6 (r	35 (0.00)	17 (0.47)	1.25
11-03	Gp3	g.chr13:30106973G>A	Missense Mutation	SLC7A1	p.L173F	solute carrier family 7 (c	110 (0.01)	24 (0.38)	0.43
11-03	Gp3	g.chr12:98850461C>T	RNA	SLC9A7P1		solute carrier family 9, s	43 (0.00)	12 (0.42)	1.11

11-03	Gp3	g.chr4:103971519G>T	Missense Mutation	SLC9B2	p.L98I	solute carrier family 9, s	23 (0.00)	26 (0.23)	0.62
11-03	Gp3	g.chr13:88327961G>A	Silent	SLITRK5	p.G106G	SLIT and NTRK-like fa	35 (0.00)	22 (0.45)	1.21
11-03	Gp3	g.chr18:48597050C>T	Intron	SMAD4		SMAD family member	27 (0.04)	32 (0.38)	1.00
11-03	Gp3	g.chrX:128640157G>A	Missense Mutation	SMARCA1	p.T333I	SWI/SNF related, matri	84 (0.00)	43 (0.35)	0.58
11-03	Gp3	g.chr22:24175818G>C	Missense Mutation	SMARCB1	p.W303S	SWI/SNF related, matri	44 (0.00)	38 (0.21)	0.56
11-03	Gp3	g.chr3:47734785G>A	Silent	SMARCC1	p.L391L	SWI/SNF related, matri	60 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr12:56567524C>T	Missense Mutation	SMARCC2	p.D536N	SWI/SNF related, matri	36 (0.00)	51 (0.16)	0.42
11-03	Gp3	g.chr10:112362364G>A	Missense Mutation	SMC3	p.G1080S	structural maintenance c	26 (0.00)	37 (0.19)	0.50
11-03	Gp3	g.chr16:18882790G>A	Missense Mutation	SMG1	p.T733I	SMG1 phosphatidylinos	29 (0.00)	28 (0.21)	0.57
11-03	Gp3	g.chr16:18891038G>T	Missense Mutation	SMG1	p.L433M	SMG1 phosphatidylinos	64 (0.00)	66 (0.15)	0.40
11-03	Gp3	g.chr1:183514371C>A	Missense Mutation	SMG7	p.T765N	SMG7 nonsense mediat	71 (0.00)	67 (0.15)	0.40
11-03	Gp3	g.chr2:88390550C>T	Missense Mutation	SMYD1	p.T183I	SET and MYND domai	23 (0.00)	27 (0.37)	0.75
11-03	Gp3	g.chr17:1715274C>A	Silent	SMYD4	p.L90L	SET and MYND domai	26 (0.00)	56 (0.14)	0.38
11-03	Gp3	g.chr17:1715346G>A	Silent	SMYD4	p.D66D	SET and MYND domai	32 (0.00)	55 (0.16)	0.44
11-03	Gp3	g.chr5:121785550G>A	Missense Mutation	SNCAIP	p.E582K	synuclein, alpha interact	17 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr15:25318347C>A	RNA	SNHG14		small nucleolar RNA ho	40 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr2:96950202G>C	Missense Mutation	SNRNP200	p.P1429R	small nuclear ribonucle	22 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr1:203832810G>A	Nonsense Mutation	SNRPE	p.W34*	small nuclear ribonucle	16 (0.00)	51 (0.22)	0.58
11-03	Gp3	g.chr5:122154641C>T	Nonsense Mutation	SNX2	p.Q262*	sorting nexin 2	25 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr16:12618628A>T	Missense Mutation	SNX29	p.I750F	sorting nexin 29	63 (0.00)	46 (0.30)	0.81
11-03	Gp3	g.chr18:8720380G>A	Silent	SOGA2	p.T441T		60 (0.00)	42 (0.19)	0.51
11-03	Gp3	g.chr18:8720427G>A	Missense Mutation	SOGA2	p.R457Q		63 (0.00)	40 (0.25)	0.67
11-03	Gp3	g.chr2:174820699C>T	Missense Mutation	SP3	p.G181S	Sp3 transcription factor	76 (0.00)	63 (0.30)	0.80
11-03	Gp3	g.chr4:88403648C>T	Silent	SPARCL1	p.K407K	SPARC-like 1 (hevin)	25 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr16:89764695C>T	Missense Mutation	SPATA2L	p.V108M	spermatogenesis associa	40 (0.00)	86 (0.21)	0.56
11-03	Gp3	g.chr16:89614427C>A	Missense Mutation	SPG7	p.N523K	spastic paraplegia 7 (pu	19 (0.00)	38 (0.29)	0.77
11-03	Gp3	g.chr17:47690840G>A	Intron	SPOP		speckle-type POZ protei	57 (0.00)	48 (0.21)	0.56
11-03	Gp3	g.chr17:47698760G>A	Intron	SPOP		speckle-type POZ protei	37 (0.00)	46 (0.15)	0.41
11-03	Gp3	g.chr17:47716199C>A	Intron	SPOP		speckle-type POZ protei	58 (0.00)	62 (0.21)	0.56
11-03	Gp3	g.chr14:78043249C>T	Silent	SPTLC2	p.G164G	serine palmitoyltransfer	52 (0.00)	48 (0.15)	0.39
11-03	Gp3	g.chr2:45826594C>T	Missense Mutation	SRBD1	p.M214I	S1 RNA binding domai	42 (0.00)	57 (0.23)	0.61
11-03	Gp3	g.chr6:36566687C>T	Missense Mutation	SRSF3	p.R90C	serine/arginine-rich spli	32 (0.00)	39 (0.23)	0.62
11-03	Gp3	g.chr2:182761670G>A	Missense Mutation	SSFA2	p.D115N	sperm specific antigen 2	92 (0.00)	74 (0.26)	0.68
11-03	Gp3	g.chr22:37603492G>A	Silent	SSTR3	p.R117R	somatostatin receptor 3	25 (0.00)	39 (0.26)	0.68
11-03	Gp3	g.chrX:48118027G>A	Missense Mutation	SSX1	p.G81R	synovial sarcoma, X bre	67 (0.00)	31 (0.52)	0.86

11-03	Gp3	g.chrX:47978999G>T	RNA	SSX6		synovial sarcoma, X bre	65 (0.02)	79 (0.24)	0.40
11-03	Gp3	g.chr5:100231424C>A	Missense Mutation	ST8SIA4	p.G60V	ST8 alpha-N-acetyl-neu	31 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr17:37370536G>A	Silent	STAC2	p.Y297Y	SH3 and cysteine rich d	23 (0.00)	29 (0.21)	0.55
11-03	Gp3	g.chr3:136323151C>A	Splice Site	STAG1	p.Q99H	stromal antigen 1	66 (0.00)	37 (0.27)	0.72
11-03	Gp3	g.chr2:96859010G>A	Silent	STARD7	p.S210S	StAR-related lipid trans	56 (0.00)	60 (0.18)	0.49
11-03	Gp3	g.chr15:42944745G>T	Missense Mutation	STARD9	p.E219D	StAR-related lipid trans	20 (0.00)	43 (0.28)	0.54
11-03	Gp3	g.chr15:42980498G>T	Missense Mutation	STARD9	p.G2241V	StAR-related lipid trans	39 (0.00)	27 (0.22)	0.43
11-03	Gp3	g.chr7:89790557C>A	Missense Mutation	STEAP1	p.H175N	six transmembrane epit	23 (0.00)	41 (0.24)	0.65
11-03	Gp3	g.chr7:87913165C>T	Nonsense Mutation	STEAP4	p.W140*	STEAP family member	40 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr11:125467004G>C	Missense Mutation	STT3A	p.E47Q	STT3A, subunit of the o	15 (0.00)	23 (0.30)	0.81
11-03	Gp3	g.chr17:27014127C>A	Missense Mutation	SUPT6H	p.P908T	suppressor of Ty 6 hom	34 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr10:70958161G>A	Missense Mutation	SUPV3L1	p.V353M	suppressor of var1, 3-lik	50 (0.02)	58 (0.26)	0.69
11-03	Gp3	g.chr10:70958170C>A	Missense Mutation	SUPV3L1	p.H356N	suppressor of var1, 3-lik	50 (0.02)	56 (0.21)	0.57
11-03	Gp3	g.chr11:67926581G>A	Missense Mutation	SUV420H1	p.T411M	suppressor of variegatio	67 (0.00)	44 (0.23)	0.61
11-03	Gp3	g.chr11:67926639C>A	Splice Site	SUV420H1		suppressor of variegatio	57 (0.00)	34 (0.35)	0.94
11-03	Gp3	g.chr5:75596700C>T	Missense Mutation	SV2C	p.P595S	synaptic vesicle glycopr	88 (0.00)	66 (0.17)	0.44
11-03	Gp3	g.chr1:25554699C>T	Missense Mutation	SYF2	p.E96K	SYF2 pre-mRNA-splici	23 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr6:86347061C>A	Missense Mutation	SYNCRIP	p.R130I	synaptotagmin binding,	17 (0.00)	17 (0.47)	0.60
11-03	Gp3	g.chr6:152558007A>T	Missense Mutation	SYNE1	p.V6715E	spectrin repeat containi	47 (0.00)	40 (0.23)	0.60
11-03	Gp3	g.chr6:152720798G>T	Missense Mutation	SYNE1	p.S2397Y	spectrin repeat containi	81 (0.00)	58 (0.24)	0.64
11-03	Gp3	g.chr6:132891733C>T	Silent	TAAR6	p.V91V	trace amine associated	51 (0.02)	33 (0.30)	0.49
11-03	Gp3	g.chr9:32634239G>A	Missense Mutation	TAF1L	p.P447S	TAF1 RNA polymerase	52 (0.00)	41 (0.54)	1.43
11-03	Gp3	g.chr18:23969868G>A	Silent	TAF4B	p.L827L	TAF4b RNA polymeras	35 (0.00)	45 (0.42)	1.13
11-03	Gp3	g.chr6:159462401G>A	Silent	TAGAP	p.L154L	T-cell activation RhoG	60 (0.00)	41 (0.17)	0.46
11-03	Gp3	g.chr11:763823C>A	Missense Mutation	TALDO1	p.F238L	transaldolase 1	116 (0.00)	59 (0.15)	0.41
11-03	Gp3	g.chr3:11858809C>A	Missense Mutation	TAMM41	p.D189Y	TAM41, mitochondrial	27 (0.00)	25 (0.36)	0.96
11-03	Gp3	g.chr17:61417516G>T	Nonsense Mutation	TANC2	p.E470*	tetratricopeptide repeat,	148 (0.01)	44 (0.27)	0.73
11-03	Gp3	g.chr17:61466750C>T	Nonsense Mutation	TANC2	p.Q892*	tetratricopeptide repeat,	19 (0.00)	29 (0.24)	0.64
11-03	Gp3	g.chr16:68901110G>C	Missense Mutation	TANGO6	p.L327F	transport and golgi orga	47 (0.02)	48 (0.35)	0.94
11-03	Gp3	g.chr17:27844660G>A	Missense Mutation	TAOK1	p.D632N	TAO kinase 1	26 (0.00)	16 (0.38)	1.00
11-03	Gp3	g.chr1:19166623G>A	Missense Mutation	TAS1R2	p.R664C	taste receptor, type 1, m	27 (0.00)	38 (0.16)	0.42
11-03	Gp3	g.chr20:13463907C>A	Missense Mutation	TASP1	p.A318S	taspase, threonine aspar	18 (0.00)	20 (0.30)	0.80
11-03	Gp3	g.chr3:10311927C>A	Missense Mutation	TATDN2	p.P354H	TatD DNase domain co	117 (0.00)	43 (0.16)	0.43
11-03	Gp3	g.chrX:48403365C>T	Silent	TBC1D25	p.S114S	TBC1 domain family, m	25 (0.00)	30 (0.23)	0.39
11-03	Gp3	g.chr17:60345538C>A	RNA	TBC1D3P2		TBC1 domain family, m	46 (0.00)	19 (0.42)	1.12

11-03	Gp3	g.chr17:80879435C>T	Silent	TBCD	p.H720H	tubulin folding cofactor	88 (0.00)	59 (0.15)	0.41
11-03	Gp3	g.chr11:67400513C>T	Missense Mutation	TBX10	p.R204H	T-box 10	67 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr15:57523433C>T	Silent	TCF12	p.F221F	transcription factor 12	43 (0.00)	52 (0.27)	0.72
11-03	Gp3	g.chr15:57574705G>A	Missense Mutation	TCF12	p.V681I	transcription factor 12	38 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr6:44253727C>A	Missense Mutation	TCTE1	p.A274S	t-complex-associated-te	19 (0.00)	25 (0.24)	0.64
11-03	Gp3	g.chr10:115980424C>A	Silent	TDRD1	p.V864V	tudor domain containing	33 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr19:33229799G>A	Missense Mutation	TDRD12	p.C74Y	tudor domain containing	23 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr14:104460920C>A	Missense Mutation	TDRD9	p.P434T	tudor domain containing	21 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr11:12923617T>A	Missense Mutation	TEAD1	p.F181Y	TEA domain family me	66 (0.00)	47 (0.30)	0.79
11-03	Gp3	g.chr22:41790185C>G	Silent	TEF	p.P187P	thyrotrophic embryonic	20 (0.00)	25 (0.48)	1.28
11-03	Gp3	g.chr22:41791868C>T	Silent	TEF	p.N272N	thyrotrophic embryonic	22 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr17:29227577C>T	Missense Mutation	TEFM	p.V167I	transcription elongation	46 (0.00)	61 (0.15)	0.39
11-03	Gp3	g.chr17:15215705G>A	Silent	TEKT3	p.D324D	tektin 3	51 (0.02)	34 (0.26)	0.71
11-03	Gp3	g.chr12:55356258C>T	Missense Mutation	TESPA1	p.R475Q	thymocyte expressed, p	52 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr1:36060057G>A	Missense Mutation	TFAP2E	p.R370H	transcription factor AP-	55 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr7:115750906T>A	Missense Mutation	TFEC	p.E18D	transcription factor EC	71 (0.00)	37 (0.30)	0.79
11-03	Gp3	g.chr7:100230631G>A	Missense Mutation	TFR2	p.A281V	transferrin receptor 2	17 (0.00)	15 (0.33)	0.89
11-03	Gp3	g.chr5:135390428C>A	Missense Mutation	TGFBI	p.H430N	transforming growth fac	107 (0.01)	64 (0.23)	0.62
11-03	Gp3	g.chr1:92161317G>A	Silent	TGFBR3	p.D783D	transforming growth fac	22 (0.00)	28 (0.21)	0.57
11-03	Gp3	g.chr3:44938259C>A	Missense Mutation	TGM4	p.P203H	transglutaminase 4	24 (0.00)	26 (0.23)	0.62
11-03	Gp3	g.chr2:85554387C>T	Silent	TGOLN2	p.A156A	trans-golgi network prot	60 (0.00)	23 (0.26)	0.53
11-03	Gp3	g.chr2:43571272C>T	Nonsense Mutation	THADA	p.W1444*	thyroid adenoma associa	52 (0.00)	60 (0.20)	0.53
11-03	Gp3	g.chr2:43625174G>A	Missense Mutation	THADA	p.S1388F	thyroid adenoma associa	59 (0.00)	18 (0.39)	1.04
11-03	Gp3	g.chr16:67877025C>A	Missense Mutation	THAP11	p.L190I	THAP domain containin	16 (0.00)	43 (0.21)	0.56
11-03	Gp3	g.chrX:122757091C>T	Missense Mutation	THOC2	p.E1183K	THO complex 2	27 (0.00)	14 (0.57)	0.95
11-03	Gp3	g.chr7:11514029G>T	Nonsense Mutation	THSD7A	p.C728*	thrombospondin, type I,	34 (0.00)	18 (0.28)	0.74
11-03	Gp3	g.chr21:32502633C>A	Splice Site	TIAM1	p.V1315L	T-cell lymphoma invasi	24 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr15:90166921C>T	Missense Mutation	TICRR	p.T1127I	TOPBP1-interacting ch	40 (0.00)	55 (0.25)	0.68
11-03	Gp3	g.chr9:35723993C>G	Missense Mutation	TLN1	p.Q246H	talin 1	16 (0.00)	28 (0.29)	0.76
11-03	Gp3	g.chr4:38798820C>T	Missense Mutation	TLR1	p.E545K	toll-like receptor 1	71 (0.00)	38 (0.16)	0.42
11-03	Gp3	g.chr13:100206623G>A	Silent	TM9SF2	p.T518T	transmembrane 9 superf	51 (0.00)	37 (0.16)	0.43
11-03	Gp3	g.chr15:81631846C>A	Splice Site	TMC3		transmembrane channel-	74 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr16:19492705C>A	Missense Mutation	TMC5	p.Q709K	transmembrane channel-	38 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr16:19032961C>A	Silent	TMC7	p.G157G	transmembrane channel-	35 (0.00)	17 (0.35)	0.94
11-03	Gp3	g.chr3:119155740A>G	Missense Mutation	TMEM39A	p.L337P	transmembrane protein	121 (0.00)	67 (0.18)	0.48

11-03	Gp3	g.chr12:83379763C>A	Missense Mutation	TMTC2	p.L670M	transmembrane and tetra	67 (0.00)	36 (0.22)	0.59
11-03	Gp3	g.chr1:201379564C>T	Splice Site	TNNI1		troponin I type 1 (skelet	32 (0.00)	26 (0.23)	0.62
11-03	Gp3	g.chr7:128640500C>T	Missense Mutation	TNPO3	p.G266S	transportin 3	39 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr16:24801918C>G	Missense Mutation	TNRC6A	p.A652G	trinucleotide repeat cont	43 (0.00)	31 (0.23)	0.60
11-03	Gp3	g.chr17:76046973G>A	Silent	TNRC6C	p.G610G	trinucleotide repeat cont	51 (0.00)	35 (0.14)	0.38
11-03	Gp3	g.chr17:76047012T>A	Missense Mutation	TNRC6C	p.S623R	trinucleotide repeat cont	77 (0.00)	37 (0.19)	0.50
11-03	Gp3	g.chr9:32542037G>C	Nonsense Mutation	TOPORS	p.S829*	topoisomerase I binding	89 (0.00)	40 (0.25)	0.67
11-03	Gp3	g.chr15:43712617G>A	Missense Mutation	TP53BP1	p.L1473F	tumor protein p53 bindi	86 (0.00)	42 (0.21)	0.41
11-03	Gp3	g.chr1:223983892C>A	Silent	TP53BP2	p.V783V	tumor protein p53 bindi	30 (0.00)	17 (0.29)	0.78
11-03	Gp3	g.chr2:24300561C>T	Missense Mutation	TP53I3	p.R296H	tumor protein p53 induc	22 (0.00)	27 (0.19)	0.49
11-03	Gp3	g.chr12:72372751G>C	Silent	TPH2	p.V275V	tryptophan hydroxylase	40 (0.03)	36 (0.19)	0.52
11-03	Gp3	g.chr20:30371644G>A	Missense Mutation	TPX2	p.E445K	TPX2, microtubule-assc	16 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr2:239234591G>T	Nonsense Mutation	TRAF3IP1	p.G112*	TNF receptor-associatec	27 (0.00)	28 (0.18)	0.48
11-03	Gp3	g.chr3:49879887G>T	Splice Site	TRAIP	p.Q168K	TRAF interacting protei	34 (0.00)	24 (0.25)	0.67
11-03	Gp3	g.chr2:202262907G>T	Silent	TRAK2	p.L217L	trafficking protein, kine	29 (0.00)	24 (0.33)	0.89
11-03	Gp3	g.chr4:184601387G>C	Silent	TRAPPC11	p.R360R	trafficking protein partic	31 (0.00)	37 (0.19)	0.50
11-03	Gp3	g.chr7:142378796G>C	RNA	TRBV25-1		T cell receptor beta vari	35 (0.00)	39 (0.31)	0.47
11-03	Gp3	g.chr6:41185558G>T	RNA	TREML3P		triggering receptor expr	57 (0.02)	71 (0.17)	0.45
11-03	Gp3	g.chr7:99490089G>T	Missense Mutation	TRIM4	p.D400E	tripartite motif containir	34 (0.00)	32 (0.19)	0.50
11-03	Gp3	g.chr11:49075405C>T	Missense Mutation	TRIM64C	p.G402D	tripartite motif containir	27 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr2:230636293C>T	Missense Mutation	TRIP12	p.R1572K	thyroid hormone recepto	24 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr1:185106757C>T	Silent	TRMT1L	p.K498K	tRNA methyltransferase	23 (0.00)	21 (0.29)	0.76
11-03	Gp3	g.chr14:61442574C>T	Missense Mutation	TRMT5	p.D355N	tRNA methyltransferase	53 (0.00)	43 (0.37)	0.99
11-03	Gp3	g.chr22:46733834G>C	Missense Mutation	TRMU	p.V81L	tRNA 5-methylaminom	83 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr11:101362308G>C	Silent	TRPC6	p.A369A	transient receptor potent	18 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr21:45821697G>A	Missense Mutation	TRPM2	p.V819M	transient receptor potent	18 (0.00)	46 (0.33)	0.87
11-03	Gp3	g.chr13:45149061C>T	Missense Mutation	TSC22D1	p.A384T	TSC22 domain family,	24 (0.00)	19 (0.32)	0.39
11-03	Gp3	g.chr19:31770012C>A	Missense Mutation	TSHZ3	p.L229F	teashirt zinc finger hom	98 (0.01)	82 (0.27)	0.72
11-03	Gp3	g.chr6:116600202G>A	Silent	TSPYL1	p.Y264Y	TSPY-like 1	80 (0.00)	21 (0.43)	0.69
11-03	Gp3	g.chr17:2227518G>C	Nonsense Mutation	TSR1	p.S796*	TSR1, 20S rRNA accun	28 (0.00)	62 (0.26)	0.69
11-03	Gp3	g.chr7:138833076C>T	Missense Mutation	TTC26	p.L193F	tetratricopeptide repeat	17 (0.00)	47 (0.47)	1.25
11-03	Gp3	g.chr21:38537914C>G	Missense Mutation	TTC3	p.A1133G	tetratricopeptide repeat	27 (0.00)	15 (0.33)	0.89
11-03	Gp3	g.chr2:178482404G>A	Silent	TTC30A	p.V342V	tetratricopeptide repeat	87 (0.01)	36 (0.33)	0.44
11-03	Gp3	g.chr5:40716421G>A	Silent	TTC33	p.D205D	tetratricopeptide repeat	15 (0.00)	19 (0.58)	1.54
11-03	Gp3	g.chr22:46685795C>T	Splice Site	TTC38	p.R439W	tetratricopeptide repeat	15 (0.00)	18 (0.44)	1.19

11-03	Gp3	g.chr14:38222441G>A	Splice Site	TTC6		tetratricopeptide repeat	30 (0.00)	16 (0.31)	0.83
11-03	Gp3	g.chr9:135266181C>A	Silent	TTF1	p.R675R	transcription terminatio	68 (0.00)	60 (0.35)	0.93
11-03	Gp3	g.chr2:179415740G>T	Missense Mutation	TTN	p.S30506R	titin	50 (0.00)	29 (0.45)	0.60
11-03	Gp3	g.chr2:179429645C>T	Missense Mutation	TTN	p.E27072K	titin	37 (0.00)	48 (0.46)	0.61
11-03	Gp3	g.chr2:179459088G>T	Missense Mutation	TTN	p.T19378N	titin	90 (0.00)	46 (0.28)	0.38
11-03	Gp3	g.chr12:49663757C>T	Silent	TUBA1C	p.L125L	tubulin, alpha 1c	47 (0.00)	45 (0.16)	0.41
11-03	Gp3	g.chr6:112393976C>A	Missense Mutation	TUBE1	p.R360L	tubulin, epsilon 1	17 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr22:31368951T>C	RNA	TUG1		taurine up-regulated 1 (	37 (0.03)	71 (0.27)	0.71
11-03	Gp3	g.chr16:11785747G>C	Missense Mutation	TXNDC11	p.H433Q	thioredoxin domain con	25 (0.00)	16 (0.44)	1.17
11-03	Gp3	g.chrX:142967353G>A	Missense Mutation	UBE2NL	p.G51R	ubiquitin-conjugating e	42 (0.00)	18 (0.44)	0.74
11-03	Gp3	g.chr1:19524266G>A	Missense Mutation	UBR4	p.P264L	ubiquitin protein ligase	32 (0.00)	66 (0.24)	0.65
11-03	Gp3	g.chr1:20517869C>T	Missense Mutation	UBXN10	p.S272L	UBX domain protein 10	27 (0.00)	19 (0.42)	1.12
11-03	Gp3	g.chr4:39512029C>T	Missense Mutation	UGDH	p.V203I	UDP-glucose 6-dehydro	26 (0.00)	24 (0.21)	0.56
11-03	Gp3	g.chr2:234628321G>A	Silent	UGT1A4	p.K285K	UDP glucuronosyltrans	17 (0.00)	12 (0.50)	1.33
11-03	Gp3	g.chr4:70152533G>A	Missense Mutation	UGT2B28	p.V312M	UDP glucuronosyltrans	70 (0.00)	72 (0.19)	0.52
11-03	Gp3	g.chr9:35310762C>T	Silent	UNC13B	p.L354L	unc-13 homolog B (C. e	32 (0.00)	24 (0.33)	0.89
11-03	Gp3	g.chr2:210678563C>T	Nonsense Mutation	UNC80	p.Q400*	unc-80 homolog (C. ele	57 (0.00)	59 (0.15)	0.41
11-03	Gp3	g.chr2:210809892G>A	Missense Mutation	UNC80	p.E2319K	unc-80 homolog (C. ele	25 (0.00)	35 (0.23)	0.61
11-03	Gp3	g.chr2:210837032A>G	Silent	UNC80	p.V2717V	unc-80 homolog (C. ele	24 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr19:18960958C>A	Missense Mutation	UPF1	p.T179K	UPF1 regulator of nons	21 (0.00)	37 (0.14)	0.48
11-03	Gp3	g.chr3:179472571G>T	Missense Mutation	USP13	p.R617M	ubiquitin specific peptid	69 (0.00)	34 (0.18)	0.47
11-03	Gp3	g.chr2:61415613G>A	Missense Mutation	USP34	p.S3422L	ubiquitin specific peptid	23 (0.00)	28 (0.36)	0.95
11-03	Gp3	g.chr15:50838704G>A	Missense Mutation	USP50	p.L7F	ubiquitin specific peptid	57 (0.00)	31 (0.19)	0.52
11-03	Gp3	g.chr10:75283448G>A	Missense Mutation	USP54	p.A752V	ubiquitin specific peptid	57 (0.00)	61 (0.15)	0.39
11-03	Gp3	g.chr13:52604240C>T	Missense Mutation	UTP14C	p.L434F	UTP14, U3 small nucle	119 (0.01)	41 (0.15)	0.39
11-03	Gp3	g.chr6:144812149G>T	Missense Mutation	UTRN	p.V1450L	utrophin	69 (0.00)	34 (0.15)	0.39
11-03	Gp3	g.chr14:77900623G>T	Missense Mutation	VIPAS39	p.N357K	VPS33B interacting pro	37 (0.00)	22 (0.27)	0.73
11-03	Gp3	g.chr15:41195226G>A	Missense Mutation	VPS18	p.C870Y	vacuolar protein sorting	21 (0.00)	33 (0.18)	0.48
11-03	Gp3	g.chr2:98736153G>A	Missense Mutation	VWA3B	p.D157N	von Willebrand factor A	46 (0.00)	48 (0.17)	0.44
11-03	Gp3	g.chr14:100826915C>T	Missense Mutation	WARS	p.R133H	tryptophanyl-tRNA syn	35 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr12:14946697C>T	Missense Mutation	WBP11	p.G294D	WW domain binding pr	99 (0.01)	87 (0.20)	0.52
11-03	Gp3	g.chr7:71130426C>T	Missense Mutation	WBSCR17	p.L371F	Williams-Beuren syndr	22 (0.00)	41 (0.12)	0.43
11-03	Gp3	g.chr4:85742503T>C	Missense Mutation	WDFY3	p.N442S	WD repeat and FYVE d	19 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr14:55455850G>T	Silent	WDHD1	p.S474S	WD repeat and HMG-b	23 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr4:39207259G>A	Missense Mutation	WDR19	p.G265S	WD repeat domain 19	29 (0.00)	37 (0.49)	1.30

11-03	Gp3	g.chr6:169982942G>T	Nonsense Mutation	WDR27	p.S838*	WD repeat domain 27	15 (0.00)	12 (0.42)	1.11
11-03	Gp3	g.chr1:118494624C>T	Missense Mutation	WDR3	p.S610F	WD repeat domain 3	16 (0.00)	27 (0.67)	1.78
11-03	Gp3	g.chr2:190332287C>T	Missense Mutation	WDR75	p.A514V	WD repeat domain 75	85 (0.00)	28 (0.39)	1.05
11-03	Gp3	g.chr17:25639388G>A	Missense Mutation	WSB1	p.R420H	WD repeat and SOCS b	63 (0.02)	92 (0.29)	0.78
11-03	Gp3	g.chr3:14191235C>G	Intron	XPC		xeroderma pigmentosun	17 (0.00)	45 (0.18)	0.47
11-03	Gp3	g.chr3:14198343G>C	Intron	XPC		xeroderma pigmentosun	87 (0.00)	69 (0.14)	0.39
11-03	Gp3	g.chr3:14203747C>A	Intron	XPC		xeroderma pigmentosun	64 (0.00)	58 (0.17)	0.46
11-03	Gp3	g.chr12:64818469G>A	Missense Mutation	XPOT	p.A425T	exportin, tRNA	17 (0.06)	33 (0.21)	0.57
11-03	Gp3	g.chr12:64827356G>T	Missense Mutation	XPOT	p.G809W	exportin, tRNA	31 (0.00)	29 (0.21)	0.55
11-03	Gp3	g.chr1:180772665G>A	Missense Mutation	XPR1	p.R122H	xenotropic and polytrop	92 (0.00)	64 (0.22)	0.58
11-03	Gp3	g.chr7:152345956G>A	Missense Mutation	XRCC2	p.S205L	X-ray repair complemer	69 (0.01)	55 (0.22)	0.58
11-03	Gp3	g.chr12:58345540G>A	Splice Site	XRCC6BP1		XRCC6 binding protein	38 (0.00)	51 (0.16)	0.42
11-03	Gp3	g.chr3:101371687C>G	Missense Mutation	ZBTB11	p.C802S	zinc finger and BTB do	38 (0.00)	47 (0.19)	0.51
11-03	Gp3	g.chr2:113081779G>A	Missense Mutation	ZC3H6	p.G464E	zinc finger CCCH-type	23 (0.00)	75 (0.23)	0.60
11-03	Gp3	g.chrX:64196205C>T	Splice Site	ZC4H2	p.R18K	zinc finger, C4H2 doma	77 (0.00)	20 (0.30)	0.50
11-03	Gp3	g.chr11:19197496C>T	Missense Mutation	ZDHHC13	p.R620C	zinc finger, DHHC-type	45 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr3:113675250C>T	Missense Mutation	ZDHHC23	p.L313F	zinc finger, DHHC-type	49 (0.00)	41 (0.15)	0.39
11-03	Gp3	g.chr6:38084406G>A	Silent	ZFAND3	p.T140T	zinc finger, AN1-type d	46 (0.02)	54 (0.22)	0.59
11-03	Gp3	g.chr8:77690561C>G	Missense Mutation	ZFHX4	p.H1071D	zinc finger homeobox 4	43 (0.00)	53 (0.19)	0.50
11-03	Gp3	g.chr8:77766054C>A	Silent	ZFHX4	p.L2299L	zinc finger homeobox 4	119 (0.01)	83 (0.33)	0.87
11-03	Gp3	g.chr19:57065981G>A	Silent	ZFP28	p.R609R	ZFP28 zinc finger prote	29 (0.00)	59 (0.31)	0.81
11-03	Gp3	g.chr19:57066228C>A	Missense Mutation	ZFP28	p.Q692K	ZFP28 zinc finger prote	35 (0.00)	29 (0.17)	0.46
11-03	Gp3	g.chr19:38126685C>A	Missense Mutation	ZFP30	p.V253F	ZFP30 zinc finger prote	34 (0.00)	47 (0.15)	0.50
11-03	Gp3	g.chrX:24228754C>T	Missense Mutation	ZFX	p.P560L	zinc finger protein, X-li	38 (0.00)	13 (0.38)	0.64
11-03	Gp3	g.chr14:68249509C>T	Missense Mutation	ZFYVE26	p.A1454T	zinc finger, FYVE doma	131 (0.00)	39 (0.31)	0.82
11-03	Gp3	g.chr8:124267013C>T	Missense Mutation	ZHX1	p.G392S	zinc fingers and homeob	26 (0.00)	45 (0.27)	0.71
11-03	Gp3	g.chr16:25268223G>A	Missense Mutation	ZKSCAN2	p.P76S	zinc finger with KRAB	36 (0.00)	54 (0.30)	0.79
11-03	Gp3	g.chr13:20567352A>T	Missense Mutation	ZMYM2	p.N47I	zinc finger, MYM-type	44 (0.00)	35 (0.17)	0.46
11-03	Gp3	g.chr2:219508388C>T	Missense Mutation	ZNF142	p.E951K	zinc finger protein 142	35 (0.00)	26 (0.19)	0.51
11-03	Gp3	g.chr2:219508511G>A	Missense Mutation	ZNF142	p.P910S	zinc finger protein 142	18 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr8:146156803C>T	Missense Mutation	ZNF16	p.G457E	zinc finger protein 16	31 (0.00)	14 (0.36)	0.95
11-03	Gp3	g.chr19:35230454G>A	Missense Mutation	ZNF181	p.V97M	zinc finger protein 181	29 (0.00)	25 (0.28)	0.75
11-03	Gp3	g.chr9:104170847G>T	Missense Mutation	ZNF189	p.G266V	zinc finger protein 189	109 (0.01)	40 (0.17)	0.47
11-03	Gp3	g.chr11:3380637G>A	Missense Mutation	ZNF195	p.S534F	zinc finger protein 195	33 (0.00)	49 (0.18)	0.49
11-03	Gp3	g.chr19:44570852G>A	Missense Mutation	ZNF223	p.E401K	zinc finger protein 223	32 (0.00)	33 (0.15)	0.40

11-03	Gp3	g.chr19:44512971G>T	Silent	ZNF230	p.V15V	zinc finger protein 230	68 (0.00)	100 (0.32)	0.85
11-03	Gp3	g.chr1:200377565T>A	Silent	ZNF281	p.T423T	zinc finger protein 281	34 (0.00)	11 (0.55)	1.45
11-03	Gp3	g.chr19:44590269G>A	Missense Mutation	ZNF284	p.S213N	zinc finger protein 284	84 (0.00)	59 (0.22)	0.59
11-03	Gp3	g.chr19:35435336G>A	Missense Mutation	ZNF30	p.C490Y	zinc finger protein 30	45 (0.02)	38 (0.24)	0.63
11-03	Gp3	g.chr19:57868681A>T	Nonsense Mutation	ZNF304	p.K482*	zinc finger protein 304	17 (0.00)	29 (0.31)	0.83
11-03	Gp3	g.chr19:7585702G>A	Missense Mutation	ZNF358	p.S525N	zinc finger protein 358	17 (0.00)	42 (0.19)	0.73
11-03	Gp3	g.chr3:21478531G>A	Missense Mutation	ZNF385D	p.R202W	zinc finger protein 385D	45 (0.00)	21 (0.24)	0.63
11-03	Gp3	g.chr18:72347341G>A	Missense Mutation	ZNF407	p.E1456K	zinc finger protein 407	37 (0.00)	22 (0.23)	0.61
11-03	Gp3	g.chr18:72589202C>T	Silent	ZNF407	p.L1643L	zinc finger protein 407	29 (0.00)	12 (0.75)	2.00
11-03	Gp3	g.chr19:58441824C>T	Silent	ZNF418	p.L35L	zinc finger protein 418	30 (0.00)	41 (0.20)	0.52
11-03	Gp3	g.chr19:52544771T>A	Missense Mutation	ZNF432	p.D35V	zinc finger protein 432	16 (0.00)	25 (0.20)	0.53
11-03	Gp3	g.chr1:23689505C>T	Missense Mutation	ZNF436	p.D124N	zinc finger protein 436	45 (0.00)	93 (0.18)	0.49
11-03	Gp3	g.chr19:11942298G>A	Missense Mutation	ZNF440	p.V103I	zinc finger protein 440	27 (0.00)	36 (0.14)	0.47
11-03	Gp3	g.chr9:109689645C>A	Missense Mutation	ZNF462	p.P1151H	zinc finger protein 462	123 (0.01)	35 (0.17)	0.46
11-03	Gp3	g.chr19:32845002A>G	Silent	ZNF507	p.E422E	zinc finger protein 507	52 (0.00)	46 (0.15)	0.41
11-03	Gp3	g.chr4:10446753T>A	Silent	ZNF518B	p.A400A	zinc finger protein 518B	72 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr18:22805909T>C	Missense Mutation	ZNF521	p.D658G	zinc finger protein 521	35 (0.00)	42 (0.14)	0.38
11-03	Gp3	g.chr19:58773675G>A	Missense Mutation	ZNF544	p.R568K	zinc finger protein 544	41 (0.00)	54 (0.31)	0.84
11-03	Gp3	g.chr19:2833810C>G	Missense Mutation	ZNF554	p.H193D	zinc finger protein 554	26 (0.00)	52 (0.19)	0.74
11-03	Gp3	g.chr19:37211053C>T	Missense Mutation	ZNF567	p.S476F	zinc finger protein 567	18 (0.00)	25 (0.20)	0.67
11-03	Gp3	g.chr19:37975011C>T	Nonsense Mutation	ZNF570	p.Q163*	zinc finger protein 570	70 (0.00)	45 (0.22)	0.75
11-03	Gp3	g.chr19:37975048C>A	Missense Mutation	ZNF570	p.P175Q	zinc finger protein 570	61 (0.00)	43 (0.14)	0.47
11-03	Gp3	g.chr19:38230204G>A	Missense Mutation	ZNF573	p.T396I	zinc finger protein 573	49 (0.00)	31 (0.16)	0.54
11-03	Gp3	g.chr16:3487317G>T	Missense Mutation	ZNF597	p.P128T	zinc finger protein 597	41 (0.00)	50 (0.20)	0.53
11-03	Gp3	g.chr15:64968186T>A	Missense Mutation	ZNF609	p.S1045T	zinc finger protein 609	24 (0.00)	32 (0.16)	0.42
11-03	Gp3	g.chr9:116812396C>T	Silent	ZNF618	p.L938L	zinc finger protein 618	118 (0.00)	49 (0.24)	0.65
11-03	Gp3	g.chr1:91405562C>T	Missense Mutation	ZNF644	p.C450Y	zinc finger protein 644	24 (0.00)	23 (0.22)	0.58
11-03	Gp3	g.chr1:91405571G>T	Missense Mutation	ZNF644	p.P447Q	zinc finger protein 644	20 (0.00)	27 (0.26)	0.69
11-03	Gp3	g.chr20:45085511C>T	RNA	ZNF663P		zinc finger protein 663,	20 (0.00)	30 (0.17)	0.44
11-03	Gp3	g.chr20:45085628C>T	RNA	ZNF663P		zinc finger protein 663,	19 (0.00)	33 (0.15)	0.40
11-03	Gp3	g.chr19:9407225C>T	Silent	ZNF699	p.G285G	zinc finger protein 699	57 (0.00)	36 (0.14)	0.47
11-03	Gp3	g.chr15:90611816C>T	Missense Mutation	ZNF710	p.L483F	zinc finger protein 710	47 (0.00)	45 (0.20)	0.53
11-03	Gp3	g.chr4:436449G>C	Missense Mutation	ZNF721	p.H603D	zinc finger protein 721	40 (0.03)	74 (0.30)	0.79
11-03	Gp3	g.chr19:22498949T>C	Silent	ZNF729	p.C910C	zinc finger protein 729	52 (0.02)	64 (0.61)	1.62
11-03	Gp3	g.chr9:130207382C>A	Missense Mutation	ZNF79	p.T468K	zinc finger protein 79	43 (0.00)	41 (0.17)	0.46

11-03	Gp3	g.chr19:12738552G>A	Missense Mutation	ZNF791	p.D50N	zinc finger protein 791	41 (0.00)	59 (0.14)	0.45
11-03	Gp3	g.chr16:21208863C>A	Missense Mutation	ZP2	p.V726L	zona pellucida glycopro	34 (0.00)	27 (0.22)	0.59
11-03	Gp3	g.chr1:238053368T>A	Missense Mutation	ZP4	p.Y95F	zona pellucida glycopro	19 (0.00)	23 (0.26)	0.70
11-03	Gp3	g.chr2:135965081G>A	Missense Mutation	ZRANB3	p.R978C	zinc finger, RAN-bindi	73 (0.00)	81 (0.15)	0.40
11-03	Gp3	g.chr6:28093328G>A	Missense Mutation	ZSCAN16	p.R36K	zinc finger and SCAN d	64 (0.00)	28 (0.29)	0.58
11-03	Gp4	g.chr12:9246060C>T	Splice Site	A2M		alpha-2-macroglobulin	40 (0.00)	69 (0.16)	0.53
11-03	Gp4	g.chr12:9268361G>C	Splice Site	A2M	p.P29A	alpha-2-macroglobulin	18 (0.00)	25 (0.24)	0.80
11-03	Gp4	g.chr12:125613909G>A	Silent	AACS	p.E484E	acetoacetyl-CoA synthe	29 (0.03)	64 (0.14)	0.49
11-03	Gp4	g.chr20:34832701C>A	Silent	AAR2	p.L280L	AAR2 splicing factor h	31 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr9:107578486C>T	Missense Mutation	ABCA1	p.D1226N	ATP-binding cassette, s	91 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr9:107620824C>T	Missense Mutation	ABCA1	p.M233I	ATP-binding cassette, s	47 (0.00)	33 (0.33)	0.89
11-03	Gp4	g.chr9:107620966C>A	Missense Mutation	ABCA1	p.G186V	ATP-binding cassette, s	41 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr7:48273670G>T	Missense Mutation	ABCA13	p.Q273H	ATP-binding cassette, s	67 (0.00)	54 (0.28)	0.74
11-03	Gp4	g.chr7:48431598G>A	Missense Mutation	ABCA13	p.R3912K	ATP-binding cassette, s	35 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr1:229661711C>A	Silent	ABCB10	p.V626V	ATP-binding cassette, s	41 (0.00)	43 (0.26)	0.68
11-03	Gp4	g.chr7:87035683C>T	Missense Mutation	ABCB4	p.S1136N	ATP-binding cassette, s	48 (0.00)	22 (0.32)	0.85
11-03	Gp4	g.chr2:220078003G>A	Missense Mutation	ABCB6	p.R589C	ATP-binding cassette, s	21 (0.00)	14 (0.71)	1.90
11-03	Gp4	g.chr16:48177949G>A	Silent	ABCC12	p.A49A	ATP-binding cassette, s	37 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr11:17434959C>A	Missense Mutation	ABCC8	p.Q819H	ATP-binding cassette, s	43 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr3:43743969G>T	Silent	ABHD5	p.V132V	abhydrolase domain con	31 (0.03)	33 (0.15)	0.40
11-03	Gp4	g.chr17:47299503G>A	Missense Mutation	ABI3	p.G279R	ABI family, member 3	40 (0.00)	39 (0.15)	0.41
11-03	Gp4	g.chr3:100469401G>C	Missense Mutation	ABI3BP	p.H1056D	ABI family, member 3 (	66 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr2:34065209C>T	lincRNA	AC009499.1			90 (0.00)	44 (0.16)	0.42
11-03	Gp4	g.chr17:16753367C>T	RNA	AC022596.2			44 (0.00)	22 (0.32)	0.85
11-03	Gp4	g.chr2:217475496C>T	lincRNA	AC073321.4			31 (0.00)	12 (0.58)	1.56
11-03	Gp4	g.chr2:89160490C>T	RNA	AC096579.13			37 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr17:35609927C>A	Missense Mutation	ACACA	p.R584L	acetyl-CoA carboxylase	35 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr12:112153696G>A	Missense Mutation	ACAD10	p.D308N	acyl-CoA dehydrogenas	51 (0.00)	54 (0.17)	0.58
11-03	Gp4	g.chr3:132277894C>T	Missense Mutation	ACAD11	p.G755E	acyl-CoA dehydrogenas	51 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr15:89401801C>T	Silent	ACAN	p.S1995S	aggrecan	34 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr14:23547381G>A	Missense Mutation	ACIN1	p.S759L	apoptotic chromatin con	86 (0.01)	44 (0.16)	0.42
11-03	Gp4	g.chr14:74062118A>C	Missense Mutation	ACOT4	p.L342F	acyl-CoA thioesterase 4	23 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr19:6156561C>T	Splice Site	ACSBG2	p.S169L	acyl-CoA synthetase bu	65 (0.00)	85 (0.16)	0.56
11-03	Gp4	g.chr19:6156562G>C	Splice Site	ACSBG2	p.S169S	acyl-CoA synthetase bu	65 (0.00)	84 (0.12)	0.40
11-03	Gp4	g.chr19:6183236C>T	Silent	ACSBG2	p.S425S	acyl-CoA synthetase bu	30 (0.00)	21 (0.33)	1.13

11-03	Gp4	g.chrX:108908668C>T	Silent	ACSL4	p.K457K	acyl-CoA synthetase lo	24 (0.00)	16 (0.31)	0.52
11-03	Gp4	g.chr16:20494380G>A	Splice Site	ACSM2A	p.V504M	acyl-CoA synthetase m	42 (0.00)	21 (0.43)	1.14
11-03	Gp4	g.chr16:20554245G>T	Silent	ACSM2B	p.V500V	acyl-CoA synthetase m	25 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr16:20554263G>T	Silent	ACSM2B	p.I494I	acyl-CoA synthetase m	29 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr12:81536982C>T	Missense Mutation	ACSS3	p.P293S	acyl-CoA synthetase sh	20 (0.00)	52 (0.15)	0.52
11-03	Gp4	g.chr2:114691921G>A	Silent	ACTR3	p.T166T	ARP3 actin-related prot	60 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr2:9676867G>C	Nonsense Mutation	ADAM17	p.Y107*	ADAM metallopeptidas	24 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr8:24181424C>A	Silent	ADAM28	p.T266T	ADAM metallopeptidas	16 (0.00)	13 (0.46)	0.46
11-03	Gp4	g.chr1:120436670C>T	Missense Mutation	ADAM30	p.A764T	ADAM metallopeptidas	105 (0.00)	80 (0.17)	0.47
11-03	Gp4	g.chr5:33616020C>A	Silent	ADAMTS12	p.L767L	ADAM metallopeptidas	33 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr5:178634632C>A	Missense Mutation	ADAMTS2	p.R258L	ADAM metallopeptidas	15 (0.00)	14 (0.43)	1.14
11-03	Gp4	g.chr12:43858433C>T	Silent	ADAMTS20	p.E490E	ADAM metallopeptidas	25 (0.00)	26 (0.58)	1.94
11-03	Gp4	g.chr12:43925967T>C	Missense Mutation	ADAMTS20	p.Y162C	ADAM metallopeptidas	23 (0.00)	73 (0.12)	0.42
11-03	Gp4	g.chr16:50349408C>A	Missense Mutation	ADCY7	p.L1079M	adenylate cyclase 7	17 (0.00)	19 (0.32)	0.84
11-03	Gp4	g.chr8:131922044C>T	Missense Mutation	ADCY8	p.C517Y	adenylate cyclase 8 (bra	26 (0.00)	44 (0.82)	2.18
11-03	Gp4	g.chr10:111892105C>T	Missense Mutation	ADD3	p.S592L	adducin 3 (gamma)	47 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr4:100232697C>T	Nonsense Mutation	ADH1B	p.W315*	alcohol dehydrogenase	33 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr18:77893677C>T	Silent	ADNP2	p.F127F	ADNP homeobox 2	32 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr15:73044806C>A	Missense Mutation	ADPGK	p.R456I	ADP-dependent glucoki	92 (0.01)	22 (0.23)	0.61
11-03	Gp4	g.chr17:10608813C>T	Silent	ADPRM	p.H190H	ADP-ribose/CDP-alcoh	45 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr7:44150334G>T	Missense Mutation	AEBP1	p.V471L	AE binding protein 1	77 (0.00)	85 (0.22)	0.60
11-03	Gp4	g.chr10:75457389C>A	Missense Mutation	AGAP5	p.G42V	ArfGAP with GTPase d	68 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr15:86687020C>A	Missense Mutation	AGBL1	p.P23Q	ATP/GTP binding prote	42 (0.02)	88 (0.30)	0.79
11-03	Gp4	g.chr11:47712013G>T	Missense Mutation	AGBL2	p.Q378K	ATP/GTP binding prote	52 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr7:134678307G>T	Missense Mutation	AGBL3	p.G63V	ATP/GTP binding prote	66 (0.00)	42 (0.21)	0.57
11-03	Gp4	g.chr5:76357600G>A	Silent	AGGF1	p.G639G	angiogenic factor with	45 (0.00)	92 (0.16)	0.43
11-03	Gp4	g.chr7:141296408C>A	Missense Mutation	AGK	p.A63D	acylglycerol kinase	35 (0.00)	70 (0.21)	0.57
11-03	Gp4	g.chr8:41476441G>T	Missense Mutation	AGPAT6	p.A403S	1-acylglycerol-3-phosp	40 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr5:35040722C>T	Silent	AGXT2	p.K45K	alanine--glyoxylate ami	37 (0.00)	64 (0.23)	0.62
11-03	Gp4	g.chr1:110558080G>A	Missense Mutation	AHCYL1	p.V237I	adenosylhomocysteinas	27 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr1:27873850G>T	Missense Mutation	AHDC1	p.H1593N	AT hook, DNA binding	23 (0.00)	36 (0.22)	0.59
11-03	Gp4	g.chr11:62300941G>T	Silent	AHNAK	p.V316V	AHNAK nucleoprotein	20 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr14:105405555C>T	Silent	AHNAK2	p.R409R	AHNAK nucleoprotein	27 (0.00)	36 (0.33)	0.89
11-03	Gp4	g.chr7:17349746T>A	Splice Site	AHR	p.D84E	aryl hydrocarbon recept	32 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr6:109814649G>A	Nonsense Mutation	AK9	p.Q1887*	adenylate kinase 9	24 (0.00)	42 (0.26)	0.70

11-03	Gp4	g.chrX:49957480G>T	Missense Mutation	AKAP4	p.N619K	A kinase (PRKA) ancho	17 (0.00)	34 (0.53)	0.88
11-03	Gp4	g.chr10:5046001C>T	Silent	AKR1C2	p.K9K	aldo-keto reductase fam	58 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr13:107773417G>T	RNA	AL445204.1			36 (0.00)	35 (0.26)	0.69
11-03	Gp4	g.chr10:97373591C>A	Missense Mutation	ALDH18A1	p.A611S	aldehyde dehydrogenase	44 (0.02)	49 (0.27)	0.71
11-03	Gp4	g.chr9:75540416G>A	Missense Mutation	ALDH1A1	p.A206V	aldehyde dehydrogenase	25 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr1:165632288C>A	Nonstop Mutation	ALDH9A1	p.*519L	aldehyde dehydrogenase	75 (0.00)	24 (0.33)	0.89
11-03	Gp4	g.chr9:104189825G>T	Missense Mutation	ALDOB	p.S160Y	aldolase B, fructose-bis	32 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr2:3745016C>T	Nonsense Mutation	ALLC	p.R274*	allantoicase	38 (0.00)	48 (0.23)	0.61
11-03	Gp4	g.chr2:73677354C>T	Missense Mutation	ALMS1	p.P1233S	Alstrom syndrome 1	62 (0.00)	49 (0.20)	0.54
11-03	Gp4	g.chr2:73677426C>A	Missense Mutation	ALMS1	p.P1257T	Alstrom syndrome 1	70 (0.00)	51 (0.27)	0.73
11-03	Gp4	g.chr2:73784412C>A	Missense Mutation	ALMS1	p.H3381N	Alstrom syndrome 1	33 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr4:113352488G>A	Nonsense Mutation	ALPK1	p.W595*	alpha-kinase 1	23 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr18:56246061C>A	Missense Mutation	ALPK2	p.W649C	alpha-kinase 2	42 (0.00)	48 (0.21)	0.56
11-03	Gp4	g.chr12:85677448G>A	Missense Mutation	ALX1	p.G109R	ALX homeobox 1	31 (0.00)	37 (0.14)	0.45
11-03	Gp4	g.chr1:110050998C>T	Silent	AMIGO1	p.K179K	adhesion molecule with	80 (0.01)	44 (0.27)	0.73
11-03	Gp4	g.chr1:115222954T>A	Silent	AMPD1	p.P260P	adenosine monophospha	41 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr2:112566758C>T	Splice Site	ANAPC1	p.G1200S	anaphase promoting con	53 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr9:140081958G>T	Missense Mutation	ANAPC2	p.Q239K	anaphase promoting con	17 (0.00)	14 (0.50)	1.33
11-03	Gp4	g.chr14:77272872C>A	Missense Mutation	ANGEL1	p.G423C	angel homolog 1 (Droso	29 (0.00)	36 (0.19)	0.52
11-03	Gp4	g.chr17:54559766A>G	Missense Mutation	ANKFN1	p.N717S	ankyrin-repeat and fibro	56 (0.02)	33 (0.21)	0.57
11-03	Gp4	g.chr17:4109634G>A	Missense Mutation	ANKFY1	p.H294Y	ankyrin repeat and FYV	30 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr4:74008375A>T	Missense Mutation	ANKRD17	p.D689E	ankyrin repeat domain 1	58 (0.00)	61 (0.26)	0.70
11-03	Gp4	g.chr9:67930395T>A	Missense Mutation	ANKRD20A1	p.L71Q	ankyrin repeat domain 2	37 (0.00)	36 (0.25)	0.67
11-03	Gp4	g.chr18:14183687G>A	RNA	ANKRD20A5P		ankyrin repeat domain 2	34 (0.00)	30 (0.43)	1.16
11-03	Gp4	g.chr4:125593285C>A	Nonsense Mutation	ANKRD50	p.E383*	ankyrin repeat domain 5	16 (0.00)	51 (0.20)	0.52
11-03	Gp4	g.chr12:100048903C>A	Missense Mutation	ANKS1B	p.W405L	ankyrin repeat and steril	20 (0.00)	71 (0.11)	0.38
11-03	Gp4	g.chr12:99640154C>T	Missense Mutation	ANKS1B	p.E749K	ankyrin repeat and steril	92 (0.00)	59 (0.34)	1.15
11-03	Gp4	g.chr7:36492158T>A	Missense Mutation	ANLN	p.D1108E	anillin, actin binding pro	31 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chr12:101491644C>T	Missense Mutation	ANO4	p.L608F	anoctamin 4	20 (0.00)	46 (0.20)	0.67
11-03	Gp4	g.chr21:28740044G>A	lincRNA	AP001604.3			16 (0.00)	18 (0.50)	1.33
11-03	Gp4	g.chr11:64942552C>T	RNA	AP003068.18			50 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr21:11181671G>A	lincRNA	AP003900.6			37 (0.03)	23 (0.22)	0.58
11-03	Gp4	g.chr16:71768576C>A	Missense Mutation	AP1G1	p.S768I	adaptor-related protein c	28 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr11:970193G>A	Missense Mutation	AP2A2	p.S54N	adaptor-related protein c	58 (0.00)	50 (0.38)	1.01
11-03	Gp4	g.chr5:112179285C>A	Missense Mutation	APC	p.P2665H	adenomatous polyposis	29 (0.00)	31 (0.19)	0.52

11-03	Gp4	g.chr2:21231703C>A	Missense Mutation	APOB	p.M2679I	apolipoprotein B	49 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr6:41029236G>A	Missense Mutation	APOBEC2	p.E101K	apolipoprotein B mRN	29 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr22:36587791C>T	Missense Mutation	APOL4	p.C126Y	apolipoprotein L, 4	16 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr1:154293649C>T	Silent	AQP10	p.A6A	aquaporin 10	44 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr5:141033987G>A	Nonsense Mutation	ARAP3	p.Q1220*	ArfGAP with RhoGAP	16 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr5:141033994C>T	Silent	ARAP3	p.K1217K	ArfGAP with RhoGAP	15 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr3:121305370G>T	Missense Mutation	ARGFX	p.A291S	arginine-fifty homeobo	35 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr15:32925235C>T	Silent	ARHGAP11A	p.L198L	Rho GTPase activating	16 (0.00)	45 (0.24)	0.65
11-03	Gp4	g.chr16:24942223T>A	Silent	ARHGAP17	p.P799P	Rho GTPase activating	17 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr6:129959555C>T	Missense Mutation	ARHGAP18	p.R179K	Rho GTPase activating	33 (0.00)	34 (0.38)	0.40
11-03	Gp4	g.chr11:128868247G>A	Silent	ARHGAP32	p.L25L	Rho GTPase activating	108 (0.00)	70 (0.14)	0.38
11-03	Gp4	g.chr11:128868279C>T	Missense Mutation	ARHGAP32	p.G14E	Rho GTPase activating	111 (0.00)	97 (0.15)	0.41
11-03	Gp4	g.chr19:47424945C>T	Silent	ARHGAP35	p.L1005L	Rho GTPase activating	77 (0.00)	72 (0.32)	0.85
11-03	Gp4	g.chrX:130219994G>T	Silent	ARHGAP36	p.G392G	Rho GTPase activating	30 (0.00)	24 (0.25)	0.42
11-03	Gp4	g.chr11:73071412C>T	Silent	ARHGEF17	p.D1418D	Rho guanine nucleotide	22 (0.05)	17 (0.65)	1.73
11-03	Gp4	g.chr1:27094450G>C	Missense Mutation	ARID1A	p.R1053P	AT rich interactive dom	42 (0.00)	48 (0.15)	0.39
11-03	Gp4	g.chr6:157528913C>T	Missense Mutation	ARID1B	p.S2213L	AT rich interactive dom	39 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr12:46244728C>A	Missense Mutation	ARID2	p.P941Q	AT rich interactive dom	101 (0.00)	72 (0.14)	0.47
11-03	Gp4	g.chr6:109179425C>T	Missense Mutation	ARMC2	p.S81L	armadillo repeat contain	23 (0.00)	53 (0.19)	0.50
11-03	Gp4	g.chr10:28223999G>T	Missense Mutation	ARMC4	p.A812D	armadillo repeat contain	16 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr2:25965888G>A	Silent	ASXL2	p.F1106F	additional sex combs lik	86 (0.00)	48 (0.29)	0.78
11-03	Gp4	g.chr18:31324142C>A	Silent	ASXL3	p.R1444R	additional sex combs lik	42 (0.00)	27 (0.37)	0.99
11-03	Gp4	g.chr18:31325531C>T	Nonsense Mutation	ASXL3	p.Q1907*	additional sex combs lik	157 (0.01)	104 (0.15)	0.41
11-03	Gp4	g.chr8:124349966C>T	Missense Mutation	ATAD2	p.D302N	ATPase family, AAA d	47 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr3:193183909G>A	Nonsense Mutation	ATP13A4	p.Q393*	ATPase type 13A4	52 (0.00)	52 (0.38)	1.03
11-03	Gp4	g.chr1:116946586G>A	Missense Mutation	ATP1A1	p.R1011Q	ATPase, Na+/K+ transp	52 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr14:92563114C>A	Silent	ATXN3	p.V31V	ataxin 3	95 (0.00)	61 (0.28)	0.74
11-03	Gp4	g.chr7:70227897C>T	Nonsense Mutation	AUTS2	p.Q262*	autism susceptibility ca	25 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chrX:69460090C>T	Missense Mutation	AWAT1	p.H313Y	acyl-CoA wax alcohol a	39 (0.00)	47 (0.26)	0.43
11-03	Gp4	g.chr3:28368342G>A	Silent	AZI2	p.T249T	5-azacytidine induced 2	29 (0.00)	25 (0.36)	0.96
11-03	Gp4	g.chr1:235628956G>T	Missense Mutation	B3GALNT2	p.Q280K	beta-1,3-N-acetylgalact	41 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr21:11047628T>A	RNA	BAGE2		B melanoma antigen fa	28 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chr20:52601880G>A	Silent	BCAS1	p.T362T	breast carcinoma amplif	26 (0.00)	58 (0.21)	0.55
11-03	Gp4	g.chr6:136597151C>T	Silent	BCLAF1	p.K504K	BCL2-associated transc	52 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr17:40963680G>A	Missense Mutation	BECN1	p.P393S	beclin 1, autophagy rela	34 (0.00)	29 (0.21)	0.55

11-03	Gp4	g.chr4:42122284G>A	Missense Mutation	BEND4	p.P392S	BEN domain containing	37 (0.00)	39 (0.51)	1.37
11-03	Gp4	g.chr12:32481052C>G	Missense Mutation	BICD1	p.P555A	bicaudal D homolog 1 (	48 (0.00)	38 (0.18)	0.62
11-03	Gp4	g.chr15:91261598C>T	Intron	BLM		Bloom syndrome, RecQ	99 (0.00)	54 (0.24)	0.64
11-03	Gp4	g.chr15:91301865C>A	Intron	BLM		Bloom syndrome, RecQ	20 (0.00)	90 (0.29)	0.77
11-03	Gp4	g.chr15:91304950T>C	Intron	BLM		Bloom syndrome, RecQ	65 (0.00)	53 (0.21)	0.55
11-03	Gp4	g.chr15:91318537A>T	Intron	BLM		Bloom syndrome, RecQ	29 (0.00)	105 (0.30)	0.81
11-03	Gp4	g.chr15:91324217G>A	Intron	BLM		Bloom syndrome, RecQ	22 (0.00)	17 (0.35)	0.94
11-03	Gp4	g.chr15:91331358G>A	Intron	BLM		Bloom syndrome, RecQ	21 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr15:91352362C>T	Intron	BLM		Bloom syndrome, RecQ	40 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr15:91354134G>A	Intron	BLM		Bloom syndrome, RecQ	47 (0.02)	12 (0.42)	1.11
11-03	Gp4	g.chr7:34094798G>A	Silent	BMPER	p.R270R	BMP binding endothelia	18 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr4:96075722C>A	Silent	BMPR1B	p.L469L	bone morphogenetic pro	40 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr15:83926343G>T	Missense Mutation	BNC1	p.H939N	basonuclin 1	65 (0.00)	82 (0.16)	0.42
11-03	Gp4	g.chr9:16418987C>A	Nonstop Mutation	BNC2	p.*1100Y	basonuclin 2	68 (0.00)	45 (0.36)	0.95
11-03	Gp4	g.chr10:133787409C>T	Missense Mutation	BNIP3	p.G29R	BCL2/adenovirus E1B 1	45 (0.02)	17 (0.47)	1.25
11-03	Gp4	g.chr4:13579075G>A	Missense Mutation	BOD1L1	p.R2946W	biorientation of chromos	36 (0.00)	29 (0.28)	0.74
11-03	Gp4	g.chr4:13602120C>T	Missense Mutation	BOD1L1	p.S2135N	biorientation of chromos	52 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr4:13603275C>A	Missense Mutation	BOD1L1	p.R1750L	biorientation of chromos	58 (0.02)	46 (0.48)	1.28
11-03	Gp4	g.chr4:13603342T>A	Missense Mutation	BOD1L1	p.T1728S	biorientation of chromos	40 (0.03)	78 (0.36)	0.96
11-03	Gp4	g.chr20:31828078G>A	Silent	BPIFA1	p.K156K	BPI fold containing fam	52 (0.02)	54 (0.28)	0.74
11-03	Gp4	g.chr7:140508737C>T	Missense Mutation	BRAF	p.R188K	B-Raf proto-oncogene, s	26 (0.00)	33 (0.27)	0.73
11-03	Gp4	g.chr12:112097112C>A	Missense Mutation	BRAP	p.C307F	BRCA1 associated prot	39 (0.00)	34 (0.15)	0.51
11-03	Gp4	g.chr17:41204180C>A	Intron	BRCA1		breast cancer 1, early on	21 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr17:41221519C>G	Intron	BRCA1		breast cancer 1, early on	91 (0.01)	33 (0.21)	0.57
11-03	Gp4	g.chr17:41222485C>T	Intron	BRCA1		breast cancer 1, early on	43 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr17:41231417C>A	Intron	BRCA1		breast cancer 1, early on	79 (0.00)	34 (0.21)	0.55
11-03	Gp4	g.chr17:41268981T>A	Intron	BRCA1		breast cancer 1, early on	38 (0.00)	55 (0.36)	0.97
11-03	Gp4	g.chr13:32927822G>T	Intron	BRCA2		breast cancer 2, early on	38 (0.00)	10 (0.50)	0.52
11-03	Gp4	g.chr5:137500629C>T	Missense Mutation	BRD8	p.R502K	bromodomain containin	35 (0.00)	28 (0.32)	0.86
11-03	Gp4	g.chr5:137500649T>C	Missense Mutation	BRD8	p.I495M	bromodomain containin	36 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr5:137503643G>T	Missense Mutation	BRD8	p.A256E	bromodomain containin	30 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr12:125497173G>C	Missense Mutation	BRI3BP	p.G103R	BRI3 binding protein	52 (0.00)	53 (0.25)	0.86
11-03	Gp4	g.chr6:36196712C>A	Missense Mutation	BRPF3	p.L1105M	bromodomain and PHD	28 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr3:49693081G>A	Missense Mutation	BSN	p.R2031H	bassoon presynaptic cyt	32 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr10:93741976C>A	Missense Mutation	BTAF1	p.A681E	BTAF1 RNA polymeras	17 (0.00)	35 (0.14)	0.38

11-03	Gp4	g.chr11:13410422C>A	Missense Mutation	BTBD10	p.G470C	BTB (POZ) domain con	51 (0.00)	32 (0.25)	0.67
11-03	Gp4	g.chr20:11900411G>A	Missense Mutation	BTBD3	p.G155R	BTB (POZ) domain con	41 (0.00)	50 (0.20)	0.53
11-03	Gp4	g.chr5:180483008C>T	Silent	BTNL9	p.G316G	butyrophilin-like 9	20 (0.00)	26 (0.42)	1.13
11-03	Gp4	g.chr10:103294593C>T	Missense Mutation	BTRC	p.H425Y	beta-transducin repeat c	62 (0.00)	63 (0.14)	0.38
11-03	Gp4	g.chr15:40494880G>A	Silent	BUB1B	p.V573V	BUB1 mitotic checkpoi	41 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr7:16737766C>A	Missense Mutation	BZW2	p.H355N	basic leucine zipper and	44 (0.02)	65 (0.38)	1.03
11-03	Gp4	g.chr10:19620454C>T	Silent	C10orf112	p.L578L		16 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr10:19636816C>G	Missense Mutation	C10orf112	p.P636A		34 (0.00)	54 (0.28)	0.74
11-03	Gp4	g.chr10:50531833C>A	Missense Mutation	C10orf71	p.H415N	chromosome 10 open re	112 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr11:62437470C>G	Missense Mutation	C11orf48	p.G12R	chromosome 11 open re	16 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr11:62437491G>A	Missense Mutation	C11orf48	p.P5S	chromosome 11 open re	15 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr11:36669607A>T	Missense Mutation	C11orf74	p.T134S	chromosome 11 open re	24 (0.00)	43 (0.33)	0.87
11-03	Gp4	g.chr12:103699827C>G	Missense Mutation	C12orf42	p.E186Q	chromosome 12 open re	53 (0.00)	40 (0.12)	0.43
11-03	Gp4	g.chr14:50559328C>A	Missense Mutation	C14orf183	p.D12Y	chromosome 14 open re	97 (0.00)	58 (0.45)	1.20
11-03	Gp4	g.chr16:67168297C>A	Silent	C16orf70	p.V196V	chromosome 16 open re	71 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr16:4793048T>A	Missense Mutation	C16orf71	p.L277H	chromosome 16 open re	16 (0.00)	21 (0.38)	1.02
11-03	Gp4	g.chr17:42744499C>A	Missense Mutation	C17orf104	p.A407E	chromosome 17 open re	62 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr17:30666870G>C	Silent	C17orf75	p.V103V	chromosome 17 open re	105 (0.00)	96 (0.18)	0.47
11-03	Gp4	g.chr17:35742986C>T	Missense Mutation	C17orf78	p.A144V	chromosome 17 open re	68 (0.00)	60 (0.15)	0.40
11-03	Gp4	g.chr1:172417595C>T	Missense Mutation	C1orf105	p.S41F	chromosome 1 open rea	75 (0.00)	66 (0.15)	0.40
11-03	Gp4	g.chr1:53684159C>T	Silent	C1orf123	p.V52V	chromosome 1 open rea	22 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr5:159776296T>G	Missense Mutation	C1QTNF2	p.E291A	C1q and tumor necrosis	56 (0.00)	42 (0.31)	0.83
11-03	Gp4	g.chr20:20056156G>A	Missense Mutation	C20orf26	p.D155N		33 (0.00)	34 (0.47)	1.25
11-03	Gp4	g.chr11:73801887G>A	Silent	C2CD3	p.I1204I	C2 calcium-dependent d	35 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr12:22646200C>G	Missense Mutation	C2CD5	p.G407R	C2 calcium-dependent d	21 (0.00)	39 (0.44)	1.46
11-03	Gp4	g.chr2:106690370C>T	Silent	C2orf40	p.A16A	chromosome 2 open rea	67 (0.01)	41 (0.37)	0.98
11-03	Gp4	g.chr3:63805244G>A	Missense Mutation	C3orf49	p.G33S	chromosome 3 open rea	55 (0.00)	34 (0.26)	0.71
11-03	Gp4	g.chr4:37591744G>A	Missense Mutation	C4orf19	p.G23S	chromosome 4 open rea	81 (0.01)	115 (0.29)	0.77
11-03	Gp4	g.chr4:113540455T>A	Missense Mutation	C4orf21	p.N248I		32 (0.00)	28 (0.32)	0.86
11-03	Gp4	g.chr4:113540845C>T	Splice Site	C4orf21	p.G118D		16 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr4:130023907G>C	Missense Mutation	C4orf33	p.E48Q	chromosome 4 open rea	24 (0.00)	27 (0.33)	0.89
11-03	Gp4	g.chr9:123737185G>T	Missense Mutation	C5	p.L1297M	complement component	48 (0.00)	26 (0.31)	0.82
11-03	Gp4	g.chr5:43453844G>A	Silent	C5orf28	p.D76D	chromosome 5 open rea	19 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr5:43509305G>C	Missense Mutation	C5orf34	p.P46R	chromosome 5 open rea	35 (0.00)	58 (0.33)	0.87
11-03	Gp4	g.chr5:37201801C>T	Silent	C5orf42	p.L1133L	chromosome 5 open rea	24 (0.04)	37 (0.16)	0.43

11-03	Gp4	g.chr5:41912268C>G	Missense Mutation	C5orf51	p.A195G	chromosome 5 open rea	22 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr5:131796276C>T	Silent	C5orf56	p.L37L	chromosome 5 open rea	32 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr6:36867264C>G	Nonsense Mutation	C6orf89	p.S22*	chromosome 6 open rea	34 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr7:134853611C>T	Missense Mutation	C7orf49	p.A22T	chromosome 7 open rea	59 (0.00)	44 (0.25)	0.67
11-03	Gp4	g.chr7:134853614C>T	Missense Mutation	C7orf49	p.V21M	chromosome 7 open rea	58 (0.00)	45 (0.24)	0.65
11-03	Gp4	g.chr7:134853617G>A	Nonsense Mutation	C7orf49	p.Q20*	chromosome 7 open rea	58 (0.00)	45 (0.18)	0.47
11-03	Gp4	g.chr8:69552743C>T	Missense Mutation	C8orf34	p.A413V	chromosome 8 open rea	17 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr9:116186533G>A	Silent	C9orf43	p.K248K	chromosome 9 open rea	68 (0.00)	17 (0.41)	1.10
11-03	Gp4	g.chr9:114510448G>A	Silent	C9orf84	p.I195I	chromosome 9 open rea	36 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr16:87921762C>A	Missense Mutation	CA5A	p.Q297H	carbonic anhydrase VA,	100 (0.00)	56 (0.21)	0.57
11-03	Gp4	g.chr12:2714934C>T	Silent	CACNA1C	p.I1066I	calcium channel, voltag	19 (0.00)	25 (0.24)	0.80
11-03	Gp4	g.chr1:181724502G>A	Missense Mutation	CACNA1E	p.D1320N	calcium channel, voltag	113 (0.00)	150 (0.17)	0.44
11-03	Gp4	g.chr1:181725190T>A	Missense Mutation	CACNA1E	p.L1363Q	calcium channel, voltag	33 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr17:48683306C>T	Silent	CACNA1G	p.N1448N	calcium channel, voltag	25 (0.00)	66 (0.24)	0.65
11-03	Gp4	g.chr3:55107474C>T	Missense Mutation	CACNA2D3	p.S997F	calcium channel, voltag	41 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr2:152737433T>C	Missense Mutation	CACNB4	p.K44E	calcium channel, voltag	51 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr3:85017094G>A	Intron	CADM2		cell adhesion molecule	17 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr3:85058257C>A	Intron	CADM2		cell adhesion molecule	49 (0.00)	36 (0.31)	0.81
11-03	Gp4	g.chr3:85097916G>A	Intron	CADM2		cell adhesion molecule	28 (0.00)	27 (0.37)	0.99
11-03	Gp4	g.chr3:85136140A>G	Intron	CADM2		cell adhesion molecule	20 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr3:85155432G>A	Intron	CADM2		cell adhesion molecule	44 (0.00)	62 (0.32)	0.86
11-03	Gp4	g.chr3:85170589A>T	Intron	CADM2		cell adhesion molecule	30 (0.00)	67 (0.24)	0.64
11-03	Gp4	g.chr3:85189251C>A	Intron	CADM2		cell adhesion molecule	28 (0.00)	34 (0.21)	0.55
11-03	Gp4	g.chr3:85225296C>T	Intron	CADM2		cell adhesion molecule	49 (0.00)	33 (0.27)	0.73
11-03	Gp4	g.chr3:85239391C>T	Intron	CADM2		cell adhesion molecule	17 (0.00)	36 (0.22)	0.59
11-03	Gp4	g.chr3:85277653G>A	Intron	CADM2		cell adhesion molecule	35 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr3:85326465C>A	Intron	CADM2		cell adhesion molecule	26 (0.00)	22 (0.82)	2.18
11-03	Gp4	g.chr3:85352660C>G	Intron	CADM2		cell adhesion molecule	21 (0.00)	14 (0.43)	1.14
11-03	Gp4	g.chr3:85426504G>T	Intron	CADM2		cell adhesion molecule	54 (0.00)	70 (0.16)	0.42
11-03	Gp4	g.chr3:85458797G>A	Intron	CADM2		cell adhesion molecule	39 (0.00)	48 (0.38)	1.00
11-03	Gp4	g.chr3:85469086G>C	Intron	CADM2		cell adhesion molecule	56 (0.00)	40 (0.25)	0.67
11-03	Gp4	g.chr3:85511302G>A	Intron	CADM2		cell adhesion molecule	47 (0.00)	35 (0.26)	0.69
11-03	Gp4	g.chr3:85557931G>C	Intron	CADM2		cell adhesion molecule	27 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr3:85616286G>A	Intron	CADM2		cell adhesion molecule	51 (0.00)	78 (0.19)	0.51
11-03	Gp4	g.chr3:85631860C>T	Intron	CADM2		cell adhesion molecule	39 (0.00)	33 (0.15)	0.40

11-03	Gp4	g.chr3:85658596A>T	Intron	CADM2		cell adhesion molecule	38 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr3:85709925G>T	Intron	CADM2		cell adhesion molecule	57 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr3:85712937C>T	Intron	CADM2		cell adhesion molecule	57 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr3:85724868G>A	Intron	CADM2		cell adhesion molecule	51 (0.02)	66 (0.24)	0.65
11-03	Gp4	g.chr3:85759384C>A	Intron	CADM2		cell adhesion molecule	54 (0.00)	75 (0.29)	0.78
11-03	Gp4	g.chr3:85808942G>C	Intron	CADM2		cell adhesion molecule	49 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr3:85822396G>T	Intron	CADM2		cell adhesion molecule	34 (0.00)	34 (0.29)	0.78
11-03	Gp4	g.chr3:85949199C>A	Intron	CADM2		cell adhesion molecule	22 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr3:86042639C>A	Intron	CADM2		cell adhesion molecule	15 (0.00)	11 (0.73)	1.94
11-03	Gp4	g.chr3:86063885C>A	Intron	CADM2		cell adhesion molecule	57 (0.00)	44 (0.20)	0.55
11-03	Gp4	g.chr3:86088161C>G	Intron	CADM2		cell adhesion molecule	60 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr3:86095933C>G	Intron	CADM2		cell adhesion molecule	38 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr3:86099192C>T	Intron	CADM2		cell adhesion molecule	21 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr10:75608858G>T	Missense Mutation	CAMK2G	p.L144M	calcium/calmodulin-dep	23 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr1:7805904G>A	Splice Site	CAMTA1		calmodulin binding tran	47 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr15:42652165C>A	Silent	CAPN3	p.I54I	calpain 3, (p94)	58 (0.00)	29 (0.28)	0.74
11-03	Gp4	g.chr3:15283043C>T	Missense Mutation	CAPN7	p.P579L	calpain 7	18 (0.00)	32 (0.41)	1.08
11-03	Gp4	g.chr11:34119301C>G	Silent	CAPRIN1	p.A686A	cell cycle associated pro	29 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr12:30906614G>T	Silent	CAPRIN2	p.S28S	caprin family member 2	35 (0.00)	37 (0.16)	0.54
11-03	Gp4	g.chr12:18891296G>A	Missense Mutation	CAPZA3	p.D32N	capping protein (actin fi	30 (0.00)	41 (0.17)	0.57
11-03	Gp4	g.chr11:104915259C>T	Missense Mutation	CARD16	p.R45H	caspase recruitment don	31 (0.00)	48 (0.33)	0.89
11-03	Gp4	g.chr2:203836374C>A	Nonsense Mutation	CARF	p.S415*	calcium responsive tran	29 (0.00)	54 (0.17)	0.44
11-03	Gp4	g.chr15:40916357A>G	Missense Mutation	CASC5	p.S1325G	cancer susceptibility car	36 (0.00)	34 (0.32)	0.86
11-03	Gp4	g.chr11:104815490G>A	Missense Mutation	CASP4	p.P319L	caspase 4, apoptosis-rel	23 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr6:90577199C>T	RNA	CASP8AP2		caspase 8 associated pro	70 (0.00)	40 (0.38)	0.43
11-03	Gp4	g.chr1:10710764G>A	Silent	CASZ1	p.S955S	castor zinc finger 1	57 (0.00)	33 (0.24)	0.65
11-03	Gp4	g.chr11:119146746G>T	Missense Mutation	CBL	p.W303C	Cbl proto-oncogene, E3	17 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr21:37444536G>A	Silent	CBR1	p.L154L	carbonyl reductase 1	54 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr19:48815311G>T	Silent	CCDC114	p.I104I	coiled-coil domain cont	22 (0.00)	32 (0.34)	0.92
11-03	Gp4	g.chr2:170502493C>A	Missense Mutation	CCDC173	p.G506V	coiled-coil domain cont	33 (0.00)	55 (0.20)	0.53
11-03	Gp4	g.chr3:14709645G>A	Silent	CCDC174	p.K303K	coiled-coil domain cont	18 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr1:3686421C>T	Silent	CCDC27	p.I606I	coiled-coil domain cont	76 (0.00)	45 (0.20)	0.53
11-03	Gp4	g.chr12:102437979G>T	Silent	CCDC53	p.I76I	coiled-coil domain cont	56 (0.00)	49 (0.12)	0.42
11-03	Gp4	g.chr4:7043833G>T	Missense Mutation	CCDC96	p.P278H	coiled-coil domain cont	18 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr4:26491060C>T	Silent	CCKAR	p.L53L	cholecystokinin A recep	20 (0.00)	20 (0.30)	0.80

11-03	Gp4	g.chr19:30308050G>A	Missense Mutation	CCNE1	p.D63N	cyclin E1	31 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr5:162868266C>A	Silent	CCNG1	p.V15V	cyclin G1	28 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr3:156866269G>A	Missense Mutation	CCNL1	p.L448F	cyclin L1	38 (0.00)	29 (0.76)	2.02
11-03	Gp4	g.chr12:49087773C>T	Silent	CCNT1	p.E408E	cyclin T1	37 (0.00)	16 (0.38)	1.26
11-03	Gp4	g.chr7:64525509G>A	RNA	CCT6P3		chaperonin containing T	42 (0.02)	38 (0.16)	0.42
11-03	Gp4	g.chr2:73466850G>A	Missense Mutation	CCT7	p.C29Y	chaperonin containing T	18 (0.00)	11 (0.82)	2.18
11-03	Gp4	g.chr2:73470227C>T	Silent	CCT7	p.I121I	chaperonin containing T	41 (0.00)	62 (0.21)	0.56
11-03	Gp4	g.chr6:47563641C>T	Missense Mutation	CD2AP	p.P385S	CD2-associated protein	87 (0.01)	98 (0.14)	0.38
11-03	Gp4	g.chr6:47573988C>A	Missense Mutation	CD2AP	p.P502Q	CD2-associated protein	31 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr1:160654748C>T	Missense Mutation	CD48	p.S105N	CD48 molecule	27 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr1:43828730C>G	Missense Mutation	CDC20	p.P477R	cell division cycle 20	24 (0.00)	27 (0.44)	1.19
11-03	Gp4	g.chr22:19506387G>A	Missense Mutation	CDC45	p.D553N	cell division cycle 45	35 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr16:68721506C>T	Silent	CDH3	p.T554T	cadherin 3, type 1, P-ca	65 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr16:61854943C>T	Missense Mutation	CDH8	p.D304N	cadherin 8, type 2	49 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr5:26881634C>T	Missense Mutation	CDH9	p.D661N	cadherin 9, type 2 (T1-c	35 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr16:29872446G>T	Missense Mutation	CDIPT	p.H60N	CDP-diacylglycerol--in	38 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr10:62544558C>A	Missense Mutation	CDK1	p.P45T	cyclin-dependent kinase	30 (0.00)	72 (0.24)	0.63
11-03	Gp4	g.chr17:37627748C>T	Missense Mutation	CDK12	p.P555S	cyclin-dependent kinase	38 (0.00)	56 (0.23)	0.62
11-03	Gp4	g.chr9:123205922C>A	Missense Mutation	CDK5RAP2	p.D1042Y	CDK5 regulatory subun	65 (0.00)	41 (0.20)	0.52
11-03	Gp4	g.chr7:92354981G>A	Missense Mutation	CDK6	p.L166F	cyclin-dependent kinase	39 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chrX:18622375G>A	Missense Mutation	CDKL5	p.R444H	cyclin-dependent kinase	29 (0.00)	20 (0.75)	1.25
11-03	Gp4	g.chr9:21970612G>T	Intron	CDKN2A		cyclin-dependent kinase	18 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr11:125880424G>A	Missense Mutation	CDON	p.S455L	cell adhesion associated	38 (0.00)	60 (0.23)	0.62
11-03	Gp4	g.chr19:42083583C>G	Silent	CEACAM21	p.T32T	carcinoembryonic antig	92 (0.00)	32 (0.28)	0.75
11-03	Gp4	g.chr19:42187837G>A	Silent	CEACAM7	p.S195S	carcinoembryonic antig	29 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr19:42190917C>T	Silent	CEACAM7	p.E100E	carcinoembryonic antig	25 (0.00)	22 (0.82)	2.18
11-03	Gp4	g.chr14:81251471G>A	Missense Mutation	CEP128	p.A660V	centrosomal protein 128	29 (0.00)	30 (0.27)	0.71
11-03	Gp4	g.chr14:81380682G>T	Missense Mutation	CEP128	p.A73E	centrosomal protein 128	31 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr4:175237336G>A	Silent	CEP44	p.E327E	centrosomal protein 44k	19 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr1:26581998C>T	Missense Mutation	CEP85	p.P182L	centrosomal protein 85k	38 (0.00)	18 (0.44)	1.19
11-03	Gp4	g.chr3:101446287C>A	Missense Mutation	CEP97	p.R83S	centrosomal protein 97k	38 (0.00)	43 (0.19)	0.50
11-03	Gp4	g.chr19:4408952C>T	Silent	CHAF1A	p.D52D	chromatin assembly fac	29 (0.00)	30 (0.23)	0.79
11-03	Gp4	g.chr5:98193903G>T	Missense Mutation	CHD1	p.H1590N	chromodomain helicase	33 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr5:98205273C>T	Intron	CHD1		chromodomain helicase	85 (0.01)	28 (0.18)	0.48
11-03	Gp4	g.chr1:146747772G>A	Missense Mutation	CHD1L	p.V464I	chromodomain helicase	48 (0.00)	27 (0.22)	0.59

11-03	Gp4	g.chr12:6692027C>A	Missense Mutation	CHD4	p.G1433V	chromodomain helicase	98 (0.00)	40 (0.15)	0.50
11-03	Gp4	g.chr1:6182255C>T	Intron	CHD5		chromodomain helicase	22 (0.00)	12 (0.67)	1.78
11-03	Gp4	g.chr1:6218004C>T	Intron	CHD5		chromodomain helicase	31 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr8:61736476G>A	Silent	CHD7	p.E1093E	chromodomain helicase	28 (0.00)	25 (0.64)	1.71
11-03	Gp4	g.chr8:61749563G>A	Missense Mutation	CHD7	p.D1393N	chromodomain helicase	82 (0.00)	67 (0.27)	0.72
11-03	Gp4	g.chr8:61765419G>A	Silent	CHD7	p.P2045P	chromodomain helicase	73 (0.00)	20 (0.25)	0.67
11-03	Gp4	g.chr16:53301261C>A	Missense Mutation	CHD9	p.A1459D	chromodomain helicase	96 (0.00)	53 (0.19)	0.50
11-03	Gp4	g.chr16:53301279C>G	Missense Mutation	CHD9	p.A1465G	chromodomain helicase	53 (0.00)	36 (0.28)	0.74
11-03	Gp4	g.chr16:53358100C>A	Missense Mutation	CHD9	p.L2647I	chromodomain helicase	26 (0.00)	35 (0.23)	0.61
11-03	Gp4	g.chr12:133433199C>T	Missense Mutation	CHFR	p.E282K	checkpoint with forkhea	20 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr1:241798796C>T	Silent	CHML	p.K91K	choroideremia-like (Ra	70 (0.01)	90 (0.21)	0.56
11-03	Gp4	g.chr7:29519959C>T	Missense Mutation	CHN2	p.T214I	chimerin 2	84 (0.00)	26 (0.54)	1.44
11-03	Gp4	g.chr7:150933562C>T	Silent	CHPF2	p.F291F	chondroitin polymerizin	16 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr15:78873281G>A	Missense Mutation	CHRNA5	p.A79T	cholinergic receptor, nic	24 (0.00)	68 (0.16)	0.43
11-03	Gp4	g.chr18:24496659C>T	Missense Mutation	CHST9	p.S299N	carbohydrate (N-acetylg	33 (0.00)	42 (0.19)	0.51
11-03	Gp4	g.chr15:101717888C>T	Missense Mutation	CHSY1	p.R705Q	chondroitin sulfate synt	21 (0.00)	37 (0.43)	1.15
11-03	Gp4	g.chr14:65390832G>A	Missense Mutation	CHURC1	p.V82I	churchill domain contai	16 (0.00)	24 (0.42)	1.11
11-03	Gp4	g.chr11:46766065C>A	Missense Mutation	CKAP5	p.G1923C	cytoskeleton associated	34 (0.03)	12 (0.50)	1.33
11-03	Gp4	g.chr11:46839959T>C	Silent	CKAP5	p.G51G	cytoskeleton associated	82 (0.00)	40 (0.42)	1.13
11-03	Gp4	g.chr2:122154727C>T	Missense Mutation	CLASP1	p.D1010N	cytoplasmic linker asso	56 (0.02)	33 (0.15)	0.40
11-03	Gp4	g.chr2:122285415G>A	Nonsense Mutation	CLASP1	p.R144*	cytoplasmic linker asso	58 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr3:33602316C>T	Missense Mutation	CLASP2	p.A980T	cytoplasmic linker asso	51 (0.00)	54 (0.15)	0.40
11-03	Gp4	g.chr7:143028688G>A	Missense Mutation	CLCN1	p.R370H	chloride channel, voltag	25 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr5:157218967C>T	Nonsense Mutation	CLINT1	p.W375*	clathrin interactor 1	23 (0.00)	50 (0.26)	0.69
11-03	Gp4	g.chr3:140140017G>A	Missense Mutation	CLSTN2	p.E230K	calsyntenin 2	46 (0.00)	32 (0.38)	1.00
11-03	Gp4	g.chr3:140282839C>G	Missense Mutation	CLSTN2	p.S840C	calsyntenin 2	71 (0.01)	59 (0.27)	0.72
11-03	Gp4	g.chr3:140282988G>A	Splice Site	CLSTN2		calsyntenin 2	34 (0.00)	17 (0.35)	0.94
11-03	Gp4	g.chr17:57738810C>T	Missense Mutation	CLTC	p.L392F	clathrin, heavy chain (H	26 (0.00)	15 (0.67)	1.78
11-03	Gp4	g.chr6:25113943C>T	RNA	CMAHP		cytidine monophospho-	15 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr6:37427455G>T	Missense Mutation	CMTR1	p.D364Y	cap methyltransferase 1	66 (0.00)	66 (0.26)	0.69
11-03	Gp4	g.chr5:79027127G>A	Missense Mutation	CMYA5	p.D847N	cardiomyopathy associa	35 (0.00)	20 (0.40)	1.07
11-03	Gp4	g.chr5:79030322G>A	Missense Mutation	CMYA5	p.G1912R	cardiomyopathy associa	74 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr5:79031254A>T	Silent	CMYA5	p.T2222T	cardiomyopathy associa	24 (0.00)	55 (0.31)	0.82
11-03	Gp4	g.chr2:99012525C>A	Missense Mutation	CNGA3	p.P302T	cyclic nucleotide gated	27 (0.00)	36 (0.19)	0.52
11-03	Gp4	g.chr8:87588129C>T	Missense Mutation	CNGB3	p.G778E	cyclic nucleotide gated	48 (0.00)	17 (0.29)	0.78

11-03	Gp4	g.chr10:101122114G>A	Silent	CNNM1	p.Q663Q	cyclin and CBS domain	51 (0.00)	64 (0.16)	0.42
11-03	Gp4	g.chr2:68544234C>T	Missense Mutation	CNRIP1	p.E129K	cannabinoid receptor int	26 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr1:230807346T>C	Missense Mutation	COG2	p.C287R	component of oligomeri	22 (0.00)	24 (0.67)	1.78
11-03	Gp4	g.chr16:70531854C>A	Nonsense Mutation	COG4	p.E434*	component of oligomeri	32 (0.00)	69 (0.16)	0.43
11-03	Gp4	g.chr7:106898775C>A	Missense Mutation	COG5	p.Q574H	component of oligomeri	43 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr8:121174731C>T	Missense Mutation	COL14A1	p.P91L	collagen, type XIV, alph	17 (0.00)	38 (0.29)	0.77
11-03	Gp4	g.chr8:121267535G>T	Missense Mutation	COL14A1	p.A937S	collagen, type XIV, alph	36 (0.00)	52 (0.19)	0.51
11-03	Gp4	g.chr9:101797384C>T	Missense Mutation	COL15A1	p.P723L	collagen, type XV, alpha	17 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr9:137619127C>T	Silent	COL5A1	p.L224L	collagen, type V, alpha	34 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr3:130159437C>T	Silent	COL6A5	p.V2085V	collagen, type VI, alpha	60 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr3:130159444G>T	Nonsense Mutation	COL6A5	p.G2088*	collagen, type VI, alpha	40 (0.03)	34 (0.18)	0.47
11-03	Gp4	g.chr1:36563397T>A	Nonsense Mutation	COL8A2	p.K629*	collagen, type VIII, alph	17 (0.00)	54 (0.19)	0.49
11-03	Gp4	g.chr3:128976598G>A	Missense Mutation	COPG1	p.E256K	coatomer protein compl	107 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr7:130295849G>A	Missense Mutation	COPG2	p.R238C	coatomer protein compl	40 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr4:84194704G>T	Missense Mutation	COQ2	p.L213I	coenzyme Q2 4-hydroxy	46 (0.02)	32 (0.31)	0.83
11-03	Gp4	g.chr7:129944393G>T	Nonsense Mutation	CPA4	p.E154*	carboxypeptidase A4	30 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr7:129989839C>G	Silent	CPA5	p.A74A	carboxypeptidase A5	37 (0.00)	40 (0.20)	0.53
11-03	Gp4	g.chr4:166405585G>A	Missense Mutation	CPE	p.E268K	carboxypeptidase E	64 (0.00)	52 (0.15)	0.41
11-03	Gp4	g.chr4:15063796G>A	Missense Mutation	CPEB2	p.G493E	cytoplasmic polyadenyla	44 (0.00)	48 (0.31)	0.83
11-03	Gp4	g.chr4:15063847G>A	Missense Mutation	CPEB2	p.R510Q	cytoplasmic polyadenyla	47 (0.02)	42 (0.31)	0.83
11-03	Gp4	g.chr10:101814146C>T	Missense Mutation	CPN1	p.A357T	carboxypeptidase N, pol	42 (0.00)	63 (0.16)	0.42
11-03	Gp4	g.chr2:207825616G>C	Missense Mutation	CPO	p.G175A	carboxypeptidase O	69 (0.00)	28 (0.39)	1.05
11-03	Gp4	g.chr1:207870972T>A	Nonsense Mutation	CR1L	p.Y329*	complement component	109 (0.00)	73 (0.30)	0.80
11-03	Gp4	g.chr12:94072758G>A	Missense Mutation	CRADD	p.D70N	CASP2 and RIPK1 dom	44 (0.00)	43 (0.12)	0.40
11-03	Gp4	g.chr9:35732839G>A	Missense Mutation	CREB3	p.G24R	cAMP responsive eleme	34 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr1:153945685C>T	Missense Mutation	CREB3L4	p.S253F	cAMP responsive eleme	18 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr7:28843861G>T	Missense Mutation	CREB5	p.G250W	cAMP responsive eleme	15 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr16:3817902C>T	Silent	CREBBP	p.E1023E	CREB binding protein	19 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr1:159683440G>A	Silent	CRP	p.L184L	C-reactive protein, pent	54 (0.00)	62 (0.18)	0.47
11-03	Gp4	g.chr3:97634475A>T	Missense Mutation	CRYBG3	p.E764D	beta-gamma crystallin d	45 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr4:71115043C>A	Missense Mutation	CSN3	p.T139N	casein kappa	50 (0.00)	17 (0.41)	1.10
11-03	Gp4	g.chr11:11374168C>T	Missense Mutation	CSNK2A3	p.E167K	casein kinase 2, alpha 3	39 (0.03)	18 (0.56)	1.48
11-03	Gp4	g.chr12:51457931G>T	Silent	CSRNP2	p.S410S	cysteine-serine-rich nuc	34 (0.00)	21 (0.33)	1.12
11-03	Gp4	g.chrX:134948111G>T	Missense Mutation	CT45A5	p.Q72K	cancer/testis antigen fan	73 (0.00)	53 (0.38)	0.63
11-03	Gp4	g.chr20:56099217C>G	Missense Mutation	CTCFL	p.K15N	CCCTC-binding factor (	27 (0.00)	61 (0.41)	1.09

11-03	Gp4	g.chr17:18418988C>T	RNA	CTD-2303H24.2			45 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr8:17947079G>A	RNA	CTD-2547L16.1			39 (0.00)	16 (0.94)	0.93
11-03	Gp4	g.chr8:64321792A>T	lincRNA	CTD-3046C4.1			38 (0.00)	56 (0.14)	0.38
11-03	Gp4	g.chr3:41275112C>A	Missense Mutation	CTNNB1	p.N426K	catenin (cadherin-associ	76 (0.00)	42 (0.26)	0.70
11-03	Gp4	g.chr7:117431983G>A	Missense Mutation	CTTNBP2	p.P423S	cortactin binding protei	67 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr10:17087063C>T	Silent	CUBN	p.L1205L	cubilin (intrinsic factor-	42 (0.00)	21 (0.33)	0.89
11-03	Gp4	g.chr17:36958406C>T	Missense Mutation	CWC25	p.R406Q	CWC25 spliceosome-as	40 (0.00)	33 (0.52)	1.37
11-03	Gp4	g.chr17:36966768G>C	Missense Mutation	CWC25	p.S193R	CWC25 spliceosome-as	17 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr5:64314095A>G	Missense Mutation	CWC27	p.R456G	CWC27 spliceosome-as	22 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr4:49034626C>T	Missense Mutation	CWH43	p.H491Y	cell wall biogenesis 43 (	38 (0.00)	48 (0.17)	0.44
11-03	Gp4	g.chrX:149100843C>T	Silent	CXorf40B	p.E132E	chromosome X open re	42 (0.00)	42 (0.26)	0.44
11-03	Gp4	g.chr10:104591337C>T	Missense Mutation	CYP17A1	p.E391K	cytochrome P450, famil	22 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr1:47279596C>T	Silent	CYP4B1	p.Y197Y	cytochrome P450, famil	55 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr4:187130045G>T	Nonsense Mutation	CYP4V2	p.E373*	cytochrome P450, famil	17 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr5:39377382C>A	Missense Mutation	DAB2	p.G503C	Dab, mitogen-responsiv	41 (0.00)	47 (0.19)	0.51
11-03	Gp4	g.chr9:124377467T>C	Intron	DAB2IP		DAB2 interacting protei	47 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr9:124413276C>T	Intron	DAB2IP		DAB2 interacting protei	51 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr9:124413310G>A	Intron	DAB2IP		DAB2 interacting protei	15 (0.00)	25 (0.32)	0.85
11-03	Gp4	g.chr9:124472322G>T	Intron	DAB2IP		DAB2 interacting protei	47 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr9:124475180G>A	Intron	DAB2IP		DAB2 interacting protei	58 (0.00)	43 (0.40)	1.05
11-03	Gp4	g.chr9:124496179G>C	Intron	DAB2IP		DAB2 interacting protei	31 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr9:124505742G>A	Intron	DAB2IP		DAB2 interacting protei	49 (0.00)	32 (0.25)	0.67
11-03	Gp4	g.chr9:124533308G>A	Intron	DAB2IP		DAB2 interacting protei	24 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr9:124533343C>A	Intron	DAB2IP		DAB2 interacting protei	18 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr9:124539518C>A	Intron	DAB2IP		DAB2 interacting protei	26 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr1:155697520C>G	Missense Mutation	DAP3	p.F198L	death associated protein	29 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr9:90262222C>A	Silent	DAPK1	p.G411G	death-associated protein	16 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr18:51025793C>T	Missense Mutation	DCC	p.L975F	DCC netrin 1 receptor	38 (0.00)	39 (0.26)	0.68
11-03	Gp4	g.chr11:108562685G>T	Missense Mutation	DDX10	p.R353I	DEAD (Asp-Glu-Ala-A	16 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr22:38890892C>T	Splice Site	DDX17	p.R347K	DEAD (Asp-Glu-Ala-A	83 (0.00)	115 (0.23)	0.60
11-03	Gp4	g.chrY:15027099G>C	Missense Mutation	DDX3Y	p.D327H	DEAD (Asp-Glu-Ala-A	20 (0.00)	18 (0.50)	0.83
11-03	Gp4	g.chr5:176943151C>A	Missense Mutation	DDX41	p.E114D	DEAD (Asp-Glu-Ala-A	18 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr20:76927G>A	Missense Mutation	DEFB125	p.E114K	defensin, beta 125	40 (0.00)	24 (0.29)	0.78
11-03	Gp4	g.chr8:142178119G>A	Silent	DENND3	p.P590P	DENN/MADD domain	37 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr15:65964221G>A	Missense Mutation	DENND4A	p.S1414F	DENN/MADD domain	56 (0.00)	46 (0.15)	0.41

11-03	Gp4	g.chr12:31604929G>T	Missense Mutation	DENND5B	p.A525D	DENN/MADD domain	42 (0.00)	24 (0.25)	0.84
11-03	Gp4	g.chr22:20077206C>T	Missense Mutation	DGCR8	p.P299S	DGCR8 microprocessor	18 (0.00)	37 (0.32)	0.86
11-03	Gp4	g.chr7:137341212C>A	Splice Site	DGKI	p.K227N	diacylglycerol kinase, ic	31 (0.00)	12 (0.50)	1.33
11-03	Gp4	g.chr4:24531368T>A	Missense Mutation	DHX15	p.H709L	DEAH (Asp-Glu-Ala-H	50 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr5:54586077C>T	Silent	DHX29	p.E292E	DEAH (Asp-Glu-Ala-H	35 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr10:127548425C>T	Missense Mutation	DHX32	p.G199E	DEAH (Asp-Glu-Ala-H	40 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr17:57647972C>T	Missense Mutation	DHX40	p.T125I	DEAH (Asp-Glu-Ala-H	24 (0.00)	45 (0.36)	0.95
11-03	Gp4	g.chr2:39046214G>A	Silent	DHX57	p.L1122L	DEAH (Asp-Glu-Ala-A	29 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr1:182853865C>T	Silent	DHX9	p.P1126P	DEAH (Asp-Glu-Ala-H	52 (0.00)	17 (0.41)	1.10
11-03	Gp4	g.chr14:95570026G>A	Missense Mutation	DICER1	p.T1236I	dicer 1, ribonuclease ty	32 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr7:96639245C>T	Silent	DLX6	p.D256D	distal-less homeobox 6	48 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr10:124339145G>A	Missense Mutation	DMBT1	p.R244Q	deleted in malignant bra	216 (0.00)	54 (0.17)	0.44
11-03	Gp4	g.chr10:124358478G>A	Missense Mutation	DMBT1	p.G1049S	deleted in malignant bra	47 (0.00)	34 (0.35)	0.94
11-03	Gp4	g.chr3:52389007C>A	Nonsense Mutation	DNAH1	p.S1210*	dynein, axonemal, heav	47 (0.00)	44 (0.18)	0.48
11-03	Gp4	g.chr3:52417499G>A	Missense Mutation	DNAH1	p.S2680N	dynein, axonemal, heav	48 (0.00)	30 (0.43)	1.16
11-03	Gp4	g.chr12:124409615C>T	Silent	DNAH10	p.L3811L	dynein, axonemal, heav	29 (0.00)	39 (0.13)	0.45
11-03	Gp4	g.chr7:21628217C>T	Nonsense Mutation	DNAH11	p.Q646*	dynein, axonemal, heav	36 (0.03)	26 (0.92)	2.46
11-03	Gp4	g.chr1:225525133G>A	Missense Mutation	DNAH14	p.E2551K	dynein, axonemal, heav	41 (0.00)	62 (0.16)	0.43
11-03	Gp4	g.chr17:11607575C>T	Missense Mutation	DNAH9	p.A1736V	dynein, axonemal, heav	46 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr17:11660950C>A	Silent	DNAH9	p.A2312A	dynein, axonemal, heav	35 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr17:11865345G>A	Silent	DNAH9	p.T4259T	dynein, axonemal, heav	17 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr1:15863266C>T	Silent	DNAJC16	p.I177I	DnaJ (Hsp40) homolog,	24 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr17:40148428C>A	Missense Mutation	DNAJC7	p.E102D	DnaJ (Hsp40) homolog,	27 (0.00)	23 (0.74)	1.97
11-03	Gp4	g.chr15:100332591C>T	RNA	DNM1P46		DNM1 pseudogene 46	43 (0.02)	14 (0.36)	0.95
11-03	Gp4	g.chr10:101716021C>A	Missense Mutation	DNMBP	p.D404Y	dynamin binding protei	18 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr19:10254555C>T	Silent	DNMT1	p.L985L	DNA (cytosine-5-)-met	88 (0.00)	47 (0.15)	0.40
11-03	Gp4	g.chr19:10274001C>A	Splice Site	DNMT1		DNA (cytosine-5-)-met	40 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr1:94343329C>T	Silent	DNTTIP2	p.K54K	deoxynucleotidyltransfe	24 (0.00)	45 (0.69)	1.84
11-03	Gp4	g.chr10:129160404G>A	Silent	DOCK1	p.L1099L	dedicator of cytokinesis	62 (0.00)	62 (0.15)	0.39
11-03	Gp4	g.chr10:129224163G>A	Missense Mutation	DOCK1	p.R1580K	dedicator of cytokinesis	99 (0.01)	48 (0.17)	0.44
11-03	Gp4	g.chrX:117815121T>C	Silent	DOCK11	p.D1924D	dedicator of cytokinesis	32 (0.00)	23 (0.26)	0.43
11-03	Gp4	g.chr3:51184027C>G	Missense Mutation	DOCK3	p.P265R	dedicator of cytokinesis	48 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr9:372261C>A	Missense Mutation	DOCK8	p.P627H	dedicator of cytokinesis	38 (0.00)	14 (0.50)	1.33
11-03	Gp4	g.chr9:446457C>T	Missense Mutation	DOCK8	p.L1790F	dedicator of cytokinesis	48 (0.00)	34 (0.38)	1.02
11-03	Gp4	g.chr18:67266663G>A	Missense Mutation	DOK6	p.R73Q	docking protein 6	66 (0.00)	30 (0.27)	0.71

11-03	Gp4	g.chr18:67406338G>A	Splice Site	DOK6	p.R246Q	docking protein 6	66 (0.00)	45 (0.16)	0.41
11-03	Gp4	g.chr19:2185912G>A	Missense Mutation	DOT1L	p.D62N	DOT1-like histone H3K	72 (0.00)	73 (0.32)	1.07
11-03	Gp4	g.chr11:66272202G>A	Silent	DPP3	p.K666K	dipeptidyl-peptidase 3	26 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr7:154143321C>T	Missense Mutation	DPP6	p.P89L	dipeptidyl-peptidase 6	61 (0.02)	38 (0.18)	0.49
11-03	Gp4	g.chr2:74749797G>A	Missense Mutation	DQX1	p.P469S	DEAQ box RNA-depen	34 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr5:31515145G>A	Nonsense Mutation	DROSHA	p.R414*	drosha, ribonuclease typ	125 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr5:31515157G>A	Missense Mutation	DROSHA	p.P410S	drosha, ribonuclease typ	125 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr6:56336905C>T	Silent	DST	p.A7050A	dystonin	84 (0.00)	38 (0.21)	0.56
11-03	Gp4	g.chr6:56380331T>C	Missense Mutation	DST	p.T5845A	dystonin	72 (0.00)	41 (0.22)	0.59
11-03	Gp4	g.chr6:56392295G>T	Missense Mutation	DST	p.P5653Q	dystonin	32 (0.00)	26 (0.42)	1.13
11-03	Gp4	g.chr6:56468769C>T	Missense Mutation	DST	p.E3342K	dystonin	61 (0.00)	42 (0.19)	0.51
11-03	Gp4	g.chr6:56470017G>A	Missense Mutation	DST	p.L2926F	dystonin	16 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr2:25803649G>A	Missense Mutation	DTNB	p.P217L	dystrobrevin, beta	20 (0.00)	14 (0.50)	1.33
11-03	Gp4	g.chr15:45408805C>T	Silent	DUOXA2	p.N144N	dual oxidase maturation	15 (0.00)	24 (0.50)	1.33
11-03	Gp4	g.chr12:89744428G>C	Missense Mutation	DUSP6	p.P259A	dual specificity phospha	90 (0.00)	52 (0.15)	0.41
11-03	Gp4	g.chr14:102494288G>A	Nonsense Mutation	DYNC1H1	p.W3093*	dynein, cytoplasmic 1,	40 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr2:172583340G>A	Missense Mutation	DYNC1I2	p.D278N	dynein, cytoplasmic 1, i	24 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr1:206821061C>T	Missense Mutation	DYRK3	p.P173L	dual-specificity tyrosine	21 (0.00)	49 (0.35)	0.93
11-03	Gp4	g.chr2:71753357G>A	Missense Mutation	DYSF	p.R386K	dysferlin	21 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr6:20481630G>A	Silent	E2F3	p.K233K	E2F transcription factor	28 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr11:19246387G>C	Splice Site	E2F8	p.P808A	E2F transcription factor	28 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr17:28414184G>A	Splice Site	EFCAB5	p.R1228K	EF-hand calcium bindin	99 (0.01)	61 (0.66)	1.75
11-03	Gp4	g.chr22:44131786T>C	Missense Mutation	EFCAB6	p.R199G	EF-hand calcium bindin	42 (0.00)	34 (0.24)	0.63
11-03	Gp4	g.chr3:19925912C>A	Missense Mutation	EFHB	p.G580V	EF-hand domain family,	21 (0.00)	32 (0.47)	1.25
11-03	Gp4	g.chr3:19926030C>G	Missense Mutation	EFHB	p.D541H	EF-hand domain family,	18 (0.00)	21 (0.52)	1.40
11-03	Gp4	g.chr13:107148106T>A	Missense Mutation	EFNB2	p.K163N	ephrin-B2	105 (0.00)	49 (0.47)	1.25
11-03	Gp4	g.chr5:137803035G>A	Silent	EGR1	p.S299S	early growth response 1	41 (0.00)	51 (0.22)	0.58
11-03	Gp4	g.chr2:63085596C>T	Silent	EHBP1	p.C230C	EH domain binding prot	30 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr3:184910690C>A	Missense Mutation	EHHADH	p.G403V	enoyl-CoA, hydratase/3	19 (0.00)	16 (0.44)	1.17
11-03	Gp4	g.chr14:75472575G>T	Nonsense Mutation	EIF2B2	p.E202*	eukaryotic translation in	27 (0.00)	24 (0.33)	0.89
11-03	Gp4	g.chr1:45446838C>T	Start Codon SNP	EIF2B3	p.M1I	eukaryotic translation in	48 (0.00)	106 (0.20)	0.53
11-03	Gp4	g.chr12:10659474C>T	Missense Mutation	EIF2S3L	p.H325Y		43 (0.00)	36 (0.33)	1.12
11-03	Gp4	g.chr10:120795727C>T	Missense Mutation	EIF3A	p.D1325N	eukaryotic translation in	22 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr7:2414233C>G	Silent	EIF3B	p.G627G	eukaryotic translation in	22 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr22:38274169C>T	Silent	EIF3L	p.Y522Y	eukaryotic translation in	40 (0.00)	34 (0.18)	0.47

11-03	Gp4	g.chr17:78109862C>T	Missense Mutation	EIF4A3	p.R387H	eukaryotic translation in	44 (0.02)	65 (0.23)	0.62
11-03	Gp4	g.chr22:31844192G>A	Missense Mutation	EIF4ENIF1	p.L424F	eukaryotic translation in	44 (0.00)	51 (0.25)	0.68
11-03	Gp4	g.chr1:21212703A>T	Silent	EIF4G3	p.I755I	eukaryotic translation in	54 (0.00)	66 (0.17)	0.44
11-03	Gp4	g.chr17:12908337G>A	Nonsense Mutation	ELAC2	p.Q318*	elaC ribonuclease Z 2	110 (0.00)	73 (0.21)	0.55
11-03	Gp4	g.chr13:41515280G>A	Silent	ELF1	p.L345L	E74-like factor 1 (ets do	76 (0.00)	66 (0.17)	0.44
11-03	Gp4	g.chr13:41533006G>A	Silent	ELF1	p.I73I	E74-like factor 1 (ets do	30 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr5:60063672G>T	Nonsense Mutation	ELOVL7	p.S92*	ELOVL fatty acid elong	27 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr18:2891553G>T	Silent	EMILIN2	p.R476R	elastin microfibril interf	45 (0.00)	13 (0.62)	1.64
11-03	Gp4	g.chr2:42488364C>T	Nonsense Mutation	EML4	p.Q148*	echinoderm microtubule	64 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr14:89094003C>G	Missense Mutation	EML5	p.W1506C	echinoderm microtubule	56 (0.00)	48 (0.23)	0.61
11-03	Gp4	g.chr19:48830116G>T	Missense Mutation	EMP3	p.L5F	epithelial membrane pro	29 (0.00)	47 (0.21)	0.57
11-03	Gp4	g.chr19:14876481G>A	Missense Mutation	EMR2	p.T257I	egf-like module contain	25 (0.00)	11 (0.64)	1.70
11-03	Gp4	g.chr3:40464871C>T	Silent	ENTPD3	p.F398F	ectonucleoside triphospl	32 (0.00)	13 (0.54)	1.44
11-03	Gp4	g.chr20:34800223C>T	Silent	EPB41L1	p.S703S	erythrocyte membrane p	44 (0.02)	47 (0.19)	0.51
11-03	Gp4	g.chr6:131277180G>C	Nonsense Mutation	EPB41L2	p.S149*	erythrocyte membrane p	93 (0.00)	23 (0.65)	0.69
11-03	Gp4	g.chr18:43535050C>T	Silent	EPG5	p.G106G	ectopic P-granules autop	24 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr4:66217208C>T	Missense Mutation	EPHA5	p.A803T	EPH receptor A5	22 (0.05)	17 (0.47)	1.25
11-03	Gp4	g.chr3:134873088C>A	Silent	EPHB1	p.I464I	EPH receptor B1	115 (0.00)	56 (0.16)	0.43
11-03	Gp4	g.chr7:100404155C>A	Missense Mutation	EPHB4	p.A791S	EPH receptor B4	26 (0.00)	10 (0.60)	1.60
11-03	Gp4	g.chr7:142568064G>A	Missense Mutation	EPHB6	p.R902H	EPH receptor B6	53 (0.00)	85 (0.22)	0.60
11-03	Gp4	g.chr7:100320671G>A	Missense Mutation	EPO	p.R166H	erythropoietin	45 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr2:26596441G>A	Missense Mutation	EPT1	p.E173K	ethanolaminephosphotra	43 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr12:91366634A>T	Missense Mutation	EPYC	p.I155N	epiphycan	33 (0.00)	29 (0.21)	0.70
11-03	Gp4	g.chr12:91366646C>T	Missense Mutation	EPYC	p.R151H	epiphycan	33 (0.00)	30 (0.30)	1.02
11-03	Gp4	g.chr17:27186026C>T	Silent	ERAL1	p.H335H	Era-like 12S mitochond	22 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr12:56478919C>T	Silent	ERBB3	p.T125T	v-erb-b2 avian erythrobl	36 (0.00)	43 (0.12)	0.39
11-03	Gp4	g.chr13:103514502C>T	Missense Mutation	ERCC5	p.P335S	excision repair cross-co	21 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr21:39787302G>A	Intron	ERG		v-ets avian erythroblast	27 (0.00)	56 (0.18)	0.48
11-03	Gp4	g.chr21:39791028G>A	Intron	ERG		v-ets avian erythroblast	90 (0.00)	69 (0.16)	0.43
11-03	Gp4	g.chr21:39806716A>T	Intron	ERG		v-ets avian erythroblast	39 (0.03)	39 (0.31)	0.82
11-03	Gp4	g.chr21:39806759G>C	Intron	ERG		v-ets avian erythroblast	43 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr21:39823302C>T	Intron	ERG		v-ets avian erythroblast	67 (0.00)	79 (0.22)	0.57
11-03	Gp4	g.chr21:39838490G>T	Intron	ERG		v-ets avian erythroblast	68 (0.00)	41 (0.22)	0.59
11-03	Gp4	g.chr21:39891562G>A	Intron	ERG		v-ets avian erythroblast	50 (0.00)	52 (0.23)	0.62
11-03	Gp4	g.chr21:39913259G>A	Intron	ERG		v-ets avian erythroblast	47 (0.00)	56 (0.14)	0.38

11-03	Gp4	g.chr21:39924649G>C	Intron	ERG		v-ets avian erythroblast	20 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr21:39932180C>T	Intron	ERG		v-ets avian erythroblast	49 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr21:39932187C>T	Intron	ERG		v-ets avian erythroblast	49 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr21:39956649G>C	Intron	ERG		v-ets avian erythroblast	31 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr21:40008495A>T	Intron	ERG		v-ets avian erythroblast	69 (0.00)	29 (0.38)	1.01
11-03	Gp4	g.chr21:40011960C>T	Intron	ERG		v-ets avian erythroblast	31 (0.00)	59 (0.29)	0.77
11-03	Gp4	g.chr21:40028074G>A	Intron	ERG		v-ets avian erythroblast	34 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr14:100604089G>T	Silent	EVL	p.V348V	Enah/Vasp-like	26 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr1:242016706G>A	Missense Mutation	EXO1	p.G110R	exonuclease 1	21 (0.00)	32 (0.44)	1.17
11-03	Gp4	g.chr7:133002072G>T	Missense Mutation	EXOC4	p.D231Y	exocyst complex compo	42 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr17:74090575G>A	Missense Mutation	EXOC7	p.S243F	exocyst complex compo	29 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr1:11147565G>A	Silent	EXOSC10	p.L343L	exosome component 10	75 (0.00)	65 (0.28)	0.74
11-03	Gp4	g.chr1:11147594G>A	Missense Mutation	EXOSC10	p.R334W	exosome component 10	67 (0.01)	62 (0.29)	0.77
11-03	Gp4	g.chr11:108381065C>T	Silent	EXPH5	p.Q1723Q	exophilin 5	26 (0.00)	33 (0.30)	0.81
11-03	Gp4	g.chr20:45811967G>T	Missense Mutation	EYA2	p.M488I	EYA transcriptional coa	55 (0.00)	30 (0.33)	0.89
11-03	Gp4	g.chr6:64472377G>A	Missense Mutation	EYS	p.T2683I	eyes shut homolog (Dro	22 (0.00)	60 (0.20)	0.53
11-03	Gp4	g.chr17:40872352C>A	Missense Mutation	EZH1	p.K131N	enhancer of zeste 1 poly	64 (0.02)	38 (0.18)	0.49
11-03	Gp4	g.chr1:207087420G>A	Silent	FAIM3	p.I19I	Fas apoptotic inhibitory	36 (0.00)	39 (0.18)	0.48
11-03	Gp4	g.chr1:184764594G>T	Silent	FAM129A	p.V768V	family with sequence si	69 (0.00)	47 (0.40)	1.08
11-03	Gp4	g.chr4:84390258C>T	Missense Mutation	FAM175A	p.E175K	family with sequence si	31 (0.00)	79 (0.18)	0.47
11-03	Gp4	g.chr12:49994397A>G	Silent	FAM186B	p.S342S	family with sequence si	27 (0.00)	46 (0.13)	0.44
11-03	Gp4	g.chr12:49994697G>A	Silent	FAM186B	p.N242N	family with sequence si	24 (0.00)	34 (0.21)	0.69
11-03	Gp4	g.chr9:71998610G>T	Missense Mutation	FAM189A2	p.V187L	family with sequence si	38 (0.03)	42 (0.14)	0.38
11-03	Gp4	g.chr9:34724476G>A	Missense Mutation	FAM205A	p.P921S	family with sequence si	90 (0.00)	38 (0.26)	0.70
11-03	Gp4	g.chr9:34835339C>T	RNA	FAM205B		family with sequence si	27 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr15:52902202G>T	Silent	FAM214A	p.G303G	family with sequence si	25 (0.00)	50 (0.18)	0.48
11-03	Gp4	g.chr20:58519761G>A	Missense Mutation	FAM217B	p.E255K	family with sequence si	75 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr10:46281060G>A	Nonsense Mutation	FAM21C	p.W931*	family with sequence si	69 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr2:24406427C>T	Missense Mutation	FAM228A	p.P105L	family with sequence si	20 (0.00)	56 (0.29)	0.76
11-03	Gp4	g.chr17:644773G>A	Missense Mutation	FAM57A	p.R214Q	family with sequence si	16 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr6:24832579C>A	Missense Mutation	FAM65B	p.S771I	family with sequence si	35 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr5:94728567C>T	Missense Mutation	FAM81B	p.P65L	family with sequence si	29 (0.00)	34 (0.26)	0.71
11-03	Gp4	g.chr8:124810380G>T	Missense Mutation	FAM91A1	p.A488S	family with sequence si	106 (0.00)	106 (0.19)	0.50
11-03	Gp4	g.chr3:10119798C>T	Silent	FANCD2	p.L965L	Fanconi anemia, comple	52 (0.02)	35 (0.46)	1.22
11-03	Gp4	g.chr3:10127575G>C	Missense Mutation	FANCD2	p.E1102Q	Fanconi anemia, comple	29 (0.00)	20 (0.25)	0.67

11-03	Gp4	g.chr9:35074390C>T	Missense Mutation	FANCG	p.G580R	Fanconi anemia, comple	24 (0.00)	35 (0.29)	0.76
11-03	Gp4	g.chr6:5545437G>A	Nonsense Mutation	FARS2	p.W310*	phenylalanyl-tRNA syn	49 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr6:5545511G>T	Nonsense Mutation	FARS2	p.E335*	phenylalanyl-tRNA syn	55 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr4:187524612G>A	Missense Mutation	FAT1	p.P3690S	FAT atypical cadherin 1	82 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr11:92087251G>A	Missense Mutation	FAT3	p.G508E	FAT atypical cadherin 3	61 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr11:92577131C>G	Missense Mutation	FAT3	p.S3383C	FAT atypical cadherin 3	29 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr22:45996264G>C	Missense Mutation	FBLN1	p.G684R	fibulin 1	86 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr5:127595246C>A	Missense Mutation	FBN2	p.K2880N	fibrillin 2	22 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr6:146127125G>T	Silent	FBXO30	p.A139A	F-box protein 30	44 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr22:32894224C>A	Missense Mutation	FBXO7	p.P426T	F-box protein 7	68 (0.01)	19 (0.32)	0.84
11-03	Gp4	g.chr22:32894225C>A	Missense Mutation	FBXO7	p.P426H	F-box protein 7	68 (0.01)	19 (0.32)	0.84
11-03	Gp4	g.chr12:117383306G>A	Silent	FBXW8	p.K187K	F-box and WD repeat d	21 (0.00)	37 (0.14)	0.47
11-03	Gp4	g.chr1:207133037C>T	Nonsense Mutation	FCAMR	p.W520*	Fc receptor, IgA, IgM,	41 (0.00)	37 (0.32)	0.86
11-03	Gp4	g.chr1:157557187C>A	Silent	FCRL4	p.T242T	Fc receptor-like 4	61 (0.00)	20 (0.55)	1.47
11-03	Gp4	g.chr20:6077588C>T	Silent	FERMT1	p.L350L	fermitin family member	40 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr4:155507487G>A	Missense Mutation	FGA	p.S365F	fibrinogen alpha chain	17 (0.00)	11 (0.64)	1.70
11-03	Gp4	g.chr11:69588238C>T	Missense Mutation	FGF4	p.E154K	fibroblast growth factor	18 (0.00)	29 (0.34)	0.92
11-03	Gp4	g.chr10:123353261G>T	Missense Mutation	FGFR2	p.S24Y	fibroblast growth factor	105 (0.00)	50 (0.18)	0.48
11-03	Gp4	g.chr1:59787369C>A	Missense Mutation	FGGY	p.H50N	FGGY carbohydrate kin	33 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr1:15692425G>T	Missense Mutation	FHAD1	p.L1028F	forkhead-associated (F	28 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr2:71012575G>C	Missense Mutation	FIGLA	p.T194S	folliculogenesis specific	27 (0.00)	26 (0.65)	1.74
11-03	Gp4	g.chr7:50513278C>T	Missense Mutation	FIGNL1	p.A570T	fidgetin-like 1	56 (0.00)	21 (0.33)	0.89
11-03	Gp4	g.chr6:76022871T>C	Missense Mutation	FILIP1	p.S893G	filamin A interacting pr	37 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr6:76023545C>A	Missense Mutation	FILIP1	p.R668I	filamin A interacting pr	90 (0.00)	68 (0.50)	1.33
11-03	Gp4	g.chr12:2906420G>A	Silent	FKBP4	p.K74K	FK506 binding protein	18 (0.00)	41 (0.12)	0.41
11-03	Gp4	g.chr1:152276060C>T	Missense Mutation	FLG	p.G3768R	filaggrin	98 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr15:33261589G>A	Silent	FMN1	p.H771H	formin 1	100 (0.00)	103 (0.29)	0.78
11-03	Gp4	g.chr2:216298075C>T	Silent	FN1	p.G129G	fibronectin 1	23 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr5:131008518G>A	Missense Mutation	FNIP1	p.T495I	folliculin interacting pro	22 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr14:65527907T>A	Silent	FNTB	p.T397T	farnesyltransferase, CA	34 (0.00)	19 (0.47)	1.26
11-03	Gp4	g.chr9:20770060G>A	Silent	FOCAD	p.A243A	focadhesin	29 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr11:89424165G>A	RNA	FOLH1B		folate hydrolase 1B	45 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr4:79301096G>T	Missense Mutation	FRAS1	p.W1170L	Fraser extracellular mat	23 (0.00)	25 (0.36)	0.96
11-03	Gp4	g.chr4:144498811C>A	Missense Mutation	FREM3	p.D2125Y	FRAS1 related extracell	18 (0.00)	12 (0.50)	1.33
11-03	Gp4	g.chr4:144618317G>C	Missense Mutation	FREM3	p.S1171C	FRAS1 related extracell	68 (0.01)	94 (0.23)	0.62

11-03	Gp4	g.chr4:48502096A>G	Silent	FRYL	p.L2912L	FRY-like	22 (0.00)	41 (0.22)	0.59
11-03	Gp4	g.chr4:48542481G>A	Missense Mutation	FRYL	p.L2062F	FRY-like	39 (0.00)	17 (0.65)	1.73
11-03	Gp4	g.chr15:83451551A>T	Missense Mutation	FSD2	p.I321K	fibronectin type III and	104 (0.00)	49 (0.22)	0.60
11-03	Gp4	g.chr15:83451553G>T	Missense Mutation	FSD2	p.F320L	fibronectin type III and	102 (0.00)	49 (0.20)	0.54
11-03	Gp4	g.chr2:186661577A>G	Silent	FSIP2	p.R3238R	fibrous sheath interactin	51 (0.00)	53 (0.21)	0.55
11-03	Gp4	g.chr17:61898798G>A	Missense Mutation	FTSJ3	p.T601I	FtsJ homolog 3 (E. coli)	53 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr16:31195577G>A	Missense Mutation	FUS	p.G128E	FUS RNA binding prot	42 (0.00)	44 (0.27)	0.73
11-03	Gp4	g.chr11:86663478G>C	Missense Mutation	FZD4	p.T107R	frizzled class receptor 4	36 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr11:77961221C>T	Missense Mutation	GAB2	p.R201Q	GRB2-associated bindi	79 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr9:101065664G>A	Silent	GABBR2	p.N757N	gamma-aminobutyric ac	51 (0.00)	54 (0.15)	0.40
11-03	Gp4	g.chr5:160757962G>A	Silent	GABRB2	p.P335P	gamma-aminobutyric ac	17 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr5:160761788T>C	Missense Mutation	GABRB2	p.Y268C	gamma-aminobutyric ac	32 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr5:161524758C>A	Missense Mutation	GABRG2	p.P148T	gamma-aminobutyric ac	27 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr3:97711741G>A	RNA	GABRR3		gamma-aminobutyric ac	47 (0.00)	162 (0.17)	0.44
11-03	Gp4	g.chr2:171713588G>A	Missense Mutation	GAD1	p.A492T	glutamate decarboxylas	82 (0.00)	41 (0.39)	1.04
11-03	Gp4	g.chr7:151791362C>A	Missense Mutation	GALNT11	p.S17Y	polypeptide N-acetylgal	30 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr3:16250017G>A	Missense Mutation	GALNT15	p.V307M	polypeptide N-acetylgal	48 (0.00)	67 (0.15)	0.40
11-03	Gp4	g.chr9:128118044A>T	Missense Mutation	GAPVD1	p.Q1272H	GTPase activating prote	16 (0.00)	30 (0.47)	1.24
11-03	Gp4	g.chr1:89524662C>A	Missense Mutation	GBP1	p.V165F	guanylate binding prote	74 (0.00)	19 (0.53)	1.40
11-03	Gp4	g.chr2:237074668G>T	Silent	GBX2	p.S312S	gastrulation brain home	55 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr6:52993052C>T	Silent	GCM1	p.L421L	glial cells missing homo	32 (0.00)	78 (0.27)	0.72
11-03	Gp4	g.chr6:10626779G>A	Missense Mutation	GCNT2	p.R383K	glucosaminyl (N-acetyl)	60 (0.02)	102 (0.17)	0.44
11-03	Gp4	g.chr6:10634658G>C	Silent	GCNT6	p.V222V	glucosaminyl (N-acetyl)	30 (0.00)	27 (0.30)	0.79
11-03	Gp4	g.chr16:30122831C>T	Missense Mutation	GDPD3	p.M195I	glycerophosphodiester	72 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chrX:14027121C>A	Missense Mutation	GEMIN8	p.A214S	gem (nuclear organelle)	23 (0.00)	11 (0.55)	0.91
11-03	Gp4	g.chr2:69556920C>G	Missense Mutation	GFPT1	p.S480T	glutamine--fructose-6-p	98 (0.00)	39 (0.18)	0.48
11-03	Gp4	g.chr3:172163191G>A	Silent	GHSR	p.S287S	growth hormone secreta	19 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chr2:233681708G>A	Missense Mutation	GIGYF2	p.R773K	GRB10 interacting GY	79 (0.01)	65 (0.22)	0.57
11-03	Gp4	g.chr7:150171621C>T	Missense Mutation	GIMAP8	p.R402W	GTPase, IMAP family	56 (0.02)	59 (0.17)	0.45
11-03	Gp4	g.chr14:24702466C>T	Missense Mutation	GMPR2	p.H3Y	guanosine monophosph	103 (0.00)	93 (0.27)	0.72
11-03	Gp4	g.chr12:102158017G>T	Missense Mutation	GNPTAB	p.P893Q	N-acetylglucosamine-1-	31 (0.00)	25 (0.28)	0.95
11-03	Gp4	g.chr15:23265489C>T	Missense Mutation	GOLGA8I	p.P611L	golgin A8 family, mem	55 (0.00)	27 (0.41)	1.09
11-03	Gp4	g.chr3:121415192C>T	Missense Mutation	GOLGB1	p.R1393K	golgin B1	63 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr6:24445970G>A	Missense Mutation	GPLD1	p.T637I	glycosylphosphatidylin	40 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr13:99947755G>A	Silent	GPR183	p.C215C	G protein-coupled recep	49 (0.00)	49 (0.18)	0.49

11-03	Gp4	g.chr2:133174867C>A	Silent	GPR39	p.L84L	G protein-coupled recep	60 (0.00)	12 (0.67)	1.78
11-03	Gp4	g.chrX:19020969C>T	Missense Mutation	GPR64	p.G739D	G protein-coupled recep	33 (0.00)	23 (0.26)	0.43
11-03	Gp4	g.chr1:145771665G>A	Silent	GPR89A	p.I325I	G protein-coupled recep	24 (0.04)	27 (0.37)	0.99
11-03	Gp4	g.chr1:145771683G>A	Silent	GPR89A	p.V319V	G protein-coupled recep	25 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr5:90072305G>A	Missense Mutation	GPR98	p.A4147T	G protein-coupled recep	22 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr1:109466666G>A	Missense Mutation	GPSM2	p.D549N	G-protein signaling moc	20 (0.00)	28 (0.36)	0.95
11-03	Gp4	g.chr12:13241842C>T	Splice Site	GSG1	p.G122G	germ cell associated 1	24 (0.00)	32 (0.19)	0.63
11-03	Gp4	g.chr12:13243599C>A	Missense Mutation	GSG1	p.A68S	germ cell associated 1	37 (0.00)	15 (0.33)	1.12
11-03	Gp4	g.chr11:18373979C>A	Missense Mutation	GTF2H1	p.P416T	general transcription fac	32 (0.00)	46 (0.26)	0.70
11-03	Gp4	g.chr7:73973268G>A	Missense Mutation	GTF2IRD1	p.E729K	GTF2I repeat domain cc	15 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr12:14774130C>T	Silent	GUCY2C	p.A874A	guanylate cyclase 2C (h	31 (0.00)	31 (0.16)	0.54
11-03	Gp4	g.chr2:127453575C>T	Missense Mutation	GYPC	p.R82C	glycophorin C (Gerbich	20 (0.00)	14 (0.50)	1.33
11-03	Gp4	g.chr5:156479604G>T	Missense Mutation	HAVCR1	p.S147R	hepatitis A virus cellulai	46 (0.00)	67 (0.48)	1.27
11-03	Gp4	g.chr19:610381C>G	Silent	HCN2	p.G520G	hyperpolarization activa	23 (0.00)	28 (0.18)	0.61
11-03	Gp4	g.chr1:32782309G>C	Missense Mutation	HDAC1	p.S69T	histone deacetylase 1	35 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr5:141009676G>A	Missense Mutation	HDAC3	p.L100F	histone deacetylase 3	60 (0.00)	42 (0.31)	0.83
11-03	Gp4	g.chr12:48179217G>T	Missense Mutation	HDAC7	p.P876H	histone deacetylase 7	58 (0.00)	76 (0.14)	0.49
11-03	Gp4	g.chr7:18548614G>A	Intron	HDAC9		histone deacetylase 9	81 (0.01)	19 (0.26)	0.70
11-03	Gp4	g.chr7:18553109G>A	Intron	HDAC9		histone deacetylase 9	46 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr7:18553235C>A	Intron	HDAC9		histone deacetylase 9	55 (0.00)	59 (0.15)	0.41
11-03	Gp4	g.chr7:18615773T>A	Intron	HDAC9		histone deacetylase 9	28 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr7:18657003G>C	Intron	HDAC9		histone deacetylase 9	149 (0.01)	55 (0.15)	0.39
11-03	Gp4	g.chr7:18657867C>T	Intron	HDAC9		histone deacetylase 9	17 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr7:18660428A>G	Intron	HDAC9		histone deacetylase 9	60 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr7:18667258G>A	Intron	HDAC9		histone deacetylase 9	34 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr7:18701009G>A	Intron	HDAC9		histone deacetylase 9	49 (0.00)	27 (0.37)	0.99
11-03	Gp4	g.chr7:18813098G>T	Intron	HDAC9		histone deacetylase 9	20 (0.00)	30 (0.50)	1.33
11-03	Gp4	g.chr7:18814673G>T	Intron	HDAC9		histone deacetylase 9	42 (0.00)	49 (0.22)	0.60
11-03	Gp4	g.chr7:18816504G>A	Intron	HDAC9		histone deacetylase 9	43 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr7:18825084G>T	Intron	HDAC9		histone deacetylase 9	27 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr7:18828680G>A	Intron	HDAC9		histone deacetylase 9	55 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr7:18843738G>A	Intron	HDAC9		histone deacetylase 9	71 (0.00)	38 (0.21)	0.56
11-03	Gp4	g.chr7:18860577G>A	Intron	HDAC9		histone deacetylase 9	31 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr2:242206282C>T	Start Codon SNP	HDLBP	p.M1I	high density lipoprotein	88 (0.00)	33 (0.21)	0.57
11-03	Gp4	g.chr14:31774331C>T	Silent	HEATR5A	p.K1673K	HEAT repeat containing	63 (0.00)	26 (0.27)	0.72

11-03	Gp4	g.chr2:37229529C>T	Missense Mutation	HEATR5B	p.R1746Q	HEAT repeat containin	56 (0.00)	67 (0.18)	0.48
11-03	Gp4	g.chr3:124731604G>A	Missense Mutation	HEG1	p.A940V	heart development prote	61 (0.00)	33 (0.33)	0.89
11-03	Gp4	g.chr17:65105572C>T	Silent	HELZ	p.Q1383Q	helicase with zinc finge	37 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr9:100692400G>A	Missense Mutation	HEMGN	p.P426L	hemogen	48 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr11:93797589C>T	Missense Mutation	HEPHL1	p.L241F	hephaestin-like 1	24 (0.00)	54 (0.19)	0.49
11-03	Gp4	g.chr11:93806497G>A	Missense Mutation	HEPHL1	p.G466S	hephaestin-like 1	42 (0.00)	55 (0.20)	0.53
11-03	Gp4	g.chr11:93844110T>A	Silent	HEPHL1	p.P1029P	hephaestin-like 1	72 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr15:63955300C>A	Missense Mutation	HERC1	p.E2928D	HECT and RLD domai	87 (0.01)	25 (0.28)	0.75
11-03	Gp4	g.chr15:64005697C>T	Missense Mutation	HERC1	p.A1440T	HECT and RLD domai	33 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr10:69682737G>A	Missense Mutation	HERC4	p.S1042F	HECT and RLD domai	34 (0.03)	34 (0.32)	0.86
11-03	Gp4	g.chr1:91843604G>T	Missense Mutation	HFM1	p.A458E	HFM1, ATP-dependent	23 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr10:102296182G>T	Silent	HIF1AN	p.L64L	hypoxia inducible facto	61 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr7:75172226G>T	Missense Mutation	HIP1	p.A894D	huntingtin interacting pr	26 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr11:33308963C>T	Missense Mutation	HIPK3	p.R335W	homeodomain interactin	70 (0.01)	99 (0.18)	0.48
11-03	Gp4	g.chr6:27114424C>A	Missense Mutation	HIST1H2BK	p.D52Y	histone cluster 1, H2bk	98 (0.00)	58 (0.16)	0.41
11-03	Gp4	g.chr6:143074331C>T	Silent	HIVEP2	p.K2418K	human immunodeficien	25 (0.04)	26 (0.19)	0.51
11-03	Gp4	g.chr10:71136764G>T	Missense Mutation	HK1	p.G317V	hexokinase 1	15 (0.00)	22 (0.45)	1.21
11-03	Gp4	g.chr10:71007159C>T	Silent	HKDC1	p.L359L	hexokinase domain cont	59 (0.02)	35 (0.23)	0.61
11-03	Gp4	g.chr20:30137041C>G	Missense Mutation	HM13	p.A191G	histocompatibility (min	30 (0.03)	21 (0.33)	0.89
11-03	Gp4	g.chr1:186088930C>T	Missense Mutation	HMCN1	p.P4004S	hemicentin 1	39 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr5:74646684C>A	Missense Mutation	HMGCR	p.A284E	3-hydroxy-3-methylglut	17 (0.00)	21 (0.76)	2.03
11-03	Gp4	g.chr16:72094749C>A	Missense Mutation	HP	p.S394Y	haptoglobin	79 (0.01)	27 (0.37)	0.99
11-03	Gp4	g.chr1:21091942G>A	Missense Mutation	HP1BP3	p.P273L	heterochromatin protein	19 (0.00)	23 (0.52)	1.39
11-03	Gp4	g.chr10:100904047C>A	Silent	HPSE2	p.L186L	heparanase 2 (inactive)	30 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr11:63257758G>A	Missense Mutation	HRASLS5	p.P76S	HRAS-like suppressor f	119 (0.00)	56 (0.16)	0.43
11-03	Gp4	g.chr17:62750640C>T	RNA	hsa-mir-6080			112 (0.00)	59 (0.25)	0.68
11-03	Gp4	g.chr5:118814534T>A	Missense Mutation	HSD17B4	p.I129N	hydroxysteroid (17-beta	30 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr5:118814550T>A	Silent	HSD17B4	p.A134A	hydroxysteroid (17-beta	31 (0.00)	23 (0.30)	0.81
11-03	Gp4	g.chr12:57178746A>G	Missense Mutation	HSD17B6	p.K228E	hydroxysteroid (17-beta	57 (0.00)	37 (0.14)	0.45
11-03	Gp4	g.chr10:38654484G>A	RNA	HSD17B7P2		hydroxysteroid (17-beta	64 (0.00)	23 (0.30)	0.81
11-03	Gp4	g.chr16:84158313C>T	Missense Mutation	HSDL1	p.M305I	hydroxysteroid dehydro	18 (0.00)	42 (0.40)	1.08
11-03	Gp4	g.chr6:44221010C>T	Silent	HSP90AB1	p.L654L	heat shock protein 90kD	38 (0.00)	41 (0.24)	0.65
11-03	Gp4	g.chr10:14881910C>T	Missense Mutation	HSPA14	p.R22W	heat shock 70kDa protei	30 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr5:132439982C>G	Missense Mutation	HSPA4	p.P793A	heat shock 70kDa protei	25 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr1:23520655G>A	Silent	HTR1D	p.L20L	5-hydroxytryptamine (s	16 (0.00)	30 (0.23)	0.62

11-03	Gp4	g.chr10:92509250G>A	Missense Mutation	HTR7	p.T214I	5-hydroxytryptamine (s	42 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr16:70843777G>T	Missense Mutation	HYDIN	p.P4931H	HYDIN, axonemal cent	26 (0.00)	46 (0.28)	0.75
11-03	Gp4	g.chr16:70916649G>A	Missense Mutation	HYDIN	p.R3377C	HYDIN, axonemal cent	59 (0.00)	9 (0.56)	1.48
11-03	Gp4	g.chr7:8198177G>A	Missense Mutation	ICA1	p.H229Y	islet cell autoantigen 1,	26 (0.00)	50 (0.26)	0.69
11-03	Gp4	g.chr6:52870065C>A	Missense Mutation	ICK	p.G594V	intestinal cell (MAK-lik	29 (0.00)	19 (0.63)	1.68
11-03	Gp4	g.chr8:39872881C>T	Silent	IDO2	p.H328H	indoleamine 2,3-dioxyg	55 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr2:27680515C>T	Silent	IFT172	p.E1073E	intraflagellar transport 1	43 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr11:68673544C>T	Nonsense Mutation	IGHMBP2	p.Q32*	immunoglobulin mu bin	61 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr14:106733340G>T	RNA	IGHV1-24		immunoglobulin heavy	44 (0.02)	22 (0.23)	0.61
11-03	Gp4	g.chr21:10862657C>A	RNA	IGHV1OR21-1		immunoglobulin heavy	153 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr14:106805281C>T	RNA	IGHV4-31		immunoglobulin heavy	21 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr14:106829645C>A	RNA	IGHV4-34		immunoglobulin heavy	19 (0.00)	11 (0.55)	1.45
11-03	Gp4	g.chr22:22550675C>A	RNA	IGLV6-57		immunoglobulin lambd	29 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr3:151154764G>A	Nonsense Mutation	IGSF10	p.R2529*	immunoglobulin superf	37 (0.03)	33 (0.42)	1.13
11-03	Gp4	g.chr15:81598313T>A	Missense Mutation	IL16	p.V1162D	interleukin 16	57 (0.00)	22 (0.27)	0.73
11-03	Gp4	g.chr2:102959757C>T	Silent	IL1RL1	p.D284D	interleukin 1 receptor-li	58 (0.02)	42 (0.17)	0.44
11-03	Gp4	g.chr3:100948289C>T	Missense Mutation	IMPG2	p.V1190M	interphotoreceptor matri	34 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr2:121107258C>T	Silent	INHBB	p.P344P	inhibin, beta B	20 (0.00)	30 (0.33)	0.89
11-03	Gp4	g.chr2:99169333G>A	Silent	INPP4A	p.L421L	inositol polyphosphate-	41 (0.00)	42 (0.19)	0.51
11-03	Gp4	g.chr4:143008521G>A	Intron	INPP4B		inositol polyphosphate-	33 (0.00)	24 (0.42)	1.11
11-03	Gp4	g.chr4:143071011G>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	25 (0.32)	0.85
11-03	Gp4	g.chr4:143072588T>A	Intron	INPP4B		inositol polyphosphate-	39 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr4:143092403C>T	Intron	INPP4B		inositol polyphosphate-	17 (0.00)	32 (0.28)	0.75
11-03	Gp4	g.chr4:143100757G>A	Intron	INPP4B		inositol polyphosphate-	31 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr4:143161529C>T	Intron	INPP4B		inositol polyphosphate-	49 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr4:143163000G>T	Intron	INPP4B		inositol polyphosphate-	27 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr4:143235493C>G	Intron	INPP4B		inositol polyphosphate-	48 (0.02)	51 (0.18)	0.47
11-03	Gp4	g.chr4:143260693G>A	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr4:143313802G>A	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	11 (0.64)	1.70
11-03	Gp4	g.chr4:143320029C>A	Intron	INPP4B		inositol polyphosphate-	64 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr4:143335840G>A	Intron	INPP4B		inositol polyphosphate-	26 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr4:143335977G>A	Intron	INPP4B		inositol polyphosphate-	33 (0.00)	32 (0.50)	1.33
11-03	Gp4	g.chr4:143370435C>A	Intron	INPP4B		inositol polyphosphate-	53 (0.00)	47 (0.23)	0.62
11-03	Gp4	g.chr4:143415080C>A	Intron	INPP4B		inositol polyphosphate-	22 (0.05)	20 (0.55)	1.47
11-03	Gp4	g.chr4:143423439G>T	Intron	INPP4B		inositol polyphosphate-	64 (0.00)	57 (0.21)	0.56

11-03	Gp4	g.chr4:143474390A>T	Intron	INPP4B		inositol polyphosphate-	25 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr4:143484918C>A	Intron	INPP4B		inositol polyphosphate-	31 (0.00)	37 (0.24)	0.65
11-03	Gp4	g.chr4:143626133T>C	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	26 (0.35)	0.92
11-03	Gp4	g.chr4:143652105C>A	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr4:143688177C>A	Intron	INPP4B		inositol polyphosphate-	28 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr4:143723315C>T	Intron	INPP4B		inositol polyphosphate-	26 (0.00)	67 (0.16)	0.44
11-03	Gp4	g.chr4:143738625C>T	Intron	INPP4B		inositol polyphosphate-	20 (0.00)	20 (0.25)	0.67
11-03	Gp4	g.chr4:143743122C>T	Intron	INPP4B		inositol polyphosphate-	35 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr6:154520888G>C	Missense Mutation	IPCEF1	p.S275C	interaction protein for c	31 (0.00)	37 (0.27)	0.72
11-03	Gp4	g.chr15:67687674G>C	Missense Mutation	IQCH	p.A560P	IQ motif containing H	35 (0.00)	51 (0.18)	0.47
11-03	Gp4	g.chr15:91027463A>G	Missense Mutation	IQGAP1	p.Q1267R	IQ motif containing GT	44 (0.00)	45 (0.40)	1.07
11-03	Gp4	g.chr12:66622127G>A	Silent	IRAK3	p.S288S	interleukin-1 receptor-a	37 (0.00)	20 (0.35)	1.17
11-03	Gp4	g.chr15:78782960G>A	Splice Site	IREB2		iron-responsive element	24 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr1:156693188C>T	Missense Mutation	ISG20L2	p.E339K	interferon stimulated ex	42 (0.00)	27 (0.33)	0.89
11-03	Gp4	g.chr19:18546675C>T	Silent	ISYNA1	p.S344S	inositol-3-phosphate sy	26 (0.00)	39 (0.15)	0.41
11-03	Gp4	g.chr5:52206093C>T	Silent	ITGA1	p.C567C	integrin, alpha 1	39 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr1:145535818G>T	Missense Mutation	ITGA10	p.R669L	integrin, alpha 10	19 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr2:187500900G>A	Silent	ITGAV	p.R241R	integrin, alpha V	47 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr10:33200440G>T	Missense Mutation	ITGB1	p.P623T	integrin, beta 1 (fibrone	40 (0.03)	28 (0.18)	0.48
11-03	Gp4	g.chr12:26709168C>T	Silent	ITPR2	p.S1654S	inositol 1,4,5-trisphosph	23 (0.00)	19 (0.58)	1.94
11-03	Gp4	g.chr9:24545033G>T	Missense Mutation	IZUMO3	p.L110I	IZUMO family member	50 (0.00)	45 (0.20)	0.53
11-03	Gp4	g.chr3:9934653G>A	Nonsense Mutation	JAGN1	p.W48*	jagunal homolog 1 (Dro	35 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr4:6055716G>A	Silent	JAKMIP1	p.L623L	janus kinase and microt	40 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr10:64966976G>A	Missense Mutation	JMJD1C	p.H1485Y	jumonji domain contain	37 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr15:42138900C>A	Missense Mutation	JMJD7-PLA2	p.T836K	JMJD7-PLA2G4B readt	25 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr17:47869267C>A	Nonsense Mutation	KAT7	p.S12*	K(lysine) acetyltransfer	21 (0.00)	53 (0.15)	0.40
11-03	Gp4	g.chr13:41766698G>A	Nonsense Mutation	KBTBD7	p.Q566*	kelch repeat and BTB (	56 (0.00)	12 (0.67)	0.65
11-03	Gp4	g.chr1:111216485G>T	Missense Mutation	KCNA3	p.A316D	potassium voltage-gated	49 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr6:73815050G>A	Missense Mutation	KCNQ5	p.G330D	potassium voltage-gated	72 (0.00)	46 (0.57)	1.51
11-03	Gp4	g.chr8:36675228C>A	Missense Mutation	KCNU1	p.F352L	potassium channel, subf	36 (0.00)	20 (0.65)	0.65
11-03	Gp4	g.chr8:36766895C>A	Missense Mutation	KCNU1	p.H725N	potassium channel, subf	135 (0.00)	19 (0.58)	0.58
11-03	Gp4	g.chr16:67327832C>T	Silent	KCTD19	p.K611K	potassium channel tetra	124 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr22:38877397C>T	Nonsense Mutation	KDELR3	p.Q178*	KDEL (Lys-Asp-Glu-L	25 (0.00)	48 (0.19)	0.50
11-03	Gp4	g.chr1:23403738C>A	Missense Mutation	KDM1A	p.F584L	lysine (K)-specific dem	37 (0.00)	28 (0.32)	0.86
11-03	Gp4	g.chr12:417122G>T	Missense Mutation	KDM5A	p.S1143Y	lysine (K)-specific dem	71 (0.00)	49 (0.14)	0.48

11-03	Gp4	g.chr17:26955535G>A	Nonsense Mutation	KIAA0100	p.Q1448*	KIAA0100	17 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr3:197431449G>A	Missense Mutation	KIAA0226	p.L143F	KIAA0226	56 (0.00)	73 (0.16)	0.44
11-03	Gp4	g.chr9:114124311T>A	Nonstop Mutation	KIAA0368	p.*1840L	KIAA0368	87 (0.00)	34 (0.24)	0.63
11-03	Gp4	g.chr16:15718953G>T	Silent	KIAA0430	p.P534P	KIAA0430	36 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr5:5457479G>T	Silent	KIAA0947	p.V242V		32 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr5:5457520C>T	Missense Mutation	KIAA0947	p.P256L		62 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr5:5462564C>T	Silent	KIAA0947	p.T1039T		80 (0.00)	38 (0.29)	0.77
11-03	Gp4	g.chr15:79749305C>A	Silent	KIAA1024	p.P272P	KIAA1024	19 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chrX:118223138G>A	Silent	KIAA1210	p.L685L	KIAA1210	25 (0.04)	28 (0.29)	0.48
11-03	Gp4	g.chr10:24825795C>G	Silent	KIAA1217	p.G852G	KIAA1217	21 (0.00)	33 (0.21)	0.57
11-03	Gp4	g.chr6:138644850G>T	Missense Mutation	KIAA1244	p.M1603I	KIAA1244	93 (0.01)	92 (0.22)	0.58
11-03	Gp4	g.chr8:95539058G>T	Missense Mutation	KIAA1429	p.Q472K	KIAA1429	36 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr9:5762588C>T	Silent	KIAA1432	p.I680I		22 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr10:30318596C>T	Missense Mutation	KIAA1462	p.E161K	KIAA1462	44 (0.00)	36 (0.47)	1.26
11-03	Gp4	g.chr1:200558355G>A	Missense Mutation	KIF14	p.A1035V	kinesin family member	18 (0.00)	22 (0.36)	0.97
11-03	Gp4	g.chr6:168439337C>T	Missense Mutation	KIF25	p.A141V	kinesin family member	36 (0.00)	42 (0.29)	0.76
11-03	Gp4	g.chr1:245766009C>T	Missense Mutation	KIF26B	p.A494V	kinesin family member	23 (0.00)	19 (0.53)	1.40
11-03	Gp4	g.chr17:51901474T>A	Nonsense Mutation	KIF2B	p.Y360*	kinesin family member	41 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chrX:69561755G>A	Missense Mutation	KIF4A	p.A414T	kinesin family member	20 (0.00)	16 (0.69)	1.15
11-03	Gp4	g.chr5:154394220C>T	Silent	KIF4B	p.L267L	kinesin family member	77 (0.00)	76 (0.47)	1.26
11-03	Gp4	g.chr12:57972050G>A	Silent	KIF5A	p.G821G	kinesin family member	34 (0.00)	38 (0.18)	0.61
11-03	Gp4	g.chr19:55263881A>T	Silent	KIR2DL3	p.T312T	killer cell immunoglobu	30 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr19:55341700G>C	Missense Mutation	KIR3DL1	p.K435N	killer cell immunoglobu	42 (0.02)	19 (0.32)	0.84
11-03	Gp4	g.chr14:104121050T>A	Missense Mutation	KLC1	p.L50Q	kinesin light chain 1	53 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr17:40010258C>T	Missense Mutation	KLHL11	p.D621N	kelch-like family memb	21 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr1:202862438G>T	Silent	KLHL12	p.V503V	kelch-like family memb	17 (0.00)	17 (0.47)	1.25
11-03	Gp4	g.chrX:117043777G>T	Missense Mutation	KLHL13	p.P234T	kelch-like family memb	23 (0.00)	29 (0.41)	0.69
11-03	Gp4	g.chr14:45415060G>A	Silent	KLHL28	p.G38G	kelch-like family memb	27 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr6:97587062C>A	Silent	KLHL32	p.S589S	kelch-like family memb	60 (0.02)	12 (0.42)	1.11
11-03	Gp4	g.chr11:118377068C>G	Silent	KMT2A	p.T3487T	lysine (K)-specific meth	45 (0.00)	22 (0.55)	1.45
11-03	Gp4	g.chr7:151879370G>A	Missense Mutation	KMT2C	p.P1859S	lysine (K)-specific meth	24 (0.00)	52 (0.23)	0.62
11-03	Gp4	g.chr12:49420608G>T	Silent	KMT2D	p.A5047A	lysine (K)-specific meth	38 (0.03)	40 (0.20)	0.67
11-03	Gp4	g.chr3:122215322C>T	Missense Mutation	KPNA1	p.E31K	karyopherin alpha 1 (im	15 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr17:66040109C>T	Silent	KPNA2	p.I362I	karyopherin alpha 2 (R	98 (0.00)	102 (0.16)	0.42
11-03	Gp4	g.chr17:8272633A>T	Nonsense Mutation	KRBA2	p.L351*	KRAB-A domain contai	47 (0.00)	40 (0.17)	0.47

11-03	Gp4	g.chrX:46332196G>A	Missense Mutation	KRBOX4	p.V89I	KRAB box domain cont	38 (0.00)	18 (0.39)	0.65
11-03	Gp4	g.chr2:88327882G>A	Silent	KRCC1	p.T67T	lysine-rich coiled-coil 1	16 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr2:88327892G>A	Missense Mutation	KRCC1	p.P64L	lysine-rich coiled-coil 1	17 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr12:75905373G>A	Missense Mutation	KRR1	p.A2V	KRR1, small subunit (S	22 (0.00)	36 (0.14)	0.47
11-03	Gp4	g.chr17:39659935T>A	Missense Mutation	KRT13	p.I180F	keratin 13	141 (0.00)	38 (0.42)	1.12
11-03	Gp4	g.chr17:18365464C>T	RNA	KRT16P4		keratin 16 pseudogene 4	76 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr17:39779282G>A	Silent	KRT17	p.I145I	keratin 17	45 (0.00)	56 (0.20)	0.52
11-03	Gp4	g.chr17:39034409C>G	Missense Mutation	KRT20	p.G376A	keratin 20	31 (0.00)	12 (0.50)	1.33
11-03	Gp4	g.chr17:38856567G>A	Silent	KRT24	p.T308T	keratin 24	61 (0.02)	53 (0.47)	1.26
11-03	Gp4	g.chr17:38950206C>T	Silent	KRT28	p.E357E	keratin 28	34 (0.00)	27 (0.30)	0.79
11-03	Gp4	g.chr17:39122962G>T	Missense Mutation	KRT39	p.H49Q	keratin 39	66 (0.00)	34 (0.32)	0.86
11-03	Gp4	g.chr12:52910902C>A	Missense Mutation	KRT5	p.V403F	keratin 5	74 (0.01)	26 (0.19)	0.40
11-03	Gp4	g.chr12:52946483G>A	Missense Mutation	KRT71	p.R127C	keratin 71	59 (0.00)	22 (0.32)	0.66
11-03	Gp4	g.chr17:39197146G>A	Silent	KRTAP1-1	p.C168C	keratin associated protei	38 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr17:39197191G>A	Silent	KRTAP1-1	p.C153C	keratin associated protei	47 (0.00)	32 (0.22)	0.58
11-03	Gp4	g.chr17:25937112C>T	Silent	KSR1	p.L634L	kinase suppressor of ras	41 (0.00)	29 (0.41)	1.10
11-03	Gp4	g.chr18:6997824C>A	Missense Mutation	LAMA1	p.V1575F	laminin, alpha 1	32 (0.00)	43 (0.28)	0.74
11-03	Gp4	g.chr6:129621993C>T	Silent	LAMA2	p.G1050G	laminin, alpha 2	34 (0.00)	11 (0.64)	0.67
11-03	Gp4	g.chr7:107603439G>A	Nonsense Mutation	LAMB1	p.R590*	laminin, beta 1	22 (0.00)	19 (0.53)	1.40
11-03	Gp4	g.chr1:183201346C>T	Nonsense Mutation	LAMC2	p.Q628*	laminin, gamma 2	29 (0.00)	34 (0.21)	0.55
11-03	Gp4	g.chr5:145543979G>T	Missense Mutation	LARS	p.S163Y	leucyl-tRNA synthetase	31 (0.00)	17 (0.41)	1.10
11-03	Gp4	g.chr1:225591089C>T	Silent	LBR	p.E588E	lamin B receptor	18 (0.06)	36 (0.17)	0.44
11-03	Gp4	g.chr1:225598103C>T	Missense Mutation	LBR	p.V402M	lamin B receptor	23 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr1:152538482G>A	Missense Mutation	LCE3E	p.S68F	late cornified envelope	40 (0.00)	12 (0.75)	2.00
11-03	Gp4	g.chr11:27401839C>A	Missense Mutation	LGR4	p.G317V	leucine-rich repeat cont	27 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr12:71978183C>A	Missense Mutation	LGR5	p.P798H	leucine-rich repeat cont	33 (0.00)	13 (0.38)	1.29
11-03	Gp4	g.chr5:38506632C>T	Missense Mutation	LIFR	p.R365H	leukemia inhibitory fact	17 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chr13:108861633C>T	Missense Mutation	LIG4	p.V662I	ligase IV, DNA, ATP-d	36 (0.00)	43 (0.21)	0.56
11-03	Gp4	g.chr19:54803554C>A	Missense Mutation	LILRA3	p.W90C	leukocyte immunoglobu	39 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr14:74567865G>T	Silent	LIN52	p.G73G	lin-52 DREAM MuvB c	33 (0.00)	37 (0.19)	0.50
11-03	Gp4	g.chr12:8519204A>G	lincRNA	LINC00937		long intergenic non-prot	150 (0.00)	109 (0.12)	0.40
11-03	Gp4	g.chr9:27949752C>T	Silent	LINGO2	p.G306G	leucine rich repeat and I	15 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr13:28134013G>T	Missense Mutation	LNX2	p.P445Q	ligand of numb-protein	33 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr13:28143253G>A	Missense Mutation	LNX2	p.R190W	ligand of numb-protein	104 (0.00)	98 (0.20)	0.54
11-03	Gp4	g.chr6:160978583C>A	Missense Mutation	LPA	p.C1551F	lipoprotein, Lp(a)	35 (0.00)	35 (0.14)	0.38

11-03	Gp4	g.chr6:161026132C>A	Missense Mutation	LPA	p.W964L	lipoprotein, Lp(a)	40 (0.03)	25 (0.20)	0.53
11-03	Gp4	g.chr19:14288369C>A	Silent	LPHN1	p.P86P	latrophilin 1	21 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr1:82447490A>G	Splice Site	LPHN2		latrophilin 2	27 (0.00)	29 (0.55)	0.63
11-03	Gp4	g.chr18:2921615G>A	Silent	LPIN2	p.F786F	lipin 2	21 (0.00)	22 (0.27)	0.73
11-03	Gp4	g.chr18:2921623C>A	Nonsense Mutation	LPIN2	p.E784*	lipin 2	20 (0.00)	22 (0.27)	0.73
11-03	Gp4	g.chr9:104071551C>G	Silent	LPPR1	p.V148V		43 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr1:111490919C>T	Missense Mutation	LRIF1	p.A658T	ligand dependent nuclea	27 (0.00)	14 (0.43)	1.14
11-03	Gp4	g.chr1:113661958C>T	Silent	LRIG2	p.D928D	leucine-rich repeats and	33 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr8:105510163G>A	Missense Mutation	LRP12	p.P206L	low density lipoprotein	18 (0.00)	21 (0.67)	1.78
11-03	Gp4	g.chr2:141093354G>A	Silent	LRP1B	p.N3982N	low density lipoprotein	32 (0.00)	32 (0.22)	0.58
11-03	Gp4	g.chr6:25450599G>C	Missense Mutation	LRRC16A	p.D168H	leucine rich repeat conta	94 (0.00)	63 (0.14)	0.38
11-03	Gp4	g.chr18:7231238G>A	Silent	LRRC30	p.L34L	leucine rich repeat conta	17 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr17:62859061C>T	Silent	LRRC37A3	p.K1043K	leucine rich repeat conta	43 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr17:43585743G>T	RNA	LRRC37A4P		leucine rich repeat conta	20 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr17:30349439T>A	Missense Mutation	LRRC37B	p.I343K	leucine rich repeat conta	31 (0.00)	22 (0.41)	1.09
11-03	Gp4	g.chr17:28960397A>T	RNA	LRRC37BP1		leucine rich repeat conta	43 (0.00)	46 (0.22)	0.58
11-03	Gp4	g.chr17:45913468G>A	Splice Site	LRRC46	p.R151H	leucine rich repeat conta	20 (0.00)	17 (0.53)	1.41
11-03	Gp4	g.chr9:130223464G>A	Missense Mutation	LRSAM1	p.E112K	leucine rich repeat and s	32 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr3:194371930C>T	Missense Mutation	LSG1	p.V397I	large 60S subunit nucle	18 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr12:96408711C>T	Missense Mutation	LTA4H	p.D376N	leukotriene A4 hydrolas	16 (0.00)	43 (0.12)	0.40
11-03	Gp4	g.chr12:6499315C>T	Missense Mutation	LTBR	p.P280L	lymphotoxin beta recept	42 (0.00)	20 (0.40)	1.34
11-03	Gp4	g.chr1:235955261T>A	Missense Mutation	LYST	p.R1427S	lysosomal trafficking re	33 (0.00)	65 (0.17)	0.45
11-03	Gp4	g.chr1:9992938C>G	Missense Mutation	LZIC	p.V119L	leucine zipper and CTN	23 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr3:119434482C>T	Nonsense Mutation	MAATS1	p.Q192*	MYCBP-associated, tes	69 (0.00)	45 (0.18)	0.47
11-03	Gp4	g.chr3:119466110G>A	Splice Site	MAATS1	p.R684H	MYCBP-associated, tes	67 (0.00)	78 (0.17)	0.44
11-03	Gp4	g.chr1:39851498C>T	Silent	MACF1	p.C4752C	microtubule-actin crossl	43 (0.00)	43 (0.19)	0.50
11-03	Gp4	g.chr11:47311022C>G	Missense Mutation	MADD	p.Q932E	MAP-kinase activating	163 (0.00)	54 (0.20)	0.54
11-03	Gp4	g.chrX:141291223C>T	Missense Mutation	MAGEC2	p.R184K	melanoma antigen famil	23 (0.00)	12 (0.42)	0.69
11-03	Gp4	g.chrX:55479424A>T	Missense Mutation	MAGEH1	p.E206V	melanoma antigen famil	25 (0.00)	36 (0.42)	0.69
11-03	Gp4	g.chr7:77667122G>T	Intron	MAGI2		membrane associated gu	44 (0.00)	48 (0.19)	0.50
11-03	Gp4	g.chr7:77671156G>A	Intron	MAGI2		membrane associated gu	63 (0.00)	28 (0.54)	1.43
11-03	Gp4	g.chr7:77703113G>A	Intron	MAGI2		membrane associated gu	54 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr7:77740171C>T	Intron	MAGI2		membrane associated gu	39 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr7:77741255G>A	Intron	MAGI2		membrane associated gu	53 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chr7:77753663G>A	Intron	MAGI2		membrane associated gu	27 (0.00)	38 (0.47)	1.26

11-03	Gp4	g.chr7:77813931G>C	Intron	MAGI2	membrane associated gu	39 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr7:77819264G>T	Intron	MAGI2	membrane associated gu	131 (0.00)	100 (0.22)	0.59
11-03	Gp4	g.chr7:77851497C>G	Intron	MAGI2	membrane associated gu	49 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr7:77925406G>A	Intron	MAGI2	membrane associated gu	24 (0.00)	32 (0.22)	0.58
11-03	Gp4	g.chr7:77983015G>T	Intron	MAGI2	membrane associated gu	55 (0.00)	69 (0.23)	0.62
11-03	Gp4	g.chr7:78045455C>T	Intron	MAGI2	membrane associated gu	47 (0.00)	38 (0.29)	0.77
11-03	Gp4	g.chr7:78064944G>C	Intron	MAGI2	membrane associated gu	44 (0.00)	32 (0.22)	0.58
11-03	Gp4	g.chr7:78064985C>T	Intron	MAGI2	membrane associated gu	80 (0.00)	54 (0.19)	0.49
11-03	Gp4	g.chr7:78074418C>G	Intron	MAGI2	membrane associated gu	34 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr7:78078546G>A	Intron	MAGI2	membrane associated gu	30 (0.00)	54 (0.15)	0.40
11-03	Gp4	g.chr7:78102856C>T	Intron	MAGI2	membrane associated gu	54 (0.00)	39 (0.21)	0.55
11-03	Gp4	g.chr7:78103170G>T	Intron	MAGI2	membrane associated gu	43 (0.00)	29 (0.34)	0.92
11-03	Gp4	g.chr7:78114109C>T	Intron	MAGI2	membrane associated gu	63 (0.00)	56 (0.23)	0.62
11-03	Gp4	g.chr7:78132234T>A	Intron	MAGI2	membrane associated gu	29 (0.00)	46 (0.20)	0.52
11-03	Gp4	g.chr7:78144121C>T	Intron	MAGI2	membrane associated gu	32 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr7:78165814C>T	Intron	MAGI2	membrane associated gu	47 (0.00)	44 (0.32)	0.85
11-03	Gp4	g.chr7:78179610C>A	Intron	MAGI2	membrane associated gu	36 (0.00)	37 (0.46)	1.23
11-03	Gp4	g.chr7:78186715C>T	Intron	MAGI2	membrane associated gu	51 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr7:78190810C>G	Intron	MAGI2	membrane associated gu	45 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr7:78218251G>A	Intron	MAGI2	membrane associated gu	63 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr7:78236980G>A	Intron	MAGI2	membrane associated gu	39 (0.00)	42 (0.19)	0.51
11-03	Gp4	g.chr7:78343381G>A	Intron	MAGI2	membrane associated gu	49 (0.00)	24 (0.42)	1.11
11-03	Gp4	g.chr7:78369553C>G	Intron	MAGI2	membrane associated gu	89 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr7:78393881G>A	Intron	MAGI2	membrane associated gu	83 (0.00)	39 (0.21)	0.55
11-03	Gp4	g.chr7:78398923C>T	Intron	MAGI2	membrane associated gu	60 (0.00)	44 (0.36)	0.97
11-03	Gp4	g.chr7:78407288C>A	Intron	MAGI2	membrane associated gu	39 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr7:78478900G>A	Intron	MAGI2	membrane associated gu	31 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr7:78582319C>G	Intron	MAGI2	membrane associated gu	40 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr7:78626260C>G	Intron	MAGI2	membrane associated gu	16 (0.06)	29 (0.24)	0.64
11-03	Gp4	g.chr7:78665920C>A	Intron	MAGI2	membrane associated gu	53 (0.00)	40 (0.25)	0.67
11-03	Gp4	g.chr7:78665921C>A	Intron	MAGI2	membrane associated gu	52 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr7:78675517C>A	Intron	MAGI2	membrane associated gu	62 (0.02)	43 (0.28)	0.74
11-03	Gp4	g.chr7:78710213C>T	Intron	MAGI2	membrane associated gu	35 (0.00)	34 (0.29)	0.78
11-03	Gp4	g.chr7:78710285C>T	Intron	MAGI2	membrane associated gu	31 (0.00)	46 (0.30)	0.81
11-03	Gp4	g.chr7:78776903G>A	Intron	MAGI2	membrane associated gu	31 (0.00)	19 (0.37)	0.98

11-03	Gp4	g.chr7:78830274C>T	Intron	MAGI2		membrane associated gu	44 (0.00)	66 (0.15)	0.40
11-03	Gp4	g.chr7:78841215G>T	Intron	MAGI2		membrane associated gu	18 (0.00)	45 (0.16)	0.41
11-03	Gp4	g.chr7:78926104G>C	Intron	MAGI2		membrane associated gu	28 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr7:78970147G>C	Intron	MAGI2		membrane associated gu	17 (0.00)	12 (0.58)	1.56
11-03	Gp4	g.chr7:78990748G>A	Intron	MAGI2		membrane associated gu	16 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr7:79061725G>T	Intron	MAGI2		membrane associated gu	50 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr1:114201841C>A	Silent	MAGI3	p.I923I	membrane associated gu	22 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr11:95825545C>G	Missense Mutation	MAML2	p.E550D	mastermind-like 2 (Dros	28 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr9:140001164C>A	Missense Mutation	MAN1B1	p.A490D	mannosidase, alpha, clas	16 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr4:103611826T>A	Missense Mutation	MANBA	p.Q259L	mannosidase, beta A, ly	36 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr1:232943729C>A	Nonsense Mutation	MAP10	p.S987*	microtubule-associated	90 (0.00)	88 (0.19)	0.52
11-03	Gp4	g.chr5:71496192C>T	Missense Mutation	MAP1B	p.A2337V	microtubule-associated	104 (0.00)	38 (0.24)	0.63
11-03	Gp4	g.chr3:185161358G>A	Missense Mutation	MAP3K13	p.G262E	mitogen-activated protei	43 (0.02)	62 (0.37)	0.99
11-03	Gp4	g.chr17:61767671G>A	Missense Mutation	MAP3K3	p.G367S	mitogen-activated protei	21 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr6:136944047C>G	Missense Mutation	MAP3K5	p.G697R	mitogen-activated protei	15 (0.00)	48 (0.31)	0.83
11-03	Gp4	g.chr3:47957578G>A	Missense Mutation	MAP4	p.S597L	microtubule-associated	15 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr6:36068028G>A	Missense Mutation	MAPK14	p.R249K	mitogen-activated protei	70 (0.00)	63 (0.17)	0.47
11-03	Gp4	g.chr12:112305462G>T	Missense Mutation	MAPKAPK5	p.E91D	mitogen-activated protei	45 (0.00)	36 (0.25)	0.87
11-03	Gp4	g.chr20:31421524G>C	Splice Site	MAPRE1	p.G41G	microtubule-associated	32 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr18:32706979G>A	Silent	MAPRE2	p.R183R	microtubule-associated	61 (0.02)	32 (0.56)	1.50
11-03	Gp4	g.chr1:220928360C>T	Missense Mutation	MARC2	p.S115F	mitochondrial amidoxin	26 (0.00)	16 (0.50)	1.33
11-03	Gp4	g.chr5:16067590G>A	Missense Mutation	MARCH11	p.T400I	membrane-associated ri	39 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr2:160605269C>T	Missense Mutation	MARCH7	p.P452S	membrane-associated ri	69 (0.00)	16 (0.44)	0.51
11-03	Gp4	g.chr1:11087348C>A	Missense Mutation	MASP2	p.C552F	mannan-binding lectin s	28 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr1:11087438C>T	Missense Mutation	MASP2	p.G522D	mannan-binding lectin s	34 (0.00)	29 (0.41)	1.10
11-03	Gp4	g.chr8:99042837G>C	Missense Mutation	MATN2	p.C835S	matrilin 2	66 (0.00)	112 (0.16)	0.43
11-03	Gp4	g.chr2:20200220C>T	Missense Mutation	MATN3	p.D384N	matrilin 3	66 (0.00)	49 (0.31)	0.82
11-03	Gp4	g.chr2:149227554C>T	Missense Mutation	MBD5	p.P681L	methyl-CpG binding do	70 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr12:57918765G>A	Silent	MBD6	p.V82V	methyl-CpG binding do	52 (0.00)	40 (0.12)	0.42
11-03	Gp4	g.chr12:57918787G>T	Missense Mutation	MBD6	p.G90W	methyl-CpG binding do	53 (0.00)	39 (0.13)	0.43
11-03	Gp4	g.chrX:131520821G>A	Silent	MBNL3	p.L264L	muscleblind-like splicin	26 (0.00)	20 (0.40)	0.67
11-03	Gp4	g.chr8:48883102G>A	Missense Mutation	MCM4	p.R489K	minichromosome maint	51 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr15:94943178C>T	Missense Mutation	MCTP2	p.P640L	multiple C2 domains, tr	37 (0.00)	85 (0.16)	0.44
11-03	Gp4	g.chr14:24683730G>A	Silent	MDP1	p.I95I	magnesium-dependent p	24 (0.00)	17 (0.35)	0.94
11-03	Gp4	g.chr12:116445361G>A	Missense Mutation	MED13L	p.P698L	mediator complex subur	30 (0.00)	45 (0.13)	0.46

11-03	Gp4	g.chr12:116445363G>A	Silent	MED13L	p.D697D	mediator complex subur	30 (0.00)	45 (0.22)	0.77
11-03	Gp4	g.chr17:38182513G>A	Silent	MED24	p.H627H	mediator complex subur	34 (0.00)	20 (0.65)	1.73
11-03	Gp4	g.chr15:66191122G>C	Missense Mutation	MEGF11	p.S973C	multiple EGF-like-doma	131 (0.00)	61 (0.16)	0.44
11-03	Gp4	g.chr16:1911985C>T	Splice Site	MEIOB		meiosis specific with O	48 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr15:81271781G>A	Missense Mutation	MESDC2	p.R162C	mesoderm development	25 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr1:171756952C>T	Silent	METTL13	p.D397D	methyltransferase like 1	28 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr1:171761295G>A	Missense Mutation	METTL13	p.G538D	methyltransferase like 1	43 (0.00)	48 (0.44)	1.17
11-03	Gp4	g.chr12:53646949C>T	Silent	MFSD5	p.L110L	major facilitator superfa	56 (0.00)	18 (0.28)	0.57
11-03	Gp4	g.chr15:42040917T>C	Silent	MGA	p.I1765I	MGA, MAX dimerizati	48 (0.00)	58 (0.16)	0.41
11-03	Gp4	g.chr7:141750635C>T	Missense Mutation	MGAM	p.P926S	maltase-glucoamylase (	56 (0.00)	66 (0.26)	0.69
11-03	Gp4	g.chr7:141755520C>A	Silent	MGAM	p.P1159P	maltase-glucoamylase (	15 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr7:141756674G>T	Missense Mutation	MGAM	p.G1209W	maltase-glucoamylase (	40 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr7:141780662C>A	Silent	MGAM	p.T1973T	maltase-glucoamylase (	51 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr16:4700395G>A	Missense Mutation	MGRN1	p.G40R	mahogunin ring finger 1	27 (0.00)	17 (0.35)	0.94
11-03	Gp4	g.chr11:12341246C>G	Missense Mutation	MICALCL	p.S477C	MICAL C-terminal like	27 (0.00)	48 (0.42)	1.11
11-03	Gp4	g.chr22:39909575C>T	Silent	MIEF1	p.N213N	mitochondrial elongatio	31 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr13:92003598G>A	RNA	MIR17HG		miR-17-92 cluster host	40 (0.00)	33 (0.52)	1.37
11-03	Gp4	g.chr10:129904768C>A	Missense Mutation	MKI67	p.G1779V	marker of proliferation	128 (0.00)	15 (0.53)	1.42
11-03	Gp4	g.chr10:129910215C>A	Missense Mutation	MKI67	p.R688S	marker of proliferation	123 (0.00)	27 (0.33)	0.89
11-03	Gp4	g.chr6:168276023C>G	Missense Mutation	MLLT4	p.S196C	myeloid/lymphoid or mi	56 (0.02)	90 (0.16)	0.41
11-03	Gp4	g.chr6:168276026G>A	Missense Mutation	MLLT4	p.R197Q	myeloid/lymphoid or mi	59 (0.00)	88 (0.18)	0.48
11-03	Gp4	g.chr16:83940674C>T	Missense Mutation	MLYCD	p.S204L	malonyl-CoA decarbox	58 (0.00)	44 (0.20)	0.55
11-03	Gp4	g.chr3:154860045T>A	Missense Mutation	MME	p.S372T	membrane metallo-endo	15 (0.00)	29 (0.28)	0.74
11-03	Gp4	g.chr11:102665970A>G	Silent	MMP1	p.C278C	matrix metallopeptidase	31 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr11:102822774C>G	Missense Mutation	MMP13	p.D256H	matrix metallopeptidase	44 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr12:56230840C>T	Missense Mutation	MMP19	p.E480K	matrix metallopeptidase	42 (0.00)	29 (0.17)	0.57
11-03	Gp4	g.chr12:56231076C>T	Missense Mutation	MMP19	p.G401E	matrix metallopeptidase	18 (0.00)	24 (0.29)	0.97
11-03	Gp4	g.chr20:49575919G>A	Silent	MOCS3	p.S180S	molybdenum cofactor s	18 (0.00)	35 (0.20)	0.53
11-03	Gp4	g.chr21:37711202C>T	Silent	MORC3	p.I197I	MORC family CW-type	25 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr21:37732521G>A	Silent	MORC3	p.L457L	MORC family CW-type	15 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr1:113242393G>A	Silent	MOV10	p.L890L	Mov10 RISC complex	68 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr2:71375221C>T	Silent	MPHOSPH10	p.A550A	M-phase phosphoprotei	15 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr12:123703013C>A	Missense Mutation	MPHOSPH9	p.K302N	M-phase phosphoprotei	32 (0.00)	37 (0.16)	0.57
11-03	Gp4	g.chr7:40172837G>C	Missense Mutation	MPLKIP	p.P121A	M-phase specific PLK1	55 (0.00)	57 (0.25)	0.65
11-03	Gp4	g.chr2:234713179G>C	Missense Mutation	MROH2A	p.D644H	maestro heat-like repeat	24 (0.00)	19 (0.42)	1.12

11-03	Gp4	g.chr1:55144951C>A	Missense Mutation	MROH7	p.L689M	maestro heat-like repeat	43 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr6:43025901G>A	Missense Mutation	MRPL2	p.S56F	mitochondrial ribosoma	47 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr10:75011548G>A	Missense Mutation	MRPS16	p.L83F	mitochondrial ribosoma	67 (0.00)	64 (0.78)	2.08
11-03	Gp4	g.chr2:95780930C>T	Missense Mutation	MRPS5	p.G53E	mitochondrial ribosoma	36 (0.00)	20 (0.50)	1.33
11-03	Gp4	g.chr11:60541320G>T	Missense Mutation	MS4A15	p.R170M	membrane-spanning 4-d	26 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr2:48016871C>T	Intron	MSH6		mutS homolog 6	33 (0.00)	50 (0.18)	0.48
11-03	Gp4	g.chr2:48024065C>G	Intron	MSH6		mutS homolog 6	21 (0.00)	26 (0.31)	0.82
11-03	Gp4	g.chr11:62362058G>A	Missense Mutation	MTA2	p.P368L	metastasis associated 1	26 (0.00)	33 (0.36)	0.97
11-03	Gp4	g.chr8:98735246G>T	Missense Mutation	MTDH	p.S498I	metadherin	43 (0.00)	42 (0.36)	0.95
11-03	Gp4	g.chr13:28014300C>T	Missense Mutation	MTIF3	p.D96N	mitochondrial translatio	61 (0.00)	62 (0.48)	1.29
11-03	Gp4	g.chr1:11205075C>G	Missense Mutation	MTOR	p.D1572H	mechanistic target of ra	51 (0.00)	12 (0.50)	1.33
11-03	Gp4	g.chr4:100515939G>T	Nonsense Mutation	MTTP	p.G297*	microsomal triglyceride	38 (0.00)	25 (0.32)	0.85
11-03	Gp4	g.chr7:100637210C>G	Missense Mutation	MUC12	p.S1265R	mucin 12, cell surface a	120 (0.00)	111 (0.16)	0.43
11-03	Gp4	g.chr19:8968941G>A	Nonsense Mutation	MUC16	p.Q14359*	mucin 16, cell surface a	43 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr19:8999488C>T	Missense Mutation	MUC16	p.D13563N	mucin 16, cell surface a	60 (0.00)	26 (0.42)	1.13
11-03	Gp4	g.chr19:9048557G>T	Missense Mutation	MUC16	p.A11025E	mucin 16, cell surface a	59 (0.00)	89 (0.16)	0.42
11-03	Gp4	g.chr19:9060915C>T	Missense Mutation	MUC16	p.R8844H	mucin 16, cell surface a	55 (0.02)	70 (0.21)	0.57
11-03	Gp4	g.chr19:9062469C>G	Missense Mutation	MUC16	p.S8326T	mucin 16, cell surface a	30 (0.03)	59 (0.17)	0.45
11-03	Gp4	g.chr19:9071793G>A	Missense Mutation	MUC16	p.T5218I	mucin 16, cell surface a	16 (0.00)	63 (0.21)	0.55
11-03	Gp4	g.chr19:9073874G>A	Silent	MUC16	p.A4524A	mucin 16, cell surface a	94 (0.01)	56 (0.14)	0.38
11-03	Gp4	g.chr19:9076935G>A	Missense Mutation	MUC16	p.A3504V	mucin 16, cell surface a	97 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr19:9077054C>G	Silent	MUC16	p.L3464L	mucin 16, cell surface a	57 (0.00)	39 (0.15)	0.41
11-03	Gp4	g.chr19:9087611C>A	Missense Mutation	MUC16	p.A1402S	mucin 16, cell surface a	58 (0.00)	45 (0.18)	0.47
11-03	Gp4	g.chr7:100677939C>A	Nonsense Mutation	MUC17	p.S1081*	mucin 17, cell surface a	204 (0.00)	217 (0.17)	0.44
11-03	Gp4	g.chr7:100685680C>T	Silent	MUC17	p.D3661D	mucin 17, cell surface a	62 (0.00)	48 (0.19)	0.50
11-03	Gp4	g.chr11:1266068C>T	Missense Mutation	MUC5B	p.P2653L	mucin 5B, oligomeric m	37 (0.00)	21 (0.38)	1.02
11-03	Gp4	g.chrX:105449868G>T	Missense Mutation	MUM1L1	p.R148M	melanoma associated an	26 (0.00)	18 (0.39)	0.65
11-03	Gp4	g.chr17:74673678C>A	Missense Mutation	MXRA7	p.D203Y	matrix-remodelling asso	27 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr6:135511455G>T	Missense Mutation	MYB	p.W166L	v-myb avian myeloblast	25 (0.00)	32 (0.31)	0.83
11-03	Gp4	g.chr6:135518283C>T	Missense Mutation	MYB	p.P463L	v-myb avian myeloblast	61 (0.00)	45 (0.24)	0.65
11-03	Gp4	g.chr8:67488537G>A	Missense Mutation	MYBL1	p.P392L	v-myb avian myeloblast	65 (0.02)	25 (0.36)	0.96
11-03	Gp4	g.chr15:48443720C>T	Missense Mutation	MYEF2	p.R419H	myelin expression facto	227 (0.00)	101 (0.21)	0.55
11-03	Gp4	g.chr3:108112897G>C	Missense Mutation	MYH15	p.A1767G	myosin, heavy chain 15	29 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr17:10363347G>T	Silent	MYH4	p.I446I	myosin, heavy chain 4,	37 (0.00)	75 (0.19)	0.50
11-03	Gp4	g.chr12:56553426C>A	Nonsense Mutation	MYL6	p.Y29*	myosin, light chain 6, al	16 (0.00)	16 (0.62)	2.08

11-03	Gp4	g.chr5:16683995G>A	Missense Mutation	MYO10	p.P1347L	myosin X	26 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr13:109707912G>T	Missense Mutation	MYO16	p.V1080F	myosin XVI	62 (0.00)	70 (0.16)	0.42
11-03	Gp4	g.chr22:26239732C>A	Missense Mutation	MYO18B	p.P1081H	myosin XVIIIB	40 (0.00)	40 (0.20)	0.53
11-03	Gp4	g.chr12:57437128C>G	Missense Mutation	MYO1A	p.G303R	myosin IA	26 (0.00)	25 (0.20)	0.66
11-03	Gp4	g.chr12:109870767G>A	Missense Mutation	MYO1H	p.R656Q	myosin IH	24 (0.00)	52 (0.13)	0.47
11-03	Gp4	g.chr10:95123745C>T	Silent	MYOF	p.K947K	myoferlin	30 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr10:95147624G>C	Missense Mutation	MYOF	p.T543S	myoferlin	31 (0.00)	13 (0.54)	1.44
11-03	Gp4	g.chr13:21331637C>T	Missense Mutation	N6AMT2	p.G34D	N-6 adenine-specific D	39 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr3:174951955C>A	Silent	NAALADL2	p.L260L	N-acetylated alpha-link	46 (0.00)	42 (0.26)	0.70
11-03	Gp4	g.chr3:174951975C>A	Missense Mutation	NAALADL2	p.S267Y	N-acetylated alpha-link	39 (0.00)	39 (0.44)	1.16
11-03	Gp4	g.chr3:175184951T>A	Silent	NAALADL2	p.I504I	N-acetylated alpha-link	25 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr17:59668264C>A	Missense Mutation	NACA2	p.R93I	nascent polypeptide-ass	25 (0.04)	45 (0.31)	0.83
11-03	Gp4	g.chr7:105913051G>T	Silent	NAMPT	p.V124V	nicotinamide phosphoril	18 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr10:36811959G>A	Missense Mutation	NAMPTL	p.P50S	nicotinamide phosphoril	71 (0.00)	34 (0.44)	1.18
11-03	Gp4	g.chr1:201777941A>T	Silent	NAV1	p.P1336P	neuron navigator 1	69 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr2:204003398G>A	Missense Mutation	NBEAL1	p.S1563N	neurobeachin-like 1	15 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr1:16890558C>T	Silent	NBPF1	p.V1100V	neuroblastoma breakpoi	26 (0.00)	42 (0.43)	1.14
11-03	Gp4	g.chr12:54925308C>T	Nonsense Mutation	NCKAP1L	p.Q880*	NCK-associated protein	54 (0.00)	77 (0.12)	0.39
11-03	Gp4	g.chr8:71039189G>A	Nonsense Mutation	NCOA2	p.Q1259*	nuclear receptor coactiv	23 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr1:54238006G>T	Missense Mutation	NDC1	p.L653M	NDC1 transmembrane	43 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr3:49060174C>T	Missense Mutation	NDUFAF3	p.L104F	NADH dehydrogenase (	32 (0.00)	25 (0.40)	1.07
11-03	Gp4	g.chr2:207008801C>T	Missense Mutation	NDUFS1	p.E310K	NADH dehydrogenase (	86 (0.00)	101 (0.15)	0.40
11-03	Gp4	g.chr2:152342296G>A	Missense Mutation	NEB	p.A8519V	nebulin	70 (0.00)	136 (0.15)	0.41
11-03	Gp4	g.chr2:152370208C>T	Splice Site	NEB		nebulin	35 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr2:152460276T>A	Missense Mutation	NEB	p.K4357M	nebulin	34 (0.00)	28 (0.32)	0.86
11-03	Gp4	g.chr2:152521038C>T	Missense Mutation	NEB	p.A1810T	nebulin	71 (0.00)	30 (0.40)	1.07
11-03	Gp4	g.chr6:11190488C>G	Silent	NEDD9	p.V538V	neural precursor cell ex	31 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr22:29881820G>A	Missense Mutation	NEFH	p.E398K	neurofilament, heavy po	25 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr14:75551363C>T	Silent	NEK9	p.Q948Q	NIMA-related kinase 9	26 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr14:50295891G>A	Silent	NEMF	p.N371N	nuclear export mediator	41 (0.00)	23 (0.30)	0.81
11-03	Gp4	g.chr16:47165899G>A	Silent	NETO2	p.A24A	neuropilin (NRP) and to	24 (0.00)	36 (0.19)	0.52
11-03	Gp4	g.chr11:74717424C>T	Nonsense Mutation	NEU3	p.Q425*	sialidase 3 (membrane s	44 (0.00)	18 (0.28)	0.74
11-03	Gp4	g.chr17:29588754C>T	Missense Mutation	NF1	p.P1535S	neurofibromin 1	27 (0.00)	32 (0.34)	0.92
11-03	Gp4	g.chr16:69681407G>A	Missense Mutation	NFAT5	p.D150N	nuclear factor of activat	51 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr16:69727290C>A	Missense Mutation	NFAT5	p.L1094I	nuclear factor of activat	18 (0.00)	34 (0.15)	0.39

11-03	Gp4	g.chr10:104157084G>T	Missense Mutation	NFKB2	p.V141L	nuclear factor of kappa	26 (0.00)	12 (0.67)	1.78
11-03	Gp4	g.chr9:33307279G>A	Missense Mutation	NFX1	p.C453Y	nuclear transcription fac	17 (0.00)	45 (0.31)	0.83
11-03	Gp4	g.chr9:33311115C>T	Missense Mutation	NFX1	p.P463L	nuclear transcription fac	91 (0.00)	85 (0.15)	0.41
11-03	Gp4	g.chr2:233839353C>A	Missense Mutation	NGEF	p.R83L	neuronal guanine nucleo	57 (0.02)	44 (0.23)	0.61
11-03	Gp4	g.chr5:156899542C>T	Silent	NIPAL4	p.L325L	NIPA-like domain conta	24 (0.00)	42 (0.19)	0.51
11-03	Gp4	g.chr5:156899653G>T	Silent	NIPAL4	p.V362V	NIPA-like domain conta	48 (0.00)	54 (0.30)	0.79
11-03	Gp4	g.chr1:247588641C>G	Nonsense Mutation	NLRP3	p.Y632*	NLR family, pyrin doma	17 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chr5:43655995G>A	Missense Mutation	NNT	p.A705T	nicotinamide nucleotide	17 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr18:31538225G>A	Missense Mutation	NOL4	p.A120V	nucleolar protein 4	31 (0.00)	13 (0.62)	1.64
11-03	Gp4	g.chr9:95076914C>A	Nonsense Mutation	NOL8	p.E665*	nucleolar protein 8	17 (0.00)	38 (0.26)	0.70
11-03	Gp4	g.chr16:18549848C>A	Splice Site	NOMO2	p.G407V	NODAL modulator 2	140 (0.00)	46 (0.17)	0.46
11-03	Gp4	g.chr16:18549930G>A	Nonsense Mutation	NOMO2	p.Q380*	NODAL modulator 2	163 (0.00)	59 (0.19)	0.50
11-03	Gp4	g.chr12:117665406G>A	Missense Mutation	NOS1	p.P1183L	nitric oxide synthase 1 (	17 (0.00)	25 (0.28)	0.98
11-03	Gp4	g.chr16:29394476G>T	Missense Mutation	NPIPB11	p.P593T	nuclear pore complex in	202 (0.00)	18 (0.28)	0.74
11-03	Gp4	g.chr18:11619759C>A	RNA	NPIPB1P		nuclear pore complex in	62 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr9:35800142C>A	Silent	NPR2	p.R371R	natriuretic peptide recep	50 (0.02)	52 (0.17)	0.46
11-03	Gp4	g.chr15:72104681G>T	RNA	NR2E3		nuclear receptor subfam	72 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr5:142779366G>T	Missense Mutation	NR3C1	p.Q347K	nuclear receptor subfam	28 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr14:80164003C>T	Missense Mutation	NRXN3	p.A843V	neurexin 3	27 (0.00)	53 (0.28)	0.75
11-03	Gp4	g.chr5:176694689A>G	Missense Mutation	NSD1	p.E1758G	nuclear receptor binding	32 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr5:176721539C>T	Silent	NSD1	p.D2390D	nuclear receptor binding	61 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr20:1445015C>T	Silent	NSFL1C	p.S54S	NSFL1 (p97) cofactor (	38 (0.00)	22 (0.23)	0.61
11-03	Gp4	g.chr5:6602574G>A	Splice Site	NSUN2	p.A631V	NOP2/Sun RNA methyl	26 (0.00)	46 (0.52)	1.39
11-03	Gp4	g.chr12:104187216G>T	Missense Mutation	NT5DC3	p.L297I	5'-nucleotidase domain	42 (0.00)	56 (0.12)	0.43
11-03	Gp4	g.chr16:77769796C>T	Silent	NUDT7	p.A87A	nudix (nucleoside dipho	30 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr11:47858454T>A	Silent	NUP160	p.R309R	nucleoporin 160kDa	37 (0.00)	35 (0.34)	0.91
11-03	Gp4	g.chr16:67902403G>T	Splice Site	NUTF2		nuclear transport factor	161 (0.00)	47 (0.15)	0.40
11-03	Gp4	g.chr1:224492452C>A	Missense Mutation	NVL	p.D271Y	nuclear VCP-like	62 (0.00)	26 (0.69)	1.85
11-03	Gp4	g.chr14:24880563G>A	Missense Mutation	NYNRIN	p.S850N	NYN domain and retrov	46 (0.00)	22 (0.36)	0.97
11-03	Gp4	g.chr9:131255028C>T	Missense Mutation	ODF2	p.R561C	outer dense fiber of sper	21 (0.00)	18 (0.28)	0.74
11-03	Gp4	g.chr19:15838882C>T	Missense Mutation	OR10H2	p.S10F	olfactory receptor, famil	29 (0.00)	47 (0.15)	0.40
11-03	Gp4	g.chr19:16059893C>T	Missense Mutation	OR10H4	p.P26S	olfactory receptor, famil	26 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr1:159410122C>T	Missense Mutation	OR10J1	p.R192C	olfactory receptor, famil	45 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr12:56030821C>T	Missense Mutation	OR10P1	p.T49I	olfactory receptor, famil	48 (0.02)	32 (0.38)	1.25
11-03	Gp4	g.chr22:16449287A>G	Missense Mutation	OR11H1	p.I173T	olfactory receptor, famil	103 (0.00)	37 (0.19)	0.50

11-03	Gp4	g.chr9:107289226T>C	Missense Mutation	OR13C4	p.K89E	olfactory receptor, famil	85 (0.01)	32 (0.19)	0.50
11-03	Gp4	g.chr1:247902145C>T	Missense Mutation	OR14K1	p.P77S	olfactory receptor, famil	32 (0.00)	42 (0.31)	0.83
11-03	Gp4	g.chr17:2996265C>A	Missense Mutation	OR1D2	p.G9V	olfactory receptor, famil	23 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr9:125424416G>A	Missense Mutation	OR1L1	p.C141Y	olfactory receptor, famil	35 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr9:125486922C>G	Silent	OR1L4	p.S218S	olfactory receptor, famil	43 (0.00)	55 (0.20)	0.53
11-03	Gp4	g.chr11:57970964G>A	Silent	OR1S2	p.S230S	olfactory receptor, famil	29 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr7:143792610G>T	Missense Mutation	OR2A12	p.W137L	olfactory receptor, famil	63 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr7:143747665C>A	Silent	OR2A5	p.P57P	olfactory receptor, famil	19 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr7:99473922C>T	Silent	OR2AE1	p.T245T	olfactory receptor, famil	28 (0.00)	17 (0.71)	1.88
11-03	Gp4	g.chr7:99474171G>A	Silent	OR2AE1	p.I162I	olfactory receptor, famil	35 (0.00)	43 (0.21)	0.56
11-03	Gp4	g.chr12:55968870G>T	Silent	OR2AP1	p.L224L	olfactory receptor, famil	32 (0.00)	50 (0.32)	1.06
11-03	Gp4	g.chr16:3406030C>T	Silent	OR2C1	p.A30A	olfactory receptor, famil	53 (0.00)	69 (0.28)	0.73
11-03	Gp4	g.chr1:248263192C>A	Missense Mutation	OR2L13	p.A172D	olfactory receptor, famil	55 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr1:248756652C>T	Missense Mutation	OR2T10	p.V140I	olfactory receptor, famil	34 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr1:248616180C>T	Missense Mutation	OR2T2	p.L28F	olfactory receptor, famil	88 (0.00)	38 (0.26)	0.70
11-03	Gp4	g.chr11:55135573C>T	Missense Mutation	OR4A15	p.L72F	olfactory receptor, famil	30 (0.00)	20 (0.60)	1.60
11-03	Gp4	g.chr15:102389858G>T	RNA	OR4F13P		olfactory receptor, famil	20 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr11:4968082C>T	Silent	OR51A4	p.V83V	olfactory receptor, famil	21 (0.00)	46 (0.17)	0.46
11-03	Gp4	g.chr11:4388863C>T	Missense Mutation	OR52B4	p.M221I	olfactory receptor, famil	28 (0.00)	48 (0.19)	0.50
11-03	Gp4	g.chr11:5862912G>C	Missense Mutation	OR52E6	p.D72E	olfactory receptor, famil	51 (0.02)	28 (0.32)	0.86
11-03	Gp4	g.chr11:5878442G>T	Missense Mutation	OR52E8	p.P164Q	olfactory receptor, famil	68 (0.00)	57 (0.16)	0.42
11-03	Gp4	g.chr11:5968859C>T	Missense Mutation	OR56A3	p.P95S	olfactory receptor, famil	20 (0.00)	48 (0.33)	0.89
11-03	Gp4	g.chr14:21109599C>A	Silent	OR6S1	p.L84L	olfactory receptor, famil	25 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr7:142750140G>T	Missense Mutation	OR6V1	p.A235S	olfactory receptor, famil	87 (0.00)	68 (0.25)	0.67
11-03	Gp4	g.chr19:9296865G>T	Missense Mutation	OR7D2	p.M136I	olfactory receptor, famil	25 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr19:9225520C>T	Missense Mutation	OR7G1	p.R307K	olfactory receptor, famil	46 (0.00)	56 (0.18)	0.48
11-03	Gp4	g.chr19:9225832C>G	Missense Mutation	OR7G1	p.S203T	olfactory receptor, famil	34 (0.00)	33 (0.27)	0.73
11-03	Gp4	g.chr19:9226308G>T	Silent	OR7G1	p.L44L	olfactory receptor, famil	22 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr11:124266452A>T	Missense Mutation	OR8B3	p.S266T	olfactory receptor, famil	41 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr11:55905102G>A	Silent	OR8J3	p.F31F	olfactory receptor, famil	24 (0.00)	15 (0.53)	1.42
11-03	Gp4	g.chr11:56085843G>C	Missense Mutation	OR8K3	p.A21P	olfactory receptor, famil	28 (0.00)	23 (0.57)	1.51
11-03	Gp4	g.chr11:55927758G>A	Silent	OR8K5	p.F12F	olfactory receptor, famil	17 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr12:48919472G>A	Missense Mutation	OR8S1	p.D20N	olfactory receptor, famil	29 (0.00)	24 (0.21)	0.70
11-03	Gp4	g.chr11:57958075C>T	Missense Mutation	OR9Q2	p.T38I	olfactory receptor, famil	60 (0.00)	36 (0.19)	0.52
11-03	Gp4	g.chr1:52854171G>A	Silent	ORC1	p.N442N	origin recognition comp	17 (0.00)	18 (0.50)	1.33

11-03	Gp4	g.chr12:76791602G>T	Missense Mutation	OSBPL8	p.Q182K	oxysterol binding protei	18 (0.00)	46 (0.17)	0.58
11-03	Gp4	g.chr8:90937611G>C	Missense Mutation	OSGIN2	p.A501P	oxidative stress induced	80 (0.00)	26 (0.46)	1.23
11-03	Gp4	g.chr12:80658958C>T	Missense Mutation	OTOGL	p.P722L	otogelin-like	27 (0.00)	51 (0.14)	0.46
11-03	Gp4	g.chr3:161221622G>C	Missense Mutation	OTOL1	p.W442C	otolin 1	21 (0.00)	26 (0.38)	1.03
11-03	Gp4	g.chr4:146059680G>T	Missense Mutation	OTUD4	p.F749L	OTU deubiquitinase 4	19 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr1:111965624C>G	Missense Mutation	OVGP1	p.R178T	oviductal glycoprotein 1	67 (0.01)	32 (0.59)	1.58
11-03	Gp4	g.chr12:133197883G>A	Silent	P2RX2	p.T316T	purinergic receptor P2X	29 (0.00)	27 (0.44)	1.19
11-03	Gp4	g.chr12:121605329C>T	Silent	P2RX7	p.N261N	purinergic receptor P2X	35 (0.00)	58 (0.22)	0.79
11-03	Gp4	g.chr1:40037021C>T	Splice Site	PABPC4	p.V130M	poly(A) binding protein	36 (0.00)	36 (0.19)	0.52
11-03	Gp4	g.chr11:65998339C>A	Silent	PACS1	p.L518L	phosphofurin acidic clus	21 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr1:17720829G>C	RNA	PADI6		peptidyl arginine deimi	27 (0.00)	16 (0.50)	1.33
11-03	Gp4	g.chr19:39879807C>T	Missense Mutation	PAF1	p.E165K	Paf1, RNA polymerase	34 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr4:57307980C>A	Silent	PAICS	p.I56I	phosphoribosylaminoim	21 (0.00)	25 (0.36)	0.96
11-03	Gp4	g.chrX:110439692C>A	Missense Mutation	PAK3	p.Q426K	p21 protein (Cdc42/Rac	15 (0.00)	17 (0.35)	0.59
11-03	Gp4	g.chr12:56726607C>T	Missense Mutation	PAN2	p.G91E	PAN2 poly(A) specific	24 (0.00)	42 (0.17)	0.55
11-03	Gp4	g.chr13:28794471C>T	Missense Mutation	PAN3	p.S319F	PAN3 poly(A) specific	19 (0.00)	23 (0.30)	0.81
11-03	Gp4	g.chr13:28841269C>A	Silent	PAN3	p.V537V	PAN3 poly(A) specific	24 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr7:4899760G>A	Missense Mutation	PAPOLB	p.A560V	poly(A) polymerase bet	25 (0.00)	24 (0.42)	1.11
11-03	Gp4	g.chr9:118973965C>A	Missense Mutation	PAPPA	p.H558N	pregnancy-associated pl	90 (0.01)	40 (0.17)	0.47
11-03	Gp4	g.chr2:205986379C>A	Missense Mutation	PARD3B	p.Q291K	par-3 family cell polarit	37 (0.00)	34 (0.26)	0.71
11-03	Gp4	g.chr3:122432380G>T	Silent	PARP14	p.V1243V	poly (ADP-ribose) poly	25 (0.00)	48 (0.21)	0.56
11-03	Gp4	g.chr15:65553229G>C	Missense Mutation	PARP16	p.P161R	poly (ADP-ribose) poly	45 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr15:72552916G>A	Missense Mutation	PARP6	p.P220L	poly (ADP-ribose) poly	45 (0.00)	90 (0.18)	0.47
11-03	Gp4	g.chr3:52582194C>A	Missense Mutation	PBRM1	p.W1615L	polybromo 1	71 (0.01)	36 (0.22)	0.59
11-03	Gp4	g.chr3:52582216C>G	Missense Mutation	PBRM1	p.E1608Q	polybromo 1	65 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr3:52620498C>A	Missense Mutation	PBRM1	p.E1125D	polybromo 1	39 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr3:52682447G>C	Nonsense Mutation	PBRM1	p.Y242*	polybromo 1	17 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr3:51992958G>A	Silent	PCBP4	p.I257I	poly(rC) binding protei	20 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr5:140249451G>T	Missense Mutation	PCDHA11	p.A255S	protocadherin alpha 11	87 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr5:140255367A>T	Missense Mutation	PCDHA12	p.I104F	protocadherin alpha 12	114 (0.00)	38 (0.32)	0.84
11-03	Gp4	g.chr5:140186800G>A	Missense Mutation	PCDHA4	p.E10K	protocadherin alpha 4	23 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr5:140201669C>A	Silent	PCDHA5	p.I103I	protocadherin alpha 5	20 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr5:140208536C>T	Missense Mutation	PCDHA6	p.A287V	protocadherin alpha 6	37 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr5:140220935G>A	Missense Mutation	PCDHA8	p.G10E	protocadherin alpha 8	36 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr5:140802433G>A	Missense Mutation	PCDHGA11	p.V547M	protocadherin gamma s	76 (0.01)	76 (0.17)	0.46

11-03	Gp4	g.chr5:140719008C>T	Missense Mutation	PCDHGA2	p.A157V	protocadherin gamma s	87 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr5:140719272C>A	Missense Mutation	PCDHGA2	p.P245H	protocadherin gamma s	22 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr5:140724028G>T	Missense Mutation	PCDHGA3	p.G143V	protocadherin gamma s	57 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr5:140754674G>T	Missense Mutation	PCDHGA6	p.D342Y	protocadherin gamma s	31 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr5:140754748C>T	Silent	PCDHGA6	p.I366I	protocadherin gamma s	59 (0.00)	53 (0.19)	0.50
11-03	Gp4	g.chr5:140740003C>A	Missense Mutation	PCDHGB2	p.L101M	protocadherin gamma s	85 (0.01)	34 (0.15)	0.39
11-03	Gp4	g.chr20:2819117G>A	Missense Mutation	PCED1A	p.P201L	PC-esterase domain con	20 (0.00)	9 (0.56)	1.48
11-03	Gp4	g.chr7:82544631G>A	Missense Mutation	PCLO	p.T4224I	piccolo presynaptic cyt	67 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr20:5098223C>T	Missense Mutation	PCNA	p.V159I	proliferating cell nuclea	42 (0.02)	63 (0.21)	0.55
11-03	Gp4	g.chr9:78947411G>T	Missense Mutation	PCSK5	p.A1518S	proprotein convertase s	69 (0.00)	49 (0.18)	0.49
11-03	Gp4	g.chr9:125582793C>T	Silent	PDCL	p.K159K	phosducin-like	104 (0.00)	81 (0.15)	0.40
11-03	Gp4	g.chr12:54967437G>A	Missense Mutation	PDE1B	p.M295I	phosphodiesterase 1B, c	44 (0.00)	23 (0.22)	0.72
11-03	Gp4	g.chr1:144921956A>T	Missense Mutation	PDE4DIP	p.L495H	phosphodiesterase 4D i	171 (0.00)	88 (0.18)	0.48
11-03	Gp4	g.chr15:85659225G>A	Missense Mutation	PDE8A	p.M470I	phosphodiesterase 8A	102 (0.00)	71 (0.25)	0.68
11-03	Gp4	g.chr4:157693880G>C	Missense Mutation	PDGFC	p.Q221E	platelet derived growth	26 (0.00)	34 (0.32)	0.86
11-03	Gp4	g.chr7:148702387C>T	Silent	PDIA4	p.E456E	protein disulfide isomer	29 (0.00)	26 (0.31)	0.82
11-03	Gp4	g.chr16:15130013G>T	Nonsense Mutation	PDXDC1	p.E750*	pyridoxal-dependent de	26 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr15:77473366C>T	Silent	PEAK1	p.L301L	pseudopodium-enriched	26 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr8:77896404C>A	Missense Mutation	PEX2	p.R4I	peroxisomal biogenesis	46 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr3:179525577C>T	Missense Mutation	PEX5L	p.G521R	peroxisomal biogenesis	39 (0.00)	22 (0.41)	1.09
11-03	Gp4	g.chr12:9086862G>T	Splice Site	PHC1		polyhomeotic homolog	34 (0.00)	67 (0.25)	0.85
11-03	Gp4	g.chr12:9091963C>T	Missense Mutation	PHC1	p.L975F	polyhomeotic homolog	71 (0.00)	24 (0.29)	0.98
11-03	Gp4	g.chr3:169840401C>A	Missense Mutation	PHC3	p.L640F	polyhomeotic homolog	32 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr18:60385153C>A	Intron	PHLPP1		PH domain and leucine	52 (0.00)	35 (0.20)	0.53
11-03	Gp4	g.chr18:60412451C>T	Intron	PHLPP1		PH domain and leucine	41 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr18:60443626C>T	Intron	PHLPP1		PH domain and leucine	36 (0.00)	19 (0.32)	0.84
11-03	Gp4	g.chr18:60463017C>T	Intron	PHLPP1		PH domain and leucine	35 (0.00)	33 (0.76)	2.02
11-03	Gp4	g.chr18:60469438C>T	Intron	PHLPP1		PH domain and leucine	23 (0.00)	24 (0.42)	1.11
11-03	Gp4	g.chr18:60481387G>A	Intron	PHLPP1		PH domain and leucine	29 (0.00)	25 (0.32)	0.85
11-03	Gp4	g.chr18:60518440G>A	Intron	PHLPP1		PH domain and leucine	67 (0.00)	43 (0.28)	0.74
11-03	Gp4	g.chr18:60520265G>A	Intron	PHLPP1		PH domain and leucine	34 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr18:60613020C>A	Intron	PHLPP1		PH domain and leucine	33 (0.00)	44 (0.16)	0.42
11-03	Gp4	g.chr18:60613514G>A	Intron	PHLPP1		PH domain and leucine	17 (0.00)	11 (0.73)	1.94
11-03	Gp4	g.chr18:60617667C>T	Intron	PHLPP1		PH domain and leucine	46 (0.02)	15 (0.80)	2.13
11-03	Gp4	g.chr18:60629368C>T	Intron	PHLPP1		PH domain and leucine	29 (0.00)	40 (0.30)	0.80

11-03	Gp4	g.chr16:71697882C>A	Intron	PHLPP2		PH domain and leucine	21 (0.00)	36 (0.17)	0.44
11-03	Gp4	g.chr16:71741177G>A	Intron	PHLPP2		PH domain and leucine	25 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr7:77569977G>A	Splice Site	PHTF2		putative homeodomain t	22 (0.00)	62 (0.16)	0.43
11-03	Gp4	g.chr22:20390411G>A	RNA	PI4KAP1		phosphatidylinositol 4-k	31 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr15:68468951C>T	Silent	PIAS1	p.T480T	protein inhibitor of activ	35 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr1:172411009C>T	Missense Mutation	PIGC	p.V252I	phosphatidylinositol gly	46 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr1:160000698G>A	Silent	PIGM	p.L278L	phosphatidylinositol gly	60 (0.00)	73 (0.29)	0.77
11-03	Gp4	g.chr12:18715702A>T	Missense Mutation	PIK3C2G	p.Q1178L	phosphatidylinositol-4-p	22 (0.00)	55 (0.22)	0.73
11-03	Gp4	g.chr2:209190185A>G	Missense Mutation	PIKFYVE	p.M884V	phosphoinositide kinase	31 (0.00)	47 (0.40)	1.08
11-03	Gp4	g.chr2:209219914G>T	Splice Site	PIKFYVE	p.G2061V	phosphoinositide kinase	37 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr9:71532526T>C	Silent	PIP5K1B	p.H278H	phosphatidylinositol-4-p	22 (0.00)	29 (0.28)	0.74
11-03	Gp4	g.chr10:3191889G>A	Missense Mutation	PITRM1	p.R599W	pitrilysin metallopeptida	15 (0.00)	20 (0.25)	0.67
11-03	Gp4	g.chr11:94328503C>T	Silent	PIWIL4	p.F393F	piwi-like RNA-mediate	17 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr11:94328505A>T	Missense Mutation	PIWIL4	p.Q394L	piwi-like RNA-mediate	16 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr16:71985626C>A	RNA	PKD1L3		polycystic kidney diseas	52 (0.00)	47 (0.15)	0.40
11-03	Gp4	g.chr16:72013971C>T	RNA	PKD1L3		polycystic kidney diseas	24 (0.00)	30 (0.30)	0.80
11-03	Gp4	g.chr10:102055897G>T	Silent	PKD2L1	p.L446L	polycystic kidney diseas	15 (0.00)	54 (0.28)	0.74
11-03	Gp4	g.chr22:46657785A>G	Missense Mutation	PKDREJ	p.F479L	polycystin (PKD) famil	34 (0.00)	25 (0.28)	0.75
11-03	Gp4	g.chr8:110495331G>A	Nonsense Mutation	PKHD1L1	p.W3191*	polycystic kidney and h	42 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr2:28742574C>T	Missense Mutation	PLB1	p.H63Y	phospholipase B1	46 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr2:28789676G>A	Missense Mutation	PLB1	p.E432K	phospholipase B1	40 (0.00)	28 (0.50)	1.33
11-03	Gp4	g.chr20:8639299A>G	Silent	PLCB1	p.Q270Q	phospholipase C, beta 1	22 (0.00)	54 (0.19)	0.49
11-03	Gp4	g.chr20:9364943C>T	Missense Mutation	PLCB4	p.H317Y	phospholipase C, beta 4	53 (0.00)	19 (0.32)	0.84
11-03	Gp4	g.chr10:95791330G>C	Missense Mutation	PLCE1	p.G176A	phospholipase C, epsilo	35 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr16:81944264G>A	Missense Mutation	PLCG2	p.A625T	phospholipase C, gamm	21 (0.00)	19 (0.42)	1.12
11-03	Gp4	g.chr16:81965173C>A	Missense Mutation	PLCG2	p.P885T	phospholipase C, gamm	38 (0.00)	37 (0.30)	0.79
11-03	Gp4	g.chr3:155241698G>A	Silent	PLCH1	p.F474F	phospholipase C, eta 1	73 (0.00)	17 (0.41)	1.10
11-03	Gp4	g.chr2:198949502C>T	Nonsense Mutation	PLCL1	p.Q421*	phospholipase C-like 1	41 (0.00)	26 (0.31)	0.82
11-03	Gp4	g.chr3:171323160G>A	Missense Mutation	PLD1	p.P939S	phospholipase D1, phos	45 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr12:19436680G>A	Splice Site	PLEKHA5		pleckstrin homology do	23 (0.00)	17 (0.29)	0.99
11-03	Gp4	g.chr12:45567488C>T	RNA	PLEKHA8P1		pleckstrin homology do	44 (0.02)	27 (0.22)	0.75
11-03	Gp4	g.chr10:115540416C>A	Missense Mutation	PLEKHS1	p.S158Y	pleckstrin homology do	89 (0.00)	32 (0.31)	0.83
11-03	Gp4	g.chr19:4511687G>A	Missense Mutation	PLIN4	p.T748I	perilipin 4	64 (0.00)	43 (0.12)	0.39
11-03	Gp4	g.chr19:4512202G>T	Silent	PLIN4	p.A576A	perilipin 4	66 (0.00)	64 (0.16)	0.53
11-03	Gp4	g.chr16:8906932C>T	Missense Mutation	PMM2	p.T176I	phosphomannomutase 2	88 (0.00)	56 (0.16)	0.43

11-03	Gp4	g.chr7:6759285C>G	RNA	PMS2CL		PMS2 C-terminal like p	116 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr6:99848558C>T	Missense Mutation	PNISR	p.R759K	PNN-interacting serine/a	17 (0.00)	15 (0.47)	0.51
11-03	Gp4	g.chr10:118351357C>T	Silent	PNLIPRP1	p.L42L	pancreatic lipase-related	35 (0.03)	43 (0.19)	0.50
11-03	Gp4	g.chr10:118389606G>T	RNA	PNLIPRP2		pancreatic lipase-related	41 (0.00)	59 (0.15)	0.41
11-03	Gp4	g.chr1:151378493C>T	Nonsense Mutation	POGZ	p.W997*	pogo transposable eleme	60 (0.00)	30 (0.30)	0.80
11-03	Gp4	g.chr11:65061712C>T	Silent	POLA2	p.L445L	polymerase (DNA direc	34 (0.00)	15 (0.73)	1.96
11-03	Gp4	g.chr6:43572359C>A	Missense Mutation	POLH	p.L298I	polymerase (DNA direc	26 (0.00)	17 (0.47)	1.25
11-03	Gp4	g.chr3:121240970G>A	Missense Mutation	POLQ	p.P379S	polymerase (DNA direc	67 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr2:86292409C>A	Missense Mutation	POLR1A	p.W682C	polymerase (RNA) I pol	15 (0.00)	18 (0.28)	0.74
11-03	Gp4	g.chr10:79741948C>T	Silent	POLR3A	p.V1241V	polymerase (RNA) III (	16 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr3:43122728G>A	Missense Mutation	POMGNT2	p.H66Y	protein O-linked manno	20 (0.00)	15 (0.53)	1.42
11-03	Gp4	g.chr8:128428991C>T	Nonsense Mutation	POU5F1B	p.R294*	POU class 5 homeobox	95 (0.00)	38 (0.29)	0.77
11-03	Gp4	g.chr12:81746960G>A	Silent	PPFIA2	p.S644S	protein tyrosine phospha	73 (0.00)	80 (0.12)	0.42
11-03	Gp4	g.chr17:57058205A>T	Missense Mutation	PPM1E	p.Q694L	protein phosphatase, Mg	33 (0.00)	30 (0.33)	0.89
11-03	Gp4	g.chr12:111160435C>A	Missense Mutation	PPP1CC	p.D197Y	protein phosphatase 1, c	27 (0.00)	31 (0.26)	0.90
11-03	Gp4	g.chr2:182928474C>T	Missense Mutation	PPP1R1C	p.P73L	protein phosphatase 1, r	36 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr11:111625719C>T	Missense Mutation	PPP2R1B	p.A315T	protein phosphatase 2, r	36 (0.00)	35 (0.49)	1.30
11-03	Gp4	g.chr18:9570610C>T	Missense Mutation	PPP4R1	p.S373N	protein phosphatase 4, r	23 (0.00)	16 (0.62)	1.67
11-03	Gp4	g.chr22:22890612C>T	Silent	PRAME	p.E469E	preferentially expressed	44 (0.00)	16 (0.56)	1.50
11-03	Gp4	g.chr1:12885096C>A	Nonsense Mutation	PRAMEF11	p.E339*	PRAME family member	68 (0.00)	12 (0.50)	1.33
11-03	Gp4	g.chr1:12887442G>A	Missense Mutation	PRAMEF11	p.H139Y	PRAME family member	94 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr1:12836137C>A	Missense Mutation	PRAMEF12	p.P247T	PRAME family member	67 (0.00)	21 (0.33)	0.89
11-03	Gp4	g.chr1:13474934G>A	Missense Mutation	PRAMEF18	p.R399C	PRAME family member	22 (0.00)	10 (0.60)	1.60
11-03	Gp4	g.chr6:106552700C>T	Splice Site	PRDM1	p.T186I	PR domain containing 1	151 (0.00)	69 (0.28)	0.73
11-03	Gp4	g.chr11:129784791G>A	Silent	PRDM10	p.S883S	PR domain containing 1	81 (0.01)	29 (0.21)	0.55
11-03	Gp4	g.chr4:81121376C>T	Missense Mutation	PRDM8	p.H48Y	PR domain containing 8	45 (0.00)	39 (0.15)	0.41
11-03	Gp4	g.chr3:64148728C>T	Silent	PRICKLE2	p.K130K	prickle homolog 2 (Dros	75 (0.00)	62 (0.50)	1.33
11-03	Gp4	g.chr10:52912978G>C	Missense Mutation	PRKG1	p.L122F	protein kinase, cGMP-d	17 (0.00)	14 (0.50)	1.33
11-03	Gp4	g.chr14:23390247C>T	Missense Mutation	PRMT5	p.E594K	protein arginine methylt	37 (0.00)	56 (0.21)	0.57
11-03	Gp4	g.chr14:23393270G>A	Missense Mutation	PRMT5	p.A441V	protein arginine methylt	61 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr17:27031116G>A	Silent	PROCA1	p.P157P	protein interacting with	22 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr14:45576808G>A	Missense Mutation	PRPF39	p.D298N	pre-mRNA processing f	61 (0.00)	23 (0.52)	1.39
11-03	Gp4	g.chr6:4032156C>T	Silent	PRPF4B	p.L135L	pre-mRNA processing f	29 (0.03)	29 (0.28)	0.74
11-03	Gp4	g.chr17:1576829C>A	Missense Mutation	PRPF8	p.R1160L	pre-mRNA processing f	38 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr17:1577779G>A	Missense Mutation	PRPF8	p.R1086C	pre-mRNA processing f	39 (0.00)	92 (0.16)	0.43

11-03	Gp4	g.chr17:1577869G>A	Missense Mutation	PRPF8	p.H1056Y	pre-mRNA processing f	31 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr7:18066805C>A	Nonsense Mutation	PRPS1L1	p.E201*	phosphoribosyl pyropho	82 (0.00)	35 (0.34)	0.91
11-03	Gp4	g.chr22:32109732C>T	Missense Mutation	PRR14L	p.D1365N	proline rich 14-like	38 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr5:126860475C>T	Missense Mutation	PRRC1	p.T119I	proline-rich coiled-coil	28 (0.00)	20 (0.45)	1.20
11-03	Gp4	g.chr1:171509420G>A	Missense Mutation	PRRC2C	p.E937K	proline-rich coiled-coil	48 (0.02)	44 (0.25)	0.67
11-03	Gp4	g.chr1:171509474G>T	Missense Mutation	PRRC2C	p.D955Y	proline-rich coiled-coil	25 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr7:142479858C>A	RNA	PRSS3P2		protease, serine, 3 pseuc	127 (0.01)	33 (0.21)	0.57
11-03	Gp4	g.chr7:142480100C>T	RNA	PRSS3P2		protease, serine, 3 pseuc	78 (0.00)	49 (0.14)	0.38
11-03	Gp4	g.chr3:46783914C>T	Missense Mutation	PRSS45	p.A205T	protease, serine, 45	36 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr9:79322731G>T	Silent	PRUNE2	p.R1487R	prune homolog 2 (Drosc	16 (0.00)	49 (0.14)	0.38
11-03	Gp4	g.chr9:80921287G>T	Missense Mutation	PSAT1	p.C152F	phosphoserine aminotra	40 (0.00)	80 (0.23)	0.60
11-03	Gp4	g.chr5:139213359G>T	Missense Mutation	PSD2	p.A448S	pleckstrin and Sec7 don	63 (0.00)	36 (0.22)	0.59
11-03	Gp4	g.chr19:43772089G>T	Missense Mutation	PSG9	p.P93T	pregnancy specific beta-	42 (0.00)	15 (0.60)	1.60
11-03	Gp4	g.chr16:74338223C>T	Missense Mutation	PSMD7	p.T154I	proteasome (prosome, n	47 (0.00)	45 (0.36)	0.95
11-03	Gp4	g.chr1:11561447G>A	Nonsense Mutation	PTCHD2	p.W133*	patched domain contain	26 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr6:47976800C>T	Silent	PTCHD4	p.V159V	patched domain contain	16 (0.00)	11 (0.55)	1.45
11-03	Gp4	g.chr10:23482786C>T	Missense Mutation	PTF1A	p.S313F	pancreas specific transc	58 (0.00)	51 (0.65)	1.73
11-03	Gp4	g.chr12:112926906C>T	Missense Mutation	PTPN11	p.A509V	protein tyrosine phospha	21 (0.00)	47 (0.13)	0.44
11-03	Gp4	g.chr7:77168543G>A	Intron	PTPN12		protein tyrosine phospha	16 (0.00)	40 (0.20)	0.53
11-03	Gp4	g.chr7:77179387C>T	Intron	PTPN12		protein tyrosine phospha	25 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr7:77193015T>A	Intron	PTPN12		protein tyrosine phospha	39 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr7:77201700G>A	Intron	PTPN12		protein tyrosine phospha	27 (0.00)	37 (0.30)	0.79
11-03	Gp4	g.chr7:77203966C>A	Intron	PTPN12		protein tyrosine phospha	95 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr7:77217973C>T	Intron	PTPN12		protein tyrosine phospha	15 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr7:77239284C>T	Intron	PTPN12		protein tyrosine phospha	53 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr7:77256781C>A	Silent	PTPN12	p.L595L	protein tyrosine phospha	33 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr4:87622657G>A	Missense Mutation	PTPN13	p.A300T	protein tyrosine phospha	71 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr4:87643573C>T	Nonsense Mutation	PTPN13	p.Q532*	protein tyrosine phospha	19 (0.00)	29 (0.55)	1.47
11-03	Gp4	g.chr1:214576281C>A	Nonsense Mutation	PTPN14	p.E176*	protein tyrosine phospha	23 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr12:70964968G>A	Nonsense Mutation	PTPRB	p.Q982*	protein tyrosine phospha	38 (0.00)	35 (0.20)	0.67
11-03	Gp4	g.chr19:55702869C>G	Splice Site	PTPRH	p.S795T	protein tyrosine phospha	36 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr18:8376528G>A	Missense Mutation	PTPRM	p.G1119E	protein tyrosine phospha	58 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr1:29585075C>A	Silent	PTPRU	p.I88I	protein tyrosine phospha	38 (0.03)	28 (0.36)	0.95
11-03	Gp4	g.chr2:61192560G>A	Silent	PUS10	p.F225F	pseudouridylate synthas	34 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr11:125765951G>A	Nonsense Mutation	PUS3	p.Q77*	pseudouridylate synthas	16 (0.00)	28 (0.39)	1.05

11-03	Gp4	g.chr3:110837619G>A	Missense Mutation	PVRL3	p.E184K	poliovirus receptor-relat	20 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr11:32987854C>T	Missense Mutation	QSER1	p.P1531S	glutamine and serine ric	34 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr9:125835889G>T	Missense Mutation	RABGAP1	p.R681M	RAB GTPase activating	45 (0.00)	30 (0.30)	0.80
11-03	Gp4	g.chr9:125835922A>T	Missense Mutation	RABGAP1	p.H692L	RAB GTPase activating	65 (0.00)	42 (0.26)	0.70
11-03	Gp4	g.chr7:100961428T>A	Silent	RABL5	p.L61L		98 (0.00)	50 (0.42)	1.12
11-03	Gp4	g.chr20:55929103G>T	Silent	RAE1	p.L3L	ribonucleic acid export	47 (0.02)	60 (0.15)	0.40
11-03	Gp4	g.chr7:39726328G>C	Missense Mutation	RALA	p.G21A	v-ral simian leukemia vi	22 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr7:39736384G>A	Missense Mutation	RALA	p.A142T	v-ral simian leukemia vi	33 (0.00)	43 (0.19)	0.50
11-03	Gp4	g.chr2:109368406C>A	Missense Mutation	RANBP2	p.Q571K	RAN binding protein 2	83 (0.01)	43 (0.28)	0.74
11-03	Gp4	g.chr2:109384206G>A	Nonsense Mutation	RANBP2	p.W2404*	RAN binding protein 2	161 (0.00)	70 (0.20)	0.53
11-03	Gp4	g.chr6:13639884C>T	Missense Mutation	RANBP9	p.R479Q	RAN binding protein 9	62 (0.00)	48 (0.15)	0.39
11-03	Gp4	g.chr12:69047999A>T	Missense Mutation	RAP1B	p.R97S	RAP1B, member of RA	23 (0.00)	20 (0.30)	1.01
11-03	Gp4	g.chr11:63312292C>G	Nonsense Mutation	RARRES3	p.Y106*	retinoic acid receptor re	37 (0.00)	42 (0.33)	0.89
11-03	Gp4	g.chr9:85640716C>T	Missense Mutation	RASEF	p.M184I	RAS and EF-hand doma	67 (0.00)	55 (0.20)	0.53
11-03	Gp4	g.chr15:38786900G>T	Silent	RASGRP1	p.R648R	RAS guanyl releasing p	25 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr2:33745738G>A	Missense Mutation	RASGRP3	p.D119N	RAS guanyl releasing p	53 (0.00)	44 (0.18)	0.48
11-03	Gp4	g.chr12:26217707G>A	Missense Mutation	RASSF8	p.R127K	Ras association (RalGD	38 (0.00)	42 (0.31)	1.04
11-03	Gp4	g.chr13:48959625G>C	Intron	RB1		retinoblastoma 1	57 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr13:49019253G>C	Intron	RB1		retinoblastoma 1	34 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr13:49020968T>C	Intron	RB1		retinoblastoma 1	98 (0.00)	67 (0.19)	0.52
11-03	Gp4	g.chr8:94746015G>A	Missense Mutation	RBM12B	p.P875L	RNA binding motif prot	98 (0.00)	40 (0.50)	1.33
11-03	Gp4	g.chr4:40440047G>A	Silent	RBM47	p.F288F	RNA binding motif prot	22 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr11:66444217C>T	Missense Mutation	RBM4B	p.D112N	RNA binding motif prot	65 (0.00)	41 (0.27)	0.72
11-03	Gp4	g.chr14:103188726C>A	Silent	RCOR1	p.S464S	REST corepressor 1	50 (0.02)	55 (0.20)	0.53
11-03	Gp4	g.chr4:39301739G>A	Silent	RFC1	p.L905L	replication factor C (acti	24 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr4:39314421G>T	Missense Mutation	RFC1	p.T445K	replication factor C (acti	46 (0.02)	63 (0.27)	0.72
11-03	Gp4	g.chr16:74666481C>T	Missense Mutation	RFWD3	p.S506N	ring finger and WD repe	77 (0.00)	62 (0.16)	0.43
11-03	Gp4	g.chr9:3248035G>A	Silent	RFX3	p.G655G	regulatory factor X, 3 (i	33 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr9:3346698C>T	Missense Mutation	RFX3	p.G62R	regulatory factor X, 3 (i	19 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr15:56388441G>T	Silent	RFX7	p.V398V	regulatory factor X, 7	42 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr8:101059721C>A	Missense Mutation	RGS22	p.G586V	regulator of G-protein si	21 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr17:63149552G>A	Missense Mutation	RGS9	p.V24M	regulator of G-protein si	63 (0.00)	53 (0.32)	0.86
11-03	Gp4	g.chr22:45818243C>T	Silent	RIBC2	p.T137T	RIB43A domain with cc	125 (0.00)	119 (0.15)	0.40
11-03	Gp4	g.chr6:72678707G>A	Silent	RIMS1	p.A62A	regulating synaptic men	76 (0.00)	59 (0.31)	0.81
11-03	Gp4	g.chr8:104778745C>A	Silent	RIMS2	p.A226A	regulating synaptic men	24 (0.00)	25 (0.48)	1.28

11-03	Gp4	g.chr1:40705348C>T	Silent	RLF	p.S1658S	rearranged L-myc fusio	25 (0.00)	44 (0.16)	0.42
11-03	Gp4	g.chrX:73811368G>A	Silent	RLIM	p.V594V	ring finger protein, LIM	15 (0.00)	38 (0.47)	0.79
11-03	Gp4	g.chr2:38231320C>T	Silent	RMDN2	p.F380F	regulator of microtubul	30 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr9:86617431G>T	Silent	RMI1	p.V510V	RecQ mediated genome	44 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chrX:106034405G>A	Missense Mutation	RNF128	p.G365E	ring finger protein 128,	24 (0.00)	42 (0.36)	0.60
11-03	Gp4	g.chr5:158585792G>A	Silent	RNF145	p.S656S	ring finger protein 145	16 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr4:141832342G>A	Missense Mutation	RNF150	p.T385I	ring finger protein 150	25 (0.00)	16 (0.62)	1.67
11-03	Gp4	g.chr17:74150395T>A	Silent	RNF157	p.I593I	ring finger protein 157	20 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr9:104302606C>T	Missense Mutation	RNF20	p.A84V	ring finger protein 20, E	25 (0.00)	13 (0.54)	1.44
11-03	Gp4	g.chr9:104307110G>T	Missense Mutation	RNF20	p.M230I	ring finger protein 20, E	42 (0.00)	41 (0.27)	0.72
11-03	Gp4	g.chr9:104323451A>T	Missense Mutation	RNF20	p.D863V	ring finger protein 20, E	23 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr1:44878363C>T	Silent	RNF220	p.A198A	ring finger protein 220	33 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr3:78700992G>A	Missense Mutation	ROBO1	p.A901V	roundabout, axon guida	32 (0.00)	49 (0.20)	0.54
11-03	Gp4	g.chr3:78701064G>T	Missense Mutation	ROBO1	p.P877H	roundabout, axon guida	26 (0.00)	44 (0.18)	0.48
11-03	Gp4	g.chr20:34288785C>A	Missense Mutation	ROMO1	p.T66N	reactive oxygen species	76 (0.00)	77 (0.31)	0.83
11-03	Gp4	g.chr8:55539476C>T	Silent	RP1	p.L1012L	retinitis pigmentosa 1 (a	71 (0.00)	55 (0.22)	0.58
11-03	Gp4	g.chr16:18810103C>A	Missense Mutation	RP11-1035H1	p.M30I		41 (0.00)	42 (0.33)	0.89
11-03	Gp4	g.chr11:18231398G>A	Missense Mutation	RP11-113D6.1	p.V62I		43 (0.00)	41 (0.29)	0.78
11-03	Gp4	g.chr16:32077314G>A	RNA	RP11-1166P10.6			51 (0.02)	40 (0.17)	0.47
11-03	Gp4	g.chr5:177398567C>A	RNA	RP11-1252I4.2			25 (0.00)	128 (0.26)	0.69
11-03	Gp4	g.chr17:45009477C>T	Missense Mutation	RP11-156P1.2	p.A83V		66 (0.00)	17 (0.35)	0.94
11-03	Gp4	g.chr9:44869117C>T	Missense Mutation	RP11-160N1.1	p.A12V		41 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr7:128108947C>A	RNA	RP11-212P7.3			24 (0.00)	39 (0.26)	0.68
11-03	Gp4	g.chr10:51816552C>A	RNA	RP11-324H6.5			17 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr10:28725815G>A	lincRNA	RP11-351M16.3			63 (0.02)	51 (0.20)	0.52
11-03	Gp4	g.chr3:125509250G>T	lincRNA	RP11-379B18.6			198 (0.00)	71 (0.17)	0.45
11-03	Gp4	g.chr12:25956474G>A	lincRNA	RP11-443N24.2			19 (0.00)	23 (0.26)	0.87
11-03	Gp4	g.chr1:247393974T>C	lincRNA	RP11-488L18.8			34 (0.00)	27 (0.30)	0.79
11-03	Gp4	g.chr3:110612121T>A	Missense Mutation	RP11-553A10.	p.K30M		45 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr3:110612158G>T	Missense Mutation	RP11-553A10.	p.H18N		46 (0.00)	21 (0.33)	0.89
11-03	Gp4	g.chr4:99877244G>T	RNA	RP11-571L19.7			45 (0.00)	36 (0.28)	0.74
11-03	Gp4	g.chr12:56110750C>G	Missense Mutation	RP11-644F5.1	p.T60S		62 (0.00)	35 (0.20)	0.66
11-03	Gp4	g.chr16:32619481C>T	RNA	RP11-652G5.1			25 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr11:82516626G>A	lincRNA	RP11-718B12.2			20 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr12:9716852G>T	RNA	RP11-726G1.1			18 (0.00)	19 (0.37)	1.23

11-03	Gp4	g.chr11:94647215G>C	RNA	RP11-856F16.2			43 (0.00)	37 (0.22)	0.58
11-03	Gp4	g.chr10:27537845C>T	lincRNA	RP11-85G18.6			58 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr20:1559180G>A	Silent	RP4-576H24.4	p.Y79Y		93 (0.00)	68 (0.44)	1.18
11-03	Gp4	g.chr14:21795806C>T	Missense Mutation	RPGRIP1	p.A912V	retinitis pigmentosa GT	66 (0.02)	34 (0.26)	0.71
11-03	Gp4	g.chr16:53698892C>A	Missense Mutation	RPGRIP1L	p.W378L	RPGRIP1-like	36 (0.00)	30 (0.27)	0.71
11-03	Gp4	g.chr22:39713578C>T	Missense Mutation	RPL3	p.V85M	ribosomal protein L3	41 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr2:101620745G>A	Splice Site	RPL31	p.R78K	ribosomal protein L31	39 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr15:66793750C>T	Silent	RPL4	p.E119E	ribosomal protein L4	63 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr3:128344434G>A	Silent	RPN1	p.F446F	ribophorin I	46 (0.02)	39 (0.46)	1.23
11-03	Gp4	g.chr1:150418788G>A	Missense Mutation	RPRD2	p.V261M	regulation of nuclear pr	61 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr1:150443968C>T	Silent	RPRD2	p.N848N	regulation of nuclear pr	33 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr1:114320399C>T	Missense Mutation	RSBN1	p.R470Q	round spermatid basic p	45 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr22:32792073G>A	Silent	RTCB	p.F326F	RNA 2',3'-cyclic phosp	69 (0.00)	54 (0.24)	0.64
11-03	Gp4	g.chr22:32792082G>A	Silent	RTCB	p.S323S	RNA 2',3'-cyclic phosp	72 (0.00)	54 (0.24)	0.64
11-03	Gp4	g.chr15:41766842G>A	Missense Mutation	RTF1	p.E410K	Rtf1, Paf1/RNA polyme	26 (0.00)	31 (0.26)	0.69
11-03	Gp4	g.chr3:46542175G>T	Missense Mutation	RTP3	p.C162F	receptor (chemosensory	16 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr4:71670070G>A	Silent	RUFY3	p.Q552Q	RUN and FYVE domai	28 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr1:237947892C>A	Missense Mutation	RYR2	p.L4294I	ryanodine receptor 2 (ca	27 (0.00)	14 (0.43)	1.14
11-03	Gp4	g.chr15:33831613C>T	Nonsense Mutation	RYR3	p.R166*	ryanodine receptor 3	22 (0.00)	63 (0.22)	0.59
11-03	Gp4	g.chr15:34118467C>T	Missense Mutation	RYR3	p.R3721C	ryanodine receptor 3	59 (0.00)	55 (0.20)	0.53
11-03	Gp4	g.chr15:34127210G>T	Missense Mutation	RYR3	p.R3835S	ryanodine receptor 3	92 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr13:23904448C>T	Missense Mutation	SACS	p.V4523I	sacsin molecular chaper	50 (0.02)	25 (0.20)	0.53
11-03	Gp4	g.chr13:23914732C>T	Missense Mutation	SACS	p.E1095K	sacsin molecular chaper	18 (0.00)	34 (0.21)	0.55
11-03	Gp4	g.chr19:5621404C>T	Missense Mutation	SAFB2	p.V64I	scaffold attachment fact	128 (0.00)	65 (0.17)	0.57
11-03	Gp4	g.chr16:51175937T>A	Missense Mutation	SALL1	p.T66S	spalt-like transcription f	35 (0.00)	18 (0.33)	0.89
11-03	Gp4	g.chr14:21992727C>A	Missense Mutation	SALL2	p.A379S	spalt-like transcription f	50 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr7:92731138T>A	Missense Mutation	SAMD9	p.T1425S	sterile alpha motif doma	49 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr7:92733365G>A	Silent	SAMD9	p.D682D	sterile alpha motif doma	71 (0.00)	58 (0.16)	0.41
11-03	Gp4	g.chr7:92762834G>T	Silent	SAMD9L	p.A817A	sterile alpha motif doma	35 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr12:108938207G>A	Silent	SART3	p.L259L	squamous cell carcinom	63 (0.00)	36 (0.14)	0.48
11-03	Gp4	g.chr21:33069058C>A	Missense Mutation	SCAF4	p.L261F	SR-related CTD-associa	38 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr6:155153172T>A	Missense Mutation	SCAF8	p.V820E	SR-related CTD-associa	23 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr1:41512203G>A	Silent	SCMH1	p.R448R	sex comb on midleg ho	19 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr3:38768514C>G	Missense Mutation	SCN10A	p.L890F	sodium channel, voltage	43 (0.00)	25 (0.32)	0.85
11-03	Gp4	g.chr3:38768529G>A	Silent	SCN10A	p.F885F	sodium channel, voltage	41 (0.00)	23 (0.35)	0.93

11-03	Gp4	g.chr3:38833661T>C	Splice Site	SCN10A		sodium channel, voltage	42 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr2:166245215T>A	Silent	SCN2A	p.I1633I	sodium channel, voltage	22 (0.00)	50 (0.18)	0.48
11-03	Gp4	g.chr2:166003315G>C	Missense Mutation	SCN3A	p.S535R	sodium channel, voltage	64 (0.00)	71 (0.17)	0.45
11-03	Gp4	g.chr12:52162966C>T	Silent	SCN8A	p.S1073S	sodium channel, voltage	28 (0.00)	17 (0.41)	0.85
11-03	Gp4	g.chr12:52180584G>A	Missense Mutation	SCN8A	p.A1401T	sodium channel, voltage	97 (0.00)	82 (0.20)	0.40
11-03	Gp4	g.chr2:167141181C>T	Missense Mutation	SCN9A	p.G586S	sodium channel, voltage	44 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr11:9096158C>A	Silent	SCUBE2	p.V129V	signal peptide, CUB do	88 (0.01)	21 (0.29)	0.76
11-03	Gp4	g.chr1:169822862T>A	Missense Mutation	SCYL3	p.N741Y	SCY1-like 3 (S. cerevisi	48 (0.00)	59 (0.19)	0.50
11-03	Gp4	g.chr10:121692579A>G	Missense Mutation	SEC23IP	p.M941V	SEC23 interacting prote	20 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr15:49325161C>T	Splice Site	SECISBP2L		SECIS binding protein	71 (0.00)	75 (0.19)	0.50
11-03	Gp4	g.chr14:81952694G>A	Silent	SEL1L	p.L579L	sel-1 suppressor of lin-1	106 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr2:74902898G>A	Missense Mutation	SEMA4F	p.R502H	sema domain, immunog	60 (0.02)	41 (0.37)	0.98
11-03	Gp4	g.chr5:9066540G>T	Silent	SEMA5A	p.S764S	sema domain, seven thr	56 (0.00)	41 (0.15)	0.39
11-03	Gp4	g.chr14:94844798G>T	Silent	SERPINA1	p.P415P	serpin peptidase inhibit	16 (0.00)	14 (0.93)	2.48
11-03	Gp4	g.chr3:47144880G>A	Missense Mutation	SETD2	p.R1625C	SET domain containing	19 (0.00)	26 (0.35)	0.92
11-03	Gp4	g.chr3:9488972G>A	Missense Mutation	SETD5	p.R588Q	SET domain containing	45 (0.02)	23 (0.61)	1.62
11-03	Gp4	g.chr1:150933049G>A	Silent	SETDB1	p.L837L	SET domain, bifurcated	19 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr9:135218141C>A	Missense Mutation	SETX	p.C145F	senataxin	18 (0.00)	54 (0.15)	0.40
11-03	Gp4	g.chr17:27286396A>T	Silent	SEZ6	p.G622G	seizure related 6 homol	23 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr22:31979931T>A	Nonsense Mutation	SFI1	p.L409*	Sfi1 homolog, spindle a	16 (0.00)	26 (0.73)	1.95
11-03	Gp4	g.chr12:132212866C>T	Missense Mutation	SFSWAP	p.P325L	splicing factor, suppress	43 (0.00)	70 (0.13)	0.45
11-03	Gp4	g.chr10:102794598C>T	Silent	SFXN3	p.I49I	sideroflexin 3	48 (0.00)	39 (0.26)	0.68
11-03	Gp4	g.chr10:120917425G>A	Silent	SFXN4	p.A143A	sideroflexin 4	26 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr10:72604314G>T	Nonsense Mutation	SGPL1	p.E38*	sphingosine-1-phosphat	27 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr22:40797615G>A	Missense Mutation	SGSM3	p.C9Y	small G protein signalin	17 (0.00)	47 (0.17)	0.45
11-03	Gp4	g.chr15:84237329G>A	Missense Mutation	SH3GL3	p.G79E	SH3-domain GRB2-like	21 (0.00)	21 (0.24)	0.63
11-03	Gp4	g.chr4:170189980G>T	Silent	SH3RF1	p.P128P	SH3 domain containing	27 (0.00)	22 (0.36)	0.97
11-03	Gp4	g.chr19:51200901T>C	Missense Mutation	SHANK1	p.K628E	SH3 and multiple ankyr	23 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr3:72802256C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	28 (0.00)	44 (0.18)	0.48
11-03	Gp4	g.chr3:72820001C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	28 (0.00)	11 (0.45)	1.21
11-03	Gp4	g.chr3:72835821G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	54 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr3:72840422C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	28 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr3:72866404G>A	Missense Mutation	SHQ1	p.R287C	SHQ1, H/ACA ribonucl	21 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr3:72867355G>C	Intron	SHQ1		SHQ1, H/ACA ribonucl	31 (0.00)	51 (0.16)	0.42
11-03	Gp4	g.chr3:72876197G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	63 (0.02)	23 (0.26)	0.70

11-03	Gp4	g.chr3:72896102C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	22 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr3:72897315G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	33 (0.00)	23 (0.96)	2.55
11-03	Gp4	g.chr4:77660974G>A	Missense Mutation	SHROOM3	p.A550T	shroom family member	34 (0.00)	15 (0.67)	1.78
11-03	Gp4	g.chr3:164760867G>A	Missense Mutation	SI	p.H662Y	sucrase-isomaltase (alph	19 (0.00)	39 (0.21)	0.55
11-03	Gp4	g.chr3:113321931C>T	Silent	SIDT1	p.S399S	SID1 transmembrane fa	18 (0.00)	27 (0.52)	1.38
11-03	Gp4	g.chr19:51769062G>T	Silent	SIGLECL1	p.V112V	SIGLEC family like 1	81 (0.01)	100 (0.19)	0.51
11-03	Gp4	g.chr11:116734442G>A	Missense Mutation	SIK3	p.A634V	SIK family kinase 3	24 (0.00)	11 (0.64)	1.70
11-03	Gp4	g.chr1:232600850A>G	Silent	SIPA1L2	p.I852I	signal-induced prolifera	34 (0.00)	51 (0.20)	0.52
11-03	Gp4	g.chr1:232601124C>G	Missense Mutation	SIPA1L2	p.G761A	signal-induced prolifera	51 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr20:1903108G>C	Missense Mutation	SIRPA	p.V302L	signal-regulatory protein	84 (0.00)	31 (0.48)	1.29
11-03	Gp4	g.chr13:21742236C>T	Missense Mutation	SKA3	p.D212N	spindle and kinetochore	53 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr15:68118514C>T	Silent	SKOR1	p.I302I	SKI family transcription	15 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr13:103718389C>T	Missense Mutation	SLC10A2	p.G71S	solute carrier family 10	17 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr15:48594964G>A	Missense Mutation	SLC12A1	p.R1061K	solute carrier family 12	114 (0.01)	27 (0.19)	0.49
11-03	Gp4	g.chr12:16397695G>A	Missense Mutation	SLC15A5	p.A265V	solute carrier family 15,	28 (0.00)	40 (0.15)	0.50
11-03	Gp4	g.chr12:60165054C>T	Missense Mutation	SLC16A7	p.A91V	solute carrier family 16	36 (0.00)	39 (0.36)	1.19
11-03	Gp4	g.chr19:49938517C>T	Silent	SLC17A7	p.E114E	solute carrier family 17	59 (0.00)	53 (0.30)	0.81
11-03	Gp4	g.chr11:35339048G>A	Silent	SLC1A2	p.P2P	solute carrier family 1 (g	27 (0.00)	29 (0.52)	1.38
11-03	Gp4	g.chr11:62984861G>A	Missense Mutation	SLC22A25	p.A252V	solute carrier family 22,	31 (0.00)	24 (0.33)	0.89
11-03	Gp4	g.chr3:48929501C>T	Missense Mutation	SLC25A20	p.R37Q	solute carrier family 25	15 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr1:108700228C>A	Silent	SLC25A24	p.G156G	solute carrier family 25	27 (0.00)	32 (0.22)	0.58
11-03	Gp4	g.chr15:45562400C>T	Missense Mutation	SLC28A2	p.A525V	solute carrier family 28	49 (0.02)	42 (0.19)	0.51
11-03	Gp4	g.chr12:40441927G>A	Silent	SLC2A13	p.L214L	solute carrier family 2 (f	56 (0.00)	19 (0.37)	1.24
11-03	Gp4	g.chr1:1601543C>A	Missense Mutation	SLC35E2B	p.R252M	solute carrier family 35,	32 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr12:46598126A>G	Silent	SLC38A1	p.N260N	solute carrier family 38,	16 (0.00)	17 (0.41)	1.39
11-03	Gp4	g.chr5:54929695C>T	Silent	SLC38A9	p.L376L	solute carrier family 38,	31 (0.00)	22 (0.32)	0.85
11-03	Gp4	g.chr18:33694112C>G	Missense Mutation	SLC39A6	p.W597C	solute carrier family 39	23 (0.00)	38 (0.21)	0.56
11-03	Gp4	g.chr2:162799378G>A	Missense Mutation	SLC4A10	p.D692N	solute carrier family 4, s	34 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr12:85266943A>G	Silent	SLC6A15	p.T237T	solute carrier family 6 (r	31 (0.00)	32 (0.16)	0.52
11-03	Gp4	g.chr3:170198520G>A	Silent	SLC7A14	p.T517T	solute carrier family 7, r	66 (0.02)	15 (0.67)	1.78
11-03	Gp4	g.chr14:23249169C>T	Silent	SLC7A7	p.A197A	solute carrier family 7 (a	33 (0.03)	47 (0.15)	0.40
11-03	Gp4	g.chr2:103148885C>T	Missense Mutation	SLC9A4	p.P712L	solute carrier family 9, s	45 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr16:67291323G>A	Missense Mutation	SLC9A5	p.E471K	solute carrier family 9, s	46 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr12:98849670C>A	RNA	SLC9A7P1		solute carrier family 9, s	40 (0.00)	13 (0.62)	2.10
11-03	Gp4	g.chr17:33679542C>G	Missense Mutation	SLFN11	p.D847H	schlafen family member	62 (0.00)	20 (0.40)	1.07

11-03	Gp4	g.chr4:20568908G>A	Missense Mutation	SLIT2	p.A917T	slit homolog 2 (Drosoph	28 (0.04)	17 (0.41)	1.10
11-03	Gp4	g.chr5:168244389C>T	Missense Mutation	SLIT3	p.G237S	slit homolog 3 (Drosoph	28 (0.00)	25 (0.48)	1.28
11-03	Gp4	g.chr13:88329349G>A	Missense Mutation	SLITRK5	p.C569Y	SLIT and NTRK-like fa	38 (0.00)	37 (0.24)	0.65
11-03	Gp4	g.chr20:43881723C>T	Missense Mutation	SLPI	p.C105Y	secretory leukocyte pept	38 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr20:43881788C>T	Silent	SLPI	p.R83R	secretory leukocyte pept	53 (0.00)	30 (0.33)	0.89
11-03	Gp4	g.chr5:159833525C>T	Missense Mutation	SLU7	p.A413T	SLU7 splicing factor ho	24 (0.00)	23 (0.35)	0.93
11-03	Gp4	g.chr18:48597013C>A	Intron	SMAD4		SMAD family member	42 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr4:95174131C>T	Silent	SMARCAD1	p.L418L	SWI/SNF-related, matri	32 (0.00)	24 (0.38)	1.00
11-03	Gp4	g.chr17:18220807G>A	Silent	SMCR8	p.E568E	Smith-Magenis syndron	41 (0.00)	33 (0.33)	0.89
11-03	Gp4	g.chr16:18845577C>A	Missense Mutation	SMG1	p.M2838I	SMG1 phosphatidylinos	24 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr17:57290884G>T	Silent	SMG8	p.L900L	SMG8 nonsense mediat	67 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr2:88367396A>G	Missense Mutation	SMYD1	p.R5G	SET and MYND domai	20 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr17:1687672G>A	Silent	SMYD4	p.D656D	SET and MYND domai	41 (0.00)	34 (0.26)	0.71
11-03	Gp4	g.chr17:1687716C>A	Nonsense Mutation	SMYD4	p.E642*	SET and MYND domai	45 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr17:47018293C>G	Silent	SNF8	p.P79P	SNF8, ESCRT-II compl	34 (0.00)	45 (0.42)	1.13
11-03	Gp4	g.chr15:25335176C>A	RNA	SNHG14		small nucleolar RNA ho	98 (0.00)	42 (0.38)	1.02
11-03	Gp4	g.chr2:96957167G>A	Missense Mutation	SNRNP200	p.T795I	small nuclear ribonucle	81 (0.00)	51 (0.16)	0.42
11-03	Gp4	g.chr1:31742050C>A	Missense Mutation	SNRNP40	p.E271D	small nuclear ribonucle	49 (0.00)	61 (0.16)	0.44
11-03	Gp4	g.chr20:16721549G>A	Missense Mutation	SNRPB2	p.E193K	small nuclear ribonucle	18 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr20:17923754C>G	Splice Site	SNX5	p.R388S	sorting nexin 5	61 (0.00)	37 (0.27)	0.72
11-03	Gp4	g.chr20:17923758G>A	Missense Mutation	SNX5	p.A387V	sorting nexin 5	60 (0.00)	36 (0.25)	0.67
11-03	Gp4	g.chr18:67992132G>A	Silent	SOCS6	p.T76T	suppressor of cytokine s	80 (0.00)	94 (0.21)	0.57
11-03	Gp4	g.chr20:35443539G>A	Missense Mutation	SOGA1	p.S769L	suppressor of glucose, a	66 (0.00)	65 (0.23)	0.62
11-03	Gp4	g.chr21:34924773C>T	Missense Mutation	SON	p.A1079V	SON DNA binding prot	20 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr10:97101048G>A	Silent	SORBS1	p.F888F	sorbin and SH3 domain	42 (0.02)	36 (0.19)	0.52
11-03	Gp4	g.chr11:16007806C>T	Silent	SOX6	p.E689E	SRY (sex determining r	66 (0.00)	61 (0.30)	0.79
11-03	Gp4	g.chr2:174819887C>T	Silent	SP3	p.Q451Q	Sp3 transcription factor	25 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr1:118583395C>A	Missense Mutation	SPAG17	p.D1042Y	sperm associated antige	30 (0.00)	27 (0.26)	0.69
11-03	Gp4	g.chr1:118642275G>A	Silent	SPAG17	p.H261H	sperm associated antige	64 (0.00)	33 (0.21)	0.57
11-03	Gp4	g.chr17:26911675G>A	Missense Mutation	SPAG5	p.A719V	sperm associated antige	44 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr9:40702756C>T	Missense Mutation	SPATA31A3	p.S138F	SPATA31 subfamily A,	54 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr9:43625020G>T	Missense Mutation	SPATA31A6	p.H1223N	SPATA31 subfamily A,	159 (0.00)	87 (0.16)	0.43
11-03	Gp4	g.chr9:84608056G>T	Nonsense Mutation	SPATA31D1	p.E891*	SPATA31 subfamily D,	24 (0.00)	49 (0.16)	0.44
11-03	Gp4	g.chr15:97328261C>A	Nonsense Mutation	SPATA8	p.S37*	spermatogenesis associa	42 (0.00)	21 (0.43)	1.14
11-03	Gp4	g.chr6:44344786C>T	Missense Mutation	SPATS1	p.P297S	spermatogenesis associa	21 (0.00)	45 (0.16)	0.41

11-03	Gp4	g.chr22:24718338G>A	Missense Mutation	SPECC1L	p.E464K	sperm antigen with calp	47 (0.02)	29 (0.34)	0.92
11-03	Gp4	g.chr2:228883162C>A	Missense Mutation	SPHKAP	p.G803V	SPHK1 interactor, AKA	53 (0.02)	17 (0.29)	0.78
11-03	Gp4	g.chr5:147693703T>A	Missense Mutation	SPINK7	p.I43N	serine peptidase inhibit	121 (0.00)	109 (0.25)	0.66
11-03	Gp4	g.chr17:47687919G>A	Intron	SPOP		speckle-type POZ protei	65 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr17:47688813C>T	Missense Mutation	SPOP	p.V163I	speckle-type POZ protei	76 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr17:47753836C>T	Intron	SPOP		speckle-type POZ protei	39 (0.00)	18 (0.28)	0.74
11-03	Gp4	g.chr12:53462013G>T	Missense Mutation	SPRYD3	p.R294S	SPRY domain containin	64 (0.00)	15 (0.47)	0.97
11-03	Gp4	g.chr1:158615088C>A	Missense Mutation	SPTA1	p.A1362S	spectrin, alpha, erythroc	19 (0.00)	13 (0.46)	1.23
11-03	Gp4	g.chr2:54858518G>A	Missense Mutation	SPTBN1	p.D1112N	spectrin, beta, non-eryth	55 (0.00)	17 (0.59)	1.57
11-03	Gp4	g.chr2:54891682C>A	Silent	SPTBN1	p.T2171T	spectrin, beta, non-eryth	22 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr5:79617046C>T	Missense Mutation	SPZ1	p.L338F	spermatogenic leucine z	55 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr2:45620101C>T	Missense Mutation	SRBD1	p.S894N	S1 RNA binding domai	31 (0.00)	31 (0.29)	0.77
11-03	Gp4	g.chr2:45826628C>G	Missense Mutation	SRBD1	p.S203T	S1 RNA binding domai	41 (0.00)	77 (0.23)	0.62
11-03	Gp4	g.chr5:65466776G>A	Splice Site	SREK1		splicing regulatory gluta	27 (0.00)	52 (0.46)	1.23
11-03	Gp4	g.chr6:35837309G>A	Missense Mutation	SRPK1	p.P454L	SRSF protein kinase 1	84 (0.00)	76 (0.20)	0.53
11-03	Gp4	g.chr1:24993341C>T	Missense Mutation	SRRM1	p.T555I	serine/arginine repetitiv	17 (0.00)	23 (0.65)	1.74
11-03	Gp4	g.chr12:120901828C>A	Missense Mutation	SRSF9	p.M149I	serine/arginine-rich spli	61 (0.00)	86 (0.14)	0.49
11-03	Gp4	g.chrX:48054258C>G	Missense Mutation	SSX5	p.E75D	synovial sarcoma, X bre	64 (0.00)	17 (0.47)	0.78
11-03	Gp4	g.chr8:53079547C>A	Splice Site	ST18		suppression of tumorige	27 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr1:44303918A>C	Silent	ST3GAL3	p.A79A	ST3 beta-galactoside al	79 (0.00)	68 (0.32)	0.86
11-03	Gp4	g.chr12:57642566G>A	Missense Mutation	STAC3	p.R119C	SH3 and cysteine rich d	156 (0.01)	127 (0.28)	0.94
11-03	Gp4	g.chrX:123164909C>T	Silent	STAG2	p.H74H	stromal antigen 2	38 (0.00)	23 (0.57)	0.94
11-03	Gp4	g.chr7:99794865G>A	Missense Mutation	STAG3	p.S343N	stromal antigen 3	36 (0.00)	38 (0.26)	0.70
11-03	Gp4	g.chr13:33859651C>T	Missense Mutation	STARD13	p.S42N	StAR-related lipid trans	70 (0.00)	27 (0.37)	0.39
11-03	Gp4	g.chr2:96859041T>A	Missense Mutation	STARD7	p.E200V	StAR-related lipid trans	55 (0.00)	33 (0.48)	1.29
11-03	Gp4	g.chr15:42953376C>A	Silent	STARD9	p.L241L	StAR-related lipid trans	21 (0.00)	18 (0.67)	1.78
11-03	Gp4	g.chr20:47740955C>A	Missense Mutation	STAU1	p.R260L	staufen double-stranded	164 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr7:89859263G>A	Missense Mutation	STEAP2	p.M366I	STEAP family member	23 (0.00)	31 (0.39)	1.03
11-03	Gp4	g.chr1:47746327G>A	Silent	STIL	p.N601N	SCL/TAL1 interrupting	24 (0.00)	19 (0.53)	1.40
11-03	Gp4	g.chr5:171481676C>A	Missense Mutation	STK10	p.R850M	serine/threonine kinase	55 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr2:48809086G>T	Silent	STON1	p.V438V	stonin 1	37 (0.00)	33 (0.30)	0.81
11-03	Gp4	g.chr14:81744357C>T	Missense Mutation	STON2	p.R433K	stonin 2	76 (0.00)	19 (0.74)	1.96
11-03	Gp4	g.chr7:129125652G>A	Silent	STRIP2	p.E829E	striatin interacting prote	26 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chr11:125479349G>A	Missense Mutation	STT3A	p.G328R	STT3A, subunit of the o	37 (0.00)	19 (0.68)	1.82
11-03	Gp4	g.chr19:19114995G>T	Missense Mutation	SUGP2	p.L971I	SURP and G patch dom	26 (0.00)	39 (0.44)	1.16

11-03	Gp4	g.chr8:70514018C>T	Missense Mutation	SULF1	p.R339C	sulfatase 1	61 (0.02)	51 (0.16)	0.42
11-03	Gp4	g.chr14:21831067C>A	Silent	SUPT16H	p.L517L	suppressor of Ty 16 hon	31 (0.00)	36 (0.31)	0.81
11-03	Gp4	g.chr14:21831107C>A	Splice Site	SUPT16H		suppressor of Ty 16 hon	33 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr17:56423627C>G	Missense Mutation	SUPT4H1	p.D71H	suppressor of Ty 4 hom	18 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr9:113166761G>T	Missense Mutation	SVEP1	p.P3148H	sushi, von Willebrand fa	33 (0.00)	73 (0.16)	0.44
11-03	Gp4	g.chr9:113170331C>A	Nonsense Mutation	SVEP1	p.G2494*	sushi, von Willebrand fa	29 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr1:185191113C>T	Missense Mutation	SWT1	p.H752Y	SWT1 RNA endoribonu	64 (0.02)	62 (0.18)	0.47
11-03	Gp4	g.chr6:10955381C>A	Missense Mutation	SYCP2L	p.Q663K	synaptonemal complex	42 (0.00)	61 (0.28)	0.74
11-03	Gp4	g.chr1:85648161G>C	Missense Mutation	SYDE2	p.R722G	synapse defective 1, Rh	23 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr1:85648614G>A	Missense Mutation	SYDE2	p.H571Y	synapse defective 1, Rh	103 (0.00)	63 (0.14)	0.38
11-03	Gp4	g.chr6:152454486G>A	Silent	SYNE1	p.L8642L	spectrin repeat containin	38 (0.00)	81 (0.33)	0.89
11-03	Gp4	g.chr6:152470649C>T	Missense Mutation	SYNE1	p.R8202H	spectrin repeat containin	42 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr6:152651080C>A	Missense Mutation	SYNE1	p.D4914Y	spectrin repeat containin	24 (0.00)	26 (0.27)	0.72
11-03	Gp4	g.chr6:152665287G>A	Missense Mutation	SYNE1	p.L4052F	spectrin repeat containin	42 (0.00)	41 (0.22)	0.59
11-03	Gp4	g.chr14:64610501G>T	Missense Mutation	SYNE2	p.M5023I	spectrin repeat containin	20 (0.00)	30 (0.20)	0.53
11-03	Gp4	g.chr21:34014273C>T	Missense Mutation	SYNJ1	p.R1213H	synaptojanin 1	15 (0.00)	48 (0.19)	0.50
11-03	Gp4	g.chr14:70842449C>G	Missense Mutation	SYNJ2BP	p.A81P	synaptojanin 2 binding p	30 (0.00)	47 (0.30)	0.79
11-03	Gp4	g.chr5:150028147G>A	Missense Mutation	SYNPO	p.V104I	synaptopodin	65 (0.00)	24 (0.62)	1.67
11-03	Gp4	g.chr6:132910619G>A	Silent	TAAR5	p.T69T	trace amine associated r	60 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr17:61683795G>T	Missense Mutation	TACO1	p.K170N	translational activator o	69 (0.00)	51 (0.16)	0.42
11-03	Gp4	g.chr4:104510923G>C	Silent	TACR3	p.G438G	tachykinin receptor 3	37 (0.00)	31 (0.35)	0.95
11-03	Gp4	g.chr11:6632450C>T	Silent	TAF10	p.T179T	TAF10 RNA polymeras	44 (0.00)	25 (0.20)	0.53
11-03	Gp4	g.chr1:222761874G>T	Missense Mutation	TAF1A	p.P11H	TATA box binding prot	33 (0.00)	29 (0.34)	0.92
11-03	Gp4	g.chr9:32634324G>A	Silent	TAF1L	p.D418D	TAF1 RNA polymerase	31 (0.00)	32 (0.31)	0.83
11-03	Gp4	g.chr9:32635303G>A	Missense Mutation	TAF1L	p.A92V	TAF1 RNA polymerase	75 (0.00)	42 (0.17)	0.44
11-03	Gp4	g.chr1:229730539G>T	Missense Mutation	TAF5L	p.H425Q	TAF5-like RNA polyme	54 (0.00)	55 (0.15)	0.39
11-03	Gp4	g.chr17:61483602G>A	Missense Mutation	TANC2	p.G1111S	tetratricopeptide repeat,	45 (0.00)	26 (0.31)	0.82
11-03	Gp4	g.chr16:68961546C>G	Missense Mutation	TANGO6	p.P735A	transport and golgi orga	36 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr7:122635565G>A	Silent	TAS2R16	p.L42L	taste receptor, type 2, m	16 (0.00)	10 (0.50)	1.33
11-03	Gp4	g.chr7:141673310G>T	Silent	TAS2R38	p.L60L	taste receptor, type 2, m	50 (0.00)	33 (0.27)	0.73
11-03	Gp4	g.chr12:11244090T>A	Missense Mutation	TAS2R43	p.I247L	taste receptor, type 2, m	151 (0.00)	91 (0.21)	0.70
11-03	Gp4	g.chr22:47308023C>A	Nonsense Mutation	TBC1D22A	p.Y318*	TBC1 domain family, m	29 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr12:65268882G>A	Missense Mutation	TBC1D30	p.A534T	TBC1 domain family, m	59 (0.00)	59 (0.19)	0.63
11-03	Gp4	g.chr2:101652523G>T	Silent	TBC1D8	p.G505G	TBC1 domain family, m	53 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr4:141578934G>A	Silent	TBC1D9	p.L652L	TBC1 domain family, m	65 (0.00)	52 (0.58)	1.54

11-03	Gp4	g.chr14:92251607C>G	Missense Mutation	TC2N	p.E421Q	tandem C2 domains, nu	18 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr3:44399328C>T	Missense Mutation	TCAIM	p.A42V	T cell activation inhibit	29 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr5:149755893G>T	Splice Site	TCOF1	p.Q714H	Treacher Collins-France	42 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr6:46657044C>T	Silent	TDRD6	p.V393V	tudor domain containing	28 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr6:46657276G>A	Missense Mutation	TDRD6	p.E471K	tudor domain containing	53 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr9:100243214C>A	Missense Mutation	TDRD7	p.S802R	tudor domain containing	79 (0.00)	34 (0.21)	0.55
11-03	Gp4	g.chr4:183675778G>A	Missense Mutation	TENM3	p.E1420K	teneurin transmembrane	50 (0.00)	36 (0.28)	0.74
11-03	Gp4	g.chr4:183713840C>A	Missense Mutation	TENM3	p.F2005L	teneurin transmembrane	121 (0.00)	76 (0.14)	0.39
11-03	Gp4	g.chr11:78380714G>A	Silent	TENM4	p.L2226L	teneurin transmembrane	70 (0.00)	51 (0.20)	0.52
11-03	Gp4	g.chr11:78412725G>A	Missense Mutation	TENM4	p.P1645S	teneurin transmembrane	16 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr14:20841282G>A	Missense Mutation	TEP1	p.S2172F	telomerase-associated p	19 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr5:1282571C>T	Nonsense Mutation	TERT	p.W581*	telomerase reverse trans	21 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr7:115891853C>A	Missense Mutation	TES	p.P248T	testis derived transcript	63 (0.02)	31 (0.48)	1.29
11-03	Gp4	g.chr4:106196661A>G	Missense Mutation	TET2	p.D1665G	tet methylcytosine diox	48 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr19:43920655C>T	Silent	TEX101	p.F131F	testis expressed 101	46 (0.00)	73 (0.15)	0.40
11-03	Gp4	g.chr17:56690796C>A	Missense Mutation	TEX14	p.V337F	testis expressed 14	41 (0.00)	44 (0.18)	0.48
11-03	Gp4	g.chr15:39885733C>A	Missense Mutation	THBS1	p.T1044N	thrombospondin 1	22 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr17:38240965C>A	Missense Mutation	THRA	p.P158Q	thyroid hormone recept	22 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr1:36766534C>T	Missense Mutation	THRAP3	p.S784F	thyroid hormone recept	36 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr1:36767216C>T	Silent	THRAP3	p.N855N	thyroid hormone recept	41 (0.00)	42 (0.24)	0.63
11-03	Gp4	g.chr7:11450854C>T	Missense Mutation	THSD7A	p.D1260N	thrombospondin, type I,	70 (0.00)	23 (0.48)	1.28
11-03	Gp4	g.chr3:9425899G>T	Missense Mutation	THUMPD3	p.M413I	THUMP domain contai	32 (0.00)	30 (0.33)	0.89
11-03	Gp4	g.chr11:134118811G>T	Missense Mutation	THYN1	p.L175M	thymocyte nuclear prote	42 (0.00)	22 (0.41)	1.09
11-03	Gp4	g.chr10:121337234A>T	Missense Mutation	TIAL1	p.L191M	TIA1 cytotoxic granule-	24 (0.00)	55 (0.15)	0.39
11-03	Gp4	g.chr10:121342065G>A	Missense Mutation	TIAL1	p.T45I	TIA1 cytotoxic granule-	47 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr15:90164642C>A	Missense Mutation	TICRR	p.P1058Q	TOPBP1-interacting ch	17 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr14:24711417A>G	Missense Mutation	TINF2	p.L41P	TERF1 (TRF1)-interact	37 (0.00)	33 (0.18)	0.48
11-03	Gp4	g.chr8:38851085C>T	Missense Mutation	TM2D2	p.R137Q	TM2 domain containing	40 (0.00)	40 (0.17)	0.47
11-03	Gp4	g.chr5:140023479C>T	Missense Mutation	TMCO6	p.L345F	transmembrane and coil	46 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr17:41368746G>T	Missense Mutation	TMEM106A	p.D201Y	transmembrane protein	25 (0.00)	45 (0.18)	0.47
11-03	Gp4	g.chr12:122199564C>T	Silent	TMEM120B	p.D157D	transmembrane protein	31 (0.00)	29 (0.17)	0.61
11-03	Gp4	g.chr4:159162717C>A	Missense Mutation	TMEM144	p.H287N	transmembrane protein	17 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr19:42824525C>A	Missense Mutation	TMEM145	p.A377D	transmembrane protein	37 (0.00)	21 (0.33)	0.89
11-03	Gp4	g.chr2:135470831C>A	Missense Mutation	TMEM163	p.K87N	transmembrane protein	50 (0.02)	34 (0.18)	0.47
11-03	Gp4	g.chr7:112424037C>T	Missense Mutation	TMEM168	p.A282T	transmembrane protein	90 (0.00)	43 (0.23)	0.62

11-03	Gp4	g.chr12:72091068A>T	Missense Mutation	TMEM19	p.R131W	transmembrane protein	42 (0.00)	68 (0.15)	0.49
11-03	Gp4	g.chr12:72094693A>G	Missense Mutation	TMEM19	p.N310S	transmembrane protein	30 (0.00)	28 (0.18)	0.60
11-03	Gp4	g.chr2:27259420G>T	Silent	TMEM214	p.L262L	transmembrane protein	19 (0.00)	15 (0.67)	1.78
11-03	Gp4	g.chr14:93652710C>A	Silent	TMEM251	p.I30I	transmembrane protein	44 (0.00)	55 (0.38)	1.02
11-03	Gp4	g.chr13:114472128C>T	Nonsense Mutation	TMEM255B	p.Q83*	transmembrane protein	27 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr14:57114023C>T	Silent	TMEM260	p.A644A	transmembrane protein	16 (0.00)	18 (0.44)	1.19
11-03	Gp4	g.chr1:25667001G>T	Missense Mutation	TMEM50A	p.L8F	transmembrane protein	23 (0.04)	35 (0.20)	0.53
11-03	Gp4	g.chr17:28656279C>A	Silent	TMIGD1	p.L117L	transmembrane and im	31 (0.00)	27 (0.19)	0.49
11-03	Gp4	g.chr9:100328187G>C	Missense Mutation	TMOD1	p.V226L	tropomodulin 1	86 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr9:100328208G>T	Missense Mutation	TMOD1	p.G233W	tropomodulin 1	83 (0.00)	34 (0.24)	0.63
11-03	Gp4	g.chr21:42877835C>A	Intron	TMPRSS2		transmembrane protease	92 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr20:7963035C>T	Missense Mutation	TMX4	p.D305N	thioredoxin-related tran	37 (0.00)	17 (0.71)	1.88
11-03	Gp4	g.chr9:117792566G>A	Silent	TNC	p.F1831F	tenascin C	19 (0.00)	32 (0.16)	0.42
11-03	Gp4	g.chr1:175097746C>T	Missense Mutation	TNN	p.P1065L	tenascin N	45 (0.02)	20 (0.30)	0.80
11-03	Gp4	g.chr7:5410015C>G	Missense Mutation	TNRC18	p.E1404Q	trinucleotide repeat cont	26 (0.00)	25 (0.24)	0.64
11-03	Gp4	g.chr17:48940405A>G	Missense Mutation	TOB1	p.L325S	transducer of ERBB2, 1	39 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr1:45808296G>T	Nonsense Mutation	TOE1	p.E245*	target of EGR1, membe	100 (0.00)	55 (0.15)	0.39
11-03	Gp4	g.chr17:18196150G>A	Nonsense Mutation	TOP3A	p.R364*	topoisomerase (DNA) I	36 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr14:21963531G>A	Silent	TOX4	p.E595E	TOX high mobility grou	42 (0.00)	35 (0.26)	0.69
11-03	Gp4	g.chr2:24305964G>A	Missense Mutation	TP53I3	p.S66F	tumor protein p53 induc	18 (0.00)	12 (0.42)	1.11
11-03	Gp4	g.chr3:188925348C>A	Missense Mutation	TPRG1	p.Q59K	tumor protein p63 regul	64 (0.00)	51 (0.16)	0.42
11-03	Gp4	g.chr13:25517100G>A	RNA	TPTE2P1		transmembrane phosph	17 (0.00)	16 (0.50)	1.33
11-03	Gp4	g.chr5:64960394G>A	Missense Mutation	TRAPPC13	p.A404T	trafficking protein partic	24 (0.00)	19 (0.37)	0.98
11-03	Gp4	g.chr14:22521090C>T	RNA	TRAV21		T cell receptor alpha va	23 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr14:22690331C>A	RNA	TRAV35		T cell receptor alpha va	18 (0.00)	28 (0.29)	0.76
11-03	Gp4	g.chr14:22237226G>A	RNA	TRAV6		T cell receptor alpha va	37 (0.00)	38 (0.32)	0.84
11-03	Gp4	g.chr7:142326966G>A	RNA	TRBV19		T cell receptor beta vari	23 (0.00)	48 (0.23)	0.61
11-03	Gp4	g.chr7:142124187C>T	RNA	TRBV6-8		T cell receptor beta vari	30 (0.00)	36 (0.25)	0.67
11-03	Gp4	g.chr14:22938138G>T	RNA	TRDV3		T cell receptor delta var	36 (0.00)	46 (0.22)	0.58
11-03	Gp4	g.chr6:42211020C>T	Missense Mutation	TRERF1	p.R942Q	transcriptional regulatin	52 (0.00)	52 (0.17)	0.46
11-03	Gp4	g.chr1:114948139T>A	Missense Mutation	TRIM33	p.E887D	tripartite motif containi	78 (0.00)	64 (0.22)	0.58
11-03	Gp4	g.chr11:89768629C>G	Missense Mutation	TRIM49C	p.L84V	tripartite motif containi	49 (0.00)	18 (0.61)	1.63
11-03	Gp4	g.chr11:4621699C>T	Missense Mutation	TRIM68	p.R422Q	tripartite motif containi	21 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr15:45050887C>T	Silent	TRIM69	p.S216S	tripartite motif containi	29 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr10:104414439G>A	Silent	TRIM8	p.L200L	tripartite motif containi	73 (0.00)	20 (0.25)	0.67

11-03	Gp4	g.chr4:189067980G>A	Silent	TRIML1	p.E287E	tripartite motif family-li	32 (0.00)	35 (0.31)	0.84
11-03	Gp4	g.chr4:189068050G>T	Missense Mutation	TRIML1	p.G311W	tripartite motif family-li	26 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr9:37763717C>T	Silent	TRMT10B	p.I129I	tRNA methyltransferase	37 (0.00)	28 (0.25)	0.67
11-03	Gp4	g.chr8:125463850G>A	Missense Mutation	TRMT12	p.V228M	tRNA methyltransferase	51 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chrX:100297166C>T	Missense Mutation	TRMT2B	p.G38E	tRNA methyltransferase	15 (0.00)	16 (0.31)	0.52
11-03	Gp4	g.chr22:46746318C>T	Silent	TRMU	p.I203I	tRNA 5-methylaminom	29 (0.00)	29 (0.17)	0.46
11-03	Gp4	g.chr4:122846224G>A	Silent	TRPC3	p.H375H	transient receptor potent	36 (0.00)	78 (0.21)	0.55
11-03	Gp4	g.chr9:73442842C>A	Silent	TRPM3	p.G298G	transient receptor potent	89 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr9:77431673G>C	Nonsense Mutation	TRPM6	p.S407*	transient receptor potent	38 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr7:130364041C>A	Missense Mutation	TSGA13	p.K113N	testis specific, 13	63 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr1:115576739G>A	Missense Mutation	TSHB	p.C103Y	thyroid stimulating horn	34 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr12:58140819C>T	Missense Mutation	TSPAN31	p.P72S	tetraspanin 31	16 (0.00)	22 (0.55)	1.81
11-03	Gp4	g.chr4:99407933C>A	Missense Mutation	TSPAN5	p.G79W	tetraspanin 5	17 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr8:98288847G>A	Missense Mutation	TSPYL5	p.T409I	TSPY-like 5	45 (0.00)	81 (0.20)	0.53
11-03	Gp4	g.chr17:2235492G>A	Silent	TSR1	p.D489D	TSR1, 20S rRNA accun	43 (0.00)	24 (0.38)	1.00
11-03	Gp4	g.chr17:2235560C>T	Missense Mutation	TSR1	p.A467T	TSR1, 20S rRNA accun	23 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr17:2236288C>A	Missense Mutation	TSR1	p.M424I	TSR1, 20S rRNA accun	55 (0.00)	35 (0.20)	0.53
11-03	Gp4	g.chr17:2238877C>T	Missense Mutation	TSR1	p.G117R	TSR1, 20S rRNA accun	61 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chr22:28379296G>A	Missense Mutation	TTC28	p.S2120L	tetratricopeptide repeat	18 (0.00)	22 (0.32)	0.85
11-03	Gp4	g.chr21:38537934G>T	Nonsense Mutation	TTC3	p.E1140*	tetratricopeptide repeat	23 (0.00)	24 (0.50)	1.33
11-03	Gp4	g.chr21:38538512G>A	Silent	TTC3	p.P1332P	tetratricopeptide repeat	19 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr2:178416190G>A	Silent	TTC30B	p.Y434Y	tetratricopeptide repeat	180 (0.00)	92 (0.21)	0.55
11-03	Gp4	g.chr5:94830422G>A	Silent	TTC37	p.L1256L	tetratricopeptide repeat	51 (0.00)	39 (0.21)	0.55
11-03	Gp4	g.chr18:21662959G>T	Missense Mutation	TTC39C	p.A300S	tetratricopeptide repeat	46 (0.02)	78 (0.15)	0.41
11-03	Gp4	g.chr9:135273583C>T	Silent	TTF1	p.E574E	transcription terminatio	39 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr9:135277901G>A	Missense Mutation	TTF1	p.T103I	transcription terminatio	21 (0.00)	16 (0.38)	1.00
11-03	Gp4	g.chr1:117617987C>G	Missense Mutation	TTF2	p.L261V	transcription terminatio	87 (0.00)	39 (0.18)	0.48
11-03	Gp4	g.chr2:179393363G>T	Silent	TTN	p.I35705I	titin	37 (0.00)	34 (0.15)	0.39
11-03	Gp4	g.chr2:179393441G>T	Missense Mutation	TTN	p.S35679R	titin	46 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr2:179400994G>A	Nonsense Mutation	TTN	p.Q33494*	titin	30 (0.00)	15 (0.47)	1.24
11-03	Gp4	g.chr2:179402363G>T	Missense Mutation	TTN	p.Q33191K	titin	63 (0.00)	61 (0.28)	0.74
11-03	Gp4	g.chr2:179404928G>A	Silent	TTN	p.T32655T	titin	100 (0.00)	75 (0.15)	0.39
11-03	Gp4	g.chr2:179407811C>A	Missense Mutation	TTN	p.V32297L	titin	121 (0.00)	83 (0.14)	0.39
11-03	Gp4	g.chr2:179428233G>T	Missense Mutation	TTN	p.F27542L	titin	46 (0.00)	47 (0.21)	0.57
11-03	Gp4	g.chr2:179432459G>A	Missense Mutation	TTN	p.R26134C	titin	62 (0.02)	17 (0.35)	0.94

11-03	Gp4	g.chr2:179443583C>A	Missense Mutation	TTN	p.G22725V	titin	44 (0.00)	31 (0.19)	0.52
11-03	Gp4	g.chr2:179443623T>A	Missense Mutation	TTN	p.M22712L	titin	37 (0.00)	19 (0.32)	0.84
11-03	Gp4	g.chr2:179449396C>T	Splice Site	TTN	p.G21658S	titin	43 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr2:179449634G>A	Silent	TTN	p.S21578S	titin	45 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr2:179451950G>T	Missense Mutation	TTN	p.L21330I	titin	58 (0.00)	15 (0.40)	1.07
11-03	Gp4	g.chr2:179458844C>A	Missense Mutation	TTN	p.D19426Y	titin	86 (0.00)	38 (0.18)	0.49
11-03	Gp4	g.chr2:179469497C>A	Missense Mutation	TTN	p.A18107S	titin	43 (0.00)	46 (0.20)	0.52
11-03	Gp4	g.chr2:179469611G>A	Missense Mutation	TTN	p.P18069S	titin	49 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr2:179486352C>T	Missense Mutation	TTN	p.D15067N	titin	50 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr2:179495647G>A	Missense Mutation	TTN	p.P14680S	titin	52 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr2:179500819C>T	Missense Mutation	TTN	p.V13827M	titin	173 (0.00)	117 (0.19)	0.50
11-03	Gp4	g.chr2:179528367G>T	Silent	TTN	p.V12173V	titin	134 (0.00)	29 (0.31)	0.83
11-03	Gp4	g.chr2:179588780C>A	Missense Mutation	TTN	p.G7069V	titin	53 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr2:179589157T>A	Missense Mutation	TTN	p.Y6982F	titin	45 (0.00)	37 (0.16)	0.43
11-03	Gp4	g.chr2:179594138C>A	Missense Mutation	TTN	p.D6249Y	titin	89 (0.00)	54 (0.17)	0.44
11-03	Gp4	g.chr2:179605503G>A	Nonsense Mutation	TTN	p.Q4153*	titin	80 (0.00)	60 (0.20)	0.53
11-03	Gp4	g.chr2:179605980C>T	Missense Mutation	TTN	p.G3994R	titin	45 (0.00)	50 (0.20)	0.53
11-03	Gp4	g.chr12:49578862C>T	Silent	TUBA1A	p.E429E	tubulin, alpha 1a	71 (0.00)	42 (0.33)	1.12
11-03	Gp4	g.chr19:6495435G>A	Missense Mutation	TUBB4A	p.R359C	tubulin, beta 4A class I	53 (0.00)	64 (0.47)	1.59
11-03	Gp4	g.chr9:140137868G>A	Missense Mutation	TUBB4B	p.G400S	tubulin, beta 4B class I	66 (0.00)	37 (0.32)	0.86
11-03	Gp4	g.chr15:22868844C>T	Silent	TUBGCP5	p.L906L	tubulin, gamma comple	17 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr22:31367706C>G	RNA	TUG1		taurine up-regulated 1 (	68 (0.01)	60 (0.27)	0.71
11-03	Gp4	g.chr22:31367707T>A	RNA	TUG1		taurine up-regulated 1 (	67 (0.01)	60 (0.27)	0.71
11-03	Gp4	g.chr17:15457102C>T	Missense Mutation	TVP23C-CDR	p.S46N	TVP23C-CDRT4 readt	25 (0.00)	22 (0.36)	0.97
11-03	Gp4	g.chr7:66479428G>T	Missense Mutation	TYW1	p.W150C	tRNA-yW synthesizing	24 (0.00)	22 (0.59)	1.58
11-03	Gp4	g.chr7:66514974C>A	Missense Mutation	TYW1	p.F341L	tRNA-yW synthesizing	79 (0.00)	26 (0.19)	0.51
11-03	Gp4	g.chr7:66703390C>T	Silent	TYW1	p.F691F	tRNA-yW synthesizing	69 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr7:72081723C>T	RNA	TYW1B		tRNA-yW synthesizing	100 (0.00)	95 (0.20)	0.53
11-03	Gp4	g.chr15:70959420G>T	Silent	UACA	p.V1201V	uveal autoantigen with	42 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr17:16285519G>A	Missense Mutation	UBB	p.E100K	ubiquitin B	80 (0.00)	24 (0.33)	0.89
11-03	Gp4	g.chr12:109967718C>G	Missense Mutation	UBE3B	p.A884G	ubiquitin protein ligase	34 (0.00)	35 (0.20)	0.70
11-03	Gp4	g.chr11:118247296C>T	Silent	UBE4A	p.D493D	ubiquitination factor E4	32 (0.00)	11 (0.55)	1.45
11-03	Gp4	g.chr1:10190817G>A	Silent	UBE4B	p.L490L	ubiquitination factor E4	111 (0.00)	68 (0.15)	0.39
11-03	Gp4	g.chr15:74751182C>T	Silent	UBL7	p.A9A	ubiquitin-like 7	21 (0.00)	27 (0.81)	2.17
11-03	Gp4	g.chr16:4924934C>A	Silent	UBN1	p.L841L	ubinuclein 1	53 (0.00)	23 (0.22)	0.58

11-03	Gp4	g.chr6:42541549G>T	Missense Mutation	UBR2	p.R52S	ubiquitin protein ligase	21 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr6:42625836G>A	Missense Mutation	UBR2	p.E983K	ubiquitin protein ligase	76 (0.00)	78 (0.14)	0.38
11-03	Gp4	g.chr1:19440262G>T	Silent	UBR4	p.I3796I	ubiquitin protein ligase	47 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr1:19443787G>A	Missense Mutation	UBR4	p.T3584I	ubiquitin protein ligase	53 (0.00)	41 (0.24)	0.65
11-03	Gp4	g.chr1:19504110C>A	Missense Mutation	UBR4	p.A828S	ubiquitin protein ligase	19 (0.00)	40 (0.25)	0.67
11-03	Gp4	g.chr2:234602464G>A	Missense Mutation	UGT1A6	p.V272I	UDP glucuronosyltrans	20 (0.00)	17 (0.47)	1.25
11-03	Gp4	g.chr4:69962496G>A	Silent	UGT2B7	p.L86L	UDP glucuronosyltrans	45 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr5:176370393G>A	Missense Mutation	UIMC1	p.P514S	ubiquitin interaction mo	39 (0.00)	36 (0.42)	1.11
11-03	Gp4	g.chr17:19699416C>T	Silent	ULK2	p.V663V	unc-51 like autophagy a	31 (0.00)	22 (0.41)	1.09
11-03	Gp4	g.chr3:41723082C>A	Missense Mutation	ULK4	p.Q965H	unc-51 like kinase 4	27 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr12:121154526C>T	Missense Mutation	UNC119B	p.R152W	unc-119 homolog B (C.	45 (0.00)	56 (0.11)	0.38
11-03	Gp4	g.chr15:54916037C>T	Missense Mutation	UNC13C	p.R2082C	unc-13 homolog C (C. e	49 (0.00)	45 (0.18)	0.47
11-03	Gp4	g.chr14:94060027C>T	Splice Site	UNC79	p.L835L	unc-79 homolog (C. ele	20 (0.00)	38 (0.16)	0.42
11-03	Gp4	g.chr2:210642204G>A	Missense Mutation	UNC80	p.R174Q	unc-80 homolog (C. ele	33 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr16:21973784G>A	Silent	UQCRC2	p.V112V	ubiquinol-cytochrome c	19 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr1:229772491G>A	Missense Mutation	URB2	p.G711S	URB2 ribosome biogen	24 (0.00)	30 (0.17)	0.44
11-03	Gp4	g.chr4:9212935C>A	Missense Mutation	USP17L10	p.R185S	ubiquitin specific peptid	30 (0.00)	23 (0.26)	0.70
11-03	Gp4	g.chr4:9212940C>G	Missense Mutation	USP17L10	p.H186Q	ubiquitin specific peptid	37 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr22:18650050G>A	Silent	USP18	p.L143L	ubiquitin specific peptid	44 (0.02)	48 (0.23)	0.61
11-03	Gp4	g.chr1:55638148C>A	Nonsense Mutation	USP24	p.E202*	ubiquitin specific peptid	16 (0.00)	28 (0.43)	1.14
11-03	Gp4	g.chr1:55638157C>A	Nonsense Mutation	USP24	p.E199*	ubiquitin specific peptid	16 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr11:113688453C>T	Missense Mutation	USP28	p.E464K	ubiquitin specific peptid	58 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr11:77919943G>A	Nonsense Mutation	USP35	p.W509*	ubiquitin specific peptid	31 (0.00)	17 (0.53)	1.41
11-03	Gp4	g.chr3:49336052G>T	Missense Mutation	USP4	p.P510Q	ubiquitin specific peptid	98 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr11:11962038T>A	Silent	USP47	p.R772R	ubiquitin specific peptid	34 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chrX:55514614G>T	Silent	USP51	p.V253V	ubiquitin specific peptid	27 (0.00)	26 (0.46)	0.77
11-03	Gp4	g.chr10:75283430C>T	Missense Mutation	USP54	p.R758Q	ubiquitin specific peptid	61 (0.00)	33 (0.27)	0.73
11-03	Gp4	g.chr10:11505380G>A	Missense Mutation	USP6NL	p.A516V	USP6 N-terminal like	49 (0.00)	22 (0.27)	0.73
11-03	Gp4	g.chr15:50782625C>T	Silent	USP8	p.L607L	ubiquitin specific peptid	20 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr11:75562985C>T	Missense Mutation	UVRAG	p.H59Y	UV radiation resistance	29 (0.00)	36 (0.22)	0.59
11-03	Gp4	g.chr2:106761800G>T	Silent	UXS1	p.G106G	UDP-glucuronate decar	32 (0.00)	20 (0.40)	1.07
11-03	Gp4	g.chr17:41168090C>T	Silent	VAT1	p.E256E	vesicle amine transport	47 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr19:6833627C>A	Missense Mutation	VAV1	p.H567N	vav 1 guanine nucleotid	22 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr10:76982145C>T	Silent	VDAC2	p.P240P	voltage-dependent anio	42 (0.00)	56 (0.21)	0.57
11-03	Gp4	g.chr4:177608541G>A	Silent	VEGFC	p.C315C	vascular endothelial gro	77 (0.00)	63 (0.25)	0.68

11-03	Gp4	g.chr12:95663889T>A	Missense Mutation	VEZT	p.L258H	vezatin, adherens juncti	19 (0.00)	30 (0.27)	0.91
11-03	Gp4	g.chr8:100791221G>A	Missense Mutation	VPS13B	p.V2606I	vacuolar protein sorting	25 (0.00)	18 (0.44)	1.19
11-03	Gp4	g.chr1:12342813C>T	Missense Mutation	VPS13D	p.L1552F	vacuolar protein sorting	44 (0.00)	76 (0.29)	0.77
11-03	Gp4	g.chr12:122716894G>A	Missense Mutation	VPS33A	p.L564F	vacuolar protein sorting	15 (0.00)	35 (0.26)	0.90
11-03	Gp4	g.chr16:46694443G>A	Missense Mutation	VPS35	p.R778C	vacuolar protein sorting	48 (0.00)	40 (0.23)	0.60
11-03	Gp4	g.chr1:151150611C>T	Silent	VPS72	p.E191E	vacuolar protein sorting	41 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr19:54561966C>A	Missense Mutation	VSTM1	p.D19Y	V-set and transmembrar	32 (0.00)	28 (0.18)	0.48
11-03	Gp4	g.chr1:119575975C>T	Missense Mutation	WARS2	p.M214I	tryptophanyl tRNA synt	72 (0.00)	34 (0.24)	0.63
11-03	Gp4	g.chr7:70885942C>T	Silent	WBSCR17	p.I271I	Williams-Beuren syndrc	145 (0.01)	71 (0.15)	0.41
11-03	Gp4	g.chr2:224746742G>T	Missense Mutation	WDFY1	p.S327R	WD repeat and FYVE d	35 (0.00)	60 (0.15)	0.40
11-03	Gp4	g.chr4:85600112G>A	Silent	WDFY3	p.P3369P	WD repeat and FYVE d	49 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr4:85600158C>T	Missense Mutation	WDFY3	p.G3354D	WD repeat and FYVE d	74 (0.00)	48 (0.15)	0.39
11-03	Gp4	g.chr10:49997937G>A	Missense Mutation	WDFY4	p.D1325N	WDFY family member	97 (0.00)	43 (0.28)	0.74
11-03	Gp4	g.chr4:39233800C>T	Missense Mutation	WDR19	p.L721F	WD repeat domain 19	77 (0.00)	35 (0.23)	0.61
11-03	Gp4	g.chr6:170070742G>A	Silent	WDR27	p.L127L	WD repeat domain 27	91 (0.01)	110 (0.35)	0.92
11-03	Gp4	g.chr1:118494663G>A	Missense Mutation	WDR3	p.G623E	WD repeat domain 3	36 (0.00)	47 (0.32)	0.85
11-03	Gp4	g.chr9:116080824C>T	Missense Mutation	WDR31	p.A292T	WD repeat domain 31	38 (0.03)	18 (0.39)	1.04
11-03	Gp4	g.chr2:29136956C>T	Missense Mutation	WDR43	p.P210S	WD repeat domain 43	56 (0.00)	26 (0.35)	0.92
11-03	Gp4	g.chr2:74652761C>T	Missense Mutation	WDR54	p.S313F	WD repeat domain 54	53 (0.02)	25 (0.36)	0.96
11-03	Gp4	g.chr7:158672619A>G	Missense Mutation	WDR60	p.Q273R	WD repeat domain 60	158 (0.00)	150 (0.16)	0.43
11-03	Gp4	g.chr5:37701233C>T	Silent	WDR70	p.T422T	WD repeat domain 70	19 (0.00)	36 (0.31)	0.81
11-03	Gp4	g.chr2:190327300G>A	Missense Mutation	WDR75	p.G290E	WD repeat domain 75	29 (0.00)	35 (0.29)	0.76
11-03	Gp4	g.chr3:52292565G>A	Missense Mutation	WDR82	p.A300V	WD repeat domain 82	62 (0.00)	61 (0.15)	0.39
11-03	Gp4	g.chr12:1005269G>T	Missense Mutation	WNK1	p.E1872D	WNK lysine deficient p	33 (0.00)	57 (0.16)	0.53
11-03	Gp4	g.chr12:993323C>A	Missense Mutation	WNK1	p.S1253Y	WNK lysine deficient p	19 (0.00)	34 (0.26)	0.89
11-03	Gp4	g.chr5:167835555C>T	Missense Mutation	WWC1	p.S255F	WW and C2 domain co	50 (0.02)	19 (0.32)	0.84
11-03	Gp4	g.chr16:69922027G>T	Silent	WWP2	p.V263V	WW domain containing	53 (0.00)	31 (0.16)	0.43
11-03	Gp4	g.chr3:14191366G>A	Intron	XPC		xeroderma pigmentosun	57 (0.02)	49 (0.24)	0.65
11-03	Gp4	g.chr16:28181087C>A	Silent	XPO6	p.V183V	exportin 6	68 (0.00)	43 (0.21)	0.56
11-03	Gp4	g.chr3:142031562T>C	Missense Mutation	XRN1	p.M1554V	5'-3' exoribonuclease 1	41 (0.00)	22 (0.50)	1.33
11-03	Gp4	g.chr18:756699C>T	Silent	YES1	p.P43P	YES proto-oncogene 1,	44 (0.00)	30 (0.37)	0.98
11-03	Gp4	g.chr10:27437934G>A	Silent	YME1L1	p.F23F	YME1-like 1 ATPase	19 (0.00)	22 (0.32)	0.85
11-03	Gp4	g.chr12:57398107G>T	Missense Mutation	ZBTB39	p.L199M	zinc finger and BTB do	51 (0.00)	32 (0.28)	0.93
11-03	Gp4	g.chr9:37440651C>A	Missense Mutation	ZBTB5	p.R633L	zinc finger and BTB do	27 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr14:75537757C>T	Missense Mutation	ZC2HC1C	p.H161Y	zinc finger, C2HC-type	39 (0.00)	49 (0.18)	0.49

11-03	Gp4	g.chrX:64722918C>A	Nonsense Mutation	ZC3H12B	p.C780*	zinc finger CCCH-type	45 (0.00)	45 (0.29)	0.48
11-03	Gp4	g.chr22:41742116C>T	Silent	ZC3H7B	p.D523D	zinc finger CCCH-type	36 (0.00)	27 (0.30)	0.79
11-03	Gp4	g.chr1:52991635C>A	Silent	ZCCHC11	p.V106V	zinc finger, CCHC dom	21 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr18:60242784G>A	Splice Site	ZCCHC2		zinc finger, CCHC dom	41 (0.02)	15 (0.60)	1.60
11-03	Gp4	g.chr9:88943337C>A	Missense Mutation	ZCCHC6	p.W509L	zinc finger, CCHC dom	17 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr12:122958321G>A	Missense Mutation	ZCCHC8	p.P378L	zinc finger, CCHC dom	137 (0.00)	151 (0.20)	0.70
11-03	Gp4	g.chr10:99212652G>C	Splice Site	ZDHHC16	p.R176S	zinc finger, DHHC-type	57 (0.00)	24 (0.25)	0.67
11-03	Gp4	g.chr4:16363283G>T	RNA	ZEB2P1		zinc finger E-box bindi	61 (0.00)	29 (0.21)	0.55
11-03	Gp4	g.chr10:46122419C>A	Silent	ZFAND4	p.G284G	zinc finger, AN1-type d	15 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr12:72050756C>T	Silent	ZFC3H1	p.L308L	zinc finger, C3H1-type	29 (0.00)	43 (0.21)	0.70
11-03	Gp4	g.chr16:72822351G>A	Missense Mutation	ZFHX3	p.P3275L	zinc finger homeobox 3	60 (0.00)	39 (0.18)	0.48
11-03	Gp4	g.chr16:72827259C>T	Missense Mutation	ZFHX3	p.A3108T	zinc finger homeobox 3	80 (0.00)	24 (0.21)	0.56
11-03	Gp4	g.chr16:72829776C>T	Missense Mutation	ZFHX3	p.D2269N	zinc finger homeobox 3	101 (0.00)	46 (0.15)	0.41
11-03	Gp4	g.chr16:72832200G>A	Nonsense Mutation	ZFHX3	p.Q1461*	zinc finger homeobox 3	39 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr16:75203240C>T	Missense Mutation	ZFP1	p.P78S	ZFP1 zinc finger protei	24 (0.00)	43 (0.30)	0.81
11-03	Gp4	g.chr1:52734137G>T	Missense Mutation	ZFYVE9	p.A820S	zinc finger, FYVE dom	31 (0.00)	19 (0.32)	0.84
11-03	Gp4	g.chr8:124265828C>T	Missense Mutation	ZHX1	p.D787N	zinc fingers and homeo	25 (0.00)	43 (0.19)	0.50
11-03	Gp4	g.chr6:28213633G>A	Missense Mutation	ZKSCAN4	p.A300V	zinc finger with KRAB	34 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr6:28217525G>T	Missense Mutation	ZKSCAN4	p.Q171K	zinc finger with KRAB	22 (0.00)	17 (0.94)	2.51
11-03	Gp4	g.chr7:99103769C>T	Silent	ZKSCAN5	p.D34D	zinc finger with KRAB	73 (0.01)	54 (0.41)	1.09
11-03	Gp4	g.chr6:28121017G>A	Missense Mutation	ZKSCAN8	p.R320K	zinc finger with KRAB	31 (0.00)	15 (0.33)	0.89
11-03	Gp4	g.chr1:35862170C>T	Missense Mutation	ZMYM4	p.P977S	zinc finger, MYM-type	19 (0.00)	23 (0.39)	1.04
11-03	Gp4	g.chr1:35480374C>T	Missense Mutation	ZMYM6	p.S240N	zinc finger, MYM-type	18 (0.00)	44 (0.30)	0.79
11-03	Gp4	g.chr1:247320685C>G	Missense Mutation	ZNF124	p.G80A	zinc finger protein 124	56 (0.00)	65 (0.22)	0.57
11-03	Gp4	g.chr17:30689996G>T	Missense Mutation	ZNF207	p.M221I	zinc finger protein 207	23 (0.00)	18 (0.39)	1.04
11-03	Gp4	g.chr10:45498907C>T	Nonsense Mutation	ZNF22	p.Q31*	zinc finger protein 22	42 (0.00)	31 (0.23)	0.60
11-03	Gp4	g.chr19:44635918C>G	Missense Mutation	ZNF225	p.A384G	zinc finger protein 225	31 (0.00)	18 (0.44)	1.19
11-03	Gp4	g.chr19:44676291G>T	Missense Mutation	ZNF226	p.L22F	zinc finger protein 226	101 (0.00)	76 (0.16)	0.42
11-03	Gp4	g.chr19:44681106G>A	Missense Mutation	ZNF226	p.C564Y	zinc finger protein 226	79 (0.00)	24 (0.50)	1.33
11-03	Gp4	g.chr17:5012793G>A	Missense Mutation	ZNF232	p.P132S	zinc finger protein 232	61 (0.00)	50 (0.62)	0.61
11-03	Gp4	g.chr19:35435295G>A	Silent	ZNF30	p.R476R	zinc finger protein 30	51 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr10:43088725C>A	Missense Mutation	ZNF33B	p.C558F	zinc finger protein 33B	34 (0.03)	34 (0.44)	1.18
11-03	Gp4	g.chr20:32344997C>G	Missense Mutation	ZNF341	p.T262R	zinc finger protein 341	42 (0.00)	23 (0.22)	0.58
11-03	Gp4	g.chr5:178506524G>T	Missense Mutation	ZNF354C	p.G364V	zinc finger protein 354C	56 (0.00)	40 (0.15)	0.40
11-03	Gp4	g.chr19:37726534C>T	Silent	ZNF383	p.Y31Y	zinc finger protein 383	19 (0.00)	15 (0.47)	1.24

11-03	Gp4	g.chr2:180309667C>T	Missense Mutation	ZNF385B	p.G378E	zinc finger protein 385B	33 (0.00)	29 (0.28)	0.74
11-03	Gp4	g.chr2:180634371C>T	Missense Mutation	ZNF385B	p.V38M	zinc finger protein 385B	69 (0.00)	35 (0.20)	0.53
11-03	Gp4	g.chr18:72345859C>T	Missense Mutation	ZNF407	p.R962C	zinc finger protein 407	38 (0.00)	28 (0.21)	0.57
11-03	Gp4	g.chr14:74364828C>A	Nonsense Mutation	ZNF410	p.S75*	zinc finger protein 410	34 (0.03)	19 (0.32)	0.84
11-03	Gp4	g.chr19:21713483C>G	Missense Mutation	ZNF429	p.P75A	zinc finger protein 429	24 (0.00)	16 (0.56)	1.50
11-03	Gp4	g.chr19:12127345C>T	Missense Mutation	ZNF433	p.G113S	zinc finger protein 433	22 (0.00)	60 (0.20)	0.53
11-03	Gp4	g.chr10:31138999G>A	Missense Mutation	ZNF438	p.S112F	zinc finger protein 438	49 (0.00)	26 (0.23)	0.62
11-03	Gp4	g.chr10:31139180G>A	Missense Mutation	ZNF438	p.P52S	zinc finger protein 438	25 (0.00)	20 (0.35)	0.93
11-03	Gp4	g.chr19:11978266G>A	Missense Mutation	ZNF439	p.V128I	zinc finger protein 439	19 (0.00)	49 (0.18)	0.49
11-03	Gp4	g.chr19:11892235G>A	Silent	ZNF441	p.K532K	zinc finger protein 441	26 (0.00)	21 (0.52)	1.40
11-03	Gp4	g.chr19:12541634C>G	Missense Mutation	ZNF443	p.C451S	zinc finger protein 443	18 (0.00)	30 (0.23)	0.62
11-03	Gp4	g.chr9:109688515C>T	Silent	ZNF462	p.F774F	zinc finger protein 462	52 (0.00)	37 (0.59)	1.59
11-03	Gp4	g.chr9:109701267C>A	Silent	ZNF462	p.S1008S	zinc finger protein 462	50 (0.00)	52 (0.25)	0.67
11-03	Gp4	g.chr10:97917991C>A	RNA	ZNF518A		zinc finger protein 518A	33 (0.00)	52 (0.17)	0.46
11-03	Gp4	g.chr10:97918006T>A	RNA	ZNF518A		zinc finger protein 518A	31 (0.00)	56 (0.16)	0.43
11-03	Gp4	g.chr19:57888537C>A	Missense Mutation	ZNF547	p.P65T	zinc finger protein 547	22 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr19:37966813G>A	Missense Mutation	ZNF570	p.D22N	zinc finger protein 570	31 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr19:52376138G>A	Missense Mutation	ZNF577	p.L369F	zinc finger protein 577	32 (0.00)	33 (0.15)	0.40
11-03	Gp4	g.chr15:85343201C>A	Missense Mutation	ZNF592	p.S1089Y	zinc finger protein 592	30 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr15:85343202C>A	Silent	ZNF592	p.S1089S	zinc finger protein 592	30 (0.00)	17 (0.29)	0.78
11-03	Gp4	g.chr19:52857025G>A	Missense Mutation	ZNF610	p.V52M	zinc finger protein 610	52 (0.00)	56 (0.23)	0.62
11-03	Gp4	g.chr19:52519922C>A	Missense Mutation	ZNF614	p.S310I	zinc finger protein 614	48 (0.00)	29 (0.24)	0.64
11-03	Gp4	g.chr3:40528997C>A	Silent	ZNF619	p.I372I	zinc finger protein 619	18 (0.00)	16 (0.31)	0.83
11-03	Gp4	g.chr17:47388778G>A	Missense Mutation	ZNF652	p.S402F	zinc finger protein 652	23 (0.00)	43 (0.16)	0.43
11-03	Gp4	g.chr19:53667850A>G	Silent	ZNF665	p.C631C	zinc finger protein 665	32 (0.00)	35 (0.14)	0.38
11-03	Gp4	g.chr19:53669234G>C	Missense Mutation	ZNF665	p.S170C	zinc finger protein 665	41 (0.00)	27 (0.22)	0.59
11-03	Gp4	g.chr19:22362974G>T	Missense Mutation	ZNF676	p.S515R	zinc finger protein 676	62 (0.00)	41 (0.17)	0.46
11-03	Gp4	g.chr19:57133006C>T	Silent	ZNF71	p.L117L	zinc finger protein 71	25 (0.00)	14 (0.36)	0.95
11-03	Gp4	g.chr6:35258160G>C	Splice Site	ZNF76		zinc finger protein 76	59 (0.00)	21 (0.29)	0.76
11-03	Gp4	g.chr7:148767525T>C	Missense Mutation	ZNF786	p.D780G	zinc finger protein 786	114 (0.00)	90 (0.21)	0.56
11-03	Gp4	g.chr9:130198252G>A	Missense Mutation	ZNF79	p.E100K	zinc finger protein 79	37 (0.00)	25 (0.36)	0.96
11-03	Gp4	g.chr2:185803416T>A	Missense Mutation	ZNF804A	p.I1098N	zinc finger protein 804A	64 (0.00)	25 (0.28)	0.75
11-03	Gp4	g.chr19:58388309C>T	Silent	ZNF814	p.E46E	zinc finger protein 814	46 (0.00)	35 (0.17)	0.46
11-03	Gp4	g.chr19:52658506C>A	Missense Mutation	ZNF836	p.E810D	zinc finger protein 836	40 (0.00)	61 (0.34)	0.92
11-03	Gp4	g.chr19:53854097G>A	Missense Mutation	ZNF845	p.E57K	zinc finger protein 845	33 (0.00)	20 (0.25)	0.67

11-03	Gp4	g.chr19:9872761G>A	Nonsense Mutation	ZNF846	p.Q76*	zinc finger protein 846	16 (0.00)	38 (0.21)	0.56
11-03	Gp4	g.chr7:149557860C>T	Silent	ZNF862	p.D537D	zinc finger protein 862	52 (0.00)	34 (0.18)	0.47
11-03	Gp4	g.chr7:149557941C>T	Silent	ZNF862	p.S564S	zinc finger protein 862	74 (0.00)	31 (0.32)	0.86
11-03	Gp4	g.chr19:22941604G>A	Silent	ZNF99	p.Y369Y	zinc finger protein 99	59 (0.00)	22 (0.36)	0.97
11-03	Gp4	g.chr20:47886882T>C	Silent	ZNFX1	p.Q489Q	zinc finger, NFX1-type	27 (0.00)	13 (0.38)	1.03
11-03	Gp4	g.chr16:21209122C>T	Missense Mutation	ZP2	p.S687N	zona pellucida glycopro	23 (0.00)	42 (0.14)	0.38
11-03	Gp4	g.chr16:21213029G>T	Missense Mutation	ZP2	p.P501Q	zona pellucida glycopro	47 (0.00)	20 (0.30)	0.80
11-03	Gp4	g.chr1:238053252C>G	Missense Mutation	ZP4	p.M105I	zona pellucida glycopro	35 (0.00)	29 (0.38)	1.01
11-03	Gp4	g.chr17:38032973G>A	Missense Mutation	ZPBP2	p.V310I	zona pellucida binding p	36 (0.00)	54 (0.17)	0.44
11-03	Gp4	g.chrX:15833900G>C	Missense Mutation	ZRSR2	p.D220H	zinc finger (CCCH type	84 (0.01)	57 (0.40)	0.67
11-03	Gp4	g.chr1:33960000C>G	Missense Mutation	ZSCAN20	p.Q686E	zinc finger and SCAN d	39 (0.00)	51 (0.24)	0.63
11-03	Gp4	g.chr15:43661997G>A	Missense Mutation	ZSCAN29	p.L39F	zinc finger and SCAN d	54 (0.00)	19 (0.26)	0.70
11-03	Gp4	g.chr17:3984693G>A	Missense Mutation	ZZEF1	p.L936F	zinc finger, ZZ-type wit	37 (0.00)	40 (0.35)	0.93
11-03	Gp4	g.chr17:3985793G>A	Silent	ZZEF1	p.V884V	zinc finger, ZZ-type wit	19 (0.00)	32 (0.19)	0.50
11-03	Gp4	g.chr1:78098746C>T	Silent	ZZZ3	p.R98R	zinc finger, ZZ-type con	52 (0.00)	23 (0.78)	0.89
11-10 Area 1	Gp3	g.chr4:87968376G>A	Missense Mutation	AFF1	p.R223Q	AF4/FMR2 family, men	76 (0.00)	38 (0.18)	0.49
11-10 Area 1	Gp3	g.chr18:14183710A>G	RNA	ANKRD20A5P		ankyrin repeat domain 2	79 (0.01)	47 (0.15)	0.40
11-10 Area 1	Gp3	g.chr21:11182670T>A	lincRNA	AP003900.6			38 (0.03)	40 (0.23)	0.60
11-10 Area 1	Gp3	g.chr14:67812524G>T	Silent	ATP6V1D	p.A84A	ATPase, H+ transportin	64 (0.00)	35 (0.14)	0.38
11-10 Area 1	Gp3	g.chr21:11094824G>A	RNA	BAGE2		B melanoma antigen fa	23 (0.00)	22 (0.27)	0.73
11-10 Area 1	Gp3	g.chr11:47179460C>T	Silent	C11orf49	p.I248I	chromosome 11 open re	79 (0.01)	68 (0.15)	0.39
11-10 Area 1	Gp3	g.chr11:10794731C>T	Nonsense Mutation	CTR9	p.Q880*	CTR9, Paf1/RNA polyn	35 (0.03)	30 (0.30)	0.80
11-10 Area 1	Gp3	g.chr11:58893250A>G	Silent	FAM111B	p.G560G	family with sequence si	98 (0.00)	42 (0.17)	0.44
11-10 Area 1	Gp3	g.chr6:116265469C>T	Missense Mutation	FRK	p.V360I	fyn-related Src family ty	15 (0.00)	29 (0.17)	0.46
11-10 Area 1	Gp3	g.chr2:207041261G>A	Silent	GPR1	p.S237S	G protein-coupled recep	35 (0.00)	30 (0.17)	0.44
11-10 Area 1	Gp3	g.chr4:143393616T>C	Intron	INPP4B		inositol polyphosphate-4	44 (0.00)	41 (0.34)	0.91
11-10 Area 1	Gp3	g.chr3:12977997C>T	Silent	IQSEC1	p.V187V	IQ motif and Sec7 doma	35 (0.00)	38 (0.34)	0.91
11-10 Area 1	Gp3	g.chr3:124160792G>A	Splice Site	KALRN	p.A1065T	kalirin, RhoGEF kinase	37 (0.00)	28 (0.25)	0.67
11-10 Area 1	Gp3	g.chr7:77740060A>G	Intron	MAGI2		membrane associated gu	72 (0.00)	58 (0.36)	0.97
11-10 Area 1	Gp3	g.chr11:82868580C>A	Missense Mutation	PCF11	p.S33R	PCF11 cleavage and pol	38 (0.00)	64 (0.19)	0.50
11-10 Area 1	Gp3	g.chr11:82868592C>A	Silent	PCF11	p.I37I	PCF11 cleavage and pol	40 (0.00)	71 (0.17)	0.45
11-10 Area 1	Gp3	g.chr2:113316998C>T	Missense Mutation	POLR1B	p.R431C	polymerase (RNA) I pol	37 (0.00)	42 (0.36)	0.95
11-10 Area 1	Gp3	g.chr18:77798574G>A	Missense Mutation	RBFA	p.A150T	ribosome binding factor	31 (0.00)	20 (0.45)	0.76
11-10 Area 1	Gp3	g.chr17:63186329G>A	Missense Mutation	RGS9	p.V241M	regulator of G-protein si	52 (0.00)	41 (0.17)	0.46
11-10 Area 1	Gp3	g.chr2:216986900G>A	Missense Mutation	XRCC5	p.E203K	X-ray repair complemen	52 (0.00)	34 (0.15)	0.39

11-10 Area 1	Gp4	g.chr12:34179259C>T	Silent	ALG10	p.G277G	ALG10, alpha-1,2-gluc	57 (0.00)	20 (0.25)	0.67
11-10 Area 1	Gp4	g.chr21:11072375T>C	RNA	BAGE2		B melanoma antigen fa	26 (0.00)	23 (0.26)	0.70
11-10 Area 1	Gp4	g.chr11:4615225T>C	Missense Mutation	OR52I1	p.L10P	olfactory receptor, famil	148 (0.00)	105 (0.25)	0.66
11-10 Area 1	Gp4	g.chr1:158687361A>G	Missense Mutation	OR6K3	p.V182A	olfactory receptor, famil	38 (0.00)	30 (0.40)	1.07
11-10 Area 1	Gp4	g.chr17:1561959C>T	Missense Mutation	PRPF8	p.R1746Q	pre-mRNA processing f	64 (0.00)	42 (0.55)	1.46
11-10 Area 1	Gp4	g.chr9:131356626C>T	Nonsense Mutation	SPTAN1	p.Q1130*	spectrin, alpha, non-eryt	31 (0.00)	23 (0.22)	0.58
11-10 Area 1	Gp4	g.chr11:64004692C>T	Silent	VEGFB	p.D136D	vascular endothelial gro	40 (0.00)	48 (0.17)	0.44
11-10 Area 1	Gp4	g.chr4:39278673G>A	Silent	WDR19	p.T1250T	WD repeat domain 19	28 (0.00)	32 (0.16)	0.42
11-10 Area 1	Gp4	g.chr4:142152631C>T	Missense Mutation	ZNF330	p.R188C	zinc finger protein 330	144 (0.00)	55 (0.29)	0.78
11-10 Area 2	Gp3	g.chr1:94502838C>A	Missense Mutation	ABCA4	p.G1226C	ATP-binding cassette, s	84 (0.01)	95 (0.41)	1.09
11-10 Area 2	Gp3	g.chr2:169814584_169814	Frame Shift Del	ABCB11	p.L745fs	ATP-binding cassette, s	311 (0.00)	45 (0.31)	0.83
11-10 Area 2	Gp3	g.chr1:179086524A>G	Missense Mutation	ABL2	p.W451R	ABL proto-oncogene 2,	27 (0.00)	40 (0.65)	1.73
11-10 Area 2	Gp3	g.chr17:34235843G>T	lincRNA	AC015849.16			52 (0.00)	19 (0.26)	0.70
11-10 Area 2	Gp3	g.chr17:35609955C>A	Missense Mutation	ACACA	p.V575L	acetyl-CoA carboxylase	81 (0.01)	190 (0.50)	1.33
11-10 Area 2	Gp3	g.chr3:179305768G>A	Silent	ACTL6A	p.G420G	actin-like 6A	53 (0.00)	128 (0.99)	2.65
11-10 Area 2	Gp3	g.chr6:11766568C>T	Missense Mutation	ADTRP	p.R110Q	androgen-dependent TF	122 (0.00)	34 (0.88)	2.35
11-10 Area 2	Gp3	g.chr10:48235974C>T	Silent	AGAP9	p.S247S	ArfGAP with GTPase d	110 (0.01)	38 (0.95)	2.00
11-10 Area 2	Gp3	g.chr5:35040740C>A	Missense Mutation	AGXT2	p.K39N	alanine--glyoxylate ami	59 (0.00)	40 (0.97)	2.60
11-10 Area 2	Gp3	g.chr14:33204927C>A	Missense Mutation	AKAP6	p.L1071M	A kinase (PRKA) ancho	33 (0.00)	42 (0.38)	1.02
11-10 Area 2	Gp3	g.chr4:74005562C>A	Missense Mutation	ANKRD17	p.G924V	ankyrin repeat domain 1	132 (0.00)	10 (0.80)	2.13
11-10 Area 2	Gp3	g.chr11:22294451G>T	Missense Mutation	ANO5	p.R717S	anoctamin 5	18 (0.00)	112 (0.47)	1.26
11-10 Area 2	Gp3	g.chr12:99097190C>A	Missense Mutation	APAF1	p.H836Q	apoptotic peptidase acti	54 (0.00)	36 (0.94)	2.52
11-10 Area 2	Gp3	g.chr1:156563749C>T	Missense Mutation	APOA1BP	p.S247F	apolipoprotein A-I bindi	119 (0.00)	295 (0.29)	0.78
11-10 Area 2	Gp3	g.chr1:156563753A>T	Silent	APOA1BP	p.A248A	apolipoprotein A-I bindi	117 (0.00)	288 (0.29)	0.78
11-10 Area 2	Gp3	g.chr22:36556813C>A	Missense Mutation	APOL3	p.V43L	apolipoprotein L, 3	71 (0.00)	160 (0.62)	1.65
11-10 Area 2	Gp3	g.chr16:24960756T>C	Missense Mutation	ARHGAP17	p.K366E	Rho GTPase activating	30 (0.00)	67 (0.28)	0.76
11-10 Area 2	Gp3	g.chr12:46215255T>C	Silent	ARID2	p.D230D	AT rich interactive dom	30 (0.00)	93 (0.16)	0.43
11-10 Area 2	Gp3	g.chr14:58814476G>A	Missense Mutation	ARID4A	p.M428I	AT rich interactive dom	65 (0.00)	26 (0.46)	1.23
11-10 Area 2	Gp3	g.chr7:95166961G>T	Missense Mutation	ASB4	p.A391S	ankyrin repeat and SOC	37 (0.00)	105 (0.55)	1.47
11-10 Area 2	Gp3	g.chr19:3918876_3918885	Splice Site	ATCAY		ataxia, cerebellar, Caym	36 (0.00)	26 (0.92)	2.46
11-10 Area 2	Gp3	g.chr18:43669649C>G	Missense Mutation	ATP5A1	p.G178A	ATP synthase, H+ trans	63 (0.00)	62 (0.98)	2.62
11-10 Area 2	Gp3	g.chr17:40639274_406392	In Frame Del	ATP6V0A1	p.H312del	ATPase, H+ transportin	40 (0.00)	47 (0.81)	1.72
11-10 Area 2	Gp3	g.chr2:32688401A>G	Silent	BIRC6	p.L1631L	baculoviral IAP repeat c	81 (0.00)	41 (0.95)	2.54
11-10 Area 2	Gp3	g.chr15:91281603G>T	Intron	BLM		Bloom syndrome, RecQ	45 (0.00)	16 (0.88)	2.33
11-10 Area 2	Gp3	g.chr1:220232224G>A	Nonsense Mutation	BPNT1	p.R297*	3'(2'), 5'-bisphosphate n	137 (0.01)	62 (0.98)	2.62

11-10 Area 2	Gp3	g.chr1:220232248_220232	Frame Shift Del	BPNT1	p.R289fs	3'(2'), 5'-bisphosphate n	127 (0.00)	73 (0.99)	2.63
11-10 Area 2	Gp3	g.chr13:32903371C>T	Intron	BRCA2		breast cancer 2, early on	88 (0.00)	80 (0.20)	0.53
11-10 Area 2	Gp3	g.chr6:26407980A>T	Missense Mutation	BTN3A1	p.Y172F	butyrophilin, subfamily	101 (0.00)	10 (0.70)	1.87
11-10 Area 2	Gp3	g.chr6:26370775G>T	Missense Mutation	BTN3A2	p.C220F	butyrophilin, subfamily	171 (0.00)	29 (0.21)	0.55
11-10 Area 2	Gp3	g.chr17:36993404C>T	Nonsense Mutation	C17orf98	p.W99*	chromosome 17 open re	45 (0.02)	66 (0.98)	2.63
11-10 Area 2	Gp3	g.chr20:3262291G>C	Missense Mutation	C20orf194	p.H870D	chromosome 20 open re	21 (0.00)	87 (0.87)	2.33
11-10 Area 2	Gp3	g.chr8:38385970C>T	Silent	C8orf86	p.E62E	chromosome 8 open rea	42 (0.02)	473 (0.42)	1.12
11-10 Area 2	Gp3	g.chr9:114510403G>T	Missense Mutation	C9orf84	p.S210R	chromosome 9 open rea	85 (0.00)	54 (0.37)	0.99
11-10 Area 2	Gp3	g.chr8:86356297_8635629	In Frame Del	CA3	p.129_130T	carbonic anhydrase III,	98 (0.00)	152 (0.93)	2.47
11-10 Area 2	Gp3	g.chr8:86356342G>A	Missense Mutation	CA3	p.G144D	carbonic anhydrase III,	61 (0.00)	145 (0.99)	2.65
11-10 Area 2	Gp3	g.chr2:27461392C>A	Missense Mutation	CAD	p.R1589S	carbamoyl-phosphate sy	31 (0.00)	127 (0.23)	0.61
11-10 Area 2	Gp3	g.chr3:85950923T>C	Intron	CADM2		cell adhesion molecule	62 (0.00)	85 (0.98)	2.60
11-10 Area 2	Gp3	g.chr17:4877782C>A	Silent	CAMTA2	p.R643R	calmodulin binding tran	65 (0.00)	66 (0.35)	0.93
11-10 Area 2	Gp3	g.chr7:2987374C>A	Nonsense Mutation	CARD11	p.E19*	caspase recruitment don	130 (0.00)	21 (0.29)	0.76
11-10 Area 2	Gp3	g.chr17:73509883C>T	Start Codon SNP	CASKIN2	p.M1I	CASK interacting prote	38 (0.00)	53 (0.98)	2.62
11-10 Area 2	Gp3	g.chr4:26487339C>A	Missense Mutation	CCKAR	p.L182F	cholecystokinin A recep	49 (0.00)	38 (0.26)	0.70
11-10 Area 2	Gp3	g.chr19:8122722C>T	Silent	CCL25	p.N121N	chemokine (C-C motif)	15 (0.00)	123 (0.44)	1.17
11-10 Area 2	Gp3	g.chr14:20784513C>A	Missense Mutation	CCNB1IP1	p.G57V	cyclin B1 interacting pr	27 (0.00)	46 (0.74)	1.97
11-10 Area 2	Gp3	g.chr12:49089839C>A	Missense Mutation	CCNT1	p.D217Y	cyclin T1	77 (0.00)	92 (0.18)	0.49
11-10 Area 2	Gp3	g.chr12:69992135G>T	Missense Mutation	CCT2	p.D457Y	chaperonin containing T	31 (0.00)	21 (0.95)	2.54
11-10 Area 2	Gp3	g.chr11:117258096C>A	Silent	CEP164	p.L634L	centrosomal protein 164	47 (0.02)	114 (0.54)	1.43
11-10 Area 2	Gp3	g.chr1:6172286T>C	Missense Mutation	CHD5	p.D1685G	chromodomain helicase	17 (0.00)	30 (0.17)	0.44
11-10 Area 2	Gp3	g.chr8:61736497C>T	Silent	CHD7	p.R1100R	chromodomain helicase	59 (0.00)	93 (0.18)	0.49
11-10 Area 2	Gp3	g.chr3:33663689T>C	Silent	CLASP2	p.A374A	cytoplasmic linker asso	78 (0.00)	117 (0.16)	0.43
11-10 Area 2	Gp3	g.chr1:36216914T>C	Silent	CLSPN	p.K655K	claspin	17 (0.00)	33 (0.18)	0.48
11-10 Area 2	Gp3	g.chr4:78663420G>T	Silent	CNOT6L	p.L249L	CCR4-NOT transcriptio	61 (0.00)	129 (0.36)	0.97
11-10 Area 2	Gp3	g.chr17:71197928G>A	Silent	COG1	p.K654K	component of oligomeri	38 (0.03)	78 (0.47)	1.26
11-10 Area 2	Gp3	g.chr3:130284355C>A	Missense Mutation	COL6A6	p.F393L	collagen, type VI, alpha	44 (0.00)	31 (0.84)	2.24
11-10 Area 2	Gp3	g.chr5:173316975C>T	Missense Mutation	CPEB4	p.A80V	cytoplasmic polyadenyl	165 (0.01)	45 (0.40)	1.07
11-10 Area 2	Gp3	g.chr3:97607285C>T	Missense Mutation	CRYBG3	p.H516Y	beta-gamma crystallin d	131 (0.00)	85 (0.25)	0.66
11-10 Area 2	Gp3	g.chr8:68070815G>A	Missense Mutation	CSPP1	p.R787K	centrosome and spindle	97 (0.00)	50 (0.96)	2.56
11-10 Area 2	Gp3	g.chr12:77259983C>A	Missense Mutation	CSRP2	p.A20S	cysteine and glycine-ric	19 (0.00)	29 (0.97)	2.57
11-10 Area 2	Gp3	g.chr20:23420953G>T	Missense Mutation	CSTL1	p.V17F	cystatin-like 1	22 (0.00)	70 (0.96)	2.55
11-10 Area 2	Gp3	g.chr10:68940103T>C	Missense Mutation	CTNNA3	p.Q340R	catenin (cadherin-associ	91 (0.01)	15 (0.33)	0.89
11-10 Area 2	Gp3	g.chr9:124457887C>A	Intron	DAB2IP		DAB2 interacting prote	46 (0.00)	19 (0.63)	1.68

11-10 Area 2	Gp3	g.chr9:124494930C>A	Intron	DAB2IP		DAB2 interacting protei	41 (0.02)	48 (0.17)	0.44
11-10 Area 2	Gp3	g.chr4:169227844G>A	Missense Mutation	DDX60	p.P98S	DEAD (Asp-Glu-Ala-A	131 (0.00)	25 (0.52)	1.39
11-10 Area 2	Gp3	g.chr8:142195275C>T	Silent	DENND3	p.H994H	DENN/MADD domain	36 (0.00)	18 (0.94)	2.52
11-10 Area 2	Gp3	g.chr9:22451753C>T	Missense Mutation	DMRTA1	p.S453L	DMRT-like family A1	145 (0.00)	15 (0.93)	2.49
11-10 Area 2	Gp3	g.chr7:86822515C>A	Splice Site	DMTF1	p.S499Y	cyclin D binding myb-li	98 (0.00)	69 (0.25)	0.66
11-10 Area 2	Gp3	g.chr11:6589778G>T	Silent	DNHD1	p.V4211V	dynein heavy chain dom	25 (0.00)	87 (0.20)	0.52
11-10 Area 2	Gp3	g.chr6:127611088C>A	Missense Mutation	ECHDC1	p.D284Y	enoyl CoA hydratase do	100 (0.00)	48 (0.52)	1.39
11-10 Area 2	Gp3	g.chr2:99980830C>A	Missense Mutation	EIF5B	p.Q412K	eukaryotic translation in	195 (0.00)	179 (0.65)	1.73
11-10 Area 2	Gp3	g.chr3:10016117C>A	Missense Mutation	EMC3	p.M121I	ER membrane protein c	25 (0.00)	173 (0.99)	2.65
11-10 Area 2	Gp3	g.chr1:8925468C>T	Silent	ENO1	p.A247A	enolase 1, (alpha)	69 (0.01)	31 (0.97)	2.58
11-10 Area 2	Gp3	g.chr21:39781516A>G	Intron	ERG		v-ets avian erythroblast	40 (0.03)	226 (0.84)	2.23
11-10 Area 2	Gp3	g.chr21:39784988G>T	Intron	ERG		v-ets avian erythroblast	33 (0.00)	94 (0.99)	2.64
11-10 Area 2	Gp3	g.chr21:39795276C>A	Intron	ERG		v-ets avian erythroblast	15 (0.00)	17 (0.82)	2.20
11-10 Area 2	Gp3	g.chr21:39978316A>G	Intron	ERG		v-ets avian erythroblast	26 (0.00)	57 (0.18)	0.47
11-10 Area 2	Gp3	g.chr10:94757300C>T	Silent	EXOC6	p.L675L	exocyst complex compo	86 (0.01)	94 (0.21)	0.57
11-10 Area 2	Gp3	g.chr10:120877051_12087	Frame Shift Del	FAM45A	p.S118fs	family with sequence si	62 (0.00)	128 (0.98)	2.62
11-10 Area 2	Gp3	g.chr17:644608G>T	Missense Mutation	FAM57A	p.C159F	family with sequence si	45 (0.02)	99 (0.17)	0.46
11-10 Area 2	Gp3	g.chr4:187540319_187540	Frame Shift Del	FAT1	p.S2475fs	FAT atypical cadherin 1	63 (0.00)	129 (0.95)	2.54
11-10 Area 2	Gp3	g.chr3:97711649C>G	RNA	GABRR3		gamma-aminobutyric ac	79 (0.00)	14 (0.43)	1.14
11-10 Area 2	Gp3	g.chr3:97711787G>A	RNA	GABRR3		gamma-aminobutyric ac	150 (0.00)	112 (0.99)	2.64
11-10 Area 2	Gp3	g.chr5:132200163A>T	Silent	GDF9	p.I21I	growth differentiation f	118 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp3	g.chr9:36234086C>T	Silent	GNE	p.E161E	glucosamine (UDP-N-a	47 (0.00)	14 (0.36)	0.95
11-10 Area 2	Gp3	g.chr1:156565355C>T	Missense Mutation	GPATCH4	p.E260K	G patch domain contain	199 (0.01)	36 (0.94)	2.52
11-10 Area 2	Gp3	g.chr12:67072664T>A	Missense Mutation	GRIP1	p.K7N	glutamate receptor inter	49 (0.00)	25 (0.96)	2.56
11-10 Area 2	Gp3	g.chr12:67072665T>A	Missense Mutation	GRIP1	p.K7I	glutamate receptor inter	49 (0.00)	24 (0.96)	2.56
11-10 Area 2	Gp3	g.chr12:67072666T>A	Nonsense Mutation	GRIP1	p.K7*	glutamate receptor inter	49 (0.00)	24 (0.96)	2.56
11-10 Area 2	Gp3	g.chrX:51487880C>T	Silent	GSPT2	p.H386H	G1 to S phase transition	42 (0.00)	94 (0.99)	1.65
11-10 Area 2	Gp3	g.chr9:135555190G>T	Splice Site	GTF3C4	p.R728R	general transcription fac	37 (0.00)	24 (0.33)	0.89
11-10 Area 2	Gp3	g.chr7:18905097C>A	Intron	HDAC9		histone deacetylase 9	147 (0.00)	7 (0.71)	1.90
11-10 Area 2	Gp3	g.chr7:18980840C>T	Intron	HDAC9		histone deacetylase 9	140 (0.01)	62 (0.95)	2.54
11-10 Area 2	Gp3	g.chr15:20620340T>A	RNA	HERC2P3		hect domain and RLD 2	24 (0.00)	26 (0.92)	2.46
11-10 Area 2	Gp3	g.chr5:74009451_7400945	Frame Shift Del	HEXB	p.W298fs	hexosaminidase B (beta	24 (0.00)	91 (0.99)	2.64
11-10 Area 2	Gp3	g.chr5:74011405T>A	Silent	HEXB	p.P324P	hexosaminidase B (beta	36 (0.03)	75 (0.55)	1.46
11-10 Area 2	Gp3	g.chr1:114483675C>A	Missense Mutation	HIPK1	p.H224N	homeodomain interactin	49 (0.00)	28 (0.21)	0.57
11-10 Area 2	Gp3	g.chr1:120298203T>C	Missense Mutation	HMGCS2	p.D345G	3-hydroxy-3-methylglut	350 (0.00)	61 (0.95)	2.54

11-10 Area 2	Gp3	g.chr10:91098875G>T	Missense Mutation	IFIT3	p.A155S	interferon-induced prote	64 (0.00)	157 (0.94)	2.51
11-10 Area 2	Gp3	g.chr11:118427653A>G	Silent	IFT46	p.D51D	intraflagellar transport 4	27 (0.00)	77 (0.51)	1.35
11-10 Area 2	Gp3	g.chr4:143002078T>C	Intron	INPP4B		inositol polyphosphate-	42 (0.00)	201 (0.39)	1.03
11-10 Area 2	Gp3	g.chr4:143053795C>T	Intron	INPP4B		inositol polyphosphate-	140 (0.00)	9 (0.78)	2.07
11-10 Area 2	Gp3	g.chr4:143171043C>T	Intron	INPP4B		inositol polyphosphate-	173 (0.01)	364 (0.54)	1.43
11-10 Area 2	Gp3	g.chr4:143171054C>T	Intron	INPP4B		inositol polyphosphate-	169 (0.01)	330 (0.56)	1.49
11-10 Area 2	Gp3	g.chr4:143252964C>T	Intron	INPP4B		inositol polyphosphate-	42 (0.00)	171 (0.99)	2.64
11-10 Area 2	Gp3	g.chr16:47195728C>A	Nonsense Mutation	ITFG1	p.E532*	integrin alpha FG-GAP	39 (0.00)	159 (0.28)	0.75
11-10 Area 2	Gp3	g.chr17:3646895C>G	Missense Mutation	ITGAE	p.C779S	integrin, alpha E (antige	50 (0.00)	81 (0.98)	2.60
11-10 Area 2	Gp3	g.chr8:73849779C>A	Missense Mutation	KCNB2	p.P730Q	potassium voltage-gated	147 (0.00)	321 (0.60)	1.59
11-10 Area 2	Gp3	g.chr11:128710049G>A	Silent	KCNJ1	p.C30C	potassium inwardly-rect	104 (0.01)	30 (0.97)	2.58
11-10 Area 2	Gp3	g.chr6:138584550C>T	Missense Mutation	KIAA1244	p.P644S	KIAA1244	37 (0.03)	104 (0.52)	1.38
11-10 Area 2	Gp3	g.chr5:154395616A>G	Missense Mutation	KIF4B	p.S733G	kinesin family member	15 (0.00)	27 (0.44)	1.19
11-10 Area 2	Gp3	g.chr3:47308478C>A	Silent	KIF9	p.L252L	kinesin family member	45 (0.00)	15 (0.93)	2.49
11-10 Area 2	Gp3	g.chr19:18779942C>A	Missense Mutation	KLHL26	p.Q579K	kelch-like family memb	15 (0.00)	31 (0.94)	2.49
11-10 Area 2	Gp3	g.chr8:124664537G>A	Silent	KLHL38	p.A210A	kelch-like family memb	93 (0.00)	31 (0.35)	0.95
11-10 Area 2	Gp3	g.chr3:160219963_160219	Frame Shift Del	KPNA4	p.PE498fs	karyopherin alpha 4 (im	135 (0.00)	50 (0.98)	2.61
11-10 Area 2	Gp3	g.chr12:52882272C>A	Missense Mutation	KRT6A	p.D422Y	keratin 6A	61 (0.00)	9 (0.56)	1.48
11-10 Area 2	Gp3	g.chr6:112493909C>A	Missense Mutation	LAMA4	p.L485F	laminin, alpha 4	71 (0.00)	28 (0.46)	1.24
11-10 Area 2	Gp3	g.chr10:98715160G>A	Missense Mutation	LCOR	p.M261I	ligand dependent nuclea	58 (0.00)	42 (0.98)	2.60
11-10 Area 2	Gp3	g.chr14:106940375C>T	lincRNA	LINC00221		long intergenic non-prot	143 (0.00)	28 (0.57)	1.52
11-10 Area 2	Gp3	g.chr2:141283869G>T	Missense Mutation	LRP1B	p.P2605T	low density lipoprotein	56 (0.00)	86 (0.99)	2.64
11-10 Area 2	Gp3	g.chr12:12318094G>T	Silent	LRP6	p.R561R	low density lipoprotein	112 (0.00)	120 (0.99)	2.12
11-10 Area 2	Gp3	g.chr1:235993708C>T	Missense Mutation	LYST	p.D4N	lysosomal trafficking re	65 (0.00)	121 (0.29)	0.77
11-10 Area 2	Gp3	g.chr12:9098021G>A	Silent	M6PR	p.F112F	mannose-6-phosphate re	16 (0.00)	64 (0.47)	1.00
11-10 Area 2	Gp3	g.chr7:77805268G>A	Intron	MAGI2		membrane associated gu	78 (0.01)	198 (0.25)	0.66
11-10 Area 2	Gp3	g.chr7:77823669G>A	Intron	MAGI2		membrane associated gu	143 (0.01)	38 (0.97)	2.60
11-10 Area 2	Gp3	g.chr7:77860844G>A	Intron	MAGI2		membrane associated gu	183 (0.01)	93 (0.42)	1.12
11-10 Area 2	Gp3	g.chr7:78024547A>G	Intron	MAGI2		membrane associated gu	30 (0.00)	45 (0.96)	2.55
11-10 Area 2	Gp3	g.chr7:78024628A>G	Intron	MAGI2		membrane associated gu	44 (0.00)	82 (0.99)	2.63
11-10 Area 2	Gp3	g.chr7:78400475C>T	Intron	MAGI2		membrane associated gu	61 (0.00)	9 (0.89)	2.37
11-10 Area 2	Gp3	g.chr7:79002060G>A	Intron	MAGI2		membrane associated gu	84 (0.00)	141 (0.17)	0.45
11-10 Area 2	Gp3	g.chr15:52356876G>A	Silent	MAPK6	p.K615K	mitogen-activated protei	104 (0.00)	46 (0.93)	2.49
11-10 Area 2	Gp3	g.chr11:63668126_636681	Frame Shift Del	MARK2	p.P256fs	MAP/microtubule affini	438 (0.00)	197 (0.94)	2.52
11-10 Area 2	Gp3	g.chr2:198571617C>T	Silent	MARS2	p.N496N	methionyl-tRNA synthe	42 (0.00)	94 (0.49)	1.30

11-10 Area 2	Gp3	g.chr7:116403181C>T	Silent	MET	p.P832P	MET proto-oncogene, r	62 (0.00)	9 (0.89)	2.37
11-10 Area 2	Gp3	g.chr7:131071990A>T	Missense Mutation	MKLN1	p.N94Y	muskelin 1, intracellula	49 (0.02)	107 (0.78)	2.07
11-10 Area 2	Gp3	g.chr21:37741753_377417	In Frame Del	MORC3	p.696_697L	MORC family CW-type	75 (0.00)	80 (0.88)	2.33
11-10 Area 2	Gp3	g.chr11:118107941G>A	Missense Mutation	MPZL3	p.T80I	myelin protein zero-like	129 (0.00)	139 (0.47)	1.25
11-10 Area 2	Gp3	g.chr7:100648662C>T	Missense Mutation	MUC12	p.P5083S	mucin 12, cell surface a	151 (0.00)	180 (0.16)	0.41
11-10 Area 2	Gp3	g.chr19:9048895A>C	Missense Mutation	MUC16	p.S10912R	mucin 16, cell surface a	120 (0.01)	115 (0.71)	1.90
11-10 Area 2	Gp3	g.chr2:171264276G>A	Missense Mutation	MYO3B	p.A858T	myosin IIIB	223 (0.00)	18 (0.94)	2.52
11-10 Area 2	Gp3	g.chr5:150056321G>A	Missense Mutation	MYOZ3	p.G214S	myozenin 3	66 (0.00)	131 (0.63)	1.67
11-10 Area 2	Gp3	g.chr20:62839452_628394	Frame Shift Del	MYT1	p.EE301fs	myelin transcription fac	27 (0.00)	36 (0.44)	1.19
11-10 Area 2	Gp3	g.chr20:62839469C>A	Missense Mutation	MYT1	p.A307E	myelin transcription fac	29 (0.00)	14 (0.36)	0.95
11-10 Area 2	Gp3	g.chr3:113440685G>A	Silent	NAA50	p.P144P	N(alpha)-acetyltransfera	23 (0.00)	77 (0.92)	2.46
11-10 Area 2	Gp3	g.chr12:6626536C>A	Silent	NCAPD2	p.L397L	non-SMC condensin I c	99 (0.00)	116 (0.66)	1.42
11-10 Area 2	Gp3	g.chr10:75563357G>A	Missense Mutation	NDST2	p.A706V	N-deacetylase/N-sulfotr	27 (0.00)	25 (0.20)	0.53
11-10 Area 2	Gp3	g.chr4:1991530G>A	Missense Mutation	NELFA	p.T150M	negative elongation fact	86 (0.01)	35 (0.40)	1.07
11-10 Area 2	Gp3	g.chr4:103505913_103505	Frame Shift Del	NFKB1	p.R336fs	nuclear factor of kappa	41 (0.00)	86 (0.98)	2.60
11-10 Area 2	Gp3	g.chr5:43700256G>A	Missense Mutation	NNT	p.G971D	nicotinamide nucleotide	83 (0.00)	172 (0.99)	2.65
11-10 Area 2	Gp3	g.chr17:65734419G>A	Missense Mutation	NOL11	p.E571K	nucleolar protein 11	86 (0.01)	279 (0.26)	0.70
11-10 Area 2	Gp3	g.chr2:203152388C>A	Missense Mutation	NOP58	p.S147Y	NOP58 ribonucleoprote	26 (0.00)	158 (0.40)	1.06
11-10 Area 2	Gp3	g.chr1:162313635T>C	Missense Mutation	NOS1AP	p.M155T	nitric oxide synthase 1 (	56 (0.00)	39 (0.26)	0.68
11-10 Area 2	Gp3	g.chr2:184024295C>A	Missense Mutation	NUP35	p.T273K	nucleoporin 35kDa	24 (0.00)	51 (0.57)	1.52
11-10 Area 2	Gp3	g.chr1:247752291T>A	Silent	OR2G2	p.L210L	olfactory receptor, famil	43 (0.00)	31 (0.97)	2.58
11-10 Area 2	Gp3	g.chr11:5863126A>G	Splice Site	OR52E6	p.M1T	olfactory receptor, famil	190 (0.01)	168 (0.18)	0.49
11-10 Area 2	Gp3	g.chr11:4608295C>T	Missense Mutation	OR52I2	p.R85W	olfactory receptor, famil	251 (0.00)	556 (0.22)	0.58
11-10 Area 2	Gp3	g.chr12:55886529C>T	Missense Mutation	OR6C68	p.A123V	olfactory receptor, famil	47 (0.00)	11 (0.73)	1.94
11-10 Area 2	Gp3	g.chr11:123676169C>T	Missense Mutation	OR6M1	p.V297M	olfactory receptor, famil	23 (0.04)	118 (0.98)	2.62
11-10 Area 2	Gp3	g.chr2:179226447A>G	Missense Mutation	OSBPL6	p.I423V	oxysterol binding protei	53 (0.00)	81 (0.58)	1.55
11-10 Area 2	Gp3	g.chr1:26314775T>A	Silent	PAFAH2	p.T96T	platelet-activating facto	53 (0.00)	82 (0.98)	2.60
11-10 Area 2	Gp3	g.chr9:112686021_112686	Frame Shift Del	PALM2-AKAI	p.Q89fs	PALM2-AKAP2 readth	34 (0.00)	24 (0.88)	2.33
11-10 Area 2	Gp3	g.chr5:140572607A>G	Missense Mutation	PCDHB10	p.D161G	protocadherin beta 10	157 (0.01)	150 (0.23)	0.62
11-10 Area 2	Gp3	g.chr13:113832532G>T	Missense Mutation	PCID2	p.P394T	PCI domain containing	30 (0.00)	40 (0.40)	1.07
11-10 Area 2	Gp3	g.chr12:130847567G>T	Missense Mutation	PIWIL1	p.E691D	piwi-like RNA-mediate	62 (0.00)	104 (0.27)	0.72
11-10 Area 2	Gp3	g.chr16:81198225C>A	RNA	PKD1L2		polycystic kidney diseas	47 (0.00)	10 (0.80)	2.13
11-10 Area 2	Gp3	g.chr2:159477503C>T	Splice Site	PKP4	p.D94D	plakophilin 4	83 (0.00)	86 (0.34)	0.90
11-10 Area 2	Gp3	g.chr14:77751910C>A	Silent	POMT2	p.R466R	protein-O-mannosyltran	47 (0.02)	17 (0.76)	2.04
11-10 Area 2	Gp3	g.chr1:13219539C>A	Nonsense Mutation	PRAMEF26	p.E15*	PRAME family membe	236 (0.00)	53 (0.98)	2.62

11-10 Area 2	Gp3	g.chr10:6527177C>T	Missense Mutation	PRKCQ	p.G319S	protein kinase C, theta	74 (0.00)	32 (0.38)	1.00
11-10 Area 2	Gp3	g.chr11:60668994C>T	Missense Mutation	PRPF19	p.V182M	pre-mRNA processing f	45 (0.00)	23 (0.91)	2.43
11-10 Area 2	Gp3	g.chr15:55916569T>A	Missense Mutation	PRTG	p.I1022F	protogenin	37 (0.00)	26 (0.19)	0.51
11-10 Area 2	Gp3	g.chr19:43382219C>T	Silent	PSG1	p.G92G	pregnancy specific beta-	98 (0.01)	117 (0.22)	0.59
11-10 Area 2	Gp3	g.chr10:89688456A>G	Intron	PTEN		phosphatase and tensin	127 (0.00)	102 (0.83)	2.22
11-10 Area 2	Gp3	g.chr1:44085377G>A	Silent	PTPRF	p.T1644T	protein tyrosine phospha	31 (0.00)	27 (0.96)	2.57
11-10 Area 2	Gp3	g.chr19:55711617G>T	Silent	PTPRH	p.V469V	protein tyrosine phospha	33 (0.00)	16 (0.50)	1.33
11-10 Area 2	Gp3	g.chr2:109383168G>A	Missense Mutation	RANBP2	p.G2058E	RAN binding protein 2	365 (0.00)	117 (0.98)	2.62
11-10 Area 2	Gp3	g.chr5:130841099C>T	Silent	RAPGEF6	p.Q353Q	Rap guanine nucleotide	36 (0.00)	291 (0.24)	0.65
11-10 Area 2	Gp3	g.chr13:48908527C>A	Intron	RB1		retinoblastoma 1	73 (0.01)	149 (0.70)	1.88
11-10 Area 2	Gp3	g.chr13:48920051_489200	Intron	RB1		retinoblastoma 1	66 (0.00)	101 (0.66)	1.77
11-10 Area 2	Gp3	g.chr2:152289658A>G	Silent	RIF1	p.T331T	replication timing regula	17 (0.00)	67 (0.49)	1.31
11-10 Area 2	Gp3	g.chr18:110349G>T	RNA	ROCK1P1		Rho-associated, coiled-	63 (0.02)	23 (0.22)	0.58
11-10 Area 2	Gp3	g.chr9:41963928T>A	lincRNA	RP11-204M4.2			371 (0.00)	186 (0.99)	2.65
11-10 Area 2	Gp3	g.chr17:17505615A>G	RNA	RP11-524F11.2			15 (0.00)	9 (0.78)	2.07
11-10 Area 2	Gp3	g.chr14:20146889G>A	lincRNA	RP11-597A11.6			82 (0.01)	132 (0.57)	1.52
11-10 Area 2	Gp3	g.chr8:10466244C>T	Silent	RP1L1	p.G1788G	retinitis pigmentosa 1-li	30 (0.00)	33 (0.97)	2.59
11-10 Area 2	Gp3	g.chr1:59361222G>A	lincRNA	RP4-794H19.1			15 (0.00)	15 (0.93)	2.49
11-10 Area 2	Gp3	g.chr1:59361227G>A	lincRNA	RP4-794H19.1			15 (0.00)	17 (0.94)	2.51
11-10 Area 2	Gp3	g.chr22:39711388C>G	Missense Mutation	RPL3	p.G225A	ribosomal protein L3	84 (0.00)	37 (0.24)	0.65
11-10 Area 2	Gp3	g.chr8:99057190_9905719	Frame Shift Del	RPL30	p.AN49fs	ribosomal protein L30	173 (0.00)	55 (0.96)	2.57
11-10 Area 2	Gp3	g.chr11:77412683C>G	Missense Mutation	RSF1	p.E531Q	remodeling and spacing	209 (0.00)	49 (0.98)	2.61
11-10 Area 2	Gp3	g.chr11:65731576C>T	Silent	SART1	p.A115A	squamous cell carcinom	18 (0.00)	17 (0.88)	2.35
11-10 Area 2	Gp3	g.chr11:121174149G>A	Nonsense Mutation	SC5D	p.W22*	sterol-C5-desaturase	104 (0.00)	13 (0.46)	1.23
11-10 Area 2	Gp3	g.chr11:121174150G>T	Missense Mutation	SC5D	p.W22C	sterol-C5-desaturase	107 (0.00)	14 (0.43)	1.14
11-10 Area 2	Gp3	g.chr12:109017877G>T	Silent	SELPLG	p.T85T	selectin P ligand	21 (0.00)	114 (0.18)	0.47
11-10 Area 2	Gp3	g.chr3:72860243G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	36 (0.03)	380 (0.78)	2.07
11-10 Area 2	Gp3	g.chr22:32614606C>T	Silent	SLC5A4	p.K625K	solute carrier family 5 (	62 (0.00)	108 (0.85)	2.27
11-10 Area 2	Gp3	g.chr13:88328385G>T	Missense Mutation	SLITRK5	p.D248Y	SLIT and NTRK-like fa	31 (0.00)	33 (0.55)	1.45
11-10 Area 2	Gp3	g.chr2:241991773C>A	Splice Site	SNED1	p.A657A	sushi, nidogen and EGF	17 (0.00)	226 (0.46)	1.23
11-10 Area 2	Gp3	g.chr1:16260257C>A	Missense Mutation	SPEN	p.P2508T	spen family transcriptio	38 (0.00)	11 (0.73)	1.94
11-10 Area 2	Gp3	g.chr17:47681620T>C	Intron	SPOP		speckle-type POZ protei	90 (0.01)	92 (0.99)	2.06
11-10 Area 2	Gp3	g.chr17:47725324A>T	Intron	SPOP		speckle-type POZ protei	71 (0.00)	58 (0.98)	2.04
11-10 Area 2	Gp3	g.chr12:57492812C>A	Missense Mutation	STAT6	p.K537N	signal transducer and ac	135 (0.00)	93 (0.24)	0.63
11-10 Area 2	Gp3	g.chr7:87910242G>A	Silent	STEAP4	p.F379F	STEAP family member	135 (0.01)	96 (0.72)	1.92

11-10 Area 2	Gp3	g.chr3:121137250T>A	Missense Mutation	STXBP5L	p.I1122K	syntaxin binding protein	41 (0.00)	138 (0.75)	1.99
11-10 Area 2	Gp3	g.chr8:38677214C>T	Missense Mutation	TACC1	p.P151L	transforming, acidic coil	77 (0.00)	298 (0.32)	0.84
11-10 Area 2	Gp3	g.chr2:162274741C>T	Missense Mutation	TBR1	p.P293S	T-box, brain, 1	53 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp3	g.chr7:139636024G>T	Missense Mutation	TBXAS1	p.S123I	thromboxane A synthas	29 (0.00)	35 (0.71)	1.90
11-10 Area 2	Gp3	g.chr4:183713942G>T	Silent	TENM3	p.L2039L	teneurin transmembrane	265 (0.00)	134 (0.97)	2.59
11-10 Area 2	Gp3	g.chr17:62265796G>T	Splice Site	TEX2	p.A726D	testis expressed 2	26 (0.00)	33 (0.21)	0.57
11-10 Area 2	Gp3	g.chr1:43783614A>G	Silent	TIE1	p.K931K	tyrosine kinase with im	133 (0.00)	196 (0.20)	0.53
11-10 Area 2	Gp3	g.chr10:63195929T>C	Splice Site	TMEM26	p.Q90R	transmembrane protein	20 (0.00)	40 (0.53)	1.40
11-10 Area 2	Gp3	g.chr3:36897445A>T	Silent	TRANK1	p.S662S	tetratricopeptide repeat	142 (0.01)	52 (0.96)	2.56
11-10 Area 2	Gp3	g.chr7:142428870G>T	RNA	TRBV28		T cell receptor beta vari	75 (0.00)	32 (0.28)	0.75
11-10 Area 2	Gp3	g.chr6:42196349C>T	Missense Mutation	TRERF1	p.E1113K	transcriptional regulatin	63 (0.00)	22 (0.91)	2.42
11-10 Area 2	Gp3	g.chr15:45059481C>A	Silent	TRIM69	p.L338L	tripartite motif containin	65 (0.02)	24 (0.54)	1.44
11-10 Area 2	Gp3	g.chr9:135797312G>A	Missense Mutation	TSC1	p.A186V	tuberous sclerosis 1	106 (0.01)	34 (0.91)	2.43
11-10 Area 2	Gp3	g.chr9:135797337C>A	Missense Mutation	TSC1	p.V178F	tuberous sclerosis 1	122 (0.01)	35 (0.91)	2.44
11-10 Area 2	Gp3	g.chr6:158923037G>C	Missense Mutation	TULP4	p.G781A	tubby like protein 4	68 (0.01)	211 (0.40)	1.06
11-10 Area 2	Gp3	g.chr6:42620252C>T	Missense Mutation	UBR2	p.P880S	ubiquitin protein ligase	116 (0.00)	54 (0.85)	2.27
11-10 Area 2	Gp3	g.chr1:45478979C>A	Missense Mutation	UROD	p.P77T	uroporphyrinogen decar	42 (0.00)	81 (0.41)	1.09
11-10 Area 2	Gp3	g.chr17:9604667A>G	Splice Site	USP43		ubiquitin specific peptid	23 (0.00)	81 (0.17)	0.46
11-10 Area 2	Gp3	g.chr11:11913582C>A	Missense Mutation	USP47	p.S162Y	ubiquitin specific peptid	60 (0.02)	446 (0.29)	0.77
11-10 Area 2	Gp3	g.chr9:2643450G>A	Missense Mutation	VLDLR	p.G247S	very low density lipopr	19 (0.00)	18 (0.83)	2.22
11-10 Area 2	Gp3	g.chr8:100831041T>C	Missense Mutation	VPS13B	p.I2874T	vacuolar protein sorting	17 (0.00)	84 (0.19)	0.51
11-10 Area 2	Gp3	g.chr2:20153627C>A	Missense Mutation	WDR35	p.Q456H	WD repeat domain 35	120 (0.01)	10 (0.80)	2.13
11-10 Area 2	Gp3	g.chr5:112889360G>T	Missense Mutation	YTHDC2	p.K647N	YTH domain containing	87 (0.00)	20 (0.50)	1.33
11-10 Area 2	Gp3	g.chr7:100365567C>T	RNA	ZAN		zonadhesin (gene/pseud	36 (0.00)	52 (0.98)	2.62
11-10 Area 2	Gp3	g.chr1:203807112C>A	Missense Mutation	ZC3H11A	p.P298Q	zinc finger CCCH-type	102 (0.01)	32 (0.19)	0.50
11-10 Area 2	Gp3	g.chr9:88959923G>T	Silent	ZCCHC6	p.I322I	zinc finger, CCHC dom	32 (0.00)	18 (0.94)	2.52
11-10 Area 2	Gp3	g.chr9:88959941C>T	Silent	ZCCHC6	p.R316R	zinc finger, CCHC dom	31 (0.00)	9 (0.89)	2.37
11-10 Area 2	Gp3	g.chr2:207171551C>A	Missense Mutation	ZDBF2	p.L767M	zinc finger, DBF-type c	193 (0.00)	38 (0.16)	0.42
11-10 Area 2	Gp3	g.chr11:9499982_9499983	Frame Shift Del	ZNF143	p.G112fs	zinc finger protein 143	50 (0.00)	189 (0.94)	2.51
11-10 Area 2	Gp3	g.chr17:15620481C>T	Silent	ZNF286A	p.L481L	zinc finger protein 286A	38 (0.00)	22 (0.91)	2.42
11-10 Area 2	Gp3	g.chr19:37117415C>T	Nonsense Mutation	ZNF382	p.Q205*	zinc finger protein 382	68 (0.00)	17 (0.94)	2.51
11-10 Area 2	Gp3	g.chr3:21706412G>T	Missense Mutation	ZNF385D	p.A44E	zinc finger protein 385D	27 (0.00)	139 (0.47)	1.27
11-10 Area 2	Gp3	g.chr19:58929145C>T	Silent	ZNF584	p.S420S	zinc finger protein 584	38 (0.00)	52 (0.23)	0.62
11-10 Area 2	Gp3	g.chr17:3969771C>A	Nonsense Mutation	ZZEF1	p.E1407*	zinc finger, ZZ-type wit	156 (0.01)	19 (0.58)	1.54
11-10 Area 2	Gp4	g.chr16:48130672C>A	Missense Mutation	ABCC12	p.L1060F	ATP-binding cassette, s	172 (0.01)	71 (0.21)	0.56

11-10 Area 2	Gp4	g.chr3:183699544C>T	Nonsense Mutation	ABCC5	p.W373*	ATP-binding cassette, s	50 (0.00)	20 (0.90)	2.40
11-10 Area 2	Gp4	g.chr12:40013054_400130	Frame Shift Del	ABCD2	p.SI121fs	ATP-binding cassette, s	48 (0.00)	56 (0.62)	1.67
11-10 Area 2	Gp4	g.chr12:40013070T>A	Silent	ABCD2	p.S116S	ATP-binding cassette, s	72 (0.00)	25 (0.76)	2.03
11-10 Area 2	Gp4	g.chr9:133738271C>T	Missense Mutation	ABL1	p.T224I	ABL proto-oncogene 1,	79 (0.00)	18 (0.72)	1.93
11-10 Area 2	Gp4	g.chr6:160196277C>G	Missense Mutation	ACAT2	p.T189R	acetyl-CoA acetyltransf	54 (0.00)	25 (0.64)	1.71
11-10 Area 2	Gp4	g.chr20:44472344C>A	Missense Mutation	ACOT8	p.K221N	acyl-CoA thioesterase 8	17 (0.00)	46 (0.72)	1.91
11-10 Area 2	Gp4	g.chr3:64644397C>T	Silent	ADAMTS9	p.L250L	ADAM metallopeptidas	56 (0.02)	13 (0.77)	2.05
11-10 Area 2	Gp4	g.chr10:88761367T>C	RNA	AGAP11		ankyrin repeat and GTP	326 (0.00)	204 (0.22)	0.59
11-10 Area 2	Gp4	g.chr1:247040534G>T	Missense Mutation	AHCTF1	p.H946N	AT hook containing trar	41 (0.00)	34 (0.29)	0.78
11-10 Area 2	Gp4	g.chr3:186330969C>G	Silent	AHSG	p.L13L	alpha-2-HS-glycoprotei	26 (0.00)	40 (0.97)	2.60
11-10 Area 2	Gp4	g.chr14:96924498G>A	Missense Mutation	AK7	p.D436N	adenylate kinase 7	27 (0.00)	19 (0.47)	1.26
11-10 Area 2	Gp4	g.chr15:86270399G>A	Missense Mutation	AKAP13	p.E2313K	A kinase (PRKA) ancho	46 (0.00)	34 (0.74)	1.96
11-10 Area 2	Gp4	g.chr9:38395790G>A	Silent	ALDH1B1	p.R15R	aldehyde dehydrogenase	26 (0.00)	95 (0.99)	2.64
11-10 Area 2	Gp4	g.chr4:114277470C>A	Missense Mutation	ANK2	p.H2533N	ankyrin 2, neuronal	92 (0.00)	12 (0.75)	2.00
11-10 Area 2	Gp4	g.chr17:64212969C>A	Missense Mutation	APOH	p.D241Y	apolipoprotein H (beta-	65 (0.00)	26 (0.23)	0.62
11-10 Area 2	Gp4	g.chr11:110450268_11045	Frame Shift Del	ARHGAP20	p.K677fs	Rho GTPase activating	19 (0.00)	17 (0.59)	1.57
11-10 Area 2	Gp4	g.chr12:58008371G>A	Missense Mutation	ARHGEF25	p.G306R	Rho guanine nucleotide	25 (0.00)	35 (0.66)	1.75
11-10 Area 2	Gp4	g.chr12:58008374G>A	Missense Mutation	ARHGEF25	p.D307N	Rho guanine nucleotide	24 (0.00)	35 (0.66)	1.75
11-10 Area 2	Gp4	g.chr19:12856303G>A	Missense Mutation	ASNA1	p.G141D	arsA arsenite transporte	16 (0.00)	13 (0.92)	2.46
11-10 Area 2	Gp4	g.chr18:55368298C>A	Missense Mutation	ATP8B1	p.R176M	ATPase, aminophospho	60 (0.00)	18 (0.44)	1.19
11-10 Area 2	Gp4	g.chr1:154316398G>A	Silent	ATP8B2	p.L629L	ATPase, aminophospho	20 (0.00)	10 (0.60)	1.60
11-10 Area 2	Gp4	g.chr1:110033653C>A	Missense Mutation	ATXN7L2	p.L490M	ataxin 7-like 2	42 (0.00)	144 (0.99)	2.65
11-10 Area 2	Gp4	g.chr12:58203454C>T	Missense Mutation	AVIL	p.G289R	advillin	48 (0.00)	21 (0.90)	2.41
11-10 Area 2	Gp4	g.chr15:91272861C>A	Intron	BLM		Bloom syndrome, RecQ	23 (0.00)	20 (0.30)	0.80
11-10 Area 2	Gp4	g.chr17:28599876G>T	Missense Mutation	BLMH	p.N281K	bleomycin hydrolase	81 (0.00)	94 (0.96)	2.55
11-10 Area 2	Gp4	g.chr19:55805469G>A	Silent	BRSK1	p.Q181Q	BR serine/threonine kin	36 (0.03)	61 (0.98)	2.62
11-10 Area 2	Gp4	g.chr3:49693118G>A	Silent	BSN	p.T2043T	bassoon presynaptic cyt	77 (0.01)	28 (0.86)	2.29
11-10 Area 2	Gp4	g.chr6:26368983G>T	Silent	BTN3A2	p.P92P	butyrophilin, subfamily	256 (0.00)	123 (0.23)	0.61
11-10 Area 2	Gp4	g.chr12:4627389A>T	Missense Mutation	C12orf4	p.L290M	chromosome 12 open re	118 (0.00)	40 (0.97)	2.60
11-10 Area 2	Gp4	g.chr16:1470338_1470339	Frame Shift Del	C16orf91	p.Q103fs	chromosome 16 open re	15 (0.00)	26 (0.96)	2.56
11-10 Area 2	Gp4	g.chr19:36255952C>T	Missense Mutation	C19orf55	p.S215F		54 (0.00)	133 (0.59)	1.58
11-10 Area 2	Gp4	g.chr2:191064793C>A	Silent	C2orf88	p.I69I	chromosome 2 open rea	143 (0.01)	116 (0.97)	2.60
11-10 Area 2	Gp4	g.chr9:100678484T>C	Silent	C9orf156	p.E71E	chromosome 9 open rea	107 (0.01)	43 (0.28)	0.74
11-10 Area 2	Gp4	g.chr3:85393734G>A	Intron	CADM2		cell adhesion molecule	19 (0.00)	140 (0.79)	2.10
11-10 Area 2	Gp4	g.chr3:85399657G>A	Intron	CADM2		cell adhesion molecule	46 (0.00)	110 (0.86)	2.30

11-10 Area 2	Gp4	g.chr3:85621721G>A	Intron	CADM2		cell adhesion molecule	37 (0.03)	173 (0.32)	0.86
11-10 Area 2	Gp4	g.chr3:85739720G>A	Intron	CADM2		cell adhesion molecule	60 (0.02)	37 (0.86)	2.31
11-10 Area 2	Gp4	g.chr3:85927176G>T	Intron	CADM2		cell adhesion molecule	33 (0.00)	68 (0.44)	1.18
11-10 Area 2	Gp4	g.chr10:106130728A>G	Missense Mutation	CCDC147	p.K336E		20 (0.00)	154 (0.23)	0.62
11-10 Area 2	Gp4	g.chr1:159860340T>A	Missense Mutation	CCDC19	p.T68S		115 (0.00)	68 (0.19)	0.51
11-10 Area 2	Gp4	g.chr17:37627800C>T	Missense Mutation	CDK12	p.A572V	cyclin-dependent kinase	105 (0.01)	94 (0.85)	2.27
11-10 Area 2	Gp4	g.chr12:96683054C>A	Missense Mutation	CDK17	p.A337S	cyclin-dependent kinase	110 (0.00)	42 (0.98)	2.60
11-10 Area 2	Gp4	g.chr9:130550317C>T	Silent	CDK9	p.V119V	cyclin-dependent kinase	71 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp4	g.chr4:119459021G>A	RNA	CEP170P1		centrosomal protein 170	276 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp4	g.chr5:98195248C>T	Intron	CHD1		chromodomain helicase	89 (0.00)	16 (0.50)	1.33
11-10 Area 2	Gp4	g.chr1:6189721A>G	Intron	CHD5		chromodomain helicase	30 (0.00)	91 (0.22)	0.59
11-10 Area 2	Gp4	g.chr1:6235320_6235320in	Intron	CHD5		chromodomain helicase	35 (0.00)	43 (0.47)	1.24
11-10 Area 2	Gp4	g.chr18:24496808G>T	Silent	CHST9	p.V249V	carbohydrate (N-acetylg	62 (0.00)	9 (0.56)	1.48
11-10 Area 2	Gp4	g.chr3:150659510G>A	Missense Mutation	CLRN1	p.H98Y	clarin 1	33 (0.00)	17 (0.76)	2.04
11-10 Area 2	Gp4	g.chr4:78663450C>T	Splice Site	CNOT6L		CCR4-NOT transcriptio	51 (0.00)	172 (0.60)	1.61
11-10 Area 2	Gp4	g.chr17:40714878C>T	Missense Mutation	COASY	p.H80Y	CoA synthase	79 (0.01)	164 (0.63)	1.69
11-10 Area 2	Gp4	g.chr13:40301650A>G	Missense Mutation	COG6	p.I597M	component of oligomeri	81 (0.01)	50 (0.32)	0.85
11-10 Area 2	Gp4	g.chr13:111088624_11108	Frame Shift Del	COL4A2	p.G246fs	collagen, type IV, alpha	44 (0.00)	77 (0.48)	1.28
11-10 Area 2	Gp4	g.chr3:130284329C>T	Nonsense Mutation	COL6A6	p.Q385*	collagen, type VI, alpha	56 (0.00)	67 (0.88)	2.35
11-10 Area 2	Gp4	g.chr16:3807954G>A	Silent	CREBBP	p.D1155D	CREB binding protein	64 (0.02)	121 (0.20)	0.53
11-10 Area 2	Gp4	g.chr3:97607290G>A	Silent	CRYBG3	p.P517P	beta-gamma crystallin d	129 (0.00)	106 (0.98)	2.62
11-10 Area 2	Gp4	g.chr10:68940144C>A	Missense Mutation	CTNNA3	p.E326D	catenin (cadherin-associ	106 (0.00)	66 (0.20)	0.53
11-10 Area 2	Gp4	g.chr3:41277291G>A	Missense Mutation	CTNNB1	p.R587Q	catenin (cadherin-associ	83 (0.00)	18 (0.78)	2.07
11-10 Area 2	Gp4	g.chr1:47399873G>T	Missense Mutation	CYP4A11	p.L355M	cytochrome P450, famil	15 (0.00)	26 (0.96)	2.56
11-10 Area 2	Gp4	g.chr9:124351296C>T	Intron	DAB2IP		DAB2 interacting protei	58 (0.02)	231 (0.18)	0.47
11-10 Area 2	Gp4	g.chr9:124421226T>A	Intron	DAB2IP		DAB2 interacting protei	41 (0.02)	77 (0.83)	2.22
11-10 Area 2	Gp4	g.chr9:124429265G>A	Intron	DAB2IP		DAB2 interacting protei	34 (0.03)	85 (0.87)	2.32
11-10 Area 2	Gp4	g.chr9:124510177G>A	Intron	DAB2IP		DAB2 interacting protei	110 (0.00)	205 (0.73)	1.94
11-10 Area 2	Gp4	g.chr1:114454692_114454	Frame Shift Del	DCLRE1B	p.L493fs	DNA cross-link repair 1	36 (0.00)	32 (0.94)	2.50
11-10 Area 2	Gp4	g.chr1:114454714A>T	Silent	DCLRE1B	p.L500L	DNA cross-link repair 1	35 (0.00)	21 (0.95)	2.54
11-10 Area 2	Gp4	g.chr13:95114311C>A	Missense Mutation	DCT	p.Q332H	dopachrome tautomeras	66 (0.00)	40 (0.15)	0.40
11-10 Area 2	Gp4	g.chr22:38890102T>A	Nonsense Mutation	DDX17	p.K417*	DEAD (Asp-Glu-Ala-A	25 (0.00)	11 (0.82)	2.18
11-10 Area 2	Gp4	g.chr19:19038822A>C	Missense Mutation	DDX49	p.K414Q	DEAD (Asp-Glu-Ala-A	18 (0.00)	46 (0.20)	0.52
11-10 Area 2	Gp4	g.chr12:56345524C>T	Missense Mutation	DGKA	p.P515L	diacylglycerol kinase, al	41 (0.00)	18 (0.89)	2.37
11-10 Area 2	Gp4	g.chr15:40659478C>T	Nonsense Mutation	DISP2	p.Q389*	dispatched homolog 2 (	50 (0.00)	86 (0.24)	0.65

11-10 Area 2	Gp4	g.chrX:31227662_3122766	In Frame Del	DMD	p.P3172del	dystrophin	34 (0.00)	17 (0.76)	1.27
11-10 Area 2	Gp4	g.chr5:78328610C>T	Missense Mutation	DMGDH	p.G473R	dimethylglycine dehydr	19 (0.00)	71 (0.21)	0.56
11-10 Area 2	Gp4	g.chr9:22451533G>A	Missense Mutation	DMRTA1	p.E380K	DMRT-like family A1	45 (0.00)	16 (0.94)	2.50
11-10 Area 2	Gp4	g.chr1:15871055C>A	Missense Mutation	DNAJC16	p.L246I	DnaJ (Hsp40) homolog,	73 (0.00)	147 (0.34)	0.91
11-10 Area 2	Gp4	g.chr1:63100520_6310052	Frame Shift Del	DOCK7	p.A321fs	dedicator of cytokinesis	31 (0.00)	35 (0.94)	2.51
11-10 Area 2	Gp4	g.chr1:221879615C>A	Missense Mutation	DUSP10	p.Q335H	dual specificity phospha	177 (0.00)	96 (0.25)	0.67
11-10 Area 2	Gp4	g.chr3:108363485G>T	Missense Mutation	DZIP3	p.R539L	DAZ interacting zinc fi	48 (0.00)	16 (0.88)	2.33
11-10 Area 2	Gp4	g.chr6:139197618G>T	Missense Mutation	ECT2L	p.V530F	epithelial cell transform	74 (0.00)	52 (0.90)	2.41
11-10 Area 2	Gp4	g.chr4:148463701C>A	Silent	EDNRA	p.I405I	endothelin receptor type	34 (0.00)	39 (0.31)	0.82
11-10 Area 2	Gp4	g.chr5:38350681C>A	Silent	EGFLAM	p.R124R	EGF-like, fibronectin ty	62 (0.00)	83 (0.75)	1.99
11-10 Area 2	Gp4	g.chr3:183855834C>A	Missense Mutation	EIF2B5	p.Q219K	eukaryotic translation in	67 (0.00)	21 (0.90)	2.41
11-10 Area 2	Gp4	g.chr10:81272837G>A	Silent	EIF5AL1	p.E144E	eukaryotic translation in	82 (0.01)	93 (0.33)	0.89
11-10 Area 2	Gp4	g.chr17:12905776G>A	Silent	ELAC2	p.L400L	elaC ribonuclease Z 2	20 (0.00)	71 (0.58)	1.54
11-10 Area 2	Gp4	g.chr22:41546114C>A	Missense Mutation	EP300	p.P910H	E1A binding protein p3	18 (0.00)	121 (0.47)	1.26
11-10 Area 2	Gp4	g.chr22:41574695C>T	Missense Mutation	EP300	p.P2327L	E1A binding protein p3	19 (0.00)	17 (0.29)	0.78
11-10 Area 2	Gp4	g.chr19:16472630G>A	Missense Mutation	EPS15L1	p.P849L	epidermal growth factor	22 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp4	g.chr2:212252698G>A	Missense Mutation	ERBB4	p.P1052L	v-erb-b2 avian erythrob	76 (0.00)	9 (0.56)	1.48
11-10 Area 2	Gp4	g.chrX:71426054C>A	Nonsense Mutation	ERCC6L	p.E732*	excision repair cross-co	25 (0.00)	35 (0.43)	0.71
11-10 Area 2	Gp4	g.chr21:39787582T>A	Intron	ERG		v-ets avian erythroblast	22 (0.00)	87 (0.99)	2.64
11-10 Area 2	Gp4	g.chr21:39814511G>T	Intron	ERG		v-ets avian erythroblast	41 (0.02)	165 (0.96)	2.57
11-10 Area 2	Gp4	g.chr21:39839066T>C	Intron	ERG		v-ets avian erythroblast	47 (0.02)	337 (0.22)	0.59
11-10 Area 2	Gp4	g.chr21:39957040C>T	Intron	ERG		v-ets avian erythroblast	51 (0.00)	51 (0.73)	1.93
11-10 Area 2	Gp4	g.chr2:158178227C>T	Silent	ERMN	p.Q137Q	ermin, ERM-like protei	21 (0.00)	53 (0.66)	1.76
11-10 Area 2	Gp4	g.chr1:11147613G>A	Silent	EXOSC10	p.C327C	exosome component 10	213 (0.00)	34 (0.76)	2.04
11-10 Area 2	Gp4	g.chr6:159191874C>T	Missense Mutation	EZR	p.E338K	ezrin	75 (0.00)	33 (0.24)	0.65
11-10 Area 2	Gp4	g.chr11:58919439G>T	Nonsense Mutation	FAM111A	p.E100*	family with sequence si	103 (0.00)	40 (0.55)	1.47
11-10 Area 2	Gp4	g.chr9:130270227C>A	Nonsense Mutation	FAM129B	p.E525*	family with sequence si	30 (0.00)	15 (0.93)	2.49
11-10 Area 2	Gp4	g.chr5:137298091_137298	Splice Site	FAM13B		family with sequence si	88 (0.00)	36 (0.97)	2.59
11-10 Area 2	Gp4	g.chr7:30931594_3093159	Frame Shift Del	FAM188B	p.W750fs	family with sequence si	121 (0.00)	114 (0.99)	2.64
11-10 Area 2	Gp4	g.chr4:159092153C>A	Silent	FAM198B	p.V125V	family with sequence si	101 (0.01)	84 (0.42)	1.11
11-10 Area 2	Gp4	g.chr3:10106096C>A	Silent	FANCD2	p.S668S	Fanconi anemia, compl	26 (0.00)	34 (0.68)	1.80
11-10 Area 2	Gp4	g.chr9:137801800T>C	Silent	FCN1	p.Q275Q	ficolin (collagen/fibrino	106 (0.00)	207 (1.00)	2.65
11-10 Area 2	Gp4	g.chr9:137801868T>A	Missense Mutation	FCN1	p.N253Y	ficolin (collagen/fibrino	115 (0.00)	220 (1.00)	2.65
11-10 Area 2	Gp4	g.chr9:108370116G>A	Missense Mutation	FKTN	p.V222I	fukutin	112 (0.00)	168 (0.45)	1.19
11-10 Area 2	Gp4	g.chr9:14859447A>T	Missense Mutation	FREM1	p.I122N	FRAS1 related extracell	152 (0.00)	16 (0.31)	0.83

11-10 Area 2	Gp4	g.chr15:44175990C>T	Missense Mutation	FRMD5	p.S349N	FERM domain containi	39 (0.00)	12 (0.92)	2.44
11-10 Area 2	Gp4	g.chr13:32745264C>A	Missense Mutation	FRY	p.L670M	furry homolog (Drosop	46 (0.00)	13 (0.38)	1.03
11-10 Area 2	Gp4	g.chr2:208632041G>A	Missense Mutation	FZD5	p.R475C	frizzled class receptor 5	15 (0.00)	20 (0.85)	2.27
11-10 Area 2	Gp4	g.chr5:151179522C>G	Missense Mutation	G3BP1	p.Q306E	GTPase activating prote	34 (0.00)	16 (0.38)	1.00
11-10 Area 2	Gp4	g.chr7:127225078C>A	Missense Mutation	GCC1	p.E53D	GRIP and coiled-coil d	128 (0.00)	14 (0.86)	2.29
11-10 Area 2	Gp4	g.chr17:651192G>C	Missense Mutation	GEMIN4	p.L31V	gem (nuclear organelle)	17 (0.00)	48 (0.98)	2.61
11-10 Area 2	Gp4	g.chr2:85783372C>A	Missense Mutation	GGCX	p.G184V	gamma-glutamyl carbox	53 (0.02)	30 (0.97)	2.58
11-10 Area 2	Gp4	g.chr5:102433387G>T	Silent	GIN1	p.I246I	gypsy retrotransposon i	64 (0.02)	163 (0.67)	1.78
11-10 Area 2	Gp4	g.chr15:75557731G>T	Missense Mutation	GOLGA6C	p.R242L	golgin A6 family, mem	225 (0.00)	14 (0.93)	2.48
11-10 Area 2	Gp4	g.chr8:145138381C>A	Missense Mutation	GPAA1	p.P115Q	glycosylphosphatidylin	52 (0.00)	20 (0.95)	2.53
11-10 Area 2	Gp4	g.chr13:27333772C>G	Missense Mutation	GPR12	p.V65L	G protein-coupled recep	50 (0.00)	31 (0.48)	1.29
11-10 Area 2	Gp4	g.chr1:6314703G>A	Missense Mutation	GPR153	p.S88F	G protein-coupled recep	20 (0.00)	54 (0.30)	0.79
11-10 Area 2	Gp4	g.chr13:99908088A>G	Silent	GPR18	p.F13F	G protein-coupled recep	47 (0.00)	227 (0.64)	1.72
11-10 Area 2	Gp4	g.chr3:151012960T>C	Missense Mutation	GPR87	p.N25S	G protein-coupled recep	28 (0.00)	25 (0.32)	0.85
11-10 Area 2	Gp4	g.chrX:51487938C>T	Missense Mutation	GSPT2	p.P406S	G1 to S phase transition	44 (0.02)	108 (0.85)	1.42
11-10 Area 2	Gp4	g.chr12:96387880G>T	Silent	HAL	p.R133R	histidine ammonia-lyas	286 (0.00)	29 (0.41)	1.10
11-10 Area 2	Gp4	g.chr4:174448477C>A	Missense Mutation	HAND2	p.G202V	heart and neural crest d	40 (0.00)	15 (0.87)	2.31
11-10 Area 2	Gp4	g.chr7:18548927G>A	Intron	HDAC9		histone deacetylase 9	103 (0.00)	63 (0.19)	0.51
11-10 Area 2	Gp4	g.chr7:18557338G>T	Intron	HDAC9		histone deacetylase 9	153 (0.00)	142 (0.39)	1.05
11-10 Area 2	Gp4	g.chr7:18660447C>A	Intron	HDAC9		histone deacetylase 9	97 (0.00)	20 (0.50)	1.33
11-10 Area 2	Gp4	g.chr7:18702043G>A	Intron	HDAC9		histone deacetylase 9	171 (0.00)	65 (0.98)	2.63
11-10 Area 2	Gp4	g.chr7:18792350C>A	Intron	HDAC9		histone deacetylase 9	49 (0.00)	31 (0.97)	2.58
11-10 Area 2	Gp4	g.chr7:18799811C>T	Intron	HDAC9		histone deacetylase 9	40 (0.00)	17 (0.59)	1.57
11-10 Area 2	Gp4	g.chr7:18897321C>T	Intron	HDAC9		histone deacetylase 9	33 (0.00)	25 (0.92)	2.45
11-10 Area 2	Gp4	g.chr7:18897323T>G	Intron	HDAC9		histone deacetylase 9	34 (0.00)	25 (0.92)	2.45
11-10 Area 2	Gp4	g.chr7:18964929G>A	Intron	HDAC9		histone deacetylase 9	74 (0.00)	17 (0.82)	2.20
11-10 Area 2	Gp4	g.chr7:18977443A>T	Intron	HDAC9		histone deacetylase 9	46 (0.00)	18 (0.61)	1.63
11-10 Area 2	Gp4	g.chr14:31828227_318282	Frame Shift Del	HEATR5A	p.D703fs	HEAT repeat containin	178 (0.00)	99 (0.97)	2.59
11-10 Area 2	Gp4	g.chr15:64021785_640217	In Frame Del	HERC1	p.977_978S	HECT and RLD domai	114 (0.00)	112 (0.96)	2.57
11-10 Area 2	Gp4	g.chr16:56976089_569760	Frame Shift Del	HERPUD1	p.F318fs	homocysteine-inducible	184 (0.00)	181 (0.99)	2.65
11-10 Area 2	Gp4	g.chr7:75186024G>A	Missense Mutation	HIP1	p.T558I	huntingtin interacting p	40 (0.00)	35 (0.91)	2.44
11-10 Area 2	Gp4	g.chr6:52880935C>T	Silent	ICK	p.Q259Q	intestinal cell (MAK-lik	46 (0.00)	10 (0.90)	2.40
11-10 Area 2	Gp4	g.chr3:129195634_129195	Frame Shift Del	IFT122	p.E380fs	intraflagellar transport 1	23 (0.00)	21 (0.71)	1.90
11-10 Area 2	Gp4	g.chr12:110572798G>A	Missense Mutation	IFT81	p.V189I	intraflagellar transport 8	34 (0.00)	7 (0.71)	1.90
11-10 Area 2	Gp4	g.chr11:18738275G>A	Splice Site	IGSF22	p.R416C	immunoglobulin superf	39 (0.03)	26 (0.27)	0.72

11-10 Area 2	Gp4	g.chr11:18738287G>A	Missense Mutation	IGSF22	p.L412F	immunoglobulin superf	39 (0.00)	25 (0.24)	0.64
11-10 Area 2	Gp4	g.chr3:159819613G>A	RNA	IL12A-AS1		IL12A antisense RNA 1	16 (0.00)	13 (0.92)	2.46
11-10 Area 2	Gp4	g.chr2:113742503C>A	Silent	IL36G	p.T129T	interleukin 36, gamma	31 (0.00)	68 (0.22)	0.59
11-10 Area 2	Gp4	g.chr4:143098074_143098	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	49 (0.37)	0.98
11-10 Area 2	Gp4	g.chr4:143273253T>A	Intron	INPP4B		inositol polyphosphate-	238 (0.00)	113 (0.97)	2.60
11-10 Area 2	Gp4	g.chr4:143273266T>A	Intron	INPP4B		inositol polyphosphate-	294 (0.00)	114 (0.93)	2.48
11-10 Area 2	Gp4	g.chr4:143290154G>T	Intron	INPP4B		inositol polyphosphate-	46 (0.00)	50 (0.30)	0.80
11-10 Area 2	Gp4	g.chr4:143365045G>A	Intron	INPP4B		inositol polyphosphate-	39 (0.00)	23 (0.57)	1.51
11-10 Area 2	Gp4	g.chr4:143508037G>A	Intron	INPP4B		inositol polyphosphate-	44 (0.00)	18 (0.83)	2.22
11-10 Area 2	Gp4	g.chr4:143561345C>T	Intron	INPP4B		inositol polyphosphate-	25 (0.00)	79 (0.68)	1.82
11-10 Area 2	Gp4	g.chr4:143561350C>T	Intron	INPP4B		inositol polyphosphate-	25 (0.00)	71 (0.69)	1.84
11-10 Area 2	Gp4	g.chr4:143680814G>T	Intron	INPP4B		inositol polyphosphate-	34 (0.03)	120 (0.45)	1.20
11-10 Area 2	Gp4	g.chr21:35144573G>A	Silent	ITSN1	p.R417R	intersectin 1 (SH3 doma	15 (0.00)	10 (0.70)	1.87
11-10 Area 2	Gp4	g.chr10:24834907C>T	Missense Mutation	KIAA1217	p.P1829L	KIAA1217	77 (0.00)	54 (0.98)	2.62
11-10 Area 2	Gp4	g.chr2:8952601C>T	Nonsense Mutation	KIDINS220	p.W143*	kinase D-interacting su	34 (0.00)	11 (0.91)	2.42
11-10 Area 2	Gp4	g.chr11:28110248G>A	Silent	KIF18A	p.D240D	kinesin family member	52 (0.00)	21 (0.76)	2.03
11-10 Area 2	Gp4	g.chr20:30898784G>A	Missense Mutation	KIF3B	p.E402K	kinesin family member	23 (0.00)	108 (0.38)	1.01
11-10 Area 2	Gp4	g.chr4:38691473T>A	Missense Mutation	KLF3	p.V223E	Kruppel-like factor 3 (b	118 (0.00)	13 (0.77)	2.05
11-10 Area 2	Gp4	g.chr11:118373290C>A	Missense Mutation	KMT2A	p.S2228Y	lysine (K)-specific meth	49 (0.00)	43 (0.33)	0.87
11-10 Area 2	Gp4	g.chr7:151849829G>T	Missense Mutation	KMT2C	p.L4163M	lysine (K)-specific meth	82 (0.00)	21 (0.62)	1.65
11-10 Area 2	Gp4	g.chr6:117053447_117053	Frame Shift Del	KPNA5	p.FQ527fs	karyopherin alpha 5 (im	79 (0.00)	66 (0.98)	2.63
11-10 Area 2	Gp4	g.chr12:52826868_528268	In Frame Del	KRT75	p.E222del	keratin 75	16 (0.00)	53 (0.40)	1.06
11-10 Area 2	Gp4	g.chr18:6943316C>A	Missense Mutation	LAMA1	p.W2977L	laminin, alpha 1	112 (0.01)	154 (0.78)	2.08
11-10 Area 2	Gp4	g.chr18:6943333C>A	Silent	LAMA1	p.V2971V	laminin, alpha 1	106 (0.00)	146 (0.44)	1.17
11-10 Area 2	Gp4	g.chr11:27390231G>A	Missense Mutation	LGR4	p.P680L	leucine-rich repeat cont	61 (0.00)	16 (0.38)	1.00
11-10 Area 2	Gp4	g.chr3:197746201C>G	Missense Mutation	LMLN	p.A474G	leishmanolysin-like (me	127 (0.00)	82 (0.56)	1.50
11-10 Area 2	Gp4	g.chr6:160913995C>T	RNA	LPAL2		lipoprotein, Lp(a)-like 2	119 (0.00)	13 (0.92)	2.46
11-10 Area 2	Gp4	g.chr16:55562327C>T	Missense Mutation	LPCAT2	p.A117V	lysophosphatidylcholin	146 (0.00)	42 (0.31)	0.83
11-10 Area 2	Gp4	g.chr2:141283887C>T	Missense Mutation	LRP1B	p.A2599T	low density lipoprotein	55 (0.02)	21 (0.95)	2.54
11-10 Area 2	Gp4	g.chr1:90178987G>A	Silent	LRRC8C	p.K286K	leucine rich repeat cont	77 (0.00)	71 (0.94)	2.52
11-10 Area 2	Gp4	g.chr2:74834292A>C	Missense Mutation	M1AP	p.L162W	meiosis 1 associated pr	29 (0.00)	56 (0.29)	0.76
11-10 Area 2	Gp4	g.chrX:140993926C>G	Missense Mutation	MAGEC1	p.L246V	melanoma antigen famil	76 (0.01)	21 (0.90)	1.51
11-10 Area 2	Gp4	g.chr7:77733015G>A	Intron	MAGI2		membrane associated g	72 (0.00)	203 (0.23)	0.62
11-10 Area 2	Gp4	g.chr7:77875926G>A	Intron	MAGI2		membrane associated g	74 (0.00)	23 (0.57)	1.51
11-10 Area 2	Gp4	g.chr7:78024631G>T	Intron	MAGI2		membrane associated g	47 (0.00)	31 (0.16)	0.43

11-10 Area 2	Gp4	g.chr7:78120245_7812024	Intron	MAGI2		membrane associated gu	124 (0.00)	248 (0.37)	0.98
11-10 Area 2	Gp4	g.chr7:78175999C>T	Intron	MAGI2		membrane associated gu	116 (0.00)	19 (0.95)	2.53
11-10 Area 2	Gp4	g.chr7:78322653A>T	Intron	MAGI2		membrane associated gu	68 (0.00)	43 (0.98)	2.60
11-10 Area 2	Gp4	g.chr7:78332375G>A	Intron	MAGI2		membrane associated gu	54 (0.00)	28 (0.29)	0.76
11-10 Area 2	Gp4	g.chr7:78371015C>A	Intron	MAGI2		membrane associated gu	29 (0.00)	36 (0.58)	1.56
11-10 Area 2	Gp4	g.chr7:78371049G>A	Intron	MAGI2		membrane associated gu	28 (0.00)	10 (0.80)	2.13
11-10 Area 2	Gp4	g.chr7:78394356G>A	Intron	MAGI2		membrane associated gu	161 (0.01)	41 (0.95)	2.54
11-10 Area 2	Gp4	g.chr7:78917941G>T	Intron	MAGI2		membrane associated gu	39 (0.00)	114 (0.18)	0.47
11-10 Area 2	Gp4	g.chr7:79043089C>T	Intron	MAGI2		membrane associated gu	39 (0.00)	231 (0.20)	0.54
11-10 Area 2	Gp4	g.chr9:139994191_139994	Frame Shift Del	MAN1B1	p.H259fs	mannosidase, alpha, cla	38 (0.00)	23 (0.91)	2.43
11-10 Area 2	Gp4	g.chr5:71491107C>A	Missense Mutation	MAP1B	p.T642K	microtubule-associated	43 (0.00)	60 (0.97)	2.58
11-10 Area 2	Gp4	g.chr2:102452364C>T	Missense Mutation	MAP4K4	p.L233F	mitogen-activated prote	50 (0.02)	62 (0.98)	2.62
11-10 Area 2	Gp4	g.chr12:57906707A>T	Missense Mutation	MARS	p.N643Y	methionyl-tRNA synthe	102 (0.00)	73 (0.41)	1.10
11-10 Area 2	Gp4	g.chr1:85487848G>A	Silent	MCOLN3	p.L409L	mucolipin 3	55 (0.00)	44 (0.39)	1.03
11-10 Area 2	Gp4	g.chr11:86219885G>T	Missense Mutation	ME3	p.D164E	malic enzyme 3, NADP	47 (0.00)	19 (0.84)	2.25
11-10 Area 2	Gp4	g.chr3:168807858C>T	Missense Mutation	MECOM	p.E914K	MDS1 and EVI1 compl	113 (0.00)	13 (0.92)	2.46
11-10 Area 2	Gp4	g.chr15:100185820G>A	Missense Mutation	MEF2A	p.V37M	myocyte enhancer facto	61 (0.00)	91 (0.44)	1.17
11-10 Area 2	Gp4	g.chr2:112702565G>A	Missense Mutation	MERTK	p.G171R	MER proto-oncogene, t	83 (0.01)	54 (0.91)	2.42
11-10 Area 2	Gp4	g.chr7:116397781G>A	Silent	MET	p.G685G	MET proto-oncogene, r	41 (0.00)	58 (0.26)	0.69
11-10 Area 2	Gp4	g.chr13:103343306T>C	Missense Mutation	METTL21C	p.K47E	methyltransferase like 2	21 (0.00)	58 (0.31)	0.83
11-10 Area 2	Gp4	g.chr4:128843045C>A	Nonsense Mutation	MFSD8	p.G358*	major facilitator superfa	19 (0.00)	39 (0.90)	2.39
11-10 Area 2	Gp4	g.chr12:56845079G>A	Silent	MIP	p.N259N	major intrinsic protein o	94 (0.00)	11 (0.91)	2.42
11-10 Area 2	Gp4	g.chr6:168325706C>A	Missense Mutation	MLLT4	p.P1005T	myeloid/lymphoid or mi	30 (0.00)	46 (0.46)	1.45
11-10 Area 2	Gp4	g.chr11:118107863G>C	Missense Mutation	MPZL3	p.P106R	myelin protein zero-like	150 (0.00)	88 (0.55)	1.45
11-10 Area 2	Gp4	g.chr11:94192640C>T	Silent	MRE11A	p.L478L	MRE11 meiotic recomb	127 (0.00)	46 (0.26)	0.70
11-10 Area 2	Gp4	g.chr8:121426231G>A	Splice Site	MRPL13	p.P172S	mitochondrial ribosoma	49 (0.02)	126 (0.52)	1.40
11-10 Area 2	Gp4	g.chr11:60183345C>T	Nonsense Mutation	MS4A14	p.Q335*	membrane-spanning 4-d	65 (0.00)	195 (0.37)	0.98
11-10 Area 2	Gp4	g.chr11:60183747C>T	Nonsense Mutation	MS4A14	p.Q469*	membrane-spanning 4-d	42 (0.00)	104 (0.20)	0.54
11-10 Area 2	Gp4	g.chr11:62362494G>A	Missense Mutation	MTA2	p.P338L	metastasis associated 1	61 (0.00)	17 (0.71)	1.88
11-10 Area 2	Gp4	g.chr7:100640008C>A	Nonsense Mutation	MUC12	p.S2198*	mucin 12, cell surface a	421 (0.00)	20 (0.90)	2.40
11-10 Area 2	Gp4	g.chr19:9046787C>A	Missense Mutation	MUC16	p.R11615M	mucin 16, cell surface a	83 (0.00)	62 (0.34)	0.90
11-10 Area 2	Gp4	g.chr7:100683893C>T	Missense Mutation	MUC17	p.L3066F	mucin 17, cell surface a	74 (0.01)	75 (0.28)	0.75
11-10 Area 2	Gp4	g.chr11:1093028C>T	Missense Mutation	MUC2	p.T1616I	mucin 2, oligomeric mu	17 (0.00)	17 (0.53)	1.41
11-10 Area 2	Gp4	g.chr11:1016931G>A	Missense Mutation	MUC6	p.A1957V	mucin 6, oligomeric mu	452 (0.00)	32 (0.16)	0.42
11-10 Area 2	Gp4	g.chr11:1017596T>G	Missense Mutation	MUC6	p.Q1735H	mucin 6, oligomeric mu	244 (0.00)	331 (0.27)	0.71

11-10 Area 2	Gp4	g.chr17:48606115G>T	Nonsense Mutation	MYCBPAP	p.E866*	MYCBP associated prot	21 (0.00)	42 (0.14)	0.38
11-10 Area 2	Gp4	g.chr6:76599938_7659995	Frame Shift Del	MYO6	p.EDEKRR	myosin VI	89 (0.00)	156 (0.68)	1.81
11-10 Area 2	Gp4	g.chr10:69934036C>T	Silent	MYPN	p.S729S	myopalladin	54 (0.02)	29 (0.93)	2.48
11-10 Area 2	Gp4	g.chr1:148754951G>A	Missense Mutation	NBPF16	p.G536E		178 (0.00)	134 (0.98)	2.61
11-10 Area 2	Gp4	g.chr10:51584746C>A	Missense Mutation	NCOA4	p.S282Y	nuclear receptor coactiv	119 (0.00)	12 (0.50)	1.33
11-10 Area 2	Gp4	g.chr4:121958011T>G	Missense Mutation	NDNF	p.Q372P	neuron-derived neurotro	135 (0.00)	17 (0.29)	0.78
11-10 Area 2	Gp4	g.chr14:35871264C>T	Silent	NFKBIA	p.L260L	nuclear factor of kappa	278 (0.00)	144 (0.30)	0.80
11-10 Area 2	Gp4	g.chr11:129739582_12973	Frame Shift Del	NFRKB	p.Q1113fs	nuclear factor related to	85 (0.00)	52 (0.94)	2.51
11-10 Area 2	Gp4	g.chr9:33318757T>C	Silent	NFX1	p.D539D	nuclear transcription fac	127 (0.00)	129 (0.24)	0.64
11-10 Area 2	Gp4	g.chr15:23006615C>A	Missense Mutation	NIPA2	p.S230I	non imprinted in Prader-	73 (0.00)	29 (0.52)	1.38
11-10 Area 2	Gp4	g.chr15:23006641C>A	Silent	NIPA2	p.L221L	non imprinted in Prader-	78 (0.00)	27 (0.48)	1.28
11-10 Area 2	Gp4	g.chr17:26370174C>A	Missense Mutation	NLK	p.P92Q	nemo-like kinase	22 (0.00)	34 (0.71)	1.88
11-10 Area 2	Gp4	g.chr19:54318211C>G	Silent	NLRP12	p.G107G	NLR family, pyrin dom	74 (0.00)	21 (0.81)	2.16
11-10 Area 2	Gp4	g.chr18:11619810T>A	RNA	NPIPB1P		nuclear pore complex in	72 (0.00)	34 (0.26)	0.71
11-10 Area 2	Gp4	g.chr14:90782932C>A	Nonsense Mutation	NRDE2	p.E133*	NRDE-2, necessary for	54 (0.00)	79 (0.18)	0.47
11-10 Area 2	Gp4	g.chr1:46810789G>A	Missense Mutation	NSUN4	p.G137E	NOP2/Sun domain fami	19 (0.00)	33 (0.73)	1.94
11-10 Area 2	Gp4	g.chr14:20404296G>T	Silent	OR4K1	p.V157V	olfactory receptor, famil	175 (0.01)	18 (0.39)	0.84
11-10 Area 2	Gp4	g.chr11:4968216_4968217	Frame Shift Del	OR51A4	p.I39fs	olfactory receptor, famil	118 (0.00)	80 (0.96)	2.57
11-10 Area 2	Gp4	g.chr11:55563602G>A	Missense Mutation	OR5D14	p.G191S	olfactory receptor, famil	236 (0.00)	86 (0.99)	2.64
11-10 Area 2	Gp4	g.chr11:55563738G>A	Missense Mutation	OR5D14	p.R236H	olfactory receptor, famil	58 (0.00)	14 (0.93)	2.48
11-10 Area 2	Gp4	g.chr2:242066295G>T	Missense Mutation	PASK	p.H679N	PAS domain containing	36 (0.00)	44 (0.23)	0.61
11-10 Area 2	Gp4	g.chr5:140262224G>T	Missense Mutation	PCDHA13	p.R124M	protocadherin alpha 13	103 (0.00)	61 (0.64)	1.70
11-10 Area 2	Gp4	g.chr5:140750423G>A	Silent	PCDHGB3	p.L154L	protocadherin gamma s	191 (0.00)	32 (0.16)	0.42
11-10 Area 2	Gp4	g.chr17:36895507C>T	Splice Site	PCGF2		polycomb group ring fir	33 (0.00)	18 (0.89)	2.37
11-10 Area 2	Gp4	g.chr8:17824535C>A	Missense Mutation	PCM1	p.P1090T	pericentriolar material 1	102 (0.00)	270 (0.24)	0.63
11-10 Area 2	Gp4	g.chr11:65384400C>A	Missense Mutation	PCNXL3	p.Q87K	pecanex-like 3 (Drosop	35 (0.00)	42 (0.52)	1.40
11-10 Area 2	Gp4	g.chr1:144915473G>T	Missense Mutation	PDE4DIP	p.S788Y	phosphodiesterase 4D i	55 (0.02)	18 (0.61)	1.63
11-10 Area 2	Gp4	g.chr18:60529883G>T	Intron	PHLPP1		PH domain and leucine	66 (0.00)	19 (0.47)	1.26
11-10 Area 2	Gp4	g.chr18:60534076C>T	Intron	PHLPP1		PH domain and leucine	74 (0.01)	90 (0.98)	2.61
11-10 Area 2	Gp4	g.chr16:71748537G>A	Silent	PHLPP2	p.S54S	PH domain and leucine	22 (0.00)	48 (0.31)	0.83
11-10 Area 2	Gp4	g.chr12:18854480T>C	Silent	PLCZ1	p.T106T	phospholipase C, zeta 1	21 (0.00)	140 (0.31)	0.67
11-10 Area 2	Gp4	g.chr12:18854481G>A	Missense Mutation	PLCZ1	p.T106I	phospholipase C, zeta 1	21 (0.00)	148 (0.34)	0.72
11-10 Area 2	Gp4	g.chr17:62818041G>A	RNA	PLEKHM1P		pleckstrin homology do	71 (0.00)	20 (0.95)	2.53
11-10 Area 2	Gp4	g.chr3:126722214G>T	Silent	PLXNA1	p.L473L	plexin A1	19 (0.00)	27 (0.44)	1.19
11-10 Area 2	Gp4	g.chr14:39648399T>A	Silent	PNN	p.A201A	pinin, desmosome assoc	96 (0.01)	108 (0.96)	2.57

11-10 Area 2	Gp4	g.chr22:38355445_383554	Frame Shift Del	POLR2F	p.R62fs	polymerase (RNA) II (	60 (0.00)	63 (0.97)	2.58
11-10 Area 2	Gp4	g.chr12:106838313C>A	Missense Mutation	POLR3B	p.H676Q	polymerase (RNA) III (	62 (0.00)	66 (0.89)	2.38
11-10 Area 2	Gp4	g.chr7:124532340G>T	Missense Mutation	POT1	p.P35Q	protection of telomeres	219 (0.00)	118 (0.36)	0.95
11-10 Area 2	Gp4	g.chr1:203024669G>T	Missense Mutation	PPFIA4	p.G626C	protein tyrosine phosph	22 (0.00)	22 (0.82)	2.18
11-10 Area 2	Gp4	g.chr2:170492639G>A	Missense Mutation	PPIG	p.R352H	peptidylprolyl isomeras	27 (0.00)	28 (0.36)	0.95
11-10 Area 2	Gp4	g.chr6:42974999_4297500	Frame Shift Del	PPP2R5D	p.E198fs	protein phosphatase 2, r	239 (0.00)	27 (0.85)	2.27
11-10 Area 2	Gp4	g.chr10:103899871A>G	Missense Mutation	PPRC1	p.S536G	peroxisome proliferator-	37 (0.00)	30 (0.97)	2.58
11-10 Area 2	Gp4	g.chr6:106553724C>T	Silent	PRDM1	p.P527P	PR domain containing 1	61 (0.00)	45 (0.24)	0.65
11-10 Area 2	Gp4	g.chr11:45246018C>T	Silent	PRDM11	p.I331I	PR domain containing 1	40 (0.00)	27 (0.89)	2.37
11-10 Area 2	Gp4	g.chr1:3160691G>C	Missense Mutation	PRDM16	p.C143S	PR domain containing 1	66 (0.00)	43 (0.79)	2.11
11-10 Area 2	Gp4	g.chr1:186277676_186277	Frame Shift Del	PRG4	p.ATTTEK	proteoglycan 4	313 (0.00)	129 (0.51)	1.36
11-10 Area 2	Gp4	g.chr1:186277712C>G	Missense Mutation	PRG4	p.T954R	proteoglycan 4	245 (0.00)	62 (0.81)	2.15
11-10 Area 2	Gp4	g.chr3:64145614A>G	Splice Site	PRICKLE2		prickle homolog 2 (Dro	100 (0.00)	22 (0.36)	0.97
11-10 Area 2	Gp4	g.chr5:35068963T>C	Missense Mutation	PRLR	p.T235A	prolactin receptor	141 (0.00)	48 (0.44)	1.17
11-10 Area 2	Gp4	g.chr12:50030598G>A	Missense Mutation	PRPF40B	p.R509Q	PRP40 pre-mRNA proc	36 (0.00)	11 (0.91)	2.42
11-10 Area 2	Gp4	g.chr12:50036134G>T	Missense Mutation	PRPF40B	p.E667D	PRP40 pre-mRNA proc	17 (0.00)	37 (0.70)	1.87
11-10 Area 2	Gp4	g.chr19:43382120T>C	Missense Mutation	PSG1	p.I125M	pregnancy specific beta-	73 (0.01)	99 (0.22)	0.59
11-10 Area 2	Gp4	g.chr5:40681513C>G	Missense Mutation	PTGER4	p.L140V	prostaglandin E recepto	155 (0.01)	155 (0.66)	1.77
11-10 Area 2	Gp4	g.chr15:55841189_558411	Frame Shift Del	PYGO1	p.G18fs	pygopus family PHD fi	17 (0.00)	38 (0.53)	1.40
11-10 Area 2	Gp4	g.chr17:29857383G>A	Missense Mutation	RAB11FIP4	p.G565R	RAB11 family interacti	34 (0.00)	103 (0.19)	0.52
11-10 Area 2	Gp4	g.chr9:125865442C>A	Missense Mutation	RABGAP1	p.L1054M	RAB GTPase activating	49 (0.00)	53 (0.25)	0.65
11-10 Area 2	Gp4	g.chr12:65082160G>T	Silent	RASSF3	p.L128L	Ras association (RalGD	76 (0.00)	14 (0.71)	1.90
11-10 Area 2	Gp4	g.chr13:48909767G>T	Intron	RB1		retinoblastoma 1	16 (0.00)	62 (0.23)	0.60
11-10 Area 2	Gp4	g.chr11:66411480C>A	Silent	RBM14-RBM	p.G299G	RBM14-RBM4 readthr	75 (0.00)	82 (0.27)	0.72
11-10 Area 2	Gp4	g.chr8:30361848T>A	Missense Mutation	RBPMS	p.F98I	RNA binding protein wi	30 (0.03)	31 (0.48)	1.29
11-10 Area 2	Gp4	g.chr4:57777211C>T	Missense Mutation	REST	p.S136L	RE1-silencing transcrip	35 (0.00)	32 (0.88)	2.33
11-10 Area 2	Gp4	g.chr2:85577329C>T	Silent	RETSAT	p.L211L	retinol saturase (all-tran	16 (0.00)	131 (0.27)	0.71
11-10 Area 2	Gp4	g.chr8:125498685C>A	Silent	RNF139	p.S265S	ring finger protein 139	34 (0.00)	23 (0.65)	1.74
11-10 Area 2	Gp4	g.chr9:104314037C>A	Silent	RNF20	p.V448V	ring finger protein 20, E	79 (0.00)	84 (0.29)	0.76
11-10 Area 2	Gp4	g.chr6:89614649C>A	Missense Mutation	RNGTT	p.A157S	RNA guanylyltransfera	40 (0.03)	94 (0.83)	2.21
11-10 Area 2	Gp4	g.chr10:90341966G>T	Missense Mutation	RNLS	p.H73N	renalase, FAD-depende	25 (0.00)	14 (0.50)	0.69
11-10 Area 2	Gp4	g.chr9:109099488C>A	lincRNA	RP11-308N19.1			27 (0.00)	14 (0.50)	1.33
11-10 Area 2	Gp4	g.chr9:6669135G>A	lincRNA	RP11-390F4.6			103 (0.00)	105 (0.87)	2.31
11-10 Area 2	Gp4	g.chr14:24621073G>A	Missense Mutation	RP11-468E2.4	p.E143K		16 (0.00)	20 (0.75)	2.00
11-10 Area 2	Gp4	g.chr18:48104T>C	Silent	RP11-683L23.	p.L173L		411 (0.00)	44 (0.98)	2.61

11-10 Area 2	Gp4	g.chr1:213415003C>A	Silent	RPS6KC1	p.A716A	ribosomal protein S6 ki	24 (0.00)	14 (0.57)	1.52
11-10 Area 2	Gp4	g.chr19:46307834G>A	Silent	RSPH6A	p.H443H	radial spoke head 6 hom	37 (0.00)	145 (0.47)	1.25
11-10 Area 2	Gp4	g.chr1:84765316T>C	Missense Mutation	SAMD13	p.L6S	sterile alpha motif doma	117 (0.00)	76 (0.55)	1.47
11-10 Area 2	Gp4	g.chr12:46319990C>T	Missense Mutation	SCAF11	p.R1165Q	SR-related CTD-associa	103 (0.01)	72 (0.99)	2.63
11-10 Area 2	Gp4	g.chr20:18541334C>A	Missense Mutation	SEC23B	p.Q752K	Sec23 homolog B (S. ce	103 (0.01)	110 (0.45)	1.21
11-10 Area 2	Gp4	g.chr10:102269147C>T	Missense Mutation	SEC31B	p.G109R	SEC31 homolog B (S. c	134 (0.00)	50 (0.28)	0.75
11-10 Area 2	Gp4	g.chr5:9202274C>T	Missense Mutation	SEMA5A	p.C242Y	sema domain, seven thr	48 (0.00)	56 (0.30)	0.81
11-10 Area 2	Gp4	g.chr2:179997128C>T	Missense Mutation	SESTD1	p.G292E	SEC14 and spectrin don	53 (0.00)	59 (0.83)	2.21
11-10 Area 2	Gp4	g.chr18:42531407G>A	Missense Mutation	SETBP1	p.G701E	SET binding protein 1	33 (0.00)	104 (0.99)	2.64
11-10 Area 2	Gp4	g.chr18:42532104C>A	Silent	SETBP1	p.L933L	SET binding protein 1	67 (0.00)	16 (0.94)	2.50
11-10 Area 2	Gp4	g.chr1:35654957G>T	Missense Mutation	SFPQ	p.A481D	splicing factor proline/g	17 (0.00)	19 (0.95)	2.53
11-10 Area 2	Gp4	g.chr4:152096257A>T	Missense Mutation	SH3D19	p.Y87N	SH3 domain containing	45 (0.00)	17 (0.94)	2.51
11-10 Area 2	Gp4	g.chr3:72833413C>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	41 (0.00)	14 (0.86)	2.29
11-10 Area 2	Gp4	g.chr4:72425819C>A	Missense Mutation	SLC4A4	p.L983I	solute carrier family 4 (	36 (0.00)	129 (0.28)	0.74
11-10 Area 2	Gp4	g.chr11:26700282C>A	Missense Mutation	SLC5A12	p.G519V	solute carrier family 5 (	76 (0.00)	35 (0.37)	0.99
11-10 Area 2	Gp4	g.chr19:49812955_498129	Frame Shift Del	SLC6A16	p.C277fs	solute carrier family 6,	73 (0.00)	41 (0.90)	2.41
11-10 Area 2	Gp4	g.chr1:27432470G>A	Missense Mutation	SLC9A1	p.S464F	solute carrier family 9,	18 (0.00)	169 (0.55)	1.47
11-10 Area 2	Gp4	g.chr16:67291323G>A	Missense Mutation	SLC9A5	p.E471K	solute carrier family 9,	95 (0.00)	155 (0.50)	1.34
11-10 Area 2	Gp4	g.chr5:159840466A>T	Missense Mutation	SLU7	p.D189E	SLU7 splicing factor ho	183 (0.00)	17 (0.76)	2.04
11-10 Area 2	Gp4	g.chr18:48560605C>T	Intron	SMAD4		SMAD family member	56 (0.02)	69 (0.17)	0.46
11-10 Area 2	Gp4	g.chr18:48560608T>C	Intron	SMAD4		SMAD family member	53 (0.00)	77 (0.16)	0.42
11-10 Area 2	Gp4	g.chr18:48560611C>T	Intron	SMAD4		SMAD family member	51 (0.00)	67 (0.16)	0.44
11-10 Area 2	Gp4	g.chr3:47702832C>A	Nonsense Mutation	SMARCC1	p.E758*	SWI/SNF related, matri	35 (0.00)	20 (0.50)	1.33
11-10 Area 2	Gp4	g.chr10:112352919G>T	Missense Mutation	SMC3	p.R634L	structural maintenance	39 (0.00)	34 (0.94)	2.51
11-10 Area 2	Gp4	g.chr7:21469455G>C	Silent	SP4	p.L224L	Sp4 transcription factor	94 (0.00)	85 (0.16)	0.44
11-10 Area 2	Gp4	g.chr1:118584573C>T	Silent	SPAG17	p.K969K	sperm associated antige	77 (0.00)	275 (0.22)	0.59
11-10 Area 2	Gp4	g.chr17:47701118A>T	Intron	SPOP		speckle-type POZ prote	42 (0.00)	209 (0.53)	1.42
11-10 Area 2	Gp4	g.chr17:47736697A>T	Intron	SPOP		speckle-type POZ prote	122 (0.00)	135 (0.99)	2.65
11-10 Area 2	Gp4	g.chr12:53468528T>C	Missense Mutation	SPRYD3	p.K175E	SPRY domain containin	66 (0.00)	28 (0.61)	1.62
11-10 Area 2	Gp4	g.chr1:158639272G>A	Silent	SPTA1	p.L587L	spectrin, alpha, erythroc	28 (0.00)	68 (0.96)	2.55
11-10 Area 2	Gp4	g.chr1:85117674C>T	Missense Mutation	SSX2IP	p.A466T	synovial sarcoma, X bre	200 (0.00)	33 (0.94)	2.51
11-10 Area 2	Gp4	g.chr15:42980654C>A	Missense Mutation	STARD9	p.T2293N	StAR-related lipid trans	59 (0.00)	99 (0.51)	1.35
11-10 Area 2	Gp4	g.chr17:40469220G>A	Silent	STAT3	p.T708T	signal transducer and ac	44 (0.00)	11 (0.91)	2.42
11-10 Area 2	Gp4	g.chr1:172525096G>A	Missense Mutation	SUCO	p.D126N	SUN domain containing	21 (0.00)	39 (0.46)	1.23
11-10 Area 2	Gp4	g.chr9:136227975G>T	Missense Mutation	SURF2	p.R244L	surfeit 2	17 (0.00)	28 (0.96)	2.57

11-10 Area 2	Gp4	g.chr14:64593328G>A	Missense Mutation	SYNE2	p.E4525K	spectrin repeat containi	87 (0.00)	35 (0.97)	2.59
11-10 Area 2	Gp4	g.chr10:8007691C>A	Missense Mutation	TAF3	p.H740N	TAF3 RNA polymerase	16 (0.00)	162 (0.17)	0.46
11-10 Area 2	Gp4	g.chr10:105139529G>A	Splice Site	TAF5		TAF5 RNA polymerase	31 (0.00)	27 (0.96)	2.57
11-10 Area 2	Gp4	g.chr7:139636004G>A	Silent	TBXAS1	p.E116E	thromboxane A synthas	20 (0.00)	32 (0.22)	0.58
11-10 Area 2	Gp4	g.chr1:152082370C>T	Missense Mutation	TCHH	p.R1108K	trichohyalin	54 (0.00)	87 (0.17)	0.46
11-10 Area 2	Gp4	g.chr4:106194060G>T	Missense Mutation	TET2	p.A1508S	tet methylcytosine diox	84 (0.00)	36 (0.64)	1.70
11-10 Area 2	Gp4	g.chr15:43569074C>T	Silent	TGM7	p.G653G	transglutaminase 7	17 (0.00)	20 (0.40)	1.07
11-10 Area 2	Gp4	g.chr14:77709261C>T	Silent	TMEM63C	p.V401V	transmembrane protein	137 (0.00)	13 (0.62)	1.64
11-10 Area 2	Gp4	g.chr8:125332413C>A	Missense Mutation	TMEM65	p.A179S	transmembrane protein	76 (0.00)	147 (0.48)	1.29
11-10 Area 2	Gp4	g.chr16:24828246G>C	Silent	TNRC6A	p.R1647R	trinucleotide repeat cont	170 (0.00)	146 (0.32)	1.04
11-10 Area 2	Gp4	g.chr1:186304252G>C	Missense Mutation	TPR	p.Q1641E	translocated promoter r	40 (0.00)	20 (0.40)	1.07
11-10 Area 2	Gp4	g.chr21:10906991G>T	Silent	TPTE	p.R524R	transmembrane phospha	47 (0.00)	27 (0.19)	0.49
11-10 Area 2	Gp4	g.chr5:911998G>A	Missense Mutation	TRIP13	p.E303K	thyroid hormone recept	40 (0.00)	64 (0.31)	0.83
11-10 Area 2	Gp4	g.chr19:31770009C>T	Silent	TSHZ3	p.T230T	teashirt zinc finger hom	129 (0.00)	40 (0.80)	2.13
11-10 Area 2	Gp4	g.chr7:19739858G>A	Missense Mutation	TWISTNB	p.H148Y	TWIST neighbor	55 (0.00)	67 (0.99)	2.63
11-10 Area 2	Gp4	g.chr16:11829917C>A	Missense Mutation	TXNDC11	p.A143S	thioredoxin domain con	91 (0.00)	34 (0.88)	2.35
11-10 Area 2	Gp4	g.chr7:138968165G>T	Silent	UBN2	p.G838G	ubinuclein 2	45 (0.00)	43 (0.47)	1.24
11-10 Area 2	Gp4	g.chr13:115057209_11505	Frame Shift Del	UPF3A	p.C263fs	UPF3 regulator of nons	15 (0.00)	106 (0.32)	0.86
11-10 Area 2	Gp4	g.chr2:61528547T>C	Missense Mutation	USP34	p.E1287G	ubiquitin specific peptid	68 (0.00)	35 (0.43)	1.14
11-10 Area 2	Gp4	g.chr2:61571009G>T	Missense Mutation	USP34	p.S814Y	ubiquitin specific peptid	54 (0.00)	36 (0.33)	0.89
11-10 Area 2	Gp4	g.chr11:75852429G>T	Missense Mutation	UVRAG	p.R319L	UV radiation resistance	96 (0.00)	26 (0.35)	0.92
11-10 Area 2	Gp4	g.chr2:37035871_3703587	Frame Shift Del	VIT	p.I486fs	vitrin	40 (0.00)	45 (0.93)	2.49
11-10 Area 2	Gp4	g.chr8:100733232A>T	Missense Mutation	VPS13B	p.E2361V	vacuolar protein sorting	44 (0.02)	151 (0.72)	1.91
11-10 Area 2	Gp4	g.chr17:531457G>T	Silent	VPS53	p.P234P	vacuolar protein sorting	38 (0.00)	9 (0.89)	2.37
11-10 Area 2	Gp4	g.chr18:60243802C>T	Missense Mutation	ZCCHC2	p.S1176F	zinc finger, CCHC dom	136 (0.00)	176 (0.33)	0.88
11-10 Area 2	Gp4	g.chr2:207171587G>T	Nonsense Mutation	ZDBF2	p.E779*	zinc finger, DBF-type c	175 (0.00)	32 (0.59)	1.58
11-10 Area 2	Gp4	g.chr16:25258351G>T	Missense Mutation	ZKSCAN2	p.T389N	zinc finger with KRAB	68 (0.00)	195 (0.48)	1.58
11-10 Area 2	Gp4	g.chr3:44612108G>A	Silent	ZKSCAN7	p.E502E	zinc finger with KRAB	51 (0.02)	63 (0.98)	2.62
11-10 Area 2	Gp4	g.chr1:40747031C>T	Silent	ZMPSTE24	p.S262S	zinc metallopeptidase S	38 (0.00)	116 (0.39)	1.03
11-10 Area 2	Gp4	g.chr13:20641451T>C	Missense Mutation	ZMYM2	p.F1125S	zinc finger, MYM-type	91 (0.01)	62 (0.21)	0.56
11-10 Area 2	Gp4	g.chr19:22154674T>C	Silent	ZNF208	p.E1054E	zinc finger protein 208	184 (0.01)	29 (0.66)	1.75
11-10 Area 2	Gp4	g.chr19:53304896C>T	Missense Mutation	ZNF28	p.S57N	zinc finger protein 28	177 (0.00)	16 (0.88)	2.33
11-10 Area 2	Gp4	g.chr1:90493196T>A	Nonsense Mutation	ZNF326	p.L473*	zinc finger protein 326	25 (0.00)	26 (0.69)	1.85
11-10 Area 2	Gp4	g.chr19:11978239A>G	Missense Mutation	ZNF439	p.K119E	zinc finger protein 439	69 (0.00)	57 (0.32)	0.84
11-10 Area 2	Gp4	g.chr19:58773270A>G	Missense Mutation	ZNF544	p.E433G	zinc finger protein 544	103 (0.00)	13 (0.54)	1.44

11-10 Area 2	Gp4	g.chr8:144732882C>T	Silent	ZNF623	p.R280R	zinc finger protein 623	62 (0.00)	13 (0.46)	1.23
11-12	Gp3	g.chr19:1043811A>G	Missense Mutation	ABCA7	p.N202D	ATP-binding cassette, s	28 (0.00)	238 (0.36)	0.96
11-12	Gp3	g.chr19:1058163C>A	Silent	ABCA7	p.R1544R	ATP-binding cassette, s	29 (0.00)	154 (0.31)	0.81
11-12	Gp3	g.chr7:20698171G>A	Missense Mutation	ABCB5	p.G527R	ATP-binding cassette, s	68 (0.00)	178 (0.21)	0.57
11-12	Gp3	g.chr12:40012909T>G	Missense Mutation	ABCD2	p.K170T	ATP-binding cassette, s	35 (0.00)	212 (0.49)	1.31
11-12	Gp3	g.chr21:43716369A>T	Missense Mutation	ABCG1	p.E623V	ATP-binding cassette, s	44 (0.00)	61 (0.43)	1.38
11-12	Gp3	g.chr2:44040375G>T	Silent	ABCG5	p.T441T	ATP-binding cassette, s	29 (0.00)	234 (0.47)	1.26
11-12	Gp3	g.chr2:204259559C>T	Nonsense Mutation	ABI2	p.R239*	abl-interactor 2	79 (0.00)	78 (0.15)	0.41
11-12	Gp3	g.chr3:127398955G>T	Missense Mutation	ABTB1	p.R386L	ankyrin repeat and BTB	35 (0.00)	360 (0.67)	1.78
11-12	Gp3	g.chr4:118497049G>T	lincRNA	AC092661.1			100 (0.00)	137 (0.73)	1.95
11-12	Gp3	g.chr2:804286C>A	lincRNA	AC113607.1			30 (0.00)	13 (0.92)	3.00
11-12	Gp3	g.chr4:8391376G>A	Silent	ACOX3	p.S462S	acyl-CoA oxidase 3, pri	64 (0.02)	283 (1.00)	2.66
11-12	Gp3	g.chr4:8398674T>C	Missense Mutation	ACOX3	p.Y349C	acyl-CoA oxidase 3, pri	43 (0.00)	104 (0.24)	0.64
11-12	Gp3	g.chr17:79478640T>C	Missense Mutation	ACTG1	p.T126A	actin, gamma 1	17 (0.00)	157 (0.19)	0.51
11-12	Gp3	g.chr9:111617457T>C	Missense Mutation	ACTL7B	p.I252V	actin-like 7B	20 (0.00)	16 (0.31)	0.83
11-12	Gp3	g.chr7:152513620T>G	Missense Mutation	ACTR3B	p.L163V	ARP3 actin-related prot	39 (0.00)	385 (0.15)	0.40
11-12	Gp3	g.chr1:155030587C>A	Missense Mutation	ADAM15	p.S559R	ADAM metallopeptidas	32 (0.00)	119 (0.75)	1.99
11-12	Gp3	g.chr9:136302880T>C	Missense Mutation	ADAMTS13	p.C483R	ADAM metallopeptidas	16 (0.00)	140 (0.24)	0.63
11-12	Gp3	g.chr22:24837148G>T	Missense Mutation	ADORA2A	p.Q310H	adenosine A2a receptor	33 (0.00)	123 (0.33)	0.89
11-12	Gp3	g.chr17:10614228T>A	Missense Mutation	ADPRM	p.W266R	ADP-ribose/CDP-alcoh	48 (0.00)	214 (0.98)	2.60
11-12	Gp3	g.chr2:64779538C>A	Missense Mutation	AFTPH	p.F310L	aftiphilin	24 (0.00)	23 (0.96)	2.55
11-12	Gp3	g.chr10:51464928A>G	Missense Mutation	AGAP7	p.S510P		90 (0.00)	153 (0.25)	0.66
11-12	Gp3	g.chr9:38396088G>T	Missense Mutation	ALDH1B1	p.D115Y	aldehyde dehydrogenas	37 (0.00)	87 (0.60)	1.59
11-12	Gp3	g.chr3:125854451C>T	Missense Mutation	ALDH1L1	p.A477T	aldehyde dehydrogenas	17 (0.00)	56 (0.20)	0.52
11-12	Gp3	g.chr8:8095880C>T	RNA	ALG1L13P		asparagine-linked glyco	33 (0.00)	58 (0.98)	2.62
11-12	Gp3	g.chr17:7976478C>G	Missense Mutation	ALOX12B	p.E638D	arachidonate 12-lipoxyg	34 (0.00)	47 (0.15)	0.40
11-12	Gp3	g.chr17:7977055T>C	Missense Mutation	ALOX12B	p.T559A	arachidonate 12-lipoxyg	26 (0.00)	152 (0.30)	0.81
11-12	Gp3	g.chr11:46564246T>A	Missense Mutation	AMBRA1	p.S351C	autophagy/beclin-1 regu	53 (0.00)	82 (0.26)	0.68
11-12	Gp3	g.chr3:49456718C>A	Missense Mutation	AMT	p.G224V	aminomethyltransferase	36 (0.00)	193 (0.45)	1.20
11-12	Gp3	g.chr13:111546513T>C	Silent	ANKRD10	p.P164P	ankyrin repeat domain 1	149 (0.00)	123 (0.34)	0.91
11-12	Gp3	g.chr3:15755149C>A	Splice Site	ANKRD28		ankyrin repeat domain 2	94 (0.00)	436 (0.19)	0.51
11-12	Gp3	g.chr16:4755106C>A	Silent	ANKS3	p.R286R	ankyrin repeat and steril	30 (0.00)	299 (0.35)	0.94
11-12	Gp3	g.chr19:10692236G>T	Missense Mutation	AP1M2	p.S158Y	adaptor-related protein c	44 (0.00)	294 (0.22)	0.58
11-12	Gp3	g.chr20:24944598T>A	Missense Mutation	APMAP	p.S368C	adipocyte plasma memb	23 (0.00)	82 (0.26)	0.68
11-12	Gp3	g.chr16:25228723G>T	Missense Mutation	AQP8	p.G73W	aquaporin 8	28 (0.00)	380 (0.69)	1.85

11-12	Gp3	g.chr16:24942457C>A	Missense Mutation	ARHGAP17	p.Q721H	Rho GTPase activating	80 (0.01)	478 (0.54)	1.44
11-12	Gp3	g.chr16:24942654A>T	Missense Mutation	ARHGAP17	p.S656T	Rho GTPase activating	69 (0.00)	394 (0.72)	1.93
11-12	Gp3	g.chr12:57872331C>A	Missense Mutation	ARHGAP9	p.A176S	Rho GTPase activating	41 (0.00)	156 (0.37)	0.97
11-12	Gp3	g.chr6:157522152A>G	Missense Mutation	ARID1B	p.Y1475C	AT rich interactive dom	26 (0.00)	22 (0.41)	1.09
11-12	Gp3	g.chr5:149677567C>A	Missense Mutation	ARSI	p.S307I	arylsulfatase family, me	21 (0.00)	67 (0.19)	0.52
11-12	Gp3	g.chr10:73912715C>A	Nonsense Mutation	ASCC1	p.E220*	activating signal cointeg	48 (0.00)	215 (0.37)	0.98
11-12	Gp3	g.chr4:47584060G>A	Silent	ATP10D	p.L1244L	ATPase, class V, type 1	23 (0.00)	118 (0.52)	1.38
11-12	Gp3	g.chr13:113510243G>C	Missense Mutation	ATP11A	p.Q754H	ATPase, class VI, type 1	42 (0.00)	164 (0.57)	1.51
11-12	Gp3	g.chr1:44441472G>A	Splice Site	ATP6V0B	p.G23E	ATPase, H+ transportin	42 (0.00)	172 (0.55)	1.46
11-12	Gp3	g.chr1:44441485C>G	Silent	ATP6V0B	p.T27T	ATPase, H+ transportin	45 (0.00)	163 (0.56)	1.51
11-12	Gp3	g.chr3:142215354T>A	Missense Mutation	ATR	p.Y1916F	ATR serine/threonine ki	25 (0.00)	31 (0.94)	2.49
11-12	Gp3	g.chr1:110031507G>C	Silent	ATXN7L2	p.R274R	ataxin 7-like 2	22 (0.00)	50 (0.16)	0.43
11-12	Gp3	g.chr1:1309405T>C	Missense Mutation	AURKAIP1	p.Q158R	aurora kinase A interact	28 (0.00)	113 (0.17)	0.45
11-12	Gp3	g.chr6:69684698G>A	Silent	BAI3	p.V523V	brain-specific angiogen	66 (0.00)	218 (0.22)	0.60
11-12	Gp3	g.chr2:160242902C>T	Missense Mutation	BAZ2B	p.A1145T	bromodomain adjacent t	73 (0.00)	37 (0.84)	2.23
11-12	Gp3	g.chr19:49299743G>C	Missense Mutation	BCAT2	p.T361S	branched chain amino-a	57 (0.00)	430 (0.32)	0.86
11-12	Gp3	g.chr2:32715162G>A	Missense Mutation	BIRC6	p.R2717Q	baculoviral IAP repeat c	128 (0.01)	429 (0.99)	2.63
11-12	Gp3	g.chr15:91263125C>T	Intron	BLM		Bloom syndrome, RecQ	85 (0.00)	40 (0.50)	1.33
11-12	Gp3	g.chr5:865696C>A	Splice Site	BRD9	p.G509V	bromodomain containin	28 (0.00)	11 (0.64)	1.70
11-12	Gp3	g.chr16:2259699C>A	Missense Mutation	BRICD5	p.E149D	BRICHOS domain cont	15 (0.00)	109 (0.24)	0.64
11-12	Gp3	g.chr19:55815088C>A	Silent	BRSK1	p.R89R	BR serine/threonine kin	50 (0.00)	206 (0.56)	1.49
11-12	Gp3	g.chr3:49695211G>T	Missense Mutation	BSN	p.S2741I	bassoon presynaptic cyt	27 (0.00)	82 (0.37)	0.98
11-12	Gp3	g.chr12:53693689C>A	Nonsense Mutation	C12orf10	p.C56*	chromosome 12 open re	15 (0.00)	119 (0.45)	1.19
11-12	Gp3	g.chr15:40855180G>A	Missense Mutation	C15orf57	p.T12I	chromosome 15 open re	26 (0.00)	38 (0.42)	1.12
11-12	Gp3	g.chr17:42744444C>A	Missense Mutation	C17orf104	p.Q389K	chromosome 17 open re	44 (0.00)	52 (0.40)	0.59
11-12	Gp3	g.chr1:150255931C>A	Nonsense Mutation	C1orf51	p.S85*		117 (0.01)	51 (0.90)	2.41
11-12	Gp3	g.chr2:232458573C>A	Missense Mutation	C2orf57	p.A304D	chromosome 2 open rea	18 (0.00)	27 (0.74)	1.98
11-12	Gp3	g.chr4:170663141C>T	Silent	C4orf27	p.Q205Q	chromosome 4 open rea	30 (0.00)	36 (0.97)	2.59
11-12	Gp3	g.chr9:130473650C>T	Nonsense Mutation	C9orf117	p.Q244*	chromosome 9 open rea	31 (0.00)	11 (0.73)	1.94
11-12	Gp3	g.chr3:54537530C>T	Silent	CACNA2D3	p.F131F	calcium channel, voltag	107 (0.01)	276 (0.99)	2.65
11-12	Gp3	g.chr12:49221371C>A	Missense Mutation	CACNB3	p.Q382K	calcium channel, voltag	17 (0.00)	105 (0.35)	0.94
11-12	Gp3	g.chr3:85131422G>A	Intron	CADM2		cell adhesion molecule	17 (0.00)	26 (0.96)	2.56
11-12	Gp3	g.chr3:85305428C>T	Intron	CADM2		cell adhesion molecule	205 (0.00)	277 (0.76)	2.03
11-12	Gp3	g.chr3:85625971A>T	Intron	CADM2		cell adhesion molecule	115 (0.00)	384 (0.88)	2.33
11-12	Gp3	g.chr3:85802189A>G	Intron	CADM2		cell adhesion molecule	46 (0.00)	263 (0.18)	0.48

11-12	Gp3	g.chr3:85984553A>T	Intron	CADM2		cell adhesion molecule	36 (0.00)	29 (0.34)	0.92
11-12	Gp3	g.chr10:5541181T>C	Missense Mutation	CALML5	p.K74R	calmodulin-like 5	19 (0.00)	102 (0.15)	0.39
11-12	Gp3	g.chr10:75608828T>C	Missense Mutation	CAMK2G	p.K154E	calcium/calmodulin-dep	51 (0.00)	75 (0.31)	0.82
11-12	Gp3	g.chr1:200827097T>A	Silent	CAMSAP2	p.S1449S	calmodulin regulated sp	21 (0.00)	29 (0.52)	1.38
11-12	Gp3	g.chr11:76831893C>A	Missense Mutation	CAPN5	p.F515L	calpain 5	44 (0.00)	23 (0.74)	1.97
11-12	Gp3	g.chr11:34482816C>A	Missense Mutation	CAT	p.P359T	catalase	36 (0.00)	268 (0.33)	0.89
11-12	Gp3	g.chr2:74701827G>T	Missense Mutation	CCDC142	p.T693K	coiled-coil domain cont	29 (0.00)	165 (0.24)	0.63
11-12	Gp3	g.chr11:124824703C>T	Silent	CCDC15	p.S25S	coiled-coil domain cont	46 (0.00)	63 (0.51)	1.35
11-12	Gp3	g.chr17:80086423G>C	Missense Mutation	CCDC57	p.H765Q	coiled-coil domain cont	15 (0.00)	83 (0.28)	0.74
11-12	Gp3	g.chr14:91770198G>C	Missense Mutation	CCDC88C	p.T1161R	coiled-coil domain cont	34 (0.00)	517 (0.15)	0.39
11-12	Gp3	g.chr14:91826016C>T	Missense Mutation	CCDC88C	p.V104I	coiled-coil domain cont	18 (0.00)	88 (0.33)	0.88
11-12	Gp3	g.chr11:6291905T>C	Missense Mutation	CCKBR	p.F228S	cholecystokinin B recep	54 (0.00)	195 (0.30)	0.81
11-12	Gp3	g.chr14:99973460T>C	Silent	CCNK	p.L365L	cyclin K	239 (0.00)	35 (0.17)	0.46
11-12	Gp3	g.chr22:17072697A>G	Silent	CCT8L2	p.F248F	chaperonin containing T	69 (0.00)	89 (0.19)	0.51
11-12	Gp3	g.chr16:30364752C>A	Missense Mutation	CD2BP2	p.D249Y	CD2 (cytoplasmic tail)	40 (0.00)	72 (0.46)	1.22
11-12	Gp3	g.chr10:73464788G>T	Nonsense Mutation	CDH23	p.E957*	cadherin-related 23	37 (0.03)	371 (0.23)	0.62
11-12	Gp3	g.chr10:73571101A>G	Missense Mutation	CDH23	p.E3041G	cadherin-related 23	44 (0.00)	75 (0.17)	0.46
11-12	Gp3	g.chr22:17990896G>T	Missense Mutation	CECR2	p.D145Y	cat eye syndrome chron	96 (0.00)	69 (0.78)	2.09
11-12	Gp3	g.chr22:46932211C>T	Missense Mutation	CELSR1	p.G286E	cadherin, EGF LAG sev	21 (0.00)	123 (0.25)	0.67
11-12	Gp3	g.chr20:34091454G>T	Missense Mutation	CEP250	p.D1753Y	centrosomal protein 250	32 (0.00)	65 (0.66)	1.76
11-12	Gp3	g.chr1:6195129C>G	Intron	CHD5		chromodomain helicase	58 (0.02)	367 (0.99)	2.64
11-12	Gp3	g.chr1:6195483T>C	Intron	CHD5		chromodomain helicase	40 (0.00)	13 (0.46)	1.23
11-12	Gp3	g.chr1:6217555C>G	Intron	CHD5		chromodomain helicase	26 (0.00)	206 (0.58)	1.54
11-12	Gp3	g.chr1:6228782C>A	Intron	CHD5		chromodomain helicase	24 (0.00)	48 (0.40)	1.06
11-12	Gp3	g.chr14:21873420A>G	Silent	CHD8	p.L1085L	chromodomain helicase	76 (0.00)	69 (0.87)	2.32
11-12	Gp3	g.chr2:220404360C>G	Silent	CHPF	p.L691L	chondroitin polymerizin	18 (0.00)	18 (0.50)	1.33
11-12	Gp3	g.chr7:150932289C>A	Missense Mutation	CHPF2	p.A132D	chondroitin polymerizin	45 (0.00)	38 (0.32)	0.84
11-12	Gp3	g.chr11:62677678C>A	Nonsense Mutation	CHRM1	p.E299*	cholinergic receptor, mu	26 (0.00)	307 (0.18)	0.47
11-12	Gp3	g.chr15:78882438C>A	Nonsense Mutation	CHRNA5	p.C235*	cholinergic receptor, nic	99 (0.00)	48 (0.23)	0.61
11-12	Gp3	g.chr7:2473390C>T	Silent	CHST12	p.T372T	carbohydrate (chondroit	75 (0.00)	35 (0.26)	0.69
11-12	Gp3	g.chr19:34263725C>A	Missense Mutation	CHST8	p.F344L	carbohydrate (N-acetylg	19 (0.00)	282 (0.60)	1.59
11-12	Gp3	g.chr19:42795789G>T	Silent	CIC	p.L1835L	capicua transcriptional r	25 (0.00)	173 (0.23)	0.60
11-12	Gp3	g.chr19:36508797T>A	Missense Mutation	CLIP3	p.Q427L	CAP-GLY domain cont	28 (0.00)	247 (0.41)	1.09
11-12	Gp3	g.chr11:66050233C>A	Silent	CNIH2	p.I60I	cornichon family AMP	24 (0.00)	52 (0.85)	2.26
11-12	Gp3	g.chr1:32164121T>A	Missense Mutation	COL16A1	p.Y118F	collagen, type XVI, alp	17 (0.00)	156 (0.96)	2.56

11-12	Gp3	g.chr2:189849504C>A	Missense Mutation	COL3A1	p.S33Y	collagen, type III, alpha	22 (0.00)	57 (0.25)	0.65
11-12	Gp3	g.chr19:10116233C>G	Splice Site	COL5A3		collagen, type V, alpha	37 (0.00)	30 (0.50)	1.33
11-12	Gp3	g.chr3:48606866G>A	Missense Mutation	COL7A1	p.P2543L	collagen, type VII, alph	35 (0.03)	98 (0.73)	1.96
11-12	Gp3	g.chr20:34219065C>T	Missense Mutation	CPNE1	p.V278M	copine I	114 (0.00)	55 (0.15)	0.39
11-12	Gp3	g.chr11:46333943G>T	Missense Mutation	CREB3L1	p.G274V	cAMP responsive eleme	19 (0.00)	219 (0.84)	2.24
11-12	Gp3	g.chr1:75172617C>T	Missense Mutation	CRYZ	p.S265N	crystallin, zeta (quinone	27 (0.00)	70 (0.90)	2.40
11-12	Gp3	g.chr17:61950564A>G	Missense Mutation	CSH2	p.L49P	chorionic somatomamm	90 (0.00)	35 (0.40)	1.07
11-12	Gp3	g.chr15:75091033C>A	Nonsense Mutation	CSK	p.C31*	c-src tyrosine kinase	26 (0.00)	70 (0.21)	0.57
11-12	Gp3	g.chr1:33985183G>A	Nonsense Mutation	CSMD2	p.Q3611*	CUB and Sushi multipl	41 (0.02)	68 (0.25)	0.67
11-12	Gp3	g.chr1:34401434G>T	Silent	CSMD2	p.G213G	CUB and Sushi multipl	27 (0.00)	145 (0.31)	0.83
11-12	Gp3	g.chr20:23669409G>T	Silent	CST4	p.R66R	cystatin S	27 (0.00)	31 (0.42)	1.12
11-12	Gp3	g.chr19:51457369G>T	RNA	CTB-147C22.8			21 (0.00)	25 (0.28)	0.75
11-12	Gp3	g.chr4:1244873C>A	RNA	CTBP1-AS2		CTBP1 antisense RNA	30 (0.00)	20 (0.30)	0.80
11-12	Gp3	g.chr10:104183294C>A	Missense Mutation	CUEDC2	p.Q251H	CUE domain containing	140 (0.00)	46 (0.96)	2.55
11-12	Gp3	g.chr22:43024266G>A	Missense Mutation	CYB5R3	p.P119S	cytochrome b5 reductas	39 (0.00)	57 (0.60)	1.59
11-12	Gp3	g.chr1:47489575C>A	Missense Mutation	CYP4X1	p.A29D	cytochrome P450, famil	20 (0.00)	58 (0.69)	1.84
11-12	Gp3	g.chr2:242689643G>T	Nonsense Mutation	D2HGDH	p.E311*	D-2-hydroxyglutarate d	27 (0.00)	299 (0.53)	1.42
11-12	Gp3	g.chr9:124362756C>G	Intron	DAB2IP		DAB2 interacting protei	52 (0.00)	223 (0.40)	1.06
11-12	Gp3	g.chr9:124408123G>A	Intron	DAB2IP		DAB2 interacting protei	40 (0.00)	64 (0.42)	1.12
11-12	Gp3	g.chr9:124408135C>T	Intron	DAB2IP		DAB2 interacting protei	40 (0.03)	89 (0.55)	1.47
11-12	Gp3	g.chr9:124430992A>G	Intron	DAB2IP		DAB2 interacting protei	39 (0.00)	23 (0.26)	0.70
11-12	Gp3	g.chr9:124463070A>G	Intron	DAB2IP		DAB2 interacting protei	54 (0.00)	10 (0.80)	2.13
11-12	Gp3	g.chr9:124495461T>A	Intron	DAB2IP		DAB2 interacting protei	48 (0.00)	55 (0.96)	2.57
11-12	Gp3	g.chr9:124505647C>A	Intron	DAB2IP		DAB2 interacting protei	116 (0.00)	43 (0.35)	0.93
11-12	Gp3	g.chr9:124526738C>T	Intron	DAB2IP		DAB2 interacting protei	19 (0.00)	48 (0.67)	1.78
11-12	Gp3	g.chr9:124542309C>T	Intron	DAB2IP		DAB2 interacting protei	192 (0.00)	66 (0.30)	0.81
11-12	Gp3	g.chr11:61105544C>A	Silent	DAK	p.L45L	dihydroxyacetone kinas	21 (0.00)	245 (0.42)	1.12
11-12	Gp3	g.chr1:173794474G>A	Missense Mutation	DARS2	p.S36N	aspartyl-tRNA syntheta	62 (0.02)	41 (0.44)	1.17
11-12	Gp3	g.chr4:41984540G>A	Missense Mutation	DCAF4L1	p.R244H	DDB1 and CUL4 associ	29 (0.00)	172 (0.91)	2.43
11-12	Gp3	g.chr11:6645409T>A	Missense Mutation	DCHS1	p.T2500S	dachsous cadherin-relat	24 (0.00)	39 (0.64)	1.71
11-12	Gp3	g.chr5:112349071G>A	Missense Mutation	DCP2	p.E385K	decapping mRNA 2	53 (0.00)	25 (0.72)	1.92
11-12	Gp3	g.chr5:112349091T>C	Silent	DCP2	p.C391C	decapping mRNA 2	41 (0.00)	38 (0.39)	1.05
11-12	Gp3	g.chr11:61089770G>T	Missense Mutation	DDB1	p.Q374K	damage-specific DNA b	34 (0.00)	97 (0.37)	0.99
11-12	Gp3	g.chr5:176942978A>T	Missense Mutation	DDX41	p.V129E	DEAD (Asp-Glu-Ala-A	54 (0.02)	233 (0.36)	0.96
11-12	Gp3	g.chr12:132625057C>A	Silent	DDX51	p.G528G	DEAD (Asp-Glu-Ala-A	15 (0.00)	319 (0.39)	1.04

11-12	Gp3	g.chr11:674589G>A	Nonsense Mutation	DEAF1	p.R484*	DEAF1 transcription fa	115 (0.00)	63 (0.41)	1.10
11-12	Gp3	g.chr8:124027752C>G	Missense Mutation	DERL1	p.A231P	derlin 1	87 (0.00)	27 (0.67)	1.78
11-12	Gp3	g.chr2:220284876C>G	Splice Site	DES	p.A213G	desmin	27 (0.00)	218 (0.25)	0.67
11-12	Gp3	g.chr7:24745816G>C	Silent	DFNA5	p.V390V	deafness, autosomal dor	105 (0.01)	348 (0.42)	1.13
11-12	Gp3	g.chr2:234368885G>T	Nonsense Mutation	DGKD	p.E959*	diacylglycerol kinase, d	67 (0.00)	11 (0.82)	2.18
11-12	Gp3	g.chr12:122701087C>T	Nonsense Mutation	DIABLO	p.W157*	diablo, IAP-binding mit	43 (0.00)	34 (0.94)	2.51
11-12	Gp3	g.chr10:403837A>G	Silent	DIP2C	p.S945S	DIP2 disco-interacting	33 (0.00)	156 (0.28)	0.74
11-12	Gp3	g.chr1:231830493T>C	Missense Mutation	DISC1	p.L330P	disrupted in schizophre	15 (0.00)	56 (0.14)	0.38
11-12	Gp3	g.chr11:111933145C>T	Silent	DLAT	p.S505S	dihydrolipoamide S-ace	117 (0.01)	152 (0.99)	2.65
11-12	Gp3	g.chr10:79581271G>T	Missense Mutation	DLG5	p.L991M	discs, large homolog 5 (	30 (0.00)	122 (0.16)	0.42
11-12	Gp3	g.chr8:1626632C>A	Silent	DLGAP2	p.P767P	discs, large (Drosophila	46 (0.00)	60 (0.83)	2.22
11-12	Gp3	g.chr7:96653759G>A	Silent	DLX5	p.C59C	distal-less homeobox 5	36 (0.00)	70 (0.79)	2.10
11-12	Gp3	g.chr14:50100192A>G	Missense Mutation	DNAAF2	p.L559S	dynein, axonemal, assen	32 (0.00)	80 (0.47)	1.27
11-12	Gp3	g.chr19:55676798C>G	Missense Mutation	DNAAF3	p.A156P	dynein, axonemal, assen	49 (0.00)	221 (0.39)	1.04
11-12	Gp3	g.chr3:57348520A>T	Splice Site	DNAH12		dynein, axonemal, heav	93 (0.00)	260 (1.00)	2.66
11-12	Gp3	g.chr3:57348521C>T	Splice Site	DNAH12		dynein, axonemal, heav	92 (0.00)	263 (1.00)	2.66
11-12	Gp3	g.chr11:6520136G>A	Missense Mutation	DNHD1	p.E231K	dynein heavy chain dom	25 (0.00)	38 (0.45)	1.19
11-12	Gp3	g.chr15:100340102G>T	RNA	DNM1P46		DNM1 pseudogene 46	24 (0.00)	147 (0.76)	2.03
11-12	Gp3	g.chr15:100340166G>C	RNA	DNM1P46		DNM1 pseudogene 46	21 (0.00)	13 (0.54)	1.44
11-12	Gp3	g.chr1:172356389G>C	Missense Mutation	DNM3	p.M721I	dynamin 3	34 (0.00)	44 (0.61)	1.64
11-12	Gp3	g.chr21:37618929G>A	Missense Mutation	DOPEY2	p.D1551N	dopey family member 2	39 (0.00)	117 (0.18)	0.48
11-12	Gp3	g.chr9:140468757C>T	Silent	DPH7	p.T181T	diphthamide biosynthes	104 (0.00)	22 (0.50)	1.33
11-12	Gp3	g.chr11:117389242G>T	Nonsense Mutation	DSCAML1	p.Y543*	Down syndrome cell ad	122 (0.00)	329 (0.77)	2.06
11-12	Gp3	g.chr6:7585834A>G	Missense Mutation	DSP	p.K2780R	desmoplakin	101 (0.00)	21 (0.43)	1.14
11-12	Gp3	g.chr15:49924476G>A	Missense Mutation	DTWD1	p.E129K	DTW domain containin	17 (0.00)	210 (0.79)	2.11
11-12	Gp3	g.chr15:45448069G>T	Missense Mutation	DUOX1	p.R1215L	dual oxidase 1	41 (0.00)	98 (0.20)	0.54
11-12	Gp3	g.chr6:348172G>T	Missense Mutation	DUSP22	p.W111C	dual specificity phospha	33 (0.00)	53 (0.36)	0.96
11-12	Gp3	g.chr11:85989556C>T	Nonsense Mutation	EED	p.R359*	embryonic ectoderm de	41 (0.00)	229 (0.22)	0.58
11-12	Gp3	g.chr11:65348738C>A	Missense Mutation	EHBP1L1	p.P254T	EH domain binding pro	16 (0.00)	77 (0.60)	1.59
11-12	Gp3	g.chr19:48244401G>A	Silent	EHD2	p.K448K	EH-domain containing	24 (0.00)	241 (0.25)	0.67
11-12	Gp3	g.chr22:36920733G>C	Missense Mutation	EIF3D	p.F72L	eukaryotic translation in	64 (0.00)	20 (0.95)	2.53
11-12	Gp3	g.chr22:29611524C>T	Missense Mutation	EMID1	p.T75I	EMI domain containing	27 (0.00)	64 (0.56)	1.50
11-12	Gp3	g.chr16:10631905C>A	Missense Mutation	EMP2	p.A66S	epithelial membrane pro	49 (0.00)	219 (0.26)	0.68
11-12	Gp3	g.chr9:130580597G>T	Missense Mutation	ENG	p.D496E	endoglin	24 (0.00)	150 (0.19)	0.52
11-12	Gp3	g.chr1:23219388G>C	Missense Mutation	EPHB2	p.E480D	EPH receptor B2	50 (0.00)	222 (0.57)	1.53

11-12	Gp3	g.chr3:184299163C>A	Missense Mutation	EPHB3	p.A952E	EPH receptor B3	16 (0.00)	127 (0.94)	2.52
11-12	Gp3	g.chr7:100417886C>A	Nonsense Mutation	EPHB4	p.G281*	EPH receptor B4	26 (0.00)	221 (0.62)	1.67
11-12	Gp3	g.chr19:56196945G>T	Missense Mutation	EPN1	p.D138Y	epsin 1	22 (0.00)	222 (0.71)	1.89
11-12	Gp3	g.chr1:220219716A>G	Silent	EPRS	p.S5S	glutamyl-prolyl-tRNA s	26 (0.00)	51 (0.18)	0.47
11-12	Gp3	g.chr10:50725100C>A	Nonsense Mutation	ERCC6-PGBD	p.E489*	ERCC6-PGBD3 readthr	21 (0.00)	43 (0.70)	1.86
11-12	Gp3	g.chr21:39782550G>T	Intron	ERG		v-ets avian erythroblast	63 (0.00)	178 (0.46)	1.23
11-12	Gp3	g.chr21:39787669A>T	Intron	ERG		v-ets avian erythroblast	22 (0.00)	55 (0.65)	1.75
11-12	Gp3	g.chr21:39839457G>A	Intron	ERG		v-ets avian erythroblast	93 (0.01)	618 (1.00)	2.66
11-12	Gp3	g.chr21:39941204G>A	Intron	ERG		v-ets avian erythroblast	170 (0.01)	28 (0.79)	2.10
11-12	Gp3	g.chr16:20809834T>A	Missense Mutation	ERI2	p.S337C	ERI1 exoribonuclease f	21 (0.00)	10 (0.50)	1.33
11-12	Gp3	g.chr6:152129092G>C	Silent	ESR1	p.L15L	estrogen receptor 1	21 (0.00)	55 (0.55)	1.45
11-12	Gp3	g.chr21:33887479A>T	Missense Mutation	EVA1C	p.R435S	eva-1 homolog C (C. el	150 (0.01)	151 (0.99)	2.65
11-12	Gp3	g.chr17:29632190A>G	Silent	EVI2B	p.F146F	ecotropic viral integrati	90 (0.00)	141 (0.99)	2.63
11-12	Gp3	g.chr14:69702849A>G	Missense Mutation	EXD2	p.Y379C	exonuclease 3'-5' domai	37 (0.00)	32 (0.19)	0.50
11-12	Gp3	g.chr11:108381552T>A	Missense Mutation	EXPH5	p.K1561M	exophilin 5	62 (0.00)	28 (0.21)	0.57
11-12	Gp3	g.chr11:108384209G>A	Silent	EXPH5	p.T675T	exophilin 5	19 (0.00)	83 (0.99)	2.63
11-12	Gp3	g.chr11:58920370T>C	Missense Mutation	FAM111A	p.V410A	family with sequence si	109 (0.00)	122 (0.25)	0.68
11-12	Gp3	g.chr10:88946944C>A	Silent	FAM35A	p.L765L	family with sequence si	113 (0.00)	12 (0.83)	2.22
11-12	Gp3	g.chr1:809550A>G	lincRNA	FAM41C		family with sequence si	145 (0.00)	58 (0.55)	1.47
11-12	Gp3	g.chr5:137681106C>A	Silent	FAM53C	p.R243R	family with sequence si	18 (0.00)	149 (0.21)	0.55
11-12	Gp3	g.chr15:59064306C>A	Missense Mutation	FAM63B	p.P238T	family with sequence si	16 (0.00)	145 (0.22)	0.59
11-12	Gp3	g.chr11:67564279G>T	RNA	FAM86C2P		family with sequence si	52 (0.00)	187 (0.17)	0.46
11-12	Gp3	g.chr3:75475710C>A	RNA	FAM86DP		family with sequence si	55 (0.00)	409 (0.19)	0.64
11-12	Gp3	g.chr12:8374609C>T	Missense Mutation	FAM90A1	p.G402R	family with sequence si	17 (0.00)	87 (0.87)	2.33
11-12	Gp3	g.chr13:99047494C>A	Missense Mutation	FARP1	p.T393N	FERM, RhoGEF (ARH	27 (0.00)	46 (0.83)	2.20
11-12	Gp3	g.chr11:92533590G>T	Missense Mutation	FAT3	p.V2321F	FAT atypical cadherin 3	123 (0.01)	224 (0.49)	1.30
11-12	Gp3	g.chr1:207134036C>T	Silent	FCAMR	p.T395T	Fc receptor, IgA, IgM,	69 (0.01)	169 (0.73)	1.96
11-12	Gp3	g.chr19:40368357C>T	Missense Mutation	FCGBP	p.A4331T	Fc fragment of IgG bind	27 (0.00)	29 (0.66)	1.75
11-12	Gp3	g.chr1:149759999G>A	Missense Mutation	FCGR1A	p.D129N	Fc fragment of IgG, hig	65 (0.00)	10 (0.70)	1.87
11-12	Gp3	g.chr19:4792640C>A	Silent	FEM1A	p.P258P	fem-1 homolog a (C. el	40 (0.00)	135 (0.22)	0.59
11-12	Gp3	g.chr19:35850519G>A	Missense Mutation	FFAR3	p.V243M	free fatty acid receptor	48 (0.02)	95 (0.16)	0.42
11-12	Gp3	g.chrX:137793040C>A	Missense Mutation	FGF13	p.K42N	fibroblast growth factor	18 (0.00)	64 (0.56)	0.94
11-12	Gp3	g.chr13:28608046C>A	Missense Mutation	FLT3	p.Q640H	fms-related tyrosine kin	30 (0.00)	47 (0.47)	1.25
11-12	Gp3	g.chr1:171303883G>A	Nonsense Mutation	FMO4	p.W387*	flavin containing mono	46 (0.00)	25 (0.52)	1.39
11-12	Gp3	g.chr14:65521361G>T	Missense Mutation	FNTB	p.G379V	farnesyltransferase, CA	21 (0.00)	86 (0.16)	0.43

11-12	Gp3	g.chr19:46375835G>T	Missense Mutation	FOXA3	p.W191L	forkhead box A3	20 (0.00)	61 (0.31)	0.83
11-12	Gp3	g.chr17:80529731G>A	Silent	FOXK2	p.A298A	forkhead box K2	15 (0.00)	11 (0.82)	2.18
11-12	Gp3	g.chr6:41555138G>A	Missense Mutation	FOXP4	p.G254S	forkhead box P4	64 (0.00)	95 (0.34)	0.90
11-12	Gp3	g.chr9:14808108C>T	Missense Mutation	FREM1	p.C973Y	FRAS1 related extracell	100 (0.00)	12 (0.75)	2.00
11-12	Gp3	g.chr14:52186954G>T	Missense Mutation	FRMD6	p.K394N	FERM domain containi	77 (0.00)	33 (0.45)	1.21
11-12	Gp3	g.chr7:5642964A>G	Silent	FSCN1	p.K303K	fascin actin-bundling pr	22 (0.00)	194 (0.15)	0.40
11-12	Gp3	g.chr5:161302580C>T	Missense Mutation	GABRA1	p.A164V	gamma-aminobutyric ac	92 (0.00)	25 (0.92)	2.45
11-12	Gp3	g.chr22:30951078G>T	Silent	GAL3ST1	p.L378L	galactose-3-O-sulfotran	15 (0.00)	25 (0.28)	0.75
11-12	Gp3	g.chr3:115394923C>G	Missense Mutation	GAP43	p.H68D	growth associated protei	104 (0.00)	47 (0.98)	2.61
11-12	Gp3	g.chr1:155184219G>A	RNA	GBAP1		glucosidase, beta, acid p	53 (0.00)	122 (0.99)	2.64
11-12	Gp3	g.chr9:136029216G>T	Silent	GBGT1	p.V264V	globoside alpha-1,3-N-a	32 (0.00)	36 (0.97)	2.59
11-12	Gp3	g.chr1:89847301C>A	Missense Mutation	GBP6	p.A307E	guanylate binding protei	42 (0.00)	35 (0.97)	2.59
11-12	Gp3	g.chr7:127224840C>A	Missense Mutation	GCC1	p.A133S	GRIP and coiled-coil d	41 (0.00)	19 (0.68)	1.82
11-12	Gp3	g.chr5:132197623T>A	Missense Mutation	GDF9	p.E341D	growth differentiation f	39 (0.00)	58 (0.50)	1.33
11-12	Gp3	g.chr7:932004T>C	Missense Mutation	GET4	p.F232S	golgi to ER traffic prote	30 (0.00)	49 (0.18)	0.49
11-12	Gp3	g.chr9:135866384C>G	Missense Mutation	GFI1B	p.Q314E	growth factor independ	20 (0.00)	88 (0.97)	2.58
11-12	Gp3	g.chr3:158408058T>C	Silent	GFM1	p.H672H	G elongation factor, mit	70 (0.00)	103 (0.22)	0.60
11-12	Gp3	g.chr17:73240742C>T	Silent	GGA3	p.K14K	golgi-associated, gamm	158 (0.00)	49 (0.39)	1.03
11-12	Gp3	g.chr12:75785024G>T	Missense Mutation	GLIPR1L2	p.R43I	GLI pathogenesis-relate	67 (0.01)	325 (0.42)	1.13
11-12	Gp3	g.chrX:102974050G>A	Silent	GLRA4	p.L290L	glycine receptor, alpha	57 (0.00)	11 (0.91)	1.52
11-12	Gp3	g.chr9:131020069C>A	Splice Site	GOLGA2	p.G844*	golgin A2	237 (0.00)	197 (0.74)	1.96
11-12	Gp3	g.chr8:145139345T>C	Silent	GPAA1	p.D281D	glycosylphosphatidylin	16 (0.00)	117 (0.39)	1.05
11-12	Gp3	g.chr17:72365659G>A	Missense Mutation	GPR142	p.G99E	G protein-coupled recep	28 (0.00)	44 (0.68)	1.82
11-12	Gp3	g.chr1:9164655G>T	Silent	GPR157	p.I277I	G protein-coupled recep	16 (0.00)	67 (0.31)	0.84
11-12	Gp3	g.chr17:36499361C>G	Missense Mutation	GPR179	p.Q104H	G protein-coupled recep	29 (0.00)	192 (0.18)	0.49
11-12	Gp3	g.chr2:133174829A>G	Missense Mutation	GPR39	p.M72V	G protein-coupled recep	94 (0.00)	21 (0.24)	0.63
11-12	Gp3	g.chr19:35500063C>A	Missense Mutation	GRAMD1A	p.P17T	GRAM domain containi	16 (0.00)	248 (0.19)	0.52
11-12	Gp3	g.chr17:37898926C>A	Missense Mutation	GRB7	p.S88Y	growth factor receptor-	21 (0.00)	20 (0.45)	1.20
11-12	Gp3	g.chr12:124144445A>G	Missense Mutation	GTF2H3	p.E263G	general transcription fac	111 (0.00)	29 (0.72)	1.93
11-12	Gp3	g.chr5:21491512C>T	RNA	GUSBP1		glucuronidase, beta pse	515 (0.00)	39 (0.18)	0.48
11-12	Gp3	g.chr1:155255575G>T	Missense Mutation	HCN3	p.D433Y	hyperpolarization activa	27 (0.00)	100 (0.42)	1.12
11-12	Gp3	g.chr2:240005875C>A	Silent	HDAC4	p.V831V	histone deacetylase 4	15 (0.00)	236 (0.38)	1.01
11-12	Gp3	g.chr7:18544475G>A	Intron	HDAC9		histone deacetylase 9	41 (0.00)	18 (0.72)	1.93
11-12	Gp3	g.chr7:18948568C>T	Intron	HDAC9		histone deacetylase 9	52 (0.00)	16 (0.94)	2.50
11-12	Gp3	g.chr6:125598297G>A	Silent	HDDC2	p.D156D	HD domain containing	78 (0.01)	112 (0.99)	2.64

11-12	Gp3	g.chr14:73989776C>A	Missense Mutation	HEATR4	p.M27I	HEAT repeat containing	47 (0.00)	103 (0.45)	1.19
11-12	Gp3	g.chr4:185941491G>T	Silent	HELT	p.L98L	helt bHLH transcription	50 (0.02)	45 (0.60)	1.60
11-12	Gp3	g.chr11:124794862G>C	Missense Mutation	HEPACAM	p.D63E	hepatic and glial cell adl	31 (0.00)	13 (0.69)	1.85
11-12	Gp3	g.chr15:20589799G>T	RNA	HERC2P3		hect domain and RLD 2	57 (0.00)	69 (0.48)	1.28
11-12	Gp3	g.chr15:28900654G>T	RNA	HERC2P9		hect domain and RLD 2	17 (0.00)	63 (0.40)	1.06
11-12	Gp3	g.chr17:80400073C>T	Missense Mutation	HEXDC	p.T425I	hexosaminidase (glycos	16 (0.00)	24 (0.75)	2.00
11-12	Gp3	g.chr7:75184835G>A	Silent	HIP1	p.A616A	huntingtin interacting pr	20 (0.00)	18 (0.78)	2.07
11-12	Gp3	g.chr7:75185426C>A	Silent	HIP1	p.R577R	huntingtin interacting pr	22 (0.00)	80 (0.95)	2.53
11-12	Gp3	g.chr6:26017621C>A	Missense Mutation	HIST1H1A	p.A114S	histone cluster 1, H1a	84 (0.00)	65 (0.32)	0.86
11-12	Gp3	g.chr6:26217213G>C	Missense Mutation	HIST1H2AE	p.R4P	histone cluster 1, H2ae	45 (0.00)	163 (0.17)	0.46
11-12	Gp3	g.chr10:71008379G>T	Missense Mutation	HKDC1	p.A489S	hexokinase domain cont	16 (0.00)	23 (0.91)	2.43
11-12	Gp3	g.chr5:74650452T>C	Missense Mutation	HMGCR	p.L498S	3-hydroxy-3-methylglut	35 (0.03)	78 (0.90)	2.39
11-12	Gp3	g.chr12:54394058C>A	Missense Mutation	HOXC9	p.P29Q	homeobox C9	32 (0.00)	159 (0.65)	1.74
11-12	Gp3	g.chr10:103827250G>T	Silent	HPS6	p.L673L	Hermansky-Pudlak sync	28 (0.00)	155 (0.19)	0.52
11-12	Gp3	g.chr10:103827253G>A	Silent	HPS6	p.L674L	Hermansky-Pudlak sync	28 (0.00)	114 (0.25)	0.65
11-12	Gp3	g.chr1:152187686G>T	Nonsense Mutation	HRNR	p.S2140*	hornerin	297 (0.00)	58 (0.48)	1.29
11-12	Gp3	g.chr6:114379119C>G	Missense Mutation	HS3ST5	p.A115P	heparan sulfate (glucosa	42 (0.00)	432 (0.49)	1.31
11-12	Gp3	g.chr4:171525876C>G	RNA	HSP90AA6P		heat shock protein 90kD	34 (0.00)	73 (0.33)	0.88
11-12	Gp3	g.chr14:65008721G>T	Missense Mutation	HSPA2	p.G385V	heat shock 70kDa protei	34 (0.00)	314 (0.23)	0.62
11-12	Gp3	g.chr1:22150160G>T	Silent	HSPG2	p.R4318R	heparan sulfate proteogl	27 (0.00)	272 (0.47)	1.25
11-12	Gp3	g.chr1:22222764G>T	Missense Mutation	HSPG2	p.P35T	heparan sulfate proteogl	112 (0.01)	564 (0.16)	0.44
11-12	Gp3	g.chr4:3234933C>A	Missense Mutation	HTT	p.T2770K	huntingtin	46 (0.00)	380 (0.43)	1.14
11-12	Gp3	g.chr3:50355883G>T	Silent	HYAL2	p.R367R	hyaluronoglucosaminida	32 (0.00)	78 (0.73)	1.95
11-12	Gp3	g.chr1:206651593G>T	Missense Mutation	IKBKE	p.E301D	inhibitor of kappa light	101 (0.00)	22 (0.95)	2.55
11-12	Gp3	g.chr4:143252352T>A	Intron	INPP4B		inositol polyphosphate-	177 (0.01)	126 (0.98)	2.62
11-12	Gp3	g.chr4:143416004C>A	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	26 (0.46)	1.23
11-12	Gp3	g.chr4:143569141C>A	Intron	INPP4B		inositol polyphosphate-	143 (0.00)	27 (0.44)	1.19
11-12	Gp3	g.chr4:143614473A>T	Intron	INPP4B		inositol polyphosphate-	69 (0.00)	32 (0.53)	1.42
11-12	Gp3	g.chr4:143670011G>T	Intron	INPP4B		inositol polyphosphate-	150 (0.00)	68 (0.19)	0.51
11-12	Gp3	g.chr11:71946748G>A	Missense Mutation	INPPL1	p.G897R	inositol polyphosphate p	21 (0.00)	71 (0.34)	0.90
11-12	Gp3	g.chr11:62416891G>C	Missense Mutation	INTS5	p.P221A	integrator complex subu	48 (0.00)	54 (0.35)	0.94
11-12	Gp3	g.chr7:128582192C>G	Silent	IRF5	p.P19P	interferon regulatory fac	38 (0.00)	208 (0.15)	0.41
11-12	Gp3	g.chr15:74467809G>T	Nonsense Mutation	ISLR	p.E204*	immunoglobulin superfa	39 (0.00)	220 (0.43)	1.14
11-12	Gp3	g.chr14:77942069G>A	Missense Mutation	ISM2	p.P529S	isthmin 2	17 (0.00)	90 (0.52)	1.39
11-12	Gp3	g.chr2:173344458G>T	Missense Mutation	ITGA6	p.S493I	integrin, alpha 6	40 (0.00)	179 (0.55)	1.47

11-12	Gp3	g.chr12:26553165C>A	Nonsense Mutation	ITPR2	p.E2476*	inositol 1,4,5-trisphosph	143 (0.00)	21 (0.48)	1.27
11-12	Gp3	g.chr2:24469137G>T	Silent	ITSN2	p.L1146L	intersectin 2	23 (0.00)	171 (0.99)	2.65
11-12	Gp3	g.chr15:42132825G>T	Missense Mutation	JMJD7-PLA2	p.Q293H	JMJD7-PLA2G4B readt	16 (0.00)	22 (0.68)	1.82
11-12	Gp3	g.chr9:711732G>A	Silent	KANK1	p.R322R	KN motif and ankyrin r	65 (0.00)	21 (0.71)	1.90
11-12	Gp3	g.chr22:24056662G>C	RNA	KB-1572G7.2			19 (0.00)	93 (0.47)	1.26
11-12	Gp3	g.chr1:110768754G>T	Silent	KCNC4	p.L591L	potassium voltage-gated	23 (0.00)	81 (0.16)	0.43
11-12	Gp3	g.chr1:112524793A>G	Missense Mutation	KCND3	p.Y186H	potassium voltage-gated	15 (0.00)	34 (0.15)	0.39
11-12	Gp3	g.chr12:49937754G>A	Missense Mutation	KCNH3	p.A294T	potassium voltage-gated	19 (0.00)	119 (0.32)	0.85
11-12	Gp3	g.chr17:61619678G>A	Silent	KCNH6	p.L677L	potassium voltage-gated	18 (0.00)	50 (0.90)	2.40
11-12	Gp3	g.chr2:155555376G>A	Missense Mutation	KCNJ3	p.G30D	potassium inwardly-rect	48 (0.02)	156 (0.99)	2.65
11-12	Gp3	g.chr16:67327724G>T	Nonsense Mutation	KCTD19	p.C647*	potassium channel tetra	194 (0.00)	46 (0.59)	0.73
11-12	Gp3	g.chr11:67018085G>A	Missense Mutation	KDM2A	p.E862K	lysine (K)-specific dem	16 (0.00)	84 (0.88)	2.35
11-12	Gp3	g.chr12:416213C>T	Missense Mutation	KDM5A	p.V1325M	lysine (K)-specific dem	19 (0.00)	50 (0.98)	2.61
11-12	Gp3	g.chr6:24596754G>A	Missense Mutation	KIAA0319	p.H50Y	KIAA0319	19 (0.00)	12 (0.83)	2.22
11-12	Gp3	g.chr10:30316264T>C	Missense Mutation	KIAA1462	p.E938G	KIAA1462	26 (0.00)	13 (0.46)	1.23
11-12	Gp3	g.chr2:8873764G>T	Missense Mutation	KIDINS220	p.P1288Q	kinase D-interacting sub	40 (0.00)	299 (0.59)	1.58
11-12	Gp3	g.chr1:245772749G>T	Silent	KIF26B	p.L611L	kinesin family member	44 (0.00)	95 (0.58)	1.54
11-12	Gp3	g.chr12:88912573A>G	Silent	KITLG	p.F88F	KIT ligand	35 (0.00)	53 (0.23)	0.60
11-12	Gp3	g.chr4:39449012C>G	Missense Mutation	KLB	p.A889G	klotho beta	40 (0.00)	175 (0.59)	1.57
11-12	Gp3	g.chr22:50986626C>T	Nonsense Mutation	KLHDC7B	p.Q11*	kelch domain containin	18 (0.00)	34 (0.21)	0.55
11-12	Gp3	g.chr1:202888969A>T	Nonsense Mutation	KLHL12	p.L88*	kelch-like family memb	46 (0.00)	50 (0.52)	1.39
11-12	Gp3	g.chr3:47385413C>A	Silent	KLHL18	p.I569I	kelch-like family memb	95 (0.00)	127 (0.30)	0.80
11-12	Gp3	g.chr19:51410255G>T	Missense Mutation	KLK4	p.P234T	kallikrein-related peptid	77 (0.00)	25 (0.44)	1.17
11-12	Gp3	g.chr12:49427573G>C	Missense Mutation	KMT2D	p.H3639D	lysine (K)-specific meth	23 (0.00)	13 (0.85)	2.26
11-12	Gp3	g.chr12:123057808G>T	Missense Mutation	KNTC1	p.E716D	kinetochore associated 1	67 (0.00)	160 (0.53)	1.42
11-12	Gp3	g.chr1:32628856C>T	Missense Mutation	KPNA6	p.A311V	karyopherin alpha 6 (im	35 (0.00)	105 (0.99)	2.64
11-12	Gp3	g.chr17:39659672C>A	Missense Mutation	KRT13	p.R201L	keratin 13	63 (0.00)	127 (0.98)	1.42
11-12	Gp3	g.chr17:39778685G>T	Silent	KRT17	p.T198T	keratin 17	48 (0.02)	516 (0.53)	0.78
11-12	Gp3	g.chr12:52841055G>T	Silent	KRT6B	p.G538G	keratin 6B	60 (0.00)	85 (0.34)	0.91
11-12	Gp3	g.chr17:39186168A>C	Missense Mutation	KRTAP1-4	p.S55A	keratin associated protei	28 (0.00)	17 (0.53)	0.77
11-12	Gp3	g.chr21:46047382C>G	Silent	KRTAP10-9	p.A98A	keratin associated protei	72 (0.00)	77 (0.47)	1.51
11-12	Gp3	g.chr17:39296254C>T	Silent	KRTAP4-6	p.P162P	keratin associated protei	38 (0.03)	185 (0.55)	0.79
11-12	Gp3	g.chr17:39383012C>T	Missense Mutation	KRTAP9-2	p.P36S	keratin associated protei	50 (0.00)	296 (1.00)	1.44
11-12	Gp3	g.chr12:6883778G>T	Nonsense Mutation	LAG3	p.G177*	lymphocyte-activation g	16 (0.00)	37 (0.38)	1.01
11-12	Gp3	g.chr3:49168206G>T	Missense Mutation	LAMB2	p.P335T	laminin, beta 2 (laminin	115 (0.00)	308 (0.76)	2.02

11-12	Gp3	g.chr1:209790888A>G	Missense Mutation	LAMB3	p.M1032T	laminin, beta 3	40 (0.00)	52 (0.46)	1.23
11-12	Gp3	g.chr1:209791819G>A	Nonsense Mutation	LAMB3	p.Q963*	laminin, beta 3	21 (0.00)	102 (0.61)	1.62
11-12	Gp3	g.chr9:133942431A>G	Missense Mutation	LAMC3	p.Q811R	laminin, gamma 3	16 (0.00)	149 (0.15)	0.39
11-12	Gp3	g.chr9:130912522G>C	Missense Mutation	LCN2	p.Q48H	lipocalin 2	32 (0.00)	43 (0.28)	0.74
11-12	Gp3	g.chr9:139639715G>T	Missense Mutation	LCN6	p.L97I	lipocalin 6	27 (0.00)	108 (0.29)	0.77
11-12	Gp3	g.chr9:139639718C>A	Nonsense Mutation	LCN6	p.E96*	lipocalin 6	25 (0.00)	112 (0.16)	0.43
11-12	Gp3	g.chr12:6940013C>G	RNA	LEPREL2		leprecan-like 2	44 (0.00)	36 (0.83)	2.22
11-12	Gp3	g.chr12:6940051C>A	RNA	LEPREL2		leprecan-like 2	46 (0.00)	26 (0.77)	2.05
11-12	Gp3	g.chr15:77907646G>T	Nonsense Mutation	LINGO1	p.C201*	leucine rich repeat and I	37 (0.00)	290 (0.68)	1.80
11-12	Gp3	g.chr8:23185916T>C	Missense Mutation	LOXL2	p.T377A	lysyl oxidase-like 2	30 (0.00)	181 (0.43)	1.13
11-12	Gp3	g.chr18:2921619T>C	Missense Mutation	LPIN2	p.K785R	lipin 2	56 (0.00)	120 (0.87)	2.31
11-12	Gp3	g.chr12:57574519G>A	Missense Mutation	LRP1	p.G1819D	low density lipoprotein	15 (0.00)	56 (0.46)	1.24
11-12	Gp3	g.chr12:57593066G>T	Nonsense Mutation	LRP1	p.E3250*	low density lipoprotein	39 (0.00)	73 (0.33)	0.88
11-12	Gp3	g.chr2:170026315G>T	Nonsense Mutation	LRP2	p.C3798*	low density lipoprotein	48 (0.02)	293 (0.27)	0.73
11-12	Gp3	g.chr11:68170999C>A	Missense Mutation	LRP5	p.L545I	low density lipoprotein	16 (0.00)	47 (0.19)	0.51
11-12	Gp3	g.chr8:145745425C>A	Missense Mutation	LRRC14	p.Q106K	leucine rich repeat cont	27 (0.00)	168 (0.14)	0.38
11-12	Gp3	g.chr8:145746650C>A	Missense Mutation	LRRC14	p.R424S	leucine rich repeat cont	20 (0.00)	137 (0.24)	0.64
11-12	Gp3	g.chr20:6022532G>T	Silent	LRRN4	p.T453T	leucine rich repeat neur	29 (0.00)	59 (0.29)	0.77
11-12	Gp3	g.chr3:115560742C>A	Missense Mutation	LSAMP	p.C290F	limbic system-associate	29 (0.00)	68 (0.34)	0.90
11-12	Gp3	g.chr22:21342384G>T	Missense Mutation	LZTR1	p.W162C	leucine-zipper-like trans	20 (0.00)	25 (0.40)	1.07
11-12	Gp3	g.chr7:77721501G>T	Intron	MAGI2		membrane associated gu	73 (0.00)	89 (0.63)	1.68
11-12	Gp3	g.chr7:77747375C>A	Intron	MAGI2		membrane associated gu	46 (0.00)	12 (0.67)	1.78
11-12	Gp3	g.chr7:77791521G>A	Intron	MAGI2		membrane associated gu	248 (0.00)	18 (0.89)	2.37
11-12	Gp3	g.chr7:77829803A>T	Intron	MAGI2		membrane associated gu	81 (0.01)	128 (0.53)	1.42
11-12	Gp3	g.chr7:77944766C>A	Intron	MAGI2		membrane associated gu	81 (0.00)	23 (0.57)	1.51
11-12	Gp3	g.chr7:77982338A>T	Intron	MAGI2		membrane associated gu	56 (0.00)	20 (0.65)	1.73
11-12	Gp3	g.chr7:77995133T>C	Intron	MAGI2		membrane associated gu	138 (0.00)	111 (0.17)	0.46
11-12	Gp3	g.chr7:78347790G>T	Intron	MAGI2		membrane associated gu	20 (0.00)	115 (0.99)	2.64
11-12	Gp3	g.chr7:78360229T>A	Intron	MAGI2		membrane associated gu	82 (0.00)	150 (0.83)	2.20
11-12	Gp3	g.chr7:78626679G>A	Intron	MAGI2		membrane associated gu	34 (0.03)	22 (0.95)	2.55
11-12	Gp3	g.chr7:78741913C>A	Intron	MAGI2		membrane associated gu	49 (0.00)	177 (0.52)	1.39
11-12	Gp3	g.chr15:91453393C>T	Missense Mutation	MAN2A2	p.P483L	mannosidase, alpha, cla	44 (0.00)	267 (0.15)	0.40
11-12	Gp3	g.chr15:91453416G>C	Missense Mutation	MAN2A2	p.G491R	mannosidase, alpha, cla	49 (0.00)	340 (0.79)	2.09
11-12	Gp3	g.chr2:102456343C>G	Missense Mutation	MAP4K4	p.S279C	mitogen-activated prote	136 (0.00)	17 (0.71)	1.88
11-12	Gp3	g.chr15:42116159C>A	Missense Mutation	MAPKBP1	p.S1371R	mitogen-activated prote	36 (0.00)	218 (0.31)	0.82

11-12	Gp3	g.chr4:164621966T>C	Splice Site	MARCH1	p.K54R	membrane-associated ri	32 (0.00)	18 (0.28)	0.74
11-12	Gp3	g.chr5:66460326C>A	Silent	MAST4	p.G1773G	microtubule associated s	25 (0.00)	125 (0.32)	0.85
11-12	Gp3	g.chr5:112399697A>T	Missense Mutation	MCC	p.S733T	mutated in colorectal ca	33 (0.00)	33 (0.21)	0.57
11-12	Gp3	g.chr21:47686052G>C	Missense Mutation	MCM3AP	p.L940V	minichromosome maint	291 (0.00)	98 (0.89)	2.87
11-12	Gp3	g.chr22:35804428A>G	Silent	MCM5	p.P208P	minichromosome maint	37 (0.00)	13 (0.38)	1.03
11-12	Gp3	g.chr12:27179376C>A	Silent	MED21	p.A22A	mediator complex subur	51 (0.00)	100 (0.49)	1.31
11-12	Gp3	g.chr15:100252658C>A	Silent	MEF2A	p.I392I	myocyte enhancer facto	70 (0.00)	57 (0.18)	0.47
11-12	Gp3	g.chr5:88056912C>A	Nonsense Mutation	MEF2C	p.E97*	myocyte enhancer facto	30 (0.00)	14 (0.79)	2.10
11-12	Gp3	g.chr15:66250057C>A	Missense Mutation	MEGF11	p.C372F	multiple EGF-like-doma	18 (0.00)	16 (0.44)	1.17
11-12	Gp3	g.chr11:12237784T>C	Missense Mutation	MICAL2	p.I289T	microtubule associated	62 (0.02)	340 (0.46)	1.23
11-12	Gp3	g.chr22:50523252C>G	Missense Mutation	MLC1	p.S27T	megalencephalic leukoe	21 (0.00)	66 (0.20)	0.53
11-12	Gp3	g.chr8:89130934A>T	Missense Mutation	MMP16	p.I289K	matrix metallopeptidase	36 (0.00)	14 (0.43)	1.14
11-12	Gp3	g.chr16:55527190T>A	Missense Mutation	MMP2	p.F410Y	matrix metallopeptidase	63 (0.00)	12 (0.67)	0.83
11-12	Gp3	g.chr17:34964848C>A	Silent	MRM1	p.G158G	mitochondrial rRNA me	19 (0.00)	108 (0.25)	0.67
11-12	Gp3	g.chr2:48018181T>C	Missense Mutation	MSH6	p.S126P	mutS homolog 6	49 (0.02)	18 (0.44)	1.19
11-12	Gp3	g.chr5:174156462G>T	Missense Mutation	MSX2	p.S227I	msh homeobox 2	46 (0.00)	125 (0.96)	2.56
11-12	Gp3	g.chr7:100647878C>T	Silent	MUC12	p.G4821G	mucin 12, cell surface a	202 (0.00)	63 (0.97)	2.58
11-12	Gp3	g.chr19:9047283G>A	Missense Mutation	MUC16	p.L11450F	mucin 16, cell surface a	104 (0.00)	222 (0.99)	2.63
11-12	Gp3	g.chr19:9057588T>C	Missense Mutation	MUC16	p.Q9953R	mucin 16, cell surface a	40 (0.00)	78 (0.14)	0.38
11-12	Gp3	g.chr19:9068830C>A	Missense Mutation	MUC16	p.D6206Y	mucin 16, cell surface a	56 (0.00)	20 (0.25)	0.67
11-12	Gp3	g.chr11:1092947C>A	Missense Mutation	MUC2	p.T1589N	mucin 2, oligomeric mu	21 (0.00)	125 (0.19)	0.51
11-12	Gp3	g.chr7:100552220G>T	Missense Mutation	MUC3A	p.G324V	mucin 3A, cell surface a	578 (0.00)	265 (0.98)	2.62
11-12	Gp3	g.chr11:1268151G>C	Silent	MUC5B	p.V3347V	mucin 5B, oligomeric m	39 (0.00)	267 (0.34)	0.90
11-12	Gp3	g.chr11:47369029C>A	Splice Site	MYBPC3	p.D285Y	myosin binding protein	60 (0.00)	17 (0.53)	1.41
11-12	Gp3	g.chr17:10404607G>T	Silent	MYH1	p.T1186T	myosin, heavy chain 1, s	79 (0.00)	77 (0.97)	2.60
11-12	Gp3	g.chr17:8381700G>A	Nonsense Mutation	MYH10	p.Q1857*	myosin, heavy chain 10,	35 (0.00)	71 (0.55)	1.46
11-12	Gp3	g.chr14:23885420C>A	Missense Mutation	MYH7	p.E1582D	myosin, heavy chain 7, c	28 (0.00)	32 (0.38)	1.00
11-12	Gp3	g.chr20:30408009C>T	Missense Mutation	MYLK2	p.P45S	myosin light chain kinas	65 (0.00)	298 (0.45)	1.20
11-12	Gp3	g.chr6:2749389G>A	Missense Mutation	MYLK4	p.S47L	myosin light chain kinas	104 (0.00)	35 (0.94)	2.51
11-12	Gp3	g.chr11:76908590G>T	Missense Mutation	MYO7A	p.R1463L	myosin VIIA	111 (0.00)	198 (0.34)	0.90
11-12	Gp3	g.chr15:72190967G>A	Missense Mutation	MYO9A	p.R1293C	myosin IXA	34 (0.00)	21 (0.52)	1.40
11-12	Gp3	g.chr8:2005567C>A	Missense Mutation	MYOM2	p.A122D	myomesin 2	23 (0.00)	55 (0.44)	1.16
11-12	Gp3	g.chr20:62843446G>A	Missense Mutation	MYT1	p.C491Y	myelin transcription fac	156 (0.00)	161 (0.51)	1.36
11-12	Gp3	g.chr12:112492219G>T	Missense Mutation	NAA25	p.A534D	N(alpha)-acetyltransfera	30 (0.00)	81 (0.47)	1.25
11-12	Gp3	g.chr9:130825933A>G	Missense Mutation	NAIF1	p.L253P	nuclear apoptosis induci	35 (0.00)	65 (0.17)	0.45

11-12	Gp3	g.chr8:144657620C>A	Missense Mutation	NAPRT1	p.A422S		16 (0.00)	47 (0.17)	0.45
11-12	Gp3	g.chr3:47043278C>A	Silent	NBEAL2	p.R1582R	neurobeachin-like 2	39 (0.00)	13 (0.85)	2.26
11-12	Gp3	g.chr1:16892290C>G	Missense Mutation	NBPF1	p.E968Q	neuroblastoma breakpoi	142 (0.00)	84 (0.60)	1.59
11-12	Gp3	g.chr17:41343599G>T	Splice Site	NBR1		neighbor of BRCA1 ger	16 (0.00)	46 (0.61)	0.88
11-12	Gp3	g.chr2:97019938A>T	Silent	NCAPH	p.V329V	non-SMC condensin I c	58 (0.00)	73 (0.42)	1.13
11-12	Gp3	g.chr12:124816977C>A	Missense Mutation	NCOR2	p.Q2264H	nuclear receptor corepre	65 (0.00)	364 (0.27)	0.72
11-12	Gp3	g.chr8:11643527C>A	Silent	NEIL2	p.L248L	nei endonuclease VIII-li	111 (0.01)	535 (0.85)	2.27
11-12	Gp3	g.chr9:127089633C>T	Silent	NEK6	p.N177N	NIMA-related kinase 6	103 (0.00)	159 (0.19)	0.52
11-12	Gp3	g.chr17:7225187A>G	Silent	NEURL4	p.F956F	neuralized E3 ubiquitin	49 (0.00)	124 (0.20)	0.54
11-12	Gp3	g.chr17:29684011C>G	Missense Mutation	NF1	p.P2591R	neurofibromin 1	102 (0.00)	35 (0.20)	0.53
11-12	Gp3	g.chr1:41236426C>G	Missense Mutation	NFYC	p.L311V	nuclear transcription fac	38 (0.00)	140 (0.59)	1.56
11-12	Gp3	g.chr6:18122238C>T	Silent	NHLRC1	p.V200V	NHL repeat containing 1	61 (0.00)	13 (0.38)	1.03
11-12	Gp3	g.chr6:138751810G>T	Silent	NHSL1	p.L1228L	NHS-like 1	15 (0.00)	352 (0.16)	0.42
11-12	Gp3	g.chr17:26370174C>G	Missense Mutation	NLK	p.P92R	nemo-like kinase	31 (0.00)	49 (0.59)	1.58
11-12	Gp3	g.chr5:43650657T>C	Missense Mutation	NNT	p.L562P	nicotinamide nucleotide	84 (0.01)	201 (0.94)	2.51
11-12	Gp3	g.chr9:33466984G>T	Splice Site	NOL6	p.H626N	nucleolar protein 6 (RN.	58 (0.02)	116 (0.81)	2.16
11-12	Gp3	g.chr7:150707327C>A	Silent	NOS3	p.T879T	nitric oxide synthase 3 (	16 (0.00)	148 (0.28)	0.74
11-12	Gp3	g.chr19:15300177C>T	Missense Mutation	NOTCH3	p.D367N	notch 3	17 (0.00)	137 (0.20)	0.55
11-12	Gp3	g.chr7:44578603T>A	Missense Mutation	NPC1L1	p.I465F	NPC1-like 1	53 (0.00)	97 (0.84)	2.23
11-12	Gp3	g.chr16:29394468C>T	Silent	NPIPB11	p.R595R	nuclear pore complex in	348 (0.00)	359 (0.88)	2.35
11-12	Gp3	g.chr1:153660686C>T	Silent	NPR1	p.R802R	natriuretic peptide recep	21 (0.00)	54 (0.30)	0.79
11-12	Gp3	g.chr11:47283157C>G	Missense Mutation	NR1H3	p.H256Q	nuclear receptor subfam	25 (0.00)	331 (0.19)	0.51
11-12	Gp3	g.chr2:27664633C>T	Missense Mutation	NRBP1	p.A521V	nuclear receptor binding	214 (0.00)	69 (0.96)	2.55
11-12	Gp3	g.chr16:67919889C>T	Missense Mutation	NRN1L	p.T2I	neuritin 1-like	51 (0.00)	31 (0.48)	0.60
11-12	Gp3	g.chr8:59514685G>T	Missense Mutation	NSMAF	p.P353T	neutral sphingomyelinas	73 (0.00)	468 (0.18)	0.48
11-12	Gp3	g.chr9:87570412T>C	Missense Mutation	NTRK2	p.Y702H	neurotrophic tyrosine ki	19 (0.00)	145 (0.68)	1.80
11-12	Gp3	g.chr11:71724571G>A	Silent	NUMA1	p.G1326G	nuclear mitotic apparatu	20 (0.00)	45 (0.62)	1.66
11-12	Gp3	g.chr3:13373839G>A	Nonsense Mutation	NUP210	p.Q1297*	nucleoporin 210kDa	61 (0.02)	325 (1.00)	2.66
11-12	Gp3	g.chr3:13429937C>A	Nonsense Mutation	NUP210	p.E184*	nucleoporin 210kDa	36 (0.00)	17 (0.59)	1.57
11-12	Gp3	g.chr19:50411977C>T	Missense Mutation	NUP62	p.R363H	nucleoporin 62kDa	47 (0.00)	48 (0.15)	0.39
11-12	Gp3	g.chr11:3712695C>T	Missense Mutation	NUP98	p.A1446T	nucleoporin 98kDa	22 (0.00)	18 (0.44)	1.19
11-12	Gp3	g.chr19:17571412C>T	Silent	NXNL1	p.L89L	nucleoredoxin-like 1	27 (0.00)	248 (0.31)	0.84
11-12	Gp3	g.chr2:226446903G>A	Missense Mutation	NYAP2	p.R257K	neuronal tyrosine-phosp	68 (0.00)	207 (0.27)	0.72
11-12	Gp3	g.chr1:228407190C>A	Missense Mutation	OBSCN	p.A940D	obscurin, cytoskeletal ca	19 (0.00)	189 (0.74)	1.96
11-12	Gp3	g.chr1:228451857G>T	Missense Mutation	OBSCN	p.R1726S	obscurin, cytoskeletal ca	25 (0.00)	519 (0.65)	1.72

11-12	Gp3	g.chr1:228475510A>G	Silent	OBSCN	p.G3649G	obscurin, cytoskeletal ca	32 (0.00)	205 (0.24)	0.65
11-12	Gp3	g.chr1:228475848G>A	Missense Mutation	OBSCN	p.A3729T	obscurin, cytoskeletal ca	81 (0.00)	149 (0.84)	2.24
11-12	Gp3	g.chr1:228509803G>T	Missense Mutation	OBSCN	p.E6044D	obscurin, cytoskeletal ca	29 (0.00)	146 (0.21)	0.57
11-12	Gp3	g.chr6:154360871T>C	Silent	OPRM1	p.S64S	opioid receptor, mu 1	16 (0.00)	12 (0.50)	1.33
11-12	Gp3	g.chr11:4928784T>C	Missense Mutation	OR51A7	p.F62S	olfactory receptor, famil	88 (0.00)	95 (0.83)	2.22
11-12	Gp3	g.chr11:4842919G>T	Nonsense Mutation	OR51F2	p.E102*	olfactory receptor, famil	23 (0.00)	18 (0.39)	1.04
11-12	Gp3	g.chr11:4842920A>T	Missense Mutation	OR51F2	p.E102V	olfactory receptor, famil	23 (0.00)	18 (0.39)	1.04
11-12	Gp3	g.chr11:4843081G>A	Missense Mutation	OR51F2	p.A156T	olfactory receptor, famil	25 (0.00)	25 (0.80)	2.13
11-12	Gp3	g.chr11:5475105C>A	Silent	OR51I2	p.P129P	olfactory receptor, famil	68 (0.00)	49 (0.14)	0.38
11-12	Gp3	g.chr8:99961446C>T	Missense Mutation	OSR2	p.P89L	odd-skipped related tran	15 (0.00)	182 (0.41)	1.08
11-12	Gp3	g.chr17:72927157A>G	Missense Mutation	OTOP2	p.E476G	otopetrin 2	58 (0.00)	400 (0.20)	0.53
11-12	Gp3	g.chr17:72927170C>A	Silent	OTOP2	p.I480I	otopetrin 2	62 (0.00)	389 (0.36)	0.95
11-12	Gp3	g.chr11:65998314G>T	Missense Mutation	PACS1	p.S510I	phosphofurin acidic clus	55 (0.02)	551 (0.15)	0.41
11-12	Gp3	g.chr12:103271329C>A	Splice Site	PAH		phenylalanine hydroxyla	43 (0.00)	132 (0.79)	2.10
11-12	Gp3	g.chr1:2450598A>G	Missense Mutation	PANK4	p.I340T	pantothenate kinase 4	24 (0.00)	145 (0.19)	0.50
11-12	Gp3	g.chr13:58209223C>G	Missense Mutation	PCDH17	p.A848G	protocadherin 17	55 (0.00)	32 (0.97)	2.58
11-12	Gp3	g.chr5:140214350G>A	Missense Mutation	PCDHA7	p.D128N	protocadherin alpha 7	60 (0.00)	43 (0.84)	2.23
11-12	Gp3	g.chr5:140811696A>T	Missense Mutation	PCDHGA12	p.Y457F	protocadherin gamma su	62 (0.02)	80 (0.16)	0.43
11-12	Gp3	g.chr5:140743983G>T	Missense Mutation	PCDHGA5	p.G29V	protocadherin gamma su	21 (0.00)	71 (0.94)	2.52
11-12	Gp3	g.chr5:140763354G>A	Silent	PCDHGA7	p.S296S	protocadherin gamma su	70 (0.00)	52 (0.98)	2.62
11-12	Gp3	g.chr21:47832787G>T	Missense Mutation	PCNT	p.A2011S	pericentrin	81 (0.00)	29 (0.90)	2.90
11-12	Gp3	g.chr1:233314895C>G	Silent	PCNXL2	p.P1031P	pecanex-like 2 (Drosoph	113 (0.00)	11 (0.91)	2.42
11-12	Gp3	g.chr17:53848468A>G	Splice Site	PCTP	p.E87E	phosphatidylcholine tran	59 (0.00)	195 (0.48)	1.29
11-12	Gp3	g.chr19:10574533G>A	Missense Mutation	PDE4A	p.R603H	phosphodiesterase 4A, c	19 (0.00)	90 (0.14)	0.39
11-12	Gp3	g.chr19:10574588C>A	Silent	PDE4A	p.R621R	phosphodiesterase 4A, c	25 (0.00)	127 (0.19)	0.50
11-12	Gp3	g.chr5:52097364A>G	Missense Mutation	PELO	p.K283R	pelota homolog (Drosop	46 (0.00)	74 (0.16)	0.43
11-12	Gp3	g.chr7:11030403G>A	Missense Mutation	PHF14	p.C325Y	PHD finger protein 14	71 (0.01)	288 (0.97)	2.59
11-12	Gp3	g.chr9:96418818T>G	Missense Mutation	PHF2	p.F363C	PHD finger protein 2	51 (0.00)	144 (0.19)	0.50
11-12	Gp3	g.chr18:60415529G>A	Intron	PHLPP1		PH domain and leucine	119 (0.00)	13 (0.92)	2.46
11-12	Gp3	g.chr18:60570347C>A	Silent	PHLPP1	p.V865V	PH domain and leucine	130 (0.01)	144 (0.47)	1.26
11-12	Gp3	g.chr18:60586604T>C	Intron	PHLPP1		PH domain and leucine	65 (0.00)	17 (0.29)	0.78
11-12	Gp3	g.chr18:60631671T>A	Intron	PHLPP1		PH domain and leucine	73 (0.00)	366 (0.20)	0.53
11-12	Gp3	g.chr18:60642763C>T	Nonsense Mutation	PHLPP1	p.R1297*	PH domain and leucine	115 (0.00)	128 (0.77)	2.57
11-12	Gp3	g.chr16:71710143T>C	Intron	PHLPP2		PH domain and leucine	64 (0.00)	13 (0.85)	1.05
11-12	Gp3	g.chr22:38471041G>A	Missense Mutation	PICK1	p.E384K	protein interacting with	20 (0.00)	121 (0.30)	0.79

11-12	Gp3	g.chr7:99957139C>T	Silent	PILRB	p.L212L	paired immunoglobin-li	22 (0.00)	121 (0.88)	2.36
11-12	Gp3	g.chr8:42037897C>A	Splice Site	PLAT		plasminogen activator, t	58 (0.00)	178 (0.51)	1.36
11-12	Gp3	g.chr8:145001465G>A	Silent	PLEC	p.V1402V	plectin	35 (0.00)	244 (0.37)	0.98
11-12	Gp3	g.chr8:145006605C>A	Missense Mutation	PLEC	p.R784L	plectin	24 (0.00)	108 (0.68)	1.80
11-12	Gp3	g.chr1:204197881T>A	Missense Mutation	PLEKHA6	p.I974F	pleckstrin homology do	43 (0.00)	107 (0.28)	0.75
11-12	Gp3	g.chr1:204198085C>T	Missense Mutation	PLEKHA6	p.D931N	pleckstrin homology do	50 (0.00)	226 (0.49)	1.31
11-12	Gp3	g.chr19:39911440G>C	Silent	PLEKHG2	p.G449G	pleckstrin homology do	74 (0.00)	231 (0.39)	1.03
11-12	Gp3	g.chr19:4510914T>C	Missense Mutation	PLIN4	p.K1006E	perilipin 4	27 (0.00)	196 (0.14)	0.38
11-12	Gp3	g.chr8:28196921G>T	Missense Mutation	PNOC	p.S164I	prepronociceptin	46 (0.00)	326 (0.33)	0.88
11-12	Gp3	g.chr6:43487140G>T	Missense Mutation	POLR1C	p.A71S	polymerase (RNA) I pol	116 (0.00)	47 (0.17)	0.45
11-12	Gp3	g.chr17:7415869G>C	Missense Mutation	POLR2A	p.Q1522H	polymerase (RNA) II (	28 (0.00)	17 (0.94)	2.51
11-12	Gp3	g.chr10:79745674C>T	Missense Mutation	POLR3A	p.D1020N	polymerase (RNA) III (	124 (0.00)	49 (0.86)	2.29
11-12	Gp3	g.chr9:4662975T>C	Silent	PPAPDC2	p.F200F	phosphatidic acid phosp	29 (0.00)	104 (0.33)	0.87
11-12	Gp3	g.chr16:4933560G>T	Nonsense Mutation	PPL	p.S1699*	periplakin	19 (0.00)	55 (0.96)	2.57
11-12	Gp3	g.chr16:4934610C>T	Missense Mutation	PPL	p.R1349K	periplakin	136 (0.01)	145 (0.19)	0.51
11-12	Gp3	g.chr16:4950973C>A	Missense Mutation	PPL	p.G186W	periplakin	24 (0.00)	259 (0.17)	0.45
11-12	Gp3	g.chr1:13001294C>A	Missense Mutation	PRAMEF6	p.R130M	PRAME family membe	219 (0.00)	6 (0.83)	2.22
11-12	Gp3	g.chr11:82550332T>A	Missense Mutation	PRCP	p.S353C	prolylcarboxypeptidase	52 (0.00)	274 (0.93)	2.48
11-12	Gp3	g.chr9:133543580C>A	Silent	PRDM12	p.I150I	PR domain containing 1	30 (0.00)	27 (0.37)	0.99
11-12	Gp3	g.chr20:47269999T>C	Missense Mutation	PREX1	p.Q749R	phosphatidylinositol-3,4	39 (0.00)	26 (0.42)	1.13
11-12	Gp3	g.chr19:54626919C>A	Silent	PRPF31	p.V169V	pre-mRNA processing f	36 (0.00)	163 (0.47)	1.26
11-12	Gp3	g.chr17:1582626C>T	Silent	PRPF8	p.L456L	pre-mRNA processing f	34 (0.00)	65 (0.40)	1.07
11-12	Gp3	g.chr19:42814014G>T	Missense Mutation	PRR19	p.G93V	proline rich 19	15 (0.00)	112 (0.28)	0.74
11-12	Gp3	g.chr9:134334707G>T	Missense Mutation	PRRC2B	p.R456S	proline-rich coiled-coil	28 (0.00)	123 (0.42)	1.13
11-12	Gp3	g.chr1:171544240T>A	Missense Mutation	PRRC2C	p.S2308T	proline-rich coiled-coil	29 (0.00)	32 (0.22)	0.58
11-12	Gp3	g.chr16:31151704G>A	Nonsense Mutation	PRSS36	p.Q734*	protease, serine, 36	44 (0.00)	256 (0.30)	0.81
11-12	Gp3	g.chr7:77246964G>T	Intron	PTPN12		protein tyrosine phosph	82 (0.00)	59 (0.71)	1.90
11-12	Gp3	g.chr7:77255250A>G	Intron	PTPN12		protein tyrosine phosph	79 (0.00)	285 (0.80)	2.13
11-12	Gp3	g.chr4:87610313G>T	Missense Mutation	PTPN13	p.L172F	protein tyrosine phosph	63 (0.00)	15 (0.40)	1.07
11-12	Gp3	g.chr1:214557856C>G	Missense Mutation	PTPN14	p.V448L	protein tyrosine phosph	41 (0.00)	347 (0.24)	0.64
11-12	Gp3	g.chr12:120650242C>T	Missense Mutation	PXN	p.A549T	paxillin	34 (0.03)	70 (0.23)	0.61
11-12	Gp3	g.chr17:17697208C>A	Missense Mutation	RAI1	p.Q316K	retinoic acid induced 1	97 (0.00)	467 (0.57)	1.52
11-12	Gp3	g.chr9:135985057G>T	Silent	RALGDS	p.L180L	ral guanine nucleotide d	28 (0.00)	201 (0.90)	2.40
11-12	Gp3	g.chr6:13622653T>C	Missense Mutation	RANBP9	p.M711V	RAN binding protein 9	39 (0.00)	280 (0.29)	0.78
11-12	Gp3	g.chr4:160274033C>T	Silent	RAPGEF2	p.T1193T	Rap guanine nucleotide	28 (0.00)	101 (0.99)	2.64

11-12	Gp3	g.chr20:34240983C>T	Missense Mutation	RBM12	p.M754I	RNA binding motif prot	16 (0.00)	11 (0.55)	1.45
11-12	Gp3	g.chr9:125004256C>T	Silent	RBM18	p.E160E	RNA binding motif prot	41 (0.00)	102 (0.57)	1.52
11-12	Gp3	g.chr9:125004301G>C	Silent	RBM18	p.A145A	RNA binding motif prot	81 (0.00)	101 (0.57)	1.53
11-12	Gp3	g.chr10:112581173T>C	Silent	RBM20	p.I932I	RNA binding motif prot	70 (0.00)	19 (0.42)	1.12
11-12	Gp3	g.chr11:63681529A>G	Missense Mutation	RCOR2	p.M263T	REST corepressor 2	18 (0.00)	73 (0.29)	0.77
11-12	Gp3	g.chr19:45532166C>T	Silent	RELB	p.L303L	v-rel avian reticuloendo	25 (0.00)	206 (0.52)	1.40
11-12	Gp3	g.chr19:45532187A>G	Missense Mutation	RELB	p.K310E	v-rel avian reticuloendo	26 (0.00)	199 (0.45)	1.21
11-12	Gp3	g.chr16:726712C>T	Missense Mutation	RHBDL1	p.A81V	rhomboid, veinlet-like 1	25 (0.00)	102 (0.54)	1.44
11-12	Gp3	g.chr8:22864834C>A	Missense Mutation	RHOBTB2	p.P381H	Rho-related BTB domai	30 (0.00)	122 (0.34)	0.92
11-12	Gp3	g.chr8:22865133G>A	Missense Mutation	RHOBTB2	p.D481N	Rho-related BTB domai	132 (0.00)	117 (0.51)	1.37
11-12	Gp3	g.chr8:22865225G>C	Silent	RHOBTB2	p.R511R	Rho-related BTB domai	65 (0.00)	82 (0.38)	1.01
11-12	Gp3	g.chr20:43385671G>T	Nonsense Mutation	RIMS4	p.Y154*	regulating synaptic men	66 (0.00)	265 (0.39)	1.04
11-12	Gp3	g.chr6:3085536G>C	Silent	RIPK1	p.G244G	receptor (TNFRSF)-inte	55 (0.00)	15 (0.40)	1.07
11-12	Gp3	g.chr3:49758704G>A	Missense Mutation	RNF123	p.G1304E	ring finger protein 123	206 (0.00)	116 (0.16)	0.44
11-12	Gp3	g.chr13:79090042G>C	RNA	RNF219-AS1		RNF219 antisense RNA	15 (0.00)	63 (0.56)	1.48
11-12	Gp3	g.chr11:119205839G>A	Missense Mutation	RNF26	p.A3T	ring finger protein 26	22 (0.00)	29 (0.69)	1.84
11-12	Gp3	g.chr3:77089984T>C	Silent	ROBO2	p.Y16Y	roundabout, axon guida	31 (0.00)	38 (0.45)	1.48
11-12	Gp3	g.chr18:110300C>A	RNA	ROCK1P1		Rho-associated, coiled-c	75 (0.00)	24 (0.33)	0.89
11-12	Gp3	g.chr18:110414A>T	RNA	ROCK1P1		Rho-associated, coiled-c	62 (0.02)	50 (0.22)	0.59
11-12	Gp3	g.chr9:94486823G>T	Missense Mutation	ROR2	p.N651K	receptor tyrosine kinase	34 (0.00)	218 (0.44)	1.19
11-12	Gp3	g.chrX:114953316C>A	Missense Mutation	RP1-241P17.4	p.M78I		48 (0.00)	22 (0.77)	1.29
11-12	Gp3	g.chr10:135233581T>A	Missense Mutation	RP11-108K14.	p.L311Q		18 (0.00)	216 (0.21)	0.57
11-12	Gp3	g.chr7:141897254C>T	Silent	RP11-1220K2.	p.L1563L		41 (0.00)	176 (0.95)	2.53
11-12	Gp3	g.chr15:85175299T>A	RNA	RP11-182J1.1			39 (0.00)	47 (0.96)	2.55
11-12	Gp3	g.chr3:153109795G>A	RNA	RP11-23D24.2			15 (0.00)	22 (0.95)	2.55
11-12	Gp3	g.chr2:96191354C>G	lincRNA	RP11-440D17.3			19 (0.00)	188 (0.36)	0.95
11-12	Gp3	g.chr3:109522760G>T	lincRNA	RP11-457K10.1			15 (0.00)	18 (0.44)	1.19
11-12	Gp3	g.chr14:24600980C>A	Missense Mutation	RP11-468E2.6	p.S257Y		32 (0.00)	120 (0.15)	0.40
11-12	Gp3	g.chr9:3641577A>G	lincRNA	RP11-509J21.1			23 (0.00)	104 (0.14)	0.38
11-12	Gp3	g.chr5:162746525G>C	RNA	RP11-541P9.3			29 (0.00)	47 (0.17)	0.45
11-12	Gp3	g.chr8:89590983C>A	RNA	RP11-586K2.1			17 (0.00)	23 (0.78)	2.09
11-12	Gp3	g.chr4:82944004G>A	lincRNA	RP11-689K5.3			17 (0.00)	12 (0.92)	2.44
11-12	Gp3	g.chr5:172190051G>T	RNA	RP11-779O18.3			43 (0.00)	122 (0.17)	0.46
11-12	Gp3	g.chr4:125467774C>T	lincRNA	RP11-93I21.3			16 (0.00)	195 (0.27)	0.71
11-12	Gp3	g.chr4:144640210A>T	RNA	RP13-578N3.3			18 (0.00)	37 (0.16)	0.43

11-12	Gp3	g.chr20:18318426C>A	lincRNA	RP4-568F9.6			21 (0.00)	30 (0.97)	2.58
11-12	Gp3	g.chr1:114310865T>C	Missense Mutation	RSBN1	p.K602R	round spermatid basic p	37 (0.00)	29 (0.97)	2.57
11-12	Gp3	g.chr2:74659693G>C	Missense Mutation	RTKN	p.A21G	rhotekin	23 (0.00)	109 (0.76)	2.03
11-12	Gp3	g.chr2:74659744C>A	Missense Mutation	RTKN	p.G4V	rhotekin	22 (0.00)	115 (0.15)	0.39
11-12	Gp3	g.chr19:39075614G>T	Missense Mutation	RYR1	p.R4893L	ryanodine receptor 1 (sk	32 (0.00)	61 (0.39)	1.05
11-12	Gp3	g.chr13:23912386G>A	Nonsense Mutation	SACS	p.R1877*	sacsin molecular chaper	55 (0.00)	184 (0.99)	2.65
11-12	Gp3	g.chr13:23915774G>A	Silent	SACS	p.I747I	sacsin molecular chaper	123 (0.00)	30 (0.63)	1.69
11-12	Gp3	g.chr22:50886784G>T	Silent	SBF1	p.T1747T	SET binding factor 1	34 (0.00)	233 (0.32)	0.86
11-12	Gp3	g.chr11:118015910C>A	Missense Mutation	SCN4B	p.E32D	sodium channel, voltage	54 (0.00)	39 (0.97)	2.60
11-12	Gp3	g.chr2:167298083T>C	Missense Mutation	SCN7A	p.I660M	sodium channel, voltage	23 (0.00)	16 (0.44)	1.17
11-12	Gp3	g.chr2:167298132A>G	Missense Mutation	SCN7A	p.F644S	sodium channel, voltage	91 (0.00)	17 (0.47)	1.25
11-12	Gp3	g.chr14:81952664T>C	Silent	SEL1L	p.A589A	sel-1 suppressor of lin-1	203 (0.00)	59 (0.39)	1.04
11-12	Gp3	g.chr22:19708360G>T	Nonsense Mutation	SEPT5	p.E229*	septin 5	23 (0.00)	114 (0.97)	2.60
11-12	Gp3	g.chr17:2280048C>A	Missense Mutation	SGSM2	p.D832E	small G protein signalin	26 (0.00)	56 (0.32)	0.86
11-12	Gp3	g.chr22:40804391C>G	Silent	SGSM3	p.S580S	small G protein signalin	29 (0.00)	122 (0.62)	1.66
11-12	Gp3	g.chr9:130536582C>A	Missense Mutation	SH2D3C	p.A68S	SH2 domain containing	23 (0.00)	87 (0.28)	0.74
11-12	Gp3	g.chr9:130536631T>C	Silent	SH2D3C	p.E51E	SH2 domain containing	51 (0.00)	84 (0.26)	0.70
11-12	Gp3	g.chr22:38046692G>T	Missense Mutation	SH3BP1	p.A520S	SH3-domain binding pr	33 (0.00)	208 (0.69)	1.85
11-12	Gp3	g.chr5:148424154A>G	Silent	SH3TC2	p.F109F	SH3 domain and tetratri	31 (0.00)	19 (0.47)	1.26
11-12	Gp3	g.chr11:70332188C>A	Missense Mutation	SHANK2	p.D808Y	SH3 and multiple ankyr	20 (0.00)	31 (0.97)	2.58
11-12	Gp3	g.chr19:51919422C>T	Splice Site	SIGLEC10		sialic acid binding Ig-lik	22 (0.00)	45 (0.31)	0.83
11-12	Gp3	g.chr1:232650656T>A	Missense Mutation	SIPA1L2	p.I144F	signal-induced prolifera	86 (0.00)	123 (0.25)	0.67
11-12	Gp3	g.chr20:45242194G>A	Silent	SLC13A3	p.L94L	solute carrier family 13	18 (0.00)	11 (0.73)	1.94
11-12	Gp3	g.chr3:38318930G>A	Missense Mutation	SLC22A13	p.A544T	solute carrier family 22	38 (0.03)	92 (0.99)	2.64
11-12	Gp3	g.chr11:62744780G>T	Missense Mutation	SLC22A6	p.L481I	solute carrier family 22	20 (0.00)	284 (0.55)	1.46
11-12	Gp3	g.chr1:16064429A>G	Silent	SLC25A34	p.K128K	solute carrier family 25,	16 (0.00)	240 (0.27)	0.72
11-12	Gp3	g.chr3:48664401G>T	Missense Mutation	SLC26A6	p.L625M	solute carrier family 26	28 (0.00)	125 (0.22)	0.60
11-12	Gp3	g.chr3:48667360C>A	Missense Mutation	SLC26A6	p.G456C	solute carrier family 26	45 (0.02)	179 (0.41)	1.09
11-12	Gp3	g.chr4:10023016C>A	Missense Mutation	SLC2A9	p.G13V	solute carrier family 2 (	126 (0.00)	156 (0.66)	1.76
11-12	Gp3	g.chr2:27481633C>A	Missense Mutation	SLC30A3	p.G89W	solute carrier family 30	24 (0.00)	195 (0.20)	0.53
11-12	Gp3	g.chr3:50252996C>A	RNA	SLC38A3		solute carrier family 38,	36 (0.00)	31 (0.55)	1.46
11-12	Gp3	g.chr1:153933168C>A	Missense Mutation	SLC39A1	p.E127D	solute carrier family 39	53 (0.00)	99 (0.91)	2.42
11-12	Gp3	g.chr19:33702437T>C	Silent	SLC7A10	p.L265L	solute carrier family 7 (	26 (0.00)	23 (0.96)	2.55
11-12	Gp3	g.chr18:48591701C>A	Intron	SMAD4		SMAD family member	103 (0.00)	82 (0.15)	0.39
11-12	Gp3	g.chr7:128850307G>T	Missense Mutation	SMO	p.A524S	smoothened, frizzled cla	38 (0.00)	485 (0.57)	1.51

11-12	Gp3	g.chr6:169051372G>T	Missense Mutation	SMOC2	p.A307S	SPARC related modular	38 (0.00)	134 (0.22)	0.60
11-12	Gp3	g.chr6:109762602G>C	Missense Mutation	SMPD2	p.R31S	sphingomyelin phospho	37 (0.00)	116 (0.78)	2.09
11-12	Gp3	g.chr15:25430825T>C	RNA	SNHG14		small nucleolar RNA ho	151 (0.00)	66 (0.98)	2.63
11-12	Gp3	g.chr15:25451413C>T	RNA	SNHG14		small nucleolar RNA ho	47 (0.00)	33 (0.33)	0.89
11-12	Gp3	g.chr15:25455051G>T	RNA	SNHG14		small nucleolar RNA ho	64 (0.00)	143 (0.35)	0.93
11-12	Gp3	g.chr15:25455053G>T	RNA	SNHG14		small nucleolar RNA ho	64 (0.00)	148 (0.35)	0.94
11-12	Gp3	g.chr15:25460752A>G	RNA	SNHG14		small nucleolar RNA ho	43 (0.00)	59 (0.46)	1.22
11-12	Gp3	g.chr15:25472303T>C	RNA	SNHG14		small nucleolar RNA ho	130 (0.00)	404 (0.22)	0.59
11-12	Gp3	g.chr20:35433266T>C	Missense Mutation	SOGA1	p.T987A	suppressor of glucose, a	37 (0.00)	333 (0.28)	0.74
11-12	Gp3	g.chr12:23999046G>T	Silent	SOX5	p.R108R	SRY (sex determining r	40 (0.00)	26 (0.46)	1.23
11-12	Gp3	g.chr11:124545299C>A	Missense Mutation	SPA17	p.L47I	sperm autoantigenic pro	76 (0.00)	299 (0.17)	0.45
11-12	Gp3	g.chr4:57677935G>A	Missense Mutation	SPINK2	p.P42L	serine peptidase inhibit	69 (0.01)	321 (0.83)	2.22
11-12	Gp3	g.chr1:32259391T>A	Missense Mutation	SPOCD1	p.M831L	SPOC domain containin	27 (0.00)	23 (0.43)	1.16
11-12	Gp3	g.chr17:47720167G>C	Intron	SPOP		speckle-type POZ prote	46 (0.00)	21 (0.29)	0.76
11-12	Gp3	g.chr14:65237774T>C	Missense Mutation	SPTB	p.N1876S	spectrin, beta, erythrocy	17 (0.00)	25 (0.60)	1.60
11-12	Gp3	g.chr14:65262333C>G	Missense Mutation	SPTB	p.A456P	spectrin, beta, erythrocy	59 (0.02)	270 (0.83)	2.22
11-12	Gp3	g.chr11:66458764G>T	Silent	SPTBN2	p.L1852L	spectrin, beta, non-eryth	36 (0.00)	90 (0.76)	2.01
11-12	Gp3	g.chr15:42169366A>G	Missense Mutation	SPTBN5	p.F1220S	spectrin, beta, non-eryth	31 (0.00)	105 (0.15)	0.41
11-12	Gp3	g.chr2:170668190G>A	Missense Mutation	SSB	p.R384K	Sjogren syndrome antig	144 (0.00)	21 (0.71)	1.90
11-12	Gp3	g.chr7:149503118C>A	RNA	SSPO		SCO-spondin	17 (0.00)	35 (0.46)	1.22
11-12	Gp3	g.chr3:98510824C>A	Missense Mutation	ST3GAL6	p.S299Y	ST3 beta-galactoside al	52 (0.00)	165 (0.72)	1.91
11-12	Gp3	g.chr11:8720510C>A	Silent	ST5	p.V483V	suppression of tumorige	70 (0.00)	118 (0.24)	0.63
11-12	Gp3	g.chr7:74303879A>G	RNA	STAG3L2		stromal antigen 3-like 2	198 (0.00)	14 (0.43)	1.14
11-12	Gp3	g.chr7:74303896A>G	RNA	STAG3L2		stromal antigen 3-like 2	28 (0.00)	9 (0.56)	1.48
11-12	Gp3	g.chr7:75651205C>T	Missense Mutation	STYXL1	p.D91N	serine/threonine/tyrosin	53 (0.00)	19 (0.53)	1.40
11-12	Gp3	g.chr9:136231733C>A	Missense Mutation	SURF4	p.D176Y	surfeit 4	63 (0.00)	32 (0.97)	2.58
11-12	Gp3	g.chr10:29839685G>T	Missense Mutation	SVIL	p.A223E	supervillin	28 (0.00)	345 (0.73)	1.96
11-12	Gp3	g.chr7:138363236C>A	Missense Mutation	SVOPL	p.E39D	SVOP-like	40 (0.00)	91 (0.25)	0.67
11-12	Gp3	g.chr19:46327091C>A	Missense Mutation	SYMPK	p.V845L	symplekin	27 (0.00)	21 (0.62)	1.65
11-12	Gp3	g.chr6:152646330G>A	Silent	SYNE1	p.S5182S	spectrin repeat containi	100 (0.00)	118 (0.47)	1.24
11-12	Gp3	g.chr15:99671498G>T	Missense Mutation	SYNM	p.G692V	synemin, intermediate fi	19 (0.00)	47 (0.19)	0.51
11-12	Gp3	g.chr12:33592330C>A	Missense Mutation	SYT10	p.G43V	synaptotagmin X	34 (0.00)	343 (0.20)	0.54
11-12	Gp3	g.chr1:229730234G>T	Missense Mutation	TAF5L	p.S527Y	TAF5-like RNA polym	42 (0.00)	132 (0.83)	2.22
11-12	Gp3	g.chr6:159458117T>C	Missense Mutation	TAGAP	p.N313S	T-cell activation RhoG	16 (0.00)	320 (0.22)	0.58
11-12	Gp3	g.chr2:160086878G>T	Silent	TANC1	p.G1647G	tetratricopeptide repeat,	96 (0.00)	73 (0.36)	0.95

11-12	Gp3	g.chr2:160086933T>C	Missense Mutation	TANC1	p.S1666P	tetratricopeptide repeat,	131 (0.00)	108 (0.54)	1.43
11-12	Gp3	g.chr12:6566645C>T	Silent	TAPBPL	p.G136G	TAP binding protein-lik	77 (0.00)	326 (0.91)	2.44
11-12	Gp3	g.chr1:6639273G>T	Nonsense Mutation	TAS1R1	p.E719*	taste receptor, type 1, m	79 (0.00)	129 (0.18)	0.48
11-12	Gp3	g.chr9:100971315G>A	Silent	TBC1D2	p.L595L	TBC1 domain family,	43 (0.02)	293 (0.17)	0.46
11-12	Gp3	g.chr17:18541992C>T	Missense Mutation	TBC1D28	p.R74H	TBC1 domain family,	83 (0.00)	255 (0.55)	1.46
11-12	Gp3	g.chr17:58089857C>T	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	50 (0.00)	129 (0.42)	1.12
11-12	Gp3	g.chr17:59556122C>A	Silent	TBX4	p.T228T	T-box 4	88 (0.00)	55 (0.31)	0.82
11-12	Gp3	g.chr22:42606933G>A	Missense Mutation	TCF20	p.P1460L	transcription factor 20 (	59 (0.02)	128 (0.69)	1.83
11-12	Gp3	g.chr1:152080373G>T	Missense Mutation	TCHH	p.R1774S	trichohyalin	44 (0.00)	8 (0.62)	1.67
11-12	Gp3	g.chr3:49449941G>T	Nonsense Mutation	TCTA	p.E28*	T-cell leukemia transloc	25 (0.00)	46 (0.39)	1.04
11-12	Gp3	g.chr2:95542422G>A	Missense Mutation	TEKT4	p.A406T	tektin 4	34 (0.00)	255 (0.22)	0.59
11-12	Gp3	g.chr14:20849765C>A	Missense Mutation	TEP1	p.R1394L	telomerase-associated p	49 (0.00)	284 (0.15)	0.39
11-12	Gp3	g.chr2:74327822C>A	Missense Mutation	TET3	p.P1168T	tet methylcytosine dioxy	88 (0.01)	172 (0.42)	1.13
11-12	Gp3	g.chr22:26895383T>C	Missense Mutation	TFIP11	p.D339G	tuftelin interacting prote	74 (0.00)	18 (0.83)	2.22
11-12	Gp3	g.chr20:36789901C>A	Missense Mutation	TGM2	p.Q37H	transglutaminase 2	53 (0.02)	225 (0.27)	0.72
11-12	Gp3	g.chr15:43552701G>A	Silent	TGM5	p.D29D	transglutaminase 5	40 (0.00)	13 (0.38)	1.03
11-12	Gp3	g.chr1:6692954C>T	Silent	THAP3	p.S179S	THAP domain containi	35 (0.00)	347 (0.17)	0.46
11-12	Gp3	g.chr1:151825993C>A	Missense Mutation	THEM5	p.G17C	thioesterase superfamily	24 (0.00)	32 (0.38)	1.00
11-12	Gp3	g.chr6:155569169G>C	Missense Mutation	TIAM2	p.A566P	T-cell lymphoma invasi	123 (0.00)	82 (0.21)	0.55
11-12	Gp3	g.chr7:75617571G>T	RNA	TMEM120A		transmembrane protein	15 (0.00)	415 (0.25)	0.67
11-12	Gp3	g.chr17:32956079G>T	Missense Mutation	TMEM132E	p.E308D	transmembrane protein	26 (0.00)	28 (0.32)	0.86
11-12	Gp3	g.chr12:57472525C>A	Missense Mutation	TMEM194A	p.A2S	transmembrane protein	15 (0.00)	162 (0.21)	0.56
11-12	Gp3	g.chr1:15546042A>G	Missense Mutation	TMEM51	p.R189G	transmembrane protein	47 (0.00)	20 (0.35)	0.93
11-12	Gp3	g.chr16:425386G>C	Missense Mutation	TMEM8A	p.S425W	transmembrane protein	24 (0.00)	106 (0.91)	2.42
11-12	Gp3	g.chr21:42851386C>A	Intron	TMPRSS2		transmembrane protease	56 (0.00)	55 (0.25)	0.68
11-12	Gp3	g.chr19:2422217G>T	Silent	TMPRSS9	p.P806P	transmembrane protease	29 (0.00)	182 (0.37)	0.98
11-12	Gp3	g.chr8:145657682G>A	Nonsense Mutation	TONSL	p.R1241*	tonsoku-like, DNA repa	57 (0.02)	501 (0.36)	0.95
11-12	Gp3	g.chr15:43748971C>T	Missense Mutation	TP53BP1	p.R612K	tumor protein p53 bindi	44 (0.00)	89 (0.76)	2.04
11-12	Gp3	g.chr3:127298894C>G	Silent	TPRA1	p.L32L	transmembrane protein,	18 (0.00)	89 (0.15)	0.39
11-12	Gp3	g.chr13:20000598C>G	Silent	TPTE2	p.L414L	transmembrane phosph	19 (0.00)	15 (0.60)	1.60
11-12	Gp3	g.chr6:42227334G>A	Missense Mutation	TRERF1	p.P671L	transcriptional regulatin	52 (0.00)	29 (0.55)	1.47
11-12	Gp3	g.chr1:155148119G>T	Missense Mutation	TRIM46	p.K107N	tripartite motif containi	42 (0.00)	371 (0.20)	0.52
11-12	Gp3	g.chr6:126329583G>A	Missense Mutation	TRMT11	p.G242E	tRNA methyltransferase	147 (0.01)	106 (0.58)	1.56
11-12	Gp3	g.chr1:28898388G>T	Nonsense Mutation	TRNAU1AP	p.E235*	tRNA selenocysteine 1	40 (0.00)	155 (0.45)	1.20
11-12	Gp3	g.chr9:77442683G>C	Missense Mutation	TRPM6	p.H284Q	transient receptor potent	36 (0.00)	11 (0.91)	2.42

11-12	Gp3	g.chr8:116427039C>A	Missense Mutation	TRPS1	p.V1033F	trichorhinophalangeal s	62 (0.00)	32 (0.97)	2.58
11-12	Gp3	g.chr17:3493169G>T	Missense Mutation	TRPV1	p.L326M	transient receptor potent	18 (0.00)	116 (0.17)	0.46
11-12	Gp3	g.chr6:116600955G>A	Silent	TSPYL1	p.L13L	TSPY-like 1	53 (0.00)	635 (0.14)	0.39
11-12	Gp3	g.chr16:1399502C>A	Missense Mutation	TSR3	p.R292L	TSR3, 20S rRNA accun	63 (0.00)	245 (0.35)	0.93
11-12	Gp3	g.chr2:166775842C>G	Missense Mutation	TTC21B	p.E540Q	tetratricopeptide repeat	36 (0.00)	37 (0.51)	1.37
11-12	Gp3	g.chr22:28503730C>A	Silent	TTC28	p.L701L	tetratricopeptide repeat	74 (0.00)	159 (0.18)	0.47
11-12	Gp3	g.chr1:117631480C>T	Missense Mutation	TTF2	p.H740Y	transcription terminatio	79 (0.00)	11 (0.91)	2.42
11-12	Gp3	g.chr1:117631523G>T	Missense Mutation	TTF2	p.C754F	transcription terminatio	91 (0.00)	12 (0.92)	2.44
11-12	Gp3	g.chr2:179464467C>T	Missense Mutation	TTN	p.A18721T	titin	90 (0.00)	398 (0.26)	0.70
11-12	Gp3	g.chr20:43109015G>A	Missense Mutation	TTPAL	p.A126T	tocopherol (alpha) trans	68 (0.00)	41 (0.93)	2.47
11-12	Gp3	g.chr20:44443087C>A	Missense Mutation	UBE2C	p.T65N	ubiquitin-conjugating e	23 (0.00)	45 (0.91)	2.43
11-12	Gp3	g.chr17:74387112C>A	Missense Mutation	UBE2O	p.G1264V	ubiquitin-conjugating e	51 (0.00)	63 (0.97)	2.58
11-12	Gp3	g.chr17:74396274C>T	Missense Mutation	UBE2O	p.C370Y	ubiquitin-conjugating e	16 (0.00)	180 (0.17)	0.46
11-12	Gp3	g.chr15:43398146C>A	Silent	UBR1	p.L25L	ubiquitin protein ligase	45 (0.00)	26 (0.85)	2.26
11-12	Gp3	g.chr1:19480291C>A	Nonsense Mutation	UBR4	p.E2201*	ubiquitin protein ligase	16 (0.00)	259 (0.27)	0.71
11-12	Gp3	g.chr10:73051242G>T	Missense Mutation	UNC5B	p.G450C	unc-5 homolog B (C. el	19 (0.00)	43 (0.26)	0.68
11-12	Gp3	g.chr3:126226900C>A	Missense Mutation	UROC1	p.E150D	urocanate hydratase 1	74 (0.00)	34 (0.50)	1.33
11-12	Gp3	g.chr10:11504945C>A	Missense Mutation	USP6NL	p.G661V	USP6 N-terminal like	55 (0.00)	136 (0.15)	0.39
11-12	Gp3	g.chr12:101773315A>G	Silent	UTP20	p.L2521L	UTP20, small subunit (	56 (0.00)	27 (0.30)	0.79
11-12	Gp3	g.chr1:151156819G>A	Missense Mutation	VPS72	p.T179I	vacuolar protein sorting	110 (0.00)	84 (0.50)	1.33
11-12	Gp3	g.chr10:104569779C>A	Missense Mutation	WBP1L	p.A87D	WW domain binding pr	157 (0.00)	462 (0.54)	1.43
11-12	Gp3	g.chr4:10090363G>T	Missense Mutation	WDR1	p.D187E	WD repeat domain 1	20 (0.00)	16 (0.38)	1.00
11-12	Gp3	g.chr9:96024979G>C	Missense Mutation	WNK2	p.G1130R	WNK lysine deficient p	34 (0.00)	151 (0.19)	0.51
11-12	Gp3	g.chr7:116937714C>T	Missense Mutation	WNT2	p.V269M	wingless-type MMTV i	118 (0.00)	122 (0.94)	2.51
11-12	Gp3	g.chr22:41303637C>T	Missense Mutation	XPNPEP3	p.A280V	X-prolyl aminopeptidas	38 (0.00)	57 (0.23)	0.61
11-12	Gp3	g.chr17:7193336G>T	Missense Mutation	YBX2	p.Q267K	Y box binding protein 2	20 (0.00)	54 (0.22)	0.59
11-12	Gp3	g.chr19:59028481G>T	Missense Mutation	ZBTB45	p.P187H	zinc finger and BTB do	15 (0.00)	28 (0.46)	1.24
11-12	Gp3	g.chr8:135614792C>A	Missense Mutation	ZFAT	p.E390D	zinc finger and AT hoo	102 (0.00)	179 (0.21)	0.55
11-12	Gp3	g.chr8:135614810G>T	Silent	ZFAT	p.V384V	zinc finger and AT hoo	112 (0.00)	224 (0.33)	0.87
11-12	Gp3	g.chr14:24001800G>A	Silent	ZFHX2	p.H845H	zinc finger homeobox 2	48 (0.00)	61 (0.33)	0.87
11-12	Gp3	g.chr14:24001808C>G	Missense Mutation	ZFHX2	p.A843P	zinc finger homeobox 2	48 (0.00)	62 (0.58)	1.55
11-12	Gp3	g.chr10:99504537G>T	Missense Mutation	ZFYVE27	p.G107V	zinc finger, FYVE dom	42 (0.00)	41 (0.27)	0.72
11-12	Gp3	g.chr11:123601271T>C	Missense Mutation	ZNF202	p.Q109R	zinc finger protein 202	37 (0.00)	16 (0.81)	2.17
11-12	Gp3	g.chr19:53432497C>T	Missense Mutation	ZNF321P	p.E121K	zinc finger protein 321,	175 (0.00)	23 (0.83)	2.20
11-12	Gp3	g.chr17:40179746G>A	Splice Site	ZNF385C	p.H390Y	zinc finger protein 385C	24 (0.00)	131 (0.60)	0.87

11-12	Gp3	g.chr7:148876156C>A	Missense Mutation	ZNF398	p.P398T	zinc finger protein 398	25 (0.00)	44 (0.45)	1.21
11-12	Gp3	g.chr16:49557538C>G	Silent	ZNF423	p.L1274L	zinc finger protein 423	42 (0.00)	58 (0.72)	0.90
11-12	Gp3	g.chr16:49670681C>A	Silent	ZNF423	p.V794V	zinc finger protein 423	30 (0.00)	26 (0.92)	1.15
11-12	Gp3	g.chr19:52538198T>A	Missense Mutation	ZNF432	p.K245M	zinc finger protein 432	116 (0.00)	244 (1.00)	2.66
11-12	Gp3	g.chr19:42730037C>A	Missense Mutation	ZNF526	p.H494Q	zinc finger protein 526	33 (0.00)	183 (0.22)	0.58
11-12	Gp3	g.chr15:85327554C>A	Missense Mutation	ZNF592	p.L550M	zinc finger protein 592	48 (0.00)	243 (0.22)	0.58
11-12	Gp3	g.chr16:30582401C>A	Missense Mutation	ZNF688	p.Q80H	zinc finger protein 688	17 (0.00)	88 (0.73)	1.94
11-12	Gp3	g.chr16:30616623G>C	Silent	ZNF689	p.G155G	zinc finger protein 689	86 (0.00)	249 (0.14)	0.39
11-12	Gp3	g.chr19:21477066G>A	Silent	ZNF708	p.N234N	zinc finger protein 708	28 (0.00)	49 (0.98)	2.61
11-12	Gp3	g.chr15:90611827G>T	Splice Site	ZNF710	p.K486N	zinc finger protein 710	66 (0.00)	288 (0.70)	1.86
11-12	Gp3	g.chr7:148767849C>G	Missense Mutation	ZNF786	p.G672A	zinc finger protein 786	139 (0.01)	685 (0.58)	1.54
11-12	Gp3	g.chr7:149559007G>A	Missense Mutation	ZNF862	p.D920N	zinc finger protein 862	63 (0.00)	238 (0.25)	0.67
11-12	Gp3	g.chr7:149559429G>T	Missense Mutation	ZNF862	p.E1060D	zinc finger protein 862	47 (0.00)	33 (0.15)	0.40
11-12	Gp3	g.chr19:23542612T>A	Nonsense Mutation	ZNF91	p.K1057*	zinc finger protein 91	61 (0.00)	16 (0.44)	1.17
11-12	Gp3	g.chr20:47886619A>G	Missense Mutation	ZNFX1	p.L577S	zinc finger, NFX1-type	67 (0.00)	40 (0.23)	0.60
11-12	Gp3	g.chr15:43661273G>A	Missense Mutation	ZSCAN29	p.P124L	zinc finger and SCAN d	32 (0.00)	32 (0.97)	2.58
11-12	Gp3	g.chr3:126180671G>T	Missense Mutation	ZXDC	p.L612M	ZXD family zinc finger	27 (0.00)	61 (0.84)	2.23
11-12	Gp4	g.chr9:133729486C>T	Missense Mutation	ABL1	p.P39S	ABL proto-oncogene 1,	45 (0.00)	45 (0.16)	0.41
11-12	Gp4	g.chr2:243037101A>G	RNA	AC093642.5			50 (0.00)	23 (0.30)	1.15
11-12	Gp4	g.chr1:4771995G>A	Missense Mutation	AJAP1	p.G22E	adherens junctions asso	30 (0.00)	149 (0.16)	0.43
11-12	Gp4	g.chr10:37422892C>A	Silent	ANKRD30A	p.G166G	ankyrin repeat domain 3	62 (0.00)	49 (0.53)	1.41
11-12	Gp4	g.chr10:47663294G>A	Splice Site	ANTXRL	p.K83K	anthrax toxin receptor-li	91 (0.00)	27 (0.41)	1.09
11-12	Gp4	g.chr19:2121284G>A	Silent	AP3D1	p.I376I	adaptor-related protein	19 (0.00)	53 (0.17)	0.45
11-12	Gp4	g.chr4:41015776T>C	Missense Mutation	APBB2	p.D220G	amyloid beta (A4) precu	122 (0.00)	18 (0.33)	0.89
11-12	Gp4	g.chr5:112173418C>T	Silent	APC	p.N709N	adenomatous polyposis	73 (0.00)	43 (0.74)	1.98
11-12	Gp4	g.chr18:24411495C>T	RNA	AQP4-AS1		AQP4 antisense RNA 1	65 (0.00)	34 (0.41)	1.10
11-12	Gp4	g.chr5:141053348C>T	Silent	ARAP3	p.R164R	ArfGAP with RhoGAP	27 (0.00)	30 (0.20)	0.53
11-12	Gp4	g.chr14:75143381T>C	Missense Mutation	AREL1	p.T186A	apoptosis resistant E3 ul	51 (0.00)	13 (0.69)	1.39
11-12	Gp4	g.chr13:111862328C>T	Silent	ARHGEF7	p.F149F	Rho guanine nucleotide	17 (0.00)	26 (0.31)	0.82
11-12	Gp4	g.chr12:46245258C>A	Missense Mutation	ARID2	p.Q1118K	AT rich interactive dom	91 (0.01)	40 (0.15)	0.40
11-12	Gp4	g.chr11:74985246C>A	Silent	ARRB1	p.V262V	arrestin, beta 1	40 (0.03)	11 (0.55)	1.45
11-12	Gp4	g.chr11:113661063C>A	RNA	ATF4P4		activating transcription	23 (0.00)	35 (0.46)	1.22
11-12	Gp4	g.chr2:220088871G>T	Missense Mutation	ATG9A	p.L408M	autophagy related 9A	79 (0.00)	145 (0.16)	0.42
11-12	Gp4	g.chr13:113487275G>A	Silent	ATP11A	p.G499G	ATPase, class VI, type	111 (0.00)	242 (0.19)	0.51
11-12	Gp4	g.chr1:154306619A>G	Missense Mutation	ATP8B2	p.D242G	ATPase, aminophospho	117 (0.00)	10 (0.80)	2.13

11-12	Gp4	g.chr19:41763489G>A	Missense Mutation	AXL	p.R763H	AXL receptor tyrosine k	37 (0.00)	19 (0.89)	2.39
11-12	Gp4	g.chr6:56857269G>T	Missense Mutation	BEND6	p.A72S	BEN domain containing	90 (0.00)	29 (0.31)	0.83
11-12	Gp4	g.chr22:43524576C>A	Missense Mutation	BIK	p.T112N	BCL2-interacting killer	18 (0.00)	74 (0.24)	0.65
11-12	Gp4	g.chr5:137480923G>A	Missense Mutation	BRD8	p.P1127L	bromodomain containin	45 (0.00)	37 (0.16)	0.43
11-12	Gp4	g.chr20:11899114C>T	Missense Mutation	BTBD3	p.A64V	BTB (POZ) domain con	242 (0.00)	101 (0.19)	0.50
11-12	Gp4	g.chr1:75072562G>C	Missense Mutation	C1orf173	p.D404E		47 (0.00)	23 (0.57)	1.51
11-12	Gp4	g.chr1:154186378G>A	Missense Mutation	C1orf43	p.R111C	chromosome 1 open rea	59 (0.02)	24 (0.33)	0.89
11-12	Gp4	g.chr1:150255762G>A	Missense Mutation	C1orf51	p.G29S		59 (0.00)	98 (0.18)	0.49
11-12	Gp4	g.chr22:19839188G>A	Silent	C22orf29	p.A199A	chromosome 22 open re	27 (0.00)	26 (0.19)	0.51
11-12	Gp4	g.chr3:112730132C>A	Missense Mutation	C3orf17	p.D225Y	chromosome 3 open rea	136 (0.00)	28 (0.18)	0.48
11-12	Gp4	g.chr9:35677799G>A	Missense Mutation	CA9	p.E285K	carbonic anhydrase IX	25 (0.00)	19 (0.84)	2.25
11-12	Gp4	g.chr1:65137348A>G	Missense Mutation	CACHD1	p.Q779R	cache domain containin	90 (0.00)	11 (0.45)	1.21
11-12	Gp4	g.chr3:85502014C>T	Intron	CADM2		cell adhesion molecule	75 (0.00)	27 (0.59)	1.58
11-12	Gp4	g.chr3:85551454G>T	Intron	CADM2		cell adhesion molecule	71 (0.00)	28 (0.43)	1.14
11-12	Gp4	g.chr1:15819512C>T	Missense Mutation	CASP9	p.V393M	caspase 9, apoptosis-rel	30 (0.00)	16 (0.38)	1.00
11-12	Gp4	g.chr12:124428006C>A	Silent	CCDC92	p.L6L	coiled-coil domain cont	27 (0.00)	55 (0.16)	0.44
11-12	Gp4	g.chr13:37011999G>A	Silent	CCNA1	p.L177L	cyclin A1	125 (0.00)	57 (0.19)	0.51
11-12	Gp4	g.chr9:4685069G>A	Missense Mutation	CDC37L1	p.E109K	cell division cycle 37-li	71 (0.00)	19 (0.47)	1.26
11-12	Gp4	g.chr10:62545434G>T	Silent	CDK1	p.V69V	cyclin-dependent kinase	114 (0.00)	39 (0.41)	1.09
11-12	Gp4	g.chr12:88500602C>A	Missense Mutation	CEP290	p.L889F	centrosomal protein 290	45 (0.00)	33 (0.15)	0.40
11-12	Gp4	g.chr5:648027C>A	Missense Mutation	CEP72	p.H592N	centrosomal protein 72k	29 (0.00)	10 (0.50)	1.85
11-12	Gp4	g.chr12:50524465C>T	Missense Mutation	CERS5	p.D348N	ceramide synthase 5	25 (0.00)	11 (0.64)	1.70
11-12	Gp4	g.chr1:6228789G>A	Intron	CHD5		chromodomain helicase	26 (0.00)	29 (0.21)	0.55
11-12	Gp4	g.chr17:17179439C>T	Missense Mutation	COPS3	p.G12E	COP9 signalosome subu	42 (0.00)	24 (0.29)	0.78
11-12	Gp4	g.chr16:57490445C>T	Silent	COQ9	p.S136S	coenzyme Q9	97 (0.00)	29 (0.41)	0.49
11-12	Gp4	g.chr19:20370053T>C	RNA	CTC-260E6.6			51 (0.00)	50 (0.32)	0.85
11-12	Gp4	g.chr20:56098977C>T	Silent	CTCFL	p.Q95Q	CCCTC-binding factor (	61 (0.00)	32 (0.16)	0.42
11-12	Gp4	g.chr5:156727772C>A	Missense Mutation	CYFIP2	p.A120D	cytoplasmic FMR1 inte	25 (0.00)	36 (0.17)	0.44
11-12	Gp4	g.chr19:15791077C>A	Missense Mutation	CYP4F12	p.L123I	cytochrome P450, famil	151 (0.00)	13 (0.54)	1.44
11-12	Gp4	g.chr9:124395930G>T	Intron	DAB2IP		DAB2 interacting protei	90 (0.00)	29 (0.38)	1.01
11-12	Gp4	g.chr9:124505422C>T	Intron	DAB2IP		DAB2 interacting protei	53 (0.00)	47 (0.17)	0.45
11-12	Gp4	g.chr3:98600510T>A	Missense Mutation	DCBLD2	p.I103F	discoidin, CUB and LC	115 (0.00)	17 (0.35)	0.94
11-12	Gp4	g.chr4:107956598C>T	Missense Mutation	DKK2	p.A51T	dickkopf WNT signalin	22 (0.00)	93 (0.15)	0.40
11-12	Gp4	g.chr3:57348553G>T	Missense Mutation	DNAH12	p.S2676Y	dynein, axonemal, heav	62 (0.00)	57 (0.18)	0.47
11-12	Gp4	g.chr17:76568955G>A	Nonsense Mutation	DNAH17	p.Q123*	dynein, axonemal, heav	19 (0.00)	41 (0.17)	0.59

11-12	Gp4	g.chr17:11696886G>A	Missense Mutation	DNAH9	p.E2710K	dynein, axonemal, heav	41 (0.00)	24 (0.62)	1.67
11-12	Gp4	g.chr18:28736056C>A	Missense Mutation	DSC1	p.A141S	desmocollin 1	29 (0.00)	28 (0.25)	0.67
11-12	Gp4	g.chr11:117301698T>A	Missense Mutation	DSCAML1	p.E1869V	Down syndrome cell ad	40 (0.03)	153 (0.31)	0.82
11-12	Gp4	g.chr2:25851158C>T	Missense Mutation	DTNB	p.E82K	dystrobrevin, beta	111 (0.00)	24 (0.33)	0.89
11-12	Gp4	g.chr10:131646681G>A	Missense Mutation	EBF3	p.P368L	early B-cell factor 3	26 (0.00)	53 (0.17)	0.61
11-12	Gp4	g.chr2:63092060T>A	Missense Mutation	EHBP1	p.Y353N	EH domain binding pro	57 (0.00)	42 (0.14)	0.38
11-12	Gp4	g.chr19:40030011A>T	Nonstop Mutation	EID2	p.*237K	EP300 interacting inhibi	16 (0.00)	35 (0.17)	0.61
11-12	Gp4	g.chr19:40030071A>C	Missense Mutation	EID2	p.S217A	EP300 interacting inhibi	17 (0.00)	36 (0.19)	0.69
11-12	Gp4	g.chr21:39811324G>T	Intron	ERG		v-ets avian erythroblast	46 (0.00)	56 (0.32)	0.86
11-12	Gp4	g.chr2:203560712G>C	Missense Mutation	FAM117B	p.S237T	family with sequence si	116 (0.00)	16 (0.31)	0.83
11-12	Gp4	g.chr4:77192805A>T	Missense Mutation	FAM47E	p.T154S	family with sequence si	35 (0.00)	19 (0.26)	0.70
11-12	Gp4	g.chr3:125643936C>A	RNA	FAM86JP		family with sequence si	55 (0.00)	210 (0.11)	0.39
11-12	Gp4	g.chr8:94713631G>T	Missense Mutation	FAM92A1	p.G69V	family with sequence si	86 (0.00)	71 (0.37)	0.98
11-12	Gp4	g.chr11:92533562G>T	Missense Mutation	FAT3	p.M2311I	FAT atypical cadherin 3	165 (0.00)	68 (0.29)	0.78
11-12	Gp4	g.chr10:5950906C>T	Silent	FBXO18	p.L258L	F-box protein, helicase,	45 (0.00)	41 (0.22)	0.59
11-12	Gp4	g.chr1:152276516C>A	Nonsense Mutation	FLG	p.E3616*	filaggrin	292 (0.00)	54 (0.24)	0.64
11-12	Gp4	g.chr2:186667617A>G	Silent	FSIP2	p.E4528E	fibrous sheath interactin	76 (0.00)	51 (0.16)	0.42
11-12	Gp4	g.chr1:78428510C>T	Missense Mutation	FUBP1	p.R430H	far upstream element (F	17 (0.00)	28 (0.39)	1.05
11-12	Gp4	g.chr20:42891935G>T	Nonsense Mutation	GDAP1L1	p.E205*	ganglioside induced dif	244 (0.00)	160 (0.34)	0.90
11-12	Gp4	g.chrX:153670993G>A	Missense Mutation	GDI1	p.D440N	GDP dissociation inhibi	16 (0.00)	25 (0.24)	0.48
11-12	Gp4	g.chr17:649564G>T	Silent	GEMIN4	p.G573G	gem (nuclear organelle)	70 (0.00)	58 (0.17)	0.46
11-12	Gp4	g.chr5:74021505G>A	Missense Mutation	GFM2	p.T663I	G elongation factor, mit	77 (0.00)	18 (0.83)	2.22
11-12	Gp4	g.chr3:37337694T>A	Missense Mutation	GOLGA4	p.S288R	golgin A4	46 (0.00)	14 (0.79)	2.10
11-12	Gp4	g.chr3:37368502C>T	Missense Mutation	GOLGA4	p.P1731S	golgin A4	221 (0.00)	59 (0.37)	0.99
11-12	Gp4	g.chr7:50671763G>A	Silent	GRB10	p.H492H	growth factor receptor-	42 (0.00)	11 (0.73)	1.94
11-12	Gp4	g.chr4:94031988A>G	Missense Mutation	GRID2	p.M207V	glutamate receptor, iono	52 (0.02)	13 (0.38)	1.03
11-12	Gp4	g.chr9:104448918C>T	Missense Mutation	GRIN3A	p.V422M	glutamate receptor, iono	88 (0.00)	40 (0.30)	0.80
11-12	Gp4	g.chr4:106647920C>T	Missense Mutation	GSTCD	p.P360L	glutathione S-transfera	92 (0.00)	41 (0.41)	1.11
11-12	Gp4	g.chr15:28456163C>A	Nonsense Mutation	HERC2	p.G2352*	HECT and RLD domai	116 (0.00)	78 (0.14)	0.50
11-12	Gp4	g.chr15:28456202G>T	Missense Mutation	HERC2	p.L2339M	HECT and RLD domai	112 (0.00)	91 (0.24)	0.86
11-12	Gp4	g.chr1:185959502G>T	Nonsense Mutation	HMCN1	p.E1102*	hemicentin 1	151 (0.00)	10 (0.70)	1.87
11-12	Gp4	g.chr5:132425288C>T	Missense Mutation	HSPA4	p.P427S	heat shock 70kDa protei	34 (0.00)	22 (0.32)	0.85
11-12	Gp4	g.chr9:21481214G>A	Silent	IFNE	p.Y160Y	interferon, epsilon	177 (0.00)	57 (0.88)	2.34
11-12	Gp4	g.chr16:1636139G>A	Nonsense Mutation	IFT140	p.Q383*	intraflagellar transport 1	37 (0.00)	72 (0.18)	0.48
11-12	Gp4	g.chr14:107083226G>A	RNA	IGHV4-59		immunoglobulin heavy	34 (0.00)	141 (0.15)	0.40

11-12	Gp4	g.chr4:143350024G>C	Intron	INPP4B		inositol polyphosphate-	48 (0.00)	34 (0.71)	1.88
11-12	Gp4	g.chr4:143366767C>T	Intron	INPP4B		inositol polyphosphate-	55 (0.00)	23 (0.26)	0.70
11-12	Gp4	g.chr4:143421469C>G	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	13 (0.69)	1.85
11-12	Gp4	g.chr4:143454394C>T	Intron	INPP4B		inositol polyphosphate-	153 (0.00)	62 (0.32)	0.86
11-12	Gp4	g.chr4:143583460G>A	Intron	INPP4B		inositol polyphosphate-	206 (0.00)	93 (0.27)	0.72
11-12	Gp4	g.chr4:143670004T>C	Intron	INPP4B		inositol polyphosphate-	150 (0.00)	26 (0.19)	0.51
11-12	Gp4	g.chr4:143733370C>T	Intron	INPP4B		inositol polyphosphate-	145 (0.00)	37 (0.24)	0.65
11-12	Gp4	g.chr4:143749506G>A	Intron	INPP4B		inositol polyphosphate-	37 (0.00)	17 (0.29)	0.78
11-12	Gp4	g.chr12:26553136G>A	Silent	ITPR2	p.C2485C	inositol 1,4,5-trisphosph	152 (0.00)	54 (0.15)	0.40
11-12	Gp4	g.chr10:133930665G>A	Missense Mutation	JAKMIP3	p.E74K	Janus kinase and microt	20 (0.00)	49 (0.16)	0.58
11-12	Gp4	g.chr13:45767983G>C	Silent	KCTD4	p.T240T	potassium channel tetra	117 (0.00)	21 (0.24)	0.63
11-12	Gp4	g.chr4:55972036G>T	Silent	KDR	p.V536V	kinase insert domain rec	91 (0.01)	77 (0.17)	0.45
11-12	Gp4	g.chr4:123145832G>T	Splice Site	KIAA1109	p.Q931H	KIAA1109	40 (0.00)	15 (0.40)	1.07
11-12	Gp4	g.chr10:3826466C>T	Intron	KLF6		Kruppel-like factor 6	34 (0.00)	45 (0.20)	0.53
11-12	Gp4	g.chr12:52881645G>T	Silent	KRT6A	p.G518G	keratin 6A	116 (0.00)	17 (0.35)	0.94
11-12	Gp4	g.chr13:76379786G>A	Silent	LMO7	p.G129G	LIM domain 7	264 (0.00)	37 (0.76)	2.02
11-12	Gp4	g.chr6:160912500C>T	RNA	LPAL2		lipoprotein, Lp(a)-like 2	228 (0.00)	83 (0.27)	0.71
11-12	Gp4	g.chr4:151829939C>T	Missense Mutation	LRBA	p.G411E	LPS-responsive vesicle	74 (0.00)	16 (0.38)	1.00
11-12	Gp4	g.chr12:57572673C>A	Splice Site	LRP1	p.A1536D	low density lipoprotein	15 (0.00)	55 (0.18)	0.48
11-12	Gp4	g.chr11:46916836T>C	Missense Mutation	LRP4	p.N397S	low density lipoprotein	60 (0.00)	160 (0.15)	0.40
11-12	Gp4	g.chr17:62892821G>C	Silent	LRRC37A3	p.S185S	leucine rich repeat conta	89 (0.00)	32 (0.22)	0.58
11-12	Gp4	g.chr1:90152066G>A	Missense Mutation	LRRC8C	p.E12K	leucine rich repeat conta	59 (0.00)	13 (0.46)	1.23
11-12	Gp4	g.chr12:85459053C>T	Missense Mutation	LRRIQ1	p.T802I	leucine-rich repeats and	48 (0.00)	23 (0.30)	0.81
11-12	Gp4	g.chr12:85459094G>A	Missense Mutation	LRRIQ1	p.E816K	leucine-rich repeats and	66 (0.00)	45 (0.20)	0.53
11-12	Gp4	g.chr7:78189297A>G	Intron	MAGI2		membrane associated gu	46 (0.00)	29 (0.41)	0.44
11-12	Gp4	g.chr7:78226064T>C	Intron	MAGI2		membrane associated gu	118 (0.01)	21 (0.38)	0.40
11-12	Gp4	g.chr7:78340555G>C	Intron	MAGI2		membrane associated gu	15 (0.00)	11 (0.82)	0.86
11-12	Gp4	g.chr7:78755317G>T	Intron	MAGI2		membrane associated gu	117 (0.01)	172 (0.52)	0.55
11-12	Gp4	g.chr7:78755319G>T	Intron	MAGI2		membrane associated gu	117 (0.01)	171 (0.52)	0.55
11-12	Gp4	g.chr7:78760599G>C	Intron	MAGI2		membrane associated gu	99 (0.00)	17 (0.65)	0.68
11-12	Gp4	g.chr7:79002426G>T	Intron	MAGI2		membrane associated gu	46 (0.00)	23 (0.91)	0.96
11-12	Gp4	g.chr1:38265350C>A	Silent	MANEAL	p.L283L	mannosidase, endo-alph	25 (0.00)	41 (0.20)	0.52
11-12	Gp4	g.chr1:242161870G>T	Missense Mutation	MAP1LC3C	p.T56N	microtubule-associated	25 (0.00)	60 (0.15)	0.40
11-12	Gp4	g.chr2:160605015G>T	Missense Mutation	MARCH7	p.G367V	membrane-associated ri	36 (0.00)	22 (0.50)	1.33
11-12	Gp4	g.chr2:149227252C>G	Silent	MBD5	p.L580L	methyl-CpG binding do	155 (0.00)	77 (0.34)	0.90

11-12	Gp4	g.chr6:90357858C>A	Nonsense Mutation	MDN1	p.E5430*	MDN1, midasin homolc	101 (0.00)	41 (0.22)	0.59
11-12	Gp4	g.chr3:151112534T>C	Missense Mutation	MED12L	p.M1865T	mediator complex subur	41 (0.00)	35 (0.37)	0.99
11-12	Gp4	g.chr15:42041983C>T	Nonsense Mutation	MGA	p.Q2060*	MGA, MAX dimerizati	81 (0.00)	32 (0.47)	1.25
11-12	Gp4	g.chr10:99236671C>T	Missense Mutation	MMS19	p.M181I	MMS19 nucleotide exci	102 (0.00)	69 (0.58)	1.55
11-12	Gp4	g.chr7:42974701G>T	Missense Mutation	MRPL32	p.R93M	mitochondrial ribosoma	67 (0.00)	62 (0.23)	0.60
11-12	Gp4	g.chr2:55490951T>A	Missense Mutation	MTIF2	p.H15L	mitochondrial translatio	187 (0.00)	41 (0.22)	0.59
11-12	Gp4	g.chr11:68480777C>A	Missense Mutation	MTL5	p.R373S	metallothionein-like 5, t	95 (0.00)	95 (0.22)	0.59
11-12	Gp4	g.chr7:100646863C>A	Missense Mutation	MUC12	p.P4483H	mucin 12, cell surface a	463 (0.00)	51 (0.25)	0.68
11-12	Gp4	g.chr11:1093412C>T	Missense Mutation	MUC2	p.T1744M	mucin 2, oligomeric mu	15 (0.00)	30 (0.43)	1.16
11-12	Gp4	g.chr1:201780824A>G	Missense Mutation	NAV1	p.S1584G	neuron navigator 1	63 (0.00)	57 (0.18)	0.47
11-12	Gp4	g.chr18:56056319G>T	Missense Mutation	NEDD4L	p.L746F	neural precursor cell ex	21 (0.00)	15 (0.60)	1.60
11-12	Gp4	g.chr12:55420282G>T	Missense Mutation	NEUROD4	p.W20L	neuronal differentiation	17 (0.00)	20 (0.40)	1.07
11-12	Gp4	g.chr17:29548914C>A	Missense Mutation	NF1	p.P563H	neurofibromin 1	58 (0.00)	38 (0.16)	0.42
11-12	Gp4	g.chr1:52257270C>T	Silent	NRD1	p.G1048G	nardilysin (N-arginine d	41 (0.00)	38 (0.24)	0.63
11-12	Gp4	g.chr11:9007322G>A	Silent	NRIP3	p.G166G	nuclear receptor interact	71 (0.00)	68 (0.15)	0.39
11-12	Gp4	g.chr7:72718745C>A	Splice Site	NSUN5	p.G252W	NOP2/Sun domain fami	42 (0.00)	64 (0.16)	0.42
11-12	Gp4	g.chr1:228482047G>A	Missense Mutation	OBSCN	p.V4205M	obscurin, cytoskeletal ca	91 (0.00)	151 (0.24)	0.64
11-12	Gp4	g.chr11:6867664C>A	Missense Mutation	OR10A5	p.L251I	olfactory receptor, famil	102 (0.00)	33 (0.24)	0.65
11-12	Gp4	g.chr12:56030691C>T	Missense Mutation	OR10P1	p.H6Y	olfactory receptor, famil	89 (0.00)	15 (0.40)	1.07
11-12	Gp4	g.chr11:57971419G>C	Missense Mutation	OR1S2	p.L79V	olfactory receptor, famil	86 (0.00)	45 (0.24)	0.65
11-12	Gp4	g.chr11:55110767C>A	Missense Mutation	OR4A16	p.L31I	olfactory receptor, famil	73 (0.00)	33 (0.33)	0.89
11-12	Gp4	g.chr11:4842807C>T	Silent	OR51F2	p.L64L	olfactory receptor, famil	84 (0.00)	17 (0.41)	1.10
11-12	Gp4	g.chr3:98188600C>T	Silent	OR5K1	p.Y60Y	olfactory receptor, famil	89 (0.01)	40 (0.20)	0.53
11-12	Gp4	g.chr7:142750000C>T	Missense Mutation	OR6V1	p.S188F	olfactory receptor, famil	248 (0.00)	49 (0.35)	0.93
11-12	Gp4	g.chr12:80633149C>T	Missense Mutation	OTOGL	p.P319S	otogelin-like	95 (0.00)	54 (0.20)	0.54
11-12	Gp4	g.chr14:94510374G>A	Silent	OTUB2	p.E92E	OTU deubiquitinase, ub	37 (0.00)	57 (0.28)	0.75
11-12	Gp4	g.chr12:29639264G>A	Missense Mutation	OVCH1	p.P304S	ovochymase 1	42 (0.00)	56 (0.93)	2.48
11-12	Gp4	g.chr21:47847547C>A	Silent	PCNT	p.T2444T	pericentrin	19 (0.00)	27 (0.19)	0.72
11-12	Gp4	g.chr9:78686726G>A	Missense Mutation	PCSK5	p.S269N	proprotein convertase su	77 (0.00)	11 (0.45)	1.21
11-12	Gp4	g.chr15:44048957G>A	Silent	PDIA3	p.R119R	protein disulfide isomer	22 (0.00)	32 (0.16)	0.42
11-12	Gp4	g.chr2:10928887C>T	Missense Mutation	PDIA6	p.G364S	protein disulfide isomer	104 (0.00)	89 (0.51)	1.35
11-12	Gp4	g.chr2:197784751G>A	Missense Mutation	PGAP1	p.L49F	post-GPI attachment to	19 (0.00)	15 (0.87)	2.31
11-12	Gp4	g.chr12:9070313G>C	Missense Mutation	PHC1	p.G14R	polyhomeotic homolog	18 (0.00)	22 (0.41)	1.09
11-12	Gp4	g.chr18:60432561C>T	Intron	PHLPP1		PH domain and leucine	183 (0.00)	241 (0.14)	0.38
11-12	Gp4	g.chr18:60469622C>A	Intron	PHLPP1		PH domain and leucine	159 (0.00)	55 (0.56)	1.50

11-12	Gp4	g.chr18:60642746G>A	Missense Mutation	PHLPP1	p.C1291Y	PH domain and leucine	134 (0.00)	26 (0.27)	0.72
11-12	Gp4	g.chr17:26881394G>C	Missense Mutation	PIGS	p.D504E	phosphatidylinositol gly	93 (0.00)	51 (0.20)	0.52
11-12	Gp4	g.chr17:26881477C>T	Missense Mutation	PIGS	p.E477K	phosphatidylinositol gly	94 (0.00)	20 (0.25)	0.67
11-12	Gp4	g.chr2:219136108T>A	Silent	PNKD	p.I24I	paroxysmal nonkinesige	59 (0.00)	99 (0.42)	1.13
11-12	Gp4	g.chr1:151381170C>A	Splice Site	POGZ	p.K678N	pogo transposable eleme	107 (0.00)	15 (0.53)	1.42
11-12	Gp4	g.chr2:130832590T>G	Missense Mutation	POTEF	p.M819L	POTE ankyrin domain f	122 (0.00)	175 (0.14)	0.56
11-12	Gp4	g.chr1:143767732C>A	Silent	PPIAL4G	p.L39L	peptidylprolyl isomerase	105 (0.01)	30 (0.23)	0.62
11-12	Gp4	g.chr16:4935946C>T	Missense Mutation	PPL	p.E904K	periplakin	23 (0.00)	70 (0.16)	0.42
11-12	Gp4	g.chr4:7435469C>A	Missense Mutation	PSAPL1	p.A380S	prosaposin-like 1 (gene/	38 (0.00)	117 (0.11)	0.39
11-12	Gp4	g.chr19:43773572G>T	Silent	PSG9	p.L4L	pregnancy specific beta-	86 (0.00)	50 (0.44)	1.17
11-12	Gp4	g.chr17:38153599C>A	Missense Mutation	PSMD3	p.P498H	proteasome (prosome, m	31 (0.00)	30 (0.50)	1.33
11-12	Gp4	g.chr1:32374508C>T	Missense Mutation	PTP4A2	p.R150Q	protein tyrosine phospha	133 (0.00)	23 (0.35)	0.93
11-12	Gp4	g.chr1:214557833C>A	Silent	PTPN14	p.G455G	protein tyrosine phospha	77 (0.00)	66 (0.18)	0.48
11-12	Gp4	g.chr12:70953228C>T	Missense Mutation	PTPRB	p.V1449M	protein tyrosine phospha	89 (0.00)	15 (0.60)	1.60
11-12	Gp4	g.chr12:44124356C>T	Silent	PUS7L	p.Q643Q	pseudouridylate synthas	88 (0.00)	47 (0.28)	0.74
11-12	Gp4	g.chr3:49095284C>A	Missense Mutation	QRICH1	p.A117S	glutamine-rich 1	35 (0.00)	75 (0.15)	0.39
11-12	Gp4	g.chr10:99995800G>T	Missense Mutation	R3HCC1L	p.K716N	R3H domain and coiled-	22 (0.00)	11 (0.82)	2.18
11-12	Gp4	g.chr13:48892501C>A	Intron	RB1		retinoblastoma 1	16 (0.00)	119 (0.22)	0.58
11-12	Gp4	g.chr13:49028602C>G	Intron	RB1		retinoblastoma 1	76 (0.00)	47 (0.23)	0.62
11-12	Gp4	g.chr20:34317279C>T	Missense Mutation	RBM39	p.R124H	RNA binding motif prot	100 (0.00)	46 (0.63)	1.68
11-12	Gp4	g.chr6:111672900G>A	Missense Mutation	REV3L	p.R2427W	REV3-like, polymerase	86 (0.00)	35 (0.17)	0.46
11-12	Gp4	g.chr16:74657849C>T	Missense Mutation	RFWD3	p.V768I	ring finger and WD repe	37 (0.00)	19 (0.47)	0.56
11-12	Gp4	g.chr3:129249773T>C	Missense Mutation	RHO	p.V139A	rhodopsin	18 (0.00)	67 (0.39)	1.03
11-12	Gp4	g.chr6:3085500C>G	Missense Mutation	RIPK1	p.I232M	receptor (TNFRSF)-inte	54 (0.00)	13 (0.85)	2.26
11-12	Gp4	g.chr6:3085559T>A	Missense Mutation	RIPK1	p.I252N	receptor (TNFRSF)-inte	57 (0.00)	25 (0.28)	0.75
11-12	Gp4	g.chr1:51735739C>A	Missense Mutation	RNF11	p.H79N	ring finger protein 11	19 (0.00)	11 (0.73)	1.94
11-12	Gp4	g.chr6:42130833G>T	Missense Mutation	RP1-139D8.6	p.G77C		20 (0.00)	26 (0.19)	0.51
11-12	Gp4	g.chr5:177398785G>A	RNA	RP11-1252I4.2			219 (0.00)	224 (0.12)	0.44
11-12	Gp4	g.chr9:41963928T>A	lincRNA	RP11-204M4.2			195 (0.00)	50 (0.26)	0.69
11-12	Gp4	g.chr13:52845561A>G	RNA	RP11-248G5.8			35 (0.00)	20 (0.30)	0.80
11-12	Gp4	g.chr14:19407833C>T	lincRNA	RP11-536C10.7			81 (0.00)	25 (0.28)	0.75
11-12	Gp4	g.chr14:20146539C>T	lincRNA	RP11-597A11.6			96 (0.00)	138 (0.23)	0.62
11-12	Gp4	g.chr14:20146580T>C	lincRNA	RP11-597A11.6			82 (0.00)	104 (0.25)	0.67
11-12	Gp4	g.chr1:143161427G>T	lincRNA	RP11-782C8.4			48 (0.00)	23 (0.26)	0.70
11-12	Gp4	g.chr12:53928375A>G	Silent	RP11-793H13.	p.P157P		78 (0.00)	48 (0.23)	0.61

11-12	Gp4	g.chr20:21147019T>C	RNA	RP4-777D9.2			71 (0.00)	13 (0.92)	2.46
11-12	Gp4	g.chr6:107076659C>T	Missense Mutation	RTN4IP1	p.A80T	reticulon 4 interacting p	58 (0.00)	51 (0.16)	0.42
11-12	Gp4	g.chr3:72487398G>A	Intron	RYBP		RING1 and YY1 bindin	120 (0.00)	29 (0.31)	0.83
11-12	Gp4	g.chr1:237660043C>T	Missense Mutation	RYR2	p.L732F	ryanodine receptor 2 (ca	190 (0.00)	198 (0.23)	0.61
11-12	Gp4	g.chr3:169644401G>T	Missense Mutation	SAMD7	p.K117N	sterile alpha motif doma	41 (0.02)	10 (0.80)	2.13
11-12	Gp4	g.chr16:30974809G>T	Missense Mutation	SETD1A	p.Q191H	SET domain containing	24 (0.00)	35 (0.14)	0.38
11-12	Gp4	g.chr3:9488945C>A	Missense Mutation	SETD5	p.T579N	SET domain containing	101 (0.00)	29 (0.17)	0.46
11-12	Gp4	g.chr1:154473937C>A	Missense Mutation	SHE	p.G189V	Src homology 2 domain	70 (0.00)	162 (0.19)	0.49
11-12	Gp4	g.chr2:196599724G>A	Missense Mutation	SLC39A10	p.A819T	solute carrier family 39	52 (0.00)	56 (0.18)	0.48
11-12	Gp4	g.chr2:162813690T>C	Silent	SLC4A10	p.V911V	solute carrier family 4, s	29 (0.00)	29 (0.86)	2.30
11-12	Gp4	g.chr2:27888076C>T	Missense Mutation	SLC4A1AP	p.S312L	solute carrier family 4 (	27 (0.00)	24 (0.33)	0.89
11-12	Gp4	g.chr6:169051392G>T	Silent	SMOC2	p.L313L	SPARC related modular	42 (0.00)	42 (0.14)	0.56
11-12	Gp4	g.chr18:8818964C>T	Nonsense Mutation	SOGA2	p.Q1274*		36 (0.03)	33 (0.33)	0.89
11-12	Gp4	g.chr5:35692811G>T	Missense Mutation	SPEF2	p.E628D	sperm flagellar 2	167 (0.01)	27 (0.22)	0.59
11-12	Gp4	g.chr1:158596702C>T	Nonsense Mutation	SPTA1	p.W1920*	spectrin, alpha, erythroc	73 (0.00)	12 (0.50)	1.33
11-12	Gp4	g.chr15:43900146G>A	Missense Mutation	STRC	p.R1237W	stereocilin	206 (0.00)	55 (0.49)	1.31
11-12	Gp4	g.chr12:65268859A>G	Missense Mutation	TBC1D30	p.K526R	TBC1 domain family, m	82 (0.00)	76 (0.26)	0.70
11-12	Gp4	g.chr17:58087945C>T	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	85 (0.00)	219 (0.19)	0.50
11-12	Gp4	g.chr6:170871248C>A	Missense Mutation	TBP	p.P142T	TATA box binding prot	17 (0.00)	29 (0.17)	0.68
11-12	Gp4	g.chrX:13681103C>A	Missense Mutation	TCEANC	p.T159N	transcription elongation	72 (0.00)	13 (0.62)	1.03
11-12	Gp4	g.chr6:167791521G>A	Silent	TCP10	p.P113P	t-complex 10	63 (0.00)	129 (0.18)	0.59
11-12	Gp4	g.chr14:24659660G>A	Silent	TM9SF1	p.A660A	transmembrane 9 superf	42 (0.00)	36 (0.31)	0.81
11-12	Gp4	g.chr3:189582029T>C	Silent	TP63	p.T102T	tumor protein p63	111 (0.00)	31 (0.29)	0.77
11-12	Gp4	g.chr17:18638278C>T	Silent	TRIM16L	p.P184P	tripartite motif containin	78 (0.00)	23 (0.48)	1.28
11-12	Gp4	g.chr15:45052007G>A	Missense Mutation	TRIM69	p.G300S	tripartite motif containin	68 (0.00)	62 (0.21)	0.56
11-12	Gp4	g.chr5:14359549C>G	Missense Mutation	TRIO	p.A767G	trio Rho guanine nucleo	20 (0.00)	50 (0.16)	0.43
11-12	Gp4	g.chr1:100606063A>G	Missense Mutation	TRMT13	p.K165R	tRNA methyltransferase	73 (0.00)	22 (0.50)	1.33
11-12	Gp4	g.chr2:179402418G>A	Silent	TTN	p.T33172T	titin	135 (0.00)	115 (0.18)	0.49
11-12	Gp4	g.chr2:179413752G>A	Silent	TTN	p.D30867D	titin	77 (0.00)	16 (0.88)	2.33
11-12	Gp4	g.chr2:179436470C>T	Missense Mutation	TTN	p.A24797T	titin	190 (0.00)	47 (0.23)	0.62
11-12	Gp4	g.chr2:179480188C>T	Missense Mutation	TTN	p.V16162I	titin	198 (0.00)	30 (0.17)	0.44
11-12	Gp4	g.chr2:179606185C>G	Silent	TTN	p.V3925V	titin	61 (0.00)	19 (0.95)	2.53
11-12	Gp4	g.chr2:179640694C>A	Missense Mutation	TTN	p.R1966I	titin	99 (0.00)	17 (0.35)	0.94
11-12	Gp4	g.chr7:72159764G>A	RNA	TYW1B		tRNA-yW synthesizing	48 (0.00)	31 (0.87)	2.32
11-12	Gp4	g.chr21:46191295C>A	Silent	UBE2G2	p.L165L	ubiquitin-conjugating e	113 (0.00)	45 (0.29)	1.13

11-12	Gp4	g.chr17:73832111C>T	Nonsense Mutation	UNC13D	p.W509*	unc-13 homolog D (C. e	40 (0.00)	111 (0.16)	0.43
11-12	Gp4	g.chr1:229772343G>T	Missense Mutation	URB2	p.K661N	URB2 ribosome biogen	207 (0.00)	61 (0.21)	0.57
11-12	Gp4	g.chr1:12423165C>G	Missense Mutation	VPS13D	p.P3437R	vacuolar protein sorting	72 (0.00)	61 (0.25)	0.66
11-12	Gp4	g.chr1:168511308C>A	Silent	XCL2	p.V33V	chemokine (C motif) lig	23 (0.00)	13 (0.69)	1.85
11-12	Gp4	g.chr9:129641959G>A	Missense Mutation	ZBTB34	p.G94E	zinc finger and BTB do	251 (0.00)	59 (0.47)	1.27
11-12	Gp4	g.chr5:79738964G>A	Missense Mutation	ZFYVE16	p.M814I	zinc finger, FYVE dom	27 (0.00)	15 (0.67)	1.78
11-12	Gp4	g.chr10:267216C>T	Missense Mutation	ZMYND11	p.R120C	zinc finger, MYND-typ	84 (0.00)	50 (0.64)	2.44
11-12	Gp4	g.chr6:87943144C>A	Missense Mutation	ZNF292	p.L214M	zinc finger protein 292	87 (0.00)	32 (0.25)	0.67
11-12	Gp4	g.chr19:53345377G>A	Missense Mutation	ZNF468	p.T57M	zinc finger protein 468	118 (0.00)	24 (0.62)	1.67
11-12	Gp4	g.chr19:40542003C>T	Missense Mutation	ZNF780B	p.G107R	zinc finger protein 780B	41 (0.00)	107 (0.16)	0.56
11-12	Gp4	g.chr19:52568452G>A	Missense Mutation	ZNF841	p.H895Y	zinc finger protein 841	76 (0.00)	65 (0.18)	0.49
11-12	Gp4	g.chr19:9874035C>A	Missense Mutation	ZNF846	p.W22L	zinc finger protein 846	180 (0.00)	25 (0.20)	0.53
11-12	Gp4	g.chr9:115759765G>A	lincRNA	ZNF883		zinc finger protein 883	69 (0.00)	38 (0.39)	1.05
11-13	Gp3	g.chr12:7273117C>T	RNA	C1RL-AS1		C1RL antisense RNA 1	102 (0.00)	90 (0.92)	0.61
11-13	Gp3	g.chr8:68084765T>C	Silent	CSPP1	p.H976H	centrosome and spindle	42 (0.00)	180 (0.11)	0.38
11-13	Gp3	g.chr7:18710691C>A	Intron	HDAC9		histone deacetylase 9	57 (0.02)	201 (0.59)	1.58
11-13	Gp3	g.chr19:55247464G>A	Silent	KIR3DL3	p.E378E	killer cell immunoglobu	60 (0.02)	18 (0.89)	0.99
11-13	Gp3	g.chr4:25005261A>G	Missense Mutation	LGI2	p.Y484H	leucine-rich repeat LGI	89 (0.00)	116 (0.16)	0.57
11-13	Gp3	g.chr2:50692626G>T	Missense Mutation	NRXN1	p.S1146R	neurexin 1	82 (0.01)	43 (0.95)	2.54
11-13	Gp3	g.chr13:111176372C>A	Silent	RAB20	p.V115V	RAB20, member RAS c	29 (0.00)	432 (0.15)	0.56
11-13	Gp3	g.chr1:36755226C>A	Missense Mutation	THRAP3	p.P536T	thyroid hormone recept	39 (0.03)	28 (0.43)	1.14
11-13	Gp3	g.chr4:38829681G>T	Missense Mutation	TLR6	p.L472M	toll-like receptor 6	175 (0.01)	242 (0.43)	1.59
11-13	Gp3	g.chr8:7215553G>A	Missense Mutation	ZNF705G	p.P283L	zinc finger protein 705	315 (0.00)	29 (0.52)	1.38
11-13	Gp4	g.chr15:89400810C>G	Missense Mutation	ACAN	p.T1665R	aggrecan	53 (0.02)	80 (0.99)	2.63
11-13	Gp4	g.chr10:24873972G>A	Missense Mutation	ARHGAP21	p.P1749L	Rho GTPase activating	45 (0.00)	54 (0.91)	2.42
11-13	Gp4	g.chr2:237150026C>A	Missense Mutation	ASB18	p.K75N	ankyrin repeat and SOC	48 (0.00)	36 (0.61)	1.63
11-13	Gp4	g.chr6:26459823G>T	Missense Mutation	BTN2A1	p.W66L	butyrophilin, subfamily	35 (0.00)	652 (0.35)	0.92
11-13	Gp4	g.chr16:57490454G>A	Silent	COQ9	p.G139G	coenzyme Q9	115 (0.00)	89 (0.75)	2.01
11-13	Gp4	g.chr7:140301370G>A	Silent	DENND2A	p.A276A	DENN/MADD domain	21 (0.00)	19 (0.84)	2.25
11-13	Gp4	g.chr2:175337764C>T	Silent	GPR155	p.T263T	G protein-coupled recep	50 (0.00)	107 (0.95)	2.54
11-13	Gp4	g.chr11:125769447C>T	Missense Mutation	HYLS1	p.P62S	hydrolethalus syndrome	70 (0.00)	57 (0.98)	2.62
11-13	Gp4	g.chr17:73016746G>T	Missense Mutation	ICT1	p.R177I	immature colon carcino	15 (0.00)	17 (0.71)	1.88
11-13	Gp4	g.chr6:84865049G>T	Missense Mutation	KIAA1009	p.R988S		49 (0.00)	225 (0.89)	2.37
11-13	Gp4	g.chr17:66040044C>T	Missense Mutation	KPNA2	p.P341S	karyopherin alpha 2 (R	259 (0.00)	77 (0.17)	0.45
11-13	Gp4	g.chr17:10546157C>T	Missense Mutation	MYH3	p.E523K	myosin, heavy chain 3,	100 (0.00)	36 (0.97)	2.59

11-13	Gp4	g.chr17:10546168G>T	Missense Mutation	MYH3	p.A519D	myosin, heavy chain 3, s	104 (0.01)	38 (0.97)	2.60
11-13	Gp4	g.chr10:69934028T>C	Missense Mutation	MYPN	p.F727L	myopalladin	90 (0.01)	260 (0.15)	0.41
11-13	Gp4	g.chr1:16893795T>A	Silent	NBPF1	p.S906S	neuroblastoma breakpoi	601 (0.00)	306 (0.65)	1.73
11-13	Gp4	g.chr12:70953257T>A	Missense Mutation	PTPRB	p.Y1439F	protein tyrosine phospha	108 (0.00)	194 (0.47)	1.25
11-13	Gp4	g.chr18:110336C>G	RNA	ROCK1P1		Rho-associated, coiled-c	75 (0.01)	34 (0.35)	0.94
11-13	Gp4	g.chr9:17083631G>C	lincRNA	RP11-132E11.2			15 (0.00)	10 (0.70)	1.87
11-13	Gp4	g.chr1:142621035G>A	lincRNA	RP11-417J8.6			50 (0.00)	15 (0.33)	0.89
11-13	Gp4	g.chr6:42913585C>A	RNA	RP3-475N16.1			18 (0.00)	43 (0.37)	0.99
11-13	Gp4	g.chr18:6462852C>A	RNA	RPL6P27		ribosomal protein L6 ps	79 (0.00)	22 (0.95)	2.55
11-13	Gp4	g.chr15:25432762C>G	RNA	SNHG14		small nucleolar RNA ho	218 (0.00)	834 (0.15)	0.39
11-13	Gp4	g.chr17:19091467T>C	lincRNA	SNORD3A		small nucleolar RNA, C	162 (0.01)	49 (0.73)	1.96
11-13	Gp4	g.chr16:29376111A>G	RNA	SNX29P2		sorting nexin 29 pseudo,	72 (0.00)	26 (0.31)	0.82
11-13	Gp4	g.chr8:9622291T>C	Silent	TNKS	p.N909N	tankyrase, TRF1-interac	57 (0.02)	149 (0.18)	0.48
11-13	Gp4	g.chr8:72964928C>A	Missense Mutation	TRPA1	p.D573Y	transient receptor potent	96 (0.00)	757 (0.21)	0.55
11-13	Gp4	g.chr10:31784716G>A	Missense Mutation	ZEB1	p.G90R	zinc finger E-box bindin	194 (0.00)	148 (0.61)	1.64
11-13	Gp4	g.chr20:57829251C>A	Missense Mutation	ZNF831	p.S1496Y	zinc finger protein 831	25 (0.00)	16 (0.56)	1.50
11-14	Gp3	g.chr7:48427505T>A	Missense Mutation	ABCA13	p.Y3808N	ATP-binding cassette, su	21 (0.00)	33 (0.85)	2.90
11-14	Gp3	g.chr19:1046345C>A	Missense Mutation	ABCA7	p.A383D	ATP-binding cassette, su	28 (0.00)	113 (0.52)	1.39
11-14	Gp3	g.chr11:17418743G>T	Missense Mutation	ABCC8	p.L1329M	ATP-binding cassette, su	18 (0.00)	121 (0.32)	0.86
11-14	Gp3	g.chr19:52102076G>A	RNA	AC018755.16			27 (0.00)	38 (0.21)	0.56
11-14	Gp3	g.chr17:20516326C>T	lincRNA	AC087499.10			34 (0.00)	24 (0.96)	2.56
11-14	Gp3	g.chr2:238341719C>T	lincRNA	AC112721.2			33 (0.00)	32 (0.25)	0.67
11-14	Gp3	g.chr3:128598582C>A	Silent	ACAD9	p.A16A	acyl-CoA dehydrogenas	57 (0.00)	325 (0.13)	0.43
11-14	Gp3	g.chr11:47264605G>A	Missense Mutation	ACP2	p.S246F	acid phosphatase 2, lyso	74 (0.01)	211 (0.50)	1.33
11-14	Gp3	g.chr1:2938907G>C	Missense Mutation	ACTRT2	p.K219N	actin-related protein T2	29 (0.00)	44 (0.16)	0.42
11-14	Gp3	g.chr19:8651745C>A	Missense Mutation	ADAMTS10	p.V732F	ADAM metallopeptidas	30 (0.00)	70 (0.96)	2.55
11-14	Gp3	g.chr19:8661067A>G	Silent	ADAMTS10	p.C409C	ADAM metallopeptidas	56 (0.00)	139 (0.20)	0.54
11-14	Gp3	g.chr9:136412171G>C	Missense Mutation	ADAMTSL2	p.E259Q	ADAMTS-like 2	84 (0.00)	390 (0.46)	1.22
11-14	Gp3	g.chr19:41206213A>G	Splice Site	ADCK4		aarF domain containing	23 (0.00)	108 (0.37)	0.99
11-14	Gp3	g.chr5:7698384A>G	Missense Mutation	ADCY2	p.I336V	adenylate cyclase 2 (bra	31 (0.00)	10 (0.80)	2.13
11-14	Gp3	g.chr16:50340969G>T	Silent	ADCY7	p.L587L	adenylate cyclase 7	18 (0.00)	68 (0.15)	0.39
11-14	Gp3	g.chr1:203134555G>T	Nonsense Mutation	ADORA1	p.E170*	adenosine A1 receptor	27 (0.00)	127 (0.35)	0.92
11-14	Gp3	g.chr7:44151156C>A	Missense Mutation	AEBP1	p.S589R	AE binding protein 1	21 (0.00)	43 (0.88)	3.02
11-14	Gp3	g.chr4:88035935C>G	Silent	AFF1	p.P643P	AF4/FMR2 family, men	18 (0.00)	38 (0.50)	1.33
11-14	Gp3	g.chr21:45400956C>T	Silent	AGPAT3	p.N310N	1-acylglycerol-3-phosph	35 (0.00)	24 (0.21)	0.56

11-14	Gp3	g.chr16:67516954A>G	Silent	AGRP	p.L64L	agouti related neuropept	48 (0.00)	179 (0.17)	0.45
11-14	Gp3	g.chr2:241814611C>T	Nonsense Mutation	AGXT	p.Q256*	alanine-glyoxylate amin	17 (0.00)	81 (0.84)	3.32
11-14	Gp3	g.chr15:86284311A>G	Missense Mutation	AKAP13	p.D2552G	A kinase (PRKA) ancho	32 (0.00)	37 (0.62)	1.66
11-14	Gp3	g.chr12:120876191G>A	Silent	AL021546.6	p.V14V		30 (0.00)	30 (0.37)	0.98
11-14	Gp3	g.chr22:50301498G>A	Missense Mutation	ALG12	p.T288M	ALG12, alpha-1,6-man	55 (0.00)	197 (0.49)	1.30
11-14	Gp3	g.chr3:183960454G>T	Missense Mutation	ALG3	p.L349M	ALG3, alpha-1,3- mann	53 (0.00)	123 (0.27)	0.87
11-14	Gp3	g.chr2:233243764G>T	Missense Mutation	ALPP	p.A54S	alkaline phosphatase, pl	26 (0.00)	152 (0.20)	0.54
11-14	Gp3	g.chr1:115223023G>A	Silent	AMPD1	p.L237L	adenosine monophosph	94 (0.00)	206 (0.69)	1.84
11-14	Gp3	g.chr17:62971206C>T	RNA	AMZ2P1		archaelysin family meta	30 (0.00)	43 (0.81)	2.17
11-14	Gp3	g.chr15:65239677G>T	Silent	ANKDD1A	p.R405R	ankyrin repeat and deat	30 (0.00)	61 (0.49)	1.31
11-14	Gp3	g.chr16:89346496C>A	Nonsense Mutation	ANKRD11	p.E2152*	ankyrin repeat domain 1	17 (0.00)	30 (0.33)	0.89
11-14	Gp3	g.chr9:38596004C>A	Missense Mutation	ANKRD18A	p.V445F	ankyrin repeat domain 1	186 (0.00)	138 (0.37)	0.99
11-14	Gp3	g.chr2:96657384G>T	Missense Mutation	ANKRD36C	p.Q25K	ankyrin repeat domain 3	77 (0.00)	324 (0.54)	1.45
11-14	Gp3	g.chr7:117864921G>A	Missense Mutation	ANKRD7	p.E13K	ankyrin repeat domain 7	116 (0.00)	248 (0.87)	3.02
11-14	Gp3	g.chr3:43642010T>C	Missense Mutation	ANO10	p.N68S	anoctamin 10	20 (0.00)	123 (0.50)	1.34
11-14	Gp3	g.chr10:47701007G>T	Missense Mutation	ANTXRL	p.C528F	anthrax toxin receptor-li	70 (0.01)	163 (0.40)	1.06
11-14	Gp3	g.chr17:40997478C>A	Silent	AOC2	p.R279R	amine oxidase, copper c	34 (0.00)	162 (0.19)	0.49
11-14	Gp3	g.chr17:41003524G>T	Missense Mutation	AOC3	p.G55V	amine oxidase, copper c	40 (0.00)	318 (0.77)	2.06
11-14	Gp3	g.chr11:125366457C>T	Missense Mutation	AP000708.1	p.P114L		42 (0.00)	76 (0.80)	2.14
11-14	Gp3	g.chr14:24030778C>T	Silent	AP1G2	p.K600K	adaptor-related protein	57 (0.00)	29 (0.97)	2.57
11-14	Gp3	g.chr19:10692500C>T	Missense Mutation	AP1M2	p.V108I	adaptor-related protein	51 (0.00)	32 (0.56)	1.50
11-14	Gp3	g.chr5:77423887G>T	Missense Mutation	AP3B1	p.D596E	adaptor-related protein	42 (0.00)	50 (0.36)	0.96
11-14	Gp3	g.chr19:2109095G>A	Silent	AP3D1	p.H1154H	adaptor-related protein	23 (0.00)	90 (0.42)	1.13
11-14	Gp3	g.chr1:114447259C>G	Silent	AP4B1	p.L27L	adaptor-related protein	335 (0.00)	830 (0.16)	0.42
11-14	Gp3	g.chr11:116661588G>T	Silent	APOA5	p.G119G	apolipoprotein A-V	26 (0.00)	92 (0.17)	0.46
11-14	Gp3	g.chr22:39418839G>T	Missense Mutation	APOBEC3D	p.E10D	apolipoprotein B mRNA	151 (0.00)	21 (0.95)	2.54
11-14	Gp3	g.chr16:24942339G>T	Missense Mutation	ARHGAP17	p.P761T	Rho GTPase activating	25 (0.00)	371 (0.23)	0.60
11-14	Gp3	g.chr16:24942390C>A	Nonsense Mutation	ARHGAP17	p.E744*	Rho GTPase activating	76 (0.01)	588 (0.22)	0.59
11-14	Gp3	g.chr11:73021502G>A	Missense Mutation	ARHGEF17	p.A607T	Rho guanine nucleotide	22 (0.00)	28 (0.46)	1.24
11-14	Gp3	g.chr1:16531908G>T	Silent	ARHGEF19	p.R532R	Rho guanine nucleotide	31 (0.00)	215 (0.18)	0.47
11-14	Gp3	g.chr19:4891504C>A	Nonsense Mutation	ARRDC5	p.E195*	arrestin domain containi	34 (0.00)	18 (0.89)	2.37
11-14	Gp3	g.chr7:95157445A>G	Missense Mutation	ASB4	p.M270V	ankyrin repeat and SOC	35 (0.00)	130 (0.37)	1.21
11-14	Gp3	g.chr2:220396534C>A	Missense Mutation	ASIC4	p.L340M	acid-sensing (proton-ga	45 (0.00)	65 (0.58)	1.56
11-14	Gp3	g.chr9:120053698G>A	Silent	ASTN2	p.S179S	astrotactin 2	18 (0.00)	18 (0.56)	1.48
11-14	Gp3	g.chr15:25958900G>A	Silent	ATP10A	p.H755H	ATPase, class V, type 1	18 (0.00)	56 (0.27)	0.71

11-14	Gp3	g.chr17:3839581A>T	Missense Mutation	ATP2A3	p.F835Y	ATPase, Ca++ transport	58 (0.00)	173 (0.51)	1.37
11-14	Gp3	g.chr3:10452323G>A	Missense Mutation	ATP2B2	p.P126S	ATPase, Ca++ transport	15 (0.00)	48 (0.71)	1.89
11-14	Gp3	g.chr16:84486977G>T	Splice Site	ATP2C2	p.K660N	ATPase, Ca++ transport	91 (0.00)	197 (0.56)	1.50
11-14	Gp3	g.chr2:71163196C>T	Missense Mutation	ATP6V1B1	p.R38C	ATPase, H+ transportin	35 (0.00)	107 (0.29)	0.77
11-14	Gp3	g.chr19:1807173G>A	Silent	ATP8B3	p.D203D	ATPase, aminophospho	29 (0.00)	242 (0.31)	0.83
11-14	Gp3	g.chr18:77097416C>A	Silent	ATP9B	p.P750P	ATPase, class II, type 9	48 (0.00)	32 (0.16)	0.42
11-14	Gp3	g.chr3:63981501C>A	Missense Mutation	ATXN7	p.S668Y	ataxin 7	106 (0.00)	191 (0.64)	1.70
11-14	Gp3	g.chr1:110033869G>T	Missense Mutation	ATXN7L2	p.G562W	ataxin 7-like 2	57 (0.00)	20 (0.95)	2.53
11-14	Gp3	g.chr7:70228290G>A	Missense Mutation	AUTS2	p.A393T	autism susceptibility car	39 (0.00)	62 (0.16)	0.43
11-14	Gp3	g.chr16:396284T>A	Nonsense Mutation	AXIN1	p.K248*	axin 1	89 (0.00)	32 (0.19)	0.50
11-14	Gp3	g.chr16:396319C>T	Missense Mutation	AXIN1	p.G236E	axin 1	97 (0.01)	28 (0.96)	2.57
11-14	Gp3	g.chr2:232263247C>T	Missense Mutation	B3GNT7	p.R273W	UDP-GlcNAc:betaGal b	33 (0.00)	171 (0.23)	0.61
11-14	Gp3	g.chr2:232263436G>T	Missense Mutation	B3GNT7	p.V336L	UDP-GlcNAc:betaGal b	26 (0.00)	446 (0.18)	0.48
11-14	Gp3	g.chr12:653562C>A	Missense Mutation	B4GALNT3	p.Q137K	beta-1,4-N-acetyl-galact	55 (0.00)	303 (0.25)	0.66
11-14	Gp3	g.chr17:79060249C>T	Silent	BAIAP2	p.L120L	BAI1-associated protein	90 (0.01)	366 (0.18)	0.58
11-14	Gp3	g.chr11:129246070T>A	Missense Mutation	BARX2	p.V47E	BARX homeobox 2	67 (0.00)	224 (0.16)	0.42
11-14	Gp3	g.chr15:73023793G>A	Missense Mutation	BBS4	p.V287M	Bardet-Biedl syndrome	17 (0.00)	174 (0.99)	2.64
11-14	Gp3	g.chr17:59118208C>A	Missense Mutation	BCAS3	p.L677I	breast carcinoma amplif	62 (0.00)	14 (0.36)	0.95
11-14	Gp3	g.chr17:6929894G>A	Silent	BCL6B	p.S336S	B-cell CLL/lymphoma	45 (0.02)	100 (0.86)	2.29
11-14	Gp3	g.chr17:6929918C>A	Silent	BCL6B	p.A344A	B-cell CLL/lymphoma	46 (0.02)	110 (0.85)	2.28
11-14	Gp3	g.chr15:91260976G>A	Intron	BLM		Bloom syndrome, RecQ	48 (0.00)	156 (0.87)	2.32
11-14	Gp3	g.chr8:22053065G>T	Missense Mutation	BMP1	p.G577V	bone morphogenetic pr	43 (0.00)	186 (0.28)	0.76
11-14	Gp3	g.chr9:16727819G>T	Missense Mutation	BNC2	p.N102K	basonuclin 2	53 (0.00)	61 (0.46)	1.22
11-14	Gp3	g.chr20:31877729T>C	Missense Mutation	BPIFB1	p.V99A	BPI fold containing fam	59 (0.00)	24 (0.50)	1.33
11-14	Gp3	g.chr13:32913822A>G	Missense Mutation	BRCA2	p.K1777R	breast cancer 2, early on	16 (0.00)	39 (0.26)	0.68
11-14	Gp3	g.chr9:121976209G>A	Silent	BRINP1	p.L304L	bone morphogenetic pr	31 (0.00)	22 (0.82)	2.18
11-14	Gp3	g.chr1:177250026T>A	Missense Mutation	BRINP2	p.L572M	bone morphogenetic pr	62 (0.02)	232 (0.16)	0.44
11-14	Gp3	g.chr1:190067835C>A	Missense Mutation	BRINP3	p.K538N	bone morphogenetic pr	53 (0.02)	195 (0.73)	1.96
11-14	Gp3	g.chr3:49692505C>T	Missense Mutation	BSN	p.A1839V	bassoon presynaptic cyt	24 (0.00)	99 (0.66)	1.75
11-14	Gp3	g.chr3:49697963G>T	Silent	BSN	p.R2895R	bassoon presynaptic cyt	45 (0.00)	102 (0.36)	0.97
11-14	Gp3	g.chr3:49698350C>G	Silent	BSN	p.G3024G	bassoon presynaptic cyt	15 (0.00)	21 (0.43)	1.14
11-14	Gp3	g.chr10:50531812G>A	Missense Mutation	C10orf71	p.G408S	chromosome 10 open re	155 (0.00)	14 (0.79)	2.10
11-14	Gp3	g.chr12:48578094G>T	Silent	C12orf68	p.G63G		17 (0.00)	169 (0.21)	0.57
11-14	Gp3	g.chr2:27360071C>A	Missense Mutation	C2orf53	p.G376V		38 (0.00)	197 (0.27)	0.72
11-14	Gp3	g.chr2:26798993C>G	Missense Mutation	C2orf70	p.R100G	chromosome 2 open rea	108 (0.00)	256 (0.19)	0.51

11-14	Gp3	g.chr4:113506755G>A	Missense Mutation	C4orf21	p.S1348F		74 (0.00)	108 (0.40)	1.06
11-14	Gp3	g.chr5:179269064C>A	Splice Site	C5orf45	p.E98*	chromosome 5 open rea	35 (0.00)	152 (0.20)	0.54
11-14	Gp3	g.chr6:165715174C>A	Missense Mutation	C6orf118	p.D213Y	chromosome 6 open rea	20 (0.00)	144 (0.49)	1.31
11-14	Gp3	g.chr9:139379282G>A	Missense Mutation	C9orf163	p.A128T	chromosome 9 open rea	15 (0.00)	141 (0.82)	2.19
11-14	Gp3	g.chr12:2787005C>A	Missense Mutation	CACNA1C	p.S1736Y	calcium channel, voltag	21 (0.00)	200 (0.47)	1.27
11-14	Gp3	g.chr3:53785838C>A	Silent	CACNA1D	p.P1193P	calcium channel, voltag	69 (0.00)	11 (0.82)	2.18
11-14	Gp3	g.chr17:48695589A>G	Missense Mutation	CACNA1G	p.D1753G	calcium channel, voltag	29 (0.00)	182 (0.28)	0.75
11-14	Gp3	g.chr22:36960712C>A	Missense Mutation	CACNG2	p.A220S	calcium channel, voltag	70 (0.00)	558 (0.23)	0.62
11-14	Gp3	g.chr3:85225229A>T	Intron	CADM2		cell adhesion molecule	125 (0.00)	42 (0.98)	2.60
11-14	Gp3	g.chr3:85225230G>T	Intron	CADM2		cell adhesion molecule	126 (0.00)	42 (0.98)	2.60
11-14	Gp3	g.chr3:86095095A>G	Intron	CADM2		cell adhesion molecule	55 (0.00)	28 (0.61)	1.62
11-14	Gp3	g.chr7:134632503C>T	Nonsense Mutation	CALD1	p.R593*	caldesmon 1	68 (0.00)	24 (0.42)	1.45
11-14	Gp3	g.chr9:138709877G>T	Missense Mutation	CAMSAP1	p.S1406Y	calmodulin regulated sp	33 (0.00)	154 (0.33)	0.88
11-14	Gp3	g.chr1:7723814G>A	Missense Mutation	CAMTA1	p.E403K	calmodulin binding tran	33 (0.00)	80 (0.93)	2.47
11-14	Gp3	g.chr11:3033480A>G	Silent	CARS	p.L671L	cysteinyl-tRNA synthet	116 (0.00)	290 (0.18)	0.49
11-14	Gp3	g.chr17:42980042C>A	Missense Mutation	CCDC103	p.Q196K	coiled-coil domain cont	23 (0.00)	54 (0.72)	1.93
11-14	Gp3	g.chr7:76916235T>C	Silent	CCDC146	p.L757L	coiled-coil domain cont	99 (0.00)	38 (0.18)	0.49
11-14	Gp3	g.chr17:78039370C>A	Silent	CCDC40	p.R509R	coiled-coil domain cont	42 (0.00)	328 (0.14)	0.45
11-14	Gp3	g.chr1:1323369G>T	Silent	CCNL2	p.G361G	cyclin L2	27 (0.00)	96 (0.50)	1.33
11-14	Gp3	g.chr5:54527362C>T	Silent	CCNO	p.S298S	cyclin O	40 (0.00)	399 (0.26)	0.68
11-14	Gp3	g.chr3:46306877G>T	Silent	CCR3	p.L76L	chemokine (C-C motif)	121 (0.00)	30 (0.93)	2.49
11-14	Gp3	g.chr22:17072648C>T	Missense Mutation	CCT8L2	p.A265T	chaperonin containing T	67 (0.00)	119 (0.47)	1.25
11-14	Gp3	g.chr1:158151292G>T	Missense Mutation	CD1D	p.A37S	CD1d molecule	142 (0.00)	623 (0.27)	0.49
11-14	Gp3	g.chr15:73995321G>A	Silent	CD276	p.R209R	CD276 molecule	30 (0.00)	196 (0.53)	1.41
11-14	Gp3	g.chr17:72691898T>A	Missense Mutation	CD300LF	p.Q228L	CD300 molecule-like fa	16 (0.00)	85 (0.33)	0.88
11-14	Gp3	g.chr3:48205807C>A	Missense Mutation	CDC25A	p.G438C	cell division cycle 25A	57 (0.00)	281 (0.29)	0.77
11-14	Gp3	g.chr11:64602830C>A	Nonsense Mutation	CDC42BPG	p.E648*	CDC42 binding protein	30 (0.00)	240 (0.43)	1.14
11-14	Gp3	g.chr11:64602831C>A	Silent	CDC42BPG	p.R647R	CDC42 binding protein	30 (0.00)	240 (0.42)	1.12
11-14	Gp3	g.chr10:73453976A>G	Missense Mutation	CDH23	p.D755G	cadherin-related 23	55 (0.00)	45 (0.20)	0.53
11-14	Gp3	g.chr1:1581157G>A	Nonsense Mutation	CDK11B	p.Q123*	cyclin-dependent kinase	630 (0.00)	476 (0.19)	0.51
11-14	Gp3	g.chr16:22358454A>G	Silent	CDR2	p.V399V	cerebellar degeneration-	40 (0.00)	68 (0.29)	0.78
11-14	Gp3	g.chr16:22358471C>T	Missense Mutation	CDR2	p.A394T	cerebellar degeneration-	32 (0.00)	72 (0.49)	1.30
11-14	Gp3	g.chr22:46930194C>A	Silent	CELSR1	p.R958R	cadherin, EGF LAG sev	60 (0.02)	333 (0.21)	0.57
11-14	Gp3	g.chr22:46930696C>G	Missense Mutation	CELSR1	p.S791T	cadherin, EGF LAG sev	20 (0.00)	102 (0.50)	1.33
11-14	Gp3	g.chr3:48699779T>A	Missense Mutation	CELSR3	p.N97Y	cadherin, EGF LAG sev	35 (0.00)	88 (0.58)	1.55

11-14	Gp3	g.chr5:640584G>T	Silent	CEP72	p.A468A	centrosomal protein 72k	25 (0.00)	79 (0.59)	1.59
11-14	Gp3	g.chr5:640637G>T	Missense Mutation	CEP72	p.S486I	centrosomal protein 72k	29 (0.00)	118 (0.42)	1.11
11-14	Gp3	g.chr22:47086028C>A	Nonsense Mutation	CERK	p.E468*	ceramide kinase	24 (0.00)	56 (0.39)	1.05
11-14	Gp3	g.chr15:57839585A>T	Missense Mutation	CGNL1	p.D1269V	cingulin-like 1	176 (0.00)	220 (0.47)	1.26
11-14	Gp3	g.chr2:27324975G>A	Missense Mutation	CGREF1	p.T111I	cell growth regulator wi	15 (0.00)	11 (0.91)	2.42
11-14	Gp3	g.chr17:48545702T>A	Missense Mutation	CHAD	p.K158M	chondroadherin	54 (0.00)	26 (0.46)	1.23
11-14	Gp3	g.chr17:7814210G>C	Missense Mutation	CHD3	p.A1993P	chromodomain helicase	69 (0.00)	271 (0.52)	1.38
11-14	Gp3	g.chr1:6182084C>T	Intron	CHD5		chromodomain helicase	60 (0.02)	143 (0.17)	0.45
11-14	Gp3	g.chr1:6182461C>A	Intron	CHD5		chromodomain helicase	153 (0.01)	87 (0.30)	0.80
11-14	Gp3	g.chr1:6189511C>G	Intron	CHD5		chromodomain helicase	48 (0.00)	81 (0.98)	2.60
11-14	Gp3	g.chr1:6205411A>G	Intron	CHD5		chromodomain helicase	42 (0.00)	113 (0.17)	0.45
11-14	Gp3	g.chr1:6221964G>T	Intron	CHD5		chromodomain helicase	30 (0.00)	58 (0.47)	1.24
11-14	Gp3	g.chr17:4805246T>C	Missense Mutation	CHRNE	p.N161D	cholinergic receptor, nic	53 (0.00)	218 (0.29)	0.78
11-14	Gp3	g.chr12:105151130A>T	Missense Mutation	CHST11	p.K198M	carbohydrate (chondroit	27 (0.00)	61 (0.80)	2.14
11-14	Gp3	g.chr15:40764290A>G	Missense Mutation	CHST14	p.Y293C	carbohydrate (N-acetylg	92 (0.00)	30 (0.20)	0.53
11-14	Gp3	g.chr16:75512610C>G	Missense Mutation	CHST6	p.D373H	carbohydrate (N-acetylg	21 (0.00)	43 (0.98)	2.60
11-14	Gp3	g.chr19:34263362G>T	Missense Mutation	CHST8	p.Q223H	carbohydrate (N-acetylg	18 (0.00)	184 (0.28)	0.75
11-14	Gp3	g.chr19:34263808G>A	Missense Mutation	CHST8	p.R372Q	carbohydrate (N-acetylg	19 (0.00)	242 (0.17)	0.46
11-14	Gp3	g.chr15:65489591A>G	Silent	CILP	p.S1011S	cartilage intermediate la	63 (0.00)	22 (0.64)	1.70
11-14	Gp3	g.chr12:106633816C>A	Missense Mutation	CKAP4	p.E265D	cytoskeleton-associated	181 (0.00)	363 (0.38)	1.01
11-14	Gp3	g.chr3:184064432C>A	Nonsense Mutation	CLCN2	p.E843*	chloride channel, voltag	27 (0.00)	44 (0.14)	0.44
11-14	Gp3	g.chr12:122812875C>A	Missense Mutation	CLIP1	p.S989I	CAP-GLY domain cont	146 (0.00)	137 (0.99)	2.63
11-14	Gp3	g.chr12:122812877C>A	Missense Mutation	CLIP1	p.Q988H	CAP-GLY domain cont	147 (0.01)	135 (0.99)	2.63
11-14	Gp3	g.chr22:19183914C>A	Missense Mutation	CLTCL1	p.A1352S	clathrin, heavy chain-lik	91 (0.00)	84 (0.98)	2.60
11-14	Gp3	g.chr1:26510592C>G	Missense Mutation	CNKSR1	p.Q296E	connector enhancer of k	30 (0.00)	97 (0.49)	1.32
11-14	Gp3	g.chr10:101147579C>A	Silent	CNNM1	p.I781I	cyclin and CBS domain	21 (0.00)	176 (0.22)	0.58
11-14	Gp3	g.chr7:135099146C>T	Silent	CNOT4	p.R165R	CCR4-NOT transcriptio	41 (0.00)	37 (0.14)	0.47
11-14	Gp3	g.chr17:40836222C>A	Missense Mutation	CNTNAP1	p.P113Q	contactin associated pro	143 (0.00)	694 (0.31)	0.83
11-14	Gp3	g.chr17:40715245G>T	Missense Mutation	COASY	p.R202L	CoA synthase	24 (0.00)	196 (0.39)	1.03
11-14	Gp3	g.chr7:101176354C>T	RNA	COL26A1		collagen, type XXVI, al	29 (0.00)	201 (0.24)	0.85
11-14	Gp3	g.chr3:139092544G>A	Silent	COPB2	p.V286V	coatomer protein compl	48 (0.00)	31 (0.97)	3.14
11-14	Gp3	g.chr16:4409542G>C	Missense Mutation	CORO7	p.A730G	coronin 7	18 (0.00)	232 (0.42)	1.11
11-14	Gp3	g.chr8:145625886G>T	Splice Site	CPSF1	p.R230S	cleavage and polyadeny	15 (0.00)	256 (0.16)	0.44
11-14	Gp3	g.chr12:69652832G>A	Missense Mutation	CPSF6	p.R386Q	cleavage and polyadeny	141 (0.00)	19 (0.84)	2.25
11-14	Gp3	g.chr12:69652840C>A	Missense Mutation	CPSF6	p.P389T	cleavage and polyadeny	133 (0.00)	19 (0.84)	2.25

11-14	Gp3	g.chr22:51008787G>T	Missense Mutation	CPT1B	p.Q693K	carnitine palmitoyltrans	17 (0.00)	53 (0.28)	0.75
11-14	Gp3	g.chr19:4157080C>A	Missense Mutation	CREB3L3	p.P82H	cAMP responsive elem	39 (0.00)	14 (0.36)	0.95
11-14	Gp3	g.chr1:16958818C>A	lincRNA	CROCCP2		ciliary rootlet coiled-coi	110 (0.00)	28 (0.25)	0.67
11-14	Gp3	g.chr19:48339507C>G	Silent	CRX	p.P36P	cone-rod homeobox	51 (0.00)	30 (0.47)	1.24
11-14	Gp3	g.chr21:44589300C>A	Missense Mutation	CRYAA	p.L31I	crystallin, alpha A	23 (0.00)	187 (0.81)	2.17
11-14	Gp3	g.chr5:149460454G>T	Nonsense Mutation	CSF1R	p.Y61*	colony stimulating facto	17 (0.00)	38 (0.42)	1.12
11-14	Gp3	g.chr1:33985261G>A	Missense Mutation	CSMD2	p.P3585S	CUB and Sushi multipl	39 (0.00)	68 (0.38)	1.02
11-14	Gp3	g.chr13:37679109G>T	Silent	CSNK1A1L	p.P95P	casein kinase 1, alpha 1	39 (0.00)	131 (0.21)	0.39
11-14	Gp3	g.chr3:39185129C>A	Missense Mutation	CSRNP1	p.S396I	cysteine-serine-rich nuc	20 (0.00)	12 (0.42)	1.11
11-14	Gp3	g.chr3:39185640G>T	Silent	CSRNP1	p.G256G	cysteine-serine-rich nuc	33 (0.00)	107 (0.45)	1.20
11-14	Gp3	g.chr3:39185645C>A	Missense Mutation	CSRNP1	p.A255S	cysteine-serine-rich nuc	34 (0.00)	107 (0.36)	0.95
11-14	Gp3	g.chr22:42523915G>T	Missense Mutation	CYP2D6	p.A305D	cytochrome P450, famil	45 (0.00)	156 (0.26)	0.70
11-14	Gp3	g.chr9:124361098C>A	Intron	DAB2IP		DAB2 interacting protei	36 (0.00)	355 (0.16)	0.42
11-14	Gp3	g.chr9:124411232C>T	Intron	DAB2IP		DAB2 interacting protei	69 (0.00)	63 (0.27)	0.72
11-14	Gp3	g.chr9:124456852G>A	Intron	DAB2IP		DAB2 interacting protei	109 (0.00)	16 (0.62)	1.67
11-14	Gp3	g.chr9:124456945T>A	Intron	DAB2IP		DAB2 interacting protei	47 (0.00)	47 (0.30)	0.79
11-14	Gp3	g.chr9:124460834C>T	Intron	DAB2IP		DAB2 interacting protei	167 (0.00)	376 (0.23)	0.61
11-14	Gp3	g.chr9:124460902C>T	Intron	DAB2IP		DAB2 interacting protei	42 (0.02)	173 (0.38)	1.02
11-14	Gp3	g.chr9:124460953T>A	Intron	DAB2IP		DAB2 interacting protei	17 (0.00)	73 (0.68)	1.83
11-14	Gp3	g.chr9:124506172C>A	Intron	DAB2IP		DAB2 interacting protei	31 (0.00)	35 (0.97)	2.59
11-14	Gp3	g.chr9:124507715A>G	Intron	DAB2IP		DAB2 interacting protei	48 (0.02)	235 (0.27)	0.71
11-14	Gp3	g.chr9:124513262C>T	Intron	DAB2IP		DAB2 interacting protei	48 (0.00)	23 (0.70)	1.86
11-14	Gp3	g.chr1:173803658G>A	Splice Site	DARS2		aspartyl-tRNA syntheta	21 (0.00)	98 (0.99)	2.64
11-14	Gp3	g.chr12:113599728C>A	Missense Mutation	DDX54	p.R757L	DEAD (Asp-Glu-Ala-A	29 (0.00)	49 (0.16)	0.44
11-14	Gp3	g.chr22:19122588G>A	Missense Mutation	DGCR14	p.T379M	DiGeorge syndrome crit	31 (0.00)	330 (0.32)	0.85
11-14	Gp3	g.chr2:234368880A>G	Missense Mutation	DGKD	p.K957R	diacylglycerol kinase, d	70 (0.00)	133 (0.28)	0.74
11-14	Gp3	g.chr11:71150080T>C	Missense Mutation	DHCR7	p.N226D	7-dehydrocholesterol re	38 (0.00)	43 (0.35)	0.93
11-14	Gp3	g.chr10:430580C>T	Splice Site	DIP2C		DIP2 disco-interacting	69 (0.00)	143 (0.85)	2.26
11-14	Gp3	g.chr1:68512885G>A	Silent	DIRAS3	p.H32H	DIRAS family, GTP-bi	54 (0.00)	144 (0.67)	1.78
11-14	Gp3	g.chr8:12957832C>A	Nonsense Mutation	DLC1	p.E672*	DLC1 Rho GTPase acti	35 (0.00)	115 (0.60)	1.60
11-14	Gp3	g.chr17:7099888C>G	Missense Mutation	DLG4	p.G361R	discs, large homolog 4 (	63 (0.00)	301 (0.14)	0.38
11-14	Gp3	g.chr20:35125142G>T	Silent	DLGAP4	p.P561P	discs, large (Drosophila	96 (0.00)	370 (0.15)	0.40
11-14	Gp3	g.chr10:124377568G>C	Missense Mutation	DMBT1	p.G1514R	deleted in malignant bra	211 (0.00)	223 (0.33)	0.88
11-14	Gp3	g.chr10:124377590G>A	Missense Mutation	DMBT1	p.R1521Q	deleted in malignant bra	271 (0.00)	287 (0.63)	1.68
11-14	Gp3	g.chr3:52417551C>T	Silent	DNAH1	p.N2697N	dynein, axonemal, heav	122 (0.00)	119 (0.22)	0.58

11-14	Gp3	g.chr17:76522751G>A	Silent	DNAH17	p.P1228P	dynein, axonemal, heav	67 (0.00)	460 (0.23)	0.61
11-14	Gp3	g.chr17:76568918G>A	Missense Mutation	DNAH17	p.S135L	dynein, axonemal, heav	17 (0.00)	83 (0.37)	1.00
11-14	Gp3	g.chr17:7681690A>G	Missense Mutation	DNAH2	p.D1815G	dynein, axonemal, heav	56 (0.00)	53 (0.17)	0.45
11-14	Gp3	g.chr3:128181963C>T	Silent	DNAJB8	p.A42A	DnaJ (Hsp40) homolog,	35 (0.00)	56 (0.34)	1.10
11-14	Gp3	g.chr11:6567428C>A	Silent	DNHD1	p.G1753G	dynein heavy chain dom	68 (0.00)	67 (0.34)	0.92
11-14	Gp3	g.chr11:6592869G>A	Missense Mutation	DNHD1	p.E4639K	dynein heavy chain dom	42 (0.00)	123 (0.28)	0.76
11-14	Gp3	g.chr9:131002263G>C	Splice Site	DNM1		dynamin 1	31 (0.00)	36 (0.22)	0.59
11-14	Gp3	g.chr21:45670788G>A	Missense Mutation	DNMT3L	p.P272S	DNA (cytosine-5-)-met	32 (0.00)	17 (0.35)	0.94
11-14	Gp3	g.chr19:11348781C>A	Missense Mutation	DOCK6	p.G591V	dedicator of cytokinesis	46 (0.00)	291 (0.71)	1.91
11-14	Gp3	g.chr20:53205136G>C	Splice Site	DOK5	p.D97H	docking protein 5	99 (0.00)	49 (0.96)	2.56
11-14	Gp3	g.chr1:44437935C>T	Missense Mutation	DPH2	p.S425L	DPH2 homolog (S. cere	36 (0.00)	57 (0.19)	0.51
11-14	Gp3	g.chr12:58001282C>A	Missense Mutation	DTX3	p.N212K	deltex 3, E3 ubiquitin li	19 (0.00)	37 (0.19)	0.50
11-14	Gp3	g.chr15:45408728C>G	Missense Mutation	DUOXA2	p.Q119E	dual oxidase maturation	71 (0.00)	102 (0.31)	0.84
11-14	Gp3	g.chr17:7132554C>A	Missense Mutation	DVL2	p.S286I	dishevelled segment pol	53 (0.00)	208 (0.15)	0.41
11-14	Gp3	g.chr2:71801492G>T	Missense Mutation	DYSF	p.E1131D	dysferlin	28 (0.00)	125 (0.62)	1.64
11-14	Gp3	g.chr15:55790521G>T	Missense Mutation	DYX1C1	p.L3I	dyslexia susceptibility 1	15 (0.00)	86 (0.90)	2.39
11-14	Gp3	g.chr16:23546598C>A	Missense Mutation	EARS2	p.R190L	glutamyl-tRNA synthet	15 (0.00)	48 (0.60)	1.61
11-14	Gp3	g.chr16:23546650C>T	Missense Mutation	EARS2	p.E173K	glutamyl-tRNA synthet	24 (0.00)	86 (0.24)	0.65
11-14	Gp3	g.chr8:110576700C>A	Missense Mutation	EBAG9	p.A230E	estrogen receptor bindin	21 (0.00)	31 (0.97)	2.58
11-14	Gp3	g.chr1:150484268C>A	Nonsense Mutation	ECM1	p.C348*	extracellular matrix prot	54 (0.00)	99 (0.51)	1.35
11-14	Gp3	g.chr1:150484292C>A	Silent	ECM1	p.T356T	extracellular matrix prot	57 (0.00)	91 (0.43)	1.14
11-14	Gp3	g.chr19:48220190C>A	Silent	EHD2	p.G107G	EH-domain containing	36 (0.00)	248 (0.17)	0.45
11-14	Gp3	g.chr15:42193109G>T	Missense Mutation	EHD4	p.L454I	EH-domain containing	19 (0.00)	101 (0.56)	1.50
11-14	Gp3	g.chr22:37770207G>A	Silent	ELFN2	p.A456A	extracellular leucine-ric	78 (0.00)	458 (0.25)	0.68
11-14	Gp3	g.chr16:67236437G>T	Splice Site	ELMO3		engulfment and cell mot	53 (0.02)	136 (0.68)	1.80
11-14	Gp3	g.chr20:39990637G>T	Missense Mutation	EMILIN3	p.S524R	elastin microfibril interf	28 (0.00)	161 (0.31)	0.83
11-14	Gp3	g.chr8:144940953G>T	Missense Mutation	EPPK1	p.L2157I	epiplakin 1	93 (0.00)	110 (0.21)	0.56
11-14	Gp3	g.chr8:642498G>A	Missense Mutation	ERICH1	p.S95F	glutamate-rich 1	58 (0.02)	362 (0.66)	1.76
11-14	Gp3	g.chr8:642530C>A	Missense Mutation	ERICH1	p.E84D	glutamate-rich 1	34 (0.00)	275 (0.61)	1.62
11-14	Gp3	g.chr21:33887342C>T	Silent	EVA1C	p.L390L	eva-1 homolog C (C. el	49 (0.00)	37 (0.30)	0.79
11-14	Gp3	g.chr4:5798801C>T	Missense Mutation	EVC	p.R647W	Ellis van Creveld syndr	23 (0.00)	20 (0.80)	2.13
11-14	Gp3	g.chr17:74004938C>A	Nonsense Mutation	EVPL	p.E1450*	envoplakin	54 (0.00)	188 (0.26)	0.68
11-14	Gp3	g.chr1:26361368T>C	Missense Mutation	EXTL1	p.L574P	exostosin-like glycosylt	71 (0.01)	134 (0.66)	1.75
11-14	Gp3	g.chr3:184062409A>T	Missense Mutation	FAM131A	p.D128V	family with sequence si	28 (0.00)	94 (0.44)	1.41
11-14	Gp3	g.chr10:15255670A>G	Silent	FAM171A1	p.S639S	family with sequence si	50 (0.00)	186 (0.17)	0.46

11-14	Gp3	g.chr12:49993506C>A	Silent	FAM186B	p.G639G	family with sequence si	75 (0.00)	109 (0.28)	0.73
11-14	Gp3	g.chr7:30915251G>T	Nonsense Mutation	FAM188B	p.E651*	family with sequence si	22 (0.00)	23 (0.96)	3.27
11-14	Gp3	g.chr3:150421425G>C	Nonsense Mutation	FAM194A	p.Y87*		24 (0.00)	91 (0.26)	0.86
11-14	Gp3	g.chr3:43073980G>C	Missense Mutation	FAM198A	p.M75I	family with sequence si	19 (0.00)	60 (0.47)	1.24
11-14	Gp3	g.chr1:113264911G>T	Missense Mutation	FAM19A3	p.C19F	family with sequence si	22 (0.00)	203 (0.19)	0.50
11-14	Gp3	g.chr22:49103589G>T	Missense Mutation	FAM19A5	p.C29F	family with sequence si	20 (0.00)	15 (0.93)	2.49
11-14	Gp3	g.chr1:809329C>A	lincRNA	FAM41C		family with sequence si	151 (0.00)	306 (0.28)	0.74
11-14	Gp3	g.chr1:212798634C>T	Silent	FAM71A	p.L139L	family with sequence si	131 (0.01)	280 (0.58)	1.55
11-14	Gp3	g.chr9:131802876G>T	Start Codon SNP	FAM73B	p.M1I	family with sequence si	28 (0.00)	38 (0.82)	2.18
11-14	Gp3	g.chr15:59752397G>A	Missense Mutation	FAM81A	p.D96N	family with sequence si	83 (0.00)	31 (0.48)	1.29
11-14	Gp3	g.chr19:49113218T>C	Missense Mutation	FAM83E	p.S225G	family with sequence si	21 (0.00)	180 (0.23)	0.62
11-14	Gp3	g.chr16:5139151G>A	Silent	FAM86A	p.T283T	family with sequence si	69 (0.00)	295 (0.47)	1.26
11-14	Gp3	g.chr14:45605483G>A	Nonsense Mutation	FANCM	p.W83*	Fanconi anemia, comple	31 (0.00)	13 (0.38)	1.03
11-14	Gp3	g.chr13:99061711T>A	Missense Mutation	FARP1	p.L512M	FERM, RhoGEF (ARH	39 (0.00)	32 (0.72)	1.92
11-14	Gp3	g.chr11:92615945A>G	Missense Mutation	FAT3	p.E3958G	FAT atypical cadherin 3	29 (0.00)	53 (0.23)	0.60
11-14	Gp3	g.chr11:64889088G>T	Missense Mutation	FAU	p.A35D	Finkel-Biskis-Reilly mu	33 (0.00)	58 (0.33)	0.87
11-14	Gp3	g.chr5:127648364C>A	Missense Mutation	FBN2	p.W1614L	fibrillin 2	157 (0.00)	110 (0.99)	1.82
11-14	Gp3	g.chr7:5521436C>A	Silent	FBXL18	p.V709V	F-box and leucine-rich r	17 (0.00)	61 (0.59)	2.04
11-14	Gp3	g.chr5:15500803C>A	Silent	FBXL7	p.G6G	F-box and leucine-rich r	23 (0.00)	17 (0.29)	0.78
11-14	Gp3	g.chr8:124992993C>G	Missense Mutation	FER1L6	p.A451G	fer-1-like family membe	25 (0.00)	74 (0.47)	1.26
11-14	Gp3	g.chr8:124993036C>T	Silent	FER1L6	p.F465F	fer-1-like family membe	25 (0.00)	71 (0.46)	1.24
11-14	Gp3	g.chr19:35941054C>A	Silent	FFAR2	p.I146I	free fatty acid receptor	38 (0.00)	27 (0.33)	0.89
11-14	Gp3	g.chr5:176524590C>T	Silent	FGFR4	p.T774T	fibroblast growth factor	30 (0.00)	178 (0.20)	0.54
11-14	Gp3	g.chr1:152279206C>A	Missense Mutation	FLG	p.S2719I	filaggrin	32 (0.00)	47 (0.36)	0.96
11-14	Gp3	g.chr7:128485109G>A	Missense Mutation	FLNC	p.G1197E	filamin C, gamma	15 (0.00)	212 (0.17)	0.61
11-14	Gp3	g.chr7:128490508C>A	Missense Mutation	FLNC	p.P1790H	filamin C, gamma	17 (0.00)	54 (0.13)	0.45
11-14	Gp3	g.chr17:43321346T>C	Missense Mutation	FMNL1	p.L801P	formin-like 1	38 (0.00)	73 (0.51)	1.35
11-14	Gp3	g.chr17:80684398C>A	Missense Mutation	FN3KRP	p.Q171K	fructosamine 3 kinase re	26 (0.00)	52 (0.25)	0.82
11-14	Gp3	g.chr14:75747543C>T	Silent	FOS	p.L187L	FBJ murine osteosarcon	79 (0.00)	19 (0.79)	2.11
11-14	Gp3	g.chr2:114257337C>A	Silent	FOXD4L1	p.I168I	forkhead box D4-like 1	28 (0.00)	190 (0.89)	2.39
11-14	Gp3	g.chr2:88748305C>T	RNA	FOXI3		forkhead box I3	44 (0.00)	138 (0.99)	2.65
11-14	Gp3	g.chr4:79328865A>T	Missense Mutation	FRAS1	p.E1393V	Fraser extracellular mat	104 (0.00)	24 (0.83)	2.22
11-14	Gp3	g.chr5:39135032C>A	Nonsense Mutation	FYB	p.G534*	FYN binding protein	242 (0.00)	212 (0.20)	0.54
11-14	Gp3	g.chr5:39135101G>A	Nonsense Mutation	FYB	p.Q511*	FYN binding protein	125 (0.01)	61 (0.41)	1.09
11-14	Gp3	g.chr3:46008622C>A	Missense Mutation	FYCO1	p.S735I	FYVE and coiled-coil d	62 (0.00)	59 (0.97)	2.58

11-14	Gp3	g.chr3:46009287C>A	Silent	FYCO1	p.R513R	FYVE and coiled-coil d	103 (0.00)	57 (0.98)	2.62
11-14	Gp3	g.chr7:90896112C>A	Missense Mutation	FZD1	p.N639K	frizzled class receptor 1	64 (0.00)	345 (0.14)	0.47
11-14	Gp3	g.chr12:130648209C>A	Silent	FZD10	p.L208L	frizzled class receptor 1	29 (0.00)	159 (0.52)	1.39
11-14	Gp3	g.chr14:69813823C>T	Silent	GALNT16	p.G446G	polypeptide N-acetylgal	42 (0.00)	12 (0.75)	2.00
11-14	Gp3	g.chr19:36034316G>T	Silent	GAPDHS	p.R272R	glyceraldehyde-3-phosp	45 (0.00)	76 (0.25)	0.67
11-14	Gp3	g.chr16:90109653G>T	Missense Mutation	GAS8	p.G446V	growth arrest-specific 8	24 (0.00)	41 (0.22)	0.59
11-14	Gp3	g.chr16:2034761T>C	Missense Mutation	GFER	p.F91S	growth factor, augment	32 (0.00)	43 (0.35)	0.93
11-14	Gp3	g.chr2:85788039A>G	Missense Mutation	GGCX	p.L38S	gamma-glutamyl carbox	118 (0.00)	358 (0.90)	2.40
11-14	Gp3	g.chr1:147230939C>A	Missense Mutation	GJA5	p.W136C	gap junction protein, al	45 (0.00)	94 (0.19)	0.51
11-14	Gp3	g.chr1:147231183T>C	Missense Mutation	GJA5	p.D55G	gap junction protein, al	30 (0.00)	49 (0.14)	0.38
11-14	Gp3	g.chr19:19745477G>A	Silent	GMIP	p.D641D	GEM interacting protei	63 (0.00)	368 (0.25)	0.67
11-14	Gp3	g.chr20:57415246G>T	Missense Mutation	GNAS	p.A29S	GNAS complex locus	17 (0.00)	292 (0.38)	1.01
11-14	Gp3	g.chr22:23465549C>T	Silent	GNAZ	p.I333I	guanine nucleotide bind	76 (0.00)	79 (0.90)	2.40
11-14	Gp3	g.chr1:27215520C>T	Missense Mutation	GPN2	p.E170K	GPN-loop GTPase 2	167 (0.00)	36 (0.97)	2.59
11-14	Gp3	g.chr1:27216323C>A	Nonsense Mutation	GPN2	p.E89*	GPN-loop GTPase 2	20 (0.00)	52 (0.17)	0.46
11-14	Gp3	g.chr14:59930491G>T	Missense Mutation	GPR135	p.P485H	G protein-coupled recep	63 (0.00)	169 (0.24)	0.65
11-14	Gp3	g.chr1:168054866C>A	Missense Mutation	GPR161	p.G366V	G protein-coupled recep	97 (0.00)	558 (0.22)	0.58
11-14	Gp3	g.chr2:133175407G>A	Silent	GPR39	p.P264P	G protein-coupled recep	34 (0.00)	198 (0.23)	0.62
11-14	Gp3	g.chr2:105859324G>A	Missense Mutation	GPR45	p.E337K	G protein-coupled recep	44 (0.00)	399 (0.19)	0.51
11-14	Gp3	g.chr1:110085906C>A	Missense Mutation	GPR61	p.L88M	G protein-coupled recep	53 (0.00)	19 (0.58)	1.54
11-14	Gp3	g.chr10:46998917C>T	Missense Mutation	GPRIN2	p.P13S	G protein regulated indu	46 (0.00)	240 (0.15)	0.39
11-14	Gp3	g.chr17:72846818C>A	Missense Mutation	GRIN2C	p.R401L	glutamate receptor, iono	33 (0.00)	264 (0.21)	0.56
11-14	Gp3	g.chr13:114321994C>A	Missense Mutation	GRK1	p.A98E	G protein-coupled recep	75 (0.00)	196 (0.23)	0.61
11-14	Gp3	g.chr6:146755359G>T	Silent	GRM1	p.L1004L	glutamate receptor, met	20 (0.00)	89 (0.24)	0.63
11-14	Gp3	g.chr14:77796680C>G	Missense Mutation	GSTZ1	p.P141A	glutathione S-transferas	112 (0.01)	543 (0.24)	0.65
11-14	Gp3	g.chr7:73961461C>T	Silent	GTF2IRD1	p.V587V	GTF2I repeat domain c	39 (0.00)	136 (0.19)	0.51
11-14	Gp3	g.chr22:46725399G>A	Missense Mutation	GTSE1	p.D691N	G-2 and S-phase expres	68 (0.01)	314 (0.29)	0.77
11-14	Gp3	g.chr5:21496928T>C	RNA	GUSBP1		glucuronidase, beta pseu	34 (0.00)	13 (0.54)	1.44
11-14	Gp3	g.chr19:49473052C>T	Missense Mutation	GYS1	p.E560K	glycogen synthase 1 (m	57 (0.00)	73 (0.85)	2.26
11-14	Gp3	g.chr22:50684774C>A	Nonsense Mutation	HDAC10	p.E535*	histone deacetylase 10	17 (0.00)	182 (0.18)	0.48
11-14	Gp3	g.chr7:18758402G>A	Intron	HDAC9		histone deacetylase 9	40 (0.00)	25 (0.28)	0.75
11-14	Gp3	g.chr7:43484961C>A	Missense Mutation	HECW1	p.S730R	HECT, C2 and WW do	61 (0.02)	551 (0.13)	0.45
11-14	Gp3	g.chr17:65074620C>A	Silent	HELZ	p.V1859V	helicase with zinc finge	119 (0.00)	131 (0.40)	1.06
11-14	Gp3	g.chr20:62192789C>A	Missense Mutation	HELZ2	p.Q2289H	helicase with zinc finge	64 (0.00)	44 (0.16)	0.42
11-14	Gp3	g.chr9:100693113G>T	Silent	HEMGN	p.S188S	hemogen	121 (0.00)	125 (0.50)	1.34

11-14	Gp3	g.chr9:100693338G>T	Missense Mutation	HEMGN	p.S113R	hemogen	37 (0.00)	121 (0.42)	1.12
11-14	Gp3	g.chr15:20645943G>T	RNA	HERC2P3		hect domain and RLD 2	46 (0.00)	32 (0.78)	2.08
11-14	Gp3	g.chr17:43227583G>A	Silent	HEXIM1	p.E342E	hexamethylene bis-acet	67 (0.00)	142 (0.41)	1.09
11-14	Gp3	g.chr1:222717021C>T	Missense Mutation	HHIPL2	p.A278T	HHIP-like 2	54 (0.00)	95 (0.25)	0.67
11-14	Gp3	g.chr6:27776079T>C	Missense Mutation	HIST1H2AI	p.V31A	histone cluster 1, H2ai	72 (0.00)	341 (0.24)	0.63
11-14	Gp3	g.chr6:27805786T>C	Missense Mutation	HIST1H2AK	p.N111S	histone cluster 1, H2ak	100 (0.00)	138 (0.20)	0.52
11-14	Gp3	g.chr6:27114214A>T	Missense Mutation	HIST1H2BK	p.Y122N	histone cluster 1, H2bk	95 (0.00)	15 (0.67)	1.78
11-14	Gp3	g.chr6:12163739T>C	Missense Mutation	HIVEP1	p.V2401A	human immunodeficien	36 (0.03)	148 (0.52)	1.39
11-14	Gp3	g.chr1:41978918A>G	Missense Mutation	HIVEP3	p.S1992P	human immunodeficien	19 (0.00)	31 (0.29)	0.77
11-14	Gp3	g.chr1:42049834C>A	Missense Mutation	HIVEP3	p.R212L	human immunodeficien	38 (0.00)	39 (0.41)	1.09
11-14	Gp3	g.chr1:42049835G>A	Missense Mutation	HIVEP3	p.R212C	human immunodeficien	38 (0.00)	38 (0.39)	1.05
11-14	Gp3	g.chr5:176317838C>A	Missense Mutation	HK3	p.Q173H	hexokinase 3 (white cell	52 (0.00)	54 (0.15)	0.40
11-14	Gp3	g.chr17:46804306T>C	Missense Mutation	HOXB13	p.E234G	homeobox B13	29 (0.00)	241 (0.17)	0.45
11-14	Gp3	g.chr17:46628137G>A	Silent	HOXB3	p.S212S	homeobox B3	36 (0.00)	436 (0.22)	0.58
11-14	Gp3	g.chr12:54403194C>A	Silent	HOXC8	p.P42P	homeobox C8	32 (0.00)	127 (0.47)	1.26
11-14	Gp3	g.chr2:176958296G>T	Missense Mutation	HOXD13	p.M226I	homeobox D13	29 (0.00)	104 (0.18)	0.49
11-14	Gp3	g.chr10:100183366A>T	Missense Mutation	HPS1	p.M531K	Hermansky-Pudlak sync	110 (0.00)	229 (0.23)	0.61
11-14	Gp3	g.chr16:67470632T>C	Missense Mutation	HSD11B2	p.M315T	hydroxysteroid (11-beta	63 (0.00)	148 (0.14)	0.38
11-14	Gp3	g.chr1:22178313G>T	Missense Mutation	HSPG2	p.T2326N	heparan sulfate proteogl	35 (0.03)	274 (0.33)	0.89
11-14	Gp3	g.chr19:10403347A>G	Missense Mutation	ICAM5	p.T341A	intercellular adhesion m	29 (0.00)	16 (0.56)	1.50
11-14	Gp3	g.chr1:23885695C>T	Missense Mutation	ID3	p.D75N	inhibitor of DNA bindin	46 (0.02)	47 (0.43)	1.13
11-14	Gp3	g.chr11:1756633G>A	Silent	IFITM10	p.D188D	interferon induced trans	30 (0.00)	26 (0.69)	1.85
11-14	Gp3	g.chr16:1570201G>T	Missense Mutation	IFT140	p.N462K	intraflagellar transport 1	27 (0.00)	11 (0.73)	1.94
11-14	Gp3	g.chr22:23101703C>G	RNA	IGLV2-14		immunoglobulin lambd	76 (0.01)	215 (0.44)	1.18
11-14	Gp3	g.chr11:117870089A>G	Silent	IL10RA	p.P490P	interleukin 10 receptor,	15 (0.00)	50 (0.24)	0.64
11-14	Gp3	g.chr13:21295934C>T	Silent	IL17D	p.A150A	interleukin 17D	17 (0.00)	222 (0.42)	1.13
11-14	Gp3	g.chr16:27460101G>A	Missense Mutation	IL21R	p.G372S	interleukin 21 receptor	31 (0.00)	36 (0.22)	0.59
11-14	Gp3	g.chr1:24447962G>T	Missense Mutation	IL22RA1	p.P353Q	interleukin 22 receptor,	39 (0.03)	163 (0.61)	1.62
11-14	Gp3	g.chr16:27374610C>T	Missense Mutation	IL4R	p.A646V	interleukin 4 receptor	28 (0.00)	40 (0.30)	0.80
11-14	Gp3	g.chr7:22767117C>A	Missense Mutation	IL6	p.A25D	interleukin 6	24 (0.00)	60 (0.13)	0.46
11-14	Gp3	g.chr2:121106712C>T	Silent	INHBB	p.F162F	inhibin, beta B	39 (0.03)	167 (0.32)	0.86
11-14	Gp3	g.chr12:57849948G>T	Missense Mutation	INHBE	p.A124S	inhibin, beta E	85 (0.00)	129 (0.38)	1.01
11-14	Gp3	g.chr4:143502111A>G	Intron	INPP4B		inositol polyphosphate-	37 (0.00)	275 (1.00)	2.66
11-14	Gp3	g.chr11:15197555C>T	Missense Mutation	INSC	p.R109C	inscuteable homolog (D	19 (0.00)	24 (0.46)	1.22
11-14	Gp3	g.chr19:7142839T>C	Missense Mutation	INSR	p.T844A	insulin receptor	76 (0.00)	157 (0.32)	0.85

11-14	Gp3	g.chr3:12977947G>T	Missense Mutation	IQSEC1	p.S204Y	IQ motif and Sec7 doma	22 (0.00)	13 (0.62)	1.64
11-14	Gp3	g.chr19:46388445G>T	Missense Mutation	IRF2BP1	p.F196L	interferon regulatory fac	19 (0.00)	322 (0.16)	0.41
11-14	Gp3	g.chr7:128588274G>T	Silent	IRF5	p.L381L	interferon regulatory fac	77 (0.00)	221 (0.73)	2.54
11-14	Gp3	g.chr2:227660476C>T	Silent	IRS1	p.Q993Q	insulin receptor substrat	67 (0.00)	244 (0.28)	0.74
11-14	Gp3	g.chr2:227660566G>T	Silent	IRS1	p.G963G	insulin receptor substrat	72 (0.00)	289 (0.47)	1.25
11-14	Gp3	g.chrX:107978383G>T	Missense Mutation	IRS4	p.R398S	insulin receptor substrat	20 (0.00)	77 (0.27)	0.45
11-14	Gp3	g.chr17:48155609C>T	Missense Mutation	ITGA3	p.T753I	integrin, alpha 3 (antige	24 (0.00)	58 (0.97)	2.57
11-14	Gp3	g.chr16:31341636C>G	Missense Mutation	ITGAM	p.S1024C	integrin, alpha M (comp	40 (0.00)	189 (0.29)	0.76
11-14	Gp3	g.chr3:52823714C>G	Missense Mutation	ITIH1	p.P722R	inter-alpha-trypsin inhib	17 (0.00)	91 (0.38)	1.03
11-14	Gp3	g.chr4:6082021G>A	Nonsense Mutation	JAKMIP1	p.Q374*	janus kinase and microt	54 (0.00)	134 (0.60)	1.61
11-14	Gp3	g.chr10:133978233G>A	Silent	JAKMIP3	p.E826E	Janus kinase and microt	69 (0.00)	225 (0.16)	0.43
11-14	Gp3	g.chr8:41845045G>T	Missense Mutation	KAT6A	p.L213I	K(lysine) acetyltransfera	56 (0.00)	27 (0.30)	0.79
11-14	Gp3	g.chr11:30034010G>C	Silent	KCNA4	p.T72T	potassium voltage-gated	36 (0.00)	135 (0.87)	2.31
11-14	Gp3	g.chr12:5153903C>T	Missense Mutation	KCNA5	p.A197V	potassium voltage-gated	21 (0.00)	340 (0.28)	0.75
11-14	Gp3	g.chrX:48825897C>T	Missense Mutation	KCND1	p.R261Q	potassium voltage-gated	21 (0.00)	46 (0.67)	1.12
11-14	Gp3	g.chr20:49626870G>A	Silent	KCNG1	p.T2T	potassium voltage-gated	20 (0.00)	22 (0.73)	1.94
11-14	Gp3	g.chr7:150656738C>A	Missense Mutation	KCNH2	p.V132L	potassium voltage-gated	32 (0.00)	86 (0.36)	1.26
11-14	Gp3	g.chr16:29918246G>T	Missense Mutation	KCTD13	p.H313N	potassium channel tetra	41 (0.02)	212 (0.33)	0.89
11-14	Gp3	g.chr5:141309205C>A	Silent	KIAA0141	p.L157L	KIAA0141	51 (0.00)	20 (0.45)	1.20
11-14	Gp3	g.chr17:73492444C>G	Silent	KIAA0195	p.A1045A	KIAA0195	26 (0.00)	200 (0.81)	2.16
11-14	Gp3	g.chr9:114246995C>T	Missense Mutation	KIAA0368	p.V11I	KIAA0368	165 (0.00)	240 (0.20)	0.52
11-14	Gp3	g.chr4:123252536G>A	Missense Mutation	KIAA1109	p.E3769K	KIAA1109	25 (0.00)	104 (0.77)	2.05
11-14	Gp3	g.chr2:61304264A>G	Missense Mutation	KIAA1841	p.E214G	KIAA1841	18 (0.00)	145 (0.34)	0.90
11-14	Gp3	g.chr17:43006314C>A	Missense Mutation	KIF18B	p.M532I	kinesin family member	28 (0.00)	34 (0.62)	1.65
11-14	Gp3	g.chr2:241700681C>G	Missense Mutation	KIF1A	p.E735Q	kinesin family member	42 (0.00)	219 (0.37)	1.48
11-14	Gp3	g.chr1:200965440G>T	Missense Mutation	KIF21B	p.L721M	kinesin family member	40 (0.00)	19 (0.42)	1.12
11-14	Gp3	g.chr9:34255750G>T	Silent	KIF24	p.P1285P	kinesin family member	64 (0.00)	17 (0.88)	2.35
11-14	Gp3	g.chr19:36351458G>T	Missense Mutation	KIRREL2	p.G273W	kin of IRRE like 2 (Dros	50 (0.00)	400 (0.19)	0.50
11-14	Gp3	g.chr1:6653517A>T	Missense Mutation	KLHL21	p.S568T	kelch-like family memb	30 (0.00)	147 (0.29)	0.78
11-14	Gp3	g.chr12:49425234T>C	Silent	KMT2D	p.E4418E	lysine (K)-specific meth	47 (0.00)	108 (0.19)	0.49
11-14	Gp3	g.chr12:49427988T>A	Silent	KMT2D	p.V3534V	lysine (K)-specific meth	129 (0.00)	12 (0.92)	2.44
11-14	Gp3	g.chr1:47016828G>A	Silent	KNCN	p.L20L	kinocilin	23 (0.00)	296 (0.36)	0.95
11-14	Gp3	g.chr10:135020245C>A	Missense Mutation	KNDC1	p.F1148L	kinase non-catalytic C-	75 (0.00)	180 (0.87)	2.33
11-14	Gp3	g.chr10:135027224A>G	Missense Mutation	KNDC1	p.I1507V	kinase non-catalytic C-	18 (0.00)	24 (0.29)	0.78
11-14	Gp3	g.chr13:50296631C>T	Missense Mutation	KPNA3	p.A180T	karyopherin alpha 3 (im	43 (0.00)	18 (0.89)	1.69

11-14	Gp3	g.chr17:39672182G>A	Silent	KRT15	p.R327R	keratin 15	40 (0.00)	27 (0.96)	2.57
11-14	Gp3	g.chr17:39619093G>A	Silent	KRT32	p.N402N	keratin 32	49 (0.00)	146 (0.29)	0.79
11-14	Gp3	g.chr17:39521473C>A	Missense Mutation	KRT33B	p.R277L	keratin 33B	43 (0.00)	103 (0.19)	0.52
11-14	Gp3	g.chr12:52566100G>A	Nonsense Mutation	KRT80	p.Q354*	keratin 80	18 (0.00)	54 (0.28)	0.74
11-14	Gp3	g.chr21:45994489G>A	Missense Mutation	KRTAP10-4	p.G285D	keratin associated protei	61 (0.00)	222 (0.14)	0.38
11-14	Gp3	g.chr21:46011829C>A	Silent	KRTAP10-6	p.V179V	keratin associated protei	45 (0.00)	232 (0.14)	0.38
11-14	Gp3	g.chr21:46047441C>T	Missense Mutation	KRTAP10-9	p.S118F	keratin associated protei	49 (0.00)	594 (0.16)	0.42
11-14	Gp3	g.chr21:46077992C>T	Silent	KRTAP12-3	p.S32S	keratin associated protei	63 (0.00)	337 (0.38)	1.00
11-14	Gp3	g.chr17:39296632G>A	Silent	KRTAP4-6	p.C36C	keratin associated protei	32 (0.00)	252 (0.20)	0.54
11-14	Gp3	g.chr11:1629496G>T	Nonsense Mutation	KRTAP5-3	p.C40*	keratin associated protei	95 (0.00)	274 (0.20)	0.53
11-14	Gp3	g.chr22:41621835G>C	Missense Mutation	L3MBTL2	p.G465A	l(3)mbt-like 2 (Drosoph	43 (0.00)	161 (0.53)	1.42
11-14	Gp3	g.chr20:60904102G>A	Silent	LAMA5	p.S1415S	laminin, alpha 5	89 (0.01)	433 (0.39)	1.05
11-14	Gp3	g.chr3:49159131G>A	Nonsense Mutation	LAMB2	p.Q1696*	laminin, beta 2 (laminin	97 (0.00)	293 (0.21)	0.56
11-14	Gp3	g.chr3:49159794G>C	Missense Mutation	LAMB2	p.A1528G	laminin, beta 2 (laminin	34 (0.00)	67 (0.28)	0.76
11-14	Gp3	g.chr9:133901723C>A	Missense Mutation	LAMC3	p.P142H	laminin, gamma 3	26 (0.00)	159 (0.27)	0.72
11-14	Gp3	g.chr9:133936508G>T	Missense Mutation	LAMC3	p.A749S	laminin, gamma 3	20 (0.00)	76 (0.50)	1.33
11-14	Gp3	g.chr1:32740402C>G	Missense Mutation	LCK	p.P57R	LCK proto-oncogene, S	42 (0.00)	49 (0.18)	0.49
11-14	Gp3	g.chr9:138415728G>A	Missense Mutation	LCN1	p.G99R	lipocalin 1	42 (0.00)	518 (0.39)	1.04
11-14	Gp3	g.chr9:138415792A>G	Missense Mutation	LCN1	p.E120G	lipocalin 1	54 (0.02)	354 (0.23)	0.63
11-14	Gp3	g.chr17:39967131G>T	Missense Mutation	LEPREL4	p.F257L	leprecan-like 4	20 (0.00)	58 (0.76)	2.02
11-14	Gp3	g.chr1:202287814G>T	Missense Mutation	LGR6	p.A795S	leucine-rich repeat conta	29 (0.00)	128 (0.23)	0.62
11-14	Gp3	g.chr19:54849721G>C	Missense Mutation	LILRA4	p.Q101E	leukocyte immunoglobu	28 (0.00)	179 (0.73)	1.94
11-14	Gp3	g.chr13:21894377G>C	lincRNA	LINC00539		long intergenic non-prot	25 (0.00)	45 (0.27)	0.71
11-14	Gp3	g.chr13:21894539G>C	lincRNA	LINC00539		long intergenic non-prot	36 (0.00)	108 (0.55)	1.46
11-14	Gp3	g.chr17:18145239C>A	Silent	LLGL1	p.S936S	lethal giant larvae homo	69 (0.00)	261 (0.43)	1.13
11-14	Gp3	g.chr17:73564664C>A	Missense Mutation	LLGL2	p.L382M	lethal giant larvae homo	20 (0.00)	102 (0.53)	1.41
11-14	Gp3	g.chr19:14266198G>C	Missense Mutation	LPHN1	p.F1094L	latrophilin 1	26 (0.00)	161 (0.31)	0.83
11-14	Gp3	g.chr3:197547272G>A	Missense Mutation	LRCH3	p.R204K	leucine-rich repeats and	44 (0.00)	12 (0.83)	2.70
11-14	Gp3	g.chr18:7231236C>G	Missense Mutation	LRRC30	p.L34V	leucine rich repeat conta	48 (0.00)	118 (0.65)	1.74
11-14	Gp3	g.chr18:7231261C>A	Missense Mutation	LRRC30	p.S42Y	leucine rich repeat conta	49 (0.00)	123 (0.34)	0.91
11-14	Gp3	g.chr18:7231658C>T	Silent	LRRC30	p.F174F	leucine rich repeat conta	124 (0.00)	136 (0.65)	1.73
11-14	Gp3	g.chr15:101605621G>T	Missense Mutation	LRRK1	p.G1660V	leucine-rich repeat kinas	49 (0.00)	100 (0.59)	1.57
11-14	Gp3	g.chr15:101605689G>T	Missense Mutation	LRRK1	p.D1683Y	leucine-rich repeat kinas	97 (0.01)	250 (0.44)	1.17
11-14	Gp3	g.chr7:102106649G>A	Missense Mutation	LRWD1	p.V122I	leucine-rich repeats and	40 (0.00)	252 (0.58)	2.01
11-14	Gp3	g.chr19:35739800G>T	Nonsense Mutation	LSR	p.G7*	lipolysis stimulated lipo	16 (0.00)	30 (0.43)	1.16

11-14	Gp3	g.chr8:20110644C>A	Silent	LZTS1	p.L266L	leucine zipper, putative	36 (0.00)	46 (0.48)	1.28
11-14	Gp3	g.chr8:20110830G>A	Silent	LZTS1	p.S204S	leucine zipper, putative	39 (0.03)	86 (0.29)	0.78
11-14	Gp3	g.chrX:140994185G>T	Missense Mutation	MAGEC1	p.G332V	melanoma antigen famil	18 (0.00)	41 (0.41)	0.69
11-14	Gp3	g.chr7:77660469A>T	Intron	MAGI2		membrane associated gu	63 (0.00)	25 (0.40)	1.07
11-14	Gp3	g.chr7:77763520G>T	Intron	MAGI2		membrane associated gu	35 (0.00)	14 (0.93)	2.48
11-14	Gp3	g.chr7:78627729C>A	Intron	MAGI2		membrane associated gu	22 (0.00)	39 (0.51)	1.37
11-14	Gp3	g.chr7:78708322C>A	Intron	MAGI2		membrane associated gu	77 (0.00)	206 (0.46)	1.23
11-14	Gp3	g.chr7:78754584A>G	Intron	MAGI2		membrane associated gu	40 (0.00)	55 (0.27)	0.73
11-14	Gp3	g.chr7:78997781C>T	Intron	MAGI2		membrane associated gu	75 (0.00)	317 (0.70)	2.29
11-14	Gp3	g.chr7:79020076C>T	Intron	MAGI2		membrane associated gu	94 (0.00)	42 (0.98)	3.21
11-14	Gp3	g.chr7:79040500T>A	Intron	MAGI2		membrane associated gu	83 (0.00)	40 (0.57)	1.89
11-14	Gp3	g.chr4:140640894C>A	Missense Mutation	MAML3	p.Q1000H	mastermind-like 3 (Dros	34 (0.00)	126 (0.77)	2.05
11-14	Gp3	g.chr9:140000636G>T	Silent	MAN1B1	p.L438L	mannosidase, alpha, cla	22 (0.00)	153 (0.16)	0.42
11-14	Gp3	g.chr18:48190830G>T	Missense Mutation	MAPK4	p.D168Y	mitogen-activated prote	142 (0.00)	111 (0.33)	0.89
11-14	Gp3	g.chr16:1793372G>A	Silent	MAPK8IP3	p.L213L	mitogen-activated prote	16 (0.00)	173 (0.25)	0.66
11-14	Gp3	g.chr19:45783647T>C	Missense Mutation	MARK4	p.M341T	MAP/microtubule affini	50 (0.00)	131 (0.33)	0.88
11-14	Gp3	g.chr1:46500535T>C	Silent	MAST2	p.R1398R	microtubule associated	73 (0.00)	24 (0.58)	1.56
11-14	Gp3	g.chr2:85769865G>T	Missense Mutation	MAT2A	p.V253F	methionine adenosyltra	36 (0.00)	34 (0.97)	2.59
11-14	Gp3	g.chr3:127325008G>T	Nonsense Mutation	MCM2	p.E241*	minichromosome maint	55 (0.00)	104 (0.14)	0.47
11-14	Gp3	g.chr17:60140614T>G	Missense Mutation	MED13	p.T39P	mediator complex subu	63 (0.00)	51 (0.90)	2.41
11-14	Gp3	g.chr22:20937154C>A	Missense Mutation	MED15	p.S439R	mediator complex subu	36 (0.00)	124 (0.20)	0.54
11-14	Gp3	g.chr15:90321545C>A	Missense Mutation	MESP2	p.R392S	mesoderm posterior bas	65 (0.02)	227 (0.15)	0.39
11-14	Gp3	g.chr3:196743199G>T	Missense Mutation	MFI2	p.S314R	antigen p97 (melanoma	20 (0.00)	49 (0.12)	0.40
11-14	Gp3	g.chr8:145736018C>T	Missense Mutation	MFSD3	p.R290C	major facilitator superfa	57 (0.00)	258 (0.22)	0.60
11-14	Gp3	g.chr12:53647517C>G	Missense Mutation	MFSD5	p.R300G	major facilitator superfa	20 (0.00)	47 (0.40)	1.08
11-14	Gp3	g.chr5:180218678C>T	Missense Mutation	MGAT1	p.A432T	mannosyl (alpha-1,3-)-g	38 (0.00)	85 (0.73)	1.95
11-14	Gp3	g.chr22:18301222G>T	Missense Mutation	MICAL3	p.P1402Q	microtubule associated	25 (0.00)	160 (0.25)	0.67
11-14	Gp3	g.chr17:4794800C>G	Missense Mutation	MINK1	p.P597R	misshapen-like kinase 1	15 (0.00)	16 (0.31)	0.83
11-14	Gp3	g.chr22:50925816C>T	Silent	MIOX	p.G6G	myo-inositol oxygenase	29 (0.00)	138 (0.49)	1.31
11-14	Gp3	g.chr3:37035084G>T	Missense Mutation	MLH1	p.V16L	mutL homolog 1	88 (0.01)	315 (0.32)	0.86
11-14	Gp3	g.chr9:20448178C>T	Silent	MLLT3	p.K121K	myeloid/lymphoid or mi	82 (0.00)	68 (0.62)	1.65
11-14	Gp3	g.chr6:168352430G>A	Missense Mutation	MLLT4	p.A1459T	myeloid/lymphoid or mi	55 (0.00)	446 (0.57)	1.53
11-14	Gp3	g.chr10:99218654G>A	Silent	MMS19	p.L990L	MMS19 nucleotide exci	105 (0.00)	19 (0.68)	1.82
11-14	Gp3	g.chr1:47078941C>A	Missense Mutation	MOB3C	p.R41L	MOB kinase activator 3	40 (0.00)	169 (0.80)	2.15
11-14	Gp3	g.chr19:4359211G>T	Nonsense Mutation	MPND	p.E430*	MPN domain containin	33 (0.00)	217 (0.17)	0.44

11-14	Gp3	g.chr2:17998115C>G	Silent	MSGN1	p.G110G	mesogenin 1	36 (0.00)	16 (0.56)	1.50
11-14	Gp3	g.chr1:76262715G>A	Silent	MSH4	p.A15A	mutS homolog 4	32 (0.00)	157 (0.68)	1.80
11-14	Gp3	g.chr17:55752373C>A	Missense Mutation	MSI2	p.N277K	musashi RNA-binding p	40 (0.00)	108 (0.73)	1.95
11-14	Gp3	g.chr3:49940121G>T	Missense Mutation	MST1R	p.R308S	macrophage stimulating	60 (0.00)	74 (0.20)	0.54
11-14	Gp3	g.chr14:105927226C>A	Missense Mutation	MTA1	p.A276D	metastasis associated 1	73 (0.00)	238 (0.42)	1.11
11-14	Gp3	g.chr1:11861447C>G	Silent	MTHFR	p.R82R	methylenetetrahydrofola	23 (0.00)	15 (0.93)	2.49
11-14	Gp3	g.chr4:187455628T>A	Missense Mutation	MTNR1A	p.N90Y	melatonin receptor 1A	94 (0.00)	95 (0.38)	1.01
11-14	Gp3	g.chr7:100682881A>G	Silent	MUC17	p.E2728E	mucin 17, cell surface a	112 (0.00)	153 (0.12)	0.41
11-14	Gp3	g.chr7:100683673G>T	Missense Mutation	MUC17	p.M2992I	mucin 17, cell surface a	116 (0.00)	330 (0.34)	1.17
11-14	Gp3	g.chr7:100683678T>C	Missense Mutation	MUC17	p.V2994A	mucin 17, cell surface a	117 (0.00)	337 (0.12)	0.41
11-14	Gp3	g.chr7:100683681G>T	Missense Mutation	MUC17	p.S2995I	mucin 17, cell surface a	118 (0.00)	344 (0.35)	1.22
11-14	Gp3	g.chr11:1094702A>T	Silent	MUC2	p.S1930S	mucin 2, oligomeric mu	47 (0.02)	418 (0.23)	0.63
11-14	Gp3	g.chr11:1094703G>T	Missense Mutation	MUC2	p.A1931S	mucin 2, oligomeric mu	49 (0.02)	418 (0.23)	0.61
11-14	Gp3	g.chr11:1261554G>T	Missense Mutation	MUC5B	p.A1307S	mucin 5B, oligomeric m	45 (0.02)	384 (0.39)	1.04
11-14	Gp3	g.chr11:1267970C>A	Missense Mutation	MUC5B	p.T3287N	mucin 5B, oligomeric m	93 (0.00)	536 (0.42)	1.11
11-14	Gp3	g.chr11:1269632C>G	Missense Mutation	MUC5B	p.A3841G	mucin 5B, oligomeric m	100 (0.00)	171 (0.21)	0.56
11-14	Gp3	g.chr11:1271682C>T	Silent	MUC5B	p.A4524A	mucin 5B, oligomeric m	134 (0.00)	149 (0.23)	0.61
11-14	Gp3	g.chr11:1025184G>T	Missense Mutation	MUC6	p.Q995K	mucin 6, oligomeric mu	31 (0.00)	130 (0.99)	2.65
11-14	Gp3	g.chr11:1025261C>G	Missense Mutation	MUC6	p.S969T	mucin 6, oligomeric mu	40 (0.03)	470 (0.34)	0.91
11-14	Gp3	g.chr17:4445915T>C	Missense Mutation	MYBBP1A	p.H1005R	MYB binding protein (	41 (0.00)	481 (0.20)	0.53
11-14	Gp3	g.chr17:4445930C>A	Missense Mutation	MYBBP1A	p.S1000I	MYB binding protein (	43 (0.00)	465 (0.16)	0.43
11-14	Gp3	g.chr17:4453572G>C	Missense Mutation	MYBBP1A	p.P367R	MYB binding protein (	47 (0.00)	416 (0.15)	0.41
11-14	Gp3	g.chr11:47360903T>C	Missense Mutation	MYBPC3	p.D707G	myosin binding protein	35 (0.00)	72 (0.21)	0.56
11-14	Gp3	g.chr16:15917212G>A	Silent	MYH11	p.Y134Y	myosin, heavy chain 11,	40 (0.00)	143 (0.69)	1.85
11-14	Gp3	g.chr17:10212649C>A	Nonsense Mutation	MYH13	p.E1691*	myosin, heavy chain 13,	19 (0.00)	187 (0.27)	0.71
11-14	Gp3	g.chr17:1381782A>C	Missense Mutation	MYO1C	p.V371G	myosin IC	20 (0.00)	289 (0.17)	0.45
11-14	Gp3	g.chr11:76892556T>C	Missense Mutation	MYO7A	p.M942T	myosin VIIA	24 (0.00)	43 (0.63)	1.67
11-14	Gp3	g.chr19:17212993G>A	Missense Mutation	MYO9B	p.E156K	myosin IXB	59 (0.00)	107 (0.87)	2.32
11-14	Gp3	g.chr1:203054786C>A	Nonsense Mutation	MYOG	p.E102*	myogenin (myogenic fa	34 (0.00)	142 (0.30)	0.79
11-14	Gp3	g.chr1:203054787G>A	Silent	MYOG	p.F101F	myogenin (myogenic fa	33 (0.00)	143 (0.29)	0.76
11-14	Gp3	g.chr1:203054811C>T	Silent	MYOG	p.R93R	myogenin (myogenic fa	17 (0.00)	114 (0.23)	0.61
11-14	Gp3	g.chr8:2040348G>C	Splice Site	MYOM2	p.R668T	myomesin 2	34 (0.00)	25 (0.92)	2.45
11-14	Gp3	g.chr9:130826001T>C	Missense Mutation	NAIF1	p.I230M	nuclear apoptosis induci	37 (0.00)	181 (0.15)	0.40
11-14	Gp3	g.chr1:201687605G>T	Missense Mutation	NAV1	p.W329C	neuron navigator 1	23 (0.00)	165 (0.15)	0.39
11-14	Gp3	g.chr13:35770326G>C	Silent	NBEA	p.V1748V	neurobeachin	142 (0.00)	14 (0.93)	1.77

11-14	Gp3	g.chr3:47039698G>A	Missense Mutation	NBEAL2	p.D1034N	neurobeachin-like 2	20 (0.00)	61 (0.18)	0.48
11-14	Gp3	g.chr20:44691488G>C	Silent	NCOA5	p.A397A	nuclear receptor coactiv	61 (0.00)	65 (0.18)	0.49
11-14	Gp3	g.chr11:67379384C>A	Missense Mutation	NDUFV1	p.A366D	NADH dehydrogenase (	16 (0.00)	79 (0.41)	1.08
11-14	Gp3	g.chr11:67379391C>A	Silent	NDUFV1	p.A368A	NADH dehydrogenase (	16 (0.00)	82 (0.20)	0.52
11-14	Gp3	g.chr8:24813106G>T	RNA	NEFL		neurofilament, light pol	72 (0.01)	464 (0.20)	0.54
11-14	Gp3	g.chr3:52773506C>T	Silent	NEK4	p.L700L	NIMA-related kinase 4	87 (0.00)	16 (0.50)	1.33
11-14	Gp3	g.chr4:1985168G>T	Missense Mutation	NELFA	p.L489M	negative elongation fact	78 (0.00)	52 (0.52)	1.38
11-14	Gp3	g.chr17:46136803C>A	Missense Mutation	NFE2L1	p.L696M	nuclear factor, erythroid	19 (0.00)	60 (0.17)	0.44
11-14	Gp3	g.chr6:44229470G>C	Missense Mutation	NFKBIE	p.A334G	nuclear factor of kappa	27 (0.00)	187 (0.14)	0.39
11-14	Gp3	g.chr2:233756155C>A	Missense Mutation	NGEF	p.E303D	neuronal guanine nucle	26 (0.00)	70 (0.21)	0.57
11-14	Gp3	g.chr20:25472010C>T	Missense Mutation	NINL	p.E488K	ninein-like	21 (0.00)	58 (0.29)	0.78
11-14	Gp3	g.chr19:54314343C>A	Missense Mutation	NLRP12	p.Q190H	NLR family, pyrin dom	28 (0.00)	134 (0.16)	0.42
11-14	Gp3	g.chr19:55451431G>A	Silent	NLRP7	p.V252V	NLR family, pyrin dom	38 (0.00)	30 (0.37)	0.98
11-14	Gp3	g.chr16:449402G>T	Missense Mutation	NME4	p.E83D	NME/NM23 nucleoside	86 (0.00)	202 (0.39)	1.03
11-14	Gp3	g.chr1:881901T>C	Missense Mutation	NOC2L	p.K562E	nucleolar complex asso	29 (0.00)	45 (0.16)	0.41
11-14	Gp3	g.chr16:50733425T>C	Missense Mutation	NOD2	p.F34L	nucleotide-binding olig	100 (0.00)	518 (0.16)	0.42
11-14	Gp3	g.chr16:50744876C>A	Missense Mutation	NOD2	p.H352N	nucleotide-binding olig	18 (0.00)	52 (0.19)	0.51
11-14	Gp3	g.chr5:175815530G>T	Missense Mutation	NOP16	p.A4D	NOP16 nucleolar prote	40 (0.00)	393 (0.15)	0.41
11-14	Gp3	g.chr19:36341975G>T	Silent	NPHS1	p.L138L	nephrosis 1, congenital,	25 (0.00)	14 (0.36)	0.95
11-14	Gp3	g.chr5:32712163C>G	Missense Mutation	NPR3	p.P94R	natriuretic peptide recep	27 (0.00)	178 (0.20)	0.54
11-14	Gp3	g.chr22:39222703G>T	Silent	NPTXR	p.I300I	neuronal pentraxin rece	20 (0.00)	119 (0.16)	0.43
11-14	Gp3	g.chr10:83635799C>A	Missense Mutation	NRG3	p.L235I	neuregulin 3	16 (0.00)	188 (0.78)	2.09
11-14	Gp3	g.chr2:206628456G>C	Silent	NRP2	p.R701R	neuropilin 2	36 (0.00)	90 (0.99)	2.64
11-14	Gp3	g.chr11:64416288G>T	Silent	NRXN2	p.A1067A	neurexin 2	25 (0.00)	165 (0.34)	0.91
11-14	Gp3	g.chr17:73126892A>G	Missense Mutation	NT5C	p.V136A	5', 3'-nucleotidase, cyto	101 (0.01)	368 (0.37)	0.99
11-14	Gp3	g.chr11:71724037C>A	Missense Mutation	NUMA1	p.E1504D	nuclear mitotic apparatu	44 (0.00)	113 (0.30)	0.80
11-14	Gp3	g.chr11:71724085C>G	Missense Mutation	NUMA1	p.E1488D	nuclear mitotic apparatu	67 (0.00)	151 (0.36)	0.95
11-14	Gp3	g.chr11:71724107G>A	Missense Mutation	NUMA1	p.A1481V	nuclear mitotic apparatu	104 (0.00)	465 (0.15)	0.40
11-14	Gp3	g.chr11:71725898G>T	Missense Mutation	NUMA1	p.A884E	nuclear mitotic apparatu	39 (0.00)	99 (0.57)	1.51
11-14	Gp3	g.chr3:13381426G>T	Silent	NUP210	p.I1133I	nucleoporin 210kDa	26 (0.00)	21 (0.71)	1.90
11-14	Gp3	g.chr9:134074179C>T	Silent	NUP214	p.S1766S	nucleoporin 214kDa	132 (0.00)	89 (0.22)	0.60
11-14	Gp3	g.chr19:50412855C>A	Missense Mutation	NUP62	p.Q70H	nucleoporin 62kDa	15 (0.00)	187 (0.18)	0.47
11-14	Gp3	g.chr10:88973937G>T	RNA	NUTM2A-AS1		NUTM2A antisense RN	31 (0.00)	101 (0.37)	0.98
11-14	Gp3	g.chr17:722742G>C	Missense Mutation	NXN	p.L253V	nucleoredoxin	37 (0.00)	103 (0.27)	0.72
11-14	Gp3	g.chr2:226446947A>G	Missense Mutation	NYAP2	p.K272E	neuronal tyrosine-phosp	46 (0.00)	304 (0.48)	1.28

11-14	Gp3	g.chr9:138440558G>A	Silent	OBP2A	p.R131R	odorant binding protein	15 (0.00)	103 (0.24)	0.65
11-14	Gp3	g.chr1:228467937G>T	Missense Mutation	OBSCN	p.W3003L	obscurin, cytoskeletal ca	27 (0.00)	37 (0.78)	1.45
11-14	Gp3	g.chr1:228558791C>G	Missense Mutation	OBSCN	p.P7728R	obscurin, cytoskeletal ca	21 (0.00)	52 (0.44)	0.82
11-14	Gp3	g.chr9:127561627G>T	Nonsense Mutation	OLFML2A	p.E176*	olfactomedin-like 2A	34 (0.00)	152 (0.18)	0.47
11-14	Gp3	g.chr9:125563187G>T	Missense Mutation	OR1K1	p.Q262H	olfactory receptor, famil	51 (0.00)	185 (0.39)	1.04
11-14	Gp3	g.chr1:248263582G>T	Missense Mutation	OR2L13	p.R302I	olfactory receptor, famil	35 (0.00)	25 (0.32)	0.85
11-14	Gp3	g.chr12:122079379T>A	Missense Mutation	ORAI1	p.F248I	ORAI calcium release-a	18 (0.00)	33 (0.18)	0.48
11-14	Gp3	g.chr2:26683876G>C	Missense Mutation	OTOF	p.N1852K	otoferlin	17 (0.00)	24 (0.54)	1.44
11-14	Gp3	g.chr2:42990470G>T	Missense Mutation	OXER1	p.L284M	oxoeicosanoid (OXE) re	17 (0.00)	89 (0.16)	0.42
11-14	Gp3	g.chr17:3806901C>T	Silent	P2RX1	p.E183E	purinergic receptor P2X	29 (0.00)	214 (0.17)	0.45
11-14	Gp3	g.chr17:79805203G>C	Missense Mutation	P4HB	p.N171K	prolyl 4-hydroxylase, be	43 (0.02)	140 (0.41)	1.33
11-14	Gp3	g.chr3:142681141G>T	Missense Mutation	PAQR9	p.F346L	progestin and adipoQ re	31 (0.00)	115 (0.45)	1.47
11-14	Gp3	g.chr3:142681367G>C	Missense Mutation	PAQR9	p.P271R	progestin and adipoQ re	59 (0.00)	470 (0.29)	0.94
11-14	Gp3	g.chr8:145059782C>A	Silent	PARP10	p.L157L	poly (ADP-ribose) poly	27 (0.00)	386 (0.22)	0.59
11-14	Gp3	g.chr3:51978520T>C	Missense Mutation	PARP3	p.F150L	poly (ADP-ribose) poly	176 (0.00)	200 (0.19)	0.51
11-14	Gp3	g.chr21:47330873G>T	Missense Mutation	PCBP3	p.A145S	poly(rC) binding protein	27 (0.00)	84 (0.37)	0.98
11-14	Gp3	g.chr3:51992148C>A	Missense Mutation	PCBP4	p.G315V	poly(rC) binding protein	67 (0.00)	320 (0.35)	0.93
11-14	Gp3	g.chr5:140248811C>G	Missense Mutation	PCDHA11	p.H41Q	protocadherin alpha 11	128 (0.00)	86 (0.20)	0.53
11-14	Gp3	g.chr5:140262261C>A	Missense Mutation	PCDHA13	p.S136R	protocadherin alpha 13	80 (0.00)	65 (0.20)	0.53
11-14	Gp3	g.chr5:140175836C>T	Silent	PCDHA2	p.D429D	protocadherin alpha 2	41 (0.00)	252 (0.44)	1.16
11-14	Gp3	g.chr5:140216220C>G	Missense Mutation	PCDHA7	p.S751C	protocadherin alpha 7	31 (0.00)	92 (0.26)	0.70
11-14	Gp3	g.chr5:140221074G>C	Silent	PCDHA8	p.L56L	protocadherin alpha 8	64 (0.00)	44 (0.16)	0.42
11-14	Gp3	g.chr5:140712533C>A	Missense Mutation	PCDHGA1	p.A761E	protocadherin gamma su	19 (0.00)	18 (0.78)	2.07
11-14	Gp3	g.chr5:140800953G>C	Silent	PCDHGA11	p.L53L	protocadherin gamma su	36 (0.00)	45 (0.87)	2.31
11-14	Gp3	g.chr5:140801248C>T	Nonsense Mutation	PCDHGA11	p.R152*	protocadherin gamma su	143 (0.00)	75 (0.96)	2.56
11-14	Gp3	g.chr5:140723623G>A	Missense Mutation	PCDHGA3	p.R8Q	protocadherin gamma su	97 (0.00)	26 (0.54)	1.44
11-14	Gp3	g.chr5:140856608C>T	Missense Mutation	PCDHGC3	p.R309W	protocadherin gamma su	49 (0.02)	61 (0.67)	1.79
11-14	Gp3	g.chr20:44575935T>A	Missense Mutation	PCIF1	p.F581I	PDX1 C-terminal inhibi	53 (0.00)	235 (0.21)	0.57
11-14	Gp3	g.chr7:94293399C>A	Silent	PEG10	p.G177G	paternally expressed 10	229 (0.00)	363 (0.50)	1.63
11-14	Gp3	g.chr22:30976063C>A	Silent	PES1	p.G243G	pescadillo ribosomal bio	24 (0.00)	176 (0.30)	0.80
11-14	Gp3	g.chr6:42934044G>C	Missense Mutation	PEX6	p.P746A	peroxisomal biogenesis	18 (0.00)	45 (0.27)	0.71
11-14	Gp3	g.chr15:99512855G>T	Missense Mutation	PGPEP1L	p.T3N	pyroglutamyl-peptidase	39 (0.03)	77 (0.30)	0.80
11-14	Gp3	g.chr11:607080C>A	Missense Mutation	PHRF1	p.Q541K	PHD and ring finger do	58 (0.00)	343 (0.77)	2.04
11-14	Gp3	g.chr11:609393A>G	Missense Mutation	PHRF1	p.S1312G	PHD and ring finger do	19 (0.00)	116 (0.25)	0.67
11-14	Gp3	g.chr1:9775634C>G	Missense Mutation	PIK3CD	p.F59L	phosphatidylinositol-4,5	15 (0.00)	179 (0.18)	0.48

11-14	Gp3	g.chr1:9777032C>A	Missense Mutation	PIK3CD	p.L266M	phosphatidylinositol-4,5	51 (0.00)	238 (0.21)	0.55
11-14	Gp3	g.chr7:106508234G>A	Silent	PIK3CG	p.L76L	phosphatidylinositol-4,5	22 (0.00)	93 (0.12)	0.41
11-14	Gp3	g.chr8:10623292A>G	Silent	PINX1	p.I202I	PIN2/TERF1 interactin	272 (0.00)	54 (0.20)	0.54
11-14	Gp3	g.chr17:6368073G>A	Missense Mutation	PITPNM3	p.R637W	PITPNM family membe	61 (0.00)	51 (0.71)	1.88
11-14	Gp3	g.chr4:111542488C>G	Silent	PITX2	p.V81V	paired-like homeodomai	17 (0.00)	40 (0.38)	1.00
11-14	Gp3	g.chr16:2153463C>A	Silent	PKD1	p.R2865R	polycystic kidney diseas	19 (0.00)	149 (0.46)	1.22
11-14	Gp3	g.chr15:72492954G>T	Silent	PKM	p.I450I	pyruvate kinase, muscle	25 (0.00)	71 (0.59)	1.58
11-14	Gp3	g.chr12:33031142G>T	Silent	PKP2	p.G224G	plakophilin 2	27 (0.00)	59 (0.19)	0.50
11-14	Gp3	g.chr22:31536299C>G	Silent	PLA2G3	p.L14L	phospholipase A2, grou	40 (0.00)	452 (0.18)	0.47
11-14	Gp3	g.chr19:48588365T>A	Missense Mutation	PLA2G4C	p.L275F	phospholipase A2, grou	16 (0.00)	101 (0.15)	0.40
11-14	Gp3	g.chr15:42363994C>A	Missense Mutation	PLA2G4D	p.E517D	phospholipase A2, grou	54 (0.00)	147 (0.18)	0.49
11-14	Gp3	g.chr15:42375431C>A	Missense Mutation	PLA2G4D	p.A213S	phospholipase A2, grou	28 (0.00)	54 (0.44)	1.19
11-14	Gp3	g.chr15:42438097C>T	Nonsense Mutation	PLA2G4F	p.W513*	phospholipase A2, grou	54 (0.00)	102 (0.18)	0.47
11-14	Gp3	g.chr19:40882517T>A	Splice Site	PLD3	p.F341I	phospholipase D family,	64 (0.02)	293 (0.38)	1.02
11-14	Gp3	g.chr14:65208320G>A	Silent	PLEKHG3	p.V695V	pleckstrin homology do	70 (0.00)	182 (0.23)	0.60
11-14	Gp3	g.chr5:169633C>A	Missense Mutation	PLEKHG4B	p.Q863K	pleckstrin homology do	65 (0.00)	92 (0.14)	0.38
11-14	Gp3	g.chr1:16059185C>A	Missense Mutation	PLEKHM2	p.L962M	pleckstrin homology do	44 (0.02)	214 (0.44)	1.17
11-14	Gp3	g.chr19:4511850C>A	Missense Mutation	PLIN4	p.V694L	perilipin 4	178 (0.00)	81 (0.20)	0.53
11-14	Gp3	g.chr3:126736316G>A	Missense Mutation	PLXNA1	p.V1109M	plexin A1	46 (0.00)	485 (0.19)	0.63
11-14	Gp3	g.chr3:48464992C>G	Silent	PLXNB1	p.R343R	plexin B1	28 (0.00)	186 (0.17)	0.44
11-14	Gp3	g.chr3:48465045G>T	Missense Mutation	PLXNB1	p.L326M	plexin B1	23 (0.00)	165 (0.24)	0.63
11-14	Gp3	g.chr1:53542922C>T	Silent	PODN	p.N262N	podocan	106 (0.00)	856 (0.24)	0.64
11-14	Gp3	g.chr21:46703416C>T	Missense Mutation	POFUT2	p.V137I	protein O-fucosyltransf	218 (0.00)	649 (0.33)	0.88
11-14	Gp3	g.chr8:22105997C>G	Missense Mutation	POLR3D	p.L164V	polymerase (RNA) III (	44 (0.00)	130 (0.80)	2.13
11-14	Gp3	g.chr16:22319488C>T	Missense Mutation	POLR3E	p.S36L	polymerase (RNA) III (	46 (0.02)	42 (0.33)	0.89
11-14	Gp3	g.chr7:75051269G>A	Missense Mutation	POM121C	p.P756S	POM121 transmembran	23 (0.00)	107 (0.30)	0.80
11-14	Gp3	g.chr22:21481051G>A	Missense Mutation	POM121L7	p.S292F	POM121 transmembran	67 (0.00)	126 (0.98)	2.60
11-14	Gp3	g.chr3:43122784G>T	Missense Mutation	POMGNT2	p.P47Q	protein O-linked manno	48 (0.02)	362 (0.18)	0.47
11-14	Gp3	g.chr5:149215908A>G	Silent	PPARGC1B	p.K630K	peroxisome proliferator-	50 (0.00)	43 (0.77)	2.05
11-14	Gp3	g.chr11:70208236T>C	Missense Mutation	PPFIA1	p.L873S	protein tyrosine phospha	107 (0.00)	43 (0.40)	1.05
11-14	Gp3	g.chr6:42974758G>T	Silent	PPP2R5D	p.V144V	protein phosphatase 2, r	47 (0.00)	48 (0.15)	0.39
11-14	Gp3	g.chr18:9550331G>C	Missense Mutation	PPP4R1	p.A786G	protein phosphatase 4, r	78 (0.00)	144 (0.85)	2.28
11-14	Gp3	g.chr10:103906794G>A	Missense Mutation	PPRC1	p.A1349T	peroxisome proliferator-	15 (0.00)	68 (0.22)	0.59
11-14	Gp3	g.chr6:106553356C>A	Missense Mutation	PRDM1	p.P405T	PR domain containing 1	21 (0.00)	39 (0.23)	0.62
11-14	Gp3	g.chr9:133542084A>G	Missense Mutation	PRDM12	p.K105E	PR domain containing 1	18 (0.00)	22 (0.73)	1.94

11-14	Gp3	g.chr21:43241425C>T	Silent	PRDM15	p.Q723Q	PR domain containing 1	100 (0.00)	345 (0.32)	0.84
11-14	Gp3	g.chr21:43241499G>T	Missense Mutation	PRDM15	p.R699S	PR domain containing 1	135 (0.00)	437 (0.36)	0.95
11-14	Gp3	g.chr21:43242364C>G	Missense Mutation	PRDM15	p.R634S	PR domain containing 1	88 (0.00)	283 (0.19)	0.50
11-14	Gp3	g.chr1:186277659G>A	Silent	PRG4	p.K936K	proteoglycan 4	183 (0.00)	358 (0.28)	0.76
11-14	Gp3	g.chr2:219694842C>G	Missense Mutation	PRKAG3	p.Q164H	protein kinase, AMP-ac	45 (0.00)	290 (0.29)	0.77
11-14	Gp3	g.chr17:1554983C>A	Missense Mutation	PRPF8	p.V2157L	pre-mRNA processing f	195 (0.00)	73 (0.85)	2.26
11-14	Gp3	g.chr16:855666C>A	Missense Mutation	PRR25	p.S75Y	proline rich 25	22 (0.00)	175 (0.19)	0.52
11-14	Gp3	g.chr10:696969G>A	Silent	PRR26	p.L154L	proline rich 26	30 (0.00)	41 (0.32)	0.85
11-14	Gp3	g.chr9:134357757G>A	Splice Site	PRRC2B		proline-rich coiled-coil	65 (0.00)	275 (0.52)	1.40
11-14	Gp3	g.chr16:67943307C>T	Missense Mutation	PSKH1	p.L219F	protein serine kinase H1	15 (0.00)	67 (0.25)	0.68
11-14	Gp3	g.chr7:103007874G>A	Missense Mutation	PSMC2	p.D287N	proteasome (prosome, m	31 (0.00)	72 (0.35)	1.21
11-14	Gp3	g.chr11:479126C>A	Missense Mutation	PTDSS2	p.L137M	phosphatidylserine synt	81 (0.00)	226 (0.20)	0.53
11-14	Gp3	g.chr11:486948G>T	Missense Mutation	PTDSS2	p.D149Y	phosphatidylserine synt	19 (0.00)	123 (0.22)	0.59
11-14	Gp3	g.chr10:89721169G>T	Intron	PTEN		phosphatase and tensin	38 (0.00)	42 (0.50)	1.33
11-14	Gp3	g.chr3:46940207C>A	Missense Mutation	PTH1R	p.L232M	parathyroid hormone 1 r	17 (0.00)	175 (0.16)	0.43
11-14	Gp3	g.chr6:43098046G>T	Silent	PTK7	p.R183R	protein tyrosine kinase 7	27 (0.00)	103 (0.19)	0.52
11-14	Gp3	g.chr19:50357730G>C	Missense Mutation	PTOV1	p.G80A	prostate tumor overexpr	24 (0.00)	164 (0.38)	1.01
11-14	Gp3	g.chr4:87685868A>G	Missense Mutation	PTPN13	p.I1380M	protein tyrosine phospha	44 (0.00)	15 (0.53)	1.42
11-14	Gp3	g.chr1:214556782G>T	Missense Mutation	PTPN14	p.P806T	protein tyrosine phospha	21 (0.00)	181 (0.97)	2.59
11-14	Gp3	g.chr14:88946502C>A	Missense Mutation	PTPN21	p.D425Y	protein tyrosine phospha	31 (0.00)	15 (0.93)	2.49
11-14	Gp3	g.chr11:18762158C>A	Nonsense Mutation	PTPN5	p.E279*	protein tyrosine phospha	117 (0.00)	97 (0.19)	0.49
11-14	Gp3	g.chr12:70964938G>T	Missense Mutation	PTPRB	p.P992T	protein tyrosine phospha	60 (0.02)	345 (0.28)	0.75
11-14	Gp3	g.chr1:44085163C>G	Silent	PTPRF	p.A1608A	protein tyrosine phospha	28 (0.00)	17 (0.47)	1.25
11-14	Gp3	g.chr2:25016153G>T	Silent	PTRHD1	p.R32R	peptidyl-tRNA hydrolas	38 (0.00)	28 (0.68)	1.81
11-14	Gp3	g.chr3:49095262G>T	Missense Mutation	QRICH1	p.T124N	glutamine-rich 1	36 (0.00)	193 (0.45)	1.20
11-14	Gp3	g.chr19:10822865C>A	Missense Mutation	QTRT1	p.F225L	queuine tRNA-ribosyltr	20 (0.00)	130 (0.17)	0.45
11-14	Gp3	g.chr2:238486800T>C	Splice Site	RAB17		RAB17, member RAS c	36 (0.00)	37 (0.27)	0.72
11-14	Gp3	g.chr3:51697005T>C	Missense Mutation	RAD54L2	p.S1325P	RAD54-like 2 (S. cerevi	112 (0.00)	29 (0.90)	2.39
11-14	Gp3	g.chr17:17700952C>T	Nonsense Mutation	RAI1	p.Q1564*	retinoic acid induced 1	51 (0.02)	323 (0.26)	0.69
11-14	Gp3	g.chrX:17819373G>T	Missense Mutation	RAI2	p.P253H	retinoic acid induced 2	37 (0.00)	105 (0.26)	0.43
11-14	Gp3	g.chr9:129928399G>T	Missense Mutation	RALGPS1	p.G221V	Ral GEF with PH doma	43 (0.00)	27 (0.81)	2.17
11-14	Gp3	g.chr7:44076343G>A	RNA	RASA4CP		RAS p21 protein activat	33 (0.00)	37 (0.59)	2.04
11-14	Gp3	g.chr10:43697339C>T	Missense Mutation	RASGEF1A	p.E134K	RasGEF domain family,	19 (0.00)	75 (0.61)	1.64
11-14	Gp3	g.chr17:34068216G>C	Silent	RASL10B	p.L168L	RAS-like, family 10, me	16 (0.00)	45 (0.18)	0.47
11-14	Gp3	g.chr13:48892938G>A	Intron	RB1		retinoblastoma 1	21 (0.00)	172 (0.63)	1.21

11-14	Gp3	g.chr1:110882754C>G	Missense Mutation	RBM15	p.R243G	RNA binding motif prot	19 (0.00)	144 (0.21)	0.56
11-14	Gp3	g.chr7:155556590C>T	Missense Mutation	RBM33	p.R1022C	RNA binding motif prot	23 (0.00)	173 (0.24)	0.85
11-14	Gp3	g.chr11:66612699T>A	Missense Mutation	RCE1	p.L228M	Ras converting CAAX	18 (0.00)	50 (0.58)	1.55
11-14	Gp3	g.chr11:66612701G>A	Silent	RCE1	p.L228L	Ras converting CAAX	16 (0.00)	50 (0.18)	0.48
11-14	Gp3	g.chr11:63681758G>T	Missense Mutation	RCOR2	p.P217H	REST corepressor 2	29 (0.00)	52 (0.40)	1.08
11-14	Gp3	g.chr14:24648636C>A	Missense Mutation	REC8	p.S428Y	REC8 meiotic recombin	91 (0.00)	79 (0.89)	2.36
11-14	Gp3	g.chr17:73659025G>A	Missense Mutation	RECQL5	p.S102L	RecQ protein-like 5	59 (0.00)	45 (0.89)	2.37
11-14	Gp3	g.chr10:43612116G>C	Missense Mutation	RET	p.A741P	ret proto-oncogene	132 (0.00)	196 (0.84)	2.23
11-14	Gp3	g.chr2:108478115C>G	Missense Mutation	RGPD4	p.C708W	RANBP2-like and GRI	152 (0.00)	17 (0.41)	1.10
11-14	Gp3	g.chr4:3319338G>T	Nonsense Mutation	RGS12	p.E481*	regulator of G-protein si	25 (0.00)	54 (0.22)	0.59
11-14	Gp3	g.chr4:3432202G>T	Nonsense Mutation	RGS12	p.E1212*	regulator of G-protein si	66 (0.00)	79 (0.18)	0.47
11-14	Gp3	g.chr9:116260312G>A	Silent	RGS3	p.L283L	regulator of G-protein si	25 (0.00)	30 (0.83)	2.22
11-14	Gp3	g.chr16:108450C>T	Silent	RHBDF1	p.V819V	rhomboid 5 homolog 1 (	104 (0.00)	46 (0.50)	1.33
11-14	Gp3	g.chr16:108452C>A	Missense Mutation	RHBDF1	p.V819L	rhomboid 5 homolog 1 (	105 (0.00)	44 (0.23)	0.61
11-14	Gp3	g.chr17:30647985G>C	Missense Mutation	RHBDL3	p.E220Q	rhomboid, veinlet-like 3	17 (0.00)	184 (0.24)	0.65
11-14	Gp3	g.chr15:41165686C>A	Missense Mutation	RHOV	p.R94L	ras homolog family mer	34 (0.00)	196 (0.28)	0.73
11-14	Gp3	g.chr19:39361561C>A	Missense Mutation	RINL	p.G225W	Ras and Rab interactor-l	25 (0.00)	377 (0.16)	0.42
11-14	Gp3	g.chr6:7404673G>T	Missense Mutation	RIOK1	p.V293F	RIO kinase 1	48 (0.00)	36 (0.19)	0.52
11-14	Gp3	g.chr15:89760355G>T	Silent	RLBP1	p.L114L	retinaldehyde binding p	17 (0.00)	103 (0.28)	0.75
11-14	Gp3	g.chr16:67679928G>T	Missense Mutation	RLTPR	p.C65F	RGD motif, leucine rich	24 (0.00)	280 (0.27)	0.72
11-14	Gp3	g.chr5:177570950G>T	Missense Mutation	RMND5B	p.V179F	required for meiotic nuc	76 (0.00)	146 (0.17)	0.46
11-14	Gp3	g.chr3:49735335C>G	Missense Mutation	RNF123	p.N120K	ring finger protein 123	101 (0.00)	21 (0.76)	2.03
11-14	Gp3	g.chr3:49739767G>A	Splice Site	RNF123	p.G520S	ring finger protein 123	44 (0.00)	51 (0.35)	0.94
11-14	Gp3	g.chr17:4848020C>A	Missense Mutation	RNF167	p.S254R	ring finger protein 167	24 (0.00)	215 (0.65)	1.74
11-14	Gp3	g.chr5:34183037G>T	RNA	RP11-1023L17.1			346 (0.00)	118 (0.41)	1.08
11-14	Gp3	g.chr4:89208850G>T	lincRNA	RP11-10L7.1			21 (0.00)	107 (0.17)	0.45
11-14	Gp3	g.chr16:12027568C>T	Splice Site	RP11-166B2.1	p.G98G		163 (0.00)	254 (0.66)	1.76
11-14	Gp3	g.chr16:2546436T>C	Missense Mutation	RP11-20I23.1	p.V96A		18 (0.00)	138 (0.24)	0.64
11-14	Gp3	g.chr16:2546535C>T	Missense Mutation	RP11-20I23.1	p.S129F		16 (0.00)	81 (0.72)	1.91
11-14	Gp3	g.chr6:73935024G>A	Missense Mutation	RP11-257K9.8	p.S139F		32 (0.00)	293 (0.29)	0.76
11-14	Gp3	g.chr1:149673394G>A	lincRNA	RP11-353N4.4			15 (0.00)	27 (0.52)	1.38
11-14	Gp3	g.chr12:13174454G>A	lincRNA	RP11-377D9.3			124 (0.00)	345 (0.14)	0.39
11-14	Gp3	g.chr10:52419547C>A	RNA	RP11-564C4.6			61 (0.02)	444 (0.42)	1.13
11-14	Gp3	g.chr1:89122750G>T	RNA	RP11-76N22.2			16 (0.00)	131 (0.24)	0.65
11-14	Gp3	g.chr8:37593816G>A	Missense Mutation	RP11-863K10.	p.S67F		87 (0.00)	69 (0.17)	0.46

11-14	Gp3	g.chr16:72762960C>G	RNA	RP5-991G20.1			133 (0.00)	45 (0.16)	0.41
11-14	Gp3	g.chr11:8704792G>T	Missense Mutation	RPL27A	p.S16I	ribosomal protein L27a	90 (0.00)	338 (0.25)	0.65
11-14	Gp3	g.chr1:150418846C>A	Missense Mutation	RPRD2	p.A280E	regulation of nuclear pr	153 (0.00)	99 (0.30)	0.81
11-14	Gp3	g.chr3:51968675G>C	Silent	RRP9	p.A384A	ribosomal RNA process	22 (0.00)	336 (0.19)	0.52
11-14	Gp3	g.chr20:948736G>T	Nonsense Mutation	RSPO4	p.S42*	R-spondin 4	19 (0.00)	34 (0.21)	0.55
11-14	Gp3	g.chr14:101349253C>T	Missense Mutation	RTL1	p.E625K	retrotransposon-like 1	53 (0.00)	12 (0.83)	2.22
11-14	Gp3	g.chr3:186917726G>T	Silent	RTP1	p.A220A	receptor (chemosensory	42 (0.00)	366 (0.19)	0.61
11-14	Gp3	g.chr17:42393753G>C	Splice Site	RUNDC3A	p.L318L	RUN domain containin	16 (0.00)	128 (0.38)	1.00
11-14	Gp3	g.chr19:39052052C>T	Silent	RYR1	p.F4194F	ryanodine receptor 1 (sk	17 (0.00)	114 (0.41)	1.10
11-14	Gp3	g.chr19:39868342C>A	Missense Mutation	SAMD4B	p.P441H	sterile alpha motif doma	22 (0.00)	173 (0.18)	0.48
11-14	Gp3	g.chr11:65732567G>A	Silent	SART1	p.A144A	squamous cell carcinom	18 (0.00)	120 (0.72)	1.91
11-14	Gp3	g.chr11:65744512G>T	Missense Mutation	SART1	p.D629Y	squamous cell carcinom	18 (0.00)	235 (0.27)	0.73
11-14	Gp3	g.chr8:27528493G>A	Silent	SCARA3	p.P482P	scavenger receptor class	15 (0.00)	62 (0.21)	0.56
11-14	Gp3	g.chr4:54231978C>T	Missense Mutation	SCFD2	p.R44H	sec1 family domain con	37 (0.00)	100 (0.80)	2.13
11-14	Gp3	g.chr19:35530043C>A	Silent	SCN1B	p.I157I	sodium channel, voltage	91 (0.00)	38 (0.71)	1.89
11-14	Gp3	g.chr17:62018666A>G	Missense Mutation	SCN4A	p.I1659T	sodium channel, voltage	94 (0.00)	172 (0.38)	1.01
11-14	Gp3	g.chr17:71394514C>G	Missense Mutation	SDK2	p.E1050Q	sidekick cell adhesion	24 (0.00)	58 (0.16)	0.41
11-14	Gp3	g.chr12:113835115C>G	Missense Mutation	SDS	p.G170R	serine dehydratase	17 (0.00)	67 (0.40)	1.07
11-14	Gp3	g.chr9:139368735C>G	Missense Mutation	SEC16A	p.Q933H	SEC16 homolog A (S. c	41 (0.00)	72 (0.71)	1.89
11-14	Gp3	g.chr1:177906422G>T	Silent	SEC16B	p.G810G	SEC16 homolog B (S. c	21 (0.00)	180 (0.62)	1.66
11-14	Gp3	g.chr3:50222909C>T	Missense Mutation	SEMA3F	p.P497L	sema domain, immunog	15 (0.00)	25 (0.28)	0.75
11-14	Gp3	g.chr19:4550167G>T	Silent	SEMA6B	p.G413G	sema domain, transmem	19 (0.00)	91 (0.20)	0.53
11-14	Gp3	g.chr17:75488708C>T	Silent	SEPT9	p.T455T	septin 9	23 (0.00)	89 (0.16)	0.42
11-14	Gp3	g.chr18:61390658G>T	RNA	SERPINB11		serpin peptidase inhibit	59 (0.00)	33 (0.70)	2.22
11-14	Gp3	g.chr2:235950150G>C	Missense Mutation	SH3BP4	p.S246T	SH3-domain binding pr	140 (0.00)	260 (0.30)	0.79
11-14	Gp3	g.chr10:105362335C>A	Silent	SH3PXD2A	p.V880V	SH3 and PX domains 2	15 (0.00)	10 (0.60)	1.60
11-14	Gp3	g.chr4:8242567T>C	Missense Mutation	SH3TC1	p.F1299S	SH3 domain and tetratri	20 (0.00)	97 (0.16)	0.44
11-14	Gp3	g.chr5:148407269A>G	Silent	SH3TC2	p.L669L	SH3 domain and tetratri	92 (0.00)	149 (0.21)	0.55
11-14	Gp3	g.chr1:154473961G>T	Missense Mutation	SHE	p.S181Y	Src homology 2 domain	56 (0.00)	62 (0.32)	0.58
11-14	Gp3	g.chr4:42403309C>A	Silent	SHISA3	p.G186G	shisa family member 3	25 (0.00)	220 (0.28)	0.74
11-14	Gp3	g.chr19:41096635G>C	Splice Site	SHKBP1		SH3KBP1 binding prot	55 (0.00)	68 (0.31)	0.82
11-14	Gp3	g.chr19:41096714C>A	Nonsense Mutation	SHKBP1	p.S616*	SH3KBP1 binding prot	16 (0.00)	101 (0.35)	0.92
11-14	Gp3	g.chr17:3514214C>A	Silent	SHPK	p.V359V	sedoheptulokinase	40 (0.00)	18 (0.50)	1.33
11-14	Gp3	g.chr19:16962273C>G	Missense Mutation	SIN3B	p.H259Q	SIN3 transcription regul	64 (0.02)	399 (0.33)	0.88
11-14	Gp3	g.chr17:79870413C>A	Missense Mutation	SIRT7	p.C361F	sirtuin 7	18 (0.00)	338 (0.26)	0.86

11-14	Gp3	g.chr5:1076888C>A	Missense Mutation	SLC12A7	p.A557S	solute carrier family 12	18 (0.00)	41 (0.34)	0.91
11-14	Gp3	g.chr7:100457779C>G	Missense Mutation	SLC12A9	p.I381M	solute carrier family 12,	71 (0.00)	217 (0.35)	1.17
11-14	Gp3	g.chr17:26824189C>T	Missense Mutation	SLC13A2	p.P561S	solute carrier family 13	27 (0.00)	215 (0.26)	0.68
11-14	Gp3	g.chr11:2943341G>A	Missense Mutation	SLC22A18	p.G292S	solute carrier family 22,	49 (0.00)	37 (0.97)	2.59
11-14	Gp3	g.chr8:23429152C>T	Silent	SLC25A37	p.N267N	solute carrier family 25	58 (0.00)	83 (0.16)	0.42
11-14	Gp3	g.chr3:48667590C>A	Splice Site	SLC26A6	p.A407S	solute carrier family 26	16 (0.00)	212 (0.15)	0.39
11-14	Gp3	g.chr3:48667591C>G	Splice Site	SLC26A6		solute carrier family 26	16 (0.00)	213 (0.14)	0.38
11-14	Gp3	g.chr19:59011980T>C	Missense Mutation	SLC27A5	p.I426V	solute carrier family 27	20 (0.00)	49 (0.37)	0.98
11-14	Gp3	g.chr10:73121911C>G	Missense Mutation	SLC29A3	p.A325G	solute carrier family 29	40 (0.00)	190 (0.48)	1.29
11-14	Gp3	g.chr5:139947295C>A	Missense Mutation	SLC35A4	p.P181T	solute carrier family 35,	38 (0.03)	233 (0.30)	0.55
11-14	Gp3	g.chr11:45832618T>C	Missense Mutation	SLC35C1	p.F276S	solute carrier family 35	26 (0.00)	52 (0.40)	1.08
11-14	Gp3	g.chr11:124955510C>A	Silent	SLC37A2	p.S455S	solute carrier family 37	56 (0.02)	190 (0.15)	0.39
11-14	Gp3	g.chr3:50255313G>T	RNA	SLC38A3		solute carrier family 38,	66 (0.00)	22 (0.64)	1.70
11-14	Gp3	g.chr3:50256283C>G	RNA	SLC38A3		solute carrier family 38,	37 (0.00)	224 (0.59)	1.58
11-14	Gp3	g.chr12:56630717G>C	Missense Mutation	SLC39A5	p.A404P	solute carrier family 39	157 (0.00)	225 (0.79)	2.10
11-14	Gp3	g.chr16:24902315C>A	Missense Mutation	SLC5A11	p.P264T	solute carrier family 5 (	69 (0.00)	272 (0.36)	0.97
11-14	Gp3	g.chr1:110709596G>T	Missense Mutation	SLC6A17	p.E15D	solute carrier family 6 (	45 (0.00)	96 (0.36)	0.97
11-14	Gp3	g.chr14:70512917G>T	Missense Mutation	SLC8A3	p.A215D	solute carrier family 8 (	15 (0.00)	51 (0.84)	2.25
11-14	Gp3	g.chr1:27426933G>T	Silent	SLC9A1	p.S771S	solute carrier family 9,	16 (0.00)	111 (0.44)	1.18
11-14	Gp3	g.chr16:3632507G>T	Missense Mutation	SLX4	p.L1781M	SLX4 structure-specific	33 (0.00)	61 (0.69)	1.84
11-14	Gp3	g.chr15:67479802G>T	Missense Mutation	SMAD3	p.C326F	SMAD family member	141 (0.01)	43 (0.33)	0.87
11-14	Gp3	g.chr19:11106910C>T	Missense Mutation	SMARCA4	p.R539C	SWI/SNF related, matri	43 (0.00)	223 (0.17)	0.45
11-14	Gp3	g.chr16:88747567C>A	Missense Mutation	SNAI3	p.C211F	snail family zinc finger	53 (0.00)	172 (0.42)	1.13
11-14	Gp3	g.chr15:25455076G>A	RNA	SNHG14		small nucleolar RNA ho	36 (0.00)	36 (0.39)	1.04
11-14	Gp3	g.chr11:64803092C>A	Silent	SNX15	p.L207L	sorting nexin 15	83 (0.00)	128 (0.25)	0.67
11-14	Gp3	g.chr5:53814508C>A	Silent	SNX18	p.A242A	sorting nexin 18	26 (0.00)	41 (0.37)	0.98
11-14	Gp3	g.chr5:53814545G>A	Missense Mutation	SNX18	p.G255R	sorting nexin 18	20 (0.00)	56 (0.71)	1.90
11-14	Gp3	g.chr18:8825449C>G	Missense Mutation	SOGA2	p.S1633C		29 (0.00)	258 (0.34)	0.92
11-14	Gp3	g.chr18:8825502G>A	Missense Mutation	SOGA2	p.E1651K		31 (0.00)	361 (0.34)	0.89
11-14	Gp3	g.chr21:34922577C>A	Missense Mutation	SON	p.P347Q	SON DNA binding prot	19 (0.00)	70 (0.19)	0.50
11-14	Gp3	g.chr12:53722238A>T	Missense Mutation	SP7	p.F312I	Sp7 transcription factor	40 (0.00)	170 (0.61)	1.62
11-14	Gp3	g.chr12:53722299C>A	Silent	SP7	p.S291S	Sp7 transcription factor	40 (0.00)	156 (0.56)	1.49
11-14	Gp3	g.chr2:214794748G>A	Missense Mutation	SPAG16	p.D427N	sperm associated antige	96 (0.01)	69 (0.14)	0.39
11-14	Gp3	g.chr17:48625735A>T	Missense Mutation	SPATA20	p.T73S	spermatogenesis associa	34 (0.00)	104 (0.26)	0.69
11-14	Gp3	g.chr17:48625795G>T	Missense Mutation	SPATA20	p.A93S	spermatogenesis associa	21 (0.00)	62 (0.32)	0.86

11-14	Gp3	g.chr2:220354296G>T	Silent	SPEG	p.L2852L	SPEG complex locus	36 (0.00)	103 (0.22)	0.60
11-14	Gp3	g.chr17:7324847T>A	Missense Mutation	SPEM1	p.Y285N	spermatid maturation 1	20 (0.00)	215 (0.46)	1.23
11-14	Gp3	g.chr16:29675326A>G	Missense Mutation	SPN	p.T93A	sialophorin	61 (0.00)	123 (0.23)	0.61
11-14	Gp3	g.chr17:47712825A>G	Intron	SPOP		speckle-type POZ protei	43 (0.00)	15 (0.33)	0.89
11-14	Gp3	g.chr14:65259982T>C	Missense Mutation	SPTB	p.E800G	spectrin, beta, erythrocy	28 (0.00)	111 (0.23)	0.60
11-14	Gp3	g.chr15:42175245G>A	Missense Mutation	SPTBN5	p.A614V	spectrin, beta, non-eryth	37 (0.03)	332 (0.32)	0.85
11-14	Gp3	g.chr19:18543795C>A	Missense Mutation	SSBP4	p.S263Y	single stranded DNA bi	49 (0.00)	55 (0.24)	0.63
11-14	Gp3	g.chr18:44260131G>A	Silent	ST8SIA5	p.H335H	ST8 alpha-N-acetyl-neu	41 (0.02)	402 (0.30)	0.80
11-14	Gp3	g.chr2:220478508G>C	Missense Mutation	STK11IP	p.A858P	serine/threonine kinase	27 (0.00)	80 (0.30)	0.80
11-14	Gp3	g.chr7:73123419C>A	Missense Mutation	STX1A	p.V22F	syntaxin 1A (brain)	162 (0.00)	647 (0.15)	0.41
11-14	Gp3	g.chr9:136234143C>T	Missense Mutation	SURF4	p.G76E	surfeit 4	30 (0.00)	222 (0.27)	0.73
11-14	Gp3	g.chr14:64610628C>A	Missense Mutation	SYNE2	p.R5066S	spectrin repeat containi	124 (0.00)	30 (0.97)	2.58
11-14	Gp3	g.chr6:158454629A>T	Missense Mutation	SYNJ2	p.S210C	synaptojanin 2	19 (0.00)	29 (0.83)	2.21
11-14	Gp3	g.chr11:64897325C>A	Missense Mutation	SYVN1	p.A490S	synovial apoptosis inhib	16 (0.00)	48 (0.19)	0.50
11-14	Gp3	g.chr1:43907705C>A	Missense Mutation	SZT2	p.P2536T	seizure threshold 2 hom	18 (0.00)	21 (0.29)	0.76
11-14	Gp3	g.chr10:123844261G>A	Missense Mutation	TACC2	p.S749N	transforming, acidic coi	15 (0.00)	12 (0.50)	1.33
11-14	Gp3	g.chr10:123845065C>A	Missense Mutation	TACC2	p.A1017D	transforming, acidic coi	26 (0.00)	116 (0.70)	1.86
11-14	Gp3	g.chr10:123845679C>G	Missense Mutation	TACC2	p.L1222V	transforming, acidic coi	76 (0.00)	142 (0.62)	1.65
11-14	Gp3	g.chr10:71174821C>T	Nonsense Mutation	TACR2	p.W156*	tachykinin receptor 2	34 (0.00)	12 (0.67)	1.78
11-14	Gp3	g.chr1:229730573T>A	Missense Mutation	TAF5L	p.D414V	TAF5-like RNA polym	101 (0.00)	291 (0.95)	1.76
11-14	Gp3	g.chr1:229730574C>A	Missense Mutation	TAF5L	p.D414Y	TAF5-like RNA polym	102 (0.00)	291 (0.95)	1.76
11-14	Gp3	g.chr1:19180963C>A	Missense Mutation	TAS1R2	p.G334V	taste receptor, type 1, m	20 (0.00)	127 (0.38)	1.01
11-14	Gp3	g.chr17:60345589G>A	RNA	TBC1D3P2		TBC1 domain family, m	99 (0.01)	179 (0.78)	2.07
11-14	Gp3	g.chr10:114925728A>G	Silent	TCF7L2	p.E596E	transcription factor 7-li	39 (0.00)	34 (0.56)	1.49
11-14	Gp3	g.chr6:167786687G>T	Silent	TCP10	p.A317A	t-complex 10	66 (0.00)	83 (0.52)	1.38
11-14	Gp3	g.chr9:100249515G>T	Missense Mutation	TDRD7	p.D993Y	tudor domain containin	51 (0.00)	79 (0.75)	1.99
11-14	Gp3	g.chr7:97875291C>A	Silent	TECPR1	p.V56V	tectonin beta-propeller	61 (0.00)	169 (0.15)	0.51
11-14	Gp3	g.chr22:41791787G>A	Silent	TEF	p.V245V	thyrotrophic embryonic	44 (0.00)	83 (0.22)	0.58
11-14	Gp3	g.chr11:78369557A>G	Missense Mutation	TENM4	p.F2619S	teneurin transmembrane	89 (0.00)	58 (0.19)	0.51
11-14	Gp3	g.chr2:74328185G>A	Missense Mutation	TET3	p.E1289K	tet methylcytosine diox	53 (0.00)	69 (0.39)	1.04
11-14	Gp3	g.chr15:72039206G>T	Missense Mutation	THSD4	p.S689I	thrombospondin, type I,	27 (0.00)	60 (0.93)	2.49
11-14	Gp3	g.chr6:155450838G>C	Missense Mutation	TIAM2	p.V161L	T-cell lymphoma invasi	29 (0.00)	40 (0.60)	1.60
11-14	Gp3	g.chr19:4817971G>A	Missense Mutation	TICAM1	p.A140V	toll-like receptor adapto	16 (0.00)	439 (0.25)	0.67
11-14	Gp3	g.chr1:43772527C>T	Silent	TIE1	p.T167T	tyrosine kinase with im	81 (0.00)	128 (0.20)	0.52
11-14	Gp3	g.chr17:76170955G>T	Missense Mutation	TK1	p.P197H	thymidine kinase 1, solu	19 (0.00)	138 (0.39)	1.04

11-14	Gp3	g.chr10:98170118T>C	Missense Mutation	TLL2	p.K388E	tolloid-like 2	63 (0.00)	54 (0.15)	0.40
11-14	Gp3	g.chr13:114202632G>T	Silent	TMCO3	p.A595A	transmembrane and coil	16 (0.00)	65 (0.42)	1.11
11-14	Gp3	g.chr17:21101797G>A	Missense Mutation	TMEM11	p.A140V	transmembrane protein	30 (0.00)	23 (0.22)	0.58
11-14	Gp3	g.chr2:85826296G>C	Missense Mutation	TMEM150A	p.A240G	transmembrane protein	27 (0.00)	148 (0.70)	1.86
11-14	Gp3	g.chr10:104230721G>A	Nonsense Mutation	TMEM180	p.W184*	transmembrane protein	18 (0.00)	13 (0.85)	2.26
11-14	Gp3	g.chr18:5891883G>A	Silent	TMEM200C	p.I60I	transmembrane protein	37 (0.00)	292 (0.22)	0.58
11-14	Gp3	g.chr6:44122610T>C	Missense Mutation	TMEM63B	p.I830T	transmembrane protein	18 (0.00)	63 (0.35)	0.93
11-14	Gp3	g.chr11:18723449C>A	Silent	TMEM86A	p.R206R	transmembrane protein	65 (0.02)	123 (0.21)	0.56
11-14	Gp3	g.chr11:117774372C>G	Missense Mutation	TMPRSS13	p.E559Q	transmembrane protease	36 (0.00)	31 (0.77)	2.06
11-14	Gp3	g.chr2:218683452C>A	Missense Mutation	TNS1	p.E1084D	tensin 1	20 (0.00)	37 (0.76)	2.02
11-14	Gp3	g.chr8:145666417C>A	Nonsense Mutation	TONSL	p.E315*	tonsoku-like, DNA repa	21 (0.00)	211 (0.22)	0.59
11-14	Gp3	g.chr8:145668622G>T	Missense Mutation	TONSL	p.T116N	tonsoku-like, DNA repa	29 (0.00)	182 (0.76)	2.02
11-14	Gp3	g.chr1:179815429G>T	Missense Mutation	TOR1AIP2	p.T397N	torsin A interacting prot	43 (0.02)	229 (0.24)	0.65
11-14	Gp3	g.chr6:83075440C>A	Missense Mutation	TPBG	p.F254L	trophoblast glycoprotei	15 (0.00)	457 (0.30)	0.80
11-14	Gp3	g.chr7:65706194G>A	Nonsense Mutation	TPST1	p.W261*	tyrosylprotein sulfotrans	61 (0.00)	14 (0.79)	2.10
11-14	Gp3	g.chr6:42236377G>C	Missense Mutation	TRERF1	p.Q318E	transcriptional regulatin	75 (0.00)	195 (0.32)	0.85
11-14	Gp3	g.chr3:48508828G>T	Missense Mutation	TREX1	p.R258S	three prime repair exonu	44 (0.00)	232 (0.67)	1.78
11-14	Gp3	g.chr2:12880545A>G	Silent	TRIB2	p.V219V	tribbles pseudokinase 2	52 (0.00)	71 (0.14)	0.38
11-14	Gp3	g.chr4:165961384C>G	Missense Mutation	TRIM60	p.P54A	tripartite motif containi	52 (0.00)	34 (0.56)	1.49
11-14	Gp3	g.chr19:6750599C>T	Missense Mutation	TRIP10	p.P482S	thyroid hormone recept	70 (0.00)	366 (0.25)	0.68
11-14	Gp3	g.chr2:230654362G>A	Missense Mutation	TRIP12	p.H1209Y	thyroid hormone recept	17 (0.00)	181 (0.33)	0.87
11-14	Gp3	g.chr21:45838409C>A	Silent	TRPM2	p.P1144P	transient receptor potent	131 (0.00)	424 (0.18)	0.48
11-14	Gp3	g.chr9:77376684G>A	Silent	TRPM6	p.V1571V	transient receptor potent	21 (0.00)	87 (0.99)	2.64
11-14	Gp3	g.chr12:110226244G>T	Silent	TRPV4	p.G723G	transient receptor potent	25 (0.00)	13 (0.38)	1.03
11-14	Gp3	g.chr18:73000363T>C	Missense Mutation	TSHZ1	p.S1001P	teashirt zinc finger hom	70 (0.00)	120 (0.57)	1.83
11-14	Gp3	g.chr19:31770384T>A	Silent	TSHZ3	p.P105P	teashirt zinc finger hom	36 (0.00)	83 (0.23)	0.61
11-14	Gp3	g.chr11:44931445C>A	Missense Mutation	TSPAN18	p.L85I	tetraspanin 18	36 (0.03)	271 (0.18)	0.49
11-14	Gp3	g.chr17:40093220G>T	RNA	TTC25		tetratricopeptide repeat	162 (0.00)	242 (0.78)	2.07
11-14	Gp3	g.chr2:74717419G>A	Missense Mutation	TTC31	p.S94N	tetratricopeptide repeat	31 (0.00)	46 (0.52)	1.39
11-14	Gp3	g.chr10:134752189C>G	Missense Mutation	TTC40	p.G147A		38 (0.00)	229 (0.19)	0.50
11-14	Gp3	g.chr17:46867418C>T	Silent	TTLL6	p.V425V	tubulin tyrosine ligase-li	31 (0.00)	40 (0.97)	2.60
11-14	Gp3	g.chr2:179534328G>T	Missense Mutation	TTN	p.P11821T	titin	95 (0.01)	218 (0.59)	1.57
11-14	Gp3	g.chr2:130949455C>G	Missense Mutation	TUBA3E	p.E434D	tubulin, alpha 3e	90 (0.00)	61 (0.15)	0.39
11-14	Gp3	g.chr2:130949480G>T	Missense Mutation	TUBA3E	p.A426E	tubulin, alpha 3e	89 (0.00)	62 (0.39)	1.03
11-14	Gp3	g.chr19:6495778G>A	Silent	TUBB4A	p.G244G	tubulin, beta 4A class I	29 (0.00)	188 (0.58)	1.55

11-14	Gp3	g.chr17:40766912C>A	Silent	TUBG1	p.A403A	tubulin, gamma 1	96 (0.00)	302 (0.19)	0.50
11-14	Gp3	g.chr15:43690249G>T	Missense Mutation	TUBGCP4	p.Q430H	tubulin, gamma comple	59 (0.00)	15 (0.87)	2.31
11-14	Gp3	g.chr6:158882749C>T	Silent	TULP4	p.D338D	tubby like protein 4	64 (0.00)	42 (0.43)	1.14
11-14	Gp3	g.chr7:72040532T>C	RNA	TYW1B		tRNA-yW synthesizing	108 (0.00)	15 (0.40)	1.07
11-14	Gp3	g.chr12:125398257C>A	Missense Mutation	UBC	p.D21Y	ubiquitin C	21 (0.00)	141 (0.95)	2.53
11-14	Gp3	g.chr1:110655387G>A	Missense Mutation	UBL4B	p.M77I	ubiquitin-like 4B	56 (0.00)	121 (0.55)	1.48
11-14	Gp3	g.chr2:234622064G>A	Missense Mutation	UGT1A5	p.A143T	UDP glucuronosyltrans	128 (0.01)	161 (0.99)	2.65
11-14	Gp3	g.chr4:70462031G>A	Silent	UGT2A1	p.V311V	UDP glucuronosyltrans	42 (0.00)	139 (0.26)	0.69
11-14	Gp3	g.chr4:70160415T>C	Missense Mutation	UGT2B28	p.V493A	UDP glucuronosyltrans	42 (0.00)	29 (0.21)	0.55
11-14	Gp3	g.chr19:4944297G>T	RNA	UHRF1		ubiquitin-like with PHD	34 (0.00)	286 (0.25)	0.67
11-14	Gp3	g.chr17:73831849G>A	Missense Mutation	UNC13D	p.R536W	unc-13 homolog D (C.	20 (0.00)	87 (0.17)	0.46
11-14	Gp3	g.chr11:17517140C>T	Silent	USH1C	p.G877G	Usher syndrome 1C (au	130 (0.01)	158 (0.21)	0.56
11-14	Gp3	g.chr9:132631604C>A	Missense Mutation	USP20	p.A431D	ubiquitin specific peptid	34 (0.00)	180 (0.19)	0.50
11-14	Gp3	g.chr11:77921513C>A	Missense Mutation	USP35	p.A871D	ubiquitin specific peptid	72 (0.00)	254 (0.64)	1.70
11-14	Gp3	g.chr11:77921604T>A	Silent	USP35	p.S901S	ubiquitin specific peptid	39 (0.00)	252 (1.00)	2.66
11-14	Gp3	g.chr15:42462036A>G	Silent	VPS39	p.P373P	vacuolar protein sorting	31 (0.00)	115 (0.15)	0.39
11-14	Gp3	g.chr11:64875144C>T	Silent	VPS51	p.S150S	vacuolar protein sorting	22 (0.00)	145 (0.23)	0.61
11-14	Gp3	g.chr19:50498156A>T	Missense Mutation	VRK3	p.L262Q	vaccinia related kinase	25 (0.00)	39 (0.56)	1.50
11-14	Gp3	g.chr1:1372331G>T	Missense Mutation	VWA1	p.G33V	von Willebrand factor A	21 (0.00)	70 (0.63)	1.68
11-14	Gp3	g.chr11:61040746C>A	Missense Mutation	VWCE	p.A542S	von Willebrand factor C	15 (0.00)	29 (0.83)	2.21
11-14	Gp3	g.chr2:114353133G>A	RNA	WASH2P		WAS protein family ho	21 (0.00)	167 (0.40)	1.05
11-14	Gp3	g.chr15:102506560G>A	RNA	WASH3P		WAS protein family ho	31 (0.00)	66 (0.17)	0.44
11-14	Gp3	g.chr7:73279708G>C	Missense Mutation	WBSCR28	p.C153S	Williams-Beuren syndr	20 (0.00)	123 (0.37)	1.00
11-14	Gp3	g.chr7:151097233G>T	Silent	WDR86	p.T86T	WD repeat domain 86	48 (0.00)	47 (0.15)	0.52
11-14	Gp3	g.chr2:68384538A>G	Missense Mutation	WDR92	p.I13T	WD repeat domain 92	29 (0.00)	123 (0.47)	1.26
11-14	Gp3	g.chr3:39227565C>G	Missense Mutation	XIRP1	p.E1124D	xin actin-binding repeat	78 (0.00)	216 (0.24)	0.63
11-14	Gp3	g.chr7:100365605C>A	RNA	ZAN		zonadhesin (gene/pseud	62 (0.00)	56 (0.30)	1.00
11-14	Gp3	g.chr2:98354018G>T	Missense Mutation	ZAP70	p.V458L	zeta-chain (TCR) associ	15 (0.00)	170 (0.15)	0.39
11-14	Gp3	g.chr22:50278527G>T	Missense Mutation	ZBED4	p.G406V	zinc finger, BED-type c	16 (0.00)	24 (0.21)	0.56
11-14	Gp3	g.chr3:114069176G>A	Silent	ZBTB20	p.C510C	zinc finger and BTB do	25 (0.00)	60 (0.28)	0.92
11-14	Gp3	g.chr17:7365468G>T	Missense Mutation	ZBTB4	p.P945T	zinc finger and BTB do	79 (0.00)	105 (0.21)	0.56
11-14	Gp3	g.chr18:45566465C>T	Silent	ZBTB7C	p.L338L	zinc finger and BTB do	30 (0.00)	51 (0.33)	0.89
11-14	Gp3	g.chr19:47593347T>C	Missense Mutation	ZC3H4	p.N198D	zinc finger CCCH-type	52 (0.00)	66 (0.35)	0.93
11-14	Gp3	g.chr16:72828969C>A	Missense Mutation	ZFHX3	p.A2538S	zinc finger homeobox 3	74 (0.00)	36 (0.36)	0.96
11-14	Gp3	g.chr16:72991579G>A	Silent	ZFHX3	p.H822H	zinc finger homeobox 3	16 (0.00)	298 (0.40)	1.07

11-14	Gp3	g.chr16:72991605T>A	Missense Mutation	ZFHX3	p.N814Y	zinc finger homeobox 3	34 (0.00)	280 (0.38)	1.02
11-14	Gp3	g.chr16:72991632G>A	Missense Mutation	ZFHX3	p.R805W	zinc finger homeobox 3	35 (0.00)	140 (0.59)	1.56
11-14	Gp3	g.chr16:72991692T>A	Missense Mutation	ZFHX3	p.N785Y	zinc finger homeobox 3	21 (0.00)	225 (0.55)	1.46
11-14	Gp3	g.chr8:106810974C>A	Silent	ZFPM2	p.S254S	zinc finger protein, FOC	35 (0.00)	10 (0.50)	1.33
11-14	Gp3	g.chr5:32403302C>G	Silent	ZFR	p.S475S	zinc finger RNA bindin	39 (0.00)	35 (0.77)	2.06
11-14	Gp3	g.chr3:15115794G>A	Missense Mutation	ZFYVE20	p.P617L	zinc finger, FYVE doma	66 (0.00)	26 (0.50)	1.33
11-14	Gp3	g.chr3:147131175C>T	Missense Mutation	ZIC1	p.S394L	Zic family member 1	19 (0.00)	31 (0.81)	2.61
11-14	Gp3	g.chr6:28120834G>T	Splice Site	ZKSCAN8	p.G259V	zinc finger with KRAB	84 (0.00)	95 (0.19)	0.51
11-14	Gp3	g.chr17:4644909C>G	Missense Mutation	ZMYND15	p.L209V	zinc finger, MYND-typ	195 (0.00)	178 (0.17)	0.46
11-14	Gp3	g.chr11:46726766C>A	Missense Mutation	ZNF408	p.R506S	zinc finger protein 408	19 (0.00)	59 (0.17)	0.45
11-14	Gp3	g.chr16:30408724C>T	Silent	ZNF48	p.F51F	zinc finger protein 48	21 (0.00)	23 (0.22)	0.58
11-14	Gp3	g.chr19:12721456T>C	Silent	ZNF490	p.R13R	zinc finger protein 490	36 (0.00)	42 (0.93)	2.48
11-14	Gp3	g.chr10:97919348C>T	RNA	ZNF518A		zinc finger protein 518A	122 (0.01)	164 (0.98)	2.62
11-14	Gp3	g.chr19:48032264C>G	Missense Mutation	ZNF541	p.R1171S	zinc finger protein 541	46 (0.00)	16 (0.88)	2.33
11-14	Gp3	g.chr16:30793437C>T	Missense Mutation	ZNF629	p.G738S	zinc finger protein 629	27 (0.00)	152 (0.86)	2.28
11-14	Gp3	g.chr8:81599579G>T	Missense Mutation	ZNF704	p.P147Q	zinc finger protein 704	19 (0.00)	65 (0.91)	2.42
11-14	Gp3	g.chr7:88965055G>T	Missense Mutation	ZNF804B	p.R920M	zinc finger protein 804B	36 (0.00)	113 (0.22)	0.73
11-14	Gp3	g.chr7:149559178G>T	Nonsense Mutation	ZNF862	p.E977*	zinc finger protein 862	129 (0.01)	549 (0.23)	0.81
11-14	Gp3	g.chr19:20229245T>C	Silent	ZNF90	p.F294F	zinc finger protein 90	53 (0.00)	14 (0.43)	1.14
11-14	Gp3	g.chr22:29446151G>T	Missense Mutation	ZNRF3	p.C661F	zinc and ring finger 3	26 (0.00)	263 (0.22)	0.59
11-14	Gp3	g.chr19:58600203C>A	Splice Site	ZSCAN18	p.G191G	zinc finger and SCAN d	56 (0.00)	325 (0.15)	0.40
11-14	Gp3	g.chr19:58189817C>A	Silent	ZSCAN4	p.S282S	zinc finger and SCAN d	22 (0.00)	82 (0.41)	1.11
11-14	Gp3	g.chr20:44507176A>G	Missense Mutation	ZSWIM3	p.E660G	zinc finger, SWIM-type	124 (0.00)	78 (0.28)	0.75
11-14	Gp4	g.chr16:2331218T>C	Missense Mutation	ABCA3	p.Y1332C	ATP-binding cassette, s	24 (0.00)	182 (0.23)	0.60
11-14	Gp4	g.chr19:1046407T>A	Splice Site	ABCA7		ATP-binding cassette, s	23 (0.00)	143 (0.79)	2.11
11-14	Gp4	g.chr16:48173146C>G	Silent	ABCC12	p.A253A	ATP-binding cassette, s	88 (0.01)	183 (0.96)	2.56
11-14	Gp4	g.chr11:119031091T>A	Missense Mutation	ABCG4	p.L531Q	ATP-binding cassette, s	61 (0.00)	51 (0.61)	1.62
11-14	Gp4	g.chr3:52021179C>T	Missense Mutation	ABHD14A-AC	p.S326F	ABHD14A-ACY1 read	65 (0.00)	316 (0.17)	0.46
11-14	Gp4	g.chr15:31093522C>A	RNA	AC004460.1			89 (0.00)	232 (0.16)	0.53
11-14	Gp4	g.chr15:31093555G>A	RNA	AC004460.1			74 (0.00)	292 (0.54)	1.73
11-14	Gp4	g.chr2:71256770T>G	RNA	AC007040.8			62 (0.00)	214 (1.00)	2.65
11-14	Gp4	g.chr22:18835246G>A	Missense Mutation	AC008132.13	p.A268T		44 (0.00)	150 (0.15)	0.39
11-14	Gp4	g.chr3:194476996A>G	lincRNA	AC090505.6			19 (0.00)	29 (0.28)	0.88
11-14	Gp4	g.chr3:194477034C>T	lincRNA	AC090505.6			19 (0.00)	26 (0.73)	2.32
11-14	Gp4	g.chr2:132257830C>T	RNA	AC093838.4			27 (0.00)	18 (0.28)	0.74

11-14	Gp4	g.chr2:135621131C>G	Missense Mutation	ACMSD	p.P139R	aminocarboxymuconate	15 (0.00)	98 (0.76)	2.01
11-14	Gp4	g.chr22:41923963C>T	Silent	ACO2	p.Y740Y	aconitase 2, mitochondr	36 (0.00)	150 (0.55)	1.48
11-14	Gp4	g.chr7:5568812T>C	Missense Mutation	ACTB	p.N115D	actin, beta	45 (0.00)	105 (0.31)	1.12
11-14	Gp4	g.chr3:169487303G>A	Silent	ACTRT3	p.N2N	actin-related protein T3	26 (0.00)	144 (0.31)	0.97
11-14	Gp4	g.chr9:136310911C>A	Missense Mutation	ADAMTS13	p.A901E	ADAM metallopeptidas	18 (0.00)	38 (0.39)	1.05
11-14	Gp4	g.chr11:130339212G>T	Missense Mutation	ADAMTS15	p.G533V	ADAM metallopeptidas	67 (0.00)	139 (0.34)	0.90
11-14	Gp4	g.chr5:178700022G>T	Missense Mutation	ADAMTS2	p.P193H	ADAM metallopeptidas	38 (0.00)	47 (0.77)	2.04
11-14	Gp4	g.chr1:161163434G>T	Silent	ADAMTS4	p.G577G	ADAM metallopeptidas	72 (0.00)	265 (0.18)	0.48
11-14	Gp4	g.chr15:84582020A>G	Missense Mutation	ADAMTSL3	p.D626G	ADAMTS-like 3	22 (0.00)	69 (0.16)	0.43
11-14	Gp4	g.chr3:123071390G>A	Silent	ADCY5	p.I24I	adenylate cyclase 5	86 (0.00)	188 (0.65)	2.06
11-14	Gp4	g.chr22:24836703G>C	Missense Mutation	ADORA2A	p.G162A	adenosine A2a receptor	32 (0.00)	49 (0.57)	1.52
11-14	Gp4	g.chr7:150839253C>A	Silent	AGAP3	p.R324R	ArfGAP with GTPase d	24 (0.00)	49 (0.65)	2.08
11-14	Gp4	g.chr10:51769855G>T	Missense Mutation	AGAP6	p.G657V	ArfGAP with GTPase d	179 (0.01)	162 (0.26)	0.69
11-14	Gp4	g.chr5:76326747C>T	Silent	AGGF1	p.H52H	angiogenic factor with	42 (0.02)	334 (0.56)	1.49
11-14	Gp4	g.chr21:45389054C>T	Missense Mutation	AGPAT3	p.T135M	1-acylglycerol-3-phosph	15 (0.00)	34 (0.88)	3.12
11-14	Gp4	g.chr1:4771960C>T	Splice Site	AJAP1	p.S10S	adherens junctions asso	36 (0.00)	126 (0.99)	2.14
11-14	Gp4	g.chr1:19593757G>T	RNA	AKR7L		aldo-keto reductase fam	16 (0.00)	61 (0.61)	1.62
11-14	Gp4	g.chr1:19200995A>G	Missense Mutation	ALDH4A1	p.I514T	aldehyde dehydrogenase	38 (0.00)	17 (0.35)	0.94
11-14	Gp4	g.chr17:6797983C>T	RNA	ALOX12P2		arachidonate 12-lipoxyg	29 (0.00)	34 (0.24)	0.63
11-14	Gp4	g.chr2:233243918G>C	Missense Mutation	ALPP	p.V68L	alkaline phosphatase, pl	24 (0.00)	32 (0.28)	0.75
11-14	Gp4	g.chr2:233272475G>A	Missense Mutation	ALPPL2	p.A158T	alkaline phosphatase, pl	31 (0.00)	75 (0.16)	0.43
11-14	Gp4	g.chr1:110604076C>T	Missense Mutation	ALX3	p.R235H	ALX homeobox 3	27 (0.00)	128 (0.74)	1.98
11-14	Gp4	g.chr11:46564528C>A	Nonsense Mutation	AMBRA1	p.E257*	autophagy/beclin-1 regu	51 (0.00)	207 (0.83)	2.22
11-14	Gp4	g.chr3:134086348G>T	Silent	AMOTL2	p.R402R	angiomotin like 2	45 (0.00)	178 (0.14)	0.45
11-14	Gp4	g.chr17:79852380C>G	Missense Mutation	ANAPC11	p.N9K	anaphase promoting co	46 (0.00)	113 (0.22)	0.59
11-14	Gp4	g.chr10:99341123G>A	Silent	ANKRD2	p.V202V	ankyrin repeat domain 2	48 (0.00)	53 (0.64)	1.71
11-14	Gp4	g.chr1:145562053G>A	Missense Mutation	ANKRD35	p.D581N	ankyrin repeat domain 3	15 (0.00)	11 (0.82)	2.18
11-14	Gp4	g.chr4:186318457G>T	Splice Site	ANKRD37		ankyrin repeat domain 3	28 (0.00)	37 (0.27)	0.72
11-14	Gp4	g.chr12:56641976C>A	Silent	ANKRD52	p.T603T	ankyrin repeat domain 5	40 (0.00)	120 (0.99)	2.64
11-14	Gp4	g.chr11:418503C>T	Silent	ANO9	p.K739K	anoctamin 9	21 (0.00)	136 (0.42)	1.12
11-14	Gp4	g.chr15:90349224C>T	Silent	ANPEP	p.E197E	alanyl (membrane) ami	40 (0.00)	136 (0.15)	0.39
11-14	Gp4	g.chr7:150555924C>T	Silent	AOC1	p.R548R	amine oxidase, copper c	51 (0.00)	150 (0.12)	0.38
11-14	Gp4	g.chr21:24473998C>T	lincRNA	AP001255.2			54 (0.02)	30 (0.80)	2.13
11-14	Gp4	g.chr21:11181137T>A	lincRNA	AP003900.6			186 (0.00)	97 (0.61)	1.62
11-14	Gp4	g.chr11:985438C>T	Missense Mutation	AP2A2	p.P273L	adaptor-related protein	77 (0.00)	114 (0.71)	1.89

11-14	Gp4	g.chr11:116691586G>T	Missense Mutation	APOA4	p.S396R	apolipoprotein A-IV	44 (0.00)	87 (0.75)	1.99
11-14	Gp4	g.chr22:36661479C>A	Missense Mutation	APOL1	p.F199L	apolipoprotein L, 1	152 (0.00)	51 (0.98)	2.61
11-14	Gp4	g.chr7:30951878C>A	Silent	AQP1	p.S118S	aquaporin 1 (Colton blo	97 (0.00)	255 (0.19)	0.64
11-14	Gp4	g.chr11:118468551C>T	Silent	ARCN1	p.S498S	archain 1	49 (0.00)	142 (0.20)	0.54
11-14	Gp4	g.chr19:47503694G>T	Missense Mutation	ARHGAP35	p.A1417S	Rho GTPase activating	67 (0.00)	227 (0.38)	1.02
11-14	Gp4	g.chr8:145770707G>A	Missense Mutation	ARHGAP39	p.P816L	Rho GTPase activating	30 (0.00)	42 (0.24)	0.63
11-14	Gp4	g.chr1:156946820G>T	Silent	ARHGEF11	p.T179T	Rho guanine nucleotide	84 (0.00)	178 (0.21)	0.57
11-14	Gp4	g.chr11:73076992G>T	Splice Site	ARHGEF17	p.G1999C	Rho guanine nucleotide	39 (0.00)	59 (0.73)	1.94
11-14	Gp4	g.chr2:131673497C>T	Missense Mutation	ARHGEF4	p.P330S	Rho guanine nucleotide	15 (0.00)	42 (0.43)	1.14
11-14	Gp4	g.chr14:21542403G>T	Missense Mutation	ARHGEF40	p.G172W	Rho guanine nucleotide	24 (0.00)	140 (0.22)	0.59
11-14	Gp4	g.chr5:149677547G>A	Missense Mutation	ARSI	p.R314C	arylsulfatase family, me	16 (0.00)	115 (0.23)	0.63
11-14	Gp4	g.chr2:220396550G>A	Missense Mutation	ASIC4	p.G345E	acid-sensing (proton-gat	46 (0.00)	20 (0.40)	1.07
11-14	Gp4	g.chr17:79954579T>A	Missense Mutation	ASPSCR1	p.S264T	alveolar soft part sarcon	23 (0.00)	104 (0.14)	0.38
11-14	Gp4	g.chr2:242606154G>C	Missense Mutation	ATG4B	p.E211D	autophagy related 4B, c	46 (0.00)	152 (0.49)	1.30
11-14	Gp4	g.chr12:7045832G>A	Missense Mutation	ATN1	p.A468T	atrophin 1	22 (0.00)	48 (0.44)	1.17
11-14	Gp4	g.chr15:25962002C>A	Missense Mutation	ATP10A	p.A551S	ATPase, class V, type 1	71 (0.00)	84 (0.29)	0.92
11-14	Gp4	g.chr5:159992823T>C	Silent	ATP10B	p.K1341K	ATPase, class V, type 1	104 (0.00)	49 (0.35)	0.93
11-14	Gp4	g.chr19:36054115G>A	Missense Mutation	ATP4A	p.T71I	ATPase, H+/K+ exchan	44 (0.00)	302 (0.17)	0.46
11-14	Gp4	g.chr19:1807188G>T	Silent	ATP8B3	p.T198T	ATPase, aminophospho	30 (0.00)	98 (0.40)	1.06
11-14	Gp4	g.chr7:70228071C>T	Missense Mutation	AUTS2	p.P320S	autism susceptibility car	35 (0.00)	199 (0.76)	2.02
11-14	Gp4	g.chr19:17922801C>A	Missense Mutation	B3GNT3	p.S330Y	UDP-GlcNAc:betaGal b	43 (0.00)	176 (0.45)	1.21
11-14	Gp4	g.chr6:90660415G>A	Silent	BACH2	p.A470A	BTB and CNC homolog	46 (0.00)	230 (0.17)	0.46
11-14	Gp4	g.chr11:64051784C>A	Missense Mutation	BAD	p.E19D	BCL2-associated agonis	22 (0.00)	180 (0.28)	0.74
11-14	Gp4	g.chr17:79077781G>T	Missense Mutation	BAIAP2	p.W176C	BAI1-associated protein	26 (0.00)	176 (0.22)	0.59
11-14	Gp4	g.chr17:6927617A>G	Missense Mutation	BCL6B	p.Q132R	B-cell CLL/lymphoma	23 (0.00)	49 (0.57)	1.52
11-14	Gp4	g.chr3:5024868G>A	Missense Mutation	BHLHE40	p.G244S	basic helix-loop-helix fa	38 (0.00)	18 (0.44)	1.19
11-14	Gp4	g.chr9:95480821C>A	Splice Site	BICD2	p.Q702H	bicaudal D homolog 2 (	20 (0.00)	24 (0.25)	0.67
11-14	Gp4	g.chr2:32743448T>C	Missense Mutation	BIRC6	p.L3826P	baculoviral IAP repeat c	48 (0.00)	19 (0.26)	0.70
11-14	Gp4	g.chr16:2259695A>G	Missense Mutation	BRICD5	p.W151R	BRICHOS domain cont	25 (0.00)	56 (0.16)	0.43
11-14	Gp4	g.chr3:49701895C>A	Missense Mutation	BSN	p.A3883D	bassoon presynaptic cyt	71 (0.00)	233 (0.36)	0.96
11-14	Gp4	g.chr20:11899001C>T	Silent	BTBD3	p.S26S	BTB (POZ) domain con	152 (0.00)	49 (0.96)	2.56
11-14	Gp4	g.chr17:56400662C>G	Missense Mutation	BZRAP1	p.E307D	benzodiazepine receptor	94 (0.00)	558 (0.20)	0.53
11-14	Gp4	g.chr11:65685238C>T	Missense Mutation	C11orf68	p.V192M	chromosome 11 open re	25 (0.00)	158 (0.50)	1.33
11-14	Gp4	g.chr11:63586075C>T	Silent	C11orf84	p.V228V	chromosome 11 open re	27 (0.00)	248 (0.67)	1.80
11-14	Gp4	g.chr15:74032975G>C	Missense Mutation	C15orf59	p.S55R	chromosome 15 open re	19 (0.00)	34 (0.15)	0.39

11-14	Gp4	g.chr17:79517420C>A	Missense Mutation	C17orf70	p.C367F	chromosome 17 open re	47 (0.02)	235 (0.68)	1.80
11-14	Gp4	g.chr1:162344195G>A	Silent	C1orf111	p.S143S	chromosome 1 open rea	94 (0.01)	239 (0.14)	0.38
11-14	Gp4	g.chr5:159776360C>T	Missense Mutation	C1QTNF2	p.A270T	C1q and tumor necrosis	74 (0.00)	106 (0.52)	1.38
11-14	Gp4	g.chr2:26798893A>T	Missense Mutation	C2orf70	p.Q66H	chromosome 2 open rea	152 (0.00)	298 (0.65)	1.74
11-14	Gp4	g.chr4:81504320C>A	Missense Mutation	C4orf22	p.R106S	chromosome 4 open rea	40 (0.00)	27 (0.26)	0.69
11-14	Gp4	g.chr9:34381396G>A	Missense Mutation	C9orf24	p.P148L	chromosome 9 open rea	88 (0.00)	338 (0.30)	0.80
11-14	Gp4	g.chr3:50416890A>G	Silent	CACNA2D2	p.F375F	calcium channel, voltag	25 (0.00)	34 (0.35)	0.94
11-14	Gp4	g.chr3:50416907C>A	Missense Mutation	CACNA2D2	p.G370C	calcium channel, voltag	19 (0.00)	33 (0.15)	0.40
11-14	Gp4	g.chr3:85225280C>T	Intron	CADM2		cell adhesion molecule	84 (0.00)	204 (0.57)	1.53
11-14	Gp4	g.chr3:85576420C>T	Intron	CADM2		cell adhesion molecule	69 (0.00)	64 (0.89)	2.38
11-14	Gp4	g.chr3:85770822C>A	Intron	CADM2		cell adhesion molecule	19 (0.00)	102 (0.44)	1.18
11-14	Gp4	g.chr12:54109733A>G	Silent	CALCOCO1	p.S368S	calcium binding and coi	40 (0.03)	194 (0.31)	0.84
11-14	Gp4	g.chr22:37903850T>C	Missense Mutation	CARD10	p.K393E	caspase recruitment don	89 (0.00)	76 (0.83)	2.21
11-14	Gp4	g.chr13:111290588G>T	Splice Site	CARKD		carbohydrate kinase don	43 (0.00)	50 (0.44)	1.17
11-14	Gp4	g.chr2:219895448G>A	Missense Mutation	CCDC108	p.T375I	coiled-coil domain conta	17 (0.00)	58 (0.26)	0.69
11-14	Gp4	g.chr2:219896289C>A	Missense Mutation	CCDC108	p.C246F	coiled-coil domain conta	91 (0.00)	161 (0.36)	0.96
11-14	Gp4	g.chr19:48801483T>A	Missense Mutation	CCDC114	p.E415V	coiled-coil domain conta	19 (0.00)	72 (0.42)	1.11
11-14	Gp4	g.chr19:48801484C>A	Nonsense Mutation	CCDC114	p.E415*	coiled-coil domain conta	19 (0.00)	71 (0.42)	1.13
11-14	Gp4	g.chr19:49920712C>A	Missense Mutation	CCDC155	p.P545Q	coiled-coil domain conta	28 (0.00)	71 (0.28)	0.75
11-14	Gp4	g.chr10:12940549G>C	Missense Mutation	CCDC3	p.S227C	coiled-coil domain conta	35 (0.00)	78 (0.18)	0.48
11-14	Gp4	g.chr3:126153074C>A	Missense Mutation	CCDC37	p.T493N	coiled-coil domain conta	22 (0.00)	28 (0.18)	0.57
11-14	Gp4	g.chr17:80159569C>A	Missense Mutation	CCDC57	p.W84C	coiled-coil domain conta	31 (0.00)	234 (0.20)	0.52
11-14	Gp4	g.chr14:91779699T>C	Missense Mutation	CCDC88C	p.K821E	coiled-coil domain conta	19 (0.00)	30 (0.70)	1.87
11-14	Gp4	g.chr11:6292368G>T	Silent	CCKBR	p.G313G	cholecystokinin B recep	23 (0.00)	188 (0.18)	0.48
11-14	Gp4	g.chr10:12291689C>A	Missense Mutation	CDC123	p.A319D	cell division cycle 123	76 (0.00)	135 (0.59)	1.58
11-14	Gp4	g.chr10:73501588C>T	Silent	CDH23	p.I1590I	cadherin-related 23	23 (0.00)	114 (0.17)	0.44
11-14	Gp4	g.chr10:73558878T>C	Silent	CDH23	p.I2360I	cadherin-related 23	36 (0.00)	37 (0.81)	2.16
11-14	Gp4	g.chr5:176002195G>T	Silent	CDHR2	p.L202L	cadherin-related family	21 (0.00)	271 (0.21)	0.56
11-14	Gp4	g.chr1:1636355A>G	Silent	CDK11A	p.I472I	cyclin-dependent kinase	51 (0.00)	49 (0.98)	2.61
11-14	Gp4	g.chr17:73000103C>T	Silent	CDR2L	p.F444F	cerebellar degeneration-	23 (0.00)	109 (0.64)	1.71
11-14	Gp4	g.chr22:46930196G>T	Silent	CELSR1	p.R958R	cadherin, EGF LAG sev	59 (0.00)	67 (0.34)	0.92
11-14	Gp4	g.chr4:68374577C>T	Missense Mutation	CENPC	p.S620N	centromere protein C	175 (0.00)	329 (0.14)	0.38
11-14	Gp4	g.chr2:65296657A>G	Missense Mutation	CEP68	p.R27G	centrosomal protein 68k	20 (0.00)	19 (0.79)	2.11
11-14	Gp4	g.chr9:131186789T>C	Missense Mutation	CERCAM	p.L221P	cerebral endothelial cell	48 (0.00)	154 (0.23)	0.62
11-14	Gp4	g.chr1:151501929C>T	Missense Mutation	CGN	p.A667V	cingulin	23 (0.00)	32 (0.84)	2.25

11-14	Gp4	g.chr1:6180986G>A	Intron	CHD5		chromodomain helicase	53 (0.00)	175 (0.85)	1.83
11-14	Gp4	g.chr1:6191065G>T	Intron	CHD5		chromodomain helicase	39 (0.00)	32 (0.28)	0.61
11-14	Gp4	g.chr1:6196517G>A	Intron	CHD5		chromodomain helicase	36 (0.00)	146 (0.19)	0.41
11-14	Gp4	g.chr1:6196522C>G	Intron	CHD5		chromodomain helicase	36 (0.00)	148 (0.51)	1.09
11-14	Gp4	g.chr1:6197092A>G	Intron	CHD5		chromodomain helicase	64 (0.00)	167 (0.19)	0.41
11-14	Gp4	g.chr1:6197107G>A	Intron	CHD5		chromodomain helicase	61 (0.00)	130 (0.28)	0.61
11-14	Gp4	g.chr1:6222543G>T	Intron	CHD5		chromodomain helicase	56 (0.00)	88 (0.41)	0.88
11-14	Gp4	g.chr1:6226942G>A	Intron	CHD5		chromodomain helicase	79 (0.00)	169 (0.40)	0.87
11-14	Gp4	g.chr11:46407132G>A	Missense Mutation	CHRM4	p.P326S	cholinergic receptor, mu	27 (0.00)	130 (0.32)	0.86
11-14	Gp4	g.chr2:233409177C>G	Missense Mutation	CHRNG	p.S379W	cholinergic receptor, nic	19 (0.00)	87 (0.31)	0.83
11-14	Gp4	g.chr19:42791859T>G	Missense Mutation	CIC	p.Y1158D	capicua transcriptional r	44 (0.02)	359 (0.43)	1.15
11-14	Gp4	g.chr19:19650507G>T	Missense Mutation	CILP2	p.E28D	cartilage intermediate la	24 (0.00)	10 (0.60)	1.60
11-14	Gp4	g.chr12:120151416G>C	Missense Mutation	CIT	p.C1448W	citron rho-interacting se	22 (0.00)	91 (0.45)	1.20
11-14	Gp4	g.chr9:130941477C>T	Missense Mutation	CIZ1	p.V337M	CDKN1A interacting zi	22 (0.00)	140 (0.18)	0.48
11-14	Gp4	g.chr7:73814765G>T	Missense Mutation	CLIP2	p.E982D	CAP-GLY domain cont	44 (0.00)	197 (0.24)	0.65
11-14	Gp4	g.chr4:10515192G>A	Missense Mutation	CLNK	p.P268S	cytokine-dependent hem	35 (0.00)	53 (0.60)	1.61
11-14	Gp4	g.chr4:56314984G>T	Missense Mutation	CLOCK	p.Q501K	clock circadian regulato	36 (0.00)	22 (0.82)	2.18
11-14	Gp4	g.chr12:7303530G>C	Missense Mutation	CLSTN3	p.V800L	calsyntenin 3	26 (0.00)	132 (0.36)	0.95
11-14	Gp4	g.chr2:97464811C>T	Missense Mutation	CNNM4	p.P567S	cyclin and CBS domain	25 (0.00)	34 (0.24)	0.63
11-14	Gp4	g.chr2:97464841C>A	Silent	CNNM4	p.R577R	cyclin and CBS domain	23 (0.00)	32 (0.25)	0.67
11-14	Gp4	g.chr7:135099146C>A	Silent	CNOT4	p.R165R	CCR4-NOT transcriptio	41 (0.00)	72 (0.42)	1.32
11-14	Gp4	g.chr1:205035623T>C	Missense Mutation	CNTN2	p.I624T	contactin 2 (axonal)	57 (0.00)	24 (0.21)	0.56
11-14	Gp4	g.chr9:39175994C>T	Silent	CNTNAP3	p.V341V	contactin associated pro	112 (0.00)	181 (0.99)	2.65
11-14	Gp4	g.chr9:117002759G>T	Missense Mutation	COL27A1	p.G943W	collagen, type XXVII, a	27 (0.00)	42 (0.17)	0.44
11-14	Gp4	g.chr9:137671980A>G	Silent	COL5A1	p.T806T	collagen, type V, alpha	109 (0.00)	253 (0.18)	0.47
11-14	Gp4	g.chr1:36565673A>G	Silent	COL8A2	p.R57R	collagen, type VIII, alph	20 (0.00)	65 (0.28)	0.74
11-14	Gp4	g.chr3:131283113A>G	Silent	CPNE4	p.N336N	copine IV	47 (0.00)	42 (0.12)	0.38
11-14	Gp4	g.chr16:3786138C>A	Missense Mutation	CREBBP	p.D1543Y	CREB binding protein	21 (0.00)	71 (0.39)	1.05
11-14	Gp4	g.chr15:75980028G>C	Nonsense Mutation	CSPG4	p.Y1126*	chondroitin sulfate prote	20 (0.00)	20 (0.85)	2.27
11-14	Gp4	g.chr8:142446166C>A	RNA	CTD-3064M3.7			20 (0.00)	61 (0.25)	0.66
11-14	Gp4	g.chr11:66281965C>G	Missense Mutation	CTD-3074O7.	p.P120R		57 (0.00)	203 (0.91)	2.42
11-14	Gp4	g.chr6:43011206A>G	Missense Mutation	CUL7	p.V1112A	cullin 7	30 (0.00)	43 (0.16)	0.43
11-14	Gp4	g.chr17:4047287A>G	Missense Mutation	CYB5D2	p.S80G	cytochrome b5 domain	40 (0.00)	17 (0.35)	0.94
11-14	Gp4	g.chr22:43023658G>T	Missense Mutation	CYB5R3	p.P167H	cytochrome b5 reductas	48 (0.00)	273 (0.15)	0.40
11-14	Gp4	g.chr15:23002908G>A	Silent	CYFIP1	p.K1210K	cytoplasmic FMR1 inter	122 (0.00)	53 (0.98)	3.16

11-14	Gp4	g.chr15:75042734C>A	Missense Mutation	CYP1A2	p.L219I	cytochrome P450, famil	37 (0.00)	113 (0.98)	2.62
11-14	Gp4	g.chr19:41704622G>T	Missense Mutation	CYP2S1	p.E221D	cytochrome P450, famil	18 (0.00)	11 (0.91)	2.42
11-14	Gp4	g.chr9:124340951C>A	Intron	DAB2IP		DAB2 interacting protei	58 (0.00)	127 (0.46)	1.22
11-14	Gp4	g.chr9:124340952C>A	Intron	DAB2IP		DAB2 interacting protei	58 (0.00)	125 (0.46)	1.22
11-14	Gp4	g.chr9:124454430G>A	Intron	DAB2IP		DAB2 interacting protei	152 (0.00)	22 (0.73)	1.94
11-14	Gp4	g.chr9:124459707C>A	Intron	DAB2IP		DAB2 interacting protei	60 (0.00)	21 (0.90)	2.41
11-14	Gp4	g.chr9:124463024A>G	Intron	DAB2IP		DAB2 interacting protei	54 (0.00)	80 (0.21)	0.57
11-14	Gp4	g.chr11:61511676G>A	Silent	DAGLA	p.E948E	diacylglycerol lipase, al	18 (0.00)	58 (0.16)	0.41
11-14	Gp4	g.chr19:14071189C>T	Silent	DCAF15	p.V539V	DDB1 and CUL4 associ	16 (0.00)	261 (0.14)	0.38
11-14	Gp4	g.chr1:154996410T>G	Missense Mutation	DCST2	p.S590R	DC-STAMP domain co	19 (0.00)	44 (0.30)	0.79
11-14	Gp4	g.chr16:461486G>T	Missense Mutation	DECR2	p.A263S	2,4-dienoyl CoA reduct	20 (0.00)	23 (0.70)	1.86
11-14	Gp4	g.chr6:35287355C>T	Nonsense Mutation	DEF6	p.Q424*	differentially expressed	44 (0.00)	43 (0.19)	0.50
11-14	Gp4	g.chr17:40260019C>A	Silent	DHX58	p.V262V	DEXH (Asp-Glu-X-His	26 (0.00)	61 (0.16)	0.44
11-14	Gp4	g.chr20:61513008A>T	Missense Mutation	DIDO1	p.L1434I	death inducer-obliterato	49 (0.00)	102 (0.50)	1.33
11-14	Gp4	g.chr15:40662336G>T	Missense Mutation	DISP2	p.W1341C	dispatched homolog 2 (	133 (0.00)	288 (0.32)	0.86
11-14	Gp4	g.chr3:38163627G>A	Missense Mutation	DLEC1	p.A1696T	deleted in lung and esop	26 (0.00)	59 (0.42)	1.13
11-14	Gp4	g.chr3:52394415C>T	Silent	DNAH1	p.L1554L	dynein, axonemal, heav	66 (0.00)	74 (0.15)	0.40
11-14	Gp4	g.chr3:52394426G>A	Silent	DNAH1	p.T1557T	dynein, axonemal, heav	64 (0.02)	73 (0.15)	0.40
11-14	Gp4	g.chr3:52425541C>A	Missense Mutation	DNAH1	p.T3325N	dynein, axonemal, heav	30 (0.00)	269 (0.33)	0.87
11-14	Gp4	g.chr12:124371836C>A	Missense Mutation	DNAH10	p.L2873I	dynein, axonemal, heav	38 (0.00)	48 (0.44)	1.17
11-14	Gp4	g.chr7:21730401A>G	Silent	DNAH11	p.E1981E	dynein, axonemal, heav	59 (0.00)	256 (0.21)	0.72
11-14	Gp4	g.chr17:76490148G>A	Silent	DNAH17	p.I2121I	dynein, axonemal, heav	32 (0.00)	97 (0.14)	0.38
11-14	Gp4	g.chr16:4492374C>A	Missense Mutation	DNAJA3	p.P246T	DnaJ (Hsp40) homolog,	24 (0.00)	21 (0.76)	2.03
11-14	Gp4	g.chr11:6588836G>T	Nonsense Mutation	DNHD1	p.E4033*	dynein heavy chain dom	25 (0.00)	84 (0.36)	0.95
11-14	Gp4	g.chr21:37618023G>A	Missense Mutation	DOPEY2	p.A1249T	dopey family member 2	17 (0.00)	65 (0.31)	0.82
11-14	Gp4	g.chr19:2225411C>A	Silent	DOT1L	p.I1207I	DOT1-like histone H3K	15 (0.00)	11 (0.73)	1.94
11-14	Gp4	g.chr7:154598750C>A	Missense Mutation	DPP6	p.L532M	dipeptidyl-peptidase 6	83 (0.00)	37 (0.16)	0.52
11-14	Gp4	g.chr19:54140154T>C	Missense Mutation	DPRX	p.L163P	divergent-paired related	71 (0.00)	181 (0.26)	0.69
11-14	Gp4	g.chr21:41505816C>T	Missense Mutation	DSCAM	p.R1176K	Down syndrome cell ad	75 (0.00)	223 (0.71)	1.89
11-14	Gp4	g.chr1:167095972G>A	Missense Mutation	DUSP27	p.S535N	dual specificity phospha	90 (0.01)	142 (0.59)	1.58
11-14	Gp4	g.chr2:71913591C>T	Missense Mutation	DYSF	p.A2110V	dysferlin	22 (0.00)	299 (0.16)	0.43
11-14	Gp4	g.chr16:67914777T>C	Silent	EDC4	p.H805H	enhancer of mRNA dec	16 (0.00)	10 (0.80)	2.13
11-14	Gp4	g.chr7:36193977C>T	Missense Mutation	EEPD1	p.P15L	endonuclease/exonuclea	52 (0.00)	32 (0.34)	1.17
11-14	Gp4	g.chr11:65350869C>T	Missense Mutation	EHBP1L1	p.P909L	EH domain binding pro	75 (0.00)	105 (0.15)	0.41
11-14	Gp4	g.chr7:6066485C>A	Silent	EIF2AK1	p.P546P	eukaryotic translation in	60 (0.00)	65 (0.14)	0.50

11-14	Gp4	g.chr1:32694150C>T	Silent	EIF3I	p.D193D	eukaryotic translation in	69 (0.00)	69 (0.43)	1.16
11-14	Gp4	g.chr3:184038496C>T	Missense Mutation	EIF4G1	p.P119S	eukaryotic translation in	21 (0.00)	18 (0.94)	3.00
11-14	Gp4	g.chr16:67237471C>A	Silent	ELMO3	p.A681A	engulfment and cell mot	40 (0.00)	336 (0.32)	0.84
11-14	Gp4	g.chr2:27306488C>T	Silent	EMILIN1	p.D683D	elastin microfibril interf	47 (0.00)	65 (0.26)	0.70
11-14	Gp4	g.chr12:132547172C>A	Missense Mutation	EP400	p.Q2754K	E1A binding protein p4	29 (0.00)	113 (0.23)	0.61
11-14	Gp4	g.chr1:23208925G>A	Silent	EPHB2	p.P459P	EPH receptor B2	69 (0.00)	215 (0.17)	0.45
11-14	Gp4	g.chr1:23236886C>A	Silent	EPHB2	p.A839A	EPH receptor B2	16 (0.00)	56 (0.14)	0.38
11-14	Gp4	g.chr3:37034287T>C	Silent	EPM2AIP1	p.E94E	EPM2A (laforin) interac	26 (0.00)	59 (0.22)	0.59
11-14	Gp4	g.chr7:100320468T>C	Splice Site	EPO		erythropoietin	43 (0.00)	227 (0.30)	0.97
11-14	Gp4	g.chr19:55597513T>C	Missense Mutation	EPS8L1	p.Y535H	EPS8-like 1	17 (0.00)	214 (0.28)	0.75
11-14	Gp4	g.chr19:55597544G>A	Missense Mutation	EPS8L1	p.S545N	EPS8-like 1	21 (0.00)	253 (0.15)	0.40
11-14	Gp4	g.chr17:37872139G>A	Missense Mutation	ERBB2	p.R487Q	v-erb-b2 avian erythrobl	19 (0.00)	68 (0.22)	0.59
11-14	Gp4	g.chr11:124624112G>C	Missense Mutation	ESAM	p.I285M	endothelial cell adhesio	102 (0.00)	296 (0.27)	0.71
11-14	Gp4	g.chr4:5798860G>T	Silent	EVC	p.G666G	Ellis van Creveld syndr	28 (0.00)	33 (0.27)	0.73
11-14	Gp4	g.chr8:28574324G>A	Missense Mutation	EXTL3	p.V250M	exostosin-like glycosylt	67 (0.00)	134 (0.95)	2.53
11-14	Gp4	g.chr9:130279226G>T	Missense Mutation	FAM129B	p.Q295K	family with sequence si	114 (0.00)	82 (0.21)	0.55
11-14	Gp4	g.chr5:137342685G>T	Missense Mutation	FAM13B	p.A281E	family with sequence si	41 (0.00)	42 (0.48)	1.27
11-14	Gp4	g.chr8:21958234A>T	Missense Mutation	FAM160B2	p.S491C	family with sequence si	33 (0.00)	71 (0.38)	1.01
11-14	Gp4	g.chr9:140138623C>T	Splice Site	FAM166A	p.A289T	family with sequence si	28 (0.00)	266 (0.16)	0.42
11-14	Gp4	g.chr5:118970001G>A	Silent	FAM170A	p.E186E	family with sequence si	19 (0.00)	34 (0.53)	1.41
11-14	Gp4	g.chr5:118970011G>A	Missense Mutation	FAM170A	p.E190K	family with sequence si	18 (0.00)	34 (0.44)	1.18
11-14	Gp4	g.chr3:43074290A>G	Missense Mutation	FAM198A	p.M179V	family with sequence si	31 (0.00)	92 (0.52)	1.39
11-14	Gp4	g.chr6:82462451G>T	Missense Mutation	FAM46A	p.P14H	family with sequence si	22 (0.00)	38 (0.47)	1.26
11-14	Gp4	g.chr20:49209715T>C	Missense Mutation	FAM65C	p.E740G	family with sequence si	70 (0.00)	46 (0.52)	1.39
11-14	Gp4	g.chr9:131831409G>A	Splice Site	FAM73B		family with sequence si	40 (0.00)	435 (0.33)	0.88
11-14	Gp4	g.chr8:144812440G>T	Missense Mutation	FAM83H	p.P105T	family with sequence si	28 (0.00)	163 (0.14)	0.38
11-14	Gp4	g.chr13:99061742G>T	Missense Mutation	FARP1	p.C522F	FERM, RhoGEF (ARH	31 (0.00)	58 (0.21)	0.69
11-14	Gp4	g.chr1:16091687C>A	Missense Mutation	FBLIM1	p.A70E	filamin binding LIM pr	18 (0.00)	111 (0.25)	0.67
11-14	Gp4	g.chr22:45958798T>A	Nonsense Mutation	FBLN1	p.C568*	fibulin 1	15 (0.00)	34 (0.97)	2.59
11-14	Gp4	g.chr22:45959095C>T	Silent	FBLN1	p.T667T	fibulin 1	46 (0.00)	54 (0.96)	2.57
11-14	Gp4	g.chr5:147817999G>A	Missense Mutation	FBXO38	p.D988N	F-box protein 38	37 (0.00)	162 (0.27)	0.71
11-14	Gp4	g.chr19:40433401G>A	Nonsense Mutation	FCGBP	p.Q290*	Fc fragment of IgG bind	41 (0.02)	38 (0.71)	1.89
11-14	Gp4	g.chr11:72600883G>A	Silent	FCHSD2	p.H208H	FCH and double SH3 d	95 (0.00)	14 (0.93)	2.48
11-14	Gp4	g.chr19:35850251A>G	Missense Mutation	FFAR3	p.I153M	free fatty acid receptor	86 (0.00)	256 (0.19)	0.50
11-14	Gp4	g.chr4:15964164C>T	Missense Mutation	FGFBP2	p.E197K	fibroblast growth factor	25 (0.00)	89 (0.34)	0.90

11-14	Gp4	g.chr4:153896226G>T	Missense Mutation	FHDC1	p.D595Y	FH2 domain containing	16 (0.00)	21 (0.29)	0.76
11-14	Gp4	g.chr19:18652541C>A	Missense Mutation	FKBP8	p.M80I	FK506 binding protein	17 (0.00)	67 (0.70)	1.87
11-14	Gp4	g.chr7:55752849G>T	RNA	FKBP9L			60 (0.00)	16 (0.75)	2.55
11-14	Gp4	g.chr1:152276699A>G	Missense Mutation	FLG	p.W3555R	filaggrin	52 (0.00)	36 (0.33)	0.89
11-14	Gp4	g.chr1:152281361C>G	Missense Mutation	FLG	p.A2001P	filaggrin	110 (0.00)	68 (0.28)	0.75
11-14	Gp4	g.chr7:128477491G>A	Missense Mutation	FLNC	p.E247K	filamin C, gamma	48 (0.00)	343 (0.34)	1.07
11-14	Gp4	g.chr7:128484816A>G	Silent	FLNC	p.V1099V	filamin C, gamma	21 (0.00)	143 (0.92)	2.93
11-14	Gp4	g.chr5:180048590G>T	Silent	FLT4	p.R658R	fms-related tyrosine kin	30 (0.00)	267 (0.15)	0.39
11-14	Gp4	g.chr17:43319754C>A	Silent	FMNL1	p.L644L	formin-like 1	46 (0.00)	148 (0.28)	0.76
11-14	Gp4	g.chr17:80696462C>T	Missense Mutation	FN3K	p.P80L	fructosamine 3 kinase	19 (0.00)	149 (0.67)	1.79
11-14	Gp4	g.chr11:65660756T>C	Silent	FOSL1	p.K103K	FOS-like antigen 1	35 (0.00)	120 (0.38)	1.00
11-14	Gp4	g.chr11:126147575C>T	Silent	FOXRED1	p.N484N	FAD-dependent oxidore	38 (0.00)	64 (0.56)	1.50
11-14	Gp4	g.chr19:3527007C>T	Silent	FZR1	p.P139P	fizzy/cell division cycle	25 (0.00)	382 (0.18)	0.47
11-14	Gp4	g.chr7:99821555G>A	Nonsense Mutation	GATS	p.Q121*	GATS, stromal antigen	75 (0.00)	242 (0.25)	0.80
11-14	Gp4	g.chr7:150846187G>T	Missense Mutation	GBX1	p.A194E	gastrulation brain home	179 (0.00)	133 (0.45)	1.43
11-14	Gp4	g.chr19:13002176C>T	Missense Mutation	GCDH	p.L20F	glutaryl-CoA dehydrog	16 (0.00)	35 (0.83)	2.21
11-14	Gp4	g.chr16:2035884C>G	Missense Mutation	GFER	p.P158R	growth factor, augment	98 (0.01)	400 (0.75)	1.99
11-14	Gp4	g.chr5:179731826C>A	Missense Mutation	GFPT2	p.K596N	glutamine-fructose-6-ph	117 (0.00)	84 (0.62)	1.65
11-14	Gp4	g.chr22:25019142A>T	Missense Mutation	GGT1	p.S268C	gamma-glutamyltransfe	20 (0.00)	133 (0.59)	1.58
11-14	Gp4	g.chr22:22989270G>A	Missense Mutation	GGTLC2	p.D75N	gamma-glutamyltransfe	46 (0.00)	16 (0.94)	2.50
11-14	Gp4	g.chr22:22989281T>C	Silent	GGTLC2	p.D78D	gamma-glutamyltransfe	49 (0.00)	19 (0.89)	2.39
11-14	Gp4	g.chr7:100284039C>A	Missense Mutation	GIGYF1	p.A238S	GRB10 interacting GY	43 (0.00)	171 (0.15)	0.46
11-14	Gp4	g.chr2:121726350T>C	Missense Mutation	GLI2	p.I235T	GLI family zinc finger	26 (0.00)	17 (0.35)	0.94
11-14	Gp4	g.chr9:36147807T>A	Missense Mutation	GLIPR2	p.V13D	GLI pathogenesis-relate	114 (0.00)	26 (0.85)	2.26
11-14	Gp4	g.chr3:50290520A>G	Missense Mutation	GNAI2	p.D123G	guanine nucleotide bind	80 (0.00)	49 (0.16)	0.44
11-14	Gp4	g.chr3:50290557T>C	Silent	GNAI2	p.H135H	guanine nucleotide bind	82 (0.00)	44 (0.27)	0.73
11-14	Gp4	g.chr15:72958604C>T	Missense Mutation	GOLGA6B	p.A668V	golgin A6 family, mem	79 (0.01)	139 (0.23)	0.61
11-14	Gp4	g.chr15:28947240C>A	Nonsense Mutation	GOLGA8M	p.G587*	golgin A8 family, mem	63 (0.00)	14 (0.79)	2.53
11-14	Gp4	g.chr15:28947674G>A	Missense Mutation	GOLGA8M	p.R502C	golgin A8 family, mem	95 (0.00)	274 (0.41)	1.33
11-14	Gp4	g.chr9:88650466G>A	Nonsense Mutation	GOLM1	p.Q278*	golgi membrane protein	116 (0.00)	240 (0.98)	2.61
11-14	Gp4	g.chr1:27216243C>A	Silent	GPN2	p.V115V	GPN-loop GTPase 2	23 (0.00)	98 (0.74)	1.99
11-14	Gp4	g.chr3:119886457G>T	Silent	GPR156	p.R623R	G protein-coupled recep	85 (0.00)	125 (0.20)	0.64
11-14	Gp4	g.chr2:128408810G>T	Silent	GPR17	p.L195L	G protein-coupled recep	16 (0.00)	190 (0.76)	2.02
11-14	Gp4	g.chr16:10273967C>T	Missense Mutation	GRIN2A	p.G101E	glutamate receptor, iono	20 (0.00)	198 (0.23)	0.61
11-14	Gp4	g.chr6:34004089C>A	Missense Mutation	GRM4	p.A600S	glutamate receptor, met	19 (0.00)	223 (0.17)	0.44

11-14	Gp4	g.chr22:24325068G>T	Missense Mutation	GSTT2	p.G120W	glutathione S-transferas	40 (0.00)	93 (0.29)	0.77
11-14	Gp4	g.chr19:6389522C>A	Missense Mutation	GTF2F1	p.V87F	general transcription fac	35 (0.00)	174 (0.15)	0.40
11-14	Gp4	g.chr2:27558890C>T	Missense Mutation	GTF3C2	p.G454D	general transcription fac	40 (0.00)	193 (0.26)	0.69
11-14	Gp4	g.chr17:7918201G>C	Silent	GUCY2D	p.T867T	guanylate cyclase 2D,	34 (0.00)	29 (0.28)	0.74
11-14	Gp4	g.chr17:7918209C>T	Missense Mutation	GUCY2D	p.P870L	guanylate cyclase 2D,	35 (0.00)	30 (0.17)	0.44
11-14	Gp4	g.chr5:21482622G>A	RNA	GUSBP1		glucuronidase, beta pse	50 (0.00)	140 (0.40)	1.29
11-14	Gp4	g.chr15:73617510C>A	Missense Mutation	HCN4	p.K588N	hyperpolarization activa	107 (0.00)	248 (0.31)	0.84
11-14	Gp4	g.chr7:18819716C>T	Intron	HDAC9		histone deacetylase 9	44 (0.00)	194 (0.98)	2.61
11-14	Gp4	g.chr20:62193019C>T	Silent	HELZ2	p.P2257P	helicase with zinc finge	40 (0.03)	198 (0.95)	2.53
11-14	Gp4	g.chr20:62196134G>T	Silent	HELZ2	p.P1347P	helicase with zinc finge	16 (0.00)	49 (0.16)	0.44
11-14	Gp4	g.chr15:28510853G>T	Missense Mutation	HERC2	p.P594Q	HECT and RLD domai	97 (0.00)	40 (0.40)	1.29
11-14	Gp4	g.chr17:43227094C>T	Silent	HEXIM1	p.D179D	hexamethylene bis-acet	98 (0.00)	186 (0.20)	0.54
11-14	Gp4	g.chr4:145567867G>A	Missense Mutation	HHIP	p.V14M	hedgehog interacting pr	68 (0.00)	36 (0.28)	0.74
11-14	Gp4	g.chr12:51354803C>T	Silent	HIGD1C	p.Y49Y	HIG1 hypoxia inducible	37 (0.03)	53 (0.89)	2.36
11-14	Gp4	g.chr6:26225708A>T	Missense Mutation	HIST1H3E	p.N109I	histone cluster 1, H3e	126 (0.00)	308 (0.15)	0.39
11-14	Gp4	g.chr6:26250615A>T	Silent	HIST1H3F	p.R73R	histone cluster 1, H3f	75 (0.01)	179 (0.31)	0.83
11-14	Gp4	g.chr17:36093592G>T	Missense Mutation	HNF1B	p.P256H	HNF1 homeobox B	106 (0.01)	72 (0.64)	1.70
11-14	Gp4	g.chr9:86588261A>G	Silent	HNRNPK	p.H152H	heterogeneous nuclear	18 (0.00)	170 (0.19)	0.50
11-14	Gp4	g.chr12:54350326G>T	Missense Mutation	HOXC12	p.R275S	homeobox C12	69 (0.01)	200 (0.39)	1.03
11-14	Gp4	g.chr1:152187628A>G	Silent	HRNR	p.Y2159Y	hornerin	174 (0.00)	209 (0.22)	0.57
11-14	Gp4	g.chr1:152188211C>T	Missense Mutation	HRNR	p.G1965D	hornerin	306 (0.00)	602 (0.15)	0.41
11-14	Gp4	g.chr1:22168502C>A	Missense Mutation	HSPG2	p.E3062D	heparan sulfate proteogl	19 (0.00)	107 (0.46)	1.22
11-14	Gp4	g.chr14:106586168G>A	RNA	IGHV3-13		immunoglobulin heavy	81 (0.00)	73 (0.48)	1.28
11-14	Gp4	g.chr3:151154702G>A	Silent	IGSF10	p.H2549H	immunoglobulin superf	18 (0.00)	27 (0.81)	2.59
11-14	Gp4	g.chr22:37524889C>A	Splice Site	IL2RB		interleukin 2 receptor, b	17 (0.00)	135 (0.23)	0.61
11-14	Gp4	g.chr8:82591408G>T	Silent	IMPA1	p.P85P	inositol(myo)-1(or 4)-m	55 (0.00)	129 (0.45)	1.20
11-14	Gp4	g.chr3:10276163T>A	Missense Mutation	IRAK2	p.D431E	interleukin-1 receptor-a	46 (0.00)	164 (0.67)	1.79
11-14	Gp4	g.chr19:46388141G>C	Missense Mutation	IRF2BP1	p.H298D	interferon regulatory fac	47 (0.00)	57 (0.16)	0.42
11-14	Gp4	g.chr2:227660544C>T	Missense Mutation	IRS1	p.G971R	insulin receptor substrat	70 (0.00)	99 (0.47)	1.27
11-14	Gp4	g.chr2:227661138G>C	Missense Mutation	IRS1	p.H773D	insulin receptor substrat	40 (0.00)	115 (0.23)	0.60
11-14	Gp4	g.chr2:227661169G>T	Silent	IRS1	p.L762L	insulin receptor substrat	46 (0.02)	154 (0.31)	0.83
11-14	Gp4	g.chr17:3660424C>A	Missense Mutation	ITGAE	p.G342V	integrin, alpha E (antige	99 (0.00)	188 (0.24)	0.65
11-14	Gp4	g.chr17:3664384G>T	Missense Mutation	ITGAE	p.A174D	integrin, alpha E (antige	82 (0.01)	98 (0.98)	2.61
11-14	Gp4	g.chr21:46320388C>T	Silent	ITGB2	p.E191E	integrin, beta 2 (comple	21 (0.00)	117 (0.66)	2.33
11-14	Gp4	g.chr6:33636791C>T	Silent	ITPR3	p.L683L	inositol 1,4,5-trisphosph	26 (0.00)	55 (0.16)	0.44

11-14	Gp4	g.chr6:33638221C>T	Missense Mutation	ITPR3	p.P770L	inositol 1,4,5-trisphosph	50 (0.00)	328 (0.20)	0.54
11-14	Gp4	g.chr20:10622452A>G	Silent	JAG1	p.N887N	jagged 1	106 (0.00)	84 (0.42)	1.11
11-14	Gp4	g.chr6:24358083G>T	Silent	KAAG1	p.T72T	kidney associated antige	24 (0.00)	177 (0.18)	0.48
11-14	Gp4	g.chr3:123988039T>C	Silent	KALRN	p.H300H	kalirin, RhoGEF kinase	45 (0.00)	27 (0.89)	2.82
11-14	Gp4	g.chr12:5153809G>A	Missense Mutation	KCNA5	p.D166N	potassium voltage-gated	24 (0.00)	144 (0.92)	2.44
11-14	Gp4	g.chr19:18096236G>T	Missense Mutation	KCNN1	p.G345C	potassium intermediate/	29 (0.00)	56 (0.84)	2.24
11-14	Gp4	g.chr20:62070966G>A	Silent	KCNQ2	p.F304F	potassium voltage-gated	24 (0.00)	257 (0.39)	1.03
11-14	Gp4	g.chr7:128548463A>C	RNA	KCP		kielin/chordin-like prote	33 (0.00)	236 (0.26)	0.83
11-14	Gp4	g.chr11:67022444C>A	Missense Mutation	KDM2A	p.A1136D	lysine (K)-specific deme	124 (0.00)	306 (0.21)	0.57
11-14	Gp4	g.chr7:142640054C>A	Missense Mutation	KEL	p.A617S	Kell blood group, metal	20 (0.05)	115 (0.99)	3.15
11-14	Gp4	g.chr17:26955373G>A	Missense Mutation	KIAA0100	p.P1502S	KIAA0100	56 (0.00)	54 (0.93)	2.47
11-14	Gp4	g.chr17:73486329G>T	Silent	KIAA0195	p.L323L	KIAA0195	27 (0.00)	126 (0.20)	0.53
11-14	Gp4	g.chr17:73494298C>A	Missense Mutation	KIAA0195	p.L1178I	KIAA0195	41 (0.00)	71 (0.54)	1.43
11-14	Gp4	g.chr4:123145810C>A	Missense Mutation	KIAA1109	p.T924K	KIAA1109	27 (0.00)	78 (0.14)	0.38
11-14	Gp4	g.chr10:24790456G>T	Missense Mutation	KIAA1217	p.Q344H	KIAA1217	19 (0.00)	260 (0.47)	1.26
11-14	Gp4	g.chr6:138615148G>A	Silent	KIAA1244	p.T1129T	KIAA1244	64 (0.00)	20 (0.80)	2.13
11-14	Gp4	g.chr9:139700974G>A	Silent	KIAA1984	p.K376K		29 (0.00)	88 (0.36)	0.97
11-14	Gp4	g.chr1:200969535G>T	Silent	KIF21B	p.V556V	kinesin family member	26 (0.00)	282 (0.17)	0.46
11-14	Gp4	g.chr2:10188476G>C	Missense Mutation	KLF11	p.A338P	Kruppel-like factor 11	34 (0.00)	39 (0.90)	2.39
11-14	Gp4	g.chr1:6653470G>T	Missense Mutation	KLHL21	p.D583E	kelch-like family memb	25 (0.00)	46 (0.41)	0.89
11-14	Gp4	g.chr15:86311790C>T	Missense Mutation	KLHL25	p.D418N	kelch-like family memb	38 (0.00)	15 (0.33)	0.89
11-14	Gp4	g.chr12:49425391G>A	Missense Mutation	KMT2D	p.A4366V	lysine (K)-specific meth	43 (0.00)	134 (0.16)	0.44
11-14	Gp4	g.chr10:135038349G>T	Silent	KNDC1	p.R1735R	kinase non-catalytic C-l	20 (0.00)	31 (0.19)	0.52
11-14	Gp4	g.chr1:152732664C>A	Silent	KPRP	p.T200T	keratinocyte proline-ric	124 (0.00)	149 (0.14)	0.38
11-14	Gp4	g.chr12:53069014T>C	Missense Mutation	KRT1	p.K633R	keratin 1	152 (0.00)	16 (0.81)	2.17
11-14	Gp4	g.chr17:38975767A>G	Splice Site	KRT10		keratin 10	53 (0.00)	148 (0.31)	0.83
11-14	Gp4	g.chr17:18344869G>T	RNA	KRT16P1		keratin 16 pseudogene 1	44 (0.00)	54 (0.15)	0.40
11-14	Gp4	g.chr17:20405890G>A	RNA	KRT16P3		keratin 16 pseudogene 3	41 (0.00)	107 (0.26)	0.70
11-14	Gp4	g.chr17:20407221C>T	RNA	KRT16P3		keratin 16 pseudogene 3	93 (0.00)	24 (0.50)	1.33
11-14	Gp4	g.chr17:39553531G>A	Silent	KRT31	p.L87L	keratin 31	56 (0.00)	13 (0.69)	1.85
11-14	Gp4	g.chr12:52908748G>C	Missense Mutation	KRT5	p.S584C	keratin 5	24 (0.00)	27 (0.19)	0.49
11-14	Gp4	g.chr17:39183407T>G	Start Codon SNP	KRTAP1-5	p.M1L	keratin associated protei	41 (0.00)	93 (0.99)	2.64
11-14	Gp4	g.chr21:45993926G>T	Silent	KRTAP10-4	p.L97L	keratin associated protei	67 (0.00)	199 (0.13)	0.44
11-14	Gp4	g.chr21:46086507G>T	Silent	KRTAP12-2	p.S99S	keratin associated protei	52 (0.00)	67 (0.15)	0.53
11-14	Gp4	g.chr17:39273987C>A	Missense Mutation	KRTAP4-11	p.C194F	keratin associated protei	26 (0.00)	222 (0.42)	1.12

11-14	Gp4	g.chr17:39274016G>T	Nonsense Mutation	KRTAP4-11	p.C184*	keratin associated protei	23 (0.00)	223 (0.55)	1.47
11-14	Gp4	g.chr5:154173706G>A	Silent	LARP1	p.E295E	La ribonucleoprotein do	27 (0.00)	16 (0.94)	2.50
11-14	Gp4	g.chr16:67977041T>C	Missense Mutation	LCAT	p.K77E	lecithin-cholesterol acyl	44 (0.02)	121 (0.33)	0.88
11-14	Gp4	g.chr1:22142481C>A	Missense Mutation	LDLRAD2	p.P186H	low density lipoprotein	59 (0.00)	28 (0.96)	2.57
11-14	Gp4	g.chr13:21894510G>A	lincRNA	LINC00539		long intergenic non-prot	37 (0.00)	28 (0.96)	2.57
11-14	Gp4	g.chr1:201868736G>A	Missense Mutation	LMOD1	p.R469C	leiomodin 1 (smooth mu	52 (0.00)	173 (0.34)	0.91
11-14	Gp4	g.chr19:14269266C>A	Missense Mutation	LPHN1	p.G755C	latrophilin 1	17 (0.00)	47 (0.47)	1.25
11-14	Gp4	g.chr8:145746727G>T	Missense Mutation	LRRC14	p.E449D	leucine rich repeat conta	26 (0.00)	150 (0.25)	0.66
11-14	Gp4	g.chr15:101605734G>A	Missense Mutation	LRRK1	p.V1698M	leucine-rich repeat kinas	85 (0.00)	54 (0.70)	1.88
11-14	Gp4	g.chr17:48818533C>A	Missense Mutation	LUC7L3	p.L93I	LUC7-like 3 (S. cerevisi	57 (0.00)	54 (0.98)	2.62
11-14	Gp4	g.chr7:77674717C>A	Intron	MAGI2		membrane associated gu	134 (0.00)	66 (0.98)	2.63
11-14	Gp4	g.chr7:78197022C>T	Intron	MAGI2		membrane associated gu	114 (0.01)	169 (0.99)	2.65
11-14	Gp4	g.chr7:78347033T>C	Intron	MAGI2		membrane associated gu	25 (0.00)	47 (0.26)	0.68
11-14	Gp4	g.chr7:78409723C>T	Intron	MAGI2		membrane associated gu	83 (0.01)	192 (0.79)	2.10
11-14	Gp4	g.chr7:78415712C>A	Intron	MAGI2		membrane associated gu	105 (0.00)	21 (0.76)	2.03
11-14	Gp4	g.chr15:43819773C>T	Silent	MAP1A	p.S2272S	microtubule-associated	65 (0.00)	68 (0.53)	1.41
11-14	Gp4	g.chr17:61770961G>T	Nonsense Mutation	MAP3K3	p.E565*	mitogen-activated protei	95 (0.00)	481 (0.19)	0.49
11-14	Gp4	g.chr19:45767964G>A	Silent	MARK4	p.E126E	MAP/microtubule affini	78 (0.00)	94 (0.78)	2.07
11-14	Gp4	g.chr19:45767968G>A	Missense Mutation	MARK4	p.E128K	MAP/microtubule affini	76 (0.00)	92 (0.79)	2.12
11-14	Gp4	g.chr3:186953985C>A	Missense Mutation	MASP1	p.Q445H	mannan-binding lectin s	43 (0.00)	131 (0.22)	0.70
11-14	Gp4	g.chr18:74696849C>T	Splice Site	MBP	p.G183E	myelin basic protein	39 (0.03)	115 (0.70)	2.40
11-14	Gp4	g.chr11:119185394C>A	Nonsense Mutation	MCAM	p.E156*	melanoma cell adhesion	25 (0.00)	44 (0.32)	0.85
11-14	Gp4	g.chr7:99693552G>A	Silent	MCM7	p.A480A	minichromosome maint	30 (0.00)	166 (0.99)	3.14
11-14	Gp4	g.chr6:119149201C>T	Missense Mutation	MCM9	p.V541M	minichromosome maint	76 (0.00)	33 (0.15)	0.40
11-14	Gp4	g.chr1:156437879C>A	Missense Mutation	MEF2D	p.R487L	myocyte enhancer facto	30 (0.00)	141 (0.17)	0.45
11-14	Gp4	g.chr15:66222218C>A	Missense Mutation	MEGF11	p.W471L	multiple EGF-like-doma	22 (0.00)	16 (0.38)	1.00
11-14	Gp4	g.chr8:8749111C>T	Silent	MFHAS1	p.V486V	malignant fibrous histio	21 (0.00)	86 (0.27)	0.71
11-14	Gp4	g.chr22:37872998C>A	Missense Mutation	MFNG	p.A195S	MFNG O-fucosylpeptid	25 (0.00)	64 (0.92)	2.46
11-14	Gp4	g.chr2:24244563C>T	Missense Mutation	MFSD2B	p.P243S	major facilitator superfa	17 (0.00)	51 (0.22)	0.58
11-14	Gp4	g.chr16:14306239A>G	Silent	MKL2	p.E83E	MKL/myocardin-like 2	19 (0.00)	35 (0.20)	0.53
11-14	Gp4	g.chr16:55519210G>A	Splice Site	MMP2		matrix metallopeptidase	27 (0.00)	78 (0.99)	2.63
11-14	Gp4	g.chr11:18955861C>T	Silent	MRGPRX1	p.E157E	MAS-related GPR, mem	62 (0.00)	187 (0.74)	1.98
11-14	Gp4	g.chr2:234737372C>A	Silent	MROH2A	p.R1404R	maestro heat-like repeat	49 (0.00)	40 (0.15)	0.40
11-14	Gp4	g.chr1:55136168A>T	Splice Site	MROH7		maestro heat-like repeat	19 (0.00)	18 (0.61)	1.63
11-14	Gp4	g.chr1:55174727T>C	Silent	MROH7	p.D1236D	maestro heat-like repeat	51 (0.00)	40 (0.40)	1.07

11-14	Gp4	g.chr19:10368911T>C	Silent	MRPL4	p.H153H	mitochondrial ribosoma	16 (0.00)	45 (0.76)	2.01
11-14	Gp4	g.chr17:55752460G>A	Silent	MSI2	p.P306P	musashi RNA-binding p	18 (0.00)	15 (0.33)	0.89
11-14	Gp4	g.chr1:237060345C>G	Nonsense Mutation	MTR	p.S1213*	5-methyltetrahydrofolat	52 (0.00)	23 (0.61)	1.62
11-14	Gp4	g.chr11:1265401G>C	Missense Mutation	MUC5B	p.G2431R	mucin 5B, oligomeric m	19 (0.00)	134 (0.76)	2.03
11-14	Gp4	g.chr11:1265418C>T	Silent	MUC5B	p.L2436L	mucin 5B, oligomeric m	19 (0.00)	132 (0.76)	2.02
11-14	Gp4	g.chr11:1018717G>C	Missense Mutation	MUC6	p.P1362A	mucin 6, oligomeric mu	28 (0.00)	40 (0.50)	1.33
11-14	Gp4	g.chr11:69063368A>G	Missense Mutation	MYEOV	p.N151D	myeloma overexpressed	18 (0.00)	119 (0.18)	0.47
11-14	Gp4	g.chr16:15814768C>G	Missense Mutation	MYH11	p.K1573N	myosin, heavy chain 11,	44 (0.00)	44 (0.18)	0.48
11-14	Gp4	g.chr17:1371298A>G	Silent	MYO1C	p.D925D	myosin IC	19 (0.00)	54 (0.19)	0.49
11-14	Gp4	g.chr19:17212916C>G	Missense Mutation	MYO9B	p.T130R	myosin IXB	44 (0.00)	130 (0.18)	0.49
11-14	Gp4	g.chr8:2027660G>A	Silent	MYOM2	p.E494E	myomesin 2	82 (0.00)	71 (0.89)	2.37
11-14	Gp4	g.chr8:2092662C>T	Silent	MYOM2	p.I1385I	myomesin 2	108 (0.00)	38 (0.71)	1.89
11-14	Gp4	g.chr8:2092675C>T	Missense Mutation	MYOM2	p.H1390Y	myomesin 2	50 (0.00)	44 (0.64)	1.70
11-14	Gp4	g.chr12:57486865C>A	Missense Mutation	NAB2	p.P388H	NGFI-A binding protein	61 (0.00)	192 (0.35)	0.94
11-14	Gp4	g.chr11:71184324G>T	Splice Site	NADSYN1	p.E154*	NAD synthetase 1	53 (0.00)	268 (0.29)	0.77
11-14	Gp4	g.chr22:42463293A>G	Splice Site	NAGA	p.V109A	N-acetylgalactosaminid	18 (0.00)	70 (0.14)	0.38
11-14	Gp4	g.chr7:100818086C>A	Start Codon SNP	NAT16	p.M1I	N-acetyltransferase 16 (	16 (0.00)	40 (0.57)	1.83
11-14	Gp4	g.chr3:47045568C>A	Splice Site	NBEAL2	p.G1961G	neurobeachin-like 2	53 (0.00)	264 (0.50)	1.33
11-14	Gp4	g.chr22:50960840A>G	Silent	NCAPH2	p.A434A	non-SMC condensin II	37 (0.00)	138 (0.72)	1.91
11-14	Gp4	g.chr3:48718768G>A	Silent	NCKIPSD	p.A348A	NCK interacting protein	51 (0.00)	263 (0.32)	0.85
11-14	Gp4	g.chr3:130799379C>T	Missense Mutation	NEK11	p.H95Y	NIMA-related kinase 11	16 (0.00)	99 (0.19)	0.61
11-14	Gp4	g.chr18:77170907C>G	Missense Mutation	NFATC1	p.S211C	nuclear factor of activat	25 (0.00)	178 (0.63)	1.69
11-14	Gp4	g.chr18:77246330C>A	Silent	NFATC1	p.L712L	nuclear factor of activat	98 (0.00)	287 (0.15)	0.40
11-14	Gp4	g.chr16:69374112G>A	Silent	NIP7	p.K53K	NIP7, nucleolar pre-rR	60 (0.00)	74 (0.57)	1.51
11-14	Gp4	g.chr3:52523622C>A	Nonsense Mutation	NISCH	p.C1128*	nischarin	37 (0.00)	42 (0.29)	0.76
11-14	Gp4	g.chr3:138023809T>G	Missense Mutation	NME9	p.T233P	NME/NM23 family me	50 (0.00)	144 (0.12)	0.40
11-14	Gp4	g.chr19:15302358C>T	Missense Mutation	NOTCH3	p.G305S	notch 3	17 (0.00)	120 (0.32)	0.84
11-14	Gp4	g.chr4:156135197C>A	Missense Mutation	NPY2R	p.P36T	neuropeptide Y receptor	34 (0.00)	126 (0.75)	2.01
11-14	Gp4	g.chr4:156135213T>A	Missense Mutation	NPY2R	p.I41K	neuropeptide Y receptor	28 (0.00)	169 (0.18)	0.47
11-14	Gp4	g.chr11:47283146C>T	Missense Mutation	NR1H3	p.R253C	nuclear receptor subfam	32 (0.00)	81 (0.37)	0.99
11-14	Gp4	g.chr5:92923765C>A	Silent	NR2F1	p.R202R	nuclear receptor subfam	35 (0.00)	59 (0.20)	0.54
11-14	Gp4	g.chr12:52448947T>C	Missense Mutation	NR4A1	p.Y279H	nuclear receptor subfam	102 (0.00)	173 (0.16)	0.43
11-14	Gp4	g.chr11:51411939G>A	Missense Mutation	OR4A5	p.H153Y	olfactory receptor, famil	34 (0.00)	15 (0.53)	1.42
11-14	Gp4	g.chr11:51412079C>T	Missense Mutation	OR4A5	p.G106D	olfactory receptor, famil	23 (0.00)	18 (0.50)	1.33
11-14	Gp4	g.chr9:125551323G>A	Missense Mutation	OR5C1	p.V38I	olfactory receptor, famil	57 (0.00)	83 (0.36)	0.96

11-14	Gp4	g.chr2:240984789C>T	Missense Mutation	OR6B3	p.C234Y	olfactory receptor, famil	48 (0.00)	62 (0.79)	2.11
11-14	Gp4	g.chr12:133196910C>T	Silent	P2RX2	p.H204H	purinergic receptor P2X	43 (0.00)	169 (0.60)	1.61
11-14	Gp4	g.chr1:26315943C>T	Silent	PAFAH2	p.A80A	platelet-activating facto	25 (0.00)	57 (0.89)	2.39
11-14	Gp4	g.chr12:56720699C>T	Missense Mutation	PAN2	p.D322N	PAN2 poly(A) specific	27 (0.00)	10 (0.90)	2.40
11-14	Gp4	g.chr3:51978417C>A	Silent	PARP3	p.G115G	poly (ADP-ribose) poly	112 (0.00)	386 (0.17)	0.46
11-14	Gp4	g.chr1:154918685G>T	Missense Mutation	PBXIP1	p.H489N	pre-B-cell leukemia hon	61 (0.00)	29 (0.45)	1.20
11-14	Gp4	g.chr1:154918775C>A	Missense Mutation	PBXIP1	p.A459S	pre-B-cell leukemia hon	70 (0.00)	60 (0.47)	1.24
11-14	Gp4	g.chr13:67477723G>A	Silent	PCDH9	p.S1017S	protocadherin 9	40 (0.00)	77 (0.99)	3.18
11-14	Gp4	g.chr5:140209338C>A	Missense Mutation	PCDHA6	p.F554L	protocadherin alpha 6	42 (0.00)	190 (0.14)	0.38
11-14	Gp4	g.chr5:140215864C>T	Silent	PCDHA7	p.S632S	protocadherin alpha 7	21 (0.00)	130 (0.69)	1.85
11-14	Gp4	g.chr5:140810756G>A	Missense Mutation	PCDHGA12	p.E144K	protocadherin gamma su	243 (0.00)	259 (0.42)	1.12
11-14	Gp4	g.chr5:140810773G>A	Silent	PCDHGA12	p.E149E	protocadherin gamma su	263 (0.00)	238 (0.75)	1.99
11-14	Gp4	g.chr20:44576197G>T	Missense Mutation	PCIF1	p.A640S	PDX1 C-terminal inhibi	31 (0.00)	87 (0.26)	0.70
11-14	Gp4	g.chr5:32087665G>A	Missense Mutation	PDZD2	p.E1371K	PDZ domain containing	28 (0.00)	19 (0.95)	3.05
11-14	Gp4	g.chr3:73433215G>A	Silent	PDZRN3	p.P551P	PDZ domain containing	24 (0.00)	75 (0.23)	0.73
11-14	Gp4	g.chr11:66238721G>T	Missense Mutation	PELI3	p.G54V	pellino E3 ubiquitin pro	31 (0.00)	86 (0.38)	1.02
11-14	Gp4	g.chr17:8052792C>T	Missense Mutation	PER1	p.G281R	period circadian clock 1	17 (0.00)	85 (0.32)	0.85
11-14	Gp4	g.chr3:179519752G>A	Missense Mutation	PEX5L	p.P582L	peroxisomal biogenesis	39 (0.00)	68 (0.99)	3.13
11-14	Gp4	g.chr17:8172503C>T	Missense Mutation	PFAS	p.P1313L	phosphoribosylformylgl	22 (0.00)	101 (0.67)	1.80
11-14	Gp4	g.chr5:133901941C>T	Missense Mutation	PHF15	p.P369S		22 (0.00)	32 (0.78)	2.08
11-14	Gp4	g.chr16:30768193C>T	Silent	PHKG2	p.T332T	phosphorylase kinase, g	41 (0.00)	168 (0.57)	1.51
11-14	Gp4	g.chr18:60501230A>G	Intron	PHLPP1		PH domain and leucine	43 (0.00)	54 (0.43)	1.14
11-14	Gp4	g.chr19:4013223G>T	Silent	PIAS4	p.V110V	protein inhibitor of activ	20 (0.05)	131 (0.23)	0.61
11-14	Gp4	g.chr16:88786872G>T	Missense Mutation	PIEZO1	p.A1957D	piezo-type mechanosens	42 (0.00)	195 (0.41)	1.09
11-14	Gp4	g.chr1:160001473G>T	Silent	PIGM	p.A19A	phosphatidylinositol gly	16 (0.00)	89 (0.20)	0.54
11-14	Gp4	g.chr10:98469522G>T	Missense Mutation	PIK3AP1	p.H78N	phosphoinositide-3-kina	32 (0.00)	112 (0.21)	0.57
11-14	Gp4	g.chr1:9777144C>T	Missense Mutation	PIK3CD	p.P303L	phosphatidylinositol-4,5	43 (0.00)	76 (0.50)	1.08
11-14	Gp4	g.chr3:130424435C>T	Missense Mutation	PIK3R4	p.A968T	phosphoinositide-3-kina	62 (0.00)	29 (0.97)	3.07
11-14	Gp4	g.chr16:81155212G>T	RNA	PKD1L2		polycystic kidney diseas	31 (0.00)	143 (0.73)	1.96
11-14	Gp4	g.chr19:40882562C>T	Missense Mutation	PLD3	p.R356C	phospholipase D family	46 (0.00)	113 (0.83)	2.22
11-14	Gp4	g.chr8:145009186C>A	Missense Mutation	PLEC	p.R410M	plectin	20 (0.00)	134 (0.69)	1.83
11-14	Gp4	g.chr12:6424816G>T	Splice Site	PLEKHG6		pleckstrin homology do	16 (0.00)	72 (0.68)	1.81
11-14	Gp4	g.chr2:43906044G>A	Missense Mutation	PLEKHH2	p.A56T	pleckstrin homology do	57 (0.00)	101 (0.83)	2.22
11-14	Gp4	g.chr19:17476251G>C	Silent	PLVAP	p.S341S	plasmalemma vesicle as	19 (0.00)	23 (0.35)	0.93
11-14	Gp4	g.chr3:126735824G>C	Missense Mutation	PLXNA1	p.A1074P	plexin A1	31 (0.00)	97 (0.12)	0.39

11-14	Gp4	g.chr3:129280708C>A	Missense Mutation	PLXND1	p.D1622Y	plexin D1	16 (0.00)	35 (0.17)	0.54
11-14	Gp4	g.chr22:44342116A>G	Missense Mutation	PNPLA3	p.K434E	patatin-like phospholipa	38 (0.00)	402 (0.63)	1.67
11-14	Gp4	g.chr19:14043542G>T	Silent	PODNL1	p.V505V	podocan-like 1	29 (0.00)	162 (0.77)	2.06
11-14	Gp4	g.chr3:121240990A>G	Missense Mutation	POLQ	p.V372A	polymerase (DNA direc	94 (0.00)	40 (0.60)	1.91
11-14	Gp4	g.chr8:22106091A>G	Missense Mutation	POLR3D	p.E195G	polymerase (RNA) III (	56 (0.00)	39 (0.95)	2.53
11-14	Gp4	g.chr2:130877612G>T	Silent	POTEF	p.V159V	POTE ankyrin domain f	123 (0.00)	288 (0.51)	1.35
11-14	Gp4	g.chr14:19553589G>T	Missense Mutation	POTEG	p.R58M	POTE ankyrin domain f	50 (0.02)	31 (0.55)	1.46
11-14	Gp4	g.chr6:35391771C>A	Missense Mutation	PPARD	p.A158E	peroxisome proliferator-	16 (0.00)	47 (0.60)	1.59
11-14	Gp4	g.chr5:149212744A>G	Missense Mutation	PPARGC1B	p.T370A	peroxisome proliferator-	18 (0.00)	50 (0.40)	1.07
11-14	Gp4	g.chr1:3102840G>T	Missense Mutation	PRDM16	p.K63N	PR domain containing 1	41 (0.00)	299 (0.21)	0.56
11-14	Gp4	g.chr7:716929G>T	Missense Mutation	PRKAR1B	p.T126N	protein kinase, cAMP-d	30 (0.00)	21 (0.95)	3.40
11-14	Gp4	g.chr1:107599753C>T	Missense Mutation	PRMT6	p.P139L	protein arginine methylt	33 (0.00)	112 (0.24)	0.64
11-14	Gp4	g.chr20:5282749G>A	Silent	PROKR2	p.D364D	prokineticin receptor 2	40 (0.03)	88 (0.77)	2.06
11-14	Gp4	g.chr11:60670102C>T	Missense Mutation	PRPF19	p.G139S	pre-mRNA processing f	60 (0.00)	109 (0.17)	0.44
11-14	Gp4	g.chr5:139192935G>T	Missense Mutation	PSD2	p.S138I	pleckstrin and Sec7 don	35 (0.00)	79 (0.16)	0.44
11-14	Gp4	g.chr10:23482635T>C	Missense Mutation	PTF1A	p.S263P	pancreas specific transc	71 (0.00)	11 (0.82)	2.18
11-14	Gp4	g.chr10:23482738C>T	Missense Mutation	PTF1A	p.T297I	pancreas specific transc	50 (0.00)	13 (0.77)	2.05
11-14	Gp4	g.chr19:46205078C>T	Silent	QPCTL	p.N303N	glutaminyl-peptide cycl	58 (0.00)	75 (0.95)	2.52
11-14	Gp4	g.chr1:180165706C>A	Missense Mutation	QSOX1	p.T593N	quiescin Q6 sulfhydryl	51 (0.00)	129 (0.16)	0.43
11-14	Gp4	g.chr20:42965835T>A	Missense Mutation	R3HDML	p.L13Q	R3H domain containing	19 (0.00)	176 (0.18)	0.47
11-14	Gp4	g.chr16:570807G>A	Missense Mutation	RAB11FIP3	p.E747K	RAB11 family interacti	22 (0.00)	77 (0.26)	0.69
11-14	Gp4	g.chr16:28926053C>A	Missense Mutation	RABEP2	p.K161N	rabaptin, RAB GTPase	21 (0.00)	41 (0.54)	1.43
11-14	Gp4	g.chr14:24736083G>T	Missense Mutation	RABGGTA	p.L65I	Rab geranylgeranyltrans	26 (0.00)	222 (0.20)	0.53
11-14	Gp4	g.chr3:120449574G>A	Missense Mutation	RABL3	p.S36L	RAB, member of RAS	49 (0.00)	111 (0.99)	3.15
11-14	Gp4	g.chr3:120449577G>A	Missense Mutation	RABL3	p.P35L	RAB, member of RAS	49 (0.00)	113 (0.99)	3.15
11-14	Gp4	g.chr3:141327352G>C	Missense Mutation	RASA2	p.E680Q	RAS p21 protein activat	45 (0.00)	31 (0.90)	2.87
11-14	Gp4	g.chr4:40440436G>A	Missense Mutation	RBM47	p.P159S	RNA binding motif prot	44 (0.00)	236 (0.49)	1.31
11-14	Gp4	g.chr12:7280979G>T	Missense Mutation	RBP5	p.L37M	retinol binding protein 5	36 (0.00)	94 (0.96)	2.55
11-14	Gp4	g.chr1:17747283C>T	Silent	RCC2	p.G262G	regulator of chromosom	82 (0.01)	17 (0.47)	1.25
11-14	Gp4	g.chr1:17752146C>A	Silent	RCC2	p.G138G	regulator of chromosom	39 (0.00)	77 (0.43)	1.14
11-14	Gp4	g.chr11:63681979T>C	Missense Mutation	RCOR2	p.Y172C	REST corepressor 2	103 (0.00)	468 (0.21)	0.57
11-14	Gp4	g.chr17:73627535G>C	Missense Mutation	RECQL5	p.F481L	RecQ protein-like 5	26 (0.00)	47 (0.36)	0.96
11-14	Gp4	g.chr1:192613530G>A	Splice Site	RGS13		regulator of G-protein si	19 (0.00)	49 (0.47)	1.25
11-14	Gp4	g.chr8:22873158G>T	Missense Mutation	RHOBTB2	p.C645F	Rho-related BTB domai	30 (0.00)	80 (0.69)	1.83
11-14	Gp4	g.chr16:67685168G>T	Missense Mutation	RLTPR	p.A755S	RGD motif, leucine rich	113 (0.00)	23 (0.35)	0.93

11-14	Gp4	g.chr9:94487198C>T	Missense Mutation	ROR2	p.M526I	receptor tyrosine kinase	67 (0.00)	166 (0.62)	1.65
11-14	Gp4	g.chr8:92883015G>A	lincRNA	RP11-122C21.1			17 (0.00)	114 (0.22)	0.58
11-14	Gp4	g.chr14:101324732C>A	RNA	RP11-123M6.2			17 (0.00)	100 (0.63)	1.68
11-14	Gp4	g.chr9:66458674T>G	lincRNA	RP11-262H14.1			21 (0.00)	42 (0.19)	0.51
11-14	Gp4	g.chr1:143426628C>T	lincRNA	RP11-435B5.4			31 (0.00)	28 (0.82)	2.19
11-14	Gp4	g.chr14:24600979T>C	Missense Mutation	RP11-468E2.6	p.S257P		31 (0.00)	30 (0.93)	2.49
11-14	Gp4	g.chr4:105708864C>A	lincRNA	RP11-556I14.2			22 (0.00)	25 (0.20)	0.53
11-14	Gp4	g.chr10:52418960G>T	RNA	RP11-564C4.6			36 (0.00)	74 (0.24)	0.65
11-14	Gp4	g.chr14:20136974C>A	RNA	RP11-597A11.1			47 (0.00)	63 (0.35)	0.93
11-14	Gp4	g.chr12:90313340A>T	lincRNA	RP11-654D12.2			85 (0.00)	320 (0.15)	0.39
11-14	Gp4	g.chr17:78820353A>G	Silent	RPTOR	p.E431E	regulatory associated pr	18 (0.00)	24 (0.42)	1.11
11-14	Gp4	g.chr3:51970353G>A	Missense Mutation	RRP9	p.R219C	ribosomal RNA process	48 (0.00)	114 (0.48)	1.29
11-14	Gp4	g.chr2:234229328G>A	Silent	SAG	p.V78V	S-antigen; retina and pir	59 (0.00)	295 (0.29)	0.77
11-14	Gp4	g.chr16:51175862G>A	Missense Mutation	SALL1	p.P91S	spalt-like transcription f	67 (0.00)	135 (0.74)	1.98
11-14	Gp4	g.chr20:50408315C>G	Missense Mutation	SALL4	p.R236P	spalt-like transcription f	28 (0.00)	57 (0.77)	2.06
11-14	Gp4	g.chr7:92733327T>A	Missense Mutation	SAMD9	p.Y695F	sterile alpha motif doma	94 (0.00)	11 (0.91)	2.89
11-14	Gp4	g.chr22:50900508C>T	Missense Mutation	SBF1	p.G813S	SET binding factor 1	21 (0.00)	16 (0.50)	1.33
11-14	Gp4	g.chr7:29963574C>T	Silent	SCRN1	p.*415*	secernin 1	82 (0.00)	26 (0.23)	0.79
11-14	Gp4	g.chr9:139298580C>T	Missense Mutation	SDCCAG3	p.V379M	serologically defined co	19 (0.00)	159 (0.64)	1.69
11-14	Gp4	g.chr9:139298593A>G	Silent	SDCCAG3	p.G374G	serologically defined co	21 (0.00)	158 (0.62)	1.65
11-14	Gp4	g.chr22:30887595T>C	Missense Mutation	SEC14L4	p.E349G	SEC14-like 4 (S. cerevis	35 (0.00)	35 (0.20)	0.53
11-14	Gp4	g.chr15:90771594A>G	Missense Mutation	SEMA4B	p.K745E	sema domain, immunog	61 (0.00)	103 (0.17)	0.47
11-14	Gp4	g.chr2:74907149C>G	Missense Mutation	SEMA4F	p.T709S	sema domain, immunog	18 (0.00)	79 (0.73)	1.96
11-14	Gp4	g.chr15:74703929T>C	Silent	SEMA7A	p.Q515Q	semaphorin 7A, GPI me	22 (0.00)	76 (0.39)	1.05
11-14	Gp4	g.chr8:22020698G>A	Missense Mutation	SFTPC	p.V50M	surfactant protein C	80 (0.00)	314 (0.28)	0.75
11-14	Gp4	g.chr17:48245326G>T	Missense Mutation	SGCA	p.D111Y	sarcoglycan, alpha (50k	20 (0.00)	149 (0.91)	2.43
11-14	Gp4	g.chr22:40804387C>G	Missense Mutation	SGSM3	p.P579R	small G protein signalin	26 (0.00)	36 (0.72)	1.93
11-14	Gp4	g.chrX:123504056C>T	Missense Mutation	SH2D1A	p.R78W	SH2 domain containing	29 (0.00)	178 (0.89)	1.49
11-14	Gp4	g.chr1:21053551C>A	Silent	SH2D5	p.R62R	SH2 domain containing	29 (0.00)	117 (0.34)	0.91
11-14	Gp4	g.chr22:38038905G>A	Silent	SH3BP1	p.K96K	SH3-domain binding pr	18 (0.00)	199 (0.32)	0.84
11-14	Gp4	g.chr19:4365564C>T	Silent	SH3GL1	p.K82K	SH3-domain GRB2-like	23 (0.00)	224 (0.17)	0.44
11-14	Gp4	g.chr11:70332059G>T	Missense Mutation	SHANK2	p.Q851K	SH3 and multiple ankyr	15 (0.00)	113 (0.19)	0.52
11-14	Gp4	g.chr1:154458520G>A	Silent	SHE	p.I400I	Src homology 2 domain	26 (0.00)	14 (0.79)	2.10
11-14	Gp4	g.chr3:72866019G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	50 (0.00)	138 (0.99)	2.65
11-14	Gp4	g.chr19:50474661G>T	RNA	SIGLEC16		sialic acid binding Ig-lik	21 (0.00)	56 (0.36)	0.95

11-14	Gp4	g.chr19:52034443G>T	Missense Mutation	SIGLEC6	p.T133K	sialic acid binding Ig-lik	85 (0.00)	47 (0.98)	2.61
11-14	Gp4	g.chr10:21805248C>A	Missense Mutation	SKIDA1	p.A502S	SKI/DACH domain con	22 (0.00)	17 (0.53)	1.41
11-14	Gp4	g.chr2:219258871C>A	Missense Mutation	SLC11A1	p.T448K	solute carrier family 11	33 (0.00)	33 (0.15)	0.40
11-14	Gp4	g.chr11:65004169G>A	RNA	SLC22A20		solute carrier family 22,	15 (0.00)	17 (0.47)	1.25
11-14	Gp4	g.chr22:18069992C>T	Missense Mutation	SLC25A18	p.T167I	solute carrier family 25	67 (0.00)	203 (0.17)	0.45
11-14	Gp4	g.chr17:8197798C>A	Missense Mutation	SLC25A35	p.A110S	solute carrier family 25,	16 (0.00)	89 (0.81)	2.16
11-14	Gp4	g.chr12:58014034G>A	Missense Mutation	SLC26A10	p.A11T	solute carrier family 26,	21 (0.00)	39 (0.41)	1.09
11-14	Gp4	g.chr20:45354527C>T	Silent	SLC2A10	p.T284T	solute carrier family 2 (	158 (0.00)	127 (0.22)	0.59
11-14	Gp4	g.chr22:24226045G>A	Silent	SLC2A11	p.V357V	solute carrier family 2 (	119 (0.00)	207 (0.20)	0.54
11-14	Gp4	g.chr6:137245505C>T	Nonsense Mutation	SLC35D3	p.Q308*	solute carrier family 35,	18 (0.00)	50 (0.30)	0.80
11-14	Gp4	g.chr11:124950604G>A	Missense Mutation	SLC37A2	p.G208S	solute carrier family 37	19 (0.00)	26 (0.31)	0.82
11-14	Gp4	g.chr17:79220703C>T	Missense Mutation	SLC38A10	p.E742K	solute carrier family 38,	18 (0.00)	257 (0.30)	0.79
11-14	Gp4	g.chr1:205628740C>A	Missense Mutation	SLC45A3	p.M428I	solute carrier family 45,	20 (0.00)	179 (0.18)	0.48
11-14	Gp4	g.chr7:150773165C>T	Silent	SLC4A2	p.A1165A	solute carrier family 4 (	42 (0.00)	89 (0.31)	1.00
11-14	Gp4	g.chr3:195955762G>A	Missense Mutation	SLC51A	p.V202I	solute carrier family 51,	58 (0.00)	61 (0.15)	0.47
11-14	Gp4	g.chr10:98803137G>A	Missense Mutation	SLIT1	p.L663F	slit homolog 1 (Drosoph	18 (0.00)	96 (0.30)	0.81
11-14	Gp4	g.chr17:18219120A>G	Missense Mutation	SMCR8	p.D6G	Smith-Magenis syndron	87 (0.00)	159 (0.36)	0.97
11-14	Gp4	g.chr22:31494659C>T	Silent	SMTN	p.F722F	smoothelin	23 (0.00)	50 (0.24)	0.64
11-14	Gp4	g.chr15:25444673G>A	RNA	SNHG14		small nucleolar RNA ho	43 (0.00)	40 (0.75)	2.42
11-14	Gp4	g.chr21:34924000G>T	Missense Mutation	SON	p.M821I	SON DNA binding prot	19 (0.00)	20 (0.75)	2.00
11-14	Gp4	g.chr17:4863076C>T	Missense Mutation	SPAG7	p.A134T	sperm associated antige	45 (0.00)	37 (0.19)	0.50
11-14	Gp4	g.chr19:11258496C>T	Missense Mutation	SPC24	p.G162D	SPC24, NDC80 kinetoc	31 (0.00)	86 (0.28)	0.74
11-14	Gp4	g.chr7:44047017C>T	Silent	SPDYE1	p.N261N	speedy/RINGO cell cyc	75 (0.00)	113 (0.12)	0.42
11-14	Gp4	g.chr2:220348890G>T	Silent	SPEG	p.L2235L	SPEG complex locus	32 (0.00)	67 (0.31)	0.84
11-14	Gp4	g.chr2:220354108A>G	Missense Mutation	SPEG	p.R2790G	SPEG complex locus	19 (0.00)	16 (0.94)	2.50
11-14	Gp4	g.chr12:64238640C>A	Missense Mutation	SRGAP1	p.A15D	SLIT-ROBO Rho GTPa	97 (0.00)	145 (0.88)	2.35
11-14	Gp4	g.chr1:206634474C>T	Silent	SRGAP2	p.D835D	SLIT-ROBO Rho GTPa	61 (0.00)	205 (0.48)	1.29
11-14	Gp4	g.chr7:149482199T>C	RNA	SSPO		SCO-spondin	20 (0.00)	52 (0.15)	0.49
11-14	Gp4	g.chr7:149524132C>T	RNA	SSPO		SCO-spondin	45 (0.00)	21 (0.24)	0.76
11-14	Gp4	g.chr1:155989883A>G	Missense Mutation	SSR2	p.S26P	signal sequence recepto	44 (0.00)	109 (0.64)	1.71
11-14	Gp4	g.chr4:98633916T>C	Silent	STPG2	p.L418L	sperm-tail PG-rich repe	41 (0.00)	19 (0.32)	0.84
11-14	Gp4	g.chr4:98633957C>A	Missense Mutation	STPG2	p.A405S	sperm-tail PG-rich repe	39 (0.00)	18 (0.33)	0.89
11-14	Gp4	g.chr7:905596C>A	Missense Mutation	SUN1	p.S661R	Sad1 and UNC84 doma	65 (0.00)	117 (0.77)	2.75
11-14	Gp4	g.chr6:10942926C>A	Nonsense Mutation	SYCP2L	p.S634*	synaptonemal complex	16 (0.00)	46 (0.15)	0.41
11-14	Gp4	g.chr19:46327053C>T	Silent	SYMPK	p.T857T	symplekin	24 (0.00)	36 (0.42)	1.11

11-14	Gp4	g.chr19:46328476C>A	Missense Mutation	SYMPK	p.A815S	symplekin	54 (0.00)	291 (0.27)	0.71
11-14	Gp4	g.chr14:74876181T>G	Silent	SYNDIG1L	p.T89T	synapse differentiation i	20 (0.00)	92 (0.48)	1.28
11-14	Gp4	g.chr14:95912318C>G	Missense Mutation	SYNE3	p.E520D	spectrin repeat containir	76 (0.00)	50 (0.24)	0.64
11-14	Gp4	g.chr14:95918626G>T	Missense Mutation	SYNE3	p.P411Q	spectrin repeat containir	17 (0.00)	108 (0.37)	0.99
11-14	Gp4	g.chr10:46961986C>G	Missense Mutation	SYT15	p.R417P	synaptotagmin XV	43 (0.00)	382 (0.23)	0.61
11-14	Gp4	g.chr10:123843200C>A	Silent	TACC2	p.G395G	transforming, acidic coil	33 (0.00)	146 (0.59)	1.57
11-14	Gp4	g.chr7:99709858G>A	Missense Mutation	TAF6	p.P235L	TAF6 RNA polymerase	16 (0.00)	49 (0.67)	2.14
11-14	Gp4	g.chr1:1267143C>A	Missense Mutation	TAS1R3	p.P106H	taste receptor, type 1, m	24 (0.00)	89 (0.31)	0.84
11-14	Gp4	g.chr17:25748606C>T	RNA	TBC1D3P5		TBC1 domain family, n	39 (0.00)	59 (0.90)	2.40
11-14	Gp4	g.chr4:141543720C>T	Missense Mutation	TBC1D9	p.G1144R	TBC1 domain family, n	24 (0.00)	262 (0.16)	0.42
11-14	Gp4	g.chr5:179318431C>G	Missense Mutation	TBC1D9B	p.C331S	TBC1 domain family, n	55 (0.00)	68 (0.37)	0.98
11-14	Gp4	g.chr2:74327794C>T	Silent	TET3	p.N1158N	tet methylcytosine diox	93 (0.00)	326 (0.22)	0.59
11-14	Gp4	g.chr6:41658524C>T	Silent	TFEB	p.P115P	transcription factor EB	54 (0.00)	97 (0.39)	1.04
11-14	Gp4	g.chr20:36759525C>A	Missense Mutation	TGM2	p.G628V	transglutaminase 2	56 (0.00)	16 (0.31)	0.83
11-14	Gp4	g.chr20:36775290A>G	Missense Mutation	TGM2	p.C230R	transglutaminase 2	16 (0.00)	75 (0.16)	0.43
11-14	Gp4	g.chr2:242572485G>A	Missense Mutation	THAP4	p.R363W	THAP domain containir	19 (0.00)	21 (0.29)	0.76
11-14	Gp4	g.chr6:169648883G>C	Missense Mutation	THBS2	p.Q80E	thrombospondin 2	17 (0.00)	100 (0.45)	1.20
11-14	Gp4	g.chr19:2790438G>A	Silent	THOP1	p.A12A	thimet oligopeptidase 1	28 (0.00)	12 (0.75)	2.00
11-14	Gp4	g.chr19:4818274C>A	Missense Mutation	TICAM1	p.G39V	toll-like receptor adapto	22 (0.00)	111 (0.49)	1.30
11-14	Gp4	g.chr16:84520355G>T	Silent	TLDC1	p.S280S	TBC/LysM-associated	39 (0.00)	60 (0.72)	1.91
11-14	Gp4	g.chr3:52255714A>G	Silent	TLR9	p.L1026L	toll-like receptor 9	29 (0.00)	159 (0.42)	1.11
11-14	Gp4	g.chr17:79288254G>T	Silent	TMEM105	p.L3L	transmembrane protein	18 (0.00)	92 (0.36)	0.96
11-14	Gp4	g.chr17:21101642C>T	Missense Mutation	TMEM11	p.V192I	transmembrane protein	68 (0.00)	75 (0.99)	2.63
11-14	Gp4	g.chr2:98409367C>A	Missense Mutation	TMEM131	p.G1209V	transmembrane protein	20 (0.00)	40 (0.57)	1.53
11-14	Gp4	g.chr11:60699230G>A	Silent	TMEM132A	p.A363A	transmembrane protein	147 (0.00)	331 (0.40)	1.07
11-14	Gp4	g.chr19:19243175C>T	Silent	TMEM161A	p.T143T	transmembrane protein	85 (0.01)	193 (0.81)	2.17
11-14	Gp4	g.chr18:5891811C>T	Silent	TMEM200C	p.E84E	transmembrane protein	20 (0.00)	26 (0.42)	1.13
11-14	Gp4	g.chr19:11453770C>A	Silent	TMEM205	p.T97T	transmembrane protein	33 (0.00)	71 (0.45)	1.20
11-14	Gp4	g.chr9:104239033G>A	Silent	TMEM246	p.G114G	transmembrane protein	25 (0.00)	46 (0.26)	0.70
11-14	Gp4	g.chr1:1849482A>G	Missense Mutation	TMEM52	p.Y157H	transmembrane protein	21 (0.00)	265 (0.25)	0.65
11-14	Gp4	g.chr19:4298054C>T	Missense Mutation	TMIGD2	p.C112Y	transmembrane and imn	29 (0.00)	42 (0.48)	1.27
11-14	Gp4	g.chr3:33135265G>C	Silent	TMPPE	p.A4A	transmembrane protein	17 (0.00)	115 (0.19)	0.51
11-14	Gp4	g.chr6:138202435G>T	Missense Mutation	TNFAIP3	p.Q784H	tumor necrosis factor, al	51 (0.00)	63 (0.32)	0.85
11-14	Gp4	g.chr11:57076064G>A	Missense Mutation	TNKS1BP1	p.P1374L	tankyrase 1 binding prot	51 (0.00)	183 (0.36)	0.96
11-14	Gp4	g.chr1:175375469C>A	Missense Mutation	TNR	p.A128S	tenascin R	59 (0.00)	130 (0.56)	1.50

11-14	Gp4	g.chr7:5347914G>A	Silent	TNRC18	p.D2910D	trinucleotide repeat cont	20 (0.00)	277 (0.29)	1.02
11-14	Gp4	g.chr7:5353485G>T	Missense Mutation	TNRC18	p.A2346D	trinucleotide repeat cont	20 (0.00)	118 (0.20)	0.73
11-14	Gp4	g.chr7:5391720C>A	Missense Mutation	TNRC18	p.D1734Y	trinucleotide repeat cont	16 (0.00)	264 (0.13)	0.47
11-14	Gp4	g.chr17:7583368G>T	Intron	TP53		tumor protein p53	130 (0.01)	270 (0.39)	1.03
11-14	Gp4	g.chr1:3662512A>G	RNA	TP73-AS1		TP73 antisense RNA 1	24 (0.00)	49 (0.55)	1.47
11-14	Gp4	g.chr11:68840124A>T	Missense Mutation	TPCN2	p.Q364L	two pore segment chann	22 (0.00)	155 (0.19)	0.50
11-14	Gp4	g.chr3:14105817C>A	Missense Mutation	TPRXL	p.S47R	tetra-peptide repeat hom	27 (0.00)	59 (0.41)	1.08
11-14	Gp4	g.chr3:36898075G>A	Silent	TRANK1	p.A452A	tetratricopeptide repeat	80 (0.00)	36 (0.97)	2.59
11-14	Gp4	g.chr11:49053187A>T	Missense Mutation	TRIM49B	p.E12D	tripartite motif containi	145 (0.00)	34 (0.50)	1.33
11-14	Gp4	g.chr7:72738598C>A	Missense Mutation	TRIM50	p.S63I	tripartite motif containi	21 (0.00)	44 (0.34)	0.91
11-14	Gp4	g.chr1:231339694T>C	Missense Mutation	TRIM67	p.F539S	tripartite motif containi	18 (0.00)	84 (0.23)	0.60
11-14	Gp4	g.chr7:75028446G>A	Missense Mutation	TRIM73	p.A77T	tripartite motif containi	18 (0.00)	53 (0.40)	1.06
11-14	Gp4	g.chr10:104414984C>T	Missense Mutation	TRIM8	p.L272F	tripartite motif containi	50 (0.00)	155 (0.19)	0.50
11-14	Gp4	g.chr10:104416056C>A	Missense Mutation	TRIM8	p.S321Y	tripartite motif containi	22 (0.00)	18 (0.67)	1.78
11-14	Gp4	g.chr7:142569511C>A	Silent	TRPV6	p.G709G	transient receptor potent	67 (0.00)	245 (0.22)	0.70
11-14	Gp4	g.chr18:72998340G>A	Missense Mutation	TSHZ1	p.M326I	teashirt zinc finger hom	28 (0.00)	10 (0.80)	2.76
11-14	Gp4	g.chr18:72998921G>A	Missense Mutation	TSHZ1	p.S520N	teashirt zinc finger hom	18 (0.00)	170 (0.18)	0.63
11-14	Gp4	g.chr18:72998925G>A	Silent	TSHZ1	p.E521E	teashirt zinc finger hom	18 (0.00)	169 (0.18)	0.63
11-14	Gp4	g.chr19:31769943C>T	Silent	TSHZ3	p.K252K	teashirt zinc finger hom	214 (0.00)	422 (0.54)	1.43
11-14	Gp4	g.chr19:31770009C>T	Silent	TSHZ3	p.T230T	teashirt zinc finger hom	183 (0.00)	391 (0.42)	1.12
11-14	Gp4	g.chr2:178483005C>T	Missense Mutation	TTC30A	p.G142E	tetratricopeptide repeat	146 (0.00)	324 (0.35)	0.94
11-14	Gp4	g.chr1:51774983C>A	Silent	TTC39A	p.V178V	tetratricopeptide repeat	67 (0.00)	101 (0.19)	0.50
11-14	Gp4	g.chr2:47278901G>A	Silent	TTC7A	p.S678S	tetratricopeptide repeat	24 (0.00)	98 (0.65)	1.74
11-14	Gp4	g.chr20:36634605C>T	Missense Mutation	TTI1	p.E833K	TELO2 interacting prot	140 (0.01)	39 (0.62)	1.64
11-14	Gp4	g.chr17:46867398T>C	Missense Mutation	TTLL6	p.D432G	tubulin tyrosine ligase-li	33 (0.00)	104 (0.26)	0.69
11-14	Gp4	g.chr2:179534373C>T	Missense Mutation	TTN	p.E11806K	titin	100 (0.00)	58 (0.98)	2.62
11-14	Gp4	g.chr17:72245499C>G	Nonsense Mutation	TTYH2	p.Y297*	tweety family member 2	31 (0.00)	67 (0.28)	0.76
11-14	Gp4	g.chr17:72246101T>C	Silent	TTYH2	p.L319L	tweety family member 2	31 (0.00)	203 (0.17)	0.45
11-14	Gp4	g.chr6:3225759C>A	Silent	TUBB2B	p.S188S	tubulin, beta 2B class II	105 (0.00)	171 (0.53)	1.42
11-14	Gp4	g.chr16:90001957C>T	Silent	TUBB3	p.T713T	tubulin, beta 3 class III	110 (0.00)	322 (0.83)	2.22
11-14	Gp4	g.chr19:6495983G>T	Nonsense Mutation	TUBB4A	p.S176*	tubulin, beta 4A class I	33 (0.00)	156 (0.35)	0.94
11-14	Gp4	g.chr10:94026G>A	Silent	TUBB8	p.A102A	tubulin, beta 8 class VII	54 (0.00)	347 (0.40)	1.08
11-14	Gp4	g.chr16:90161490C>A	RNA	TUBB8P7		tubulin, beta 8 class VII	20 (0.00)	18 (0.44)	1.19
11-14	Gp4	g.chr22:50659377C>G	Silent	TUBGCP6	p.V1137V	tubulin, gamma comple	26 (0.00)	51 (0.65)	1.73
11-14	Gp4	g.chr17:74387662C>G	Missense Mutation	UBE2O	p.E1081Q	ubiquitin-conjugating en	36 (0.00)	59 (0.66)	1.76

11-14	Gp4	g.chr19:4929264G>T	RNA	UHRF1		ubiquitin-like with PHD	29 (0.00)	155 (0.63)	1.69
11-14	Gp4	g.chr19:4929573G>A	RNA	UHRF1		ubiquitin-like with PHD	30 (0.00)	34 (0.32)	0.86
11-14	Gp4	g.chr15:91496525C>A	Missense Mutation	UNC45A	p.S854R	unc-45 homolog A (C. e	60 (0.00)	294 (0.29)	0.76
11-14	Gp4	g.chr4:96104198G>T	Nonsense Mutation	UNC5C	p.Y767*	unc-5 homolog C (C. el	66 (0.00)	36 (0.97)	2.59
11-14	Gp4	g.chr6:167719436G>A	Missense Mutation	UNC93A	p.V292I	unc-93 homolog A (C. e	178 (0.00)	720 (0.27)	0.71
11-14	Gp4	g.chr11:113704196C>T	Silent	USP28	p.P235P	ubiquitin specific peptid	90 (0.00)	129 (0.58)	1.55
11-14	Gp4	g.chr17:76799835C>A	Missense Mutation	USP36	p.K814N	ubiquitin specific peptid	32 (0.00)	139 (0.73)	1.96
11-14	Gp4	g.chr17:9604721G>T	Missense Mutation	USP43	p.G572V	ubiquitin specific peptid	43 (0.00)	203 (0.29)	0.78
11-14	Gp4	g.chr17:9604779G>T	Missense Mutation	USP43	p.R591S	ubiquitin specific peptid	35 (0.00)	129 (0.33)	0.89
11-14	Gp4	g.chr4:1374749C>A	Silent	UVSSA	p.R612R	UV-stimulated scaffold	24 (0.00)	110 (0.31)	0.82
11-14	Gp4	g.chr3:38048166A>G	Missense Mutation	VILL	p.E811G	villin-like	17 (0.00)	120 (0.33)	0.87
11-14	Gp4	g.chr3:38048460G>T	Missense Mutation	VILL	p.D829Y	villin-like	92 (0.00)	37 (0.22)	0.58
11-14	Gp4	g.chr3:38048515G>C	Missense Mutation	VILL	p.R847P	villin-like	93 (0.00)	40 (0.20)	0.53
11-14	Gp4	g.chr3:42568929T>C	Silent	VIPR1	p.I148I	vasoactive intestinal pe	29 (0.00)	33 (0.82)	2.18
11-14	Gp4	g.chr22:22599388C>A	Missense Mutation	VPREB1	p.P26Q	pre-B lymphocyte 1	25 (0.00)	141 (0.21)	0.57
11-14	Gp4	g.chr8:100883812G>A	Missense Mutation	VPS13B	p.D3903N	vacuolar protein sorting	118 (0.00)	90 (0.26)	0.68
11-14	Gp4	g.chr16:22144318C>T	Missense Mutation	VWA3A	p.T657I	von Willebrand factor A	46 (0.00)	163 (0.51)	1.36
11-14	Gp4	g.chr7:73280023G>A	Nonsense Mutation	WBSCR28	p.W206*	Williams-Beuren syndr	55 (0.00)	284 (0.20)	0.53
11-14	Gp4	g.chrX:48463283G>A	Missense Mutation	WDR13	p.A441T	WD repeat domain 13	19 (0.00)	74 (0.51)	0.86
11-14	Gp4	g.chr2:20189764G>T	Missense Mutation	WDR35	p.L5M	WD repeat domain 35	16 (0.00)	139 (0.22)	0.58
11-14	Gp4	g.chr8:38187062G>A	Missense Mutation	WHSC1L1	p.T472I	Wolf-Hirschhorn syndr	46 (0.00)	115 (0.82)	2.18
11-14	Gp4	g.chr3:13860650C>G	Missense Mutation	WNT7A	p.D281H	wingless-type MMTV i	19 (0.00)	195 (0.31)	0.82
11-14	Gp4	g.chr16:69922018C>A	Silent	WWP2	p.P260P	WW domain containing	95 (0.00)	373 (0.23)	0.61
11-14	Gp4	g.chr3:39225796C>T	Missense Mutation	XIRP1	p.G1714D	xin actin-binding repeat	20 (0.00)	42 (0.40)	1.08
11-14	Gp4	g.chr20:30556212G>T	Silent	XKR7	p.A78A	XK, Kell blood group c	18 (0.00)	69 (0.64)	1.70
11-14	Gp4	g.chr3:14216796G>T	Intron	XPC		xeroderma pigmentosu	222 (0.00)	431 (0.48)	1.29
11-14	Gp4	g.chr17:48431848C>A	Nonsense Mutation	XYLT2	p.Y236*	xylosyltransferase II	39 (0.00)	45 (0.16)	0.41
11-14	Gp4	g.chr7:100364752G>A	RNA	ZAN		zonadhesin (gene/pseud	30 (0.00)	226 (0.67)	2.12
11-14	Gp4	g.chr22:50277393A>G	Missense Mutation	ZBED4	p.D28G	zinc finger, BED-type c	62 (0.02)	96 (0.68)	1.81
11-14	Gp4	g.chr20:56191369C>T	Missense Mutation	ZBP1	p.A64T	Z-DNA binding protein	36 (0.00)	146 (0.77)	2.05
11-14	Gp4	g.chr3:114069208C>A	Missense Mutation	ZBTB20	p.G500C	zinc finger and BTB do	23 (0.00)	145 (0.37)	1.16
11-14	Gp4	g.chr3:114069245C>A	Silent	ZBTB20	p.L487L	zinc finger and BTB do	18 (0.00)	125 (0.61)	1.93
11-14	Gp4	g.chr9:129595408G>C	Missense Mutation	ZBTB43	p.S207T	zinc finger and BTB do	36 (0.00)	223 (0.30)	0.81
11-14	Gp4	g.chr16:88694427C>A	Missense Mutation	ZC3H18	p.S790Y	zinc finger CCCH-type	43 (0.00)	80 (0.17)	0.47
11-14	Gp4	g.chr8:144620183T>C	Missense Mutation	ZC3H3	p.S452G	zinc finger CCCH-type	48 (0.00)	61 (0.52)	1.40

11-14	Gp4	g.chr19:47593368C>T	Missense Mutation	ZC3H4	p.G191S	zinc finger CCCH-type	52 (0.02)	270 (0.23)	0.62
11-14	Gp4	g.chr16:72991941C>T	Missense Mutation	ZFHX3	p.V702I	zinc finger homeobox 3	47 (0.00)	223 (0.17)	0.47
11-14	Gp4	g.chr4:2306934C>G	Missense Mutation	ZFYVE28	p.S378T	zinc finger, FYVE dom	20 (0.00)	126 (0.14)	0.38
11-14	Gp4	g.chr4:2306949G>A	Missense Mutation	ZFYVE28	p.P373L	zinc finger, FYVE dom	22 (0.00)	128 (0.20)	0.54
11-14	Gp4	g.chr10:81052035C>G	Silent	ZMIZ1	p.A293A	zinc finger, MIZ-type c	38 (0.00)	116 (0.16)	0.44
11-14	Gp4	g.chr7:44802560G>T	Silent	ZMIZ2	p.L559L	zinc finger, MIZ-type c	28 (0.00)	279 (0.27)	0.93
11-14	Gp4	g.chr19:44384253G>A	Silent	ZNF404	p.F15F	zinc finger protein 404	42 (0.00)	557 (1.00)	2.66
11-14	Gp4	g.chr16:49672520A>G	Silent	ZNF423	p.R181R	zinc finger protein 423	21 (0.00)	116 (0.73)	1.95
11-14	Gp4	g.chr19:42729094C>A	Missense Mutation	ZNF526	p.P180Q	zinc finger protein 526	20 (0.00)	37 (0.62)	1.66
11-14	Gp4	g.chr19:42730358G>T	Missense Mutation	ZNF526	p.L601F	zinc finger protein 526	57 (0.00)	88 (0.17)	0.45
11-14	Gp4	g.chr19:30935911C>A	Missense Mutation	ZNF536	p.P481Q	zinc finger protein 536	60 (0.00)	289 (0.25)	0.67
11-14	Gp4	g.chr16:31072478C>A	Nonsense Mutation	ZNF668	p.E591*	zinc finger protein 668	39 (0.00)	290 (0.26)	0.70
11-14	Gp4	g.chr1:151260561C>A	Silent	ZNF687	p.V598V	zinc finger protein 687	36 (0.00)	73 (0.75)	2.01
11-14	Gp4	g.chr7:143079727T>C	Silent	ZYX	p.S150S	zyxin	15 (0.00)	40 (0.55)	1.75
12-01	Gp3	g.chr5:178208183A>T	RNA	AACSP1		acetoacetyl-CoA synthe	149 (0.00)	182 (0.19)	0.51
12-01	Gp3	g.chr2:69784070C>A	Silent	AAK1	p.G68G	AP2 associated kinase 1	172 (0.00)	133 (0.30)	0.80
12-01	Gp3	g.chr17:67004275C>A	Silent	ABCA9	p.L1083L	ATP-binding cassette, s	37 (0.00)	37 (0.65)	1.73
12-01	Gp3	g.chr11:119024787T>A	Missense Mutation	ABCG4	p.L97Q	ATP-binding cassette, s	125 (0.00)	25 (0.20)	0.53
12-01	Gp3	g.chr6:26597387C>A	Silent	ABT1	p.P59P	activator of basal transc	24 (0.00)	38 (0.24)	0.63
12-01	Gp3	g.chr11:34192524C>A	Missense Mutation	ABTB2	p.G498W	ankyrin repeat and BTB	164 (0.01)	55 (0.22)	0.58
12-01	Gp3	g.chr7:131625973G>A	lincRNA	AC009518.4			174 (0.00)	90 (0.17)	0.44
12-01	Gp3	g.chr12:109680301T>C	Silent	ACACB	p.T1694T	acetyl-CoA carboxylase	52 (0.00)	45 (0.27)	0.71
12-01	Gp3	g.chr14:23531672C>A	Nonsense Mutation	ACIN1	p.E1040*	apoptotic chromatin con	318 (0.00)	112 (0.24)	0.64
12-01	Gp3	g.chr2:237489420C>A	Silent	ACKR3	p.L104L	atypical chemokine rece	40 (0.00)	61 (0.16)	0.44
12-01	Gp3	g.chr10:114154707G>A	Start Codon SNP	ACSL5	p.M1I	acyl-CoA synthetase lo	75 (0.00)	30 (0.43)	1.16
12-01	Gp3	g.chr20:33507279C>A	Silent	ACSS2	p.L292L	acyl-CoA synthetase sh	40 (0.00)	30 (0.30)	0.80
12-01	Gp3	g.chr19:1507357C>A	Missense Mutation	ADAMTSL5	p.V246F	ADAMTS-like 5	18 (0.00)	37 (0.16)	0.43
12-01	Gp3	g.chr5:7709333C>T	Missense Mutation	ADCY2	p.R471W	adenylate cyclase 2 (bra	118 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr4:88047331C>A	Missense Mutation	AFF1	p.A878D	AF4/FMR2 family, me	149 (0.00)	85 (0.21)	0.56
12-01	Gp3	g.chr3:186338393C>A	Missense Mutation	AHSG	p.Q261K	alpha-2-HS-glycoprotei	106 (0.00)	111 (0.25)	0.67
12-01	Gp3	g.chr6:151672044G>T	Missense Mutation	AKAP12	p.D840Y	A kinase (PRKA) ancho	55 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr7:91732060G>A	Silent	AKAP9	p.T3750T	A kinase (PRKA) ancho	46 (0.00)	15 (0.33)	0.89
12-01	Gp3	g.chr22:50302947G>A	Missense Mutation	ALG12	p.P238L	ALG12, alpha-1,6-man	24 (0.00)	63 (0.13)	0.42
12-01	Gp3	g.chr2:73676031G>A	Missense Mutation	ALMS1	p.V792I	Alstrom syndrome 1	153 (0.00)	38 (0.76)	2.04
12-01	Gp3	g.chr15:85399786G>C	Missense Mutation	ALPK3	p.S808T	alpha-kinase 3	32 (0.00)	11 (0.55)	1.45

12-01	Gp3	g.chr3:134078321G>C	Missense Mutation	AMOTL2	p.I694M	angiomotin like 2	23 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr1:104162289C>T	Silent	AMY2A	p.F209F	amylase, alpha 2A (panc	108 (0.00)	31 (0.48)	1.29
12-01	Gp3	g.chr12:121783726G>T	Missense Mutation	ANAPC5	p.T169K	anaphase promoting com	70 (0.00)	18 (0.39)	1.04
12-01	Gp3	g.chr4:73990681T>A	Missense Mutation	ANKRD17	p.E1147D	ankyrin repeat domain 1	133 (0.00)	54 (0.39)	1.04
12-01	Gp3	g.chr9:95649232C>T	RNA	ANKRD19P		ankyrin repeat domain 1	277 (0.00)	61 (0.41)	1.09
12-01	Gp3	g.chr19:33117728C>G	Missense Mutation	ANKRD27	p.A476P	ankyrin repeat domain 2	59 (0.00)	51 (0.24)	0.63
12-01	Gp3	g.chr18:12125849C>T	Silent	ANKRD62	p.L677L	ankyrin repeat domain 6	88 (0.00)	15 (0.33)	0.89
12-01	Gp3	g.chr7:4823046G>C	Missense Mutation	AP5Z1	p.V156L	adaptor-related protein c	19 (0.00)	42 (0.14)	0.38
12-01	Gp3	g.chr22:36661639G>A	Missense Mutation	APOL1	p.E253K	apolipoprotein L, 1	152 (0.01)	33 (0.21)	0.57
12-01	Gp3	g.chr22:36662016G>T	Silent	APOL1	p.L378L	apolipoprotein L, 1	96 (0.00)	34 (0.29)	0.78
12-01	Gp3	g.chr22:36587797C>T	Missense Mutation	APOL4	p.C124Y	apolipoprotein L, 4	113 (0.00)	19 (0.26)	0.70
12-01	Gp3	g.chr9:33395109G>T	Missense Mutation	AQP7	p.F37L	aquaporin 7	84 (0.00)	35 (0.17)	0.46
12-01	Gp3	g.chr11:72424286C>G	Missense Mutation	ARAP1	p.D228H	ArfGAP with RhoGAP	19 (0.00)	30 (0.20)	0.53
12-01	Gp3	g.chr19:47423471C>A	Missense Mutation	ARHGAP35	p.S513R	Rho GTPase activating	185 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr19:42398600G>C	Missense Mutation	ARHGEF1	p.W289S	Rho guanine nucleotide	25 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr8:1814720G>T	Missense Mutation	ARHGEF10	p.A192S	Rho guanine nucleotide	93 (0.00)	153 (0.12)	0.40
12-01	Gp3	g.chr8:1851503C>G	Silent	ARHGEF10	p.A569A	Rho guanine nucleotide	167 (0.00)	38 (0.26)	0.89
12-01	Gp3	g.chr6:157405805G>T	Missense Mutation	ARID1B	p.G683C	AT rich interactive dom	89 (0.00)	24 (0.33)	0.89
12-01	Gp3	g.chrX:101857520G>A	Missense Mutation	ARMCX5	p.D151N	armadillo repeat contain	68 (0.00)	11 (0.73)	1.21
12-01	Gp3	g.chr12:27521205G>A	Silent	ARNTL2	p.L25L	aryl hydrocarbon recepto	25 (0.00)	22 (0.32)	0.85
12-01	Gp3	g.chr1:23769064C>A	Missense Mutation	ASAP3	p.G172V	ArfGAP with SH3 doma	72 (0.00)	41 (0.15)	0.39
12-01	Gp3	g.chr6:100957933G>A	Silent	ASCC3	p.D2112D	activating signal cointeg	98 (0.00)	60 (0.18)	0.49
12-01	Gp3	g.chr1:197070968C>T	Silent	ASPM	p.L2471L	asp (abnormal spindle)	34 (0.00)	39 (0.33)	0.89
12-01	Gp3	g.chr2:70188620C>A	Silent	ASPRV1	p.G67G	aspartic peptidase, retro	28 (0.00)	37 (0.16)	0.43
12-01	Gp3	g.chr22:39918599G>A	Missense Mutation	ATF4	p.V350I	activating transcription	71 (0.00)	40 (0.28)	0.73
12-01	Gp3	g.chr14:96761368C>T	Silent	ATG2B	p.V1785V	autophagy related 2B	169 (0.00)	44 (0.20)	0.55
12-01	Gp3	g.chr15:25925348G>A	Silent	ATP10A	p.Y1262Y	ATPase, class V, type 1	47 (0.00)	107 (0.13)	0.44
12-01	Gp3	g.chr5:160097616G>T	Missense Mutation	ATP10B	p.Q177K	ATPase, class V, type 1	140 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr13:113505450G>A	Missense Mutation	ATP11A	p.D637N	ATPase, class VI, type 1	145 (0.00)	102 (0.12)	0.38
12-01	Gp3	g.chr1:17322651C>G	Silent	ATP13A2	p.L454L	ATPase type 13A2	61 (0.00)	100 (0.20)	0.53
12-01	Gp3	g.chr12:90028882G>A	Nonsense Mutation	ATP2B1	p.Q185*	ATPase, Ca++ transport	51 (0.02)	24 (0.21)	0.56
12-01	Gp3	g.chr7:97949382C>G	Silent	BAIAP2L1	p.V112V	BAI1-associated protein	134 (0.00)	111 (0.20)	0.53
12-01	Gp3	g.chr7:72892611G>A	Missense Mutation	BAZ1B	p.P394S	bromodomain adjacent t	45 (0.00)	12 (0.83)	2.22
12-01	Gp3	g.chr4:42145676G>A	Missense Mutation	BEND4	p.H275Y	BEN domain containing	57 (0.00)	13 (0.54)	1.44
12-01	Gp3	g.chrX:102564541C>A	Missense Mutation	BEX2	p.D122Y	brain expressed X-linke	49 (0.00)	29 (0.62)	1.03

12-01	Gp3	g.chr12:51685998C>T	Missense Mutation	BIN2	p.D298N	bridging integrator 2	163 (0.00)	55 (0.15)	0.39
12-01	Gp3	g.chr6:3127631G>A	Missense Mutation	BPHL	p.D106N	biphenyl hydrolase-like	59 (0.00)	20 (0.30)	0.80
12-01	Gp3	g.chr20:31767473G>A	Splice Site	BPIFA2	p.D237N	BPI fold containing fam	99 (0.00)	44 (0.16)	0.42
12-01	Gp3	g.chr17:65850149T>A	Nonsense Mutation	BPTF	p.L236*	bromodomain PHD fing	144 (0.01)	128 (0.41)	1.10
12-01	Gp3	g.chr13:32907863C>T	Intron	BRCA2		breast cancer 2, early on	76 (0.00)	49 (0.14)	0.38
12-01	Gp3	g.chr1:55464905C>T	Missense Mutation	BSND	p.L16F	barttin CLCNK-type ch	31 (0.00)	30 (0.17)	0.44
12-01	Gp3	g.chr15:74032542C>A	Missense Mutation	C15orf59	p.D200Y	chromosome 15 open re	32 (0.00)	48 (0.15)	0.39
12-01	Gp3	g.chr19:14193358C>T	Silent	C19orf67	p.S275S	chromosome 19 open re	63 (0.00)	54 (0.24)	0.64
12-01	Gp3	g.chr1:244715787C>A	Missense Mutation	C1orf101	p.P234T	chromosome 1 open rea	30 (0.00)	41 (0.22)	0.59
12-01	Gp3	g.chr1:223568584C>A	Silent	C1orf65	p.L589L		140 (0.00)	111 (0.15)	0.41
12-01	Gp3	g.chr1:22986089C>A	Missense Mutation	C1QB	p.P45H	complement component	26 (0.00)	43 (0.30)	0.81
12-01	Gp3	g.chr3:112732805A>C	Silent	C3orf17	p.S112S	chromosome 3 open rea	88 (0.00)	47 (0.15)	0.40
12-01	Gp3	g.chr6:165713887G>A	Missense Mutation	C6orf118	p.S281F	chromosome 6 open rea	129 (0.01)	42 (0.36)	0.95
12-01	Gp3	g.chr9:100672565C>A	Missense Mutation	C9orf156	p.R248M	chromosome 9 open rea	268 (0.00)	45 (0.18)	0.47
12-01	Gp3	g.chr9:100672574G>A	Missense Mutation	C9orf156	p.P245L	chromosome 9 open rea	222 (0.00)	37 (0.22)	0.58
12-01	Gp3	g.chr13:49906199G>A	Missense Mutation	CAB39L	p.H240Y	calcium binding protein	105 (0.01)	29 (0.21)	0.55
12-01	Gp3	g.chr12:2690949C>G	Missense Mutation	CACNA1C	p.L697V	calcium channel, voltag	132 (0.00)	35 (0.29)	0.76
12-01	Gp3	g.chr3:85069393G>T	Intron	CADM2		cell adhesion molecule	18 (0.00)	12 (0.42)	1.11
12-01	Gp3	g.chr3:85225383T>C	Intron	CADM2		cell adhesion molecule	176 (0.00)	99 (0.14)	0.38
12-01	Gp3	g.chr3:85369591G>A	Intron	CADM2		cell adhesion molecule	36 (0.00)	19 (0.26)	0.70
12-01	Gp3	g.chr3:85463289A>T	Intron	CADM2		cell adhesion molecule	56 (0.00)	17 (0.41)	1.10
12-01	Gp3	g.chr14:90867621C>G	Missense Mutation	CALM1	p.S19C	calmodulin 1 (phosphor	90 (0.00)	20 (0.30)	0.80
12-01	Gp3	g.chr1:7811317G>A	Missense Mutation	CAMTA1	p.S1583N	calmodulin binding tran	281 (0.00)	110 (0.15)	0.39
12-01	Gp3	g.chr19:48737660C>T	Splice Site	CARD8	p.S117N	caspase recruitment don	43 (0.00)	28 (0.61)	1.62
12-01	Gp3	g.chr15:43928376G>A	Missense Mutation	CATSPER2	p.T295I	cation channel, sperm a	133 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr19:14041075C>A	Silent	CC2D1A	p.L936L	coiled-coil and C2 dom	67 (0.00)	132 (0.14)	0.38
12-01	Gp3	g.chr13:103383002C>T	Missense Mutation	CCDC168	p.S2053N	coiled-coil domain cont	59 (0.00)	21 (0.67)	1.78
12-01	Gp3	g.chr12:102433670G>T	Silent	CCDC53	p.A137A	coiled-coil domain cont	37 (0.00)	49 (0.18)	0.49
12-01	Gp3	g.chr13:37007270C>G	Missense Mutation	CCNA1	p.T70S	cyclin A1	76 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr6:41905075G>A	Missense Mutation	CCND3	p.H158Y	cyclin D3	59 (0.00)	23 (0.43)	1.16
12-01	Gp3	g.chr5:159686680G>T	Missense Mutation	CCNJL	p.L127M	cyclin J-like	88 (0.01)	115 (0.16)	0.42
12-01	Gp3	g.chr1:1333999G>T	Missense Mutation	CCNL2	p.S114Y	cyclin L2	70 (0.00)	44 (0.30)	0.79
12-01	Gp3	g.chr7:5949671G>A	Missense Mutation	CCZ1	p.G235E	CCZ1 vacuolar protein	138 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr1:111437592A>T	Missense Mutation	CD53	p.Y113F	CD53 molecule	36 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr5:149782185G>A	Missense Mutation	CD74	p.S274L	CD74 molecule, major	42 (0.00)	35 (0.17)	0.46

12-01	Gp3	g.chr5:149782189C>A	Splice Site	CD74		CD74 molecule, major	27 (0.00)	29 (0.28)	0.74
12-01	Gp3	g.chr13:49823078G>A	Missense Mutation	CDADC1	p.E52K	cytidine and dCMP dea	48 (0.00)	24 (0.29)	0.78
12-01	Gp3	g.chr10:73377012G>A	Silent	CDH23	p.T337T	cadherin-related 23	164 (0.00)	55 (0.15)	0.39
12-01	Gp3	g.chr10:73556927T>A	Missense Mutation	CDH23	p.V2265E	cadherin-related 23	67 (0.00)	28 (0.32)	0.86
12-01	Gp3	g.chr6:4943871C>A	Missense Mutation	CDYL	p.L405I	chromodomain protein,	145 (0.00)	34 (0.26)	0.71
12-01	Gp3	g.chr22:17662410C>T	Missense Mutation	CECR1	p.R500K	cat eye syndrome chrom	351 (0.00)	162 (0.19)	0.49
12-01	Gp3	g.chr20:3765602G>A	Missense Mutation	CENPB	p.S510F	centromere protein B, 8	20 (0.00)	12 (0.42)	0.49
12-01	Gp3	g.chr4:119459182G>A	RNA	CEP170P1		centrosomal protein 170	208 (0.00)	55 (0.95)	2.52
12-01	Gp3	g.chr1:180022984C>A	Missense Mutation	CEP350	p.H1697N	centrosomal protein 350	73 (0.00)	45 (0.53)	1.42
12-01	Gp3	g.chr19:33417172A>T	Missense Mutation	CEP89	p.I363K	centrosomal protein 89k	16 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr3:101446313C>G	Missense Mutation	CEP97	p.S91R	centrosomal protein 97k	89 (0.00)	143 (0.33)	0.88
12-01	Gp3	g.chr22:47116908G>T	Silent	CERK	p.A49A	ceramide kinase	149 (0.00)	68 (0.12)	0.39
12-01	Gp3	g.chr16:67000658G>T	Missense Mutation	CES3	p.G318C	carboxylesterase 3	219 (0.00)	117 (0.15)	0.39
12-01	Gp3	g.chr17:7806761C>T	Nonsense Mutation	CHD3	p.Q1282*	chromodomain helicase	39 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr12:6704596C>A	Splice Site	CHD4	p.R672S	chromodomain helicase	152 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr1:6183217G>C	Intron	CHD5		chromodomain helicase	79 (0.00)	84 (0.15)	0.41
12-01	Gp3	g.chr20:40113205G>T	Silent	CHD6	p.R682R	chromodomain helicase	85 (0.00)	26 (0.19)	0.51
12-01	Gp3	g.chr19:34263935C>T	Silent	CHST8	p.F414F	carbohydrate (N-acetylg	17 (0.00)	36 (0.17)	0.44
12-01	Gp3	g.chr19:42798111C>G	Missense Mutation	CIC	p.F2261L	capicua transcriptional r	65 (0.00)	118 (0.16)	0.43
12-01	Gp3	g.chr11:46765573T>A	Nonstop Mutation	CKAP5	p.*2033C	cytoskeleton associated	26 (0.00)	22 (0.59)	1.58
12-01	Gp3	g.chr2:122286336T>C	Missense Mutation	CLASP1	p.R99G	cytoplasmic linker asso	82 (0.00)	32 (0.16)	0.42
12-01	Gp3	g.chr17:6978698C>G	Missense Mutation	CLEC10A	p.D231H	C-type lectin domain fa	99 (0.00)	41 (0.29)	0.78
12-01	Gp3	g.chr1:9795634C>A	Nonsense Mutation	CLSTN1	p.G592*	calsyntenin 1	59 (0.00)	40 (0.15)	0.40
12-01	Gp3	g.chr22:19171099G>A	Missense Mutation	CLTCL1	p.S1544L	clathrin, heavy chain-lik	21 (0.00)	42 (0.21)	0.57
12-01	Gp3	g.chr22:19209500C>A	Missense Mutation	CLTCL1	p.L845F	clathrin, heavy chain-lik	166 (0.00)	28 (0.39)	1.05
12-01	Gp3	g.chr8:87738765G>A	Missense Mutation	CNGB3	p.P111L	cyclic nucleotide gated	186 (0.00)	25 (0.40)	1.07
12-01	Gp3	g.chr9:116958249G>T	Missense Mutation	COL27A1	p.G694V	collagen, type XXVII, a	71 (0.00)	47 (0.15)	0.40
12-01	Gp3	g.chr21:47409035G>A	Missense Mutation	COL6A1	p.G281E	collagen, type VI, alpha	78 (0.00)	119 (0.12)	0.43
12-01	Gp3	g.chr8:87567195C>T	Nonsense Mutation	CPNE3	p.Q413*	copine III	90 (0.00)	48 (0.38)	1.00
12-01	Gp3	g.chr1:153941837C>A	Missense Mutation	CREB3L4	p.P150H	cAMP responsive eleme	130 (0.00)	47 (0.51)	1.36
12-01	Gp3	g.chr8:75928863C>A	Nonsense Mutation	CRISPLD1	p.S264*	cysteine-rich secretory	75 (0.01)	25 (0.40)	1.07
12-01	Gp3	g.chr8:75928865C>A	Missense Mutation	CRISPLD1	p.Q265K	cysteine-rich secretory	75 (0.01)	24 (0.42)	1.11
12-01	Gp3	g.chr17:29123236G>T	Missense Mutation	CRLF3	p.P182Q	cytokine receptor-like fa	52 (0.00)	36 (0.17)	0.44
12-01	Gp3	g.chr12:107391359G>A	Missense Mutation	CRY1	p.P467S	cryptochrome circadian	35 (0.00)	25 (0.36)	0.96
12-01	Gp3	g.chr8:4851897G>A	Silent	CSMD1	p.L14L	CUB and Sushi multiple	29 (0.00)	42 (0.14)	0.38

12-01	Gp3	g.chr15:75980795C>A	Missense Mutation	CSPG4	p.D871Y	chondroitin sulfate prote	103 (0.00)	109 (0.17)	0.44
12-01	Gp3	g.chr12:51467623G>T	Missense Mutation	CSRNP2	p.H132N	cysteine-serine-rich nuc	118 (0.00)	37 (0.49)	1.30
12-01	Gp3	g.chr19:20370054C>T	RNA	CTC-260E6.6			120 (0.00)	70 (0.17)	0.46
12-01	Gp3	g.chr11:66278531C>A	Missense Mutation	CTD-3074O7.	p.A69D		69 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr11:57576006T>C	Silent	CTNND1	p.L740L	catenin (cadherin-associ	248 (0.00)	116 (0.19)	0.51
12-01	Gp3	g.chr6:43190092C>T	Silent	CUL9	p.D2267D	cullin 9	72 (0.00)	63 (0.29)	0.76
12-01	Gp3	g.chr18:47812995C>A	Missense Mutation	CXXC1	p.C46F	CXXC finger protein 1	71 (0.00)	77 (0.17)	0.45
12-01	Gp3	g.chr5:139622891G>A	Splice Site	CYSTM1	p.V63V	cysteine-rich transmemb	34 (0.00)	15 (0.40)	1.07
12-01	Gp3	g.chr9:124336763A>G	Intron	DAB2IP		DAB2 interacting protei	146 (0.00)	139 (0.19)	0.50
12-01	Gp3	g.chr9:124341980C>A	Intron	DAB2IP		DAB2 interacting protei	236 (0.00)	154 (0.19)	0.52
12-01	Gp3	g.chr9:124362740C>G	Intron	DAB2IP		DAB2 interacting protei	149 (0.00)	134 (0.23)	0.62
12-01	Gp3	g.chr9:124395596T>A	Intron	DAB2IP		DAB2 interacting protei	226 (0.00)	32 (0.34)	0.92
12-01	Gp3	g.chr9:124442964C>T	Intron	DAB2IP		DAB2 interacting protei	47 (0.00)	73 (0.23)	0.62
12-01	Gp3	g.chr9:124450272C>G	Intron	DAB2IP		DAB2 interacting protei	87 (0.00)	28 (0.32)	0.86
12-01	Gp3	g.chr9:124479240C>A	Intron	DAB2IP		DAB2 interacting protei	183 (0.00)	41 (0.24)	0.65
12-01	Gp3	g.chr14:59112231G>A	Missense Mutation	DACT1	p.R260K	dishevelled-binding anta	151 (0.00)	73 (0.16)	0.44
12-01	Gp3	g.chr1:155707979G>T	Silent	DAP3	p.L381L	death associated protein	57 (0.00)	15 (0.33)	0.89
12-01	Gp3	g.chr4:155256100C>G	Missense Mutation	DCHS2	p.R379T	dachsous cadherin-relat	98 (0.00)	21 (0.29)	0.76
12-01	Gp3	g.chr12:57926417C>T	Missense Mutation	DCTN2	p.G288R	dynactin 2 (p50)	174 (0.00)	45 (0.16)	0.41
12-01	Gp3	g.chr12:57926425C>G	Splice Site	DCTN2	p.S285T	dynactin 2 (p50)	168 (0.00)	44 (0.23)	0.61
12-01	Gp3	g.chr1:85817243G>T	Silent	DDAH1	p.G141G	dimethylarginine dimeth	34 (0.00)	11 (0.45)	1.21
12-01	Gp3	g.chr11:125791238G>A	Missense Mutation	DDX25	p.E452K	DEAD (Asp-Glu-Ala-A	223 (0.00)	47 (0.19)	0.51
12-01	Gp3	g.chrX:41206962G>A	Nonsense Mutation	DDX3X	p.W660*	DEAD (Asp-Glu-Ala-A	86 (0.00)	24 (0.38)	0.62
12-01	Gp3	g.chr5:134147010G>A	Missense Mutation	DDX46	p.E750K	DEAD (Asp-Glu-Ala-A	15 (0.00)	13 (0.62)	1.64
12-01	Gp3	g.chr12:12974945C>T	Silent	DDX47	p.F163F	DEAD (Asp-Glu-Ala-A	45 (0.00)	26 (0.31)	0.38
12-01	Gp3	g.chr12:113618843C>A	Silent	DDX54	p.L65L	DEAD (Asp-Glu-Ala-A	42 (0.00)	45 (0.16)	0.41
12-01	Gp3	g.chr11:33053022G>A	Missense Mutation	DEPDC7	p.R294Q	DEP domain containing	74 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr10:12162191G>C	Missense Mutation	DHTKD1	p.W861C	dehydrogenase E1 and t	31 (0.00)	76 (0.16)	0.42
12-01	Gp3	g.chr5:54579076G>A	Silent	DHX29	p.N640N	DEAH (Asp-Glu-Ala-H	32 (0.00)	12 (0.75)	2.00
12-01	Gp3	g.chr12:125461922C>A	Missense Mutation	DHX37	p.V72L	DEAH (Asp-Glu-Ala-H	228 (0.00)	210 (0.23)	0.61
12-01	Gp3	g.chr13:60453513G>T	Missense Mutation	DIAPH3	p.D819E	diaphanous-related form	57 (0.00)	31 (0.52)	1.38
12-01	Gp3	g.chr13:60453525G>C	Missense Mutation	DIAPH3	p.N815K	diaphanous-related form	53 (0.00)	29 (0.45)	1.20
12-01	Gp3	g.chr14:95556924C>T	Missense Mutation	DICER1	p.G1894S	dicer 1, ribonuclease typ	49 (0.00)	27 (0.67)	1.78
12-01	Gp3	g.chr20:61526210C>T	Silent	DIDO1	p.Q796Q	death inducer-obliterato	25 (0.00)	18 (0.39)	1.04
12-01	Gp3	g.chr21:47918523C>G	Silent	DIP2A	p.G144G	DIP2 disco-interacting p	48 (0.00)	26 (0.19)	0.70

12-01	Gp3	g.chr21:47931487C>A	Silent	DIP2A	p.A350A	DIP2 disco-interacting p	94 (0.00)	74 (0.22)	0.78
12-01	Gp3	g.chr12:51127927G>T	Missense Mutation	DIP2B	p.G1331W	DIP2 disco-interacting p	47 (0.00)	12 (0.42)	1.11
12-01	Gp3	g.chr15:51829823C>T	Silent	DMXL2	p.R493R	Dmx-like 2	64 (0.00)	23 (0.39)	1.04
12-01	Gp3	g.chr12:124418676C>G	Missense Mutation	DNAH10OS	p.S152T	dynein, axonemal, heav	35 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr16:20963773C>G	Missense Mutation	DNAH3	p.A3724P	dynein, axonemal, heav	108 (0.00)	22 (0.23)	0.39
12-01	Gp3	g.chr9:33026932T>C	Missense Mutation	DNAJA1	p.M85T	DnaJ (Hsp40) homolog,	198 (0.00)	51 (0.27)	0.73
12-01	Gp3	g.chr15:100339976C>A	RNA	DNM1P46		DNM1 pseudogene 46	22 (0.00)	44 (0.23)	0.61
12-01	Gp3	g.chr21:45674513G>C	Missense Mutation	DNMT3L	p.T227R	DNA (cytosine-5-)-metl	67 (0.00)	64 (0.16)	0.56
12-01	Gp3	g.chr17:1939270G>A	Silent	DPH1	p.T100T	diphthamide biosynthesi	22 (0.00)	73 (0.15)	0.40
12-01	Gp3	g.chr1:168698307C>T	Missense Mutation	DPT	p.D36N	dermatopontin	90 (0.00)	11 (0.55)	1.45
12-01	Gp3	g.chr1:97771741G>T	Missense Mutation	DPYD	p.A724E	dihydropyrimidine dehy	80 (0.00)	23 (0.26)	0.70
12-01	Gp3	g.chr11:113281583C>G	Missense Mutation	DRD2	p.D400H	dopamine receptor D2	60 (0.00)	50 (0.24)	0.64
12-01	Gp3	g.chr4:9784579G>T	Missense Mutation	DRD5	p.W309L	dopamine receptor D5	76 (0.00)	104 (0.14)	0.38
12-01	Gp3	g.chr2:25376592C>G	Silent	EFR3B	p.L770L	EFR3 homolog B (S. ce	26 (0.00)	20 (0.25)	0.67
12-01	Gp3	g.chr14:75470326C>G	Missense Mutation	EIF2B2	p.N119K	eukaryotic translation in	36 (0.00)	22 (0.32)	0.85
12-01	Gp3	g.chr22:31864207C>T	Silent	EIF4ENIF1	p.K84K	eukaryotic translation in	78 (0.00)	34 (0.26)	0.71
12-01	Gp3	g.chr11:34527213G>T	Missense Mutation	ELF5	p.S28R	E74-like factor 5 (ets do	41 (0.00)	48 (0.17)	0.44
12-01	Gp3	g.chr18:2890818G>T	Missense Mutation	EMILIN2	p.Q231H	elastin microfibril interf	44 (0.00)	10 (0.50)	1.33
12-01	Gp3	g.chr20:39993761G>A	Silent	EMILIN3	p.T68T	elastin microfibril interf	20 (0.00)	26 (0.23)	0.62
12-01	Gp3	g.chr18:43505724T>A	Missense Mutation	EPG5	p.N900Y	ectopic P-granules autop	24 (0.00)	28 (0.79)	2.10
12-01	Gp3	g.chr3:96706696G>A	Missense Mutation	EPHA6	p.E325K	EPH receptor A6	134 (0.00)	171 (0.27)	0.73
12-01	Gp3	g.chr7:142561841G>C	Missense Mutation	EPHB6	p.V95L	EPH receptor B6	18 (0.00)	27 (0.30)	0.79
12-01	Gp3	g.chr1:110295773G>T	Nonsense Mutation	EPS8L3	p.S390*	EPS8-like 3	50 (0.00)	13 (0.46)	1.23
12-01	Gp3	g.chr17:56281674G>A	Missense Mutation	EPX	p.G680S	eosinophil peroxidase	42 (0.00)	13 (0.38)	1.03
12-01	Gp3	g.chr17:27183528C>T	Silent	ERAL1	p.F139F	Era-like 12S mitochond	77 (0.00)	20 (0.30)	0.80
12-01	Gp3	g.chr21:39798127C>A	Intron	ERG		v-ets avian erythroblast	71 (0.00)	45 (0.49)	1.30
12-01	Gp3	g.chr21:39834529C>G	Intron	ERG		v-ets avian erythroblast	43 (0.00)	12 (0.50)	1.33
12-01	Gp3	g.chr21:39842686C>T	Intron	ERG		v-ets avian erythroblast	42 (0.00)	25 (0.36)	0.96
12-01	Gp3	g.chr21:39904646G>C	Intron	ERG		v-ets avian erythroblast	71 (0.00)	33 (0.21)	0.57
12-01	Gp3	g.chr21:39940521A>T	Intron	ERG		v-ets avian erythroblast	324 (0.00)	124 (0.16)	0.43
12-01	Gp3	g.chr21:39966483G>A	Intron	ERG		v-ets avian erythroblast	132 (0.00)	11 (0.45)	1.21
12-01	Gp3	g.chr16:23711896G>T	Missense Mutation	ERN2	p.P445T	endoplasmic reticulum t	76 (0.00)	73 (0.15)	0.40
12-01	Gp3	g.chr12:112460064T>C	Missense Mutation	ERP29	p.Y31H	endoplasmic reticulum p	83 (0.00)	32 (0.81)	2.17
12-01	Gp3	g.chr1:6511797C>A	Missense Mutation	ESPN	p.P684T	espin	25 (0.00)	35 (0.14)	0.38
12-01	Gp3	g.chr21:40190521C>A	Silent	ETS2	p.V254V	v-ets avian erythroblast	365 (0.00)	206 (0.51)	1.37

12-01	Gp3	g.chr1:157095303C>A	Missense Mutation	ETV3	p.C290F	ets variant 3	49 (0.00)	23 (0.43)	1.16
12-01	Gp3	g.chr5:453982G>T	Missense Mutation	EXOC3	p.D288Y	exocyst complex compo	167 (0.00)	124 (0.17)	0.45
12-01	Gp3	g.chr2:72968466C>A	Silent	EXOC6B	p.L82L	exocyst complex compo	89 (0.00)	41 (0.20)	0.52
12-01	Gp3	g.chr1:231472972G>T	Missense Mutation	EXOC8	p.H170N	exocyst complex compo	27 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr9:133573613C>A	Missense Mutation	EXOSC2	p.S112Y	exosome component 2	106 (0.00)	57 (0.19)	0.51
12-01	Gp3	g.chr6:64431213C>T	Nonsense Mutation	EYS	p.W2905*	eyes shut homolog (Dro	123 (0.00)	50 (0.22)	0.59
12-01	Gp3	g.chr1:197032096G>T	Missense Mutation	F13B	p.D52E	coagulation factor XIII,	40 (0.00)	24 (0.46)	1.22
12-01	Gp3	g.chr7:143417213G>C	Missense Mutation	FAM115C	p.G354A	family with sequence si	39 (0.00)	42 (0.21)	0.57
12-01	Gp3	g.chr11:6243787C>T	Missense Mutation	FAM160A2	p.R359Q	family with sequence si	170 (0.00)	19 (0.58)	1.54
12-01	Gp3	g.chr11:6244338G>A	Missense Mutation	FAM160A2	p.S303F	family with sequence si	204 (0.00)	86 (0.17)	0.47
12-01	Gp3	g.chr10:116595951C>A	Nonsense Mutation	FAM160B1	p.C156*	family with sequence si	47 (0.00)	30 (0.20)	0.53
12-01	Gp3	g.chr14:74409236G>A	Missense Mutation	FAM161B	p.P433S	family with sequence si	178 (0.00)	171 (0.28)	0.75
12-01	Gp3	g.chr7:30931608C>T	Silent	FAM188B	p.D754D	family with sequence si	180 (0.00)	183 (0.17)	0.45
12-01	Gp3	g.chr4:2698255A>T	Missense Mutation	FAM193A	p.S879C	family with sequence si	90 (0.00)	77 (0.16)	0.42
12-01	Gp3	g.chr20:33879708C>A	Nonsense Mutation	FAM83C	p.E134*	family with sequence si	76 (0.00)	84 (0.20)	0.54
12-01	Gp3	g.chr20:37580841C>A	Missense Mutation	FAM83D	p.S509Y	family with sequence si	207 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr3:125647388T>A	RNA	FAM86JP		family with sequence si	64 (0.00)	19 (0.26)	0.70
12-01	Gp3	g.chr11:92533807G>A	Missense Mutation	FAT3	p.R2393Q	FAT atypical cadherin 3	69 (0.00)	13 (0.69)	1.85
12-01	Gp3	g.chr8:413089C>T	Missense Mutation	FBXO25	p.A309V	F-box protein 25	99 (0.00)	48 (0.25)	0.85
12-01	Gp3	g.chr3:121340958G>T	Missense Mutation	FBXO40	p.A228S	F-box protein 40	89 (0.00)	53 (0.17)	0.45
12-01	Gp3	g.chr1:149760137C>T	Missense Mutation	FCGR1A	p.R175C	Fc fragment of IgG, hig	145 (0.00)	28 (0.79)	2.10
12-01	Gp3	g.chr1:157660153C>G	Missense Mutation	FCRL3	p.A528P	Fc receptor-like 3	201 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr4:155507149C>G	Missense Mutation	FGA	p.V478L	fibrinogen alpha chain	165 (0.00)	27 (0.19)	0.49
12-01	Gp3	g.chr3:14860748C>A	Missense Mutation	FGD5	p.S57Y	FYVE, RhoGEF and P	20 (0.00)	39 (0.15)	0.41
12-01	Gp3	g.chr12:95603866G>A	Silent	FGD6	p.V398V	FYVE, RhoGEF and P	59 (0.00)	32 (0.19)	0.50
12-01	Gp3	g.chr8:16850747T>A	Missense Mutation	FGF20	p.K157I	fibroblast growth factor	36 (0.00)	26 (0.27)	0.72
12-01	Gp3	g.chr2:164467941C>A	Missense Mutation	FIGN	p.G134V	fidgetin	109 (0.00)	21 (0.24)	0.63
12-01	Gp3	g.chr1:152327883G>A	Silent	FLG2	p.G793G	filaggrin family membe	69 (0.00)	34 (0.18)	0.47
12-01	Gp3	g.chr6:159653123G>T	Missense Mutation	FNDC1	p.A527S	fibronectin type III dom	40 (0.00)	32 (0.50)	1.33
12-01	Gp3	g.chr9:117927G>T	Missense Mutation	FOXD4	p.L65I	forkhead box D4	27 (0.00)	50 (0.18)	0.48
12-01	Gp3	g.chr7:114282582C>T	Missense Mutation	FOXP2	p.S298L	forkhead box P2	115 (0.01)	33 (0.27)	0.73
12-01	Gp3	g.chrX:49116597G>A	Intron	FOXP3		forkhead box P3	174 (0.00)	26 (0.31)	0.51
12-01	Gp3	g.chr9:14801763C>G	Missense Mutation	FREM1	p.G1194A	FRAS1 related extracell	52 (0.00)	15 (0.33)	0.89
12-01	Gp3	g.chr9:14841545C>T	Missense Mutation	FREM1	p.G594E	FRAS1 related extracell	41 (0.00)	76 (0.25)	0.67
12-01	Gp3	g.chr3:69231780T>A	Missense Mutation	FRMD4B	p.T670S	FERM domain containi	216 (0.00)	37 (0.43)	1.15

12-01	Gp3	g.chr3:46021209C>A	Missense Mutation	FYCO1	p.K92N	FYVE and coiled-coil d	207 (0.00)	76 (0.21)	0.56
12-01	Gp3	g.chr11:77936213C>T	Missense Mutation	GAB2	p.G415S	GRB2-associated bindi	53 (0.00)	30 (0.23)	0.62
12-01	Gp3	g.chr15:50596193G>T	Silent	GABPB1	p.G82G	GA binding protein tran	125 (0.00)	35 (0.31)	0.84
12-01	Gp3	g.chrX:151123968T>A	Missense Mutation	GABRE	p.I337F	gamma-aminobutyric ac	137 (0.00)	26 (0.46)	0.77
12-01	Gp3	g.chr9:130027298C>T	Silent	GARNL3	p.L48L	GTPase activating Rap/	180 (0.00)	98 (0.43)	1.14
12-01	Gp3	g.chr4:22737729G>A	RNA	GBA3		glucosidase, beta, acid 3	47 (0.02)	30 (0.30)	0.80
12-01	Gp3	g.chr1:89615153G>A	Missense Mutation	GBP7	p.A325V	guanylate binding protei	46 (0.00)	21 (0.29)	0.76
12-01	Gp3	g.chr7:127223226G>A	Silent	GCC1	p.A390A	GRIP and coiled-coil d	93 (0.00)	32 (0.34)	0.92
12-01	Gp3	g.chr2:85777799G>A	Silent	GGCX	p.L655L	gamma-glutamyl carbox	132 (0.00)	27 (0.19)	0.49
12-01	Gp3	g.chr1:29040860C>A	Missense Mutation	GMEB1	p.P423T	glucocorticoid modulat	211 (0.00)	58 (0.19)	0.51
12-01	Gp3	g.chr15:28947164C>T	Missense Mutation	GOLGA8M	p.G612D	golgin A8 family, mem	323 (0.00)	167 (0.14)	0.38
12-01	Gp3	g.chr2:133402925C>A	Missense Mutation	GPR39	p.H370N	G protein-coupled recep	21 (0.00)	33 (0.15)	0.58
12-01	Gp3	g.chr5:90124957G>A	Missense Mutation	GPR98	p.R5522K	G protein-coupled recep	183 (0.00)	82 (0.27)	0.72
12-01	Gp3	g.chr21:31015243G>A	Missense Mutation	GRIK1	p.A334V	glutamate receptor, ion	87 (0.00)	15 (0.40)	1.07
12-01	Gp3	g.chr16:10273995C>A	Missense Mutation	GRIN2A	p.G92W	glutamate receptor, ion	98 (0.00)	131 (0.18)	0.49
12-01	Gp3	g.chr7:86416078G>T	Nonsense Mutation	GRM3	p.E324*	glutamate receptor, met	31 (0.00)	35 (0.14)	0.38
12-01	Gp3	g.chr13:51598437C>T	RNA	GUCY1B2		guanylate cyclase 1, sol	18 (0.00)	15 (0.67)	1.78
12-01	Gp3	g.chr19:17160684C>A	Nonstop Mutation	HAUS8	p.*411L	HAUS augmin-like co	23 (0.00)	38 (0.32)	0.84
12-01	Gp3	g.chr7:18737505A>G	Intron	HDAC9		histone deacetylase 9	46 (0.00)	43 (0.21)	0.56
12-01	Gp3	g.chr7:18779853G>T	Intron	HDAC9		histone deacetylase 9	65 (0.02)	31 (0.16)	0.43
12-01	Gp3	g.chr7:18780242T>A	Intron	HDAC9		histone deacetylase 9	296 (0.00)	131 (0.20)	0.53
12-01	Gp3	g.chr7:18834307G>A	Intron	HDAC9		histone deacetylase 9	17 (0.00)	23 (0.43)	1.16
12-01	Gp3	g.chr7:18993390C>T	Intron	HDAC9		histone deacetylase 9	65 (0.00)	14 (0.57)	1.52
12-01	Gp3	g.chr7:18994953C>A	Intron	HDAC9		histone deacetylase 9	35 (0.00)	71 (0.32)	0.86
12-01	Gp3	g.chr7:19023413G>A	Intron	HDAC9		histone deacetylase 9	35 (0.00)	21 (0.43)	1.14
12-01	Gp3	g.chr17:58121370C>A	Missense Mutation	HEATR6	p.G1034W	HEAT repeat containin	184 (0.00)	27 (0.33)	0.89
12-01	Gp3	g.chr12:66700236T>C	Missense Mutation	HELB	p.M240T	helicase (DNA) B	17 (0.00)	12 (0.58)	1.56
12-01	Gp3	g.chr15:20644181C>T	RNA	HERC2P3		hect domain and RLD 2	81 (0.00)	27 (0.30)	0.79
12-01	Gp3	g.chr17:46669654G>A	Nonsense Mutation	HOXB5	p.Q243*	homeobox B5	89 (0.00)	143 (0.20)	0.54
12-01	Gp3	g.chr12:54403431C>A	Missense Mutation	HOXC8	p.N121K	homeobox C8	115 (0.00)	191 (0.21)	0.57
12-01	Gp3	g.chrX:131763005G>T	Missense Mutation	HS6ST2	p.P395H	heparan sulfate 6-O-sul	88 (0.00)	51 (0.63)	1.05
12-01	Gp3	g.chr4:3148669C>T	Missense Mutation	HTT	p.L1097F	huntingtin	91 (0.00)	20 (0.30)	0.80
12-01	Gp3	g.chr19:10403522G>A	Missense Mutation	ICAM5	p.S399N	intercellular adhesion m	33 (0.00)	49 (0.22)	0.60
12-01	Gp3	g.chr9:21077505C>A	Missense Mutation	IFNB1	p.V122F	interferon, beta 1, fibro	110 (0.00)	30 (0.17)	0.44
12-01	Gp3	g.chr19:36230666G>A	Silent	IGFLR1	p.A222A	IGF-like family recepto	49 (0.00)	88 (0.15)	0.39

12-01	Gp3	g.chr2:89442310G>A	RNA	IGKV3-20		immunoglobulin kappa	239 (0.00)	70 (0.17)	0.46
12-01	Gp3	g.chr22:23077316G>T	RNA	IGLV2-18		immunoglobulin lambd	109 (0.00)	34 (0.21)	0.55
12-01	Gp3	g.chr22:17583114C>A	Silent	IL17RA	p.T228T	interleukin 17 receptor	111 (0.00)	130 (0.15)	0.41
12-01	Gp3	g.chr10:6061883C>T	Missense Mutation	IL2RA	p.S202N	interleukin 2 receptor, a	90 (0.00)	28 (0.36)	0.95
12-01	Gp3	g.chr16:3117404G>A	Silent	IL32	p.L14L	interleukin 32	86 (0.00)	103 (0.26)	0.70
12-01	Gp3	g.chr7:128035248C>A	Missense Mutation	IMPDH1	p.A358S	IMP (inosine 5'-monoph	54 (0.00)	57 (0.16)	0.42
12-01	Gp3	g.chr4:142974971C>T	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	18 (0.50)	1.33
12-01	Gp3	g.chr4:143094332C>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	19 (0.26)	0.70
12-01	Gp3	g.chr4:143150775C>A	Intron	INPP4B		inositol polyphosphate-	82 (0.00)	36 (0.28)	0.74
12-01	Gp3	g.chr4:143181429G>A	Intron	INPP4B		inositol polyphosphate-	53 (0.00)	35 (0.14)	0.38
12-01	Gp3	g.chr4:143217930C>A	Intron	INPP4B		inositol polyphosphate-	16 (0.00)	31 (0.16)	0.43
12-01	Gp3	g.chr4:143254386C>A	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr4:143254397G>A	Intron	INPP4B		inositol polyphosphate-	60 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr4:143260019C>G	Intron	INPP4B		inositol polyphosphate-	196 (0.00)	27 (0.70)	1.88
12-01	Gp3	g.chr4:143318370C>T	Intron	INPP4B		inositol polyphosphate-	106 (0.01)	82 (0.24)	0.65
12-01	Gp3	g.chr4:143444386C>T	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	50 (0.58)	1.55
12-01	Gp3	g.chr4:143458232G>T	Intron	INPP4B		inositol polyphosphate-	57 (0.00)	13 (0.54)	1.44
12-01	Gp3	g.chr4:143484903C>T	Intron	INPP4B		inositol polyphosphate-	49 (0.00)	27 (0.74)	1.98
12-01	Gp3	g.chr4:143544222C>A	Intron	INPP4B		inositol polyphosphate-	83 (0.00)	29 (0.66)	1.75
12-01	Gp3	g.chr4:143611965G>T	Intron	INPP4B		inositol polyphosphate-	27 (0.00)	29 (0.28)	0.74
12-01	Gp3	g.chr4:143708500C>A	Intron	INPP4B		inositol polyphosphate-	59 (0.00)	24 (0.21)	0.56
12-01	Gp3	g.chr4:143708512C>A	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	17 (0.29)	0.78
12-01	Gp3	g.chr10:134511343G>A	Missense Mutation	INPP5A	p.G132S	inositol polyphosphate-	71 (0.00)	43 (0.26)	0.68
12-01	Gp3	g.chr1:38341283G>A	Nonsense Mutation	INPP5B	p.R595*	inositol polyphosphate-	105 (0.00)	18 (0.28)	0.74
12-01	Gp3	g.chr8:19694646G>A	Silent	INTS10	p.S538S	integrator complex subu	39 (0.00)	30 (0.23)	0.62
12-01	Gp3	g.chr8:95839632G>A	Splice Site	INTS8		integrator complex subu	64 (0.00)	23 (0.22)	0.58
12-01	Gp3	g.chr1:201841963G>A	Missense Mutation	IPO9	p.A862T	importin 9	32 (0.00)	11 (0.45)	1.21
12-01	Gp3	g.chr16:31341876G>T	Missense Mutation	ITGAM	p.D1077Y	integrin, alpha M (comp	66 (0.00)	44 (0.14)	0.45
12-01	Gp3	g.chr3:52813449G>A	Splice Site	ITIH1	p.A138T	inter-alpha-trypsin inhib	61 (0.00)	53 (0.17)	0.45
12-01	Gp3	g.chr1:160920895C>A	Missense Mutation	ITLN2	p.G127C	intelectin 2	56 (0.00)	51 (0.18)	0.47
12-01	Gp3	g.chr3:4714915G>T	Missense Mutation	ITPR1	p.R752L	inositol 1,4,5-trisphosph	269 (0.00)	95 (0.23)	0.62
12-01	Gp3	g.chr12:26816730G>A	Missense Mutation	ITPR2	p.S534L	inositol 1,4,5-trisphosph	21 (0.00)	14 (0.36)	0.95
12-01	Gp3	g.chr17:74717917C>G	Missense Mutation	JMJD6	p.V302L	jumonji domain contain	25 (0.00)	17 (0.29)	0.78
12-01	Gp3	g.chr19:11287414G>C	Missense Mutation	KANK2	p.P542A	KN motif and ankyrin r	20 (0.00)	30 (0.37)	0.98
12-01	Gp3	g.chr8:41791414C>A	Missense Mutation	KAT6A	p.A1442S	K(lysine) acetyltransfer	162 (0.00)	32 (0.19)	0.50

12-01	Gp3	g.chr5:169931626G>A	Missense Mutation	KCNIP1	p.R17Q	Kv channel interacting p	32 (0.00)	63 (0.32)	0.67
12-01	Gp3	g.chr17:21318821A>C	Missense Mutation	KCNJ12	p.E56A	potassium inwardly-rect	51 (0.02)	83 (0.17)	0.45
12-01	Gp3	g.chr11:2604727C>A	Silent	KCNQ1	p.I328I	potassium voltage-gated	39 (0.00)	27 (0.22)	0.59
12-01	Gp3	g.chr5:143853540G>A	Missense Mutation	KCTD16	p.A384T	potassium channel tetra	71 (0.00)	61 (0.15)	0.39
12-01	Gp3	g.chr12:121970853C>A	Silent	KDM2B	p.L32L	lysine (K)-specific deme	50 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr5:137727273G>T	Missense Mutation	KDM3B	p.S651I	lysine (K)-specific deme	148 (0.00)	55 (0.27)	0.73
12-01	Gp3	g.chr13:46924365G>T	Nonsense Mutation	KIAA0226L	p.Y327*	KIAA0226-like	100 (0.01)	19 (0.26)	0.70
12-01	Gp3	g.chr14:58965518G>T	Silent	KIAA0586	p.V1389V	KIAA0586	24 (0.00)	17 (0.41)	1.10
12-01	Gp3	g.chr4:37440644G>C	Missense Mutation	KIAA1239	p.V310L		79 (0.00)	15 (0.33)	0.89
12-01	Gp3	g.chr7:138604131G>A	Silent	KIAA1549	p.L81L	KIAA1549	180 (0.00)	36 (0.44)	1.19
12-01	Gp3	g.chr8:29003917G>T	Missense Mutation	KIF13B	p.S722Y	kinesin family member	206 (0.00)	18 (0.28)	0.74
12-01	Gp3	g.chr1:10316334G>A	Missense Mutation	KIF1B	p.A46T	kinesin family member	27 (0.00)	44 (0.36)	0.97
12-01	Gp3	g.chr5:61659025G>T	Missense Mutation	KIF2A	p.R360S	kinesin heavy chain mer	89 (0.00)	18 (0.28)	0.74
12-01	Gp3	g.chr19:55330021G>T	Missense Mutation	KIR3DL1	p.A108S	killer cell immunoglobu	50 (0.00)	37 (0.22)	0.58
12-01	Gp3	g.chr6:43029222C>A	Missense Mutation	KLC4	p.T50N	kinesin light chain 4	71 (0.00)	97 (0.15)	0.41
12-01	Gp3	g.chr16:87795572G>A	Silent	KLHDC4	p.C58C	kelch domain containing	72 (0.00)	11 (0.82)	0.96
12-01	Gp3	g.chr7:98786164G>A	Missense Mutation	KPNA7	p.T220M	karyopherin alpha 7 (im	83 (0.00)	51 (0.22)	0.58
12-01	Gp3	g.chr1:152732258G>T	Missense Mutation	KPRP	p.C65F	keratinocyte proline-ricl	69 (0.00)	28 (0.18)	0.48
12-01	Gp3	g.chr12:53343293C>A	Silent	KRT18	p.I112I	keratin 18	25 (0.00)	53 (0.17)	0.45
12-01	Gp3	g.chr21:46078008G>A	Missense Mutation	KRTAP12-3	p.V38M	keratin associated protei	150 (0.00)	234 (0.14)	0.49
12-01	Gp3	g.chr21:46078009T>A	Missense Mutation	KRTAP12-3	p.V38E	keratin associated protei	150 (0.00)	233 (0.14)	0.50
12-01	Gp3	g.chr17:39296558C>A	Missense Mutation	KRTAP4-6	p.C61F	keratin associated protei	76 (0.00)	75 (0.15)	0.39
12-01	Gp3	g.chr22:41605776G>A	Missense Mutation	L3MBTL2	p.R34Q	l(3)mbt-like 2 (Drosoph	83 (0.00)	16 (0.31)	0.83
12-01	Gp3	g.chr22:41616870G>A	Missense Mutation	L3MBTL2	p.R284Q	l(3)mbt-like 2 (Drosoph	83 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr6:112493842C>T	Missense Mutation	LAMA4	p.A508T	laminin, alpha 4	65 (0.00)	29 (0.31)	0.83
12-01	Gp3	g.chr7:107605030G>T	Nonsense Mutation	LAMB1	p.Y555*	laminin, beta 1	224 (0.00)	50 (0.26)	0.69
12-01	Gp3	g.chr1:209824266A>G	Silent	LAMB3	p.C8C	laminin, beta 3	97 (0.00)	53 (0.34)	0.91
12-01	Gp3	g.chr1:183109562C>T	Silent	LAMC1	p.A1499A	laminin, gamma 1 (form	28 (0.00)	21 (0.43)	0.85
12-01	Gp3	g.chr10:909706G>A	Missense Mutation	LARP4B	p.S136F	La ribonucleoprotein do	20 (0.00)	21 (0.29)	0.76
12-01	Gp3	g.chr19:11230873G>T	Missense Mutation	LDLR	p.D651Y	low density lipoprotein	56 (0.00)	42 (0.19)	0.51
12-01	Gp3	g.chr3:189681794A>G	Missense Mutation	LEPREL1	p.C663R	leprecan-like 1	49 (0.00)	42 (0.14)	0.38
12-01	Gp3	g.chr19:55106760G>T	Missense Mutation	LILRA1	p.G185V	leukocyte immunoglobu	121 (0.00)	47 (0.19)	0.51
12-01	Gp3	g.chr4:41687784C>A	Missense Mutation	LIMCH1	p.P798Q	LIM and calponin homo	31 (0.00)	34 (0.76)	2.04
12-01	Gp3	g.chr11:74203281G>T	Missense Mutation	LIPT2	p.L199I	lipoyl(octanoyl) transfe	61 (0.02)	38 (0.16)	0.42
12-01	Gp3	g.chr7:97820077G>T	Missense Mutation	LMTK2	p.A346S	lemur tyrosine kinase 2	127 (0.00)	25 (0.60)	1.60

12-01	Gp3	g.chr4:62758388G>C	Missense Mutation	LPHN3	p.G431R	latrophilin 3	241 (0.00)	43 (0.51)	0.63
12-01	Gp3	g.chr3:197597030G>A	Splice Site	LRCH3		leucine-rich repeats and	211 (0.00)	83 (0.16)	0.42
12-01	Gp3	g.chr4:110772898G>A	Missense Mutation	LRIT3	p.A119T	leucine-rich repeat, imm	31 (0.00)	31 (0.26)	0.69
12-01	Gp3	g.chr11:46921925T>A	Silent	LRP4	p.L68L	low density lipoprotein	74 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr1:90048293G>A	Nonsense Mutation	LRRC8B	p.W28*	leucine rich repeat conta	103 (0.00)	53 (0.23)	0.60
12-01	Gp3	g.chr3:3888041C>A	Silent	LRRN1	p.A572A	leucine rich repeat neur	191 (0.00)	48 (0.17)	0.44
12-01	Gp3	g.chr3:119463031G>T	Missense Mutation	MAATS1	p.E630D	MYCBP-associated, tes	72 (0.01)	55 (0.16)	0.44
12-01	Gp3	g.chr1:39852997G>T	Missense Mutation	MACF1	p.R4833L	microtubule-actin crossl	243 (0.00)	39 (0.33)	0.89
12-01	Gp3	g.chr11:47311768G>A	Silent	MADD	p.Q1024Q	MAP-kinase activating	109 (0.00)	115 (0.25)	0.67
12-01	Gp3	g.chrX:75648715C>T	Missense Mutation	MAGEE1	p.A131V	melanoma antigen famil	16 (0.00)	19 (0.26)	0.44
12-01	Gp3	g.chr7:77734131C>G	Intron	MAGI2		membrane associated gu	102 (0.00)	64 (0.30)	0.79
12-01	Gp3	g.chr7:77804907G>T	Intron	MAGI2		membrane associated gu	63 (0.00)	31 (0.39)	1.03
12-01	Gp3	g.chr7:77839650C>T	Intron	MAGI2		membrane associated gu	77 (0.01)	49 (0.39)	1.03
12-01	Gp3	g.chr7:77875724G>T	Intron	MAGI2		membrane associated gu	201 (0.00)	54 (0.26)	0.69
12-01	Gp3	g.chr7:77975239C>T	Splice Site	MAGI2	p.E409K	membrane associated gu	277 (0.00)	153 (0.18)	0.47
12-01	Gp3	g.chr7:78047539C>A	Intron	MAGI2		membrane associated gu	68 (0.00)	21 (0.33)	0.89
12-01	Gp3	g.chr7:78095867G>T	Intron	MAGI2		membrane associated gu	22 (0.00)	26 (0.50)	1.33
12-01	Gp3	g.chr7:78131841G>T	Intron	MAGI2		membrane associated gu	17 (0.00)	31 (0.35)	0.95
12-01	Gp3	g.chr7:78162223G>C	Intron	MAGI2		membrane associated gu	73 (0.00)	36 (0.19)	0.52
12-01	Gp3	g.chr7:78192650G>T	Intron	MAGI2		membrane associated gu	67 (0.00)	41 (0.51)	1.37
12-01	Gp3	g.chr7:78288315C>T	Intron	MAGI2		membrane associated gu	34 (0.00)	47 (0.15)	0.40
12-01	Gp3	g.chr7:78361525C>A	Intron	MAGI2		membrane associated gu	57 (0.00)	56 (0.46)	1.24
12-01	Gp3	g.chr7:78408631C>T	Intron	MAGI2		membrane associated gu	44 (0.00)	42 (0.40)	1.08
12-01	Gp3	g.chr7:78408648G>C	Intron	MAGI2		membrane associated gu	43 (0.00)	37 (0.46)	1.23
12-01	Gp3	g.chr7:78536441G>A	Intron	MAGI2		membrane associated gu	83 (0.00)	95 (0.22)	0.59
12-01	Gp3	g.chr7:78619941C>T	Intron	MAGI2		membrane associated gu	55 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr7:78871332G>T	Intron	MAGI2		membrane associated gu	48 (0.00)	21 (0.48)	1.27
12-01	Gp3	g.chr7:78953290G>C	Intron	MAGI2		membrane associated gu	177 (0.00)	70 (0.16)	0.42
12-01	Gp3	g.chr7:79043588C>T	Intron	MAGI2		membrane associated gu	43 (0.00)	104 (0.17)	0.46
12-01	Gp3	g.chr7:79062233G>T	Intron	MAGI2		membrane associated gu	376 (0.00)	111 (0.19)	0.50
12-01	Gp3	g.chr19:17838858C>A	Missense Mutation	MAP1S	p.L889I	microtubule-associated	20 (0.00)	30 (0.20)	0.53
12-01	Gp3	g.chr3:185167723G>A	Missense Mutation	MAP3K13	p.G349E	mitogen-activated protei	151 (0.00)	27 (0.19)	0.49
12-01	Gp3	g.chr1:27682174G>A	Silent	MAP3K6	p.I1258I	mitogen-activated protei	80 (0.00)	71 (0.20)	0.53
12-01	Gp3	g.chr6:90388331G>A	Silent	MDN1	p.H4133H	MDN1, midasin homolo	197 (0.00)	47 (0.19)	0.51
12-01	Gp3	g.chr18:48473499C>T	Missense Mutation	ME2	p.P567L	malic enzyme 2, NAD(	72 (0.00)	34 (0.18)	0.47

12-01	Gp3	g.chr15:100211603G>A	Missense Mutation	MEF2A	p.E112K	myocyte enhancer facto	217 (0.00)	68 (0.21)	0.55
12-01	Gp3	g.chr15:66190367C>T	Missense Mutation	MEGF11	p.D1014N	multiple EGF-like-dom	87 (0.00)	11 (0.64)	1.70
12-01	Gp3	g.chr18:29790595G>T	Nonsense Mutation	MEP1B	p.E351*	meprin A, beta	133 (0.00)	68 (0.28)	0.75
12-01	Gp3	g.chr4:170913335C>T	Missense Mutation	MFAP3L	p.V142I	microfibrillar-associate	67 (0.00)	23 (0.26)	0.70
12-01	Gp3	g.chr12:53647534G>A	Silent	MFSD5	p.K305K	major facilitator superfa	50 (0.02)	115 (0.21)	0.56
12-01	Gp3	g.chr14:39703397G>T	Missense Mutation	MIA2	p.A27S	melanoma inhibitory ac	86 (0.00)	47 (0.32)	0.85
12-01	Gp3	g.chr1:222828015A>T	Missense Mutation	MIA3	p.E1496V	melanoma inhibitory ac	112 (0.01)	15 (0.47)	1.24
12-01	Gp3	g.chr22:18374282C>T	Missense Mutation	MICAL3	p.A555T	microtubule associated	196 (0.00)	70 (0.19)	0.50
12-01	Gp3	g.chr22:39909592C>T	Missense Mutation	MIEF1	p.P219L	mitochondrial elongatio	178 (0.00)	66 (0.23)	0.61
12-01	Gp3	g.chr9:20365683G>A	Silent	MLLT3	p.S395S	myeloid/lymphoid or mi	81 (0.00)	46 (0.20)	0.52
12-01	Gp3	g.chr15:56735936C>T	Missense Mutation	MNS1	p.R268K	meiosis-specific nuclear	17 (0.00)	9 (0.67)	1.78
12-01	Gp3	g.chr9:13193278C>T	Missense Mutation	MPDZ	p.G564E	multiple PDZ domain p	102 (0.00)	52 (0.27)	0.72
12-01	Gp3	g.chr11:18955858C>A	Missense Mutation	MRGPRX1	p.W158C	MAS-related GPR, men	79 (0.00)	45 (0.20)	0.53
12-01	Gp3	g.chr20:35783489G>A	Silent	MROH8	p.L351L	maestro heat-like repeat	243 (0.00)	31 (0.19)	0.52
12-01	Gp3	g.chr9:138395749G>T	Missense Mutation	MRPS2	p.G221C	mitochondrial ribosoma	43 (0.00)	62 (0.15)	0.39
12-01	Gp3	g.chr9:125033207C>A	Missense Mutation	MRRF	p.P13T	mitochondrial ribosome	284 (0.00)	37 (0.49)	1.30
12-01	Gp3	g.chr11:10626069C>A	Missense Mutation	MRVI1	p.L542F	murine retrovirus integr	182 (0.00)	14 (0.71)	1.90
12-01	Gp3	g.chr3:9695422G>A	Missense Mutation	MTMR14	p.E93K	myotubularin related pr	160 (0.00)	47 (0.19)	0.51
12-01	Gp3	g.chr7:100646425G>T	Missense Mutation	MUC12	p.S4337I	mucin 12, cell surface a	191 (0.00)	81 (0.20)	0.53
12-01	Gp3	g.chr7:100656311G>T	Missense Mutation	MUC12	p.D5319Y	mucin 12, cell surface a	44 (0.00)	31 (0.23)	0.60
12-01	Gp3	g.chr7:100682238G>T	Missense Mutation	MUC17	p.S2514I	mucin 17, cell surface a	216 (0.00)	52 (0.15)	0.41
12-01	Gp3	g.chr7:100683734G>T	Missense Mutation	MUC17	p.D3013Y	mucin 17, cell surface a	155 (0.00)	44 (0.23)	0.61
12-01	Gp3	g.chr3:195453080C>A	Missense Mutation	MUC20	p.L536I	mucin 20, cell surface a	72 (0.00)	77 (0.21)	0.55
12-01	Gp3	g.chr7:100551653C>A	Missense Mutation	MUC3A	p.P135H	mucin 3A, cell surface a	512 (0.00)	16 (0.31)	0.83
12-01	Gp3	g.chr19:54377419C>T	Silent	MYADM	p.I212I	myeloid-associated diff	75 (0.00)	114 (0.17)	0.44
12-01	Gp3	g.chr20:42320821C>A	Missense Mutation	MYBL2	p.H175Q	v-myb avian myeloblast	156 (0.00)	48 (0.19)	0.50
12-01	Gp3	g.chr16:15835664G>A	Nonsense Mutation	MYH11	p.Q869*	myosin, heavy chain 11,	129 (0.00)	66 (0.29)	0.77
12-01	Gp3	g.chr17:10441084G>A	Silent	MYH2	p.H495H	myosin, heavy chain 2,	146 (0.00)	39 (0.23)	0.62
12-01	Gp3	g.chr7:44180602G>A	Silent	MYL7	p.V25V	myosin, light chain 7, re	20 (0.00)	24 (0.21)	0.56
12-01	Gp3	g.chr12:56620165C>A	Missense Mutation	NABP2	p.A133D	nucleic acid binding pro	147 (0.00)	39 (0.49)	1.30
12-01	Gp3	g.chr12:78511838C>G	Missense Mutation	NAV3	p.T934R	neuron navigator 3	71 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr12:78579392G>C	Missense Mutation	NAV3	p.D1880H	neuron navigator 3	50 (0.00)	28 (0.21)	0.57
12-01	Gp3	g.chr3:47039994C>A	Missense Mutation	NBEAL2	p.Q1054K	neurobeachin-like 2	63 (0.00)	60 (0.15)	0.40
12-01	Gp3	g.chr11:134037897G>A	Silent	NCAPD3	p.I1189I	non-SMC condensin II	132 (0.00)	79 (0.22)	0.57
12-01	Gp3	g.chr18:9122560C>T	Missense Mutation	NDUFV2	p.T117I	NADH dehydrogenase (	115 (0.00)	55 (0.44)	1.16

12-01	Gp3	g.chr2:152470939G>A	Missense Mutation	NEB	p.P3818S	nebulin	154 (0.00)	159 (0.43)	1.14
12-01	Gp3	g.chr9:127089719C>T	Missense Mutation	NEK6	p.S206F	NIMA-related kinase 6	37 (0.00)	70 (0.19)	0.50
12-01	Gp3	g.chr1:204970303G>C	Missense Mutation	NFASC	p.D1009H	neurofascin	89 (0.00)	64 (0.20)	0.54
12-01	Gp3	g.chr14:24839423C>A	Missense Mutation	NFATC4	p.S336R	nuclear factor of activat	19 (0.00)	48 (0.17)	0.44
12-01	Gp3	g.chrX:17744321G>C	Missense Mutation	NHS	p.A678P	Nance-Horan syndrome	130 (0.00)	48 (0.23)	0.38
12-01	Gp3	g.chr1:24782668G>T	Missense Mutation	NIPAL3	p.M226I	NIPA-like domain conta	130 (0.00)	56 (0.29)	0.76
12-01	Gp3	g.chr17:33464104C>A	Silent	NLE1	p.S248S	notchless homolog 1 (D	62 (0.00)	99 (0.15)	0.40
12-01	Gp3	g.chr19:55451785C>T	Nonsense Mutation	NLRP7	p.W134*	NLR family, pyrin doma	412 (0.00)	267 (0.14)	0.38
12-01	Gp3	g.chr2:10712206C>T	Silent	NOL10	p.S686S	nucleolar protein 10	167 (0.00)	19 (0.53)	1.40
12-01	Gp3	g.chr7:156746821C>T	Silent	NOM1	p.S379S	nucleolar protein with M	48 (0.00)	28 (0.18)	0.48
12-01	Gp3	g.chr9:139409088T>C	Missense Mutation	NOTCH1	p.E694G	notch 1	18 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr11:89135595C>A	Nonsense Mutation	NOX4	p.E249*	NADPH oxidase 4	21 (0.00)	22 (0.23)	0.61
12-01	Gp3	g.chr19:36326618T>A	Missense Mutation	NPHS1	p.E1052V	nephrosis 1, congenital,	148 (0.00)	20 (0.25)	0.67
12-01	Gp3	g.chr11:9009143G>A	Missense Mutation	NRIP3	p.T125I	nuclear receptor interact	107 (0.00)	37 (0.30)	0.79
12-01	Gp3	g.chr12:5603677C>A	Nonsense Mutation	NTF3	p.Y112*	neurotrophin 3	164 (0.00)	136 (0.16)	0.43
12-01	Gp3	g.chr16:2522444G>A	Missense Mutation	NTN3	p.D248N	netrin 3	17 (0.00)	35 (0.51)	1.37
12-01	Gp3	g.chr15:88678366G>T	Silent	NTRK3	p.T292T	neurotrophic tyrosine ki	148 (0.00)	42 (0.14)	0.38
12-01	Gp3	g.chr20:61341075C>A	Missense Mutation	NTSR1	p.H172Q	neurotensin receptor 1 (	126 (0.00)	73 (0.29)	0.77
12-01	Gp3	g.chr6:17675580G>A	Silent	NUP153	p.N201N	nucleoporin 153kDa	46 (0.00)	12 (0.75)	2.00
12-01	Gp3	g.chr9:131756722G>T	Splice Site	NUP188		nucleoporin 188kDa	52 (0.00)	38 (0.32)	0.84
12-01	Gp3	g.chr15:34648513G>C	Missense Mutation	NUTM1	p.E768D	NUT midline carcinoma	151 (0.00)	82 (0.15)	0.39
12-01	Gp3	g.chr1:228471276G>T	Missense Mutation	OBSCN	p.C3366F	obscurin, cytoskeletal ca	69 (0.00)	130 (0.16)	0.43
12-01	Gp3	g.chr1:228491480C>A	Silent	OBSCN	p.R4615R	obscurin, cytoskeletal ca	124 (0.00)	114 (0.15)	0.40
12-01	Gp3	g.chr2:220418334C>T	Missense Mutation	OBSL1	p.E1651K	obscurin-like 1	90 (0.00)	160 (0.21)	0.55
12-01	Gp3	g.chr8:103564040G>A	Missense Mutation	ODF1	p.D29N	outer dense fiber of sper	86 (0.00)	35 (0.49)	1.30
12-01	Gp3	g.chr8:103564067G>A	Missense Mutation	ODF1	p.D38N	outer dense fiber of sper	104 (0.00)	36 (0.28)	0.74
12-01	Gp3	g.chr9:107380179G>A	Missense Mutation	OR13C9	p.L103F	olfactory receptor, famil	144 (0.00)	59 (0.17)	0.45
12-01	Gp3	g.chr9:125512165C>A	Missense Mutation	OR1L6	p.F13L	olfactory receptor, famil	422 (0.00)	154 (0.16)	0.42
12-01	Gp3	g.chr11:6007591G>A	Silent	OR52L1	p.T190T	olfactory receptor, famil	200 (0.00)	159 (0.26)	0.69
12-01	Gp3	g.chr11:55563529C>T	Silent	OR5D14	p.L166L	olfactory receptor, famil	126 (0.00)	29 (0.31)	0.83
12-01	Gp3	g.chr11:124253192T>A	Silent	OR8B2	p.G16G	olfactory receptor, famil	87 (0.00)	53 (0.26)	0.70
12-01	Gp3	g.chr11:124266460G>A	Missense Mutation	OR8B3	p.S263F	olfactory receptor, famil	39 (0.00)	21 (0.24)	0.63
12-01	Gp3	g.chr2:241078677G>T	Nonsense Mutation	OTOS	p.Y60*	otospiralin	61 (0.00)	86 (0.17)	0.66
12-01	Gp3	g.chr8:101716543C>A	Missense Mutation	PABPC1	p.G632C	poly(A) binding protein,	251 (0.00)	60 (0.17)	0.44
12-01	Gp3	g.chr4:79856274C>T	Splice Site	PAQR3		progestin and adipoQ re	53 (0.00)	11 (0.45)	1.21

12-01	Gp3	g.chr16:3021827G>C	Missense Mutation	PAQR4	p.D160H	progestin and adipoQ re	27 (0.00)	84 (0.17)	0.44
12-01	Gp3	g.chr4:30725888C>G	Nonsense Mutation	PCDH7	p.Y948*	protocadherin 7	148 (0.01)	25 (0.24)	0.64
12-01	Gp3	g.chr4:30725902C>A	Missense Mutation	PCDH7	p.T953N	protocadherin 7	164 (0.01)	24 (0.25)	0.67
12-01	Gp3	g.chr5:140626553C>A	Missense Mutation	PCDHB15	p.H469Q	protocadherin beta 15	67 (0.00)	37 (0.22)	0.58
12-01	Gp3	g.chr5:140614250C>A	RNA	PCDHB18		protocadherin beta 18 ps	45 (0.00)	12 (0.58)	1.56
12-01	Gp3	g.chr5:140482140C>A	Missense Mutation	PCDHB3	p.A636D	protocadherin beta 3	67 (0.00)	37 (0.19)	0.50
12-01	Gp3	g.chr5:140745656C>A	Missense Mutation	PCDHGA5	p.L587M	protocadherin gamma su	17 (0.00)	38 (0.21)	0.56
12-01	Gp3	g.chr5:140864852G>T	Nonsense Mutation	PCDHGC4	p.E38*	protocadherin gamma su	48 (0.00)	58 (0.16)	0.41
12-01	Gp3	g.chr5:140866177C>A	Silent	PCDHGC4	p.A479A	protocadherin gamma su	86 (0.00)	39 (0.15)	0.41
12-01	Gp3	g.chr7:82584108T>A	Missense Mutation	PCLO	p.E2054V	piccolo presynaptic cyto	58 (0.00)	25 (0.20)	0.53
12-01	Gp3	g.chr11:72299946G>C	Missense Mutation	PDE2A	p.Q318E	phosphodiesterase 2A, c	29 (0.00)	27 (0.22)	0.59
12-01	Gp3	g.chr5:149504373G>T	Missense Mutation	PDGFRB	p.A610D	platelet-derived growth	37 (0.00)	50 (0.16)	0.43
12-01	Gp3	g.chr4:39868480C>G	Splice Site	PDS5A		PDS5, regulator of cohe	34 (0.00)	18 (0.33)	0.89
12-01	Gp3	g.chr17:4585825T>A	Missense Mutation	PELP1	p.Y205F	proline, glutamate and le	175 (0.00)	87 (0.21)	0.55
12-01	Gp3	g.chr11:61017249G>T	Missense Mutation	PGA5	p.Q294H	pepsinogen 5, group I (p	231 (0.00)	158 (0.16)	0.42
12-01	Gp3	g.chr6:49753804C>A	Missense Mutation	PGK2	p.G366V	phosphoglycerate kinase	23 (0.00)	16 (0.31)	0.83
12-01	Gp3	g.chr18:60434916G>T	Intron	PHLPP1		PH domain and leucine	44 (0.00)	39 (0.28)	0.75
12-01	Gp3	g.chr18:60520230G>A	Intron	PHLPP1		PH domain and leucine	143 (0.00)	115 (0.16)	0.42
12-01	Gp3	g.chr18:60550539G>A	Intron	PHLPP1		PH domain and leucine	149 (0.00)	40 (0.23)	0.60
12-01	Gp3	g.chr18:60640195C>T	Intron	PHLPP1		PH domain and leucine	205 (0.00)	59 (0.69)	1.85
12-01	Gp3	g.chr11:581545C>A	Silent	PHRF1	p.A11A	PHD and ring finger do	66 (0.00)	90 (0.14)	0.39
12-01	Gp3	g.chr1:151274741C>A	Silent	PI4KB	p.P503P	phosphatidylinositol 4-k	178 (0.00)	43 (0.23)	0.62
12-01	Gp3	g.chr17:34893379T>A	Silent	PIGW	p.A143A	phosphatidylinositol gly	197 (0.00)	23 (0.78)	2.09
12-01	Gp3	g.chr1:204409429C>A	Missense Mutation	PIK3C2B	p.Q1090H	phosphatidylinositol-4-p	151 (0.00)	20 (0.30)	0.80
12-01	Gp3	g.chr5:67569288C>T	Silent	PIK3R1	p.L135L	phosphoinositide-3-kina	50 (0.00)	35 (0.69)	1.83
12-01	Gp3	g.chr15:42374482G>T	Missense Mutation	PLA2G4D	p.P260T	phospholipase A2, grou	194 (0.00)	43 (0.21)	0.56
12-01	Gp3	g.chr15:42276721G>A	Silent	PLA2G4E	p.L767L	phospholipase A2, grou	289 (0.00)	176 (0.15)	0.39
12-01	Gp3	g.chr16:81944217G>T	Missense Mutation	PLCG2	p.S609I	phospholipase C, gamm	178 (0.00)	91 (0.34)	0.40
12-01	Gp3	g.chr17:4718809A>T	Missense Mutation	PLD2	p.E404D	phospholipase D2	287 (0.00)	123 (0.24)	0.65
12-01	Gp3	g.chr6:151161377G>A	Missense Mutation	PLEKHG1	p.R1168Q	pleckstrin homology do	70 (0.01)	27 (0.67)	1.78
12-01	Gp3	g.chr2:43937144C>T	Missense Mutation	PLEKHH2	p.S661F	pleckstrin homology do	280 (0.00)	111 (0.24)	0.65
12-01	Gp3	g.chr6:161128774G>A	Missense Mutation	PLG	p.M76I	plasminogen	37 (0.00)	63 (0.37)	0.97
12-01	Gp3	g.chr7:131844284G>A	Silent	PLXNA4	p.I1536I	plexin A4	226 (0.00)	51 (0.25)	0.68
12-01	Gp3	g.chr14:39645351G>T	Silent	PNN	p.L61L	pinin, desmosome assoc	124 (0.00)	38 (0.18)	0.49
12-01	Gp3	g.chr7:108154879C>G	Splice Site	PNPLA8		patatin-like phospholipa	48 (0.00)	38 (0.21)	0.56

12-01	Gp3	g.chr1:166818232C>T	Missense Mutation	POGK	p.S139F	pogo transposable elem	307 (0.00)	133 (0.15)	0.40
12-01	Gp3	g.chr8:43173753A>T	RNA	POTEA		POTE ankyrin domain f	35 (0.00)	13 (0.85)	2.26
12-01	Gp3	g.chr12:51589884C>A	Missense Mutation	POU6F1	p.V40F	POU class 6 homeobox	50 (0.00)	31 (0.16)	0.43
12-01	Gp3	g.chr18:9557302G>T	Missense Mutation	PPP4R1	p.L703M	protein phosphatase 4, r	89 (0.00)	13 (0.38)	1.03
12-01	Gp3	g.chr8:69032499C>A	Silent	PREX2	p.L1191L	phosphatidylinositol-3,4	39 (0.00)	12 (0.75)	2.00
12-01	Gp3	g.chr12:49398911G>A	Missense Mutation	PRKAG1	p.T116I	protein kinase, AMP-ac	26 (0.00)	14 (0.50)	1.33
12-01	Gp3	g.chr21:48071884G>A	Missense Mutation	PRMT2	p.G274D	protein arginine methylt	149 (0.01)	154 (0.21)	0.75
12-01	Gp3	g.chr14:75323582G>T	Silent	PROX2	p.P510P	prospero homeobox 2	109 (0.00)	45 (0.60)	1.60
12-01	Gp3	g.chr14:75323583G>T	Missense Mutation	PROX2	p.P510H	prospero homeobox 2	111 (0.00)	45 (0.60)	1.60
12-01	Gp3	g.chr10:13647645G>T	Missense Mutation	PRPF18	p.L88F	pre-mRNA processing f	73 (0.00)	93 (0.24)	0.63
12-01	Gp3	g.chr7:18067083G>T	Missense Mutation	PRPS1L1	p.S108Y	phosphoribosyl pyropho	256 (0.00)	65 (0.17)	0.45
12-01	Gp3	g.chr16:31143612C>A	Missense Mutation	PRSS8	p.W250C	protease, serine, 8	15 (0.00)	39 (0.13)	0.42
12-01	Gp3	g.chr9:79325463C>T	Missense Mutation	PRUNE2	p.S576N	prune homolog 2 (Dros	81 (0.00)	11 (0.45)	1.21
12-01	Gp3	g.chr9:79328500T>C	Silent	PRUNE2	p.E298E	prune homolog 2 (Dros	54 (0.00)	21 (0.24)	0.63
12-01	Gp3	g.chr4:7435328A>G	Missense Mutation	PSAPL1	p.C427R	prosaposin-like 1 (gene/	48 (0.00)	75 (0.15)	0.39
12-01	Gp3	g.chr4:7436229C>G	Silent	PSAPL1	p.P126P	prosaposin-like 1 (gene/	27 (0.00)	35 (0.14)	0.38
12-01	Gp3	g.chr10:104176528C>A	Missense Mutation	PSD	p.G90W	pleckstrin and Sec7 dom	26 (0.00)	28 (0.21)	0.57
12-01	Gp3	g.chr5:139222055C>A	Missense Mutation	PSD2	p.T771N	pleckstrin and Sec7 dom	91 (0.00)	57 (0.18)	0.47
12-01	Gp3	g.chr19:43258539G>A	Missense Mutation	PSG8	p.R397C	pregnancy specific beta-	36 (0.00)	28 (0.64)	1.71
12-01	Gp3	g.chrX:107330994C>T	Missense Mutation	PSMD10	p.G150D	proteasome (prosome, n	64 (0.00)	32 (0.78)	1.30
12-01	Gp3	g.chr10:29710429G>A	RNA	PTCHD3P1		patched domain contain	28 (0.00)	38 (0.24)	0.63
12-01	Gp3	g.chr8:27278239C>T	Missense Mutation	PTK2B	p.T150M	protein tyrosine kinase	187 (0.00)	39 (0.21)	0.55
12-01	Gp3	g.chr7:77186657C>A	Intron	PTPN12		protein tyrosine phospha	307 (0.00)	80 (0.34)	0.90
12-01	Gp3	g.chr15:75772216G>A	Nonsense Mutation	PTPN9	p.Q368*	protein tyrosine phospha	77 (0.01)	22 (0.36)	0.97
12-01	Gp3	g.chr19:55711800G>A	Silent	PTPRH	p.V408V	protein tyrosine phospha	44 (0.00)	27 (0.26)	0.69
12-01	Gp3	g.chr2:220160947C>T	Splice Site	PTPRN		protein tyrosine phospha	78 (0.00)	53 (0.17)	0.45
12-01	Gp3	g.chr2:220167475C>A	Missense Mutation	PTPRN	p.Q154H	protein tyrosine phospha	75 (0.00)	60 (0.17)	0.44
12-01	Gp3	g.chr19:5210584G>T	Missense Mutation	PTPRS	p.P1795T	protein tyrosine phospha	35 (0.00)	139 (0.17)	0.46
12-01	Gp3	g.chr11:125765836C>T	Missense Mutation	PUS3	p.G115E	pseudouridylate synthas	116 (0.00)	66 (0.29)	0.77
12-01	Gp3	g.chr10:99967948G>A	Missense Mutation	R3HCC1L	p.R26K	R3H domain and coiled-	20 (0.00)	29 (0.21)	0.55
12-01	Gp3	g.chr15:66170242G>A	Missense Mutation	RAB11A	p.D127N	RAB11A, member RAS	70 (0.00)	24 (0.25)	0.67
12-01	Gp3	g.chr15:66170275G>A	Missense Mutation	RAB11A	p.E138K	RAB11A, member RAS	75 (0.00)	21 (0.24)	0.63
12-01	Gp3	g.chr1:156039504C>T	Missense Mutation	RAB25	p.S159F	RAB25, member RAS c	50 (0.00)	50 (0.24)	0.64
12-01	Gp3	g.chr19:11448054G>A	Nonsense Mutation	RAB3D	p.Q8*	RAB3D, member RAS	183 (0.00)	98 (0.17)	0.46
12-01	Gp3	g.chr2:114399664C>G	Missense Mutation	RABL2A	p.S215R	RAB, member of RAS	80 (0.00)	31 (0.26)	0.69

12-01	Gp3	g.chr17:33430524C>A	Missense Mutation	RAD51D	p.D206Y	RAD51 paralog D	26 (0.00)	28 (0.25)	0.67
12-01	Gp3	g.chr20:37154645G>T	Missense Mutation	RALGAPB	p.L670F	Ral GTPase activating p	53 (0.00)	27 (0.30)	0.79
12-01	Gp3	g.chr2:109383844G>A	Silent	RANBP2	p.K2283K	RAN binding protein 2	121 (0.00)	25 (0.20)	0.53
12-01	Gp3	g.chr19:5941661G>A	Missense Mutation	RANBP3	p.S126F	RAN binding protein 3	76 (0.00)	115 (0.23)	0.63
12-01	Gp3	g.chr6:13657431C>G	Missense Mutation	RANBP9	p.G272R	RAN binding protein 9	42 (0.00)	33 (0.27)	0.73
12-01	Gp3	g.chr12:48143207C>T	Missense Mutation	RAPGEF3	p.R336H	Rap guanine nucleotide	46 (0.02)	37 (0.27)	0.72
12-01	Gp3	g.chr11:63304344G>T	Missense Mutation	RARRES3	p.A2S	retinoic acid receptor re	53 (0.00)	12 (0.42)	1.11
12-01	Gp3	g.chr11:64497272T>A	Splice Site	RASGRP2		RAS guanyl releasing p	54 (0.00)	55 (0.36)	0.97
12-01	Gp3	g.chr17:9801464C>T	Missense Mutation	RCVRN	p.R184Q	recoverin	388 (0.00)	149 (0.44)	1.16
12-01	Gp3	g.chr7:103155642G>A	Silent	RELN	p.D2703D	reelin	94 (0.00)	50 (0.22)	0.59
12-01	Gp3	g.chr7:103155675G>A	Silent	RELN	p.V2692V	reelin	94 (0.00)	47 (0.15)	0.40
12-01	Gp3	g.chr6:111694907A>T	Missense Mutation	REV3L	p.L1551I	REV3-like, polymerase	40 (0.00)	23 (0.22)	0.58
12-01	Gp3	g.chr22:29834904G>A	Missense Mutation	RFPL1	p.V42I	ret finger protein-like 1	82 (0.00)	11 (0.55)	1.45
12-01	Gp3	g.chr2:113146807C>A	Missense Mutation	RGPD8	p.A1099S	RANBP2-like and GRII	173 (0.00)	44 (0.18)	0.48
12-01	Gp3	g.chr12:107208831G>A	Missense Mutation	RIC8B	p.D164N	RIC8 guanine nucleotid	36 (0.00)	21 (0.43)	1.14
12-01	Gp3	g.chr1:41094961C>A	Missense Mutation	RIMS3	p.G186C	regulating synaptic mem	152 (0.00)	61 (0.15)	0.39
12-01	Gp3	g.chr9:5335448C>A	Missense Mutation	RLN1	p.D121Y	relaxin 1	71 (0.00)	74 (0.41)	1.08
12-01	Gp3	g.chr9:116060414C>A	Missense Mutation	RNF183	p.W17C	ring finger protein 183	31 (0.00)	49 (0.16)	0.44
12-01	Gp3	g.chr1:33407878A>G	Missense Mutation	RNF19B	p.S530P	ring finger protein 19B	84 (0.00)	48 (0.23)	0.61
12-01	Gp3	g.chr7:5662524C>A	Missense Mutation	RNF216	p.M913I	ring finger protein 216	38 (0.00)	105 (0.15)	0.41
12-01	Gp3	g.chr1:45115366G>A	Silent	RNF220	p.E493E	ring finger protein 220	161 (0.00)	48 (0.29)	0.78
12-01	Gp3	g.chr12:56604352C>A	Splice Site	RNF41	p.A31S	ring finger protein 41, E	24 (0.00)	26 (0.19)	0.51
12-01	Gp3	g.chr1:172955526C>T	lincRNA	RP1-15D23.2			33 (0.00)	25 (0.20)	0.53
12-01	Gp3	g.chr8:84932238C>G	lincRNA	RP11-120I21.2			20 (0.00)	24 (0.21)	0.56
12-01	Gp3	g.chr9:67293622C>A	RNA	RP11-236F9.2			116 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr2:74588656C>T	Silent	RP11-287D1.3	p.L182L		46 (0.00)	41 (0.24)	0.65
12-01	Gp3	g.chr16:30309884C>A	RNA	RP11-347C12.2			79 (0.00)	27 (0.19)	0.49
12-01	Gp3	g.chr3:125509447C>A	lincRNA	RP11-379B18.6			70 (0.00)	75 (0.21)	0.57
12-01	Gp3	g.chr16:59041137G>A	lincRNA	RP11-410D17.2			29 (0.00)	12 (0.42)	1.11
12-01	Gp3	g.chr17:20449242G>A	lincRNA	RP11-434D2.3			59 (0.00)	26 (0.19)	0.51
12-01	Gp3	g.chr3:196043072G>A	Silent	RP11-447L10.	p.I48I		50 (0.00)	13 (0.46)	1.23
12-01	Gp3	g.chr1:145381782G>T	lincRNA	RP11-458D21.1			47 (0.00)	37 (0.22)	0.58
12-01	Gp3	g.chr11:49747451G>T	RNA	RP11-707M1.1			28 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr14:47120402C>A	Nonsense Mutation	RPL10L	p.E180*	ribosomal protein L10-l	144 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr22:39710730C>A	Silent	RPL3	p.G270G	ribosomal protein L3	27 (0.00)	40 (0.15)	0.40

12-01	Gp3	g.chr6:166836783G>T	Silent	RPS6KA2	p.L479L	ribosomal protein S6 ki	44 (0.00)	52 (0.17)	0.46
12-01	Gp3	g.chr12:66152204G>A	RNA	RPSAP52		ribosomal protein SA ps	30 (0.00)	14 (0.43)	1.14
12-01	Gp3	g.chr8:108970322C>A	Missense Mutation	RSPO2	p.R201M	R-spondin 2	65 (0.00)	33 (0.58)	1.54
12-01	Gp3	g.chr8:108970358G>A	Missense Mutation	RSPO2	p.T189I	R-spondin 2	62 (0.00)	30 (0.87)	2.31
12-01	Gp3	g.chr14:60074113C>G	Silent	RTN1	p.V38V	reticulon 1	28 (0.00)	31 (0.16)	0.43
12-01	Gp3	g.chr3:72437543C>G	Intron	RYBP		RING1 and YY1 bindin	122 (0.00)	26 (0.81)	2.15
12-01	Gp3	g.chr3:72459763C>T	Intron	RYBP		RING1 and YY1 bindin	83 (0.00)	93 (0.26)	0.69
12-01	Gp3	g.chr3:72459871G>A	Intron	RYBP		RING1 and YY1 bindin	58 (0.00)	70 (0.23)	0.61
12-01	Gp3	g.chr19:38980901C>A	Silent	RYR1	p.S2000S	ryanodine receptor 1 (sk	33 (0.00)	28 (0.18)	0.48
12-01	Gp3	g.chr16:51171162G>A	Missense Mutation	SALL1	p.T1279M	spalt-like transcription f	188 (0.00)	110 (0.26)	0.70
12-01	Gp3	g.chr5:133942752C>G	Missense Mutation	SAR1B	p.S162T	secretion associated, Ra	117 (0.00)	23 (0.30)	0.81
12-01	Gp3	g.chr19:1119568G>A	Silent	SBNO2	p.G440G	strawberry notch homol	15 (0.00)	37 (0.22)	0.58
12-01	Gp3	g.chr15:76646419C>A	Missense Mutation	SCAPER	p.Q1306H	S-phase cyclin A-associ	142 (0.00)	235 (0.15)	0.40
12-01	Gp3	g.chr4:54140068G>T	Silent	SCFD2	p.A412A	sec1 family domain con	58 (0.00)	27 (0.48)	1.28
12-01	Gp3	g.chr2:224463986C>A	Missense Mutation	SCG2	p.K5N	secretogranin II	105 (0.00)	27 (0.33)	0.89
12-01	Gp3	g.chr17:62018427G>A	Missense Mutation	SCN4A	p.R1739C	sodium channel, voltage	123 (0.00)	173 (0.53)	1.40
12-01	Gp3	g.chr2:167298231G>A	Missense Mutation	SCN7A	p.P611L	sodium channel, voltage	23 (0.00)	32 (0.34)	0.92
12-01	Gp3	g.chr11:9069506G>C	Missense Mutation	SCUBE2	p.N593K	signal peptide, CUB do	203 (0.00)	126 (0.18)	0.49
12-01	Gp3	g.chr2:192701174G>A	Silent	SDPR	p.I251I	serum deprivation respo	151 (0.00)	69 (0.22)	0.58
12-01	Gp3	g.chr9:139369422G>T	Missense Mutation	SEC16A	p.N704K	SEC16 homolog A (S. c	163 (0.00)	109 (0.20)	0.54
12-01	Gp3	g.chr1:177934200T>A	Missense Mutation	SEC16B	p.N172I	SEC16 homolog B (S. c	108 (0.00)	33 (0.24)	0.65
12-01	Gp3	g.chr1:169582205G>A	Missense Mutation	SELP	p.A246V	selectin P (granule mem	30 (0.00)	24 (0.75)	2.00
12-01	Gp3	g.chr14:94849047C>A	Missense Mutation	SERPINA1	p.E176D	serpin peptidase inhibit	88 (0.00)	54 (0.26)	0.69
12-01	Gp3	g.chr22:26692864T>C	Missense Mutation	SEZ6L	p.V327A	seizure related 6 homol	70 (0.00)	22 (0.27)	0.73
12-01	Gp3	g.chr1:162367101C>T	Missense Mutation	SH2D1B	p.S123N	SH2 domain containing	25 (0.04)	16 (0.75)	2.00
12-01	Gp3	g.chr11:70319127G>A	Silent	SHANK2	p.N1203N	SH3 and multiple ankyr	39 (0.00)	21 (0.33)	0.89
12-01	Gp3	g.chr17:18238886G>T	Missense Mutation	SHMT1	p.N306K	serine hydroxymethyltr	174 (0.00)	20 (0.55)	1.47
12-01	Gp3	g.chr12:57626052G>A	Missense Mutation	SHMT2	p.E191K	serine hydroxymethyltr	95 (0.00)	49 (0.14)	0.38
12-01	Gp3	g.chr3:72841297G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	44 (0.00)	24 (0.46)	1.22
12-01	Gp3	g.chr3:72861294G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	132 (0.01)	32 (0.28)	0.75
12-01	Gp3	g.chr5:132159863C>T	Missense Mutation	SHROOM1	p.S497N	shroom family member	117 (0.01)	52 (0.29)	0.77
12-01	Gp3	g.chr19:51769078G>T	Missense Mutation	SIGLECL1	p.G118C	SIGLEC family like 1	202 (0.00)	18 (0.44)	1.19
12-01	Gp3	g.chr14:72117064C>T	Nonsense Mutation	SIPA1L1	p.Q611*	signal-induced prolifera	223 (0.00)	24 (0.54)	1.44
12-01	Gp3	g.chr1:232650844G>A	Missense Mutation	SIPA1L2	p.S81F	signal-induced prolifera	109 (0.00)	27 (0.22)	0.59
12-01	Gp3	g.chr19:38643554C>A	Missense Mutation	SIPA1L3	p.S1203Y	signal-induced prolifera	15 (0.00)	49 (0.31)	0.82

12-01	Gp3	g.chr10:69651254C>T	Missense Mutation	SIRT1	p.A295V	sirtuin 1	191 (0.00)	71 (0.23)	0.60
12-01	Gp3	g.chr3:170078687C>G	Missense Mutation	SKIL	p.L170V	SKI-like proto-oncogen	36 (0.00)	19 (0.26)	0.70
12-01	Gp3	g.chr8:42294731G>T	Nonsense Mutation	SLC20A2	p.Y433*	solute carrier family 20	57 (0.00)	67 (0.15)	0.40
12-01	Gp3	g.chr6:160828158G>A	Missense Mutation	SLC22A3	p.V207M	solute carrier family 22	33 (0.00)	28 (0.36)	0.95
12-01	Gp3	g.chr17:78210806A>T	Silent	SLC26A11	p.L272L	solute carrier family 26	71 (0.00)	119 (0.17)	0.45
12-01	Gp3	g.chr1:9083102C>A	Missense Mutation	SLC2A7	p.E62D	solute carrier family 2 (	145 (0.00)	60 (0.17)	0.44
12-01	Gp3	g.chr4:25678140C>A	Missense Mutation	SLC34A2	p.F614L	solute carrier family 34	52 (0.00)	33 (0.24)	0.65
12-01	Gp3	g.chr21:43987130C>A	Missense Mutation	SLC37A1	p.P436T	solute carrier family 37	26 (0.00)	42 (0.19)	0.51
12-01	Gp3	g.chr3:50255458G>C	RNA	SLC38A3		solute carrier family 38,	49 (0.00)	55 (0.15)	0.39
12-01	Gp3	g.chr17:19470102G>A	Splice Site	SLC47A1		solute carrier family 47	136 (0.01)	52 (0.25)	0.67
12-01	Gp3	g.chr19:33324146C>T	Silent	SLC7A9	p.E436E	solute carrier family 7 (	65 (0.00)	58 (0.29)	0.78
12-01	Gp3	g.chr18:48561507G>A	Intron	SMAD4		SMAD family member	84 (0.00)	42 (0.83)	2.22
12-01	Gp3	g.chr18:48604728G>T	Missense Mutation	SMAD4	p.S421I	SMAD family member	73 (0.00)	35 (0.17)	0.46
12-01	Gp3	g.chrX:21772366G>A	Nonsense Mutation	SMPX	p.Q15*	small muscle protein, X	57 (0.00)	37 (0.46)	0.77
12-01	Gp3	g.chr2:242021191G>A	Missense Mutation	SNED1	p.G1339D	sushi, nidogen and EGF	23 (0.00)	89 (0.16)	0.60
12-01	Gp3	g.chr15:25427604G>A	RNA	SNHG14		small nucleolar RNA ho	73 (0.00)	95 (0.18)	0.48
12-01	Gp3	g.chr15:25432793C>A	RNA	SNHG14		small nucleolar RNA ho	277 (0.00)	339 (0.20)	0.54
12-01	Gp3	g.chr11:130784574C>A	Nonsense Mutation	SNX19	p.G421*	sorting nexin 19	66 (0.00)	24 (0.29)	0.78
12-01	Gp3	g.chr11:65618614T>A	Missense Mutation	SNX32	p.V231D	sorting nexin 32	41 (0.00)	57 (0.16)	0.42
12-01	Gp3	g.chr20:35443684G>T	Missense Mutation	SOGA1	p.Q721K	suppressor of glucose, a	41 (0.02)	31 (0.19)	0.52
12-01	Gp3	g.chr4:7668877C>T	Silent	SORCS2	p.Y366Y	sortilin-related VPS10 d	143 (0.01)	43 (0.19)	0.50
12-01	Gp3	g.chr9:40702801C>T	Missense Mutation	SPATA31A3	p.A153V	SPATA31 subfamily A,	305 (0.00)	198 (0.16)	0.43
12-01	Gp3	g.chr9:43625308G>A	Missense Mutation	SPATA31A6	p.P1127S	SPATA31 subfamily A,	170 (0.00)	46 (0.50)	1.33
12-01	Gp3	g.chr11:74676917A>G	Missense Mutation	SPCS2	p.Y103C	signal peptidase comple	47 (0.00)	25 (0.28)	0.75
12-01	Gp3	g.chr22:24761523G>C	Missense Mutation	SPECC1L	p.M969I	sperm antigen with calp	56 (0.00)	28 (0.25)	0.67
12-01	Gp3	g.chr13:46288393G>A	Silent	SPERT	p.K375K	spermatid associated	26 (0.00)	29 (0.17)	0.46
12-01	Gp3	g.chr17:47705265A>C	Intron	SPOP		speckle-type POZ protei	73 (0.00)	12 (0.42)	1.11
12-01	Gp3	g.chr1:9427513C>A	Missense Mutation	SPSB1	p.P234Q	splA/ryanodine receptor	38 (0.00)	82 (0.27)	0.72
12-01	Gp3	g.chr12:109182168G>A	Silent	SSH1	p.L916L	slingshot protein phosp	124 (0.00)	147 (0.20)	0.53
12-01	Gp3	g.chr3:52537397G>T	Silent	STAB1	p.L244L	stabilin 1	39 (0.00)	44 (0.20)	0.55
12-01	Gp3	g.chr17:40369412C>A	Missense Mutation	STAT5B	p.A414S	signal transducer and ac	78 (0.00)	12 (0.50)	0.53
12-01	Gp3	g.chr12:57492850C>A	Missense Mutation	STAT6	p.G525C	signal transducer and ac	125 (0.00)	36 (0.22)	0.59
12-01	Gp3	g.chr5:171532736A>T	Missense Mutation	STK10	p.V265E	serine/threonine kinase	80 (0.00)	66 (0.18)	0.48
12-01	Gp3	g.chr4:184931376G>A	Missense Mutation	STOX2	p.S462N	storkhead box 2	82 (0.00)	38 (0.18)	0.49
12-01	Gp3	g.chr7:129122825C>T	Missense Mutation	STRIP2	p.T731I	striatin interacting prote	29 (0.00)	28 (0.25)	0.67

12-01	Gp3	g.chr12:118829065G>A	Silent	SUDS3	p.K165K	suppressor of defective	167 (0.00)	38 (0.24)	0.63
12-01	Gp3	g.chr6:149721679G>A	Missense Mutation	SUMO4	p.R51Q	small ubiquitin-like mo	85 (0.00)	48 (0.35)	0.94
12-01	Gp3	g.chr17:27005098G>T	Missense Mutation	SUPT6H	p.S335I	suppressor of Ty 6 hom	104 (0.01)	24 (0.42)	1.11
12-01	Gp3	g.chr6:152737726C>T	Missense Mutation	SYNE1	p.R1949K	spectrin repeat containi	206 (0.00)	23 (0.74)	1.97
12-01	Gp3	g.chr14:64453260G>T	Silent	SYNE2	p.V746V	spectrin repeat containi	45 (0.00)	44 (0.16)	0.42
12-01	Gp3	g.chr11:61291406C>T	Missense Mutation	SYT7	p.R311Q	synaptotagmin VII	122 (0.00)	100 (0.29)	0.77
12-01	Gp3	g.chr11:61323656G>A	Silent	SYT7	p.L19L	synaptotagmin VII	34 (0.00)	38 (0.21)	0.56
12-01	Gp3	g.chr17:35797857C>T	Missense Mutation	TADA2A	p.L71F	transcriptional adaptor 2	89 (0.00)	43 (0.16)	0.43
12-01	Gp3	g.chr3:9822170C>A	Missense Mutation	TADA3	p.E390D	transcriptional adaptor 3	23 (0.00)	43 (0.16)	0.43
12-01	Gp3	g.chr1:159889622G>T	Missense Mutation	TAGLN2	p.L62I	transgelin 2	26 (0.00)	34 (0.53)	1.41
12-01	Gp3	g.chr17:61483633C>G	Missense Mutation	TANC2	p.A1121G	tetratricopeptide repeat,	218 (0.00)	34 (0.32)	0.86
12-01	Gp3	g.chr17:58088526C>T	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	83 (0.00)	77 (0.18)	0.48
12-01	Gp3	g.chr16:30098137C>A	Missense Mutation	TBX6	p.G292V	T-box 6	24 (0.00)	21 (0.38)	1.02
12-01	Gp3	g.chr5:149755349G>T	Missense Mutation	TCOF1	p.Q590H	Treacher Collins-France	89 (0.00)	109 (0.28)	0.76
12-01	Gp3	g.chr19:33233721C>T	Missense Mutation	TDRD12	p.P119S	tudor domain containing	40 (0.00)	44 (0.43)	1.15
12-01	Gp3	g.chr11:121023691G>A	Missense Mutation	TECTA	p.V1403M	tectorin alpha	36 (0.00)	47 (0.53)	1.42
12-01	Gp3	g.chr17:73987605G>T	Missense Mutation	TEN1	p.D51Y	TEN1 CST complex sul	195 (0.00)	140 (0.19)	0.51
12-01	Gp3	g.chr6:155579140G>A	Missense Mutation	TFB1M	p.R291W	transcription factor B1,	178 (0.00)	42 (0.45)	1.21
12-01	Gp3	g.chr11:134119730G>A	Missense Mutation	THYN1	p.L126F	thymocyte nuclear prote	36 (0.00)	26 (0.50)	1.33
12-01	Gp3	g.chr9:35707480T>A	Silent	TLN1	p.L1546L	talin 1	42 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr10:98292808C>A	Splice Site	TM9SF3	p.W442L	transmembrane 9 superf	95 (0.00)	18 (0.67)	1.78
12-01	Gp3	g.chr11:66061832C>T	Missense Mutation	TMEM151A	p.R39C	transmembrane protein	17 (0.00)	14 (0.43)	1.14
12-01	Gp3	g.chr6:11575678G>A	Missense Mutation	TMEM170B	p.G95S	transmembrane protein	57 (0.00)	22 (0.27)	0.73
12-01	Gp3	g.chr7:150490234C>A	Missense Mutation	TMEM176B	p.R181L	transmembrane protein	49 (0.00)	24 (0.21)	0.56
12-01	Gp3	g.chr16:29979483G>A	Missense Mutation	TMEM219	p.A165T	transmembrane protein	128 (0.00)	70 (0.14)	0.38
12-01	Gp3	g.chr11:129724538C>T	Missense Mutation	TMEM45B	p.P71L	transmembrane protein	66 (0.00)	13 (0.38)	1.03
12-01	Gp3	g.chr1:205052779C>A	Missense Mutation	TMEM81	p.V224L	transmembrane protein	52 (0.00)	20 (0.65)	1.73
12-01	Gp3	g.chr21:42838816G>A	Intron	TMPRSS2		transmembrane protease	96 (0.00)	77 (0.19)	0.52
12-01	Gp3	g.chr11:128806508C>T	Missense Mutation	TP53AIP1	p.G60R	tumor protein p53 regul	112 (0.01)	56 (0.18)	0.48
12-01	Gp3	g.chr2:24300455G>T	Silent	TP53I3	p.P331P	tumor protein p53 induc	42 (0.00)	49 (0.33)	0.87
12-01	Gp3	g.chr21:45494987G>C	Missense Mutation	TRAPPC10	p.R418T	trafficking protein partic	187 (0.00)	42 (0.14)	0.52
12-01	Gp3	g.chr7:38370227C>A	RNA	TRGV8		T cell receptor gamma v	189 (0.00)	38 (0.18)	0.49
12-01	Gp3	g.chr5:64920090C>A	Silent	TRIM23	p.L4L	tripartite motif containi	19 (0.00)	41 (0.20)	0.52
12-01	Gp3	g.chr11:119996523C>A	Missense Mutation	TRIM29	p.E403D	tripartite motif containi	27 (0.00)	17 (0.29)	0.78
12-01	Gp3	g.chr17:57093091C>T	Missense Mutation	TRIM37	p.G819D	tripartite motif containi	158 (0.00)	39 (0.15)	0.41

12-01	Gp3	g.chr11:55032423G>T	Missense Mutation	TRIM48	p.C31F	tripartite motif containi	64 (0.00)	33 (0.33)	0.89
12-01	Gp3	g.chr11:89537510C>G	Missense Mutation	TRIM49	p.W43S	tripartite motif containi	54 (0.00)	27 (0.26)	0.69
12-01	Gp3	g.chr22:38120367T>A	Missense Mutation	TRIOBP	p.C602S	TRIO and F-actin bindi	156 (0.01)	52 (0.19)	0.51
12-01	Gp3	g.chr22:38120401C>A	Missense Mutation	TRIOBP	p.T613N	TRIO and F-actin bindi	146 (0.00)	28 (0.36)	0.95
12-01	Gp3	g.chr22:38121921C>G	Missense Mutation	TRIOBP	p.P1120A	TRIO and F-actin bindi	18 (0.00)	19 (0.32)	0.84
12-01	Gp3	g.chr2:230656782C>T	Splice Site	TRIP12		thyroid hormone recept	63 (0.00)	51 (0.16)	0.42
12-01	Gp3	g.chr5:901529G>T	Missense Mutation	TRIP13	p.R173L	thyroid hormone recept	172 (0.00)	92 (0.18)	0.49
12-01	Gp3	g.chr8:116599252C>A	Missense Mutation	TRPS1	p.K892N	trichorhinophalangeal s	116 (0.00)	99 (0.18)	0.48
12-01	Gp3	g.chr7:98586559C>T	Silent	TRRAP	p.N3162N	transformation/transcrip	52 (0.00)	69 (0.17)	0.46
12-01	Gp3	g.chr7:98591177G>A	Silent	TRRAP	p.Q3263Q	transformation/transcrip	16 (0.00)	48 (0.19)	0.50
12-01	Gp3	g.chr9:135781061G>A	Missense Mutation	TSC1	p.T635I	tuberous sclerosis 1	167 (0.00)	17 (0.29)	0.78
12-01	Gp3	g.chr9:135798868G>T	Missense Mutation	TSC1	p.D125E	tuberous sclerosis 1	85 (0.01)	54 (0.26)	0.69
12-01	Gp3	g.chr18:72998899G>A	Missense Mutation	TSHZ1	p.A513T	teashirt zinc finger hom	58 (0.00)	75 (0.12)	0.41
12-01	Gp3	g.chr18:73000430T>A	Missense Mutation	TSHZ1	p.L1023Q	teashirt zinc finger hom	210 (0.00)	81 (0.16)	0.55
12-01	Gp3	g.chr7:138872248G>A	Missense Mutation	TTC26	p.G475S	tetratricopeptide repeat	177 (0.00)	42 (0.19)	0.51
12-01	Gp3	g.chr22:28379216C>T	Missense Mutation	TTC28	p.V2147M	tetratricopeptide repeat	73 (0.00)	110 (0.16)	0.44
12-01	Gp3	g.chr14:20770017G>A	Silent	TTC5	p.T53T	tetratricopeptide repeat	93 (0.00)	36 (0.22)	0.59
12-01	Gp3	g.chr14:91113307G>T	Silent	TTC7B	p.A526A	tetratricopeptide repeat	218 (0.00)	41 (0.24)	0.65
12-01	Gp3	g.chr14:91113315G>T	Missense Mutation	TTC7B	p.Q524K	tetratricopeptide repeat	222 (0.00)	43 (0.30)	0.81
12-01	Gp3	g.chr14:91113318G>T	Missense Mutation	TTC7B	p.L523M	tetratricopeptide repeat	220 (0.00)	44 (0.20)	0.55
12-01	Gp3	g.chr22:43447846G>A	Silent	TTLL1	p.D313D	tubulin tyrosine ligase-li	73 (0.00)	140 (0.14)	0.38
12-01	Gp3	g.chr2:179588737C>A	Missense Mutation	TTN	p.K7083N	titin	73 (0.00)	29 (0.34)	0.92
12-01	Gp3	g.chr19:54942359G>T	Missense Mutation	TTYH1	p.S372I	tweety family member 1	17 (0.00)	50 (0.20)	0.53
12-01	Gp3	g.chr6:158902276C>A	Silent	TULP4	p.R481R	tubby like protein 4	35 (0.00)	70 (0.20)	0.53
12-01	Gp3	g.chr8:15605909G>A	Silent	TUSC3	p.L321L	tumor suppressor candi	39 (0.00)	19 (0.32)	0.84
12-01	Gp3	g.chr16:11785415T>C	Missense Mutation	TXNDC11	p.D544G	thioredoxin domain con	100 (0.00)	63 (0.21)	0.55
12-01	Gp3	g.chr15:41865963C>A	Nonsense Mutation	TYRO3	p.Y744*	TYRO3 protein tyrosin	23 (0.00)	15 (0.40)	1.07
12-01	Gp3	g.chr7:66479516G>T	Nonsense Mutation	TYW1	p.G180*	tRNA-yW synthesizing	93 (0.00)	25 (0.28)	0.75
12-01	Gp3	g.chr1:1198729C>A	Nonsense Mutation	UBE2J2	p.E73*	ubiquitin-conjugating e	134 (0.00)	46 (0.22)	0.58
12-01	Gp3	g.chr11:118255624G>T	Missense Mutation	UBE4A	p.M799I	ubiquitination factor E4	45 (0.00)	38 (0.21)	0.56
12-01	Gp3	g.chr1:10161208G>T	Missense Mutation	UBE4B	p.E130D	ubiquitination factor E4	74 (0.00)	18 (0.61)	1.63
12-01	Gp3	g.chr16:4910682C>T	Missense Mutation	UBN1	p.A230V	ubinuclein 1	175 (0.00)	87 (0.16)	0.43
12-01	Gp3	g.chr16:4918879C>G	Missense Mutation	UBN1	p.Q386E	ubinuclein 1	100 (0.00)	25 (0.64)	1.71
12-01	Gp3	g.chrX:56591114C>T	Missense Mutation	UBQLN2	p.R270C	ubiquilin 2	151 (0.00)	39 (0.28)	0.47
12-01	Gp3	g.chr10:99327732C>A	Missense Mutation	UBTD1	p.D44E	ubiquitin domain contai	80 (0.00)	96 (0.24)	0.64

12-01	Gp3	g.chr12:132393747G>A	Missense Mutation	ULK1	p.V211I	unc-51 like autophagy a	23 (0.00)	34 (0.15)	0.39
12-01	Gp3	g.chr19:17750005G>A	Missense Mutation	UNC13A	p.P990S	unc-13 homolog A (C. e	43 (0.00)	23 (0.43)	1.16
12-01	Gp3	g.chr9:35375170C>A	Missense Mutation	UNC13B	p.T447K	unc-13 homolog B (C. e	296 (0.00)	33 (0.21)	0.57
12-01	Gp3	g.chr2:99227304G>T	Missense Mutation	UNC50	p.W116L	unc-50 homolog (C. ele	49 (0.00)	18 (0.33)	0.89
12-01	Gp3	g.chr16:21973827C>T	Missense Mutation	UQCRC2	p.R127W	ubiquinol-cytochrome c	32 (0.00)	51 (0.16)	0.42
12-01	Gp3	g.chrX:47106604G>A	Missense Mutation	USP11	p.V802M	ubiquitin specific peptid	66 (0.02)	33 (0.30)	0.51
12-01	Gp3	g.chr1:55591349G>A	Silent	USP24	p.L1240L	ubiquitin specific peptid	24 (0.00)	18 (0.50)	1.33
12-01	Gp3	g.chr12:109520792C>A	Missense Mutation	USP30	p.Q334K	ubiquitin specific peptid	52 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr17:49353277C>T	Silent	UTP18	p.I254I	UTP18 small subunit (S	24 (0.00)	18 (0.44)	1.19
12-01	Gp3	g.chr6:144820421G>A	Missense Mutation	UTRN	p.R1541K	utrophin	98 (0.00)	22 (0.95)	2.55
12-01	Gp3	g.chr8:100789139C>T	Missense Mutation	VPS13B	p.H2487Y	vacuolar protein sorting	48 (0.00)	39 (0.31)	0.82
12-01	Gp3	g.chr20:25059476C>A	Missense Mutation	VSX1	p.D206Y	visual system homeobo	160 (0.00)	43 (0.30)	0.81
12-01	Gp3	g.chr6:142519639C>A	Nonsense Mutation	VTA1	p.S195*	vesicle (multivesicular	80 (0.00)	30 (0.20)	0.53
12-01	Gp3	g.chr9:137006631G>A	Splice Site	WDR5		WD repeat domain 5	66 (0.00)	18 (0.39)	1.04
12-01	Gp3	g.chr2:74650021C>G	Missense Mutation	WDR54	p.R83G	WD repeat domain 54	87 (0.00)	37 (0.27)	0.72
12-01	Gp3	g.chr7:158695106G>A	Missense Mutation	WDR60	p.D393N	WD repeat domain 60	46 (0.00)	24 (0.50)	1.33
12-01	Gp3	g.chr3:14193605G>C	Intron	XPC		xeroderma pigmentosu	86 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr3:14206569C>T	Intron	XPC		xeroderma pigmentosu	138 (0.01)	15 (0.40)	1.07
12-01	Gp3	g.chr6:43483678G>A	Silent	YIPF3	p.F85F	Yip1 domain family, m	276 (0.00)	64 (0.16)	0.42
12-01	Gp3	g.chr10:27431328G>T	Missense Mutation	YME1L1	p.Q140K	YME1-like 1 ATPase	22 (0.00)	31 (0.19)	0.52
12-01	Gp3	g.chr11:57413834G>A	Missense Mutation	YPEL4	p.T77M	yippee-like 4 (Drosophi	92 (0.00)	47 (0.21)	0.57
12-01	Gp3	g.chr7:100371392T>C	RNA	ZAN		zonadhesin (gene/pseud	43 (0.00)	33 (0.15)	0.40
12-01	Gp3	g.chr22:50280049C>T	Silent	ZBED4	p.S913S	zinc finger, BED-type c	113 (0.01)	180 (0.13)	0.44
12-01	Gp3	g.chr6:109802892G>T	Missense Mutation	ZBTB24	p.A113D	zinc finger and BTB do	157 (0.00)	67 (0.39)	1.03
12-01	Gp3	g.chr1:173854900C>A	Missense Mutation	ZBTB37	p.Q384K	zinc finger and BTB do	47 (0.00)	54 (0.52)	1.38
12-01	Gp3	g.chr12:56515147A>T	Silent	ZC3H10	p.V267V	zinc finger CCCH-type	37 (0.00)	39 (0.18)	0.48
12-01	Gp3	g.chr12:56515187G>C	Missense Mutation	ZC3H10	p.V281L	zinc finger CCCH-type	23 (0.00)	31 (0.19)	0.52
12-01	Gp3	g.chr9:88954955G>T	Missense Mutation	ZCCHC6	p.Q402K	zinc finger, CCHC dom	48 (0.00)	14 (0.43)	1.14
12-01	Gp3	g.chr12:122958295C>A	Missense Mutation	ZCCHC8	p.D387Y	zinc finger, CCHC dom	470 (0.00)	229 (0.16)	0.42
12-01	Gp3	g.chr2:207170355G>A	Missense Mutation	ZDBF2	p.C368Y	zinc finger, DBF-type c	89 (0.00)	66 (0.53)	1.41
12-01	Gp3	g.chr8:77776189T>A	Silent	ZFHX4	p.T3413T	zinc finger homeobox 4	33 (0.00)	41 (0.22)	0.59
12-01	Gp3	g.chr8:77776200C>A	Missense Mutation	ZFHX4	p.A3417D	zinc finger homeobox 4	33 (0.00)	44 (0.20)	0.55
12-01	Gp3	g.chr14:68274532G>T	Missense Mutation	ZFYVE26	p.L157I	zinc finger, FYVE dom	40 (0.00)	67 (0.25)	0.68
12-01	Gp3	g.chr8:124267313C>T	Missense Mutation	ZHX1	p.A292T	zinc fingers and homeo	98 (0.00)	54 (0.17)	0.44
12-01	Gp3	g.chr19:44680469G>A	Missense Mutation	ZNF226	p.V352I	zinc finger protein 226	130 (0.00)	29 (0.55)	1.47

12-01	Gp3	g.chr19:35434428C>T	Silent	ZNF30	p.I187I	zinc finger protein 30	17 (0.00)	11 (0.73)	1.94
12-01	Gp3	g.chr8:28206746C>G	Splice Site	ZNF395		zinc finger protein 395	41 (0.00)	36 (0.17)	0.44
12-01	Gp3	g.chr19:58437880G>T	Missense Mutation	ZNF418	p.Q557K	zinc finger protein 418	64 (0.00)	22 (0.36)	0.97
12-01	Gp3	g.chr18:74091529G>A	Silent	ZNF516	p.S847S	zinc finger protein 516	44 (0.00)	96 (0.11)	0.40
12-01	Gp3	g.chr10:97916509C>A	RNA	ZNF518A		zinc finger protein 518A	58 (0.00)	27 (0.26)	0.69
12-01	Gp3	g.chr19:58371227C>A	Missense Mutation	ZNF587	p.Q483K	zinc finger protein 587	46 (0.00)	28 (0.32)	0.86
12-01	Gp3	g.chr19:53210019G>T	Missense Mutation	ZNF611	p.H97N	zinc finger protein 611	119 (0.00)	18 (0.50)	1.33
12-01	Gp3	g.chr19:52619239C>T	Missense Mutation	ZNF616	p.R393H	zinc finger protein 616	44 (0.00)	22 (0.36)	0.97
12-01	Gp3	g.chr19:53912051G>A	Missense Mutation	ZNF765	p.E415K	zinc finger protein 765	31 (0.00)	12 (0.50)	1.33
12-01	Gp3	g.chr7:88956751C>A	Missense Mutation	ZNF804B	p.L115I	zinc finger protein 804B	25 (0.00)	24 (0.38)	1.00
12-01	Gp3	g.chr19:53056527G>A	Missense Mutation	ZNF808	p.D120N	zinc finger protein 808	78 (0.00)	26 (0.23)	0.62
12-01	Gp3	g.chr14:102793059C>A	Missense Mutation	ZNF839	p.D342E	zinc finger protein 839	60 (0.00)	31 (0.16)	0.43
12-01	Gp3	g.chr19:56755757G>T	Nonsense Mutation	ZSCAN5D	p.E113*		68 (0.00)	31 (0.16)	0.43
12-01	Gp4	g.chr12:9221390G>A	Missense Mutation	A2M	p.P1438S	alpha-2-macroglobulin	20 (0.00)	23 (0.91)	0.93
12-01	Gp4	g.chr5:178201004G>A	RNA	AACSP1		acetoacetyl-CoA synthe	17 (0.00)	26 (0.58)	1.54
12-01	Gp4	g.chr2:69784027C>A	Missense Mutation	AAK1	p.D83Y	AP2 associated kinase 1	147 (0.00)	47 (0.98)	2.61
12-01	Gp4	g.chr6:44272032C>G	Missense Mutation	AARS2	p.K631N	alanyl-tRNA synthetase	64 (0.00)	97 (0.43)	1.15
12-01	Gp4	g.chr4:57220237C>A	Missense Mutation	AASDH	p.G451C	aminoadipate-semialdeh	24 (0.00)	33 (0.24)	0.65
12-01	Gp4	g.chr7:48318070C>A	Missense Mutation	ABCA13	p.L2427M	ATP-binding cassette, s	30 (0.00)	31 (0.26)	0.69
12-01	Gp4	g.chr9:139907033G>T	Silent	ABCA2	p.A1697A	ATP-binding cassette, s	23 (0.00)	50 (0.32)	0.85
12-01	Gp4	g.chr9:139911480A>T	Missense Mutation	ABCA2	p.S884T	ATP-binding cassette, s	55 (0.00)	80 (0.23)	0.60
12-01	Gp4	g.chr1:94508432C>A	Silent	ABCA4	p.S1071S	ATP-binding cassette, s	224 (0.00)	46 (0.22)	0.58
12-01	Gp4	g.chr17:66979880C>T	Missense Mutation	ABCA9	p.R1537K	ATP-binding cassette, s	184 (0.00)	34 (0.38)	1.02
12-01	Gp4	g.chr1:229683272G>T	Missense Mutation	ABCB10	p.Q299K	ATP-binding cassette, s	109 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr7:150730774G>A	Missense Mutation	ABCB8	p.A60T	ATP-binding cassette, s	40 (0.00)	244 (0.39)	1.04
12-01	Gp4	g.chr12:123430600G>T	Missense Mutation	ABCB9	p.A408D	ATP-binding cassette, s	22 (0.00)	84 (0.20)	0.54
12-01	Gp4	g.chr16:16215929G>T	Missense Mutation	ABCC1	p.S1163I	ATP-binding cassette, s	36 (0.00)	32 (0.28)	0.75
12-01	Gp4	g.chr6:43414029A>G	Missense Mutation	ABCC10	p.N1130S	ATP-binding cassette, s	22 (0.00)	72 (0.32)	0.85
12-01	Gp4	g.chr16:48226479C>T	Silent	ABCC11	p.K886K	ATP-binding cassette, s	114 (0.00)	187 (0.59)	1.57
12-01	Gp4	g.chr10:101557005G>T	Nonsense Mutation	ABCC2	p.E262*	ATP-binding cassette, s	51 (0.00)	14 (0.93)	2.48
12-01	Gp4	g.chr16:16272669G>A	Silent	ABCC6	p.L801L	ATP-binding cassette, s	139 (0.00)	238 (0.19)	0.52
12-01	Gp4	g.chr11:17428451T>A	Missense Mutation	ABCC8	p.N1049I	ATP-binding cassette, s	102 (0.00)	27 (0.56)	1.48
12-01	Gp4	g.chr11:17449907G>T	Silent	ABCC8	p.R657R	ATP-binding cassette, s	47 (0.00)	66 (0.27)	0.73
12-01	Gp4	g.chr12:40001460G>A	Nonsense Mutation	ABCD2	p.R393*	ATP-binding cassette, s	49 (0.00)	30 (0.97)	2.58
12-01	Gp4	g.chr11:119020722G>T	Missense Mutation	ABCG4	p.G16V	ATP-binding cassette, s	17 (0.00)	76 (0.54)	1.44

12-01	Gp4	g.chr20:25282925G>A	Missense Mutation	ABHD12	p.P363S	abhydrolase domain con	146 (0.00)	263 (0.25)	0.67
12-01	Gp4	g.chr15:89738637G>T	Nonsense Mutation	ABHD2	p.E421*	abhydrolase domain con	49 (0.00)	55 (0.27)	0.73
12-01	Gp4	g.chr10:116307527C>T	Missense Mutation	ABLIM1	p.G228S	actin binding LIM prote	52 (0.00)	112 (0.29)	0.79
12-01	Gp4	g.chr22:19112662T>A	lincRNA	AC004471.10			56 (0.00)	43 (0.33)	0.87
12-01	Gp4	g.chr19:29213655T>G	lincRNA	AC005307.3			33 (0.00)	37 (0.97)	2.59
12-01	Gp4	g.chr2:51820153C>A	lincRNA	AC007682.1			25 (0.00)	30 (0.27)	0.71
12-01	Gp4	g.chr2:231013625G>A	RNA	AC009950.2			19 (0.00)	25 (0.64)	1.71
12-01	Gp4	g.chr2:96906551C>A	RNA	AC012307.3			83 (0.00)	54 (0.48)	1.28
12-01	Gp4	g.chr2:62373709T>C	RNA	AC018462.2			406 (0.00)	70 (0.39)	1.03
12-01	Gp4	g.chr2:130989055G>T	RNA	AC018804.7			44 (0.00)	50 (0.16)	0.43
12-01	Gp4	g.chr2:199578710C>A	lincRNA	AC019330.1			39 (0.00)	22 (0.32)	0.85
12-01	Gp4	g.chr2:219219090G>T	RNA	AC021016.8			59 (0.00)	42 (0.45)	1.21
12-01	Gp4	g.chr8:61850709C>A	lincRNA	AC022182.1			63 (0.02)	38 (0.24)	0.63
12-01	Gp4	g.chr8:61850759G>A	lincRNA	AC022182.1			66 (0.00)	45 (0.96)	2.55
12-01	Gp4	g.chr3:6042052C>A	lincRNA	AC027119.1			22 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr2:11242862C>A	lincRNA	AC062028.1			32 (0.00)	21 (0.52)	1.40
12-01	Gp4	g.chr2:178062912G>T	RNA	AC079305.8			32 (0.00)	127 (0.15)	0.40
12-01	Gp4	g.chr2:132277807C>G	RNA	AC093838.4			16 (0.00)	39 (0.26)	0.68
12-01	Gp4	g.chr2:221143741G>C	lincRNA	AC114765.1			17 (0.00)	18 (0.39)	1.04
12-01	Gp4	g.chr15:62535599C>A	RNA	AC126323.1			265 (0.00)	291 (0.20)	0.53
12-01	Gp4	g.chr5:179078974C>A	Missense Mutation	AC136604.1	p.P153T		140 (0.00)	54 (0.46)	1.23
12-01	Gp4	g.chr3:38168087T>C	Missense Mutation	ACAA1	p.Q244R	acetyl-CoA acyltransfer	154 (0.00)	238 (0.56)	1.50
12-01	Gp4	g.chr12:109616974G>T	Missense Mutation	ACACB	p.A507S	acetyl-CoA carboxylase	75 (0.00)	48 (0.98)	2.61
12-01	Gp4	g.chr17:7124374C>A	Silent	ACADVL	p.T158T	acyl-CoA dehydrogenas	38 (0.00)	24 (0.33)	0.89
12-01	Gp4	g.chr15:89402437G>A	Silent	ACAN	p.S2207S	aggrecan	255 (0.00)	163 (0.20)	0.54
12-01	Gp4	g.chr17:61561219G>T	Silent	ACE	p.V532V	angiotensin I converting	41 (0.00)	38 (0.32)	0.84
12-01	Gp4	g.chr17:40024143G>A	Nonsense Mutation	ACLY	p.Q1076*	ATP citrate lyase	200 (0.00)	91 (0.56)	0.47
12-01	Gp4	g.chr1:6378555C>A	Nonsense Mutation	ACOT7	p.G247*	acyl-CoA thioesterase 7	84 (0.00)	44 (0.32)	0.85
12-01	Gp4	g.chr20:44483925C>A	Missense Mutation	ACOT8	p.R45S	acyl-CoA thioesterase 8	27 (0.00)	58 (0.45)	1.20
12-01	Gp4	g.chr20:33470628C>A	Nonsense Mutation	ACSS2	p.Y70*	acyl-CoA synthetase sh	44 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr17:79478032C>T	Missense Mutation	ACTG1	p.G302D	actin, gamma 1	70 (0.00)	245 (0.18)	0.49
12-01	Gp4	g.chr19:8808632G>T	Silent	ACTL9	p.A140A	actin-like 9	28 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr14:69341826G>C	Missense Mutation	ACTN1	p.A848G	actinin, alpha 1	44 (0.00)	35 (0.46)	1.22
12-01	Gp4	g.chr14:69352243C>T	Silent	ACTN1	p.S428S	actinin, alpha 1	67 (0.00)	70 (0.14)	0.38
12-01	Gp4	g.chr1:236902650C>G	Missense Mutation	ACTN2	p.P309A	actinin, alpha 2	141 (0.00)	321 (0.17)	0.45

12-01	Gp4	g.chr1:2938533G>T	Nonsense Mutation	ACTRT2	p.E95*	actin-related protein T2	88 (0.00)	110 (0.18)	0.48
12-01	Gp4	g.chr5:156915309C>G	Silent	ADAM19	p.R838R	ADAM metallopeptidas	58 (0.00)	20 (0.85)	2.27
12-01	Gp4	g.chr7:87772441G>T	Splice Site	ADAM22		ADAM metallopeptidas	31 (0.00)	28 (0.79)	2.10
12-01	Gp4	g.chr8:38928919C>A	Missense Mutation	ADAM9	p.T565N	ADAM metallopeptidas	44 (0.00)	78 (0.94)	2.50
12-01	Gp4	g.chr19:8661458C>T	Missense Mutation	ADAMTS10	p.C351Y	ADAM metallopeptidas	67 (0.00)	198 (0.15)	0.40
12-01	Gp4	g.chr10:72462200C>A	Missense Mutation	ADAMTS14	p.P219T	ADAM metallopeptidas	96 (0.00)	219 (0.16)	0.41
12-01	Gp4	g.chr11:130331409A>G	Missense Mutation	ADAMTS15	p.D328G	ADAM metallopeptidas	144 (0.01)	143 (0.50)	1.34
12-01	Gp4	g.chr11:130341189G>T	Silent	ADAMTS15	p.L663L	ADAM metallopeptidas	30 (0.00)	78 (0.28)	0.75
12-01	Gp4	g.chr11:130286860C>T	Silent	ADAMTS8	p.A357A	ADAM metallopeptidas	183 (0.00)	154 (0.16)	0.42
12-01	Gp4	g.chr9:18574196C>T	Missense Mutation	ADAMTSL1	p.P136S	ADAMTS-like 1	48 (0.00)	13 (0.77)	2.05
12-01	Gp4	g.chr12:49165675C>A	Missense Mutation	ADCY6	p.A957S	adenylate cyclase 6	135 (0.00)	34 (0.21)	0.55
12-01	Gp4	g.chr7:31142904C>T	Missense Mutation	ADCYAP1R1	p.T395I	adenylate cyclase activa	188 (0.00)	276 (0.43)	1.16
12-01	Gp4	g.chr4:2928373C>A	Missense Mutation	ADD1	p.D653E	adducin 1 (alpha)	56 (0.00)	71 (0.49)	1.31
12-01	Gp4	g.chr6:147045455G>T	Silent	ADGB	p.L743L	androglobin	115 (0.00)	259 (0.94)	2.51
12-01	Gp4	g.chr11:67049350G>T	Missense Mutation	ADRBK1	p.R295L	adrenergic, beta, recepto	45 (0.00)	250 (0.36)	0.96
12-01	Gp4	g.chr20:60878835G>T	Missense Mutation	ADRM1	p.D71Y	adhesion regulating mol	17 (0.00)	11 (0.45)	1.21
12-01	Gp4	g.chr22:40759001G>A	Missense Mutation	ADSL	p.E343K	adenylosuccinate lyase	142 (0.00)	123 (0.36)	0.95
12-01	Gp4	g.chr5:132234024A>T	Missense Mutation	AFF4	p.S429R	AF4/FMR2 family, men	93 (0.00)	41 (0.37)	0.98
12-01	Gp4	g.chr4:178354463G>T	Missense Mutation	AGA	p.P282Q	aspartylglucosaminidas	15 (0.00)	13 (0.46)	1.23
12-01	Gp4	g.chr10:88764074T>C	RNA	AGAP11		ankyrin repeat and GTP	94 (0.00)	14 (0.43)	1.14
12-01	Gp4	g.chr7:150840862G>T	Silent	AGAP3	p.L525L	ArfGAP with GTPase d	30 (0.00)	45 (0.31)	0.83
12-01	Gp4	g.chr10:46322410G>A	Silent	AGAP4	p.I315I	ArfGAP with GTPase d	242 (0.00)	49 (0.22)	0.60
12-01	Gp4	g.chr5:76326750A>G	Silent	AGGF1	p.T53T	angiogenic factor with	149 (0.00)	222 (0.27)	0.72
12-01	Gp4	g.chr11:62300932C>A	Silent	AHNAK	p.G319G	AHNAK nucleoprotein	110 (0.00)	131 (0.17)	0.45
12-01	Gp4	g.chr3:186338667C>A	Missense Mutation	AHSG	p.A352D	alpha-2-HS-glycoprotei	24 (0.00)	71 (0.61)	1.62
12-01	Gp4	g.chr22:21333968G>T	Silent	AIFM3	p.L549L	apoptosis-inducing facto	40 (0.00)	36 (0.33)	0.89
12-01	Gp4	g.chr17:55189869G>T	Missense Mutation	AKAP1	p.D665Y	A kinase (PRKA) ancho	86 (0.00)	63 (0.14)	0.38
12-01	Gp4	g.chr17:55191902C>A	Missense Mutation	AKAP1	p.T729K	A kinase (PRKA) ancho	91 (0.00)	129 (0.15)	0.39
12-01	Gp4	g.chr7:91724467C>T	Missense Mutation	AKAP9	p.R3237W	A kinase (PRKA) ancho	47 (0.00)	148 (0.20)	0.52
12-01	Gp4	g.chr7:91737817C>A	Silent	AKAP9	p.G3852G	A kinase (PRKA) ancho	102 (0.00)	33 (0.58)	1.54
12-01	Gp4	g.chr9:117138998C>A	Missense Mutation	AKNA	p.K363N	AT-hook transcription f	38 (0.00)	80 (0.84)	2.23
12-01	Gp4	g.chr7:134136346C>A	Missense Mutation	AKR1B1	p.V76F	aldo-keto reductase fam	248 (0.00)	214 (0.29)	0.76
12-01	Gp4	g.chr19:40741185G>A	Silent	AKT2	p.D416D	v-akt murine thymoma	126 (0.00)	84 (0.18)	0.48
12-01	Gp4	g.chr17:18325821G>T	RNA	AL353997.3			28 (0.00)	26 (0.65)	1.74
12-01	Gp4	g.chr19:49967903T>A	Nonsense Mutation	ALDH16A1	p.Y484*	aldehyde dehydrogenas	90 (0.00)	49 (0.59)	1.58

12-01	Gp4	g.chr3:125822689C>A	Splice Site	ALDH1L1	p.G895V	aldehyde dehydrogenase	15 (0.00)	34 (0.56)	1.49
12-01	Gp4	g.chr3:125850275C>A	Missense Mutation	ALDH1L1	p.M535I	aldehyde dehydrogenase	187 (0.00)	122 (0.24)	0.63
12-01	Gp4	g.chr11:111749334C>A	Missense Mutation	ALG9	p.G92V	ALG9, alpha-1,2-manno	99 (0.00)	18 (0.67)	1.78
12-01	Gp4	g.chr2:29445428C>T	Silent	ALK	p.V1135V	anaplastic lymphoma re	43 (0.00)	18 (0.50)	1.33
12-01	Gp4	g.chr19:36501505C>A	Missense Mutation	ALKBH6	p.E139D	alkB, alkylation repair h	80 (0.00)	75 (0.65)	1.74
12-01	Gp4	g.chr2:73784349G>A	Missense Mutation	ALMS1	p.A3360T	Alstrom syndrome 1	81 (0.00)	223 (0.17)	0.45
12-01	Gp4	g.chr2:73874844C>A	RNA	ALMS1P		Alstrom syndrome 1 pse	20 (0.00)	40 (0.30)	0.80
12-01	Gp4	g.chr10:45920564T>A	Nonsense Mutation	ALOX5	p.L273*	arachidonate 5-lipoxyge	35 (0.00)	77 (0.38)	1.00
12-01	Gp4	g.chr1:21889647C>A	Silent	ALPL	p.A114A	alkaline phosphatase, liv	31 (0.00)	13 (0.69)	1.85
12-01	Gp4	g.chr3:46713040G>A	Missense Mutation	ALS2CL	p.R907C	ALS2 C-terminal like	82 (0.00)	121 (0.28)	0.75
12-01	Gp4	g.chr2:131519739G>T	Nonsense Mutation	AMER3	p.E32*	APC membrane recruitm	20 (0.00)	23 (0.43)	1.16
12-01	Gp4	g.chr12:53819007G>C	Silent	AMHR2	p.L161L	anti-Mullerian hormone	36 (0.00)	133 (0.30)	0.80
12-01	Gp4	g.chr3:49756598C>A	Missense Mutation	AMIGO3	p.G101C	adhesion molecule with	69 (0.00)	74 (0.15)	0.40
12-01	Gp4	g.chr11:94533444G>A	Missense Mutation	AMOTL1	p.R363Q	angiomotin like 1	123 (0.00)	34 (0.38)	1.02
12-01	Gp4	g.chr11:10527309G>A	Missense Mutation	AMPD3	p.D737N	adenosine monophospha	23 (0.00)	119 (0.47)	1.25
12-01	Gp4	g.chr11:10527352G>A	Missense Mutation	AMPD3	p.R751Q	adenosine monophospha	22 (0.00)	115 (0.23)	0.63
12-01	Gp4	g.chr3:49457154A>T	Missense Mutation	AMT	p.L180Q	aminomethyltransferase	175 (0.00)	96 (0.29)	0.78
12-01	Gp4	g.chr8:41581104G>A	Silent	ANK1	p.I253I	ankyrin 1, erythrocytic	30 (0.00)	38 (0.39)	1.05
12-01	Gp4	g.chr2:190561043G>A	Silent	ANKAR	p.L552L	ankyrin and armadillo re	46 (0.00)	144 (0.73)	1.94
12-01	Gp4	g.chr15:65235729T>A	Missense Mutation	ANKDD1A	p.I339K	ankyrin repeat and death	401 (0.00)	25 (0.36)	0.96
12-01	Gp4	g.chr17:4071182C>A	Missense Mutation	ANKFY1	p.C1135F	ankyrin repeat and FYV	85 (0.01)	11 (0.73)	1.94
12-01	Gp4	g.chr17:4080518A>G	Missense Mutation	ANKFY1	p.V894A	ankyrin repeat and FYV	93 (0.00)	59 (0.17)	0.45
12-01	Gp4	g.chr12:133324805T>C	Silent	ANKLE2	p.G320G	ankyrin repeat and LEM	58 (0.00)	133 (0.23)	0.60
12-01	Gp4	g.chr18:14179469G>T	RNA	ANKRD20A5P		ankyrin repeat domain 2	24 (0.00)	125 (0.17)	0.45
12-01	Gp4	g.chr19:4202924G>A	Splice Site	ANKRD24		ankyrin repeat domain 2	22 (0.00)	46 (0.22)	0.58
12-01	Gp4	g.chr19:33089209T>A	Missense Mutation	ANKRD27	p.N999Y	ankyrin repeat domain 2	308 (0.00)	41 (0.27)	0.72
12-01	Gp4	g.chr19:33130319G>T	Silent	ANKRD27	p.T353T	ankyrin repeat domain 2	67 (0.00)	76 (0.20)	0.53
12-01	Gp4	g.chr21:14415158C>G	RNA	ANKRD30BP2		ankyrin repeat domain 3	89 (0.00)	29 (0.62)	1.66
12-01	Gp4	g.chr12:56646000G>T	Nonsense Mutation	ANKRD52	p.C490*	ankyrin repeat domain 5	155 (0.00)	48 (0.54)	1.44
12-01	Gp4	g.chr12:56647182G>A	Silent	ANKRD52	p.S330S	ankyrin repeat domain 5	120 (0.00)	144 (0.30)	0.80
12-01	Gp4	g.chr11:69933999C>G	Missense Mutation	ANO1	p.Q84E	anoctamin 1, calcium ac	40 (0.00)	158 (0.25)	0.68
12-01	Gp4	g.chr11:69957812G>T	Splice Site	ANO1		anoctamin 1, calcium ac	247 (0.00)	70 (0.47)	1.26
12-01	Gp4	g.chr12:5744406C>A	Silent	ANO2	p.V577V	anoctamin 2, calcium ac	121 (0.00)	67 (0.46)	1.23
12-01	Gp4	g.chr15:69079785G>A	Silent	ANP32A	p.N98N	acidic (leucine-rich) nuc	208 (0.00)	97 (0.90)	2.39
12-01	Gp4	g.chr15:90335765C>T	Missense Mutation	ANPEP	p.A760T	alanyl (membrane) amin	179 (0.01)	285 (0.29)	0.78

12-01	Gp4	g.chr5:43040013C>G	Missense Mutation	ANXA2R	p.E46Q	annexin A2 receptor	55 (0.00)	31 (0.94)	2.49
12-01	Gp4	g.chr7:150554808G>C	Missense Mutation	AOC1	p.C417S	amine oxidase, copper c	38 (0.00)	17 (0.35)	0.94
12-01	Gp4	g.chr11:64856220G>T	Missense Mutation	AP003068.6	p.F59L		143 (0.00)	63 (0.33)	0.89
12-01	Gp4	g.chr19:16317194T>A	Missense Mutation	AP1M1	p.F81Y	adaptor-related protein c	135 (0.00)	163 (0.43)	1.15
12-01	Gp4	g.chr11:984682C>G	Missense Mutation	AP2A2	p.T248S	adaptor-related protein c	362 (0.00)	185 (0.72)	1.92
12-01	Gp4	g.chr19:2112914G>T	Missense Mutation	AP3D1	p.A911D	adaptor-related protein c	54 (0.00)	119 (0.51)	1.37
12-01	Gp4	g.chr19:2120959C>A	Silent	AP3D1	p.A461A	adaptor-related protein c	51 (0.00)	79 (0.91)	2.43
12-01	Gp4	g.chr15:29397714T>C	Missense Mutation	APBA2	p.Y553H	amyloid beta (A4) precu	68 (0.00)	114 (0.20)	0.64
12-01	Gp4	g.chr19:1456374G>A	Missense Mutation	APC2	p.D263N	adenomatosis polyposis	21 (0.00)	48 (0.23)	0.61
12-01	Gp4	g.chr3:49713857C>T	Missense Mutation	APEH	p.S218F	acylaminoacyl-peptide	91 (0.00)	56 (0.14)	0.38
12-01	Gp4	g.chr20:24959413T>C	Silent	APMAP	p.A106A	adipocyte plasma memb	66 (0.00)	39 (0.21)	0.55
12-01	Gp4	g.chr6:41029071C>T	Missense Mutation	APOBEC2	p.R46W	apolipoprotein B mRNA	103 (0.00)	175 (0.22)	0.58
12-01	Gp4	g.chr22:39482504G>T	Missense Mutation	APOBEC3G	p.G319V	apolipoprotein B mRNA	58 (0.00)	17 (0.88)	2.35
12-01	Gp4	g.chr12:12940585G>T	Nonstop Mutation	APOLD1	p.*249L	apolipoprotein L domai	126 (0.00)	213 (0.38)	0.39
12-01	Gp4	g.chr5:141051745C>G	Missense Mutation	ARAP3	p.Q425H	ArfGAP with RhoGAP	337 (0.00)	379 (0.25)	0.66
12-01	Gp4	g.chr1:228285044C>A	Splice Site	ARF1	p.G50G	ADP-ribosylation factor	72 (0.00)	45 (0.24)	0.65
12-01	Gp4	g.chr22:43231398G>A	Silent	ARFGAP3	p.A121A	ADP-ribosylation factor	167 (0.00)	139 (0.17)	0.46
12-01	Gp4	g.chr11:46703728G>C	Missense Mutation	ARHGAP1	p.L108V	Rho GTPase activating	133 (0.00)	171 (0.18)	0.48
12-01	Gp4	g.chr1:161018853G>T	Missense Mutation	ARHGAP30	p.A653E	Rho GTPase activating	79 (0.00)	94 (0.27)	0.71
12-01	Gp4	g.chrX:153175669G>C	Silent	ARHGAP4	p.P744P	Rho GTPase activating	18 (0.00)	14 (0.50)	0.83
12-01	Gp4	g.chr22:45210574C>A	Missense Mutation	ARHGAP8	p.L108I	Rho GTPase activating	57 (0.00)	122 (0.62)	1.66
12-01	Gp4	g.chr17:79827055C>T	Missense Mutation	ARHGDIA	p.V137I	Rho GDP dissociation i	45 (0.00)	20 (0.35)	0.93
12-01	Gp4	g.chr19:42406125C>A	Missense Mutation	ARHGEF1	p.F467L	Rho guanine nucleotide	52 (0.00)	126 (0.18)	0.49
12-01	Gp4	g.chr19:42407906G>T	Missense Mutation	ARHGEF1	p.Q644H	Rho guanine nucleotide	112 (0.00)	61 (0.16)	0.44
12-01	Gp4	g.chr8:1808165C>A	Missense Mutation	ARHGEF10	p.P99Q	Rho guanine nucleotide	190 (0.00)	391 (0.16)	0.52
12-01	Gp4	g.chr8:1877554G>T	Missense Mutation	ARHGEF10	p.Q1008H	Rho guanine nucleotide	170 (0.01)	95 (0.77)	2.52
12-01	Gp4	g.chr1:16525650C>A	Missense Mutation	ARHGEF19	p.S749I	Rho guanine nucleotide	47 (0.00)	97 (0.14)	0.38
12-01	Gp4	g.chr2:39162918C>T	Nonsense Mutation	ARHGEF33	p.Q170*	Rho guanine nucleotide	16 (0.00)	73 (0.97)	2.59
12-01	Gp4	g.chr5:149011716C>A	Silent	ARHGEF37	p.R664R	Rho guanine nucleotide	80 (0.00)	47 (0.15)	0.40
12-01	Gp4	g.chr1:27105715G>A	Missense Mutation	ARID1A	p.E1559K	AT rich interactive dom	148 (0.00)	63 (0.81)	2.16
12-01	Gp4	g.chr12:46244802C>T	Missense Mutation	ARID2	p.P966S	AT rich interactive dom	93 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr19:968490C>G	Silent	ARID3A	p.G527G	AT rich interactive dom	47 (0.00)	109 (0.35)	0.93
12-01	Gp4	g.chr15:74883559G>T	Missense Mutation	ARID3B	p.A317S	AT rich interactive dom	154 (0.01)	115 (0.19)	0.51
12-01	Gp4	g.chr2:97215175C>A	Missense Mutation	ARID5A	p.P12T	AT rich interactive dom	49 (0.00)	41 (0.27)	0.72
12-01	Gp4	g.chr10:63851460C>T	Silent	ARID5B	p.V746V	AT rich interactive dom	107 (0.00)	13 (0.92)	2.46

12-01	Gp4	g.chr10:63852555G>T	Silent	ARID5B	p.V1111V	AT rich interactive dom	167 (0.00)	89 (0.47)	1.26
12-01	Gp4	g.chr17:73124810G>A	Silent	ARMC7	p.R70R	armadillo repeat contain	33 (0.00)	135 (0.50)	1.32
12-01	Gp4	g.chr15:80869239G>T	Missense Mutation	ARNT2	p.A516S	aryl-hydrocarbon recept	116 (0.00)	109 (0.23)	0.61
12-01	Gp4	g.chr7:98951695G>C	Missense Mutation	ARPC1A	p.V222L	actin related protein 2/3	69 (0.00)	36 (0.47)	1.26
12-01	Gp4	g.chr17:4619285C>G	Silent	ARRB2	p.G24G	arrestin, beta 2	112 (0.01)	10 (0.90)	2.40
12-01	Gp4	g.chr1:23782630G>T	Missense Mutation	ASAP3	p.H63N	ArfGAP with SH3 dom	124 (0.00)	40 (0.65)	1.73
12-01	Gp4	g.chr17:7077136G>T	Missense Mutation	ASGR1	p.Q240K	asialoglycoprotein recep	26 (0.00)	99 (0.29)	0.78
12-01	Gp4	g.chr17:32483084G>T	Missense Mutation	ASIC2	p.F156L	acid-sensing (proton-ga	236 (0.00)	78 (0.49)	1.30
12-01	Gp4	g.chr17:32483090C>T	Silent	ASIC2	p.L154L	acid-sensing (proton-ga	228 (0.00)	77 (0.16)	0.42
12-01	Gp4	g.chr7:65553845C>G	Missense Mutation	ASL	p.A257G	argininosuccinate lyase	76 (0.00)	138 (0.15)	0.41
12-01	Gp4	g.chr2:70188309G>T	Missense Mutation	ASPRV1	p.A171D	aspartic peptidase, retro	15 (0.00)	13 (0.77)	2.05
12-01	Gp4	g.chr9:133329755A>G	Missense Mutation	ASS1	p.K57E	argininosuccinate synth	71 (0.00)	30 (0.17)	0.44
12-01	Gp4	g.chr9:133355122C>A	Silent	ASS1	p.T236T	argininosuccinate synth	23 (0.00)	15 (0.40)	1.07
12-01	Gp4	g.chr2:96789893C>A	Missense Mutation	ASTL	p.G331V	astacin-like metallo-end	28 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr8:124340703C>G	Missense Mutation	ATAD2	p.E517Q	ATPase family, AAA d	79 (0.00)	28 (0.54)	1.43
12-01	Gp4	g.chr1:1469448C>A	Missense Mutation	ATAD3A	p.S586Y	ATPase family, AAA d	19 (0.00)	30 (0.27)	0.71
12-01	Gp4	g.chr17:29196592C>A	Missense Mutation	ATAD5	p.Q1179K	ATPase family, AAA d	15 (0.07)	97 (0.20)	0.52
12-01	Gp4	g.chr11:64670805C>A	Missense Mutation	ATG2A	p.L1189F	autophagy related 2A	57 (0.00)	25 (0.24)	0.64
12-01	Gp4	g.chr2:220088693G>T	Silent	ATG9A	p.R439R	autophagy related 9A	151 (0.01)	157 (0.75)	1.99
12-01	Gp4	g.chr13:25263454T>C	Missense Mutation	ATP12A	p.Y163H	ATPase, H+/K+ transpo	84 (0.00)	65 (0.23)	0.62
12-01	Gp4	g.chr3:193153437C>G	Splice Site	ATP13A4	p.W923C	ATPase type 13A4	178 (0.00)	139 (0.56)	1.50
12-01	Gp4	g.chr3:193153476G>A	Silent	ATP13A4	p.Y910Y	ATPase type 13A4	140 (0.00)	125 (0.66)	1.77
12-01	Gp4	g.chr3:10417176C>T	Missense Mutation	ATP2B2	p.V407M	ATPase, Ca++ transport	48 (0.00)	61 (0.21)	0.57
12-01	Gp4	g.chrX:152845640A>G	Missense Mutation	ATP2B3	p.N1183D	ATPase, Ca++ transport	98 (0.00)	41 (0.41)	0.69
12-01	Gp4	g.chr2:71191620C>G	Missense Mutation	ATP6V1B1	p.A399G	ATPase, H+ transportin	92 (0.00)	56 (0.43)	1.14
12-01	Gp4	g.chr2:10922459C>T	Silent	ATP6V1C2	p.V338V	ATPase, H+ transportin	141 (0.00)	364 (0.29)	0.76
12-01	Gp4	g.chr13:52544768G>A	Missense Mutation	ATP7B	p.A468V	ATPase, Cu++ transport	198 (0.00)	28 (0.96)	2.57
12-01	Gp4	g.chr13:52548229G>A	Missense Mutation	ATP7B	p.S376F	ATPase, Cu++ transport	223 (0.00)	17 (0.94)	2.51
12-01	Gp4	g.chr1:154320937A>T	Missense Mutation	ATP8B2	p.T1106S	ATPase, aminophospho	20 (0.00)	31 (0.81)	2.15
12-01	Gp4	g.chr19:1785575T>A	Missense Mutation	ATP8B3	p.M1096L	ATPase, aminophospho	104 (0.00)	47 (0.28)	0.74
12-01	Gp4	g.chr10:99439410G>T	Missense Mutation	AVPI1	p.L85M	arginine vasopressin-inc	25 (0.00)	96 (0.34)	0.92
12-01	Gp4	g.chr10:99439583G>T	Nonsense Mutation	AVPI1	p.S27*	arginine vasopressin-inc	21 (0.00)	49 (0.35)	0.93
12-01	Gp4	g.chr12:668532A>G	Missense Mutation	B4GALNT3	p.N945D	beta-1,4-N-acetyl-galac	234 (0.00)	26 (0.23)	0.62
12-01	Gp4	g.chr6:90642230C>A	Missense Mutation	BACH2	p.G808V	BTB and CNC homolog	114 (0.00)	191 (0.17)	0.46
12-01	Gp4	g.chr6:90661099G>T	Silent	BACH2	p.V242V	BTB and CNC homolog	30 (0.00)	183 (0.25)	0.66

12-01	Gp4	g.chr21:11097383C>G	RNA	BAGE2		B melanoma antigen far	50 (0.00)	29 (0.34)	0.92
12-01	Gp4	g.chr8:143561153C>A	Missense Mutation	BAI1	p.T609K	brain-specific angiogen	94 (0.00)	106 (0.27)	0.73
12-01	Gp4	g.chr1:32196611G>T	Silent	BAI2	p.A1357A	brain-specific angiogen	31 (0.00)	70 (0.39)	1.03
12-01	Gp4	g.chr1:32205552G>T	Missense Mutation	BAI2	p.S714R	brain-specific angiogen	53 (0.00)	28 (0.21)	0.57
12-01	Gp4	g.chr17:79077416A>C	Missense Mutation	BAIAP2	p.T116P	BAI1-associated protein	29 (0.03)	85 (0.14)	0.38
12-01	Gp4	g.chr5:17275950C>A	Missense Mutation	BASP1	p.P209T	brain abundant, membra	54 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr11:64756889C>T	Silent	BATF2	p.S94S	basic leucine zipper tran	28 (0.00)	95 (0.27)	0.73
12-01	Gp4	g.chr11:64756926G>T	Missense Mutation	BATF2	p.P82H	basic leucine zipper tran	21 (0.00)	88 (0.16)	0.42
12-01	Gp4	g.chr12:56995921C>G	Silent	BAZ2A	p.A1160A	bromodomain adjacent t	46 (0.00)	132 (0.50)	1.33
12-01	Gp4	g.chr7:33427732C>T	Silent	BBS9	p.T697T	Bardet-Biedl syndrome	226 (0.00)	122 (0.77)	2.05
12-01	Gp4	g.chr1:156622373C>G	Missense Mutation	BCAN	p.P544R	brevican	47 (0.00)	34 (0.15)	0.39
12-01	Gp4	g.chr2:60687850G>T	Missense Mutation	BCL11A	p.P699T	B-cell CLL/lymphoma 1	98 (0.01)	225 (0.24)	0.63
12-01	Gp4	g.chr20:30309610C>A	Missense Mutation	BCL2L1	p.G138C	BCL2-like 1	187 (0.00)	116 (0.70)	1.86
12-01	Gp4	g.chr20:30309750C>G	Missense Mutation	BCL2L1	p.R91T	BCL2-like 1	148 (0.00)	229 (0.14)	0.38
12-01	Gp4	g.chr12:122497069G>A	Silent	BCL7A	p.*211*	B-cell CLL/lymphoma 7	180 (0.00)	103 (0.37)	0.98
12-01	Gp4	g.chrX:129171491T>A	Missense Mutation	BCORL1	p.S1485R	BCL6 corepressor-like 1	61 (0.00)	14 (0.71)	1.19
12-01	Gp4	g.chrX:129173127G>T	Silent	BCORL1	p.A1496A	BCL6 corepressor-like 1	76 (0.00)	19 (0.58)	0.96
12-01	Gp4	g.chr22:23656186C>A	Nonsense Mutation	BCR	p.C1163*	breakpoint cluster regio	137 (0.00)	57 (0.16)	0.42
12-01	Gp4	g.chr11:205463C>G	Missense Mutation	BET1L	p.D59H	Bet1 golgi vesicular me	33 (0.00)	53 (0.45)	1.21
12-01	Gp4	g.chr11:205632C>A	Missense Mutation	BET1L	p.Q49H	Bet1 golgi vesicular me	38 (0.00)	82 (0.18)	0.49
12-01	Gp4	g.chr3:5024952G>T	Nonsense Mutation	BHLHE40	p.G272*	basic helix-loop-helix fa	151 (0.01)	32 (0.19)	0.50
12-01	Gp4	g.chr12:32481146C>T	Missense Mutation	BICD1	p.T586I	bicaudal D homolog 1 (	113 (0.00)	95 (0.41)	1.09
12-01	Gp4	g.chr2:127828158C>T	Missense Mutation	BIN1	p.G96S	bridging integrator 1	186 (0.00)	243 (0.28)	0.75
12-01	Gp4	g.chr15:91261007C>A	Intron	BLM		Bloom syndrome, RecQ	182 (0.00)	204 (0.49)	1.29
12-01	Gp4	g.chr15:91261310G>A	Intron	BLM		Bloom syndrome, RecQ	442 (0.00)	118 (0.75)	2.01
12-01	Gp4	g.chr15:91262142G>T	Intron	BLM		Bloom syndrome, RecQ	129 (0.00)	172 (0.16)	0.42
12-01	Gp4	g.chr15:91291974C>A	Intron	BLM		Bloom syndrome, RecQ	41 (0.00)	27 (0.19)	0.49
12-01	Gp4	g.chr15:91348301G>T	Intron	BLM		Bloom syndrome, RecQ	82 (0.00)	33 (0.58)	1.54
12-01	Gp4	g.chr15:91348397G>T	Intron	BLM		Bloom syndrome, RecQ	99 (0.00)	50 (0.36)	0.96
12-01	Gp4	g.chr15:91356923G>A	Intron	BLM		Bloom syndrome, RecQ	67 (0.00)	138 (0.56)	1.49
12-01	Gp4	g.chr7:43827622G>T	Silent	BLVRA	p.S44S	biliverdin reductase A	142 (0.00)	35 (0.74)	1.98
12-01	Gp4	g.chr8:22034109T>C	Missense Mutation	BMP1	p.F166S	bone morphogenetic pro	67 (0.00)	25 (0.84)	2.24
12-01	Gp4	g.chr3:113002368G>T	Missense Mutation	BOC	p.A848S	BOC cell adhesion asso	73 (0.00)	41 (0.80)	2.15
12-01	Gp4	g.chr4:13604192T>A	Silent	BOD1L1	p.V1444V	biorientation of chromo	57 (0.00)	61 (0.44)	1.18
12-01	Gp4	g.chr2:74372373G>A	Nonsense Mutation	BOLA3	p.Q38*	bolA family member 3	84 (0.00)	115 (0.22)	0.58

12-01	Gp4	g.chr2:198593232C>T	Missense Mutation	BOLL	p.D321N	boule-like RNA-binding	176 (0.00)	25 (0.76)	2.03
12-01	Gp4	g.chr20:31606505G>T	Missense Mutation	BPIFB2	p.L244F	BPI fold containing fam	178 (0.00)	159 (0.35)	0.94
12-01	Gp4	g.chr20:31671474C>A	Silent	BPIFB4	p.I157I	BPI fold containing fam	30 (0.00)	42 (0.19)	0.51
12-01	Gp4	g.chr13:32896748C>A	Intron	BRCA2		breast cancer 2, early on	66 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr13:32922870C>A	Intron	BRCA2		breast cancer 2, early on	66 (0.00)	33 (0.39)	1.05
12-01	Gp4	g.chr13:32935136G>A	Intron	BRCA2		breast cancer 2, early on	128 (0.00)	15 (0.73)	1.96
12-01	Gp4	g.chr22:50217789G>C	Missense Mutation	BRD1	p.I59M	bromodomain containin	159 (0.00)	171 (0.18)	0.47
12-01	Gp4	g.chr9:136899836C>G	Missense Mutation	BRD3	p.K684N	bromodomain containin	137 (0.00)	41 (0.56)	1.50
12-01	Gp4	g.chr3:9786728C>T	Missense Mutation	BRPF1	p.P979L	bromodomain and PHD	150 (0.00)	104 (0.15)	0.41
12-01	Gp4	g.chr3:9787360T>A	Missense Mutation	BRPF1	p.S1051T	bromodomain and PHD	70 (0.01)	71 (0.18)	0.49
12-01	Gp4	g.chr3:9787377C>T	Silent	BRPF1	p.R1056R	bromodomain and PHD	65 (0.00)	63 (0.14)	0.38
12-01	Gp4	g.chr11:1459572C>A	Missense Mutation	BRSK2	p.H75N	BR serine/threonine kin	62 (0.00)	46 (0.48)	1.28
12-01	Gp4	g.chr21:40627701G>A	Missense Mutation	BRWD1	p.R709C	bromodomain and WD	79 (0.00)	49 (0.49)	1.31
12-01	Gp4	g.chr21:40667701C>A	Missense Mutation	BRWD1	p.A193S	bromodomain and WD	17 (0.00)	40 (0.38)	1.00
12-01	Gp4	g.chr3:49690477C>A	Nonsense Mutation	BSN	p.S1163*	bassoon presynaptic cyt	58 (0.00)	291 (0.14)	0.38
12-01	Gp4	g.chr10:124050595C>A	Splice Site	BTBD16	p.A159D	BTB (POZ) domain con	63 (0.02)	20 (0.70)	1.87
12-01	Gp4	g.chr14:93708908G>A	Missense Mutation	BTBD7	p.S1037L	BTB (POZ) domain con	242 (0.00)	22 (0.95)	2.55
12-01	Gp4	g.chr6:38142769G>T	Missense Mutation	BTBD9	p.H581N	BTB (POZ) domain con	105 (0.00)	51 (0.29)	0.78
12-01	Gp4	g.chr6:38142873G>C	Missense Mutation	BTBD9	p.T546S	BTB (POZ) domain con	51 (0.00)	19 (0.63)	1.68
12-01	Gp4	g.chr1:228699464G>C	RNA	BTNL10		butyrophilin-like 10	18 (0.00)	88 (0.25)	0.67
12-01	Gp4	g.chr10:124914611C>T	Silent	BUB3	p.L60L	BUB3 mitotic checkpoi	44 (0.00)	15 (0.47)	1.24
12-01	Gp4	g.chr17:56389008G>T	Missense Mutation	BZRAP1	p.P942Q	benzodiazepine receptor	65 (0.00)	42 (0.45)	1.21
12-01	Gp4	g.chr10:50533734G>T	Silent	C10orf71	p.L1048L	chromosome 10 open re	21 (0.00)	24 (0.25)	0.67
12-01	Gp4	g.chr10:124697365A>T	Missense Mutation	C10orf88	p.V320E	chromosome 10 open re	36 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr12:110511356G>T	De novo Start InFran	C12orf76		chromosome 12 open re	52 (0.00)	119 (0.50)	1.34
12-01	Gp4	g.chr14:105461055C>T	Missense Mutation	C14orf79	p.R313C	chromosome 14 open re	144 (0.00)	121 (0.69)	1.83
12-01	Gp4	g.chr14:23465206C>G	Missense Mutation	C14orf93	p.R290T	chromosome 14 open re	72 (0.00)	200 (0.69)	1.83
12-01	Gp4	g.chr15:41062991C>A	Missense Mutation	C15orf62	p.P100T	chromosome 15 open re	25 (0.00)	47 (0.36)	0.96
12-01	Gp4	g.chr16:31505033G>T	Silent	C16orf58	p.V283V	chromosome 16 open re	135 (0.00)	216 (0.22)	0.59
12-01	Gp4	g.chr16:31505071G>T	Missense Mutation	C16orf58	p.H271N	chromosome 16 open re	105 (0.00)	243 (0.38)	1.01
12-01	Gp4	g.chr16:2510921G>T	Missense Mutation	C16orf59	p.D101Y	chromosome 16 open re	98 (0.01)	232 (0.47)	1.24
12-01	Gp4	g.chr16:4787830C>A	Silent	C16orf71	p.I53I	chromosome 16 open re	103 (0.00)	90 (0.79)	2.10
12-01	Gp4	g.chr16:30770738C>T	Silent	C16orf93	p.L194L	chromosome 16 open re	25 (0.00)	42 (0.83)	2.22
12-01	Gp4	g.chr17:79512837G>A	Nonsense Mutation	C17orf70	p.R749*	chromosome 17 open re	17 (0.00)	22 (0.55)	1.45
12-01	Gp4	g.chr17:72588212C>T	Silent	C17orf77	p.S9S	chromosome 17 open re	135 (0.00)	75 (0.29)	0.78

12-01	Gp4	g.chr17:3746432C>T	Missense Mutation	C17orf85	p.R66K	chromosome 17 open re	92 (0.00)	24 (0.96)	2.56
12-01	Gp4	g.chr19:58485557G>A	Nonsense Mutation	C19orf18	p.Q46*	chromosome 19 open re	94 (0.00)	102 (0.52)	1.39
12-01	Gp4	g.chr1:34663074C>A	Missense Mutation	C1orf94	p.A190D	chromosome 1 open rea	99 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr1:22974231G>A	Silent	C1QC	p.Q231Q	complement component	162 (0.00)	66 (0.92)	2.46
12-01	Gp4	g.chr22:19431809C>T	Silent	C22orf39	p.L99L	chromosome 22 open re	65 (0.00)	84 (0.19)	0.51
12-01	Gp4	g.chr21:43338314G>A	Missense Mutation	C2CD2	p.A207V	C2 calcium-dependent d	107 (0.00)	38 (0.34)	0.91
12-01	Gp4	g.chr11:118986739C>G	Silent	C2CD2L	p.S386S	C2CD2-like	41 (0.00)	34 (0.15)	0.39
12-01	Gp4	g.chr2:29295108A>G	Missense Mutation	C2orf71	p.F674L	chromosome 2 open rea	165 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr19:6718162G>C	Missense Mutation	C3	p.I149M	complement component	35 (0.00)	87 (0.41)	1.10
12-01	Gp4	g.chr3:128292344C>A	Missense Mutation	C3orf27	p.D77Y	chromosome 3 open rea	33 (0.00)	44 (0.73)	1.94
12-01	Gp4	g.chr3:118865484T>C	Silent	C3orf30	p.L150L	chromosome 3 open rea	147 (0.00)	106 (0.27)	0.73
12-01	Gp4	g.chr3:126915564G>T	Missense Mutation	C3orf56	p.Q12H	chromosome 3 open rea	64 (0.00)	159 (0.16)	0.44
12-01	Gp4	g.chr3:126915757G>T	Missense Mutation	C3orf56	p.A77S	chromosome 3 open rea	156 (0.00)	122 (0.36)	0.96
12-01	Gp4	g.chr3:126915858C>G	Missense Mutation	C3orf56	p.S110R	chromosome 3 open rea	280 (0.00)	286 (0.18)	0.48
12-01	Gp4	g.chr5:102611623G>A	Start Codon SNP	C5orf30	p.M1I	chromosome 5 open rea	29 (0.00)	55 (0.22)	0.58
12-01	Gp4	g.chr7:40899964C>T	Silent	C7orf10	p.P408P		166 (0.00)	123 (0.70)	1.86
12-01	Gp4	g.chr7:99754797A>G	Silent	C7orf43	p.D255D	chromosome 7 open rea	132 (0.00)	78 (0.38)	1.03
12-01	Gp4	g.chr7:99754803G>A	Silent	C7orf43	p.I253I	chromosome 7 open rea	129 (0.00)	75 (0.51)	1.35
12-01	Gp4	g.chr8:96281283G>T	Silent	C8orf37	p.A45A	chromosome 8 open rea	145 (0.00)	61 (0.79)	2.10
12-01	Gp4	g.chr9:139379340G>C	Missense Mutation	C9orf163	p.R147T	chromosome 9 open rea	55 (0.00)	72 (0.57)	1.52
12-01	Gp4	g.chr9:135763691T>C	Missense Mutation	C9orf9	p.V121A	chromosome 9 open rea	51 (0.00)	35 (0.77)	2.06
12-01	Gp4	g.chr17:58236715C>A	Missense Mutation	CA4	p.P290Q	carbonic anhydrase IV	33 (0.00)	100 (0.26)	0.69
12-01	Gp4	g.chr9:136328678G>T	Splice Site	CACFD1		calcium channel flower	43 (0.00)	20 (0.30)	0.80
12-01	Gp4	g.chr9:140919450G>T	Missense Mutation	CACNA1B	p.G1038C	calcium channel, voltag	111 (0.00)	39 (0.23)	0.62
12-01	Gp4	g.chr12:2690912C>A	Silent	CACNA1C	p.T684T	calcium channel, voltag	147 (0.00)	15 (0.40)	1.07
12-01	Gp4	g.chr1:181767706C>A	Silent	CACNA1E	p.R2183R	calcium channel, voltag	20 (0.00)	21 (0.38)	1.02
12-01	Gp4	g.chr1:201009822A>G	Silent	CACNA1S	p.C1718C	calcium channel, voltag	75 (0.01)	112 (0.21)	0.57
12-01	Gp4	g.chr1:201043694T>A	Missense Mutation	CACNA1S	p.E668V	calcium channel, voltag	95 (0.00)	35 (0.17)	0.46
12-01	Gp4	g.chr17:65050143C>A	Missense Mutation	CACNG1	p.N87K	calcium channel, voltag	66 (0.00)	24 (0.25)	0.67
12-01	Gp4	g.chr17:64881354C>G	Missense Mutation	CACNG5	p.C275W	calcium channel, voltag	83 (0.00)	92 (0.71)	1.88
12-01	Gp4	g.chr3:85081495G>A	Intron	CADM2		cell adhesion molecule	114 (0.01)	85 (0.25)	0.66
12-01	Gp4	g.chr3:85265256G>A	Intron	CADM2		cell adhesion molecule	37 (0.00)	21 (0.90)	2.41
12-01	Gp4	g.chr3:85340415C>A	Intron	CADM2		cell adhesion molecule	34 (0.00)	13 (0.54)	1.44
12-01	Gp4	g.chr3:85397224T>C	Intron	CADM2		cell adhesion molecule	157 (0.00)	126 (0.46)	1.23
12-01	Gp4	g.chr3:85468339C>A	Intron	CADM2		cell adhesion molecule	141 (0.00)	132 (0.39)	1.03

12-01	Gp4	g.chr3:85470335T>A	Intron	CADM2		cell adhesion molecule	131 (0.00)	68 (0.49)	1.29
12-01	Gp4	g.chr3:85470343T>A	Intron	CADM2		cell adhesion molecule	127 (0.00)	62 (0.47)	1.25
12-01	Gp4	g.chr3:85553123T>C	Intron	CADM2		cell adhesion molecule	92 (0.01)	24 (0.54)	1.44
12-01	Gp4	g.chr3:85652795A>T	Intron	CADM2		cell adhesion molecule	72 (0.00)	25 (0.32)	0.85
12-01	Gp4	g.chr3:85839843G>T	Intron	CADM2		cell adhesion molecule	134 (0.00)	76 (0.75)	2.00
12-01	Gp4	g.chr3:85910038G>T	Intron	CADM2		cell adhesion molecule	27 (0.00)	92 (0.52)	1.39
12-01	Gp4	g.chr3:85939302A>T	Intron	CADM2		cell adhesion molecule	23 (0.00)	22 (0.41)	1.09
12-01	Gp4	g.chr3:86017180G>T	Intron	CADM2		cell adhesion molecule	113 (0.00)	21 (0.33)	0.89
12-01	Gp4	g.chr3:86073299T>A	Intron	CADM2		cell adhesion molecule	22 (0.00)	114 (0.35)	0.94
12-01	Gp4	g.chr7:128399029G>T	Nonsense Mutation	CALU	p.E174*	calumenin	300 (0.00)	44 (0.30)	0.79
12-01	Gp4	g.chr10:75583809C>A	Missense Mutation	CAMK2G	p.D342Y	calcium/calmodulin-dep	112 (0.00)	93 (0.23)	0.60
12-01	Gp4	g.chr9:138709867C>T	Silent	CAMSAP1	p.T1409T	calmodulin regulated sp	121 (0.00)	125 (0.40)	1.07
12-01	Gp4	g.chr1:7723585G>C	Missense Mutation	CAMTA1	p.R326S	calmodulin binding tran	140 (0.00)	105 (0.42)	1.12
12-01	Gp4	g.chr2:241533998C>A	Missense Mutation	CAPN10	p.S290Y	calpain 10	216 (0.00)	249 (0.16)	0.43
12-01	Gp4	g.chr2:203818807C>T	Silent	CARF	p.Y67Y	calcium responsive tran	41 (0.02)	138 (0.99)	2.63
12-01	Gp4	g.chr13:111287909G>T	Missense Mutation	CARKD	p.R249L	carbohydrate kinase do	47 (0.00)	138 (0.20)	0.54
12-01	Gp4	g.chr19:11024585C>T	Silent	CARM1	p.R234R	coactivator-associated a	90 (0.00)	181 (0.19)	0.52
12-01	Gp4	g.chr16:2240150C>A	Silent	CASKIN1	p.A56A	CASK interacting protei	23 (0.00)	27 (0.30)	0.79
12-01	Gp4	g.chr20:55012382C>T	Missense Mutation	CASS4	p.R67C	Cas scaffolding protein	93 (0.00)	348 (0.39)	1.03
12-01	Gp4	g.chr19:38853198G>A	Silent	CATSPERG	p.R780R	catsper channel auxiliar	40 (0.00)	126 (0.62)	1.65
12-01	Gp4	g.chr21:44485369C>A	Missense Mutation	CBS	p.S227I	cystathionine-beta-synt	106 (0.00)	25 (0.20)	0.53
12-01	Gp4	g.chr17:77809072G>A	Silent	CBX4	p.N123N	chromobox homolog 4	42 (0.02)	150 (0.45)	1.19
12-01	Gp4	g.chr1:52824943G>C	Missense Mutation	CC2D1B	p.P369A	coiled-coil and C2 dom	33 (0.00)	182 (0.18)	0.48
12-01	Gp4	g.chr1:52828337C>G	Missense Mutation	CC2D1B	p.E51Q	coiled-coil and C2 dom	148 (0.00)	172 (0.22)	0.57
12-01	Gp4	g.chr8:22473642G>T	Nonsense Mutation	CCAR2	p.E576*	cell cycle and apoptosis	202 (0.00)	377 (0.36)	0.96
12-01	Gp4	g.chr9:131597777G>A	Missense Mutation	CCBL1	p.T342I	cysteine conjugate-beta	84 (0.00)	140 (0.36)	0.95
12-01	Gp4	g.chr19:15133778C>A	Nonsense Mutation	CCDC105	p.C449*	coiled-coil domain cont	20 (0.00)	76 (0.92)	2.46
12-01	Gp4	g.chr4:186380382T>C	Silent	CCDC110	p.L453L	coiled-coil domain cont	18 (0.00)	20 (0.30)	0.80
12-01	Gp4	g.chr5:205810G>A	Nonsense Mutation	CCDC127	p.Q129*	coiled-coil domain cont	149 (0.00)	120 (0.79)	2.11
12-01	Gp4	g.chr5:206008T>C	Missense Mutation	CCDC127	p.T63A	coiled-coil domain cont	52 (0.00)	23 (0.22)	0.58
12-01	Gp4	g.chr3:42754685G>T	Silent	CCDC13	p.A614A	coiled-coil domain cont	88 (0.00)	56 (0.39)	1.05
12-01	Gp4	g.chr22:42221756C>T	Nonsense Mutation	CCDC134	p.R207*	coiled-coil domain cont	87 (0.00)	72 (0.18)	0.48
12-01	Gp4	g.chr7:128457886G>A	Nonsense Mutation	CCDC136	p.W507*	coiled-coil domain cont	311 (0.00)	15 (0.73)	1.96
12-01	Gp4	g.chr2:109405307G>A	Splice Site	CCDC138		coiled-coil domain cont	168 (0.00)	27 (0.93)	2.47
12-01	Gp4	g.chr1:3673374C>A	Missense Mutation	CCDC27	p.P211T	coiled-coil domain cont	30 (0.00)	303 (0.18)	0.49

12-01	Gp4	g.chr10:12940485C>A	Missense Mutation	CCDC3	p.K248N	coiled-coil domain cont	78 (0.00)	58 (0.67)	1.79
12-01	Gp4	g.chr15:74623047G>T	Missense Mutation	CCDC33	p.K500N	coiled-coil domain cont	56 (0.00)	9 (0.67)	1.78
12-01	Gp4	g.chr17:78055545T>C	Missense Mutation	CCDC40	p.L588P	coiled-coil domain cont	62 (0.00)	15 (0.60)	1.60
12-01	Gp4	g.chr3:48474523C>A	Missense Mutation	CCDC51	p.E177D	coiled-coil domain cont	109 (0.00)	41 (0.39)	1.04
12-01	Gp4	g.chr12:49310829A>T	Missense Mutation	CCDC65	p.I183L	coiled-coil domain cont	34 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr2:130899949G>T	Missense Mutation	CCDC74B	p.P101T	coiled-coil domain cont	33 (0.00)	27 (0.67)	1.78
12-01	Gp4	g.chr3:112356993T>C	Missense Mutation	CCDC80	p.K587R	coiled-coil domain cont	69 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr3:112358193A>G	Missense Mutation	CCDC80	p.I187T	coiled-coil domain cont	181 (0.00)	164 (0.23)	0.60
12-01	Gp4	g.chr11:66359184G>T	Missense Mutation	CCDC87	p.L435I	coiled-coil domain cont	131 (0.01)	75 (0.60)	1.60
12-01	Gp4	g.chr11:66359736C>T	Missense Mutation	CCDC87	p.E251K	coiled-coil domain cont	77 (0.00)	141 (0.57)	1.53
12-01	Gp4	g.chr11:66360217C>A	Missense Mutation	CCDC87	p.E90D	coiled-coil domain cont	60 (0.00)	103 (0.19)	0.52
12-01	Gp4	g.chr11:64108922C>G	Missense Mutation	CCDC88B	p.H159Q	coiled-coil domain cont	80 (0.00)	111 (0.53)	1.42
12-01	Gp4	g.chr14:91779598G>C	Silent	CCDC88C	p.V854V	coiled-coil domain cont	136 (0.00)	218 (0.44)	1.17
12-01	Gp4	g.chr6:31118579C>T	Missense Mutation	CCHCR1	p.V342I	coiled-coil alpha-helical	263 (0.00)	623 (0.15)	0.40
12-01	Gp4	g.chr1:1322697G>T	Missense Mutation	CCNL2	p.Q493K	cyclin L2	51 (0.00)	38 (0.42)	1.12
12-01	Gp4	g.chr10:35857984C>A	Silent	CCNY	p.A304A	cyclin Y	126 (0.00)	23 (0.30)	0.81
12-01	Gp4	g.chr1:167407822C>A	Missense Mutation	CD247	p.E95D	CD247 molecule	151 (0.00)	52 (0.21)	0.56
12-01	Gp4	g.chr15:73994877A>T	Missense Mutation	CD276	p.T121S	CD276 molecule	30 (0.00)	29 (0.59)	1.56
12-01	Gp4	g.chr19:8367431G>T	Silent	CD320	p.A255A	CD320 molecule	76 (0.00)	81 (0.22)	0.59
12-01	Gp4	g.chr19:8367485C>A	Silent	CD320	p.V237V	CD320 molecule	76 (0.00)	104 (0.32)	0.85
12-01	Gp4	g.chr11:118178017C>T	Nonsense Mutation	CD3E	p.Q22*	CD3e molecule, epsilon	32 (0.00)	15 (0.87)	2.31
12-01	Gp4	g.chr17:7484696G>T	Splice Site	CD68	p.S311I	CD68 molecule	196 (0.00)	139 (0.20)	0.54
12-01	Gp4	g.chr19:14516700C>A	Silent	CD97	p.L590L	CD97 molecule	76 (0.01)	164 (0.22)	0.59
12-01	Gp4	g.chr17:45234397G>A	Missense Mutation	CDC27	p.P242S	cell division cycle 27	38 (0.00)	22 (0.64)	1.70
12-01	Gp4	g.chr8:25364876G>A	Silent	CDCA2	p.K898K	cell division cycle assoc	49 (0.00)	128 (0.20)	0.54
12-01	Gp4	g.chr10:73490328G>C	Missense Mutation	CDH23	p.V1233L	cadherin-related 23	32 (0.00)	75 (0.23)	0.60
12-01	Gp4	g.chr10:73563067G>T	Nonsense Mutation	CDH23	p.E2593*	cadherin-related 23	74 (0.00)	101 (0.38)	1.00
12-01	Gp4	g.chr10:73571307G>T	Missense Mutation	CDH23	p.A3085S	cadherin-related 23	74 (0.00)	291 (0.17)	0.45
12-01	Gp4	g.chr3:49836530C>A	Missense Mutation	CDHR4	p.Q100H	cadherin-related family	87 (0.00)	97 (0.51)	1.35
12-01	Gp4	g.chr1:1636385G>T	Missense Mutation	CDK11A	p.N462K	cyclin-dependent kinase	171 (0.00)	18 (0.33)	0.89
12-01	Gp4	g.chr17:37667845G>A	Silent	CDK12	p.E910E	cyclin-dependent kinase	34 (0.00)	17 (0.82)	2.20
12-01	Gp4	g.chr9:123171416C>T	Silent	CDK5RAP2	p.Q1531Q	CDK5 regulatory subun	55 (0.00)	56 (0.73)	1.95
12-01	Gp4	g.chr9:21970587C>A	Intron	CDKN2A		cyclin-dependent kinase	163 (0.00)	350 (0.30)	0.80
12-01	Gp4	g.chr19:43023273C>T	Missense Mutation	CEACAM1	p.R358H	carcinoembryonic antig	26 (0.00)	53 (0.36)	0.96
12-01	Gp4	g.chr19:45211335G>A	Silent	CEACAM16	p.V381V	carcinoembryonic antig	64 (0.02)	25 (0.20)	0.67

12-01	Gp4	g.chr19:45185857C>A	Missense Mutation	CEACAM19	p.H271N	carcinoembryonic antig	27 (0.00)	25 (0.20)	0.67
12-01	Gp4	g.chr22:18028306G>C	Missense Mutation	CECR2	p.G946A	cat eye syndrome chrom	136 (0.00)	23 (0.35)	0.93
12-01	Gp4	g.chr22:46782336C>A	Silent	CELSR1	p.T2234T	cadherin, EGF LAG sev	29 (0.00)	31 (0.29)	0.77
12-01	Gp4	g.chr1:109794179T>G	Missense Mutation	CELSR2	p.V493G	cadherin, EGF LAG sev	177 (0.01)	28 (0.18)	0.48
12-01	Gp4	g.chr1:109794380G>T	Missense Mutation	CELSR2	p.G560V	cadherin, EGF LAG sev	184 (0.00)	11 (0.55)	1.45
12-01	Gp4	g.chr1:109812340G>A	Silent	CELSR2	p.S2335S	cadherin, EGF LAG sev	90 (0.00)	87 (0.23)	0.61
12-01	Gp4	g.chr1:109815899C>A	Missense Mutation	CELSR2	p.A2817D	cadherin, EGF LAG sev	175 (0.00)	69 (0.16)	0.43
12-01	Gp4	g.chr3:48698833C>T	Missense Mutation	CELSR3	p.R412H	cadherin, EGF LAG sev	60 (0.00)	87 (0.16)	0.43
12-01	Gp4	g.chr1:3732008G>T	Silent	CEP104	p.G912G	centrosomal protein 104	43 (0.00)	89 (0.24)	0.63
12-01	Gp4	g.chr11:117246437G>T	Missense Mutation	CEP164	p.R416L	centrosomal protein 164	338 (0.00)	111 (0.31)	0.82
12-01	Gp4	g.chr14:105360133C>A	Silent	CEP170B	p.S1406S	centrosomal protein 170	64 (0.00)	63 (0.43)	1.14
12-01	Gp4	g.chr1:179983300G>C	Missense Mutation	CEP350	p.R571T	centrosomal protein 350	29 (0.00)	53 (0.26)	0.70
12-01	Gp4	g.chr2:65299081C>A	Missense Mutation	CEP68	p.P284Q	centrosomal protein 68k	149 (0.00)	98 (0.18)	0.49
12-01	Gp4	g.chr2:65299570C>A	Nonsense Mutation	CEP68	p.S447*	centrosomal protein 68k	70 (0.00)	167 (0.17)	0.45
12-01	Gp4	g.chr3:101484353T>A	Nonsense Mutation	CEP97	p.C793*	centrosomal protein 97k	56 (0.00)	34 (0.35)	0.94
12-01	Gp4	g.chr1:151491246G>T	Missense Mutation	CGN	p.G84V	cingulin	43 (0.00)	57 (0.28)	0.75
12-01	Gp4	g.chr22:41631235C>A	Missense Mutation	CHADL	p.A726S	chondroadherin-like	23 (0.00)	81 (0.16)	0.43
12-01	Gp4	g.chr17:7806693G>T	Missense Mutation	CHD3	p.R1259I	chromodomain helicase	52 (0.02)	174 (0.80)	2.15
12-01	Gp4	g.chr1:6175847C>A	Intron	CHD5		chromodomain helicase	154 (0.00)	64 (0.47)	1.25
12-01	Gp4	g.chr1:6186649G>T	Missense Mutation	CHD5	p.A1354D	chromodomain helicase	37 (0.00)	156 (0.14)	0.38
12-01	Gp4	g.chr1:6190747C>A	Intron	CHD5		chromodomain helicase	20 (0.00)	80 (0.21)	0.57
12-01	Gp4	g.chr1:6196982C>G	Intron	CHD5		chromodomain helicase	85 (0.00)	91 (0.19)	0.50
12-01	Gp4	g.chr1:6202910G>A	Intron	CHD5		chromodomain helicase	19 (0.00)	80 (0.94)	2.50
12-01	Gp4	g.chr1:6202938C>A	Intron	CHD5		chromodomain helicase	33 (0.00)	94 (0.34)	0.91
12-01	Gp4	g.chr1:6204081C>A	Intron	CHD5		chromodomain helicase	107 (0.00)	29 (0.28)	0.74
12-01	Gp4	g.chr1:6204837G>T	Intron	CHD5		chromodomain helicase	53 (0.00)	62 (0.82)	2.19
12-01	Gp4	g.chr1:6206859C>A	Missense Mutation	CHD5	p.V486L	chromodomain helicase	23 (0.00)	66 (0.30)	0.81
12-01	Gp4	g.chr1:6213765C>A	Intron	CHD5		chromodomain helicase	39 (0.00)	48 (0.15)	0.39
12-01	Gp4	g.chr1:6225459C>A	Intron	CHD5		chromodomain helicase	72 (0.01)	132 (0.38)	1.01
12-01	Gp4	g.chr1:6225712C>A	Intron	CHD5		chromodomain helicase	52 (0.00)	41 (0.24)	0.65
12-01	Gp4	g.chr1:6228372G>C	Intron	CHD5		chromodomain helicase	226 (0.00)	150 (0.25)	0.66
12-01	Gp4	g.chr1:6236762C>A	Intron	CHD5		chromodomain helicase	50 (0.00)	111 (0.37)	0.98
12-01	Gp4	g.chr1:6236820C>T	Intron	CHD5		chromodomain helicase	60 (0.02)	117 (0.48)	1.28
12-01	Gp4	g.chr14:21899231A>G	Missense Mutation	CHD8	p.V191A	chromodomain helicase	174 (0.00)	182 (0.60)	1.60
12-01	Gp4	g.chr2:175666458C>A	Silent	CHN1	p.R395R	chimerin 1	64 (0.00)	18 (0.72)	1.93

12-01	Gp4	g.chr16:23767003G>T	Missense Mutation	CHP2	p.R30L	calcineurin-like EF-hand	32 (0.00)	14 (0.57)	1.52
12-01	Gp4	g.chr2:220404158G>A	Nonsense Mutation	CHPF	p.R759*	chondroitin polymerizin	35 (0.00)	32 (0.31)	0.83
12-01	Gp4	g.chr3:184102977C>A	Missense Mutation	CHRD	p.P590H	chordin	139 (0.00)	177 (0.19)	0.50
12-01	Gp4	g.chr11:74415590C>A	Missense Mutation	CHRDL2	p.R231I	chordin-like 2	139 (0.00)	99 (0.26)	0.70
12-01	Gp4	g.chr1:240071404C>T	Missense Mutation	CHRM3	p.P218L	cholinergic receptor, mu	190 (0.01)	78 (0.97)	2.60
12-01	Gp4	g.chr15:78894182C>G	Missense Mutation	CHRNA3	p.D268H	cholinergic receptor, nic	66 (0.00)	72 (0.62)	1.67
12-01	Gp4	g.chr2:233409184G>A	Nonsense Mutation	CHRNG	p.W381*	cholinergic receptor, nic	67 (0.00)	177 (0.23)	0.62
12-01	Gp4	g.chr10:125805347G>A	Missense Mutation	CHST15	p.P128S	carbohydrate (N-acetylg	182 (0.00)	40 (0.15)	0.40
12-01	Gp4	g.chr16:844115G>T	Missense Mutation	CHTF18	p.A622S	CTF18, chromosome tra	96 (0.00)	83 (0.39)	1.03
12-01	Gp4	g.chr18:12264364G>A	Missense Mutation	CIDEA	p.G81D	cell death-inducing DFF	43 (0.00)	9 (0.89)	2.37
12-01	Gp4	g.chr18:12274154C>A	Missense Mutation	CIDEA	p.F131L	cell death-inducing DFF	20 (0.00)	51 (0.18)	0.47
12-01	Gp4	g.chr16:11000509G>T	Missense Mutation	CIITA	p.W387L	class II, major histocom	24 (0.00)	26 (0.50)	1.33
12-01	Gp4	g.chr15:65499141C>T	Missense Mutation	CILP	p.V135I	cartilage intermediate la	59 (0.00)	67 (0.99)	2.63
12-01	Gp4	g.chr19:1271421G>T	Missense Mutation	CIRBP	p.G102C	cold inducible RNA bin	20 (0.00)	197 (0.19)	0.51
12-01	Gp4	g.chr12:106633584C>G	Missense Mutation	CKAP4	p.D343H	cytoskeleton-associated	22 (0.00)	32 (0.25)	0.67
12-01	Gp4	g.chr11:46806088C>T	Missense Mutation	CKAP5	p.A702T	cytoskeleton associated	161 (0.00)	111 (0.84)	2.23
12-01	Gp4	g.chr19:40222116G>A	Silent	CLC	p.T111T	Charcot-Leyden crystal	78 (0.00)	23 (0.91)	2.43
12-01	Gp4	g.chr14:95670650G>T	Missense Mutation	CLMN	p.P346T	calmin (calponin-like, tr	122 (0.00)	14 (0.79)	2.10
12-01	Gp4	g.chr1:9794180C>T	Missense Mutation	CLSTN1	p.E711K	calsyntenin 1	35 (0.00)	55 (0.16)	0.44
12-01	Gp4	g.chr16:3580616G>T	Missense Mutation	CLUAP1	p.S326I	clusterin associated prot	52 (0.00)	122 (0.29)	0.77
12-01	Gp4	g.chr18:72228192G>C	Silent	CNDP1	p.V92V	carnosine dipeptidase 1	58 (0.00)	40 (0.20)	0.53
12-01	Gp4	g.chr18:72178216G>A	Missense Mutation	CNDP2	p.G209S	CNDP dipeptidase 2 (m	66 (0.00)	90 (0.33)	0.89
12-01	Gp4	g.chr1:224804942C>T	Silent	CNIH3	p.F22F	cornichon family AMPA	65 (0.00)	19 (0.68)	1.82
12-01	Gp4	g.chr2:220037524G>T	Nonsense Mutation	CNPPD1	p.C339*	cyclin Pas1/PHO80 dom	16 (0.00)	100 (0.20)	0.53
12-01	Gp4	g.chr1:24201300C>G	Missense Mutation	CNR2	p.A270P	cannabinoid receptor 2 (	28 (0.00)	33 (0.76)	2.02
12-01	Gp4	g.chr1:246811195C>A	Silent	CNST	p.S564S	consortin, connexin sort	85 (0.00)	30 (0.93)	2.49
12-01	Gp4	g.chr3:3084072T>C	Missense Mutation	CNTN4	p.L826P	contactin 4	31 (0.00)	51 (0.20)	0.52
12-01	Gp4	g.chr16:76587202T>G	Missense Mutation	CNTNAP4	p.D1158E	contactin associated pro	132 (0.00)	46 (0.37)	0.41
12-01	Gp4	g.chr7:51096038G>C	Missense Mutation	COBL	p.H919D	cordon-bleu WH2 repea	128 (0.01)	74 (0.51)	1.37
12-01	Gp4	g.chr7:51096171C>A	Missense Mutation	COBL	p.K874N	cordon-bleu WH2 repea	194 (0.00)	156 (0.17)	0.46
12-01	Gp4	g.chr7:51096182C>A	Missense Mutation	COBL	p.A871S	cordon-bleu WH2 repea	191 (0.00)	155 (0.17)	0.46
12-01	Gp4	g.chr16:70530276G>T	Missense Mutation	COG4	p.Q514K	component of oligomeri	105 (0.00)	53 (0.42)	1.11
12-01	Gp4	g.chr6:116441778A>T	Missense Mutation	COL10A1	p.S501T	collagen, type X, alpha	104 (0.00)	44 (0.16)	0.42
12-01	Gp4	g.chr1:32119206G>T	Missense Mutation	COL16A1	p.P1536T	collagen, type XVI, alph	111 (0.00)	124 (0.71)	1.89
12-01	Gp4	g.chr1:32119510G>T	Missense Mutation	COL16A1	p.Q1498K	collagen, type XVI, alph	44 (0.00)	346 (0.28)	0.74

12-01	Gp4	g.chr9:116930426C>A	Missense Mutation	COL27A1	p.F197L	collagen, type XXVII, a	117 (0.00)	16 (0.38)	1.00
12-01	Gp4	g.chr12:48369152G>T	Missense Mutation	COL2A1	p.N1278K	collagen, type II, alpha	143 (0.00)	228 (0.25)	0.68
12-01	Gp4	g.chr12:48369836G>C	Silent	COL2A1	p.V1169V	collagen, type II, alpha	60 (0.02)	28 (0.54)	1.43
12-01	Gp4	g.chr12:48379370C>A	Splice Site	COL2A1	p.G561C	collagen, type II, alpha	160 (0.00)	226 (0.31)	0.83
12-01	Gp4	g.chr19:10087958C>A	Splice Site	COL5A3	p.G1079W	collagen, type V, alpha	130 (0.00)	167 (0.72)	1.92
12-01	Gp4	g.chr3:130368301G>T	Silent	COL6A6	p.A1876A	collagen, type VI, alpha	31 (0.00)	10 (0.70)	1.87
12-01	Gp4	g.chr3:48605162G>C	Missense Mutation	COL7A1	p.A2655G	collagen, type VII, alph	104 (0.00)	281 (0.41)	1.08
12-01	Gp4	g.chr3:48619924C>A	Missense Mutation	COL7A1	p.R1529L	collagen, type VII, alph	55 (0.00)	97 (0.27)	0.71
12-01	Gp4	g.chr11:14490271G>T	Missense Mutation	COPB1	p.Q701K	coatomer protein compl	82 (0.00)	23 (0.22)	0.58
12-01	Gp4	g.chr19:19023796C>A	Silent	COPE	p.A62A	coatomer protein compl	47 (0.00)	100 (0.19)	0.51
12-01	Gp4	g.chr19:19023829C>A	Missense Mutation	COPE	p.E51D	coatomer protein compl	45 (0.00)	94 (0.22)	0.60
12-01	Gp4	g.chr6:99828181G>A	Silent	COQ3	p.T90T	coenzyme Q3 methyltra	39 (0.00)	48 (0.75)	2.00
12-01	Gp4	g.chr16:4409487G>T	Silent	CORO7	p.T748T	coronin 7	43 (0.00)	86 (0.15)	0.40
12-01	Gp4	g.chr16:4409538G>T	Silent	CORO7	p.P731P	coronin 7	29 (0.00)	22 (0.68)	1.82
12-01	Gp4	g.chr17:14095376A>T	Missense Mutation	COX10	p.N256Y	cytochrome c oxidase as	403 (0.00)	96 (0.17)	0.44
12-01	Gp4	g.chr17:14110285G>C	Missense Mutation	COX10	p.A363P	cytochrome c oxidase as	69 (0.00)	62 (0.24)	0.65
12-01	Gp4	g.chr17:13928606T>G	RNA	COX10-AS1		COX10 antisense RNA	25 (0.00)	62 (0.24)	0.65
12-01	Gp4	g.chr6:75950975G>A	Missense Mutation	COX7A2	p.R9C	cytochrome c oxidase su	55 (0.00)	31 (0.23)	0.60
12-01	Gp4	g.chr19:17025496C>A	Missense Mutation	CPAMD8	p.V1300L	C3 and PZP-like, alpha-	55 (0.00)	45 (0.24)	0.65
12-01	Gp4	g.chr19:17057993C>T	Silent	CPAMD8	p.G898G	C3 and PZP-like, alpha-	65 (0.00)	49 (0.14)	0.38
12-01	Gp4	g.chr19:17120112C>A	Splice Site	CPAMD8		C3 and PZP-like, alpha-	83 (0.00)	88 (0.65)	1.73
12-01	Gp4	g.chr6:36710075G>C	Silent	CPNE5	p.P584P	copine V	25 (0.00)	57 (0.96)	2.57
12-01	Gp4	g.chr6:36710218G>T	Missense Mutation	CPNE5	p.L537M	copine V	34 (0.00)	139 (0.60)	1.59
12-01	Gp4	g.chr16:12798877C>A	Missense Mutation	CPPED1	p.D107Y	calcineurin-like phosph	172 (0.01)	197 (0.21)	0.55
12-01	Gp4	g.chr1:1248467C>A	Missense Mutation	CPSF3L	p.G360V	cleavage and polyadeny	29 (0.00)	88 (0.33)	0.88
12-01	Gp4	g.chr22:51010451C>T	Nonsense Mutation	CPT1B	p.W520*	carnitine palmitoyltrans	95 (0.01)	157 (0.19)	0.51
12-01	Gp4	g.chr20:2777258G>T	Silent	CPXM1	p.T320T	carboxypeptidase X (M	75 (0.00)	67 (0.70)	0.57
12-01	Gp4	g.chr10:125528110C>A	Missense Mutation	CPXM2	p.V411L	carboxypeptidase X (M	89 (0.00)	43 (0.33)	0.87
12-01	Gp4	g.chr10:125528127G>A	Missense Mutation	CPXM2	p.A405V	carboxypeptidase X (M	85 (0.00)	40 (0.47)	1.27
12-01	Gp4	g.chr16:1706100C>A	Missense Mutation	CRAMP1L	p.L448M	Crm, cramped-like (Dro	20 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr9:131864256C>G	Missense Mutation	CRAT	p.W237C	carnitine O-acetyltransf	151 (0.00)	85 (0.25)	0.66
12-01	Gp4	g.chr16:3789659C>T	Silent	CREBBP	p.E1400E	CREB binding protein	46 (0.00)	12 (0.92)	2.44
12-01	Gp4	g.chr19:18707748G>T	Missense Mutation	CRLF1	p.A270D	cytokine receptor-like fa	31 (0.00)	45 (0.71)	1.90
12-01	Gp4	g.chr19:18709362G>T	Missense Mutation	CRLF1	p.H193N	cytokine receptor-like fa	35 (0.00)	281 (0.15)	0.39
12-01	Gp4	g.chr1:16950915C>A	lincRNA	CROCCP2		ciliary rootlet coiled-coi	16 (0.00)	42 (0.29)	0.76

12-01	Gp4	g.chr1:16812197C>A	RNA	CROCCP3		ciliary rootlet coiled-coi	72 (0.00)	66 (0.29)	0.77
12-01	Gp4	g.chr2:209010500G>T	Missense Mutation	CRYGB	p.P84T	crystallin, gamma B	52 (0.00)	110 (0.47)	1.26
12-01	Gp4	g.chr2:209010502G>T	Missense Mutation	CRYGB	p.P83H	crystallin, gamma B	52 (0.00)	110 (0.48)	1.28
12-01	Gp4	g.chr1:110466466T>C	Missense Mutation	CSF1	p.L408P	colony stimulating facto	146 (0.00)	54 (0.81)	2.17
12-01	Gp4	g.chr5:149457674C>G	Splice Site	CSF1R		colony stimulating facto	80 (0.00)	33 (0.39)	1.05
12-01	Gp4	g.chr8:19266192T>C	Missense Mutation	CSGALNACT	p.E414G	chondroitin sulfate N-ac	54 (0.00)	14 (0.43)	1.14
12-01	Gp4	g.chr17:61988255C>G	Missense Mutation	CSHL1	p.A14P	chorionic somatomamm	64 (0.00)	63 (0.84)	2.24
12-01	Gp4	g.chr22:38710090G>T	Missense Mutation	CSNK1E	p.L25M	casein kinase 1, epsilon	95 (0.00)	106 (0.58)	1.56
12-01	Gp4	g.chr15:75977140G>T	Missense Mutation	CSPG4	p.F1462L	chondroitin sulfate prote	48 (0.00)	62 (0.66)	1.76
12-01	Gp4	g.chr15:75980925C>T	Silent	CSPG4	p.Q827Q	chondroitin sulfate prote	88 (0.00)	20 (0.95)	2.53
12-01	Gp4	g.chr15:85741271G>A	RNA	CSPG4P12		chondroitin sulfate prote	16 (0.00)	21 (0.71)	1.90
12-01	Gp4	g.chr15:85747574C>G	RNA	CSPG4P12		chondroitin sulfate prote	25 (0.00)	22 (0.23)	0.61
12-01	Gp4	g.chr11:65780420G>C	Missense Mutation	CST6	p.E122Q	cystatin E/M	25 (0.00)	54 (0.33)	0.89
12-01	Gp4	g.chr4:1244716G>T	RNA	CTBP1-AS2		CTBP1 antisense RNA	58 (0.00)	35 (0.14)	0.38
12-01	Gp4	g.chr19:20370002A>T	RNA	CTC-260E6.6			135 (0.00)	261 (0.40)	1.06
12-01	Gp4	g.chr19:20370033A>T	RNA	CTC-260E6.6			112 (0.00)	118 (0.35)	0.93
12-01	Gp4	g.chr5:68247610G>T	lincRNA	CTC-340D7.1			32 (0.00)	34 (0.15)	0.39
12-01	Gp4	g.chr19:22790752C>A	RNA	CTC-457E21.6			61 (0.00)	105 (0.36)	0.97
12-01	Gp4	g.chr17:8135724C>A	Missense Mutation	CTC1	p.W672L	CTS telomere maintena	88 (0.00)	164 (0.34)	0.91
12-01	Gp4	g.chr5:99799661C>T	lincRNA	CTD-2001C12.1			40 (0.00)	16 (0.88)	2.33
12-01	Gp4	g.chr5:38174988G>T	lincRNA	CTD-2116N24.1			41 (0.00)	84 (0.18)	0.48
12-01	Gp4	g.chr14:65746158C>T	lincRNA	CTD-2509G16.5			33 (0.00)	16 (0.88)	2.33
12-01	Gp4	g.chr8:17947160G>T	RNA	CTD-2547L16.1			66 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr19:48267963C>A	RNA	CTD-2571L23.6			15 (0.00)	43 (0.67)	1.80
12-01	Gp4	g.chr11:66276650C>G	Missense Mutation	CTD-3074O7.	p.S8C		116 (0.00)	104 (0.17)	0.46
12-01	Gp4	g.chr19:51658645C>T	RNA	CTD-3187F8.14			102 (0.00)	39 (0.85)	2.26
12-01	Gp4	g.chr18:46163003G>T	Nonsense Mutation	CTIF	p.E67*	CBP80/20-dependent tra	43 (0.00)	50 (0.16)	0.43
12-01	Gp4	g.chr18:46287962C>A	Missense Mutation	CTIF	p.R425S	CBP80/20-dependent tra	37 (0.00)	41 (0.73)	1.95
12-01	Gp4	g.chr7:117432137G>A	Silent	CTTNBP2	p.P371P	cortactin binding protei	136 (0.01)	47 (0.83)	2.21
12-01	Gp4	g.chr17:55962703C>A	Missense Mutation	CUEDC1	p.G75C	CUE domain containing	82 (0.01)	138 (0.36)	0.97
12-01	Gp4	g.chr10:104184476C>A	Nonsense Mutation	CUEDC2	p.E50*	CUE domain containing	90 (0.00)	74 (0.18)	0.47
12-01	Gp4	g.chr10:104184891G>A	Missense Mutation	CUEDC2	p.L19F	CUE domain containing	32 (0.00)	71 (0.34)	0.90
12-01	Gp4	g.chr7:148487438G>A	Missense Mutation	CUL1	p.A571T	cullin 1	130 (0.01)	129 (0.98)	2.63
12-01	Gp4	g.chr12:111779748C>T	Missense Mutation	CUX2	p.R1184W	cut-like homeobox 2	21 (0.00)	82 (0.17)	0.46
12-01	Gp4	g.chr17:36963078G>C	Missense Mutation	CWC25	p.S281C	CWC25 spliceosome-as	101 (0.00)	25 (0.44)	1.17

12-01	Gp4	g.chr15:22928456C>T	Silent	CYFIP1	p.T111T	cytoplasmic FMR1 inte	354 (0.00)	261 (0.33)	1.03
12-01	Gp4	g.chr5:156738692G>C	Missense Mutation	CYFIP2	p.S312T	cytoplasmic FMR1 inte	121 (0.00)	10 (0.70)	1.87
12-01	Gp4	g.chr15:74631065G>T	Silent	CYP11A1	p.T269T	cytochrome P450, famil	56 (0.00)	14 (0.71)	1.90
12-01	Gp4	g.chr10:94834153G>T	Missense Mutation	CYP26A1	p.G93V	cytochrome P450, famil	50 (0.00)	41 (0.41)	1.11
12-01	Gp4	g.chr19:41405884C>A	RNA	CYP2G1P		cytochrome P450, famil	98 (0.00)	230 (0.16)	0.42
12-01	Gp4	g.chr1:47610079G>A	Missense Mutation	CYP4A22	p.E281K	cytochrome P450, famil	289 (0.00)	25 (0.84)	2.24
12-01	Gp4	g.chr1:47283664C>G	Missense Mutation	CYP4B1	p.A397G	cytochrome P450, famil	158 (0.01)	67 (0.97)	2.59
12-01	Gp4	g.chr19:15760993G>T	Splice Site	CYP4F3	p.K306N	cytochrome P450, famil	59 (0.00)	43 (0.63)	1.67
12-01	Gp4	g.chr3:42916694C>A	Missense Mutation	CYP8B1	p.E205D	cytochrome P450, famil	97 (0.00)	22 (0.55)	1.45
12-01	Gp4	g.chr9:124331135G>C	Intron	DAB2IP		DAB2 interacting protei	67 (0.00)	85 (0.14)	0.38
12-01	Gp4	g.chr9:124332874C>G	Intron	DAB2IP		DAB2 interacting protei	106 (0.00)	105 (0.21)	0.56
12-01	Gp4	g.chr9:124333628G>A	Intron	DAB2IP		DAB2 interacting protei	168 (0.00)	25 (0.88)	2.35
12-01	Gp4	g.chr9:124334762T>C	Intron	DAB2IP		DAB2 interacting protei	89 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr9:124383034C>A	Intron	DAB2IP		DAB2 interacting protei	210 (0.00)	234 (0.15)	0.41
12-01	Gp4	g.chr9:124391153A>G	Intron	DAB2IP		DAB2 interacting protei	48 (0.00)	32 (0.62)	1.67
12-01	Gp4	g.chr9:124391753G>T	Intron	DAB2IP		DAB2 interacting protei	191 (0.00)	87 (0.98)	2.61
12-01	Gp4	g.chr9:124393609C>T	Intron	DAB2IP		DAB2 interacting protei	190 (0.00)	212 (0.34)	0.91
12-01	Gp4	g.chr9:124394259C>A	Intron	DAB2IP		DAB2 interacting protei	209 (0.00)	151 (0.16)	0.42
12-01	Gp4	g.chr9:124399202G>T	Intron	DAB2IP		DAB2 interacting protei	223 (0.00)	97 (0.15)	0.41
12-01	Gp4	g.chr9:124401383C>A	Intron	DAB2IP		DAB2 interacting protei	110 (0.00)	49 (0.41)	1.09
12-01	Gp4	g.chr9:124401482G>T	Intron	DAB2IP		DAB2 interacting protei	136 (0.00)	68 (0.18)	0.47
12-01	Gp4	g.chr9:124402833C>A	Intron	DAB2IP		DAB2 interacting protei	104 (0.00)	47 (0.64)	1.70
12-01	Gp4	g.chr9:124417663C>A	Intron	DAB2IP		DAB2 interacting protei	103 (0.01)	346 (0.66)	1.75
12-01	Gp4	g.chr9:124418819C>T	Intron	DAB2IP		DAB2 interacting protei	298 (0.00)	506 (0.17)	0.44
12-01	Gp4	g.chr9:124441591A>T	Intron	DAB2IP		DAB2 interacting protei	334 (0.00)	248 (0.37)	0.98
12-01	Gp4	g.chr9:124442448G>C	Intron	DAB2IP		DAB2 interacting protei	142 (0.00)	88 (0.27)	0.73
12-01	Gp4	g.chr9:124445300C>A	Intron	DAB2IP		DAB2 interacting protei	75 (0.00)	93 (0.40)	1.06
12-01	Gp4	g.chr9:124446637C>A	Intron	DAB2IP		DAB2 interacting protei	222 (0.00)	32 (0.72)	1.92
12-01	Gp4	g.chr9:124449739C>A	Intron	DAB2IP		DAB2 interacting protei	177 (0.00)	102 (0.36)	0.97
12-01	Gp4	g.chr9:124451741C>A	Intron	DAB2IP		DAB2 interacting protei	106 (0.00)	91 (0.70)	1.88
12-01	Gp4	g.chr9:124463956G>T	Intron	DAB2IP		DAB2 interacting protei	113 (0.00)	45 (0.33)	0.89
12-01	Gp4	g.chr9:124469901G>T	Intron	DAB2IP		DAB2 interacting protei	111 (0.01)	144 (0.72)	1.93
12-01	Gp4	g.chr9:124474241G>A	Intron	DAB2IP		DAB2 interacting protei	49 (0.00)	49 (0.41)	1.09
12-01	Gp4	g.chr9:124478021C>A	Intron	DAB2IP		DAB2 interacting protei	155 (0.00)	20 (0.75)	2.00
12-01	Gp4	g.chr9:124496863C>A	Intron	DAB2IP		DAB2 interacting protei	38 (0.03)	101 (0.81)	2.17

12-01	Gp4	g.chr9:124498434C>A	Intron	DAB2IP		DAB2 interacting protei	45 (0.00)	135 (0.97)	2.59
12-01	Gp4	g.chr9:124509435G>T	Intron	DAB2IP		DAB2 interacting protei	147 (0.00)	344 (0.37)	0.99
12-01	Gp4	g.chr9:124521622C>G	Intron	DAB2IP		DAB2 interacting protei	99 (0.00)	60 (0.57)	1.51
12-01	Gp4	g.chr9:124523357C>A	Intron	DAB2IP		DAB2 interacting protei	117 (0.00)	129 (0.16)	0.43
12-01	Gp4	g.chr9:124524103C>G	Intron	DAB2IP		DAB2 interacting protei	155 (0.00)	90 (0.36)	0.95
12-01	Gp4	g.chr9:124527243G>A	Intron	DAB2IP		DAB2 interacting protei	123 (0.00)	34 (0.32)	0.86
12-01	Gp4	g.chr9:124543159G>A	Intron	DAB2IP		DAB2 interacting protei	91 (0.00)	72 (0.33)	0.89
12-01	Gp4	g.chrX:85969563C>T	Missense Mutation	DACH2	p.P315L	dachshund family transc	90 (0.00)	12 (0.83)	1.39
12-01	Gp4	g.chr3:49053390G>A	Missense Mutation	DALRD3	p.P320S	DALR anticodon bindin	151 (0.00)	39 (0.18)	0.48
12-01	Gp4	g.chr19:3963887C>A	Missense Mutation	DAPK3	p.G195V	death-associated protein	24 (0.00)	32 (0.19)	0.50
12-01	Gp4	g.chr1:173808538G>T	Missense Mutation	DARS2	p.G292W	aspartyl-tRNA syntheta	94 (0.00)	21 (0.62)	1.65
12-01	Gp4	g.chr19:1421256T>C	Splice Site	DAZAP1	p.V138A	DAZ associated protein	34 (0.00)	83 (0.34)	0.90
12-01	Gp4	g.chr7:44099706C>A	Silent	DBNL	p.L345L	drebrin-like	36 (0.00)	26 (0.50)	1.33
12-01	Gp4	g.chr11:20180804G>C	Silent	DBX1	p.P134P	developing brain homeo	40 (0.00)	176 (0.80)	2.12
12-01	Gp4	g.chrX:125685397T>C	Missense Mutation	DCAF12L1	p.R399G	DDB1 and CUL4 associ	68 (0.00)	23 (0.61)	1.01
12-01	Gp4	g.chr19:14070099C>T	Missense Mutation	DCAF15	p.R343W	DDB1 and CUL4 associ	65 (0.00)	59 (0.15)	0.41
12-01	Gp4	g.chr17:61628058G>T	Missense Mutation	DCAF7	p.R7L	DDB1 and CUL4 associ	48 (0.00)	113 (0.21)	0.57
12-01	Gp4	g.chr17:61628117C>T	Missense Mutation	DCAF7	p.R27W	DDB1 and CUL4 associ	55 (0.00)	148 (0.20)	0.52
12-01	Gp4	g.chr1:160188708G>T	Silent	DCAF8	p.G651G	DDB1 and CUL4 associ	48 (0.02)	126 (0.36)	0.95
12-01	Gp4	g.chr1:160209565C>A	Silent	DCAF8	p.L369L	DDB1 and CUL4 associ	122 (0.00)	54 (0.96)	2.57
12-01	Gp4	g.chr1:32681460G>T	Missense Mutation	DCDC2B	p.A338S	doublecortin domain co	27 (0.00)	53 (0.32)	0.86
12-01	Gp4	g.chr11:6645376C>A	Nonsense Mutation	DCHS1	p.G2511*	dachsous cadherin-relat	93 (0.00)	152 (0.29)	0.77
12-01	Gp4	g.chr11:6661560G>T	Silent	DCHS1	p.R429R	dachsous cadherin-relat	50 (0.00)	82 (0.72)	1.92
12-01	Gp4	g.chr5:112337305C>A	Nonsense Mutation	DCP2	p.S247*	decapping mRNA 2	15 (0.00)	66 (0.47)	1.25
12-01	Gp4	g.chr2:74607148C>A	Missense Mutation	DCTN1	p.R6M	dynactin 1	37 (0.00)	27 (0.30)	0.79
12-01	Gp4	g.chr11:61097485T>G	Missense Mutation	DDB1	p.Y91S	damage-specific DNA b	102 (0.00)	39 (0.62)	1.64
12-01	Gp4	g.chr17:76887376C>A	Missense Mutation	DDC8	p.G404W		60 (0.00)	33 (0.15)	0.40
12-01	Gp4	g.chr1:15957000C>A	Missense Mutation	DDI2	p.S150Y	DNA-damage inducible	74 (0.00)	40 (0.35)	0.93
12-01	Gp4	g.chr1:15957036C>A	Missense Mutation	DDI2	p.A162D	DNA-damage inducible	66 (0.00)	27 (0.89)	2.37
12-01	Gp4	g.chr10:70723164T>A	Missense Mutation	DDX21	p.I242N	DEAD (Asp-Glu-Ala-A	57 (0.00)	14 (0.86)	2.29
12-01	Gp4	g.chr12:49228187C>T	Silent	DDX23	p.G492G	DEAD (Asp-Glu-Ala-A	65 (0.00)	35 (0.51)	1.37
12-01	Gp4	g.chr17:61864461G>T	Missense Mutation	DDX42	p.G18C	DEAD (Asp-Glu-Ala-A	134 (0.01)	41 (0.15)	0.39
12-01	Gp4	g.chr19:19033189G>T	Missense Mutation	DDX49	p.D168Y	DEAD (Asp-Glu-Ala-A	23 (0.00)	17 (0.65)	1.73
12-01	Gp4	g.chr12:132624673G>T	Missense Mutation	DDX51	p.A582D	DEAD (Asp-Glu-Ala-A	32 (0.00)	69 (0.20)	0.54
12-01	Gp4	g.chr9:32526140G>T	Missense Mutation	DDX58	p.L9M	DEAD (Asp-Glu-Ala-A	55 (0.00)	137 (0.29)	0.78

12-01	Gp4	g.chr4:169340505G>A	Missense Mutation	DDX60L	p.A853V	DEAD (Asp-Glu-Ala-A	26 (0.00)	18 (0.89)	2.37
12-01	Gp4	g.chr15:65960405C>G	Missense Mutation	DENND4A	p.R1571T	DENN/MADD domain	188 (0.00)	33 (0.79)	2.10
12-01	Gp4	g.chr22:50756412G>T	Silent	DENND6B	p.R99R	DENN/MADD domain	32 (0.00)	39 (0.46)	1.23
12-01	Gp4	g.chr15:89070907A>T	Silent	DET1	p.R398R	de-etiolated homolog 1 (	42 (0.02)	183 (0.36)	0.95
12-01	Gp4	g.chr9:117266780G>A	Missense Mutation	DFNB31	p.S101F	deafness, autosomal rec	21 (0.00)	46 (0.28)	0.75
12-01	Gp4	g.chr22:19127227G>T	Missense Mutation	DGCR14	p.L196I	DiGeorge syndrome crit	85 (0.00)	136 (0.41)	1.10
12-01	Gp4	g.chr22:20074004G>A	Missense Mutation	DGCR8	p.G173D	DGCR8 microprocessor	240 (0.00)	263 (0.17)	0.47
12-01	Gp4	g.chr2:234371289G>T	Splice Site	DGKD	p.G1032W	diacylglycerol kinase, d	208 (0.00)	70 (0.23)	0.61
12-01	Gp4	g.chr11:46398625G>T	Missense Mutation	DGKZ	p.E923D	diacylglycerol kinase, ze	52 (0.00)	25 (0.28)	0.75
12-01	Gp4	g.chr11:71149955G>C	Silent	DHCR7	p.T267T	7-dehydrocholesterol re	35 (0.00)	41 (0.24)	0.65
12-01	Gp4	g.chr12:49488123C>A	Missense Mutation	DHH	p.G58V	desert hedgehog	74 (0.00)	59 (0.34)	0.90
12-01	Gp4	g.chr19:47858373G>C	Silent	DHX34	p.L261L	DEAH (Asp-Glu-Ala-H	111 (0.00)	59 (0.63)	1.67
12-01	Gp4	g.chr12:125451714G>T	Missense Mutation	DHX37	p.R274S	DEAH (Asp-Glu-Ala-H	87 (0.00)	72 (0.81)	2.15
12-01	Gp4	g.chr14:95560281C>A	Missense Mutation	DICER1	p.D1770Y	dicer 1, ribonuclease typ	57 (0.00)	80 (0.69)	1.83
12-01	Gp4	g.chr1:210010208C>A	Silent	DIEXF	p.P238P	digestive organ expansi	59 (0.00)	54 (0.59)	1.58
12-01	Gp4	g.chr12:51127926A>G	Silent	DIP2B	p.S1330S	DIP2 disco-interacting p	47 (0.00)	199 (0.42)	1.11
12-01	Gp4	g.chr1:68512639C>T	Silent	DIRAS3	p.L114L	DIRAS family, GTP-bin	265 (0.00)	340 (0.35)	0.93
12-01	Gp4	g.chr1:231829605T>C	Missense Mutation	DISC1	p.F34S	disrupted in schizophrer	151 (0.00)	16 (0.38)	1.00
12-01	Gp4	g.chr11:111844816G>T	Missense Mutation	DIXDC1	p.G128V	DIX domain containing	79 (0.00)	260 (0.72)	1.93
12-01	Gp4	g.chr10:54075346G>A	Intron	DKK1		dickkopf WNT signalin	397 (0.00)	86 (0.30)	0.81
12-01	Gp4	g.chr8:42231674T>A	Missense Mutation	DKK4	p.T207S	dickkopf WNT signalin	47 (0.00)	125 (0.34)	0.92
12-01	Gp4	g.chr3:38163602C>A	Silent	DLEC1	p.V1687V	deleted in lung and esop	136 (0.00)	223 (0.16)	0.42
12-01	Gp4	g.chr8:1581043C>A	Silent	DLGAP2	p.V467V	discs, large (Drosophila	30 (0.00)	47 (0.17)	0.56
12-01	Gp4	g.chr8:1581180C>A	Missense Mutation	DLGAP2	p.S513Y	discs, large (Drosophila	133 (0.00)	98 (0.18)	0.60
12-01	Gp4	g.chr6:170592127C>A	Missense Mutation	DLL1	p.Q705H	delta-like 1 (Drosophila	80 (0.00)	24 (0.21)	0.56
12-01	Gp4	g.chr6:170595358C>G	Missense Mutation	DLL1	p.Q233H	delta-like 1 (Drosophila	237 (0.00)	276 (0.25)	0.67
12-01	Gp4	g.chr7:96651665C>A	Missense Mutation	DLX5	p.E124D	distal-less homeobox 5	52 (0.00)	45 (0.60)	1.60
12-01	Gp4	g.chr7:96639306C>T	Missense Mutation	DLX6	p.H277Y	distal-less homeobox 6	87 (0.00)	17 (0.35)	0.94
12-01	Gp4	g.chr10:124390489G>A	Missense Mutation	DMBT1	p.R1884K	deleted in malignant bra	198 (0.00)	102 (0.27)	0.73
12-01	Gp4	g.chr10:124399854A>G	Missense Mutation	DMBT1	p.Q2285R	deleted in malignant bra	288 (0.00)	53 (0.45)	1.21
12-01	Gp4	g.chr19:42351930C>A	Silent	DMRTC2	p.T117T	DMRT-like family C2	28 (0.00)	65 (0.15)	0.41
12-01	Gp4	g.chr3:52403955G>T	Nonsense Mutation	DNAH1	p.E2020*	dynein, axonemal, heav	210 (0.00)	289 (0.49)	1.31
12-01	Gp4	g.chr12:124272404G>T	Missense Mutation	DNAH10	p.R431M	dynein, axonemal, heav	74 (0.00)	60 (0.18)	0.49
12-01	Gp4	g.chr7:21678616C>A	Missense Mutation	DNAH11	p.P1626H	dynein, axonemal, heav	50 (0.02)	259 (0.64)	1.70
12-01	Gp4	g.chr17:76455273G>A	Missense Mutation	DNAH17	p.P3219L	dynein, axonemal, heav	131 (0.00)	74 (0.32)	0.86

12-01	Gp4	g.chr17:76481803G>A	Missense Mutation	DNAH17	p.R2433C	dynein, axonemal, heav	104 (0.00)	141 (0.18)	0.49
12-01	Gp4	g.chr17:76490741C>A	Missense Mutation	DNAH17	p.M2063I	dynein, axonemal, heav	97 (0.00)	30 (0.90)	2.40
12-01	Gp4	g.chr17:76547654G>T	Missense Mutation	DNAH17	p.A785E	dynein, axonemal, heav	176 (0.00)	152 (0.43)	1.16
12-01	Gp4	g.chr17:76557910G>A	Silent	DNAH17	p.N574N	dynein, axonemal, heav	148 (0.00)	49 (0.82)	2.18
12-01	Gp4	g.chr17:11671874G>T	Missense Mutation	DNAH9	p.E2425D	dynein, axonemal, heav	86 (0.00)	32 (0.16)	0.42
12-01	Gp4	g.chr19:14627332G>A	Silent	DNAJB1	p.I246I	DnaJ (Hsp40) homolog,	98 (0.00)	13 (0.54)	1.44
12-01	Gp4	g.chr12:49742670C>G	Silent	DNAJC22	p.L5L	DnaJ (Hsp40) homolog,	111 (0.00)	16 (0.56)	1.50
12-01	Gp4	g.chr12:49743023C>A	Missense Mutation	DNAJC22	p.A123D	DnaJ (Hsp40) homolog,	141 (0.00)	157 (0.31)	0.83
12-01	Gp4	g.chr11:6588321T>C	Missense Mutation	DNHD1	p.V3861A	dynein heavy chain dom	298 (0.00)	133 (0.16)	0.42
12-01	Gp4	g.chr11:6593059T>C	Missense Mutation	DNHD1	p.L4702P	dynein heavy chain dom	123 (0.00)	66 (0.24)	0.65
12-01	Gp4	g.chr11:6593193G>T	Missense Mutation	DNHD1	p.V4747L	dynein heavy chain dom	531 (0.00)	210 (0.34)	0.90
12-01	Gp4	g.chr9:130985072A>T	Splice Site	DNM1	p.M377L	dynamin 1	21 (0.00)	51 (0.31)	0.84
12-01	Gp4	g.chr12:32895669C>T	Missense Mutation	DNM1L	p.A677V	dynamin 1-like	75 (0.00)	220 (0.19)	0.51
12-01	Gp4	g.chr15:100340393T>G	RNA	DNM1P46		DNM1 pseudogene 46	47 (0.02)	16 (0.38)	1.00
12-01	Gp4	g.chr15:100340405C>G	RNA	DNM1P46		DNM1 pseudogene 46	49 (0.02)	17 (0.29)	0.78
12-01	Gp4	g.chr15:84957391T>C	RNA	DNM1P51		DNM1 pseudogene 51	82 (0.00)	22 (0.23)	0.61
12-01	Gp4	g.chr19:10940965G>T	Silent	DNM2	p.V814V	dynamin 2	25 (0.00)	40 (0.42)	1.13
12-01	Gp4	g.chr19:10248595G>T	Silent	DNMT1	p.I1386I	DNA (cytosine-5-)-metl	36 (0.00)	62 (0.23)	0.60
12-01	Gp4	g.chr19:10257071T>G	Silent	DNMT1	p.R934R	DNA (cytosine-5-)-metl	69 (0.01)	123 (0.26)	0.69
12-01	Gp4	g.chr19:10291528C>T	Missense Mutation	DNMT1	p.E51K	DNA (cytosine-5-)-metl	52 (0.00)	51 (0.27)	0.73
12-01	Gp4	g.chr21:45666412C>G	Missense Mutation	DNMT3L	p.L344F	DNA (cytosine-5-)-metl	19 (0.00)	47 (0.66)	1.76
12-01	Gp4	g.chr7:111368610G>T	Missense Mutation	DOCK4	p.A1874D	dedicator of cytokinesis	212 (0.00)	50 (0.38)	1.01
12-01	Gp4	g.chr19:11344034G>T	Missense Mutation	DOCK6	p.P855T	dedicator of cytokinesis	54 (0.00)	43 (0.56)	1.49
12-01	Gp4	g.chr17:1936940A>T	Missense Mutation	DPH1	p.Q73L	diphthamide biosynthesi	140 (0.00)	75 (0.15)	0.39
12-01	Gp4	g.chr1:44436343T>C	Missense Mutation	DPH2	p.S75P	DPH2 homolog (S. cere	177 (0.00)	80 (0.20)	0.53
12-01	Gp4	g.chr15:36026969G>T	lincRNA	DPH6-AS1		DPH6 antisense RNA 1	38 (0.03)	22 (0.41)	1.09
12-01	Gp4	g.chr9:140468736C>A	Silent	DPH7	p.V188V	diphthamide biosynthesi	301 (0.00)	230 (0.16)	0.43
12-01	Gp4	g.chr7:154461117A>G	Missense Mutation	DPP6	p.Q243R	dipeptidyl-peptidase 6	123 (0.00)	22 (0.82)	2.18
12-01	Gp4	g.chr12:64061882C>T	Missense Mutation	DPY19L2	p.E98K	dpy-19-like 2 (C. elegan	79 (0.00)	100 (0.17)	0.45
12-01	Gp4	g.chr10:134015485G>A	Silent	DPYSL4	p.A382A	dihydropyrimidinase-lik	32 (0.00)	41 (0.41)	1.11
12-01	Gp4	g.chr4:9784709C>G	Silent	DRD5	p.S352S	dopamine receptor D5	118 (0.00)	128 (0.57)	1.52
12-01	Gp4	g.chr11:117387231G>C	Silent	DSCAML1	p.L638L	Down syndrome cell adl	52 (0.00)	96 (0.27)	0.72
12-01	Gp4	g.chr21:38610870G>A	Missense Mutation	DSCR3	p.P81L	Down syndrome critical	38 (0.00)	123 (0.48)	1.28
12-01	Gp4	g.chr6:15533617T>A	Missense Mutation	DTNBP1	p.D174V	dystrobrevin binding pr	191 (0.00)	190 (0.73)	1.95
12-01	Gp4	g.chr7:76132886C>A	Missense Mutation	DTX2	p.S511R	deltex 2, E3 ubiquitin li	89 (0.00)	63 (0.19)	0.51

12-01	Gp4	g.chr15:45436406G>A	Silent	DUOX1	p.L703L	dual oxidase 1	130 (0.00)	182 (0.19)	0.50
12-01	Gp4	g.chr15:45454021G>A	Silent	DUOX1	p.G1314G	dual oxidase 1	62 (0.00)	188 (0.25)	0.67
12-01	Gp4	g.chr15:45398386G>T	Silent	DUOX2	p.L695L	dual oxidase 2	53 (0.00)	39 (0.49)	1.30
12-01	Gp4	g.chr10:76797597C>A	Silent	DUPD1	p.L220L	dual specificity phospha	27 (0.00)	33 (0.18)	0.48
12-01	Gp4	g.chr19:5786764C>T	Silent	DUS3L	p.L494L	dihydrouridine synthase	36 (0.00)	103 (0.41)	1.09
12-01	Gp4	g.chr17:7132758G>A	Silent	DVL2	p.S252S	dishevelled segment pol	118 (0.00)	224 (0.36)	0.95
12-01	Gp4	g.chr14:102467555T>C	Missense Mutation	DYNC1H1	p.L1420P	dynein, cytoplasmic 1, h	338 (0.00)	125 (0.51)	1.37
12-01	Gp4	g.chr14:102486280A>G	Silent	DYNC1H1	p.E2798E	dynein, cytoplasmic 1, h	265 (0.00)	257 (0.15)	0.39
12-01	Gp4	g.chr14:102516850G>A	Missense Mutation	DYNC1H1	p.D4631N	dynein, cytoplasmic 1, h	148 (0.00)	231 (0.20)	0.54
12-01	Gp4	g.chr2:172549359G>A	Missense Mutation	DYNC1I2	p.E61K	dynein, cytoplasmic 1, i	20 (0.00)	108 (0.54)	1.43
12-01	Gp4	g.chr2:71791251C>A	Missense Mutation	DYSF	p.Q825K	dysferlin	94 (0.00)	114 (0.27)	0.73
12-01	Gp4	g.chr1:21584052C>A	Missense Mutation	ECE1	p.R265I	endothelin converting en	41 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr16:67917488C>A	Missense Mutation	EDC4	p.D1289E	enhancer of mRNA deca	282 (0.00)	217 (0.26)	0.70
12-01	Gp4	g.chr16:67917594C>A	Missense Mutation	EDC4	p.L1325M	enhancer of mRNA deca	217 (0.00)	144 (0.82)	2.19
12-01	Gp4	g.chr9:139758280G>A	Missense Mutation	EDF1	p.S41F	endothelial differentiatio	111 (0.00)	56 (0.62)	1.67
12-01	Gp4	g.chr5:137803020C>A	Silent	EGR1	p.A294A	early growth response 1	277 (0.00)	209 (0.34)	0.92
12-01	Gp4	g.chr10:64573250T>A	Missense Mutation	EGR2	p.D383V	early growth response 2	232 (0.00)	304 (0.34)	0.89
12-01	Gp4	g.chr9:140669589A>G	Missense Mutation	EHMT1	p.K559R	euchromatic histone-lys	36 (0.00)	63 (0.56)	1.48
12-01	Gp4	g.chr2:27592369C>T	Silent	EIF2B4	p.K41K	eukaryotic translation in	199 (0.00)	182 (0.15)	0.41
12-01	Gp4	g.chr10:120803576G>A	Missense Mutation	EIF3A	p.P913S	eukaryotic translation in	99 (0.00)	65 (0.68)	1.81
12-01	Gp4	g.chr7:2414236G>A	Silent	EIF3B	p.L628L	eukaryotic translation in	164 (0.00)	103 (0.23)	0.62
12-01	Gp4	g.chr19:39127547C>A	Missense Mutation	EIF3K	p.A128D	eukaryotic translation in	92 (0.00)	60 (0.20)	0.53
12-01	Gp4	g.chr5:176072377G>T	Splice Site	EIF4E1B		eukaryotic translation in	33 (0.00)	11 (0.82)	2.18
12-01	Gp4	g.chr3:184039377T>C	Silent	EIF4G1	p.V248V	eukaryotic translation in	68 (0.00)	81 (0.41)	1.09
12-01	Gp4	g.chr16:67236557G>T	Missense Mutation	ELMO3	p.A512S	engulfment and cell mot	48 (0.00)	38 (0.16)	0.42
12-01	Gp4	g.chr7:73457333C>A	Silent	ELN	p.V115V	elastin	94 (0.00)	12 (0.83)	2.22
12-01	Gp4	g.chr7:73474349T>C	Silent	ELN	p.A516A	elastin	93 (0.00)	24 (0.71)	1.89
12-01	Gp4	g.chr4:110980852G>T	Missense Mutation	ELOVL6	p.L94M	ELOVL fatty acid elong	18 (0.00)	10 (0.60)	1.60
12-01	Gp4	g.chr22:29611613G>A	Missense Mutation	EMID1	p.E105K	EMI domain containing	68 (0.00)	123 (0.15)	0.39
12-01	Gp4	g.chr22:29627061C>A	Missense Mutation	EMID1	p.P173H	EMI domain containing	24 (0.00)	154 (0.25)	0.68
12-01	Gp4	g.chr20:39990484C>A	Silent	EMILIN3	p.G575G	elastin microfibril interf	89 (0.00)	62 (0.42)	1.12
12-01	Gp4	g.chr14:89087539C>A	Missense Mutation	EML5	p.G1707V	echinoderm microtubule	345 (0.00)	31 (0.48)	1.29
12-01	Gp4	g.chr14:89181368G>T	Missense Mutation	EML5	p.F453L	echinoderm microtubule	39 (0.00)	15 (0.40)	1.07
12-01	Gp4	g.chr19:14884860G>T	Missense Mutation	EMR2	p.A30D	egf-like module contain	33 (0.00)	78 (0.88)	2.36
12-01	Gp4	g.chr10:119305213C>A	Silent	EMX2	p.T159T	empty spiracles homeob	24 (0.00)	14 (0.57)	1.52

12-01	Gp4	g.chr5:73931336G>A	Silent	ENC1	p.D252D	ectodermal-neural corte	140 (0.00)	21 (0.24)	0.63
12-01	Gp4	g.chr1:8926429C>A	Silent	ENO1	p.L192L	enolase 1, (alpha)	82 (0.00)	85 (0.14)	0.38
12-01	Gp4	g.chr12:7025011G>A	Silent	ENO2	p.K5K	enolase 2 (gamma, neur	30 (0.00)	23 (0.65)	1.74
12-01	Gp4	g.chr22:41574581C>A	Missense Mutation	EP300	p.A2289D	E1A binding protein p3	119 (0.00)	56 (0.16)	0.43
12-01	Gp4	g.chr12:132479459G>A	Missense Mutation	EP400	p.V929I	E1A binding protein p4	101 (0.00)	38 (0.24)	0.63
12-01	Gp4	g.chr12:132547047C>A	Missense Mutation	EP400	p.P2712H	E1A binding protein p4	58 (0.00)	78 (0.29)	0.79
12-01	Gp4	g.chr12:132547159G>A	Silent	EP400	p.T2749T	E1A binding protein p4	62 (0.00)	144 (0.27)	0.72
12-01	Gp4	g.chr3:96706609G>A	Missense Mutation	EPHA6	p.V296I	EPH receptor A6	165 (0.00)	33 (0.27)	0.73
12-01	Gp4	g.chr1:23111349C>A	Nonsense Mutation	EPHB2	p.C197*	EPH receptor B2	44 (0.00)	84 (0.40)	1.08
12-01	Gp4	g.chr3:184290477C>T	Silent	EPHB3	p.P123P	EPH receptor B3	84 (0.00)	60 (0.47)	1.24
12-01	Gp4	g.chr3:184294797G>C	Missense Mutation	EPHB3	p.D394H	EPH receptor B3	172 (0.00)	128 (0.70)	1.85
12-01	Gp4	g.chr7:142566105C>A	Silent	EPHB6	p.V675V	EPH receptor B6	65 (0.00)	152 (0.25)	0.67
12-01	Gp4	g.chr3:37033464T>C	Missense Mutation	EPM2AIP1	p.T369A	EPM2A (laforin) intera	153 (0.00)	26 (0.69)	1.85
12-01	Gp4	g.chr3:37033875G>C	Missense Mutation	EPM2AIP1	p.Q232E	EPM2A (laforin) intera	23 (0.00)	59 (0.24)	0.63
12-01	Gp4	g.chr8:144941145C>T	Missense Mutation	EPPK1	p.E2093K	epiplakin 1	117 (0.00)	207 (0.28)	0.73
12-01	Gp4	g.chr19:16488032C>G	Missense Mutation	EPS15L1	p.G761R	epidermal growth factor	45 (0.00)	23 (0.70)	1.86
12-01	Gp4	g.chr19:16513210G>T	Silent	EPS15L1	p.A571A	epidermal growth factor	31 (0.00)	176 (0.39)	1.05
12-01	Gp4	g.chr12:91363833G>A	Silent	EPYC	p.A262A	epiphycan	53 (0.00)	14 (0.79)	2.10
12-01	Gp4	g.chr17:37872078C>A	Missense Mutation	ERBB2	p.L467I	v-erb-b2 avian erythrobl	192 (0.00)	20 (0.80)	2.13
12-01	Gp4	g.chr19:45871949T>C	Missense Mutation	ERCC2	p.E100G	excision repair cross-co	32 (0.00)	51 (0.20)	0.66
12-01	Gp4	g.chr9:98774903G>T	Missense Mutation	ERCC6L2	p.K338N	excision repair cross-co	17 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr21:39777217C>G	Intron	ERG		v-ets avian erythroblast	65 (0.00)	42 (0.26)	0.70
12-01	Gp4	g.chr21:39797669G>T	Intron	ERG		v-ets avian erythroblast	93 (0.00)	48 (0.92)	2.44
12-01	Gp4	g.chr21:39797756G>T	Intron	ERG		v-ets avian erythroblast	186 (0.00)	69 (0.93)	2.47
12-01	Gp4	g.chr21:39812675G>T	Intron	ERG		v-ets avian erythroblast	15 (0.00)	44 (0.68)	1.82
12-01	Gp4	g.chr21:39845103G>T	Intron	ERG		v-ets avian erythroblast	54 (0.00)	26 (0.27)	0.72
12-01	Gp4	g.chr21:39934778T>A	Intron	ERG		v-ets avian erythroblast	45 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr21:39940838C>G	Intron	ERG		v-ets avian erythroblast	184 (0.00)	48 (0.19)	0.50
12-01	Gp4	g.chr21:39953573C>T	Intron	ERG		v-ets avian erythroblast	124 (0.00)	19 (0.68)	1.82
12-01	Gp4	g.chr21:39984017G>T	Intron	ERG		v-ets avian erythroblast	108 (0.00)	36 (0.89)	2.37
12-01	Gp4	g.chr21:39998401C>A	Intron	ERG		v-ets avian erythroblast	37 (0.00)	20 (0.35)	0.93
12-01	Gp4	g.chr21:40021675C>T	Intron	ERG		v-ets avian erythroblast	182 (0.00)	54 (0.24)	0.64
12-01	Gp4	g.chr11:124622563G>T	Missense Mutation	ESAM	p.L114I	endothelial cell adhesio	141 (0.01)	328 (0.18)	0.48
12-01	Gp4	g.chr1:17030463G>T	RNA	ESPNP		espin pseudogene	60 (0.00)	94 (0.23)	0.62
12-01	Gp4	g.chr7:158534543G>A	Silent	ESYT2	p.H640H	extended synaptotagmin	120 (0.00)	147 (0.19)	0.51

12-01	Gp4	g.chr7:158536271C>A	Missense Mutation	ESYT2	p.Q608H	extended synaptotagmin	48 (0.00)	9 (0.78)	2.07
12-01	Gp4	g.chr19:44030412T>C	Missense Mutation	ETHE1	p.S106G	ethylmalonic encephalo	29 (0.00)	30 (0.23)	0.62
12-01	Gp4	g.chr3:185775264T>A	Missense Mutation	ETV5	p.K329N	ets variant 5	113 (0.00)	40 (0.47)	1.27
12-01	Gp4	g.chr6:36336763G>C	Silent	ETV7	p.A250A	ets variant 7	43 (0.00)	29 (0.34)	0.92
12-01	Gp4	g.chr17:29631316C>A	Nonsense Mutation	EVI2B	p.E438*	ecotropic viral integrati	34 (0.00)	34 (0.35)	0.94
12-01	Gp4	g.chr1:40980338T>A	Missense Mutation	EXO5	p.V41D	exonuclease 5	148 (0.00)	208 (0.61)	1.62
12-01	Gp4	g.chr4:56724546C>A	Silent	EXOC1	p.R19R	exocyst complex compo	20 (0.00)	97 (0.45)	1.21
12-01	Gp4	g.chr5:453673G>T	Missense Mutation	EXOC3	p.D185Y	exocyst complex compo	133 (0.00)	40 (0.28)	0.73
12-01	Gp4	g.chr5:454125G>T	Missense Mutation	EXOC3	p.E335D	exocyst complex compo	143 (0.00)	21 (0.57)	1.52
12-01	Gp4	g.chr17:74084184T>C	Missense Mutation	EXOC7	p.Y440C	exocyst complex compo	17 (0.00)	84 (0.30)	0.79
12-01	Gp4	g.chr1:231472597G>T	Silent	EXOC8	p.R295R	exocyst complex compo	129 (0.00)	75 (0.21)	0.57
12-01	Gp4	g.chr8:28574275C>A	Missense Mutation	EXTL3	p.D233E	exostosin-like glycosylt	193 (0.00)	42 (0.14)	0.38
12-01	Gp4	g.chr8:72184121T>C	Missense Mutation	EYA1	p.I280V	EYA transcriptional coa	71 (0.00)	33 (0.21)	0.57
12-01	Gp4	g.chr11:46751050G>C	Silent	F2	p.V531V	coagulation factor II (th	65 (0.00)	39 (0.36)	0.96
12-01	Gp4	g.chr16:74750249C>A	Missense Mutation	FA2H	p.K345N	fatty acid 2-hydroxylase	59 (0.00)	33 (0.64)	0.70
12-01	Gp4	g.chr10:14816527C>A	Missense Mutation	FAM107B	p.A46S	family with sequence si	52 (0.00)	19 (0.58)	1.54
12-01	Gp4	g.chr8:59059472C>A	Missense Mutation	FAM110B	p.P228H	family with sequence si	67 (0.00)	127 (0.17)	0.44
12-01	Gp4	g.chr4:187078859C>A	Missense Mutation	FAM149A	p.L239M	family with sequence si	205 (0.00)	387 (0.17)	0.45
12-01	Gp4	g.chr1:55076206C>A	Missense Mutation	FAM151A	p.M321I	family with sequence si	63 (0.00)	142 (0.31)	0.83
12-01	Gp4	g.chr11:6235670C>T	Missense Mutation	FAM160A2	p.G857E	family with sequence si	199 (0.00)	289 (0.16)	0.42
12-01	Gp4	g.chr11:6235677C>T	Missense Mutation	FAM160A2	p.A855T	family with sequence si	186 (0.00)	229 (0.39)	1.05
12-01	Gp4	g.chr11:6245392C>A	Missense Mutation	FAM160A2	p.Q75H	family with sequence si	34 (0.00)	94 (0.47)	1.25
12-01	Gp4	g.chr2:29237351C>A	Missense Mutation	FAM179A	p.T323K	family with sequence si	175 (0.00)	85 (0.14)	0.38
12-01	Gp4	g.chr12:49993528G>T	Missense Mutation	FAM186B	p.S632Y	family with sequence si	190 (0.01)	224 (0.57)	1.51
12-01	Gp4	g.chr19:35719251C>A	Missense Mutation	FAM187B	p.Q111H	family with sequence si	292 (0.00)	47 (0.53)	1.42
12-01	Gp4	g.chr5:176952200C>A	Nonsense Mutation	FAM193B	p.E428*	family with sequence si	84 (0.00)	145 (0.24)	0.64
12-01	Gp4	g.chr17:16347230G>A	Silent	FAM211A	p.G197G		168 (0.00)	205 (0.20)	0.52
12-01	Gp4	g.chr3:49841650G>T	Missense Mutation	FAM212A	p.G32C	family with sequence si	101 (0.00)	21 (0.24)	0.63
12-01	Gp4	g.chr10:88930289C>A	Nonsense Mutation	FAM35A	p.S563*	family with sequence si	123 (0.00)	101 (0.52)	1.40
12-01	Gp4	g.chr1:808748C>A	lincRNA	FAM41C		family with sequence si	31 (0.00)	33 (0.21)	0.57
12-01	Gp4	g.chr1:808820G>T	lincRNA	FAM41C		family with sequence si	46 (0.00)	31 (0.19)	0.52
12-01	Gp4	g.chr3:194407816C>A	Silent	FAM43A	p.G87G	family with sequence si	66 (0.00)	105 (0.28)	0.74
12-01	Gp4	g.chrX:34148368G>T	Silent	FAM47A	p.G676G	family with sequence si	42 (0.00)	134 (0.98)	1.63
12-01	Gp4	g.chr6:3850964G>T	Missense Mutation	FAM50B	p.A307S	family with sequence si	73 (0.00)	150 (0.15)	0.49
12-01	Gp4	g.chr5:137681035G>T	Nonsense Mutation	FAM53C	p.E220*	family with sequence si	100 (0.01)	105 (0.51)	1.37

12-01	Gp4	g.chr16:67574520G>A	Silent	FAM65A	p.R252R	family with sequence si	162 (0.01)	36 (0.25)	0.67
12-01	Gp4	g.chr16:67578707A>G	Missense Mutation	FAM65A	p.E962G	family with sequence si	133 (0.00)	131 (0.39)	1.04
12-01	Gp4	g.chr20:49225247C>G	Missense Mutation	FAM65C	p.W234S	family with sequence si	16 (0.00)	10 (0.60)	1.60
12-01	Gp4	g.chr20:49225873C>A	Silent	FAM65C	p.G195G	family with sequence si	42 (0.00)	87 (0.90)	2.39
12-01	Gp4	g.chr9:134151502C>T	Missense Mutation	FAM78A	p.G22D	family with sequence si	17 (0.00)	42 (0.93)	2.48
12-01	Gp4	g.chr16:5143523T>C	Missense Mutation	FAM86A	p.K68E	family with sequence si	173 (0.00)	114 (0.15)	0.40
12-01	Gp4	g.chr11:71507148T>C	Missense Mutation	FAM86C1	p.L116P	family with sequence si	234 (0.00)	365 (0.15)	0.41
12-01	Gp4	g.chr3:129821650G>A	RNA	FAM86HP		family with sequence si	210 (0.00)	230 (0.23)	0.61
12-01	Gp4	g.chr19:53786581C>A	RNA	FAM90A27P		family with sequence si	52 (0.00)	81 (0.32)	0.86
12-01	Gp4	g.chr16:89838171C>A	Missense Mutation	FANCA	p.G689V	Fanconi anemia, comple	81 (0.00)	18 (0.67)	0.73
12-01	Gp4	g.chrX:14882828G>A	Nonsense Mutation	FANCB	p.Q269*	Fanconi anemia, comple	16 (0.00)	22 (0.27)	0.45
12-01	Gp4	g.chr6:35424089A>T	Nonsense Mutation	FANCE	p.K272*	Fanconi anemia, comple	242 (0.00)	184 (0.25)	0.67
12-01	Gp4	g.chr11:22647124G>A	Missense Mutation	FANCF	p.P78L	Fanconi anemia, comple	69 (0.01)	181 (0.46)	1.24
12-01	Gp4	g.chr13:99083410G>T	Silent	FARP1	p.V673V	FERM, RhoGEF (ARH	17 (0.00)	30 (0.33)	0.89
12-01	Gp4	g.chr17:80039948A>G	Missense Mutation	FASN	p.Y2034H	fatty acid synthase	30 (0.00)	52 (0.15)	0.41
12-01	Gp4	g.chr11:92086632G>A	Missense Mutation	FAT3	p.G302R	FAT atypical cadherin 3	127 (0.00)	14 (0.93)	2.48
12-01	Gp4	g.chr11:92531991G>T	Missense Mutation	FAT3	p.V1788L	FAT atypical cadherin 3	46 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr4:126238327A>G	Missense Mutation	FAT4	p.H254R	FAT atypical cadherin 4	60 (0.00)	26 (0.23)	0.62
12-01	Gp4	g.chr4:126336809G>A	Missense Mutation	FAT4	p.A2231T	FAT atypical cadherin 4	49 (0.00)	21 (0.76)	2.03
12-01	Gp4	g.chr3:13663344C>A	Missense Mutation	FBLN2	p.S742Y	fibulin 2	69 (0.00)	38 (0.16)	0.42
12-01	Gp4	g.chr3:13678033C>T	Silent	FBLN2	p.F1101F	fibulin 2	127 (0.01)	291 (0.26)	0.70
12-01	Gp4	g.chr19:8176939C>A	Missense Mutation	FBN3	p.A1295S	fibrillin 3	164 (0.01)	164 (0.44)	1.17
12-01	Gp4	g.chr19:8191714C>G	Missense Mutation	FBN3	p.V767L	fibrillin 3	45 (0.00)	51 (0.31)	0.84
12-01	Gp4	g.chr9:97372207T>C	Missense Mutation	FBP1	p.D188G	fructose-1,6-bisphospha	25 (0.00)	30 (0.17)	0.44
12-01	Gp4	g.chr16:30671626C>A	Missense Mutation	FBRS	p.L168M	fibrosin	60 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr13:77595843C>A	Missense Mutation	FBXL3	p.L51F	F-box and leucine-rich r	24 (0.00)	20 (0.25)	0.67
12-01	Gp4	g.chr9:37512663G>T	Missense Mutation	FBXO10	p.L918I	F-box protein 10	115 (0.00)	87 (0.41)	1.10
12-01	Gp4	g.chr7:100198172T>C	Missense Mutation	FBXO24	p.C465R	F-box protein 24	87 (0.00)	50 (0.28)	0.75
12-01	Gp4	g.chr1:11721233G>T	Missense Mutation	FBXO44	p.W224L	F-box protein 44	80 (0.00)	72 (0.22)	0.59
12-01	Gp4	g.chr19:40368748C>A	Silent	FCGBP	p.R4200R	Fc fragment of IgG bind	235 (0.00)	323 (0.52)	1.40
12-01	Gp4	g.chr19:40408426C>G	Silent	FCGBP	p.L1471L	Fc fragment of IgG bind	110 (0.00)	25 (0.20)	0.53
12-01	Gp4	g.chr19:40412083G>T	Missense Mutation	FCGBP	p.S1182Y	Fc fragment of IgG bind	20 (0.00)	53 (0.17)	0.45
12-01	Gp4	g.chr1:120930076G>A	Silent	FCGR1B	p.R175R	Fc fragment of IgG, hig	156 (0.00)	105 (0.15)	0.41
12-01	Gp4	g.chr19:17877530C>A	Missense Mutation	FCHO1	p.L83M	FCH domain only 1	48 (0.00)	211 (0.38)	1.01
12-01	Gp4	g.chr5:141028989C>A	Silent	FCHSD1	p.R40R	FCH and double SH3 d	293 (0.00)	162 (0.18)	0.48

12-01	Gp4	g.chr1:157660073G>A	Silent	FCRL3	p.H554H	Fc receptor-like 3	158 (0.00)	110 (0.20)	0.53
12-01	Gp4	g.chr1:161695667C>A	Missense Mutation	FCRLB	p.L122M	Fc receptor-like B	35 (0.00)	41 (0.24)	0.65
12-01	Gp4	g.chr1:155290344C>G	Missense Mutation	FDPS	p.L402V	farnesyl diphosphate sy	26 (0.00)	32 (0.28)	0.75
12-01	Gp4	g.chr11:111746434C>T	Missense Mutation	FDXACB1	p.D363N	ferredoxin-fold anticod	349 (0.00)	80 (0.74)	1.97
12-01	Gp4	g.chr11:61563023C>A	Missense Mutation	FEN1	p.L64M	flap structure-specific e	100 (0.00)	64 (0.19)	0.50
12-01	Gp4	g.chr20:34191789C>G	RNA	FER1L4		fer-1-like family memb	52 (0.00)	33 (0.42)	1.13
12-01	Gp4	g.chr2:97368417G>T	RNA	FER1L5		fer-1-like family memb	70 (0.00)	79 (0.30)	0.81
12-01	Gp4	g.chr2:97369184T>A	RNA	FER1L5		fer-1-like family memb	172 (0.00)	43 (0.44)	1.18
12-01	Gp4	g.chr8:38273490G>C	Missense Mutation	FGFR1	p.C495W	fibroblast growth factor	39 (0.00)	40 (0.42)	1.13
12-01	Gp4	g.chr4:1806223C>A	Silent	FGFR3	p.I414I	fibroblast growth factor	243 (0.00)	280 (0.16)	0.43
12-01	Gp4	g.chr1:27941967G>T	Silent	FGR	p.I332I	FGR proto-oncogene, S	85 (0.00)	92 (0.46)	1.22
12-01	Gp4	g.chr16:67265117T>C	Missense Mutation	FHOD1	p.I881V	formin homology 2 dom	24 (0.00)	25 (0.28)	0.75
12-01	Gp4	g.chr16:67271462G>T	Silent	FHOD1	p.P255P	formin homology 2 dom	90 (0.00)	32 (0.28)	0.75
12-01	Gp4	g.chr16:67271573C>A	Silent	FHOD1	p.V247V	formin homology 2 dom	135 (0.00)	55 (0.29)	0.78
12-01	Gp4	g.chr2:164466520C>T	Missense Mutation	FIGN	p.E608K	fidgetin	100 (0.00)	58 (0.88)	2.34
12-01	Gp4	g.chr20:42935854C>T	Nonsense Mutation	FITM2	p.W67*	fat storage-inducing tra	139 (0.00)	49 (0.22)	0.60
12-01	Gp4	g.chr9:115935823G>T	Silent	FKBP15	p.A814A	FK506 binding protein	128 (0.00)	51 (0.96)	2.56
12-01	Gp4	g.chr12:2910436T>C	Missense Mutation	FKBP4	p.C396R	FK506 binding protein	121 (0.00)	17 (0.41)	1.10
12-01	Gp4	g.chr1:152281450G>T	Missense Mutation	FLG	p.A1971E	filaggrin	148 (0.00)	579 (0.22)	0.60
12-01	Gp4	g.chrX:153586707C>T	Missense Mutation	FLNA	p.V1539M	filamin A, alpha	44 (0.00)	141 (0.32)	0.53
12-01	Gp4	g.chrX:153594432C>A	Silent	FLNA	p.V463V	filamin A, alpha	19 (0.00)	48 (0.27)	0.45
12-01	Gp4	g.chr3:58108844G>T	Nonsense Mutation	FLNB	p.E1051*	filamin B, beta	177 (0.01)	106 (0.16)	0.43
12-01	Gp4	g.chr7:128493020G>A	Missense Mutation	FLNC	p.G2048D	filamin C, gamma	151 (0.00)	282 (0.25)	0.67
12-01	Gp4	g.chr7:128493063C>G	Missense Mutation	FLNC	p.F2062L	filamin C, gamma	153 (0.00)	242 (0.38)	1.01
12-01	Gp4	g.chr7:128496574G>T	Missense Mutation	FLNC	p.E2418D	filamin C, gamma	35 (0.00)	34 (0.38)	1.02
12-01	Gp4	g.chr5:180057024G>T	Missense Mutation	FLT4	p.H199N	fms-related tyrosine kin	35 (0.00)	107 (0.16)	0.42
12-01	Gp4	g.chr1:213058696C>A	Missense Mutation	FLVCR1	p.S385Y	feline leukemia virus su	33 (0.00)	170 (0.26)	0.71
12-01	Gp4	g.chr15:33256353T>C	Silent	FMN1	p.K1031K	formin 1	36 (0.00)	34 (0.15)	0.47
12-01	Gp4	g.chr2:153468117G>T	Missense Mutation	FMNL2	p.D354Y	formin-like 2	116 (0.00)	26 (0.27)	0.72
12-01	Gp4	g.chr17:80685017C>T	Silent	FN3KRP	p.S300S	fructosamine 3 kinase r	80 (0.00)	283 (0.30)	0.80
12-01	Gp4	g.chr6:159654079C>T	Silent	FNDC1	p.P845P	fibronectin type III dom	92 (0.00)	54 (0.30)	0.79
12-01	Gp4	g.chr6:159657323C>G	Missense Mutation	FNDC1	p.I1348M	fibronectin type III dom	116 (0.00)	165 (0.19)	0.52
12-01	Gp4	g.chr6:159659697G>T	Splice Site	FNDC1	p.D1394Y	fibronectin type III dom	176 (0.00)	209 (0.50)	1.33
12-01	Gp4	g.chr1:33330239C>A	Missense Mutation	FNDC5	p.W145L	fibronectin type III dom	133 (0.01)	28 (0.71)	1.90
12-01	Gp4	g.chr17:33454077G>T	Nonsense Mutation	FNDC8	p.E76*	fibronectin type III dom	136 (0.00)	99 (0.34)	0.92

12-01	Gp4	g.chr5:156770451A>G	Missense Mutation	FNDC9	p.Y32H	fibronectin type III dom	71 (0.01)	40 (0.88)	2.33
12-01	Gp4	g.chr4:159790335G>C	Silent	FNIP2	p.V849V	folliculin interacting prc	88 (0.00)	52 (0.48)	1.28
12-01	Gp4	g.chr14:29237161C>A	Missense Mutation	FOXG1	p.Q226K	forkhead box G1	21 (0.00)	37 (0.32)	0.86
12-01	Gp4	g.chr6:108985100C>G	Nonsense Mutation	FOXO3	p.S355*	forkhead box O3	58 (0.00)	102 (0.26)	0.71
12-01	Gp4	g.chrX:49113934G>C	Missense Mutation	FOXP3	p.T135S	forkhead box P3	60 (0.00)	49 (0.51)	0.85
12-01	Gp4	g.chr9:130571977G>T	Nonsense Mutation	FPGS	p.E359*	folylpolyglutamate synt	16 (0.00)	116 (0.51)	1.36
12-01	Gp4	g.chr7:127233973C>G	Missense Mutation	FSCN3	p.S22R	fascin actin-bundling pr	40 (0.00)	14 (0.36)	0.95
12-01	Gp4	g.chr9:133493183G>T	Splice Site	FUBP3		far upstream element (F	183 (0.00)	55 (0.25)	0.68
12-01	Gp4	g.chr16:70512224G>T	Silent	FUK	p.V388V	fucokinase	104 (0.01)	99 (0.18)	0.48
12-01	Gp4	g.chr16:70513512G>T	Nonsense Mutation	FUK	p.E553*	fucokinase	91 (0.00)	27 (0.19)	0.49
12-01	Gp4	g.chr2:84518192G>A	RNA	FUNDC2P2		FUN14 domain containi	151 (0.00)	146 (0.16)	0.42
12-01	Gp4	g.chr2:202900651G>A	Silent	FZD7	p.A427A	frizzled class receptor 7	206 (0.00)	219 (0.26)	0.71
12-01	Gp4	g.chr2:202900660C>G	Missense Mutation	FZD7	p.F430L	frizzled class receptor 7	225 (0.00)	241 (0.14)	0.38
12-01	Gp4	g.chr19:3533324C>A	Silent	FZR1	p.I425I	fizzy/cell division cycle	47 (0.00)	63 (0.40)	1.06
12-01	Gp4	g.chr4:46388155G>A	Silent	GABRA2	p.I41I	gamma-aminobutyric ac	15 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr3:30842485G>T	Silent	GADL1	p.I382I	glutamate decarboxylas	43 (0.00)	31 (0.19)	0.52
12-01	Gp4	g.chr17:73760120C>T	Silent	GALK1	p.G71G	galactokinase 1	21 (0.00)	83 (0.22)	0.58
12-01	Gp4	g.chr11:11394156C>A	Missense Mutation	GALNT18	p.C333F	polypeptide N-acetylgal	91 (0.00)	17 (0.76)	2.04
12-01	Gp4	g.chr12:6647054C>G	Missense Mutation	GAPDH	p.T277S	glyceraldehyde-3-phosp	71 (0.00)	109 (0.22)	0.59
12-01	Gp4	g.chr2:26411090C>A	Silent	GAREML	p.I653I	GRB2 associated, regul	37 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr9:130111223C>A	Missense Mutation	GARNL3	p.F484L	GTPase activating Rap/	81 (0.00)	280 (0.15)	0.40
12-01	Gp4	g.chr7:30662010G>A	Silent	GARS	p.V515V	glycyl-tRNA synthetase	146 (0.00)	32 (0.19)	0.50
12-01	Gp4	g.chr17:34072865C>A	Missense Mutation	GAS2L2	p.G551W	growth arrest-specific 2	71 (0.00)	95 (0.16)	0.42
12-01	Gp4	g.chr3:128200781C>A	Missense Mutation	GATA2	p.A342S	GATA binding protein	54 (0.00)	40 (0.25)	0.67
12-01	Gp4	g.chr8:11606470G>T	Missense Mutation	GATA4	p.C220F	GATA binding protein	106 (0.00)	75 (0.87)	2.31
12-01	Gp4	g.chr10:104111673C>A	Missense Mutation	GBF1	p.S163Y	golgi brefeldin A resista	120 (0.00)	27 (0.30)	0.79
12-01	Gp4	g.chr7:127224686G>A	Missense Mutation	GCC1	p.A184V	GRIP and coiled-coil d	243 (0.00)	569 (0.21)	0.55
12-01	Gp4	g.chr12:56143659G>T	Missense Mutation	GDF11	p.C406F	growth differentiation f	330 (0.00)	187 (0.14)	0.39
12-01	Gp4	g.chr8:97172721G>A	Missense Mutation	GDF6	p.P67L	growth differentiation f	70 (0.01)	85 (0.89)	2.38
12-01	Gp4	g.chrX:153668373T>C	Silent	GDI1	p.F158F	GDP dissociation inhibi	238 (0.00)	188 (0.34)	0.57
12-01	Gp4	g.chr15:90784504G>T	Missense Mutation	GDPGP1	p.V122L	GDP-D-glucose phosph	129 (0.00)	38 (0.16)	0.42
12-01	Gp4	g.chr7:932000C>A	Missense Mutation	GET4	p.P231T	golgi to ER traffic prote	95 (0.00)	100 (0.60)	1.60
12-01	Gp4	g.chr1:92941638T>C	Missense Mutation	GFI1	p.Q406R	growth factor independe	111 (0.00)	161 (0.18)	0.48
12-01	Gp4	g.chr2:69590792A>G	Silent	GFPT1	p.D78D	glutamine--fructose-6-p	29 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr5:179729474C>A	Silent	GFPT2	p.V651V	glutamine-fructose-6-ph	96 (0.00)	76 (0.28)	0.74

12-01	Gp4	g.chr5:179762902G>T	Missense Mutation	GFPT2	p.A89D	glutamine-fructose-6-ph	63 (0.00)	80 (0.39)	1.03
12-01	Gp4	g.chr17:61958867G>T	Missense Mutation	GH2	p.S8Y	growth hormone 2	129 (0.00)	195 (0.43)	1.15
12-01	Gp4	g.chr7:100279366C>A	Missense Mutation	GIGYF1	p.E1028D	GRB10 interacting GY	23 (0.00)	12 (0.42)	1.11
12-01	Gp4	g.chr7:100279523G>T	Silent	GIGYF1	p.R1007R	GRB10 interacting GY	28 (0.00)	32 (0.31)	0.83
12-01	Gp4	g.chr7:100279602G>A	Silent	GIGYF1	p.S980S	GRB10 interacting GY	34 (0.00)	47 (0.53)	1.42
12-01	Gp4	g.chr7:150325503G>A	Silent	GIMAP6	p.L61L	GTPase, IMAP family	251 (0.00)	129 (0.90)	2.40
12-01	Gp4	g.chr6:149903591A>T	Missense Mutation	GINM1	p.M245L	glycoprotein integral m	16 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr1:147231201T>C	Missense Mutation	GJA5	p.Q49R	gap junction protein, al	122 (0.00)	91 (0.20)	0.53
12-01	Gp4	g.chr7:99526695G>A	Silent	GJC3	p.S183S	gap junction protein, ga	98 (0.00)	65 (0.28)	0.74
12-01	Gp4	g.chr11:134244891C>T	Missense Mutation	GLB1L2	p.A617V	galactosidase, beta 1-lik	49 (0.00)	71 (0.80)	2.14
12-01	Gp4	g.chr1:1263140C>A	Silent	GLTPD1	p.P214P		19 (0.00)	24 (0.29)	0.78
12-01	Gp4	g.chr20:62234356T>C	Missense Mutation	GMEB2	p.K107E	glucocorticoid modulat	158 (0.00)	88 (0.41)	1.09
12-01	Gp4	g.chr19:3162860G>T	Missense Mutation	GNA15	p.C323F	guanine nucleotide bind	17 (0.00)	32 (0.84)	2.25
12-01	Gp4	g.chr20:57415432G>T	Missense Mutation	GNAS	p.A91S	GNAS complex locus	21 (0.00)	41 (0.85)	2.28
12-01	Gp4	g.chr20:57430127C>A	Missense Mutation	GNAS	p.P603T	GNAS complex locus	44 (0.00)	31 (0.52)	1.38
12-01	Gp4	g.chr7:100275190G>A	Missense Mutation	GNB2	p.A113T	guanine nucleotide bind	92 (0.00)	108 (0.25)	0.67
12-01	Gp4	g.chr12:133365693C>T	Missense Mutation	GOLGA3	p.V911I	golgin A3	30 (0.00)	34 (0.24)	0.63
12-01	Gp4	g.chr14:93282601G>T	Missense Mutation	GOLGA5	p.K442N	golgin A5	62 (0.00)	16 (0.69)	1.83
12-01	Gp4	g.chr3:121409730T>A	Silent	GOLGB1	p.S2827S	golgin B1	27 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr3:121414616G>A	Missense Mutation	GOLGB1	p.T1585I	golgin B1	45 (0.00)	14 (0.71)	1.90
12-01	Gp4	g.chr17:42477590C>T	Missense Mutation	GPATCH8	p.G619R	G patch domain contain	71 (0.00)	21 (0.81)	0.67
12-01	Gp4	g.chr7:1131454G>T	Missense Mutation	GPER1	p.E30D	G protein-coupled estro	42 (0.02)	76 (0.33)	0.88
12-01	Gp4	g.chr19:34890923C>T	Silent	GPI	p.R553R	glucose-6-phosphate iso	21 (0.00)	72 (0.31)	0.81
12-01	Gp4	g.chrX:129518973G>T	Missense Mutation	GPR119	p.A150D	G protein-coupled recep	107 (0.00)	522 (0.36)	0.59
12-01	Gp4	g.chr8:37672423C>A	Missense Mutation	GPR124	p.S92R	G protein-coupled recep	59 (0.00)	34 (0.35)	0.94
12-01	Gp4	g.chr1:6314868C>G	Missense Mutation	GPR153	p.G33A	G protein-coupled recep	50 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr2:175346384A>G	Missense Mutation	GPR155	p.S101P	G protein-coupled recep	18 (0.00)	38 (0.24)	0.63
12-01	Gp4	g.chr17:36499008C>A	Missense Mutation	GPR179	p.G222V	G protein-coupled recep	171 (0.00)	143 (0.34)	0.91
12-01	Gp4	g.chr1:202097478G>T	Missense Mutation	GPR37L1	p.V414L	G protein-coupled recep	50 (0.00)	19 (0.42)	1.12
12-01	Gp4	g.chrX:19018024C>A	Missense Mutation	GPR64	p.G759V	G protein-coupled recep	137 (0.00)	143 (0.49)	0.82
12-01	Gp4	g.chr16:57713101G>C	Missense Mutation	GPR97	p.G169R	G protein-coupled recep	42 (0.00)	29 (0.38)	1.01
12-01	Gp4	g.chr5:176026731C>T	Silent	GPRIN1	p.L35L	G protein regulated ind	24 (0.00)	71 (0.30)	0.79
12-01	Gp4	g.chr19:35501033G>C	Missense Mutation	GRAMD1A	p.Q114H	GRAM domain containi	127 (0.00)	46 (0.54)	1.45
12-01	Gp4	g.chr12:52407694G>T	Missense Mutation	GRASP	p.K194N	GRP1 (general receptor	221 (0.00)	300 (0.20)	0.52
12-01	Gp4	g.chr7:50660759C>T	Missense Mutation	GRB10	p.D559N	growth factor receptor-	79 (0.00)	20 (0.25)	0.67

12-01	Gp4	g.chr17:37900322G>T	Splice Site	GRB7		growth factor receptor-b	185 (0.00)	9 (0.67)	1.78
12-01	Gp4	g.chr2:11758601C>T	Silent	GREB1	p.P1200P	growth regulation by est	26 (0.00)	68 (0.22)	0.59
12-01	Gp4	g.chr2:11778031C>A	Missense Mutation	GREB1	p.L1846M	growth regulation by est	109 (0.00)	41 (0.83)	2.21
12-01	Gp4	g.chr2:10101415A>T	Silent	GRHL1	p.A173A	grainyhead-like 1 (Dros	114 (0.00)	27 (0.52)	1.38
12-01	Gp4	g.chr2:10101474A>G	Missense Mutation	GRHL1	p.D193G	grainyhead-like 1 (Dros	109 (0.00)	36 (0.58)	1.56
12-01	Gp4	g.chr11:120531057G>T	Silent	GRIK4	p.L10L	glutamate receptor, iono	65 (0.00)	26 (0.42)	1.13
12-01	Gp4	g.chr11:120673486C>A	Missense Mutation	GRIK4	p.P56H	glutamate receptor, iono	169 (0.00)	305 (0.37)	0.99
12-01	Gp4	g.chr8:145066891G>C	Missense Mutation	GRINA	p.G333A	glutamate receptor, iono	52 (0.00)	63 (0.54)	1.44
12-01	Gp4	g.chr12:66838489C>A	Missense Mutation	GRIP1	p.G469V	glutamate receptor inter	65 (0.00)	35 (0.29)	0.76
12-01	Gp4	g.chr3:14565978G>C	RNA	GRIP2		glutamate receptor inter	45 (0.00)	20 (0.55)	1.47
12-01	Gp4	g.chr4:3011390G>A	Silent	GRK4	p.K184K	G protein-coupled recep	81 (0.00)	72 (0.53)	1.41
12-01	Gp4	g.chr5:176867836G>C	Missense Mutation	GRK6	p.E480Q	G protein-coupled recep	55 (0.00)	108 (0.27)	0.72
12-01	Gp4	g.chr6:146351275G>T	Missense Mutation	GRM1	p.D208Y	glutamate receptor, meta	239 (0.00)	166 (0.70)	1.86
12-01	Gp4	g.chr6:146755377C>A	Silent	GRM1	p.P1010P	glutamate receptor, meta	141 (0.00)	18 (0.56)	1.48
12-01	Gp4	g.chr3:51746729C>T	Missense Mutation	GRM2	p.R231C	glutamate receptor, meta	38 (0.00)	61 (0.39)	1.05
12-01	Gp4	g.chr8:144641663G>A	Missense Mutation	GSDMD	p.R53H	gasdermin D	117 (0.01)	210 (0.37)	0.99
12-01	Gp4	g.chr19:42740862C>T	Missense Mutation	GSK3A	p.E188K	glycogen synthase kinas	224 (0.00)	158 (0.22)	0.59
12-01	Gp4	g.chr7:73960133C>G	Missense Mutation	GTF2IRD1	p.R576G	GTF2I repeat domain c	76 (0.00)	20 (0.60)	1.60
12-01	Gp4	g.chr7:74015455C>A	Missense Mutation	GTF2IRD1	p.S905Y	GTF2I repeat domain c	107 (0.00)	52 (0.58)	1.54
12-01	Gp4	g.chr7:72663632G>T	RNA	GTF2IRD2P1		GTF2I repeat domain c	45 (0.00)	25 (0.48)	1.28
12-01	Gp4	g.chr22:39112955A>G	Missense Mutation	GTPBP1	p.T262A	GTP binding protein 1	25 (0.00)	42 (0.19)	0.51
12-01	Gp4	g.chr6:42141344C>A	De novo Start OutOf	GUCA1A		guanylate cyclase activa	34 (0.00)	24 (0.79)	2.11
12-01	Gp4	g.chr22:23994828C>A	RNA	GUSBP11		glucuronidase, beta pseu	19 (0.00)	33 (0.67)	1.78
12-01	Gp4	g.chr17:73774702G>T	Missense Mutation	H3F3B	p.R129S	H3 histone, family 3B (	163 (0.00)	15 (0.80)	2.13
12-01	Gp4	g.chr10:115343033T>A	Missense Mutation	HABP2	p.F385I	hyaluronan binding prot	73 (0.00)	10 (0.50)	1.33
12-01	Gp4	g.chr5:140076196C>A	Missense Mutation	HARS2	p.H275N	histidyl-tRNA synthetas	80 (0.00)	13 (0.54)	1.44
12-01	Gp4	g.chr19:17160833G>T	Silent	HAUS8	p.P361P	HAUS augmin-like com	38 (0.00)	58 (0.38)	1.01
12-01	Gp4	g.chr5:156533798C>A	Missense Mutation	HAVCR2	p.W78C	hepatitis A virus cellula	43 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr12:123187369G>A	Silent	HCAR2	p.I154I	hydroxycarboxylic acid	30 (0.00)	26 (0.96)	2.56
12-01	Gp4	g.chr1:32798625G>A	Missense Mutation	HDAC1	p.E477K	histone deacetylase 1	62 (0.00)	59 (0.66)	1.76
12-01	Gp4	g.chr17:42164884C>A	Missense Mutation	HDAC5	p.D595Y	histone deacetylase 5	38 (0.00)	59 (0.58)	0.48
12-01	Gp4	g.chr7:18536059T>A	Intron	HDAC9		histone deacetylase 9	62 (0.00)	128 (0.37)	0.98
12-01	Gp4	g.chr7:18653016T>C	Intron	HDAC9		histone deacetylase 9	41 (0.00)	18 (0.33)	0.89
12-01	Gp4	g.chr7:18834294G>A	Intron	HDAC9		histone deacetylase 9	19 (0.00)	30 (0.97)	2.58
12-01	Gp4	g.chr7:18928188C>G	Intron	HDAC9		histone deacetylase 9	112 (0.00)	200 (0.19)	0.51

12-01	Gp4	g.chr1:156714014G>A	Missense Mutation	HDGF	p.P144S	hepatoma-derived grow	194 (0.00)	106 (0.22)	0.58
12-01	Gp4	g.chrX:83724041T>C	Silent	HDX	p.S230S	highly divergent homeo	94 (0.01)	20 (0.30)	0.50
12-01	Gp4	g.chr17:58147124C>A	Missense Mutation	HEATR6	p.R296L	HEAT repeat containing	22 (0.00)	23 (0.74)	1.97
12-01	Gp4	g.chr12:112605667G>T	Nonsense Mutation	HECTD4	p.S3942*	HECT domain containin	71 (0.00)	68 (0.26)	0.71
12-01	Gp4	g.chr20:62195450G>T	Silent	HELZ2	p.P1575P	helicase with zinc finge	37 (0.00)	57 (0.18)	0.47
12-01	Gp4	g.chr15:63961749C>G	Missense Mutation	HERC1	p.A2732P	HECT and RLD domain	98 (0.00)	35 (0.86)	2.29
12-01	Gp4	g.chr15:64045210G>T	Missense Mutation	HERC1	p.R617S	HECT and RLD domain	29 (0.00)	44 (0.86)	2.30
12-01	Gp4	g.chr15:28421857G>A	Nonsense Mutation	HERC2	p.Q3164*	HECT and RLD domain	198 (0.00)	95 (0.48)	1.53
12-01	Gp4	g.chr15:28465677T>C	Silent	HERC2	p.G1922G	HECT and RLD domain	65 (0.00)	404 (0.14)	0.45
12-01	Gp4	g.chr15:20645820C>A	RNA	HERC2P3		hect domain and RLD 2	67 (0.00)	73 (0.26)	0.69
12-01	Gp4	g.chr8:43033312G>C	Missense Mutation	HGSNAT	p.W316S	heparan-alpha-glucosam	86 (0.01)	481 (0.62)	1.66
12-01	Gp4	g.chr14:100129278G>A	Missense Mutation	HHIPL1	p.G523D	HHIP-like 1	28 (0.00)	32 (0.16)	0.42
12-01	Gp4	g.chr1:222717022C>T	Silent	HHIPL2	p.L277L	HHIP-like 2	231 (0.00)	213 (0.20)	0.53
12-01	Gp4	g.chr1:222717079G>T	Silent	HHIPL2	p.L258L	HHIP-like 2	153 (0.00)	160 (0.18)	0.48
12-01	Gp4	g.chr1:114515787C>A	Missense Mutation	HIPK1	p.P1096T	homeodomain interactin	250 (0.00)	107 (0.31)	0.82
12-01	Gp4	g.chr19:40895462G>T	Silent	HIPK4	p.V116V	homeodomain interactin	78 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr6:26017380G>T	Missense Mutation	HIST1H1A	p.A194E	histone cluster 1, H1a	338 (0.00)	355 (0.15)	0.40
12-01	Gp4	g.chr6:26217216G>T	Missense Mutation	HIST1H2AE	p.G5V	histone cluster 1, H2ae	143 (0.00)	83 (0.37)	1.00
12-01	Gp4	g.chr6:27782177G>A	Silent	HIST1H2AJ	p.A114A	histone cluster 1, H2aj	351 (0.00)	640 (0.23)	0.61
12-01	Gp4	g.chr1:228646069G>T	Missense Mutation	HIST3H2BB	p.R80L	histone cluster 3, H2bb	242 (0.00)	49 (0.57)	1.52
12-01	Gp4	g.chr1:42049227G>A	Silent	HIVEP3	p.Y414Y	human immunodeficien	110 (0.00)	180 (0.21)	0.56
12-01	Gp4	g.chr10:71005875G>A	Missense Mutation	HKDC1	p.V306I	hexokinase domain cont	147 (0.00)	60 (0.48)	1.29
12-01	Gp4	g.chr5:149391885C>A	Nonsense Mutation	HMGXB3	p.S293*	HMG box domain conta	128 (0.00)	112 (0.84)	2.24
12-01	Gp4	g.chr22:35782782G>T	Silent	HMOX1	p.L83L	heme oxygenase (decyc	118 (0.00)	104 (0.14)	0.38
12-01	Gp4	g.chr5:137089356G>T	Missense Mutation	HNRNPA0	p.Q134K	heterogeneous nuclear r	46 (0.00)	88 (0.72)	1.91
12-01	Gp4	g.chr5:177632851T>A	Missense Mutation	HNRNPAB	p.F73Y	heterogeneous nuclear r	78 (0.00)	12 (0.92)	2.44
12-01	Gp4	g.chr19:39329574G>T	Missense Mutation	HNRNPL	p.L439I	heterogeneous nuclear r	191 (0.00)	65 (0.26)	0.70
12-01	Gp4	g.chr19:8550618C>A	Missense Mutation	HNRNPM	p.R436S	heterogeneous nuclear r	35 (0.00)	126 (0.98)	2.62
12-01	Gp4	g.chr7:27237952A>T	Missense Mutation	HOXA13	p.N344K	homeobox A13	83 (0.00)	19 (0.47)	1.26
12-01	Gp4	g.chr17:46628084G>T	Missense Mutation	HOXB3	p.A230E	homeobox B3	174 (0.00)	155 (0.20)	0.53
12-01	Gp4	g.chr17:46628302C>G	Silent	HOXB3	p.R157R	homeobox B3	222 (0.00)	100 (0.59)	1.57
12-01	Gp4	g.chr17:46673918C>A	Nonsense Mutation	HOXB6	p.E178*	homeobox B6	141 (0.00)	139 (0.32)	0.84
12-01	Gp4	g.chr2:176996285C>A	Missense Mutation	HOXD8	p.T89K	homeobox D8	228 (0.00)	23 (0.70)	1.86
12-01	Gp4	g.chr19:35551373C>A	Missense Mutation	HPN	p.L193I	hepsin	59 (0.00)	15 (0.53)	1.42
12-01	Gp4	g.chr10:100183562C>A	Nonsense Mutation	HPS1	p.G494*	Hermansky-Pudlak sync	78 (0.00)	118 (0.25)	0.66

12-01	Gp4	g.chr10:100185633G>T	Missense Mutation	HPS1	p.P366H	Hermansky-Pudlak sync	113 (0.00)	234 (0.35)	0.92
12-01	Gp4	g.chr10:103825928C>T	Missense Mutation	HPS6	p.L233F	Hermansky-Pudlak sync	41 (0.00)	66 (0.26)	0.69
12-01	Gp4	g.chr10:100242409C>A	Nonsense Mutation	HPSE2	p.E533*	heparanase 2 (inactive)	96 (0.00)	25 (0.88)	2.35
12-01	Gp4	g.chr20:60791752G>T	Missense Mutation	HRH3	p.F216L	histamine receptor H3	59 (0.00)	65 (0.28)	0.74
12-01	Gp4	g.chr1:152187003C>A	Nonsense Mutation	HRNR	p.E2368*	hornerin	305 (0.00)	352 (0.43)	1.14
12-01	Gp4	g.chr2:20818775G>T	Missense Mutation	HS1BP3	p.P384Q	HCLS1 binding protein	20 (0.00)	78 (0.42)	1.13
12-01	Gp4	g.chrX:131763087C>T	Missense Mutation	HS6ST2	p.V368M	heparan sulfate 6-O-sulf	81 (0.00)	125 (0.57)	0.95
12-01	Gp4	g.chr15:62538122G>A	RNA	hsa-mir-7162			19 (0.00)	43 (0.44)	1.18
12-01	Gp4	g.chr12:104335293G>T	Nonsense Mutation	HSP90B1	p.E400*	heat shock protein 90kD	45 (0.00)	16 (0.50)	1.33
12-01	Gp4	g.chr1:22151052C>A	Missense Mutation	HSPG2	p.G4241V	heparan sulfate proteogl	16 (0.00)	28 (0.43)	1.14
12-01	Gp4	g.chr6:78172847C>A	Missense Mutation	HTR1B	p.A92S	5-hydroxytryptamine (s	165 (0.00)	145 (0.52)	1.38
12-01	Gp4	g.chr2:118629096T>C	RNA	HTR5BP		5-hydroxytryptamine (s	26 (0.00)	22 (0.36)	0.97
12-01	Gp4	g.chr21:33347027G>C	Missense Mutation	HUNK	p.G391R	hormonally up-regulate	190 (0.00)	107 (0.30)	0.80
12-01	Gp4	g.chr6:656356C>T	Missense Mutation	HUS1B	p.V197M	HUS1 checkpoint homo	59 (0.00)	604 (0.27)	0.71
12-01	Gp4	g.chr11:118919222G>T	Missense Mutation	HYOU1	p.A678D	hypoxia up-regulated 1	145 (0.00)	295 (0.19)	0.51
12-01	Gp4	g.chr9:21304776G>C	Missense Mutation	IFNA5	p.S160R	interferon, alpha 5	67 (0.00)	43 (0.95)	2.54
12-01	Gp4	g.chr19:39759354G>T	Missense Mutation	IFNL2	p.M16I	interferon, lambda 2	34 (0.00)	52 (0.58)	1.54
12-01	Gp4	g.chr1:24483654C>G	Missense Mutation	IFNLR1	p.R510T	interferon, lambda recep	67 (0.00)	141 (0.30)	0.79
12-01	Gp4	g.chr16:1573590G>T	Missense Mutation	IFT140	p.R322S	intraflagellar transport 1	33 (0.00)	18 (0.39)	1.04
12-01	Gp4	g.chr16:1573650C>A	Missense Mutation	IFT140	p.V302L	intraflagellar transport 1	33 (0.00)	35 (0.71)	1.90
12-01	Gp4	g.chr14:76488689C>A	Missense Mutation	IFT43	p.P56H	intraflagellar transport 4	297 (0.00)	218 (0.52)	1.38
12-01	Gp4	g.chr6:160461622C>T	Missense Mutation	IGF2R	p.T449I	insulin-like growth fact	192 (0.01)	47 (0.77)	2.04
12-01	Gp4	g.chr14:106311243C>A	RNA	IGHD		immunoglobulin heavy	15 (0.00)	82 (0.16)	0.42
12-01	Gp4	g.chr14:106110267C>A	RNA	IGHG2		immunoglobulin heavy	261 (0.00)	116 (0.17)	0.46
12-01	Gp4	g.chr14:106610440C>A	RNA	IGHV3-15		immunoglobulin heavy	215 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr14:106780822G>T	RNA	IGHV4-28		immunoglobulin heavy	66 (0.00)	27 (0.26)	0.69
12-01	Gp4	g.chr2:87565706T>C	RNA	IGKV3OR2-268		immunoglobulin kappa	137 (0.00)	187 (0.21)	0.57
12-01	Gp4	g.chr22:22677244C>T	RNA	IGLV1-51		immunoglobulin lambda	70 (0.00)	53 (0.17)	0.45
12-01	Gp4	g.chr22:23135410C>T	RNA	IGLV2-11		immunoglobulin lambda	386 (0.00)	59 (0.66)	1.76
12-01	Gp4	g.chr3:118645055C>T	Missense Mutation	IGSF11	p.G158D	immunoglobulin superfa	67 (0.00)	32 (0.22)	0.58
12-01	Gp4	g.chr1:18688614C>T	Missense Mutation	IGSF21	p.P144S	immunoglobin superfan	94 (0.00)	85 (0.41)	1.10
12-01	Gp4	g.chr7:50450332C>G	Silent	IKZF1	p.P172P	IKAROS family zinc fir	53 (0.00)	14 (0.93)	2.48
12-01	Gp4	g.chr2:102851700C>A	Silent	IL1RL2	p.V547V	interleukin 1 receptor-lil	146 (0.00)	139 (0.17)	0.44
12-01	Gp4	g.chr16:27457345G>T	Missense Mutation	IL21R	p.W268L	interleukin 21 receptor	63 (0.00)	226 (0.35)	0.92
12-01	Gp4	g.chr3:49062441C>A	Nonsense Mutation	IMPDH2	p.E395*	IMP (inosine 5'-monoph	74 (0.00)	24 (0.21)	0.56

12-01	Gp4	g.chr14:105173672C>A	Silent	INF2	p.A356A	inverted formin, FH2 an	20 (0.00)	21 (0.57)	1.52
12-01	Gp4	g.chr7:30795187G>T	Missense Mutation	INMT	p.C171F	indolethylamine N-meth	42 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr2:206874360G>A	Silent	INO80D	p.P567P	INO80 complex subunit	49 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr2:99170746G>T	Missense Mutation	INPP4A	p.V459F	inositol polyphosphate-4	50 (0.00)	74 (0.24)	0.65
12-01	Gp4	g.chr4:142986771A>T	Intron	INPP4B		inositol polyphosphate-4	201 (0.00)	19 (0.74)	1.96
12-01	Gp4	g.chr4:143079223G>C	Intron	INPP4B		inositol polyphosphate-4	67 (0.00)	171 (0.99)	2.65
12-01	Gp4	g.chr4:143103814C>A	Intron	INPP4B		inositol polyphosphate-4	118 (0.01)	370 (0.31)	0.81
12-01	Gp4	g.chr4:143133465C>A	Intron	INPP4B		inositol polyphosphate-4	87 (0.00)	159 (0.24)	0.64
12-01	Gp4	g.chr4:143253613G>A	Intron	INPP4B		inositol polyphosphate-4	31 (0.00)	89 (0.35)	0.93
12-01	Gp4	g.chr4:143253738T>C	Intron	INPP4B		inositol polyphosphate-4	158 (0.00)	53 (0.47)	1.26
12-01	Gp4	g.chr4:143254373G>A	Intron	INPP4B		inositol polyphosphate-4	64 (0.00)	83 (0.81)	2.15
12-01	Gp4	g.chr4:143486592G>T	Intron	INPP4B		inositol polyphosphate-4	34 (0.00)	14 (0.50)	1.33
12-01	Gp4	g.chr10:134511411C>T	Silent	INPP5A	p.D154D	inositol polyphosphate-5	68 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr10:134595414C>G	Missense Mutation	INPP5A	p.A403G	inositol polyphosphate-5	58 (0.00)	116 (0.17)	0.46
12-01	Gp4	g.chr1:38341328C>T	Missense Mutation	INPP5B	p.D580N	inositol polyphosphate-5	142 (0.00)	30 (0.23)	0.62
12-01	Gp4	g.chr1:156814916C>T	Missense Mutation	INSRR	p.V797M	insulin receptor-related r	16 (0.00)	14 (0.71)	1.90
12-01	Gp4	g.chr7:1539625G>T	Silent	INTS1	p.S193S	integrator complex subu	57 (0.00)	136 (0.22)	0.59
12-01	Gp4	g.chr7:1539838G>T	Missense Mutation	INTS1	p.P172T	integrator complex subu	17 (0.00)	22 (0.64)	1.70
12-01	Gp4	g.chr7:1539973C>G	Missense Mutation	INTS1	p.E127Q	integrator complex subu	22 (0.00)	30 (0.63)	1.69
12-01	Gp4	g.chr6:33703133T>C	Missense Mutation	IP6K3	p.K41E	inositol hexakisphospha	102 (0.00)	30 (0.27)	0.71
12-01	Gp4	g.chr14:24652863C>T	Missense Mutation	IPO4	p.E666K	importin 4	76 (0.01)	49 (0.29)	0.76
12-01	Gp4	g.chr2:237240106G>A	Nonsense Mutation	IQCA1	p.Q757*	IQ motif containing with	75 (0.01)	41 (0.15)	0.39
12-01	Gp4	g.chr1:156524042C>A	Missense Mutation	IQGAP3	p.G478V	IQ motif containing GT	232 (0.00)	120 (0.44)	1.18
12-01	Gp4	g.chr3:10242180G>C	Missense Mutation	IRAK2	p.M135I	interleukin-1 receptor-as	111 (0.00)	79 (0.24)	0.64
12-01	Gp4	g.chr2:227663199G>T	Missense Mutation	IRS1	p.L86I	insulin receptor substrat	101 (0.00)	65 (0.20)	0.53
12-01	Gp4	g.chr16:313345G>T	Silent	ITFG3	p.L352L	integrin alpha FG-GAP	81 (0.00)	68 (0.31)	0.82
12-01	Gp4	g.chr16:313357G>T	Missense Mutation	ITFG3	p.Q356H	integrin alpha FG-GAP	76 (0.00)	62 (0.15)	0.39
12-01	Gp4	g.chr17:48165116G>T	Silent	ITGA3	p.V976V	integrin, alpha 3 (antigen	15 (0.00)	103 (0.74)	1.97
12-01	Gp4	g.chr2:173344450G>A	Silent	ITGA6	p.G490G	integrin, alpha 6	203 (0.00)	28 (0.75)	2.00
12-01	Gp4	g.chr12:56088645C>T	Missense Mutation	ITGA7	p.G709R	integrin, alpha 7	24 (0.00)	57 (0.16)	0.42
12-01	Gp4	g.chr10:15760847G>T	Silent	ITGA8	p.I87I	integrin, alpha 8	107 (0.00)	31 (0.29)	0.77
12-01	Gp4	g.chr16:30500650G>A	Missense Mutation	ITGAL	p.D386N	integrin, alpha L (antige	169 (0.00)	222 (0.79)	2.10
12-01	Gp4	g.chr16:31374362G>T	Missense Mutation	ITGAX	p.G489V	integrin, alpha X (comp	39 (0.00)	28 (0.93)	2.48
12-01	Gp4	g.chr16:31374687C>A	Missense Mutation	ITGAX	p.H568N	integrin, alpha X (comp	25 (0.00)	75 (0.67)	1.78
12-01	Gp4	g.chr17:45360756G>T	Nonsense Mutation	ITGB3	p.E68*	integrin, beta 3 (platelet	157 (0.00)	43 (0.53)	1.43

12-01	Gp4	g.chr17:45360782C>A	Missense Mutation	ITGB3	p.P65T	integrin, beta 3 (platelet	142 (0.00)	41 (0.37)	0.98
12-01	Gp4	g.chr17:73720822C>G	Silent	ITGB4	p.L13L	integrin, beta 4	48 (0.00)	33 (0.82)	2.18
12-01	Gp4	g.chr13:102345046G>T	Missense Mutation	ITGBL1	p.C376F	integrin, beta-like 1 (wit	33 (0.00)	36 (0.97)	2.59
12-01	Gp4	g.chr3:4735230G>A	Silent	ITPR1	p.Q1347Q	inositol 1,4,5-trisphosph	57 (0.00)	302 (0.31)	0.83
12-01	Gp4	g.chr3:4777015G>C	Missense Mutation	ITPR1	p.E1826Q	inositol 1,4,5-trisphosph	160 (0.00)	32 (0.16)	0.42
12-01	Gp4	g.chr6:33632693C>G	Missense Mutation	ITPR3	p.Q399E	inositol 1,4,5-trisphosph	42 (0.00)	71 (0.69)	1.84
12-01	Gp4	g.chr21:35144397G>A	Missense Mutation	ITSN1	p.E359K	intersectin 1 (SH3 doma	155 (0.00)	113 (0.20)	0.54
12-01	Gp4	g.chr20:10620269C>T	Silent	JAG1	p.L1178L	jagged 1	257 (0.00)	84 (0.93)	2.48
12-01	Gp4	g.chr19:17945438C>A	Silent	JAK3	p.P764P	Janus kinase 3	49 (0.00)	52 (0.52)	1.38
12-01	Gp4	g.chr4:6066665G>A	Missense Mutation	JAKMIP1	p.S458F	janus kinase and microt	16 (0.00)	81 (0.84)	2.24
12-01	Gp4	g.chr10:133978212G>A	Silent	JAKMIP3	p.K819K	Janus kinase and microt	119 (0.00)	160 (0.16)	0.42
12-01	Gp4	g.chr14:59970655C>G	Silent	JKAMP	p.S267S	JNK1/MAPK8-associat	24 (0.00)	11 (0.82)	2.18
12-01	Gp4	g.chr9:711775C>T	Missense Mutation	KANK1	p.R337W	KN motif and ankyrin r	113 (0.00)	222 (0.17)	0.44
12-01	Gp4	g.chr12:49065621G>A	Nonsense Mutation	KANSL2	p.R224*	KAT8 regulatory NSL c	354 (0.00)	21 (0.38)	1.02
12-01	Gp4	g.chr12:49075351G>A	Missense Mutation	KANSL2	p.S22F	KAT8 regulatory NSL c	80 (0.01)	87 (0.20)	0.52
12-01	Gp4	g.chr16:31141380G>A	Missense Mutation	KAT8	p.D272N	K(lysine) acetyltransfer	149 (0.00)	166 (0.53)	1.41
12-01	Gp4	g.chr22:24057376G>T	RNA	KB-1572G7.2			54 (0.00)	107 (0.19)	0.50
12-01	Gp4	g.chr13:41705742G>T	Silent	KBTBD6	p.R302R	kelch repeat and BTB (	191 (0.00)	15 (0.53)	1.42
12-01	Gp4	g.chr13:41767330G>A	Missense Mutation	KBTBD7	p.P355L	kelch repeat and BTB (	200 (0.01)	166 (0.40)	1.06
12-01	Gp4	g.chr13:41768210G>T	Missense Mutation	KBTBD7	p.L62M	kelch repeat and BTB (	51 (0.00)	16 (0.50)	1.33
12-01	Gp4	g.chr11:30034154C>A	Missense Mutation	KCNA4	p.Q24H	potassium voltage-gated	96 (0.00)	132 (0.15)	0.40
12-01	Gp4	g.chr7:119914831G>A	Missense Mutation	KCND2	p.G49S	potassium voltage-gated	215 (0.00)	72 (0.58)	1.56
12-01	Gp4	g.chr2:223917781G>A	Missense Mutation	KCNE4	p.R129Q	potassium voltage-gated	111 (0.00)	103 (0.24)	0.65
12-01	Gp4	g.chr12:49944024C>A	Silent	KCNH3	p.I610I	potassium voltage-gated	105 (0.00)	36 (0.31)	0.81
12-01	Gp4	g.chr2:155555618G>A	Missense Mutation	KCNJ3	p.D111N	potassium inwardly-rect	29 (0.00)	138 (0.78)	2.09
12-01	Gp4	g.chr6:39159201C>A	Missense Mutation	KCNK5	p.G322V	potassium channel, subf	63 (0.02)	131 (0.49)	1.30
12-01	Gp4	g.chr20:62065176G>T	Silent	KCNQ2	p.T368T	potassium voltage-gated	63 (0.00)	254 (0.29)	0.78
12-01	Gp4	g.chr20:43723847G>T	Silent	KCNS1	p.G415G	potassium voltage-gated	70 (0.00)	52 (0.19)	0.51
12-01	Gp4	g.chr9:138676699C>T	Silent	KCNT1	p.I1040I	potassium channel, subf	102 (0.00)	132 (0.17)	0.46
12-01	Gp4	g.chr8:36694435C>A	Missense Mutation	KCNU1	p.T497K	potassium channel, subf	37 (0.00)	21 (0.29)	0.76
12-01	Gp4	g.chr9:2718265C>T	Silent	KCNV2	p.L176L	potassium channel, subf	39 (0.00)	103 (0.20)	0.54
12-01	Gp4	g.chr11:67017668C>A	Missense Mutation	KDM2A	p.L723M	lysine (K)-specific dem	51 (0.00)	60 (0.40)	1.07
12-01	Gp4	g.chr12:121877717G>T	Missense Mutation	KDM2B	p.L1258M	lysine (K)-specific dem	20 (0.00)	51 (0.16)	0.42
12-01	Gp4	g.chr12:121880349C>A	Silent	KDM2B	p.L965L	lysine (K)-specific dem	47 (0.00)	32 (0.38)	1.00
12-01	Gp4	g.chr1:44137344G>A	Missense Mutation	KDM4A	p.S511N	lysine (K)-specific dem	92 (0.00)	127 (0.65)	1.74

12-01	Gp4	g.chrY:21871395C>G	Missense Mutation	KDM5D	p.E962Q	lysine (K)-specific dem	68 (0.00)	36 (0.36)	0.60
12-01	Gp4	g.chr19:10602816C>A	Missense Mutation	KEAP1	p.K254N	kelch-like ECH-associat	20 (0.00)	29 (0.55)	1.47
12-01	Gp4	g.chr17:26960924T>A	Missense Mutation	KIAA0100	p.H1084L	KIAA0100	206 (0.00)	218 (0.14)	0.38
12-01	Gp4	g.chr3:197409461G>T	Missense Mutation	KIAA0226	p.P669H	KIAA0226	34 (0.00)	52 (0.27)	0.72
12-01	Gp4	g.chr3:197411072C>A	Missense Mutation	KIAA0226	p.R601S	KIAA0226	375 (0.00)	50 (0.90)	2.40
12-01	Gp4	g.chr3:197411073C>G	Missense Mutation	KIAA0226	p.R601T	KIAA0226	376 (0.00)	50 (0.90)	2.40
12-01	Gp4	g.chr6:24570198C>A	Missense Mutation	KIAA0319	p.A642S	KIAA0319	157 (0.00)	112 (0.24)	0.64
12-01	Gp4	g.chr1:35900546G>T	Silent	KIAA0319L	p.P1033P	KIAA0319-like	24 (0.00)	56 (0.46)	1.24
12-01	Gp4	g.chr4:154504783C>A	Missense Mutation	KIAA0922	p.S340Y	KIAA0922	15 (0.00)	21 (0.67)	1.78
12-01	Gp4	g.chr22:45601572G>T	Missense Mutation	KIAA0930	p.T118N	KIAA0930	41 (0.02)	35 (0.46)	1.22
12-01	Gp4	g.chr7:141364773T>C	Missense Mutation	KIAA1147	p.D345G	KIAA1147	121 (0.00)	76 (0.14)	0.39
12-01	Gp4	g.chr5:175786508C>A	Missense Mutation	KIAA1191	p.A2S	KIAA1191	52 (0.00)	92 (0.84)	2.23
12-01	Gp4	g.chr2:99449372G>C	Missense Mutation	KIAA1211L	p.R110G	KIAA1211-like	121 (0.00)	25 (0.96)	2.56
12-01	Gp4	g.chr10:24790385G>C	Missense Mutation	KIAA1217	p.G321R	KIAA1217	53 (0.00)	135 (0.20)	0.53
12-01	Gp4	g.chr6:138649248G>T	Missense Mutation	KIAA1244	p.D1698Y	KIAA1244	55 (0.00)	21 (0.81)	2.16
12-01	Gp4	g.chr10:30315979G>C	Missense Mutation	KIAA1462	p.P1033R	KIAA1462	95 (0.00)	338 (0.23)	0.61
12-01	Gp4	g.chr11:33564204T>A	Silent	KIAA1549L	p.L68L	KIAA1549-like	167 (0.01)	101 (0.34)	0.90
12-01	Gp4	g.chr10:118704478A>G	Missense Mutation	KIAA1598	p.L223P	KIAA1598	38 (0.00)	71 (0.15)	0.41
12-01	Gp4	g.chr10:118704485G>A	Silent	KIAA1598	p.L221L	KIAA1598	41 (0.00)	79 (0.96)	2.57
12-01	Gp4	g.chr19:18375564G>T	Missense Mutation	KIAA1683	p.P929H	KIAA1683	16 (0.00)	16 (0.50)	1.33
12-01	Gp4	g.chr20:36841588C>A	Missense Mutation	KIAA1755	p.L1153F	KIAA1755	49 (0.00)	87 (0.28)	0.74
12-01	Gp4	g.chr9:115380721A>T	Missense Mutation	KIAA1958	p.Y581F	KIAA1958	201 (0.00)	61 (0.28)	0.74
12-01	Gp4	g.chr9:116859896G>A	Silent	KIF12	p.Y29Y	kinesin family member	57 (0.00)	63 (0.97)	2.58
12-01	Gp4	g.chr6:17764413C>A	Missense Mutation	KIF13A	p.Q1782H	kinesin family member	49 (0.00)	103 (0.19)	0.52
12-01	Gp4	g.chr8:28974376C>T	Missense Mutation	KIF13B	p.R1270K	kinesin family member	94 (0.00)	122 (0.95)	2.54
12-01	Gp4	g.chr6:168440757C>A	Missense Mutation	KIF25	p.S169R	kinesin family member	62 (0.00)	48 (0.48)	1.28
12-01	Gp4	g.chr1:245847643G>T	Silent	KIF26B	p.L789L	kinesin family member	17 (0.00)	58 (0.17)	0.46
12-01	Gp4	g.chr1:245849618C>G	Silent	KIF26B	p.S1111S	kinesin family member	63 (0.00)	142 (0.18)	0.47
12-01	Gp4	g.chr2:26204495G>C	Missense Mutation	KIF3C	p.Q98E	kinesin family member	124 (0.00)	20 (0.60)	1.60
12-01	Gp4	g.chr10:32344791G>C	Missense Mutation	KIF5B	p.D37E	kinesin family member	22 (0.00)	23 (0.96)	2.55
12-01	Gp4	g.chr2:149868143C>A	Silent	KIF5C	p.R943R	kinesin family member	234 (0.00)	107 (0.21)	0.55
12-01	Gp4	g.chr2:149868162C>A	Missense Mutation	KIF5C	p.S949Y	kinesin family member	122 (0.00)	94 (0.66)	1.76
12-01	Gp4	g.chr1:158064860C>A	Missense Mutation	KIRREL	p.H556N	kin of IRRE like (Droso	19 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr19:36352045C>A	Missense Mutation	KIRREL2	p.L360M	kin of IRRE like 2 (Dro	25 (0.00)	42 (0.38)	1.02
12-01	Gp4	g.chr19:36355562C>T	Missense Mutation	KIRREL2	p.H580Y	kin of IRRE like 2 (Dro	31 (0.00)	27 (0.30)	0.79

12-01	Gp4	g.chr3:126071183G>A	Missense Mutation	KLF15	p.P195S	Kruppel-like factor 15	26 (0.00)	16 (0.44)	1.17
12-01	Gp4	g.chr3:47385082C>A	Missense Mutation	KLHL18	p.P459H	kelch-like family memb	133 (0.00)	38 (0.26)	0.70
12-01	Gp4	g.chr22:20796616C>T	Missense Mutation	KLHL22	p.G550D	kelch-like family memb	36 (0.00)	152 (0.38)	1.02
12-01	Gp4	g.chr15:86311695G>A	Silent	KLHL25	p.F449F	kelch-like family memb	116 (0.01)	63 (0.43)	1.14
12-01	Gp4	g.chr8:124664814T>A	Missense Mutation	KLHL38	p.K118M	kelch-like family memb	70 (0.00)	22 (0.59)	1.58
12-01	Gp4	g.chr19:36228072G>T	Missense Mutation	KMT2B	p.Q2486H	lysine (K)-specific meth	34 (0.00)	131 (0.41)	1.10
12-01	Gp4	g.chr12:49421034C>G	Missense Mutation	KMT2D	p.Q4905H	lysine (K)-specific meth	241 (0.00)	36 (0.67)	1.78
12-01	Gp4	g.chr12:49431455T>A	Silent	KMT2D	p.A3228A	lysine (K)-specific meth	36 (0.00)	46 (0.52)	1.39
12-01	Gp4	g.chr12:49432115C>A	Missense Mutation	KMT2D	p.E3008D	lysine (K)-specific meth	95 (0.00)	61 (0.21)	0.57
12-01	Gp4	g.chr12:49438082C>A	Missense Mutation	KMT2D	p.G1697C	lysine (K)-specific meth	56 (0.00)	39 (0.21)	0.55
12-01	Gp4	g.chr19:47986586C>A	Missense Mutation	KPTN	p.E120D	kaptin (actin binding pr	41 (0.00)	109 (0.18)	0.49
12-01	Gp4	g.chr17:39023105T>C	Missense Mutation	KRT12	p.I112V	keratin 12	467 (0.00)	16 (0.31)	0.83
12-01	Gp4	g.chr17:39502471C>G	Missense Mutation	KRT33A	p.C372S	keratin 33A	193 (0.00)	110 (0.97)	2.59
12-01	Gp4	g.chr17:39578538C>A	Missense Mutation	KRT37	p.W294L	keratin 37	139 (0.00)	176 (0.38)	1.02
12-01	Gp4	g.chr12:52863639C>A	Missense Mutation	KRT6C	p.E413D	keratin 6C	86 (0.00)	28 (0.36)	0.95
12-01	Gp4	g.chr12:53170963C>A	Missense Mutation	KRT76	p.G38V	keratin 76	92 (0.00)	210 (0.48)	1.28
12-01	Gp4	g.chr12:53233610C>A	Silent	KRT78	p.T402T	keratin 78	147 (0.00)	56 (0.30)	0.81
12-01	Gp4	g.chr12:53227700C>A	Missense Mutation	KRT79	p.Q115H	keratin 79	46 (0.00)	59 (0.24)	0.63
12-01	Gp4	g.chr12:52567401C>G	Missense Mutation	KRT80	p.A272P	keratin 80	61 (0.00)	38 (0.29)	0.77
12-01	Gp4	g.chr12:52695720G>A	Missense Mutation	KRT86	p.C7Y	keratin 86	140 (0.00)	72 (0.26)	0.70
12-01	Gp4	g.chr17:39197554G>A	Silent	KRTAP1-1	p.T32T	keratin associated protei	63 (0.00)	175 (0.98)	2.61
12-01	Gp4	g.chr21:46117767C>A	Silent	KRTAP10-12	p.P217P	keratin associated protei	83 (0.00)	62 (0.35)	0.95
12-01	Gp4	g.chr21:46021588G>T	Missense Mutation	KRTAP10-7	p.R356L	keratin associated protei	93 (0.00)	51 (0.16)	0.42
12-01	Gp4	g.chr21:46032355C>A	Missense Mutation	KRTAP10-8	p.P113H	keratin associated protei	110 (0.00)	234 (0.16)	0.43
12-01	Gp4	g.chr21:46047178C>A	Silent	KRTAP10-9	p.P30P	keratin associated protei	31 (0.00)	83 (0.16)	0.42
12-01	Gp4	g.chr21:46086467C>A	Missense Mutation	KRTAP12-2	p.V113F	keratin associated protei	102 (0.00)	129 (0.40)	1.05
12-01	Gp4	g.chr21:32127545C>G	Missense Mutation	KRTAP21-1	p.G51A	keratin associated protei	61 (0.00)	93 (0.95)	2.52
12-01	Gp4	g.chr21:31973565T>C	Silent	KRTAP22-1	p.S42S	keratin associated protei	82 (0.00)	20 (0.50)	1.33
12-01	Gp4	g.chr17:39316477T>C	Missense Mutation	KRTAP4-4	p.Y156C	keratin associated protei	99 (0.00)	96 (0.16)	0.42
12-01	Gp4	g.chr11:71276967G>T	Missense Mutation	KRTAP5-10	p.G112W	keratin associated protei	92 (0.00)	43 (0.16)	0.43
12-01	Gp4	g.chr11:71293483G>T	Missense Mutation	KRTAP5-11	p.S134Y	keratin associated protei	128 (0.00)	86 (0.26)	0.68
12-01	Gp4	g.chr11:1718786G>T	Missense Mutation	KRTAP5-6	p.C104F	keratin associated protei	153 (0.00)	148 (0.41)	1.08
12-01	Gp4	g.chr17:39388899C>G	Missense Mutation	KRTAP9-3	p.P49R	keratin associated protei	67 (0.00)	248 (0.57)	1.52
12-01	Gp4	g.chrX:153130125C>T	Silent	L1CAM	p.A1027A	L1 cell adhesion molecu	92 (0.01)	153 (0.26)	0.44
12-01	Gp4	g.chr22:41605757G>A	Missense Mutation	L3MBTL2	p.G28S	l(3)mbt-like 2 (Drosoph	91 (0.00)	129 (0.51)	1.36

12-01	Gp4	g.chr22:41625645C>A	Missense Mutation	L3MBTL2	p.P664T	l(3)mbt-like 2 (Drosoph	53 (0.00)	110 (0.19)	0.51
12-01	Gp4	g.chr1:201356225G>T	Silent	LAD1	p.I88I	ladinin 1	17 (0.00)	30 (0.23)	0.62
12-01	Gp4	g.chr12:6884591G>A	Missense Mutation	LAG3	p.D312N	lymphocyte-activation g	40 (0.00)	17 (0.88)	2.35
12-01	Gp4	g.chr18:21427476G>T	Missense Mutation	LAMA3	p.R1327L	laminin, alpha 3	60 (0.00)	18 (0.28)	0.74
12-01	Gp4	g.chr18:21464765G>T	Nonsense Mutation	LAMA3	p.G1751*	laminin, alpha 3	64 (0.00)	155 (0.41)	1.08
12-01	Gp4	g.chr20:60888053C>G	Missense Mutation	LAMA5	p.C2990S	laminin, alpha 5	20 (0.00)	16 (0.94)	2.50
12-01	Gp4	g.chr20:60902686C>A	Missense Mutation	LAMA5	p.G1613W	laminin, alpha 5	64 (0.00)	42 (0.38)	1.02
12-01	Gp4	g.chr7:107605018C>A	Silent	LAMB1	p.A559A	laminin, beta 1	226 (0.00)	66 (0.53)	1.41
12-01	Gp4	g.chr7:107605071C>A	Nonsense Mutation	LAMB1	p.E542*	laminin, beta 1	174 (0.00)	50 (0.38)	1.01
12-01	Gp4	g.chr3:49169089C>A	Missense Mutation	LAMB2	p.R176L	laminin, beta 2 (laminin	55 (0.00)	125 (0.22)	0.58
12-01	Gp4	g.chr9:133911586C>A	Silent	LAMC3	p.G281G	laminin, gamma 3	40 (0.00)	43 (0.63)	1.67
12-01	Gp4	g.chr16:28997042G>T	Missense Mutation	LAT	p.D73Y	linker for activation of	157 (0.00)	88 (0.55)	1.45
12-01	Gp4	g.chr2:30546398C>T	Missense Mutation	LBH	p.P48L	limb bud and heart deve	202 (0.00)	42 (0.31)	0.83
12-01	Gp4	g.chr16:67973905G>T	Missense Mutation	LCAT	p.L409M	lecithin-cholesterol acyl	163 (0.00)	157 (0.15)	0.39
12-01	Gp4	g.chr9:139640340A>G	Missense Mutation	LCN6	p.M76T	lipocalin 6	40 (0.00)	46 (0.22)	0.58
12-01	Gp4	g.chr2:136594327G>T	Missense Mutation	LCT	p.A138D	lactase	64 (0.00)	29 (0.62)	1.66
12-01	Gp4	g.chr15:66853625T>C	Missense Mutation	LCTL	p.Q170R	lactase-like	254 (0.00)	21 (0.24)	0.63
12-01	Gp4	g.chr4:1817448C>G	Silent	LETM1	p.L671L	leucine zipper-EF-hand	31 (0.00)	146 (0.90)	2.39
12-01	Gp4	g.chr7:103969564G>T	Missense Mutation	LHFPL3	p.G99C	lipoma HMGIC fusion	221 (0.00)	252 (0.29)	0.78
12-01	Gp4	g.chr9:124971908G>T	Silent	LHX6	p.S381S	LIM homeobox 6	104 (0.00)	49 (0.55)	1.47
12-01	Gp4	g.chr19:55220820G>T	RNA	LILRP2		leukocyte immunoglobu	45 (0.00)	75 (0.27)	0.71
12-01	Gp4	g.chr4:41648511A>T	Missense Mutation	LIMCH1	p.R263S	LIM and calponin homo	107 (0.00)	28 (0.96)	2.57
12-01	Gp4	g.chr7:73511451C>A	Nonsense Mutation	LIMK1	p.C141*	LIM domain kinase 1	21 (0.00)	147 (0.15)	0.40
12-01	Gp4	g.chr7:73526308C>A	Missense Mutation	LIMK1	p.H494N	LIM domain kinase 1	44 (0.00)	19 (0.63)	1.68
12-01	Gp4	g.chr9:136893736G>C	RNA	LINC00094		long intergenic non-prot	37 (0.00)	40 (0.35)	0.93
12-01	Gp4	g.chr12:116972554G>A	RNA	LINC00173		long intergenic non-prot	124 (0.01)	46 (0.39)	1.04
12-01	Gp4	g.chr21:46713421G>T	lincRNA	LINC00205		long intergenic non-prot	30 (0.00)	88 (0.77)	2.06
12-01	Gp4	g.chr13:51660161G>T	lincRNA	LINC00371		long intergenic non-prot	31 (0.00)	39 (0.38)	1.03
12-01	Gp4	g.chr13:51660307G>T	lincRNA	LINC00371		long intergenic non-prot	38 (0.00)	30 (0.33)	0.89
12-01	Gp4	g.chr14:101138472G>T	lincRNA	LINC00523		long intergenic non-prot	79 (0.00)	135 (0.52)	1.38
12-01	Gp4	g.chr14:48238932A>G	lincRNA	LINC00648		long intergenic non-prot	27 (0.00)	23 (0.22)	0.58
12-01	Gp4	g.chr3:106824178C>T	lincRNA	LINC00882		long intergenic non-prot	68 (0.00)	75 (0.83)	2.20
12-01	Gp4	g.chr22:48025157C>T	lincRNA	LINC00898		long intergenic non-prot	33 (0.00)	114 (0.79)	2.11
12-01	Gp4	g.chr15:80588214G>T	lincRNA	LINC00927		long intergenic non-prot	22 (0.00)	18 (0.39)	1.04
12-01	Gp4	g.chr1:156104716G>A	Missense Mutation	LMNA	p.D254N	lamin A/C	95 (0.00)	350 (0.47)	1.26

12-01	Gp4	g.chr7:97822238G>A	Missense Mutation	LMTK2	p.E821K	lemur tyrosine kinase 2	41 (0.00)	68 (0.25)	0.67
12-01	Gp4	g.chr18:44063569C>T	Missense Mutation	LOXHD1	p.E997K	lipoxygenase homology	239 (0.00)	29 (0.24)	0.64
12-01	Gp4	g.chr18:44109173T>C	Silent	LOXHD1	p.S388S	lipoxygenase homology	209 (0.00)	223 (0.19)	0.50
12-01	Gp4	g.chr15:74235209G>T	Missense Mutation	LOXL1	p.V373F	lysyl oxidase-like 1	382 (0.00)	197 (0.59)	1.58
12-01	Gp4	g.chr8:23186055G>T	Silent	LOXL2	p.G330G	lysyl oxidase-like 2	150 (0.00)	28 (0.36)	0.95
12-01	Gp4	g.chr19:14266250A>G	Missense Mutation	LPHN1	p.V1077A	latrophilin 1	59 (0.00)	33 (0.36)	0.97
12-01	Gp4	g.chr18:2920423C>A	Silent	LPIN2	p.L853L	lipin 2	43 (0.00)	39 (0.15)	0.41
12-01	Gp4	g.chr20:39974517C>A	Missense Mutation	LPIN3	p.A25D	lipin 3	122 (0.01)	93 (0.24)	0.63
12-01	Gp4	g.chr4:151236723A>T	Missense Mutation	LRBA	p.D2561E	LPS-responsive vesicle	35 (0.00)	17 (0.41)	1.10
12-01	Gp4	g.chr19:36430821A>T	Missense Mutation	LRFN3	p.Y165F	leucine rich repeat and f	44 (0.00)	39 (0.15)	0.41
12-01	Gp4	g.chr10:85992155C>A	Missense Mutation	LRIT1	p.G467V	leucine-rich repeat, imm	56 (0.00)	49 (0.14)	0.38
12-01	Gp4	g.chr4:3521914A>G	Missense Mutation	LRPAP1	p.L119S	low density lipoprotein	89 (0.00)	41 (0.98)	2.60
12-01	Gp4	g.chr8:145745638G>C	Missense Mutation	LRRC14	p.V116L	leucine rich repeat conta	224 (0.00)	343 (0.40)	1.06
12-01	Gp4	g.chr8:145745872C>T	Missense Mutation	LRRC14	p.R194W	leucine rich repeat conta	25 (0.00)	112 (0.19)	0.50
12-01	Gp4	g.chr3:194080696G>T	Missense Mutation	LRRC15	p.N359K	leucine rich repeat conta	93 (0.00)	153 (0.14)	0.38
12-01	Gp4	g.chr10:134165126C>A	Silent	LRRC27	p.S314S	leucine rich repeat conta	203 (0.00)	230 (0.17)	0.45
12-01	Gp4	g.chr21:45876542C>A	Silent	LRRC3	p.R5R	leucine rich repeat conta	29 (0.00)	46 (0.24)	0.64
12-01	Gp4	g.chr21:45876658G>T	Missense Mutation	LRRC3	p.G44V	leucine rich repeat conta	16 (0.00)	39 (0.15)	0.41
12-01	Gp4	g.chr18:29304956C>A	RNA	LRRC37A7P		leucine rich repeat conta	16 (0.00)	11 (0.55)	1.45
12-01	Gp4	g.chr17:45913795C>G	Missense Mutation	LRRC46	p.S183R	leucine rich repeat conta	76 (0.01)	114 (0.47)	1.26
12-01	Gp4	g.chr7:150034430C>A	Silent	LRRC61	p.I160I	leucine rich repeat conta	113 (0.00)	183 (0.32)	0.85
12-01	Gp4	g.chr9:131670277C>A	Silent	LRRC8A	p.I278I	leucine rich repeat conta	238 (0.00)	126 (0.21)	0.57
12-01	Gp4	g.chr19:7963706G>A	Missense Mutation	LRRC8E	p.S100N	leucine rich repeat conta	160 (0.00)	42 (0.19)	0.51
12-01	Gp4	g.chr3:169539907G>A	Silent	LRRIQ4	p.E66E	leucine-rich repeats and	312 (0.00)	60 (0.52)	1.38
12-01	Gp4	g.chr15:101523787C>A	Missense Mutation	LRRK1	p.L106I	leucine-rich repeat kinas	215 (0.00)	34 (0.82)	2.20
12-01	Gp4	g.chr1:204587243C>G	Silent	LRRN2	p.G626G	leucine rich repeat neur	47 (0.00)	104 (0.15)	0.41
12-01	Gp4	g.chr1:204588896G>T	Silent	LRRN2	p.L75L	leucine rich repeat neur	126 (0.00)	207 (0.21)	0.57
12-01	Gp4	g.chr10:68687910C>A	Silent	LRRTM3	p.A412A	leucine rich repeat trans	167 (0.00)	41 (0.59)	1.56
12-01	Gp4	g.chr21:47615649G>T	Silent	LSS	p.T586T	lanosterol synthase (2,3-	114 (0.00)	120 (0.21)	0.56
12-01	Gp4	g.chr9:12775726C>A	Missense Mutation	LURAP1L	p.S4R	leucine rich adaptor pro	91 (0.00)	64 (0.66)	1.75
12-01	Gp4	g.chr8:144102384G>A	Missense Mutation	LY6E	p.A10T	lymphocyte antigen 6 c	41 (0.00)	24 (0.21)	0.56
12-01	Gp4	g.chr12:69742241G>A	Missense Mutation	LYZ	p.G18D	lysozyme	40 (0.00)	18 (0.28)	0.74
12-01	Gp4	g.chr8:20110307C>A	Nonsense Mutation	LZTS1	p.E379*	leucine zipper, putative	73 (0.00)	51 (0.16)	0.42
12-01	Gp4	g.chr19:35800857C>A	Missense Mutation	MAG	p.P438T	myelin associated glyco	17 (0.00)	40 (0.50)	1.33
12-01	Gp4	g.chr7:77650450G>T	Intron	MAGI2		membrane associated gu	262 (0.00)	11 (0.45)	1.21

12-01	Gp4	g.chr7:77670385G>T	Intron	MAGI2		membrane associated gu	69 (0.00)	21 (0.43)	1.14
12-01	Gp4	g.chr7:77753619A>G	Intron	MAGI2		membrane associated gu	149 (0.00)	74 (0.27)	0.72
12-01	Gp4	g.chr7:77788641C>T	Intron	MAGI2		membrane associated gu	95 (0.00)	13 (0.46)	1.23
12-01	Gp4	g.chr7:77809383A>T	Intron	MAGI2		membrane associated gu	56 (0.00)	20 (0.40)	1.07
12-01	Gp4	g.chr7:77817116C>T	Intron	MAGI2		membrane associated gu	33 (0.00)	55 (0.98)	2.62
12-01	Gp4	g.chr7:77892234C>A	Intron	MAGI2		membrane associated gu	39 (0.00)	37 (0.43)	1.15
12-01	Gp4	g.chr7:77974777C>T	Intron	MAGI2		membrane associated gu	67 (0.00)	31 (0.19)	0.52
12-01	Gp4	g.chr7:77975855G>T	Intron	MAGI2		membrane associated gu	117 (0.00)	47 (0.96)	2.55
12-01	Gp4	g.chr7:78019114C>A	Intron	MAGI2		membrane associated gu	51 (0.00)	136 (0.80)	2.14
12-01	Gp4	g.chr7:78096946G>A	Intron	MAGI2		membrane associated gu	21 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr7:78415978C>T	Intron	MAGI2		membrane associated gu	340 (0.00)	337 (0.24)	0.64
12-01	Gp4	g.chr7:78442911C>A	Intron	MAGI2		membrane associated gu	65 (0.00)	68 (0.44)	1.18
12-01	Gp4	g.chr7:78445273G>A	Intron	MAGI2		membrane associated gu	41 (0.00)	29 (0.76)	2.02
12-01	Gp4	g.chr7:78528899G>T	Intron	MAGI2		membrane associated gu	49 (0.00)	45 (0.96)	2.55
12-01	Gp4	g.chr7:78532811G>T	Intron	MAGI2		membrane associated gu	68 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr7:78619915T>C	Intron	MAGI2		membrane associated gu	37 (0.00)	135 (0.19)	0.49
12-01	Gp4	g.chr7:78706544C>A	Intron	MAGI2		membrane associated gu	259 (0.00)	190 (0.17)	0.45
12-01	Gp4	g.chr7:78804326C>T	Intron	MAGI2		membrane associated gu	20 (0.00)	40 (0.28)	0.73
12-01	Gp4	g.chr7:78847167T>A	Intron	MAGI2		membrane associated gu	33 (0.00)	39 (0.36)	0.96
12-01	Gp4	g.chr7:78852152G>A	Intron	MAGI2		membrane associated gu	33 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr7:78884244C>G	Intron	MAGI2		membrane associated gu	21 (0.00)	80 (0.49)	1.30
12-01	Gp4	g.chr7:78884275C>T	Intron	MAGI2		membrane associated gu	22 (0.00)	88 (0.36)	0.97
12-01	Gp4	g.chr7:78910719G>A	Intron	MAGI2		membrane associated gu	24 (0.00)	21 (0.90)	2.41
12-01	Gp4	g.chr7:78940079G>A	Intron	MAGI2		membrane associated gu	28 (0.00)	45 (0.98)	2.61
12-01	Gp4	g.chr7:78951047G>T	Intron	MAGI2		membrane associated gu	69 (0.00)	16 (0.31)	0.83
12-01	Gp4	g.chr7:78967307G>A	Intron	MAGI2		membrane associated gu	46 (0.00)	75 (0.88)	2.35
12-01	Gp4	g.chr7:78983836G>C	Intron	MAGI2		membrane associated gu	386 (0.00)	41 (0.39)	1.04
12-01	Gp4	g.chr4:141074103C>A	Missense Mutation	MAML3	p.A127S	mastermind-like 3 (Dros	45 (0.00)	141 (0.38)	1.00
12-01	Gp4	g.chr9:140001711G>T	Missense Mutation	MAN1B1	p.V526L	mannosidase, alpha, cla	27 (0.00)	86 (0.19)	0.50
12-01	Gp4	g.chr15:43821153G>T	Silent	MAP1A	p.V2732V	microtubule-associated	92 (0.00)	209 (0.17)	0.46
12-01	Gp4	g.chr15:43821264C>A	Silent	MAP1A	p.L2769L	microtubule-associated	53 (0.00)	190 (0.19)	0.52
12-01	Gp4	g.chr5:71496153C>A	Missense Mutation	MAP1B	p.A2324D	microtubule-associated	302 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr1:27684746G>T	Nonsense Mutation	MAP3K6	p.C947*	mitogen-activated protei	67 (0.01)	25 (0.40)	1.07
12-01	Gp4	g.chr1:27689968A>G	Silent	MAP3K6	p.H312H	mitogen-activated protei	40 (0.00)	30 (0.70)	1.87
12-01	Gp4	g.chr14:71209168G>T	Missense Mutation	MAP3K9	p.H183Q	mitogen-activated protei	48 (0.00)	16 (0.44)	1.17

12-01	Gp4	g.chr4:156289900C>A	Missense Mutation	MAP9	p.L182F	microtubule-associated	47 (0.00)	49 (0.53)	1.41
12-01	Gp4	g.chr22:50703775C>A	Missense Mutation	MAPK11	p.K330N	mitogen-activated protei	142 (0.00)	35 (0.34)	0.91
12-01	Gp4	g.chr8:144801075G>A	Splice Site	MAPK15	p.K139K	mitogen-activated protei	28 (0.00)	78 (0.14)	0.38
12-01	Gp4	g.chr16:30129005A>G	Missense Mutation	MAPK3	p.L186P	mitogen-activated protei	165 (0.00)	46 (0.20)	0.52
12-01	Gp4	g.chr15:42111838A>G	Missense Mutation	MAPKBP1	p.E824G	mitogen-activated protei	154 (0.00)	136 (0.29)	0.76
12-01	Gp4	g.chr15:42116236G>T	Missense Mutation	MAPKBP1	p.G1397V	mitogen-activated protei	61 (0.00)	161 (0.24)	0.63
12-01	Gp4	g.chr5:126250730T>A	Silent	MARCH3	p.T95T	membrane-associated ri	92 (0.00)	80 (0.79)	2.10
12-01	Gp4	g.chr16:71674893G>T	Missense Mutation	MARVELD3	p.S399I	MARVEL domain conta	52 (0.00)	149 (0.36)	0.95
12-01	Gp4	g.chr1:11103042C>A	Missense Mutation	MASP2	p.G260V	mannan-binding lectin s	100 (0.00)	97 (0.14)	0.38
12-01	Gp4	g.chr1:46497205C>A	Missense Mutation	MAST2	p.N1045K	microtubule associated	34 (0.00)	89 (0.45)	1.20
12-01	Gp4	g.chr5:66459228C>A	Silent	MAST4	p.S1407S	microtubule associated	143 (0.00)	162 (0.28)	0.74
12-01	Gp4	g.chr22:36007029C>A	Missense Mutation	MB	p.G74C	myoglobin	141 (0.00)	179 (0.92)	2.44
12-01	Gp4	g.chr12:57919388G>T	Missense Mutation	MBD6	p.A213S	methyl-CpG binding do	74 (0.00)	17 (0.35)	0.94
12-01	Gp4	g.chr5:112399775G>T	Missense Mutation	MCC	p.L707I	mutated in colorectal ca	80 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr6:90384229C>A	Missense Mutation	MDN1	p.D4281Y	MDN1, midasin homol	97 (0.00)	65 (0.60)	1.60
12-01	Gp4	g.chr6:90405690C>A	Missense Mutation	MDN1	p.Q3135H	MDN1, midasin homol	132 (0.00)	23 (0.61)	1.62
12-01	Gp4	g.chr11:86267666G>T	Missense Mutation	ME3	p.F132L	malic enzyme 3, NADP	112 (0.00)	76 (0.34)	0.91
12-01	Gp4	g.chrX:70350046C>T	Silent	MED12	p.R1343R	mediator complex subu	26 (0.00)	21 (0.33)	0.56
12-01	Gp4	g.chrX:70357789C>A	Missense Mutation	MED12	p.Q2014K	mediator complex subu	64 (0.00)	31 (0.42)	0.70
12-01	Gp4	g.chr17:60040210G>T	Missense Mutation	MED13	p.T1656N	mediator complex subu	107 (0.00)	216 (0.45)	1.21
12-01	Gp4	g.chr19:39882130C>A	Missense Mutation	MED29	p.A44D	mediator complex subu	24 (0.00)	34 (0.47)	1.25
12-01	Gp4	g.chr15:66206204G>A	Missense Mutation	MEGF11	p.L861F	multiple EGF-like-doma	96 (0.00)	12 (0.42)	1.11
12-01	Gp4	g.chr1:3428184G>A	Silent	MEGF6	p.H348H	multiple EGF-like-doma	32 (0.00)	24 (0.88)	2.33
12-01	Gp4	g.chr9:123421791C>T	Missense Mutation	MEGF9	p.G222R	multiple EGF-like-doma	32 (0.00)	62 (0.53)	1.42
12-01	Gp4	g.chr22:42180628C>A	Missense Mutation	MEI1	p.F1062L	meiosis inhibitor 1	101 (0.00)	82 (0.15)	0.39
12-01	Gp4	g.chr22:42190390C>A	Missense Mutation	MEI1	p.S1148Y	meiosis inhibitor 1	191 (0.00)	119 (0.24)	0.63
12-01	Gp4	g.chr9:36589578C>A	Missense Mutation	MELK	p.L64M	maternal embryonic leu	197 (0.00)	134 (0.62)	1.65
12-01	Gp4	g.chr7:100028414C>G	Missense Mutation	MEPCE	p.T258S	methylphosphate cappin	49 (0.00)	39 (0.62)	1.64
12-01	Gp4	g.chr1:171759624C>T	Nonsense Mutation	METTL13	p.Q448*	methyltransferase like 1	47 (0.00)	23 (0.43)	1.16
12-01	Gp4	g.chr14:21458389G>A	Splice Site	METTL17	p.A26T	methyltransferase like 1	59 (0.02)	148 (0.59)	1.59
12-01	Gp4	g.chr16:8738489G>T	Silent	METTL22	p.L362L	methyltransferase like 2	332 (0.00)	214 (0.24)	0.65
12-01	Gp4	g.chr15:82336281C>T	Silent	MEX3B	p.A310A	mex-3 RNA binding fa	87 (0.01)	149 (0.38)	1.02
12-01	Gp4	g.chr15:89448988C>T	Splice Site	MFGE8	p.G229R	milk fat globule-EGF fa	60 (0.00)	156 (0.27)	0.72
12-01	Gp4	g.chr8:8749293G>A	Missense Mutation	MFHAS1	p.R426C	malignant fibrous histi	91 (0.00)	70 (0.14)	0.38
12-01	Gp4	g.chr1:12069657C>G	Missense Mutation	MFN2	p.S693C	mitofusin 2	155 (0.00)	142 (0.43)	1.15

12-01	Gp4	g.chr22:37876276C>A	Missense Mutation	MFNG	p.K122N	MFNG O-fucosylpeptid	54 (0.00)	17 (0.76)	2.04
12-01	Gp4	g.chr16:4731577C>A	Nonsense Mutation	MGRN1	p.Y386*	mahogunin ring finger 1	26 (0.00)	19 (0.53)	1.40
12-01	Gp4	g.chr11:62346066G>T	Nonsense Mutation	MIR3654	p.S376*	microRNA 3654	66 (0.00)	22 (0.36)	0.97
12-01	Gp4	g.chr14:45687505G>A	Missense Mutation	MIS18BP1	p.A941V	MIS18 binding protein	61 (0.00)	26 (0.96)	2.56
12-01	Gp4	g.chr22:40820231G>T	Silent	MKL1	p.A152A	megakaryoblastic leuke	70 (0.00)	308 (0.32)	0.87
12-01	Gp4	g.chr19:2039759C>G	Missense Mutation	MKNK2	p.E417D	MAP kinase interacting	28 (0.00)	60 (0.58)	1.56
12-01	Gp4	g.chr19:2041144G>T	Silent	MKNK2	p.A335A	MAP kinase interacting	136 (0.00)	241 (0.23)	0.62
12-01	Gp4	g.chr22:50523163G>A	Silent	MLC1	p.L57L	megalencephalic leukoe	139 (0.01)	110 (0.18)	0.48
12-01	Gp4	g.chr19:6270703C>A	Missense Mutation	MLLT1	p.G27V	myeloid/lymphoid or mi	32 (0.00)	53 (0.62)	1.66
12-01	Gp4	g.chr10:21962675G>T	Missense Mutation	MLLT10	p.G483V	myeloid/lymphoid or mi	200 (0.00)	57 (0.93)	2.48
12-01	Gp4	g.chr6:168315850G>T	Missense Mutation	MLLT4	p.D761Y	myeloid/lymphoid or mi	202 (0.00)	57 (0.40)	1.08
12-01	Gp4	g.chr6:168352666C>A	Missense Mutation	MLLT4	p.S1537R	myeloid/lymphoid or mi	124 (0.00)	83 (0.20)	0.55
12-01	Gp4	g.chr17:36872641C>G	Missense Mutation	MLLT6	p.P353R	myeloid/lymphoid or mi	68 (0.00)	213 (0.24)	0.65
12-01	Gp4	g.chr16:2258510C>A	Missense Mutation	MLST8	p.S253Y	MTOR associated prote	59 (0.00)	146 (0.45)	1.21
12-01	Gp4	g.chr12:132334465C>A	Missense Mutation	MMP17	p.D441E	matrix metallopeptidase	107 (0.00)	172 (0.15)	0.39
12-01	Gp4	g.chr12:56234665G>T	Splice Site	MMP19	p.G102G	matrix metallopeptidase	92 (0.00)	240 (0.32)	0.86
12-01	Gp4	g.chr18:33831177G>A	Missense Mutation	MOCOS	p.G699S	molybdenum cofactor s	65 (0.00)	15 (0.93)	2.49
12-01	Gp4	g.chr2:74688686C>A	Nonsense Mutation	MOGS	p.E744*	mannosyl-oligosacchari	224 (0.00)	374 (0.17)	0.46
12-01	Gp4	g.chr22:31328363G>T	Missense Mutation	MORC2	p.L942I	MORC family CW-type	70 (0.00)	116 (0.34)	0.90
12-01	Gp4	g.chr22:31328421G>A	Silent	MORC2	p.F922F	MORC family CW-type	62 (0.00)	148 (0.47)	1.24
12-01	Gp4	g.chr22:31330954C>A	Missense Mutation	MORC2	p.Q669H	MORC family CW-type	124 (0.00)	349 (0.36)	0.96
12-01	Gp4	g.chr8:57026131G>T	Silent	MOS	p.I137I	v-mos Moloney murine	138 (0.00)	36 (0.28)	0.74
12-01	Gp4	g.chr7:100210848G>C	Silent	MOSPD3	p.V79V	motile sperm domain co	225 (0.00)	179 (0.22)	0.60
12-01	Gp4	g.chr22:50584204C>G	Missense Mutation	MOV10L1	p.C864W	Mov10 RISC complex	307 (0.00)	438 (0.18)	0.47
12-01	Gp4	g.chr16:135469G>A	Missense Mutation	MPG	p.R197H	N-methylpurine-DNA g	159 (0.00)	128 (0.27)	0.71
12-01	Gp4	g.chr15:75189994G>T	Missense Mutation	MPI	p.G399W	mannose phosphate iso	167 (0.01)	36 (0.47)	1.26
12-01	Gp4	g.chr19:4358087C>A	Missense Mutation	MPND	p.P365H	MPN domain containin	61 (0.00)	52 (0.31)	0.82
12-01	Gp4	g.chr19:4359253G>T	Splice Site	MPND		MPN domain containin	60 (0.00)	69 (0.29)	0.77
12-01	Gp4	g.chr17:41956762C>A	Missense Mutation	MPP2	p.V472L	membrane protein, pal	104 (0.00)	50 (0.76)	0.63
12-01	Gp4	g.chr1:161276204C>T	Missense Mutation	MPZ	p.G167R	myelin protein zero	71 (0.00)	61 (0.23)	0.61
12-01	Gp4	g.chr11:118122982G>T	Missense Mutation	MPZL3	p.R10S	myelin protein zero-like	122 (0.01)	258 (0.19)	0.52
12-01	Gp4	g.chr17:60757223C>A	Missense Mutation	MRC2	p.P753H	mannose receptor, C ty	71 (0.00)	75 (0.35)	0.92
12-01	Gp4	g.chr2:216810376C>G	Missense Mutation	MREG	p.R143P	melanoregulin	85 (0.00)	18 (0.28)	0.74
12-01	Gp4	g.chr11:18955730C>A	Missense Mutation	MRGPRX1	p.R201M	MAS-related GPR, me	89 (0.01)	18 (0.39)	1.04
12-01	Gp4	g.chr8:142444091G>T	RNA	MROH5		maestro heat-like repeat	25 (0.00)	83 (0.71)	1.90

12-01	Gp4	g.chr1:17083969C>A	RNA	MST1L		macrophage stimulating	98 (0.00)	36 (0.17)	0.44
12-01	Gp4	g.chr1:17084158G>T	RNA	MST1L		macrophage stimulating	174 (0.00)	97 (0.72)	1.92
12-01	Gp4	g.chr3:49936678T>C	Missense Mutation	MST1R	p.S417G	macrophage stimulating	35 (0.00)	30 (0.53)	1.42
12-01	Gp4	g.chr1:155582305G>T	Missense Mutation	MSTO1	p.G304W	misato 1, mitochondrial	88 (0.00)	75 (0.56)	1.49
12-01	Gp4	g.chr1:155717686G>C	Missense Mutation	MSTO1	p.G298A	misato 1, mitochondrial	98 (0.00)	56 (0.54)	1.43
12-01	Gp4	g.chr1:26153144G>T	Missense Mutation	MTFR1L	p.S93I	mitochondrial fission re	239 (0.00)	194 (0.45)	1.21
12-01	Gp4	g.chr5:7897191C>T	Missense Mutation	MTRR	p.H595Y	5-methyltetrahydrofolat	43 (0.00)	26 (0.77)	2.05
12-01	Gp4	g.chr13:29599481C>A	Missense Mutation	MTUS2	p.P226T	microtubule associated t	31 (0.00)	70 (0.27)	0.72
12-01	Gp4	g.chr7:100683715C>A	Silent	MUC17	p.T3006T	mucin 17, cell surface a	147 (0.00)	120 (0.47)	1.27
12-01	Gp4	g.chr11:1082692G>T	Missense Mutation	MUC2	p.W647C	mucin 2, oligomeric mu	27 (0.00)	49 (0.31)	0.82
12-01	Gp4	g.chr11:1090342G>T	Missense Mutation	MUC2	p.C1213F	mucin 2, oligomeric mu	34 (0.00)	19 (0.47)	1.26
12-01	Gp4	g.chr11:1093761G>T	Missense Mutation	MUC2	p.Q1860H	mucin 2, oligomeric mu	58 (0.00)	138 (0.48)	1.28
12-01	Gp4	g.chr11:1268151G>T	Silent	MUC5B	p.V3347V	mucin 5B, oligomeric m	179 (0.00)	183 (0.42)	1.12
12-01	Gp4	g.chr11:1269656C>A	Missense Mutation	MUC5B	p.S3849Y	mucin 5B, oligomeric m	255 (0.00)	280 (0.23)	0.61
12-01	Gp4	g.chr21:42749082G>A	Splice Site	MX2	p.M83I	MX dynamin-like GTPa	159 (0.00)	58 (0.33)	0.87
12-01	Gp4	g.chrX:3228421G>T	Nonsense Mutation	MXRA5	p.S2608*	matrix-remodelling asso	35 (0.00)	28 (0.93)	1.55
12-01	Gp4	g.chr20:42320949C>T	Missense Mutation	MYBL2	p.T218M	v-myb avian myeloblast	41 (0.02)	16 (0.38)	1.00
12-01	Gp4	g.chr12:81110968C>A	Missense Mutation	MYF5	p.H42Q	myogenic factor 5	36 (0.00)	75 (0.20)	0.53
12-01	Gp4	g.chr16:15851755C>A	Nonsense Mutation	MYH11	p.E502*	myosin, heavy chain 11,	75 (0.00)	138 (0.37)	0.99
12-01	Gp4	g.chr17:10536025C>A	Missense Mutation	MYH3	p.R1575I	myosin, heavy chain 3,	212 (0.00)	132 (0.37)	0.99
12-01	Gp4	g.chr17:10355767G>A	Missense Mutation	MYH4	p.A1105V	myosin, heavy chain 4,	67 (0.00)	38 (0.74)	1.96
12-01	Gp4	g.chr6:16145171G>A	Missense Mutation	MYLIP	p.D291N	myosin regulatory light	59 (0.00)	47 (0.15)	0.40
12-01	Gp4	g.chr3:123452619C>A	Missense Mutation	MYLK	p.Q408H	myosin light chain kinas	118 (0.00)	55 (0.27)	0.73
12-01	Gp4	g.chr20:30408033G>C	Missense Mutation	MYLK2	p.D53H	myosin light chain kinas	161 (0.00)	308 (0.43)	1.13
12-01	Gp4	g.chr16:30387844C>A	Silent	MYLPF	p.L91L	myosin light chain, phos	65 (0.00)	206 (0.25)	0.66
12-01	Gp4	g.chr5:16694659G>C	Missense Mutation	MYO10	p.F1207L	myosin X	261 (0.00)	69 (0.23)	0.62
12-01	Gp4	g.chr5:16703217T>A	Missense Mutation	MYO10	p.Y776F	myosin X	176 (0.00)	47 (0.45)	1.19
12-01	Gp4	g.chr17:18045521C>A	Silent	MYO15A	p.R1926R	myosin XVA	39 (0.00)	39 (0.15)	0.41
12-01	Gp4	g.chr17:18051389C>A	Missense Mutation	MYO15A	p.H2186N	myosin XVA	98 (0.00)	41 (0.17)	0.46
12-01	Gp4	g.chr17:18054605G>A	Splice Site	MYO15A		myosin XVA	75 (0.00)	65 (0.54)	1.44
12-01	Gp4	g.chr17:18058536C>A	Silent	MYO15A	p.A43A	myosin XVA	99 (0.00)	145 (0.60)	1.60
12-01	Gp4	g.chr17:34857010G>T	Missense Mutation	MYO19	p.P716T	myosin XIX	115 (0.00)	72 (0.46)	1.22
12-01	Gp4	g.chr12:57431694C>A	Missense Mutation	MYO1A	p.L640F	myosin IA	117 (0.01)	107 (0.16)	0.42
12-01	Gp4	g.chr19:8616999C>A	Missense Mutation	MYO1F	p.G185V	myosin IF	169 (0.00)	14 (0.43)	1.14
12-01	Gp4	g.chr11:76867976T>C	Missense Mutation	MYO7A	p.F221L	myosin VIIA	111 (0.00)	204 (0.39)	1.05

12-01	Gp4	g.chr19:17308649G>A	Silent	MYO9B	p.P1365P	myosin IXB	98 (0.00)	167 (0.99)	2.63
12-01	Gp4	g.chr17:12647554C>A	Missense Mutation	MYOCD	p.P258T	myocardin	195 (0.00)	136 (0.40)	1.06
12-01	Gp4	g.chr1:24413144C>A	Silent	MYOM3	p.R596R	myomesin 3	78 (0.00)	76 (0.17)	0.46
12-01	Gp4	g.chr11:61545899G>T	Missense Mutation	MYRF	p.D651Y	myelin regulatory factor	146 (0.00)	26 (0.65)	1.74
12-01	Gp4	g.chr20:62837070C>T	Missense Mutation	MYT1	p.S105L	myelin transcription fac	18 (0.00)	22 (0.45)	1.21
12-01	Gp4	g.chr5:177546686C>G	Silent	N4BP3	p.A34A	NEDD4 binding protein	79 (0.00)	95 (0.21)	0.56
12-01	Gp4	g.chr13:101714339C>A	Missense Mutation	NALCN	p.C1579F	sodium leak channel, no	105 (0.00)	137 (0.34)	0.90
12-01	Gp4	g.chr17:72771825G>T	Missense Mutation	NAT9	p.Q5K	N-acetyltransferase 9 (G	94 (0.00)	109 (0.29)	0.78
12-01	Gp4	g.chr1:201751481C>A	Missense Mutation	NAV1	p.T627K	neuron navigator 1	203 (0.00)	159 (0.21)	0.57
12-01	Gp4	g.chr11:19954747C>A	Silent	NAV2	p.S255S	neuron navigator 2	396 (0.00)	569 (0.18)	0.47
12-01	Gp4	g.chr3:47030865G>C	Missense Mutation	NBEAL2	p.R156P	neurobeachin-like 2	20 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr3:47040873G>T	Missense Mutation	NBEAL2	p.E1204D	neurobeachin-like 2	74 (0.00)	65 (0.20)	0.53
12-01	Gp4	g.chr3:47045779C>T	Missense Mutation	NBEAL2	p.R2032W	neurobeachin-like 2	93 (0.00)	115 (0.23)	0.63
12-01	Gp4	g.chr1:16913567C>T	Silent	NBPF1	p.Q252Q	neuroblastoma breakpoi	174 (0.00)	38 (0.16)	0.42
12-01	Gp4	g.chr7:72639991G>T	RNA	NCF1B		neutrophil cytosolic fact	30 (0.00)	73 (0.22)	0.58
12-01	Gp4	g.chr22:37263442T>C	Missense Mutation	NCF4	p.Y94H	neutrophil cytosolic fact	141 (0.00)	20 (0.25)	0.67
12-01	Gp4	g.chr2:133539713C>A	Missense Mutation	NCKAP5	p.K1557N	NCK-associated protein	212 (0.00)	35 (0.51)	1.37
12-01	Gp4	g.chr12:50188693C>A	Nonsense Mutation	NCKAP5L	p.E984*	NCK-associated protein	24 (0.00)	61 (0.18)	0.48
12-01	Gp4	g.chr2:24985575G>T	Missense Mutation	NCOA1	p.R1362I	nuclear receptor coactiv	321 (0.00)	44 (0.20)	0.55
12-01	Gp4	g.chr20:33329421G>A	Silent	NCOA6	p.L1547L	nuclear receptor coactiv	116 (0.00)	32 (0.97)	2.58
12-01	Gp4	g.chr14:21486660C>G	Missense Mutation	NDRG2	p.E273Q	NDRG family member	35 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr12:95397378A>G	Missense Mutation	NDUFA12	p.F27L	NADH dehydrogenase (	141 (0.00)	46 (0.26)	0.70
12-01	Gp4	g.chr22:42488722G>T	RNA	NDUFA6-AS1		NDUFA6 antisense RN	21 (0.05)	24 (0.25)	0.67
12-01	Gp4	g.chr16:2011233G>T	Missense Mutation	NDUFB10	p.E70D	NADH dehydrogenase (	85 (0.00)	173 (0.18)	0.49
12-01	Gp4	g.chr18:9126888C>A	Silent	NDUFV2	p.I213I	NADH dehydrogenase (	41 (0.00)	86 (0.41)	1.09
12-01	Gp4	g.chr8:11643730C>A	Missense Mutation	NEIL2	p.P316Q	nei endonuclease VIII-li	82 (0.00)	88 (0.51)	1.36
12-01	Gp4	g.chr13:52673885G>T	Silent	NEK5	p.A340A	NIMA-related kinase 5	120 (0.00)	79 (0.97)	2.60
12-01	Gp4	g.chr17:7224213G>A	Silent	NEURL4	p.T1130T	neuralized E3 ubiquitin	162 (0.00)	261 (0.42)	1.11
12-01	Gp4	g.chr1:204957880C>A	Missense Mutation	NFASC	p.Q905K	neurofascin	91 (0.00)	141 (0.89)	2.36
12-01	Gp4	g.chr1:204985623T>C	Missense Mutation	NFASC	p.S1227P	neurofascin	108 (0.00)	76 (0.20)	0.53
12-01	Gp4	g.chr14:24845294C>A	Missense Mutation	NFATC4	p.F744L	nuclear factor of activat	250 (0.00)	198 (0.17)	0.46
12-01	Gp4	g.chr17:46135794C>A	Silent	NFE2L1	p.G359G	nuclear factor, erythroid	210 (0.00)	310 (0.27)	0.73
12-01	Gp4	g.chr4:47880574T>G	Missense Mutation	NFXL1	p.T683P	nuclear transcription fac	34 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr1:41223792G>C	Splice Site	NFYC		nuclear transcription fac	76 (0.00)	22 (0.50)	1.33
12-01	Gp4	g.chr2:233750042C>A	Missense Mutation	NGEF	p.S370I	neuronal guanine nucle	30 (0.00)	46 (0.59)	1.57

12-01	Gp4	g.chr5:177576825G>T	Silent	NHP2	p.A117A	NHP2 ribonucleoprotei	107 (0.00)	129 (0.16)	0.41
12-01	Gp4	g.chr20:25459597G>T	Silent	NINL	p.G721G	ninein-like	84 (0.00)	92 (0.20)	0.52
12-01	Gp4	g.chr15:23052595C>T	Splice Site	NIPA1	p.V160M	non imprinted in Prader-	141 (0.00)	74 (0.46)	1.46
12-01	Gp4	g.chr3:52522112G>T	Silent	NISCH	p.V868V	nischarin	40 (0.00)	40 (0.25)	0.67
12-01	Gp4	g.chr3:52526285C>G	Missense Mutation	NISCH	p.F1434L	nischarin	233 (0.00)	317 (0.25)	0.67
12-01	Gp4	g.chr3:42660563C>A	Missense Mutation	NKTR	p.S62Y	natural killer cell trigge	19 (0.00)	18 (0.94)	2.52
12-01	Gp4	g.chr17:33462450C>A	Silent	NLE1	p.L344L	notchless homolog 1 (D	23 (0.00)	11 (0.64)	1.70
12-01	Gp4	g.chr17:7318084G>T	Missense Mutation	NLGN2	p.G254V	neuroligin 2	172 (0.00)	168 (0.55)	1.46
12-01	Gp4	g.chr16:57060053C>G	Missense Mutation	NLRC5	p.R400G	NLR family, CARD do	131 (0.00)	479 (0.31)	0.84
12-01	Gp4	g.chr16:57095360G>T	Splice Site	NLRC5	p.R1329S	NLR family, CARD do	52 (0.00)	36 (0.22)	0.59
12-01	Gp4	g.chr17:5436178G>T	Missense Mutation	NLRP1	p.A1087D	NLR family, pyrin dom	82 (0.01)	58 (0.31)	0.83
12-01	Gp4	g.chr17:5436192G>T	Silent	NLRP1	p.P1082P	NLR family, pyrin dom	107 (0.00)	106 (0.16)	0.43
12-01	Gp4	g.chr19:54314308G>T	Missense Mutation	NLRP12	p.P202Q	NLR family, pyrin dom	138 (0.00)	211 (0.22)	0.58
12-01	Gp4	g.chr19:56370124C>A	Silent	NLRP4	p.I455I	NLR family, pyrin dom	256 (0.00)	22 (0.27)	0.73
12-01	Gp4	g.chr19:56544013A>G	Silent	NLRP5	p.E771E	NLR family, pyrin dom	117 (0.01)	195 (0.24)	0.64
12-01	Gp4	g.chr11:284592C>G	Silent	NLRP6	p.T830T	NLR family, pyrin dom	25 (0.00)	105 (0.18)	0.48
12-01	Gp4	g.chr11:119053972C>A	Missense Mutation	NLRX1	p.Q918K	NLR family member X1	101 (0.00)	120 (0.24)	0.64
12-01	Gp4	g.chr1:183387378C>G	Missense Mutation	NMNAT2	p.V9L	nicotinamide nucleotide	40 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr2:232389866C>A	Missense Mutation	NMUR1	p.S390I	neuromedin U receptor	38 (0.00)	32 (0.94)	2.50
12-01	Gp4	g.chr7:30491972G>T	Missense Mutation	NOD1	p.P354H	nucleotide-binding olig	33 (0.00)	48 (0.60)	1.61
12-01	Gp4	g.chr9:33469562C>A	Missense Mutation	NOL6	p.G221V	nucleolar protein 6 (RN	50 (0.00)	16 (0.88)	2.33
12-01	Gp4	g.chr16:14951417C>G	Nonsense Mutation	NOMO1	p.Y375*	NODAL modulator 1	291 (0.00)	23 (0.96)	2.55
12-01	Gp4	g.chr16:18544427A>T	Missense Mutation	NOMO2	p.V432D	NODAL modulator 2	46 (0.00)	14 (0.71)	1.90
12-01	Gp4	g.chr12:117681232A>G	Silent	NOS1	p.C978C	nitric oxide synthase 1 (	70 (0.00)	19 (0.84)	2.25
12-01	Gp4	g.chr17:26092655G>T	Silent	NOS2	p.G778G	nitric oxide synthase 2,	21 (0.00)	49 (0.24)	0.65
12-01	Gp4	g.chr1:120458604G>T	Silent	NOTCH2	p.V2247V	notch 2	144 (0.00)	115 (0.37)	1.00
12-01	Gp4	g.chr17:79910956C>A	Missense Mutation	NOTUM	p.G458W	notum pectinacetyleste	47 (0.00)	91 (0.26)	0.70
12-01	Gp4	g.chr19:46457135G>T	Missense Mutation	NOVA2	p.A100D	neuro-oncological ventr	213 (0.00)	146 (0.21)	0.71
12-01	Gp4	g.chr17:45608828G>T	Silent	NPEPPS	p.L54L	aminopeptidase puromy	21 (0.00)	71 (0.17)	0.45
12-01	Gp4	g.chr1:6038427G>T	Missense Mutation	NPHP4	p.S61Y	nephronophthisis 4	175 (0.00)	276 (0.33)	0.87
12-01	Gp4	g.chr16:21848756C>A	Missense Mutation	NPIPB4	p.D318Y	nuclear pore complex in	245 (0.00)	34 (0.29)	0.78
12-01	Gp4	g.chr1:153660625G>T	Missense Mutation	NPR1	p.R782L	natriuretic peptide recep	109 (0.00)	82 (0.16)	0.42
12-01	Gp4	g.chr9:35792515G>T	Missense Mutation	NPR2	p.S37I	natriuretic peptide recep	18 (0.00)	63 (0.54)	1.44
12-01	Gp4	g.chr9:35801065A>G	Splice Site	NPR2		natriuretic peptide recep	44 (0.00)	45 (0.42)	1.13
12-01	Gp4	g.chr5:32712582T>A	Missense Mutation	NPR3	p.Y234N	natriuretic peptide recep	137 (0.00)	21 (0.76)	2.03

12-01	Gp4	g.chr3:50385646C>A	Missense Mutation	NPRL2	p.V281L	nitrogen permease regul	181 (0.01)	159 (0.18)	0.49
12-01	Gp4	g.chr15:73889565C>A	Missense Mutation	NPTN	p.W79C	neuroplastin	79 (0.00)	145 (0.70)	1.88
12-01	Gp4	g.chr2:27664574G>T	Splice Site	NRBP1		nuclear receptor binding	292 (0.00)	334 (0.26)	0.69
12-01	Gp4	g.chr21:16339748A>T	Missense Mutation	NRIP1	p.S256T	nuclear receptor interact	18 (0.00)	29 (0.21)	0.55
12-01	Gp4	g.chr2:206656968C>A	Missense Mutation	NRP2	p.P812Q	neuropilin 2	27 (0.00)	153 (0.18)	0.49
12-01	Gp4	g.chr3:196388185C>A	Missense Mutation	NRROS	p.S557R	negative regulator of re	118 (0.00)	31 (0.35)	0.95
12-01	Gp4	g.chr4:4411317C>A	Silent	NSG1	p.L49L		48 (0.00)	29 (0.62)	1.66
12-01	Gp4	g.chr4:4419140A>G	Missense Mutation	NSG1	p.E140G		87 (0.00)	42 (0.19)	0.51
12-01	Gp4	g.chr17:73127370C>A	Missense Mutation	NT5C	p.V61L	5', 3'-nucleotidase, cyto	32 (0.00)	112 (0.43)	1.14
12-01	Gp4	g.chr3:52562548G>A	Nonsense Mutation	NT5DC2	p.Q186*	5'-nucleotidase domain	29 (0.00)	97 (0.58)	1.54
12-01	Gp4	g.chr2:113479424G>T	Missense Mutation	NT5DC4	p.G14V	5'-nucleotidase domain	64 (0.00)	198 (0.21)	0.55
12-01	Gp4	g.chr16:2096129C>A	Splice Site	NTHL1	p.K126N	nth endonuclease III-lik	62 (0.00)	64 (0.53)	1.42
12-01	Gp4	g.chr1:156849012C>A	Missense Mutation	NTRK1	p.A635D	neurotrophic tyrosine ki	28 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr1:156849811G>T	Silent	NTRK1	p.L689L	neurotrophic tyrosine ki	78 (0.00)	358 (0.23)	0.63
12-01	Gp4	g.chr9:87285722G>A	Nonsense Mutation	NTRK2	p.W20*	neurotrophic tyrosine ki	53 (0.00)	79 (0.72)	1.92
12-01	Gp4	g.chr1:205290701A>T	Missense Mutation	NUAK2	p.L19Q	NUAK family, SNF1-li	47 (0.00)	39 (0.38)	1.03
12-01	Gp4	g.chr10:12209810G>T	Splice Site	NUDT5	p.A184D	nudix (nucleoside dipho	167 (0.00)	139 (0.32)	0.84
12-01	Gp4	g.chr4:123838775G>T	Missense Mutation	NUDT6	p.A108D	nudix (nucleoside dipho	19 (0.00)	29 (0.86)	2.30
12-01	Gp4	g.chr11:71726956C>A	Missense Mutation	NUMA1	p.K531N	nuclear mitotic apparatu	153 (0.00)	494 (0.17)	0.46
12-01	Gp4	g.chr9:131720319G>A	Missense Mutation	NUP188	p.A120T	nucleoporin 188kDa	21 (0.00)	89 (0.81)	2.16
12-01	Gp4	g.chr9:131760497C>T	Missense Mutation	NUP188	p.T1140I	nucleoporin 188kDa	47 (0.00)	158 (0.27)	0.71
12-01	Gp4	g.chr9:131760506T>C	Splice Site	NUP188	p.L1143S	nucleoporin 188kDa	45 (0.00)	126 (0.17)	0.44
12-01	Gp4	g.chr9:131763998G>T	Missense Mutation	NUP188	p.R1345L	nucleoporin 188kDa	42 (0.00)	51 (0.33)	0.89
12-01	Gp4	g.chr3:13363741G>A	Missense Mutation	NUP210	p.P1623S	nucleoporin 210kDa	114 (0.01)	81 (0.15)	0.40
12-01	Gp4	g.chr17:73222224G>A	Missense Mutation	NUP85	p.D311N	nucleoporin 85kDa	55 (0.00)	82 (0.39)	1.04
12-01	Gp4	g.chr10:88974004G>T	RNA	NUTM2A-AS1		NUTM2A antisense RN	30 (0.00)	26 (0.77)	2.05
12-01	Gp4	g.chr10:88974038G>T	RNA	NUTM2A-AS1		NUTM2A antisense RN	32 (0.00)	41 (0.34)	0.91
12-01	Gp4	g.chr10:88975818C>A	RNA	NUTM2A-AS1		NUTM2A antisense RN	164 (0.00)	217 (0.47)	1.25
12-01	Gp4	g.chr10:89054928C>A	RNA	NUTM2A-AS1		NUTM2A antisense RN	24 (0.00)	37 (0.46)	1.23
12-01	Gp4	g.chr17:47656251G>C	Silent	NXPH3	p.L116L	neurexophilin 3	58 (0.00)	40 (0.15)	0.40
12-01	Gp4	g.chr7:100086891G>T	Missense Mutation	NYAP1	p.G516V	neuronal tyrosine-phosp	23 (0.00)	12 (0.92)	2.44
12-01	Gp4	g.chr14:24878677C>A	Silent	NYNRIN	p.S559S	NYN domain and retrov	79 (0.01)	146 (0.22)	0.58
12-01	Gp4	g.chr14:24885969G>T	Missense Mutation	NYNRIN	p.G1672C	NYN domain and retrov	108 (0.01)	119 (0.24)	0.65
12-01	Gp4	g.chr12:113400583G>T	Missense Mutation	OAS3	p.G654C	2'-5'-oligoadenylate syn	260 (0.00)	169 (0.14)	0.38
12-01	Gp4	g.chr9:136082710C>A	Missense Mutation	OBP2B	p.K97N	odorant binding protein	73 (0.01)	93 (0.37)	0.97

12-01	Gp4	g.chr1:228412255G>T	Missense Mutation	OBSCN	p.A1009S	obscurin, cytoskeletal ca	62 (0.00)	19 (0.84)	2.25
12-01	Gp4	g.chr1:228432086G>T	Missense Mutation	OBSCN	p.A1191S	obscurin, cytoskeletal ca	231 (0.00)	94 (0.57)	1.53
12-01	Gp4	g.chr1:228434477C>T	Missense Mutation	OBSCN	p.R1428W	obscurin, cytoskeletal ca	71 (0.00)	170 (0.23)	0.61
12-01	Gp4	g.chr1:228505240C>A	Missense Mutation	OBSCN	p.P5503H	obscurin, cytoskeletal ca	66 (0.00)	40 (0.82)	2.20
12-01	Gp4	g.chr1:228523972G>C	Splice Site	OBSCN		obscurin, cytoskeletal ca	161 (0.00)	67 (0.39)	1.03
12-01	Gp4	g.chr1:228528908A>G	Missense Mutation	OBSCN	p.D6894G	obscurin, cytoskeletal ca	22 (0.00)	65 (0.51)	1.35
12-01	Gp4	g.chr1:228558397G>C	Missense Mutation	OBSCN	p.E7685D	obscurin, cytoskeletal ca	122 (0.00)	247 (0.45)	1.19
12-01	Gp4	g.chr8:103572768G>T	Missense Mutation	ODF1	p.D137Y	outer dense fiber of sper	273 (0.00)	127 (0.32)	0.86
12-01	Gp4	g.chr8:103572848G>T	Silent	ODF1	p.S163S	outer dense fiber of sper	199 (0.00)	171 (0.34)	0.90
12-01	Gp4	g.chr9:131231612G>A	Missense Mutation	ODF2	p.V129I	outer dense fiber of sper	149 (0.00)	70 (0.14)	0.38
12-01	Gp4	g.chr10:50946023G>T	Silent	OGDHL	p.R829R	oxoglutarate dehydroger	90 (0.00)	380 (0.15)	0.41
12-01	Gp4	g.chr9:138011703C>A	Silent	OLFM1	p.V352V	olfactomedin 1	57 (0.00)	128 (0.77)	2.04
12-01	Gp4	g.chr1:114523127T>A	Nonsense Mutation	OLFML3	p.Y96*	olfactomedin-like 3	92 (0.00)	44 (0.36)	0.97
12-01	Gp4	g.chr6:137815214G>C	Missense Mutation	OLIG3	p.H32D	oligodendrocyte transcri	140 (0.00)	260 (0.49)	1.31
12-01	Gp4	g.chr14:22038403G>T	Missense Mutation	OR10G3	p.A158D	olfactory receptor, famil	205 (0.00)	24 (0.33)	0.89
12-01	Gp4	g.chr19:15918781G>A	Missense Mutation	OR10H1	p.L23F	olfactory receptor, famil	155 (0.01)	207 (0.17)	0.45
12-01	Gp4	g.chr11:123848059G>A	Nonsense Mutation	OR10S1	p.Q114*	olfactory receptor, famil	92 (0.00)	55 (0.45)	1.21
12-01	Gp4	g.chr1:248436529G>T	Silent	OR2T33	p.A196A	olfactory receptor, famil	116 (0.00)	32 (0.19)	0.50
12-01	Gp4	g.chr1:248737322C>A	Missense Mutation	OR2T34	p.C246F	olfactory receptor, famil	102 (0.00)	12 (0.42)	1.11
12-01	Gp4	g.chr5:180581978C>A	Silent	OR2V2	p.G12G	olfactory receptor, famil	142 (0.00)	109 (0.16)	0.42
12-01	Gp4	g.chr5:180582620G>A	Silent	OR2V2	p.V226V	olfactory receptor, famil	133 (0.00)	138 (0.36)	0.95
12-01	Gp4	g.chr1:247654410T>A	RNA	OR2W5		olfactory receptor, famil	50 (0.00)	23 (0.52)	1.39
12-01	Gp4	g.chr1:247655188G>T	RNA	OR2W5		olfactory receptor, famil	241 (0.00)	74 (0.93)	2.49
12-01	Gp4	g.chr11:4661100T>A	Missense Mutation	OR51D1	p.V27E	olfactory receptor, famil	110 (0.00)	12 (0.92)	2.44
12-01	Gp4	g.chr11:4703027C>T	Missense Mutation	OR51E2	p.M305I	olfactory receptor, famil	103 (0.00)	27 (0.96)	2.57
12-01	Gp4	g.chr11:6221104G>A	Silent	OR52W1	p.L217L	olfactory receptor, famil	95 (0.00)	33 (0.15)	0.40
12-01	Gp4	g.chr11:59211077C>T	Missense Mutation	OR5A1	p.R146C	olfactory receptor, famil	195 (0.00)	36 (0.50)	1.33
12-01	Gp4	g.chr3:97868365A>T	Missense Mutation	OR5H14	p.I46F	olfactory receptor, famil	80 (0.00)	124 (0.48)	1.29
12-01	Gp4	g.chr2:240969831C>T	Missense Mutation	OR6B2	p.V6I	olfactory receptor, famil	92 (0.01)	162 (0.15)	0.41
12-01	Gp4	g.chr2:240969844C>A	Start Codon SNP	OR6B2	p.M1I	olfactory receptor, famil	92 (0.00)	165 (0.22)	0.60
12-01	Gp4	g.chr2:240984550C>T	Missense Mutation	OR6B3	p.G314R	olfactory receptor, famil	435 (0.00)	508 (0.17)	0.44
12-01	Gp4	g.chr1:247876006G>A	Missense Mutation	OR6F1	p.P18S	olfactory receptor, famil	329 (0.00)	99 (0.92)	2.45
12-01	Gp4	g.chr19:9225567G>A	Silent	OR7G1	p.S291S	olfactory receptor, famil	154 (0.00)	129 (0.90)	2.40
12-01	Gp4	g.chr22:31289631G>A	Missense Mutation	OSBP2	p.D701N	oxysterol binding protei	83 (0.00)	96 (0.16)	0.42
12-01	Gp4	g.chr19:54600416C>A	Nonsense Mutation	OSCAR	p.G40*	osteoclast associated, in	47 (0.00)	25 (0.28)	0.75

12-01	Gp4	g.chr2:241078694G>C	Missense Mutation	OTOS	p.Q55E	otospiralin	68 (0.00)	21 (0.67)	1.78
12-01	Gp4	g.chr2:63282914C>A	Silent	OTX1	p.I176I	orthodenticle homeobox	27 (0.00)	62 (0.29)	0.77
12-01	Gp4	g.chr11:65562071C>G	Missense Mutation	OVOL1	p.F127L	ovo-like zinc finger 1	50 (0.00)	31 (0.19)	0.52
12-01	Gp4	g.chr17:3801344G>T	Missense Mutation	P2RX1	p.Q365K	purinergic receptor P2X	44 (0.00)	58 (0.26)	0.69
12-01	Gp4	g.chr17:3591929T>C	Missense Mutation	P2RX5-TAX1	p.Y293C	P2RX5-TAX1BP3 read	62 (0.00)	171 (0.19)	0.50
12-01	Gp4	g.chr11:72945588C>G	Missense Mutation	P2RY2	p.S128R	purinergic receptor P2Y	44 (0.02)	202 (0.57)	1.52
12-01	Gp4	g.chr11:65988215G>A	Silent	PACS1	p.E384E	phosphofurin acidic clu	56 (0.00)	138 (0.21)	0.56
12-01	Gp4	g.chr22:43280495G>C	Missense Mutation	PACSIN2	p.Q228E	protein kinase C and ca	137 (0.00)	28 (0.93)	2.48
12-01	Gp4	g.chr11:47202016C>A	Missense Mutation	PACSIN3	p.R146M	protein kinase C and ca	58 (0.00)	24 (0.54)	1.44
12-01	Gp4	g.chr1:17555137G>T	Missense Mutation	PADI1	p.D224Y	peptidyl arginine deimi	185 (0.00)	48 (0.54)	1.44
12-01	Gp4	g.chr1:17674447G>T	Missense Mutation	PADI4	p.E353D	peptidyl arginine deimi	52 (0.00)	205 (0.16)	0.43
12-01	Gp4	g.chr1:17701952G>T	RNA	PADI6		peptidyl arginine deimi	61 (0.00)	44 (0.18)	0.48
12-01	Gp4	g.chr17:2577502G>T	Nonsense Mutation	PAFAH1B1	p.E274*	platelet-activating facto	143 (0.00)	10 (0.70)	1.87
12-01	Gp4	g.chr10:72326411G>C	Missense Mutation	PALD1	p.Q831H	phosphatase domain co	22 (0.00)	23 (0.65)	1.74
12-01	Gp4	g.chr9:118950120C>A	Missense Mutation	PAPPA	p.P368Q	pregnancy-associated pl	41 (0.00)	27 (0.70)	1.88
12-01	Gp4	g.chr9:119097242G>T	Missense Mutation	PAPPA	p.S1167I	pregnancy-associated pl	89 (0.00)	90 (0.18)	0.47
12-01	Gp4	g.chr4:75858577G>T	Missense Mutation	PARM1	p.A14S	prostate androgen-regul	37 (0.03)	287 (0.24)	0.65
12-01	Gp4	g.chr16:14576539C>A	Missense Mutation	PARN	p.Q542H	poly(A)-specific ribonu	107 (0.01)	240 (0.28)	0.73
12-01	Gp4	g.chr16:14576633T>A	Missense Mutation	PARN	p.E511V	poly(A)-specific ribonu	63 (0.00)	241 (0.16)	0.43
12-01	Gp4	g.chr1:226568822C>T	Missense Mutation	PARP1	p.G416E	poly (ADP-ribose) poly	79 (0.00)	57 (0.19)	0.51
12-01	Gp4	g.chr7:139741597A>G	Silent	PARP12	p.C343C	poly (ADP-ribose) poly	157 (0.01)	129 (0.43)	1.14
12-01	Gp4	g.chr3:122420148T>C	Missense Mutation	PARP14	p.I916T	poly (ADP-ribose) poly	102 (0.00)	16 (0.44)	1.17
12-01	Gp4	g.chr5:50090811G>T	Missense Mutation	PARP8	p.D330Y	poly (ADP-ribose) poly	33 (0.00)	184 (0.83)	2.22
12-01	Gp4	g.chr1:55223849C>A	Missense Mutation	PARS2	p.C329F	prolyl-tRNA synthetase	335 (0.00)	452 (0.23)	0.62
12-01	Gp4	g.chr22:31723240G>T	Missense Mutation	PATZ1	p.D567E	POZ (BTB) and AT ho	35 (0.00)	168 (0.17)	0.44
12-01	Gp4	g.chr21:34101853C>A	RNA	PAXBP1-AS1		PAXBP1 antisense RN	30 (0.00)	89 (0.53)	1.41
12-01	Gp4	g.chr3:52643843G>A	Silent	PBRM1	p.L700L	polybromo 1	62 (0.00)	38 (0.24)	0.63
12-01	Gp4	g.chr3:142895370C>T	RNA	PBX2P1		pre-B-cell leukemia ho	46 (0.00)	35 (0.17)	0.46
12-01	Gp4	g.chr1:154918089G>C	Missense Mutation	PBXIP1	p.F687L	pre-B-cell leukemia ho	132 (0.00)	310 (0.45)	1.20
12-01	Gp4	g.chr1:154918326G>T	Silent	PBXIP1	p.A608A	pre-B-cell leukemia ho	89 (0.00)	71 (0.28)	0.75
12-01	Gp4	g.chr1:154920826C>G	Missense Mutation	PBXIP1	p.E142D	pre-B-cell leukemia ho	28 (0.00)	31 (0.23)	0.60
12-01	Gp4	g.chr2:70248739C>A	RNA	PCBP1-AS1		PCBP1 antisense RNA	46 (0.00)	18 (0.28)	0.74
12-01	Gp4	g.chr21:47330866G>T	Silent	PCBP3	p.T142T	poly(rC) binding protei	43 (0.00)	25 (0.20)	0.53
12-01	Gp4	g.chr13:58208024C>A	Silent	PCDH17	p.G448G	protocadherin 17	68 (0.00)	199 (0.32)	0.84
12-01	Gp4	g.chr5:140236978G>T	Missense Mutation	PCDHA10	p.D449Y	protocadherin alpha 10	165 (0.00)	153 (0.25)	0.66

12-01	Gp4	g.chr5:140248961C>G	Missense Mutation	PCDHA11	p.D91E	protocadherin alpha 11	279 (0.00)	555 (0.40)	1.06
12-01	Gp4	g.chr5:140250671G>T	Silent	PCDHA11	p.T661T	protocadherin alpha 11	44 (0.00)	49 (0.24)	0.65
12-01	Gp4	g.chr5:140255554C>T	Missense Mutation	PCDHA12	p.S166F	protocadherin alpha 12	181 (0.00)	40 (0.28)	0.73
12-01	Gp4	g.chr5:140187637G>A	Missense Mutation	PCDHA4	p.V289M	protocadherin alpha 4	48 (0.00)	107 (0.42)	1.12
12-01	Gp4	g.chr5:140215854G>A	Missense Mutation	PCDHA7	p.G629D	protocadherin alpha 7	81 (0.00)	31 (0.52)	1.38
12-01	Gp4	g.chr5:140221347G>A	Missense Mutation	PCDHA8	p.M147I	protocadherin alpha 8	71 (0.00)	378 (0.49)	1.32
12-01	Gp4	g.chr5:140221365G>A	Silent	PCDHA8	p.P153P	protocadherin alpha 8	59 (0.00)	411 (0.29)	0.78
12-01	Gp4	g.chr5:140228458T>A	Silent	PCDHA9	p.I126I	protocadherin alpha 9	174 (0.00)	35 (0.49)	1.30
12-01	Gp4	g.chr5:140615556A>T	RNA	PCDHB18		protocadherin beta 18 ps	15 (0.00)	37 (0.19)	0.50
12-01	Gp4	g.chr5:140531466C>A	Missense Mutation	PCDHB6	p.A543E	protocadherin beta 6	42 (0.00)	110 (0.26)	0.70
12-01	Gp4	g.chr5:140532185G>T	Nonsense Mutation	PCDHB6	p.E783*	protocadherin beta 6	145 (0.01)	177 (0.57)	1.52
12-01	Gp4	g.chr5:140794569C>G	Silent	PCDHGA10	p.S609S	protocadherin gamma su	24 (0.00)	173 (0.37)	0.99
12-01	Gp4	g.chr5:140801717T>A	Missense Mutation	PCDHGA11	p.L308Q	protocadherin gamma su	216 (0.00)	23 (0.57)	1.51
12-01	Gp4	g.chr5:140810571G>A	Missense Mutation	PCDHGA12	p.G82D	protocadherin gamma su	93 (0.00)	35 (0.40)	1.07
12-01	Gp4	g.chr5:140811710C>T	Missense Mutation	PCDHGA12	p.P462S	protocadherin gamma su	144 (0.00)	149 (0.53)	1.41
12-01	Gp4	g.chr5:140890686C>A	Silent	PCDHGA12	p.A915A	protocadherin gamma su	88 (0.00)	93 (0.30)	0.80
12-01	Gp4	g.chr5:140719935C>A	Missense Mutation	PCDHGA2	p.P466H	protocadherin gamma su	88 (0.00)	59 (0.31)	0.81
12-01	Gp4	g.chr5:140772810G>T	Nonsense Mutation	PCDHGA8	p.E144*	protocadherin gamma su	233 (0.00)	197 (0.34)	0.89
12-01	Gp4	g.chr5:140768078C>T	Silent	PCDHGB4	p.H209H	protocadherin gamma su	114 (0.00)	48 (0.98)	2.61
12-01	Gp4	g.chr5:140869414G>A	Missense Mutation	PCDHGC5	p.E203K	protocadherin gamma su	157 (0.00)	13 (0.77)	2.05
12-01	Gp4	g.chr5:140871163G>T	Missense Mutation	PCDHGC5	p.D786Y	protocadherin gamma su	26 (0.00)	81 (0.22)	0.59
12-01	Gp4	g.chr11:82880692T>C	Silent	PCF11	p.F1105F	PCF11 cleavage and pol	71 (0.00)	135 (0.20)	0.53
12-01	Gp4	g.chr20:44569748C>A	Nonsense Mutation	PCIF1	p.S192*	PDX1 C-terminal inhibi	98 (0.00)	75 (0.67)	1.78
12-01	Gp4	g.chr7:82584608G>T	Silent	PCLO	p.P1887P	piccolo presynaptic cyto	59 (0.00)	26 (0.50)	1.33
12-01	Gp4	g.chr7:82784924G>A	Nonsense Mutation	PCLO	p.Q345*	piccolo presynaptic cyto	93 (0.00)	151 (0.83)	2.23
12-01	Gp4	g.chr21:47808738G>T	Silent	PCNT	p.R1182R	pericentrin	26 (0.00)	16 (0.31)	0.83
12-01	Gp4	g.chr21:47809289G>T	Missense Mutation	PCNT	p.Q1261H	pericentrin	80 (0.00)	94 (0.30)	0.79
12-01	Gp4	g.chr21:47847700C>A	Silent	PCNT	p.I2495I	pericentrin	30 (0.00)	31 (0.16)	0.43
12-01	Gp4	g.chr14:71443720G>T	Missense Mutation	PCNX	p.Q222H	pecanex homolog (Dros	46 (0.02)	161 (0.58)	1.56
12-01	Gp4	g.chr14:71444788G>A	Silent	PCNX	p.R578R	pecanex homolog (Dros	168 (0.00)	43 (0.98)	2.60
12-01	Gp4	g.chr11:65386293G>T	Missense Mutation	PCNXL3	p.G487V	pecanex-like 3 (Drosoph	30 (0.00)	102 (0.15)	0.39
12-01	Gp4	g.chr11:65397067C>T	Silent	PCNXL3	p.D1359D	pecanex-like 3 (Drosoph	26 (0.00)	30 (0.30)	0.80
12-01	Gp4	g.chr11:65403976C>A	Missense Mutation	PCNXL3	p.P1903H	pecanex-like 3 (Drosoph	28 (0.00)	22 (0.64)	1.70
12-01	Gp4	g.chr14:60600773G>T	Missense Mutation	PCNXL4	p.W1118L	pecanex-like 4 (Drosoph	33 (0.03)	42 (0.74)	1.97
12-01	Gp4	g.chr19:1490161C>A	Missense Mutation	PCSK4	p.G62V	proprotein convertase su	16 (0.00)	25 (0.52)	1.39

12-01	Gp4	g.chr11:117097987G>A	Missense Mutation	PCSK7	p.H219Y	proprotein convertase su	158 (0.00)	383 (0.27)	0.72
12-01	Gp4	g.chr5:148743705G>T	Missense Mutation	PCYOX1L	p.W134C	prenylcysteine oxidase 1	50 (0.00)	61 (0.34)	0.92
12-01	Gp4	g.chr3:57542385G>T	Missense Mutation	PDE12	p.K93N	phosphodiesterase 12	19 (0.00)	114 (0.34)	0.91
12-01	Gp4	g.chr3:57542725G>T	Nonsense Mutation	PDE12	p.E207*	phosphodiesterase 12	173 (0.00)	484 (0.20)	0.52
12-01	Gp4	g.chr12:54963391C>T	Missense Mutation	PDE1B	p.L117F	phosphodiesterase 1B, c	46 (0.00)	40 (0.20)	0.53
12-01	Gp4	g.chr11:72295920T>A	Missense Mutation	PDE2A	p.D452V	phosphodiesterase 2A, c	43 (0.00)	38 (0.29)	0.77
12-01	Gp4	g.chr19:18329026G>T	Silent	PDE4C	p.A421A	phosphodiesterase 4C, c	70 (0.00)	75 (0.47)	1.24
12-01	Gp4	g.chr19:18329296G>T	Missense Mutation	PDE4C	p.L360M	phosphodiesterase 4C, c	95 (0.00)	69 (0.48)	1.28
12-01	Gp4	g.chr21:44152210C>T	Missense Mutation	PDE9A	p.A98V	phosphodiesterase 9A	126 (0.00)	95 (0.16)	0.42
12-01	Gp4	g.chr5:149497301G>A	Missense Mutation	PDGFRB	p.S1006F	platelet-derived growth	118 (0.00)	106 (0.21)	0.55
12-01	Gp4	g.chr8:94934980T>A	Missense Mutation	PDP1	p.D231E	pyruvate dehyrogenase	32 (0.00)	16 (0.94)	2.50
12-01	Gp4	g.chr16:70011867T>A	RNA	PDXDC2P		pyridoxal-dependent de	277 (0.00)	18 (0.44)	1.19
12-01	Gp4	g.chr5:32072383C>A	Nonsense Mutation	PDZD2	p.C895*	PDZ domain containing	127 (0.00)	142 (0.23)	0.62
12-01	Gp4	g.chr5:32072424G>T	Splice Site	PDZD2		PDZ domain containing	91 (0.00)	109 (0.23)	0.61
12-01	Gp4	g.chr1:145762298C>A	Nonsense Mutation	PDZK1	p.S492*	PDZ domain containing	137 (0.00)	9 (0.67)	1.78
12-01	Gp4	g.chr1:156883050C>G	Silent	PEAR1	p.S829S	platelet endothelial aggr	95 (0.00)	196 (0.60)	1.61
12-01	Gp4	g.chr1:32101038C>G	Missense Mutation	PEF1	p.G37A	penta-EF-hand domain	48 (0.00)	14 (0.86)	2.29
12-01	Gp4	g.chr7:94293188G>T	Missense Mutation	PEG10	p.S107I	paternally expressed 10	212 (0.00)	229 (0.76)	2.03
12-01	Gp4	g.chr19:57325096G>T	Missense Mutation	PEG3	p.L1572I	paternally expressed 3	84 (0.00)	48 (0.75)	2.00
12-01	Gp4	g.chr5:52096402C>G	Missense Mutation	PELO	p.S58R	pelota homolog (Drosop	29 (0.00)	96 (0.42)	1.11
12-01	Gp4	g.chr17:8048289C>G	Silent	PER1	p.L747L	period circadian clock 1	41 (0.00)	35 (0.46)	1.22
12-01	Gp4	g.chr19:7550724C>A	Splice Site	PEX11G	p.Q83H	peroxisomal biogenesis	137 (0.00)	102 (0.38)	1.02
12-01	Gp4	g.chrX:77224622C>T	Missense Mutation	PGAM4	p.V172I	phosphoglycerate mutas	40 (0.00)	11 (0.82)	1.36
12-01	Gp4	g.chr19:46522564G>A	Missense Mutation	PGLYRP1	p.R175C	peptidoglycan recogniti	23 (0.00)	75 (0.44)	1.47
12-01	Gp4	g.chr11:74109174G>T	Silent	PGM2L1	p.S11S	phosphoglucomutase 2-	51 (0.00)	124 (0.23)	0.60
12-01	Gp4	g.chr20:58348339G>T	Missense Mutation	PHACTR3	p.A253S	phosphatase and actin re	124 (0.00)	58 (0.19)	0.51
12-01	Gp4	g.chr9:123620515G>A	Missense Mutation	PHF19	p.P484S	PHD finger protein 19	63 (0.00)	25 (0.44)	1.17
12-01	Gp4	g.chr22:41864145C>A	Missense Mutation	PHF5A	p.G20V	PHD finger protein 5A	128 (0.00)	53 (0.47)	1.26
12-01	Gp4	g.chr1:120277283C>A	Silent	PHGDH	p.S179S	phosphoglycerate dehyd	387 (0.00)	136 (0.16)	0.43
12-01	Gp4	g.chr16:30768413G>T	Missense Mutation	PHKG2	p.G406C	phosphorylase kinase, g	65 (0.00)	54 (0.59)	1.58
12-01	Gp4	g.chr1:201437722C>A	Nonsense Mutation	PHLDA3	p.E65*	pleckstrin homology-lik	31 (0.00)	79 (0.54)	1.45
12-01	Gp4	g.chr11:118516514G>T	Missense Mutation	PHLDB1	p.A1160S	pleckstrin homology-lik	119 (0.00)	170 (0.36)	0.96
12-01	Gp4	g.chr18:60518494T>C	Intron	PHLPP1		PH domain and leucine	112 (0.00)	74 (0.16)	0.43
12-01	Gp4	g.chr18:60518518G>T	Intron	PHLPP1		PH domain and leucine	120 (0.00)	96 (0.28)	0.75
12-01	Gp4	g.chr18:60543610T>A	Intron	PHLPP1		PH domain and leucine	23 (0.00)	64 (0.44)	1.17

12-01	Gp4	g.chr18:60599443C>G	Intron	PHLPP1		PH domain and leucine	21 (0.00)	40 (0.33)	0.87
12-01	Gp4	g.chr18:60645899G>T	Silent	PHLPP1	p.G1463G	PH domain and leucine	151 (0.00)	142 (0.27)	0.73
12-01	Gp4	g.chr11:605173G>A	Missense Mutation	PHRF1	p.V403I	PHD and ring finger do	85 (0.00)	94 (0.20)	0.54
12-01	Gp4	g.chr22:21096918G>A	Silent	PI4KA	p.T1197T	phosphatidylinositol 4-k	93 (0.00)	114 (0.16)	0.42
12-01	Gp4	g.chr1:145578455G>T	Nonsense Mutation	PIAS3	p.E140*	protein inhibitor of activ	90 (0.00)	32 (0.34)	0.92
12-01	Gp4	g.chr15:65114565C>A	Missense Mutation	PIF1	p.K239N	PIF1 5'-to-3' DNA helic	61 (0.00)	82 (0.20)	0.52
12-01	Gp4	g.chr9:35091480G>T	Silent	PIGO	p.R802R	phosphatidylinositol gly	114 (0.00)	53 (0.17)	0.45
12-01	Gp4	g.chr9:35092045G>T	Silent	PIGO	p.P613P	phosphatidylinositol gly	110 (0.00)	157 (0.24)	0.63
12-01	Gp4	g.chr9:35092108G>T	Silent	PIGO	p.G592G	phosphatidylinositol gly	112 (0.00)	132 (0.36)	0.95
12-01	Gp4	g.chr20:44047974G>T	Missense Mutation	PIGT	p.R178L	phosphatidylinositol gly	69 (0.00)	60 (0.30)	0.80
12-01	Gp4	g.chr1:9780040G>A	Missense Mutation	PIK3CD	p.G435E	phosphatidylinositol-4,5	135 (0.00)	145 (0.22)	0.59
12-01	Gp4	g.chr19:18272788C>A	Missense Mutation	PIK3R2	p.S276R	phosphoinositide-3-kina	81 (0.00)	73 (0.26)	0.69
12-01	Gp4	g.chr7:99987565G>A	Missense Mutation	PILRA	p.S170N	paired immunoglobin-li	37 (0.00)	19 (0.89)	2.39
12-01	Gp4	g.chr22:50356413G>T	Silent	PIM3	p.L231L	Pim-3 proto-oncogene,	46 (0.00)	25 (0.52)	1.39
12-01	Gp4	g.chr1:151214647G>T	Missense Mutation	PIP5K1A	p.R459L	phosphatidylinositol-4-	234 (0.00)	89 (0.52)	1.38
12-01	Gp4	g.chr10:95719178G>T	RNA	PIPSL		PIP5K1A and PSMD4-l	261 (0.00)	247 (0.40)	1.06
12-01	Gp4	g.chr12:123472830G>T	Nonsense Mutation	PITPNM2	p.S983*	phosphatidylinositol tra	184 (0.00)	283 (0.19)	0.52
12-01	Gp4	g.chr5:134364583C>T	Silent	PITX1	p.T277T	paired-like homeodoma	40 (0.00)	26 (0.27)	0.72
12-01	Gp4	g.chr16:2160900G>A	Missense Mutation	PKD1	p.P1423L	polycystic kidney diseas	35 (0.00)	14 (0.36)	0.95
12-01	Gp4	g.chr16:72005941C>A	RNA	PKD1L3		polycystic kidney diseas	31 (0.00)	15 (0.40)	0.44
12-01	Gp4	g.chr2:42282441G>T	Missense Mutation	PKDCC	p.G377V	protein kinase domain c	30 (0.00)	64 (0.17)	0.46
12-01	Gp4	g.chr6:51890152G>A	Missense Mutation	PKHD1	p.P1486S	polycystic kidney and h	27 (0.00)	16 (0.69)	1.83
12-01	Gp4	g.chr6:51890639G>T	Missense Mutation	PKHD1	p.N1323K	polycystic kidney and h	67 (0.00)	146 (0.43)	1.15
12-01	Gp4	g.chr20:43246989G>T	Missense Mutation	PKIG	p.G72V	protein kinase (cAMP-d	85 (0.00)	10 (0.50)	1.33
12-01	Gp4	g.chr2:159526278T>A	Missense Mutation	PKP4	p.N925K	plakophilin 4	165 (0.00)	124 (0.21)	0.56
12-01	Gp4	g.chr22:31531801G>T	Missense Mutation	PLA2G3	p.L480M	phospholipase A2, grou	155 (0.01)	41 (0.49)	1.30
12-01	Gp4	g.chr22:31534342C>T	Silent	PLA2G3	p.V234V	phospholipase A2, grou	18 (0.00)	56 (0.27)	0.71
12-01	Gp4	g.chr20:30784556G>T	Missense Mutation	PLAGL2	p.A397D	pleiomorphic adenoma	60 (0.00)	39 (0.74)	1.98
12-01	Gp4	g.chr12:113825651C>A	Silent	PLBD2	p.A482A	phospholipase B domai	326 (0.00)	454 (0.17)	0.46
12-01	Gp4	g.chr10:96006154G>C	Missense Mutation	PLCE1	p.V958L	phospholipase C, epsilo	197 (0.00)	39 (0.69)	1.85
12-01	Gp4	g.chr17:4722075G>T	Silent	PLD2	p.L710L	phospholipase D2	36 (0.00)	66 (0.45)	1.21
12-01	Gp4	g.chr8:144994818C>A	Silent	PLEC	p.L3194L	plectin	89 (0.00)	187 (0.17)	0.46
12-01	Gp4	g.chr8:144998374C>G	Missense Mutation	PLEC	p.R2045P	plectin	15 (0.00)	83 (0.17)	0.45
12-01	Gp4	g.chr5:143317C>A	Missense Mutation	PLEKHG4B	p.Q189K	pleckstrin homology do	89 (0.00)	19 (0.58)	1.54
12-01	Gp4	g.chr19:4510571G>A	Missense Mutation	PLIN4	p.T1120M	perilipin 4	50 (0.00)	24 (0.71)	1.89

12-01	Gp4	g.chr19:4512431T>G	Missense Mutation	PLIN4	p.K500T	perilipin 4	95 (0.00)	44 (0.30)	0.79
12-01	Gp4	g.chr1:45271225G>T	Missense Mutation	PLK3	p.V606L	polo-like kinase 3	306 (0.00)	155 (0.37)	1.00
12-01	Gp4	g.chrX:153697457T>C	Missense Mutation	PLXNA3	p.L1498P	plexin A3	35 (0.00)	23 (0.57)	0.94
12-01	Gp4	g.chr15:74336687C>A	Missense Mutation	PML	p.L663I	promyelocytic leukemia	121 (0.00)	391 (0.14)	0.38
12-01	Gp4	g.chr15:74336952G>T	Missense Mutation	PML	p.R751L	promyelocytic leukemia	65 (0.00)	85 (0.21)	0.56
12-01	Gp4	g.chr22:41973894C>T	Missense Mutation	PMM1	p.G195D	phosphomannomutase 1	87 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr9:139311552G>T	Missense Mutation	PMPCA	p.E261D	peptidase (mitochondria	145 (0.00)	188 (0.26)	0.68
12-01	Gp4	g.chr10:118385618C>T	RNA	PNLIPRP2		pancreatic lipase-related	223 (0.00)	235 (0.63)	1.69
12-01	Gp4	g.chr19:46973623G>T	Missense Mutation	PNMAL1	p.Q224K	paraneoplastic Ma antig	73 (0.00)	89 (0.61)	2.03
12-01	Gp4	g.chr8:28196592C>A	Silent	PNOC	p.P54P	prepronociceptin	88 (0.00)	105 (0.34)	0.91
12-01	Gp4	g.chr3:52183318G>T	Silent	POC1A	p.A121A	POC1 centriolar protein	120 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr12:89918910G>T	Missense Mutation	POC1B-GALN	p.N29K	POC1B-GALNT4 readt	26 (0.00)	10 (0.50)	1.33
12-01	Gp4	g.chr22:42995743C>G	Missense Mutation	POLDIP3	p.Q198H	polymerase (DNA-direc	75 (0.00)	37 (0.19)	0.50
12-01	Gp4	g.chr15:89867343G>A	Nonsense Mutation	POLG	p.Q689*	polymerase (DNA direc	231 (0.00)	103 (0.54)	1.45
12-01	Gp4	g.chr4:2073962G>T	Missense Mutation	POLN	p.A861D	polymerase (DNA direc	30 (0.00)	142 (0.19)	0.51
12-01	Gp4	g.chr13:28239886G>A	Silent	POLR1D	p.L55L	polymerase (RNA) I pol	130 (0.01)	63 (0.94)	2.50
12-01	Gp4	g.chr17:7416866C>A	Missense Mutation	POLR2A	p.S1761R	polymerase (RNA) II (D	660 (0.00)	544 (0.32)	0.86
12-01	Gp4	g.chr11:62533149G>A	Missense Mutation	POLR2G	p.E142K	polymerase (RNA) II (D	124 (0.00)	12 (0.92)	2.44
12-01	Gp4	g.chr7:44027773G>C	RNA	POLR2J4		polymerase (RNA) II (D	71 (0.00)	48 (0.15)	0.39
12-01	Gp4	g.chr7:44054330G>A	RNA	POLR2J4		polymerase (RNA) II (D	236 (0.00)	165 (0.52)	1.39
12-01	Gp4	g.chr3:43122095C>G	Missense Mutation	POMGNT2	p.V277L	protein O-linked manno	168 (0.00)	13 (0.85)	2.26
12-01	Gp4	g.chr9:134393900C>A	Missense Mutation	POMT1	p.H447Q	protein-O-mannosyltran	388 (0.00)	38 (0.55)	1.47
12-01	Gp4	g.chr1:167381230C>T	Silent	POU2F1	p.T519T	POU class 2 homeobox	72 (0.00)	19 (0.79)	2.11
12-01	Gp4	g.chr1:203014590C>A	Missense Mutation	PPFIA4	p.T254K	protein tyrosine phospha	25 (0.00)	71 (0.17)	0.45
12-01	Gp4	g.chr16:4944480G>T	Missense Mutation	PPL	p.A461D	periplakin	28 (0.00)	85 (0.18)	0.47
12-01	Gp4	g.chr19:55614909G>T	Missense Mutation	PPP1R12C	p.A200E	protein phosphatase 1, r	122 (0.00)	109 (0.83)	2.23
12-01	Gp4	g.chr14:104202478C>A	Missense Mutation	PPP1R13B	p.E1031D	protein phosphatase 1, r	97 (0.00)	103 (0.63)	1.68
12-01	Gp4	g.chr14:104208394G>T	Missense Mutation	PPP1R13B	p.Q519K	protein phosphatase 1, r	265 (0.00)	364 (0.24)	0.63
12-01	Gp4	g.chr19:52709250C>G	Silent	PPP2R1A	p.A68A	protein phosphatase 2, r	125 (0.00)	49 (0.33)	0.87
12-01	Gp4	g.chr16:30094142A>G	Missense Mutation	PPP4C	p.T93A	protein phosphatase 4, c	31 (0.00)	15 (0.60)	1.60
12-01	Gp4	g.chr22:50832488C>A	Missense Mutation	PPP6R2	p.Q51K	protein phosphatase 6, r	276 (0.00)	153 (0.35)	0.92
12-01	Gp4	g.chr22:50876638C>A	Missense Mutation	PPP6R2	p.D598E	protein phosphatase 6, r	113 (0.00)	430 (0.22)	0.58
12-01	Gp4	g.chr10:103900170C>A	Silent	PPRC1	p.V635V	peroxisome proliferator-	34 (0.00)	51 (0.25)	0.68
12-01	Gp4	g.chr19:8563824G>C	Missense Mutation	PRAM1	p.L290V	PML-RARA regulated a	43 (0.00)	41 (0.59)	1.56
12-01	Gp4	g.chr1:12887323C>T	Silent	PRAMEF11	p.L178L	PRAME family membe	357 (0.00)	26 (0.46)	1.23

12-01	Gp4	g.chr21:43236080C>A	Missense Mutation	PRDM15	p.K828N	PR domain containing 1	23 (0.00)	43 (0.19)	0.50
12-01	Gp4	g.chr1:14108202G>A	Silent	PRDM2	p.Q1304Q	PR domain containing 2	129 (0.00)	119 (0.48)	1.28
12-01	Gp4	g.chr6:126965353G>T	RNA	PRELID1P1		PRELI domain containi	79 (0.00)	43 (0.23)	0.62
12-01	Gp4	g.chr10:72358597G>C	Missense Mutation	PRF1	p.Q294E	perforin 1 (pore forming	187 (0.00)	490 (0.31)	0.84
12-01	Gp4	g.chr3:64084742G>T	Missense Mutation	PRICKLE2	p.N896K	prickle homolog 2 (Dros	89 (0.00)	53 (0.15)	0.40
12-01	Gp4	g.chr12:57135571G>A	Nonsense Mutation	PRIM1	p.Q267*	primase, DNA, polypep	93 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr12:57135574G>C	Missense Mutation	PRIM1	p.L266V	primase, DNA, polypep	93 (0.00)	27 (0.19)	0.49
12-01	Gp4	g.chr12:57135576G>A	Missense Mutation	PRIM1	p.S265L	primase, DNA, polypep	93 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr3:53217164G>T	Missense Mutation	PRKCD	p.C200F	protein kinase C, delta	62 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr3:53222774G>T	Missense Mutation	PRKCD	p.G485V	protein kinase C, delta	108 (0.00)	106 (0.48)	1.28
12-01	Gp4	g.chr16:68387463G>T	Missense Mutation	PRMT7	p.M548I	protein arginine methylt	102 (0.00)	78 (0.28)	0.75
12-01	Gp4	g.chr22:18918535C>T	Silent	PRODH	p.L150L	proline dehydrogenase (	86 (0.00)	47 (0.34)	0.91
12-01	Gp4	g.chr19:36297597T>C	Missense Mutation	PRODH2	p.T348A	proline dehydrogenase (	42 (0.00)	67 (0.19)	0.52
12-01	Gp4	g.chr3:93692526T>A	Missense Mutation	PROS1	p.E23V	protein S (alpha)	46 (0.00)	32 (0.56)	1.50
12-01	Gp4	g.chr14:75330160C>A	Missense Mutation	PROX2	p.R126S	prospero homeobox 2	92 (0.00)	167 (0.24)	0.64
12-01	Gp4	g.chr19:54625248C>A	Missense Mutation	PRPF31	p.P83Q	pre-mRNA processing f	22 (0.00)	54 (0.70)	1.88
12-01	Gp4	g.chr12:49689213G>A	Missense Mutation	PRPH	p.R77H	peripherin	19 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr3:138724820G>C	Silent	PRR23A	p.L97L	proline rich 23A	22 (0.00)	11 (0.64)	1.70
12-01	Gp4	g.chr9:134353300G>T	Nonsense Mutation	PRRC2B	p.G832*	proline-rich coiled-coil	150 (0.00)	117 (0.50)	1.34
12-01	Gp4	g.chr9:79322352C>T	Missense Mutation	PRUNE2	p.S1613N	prune homolog 2 (Dros	33 (0.00)	44 (0.64)	1.70
12-01	Gp4	g.chr10:104172151G>T	Missense Mutation	PSD	p.H579N	pleckstrin and Sec7 do	85 (0.00)	122 (0.23)	0.61
12-01	Gp4	g.chr10:104173622T>C	Missense Mutation	PSD	p.E486G	pleckstrin and Sec7 do	78 (0.00)	91 (0.24)	0.64
12-01	Gp4	g.chr2:113958776C>A	Silent	PSD4	p.R956R	pleckstrin and Sec7 do	291 (0.00)	136 (0.32)	0.84
12-01	Gp4	g.chr14:23511540C>A	Missense Mutation	PSMB11	p.Q36K	proteasome (prosome,	118 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr17:61907739C>T	Missense Mutation	PSMC5	p.P144S	proteasome (prosome,	151 (0.00)	399 (0.51)	1.36
12-01	Gp4	g.chr15:77322885G>T	Missense Mutation	PSTPIP1	p.R202L	proline-serine-threonine	54 (0.00)	167 (0.39)	1.04
12-01	Gp4	g.chr6:42883815G>T	Missense Mutation	PTCRA	p.G3V	pre T-cell antigen recep	101 (0.00)	242 (0.43)	1.13
12-01	Gp4	g.chr10:23482773C>T	Missense Mutation	PTF1A	p.L309F	pancreas specific transc	281 (0.00)	118 (0.49)	1.31
12-01	Gp4	g.chr9:132502052G>T	Silent	PTGES	p.A99A	prostaglandin E synthas	15 (0.00)	43 (0.23)	0.62
12-01	Gp4	g.chr9:132515204C>G	Missense Mutation	PTGES	p.V30L	prostaglandin E synthas	65 (0.00)	18 (0.33)	0.89
12-01	Gp4	g.chr9:130885298C>A	Missense Mutation	PTGES2	p.G268C	prostaglandin E synthas	27 (0.00)	151 (0.48)	1.29
12-01	Gp4	g.chr1:117484557C>A	Silent	PTGFRN	p.G90G	prostaglandin F2 recept	109 (0.00)	128 (0.53)	1.42
12-01	Gp4	g.chr1:117504142G>A	Silent	PTGFRN	p.T497T	prostaglandin F2 recept	214 (0.00)	177 (0.47)	1.27
12-01	Gp4	g.chr3:46945134G>T	Missense Mutation	PTH1R	p.E590D	parathyroid hormone 1	44 (0.00)	86 (0.45)	1.21
12-01	Gp4	g.chr20:49195833T>C	Silent	PTPN1	p.G277G	protein tyrosine phospha	73 (0.00)	58 (0.60)	1.61

12-01	Gp4	g.chr4:87622813G>A	Missense Mutation	PTPN13	p.D352N	protein tyrosine phospha	63 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr4:87729008G>C	Silent	PTPN13	p.L2352L	protein tyrosine phospha	38 (0.00)	80 (0.65)	1.73
12-01	Gp4	g.chr3:47447984A>T	Missense Mutation	PTPN23	p.Y214F	protein tyrosine phospha	26 (0.00)	30 (0.30)	0.80
12-01	Gp4	g.chr3:47450951G>T	Silent	PTPN23	p.V614V	protein tyrosine phospha	37 (0.00)	135 (0.52)	1.38
12-01	Gp4	g.chr11:18754241G>T	Silent	PTPN5	p.T385T	protein tyrosine phospha	64 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr1:44064476C>A	Missense Mutation	PTPRF	p.S735R	protein tyrosine phospha	24 (0.00)	55 (0.45)	1.21
12-01	Gp4	g.chr1:44069477G>T	Missense Mutation	PTPRF	p.G876V	protein tyrosine phospha	194 (0.01)	126 (0.33)	0.87
12-01	Gp4	g.chr1:44069529G>T	Missense Mutation	PTPRF	p.E893D	protein tyrosine phospha	112 (0.00)	84 (0.60)	1.59
12-01	Gp4	g.chr1:44072039G>T	Missense Mutation	PTPRF	p.K1195N	protein tyrosine phospha	183 (0.00)	377 (0.74)	1.98
12-01	Gp4	g.chr1:29606101C>A	Missense Mutation	PTPRU	p.S566Y	protein tyrosine phospha	86 (0.00)	55 (0.65)	1.75
12-01	Gp4	g.chr3:157154771G>A	Missense Mutation	PTX3	p.A17T	pentraxin 3, long	51 (0.00)	69 (0.72)	1.93
12-01	Gp4	g.chr21:45548143C>A	Missense Mutation	PWP2	p.S792Y	PWP2 periodic tryptoph	141 (0.00)	94 (0.18)	0.48
12-01	Gp4	g.chr20:32302503C>T	Missense Mutation	PXMP4	p.M51I	peroxisomal membrane	169 (0.00)	124 (0.44)	1.18
12-01	Gp4	g.chr3:49094994G>T	Silent	QRICH1	p.I213I	glutamine-rich 1	87 (0.00)	13 (0.92)	2.46
12-01	Gp4	g.chr15:66161939G>T	Missense Mutation	RAB11A	p.D6Y	RAB11A, member RAS	57 (0.00)	145 (0.64)	1.71
12-01	Gp4	g.chr17:29848279G>T	Missense Mutation	RAB11FIP4	p.G220V	RAB11 family interacti	101 (0.00)	17 (0.29)	0.78
12-01	Gp4	g.chr17:29855463C>A	Missense Mutation	RAB11FIP4	p.L466M	RAB11 family interacti	83 (0.00)	170 (0.19)	0.50
12-01	Gp4	g.chr22:23492292C>A	Missense Mutation	RAB36	p.H104N	RAB36, member RAS c	37 (0.00)	53 (0.25)	0.65
12-01	Gp4	g.chr19:18308470C>G	Splice Site	RAB3A	p.G158A	RAB3A, member RAS	117 (0.00)	81 (0.19)	0.49
12-01	Gp4	g.chr3:128809940C>A	Nonstop Mutation	RAB43	p.*213L	RAB43, member RAS c	30 (0.00)	128 (0.38)	1.00
12-01	Gp4	g.chr3:133558382C>A	Silent	RAB6B	p.L123L	RAB6B, member RAS	34 (0.00)	35 (0.14)	0.38
12-01	Gp4	g.chr16:28922458G>A	Missense Mutation	RABEP2	p.R313W	rabaptin, RAB GTPase	132 (0.00)	52 (0.52)	1.38
12-01	Gp4	g.chr16:28935786G>T	Missense Mutation	RABEP2	p.A71D	rabaptin, RAB GTPase	190 (0.00)	70 (0.57)	1.52
12-01	Gp4	g.chr22:37637674G>A	Silent	RAC2	p.L13L	ras-related C3 botulinu	51 (0.00)	36 (0.33)	0.89
12-01	Gp4	g.chr7:4917283G>A	Missense Mutation	RADIL	p.S163L	Ras association and DIL	64 (0.00)	174 (0.22)	0.58
12-01	Gp4	g.chr9:135974071C>A	Missense Mutation	RALGDS	p.R883L	ral guanine nucleotide d	69 (0.00)	60 (0.23)	0.62
12-01	Gp4	g.chr9:129937045C>T	Silent	RALGPS1	p.S298S	Ral GEF with PH doma	171 (0.00)	160 (0.26)	0.70
12-01	Gp4	g.chr16:67762370A>G	Missense Mutation	RANBP10	p.V466A	RAN binding protein 10	51 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr19:5931427C>T	Silent	RANBP3	p.V227V	RAN binding protein 3	74 (0.00)	58 (0.16)	0.41
12-01	Gp4	g.chr19:5941630A>C	Splice Site	RANBP3		RAN binding protein 3	77 (0.00)	61 (0.30)	0.79
12-01	Gp4	g.chr22:41648966A>G	Silent	RANGAP1	p.P430P	Ran GTPase activating	38 (0.00)	48 (0.15)	0.39
12-01	Gp4	g.chr9:134455675C>A	Missense Mutation	RAPGEF1	p.D1037Y	Rap guanine nucleotide	81 (0.00)	68 (0.37)	0.98
12-01	Gp4	g.chr9:134497311C>T	Missense Mutation	RAPGEF1	p.E593K	Rap guanine nucleotide	73 (0.00)	103 (0.25)	0.67
12-01	Gp4	g.chr12:48141332G>T	Nonsense Mutation	RAPGEF3	p.C517*	Rap guanine nucleotide	16 (0.00)	46 (0.43)	1.16
12-01	Gp4	g.chr5:179545850G>T	Missense Mutation	RASGEF1C	p.S308R	RasGEF domain family,	36 (0.03)	108 (0.59)	1.58

12-01	Gp4	g.chr15:79307748C>A	Missense Mutation	RASGRF1	p.V583L	Ras protein-specific gua	102 (0.00)	59 (0.98)	2.62
12-01	Gp4	g.chr11:64508450C>A	Missense Mutation	RASGRP2	p.R114L	RAS guanyl releasing pr	339 (0.00)	335 (0.18)	0.47
12-01	Gp4	g.chr19:38903677T>C	Missense Mutation	RASGRP4	p.N477D	RAS guanyl releasing pr	117 (0.00)	67 (0.22)	0.60
12-01	Gp4	g.chr19:38903686C>G	Missense Mutation	RASGRP4	p.V474L	RAS guanyl releasing pr	118 (0.00)	66 (0.24)	0.65
12-01	Gp4	g.chr13:48913138G>T	Intron	RB1		retinoblastoma 1	32 (0.00)	59 (0.17)	0.45
12-01	Gp4	g.chr1:110884306C>A	Missense Mutation	RBM15	p.S760Y	RNA binding motif prot	65 (0.00)	74 (0.59)	1.59
12-01	Gp4	g.chr7:155504151T>C	Splice Site	RBM33		RNA binding motif prot	44 (0.00)	74 (0.49)	1.30
12-01	Gp4	g.chr1:235324256G>T	Missense Mutation	RBM34	p.F60L	RNA binding motif prot	158 (0.00)	70 (0.24)	0.65
12-01	Gp4	g.chr3:50005997C>A	Nonsense Mutation	RBM6	p.S380*	RNA binding motif prot	38 (0.00)	93 (0.45)	1.20
12-01	Gp4	g.chr3:50107953G>C	Missense Mutation	RBM6	p.G15A	RNA binding motif prot	25 (0.00)	118 (0.38)	1.02
12-01	Gp4	g.chr15:65043822C>A	Missense Mutation	RBPMS2	p.V35F	RNA binding protein wi	86 (0.00)	118 (0.43)	1.15
12-01	Gp4	g.chr1:211486246G>T	Missense Mutation	RCOR3	p.E420D	REST corepressor 3	206 (0.00)	24 (0.38)	1.00
12-01	Gp4	g.chr17:9801487T>C	Silent	RCVRN	p.T176T	recoverin	400 (0.00)	401 (0.15)	0.41
12-01	Gp4	g.chr17:73627280G>T	Missense Mutation	RECQL5	p.H500N	RecQ protein-like 5	101 (0.00)	78 (0.21)	0.55
12-01	Gp4	g.chr5:137781285G>C	Missense Mutation	REEP2	p.E192Q	receptor accessory prote	23 (0.00)	224 (0.17)	0.44
12-01	Gp4	g.chr1:204128634C>A	Silent	REN	p.V194V	renin	82 (0.00)	54 (0.56)	1.48
12-01	Gp4	g.chr1:204128658C>A	Missense Mutation	REN	p.M186I	renin	88 (0.00)	49 (0.24)	0.65
12-01	Gp4	g.chr1:204128702G>A	Nonsense Mutation	REN	p.Q172*	renin	102 (0.00)	54 (0.57)	1.53
12-01	Gp4	g.chr10:43598027C>G	Missense Mutation	RET	p.P192R	ret proto-oncogene	146 (0.00)	191 (0.21)	0.57
12-01	Gp4	g.chr2:85576639C>G	Missense Mutation	RETSAT	p.G289R	retinol saturase (all-trans	97 (0.00)	87 (0.21)	0.55
12-01	Gp4	g.chr6:111643790A>T	Missense Mutation	REV3L	p.V2778E	REV3-like, polymerase	74 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr17:80008620T>A	Missense Mutation	RFNG	p.N113Y	RFNG O-fucosylpeptide	52 (0.00)	40 (0.25)	0.67
12-01	Gp4	g.chr3:53126469G>T	Silent	RFT1	p.P419P	RFT1 homolog (S. cerev	62 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr19:11513383C>T	Splice Site	RGL3		ral guanine nucleotide d	41 (0.00)	58 (0.16)	0.41
12-01	Gp4	g.chr2:113157289C>A	Missense Mutation	RGPD8	p.A519S	RANBP2-like and GRIP	55 (0.00)	33 (0.48)	1.29
12-01	Gp4	g.chr4:3318888G>T	Missense Mutation	RGS12	p.G331C	regulator of G-protein si	119 (0.00)	177 (0.40)	1.05
12-01	Gp4	g.chr4:3417846C>A	Missense Mutation	RGS12	p.Q809K	regulator of G-protein si	23 (0.00)	29 (0.41)	1.10
12-01	Gp4	g.chr4:3419237G>T	Missense Mutation	RGS12	p.Q910H	regulator of G-protein si	30 (0.00)	93 (0.54)	1.43
12-01	Gp4	g.chr17:30615876C>A	Missense Mutation	RHBDL3	p.S22R	rhomboid, veinlet-like 3	121 (0.00)	84 (0.20)	0.54
12-01	Gp4	g.chr12:124008049C>A	Missense Mutation	RILPL1	p.K151N	Rab interacting lysosom	174 (0.01)	95 (0.81)	2.16
12-01	Gp4	g.chr12:130927050C>T	Missense Mutation	RIMBP2	p.D266N	RIMS binding protein 2	140 (0.00)	46 (0.22)	0.58
12-01	Gp4	g.chr11:66100009C>A	Missense Mutation	RIN1	p.G531V	Ras and Rab interactor 1	114 (0.00)	30 (0.63)	1.69
12-01	Gp4	g.chr14:93022193C>T	Missense Mutation	RIN3	p.R48W	Ras and Rab interactor 3	70 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr6:3078037G>T	Missense Mutation	RIPK1	p.E63D	receptor (TNFRSF)-inte	141 (0.00)	235 (0.12)	0.39
12-01	Gp4	g.chr16:67691373C>A	Missense Mutation	RLTPR	p.S1420R	RGD motif, leucine rich	44 (0.00)	115 (0.17)	0.44

12-01	Gp4	g.chr17:74150380T>C	Silent	RNF157	p.G598G	ring finger protein 157	180 (0.00)	38 (0.55)	1.47
12-01	Gp4	g.chr18:44013351C>A	Missense Mutation	RNF165	p.T87N	ring finger protein 165	37 (0.00)	41 (0.20)	0.52
12-01	Gp4	g.chr3:196210760G>A	Silent	RNF168	p.N187N	ring finger protein 168,	32 (0.00)	27 (0.26)	0.69
12-01	Gp4	g.chr1:45101747C>A	Missense Mutation	RNF220	p.H347N	ring finger protein 220	447 (0.00)	549 (0.23)	0.60
12-01	Gp4	g.chr1:151789697C>T	Missense Mutation	RORC	p.G44R	RAR-related orphan rec	76 (0.01)	12 (0.92)	2.44
12-01	Gp4	g.chr8:33832298G>T	lincRNA	RP1-273G13.3			19 (0.00)	34 (0.38)	1.02
12-01	Gp4	g.chr17:29934869G>T	lincRNA	RP1-41C23.1			48 (0.00)	28 (0.29)	0.76
12-01	Gp4	g.chr12:110323443C>T	lincRNA	RP1-7G5.6			17 (0.00)	30 (0.33)	0.89
12-01	Gp4	g.chr10:135215740G>T	Missense Mutation	RP11-108K14.	p.A226S		46 (0.00)	66 (0.86)	2.30
12-01	Gp4	g.chr11:76093241G>A	Silent	RP11-111M22	p.S123S		94 (0.00)	141 (0.38)	1.02
12-01	Gp4	g.chr12:23229453C>A	lincRNA	RP11-114G22.1			19 (0.00)	23 (0.57)	1.51
12-01	Gp4	g.chr16:31995213G>T	RNA	RP11-1166P10.1			19 (0.00)	31 (0.35)	0.95
12-01	Gp4	g.chr16:32077287G>T	RNA	RP11-1166P10.6			99 (0.00)	69 (0.32)	0.85
12-01	Gp4	g.chr4:178392930G>T	RNA	RP11-130F10.1			35 (0.00)	31 (0.65)	1.72
12-01	Gp4	g.chr4:178611456G>C	lincRNA	RP11-140M13.1			25 (0.00)	66 (0.55)	1.45
12-01	Gp4	g.chr13:34196860C>A	lincRNA	RP11-141M1.3			44 (0.00)	44 (0.23)	0.61
12-01	Gp4	g.chr3:192874368T>C	lincRNA	RP11-143P4.2			102 (0.00)	21 (0.33)	0.89
12-01	Gp4	g.chr4:133557567C>T	lincRNA	RP11-149A7.2			30 (0.00)	30 (0.80)	2.13
12-01	Gp4	g.chr17:55156215G>T	lincRNA	RP11-166P13.3			15 (0.00)	44 (0.25)	0.67
12-01	Gp4	g.chr8:57390259G>T	RNA	RP11-17A4.2			93 (0.01)	49 (0.90)	2.39
12-01	Gp4	g.chr8:57390296G>T	RNA	RP11-17A4.2			82 (0.00)	48 (0.96)	2.56
12-01	Gp4	g.chr1:238067929C>G	RNA	RP11-193H5.1			16 (0.00)	14 (0.43)	1.14
12-01	Gp4	g.chr16:2546942G>A	Missense Mutation	RP11-20I23.1	p.V265M		60 (0.00)	142 (0.20)	0.54
12-01	Gp4	g.chr4:167385173C>T	lincRNA	RP11-217C7.1			52 (0.00)	37 (0.22)	0.58
12-01	Gp4	g.chr8:139060196C>A	lincRNA	RP11-238K6.1			22 (0.00)	42 (0.55)	1.46
12-01	Gp4	g.chr13:52849788C>T	RNA	RP11-248G5.8			22 (0.00)	48 (0.33)	0.89
12-01	Gp4	g.chr12:8388071C>T	lincRNA	RP11-266K4.9			246 (0.00)	67 (0.97)	0.99
12-01	Gp4	g.chr9:89628014G>A	lincRNA	RP11-276H19.2			44 (0.00)	67 (0.15)	0.40
12-01	Gp4	g.chr10:51785778A>G	RNA	RP11-324H6.5			54 (0.00)	103 (0.24)	0.65
12-01	Gp4	g.chr15:89592144T>C	lincRNA	RP11-326A19.4			38 (0.00)	18 (0.67)	1.78
12-01	Gp4	g.chr4:13801403G>T	lincRNA	RP11-341G5.1			15 (0.00)	22 (0.73)	1.94
12-01	Gp4	g.chr15:93255340A>G	RNA	RP11-386M24.8			99 (0.00)	139 (0.24)	0.63
12-01	Gp4	g.chr13:64413507C>A	lincRNA	RP11-394A14.2			54 (0.00)	23 (0.35)	0.93
12-01	Gp4	g.chr17:40699415C>A	RNA	RP11-400F19.8			50 (0.00)	23 (0.61)	0.51
12-01	Gp4	g.chr1:142813228C>T	lincRNA	RP11-423O2.5			271 (0.00)	74 (0.95)	2.52

12-01	Gp4	g.chr17:50486787C>A	lincRNA	RP11-429O1.1	19 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr1:246940638G>T	RNA	RP11-439E19.8	98 (0.00)	41 (0.95)	2.54
12-01	Gp4	g.chr1:246943618G>T	RNA	RP11-439E19.8	221 (0.00)	330 (0.41)	1.10
12-01	Gp4	g.chr12:46986693T>A	lincRNA	RP11-446N19.1	32 (0.00)	29 (0.66)	1.75
12-01	Gp4	g.chr3:109479074C>A	lincRNA	RP11-457K10.1	41 (0.00)	41 (0.32)	0.85
12-01	Gp4	g.chr16:56188615C>A	lincRNA	RP11-461O7.1	20 (0.00)	11 (0.64)	1.70
12-01	Gp4	g.chr7:76687141C>A	RNA	RP11-467H10.2	143 (0.01)	76 (0.61)	1.61
12-01	Gp4	g.chr7:76689864G>A	RNA	RP11-467H10.2	71 (0.00)	252 (0.27)	0.71
12-01	Gp4	g.chr4:121569078A>G	lincRNA	RP11-501E14.1	24 (0.00)	31 (0.23)	0.60
12-01	Gp4	g.chr7:102210313C>A	Missense Mutation	RP11-514P8.7 p.R159I	344 (0.00)	137 (0.88)	2.36
12-01	Gp4	g.chr7:102210336G>A	Silent	RP11-514P8.7 p.C151C	362 (0.00)	139 (0.88)	2.36
12-01	Gp4	g.chr14:19412668G>A	lincRNA	RP11-536C10.16	168 (0.00)	66 (0.26)	0.69
12-01	Gp4	g.chr14:19413431A>G	lincRNA	RP11-536C10.16	240 (0.00)	78 (0.14)	0.38
12-01	Gp4	g.chr10:8464319A>G	lincRNA	RP11-543F8.2	55 (0.02)	53 (0.25)	0.65
12-01	Gp4	g.chr10:54495176G>C	RNA	RP11-556E13.1	27 (0.00)	49 (0.16)	0.44
12-01	Gp4	g.chr4:105708844G>T	lincRNA	RP11-556I14.2	59 (0.00)	41 (0.15)	0.39
12-01	Gp4	g.chr10:52419182C>G	RNA	RP11-564C4.6	20 (0.00)	11 (0.64)	1.70
12-01	Gp4	g.chr15:23101410G>T	RNA	RP11-566K19.6	25 (0.00)	33 (0.21)	0.67
12-01	Gp4	g.chr4:68312176T>C	lincRNA	RP11-584P21.2	42 (0.00)	108 (0.30)	0.79
12-01	Gp4	g.chr11:30078450C>A	lincRNA	RP11-624D11.2	19 (0.00)	32 (0.19)	0.50
12-01	Gp4	g.chr12:90313312G>T	lincRNA	RP11-654D12.2	144 (0.00)	318 (0.27)	0.73
12-01	Gp4	g.chr18:976002G>A	lincRNA	RP11-689C9.1	31 (0.00)	11 (0.73)	1.94
12-01	Gp4	g.chr4:100020561G>A	RNA	RP11-696N14.1	24 (0.00)	25 (0.80)	2.13
12-01	Gp4	g.chr3:81072297C>A	lincRNA	RP11-6B4.1	27 (0.00)	17 (0.35)	1.13
12-01	Gp4	g.chr3:128664602T>C	Missense Mutation	RP11-723O4.6 p.K70E	37 (0.00)	34 (0.21)	0.55
12-01	Gp4	g.chr18:12076002A>T	RNA	RP11-815J4.6	21 (0.00)	17 (0.41)	1.10
12-01	Gp4	g.chr18:12076234G>T	RNA	RP11-815J4.6	42 (0.00)	20 (0.30)	0.80
12-01	Gp4	g.chr5:175467761G>T	RNA	RP11-826N14.1	84 (0.00)	20 (0.50)	1.33
12-01	Gp4	g.chr11:94646260G>A	RNA	RP11-856F16.2	60 (0.00)	96 (0.67)	1.78
12-01	Gp4	g.chr3:165290761C>A	lincRNA	RP11-85M11.2	37 (0.00)	31 (0.16)	0.43
12-01	Gp4	g.chr8:81213300C>A	lincRNA	RP11-941H19.3	21 (0.00)	121 (0.40)	1.08
12-01	Gp4	g.chr8:111991317T>C	lincRNA	RP11-946L20.2	47 (0.00)	46 (0.17)	0.46
12-01	Gp4	g.chr16:4303169G>A	lincRNA	RP11-95P2.1	18 (0.00)	33 (0.42)	1.13
12-01	Gp4	g.chr3:49025126C>G	RNA	RP13-131K19.2	21 (0.00)	20 (0.60)	1.60
12-01	Gp4	g.chr12:122029621G>A	lincRNA	RP13-941N14.1	17 (0.00)	27 (0.26)	0.69

12-01	Gp4	g.chr6:134138214C>A	RNA	RP3-323P13.2			36 (0.03)	24 (0.25)	0.67
12-01	Gp4	g.chr1:44570020G>T	lincRNA	RP5-1198O20.4			48 (0.00)	35 (0.54)	1.45
12-01	Gp4	g.chr1:143663747T>C	lincRNA	RP6-206I17.1			93 (0.00)	77 (0.19)	0.52
12-01	Gp4	g.chr15:41823296T>C	Missense Mutation	RPAP1	p.T290A	RNA polymerase II ass	195 (0.00)	43 (0.16)	0.43
12-01	Gp4	g.chr1:84945089C>A	Missense Mutation	RPF1	p.P42H	ribosome production fac	72 (0.00)	46 (0.17)	0.46
12-01	Gp4	g.chr19:5691439G>A	Missense Mutation	RPL36	p.R68Q	ribosomal protein L36	100 (0.00)	150 (0.54)	1.44
12-01	Gp4	g.chr6:34386171G>T	Missense Mutation	RPS10-NUDT	p.A144D	RPS10-NUDT3 readthr	127 (0.00)	96 (0.19)	0.50
12-01	Gp4	g.chr6:166833424T>C	Missense Mutation	RPS6KA2	p.D500G	ribosomal protein S6 ki	72 (0.00)	137 (0.27)	0.72
12-01	Gp4	g.chr14:75373777G>T	Silent	RPS6KL1	p.V530V	ribosomal protein S6 ki	53 (0.00)	318 (0.17)	0.44
12-01	Gp4	g.chr15:40866098G>T	Missense Mutation	RPUSD2	p.D365Y	RNA pseudouridylate s	39 (0.03)	57 (0.16)	0.42
12-01	Gp4	g.chr20:17600974C>A	Missense Mutation	RRBP1	p.K750N	ribosome binding protei	73 (0.00)	19 (0.58)	0.86
12-01	Gp4	g.chr6:7231300G>T	Nonsense Mutation	RREB1	p.E990*	ras responsive element	20 (0.00)	39 (0.51)	1.64
12-01	Gp4	g.chr6:7231571C>T	Missense Mutation	RREB1	p.T1080I	ras responsive element	30 (0.00)	26 (0.73)	2.34
12-01	Gp4	g.chr16:29113395C>T	RNA	RRN3P2		RNA polymerase I trans	64 (0.00)	464 (0.33)	0.89
12-01	Gp4	g.chr17:48559483G>A	Missense Mutation	RSAD1	p.G169E	radical S-adenosyl meth	87 (0.00)	239 (0.74)	1.97
12-01	Gp4	g.chr7:77320873G>T	lincRNA	RSBN1L-AS1			19 (0.00)	89 (0.39)	1.05
12-01	Gp4	g.chr15:55489055G>T	Missense Mutation	RSL24D1	p.P12T	ribosomal L24 domain	55 (0.00)	11 (0.82)	2.18
12-01	Gp4	g.chr6:159407420G>A	Nonsense Mutation	RSPH3	p.Q80*	radial spoke 3 homolog	152 (0.00)	17 (0.53)	1.41
12-01	Gp4	g.chr14:101347709C>T	Silent	RTL1	p.T1139T	retrotransposon-like 1	52 (0.02)	25 (0.40)	1.07
12-01	Gp4	g.chr5:179032905G>A	Missense Mutation	RUFY1	p.E521K	RUN and FYVE domai	82 (0.00)	26 (0.69)	1.85
12-01	Gp4	g.chr1:25233851A>G	Missense Mutation	RUNX3	p.L215P	runt-related transcriptio	45 (0.00)	60 (0.25)	0.67
12-01	Gp4	g.chr9:35561362G>T	Nonsense Mutation	RUSC2	p.G1512*	RUN and SH3 domain c	24 (0.00)	61 (0.20)	0.52
12-01	Gp4	g.chr1:95712377C>A	Missense Mutation	RWDD3	p.A252E	RWD domain containin	23 (0.00)	65 (0.94)	2.50
12-01	Gp4	g.chr9:137293533G>T	Missense Mutation	RXRA	p.M28I	retinoid X receptor, alp	71 (0.00)	132 (0.29)	0.77
12-01	Gp4	g.chr9:137321019C>A	Missense Mutation	RXRA	p.L326M	retinoid X receptor, alp	63 (0.00)	73 (0.64)	1.72
12-01	Gp4	g.chr3:72438567G>T	Intron	RYBP		RING1 and YY1 bindin	19 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr3:72455960C>T	Intron	RYBP		RING1 and YY1 bindin	72 (0.00)	9 (0.78)	2.07
12-01	Gp4	g.chr3:72477053T>C	Intron	RYBP		RING1 and YY1 bindin	20 (0.00)	18 (0.44)	1.19
12-01	Gp4	g.chr19:38934416G>T	Missense Mutation	RYR1	p.G135V	ryanodine receptor 1 (sk	70 (0.00)	368 (0.55)	1.47
12-01	Gp4	g.chr19:39001164G>A	Missense Mutation	RYR1	p.E2987K	ryanodine receptor 1 (sk	86 (0.00)	77 (0.14)	0.38
12-01	Gp4	g.chr19:39008282C>A	Silent	RYR1	p.I3323I	ryanodine receptor 1 (sk	47 (0.00)	23 (0.30)	0.81
12-01	Gp4	g.chr1:237870499A>G	Silent	RYR2	p.L3277L	ryanodine receptor 2 (ca	109 (0.00)	80 (0.38)	1.00
12-01	Gp4	g.chr15:33954469C>A	Missense Mutation	RYR3	p.L1580M	ryanodine receptor 3	43 (0.00)	34 (0.18)	0.47
12-01	Gp4	g.chr1:153512617G>A	Silent	S100A5	p.H17H	S100 calcium binding p	119 (0.00)	211 (0.35)	0.92
12-01	Gp4	g.chr16:51175304T>C	Missense Mutation	SALL1	p.T277A	spalt-like transcription f	190 (0.00)	299 (0.38)	1.03

12-01	Gp4	g.chr20:50408009G>T	Missense Mutation	SALL4	p.A338D	spalt-like transcription f	120 (0.00)	172 (0.42)	1.12
12-01	Gp4	g.chr20:50408295C>A	Missense Mutation	SALL4	p.A243S	spalt-like transcription f	72 (0.00)	71 (0.41)	1.09
12-01	Gp4	g.chr19:39871716C>A	Silent	SAMD4B	p.V645V	sterile alpha motif doma	51 (0.00)	135 (0.19)	0.49
12-01	Gp4	g.chr22:50903476A>G	Missense Mutation	SBF1	p.V429A	SET binding factor 1	25 (0.00)	51 (0.24)	0.63
12-01	Gp4	g.chr3:47459246C>A	Missense Mutation	SCAP	p.G840C	SREBF chaperone	21 (0.00)	38 (0.18)	0.49
12-01	Gp4	g.chr11:193881A>G	Silent	SCGB1C1	p.P75P	secretoglobin, family 1C	76 (0.00)	94 (0.16)	0.43
12-01	Gp4	g.chr3:38949576G>T	Missense Mutation	SCN11A	p.T446N	sodium channel, voltage	16 (0.00)	20 (0.50)	1.33
12-01	Gp4	g.chr8:144876073C>A	Missense Mutation	SCRIB	p.Q1302H	scribbled planar cell pol	76 (0.00)	342 (0.24)	0.63
12-01	Gp4	g.chr11:65303528C>T	Silent	SCYL1	p.L497L	SCY1-like 1 (S. cerevisi	63 (0.00)	69 (0.41)	1.08
12-01	Gp4	g.chr2:20403955G>T	Silent	SDC1	p.G82G	syndecan 1	140 (0.00)	218 (0.19)	0.50
12-01	Gp4	g.chr5:226017C>G	Missense Mutation	SDHA	p.P159R	succinate dehydrogenase	166 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr3:195712471G>C	RNA	SDHAP1		succinate dehydrogenase	302 (0.00)	56 (0.57)	1.52
12-01	Gp4	g.chr7:4218193C>A	Silent	SDK1	p.P1671P	sidekick cell adhesion m	139 (0.01)	392 (0.28)	0.76
12-01	Gp4	g.chr2:192711595C>A	Silent	SDPR	p.R19R	serum deprivation respo	172 (0.00)	134 (0.30)	0.80
12-01	Gp4	g.chr14:24909526C>T	Silent	SDR39U1	p.L48L	short chain dehydrogena	116 (0.00)	55 (0.24)	0.63
12-01	Gp4	g.chr22:30891381C>A	Missense Mutation	SEC14L4	p.G95C	SEC14-like 4 (S. cerevis	29 (0.00)	44 (0.43)	1.15
12-01	Gp4	g.chr9:139341421G>T	Silent	SEC16A	p.L254L	SEC16 homolog A (S. c	133 (0.00)	57 (0.33)	0.89
12-01	Gp4	g.chr5:133996842A>G	Missense Mutation	SEC24A	p.E44G	SEC24 family member A	90 (0.00)	104 (0.16)	0.44
12-01	Gp4	g.chr17:80280072G>A	Missense Mutation	SECTM1	p.P238S	secreted and transmemb	21 (0.00)	54 (0.20)	0.54
12-01	Gp4	g.chr2:97527188C>G	Missense Mutation	SEMA4C	p.R559S	sema domain, immunog	39 (0.00)	30 (0.77)	2.04
12-01	Gp4	g.chr10:102740959C>T	Nonsense Mutation	SEMA4G	p.R560*	sema domain, immunog	117 (0.00)	35 (0.14)	0.38
12-01	Gp4	g.chr1:151108156C>A	Silent	SEMA6C	p.G448G	sema domain, transmem	84 (0.00)	62 (0.31)	0.82
12-01	Gp4	g.chr1:151115058G>T	Missense Mutation	SEMA6C	p.L14M	sema domain, transmem	71 (0.00)	99 (0.15)	0.40
12-01	Gp4	g.chr1:26135179G>A	Missense Mutation	SEPN1	p.E182K	selenoprotein N, 1	127 (0.00)	199 (0.50)	1.33
12-01	Gp4	g.chr1:26140375C>G	Nonsense Mutation	SEPN1	p.S430*	selenoprotein N, 1	100 (0.00)	47 (0.30)	0.79
12-01	Gp4	g.chr16:4829721C>A	Missense Mutation	SEPT12	p.G265C	septin 12	79 (0.00)	43 (0.21)	0.56
12-01	Gp4	g.chr7:55910680G>T	Silent	SEPT14	p.S171S	septin 14	236 (0.00)	294 (0.14)	0.38
12-01	Gp4	g.chr10:38681993C>T	RNA	SEPT7P9		septin 7 pseudogene 9	27 (0.00)	123 (0.44)	1.17
12-01	Gp4	g.chr1:67878912T>C	Missense Mutation	SERBP1	p.E402G	SERPINE1 mRNA bind	15 (0.00)	21 (0.67)	1.78
12-01	Gp4	g.chr14:95107149G>A	RNA	SERPINA13P		serpin peptidase inhibito	45 (0.00)	20 (0.60)	1.60
12-01	Gp4	g.chr1:28598236C>G	Missense Mutation	SESN2	p.L70V	sestrin 2	147 (0.00)	134 (0.33)	0.88
12-01	Gp4	g.chr16:30970069G>C	Missense Mutation	SETD1A	p.G6A	SET domain containing	85 (0.00)	39 (0.23)	0.62
12-01	Gp4	g.chr21:37408451G>T	Silent	SETD4	p.A429A	SET domain containing	195 (0.00)	105 (0.37)	0.99
12-01	Gp4	g.chr9:135224765G>A	Silent	SETX	p.F17F	senataxin	79 (0.00)	67 (0.15)	0.40
12-01	Gp4	g.chr16:29898974C>G	Missense Mutation	SEZ6L2	p.D402H	seizure related 6 homolo	190 (0.00)	129 (0.98)	2.60

12-01	Gp4	g.chr22:32009652G>T	Missense Mutation	SFI1	p.G905V	Sfi1 homolog, spindle a	15 (0.00)	17 (0.35)	0.94
12-01	Gp4	g.chr1:27189928G>T	Missense Mutation	SFN	p.E75D	stratifin	131 (0.00)	193 (0.15)	0.40
12-01	Gp4	g.chr10:102795264G>A	Missense Mutation	SFXN3	p.V58M	sideroflexin 3	94 (0.00)	85 (0.15)	0.41
12-01	Gp4	g.chr2:73198714C>A	Missense Mutation	SFXN5	p.K242N	sideroflexin 5	84 (0.00)	26 (0.42)	1.13
12-01	Gp4	g.chr17:26939690G>T	Missense Mutation	SGK494	p.P165T		61 (0.02)	30 (0.97)	2.58
12-01	Gp4	g.chr3:20225108G>A	Missense Mutation	SGOL1	p.P111S	shugoshin-like 1 (S. por	15 (0.00)	10 (0.70)	1.87
12-01	Gp4	g.chr22:40800295A>G	Missense Mutation	SGSM3	p.M68V	small G protein signalin	135 (0.00)	103 (0.19)	0.52
12-01	Gp4	g.chr19:6760818G>A	Nonsense Mutation	SH2D3A	p.Q84*	SH2 domain containing	89 (0.00)	140 (0.71)	1.89
12-01	Gp4	g.chr9:130540871G>T	Splice Site	SH2D3C	p.F12L	SH2 domain containing	112 (0.00)	51 (0.24)	0.63
12-01	Gp4	g.chr1:21050953G>T	Missense Mutation	SH2D5	p.S189Y	SH2 domain containing	36 (0.00)	120 (0.26)	0.69
12-01	Gp4	g.chr22:38046570G>T	Missense Mutation	SH3BP1	p.G479V	SH3-domain binding pr	78 (0.00)	100 (0.50)	1.33
12-01	Gp4	g.chr2:235950235C>A	Silent	SH3BP4	p.P274P	SH3-domain binding pr	207 (0.00)	350 (0.20)	0.54
12-01	Gp4	g.chr2:235950313G>A	Silent	SH3BP4	p.L300L	SH3-domain binding pr	137 (0.00)	207 (0.61)	1.64
12-01	Gp4	g.chr2:235950991G>T	Missense Mutation	SH3BP4	p.K526N	SH3-domain binding pr	109 (0.00)	44 (0.68)	1.82
12-01	Gp4	g.chr10:105376974C>T	Silent	SH3PXD2A	p.L300L	SH3 and PX domains 2	30 (0.00)	12 (0.42)	1.11
12-01	Gp4	g.chr2:110048983C>A	Missense Mutation	SH3RF3	p.P477H	SH3 domain containing	41 (0.00)	56 (0.71)	1.90
12-01	Gp4	g.chr4:8218773G>T	Missense Mutation	SH3TC1	p.A240S	SH3 domain and tetratri	60 (0.00)	70 (0.26)	0.69
12-01	Gp4	g.chr22:51121794C>G	Missense Mutation	SHANK3	p.F304L	SH3 and multiple ankyr	34 (0.00)	57 (0.23)	0.61
12-01	Gp4	g.chr9:37974820C>T	Missense Mutation	SHB	p.E285K	Src homology 2 domain	60 (0.00)	36 (0.83)	2.22
12-01	Gp4	g.chr17:7534663C>A	Missense Mutation	SHBG	p.S180Y	sex hormone-binding gl	97 (0.00)	149 (0.32)	0.86
12-01	Gp4	g.chr9:91692803G>A	Silent	SHC3	p.R187R	SHC (Src homology 2 d	65 (0.00)	21 (0.43)	1.14
12-01	Gp4	g.chr19:41096189A>G	Silent	SHKBP1	p.T543T	SH3KBP1 binding prot	15 (0.00)	14 (0.64)	1.71
12-01	Gp4	g.chr17:18250870G>T	Missense Mutation	SHMT1	p.F153L	serine hydroxymethyltra	304 (0.00)	235 (0.17)	0.45
12-01	Gp4	g.chr17:3527387G>T	Missense Mutation	SHPK	p.A150D	sedoheptulokinase	48 (0.00)	129 (0.58)	1.55
12-01	Gp4	g.chr3:72858192G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	140 (0.00)	51 (0.96)	2.56
12-01	Gp4	g.chr3:72872170G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	40 (0.00)	149 (0.31)	0.82
12-01	Gp4	g.chr4:77476834G>A	Missense Mutation	SHROOM3	p.E81K	shroom family member	36 (0.00)	114 (0.24)	0.63
12-01	Gp4	g.chrX:50378477G>T	Missense Mutation	SHROOM4	p.A199D	shroom family member	37 (0.00)	23 (0.26)	0.43
12-01	Gp4	g.chr20:3674170G>T	Silent	SIGLEC1	p.A1144A	sialic acid binding Ig-lik	39 (0.00)	25 (0.52)	0.43
12-01	Gp4	g.chr11:111594286G>A	Silent	SIK2	p.Q738Q	salt-inducible kinase 2	39 (0.00)	106 (0.21)	0.55
12-01	Gp4	g.chr14:72055593A>G	Missense Mutation	SIPA1L1	p.D335G	signal-induced prolifera	41 (0.00)	35 (0.29)	0.76
12-01	Gp4	g.chr19:38633254C>A	Missense Mutation	SIPA1L3	p.A1146E	signal-induced prolifera	127 (0.01)	507 (0.15)	0.41
12-01	Gp4	g.chr9:35650510C>A	Silent	SIT1	p.P75P	signaling threshold regu	68 (0.00)	87 (0.17)	0.46
12-01	Gp4	g.chr16:67979417C>A	Nonsense Mutation	SLC12A4	p.E963*	solute carrier family 12	61 (0.00)	45 (0.38)	1.01
12-01	Gp4	g.chr16:67979685C>A	Missense Mutation	SLC12A4	p.K943N	solute carrier family 12	106 (0.00)	40 (0.68)	1.80

12-01	Gp4	g.chr5:1053510C>A	Silent	SLC12A7	p.L1038L	solute carrier family 12	65 (0.00)	88 (0.41)	1.09
12-01	Gp4	g.chr17:26821068C>T	Silent	SLC13A2	p.I377I	solute carrier family 13	42 (0.00)	86 (0.55)	1.46
12-01	Gp4	g.chr12:60165049G>A	Silent	SLC16A7	p.V89V	solute carrier family 16	115 (0.00)	53 (0.45)	1.21
12-01	Gp4	g.chr2:113417995T>A	Missense Mutation	SLC20A1	p.L547M	solute carrier family 20	131 (0.00)	11 (0.45)	1.21
12-01	Gp4	g.chr3:38350536C>T	Silent	SLC22A14	p.I289I	solute carrier family 22,	219 (0.00)	13 (0.85)	2.26
12-01	Gp4	g.chr17:73269562G>A	Silent	SLC25A19	p.H311H	solute carrier family 25	50 (0.02)	23 (0.26)	0.70
12-01	Gp4	g.chr1:16063339T>C	Missense Mutation	SLC25A34	p.V120A	solute carrier family 25,	44 (0.02)	59 (0.20)	0.54
12-01	Gp4	g.chr4:186066959G>T	Missense Mutation	SLC25A4	p.M215I	solute carrier family 25	56 (0.00)	29 (0.97)	2.57
12-01	Gp4	g.chr17:78196544T>C	Missense Mutation	SLC26A11	p.S109P	solute carrier family 26	46 (0.02)	97 (0.29)	0.77
12-01	Gp4	g.chr9:131118037C>A	Missense Mutation	SLC27A4	p.P579H	solute carrier family 27	141 (0.01)	415 (0.16)	0.44
12-01	Gp4	g.chr22:24219239G>T	Missense Mutation	SLC2A11	p.M139I	solute carrier family 2 (	70 (0.00)	183 (0.49)	1.31
12-01	Gp4	g.chr1:9085105G>A	Missense Mutation	SLC2A7	p.T27I	solute carrier family 2 (	25 (0.00)	25 (0.84)	2.24
12-01	Gp4	g.chr9:130166243C>A	Missense Mutation	SLC2A8	p.S291R	solute carrier family 2 (	17 (0.00)	24 (0.29)	0.78
12-01	Gp4	g.chr20:37353567G>T	Missense Mutation	SLC32A1	p.G67V	solute carrier family 32	57 (0.02)	97 (0.15)	0.41
12-01	Gp4	g.chr5:176815108C>A	Missense Mutation	SLC34A1	p.A253D	solute carrier family 34	44 (0.00)	12 (0.42)	1.11
12-01	Gp4	g.chr5:139947340T>C	Missense Mutation	SLC35A4	p.C196R	solute carrier family 35,	105 (0.00)	138 (0.32)	0.85
12-01	Gp4	g.chr20:44979458G>A	Silent	SLC35C2	p.F303F	solute carrier family 35	64 (0.00)	52 (0.69)	1.85
12-01	Gp4	g.chr20:44979499G>A	Silent	SLC35C2	p.L290L	solute carrier family 35	50 (0.00)	64 (0.73)	1.96
12-01	Gp4	g.chr5:150867733T>A	Missense Mutation	SLC36A1	p.V450E	solute carrier family 36	73 (0.00)	17 (0.35)	0.94
12-01	Gp4	g.chr17:79226916G>A	Silent	SLC38A10	p.G471G	solute carrier family 38,	63 (0.00)	93 (0.18)	0.49
12-01	Gp4	g.chr10:18284589G>A	Missense Mutation	SLC39A12	p.S512N	solute carrier family 39	48 (0.00)	153 (0.15)	0.40
12-01	Gp4	g.chr8:145642046G>T	Missense Mutation	SLC39A4	p.A43D	solute carrier family 39	19 (0.00)	27 (0.59)	1.58
12-01	Gp4	g.chr3:125786883C>A	Missense Mutation	SLC41A3	p.E60D	solute carrier family 41,	117 (0.00)	210 (0.21)	0.56
12-01	Gp4	g.chr11:57268659G>T	Missense Mutation	SLC43A1	p.R100S	solute carrier family 43	20 (0.00)	40 (0.35)	0.93
12-01	Gp4	g.chr19:10748356G>A	Missense Mutation	SLC44A2	p.C543Y	solute carrier family 44	77 (0.01)	156 (0.22)	0.58
12-01	Gp4	g.chr1:205633637C>A	Nonsense Mutation	SLC45A3	p.E50*	solute carrier family 45,	271 (0.00)	365 (0.20)	0.53
12-01	Gp4	g.chr8:142226039T>C	Missense Mutation	SLC45A4	p.D536G	solute carrier family 45,	51 (0.00)	44 (0.25)	0.67
12-01	Gp4	g.chr8:142231806G>T	Silent	SLC45A4	p.I49I	solute carrier family 45,	175 (0.00)	199 (0.15)	0.39
12-01	Gp4	g.chr17:19459328C>A	Missense Mutation	SLC47A1	p.L269M	solute carrier family 47	71 (0.00)	47 (0.15)	0.40
12-01	Gp4	g.chr2:162805754G>T	Missense Mutation	SLC4A10	p.V788L	solute carrier family 4,	51 (0.00)	30 (0.80)	2.13
12-01	Gp4	g.chr2:220501572C>A	Nonsense Mutation	SLC4A3	p.Y837*	solute carrier family 4 (	184 (0.00)	169 (0.33)	0.87
12-01	Gp4	g.chr1:110735274C>A	Nonsense Mutation	SLC6A17	p.S418*	solute carrier family 6 (	97 (0.00)	131 (0.19)	0.51
12-01	Gp4	g.chr5:1210591G>T	Nonsense Mutation	SLC6A19	p.G126*	solute carrier family 6 (	38 (0.00)	27 (0.44)	1.19
12-01	Gp4	g.chr5:1443079C>A	Silent	SLC6A3	p.V78V	solute carrier family 6 (	111 (0.00)	39 (0.18)	0.48
12-01	Gp4	g.chr16:87873414A>G	Missense Mutation	SLC7A5	p.I278T	solute carrier family 7 (	52 (0.00)	12 (0.42)	0.46

12-01	Gp4	g.chr2:40241136G>T	RNA	SLC8A1-AS1		SLC8A1 antisense RNA	16 (0.00)	40 (0.40)	1.07
12-01	Gp4	g.chr2:103274251C>G	Missense Mutation	SLC9A2	p.A173G	solute carrier family 9, s	128 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr5:476193G>T	Silent	SLC9A3	p.I694I	solute carrier family 9, s	48 (0.00)	40 (0.15)	0.40
12-01	Gp4	g.chr16:67304847G>T	Missense Mutation	SLC9A5	p.A809S	solute carrier family 9, s	166 (0.00)	279 (0.34)	0.92
12-01	Gp4	g.chr20:61299469G>A	Missense Mutation	SLCO4A1	p.V582I	solute carrier organic an	256 (0.00)	119 (0.28)	0.74
12-01	Gp4	g.chr10:98819843C>G	Splice Site	SLIT1		slit homolog 1 (Drosoph	132 (0.00)	125 (0.33)	0.87
12-01	Gp4	g.chr16:3633274A>G	Silent	SLX4	p.P1659P	SLX4 structure-specific	143 (0.00)	107 (0.28)	0.75
12-01	Gp4	g.chr16:3639256G>T	Silent	SLX4	p.A1461A	SLX4 structure-specific	30 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr18:48578728C>A	Intron	SMAD4		SMAD family member	89 (0.00)	18 (0.50)	1.33
12-01	Gp4	g.chr18:48589408G>T	Intron	SMAD4		SMAD family member	55 (0.00)	30 (0.57)	1.51
12-01	Gp4	g.chr19:11098366C>A	Missense Mutation	SMARCA4	p.P295H	SWI/SNF related, matri	29 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr19:11136143C>G	Missense Mutation	SMARCA4	p.R1043G	SWI/SNF related, matri	44 (0.00)	18 (0.44)	1.19
12-01	Gp4	g.chr3:160119743G>T	Missense Mutation	SMC4	p.E60D	structural maintenance c	124 (0.00)	144 (0.92)	2.44
12-01	Gp4	g.chr17:18221307T>C	Missense Mutation	SMCR8	p.V735A	Smith-Magenis syndron	233 (0.00)	149 (0.19)	0.52
12-01	Gp4	g.chr17:18226372G>T	Missense Mutation	SMCR8	p.L934F	Smith-Magenis syndron	63 (0.00)	20 (0.60)	1.60
12-01	Gp4	g.chr16:18848746C>T	Missense Mutation	SMG1	p.R2478K	SMG1 phosphatidylinos	102 (0.00)	14 (0.79)	2.10
12-01	Gp4	g.chr19:44251828G>T	Silent	SMG9	p.I149I	SMG9 nonsense mediat	22 (0.00)	37 (0.16)	0.43
12-01	Gp4	g.chr6:84303301G>T	Missense Mutation	SNAP91	p.A531D	synaptosomal-associate	51 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr9:139276382C>A	Silent	SNAPC4	p.R737R	small nuclear RNA acti	29 (0.00)	32 (0.19)	0.50
12-01	Gp4	g.chr17:47018391G>C	Missense Mutation	SNF8	p.L47V	SNF8, ESCRT-II compl	81 (0.00)	32 (0.25)	0.67
12-01	Gp4	g.chr1:28909493C>A	RNA	SNHG12		small nucleolar RNA ho	27 (0.00)	56 (0.14)	0.38
12-01	Gp4	g.chr15:25440150G>T	RNA	SNHG14		small nucleolar RNA ho	124 (0.00)	113 (0.28)	0.90
12-01	Gp4	g.chr2:27596151C>G	Missense Mutation	SNX17	p.F98L	sorting nexin 17	53 (0.00)	52 (0.33)	0.87
12-01	Gp4	g.chr11:130784841C>A	Missense Mutation	SNX19	p.G332C	sorting nexin 19	108 (0.00)	56 (0.96)	2.57
12-01	Gp4	g.chr15:75942072A>T	Missense Mutation	SNX33	p.E210V	sorting nexin 33	113 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr20:35444275C>T	Missense Mutation	SOGA1	p.E524K	suppressor of glucose, a	30 (0.00)	83 (0.14)	0.39
12-01	Gp4	g.chr20:35444293A>T	Missense Mutation	SOGA1	p.F518I	suppressor of glucose, a	35 (0.00)	83 (0.14)	0.39
12-01	Gp4	g.chr6:127796884C>T	Missense Mutation	SOGA3	p.D763N	SOGA family member	35 (0.03)	71 (0.55)	1.46
12-01	Gp4	g.chr21:34922829C>A	Missense Mutation	SON	p.P431H	SON DNA binding prot	59 (0.00)	11 (0.73)	1.94
12-01	Gp4	g.chr10:97174587C>T	Silent	SORBS1	p.E158E	sorbin and SH3 domain	108 (0.00)	45 (0.16)	0.41
12-01	Gp4	g.chr4:7640180G>T	Missense Mutation	SORCS2	p.K258N	sortilin-related VPS10 d	43 (0.00)	51 (0.80)	2.14
12-01	Gp4	g.chr11:121498353G>T	Missense Mutation	SORL1	p.G1062W	sortilin-related receptor,	114 (0.00)	50 (0.62)	1.65
12-01	Gp4	g.chr2:110373571G>A	Missense Mutation	SOWAHC	p.G502E	sosondowah ankyrin rep	67 (0.00)	22 (0.59)	1.58
12-01	Gp4	g.chr5:157073789G>C	Missense Mutation	SOX30	p.R415G	SRY (sex determining r	44 (0.00)	29 (0.93)	2.48
12-01	Gp4	g.chr17:45994332C>A	Missense Mutation	SP2	p.Q299K	Sp2 transcription factor	145 (0.00)	420 (0.28)	0.74

12-01	Gp4	g.chr17:4863391C>A	Missense Mutation	SPAG7	p.D64Y	sperm associated antige	15 (0.00)	115 (0.41)	1.09
12-01	Gp4	g.chr20:48524731G>T	Silent	SPATA2	p.L99L	spermatogenesis associa	172 (0.00)	514 (0.35)	0.93
12-01	Gp4	g.chr9:90535414C>A	RNA	SPATA31C1		SPATA31 subfamily C,	268 (0.00)	270 (0.26)	0.69
12-01	Gp4	g.chr19:11258541C>T	Missense Mutation	SPC24	p.S147N	SPC24, NDC80 kinetoc	57 (0.00)	26 (0.69)	1.85
12-01	Gp4	g.chr7:44042271G>A	Silent	SPDYE1	p.S114S	speedy/RINGO cell cyc	140 (0.00)	272 (0.21)	0.57
12-01	Gp4	g.chr7:99917286C>A	Missense Mutation	SPDYE3	p.P482H	speedy/RINGO cell cyc	319 (0.00)	162 (0.38)	1.00
12-01	Gp4	g.chr2:220355169C>A	Missense Mutation	SPEG	p.A2987D	SPEG complex locus	43 (0.00)	59 (0.22)	0.59
12-01	Gp4	g.chr13:46287767C>G	Missense Mutation	SPERT	p.H167D	spermatid associated	53 (0.00)	75 (0.19)	0.50
12-01	Gp4	g.chr15:65256016G>T	Missense Mutation	SPG21	p.A264D	spastic paraplegia 21 (a	40 (0.00)	48 (0.25)	0.67
12-01	Gp4	g.chr2:228882473C>A	Missense Mutation	SPHKAP	p.D1033Y	SPHK1 interactor, AKA	71 (0.00)	15 (0.67)	1.78
12-01	Gp4	g.chr19:38774352G>T	Missense Mutation	SPINT2	p.Q14H	serine peptidase inhibito	125 (0.00)	165 (0.21)	0.55
12-01	Gp4	g.chr17:4435939C>A	Silent	SPNS2	p.R299R	spinster homolog 2 (Dro	74 (0.00)	104 (0.37)	0.97
12-01	Gp4	g.chr1:32263855G>C	Missense Mutation	SPOCD1	p.L700V	SPOC domain containin	55 (0.00)	18 (0.28)	0.74
12-01	Gp4	g.chr4:168155202A>G	Silent	SPOCK3	p.D41D	sparc/osteonectin, cwcv	34 (0.00)	47 (0.53)	1.42
12-01	Gp4	g.chr12:56863182G>C	Missense Mutation	SPRYD4	p.E149Q	SPRY domain containin	113 (0.00)	55 (0.51)	1.36
12-01	Gp4	g.chr12:56863233G>C	Missense Mutation	SPRYD4	p.D166H	SPRY domain containin	119 (0.00)	69 (0.32)	0.85
12-01	Gp4	g.chr16:1827820C>A	Missense Mutation	SPSB3	p.G217C	splA/ryanodine receptor	31 (0.00)	45 (0.24)	0.65
12-01	Gp4	g.chr9:131388141C>G	Missense Mutation	SPTAN1	p.Q2050E	spectrin, alpha, non-eryt	103 (0.00)	38 (0.32)	0.84
12-01	Gp4	g.chr14:65246559C>A	Missense Mutation	SPTB	p.D1453Y	spectrin, beta, erythrocy	188 (0.00)	265 (0.18)	0.49
12-01	Gp4	g.chr14:65263308G>C	Silent	SPTB	p.T436T	spectrin, beta, erythrocy	135 (0.00)	223 (0.18)	0.48
12-01	Gp4	g.chr11:66455692G>C	Missense Mutation	SPTBN2	p.P2108A	spectrin, beta, non-eryth	37 (0.00)	67 (0.31)	0.84
12-01	Gp4	g.chr11:66463814G>T	Silent	SPTBN2	p.A1404A	spectrin, beta, non-eryth	21 (0.00)	21 (0.29)	0.76
12-01	Gp4	g.chr15:42171490C>A	Missense Mutation	SPTBN5	p.R1050S	spectrin, beta, non-eryth	83 (0.00)	84 (0.35)	0.92
12-01	Gp4	g.chr17:17720274G>T	Silent	SREBF1	p.R595R	sterol regulatory elemen	103 (0.00)	46 (0.67)	1.80
12-01	Gp4	g.chr11:126135925C>T	Silent	SRPR	p.V300V	signal recognition partic	173 (0.00)	50 (0.60)	1.60
12-01	Gp4	g.chr16:2812617A>G	Silent	SRRM2	p.T696T	serine/arginine repetitiv	110 (0.00)	45 (0.58)	1.54
12-01	Gp4	g.chr19:56009339G>T	Missense Mutation	SSC5D	p.D494Y	scavenger receptor cyste	58 (0.02)	30 (0.43)	1.16
12-01	Gp4	g.chr19:56009353G>T	Missense Mutation	SSC5D	p.M498I	scavenger receptor cyste	41 (0.00)	22 (0.23)	0.61
12-01	Gp4	g.chr2:182786713T>C	Silent	SSFA2	p.S592S	sperm specific antigen 2	49 (0.00)	10 (0.90)	2.40
12-01	Gp4	g.chr9:140084363C>A	Missense Mutation	SSNA1	p.S119R	Sjogren syndrome nucle	52 (0.02)	50 (0.32)	0.85
12-01	Gp4	g.chr7:149486155G>T	RNA	SSPO		SCO-spondin	25 (0.00)	15 (0.33)	0.89
12-01	Gp4	g.chr7:149491836G>T	RNA	SSPO		SCO-spondin	35 (0.00)	47 (0.15)	0.40
12-01	Gp4	g.chr7:149509641G>T	RNA	SSPO		SCO-spondin	273 (0.00)	442 (0.28)	0.75
12-01	Gp4	g.chr7:149515705C>T	RNA	SSPO		SCO-spondin	20 (0.00)	26 (0.23)	0.62
12-01	Gp4	g.chr7:149523990C>A	RNA	SSPO		SCO-spondin	130 (0.00)	81 (0.19)	0.49

12-01	Gp4	g.chr8:134472140C>G	Missense Mutation	ST3GAL1	p.W297S	ST3 beta-galactoside al	71 (0.00)	17 (0.29)	0.78
12-01	Gp4	g.chr16:70422386G>A	Silent	ST3GAL2	p.F199F	ST3 beta-galactoside al	42 (0.00)	188 (0.88)	2.34
12-01	Gp4	g.chr9:130674765C>A	Silent	ST6GALNAC	p.L131L	ST6 (alpha-N-acetyl-ne	78 (0.00)	121 (0.19)	0.51
12-01	Gp4	g.chr3:52550388T>A	Missense Mutation	STAB1	p.H1387Q	stabilin 1	27 (0.00)	38 (0.18)	0.49
12-01	Gp4	g.chr12:104048393G>A	Missense Mutation	STAB2	p.D490N	stabilin 2	23 (0.00)	20 (0.90)	2.40
12-01	Gp4	g.chr12:57640619C>T	Missense Mutation	STAC3	p.E191K	SH3 and cysteine rich d	220 (0.00)	91 (0.97)	2.58
12-01	Gp4	g.chr7:99798717C>A	Missense Mutation	STAG3	p.S689Y	stromal antigen 3	61 (0.00)	24 (0.29)	0.78
12-01	Gp4	g.chr7:72470019C>T	RNA	STAG3L3		stromal antigen 3-like 3	24 (0.00)	166 (0.85)	2.27
12-01	Gp4	g.chr13:33704288C>A	Missense Mutation	STARD13	p.G176W	StAR-related lipid trans	15 (0.00)	32 (0.25)	0.67
12-01	Gp4	g.chrX:67941976G>T	Missense Mutation	STARD8	p.M849I	StAR-related lipid trans	30 (0.00)	12 (0.92)	1.53
12-01	Gp4	g.chr2:219563523G>T	Missense Mutation	STK36	p.A1086S	serine/threonine kinase	189 (0.01)	208 (0.23)	0.60
12-01	Gp4	g.chr1:36807503C>G	Missense Mutation	STK40	p.E387D	serine/threonine kinase	21 (0.00)	43 (0.33)	0.87
12-01	Gp4	g.chr11:62594833G>T	Missense Mutation	STX5	p.L112M	syntaxin 5	222 (0.00)	169 (0.21)	0.57
12-01	Gp4	g.chr19:19414559C>T	Silent	SUGP1	p.E212E	SURP and G patch dom	282 (0.00)	133 (0.55)	1.46
12-01	Gp4	g.chr19:19115120G>A	Missense Mutation	SUGP2	p.A929V	SURP and G patch dom	23 (0.00)	44 (0.36)	0.97
12-01	Gp4	g.chr19:19115393C>T	Missense Mutation	SUGP2	p.C838Y	SURP and G patch dom	85 (0.00)	76 (0.17)	0.46
12-01	Gp4	g.chr19:19120909G>A	Missense Mutation	SUGP2	p.T698I	SURP and G patch dom	129 (0.00)	103 (0.19)	0.52
12-01	Gp4	g.chr7:883044G>T	Missense Mutation	SUN1	p.G182V	Sad1 and UNC84 doma	309 (0.00)	35 (0.31)	0.84
12-01	Gp4	g.chr12:56398781G>T	Missense Mutation	SUOX	p.W536C	sulfite oxidase	222 (0.00)	269 (0.20)	0.54
12-01	Gp4	g.chr14:21827706C>A	Missense Mutation	SUPT16H	p.E746D	suppressor of Ty 16 hon	78 (0.00)	64 (0.22)	0.58
12-01	Gp4	g.chr10:70940087G>T	Missense Mutation	SUPV3L1	p.A14S	suppressor of var1, 3-lik	27 (0.00)	36 (0.92)	2.44
12-01	Gp4	g.chr22:24583665C>A	Missense Mutation	SUSD2	p.P673H	sushi domain containing	86 (0.00)	161 (0.15)	0.40
12-01	Gp4	g.chr19:55853327C>A	Missense Mutation	SUV420H2	p.A8E	suppressor of variegatio	37 (0.00)	11 (0.91)	2.42
12-01	Gp4	g.chr1:149880756G>T	Missense Mutation	SV2A	p.T456N	synaptic vesicle glycopr	142 (0.00)	74 (0.34)	0.90
12-01	Gp4	g.chr9:113197580T>A	Missense Mutation	SVEP1	p.D1587V	sushi, von Willebrand f	40 (0.00)	12 (0.50)	1.33
12-01	Gp4	g.chr1:85656385C>A	Nonsense Mutation	SYDE2	p.E266*	synapse defective 1, Rh	29 (0.00)	27 (0.93)	2.47
12-01	Gp4	g.chr22:32914133C>A	Missense Mutation	SYN3	p.G503C	synapsin III	153 (0.00)	63 (0.35)	0.93
12-01	Gp4	g.chr6:152462340G>T	Missense Mutation	SYNE1	p.A8415D	spectrin repeat containi	162 (0.00)	159 (0.35)	0.92
12-01	Gp4	g.chr6:152757094T>C	Missense Mutation	SYNE1	p.E1431G	spectrin repeat containi	21 (0.00)	15 (0.53)	1.42
12-01	Gp4	g.chr14:64470001C>T	Silent	SYNE2	p.I1450I	spectrin repeat containi	15 (0.00)	36 (0.22)	0.59
12-01	Gp4	g.chr14:64679535C>T	Nonsense Mutation	SYNE2	p.Q6249*	spectrin repeat containi	44 (0.00)	97 (0.22)	0.58
12-01	Gp4	g.chr14:95884178G>T	Silent	SYNE3	p.G971G	spectrin repeat containi	227 (0.00)	137 (0.68)	1.81
12-01	Gp4	g.chr19:48879348C>A	Missense Mutation	SYNGR4	p.Q160K	synaptogyrin 4	42 (0.00)	13 (0.85)	2.26
12-01	Gp4	g.chr5:150027979C>A	Silent	SYNPO	p.R48R	synaptopodin	200 (0.01)	54 (0.15)	0.40
12-01	Gp4	g.chr10:75406933C>A	Missense Mutation	SYNPO2L	p.R826L	synaptopodin 2-like	72 (0.00)	50 (0.16)	0.43

12-01	Gp4	g.chr10:75413315T>C	Silent	SYNPO2L	p.P118P	synaptopodin 2-like	72 (0.00)	78 (0.37)	0.99
12-01	Gp4	g.chr19:55687401G>T	Missense Mutation	SYT5	p.S115Y	synaptotagmin V	280 (0.00)	284 (0.54)	1.45
12-01	Gp4	g.chr11:61290697C>T	Silent	SYT7	p.K363K	synaptotagmin VII	78 (0.00)	175 (0.27)	0.72
12-01	Gp4	g.chr6:166580079C>T	Splice Site	T		T, brachyury homolog (	147 (0.00)	123 (0.33)	0.87
12-01	Gp4	g.chr10:123843705G>T	Missense Mutation	TACC2	p.V564L	transforming, acidic coil	108 (0.00)	132 (0.45)	1.21
12-01	Gp4	g.chr17:35837040A>G	Missense Mutation	TADA2A	p.K429E	transcriptional adaptor 2	171 (0.00)	131 (0.99)	2.65
12-01	Gp4	g.chr4:7056437G>C	Missense Mutation	TADA2B	p.E307Q	transcriptional adaptor 2	83 (0.00)	169 (0.22)	0.60
12-01	Gp4	g.chr9:32635219C>A	Missense Mutation	TAF1L	p.S120I	TAF1 RNA polymerase	145 (0.00)	92 (0.67)	1.80
12-01	Gp4	g.chr11:62553754C>T	Missense Mutation	TAF6L	p.P328L	TAF6-like RNA polyme	49 (0.00)	38 (0.74)	1.96
12-01	Gp4	g.chr17:27844560A>G	Silent	TAOK1	p.E598E	TAO kinase 1	175 (0.00)	75 (0.57)	1.53
12-01	Gp4	g.chr12:6566867C>A	Missense Mutation	TAPBPL	p.L169I	TAP binding protein-lik	54 (0.00)	196 (0.26)	0.68
12-01	Gp4	g.chr7:141491011C>A	Missense Mutation	TAS2R5	p.Q284K	taste receptor, type 2, m	154 (0.00)	48 (0.52)	1.39
12-01	Gp4	g.chr4:7026857C>A	Missense Mutation	TBC1D14	p.D400E	TBC1 domain family, m	128 (0.00)	255 (0.36)	0.97
12-01	Gp4	g.chr19:50381797G>T	Nonsense Mutation	TBC1D17	p.G55*	TBC1 domain family, m	111 (0.01)	71 (0.35)	0.94
12-01	Gp4	g.chr9:100995760G>T	Missense Mutation	TBC1D2	p.S240Y	TBC1 domain family, m	111 (0.00)	173 (0.17)	0.45
12-01	Gp4	g.chr15:74177361C>A	Missense Mutation	TBC1D21	p.H130N	TBC1 domain family, m	89 (0.00)	26 (0.73)	1.95
12-01	Gp4	g.chr22:47287201C>A	Missense Mutation	TBC1D22A	p.L250I	TBC1 domain family, m	198 (0.00)	125 (0.46)	1.22
12-01	Gp4	g.chr2:101645961G>A	Silent	TBC1D8	p.I723I	TBC1 domain family, m	63 (0.00)	48 (0.50)	1.33
12-01	Gp4	g.chr5:179296817C>G	Missense Mutation	TBC1D9B	p.D915H	TBC1 domain family, m	23 (0.00)	70 (0.14)	0.38
12-01	Gp4	g.chr5:179315177G>A	Missense Mutation	TBC1D9B	p.L394F	TBC1 domain family, m	132 (0.00)	154 (0.18)	0.48
12-01	Gp4	g.chr17:80758753C>A	Silent	TBCD	p.L277L	tubulin folding cofactor	20 (0.00)	124 (0.15)	0.41
12-01	Gp4	g.chr7:45145349C>G	Missense Mutation	TBRG4	p.W142C	transforming growth fac	33 (0.00)	98 (0.81)	2.15
12-01	Gp4	g.chr17:59557490G>T	Missense Mutation	TBX4	p.Q277H	T-box 4	49 (0.00)	27 (0.44)	1.19
12-01	Gp4	g.chr17:59557531G>T	Missense Mutation	TBX4	p.G291V	T-box 4	49 (0.00)	26 (0.54)	1.44
12-01	Gp4	g.chr17:59560397G>A	Silent	TBX4	p.V386V	T-box 4	51 (0.02)	22 (0.95)	2.55
12-01	Gp4	g.chrX:102529116C>T	Missense Mutation	TCEAL5	p.D126N	transcription elongation	67 (0.00)	20 (0.40)	0.48
12-01	Gp4	g.chr12:110353212C>G	Missense Mutation	TCHP	p.A442G	trichoplein, keratin filan	142 (0.00)	38 (0.18)	0.49
12-01	Gp4	g.chr6:170151519G>T	Silent	TCTE3	p.P12P	t-complex-associated-te	36 (0.00)	277 (0.51)	1.35
12-01	Gp4	g.chr19:33229899G>A	Splice Site	TDRD12		tudor domain containing	77 (0.00)	173 (0.16)	0.42
12-01	Gp4	g.chr6:46660550G>T	Missense Mutation	TDRD6	p.R1562I	tudor domain containing	55 (0.00)	21 (0.33)	0.89
12-01	Gp4	g.chr6:35447084G>T	Missense Mutation	TEAD3	p.L54M	TEA domain family me	107 (0.00)	104 (0.20)	0.54
12-01	Gp4	g.chr7:97874210G>T	Missense Mutation	TECPR1	p.P132H	tectonin beta-propeller r	86 (0.00)	121 (0.21)	0.57
12-01	Gp4	g.chr14:102901309G>T	Missense Mutation	TECPR2	p.G719W	tectonin beta-propeller r	31 (0.00)	39 (0.31)	0.82
12-01	Gp4	g.chr1:36552559C>A	Missense Mutation	TEKT2	p.D220E	tektin 2 (testicular)	126 (0.00)	41 (0.41)	1.11
12-01	Gp4	g.chrX:123554640C>A	Missense Mutation	TENM1	p.M1494I	teneurin transmembrane	41 (0.00)	15 (0.33)	0.56

12-01	Gp4	g.chr5:167671452G>A	Missense Mutation	TENM2	p.D1611N	teneurin transmembrane	119 (0.00)	159 (0.45)	1.21
12-01	Gp4	g.chr11:78433797G>T	Missense Mutation	TENM4	p.S1239Y	teneurin transmembrane	277 (0.00)	47 (0.26)	0.68
12-01	Gp4	g.chr11:78574162C>G	Missense Mutation	TENM4	p.G367A	teneurin transmembrane	89 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr9:35608178G>T	Missense Mutation	TESK1	p.A273S	testis-specific kinase 1	108 (0.01)	40 (0.57)	1.53
12-01	Gp4	g.chr1:45810693G>T	Missense Mutation	TESK2	p.A512D	testis-specific kinase 2	201 (0.00)	55 (0.18)	0.48
12-01	Gp4	g.chr2:74274626C>G	Missense Mutation	TET3	p.L393V	tet methylcytosine dioxy	175 (0.00)	87 (0.63)	1.69
12-01	Gp4	g.chr9:103092418T>G	Silent	TEX10	p.I428I	testis expressed 10	18 (0.00)	18 (0.94)	2.52
12-01	Gp4	g.chr17:56676237C>A	Splice Site	TEX14	p.M829I	testis expressed 14	47 (0.00)	310 (0.97)	2.59
12-01	Gp4	g.chr6:50791197C>G	Missense Mutation	TFAP2B	p.S53R	transcription factor AP-	20 (0.00)	30 (0.83)	2.22
12-01	Gp4	g.chr2:122038798G>T	Missense Mutation	TFCP2L1	p.P38T	transcription factor CP2	85 (0.00)	61 (0.36)	0.96
12-01	Gp4	g.chr8:133995605T>A	Missense Mutation	TG	p.N2070K	thyroglobulin	200 (0.00)	90 (0.33)	0.89
12-01	Gp4	g.chr14:24724386C>G	Silent	TGM1	p.R573R	transglutaminase 1	141 (0.00)	331 (0.27)	0.73
12-01	Gp4	g.chr15:43568733G>T	Missense Mutation	TGM7	p.Q685K	transglutaminase 7	174 (0.00)	486 (0.69)	1.83
12-01	Gp4	g.chr15:43574785G>A	Silent	TGM7	p.I346I	transglutaminase 7	29 (0.00)	23 (0.39)	1.04
12-01	Gp4	g.chr15:43579606T>C	Missense Mutation	TGM7	p.D246G	transglutaminase 7	63 (0.00)	86 (0.34)	0.90
12-01	Gp4	g.chr16:67877401G>T	Nonstop Mutation	THAP11	p.*315L	THAP domain containir	124 (0.00)	101 (0.19)	0.50
12-01	Gp4	g.chr1:155172743C>A	Nonsense Mutation	THBS3	p.E273*	thrombospondin 3	61 (0.00)	37 (0.81)	2.16
12-01	Gp4	g.chr5:79355571C>T	Missense Mutation	THBS4	p.P186L	thrombospondin 4	193 (0.01)	43 (0.44)	1.18
12-01	Gp4	g.chr5:79372787G>T	Missense Mutation	THBS4	p.D577Y	thrombospondin 4	184 (0.00)	38 (0.84)	2.25
12-01	Gp4	g.chr1:36758270C>A	Missense Mutation	THRAP3	p.Q664K	thyroid hormone recept	89 (0.00)	16 (0.50)	1.33
12-01	Gp4	g.chr7:11452317G>T	Missense Mutation	THSD7A	p.N1216K	thrombospondin, type I,	85 (0.00)	22 (0.32)	0.85
12-01	Gp4	g.chr6:155451381C>A	Missense Mutation	TIAM2	p.P342T	T-cell lymphoma invasi	101 (0.00)	29 (0.38)	1.01
12-01	Gp4	g.chr6:155490003G>A	Missense Mutation	TIAM2	p.G108R	T-cell lymphoma invasi	36 (0.03)	140 (0.92)	2.46
12-01	Gp4	g.chr6:155490004G>A	Missense Mutation	TIAM2	p.G108E	T-cell lymphoma invasi	36 (0.03)	139 (0.93)	2.47
12-01	Gp4	g.chr19:4817417G>T	Missense Mutation	TICAM1	p.P325T	toll-like receptor adapto	140 (0.00)	58 (0.19)	0.51
12-01	Gp4	g.chr1:43777670C>A	Missense Mutation	TIE1	p.P500T	tyrosine kinase with im	281 (0.00)	480 (0.30)	0.79
12-01	Gp4	g.chr12:56818695A>T	Missense Mutation	TIMELESS	p.N573K	timeless circadian clock	126 (0.00)	18 (0.39)	1.04
12-01	Gp4	g.chr14:24711434C>A	Silent	TINF2	p.L35L	TERF1 (TRF1)-interacti	136 (0.00)	202 (0.19)	0.50
12-01	Gp4	g.chr1:168160676G>A	Missense Mutation	TIPRL	p.E152K	TOR signaling pathway	96 (0.00)	28 (0.68)	1.81
12-01	Gp4	g.chr3:53263048G>A	Missense Mutation	TKT	p.A457V	transketolase	111 (0.00)	35 (0.43)	1.14
12-01	Gp4	g.chr20:35517694G>A	Missense Mutation	TLDC2	p.G185R	TBC/LysM-associated	210 (0.00)	156 (0.22)	0.58
12-01	Gp4	g.chr19:2991967C>T	Silent	TLE6	p.Y457Y	transducin-like enhance	167 (0.01)	74 (0.70)	1.87
12-01	Gp4	g.chr9:35698141G>T	Nonsense Mutation	TLN1	p.S2467*	talin 1	236 (0.00)	149 (0.72)	1.91
12-01	Gp4	g.chr9:35712840G>C	Missense Mutation	TLN1	p.L1185V	talin 1	19 (0.00)	10 (0.80)	2.13
12-01	Gp4	g.chr3:52256600G>T	Missense Mutation	TLR9	p.A731E	toll-like receptor 9	42 (0.00)	84 (0.19)	0.51

12-01	Gp4	g.chr1:62190904A>T	Silent	TM2D1	p.T25T	TM2 domain containing	70 (0.00)	25 (0.40)	1.07
12-01	Gp4	g.chr14:24658665G>T	Missense Mutation	TM9SF1	p.L802I	transmembrane 9 superf	202 (0.00)	34 (0.62)	1.65
12-01	Gp4	g.chr14:24664063G>A	Missense Mutation	TM9SF1	p.P264S	transmembrane 9 superf	237 (0.00)	17 (0.59)	1.57
12-01	Gp4	g.chr19:54669202C>A	Missense Mutation	TMC4	p.G305V	transmembrane channel-	28 (0.00)	42 (0.31)	0.83
12-01	Gp4	g.chr17:79287656C>A	Missense Mutation	TMEM105	p.R62L	transmembrane protein	53 (0.00)	46 (0.15)	0.41
12-01	Gp4	g.chr7:75617499C>A	RNA	TMEM120A		transmembrane protein	81 (0.00)	141 (0.50)	1.32
12-01	Gp4	g.chr11:102272666A>T	Silent	TMEM123	p.S143S	transmembrane protein	35 (0.00)	97 (0.58)	1.54
12-01	Gp4	g.chr11:60698013G>T	Missense Mutation	TMEM132A	p.A300S	transmembrane protein	204 (0.00)	178 (0.34)	0.90
12-01	Gp4	g.chr11:60703337A>G	Splice Site	TMEM132A	p.E678G	transmembrane protein	206 (0.00)	107 (0.31)	0.82
12-01	Gp4	g.chr17:32964330C>A	Silent	TMEM132E	p.A678A	transmembrane protein	80 (0.00)	243 (0.29)	0.78
12-01	Gp4	g.chr11:87020584A>G	Missense Mutation	TMEM135	p.Q269R	transmembrane protein	70 (0.00)	34 (0.24)	0.63
12-01	Gp4	g.chr7:134849514C>G	Missense Mutation	TMEM140	p.N107K	transmembrane protein	41 (0.00)	21 (0.57)	1.52
12-01	Gp4	g.chr19:36037587C>A	Missense Mutation	TMEM147	p.A74D	transmembrane protein	85 (0.00)	81 (0.27)	0.72
12-01	Gp4	g.chr19:36037641C>A	Missense Mutation	TMEM147	p.A92D	transmembrane protein	93 (0.01)	65 (0.23)	0.62
12-01	Gp4	g.chr4:944275A>G	Missense Mutation	TMEM175	p.I87V	transmembrane protein	50 (0.00)	14 (0.43)	1.14
12-01	Gp4	g.chr1:202989937G>T	Missense Mutation	TMEM183A	p.S269I	transmembrane protein	34 (0.00)	12 (0.58)	1.56
12-01	Gp4	g.chr18:5891696C>T	Missense Mutation	TMEM200C	p.V123I	transmembrane protein	93 (0.00)	160 (0.77)	2.05
12-01	Gp4	g.chr3:190159255C>A	Missense Mutation	TMEM207	p.D44Y	transmembrane protein	15 (0.00)	93 (0.38)	1.00
12-01	Gp4	g.chr2:27262658C>A	Missense Mutation	TMEM214	p.S525R	transmembrane protein	132 (0.00)	182 (0.22)	0.59
12-01	Gp4	g.chr1:27660546G>C	Splice Site	TMEM222		transmembrane protein	126 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr9:104239212G>T	Missense Mutation	TMEM246	p.H55N	transmembrane protein	83 (0.00)	99 (0.20)	0.54
12-01	Gp4	g.chr3:12783999C>T	Silent	TMEM40	p.G103G	transmembrane protein	211 (0.00)	406 (0.24)	0.65
12-01	Gp4	g.chr3:14183207G>A	Missense Mutation	TMEM43	p.R372Q	transmembrane protein	22 (0.00)	24 (0.21)	0.56
12-01	Gp4	g.chr3:194344317G>T	Missense Mutation	TMEM44	p.P156T	transmembrane protein	89 (0.00)	117 (0.21)	0.55
12-01	Gp4	g.chr1:55451911C>A	Missense Mutation	TMEM61	p.P53T	transmembrane protein	78 (0.00)	50 (0.52)	1.39
12-01	Gp4	g.chr1:226034855C>G	Missense Mutation	TMEM63A	p.Q770H	transmembrane protein	57 (0.00)	43 (0.19)	0.50
12-01	Gp4	g.chr3:48658434G>A	Silent	TMEM89	p.C107C	transmembrane protein	60 (0.00)	54 (0.19)	0.49
12-01	Gp4	g.chr21:42840264C>A	Intron	TMPRSS2		transmembrane protease	102 (0.00)	13 (0.77)	2.05
12-01	Gp4	g.chr21:42850217C>A	Intron	TMPRSS2		transmembrane protease	16 (0.00)	19 (0.68)	1.82
12-01	Gp4	g.chr21:42862098C>A	Intron	TMPRSS2		transmembrane protease	82 (0.00)	35 (0.97)	2.59
12-01	Gp4	g.chrX:12994920G>A	Missense Mutation	TMSB4X	p.G42D	thymosin beta 4, X-link	118 (0.00)	282 (0.46)	0.77
12-01	Gp4	g.chr1:2494682C>A	Silent	TNFRSF14	p.P274P	tumor necrosis factor re	26 (0.00)	40 (0.28)	0.73
12-01	Gp4	g.chr4:2749410C>A	Missense Mutation	TNIP2	p.R180M	TNFAIP3 interacting pr	238 (0.00)	625 (0.35)	0.93
12-01	Gp4	g.chr17:7286754G>T	Missense Mutation	TNK1	p.G82V	tyrosine kinase, non-rec	55 (0.00)	63 (0.17)	0.47
12-01	Gp4	g.chr17:7287096C>A	Missense Mutation	TNK1	p.F165L	tyrosine kinase, non-rec	53 (0.00)	14 (0.57)	1.52

12-01	Gp4	g.chr11:57076997C>A	Missense Mutation	TNKS1BP1	p.R1063I	tankyrase 1 binding prot	49 (0.00)	57 (0.18)	0.47
12-01	Gp4	g.chr19:12830080G>T	Nonsense Mutation	TNPO2	p.S57*	transportin 2	62 (0.00)	53 (0.68)	1.81
12-01	Gp4	g.chr7:5396764G>T	Missense Mutation	TNRC18	p.S1659R	trinucleotide repeat cont	73 (0.00)	22 (0.23)	0.61
12-01	Gp4	g.chr22:40658175C>T	Missense Mutation	TNRC6B	p.P188L	trinucleotide repeat cont	31 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr2:218713744G>A	Missense Mutation	TNS1	p.S374F	tensin 1	51 (0.02)	269 (0.24)	0.63
12-01	Gp4	g.chr17:38635997G>T	Silent	TNS4	p.I613I	tensin 4	130 (0.00)	134 (0.14)	0.38
12-01	Gp4	g.chr8:145659074G>A	Silent	TONSL	p.L1152L	tonsoku-like, DNA repa	42 (0.00)	100 (0.79)	2.11
12-01	Gp4	g.chr8:145664071G>T	Missense Mutation	TONSL	p.L510I	tonsoku-like, DNA repa	21 (0.00)	44 (0.27)	0.73
12-01	Gp4	g.chr8:145665733C>A	Splice Site	TONSL		tonsoku-like, DNA repa	48 (0.00)	222 (0.23)	0.61
12-01	Gp4	g.chr8:144407700G>T	Missense Mutation	TOP1MT	p.L65I	topoisomerase (DNA) I,	54 (0.00)	54 (0.39)	1.04
12-01	Gp4	g.chr17:7578488C>A	Missense Mutation	TP53	p.D148Y	tumor protein p53	89 (0.00)	110 (0.70)	1.87
12-01	Gp4	g.chr17:27898875C>A	Splice Site	TP53I13	p.P105T	tumor protein p53 induc	90 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr2:24300466G>T	Missense Mutation	TP53I3	p.L328M	tumor protein p53 induc	47 (0.00)	79 (0.27)	0.71
12-01	Gp4	g.chr12:113711392G>T	Missense Mutation	TPCN1	p.M219I	two pore segment chann	177 (0.00)	102 (0.46)	1.23
12-01	Gp4	g.chr9:6328623G>A	Missense Mutation	TPD52L3	p.V10M	tumor protein D52-like	113 (0.00)	100 (0.16)	0.43
12-01	Gp4	g.chr9:35685671G>T	Missense Mutation	TPM2	p.A116D	tropomyosin 2 (beta)	93 (0.01)	91 (0.18)	0.47
12-01	Gp4	g.chr14:23020638T>C	RNA	TRAC		T cell receptor alpha co	254 (0.00)	42 (0.90)	2.41
12-01	Gp4	g.chr9:123675765C>A	Missense Mutation	TRAF1	p.M182I	TNF receptor-associatec	45 (0.00)	286 (0.14)	0.38
12-01	Gp4	g.chr3:36875170C>G	Silent	TRANK1	p.L1374L	tetratricopeptide repeat a	165 (0.00)	20 (0.50)	1.33
12-01	Gp4	g.chr14:22090576C>T	RNA	TRAV1-1		T cell receptor alpha va	92 (0.00)	195 (0.59)	1.59
12-01	Gp4	g.chr7:142499076C>A	RNA	TRBC2		T cell receptor beta cons	72 (0.00)	42 (0.31)	0.83
12-01	Gp4	g.chr7:38299670C>A	RNA	TRGC1		T cell receptor gamma c	62 (0.00)	45 (0.22)	0.59
12-01	Gp4	g.chr2:12880850C>T	Missense Mutation	TRIB2	p.A321V	tribbles pseudokinase 2	134 (0.00)	78 (0.22)	0.58
12-01	Gp4	g.chr17:18638680C>A	Missense Mutation	TRIM16L	p.F318L	tripartite motif containir	56 (0.00)	71 (0.15)	0.41
12-01	Gp4	g.chr11:6477701G>T	Missense Mutation	TRIM3	p.L419M	tripartite motif containir	28 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr15:45059829G>A	Silent	TRIM69	p.L454L	tripartite motif containir	20 (0.00)	111 (0.96)	2.57
12-01	Gp4	g.chr3:32931860G>A	Silent	TRIM71	p.K388K	tripartite motif containir	283 (0.00)	260 (0.22)	0.57
12-01	Gp4	g.chr7:72430629C>G	Missense Mutation	TRIM74	p.G217R	tripartite motif containir	95 (0.00)	44 (0.59)	1.58
12-01	Gp4	g.chr2:230679838C>A	Missense Mutation	TRIP12	p.A225S	thyroid hormone recepto	26 (0.00)	21 (0.90)	2.41
12-01	Gp4	g.chr7:100466183C>A	Missense Mutation	TRIP6	p.L144I	thyroid hormone recepto	27 (0.00)	35 (0.17)	0.46
12-01	Gp4	g.chr22:20100285C>A	Missense Mutation	TRMT2A	p.G560V	tRNA methyltransferase	46 (0.00)	42 (0.38)	1.02
12-01	Gp4	g.chr22:20103951G>A	Missense Mutation	TRMT2A	p.S70F	tRNA methyltransferase	29 (0.00)	33 (0.97)	2.59
12-01	Gp4	g.chr12:49719581G>T	Missense Mutation	TROAP	p.D183Y	trophinin associated pro	108 (0.00)	81 (0.36)	0.95
12-01	Gp4	g.chr20:33594373G>A	Silent	TRPC4AP	p.I564I	transient receptor potent	32 (0.00)	30 (0.33)	0.89
12-01	Gp4	g.chr21:45795880G>T	Missense Mutation	TRPM2	p.Q312H	transient receptor potent	143 (0.00)	243 (0.14)	0.38

12-01	Gp4	g.chr7:142571225C>A	Missense Mutation	TRPV6	p.E588D	transient receptor potent	159 (0.00)	164 (0.35)	0.94
12-01	Gp4	g.chr7:98558953G>T	Missense Mutation	TRRAP	p.V2161F	transformation/transcrip	63 (0.00)	16 (0.38)	1.00
12-01	Gp4	g.chr7:98567749G>T	Silent	TRRAP	p.V2484V	transformation/transcrip	76 (0.00)	88 (0.35)	0.94
12-01	Gp4	g.chr7:98608756C>A	Missense Mutation	TRRAP	p.P3649T	transformation/transcrip	32 (0.00)	122 (0.35)	0.94
12-01	Gp4	g.chr3:150128183C>A	Missense Mutation	TSC22D2	p.P349H	TSC22 domain family,	21 (0.00)	25 (0.20)	0.53
12-01	Gp4	g.chrX:107018425C>A	Missense Mutation	TSC22D3	p.E75D	TSC22 domain family,	222 (0.00)	76 (0.43)	0.52
12-01	Gp4	g.chr11:65714762G>A	RNA	TSGA10IP		testis specific, 10 intera	26 (0.00)	164 (0.18)	0.47
12-01	Gp4	g.chr18:72999314A>G	Missense Mutation	TSHZ1	p.N651S	teashirt zinc finger hom	98 (0.00)	78 (0.18)	0.63
12-01	Gp4	g.chr19:31770017C>G	Missense Mutation	TSHZ3	p.E228Q	teashirt zinc finger hom	398 (0.00)	207 (0.46)	1.22
12-01	Gp4	g.chr17:79612084C>A	RNA	TSPAN10		tetraspanin 10	15 (0.00)	93 (0.31)	0.83
12-01	Gp4	g.chr12:31116942G>T	Missense Mutation	TSPAN11	p.C89F	tetraspanin 11	26 (0.00)	24 (0.54)	1.44
12-01	Gp4	g.chr5:176083945T>C	Missense Mutation	TSPAN17	p.V246A	tetraspanin 17	34 (0.00)	16 (0.81)	2.17
12-01	Gp4	g.chr11:44931363C>A	Silent	TSPAN18	p.I57I	tetraspanin 18	155 (0.00)	177 (0.28)	0.74
12-01	Gp4	g.chr12:3389617C>A	Missense Mutation	TSPAN9	p.L134M	tetraspanin 9	15 (0.00)	229 (0.17)	0.44
12-01	Gp4	g.chr8:98289446C>A	Missense Mutation	TSPYL5	p.Q209H	TSPY-like 5	153 (0.01)	57 (0.61)	1.64
12-01	Gp4	g.chr8:98289625G>T	Missense Mutation	TSPYL5	p.P150T	TSPY-like 5	25 (0.04)	23 (0.30)	0.81
12-01	Gp4	g.chr22:19119448C>A	Missense Mutation	TSSK2	p.A179E	testis-specific serine kin	187 (0.00)	83 (0.94)	2.51
12-01	Gp4	g.chr6:43220530G>T	Silent	TTBK1	p.L3L	tau tubulin kinase 1	41 (0.00)	17 (0.76)	2.04
12-01	Gp4	g.chr6:43230717G>T	Missense Mutation	TTBK1	p.D488Y	tau tubulin kinase 1	23 (0.00)	44 (0.16)	0.42
12-01	Gp4	g.chr1:231060705C>T	Missense Mutation	TTC13	p.A535T	tetratricopeptide repeat	240 (0.00)	94 (0.37)	0.99
12-01	Gp4	g.chr9:130478437G>T	Missense Mutation	TTC16	p.D5Y	tetratricopeptide repeat	44 (0.00)	63 (0.21)	0.55
12-01	Gp4	g.chr9:130485499G>T	Missense Mutation	TTC16	p.Q253H	tetratricopeptide repeat	29 (0.00)	63 (0.35)	0.93
12-01	Gp4	g.chr3:39180080A>G	Missense Mutation	TTC21A	p.K1284R	tetratricopeptide repeat	145 (0.00)	163 (0.20)	0.54
12-01	Gp4	g.chr22:28504121T>A	Missense Mutation	TTC28	p.D571V	tetratricopeptide repeat	83 (0.00)	55 (0.44)	1.16
12-01	Gp4	g.chr2:74717511C>A	Missense Mutation	TTC31	p.Q125K	tetratricopeptide repeat	18 (0.00)	67 (0.63)	1.67
12-01	Gp4	g.chr10:134673934C>T	Missense Mutation	TTC40	p.D1729N		273 (0.00)	203 (0.92)	2.44
12-01	Gp4	g.chr10:134752209C>A	Silent	TTC40	p.V140V		81 (0.01)	295 (0.27)	0.73
12-01	Gp4	g.chr2:47184122C>A	Missense Mutation	TTC7A	p.L165M	tetratricopeptide repeat	269 (0.00)	81 (0.43)	1.15
12-01	Gp4	g.chr14:91123518C>G	Splice Site	TTC7B	p.W447C	tetratricopeptide repeat	46 (0.00)	14 (0.36)	0.95
12-01	Gp4	g.chr1:117618030C>T	Missense Mutation	TTF2	p.P275L	transcription terminatio	210 (0.00)	65 (0.35)	0.94
12-01	Gp4	g.chr1:117618806C>A	Missense Mutation	TTF2	p.T427K	transcription terminatio	177 (0.01)	159 (0.64)	1.71
12-01	Gp4	g.chr17:46868770C>T	Silent	TTLL6	p.L398L	tubulin tyrosine ligase-li	44 (0.00)	35 (0.40)	1.07
12-01	Gp4	g.chr2:179407626G>A	Missense Mutation	TTN	p.P32319S	titin	110 (0.00)	12 (0.75)	2.00
12-01	Gp4	g.chr2:179423271C>A	Missense Mutation	TTN	p.S28972I	titin	41 (0.00)	18 (0.44)	1.19
12-01	Gp4	g.chr2:179442018G>T	Missense Mutation	TTN	p.A23015E	titin	117 (0.00)	291 (0.44)	1.16

12-01	Gp4	g.chr2:179459148C>T	Missense Mutation	TTN	p.R19358H	titin	113 (0.00)	71 (0.42)	1.13
12-01	Gp4	g.chr2:179542371G>T	Missense Mutation	TTN	p.P11423H	titin	70 (0.00)	30 (0.63)	1.69
12-01	Gp4	g.chr2:179542443G>T	Missense Mutation	TTN	p.P11399H	titin	166 (0.00)	45 (0.16)	0.41
12-01	Gp4	g.chr12:49522069A>G	Missense Mutation	TUBA1B	p.F343S	tubulin, alpha 1b	152 (0.00)	93 (0.16)	0.43
12-01	Gp4	g.chr2:132237671C>A	Missense Mutation	TUBA3D	p.F135L	tubulin, alpha 3d	241 (0.00)	230 (0.43)	1.16
12-01	Gp4	g.chr2:132240304C>A	Silent	TUBA3D	p.G412G	tubulin, alpha 3d	280 (0.00)	285 (0.15)	0.41
12-01	Gp4	g.chr2:220115948G>T	Missense Mutation	TUBA4A	p.S143Y	tubulin, alpha 4a	112 (0.01)	164 (0.23)	0.60
12-01	Gp4	g.chr20:57597927G>T	Missense Mutation	TUBB1	p.G29W	tubulin, beta 1 class VI	89 (0.00)	73 (0.53)	1.42
12-01	Gp4	g.chr19:6495404C>A	Missense Mutation	TUBB4A	p.G369V	tubulin, beta 4A class I	360 (0.00)	83 (0.46)	1.22
12-01	Gp4	g.chr9:140137623G>T	Missense Mutation	TUBB4B	p.R318M	tubulin, beta 4B class I	265 (0.00)	176 (0.14)	0.38
12-01	Gp4	g.chr16:90161642C>A	RNA	TUBB8P7		tubulin, beta 8 class VII	84 (0.00)	259 (0.42)	1.12
12-01	Gp4	g.chr13:113212640G>T	Missense Mutation	TUBGCP3	p.P140T	tubulin, gamma comple	77 (0.00)	127 (0.47)	1.26
12-01	Gp4	g.chr22:50656963G>T	Silent	TUBGCP6	p.L1636L	tubulin, gamma comple	60 (0.00)	157 (0.21)	0.56
12-01	Gp4	g.chr22:50659050G>A	Silent	TUBGCP6	p.S1246S	tubulin, gamma comple	71 (0.00)	78 (0.26)	0.68
12-01	Gp4	g.chr22:50682717G>A	Nonsense Mutation	TUBGCP6	p.Q58*	tubulin, gamma comple	54 (0.00)	377 (0.24)	0.63
12-01	Gp4	g.chr1:32646027C>T	Silent	TXLNA	p.P27P	taxilin alpha	23 (0.00)	31 (0.26)	0.69
12-01	Gp4	g.chr1:145440782C>T	Missense Mutation	TXNIP	p.P328S	thioredoxin interacting	28 (0.00)	24 (0.21)	0.56
12-01	Gp4	g.chr19:10479065C>G	Missense Mutation	TYK2	p.A75P	tyrosine kinase 2	113 (0.00)	49 (0.51)	1.36
12-01	Gp4	g.chr15:41865220G>A	Silent	TYRO3	p.L632L	TYRO3 protein tyrosin	46 (0.00)	68 (0.22)	0.59
12-01	Gp4	g.chr19:34943050A>T	Nonsense Mutation	UBA2	p.K346*	ubiquitin-like modifier	79 (0.00)	19 (0.37)	0.98
12-01	Gp4	g.chr3:23848833G>A	Missense Mutation	UBE2E1	p.E25K	ubiquitin-conjugating e	166 (0.00)	115 (0.30)	0.81
12-01	Gp4	g.chr1:154523944C>A	Nonsense Mutation	UBE2Q1	p.E367*	ubiquitin-conjugating e	45 (0.00)	23 (0.65)	1.74
12-01	Gp4	g.chr12:109961873C>A	Missense Mutation	UBE3B	p.L819M	ubiquitin protein ligase	78 (0.00)	108 (0.31)	0.84
12-01	Gp4	g.chr12:109962283C>A	Missense Mutation	UBE3B	p.S848Y	ubiquitin protein ligase	95 (0.01)	25 (0.28)	0.75
12-01	Gp4	g.chr1:19467887G>C	Silent	UBR4	p.T2814T	ubiquitin protein ligase	90 (0.00)	16 (0.31)	0.83
12-01	Gp4	g.chr1:19467890C>T	Silent	UBR4	p.E2813E	ubiquitin protein ligase	87 (0.00)	19 (0.26)	0.70
12-01	Gp4	g.chr8:103284937G>A	Nonsense Mutation	UBR5	p.R2259*	ubiquitin protein ligase	46 (0.00)	27 (0.96)	2.57
12-01	Gp4	g.chr11:62445472G>T	Silent	UBXN1	p.R137R	UBX domain protein 1	62 (0.00)	21 (0.67)	1.78
12-01	Gp4	g.chr1:165865459A>G	Missense Mutation	UCK2	p.D130G	uridine-cytidine kinase	105 (0.00)	178 (0.62)	1.66
12-01	Gp4	g.chr1:165876983C>A	Missense Mutation	UCK2	p.Q237K	uridine-cytidine kinase	92 (0.00)	13 (0.46)	1.23
12-01	Gp4	g.chr1:165876988C>A	Silent	UCK2	p.T238T	uridine-cytidine kinase	92 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr6:96974292C>A	Missense Mutation	UFL1	p.P149H	UFM1-specific ligase 1	20 (0.00)	30 (0.80)	2.13
12-01	Gp4	g.chr2:234680989G>C	Silent	UGT1A6	p.V461V	UDP glucuronosyltrans	46 (0.00)	35 (0.23)	0.61
12-01	Gp4	g.chr19:4929259A>G	RNA	UHRF1		ubiquitin-like with PHD	121 (0.00)	215 (0.19)	0.51
12-01	Gp4	g.chr15:75131713G>T	Splice Site	ULK3	p.T285N	unc-51 like kinase 3	19 (0.00)	24 (0.33)	0.89

12-01	Gp4	g.chr16:20355481T>C	Missense Mutation	UMOD	p.H399R	uromodulin	69 (0.00)	13 (0.38)	1.03
12-01	Gp4	g.chr17:73832338C>A	Splice Site	UNC13D		unc-13 homolog D (C. e	37 (0.00)	43 (0.47)	1.24
12-01	Gp4	g.chr15:91483553G>T	Silent	UNC45A	p.V179V	unc-45 homolog A (C. e	119 (0.00)	81 (0.16)	0.43
12-01	Gp4	g.chr15:91491979G>T	Missense Mutation	UNC45A	p.E611D	unc-45 homolog A (C. e	76 (0.00)	89 (0.37)	0.99
12-01	Gp4	g.chr2:210808115C>T	Silent	UNC80	p.D2238D	unc-80 homolog (C. ele	128 (0.00)	18 (0.83)	2.22
12-01	Gp4	g.chr22:45681854A>G	Missense Mutation	UPK3A	p.T29A	uroplakin 3A	112 (0.00)	35 (0.34)	0.91
12-01	Gp4	g.chr2:158974394A>T	Missense Mutation	UPP2	p.H133L	uridine phosphorylase 2	40 (0.00)	25 (0.32)	0.85
12-01	Gp4	g.chr6:33679349A>G	Missense Mutation	UQCC2	p.F39L	ubiquinol-cytochrome c	69 (0.00)	45 (0.20)	0.53
12-01	Gp4	g.chr8:11995456A>G	Missense Mutation	USP17L2	p.S272P	ubiquitin specific peptid	286 (0.00)	54 (0.67)	1.78
12-01	Gp4	g.chr22:18652644G>T	Nonsense Mutation	USP18	p.E221*	ubiquitin specific peptid	191 (0.00)	134 (0.24)	0.64
12-01	Gp4	g.chr9:132631951G>A	Splice Site	USP20	p.V465I	ubiquitin specific peptid	85 (0.01)	78 (0.19)	0.51
12-01	Gp4	g.chr1:161130717C>A	Missense Mutation	USP21	p.P96Q	ubiquitin specific peptid	54 (0.00)	122 (0.16)	0.42
12-01	Gp4	g.chr5:72868391G>A	Missense Mutation	UTP15	p.V251M	UTP15, U3 small nucle	85 (0.00)	13 (0.62)	1.64
12-01	Gp4	g.chr4:1369171G>A	Silent	UVSSA	p.E436E	UV-stimulated scaffold	80 (0.00)	43 (0.19)	0.50
12-01	Gp4	g.chr1:160389064G>T	Missense Mutation	VANGL2	p.K155N	VANGL planar cell pol	79 (0.00)	77 (0.16)	0.42
12-01	Gp4	g.chr14:77242571C>A	Missense Mutation	VASH1	p.D289E	vasohibin 1	19 (0.00)	27 (0.26)	0.69
12-01	Gp4	g.chr9:136637135C>T	Silent	VAV2	p.V713V	vav 2 guanine nucleotid	28 (0.00)	21 (0.29)	0.76
12-01	Gp4	g.chr2:71148320C>A	Missense Mutation	VAX2	p.L114M	ventral anterior homeob	49 (0.00)	33 (0.33)	0.89
12-01	Gp4	g.chr9:35057443C>A	Missense Mutation	VCP	p.D749Y	valosin containing prote	104 (0.01)	24 (0.54)	1.44
12-01	Gp4	g.chr6:43749815G>A	Missense Mutation	VEGFA	p.R182H	vascular endothelial gro	52 (0.00)	35 (0.23)	0.61
12-01	Gp4	g.chr12:95656693C>T	Silent	VEZT	p.F90F	vezatin, adherens juncti	22 (0.00)	25 (0.56)	1.49
12-01	Gp4	g.chr3:38042968C>A	Missense Mutation	VILL	p.H402N	villin-like	115 (0.00)	64 (0.36)	0.96
12-01	Gp4	g.chr3:38044027G>T	Missense Mutation	VILL	p.L540F	villin-like	198 (0.00)	234 (0.38)	1.00
12-01	Gp4	g.chr1:12566906G>T	Splice Site	VPS13D		vacuolar protein sorting	76 (0.00)	79 (0.27)	0.71
12-01	Gp4	g.chr13:53013285G>A	Missense Mutation	VPS36	p.L62F	vacuolar protein sorting	83 (0.00)	16 (0.75)	2.00
12-01	Gp4	g.chr16:69358127C>A	Missense Mutation	VPS4A	p.S410Y	vacuolar protein sorting	114 (0.00)	77 (0.56)	1.49
12-01	Gp4	g.chr16:69358129C>A	Missense Mutation	VPS4A	p.L411M	vacuolar protein sorting	114 (0.00)	79 (0.56)	1.49
12-01	Gp4	g.chr11:64875841G>T	Missense Mutation	VPS51	p.V300L	vacuolar protein sorting	23 (0.00)	138 (0.17)	0.44
12-01	Gp4	g.chr19:50512547C>A	Missense Mutation	VRK3	p.D79Y	vaccinia related kinase	37 (0.00)	38 (0.47)	1.26
12-01	Gp4	g.chr14:74824305G>T	Silent	VRTN	p.L273L	vertebrae development	55 (0.00)	82 (0.17)	0.46
12-01	Gp4	g.chr12:118517295C>A	Nonsense Mutation	VSIG10	p.E261*	V-set and immunoglobu	116 (0.00)	46 (0.24)	0.64
12-01	Gp4	g.chr12:118520091C>A	Missense Mutation	VSIG10	p.A169S	V-set and immunoglobu	92 (0.00)	258 (0.22)	0.59
12-01	Gp4	g.chr10:116038550C>A	Missense Mutation	VWA2	p.P258Q	von Willebrand factor A	142 (0.00)	183 (0.54)	1.43
12-01	Gp4	g.chr10:116048924C>A	Missense Mutation	VWA2	p.Q600K	von Willebrand factor A	23 (0.00)	43 (0.40)	1.05
12-01	Gp4	g.chr3:183954260C>T	Silent	VWA5B2	p.L448L	von Willebrand factor A	23 (0.00)	12 (0.75)	2.00

12-01	Gp4	g.chr2:114353383G>T	RNA	WASH2P		WAS protein family hor	157 (0.00)	213 (0.29)	0.78
12-01	Gp4	g.chr10:104572508C>A	Missense Mutation	WBP1L	p.T150N	WW domain binding pro	49 (0.00)	70 (0.14)	0.38
12-01	Gp4	g.chr10:104572614C>A	Missense Mutation	WBP1L	p.D185E	WW domain binding pro	50 (0.00)	59 (0.17)	0.45
12-01	Gp4	g.chr10:49986694T>C	Missense Mutation	WDFY4	p.F1072L	WDFY family member	33 (0.00)	51 (0.37)	0.99
12-01	Gp4	g.chrX:48463342C>A	Missense Mutation	WDR13	p.S460R	WD repeat domain 13	29 (0.00)	44 (0.23)	0.38
12-01	Gp4	g.chr16:739581G>T	Silent	WDR24	p.T20T	WD repeat domain 24	22 (0.00)	26 (0.19)	0.51
12-01	Gp4	g.chr14:100996330C>A	Silent	WDR25	p.S529S	WD repeat domain 25	70 (0.00)	77 (0.26)	0.69
12-01	Gp4	g.chr10:1132244G>A	Nonsense Mutation	WDR37	p.W184*	WD repeat domain 37	82 (0.00)	58 (0.17)	0.46
12-01	Gp4	g.chr3:49051533G>T	Missense Mutation	WDR6	p.V304L	WD repeat domain 6	131 (0.00)	61 (0.38)	1.01
12-01	Gp4	g.chr7:158683955G>T	Splice Site	WDR60		WD repeat domain 60	135 (0.00)	17 (0.29)	0.78
12-01	Gp4	g.chr7:158695287G>A	Splice Site	WDR60		WD repeat domain 60	121 (0.00)	57 (0.98)	2.62
12-01	Gp4	g.chr19:38385558G>T	Missense Mutation	WDR87	p.A223D	WD repeat domain 87	46 (0.00)	18 (0.56)	1.48
12-01	Gp4	g.chr16:700569G>T	Missense Mutation	WDR90	p.R140L	WD repeat domain 90	41 (0.00)	63 (0.71)	1.90
12-01	Gp4	g.chr15:90281301G>T	Missense Mutation	WDR93	p.D599Y	WD repeat domain 93	346 (0.00)	16 (0.31)	0.83
12-01	Gp4	g.chr20:43739165G>T	Nonsense Mutation	WFDC5	p.C81*	WAP four-disulfide cor	22 (0.00)	52 (0.15)	0.41
12-01	Gp4	g.chr16:684043C>A	Missense Mutation	WFIKKN1	p.R545S	WAP, follistatin/kazal, i	26 (0.00)	66 (0.30)	0.81
12-01	Gp4	g.chr19:15558932C>A	Missense Mutation	WIZ	p.G63C	widely interspaced zinc	210 (0.00)	40 (0.23)	0.60
12-01	Gp4	g.chr9:96061537G>C	Missense Mutation	WNK2	p.G2074R	WNK lysine deficient p	66 (0.00)	119 (0.21)	0.56
12-01	Gp4	g.chr12:1741846C>A	Missense Mutation	WNT5B	p.Q35K	wingless-type MMTV i	266 (0.00)	330 (0.31)	0.82
12-01	Gp4	g.chr22:46345952C>G	Missense Mutation	WNT7B	p.R53P	wingless-type MMTV i	28 (0.00)	26 (0.27)	0.72
12-01	Gp4	g.chr10:102241759G>T	Missense Mutation	WNT8B	p.G153V	wingless-type MMTV i	99 (0.01)	51 (0.33)	0.89
12-01	Gp4	g.chr17:7605095C>A	Silent	WRAP53	p.R282R	WD repeat containing, a	20 (0.00)	12 (0.83)	2.22
12-01	Gp4	g.chr1:3552530G>C	Missense Mutation	WRAP73	p.A194G	WD repeat containing, a	73 (0.00)	67 (0.18)	0.48
12-01	Gp4	g.chr19:34981288C>A	Nonsense Mutation	WTIP	p.C225*	Wilms tumor 1 interacti	25 (0.00)	47 (0.21)	0.57
12-01	Gp4	g.chr19:7685834C>G	Silent	XAB2	p.V623V	XPA binding protein 2	28 (0.00)	47 (0.32)	0.85
12-01	Gp4	g.chr3:46062850G>T	Missense Mutation	XCR1	p.S197Y	chemokine (C motif) rec	142 (0.00)	37 (0.30)	0.79
12-01	Gp4	g.chr3:39228468C>A	Silent	XIRP1	p.V823V	xin actin-binding repeat	83 (0.00)	58 (0.26)	0.69
12-01	Gp4	g.chr8:56436138G>T	Missense Mutation	XKR4	p.M435I	XK, Kell blood group co	268 (0.00)	221 (0.17)	0.45
12-01	Gp4	g.chr8:6673254C>A	RNA	XKR5		XK, Kell blood group co	48 (0.00)	43 (0.23)	0.76
12-01	Gp4	g.chr3:14193320C>G	Intron	XPC		xeroderma pigmentosun	133 (0.00)	42 (0.31)	0.83
12-01	Gp4	g.chr22:42018080T>A	Silent	XRCC6	p.L24L	X-ray repair complemer	23 (0.00)	83 (0.33)	0.87
12-01	Gp4	g.chr3:142166742G>T	Silent	XRN1	p.P15P	5'-3' exoribonuclease 1	57 (0.00)	77 (0.18)	0.48
12-01	Gp4	g.chr17:48431795G>T	Missense Mutation	XYLT2	p.D219Y	xylosyltransferase II	87 (0.00)	89 (0.20)	0.54
12-01	Gp4	g.chr11:66052999G>C	Missense Mutation	YIF1A	p.P22R	Yip1 interacting factor h	64 (0.00)	39 (0.23)	0.62
12-01	Gp4	g.chr18:72913949C>A	Missense Mutation	ZADH2	p.G63C	zinc binding alcohol deh	302 (0.00)	27 (0.52)	1.82

12-01	Gp4	g.chr2:98354259C>A	Missense Mutation	ZAP70	p.P508T	zeta-chain (TCR) associ	99 (0.00)	185 (0.23)	0.61
12-01	Gp4	g.chr22:50278508C>A	Missense Mutation	ZBED4	p.H400N	zinc finger, BED-type c	98 (0.00)	237 (0.24)	0.65
12-01	Gp4	g.chr1:244218593C>T	Missense Mutation	ZBTB18	p.S506L	zinc finger and BTB do	176 (0.00)	173 (0.35)	0.94
12-01	Gp4	g.chr3:114069707G>T	Silent	ZBTB20	p.P333P	zinc finger and BTB do	109 (0.01)	177 (0.40)	1.05
12-01	Gp4	g.chr6:109802293G>T	Missense Mutation	ZBTB24	p.Q313K	zinc finger and BTB do	69 (0.01)	37 (0.24)	0.65
12-01	Gp4	g.chr6:109802923C>A	Nonsense Mutation	ZBTB24	p.E103*	zinc finger and BTB do	176 (0.00)	12 (0.67)	1.78
12-01	Gp4	g.chrX:119387348T>C	Silent	ZBTB33	p.R26R	zinc finger and BTB do	38 (0.00)	91 (0.31)	0.51
12-01	Gp4	g.chr1:173840129C>A	Missense Mutation	ZBTB37	p.P256T	zinc finger and BTB do	56 (0.02)	13 (0.62)	1.64
12-01	Gp4	g.chr17:7369475C>T	Missense Mutation	ZBTB4	p.D216N	zinc finger and BTB do	45 (0.00)	81 (0.31)	0.82
12-01	Gp4	g.chr3:42701239C>A	Silent	ZBTB47	p.I464I	zinc finger and BTB do	93 (0.00)	279 (0.15)	0.39
12-01	Gp4	g.chr14:89039251T>C	Missense Mutation	ZC3H14	p.V254A	zinc finger CCCH-type	93 (0.00)	128 (0.18)	0.48
12-01	Gp4	g.chr2:113090024G>T	Missense Mutation	ZC3H6	p.V1177F	zinc finger CCCH-type	138 (0.00)	39 (0.31)	0.82
12-01	Gp4	g.chr22:41723277C>T	Missense Mutation	ZC3H7B	p.A118V	zinc finger CCCH-type	61 (0.00)	114 (0.18)	0.49
12-01	Gp4	g.chr18:60242771G>A	Missense Mutation	ZCCHC2	p.A1153T	zinc finger, CCHC dom	88 (0.00)	11 (0.45)	1.21
12-01	Gp4	g.chr5:825300C>A	Missense Mutation	ZDHHC11	p.Q334H	zinc finger, DHHC-type	103 (0.00)	33 (0.27)	0.73
12-01	Gp4	g.chr10:99212678G>T	Missense Mutation	ZDHHC16	p.C185F	zinc finger, DHHC-type	207 (0.00)	294 (1.00)	2.66
12-01	Gp4	g.chr3:113672876G>T	Missense Mutation	ZDHHC23	p.G164V	zinc finger, DHHC-type	352 (0.00)	32 (0.84)	2.25
12-01	Gp4	g.chr3:44986745C>A	Nonsense Mutation	ZDHHC3	p.E150*	zinc finger, DHHC-type	242 (0.00)	29 (0.28)	0.74
12-01	Gp4	g.chr9:131513724G>T	Missense Mutation	ZER1	p.L336M	zyg-11 related, cell cycl	142 (0.00)	37 (0.16)	0.43
12-01	Gp4	g.chr8:135614438C>A	Missense Mutation	ZFAT	p.Q508H	zinc finger and AT hoo	96 (0.00)	199 (0.24)	0.64
12-01	Gp4	g.chr14:23993379C>A	Silent	ZFHX2	p.V1924V	zinc finger homeobox 2	67 (0.00)	17 (0.47)	1.25
12-01	Gp4	g.chr16:72831290G>T	Missense Mutation	ZFHX3	p.A1764D	zinc finger homeobox 3	86 (0.00)	31 (0.55)	0.60
12-01	Gp4	g.chr16:72845620C>T	Silent	ZFHX3	p.V1240V	zinc finger homeobox 3	125 (0.00)	39 (0.79)	0.87
12-01	Gp4	g.chr16:72923701T>C	Missense Mutation	ZFHX3	p.K1126R	zinc finger homeobox 3	41 (0.00)	24 (0.71)	0.78
12-01	Gp4	g.chr15:41106005C>A	Missense Mutation	ZFYVE19	p.P227H	zinc finger, FYVE dom	114 (0.00)	144 (0.43)	1.15
12-01	Gp4	g.chr14:68249985G>T	Nonsense Mutation	ZFYVE26	p.S1295*	zinc finger, FYVE dom	126 (0.00)	56 (0.39)	1.05
12-01	Gp4	g.chr14:68265093T>C	Missense Mutation	ZFYVE26	p.K629R	zinc finger, FYVE dom	51 (0.00)	20 (0.30)	0.80
12-01	Gp4	g.chr14:68270908G>A	Missense Mutation	ZFYVE26	p.H449Y	zinc finger, FYVE dom	81 (0.00)	19 (0.42)	1.12
12-01	Gp4	g.chr4:2343238G>C	Missense Mutation	ZFYVE28	p.D48E	zinc finger, FYVE dom	47 (0.00)	28 (0.32)	0.86
12-01	Gp4	g.chr13:100635086A>G	Silent	ZIC2	p.L256L	Zic family member 2	82 (0.00)	41 (0.20)	0.52
12-01	Gp4	g.chr10:80968173G>T	Silent	ZMIZ1	p.R47R	zinc finger, MIZ-type c	21 (0.00)	87 (0.57)	1.53
12-01	Gp4	g.chr7:44805848G>T	Silent	ZMIZ2	p.P776P	zinc finger, MIZ-type c	44 (0.00)	44 (0.84)	2.24
12-01	Gp4	g.chr20:45853003A>G	Missense Mutation	ZMYND8	p.W923R	zinc finger, MYND-typ	89 (0.00)	85 (0.20)	0.53
12-01	Gp4	g.chr20:45853052G>A	Silent	ZMYND8	p.Y906Y	zinc finger, MYND-typ	160 (0.00)	115 (0.69)	1.83
12-01	Gp4	g.chr16:3169658G>C	Missense Mutation	ZNF205	p.E333Q	zinc finger protein 205	78 (0.00)	150 (0.31)	0.84

12-01	Gp4	g.chr7:148947284C>T	Missense Mutation	ZNF212	p.S20F	zinc finger protein 212	58 (0.00)	31 (0.48)	1.29
12-01	Gp4	g.chr16:3187400A>G	Missense Mutation	ZNF213	p.D40G	zinc finger protein 213	216 (0.00)	174 (0.23)	0.61
12-01	Gp4	g.chr19:44610610C>A	Silent	ZNF224	p.S99S	zinc finger protein 224	38 (0.00)	27 (0.37)	0.99
12-01	Gp4	g.chr10:38241329C>A	Missense Mutation	ZNF25	p.G366V	zinc finger protein 25	32 (0.00)	22 (0.50)	1.33
12-01	Gp4	g.chr22:22869000G>T	Missense Mutation	ZNF280A	p.H319N	zinc finger protein 280A	66 (0.00)	19 (0.37)	0.98
12-01	Gp4	g.chr1:200378282G>T	Silent	ZNF281	p.V184V	zinc finger protein 281	138 (0.00)	102 (0.33)	0.89
12-01	Gp4	g.chr19:45575076T>C	Missense Mutation	ZNF296	p.H404R	zinc finger protein 296	100 (0.00)	28 (0.61)	2.03
12-01	Gp4	g.chr19:45575090G>T	Missense Mutation	ZNF296	p.S399R	zinc finger protein 296	98 (0.00)	26 (0.58)	1.93
12-01	Gp4	g.chr5:71756240C>G	Missense Mutation	ZNF366	p.G362R	zinc finger protein 366	86 (0.00)	115 (0.15)	0.39
12-01	Gp4	g.chr12:6778352G>T	Missense Mutation	ZNF384	p.H277N	zinc finger protein 384	91 (0.00)	33 (0.67)	1.78
12-01	Gp4	g.chr19:12358753C>T	Missense Mutation	ZNF44	p.C321Y	zinc finger protein 44	20 (0.00)	24 (0.88)	2.33
12-01	Gp4	g.chr9:109689842C>G	Missense Mutation	ZNF462	p.R62G	zinc finger protein 462	411 (0.00)	88 (0.32)	0.85
12-01	Gp4	g.chr19:50549664T>A	Missense Mutation	ZNF473	p.F655Y	zinc finger protein 473	40 (0.00)	30 (0.33)	0.89
12-01	Gp4	g.chr9:114293204G>A	Silent	ZNF483	p.E154E	zinc finger protein 483	20 (0.00)	35 (0.71)	1.90
12-01	Gp4	g.chr10:48371065C>A	Nonsense Mutation	ZNF488	p.S178*	zinc finger protein 488	53 (0.00)	27 (0.22)	0.59
12-01	Gp4	g.chr18:74154264C>T	Silent	ZNF516	p.P249P	zinc finger protein 516	33 (0.00)	25 (0.24)	0.84
12-01	Gp4	g.chr19:42728937G>T	Missense Mutation	ZNF526	p.D128Y	zinc finger protein 526	35 (0.00)	52 (0.48)	1.28
12-01	Gp4	g.chr19:30934755C>A	Missense Mutation	ZNF536	p.L96I	zinc finger protein 536	49 (0.00)	51 (0.29)	0.78
12-01	Gp4	g.chr19:30935687C>A	Silent	ZNF536	p.P406P	zinc finger protein 536	53 (0.00)	116 (0.47)	1.26
12-01	Gp4	g.chr19:48047660G>T	Missense Mutation	ZNF541	p.P709Q	zinc finger protein 541	25 (0.00)	31 (0.39)	1.03
12-01	Gp4	g.chr19:2876206C>A	Silent	ZNF556	p.S82S	zinc finger protein 556	81 (0.00)	41 (0.46)	1.24
12-01	Gp4	g.chr19:53208414G>A	Missense Mutation	ZNF611	p.R632C	zinc finger protein 611	119 (0.01)	22 (0.36)	0.97
12-01	Gp4	g.chr19:55993076C>T	Silent	ZNF628	p.G172G	zinc finger protein 628	16 (0.00)	48 (0.29)	0.78
12-01	Gp4	g.chr16:31072452C>G	Silent	ZNF668	p.G599G	zinc finger protein 668	98 (0.00)	164 (0.26)	0.70
12-01	Gp4	g.chr17:80788076G>T	Missense Mutation	ZNF750	p.A705E	zinc finger protein 750	93 (0.00)	59 (0.42)	1.13
12-01	Gp4	g.chr6:35261578G>A	Missense Mutation	ZNF76	p.M460I	zinc finger protein 76	63 (0.00)	183 (0.22)	0.58
12-01	Gp4	g.chr19:53926326G>A	Missense Mutation	ZNF765	p.E52K	zinc finger protein 765	216 (0.00)	47 (0.34)	0.91
12-01	Gp4	g.chr16:30537210G>A	Missense Mutation	ZNF768	p.P84L	zinc finger protein 768	47 (0.00)	15 (0.60)	1.60
12-01	Gp4	g.chr7:148769441T>A	Silent	ZNF786	p.P141P	zinc finger protein 786	52 (0.00)	158 (0.41)	1.10
12-01	Gp4	g.chr4:206511C>G	RNA	ZNF876P		zinc finger protein 876,	30 (0.00)	81 (0.32)	0.86
12-01	Gp4	g.chr19:22605020C>T	Missense Mutation	ZNF98	p.G3R	zinc finger protein 98	52 (0.00)	54 (0.41)	1.09
12-01	Gp4	g.chr22:29445231C>T	Silent	ZNRF3	p.L354L	zinc and ring finger 3	158 (0.01)	123 (0.47)	1.26
12-01	Gp4	g.chr7:76062786G>T	Splice Site	ZP3		zona pellucida glycopro	108 (0.00)	43 (0.23)	0.62
12-01	Gp4	g.chr16:3142137C>A	Nonsense Mutation	ZSCAN10	p.E138*	zinc finger and SCAN d	16 (0.00)	42 (0.40)	1.08
12-01	Gp4	g.chr20:44512362G>C	Missense Mutation	ZSWIM1	p.Q377H	zinc finger, SWIM-type	188 (0.00)	34 (0.21)	0.55

12-01	Gp4	g.chr20:44506974G>T	Missense Mutation	ZSWIM3	p.G593W	zinc finger, SWIM-type	157 (0.00)	259 (0.20)	0.54
12-01	Gp4	g.chr19:13919965C>G	Missense Mutation	ZSWIM4	p.R315G	zinc finger, SWIM-type	21 (0.00)	101 (0.18)	0.48
12-01	Gp4	g.chr10:75558854A>T	Missense Mutation	ZSWIM8	p.Q1419L	zinc finger, SWIM-type	102 (0.01)	173 (0.50)	1.34
12-01	Gp4	g.chr3:126193916C>A	Nonsense Mutation	ZXDC	p.E265*	ZXD family zinc finger	29 (0.00)	27 (0.19)	0.49
12-01	Gp4	g.chr7:143079462G>T	Missense Mutation	ZYX	p.E110D	zyxin	28 (0.00)	15 (0.53)	1.42
12-01	Gp4	g.chr17:3920698G>T	Missense Mutation	ZZEF1	p.F2656L	zinc finger, ZZ-type wit	70 (0.00)	104 (0.41)	1.10
12-01	Gp4	g.chr17:3968075G>A	Missense Mutation	ZZEF1	p.T1433M	zinc finger, ZZ-type wit	73 (0.00)	54 (0.74)	1.98
12-02	Gp3	g.chr12:53702526G>A	Missense Mutation	AAAS	p.S357F	achalasia, adrenocortica	46 (0.00)	51 (0.27)	0.73
12-02	Gp3	g.chr17:35346709C>A	Splice Site	AATF	p.P438Q	apoptosis antagonizing t	57 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr2:215876760G>T	Missense Mutation	ABCA12	p.P686T	ATP-binding cassette, s	174 (0.00)	109 (0.15)	0.39
12-02	Gp3	g.chr13:95715088G>T	Missense Mutation	ABCC4	p.A1079D	ATP-binding cassette, s	57 (0.00)	35 (0.17)	0.46
12-02	Gp3	g.chr15:89695016C>T	Silent	ABHD2	p.I101I	abhydrolase domain con	30 (0.00)	78 (0.23)	0.62
12-02	Gp3	g.chr2:58688928C>A	lincRNA	AC007092.1			37 (0.00)	33 (0.39)	1.05
12-02	Gp3	g.chr2:62373999G>T	RNA	AC018462.2			35 (0.00)	47 (0.57)	1.53
12-02	Gp3	g.chr8:61851023T>A	lincRNA	AC022182.1			56 (0.00)	17 (0.53)	1.41
12-02	Gp3	g.chr10:15120564T>A	Nonsense Mutation	ACBD7	p.K78*	acyl-CoA binding doma	40 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr4:8416616G>A	Missense Mutation	ACOX3	p.H140Y	acyl-CoA oxidase 3, pri	80 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr3:38520636G>T	Missense Mutation	ACVR2B	p.Q228H	activin A receptor, type	28 (0.00)	49 (0.16)	0.44
12-02	Gp3	g.chr10:127806666T>A	Missense Mutation	ADAM12	p.T185S	ADAM metallopeptidas	52 (0.00)	56 (0.21)	0.57
12-02	Gp3	g.chr7:87795245C>A	Silent	ADAM22	p.I725I	ADAM metallopeptidas	140 (0.00)	42 (0.31)	0.83
12-02	Gp3	g.chr8:24207412G>C	Missense Mutation	ADAM28	p.A676P	ADAM metallopeptidas	41 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr3:64641251C>T	Splice Site	ADAMTS9		ADAM metallopeptidas	115 (0.00)	55 (0.20)	0.53
12-02	Gp3	g.chr7:140373855C>G	Nonsense Mutation	ADCK2	p.S242*	aarF domain containing	22 (0.00)	99 (0.18)	0.48
12-02	Gp3	g.chr5:7727281G>T	Missense Mutation	ADCY2	p.R593L	adenylate cyclase 2 (bra	20 (0.00)	43 (0.21)	0.56
12-02	Gp3	g.chr14:24799097C>A	Missense Mutation	ADCY4	p.A396S	adenylate cyclase 4	20 (0.00)	53 (0.15)	0.40
12-02	Gp3	g.chr16:4163766C>G	Missense Mutation	ADCY9	p.A560P	adenylate cyclase 9	20 (0.00)	31 (0.16)	0.59
12-02	Gp3	g.chr6:147012420G>T	Missense Mutation	ADGB	p.A494S	androglobin	27 (0.00)	24 (0.38)	1.00
12-02	Gp3	g.chr4:100129871G>A	Missense Mutation	ADH6	p.A261V	alcohol dehydrogenase (	37 (0.00)	46 (0.43)	1.16
12-02	Gp3	g.chr20:49509396C>A	Missense Mutation	ADNP	p.V619F	activity-dependent neur	56 (0.00)	37 (0.19)	0.50
12-02	Gp3	g.chr10:88769239G>T	RNA	AGAP11		ankyrin repeat and GTP	23 (0.00)	91 (0.18)	0.47
12-02	Gp3	g.chr2:27277675G>T	Splice Site	AGBL5	p.R243S	ATP/GTP binding prote	81 (0.00)	44 (0.30)	0.79
12-02	Gp3	g.chr1:100350183C>G	Missense Mutation	AGL	p.Q869E	amylo-alpha-1, 6-glucos	69 (0.00)	27 (0.19)	0.49
12-02	Gp3	g.chr1:36492776C>A	Missense Mutation	AGO3	p.P490T	argonaute RISC catalyti	48 (0.00)	73 (0.25)	0.66
12-02	Gp3	g.chr1:36298166A>T	Missense Mutation	AGO4	p.L458F	argonaute RISC catalyti	30 (0.00)	16 (0.50)	1.33
12-02	Gp3	g.chr8:41472523G>A	Missense Mutation	AGPAT6	p.G337R	1-acylglycerol-3-phosph	47 (0.00)	39 (0.26)	0.68

12-02	Gp3	g.chr6:135787113T>C	Silent	AHI1	p.V196V	Abelson helper integrati	35 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr11:62290929G>A	Silent	AHNAK	p.L3654L	AHNAK nucleoprotein	34 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr4:107249301C>A	Missense Mutation	AIMP1	p.Q98K	aminoacyl tRNA synthe	23 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr1:33480184G>T	Missense Mutation	AK2	p.P146H	adenylate kinase 2	85 (0.00)	46 (0.20)	0.52
12-02	Gp3	g.chr13:42876393T>A	Missense Mutation	AKAP11	p.S1171T	A kinase (PRKA) ancho	129 (0.00)	23 (0.48)	1.28
12-02	Gp3	g.chr6:151670408A>G	Silent	AKAP12	p.S294S	A kinase (PRKA) ancho	22 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr7:91714173C>A	Missense Mutation	AKAP9	p.H2917Q	A kinase (PRKA) ancho	162 (0.00)	60 (0.15)	0.40
12-02	Gp3	g.chr7:91727092C>A	Missense Mutation	AKAP9	p.Q3531K	A kinase (PRKA) ancho	74 (0.00)	17 (0.35)	0.94
12-02	Gp3	g.chr9:117121939C>G	Missense Mutation	AKNA	p.E809D	AT-hook transcription f	23 (0.00)	33 (0.21)	0.57
12-02	Gp3	g.chr17:18326044G>A	RNA	AL353997.3			32 (0.00)	72 (0.19)	0.52
12-02	Gp3	g.chr10:97373730G>T	Silent	ALDH18A1	p.T598T	aldehyde dehydrogenas	60 (0.00)	37 (0.27)	0.72
12-02	Gp3	g.chr2:202357544C>A	Missense Mutation	ALS2CR11	p.D1174Y	amyotrophic lateral scle	35 (0.00)	29 (0.31)	0.83
12-02	Gp3	g.chrX:112033824G>T	Missense Mutation	AMOT	p.Q705K	angiomotin	47 (0.02)	33 (0.64)	1.06
12-02	Gp3	g.chr11:94533280T>C	Silent	AMOTL1	p.G308G	angiomotin like 1	21 (0.00)	72 (0.15)	0.41
12-02	Gp3	g.chr12:121773445G>A	Silent	ANAPC5	p.L281L	anaphase promoting con	31 (0.00)	15 (0.47)	0.74
12-02	Gp3	g.chr8:41545725C>A	Missense Mutation	ANK1	p.A1403S	ankyrin 1, erythrocytic	22 (0.00)	42 (0.36)	0.95
12-02	Gp3	g.chr5:139909183G>T	Missense Mutation	ANKHD1	p.D2218Y	ankyrin repeat and KH	53 (0.00)	37 (0.27)	0.72
12-02	Gp3	g.chr2:241419029C>A	Missense Mutation	ANKMY1	p.Q843H	ankyrin repeat and MY	17 (0.00)	109 (0.18)	0.49
12-02	Gp3	g.chr4:73979546T>C	Missense Mutation	ANKRD17	p.N1455S	ankyrin repeat domain 1	87 (0.00)	43 (0.19)	0.50
12-02	Gp3	g.chr4:74026963G>T	Missense Mutation	ANKRD17	p.A217D	ankyrin repeat domain 1	22 (0.00)	30 (0.20)	0.53
12-02	Gp3	g.chr9:33548198G>T	Missense Mutation	ANKRD18B	p.R409M	ankyrin repeat domain 1	61 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr9:67951956G>T	Nonsense Mutation	ANKRD20A1	p.E307*	ankyrin repeat domain 2	49 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr21:15347490T>A	RNA	ANKRD20A11P		ankyrin repeat domain 2	23 (0.00)	16 (0.44)	1.17
12-02	Gp3	g.chr2:95484533G>A	RNA	ANKRD20A8P		ankyrin repeat domain 2	181 (0.00)	37 (0.51)	1.37
12-02	Gp3	g.chr4:80898856C>A	Splice Site	ANTXR2		anthrax toxin receptor 2	56 (0.00)	27 (0.37)	0.99
12-02	Gp3	g.chr7:36588256G>A	Silent	AOAH	p.I365I	acyloxyacyl hydrolase (	36 (0.00)	75 (0.15)	0.39
12-02	Gp3	g.chr17:33977734T>A	Nonsense Mutation	AP2B1	p.Y574*	adaptor-related protein	21 (0.00)	18 (0.56)	1.48
12-02	Gp3	g.chr1:114442525C>T	Splice Site	AP4B1		adaptor-related protein	109 (0.00)	142 (0.16)	0.43
12-02	Gp3	g.chr1:114445397C>G	Missense Mutation	AP4B1	p.L67F	adaptor-related protein	29 (0.00)	23 (0.26)	0.70
12-02	Gp3	g.chr4:41015885C>T	Missense Mutation	APBB2	p.G184R	amyloid beta (A4) precu	69 (0.00)	64 (0.33)	0.88
12-02	Gp3	g.chr5:112163668G>C	Missense Mutation	APC	p.A531P	adenomatous polyposis	32 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr2:68765332C>T	Missense Mutation	APLF	p.S378F	aprataxin and PNKP lik	31 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr2:21231802G>T	Silent	APOB	p.S2646S	apolipoprotein B	37 (0.00)	29 (0.38)	1.01
12-02	Gp3	g.chr17:64224221G>T	Missense Mutation	APOH	p.P53Q	apolipoprotein H (beta-	77 (0.00)	37 (0.19)	0.50
12-02	Gp3	g.chr22:36054723G>C	Missense Mutation	APOL6	p.E38Q	apolipoprotein L, 6	50 (0.00)	34 (0.15)	0.39

12-02	Gp3	g.chr15:30927766G>T	Missense Mutation	ARHGAP11B	p.W246L	Rho GTPase activating	114 (0.00)	54 (0.17)	0.44
12-02	Gp3	g.chr19:47425251G>C	Missense Mutation	ARHGAP35	p.V1107L	Rho GTPase activating	57 (0.00)	35 (0.14)	0.54
12-02	Gp3	g.chr1:156939823G>A	Silent	ARHGEF11	p.L239L	Rho guanine nucleotide	34 (0.00)	27 (0.37)	0.99
12-02	Gp3	g.chr3:56766320C>A	Nonsense Mutation	ARHGEF3	p.G363*	Rho guanine nucleotide	26 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr3:56779291C>G	Missense Mutation	ARHGEF3	p.R242P	Rho guanine nucleotide	64 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr2:39184082C>T	Silent	ARHGEF33	p.L422L	Rho guanine nucleotide	29 (0.00)	16 (0.62)	1.67
12-02	Gp3	g.chr10:63662148G>A	Silent	ARID5B	p.Q84Q	AT rich interactive dom	86 (0.00)	67 (0.15)	0.40
12-02	Gp3	g.chr4:57384934G>A	Missense Mutation	ARL9	p.S36N	ADP-ribosylation factor	49 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr6:109225507A>T	Missense Mutation	ARMC2	p.N308Y	armadillo repeat contain	25 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr6:109285451C>A	Missense Mutation	ARMC2	p.L741I	armadillo repeat contain	102 (0.00)	17 (0.41)	1.10
12-02	Gp3	g.chr3:137991858G>A	Missense Mutation	ARMC8	p.S510N	armadillo repeat contain	79 (0.00)	25 (0.32)	0.85
12-02	Gp3	g.chr8:131127954T>C	Missense Mutation	ASAP1	p.N698D	ArfGAP with SH3 dom	61 (0.00)	19 (0.42)	1.12
12-02	Gp3	g.chr8:131149254G>A	Missense Mutation	ASAP1	p.L371F	ArfGAP with SH3 dom	21 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr2:9498901C>G	Silent	ASAP2	p.S448S	ArfGAP with SH3 dom	59 (0.00)	72 (0.18)	0.48
12-02	Gp3	g.chr6:100988236C>A	Missense Mutation	ASCC3	p.V1860L	activating signal cointeg	56 (0.00)	15 (0.53)	1.42
12-02	Gp3	g.chr1:155385639C>G	Missense Mutation	ASH1L	p.L1968F	ash1 (absent, small, or h	37 (0.00)	52 (0.25)	0.67
12-02	Gp3	g.chr2:25973096T>C	Silent	ASXL2	p.R443R	additional sex combs lik	164 (0.00)	92 (0.14)	0.38
12-02	Gp3	g.chr12:51203271C>A	Missense Mutation	ATF1	p.T76K	activating transcription	52 (0.00)	39 (0.18)	0.48
12-02	Gp3	g.chr12:51203274G>A	Missense Mutation	ATF1	p.R77Q	activating transcription	51 (0.00)	39 (0.18)	0.48
12-02	Gp3	g.chr3:11340197C>T	Missense Mutation	ATG7	p.L10F	autophagy related 7	31 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr3:11402250C>A	Missense Mutation	ATG7	p.P559T	autophagy related 7	70 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr5:159992538G>C	Nonsense Mutation	ATP10B	p.Y1436*	ATPase, class V, type 1	31 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr13:25276103A>G	Missense Mutation	ATP12A	p.T638A	ATPase, H+/K+ transpo	18 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr3:193039476C>A	Nonsense Mutation	ATP13A5	p.E637*	ATPase type 13A5	26 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr3:142279163C>T	Missense Mutation	ATR	p.V495I	ATR serine/threonine ki	49 (0.00)	21 (0.29)	0.76
12-02	Gp3	g.chr3:48493230G>T	Missense Mutation	ATRIP	p.Q159H	ATR interacting protein	27 (0.00)	19 (0.37)	0.98
12-02	Gp3	g.chr17:47218700G>A	Missense Mutation	B4GALNT2	p.V36M	beta-1,4-N-acetyl-galact	41 (0.00)	71 (0.17)	0.54
12-02	Gp3	g.chr14:96731042C>G	Silent	BDKRB1	p.S341S	bradykinin receptor B1	53 (0.00)	57 (0.16)	0.42
12-02	Gp3	g.chr2:32667164G>T	Nonsense Mutation	BIRC6	p.E1326*	baculoviral IAP repeat c	100 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr2:32670588G>T	Splice Site	BIRC6		baculoviral IAP repeat c	20 (0.00)	29 (0.28)	0.74
12-02	Gp3	g.chr19:53793356A>T	Missense Mutation	BIRC8	p.L91Q	baculoviral IAP repeat c	37 (0.00)	51 (0.29)	0.78
12-02	Gp3	g.chr15:91266392G>T	Intron	BLM		Bloom syndrome, RecQ	35 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr15:91293735C>G	Intron	BLM		Bloom syndrome, RecQ	97 (0.00)	35 (0.17)	0.46
12-02	Gp3	g.chr15:91341902C>A	Intron	BLM		Bloom syndrome, RecQ	38 (0.00)	68 (0.18)	0.47
12-02	Gp3	g.chr4:81967497C>A	Missense Mutation	BMP3	p.Q308K	bone morphogenetic pro	29 (0.00)	15 (0.33)	0.89

12-02	Gp3	g.chr17:41202207G>A	Intron	BRCA1		breast cancer 1, early on	24 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr17:41216145G>A	Intron	BRCA1		breast cancer 1, early on	27 (0.00)	24 (0.29)	0.78
12-02	Gp3	g.chr17:41216420C>A	Intron	BRCA1		breast cancer 1, early on	31 (0.00)	31 (0.32)	0.86
12-02	Gp3	g.chr17:41268923C>T	Intron	BRCA1		breast cancer 1, early on	25 (0.00)	42 (0.50)	1.33
12-02	Gp3	g.chr13:32890373C>G	Intron	BRCA2		breast cancer 2, early on	21 (0.00)	73 (0.18)	0.47
12-02	Gp3	g.chr13:32894937T>A	Intron	BRCA2		breast cancer 2, early on	25 (0.00)	22 (0.45)	1.21
12-02	Gp3	g.chr13:32931514G>C	Intron	BRCA2		breast cancer 2, early on	24 (0.00)	17 (0.47)	1.25
12-02	Gp3	g.chr2:28117470C>A	Missense Mutation	BRE	p.P16H	brain and reproductive c	85 (0.00)	40 (0.25)	0.67
12-02	Gp3	g.chr10:93749100A>T	Nonsense Mutation	BTAF1	p.K873*	BTAF1 RNA polymeras	53 (0.00)	15 (0.47)	1.24
12-02	Gp3	g.chr10:93749115A>T	Missense Mutation	BTAF1	p.I878L	BTAF1 RNA polymeras	53 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr10:93749220C>T	Missense Mutation	BTAF1	p.P913S	BTAF1 RNA polymeras	49 (0.00)	36 (0.44)	1.19
12-02	Gp3	g.chr10:103291068C>A	Missense Mutation	BTRC	p.P273H	beta-transducin repeat c	22 (0.00)	24 (0.21)	0.56
12-02	Gp3	g.chr6:105577347G>T	Silent	BVES	p.L86L	blood vessel epicardial s	66 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr10:98744500C>A	Missense Mutation	C10orf12	p.A1118D	chromosome 10 open re	54 (0.00)	48 (0.27)	0.72
12-02	Gp3	g.chr10:127411671G>T	Nonsense Mutation	C10orf137	p.G118*		19 (0.00)	11 (0.73)	1.94
12-02	Gp3	g.chr10:102748712G>A	Missense Mutation	C10orf2	p.G249R	chromosome 10 open re	16 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr11:76253347C>A	Missense Mutation	C11orf30	p.T791N	chromosome 11 open re	24 (0.00)	47 (0.23)	0.62
12-02	Gp3	g.chr11:66581456A>T	Missense Mutation	C11orf80	p.I169L	chromosome 11 open re	26 (0.00)	56 (0.12)	0.44
12-02	Gp3	g.chr11:82643602G>A	Missense Mutation	C11orf82	p.G408S		33 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr11:82643681C>A	Missense Mutation	C11orf82	p.A434D		53 (0.00)	14 (0.43)	1.14
12-02	Gp3	g.chr12:64587965T>A	Missense Mutation	C12orf66	p.H332L	chromosome 12 open re	51 (0.00)	49 (0.16)	0.44
12-02	Gp3	g.chr15:73848676G>T	Missense Mutation	C15orf60	p.V194L		99 (0.00)	68 (0.26)	0.71
12-02	Gp3	g.chr16:4790271G>A	Missense Mutation	C16orf71	p.E146K	chromosome 16 open re	18 (0.00)	45 (0.31)	1.15
12-02	Gp3	g.chr17:30660511C>A	Missense Mutation	C17orf75	p.M300I	chromosome 17 open re	92 (0.00)	92 (0.16)	0.43
12-02	Gp3	g.chr1:38149007G>A	Silent	C1orf109	p.H186H	chromosome 1 open rea	30 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr1:109649720G>A	Missense Mutation	C1orf194	p.R36C	chromosome 1 open rea	99 (0.00)	131 (0.15)	0.39
12-02	Gp3	g.chr1:109649730G>T	Missense Mutation	C1orf194	p.D32E	chromosome 1 open rea	101 (0.00)	125 (0.25)	0.66
12-02	Gp3	g.chr1:152692423C>G	Missense Mutation	C1orf68	p.S142R	chromosome 1 open rea	21 (0.00)	36 (0.14)	0.48
12-02	Gp3	g.chr12:7177888G>A	Missense Mutation	C1S	p.R500Q	complement component	52 (0.00)	65 (0.34)	0.63
12-02	Gp3	g.chr2:29296933C>A	Missense Mutation	C2orf71	p.R65S	chromosome 2 open rea	34 (0.00)	35 (0.46)	1.22
12-02	Gp3	g.chr3:14725786G>C	Silent	C3orf20	p.V174V	chromosome 3 open rea	22 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr4:81283919G>A	Silent	C4orf22	p.L41L	chromosome 4 open rea	45 (0.00)	24 (0.21)	0.56
12-02	Gp3	g.chr4:170669928A>G	Missense Mutation	C4orf27	p.V155A	chromosome 4 open rea	40 (0.00)	19 (0.47)	1.26
12-02	Gp3	g.chr5:41199892C>A	Missense Mutation	C6	p.K141N	complement component	53 (0.00)	32 (0.50)	1.33
12-02	Gp3	g.chr6:36294495T>C	Silent	C6orf222	p.P276P	chromosome 6 open rea	36 (0.00)	50 (0.22)	0.59

12-02	Gp3	g.chr5:40979868G>A	Missense Mutation	C7	p.R736K	complement component	60 (0.00)	63 (0.16)	0.42
12-02	Gp3	g.chr9:97718199C>T	Missense Mutation	C9orf3	p.L493F	chromosome 9 open rea	37 (0.00)	16 (0.50)	1.60
12-02	Gp3	g.chr9:114521510C>T	Missense Mutation	C9orf84	p.R20K	chromosome 9 open rea	31 (0.00)	36 (0.19)	0.52
12-02	Gp3	g.chr22:24459472G>T	Missense Mutation	CABIN1	p.D533Y	calcineurin binding prot	26 (0.00)	37 (0.35)	0.94
12-02	Gp3	g.chr1:181727133G>T	Missense Mutation	CACNA1E	p.M1460I	calcium channel, voltag	73 (0.00)	97 (0.15)	0.41
12-02	Gp3	g.chr3:85092116C>A	Intron	CADM2		cell adhesion molecule	51 (0.02)	48 (0.44)	1.17
12-02	Gp3	g.chr3:85220097T>A	Intron	CADM2		cell adhesion molecule	75 (0.00)	19 (0.37)	0.98
12-02	Gp3	g.chr3:85221888C>A	Intron	CADM2		cell adhesion molecule	79 (0.00)	32 (0.19)	0.50
12-02	Gp3	g.chr3:85258504G>T	Intron	CADM2		cell adhesion molecule	37 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr3:85265097G>T	Intron	CADM2		cell adhesion molecule	25 (0.00)	45 (0.47)	1.24
12-02	Gp3	g.chr3:85338882G>A	Intron	CADM2		cell adhesion molecule	19 (0.00)	17 (0.41)	1.10
12-02	Gp3	g.chr3:85362316G>A	Intron	CADM2		cell adhesion molecule	39 (0.00)	36 (0.39)	1.04
12-02	Gp3	g.chr3:85404010G>A	Intron	CADM2		cell adhesion molecule	81 (0.00)	51 (0.25)	0.68
12-02	Gp3	g.chr3:85437794T>A	Intron	CADM2		cell adhesion molecule	33 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr3:85456513G>C	Intron	CADM2		cell adhesion molecule	158 (0.00)	39 (0.28)	0.75
12-02	Gp3	g.chr3:85472954A>T	Intron	CADM2		cell adhesion molecule	53 (0.00)	37 (0.19)	0.50
12-02	Gp3	g.chr3:85480578C>T	Intron	CADM2		cell adhesion molecule	44 (0.00)	28 (0.54)	1.43
12-02	Gp3	g.chr3:85591539T>G	Intron	CADM2		cell adhesion molecule	83 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr3:85591549C>T	Intron	CADM2		cell adhesion molecule	53 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr3:85802714A>T	Intron	CADM2		cell adhesion molecule	38 (0.00)	42 (0.31)	0.83
12-02	Gp3	g.chr3:85830168C>A	Intron	CADM2		cell adhesion molecule	58 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr3:85837215T>A	Intron	CADM2		cell adhesion molecule	63 (0.00)	27 (0.30)	0.79
12-02	Gp3	g.chr3:85869532G>T	Intron	CADM2		cell adhesion molecule	74 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr3:85870500C>T	Intron	CADM2		cell adhesion molecule	43 (0.00)	39 (0.46)	1.23
12-02	Gp3	g.chr3:85872649C>A	Intron	CADM2		cell adhesion molecule	116 (0.00)	41 (0.22)	0.59
12-02	Gp3	g.chr3:85899077G>A	Intron	CADM2		cell adhesion molecule	22 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr3:85912692C>T	Intron	CADM2		cell adhesion molecule	27 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr3:85931489C>A	Intron	CADM2		cell adhesion molecule	50 (0.00)	30 (0.20)	0.53
12-02	Gp3	g.chr3:85932976C>T	Intron	CADM2		cell adhesion molecule	67 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr3:85953582C>T	Intron	CADM2		cell adhesion molecule	76 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr3:86022566G>T	Intron	CADM2		cell adhesion molecule	62 (0.00)	31 (0.16)	0.43
12-02	Gp3	g.chr3:86022585G>T	Intron	CADM2		cell adhesion molecule	32 (0.00)	17 (0.35)	0.94
12-02	Gp3	g.chr3:86043867G>T	Intron	CADM2		cell adhesion molecule	50 (0.02)	34 (0.32)	0.86
12-02	Gp3	g.chr3:86050383C>G	Intron	CADM2		cell adhesion molecule	84 (0.00)	69 (0.14)	0.39
12-02	Gp3	g.chr3:86050644T>A	Intron	CADM2		cell adhesion molecule	62 (0.00)	44 (0.18)	0.48

12-02	Gp3	g.chr3:86062265C>A	Intron	CADM2		cell adhesion molecule	23 (0.00)	68 (0.15)	0.39
12-02	Gp3	g.chr3:86105340G>A	Intron	CADM2		cell adhesion molecule	98 (0.00)	18 (0.50)	1.33
12-02	Gp3	g.chr7:121985693G>A	Missense Mutation	CADPS2	p.R1142W	Ca++-dependent secreti	82 (0.00)	31 (0.26)	0.69
12-02	Gp3	g.chr3:48266863C>G	Silent	CAMP	p.V157V	cathelicidin antimicrobi	36 (0.00)	43 (0.19)	0.50
12-02	Gp3	g.chr11:64978328C>A	Silent	CAPN1	p.T701T	calpain 1, (mu/I) large s	20 (0.00)	116 (0.20)	0.69
12-02	Gp3	g.chr12:30869499G>C	Missense Mutation	CAPRIN2	p.P768A	caprin family member 2	35 (0.00)	25 (0.32)	0.85
12-02	Gp3	g.chr12:30869589G>A	Silent	CAPRIN2	p.L738L	caprin family member 2	43 (0.00)	38 (0.50)	1.33
12-02	Gp3	g.chr12:30906390G>T	Missense Mutation	CAPRIN2	p.P103H	caprin family member 2	25 (0.00)	34 (0.18)	0.47
12-02	Gp3	g.chr13:111353817C>A	Missense Mutation	CARS2	p.V121L	cysteinyl-tRNA synthet	67 (0.00)	46 (0.22)	0.58
12-02	Gp3	g.chr12:25263171G>T	Missense Mutation	CASC1	p.P595T	cancer susceptibility car	41 (0.00)	10 (0.90)	2.40
12-02	Gp3	g.chr2:202149705C>A	Silent	CASP8	p.I382I	caspase 8, apoptosis-rel	45 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr2:202149719G>A	Missense Mutation	CASP8	p.G387E	caspase 8, apoptosis-rel	47 (0.00)	21 (0.33)	0.89
12-02	Gp3	g.chr6:90566808C>T	RNA	CASP8AP2		caspase 8 associated pro	31 (0.00)	40 (0.20)	0.53
12-02	Gp3	g.chr6:90572272C>A	RNA	CASP8AP2		caspase 8 associated pro	97 (0.00)	145 (0.17)	0.44
12-02	Gp3	g.chr1:26524225C>G	Missense Mutation	CATSPER4	p.R170G	cation channel, sperm a	19 (0.00)	64 (0.30)	0.99
12-02	Gp3	g.chr14:92088185T>A	Missense Mutation	CATSPERB	p.N676I	catsper channel auxiliar	51 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr7:107399174C>T	Missense Mutation	CBLL1	p.P343S	Cbl proto-oncogene-lik	31 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr14:24897018C>A	Missense Mutation	CBLN3	p.G148C	cerebellin 3 precursor	44 (0.00)	143 (0.15)	0.39
12-02	Gp3	g.chr1:52828401C>T	Silent	CC2D1B	p.E29E	coiled-coil and C2 dom	19 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr2:219900333C>T	Silent	CCDC108	p.V137V	coiled-coil domain cont	40 (0.00)	18 (0.56)	1.48
12-02	Gp3	g.chr2:179912034C>G	Missense Mutation	CCDC141	p.E68Q	coiled-coil domain cont	102 (0.00)	24 (0.33)	0.52
12-02	Gp3	g.chr17:20230400G>T	RNA	CCDC144CP		coiled-coil domain cont	15 (0.00)	20 (0.30)	0.80
12-02	Gp3	g.chr11:124824666C>A	Missense Mutation	CCDC15	p.T13N	coiled-coil domain cont	43 (0.00)	53 (0.23)	0.60
12-02	Gp3	g.chr11:124824709C>A	Missense Mutation	CCDC15	p.D27E	coiled-coil domain cont	42 (0.00)	52 (0.23)	0.62
12-02	Gp3	g.chr4:77305725C>A	Missense Mutation	CCDC158	p.A128S	coiled-coil domain cont	62 (0.00)	18 (0.39)	1.04
12-02	Gp3	g.chr1:169390848G>A	Missense Mutation	CCDC181	p.A274V	coiled-coil domain cont	71 (0.00)	38 (0.24)	0.63
12-02	Gp3	g.chr1:169390877G>A	Silent	CCDC181	p.V264V	coiled-coil domain cont	67 (0.00)	43 (0.21)	0.56
12-02	Gp3	g.chr11:93088627G>C	Missense Mutation	CCDC67	p.M40I	coiled-coil domain cont	146 (0.00)	50 (0.16)	0.43
12-02	Gp3	g.chr12:91347464C>A	Missense Mutation	CCER1	p.Q352H	coiled-coil glutamate-ri	46 (0.00)	48 (0.17)	0.44
12-02	Gp3	g.chr4:77987414C>G	Missense Mutation	CCNI	p.M34I	cyclin I	45 (0.00)	36 (0.17)	0.44
12-02	Gp3	g.chr6:74497065G>A	Missense Mutation	CD109	p.A816T	CD109 molecule	44 (0.00)	29 (0.34)	0.92
12-02	Gp3	g.chr12:7647748C>T	Nonsense Mutation	CD163	p.W450*	CD163 molecule	81 (0.00)	36 (0.28)	0.52
12-02	Gp3	g.chr12:7647887G>T	Missense Mutation	CD163	p.L404M	CD163 molecule	61 (0.00)	32 (0.34)	0.64
12-02	Gp3	g.chr19:7807938G>T	Missense Mutation	CD209	p.P401H	CD209 molecule	33 (0.00)	36 (0.17)	0.62
12-02	Gp3	g.chr1:160654923C>A	Nonsense Mutation	CD48	p.E47*	CD48 molecule	17 (0.00)	16 (0.62)	1.67

12-02	Gp3	g.chr5:19473673G>T	Missense Mutation	CDH18	p.P679T	cadherin 18, type 2	100 (0.00)	42 (0.12)	0.41
12-02	Gp3	g.chr20:58557977G>T	Splice Site	CDH26		cadherin 26	57 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr5:31294336G>T	Missense Mutation	CDH6	p.A166S	cadherin 6, type 2, K-ca	57 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr5:26903797G>C	Missense Mutation	CDH9	p.F316L	cadherin 9, type 2 (T1-c	32 (0.00)	41 (0.59)	2.03
12-02	Gp3	g.chr7:105603783C>T	Missense Mutation	CDHR3	p.L7F	cadherin-related family	43 (0.00)	35 (0.29)	0.76
12-02	Gp3	g.chr7:105658337C>T	Missense Mutation	CDHR3	p.P491L	cadherin-related family	28 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr7:40133798G>A	Missense Mutation	CDK13	p.R1253Q	cyclin-dependent kinase	72 (0.01)	30 (0.17)	0.44
12-02	Gp3	g.chr22:18018355G>A	Missense Mutation	CECR2	p.D272N	cat eye syndrome chrom	32 (0.00)	36 (0.28)	0.96
12-02	Gp3	g.chr11:47508319T>A	Missense Mutation	CELF1	p.D98V	CUGBP, Elav-like fami	32 (0.00)	50 (0.28)	0.75
12-02	Gp3	g.chr1:214787190G>A	Silent	CENPF	p.K31K	centromere protein F, 3	31 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr9:95375347C>A	Missense Mutation	CENPP	p.S261R	centromere protein P	46 (0.00)	34 (0.44)	1.18
12-02	Gp3	g.chr1:243385051A>G	Missense Mutation	CEP170	p.V57A	centrosomal protein 170	29 (0.00)	34 (0.21)	0.55
12-02	Gp3	g.chr1:179993618G>T	Missense Mutation	CEP350	p.D1151Y	centrosomal protein 350	24 (0.00)	25 (0.36)	0.96
12-02	Gp3	g.chr17:62529082G>A	Missense Mutation	CEP95	p.E600K	centrosomal protein 95k	92 (0.00)	49 (0.16)	0.44
12-02	Gp3	g.chr1:111703849T>A	Missense Mutation	CEPT1	p.F187Y	choline/ethanolamine p	56 (0.00)	18 (0.44)	1.19
12-02	Gp3	g.chr5:98245171C>T	Intron	CHD1		chromodomain helicase	58 (0.00)	51 (0.24)	0.63
12-02	Gp3	g.chr5:98258899C>G	Intron	CHD1		chromodomain helicase	26 (0.00)	65 (0.17)	0.45
12-02	Gp3	g.chr12:6680080A>G	Silent	CHD4	p.I1917I	chromodomain helicase	73 (0.00)	25 (0.24)	0.45
12-02	Gp3	g.chr12:6704542C>A	Missense Mutation	CHD4	p.K690N	chromodomain helicase	68 (0.00)	14 (0.36)	0.66
12-02	Gp3	g.chr1:6210803C>T	Intron	CHD5		chromodomain helicase	19 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr16:53301341C>A	Missense Mutation	CHD9	p.R1486S	chromodomain helicase	180 (0.01)	35 (0.57)	0.74
12-02	Gp3	g.chr18:24496571G>A	Silent	CHST9	p.V328V	carbohydrate (N-acetylg	23 (0.00)	22 (0.45)	1.21
12-02	Gp3	g.chr15:65489731C>A	Nonsense Mutation	CILP	p.E965*	cartilage intermediate la	18 (0.00)	52 (0.15)	0.41
12-02	Gp3	g.chr2:122205862G>T	Silent	CLASP1	p.T577T	cytoplasmic linker assoc	20 (0.00)	23 (0.22)	0.39
12-02	Gp3	g.chr19:45573813C>T	Missense Mutation	CLASRP	p.S659F	CLK4-associating serin	20 (0.00)	87 (0.29)	1.09
12-02	Gp3	g.chr19:40225024C>A	Nonsense Mutation	CLC	p.E68*	Charcot-Leyden crystal	38 (0.00)	64 (0.11)	0.38
12-02	Gp3	g.chr1:11875953G>T	Missense Mutation	CLCN6	p.E66D	chloride channel, voltag	29 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr12:8672900C>T	Missense Mutation	CLEC4D	p.R155C	C-type lectin domain fa	22 (0.00)	24 (0.25)	0.46
12-02	Gp3	g.chr22:19223265G>A	Missense Mutation	CLTCL1	p.P308L	clathrin, heavy chain-lik	82 (0.00)	116 (0.20)	0.68
12-02	Gp3	g.chr6:37411778C>A	Missense Mutation	CMTR1	p.S46Y	cap methyltransferase 1	37 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr8:87588116T>A	Missense Mutation	CNGB3	p.Q782H	cyclic nucleotide gated	73 (0.01)	43 (0.23)	0.62
12-02	Gp3	g.chr2:68544265C>A	Missense Mutation	CNRIP1	p.R118S	cannabinoid receptor int	37 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr3:2777934G>C	Missense Mutation	CNTN4	p.E31Q	contactin 4	71 (0.00)	55 (0.55)	1.45
12-02	Gp3	g.chr3:1424745C>T	Silent	CNTN6	p.V762V	contactin 6	44 (0.00)	20 (0.60)	1.60
12-02	Gp3	g.chr6:70850853C>A	Missense Mutation	COL19A1	p.P485H	collagen, type XIX, alp	38 (0.00)	46 (0.80)	2.14

12-02	Gp3	g.chr6:56044706C>A	Missense Mutation	COL21A1	p.V104L	collagen, type XXI, alph	75 (0.00)	20 (0.35)	0.93
12-02	Gp3	g.chr1:86249945C>G	Missense Mutation	COL24A1	p.Q1388H	collagen, type XXIV, al	46 (0.00)	26 (0.27)	0.72
12-02	Gp3	g.chr9:116956714G>C	Missense Mutation	COL27A1	p.G683R	collagen, type XXVII, a	24 (0.00)	15 (0.40)	1.07
12-02	Gp3	g.chr2:228159707G>A	Missense Mutation	COL4A3	p.G1149E	collagen, type IV, alpha	147 (0.00)	80 (0.29)	0.77
12-02	Gp3	g.chr2:228173717G>T	Missense Mutation	COL4A3	p.W1522L	collagen, type IV, alpha	36 (0.00)	40 (0.15)	0.40
12-02	Gp3	g.chr3:130292950A>T	Missense Mutation	COL6A6	p.Q1043L	collagen, type VI, alpha	84 (0.00)	47 (0.19)	0.51
12-02	Gp3	g.chr3:130305424G>T	Nonsense Mutation	COL6A6	p.E1349*	collagen, type VI, alpha	164 (0.00)	137 (0.20)	0.53
12-02	Gp3	g.chr11:14501200G>A	Missense Mutation	COPB1	p.R425C	coatomer protein compl	80 (0.00)	33 (0.21)	0.57
12-02	Gp3	g.chr3:139080043C>A	Missense Mutation	COPB2	p.G697V	coatomer protein compl	64 (0.00)	33 (0.48)	1.29
12-02	Gp3	g.chr9:100899930T>C	Missense Mutation	CORO2A	p.H81R	coronin, actin binding p	40 (0.00)	41 (0.17)	0.46
12-02	Gp3	g.chr8:100904156C>T	Missense Mutation	COX6C	p.G32R	cytochrome c oxidase su	117 (0.00)	55 (0.35)	0.92
12-02	Gp3	g.chr2:9588410C>G	Missense Mutation	CPSF3	p.H442Q	cleavage and polyadeny	30 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr1:207680076C>A	Missense Mutation	CR1	p.P107T	complement component	98 (0.00)	47 (0.32)	0.85
12-02	Gp3	g.chr2:209007629G>A	Silent	CRYGB	p.G87G	crystallin, gamma B	60 (0.00)	33 (0.58)	1.54
12-02	Gp3	g.chr8:2965247G>T	Missense Mutation	CSMD1	p.F2277L	CUB and Sushi multiple	46 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr8:68049813C>G	Silent	CSPP1	p.L645L	centrosome and spindle	22 (0.00)	12 (0.75)	2.00
12-02	Gp3	g.chr18:19995815C>G	Missense Mutation	CTAGE1	p.E654Q	cutaneous T-cell lymph	46 (0.00)	27 (0.33)	0.89
12-02	Gp3	g.chr18:19996503G>T	Silent	CTAGE1	p.L424L	cutaneous T-cell lymph	67 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr18:19997438G>A	Missense Mutation	CTAGE1	p.H113Y	cutaneous T-cell lymph	71 (0.00)	35 (0.17)	0.46
12-02	Gp3	g.chr19:20368624C>A	RNA	CTC-260E6.6			24 (0.00)	20 (0.40)	1.39
12-02	Gp3	g.chr19:20370065G>T	RNA	CTC-260E6.6			78 (0.00)	62 (0.34)	1.17
12-02	Gp3	g.chr19:20405969G>A	RNA	CTC-260E6.6			45 (0.00)	49 (0.24)	0.85
12-02	Gp3	g.chr11:10785366G>A	Missense Mutation	CTR9	p.M378I	CTR9, Paf1/RNA polyn	69 (0.00)	77 (0.31)	0.83
12-02	Gp3	g.chr17:36971241C>A	Nonsense Mutation	CWC25	p.E101*	CWC25 spliceosome-as	32 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr19:41386040C>G	Silent	CYP2A7	p.L201L	cytochrome P450, famil	15 (0.00)	81 (0.21)	0.74
12-02	Gp3	g.chr19:15734190G>T	RNA	CYP4F8		cytochrome P450, famil	50 (0.00)	36 (0.14)	0.48
12-02	Gp3	g.chr9:124345213C>G	Intron	DAB2IP		DAB2 interacting protei	22 (0.00)	39 (0.15)	0.41
12-02	Gp3	g.chr9:124352024C>A	Intron	DAB2IP		DAB2 interacting protei	24 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr9:124360008G>T	Intron	DAB2IP		DAB2 interacting protei	63 (0.00)	104 (0.19)	0.51
12-02	Gp3	g.chr9:124378863C>T	Intron	DAB2IP		DAB2 interacting protei	50 (0.00)	62 (0.27)	0.73
12-02	Gp3	g.chr9:124382859T>A	Intron	DAB2IP		DAB2 interacting protei	31 (0.00)	80 (0.15)	0.40
12-02	Gp3	g.chr9:124386401C>A	Intron	DAB2IP		DAB2 interacting protei	39 (0.00)	46 (0.15)	0.41
12-02	Gp3	g.chr9:124417728G>T	Intron	DAB2IP		DAB2 interacting protei	16 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr9:124446197G>T	Intron	DAB2IP		DAB2 interacting protei	41 (0.00)	88 (0.20)	0.55
12-02	Gp3	g.chr9:124488107G>A	Intron	DAB2IP		DAB2 interacting protei	17 (0.00)	58 (0.22)	0.60

12-02	Gp3	g.chr9:124489428C>G	Intron	DAB2IP		DAB2 interacting protei	52 (0.00)	36 (0.19)	0.52
12-02	Gp3	g.chr9:124518877C>A	Intron	DAB2IP		DAB2 interacting protei	15 (0.00)	142 (0.14)	0.38
12-02	Gp3	g.chr8:104453695G>A	Missense Mutation	DCAF13	p.E519K	DDB1 and CUL4 associ	51 (0.00)	37 (0.19)	0.50
12-02	Gp3	g.chr10:14950782C>A	Silent	DCLRE1C	p.G568G	DNA cross-link repair 1	60 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr1:112308953T>C	Missense Mutation	DDX20	p.I636T	DEAD (Asp-Glu-Ala-A	25 (0.00)	16 (0.38)	1.00
12-02	Gp3	g.chr12:49227201C>G	Missense Mutation	DDX23	p.M554I	DEAD (Asp-Glu-Ala-A	30 (0.00)	40 (0.15)	0.40
12-02	Gp3	g.chr12:49230747G>T	Silent	DDX23	p.R314R	DEAD (Asp-Glu-Ala-A	36 (0.00)	97 (0.15)	0.41
12-02	Gp3	g.chr20:47839898G>A	Missense Mutation	DDX27	p.E163K	DEAD (Asp-Glu-Ala-A	76 (0.01)	40 (0.35)	0.93
12-02	Gp3	g.chr5:134120145G>T	Missense Mutation	DDX46	p.G419V	DEAD (Asp-Glu-Ala-A	51 (0.00)	48 (0.21)	0.56
12-02	Gp3	g.chr11:118630702G>T	Missense Mutation	DDX6	p.L265I	DEAD (Asp-Glu-Ala-A	31 (0.00)	10 (0.50)	1.33
12-02	Gp3	g.chr4:169343746G>T	Missense Mutation	DDX60L	p.H725N	DEAD (Asp-Glu-Ala-A	63 (0.00)	30 (0.23)	0.62
12-02	Gp3	g.chr22:32293567C>G	Missense Mutation	DEPDC5	p.L1426V	DEP domain containing	27 (0.00)	22 (0.36)	0.97
12-02	Gp3	g.chr1:10523648C>G	Silent	DFFA	p.L157L	DNA fragmentation fac	20 (0.00)	44 (0.23)	0.61
12-02	Gp3	g.chr22:20074154C>A	Missense Mutation	DGCR8	p.A223E	DGCR8 microprocessor	54 (0.00)	286 (0.15)	0.52
12-02	Gp3	g.chr2:234343109G>T	Silent	DGKD	p.V144V	diacylglycerol kinase, d	17 (0.00)	24 (0.46)	1.22
12-02	Gp3	g.chr1:26764725C>A	Missense Mutation	DHDDS	p.Q44K	dehydrodolichyl diphos	45 (0.00)	63 (0.14)	0.47
12-02	Gp3	g.chr14:24429198G>T	Nonsense Mutation	DHRS4	p.E132*	dehydrogenase/reductas	26 (0.00)	11 (0.55)	1.45
12-02	Gp3	g.chr10:12160844C>T	Silent	DHTKD1	p.I833I	dehydrogenase E1 and t	61 (0.00)	132 (0.15)	0.40
12-02	Gp3	g.chr21:47954555C>A	Missense Mutation	DIP2A	p.L529M	DIP2 disco-interacting	52 (0.00)	41 (0.17)	0.61
12-02	Gp3	g.chr12:51125183C>A	Missense Mutation	DIP2B	p.P1225T	DIP2 disco-interacting	44 (0.00)	29 (0.24)	0.64
12-02	Gp3	g.chr12:51125215C>A	Silent	DIP2B	p.L1235L	DIP2 disco-interacting	40 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr12:51127918G>A	Splice Site	DIP2B	p.G1328R	DIP2 disco-interacting	34 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr12:51127936C>A	Missense Mutation	DIP2B	p.P1334T	DIP2 disco-interacting	34 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr3:38129832C>A	Missense Mutation	DLEC1	p.L540M	deleted in lung and esop	18 (0.00)	14 (0.71)	1.90
12-02	Gp3	g.chr3:38129836C>A	Missense Mutation	DLEC1	p.P541H	deleted in lung and esop	18 (0.00)	14 (0.71)	1.90
12-02	Gp3	g.chr14:55636201C>A	Silent	DLGAP5	p.L488L	discs, large (Drosophila	29 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr12:124350525G>A	Missense Mutation	DNAH10	p.A2240T	dynein, axonemal, heav	38 (0.00)	18 (0.39)	0.62
12-02	Gp3	g.chr7:21584685G>A	Missense Mutation	DNAH11	p.G138E	dynein, axonemal, heav	87 (0.01)	39 (0.28)	0.75
12-02	Gp3	g.chr7:21657342C>T	Nonsense Mutation	DNAH11	p.Q1401*	dynein, axonemal, heav	54 (0.00)	35 (0.46)	1.22
12-02	Gp3	g.chr7:21892211G>A	Missense Mutation	DNAH11	p.E3675K	dynein, axonemal, heav	66 (0.00)	32 (0.28)	0.75
12-02	Gp3	g.chr3:57335933G>A	Missense Mutation	DNAH12	p.L2874F	dynein, axonemal, heav	20 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr16:21014437C>A	Missense Mutation	DNAH3	p.A2039S	dynein, axonemal, heav	48 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr2:84954888C>A	Silent	DNAH6	p.V3356V	dynein, axonemal, heav	74 (0.00)	44 (0.25)	0.67
12-02	Gp3	g.chr2:196636563C>A	Missense Mutation	DNAH7	p.V3752F	dynein, axonemal, heav	82 (0.00)	20 (0.30)	0.80
12-02	Gp3	g.chr2:196771469C>T	Missense Mutation	DNAH7	p.E1417K	dynein, axonemal, heav	43 (0.00)	31 (0.35)	0.95

12-02	Gp3	g.chr1:78481827C>A	Missense Mutation	DNAJB4	p.P304T	DnaJ (Hsp40) homolog,	41 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr7:102953424C>A	Missense Mutation	DNAJC2	p.R587S	DnaJ (Hsp40) homolog,	93 (0.00)	86 (0.27)	0.71
12-02	Gp3	g.chr17:40146922G>A	Missense Mutation	DNAJC7	p.A149V	DnaJ (Hsp40) homolog,	68 (0.00)	47 (0.28)	0.99
12-02	Gp3	g.chr1:94342611G>A	Nonsense Mutation	DNTTIP2	p.Q294*	deoxynucleotidyltransfe	56 (0.00)	23 (0.70)	1.86
12-02	Gp3	g.chr10:129242509A>G	Silent	DOCK1	p.T1772T	dedicator of cytokinesis	41 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chrX:117814575T>C	Missense Mutation	DOCK11	p.V1864A	dedicator of cytokinesis	106 (0.00)	27 (0.63)	1.05
12-02	Gp3	g.chr7:111387401C>A	Missense Mutation	DOCK4	p.Q1496H	dedicator of cytokinesis	103 (0.00)	79 (0.23)	0.61
12-02	Gp3	g.chr8:25216521G>T	Missense Mutation	DOCK5	p.D965Y	dedicator of cytokinesis	30 (0.00)	26 (0.23)	0.62
12-02	Gp3	g.chr18:67266663G>C	Missense Mutation	DOK6	p.R73P	docking protein 6	116 (0.00)	79 (0.23)	0.61
12-02	Gp3	g.chr15:65793030C>A	Missense Mutation	DPP8	p.D170Y	dipeptidyl-peptidase 8	36 (0.00)	39 (0.28)	0.75
12-02	Gp3	g.chr3:109028053G>A	Silent	DPPA2	p.D102D	developmental pluripote	29 (0.00)	77 (0.18)	0.48
12-02	Gp3	g.chr19:32954790G>A	Nonsense Mutation	DPY19L3	p.W487*	dpy-19-like 3 (C. elegan	114 (0.01)	40 (0.30)	0.80
12-02	Gp3	g.chr5:146785246G>A	Silent	DPYSL3	p.T246T	dihydropyrimidinase-lik	31 (0.00)	51 (0.27)	0.73
12-02	Gp3	g.chr18:65180559G>T	Silent	DSEL	p.T439T	dermatan sulfate epimer	26 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr6:7568742C>A	Missense Mutation	DSP	p.Q447K	desmoplakin	59 (0.00)	24 (0.29)	0.78
12-02	Gp3	g.chr6:7581663C>A	Missense Mutation	DSP	p.A1747E	desmoplakin	104 (0.00)	54 (0.26)	0.69
12-02	Gp3	g.chr6:56373402A>T	Silent	DST	p.T6068T	dystonin	72 (0.00)	119 (0.24)	0.63
12-02	Gp3	g.chr6:56417893G>A	Missense Mutation	DST	p.L5022F	dystonin	55 (0.00)	23 (0.26)	0.70
12-02	Gp3	g.chr6:56471493G>T	Missense Mutation	DST	p.Q2434K	dystonin	19 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr19:57670572C>A	Missense Mutation	DUXA	p.Q85H	double homeobox A	22 (0.00)	13 (0.92)	2.46
12-02	Gp3	g.chr1:206822096G>T	Missense Mutation	DYRK3	p.R518I	dual-specificity tyrosine	28 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr20:18370424C>A	Missense Mutation	DZANK1	p.V647L	double zinc ribbon and	47 (0.00)	46 (0.15)	0.41
12-02	Gp3	g.chr3:137783535C>A	Missense Mutation	DZIP1L	p.V693F	DAZ interacting zinc fir	43 (0.00)	21 (0.29)	0.76
12-02	Gp3	g.chr11:19251050G>T	Missense Mutation	E2F8	p.S615Y	E2F transcription factor	72 (0.01)	41 (0.22)	0.59
12-02	Gp3	g.chr3:73111890G>A	Missense Mutation	EBLN2	p.G220R	endogenous Bornavirus-	78 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr3:73111939C>A	Missense Mutation	EBLN2	p.A236E	endogenous Bornavirus-	75 (0.00)	47 (0.15)	0.40
12-02	Gp3	g.chr1:236645864G>C	Missense Mutation	EDARADD	p.R178T	EDAR-associated death	18 (0.00)	55 (0.16)	0.44
12-02	Gp3	g.chr13:78492253G>T	Silent	EDNRB	p.V242V	endothelin receptor type	22 (0.00)	50 (0.16)	0.43
12-02	Gp3	g.chr2:63053353C>T	Silent	EHBP1	p.A148A	EH domain binding prot	140 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr19:40030083C>A	Missense Mutation	EID2	p.A213S	EP300 interacting inhibi	21 (0.00)	52 (0.21)	0.74
12-02	Gp3	g.chr3:184039723C>A	Missense Mutation	EIF4G1	p.P364T	eukaryotic translation in	22 (0.00)	54 (0.24)	0.64
12-02	Gp3	g.chr4:139981694G>A	Missense Mutation	ELF2	p.T302I	E74-like factor 2 (ets do	64 (0.00)	58 (0.66)	1.75
12-02	Gp3	g.chr14:24608639G>A	Nonsense Mutation	EMC9	p.Q50*	ER membrane protein c	34 (0.00)	17 (0.35)	0.94
12-02	Gp3	g.chr19:6926575G>T	Missense Mutation	EMR1	p.A729S	egf-like module contain	17 (0.00)	18 (0.61)	2.26
12-02	Gp3	g.chr1:29314147G>T	Missense Mutation	EPB41	p.L66F	erythrocyte membrane p	36 (0.00)	19 (0.42)	1.40

12-02	Gp3	g.chr7:37988491G>A	Missense Mutation	EPDR1	p.D46N	ependymin related 1	70 (0.00)	52 (0.15)	0.41
12-02	Gp3	g.chr7:100411274C>G	Splice Site	EPHB4	p.G586R	EPH receptor B4	37 (0.00)	44 (0.18)	0.48
12-02	Gp3	g.chr13:43491697T>A	Nonsense Mutation	EPSTI1	p.K241*	epithelial stromal intera	105 (0.00)	56 (0.23)	0.62
12-02	Gp3	g.chr16:14021912A>T	Missense Mutation	ERCC4	p.L204F	excision repair cross-co	90 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr16:14021913G>T	Nonsense Mutation	ERCC4	p.E205*	excision repair cross-co	91 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr10:50714016C>A	Silent	ERCC6	p.L480L	excision repair cross-co	102 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr21:39820911C>T	Intron	ERG		v-ets avian erythroblast	43 (0.00)	21 (0.52)	0.46
12-02	Gp3	g.chr21:39907944C>A	Intron	ERG		v-ets avian erythroblast	127 (0.00)	11 (0.73)	0.65
12-02	Gp3	g.chr21:39932328C>T	Intron	ERG		v-ets avian erythroblast	74 (0.00)	77 (0.44)	0.39
12-02	Gp3	g.chr21:39961676G>A	Intron	ERG		v-ets avian erythroblast	81 (0.00)	52 (0.56)	0.49
12-02	Gp3	g.chr12:56536626G>A	Missense Mutation	ESYT1	p.E976K	extended synaptotagmin	33 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr7:158528218G>C	Silent	ESYT2	p.S854S	extended synaptotagmin	20 (0.00)	48 (0.27)	0.72
12-02	Gp3	g.chr3:185783746G>C	Missense Mutation	ETV5	p.P256A	ets variant 5	18 (0.00)	13 (0.62)	1.64
12-02	Gp3	g.chr2:72958316G>T	Missense Mutation	EXOC6B	p.A129D	exocyst complex compo	62 (0.00)	28 (0.21)	0.57
12-02	Gp3	g.chr8:72127948G>T	Missense Mutation	EYA1	p.A459D	EYA transcriptional coa	40 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr11:61570870C>T	Missense Mutation	FADS1	p.D405N	fatty acid desaturase 1	88 (0.00)	50 (0.18)	0.48
12-02	Gp3	g.chr1:50956312G>T	Missense Mutation	FAF1	p.A534E	Fas (TNFRSF6) associa	55 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr4:38907156G>A	Silent	FAM114A1	p.T150T	family with sequence si	35 (0.00)	22 (0.45)	1.21
12-02	Gp3	g.chr17:40734785C>T	Missense Mutation	FAM134C	p.D284N	family with sequence si	23 (0.00)	43 (0.30)	1.08
12-02	Gp3	g.chr5:177468764G>T	Splice Site	FAM153C	p.M97I	family with sequence si	99 (0.01)	53 (0.17)	0.45
12-02	Gp3	g.chr4:152499103C>T	Missense Mutation	FAM160A1	p.P203S	family with sequence si	41 (0.00)	32 (0.22)	0.58
12-02	Gp3	g.chr14:45475279C>G	Missense Mutation	FAM179B	p.R905G	family with sequence si	66 (0.00)	15 (0.53)	1.42
12-02	Gp3	g.chr10:5789182T>C	Silent	FAM208B	p.S1266S	family with sequence si	19 (0.00)	14 (0.43)	1.14
12-02	Gp3	g.chr10:46245581A>G	Missense Mutation	FAM21C	p.D257G	family with sequence si	49 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr6:116875168G>C	Missense Mutation	FAM26D	p.R71T	family with sequence si	76 (0.00)	33 (0.36)	0.97
12-02	Gp3	g.chr1:809826C>A	lincRNA	FAM41C		family with sequence si	15 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr6:24850926G>A	Missense Mutation	FAM65B	p.R233W	family with sequence si	89 (0.00)	80 (0.19)	0.50
12-02	Gp3	g.chr6:24873108C>G	Splice Site	FAM65B		family with sequence si	26 (0.00)	20 (0.40)	1.07
12-02	Gp3	g.chr15:89828379G>T	Missense Mutation	FANCI	p.C584F	Fanconi anemia, compl	43 (0.00)	39 (0.21)	0.55
12-02	Gp3	g.chr15:89843558G>A	Missense Mutation	FANCI	p.R944K	Fanconi anemia, compl	62 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr2:207636648T>A	Missense Mutation	FASTKD2	p.S341T	FAST kinase domains 2	51 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr2:207636679T>A	Missense Mutation	FASTKD2	p.V351E	FAST kinase domains 2	55 (0.02)	58 (0.31)	0.83
12-02	Gp3	g.chr20:3128413C>A	Missense Mutation	FASTKD5	p.W435L	FAST kinase domains 5	55 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr4:187629074T>C	Silent	FAT1	p.A636A	FAT atypical cadherin 1	81 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr11:92086159C>T	Missense Mutation	FAT3	p.A144V	FAT atypical cadherin 3	71 (0.00)	47 (0.23)	0.62

12-02	Gp3	g.chr11:92088454G>T	Missense Mutation	FAT3	p.G909V	FAT atypical cadherin 3	87 (0.00)	41 (0.17)	0.46
12-02	Gp3	g.chr9:37516023G>T	Silent	FBXO10	p.A858A	F-box protein 10	24 (0.00)	41 (0.15)	0.39
12-02	Gp3	g.chr6:146125839C>A	Missense Mutation	FBXO30	p.R568I	F-box protein 30	55 (0.00)	31 (0.16)	0.43
12-02	Gp3	g.chr6:146127424C>T	Missense Mutation	FBXO30	p.V40I	F-box protein 30	47 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr6:52943664G>A	Silent	FBXO9	p.R125R	F-box protein 9	30 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr9:123526906C>T	Silent	FBXW2	p.T432T	F-box and WD repeat d	19 (0.00)	47 (0.43)	1.13
12-02	Gp3	g.chr11:72598541C>A	Missense Mutation	FCHSD2	p.A238S	FCH and double SH3 d	76 (0.00)	58 (0.19)	0.66
12-02	Gp3	g.chr4:71099779C>T	Missense Mutation	FDCSP	p.P45S	follicular dendritic cell	123 (0.00)	66 (0.32)	0.85
12-02	Gp3	g.chr1:60106969G>T	Silent	FGGY	p.L413L	FGGY carbohydrate kin	50 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr11:27016670C>A	Silent	FIBIN	p.T199T	fin bud initiation factor	28 (0.00)	60 (0.18)	0.49
12-02	Gp3	g.chr3:99643091T>C	Silent	FILIP1L	p.L196L	filamin A interacting pr	120 (0.01)	56 (0.21)	0.57
12-02	Gp3	g.chr1:154960931C>A	Missense Mutation	FLAD1	p.F144L	flavin adenine dinucleot	16 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr1:152278858C>G	Missense Mutation	FLG	p.R2835T	filaggrin	58 (0.00)	41 (0.15)	0.51
12-02	Gp3	g.chr1:152281880G>C	Missense Mutation	FLG	p.H1828D	filaggrin	45 (0.00)	58 (0.12)	0.42
12-02	Gp3	g.chr1:152284273C>A	Missense Mutation	FLG	p.G1030V	filaggrin	42 (0.00)	52 (0.15)	0.53
12-02	Gp3	g.chr1:152285412C>T	Silent	FLG	p.Q650Q	filaggrin	41 (0.00)	52 (0.19)	0.67
12-02	Gp3	g.chr1:152329369C>G	Missense Mutation	FLG2	p.C298S	filaggrin family membe	57 (0.00)	67 (0.24)	0.83
12-02	Gp3	g.chr13:28897033C>A	Silent	FLT1	p.L949L	fms-related tyrosine kin	60 (0.00)	63 (0.24)	0.63
12-02	Gp3	g.chr9:132720771G>A	Splice Site	FNBP1	p.S136F	formin binding protein 1	38 (0.03)	51 (0.41)	1.38
12-02	Gp3	g.chr12:2981323C>G	Missense Mutation	FOXM1	p.R198P	forkhead box M1	52 (0.02)	38 (0.21)	0.39
12-02	Gp3	g.chr4:79350252C>T	Missense Mutation	FRAS1	p.S1572L	Fraser extracellular mat	38 (0.00)	24 (0.29)	0.78
12-02	Gp3	g.chr4:144618097C>A	Missense Mutation	FREM3	p.Q1244H	FRAS1 related extracell	29 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr7:127239473T>A	Missense Mutation	FSCN3	p.S387T	fascin actin-bundling pr	19 (0.00)	29 (0.28)	0.74
12-02	Gp3	g.chr2:186657964C>A	Missense Mutation	FSIP2	p.S2034Y	fibrous sheath interactin	79 (0.00)	44 (0.23)	0.42
12-02	Gp3	g.chr19:49469861C>A	Missense Mutation	FTL	p.H133N	ferritin, light polypeptid	18 (0.00)	25 (0.20)	0.76
12-02	Gp3	g.chr5:161324315G>A	Missense Mutation	GABRA1	p.D420N	gamma-aminobutyric ac	65 (0.00)	39 (0.36)	0.96
12-02	Gp3	g.chr9:101606471C>T	Missense Mutation	GALNT12	p.H480Y	polypeptide N-acetylgal	23 (0.00)	35 (0.23)	0.61
12-02	Gp3	g.chr9:130155488C>A	Missense Mutation	GARNL3	p.F999L	GTPase activating Rap/	28 (0.00)	35 (0.14)	0.48
12-02	Gp3	g.chr21:34883690G>A	Missense Mutation	GART	p.A728V	phosphoribosylglycinam	109 (0.00)	97 (0.23)	0.60
12-02	Gp3	g.chr11:22759284G>T	Missense Mutation	GAS2	p.C148F	growth arrest-specific 2	54 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr1:155207363C>A	Silent	GBA	p.L256L	glucosidase, beta, acid	36 (0.00)	49 (0.18)	0.49
12-02	Gp3	g.chr1:89524685G>A	Missense Mutation	GBP1	p.S157L	guanylate binding prote	102 (0.00)	61 (0.16)	0.44
12-02	Gp3	g.chr6:10874852A>G	Silent	GCM2	p.P299P	glial cells missing homo	98 (0.00)	59 (0.36)	0.95
12-02	Gp3	g.chr17:57326130T>A	Missense Mutation	GDPD1	p.D117E	glycerophosphodiester p	55 (0.00)	29 (0.31)	1.03
12-02	Gp3	g.chr2:17962283C>T	Nonsense Mutation	GEN1	p.Q602*	GEN1 Holliday junctio	21 (0.00)	20 (0.30)	0.80

12-02	Gp3	g.chr3:158370014C>A	Silent	GFM1	p.I273I	G elongation factor, mit	25 (0.00)	27 (0.19)	0.49
12-02	Gp3	g.chr8:63930103G>C	Missense Mutation	GGH	p.P262A	gamma-glutamyl hydrol	70 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr2:233671277G>A	Silent	GIGYF2	p.A566A	GRB10 interacting GYF	48 (0.00)	44 (0.27)	0.73
12-02	Gp3	g.chr7:150171491C>A	Nonsense Mutation	GIMAP8	p.Y358*	GTPase, IMAP family n	62 (0.00)	37 (0.24)	0.65
12-02	Gp3	g.chr7:99526489T>A	Missense Mutation	GJC3	p.E252V	gap junction protein, ga	23 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr15:69548542G>T	Missense Mutation	GLCE	p.V69F	glucuronic acid epimera	73 (0.00)	22 (0.36)	0.97
12-02	Gp3	g.chr16:74525108G>T	Missense Mutation	GLG1	p.Q403K	golgi glycoprotein 1	66 (0.00)	10 (0.50)	0.79
12-02	Gp3	g.chr6:39053733C>A	Missense Mutation	GLP1R	p.H426N	glucagon-like peptide 1	19 (0.00)	84 (0.21)	0.57
12-02	Gp3	g.chr9:138516483G>T	Missense Mutation	GLT6D1	p.H97Q	glycosyltransferase 6 do	15 (0.00)	37 (0.16)	0.43
12-02	Gp3	g.chr1:231396412G>A	Missense Mutation	GNPAT	p.E141K	glyceronephosphate O-a	18 (0.00)	25 (0.48)	1.28
12-02	Gp3	g.chr9:127650591G>T	Missense Mutation	GOLGA1	p.L616I	golgin A1	26 (0.00)	67 (0.19)	0.52
12-02	Gp3	g.chr15:23610236T>A	Nonsense Mutation	GOLGA8S	p.C611*	golgin A8 family, memb	29 (0.00)	243 (0.20)	0.69
12-02	Gp3	g.chr6:24456783T>A	Missense Mutation	GPLD1	p.H364L	glycosylphosphatidylinc	63 (0.00)	39 (0.15)	0.41
12-02	Gp3	g.chrX:129519013C>T	Missense Mutation	GPR119	p.G137S	G protein-coupled recep	23 (0.00)	15 (0.40)	0.67
12-02	Gp3	g.chr4:22390430G>T	Missense Mutation	GPR125	p.P955H	G protein-coupled recep	87 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr5:90073777C>A	Missense Mutation	GPR98	p.P4195T	G protein-coupled recep	69 (0.00)	26 (0.23)	0.62
12-02	Gp3	g.chr4:90170285G>A	Missense Mutation	GPRIN3	p.A326V	GPRIN family member	32 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr1:109461321G>T	Silent	GPSM2	p.L450L	G-protein signaling moc	45 (0.00)	36 (0.33)	0.89
12-02	Gp3	g.chr11:105483024C>T	Missense Mutation	GRIA4	p.T37I	glutamate receptor, iono	81 (0.00)	34 (0.15)	0.39
12-02	Gp3	g.chr16:9934877C>A	Silent	GRIN2A	p.V471V	glutamate receptor, iono	46 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr10:121207737G>T	Nonsense Mutation	GRK5	p.E457*	G protein-coupled recep	19 (0.00)	128 (0.21)	0.56
12-02	Gp3	g.chr10:121207763C>T	Silent	GRK5	p.F465F	G protein-coupled recep	21 (0.00)	126 (0.20)	0.53
12-02	Gp3	g.chr4:71691024C>A	Missense Mutation	GRSF1	p.R299L	G-rich RNA sequence b	105 (0.01)	168 (0.20)	0.54
12-02	Gp3	g.chr7:76982948C>G	Missense Mutation	GSAP	p.W450S	gamma-secretase activat	110 (0.00)	17 (0.53)	1.41
12-02	Gp3	g.chr7:74114711C>T	Silent	GTF2I	p.L170L	general transcription fac	101 (0.00)	119 (0.32)	0.85
12-02	Gp3	g.chr7:74148271G>A	Silent	GTF2I	p.E437E	general transcription fac	22 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr7:72657836C>G	RNA	GTF2IRD2P1		GTF2I repeat domain cc	20 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr16:27512521G>T	Silent	GTF3C1	p.I684I	general transcription fac	38 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr13:51599601G>T	RNA	GUCY1B2		guanylate cyclase 1, solu	19 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr4:156723633T>A	Missense Mutation	GUCY1B3	p.S414T	guanylate cyclase 1, solu	76 (0.00)	42 (0.64)	1.71
12-02	Gp3	g.chr6:135360761C>T	Missense Mutation	HBS1L	p.S127N	HBS1-like translational	102 (0.00)	103 (0.24)	0.65
12-02	Gp3	g.chr3:121366177G>A	Nonsense Mutation	HCLS1	p.R93*	hematopoietic cell-speci	22 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr1:155253884G>T	Missense Mutation	HCN3	p.Q276H	hyperpolarization activa	16 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr7:18631668G>A	Intron	HDAC9		histone deacetylase 9	101 (0.00)	53 (0.45)	1.21
12-02	Gp3	g.chr7:18641180C>T	Intron	HDAC9		histone deacetylase 9	83 (0.00)	35 (0.17)	0.46

12-02	Gp3	g.chr7:18659336C>A	Intron	HDAC9		histone deacetylase 9	31 (0.00)	26 (0.77)	2.05
12-02	Gp3	g.chr7:18661878G>T	Intron	HDAC9		histone deacetylase 9	28 (0.00)	37 (0.22)	0.58
12-02	Gp3	g.chr7:18668145G>A	Intron	HDAC9		histone deacetylase 9	18 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr7:18702390G>A	Intron	HDAC9		histone deacetylase 9	59 (0.00)	43 (0.28)	0.74
12-02	Gp3	g.chr7:18743839A>G	Intron	HDAC9		histone deacetylase 9	48 (0.00)	27 (0.52)	1.38
12-02	Gp3	g.chr7:18761272G>A	Intron	HDAC9		histone deacetylase 9	104 (0.00)	43 (0.44)	1.18
12-02	Gp3	g.chr7:18785009C>G	Intron	HDAC9		histone deacetylase 9	35 (0.00)	76 (0.17)	0.46
12-02	Gp3	g.chr7:18796440C>A	Intron	HDAC9		histone deacetylase 9	99 (0.00)	33 (0.36)	0.97
12-02	Gp3	g.chr7:18800288C>A	Intron	HDAC9		histone deacetylase 9	68 (0.00)	15 (0.47)	1.24
12-02	Gp3	g.chr7:18806910T>C	Intron	HDAC9		histone deacetylase 9	25 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr7:18822104T>C	Intron	HDAC9		histone deacetylase 9	63 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr7:18826164C>T	Intron	HDAC9		histone deacetylase 9	67 (0.00)	28 (0.39)	1.05
12-02	Gp3	g.chr7:18829835A>C	Intron	HDAC9		histone deacetylase 9	191 (0.00)	76 (0.43)	1.16
12-02	Gp3	g.chr7:18835989C>A	Intron	HDAC9		histone deacetylase 9	163 (0.01)	39 (0.21)	0.55
12-02	Gp3	g.chr7:18854251C>A	Intron	HDAC9		histone deacetylase 9	72 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr7:18877874T>G	Intron	HDAC9		histone deacetylase 9	57 (0.00)	30 (0.20)	0.53
12-02	Gp3	g.chr7:18912078T>C	Intron	HDAC9		histone deacetylase 9	134 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr7:18918493T>C	Intron	HDAC9		histone deacetylase 9	20 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr7:18935085G>T	Intron	HDAC9		histone deacetylase 9	55 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr7:18945420C>T	Intron	HDAC9		histone deacetylase 9	21 (0.00)	40 (0.20)	0.53
12-02	Gp3	g.chr7:18980816C>A	Intron	HDAC9		histone deacetylase 9	87 (0.01)	32 (0.25)	0.67
12-02	Gp3	g.chr7:19001488C>G	Intron	HDAC9		histone deacetylase 9	117 (0.00)	52 (0.19)	0.51
12-02	Gp3	g.chr1:156714066C>T	Silent	HDGF	p.K126K	hepatoma-derived growt	25 (0.00)	164 (0.15)	0.41
12-02	Gp3	g.chr2:242186232T>C	Missense Mutation	HDLBP	p.I629V	high density lipoprotein	33 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr2:242186244C>A	Nonsense Mutation	HDLBP	p.E625*	high density lipoprotein	44 (0.00)	38 (0.24)	0.63
12-02	Gp3	g.chr2:242194556G>C	Silent	HDLBP	p.V366V	high density lipoprotein	197 (0.00)	154 (0.15)	0.40
12-02	Gp3	g.chr16:50109596C>G	Missense Mutation	HEATR3	p.S246C	HEAT repeat containing	33 (0.00)	18 (0.50)	0.65
12-02	Gp3	g.chr14:73976125A>G	Silent	HEATR4	p.A537A	HEAT repeat containing	66 (0.00)	109 (0.21)	0.56
12-02	Gp3	g.chr2:37265078C>A	Missense Mutation	HEATR5B	p.A1046S	HEAT repeat containing	45 (0.00)	48 (0.15)	0.39
12-02	Gp3	g.chr2:37302644C>T	Missense Mutation	HEATR5B	p.R194Q	HEAT repeat containing	40 (0.00)	39 (0.18)	0.48
12-02	Gp3	g.chr14:31598357C>T	Missense Mutation	HECTD1	p.R1407K	HECT domain containin	65 (0.00)	62 (0.15)	0.39
12-02	Gp3	g.chr17:65103787A>T	Missense Mutation	HELZ	p.I1580N	helicase with zinc finger	43 (0.00)	27 (0.41)	1.09
12-02	Gp3	g.chr15:28375413G>T	Nonsense Mutation	HERC2	p.S4233*	HECT and RLD domain	17 (0.00)	40 (0.15)	0.52
12-02	Gp3	g.chr15:28483316G>T	Missense Mutation	HERC2	p.Q1266K	HECT and RLD domain	185 (0.00)	93 (0.23)	0.78
12-02	Gp3	g.chr15:20663005A>G	RNA	HERC2P3		hect domain and RLD 2	52 (0.00)	39 (0.18)	0.48

12-02	Gp3	g.chr8:43002176C>G	Silent	HGSNAT	p.T68T	heparan-alpha-glucosam	154 (0.00)	39 (0.23)	0.62
12-02	Gp3	g.chr11:33308434G>A	Missense Mutation	HIPK3	p.M158I	homeodomain interactin	51 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr6:26234986G>A	Missense Mutation	HIST1H1D	p.S59F	histone cluster 1, H1d	29 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr6:26235014C>T	Missense Mutation	HIST1H1D	p.A50T	histone cluster 1, H1d	28 (0.00)	35 (0.26)	0.69
12-02	Gp3	g.chr6:143092886T>C	Missense Mutation	HIVEP2	p.Q997R	human immunodeficien	23 (0.00)	45 (0.18)	0.47
12-02	Gp3	g.chr5:176317669G>T	Silent	HK3	p.V199V	hexokinase 3 (white cell	44 (0.00)	76 (0.20)	0.53
12-02	Gp3	g.chr5:149410360C>G	Silent	HMGXB3	p.P597P	HMG box domain conta	54 (0.00)	37 (0.16)	0.43
12-02	Gp3	g.chr5:179045005C>A	Missense Mutation	HNRNPH1	p.D258Y	heterogeneous nuclear r	111 (0.00)	49 (0.16)	0.44
12-02	Gp3	g.chr9:86586607C>G	Missense Mutation	HNRNPK	p.G330R	heterogeneous nuclear r	195 (0.00)	48 (0.15)	0.39
12-02	Gp3	g.chr1:245009916C>A	RNA	HNRNPU-AS1		HNRNPU antisense RN	29 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr19:41807520C>A	Missense Mutation	HNRNPUL1	p.P533H	heterogeneous nuclear r	56 (0.00)	66 (0.14)	0.48
12-02	Gp3	g.chr8:42841907C>G	Missense Mutation	HOOK3	p.L501V	hook microtubule-tether	56 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr10:100904139C>A	Missense Mutation	HPSE2	p.V156F	heparanase 2 (inactive)	81 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr11:63327587C>G	Missense Mutation	HRASLS2	p.D30H	HRAS-like suppressor 2	23 (0.00)	42 (0.17)	0.44
12-02	Gp3	g.chr7:136516907G>A	RNA	hsa-mir-490			16 (0.00)	15 (0.60)	1.60
12-02	Gp3	g.chr14:102552133G>A	Missense Mutation	HSP90AA1	p.S164F	heat shock protein 90kD	24 (0.00)	45 (0.20)	0.53
12-02	Gp3	g.chr6:44219765G>C	Missense Mutation	HSP90AB1	p.A498P	heat shock protein 90kD	55 (0.00)	42 (0.14)	0.38
12-02	Gp3	g.chr11:113856770C>A	Missense Mutation	HTR3A	p.P193Q	5-hydroxytryptamine (s	92 (0.00)	65 (0.23)	0.62
12-02	Gp3	g.chr4:3180151T>A	Missense Mutation	HTT	p.S1530R	huntingtin	68 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr4:3180152G>A	Missense Mutation	HTT	p.G1531R	huntingtin	68 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr10:91162675G>A	Missense Mutation	IFIT1	p.D215N	interferon-induced prote	132 (0.00)	113 (0.55)	1.46
12-02	Gp3	g.chr10:91143487A>G	Silent	IFIT1B	p.P139P	interferon-induced prote	42 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr10:91144375G>A	Silent	IFIT1B	p.R435R	interferon-induced prote	34 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr2:27684239G>C	Missense Mutation	IFT172	p.A780G	intraflagellar transport 1	20 (0.00)	20 (0.35)	0.93
12-02	Gp3	g.chr6:160517540C>G	Missense Mutation	IGF2R	p.S2242C	insulin-like growth fact	110 (0.00)	56 (0.21)	0.57
12-02	Gp3	g.chr15:20169940G>A	RNA	IGHV1OR15-9		immunoglobulin heavy	50 (0.00)	18 (0.61)	1.63
12-02	Gp3	g.chr21:10862961G>T	RNA	IGHV1OR21-1		immunoglobulin heavy	31 (0.00)	64 (0.28)	0.75
12-02	Gp3	g.chr16:33629752G>A	RNA	IGHV3OR16-13		immunoglobulin heavy	82 (0.00)	68 (0.13)	0.46
12-02	Gp3	g.chr2:89442617A>T	RNA	IGKV3-20		immunoglobulin kappa	35 (0.00)	44 (0.18)	0.48
12-02	Gp3	g.chr2:90211931G>T	RNA	IGKV3D-11		immunoglobulin kappa	32 (0.00)	31 (0.16)	0.43
12-02	Gp3	g.chr2:90077921C>A	RNA	IGKV3D-20		immunoglobulin kappa	57 (0.00)	40 (0.40)	1.07
12-02	Gp3	g.chr3:151171507C>T	Missense Mutation	IGSF10	p.G127D	immunoglobulin superf	40 (0.00)	41 (0.22)	0.59
12-02	Gp3	g.chr5:140038682G>T	Missense Mutation	IK	p.R370L	IK cytokine, down-regu	38 (0.00)	37 (0.16)	0.43
12-02	Gp3	g.chr12:99020266C>T	Silent	IKBIP	p.E192E	IKBKB interacting prot	22 (0.00)	14 (0.71)	1.13
12-02	Gp3	g.chr12:99020316C>T	Missense Mutation	IKBIP	p.E176K	IKBKB interacting prot	35 (0.00)	26 (0.65)	1.04

12-02	Gp3	g.chr8:42183529G>T	Missense Mutation	IKBKB	p.M676I	inhibitor of kappa light	36 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr7:50455105G>A	Missense Mutation	IKZF1	p.E218K	IKAROS family zinc fir	28 (0.00)	39 (0.44)	1.16
12-02	Gp3	g.chr10:124754007C>T	Silent	IKZF5	p.Q183Q	IKAROS family zinc fir	53 (0.00)	47 (0.17)	0.45
12-02	Gp3	g.chr3:53899134C>A	Missense Mutation	IL17RB	p.S436R	interleukin 17 receptor	28 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr2:102849562C>A	Silent	IL1RL2	p.G425G	interleukin 1 receptor-li	18 (0.00)	26 (0.62)	1.64
12-02	Gp3	g.chr7:22769184C>A	Missense Mutation	IL6	p.L126I	interleukin 6	47 (0.00)	30 (0.30)	0.80
12-02	Gp3	g.chr3:101038608C>T	Missense Mutation	IMPG2	p.E52K	interphotoreceptor matri	60 (0.00)	27 (0.33)	0.89
12-02	Gp3	g.chr2:242650841C>T	Missense Mutation	ING5	p.A109V	inhibitor of growth fami	36 (0.00)	25 (0.24)	0.64
12-02	Gp3	g.chr2:206911279G>A	Missense Mutation	INO80D	p.P341L	INO80 complex subunit	28 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr4:142955280G>A	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	51 (0.25)	0.68
12-02	Gp3	g.chr4:142977728G>C	Intron	INPP4B		inositol polyphosphate-	99 (0.00)	52 (0.19)	0.51
12-02	Gp3	g.chr4:142986525A>G	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	67 (0.18)	0.48
12-02	Gp3	g.chr4:143010160C>G	Intron	INPP4B		inositol polyphosphate-	52 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr4:143069039C>T	Intron	INPP4B		inositol polyphosphate-	233 (0.00)	99 (0.16)	0.43
12-02	Gp3	g.chr4:143072551C>T	Intron	INPP4B		inositol polyphosphate-	67 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr4:143073189C>A	Intron	INPP4B		inositol polyphosphate-	38 (0.00)	30 (0.23)	0.62
12-02	Gp3	g.chr4:143086198C>G	Intron	INPP4B		inositol polyphosphate-	36 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr4:143118521C>A	Intron	INPP4B		inositol polyphosphate-	56 (0.00)	32 (0.16)	0.42
12-02	Gp3	g.chr4:143124042G>A	Intron	INPP4B		inositol polyphosphate-	67 (0.00)	28 (0.36)	0.95
12-02	Gp3	g.chr4:143134312G>T	Intron	INPP4B		inositol polyphosphate-	105 (0.00)	77 (0.14)	0.38
12-02	Gp3	g.chr4:143136507T>A	Intron	INPP4B		inositol polyphosphate-	55 (0.00)	13 (0.62)	1.64
12-02	Gp3	g.chr4:143147505C>A	Intron	INPP4B		inositol polyphosphate-	81 (0.00)	44 (0.36)	0.97
12-02	Gp3	g.chr4:143150913T>A	Intron	INPP4B		inositol polyphosphate-	84 (0.00)	29 (0.28)	0.74
12-02	Gp3	g.chr4:143174336C>T	Intron	INPP4B		inositol polyphosphate-	17 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr4:143181650T>C	Missense Mutation	INPP4B	p.N228S	inositol polyphosphate-	41 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr4:143188696T>A	Intron	INPP4B		inositol polyphosphate-	81 (0.00)	26 (0.58)	1.54
12-02	Gp3	g.chr4:143202378G>A	Intron	INPP4B		inositol polyphosphate-	18 (0.00)	39 (0.69)	1.85
12-02	Gp3	g.chr4:143206475C>A	Intron	INPP4B		inositol polyphosphate-	33 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr4:143230129C>A	Intron	INPP4B		inositol polyphosphate-	37 (0.00)	13 (0.46)	1.23
12-02	Gp3	g.chr4:143243930G>T	Intron	INPP4B		inositol polyphosphate-	36 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr4:143244144A>T	Intron	INPP4B		inositol polyphosphate-	52 (0.00)	40 (0.23)	0.60
12-02	Gp3	g.chr4:143252462C>A	Intron	INPP4B		inositol polyphosphate-	58 (0.00)	67 (0.15)	0.40
12-02	Gp3	g.chr4:143282307C>A	Intron	INPP4B		inositol polyphosphate-	245 (0.00)	57 (0.21)	0.56
12-02	Gp3	g.chr4:143322192C>T	Intron	INPP4B		inositol polyphosphate-	64 (0.00)	20 (0.50)	1.33
12-02	Gp3	g.chr4:143335952G>A	Intron	INPP4B		inositol polyphosphate-	64 (0.00)	26 (0.31)	0.82

12-02	Gp3	g.chr4:143344784G>C	Intron	INPP4B		inositol polyphosphate-4	92 (0.00)	41 (0.29)	0.78
12-02	Gp3	g.chr4:143415148C>A	Intron	INPP4B		inositol polyphosphate-4	91 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr4:143438863A>T	Intron	INPP4B		inositol polyphosphate-4	83 (0.01)	34 (0.18)	0.47
12-02	Gp3	g.chr4:143492397C>A	Intron	INPP4B		inositol polyphosphate-4	81 (0.00)	26 (0.38)	1.03
12-02	Gp3	g.chr4:143506954A>T	Intron	INPP4B		inositol polyphosphate-4	33 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr4:143552050C>T	Intron	INPP4B		inositol polyphosphate-4	46 (0.00)	18 (0.56)	1.48
12-02	Gp3	g.chr4:143585215T>A	Intron	INPP4B		inositol polyphosphate-4	26 (0.00)	33 (0.24)	0.65
12-02	Gp3	g.chr4:143594867C>G	Intron	INPP4B		inositol polyphosphate-4	143 (0.00)	44 (0.25)	0.67
12-02	Gp3	g.chr4:143601919T>C	Intron	INPP4B		inositol polyphosphate-4	149 (0.00)	13 (0.38)	1.03
12-02	Gp3	g.chr4:143618450A>G	Intron	INPP4B		inositol polyphosphate-4	107 (0.00)	77 (0.14)	0.38
12-02	Gp3	g.chr4:143627491T>G	Intron	INPP4B		inositol polyphosphate-4	57 (0.00)	24 (0.29)	0.78
12-02	Gp3	g.chr4:143635671G>T	Intron	INPP4B		inositol polyphosphate-4	108 (0.00)	34 (0.62)	1.65
12-02	Gp3	g.chr4:143656117G>A	Intron	INPP4B		inositol polyphosphate-4	31 (0.00)	18 (0.39)	1.04
12-02	Gp3	g.chr4:143662946G>A	Intron	INPP4B		inositol polyphosphate-4	54 (0.00)	58 (0.22)	0.60
12-02	Gp3	g.chr4:143662978G>A	Intron	INPP4B		inositol polyphosphate-4	79 (0.00)	52 (0.21)	0.56
12-02	Gp3	g.chr4:143664319G>C	Intron	INPP4B		inositol polyphosphate-4	59 (0.00)	30 (0.30)	0.80
12-02	Gp3	g.chr4:143693345C>G	Intron	INPP4B		inositol polyphosphate-4	39 (0.00)	23 (0.26)	0.70
12-02	Gp3	g.chr4:143702365C>A	Intron	INPP4B		inositol polyphosphate-4	28 (0.00)	95 (0.60)	1.60
12-02	Gp3	g.chr4:143757307C>T	Intron	INPP4B		inositol polyphosphate-4	32 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr4:143762563C>T	Intron	INPP4B		inositol polyphosphate-4	84 (0.00)	42 (0.31)	0.83
12-02	Gp3	g.chr4:143765828C>T	Intron	INPP4B		inositol polyphosphate-4	114 (0.00)	60 (0.43)	1.16
12-02	Gp3	g.chr10:134463943G>A	Silent	INPP5A	p.A80A	inositol polyphosphate-5	17 (0.00)	38 (0.34)	0.91
12-02	Gp3	g.chr9:103035223C>T	Missense Mutation	INVS	p.S550F	inversin	72 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr11:9450613G>A	Silent	IPO7	p.K487K	importin 7	25 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr15:67713895C>A	Missense Mutation	IQCH	p.P829T	IQ motif containing H	30 (0.00)	37 (0.27)	0.72
12-02	Gp3	g.chr5:131822533C>A	Missense Mutation	IRF1	p.R123I	interferon regulatory fac	15 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr16:31284817G>A	Missense Mutation	ITGAM	p.G279E	integrin, alpha M (comp	54 (0.00)	57 (0.18)	0.61
12-02	Gp3	g.chr3:4821260C>T	Silent	ITPR1	p.A2091A	inositol 1,4,5-trisphosph	33 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr3:124390715C>T	Silent	KALRN	p.H606H	kalirin, RhoGEF kinase	42 (0.00)	45 (0.24)	0.65
12-02	Gp3	g.chr10:76790380C>A	Nonsense Mutation	KAT6B	p.S1933*	K(lysine) acetyltransfera	33 (0.00)	40 (0.23)	0.60
12-02	Gp3	g.chr12:5021491G>T	Missense Mutation	KCNA1	p.G316V	potassium voltage-gated	23 (0.00)	39 (0.23)	0.43
12-02	Gp3	g.chr3:156249257C>G	Missense Mutation	KCNAB1	p.Q363E	potassium voltage-gated	125 (0.00)	77 (0.18)	0.48
12-02	Gp3	g.chr1:23406133C>A	Missense Mutation	KDM1A	p.L715I	lysine (K)-specific deme	21 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr17:26943699C>G	Missense Mutation	KIAA0100	p.G2032R	KIAA0100	64 (0.00)	27 (0.19)	0.49
12-02	Gp3	g.chr8:126061330C>A	Missense Mutation	KIAA0196	p.G766V	KIAA0196	42 (0.00)	30 (0.20)	0.53

12-02	Gp3	g.chr14:70175797C>G	Missense Mutation	KIAA0247	p.L288V	KIAA0247	38 (0.00)	49 (0.18)	0.49
12-02	Gp3	g.chr6:24596620G>T	Silent	KIAA0319	p.G94G	KIAA0319	16 (0.00)	26 (0.23)	0.62
12-02	Gp3	g.chr16:27720099G>T	Missense Mutation	KIAA0556	p.G488V	KIAA0556	30 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr5:93489804G>T	Missense Mutation	KIAA0825	p.L1246I	KIAA0825	16 (0.00)	25 (0.24)	0.64
12-02	Gp3	g.chr7:36366393G>T	Missense Mutation	KIAA0895	p.D410E	KIAA0895	87 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr7:36366525A>T	Silent	KIAA0895	p.V366V	KIAA0895	73 (0.00)	31 (0.39)	1.03
12-02	Gp3	g.chrX:118221298G>C	Missense Mutation	KIAA1210	p.Q1299E	KIAA1210	103 (0.00)	42 (0.52)	0.87
12-02	Gp3	g.chr12:32137835C>A	Missense Mutation	KIAA1551	p.Q1316K	KIAA1551	39 (0.00)	19 (0.58)	1.54
12-02	Gp3	g.chr2:61324885G>T	Silent	KIAA1841	p.V421V	KIAA1841	33 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr9:115381001G>C	Missense Mutation	KIAA1958	p.K674N	KIAA1958	21 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr6:17837186C>A	Nonsense Mutation	KIF13A	p.E360*	kinesin family member	66 (0.00)	53 (0.15)	0.40
12-02	Gp3	g.chr3:44856518C>A	Missense Mutation	KIF15	p.N833K	kinesin family member	45 (0.02)	36 (0.19)	0.52
12-02	Gp3	g.chr11:28058069G>T	Missense Mutation	KIF18A	p.S697R	kinesin family member	28 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr1:10425199G>A	Missense Mutation	KIF1B	p.A1470T	kinesin family member	26 (0.00)	17 (0.35)	0.94
12-02	Gp3	g.chr9:34255883G>C	Missense Mutation	KIF24	p.P1241R	kinesin family member	58 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr5:61659107G>T	Nonsense Mutation	KIF2A	p.E388*	kinesin heavy chain me	110 (0.00)	69 (0.16)	0.43
12-02	Gp3	g.chr5:154393709C>A	Nonsense Mutation	KIF4B	p.S97*	kinesin family member	46 (0.00)	76 (0.16)	0.42
12-02	Gp3	g.chr5:154393725C>G	Nonsense Mutation	KIF4B	p.Y102*	kinesin family member	56 (0.00)	71 (0.20)	0.53
12-02	Gp3	g.chr13:73636580G>T	Missense Mutation	KLF5	p.M281I	Kruppel-like factor 5 (i	59 (0.00)	12 (0.50)	1.33
12-02	Gp3	g.chr1:173702928C>A	Missense Mutation	KLHL20	p.P34T	kelch-like family memb	70 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr14:45398260G>A	Missense Mutation	KLHL28	p.R577C	kelch-like family memb	64 (0.00)	33 (0.27)	0.73
12-02	Gp3	g.chr14:45398264G>A	Silent	KLHL28	p.Y575Y	kelch-like family memb	64 (0.00)	34 (0.26)	0.71
12-02	Gp3	g.chr11:118343170G>T	Missense Mutation	KMT2A	p.E432D	lysine (K)-specific meth	26 (0.00)	12 (0.58)	1.56
12-02	Gp3	g.chr12:123042036G>C	Missense Mutation	KNTC1	p.E423Q	kinetochore associated 1	64 (0.00)	19 (0.32)	0.50
12-02	Gp3	g.chr17:39022897G>T	Missense Mutation	KRT12	p.P181Q	keratin 12	79 (0.00)	82 (0.24)	0.87
12-02	Gp3	g.chr17:39114901A>T	Silent	KRT39	p.S476S	keratin 39	88 (0.00)	74 (0.14)	0.48
12-02	Gp3	g.chr17:39137266T>C	Silent	KRT40	p.E275E	keratin 40	51 (0.00)	43 (0.12)	0.42
12-02	Gp3	g.chr17:39137297C>T	Missense Mutation	KRT40	p.C265Y	keratin 40	54 (0.00)	46 (0.20)	0.70
12-02	Gp3	g.chr17:39388852T>C	Silent	KRTAP9-3	p.C33C	keratin associated protei	22 (0.00)	49 (0.27)	0.95
12-02	Gp3	g.chr6:130415446G>T	Missense Mutation	L3MBTL3	p.G557V	l(3)mbt-like 3 (Drosoph	21 (0.00)	16 (0.50)	1.33
12-02	Gp3	g.chr18:21487836G>T	Missense Mutation	LAMA3	p.D2318Y	laminin, alpha 3	34 (0.00)	32 (0.41)	1.08
12-02	Gp3	g.chr7:107746371T>A	Missense Mutation	LAMB4	p.Y254F	laminin, beta 4	35 (0.00)	45 (0.36)	0.95
12-02	Gp3	g.chr1:183212360G>T	Missense Mutation	LAMC2	p.S1136I	laminin, gamma 2	51 (0.00)	25 (0.64)	1.71
12-02	Gp3	g.chr1:183212452C>T	Silent	LAMC2	p.L1167L	laminin, gamma 2	33 (0.00)	30 (0.80)	2.13
12-02	Gp3	g.chr1:236706082C>G	Missense Mutation	LGALS8	p.Q182E	lectin, galactoside-bindi	34 (0.00)	57 (0.26)	0.70

12-02	Gp3	g.chr2:48915070C>A	Silent	LHCGR	p.L622L	luteinizing hormone/ch	96 (0.00)	25 (0.24)	0.64
12-02	Gp3	g.chr11:60388643C>T	lincRNA	LINC00301		long intergenic non-prot	39 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr3:52097311G>A	Missense Mutation	LINC00696	p.A86V	long intergenic non-prot	52 (0.00)	57 (0.32)	0.84
12-02	Gp3	g.chr14:46701262C>A	lincRNA	LINC00871		long intergenic non-prot	18 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr10:131906519A>G	lincRNA	LINC00959		long intergenic non-prot	18 (0.00)	24 (0.50)	1.33
12-02	Gp3	g.chr6:2990689C>A	lincRNA	LINC01011		long intergenic non-prot	91 (0.00)	41 (0.27)	0.72
12-02	Gp3	g.chr1:145487402T>A	Missense Mutation	LIX1L	p.S131T	Lix1 homolog (chicken)	31 (0.00)	43 (0.16)	0.43
12-02	Gp3	g.chr1:145487403C>A	Missense Mutation	LIX1L	p.S131Y	Lix1 homolog (chicken)	31 (0.00)	42 (0.17)	0.44
12-02	Gp3	g.chr7:156556396C>A	Missense Mutation	LMBR1	p.D173Y	limb development mem	26 (0.00)	22 (0.27)	0.73
12-02	Gp3	g.chr13:28136712T>A	Missense Mutation	LNX2	p.K354N	ligand of numb-protein	35 (0.00)	13 (0.38)	1.03
12-02	Gp3	g.chr2:100915391A>G	Silent	LONRF2	p.T461T	LON peptidase N-termi	127 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr6:161015111G>A	Missense Mutation	LPA	p.H1170Y	lipoprotein, Lp(a)	43 (0.00)	16 (0.44)	1.17
12-02	Gp3	g.chr6:160906978C>T	RNA	LPAL2		lipoprotein, Lp(a)-like 2	66 (0.00)	31 (0.29)	0.77
12-02	Gp3	g.chr4:62758418A>T	Missense Mutation	LPHN3	p.S441C	latrophilin 3	63 (0.00)	130 (0.15)	0.39
12-02	Gp3	g.chr12:12274277G>A	Missense Mutation	LRP6	p.A1497V	low density lipoprotein	58 (0.00)	15 (0.40)	0.74
12-02	Gp3	g.chr17:30358430C>G	Missense Mutation	LRRC37B	p.S561R	leucine rich repeat cont	37 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr1:90178399C>T	Silent	LRRC8C	p.N90N	leucine rich repeat cont	23 (0.00)	21 (0.33)	0.89
12-02	Gp3	g.chr19:34706522G>A	Missense Mutation	LSM14A	p.R205K	LSM14A, SCD6 homol	19 (0.00)	47 (0.19)	0.51
12-02	Gp3	g.chr1:23419518T>C	Missense Mutation	LUZP1	p.N413D	leucine zipper protein 1	56 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr2:160714872C>T	Splice Site	LY75-CD302		LY75-CD302 readthrou	68 (0.00)	34 (0.32)	0.50
12-02	Gp3	g.chr8:74903745G>T	Missense Mutation	LY96	p.W23L	lymphocyte antigen 96	49 (0.00)	36 (0.28)	0.74
12-02	Gp3	g.chr8:74903746G>T	Missense Mutation	LY96	p.W23C	lymphocyte antigen 96	49 (0.00)	36 (0.28)	0.74
12-02	Gp3	g.chr1:39888456C>G	Missense Mutation	MACF1	p.Q5350E	microtubule-actin crossl	51 (0.00)	10 (0.80)	2.13
12-02	Gp3	g.chrX:140996422G>A	Missense Mutation	MAGEC1	p.E1078K	melanoma antigen famil	40 (0.00)	82 (0.45)	0.75
12-02	Gp3	g.chr7:77654110A>G	Intron	MAGI2		membrane associated g	40 (0.00)	55 (0.38)	1.02
12-02	Gp3	g.chr7:77654148T>C	Intron	MAGI2		membrane associated g	46 (0.00)	59 (0.49)	1.31
12-02	Gp3	g.chr7:77663725C>A	Intron	MAGI2		membrane associated g	51 (0.00)	42 (0.31)	0.83
12-02	Gp3	g.chr7:77667225C>A	Intron	MAGI2		membrane associated g	22 (0.00)	23 (0.61)	1.62
12-02	Gp3	g.chr7:77677204C>T	Intron	MAGI2		membrane associated g	41 (0.00)	44 (0.18)	0.48
12-02	Gp3	g.chr7:77686838G>T	Intron	MAGI2		membrane associated g	45 (0.00)	43 (0.21)	0.56
12-02	Gp3	g.chr7:77686861G>T	Intron	MAGI2		membrane associated g	48 (0.00)	53 (0.19)	0.50
12-02	Gp3	g.chr7:77694860G>T	Intron	MAGI2		membrane associated g	42 (0.00)	31 (0.26)	0.69
12-02	Gp3	g.chr7:77694878A>T	Intron	MAGI2		membrane associated g	60 (0.00)	42 (0.14)	0.38
12-02	Gp3	g.chr7:77754547G>A	Intron	MAGI2		membrane associated g	40 (0.00)	63 (0.84)	2.24
12-02	Gp3	g.chr7:77755126T>C	Missense Mutation	MAGI2	p.E1151G	membrane associated g	41 (0.00)	23 (0.30)	0.81

12-02	Gp3	g.chr7:77755597G>C	Intron	MAGI2	membrane associated gu	29 (0.00)	11 (0.64)	1.70
12-02	Gp3	g.chr7:77770970C>G	Intron	MAGI2	membrane associated gu	74 (0.01)	49 (0.18)	0.49
12-02	Gp3	g.chr7:77779861C>A	Intron	MAGI2	membrane associated gu	96 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr7:77782609C>G	Intron	MAGI2	membrane associated gu	89 (0.00)	19 (0.32)	0.84
12-02	Gp3	g.chr7:77799627C>A	Intron	MAGI2	membrane associated gu	68 (0.00)	34 (0.32)	0.86
12-02	Gp3	g.chr7:77818474C>T	Intron	MAGI2	membrane associated gu	42 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr7:77841678A>T	Intron	MAGI2	membrane associated gu	59 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr7:77855981C>T	Intron	MAGI2	membrane associated gu	120 (0.01)	95 (0.19)	0.51
12-02	Gp3	g.chr7:77892735C>A	Intron	MAGI2	membrane associated gu	80 (0.00)	42 (0.17)	0.44
12-02	Gp3	g.chr7:77914165G>T	Intron	MAGI2	membrane associated gu	155 (0.00)	56 (0.36)	0.95
12-02	Gp3	g.chr7:77916281G>A	Intron	MAGI2	membrane associated gu	139 (0.00)	82 (0.35)	0.94
12-02	Gp3	g.chr7:77934909C>A	Intron	MAGI2	membrane associated gu	76 (0.00)	46 (0.17)	0.46
12-02	Gp3	g.chr7:77955528T>C	Intron	MAGI2	membrane associated gu	100 (0.00)	70 (0.19)	0.50
12-02	Gp3	g.chr7:77965253C>G	Intron	MAGI2	membrane associated gu	68 (0.00)	35 (0.23)	0.61
12-02	Gp3	g.chr7:77983177C>G	Intron	MAGI2	membrane associated gu	41 (0.00)	16 (0.44)	1.17
12-02	Gp3	g.chr7:77990023C>A	Intron	MAGI2	membrane associated gu	50 (0.00)	31 (0.32)	0.86
12-02	Gp3	g.chr7:77996737G>A	Intron	MAGI2	membrane associated gu	129 (0.01)	44 (0.50)	1.33
12-02	Gp3	g.chr7:77998895C>T	Intron	MAGI2	membrane associated gu	17 (0.00)	32 (0.25)	0.67
12-02	Gp3	g.chr7:78002354G>T	Intron	MAGI2	membrane associated gu	88 (0.00)	43 (0.21)	0.56
12-02	Gp3	g.chr7:78019019C>A	Intron	MAGI2	membrane associated gu	149 (0.00)	44 (0.27)	0.73
12-02	Gp3	g.chr7:78019954G>T	Intron	MAGI2	membrane associated gu	84 (0.01)	24 (0.46)	1.22
12-02	Gp3	g.chr7:78020090C>A	Intron	MAGI2	membrane associated gu	64 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr7:78022544C>A	Intron	MAGI2	membrane associated gu	63 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr7:78023841G>A	Intron	MAGI2	membrane associated gu	37 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr7:78024045C>G	Intron	MAGI2	membrane associated gu	98 (0.00)	32 (0.34)	0.92
12-02	Gp3	g.chr7:78025817T>C	Intron	MAGI2	membrane associated gu	115 (0.00)	20 (0.45)	1.20
12-02	Gp3	g.chr7:78038943G>T	Intron	MAGI2	membrane associated gu	30 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr7:78039802G>T	Intron	MAGI2	membrane associated gu	65 (0.00)	36 (0.22)	0.59
12-02	Gp3	g.chr7:78070434A>G	Intron	MAGI2	membrane associated gu	25 (0.00)	16 (0.44)	1.17
12-02	Gp3	g.chr7:78094657G>T	Intron	MAGI2	membrane associated gu	133 (0.00)	55 (0.22)	0.58
12-02	Gp3	g.chr7:78096658G>T	Intron	MAGI2	membrane associated gu	76 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr7:78096662C>T	Intron	MAGI2	membrane associated gu	76 (0.00)	26 (0.46)	1.23
12-02	Gp3	g.chr7:78162921C>T	Intron	MAGI2	membrane associated gu	25 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr7:78195659C>T	Intron	MAGI2	membrane associated gu	45 (0.00)	17 (0.82)	2.20
12-02	Gp3	g.chr7:78197986C>A	Intron	MAGI2	membrane associated gu	111 (0.00)	65 (0.22)	0.57

12-02	Gp3	g.chr7:78220652G>A	Intron	MAGI2	membrane associated gu	99 (0.00)	17 (0.53)	1.41
12-02	Gp3	g.chr7:78295348C>G	Intron	MAGI2	membrane associated gu	110 (0.00)	75 (0.25)	0.68
12-02	Gp3	g.chr7:78339199C>T	Intron	MAGI2	membrane associated gu	147 (0.00)	106 (0.23)	0.60
12-02	Gp3	g.chr7:78356982G>T	Intron	MAGI2	membrane associated gu	42 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr7:78359263G>T	Intron	MAGI2	membrane associated gu	46 (0.00)	11 (0.73)	1.94
12-02	Gp3	g.chr7:78385398C>A	Intron	MAGI2	membrane associated gu	59 (0.00)	27 (0.19)	0.49
12-02	Gp3	g.chr7:78389980G>A	Intron	MAGI2	membrane associated gu	147 (0.00)	40 (0.15)	0.40
12-02	Gp3	g.chr7:78397837C>T	Intron	MAGI2	membrane associated gu	85 (0.00)	25 (0.28)	0.75
12-02	Gp3	g.chr7:78446769A>T	Intron	MAGI2	membrane associated gu	31 (0.00)	12 (0.75)	2.00
12-02	Gp3	g.chr7:78563708C>T	Intron	MAGI2	membrane associated gu	40 (0.00)	29 (0.31)	0.83
12-02	Gp3	g.chr7:78607358G>T	Intron	MAGI2	membrane associated gu	53 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr7:78632353G>A	Intron	MAGI2	membrane associated gu	64 (0.00)	23 (0.26)	0.70
12-02	Gp3	g.chr7:78649486C>A	Intron	MAGI2	membrane associated gu	19 (0.00)	17 (0.47)	1.25
12-02	Gp3	g.chr7:78674202C>A	Intron	MAGI2	membrane associated gu	62 (0.00)	60 (0.28)	0.76
12-02	Gp3	g.chr7:78692772C>A	Intron	MAGI2	membrane associated gu	119 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr7:78692787C>A	Intron	MAGI2	membrane associated gu	114 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr7:78693958C>A	Intron	MAGI2	membrane associated gu	102 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr7:78704369G>A	Intron	MAGI2	membrane associated gu	36 (0.00)	40 (0.38)	1.00
12-02	Gp3	g.chr7:78704373C>A	Intron	MAGI2	membrane associated gu	63 (0.00)	44 (0.27)	0.73
12-02	Gp3	g.chr7:78706524A>T	Intron	MAGI2	membrane associated gu	77 (0.00)	68 (0.16)	0.43
12-02	Gp3	g.chr7:78710205C>G	Intron	MAGI2	membrane associated gu	67 (0.00)	17 (0.41)	1.10
12-02	Gp3	g.chr7:78740143C>A	Intron	MAGI2	membrane associated gu	81 (0.00)	27 (0.33)	0.89
12-02	Gp3	g.chr7:78754062C>A	Intron	MAGI2	membrane associated gu	136 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr7:78773505T>C	Intron	MAGI2	membrane associated gu	34 (0.00)	43 (0.23)	0.62
12-02	Gp3	g.chr7:78786400C>A	Intron	MAGI2	membrane associated gu	69 (0.00)	19 (0.37)	0.98
12-02	Gp3	g.chr7:78786401T>A	Intron	MAGI2	membrane associated gu	68 (0.00)	19 (0.32)	0.84
12-02	Gp3	g.chr7:78788564G>T	Intron	MAGI2	membrane associated gu	40 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr7:78841051G>T	Intron	MAGI2	membrane associated gu	37 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr7:78895046G>T	Intron	MAGI2	membrane associated gu	54 (0.02)	40 (0.33)	0.87
12-02	Gp3	g.chr7:78908180G>T	Intron	MAGI2	membrane associated gu	62 (0.00)	37 (0.32)	0.86
12-02	Gp3	g.chr7:78913542G>T	Intron	MAGI2	membrane associated gu	88 (0.00)	68 (0.16)	0.43
12-02	Gp3	g.chr7:78916423G>T	Intron	MAGI2	membrane associated gu	77 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr7:78920318A>T	Intron	MAGI2	membrane associated gu	27 (0.00)	18 (0.50)	1.33
12-02	Gp3	g.chr7:78927021G>A	Intron	MAGI2	membrane associated gu	104 (0.00)	104 (0.22)	0.59
12-02	Gp3	g.chr7:78945243C>G	Intron	MAGI2	membrane associated gu	25 (0.00)	25 (0.20)	0.53

12-02	Gp3	g.chr7:78981504T>C	Intron	MAGI2		membrane associated gu	55 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr7:78982789G>T	Intron	MAGI2		membrane associated gu	29 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr7:78995588T>A	Intron	MAGI2		membrane associated gu	35 (0.00)	26 (0.69)	1.85
12-02	Gp3	g.chr7:78998973G>A	Intron	MAGI2		membrane associated gu	105 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr7:79015073G>A	Intron	MAGI2		membrane associated gu	95 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr7:79023825C>A	Intron	MAGI2		membrane associated gu	98 (0.00)	14 (0.71)	1.90
12-02	Gp3	g.chr7:79028788T>A	Intron	MAGI2		membrane associated gu	22 (0.00)	33 (0.24)	0.65
12-02	Gp3	g.chr7:79028803G>A	Intron	MAGI2		membrane associated gu	22 (0.00)	31 (0.26)	0.69
12-02	Gp3	g.chr7:79028824G>A	Intron	MAGI2		membrane associated gu	23 (0.00)	44 (0.23)	0.61
12-02	Gp3	g.chr7:79035867G>A	Intron	MAGI2		membrane associated gu	112 (0.00)	62 (0.16)	0.43
12-02	Gp3	g.chr7:79042179C>A	Intron	MAGI2		membrane associated gu	47 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr7:79059784A>T	Intron	MAGI2		membrane associated gu	19 (0.00)	12 (0.50)	1.33
12-02	Gp3	g.chr11:95826314C>T	Missense Mutation	MAML2	p.G294E	mastermind-like 2 (Dros	19 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr4:140811863G>A	Silent	MAML3	p.L243L	mastermind-like 3 (Dros	63 (0.00)	39 (0.41)	1.09
12-02	Gp3	g.chr5:109117251C>T	Missense Mutation	MAN2A1	p.S510F	mannosidase, alpha, clas	60 (0.00)	11 (0.64)	1.70
12-02	Gp3	g.chr2:210559026C>G	Missense Mutation	MAP2	p.S711C	microtubule-associated	50 (0.02)	75 (0.60)	1.60
12-02	Gp3	g.chr6:161529815C>A	Missense Mutation	MAP3K4	p.T1387N	mitogen-activated protei	45 (0.00)	23 (0.26)	0.70
12-02	Gp3	g.chr9:128305365G>A	Nonsense Mutation	MAPKAP1	p.R311*	mitogen-activated protei	44 (0.00)	29 (0.24)	0.64
12-02	Gp3	g.chr11:63665702A>G	Splice Site	MARK2		MAP/microtubule affini	31 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr1:11087099C>T	Missense Mutation	MASP2	p.G635E	mannan-binding lectin s	20 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr3:152174109G>T	Missense Mutation	MBNL1	p.A351S	muscleblind-like splicin	67 (0.00)	59 (0.20)	0.54
12-02	Gp3	g.chr6:52142393C>T	Missense Mutation	MCM3	p.V325M	minichromosome maint	75 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr6:90494761C>A	Silent	MDN1	p.L473L	MDN1, midasin homolo	61 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr17:60039055G>A	Missense Mutation	MED13	p.S1717L	mediator complex subu	78 (0.01)	83 (0.13)	0.44
12-02	Gp3	g.chr15:37187357G>A	Missense Mutation	MEIS2	p.P374L	Meis homeobox 2	21 (0.00)	26 (0.27)	0.72
12-02	Gp3	g.chr18:29790522G>T	Silent	MEP1B	p.V326V	meprin A, beta	63 (0.00)	84 (0.19)	0.51
12-02	Gp3	g.chr10:126454042T>C	Missense Mutation	METTL10	p.R179G	methyltransferase like 1	77 (0.00)	58 (0.16)	0.41
12-02	Gp3	g.chr11:28318444C>A	Silent	METTL15	p.I248I	methyltransferase like 1	41 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr15:42052536C>A	Missense Mutation	MGA	p.L2403I	MGA, MAX dimerizati	16 (0.00)	20 (0.35)	0.93
12-02	Gp3	g.chr7:141734557G>T	Missense Mutation	MGAM	p.W625C	maltase-glucoamylase (	58 (0.00)	43 (0.42)	1.12
12-02	Gp3	g.chr18:19371374T>A	Silent	MIB1	p.I316I	mindbomb E3 ubiquitin	52 (0.00)	71 (0.18)	0.49
12-02	Gp3	g.chr6:109773601A>G	Missense Mutation	MICAL1	p.F227S	microtubule associated	15 (0.00)	16 (0.44)	1.17
12-02	Gp3	g.chr11:12315226C>T	Missense Mutation	MICALCL	p.P83L	MICAL C-terminal like	77 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr10:74183031G>T	Silent	MICU1	p.A344A	mitochondrial calcium u	52 (0.00)	147 (0.14)	0.38
12-02	Gp3	g.chr7:7625274G>A	Silent	MIOS	p.L552L	missing oocyte, meiosis	58 (0.00)	24 (0.54)	1.08

12-02	Gp3	g.chr6:168276056C>G	Missense Mutation	MLLT4	p.P207R	myeloid/lymphoid or mi	137 (0.00)	42 (0.21)	0.57
12-02	Gp3	g.chr21:37741608G>A	Missense Mutation	MORC3	p.V648I	MORC family CW-type	51 (0.00)	44 (0.39)	1.03
12-02	Gp3	g.chr9:124931935G>C	Silent	MORN5	p.T69T	MORN repeat containin	22 (0.00)	37 (0.51)	1.37
12-02	Gp3	g.chr5:41004471G>A	Nonsense Mutation	MROH2B	p.Q1391*	maestro heat-like repeat	98 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr2:86433369A>G	Missense Mutation	MRPL35	p.T62A	mitochondrial ribosoma	27 (0.00)	45 (0.42)	1.13
12-02	Gp3	g.chr1:54678305C>G	Missense Mutation	MRPL37	p.L322V	mitochondrial ribosoma	32 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr2:224824599G>A	Silent	MRPL44	p.E176E	mitochondrial ribosoma	41 (0.00)	36 (0.25)	0.67
12-02	Gp3	g.chr2:48013130G>A	Intron	MSH6		mutS homolog 6	55 (0.00)	36 (0.36)	0.96
12-02	Gp3	g.chr2:48027325C>A	Missense Mutation	MSH6	p.L735I	mutS homolog 6	20 (0.00)	27 (0.33)	0.89
12-02	Gp3	g.chr13:28014376C>T	Silent	MTIF3	p.K70K	mitochondrial translatio	92 (0.01)	70 (0.36)	0.95
12-02	Gp3	g.chr22:30416263G>C	Missense Mutation	MTMR3	p.G736A	myotubularin related pr	17 (0.00)	36 (0.17)	0.44
12-02	Gp3	g.chr4:187455076C>A	Nonsense Mutation	MTNR1A	p.E274*	melatonin receptor 1A	23 (0.00)	34 (0.15)	0.39
12-02	Gp3	g.chr1:237060884C>T	Silent	MTR	p.N1246N	5-methyltetrahydrofolat	27 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr13:29608061C>A	Missense Mutation	MTUS2	p.P759T	microtubule associated t	78 (0.00)	79 (0.68)	1.82
12-02	Gp3	g.chr19:9027552G>C	Missense Mutation	MUC16	p.P12198A	mucin 16, cell surface a	33 (0.00)	40 (0.25)	0.67
12-02	Gp3	g.chr19:9070079C>G	Silent	MUC16	p.T5789T	mucin 16, cell surface a	33 (0.00)	22 (0.41)	1.09
12-02	Gp3	g.chr19:9075406T>A	Missense Mutation	MUC16	p.T4014S	mucin 16, cell surface a	16 (0.00)	14 (0.57)	1.52
12-02	Gp3	g.chr19:9075758C>A	Missense Mutation	MUC16	p.E3896D	mucin 16, cell surface a	17 (0.00)	22 (0.27)	0.73
12-02	Gp3	g.chr19:9076754C>A	Missense Mutation	MUC16	p.M3564I	mucin 16, cell surface a	52 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr7:100676618G>A	Missense Mutation	MUC17	p.V641M	mucin 17, cell surface a	37 (0.00)	30 (0.30)	0.80
12-02	Gp3	g.chr7:100678412C>T	Missense Mutation	MUC17	p.L1239F	mucin 17, cell surface a	91 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr7:100678998C>G	Missense Mutation	MUC17	p.T1434S	mucin 17, cell surface a	50 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr7:100680511G>T	Silent	MUC17	p.V1938V	mucin 17, cell surface a	64 (0.02)	44 (0.48)	1.27
12-02	Gp3	g.chr7:100551722A>T	Missense Mutation	MUC3A	p.D158V	mucin 3A, cell surface a	360 (0.00)	239 (0.23)	0.62
12-02	Gp3	g.chr6:135521492C>T	Missense Mutation	MYB	p.S630F	v-myb avian myeloblast	74 (0.00)	48 (0.23)	0.61
12-02	Gp3	g.chr1:109839792C>G	Missense Mutation	MYBPHL	p.Q150H	myosin binding protein	17 (0.00)	32 (0.25)	0.67
12-02	Gp3	g.chr15:48443700G>C	Missense Mutation	MYEF2	p.Q426E	myelin expression facto	312 (0.00)	85 (0.55)	1.47
12-02	Gp3	g.chr17:10542235C>A	Missense Mutation	MYH3	p.E1098D	myosin, heavy chain 3, s	39 (0.00)	18 (0.28)	0.50
12-02	Gp3	g.chr2:211159091G>C	Missense Mutation	MYL1	p.A75G	myosin, light chain 1, al	26 (0.00)	36 (0.67)	1.78
12-02	Gp3	g.chr22:26239710G>A	Missense Mutation	MYO18B	p.A1074T	myosin XVIIIB	34 (0.00)	16 (0.38)	1.00
12-02	Gp3	g.chr2:192250614C>T	Missense Mutation	MYO1B	p.T453I	myosin IB	93 (0.00)	59 (0.36)	0.66
12-02	Gp3	g.chr17:30986230C>A	Missense Mutation	MYO1D	p.V662F	myosin ID	58 (0.00)	42 (0.14)	0.38
12-02	Gp3	g.chr2:171264324C>A	Missense Mutation	MYO3B	p.Q874K	myosin IIIB	97 (0.00)	44 (0.27)	0.42
12-02	Gp3	g.chr15:52529831G>T	Missense Mutation	MYO5C	p.H906N	myosin VC	72 (0.00)	25 (0.32)	0.85
12-02	Gp3	g.chr19:17256230C>A	Silent	MYO9B	p.A288A	myosin IXB	29 (0.00)	44 (0.11)	0.39

12-02	Gp3	g.chr13:21331659G>C	Missense Mutation	N6AMT2	p.Q27E	N-6 adenine-specific D	53 (0.00)	24 (0.21)	0.71
12-02	Gp3	g.chr13:41929301G>T	Missense Mutation	NAA16	p.V346F	N(alpha)-acetyltransfera	16 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr12:56619448G>T	Missense Mutation	NABP2	p.G87C	nucleic acid binding pro	43 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr13:35738568C>A	Silent	NBEA	p.L1385L	neurobeachin	70 (0.00)	20 (0.40)	1.07
12-02	Gp3	g.chr13:36167547C>T	Missense Mutation	NBEA	p.S2417F	neurobeachin	62 (0.00)	21 (0.57)	1.52
12-02	Gp3	g.chr1:16890529C>A	Missense Mutation	NBPF1	p.S1110I	neuroblastoma breakpoi	65 (0.00)	51 (0.25)	0.68
12-02	Gp3	g.chr12:6626552C>A	Missense Mutation	NCAPD2	p.Q403K	non-SMC condensin I c	48 (0.02)	30 (0.27)	0.50
12-02	Gp3	g.chr11:134072770C>T	Missense Mutation	NCAPD3	p.R519H	non-SMC condensin II c	58 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr2:97020022C>A	Silent	NCAPH	p.S357S	non-SMC condensin I c	48 (0.00)	49 (0.37)	0.98
12-02	Gp3	g.chr1:183533160T>C	Missense Mutation	NCF2	p.K336E	neutrophil cytosolic fact	25 (0.00)	28 (0.32)	0.86
12-02	Gp3	g.chr8:71068389G>T	Silent	NCOA2	p.P737P	nuclear receptor coactiv	158 (0.00)	176 (0.20)	0.55
12-02	Gp3	g.chr8:71087012C>T	Silent	NCOA2	p.A114A	nuclear receptor coactiv	263 (0.00)	113 (0.19)	0.50
12-02	Gp3	g.chr20:33329126G>A	Missense Mutation	NCOA6	p.S1645L	nuclear receptor coactiv	45 (0.00)	25 (0.40)	1.07
12-02	Gp3	g.chr9:132980150G>C	Silent	NCS1	p.L43L	neuronal calcium sensor	26 (0.00)	25 (0.20)	0.67
12-02	Gp3	g.chr1:54238006G>T	Missense Mutation	NDC1	p.L653M	NDC1 transmembrane n	80 (0.00)	37 (0.30)	0.79
12-02	Gp3	g.chr2:152548609G>A	Silent	NEB	p.H690H	nebulin	91 (0.00)	26 (0.23)	0.43
12-02	Gp3	g.chr8:24775274G>T	Nonsense Mutation	NEFM	p.E636*	neurofilament, medium	42 (0.00)	29 (0.31)	0.83
12-02	Gp3	g.chr4:170359313A>T	Missense Mutation	NEK1	p.D895E	NIMA-related kinase 1	77 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr3:130947490C>A	Silent	NEK11	p.I401I	NIMA-related kinase 11	63 (0.00)	48 (0.19)	0.50
12-02	Gp3	g.chr13:52709999C>A	Splice Site	NEK3	p.G375V	NIMA-related kinase 3	46 (0.00)	30 (0.33)	0.89
12-02	Gp3	g.chr3:52773513T>A	Missense Mutation	NEK4	p.D698V	NIMA-related kinase 4	59 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr14:75553807C>G	Missense Mutation	NEK9	p.A911P	NIMA-related kinase 9	118 (0.00)	62 (0.15)	0.39
12-02	Gp3	g.chr14:75553829C>A	Missense Mutation	NEK9	p.Q903H	NIMA-related kinase 9	109 (0.01)	47 (0.17)	0.45
12-02	Gp3	g.chr14:75580067G>A	Missense Mutation	NEK9	p.R305C	NIMA-related kinase 9	96 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr12:44915795C>A	Missense Mutation	NELL2	p.Q721H	NEL-like 2 (chicken)	25 (0.00)	20 (0.30)	0.80
12-02	Gp3	g.chr11:74705641C>A	Missense Mutation	NEU3	p.A61D	sialidase 3 (membrane s	35 (0.00)	81 (0.42)	1.12
12-02	Gp3	g.chr13:39621997A>C	Missense Mutation	NHLRC3	p.E129D	NHL repeat containing	41 (0.00)	19 (0.47)	1.26
12-02	Gp3	g.chr14:51223253G>T	Missense Mutation	NIN	p.Q1499K	ninein (GSK3B interacti	15 (0.00)	34 (0.21)	0.55
12-02	Gp3	g.chr5:36976361C>T	Missense Mutation	NIPBL	p.S451F	Nipped-B homolog (Dro	32 (0.00)	25 (0.36)	0.96
12-02	Gp3	g.chr15:85198635C>A	Missense Mutation	NMB	p.R112S	neuromedin B	29 (0.00)	34 (0.15)	0.39
12-02	Gp3	g.chr1:6592071A>G	Missense Mutation	NOL9	p.M535T	nucleolar protein 9	39 (0.00)	42 (0.14)	0.38
12-02	Gp3	g.chr16:18549858C>T	Missense Mutation	NOMO2	p.V404I	NODAL modulator 2	70 (0.00)	52 (0.17)	0.46
12-02	Gp3	g.chr12:117660574C>A	Missense Mutation	NOS1	p.K1341N	nitric oxide synthase 1 (	23 (0.00)	43 (0.42)	0.66
12-02	Gp3	g.chr2:101582125A>T	Silent	NPAS2	p.A268A	neuronal PAS domain p	40 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr4:106861271G>T	Missense Mutation	NPNT	p.R212I	nephronectin	44 (0.00)	27 (0.19)	0.49

12-02	Gp3	g.chr4:164271943C>A	Missense Mutation	NPY5R	p.P173H	neuropeptide Y receptor	17 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr5:137143848C>A	RNA	NPY6R		neuropeptide Y receptor	24 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr2:27663733G>T	Nonsense Mutation	NRBP1	p.E419*	nuclear receptor binding	23 (0.00)	40 (0.25)	0.67
12-02	Gp3	g.chr10:84744877C>A	Missense Mutation	NRG3	p.T536N	neuregulin 3	75 (0.00)	59 (0.17)	0.45
12-02	Gp3	g.chr2:50723149C>A	Missense Mutation	NRXN1	p.W1028C	neurexin 1	123 (0.00)	37 (0.16)	0.43
12-02	Gp3	g.chr2:50765399C>A	Missense Mutation	NRXN1	p.C752F	neurexin 1	94 (0.00)	78 (0.15)	0.41
12-02	Gp3	g.chr17:28445147C>T	Nonsense Mutation	NSRP1	p.Q24*	nuclear speckle splicing	41 (0.00)	26 (0.73)	1.95
12-02	Gp3	g.chr4:40778121A>T	Missense Mutation	NSUN7	p.D294V	NOP2/Sun domain fami	15 (0.00)	24 (0.54)	1.44
12-02	Gp3	g.chr12:104187031C>T	Missense Mutation	NT5DC3	p.M310I	5'-nucleotidase domain	99 (0.00)	44 (0.59)	0.94
12-02	Gp3	g.chr12:104187755G>C	Missense Mutation	NT5DC3	p.H258Q	5'-nucleotidase domain	35 (0.00)	27 (0.26)	0.41
12-02	Gp3	g.chr8:27891131C>T	Silent	NUGGC	p.A565A	nuclear GTPase, germin	24 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr9:134019861G>A	Missense Mutation	NUP214	p.G497R	nucleoporin 214kDa	97 (0.00)	117 (0.25)	0.66
12-02	Gp3	g.chr9:134021619A>T	Missense Mutation	NUP214	p.S625C	nucleoporin 214kDa	82 (0.00)	47 (0.15)	0.40
12-02	Gp3	g.chrX:106418365G>A	Silent	NUP62CL	p.T4T	nucleoporin 62kDa C-te	56 (0.00)	17 (0.29)	0.49
12-02	Gp3	g.chr10:88971944T>G	RNA	NUTM2A-AS1		NUTM2A antisense RN	30 (0.00)	52 (0.15)	0.41
12-02	Gp3	g.chr1:228432058G>C	Silent	OBSCN	p.G1181G	obscurin, cytoskeletal c	59 (0.00)	81 (0.15)	0.40
12-02	Gp3	g.chr10:74658447C>A	Silent	OIT3	p.I29I	oncoprotein induced tra	17 (0.00)	38 (0.18)	0.49
12-02	Gp3	g.chr1:161954601G>A	Silent	OLFML2B	p.F549F	olfactomedin-like 2B	26 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr12:10313444G>T	Missense Mutation	OLR1	p.Q169K	oxidized low density lip	98 (0.00)	31 (0.29)	0.54
12-02	Gp3	g.chr12:10313445G>C	Missense Mutation	OLR1	p.S168R	oxidized low density lip	99 (0.00)	31 (0.29)	0.54
12-02	Gp3	g.chr10:13151224G>A	Silent	OPTN	p.T34T	optineurin	47 (0.00)	41 (0.17)	0.46
12-02	Gp3	g.chr14:22038437C>A	Missense Mutation	OR10G3	p.A147S	olfactory receptor, famil	49 (0.00)	39 (0.15)	0.41
12-02	Gp3	g.chr1:158435747C>T	Silent	OR10K1	p.Y132Y	olfactory receptor, famil	29 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr1:247902698G>T	Missense Mutation	OR14K1	p.G261V	olfactory receptor, famil	96 (0.01)	42 (0.14)	0.38
12-02	Gp3	g.chr7:143792432C>A	Missense Mutation	OR2A12	p.P78T	olfactory receptor, famil	63 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr11:6806496T>C	Silent	OR2AG1	p.V76V	olfactory receptor, famil	21 (0.00)	32 (0.22)	0.58
12-02	Gp3	g.chr1:248308957G>T	Missense Mutation	OR2M5	p.G170W	olfactory receptor, famil	22 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr8:116685G>A	Silent	OR4F21	p.L114L	olfactory receptor, famil	92 (0.00)	59 (0.17)	0.45
12-02	Gp3	g.chr14:20612573G>C	Missense Mutation	OR4N5	p.E227Q	olfactory receptor, famil	46 (0.00)	42 (0.17)	0.44
12-02	Gp3	g.chr11:55418740T>A	Missense Mutation	OR4S2	p.Y121N	olfactory receptor, famil	75 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr11:55798515G>T	Missense Mutation	OR5AS1	p.Q207H	olfactory receptor, famil	102 (0.00)	52 (0.15)	0.41
12-02	Gp3	g.chr9:125551909G>T	Missense Mutation	OR5C1	p.R233L	olfactory receptor, famil	17 (0.00)	60 (0.22)	0.58
12-02	Gp3	g.chr14:23103413A>G	Missense Mutation	OR6J1	p.F102L	olfactory receptor, famil	64 (0.00)	76 (0.30)	0.81
12-02	Gp3	g.chr1:158532490C>T	Missense Mutation	OR6P1	p.R302K	olfactory receptor, famil	86 (0.00)	51 (0.16)	0.42
12-02	Gp3	g.chr1:36886182T>C	Missense Mutation	OSCP1	p.E240G	organic solute carrier pa	20 (0.00)	23 (0.35)	0.93

12-02	Gp3	g.chr2:190618749C>T	Missense Mutation	OSGEPL1	p.A286T	O-sialoglycoprotein end	62 (0.00)	23 (0.26)	0.48
12-02	Gp3	g.chr12:80762090G>A	Splice Site	OTOGL		otogelin-like	50 (0.00)	17 (0.35)	0.94
12-02	Gp3	g.chr20:9546692C>G	Missense Mutation	PAK7	p.D444H	p21 protein (Cdc42/Rac	105 (0.00)	80 (0.15)	0.40
12-02	Gp3	g.chr12:56726643G>T	Missense Mutation	PAN2	p.S79Y	PAN2 poly(A) specific	43 (0.00)	58 (0.16)	0.41
12-02	Gp3	g.chr10:91353592G>T	Missense Mutation	PANK1	p.Q264K	pantothenate kinase 1	92 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr14:96998882C>T	Silent	PAPOLA	p.L244L	poly(A) polymerase alp	142 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr16:14676106T>C	Missense Mutation	PARN	p.Q375R	poly(A)-specific ribonu	30 (0.00)	24 (0.21)	0.56
12-02	Gp3	g.chr3:122437773G>T	Missense Mutation	PARP14	p.S1592I	poly (ADP-ribose) poly	59 (0.00)	32 (0.25)	0.67
12-02	Gp3	g.chr12:102558357G>A	Missense Mutation	PARPBP	p.A213T	PARP1 binding protein	16 (0.00)	22 (0.32)	0.50
12-02	Gp3	g.chr7:154752661C>T	Silent	PAXIP1	p.T792T	PAX interacting (with t	56 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr1:154918776C>A	Missense Mutation	PBXIP1	p.K458N	pre-B-cell leukemia hon	20 (0.00)	264 (0.16)	0.43
12-02	Gp3	g.chr13:100953726G>A	Missense Mutation	PCCA	p.V360I	propionyl CoA carboxyl	53 (0.00)	27 (0.52)	1.38
12-02	Gp3	g.chr13:58298918G>T	Silent	PCDH17	p.V990V	protocadherin 17	19 (0.00)	15 (0.40)	1.33
12-02	Gp3	g.chr13:61987623A>T	Missense Mutation	PCDH20	p.N203K	protocadherin 20	30 (0.00)	79 (0.11)	0.38
12-02	Gp3	g.chr13:61987699A>G	Missense Mutation	PCDH20	p.L178S	protocadherin 20	20 (0.00)	63 (0.13)	0.42
12-02	Gp3	g.chr5:140202131G>T	Silent	PCDHA5	p.G257G	protocadherin alpha 5	27 (0.00)	44 (0.16)	0.42
12-02	Gp3	g.chr5:140588856T>C	Missense Mutation	PCDHB12	p.I126T	protocadherin beta 12	32 (0.00)	49 (0.14)	0.38
12-02	Gp3	g.chr5:140603352G>A	Missense Mutation	PCDHB14	p.R92Q	protocadherin beta 14	106 (0.01)	70 (0.24)	0.65
12-02	Gp3	g.chr5:140625702G>C	Missense Mutation	PCDHB15	p.G186R	protocadherin beta 15	35 (0.00)	35 (0.23)	0.61
12-02	Gp3	g.chr5:140502098C>A	Missense Mutation	PCDHB4	p.P173H	protocadherin beta 4	34 (0.00)	56 (0.16)	0.43
12-02	Gp3	g.chr5:140773411G>T	Missense Mutation	PCDHGA8	p.R344I	protocadherin gamma s	42 (0.00)	30 (0.30)	0.80
12-02	Gp3	g.chr7:82545785C>A	Silent	PCLO	p.V3839V	piccolo presynaptic cyt	269 (0.00)	198 (0.23)	0.62
12-02	Gp3	g.chr7:82545810C>G	Missense Mutation	PCLO	p.R3831P	piccolo presynaptic cyt	253 (0.00)	188 (0.21)	0.57
12-02	Gp3	g.chr20:5096162G>T	Missense Mutation	PCNA	p.N213K	proliferating cell nuclea	50 (0.00)	32 (0.19)	0.50
12-02	Gp3	g.chr1:233314821G>A	Missense Mutation	PCNXL2	p.S1056F	pecanex-like 2 (Drosop	53 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr1:233397911G>T	Splice Site	PCNXL2	p.S120R	pecanex-like 2 (Drosop	129 (0.00)	72 (0.24)	0.63
12-02	Gp3	g.chr14:60591120C>A	Nonsense Mutation	PCNXL4	p.S744*	pecanex-like 4 (Drosop	109 (0.00)	65 (0.28)	0.74
12-02	Gp3	g.chr9:78710854G>T	Nonsense Mutation	PCSK5	p.G315*	proprotein convertase s	41 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr9:78804597C>G	Missense Mutation	PCSK5	p.T854R	proprotein convertase s	65 (0.00)	23 (0.39)	1.04
12-02	Gp3	g.chr1:144918855C>T	Missense Mutation	PDE4DIP	p.S581N	phosphodiesterase 4D i	67 (0.00)	39 (0.15)	0.41
12-02	Gp3	g.chr4:96761510G>A	Missense Mutation	PDHA2	p.R70H	pyruvate dehydrogenase	18 (0.00)	53 (0.25)	0.65
12-02	Gp3	g.chr2:10927421G>A	Silent	PDIA6	p.I433I	protein disulfide isomer	31 (0.00)	48 (0.23)	0.61
12-02	Gp3	g.chr2:10927442G>T	Silent	PDIA6	p.G426G	protein disulfide isomer	32 (0.00)	45 (0.20)	0.53
12-02	Gp3	g.chr16:70164393G>T	Silent	PDPR	p.V225V	pyruvate dehydrogenase	15 (0.00)	23 (0.35)	0.55
12-02	Gp3	g.chr4:39846316C>A	Missense Mutation	PDS5A	p.V1170L	PDS5, regulator of cohe	115 (0.00)	126 (0.43)	1.14

12-02	Gp3	g.chr2:61245391C>T	Missense Mutation	PEX13	p.P63S	peroxisomal biogenesis	43 (0.00)	51 (0.16)	0.42
12-02	Gp3	g.chr1:28792271C>G	Nonsense Mutation	PHACTR4	p.S126*	phosphatase and actin re	78 (0.00)	34 (0.15)	0.49
12-02	Gp3	g.chr3:169847213G>A	Silent	PHC3	p.I349I	polyhomeotic homolog	139 (0.01)	80 (0.50)	1.33
12-02	Gp3	g.chr4:129764120C>A	Missense Mutation	PHF17	p.T22N		60 (0.00)	52 (0.15)	0.41
12-02	Gp3	g.chr11:46001518C>A	Splice Site	PHF21A		PHD finger protein 21A	80 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr6:79655070G>T	Missense Mutation	PHIP	p.S1592Y	pleckstrin homology do	36 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr18:60393544C>G	Intron	PHLPP1		PH domain and leucine	51 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr18:60518401C>A	Intron	PHLPP1		PH domain and leucine	63 (0.00)	42 (0.33)	0.89
12-02	Gp3	g.chr18:60525124G>A	Intron	PHLPP1		PH domain and leucine	69 (0.00)	38 (0.42)	1.12
12-02	Gp3	g.chr18:60564789G>A	Intron	PHLPP1		PH domain and leucine	69 (0.00)	22 (0.27)	0.73
12-02	Gp3	g.chr18:60634120C>T	Intron	PHLPP1		PH domain and leucine	137 (0.01)	223 (0.16)	0.43
12-02	Gp3	g.chr16:71698289G>C	Intron	PHLPP2		PH domain and leucine	71 (0.00)	22 (0.36)	0.58
12-02	Gp3	g.chr16:71718812G>T	Intron	PHLPP2		PH domain and leucine	64 (0.00)	27 (0.37)	0.59
12-02	Gp3	g.chr16:71726554C>G	Intron	PHLPP2		PH domain and leucine	19 (0.00)	29 (0.28)	0.44
12-02	Gp3	g.chr16:71736919G>A	Intron	PHLPP2		PH domain and leucine	40 (0.00)	37 (0.51)	0.82
12-02	Gp3	g.chr1:114255962T>A	Missense Mutation	PHTF1	p.E241V	putative homeodomain t	34 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr7:77538240C>T	Silent	PHTF2	p.P154P	putative homeodomain t	88 (0.01)	59 (0.27)	0.72
12-02	Gp3	g.chr1:151271482T>C	Missense Mutation	PI4KB	p.D591G	phosphatidylinositol 4-k	24 (0.00)	16 (0.38)	1.30
12-02	Gp3	g.chr18:10671651C>T	Missense Mutation	PIEZO2	p.C2711Y	piezo-type mechanosens	26 (0.00)	40 (0.38)	1.00
12-02	Gp3	g.chr9:71478883G>A	Splice Site	PIP5K1B	p.S67N	phosphatidylinositol-4-p	115 (0.01)	24 (0.42)	1.11
12-02	Gp3	g.chr12:130855828G>A	Missense Mutation	PIWIL1	p.R810H	piwi-like RNA-mediate	59 (0.00)	43 (0.37)	0.59
12-02	Gp3	g.chr5:108672946C>T	Missense Mutation	PJA2	p.A705T	praja ring finger 2, E3 u	25 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr16:71967302G>A	RNA	PKD1L3		polycystic kidney diseas	32 (0.00)	26 (0.54)	0.86
12-02	Gp3	g.chr16:71977987G>T	RNA	PKD1L3		polycystic kidney diseas	70 (0.01)	20 (0.40)	0.64
12-02	Gp3	g.chr4:88957446G>T	Missense Mutation	PKD2	p.V262L	polycystic kidney diseas	34 (0.00)	38 (0.61)	1.61
12-02	Gp3	g.chr8:110437349C>T	Silent	PKHD1L1	p.Y911Y	polycystic kidney and h	55 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr8:110457011A>G	Missense Mutation	PKHD1L1	p.Y1638C	polycystic kidney and h	140 (0.00)	28 (0.43)	1.14
12-02	Gp3	g.chr8:110476739G>T	Missense Mutation	PKHD1L1	p.A2560S	polycystic kidney and h	78 (0.00)	58 (0.60)	1.61
12-02	Gp3	g.chr15:72502132C>G	Missense Mutation	PKM	p.M149I	pyruvate kinase, muscle	55 (0.00)	44 (0.27)	0.73
12-02	Gp3	g.chr9:26928113C>A	Nonsense Mutation	PLAA	p.E184*	phospholipase A2-activa	47 (0.02)	33 (0.18)	0.48
12-02	Gp3	g.chr20:9388599G>T	Missense Mutation	PLCB4	p.M549I	phospholipase C, beta 4	43 (0.02)	21 (0.24)	0.63
12-02	Gp3	g.chr3:155267631C>T	Missense Mutation	PLCH1	p.G424E	phospholipase C, eta 1	39 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr17:4718784G>T	Missense Mutation	PLD2	p.R396L	phospholipase D2	24 (0.00)	26 (0.31)	0.56
12-02	Gp3	g.chr14:68052725G>A	Missense Mutation	PLEKHH1	p.D1282N	pleckstrin homology do	90 (0.00)	79 (0.33)	0.88
12-02	Gp3	g.chr15:65140865G>T	Missense Mutation	PLEKHO2	p.S29I	pleckstrin homology do	52 (0.02)	54 (0.17)	0.44

12-02	Gp3	g.chr6:161152119C>A	Silent	PLG	p.A431A	plasminogen	82 (0.00)	19 (0.37)	0.98
12-02	Gp3	g.chr3:145839001T>A	Missense Mutation	PLOD2	p.D79V	procollagen-lysine, 2-ox	102 (0.00)	34 (0.21)	0.55
12-02	Gp3	g.chr3:145914465C>T	Missense Mutation	PLSCR4	p.R247H	phospholipid scramblas	59 (0.00)	17 (0.41)	1.10
12-02	Gp3	g.chr1:208201461C>A	Missense Mutation	PLXNA2	p.D1828Y	plexin A2	22 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr15:89870229G>T	Missense Mutation	POLG	p.A500D	polymerase (DNA direc	36 (0.00)	87 (0.22)	0.58
12-02	Gp3	g.chr2:86292400T>C	Silent	POLR1A	p.K685K	polymerase (RNA) I pol	20 (0.00)	15 (0.47)	1.24
12-02	Gp3	g.chr10:79742029A>G	Silent	POLR3A	p.I1214I	polymerase (RNA) III (	132 (0.00)	21 (0.29)	0.76
12-02	Gp3	g.chr7:72418911C>T	Missense Mutation	POM121	p.P968S	POM121 transmembran	25 (0.00)	172 (0.21)	0.56
12-02	Gp3	g.chr6:27278850G>A	Missense Mutation	POM121L2	p.T367I	POM121 transmembran	47 (0.00)	56 (0.18)	0.61
12-02	Gp3	g.chr7:124503538C>G	Missense Mutation	POT1	p.V138L	protection of telomeres	69 (0.00)	32 (0.16)	0.42
12-02	Gp3	g.chr7:124503612G>A	Missense Mutation	POT1	p.P113L	protection of telomeres	95 (0.00)	40 (0.20)	0.53
12-02	Gp3	g.chr11:70178095G>T	Missense Mutation	PPFIA1	p.E369D	protein tyrosine phospha	76 (0.00)	92 (0.11)	0.38
12-02	Gp3	g.chr11:70202283G>A	Silent	PPFIA1	p.T835T	protein tyrosine phospha	97 (0.00)	46 (0.17)	0.61
12-02	Gp3	g.chr2:170493509G>A	Missense Mutation	PPIG	p.D581N	peptidylprolyl isomeras	57 (0.00)	21 (0.48)	0.74
12-02	Gp3	g.chr1:113253214G>T	Missense Mutation	PPM1J	p.T413K	protein phosphatase, Mg	39 (0.00)	30 (0.23)	0.62
12-02	Gp3	g.chr14:102229246C>A	Nonsense Mutation	PPP2R5C	p.S11*	protein phosphatase 2, r	15 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr6:105800850C>T	Missense Mutation	PREP	p.A274T	prolyl endopeptidase	31 (0.00)	11 (0.73)	1.94
12-02	Gp3	g.chr12:49398769C>G	Missense Mutation	PRKAG1	p.V130L	protein kinase, AMP-ac	43 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr3:53223971C>A	Missense Mutation	PRKCD	p.T609N	protein kinase C, delta	34 (0.00)	83 (0.36)	0.96
12-02	Gp3	g.chr10:6498699C>A	Missense Mutation	PRKCQ	p.E528D	protein kinase C, theta	30 (0.00)	32 (0.22)	0.58
12-02	Gp3	g.chr14:23393293G>A	Silent	PRMT5	p.V433V	protein arginine methylt	42 (0.00)	39 (0.23)	0.62
12-02	Gp3	g.chr14:23393523C>G	Silent	PRMT5	p.R385R	protein arginine methylt	51 (0.00)	47 (0.30)	0.79
12-02	Gp3	g.chr14:75329308G>T	Silent	PROX2	p.P410P	prospero homeobox 2	23 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr9:116053081C>T	Missense Mutation	PRPF4	p.P417L	pre-mRNA processing f	69 (0.00)	40 (0.20)	0.53
12-02	Gp3	g.chr2:153526894T>C	Splice Site	PRPF40A	p.E494G	PRP40 pre-mRNA proc	22 (0.00)	10 (0.50)	0.92
12-02	Gp3	g.chr6:4056660C>A	Missense Mutation	PRPF4B	p.P858T	pre-mRNA processing f	46 (0.00)	25 (0.24)	0.64
12-02	Gp3	g.chr1:171553315C>G	Missense Mutation	PRRC2C	p.H2542D	proline-rich coiled-coil	76 (0.00)	18 (0.44)	1.19
12-02	Gp3	g.chr1:171556814G>T	Nonsense Mutation	PRRC2C	p.G2664*	proline-rich coiled-coil	83 (0.00)	15 (0.40)	1.07
12-02	Gp3	g.chr1:171560972G>A	Missense Mutation	PRRC2C	p.E2814K	proline-rich coiled-coil	42 (0.00)	11 (0.55)	1.45
12-02	Gp3	g.chr7:127998779G>C	Missense Mutation	PRRT4	p.P278R	proline-rich transmemb	15 (0.00)	36 (0.22)	0.59
12-02	Gp3	g.chr9:79318319G>A	Missense Mutation	PRUNE2	p.P2737L	prune homolog 2 (Dros	81 (0.00)	50 (0.40)	1.07
12-02	Gp3	g.chr8:18729517C>T	Missense Mutation	PSD3	p.R286Q	pleckstrin and Sec7 dom	26 (0.00)	18 (0.28)	0.57
12-02	Gp3	g.chr3:184021134G>A	Missense Mutation	PSMD2	p.D366N	proteasome (prosome, n	18 (0.00)	18 (0.78)	2.07
12-02	Gp3	g.chr17:40990984G>A	Missense Mutation	PSME3	p.R105K	proteasome (prosome, n	68 (0.00)	59 (0.14)	0.49
12-02	Gp3	g.chr18:43570708G>T	Missense Mutation	PSTPIP2	p.P312Q	proline-serine-threonine	53 (0.00)	43 (0.28)	0.74

12-02	Gp3	g.chr9:72338414C>A	Nonsense Mutation	PTAR1	p.E259*	protein prenyltransfera	28 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr9:114994438G>T	Missense Mutation	PTBP3	p.P321T	polypyrimidine tract bin	37 (0.00)	29 (0.31)	0.83
12-02	Gp3	g.chr10:89675566C>T	Intron	PTEN		phosphatase and tensin	143 (0.01)	29 (0.21)	0.55
12-02	Gp3	g.chr10:89700596C>T	Intron	PTEN		phosphatase and tensin	122 (0.01)	33 (0.39)	1.05
12-02	Gp3	g.chr1:32374508C>T	Missense Mutation	PTP4A2	p.R150Q	protein tyrosine phospha	114 (0.00)	49 (0.22)	0.60
12-02	Gp3	g.chr7:77172424C>A	Intron	PTPN12		protein tyrosine phospha	143 (0.00)	46 (0.15)	0.41
12-02	Gp3	g.chr7:77206842A>G	Intron	PTPN12		protein tyrosine phospha	69 (0.00)	40 (0.60)	1.60
12-02	Gp3	g.chr7:77239312C>A	Intron	PTPN12		protein tyrosine phospha	66 (0.02)	140 (0.15)	0.40
12-02	Gp3	g.chr7:77260708G>T	Intron	PTPN12		protein tyrosine phospha	100 (0.00)	40 (0.28)	0.73
12-02	Gp3	g.chr9:112172311C>A	Missense Mutation	PTPN3	p.D516Y	protein tyrosine phospha	18 (0.00)	25 (0.36)	0.96
12-02	Gp3	g.chr12:70949895G>T	Missense Mutation	PTPRB	p.P1495H	protein tyrosine phospha	124 (0.00)	63 (0.16)	0.42
12-02	Gp3	g.chr12:70953334C>G	Silent	PTPRB	p.G1413G	protein tyrosine phospha	40 (0.00)	35 (0.26)	0.69
12-02	Gp3	g.chr11:48146547C>G	Missense Mutation	PTPRJ	p.A301G	protein tyrosine phospha	17 (0.00)	37 (0.19)	0.50
12-02	Gp3	g.chr2:136481625C>T	Silent	R3HDM1	p.P966P	R3H domain containing	32 (0.00)	23 (0.26)	0.48
12-02	Gp3	g.chr15:66170279C>T	Missense Mutation	RAB11A	p.A139V	RAB11A, member RAS	59 (0.00)	73 (0.16)	0.44
12-02	Gp3	g.chr12:1042175G>T	Missense Mutation	RAD52	p.A17D	RAD52 homolog (S. ce	49 (0.00)	75 (0.17)	0.46
12-02	Gp3	g.chr20:55949751G>A	Missense Mutation	RAE1	p.R305K	ribonucleic acid export	66 (0.00)	82 (0.30)	0.81
12-02	Gp3	g.chr11:36596172C>A	Missense Mutation	RAG1	p.L440M	recombination activatin	17 (0.00)	47 (0.17)	0.45
12-02	Gp3	g.chr9:129937044C>G	Missense Mutation	RALGPS1	p.S298C	Ral GEF with PH doma	28 (0.00)	36 (0.19)	0.65
12-02	Gp3	g.chr2:109368009C>T	Missense Mutation	RANBP2	p.T494I	RAN binding protein 2	132 (0.00)	21 (0.62)	1.08
12-02	Gp3	g.chr2:109382892C>A	Missense Mutation	RANBP2	p.P1966H	RAN binding protein 2	100 (0.01)	93 (0.44)	0.77
12-02	Gp3	g.chr2:109382893C>A	Silent	RANBP2	p.P1966P	RAN binding protein 2	99 (0.01)	94 (0.45)	0.78
12-02	Gp3	g.chr3:25502708C>A	Missense Mutation	RARB	p.S61Y	retinoic acid receptor, b	62 (0.00)	29 (0.38)	1.01
12-02	Gp3	g.chr1:178414707G>A	Missense Mutation	RASAL2	p.V513I	RAS protein activator li	21 (0.00)	31 (0.32)	0.86
12-02	Gp3	g.chr15:38805029C>A	Silent	RASGRP1	p.P268P	RAS guanyl releasing p	44 (0.00)	43 (0.26)	0.68
12-02	Gp3	g.chr2:33780625A>G	Missense Mutation	RASGRP3	p.K524E	RAS guanyl releasing p	32 (0.00)	39 (0.28)	0.75
12-02	Gp3	g.chr13:48884204G>A	Intron	RB1		retinoblastoma 1	118 (0.00)	50 (0.48)	1.28
12-02	Gp3	g.chr13:48907768G>A	Intron	RB1		retinoblastoma 1	101 (0.00)	57 (0.61)	1.64
12-02	Gp3	g.chr13:48907819A>T	Intron	RB1		retinoblastoma 1	119 (0.00)	55 (0.45)	1.21
12-02	Gp3	g.chr13:48914203C>A	Intron	RB1		retinoblastoma 1	28 (0.00)	21 (0.43)	1.14
12-02	Gp3	g.chr13:48952663C>A	Intron	RB1		retinoblastoma 1	61 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr13:49020488T>A	Intron	RB1		retinoblastoma 1	21 (0.00)	40 (0.42)	1.13
12-02	Gp3	g.chr13:49023699G>A	Intron	RB1		retinoblastoma 1	80 (0.00)	36 (0.25)	0.67
12-02	Gp3	g.chr13:49032753A>G	Intron	RB1		retinoblastoma 1	59 (0.00)	73 (0.16)	0.44
12-02	Gp3	g.chr10:112541497G>A	Missense Mutation	RBM20	p.G377D	RNA binding motif prot	22 (0.00)	38 (0.24)	0.63

12-02	Gp3	g.chr7:127961425C>T	Missense Mutation	RBM28	p.R486Q	RNA binding motif prot	35 (0.00)	33 (0.39)	1.05
12-02	Gp3	g.chr1:89449143G>A	Missense Mutation	RBMXL1	p.P123S	RNA binding motif prot	68 (0.00)	16 (0.38)	1.00
12-02	Gp3	g.chr2:61144116C>A	Missense Mutation	REL	p.L167I	v-rel avian reticuloendo	48 (0.00)	35 (0.31)	0.84
12-02	Gp3	g.chr11:65426188C>A	Splice Site	RELA		v-rel avian reticuloendo	17 (0.00)	79 (0.15)	0.53
12-02	Gp3	g.chr4:37651083G>A	Missense Mutation	RELL1	p.T43M	RELT-like 1	40 (0.00)	48 (0.69)	1.83
12-02	Gp3	g.chr6:111701373T>C	Silent	REV3L	p.E422E	REV3-like, polymerase	100 (0.00)	41 (0.15)	0.39
12-02	Gp3	g.chr6:111701410G>T	Missense Mutation	REV3L	p.P410H	REV3-like, polymerase	42 (0.00)	40 (0.15)	0.40
12-02	Gp3	g.chr9:136279840C>T	Missense Mutation	REXO4	p.D173N	REX4, RNA exonucleas	28 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr3:186518960A>G	Silent	RFC4	p.V52V	replication factor C (acti	23 (0.00)	24 (0.50)	1.33
12-02	Gp3	g.chr22:32754341C>A	Missense Mutation	RFPL3	p.Q66K	ret finger protein-like 3	52 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr19:56274496C>T	Silent	RFPL4A	p.I273I	ret finger protein-like 4	29 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr2:198540155C>A	Missense Mutation	RFTN2	p.D10Y	raftlin family member 2	108 (0.00)	105 (0.17)	0.46
12-02	Gp3	g.chr5:38982138G>A	Splice Site	RICTOR	p.A195V	RPTOR independent co	18 (0.00)	15 (0.87)	2.31
12-02	Gp3	g.chr8:104948876C>T	Missense Mutation	RIMS2	p.R603W	regulating synaptic mem	21 (0.00)	23 (0.39)	1.04
12-02	Gp3	g.chr2:7154590G>A	Silent	RNF144A	p.L47L	ring finger protein 144A	29 (0.00)	24 (0.21)	0.56
12-02	Gp3	g.chr9:104316328C>A	Missense Mutation	RNF20	p.P654T	ring finger protein 20, E	37 (0.00)	19 (0.32)	0.84
12-02	Gp3	g.chr13:79190110G>T	Missense Mutation	RNF219	p.L596I	ring finger protein 219	55 (0.00)	40 (0.38)	1.00
12-02	Gp3	g.chr17:58040337T>C	Missense Mutation	RNFT1	p.E122G	ring finger protein, trans	36 (0.00)	30 (0.17)	0.56
12-02	Gp3	g.chr3:78656014C>T	Missense Mutation	ROBO1	p.R1538K	roundabout, axon guida	164 (0.00)	105 (0.43)	1.45
12-02	Gp3	g.chr15:78217424C>A	RNA	RP11-114H24.2			34 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr5:177059237G>T	RNA	RP11-1277A3.2			23 (0.00)	45 (0.16)	0.41
12-02	Gp3	g.chr15:76074939G>T	RNA	RP11-24M17.5			21 (0.00)	34 (0.15)	0.39
12-02	Gp3	g.chr3:139213532G>T	RNA	RP11-319G6.1			31 (0.00)	22 (0.36)	0.97
12-02	Gp3	g.chr10:51822502C>A	RNA	RP11-324H6.5			34 (0.00)	83 (0.28)	0.74
12-02	Gp3	g.chr3:97957312C>A	lincRNA	RP11-325B23.2			62 (0.02)	33 (0.24)	0.65
12-02	Gp3	g.chr3:97957351C>A	lincRNA	RP11-325B23.2			78 (0.00)	34 (0.26)	0.71
12-02	Gp3	g.chr3:9390341G>T	RNA	RP11-380O24.1			25 (0.00)	36 (0.22)	0.59
12-02	Gp3	g.chr9:84547687C>G	lincRNA	RP11-383M4.6			33 (0.00)	18 (0.72)	1.93
12-02	Gp3	g.chr1:159320979G>A	RNA	RP11-550P17.5			69 (0.00)	23 (0.74)	1.97
12-02	Gp3	g.chr10:89402608A>T	RNA	RP11-57C13.3			64 (0.00)	52 (0.23)	0.62
12-02	Gp3	g.chr4:68312079G>A	lincRNA	RP11-584P21.2			24 (0.00)	40 (0.20)	0.53
12-02	Gp3	g.chr14:20151707G>A	lincRNA	RP11-597A11.2			79 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr17:43626627C>A	lincRNA	RP11-798G7.6			41 (0.00)	30 (0.27)	0.86
12-02	Gp3	g.chr18:11913879C>G	lincRNA	RP11-820I16.1			19 (0.00)	29 (0.48)	1.29
12-02	Gp3	g.chr11:94647279T>A	RNA	RP11-856F16.2			28 (0.00)	21 (0.24)	0.63

12-02	Gp3	g.chr20:26173969C>A	lincRNA	RP3-410C9.2			53 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr14:21788274C>A	Missense Mutation	RPGRIP1	p.P469T	retinitis pigmentosa GT	36 (0.00)	44 (0.16)	0.42
12-02	Gp3	g.chr14:21793132C>G	Silent	RPGRIP1	p.A706A	retinitis pigmentosa GT	29 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr14:21796675G>T	Missense Mutation	RPGRIP1	p.E996D	retinitis pigmentosa GT	39 (0.00)	27 (0.33)	0.89
12-02	Gp3	g.chr16:53698861C>A	Missense Mutation	RPGRIP1L	p.Q388H	RPGRIP1-like	50 (0.00)	37 (0.43)	0.56
12-02	Gp3	g.chrX:153628858G>C	Missense Mutation	RPL10	p.R128T	ribosomal protein L10	29 (0.00)	31 (0.29)	0.48
12-02	Gp3	g.chr1:93299218G>C	Splice Site	RPL5		ribosomal protein L5	79 (0.00)	27 (0.59)	1.58
12-02	Gp3	g.chr17:57990151G>T	Missense Mutation	RPS6KB1	p.G100W	ribosomal protein S6 ki	67 (0.00)	65 (0.35)	1.18
12-02	Gp3	g.chr17:78796977C>T	Missense Mutation	RPTOR	p.P364S	regulatory associated pr	18 (0.00)	51 (0.12)	0.43
12-02	Gp3	g.chr6:7187672G>A	Silent	RREB1	p.T59T	ras responsive element	42 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr2:74654385C>A	Missense Mutation	RTKN	p.C374F	rhotekin	58 (0.02)	28 (0.18)	0.48
12-02	Gp3	g.chr2:55253061T>C	Missense Mutation	RTN4	p.E725G	reticulon 4	45 (0.00)	30 (0.23)	0.62
12-02	Gp3	g.chr3:72451231G>A	Intron	RYBP		RING1 and YY1 bindin	50 (0.00)	23 (0.48)	1.28
12-02	Gp3	g.chr3:72456786C>A	Intron	RYBP		RING1 and YY1 bindin	68 (0.00)	21 (0.29)	0.76
12-02	Gp3	g.chr3:72460893C>T	Intron	RYBP		RING1 and YY1 bindin	107 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr3:72463462C>A	Intron	RYBP		RING1 and YY1 bindin	51 (0.00)	61 (0.15)	0.39
12-02	Gp3	g.chr3:72476605C>A	Intron	RYBP		RING1 and YY1 bindin	22 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr1:237955549C>A	Missense Mutation	RYR2	p.P4570T	ryanodine receptor 2 (ca	102 (0.00)	83 (0.17)	0.45
12-02	Gp3	g.chr1:237993849G>A	Missense Mutation	RYR2	p.G4892E	ryanodine receptor 2 (ca	73 (0.00)	11 (0.64)	1.70
12-02	Gp3	g.chr13:23904861G>T	Missense Mutation	SACS	p.S4385Y	sacsin molecular chaper	18 (0.00)	23 (0.30)	0.81
12-02	Gp3	g.chr7:92764166C>G	Silent	SAMD9L	p.L373L	sterile alpha motif doma	131 (0.00)	92 (0.34)	0.90
12-02	Gp3	g.chr6:148854045C>A	Silent	SASH1	p.A559A	SAM and SH3 domain	17 (0.00)	22 (0.27)	0.73
12-02	Gp3	g.chr3:18393591G>T	Missense Mutation	SATB1	p.L558I	SATB homeobox 1	26 (0.00)	12 (0.42)	1.11
12-02	Gp3	g.chr11:9864315G>C	Missense Mutation	SBF2	p.T1038S	SET binding factor 2	55 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr12:46316847G>T	Missense Mutation	SCAF11	p.Q1333K	SR-related CTD-associa	136 (0.00)	64 (0.28)	0.75
12-02	Gp3	g.chr6:155114050C>A	Missense Mutation	SCAF8	p.P139T	SR-related CTD-associa	46 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr2:166848812G>A	Missense Mutation	SCN1A	p.T1630M	sodium channel, voltage	64 (0.00)	53 (0.58)	0.91
12-02	Gp3	g.chr2:165971986G>A	Missense Mutation	SCN3A	p.P1165S	sodium channel, voltage	49 (0.00)	16 (0.50)	0.78
12-02	Gp3	g.chr12:52082631C>A	Missense Mutation	SCN8A	p.P235Q	sodium channel, voltage	81 (0.00)	42 (0.29)	0.76
12-02	Gp3	g.chr12:52159756G>T	Missense Mutation	SCN8A	p.G949V	sodium channel, voltage	100 (0.00)	71 (0.23)	0.60
12-02	Gp3	g.chr6:35210032C>A	Missense Mutation	SCUBE3	p.A490D	signal peptide, CUB do	16 (0.00)	59 (0.17)	0.45
12-02	Gp3	g.chr1:169833544C>G	Missense Mutation	SCYL3	p.K307N	SCY1-like 3 (S. cerevisi	119 (0.00)	35 (0.37)	0.99
12-02	Gp3	g.chr17:75196707C>A	Missense Mutation	SEC14L1	p.Q321K	SEC14-like 1 (S. cerevis	106 (0.00)	92 (0.12)	0.43
12-02	Gp3	g.chr1:169586609G>T	Nonsense Mutation	SELP	p.Y46*	selectin P (granule mem	72 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr9:91994412G>T	Missense Mutation	SEMA4D	p.P599H	sema domain, immunog	50 (0.00)	35 (0.14)	0.38

12-02	Gp3	g.chr5:115818270T>C	Splice Site	SEMA6A	p.I322V	sema domain, transmem	39 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr3:101136460G>A	Silent	SENP7	p.R153R	SUMO1/sentrin specific	36 (0.00)	27 (0.26)	0.69
12-02	Gp3	g.chr14:94942472C>A	Splice Site	SERPINA9		serpin peptidase inhibit	46 (0.00)	50 (0.16)	0.43
12-02	Gp3	g.chr6:2890693C>A	Missense Mutation	SERPINB9	p.D279Y	serpin peptidase inhibit	71 (0.00)	74 (0.20)	0.54
12-02	Gp3	g.chr11:94911882G>A	Nonsense Mutation	SESN3	p.R211*	sestrin 3	21 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr3:9482249G>C	Missense Mutation	SETD5	p.S226T	SET domain containing	33 (0.00)	21 (0.38)	1.02
12-02	Gp3	g.chr3:9515086G>T	Missense Mutation	SETD5	p.R1121L	SET domain containing	45 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr22:26707870C>A	Silent	SEZ6L	p.I606I	seizure related 6 homol	19 (0.00)	48 (0.65)	1.72
12-02	Gp3	g.chr2:198267383C>T	Nonsense Mutation	SF3B1	p.W658*	splicing factor 3b, subu	42 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr8:13947965C>A	Missense Mutation	SGCZ	p.C309F	sarcoglycan, zeta	46 (0.00)	49 (0.43)	1.14
12-02	Gp3	g.chr8:67743543C>A	Silent	SGK3	p.G174G	serum/glucocorticoid re	47 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr8:19218765G>T	Nonsense Mutation	SH2D4A	p.E171*	SH2 domain containing	30 (0.00)	12 (0.42)	0.86
12-02	Gp3	g.chr3:72850756A>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	55 (0.00)	26 (0.23)	0.62
12-02	Gp3	g.chr3:72855317C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	58 (0.00)	22 (0.36)	0.97
12-02	Gp3	g.chr3:72855320G>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	57 (0.00)	21 (0.38)	1.02
12-02	Gp3	g.chr3:72886137C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	109 (0.00)	41 (0.22)	0.59
12-02	Gp3	g.chr19:52034653C>G	Missense Mutation	SIGLEC6	p.G63A	sialic acid binding Ig-lik	21 (0.00)	121 (0.18)	0.69
12-02	Gp3	g.chr17:46257462C>T	Silent	SKAP1	p.E260E	src kinase associated ph	21 (0.00)	40 (0.23)	0.72
12-02	Gp3	g.chr5:127466891T>A	Nonsense Mutation	SLC12A2	p.L394*	solute carrier family 12	33 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr6:133108662C>A	Missense Mutation	SLC18B1	p.V138L	solute carrier family 18,	51 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr2:228564171C>T	Missense Mutation	SLC19A3	p.G87D	solute carrier family 19	29 (0.00)	32 (0.25)	0.67
12-02	Gp3	g.chr1:9640219C>T	Silent	SLC25A33	p.S230S	solute carrier family 25	36 (0.00)	30 (0.23)	0.78
12-02	Gp3	g.chr1:75805306C>T	Missense Mutation	SLC44A5	p.R21K	solute carrier family 44,	104 (0.00)	80 (0.25)	0.67
12-02	Gp3	g.chr13:29291966G>A	Missense Mutation	SLC46A3	p.P57L	solute carrier family 46,	23 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr22:32477903T>A	Missense Mutation	SLC5A1	p.N176K	solute carrier family 5 (	68 (0.00)	73 (0.21)	0.55
12-02	Gp3	g.chr22:32498086G>A	Silent	SLC5A1	p.G509G	solute carrier family 5 (	25 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr21:35468322C>G	Nonsense Mutation	SLC5A3	p.Y275*	solute carrier family 5 (	82 (0.00)	51 (0.20)	0.52
12-02	Gp3	g.chr8:87242406G>T	Missense Mutation	SLC7A13	p.S34Y	solute carrier family 7 (	24 (0.00)	56 (0.21)	0.57
12-02	Gp3	g.chr16:67291338G>A	Splice Site	SLC9A5		solute carrier family 9, s	16 (0.00)	18 (0.28)	0.44
12-02	Gp3	g.chr17:33802396T>A	Missense Mutation	SLFN12L	p.K438M	schlafen family member	117 (0.00)	107 (0.25)	0.67
12-02	Gp3	g.chr17:33802417T>A	Missense Mutation	SLFN12L	p.E431V	schlafen family member	113 (0.00)	107 (0.24)	0.65
12-02	Gp3	g.chr3:57882601C>T	Splice Site	SLMAP	p.D447D	sarcolemma associated	124 (0.00)	72 (0.26)	0.70
12-02	Gp3	g.chr22:24145550G>T	Missense Mutation	SMARCB1	p.R144L	SWI/SNF related, matri	37 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr3:47755931G>T	Missense Mutation	SMARCC1	p.P256T	SWI/SNF related, matri	39 (0.00)	28 (0.21)	0.57
12-02	Gp3	g.chr10:112361622C>A	Missense Mutation	SMC3	p.Q958K	structural maintenance	63 (0.00)	33 (0.27)	0.73

12-02	Gp3	g.chr3:160120546C>A	Missense Mutation	SMC4	p.A134E	structural maintenance c	39 (0.00)	45 (0.51)	1.36
12-02	Gp3	g.chr18:73139411C>G	Silent	SMIM21	p.L36L	small integral membran	62 (0.00)	36 (0.42)	1.11
12-02	Gp3	g.chr1:28280984C>G	Missense Mutation	SMPDL3B	p.Q213E	sphingomyelin phospho	33 (0.00)	29 (0.28)	0.92
12-02	Gp3	g.chr1:153633687A>G	Silent	SNAPIN	p.R107R	SNAP-associated protei	15 (0.00)	28 (0.39)	1.05
12-02	Gp3	g.chr5:121785594C>A	Silent	SNCAIP	p.A596A	synuclein, alpha interact	23 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr7:127544868C>A	Missense Mutation	SND1	p.S508Y	staphylococcal nuclease	29 (0.00)	12 (0.50)	1.33
12-02	Gp3	g.chr17:47010675C>A	Missense Mutation	SNF8	p.K152N	SNF8, ESCRT-II compl	44 (0.00)	43 (0.19)	0.60
12-02	Gp3	g.chr15:25436590C>A	RNA	SNHG14		small nucleolar RNA ho	17 (0.00)	64 (0.33)	1.13
12-02	Gp3	g.chr15:25442760G>A	RNA	SNHG14		small nucleolar RNA ho	20 (0.00)	49 (0.20)	0.70
12-02	Gp3	g.chr20:37062515A>G	RNA	SNORA71D		small nucleolar RNA, H	20 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr2:96956098G>T	Missense Mutation	SNRNP200	p.A903E	small nuclear ribonucle	37 (0.00)	40 (0.47)	1.27
12-02	Gp3	g.chr2:27596984C>T	Silent	SNX17	p.D155D	sorting nexin 17	27 (0.00)	54 (0.22)	0.59
12-02	Gp3	g.chr2:27596987G>T	Missense Mutation	SNX17	p.L156F	sorting nexin 17	27 (0.00)	56 (0.23)	0.62
12-02	Gp3	g.chr8:101608959C>A	Nonsense Mutation	SNX31	p.E296*	sorting nexin 31	68 (0.00)	51 (0.20)	0.52
12-02	Gp3	g.chr10:97101359G>A	Missense Mutation	SORBS1	p.H836Y	sorbin and SH3 domain	39 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr2:231307730G>C	Silent	SP100	p.V62V	SP100 nuclear antigen	43 (0.02)	20 (0.30)	0.80
12-02	Gp3	g.chr2:231150502G>A	Missense Mutation	SP140	p.E474K	SP140 nuclear body pro	45 (0.02)	20 (0.25)	0.67
12-02	Gp3	g.chr2:174820638C>A	Missense Mutation	SP3	p.S201I	Sp3 transcription factor	63 (0.00)	55 (0.42)	0.65
12-02	Gp3	g.chr7:123595132C>T	Nonsense Mutation	SPAM1	p.R346*	sperm adhesion molecul	62 (0.00)	19 (0.32)	0.84
12-02	Gp3	g.chr9:43624970G>T	Silent	SPATA31A6	p.V1239V	SPATA31 subfamily A,	87 (0.00)	90 (0.40)	1.40
12-02	Gp3	g.chr9:84608706G>C	Silent	SPATA31D1	p.L1107L	SPATA31 subfamily D,	38 (0.00)	48 (0.19)	0.50
12-02	Gp3	g.chr9:84534432C>T	RNA	SPATA31D5P		SPATA31 subfamily D,	46 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr3:52741771C>A	Missense Mutation	SPCS1	p.S84R	signal peptidase comple	69 (0.00)	34 (0.35)	0.94
12-02	Gp3	g.chr15:44890856G>T	Missense Mutation	SPG11	p.Q1289K	spastic paraplegia 11 (au	15 (0.00)	17 (0.47)	1.25
12-02	Gp3	g.chr15:65273278G>A	Missense Mutation	SPG21	p.P50L	spastic paraplegia 21 (au	26 (0.00)	24 (0.62)	1.67
12-02	Gp3	g.chr5:147715203C>A	Silent	SPINK9	p.L9L	serine peptidase inhibitc	25 (0.00)	44 (0.36)	0.97
12-02	Gp3	g.chr17:47690822G>T	Intron	SPOP		speckle-type POZ protei	116 (0.00)	99 (0.21)	0.57
12-02	Gp3	g.chr17:47716368G>T	Intron	SPOP		speckle-type POZ protei	32 (0.00)	28 (0.29)	0.76
12-02	Gp3	g.chr17:47748965G>A	Intron	SPOP		speckle-type POZ protei	53 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr15:51041898T>A	Missense Mutation	SPPL2A	p.T38S	signal peptide peptidase	59 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr9:131374506T>A	Missense Mutation	SPTAN1	p.F1670Y	spectrin, alpha, non-eryt	41 (0.00)	25 (0.32)	1.07
12-02	Gp3	g.chr14:65216805G>T	Missense Mutation	SPTB	p.L2224M	spectrin, beta, erythrocy	33 (0.00)	106 (0.20)	0.53
12-02	Gp3	g.chr19:41008789G>A	Silent	SPTBN4	p.K437K	spectrin, beta, non-eryth	18 (0.00)	37 (0.32)	1.14
12-02	Gp3	g.chr16:30731516C>T	Silent	SRCAP	p.L951L	Snf2-related CREBBP a	112 (0.00)	313 (0.15)	0.54
12-02	Gp3	g.chr5:121356079G>A	Missense Mutation	SRFBP1	p.E217K	serum response factor bi	30 (0.00)	13 (0.62)	1.64

12-02	Gp3	g.chr10:70856979C>G	Missense Mutation	SRGN	p.D73E	serglycin	56 (0.00)	47 (0.19)	0.51
12-02	Gp3	g.chr7:87839339G>T	Missense Mutation	SRI	p.T119K	sorcin	89 (0.00)	60 (0.27)	0.71
12-02	Gp3	g.chr6:35806147C>A	Nonsense Mutation	SRPK1	p.G584*	SRSF protein kinase 1	15 (0.00)	28 (0.32)	0.86
12-02	Gp3	g.chr6:35837363G>A	Missense Mutation	SRPK1	p.S436L	SRSF protein kinase 1	116 (0.00)	67 (0.30)	0.80
12-02	Gp3	g.chr1:29476663C>A	Missense Mutation	SRSF4	p.R207L	serine/arginine-rich spli	25 (0.00)	36 (0.39)	1.29
12-02	Gp3	g.chrX:48047112C>A	Silent	SSX5	p.L215L	synovial sarcoma, X bre	29 (0.00)	50 (0.26)	0.43
12-02	Gp3	g.chr11:8747652G>T	Missense Mutation	ST5	p.T482N	suppression of tumorige	72 (0.00)	68 (0.18)	0.47
12-02	Gp3	g.chr12:104121073C>A	Missense Mutation	STAB2	p.P1627Q	stabilin 2	48 (0.00)	24 (0.29)	0.46
12-02	Gp3	g.chr13:33686946C>T	Missense Mutation	STARD13	p.E802K	StAR-related lipid trans	39 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr17:40474502C>T	Silent	STAT3	p.Q633Q	signal transducer and ac	44 (0.00)	35 (0.14)	0.51
12-02	Gp3	g.chr7:87910242G>A	Silent	STEAP4	p.F379F	STEAP family member	109 (0.00)	65 (0.18)	0.49
12-02	Gp3	g.chr19:19119186T>C	Missense Mutation	SUGP2	p.Q797R	SURP and G patch dom	63 (0.00)	76 (0.28)	0.96
12-02	Gp3	g.chr12:56397724C>T	Missense Mutation	SUOX	p.P184L	sulfite oxidase	25 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr1:223441958C>A	Nonsense Mutation	SUSD4	p.E141*	sushi domain containing	54 (0.00)	39 (0.15)	0.41
12-02	Gp3	g.chr11:67957491C>T	Missense Mutation	SUV420H1	p.G18E	suppressor of variegatio	58 (0.02)	37 (0.43)	1.51
12-02	Gp3	g.chr9:113169630T>C	Silent	SVEP1	p.A2727A	sushi, von Willebrand f	86 (0.00)	72 (0.33)	0.89
12-02	Gp3	g.chr6:10961598G>A	Silent	SYCP2L	p.Q772Q	synaptonemal complex	17 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr6:152690127C>A	Missense Mutation	SYNE1	p.A3263S	spectrin repeat containi	41 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr6:152757134G>C	Missense Mutation	SYNE1	p.Q1418E	spectrin repeat containi	21 (0.00)	23 (0.22)	0.58
12-02	Gp3	g.chr14:64443362G>A	Missense Mutation	SYNE2	p.E404K	spectrin repeat containi	47 (0.00)	36 (0.19)	0.52
12-02	Gp3	g.chr14:64634243G>A	Silent	SYNE2	p.K5472K	spectrin repeat containi	72 (0.00)	41 (0.22)	0.59
12-02	Gp3	g.chr14:64683042G>T	Missense Mutation	SYNE2	p.M6412I	spectrin repeat containi	40 (0.00)	23 (0.39)	1.04
12-02	Gp3	g.chr14:64683054G>C	Missense Mutation	SYNE2	p.R6416S	spectrin repeat containi	42 (0.00)	24 (0.38)	1.00
12-02	Gp3	g.chr14:70842443C>A	Missense Mutation	SYNJ2BP	p.D83Y	synaptojanin 2 binding	65 (0.00)	19 (0.26)	0.70
12-02	Gp3	g.chr17:35879117C>A	Missense Mutation	SYNRG	p.A1236S	synergin, gamma	46 (0.00)	41 (0.37)	0.98
12-02	Gp3	g.chr12:33579132T>A	Missense Mutation	SYT10	p.E150D	synaptotagmin X	149 (0.00)	92 (0.36)	0.96
12-02	Gp3	g.chr12:33579178T>C	Missense Mutation	SYT10	p.H135R	synaptotagmin X	130 (0.00)	100 (0.17)	0.45
12-02	Gp3	g.chr11:85407428G>A	Silent	SYTL2	p.T820T	synaptotagmin-like 2	44 (0.02)	34 (0.56)	1.49
12-02	Gp3	g.chr6:132892049A>G	Missense Mutation	TAAR6	p.N197D	trace amine associated	26 (0.00)	17 (0.41)	1.10
12-02	Gp3	g.chr10:71166902G>C	Silent	TACR2	p.L292L	tachykinin receptor 2	15 (0.00)	37 (0.24)	0.65
12-02	Gp3	g.chr18:23845190A>G	Missense Mutation	TAF4B	p.T134A	TAF4b RNA polymeras	142 (0.00)	43 (0.21)	0.56
12-02	Gp3	g.chrX:77394376G>T	Missense Mutation	TAF9B	p.P33T	TAF9B RNA polymera	36 (0.03)	63 (0.24)	0.40
12-02	Gp3	g.chr17:61466060C>T	Missense Mutation	TANC2	p.T845I	tetratricopeptide repeat,	49 (0.00)	33 (0.21)	0.57
12-02	Gp3	g.chr17:27857622G>A	Missense Mutation	TAOK1	p.M782I	TAO kinase 1	49 (0.00)	45 (0.18)	0.47
12-02	Gp3	g.chr5:33461303C>T	Missense Mutation	TARS	p.T518M	threonyl-tRNA syntheta	40 (0.00)	30 (0.17)	0.44

12-02	Gp3	g.chr12:10954406G>A	Missense Mutation	TAS2R7	p.T255I	taste receptor, type 2, m	18 (0.00)	12 (0.50)	0.93
12-02	Gp3	g.chr12:65269534C>A	Missense Mutation	TBC1D30	p.P751H	TBC1 domain family,	28 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr3:17349593G>A	Silent	TBC1D5	p.F343F	TBC1 domain family,	63 (0.00)	13 (0.54)	1.44
12-02	Gp3	g.chr4:141600967C>T	Missense Mutation	TBC1D9	p.D131N	TBC1 domain family,	92 (0.00)	25 (0.28)	0.75
12-02	Gp3	g.chr1:235599871C>A	Missense Mutation	TBCE	p.S304Y	tubulin folding cofactor	58 (0.00)	26 (0.27)	0.72
12-02	Gp3	g.chr1:168260401G>C	Silent	TBX19	p.R69R	T-box 19	69 (0.00)	28 (0.18)	0.48
12-02	Gp3	g.chr22:42608730G>A	Missense Mutation	TCF20	p.S861F	transcription factor 20 (	41 (0.00)	71 (0.24)	0.82
12-02	Gp3	g.chr1:152057504T>C	Missense Mutation	TCHHL1	p.Q885R	trichohyalin-like 1	23 (0.00)	29 (0.21)	0.72
12-02	Gp3	g.chr1:152058269C>A	Missense Mutation	TCHHL1	p.R630I	trichohyalin-like 1	59 (0.00)	58 (0.12)	0.42
12-02	Gp3	g.chr14:104490960C>G	Missense Mutation	TDRD9	p.N887K	tudor domain containing	47 (0.00)	47 (0.47)	1.25
12-02	Gp3	g.chrX:123516567C>T	Missense Mutation	TENM1	p.E2458K	teneurin transmembrane	47 (0.00)	21 (0.48)	0.79
12-02	Gp3	g.chrX:123518535C>A	Missense Mutation	TENM1	p.E2075D	teneurin transmembrane	36 (0.00)	16 (0.94)	1.56
12-02	Gp3	g.chr4:183673017G>A	Missense Mutation	TENM3	p.D1232N	teneurin transmembrane	76 (0.00)	78 (0.27)	0.72
12-02	Gp3	g.chr4:183673030G>A	Missense Mutation	TENM3	p.R1236H	teneurin transmembrane	76 (0.01)	79 (0.27)	0.71
12-02	Gp3	g.chr5:1278815G>A	Missense Mutation	TERT	p.R743W	telomerase reverse trans	17 (0.00)	116 (0.28)	0.76
12-02	Gp3	g.chr10:70333434T>C	Missense Mutation	TET1	p.S447P	tet methylcytosine dioxy	19 (0.00)	29 (0.17)	0.46
12-02	Gp3	g.chr17:56707861G>T	Missense Mutation	TEX14	p.A64E	testis expressed 14	70 (0.00)	64 (0.47)	1.25
12-02	Gp3	g.chr17:62290437C>A	Nonsense Mutation	TEX2	p.E381*	testis expressed 2	39 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr3:133476651A>T	Silent	TF	p.L303L	transferrin	16 (0.00)	18 (0.44)	1.19
12-02	Gp3	g.chr6:50803808G>A	Missense Mutation	TFAP2B	p.M212I	transcription factor AP-	44 (0.00)	70 (0.30)	0.80
12-02	Gp3	g.chr21:43771015A>T	Missense Mutation	TFF2	p.C18S	trefoil factor 2	15 (0.00)	46 (0.22)	0.77
12-02	Gp3	g.chr3:195780359G>T	Missense Mutation	TFRC	p.T657K	transferrin receptor	24 (0.00)	14 (0.50)	1.33
12-02	Gp3	g.chr8:133945878A>G	Missense Mutation	TG	p.Y1630C	thyroglobulin	21 (0.00)	13 (0.38)	1.03
12-02	Gp3	g.chr3:30686397G>C	Missense Mutation	TGFBR2	p.V85L	transforming growth fac	27 (0.00)	20 (0.25)	0.67
12-02	Gp3	g.chr11:134119082C>A	Missense Mutation	THYN1	p.E153D	thymocyte nuclear prote	55 (0.00)	19 (0.42)	1.12
12-02	Gp3	g.chr15:90167004G>T	Nonsense Mutation	TICRR	p.E1155*	TOPBP1-interacting ch	32 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr3:114026778C>A	Missense Mutation	TIGIT	p.L179I	T cell immunoreceptor	70 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr6:54254647G>A	Missense Mutation	TINAG	p.R452Q	tubulointerstitial nephrit	31 (0.00)	22 (0.32)	0.85
12-02	Gp3	g.chr6:43468505G>T	Missense Mutation	TJAP1	p.R41S	tight junction associated	32 (0.00)	56 (0.25)	0.67
12-02	Gp3	g.chr15:30053453G>T	Missense Mutation	TJP1	p.S304Y	tight junction protein 1	17 (0.00)	11 (0.73)	1.94
12-02	Gp3	g.chr9:35721775A>T	Missense Mutation	TLN1	p.L325Q	talin 1	29 (0.00)	10 (0.60)	1.60
12-02	Gp3	g.chrX:12905384C>T	Missense Mutation	TLR7	p.T586I	toll-like receptor 7	23 (0.00)	11 (0.91)	1.52
12-02	Gp3	g.chr15:102182682C>T	Silent	TM2D3	p.*222*	TM2 domain containing	54 (0.00)	48 (0.42)	1.11
12-02	Gp3	g.chr10:98287907T>A	Silent	TM9SF3	p.A474A	transmembrane 9 superf	124 (0.01)	17 (0.29)	0.78
12-02	Gp3	g.chr17:41368509G>T	Missense Mutation	TMEM106A	p.M157I	transmembrane protein	72 (0.00)	77 (0.13)	0.42

12-02	Gp3	g.chr7:12263868G>A	Missense Mutation	TMEM106B	p.A100T	transmembrane protein	89 (0.00)	36 (0.64)	1.70
12-02	Gp3	g.chr12:44770413T>C	Silent	TMEM117	p.D268D	transmembrane protein	26 (0.00)	24 (0.33)	0.89
12-02	Gp3	g.chr19:36038275C>T	Nonsense Mutation	TMEM147	p.R201*	transmembrane protein	18 (0.00)	38 (0.21)	0.56
12-02	Gp3	g.chr6:130762909G>A	Missense Mutation	TMEM200A	p.V448I	transmembrane protein	19 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr3:100277349C>A	Missense Mutation	TMEM45A	p.F184L	transmembrane protein	43 (0.00)	34 (0.21)	0.55
12-02	Gp3	g.chr21:34823166G>T	Missense Mutation	TMEM50B	p.L146M	transmembrane protein	23 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr21:34832806C>T	Missense Mutation	TMEM50B	p.R96Q	transmembrane protein	70 (0.00)	40 (0.17)	0.47
12-02	Gp3	g.chr10:45430320T>A	Missense Mutation	TMEM72	p.I71N	transmembrane protein	19 (0.00)	35 (0.23)	0.61
12-02	Gp3	g.chr8:109797266C>A	Missense Mutation	TMEM74	p.W21L	transmembrane protein	33 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr3:69092059A>C	Missense Mutation	TMF1	p.I528S	TATA element modulat	50 (0.02)	34 (0.15)	0.39
12-02	Gp3	g.chr21:42854759C>G	Intron	TMPRSS2		transmembrane protease	86 (0.00)	24 (0.62)	0.55
12-02	Gp3	g.chr6:47251962T>G	Missense Mutation	TNFRSF21	p.T319P	tumor necrosis factor re	31 (0.00)	25 (0.28)	0.75
12-02	Gp3	g.chr16:24817028C>A	Missense Mutation	TNRC6A	p.Q1409K	trinucleotide repeat cont	44 (0.00)	29 (0.21)	0.55
12-02	Gp3	g.chr17:76060904G>C	Missense Mutation	TNRC6C	p.A830P	trinucleotide repeat cont	20 (0.00)	44 (0.16)	0.58
12-02	Gp3	g.chr20:39750417G>A	Missense Mutation	TOP1	p.A678T	topoisomerase (DNA) I	88 (0.00)	34 (0.18)	0.47
12-02	Gp3	g.chr17:38555073A>G	Silent	TOP2A	p.Y1135Y	topoisomerase (DNA) I	64 (0.00)	46 (0.15)	0.41
12-02	Gp3	g.chr17:38569100C>A	Missense Mutation	TOP2A	p.D234Y	topoisomerase (DNA) I	44 (0.00)	33 (0.27)	0.73
12-02	Gp3	g.chr3:133368251A>T	Missense Mutation	TOPBP1	p.Y494N	topoisomerase (DNA) I	48 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr17:7583487C>A	Intron	TP53		tumor protein p53	83 (0.00)	30 (0.23)	0.42
12-02	Gp3	g.chr12:72366489C>A	Missense Mutation	TPH2	p.L267M	tryptophan hydroxylase	38 (0.00)	21 (0.24)	0.63
12-02	Gp3	g.chr1:186304610G>C	Missense Mutation	TPR	p.Q1591E	translocated promoter re	103 (0.00)	50 (0.22)	0.59
12-02	Gp3	g.chr13:41407011G>A	RNA	TPTE2P5		transmembrane phospho	16 (0.00)	45 (0.27)	0.71
12-02	Gp3	g.chr11:36511543C>A	Missense Mutation	TRAF6	p.G472C	TNF receptor-associate	88 (0.00)	35 (0.20)	0.53
12-02	Gp3	g.chr3:42235335A>G	Missense Mutation	TRAK1	p.E233G	trafficking protein, kine	44 (0.00)	28 (0.46)	1.24
12-02	Gp3	g.chr3:36873409G>T	Silent	TRANK1	p.V1961V	tetratricopeptide repeat	47 (0.00)	34 (0.21)	0.55
12-02	Gp3	g.chr3:36873876C>T	Missense Mutation	TRANK1	p.D1806N	tetratricopeptide repeat	57 (0.00)	50 (0.30)	0.80
12-02	Gp3	g.chr3:36887807C>A	Missense Mutation	TRANK1	p.R1114L	tetratricopeptide repeat	53 (0.00)	32 (0.16)	0.42
12-02	Gp3	g.chr3:36898759G>T	Missense Mutation	TRANK1	p.S224R	tetratricopeptide repeat	118 (0.00)	134 (0.37)	1.00
12-02	Gp3	g.chr14:22690311C>A	RNA	TRAV35		T cell receptor alpha va	27 (0.00)	34 (0.24)	0.63
12-02	Gp3	g.chr3:140407162C>A	Missense Mutation	TRIM42	p.D546E	tripartite motif containi	16 (0.00)	39 (0.23)	0.62
12-02	Gp3	g.chr1:248039662T>A	Silent	TRIM58	p.L444L	tripartite motif containi	19 (0.00)	25 (0.92)	2.45
12-02	Gp3	g.chr3:32933116G>A	Missense Mutation	TRIM71	p.R807H	tripartite motif containi	16 (0.00)	43 (0.19)	0.50
12-02	Gp3	g.chr5:14391099C>G	Splice Site	TRIO	p.D1406E	trio Rho guanine nucleo	48 (0.00)	37 (0.16)	0.43
12-02	Gp3	g.chrX:100278457A>G	Splice Site	TRMT2B		tRNA methyltransferase	37 (0.00)	16 (0.31)	0.52
12-02	Gp3	g.chr4:8453703C>A	Missense Mutation	TRMT44	p.T324N	tRNA methyltransferase	51 (0.00)	74 (0.20)	0.54

12-02	Gp3	g.chr3:142511685G>A	Missense Mutation	TRPC1	p.R486Q	transient receptor potent	69 (0.00)	14 (0.43)	1.14
12-02	Gp3	g.chr11:101341937G>C	Missense Mutation	TRPC6	p.Q718E	transient receptor potent	64 (0.00)	31 (0.39)	1.03
12-02	Gp3	g.chr9:73442927C>T	Missense Mutation	TRPM3	p.R270Q	transient receptor potent	56 (0.00)	25 (0.20)	0.53
12-02	Gp3	g.chr9:135781021C>A	Silent	TSC1	p.V648V	tuberous sclerosis 1	43 (0.00)	30 (0.27)	0.71
12-02	Gp3	g.chr14:81554324C>T	Missense Mutation	TSHR	p.T115I	thyroid stimulating horn	27 (0.00)	18 (0.28)	0.74
12-02	Gp3	g.chr14:81609744G>C	Missense Mutation	TSHR	p.V448L	thyroid stimulating horn	83 (0.00)	32 (0.16)	0.42
12-02	Gp3	g.chr18:73000416C>T	Silent	TSHZ1	p.L1018L	teashirt zinc finger hom	38 (0.00)	95 (0.16)	0.42
12-02	Gp3	g.chr20:51870976G>T	Missense Mutation	TSHZ2	p.V327F	teashirt zinc finger hom	24 (0.00)	35 (0.14)	0.38
12-02	Gp3	g.chr19:31769454G>T	Silent	TSHZ3	p.T415T	teashirt zinc finger hom	16 (0.00)	68 (0.21)	0.55
12-02	Gp3	g.chr9:135277342C>T	Silent	TTF1	p.E289E	transcription terminatio	25 (0.00)	32 (0.31)	0.83
12-02	Gp3	g.chr1:117617738C>A	Missense Mutation	TTF2	p.L178I	transcription terminatio	61 (0.00)	73 (0.18)	0.47
12-02	Gp3	g.chr2:179397138G>A	Missense Mutation	TTN	p.T34735M	titin	43 (0.00)	48 (0.40)	0.62
12-02	Gp3	g.chr2:179442145C>A	Missense Mutation	TTN	p.G22973C	titin	47 (0.00)	28 (0.29)	0.44
12-02	Gp3	g.chr2:179486027C>G	Missense Mutation	TTN	p.V15140L	titin	58 (0.00)	17 (0.71)	1.10
12-02	Gp3	g.chr2:179501181C>A	Missense Mutation	TTN	p.C13758F	titin	42 (0.00)	22 (0.77)	1.20
12-02	Gp3	g.chr2:179501436G>A	Missense Mutation	TTN	p.P13673L	titin	58 (0.00)	16 (0.31)	0.49
12-02	Gp3	g.chr12:49579161C>A	Missense Mutation	TUBA1A	p.A330S	tubulin, alpha 1a	22 (0.00)	81 (0.19)	0.49
12-02	Gp3	g.chr12:49522361C>A	Nonsense Mutation	TUBA1B	p.G246*	tubulin, alpha 1b	49 (0.00)	38 (0.16)	0.42
12-02	Gp3	g.chr12:49666937C>A	Missense Mutation	TUBA1C	p.A426D	tubulin, alpha 1c	67 (0.00)	75 (0.20)	0.53
12-02	Gp3	g.chr18:9886890A>G	Silent	TXNDC2	p.S138S	thioredoxin domain con	35 (0.00)	28 (0.46)	1.24
12-02	Gp3	g.chr18:672920G>T	Missense Mutation	TYMS	p.D255Y	thymidylate synthetase	64 (0.00)	36 (0.31)	0.81
12-02	Gp3	g.chr7:66514944G>A	Silent	TYW1	p.K331K	tRNA-yW synthesizing	57 (0.00)	72 (0.28)	0.74
12-02	Gp3	g.chr7:66515021C>A	Missense Mutation	TYW1	p.T357N	tRNA-yW synthesizing	37 (0.00)	27 (0.19)	0.49
12-02	Gp3	g.chr3:142751748C>G	Missense Mutation	U2SURP	p.T578S	U2 snRNP-associated S	19 (0.00)	17 (0.29)	0.78
12-02	Gp3	g.chr9:33944417C>A	Missense Mutation	UBAP2	p.Q497H	ubiquitin associated pro	38 (0.00)	32 (0.22)	0.58
12-02	Gp3	g.chr11:118263500C>T	Silent	UBE4A	p.A995A	ubiquitination factor E4.	24 (0.00)	25 (0.64)	1.71
12-02	Gp3	g.chr6:42619772G>T	Silent	UBR2	p.A859A	ubiquitin protein ligase	24 (0.00)	16 (0.38)	1.00
12-02	Gp3	g.chr8:103323643C>A	Missense Mutation	UBR5	p.D828Y	ubiquitin protein ligase	130 (0.00)	55 (0.15)	0.39
12-02	Gp3	g.chr13:76141399C>T	Missense Mutation	UCHL3	p.S126F	ubiquitin carboxyl-termi	57 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr4:39507325C>A	Missense Mutation	UGDH	p.R317L	UDP-glucose 6-dehydro	69 (0.00)	25 (0.28)	0.75
12-02	Gp3	g.chr4:69426370A>T	Missense Mutation	UGT2B17	p.V297E	UDP glucuronosyltrans	36 (0.00)	21 (0.57)	1.52
12-02	Gp3	g.chr4:70146274G>A	Missense Mutation	UGT2B28	p.S19N	UDP glucuronosyltrans	227 (0.00)	50 (0.24)	0.64
12-02	Gp3	g.chr17:19698941C>T	Missense Mutation	ULK2	p.D699N	unc-51 like autophagy a	51 (0.00)	13 (0.46)	1.23
12-02	Gp3	g.chr8:35579755T>C	Missense Mutation	UNC5D	p.L326S	unc-5 homolog D (C. el	19 (0.00)	33 (0.15)	0.40
12-02	Gp3	g.chr2:210698857G>T	Missense Mutation	UNC80	p.E964D	unc-80 homolog (C. ele	67 (0.00)	42 (0.36)	0.95

12-02	Gp3	g.chr2:210837021G>C	Missense Mutation	UNC80	p.V2714L	unc-80 homolog (C. ele	36 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr7:48141508G>T	Missense Mutation	UPP1	p.D84Y	uridine phosphorylase 1	24 (0.00)	73 (0.26)	0.69
12-02	Gp3	g.chr16:21968622C>G	Missense Mutation	UQCRC2	p.Q34E	ubiquinol-cytochrome c	37 (0.00)	30 (0.17)	0.44
12-02	Gp3	g.chr1:229772149C>A	Missense Mutation	URB2	p.L597M	URB2 ribosome biogen	33 (0.00)	34 (0.15)	0.39
12-02	Gp3	g.chr16:84778667G>A	Missense Mutation	USP10	p.A194T	ubiquitin specific peptid	29 (0.00)	55 (0.40)	0.64
12-02	Gp3	g.chr3:49155192C>A	Missense Mutation	USP19	p.A124S	ubiquitin specific peptid	33 (0.00)	65 (0.20)	0.53
12-02	Gp3	g.chr1:55620435G>A	Missense Mutation	USP24	p.T488I	ubiquitin specific peptid	44 (0.00)	22 (0.27)	0.73
12-02	Gp3	g.chr2:219362537C>T	Missense Mutation	USP37	p.E329K	ubiquitin specific peptid	25 (0.00)	21 (0.33)	0.89
12-02	Gp3	g.chr3:49335984C>T	Splice Site	USP4		ubiquitin specific peptid	63 (0.00)	38 (0.29)	0.77
12-02	Gp3	g.chr10:11531171C>T	Missense Mutation	USP6NL	p.M198I	USP6 N-terminal like	38 (0.00)	13 (0.54)	1.44
12-02	Gp3	g.chr6:144809821C>T	Nonsense Mutation	UTRN	p.Q1329*	utrophin	83 (0.00)	33 (0.18)	0.48
12-02	Gp3	g.chr1:7839694G>A	Missense Mutation	VAMP3	p.V70I	vesicle-associated mem	42 (0.00)	44 (0.32)	1.06
12-02	Gp3	g.chr19:6843173C>A	Missense Mutation	VAV1	p.L670I	vav 1 guanine nucleotid	38 (0.00)	18 (0.33)	1.24
12-02	Gp3	g.chr19:53762707C>T	Missense Mutation	VN1R2	p.P360L	vomeronasal 1 receptor	62 (0.00)	23 (0.35)	0.93
12-02	Gp3	g.chr3:51517767G>A	Silent	VPRBP	p.G26G	Vpr (HIV-1) binding pr	37 (0.00)	62 (0.29)	0.77
12-02	Gp3	g.chr9:79954534C>T	Missense Mutation	VPS13A	p.L2161F	vacuolar protein sorting	43 (0.00)	16 (0.38)	1.00
12-02	Gp3	g.chr12:122745868G>C	Missense Mutation	VPS33A	p.S141R	vacuolar protein sorting	23 (0.00)	53 (0.28)	0.45
12-02	Gp3	g.chr11:123988985C>A	Nonsense Mutation	VWA5A	p.C128*	von Willebrand factor A	26 (0.00)	34 (0.24)	0.63
12-02	Gp3	g.chr4:85678111C>A	Missense Mutation	WDFY3	p.V1798F	WD repeat and FYVE d	15 (0.00)	36 (0.28)	0.74
12-02	Gp3	g.chr4:177069470C>A	Missense Mutation	WDR17	p.H627Q	WD repeat domain 17	34 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr4:39274642C>A	Missense Mutation	WDR19	p.L1176I	WD repeat domain 19	80 (0.00)	52 (0.21)	0.56
12-02	Gp3	g.chr1:118483795G>T	Missense Mutation	WDR3	p.D280Y	WD repeat domain 3	53 (0.00)	15 (0.33)	0.89
12-02	Gp3	g.chr12:122404860G>A	Splice Site	WDR66		WD repeat domain 66	36 (0.00)	118 (0.31)	0.48
12-02	Gp3	g.chr19:38379838C>A	Missense Mutation	WDR87	p.E1452D	WD repeat domain 87	50 (0.00)	46 (0.22)	0.58
12-02	Gp3	g.chr19:33651330C>A	Silent	WDR88	p.L336L	WD repeat domain 88	77 (0.00)	49 (0.24)	0.65
12-02	Gp3	g.chr8:38146035C>A	Missense Mutation	WHSC1L1	p.W1157C	Wolf-Hirschhorn syndr	59 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr6:112382276G>A	Missense Mutation	WISP3	p.R44H	WNT1 inducible signali	31 (0.00)	26 (0.31)	0.82
12-02	Gp3	g.chr12:990024C>A	Nonsense Mutation	WNK1	p.Y990*	WNK lysine deficient p	27 (0.00)	13 (0.38)	1.03
12-02	Gp3	g.chr17:40940179C>T	Missense Mutation	WNK4	p.P632L	WNK lysine deficient p	32 (0.00)	37 (0.22)	0.77
12-02	Gp3	g.chr4:184236868G>A	Missense Mutation	WWC2	p.A1189T	WW and C2 domain co	58 (0.00)	47 (0.17)	0.45
12-02	Gp3	g.chr8:87473466C>G	Missense Mutation	WWP1	p.T838R	WW domain containing	32 (0.00)	27 (0.22)	0.59
12-02	Gp3	g.chr3:14200805G>T	Intron	XPC		xeroderma pigmentosu	54 (0.00)	47 (0.17)	0.45
12-02	Gp3	g.chr3:14205299C>G	Intron	XPC		xeroderma pigmentosu	64 (0.00)	47 (0.36)	0.96
12-02	Gp3	g.chr3:14213076G>A	Intron	XPC		xeroderma pigmentosu	15 (0.00)	18 (0.61)	1.63
12-02	Gp3	g.chr3:141162384G>T	Missense Mutation	ZBTB38	p.R385M	zinc finger and BTB do	144 (0.00)	59 (0.34)	0.90

12-02	Gp3	g.chr16:11857362C>G	Silent	ZC3H7A	p.L658L	zinc finger CCCH-type	36 (0.00)	43 (0.30)	0.81
12-02	Gp3	g.chr9:37304241C>G	Silent	ZCCHC7	p.A237A	zinc finger, CCHC dom	69 (0.00)	80 (0.28)	0.73
12-02	Gp3	g.chr3:44975392G>A	Silent	ZDHHC3	p.F206F	zinc finger, DHHC-type	42 (0.00)	50 (0.38)	1.01
12-02	Gp3	g.chr10:46122064A>T	Missense Mutation	ZFAND4	p.S403T	zinc finger, AN1-type d	25 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr19:57065950G>A	Missense Mutation	ZFP28	p.R599K	ZFP28 zinc finger prote	62 (0.00)	25 (0.40)	1.07
12-02	Gp3	g.chr3:15127415C>A	Missense Mutation	ZFYVE20	p.D115Y	zinc finger, FYVE dom	65 (0.00)	37 (0.41)	1.08
12-02	Gp3	g.chr1:52810518G>T	Missense Mutation	ZFYVE9	p.A1340S	zinc finger, FYVE dom	26 (0.00)	30 (0.37)	0.98
12-02	Gp3	g.chr8:124268084G>C	Missense Mutation	ZHX1	p.L35V	zinc fingers and homeob	61 (0.00)	17 (0.53)	1.41
12-02	Gp3	g.chr8:123964256G>T	Missense Mutation	ZHX2	p.G169V	zinc fingers and homeob	17 (0.00)	38 (0.18)	0.49
12-02	Gp3	g.chr20:39833311G>T	Nonsense Mutation	ZHX3	p.C82*	zinc fingers and homeob	65 (0.00)	72 (0.15)	0.41
12-02	Gp3	g.chr19:57654000G>T	Silent	ZIM3	p.S4S	zinc finger, imprinted 3	30 (0.00)	64 (0.16)	0.42
12-02	Gp3	g.chr3:178745465G>T	Silent	ZMAT3	p.R176R	zinc finger, matrin-type	35 (0.00)	18 (0.33)	0.89
12-02	Gp3	g.chr7:64168806T>C	Silent	ZNF107	p.T708T	zinc finger protein 107	30 (0.00)	36 (0.33)	1.11
12-02	Gp3	g.chr3:44670656G>A	Missense Mutation	ZNF197	p.E4K	zinc finger protein 197	71 (0.00)	40 (0.47)	1.27
12-02	Gp3	g.chr19:12246643G>A	Missense Mutation	ZNF20	p.S27F	zinc finger protein 20	92 (0.00)	106 (0.12)	0.42
12-02	Gp3	g.chr19:12246665C>A	Nonsense Mutation	ZNF20	p.E20*	zinc finger protein 20	88 (0.00)	99 (0.11)	0.38
12-02	Gp3	g.chr19:22156230T>A	Missense Mutation	ZNF208	p.T536S	zinc finger protein 208	55 (0.00)	49 (0.24)	0.85
12-02	Gp3	g.chr19:53304387G>A	Silent	ZNF28	p.H237H	zinc finger protein 28	45 (0.00)	28 (0.25)	0.67
12-02	Gp3	g.chr5:150322148C>G	RNA	ZNF300P1		zinc finger protein 300	42 (0.00)	22 (0.23)	0.61
12-02	Gp3	g.chr10:38345036G>T	Nonsense Mutation	ZNF33A	p.E662*	zinc finger protein 33A	50 (0.00)	46 (0.17)	0.46
12-02	Gp3	g.chr19:53651958C>G	Missense Mutation	ZNF347	p.E84Q	zinc finger protein 347	98 (0.00)	24 (0.25)	0.67
12-02	Gp3	g.chr3:21552471C>A	Missense Mutation	ZNF385D	p.K107N	zinc finger protein 385D	17 (0.00)	16 (0.31)	0.83
12-02	Gp3	g.chr10:31138920G>C	Missense Mutation	ZNF438	p.I138M	zinc finger protein 438	55 (0.00)	49 (0.14)	0.38
12-02	Gp3	g.chr9:109689859T>C	Silent	ZNF462	p.N67N	zinc finger protein 462	108 (0.00)	94 (0.18)	0.48
12-02	Gp3	g.chr9:109701274G>T	Missense Mutation	ZNF462	p.V1011F	zinc finger protein 462	88 (0.00)	68 (0.60)	1.61
12-02	Gp3	g.chr9:95609765G>C	Missense Mutation	ZNF484	p.T435S	zinc finger protein 484	53 (0.00)	20 (0.25)	0.80
12-02	Gp3	g.chr19:31039081G>T	Missense Mutation	ZNF536	p.G852V	zinc finger protein 536	21 (0.00)	26 (0.19)	0.51
12-02	Gp3	g.chr19:12639427G>C	Nonsense Mutation	ZNF564	p.Y29*	zinc finger protein 564	34 (0.00)	24 (0.38)	1.30
12-02	Gp3	g.chr19:58929080C>A	Missense Mutation	ZNF584	p.Q399K	zinc finger protein 584	22 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr15:85341118C>T	Silent	ZNF592	p.V806V	zinc finger protein 592	21 (0.00)	26 (0.42)	1.13
12-02	Gp3	g.chr5:123977099C>T	Splice Site	ZNF608		zinc finger protein 608	39 (0.00)	31 (0.23)	0.60
12-02	Gp3	g.chr1:91405466C>T	Missense Mutation	ZNF644	p.R482H	zinc finger protein 644	59 (0.00)	20 (0.40)	1.07
12-02	Gp3	g.chr9:40772410T>A	Silent	ZNF658	p.V955V	zinc finger protein 658	35 (0.00)	34 (0.29)	1.03
12-02	Gp3	g.chr19:53669557C>T	Silent	ZNF665	p.G62G	zinc finger protein 665	58 (0.00)	92 (0.17)	0.46
12-02	Gp3	g.chr19:12015784C>A	Missense Mutation	ZNF69	p.P191H	zinc finger protein 69	25 (0.00)	18 (0.50)	1.73

12-02	Gp3	g.chr19:21281633C>G	Missense Mutation	ZNF714	p.S20C	zinc finger protein 714	114 (0.00)	30 (0.37)	1.27
12-02	Gp3	g.chr19:53959648C>T	RNA	ZNF761		zinc finger protein 761	37 (0.00)	44 (0.32)	0.85
12-02	Gp3	g.chr16:89289592G>C	Missense Mutation	ZNF778	p.V49L	zinc finger protein 778	17 (0.00)	29 (0.34)	0.55
12-02	Gp3	g.chr19:40541505C>A	Nonsense Mutation	ZNF780B	p.E273*	zinc finger protein 780B	56 (0.00)	66 (0.30)	1.06
12-02	Gp3	g.chr19:52663830G>T	Missense Mutation	ZNF836	p.F10L	zinc finger protein 836	83 (0.00)	88 (0.22)	0.58
12-02	Gp3	g.chr19:52580251C>T	Silent	ZNF841	p.R34R	zinc finger protein 841	74 (0.01)	58 (0.33)	0.87
12-02	Gp3	g.chr9:115760372A>G	lincRNA	ZNF883		zinc finger protein 883	17 (0.00)	14 (0.43)	1.14
12-02	Gp3	g.chr19:23542697G>C	Silent	ZNF91	p.G1028G	zinc finger protein 91	51 (0.00)	57 (0.21)	0.73
12-02	Gp3	g.chr19:22574433C>A	Missense Mutation	ZNF98	p.R535I	zinc finger protein 98	26 (0.00)	15 (0.33)	1.15
12-02	Gp3	g.chr20:47887522G>T	Missense Mutation	ZNFX1	p.S276Y	zinc finger, NFX1-type	33 (0.00)	14 (0.36)	0.95
12-02	Gp3	g.chr15:43653933T>A	Nonsense Mutation	ZSCAN29	p.K633*	zinc finger and SCAN d	91 (0.00)	31 (0.19)	0.52
12-02	Gp3	g.chr5:60839313C>A	Silent	ZSWIM6	p.T939T	zinc finger, SWIM-type	45 (0.00)	39 (0.21)	0.55
12-02	Gp3	g.chr17:3967998G>A	Missense Mutation	ZZEF1	p.R1459C	zinc finger, ZZ-type wit	17 (0.00)	23 (0.22)	0.39
12-02	Gp4	g.chr17:67178897C>T	Silent	ABCA10	p.L850L	ATP-binding cassette, s	50 (0.00)	37 (0.30)	0.79
12-02	Gp4	g.chr5:5209280G>A	Missense Mutation	ADAMTS16	p.G509E	ADAM metallopeptidas	130 (0.00)	28 (0.18)	0.48
12-02	Gp4	g.chr1:202914155G>T	Missense Mutation	ADIPOR1	p.H191Q	adiponectin receptor 1	110 (0.00)	19 (0.32)	0.84
12-02	Gp4	g.chr10:76468088C>A	Missense Mutation	ADK	p.S325Y	adenosine kinase	33 (0.00)	33 (0.24)	0.65
12-02	Gp4	g.chr1:36492763C>T	Silent	AGO3	p.P485P	argonaute RISC catalyti	45 (0.00)	53 (0.25)	0.65
12-02	Gp4	g.chr4:114278572C>G	Missense Mutation	ANK2	p.S2900C	ankyrin 2, neuronal	126 (0.00)	44 (0.20)	0.55
12-02	Gp4	g.chr9:95650549C>G	RNA	ANKRD19P		ankyrin repeat domain 1	57 (0.00)	30 (0.20)	0.85
12-02	Gp4	g.chr16:4780000C>A	Missense Mutation	ANKS3	p.V51L	ankyrin repeat and steril	107 (0.00)	133 (0.14)	0.48
12-02	Gp4	g.chr12:57874614C>A	Missense Mutation	ARHGAP9	p.S28I	Rho GTPase activating	37 (0.00)	17 (0.29)	0.78
12-02	Gp4	g.chr1:183596706C>T	Silent	ARPC5	p.G142G	actin related protein 2/3	82 (0.00)	25 (0.24)	0.50
12-02	Gp4	g.chr9:119488112G>A	Missense Mutation	ASTN2	p.T864I	astrotactin 2	26 (0.00)	35 (0.23)	0.97
12-02	Gp4	g.chr2:25965484G>A	Missense Mutation	ASXL2	p.T1241I	additional sex combs lik	91 (0.00)	36 (0.22)	0.59
12-02	Gp4	g.chr3:11402189G>C	Silent	ATG7	p.S538S	autophagy related 7	100 (0.00)	29 (0.34)	0.92
12-02	Gp4	g.chr15:25924600G>C	Missense Mutation	ATP10A	p.A1463G	ATPase, class V, type 1	34 (0.00)	44 (0.18)	0.64
12-02	Gp4	g.chr4:47578884T>A	Missense Mutation	ATP10D	p.L1154H	ATPase, class V, type 1	40 (0.00)	47 (0.28)	0.74
12-02	Gp4	g.chr1:160145974C>A	Missense Mutation	ATP1A4	p.L802I	ATPase, Na+/K+ transp	47 (0.00)	47 (0.23)	0.62
12-02	Gp4	g.chrX:119504659C>A	Missense Mutation	ATP1B4	p.P140T	ATPase, Na+/K+ transp	40 (0.00)	15 (0.60)	1.00
12-02	Gp4	g.chr10:7841022C>A	Nonsense Mutation	ATP5C1	p.S98*	ATP synthase, H+ trans	46 (0.00)	35 (0.14)	0.38
12-02	Gp4	g.chr3:63973759G>C	Missense Mutation	ATXN7	p.A374P	ataxin 7	33 (0.00)	12 (0.42)	1.11
12-02	Gp4	g.chr17:63554478G>A	Silent	AXIN2	p.G87G	axin 2	17 (0.00)	108 (0.17)	0.44
12-02	Gp4	g.chr20:48259037G>T	Missense Mutation	B4GALT5	p.R192S	UDP-Gal:betaGlcNAc b	18 (0.00)	14 (0.43)	1.14
12-02	Gp4	g.chr21:11072874G>A	RNA	BAGE2		B melanoma antigen far	24 (0.00)	41 (0.22)	0.59

12-02	Gp4	g.chr2:32670704G>A	Silent	BIRC6	p.R1484R	baculoviral IAP repeat c	66 (0.00)	51 (0.24)	0.63
12-02	Gp4	g.chr2:32800247C>A	Missense Mutation	BIRC6	p.P4390Q	baculoviral IAP repeat c	160 (0.01)	50 (0.20)	0.53
12-02	Gp4	g.chr15:91348569T>C	Intron	BLM		Bloom syndrome, RecQ	46 (0.00)	181 (0.17)	0.44
12-02	Gp4	g.chr15:91358394G>T	Missense Mutation	BLM	p.S1249I	Bloom syndrome, RecQ	43 (0.00)	36 (0.17)	0.44
12-02	Gp4	g.chr2:198646561G>A	Missense Mutation	BOLL	p.S5L	boule-like RNA-binding	44 (0.00)	14 (0.43)	1.14
12-02	Gp4	g.chr17:41230870G>T	Intron	BRCA1		breast cancer 1, early on	28 (0.00)	25 (0.20)	0.53
12-02	Gp4	g.chr17:41230871G>T	Intron	BRCA1		breast cancer 1, early on	28 (0.00)	25 (0.20)	0.53
12-02	Gp4	g.chr10:98741863C>A	Missense Mutation	C10orf12	p.P239Q	chromosome 10 open re	55 (0.00)	22 (0.27)	0.73
12-02	Gp4	g.chr11:76183749G>A	Missense Mutation	C11orf30	p.A339T	chromosome 11 open re	48 (0.00)	12 (0.50)	1.33
12-02	Gp4	g.chr6:4087934G>C	Missense Mutation	C6orf201	p.R20P	chromosome 6 open rea	44 (0.00)	45 (0.24)	0.65
12-02	Gp4	g.chr8:86250662G>A	Silent	CA1	p.S18S	carbonic anhydrase I	26 (0.00)	21 (0.24)	0.63
12-02	Gp4	g.chr19:13563723C>A	Missense Mutation	CACNA1A	p.W169L	calcium channel, voltag	147 (0.00)	75 (0.20)	0.69
12-02	Gp4	g.chr3:85044605C>T	Intron	CADM2		cell adhesion molecule	47 (0.00)	16 (0.31)	0.83
12-02	Gp4	g.chr3:85092397A>G	Intron	CADM2		cell adhesion molecule	117 (0.00)	48 (0.17)	0.44
12-02	Gp4	g.chr3:85155585C>T	Intron	CADM2		cell adhesion molecule	56 (0.00)	35 (0.34)	0.91
12-02	Gp4	g.chr3:85314627A>G	Intron	CADM2		cell adhesion molecule	24 (0.00)	29 (0.62)	1.66
12-02	Gp4	g.chr3:85457847C>T	Intron	CADM2		cell adhesion molecule	45 (0.02)	11 (0.64)	1.70
12-02	Gp4	g.chr3:85469207G>T	Intron	CADM2		cell adhesion molecule	76 (0.00)	21 (0.24)	0.63
12-02	Gp4	g.chr3:85481342G>A	Intron	CADM2		cell adhesion molecule	37 (0.00)	46 (0.57)	1.51
12-02	Gp4	g.chr3:85593815C>G	Intron	CADM2		cell adhesion molecule	26 (0.00)	41 (0.15)	0.39
12-02	Gp4	g.chr3:85961994C>T	Intron	CADM2		cell adhesion molecule	27 (0.00)	15 (0.60)	1.60
12-02	Gp4	g.chr12:121690493C>T	Missense Mutation	CAMKK2	p.V378M	calcium/calmodulin-dep	17 (0.00)	16 (0.31)	0.83
12-02	Gp4	g.chr15:44671956G>A	Missense Mutation	CASC4	p.G291R	cancer susceptibility car	100 (0.00)	13 (0.38)	1.03
12-02	Gp4	g.chr19:38847451G>A	Missense Mutation	CATSPERG	p.S422N	catsper channel auxiliar	15 (0.00)	27 (0.26)	0.88
12-02	Gp4	g.chr5:114611244C>A	Missense Mutation	CCDC112	p.R113I	coiled-coil domain conta	71 (0.00)	16 (0.31)	0.83
12-02	Gp4	g.chr5:205685C>T	Silent	CCDC127	p.Q170Q	coiled-coil domain conta	35 (0.00)	41 (0.15)	0.39
12-02	Gp4	g.chr1:117568275G>T	Missense Mutation	CD101	p.G858V	CD101 molecule	33 (0.00)	15 (0.33)	0.89
12-02	Gp4	g.chr11:118223137G>A	Missense Mutation	CD3G	p.D168N	CD3g molecule, gamma	61 (0.00)	46 (0.15)	0.41
12-02	Gp4	g.chr8:25341691C>G	Missense Mutation	CDCA2	p.P444A	cell division cycle assoc	42 (0.00)	19 (0.47)	1.26
12-02	Gp4	g.chr9:123280906C>T	Silent	CDK5RAP2	p.E370E	CDK5 regulatory subun	38 (0.00)	65 (0.09)	0.39
12-02	Gp4	g.chr18:13059180C>G	Missense Mutation	CEP192	p.P1453A	centrosomal protein 192	52 (0.00)	29 (0.21)	0.55
12-02	Gp4	g.chr20:40083367C>T	Missense Mutation	CHD6	p.V1007M	chromodomain helicase	63 (0.00)	18 (0.28)	0.44
12-02	Gp4	g.chr8:61735108C>A	Missense Mutation	CHD7	p.Q1002K	chromodomain helicase	231 (0.00)	38 (0.29)	0.77
12-02	Gp4	g.chr1:111825123C>T	RNA	CHIAP2		chitinase, acidic pseudo	57 (0.00)	28 (0.18)	0.48
12-02	Gp4	g.chr8:42587020C>T	Silent	CHRNB3	p.V190V	cholinergic receptor, nic	39 (0.00)	21 (0.48)	1.27

12-02	Gp4	g.chr2:175213326T>A	Nonsense Mutation	CIR1	p.R418*	corepressor interacting \	54 (0.00)	14 (0.36)	0.95
12-02	Gp4	g.chr16:69184788G>C	Missense Mutation	CIRH1A	p.R328P	cirrhosis, autosomal rec	80 (0.00)	18 (0.33)	0.40
12-02	Gp4	g.chr2:113509909C>A	Missense Mutation	CKAP2L	p.A513S	cytoskeleton associated	106 (0.00)	22 (0.32)	0.60
12-02	Gp4	g.chr7:155301689C>G	Missense Mutation	CNPY1	p.R15T	canopy FGF signaling r	28 (0.00)	34 (0.18)	0.47
12-02	Gp4	g.chr17:55028133G>A	Missense Mutation	COIL	p.T157I	coilin	76 (0.00)	32 (0.25)	0.67
12-02	Gp4	g.chr16:3786692G>A	Silent	CREBBP	p.L1507L	CREB binding protein	18 (0.00)	55 (0.27)	0.97
12-02	Gp4	g.chr13:37678938C>T	Silent	CSNK1A1L	p.K152K	casein kinase 1, alpha 1-	30 (0.00)	43 (0.37)	0.99
12-02	Gp4	g.chr18:19995842G>A	Missense Mutation	CTAGE1	p.P645S	cutaneous T-cell lymph	43 (0.00)	31 (0.16)	0.43
12-02	Gp4	g.chr10:102016176G>A	Missense Mutation	CWF19L1	p.T116I	CWF19-like 1, cell cycl	41 (0.00)	46 (0.37)	0.99
12-02	Gp4	g.chr3:45988339C>T	Silent	CXCR6	p.C122C	chemokine (C-X-C moti	40 (0.00)	23 (0.48)	1.28
12-02	Gp4	g.chr9:124356861C>A	Intron	DAB2IP		DAB2 interacting protei	21 (0.00)	80 (0.23)	0.60
12-02	Gp4	g.chr9:124466813C>T	Intron	DAB2IP		DAB2 interacting protei	44 (0.00)	46 (0.15)	0.41
12-02	Gp4	g.chr12:2061951G>A	Silent	DCP1B	p.S259S	decapping mRNA 1B	25 (0.00)	39 (0.18)	0.48
12-02	Gp4	g.chr9:135522228G>T	Missense Mutation	DDX31	p.F500L	DEAD (Asp-Glu-Ala-A	36 (0.00)	57 (0.11)	0.51
12-02	Gp4	g.chr6:74117334C>G	Missense Mutation	DDX43	p.R345G	DEAD (Asp-Glu-Ala-A	111 (0.00)	24 (0.33)	0.89
12-02	Gp4	g.chrX:50147175G>A	RNA	DGKK		diacylglycerol kinase, k	31 (0.00)	18 (0.28)	0.46
12-02	Gp4	g.chr11:117389208C>T	Missense Mutation	DSCAML1	p.E555K	Down syndrome cell ad	47 (0.02)	53 (0.15)	0.40
12-02	Gp4	g.chr6:56469416G>A	Missense Mutation	DST	p.S3126F	dystonin	49 (0.00)	32 (0.16)	0.42
12-02	Gp4	g.chr14:31917441C>G	Missense Mutation	DTD2	p.S134T	D-tyrosyl-tRNA deacyl	54 (0.00)	26 (0.31)	0.82
12-02	Gp4	g.chr14:102486374C>A	Missense Mutation	DYNC1H1	p.L2830M	dynein, cytoplasmic 1, h	38 (0.00)	35 (0.20)	0.53
12-02	Gp4	g.chr14:102498632C>G	Missense Mutation	DYNC1H1	p.H3303D	dynein, cytoplasmic 1, h	45 (0.00)	96 (0.16)	0.42
12-02	Gp4	g.chr10:74899103G>C	Missense Mutation	ECD	p.S462C	ecdysoneless homolog (	20 (0.00)	34 (0.15)	0.39
12-02	Gp4	g.chr6:8097537C>G	Missense Mutation	EEF1E1	p.G84A	eukaryotic translation el	105 (0.00)	22 (0.36)	0.56
12-02	Gp4	g.chr12:10659443C>T	Silent	EIF2S3L	p.I314I		55 (0.00)	33 (0.15)	0.40
12-02	Gp4	g.chr10:120809362C>T	Missense Mutation	EIF3A	p.R870Q	eukaryotic translation in	157 (0.01)	79 (0.28)	0.74
12-02	Gp4	g.chr3:184043696G>A	Missense Mutation	EIF4G1	p.G973D	eukaryotic translation in	18 (0.00)	26 (0.19)	0.71
12-02	Gp4	g.chr13:41515174G>A	Missense Mutation	ELF1	p.T380I	E74-like factor 1 (ets do	71 (0.00)	20 (0.35)	0.93
12-02	Gp4	g.chr1:19563635C>A	Splice Site	EMC1		ER membrane protein c	25 (0.00)	27 (0.26)	0.69
12-02	Gp4	g.chr22:41569731C>G	Silent	EP300	p.P1574P	E1A binding protein p3	48 (0.00)	77 (0.14)	0.38
12-02	Gp4	g.chr3:37033529G>T	Missense Mutation	EPM2AIP1	p.T347N	EPM2A (laforin) intera	95 (0.00)	64 (0.16)	0.42
12-02	Gp4	g.chr1:220170441C>G	Missense Mutation	EPRS	p.G809R	glutamyl-prolyl-tRNA s	108 (0.00)	28 (0.18)	0.48
12-02	Gp4	g.chr12:53673595C>A	Missense Mutation	ESPL1	p.S815Y	extra spindle pole bodie	24 (0.00)	56 (0.14)	0.38
12-02	Gp4	g.chr1:11148256C>T	Splice Site	EXOSC10		exosome component 10	42 (0.00)	11 (0.45)	1.21
12-02	Gp4	g.chr2:203630211C>A	Missense Mutation	FAM117B	p.D498E	family with sequence si	108 (0.01)	39 (0.28)	0.75
12-02	Gp4	g.chr11:92087946G>A	Missense Mutation	FAT3	p.D740N	FAT atypical cadherin 3	112 (0.00)	22 (0.41)	1.09

12-02	Gp4	g.chr11:92523136G>T	Missense Mutation	FAT3	p.D1305Y	FAT atypical cadherin 3	53 (0.00)	33 (0.24)	0.65
12-02	Gp4	g.chr17:73922903C>T	Silent	FBF1	p.K163K	Fas (TNFRSF6) binding	74 (0.00)	89 (0.15)	0.49
12-02	Gp4	g.chr9:37537764G>A	Silent	FBXO10	p.N254N	F-box protein 10	34 (0.00)	61 (0.15)	0.59
12-02	Gp4	g.chr8:17726142T>G	Missense Mutation	FGL1	p.M232L	fibrinogen-like 1	34 (0.00)	19 (0.37)	0.69
12-02	Gp4	g.chr4:159756585C>T	Silent	FNIP2	p.S228S	folliculin interacting pro	122 (0.00)	14 (0.64)	1.71
12-02	Gp4	g.chr9:85928634T>C	Missense Mutation	FRMD3	p.N209D	FERM domain containi	19 (0.00)	22 (0.23)	0.98
12-02	Gp4	g.chr9:37745173C>A	Silent	FRMPD1	p.P1048P	FERM and PDZ domain	25 (0.00)	46 (0.17)	0.69
12-02	Gp4	g.chr15:83455866C>T	Missense Mutation	FSD2	p.E93K	fibronectin type III and	27 (0.00)	62 (0.15)	0.39
12-02	Gp4	g.chr15:27572045C>T	Silent	GABRG3	p.S120S	gamma-aminobutyric ac	50 (0.00)	35 (0.43)	1.51
12-02	Gp4	g.chr7:151791346G>A	Missense Mutation	GALNT11	p.G12R	polypeptide N-acetylgal	32 (0.00)	20 (0.30)	0.80
12-02	Gp4	g.chr15:42585049T>A	Missense Mutation	GANC	p.V149D	glucosidase, alpha; neut	30 (0.00)	10 (0.60)	1.60
12-02	Gp4	g.chr5:74021580C>T	Splice Site	GFM2	p.G638E	G elongation factor, mit	48 (0.00)	16 (0.31)	0.83
12-02	Gp4	g.chr7:150389580G>A	Missense Mutation	GIMAP2	p.G69E	GTPase, IMAP family	32 (0.00)	24 (0.25)	0.67
12-02	Gp4	g.chr19:3157839C>T	Silent	GNA15	p.I286I	guanine nucleotide bind	16 (0.00)	54 (0.17)	0.62
12-02	Gp4	g.chr12:131476852G>A	Missense Mutation	GPR133	p.G326E	G protein-coupled recep	47 (0.00)	60 (0.15)	0.40
12-02	Gp4	g.chrX:101909343G>A	Missense Mutation	GPRASP1	p.E168K	G protein-coupled recep	31 (0.00)	11 (0.45)	0.76
12-02	Gp4	g.chr5:150406521G>T	Missense Mutation	GPX3	p.C101F	glutathione peroxidase	30 (0.00)	10 (0.50)	1.33
12-02	Gp4	g.chr7:18656874A>G	Intron	HDAC9		histone deacetylase 9	207 (0.00)	50 (0.18)	0.48
12-02	Gp4	g.chr7:18784008C>A	Intron	HDAC9		histone deacetylase 9	41 (0.00)	27 (0.33)	0.89
12-02	Gp4	g.chr7:18886891C>G	Intron	HDAC9		histone deacetylase 9	122 (0.00)	22 (0.32)	0.85
12-02	Gp4	g.chr7:18969728C>G	Intron	HDAC9		histone deacetylase 9	52 (0.00)	57 (0.16)	0.42
12-02	Gp4	g.chr7:19003571G>A	Intron	HDAC9		histone deacetylase 9	51 (0.00)	24 (0.25)	0.67
12-02	Gp4	g.chr5:74655013G>A	Missense Mutation	HMGCR	p.E726K	3-hydroxy-3-methylglut	36 (0.00)	20 (0.70)	1.87
12-02	Gp4	g.chr11:6461442C>G	Missense Mutation	HPX	p.V97L	hemopexin	25 (0.00)	18 (0.44)	1.19
12-02	Gp4	g.chr14:102551084A>T	Silent	HSP90AA1	p.T305T	heat shock protein 90kD	121 (0.00)	27 (0.26)	0.69
12-02	Gp4	g.chr6:52880914C>T	Silent	ICK	p.Q266Q	intestinal cell (MAK-lik	43 (0.00)	19 (0.26)	0.70
12-02	Gp4	g.chr8:39781054G>A	Missense Mutation	IDO1	p.E202K	indoleamine 2,3-dioxyg	35 (0.00)	35 (0.14)	0.38
12-02	Gp4	g.chr9:21350427G>A	Silent	IFNA6	p.L154L	interferon, alpha 6	25 (0.00)	18 (0.39)	0.51
12-02	Gp4	g.chr15:99491860C>T	Silent	IGF1R	p.G1214G	insulin-like growth fact	20 (0.00)	32 (0.16)	0.42
12-02	Gp4	g.chr2:90193192G>T	RNA	IGKV1D-13		immunoglobulin kappa	40 (0.00)	21 (0.29)	0.76
12-02	Gp4	g.chr2:89278001C>A	RNA	IGKV3-7		immunoglobulin kappa	39 (0.00)	17 (0.41)	1.10
12-02	Gp4	g.chr6:137325851C>T	Silent	IL20RA	p.L257L	interleukin 20 receptor,	174 (0.00)	46 (0.35)	0.93
12-02	Gp4	g.chr4:142955243G>A	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	57 (0.26)	0.70
12-02	Gp4	g.chr4:142974221G>A	Intron	INPP4B		inositol polyphosphate-	99 (0.00)	14 (0.50)	1.33
12-02	Gp4	g.chr4:143250138A>T	Intron	INPP4B		inositol polyphosphate-	104 (0.00)	33 (0.15)	0.40

12-02	Gp4	g.chr4:143250196G>T	Intron	INPP4B		inositol polyphosphate-	88 (0.00)	26 (0.19)	0.51
12-02	Gp4	g.chr4:143343025C>T	Intron	INPP4B		inositol polyphosphate-	202 (0.00)	35 (0.17)	0.46
12-02	Gp4	g.chr4:143538217C>T	Intron	INPP4B		inositol polyphosphate-	80 (0.00)	14 (0.50)	1.33
12-02	Gp4	g.chr4:143717867G>A	Intron	INPP4B		inositol polyphosphate-	85 (0.00)	20 (0.35)	0.93
12-02	Gp4	g.chr4:143738648C>A	Intron	INPP4B		inositol polyphosphate-	62 (0.00)	19 (0.26)	0.70
12-02	Gp4	g.chr13:103443683C>G	Missense Mutation	KDELC1	p.C257S	KDEL (Lys-Asp-Glu-L	109 (0.00)	64 (0.16)	0.42
12-02	Gp4	g.chr11:67013573C>T	Missense Mutation	KDM2A	p.P651S	lysine (K)-specific dem	41 (0.00)	26 (0.19)	0.66
12-02	Gp4	g.chr9:114176866C>G	Missense Mutation	KIAA0368	p.L610F	KIAA0368	73 (0.00)	62 (0.10)	0.41
12-02	Gp4	g.chr9:5919759G>A	Silent	KIAA2026	p.A2079A	KIAA2026	156 (0.00)	23 (0.30)	0.40
12-02	Gp4	g.chr2:8918773C>A	Missense Mutation	KIDINS220	p.R900I	kinase D-interacting sub	94 (0.01)	24 (0.25)	0.67
12-02	Gp4	g.chr1:202897667T>A	Missense Mutation	KLHL12	p.N4I	kelch-like family memb	32 (0.00)	70 (0.23)	0.61
12-02	Gp4	g.chr21:31654967C>A	Missense Mutation	KRTAP24-1	p.C95F	keratin associated protei	29 (0.00)	34 (0.15)	0.39
12-02	Gp4	g.chr6:105405131C>T	Silent	LIN28B	p.A2A	lin-28 homolog B (C. el	44 (0.00)	20 (0.35)	0.93
12-02	Gp4	g.chr13:76379776C>T	Missense Mutation	LMO7	p.P126L	LIM domain 7	208 (0.00)	62 (0.18)	0.47
12-02	Gp4	g.chr4:62758425C>T	Missense Mutation	LPHN3	p.T443I	latrophilin 3	62 (0.00)	50 (0.24)	0.82
12-02	Gp4	g.chr2:170060624C>T	Missense Mutation	LRP2	p.G2625S	low density lipoprotein	86 (0.00)	17 (0.41)	0.80
12-02	Gp4	g.chr1:53716424C>A	Nonsense Mutation	LRP8	p.E425*	low density lipoprotein	55 (0.00)	21 (0.29)	0.76
12-02	Gp4	g.chr6:25280058T>G	Missense Mutation	LRRC16A	p.L12W	leucine rich repeat cont	42 (0.00)	88 (0.16)	0.42
12-02	Gp4	g.chr9:114371364G>A	RNA	LRRC37A5P		leucine rich repeat cont	68 (0.00)	52 (0.12)	0.49
12-02	Gp4	g.chr2:33246083G>A	Missense Mutation	LTBP1	p.D225N	latent transforming grov	18 (0.00)	35 (0.26)	0.69
12-02	Gp4	g.chr7:77702670G>A	Intron	MAGI2		membrane associated gu	33 (0.00)	54 (0.19)	0.49
12-02	Gp4	g.chr7:77779487T>C	Intron	MAGI2		membrane associated gu	77 (0.00)	19 (0.26)	0.70
12-02	Gp4	g.chr7:77781887A>G	Intron	MAGI2		membrane associated gu	44 (0.00)	14 (0.36)	0.95
12-02	Gp4	g.chr7:77937521C>T	Intron	MAGI2		membrane associated gu	50 (0.00)	15 (0.33)	0.89
12-02	Gp4	g.chr7:77976137C>G	Intron	MAGI2		membrane associated gu	97 (0.00)	30 (0.17)	0.44
12-02	Gp4	g.chr7:78059243G>C	Intron	MAGI2		membrane associated gu	67 (0.00)	13 (0.38)	1.03
12-02	Gp4	g.chr7:78080259G>A	Intron	MAGI2		membrane associated gu	16 (0.00)	21 (0.24)	0.63
12-02	Gp4	g.chr7:78140161C>T	Intron	MAGI2		membrane associated gu	62 (0.00)	20 (0.35)	0.93
12-02	Gp4	g.chr7:78324750C>A	Intron	MAGI2		membrane associated gu	69 (0.00)	71 (0.32)	0.86
12-02	Gp4	g.chr7:78338719C>G	Intron	MAGI2		membrane associated gu	99 (0.00)	48 (0.15)	0.39
12-02	Gp4	g.chr7:78350214T>A	Intron	MAGI2		membrane associated gu	51 (0.00)	20 (0.40)	1.07
12-02	Gp4	g.chr7:78394436G>A	Intron	MAGI2		membrane associated gu	74 (0.00)	12 (0.42)	1.11
12-02	Gp4	g.chr7:78511714C>A	Intron	MAGI2		membrane associated gu	54 (0.00)	28 (0.21)	0.57
12-02	Gp4	g.chr7:79025668C>T	Intron	MAGI2		membrane associated gu	70 (0.01)	33 (0.33)	0.89
12-02	Gp4	g.chr11:64566296C>A	Missense Mutation	MAP4K2	p.W356L	mitogen-activated protei	19 (0.00)	110 (0.25)	0.68

12-02	Gp4	g.chr2:160599672G>A	Missense Mutation	MARCH7	p.R47Q	membrane-associated ri	62 (0.02)	28 (0.21)	0.57
12-02	Gp4	g.chr5:112720806C>A	Missense Mutation	MCC	p.D92Y	mutated in colorectal ca	49 (0.00)	40 (0.15)	0.40
12-02	Gp4	g.chr7:128141898G>T	Silent	METTL2B	p.G355G	methyltransferase like 2	31 (0.00)	42 (0.19)	0.51
12-02	Gp4	g.chr3:179103507G>C	Missense Mutation	MFN1	p.V605L	mitofusin 1	66 (0.00)	45 (0.13)	0.50
12-02	Gp4	g.chr4:128865097A>T	Nonsense Mutation	MFSD8	p.Y83*	major facilitator superfa	82 (0.01)	34 (0.24)	0.63
12-02	Gp4	g.chrX:10427723G>T	Silent	MID1	p.G470G	midline 1	27 (0.00)	22 (0.27)	0.45
12-02	Gp4	g.chr20:10393719C>A	Missense Mutation	MKKS	p.Q148H	McKusick-Kaufman sy	55 (0.00)	21 (0.24)	0.63
12-02	Gp4	g.chr8:89128948C>A	Splice Site	MMP16		matrix metallopeptidase	40 (0.00)	29 (0.24)	0.64
12-02	Gp4	g.chr21:37710234C>G	Missense Mutation	MORC3	p.F150L	MORC family CW-type	31 (0.00)	22 (0.41)	1.09
12-02	Gp4	g.chr2:202546268A>G	Missense Mutation	MPP4	p.M201T	membrane protein, pal	87 (0.00)	38 (0.21)	0.56
12-02	Gp4	g.chr10:30615413G>A	Missense Mutation	MTPAP	p.P311L	mitochondrial poly(A)	29 (0.00)	16 (0.50)	1.33
12-02	Gp4	g.chr13:41791344C>A	Missense Mutation	MTRF1	p.K415N	mitochondrial translatio	71 (0.00)	21 (0.33)	0.89
12-02	Gp4	g.chr19:8969326G>A	Nonsense Mutation	MUC16	p.Q14340*	mucin 16, cell surface a	42 (0.00)	60 (0.17)	0.62
12-02	Gp4	g.chr19:9026244G>A	Missense Mutation	MUC16	p.R12248C	mucin 16, cell surface a	23 (0.00)	32 (0.25)	0.67
12-02	Gp4	g.chr19:9048863G>A	Missense Mutation	MUC16	p.T10923I	mucin 16, cell surface a	53 (0.00)	68 (0.16)	0.43
12-02	Gp4	g.chr19:9067082T>A	Silent	MUC16	p.L6788L	mucin 16, cell surface a	23 (0.00)	25 (0.28)	0.75
12-02	Gp4	g.chr19:9087268G>A	Missense Mutation	MUC16	p.T1516M	mucin 16, cell surface a	77 (0.00)	41 (0.29)	0.78
12-02	Gp4	g.chr7:100680746A>G	Missense Mutation	MUC17	p.T2017A	mucin 17, cell surface a	67 (0.00)	26 (0.19)	0.51
12-02	Gp4	g.chr3:195453120C>A	Missense Mutation	MUC20	p.A549E	mucin 20, cell surface a	21 (0.00)	65 (0.12)	0.46
12-02	Gp4	g.chr9:113538176G>T	Silent	MUSK	p.V431V	muscle, skeletal, recept	115 (0.01)	58 (0.12)	0.51
12-02	Gp4	g.chr8:67492498A>T	Missense Mutation	MYBL1	p.M324K	v-myb avian myeloblast	32 (0.00)	28 (0.46)	1.24
12-02	Gp4	g.chr17:10363323C>A	Missense Mutation	MYH4	p.Q454H	myosin, heavy chain 4,	47 (0.00)	25 (0.28)	0.41
12-02	Gp4	g.chr3:175293950C>A	Missense Mutation	NAALADL2	p.A592D	N-acetylated alpha-link	85 (0.00)	28 (0.18)	0.66
12-02	Gp4	g.chr12:54894352G>A	Silent	NCKAP1L	p.E83E	NCK-associated protein	41 (0.00)	29 (0.28)	0.74
12-02	Gp4	g.chr2:152497061C>A	Missense Mutation	NEB	p.E2831D	nebulin	128 (0.01)	112 (0.19)	0.50
12-02	Gp4	g.chr2:152563433G>A	Missense Mutation	NEB	p.L372F	nebulin	43 (0.00)	19 (0.32)	0.84
12-02	Gp4	g.chr1:16774394C>G	Nonsense Mutation	NECAP2	p.S41*	NECAP endocytosis ass	15 (0.00)	18 (0.50)	1.33
12-02	Gp4	g.chr1:115828948C>T	Missense Mutation	NGF	p.V157M	nerve growth factor (bet	18 (0.00)	31 (0.23)	0.60
12-02	Gp4	g.chr11:7067911C>T	Silent	NLRP14	p.R657R	NLR family, pyrin dom	58 (0.00)	27 (0.19)	0.49
12-02	Gp4	g.chr5:176700786G>A	Splice Site	NSD1		nuclear receptor binding	43 (0.00)	17 (0.35)	0.94
12-02	Gp4	g.chr22:45571948C>T	Silent	NUP50	p.P109P	nucleoporin 50kDa	49 (0.00)	29 (0.21)	0.55
12-02	Gp4	g.chr11:3765738C>A	Splice Site	NUP98		nucleoporin 98kDa	33 (0.00)	15 (0.53)	1.42
12-02	Gp4	g.chr1:161954665C>T	Missense Mutation	OLFML2B	p.R528Q	olfactomedin-like 2B	28 (0.00)	16 (0.75)	2.00
12-02	Gp4	g.chr1:158576521C>T	Missense Mutation	OR10Z1	p.A98V	olfactory receptor, famil	37 (0.00)	11 (0.45)	1.21
12-02	Gp4	g.chr9:107380150A>G	Silent	OR13C9	p.C112C	olfactory receptor, famil	102 (0.00)	48 (0.12)	0.53

12-02	Gp4	g.chr14:20295635A>G	Missense Mutation	OR4N2	p.R10G	olfactory receptor, famil	86 (0.00)	45 (0.24)	0.65
12-02	Gp4	g.chr11:5863080C>A	Silent	OR52E6	p.L16L	olfactory receptor, famil	166 (0.00)	42 (0.19)	0.51
12-02	Gp4	g.chr11:4615930C>T	Missense Mutation	OR52I1	p.S221F	olfactory receptor, famil	86 (0.01)	28 (0.29)	0.76
12-02	Gp4	g.chr11:4615957T>C	Missense Mutation	OR52I1	p.F230S	olfactory receptor, famil	129 (0.00)	35 (0.17)	0.46
12-02	Gp4	g.chr11:5758669G>A	Missense Mutation	OR56B1	p.R308K	olfactory receptor, famil	54 (0.00)	22 (0.27)	0.73
12-02	Gp4	g.chr3:97806122G>T	Missense Mutation	OR5AC2	p.V36F	olfactory receptor, famil	23 (0.00)	18 (0.50)	1.33
12-02	Gp4	g.chr12:29630384G>T	Nonsense Mutation	OVCH1	p.S379*	ovochymase 1	95 (0.00)	27 (0.19)	0.49
12-02	Gp4	g.chr8:101724959G>A	Missense Mutation	PABPC1	p.A266V	poly(A) binding protein,	129 (0.01)	36 (0.17)	0.44
12-02	Gp4	g.chr20:3903910G>A	Missense Mutation	PANK2	p.G561E	pantothenate kinase 2	18 (0.00)	23 (0.22)	0.58
12-02	Gp4	g.chr14:20825866C>G	Silent	PARP2	p.L541L	poly (ADP-ribose) poly	45 (0.00)	28 (0.25)	0.67
12-02	Gp4	g.chr7:154790397C>G	Missense Mutation	PAXIP1	p.G60A	PAX interacting (with t	109 (0.00)	55 (0.15)	0.39
12-02	Gp4	g.chr5:140711891C>T	Missense Mutation	PCDHGA1	p.S547F	protocadherin gamma s	48 (0.00)	164 (0.15)	0.39
12-02	Gp4	g.chr7:82579281T>A	Silent	PCLO	p.A3541A	piccolo presynaptic cyt	49 (0.00)	35 (0.37)	0.99
12-02	Gp4	g.chr1:144915505T>C	Silent	PDE4DIP	p.E777E	phosphodiesterase 4D i	62 (0.00)	49 (0.16)	0.44
12-02	Gp4	g.chr16:15120546A>T	Missense Mutation	PDXDC1	p.Q396L	pyridoxal-dependent de	25 (0.00)	10 (0.50)	1.33
12-02	Gp4	g.chr3:130427220T>A	Missense Mutation	PIK3R4	p.K816N	phosphoinositide-3-kina	54 (0.00)	12 (0.42)	1.11
12-02	Gp4	g.chr7:6754237G>T	RNA	PMS2CL		PMS2 C-terminal like p	67 (0.00)	51 (0.18)	0.47
12-02	Gp4	g.chr11:70221163G>A	Silent	PPFIA1	p.L1093L	protein tyrosine phospha	33 (0.00)	13 (0.46)	1.57
12-02	Gp4	g.chr12:81733001G>A	Missense Mutation	PPFIA2	p.R836C	protein tyrosine phospha	94 (0.00)	36 (0.22)	0.59
12-02	Gp4	g.chr12:63060964G>A	Missense Mutation	PPM1H	p.P464L	protein phosphatase, M	31 (0.00)	16 (0.44)	1.17
12-02	Gp4	g.chr14:102375951G>T	Missense Mutation	PPP2R5C	p.A393S	protein phosphatase 2, r	23 (0.00)	38 (0.16)	0.42
12-02	Gp4	g.chr14:63888807A>G	Silent	PPP2R5E	p.S120S	protein phosphatase 2, r	66 (0.00)	34 (0.18)	0.47
12-02	Gp4	g.chr12:110989697C>T	Silent	PPTC7	p.T100T	PTC7 protein phosphata	37 (0.00)	27 (0.26)	0.69
12-02	Gp4	g.chr1:13695844C>A	Missense Mutation	PRAMEF19	p.S305I	PRAME family membe	40 (0.00)	40 (0.23)	0.60
12-02	Gp4	g.chr1:57161789C>A	Missense Mutation	PRKAA2	p.L249M	protein kinase, AMP-ac	91 (0.00)	28 (0.25)	0.67
12-02	Gp4	g.chr17:74326715G>A	Nonsense Mutation	PRPSAP1	p.Q166*	phosphoribosyl pyropho	51 (0.00)	32 (0.16)	0.53
12-02	Gp4	g.chr1:171486749T>C	Silent	PRRC2C	p.D180D	proline-rich coiled-coil	92 (0.00)	33 (0.52)	1.37
12-02	Gp4	g.chr1:171510825G>A	Missense Mutation	PRRC2C	p.R1405Q	proline-rich coiled-coil	43 (0.00)	21 (0.48)	1.27
12-02	Gp4	g.chr10:89707792C>A	Intron	PTEN		phosphatase and tensin	148 (0.00)	30 (0.17)	0.44
12-02	Gp4	g.chr7:77239323C>T	Intron	PTPN12		protein tyrosine phospha	70 (0.00)	69 (0.17)	0.46
12-02	Gp4	g.chr11:48186036G>A	Missense Mutation	PTPRJ	p.R1275Q	protein tyrosine phospha	23 (0.00)	32 (0.22)	0.58
12-02	Gp4	g.chr2:136396651G>A	Missense Mutation	R3HDM1	p.S337N	R3H domain containing	220 (0.00)	45 (0.20)	0.53
12-02	Gp4	g.chr9:125760971T>C	Missense Mutation	RABGAP1	p.S434P	RAB GTPase activating	51 (0.00)	96 (0.35)	1.65
12-02	Gp4	g.chr2:109352147C>T	Missense Mutation	RANBP2	p.H189Y	RAN binding protein 2	255 (0.00)	108 (0.40)	1.06
12-02	Gp4	g.chr2:109380572G>A	Missense Mutation	RANBP2	p.E1193K	RAN binding protein 2	34 (0.00)	25 (0.20)	0.53

12-02	Gp4	g.chr3:25635044C>T	Silent	RARB	p.F279F	retinoic acid receptor, b	100 (0.00)	38 (0.53)	1.40
12-02	Gp4	g.chr13:48963428C>G	Intron	RB1		retinoblastoma 1	86 (0.00)	22 (0.23)	0.61
12-02	Gp4	g.chr13:49029541T>A	Intron	RB1		retinoblastoma 1	147 (0.00)	32 (0.16)	0.42
12-02	Gp4	g.chr4:57796227G>T	Missense Mutation	REST	p.K401N	RE1-silencing transcript	48 (0.00)	26 (0.23)	0.62
12-02	Gp4	g.chr2:85577921C>T	Silent	RETSAT	p.K193K	retinol saturase (all-tran	44 (0.00)	24 (0.29)	0.59
12-02	Gp4	g.chr3:49735329C>A	Missense Mutation	RNF123	p.H118Q	ring finger protein 123	36 (0.00)	25 (0.24)	0.43
12-02	Gp4	g.chr4:1066870A>T	Missense Mutation	RNF212	p.V229D	ring finger protein 212	24 (0.00)	22 (0.55)	1.45
12-02	Gp4	g.chr17:78357548G>T	Silent	RNF213	p.V4763V	ring finger protein 213	23 (0.00)	23 (0.22)	0.73
12-02	Gp4	g.chr3:97957237C>T	lincRNA	RP11-325B23.2			116 (0.01)	39 (0.38)	1.03
12-02	Gp4	g.chr14:58751736C>T	RNA	RP11-349A22.5			47 (0.00)	22 (0.27)	0.73
12-02	Gp4	g.chr17:46952366G>T	RNA	RP11-463M16.4			27 (0.00)	25 (0.32)	0.85
12-02	Gp4	g.chr15:22332556C>T	RNA	RP11-69H14.6			55 (0.00)	33 (0.39)	1.39
12-02	Gp4	g.chr14:21792916G>T	Missense Mutation	RPGRIP1	p.Q634H	retinitis pigmentosa GT	112 (0.00)	58 (0.29)	0.78
12-02	Gp4	g.chr3:72430250A>T	Intron	RYBP		RING1 and YY1 bindin	104 (0.00)	31 (0.35)	0.95
12-02	Gp4	g.chr11:9834089C>A	Missense Mutation	SBF2	p.W1382L	SET binding factor 2	28 (0.00)	35 (0.14)	0.38
12-02	Gp4	g.chr12:52156321T>C	Missense Mutation	SCN8A	p.L802P	sodium channel, voltage	33 (0.00)	27 (0.22)	0.59
12-02	Gp4	g.chr1:169822878C>G	Silent	SCYL3	p.L735L	SCY1-like 3 (S. cerevisi	67 (0.00)	20 (0.25)	0.67
12-02	Gp4	g.chr4:76896991G>A	Nonsense Mutation	SDAD1	p.Q162*	SDA1 domain containin	41 (0.00)	18 (0.28)	0.55
12-02	Gp4	g.chr4:25160619C>T	Silent	SEPSECS	p.R75R	Sep (O-phosphoserine)	108 (0.00)	43 (0.21)	0.56
12-02	Gp4	g.chr6:109323481C>A	Splice Site	SESN1	p.E115D	sestrin 1	57 (0.00)	14 (0.36)	0.95
12-02	Gp4	g.chr7:94259056C>T	Silent	SGCE	p.G69G	sarcoglycan, epsilon	113 (0.00)	19 (0.68)	1.82
12-02	Gp4	g.chr3:72811696G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	119 (0.00)	19 (0.26)	0.70
12-02	Gp4	g.chr19:52034515C>T	Missense Mutation	SIGLEC6	p.R109K	sialic acid binding Ig-lik	22 (0.00)	83 (0.11)	0.39
12-02	Gp4	g.chr2:113405031G>A	Silent	SLC20A1	p.L155L	solute carrier family 20	37 (0.03)	24 (0.42)	0.78
12-02	Gp4	g.chr16:18875446T>A	Missense Mutation	SMG1	p.E1124V	SMG1 phosphatidylinos	69 (0.00)	31 (0.23)	0.60
12-02	Gp4	g.chr16:12571627G>T	Nonsense Mutation	SNX29	p.E697*	sorting nexin 29	84 (0.00)	46 (0.22)	0.58
12-02	Gp4	g.chr2:201305478C>A	Silent	SPATS2L	p.I253I	spermatogenesis associa	74 (0.00)	23 (0.26)	0.70
12-02	Gp4	g.chr1:16257403T>C	Silent	SPEN	p.I1556I	spen family transcriptio	59 (0.00)	27 (0.19)	0.49
12-02	Gp4	g.chr17:47724151G>A	Intron	SPOP		speckle-type POZ protei	48 (0.00)	34 (0.18)	0.47
12-02	Gp4	g.chr14:65246611C>T	Silent	SPTB	p.L1435L	spectrin, beta, erythrocy	15 (0.00)	23 (0.30)	0.81
12-02	Gp4	g.chr7:99780423T>C	Silent	STAG3	p.D99D	stromal antigen 3	69 (0.00)	23 (0.22)	0.58
12-02	Gp4	g.chr2:219540126C>T	Silent	STK36	p.L122L	serine/threonine kinase	62 (0.02)	57 (0.23)	0.61
12-02	Gp4	g.chr13:37619400C>T	Silent	SUPT20H	p.R92R	suppressor of Ty 20 hon	33 (0.00)	14 (0.43)	1.14
12-02	Gp4	g.chr6:10931677G>A	Silent	SYCP2L	p.L546L	synaptonemal complex	33 (0.00)	16 (0.44)	0.67
12-02	Gp4	g.chr14:64453263A>G	Silent	SYNE2	p.E747E	spectrin repeat containi	62 (0.00)	41 (0.24)	0.65

12-02	Gp4	g.chr6:132874693C>A	Missense Mutation	TAAR8	p.P288T	trace amine associated r	87 (0.00)	42 (0.17)	0.44
12-02	Gp4	g.chr12:11286236C>T	Missense Mutation	TAS2R30	p.C203Y	taste receptor, type 2, m	128 (0.01)	42 (0.17)	0.44
12-02	Gp4	g.chr12:11286494A>G	Missense Mutation	TAS2R30	p.I117T	taste receptor, type 2, m	105 (0.00)	49 (0.20)	0.54
12-02	Gp4	g.chr20:13463913G>T	Missense Mutation	TASP1	p.H316N	taspase, threonine aspar	41 (0.00)	27 (0.22)	0.59
12-02	Gp4	g.chr8:124153142G>A	Splice Site	TBC1D31		TBC1 domain family, m	52 (0.00)	26 (0.23)	0.62
12-02	Gp4	g.chr2:43797599C>A	Missense Mutation	THADA	p.Q705H	thyroid adenoma associa	55 (0.00)	28 (0.18)	0.48
12-02	Gp4	g.chr4:159162721C>A	Missense Mutation	TMEM144	p.S288Y	transmembrane protein	49 (0.00)	16 (0.44)	1.17
12-02	Gp4	g.chr14:93652732G>T	Missense Mutation	TMEM251	p.A38S	transmembrane protein	103 (0.00)	31 (0.16)	0.43
12-02	Gp4	g.chr1:25810707C>A	Silent	TMEM57	p.R419R	transmembrane protein	29 (0.00)	29 (0.17)	0.46
12-02	Gp4	g.chr11:117984061C>T	Missense Mutation	TMPRSS4	p.A274V	transmembrane protease	21 (0.00)	21 (0.48)	1.27
12-02	Gp4	g.chr1:173013078C>T	Splice Site	TNFSF18		tumor necrosis factor (li	82 (0.00)	23 (0.30)	0.81
12-02	Gp4	g.chr3:170811651C>T	Missense Mutation	TNIK	p.E900K	TRAF2 and NCK intera	95 (0.00)	111 (0.14)	0.54
12-02	Gp4	g.chr4:189063507G>A	Silent	TRIML1	p.Q202Q	tripartite motif family-li	26 (0.00)	41 (0.15)	0.39
12-02	Gp4	g.chr8:116599540C>A	Missense Mutation	TRPS1	p.E796D	trichorhinophalangeal sy	16 (0.00)	13 (0.62)	1.64
12-02	Gp4	g.chr9:100372670G>A	Missense Mutation	TSTD2	p.P265S	thiosulfate sulfurtransfe	95 (0.00)	69 (0.12)	0.49
12-02	Gp4	g.chr6:167754522C>T	Silent	TTLL2	p.D378D	tubulin tyrosine ligase-li	76 (0.00)	42 (0.14)	0.38
12-02	Gp4	g.chr2:179393363G>A	Silent	TTN	p.I35705I	titin	44 (0.00)	34 (0.15)	0.39
12-02	Gp4	g.chr2:179500795G>A	Missense Mutation	TTN	p.R13835W	titin	144 (0.00)	26 (0.27)	0.72
12-02	Gp4	g.chr2:179599232T>A	Missense Mutation	TTN	p.S5107C	titin	178 (0.00)	56 (0.20)	0.52
12-02	Gp4	g.chr6:112393229G>T	Missense Mutation	TUBE1	p.T382N	tubulin, epsilon 1	108 (0.00)	30 (0.33)	0.89
12-02	Gp4	g.chr18:9887013C>G	Missense Mutation	TXNDC2	p.I179M	thioredoxin domain con	26 (0.00)	25 (0.32)	0.85
12-02	Gp4	g.chr12:104715056C>T	Missense Mutation	TXNRD1	p.H205Y	thioredoxin reductase 1	41 (0.00)	29 (0.17)	0.46
12-02	Gp4	g.chr21:43838522C>A	Missense Mutation	UBASH3A	p.L246I	ubiquitin associated and	20 (0.00)	85 (0.13)	0.44
12-02	Gp4	g.chr7:43988316C>A	Missense Mutation	UBE2D4	p.P95Q	ubiquitin-conjugating en	58 (0.02)	14 (0.57)	1.52
12-02	Gp4	g.chr15:43258468T>A	Missense Mutation	UBR1	p.I1492F	ubiquitin protein ligase	36 (0.00)	22 (0.23)	0.61
12-02	Gp4	g.chr2:234628188G>A	Missense Mutation	UGT1A4	p.R241K	UDP glucuronosyltrans	44 (0.00)	73 (0.21)	0.55
12-02	Gp4	g.chr2:234669531C>A	Missense Mutation	UGT1A8	p.H200N	UDP glucuronosyltrans	49 (0.00)	23 (0.30)	0.81
12-02	Gp4	g.chr4:69434083C>A	Missense Mutation	UGT2B17	p.K40N	UDP glucuronosyltrans	129 (0.00)	48 (0.21)	0.56
12-02	Gp4	g.chr1:12342880C>T	Missense Mutation	VPS13D	p.P1574L	vacuolar protein sorting	37 (0.00)	14 (0.57)	1.52
12-02	Gp4	g.chr13:42442517T>A	Missense Mutation	VWA8	p.T393S	von Willebrand factor A	72 (0.00)	39 (0.21)	0.55
12-02	Gp4	g.chr18:30093566C>A	RNA	WBP11P1		WW domain binding pr	105 (0.00)	10 (0.50)	0.59
12-02	Gp4	g.chr7:73105305G>T	Missense Mutation	WBSCR22	p.R141L	Williams Beuren syndro	30 (0.00)	31 (0.16)	0.43
12-02	Gp4	g.chr19:38384843G>T	Missense Mutation	WDR87	p.F461L	WD repeat domain 87	32 (0.00)	33 (0.18)	0.48
12-02	Gp4	g.chr12:1009828C>A	Missense Mutation	WNK1	p.P2212Q	WNK lysine deficient p	22 (0.00)	21 (0.24)	0.63
12-02	Gp4	g.chr12:989939C>T	Missense Mutation	WNK1	p.P962L	WNK lysine deficient p	65 (0.00)	33 (0.24)	0.65

12-02	Gp4	g.chr1:180853191G>T	Missense Mutation	XPR1	p.A694S	xenotropic and polytrop	40 (0.00)	18 (0.39)	1.04
12-02	Gp4	g.chr14:75277082C>T	Silent	YLPM1	p.D1023D	YLP motif containing 1	160 (0.00)	29 (0.17)	0.46
12-02	Gp4	g.chr12:57397637G>C	Missense Mutation	ZBTB39	p.N355K	zinc finger and BTB do	37 (0.00)	30 (0.23)	0.62
12-02	Gp4	g.chr9:129594970A>T	Missense Mutation	ZBTB43	p.Q61L	zinc finger and BTB do	23 (0.00)	69 (0.13)	0.61
12-02	Gp4	g.chr11:110035901C>A	Missense Mutation	ZC3H12C	p.F698L	zinc finger CCCH-type	59 (0.00)	77 (0.16)	0.42
12-02	Gp4	g.chr2:207175052G>A	Missense Mutation	ZDBF2	p.A1934T	zinc finger, DBF-type c	122 (0.00)	53 (0.23)	0.60
12-02	Gp4	g.chr2:207175563C>G	Nonsense Mutation	ZDBF2	p.S2104*	zinc finger, DBF-type c	66 (0.00)	31 (0.26)	0.69
12-02	Gp4	g.chr8:124266157C>A	Missense Mutation	ZHX1	p.S677I	zinc fingers and homeo	88 (0.01)	18 (0.28)	0.74
12-02	Gp4	g.chr3:178742869T>C	Missense Mutation	ZMAT3	p.Q269R	zinc finger, matrin-type	73 (0.00)	49 (0.10)	0.38
12-02	Gp4	g.chr19:44681660C>A	Missense Mutation	ZNF226	p.H749N	zinc finger protein 226	79 (0.00)	26 (0.35)	0.92
12-02	Gp4	g.chr6:109107803G>T	RNA	ZNF259P1		zinc finger protein 259	30 (0.00)	41 (0.20)	0.52
12-02	Gp4	g.chr9:109736502C>A	Silent	ZNF462	p.L1166L	zinc finger protein 462	39 (0.00)	21 (0.24)	1.01
12-02	Gp4	g.chr9:116731399T>C	Silent	ZNF618	p.A12A	zinc finger protein 618	51 (0.00)	63 (0.10)	0.40
12-02	Gp4	g.chr19:52400204C>A	Missense Mutation	ZNF649	p.V15L	zinc finger protein 649	116 (0.00)	30 (0.27)	0.71
12-02	Gp4	g.chr9:40774498G>A	Silent	ZNF658	p.N259N	zinc finger protein 658	41 (0.00)	51 (0.16)	0.62
12-02	Gp4	g.chr9:130207384G>A	Missense Mutation	ZNF79	p.G469S	zinc finger protein 79	24 (0.00)	40 (0.12)	0.58
12-02	Gp4	g.chr19:53056508T>A	Silent	ZNF808	p.I113I	zinc finger protein 808	110 (0.00)	48 (0.33)	0.89
12-02	Gp4	g.chr19:53056549C>A	Missense Mutation	ZNF808	p.A127E	zinc finger protein 808	161 (0.00)	58 (0.34)	0.92
12-03	Gp3	g.chr12:9232276G>A	Missense Mutation	A2M	p.T997I	alpha-2-macroglobulin	104 (0.00)	80 (0.23)	0.60
12-03	Gp3	g.chr12:53701348G>T	Silent	AAAS	p.S522S	achalasia, adrenocortica	21 (0.00)	29 (0.17)	0.46
12-03	Gp3	g.chr12:53701398C>A	Missense Mutation	AAAS	p.A506S	achalasia, adrenocortica	43 (0.00)	45 (0.22)	0.59
12-03	Gp3	g.chr2:215843575C>A	Missense Mutation	ABCA12	p.D1644Y	ATP-binding cassette, s	53 (0.00)	88 (0.43)	1.15
12-03	Gp3	g.chr7:48550702G>A	Missense Mutation	ABCA13	p.C4516Y	ATP-binding cassette, s	40 (0.00)	149 (0.97)	2.58
12-03	Gp3	g.chr19:1046228G>T	Splice Site	ABCA7		ATP-binding cassette, s	28 (0.00)	640 (0.14)	0.38
12-03	Gp3	g.chr17:67031489C>A	Missense Mutation	ABCA9	p.W342C	ATP-binding cassette, s	15 (0.00)	29 (0.31)	0.83
12-03	Gp3	g.chr17:67031490C>A	Missense Mutation	ABCA9	p.W342L	ATP-binding cassette, s	15 (0.00)	30 (0.30)	0.80
12-03	Gp3	g.chr2:169850316C>G	Missense Mutation	ABCB11	p.G230R	ATP-binding cassette, s	41 (0.00)	26 (0.19)	0.51
12-03	Gp3	g.chr15:89728718C>T	Silent	ABHD2	p.D262D	abhydrolase domain con	27 (0.00)	94 (0.53)	1.42
12-03	Gp3	g.chr15:89738481G>A	Missense Mutation	ABHD2	p.V369M	abhydrolase domain con	52 (0.00)	63 (0.24)	0.63
12-03	Gp3	g.chr9:133760977C>T	Silent	ABL1	p.C1100C	ABL proto-oncogene 1,	24 (0.00)	136 (0.16)	0.43
12-03	Gp3	g.chr9:133761021G>T	Missense Mutation	ABL1	p.S1115I	ABL proto-oncogene 1,	19 (0.00)	127 (0.24)	0.63
12-03	Gp3	g.chr15:31093540G>T	RNA	AC004460.1			46 (0.02)	549 (0.24)	0.80
12-03	Gp3	g.chr19:52097529C>A	Nonsense Mutation	AC018755.1	p.E16*		21 (0.00)	67 (0.27)	0.96
12-03	Gp3	g.chr17:20418719C>T	RNA	AC025627.9			31 (0.00)	29 (0.59)	1.56
12-03	Gp3	g.chr3:10029647G>A	RNA	AC034193.5			24 (0.00)	29 (0.45)	1.20

12-03	Gp3	g.chr3:194476404G>T	lincRNA	AC090505.6			20 (0.00)	139 (0.14)	0.38
12-03	Gp3	g.chr3:38167325C>A	Missense Mutation	ACAA1	p.A349S	acetyl-CoA acyltransfer	55 (0.00)	63 (0.32)	0.59
12-03	Gp3	g.chr17:35632928C>G	Missense Mutation	ACACA	p.A236P	acetyl-CoA carboxylase	109 (0.00)	267 (0.37)	0.98
12-03	Gp3	g.chr12:112184045C>T	Missense Mutation	ACAD10	p.A738V	acyl-CoA dehydrogenas	46 (0.00)	63 (0.19)	0.51
12-03	Gp3	g.chr9:19434989C>T	Missense Mutation	ACER2	p.T137M	alkaline ceramidase 2	128 (0.00)	264 (0.19)	0.52
12-03	Gp3	g.chr1:55050454C>T	Silent	ACOT11	p.L54L	acyl-CoA thioesterase 1	24 (0.00)	89 (0.22)	0.60
12-03	Gp3	g.chr4:8398676C>G	Missense Mutation	ACOX3	p.E348D	acyl-CoA oxidase 3, pri	44 (0.00)	146 (0.23)	0.60
12-03	Gp3	g.chr11:125547761C>A	Nonsense Mutation	ACRV1	p.E162*	acrosomal vesicle protei	45 (0.00)	21 (0.76)	2.03
12-03	Gp3	g.chr11:66330275G>A	RNA	ACTN3		actinin, alpha 3 (gene/ps	32 (0.00)	319 (0.20)	0.73
12-03	Gp3	g.chr20:37400256G>T	Missense Mutation	ACTR5	p.A541S	ARP5 actin-related prot	108 (0.00)	323 (0.18)	0.49
12-03	Gp3	g.chr5:33616134T>A	Silent	ADAMTS12	p.I729I	ADAM metallopeptidas	33 (0.00)	31 (0.19)	0.52
12-03	Gp3	g.chr5:33649724G>C	Silent	ADAMTS12	p.L423L	ADAM metallopeptidas	46 (0.00)	24 (0.33)	0.89
12-03	Gp3	g.chr10:72498603C>A	Nonsense Mutation	ADAMTS14	p.C538*	ADAM metallopeptidas	29 (0.00)	300 (0.25)	0.66
12-03	Gp3	g.chr1:150529111G>A	Missense Mutation	ADAMTSL4	p.G531R	ADAMTS-like 4	25 (0.00)	381 (0.25)	0.82
12-03	Gp3	g.chr21:46603337G>T	Silent	ADARB1	p.L436L	adenosine deaminase, R	18 (0.00)	20 (0.50)	1.89
12-03	Gp3	g.chr1:227174223G>T	Missense Mutation	ADCK3	p.D577Y	aarF domain containing	20 (0.00)	94 (0.57)	1.53
12-03	Gp3	g.chr3:123071338G>C	Missense Mutation	ADCY5	p.Q42E	adenylate cyclase 5	41 (0.00)	227 (0.31)	0.64
12-03	Gp3	g.chr5:132228792C>A	Missense Mutation	AFF4	p.A776S	AF4/FMR2 family, men	194 (0.00)	68 (0.49)	1.29
12-03	Gp3	g.chr10:51748572G>T	Nonsense Mutation	AGAP6	p.E33*	ArfGAP with GTPase d	47 (0.00)	374 (0.41)	1.08
12-03	Gp3	g.chr1:49100186G>T	Silent	AGBL4	p.I310I	ATP/GTP binding prote	50 (0.00)	56 (0.18)	0.48
12-03	Gp3	g.chr1:247040570G>T	Missense Mutation	AHCTF1	p.H934N	AT hook containing trar	22 (0.00)	77 (0.16)	0.42
12-03	Gp3	g.chr14:105405701C>A	Missense Mutation	AHNAK2	p.D361Y	AHNAK nucleoprotein	35 (0.00)	25 (0.80)	2.13
12-03	Gp3	g.chr6:143457998C>T	Silent	AIG1	p.I56I	androgen-induced 1	17 (0.00)	119 (0.37)	0.99
12-03	Gp3	g.chr6:143654546G>T	Nonsense Mutation	AIG1	p.E215*	androgen-induced 1	34 (0.00)	44 (0.77)	2.06
12-03	Gp3	g.chr15:86225398C>T	Missense Mutation	AKAP13	p.P1708L	A kinase (PRKA) ancho	16 (0.00)	19 (0.37)	0.98
12-03	Gp3	g.chr15:86236564G>A	Silent	AKAP13	p.K1786K	A kinase (PRKA) ancho	39 (0.00)	38 (0.97)	2.60
12-03	Gp3	g.chr19:15507988C>T	Silent	AKAP8L	p.K503K	A kinase (PRKA) ancho	44 (0.00)	52 (0.38)	1.32
12-03	Gp3	g.chr15:101427809G>T	Missense Mutation	ALDH1A3	p.Q79H	aldehyde dehydrogenase	25 (0.00)	204 (0.19)	0.51
12-03	Gp3	g.chr3:125843285G>A	Missense Mutation	ALDH1L1	p.L614F	aldehyde dehydrogenase	15 (0.00)	81 (0.17)	0.46
12-03	Gp3	g.chr2:3730654C>T	Silent	ALLC	p.N167N	allantoicase	36 (0.00)	182 (0.69)	1.83
12-03	Gp3	g.chr2:73678225C>T	Missense Mutation	ALMS1	p.S1523L	Alstrom syndrome 1	16 (0.00)	26 (0.23)	0.62
12-03	Gp3	g.chr2:73679655G>A	Missense Mutation	ALMS1	p.V2000M	Alstrom syndrome 1	39 (0.00)	39 (0.44)	1.16
12-03	Gp3	g.chr1:110172024G>A	Missense Mutation	AMPD2	p.E646K	adenosine monophospha	25 (0.00)	73 (0.16)	0.44
12-03	Gp3	g.chr2:112636548C>T	Splice Site	ANAPC1	p.E72K	anaphase promoting con	31 (0.00)	19 (0.47)	1.26
12-03	Gp3	g.chr4:25392602T>A	Missense Mutation	ANAPC4	p.S224T	anaphase promoting con	18 (0.00)	27 (0.22)	0.59

12-03	Gp3	g.chr19:10204068G>T	Missense Mutation	ANGPTL6	p.D393E	angiopoietin-like 6	18 (0.00)	47 (0.51)	1.36
12-03	Gp3	g.chr5:139908027T>C	Silent	ANKHD1	p.N1832N	ankyrin repeat and KH	82 (0.00)	72 (0.18)	0.48
12-03	Gp3	g.chr12:110466351C>T	Missense Mutation	ANKRD13A	p.P327L	ankyrin repeat domain 1	19 (0.00)	59 (0.61)	1.63
12-03	Gp3	g.chr4:73979530T>A	Missense Mutation	ANKRD17	p.L1460F	ankyrin repeat domain 1	69 (0.00)	46 (0.57)	1.51
12-03	Gp3	g.chr9:38595861C>T	Silent	ANKRD18A	p.E492E	ankyrin repeat domain 1	108 (0.00)	107 (0.41)	1.10
12-03	Gp3	g.chr10:90583080G>T	Missense Mutation	ANKRD22	p.P152H	ankyrin repeat domain 2	68 (0.00)	366 (0.24)	0.63
12-03	Gp3	g.chr21:14414971G>A	RNA	ANKRD30BP2		ankyrin repeat domain 3	148 (0.00)	37 (0.16)	0.43
12-03	Gp3	g.chr1:145561771G>A	Missense Mutation	ANKRD35	p.A487T	ankyrin repeat domain 3	35 (0.00)	97 (0.15)	0.41
12-03	Gp3	g.chr2:89084116G>A	RNA	ANKRD36BP2		ankyrin repeat domain 3	93 (0.00)	59 (0.58)	1.22
12-03	Gp3	g.chr2:96521530C>T	Silent	ANKRD36C	p.Q1493Q	ankyrin repeat domain 3	55 (0.00)	44 (0.57)	1.52
12-03	Gp3	g.chr15:90335721G>A	Silent	ANPEP	p.G774G	alanyl (membrane) amin	30 (0.00)	75 (0.29)	0.78
12-03	Gp3	g.chr11:970258C>A	Missense Mutation	AP2A2	p.H76N	adaptor-related protein	64 (0.00)	246 (0.18)	0.48
12-03	Gp3	g.chr15:51289744G>A	Silent	AP4E1	p.E856E	adaptor-related protein	15 (0.00)	38 (0.16)	0.42
12-03	Gp3	g.chr12:99061338G>A	Silent	APAF1	p.P470P	apoptotic peptidase acti	53 (0.00)	32 (0.88)	2.33
12-03	Gp3	g.chr5:139940648A>G	Missense Mutation	APBB3	p.Y289H	amyloid beta (A4) precu	55 (0.00)	56 (0.57)	1.52
12-03	Gp3	g.chr1:159558435C>T	Silent	APCS	p.D203D	amyloid P component, s	19 (0.05)	14 (0.79)	1.66
12-03	Gp3	g.chr22:39496332C>A	Missense Mutation	APOBEC3H	p.R17S	apolipoprotein B mRNA	16 (0.00)	84 (0.20)	0.54
12-03	Gp3	g.chr22:36122931G>T	Silent	APOL5	p.T272T	apolipoprotein L, 5	91 (0.00)	46 (0.30)	0.81
12-03	Gp3	g.chr11:47196609G>T	Missense Mutation	ARFGAP2	p.S146Y	ADP-ribosylation factor	15 (0.00)	63 (0.68)	1.82
12-03	Gp3	g.chr22:43218332C>T	Silent	ARFGAP3	p.A252A	ADP-ribosylation factor	71 (0.00)	75 (0.16)	0.43
12-03	Gp3	g.chr15:32929968G>C	Missense Mutation	ARHGAP11A	p.R809S	Rho GTPase activating	23 (0.00)	24 (0.54)	1.78
12-03	Gp3	g.chr10:24908855G>A	Nonsense Mutation	ARHGAP21	p.Q657*	Rho GTPase activating	39 (0.00)	41 (0.71)	1.89
12-03	Gp3	g.chr17:12819263G>T	Nonsense Mutation	ARHGAP44	p.E108*	Rho GTPase activating	30 (0.00)	14 (0.36)	0.95
12-03	Gp3	g.chr17:12847463C>A	Missense Mutation	ARHGAP44	p.P271T	Rho GTPase activating	15 (0.00)	25 (0.32)	0.85
12-03	Gp3	g.chr8:1812554C>T	Missense Mutation	ARHGEF10	p.T166I	Rho guanine nucleotide	35 (0.00)	25 (0.24)	0.64
12-03	Gp3	g.chr1:156909367C>T	Missense Mutation	ARHGEF11	p.A1357T	Rho guanine nucleotide	27 (0.00)	32 (0.75)	1.58
12-03	Gp3	g.chr11:73063887C>G	Missense Mutation	ARHGEF17	p.P1095A	Rho guanine nucleotide	17 (0.00)	76 (0.20)	0.53
12-03	Gp3	g.chr11:73066629C>A	Missense Mutation	ARHGEF17	p.L1169I	Rho guanine nucleotide	23 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chr11:73066916G>A	Missense Mutation	ARHGEF17	p.R1194H	Rho guanine nucleotide	132 (0.00)	264 (0.15)	0.39
12-03	Gp3	g.chr12:101790300T>C	Missense Mutation	ARL1	p.E114G	ADP-ribosylation factor	45 (0.00)	22 (0.45)	1.21
12-03	Gp3	g.chr6:109274326A>G	Missense Mutation	ARMC2	p.I563V	armadillo repeat contain	31 (0.00)	70 (0.67)	1.05
12-03	Gp3	g.chr19:4891568C>T	Silent	ARRDC5	p.E173E	arrestin domain containi	19 (0.00)	40 (0.12)	0.45
12-03	Gp3	g.chr22:51063793G>T	Missense Mutation	ARSA	p.P437H	arylsulfatase A	25 (0.00)	252 (0.17)	0.65
12-03	Gp3	g.chr1:155408730G>A	Missense Mutation	ASH1L	p.A1739V	ash1 (absent, small, or h	28 (0.00)	21 (0.24)	0.50
12-03	Gp3	g.chr22:26830448C>G	Missense Mutation	ASPHD2	p.I289M	aspartate beta-hydroxyla	40 (0.00)	26 (0.35)	0.92

12-03	Gp3	g.chr9:133364742C>G	Silent	ASS1	p.G287G	argininosuccinate synth	40 (0.00)	80 (0.41)	1.10
12-03	Gp3	g.chr2:96789818G>T	Missense Mutation	ASTL	p.A356E	astacin-like metallo-end	19 (0.00)	57 (0.33)	0.89
12-03	Gp3	g.chr18:31323689A>G	Missense Mutation	ASXL3	p.I1293V	additional sex combs lik	48 (0.00)	25 (0.28)	0.75
12-03	Gp3	g.chr18:31324919C>T	Nonsense Mutation	ASXL3	p.Q1703*	additional sex combs lik	34 (0.00)	54 (0.70)	1.88
12-03	Gp3	g.chr17:29161625A>G	Missense Mutation	ATAD5	p.K176E	ATPase family, AAA d	46 (0.00)	28 (0.25)	0.67
12-03	Gp3	g.chr1:161833037T>C	Missense Mutation	ATF6	p.Y552H	activating transcription	50 (0.00)	27 (0.41)	1.09
12-03	Gp3	g.chr11:108142092G>A	Silent	ATM	p.R1012R	ATM serine/threonine k	27 (0.00)	35 (0.23)	0.61
12-03	Gp3	g.chr11:108163472T>A	Silent	ATM	p.V1521V	ATM serine/threonine k	47 (0.00)	69 (0.16)	0.43
12-03	Gp3	g.chr4:94751026G>C	Missense Mutation	ATOH1	p.G317R	atonal homolog 1 (Dros	48 (0.00)	182 (0.24)	0.63
12-03	Gp3	g.chr15:25940161C>A	Missense Mutation	ATP10A	p.A965S	ATPase, class V, type 1	16 (0.00)	108 (0.37)	1.22
12-03	Gp3	g.chr18:43664288T>C	Missense Mutation	ATP5A1	p.K541R	ATP synthase, H+ trans	18 (0.00)	23 (0.26)	0.70
12-03	Gp3	g.chr13:26436522C>A	Silent	ATP8A2	p.P1053P	ATPase, aminophospho	39 (0.00)	14 (0.43)	1.14
12-03	Gp3	g.chr1:154300325C>T	Missense Mutation	ATP8B2	p.S17F	ATPase, aminophospho	31 (0.00)	106 (0.62)	1.31
12-03	Gp3	g.chr17:17921958G>T	Missense Mutation	ATPAF2	p.L259M	ATP synthase mitochon	15 (0.00)	203 (0.33)	0.89
12-03	Gp3	g.chr17:8110573C>T	Missense Mutation	AURKB	p.V107I	aurora kinase B	18 (0.00)	75 (0.29)	0.78
12-03	Gp3	g.chr11:66114009G>T	Silent	B3GNT1	p.P336P	UDP-GlcNAc:betaGal	33 (0.00)	218 (0.12)	0.44
12-03	Gp3	g.chr3:182987909G>T	Missense Mutation	B3GNT5	p.R108I	UDP-GlcNAc:betaGal	38 (0.00)	60 (0.80)	2.13
12-03	Gp3	g.chr1:44456019G>T	Missense Mutation	B4GALT2	p.G340W	UDP-Gal:betaGlcNAc	125 (0.00)	90 (0.21)	0.56
12-03	Gp3	g.chr15:40758173C>G	Silent	BAHD1	p.G729G	bromo adjacent homolo	73 (0.00)	366 (0.27)	0.73
12-03	Gp3	g.chr14:76012836C>T	Missense Mutation	BATF	p.A67V	basic leucine zipper tran	30 (0.00)	118 (0.16)	0.43
12-03	Gp3	g.chr12:56995476C>A	Missense Mutation	BAZ2A	p.D1309Y	bromodomain adjacent	88 (0.00)	110 (0.29)	0.78
12-03	Gp3	g.chr12:56995513G>A	Silent	BAZ2A	p.D1296D	bromodomain adjacent	76 (0.00)	99 (0.34)	0.92
12-03	Gp3	g.chr19:49309921G>A	Silent	BCAT2	p.P51P	branched chain amino-a	49 (0.00)	549 (0.15)	0.53
12-03	Gp3	g.chr14:96707517G>T	Silent	BDKRB2	p.L284L	bradykinin receptor B2	21 (0.00)	37 (0.19)	0.50
12-03	Gp3	g.chr10:60549449C>T	Missense Mutation	BICC1	p.T268I	BicC family RNA bindi	40 (0.00)	25 (0.68)	1.81
12-03	Gp3	g.chr2:32726915C>T	Missense Mutation	BIRC6	p.P3056L	baculoviral IAP repeat c	29 (0.00)	11 (0.73)	1.94
12-03	Gp3	g.chr15:91272171G>T	Intron	BLM		Bloom syndrome, RecQ	20 (0.00)	30 (0.23)	0.62
12-03	Gp3	g.chr15:91290088G>A	Intron	BLM		Bloom syndrome, RecQ	172 (0.00)	245 (0.60)	1.60
12-03	Gp3	g.chr15:91305040A>T	Intron	BLM		Bloom syndrome, RecQ	66 (0.00)	30 (0.23)	0.62
12-03	Gp3	g.chr15:91335591C>T	Intron	BLM		Bloom syndrome, RecQ	86 (0.00)	121 (0.21)	0.57
12-03	Gp3	g.chr10:133787448C>T	Splice Site	BNIP3		BCL2/adenovirus E1B	129 (0.00)	92 (0.15)	0.41
12-03	Gp3	g.chr7:134363641C>A	Missense Mutation	BPGM	p.P213H	2,3-bisphosphoglycerat	15 (0.00)	40 (0.47)	1.27
12-03	Gp3	g.chr17:41200633G>A	Intron	BRCA1		breast cancer 1, early on	40 (0.00)	66 (0.26)	0.48
12-03	Gp3	g.chr17:41203400C>T	Intron	BRCA1		breast cancer 1, early on	63 (0.00)	73 (0.37)	0.69
12-03	Gp3	g.chr17:41213189T>C	Intron	BRCA1		breast cancer 1, early on	81 (0.00)	24 (0.42)	0.78

12-03	Gp3	g.chr17:41236912T>C	Intron	BRCA1		breast cancer 1, early on	66 (0.00)	23 (0.48)	0.89
12-03	Gp3	g.chr17:41237033C>A	Intron	BRCA1		breast cancer 1, early on	48 (0.00)	19 (0.95)	1.77
12-03	Gp3	g.chr17:41259688G>T	Intron	BRCA1		breast cancer 1, early on	34 (0.00)	55 (0.24)	0.44
12-03	Gp3	g.chr13:32904642G>C	Intron	BRCA2		breast cancer 2, early on	24 (0.00)	37 (0.92)	2.45
12-03	Gp3	g.chr13:32928700G>A	Intron	BRCA2		breast cancer 2, early on	168 (0.01)	73 (0.96)	2.56
12-03	Gp3	g.chr22:50217813G>A	Silent	BRD1	p.I51I	bromodomain containin	37 (0.00)	269 (0.20)	0.78
12-03	Gp3	g.chr1:177250157G>A	Silent	BRINP2	p.R615R	bone morphogenetic pro	55 (0.00)	134 (0.14)	0.38
12-03	Gp3	g.chr10:93751924G>T	Missense Mutation	BTAF1	p.R968I	BTAF1 RNA polymeras	22 (0.00)	40 (0.30)	0.80
12-03	Gp3	g.chr15:40509749G>C	Missense Mutation	BUB1B	p.D911H	BUB1 mitotic checkpoi	94 (0.00)	46 (0.20)	0.52
12-03	Gp3	g.chr15:40509808T>C	Silent	BUB1B	p.F930F	BUB1 mitotic checkpoi	86 (0.00)	53 (0.30)	0.81
12-03	Gp3	g.chr15:40509855C>T	Missense Mutation	BUB1B	p.S946F	BUB1 mitotic checkpoi	70 (0.00)	41 (0.49)	1.30
12-03	Gp3	g.chr10:50533032G>A	Silent	C10orf71	p.K814K	chromosome 10 open re	33 (0.00)	14 (0.36)	0.95
12-03	Gp3	g.chr10:124712521G>A	Silent	C10orf88	p.N64N	chromosome 10 open re	15 (0.00)	72 (0.39)	1.04
12-03	Gp3	g.chr11:66571578G>T	Nonsense Mutation	C11orf80	p.E100*	chromosome 11 open re	43 (0.00)	73 (0.58)	2.13
12-03	Gp3	g.chr11:66581364C>A	Missense Mutation	C11orf80	p.P138H	chromosome 11 open re	22 (0.00)	64 (0.83)	3.07
12-03	Gp3	g.chr14:105460983C>T	Missense Mutation	C14orf79	p.R289C	chromosome 14 open re	42 (0.00)	142 (0.19)	0.51
12-03	Gp3	g.chr1:169792600C>G	Missense Mutation	C1orf112	p.L279V	chromosome 1 open rea	25 (0.00)	119 (0.40)	1.08
12-03	Gp3	g.chr1:150255890C>A	Silent	C1orf51	p.S71S		55 (0.00)	193 (0.42)	1.41
12-03	Gp3	g.chr1:197874965G>A	Missense Mutation	C1orf53	p.V102M	chromosome 1 open rea	131 (0.00)	30 (0.40)	1.07
12-03	Gp3	g.chr5:34043179G>A	Missense Mutation	C1QTNF3	p.P18S	C1q and tumor necrosis	91 (0.00)	27 (0.19)	0.49
12-03	Gp3	g.chr11:73745033C>A	Missense Mutation	C2CD3	p.A2058S	C2 calcium-dependent d	102 (0.00)	33 (0.33)	0.89
12-03	Gp3	g.chr2:29296413C>A	Missense Mutation	C2orf71	p.D239Y	chromosome 2 open rea	55 (0.00)	188 (0.22)	0.58
12-03	Gp3	g.chr2:29296446C>A	Nonsense Mutation	C2orf71	p.E228*	chromosome 2 open rea	47 (0.00)	207 (0.17)	0.45
12-03	Gp3	g.chr4:128938627G>A	Missense Mutation	C4orf29	p.G194R	chromosome 4 open rea	74 (0.00)	151 (0.36)	0.95
12-03	Gp3	g.chr4:71024361C>A	Missense Mutation	C4orf40	p.A131D		57 (0.00)	59 (0.27)	0.72
12-03	Gp3	g.chr5:37244595G>A	Missense Mutation	C5orf42	p.S151F	chromosome 5 open rea	94 (0.00)	57 (0.25)	0.65
12-03	Gp3	g.chr5:40958231G>T	Missense Mutation	C7	p.D453Y	complement component	57 (0.00)	117 (0.70)	1.87
12-03	Gp3	g.chr9:35043869G>A	Missense Mutation	C9orf131	p.E415K	chromosome 9 open rea	15 (0.00)	57 (0.49)	1.31
12-03	Gp3	g.chr8:86249288C>A	Silent	CA1	p.L80L	carbonic anhydrase I	54 (0.00)	106 (0.69)	1.84
12-03	Gp3	g.chr9:140904511C>T	Silent	CACNA1B	p.N714N	calcium channel, voltag	15 (0.00)	218 (0.17)	0.44
12-03	Gp3	g.chr12:2717735C>T	Missense Mutation	CACNA1C	p.R1159C	calcium channel, voltag	15 (0.00)	64 (0.22)	0.58
12-03	Gp3	g.chr22:40068279G>A	Missense Mutation	CACNA1I	p.V1539M	calcium channel, voltag	97 (0.00)	19 (0.42)	1.12
12-03	Gp3	g.chr12:49220620C>G	Missense Mutation	CACNB3	p.L325V	calcium channel, voltag	50 (0.00)	101 (0.15)	0.40
12-03	Gp3	g.chr2:27454967G>A	Missense Mutation	CAD	p.M777I	carbamoyl-phosphate sy	49 (0.00)	37 (0.92)	2.45
12-03	Gp3	g.chr2:27455093G>A	Splice Site	CAD		carbamoyl-phosphate sy	50 (0.00)	36 (0.89)	2.37

12-03	Gp3	g.chr11:115049409G>A	Silent	CADM1	p.L389L	cell adhesion molecule	38 (0.00)	28 (0.57)	1.52
12-03	Gp3	g.chr3:85014467C>T	Intron	CADM2		cell adhesion molecule	24 (0.00)	18 (0.33)	0.89
12-03	Gp3	g.chr3:85117354C>A	Intron	CADM2		cell adhesion molecule	27 (0.00)	13 (0.38)	1.03
12-03	Gp3	g.chr3:85252347C>T	Intron	CADM2		cell adhesion molecule	21 (0.00)	34 (0.18)	0.47
12-03	Gp3	g.chr3:85438297C>T	Intron	CADM2		cell adhesion molecule	100 (0.00)	253 (0.28)	0.75
12-03	Gp3	g.chr3:85553090G>A	Intron	CADM2		cell adhesion molecule	50 (0.00)	17 (0.59)	1.57
12-03	Gp3	g.chr3:85611350A>G	Intron	CADM2		cell adhesion molecule	25 (0.00)	26 (0.23)	0.62
12-03	Gp3	g.chr3:85660780G>T	Intron	CADM2		cell adhesion molecule	69 (0.00)	20 (0.25)	0.67
12-03	Gp3	g.chr3:85763408C>T	Intron	CADM2		cell adhesion molecule	121 (0.00)	25 (0.32)	0.85
12-03	Gp3	g.chr3:85800359G>A	Intron	CADM2		cell adhesion molecule	49 (0.00)	135 (0.37)	0.99
12-03	Gp3	g.chr3:85827052C>A	Intron	CADM2		cell adhesion molecule	57 (0.00)	30 (0.17)	0.44
12-03	Gp3	g.chr3:86064622G>A	Intron	CADM2		cell adhesion molecule	35 (0.00)	43 (0.21)	0.56
12-03	Gp3	g.chr10:105215306C>A	Nonsense Mutation	CALHM1	p.E252*	calcium homeostasis m	21 (0.00)	186 (0.22)	0.57
12-03	Gp3	g.chr15:68491943C>A	Missense Mutation	CALML4	p.M80I	calmodulin-like 4	26 (0.00)	177 (0.31)	0.83
12-03	Gp3	g.chr3:49898725G>A	Silent	CAMKV	p.N150N	CaM kinase-like vesicle	16 (0.00)	189 (0.23)	0.62
12-03	Gp3	g.chr1:40527459C>A	Missense Mutation	CAP1	p.A90D	CAP, adenylate cyclase-	41 (0.00)	132 (0.70)	1.86
12-03	Gp3	g.chr11:64978313G>A	Silent	CAPN1	p.L696L	calpain 1, (mu/I) large s	36 (0.00)	229 (0.59)	2.19
12-03	Gp3	g.chr19:36633202C>A	Splice Site	CAPNS1	p.S70R	calpain, small subunit 1	27 (0.00)	137 (0.16)	0.43
12-03	Gp3	g.chr13:111296779A>T	Missense Mutation	CARS2	p.F457I	cysteinyl-tRNA synthet	22 (0.00)	35 (0.14)	0.38
12-03	Gp3	g.chr10:115489176C>T	Silent	CASP7	p.T263T	caspase 7, apoptosis-rel	24 (0.00)	94 (0.96)	2.55
12-03	Gp3	g.chr3:121973109C>A	Silent	CASR	p.R25R	calcium-sensing recepto	23 (0.00)	22 (0.95)	2.55
12-03	Gp3	g.chr11:65790440G>A	Missense Mutation	CATSPER1	p.R437W	cation channel, sperm a	15 (0.00)	54 (0.19)	0.69
12-03	Gp3	g.chr19:45293302C>T	Missense Mutation	CBLC	p.T320I	Cbl proto-oncogene C,	20 (0.00)	111 (0.26)	0.70
12-03	Gp3	g.chr19:14034152C>A	Missense Mutation	CC2D1A	p.P550T	coiled-coil and C2 dom	16 (0.00)	236 (0.11)	0.40
12-03	Gp3	g.chr1:52826803G>A	Splice Site	CC2D1B	p.T107M	coiled-coil and C2 dom	20 (0.00)	157 (0.17)	0.44
12-03	Gp3	g.chr9:131600404C>T	Missense Mutation	CCBL1	p.E122K	cysteine conjugate-beta	97 (0.00)	81 (0.54)	1.45
12-03	Gp3	g.chr7:31617838C>G	Silent	CCDC129	p.A228A	coiled-coil domain cont	49 (0.00)	72 (0.64)	1.70
12-03	Gp3	g.chr17:79638778C>G	Missense Mutation	CCDC137	p.Q168E	coiled-coil domain cont	15 (0.00)	110 (0.25)	0.91
12-03	Gp3	g.chr2:179742714C>A	Nonsense Mutation	CCDC141	p.E626*	coiled-coil domain cont	34 (0.00)	39 (0.51)	1.37
12-03	Gp3	g.chr2:170537558G>A	Nonsense Mutation	CCDC173	p.R85*	coiled-coil domain cont	75 (0.00)	57 (0.16)	0.42
12-03	Gp3	g.chr1:159860329G>A	Silent	CCDC19	p.G71G		103 (0.00)	63 (0.71)	1.51
12-03	Gp3	g.chr17:42761312G>A	Missense Mutation	CCDC43	p.L74F	coiled-coil domain cont	18 (0.00)	15 (0.33)	0.89
12-03	Gp3	g.chr3:56628052A>T	Missense Mutation	CCDC66	p.H467L	coiled-coil domain cont	37 (0.00)	33 (0.21)	0.57
12-03	Gp3	g.chr17:34304676G>C	Missense Mutation	CCL16	p.P97A	chemokine (C-C motif)	21 (0.00)	34 (0.26)	0.71
12-03	Gp3	g.chr10:42928724G>A	RNA	CCNYL2		cyclin Y-like 2	29 (0.00)	11 (0.45)	1.21

12-03	Gp3	g.chr10:42928727G>A	RNA	CCNYL2		cyclin Y-like 2	29 (0.00)	11 (0.45)	1.21
12-03	Gp3	g.chr17:38711666G>A	Silent	CCR7	p.Y155Y	chemokine (C-C motif)	35 (0.00)	35 (0.40)	1.07
12-03	Gp3	g.chr12:7556307C>T	Missense Mutation	CD163L1	p.G421E	CD163 molecule-like 1	18 (0.00)	10 (0.60)	1.60
12-03	Gp3	g.chr17:72537783C>A	Missense Mutation	CD300C	p.R207I	CD300c molecule	29 (0.00)	110 (0.71)	1.89
12-03	Gp3	g.chr11:60885884T>A	Missense Mutation	CD5	p.L111Q	CD5 molecule	25 (0.00)	201 (0.21)	0.42
12-03	Gp3	g.chr3:121822515A>G	Missense Mutation	CD86	p.K68R	CD86 molecule	15 (0.00)	13 (0.46)	1.23
12-03	Gp3	g.chr11:64594624G>A	Silent	CDC42BPG	p.D1429D	CDC42 binding protein	16 (0.00)	496 (0.17)	0.61
12-03	Gp3	g.chr22:19471492G>A	Silent	CDC45	p.G150G	cell division cycle 45	51 (0.00)	35 (0.46)	1.22
12-03	Gp3	g.chr1:91967349G>A	Missense Mutation	CDC7	p.G26S	cell division cycle 7	126 (0.00)	209 (0.22)	0.57
12-03	Gp3	g.chr16:66413301G>T	Missense Mutation	CDH5	p.A21S	cadherin 5, type 2 (vasc	34 (0.00)	236 (0.17)	0.45
12-03	Gp3	g.chr10:85971996G>T	Nonsense Mutation	CDHR1	p.E539*	cadherin-related family	44 (0.02)	39 (0.21)	0.55
12-03	Gp3	g.chr5:176017140G>A	Missense Mutation	CDHR2	p.A1090T	cadherin-related family	142 (0.00)	255 (0.15)	0.41
12-03	Gp3	g.chr1:1581160G>A	Nonsense Mutation	CDK11B	p.Q122*	cyclin-dependent kinase	397 (0.00)	691 (0.17)	0.44
12-03	Gp3	g.chr11:67274909G>T	Silent	CDK2AP2	p.V80V	cyclin-dependent kinase	21 (0.00)	76 (0.13)	0.49
12-03	Gp3	g.chr17:30815524G>A	Missense Mutation	CDK5R1	p.E296K	cyclin-dependent kinase	76 (0.00)	145 (0.35)	0.94
12-03	Gp3	g.chr20:31973458G>T	Missense Mutation	CDK5RAP1	p.Q292K	CDK5 regulatory subun	33 (0.00)	27 (0.19)	0.49
12-03	Gp3	g.chr9:123307991C>G	Splice Site	CDK5RAP2		CDK5 regulatory subun	22 (0.00)	10 (0.50)	1.33
12-03	Gp3	g.chr12:12870966C>A	Missense Mutation	CDKN1B	p.Q65K	cyclin-dependent kinase	22 (0.00)	64 (0.17)	0.46
12-03	Gp3	g.chr6:4892219C>T	Silent	CDYL	p.L99L	chromodomain protein,	39 (0.00)	69 (0.26)	0.70
12-03	Gp3	g.chr19:43093649C>T	Silent	CEACAM8	p.A221A	carcinoembryonic antig	26 (0.00)	15 (0.67)	1.78
12-03	Gp3	g.chr2:37454720G>A	Missense Mutation	CEBPZ	p.T539I	CCAAT/enhancer bindi	50 (0.00)	34 (0.21)	0.55
12-03	Gp3	g.chr22:18028002T>C	Missense Mutation	CECR2	p.S845P	cat eye syndrome chrom	24 (0.00)	60 (0.17)	0.44
12-03	Gp3	g.chr22:18029103G>T	Missense Mutation	CECR2	p.G1212W	cat eye syndrome chrom	36 (0.00)	80 (0.17)	0.47
12-03	Gp3	g.chr1:109794243C>A	Silent	CELSR2	p.V514V	cadherin, EGF LAG sev	64 (0.00)	50 (0.60)	1.60
12-03	Gp3	g.chr1:109795490T>C	Missense Mutation	CELSR2	p.V930A	cadherin, EGF LAG sev	19 (0.00)	71 (0.14)	0.38
12-03	Gp3	g.chr3:48691351G>T	Nonsense Mutation	CELSR3	p.C1746*	cadherin, EGF LAG sev	79 (0.00)	353 (0.16)	0.42
12-03	Gp3	g.chr1:179966068C>A	Missense Mutation	CEP350	p.P259Q	centrosomal protein 350	28 (0.00)	15 (0.67)	1.78
12-03	Gp3	g.chr1:111725522C>T	Silent	CEPT1	p.P316P	choline/ethanolamine p	64 (0.00)	76 (0.25)	0.48
12-03	Gp3	g.chr19:4408937G>A	Silent	CHAF1A	p.K47K	chromatin assembly fac	43 (0.00)	68 (0.34)	1.22
12-03	Gp3	g.chr1:6206355G>A	Silent	CHD5	p.P573P	chromodomain helicase	31 (0.00)	292 (0.17)	0.46
12-03	Gp3	g.chr1:6217433G>T	Intron	CHD5		chromodomain helicase	33 (0.00)	65 (0.26)	0.70
12-03	Gp3	g.chr1:6235413A>G	Intron	CHD5		chromodomain helicase	22 (0.00)	234 (0.15)	0.41
12-03	Gp3	g.chr20:32438854T>C	Silent	CHMP4B	p.F155F	charged multivesicular	87 (0.00)	97 (0.22)	0.58
12-03	Gp3	g.chr11:46407104G>A	Missense Mutation	CHRM4	p.P335L	cholinergic receptor, mu	24 (0.00)	360 (0.20)	0.53
12-03	Gp3	g.chr2:233407730T>A	Missense Mutation	CHRNG	p.I248N	cholinergic receptor, nic	97 (0.00)	222 (0.21)	0.55

12-03	Gp3	g.chr16:57473196C>T	Missense Mutation	CIAPIN1	p.G70R	cytokine induced apopt	30 (0.00)	137 (0.16)	0.43
12-03	Gp3	g.chr11:46774920C>T	Missense Mutation	CKAP5	p.R1666H	cytoskeleton associated	44 (0.00)	25 (0.88)	2.35
12-03	Gp3	g.chr16:74447519C>A	Missense Mutation	CLEC18B	p.G171V	C-type lectin domain fa	20 (0.00)	60 (0.20)	0.53
12-03	Gp3	g.chr16:70211247G>T	Missense Mutation	CLEC18C	p.G107V	C-type lectin domain fa	20 (0.00)	82 (0.17)	0.46
12-03	Gp3	g.chr1:25166356G>A	Missense Mutation	CLIC4	p.E141K	chloride intracellular ch	42 (0.00)	35 (0.94)	2.51
12-03	Gp3	g.chr19:45489754G>A	Nonsense Mutation	CLPTM1	p.W224*	cleft lip and palate asso	53 (0.00)	68 (0.18)	0.47
12-03	Gp3	g.chr18:72186248G>T	Missense Mutation	CNDP2	p.Q425H	CNDP dipeptidase 2 (m	42 (0.00)	197 (0.22)	0.60
12-03	Gp3	g.chr2:99013190G>A	Missense Mutation	CNGA3	p.M523I	cyclic nucleotide gated	37 (0.00)	67 (0.19)	0.52
12-03	Gp3	g.chr6:154762429C>A	Missense Mutation	CNKSR3	p.Q88H	CNKSR family member	51 (0.00)	95 (0.22)	0.59
12-03	Gp3	g.chr10:104679750C>A	Missense Mutation	CNNM2	p.P505T	cyclin and CBS domain	37 (0.00)	33 (0.76)	2.02
12-03	Gp3	g.chr10:104836919C>G	Missense Mutation	CNNM2	p.H870Q	cyclin and CBS domain	37 (0.00)	243 (0.22)	0.59
12-03	Gp3	g.chr2:97493599C>T	Missense Mutation	CNNM3	p.R551C	cyclin and CBS domain	19 (0.00)	98 (0.19)	0.52
12-03	Gp3	g.chr11:99690407G>T	Missense Mutation	CNTN5	p.S63I	contactin 5	75 (0.00)	34 (0.38)	1.02
12-03	Gp3	g.chr17:40850669G>T	Missense Mutation	CNTNAP1	p.G1299V	contactin associated pro	53 (0.00)	104 (0.21)	0.39
12-03	Gp3	g.chr6:56044694G>T	Missense Mutation	COL21A1	p.L108I	collagen, type XXI, alp	64 (0.00)	74 (0.35)	0.94
12-03	Gp3	g.chr9:116930954G>A	Silent	COL27A1	p.S373S	collagen, type XXVII, a	26 (0.00)	112 (0.23)	0.62
12-03	Gp3	g.chr13:110864017G>A	Missense Mutation	COL4A1	p.P149S	collagen, type IV, alpha	15 (0.00)	31 (0.84)	2.24
12-03	Gp3	g.chr9:137622306C>T	Silent	COL5A1	p.T383T	collagen, type V, alpha	22 (0.00)	56 (0.55)	1.90
12-03	Gp3	g.chr3:130289760G>T	Missense Mutation	COL6A6	p.G834C	collagen, type VI, alpha	122 (0.00)	14 (0.50)	1.33
12-03	Gp3	g.chr2:62227970C>T	Silent	COMMD1	p.I105I	copper metabolism (Mu	38 (0.00)	85 (0.52)	1.38
12-03	Gp3	g.chr3:149459389G>T	Silent	COMMD2	p.L173L	COMM domain contain	46 (0.00)	106 (0.34)	0.91
12-03	Gp3	g.chr9:131095789G>T	Missense Mutation	COQ4	p.W221C	coenzyme Q4	56 (0.00)	174 (0.19)	0.51
12-03	Gp3	g.chr5:173380246C>A	Missense Mutation	CPEB4	p.Q645K	cytoplasmic polyadenyl	48 (0.02)	141 (0.97)	2.59
12-03	Gp3	g.chr12:94072767C>A	Missense Mutation	CRADD	p.L73I	CASP2 and RIPK1 dom	70 (0.00)	73 (0.75)	2.01
12-03	Gp3	g.chr22:50315393C>A	Silent	CRELD2	p.T192T	cysteine-rich with EGF-	26 (0.00)	251 (0.14)	0.53
12-03	Gp3	g.chr6:49665656C>A	Silent	CRISP2	p.S144S	cysteine-rich secretory	59 (0.00)	28 (0.25)	0.67
12-03	Gp3	g.chr16:84911053T>A	Nonsense Mutation	CRISPLD2	p.L389*	cysteine-rich secretory	22 (0.00)	47 (0.26)	0.68
12-03	Gp3	g.chr4:5843070C>A	Missense Mutation	CRMP1	p.S257I	collapsin response medi	64 (0.00)	232 (0.16)	0.44
12-03	Gp3	g.chr22:27008142C>A	Nonsense Mutation	CRYBB1	p.E65*	crystallin, beta B1	25 (0.00)	112 (0.21)	0.55
12-03	Gp3	g.chr22:27008143G>A	Silent	CRYBB1	p.F64F	crystallin, beta B1	25 (0.00)	113 (0.20)	0.54
12-03	Gp3	g.chr17:61987865G>T	Nonsense Mutation	CSHL1	p.S74*	chorionic somatomamm	18 (0.00)	144 (0.28)	0.74
12-03	Gp3	g.chr1:34006200A>G	Missense Mutation	CSMD2	p.Y3186H	CUB and Sushi multipl	26 (0.00)	37 (0.54)	1.44
12-03	Gp3	g.chr8:113353768G>C	Missense Mutation	CSMD3	p.T2197S	CUB and Sushi multipl	50 (0.00)	18 (0.89)	2.37
12-03	Gp3	g.chr17:80213332T>A	Missense Mutation	CSNK1D	p.K103N	casein kinase 1, delta	30 (0.00)	182 (0.13)	0.47
12-03	Gp3	g.chr11:33108599C>T	Missense Mutation	CSTF3	p.R577K	cleavage stimulation fac	97 (0.00)	63 (0.40)	1.06

12-03	Gp3	g.chr17:8141356T>A	Missense Mutation	CTC1	p.R214W	CTS telomere maintena	25 (0.00)	14 (0.43)	1.14
12-03	Gp3	g.chr5:56817007G>A	RNA	CTD-2023N9.1			23 (0.00)	64 (0.95)	1.45
12-03	Gp3	g.chr5:138261016G>T	Missense Mutation	CTNNA1	p.D607Y	catenin (cadherin-associ	29 (0.00)	15 (0.67)	1.78
12-03	Gp3	g.chr11:57575702A>G	Missense Mutation	CTNND1	p.T671A	catenin (cadherin-associ	51 (0.00)	53 (0.19)	0.38
12-03	Gp3	g.chr11:88029405G>C	Missense Mutation	CTSC	p.A262G	cathepsin C	46 (0.00)	92 (0.28)	0.75
12-03	Gp3	g.chr1:150772142C>A	Missense Mutation	CTSK	p.C221F	cathepsin K	15 (0.00)	13 (0.62)	2.04
12-03	Gp3	g.chr6:43013099G>T	Silent	CUL7	p.G968G	cullin 7	36 (0.00)	199 (0.15)	0.40
12-03	Gp3	g.chr17:61514738C>T	Missense Mutation	CYB561	p.M57I	cytochrome b561	15 (0.00)	117 (0.15)	0.41
12-03	Gp3	g.chr5:156727766G>T	Missense Mutation	CYFIP2	p.C118F	cytoplasmic FMR1 inte	27 (0.00)	76 (0.25)	0.67
12-03	Gp3	g.chr19:41352813G>A	Silent	CYP2A6	p.D266D	cytochrome P450, famil	50 (0.00)	14 (0.57)	1.52
12-03	Gp3	g.chr7:99264276C>T	Missense Mutation	CYP3A5	p.V157M	cytochrome P450, famil	39 (0.00)	40 (0.97)	2.60
12-03	Gp3	g.chr7:99270203C>A	Splice Site	CYP3A5	p.R106S	cytochrome P450, famil	50 (0.00)	12 (0.75)	2.00
12-03	Gp3	g.chr1:47348888G>A	RNA	CYP4Z2P		cytochrome P450, famil	65 (0.00)	51 (0.18)	0.47
12-03	Gp3	g.chr6:39846004C>A	Missense Mutation	DAAM2	p.Q443K	dishevelled associated a	42 (0.00)	16 (0.38)	1.00
12-03	Gp3	g.chr9:124329988C>G	Intron	DAB2IP		DAB2 interacting protei	20 (0.00)	31 (0.16)	0.43
12-03	Gp3	g.chr9:124336181C>A	Intron	DAB2IP		DAB2 interacting protei	32 (0.00)	67 (0.36)	0.96
12-03	Gp3	g.chr9:124338196C>A	Intron	DAB2IP		DAB2 interacting protei	23 (0.00)	26 (0.58)	1.54
12-03	Gp3	g.chr9:124338526C>T	Intron	DAB2IP		DAB2 interacting protei	140 (0.00)	28 (0.21)	0.57
12-03	Gp3	g.chr9:124362657C>T	Intron	DAB2IP		DAB2 interacting protei	26 (0.00)	132 (0.17)	0.44
12-03	Gp3	g.chr9:124396080C>T	Intron	DAB2IP		DAB2 interacting protei	28 (0.00)	28 (0.36)	0.95
12-03	Gp3	g.chr9:124399239G>A	Intron	DAB2IP		DAB2 interacting protei	63 (0.00)	81 (0.28)	0.76
12-03	Gp3	g.chr9:124399257T>A	Intron	DAB2IP		DAB2 interacting protei	60 (0.02)	80 (0.30)	0.80
12-03	Gp3	g.chr9:124411424G>T	Intron	DAB2IP		DAB2 interacting protei	40 (0.00)	18 (0.28)	0.74
12-03	Gp3	g.chr9:124463308C>A	Intron	DAB2IP		DAB2 interacting protei	53 (0.00)	52 (0.62)	1.64
12-03	Gp3	g.chr9:124480364G>T	Intron	DAB2IP		DAB2 interacting protei	21 (0.00)	135 (0.15)	0.40
12-03	Gp3	g.chr9:124499260A>G	Intron	DAB2IP		DAB2 interacting protei	41 (0.00)	87 (0.57)	1.53
12-03	Gp3	g.chr9:124528073G>A	Intron	DAB2IP		DAB2 interacting protei	36 (0.00)	58 (0.50)	1.33
12-03	Gp3	g.chr9:124539015G>A	Intron	DAB2IP		DAB2 interacting protei	35 (0.00)	140 (0.15)	0.40
12-03	Gp3	g.chr1:159176066G>A	Silent	DARC	p.Q279Q		93 (0.00)	223 (0.30)	0.63
12-03	Gp3	g.chr19:14070662C>T	Silent	DCAF15	p.G465G	DDB1 and CUL4 associ	19 (0.00)	194 (0.22)	0.76
12-03	Gp3	g.chr14:69521518G>T	Missense Mutation	DCAF5	p.P629T	DDB1 and CUL4 associ	30 (0.00)	35 (0.23)	0.61
12-03	Gp3	g.chr11:6646869C>T	Missense Mutation	DCHS1	p.R2274H	dachsous cadherin-relat	32 (0.00)	78 (0.36)	0.71
12-03	Gp3	g.chr3:36780099G>A	Silent	DCLK3	p.L18L	doublecortin-like kinase	75 (0.00)	51 (0.49)	0.91
12-03	Gp3	g.chr10:115609914T>C	Missense Mutation	DCLRE1A	p.D317G	DNA cross-link repair 1	39 (0.03)	10 (0.60)	1.60
12-03	Gp3	g.chr10:115612767C>A	Nonsense Mutation	DCLRE1A	p.E59*	DNA cross-link repair 1	21 (0.00)	12 (0.42)	1.11

12-03	Gp3	g.chr12:2061868G>T	Missense Mutation	DCP1B	p.P287Q	decapping mRNA 1B	147 (0.00)	112 (0.74)	1.98
12-03	Gp3	g.chr12:31256745A>G	Missense Mutation	DDX11	p.H899R	DEAD/H (Asp-Glu-Ala	24 (0.00)	44 (0.16)	0.42
12-03	Gp3	g.chr5:134120077G>A	Silent	DDX46	p.T396T	DEAD (Asp-Glu-Ala-A	32 (0.00)	74 (0.24)	0.65
12-03	Gp3	g.chr11:688452C>A	Missense Mutation	DEAF1	p.R132S	DEAF1 transcription fa	20 (0.00)	248 (0.38)	1.01
12-03	Gp3	g.chr15:65960313G>A	Nonsense Mutation	DENND4A	p.Q1602*	DENN/MADD domain	15 (0.00)	32 (0.62)	1.67
12-03	Gp3	g.chr12:16189209C>A	Missense Mutation	DERA	p.S265Y	deoxyribose-phosphate	23 (0.00)	54 (0.48)	1.28
12-03	Gp3	g.chr22:20073458C>A	De novo Start OutOf	DGCR8		DGCR8 microprocessor	92 (0.00)	660 (0.10)	0.40
12-03	Gp3	g.chr10:12131126C>A	Missense Mutation	DHTKD1	p.P287T	dehydrogenase E1 and t	30 (0.00)	86 (0.16)	0.43
12-03	Gp3	g.chr3:154041970C>T	Missense Mutation	DHX36	p.R79K	DEAH (Asp-Glu-Ala-H	38 (0.00)	78 (0.28)	0.75
12-03	Gp3	g.chr17:57682898G>A	Missense Mutation	DHX40	p.R688H	DEAH (Asp-Glu-Ala-H	41 (0.00)	52 (0.38)	1.03
12-03	Gp3	g.chr15:40657102C>T	Missense Mutation	DISP2	p.L223F	dispatched homolog 2 (	34 (0.00)	84 (0.21)	0.57
12-03	Gp3	g.chr15:41223879C>T	Silent	DLL4	p.R191R	delta-like 4 (Drosophila	59 (0.00)	91 (0.15)	0.41
12-03	Gp3	g.chr22:38934582C>A	Missense Mutation	DMC1	p.A208S	DNA meiotic recombina	17 (0.00)	15 (0.33)	0.89
12-03	Gp3	g.chr5:118468880G>A	Missense Mutation	DMXL1	p.G457S	Dmx-like 1	52 (0.00)	20 (0.35)	0.93
12-03	Gp3	g.chr5:118525494C>A	Silent	DMXL1	p.S2409S	Dmx-like 1	52 (0.00)	88 (0.30)	0.79
12-03	Gp3	g.chr10:70196864C>T	Missense Mutation	DNA2	p.R517K	DNA replication helicas	23 (0.00)	51 (0.86)	2.30
12-03	Gp3	g.chr12:124320011A>T	Missense Mutation	DNAH10	p.D1495V	dynein, axonemal, heav	50 (0.00)	39 (0.18)	0.48
12-03	Gp3	g.chr7:21621614G>A	Missense Mutation	DNAH11	p.C562Y	dynein, axonemal, heav	48 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chr7:21882318G>A	Silent	DNAH11	p.L3616L	dynein, axonemal, heav	20 (0.00)	33 (0.85)	2.26
12-03	Gp3	g.chr17:7674092G>A	Silent	DNAH2	p.Q1401Q	dynein, axonemal, heav	42 (0.00)	22 (0.36)	0.78
12-03	Gp3	g.chr17:7728046G>A	Splice Site	DNAH2		dynein, axonemal, heav	21 (0.00)	27 (0.19)	0.40
12-03	Gp3	g.chr17:11593496C>T	Missense Mutation	DNAH9	p.P1453S	dynein, axonemal, heav	66 (0.00)	24 (0.25)	0.67
12-03	Gp3	g.chr10:74103203C>A	Silent	DNAJB12	p.L126L	DnaJ (Hsp40) homolog,	16 (0.00)	18 (0.44)	1.19
12-03	Gp3	g.chr14:74154076G>T	Missense Mutation	DNAL1	p.V127L	dynein, axonemal, light	58 (0.00)	131 (0.16)	0.43
12-03	Gp3	g.chr22:39176991C>A	Missense Mutation	DNAL4	p.M31I	dynein, axonemal, light	56 (0.00)	152 (0.18)	0.47
12-03	Gp3	g.chr19:12986871G>A	Missense Mutation	DNASE2	p.P339L	deoxyribonuclease II, ly	34 (0.00)	24 (0.46)	1.60
12-03	Gp3	g.chr9:131008723C>T	Silent	DNM1	p.D574D	dynamin 1	27 (0.00)	170 (0.15)	0.41
12-03	Gp3	g.chr1:172376923C>T	Missense Mutation	DNM3	p.P841L	dynamin 3	17 (0.00)	44 (0.34)	0.91
12-03	Gp3	g.chr10:101659743G>A	Silent	DNMBP	p.L879L	dynamin binding protei	22 (0.00)	20 (0.40)	1.07
12-03	Gp3	g.chr10:101667792C>T	Silent	DNMBP	p.S838S	dynamin binding protei	47 (0.00)	13 (0.38)	1.03
12-03	Gp3	g.chr10:129231674C>T	Missense Mutation	DOCK1	p.S1660F	dedicator of cytokinesis	65 (0.00)	22 (0.73)	1.94
12-03	Gp3	g.chr5:169141387T>C	Missense Mutation	DOCK2	p.W115R	dedicator of cytokinesis	23 (0.00)	39 (0.21)	0.55
12-03	Gp3	g.chr9:377069G>T	Missense Mutation	DOCK8	p.E698D	dedicator of cytokinesis	40 (0.00)	85 (0.26)	0.69
12-03	Gp3	g.chr21:37618314G>A	Missense Mutation	DOPEY2	p.V1346I	dopey family member 2	61 (0.00)	384 (0.19)	0.51
12-03	Gp3	g.chr11:118968223G>A	Missense Mutation	DPAGT1	p.S319F	dolichyl-phosphate (UD	86 (0.00)	14 (0.86)	2.29

12-03	Gp3	g.chr5:146785271C>T	Missense Mutation	DPYSL3	p.R238H	dihydropyrimidinase-lik	25 (0.00)	28 (0.21)	0.57
12-03	Gp3	g.chr4:9784727C>A	Silent	DRD5	p.I358I	dopamine receptor D5	23 (0.00)	20 (0.30)	0.80
12-03	Gp3	g.chr22:31796709G>A	Missense Mutation	DRG1	p.G49D	developmentally regulat	19 (0.00)	93 (0.26)	0.69
12-03	Gp3	g.chr5:31424540T>A	Silent	DROSHA	p.P1085P	drosha, ribonuclease typ	83 (0.00)	78 (0.23)	0.62
12-03	Gp3	g.chr18:28991402C>A	Nonsense Mutation	DSG4	p.Y782*	desmoglein 4	43 (0.00)	65 (0.42)	1.11
12-03	Gp3	g.chr6:56417846C>T	Silent	DST	p.K5037K	dystonin	48 (0.00)	41 (0.17)	0.46
12-03	Gp3	g.chr6:56470602C>T	Missense Mutation	DST	p.D2731N	dystonin	57 (0.00)	72 (0.25)	0.67
12-03	Gp3	g.chr1:205119918T>A	Missense Mutation	DSTYK	p.D786V	dual serine/threonine an	50 (0.00)	13 (0.38)	0.83
12-03	Gp3	g.chr6:15533626G>A	Splice Site	DTNBP1	p.A171V	dystrobrevin binding pr	79 (0.00)	95 (0.15)	0.39
12-03	Gp3	g.chr7:76112178G>C	Missense Mutation	DTX2	p.G208R	deltex 2, E3 ubiquitin li	20 (0.00)	301 (0.21)	0.57
12-03	Gp3	g.chr15:45454558C>G	Missense Mutation	DUOX1	p.Q1411E	dual oxidase 1	51 (0.00)	195 (0.20)	0.53
12-03	Gp3	g.chr15:45386378G>T	Silent	DUOX2	p.A1539A	dual oxidase 2	17 (0.00)	25 (0.28)	0.75
12-03	Gp3	g.chr15:45408835G>T	Silent	DUOXA2	p.V154V	dual oxidase maturation	22 (0.00)	273 (0.21)	0.57
12-03	Gp3	g.chr19:5790080C>T	Missense Mutation	DUS3L	p.R122K	dihydrouridine synthase	21 (0.00)	140 (0.12)	0.44
12-03	Gp3	g.chr1:167097166G>T	Missense Mutation	DUSP27	p.S933I	dual specificity phospha	29 (0.00)	11 (0.45)	1.21
12-03	Gp3	g.chr11:102987413T>A	Missense Mutation	DYNC2H1	p.S246T	dynein, cytoplasmic 2,	47 (0.00)	14 (0.57)	1.52
12-03	Gp3	g.chr1:43632541T>G	Silent	EBNA1BP2	p.A221A	EBNA1 binding protein	22 (0.00)	54 (0.17)	0.44
12-03	Gp3	g.chr1:21586870C>A	Missense Mutation	ECE1	p.S170I	endothelin converting e	63 (0.00)	96 (0.25)	0.67
12-03	Gp3	g.chr20:62127356C>G	Silent	EEF1A2	p.V59V	eukaryotic translation el	19 (0.00)	270 (0.26)	0.68
12-03	Gp3	g.chr17:42953319C>T	Silent	EFTUD2	p.E284E	elongation factor Tu GT	91 (0.00)	108 (0.64)	1.70
12-03	Gp3	g.chr7:55241619G>A	Silent	EGFR	p.V644V	epidermal growth factor	34 (0.00)	86 (0.36)	0.96
12-03	Gp3	g.chr10:64573853T>G	Missense Mutation	EGR2	p.Y182S	early growth response 2	93 (0.00)	237 (0.19)	0.51
12-03	Gp3	g.chr19:40030044C>A	Nonsense Mutation	EID2	p.E226*	EP300 interacting inhibi	27 (0.00)	146 (0.15)	0.56
12-03	Gp3	g.chr12:10658908C>A	Missense Mutation	EIF2S3L	p.P136H		112 (0.00)	408 (0.30)	0.81
12-03	Gp3	g.chr10:120795741C>T	Missense Mutation	EIF3A	p.R1320Q	eukaryotic translation in	17 (0.00)	98 (0.40)	1.06
12-03	Gp3	g.chr19:8038698G>A	Missense Mutation	ELAVL1	p.P114L	ELAV like RNA bindin	21 (0.00)	124 (0.15)	0.52
12-03	Gp3	g.chr20:45000036C>T	Missense Mutation	ELMO2	p.D586N	engulfment and cell mot	75 (0.00)	47 (0.23)	0.62
12-03	Gp3	g.chr20:45022210G>A	Silent	ELMO2	p.T50T	engulfment and cell mot	60 (0.00)	85 (0.15)	0.41
12-03	Gp3	g.chr1:43830123C>A	Missense Mutation	ELOVL1	p.G164C	ELOVL fatty acid elong	30 (0.00)	17 (0.35)	0.94
12-03	Gp3	g.chr14:24608635G>A	Missense Mutation	EMC9	p.P51L	ER membrane protein c	65 (0.00)	90 (0.60)	1.25
12-03	Gp3	g.chr19:14883162G>A	Missense Mutation	EMR2	p.T116M	egf-like module contain	37 (0.00)	30 (0.50)	1.33
12-03	Gp3	g.chr16:67698993C>T	Missense Mutation	ENKD1	p.R120H	enkurin domain contain	98 (0.00)	50 (0.24)	0.64
12-03	Gp3	g.chr16:67698997C>T	Missense Mutation	ENKD1	p.E119K	enkurin domain contain	98 (0.00)	49 (0.24)	0.65
12-03	Gp3	g.chr4:83372341A>G	Missense Mutation	ENOPH1	p.K111R	enolase-phosphatase 1	21 (0.00)	11 (0.64)	1.70
12-03	Gp3	g.chr18:685969C>A	Missense Mutation	ENOSF1	p.M231I	enolase superfamily me	43 (0.00)	38 (0.66)	1.75

12-03	Gp3	g.chrX:129761981C>T	Missense Mutation	ENOX2	p.G522E	ecto-NOX disulfide-thic	37 (0.00)	66 (0.86)	1.44
12-03	Gp3	g.chr4:111398046G>C	Missense Mutation	ENPEP	p.R159T	glutamyl aminopeptidas	45 (0.00)	194 (0.15)	0.41
12-03	Gp3	g.chr17:77710896C>T	Silent	ENPP7	p.D361D	ectonucleotide pyrophos	18 (0.00)	109 (0.15)	0.39
12-03	Gp3	g.chr12:132514632G>A	Missense Mutation	EP400	p.E1895K	E1A binding protein p4	47 (0.00)	211 (0.18)	0.47
12-03	Gp3	g.chr3:96706794C>A	Nonsense Mutation	EPHA6	p.C357*	EPH receptor A6	33 (0.00)	41 (0.85)	2.28
12-03	Gp3	g.chr8:144940958G>A	Missense Mutation	EPPK1	p.A2155V	epiplakin 1	47 (0.00)	522 (0.17)	0.45
12-03	Gp3	g.chr1:220162088T>C	Missense Mutation	EPRS	p.I873M	glutamyl-prolyl-tRNA s	25 (0.00)	15 (0.87)	2.31
12-03	Gp3	g.chr1:51873840C>T	Silent	EPS15	p.Q480Q	epidermal growth factor	30 (0.00)	78 (0.83)	2.22
12-03	Gp3	g.chr1:51910667G>T	Missense Mutation	EPS15	p.A283D	epidermal growth factor	37 (0.00)	51 (0.25)	0.68
12-03	Gp3	g.chr17:27185164G>A	Splice Site	ERAL1	p.R179R	Era-like 12S mitochond	20 (0.00)	35 (0.80)	2.13
12-03	Gp3	g.chr2:212426655C>A	Silent	ERBB4	p.L820L	v-erb-b2 avian erythrob	95 (0.00)	40 (0.55)	1.47
12-03	Gp3	g.chr21:39756251C>A	Intron	ERG		v-ets avian erythroblast	82 (0.00)	294 (0.20)	0.54
12-03	Gp3	g.chr21:39771470C>A	Intron	ERG		v-ets avian erythroblast	34 (0.00)	23 (0.35)	0.43
12-03	Gp3	g.chr21:39811206C>T	Intron	ERG		v-ets avian erythroblast	48 (0.00)	20 (0.60)	0.73
12-03	Gp3	g.chr21:39811743C>T	Intron	ERG		v-ets avian erythroblast	83 (0.00)	276 (0.37)	0.45
12-03	Gp3	g.chr21:39844702C>A	Intron	ERG		v-ets avian erythroblast	29 (0.00)	94 (0.46)	0.56
12-03	Gp3	g.chr21:39947736G>T	Intron	ERG		v-ets avian erythroblast	94 (0.00)	25 (0.36)	0.44
12-03	Gp3	g.chr21:39985671C>A	Intron	ERG		v-ets avian erythroblast	31 (0.00)	10 (0.60)	0.73
12-03	Gp3	g.chr21:39993026A>G	Intron	ERG		v-ets avian erythroblast	20 (0.00)	28 (0.36)	0.44
12-03	Gp3	g.chr6:11105502T>C	Silent	ERVFRD-1	p.L14L	endogenous retrovirus g	26 (0.00)	68 (0.19)	0.51
12-03	Gp3	g.chr20:13695658C>A	Missense Mutation	ESF1	p.A807S	ESF1, nucleolar pre-rR	54 (0.00)	16 (0.44)	1.17
12-03	Gp3	g.chr2:67630708C>T	Silent	ETAA1	p.S298S	Ewing tumor-associated	15 (0.00)	31 (0.32)	0.86
12-03	Gp3	g.chr22:29688580G>A	Silent	EWSR1	p.Q388Q	EWS RNA-binding prot	29 (0.00)	24 (0.21)	0.56
12-03	Gp3	g.chr1:40980709G>A	Missense Mutation	EXO5	p.E165K	exonuclease 5	50 (0.00)	46 (0.72)	1.91
12-03	Gp3	g.chr8:72127952G>T	Missense Mutation	EYA1	p.P458T	EYA transcriptional coa	36 (0.00)	39 (0.92)	2.46
12-03	Gp3	g.chr7:92207661C>T	Missense Mutation	FAM133B	p.G83E	family with sequence si	36 (0.00)	66 (0.92)	2.46
12-03	Gp3	g.chr4:89711766G>A	Silent	FAM13A	p.P354P	family with sequence si	64 (0.00)	47 (0.32)	0.85
12-03	Gp3	g.chr4:89772331G>A	Missense Mutation	FAM13A	p.P283S	family with sequence si	25 (0.00)	52 (0.23)	0.62
12-03	Gp3	g.chr10:15256153C>T	Silent	FAM171A1	p.E478E	family with sequence si	15 (0.00)	143 (0.26)	0.69
12-03	Gp3	g.chr7:38725428C>G	Missense Mutation	FAM183B	p.E60Q	family with sequence si	40 (0.00)	151 (0.39)	1.04
12-03	Gp3	g.chr3:56658955G>A	Missense Mutation	FAM208A	p.H1407Y	family with sequence si	30 (0.00)	19 (0.53)	1.40
12-03	Gp3	g.chrX:34150275G>T	Missense Mutation	FAM47A	p.P41T	family with sequence si	63 (0.02)	265 (0.25)	0.42
12-03	Gp3	g.chr16:67575558C>T	Missense Mutation	FAM65A	p.P332L	family with sequence si	22 (0.00)	81 (0.22)	0.59
12-03	Gp3	g.chr8:11990220G>A	RNA	FAM66D		family with sequence si	125 (0.00)	76 (0.24)	0.63
12-03	Gp3	g.chr16:5139188T>A	Missense Mutation	FAM86A	p.E271V	family with sequence si	58 (0.00)	465 (0.12)	0.41

12-03	Gp3	g.chr3:125643728C>G	RNA	FAM86JP		family with sequence si	23 (0.00)	113 (0.14)	0.38
12-03	Gp3	g.chr16:89805341C>T	Silent	FANCA	p.L1403L	Fanconi anemia, comple	46 (0.00)	75 (0.15)	0.39
12-03	Gp3	g.chr2:242375932G>T	Silent	FARP2	p.L379L	FERM, RhoGEF and pl	45 (0.00)	237 (0.24)	0.65
12-03	Gp3	g.chr2:170425723T>A	Silent	FASTKD1	p.L139L	FAST kinase domains 1	73 (0.00)	94 (0.44)	1.16
12-03	Gp3	g.chr4:187510146C>T	Missense Mutation	FAT1	p.S4456N	FAT atypical cadherin 1	265 (0.00)	321 (0.41)	1.10
12-03	Gp3	g.chr5:150885489G>T	Silent	FAT2	p.P4229P	FAT atypical cadherin 2	45 (0.00)	341 (0.15)	0.39
12-03	Gp3	g.chr5:107197503G>A	Missense Mutation	FBXL17	p.T277I	F-box and leucine-rich r	18 (0.00)	65 (0.51)	1.35
12-03	Gp3	g.chr5:15936651G>T	Missense Mutation	FBXL7	p.D278Y	F-box and leucine-rich r	40 (0.00)	363 (0.26)	0.69
12-03	Gp3	g.chr1:224345289G>A	Silent	FBXO28	p.R316R	F-box protein 28	72 (0.00)	108 (0.18)	0.47
12-03	Gp3	g.chr1:224345294C>A	Missense Mutation	FBXO28	p.A318E	F-box protein 28	68 (0.00)	116 (0.32)	0.85
12-03	Gp3	g.chr6:146125988C>T	Missense Mutation	FBXO30	p.M518I	F-box protein 30	24 (0.00)	11 (0.91)	2.42
12-03	Gp3	g.chr8:124546989G>T	Missense Mutation	FBXO32	p.A61D	F-box protein 32	45 (0.00)	24 (0.21)	0.56
12-03	Gp3	g.chr19:40368684G>A	Missense Mutation	FCGBP	p.R4222C	Fc fragment of IgG bind	52 (0.00)	478 (0.14)	0.52
12-03	Gp3	g.chr1:149755757G>A	Missense Mutation	FCGR1A	p.R84K	Fc fragment of IgG, hig	89 (0.00)	32 (0.47)	1.56
12-03	Gp3	g.chr1:155279985C>T	Missense Mutation	FDPS	p.R110W	farnesyl diphosphate sy	59 (0.00)	212 (0.19)	0.41
12-03	Gp3	g.chr17:72860021G>T	Missense Mutation	FDXR	p.P339T	ferredoxin reductase	28 (0.00)	240 (0.15)	0.41
12-03	Gp3	g.chr2:97370023A>G	RNA	FER1L5		fer-1-like family membe	70 (0.00)	79 (0.47)	1.25
12-03	Gp3	g.chr1:241675343C>T	Missense Mutation	FH	p.R160K	fumarate hydratase	30 (0.00)	17 (0.65)	1.73
12-03	Gp3	g.chr6:76124517G>A	Missense Mutation	FILIP1	p.H58Y	filamin A interacting pr	15 (0.00)	22 (0.95)	2.55
12-03	Gp3	g.chr3:99568958G>A	Missense Mutation	FILIP1L	p.A521V	filamin A interacting pr	19 (0.00)	16 (0.88)	2.33
12-03	Gp3	g.chr9:115952825G>A	Missense Mutation	FKBP15	p.R367W	FK506 binding protein	40 (0.00)	23 (0.22)	0.58
12-03	Gp3	g.chr1:152281246T>G	Missense Mutation	FLG	p.Y2039S	filaggrin	30 (0.00)	70 (0.16)	0.42
12-03	Gp3	g.chr1:152285802C>T	Silent	FLG	p.P520P	filaggrin	89 (0.00)	290 (0.54)	1.44
12-03	Gp3	g.chr11:128680581G>C	Missense Mutation	FLI1	p.G160R	Fli-1 proto-oncogene, E	221 (0.00)	460 (0.51)	1.36
12-03	Gp3	g.chr11:128680780C>T	Missense Mutation	FLI1	p.A226V	Fli-1 proto-oncogene, E	122 (0.00)	135 (0.17)	0.45
12-03	Gp3	g.chr17:27209590C>T	Splice Site	FLOT2		flotillin 2	33 (0.00)	149 (0.54)	1.43
12-03	Gp3	g.chr15:33192221T>C	Missense Mutation	FMN1	p.S1205G	formin 1	40 (0.00)	45 (0.27)	0.88
12-03	Gp3	g.chr15:33261508C>A	Missense Mutation	FMN1	p.K798N	formin 1	268 (0.00)	213 (0.64)	2.10
12-03	Gp3	g.chr11:71932513G>C	Splice Site	FOLR2		folate receptor 2 (fetal)	30 (0.00)	34 (0.41)	1.10
12-03	Gp3	g.chr9:130575758C>A	Missense Mutation	FPGS	p.H547N	folylpolyglutamate synt	37 (0.03)	288 (0.19)	0.52
12-03	Gp3	g.chr9:37746020A>T	Missense Mutation	FRMPD1	p.M1331L	FERM and PDZ domain	48 (0.00)	141 (0.20)	0.53
12-03	Gp3	g.chr14:44974030C>T	Missense Mutation	FSCB	p.A721T	fibrous sheath CABYR	36 (0.03)	65 (0.88)	2.34
12-03	Gp3	g.chr2:186665472C>A	Nonsense Mutation	FSIP2	p.C3813*	fibrous sheath interactin	41 (0.00)	34 (0.21)	0.55
12-03	Gp3	g.chr2:186667217C>T	Missense Mutation	FSIP2	p.S4395F	fibrous sheath interactin	19 (0.00)	47 (0.94)	2.50
12-03	Gp3	g.chr5:132561473G>A	Nonsense Mutation	FSTL4	p.Q352*	follistatin-like 4	38 (0.00)	25 (0.32)	0.85

12-03	Gp3	g.chr17:7509003G>T	Missense Mutation	FXR2	p.A63D	fragile X mental retarda	51 (0.00)	115 (0.37)	0.79
12-03	Gp3	g.chr3:45999947G>A	Missense Mutation	FYCO1	p.P1251L	FYVE and coiled-coil d	15 (0.00)	13 (0.62)	1.64
12-03	Gp3	g.chr14:31066724T>C	Silent	G2E3	p.I209I	G2/M-phase specific E3	31 (0.00)	27 (0.63)	1.68
12-03	Gp3	g.chr5:151178813C>A	Missense Mutation	G3BP1	p.P261H	GTPase activating prote	37 (0.00)	97 (0.63)	1.68
12-03	Gp3	g.chr10:26589852C>A	Missense Mutation	GAD2	p.L574M	glutamate decarboxylase	26 (0.00)	31 (0.26)	0.69
12-03	Gp3	g.chr4:173930381G>A	Missense Mutation	GALNTL6	p.G475E	polypeptide N-acetylgal	27 (0.00)	17 (0.29)	0.78
12-03	Gp3	g.chr12:6647301G>T	Missense Mutation	GAPDH	p.V325L	glyceraldehyde-3-phosp	30 (0.00)	57 (0.18)	0.47
12-03	Gp3	g.chr16:90094107C>G	Missense Mutation	GAS8	p.P23A	growth arrest-specific 8	25 (0.00)	284 (0.22)	0.59
12-03	Gp3	g.chr1:89729549T>A	Missense Mutation	GBP5	p.D411V	guanylate binding protei	26 (0.00)	24 (0.25)	0.67
12-03	Gp3	g.chr1:89729579G>A	Missense Mutation	GBP5	p.S401F	guanylate binding protei	28 (0.00)	24 (0.54)	1.44
12-03	Gp3	g.chr20:34025300C>A	Missense Mutation	GDF5	p.A137S	growth differentiation fa	22 (0.00)	96 (0.20)	0.53
12-03	Gp3	g.chr17:649497G>T	Missense Mutation	GEMIN4	p.P596T	gem (nuclear organelle)	70 (0.00)	109 (0.50)	1.35
12-03	Gp3	g.chr17:650787C>A	Nonsense Mutation	GEMIN4	p.E166*	gem (nuclear organelle)	147 (0.00)	444 (0.18)	0.47
12-03	Gp3	g.chr17:650802G>A	Silent	GEMIN4	p.L161L	gem (nuclear organelle)	145 (0.00)	371 (0.22)	0.58
12-03	Gp3	g.chr17:651077G>A	Missense Mutation	GEMIN4	p.A69V	gem (nuclear organelle)	16 (0.00)	23 (0.61)	1.62
12-03	Gp3	g.chr5:154316707C>T	Missense Mutation	GEMIN5	p.G69S	gem (nuclear organelle)	53 (0.00)	20 (0.95)	2.53
12-03	Gp3	g.chr5:179762889C>A	Missense Mutation	GFPT2	p.W93C	glutamine-fructose-6-ph	21 (0.00)	145 (0.19)	0.60
12-03	Gp3	g.chr8:21608281G>A	Missense Mutation	GFRA2	p.R205C	GDNF family receptor a	25 (0.00)	67 (0.22)	0.60
12-03	Gp3	g.chr17:73235056G>A	Missense Mutation	GGA3	p.S558F	golgi-associated, gamma	22 (0.00)	74 (0.18)	0.47
12-03	Gp3	g.chr2:85777855G>T	Missense Mutation	GGCX	p.P636Q	gamma-glutamyl carbox	32 (0.00)	277 (0.23)	0.49
12-03	Gp3	g.chr22:22989348C>A	Missense Mutation	GGTLC2	p.P101T	gamma-glutamyltransfe	42 (0.00)	214 (0.33)	0.87
12-03	Gp3	g.chr17:17957461C>A	Silent	GID4	p.T173T	GID complex subunit 4	18 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr2:233671368G>A	Splice Site	GIGYF2		GRB10 interacting GYF	20 (0.00)	24 (0.79)	2.11
12-03	Gp3	g.chr1:39341707C>T	Missense Mutation	GJA9	p.G22R	gap junction protein, alp	97 (0.01)	176 (0.45)	1.21
12-03	Gp3	g.chr6:42821405G>A	Missense Mutation	GLTSCR1L	p.A659T	GLTSCR1-like	53 (0.00)	48 (0.15)	0.39
12-03	Gp3	g.chr2:220368914G>T	Missense Mutation	GMPPA	p.R200L	GDP-mannose pyrophos	28 (0.00)	18 (0.72)	1.93
12-03	Gp3	g.chr3:50294181C>T	Missense Mutation	GNAI2	p.S207F	guanine nucleotide bind	29 (0.00)	103 (0.15)	0.39
12-03	Gp3	g.chr3:50294196G>A	Nonsense Mutation	GNAI2	p.W212*	guanine nucleotide bind	26 (0.00)	117 (0.22)	0.59
12-03	Gp3	g.chr16:56226488G>A	Missense Mutation	GNAO1	p.A41T	guanine nucleotide bind	33 (0.00)	57 (0.18)	0.47
12-03	Gp3	g.chr1:1720564C>T	Missense Mutation	GNB1	p.G282R	guanine nucleotide bind	43 (0.00)	26 (0.77)	2.05
12-03	Gp3	g.chrX:109590018C>A	Silent	GNG5P2	p.L40L	guanine nucleotide bind	29 (0.00)	122 (0.70)	1.16
12-03	Gp3	g.chr1:38053043A>G	Silent	GNL2	p.P146P	guanine nucleotide bind	29 (0.00)	30 (0.23)	0.62
12-03	Gp3	g.chr3:52727021G>T	Nonsense Mutation	GNL3	p.E335*	guanine nucleotide bind	49 (0.00)	40 (0.23)	0.60
12-03	Gp3	g.chr3:37379195G>A	Silent	GOLGA4	p.S2137S	golgin A4	33 (0.00)	13 (0.38)	0.72
12-03	Gp3	g.chr15:28947196C>A	Missense Mutation	GOLGA8M	p.Q601H	golgin A8 family, memb	58 (0.00)	291 (0.33)	1.10

12-03	Gp3	g.chr3:121396172G>C	Missense Mutation	GOLGB1	p.S3000C	golgin B1	15 (0.00)	30 (0.60)	1.60
12-03	Gp3	g.chr3:121400536G>T	Silent	GOLGB1	p.L2957L	golgin B1	28 (0.00)	18 (0.56)	1.48
12-03	Gp3	g.chr3:121410638C>T	Missense Mutation	GOLGB1	p.D2525N	golgin B1	46 (0.00)	16 (0.94)	2.50
12-03	Gp3	g.chr2:171806173G>A	Nonsense Mutation	GORASP2	p.W90*	golgi reassembly stackir	31 (0.00)	95 (0.57)	1.52
12-03	Gp3	g.chr10:113917033C>T	Missense Mutation	GPAM	p.E699K	glycerol-3-phosphate ac	23 (0.00)	16 (0.50)	1.33
12-03	Gp3	g.chr19:34857334G>A	Silent	GPI	p.V69V	glucose-6-phosphate iso	34 (0.00)	80 (0.20)	0.53
12-03	Gp3	g.chr17:36499047A>T	Missense Mutation	GPR179	p.L209H	G protein-coupled recep	19 (0.00)	55 (0.33)	0.87
12-03	Gp3	g.chr13:99907971C>A	Missense Mutation	GPR18	p.K52N	G protein-coupled recep	29 (0.00)	73 (0.60)	1.61
12-03	Gp3	g.chr5:90084016G>A	Silent	GPR98	p.L4594L	G protein-coupled recep	27 (0.00)	14 (0.64)	1.71
12-03	Gp3	g.chr12:52407715G>A	Silent	GRASP	p.L201L	GRP1 (general receptor	60 (0.00)	228 (0.16)	0.43
12-03	Gp3	g.chr7:50800005G>A	Silent	GRB10	p.G5G	growth factor receptor-b	31 (0.00)	12 (0.50)	1.33
12-03	Gp3	g.chr7:50800007C>A	Missense Mutation	GRB10	p.G5C	growth factor receptor-b	31 (0.00)	12 (0.50)	1.33
12-03	Gp3	g.chr17:37898867C>A	Silent	GRB7	p.P68P	growth factor receptor-b	26 (0.00)	127 (0.34)	0.90
12-03	Gp3	g.chr2:10104151C>T	Missense Mutation	GRHL1	p.H295Y	grainyhead-like 1 (Dros	69 (0.00)	178 (0.15)	0.39
12-03	Gp3	g.chr12:66770994A>G	Missense Mutation	GRIP1	p.L846S	glutamate receptor inter	74 (0.00)	13 (0.69)	1.85
12-03	Gp3	g.chr5:176860627A>G	Missense Mutation	GRK6	p.M230V	G protein-coupled recep	43 (0.00)	211 (0.35)	1.11
12-03	Gp3	g.chr16:85697000G>T	Missense Mutation	GSE1	p.E808D	Gse1 coiled-coil protein	25 (0.00)	41 (0.22)	0.59
12-03	Gp3	g.chr17:3629258C>T	Missense Mutation	GSG2	p.P677S	germ cell associated 2 (	18 (0.00)	18 (0.61)	1.63
12-03	Gp3	g.chr19:42738519T>C	Missense Mutation	GSK3A	p.Y297C	glycogen synthase kinas	48 (0.00)	60 (0.28)	0.76
12-03	Gp3	g.chr4:106639075G>A	Missense Mutation	GSTCD	p.R102K	glutathione S-transferas	25 (0.00)	11 (0.45)	1.21
12-03	Gp3	g.chr8:30510973G>A	Missense Mutation	GTF2E2	p.S48L	general transcription fac	27 (0.00)	26 (0.92)	2.46
12-03	Gp3	g.chr3:148714114G>A	Missense Mutation	GYG1	p.E57K	glycogenin 1	83 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chr20:23345887G>A	Silent	GZF1	p.E289E	GDNF-inducible zinc fi	21 (0.00)	75 (0.52)	1.39
12-03	Gp3	g.chr15:89424944C>T	Missense Mutation	HAPLN3	p.G108E	hyaluronan and proteogl	27 (0.00)	200 (0.23)	0.63
12-03	Gp3	g.chr7:18536872T>C	Intron	HDAC9		histone deacetylase 9	110 (0.00)	32 (0.34)	0.92
12-03	Gp3	g.chr7:18537704C>A	Intron	HDAC9		histone deacetylase 9	35 (0.00)	108 (0.31)	0.81
12-03	Gp3	g.chr7:18575893T>A	Intron	HDAC9		histone deacetylase 9	89 (0.00)	99 (0.29)	0.78
12-03	Gp3	g.chr7:18633266G>T	Intron	HDAC9		histone deacetylase 9	29 (0.00)	104 (0.49)	1.31
12-03	Gp3	g.chr7:18712973G>T	Intron	HDAC9		histone deacetylase 9	66 (0.00)	164 (0.16)	0.42
12-03	Gp3	g.chr7:18829657G>A	Intron	HDAC9		histone deacetylase 9	56 (0.00)	22 (0.23)	0.61
12-03	Gp3	g.chr7:18883013G>T	Intron	HDAC9		histone deacetylase 9	26 (0.00)	27 (0.26)	0.69
12-03	Gp3	g.chr7:18887154C>T	Intron	HDAC9		histone deacetylase 9	33 (0.00)	36 (0.44)	1.19
12-03	Gp3	g.chr7:18901463G>A	Intron	HDAC9		histone deacetylase 9	29 (0.00)	18 (0.39)	1.04
12-03	Gp3	g.chr7:18988883C>G	Intron	HDAC9		histone deacetylase 9	65 (0.00)	80 (0.57)	1.53
12-03	Gp3	g.chr15:91475030C>T	Missense Mutation	HDDC3	p.V105M	HD domain containing	20 (0.00)	71 (0.28)	0.75

12-03	Gp3	g.chr14:31598644A>C	Missense Mutation	HECTD1	p.D1311E	HECT domain containir	38 (0.00)	66 (0.15)	0.40
12-03	Gp3	g.chr12:112681776G>T	Missense Mutation	HECTD4	p.H1371Q	HECT domain containir	156 (0.00)	127 (0.60)	1.60
12-03	Gp3	g.chr7:43351662G>T	Missense Mutation	HECW1	p.D110Y	HECT, C2 and WW dor	29 (0.00)	51 (0.16)	0.42
12-03	Gp3	g.chr17:65083037G>A	Missense Mutation	HELZ	p.P1801L	helicase with zinc finger	21 (0.00)	21 (0.43)	1.14
12-03	Gp3	g.chr9:100692844G>C	Missense Mutation	HEMGN	p.P278R	hemogen	68 (0.00)	33 (0.15)	0.40
12-03	Gp3	g.chr3:50608670C>G	Silent	HEMK1	p.V45V	HemK methyltransferas	34 (0.00)	44 (0.43)	1.15
12-03	Gp3	g.chr15:28375700C>G	Missense Mutation	HERC2	p.C4204S	HECT and RLD domair	113 (0.00)	149 (0.21)	0.68
12-03	Gp3	g.chr15:28375725C>G	Missense Mutation	HERC2	p.G4196R	HECT and RLD domair	104 (0.00)	166 (0.16)	0.54
12-03	Gp3	g.chr15:28424295C>T	Silent	HERC2	p.L3004L	HECT and RLD domair	23 (0.00)	23 (0.57)	1.86
12-03	Gp3	g.chr15:23311659C>T	RNA	HERC2P2		hect domain and RLD 2	16 (0.00)	61 (0.48)	1.27
12-03	Gp3	g.chr15:23318695G>A	RNA	HERC2P2		hect domain and RLD 2	158 (0.00)	82 (0.15)	0.39
12-03	Gp3	g.chr15:20644845C>A	RNA	HERC2P3		hect domain and RLD 2	39 (0.00)	186 (0.17)	0.44
12-03	Gp3	g.chr15:20651283G>A	RNA	HERC2P3		hect domain and RLD 2	75 (0.01)	132 (0.23)	0.63
12-03	Gp3	g.chr1:145416531G>A	Silent	HFE2	p.G292G	hemochromatosis type 2	62 (0.00)	66 (0.27)	0.73
12-03	Gp3	g.chr22:21799299C>T	Nonsense Mutation	HIC2	p.Q39*	hypermethylated in canc	40 (0.00)	605 (0.14)	0.54
12-03	Gp3	g.chr19:40886789C>A	Missense Mutation	HIPK4	p.R370L	homeodomain interactin	26 (0.00)	215 (0.16)	0.59
12-03	Gp3	g.chr6:27101235G>A	Missense Mutation	HIST1H2AG	p.G129S	histone cluster 1, H2ag	39 (0.00)	254 (0.21)	0.56
12-03	Gp3	g.chr6:27100359G>A	Silent	HIST1H2BJ	p.S57S	histone cluster 1, H2bj	125 (0.00)	146 (0.18)	0.49
12-03	Gp3	g.chr6:27783169C>A	Silent	HIST1H2BM	p.T116T	histone cluster 1, H2bm	41 (0.00)	272 (0.15)	0.39
12-03	Gp3	g.chr1:42046859G>A	Missense Mutation	HIVEP3	p.H1204Y	human immunodeficienc	28 (0.00)	31 (0.19)	0.52
12-03	Gp3	g.chr1:42047121G>C	Silent	HIVEP3	p.P1116P	human immunodeficienc	22 (0.00)	248 (0.29)	0.77
12-03	Gp3	g.chr1:42049618G>A	Missense Mutation	HIVEP3	p.S284F	human immunodeficienc	64 (0.00)	294 (0.29)	0.77
12-03	Gp3	g.chr5:177632986T>C	Missense Mutation	HNRNPAB	p.F118S	heterogeneous nuclear r	46 (0.00)	172 (0.12)	0.39
12-03	Gp3	g.chr19:41811583G>T	Silent	HNRNPUL1	p.P755P	heterogeneous nuclear r	58 (0.00)	50 (0.48)	1.28
12-03	Gp3	g.chr22:30517718G>A	Missense Mutation	HORMAD2	p.D170N	HORMA domain contai	41 (0.00)	20 (0.25)	0.67
12-03	Gp3	g.chr7:27134122G>C	Missense Mutation	HOXA1	p.S315R	homeobox A1	37 (0.00)	20 (0.65)	1.73
12-03	Gp3	g.chr7:27135110T>C	Missense Mutation	HOXA1	p.Q141R	homeobox A1	35 (0.00)	30 (0.33)	0.89
12-03	Gp3	g.chr2:177033967G>T	Missense Mutation	HOXD3	p.G42V	homeobox D3	60 (0.00)	246 (0.15)	0.39
12-03	Gp3	g.chr10:100195426G>A	Missense Mutation	HPS1	p.T74M	Hermansky-Pudlak sync	30 (0.00)	41 (0.22)	0.59
12-03	Gp3	g.chr3:192980799C>T	Silent	HRASLS	p.F165F	HRAS-like suppressor	36 (0.03)	148 (0.97)	2.59
12-03	Gp3	g.chr3:192980800A>T	Missense Mutation	HRASLS	p.S166C	HRAS-like suppressor	36 (0.03)	148 (0.97)	2.59
12-03	Gp3	g.chr1:152191816C>T	Silent	HRNR	p.S763S	hornerin	22 (0.00)	238 (0.21)	0.57
12-03	Gp3	g.chr6:44219568C>G	Nonsense Mutation	HSP90AB1	p.S470*	heat shock protein 90kD	18 (0.00)	21 (0.29)	0.76
12-03	Gp3	g.chr5:132406110G>A	Silent	HSPA4	p.V117V	heat shock 70kDa protei	26 (0.00)	17 (0.41)	1.10
12-03	Gp3	g.chr9:128002979C>A	Missense Mutation	HSPA5	p.Q110H	heat shock 70kDa protei	38 (0.00)	59 (0.51)	1.36

12-03	Gp3	g.chr4:3174103G>A	Missense Mutation	HTT	p.M1307I	huntingtin	44 (0.02)	21 (0.52)	1.40
12-03	Gp3	g.chr21:33296872C>T	Silent	HUNK	p.I118I	hormonally up-regulate	57 (0.00)	120 (0.37)	0.98
12-03	Gp3	g.chr8:39785498G>A	Missense Mutation	IDO1	p.V336M	indoleamine 2,3-dioxyg	22 (0.00)	55 (0.27)	0.73
12-03	Gp3	g.chr14:106207828G>T	RNA	IGHG1		immunoglobulin heavy	32 (0.00)	35 (0.37)	0.99
12-03	Gp3	g.chr14:106208215C>G	RNA	IGHG1		immunoglobulin heavy	34 (0.00)	466 (0.31)	0.82
12-03	Gp3	g.chr21:10862766T>A	RNA	IGHV1OR21-1		immunoglobulin heavy	128 (0.00)	62 (0.15)	0.39
12-03	Gp3	g.chr14:107013175G>T	RNA	IGHV3-49		immunoglobulin heavy	18 (0.00)	36 (0.58)	1.56
12-03	Gp3	g.chr14:106805490C>A	RNA	IGHV4-31		immunoglobulin heavy	16 (0.00)	87 (0.18)	0.49
12-03	Gp3	g.chr14:107083464G>T	RNA	IGHV4-59		immunoglobulin heavy	17 (0.00)	82 (0.22)	0.59
12-03	Gp3	g.chr3:53894167G>A	Silent	IL17RB	p.K286K	interleukin 17 receptor	47 (0.00)	52 (0.65)	1.74
12-03	Gp3	g.chr15:41277590C>T	Silent	INO80	p.E1289E	INO80 complex subunit	35 (0.00)	31 (0.42)	1.12
12-03	Gp3	g.chr2:99193523G>T	Silent	INPP4A	p.V867V	inositol polyphosphate-	16 (0.00)	146 (0.25)	0.66
12-03	Gp3	g.chr4:142972477G>A	Intron	INPP4B		inositol polyphosphate-	19 (0.00)	45 (0.16)	0.41
12-03	Gp3	g.chr4:142983212T>A	Intron	INPP4B		inositol polyphosphate-	28 (0.00)	38 (0.32)	0.84
12-03	Gp3	g.chr4:143014481C>T	Intron	INPP4B		inositol polyphosphate-	196 (0.00)	64 (0.88)	2.33
12-03	Gp3	g.chr4:143069254C>A	Intron	INPP4B		inositol polyphosphate-	52 (0.00)	27 (0.30)	0.79
12-03	Gp3	g.chr4:143070358C>T	Intron	INPP4B		inositol polyphosphate-	15 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr4:143076609C>A	Intron	INPP4B		inositol polyphosphate-	140 (0.00)	21 (0.57)	1.52
12-03	Gp3	g.chr4:143163368G>T	Intron	INPP4B		inositol polyphosphate-	32 (0.00)	22 (0.64)	1.70
12-03	Gp3	g.chr4:143188903G>A	Intron	INPP4B		inositol polyphosphate-	61 (0.00)	30 (0.83)	2.22
12-03	Gp3	g.chr4:143214569C>G	Intron	INPP4B		inositol polyphosphate-	43 (0.00)	13 (0.85)	2.26
12-03	Gp3	g.chr4:143272252C>T	Intron	INPP4B		inositol polyphosphate-	23 (0.00)	42 (0.17)	0.44
12-03	Gp3	g.chr4:143305132G>A	Intron	INPP4B		inositol polyphosphate-	110 (0.01)	278 (0.21)	0.55
12-03	Gp3	g.chr4:143402956C>T	Intron	INPP4B		inositol polyphosphate-	38 (0.03)	16 (0.75)	2.00
12-03	Gp3	g.chr4:143501916C>A	Intron	INPP4B		inositol polyphosphate-	90 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chr4:143501929G>T	Intron	INPP4B		inositol polyphosphate-	86 (0.00)	16 (0.38)	1.00
12-03	Gp3	g.chr4:143674663A>T	Intron	INPP4B		inositol polyphosphate-	94 (0.00)	24 (0.42)	1.11
12-03	Gp3	g.chr1:212161253G>T	Silent	INTS7	p.I324I	integrator complex subu	19 (0.00)	30 (0.17)	0.44
12-03	Gp3	g.chr1:212161285C>A	Missense Mutation	INTS7	p.V314F	integrator complex subu	19 (0.00)	30 (0.23)	0.62
12-03	Gp3	g.chr8:95885700G>A	Missense Mutation	INTS8	p.D878N	integrator complex subu	16 (0.00)	50 (0.88)	2.35
12-03	Gp3	g.chr2:237240148G>A	Nonsense Mutation	IQCA1	p.Q743*	IQ motif containing wit	51 (0.00)	47 (0.70)	1.87
12-03	Gp3	g.chr7:2634571G>A	Silent	IQCE	p.K467K	IQ motif containing E	83 (0.00)	466 (0.20)	0.52
12-03	Gp3	g.chr15:76632812G>T	Missense Mutation	ISL2	p.R236L	ISL LIM homeobox 2	15 (0.00)	20 (0.40)	0.55
12-03	Gp3	g.chr16:304412G>A	De novo Start InFran	ITFG3		integrin alpha FG-GAP	52 (0.02)	353 (0.33)	1.12
12-03	Gp3	g.chr16:30529005G>T	Missense Mutation	ITGAL	p.E1004D	integrin, alpha L (antige	25 (0.00)	248 (0.21)	0.72

12-03	Gp3	g.chr16:31284706C>T	Missense Mutation	ITGAM	p.T242I	integrin, alpha M (comp	50 (0.00)	16 (0.31)	1.07
12-03	Gp3	g.chr7:20420383C>T	Nonsense Mutation	ITGB8	p.Q244*	integrin, beta 8	53 (0.00)	19 (0.26)	0.70
12-03	Gp3	g.chr10:7621734C>A	Missense Mutation	ITIH5	p.G468C	inter-alpha-trypsin inhib	17 (0.00)	236 (0.17)	0.45
12-03	Gp3	g.chr2:24432795G>A	Silent	ITSN2	p.F1455F	intersectin 2	52 (0.00)	160 (0.68)	1.80
12-03	Gp3	g.chr14:105618538G>C	Missense Mutation	JAG2	p.C293W	jagged 2	21 (0.00)	161 (0.22)	0.58
12-03	Gp3	g.chr10:133950582G>T	Missense Mutation	JAKMIP3	p.Q392H	Janus kinase and microt	85 (0.00)	351 (0.35)	0.94
12-03	Gp3	g.chr1:153949242G>T	Nonsense Mutation	JTB	p.S44*	jumping translocation b	46 (0.00)	53 (0.19)	0.40
12-03	Gp3	g.chr8:41790017G>T	Silent	KAT6A	p.P1907P	K(lysine) acetyltransfer	34 (0.00)	59 (0.27)	0.72
12-03	Gp3	g.chr16:57785929C>G	Missense Mutation	KATNB1	p.H198Q	katanin p80 (WD repeat	48 (0.02)	386 (0.32)	0.85
12-03	Gp3	g.chr12:5021796G>T	Nonsense Mutation	KCNA1	p.E418*	potassium voltage-gated	100 (0.00)	68 (0.78)	2.08
12-03	Gp3	g.chr12:4920705G>A	Missense Mutation	KCNA6	p.D500N	potassium voltage-gated	39 (0.00)	79 (0.61)	1.62
12-03	Gp3	g.chr3:156249238G>A	Silent	KCNAB1	p.L356L	potassium voltage-gated	127 (0.00)	75 (0.64)	1.71
12-03	Gp3	g.chr12:75444510G>T	Silent	KCNC2	p.P425P	potassium voltage-gated	30 (0.00)	15 (0.40)	1.07
12-03	Gp3	g.chr16:84255908G>A	Missense Mutation	KCNG4	p.P492L	potassium voltage-gated	91 (0.00)	137 (0.35)	0.93
12-03	Gp3	g.chr20:62073870G>A	Silent	KCNQ2	p.A235A	potassium voltage-gated	22 (0.00)	490 (0.27)	0.71
12-03	Gp3	g.chr8:99440869C>A	Missense Mutation	KCNS2	p.P221H	potassium voltage-gated	40 (0.00)	133 (0.20)	0.52
12-03	Gp3	g.chr2:18112555C>A	Missense Mutation	KCNS3	p.L94M	potassium voltage-gated	68 (0.00)	15 (0.80)	2.13
12-03	Gp3	g.chr8:36766868A>T	Missense Mutation	KCNU1	p.I716F	potassium channel, subf	140 (0.00)	71 (0.28)	0.75
12-03	Gp3	g.chr7:128530297A>G	RNA	KCP		kielin/chordin-like prot	18 (0.00)	58 (0.19)	0.51
12-03	Gp3	g.chr6:36447443C>T	Missense Mutation	KCTD20	p.L205F	potassium channel tetra	101 (0.00)	57 (0.35)	0.94
12-03	Gp3	g.chr6:36454928G>A	Missense Mutation	KCTD20	p.M412I	potassium channel tetra	73 (0.00)	35 (0.17)	0.46
12-03	Gp3	g.chr12:431710G>A	Silent	KDM5A	p.L767L	lysine (K)-specific dem	26 (0.00)	23 (0.96)	2.55
12-03	Gp3	g.chr2:27319603G>A	Silent	KHK	p.L117L	ketohexokinase (fructok	56 (0.00)	62 (0.66)	1.76
12-03	Gp3	g.chr19:6418508G>T	Missense Mutation	KHSRP	p.P289T	KH-type splicing regula	15 (0.00)	212 (0.56)	2.02
12-03	Gp3	g.chr19:6418559C>T	Missense Mutation	KHSRP	p.D272N	KH-type splicing regula	17 (0.00)	216 (0.69)	2.47
12-03	Gp3	g.chr9:114184267C>T	Silent	KIAA0368	p.A463A	KIAA0368	19 (0.00)	12 (0.75)	2.00
12-03	Gp3	g.chr12:105557951C>A	Missense Mutation	KIAA1033	p.Q1074K	KIAA1033	17 (0.00)	12 (0.50)	1.33
12-03	Gp3	g.chr15:81234199C>T	Silent	KIAA1199	p.F1139F		37 (0.00)	35 (0.77)	2.06
12-03	Gp3	g.chr3:128711914G>A	Silent	KIAA1257	p.T78T	KIAA1257	50 (0.00)	104 (0.15)	0.41
12-03	Gp3	g.chr10:30317271G>A	Silent	KIAA1462	p.D602D	KIAA1462	34 (0.00)	84 (0.50)	1.33
12-03	Gp3	g.chr11:33667258C>A	Silent	KIAA1549L	p.T1515T	KIAA1549-like	134 (0.00)	317 (0.31)	0.82
12-03	Gp3	g.chr17:43006346G>C	Missense Mutation	KIF18B	p.L522V	kinesin family member	21 (0.00)	98 (0.16)	0.44
12-03	Gp3	g.chr2:241666289G>A	Missense Mutation	KIF1A	p.T1258I	kinesin family member	22 (0.00)	197 (0.18)	0.49
12-03	Gp3	g.chr16:29810009G>T	Nonsense Mutation	KIF22	p.E96*	kinesin family member	23 (0.00)	88 (0.33)	0.88
12-03	Gp3	g.chr5:154393459C>A	Missense Mutation	KIF4B	p.L14M	kinesin family member	40 (0.00)	60 (0.17)	0.44

12-03	Gp3	g.chr19:36216440C>A	Silent	KMT2B	p.R1235R	lysine (K)-specific meth	26 (0.00)	113 (0.34)	0.90
12-03	Gp3	g.chr17:45752013C>A	Silent	KPNB1	p.R448R	karyopherin (importin)	105 (0.00)	32 (0.94)	2.50
12-03	Gp3	g.chr17:39741258C>T	Missense Mutation	KRT14	p.A193T	keratin 14	30 (0.00)	23 (0.52)	0.97
12-03	Gp3	g.chr11:124984248G>A	RNA	KRT18P59		keratin 18 pseudogene 5	27 (0.00)	14 (0.57)	1.52
12-03	Gp3	g.chr17:38906659T>C	Missense Mutation	KRT25	p.Y383C	keratin 25	51 (0.00)	59 (0.20)	0.54
12-03	Gp3	g.chr12:53185179G>A	Missense Mutation	KRT3	p.A449V	keratin 3	51 (0.00)	351 (0.26)	0.69
12-03	Gp3	g.chr17:39502390C>G	Missense Mutation	KRT33A	p.C399S	keratin 33A	35 (0.00)	50 (0.18)	0.48
12-03	Gp3	g.chr17:39502394G>C	Missense Mutation	KRT33A	p.P398A	keratin 33A	37 (0.00)	48 (0.15)	0.39
12-03	Gp3	g.chr17:39502754C>T	Missense Mutation	KRT33A	p.R348Q	keratin 33A	48 (0.00)	167 (0.16)	0.42
12-03	Gp3	g.chr17:39521222C>A	Missense Mutation	KRT33B	p.E302D	keratin 33B	15 (0.00)	112 (0.22)	0.60
12-03	Gp3	g.chr17:39538014C>T	Missense Mutation	KRT34	p.V170M	keratin 34	29 (0.00)	191 (0.15)	0.39
12-03	Gp3	g.chr17:39594998G>A	Missense Mutation	KRT38	p.A282V	keratin 38	46 (0.00)	116 (0.35)	0.94
12-03	Gp3	g.chr12:52841686G>A	Silent	KRT6B	p.L434L	keratin 6B	59 (0.00)	151 (0.32)	0.87
12-03	Gp3	g.chr12:52967121C>T	Silent	KRT74	p.L147L	keratin 74	15 (0.00)	39 (0.46)	1.23
12-03	Gp3	g.chr12:52681812C>G	Missense Mutation	KRT81	p.V286L	keratin 81	19 (0.00)	28 (0.18)	0.48
12-03	Gp3	g.chr12:52778955C>T	Missense Mutation	KRT84	p.A139T	keratin 84	42 (0.00)	22 (0.95)	2.55
12-03	Gp3	g.chr17:39334070T>C	Missense Mutation	KRTAP4-2	p.Y116C	keratin associated protei	34 (0.00)	175 (0.18)	0.47
12-03	Gp3	g.chr11:1628993C>A	Missense Mutation	KRTAP5-3	p.G208V	keratin associated protei	66 (0.00)	556 (0.20)	0.53
12-03	Gp3	g.chr17:39346851C>A	Missense Mutation	KRTAP9-1	p.P238H	keratin associated protei	25 (0.00)	72 (0.43)	1.15
12-03	Gp3	g.chr17:39346885C>A	Nonsense Mutation	KRTAP9-1	p.C249*	keratin associated protei	22 (0.00)	51 (0.55)	1.46
12-03	Gp3	g.chr1:201355923G>A	Missense Mutation	LAD1	p.T189M	ladinin 1	47 (0.02)	157 (0.19)	0.51
12-03	Gp3	g.chr7:107613517C>A	Splice Site	LAMB1		laminin, beta 1	27 (0.00)	24 (0.83)	2.22
12-03	Gp3	g.chr1:209807795C>A	Silent	LAMB3	p.G187G	laminin, beta 3	39 (0.00)	216 (0.29)	0.77
12-03	Gp3	g.chr6:150004585G>T	Missense Mutation	LATS1	p.A547D	large tumor suppressor	34 (0.00)	44 (0.20)	0.55
12-03	Gp3	g.chr20:36982723C>A	Silent	LBP	p.I136I	lipopolysaccharide bind	22 (0.00)	68 (0.41)	1.10
12-03	Gp3	g.chr1:152636701T>C	Silent	LCE2D	p.C40C	late cornified envelope	46 (0.00)	494 (0.16)	0.43
12-03	Gp3	g.chr9:139641878G>A	Silent	LCN6	p.H66H	lipocalin 6	15 (0.00)	191 (0.12)	0.41
12-03	Gp3	g.chr4:17885391C>T	Missense Mutation	LCORL	p.M503I	ligand dependent nuclea	23 (0.00)	16 (0.56)	1.50
12-03	Gp3	g.chr19:11230902G>A	Silent	LDLR	p.Q660Q	low density lipoprotein	23 (0.00)	27 (0.33)	1.17
12-03	Gp3	g.chr4:1818635G>T	Missense Mutation	LETM1	p.Q584K	leucine zipper-EF-hand	97 (0.00)	287 (0.17)	0.46
12-03	Gp3	g.chr1:180235614G>T	Silent	LHX4	p.L112L	LIM homeobox 4	17 (0.00)	57 (0.32)	0.84
12-03	Gp3	g.chr13:108860946C>T	Missense Mutation	LIG4	p.E891K	ligase IV, DNA, ATP-d	31 (0.00)	18 (0.67)	1.78
12-03	Gp3	g.chr9:132252823C>A	RNA	LINC00963		long intergenic non-prot	50 (0.00)	48 (0.54)	1.44
12-03	Gp3	g.chr3:69168170A>G	Missense Mutation	LMOD3	p.F446L	leiomodin 3 (fetal)	147 (0.00)	33 (0.27)	0.73
12-03	Gp3	g.chr7:97833269G>T	Missense Mutation	LMTK2	p.E1418D	lemur tyrosine kinase 2	57 (0.00)	360 (0.15)	0.41

12-03	Gp3	g.chr18:44173690T>A	Missense Mutation	LOXHD1	p.D435V	lipoxygenase homology	42 (0.00)	25 (0.44)	1.17
12-03	Gp3	g.chr10:100016597G>C	Silent	LOXL4	p.L456L	lysyl oxidase-like 4	16 (0.00)	53 (0.15)	0.40
12-03	Gp3	g.chr6:160978444G>C	Missense Mutation	LPA	p.S1597R	lipoprotein, Lp(a)	15 (0.00)	39 (0.56)	1.50
12-03	Gp3	g.chr12:7087653A>G	Missense Mutation	LPCAT3	p.L297S	lysophosphatidylcholine	78 (0.00)	38 (0.50)	1.33
12-03	Gp3	g.chr3:197547201G>C	Silent	LRCH3	p.V180V	leucine-rich repeats and	32 (0.00)	19 (0.95)	2.53
12-03	Gp3	g.chr3:66436710G>A	Missense Mutation	LRIG1	p.P495L	leucine-rich repeats and	106 (0.00)	28 (0.93)	2.48
12-03	Gp3	g.chr12:57567585G>T	Missense Mutation	LRP1	p.W1123C	low density lipoprotein	19 (0.00)	164 (0.23)	0.60
12-03	Gp3	g.chr2:141598606C>A	Missense Mutation	LRP1B	p.W1665C	low density lipoprotein	19 (0.00)	15 (0.80)	2.13
12-03	Gp3	g.chr2:170009391G>A	Missense Mutation	LRP2	p.R4127C	low density lipoprotein	61 (0.00)	50 (0.60)	1.60
12-03	Gp3	g.chr2:170010976C>T	Missense Mutation	LRP2	p.G4097S	low density lipoprotein	22 (0.00)	10 (0.60)	1.60
12-03	Gp3	g.chr3:194081160A>T	Missense Mutation	LRRC15	p.Y205N	leucine rich repeat conta	57 (0.00)	347 (0.18)	0.48
12-03	Gp3	g.chr1:70671093G>C	Missense Mutation	LRRC40	p.S44W	leucine rich repeat conta	22 (0.00)	115 (0.23)	0.60
12-03	Gp3	g.chr17:45913442C>T	Silent	LRRC46	p.N142N	leucine rich repeat conta	60 (0.00)	80 (0.42)	1.13
12-03	Gp3	g.chr1:70505212G>T	Missense Mutation	LRRC7	p.R1197S	leucine rich repeat conta	15 (0.00)	32 (0.38)	1.00
12-03	Gp3	g.chr9:131670298C>T	Silent	LRRC8A	p.Y285Y	leucine rich repeat conta	73 (0.00)	43 (0.35)	0.93
12-03	Gp3	g.chr10:68687867C>A	Missense Mutation	LRRTM3	p.T398K	leucine rich repeat trans	34 (0.00)	207 (0.32)	0.86
12-03	Gp3	g.chr20:60706520C>A	Missense Mutation	LSM14B	p.S315Y	LSM14B, SCD6 homol	31 (0.00)	33 (0.67)	1.78
12-03	Gp3	g.chr14:74971527G>A	Silent	LTBP2	p.Y1425Y	latent transforming grow	31 (0.00)	67 (0.18)	0.48
12-03	Gp3	g.chr21:30343592C>T	Splice Site	LTN1		listerin E3 ubiquitin pro	17 (0.00)	19 (0.95)	2.53
12-03	Gp3	g.chr22:21337335G>A	Missense Mutation	LZTR1	p.V74M	leucine-zipper-like trans	28 (0.00)	172 (0.12)	0.47
12-03	Gp3	g.chr1:39753017G>A	Missense Mutation	MACF1	p.R528Q	microtubule-actin crossl	36 (0.00)	13 (0.62)	1.64
12-03	Gp3	g.chr1:39853268G>A	Nonsense Mutation	MACF1	p.W4923*	microtubule-actin crossl	16 (0.00)	13 (0.38)	1.03
12-03	Gp3	g.chr11:63919788G>T	Missense Mutation	MACROD1	p.P126T	MACRO domain contai	20 (0.00)	88 (0.32)	0.85
12-03	Gp3	g.chr7:77695969G>C	Intron	MAGI2		membrane associated gu	39 (0.03)	15 (0.47)	1.24
12-03	Gp3	g.chr7:77738387C>T	Intron	MAGI2		membrane associated gu	41 (0.02)	80 (0.56)	1.50
12-03	Gp3	g.chr7:77741822A>G	Intron	MAGI2		membrane associated gu	35 (0.00)	97 (0.14)	0.38
12-03	Gp3	g.chr7:77770678C>T	Intron	MAGI2		membrane associated gu	24 (0.00)	15 (0.33)	0.89
12-03	Gp3	g.chr7:77791478G>C	Intron	MAGI2		membrane associated gu	217 (0.00)	51 (0.61)	1.62
12-03	Gp3	g.chr7:77810564G>A	Intron	MAGI2		membrane associated gu	32 (0.00)	24 (0.42)	1.11
12-03	Gp3	g.chr7:77838934C>T	Intron	MAGI2		membrane associated gu	34 (0.00)	29 (0.17)	0.46
12-03	Gp3	g.chr7:77890734C>A	Intron	MAGI2		membrane associated gu	69 (0.01)	15 (0.53)	1.42
12-03	Gp3	g.chr7:77916139T>C	Intron	MAGI2		membrane associated gu	144 (0.00)	85 (0.26)	0.69
12-03	Gp3	g.chr7:77926466A>T	Intron	MAGI2		membrane associated gu	78 (0.00)	25 (0.24)	0.64
12-03	Gp3	g.chr7:78011141T>C	Intron	MAGI2		membrane associated gu	91 (0.00)	13 (0.38)	1.03
12-03	Gp3	g.chr7:78045083C>T	Intron	MAGI2		membrane associated gu	44 (0.00)	53 (0.96)	2.57

12-03	Gp3	g.chr7:78131712A>T	Intron	MAGI2		membrane associated gu	33 (0.00)	27 (0.26)	0.69
12-03	Gp3	g.chr7:78164827T>C	Intron	MAGI2		membrane associated gu	45 (0.00)	29 (0.31)	0.83
12-03	Gp3	g.chr7:78413195G>A	Intron	MAGI2		membrane associated gu	33 (0.00)	80 (0.81)	2.17
12-03	Gp3	g.chr7:78415267G>A	Intron	MAGI2		membrane associated gu	32 (0.00)	23 (0.52)	1.39
12-03	Gp3	g.chr7:78619303C>T	Intron	MAGI2		membrane associated gu	27 (0.00)	11 (0.55)	1.45
12-03	Gp3	g.chr7:78625389C>T	Intron	MAGI2		membrane associated gu	16 (0.00)	26 (0.23)	0.62
12-03	Gp3	g.chr7:78645532C>A	Intron	MAGI2		membrane associated gu	49 (0.00)	14 (0.50)	1.33
12-03	Gp3	g.chr7:78790622G>A	Intron	MAGI2		membrane associated gu	77 (0.00)	16 (0.81)	2.17
12-03	Gp3	g.chr7:78916533C>T	Intron	MAGI2		membrane associated gu	74 (0.00)	113 (0.64)	1.70
12-03	Gp3	g.chr7:78941087G>A	Intron	MAGI2		membrane associated gu	39 (0.00)	193 (0.17)	0.44
12-03	Gp3	g.chr7:78973435A>T	Intron	MAGI2		membrane associated gu	63 (0.00)	10 (0.80)	2.13
12-03	Gp3	g.chr7:78981162T>A	Intron	MAGI2		membrane associated gu	77 (0.00)	14 (0.36)	0.95
12-03	Gp3	g.chr7:78994867G>T	Intron	MAGI2		membrane associated gu	111 (0.00)	24 (0.71)	1.89
12-03	Gp3	g.chr7:79029435C>T	Intron	MAGI2		membrane associated gu	19 (0.00)	54 (0.98)	2.62
12-03	Gp3	g.chr7:79081101G>A	Intron	MAGI2		membrane associated gu	33 (0.00)	31 (0.19)	0.52
12-03	Gp3	g.chr11:65265490G>A	lincRNA	MALAT1		metastasis associated lu	23 (0.00)	257 (0.26)	0.97
12-03	Gp3	g.chr11:65272573G>A	lincRNA	MALAT1		metastasis associated lu	37 (0.03)	70 (0.36)	1.32
12-03	Gp3	g.chr15:91461446G>A	Missense Mutation	MAN2A2	p.S1006N	mannosidase, alpha, cla	24 (0.00)	69 (0.51)	1.35
12-03	Gp3	g.chr4:103611779C>G	Missense Mutation	MANBA	p.V275L	mannosidase, beta A, ly	20 (0.00)	22 (0.50)	1.33
12-03	Gp3	g.chr15:43815595G>T	Nonsense Mutation	MAP1A	p.E880*	microtubule-associated	19 (0.00)	56 (0.66)	1.76
12-03	Gp3	g.chr15:43818745G>A	Missense Mutation	MAP1A	p.E1930K	microtubule-associated	44 (0.00)	52 (0.44)	1.18
12-03	Gp3	g.chr6:137019627C>T	Splice Site	MAP3K5	p.S269N	mitogen-activated prote	31 (0.00)	20 (0.65)	1.73
12-03	Gp3	g.chr3:47910732G>T	Missense Mutation	MAP4	p.A2127E	microtubule-associated	20 (0.00)	95 (0.27)	0.73
12-03	Gp3	g.chr3:47951053C>A	Missense Mutation	MAP4	p.V1637F	microtubule-associated	35 (0.00)	17 (0.76)	2.04
12-03	Gp3	g.chr12:58152446C>T	Silent	MARCH9	p.D269D	membrane-associated ri	28 (0.00)	76 (0.16)	0.42
12-03	Gp3	g.chr3:186954276G>A	Silent	MASP1	p.F348F	mannan-binding lectin s	26 (0.00)	96 (0.16)	0.42
12-03	Gp3	g.chr1:46491395G>A	Silent	MAST2	p.V609V	microtubule associated	51 (0.00)	19 (0.89)	2.39
12-03	Gp3	g.chr10:27462131C>A	Silent	MASTL	p.R737R	microtubule associated	91 (0.00)	29 (0.31)	0.83
12-03	Gp3	g.chr8:99015924G>T	Nonsense Mutation	MATN2	p.E414*	matrilin 2	15 (0.00)	24 (0.92)	2.44
12-03	Gp3	g.chr5:138643226C>T	Missense Mutation	MATR3	p.S41F	matrin 3	27 (0.00)	36 (0.69)	1.85
12-03	Gp3	g.chr16:84088135G>A	Silent	MBTPS1	p.S1026S	membrane-bound transc	16 (0.00)	195 (0.14)	0.38
12-03	Gp3	g.chr13:113738348C>A	Nonsense Mutation	MCF2L	p.C676*	MCF.2 cell line derived	34 (0.00)	163 (0.29)	0.79
12-03	Gp3	g.chr3:127338061C>A	Silent	MCM2	p.L735L	minichromosome maint	18 (0.00)	209 (0.22)	0.60
12-03	Gp3	g.chr21:47705176C>T	Missense Mutation	MCM3AP	p.G9R	minichromosome maint	85 (0.00)	197 (0.17)	0.63
12-03	Gp3	g.chr1:85498408G>A	Missense Mutation	MCOLN3	p.L235F	mucolipin 3	104 (0.00)	165 (0.96)	2.57

12-03	Gp3	g.chr6:41617363C>A	Missense Mutation	MDFI	p.P28H	MyoD family inhibitor	24 (0.00)	34 (0.26)	0.71
12-03	Gp3	g.chrX:153296800G>A	Missense Mutation	MECP2	p.T160I	methyl CpG binding pro	21 (0.00)	74 (0.23)	0.38
12-03	Gp3	g.chr1:28661384C>A	Missense Mutation	MED18	p.A177D	mediator complex subun	28 (0.00)	28 (0.79)	2.10
12-03	Gp3	g.chr2:112722818C>T	Silent	MERTK	p.L270L	MER proto-oncogene, t	17 (0.00)	37 (0.41)	1.08
12-03	Gp3	g.chr7:116381016G>A	Silent	MET	p.V546V	MET proto-oncogene, r	67 (0.00)	67 (0.61)	1.63
12-03	Gp3	g.chr17:74729198C>T	Nonsense Mutation	METTL23	p.Q75*	methyltransferase like 2	92 (0.00)	18 (0.28)	0.74
12-03	Gp3	g.chr15:89449895C>T	Missense Mutation	MFGE8	p.E168K	milk fat globule-EGF fa	16 (0.00)	53 (0.83)	2.21
12-03	Gp3	g.chr1:12069697C>A	Silent	MFN2	p.T706T	mitofusin 2	27 (0.00)	86 (0.17)	0.47
12-03	Gp3	g.chr1:40422854G>A	Silent	MFSD2A	p.L63L	major facilitator superfa	39 (0.00)	38 (0.76)	2.04
12-03	Gp3	g.chr1:205555320G>A	Missense Mutation	MFSD4	p.M378I	major facilitator superfa	21 (0.00)	35 (0.20)	0.43
12-03	Gp3	g.chr16:14339488C>T	Missense Mutation	MKL2	p.P395S	MKL/myocardin-like 2	35 (0.00)	99 (0.60)	1.23
12-03	Gp3	g.chr14:75489567C>T	Missense Mutation	MLH3	p.G1347E	mutL homolog 3	61 (0.02)	78 (0.22)	0.58
12-03	Gp3	g.chr1:233498008C>A	Silent	MLK4	p.L507L		38 (0.00)	37 (0.73)	1.95
12-03	Gp3	g.chr16:58074478C>G	Silent	MMP15	p.G262G	matrix metallopeptidase	27 (0.00)	313 (0.20)	0.55
12-03	Gp3	g.chr14:93650221C>T	Missense Mutation	MOAP1	p.A123T	modulator of apoptosis	46 (0.02)	210 (0.15)	0.39
12-03	Gp3	g.chr15:79186416G>T	Nonsense Mutation	MORF4L1	p.E241*	mortality factor 4 like 1	38 (0.00)	9 (0.56)	1.48
12-03	Gp3	g.chr17:41960303C>G	Missense Mutation	MPP2	p.V158L	membrane protein, palm	72 (0.00)	213 (0.43)	0.81
12-03	Gp3	g.chr14:67799615G>A	Missense Mutation	MPP5	p.R657K	membrane protein, palm	27 (0.00)	21 (0.86)	2.29
12-03	Gp3	g.chr1:54665952A>G	Silent	MRPL37	p.L12L	mitochondrial ribosoma	17 (0.00)	109 (0.16)	0.42
12-03	Gp3	g.chr10:75011562C>T	Missense Mutation	MRPS16	p.G78D	mitochondrial ribosoma	70 (0.00)	113 (0.50)	1.32
12-03	Gp3	g.chr2:48023682C>A	Intron	MSH6		mutS homolog 6	29 (0.00)	51 (0.45)	1.20
12-03	Gp3	g.chr14:105920584G>A	Missense Mutation	MTA1	p.D146N	metastasis associated 1	21 (0.00)	147 (0.18)	0.47
12-03	Gp3	g.chr8:11172573G>T	Splice Site	MTMR9	p.Q286H	myotubularin related pr	81 (0.01)	142 (0.34)	0.90
12-03	Gp3	g.chr7:100616205A>G	Silent	MUC12	p.R56R	mucin 12, cell surface a	34 (0.00)	33 (0.27)	0.73
12-03	Gp3	g.chr7:100643821C>A	Missense Mutation	MUC12	p.S3469Y	mucin 12, cell surface a	433 (0.00)	192 (0.21)	0.57
12-03	Gp3	g.chr19:9028332C>A	Missense Mutation	MUC16	p.D12154Y	mucin 16, cell surface a	41 (0.00)	84 (0.40)	1.08
12-03	Gp3	g.chr19:9048971G>T	Missense Mutation	MUC16	p.A10887E	mucin 16, cell surface a	43 (0.00)	73 (0.26)	0.69
12-03	Gp3	g.chr19:9049125G>A	Missense Mutation	MUC16	p.P10836S	mucin 16, cell surface a	184 (0.00)	97 (0.70)	1.87
12-03	Gp3	g.chr19:9056358G>C	Missense Mutation	MUC16	p.T10363S	mucin 16, cell surface a	34 (0.00)	95 (0.22)	0.59
12-03	Gp3	g.chr19:9056407C>T	Missense Mutation	MUC16	p.A10347T	mucin 16, cell surface a	29 (0.00)	71 (0.31)	0.83
12-03	Gp3	g.chr19:9061641G>A	Missense Mutation	MUC16	p.T8602I	mucin 16, cell surface a	76 (0.00)	76 (0.16)	0.42
12-03	Gp3	g.chr19:9063147G>T	Missense Mutation	MUC16	p.T8100K	mucin 16, cell surface a	39 (0.00)	24 (0.92)	2.44
12-03	Gp3	g.chr19:9068127G>A	Missense Mutation	MUC16	p.S6440F	mucin 16, cell surface a	35 (0.00)	85 (0.80)	2.13
12-03	Gp3	g.chr19:9076162C>T	Missense Mutation	MUC16	p.E3762K	mucin 16, cell surface a	111 (0.00)	110 (0.35)	0.92
12-03	Gp3	g.chr19:9082356C>T	Silent	MUC16	p.K3153K	mucin 16, cell surface a	18 (0.00)	15 (0.33)	0.89

12-03	Gp3	g.chr19:9085795G>T	Missense Mutation	MUC16	p.S2007Y	mucin 16, cell surface a	61 (0.02)	84 (0.74)	1.97
12-03	Gp3	g.chr19:9085919G>A	Missense Mutation	MUC16	p.P1966S	mucin 16, cell surface a	99 (0.01)	25 (0.80)	2.13
12-03	Gp3	g.chr19:9091111G>T	Missense Mutation	MUC16	p.S235Y	mucin 16, cell surface a	53 (0.00)	127 (0.20)	0.55
12-03	Gp3	g.chr7:100677108G>T	Missense Mutation	MUC17	p.G804V	mucin 17, cell surface a	39 (0.03)	32 (0.44)	1.17
12-03	Gp3	g.chr7:100678672C>G	Silent	MUC17	p.T1325T	mucin 17, cell surface a	54 (0.00)	21 (0.62)	1.65
12-03	Gp3	g.chr7:100678718A>G	Missense Mutation	MUC17	p.S1341G	mucin 17, cell surface a	70 (0.00)	21 (0.33)	0.89
12-03	Gp3	g.chr11:1094770C>A	Missense Mutation	MUC2	p.S1953Y	mucin 2, oligomeric mu	39 (0.00)	486 (0.14)	0.38
12-03	Gp3	g.chr11:1094771C>A	Silent	MUC2	p.S1953S	mucin 2, oligomeric mu	40 (0.00)	482 (0.15)	0.39
12-03	Gp3	g.chr3:195474218G>A	Silent	MUC4	p.G1120G	mucin 4, cell surface ass	27 (0.00)	222 (0.27)	0.71
12-03	Gp3	g.chr11:1016403G>A	Missense Mutation	MUC6	p.P2133L	mucin 6, oligomeric mu	39 (0.00)	46 (0.74)	1.97
12-03	Gp3	g.chr12:102067331G>C	Missense Mutation	MYBPC1	p.G907R	myosin binding protein	56 (0.00)	51 (0.24)	0.63
12-03	Gp3	g.chr13:77672413C>G	Missense Mutation	MYCBP2	p.S2921T	MYC binding protein 2,	79 (0.00)	52 (0.42)	1.13
12-03	Gp3	g.chr17:48603275C>A	Missense Mutation	MYCBPAP	p.H649N	MYCBP associated prot	62 (0.00)	80 (0.23)	0.60
12-03	Gp3	g.chr17:10213100C>A	Missense Mutation	MYH13	p.E1568D	myosin, heavy chain 13,	18 (0.00)	80 (0.74)	1.97
12-03	Gp3	g.chr17:10258045C>T	Silent	MYH13	p.E319E	myosin, heavy chain 13,	27 (0.00)	18 (0.61)	1.63
12-03	Gp3	g.chr19:50720907G>A	Silent	MYH14	p.P147P	myosin, heavy chain 14,	45 (0.00)	125 (0.11)	0.40
12-03	Gp3	g.chr14:23893195G>T	Nonsense Mutation	MYH7	p.S948*	myosin, heavy chain 7,	21 (0.00)	13 (0.85)	1.77
12-03	Gp3	g.chr20:30414434C>A	Silent	MYLK2	p.V333V	myosin light chain kinas	15 (0.00)	24 (0.25)	0.67
12-03	Gp3	g.chr2:171264264G>A	Missense Mutation	MYO3B	p.D854N	myosin IIIB	138 (0.00)	45 (0.31)	0.83
12-03	Gp3	g.chr2:128341745C>A	Missense Mutation	MYO7B	p.F464L	myosin VIIB	37 (0.00)	121 (0.15)	0.40
12-03	Gp3	g.chr15:72180387G>A	Missense Mutation	MYO9A	p.T1738I	myosin IXA	31 (0.00)	86 (0.41)	1.09
12-03	Gp3	g.chr17:12656345T>C	Silent	MYOCD	p.P580P	myocardin	25 (0.00)	104 (0.15)	0.41
12-03	Gp3	g.chr11:64815634G>C	Missense Mutation	NAALADL1	p.I405M	N-acetylated alpha-link	19 (0.00)	206 (0.12)	0.43
12-03	Gp3	g.chr4:164054346A>G	Silent	NAF1	p.I331I	nuclear assembly factor	24 (0.00)	33 (0.15)	0.40
12-03	Gp3	g.chr19:50862309C>T	Missense Mutation	NAPSA	p.G332R	napsin A aspartic peptid	29 (0.00)	86 (0.26)	0.91
12-03	Gp3	g.chr12:78522592T>A	Missense Mutation	NAV3	p.S1463T	neuron navigator 3	25 (0.00)	80 (0.20)	0.53
12-03	Gp3	g.chr13:35770243G>A	Missense Mutation	NBEA	p.E1721K	neurobeachin	132 (0.00)	17 (0.35)	0.94
12-03	Gp3	g.chr3:47049370C>A	Silent	NBEAL2	p.T2524T	neurobeachin-like 2	23 (0.00)	105 (0.14)	0.38
12-03	Gp3	g.chr1:16914274T>A	Missense Mutation	NBPF1	p.D171V	neuroblastoma breakpoi	102 (0.00)	39 (0.15)	0.41
12-03	Gp3	g.chr1:146401749T>A	Missense Mutation	NBPF12	p.M286K	neuroblastoma breakpoi	77 (0.00)	75 (0.39)	1.03
12-03	Gp3	g.chr1:148251901G>T	Missense Mutation	NBPF20	p.Q4614K	neuroblastoma breakpoi	51 (0.00)	85 (0.18)	0.47
12-03	Gp3	g.chr1:144220791A>T	Missense Mutation	NBPF8	p.S20C	neuroblastoma breakpoi	38 (0.00)	28 (0.21)	0.57
12-03	Gp3	g.chr17:41345270G>A	Splice Site	NBR1	p.K411K	neighbor of BRCA1 ger	67 (0.00)	18 (0.44)	0.83
12-03	Gp3	g.chr7:158443536G>A	Silent	NCAPG2	p.H1021H	non-SMC condensin II	41 (0.00)	28 (0.96)	2.57
12-03	Gp3	g.chr7:158485576C>A	Nonsense Mutation	NCAPG2	p.E114*	non-SMC condensin II	32 (0.00)	24 (0.58)	1.56

12-03	Gp3	g.chr2:97031743G>T	Nonsense Mutation	NCAPH	p.G599*	non-SMC condensin I c	56 (0.00)	31 (0.42)	1.12
12-03	Gp3	g.chr12:54914948C>A	Missense Mutation	NCKAP1L	p.L602M	NCK-associated protein	18 (0.00)	44 (0.20)	0.55
12-03	Gp3	g.chr20:46262893G>A	Missense Mutation	NCOA3	p.V356I	nuclear receptor coactiv	19 (0.00)	72 (0.82)	2.19
12-03	Gp3	g.chr6:126206490G>A	Splice Site	NCOA7		nuclear receptor coactiv	26 (0.00)	28 (0.57)	1.52
12-03	Gp3	g.chr19:55418091G>T	Missense Mutation	NCR1	p.G94V	natural cytotoxicity trig	15 (0.00)	104 (0.24)	0.64
12-03	Gp3	g.chr1:54273410G>A	Silent	NDC1	p.L270L	NDC1 transmembrane	34 (0.03)	306 (0.54)	1.43
12-03	Gp3	g.chr10:75564553G>A	Silent	NDST2	p.L607L	N-deacetylase/N-sulfotr	39 (0.00)	13 (0.46)	1.23
12-03	Gp3	g.chr7:140421480C>T	Missense Mutation	NDUFB2	p.P76L	NADH dehydrogenase (	38 (0.00)	24 (0.96)	2.56
12-03	Gp3	g.chr2:206991475C>T	Missense Mutation	NDUFS1	p.E660K	NADH dehydrogenase (	25 (0.00)	15 (0.47)	1.24
12-03	Gp3	g.chr15:56208054G>A	Missense Mutation	NEDD4	p.L326F	neural precursor cell ex	24 (0.00)	46 (0.37)	0.99
12-03	Gp3	g.chr4:170477213G>A	Missense Mutation	NEK1	p.P434S	NIMA-related kinase 1	41 (0.00)	109 (0.96)	2.57
12-03	Gp3	g.chr3:52778283C>A	Missense Mutation	NEK4	p.K576N	NIMA-related kinase 4	39 (0.00)	109 (0.40)	1.08
12-03	Gp3	g.chr11:21594918C>T	Missense Mutation	NELL1	p.T782M	NEL-like 1 (chicken)	39 (0.00)	49 (0.43)	1.14
12-03	Gp3	g.chr17:7224197C>T	Missense Mutation	NEURL4	p.E1136K	neuralized E3 ubiquitin	58 (0.00)	220 (0.28)	0.60
12-03	Gp3	g.chr17:7225047T>C	Silent	NEURL4	p.T977T	neuralized E3 ubiquitin	29 (0.00)	157 (0.20)	0.43
12-03	Gp3	g.chr19:39395662C>A	Missense Mutation	NFKBIB	p.H63N	nuclear factor of kappa	99 (0.00)	95 (0.61)	2.26
12-03	Gp3	g.chr1:115828991C>T	Nonsense Mutation	NGF	p.W142*	nerve growth factor (bet	33 (0.00)	90 (0.16)	0.41
12-03	Gp3	g.chr5:36962287T>G	Missense Mutation	NIPBL	p.V174G	Nipped-B homolog (Dr	16 (0.00)	19 (0.53)	1.40
12-03	Gp3	g.chrX:118724452C>T	Silent	NKRF	p.K312K	NFKB repressing factor	23 (0.00)	45 (0.47)	0.78
12-03	Gp3	g.chr11:7981840C>G	Missense Mutation	NLRP10	p.G440A	NLR family, pyrin dom	30 (0.00)	41 (0.68)	1.35
12-03	Gp3	g.chr3:160942774C>G	Missense Mutation	NMD3	p.A34G	NMD3 ribosome export	63 (0.00)	101 (0.40)	1.06
12-03	Gp3	g.chr17:65733982G>T	Nonsense Mutation	NOL11	p.E475*	nucleolar protein 11	28 (0.00)	28 (0.54)	1.43
12-03	Gp3	g.chr20:2635091G>T	Missense Mutation	NOP56	p.L80F	NOP56 ribonucleoprote	45 (0.00)	29 (0.24)	0.64
12-03	Gp3	g.chr20:2635401G>A	Missense Mutation	NOP56	p.R126H	NOP56 ribonucleoprote	110 (0.01)	398 (0.36)	0.95
12-03	Gp3	g.chr1:5923353G>A	Missense Mutation	NPHP4	p.A1418V	nephronophthisis 4	85 (0.00)	305 (0.29)	0.77
12-03	Gp3	g.chr16:29394442C>T	Missense Mutation	NPIPB11	p.S604N	nuclear pore complex in	178 (0.00)	115 (0.15)	0.39
12-03	Gp3	g.chr16:29394444C>T	Silent	NPIPB11	p.P603P	nuclear pore complex in	180 (0.00)	113 (0.15)	0.40
12-03	Gp3	g.chr17:38250185G>A	Missense Mutation	NR1D1	p.A542V	nuclear receptor subfam	37 (0.00)	125 (0.30)	0.81
12-03	Gp3	g.chr19:19313142G>A	Nonsense Mutation	NR2C2AP	p.Q101*	nuclear receptor 2C2-as	85 (0.00)	231 (0.19)	0.67
12-03	Gp3	g.chr9:102590455G>C	Missense Mutation	NR4A3	p.S44T	nuclear receptor subfam	47 (0.00)	240 (0.23)	0.60
12-03	Gp3	g.chr1:200017627T>C	Missense Mutation	NR5A2	p.F264S	nuclear receptor subfam	96 (0.00)	36 (0.22)	0.59
12-03	Gp3	g.chr2:27664599C>T	Silent	NRBP1	p.L510L	nuclear receptor binding	113 (0.00)	369 (0.44)	1.18
12-03	Gp3	g.chr1:52266242G>A	Silent	NRD1	p.P877P	nardilysin (N-arginine d	58 (0.00)	87 (0.67)	1.78
12-03	Gp3	g.chr14:90764725C>A	Splice Site	NRDE2		NRDE-2, necessary for	25 (0.00)	35 (0.14)	0.38
12-03	Gp3	g.chr7:129350236G>A	Missense Mutation	NRF1	p.R263Q	nuclear respiratory fact	66 (0.00)	65 (0.37)	0.98

12-03	Gp3	g.chr5:173473835C>T	Missense Mutation	NSG2	p.P26L		25 (0.00)	16 (0.69)	1.83
12-03	Gp3	g.chr9:132397728C>T	Silent	NTMT1	p.S219S	N-terminal Xaa-Pro-Lys	18 (0.00)	73 (0.34)	0.91
12-03	Gp3	g.chr12:106461034C>A	Missense Mutation	NUAK1	p.R511M	NUAK family, SNF1-lil	40 (0.00)	196 (0.16)	0.44
12-03	Gp3	g.chr1:153973460G>C	Missense Mutation	NUP210L	p.S1753C	nucleoporin 210kDa-lik	64 (0.02)	80 (0.36)	0.77
12-03	Gp3	g.chr1:153995680G>T	Missense Mutation	NUP210L	p.L1406I	nucleoporin 210kDa-lik	48 (0.00)	34 (0.26)	0.56
12-03	Gp3	g.chr9:134008581G>T	Silent	NUP214	p.V272V	nucleoporin 214kDa	50 (0.00)	30 (0.73)	1.96
12-03	Gp3	g.chr12:113400461C>T	Missense Mutation	OAS3	p.A613V	2'-5'-oligoadenylate syn	84 (0.01)	94 (0.24)	0.65
12-03	Gp3	g.chr1:228433208G>C	Missense Mutation	OBSCN	p.Q1284H	obscurin, cytoskeletal ca	68 (0.00)	37 (0.54)	1.44
12-03	Gp3	g.chr17:29622212G>A	Silent	OMG	p.L380L	oligodendrocyte myelin	20 (0.00)	22 (0.50)	1.33
12-03	Gp3	g.chr22:16449261G>A	Missense Mutation	OR11H1	p.P182S	olfactory receptor, famil	97 (0.00)	36 (0.94)	2.52
12-03	Gp3	g.chr22:16449670G>T	Silent	OR11H1	p.L45L	olfactory receptor, famil	145 (0.00)	162 (0.54)	1.43
12-03	Gp3	g.chr9:107380318G>A	Silent	OR13C9	p.H56H	olfactory receptor, famil	29 (0.00)	51 (0.39)	1.05
12-03	Gp3	g.chr1:247902370G>A	Missense Mutation	OR14K1	p.A152T	olfactory receptor, famil	30 (0.00)	65 (0.25)	0.66
12-03	Gp3	g.chr17:3181747G>C	Silent	OR3A2	p.A161A	olfactory receptor, famil	15 (0.00)	27 (0.22)	0.59
12-03	Gp3	g.chr17:56233241C>T	Missense Mutation	OR4D1	p.H243Y	olfactory receptor, famil	26 (0.00)	46 (0.89)	2.38
12-03	Gp3	g.chr14:22133982C>G	Nonsense Mutation	OR4E2	p.S229*	olfactory receptor, famil	26 (0.00)	69 (0.83)	1.73
12-03	Gp3	g.chr11:5968768C>G	Nonsense Mutation	OR56A3	p.Y64*	olfactory receptor, famil	18 (0.00)	26 (0.27)	0.44
12-03	Gp3	g.chr9:125551593G>T	Missense Mutation	OR5C1	p.V128L	olfactory receptor, famil	84 (0.00)	216 (0.25)	0.68
12-03	Gp3	g.chr18:21957416T>C	Missense Mutation	OSBPL1A	p.M28V	oxysterol binding protei	16 (0.00)	14 (0.36)	0.95
12-03	Gp3	g.chr1:36904390G>T	Silent	OSCP1	p.S33S	organic solute carrier pa	48 (0.00)	92 (0.14)	0.38
12-03	Gp3	g.chr17:79804873C>T	Missense Mutation	P4HB	p.D225N	prolyl 4-hydroxylase, be	41 (0.00)	412 (0.30)	1.12
12-03	Gp3	g.chr8:101716597G>A	Silent	PABPC1	p.L614L	poly(A) binding protein,	57 (0.00)	17 (0.29)	0.78
12-03	Gp3	g.chr13:25671613G>A	Missense Mutation	PABPC3	p.R426K	poly(A) binding protein,	90 (0.00)	80 (0.40)	1.07
12-03	Gp3	g.chr1:17555135C>T	Missense Mutation	PADI1	p.S223L	peptidyl arginine deimir	45 (0.00)	103 (0.17)	0.47
12-03	Gp3	g.chr1:17555157G>T	Silent	PADI1	p.G230G	peptidyl arginine deimir	52 (0.00)	107 (0.18)	0.47
12-03	Gp3	g.chr2:71429663C>G	Missense Mutation	PAIP2B	p.Q19H	poly(A) binding protein	54 (0.00)	127 (0.99)	2.65
12-03	Gp3	g.chr19:14165076C>G	Missense Mutation	PALM3	p.G455R	paralemmin 3	19 (0.00)	30 (0.33)	1.17
12-03	Gp3	g.chr11:93911752G>A	Missense Mutation	PANX1	p.G180E	pannexin 1	23 (0.00)	68 (0.40)	1.06
12-03	Gp3	g.chr14:20824096C>T	Missense Mutation	PARP2	p.T336I	poly (ADP-ribose) poly	55 (0.00)	28 (0.61)	1.27
12-03	Gp3	g.chr3:122247339C>T	Missense Mutation	PARP9	p.A813T	poly (ADP-ribose) poly	22 (0.00)	21 (0.95)	1.94
12-03	Gp3	g.chr2:242066757G>A	Missense Mutation	PASK	p.P525S	PAS domain containing	75 (0.00)	262 (0.15)	0.41
12-03	Gp3	g.chr2:242075323G>T	Missense Mutation	PASK	p.D423E	PAS domain containing	20 (0.00)	132 (0.42)	1.11
12-03	Gp3	g.chr19:19680257C>A	Splice Site	PBX4		pre-B-cell leukemia hon	25 (0.00)	16 (0.44)	1.50
12-03	Gp3	g.chr10:56138644G>T	Silent	PCDH15	p.T72T	protocadherin-related 1	48 (0.00)	17 (0.94)	2.51
12-03	Gp3	g.chr5:140235926G>A	Missense Mutation	PCDHA10	p.S98N	protocadherin alpha 10	39 (0.00)	481 (0.19)	0.51

12-03	Gp3	g.chr5:140249766G>A	Missense Mutation	PCDHA11	p.E360K	protocadherin alpha 11	20 (0.00)	151 (0.46)	1.24
12-03	Gp3	g.chr5:140502617T>C	Missense Mutation	PCDHB4	p.L346P	protocadherin beta 4	110 (0.00)	140 (0.21)	0.55
12-03	Gp3	g.chr5:140502697G>T	Missense Mutation	PCDHB4	p.D373Y	protocadherin beta 4	70 (0.00)	155 (0.32)	0.86
12-03	Gp3	g.chr5:140558294G>A	Missense Mutation	PCDHB8	p.A227T	protocadherin beta 8	33 (0.00)	28 (0.68)	1.81
12-03	Gp3	g.chr5:140755146C>A	Missense Mutation	PCDHGA6	p.A499E	protocadherin gamma su	96 (0.00)	274 (0.27)	0.71
12-03	Gp3	g.chr5:140773133C>T	Silent	PCDHGA8	p.V251V	protocadherin gamma su	25 (0.00)	168 (0.21)	0.57
12-03	Gp3	g.chr5:140774729G>T	Missense Mutation	PCDHGA8	p.E783D	protocadherin gamma su	57 (0.00)	62 (0.24)	0.65
12-03	Gp3	g.chr5:140783613T>G	Missense Mutation	PCDHGA9	p.V365G	protocadherin gamma su	18 (0.00)	39 (0.44)	1.16
12-03	Gp3	g.chr5:140750776G>T	Missense Mutation	PCDHGB3	p.G272V	protocadherin gamma su	183 (0.01)	254 (0.23)	0.62
12-03	Gp3	g.chr5:140750953G>A	Missense Mutation	PCDHGB3	p.C331Y	protocadherin gamma su	124 (0.00)	141 (0.28)	0.76
12-03	Gp3	g.chr5:140751956A>G	Silent	PCDHGB3	p.A665A	protocadherin gamma su	34 (0.03)	161 (0.55)	1.47
12-03	Gp3	g.chr5:140789966G>T	Missense Mutation	PCDHGB6	p.V733F	protocadherin gamma su	33 (0.00)	99 (0.28)	0.75
12-03	Gp3	g.chr7:82584247T>C	Missense Mutation	PCLO	p.T2008A	piccolo presynaptic cyto	112 (0.00)	38 (0.18)	0.49
12-03	Gp3	g.chr21:47831244C>T	Silent	PCNT	p.L1753L	pericentrin	20 (0.00)	397 (0.27)	1.02
12-03	Gp3	g.chr15:65421503C>A	Missense Mutation	PDCD7	p.Q292H	programmed cell death	57 (0.00)	35 (0.40)	1.07
12-03	Gp3	g.chr9:125582601G>A	Silent	PDCL	p.G223G	phosducin-like	37 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr1:144881455C>T	Silent	PDE4DIP	p.E1384E	phosphodiesterase 4D in	87 (0.00)	57 (0.82)	2.20
12-03	Gp3	g.chr4:120549713C>T	Nonsense Mutation	PDE5A	p.W38*	phosphodiesterase 5A, c	30 (0.00)	107 (0.22)	0.60
12-03	Gp3	g.chr5:149513155C>T	Missense Mutation	PDGFRB	p.V310M	platelet-derived growth	15 (0.00)	78 (0.83)	2.22
12-03	Gp3	g.chr4:39874689T>C	Missense Mutation	PDS5A	p.M785V	PDS5, regulator of cohe	18 (0.00)	26 (0.35)	0.92
12-03	Gp3	g.chr16:70044698G>A	RNA	PDXDC2P		pyridoxal-dependent dec	31 (0.00)	34 (0.18)	0.47
12-03	Gp3	g.chr7:94293076C>T	Missense Mutation	PEG10	p.P70S	paternally expressed 10	47 (0.02)	56 (0.14)	0.38
12-03	Gp3	g.chr17:33903046G>A	Silent	PEX12	p.L279L	peroxisomal biogenesis	40 (0.00)	14 (0.71)	1.90
12-03	Gp3	g.chr6:42932837C>T	Missense Mutation	PEX6	p.R881H	peroxisomal biogenesis	55 (0.00)	37 (0.65)	1.73
12-03	Gp3	g.chr12:48536644G>T	Missense Mutation	PFKM	p.G578V	phosphofructokinase, m	71 (0.00)	31 (0.29)	0.77
12-03	Gp3	g.chr6:13228136C>A	Missense Mutation	PHACTR1	p.L359I	phosphatase and actin re	65 (0.00)	35 (0.69)	1.83
12-03	Gp3	g.chr5:125939285T>C	Silent	PHAX	p.A40A	phosphorylated adaptor	23 (0.00)	21 (0.52)	1.40
12-03	Gp3	g.chr3:169847266C>T	Missense Mutation	PHC3	p.V332I	polyhomeotic homolog	138 (0.00)	102 (0.38)	1.02
12-03	Gp3	g.chr9:96425286C>T	Missense Mutation	PHF2	p.S599L	PHD finger protein 2	86 (0.00)	26 (0.96)	2.56
12-03	Gp3	g.chr1:120277286A>T	Silent	PHGDH	p.P180P	phosphoglycerate dehyd	105 (0.00)	121 (0.24)	0.64
12-03	Gp3	g.chr18:60384566C>A	Intron	PHLPP1		PH domain and leucine	58 (0.00)	242 (0.18)	0.48
12-03	Gp3	g.chr18:60384723A>G	Intron	PHLPP1		PH domain and leucine	76 (0.00)	122 (0.15)	0.39
12-03	Gp3	g.chr18:60384790C>T	Intron	PHLPP1		PH domain and leucine	112 (0.00)	126 (0.18)	0.49
12-03	Gp3	g.chr18:60522888T>G	Intron	PHLPP1		PH domain and leucine	77 (0.00)	67 (0.45)	1.19
12-03	Gp3	g.chr18:60525132G>T	Intron	PHLPP1		PH domain and leucine	44 (0.00)	124 (0.87)	2.32

12-03	Gp3	g.chr18:60561766G>A	Intron	PHLPP1		PH domain and leucine	30 (0.00)	99 (0.84)	2.24
12-03	Gp3	g.chr18:60609120G>C	Missense Mutation	PHLPP1	p.A1044P	PH domain and leucine	59 (0.00)	109 (0.28)	0.73
12-03	Gp3	g.chr18:60620171G>A	Intron	PHLPP1		PH domain and leucine	32 (0.00)	15 (0.33)	0.89
12-03	Gp3	g.chr18:60644301G>A	Intron	PHLPP1		PH domain and leucine	39 (0.00)	206 (0.43)	1.14
12-03	Gp3	g.chr16:71678766C>A	Intron	PHLPP2		PH domain and leucine	25 (0.00)	88 (0.33)	0.88
12-03	Gp3	g.chr16:71706636C>T	Intron	PHLPP2		PH domain and leucine	68 (0.00)	57 (0.16)	0.42
12-03	Gp3	g.chr11:607871T>A	Missense Mutation	PHRF1	p.D804E	PHD and ring finger do	42 (0.00)	517 (0.17)	0.46
12-03	Gp3	g.chr22:21064997G>T	Missense Mutation	PI4KA	p.L2025M	phosphatidylinositol 4-k	32 (0.00)	140 (0.11)	0.41
12-03	Gp3	g.chr22:21087360C>A	Missense Mutation	PI4KA	p.G1396V	phosphatidylinositol 4-k	25 (0.00)	137 (0.31)	1.20
12-03	Gp3	g.chr15:65113701G>T	Missense Mutation	PIF1	p.A279D	PIF1 5'-to-3' DNA helic	25 (0.00)	15 (0.33)	0.89
12-03	Gp3	g.chr17:26881273G>A	Missense Mutation	PIGS	p.R545C	phosphatidylinositol gly	48 (0.00)	32 (0.34)	0.92
12-03	Gp3	g.chr3:178917582C>T	Missense Mutation	PIK3CA	p.L153F	phosphatidylinositol-4,5	81 (0.00)	22 (0.41)	1.09
12-03	Gp3	g.chr3:130403129G>A	Missense Mutation	PIK3R4	p.S1191L	phosphoinositide-3-kina	41 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chr3:130435326G>C	Missense Mutation	PIK3R4	p.Q749E	phosphoinositide-3-kina	27 (0.00)	17 (0.59)	1.57
12-03	Gp3	g.chr2:209217467T>C	Silent	PIKFYVE	p.L1935L	phosphoinositide kinase	64 (0.00)	98 (0.17)	0.46
12-03	Gp3	g.chr1:24105927G>T	Splice Site	PITHD1		PITH (C-terminal prote	23 (0.00)	36 (0.61)	1.63
12-03	Gp3	g.chr17:65548431G>T	Missense Mutation	PITPNC1	p.A86S	phosphatidylinositol tra	24 (0.00)	36 (0.89)	2.37
12-03	Gp3	g.chr11:67267228G>T	Silent	PITPNM1	p.A379A	phosphatidylinositol tra	35 (0.00)	69 (0.48)	1.77
12-03	Gp3	g.chr22:25144934A>T	Missense Mutation	PIWIL3	p.N463K	piwi-like RNA-mediate	37 (0.00)	58 (0.79)	2.11
12-03	Gp3	g.chr22:25144969A>T	Missense Mutation	PIWIL3	p.L452I	piwi-like RNA-mediate	40 (0.00)	52 (0.83)	2.21
12-03	Gp3	g.chr11:94328517C>T	Missense Mutation	PIWIL4	p.A398V	piwi-like RNA-mediate	25 (0.00)	114 (0.97)	2.60
12-03	Gp3	g.chr8:110510941G>A	Missense Mutation	PKHD1L1	p.R3590Q	polycystic kidney and h	50 (0.00)	157 (0.75)	2.00
12-03	Gp3	g.chr20:30785364G>A	Missense Mutation	PLAGL2	p.H128Y	pleiomorphic adenoma	28 (0.00)	187 (0.18)	0.48
12-03	Gp3	g.chr12:113825565C>G	Missense Mutation	PLBD2	p.H454D	phospholipase B domai	118 (0.00)	505 (0.15)	0.39
12-03	Gp3	g.chr6:151153168G>A	Missense Mutation	PLEKHG1	p.S974N	pleckstrin homology do	86 (0.00)	285 (0.22)	0.59
12-03	Gp3	g.chr6:151153253G>A	Silent	PLEKHG1	p.E1002E	pleckstrin homology do	35 (0.00)	27 (0.19)	0.49
12-03	Gp3	g.chr19:39915368G>A	Missense Mutation	PLEKHG2	p.E1199K	pleckstrin homology do	51 (0.00)	242 (0.29)	1.07
12-03	Gp3	g.chr19:39915434C>G	Missense Mutation	PLEKHG2	p.L1221V	pleckstrin homology do	40 (0.00)	271 (0.22)	0.81
12-03	Gp3	g.chr16:67322069G>T	Splice Site	PLEKHG4		pleckstrin homology do	36 (0.00)	145 (0.30)	0.79
12-03	Gp3	g.chr14:68040543G>T	Missense Mutation	PLEKHH1	p.G622V	pleckstrin homology do	16 (0.00)	44 (0.32)	0.85
12-03	Gp3	g.chr2:43927544A>G	Missense Mutation	PLEKHH2	p.R483G	pleckstrin homology do	19 (0.00)	126 (0.40)	1.08
12-03	Gp3	g.chr19:4512763C>G	Missense Mutation	PLIN4	p.M389I	perilipin 4	39 (0.00)	67 (0.57)	2.04
12-03	Gp3	g.chr7:131872332C>A	Missense Mutation	PLXNA4	p.G964V	plexin A4	38 (0.00)	96 (0.39)	1.03
12-03	Gp3	g.chr3:48454343G>A	Silent	PLXNB1	p.L1554L	plexin B1	31 (0.00)	158 (0.15)	0.39
12-03	Gp3	g.chr3:129278594G>A	Silent	PLXND1	p.F1722F	plexin D1	25 (0.00)	98 (0.18)	0.49

12-03	Gp3	g.chr22:41980050G>A	Silent	PMM1	p.I129I	phosphomannomutase 1	17 (0.00)	20 (0.55)	1.47
12-03	Gp3	g.chr19:50369667C>T	Missense Mutation	PNKP	p.A63T	polynucleotide kinase 3'	41 (0.00)	44 (0.11)	0.40
12-03	Gp3	g.chr6:160237044G>A	Missense Mutation	PNLDC1	p.A347T	poly(A)-specific ribonu	126 (0.00)	52 (0.23)	0.62
12-03	Gp3	g.chr6:160237612C>T	Silent	PNLDC1	p.A366A	poly(A)-specific ribonu	73 (0.00)	90 (0.30)	0.80
12-03	Gp3	g.chr7:131189226G>A	Silent	PODXL	p.Y507Y	podocalyxin-like	58 (0.00)	36 (0.19)	0.52
12-03	Gp3	g.chr7:44116147G>A	Nonsense Mutation	POLM	p.R266*	polymerase (DNA direc	18 (0.00)	219 (0.18)	0.47
12-03	Gp3	g.chr3:121187228C>T	Missense Mutation	POLQ	p.E2257K	polymerase (DNA direc	54 (0.00)	60 (0.50)	1.33
12-03	Gp3	g.chr3:121206962G>A	Nonsense Mutation	POLQ	p.Q1606*	polymerase (DNA direc	62 (0.00)	45 (0.20)	0.53
12-03	Gp3	g.chr15:21051183G>A	Missense Mutation	POTEB2	p.T426I	POTE ankyrin domain f	23 (0.00)	17 (0.41)	1.10
12-03	Gp3	g.chr2:131414319C>A	Silent	POTEJ	p.L662L	POTE ankyrin domain f	135 (0.00)	248 (0.23)	0.94
12-03	Gp3	g.chr5:149212302G>T	Silent	PPARGC1B	p.S222S	peroxisome proliferator-	21 (0.00)	189 (0.40)	1.07
12-03	Gp3	g.chr12:81657105T>A	Missense Mutation	PPFIA2	p.H1207L	protein tyrosine phospha	26 (0.00)	71 (0.18)	0.49
12-03	Gp3	g.chr12:81657129C>A	Missense Mutation	PPFIA2	p.R1199M	protein tyrosine phospha	27 (0.00)	70 (0.17)	0.46
12-03	Gp3	g.chr1:143767495C>A	Missense Mutation	PPIAL4G	p.K118N	peptidylprolyl isomeras	115 (0.00)	141 (0.77)	2.04
12-03	Gp3	g.chr11:73933390G>A	Missense Mutation	PPME1	p.V108I	protein phosphatase met	29 (0.00)	41 (0.15)	0.39
12-03	Gp3	g.chr12:111158930C>G	Missense Mutation	PPP1CC	p.R308T	protein phosphatase 1, c	34 (0.00)	35 (0.40)	1.07
12-03	Gp3	g.chr14:104206734G>T	Silent	PPP1R13B	p.T673T	protein phosphatase 1, r	43 (0.00)	219 (0.23)	0.61
12-03	Gp3	g.chr19:49379064G>A	Missense Mutation	PPP1R15A	p.R620K	protein phosphatase 1, r	52 (0.00)	439 (0.15)	0.55
12-03	Gp3	g.chr9:138379876C>A	Silent	PPP1R26	p.R1174R	protein phosphatase 1, r	22 (0.00)	261 (0.13)	0.43
12-03	Gp3	g.chr14:102384285G>A	Splice Site	PPP2R5C		protein phosphatase 2, r	31 (0.00)	95 (0.26)	0.70
12-03	Gp3	g.chr1:13036378G>T	Missense Mutation	PRAMEF22	p.K150N	PRAME family membe	139 (0.01)	68 (0.18)	0.47
12-03	Gp3	g.chr1:12939704G>T	Missense Mutation	PRAMEF4	p.D366E	PRAME family membe	62 (0.00)	26 (0.27)	0.72
12-03	Gp3	g.chr1:14108692G>A	Missense Mutation	PRDM2	p.G1468R	PR domain containing 2	88 (0.00)	44 (0.77)	2.06
12-03	Gp3	g.chr2:27355172G>T	Silent	PREB	p.A284A	prolactin regulatory ele	22 (0.00)	68 (0.28)	0.75
12-03	Gp3	g.chr12:57135306G>A	Nonsense Mutation	PRIM1	p.Q299*	primase, DNA, polypep	39 (0.00)	107 (0.59)	1.57
12-03	Gp3	g.chr12:57135324C>A	Nonsense Mutation	PRIM1	p.E293*	primase, DNA, polypep	35 (0.00)	92 (0.52)	1.39
12-03	Gp3	g.chr9:71628798C>G	Missense Mutation	PRKACG	p.A71P	protein kinase, cAMP-d	38 (0.00)	212 (0.17)	0.45
12-03	Gp3	g.chr14:30132925C>T	Missense Mutation	PRKD1	p.A226T	protein kinase D1	32 (0.00)	119 (0.29)	0.76
12-03	Gp3	g.chr21:48083360T>A	Missense Mutation	PRMT2	p.V388E	protein arginine methylt	17 (0.00)	90 (0.12)	0.46
12-03	Gp3	g.chr11:20419210G>T	Missense Mutation	PRMT3	p.E216D	protein arginine methylt	36 (0.00)	11 (0.82)	2.18
12-03	Gp3	g.chr12:50027302C>A	Silent	PRPF40B	p.T184T	PRP40 pre-mRNA proc	35 (0.00)	97 (0.15)	0.41
12-03	Gp3	g.chr19:50118217G>A	Missense Mutation	PRR12	p.V1659M	proline rich 12	29 (0.00)	286 (0.24)	0.85
12-03	Gp3	g.chr22:32108724T>C	Missense Mutation	PRR14L	p.I1701V	proline rich 14-like	84 (0.00)	18 (0.28)	0.74
12-03	Gp3	g.chr9:134353271A>G	Missense Mutation	PRRC2B	p.K822R	proline-rich coiled-coil	37 (0.00)	102 (0.32)	0.86
12-03	Gp3	g.chr16:29825220C>G	Missense Mutation	PRRT2	p.P282R	proline-rich transmemb	19 (0.00)	150 (0.16)	0.43

12-03	Gp3	g.chr16:2871061G>A	Missense Mutation	PRSS21	p.G219E	protease, serine, 21 (test	17 (0.00)	225 (0.15)	0.49
12-03	Gp3	g.chr1:151006411C>A	Missense Mutation	PRUNE	p.L355I	prune exopolyphosphata	19 (0.00)	27 (0.37)	1.23
12-03	Gp3	g.chr10:73588712C>A	Missense Mutation	PSAP	p.E166D	prosaposin	19 (0.00)	16 (0.94)	2.50
12-03	Gp3	g.chr19:43530491G>A	Missense Mutation	PSG11	p.H12Y	pregnancy specific beta-	60 (0.00)	79 (0.72)	1.92
12-03	Gp3	g.chr17:4700783G>A	Missense Mutation	PSMB6	p.R74H	proteasome (prosome, n	74 (0.00)	23 (0.83)	2.20
12-03	Gp3	g.chr3:64004695T>C	Silent	PSMD6	p.G172G	proteasome (prosome, n	63 (0.00)	27 (0.19)	0.49
12-03	Gp3	g.chr10:89648131C>T	Intron	PTEN		phosphatase and tensin	29 (0.00)	56 (0.43)	1.14
12-03	Gp3	g.chr10:89695737G>A	Intron	PTEN		phosphatase and tensin	108 (0.00)	61 (0.72)	1.92
12-03	Gp3	g.chr10:89700707C>A	Intron	PTEN		phosphatase and tensin	61 (0.00)	17 (0.41)	1.10
12-03	Gp3	g.chr10:89722752C>T	Intron	PTEN		phosphatase and tensin	92 (0.00)	46 (0.20)	0.52
12-03	Gp3	g.chr5:40681479C>G	Missense Mutation	PTGER4	p.S128R	prostaglandin E receptor	141 (0.00)	497 (0.16)	0.42
12-03	Gp3	g.chr1:117529476A>G	Missense Mutation	PTGFRN	p.I843V	prostaglandin F2 recept	35 (0.00)	73 (0.18)	0.47
12-03	Gp3	g.chr9:96847022G>A	Silent	PTPDC1	p.E70E	protein tyrosine phospha	79 (0.00)	203 (0.14)	0.38
12-03	Gp3	g.chr9:96857666G>A	Silent	PTPDC1	p.V226V	protein tyrosine phospha	49 (0.00)	78 (0.38)	1.03
12-03	Gp3	g.chr7:77195520G>A	Intron	PTPN12		protein tyrosine phospha	20 (0.00)	24 (0.67)	1.78
12-03	Gp3	g.chr7:77218232C>A	Intron	PTPN12		protein tyrosine phospha	57 (0.02)	107 (0.54)	1.45
12-03	Gp3	g.chr7:77226350C>A	Intron	PTPN12		protein tyrosine phospha	35 (0.00)	30 (0.47)	1.24
12-03	Gp3	g.chr3:47453028G>A	Missense Mutation	PTPN23	p.S1247N	protein tyrosine phospha	29 (0.00)	257 (0.18)	0.47
12-03	Gp3	g.chr9:112216810G>A	Missense Mutation	PTPN3	p.P112S	protein tyrosine phospha	60 (0.00)	33 (0.88)	2.34
12-03	Gp3	g.chr1:44085824T>A	Missense Mutation	PTPRF	p.W1715R	protein tyrosine phospha	26 (0.00)	29 (0.21)	0.55
12-03	Gp3	g.chr19:55718140C>T	Missense Mutation	PTPRH	p.G90E	protein tyrosine phospha	56 (0.00)	134 (0.21)	0.56
12-03	Gp3	g.chr19:5219985G>T	Missense Mutation	PTPRS	p.L1244I	protein tyrosine phospha	36 (0.00)	342 (0.26)	0.94
12-03	Gp3	g.chr2:20490431G>T	Missense Mutation	PUM2	p.L425I	pumilio RNA-binding fa	33 (0.00)	10 (0.80)	2.13
12-03	Gp3	g.chr11:125765837C>T	Missense Mutation	PUS3	p.G115R	pseudouridylate synthas	85 (0.00)	89 (0.15)	0.39
12-03	Gp3	g.chr19:45162096G>A	Missense Mutation	PVR	p.G360R	poliovirus receptor	16 (0.00)	18 (0.78)	2.07
12-03	Gp3	g.chr19:45162159T>C	Missense Mutation	PVR	p.C381R	poliovirus receptor	16 (0.00)	23 (0.30)	0.81
12-03	Gp3	g.chr1:226109270G>A	Silent	PYCR2	p.L205L	pyrroline-5-carboxylate	22 (0.00)	181 (0.17)	0.44
12-03	Gp3	g.chr1:154932271C>A	Missense Mutation	PYGO2	p.V69L	pygopus family PHD fin	19 (0.00)	72 (0.18)	0.38
12-03	Gp3	g.chr17:74283947T>A	Missense Mutation	QRICH2	p.E1111V	glutamine rich 2	33 (0.03)	23 (0.22)	0.58
12-03	Gp3	g.chr2:136396529G>T	Missense Mutation	R3HDM1	p.L296F	R3H domain containing	55 (0.00)	19 (0.79)	1.20
12-03	Gp3	g.chr3:128813861T>A	Missense Mutation	RAB43	p.Y119F	RAB43, member RAS c	31 (0.00)	80 (0.40)	1.07
12-03	Gp3	g.chr15:40993312C>T	Silent	RAD51	p.F46F	RAD51 recombinase	35 (0.00)	32 (0.19)	0.50
12-03	Gp3	g.chr5:34823315G>A	Silent	RAI14	p.Q456Q	retinoic acid induced 14	24 (0.00)	57 (0.35)	0.94
12-03	Gp3	g.chr9:6015529T>A	Missense Mutation	RANBP6	p.I27F	RAN binding protein 6	17 (0.00)	139 (0.29)	0.79
12-03	Gp3	g.chr9:134526309A>T	Missense Mutation	RAPGEF1	p.F30Y	Rap guanine nucleotide	18 (0.00)	12 (0.67)	1.78

12-03	Gp3	g.chr6:88240535G>A	Silent	RARS2	p.D246D	arginyl-tRNA synthetas	41 (0.00)	223 (0.64)	0.91
12-03	Gp3	g.chr5:179548150C>A	Splice Site	RASGEF1C		RasGEF domain family,	15 (0.00)	15 (0.67)	2.14
12-03	Gp3	g.chr13:48890459C>A	Intron	RB1		retinoblastoma 1	25 (0.00)	170 (0.16)	0.44
12-03	Gp3	g.chr13:48890593G>T	Intron	RB1		retinoblastoma 1	17 (0.00)	20 (0.45)	1.20
12-03	Gp3	g.chr13:48902905C>T	Intron	RB1		retinoblastoma 1	56 (0.00)	16 (0.44)	1.17
12-03	Gp3	g.chr20:34241613G>C	Silent	RBM12	p.V544V	RNA binding motif prot	134 (0.00)	102 (0.98)	2.61
12-03	Gp3	g.chr8:94745914C>T	Missense Mutation	RBM12B	p.G909R	RNA binding motif prot	68 (0.00)	240 (0.16)	0.43
12-03	Gp3	g.chr10:6155489A>T	Missense Mutation	RBM17	p.D292V	RNA binding motif prot	22 (0.00)	38 (0.21)	0.56
12-03	Gp3	g.chr19:36120463C>T	Missense Mutation	RBM42	p.P57L	RNA binding motif prot	33 (0.00)	53 (0.42)	1.11
12-03	Gp3	g.chr19:50040307G>A	Missense Mutation	RCN3	p.V155M	reticulocalbin 3, EF-han	46 (0.02)	368 (0.26)	0.92
12-03	Gp3	g.chr12:57346727C>T	Missense Mutation	RDH16	p.G207D	retinol dehydrogenase 1	51 (0.00)	40 (0.85)	2.27
12-03	Gp3	g.chr17:73661160C>A	Missense Mutation	RECQL5	p.V75L	RecQ protein-like 5	64 (0.00)	62 (0.53)	1.42
12-03	Gp3	g.chrX:71350203C>T	Silent	RGAG4	p.E396E	retrotransposon gag don	25 (0.00)	70 (0.53)	0.88
12-03	Gp3	g.chr2:107040815T>C	Missense Mutation	RGPD3	p.K1203R	RANBP2-like and GRI	117 (0.01)	63 (0.29)	0.76
12-03	Gp3	g.chr2:108489230G>A	Silent	RGPD4	p.Q1590Q	RANBP2-like and GRI	53 (0.00)	62 (0.53)	1.42
12-03	Gp3	g.chr4:3430435G>A	Missense Mutation	RGS12	p.E1188K	regulator of G-protein si	27 (0.00)	85 (0.40)	1.07
12-03	Gp3	g.chr12:2997475T>C	Silent	RHNO1	p.P175P	RAD9-HUS1-RAD1 int	25 (0.00)	20 (0.50)	1.33
12-03	Gp3	g.chr20:19955473C>T	Silent	RIN2	p.A317A	Ras and Rab interactor	35 (0.03)	167 (0.29)	0.78
12-03	Gp3	g.chr17:41180496C>A	Nonsense Mutation	RND2	p.C161*	Rho family GTPase 2	18 (0.00)	89 (0.22)	0.42
12-03	Gp3	g.chr1:20141544G>C	Silent	RNF186	p.A17A	ring finger protein 186	15 (0.00)	250 (0.22)	0.59
12-03	Gp3	g.chr12:121861260G>C	Missense Mutation	RNF34	p.D334H	ring finger protein 34, E	20 (0.00)	38 (0.24)	0.63
12-03	Gp3	g.chr1:201958113G>T	Missense Mutation	RNPEP	p.A177S	arginyl aminopeptidase	74 (0.00)	60 (0.78)	2.09
12-03	Gp3	g.chr18:110299G>T	RNA	ROCK1P1		Rho-associated, coiled-	48 (0.02)	30 (0.17)	0.44
12-03	Gp3	g.chr18:110501C>T	RNA	ROCK1P1		Rho-associated, coiled-	25 (0.00)	18 (0.28)	0.74
12-03	Gp3	g.chr18:110527T>C	RNA	ROCK1P1		Rho-associated, coiled-	21 (0.00)	16 (0.31)	0.83
12-03	Gp3	g.chrX:114953381G>T	Missense Mutation	RP1-241P17.4	p.Q57K		31 (0.00)	14 (0.50)	0.83
12-03	Gp3	g.chr22:44761504G>T	Nonsense Mutation	RP1-32I10.10	p.G4*		19 (0.00)	20 (0.95)	2.53
12-03	Gp3	g.chr5:177059252G>A	RNA	RP11-1277A3.2			19 (0.00)	19 (0.42)	1.35
12-03	Gp3	g.chr4:9386263G>A	Silent	RP11-1396O1	p.H127H		50 (0.00)	20 (0.45)	1.20
12-03	Gp3	g.chr16:74382953A>C	RNA	RP11-252A24.2			30 (0.00)	73 (0.71)	1.90
12-03	Gp3	g.chr4:40045277T>C	RNA	RP11-333E13.4			15 (0.00)	148 (0.23)	0.61
12-03	Gp3	g.chr1:142810463A>T	lincRNA	RP11-423O2.5			19 (0.00)	42 (0.67)	1.78
12-03	Gp3	g.chr1:142810475C>T	lincRNA	RP11-423O2.5			19 (0.00)	38 (0.66)	1.75
12-03	Gp3	g.chr3:185689679G>T	RNA	RP11-443P15.2			33 (0.00)	29 (0.72)	1.93
12-03	Gp3	g.chr3:196043067G>T	Missense Mutation	RP11-447L10.	p.A50D		15 (0.00)	31 (0.26)	0.69

12-03	Gp3	g.chr1:145281510G>A	Missense Mutation	RP11-458D21.	p.C147Y		115 (0.00)	122 (0.39)	1.03
12-03	Gp3	g.chr1:202794939G>A	Missense Mutation	RP11-480I12.4	p.C102Y		36 (0.00)	57 (0.61)	1.33
12-03	Gp3	g.chr9:95647313C>A	RNA	RP11-526D8.7			66 (0.00)	238 (0.53)	1.40
12-03	Gp3	g.chr9:95647769A>G	RNA	RP11-526D8.7			67 (0.00)	71 (0.30)	0.79
12-03	Gp3	g.chr9:95648403G>A	RNA	RP11-526D8.7			22 (0.00)	12 (0.58)	1.56
12-03	Gp3	g.chr5:162843571C>A	RNA	RP11-541P9.3			21 (0.00)	31 (0.29)	0.77
12-03	Gp3	g.chr18:48445G>A	Nonsense Mutation	RP11-683L23.	p.Q60*		59 (0.00)	201 (0.23)	0.62
12-03	Gp3	g.chr15:67293200G>A	lincRNA	RP11-798K3.2			31 (0.00)	51 (0.20)	0.52
12-03	Gp3	g.chr1:143743198G>A	lincRNA	RP6-206I17.1			18 (0.00)	38 (0.32)	0.84
12-03	Gp3	g.chr14:21788274C>T	Missense Mutation	RPGRIP1	p.P469S	retinitis pigmentosa GT	42 (0.00)	287 (0.29)	0.61
12-03	Gp3	g.chr1:24019171G>A	Missense Mutation	RPL11	p.G27R	ribosomal protein L11	22 (0.00)	35 (0.91)	2.44
12-03	Gp3	g.chr10:15145642G>A	Missense Mutation	RPP38	p.R110K	ribonuclease P/MRP 38	25 (0.00)	20 (0.70)	1.87
12-03	Gp3	g.chr6:166914393C>T	Missense Mutation	RPS6KA2	p.G107R	ribosomal protein S6 ki	55 (0.00)	212 (0.20)	0.53
12-03	Gp3	g.chr15:41770811C>T	Silent	RTF1	p.T602T	Rtf1, Paf1/RNA polyme	121 (0.01)	71 (0.68)	1.80
12-03	Gp3	g.chr14:101348835G>T	Missense Mutation	RTL1	p.S764Y	retrotransposon-like 1	39 (0.00)	37 (0.19)	0.50
12-03	Gp3	g.chr3:72434321C>G	Intron	RYBP		RING1 and YY1 bindin	108 (0.00)	26 (0.54)	1.44
12-03	Gp3	g.chr3:72443909C>A	Intron	RYBP		RING1 and YY1 bindin	51 (0.00)	50 (0.26)	0.69
12-03	Gp3	g.chr3:72464017G>A	Intron	RYBP		RING1 and YY1 bindin	43 (0.00)	31 (0.23)	0.60
12-03	Gp3	g.chr3:72489962G>A	Intron	RYBP		RING1 and YY1 bindin	58 (0.00)	31 (0.81)	2.15
12-03	Gp3	g.chr19:39051920G>T	Silent	RYR1	p.S4150S	ryanodine receptor 1 (sk	37 (0.00)	352 (0.14)	0.39
12-03	Gp3	g.chr1:237664166C>T	Missense Mutation	RYR2	p.L787F	ryanodine receptor 2 (ca	19 (0.00)	65 (0.38)	1.03
12-03	Gp3	g.chr13:23904372G>C	Missense Mutation	SACS	p.P4548R	sacsin molecular chaper	77 (0.00)	153 (0.66)	1.76
12-03	Gp3	g.chr20:50408682C>T	Missense Mutation	SALL4	p.D114N	spalt-like transcription f	41 (0.00)	342 (0.29)	0.77
12-03	Gp3	g.chr7:92763751G>T	Missense Mutation	SAMD9L	p.L512I	sterile alpha motif doma	40 (0.00)	33 (0.45)	1.21
12-03	Gp3	g.chr1:100550901G>T	Missense Mutation	SASS6	p.Q653K	spindle assembly 6 hom	93 (0.00)	52 (0.23)	0.62
12-03	Gp3	g.chr15:32972104G>A	Missense Mutation	SCG5	p.V122I	secretogranin V (7B2 pr	43 (0.00)	162 (0.36)	1.20
12-03	Gp3	g.chr5:147261104C>A	Missense Mutation	SCGB3A2	p.L51I	secretoglobin, family 3	66 (0.00)	22 (0.27)	0.73
12-03	Gp3	g.chr17:5126670C>A	Missense Mutation	SCIMP	p.G35C	SLP adaptor and CSK i	67 (0.00)	23 (0.35)	0.75
12-03	Gp3	g.chr2:238999877G>T	Missense Mutation	SCLY	p.M309I	selenocysteine lyase	52 (0.00)	101 (0.15)	0.40
12-03	Gp3	g.chr2:166901664C>T	Silent	SCN1A	p.E517E	sodium channel, voltage	107 (0.00)	85 (0.89)	2.38
12-03	Gp3	g.chr2:166904278G>A	Splice Site	SCN1A	p.G343G	sodium channel, voltage	30 (0.00)	21 (0.48)	1.27
12-03	Gp3	g.chr17:62020457C>A	Splice Site	SCN4A		sodium channel, voltage	17 (0.00)	37 (0.22)	0.58
12-03	Gp3	g.chr16:23197820C>T	Silent	SCNN1G	p.F76F	sodium channel, non-vo	34 (0.00)	302 (0.21)	0.55
12-03	Gp3	g.chr16:23197897T>A	Missense Mutation	SCNN1G	p.I102N	sodium channel, non-vo	25 (0.00)	112 (0.44)	1.17
12-03	Gp3	g.chr22:50962107C>G	Missense Mutation	SCO2	p.R245T	SCO2 cytochrome c oxi	38 (0.00)	104 (0.22)	0.84

12-03	Gp3	g.chr11:9069533G>A	Silent	SCUBE2	p.I584I	signal peptide, CUB dor	67 (0.01)	89 (0.24)	0.47
12-03	Gp3	g.chr11:65303577C>G	Missense Mutation	SCYL1	p.L514V	SCY1-like 1 (S. cerevisi	23 (0.00)	91 (0.42)	1.55
12-03	Gp3	g.chr5:134059326C>T	Nonsense Mutation	SEC24A	p.Q1045*	SEC24 family member	25 (0.00)	26 (0.35)	0.92
12-03	Gp3	g.chr4:83763348A>G	Silent	SEC31A	p.P971P	SEC31 homolog A (S. c	16 (0.00)	16 (0.88)	2.33
12-03	Gp3	g.chr1:169676499C>A	Silent	SELL	p.G201G	selectin L	49 (0.00)	46 (0.65)	1.74
12-03	Gp3	g.chr22:31501643C>T	Splice Site	SELM			39 (0.00)	76 (0.46)	1.23
12-03	Gp3	g.chr2:74902904A>T	Missense Mutation	SEMA4F	p.E504V	sema domain, immunog	73 (0.00)	53 (0.21)	0.55
12-03	Gp3	g.chr2:74906743G>T	Nonsense Mutation	SEMA4F	p.E574*	sema domain, immunog	69 (0.00)	319 (0.15)	0.39
12-03	Gp3	g.chr16:4835815C>T	Missense Mutation	SEPT12	p.D123N	septin 12	43 (0.00)	369 (0.27)	0.90
12-03	Gp3	g.chr20:43132544G>A	Missense Mutation	SERINC3	p.P323S	serine incorporator 3	41 (0.00)	53 (0.49)	1.31
12-03	Gp3	g.chr14:94914981G>A	Missense Mutation	SERPINA11	p.A44V	serpin peptidase inhibitc	96 (0.01)	248 (0.60)	1.61
12-03	Gp3	g.chr22:21141334G>A	Missense Mutation	SERPIND1	p.A494T	serpin peptidase inhibitc	18 (0.00)	12 (0.92)	3.50
12-03	Gp3	g.chr16:30976227A>G	Silent	SETD1A	p.T388T	SET domain containing	54 (0.00)	392 (0.15)	0.52
12-03	Gp3	g.chr14:99879350C>A	Missense Mutation	SETD3	p.G263C	SET domain containing	19 (0.00)	100 (0.98)	2.61
12-03	Gp3	g.chr9:135139653G>A	Silent	SETX	p.S2669S	senataxin	95 (0.00)	244 (0.21)	0.57
12-03	Gp3	g.chr9:135204715T>C	Missense Mutation	SETX	p.K757R	senataxin	71 (0.00)	60 (0.20)	0.53
12-03	Gp3	g.chr1:149898653C>A	Silent	SF3B4	p.L107L	splicing factor 3b, subur	85 (0.00)	65 (0.62)	2.04
12-03	Gp3	g.chr10:81372071C>T	Missense Mutation	SFTPA1	p.P74L	surfactant protein A1	67 (0.00)	178 (0.19)	0.49
12-03	Gp3	g.chr10:81372122C>T	Missense Mutation	SFTPA1	p.P91L	surfactant protein A1	32 (0.00)	149 (0.17)	0.45
12-03	Gp3	g.chr3:72862295G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	23 (0.00)	33 (0.91)	2.42
12-03	Gp3	g.chr3:72864323A>G	Intron	SHQ1		SHQ1, H/ACA ribonucl	53 (0.00)	84 (0.24)	0.63
12-03	Gp3	g.chr3:72880779C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	125 (0.00)	87 (0.36)	0.95
12-03	Gp3	g.chr3:72886353G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	18 (0.00)	44 (0.93)	2.48
12-03	Gp3	g.chr3:113329868G>A	Missense Mutation	SIDT1	p.M578I	SID1 transmembrane fa	19 (0.00)	56 (0.91)	2.43
12-03	Gp3	g.chr9:34635815C>A	Silent	SIGMAR1	p.V162V	sigma non-opioid intrac	35 (0.00)	148 (0.18)	0.47
12-03	Gp3	g.chr10:21804823T>C	Silent	SKIDA1	p.E643E	SKI/DACH domain con	49 (0.00)	17 (0.47)	1.25
12-03	Gp3	g.chr1:160466130C>A	Missense Mutation	SLAMF6	p.G35W	SLAM family member	32 (0.00)	106 (0.78)	1.65
12-03	Gp3	g.chr4:48490471C>A	Missense Mutation	SLC10A4	p.L277M	solute carrier family 10,	36 (0.00)	26 (0.73)	1.95
12-03	Gp3	g.chr11:60714088G>A	Missense Mutation	SLC15A3	p.P255L	solute carrier family 15	59 (0.00)	125 (0.21)	0.42
12-03	Gp3	g.chr10:61413929C>T	Silent	SLC16A9	p.R285R	solute carrier family 16,	28 (0.00)	50 (0.20)	0.53
12-03	Gp3	g.chr8:42297033G>T	Missense Mutation	SLC20A2	p.A290E	solute carrier family 20	20 (0.00)	23 (0.30)	0.81
12-03	Gp3	g.chr7:107415284G>A	Missense Mutation	SLC26A3	p.R571C	solute carrier family 26	78 (0.00)	79 (0.54)	1.45
12-03	Gp3	g.chr19:59012760C>A	Missense Mutation	SLC27A5	p.A359S	solute carrier family 27	26 (0.00)	50 (0.36)	0.96
12-03	Gp3	g.chr1:9098033G>C	Missense Mutation	SLC2A5	p.P409A	solute carrier family 2 (	116 (0.00)	62 (0.23)	0.60
12-03	Gp3	g.chr12:46764389C>T	Missense Mutation	SLC38A2	p.G74R	solute carrier family 38,	29 (0.00)	77 (0.17)	0.45

12-03	Gp3	g.chr1:153933100C>A	Missense Mutation	SLC39A1	p.G150V	solute carrier family 39	40 (0.00)	166 (0.48)	1.00
12-03	Gp3	g.chr17:70943930C>T	Missense Mutation	SLC39A11	p.A131T	solute carrier family 39,	31 (0.00)	18 (0.50)	1.33
12-03	Gp3	g.chr19:10745708G>A	Silent	SLC44A2	p.K338K	solute carrier family 44	83 (0.00)	15 (0.93)	3.27
12-03	Gp3	g.chr19:10746155C>A	Missense Mutation	SLC44A2	p.S399R	solute carrier family 44	22 (0.00)	50 (0.14)	0.49
12-03	Gp3	g.chr2:162735756C>T	Missense Mutation	SLC4A10	p.A355V	solute carrier family 4, s	32 (0.00)	34 (0.18)	0.47
12-03	Gp3	g.chr2:162815024G>T	Missense Mutation	SLC4A10	p.V941L	solute carrier family 4, s	56 (0.00)	27 (0.33)	0.89
12-03	Gp3	g.chr11:26734241G>T	Silent	SLC5A12	p.R118R	solute carrier family 5 (	93 (0.00)	40 (0.40)	1.07
12-03	Gp3	g.chr1:44474270C>G	Silent	SLC6A9	p.V50V	solute carrier family 6 (	19 (0.00)	18 (0.44)	1.19
12-03	Gp3	g.chr1:27428982G>A	Nonsense Mutation	SLC9A1	p.Q572*	solute carrier family 9, s	18 (0.00)	414 (0.27)	0.71
12-03	Gp3	g.chr18:48567417C>A	Intron	SMAD4		SMAD family member	57 (0.00)	83 (0.88)	2.35
12-03	Gp3	g.chr19:11100023G>A	Silent	SMARCA4	p.Q383Q	SWI/SNF related, matri	19 (0.00)	186 (0.28)	0.98
12-03	Gp3	g.chr22:24145499C>T	Missense Mutation	SMARCB1	p.P127L	SWI/SNF related, matri	76 (0.00)	156 (0.62)	1.66
12-03	Gp3	g.chr12:50481239C>T	Missense Mutation	SMARCD1	p.L209F	SWI/SNF related, matri	57 (0.00)	81 (0.31)	0.82
12-03	Gp3	g.chr17:61911866T>C	Missense Mutation	SMARCD2	p.K297E	SWI/SNF related, matri	34 (0.00)	115 (0.50)	1.32
12-03	Gp3	g.chr22:45748455C>T	Missense Mutation	SMC1B	p.E1101K	structural maintenance c	19 (0.00)	75 (0.92)	2.45
12-03	Gp3	g.chr17:18219115C>A	Silent	SMCR8	p.A4A	Smith-Magenis syndron	67 (0.01)	162 (0.40)	1.07
12-03	Gp3	g.chr17:57288171C>T	Silent	SMG8	p.D253D	SMG8 nonsense mediat	17 (0.00)	34 (0.15)	0.39
12-03	Gp3	g.chr16:12662374C>T	Missense Mutation	SNX29	p.P777L	sorting nexin 29	68 (0.00)	222 (0.26)	0.54
12-03	Gp3	g.chr16:29342511C>T	lincRNA	SNX29P2		sorting nexin 29 pseudo	32 (0.00)	45 (0.47)	1.24
12-03	Gp3	g.chr8:22421558G>A	Missense Mutation	SORBS3	p.A215T	sorbin and SH3 domain	43 (0.00)	40 (0.35)	0.93
12-03	Gp3	g.chr11:16208371T>A	Missense Mutation	SOX6	p.K222N	SRY (sex determining r	91 (0.00)	68 (0.21)	0.55
12-03	Gp3	g.chr17:26912597G>T	Silent	SPAG5	p.S605S	sperm associated antige	27 (0.00)	11 (0.82)	2.18
12-03	Gp3	g.chr5:169021187A>G	Silent	SPDL1	p.R190R	spindle apparatus coiled	39 (0.00)	23 (0.26)	0.70
12-03	Gp3	g.chr20:3761827T>C	Splice Site	SPEF1	p.G36G	sperm flagellar 1	39 (0.00)	156 (0.17)	0.46
12-03	Gp3	g.chr1:16257957C>T	Missense Mutation	SPEN	p.S1741L	spen family transcriptio	233 (0.00)	414 (0.66)	1.75
12-03	Gp3	g.chr18:12506635T>A	Silent	SPIRE1	p.R271R	spire-type actin nucleati	38 (0.00)	56 (0.98)	2.62
12-03	Gp3	g.chr1:32280421T>C	Missense Mutation	SPOCD1	p.M172V	SPOC domain containin	22 (0.00)	138 (0.16)	0.43
12-03	Gp3	g.chr17:47679363G>A	Silent	SPOP	p.L282L	speckle-type POZ protei	100 (0.00)	40 (0.20)	0.53
12-03	Gp3	g.chr19:2351471C>T	RNA	SPPL2B		signal peptide peptidase	39 (0.00)	469 (0.19)	0.70
12-03	Gp3	g.chr19:41008192C>T	Missense Mutation	SPTBN4	p.T352M	spectrin, beta, non-eryth	25 (0.00)	192 (0.22)	0.83
12-03	Gp3	g.chr17:2218918T>A	Missense Mutation	SRR	p.S22T	serine racemase	32 (0.00)	14 (0.50)	1.33
12-03	Gp3	g.chr17:2221228C>T	Missense Mutation	SRR	p.A78V	serine racemase	56 (0.00)	76 (0.26)	0.70
12-03	Gp3	g.chr20:60749702C>A	Splice Site	SS18L1		synovial sarcoma transl	65 (0.00)	422 (0.29)	0.78
12-03	Gp3	g.chr7:149481207A>G	RNA	SSPO		SCO-spondin	19 (0.00)	165 (0.16)	0.42
12-03	Gp3	g.chr7:149485105G>A	RNA	SSPO		SCO-spondin	16 (0.00)	71 (0.24)	0.64

12-03	Gp3	g.chr11:8736234G>A	Missense Mutation	ST5	p.S135F	suppression of tumorige	44 (0.00)	17 (0.47)	0.93
12-03	Gp3	g.chr18:55020109G>A	Missense Mutation	ST8SIA3	p.S11N	ST8 alpha-N-acetyl-neu	19 (0.00)	58 (0.26)	0.69
12-03	Gp3	g.chr15:42981838G>A	Missense Mutation	STARD9	p.A2688T	StAR-related lipid trans	21 (0.00)	14 (0.79)	2.10
12-03	Gp3	g.chr2:191926534C>A	Nonsense Mutation	STAT4	p.E319*	signal transducer and ac	37 (0.00)	128 (0.15)	0.40
12-03	Gp3	g.chr4:27019575G>C	Missense Mutation	STIM2	p.E578Q	stromal interaction mol	72 (0.00)	46 (0.63)	1.68
12-03	Gp3	g.chr11:63967417G>A	Silent	STIP1	p.E390E	stress-induced phospho	52 (0.00)	124 (0.15)	0.39
12-03	Gp3	g.chr5:146752735C>A	Missense Mutation	STK32A	p.L261I	serine/threonine kinase	16 (0.00)	11 (0.82)	2.18
12-03	Gp3	g.chr4:184930504C>T	Silent	STOX2	p.T171T	storkhead box 2	22 (0.00)	41 (0.83)	2.21
12-03	Gp3	g.chr2:37082396G>A	Missense Mutation	STRN	p.T646I	striatin, calmodulin bin	21 (0.00)	19 (0.42)	1.12
12-03	Gp3	g.chr10:104386940G>A	Silent	SUFU	p.L435L	suppressor of fused hom	92 (0.00)	40 (0.20)	0.53
12-03	Gp3	g.chr20:46311807G>T	Missense Mutation	SULF2	p.S332Y	sulfatase 2	33 (0.00)	130 (0.16)	0.43
12-03	Gp3	g.chr16:28617477C>A	Missense Mutation	SULT1A1	p.Q225H	sulfotransferase family,	24 (0.00)	224 (0.29)	0.76
12-03	Gp3	g.chr14:21836520C>A	Missense Mutation	SUPT16H	p.R288L	suppressor of Ty 16 hon	33 (0.00)	20 (0.85)	1.78
12-03	Gp3	g.chr13:37591392G>C	Missense Mutation	SUPT20H	p.P661R	suppressor of Ty 20 hon	61 (0.02)	131 (0.56)	1.49
12-03	Gp3	g.chr17:56424548C>T	Splice Site	SUPT4H1		suppressor of Ty 4 hom	55 (0.00)	69 (0.42)	1.12
12-03	Gp3	g.chr17:56424592C>T	Silent	SUPT4H1	p.K40K	suppressor of Ty 4 hom	54 (0.00)	69 (0.19)	0.50
12-03	Gp3	g.chr9:95846929C>A	Missense Mutation	SUSD3	p.A223D	sushi domain containing	24 (0.00)	489 (0.22)	0.58
12-03	Gp3	g.chr9:95846930C>A	Silent	SUSD3	p.A223A	sushi domain containing	24 (0.00)	486 (0.22)	0.58
12-03	Gp3	g.chr1:223402550C>T	Missense Mutation	SUSD4	p.C302Y	sushi domain containing	56 (0.00)	40 (0.50)	1.33
12-03	Gp3	g.chr9:113252008C>A	Nonsense Mutation	SVEP1	p.G595*	sushi, von Willebrand f	29 (0.00)	23 (0.48)	1.28
12-03	Gp3	g.chr3:12209987G>A	RNA	SYN2		synapsin II	45 (0.00)	86 (0.30)	0.81
12-03	Gp3	g.chr22:32914038C>T	Silent	SYN3	p.P534P	synapsin III	29 (0.00)	168 (0.22)	0.59
12-03	Gp3	g.chr14:64678678G>A	Splice Site	SYNE2		spectrin repeat containi	154 (0.00)	184 (0.21)	0.57
12-03	Gp3	g.chr6:158517268G>A	Missense Mutation	SYNJ2	p.G1455S	synaptojanin 2	27 (0.00)	71 (0.15)	0.41
12-03	Gp3	g.chr6:158517325C>A	Missense Mutation	SYNJ2	p.H1474N	synaptojanin 2	36 (0.00)	69 (0.39)	1.04
12-03	Gp3	g.chr11:61291372G>T	Silent	SYT7	p.P322P	synaptotagmin VII	51 (0.02)	138 (0.65)	1.32
12-03	Gp3	g.chr11:64898767G>A	Missense Mutation	SYVN1	p.R246W	synovial apoptosis inhib	41 (0.00)	165 (0.15)	0.56
12-03	Gp3	g.chr1:43891306C>T	Missense Mutation	SZT2	p.P936L	seizure threshold 2 hom	23 (0.00)	63 (0.27)	0.72
12-03	Gp3	g.chr17:35797843C>T	Missense Mutation	TADA2A	p.S66L	transcriptional adaptor 2	38 (0.00)	50 (0.22)	0.59
12-03	Gp3	g.chr2:160086806G>C	Missense Mutation	TANC1	p.K1623N	tetratricopeptide repeat,	56 (0.00)	71 (0.18)	0.49
12-03	Gp3	g.chr16:29990384A>G	Missense Mutation	TAOK2	p.I148V	TAO kinase 2	92 (0.00)	21 (0.57)	1.52
12-03	Gp3	g.chr1:6631099G>T	Missense Mutation	TAS1R1	p.D108Y	taste receptor, type 1, m	43 (0.00)	100 (0.62)	1.65
12-03	Gp3	g.chr1:6639250G>A	Missense Mutation	TAS1R1	p.R711H	taste receptor, type 1, m	28 (0.00)	115 (0.21)	0.56
12-03	Gp3	g.chr7:141673253G>A	Silent	TAS2R38	p.T79T	taste receptor, type 2, m	53 (0.02)	19 (0.84)	2.25
12-03	Gp3	g.chr7:142919670G>A	Missense Mutation	TAS2R40	p.V167M	taste receptor, type 2, m	53 (0.00)	19 (0.63)	1.11

12-03	Gp3	g.chr3:10312656A>G	Missense Mutation	TATDN2	p.D597G	TatD DNase domain co	59 (0.00)	30 (0.27)	0.71
12-03	Gp3	g.chr4:7026740C>T	Silent	TBC1D14	p.T361T	TBC1 domain family,	47 (0.00)	178 (0.22)	0.58
12-03	Gp3	g.chr17:58088018G>A	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	79 (0.00)	221 (0.26)	0.70
12-03	Gp3	g.chr17:60344564C>T	RNA	TBC1D3P2		TBC1 domain family,	68 (0.00)	362 (0.19)	0.50
12-03	Gp3	g.chr1:23724430T>C	Silent	TCEA3	p.S154S	transcription elongation	31 (0.00)	21 (0.52)	1.40
12-03	Gp3	g.chr22:42606957T>C	Missense Mutation	TCF20	p.E1452G	transcription factor 20 (	28 (0.00)	22 (0.23)	0.61
12-03	Gp3	g.chr16:89952281G>A	Missense Mutation	TCF25	p.R152H	transcription factor 25 (	129 (0.00)	388 (0.20)	0.53
12-03	Gp3	g.chr1:152080041G>A	Silent	TCHH	p.H1884H	trichohyalin	35 (0.00)	219 (0.17)	0.45
12-03	Gp3	g.chr1:152082008G>T	Missense Mutation	TCHH	p.P1229T	trichohyalin	55 (0.00)	96 (0.28)	0.75
12-03	Gp3	g.chr6:44250173C>A	Missense Mutation	TCTE1	p.A324S	t-complex-associated-te	24 (0.00)	51 (0.20)	0.52
12-03	Gp3	g.chr10:97453182C>G	Missense Mutation	TCTN3	p.C103S	tectonic family member	39 (0.00)	78 (0.45)	1.20
12-03	Gp3	g.chr6:46657117G>A	Missense Mutation	TDRD6	p.V418M	tudor domain containin	31 (0.00)	41 (0.68)	1.82
12-03	Gp3	g.chr14:104472799G>C	Missense Mutation	TDRD9	p.R596T	tudor domain containin	31 (0.00)	35 (0.69)	1.83
12-03	Gp3	g.chr8:442579G>A	Silent	TDRP	p.T126T	testis development relat	59 (0.00)	194 (0.21)	0.56
12-03	Gp3	g.chr19:14674861T>C	Missense Mutation	TECR	p.I112T	trans-2,3-enoyl-CoA re	23 (0.00)	125 (0.15)	0.41
12-03	Gp3	g.chr11:78369627C>A	Missense Mutation	TENM4	p.A2596S	teneurin transmembrane	67 (0.00)	349 (0.17)	0.46
12-03	Gp3	g.chr11:78380165G>C	Missense Mutation	TENM4	p.P2409A	teneurin transmembrane	61 (0.00)	142 (0.18)	0.49
12-03	Gp3	g.chr2:122007190C>T	Missense Mutation	TFCP2L1	p.R83Q	transcription factor CP2	40 (0.00)	47 (0.66)	1.76
12-03	Gp3	g.chr15:43585699G>T	Missense Mutation	TGM7	p.F47L	transglutaminase 7	23 (0.00)	85 (0.19)	0.50
12-03	Gp3	g.chr2:242572929C>A	Missense Mutation	THAP4	p.G215C	THAP domain containi	37 (0.00)	382 (0.15)	0.40
12-03	Gp3	g.chr5:79354583G>A	Silent	THBS4	p.L143L	thrombospondin 4	22 (0.00)	82 (0.44)	0.55
12-03	Gp3	g.chr2:88478407C>T	Missense Mutation	THNSL2	p.S194F	threonine synthase-like	82 (0.00)	13 (0.77)	1.62
12-03	Gp3	g.chr7:11675809G>T	Missense Mutation	THSD7A	p.Q324K	thrombospondin, type I,	241 (0.00)	609 (0.14)	0.38
12-03	Gp3	g.chr14:24026365G>A	Silent	THTPA	p.L133L	thiamine triphosphatase	31 (0.00)	40 (0.42)	0.89
12-03	Gp3	g.chr1:32042961G>C	Missense Mutation	TINAGL1	p.C71S	tubulointerstitial nephrit	35 (0.00)	189 (0.40)	1.06
12-03	Gp3	g.chr3:53263145C>T	Missense Mutation	TKT	p.G425R	transketolase	18 (0.00)	40 (0.17)	0.47
12-03	Gp3	g.chr15:63000704G>C	Missense Mutation	TLN2	p.V726L	talin 2	43 (0.00)	333 (0.14)	0.38
12-03	Gp3	g.chr1:62175008G>A	Nonsense Mutation	TM2D1	p.R114*	TM2 domain containing	72 (0.01)	82 (0.99)	2.63
12-03	Gp3	g.chr14:24664017T>C	Missense Mutation	TM9SF1	p.E279G	transmembrane 9 superf	95 (0.00)	370 (0.63)	1.31
12-03	Gp3	g.chr13:100196145A>G	Missense Mutation	TM9SF2	p.K349R	transmembrane 9 superf	23 (0.00)	20 (0.65)	1.73
12-03	Gp3	g.chr12:125834725G>A	Silent	TMEM132B	p.G260G	transmembrane protein	71 (0.00)	155 (0.30)	0.79
12-03	Gp3	g.chr19:42819230G>A	Splice Site	TMEM145		transmembrane protein	25 (0.00)	69 (0.29)	0.77
12-03	Gp3	g.chr1:202989993C>A	Missense Mutation	TMEM183A	p.P288T	transmembrane protein	43 (0.00)	30 (0.63)	1.37
12-03	Gp3	g.chr12:10342524C>T	Missense Mutation	TMEM52B	p.R93W	transmembrane protein	15 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr6:44106248G>T	Missense Mutation	TMEM63B	p.R134M	transmembrane protein	44 (0.00)	124 (0.40)	1.08

12-03	Gp3	g.chr10:45430114C>G	Silent	TMEM72	p.L2L	transmembrane protein	30 (0.00)	55 (0.38)	1.02
12-03	Gp3	g.chr17:48356617G>T	Missense Mutation	TMEM92	p.R143M	transmembrane protein	25 (0.00)	135 (0.73)	1.94
12-03	Gp3	g.chr3:33135035C>T	Missense Mutation	TMPPE	p.G81D	transmembrane protein	30 (0.00)	146 (0.23)	0.62
12-03	Gp3	g.chr21:42843367G>A	Intron	TMPRSS2		transmembrane protease	101 (0.00)	25 (0.32)	0.39
12-03	Gp3	g.chr21:42852003C>T	Intron	TMPRSS2		transmembrane protease	48 (0.00)	17 (0.65)	0.79
12-03	Gp3	g.chr22:37480371G>T	Missense Mutation	TMPRSS6	p.P387Q	transmembrane protease	33 (0.00)	35 (0.20)	0.53
12-03	Gp3	g.chr17:7286287C>T	Silent	TNK1	p.L14L	tyrosine kinase, non-rec	41 (0.00)	141 (0.33)	0.72
12-03	Gp3	g.chr19:12817476G>A	Silent	TNPO2	p.S468S	transportin 2	27 (0.00)	208 (0.35)	1.23
12-03	Gp3	g.chr2:218758250G>C	Missense Mutation	TNS1	p.P85R	tensin 1	89 (0.00)	214 (0.20)	0.54
12-03	Gp3	g.chr3:25659950C>T	Missense Mutation	TOP2B	p.E1099K	topoisomerase (DNA) II	37 (0.00)	19 (0.89)	2.39
12-03	Gp3	g.chr3:133368465C>A	Silent	TOPBP1	p.V422V	topoisomerase (DNA) II	73 (0.00)	26 (0.62)	1.64
12-03	Gp3	g.chr17:7582909G>A	Intron	TP53		tumor protein p53	38 (0.00)	115 (0.23)	0.51
12-03	Gp3	g.chr17:7585446C>T	Intron	TP53		tumor protein p53	27 (0.00)	79 (0.19)	0.41
12-03	Gp3	g.chr7:144320302C>T	Missense Mutation	TPK1	p.C104Y	thiamin pyrophosphokir	28 (0.00)	25 (0.20)	0.53
12-03	Gp3	g.chr22:26932403G>T	Missense Mutation	TPST2	p.L298I	tyrosylprotein sulfotrans	15 (0.00)	84 (0.20)	0.54
12-03	Gp3	g.chr13:45964978C>G	RNA	TPT1-AS1		TPT1 antisense RNA 1	96 (0.00)	373 (0.16)	0.44
12-03	Gp3	g.chr12:112589728C>A	Nonsense Mutation	TRAFD1	p.S468*	TRAF-type zinc finger	94 (0.00)	41 (0.85)	2.28
12-03	Gp3	g.chr21:45513967G>A	Silent	TRAPPC10	p.V1007V	trafficking protein partic	34 (0.00)	31 (0.19)	0.73
12-03	Gp3	g.chr4:184587563A>G	Missense Mutation	TRAPPC11	p.R120G	trafficking protein partic	72 (0.00)	25 (0.72)	1.92
12-03	Gp3	g.chr11:118889562G>T	Missense Mutation	TRAPPC4	p.L19F	trafficking protein partic	37 (0.00)	656 (0.20)	0.54
12-03	Gp3	g.chr8:141407832C>T	Missense Mutation	TRAPPC9	p.G439R	trafficking protein partic	24 (0.00)	17 (0.65)	1.73
12-03	Gp3	g.chr7:142428798G>T	RNA	TRBV28		T cell receptor beta vari	37 (0.00)	22 (0.41)	0.72
12-03	Gp3	g.chr7:142180644C>G	RNA	TRBV6-5		T cell receptor beta vari	71 (0.00)	54 (0.35)	0.62
12-03	Gp3	g.chr6:42227381C>A	Silent	TRERF1	p.R655R	transcriptional regulatin	36 (0.00)	179 (0.17)	0.46
12-03	Gp3	g.chr6:42237063G>C	Missense Mutation	TRERF1	p.A89G	transcriptional regulatin	50 (0.00)	92 (0.25)	0.67
12-03	Gp3	g.chr20:368679C>T	Missense Mutation	TRIB3	p.P9S	tribbles pseudokinase 3	17 (0.00)	57 (0.28)	0.75
12-03	Gp3	g.chr4:154216772C>A	Missense Mutation	TRIM2	p.T338N	tripartite motif containir	35 (0.00)	149 (0.15)	0.41
12-03	Gp3	g.chr11:6477385C>T	Missense Mutation	TRIM3	p.G484S	tripartite motif containir	41 (0.00)	174 (0.33)	0.87
12-03	Gp3	g.chr17:57128689C>T	Splice Site	TRIM37	p.R400R	tripartite motif containir	63 (0.00)	82 (0.38)	1.01
12-03	Gp3	g.chr1:155149451G>A	Missense Mutation	TRIM46	p.C238Y	tripartite motif containir	39 (0.00)	18 (0.33)	0.70
12-03	Gp3	g.chr11:55655689A>T	Missense Mutation	TRIM51	p.Y230F	tripartite motif-containir	74 (0.00)	18 (0.33)	0.68
12-03	Gp3	g.chr5:14420040C>A	Missense Mutation	TRIO	p.P1705T	trio Rho guanine nucleo	16 (0.00)	194 (0.19)	0.51
12-03	Gp3	g.chr5:14508190C>T	Missense Mutation	TRIO	p.L2985F	trio Rho guanine nucleo	39 (0.03)	35 (0.69)	1.83
12-03	Gp3	g.chr1:185114625C>A	Nonsense Mutation	TRMT1L	p.G201*	tRNA methyltransferase	18 (0.00)	10 (0.50)	1.33
12-03	Gp3	g.chr20:33637752T>A	Missense Mutation	TRPC4AP	p.I192F	transient receptor potent	61 (0.00)	29 (0.21)	0.55

12-03	Gp3	g.chr20:33637774C>G	Missense Mutation	TRPC4AP	p.L184F	transient receptor potent	67 (0.00)	30 (0.27)	0.71
12-03	Gp3	g.chr7:98497386G>A	Missense Mutation	TRRAP	p.A266T	transformation/transcrip	33 (0.00)	27 (0.52)	1.38
12-03	Gp3	g.chr7:98553914T>A	Missense Mutation	TRRAP	p.I2002N	transformation/transcrip	16 (0.00)	15 (0.47)	1.24
12-03	Gp3	g.chr7:98553915C>A	Silent	TRRAP	p.I2002I	transformation/transcrip	15 (0.00)	15 (0.47)	1.24
12-03	Gp3	g.chr16:2115615G>A	Silent	TSC2	p.L565L	tuberous sclerosis 2	37 (0.03)	331 (0.23)	0.76
12-03	Gp3	g.chr20:51871034C>T	Missense Mutation	TSHZ2	p.S346F	teashirt zinc finger hom	36 (0.00)	48 (0.23)	0.61
12-03	Gp3	g.chr20:51871440C>T	Silent	TSHZ2	p.S481S	teashirt zinc finger hom	143 (0.00)	35 (0.34)	0.91
12-03	Gp3	g.chr20:51871863G>A	Silent	TSHZ2	p.E622E	teashirt zinc finger hom	51 (0.00)	185 (0.17)	0.45
12-03	Gp3	g.chr16:67854759G>T	Start Codon SNP	TSNAXIP1	p.M1I	translin-associated facto	101 (0.01)	478 (0.25)	0.66
12-03	Gp3	g.chr1:115593112C>A	Nonstop Mutation	TSPAN2	p.*222L	tetraspanin 2	62 (0.00)	25 (0.36)	0.96
12-03	Gp3	g.chr5:112770251C>G	Missense Mutation	TSSK1B	p.G96R	testis-specific serine kin	19 (0.00)	32 (0.16)	0.42
12-03	Gp3	g.chr9:130488548C>A	Silent	TTC16	p.S430S	tetratricopeptide repeat	15 (0.00)	72 (0.56)	1.48
12-03	Gp3	g.chr7:138832959C>T	Missense Mutation	TTC26	p.L154F	tetratricopeptide repeat	68 (0.00)	61 (0.98)	2.62
12-03	Gp3	g.chr2:32875282G>T	Nonsense Mutation	TTC27	p.E208*	tetratricopeptide repeat	51 (0.00)	125 (0.16)	0.43
12-03	Gp3	g.chr22:28378553G>A	Missense Mutation	TTC28	p.P2368S	tetratricopeptide repeat	29 (0.00)	60 (0.20)	0.53
12-03	Gp3	g.chr2:179408047G>T	Missense Mutation	TTN	p.T32218N	titin	28 (0.00)	11 (0.73)	1.94
12-03	Gp3	g.chr2:179428161A>G	Silent	TTN	p.D27566D	titin	54 (0.02)	27 (0.74)	1.98
12-03	Gp3	g.chr2:179431610C>A	Nonsense Mutation	TTN	p.E26417*	titin	43 (0.00)	28 (0.86)	2.29
12-03	Gp3	g.chr2:179449409C>A	Silent	TTN	p.A21653A	titin	54 (0.00)	34 (0.21)	0.55
12-03	Gp3	g.chr2:179500726T>A	Missense Mutation	TTN	p.N13858Y	titin	177 (0.00)	144 (0.19)	0.52
12-03	Gp3	g.chr2:179582046C>T	Missense Mutation	TTN	p.S8472N	titin	59 (0.00)	51 (0.55)	1.46
12-03	Gp3	g.chr20:57599649C>A	Missense Mutation	TUBB1	p.F389L	tubulin, beta 1 class VI	38 (0.00)	117 (0.18)	0.48
12-03	Gp3	g.chr13:113170869C>T	Missense Mutation	TUBGCP3	p.M657I	tubulin, gamma comple	64 (0.00)	74 (0.62)	1.66
12-03	Gp3	g.chr22:50659099G>A	Missense Mutation	TUBGCP6	p.S1230L	tubulin, gamma comple	19 (0.00)	386 (0.20)	0.75
12-03	Gp3	g.chr22:50682685G>A	Silent	TUBGCP6	p.N68N	tubulin, gamma comple	22 (0.00)	118 (0.10)	0.39
12-03	Gp3	g.chr16:28856784C>T	Missense Mutation	TUFM	p.G89R	Tu translation elongatio	22 (0.00)	96 (0.15)	0.39
12-03	Gp3	g.chr1:32658891A>G	Missense Mutation	TXLNA	p.E414G	taxilin alpha	33 (0.00)	34 (0.15)	0.39
12-03	Gp3	g.chr15:70960206C>T	Missense Mutation	UACA	p.M939I	uveal autoantigen with	35 (0.00)	13 (0.54)	1.44
12-03	Gp3	g.chr9:33943554C>A	Missense Mutation	UBAP2	p.A527S	ubiquitin associated pro	33 (0.00)	53 (0.43)	1.16
12-03	Gp3	g.chr17:16285515C>T	Silent	UBB	p.T98T	ubiquitin B	63 (0.00)	13 (0.54)	1.44
12-03	Gp3	g.chr17:74392554C>G	Missense Mutation	UBE2O	p.E822Q	ubiquitin-conjugating e	18 (0.00)	220 (0.16)	0.42
12-03	Gp3	g.chr17:47000256T>A	Missense Mutation	UBE2Z	p.V284E	ubiquitin-conjugating e	71 (0.00)	43 (0.33)	0.87
12-03	Gp3	g.chr12:109971326C>T	Missense Mutation	UBE3B	p.P993L	ubiquitin protein ligase	51 (0.00)	206 (0.44)	1.18
12-03	Gp3	g.chr8:103301764G>A	Nonsense Mutation	UBR5	p.Q1538*	ubiquitin protein ligase	42 (0.00)	29 (0.24)	0.64
12-03	Gp3	g.chr2:128870680G>C	Missense Mutation	UGGT1	p.G182R	UDP-glucose glycoprot	67 (0.00)	46 (0.17)	0.46

12-03	Gp3	g.chr21:43541214A>G	Missense Mutation	UMODL1	p.R903G	uromodulin-like 1	80 (0.00)	67 (0.16)	0.62
12-03	Gp3	g.chr11:67766642C>T	Splice Site	UNC93B1		unc-93 homolog B1 (C.	37 (0.00)	140 (0.16)	0.58
12-03	Gp3	g.chr1:229771540G>T	Missense Mutation	URB2	p.A394S	URB2 ribosome biogen	37 (0.00)	98 (0.50)	1.33
12-03	Gp3	g.chr1:229772893G>T	Missense Mutation	URB2	p.D845Y	URB2 ribosome biogen	24 (0.00)	22 (0.82)	2.18
12-03	Gp3	g.chr19:30477200C>T	Silent	URI1	p.G63G	URI1, prefoldin-like ch	42 (0.00)	143 (0.32)	0.86
12-03	Gp3	g.chr2:61415485C>A	Nonsense Mutation	USP34	p.E3465*	ubiquitin specific peptid	19 (0.00)	35 (0.46)	1.22
12-03	Gp3	g.chr11:77910653G>C	Missense Mutation	USP35	p.W273C	ubiquitin specific peptid	20 (0.00)	103 (0.72)	1.92
12-03	Gp3	g.chr13:31233133G>A	Silent	USPL1	p.A973A	ubiquitin specific peptid	27 (0.00)	15 (0.47)	1.24
12-03	Gp3	g.chr12:101768611T>A	Missense Mutation	UTP20	p.L2386Q	UTP20, small subunit (	35 (0.00)	56 (0.55)	1.48
12-03	Gp3	g.chr4:71555748C>T	Missense Mutation	UTP3	p.R452C	UTP3, small subunit (S	88 (0.00)	80 (0.23)	0.60
12-03	Gp3	g.chr9:2646430C>T	Silent	VLDLR	p.I527I	very low density lipopr	36 (0.00)	69 (0.52)	1.39
12-03	Gp3	g.chr9:2652856C>G	Missense Mutation	VLDLR	p.N831K	very low density lipopr	55 (0.00)	63 (0.16)	0.42
12-03	Gp3	g.chr1:12398321C>A	Missense Mutation	VPS13D	p.T2862K	vacuolar protein sorting	31 (0.00)	99 (0.91)	2.42
12-03	Gp3	g.chr15:42476770T>C	Silent	VPS39	p.E221E	vacuolar protein sorting	17 (0.00)	48 (0.19)	0.50
12-03	Gp3	g.chr1:151149186C>A	Silent	VPS72	p.P354P	vacuolar protein sorting	60 (0.02)	102 (0.24)	0.63
12-03	Gp3	g.chr12:118520003T>C	Missense Mutation	VSIG10	p.N198S	V-set and immunoglobu	17 (0.00)	51 (0.16)	0.42
12-03	Gp3	g.chr12:118520231C>A	Missense Mutation	VSIG10	p.G122V	V-set and immunoglobu	36 (0.00)	64 (0.36)	0.96
12-03	Gp3	g.chr14:68126485A>G	Missense Mutation	VTI1B	p.M110T	vesicle transport throug	25 (0.00)	17 (0.53)	1.41
12-03	Gp3	g.chr2:98736149G>A	Silent	VWA3B	p.E155E	von Willebrand factor A	76 (0.01)	38 (0.71)	1.89
12-03	Gp3	g.chr2:98750330G>T	Missense Mutation	VWA3B	p.A306S	von Willebrand factor A	77 (0.00)	165 (0.79)	2.12
12-03	Gp3	g.chr7:12379974C>T	Missense Mutation	VWDE	p.G1447E	von Willebrand factor D	37 (0.00)	51 (0.41)	1.10
12-03	Gp3	g.chr2:74686783G>A	Missense Mutation	WBP1	p.C62Y	WW domain binding pr	43 (0.02)	168 (0.17)	0.46
12-03	Gp3	g.chr1:224581562G>A	Missense Mutation	WDR26	p.P643L	WD repeat domain 26	58 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr6:170064338C>T	Silent	WDR27	p.V276V	WD repeat domain 27	18 (0.00)	134 (0.27)	0.72
12-03	Gp3	g.chr1:43652390C>A	Missense Mutation	WDR65	p.P328T		19 (0.00)	15 (0.93)	2.49
12-03	Gp3	g.chr12:122396317G>C	Missense Mutation	WDR66	p.G624R	WD repeat domain 66	47 (0.00)	107 (0.24)	0.65
12-03	Gp3	g.chr12:122404946C>A	Missense Mutation	WDR66	p.R860S	WD repeat domain 66	25 (0.00)	226 (0.17)	0.45
12-03	Gp3	g.chr7:141408640A>G	Missense Mutation	WEE2	p.K28E	WEE1 homolog 2 (S. p	181 (0.00)	29 (0.31)	0.83
12-03	Gp3	g.chr7:141422936G>T	Missense Mutation	WEE2	p.G295W	WEE1 homolog 2 (S. p	24 (0.00)	97 (0.53)	1.40
12-03	Gp3	g.chr15:23205207C>G	RNA	WHAMMP3		WAS protein homolog	46 (0.02)	69 (0.49)	1.31
12-03	Gp3	g.chr1:13052819C>T	Silent	WI2-3308P17.	p.R60R		225 (0.00)	124 (0.31)	0.84
12-03	Gp3	g.chr12:994912G>T	Nonsense Mutation	WNK1	p.G1648*	WNK lysine deficient p	16 (0.00)	23 (0.30)	0.81
12-03	Gp3	g.chr9:96000573G>A	Missense Mutation	WNK2	p.G431E	WNK lysine deficient p	24 (0.00)	57 (0.37)	0.98
12-03	Gp3	g.chr17:5991423C>A	Splice Site	WSCD1	p.R181R	WSC domain containin	38 (0.00)	115 (0.57)	1.22
12-03	Gp3	g.chr5:167824751C>A	Missense Mutation	WWC1	p.S152R	WW and C2 domain co	26 (0.00)	90 (0.46)	1.21

12-03	Gp3	g.chr16:69973284C>T	Silent	WWP2	p.G827G	WW domain containing	41 (0.00)	228 (0.20)	0.53
12-03	Gp3	g.chr8:11052698C>T	Missense Mutation	XKR6	p.R266K	XK, Kell blood group c	17 (0.00)	30 (0.27)	0.71
12-03	Gp3	g.chr3:14189955C>T	Intron	XPC		xeroderma pigmentosun	26 (0.00)	160 (0.33)	0.57
12-03	Gp3	g.chr3:14194702C>T	Intron	XPC		xeroderma pigmentosun	70 (0.00)	74 (0.96)	1.66
12-03	Gp3	g.chr3:14218929G>A	Intron	XPC		xeroderma pigmentosun	74 (0.00)	39 (0.23)	0.40
12-03	Gp3	g.chr1:180775682G>T	Nonsense Mutation	XPR1	p.G224*	xenotropic and polytrop	40 (0.00)	21 (0.38)	1.02
12-03	Gp3	g.chr11:74563037G>C	Missense Mutation	XRRA1	p.R413G	X-ray radiation resistan	68 (0.00)	12 (0.42)	1.11
12-03	Gp3	g.chr5:112920157C>T	Missense Mutation	YTHDC2	p.S1269F	YTH domain containing	53 (0.00)	36 (0.67)	1.78
12-03	Gp3	g.chrX:21875213C>T	Missense Mutation	YY2	p.A204V	YY2 transcription facto	59 (0.02)	110 (0.39)	0.65
12-03	Gp3	g.chr9:129642742G>T	Missense Mutation	ZBTB34	p.G355V	zinc finger and BTB do	63 (0.00)	248 (0.25)	0.68
12-03	Gp3	g.chr9:37442280A>T	Missense Mutation	ZBTB5	p.M90K	zinc finger and BTB do	67 (0.00)	123 (0.17)	0.46
12-03	Gp3	g.chr16:11852303G>T	Nonsense Mutation	ZC3H7A	p.Y804*	zinc finger CCCH-type	62 (0.00)	89 (0.51)	1.35
12-03	Gp3	g.chr16:11864763G>A	Silent	ZC3H7A	p.T328T	zinc finger CCCH-type	58 (0.02)	23 (0.30)	0.81
12-03	Gp3	g.chr18:60242266C>A	Missense Mutation	ZCCHC2	p.D984E	zinc finger, CCHC dom	48 (0.00)	204 (0.24)	0.64
12-03	Gp3	g.chr10:99211642G>A	Nonsense Mutation	ZDHHC16	p.W70*	zinc finger, DHHC-type	20 (0.00)	89 (0.19)	0.51
12-03	Gp3	g.chr2:145161573C>A	Missense Mutation	ZEB2	p.E239D	zinc finger E-box bindir	39 (0.00)	141 (0.40)	1.08
12-03	Gp3	g.chr8:135613793C>A	Missense Mutation	ZFAT	p.Q723H	zinc finger and AT hook	41 (0.00)	57 (0.44)	1.17
12-03	Gp3	g.chr16:72828689C>T	Missense Mutation	ZFHX3	p.S2631N	zinc finger homeobox 3	154 (0.00)	367 (0.19)	0.49
12-03	Gp3	g.chr8:106813788C>T	Missense Mutation	ZFPM2	p.P493L	zinc finger protein, FOC	146 (0.00)	72 (0.74)	1.96
12-03	Gp3	g.chr3:50379446C>A	Splice Site	ZMYND10	p.Q333H	zinc finger, MYND-typ	36 (0.00)	148 (0.16)	0.43
12-03	Gp3	g.chr9:140477000G>T	Silent	ZMYND19	p.R227R	zinc finger, MYND-typ	34 (0.03)	138 (0.27)	0.71
12-03	Gp3	g.chr2:219510997T>A	Missense Mutation	ZNF142	p.T450S	zinc finger protein 142	31 (0.00)	30 (0.33)	0.89
12-03	Gp3	g.chr19:22271438T>A	Missense Mutation	ZNF257	p.W296R	zinc finger protein 257	32 (0.00)	12 (0.58)	2.00
12-03	Gp3	g.chr19:44590076C>A	Missense Mutation	ZNF284	p.H149N	zinc finger protein 284	56 (0.00)	15 (0.53)	1.42
12-03	Gp3	g.chr7:148802424C>T	Missense Mutation	ZNF425	p.R180H	zinc finger protein 425	33 (0.00)	47 (0.70)	1.87
12-03	Gp3	g.chr1:23688751G>A	Missense Mutation	ZNF436	p.S375F	zinc finger protein 436	21 (0.00)	23 (0.43)	1.16
12-03	Gp3	g.chr19:56669911G>A	Missense Mutation	ZNF444	p.D116N	zinc finger protein 444	17 (0.00)	138 (0.59)	1.58
12-03	Gp3	g.chr20:62597809A>G	Missense Mutation	ZNF512B	p.V240A	zinc finger protein 512B	22 (0.00)	76 (0.28)	0.74
12-03	Gp3	g.chr4:10445193T>C	Silent	ZNF518B	p.A920A	zinc finger protein 518B	29 (0.00)	18 (0.50)	1.33
12-03	Gp3	g.chr19:58774037G>T	Nonsense Mutation	ZNF544	p.E689*	zinc finger protein 544	49 (0.00)	29 (0.21)	0.55
12-03	Gp3	g.chr19:12429570G>T	Nonsense Mutation	ZNF563	p.C423*	zinc finger protein 563	31 (0.00)	15 (0.47)	1.63
12-03	Gp3	g.chr19:42582791C>T	Silent	ZNF574	p.Y11Y	zinc finger protein 574	39 (0.00)	140 (0.22)	0.59
12-03	Gp3	g.chr19:56895687A>T	Missense Mutation	ZNF582	p.Y367N	zinc finger protein 582	32 (0.00)	38 (0.55)	1.47
12-03	Gp3	g.chr19:58301683G>A	Silent	ZNF586	p.L26L	zinc finger protein 586	24 (0.00)	66 (0.29)	0.77
12-03	Gp3	g.chr15:85327490G>T	Silent	ZNF592	p.R528R	zinc finger protein 592	20 (0.00)	42 (0.52)	1.40

12-03	Gp3	g.chr16:3486895G>T	Nonsense Mutation	ZNF597	p.Y268*	zinc finger protein 597	43 (0.00)	14 (0.50)	1.69
12-03	Gp3	g.chr19:58491321G>T	Missense Mutation	ZNF606	p.H243N	zinc finger protein 606	28 (0.00)	16 (0.44)	1.17
12-03	Gp3	g.chr8:144732085G>T	Missense Mutation	ZNF623	p.G15C	zinc finger protein 623	27 (0.00)	12 (0.50)	1.33
12-03	Gp3	g.chr19:23405334A>T	Missense Mutation	ZNF724P	p.F571L	zinc finger protein 724,	17 (0.00)	40 (0.50)	1.71
12-03	Gp3	g.chr19:22497606G>T	Nonsense Mutation	ZNF729	p.E463*	zinc finger protein 729	57 (0.00)	48 (0.83)	2.86
12-03	Gp3	g.chr19:22497721C>A	Nonsense Mutation	ZNF729	p.S501*	zinc finger protein 729	55 (0.00)	35 (0.69)	2.35
12-03	Gp3	g.chr19:22497733G>A	Missense Mutation	ZNF729	p.R505K	zinc finger protein 729	49 (0.00)	34 (0.68)	2.32
12-03	Gp3	g.chr17:80789407G>A	Silent	ZNF750	p.F308F	zinc finger protein 750	59 (0.00)	404 (0.15)	0.54
12-03	Gp3	g.chr19:58806781G>T	Missense Mutation	ZNF8	p.R536I	zinc finger protein 8	56 (0.00)	82 (0.90)	2.41
12-03	Gp3	g.chr19:20045249C>T	Silent	ZNF93	p.S495S	zinc finger protein 93	40 (0.00)	29 (0.62)	2.13
12-03	Gp3	g.chr7:99217360G>C	Missense Mutation	ZSCAN25	p.R44T	zinc finger and SCAN d	47 (0.00)	169 (0.15)	0.39
12-03	Gp3	g.chr1:45499992G>A	Missense Mutation	ZSWIM5	p.A814V	zinc finger, SWIM-type	79 (0.00)	64 (0.30)	0.79
12-03	Gp3	g.chr10:75558820G>A	Missense Mutation	ZSWIM8	p.V1408M	zinc finger, SWIM-type	30 (0.00)	191 (0.28)	0.75
12-03	Gp3	g.chr17:3947568G>A	Missense Mutation	ZZEF1	p.T2039I	zinc finger, ZZ-type wit	40 (0.00)	15 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr7:48287931G>A	Silent	ABCA13	p.L585L	ATP-binding cassette, s	46 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr16:16225765C>G	Missense Mutation	ABCC1	p.I1313M	ATP-binding cassette, s	34 (0.00)	17 (0.29)	0.62
12-03	Gp4 Focus 1	g.chr16:48162417C>T	Missense Mutation	ABCC12	p.D490N	ATP-binding cassette, s	32 (0.00)	15 (0.80)	2.13
12-03	Gp4 Focus 1	g.chr10:101569933G>T	Missense Mutation	ABCC2	p.D620Y	ATP-binding cassette, s	20 (0.00)	34 (0.82)	2.20
12-03	Gp4 Focus 1	g.chr3:58260497A>G	Silent	ABHD6	p.E212E	abhydrolase domain con	61 (0.00)	31 (0.32)	0.86
12-03	Gp4 Focus 1	g.chr4:8009854G>T	Missense Mutation	ABLIM2	p.S517Y	actin binding LIM prote	117 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr7:80805255T>C	Missense Mutation	AC005008.2	p.I42T		21 (0.00)	26 (0.27)	0.44
12-03	Gp4 Focus 1	g.chr4:118496939C>T	lincRNA	AC092661.1			52 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr18:47318542C>A	Missense Mutation	ACAA2	p.V242F	acetyl-CoA acyltransfer	16 (0.00)	27 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr17:35506888C>T	Missense Mutation	ACACA	p.R1823Q	acetyl-CoA carboxylase	38 (0.00)	48 (0.15)	0.51
12-03	Gp4 Focus 1	g.chr3:195022739G>T	Silent	ACAP2	p.I427I	ArfGAP with coiled-coi	111 (0.00)	18 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr9:32430506C>T	Missense Mutation	ACO1	p.P554S	aconitase 1, soluble	62 (0.00)	12 (0.58)	1.56
12-03	Gp4 Focus 1	g.chr22:41914513G>A	Silent	ACO2	p.K348K	aconitase 2, mitochondr	66 (0.02)	67 (0.39)	1.30
12-03	Gp4 Focus 1	g.chr15:78475099G>A	Missense Mutation	ACSBG1	p.A231V	acyl-CoA synthetase bu	55 (0.00)	118 (0.37)	0.99
12-03	Gp4 Focus 1	g.chr11:67412598C>A	Missense Mutation	ACY3	p.Q63H	aspartoacylase (aminoc	23 (0.00)	121 (0.18)	0.63
12-03	Gp4 Focus 1	g.chr1:155030345C>T	Nonsense Mutation	ADAM15	p.Q479*	ADAM metallopeptidas	28 (0.00)	307 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr1:155033241C>A	Missense Mutation	ADAM15	p.A737E	ADAM metallopeptidas	28 (0.00)	68 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr1:120438695G>T	Missense Mutation	ADAM30	p.R89S	ADAM metallopeptidas	19 (0.00)	51 (0.35)	0.94
12-03	Gp4 Focus 1	g.chr8:39181648G>A	RNA	ADAM5		ADAM metallopeptidas	28 (0.00)	78 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr8:39181682C>T	RNA	ADAM5		ADAM metallopeptidas	29 (0.00)	86 (0.17)	0.47
12-03	Gp4 Focus 1	g.chr5:5306619C>T	Silent	ADAMTS16	p.C1063C	ADAM metallopeptidas	40 (0.00)	42 (0.14)	0.38

12-03	Gp4 Focus 1	g.chr6:143771730G>T	Silent	ADAT2	p.T22T	adenosine deaminase, t	33 (0.00)	85 (0.53)	1.41
12-03	Gp4 Focus 1	g.chr7:31142854A>T	Silent	ADCYAP1R1	p.R378R	adenylate cyclase activa	48 (0.00)	20 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr20:49510855G>A	Silent	ADNP	p.N132N	activity-dependent neur	63 (0.00)	26 (0.46)	1.23
12-03	Gp4 Focus 1	g.chr18:77895561G>A	Silent	ADNP2	p.L755L	ADNP homeobox 2	39 (0.00)	113 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr2:64779863A>G	Missense Mutation	AFTPH	p.N419D	aftiphilin	40 (0.00)	36 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr10:88768865C>A	RNA	AGAP11		ankyrin repeat and GTP	79 (0.00)	113 (0.44)	1.18
12-03	Gp4 Focus 1	g.chr10:51465828C>T	Missense Mutation	AGAP7	p.V210I		64 (0.00)	56 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr1:36372651C>T	Missense Mutation	AGO1	p.H505Y	argonaute RISC catalyti	33 (0.00)	11 (0.55)	1.80
12-03	Gp4 Focus 1	g.chr1:230846111C>G	Silent	AGT	p.L162L	angiotensinogen (serpin	37 (0.00)	22 (0.36)	0.97
12-03	Gp4 Focus 1	g.chr5:432614G>A	Silent	AHRR	p.L337L	aryl-hydrocarbon recept	40 (0.00)	82 (0.27)	0.72
12-03	Gp4 Focus 1	g.chr7:91631003C>A	Missense Mutation	AKAP9	p.A591E	A kinase (PRKA) ancho	49 (0.00)	13 (0.46)	1.23
12-03	Gp4 Focus 1	g.chr7:134216677T>A	Missense Mutation	AKR1B10	p.F84L	aldo-keto reductase fam	131 (0.00)	30 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr10:5138681A>T	Missense Mutation	AKR1C3	p.Y55F	aldo-keto reductase fam	71 (0.00)	52 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr2:31756476C>T	RNA	AL133247.2			26 (0.00)	37 (0.70)	1.87
12-03	Gp4 Focus 1	g.chr2:73896260C>T	RNA	ALMS1P		Alstrom syndrome 1 ps	21 (0.00)	29 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr15:85400130G>T	Nonsense Mutation	ALPK3	p.E923*	alpha-kinase 3	57 (0.00)	120 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr11:46529791G>A	Silent	AMBRA1	p.D673D	autophagy/beclin-1 regu	60 (0.00)	52 (0.31)	0.82
12-03	Gp4 Focus 1	g.chr12:121747602G>T	Missense Mutation	ANAPC5	p.A653D	anaphase promoting con	39 (0.00)	59 (0.14)	0.47
12-03	Gp4 Focus 1	g.chr8:41557967C>G	Missense Mutation	ANK1	p.A856P	ankyrin 1, erythrocytic	98 (0.00)	32 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr4:114257154C>G	Missense Mutation	ANK2	p.Q1145E	ankyrin 2, neuronal	45 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr9:95575834G>A	RNA	ANKRD19P		ankyrin repeat domain 1	26 (0.00)	13 (0.54)	1.80
12-03	Gp4 Focus 1	g.chr7:36435874G>A	Splice Site	ANLN		anillin, actin binding pr	40 (0.00)	15 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr15:90335720G>T	Missense Mutation	ANPEP	p.L775I	alanyl (membrane) ami	29 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 1	g.chr7:150554105G>T	Missense Mutation	AOC1	p.A183S	amine oxidase, copper c	27 (0.00)	38 (0.32)	1.18
12-03	Gp4 Focus 1	g.chr17:41003592C>A	Silent	AOC3	p.R78R	amine oxidase, copper c	50 (0.00)	307 (0.18)	0.62
12-03	Gp4 Focus 1	g.chr11:64942742C>A	RNA	AP003068.18			20 (0.00)	54 (0.59)	2.05
12-03	Gp4 Focus 1	g.chr19:2138654T>G	Silent	AP3D1	p.I52I	adaptor-related protein	61 (0.00)	223 (0.14)	0.55
12-03	Gp4 Focus 1	g.chr11:129996682C>A	Missense Mutation	APLP2	p.A393D	amyloid beta (A4) precu	96 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr12:56755618G>T	Silent	APOF	p.I124I	apolipoprotein F	45 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr11:46700752G>A	Silent	ARHGAP1	p.N385N	Rho GTPase activating	28 (0.00)	246 (0.48)	1.29
12-03	Gp4 Focus 1	g.chr10:24908662G>A	Missense Mutation	ARHGAP21	p.A721V	Rho GTPase activating	45 (0.00)	19 (0.79)	2.11
12-03	Gp4 Focus 1	g.chr19:47425554G>A	Missense Mutation	ARHGAP35	p.E1208K	Rho GTPase activating	168 (0.01)	54 (0.41)	1.46
12-03	Gp4 Focus 1	g.chr11:73063938G>T	Nonsense Mutation	ARHGEF17	p.E1112*	Rho guanine nucleotide	16 (0.00)	95 (0.15)	0.53
12-03	Gp4 Focus 1	g.chr7:144063460C>T	Missense Mutation	ARHGEF5	p.P1056L	Rho guanine nucleotide	117 (0.00)	14 (0.57)	0.91
12-03	Gp4 Focus 1	g.chr12:50472324G>T	Missense Mutation	ASIC1	p.V320L	acid-sensing (proton-ga	30 (0.00)	69 (0.20)	0.54

12-03	Gp4 Focus 1	g.chr9:133364740G>A	Missense Mutation	ASS1	p.G287S	argininosuccinate synth	41 (0.00)	31 (0.19)	0.66
12-03	Gp4 Focus 1	g.chr2:25966265G>A	Missense Mutation	ASXL2	p.P981S	additional sex combs lik	61 (0.00)	45 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr15:25924550A>G	Missense Mutation	ATP10A	p.S1480P	ATPase, class V, type 1	35 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr19:19756736C>A	Missense Mutation	ATP13A1	p.V1103F	ATPase type 13A1	20 (0.00)	103 (0.12)	0.41
12-03	Gp4 Focus 1	g.chr1:160106789C>A	Silent	ATP1A2	p.T936T	ATPase, Na+/K+ transp	25 (0.00)	44 (0.34)	0.67
12-03	Gp4 Focus 1	g.chr1:203667323C>T	Nonsense Mutation	ATP2B4	p.Q78*	ATPase, Ca++ transport	29 (0.00)	18 (0.72)	1.93
12-03	Gp4 Focus 1	g.chr2:176043958C>T	Silent	ATP5G3	p.G47G	ATP synthase, H+ trans	38 (0.00)	28 (0.29)	0.76
12-03	Gp4 Focus 1	g.chrX:77243862C>T	Missense Mutation	ATP7A	p.P82L	ATPase, Cu++ transport	75 (0.00)	17 (0.47)	0.78
12-03	Gp4 Focus 1	g.chrX:77245118G>T	Missense Mutation	ATP7A	p.A334S	ATPase, Cu++ transport	34 (0.00)	21 (0.24)	0.40
12-03	Gp4 Focus 1	g.chr18:77108169C>T	Missense Mutation	ATP9B	p.P959L	ATPase, class II, type 9	56 (0.00)	73 (0.25)	0.66
12-03	Gp4 Focus 1	g.chr20:3581671G>T	Splice Site	ATRN	p.A1215S	attractin	52 (0.00)	71 (0.51)	1.35
12-03	Gp4 Focus 1	g.chr1:26161605C>T	Missense Mutation	AUNIP	p.G318E	aurora kinase A and nin	84 (0.00)	89 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr19:41727125C>T	Missense Mutation	AXL	p.S128F	AXL receptor tyrosine k	19 (0.00)	35 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr1:193150193C>A	Missense Mutation	B3GALT2	p.R167I	UDP-Gal:betaGlcNAc b	45 (0.00)	15 (0.80)	2.13
12-03	Gp4 Focus 1	g.chr14:104026416C>T	Silent	BAG5	p.E362E	BCL2-associated athanc	57 (0.00)	39 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr22:23656244C>T	Silent	BCR	p.L1183L	breakpoint cluster regio	30 (0.00)	338 (0.15)	0.52
12-03	Gp4 Focus 1	g.chr10:60577443G>A	Silent	BICC1	p.L885L	BicC family RNA bindi	35 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr9:95482761C>A	Missense Mutation	BICD2	p.D295Y	bicaudal D homolog 2 (	36 (0.00)	200 (0.22)	0.74
12-03	Gp4 Focus 1	g.chr2:32626388C>A	Missense Mutation	BIRC6	p.H398N	baculoviral IAP repeat c	94 (0.00)	273 (0.39)	1.05
12-03	Gp4 Focus 1	g.chr2:32626433G>A	Missense Mutation	BIRC6	p.D413N	baculoviral IAP repeat c	100 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr2:32694588C>A	Missense Mutation	BIRC6	p.L2085M	baculoviral IAP repeat c	98 (0.00)	26 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr15:91267806C>A	Intron	BLM		Bloom syndrome, RecQ	108 (0.00)	30 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr15:91287530T>A	Intron	BLM		Bloom syndrome, RecQ	29 (0.00)	10 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr15:91339973G>T	Intron	BLM		Bloom syndrome, RecQ	86 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 1	g.chr5:172586971G>T	Missense Mutation	BNIP1	p.S136I	BCL2/adenovirus E1B	27 (0.00)	48 (0.52)	1.39
12-03	Gp4 Focus 1	g.chr18:54814880G>A	Missense Mutation	BOD1L2	p.E113K	biorientation of chromo	16 (0.00)	78 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr17:41210973G>A	Intron	BRCA1		breast cancer 1, early on	38 (0.00)	29 (0.41)	1.10
12-03	Gp4 Focus 1	g.chr17:41235586A>G	Intron	BRCA1		breast cancer 1, early on	45 (0.00)	16 (0.62)	1.67
12-03	Gp4 Focus 1	g.chr17:41242240C>T	Intron	BRCA1		breast cancer 1, early on	37 (0.00)	137 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr13:32928595G>C	Intron	BRCA2		breast cancer 2, early on	100 (0.00)	24 (0.62)	0.81
12-03	Gp4 Focus 1	g.chr19:15355544G>C	Missense Mutation	BRD4	p.H730D	bromodomain containin	27 (0.00)	51 (0.22)	0.76
12-03	Gp4 Focus 1	g.chr19:15375568C>T	Missense Mutation	BRD4	p.G287R	bromodomain containin	63 (0.00)	268 (0.32)	1.14
12-03	Gp4 Focus 1	g.chr5:886707C>T	Splice Site	BRD9	p.S278N	bromodomain containin	99 (0.00)	287 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr21:40572285G>T	Missense Mutation	BRWD1	p.T1538N	bromodomain and WD	36 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr3:49689913C>A	Missense Mutation	BSN	p.S975Y	bassoon presynaptic cyt	15 (0.00)	412 (0.18)	0.47

12-03	Gp4 Focus 1	g.chr6:26423195C>T	RNA	BTN2A3P		butyrophilin, subfamily	32 (0.00)	46 (0.33)	0.87
12-03	Gp4 Focus 1	g.chr6:105563609C>T	Missense Mutation	BVES	p.D304N	blood vessel epicardial	30 (0.00)	19 (0.37)	0.46
12-03	Gp4 Focus 1	g.chr10:115885779G>A	Missense Mutation	C10orf118	p.R827W		53 (0.00)	14 (0.93)	2.48
12-03	Gp4 Focus 1	g.chr10:98744457G>A	Missense Mutation	C10orf12	p.G1104R	chromosome 10 open re	50 (0.00)	31 (0.32)	0.86
12-03	Gp4 Focus 1	g.chr16:67166423C>T	Missense Mutation	C16orf70	p.P117L	chromosome 16 open re	34 (0.00)	37 (0.78)	2.09
12-03	Gp4 Focus 1	g.chr16:67180219C>A	Missense Mutation	C16orf70	p.T383K	chromosome 16 open re	27 (0.00)	14 (0.86)	2.29
12-03	Gp4 Focus 1	g.chr16:5115803G>C	Missense Mutation	C16orf89	p.A36G	chromosome 16 open re	23 (0.00)	123 (0.15)	0.51
12-03	Gp4 Focus 1	g.chr17:42744869T>A	Missense Mutation	C17orf104	p.N530K	chromosome 17 open re	28 (0.00)	36 (0.31)	1.10
12-03	Gp4 Focus 1	g.chr1:244803275G>T	Silent	C1orf101	p.L916L	chromosome 1 open rea	122 (0.00)	13 (0.46)	1.23
12-03	Gp4 Focus 1	g.chr1:150259248G>A	Missense Mutation	C1orf51	p.S347N		64 (0.00)	111 (0.42)	1.58
12-03	Gp4 Focus 1	g.chr1:25571693G>A	Missense Mutation	C1orf63	p.A207V		70 (0.00)	84 (0.30)	0.79
12-03	Gp4 Focus 1	g.chr1:22974246C>A	Silent	C1QC	p.V236V	complement component	48 (0.00)	64 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr21:43523939G>T	Silent	C21orf128	p.V98V	chromosome 21 open re	59 (0.00)	199 (0.16)	0.61
12-03	Gp4 Focus 1	g.chr2:200820968G>A	Silent	C2orf47	p.K149K	chromosome 2 open rea	62 (0.00)	87 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr2:232457708T>C	Missense Mutation	C2orf57	p.S16P	chromosome 2 open rea	26 (0.00)	56 (0.38)	1.00
12-03	Gp4 Focus 1	g.chr2:29294779A>G	Silent	C2orf71	p.I783I	chromosome 2 open rea	22 (0.00)	38 (0.37)	0.98
12-03	Gp4 Focus 1	g.chr3:118865414G>T	Missense Mutation	C3orf30	p.Q126H	chromosome 3 open rea	23 (0.00)	12 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr3:138669336G>T	Missense Mutation	C3orf72	p.E150D		19 (0.00)	28 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr7:99754574A>T	Missense Mutation	C7orf43	p.L296Q	chromosome 7 open rea	23 (0.00)	60 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr9:35044926G>A	Nonsense Mutation	C9orf131	p.W767*	chromosome 9 open rea	69 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr17:50008368G>A	Silent	CA10	p.I87I	carbonic anhydrase X	104 (0.00)	36 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr8:86354387G>T	Missense Mutation	CA3	p.E106D	carbonic anhydrase III,	19 (0.00)	14 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr17:58234870C>T	Silent	CA4	p.H117H	carbonic anhydrase IV	43 (0.00)	104 (0.12)	0.41
12-03	Gp4 Focus 1	g.chr1:65047903T>C	Missense Mutation	CACHD1	p.V58A	cache domain containin	45 (0.00)	13 (0.62)	1.64
12-03	Gp4 Focus 1	g.chr3:85037443C>A	Intron	CADM2		cell adhesion molecule	64 (0.00)	32 (0.41)	1.08
12-03	Gp4 Focus 1	g.chr3:85117375C>A	Intron	CADM2		cell adhesion molecule	30 (0.00)	29 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr3:85133189C>T	Intron	CADM2		cell adhesion molecule	51 (0.00)	14 (0.79)	2.10
12-03	Gp4 Focus 1	g.chr3:85155437T>C	Intron	CADM2		cell adhesion molecule	115 (0.00)	100 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr3:85165016C>A	Intron	CADM2		cell adhesion molecule	48 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr3:85219259T>A	Intron	CADM2		cell adhesion molecule	33 (0.00)	17 (0.76)	2.04
12-03	Gp4 Focus 1	g.chr3:85219260T>A	Intron	CADM2		cell adhesion molecule	33 (0.00)	17 (0.41)	1.10
12-03	Gp4 Focus 1	g.chr3:85348943G>A	Intron	CADM2		cell adhesion molecule	26 (0.00)	15 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr3:85387326G>A	Intron	CADM2		cell adhesion molecule	34 (0.00)	26 (0.54)	1.44
12-03	Gp4 Focus 1	g.chr3:85408116C>G	Intron	CADM2		cell adhesion molecule	39 (0.00)	47 (0.30)	0.79
12-03	Gp4 Focus 1	g.chr3:85593887G>T	Intron	CADM2		cell adhesion molecule	33 (0.00)	25 (0.64)	1.71

12-03	Gp4 Focus 1	g.chr3:85830339T>C	Intron	CADM2		cell adhesion molecule	34 (0.00)	16 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr3:85953016G>C	Intron	CADM2		cell adhesion molecule	49 (0.00)	40 (0.93)	2.47
12-03	Gp4 Focus 1	g.chr4:114378594G>T	Missense Mutation	CAMK2D	p.P444T	calcium/calmodulin-dep	17 (0.00)	12 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr1:7737671G>A	Missense Mutation	CAMTA1	p.G931D	calmodulin binding tran	37 (0.00)	72 (0.36)	0.96
12-03	Gp4 Focus 1	g.chr17:38320272C>T	Missense Mutation	CASC3	p.P442S	cancer susceptibility car	65 (0.00)	59 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr17:38325576G>A	Splice Site	CASC3		cancer susceptibility car	26 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr19:15164721G>A	Missense Mutation	CASP14	p.A119T	caspase 14, apoptosis-re	18 (0.00)	17 (0.29)	1.04
12-03	Gp4 Focus 1	g.chr10:115489137G>A	Silent	CASP7	p.E250E	caspase 7, apoptosis-rel	26 (0.00)	30 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr3:122003300C>T	Silent	CASR	p.V833V	calcium-sensing recepto	18 (0.00)	93 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr19:15132436A>G	Silent	CCDC105	p.L350L	coiled-coil domain cont	38 (0.00)	184 (0.12)	0.44
12-03	Gp4 Focus 1	g.chr7:23682712A>G	Missense Mutation	CCDC126	p.N134S	coiled-coil domain cont	31 (0.00)	12 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr9:100132942T>C	Missense Mutation	CCDC180	p.L1501P	coiled-coil domain cont	19 (0.00)	57 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr17:61843313C>T	Missense Mutation	CCDC47	p.D75N	coiled-coil domain cont	22 (0.00)	21 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr12:49308336C>A	Silent	CCDC65	p.T150T	coiled-coil domain cont	20 (0.00)	44 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr3:56627971G>A	Splice Site	CCDC66		coiled-coil domain cont	48 (0.00)	23 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr5:150563988C>T	Silent	CCDC69	p.L210L	coiled-coil domain cont	24 (0.00)	52 (0.33)	0.58
12-03	Gp4 Focus 1	g.chr2:132289323C>G	Missense Mutation	CCDC74A	p.L211V	coiled-coil domain cont	78 (0.00)	120 (0.23)	0.83
12-03	Gp4 Focus 1	g.chr3:112358219C>A	Missense Mutation	CCDC80	p.E178D	coiled-coil domain cont	37 (0.00)	11 (0.82)	2.18
12-03	Gp4 Focus 1	g.chr11:85627204G>A	Silent	CCDC83	p.E336E	coiled-coil domain cont	48 (0.00)	17 (0.76)	2.04
12-03	Gp4 Focus 1	g.chr12:124427326G>A	Missense Mutation	CCDC92	p.T46I	coiled-coil domain cont	56 (0.00)	54 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr10:97816730G>A	Missense Mutation	CCNJ	p.D185N	cyclin J	26 (0.00)	51 (0.31)	0.84
12-03	Gp4 Focus 1	g.chr3:46414922A>G	Missense Mutation	CCR5	p.T177A	chemokine (C-C motif)	53 (0.00)	169 (0.40)	1.35
12-03	Gp4 Focus 1	g.chr7:56122136G>A	Silent	CCT6A	p.T92T	chaperonin containing T	38 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr7:5944759T>A	Missense Mutation	CCZ1	p.L186Q	CCZ1 vacuolar protein	98 (0.00)	13 (0.85)	2.26
12-03	Gp4 Focus 1	g.chr1:117556076G>C	Missense Mutation	CD101	p.G297A	CD101 molecule	65 (0.00)	122 (0.41)	1.09
12-03	Gp4 Focus 1	g.chr1:167400948G>A	Silent	CD247	p.A155A	CD247 molecule	55 (0.00)	26 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr12:6554606G>A	Silent	CD27	p.K51K	CD27 molecule	46 (0.00)	44 (0.43)	1.15
12-03	Gp4 Focus 1	g.chr1:207510097C>T	Missense Mutation	CD55	p.P241S	CD55 molecule, decay	55 (0.00)	58 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr9:35612930G>A	Missense Mutation	CD72	p.T250I	CD72 molecule	29 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr14:103466000G>A	Silent	CDC42BPB	p.S166S	CDC42 binding protein	18 (0.00)	30 (0.37)	0.98
12-03	Gp4 Focus 1	g.chr17:38445782C>T	Missense Mutation	CDC6	p.T37I	cell division cycle 6	33 (0.00)	26 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr16:68849596G>C	Missense Mutation	CDH1	p.G500A	cadherin 1, type 1, E-ca	35 (0.00)	28 (0.18)	0.61
12-03	Gp4 Focus 1	g.chr10:73491815G>A	Missense Mutation	CDH23	p.G1268R	cadherin-related 23	62 (0.00)	44 (0.43)	1.48
12-03	Gp4 Focus 1	g.chr5:176011676G>T	Silent	CDHR2	p.V798V	cadherin-related family	28 (0.00)	82 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr7:105658411C>A	Missense Mutation	CDHR3	p.P516T	cadherin-related family	62 (0.00)	19 (0.37)	0.98

12-03	Gp4 Focus 1	g.chr17:37686906C>A	Silent	CDK12	p.P1270P	cyclin-dependent kinase	43 (0.00)	45 (0.16)	0.41
12-03	Gp4 Focus 1	g.chr17:37687013C>A	Missense Mutation	CDK12	p.S1306Y	cyclin-dependent kinase	55 (0.00)	32 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr19:51983921G>T	Missense Mutation	CEACAM18	p.W129C	carcinoembryonic antig	108 (0.00)	32 (0.25)	0.89
12-03	Gp4 Focus 1	g.chr1:109794090C>A	Missense Mutation	CELSR2	p.D463E	cadherin, EGF LAG sev	34 (0.00)	42 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr1:109804193C>G	Missense Mutation	CELSR2	p.H1414D	cadherin, EGF LAG sev	55 (0.00)	90 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr3:48691068C>A	Missense Mutation	CELSR3	p.S1811I	cadherin, EGF LAG sev	64 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr16:67862671C>A	Silent	CENPT	p.R452R	centromere protein T	23 (0.00)	84 (0.29)	0.97
12-03	Gp4 Focus 1	g.chr14:81251425C>T	Silent	CEP128	p.R675R	centrosomal protein 128	29 (0.00)	25 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr4:56886910C>T	Missense Mutation	CEP135	p.A1095V	centrosomal protein 135	62 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr11:117265692G>A	Silent	CEP164	p.K939K	centrosomal protein 164	34 (0.00)	294 (0.32)	0.86
12-03	Gp4 Focus 1	g.chr11:117267908G>A	Missense Mutation	CEP164	p.R1127Q	centrosomal protein 164	22 (0.00)	92 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr9:131186753G>A	Missense Mutation	CERCAM	p.R209H	cerebral endothelial cell	20 (0.00)	50 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr16:55860091G>T	Missense Mutation	CES1	p.A126D	carboxylesterase 1	131 (0.00)	46 (0.91)	2.43
12-03	Gp4 Focus 1	g.chr1:6167647G>A	Intron	CHD5		chromodomain helicase	18 (0.00)	325 (0.36)	0.95
12-03	Gp4 Focus 1	g.chr1:6182469C>A	Intron	CHD5		chromodomain helicase	83 (0.00)	272 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr1:6186930C>T	Intron	CHD5		chromodomain helicase	39 (0.00)	242 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr1:6212402C>G	Intron	CHD5		chromodomain helicase	20 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 1	g.chr1:6222685G>A	Intron	CHD5		chromodomain helicase	28 (0.00)	177 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr1:6227543C>A	Intron	CHD5		chromodomain helicase	22 (0.00)	93 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr1:6228706T>C	Intron	CHD5		chromodomain helicase	109 (0.00)	53 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr15:20490628G>A	RNA	CHEK2P2		checkpoint kinase 2 pse	68 (0.01)	87 (0.86)	2.30
12-03	Gp4 Focus 1	g.chr12:102108351C>T	Missense Mutation	CHPT1	p.S164F	choline phosphotransfer	60 (0.02)	32 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr12:102108364G>T	Missense Mutation	CHPT1	p.M168I	choline phosphotransfer	61 (0.00)	33 (0.55)	1.45
12-03	Gp4 Focus 1	g.chr2:101023073C>A	Missense Mutation	CHST10	p.S22I	carbohydrate sulfotrans	36 (0.00)	16 (0.44)	1.17
12-03	Gp4 Focus 1	g.chr16:75563275C>A	Missense Mutation	CHST5	p.K336N	carbohydrate (N-acetylg	15 (0.00)	148 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr19:42793042T>A	Missense Mutation	CIC	p.S1221T	capicua transcriptional r	15 (0.00)	78 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr2:122125391C>A	Missense Mutation	CLASP1	p.G1153V	cytoplasmic linker asso	63 (0.00)	127 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr1:11897448C>T	Silent	CLCN6	p.D729D	chloride channel, voltag	30 (0.00)	112 (0.45)	1.19
12-03	Gp4 Focus 1	g.chr15:65450140G>T	Missense Mutation	CLPX	p.S334Y	caseinolytic mitochondr	43 (0.00)	41 (0.46)	1.24
12-03	Gp4 Focus 1	g.chr17:57744250G>A	Silent	CLTC	p.Q680Q	clathrin, heavy chain (H	17 (0.00)	22 (0.32)	1.13
12-03	Gp4 Focus 1	g.chr22:19188971C>A	Nonsense Mutation	CLTCL1	p.E1212*	clathrin, heavy chain-lik	46 (0.00)	138 (0.20)	0.69
12-03	Gp4 Focus 1	g.chr10:104831549G>C	Missense Mutation	CNNM2	p.R729P	cyclin and CBS domain	21 (0.00)	70 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr10:104836785C>T	Nonsense Mutation	CNNM2	p.Q826*	cyclin and CBS domain	62 (0.00)	129 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr5:179994905C>T	Missense Mutation	CNOT6	p.S310F	CCR4-NOT transcriptio	26 (0.00)	49 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr4:78652577C>A	Missense Mutation	CNOT6L	p.V330L	CCR4-NOT transcriptio	45 (0.00)	42 (0.48)	1.27

12-03	Gp4 Focus 1	g.chr12:41419113G>A	Missense Mutation	CNTN1	p.M895I	contactin 1	64 (0.02)	209 (0.38)	1.01
12-03	Gp4 Focus 1	g.chr11:99932034G>C	Silent	CNTN5	p.P357P	contactin 5	63 (0.00)	9 (0.89)	2.37
12-03	Gp4 Focus 1	g.chr3:1363333G>A	Splice Site	CNTN6		contactin 6	40 (0.00)	15 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr16:76528814C>A	Silent	CNTNAP4	p.T699T	contactin associated pro	36 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr16:76587188G>A	Missense Mutation	CNTNAP4	p.D1154N	contactin associated pro	66 (0.00)	28 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr2:125555867G>A	Missense Mutation	CNTNAP5	p.D1062N	contactin associated pro	34 (0.00)	46 (0.65)	1.74
12-03	Gp4 Focus 1	g.chr2:125555879G>A	Missense Mutation	CNTNAP5	p.V1066I	contactin associated pro	34 (0.00)	41 (0.66)	1.76
12-03	Gp4 Focus 1	g.chr17:7836560C>A	Missense Mutation	CNTROB	p.Q55K	centrobin, centrosomal	45 (0.00)	69 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr7:51097190C>A	Missense Mutation	COBL	p.D535Y	cordon-bleu WH2 repea	29 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr17:48264051G>T	Missense Mutation	COL1A1	p.P1255H	collagen, type I, alpha 1	26 (0.00)	62 (0.77)	2.06
12-03	Gp4 Focus 1	g.chr8:139749787G>A	Missense Mutation	COL22A1	p.P707S	collagen, type XXII, alp	28 (0.00)	27 (0.74)	1.98
12-03	Gp4 Focus 1	g.chr8:139820045C>A	Missense Mutation	COL22A1	p.G487V	collagen, type XXII, alp	29 (0.00)	17 (0.35)	0.94
12-03	Gp4 Focus 1	g.chr2:228012192G>A	Missense Mutation	COL4A4	p.S3F	collagen, type IV, alpha	42 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr19:10078737C>T	Missense Mutation	COL5A3	p.G1445S	collagen, type V, alpha	30 (0.00)	16 (0.94)	3.32
12-03	Gp4 Focus 1	g.chr2:238265999A>G	Silent	COL6A3	p.P2191P	collagen, type VI, alpha	87 (0.00)	137 (0.31)	0.84
12-03	Gp4 Focus 1	g.chr2:238266029G>C	Silent	COL6A3	p.V2181V	collagen, type VI, alpha	33 (0.00)	122 (0.54)	1.44
12-03	Gp4 Focus 1	g.chr3:130289888C>A	Silent	COL6A6	p.L876L	collagen, type VI, alpha	140 (0.01)	14 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr4:8608508G>T	Missense Mutation	CPZ	p.Q306H	carboxypeptidase Z	37 (0.00)	47 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr1:207867792C>A	Missense Mutation	CR1L	p.H186Q	complement component	107 (0.00)	13 (0.38)	1.03
12-03	Gp4 Focus 1	g.chr1:207867826G>A	Missense Mutation	CR1L	p.E198K	complement component	97 (0.00)	16 (0.38)	1.00
12-03	Gp4 Focus 1	g.chr17:1326921C>T	Silent	CRK	p.T267T	v-crk avian sarcoma vir	22 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr1:16958870G>T	lincRNA	CROCCP2		ciliary rootlet coiled-coi	58 (0.00)	170 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr5:131409781C>G	Missense Mutation	CSF2	p.T56R	colony stimulating facto	19 (0.00)	112 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr17:80209349G>T	Missense Mutation	CSNK1D	p.P264H	casein kinase 1, delta	17 (0.00)	39 (0.31)	1.08
12-03	Gp4 Focus 1	g.chr8:68102933C>T	Missense Mutation	CSPP1	p.P1085L	centrosome and spindle	23 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr21:45194562C>T	Missense Mutation	CSTB	p.A49T	cystatin B (stefin B)	22 (0.00)	31 (0.16)	0.61
12-03	Gp4 Focus 1	g.chr17:34292222C>A	RNA	CTB-186H2.2			41 (0.00)	44 (0.86)	2.30
12-03	Gp4 Focus 1	g.chr17:3558346G>A	Missense Mutation	CTNS	p.V94I	cystinosin, lysosomal cy	20 (0.00)	55 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr1:112998924A>T	Missense Mutation	CTTNBP2NL	p.L270F	CTTNBP2 N-terminal li	36 (0.00)	49 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr1:112998925A>T	Nonsense Mutation	CTTNBP2NL	p.K271*	CTTNBP2 N-terminal li	36 (0.00)	49 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr4:105412001C>A	Missense Mutation	CXXC4	p.C320F	CXXC finger protein 4	93 (0.00)	96 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr1:47610043C>T	Silent	CYP4A22	p.L269L	cytochrome P450, famil	74 (0.00)	28 (0.93)	2.48
12-03	Gp4 Focus 1	g.chr9:124408153G>A	Intron	DAB2IP		DAB2 interacting protei	53 (0.00)	16 (0.94)	0.62
12-03	Gp4 Focus 1	g.chr9:124422733G>A	Intron	DAB2IP		DAB2 interacting protei	37 (0.00)	26 (0.73)	0.49
12-03	Gp4 Focus 1	g.chr9:124434271G>T	Intron	DAB2IP		DAB2 interacting protei	29 (0.00)	66 (0.58)	0.38

12-03	Gp4 Focus 1	g.chr14:69521328C>A	Missense Mutation	DCAF5	p.G692V	DDB1 and CUL4 associ	54 (0.00)	19 (0.32)	0.84
12-03	Gp4 Focus 1	g.chr11:6647863G>A	Missense Mutation	DCHS1	p.A2095V	dachsous cadherin-relat	21 (0.00)	53 (0.25)	0.49
12-03	Gp4 Focus 1	g.chr4:155254449C>T	Missense Mutation	DCHS2	p.D472N	dachsous cadherin-relat	18 (0.00)	16 (0.38)	1.00
12-03	Gp4 Focus 1	g.chr13:95121290G>T	Missense Mutation	DCT	p.A102D	dopachrome tautomeras	46 (0.00)	54 (0.91)	1.35
12-03	Gp4 Focus 1	g.chr2:74597751T>C	Missense Mutation	DCTN1	p.K349E	dynactin 1	26 (0.00)	56 (0.38)	1.00
12-03	Gp4 Focus 1	g.chr13:114112385C>A	Missense Mutation	DCUN1D2	p.A247S	DCN1, defective in cull	77 (0.00)	206 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr4:101108898C>A	Missense Mutation	DDIT4L	p.G173V	DNA-damage-inducible	48 (0.00)	13 (0.69)	1.85
12-03	Gp4 Focus 1	g.chr12:31236927G>T	Nonsense Mutation	DDX11	p.G109*	DEAD/H (Asp-Glu-Ala	16 (0.06)	30 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr1:112303725G>A	Missense Mutation	DDX20	p.V314I	DEAD (Asp-Glu-Ala-A	21 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr5:134120150G>T	Nonsense Mutation	DDX46	p.G421*	DEAD (Asp-Glu-Ala-A	58 (0.00)	46 (0.35)	0.93
12-03	Gp4 Focus 1	g.chr8:142176361G>T	Silent	DENND3	p.L542L	DENN/MADD domain	31 (0.00)	97 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr9:19300235C>A	Missense Mutation	DENND4C	p.A406E	DENN/MADD domain	23 (0.00)	14 (0.64)	1.71
12-03	Gp4 Focus 1	g.chr1:68947917A>G	Missense Mutation	DEPDC1	p.I525T	DEP domain containing	55 (0.00)	99 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr22:19050790A>G	Splice Site	DGCR2	p.L184L	DiGeorge syndrome crit	16 (0.00)	19 (0.26)	0.89
12-03	Gp4 Focus 1	g.chr19:12790981G>A	Silent	DHPS	p.H122H	deoxyhypusine synthase	104 (0.00)	121 (0.56)	1.99
12-03	Gp4 Focus 1	g.chr19:12791003G>A	Missense Mutation	DHPS	p.T115I	deoxyhypusine synthase	100 (0.00)	113 (0.58)	2.04
12-03	Gp4 Focus 1	g.chr14:24424349G>T	Silent	DHRS4	p.G78G	dehydrogenase/reductas	20 (0.00)	143 (0.22)	0.43
12-03	Gp4 Focus 1	g.chr1:182841587G>A	Missense Mutation	DHX9	p.C558Y	DEAH (Asp-Glu-Ala-H	50 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr10:54075458C>T	Intron	DKK1		dickkopf WNT signalin	60 (0.00)	107 (0.31)	0.82
12-03	Gp4 Focus 1	g.chr3:38153780C>T	Silent	DLEC1	p.Y1198Y	deleted in lung and esop	61 (0.00)	79 (0.25)	0.41
12-03	Gp4 Focus 1	g.chr10:124377594G>A	Silent	DMBT1	p.V1522V	deleted in malignant bra	262 (0.00)	20 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr17:7701021G>A	Missense Mutation	DNAH2	p.V2702M	dynein, axonemal, heav	17 (0.00)	15 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr16:21132173C>A	Silent	DNAH3	p.L529L	dynein, axonemal, heav	98 (0.00)	64 (0.89)	2.38
12-03	Gp4 Focus 1	g.chr22:41257419C>T	Missense Mutation	DNAJB7	p.V194I	DnaJ (Hsp40) homolog,	25 (0.00)	36 (0.17)	0.56
12-03	Gp4 Focus 1	g.chr15:41068474T>C	Missense Mutation	DNAJC17	p.E133G	DnaJ (Hsp40) homolog,	16 (0.00)	26 (0.27)	0.72
12-03	Gp4 Focus 1	g.chr11:6591252C>T	Silent	DNHD1	p.L4293L	dynein heavy chain dom	22 (0.00)	47 (0.36)	0.96
12-03	Gp4 Focus 1	g.chr9:131012393G>T	Splice Site	DNM1		dynamin 1	23 (0.00)	253 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr10:128798486G>A	Silent	DOCK1	p.Q300Q	dedicator of cytokinesis	53 (0.00)	73 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr2:225637885C>A	Missense Mutation	DOCK10	p.V2065F	dedicator of cytokinesis	30 (0.00)	34 (0.74)	1.96
12-03	Gp4 Focus 1	g.chr2:225710285G>A	Silent	DOCK10	p.D770D	dedicator of cytokinesis	72 (0.00)	28 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr1:63008323G>A	Missense Mutation	DOCK7	p.R970W	dedicator of cytokinesis	25 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr1:63100516G>A	Silent	DOCK7	p.A321A	dedicator of cytokinesis	15 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr6:7580524G>A	Silent	DSP	p.E1367E	desmoplakin	49 (0.00)	13 (0.38)	1.03
12-03	Gp4 Focus 1	g.chr6:56334985G>C	Missense Mutation	DST	p.L7153V	dystonin	84 (0.00)	18 (0.44)	0.88
12-03	Gp4 Focus 1	g.chr6:56382052T>A	Nonsense Mutation	DST	p.K5781*	dystonin	29 (0.00)	23 (0.43)	0.86

12-03	Gp4 Focus 1	g.chr15:45448008G>A	Missense Mutation	DUOX1	p.G1195R	dual oxidase 1	81 (0.00)	13 (0.92)	2.46
12-03	Gp4 Focus 1	g.chr15:45457018G>A	Missense Mutation	DUOX1	p.M1525I	dual oxidase 1	27 (0.00)	50 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr15:45397870C>A	Nonsense Mutation	DUOX2	p.E769*	dual oxidase 2	52 (0.00)	62 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr11:103339377C>A	Missense Mutation	DYNC2H1	p.L4237I	dynein, cytoplasmic 2, h	139 (0.01)	28 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr21:38877851C>T	Missense Mutation	DYRK1A	p.S502F	dual-specificity tyrosine	36 (0.00)	25 (0.68)	1.81
12-03	Gp4 Focus 1	g.chr2:71778223C>A	Silent	DYSF	p.L543L	dysferlin	60 (0.00)	116 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr11:65636079G>A	Missense Mutation	EFEMP2	p.S250F	EGF containing fibulin-	23 (0.00)	137 (0.20)	0.68
12-03	Gp4 Focus 1	g.chr8:132996459T>A	Missense Mutation	EFR3A	p.L550Q	EFR3 homolog A (S. ce	22 (0.00)	34 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr15:40282545T>C	Silent	EIF2AK4	p.D866D	eukaryotic translation in	23 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr12:10658875G>A	Missense Mutation	EIF2S3L	p.R125K		107 (0.00)	98 (0.28)	0.73
12-03	Gp4 Focus 1	g.chr17:78117976G>T	Silent	EIF4A3	p.I79I	eukaryotic translation in	45 (0.00)	43 (0.12)	0.41
12-03	Gp4 Focus 1	g.chr13:41507692G>A	Missense Mutation	ELF1	p.H577Y	E74-like factor 1 (ets do	47 (0.00)	34 (0.50)	0.65
12-03	Gp4 Focus 1	g.chr14:89109332C>A	Missense Mutation	EML5	p.G1381V	echinoderm microtubule	45 (0.00)	35 (0.31)	0.84
12-03	Gp4 Focus 1	g.chr19:6904129C>A	Silent	EMR1	p.G295G	egf-like module contain	27 (0.00)	39 (0.36)	1.37
12-03	Gp4 Focus 1	g.chr8:120606044C>A	Silent	ENPP2	p.L395L	ectonucleotide pyrophos	38 (0.00)	44 (0.48)	1.27
12-03	Gp4 Focus 1	g.chr22:41569780C>A	Missense Mutation	EP300	p.H1591N	E1A binding protein p3	25 (0.00)	60 (0.37)	1.23
12-03	Gp4 Focus 1	g.chr12:132502860G>A	Missense Mutation	EP400	p.E1406K	E1A binding protein p4	22 (0.00)	28 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr7:100411302G>A	Silent	EPHB4	p.D576D	EPH receptor B4	35 (0.00)	25 (0.76)	2.03
12-03	Gp4 Focus 1	g.chr16:14021961A>G	Missense Mutation	ERCC4	p.T221A	excision repair cross-co	50 (0.00)	17 (0.29)	0.62
12-03	Gp4 Focus 1	g.chr21:39756338G>A	Intron	ERG		v-ets avian erythroblast	53 (0.00)	60 (0.35)	0.93
12-03	Gp4 Focus 1	g.chr21:39770177G>A	Intron	ERG		v-ets avian erythroblast	156 (0.00)	27 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr21:39806293C>T	Intron	ERG		v-ets avian erythroblast	92 (0.00)	44 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr21:39813879G>T	Intron	ERG		v-ets avian erythroblast	52 (0.00)	33 (0.39)	1.05
12-03	Gp4 Focus 1	g.chr21:39834713G>T	Intron	ERG		v-ets avian erythroblast	43 (0.00)	47 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr21:39863587C>T	Intron	ERG		v-ets avian erythroblast	73 (0.00)	25 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr21:39867733G>A	Intron	ERG		v-ets avian erythroblast	22 (0.00)	34 (0.82)	2.20
12-03	Gp4 Focus 1	g.chr21:39998480A>G	Intron	ERG		v-ets avian erythroblast	17 (0.00)	24 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr21:40008305G>A	Intron	ERG		v-ets avian erythroblast	93 (0.00)	49 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr21:40008408G>A	Intron	ERG		v-ets avian erythroblast	73 (0.00)	37 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr12:53664539G>T	Missense Mutation	ESPL1	p.E442D	extra spindle pole bodie	33 (0.00)	37 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr12:56531994G>A	Missense Mutation	ESYT1	p.G769S	extended synaptotagmin	41 (0.00)	18 (0.61)	1.63
12-03	Gp4 Focus 1	g.chr4:159627967T>A	Missense Mutation	ETFDH	p.I505K	electron-transferring-fla	51 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr14:69695766C>T	Silent	EXD2	p.L189L	exonuclease 3'-5' domai	37 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr5:453492G>T	Missense Mutation	EXOC3	p.E124D	exocyst complex compo	26 (0.00)	20 (0.35)	0.93
12-03	Gp4 Focus 1	g.chr1:11147588C>T	Missense Mutation	EXOSC10	p.E336K	exosome component 10	71 (0.00)	144 (0.17)	0.46

12-03	Gp4 Focus 1	g.chr8:28574353G>A	Silent	EXTL3	p.Q259Q	exostosin-like glycosylt	54 (0.00)	83 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr1:50941195C>T	Missense Mutation	FAF1	p.A604T	Fas (TNFRSF6) associa	29 (0.00)	34 (0.26)	0.71
12-03	Gp4 Focus 1	g.chr12:50295054C>A	Nonsense Mutation	FAIM2	p.E24*	Fas apoptotic inhibitory	36 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr7:22999935G>A	Nonsense Mutation	FAM126A	p.R311*	family with sequence si	48 (0.00)	19 (0.47)	1.26
12-03	Gp4 Focus 1	g.chr4:152499069C>T	Silent	FAM160A1	p.G191G	family with sequence si	48 (0.02)	49 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr2:62067273G>A	Missense Mutation	FAM161A	p.A289V	family with sequence si	103 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 1	g.chr7:135433285G>T	Missense Mutation	FAM180A	p.A15D	family with sequence si	109 (0.00)	99 (0.43)	1.16
12-03	Gp4 Focus 1	g.chr10:82185747C>T	Silent	FAM213A	p.I132I	family with sequence si	58 (0.00)	43 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr10:120889053G>A	Missense Mutation	FAM45A	p.E241K	family with sequence si	18 (0.00)	26 (0.54)	1.44
12-03	Gp4 Focus 1	g.chr9:97873814C>A	Silent	FANCC	p.T420T	Fanconi anemia, comple	46 (0.00)	136 (0.21)	0.69
12-03	Gp4 Focus 1	g.chr2:207655327T>C	Missense Mutation	FASTKD2	p.Y644H	FAST kinase domains 2	88 (0.00)	34 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr11:92087620G>T	Missense Mutation	FAT3	p.G631V	FAT atypical cadherin 3	38 (0.00)	38 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr9:97382637C>T	Missense Mutation	FBP1	p.A103T	fructose-1,6-bisphospha	30 (0.00)	38 (0.18)	0.62
12-03	Gp4 Focus 1	g.chr8:28340939T>G	Missense Mutation	FBXO16	p.N9H	F-box protein 16	26 (0.00)	27 (0.52)	1.38
12-03	Gp4 Focus 1	g.chr5:171326957G>A	Missense Mutation	FBXW11	p.T161I	F-box and WD repeat d	76 (0.00)	59 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr3:48421044C>T	Missense Mutation	FBXW12	p.P100L	F-box and WD repeat d	58 (0.00)	118 (0.75)	2.50
12-03	Gp4 Focus 1	g.chr11:72600965C>A	Missense Mutation	FCHSD2	p.G181V	FCH and double SH3 d	24 (0.00)	38 (0.32)	1.13
12-03	Gp4 Focus 1	g.chr9:95780479C>A	Missense Mutation	FGD3	p.S446Y	FYVE, RhoGEF and P	51 (0.00)	42 (0.17)	0.56
12-03	Gp4 Focus 1	g.chr11:65655135G>A	Missense Mutation	FIBP	p.T116I	fibroblast growth factor	141 (0.00)	288 (0.19)	0.66
12-03	Gp4 Focus 1	g.chr14:24601739C>A	Missense Mutation	FITM1	p.L196I	fat storage-inducing tra	15 (0.00)	104 (0.33)	0.63
12-03	Gp4 Focus 1	g.chr1:152276956G>C	Missense Mutation	FLG	p.S3469C	filaggrin	66 (0.00)	77 (0.88)	2.35
12-03	Gp4 Focus 1	g.chr1:152278970G>A	Nonsense Mutation	FLG	p.Q2798*	filaggrin	64 (0.00)	130 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr1:152279013C>T	Silent	FLG	p.Q2783Q	filaggrin	63 (0.00)	166 (0.14)	0.39
12-03	Gp4 Focus 1	g.chr1:152279701G>T	Nonsense Mutation	FLG	p.S2554*	filaggrin	37 (0.00)	28 (0.61)	1.62
12-03	Gp4 Focus 1	g.chr1:152281235G>A	Nonsense Mutation	FLG	p.Q2043*	filaggrin	24 (0.00)	39 (0.54)	1.44
12-03	Gp4 Focus 1	g.chr1:152282690C>A	Missense Mutation	FLG	p.G1558W	filaggrin	90 (0.00)	135 (0.45)	1.20
12-03	Gp4 Focus 1	g.chr1:152284551C>T	Silent	FLG	p.R937R	filaggrin	25 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr1:152285771G>T	Missense Mutation	FLG	p.H531N	filaggrin	102 (0.00)	186 (0.23)	0.60
12-03	Gp4 Focus 1	g.chr1:152286362T>A	Nonsense Mutation	FLG	p.R334*	filaggrin	81 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr11:128680806G>A	Missense Mutation	FLI1	p.G235R	Fli-1 proto-oncogene, E	136 (0.00)	42 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr7:128481553G>T	Missense Mutation	FLNC	p.D685Y	filamin C, gamma	64 (0.00)	200 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr2:153471419G>T	Missense Mutation	FMNL2	p.D373Y	formin-like 2	70 (0.00)	44 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr1:171079979G>A	Missense Mutation	FMO3	p.R223Q	flavin containing monoc	28 (0.00)	12 (0.75)	2.00
12-03	Gp4 Focus 1	g.chr9:132740819G>T	Silent	FNBP1	p.I90I	formin binding protein 1	22 (0.00)	50 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr16:86612605C>A	Silent	FOXL1	p.G92G	forkhead box L1	16 (0.00)	254 (0.12)	0.39

12-03	Gp4 Focus 1	g.chr4:79455636C>A	Missense Mutation	FRAS1	p.N3653K	Fraser extracellular mat	83 (0.00)	29 (0.62)	1.66
12-03	Gp4 Focus 1	g.chr9:14824824G>A	Missense Mutation	FREM1	p.T683I	FRAS1 related extracell	39 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr14:44975381C>A	Missense Mutation	FSCB	p.Q270H	fibrous sheath CABYR	29 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr2:186665487C>A	Nonsense Mutation	FSIP2	p.Y3818*	fibrous sheath interactin	41 (0.00)	21 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr2:84518109G>T	RNA	FUNDC2P2		FUN14 domain containi	57 (0.00)	143 (0.31)	0.82
12-03	Gp4 Focus 1	g.chr5:151176938T>A	Missense Mutation	G3BP1	p.S230R	GTPase activating prote	28 (0.00)	13 (0.38)	1.03
12-03	Gp4 Focus 1	g.chrX:49355887G>T	Nonsense Mutation	GAGE2A	p.E57*	G antigen 2A	93 (0.00)	67 (0.58)	0.74
12-03	Gp4 Focus 1	g.chr7:99758258G>T	Missense Mutation	GAL3ST4	p.Q252K	galactose-3-O-sulfotran	48 (0.00)	84 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr14:88414128G>A	Missense Mutation	GALC	p.P478L	galactosylceramidase	23 (0.00)	22 (0.36)	0.97
12-03	Gp4 Focus 1	g.chr14:88414134C>G	Missense Mutation	GALC	p.S476T	galactosylceramidase	23 (0.00)	21 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr9:35741680G>T	Missense Mutation	GBA2	p.H259N	glucosidase, beta (bile a	103 (0.00)	53 (0.70)	1.86
12-03	Gp4 Focus 1	g.chr4:22749311G>T	RNA	GBA3		glucosidase, beta, acid 3	115 (0.00)	19 (0.47)	1.26
12-03	Gp4 Focus 1	g.chr6:10874765G>A	Silent	GCM2	p.N328N	glial cells missing homo	60 (0.00)	27 (0.41)	1.09
12-03	Gp4 Focus 1	g.chr6:10874855G>C	Missense Mutation	GCM2	p.I298M	glial cells missing homo	138 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr12:120602254C>G	Missense Mutation	GCN1L1	p.W578C	GCN1 general control o	19 (0.00)	127 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr12:7843151C>A	Nonsense Mutation	GDF3	p.G140*	growth differentiation f	29 (0.00)	20 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr11:76982220G>A	Missense Mutation	GDPD4	p.L119F	glycerophosphodiester	39 (0.00)	61 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr11:76982232C>G	Missense Mutation	GDPD4	p.V115L	glycerophosphodiester	38 (0.00)	64 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr11:76982245C>G	Silent	GDPD4	p.L110L	glycerophosphodiester	36 (0.00)	65 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr2:233613701C>A	Missense Mutation	GIGYF2	p.P59H	GRB10 interacting GY	64 (0.00)	47 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr7:150325230C>A	Silent	GIMAP6	p.V152V	GTPase, IMAP family	23 (0.00)	61 (0.36)	1.35
12-03	Gp4 Focus 1	g.chr1:35250424G>A	Missense Mutation	GJB3	p.G21R	gap junction protein, be	39 (0.00)	115 (0.21)	0.69
12-03	Gp4 Focus 1	g.chr7:99526772G>A	Silent	GJC3	p.L158L	gap junction protein, ga	27 (0.00)	39 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr4:80328975C>T	Missense Mutation	GK2	p.S127N	glycerol kinase 2	55 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr11:134243635C>A	Missense Mutation	GLB1L2	p.L510M	galactosidase, beta 1-lik	52 (0.00)	236 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr11:134243637G>A	Silent	GLB1L2	p.L510L	galactosidase, beta 1-lik	52 (0.00)	236 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr3:52325877T>C	Missense Mutation	GLYCTK	p.I131T	glycerate kinase	19 (0.00)	71 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr6:16254845G>A	Missense Mutation	GMPR	p.S115N	guanosine monophosph	46 (0.00)	15 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr6:16290798G>T	Missense Mutation	GMPR	p.G268V	guanosine monophosph	65 (0.00)	10 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr15:30906722G>C	Silent	GOLGA8H	p.V619V	golgin A8 family, mem	44 (0.00)	82 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr1:155724239G>C	Missense Mutation	GON4L	p.S1853C	gon-4-like (C. elegans)	141 (0.00)	98 (0.36)	0.71
12-03	Gp4 Focus 1	g.chr2:171806120T>A	Nonsense Mutation	GORASP2	p.Y72*	golgi reassembly stacki	24 (0.00)	24 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr3:194118732A>T	Missense Mutation	GP5	p.F94I	glycoprotein V (platelet	27 (0.00)	114 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr1:217671729A>C	Missense Mutation	GPATCH2	p.F392C	G patch domain contain	43 (0.00)	101 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr1:27223868T>C	Missense Mutation	GPATCH3	p.D267G	G patch domain contain	47 (0.00)	38 (0.18)	0.65

12-03	Gp4 Focus 1	g.chr1:46099767C>A	Splice Site	GPBP1L1		GC-rich promoter bindi	22 (0.00)	13 (0.38)	1.03
12-03	Gp4 Focus 1	g.chr3:154145383G>A	Missense Mutation	GPR149	p.R366C	G protein-coupled recep	18 (0.00)	83 (0.14)	0.39
12-03	Gp4 Focus 1	g.chr10:25885654C>T	Missense Mutation	GPR158	p.S694F	G protein-coupled recep	15 (0.00)	12 (0.58)	1.56
12-03	Gp4 Focus 1	g.chr1:168054913C>A	Missense Mutation	GPR161	p.E350D	G protein-coupled recep	96 (0.00)	185 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr17:36483720G>A	Missense Mutation	GPR179	p.T1911I	G protein-coupled recep	51 (0.00)	31 (0.84)	2.93
12-03	Gp4 Focus 1	g.chr17:36484024C>A	Missense Mutation	GPR179	p.A1810S	G protein-coupled recep	83 (0.00)	115 (0.32)	1.12
12-03	Gp4 Focus 1	g.chr1:202092242G>C	Missense Mutation	GPR37L1	p.E51Q	G protein-coupled recep	16 (0.00)	46 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr5:89931108G>A	Splice Site	GPR98		G protein-coupled recep	36 (0.00)	28 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr17:7217019C>A	Missense Mutation	GPS2	p.A168S	G protein pathway supp	99 (0.00)	35 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr16:9927968C>G	Missense Mutation	GRIN2A	p.G591R	glutamate receptor, iono	55 (0.00)	51 (0.47)	1.25
12-03	Gp4 Focus 1	g.chr12:13717335C>T	Missense Mutation	GRIN2B	p.C946Y	glutamate receptor, iono	27 (0.00)	46 (0.30)	0.81
12-03	Gp4 Focus 1	g.chr12:66838487C>T	Missense Mutation	GRIP1	p.D470N	glutamate receptor inter	18 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr7:86394687A>G	Missense Mutation	GRM3	p.I76V	glutamate receptor, meta	32 (0.00)	22 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr3:7188256G>T	Missense Mutation	GRM7	p.V213L	glutamate receptor, meta	20 (0.00)	59 (0.71)	1.90
12-03	Gp4 Focus 1	g.chr4:71698039C>A	Missense Mutation	GRSF1	p.V105L	G-rich RNA sequence b	44 (0.00)	20 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr1:110282087C>A	Silent	GSTM3	p.L51L	glutathione S-transferas	58 (0.00)	162 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr7:65432717C>T	Splice Site	GUSB		glucuronidase, beta	33 (0.00)	56 (0.14)	0.54
12-03	Gp4 Focus 1	g.chr6:26867283C>T	RNA	GUSBP2		glucuronidase, beta pseu	16 (0.00)	172 (0.22)	0.72
12-03	Gp4 Focus 1	g.chr12:21721851C>A	Silent	GYS2	p.T257T	glycogen synthase 2 (liv	57 (0.00)	34 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr12:21721944C>T	Splice Site	GYS2		glycogen synthase 2 (liv	22 (0.00)	29 (0.45)	1.20
12-03	Gp4 Focus 1	g.chr15:89424958T>A	Splice Site	HAPLN3		hyaluronan and proteogl	24 (0.00)	36 (0.39)	1.04
12-03	Gp4 Focus 1	g.chr7:18593249C>A	Intron	HDAC9		histone deacetylase 9	23 (0.00)	17 (0.53)	1.41
12-03	Gp4 Focus 1	g.chr7:18598347C>T	Intron	HDAC9		histone deacetylase 9	32 (0.00)	71 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr7:18671041T>C	Intron	HDAC9		histone deacetylase 9	36 (0.00)	21 (0.48)	1.27
12-03	Gp4 Focus 1	g.chr7:18750234C>A	Intron	HDAC9		histone deacetylase 9	58 (0.00)	55 (0.67)	1.79
12-03	Gp4 Focus 1	g.chr7:18794308C>G	Intron	HDAC9		histone deacetylase 9	16 (0.00)	47 (0.45)	1.19
12-03	Gp4 Focus 1	g.chr7:18809306T>A	Intron	HDAC9		histone deacetylase 9	19 (0.00)	17 (0.47)	1.25
12-03	Gp4 Focus 1	g.chr7:18920810A>T	Intron	HDAC9		histone deacetylase 9	90 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr7:18979385C>A	Intron	HDAC9		histone deacetylase 9	21 (0.00)	35 (0.74)	1.98
12-03	Gp4 Focus 1	g.chr15:91474538C>T	Silent	HDDC3	p.K169K	HD domain containing	36 (0.00)	137 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr2:242173294G>T	Missense Mutation	HDLBP	p.Q1077K	high density lipoprotein	28 (0.00)	31 (0.29)	0.77
12-03	Gp4 Focus 1	g.chr14:31785131C>T	Missense Mutation	HEATR5A	p.G1355R	HEAT repeat containing	44 (0.00)	26 (0.58)	1.54
12-03	Gp4 Focus 1	g.chr14:31597825G>A	Silent	HECTD1	p.S1584S	HECT domain containir	33 (0.00)	30 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr12:66725034A>T	Missense Mutation	HELB	p.Y924F	helicase (DNA) B	16 (0.00)	12 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr1:109192975A>T	Missense Mutation	HENMT1	p.V205E	HEN1 methyltransferas	15 (0.00)	11 (0.55)	1.45

12-03	Gp4 Focus 1	g.chr15:64045275C>T	Missense Mutation	HERC1	p.G595D	HECT and RLD domair	22 (0.00)	35 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr15:28544659C>T	Missense Mutation	HERC2	p.A26T	HECT and RLD domair	56 (0.00)	28 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr4:89311842C>A	Missense Mutation	HERC6	p.Q159K	HECT and RLD domair	112 (0.00)	39 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr3:42740618C>A	Missense Mutation	HHATL	p.W65L	hedgehog acyltransferas	50 (0.00)	13 (0.62)	1.64
12-03	Gp4 Focus 1	g.chr1:222717495C>T	Missense Mutation	HHIPL2	p.E120K	HHIP-like 2	77 (0.00)	22 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr16:30005829C>T	Missense Mutation	HIRIP3	p.G213R	HIRA interacting protei	67 (0.00)	46 (0.59)	2.02
12-03	Gp4 Focus 1	g.chr6:12122658A>T	Missense Mutation	HIVEP1	p.D877V	human immunodeficien	40 (0.00)	40 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr10:71158398G>T	Missense Mutation	HK1	p.G808V	hexokinase 1	22 (0.00)	23 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr1:185935017A>T	Missense Mutation	HMCN1	p.I728F	hemicentin 1	19 (0.00)	14 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr4:174254252C>T	Silent	HMGB2	p.K88K	high mobility group box	86 (0.00)	69 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr20:43048382G>A	Missense Mutation	HNF4A	p.R253Q	hepatocyte nuclear facto	42 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr19:41810159C>G	Missense Mutation	HNRNPUL1	p.P752R	heterogeneous nuclear r	42 (0.00)	110 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr1:152191859G>C	Missense Mutation	HRNR	p.S749C	hornerin	56 (0.00)	245 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr16:83842296C>A	Silent	HSBP1	p.L19L	heat shock factor bindin	54 (0.00)	92 (0.30)	0.81
12-03	Gp4 Focus 1	g.chr5:63257006G>A	Missense Mutation	HTR1A	p.R181C	5-hydroxytryptamine (s	58 (0.00)	99 (0.30)	0.45
12-03	Gp4 Focus 1	g.chr6:87725250G>T	Silent	HTR1E	p.V66V	5-hydroxytryptamine (s	44 (0.00)	16 (0.56)	0.66
12-03	Gp4 Focus 1	g.chr4:3131750G>T	Nonsense Mutation	HTT	p.E615*	huntingtin	54 (0.00)	35 (0.37)	0.99
12-03	Gp4 Focus 1	g.chr7:123509039C>T	Missense Mutation	HYAL4	p.P238S	hyaluronoglucosaminid	51 (0.00)	11 (0.45)	1.21
12-03	Gp4 Focus 1	g.chr9:95027762C>A	Splice Site	IARS	p.S502I	isoleucyl-tRNA synthet	59 (0.00)	36 (0.22)	0.74
12-03	Gp4 Focus 1	g.chr19:10445026C>A	Silent	ICAM3	p.T417T	intercellular adhesion m	24 (0.00)	197 (0.12)	0.43
12-03	Gp4 Focus 1	g.chr21:45656927C>G	Missense Mutation	ICOSLG	p.D77H	inducible T-cell co-stim	29 (0.00)	71 (0.34)	1.29
12-03	Gp4 Focus 1	g.chr8:39785369C>A	Missense Mutation	IDO1	p.Q293K	indoleamine 2,3-dioxyg	36 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 1	g.chr2:27672588G>A	Missense Mutation	IFT172	p.A1377V	intraflagellar transport 1	40 (0.00)	12 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr17:26658941G>A	Missense Mutation	IFT20	p.P24L	intraflagellar transport 2	15 (0.00)	10 (0.70)	1.87
12-03	Gp4 Focus 1	g.chr15:99456489G>A	Silent	IGF1R	p.L602L	insulin-like growth facto	37 (0.00)	18 (0.39)	1.04
12-03	Gp4 Focus 1	g.chr14:106208090C>A	RNA	IGHG1		immunoglobulin heavy	28 (0.00)	195 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr14:106235613G>A	RNA	IGHG3		immunoglobulin heavy	25 (0.00)	170 (0.34)	0.91
12-03	Gp4 Focus 1	g.chr15:20169986C>T	RNA	IGHV1OR15-9		immunoglobulin heavy	30 (0.00)	45 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr14:107113965C>T	RNA	IGHV3-64		immunoglobulin heavy	33 (0.00)	135 (0.29)	0.77
12-03	Gp4 Focus 1	g.chr22:22556511G>A	RNA	IGLV11-55		immunoglobulin lambda	31 (0.00)	27 (0.22)	0.75
12-03	Gp4 Focus 1	g.chr10:124753940C>T	Missense Mutation	IKZF5	p.V206I	IKAROS family zinc fir	63 (0.00)	34 (0.71)	1.88
12-03	Gp4 Focus 1	g.chr15:81592159G>A	Missense Mutation	IL16	p.R831Q	interleukin 16	44 (0.00)	74 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr3:190373908G>T	Nonsense Mutation	IL1RAP	p.G526*	interleukin 1 receptor ac	42 (0.00)	12 (0.75)	2.00
12-03	Gp4 Focus 1	g.chr5:55237528C>T	Silent	IL6ST	p.L713L	interleukin 6 signal tran	53 (0.00)	22 (0.82)	1.20
12-03	Gp4 Focus 1	g.chr1:153640086C>T	Missense Mutation	ILF2	p.M113I	interleukin enhancer bin	137 (0.00)	19 (0.74)	1.96

12-03	Gp4 Focus 1	g.chr19:15227298C>A	Missense Mutation	ILVBL	p.G408C	ilvB (bacterial acetolact	28 (0.00)	223 (0.13)	0.48
12-03	Gp4 Focus 1	g.chr2:131102245C>T	Silent	IMP4	p.A52A	IMP4, U3 small nucleol	31 (0.00)	17 (0.29)	1.05
12-03	Gp4 Focus 1	g.chr3:100949923C>A	Silent	IMPG2	p.V1100V	interphotoreceptor matri	40 (0.00)	28 (0.25)	0.47
12-03	Gp4 Focus 1	g.chr4:142978119C>A	Intron	INPP4B		inositol polyphosphate-4	66 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr4:143123959C>A	Intron	INPP4B		inositol polyphosphate-4	16 (0.00)	13 (0.77)	2.05
12-03	Gp4 Focus 1	g.chr4:143134383T>C	Intron	INPP4B		inositol polyphosphate-4	160 (0.00)	96 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr4:143160330G>A	Intron	INPP4B		inositol polyphosphate-4	47 (0.00)	21 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr4:143277264C>A	Intron	INPP4B		inositol polyphosphate-4	25 (0.00)	21 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr4:143293768C>A	Intron	INPP4B		inositol polyphosphate-4	132 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr4:143322271C>T	Intron	INPP4B		inositol polyphosphate-4	50 (0.02)	136 (0.97)	2.59
12-03	Gp4 Focus 1	g.chr4:143344458G>A	Intron	INPP4B		inositol polyphosphate-4	57 (0.00)	28 (0.79)	2.10
12-03	Gp4 Focus 1	g.chr4:143393538C>T	Intron	INPP4B		inositol polyphosphate-4	70 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr4:143501079G>A	Intron	INPP4B		inositol polyphosphate-4	30 (0.00)	19 (0.53)	1.40
12-03	Gp4 Focus 1	g.chr4:143639464C>T	Intron	INPP4B		inositol polyphosphate-4	67 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr4:143705235G>T	Intron	INPP4B		inositol polyphosphate-4	44 (0.00)	19 (0.58)	1.54
12-03	Gp4 Focus 1	g.chr4:143733226C>T	Intron	INPP4B		inositol polyphosphate-4	44 (0.00)	35 (0.63)	1.68
12-03	Gp4 Focus 1	g.chr8:19688022G>A	Missense Mutation	INTS10	p.A416T	integrator complex subu	31 (0.00)	12 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr9:103055230G>A	Silent	INVS	p.E897E	inversin	17 (0.00)	27 (0.63)	1.68
12-03	Gp4 Focus 1	g.chr1:201845101T>A	Missense Mutation	IPO9	p.F1015L	importin 9	24 (0.00)	21 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr1:32672130C>T	Silent	IQCC	p.T69T	IQ motif containing C	42 (0.00)	48 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr7:2629540G>A	Splice Site	IQCE		IQ motif containing E	24 (0.00)	193 (0.16)	0.59
12-03	Gp4 Focus 1	g.chr3:51937085C>T	Silent	IQCF1	p.K8K	IQ motif containing F1	49 (0.02)	18 (0.83)	2.22
12-03	Gp4 Focus 1	g.chr3:159605525G>A	Missense Mutation	IQCJ-SCHIP1	p.R302K	IQCJ-SCHIP1 readthrou	17 (0.00)	41 (0.54)	1.43
12-03	Gp4 Focus 1	g.chr3:12978055C>A	Missense Mutation	IQSEC1	p.R168L	IQ motif and Sec7 doma	24 (0.00)	91 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr15:74467808G>A	Silent	ISLR	p.P203P	immunoglobulin superfa	16 (0.00)	101 (0.46)	0.70
12-03	Gp4 Focus 1	g.chr2:182358067C>G	Missense Mutation	ITGA4	p.A390G	integrin, alpha 4 (antige	26 (0.00)	17 (0.65)	1.73
12-03	Gp4 Focus 1	g.chr17:3632827C>A	Missense Mutation	ITGAE	p.A953S	integrin, alpha E (antige	74 (0.00)	41 (0.39)	1.04
12-03	Gp4 Focus 1	g.chr3:4703770G>A	Missense Mutation	ITPR1	p.G404D	inositol 1,4,5-trisphosph	34 (0.00)	15 (0.73)	1.96
12-03	Gp4 Focus 1	g.chr12:26834927G>A	Missense Mutation	ITPR2	p.A430V	inositol 1,4,5-trisphosph	49 (0.00)	18 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr17:39919444T>A	Missense Mutation	JUP	p.T430S	junction plakoglobin	33 (0.00)	141 (0.14)	0.50
12-03	Gp4 Focus 1	g.chr1:62739133G>A	Missense Mutation	KANK4	p.P548L	KN motif and ankyrin r	20 (0.00)	178 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr2:210908705C>G	Missense Mutation	KANSL1L	p.E627Q	KAT8 regulatory NSL c	15 (0.00)	21 (0.52)	1.40
12-03	Gp4 Focus 1	g.chr12:5021316G>A	Missense Mutation	KCNA1	p.D258N	potassium voltage-gated	75 (0.01)	135 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr12:5021732T>C	Silent	KCNA1	p.G396G	potassium voltage-gated	144 (0.00)	23 (0.65)	1.74
12-03	Gp4 Focus 1	g.chr3:156175287C>T	Missense Mutation	KCNAB1	p.L117F	potassium voltage-gated	16 (0.00)	42 (0.98)	2.60

12-03	Gp4 Focus 1	g.chr12:49937847G>A	Missense Mutation	KCNH3	p.V325I	potassium voltage-gated	16 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr17:68172233C>T	Silent	KCNJ2	p.P351P	potassium inwardly-rect	67 (0.00)	21 (0.90)	2.41
12-03	Gp4 Focus 1	g.chr6:39271757C>G	Missense Mutation	KCNK17	p.V222L	potassium channel, subf	33 (0.00)	290 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr20:62073854G>A	Missense Mutation	KCNQ2	p.L241F	potassium voltage-gated	43 (0.00)	493 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr7:128530321C>G	RNA	KCP		kielin/chordin-like prote	22 (0.00)	43 (0.35)	0.93
12-03	Gp4 Focus 1	g.chr22:37455385C>A	Silent	KCTD17	p.G180G	potassium channel tetra	25 (0.00)	222 (0.14)	0.47
12-03	Gp4 Focus 1	g.chr11:94731479G>A	Missense Mutation	KDM4D	p.A315T	lysine (K)-specific dem	19 (0.00)	36 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr4:55971030C>A	Missense Mutation	KDR	p.Q589H	kinase insert domain rec	46 (0.00)	56 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr14:24900756G>T	Missense Mutation	KHNYN	p.G97C	KH and NYN domain c	41 (0.00)	186 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr17:26950898G>T	Silent	KIAA0100	p.A1613A	KIAA0100	85 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr15:64673232C>A	Missense Mutation	KIAA0101	p.A18S	KIAA0101	33 (0.00)	83 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr6:24576729C>A	Missense Mutation	KIAA0319	p.G534V	KIAA0319	56 (0.00)	150 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr19:34791840G>A	Silent	KIAA0355	p.T154T	KIAA0355	50 (0.00)	38 (0.21)	0.77
12-03	Gp4 Focus 1	g.chr4:123274126C>T	Silent	KIAA1109	p.S4639S	KIAA1109	55 (0.00)	56 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr15:81214425G>A	Missense Mutation	KIAA1199	p.E717K		66 (0.00)	12 (0.92)	2.44
12-03	Gp4 Focus 1	g.chr9:5763412T>C	Silent	KIAA1432	p.T795T		84 (0.00)	60 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr10:30316246G>T	Missense Mutation	KIAA1462	p.P944H	KIAA1462	27 (0.00)	148 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr10:30317100T>C	Silent	KIAA1462	p.R659R	KIAA1462	24 (0.00)	33 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr9:115337178C>A	Missense Mutation	KIAA1958	p.P273H	KIAA1958	65 (0.00)	45 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr9:115422252T>C	Missense Mutation	KIAA1958	p.L685S	KIAA1958	33 (0.00)	54 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr8:29018297G>A	Silent	KIF13B	p.L453L	kinesin family member	25 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr16:29810762C>A	Missense Mutation	KIF22	p.Q245K	kinesin family member	27 (0.00)	42 (0.24)	0.82
12-03	Gp4 Focus 1	g.chr6:168430296G>C	Missense Mutation	KIF25	p.E11Q	kinesin family member	24 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr1:18808178G>A	Missense Mutation	KLHDC7A	p.E235K	kelch domain containin	17 (0.00)	178 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr17:40004382G>T	Missense Mutation	KLHL10	p.K550N	kelch-like family memb	85 (0.00)	139 (0.14)	0.48
12-03	Gp4 Focus 1	g.chr8:124659190G>A	Missense Mutation	KLHL38	p.A472V	kelch-like family memb	18 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr1:152732461G>A	Missense Mutation	KPRP	p.V133I	keratinocyte proline-ric	61 (0.00)	50 (0.34)	0.91
12-03	Gp4 Focus 1	g.chr17:39635959G>A	Silent	KRT35	p.F152F	keratin 35	69 (0.00)	33 (0.27)	0.96
12-03	Gp4 Focus 1	g.chr12:53207575C>A	Missense Mutation	KRT4	p.G90W	keratin 4	31 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr12:53001984C>T	Missense Mutation	KRT73	p.R540K	keratin 73	18 (0.00)	14 (0.64)	1.71
12-03	Gp4 Focus 1	g.chr12:52774911G>A	Missense Mutation	KRT84	p.R386C	keratin 84	54 (0.00)	46 (0.61)	1.62
12-03	Gp4 Focus 1	g.chr17:39323867G>T	Missense Mutation	KRTAP4-3	p.H186Q	keratin associated protei	19 (0.00)	107 (0.24)	0.85
12-03	Gp4 Focus 1	g.chr11:1606289C>T	Missense Mutation	KRTAP5-1	p.C64Y	keratin associated protei	19 (0.00)	183 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr11:71276671G>T	Missense Mutation	KRTAP5-10	p.G13V	keratin associated protei	30 (0.00)	537 (0.14)	0.49
12-03	Gp4 Focus 1	g.chr11:71276674G>T	Missense Mutation	KRTAP5-10	p.C14F	keratin associated protei	30 (0.00)	546 (0.14)	0.50

12-03	Gp4 Focus 1	g.chr11:1642759A>G	Missense Mutation	KRTAP5-4	p.C189R	keratin associated protei	19 (0.00)	209 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr17:39431995A>T	Missense Mutation	KRTAP9-7	p.T16S	keratin associated protei	21 (0.00)	50 (0.12)	0.42
12-03	Gp4 Focus 1	g.chr3:49160275C>T	Missense Mutation	LAMB2	p.E1479K	laminin, beta 2 (laminin	15 (0.00)	46 (0.37)	0.99
12-03	Gp4 Focus 1	g.chr3:49169590C>T	Missense Mutation	LAMB2	p.E140K	laminin, beta 2 (laminin	24 (0.00)	112 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr16:67973926G>C	Missense Mutation	LCAT	p.L402V	lecithin-cholesterol acyl	18 (0.00)	162 (0.16)	0.55
12-03	Gp4 Focus 1	g.chr1:152749133T>A	Missense Mutation	LCE1F	p.C96S	late cornified envelope	16 (0.00)	45 (0.16)	0.41
12-03	Gp4 Focus 1	g.chr16:25162893C>T	Silent	LCMT1	p.S141S	leucine carboxyl methyl	34 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr2:48950801C>G	Missense Mutation	LHCGR	p.D140H	luteinizing hormone/chc	51 (0.00)	20 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr19:54758798G>A	Missense Mutation	LILRB5	p.T352I	leukocyte immunoglobu	25 (0.00)	62 (0.16)	0.58
12-03	Gp4 Focus 1	g.chr12:127229479T>G	lincRNA	LINC00943		long intergenic non-prot	53 (0.00)	13 (0.62)	1.64
12-03	Gp4 Focus 1	g.chr12:49494414G>A	Silent	LMBR1L	p.S366S	limb development meml	34 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr12:49496292C>A	Missense Mutation	LMBR1L	p.C243F	limb development meml	94 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr8:12595506G>A	Nonsense Mutation	LONRF1	p.Q371*	LON peptidase N-termi	23 (0.00)	15 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr6:160969557G>A	Missense Mutation	LPA	p.P1703L	lipoprotein, Lp(a)	52 (0.00)	33 (0.64)	1.70
12-03	Gp4 Focus 1	g.chr4:62758537G>A	Missense Mutation	LPHN3	p.M480I	latrophilin 3	16 (0.00)	91 (0.34)	0.91
12-03	Gp4 Focus 1	g.chr3:197598227C>T	Missense Mutation	LRCH3	p.P675L	leucine-rich repeats and	56 (0.00)	32 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr1:113657309C>A	Missense Mutation	LRIG2	p.L781I	leucine-rich repeats and	22 (0.00)	18 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr10:134161600G>C	Silent	LRRC27	p.G222G	leucine rich repeat conta	15 (0.00)	55 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr16:67401226G>T	Missense Mutation	LRRC36	p.S233I	leucine rich repeat conta	80 (0.00)	130 (0.12)	0.42
12-03	Gp4 Focus 1	g.chr17:30349165G>A	Missense Mutation	LRRC37B	p.A252T	leucine rich repeat conta	17 (0.00)	25 (0.48)	1.28
12-03	Gp4 Focus 1	g.chr1:156902658C>T	Missense Mutation	LRRC71	p.A526V	leucine rich repeat conta	38 (0.00)	44 (0.55)	1.08
12-03	Gp4 Focus 1	g.chr15:101569273G>T	Missense Mutation	LRRK1	p.R933S	leucine-rich repeat kinas	34 (0.00)	26 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr9:130243480G>A	Silent	LRSAM1	p.E354E	leucine rich repeat and s	21 (0.00)	39 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr7:77656655G>A	Intron	MAGI2		membrane associated gu	17 (0.00)	19 (0.58)	0.94
12-03	Gp4 Focus 1	g.chr7:77676744T>C	Intron	MAGI2		membrane associated gu	34 (0.00)	8 (0.75)	1.22
12-03	Gp4 Focus 1	g.chr7:77733821G>A	Intron	MAGI2		membrane associated gu	59 (0.00)	174 (0.35)	0.57
12-03	Gp4 Focus 1	g.chr7:77850135T>A	Intron	MAGI2		membrane associated gu	34 (0.00)	25 (0.36)	0.58
12-03	Gp4 Focus 1	g.chr7:77850562C>A	Intron	MAGI2		membrane associated gu	51 (0.00)	23 (0.26)	0.42
12-03	Gp4 Focus 1	g.chr7:77892267G>A	Intron	MAGI2		membrane associated gu	29 (0.00)	27 (0.74)	1.20
12-03	Gp4 Focus 1	g.chr7:77909529C>G	Intron	MAGI2		membrane associated gu	81 (0.00)	18 (0.33)	0.54
12-03	Gp4 Focus 1	g.chr7:78071066G>A	Intron	MAGI2		membrane associated gu	54 (0.00)	14 (0.43)	0.70
12-03	Gp4 Focus 1	g.chr7:78175397C>T	Intron	MAGI2		membrane associated gu	36 (0.00)	26 (0.31)	0.50
12-03	Gp4 Focus 1	g.chr7:78222826G>A	Intron	MAGI2		membrane associated gu	74 (0.00)	74 (0.51)	0.83
12-03	Gp4 Focus 1	g.chr7:78267807C>T	Intron	MAGI2		membrane associated gu	46 (0.00)	13 (0.38)	0.62
12-03	Gp4 Focus 1	g.chr7:78320551G>T	Intron	MAGI2		membrane associated gu	74 (0.00)	37 (0.81)	1.32

12-03	Gp4 Focus 1	g.chr7:78330881G>C	Intron	MAGI2		membrane associated gu	72 (0.00)	19 (0.32)	0.51
12-03	Gp4 Focus 1	g.chr7:78347325C>T	Intron	MAGI2		membrane associated gu	54 (0.00)	18 (0.33)	0.54
12-03	Gp4 Focus 1	g.chr7:78358257T>A	Intron	MAGI2		membrane associated gu	24 (0.00)	28 (0.57)	0.93
12-03	Gp4 Focus 1	g.chr7:78394117C>T	Intron	MAGI2		membrane associated gu	72 (0.00)	28 (0.32)	0.52
12-03	Gp4 Focus 1	g.chr7:78452926G>T	Intron	MAGI2		membrane associated gu	33 (0.00)	16 (0.69)	1.12
12-03	Gp4 Focus 1	g.chr7:78576569C>A	Intron	MAGI2		membrane associated gu	64 (0.00)	51 (0.84)	1.37
12-03	Gp4 Focus 1	g.chr7:78623290C>T	Intron	MAGI2		membrane associated gu	51 (0.00)	58 (0.62)	1.01
12-03	Gp4 Focus 1	g.chr7:78632469C>T	Intron	MAGI2		membrane associated gu	29 (0.00)	24 (0.25)	0.41
12-03	Gp4 Focus 1	g.chr7:78744128G>A	Intron	MAGI2		membrane associated gu	83 (0.00)	21 (0.71)	1.16
12-03	Gp4 Focus 1	g.chr7:78907790C>A	Intron	MAGI2		membrane associated gu	85 (0.00)	31 (0.48)	0.79
12-03	Gp4 Focus 1	g.chr7:78929586G>A	Intron	MAGI2		membrane associated gu	56 (0.00)	26 (0.38)	0.62
12-03	Gp4 Focus 1	g.chr7:79007288C>A	Intron	MAGI2		membrane associated gu	57 (0.02)	16 (0.38)	0.61
12-03	Gp4 Focus 1	g.chr1:26109087A>G	Silent	MAN1C1	p.K554K	mannosidase, alpha, cla	49 (0.00)	41 (0.54)	1.43
12-03	Gp4 Focus 1	g.chr2:210574820C>G	Missense Mutation	MAP2	p.P1639A	microtubule-associated	36 (0.00)	41 (0.68)	1.82
12-03	Gp4 Focus 1	g.chr12:53875875G>A	Silent	MAP3K12	p.S810S	mitogen-activated protei	126 (0.00)	202 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr2:128065234A>G	Missense Mutation	MAP3K2	p.L594P	mitogen-activated protei	52 (0.00)	63 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr2:102493508G>T	Silent	MAP4K4	p.L865L	mitogen-activated protei	120 (0.00)	21 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr10:49618192C>T	Missense Mutation	MAPK8	p.S144F	mitogen-activated protei	90 (0.00)	14 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr11:45926046G>T	Silent	MAPK8IP1	p.V559V	mitogen-activated protei	32 (0.00)	114 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr19:8491618C>T	Missense Mutation	MARCH2	p.S101F	membrane-associated ri	24 (0.00)	110 (0.22)	0.83
12-03	Gp4 Focus 1	g.chr2:160605253C>T	Silent	MARCH7	p.F446F	membrane-associated ri	87 (0.00)	99 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr12:57906703G>C	Missense Mutation	MARS	p.K641N	methionyl-tRNA synthe	78 (0.00)	71 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr2:198571547T>C	Missense Mutation	MARS2	p.L473P	methionyl-tRNA synthe	47 (0.02)	24 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr10:27462169G>T	Silent	MASTL	p.L749L	microtubule associated	56 (0.00)	16 (0.56)	1.50
12-03	Gp4 Focus 1	g.chr2:149227461C>G	Missense Mutation	MBD5	p.S650C	methyl-CpG binding do	86 (0.00)	20 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr8:48874231C>T	Missense Mutation	MCM4	p.H76Y	minichromosome maint	36 (0.00)	196 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr17:60043897G>C	Missense Mutation	MED13	p.S1436C	mediator complex subu	22 (0.00)	36 (0.14)	0.50
12-03	Gp4 Focus 1	g.chr22:42112059C>T	Silent	MEI1	p.P146P	meiosis inhibitor 1	71 (0.00)	93 (0.44)	1.48
12-03	Gp4 Focus 1	g.chr18:29793225C>A	Missense Mutation	MEP1B	p.P428T	meprin A, beta	30 (0.00)	108 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr7:116435748G>T	Nonsense Mutation	MET	p.G1298*	MET proto-oncogene, r	58 (0.00)	52 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr14:21969941A>T	Nonsense Mutation	METTL3	p.C276*	methyltransferase like 3	35 (0.00)	19 (0.26)	0.51
12-03	Gp4 Focus 1	g.chr17:8701456G>A	Missense Mutation	MFSD6L	p.S328L	major facilitator superfa	24 (0.00)	101 (0.35)	0.92
12-03	Gp4 Focus 1	g.chr15:42058719G>C	Missense Mutation	MGA	p.M2813I	MGA, MAX dimerizati	16 (0.00)	34 (0.32)	0.86
12-03	Gp4 Focus 1	g.chr15:42058770T>A	Silent	MGA	p.I2830I	MGA, MAX dimerizati	16 (0.00)	18 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr22:39883477G>T	Missense Mutation	MGAT3	p.S42I	mannosyl (beta-1,4-)-gl	43 (0.00)	208 (0.13)	0.45

12-03	Gp4 Focus 1	g.chr10:103557825G>T	Silent	MGEA5	p.A632A	meningioma expressed	31 (0.00)	45 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr1:9211787G>T	RNA	MIR34A		microRNA 34a	115 (0.00)	259 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr10:99227308G>T	Silent	MMS19	p.L417L	MMS19 nucleotide exci	34 (0.03)	25 (0.56)	1.49
12-03	Gp4 Focus 1	g.chr14:93650183C>A	Missense Mutation	MOAP1	p.Q135H	modulator of apoptosis	31 (0.00)	51 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr12:62919843T>C	Missense Mutation	MON2	p.I454T	MON2 homolog (S. cer	45 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr10:99377032A>T	Missense Mutation	MORN4	p.Y39N	MORN repeat containin	61 (0.00)	27 (0.30)	0.79
12-03	Gp4 Focus 1	g.chr16:133110G>T	Missense Mutation	MPG	p.E125D	N-methylpurine-DNA g	21 (0.00)	93 (0.18)	0.64
12-03	Gp4 Focus 1	g.chr11:118107927G>A	Missense Mutation	MPZL3	p.R85W	myelin protein zero-like	79 (0.00)	15 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr5:41015568T>G	Missense Mutation	MROH2B	p.E966A	maestro heat-like repeat	33 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr20:35752035C>A	Silent	MROH8	p.V651V	maestro heat-like repeat	23 (0.00)	48 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr20:35752096C>A	Missense Mutation	MROH8	p.S631I	maestro heat-like repeat	29 (0.00)	57 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr1:38283131C>T	Silent	MTF1	p.K597K	metal-regulatory transcr	34 (0.00)	64 (0.42)	1.39
12-03	Gp4 Focus 1	g.chr1:11181417C>T	Silent	MTOR	p.P2273P	mechanistic target of ra	31 (0.00)	10 (0.70)	1.87
12-03	Gp4 Focus 1	g.chr1:155160711G>T	Silent	MUC1	p.L272L	mucin 1, cell surface ass	38 (0.00)	70 (0.36)	0.95
12-03	Gp4 Focus 1	g.chr19:9065791C>T	Missense Mutation	MUC16	p.E7219K	mucin 16, cell surface a	18 (0.00)	33 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr19:9073305C>T	Missense Mutation	MUC16	p.G4714E	mucin 16, cell surface a	70 (0.01)	18 (0.44)	1.19
12-03	Gp4 Focus 1	g.chr19:9083366G>A	Missense Mutation	MUC16	p.L2817F	mucin 16, cell surface a	32 (0.00)	42 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr19:9086956G>A	Missense Mutation	MUC16	p.T1620I	mucin 16, cell surface a	26 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr19:9088933G>C	Missense Mutation	MUC16	p.A961G	mucin 16, cell surface a	63 (0.00)	43 (0.49)	1.30
12-03	Gp4 Focus 1	g.chr19:9091090G>T	Missense Mutation	MUC16	p.P242H	mucin 16, cell surface a	52 (0.00)	66 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr7:100551962C>T	Missense Mutation	MUC3A	p.T238I	mucin 3A, cell surface a	220 (0.00)	49 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr11:1263688G>T	Nonsense Mutation	MUC5B	p.E1860*	mucin 5B, oligomeric m	21 (0.00)	184 (0.32)	0.84
12-03	Gp4 Focus 1	g.chr11:1018152G>A	Missense Mutation	MUC6	p.T1550I	mucin 6, oligomeric mu	146 (0.00)	32 (0.59)	1.58
12-03	Gp4 Focus 1	g.chr17:74673707C>T	Missense Mutation	MXRA7	p.G193D	matrix-remodelling asso	60 (0.00)	44 (0.11)	0.40
12-03	Gp4 Focus 1	g.chr8:67492521C>A	Missense Mutation	MYBL1	p.E316D	v-myb avian myeloblast	17 (0.00)	22 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr20:42331459C>A	Missense Mutation	MYBL2	p.S427R	v-myb avian myeloblast	19 (0.00)	31 (0.23)	0.60
12-03	Gp4 Focus 1	g.chr2:241069366G>T	Missense Mutation	MYEOV2	p.R115S	myeloma overexpressed	21 (0.00)	93 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr3:108216932G>A	Silent	MYH15	p.T215T	myosin, heavy chain 15	43 (0.00)	35 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr17:10369730C>T	Missense Mutation	MYH4	p.V70I	myosin, heavy chain 4,	17 (0.00)	29 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr14:23871723T>C	Missense Mutation	MYH6	p.K364R	myosin, heavy chain 6,	17 (0.00)	59 (0.20)	0.39
12-03	Gp4 Focus 1	g.chr14:23871750C>T	Missense Mutation	MYH6	p.G355E	myosin, heavy chain 6,	18 (0.00)	104 (0.23)	0.44
12-03	Gp4 Focus 1	g.chr17:45297317A>T	Missense Mutation	MYL4	p.M71L	myosin, light chain 4, al	36 (0.00)	41 (0.20)	0.70
12-03	Gp4 Focus 1	g.chr3:123452570C>T	Missense Mutation	MYLK	p.V425I	myosin light chain kina	31 (0.00)	31 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr16:46761162G>T	Missense Mutation	MYLK3	p.H293N	myosin light chain kina	25 (0.00)	25 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr17:27417925C>T	Missense Mutation	MYO18A	p.R1736H	myosin XVIIIA	66 (0.00)	21 (0.52)	1.73

12-03	Gp4 Focus 1	g.chr17:27438822C>T	Silent	MYO18A	p.E886E	myosin XVIIIA	40 (0.00)	60 (0.22)	0.72
12-03	Gp4 Focus 1	g.chr17:34854268C>G	Missense Mutation	MYO19	p.G867R	myosin XIX	59 (0.00)	80 (0.41)	1.44
12-03	Gp4 Focus 1	g.chr12:57441853G>T	Silent	MYO1A	p.P50P	myosin IA	46 (0.00)	19 (0.37)	0.98
12-03	Gp4 Focus 1	g.chr2:171264245G>A	Silent	MYO3B	p.G847G	myosin IIIB	115 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr18:3083883G>T	Missense Mutation	MYOM1	p.A1463D	myomesin 1	20 (0.00)	34 (0.85)	2.27
12-03	Gp4 Focus 1	g.chr8:2027652G>T	Nonsense Mutation	MYOM2	p.E492*	myomesin 2	66 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 1	g.chr16:5081798G>T	Missense Mutation	NAGPA	p.S210R	N-acetylglucosamine-1-	176 (0.00)	127 (0.13)	0.44
12-03	Gp4 Focus 1	g.chr11:34153768G>A	Splice Site	NAT10	p.K539K	N-acetyltransferase 10 (	86 (0.00)	151 (0.62)	1.66
12-03	Gp4 Focus 1	g.chr12:78513335A>G	Missense Mutation	NAV3	p.Q1120R	neuron navigator 3	109 (0.00)	33 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr2:203972381C>T	Silent	NBEAL1	p.V444V	neurobeachin-like 1	23 (0.00)	43 (0.26)	0.68
12-03	Gp4 Focus 1	g.chr5:85589147G>T	RNA	NBPF22P		neuroblastoma breakpoi	20 (0.00)	20 (0.85)	2.27
12-03	Gp4 Focus 1	g.chr12:124885101C>T	Missense Mutation	NCOR2	p.A587T	nuclear receptor corepre	48 (0.00)	258 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr22:42483072C>A	Missense Mutation	NDUFA6	p.V83F	NADH dehydrogenase (	56 (0.00)	138 (0.51)	1.73
12-03	Gp4 Focus 1	g.chr2:152515602C>A	Missense Mutation	NEB	p.A2018S	nebulin	35 (0.00)	31 (0.35)	0.95
12-03	Gp4 Focus 1	g.chr1:72748156G>T	Missense Mutation	NEGR1	p.Q8K	neuronal growth regulat	26 (0.00)	18 (0.56)	1.48
12-03	Gp4 Focus 1	g.chr15:73547154G>T	Silent	NEO1	p.L692L	neogenin 1	99 (0.00)	46 (0.20)	0.52
12-03	Gp4 Focus 1	g.chr12:54687011G>A	Missense Mutation	NFE2	p.S90F	nuclear factor, erythroid	26 (0.00)	103 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr10:104157838G>A	Silent	NFKB2	p.Q254Q	nuclear factor of kappa l	48 (0.02)	131 (0.35)	0.94
12-03	Gp4 Focus 1	g.chr6:138768235C>A	Silent	NHSL1	p.T193T	NHS-like 1	32 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr14:51225021G>A	Silent	NIN	p.V909V	ninein (GSK3B interacti	38 (0.00)	84 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr6:28228057G>A	Missense Mutation	NKAPL	p.G303D	NFKB activating protei	22 (0.00)	57 (0.30)	1.00
12-03	Gp4 Focus 1	g.chr8:23539058G>A	Silent	NKX3-1	p.S127S	NK3 homeobox 1	22 (0.00)	55 (0.33)	0.41
12-03	Gp4 Focus 1	g.chr17:5462474C>G	Missense Mutation	NLRP1	p.W514C	NLR family, pyrin doma	49 (0.00)	23 (0.39)	1.04
12-03	Gp4 Focus 1	g.chr17:5485186G>A	Silent	NLRP1	p.Y215Y	NLR family, pyrin doma	19 (0.00)	19 (0.37)	0.98
12-03	Gp4 Focus 1	g.chr19:54313438G>A	Missense Mutation	NLRP12	p.S492F	NLR family, pyrin doma	33 (0.00)	174 (0.11)	0.41
12-03	Gp4 Focus 1	g.chr11:119052829C>A	Missense Mutation	NLRX1	p.A794E	NLR family member X1	80 (0.00)	159 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr9:33466983T>C	Missense Mutation	NOL6	p.H626R	nucleolar protein 6 (RN.	34 (0.00)	95 (0.44)	1.18
12-03	Gp4 Focus 1	g.chr4:2955285G>A	Missense Mutation	NOP14	p.H234Y	NOP14 nucleolar protei	28 (0.00)	35 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr20:2635483C>T	Silent	NOP56	p.S153S	NOP56 ribonucleoprote	41 (0.00)	47 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr7:150696168C>A	Missense Mutation	NOS3	p.H317Q	nitric oxide synthase 3 (	17 (0.00)	175 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr1:120468186G>T	Missense Mutation	NOTCH2	p.P1418H	notch 2	25 (0.00)	79 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr15:24921972G>T	Missense Mutation	NPAP1	p.A320S	nuclear pore associated	30 (0.00)	117 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr18:21119842C>T	Missense Mutation	NPC1	p.G910S	Niemann-Pick disease, t	31 (0.00)	12 (0.75)	2.00
12-03	Gp4 Focus 1	g.chr17:45695820T>C	Silent	NPEPPS	p.L800L	aminopeptidase puromy	34 (0.00)	41 (0.15)	0.53
12-03	Gp4 Focus 1	g.chr18:11621260G>A	RNA	NPIPB1P		nuclear pore complex in	77 (0.00)	52 (0.90)	2.41

12-03	Gp4 Focus 1	g.chr16:21848648C>T	Missense Mutation	NPIPB4	p.A354T	nuclear pore complex in	109 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr3:50387232G>T	Missense Mutation	NPRL2	p.P68H	nitrogen permease regul	45 (0.00)	197 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr19:50881430C>T	Missense Mutation	NR1H2	p.P69L	nuclear receptor subfam	41 (0.00)	353 (0.11)	0.38
12-03	Gp4 Focus 1	g.chr1:52266322C>G	Missense Mutation	NRD1	p.E851Q	nardilysin (N-arginine d	31 (0.00)	46 (0.15)	0.41
12-03	Gp4 Focus 1	g.chr2:11802161T>C	Missense Mutation	NTSR2	p.Q277R	neurotensin receptor 2	68 (0.00)	50 (0.42)	1.12
12-03	Gp4 Focus 1	g.chr1:205274349G>T	Nonsense Mutation	NUAK2	p.Y267*	NUAK family, SNF1-lil	32 (0.00)	68 (0.84)	2.24
12-03	Gp4 Focus 1	g.chr3:13407560G>T	Missense Mutation	NUP210	p.S606R	nucleoporin 210kDa	18 (0.00)	61 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr9:134073349G>A	Missense Mutation	NUP214	p.G1490S	nucleoporin 214kDa	54 (0.00)	83 (0.29)	0.98
12-03	Gp4 Focus 1	g.chr4:77053744G>A	Missense Mutation	NUP54	p.T232I	nucleoporin 54kDa	62 (0.02)	36 (0.92)	2.44
12-03	Gp4 Focus 1	g.chr4:77053751C>A	Missense Mutation	NUP54	p.G230C	nucleoporin 54kDa	62 (0.00)	32 (0.81)	2.17
12-03	Gp4 Focus 1	g.chr15:34648611G>C	Missense Mutation	NUTM1	p.G801A	NUT midline carcinoma	55 (0.00)	57 (0.58)	1.54
12-03	Gp4 Focus 1	g.chr11:62560130C>T	Missense Mutation	NXF1	p.A602T	nuclear RNA export fac	26 (0.00)	27 (0.22)	0.47
12-03	Gp4 Focus 1	g.chr11:62571376C>A	Nonsense Mutation	NXF1	p.E35*	nuclear RNA export fac	38 (0.00)	67 (0.45)	0.95
12-03	Gp4 Focus 1	g.chr2:226446931C>T	Silent	NYAP2	p.A266A	neuronal tyrosine-phosp	44 (0.00)	94 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr12:113355463T>C	Silent	OAS1	p.F332F	2'-5'-oligoadenylate syn	37 (0.00)	21 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr12:121465503C>A	Missense Mutation	OASL	p.G259C	2'-5'-oligoadenylate syn	21 (0.00)	15 (0.47)	1.63
12-03	Gp4 Focus 1	g.chr1:228437805C>G	Missense Mutation	OBSCN	p.S1483R	obscurin, cytoskeletal c	24 (0.00)	112 (0.17)	0.59
12-03	Gp4 Focus 1	g.chr1:228481986G>A	Silent	OBSCN	p.G4184G	obscurin, cytoskeletal c	101 (0.00)	103 (0.29)	1.00
12-03	Gp4 Focus 1	g.chr2:220432687G>T	Silent	OBSL1	p.P429P	obscurin-like 1	16 (0.00)	96 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr9:138011508G>A	Silent	OLFM1	p.K287K	olfactomedin 1	35 (0.00)	52 (0.15)	0.52
12-03	Gp4 Focus 1	g.chr19:15838887T>C	Missense Mutation	OR10H2	p.F12L	olfactory receptor, famil	38 (0.00)	115 (0.17)	0.62
12-03	Gp4 Focus 1	g.chr11:123847475C>T	Silent	OR10S1	p.E308E	olfactory receptor, famil	42 (0.00)	14 (0.36)	0.75
12-03	Gp4 Focus 1	g.chr11:123848358G>A	Missense Mutation	OR10S1	p.T14M	olfactory receptor, famil	61 (0.00)	26 (0.96)	2.01
12-03	Gp4 Focus 1	g.chr1:158368708T>C	Silent	OR10T2	p.A183A	olfactory receptor, famil	29 (0.00)	17 (0.47)	0.93
12-03	Gp4 Focus 1	g.chr10:45799184G>T	Missense Mutation	OR13A1	p.F229L	olfactory receptor, famil	50 (0.00)	53 (0.32)	0.86
12-03	Gp4 Focus 1	g.chr17:2996112T>C	Missense Mutation	OR1D2	p.Y60C	olfactory receptor, famil	109 (0.00)	36 (0.31)	0.81
12-03	Gp4 Focus 1	g.chr6:27879265C>T	Missense Mutation	OR2B2	p.C278Y	olfactory receptor, famil	25 (0.00)	29 (0.28)	0.93
12-03	Gp4 Focus 1	g.chr16:3406177C>T	Silent	OR2C1	p.P79P	olfactory receptor, famil	39 (0.00)	64 (0.69)	2.40
12-03	Gp4 Focus 1	g.chr1:248059704G>A	Missense Mutation	OR2W3	p.M272I	olfactory receptor, famil	19 (0.00)	64 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr12:55820487C>A	Missense Mutation	OR6C76	p.F150L	olfactory receptor, famil	41 (0.00)	72 (0.62)	1.67
12-03	Gp4 Focus 1	g.chr11:124179969C>A	Nonsense Mutation	OR8D1	p.E232*	olfactory receptor, famil	15 (0.00)	11 (0.45)	1.21
12-03	Gp4 Focus 1	g.chr11:124180573C>T	Silent	OR8D1	p.L30L	olfactory receptor, famil	66 (0.02)	42 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr11:55979081G>T	RNA	OR8J2		olfactory receptor, famil	22 (0.00)	46 (0.30)	0.65
12-03	Gp4 Focus 1	g.chr2:148693231G>T	Missense Mutation	ORC4	p.P387T	origin recognition comp	54 (0.00)	32 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr11:59375994G>T	Missense Mutation	OSBP	p.A262D	oxysterol binding protei	75 (0.00)	26 (0.19)	0.41

12-03	Gp4 Focus 1	g.chr22:31285623G>T	Splice Site	OSBP2	p.P541P	oxysterol binding protei	21 (0.00)	49 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr17:72926558C>A	Missense Mutation	OTOP2	p.S276R	otopetrin 2	52 (0.00)	229 (0.13)	0.46
12-03	Gp4 Focus 1	g.chr12:56715869G>A	Silent	PAN2	p.N931N	PAN2 poly(A) specific	29 (0.00)	31 (0.90)	2.41
12-03	Gp4 Focus 1	g.chr3:142681301C>A	Missense Mutation	PAQR9	p.S293I	progestin and adipoQ re	50 (0.00)	147 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr3:122418412G>A	Silent	PARP14	p.K337K	poly (ADP-ribose) poly	19 (0.00)	13 (0.54)	1.44
12-03	Gp4 Focus 1	g.chr11:59410430G>A	Nonsense Mutation	PATL1	p.Q658*	protein associated with	30 (0.00)	33 (0.24)	0.51
12-03	Gp4 Focus 1	g.chr22:31723065T>C	Missense Mutation	PATZ1	p.K626E	POZ (BTB) and AT hoc	34 (0.00)	94 (0.46)	1.22
12-03	Gp4 Focus 1	g.chr6:138539221G>A	Silent	PBOV1	p.A104A	prostate and breast canc	19 (0.00)	153 (0.61)	1.62
12-03	Gp4 Focus 1	g.chr5:141336844G>A	Silent	PCDH12	p.T191T	protocadherin 12	59 (0.00)	107 (0.55)	1.47
12-03	Gp4 Focus 1	g.chr4:30725726C>T	Silent	PCDH7	p.I894I	protocadherin 7	18 (0.00)	14 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr5:140255823C>T	Nonsense Mutation	PCDHA12	p.Q256*	protocadherin alpha 12	74 (0.00)	169 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr5:140187130G>A	Missense Mutation	PCDHA4	p.D120N	protocadherin alpha 4	41 (0.00)	78 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr5:140222601G>A	Silent	PCDHA8	p.L565L	protocadherin alpha 8	29 (0.00)	333 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr5:140626167A>G	Missense Mutation	PCDHB15	p.N341D	protocadherin beta 15	72 (0.00)	34 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr5:140626362G>C	Missense Mutation	PCDHB15	p.E406Q	protocadherin beta 15	22 (0.00)	18 (0.78)	2.07
12-03	Gp4 Focus 1	g.chr5:140476709C>A	Missense Mutation	PCDHB2	p.Q779K	protocadherin beta 2	46 (0.02)	10 (0.80)	2.13
12-03	Gp4 Focus 1	g.chr5:140530297G>A	Silent	PCDHB6	p.L153L	protocadherin beta 6	38 (0.00)	47 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr5:140711911G>T	Missense Mutation	PCDHGA1	p.D554Y	protocadherin gamma s	63 (0.00)	35 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr5:140744399C>T	Missense Mutation	PCDHGA5	p.R168W	protocadherin gamma s	40 (0.00)	89 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr5:140750396G>A	Silent	PCDHGB3	p.L145L	protocadherin gamma s	114 (0.00)	95 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr5:140799690G>T	Missense Mutation	PCDHGB7	p.C755F	protocadherin gamma s	21 (0.00)	30 (0.30)	0.80
12-03	Gp4 Focus 1	g.chr5:140865638G>A	Missense Mutation	PCDHGC4	p.G300R	protocadherin gamma s	35 (0.00)	131 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr14:71540492G>T	Missense Mutation	PCNX	p.V1695L	pecanex homolog (Dros	34 (0.00)	46 (0.17)	0.46
12-03	Gp4 Focus 1	g.chr9:78936393T>C	Missense Mutation	PCSK5	p.C1287R	proprotein convertase s	115 (0.00)	63 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr3:57542947C>A	Missense Mutation	PDE12	p.H281N	phosphodiesterase 12	40 (0.00)	182 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr3:57542959T>C	Missense Mutation	PDE12	p.Y285H	phosphodiesterase 12	45 (0.00)	174 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr19:10577584G>A	Missense Mutation	PDE4A	p.V650M	phosphodiesterase 4A, c	75 (0.00)	89 (0.11)	0.40
12-03	Gp4 Focus 1	g.chr8:17486174G>A	Silent	PDGFRL	p.K228K	platelet-derived growth	86 (0.00)	64 (0.47)	1.25
12-03	Gp4 Focus 1	g.chr8:17486175C>A	Silent	PDGFRL	p.R229R	platelet-derived growth	87 (0.00)	66 (0.39)	1.05
12-03	Gp4 Focus 1	g.chr1:161070520C>G	Missense Mutation	PFDN2	p.E140Q	prefoldin subunit 2	21 (0.00)	20 (0.85)	1.68
12-03	Gp4 Focus 1	g.chr3:48573745G>T	Missense Mutation	PFKFB4	p.L262I	6-phosphofructo-2-kina	33 (0.00)	150 (0.36)	1.21
12-03	Gp4 Focus 1	g.chr12:48536630G>T	Missense Mutation	PFKM	p.M573I	phosphofructokinase, m	61 (0.00)	33 (0.27)	0.73
12-03	Gp4 Focus 1	g.chr15:99512839G>A	Silent	PGPEP1L	p.I8I	pyroglutamyl-peptidase	16 (0.00)	98 (0.16)	0.44
12-03	Gp4 Focus 1	g.chr3:169847257G>C	Missense Mutation	PHC3	p.H335D	polyhomeotic homolog	140 (0.00)	218 (0.44)	1.16
12-03	Gp4 Focus 1	g.chr9:96416762C>A	Missense Mutation	PHF2	p.S286Y	PHD finger protein 2	64 (0.00)	57 (0.12)	0.41

12-03	Gp4 Focus 1	g.chr18:60408951C>T	Intron	PHLPP1		PH domain and leucine	103 (0.00)	20 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr18:60450726G>T	Intron	PHLPP1		PH domain and leucine	62 (0.00)	39 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr18:60465436G>A	Intron	PHLPP1		PH domain and leucine	30 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr18:60470023G>A	Intron	PHLPP1		PH domain and leucine	39 (0.00)	44 (0.73)	1.94
12-03	Gp4 Focus 1	g.chr18:60571436G>A	Intron	PHLPP1		PH domain and leucine	40 (0.00)	25 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr18:60609947C>T	Intron	PHLPP1		PH domain and leucine	60 (0.00)	49 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr16:71683836C>G	Missense Mutation	PHLPP2	p.D910H	PH domain and leucine	52 (0.00)	20 (0.70)	1.87
12-03	Gp4 Focus 1	g.chr16:71688544C>T	Intron	PHLPP2		PH domain and leucine	31 (0.00)	57 (0.91)	2.43
12-03	Gp4 Focus 1	g.chr16:71689764T>A	Intron	PHLPP2		PH domain and leucine	85 (0.00)	21 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr16:71704259G>A	Intron	PHLPP2		PH domain and leucine	76 (0.00)	68 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr16:71734915G>A	Intron	PHLPP2		PH domain and leucine	81 (0.00)	29 (0.66)	1.75
12-03	Gp4 Focus 1	g.chr16:71736150C>A	Intron	PHLPP2		PH domain and leucine	23 (0.00)	14 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr22:21097030G>A	Missense Mutation	PI4KA	p.S1160L	phosphatidylinositol 4-k	52 (0.00)	25 (0.72)	2.44
12-03	Gp4 Focus 1	g.chr22:21174007G>A	Silent	PI4KA	p.I237I	phosphatidylinositol 4-k	35 (0.00)	74 (0.61)	2.06
12-03	Gp4 Focus 1	g.chr4:517287C>T	Missense Mutation	PIGG	p.L544F	phosphatidylinositol gly	77 (0.00)	90 (0.38)	1.01
12-03	Gp4 Focus 1	g.chr7:106508258G>A	Silent	PIK3CG	p.A84A	phosphatidylinositol-4,5	19 (0.00)	31 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr10:95720995A>G	RNA	PIPSL		PIP5K1A and PSMD4-l	123 (0.00)	45 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr8:22168777T>A	Silent	PIWIL2	p.T651T	piwi-like RNA-mediate	24 (0.00)	43 (0.33)	0.41
12-03	Gp4 Focus 1	g.chr16:71976451C>T	RNA	PKD1L3		polycystic kidney diseas	111 (0.00)	22 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr22:46655725C>T	Silent	PKDREJ	p.V1165V	polycystin (PKD) famil	68 (0.01)	107 (0.57)	1.92
12-03	Gp4 Focus 1	g.chr12:33031236C>A	Missense Mutation	PKP2	p.R193I	plakophilin 2	25 (0.00)	57 (0.18)	0.47
12-03	Gp4 Focus 1	g.chr16:68293272G>T	Silent	PLA2G15	p.L223L	phospholipase A2, grou	60 (0.00)	205 (0.20)	0.68
12-03	Gp4 Focus 1	g.chr9:26925891G>T	Silent	PLAA	p.I267I	phospholipase A2-activ	38 (0.00)	47 (0.34)	0.91
12-03	Gp4 Focus 1	g.chr20:9400537C>T	Missense Mutation	PLCB4	p.A700V	phospholipase C, beta 4	59 (0.00)	42 (0.98)	2.60
12-03	Gp4 Focus 1	g.chr17:62811087G>T	RNA	PLEKHM1P		pleckstrin homology do	20 (0.00)	22 (0.45)	1.21
12-03	Gp4 Focus 1	g.chr17:62818531G>A	RNA	PLEKHM1P		pleckstrin homology do	21 (0.00)	88 (0.34)	0.91
12-03	Gp4 Focus 1	g.chr10:115540460C>T	Silent	PLEKHS1	p.L173L	pleckstrin homology do	46 (0.00)	48 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr16:23690575C>T	Missense Mutation	PLK1	p.L108F	polo-like kinase 1	16 (0.00)	107 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr7:75144122T>A	RNA	PMS2P3		postmeiotic segregation	19 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr22:44340662C>T	Missense Mutation	PNPLA3	p.L402F	patatin-like phospholipa	62 (0.00)	40 (0.23)	0.76
12-03	Gp4 Focus 1	g.chr6:43582225C>T	Silent	POLH	p.C691C	polymerase (DNA direc	29 (0.00)	21 (0.62)	1.65
12-03	Gp4 Focus 1	g.chr1:145608420G>A	Silent	POLR3C	p.L129L	polymerase (RNA) III (	190 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr22:24656894G>T	RNA	POM121L9P		POM121 transmembran	32 (0.00)	102 (0.13)	0.43
12-03	Gp4 Focus 1	g.chr18:14542675G>T	Silent	POTEC	p.L157L	POTE ankyrin domain f	96 (0.00)	69 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr2:130832635G>T	Missense Mutation	POTEF	p.L804M	POTE ankyrin domain f	73 (0.00)	248 (0.20)	0.72

12-03	Gp4 Focus 1	g.chr5:93076939G>A	Missense Mutation	POU5F2	p.P111S	POU domain class 5, tra	39 (0.00)	147 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr19:287744G>T	Missense Mutation	PPAP2C	p.A71D	phosphatidic acid phosp	28 (0.00)	469 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr12:81657080G>A	Silent	PPFIA2	p.S1215S	protein tyrosine phospha	26 (0.00)	18 (0.39)	1.04
12-03	Gp4 Focus 1	g.chr12:80199415C>A	Missense Mutation	PPP1R12A	p.A653S	protein phosphatase 1, r	63 (0.00)	14 (0.71)	1.90
12-03	Gp4 Focus 1	g.chr12:80199417G>A	Missense Mutation	PPP1R12A	p.T652I	protein phosphatase 1, r	63 (0.00)	14 (0.71)	1.90
12-03	Gp4 Focus 1	g.chr19:49377782C>T	Missense Mutation	PPP1R15A	p.A431V	protein phosphatase 1, r	49 (0.00)	67 (0.12)	0.43
12-03	Gp4 Focus 1	g.chr11:61254629G>A	Silent	PPP1R32	p.G320G	protein phosphatase 1, r	18 (0.00)	75 (0.29)	0.62
12-03	Gp4 Focus 1	g.chr19:52722972C>T	Missense Mutation	PPP2R1A	p.S386F	protein phosphatase 2, r	59 (0.00)	61 (0.51)	1.82
12-03	Gp4 Focus 1	g.chr5:145972568C>T	Missense Mutation	PPP2R2B	p.D340N	protein phosphatase 2, r	57 (0.00)	32 (0.72)	1.92
12-03	Gp4 Focus 1	g.chr9:127920549C>T	Missense Mutation	PPP6C	p.R117K	protein phosphatase 6, c	37 (0.00)	32 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr1:12835759G>T	Missense Mutation	PRAMEF12	p.A121S	PRAME family membe	44 (0.00)	27 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr1:12942131C>T	Missense Mutation	PRAMEF4	p.C140Y	PRAME family membe	70 (0.01)	36 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr1:14109327G>A	Splice Site	PRDM2		PR domain containing 2	73 (0.00)	72 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr10:120934040G>A	Silent	PRDX3	p.V78V	peroxiredoxin 3	37 (0.03)	16 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr19:54403952C>T	Silent	PRKCG	p.P508P	protein kinase C, gamm	36 (0.00)	45 (0.24)	0.87
12-03	Gp4 Focus 1	g.chr14:75330470G>A	Missense Mutation	PROX2	p.T23M	prospero homeobox 2	36 (0.00)	41 (0.20)	0.52
12-03	Gp4 Focus 1	g.chr1:150318933G>A	Silent	PRPF3	p.K603K	pre-mRNA processing f	19 (0.00)	24 (0.83)	3.12
12-03	Gp4 Focus 1	g.chr17:1563726C>T	Splice Site	PRPF8	p.Q1595Q	pre-mRNA processing f	63 (0.00)	19 (0.74)	1.96
12-03	Gp4 Focus 1	g.chr17:1586909G>T	Missense Mutation	PRPF8	p.P63T	pre-mRNA processing f	36 (0.03)	77 (0.25)	0.66
12-03	Gp4 Focus 1	g.chrX:106884137G>T	Silent	PRPS1	p.R104R	phosphoribosyl pyropho	47 (0.00)	69 (0.49)	0.82
12-03	Gp4 Focus 1	g.chr22:32081569C>T	Missense Mutation	PRR14L	p.E2134K	proline rich 14-like	20 (0.00)	55 (0.25)	0.68
12-03	Gp4 Focus 1	g.chr15:55931897G>A	Missense Mutation	PRTG	p.T756I	protogenin	50 (0.00)	11 (0.64)	1.70
12-03	Gp4 Focus 1	g.chr19:43528951G>A	Silent	PSG11	p.L108L	pregnancy specific beta-	16 (0.00)	10 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr19:43680297T>A	Missense Mutation	PSG5	p.K238M	pregnancy specific beta-	19 (0.00)	16 (0.69)	1.83
12-03	Gp4 Focus 1	g.chr19:43766063G>A	Missense Mutation	PSG9	p.R220W	pregnancy specific beta-	190 (0.01)	12 (0.83)	2.22
12-03	Gp4 Focus 1	g.chr14:23511437G>A	Start Codon SNP	PSMB11	p.M1I	proteasome (prosome, n	17 (0.00)	100 (0.34)	0.65
12-03	Gp4 Focus 1	g.chr2:231937101G>T	Missense Mutation	PSMD1	p.G285C	proteasome (prosome, n	66 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr2:120567493C>T	Nonsense Mutation	PTPN4	p.R22*	protein tyrosine phospha	31 (0.00)	17 (0.59)	1.57
12-03	Gp4 Focus 1	g.chr1:44084308G>C	Missense Mutation	PTPRF	p.C1451S	protein tyrosine phospha	80 (0.00)	181 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr1:31414856G>A	Nonsense Mutation	PUM1	p.Q1035*	pumilio RNA-binding fa	33 (0.00)	65 (0.38)	1.03
12-03	Gp4 Focus 1	g.chr2:1653251C>T	Silent	PXDN	p.L767L	peroxidasin homolog (D	18 (0.00)	83 (0.20)	0.55
12-03	Gp4 Focus 1	g.chr20:25271166C>A	Missense Mutation	PYGB	p.S626Y	phosphorylase, glycoge	82 (0.00)	155 (0.34)	0.89
12-03	Gp4 Focus 1	g.chr20:25271188T>A	Missense Mutation	PYGB	p.H633Q	phosphorylase, glycoge	88 (0.00)	166 (0.30)	0.79
12-03	Gp4 Focus 1	g.chr12:9317761G>A	Silent	PZP	p.L821L	pregnancy-zone protein	53 (0.00)	16 (0.75)	2.00
12-03	Gp4 Focus 1	g.chr3:49094494G>A	Missense Mutation	QRICH1	p.A380V	glutamine-rich 1	24 (0.00)	63 (0.40)	1.06

12-03	Gp4 Focus 1	g.chr19:10812626G>A	Splice Site	QTRT1	p.G82R	queuine tRNA-ribosyltr	41 (0.00)	461 (0.13)	0.47
12-03	Gp4 Focus 1	g.chr13:111176219C>G	Missense Mutation	RAB20	p.M166I	RAB20, member RAS c	42 (0.00)	18 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr1:46740280G>A	Missense Mutation	RAD54L	p.R587Q	RAD54-like (S. cerevisi	25 (0.00)	19 (0.74)	1.96
12-03	Gp4 Focus 1	g.chr1:46740321G>A	Missense Mutation	RAD54L	p.E601K	RAD54-like (S. cerevisi	29 (0.00)	38 (0.79)	2.11
12-03	Gp4 Focus 1	g.chr5:34824438G>A	Missense Mutation	RAI14	p.V831M	retinoic acid induced 14	51 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 1	g.chrX:17819626G>T	Missense Mutation	RAI2	p.L169M	retinoic acid induced 2	20 (0.00)	101 (0.29)	0.48
12-03	Gp4 Focus 1	g.chr7:45222938T>C	Missense Mutation	RAMP3	p.I125T	receptor (G protein-cou	43 (0.02)	70 (0.27)	0.72
12-03	Gp4 Focus 1	g.chr4:53730645G>A	Splice Site	RASL11B	p.G67D	RAS-like, family 11, m	55 (0.00)	92 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr1:205065957C>T	Missense Mutation	RBBP5	p.G417S	retinoblastoma binding	118 (0.00)	67 (0.94)	2.51
12-03	Gp4 Focus 1	g.chr1:110883009G>A	Missense Mutation	RBM15	p.E328K	RNA binding motif prot	44 (0.00)	136 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr1:110883011G>A	Silent	RBM15	p.E328E	RNA binding motif prot	44 (0.00)	136 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr1:89449327G>A	Silent	RBMXL1	p.D61D	RNA binding motif prot	122 (0.00)	155 (0.66)	1.77
12-03	Gp4 Focus 1	g.chr7:73663425G>A	Silent	RFC2	p.T83T	replication factor C (act	22 (0.00)	23 (0.91)	2.43
12-03	Gp4 Focus 1	g.chr3:53155717G>A	Nonsense Mutation	RFT1	p.Q147*	RFT1 homolog (S. cere	37 (0.00)	33 (0.48)	1.29
12-03	Gp4 Focus 1	g.chr1:163117172C>A	Missense Mutation	RGS5	p.R173L	regulator of G-protein si	18 (0.00)	15 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr3:129247680G>T	Missense Mutation	RHO	p.W35L	rhodopsin	34 (0.00)	145 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr3:129247693G>T	Missense Mutation	RHO	p.M39I	rhodopsin	34 (0.00)	147 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr18:40503578C>A	Missense Mutation	RIT2	p.V129L	Ras-like without CAAX	155 (0.00)	168 (0.56)	1.49
12-03	Gp4 Focus 1	g.chr15:41043663G>T	Missense Mutation	RMDN3	p.S162Y	regulator of microtubul	105 (0.00)	209 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr15:59350599G>C	Missense Mutation	RNF111	p.A406P	ring finger protein 111	95 (0.00)	44 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr9:104323206A>T	Nonsense Mutation	RNF20	p.K836*	ring finger protein 20, E	17 (0.00)	15 (0.87)	2.31
12-03	Gp4 Focus 1	g.chr1:45115368C>T	Missense Mutation	RNF220	p.A494V	ring finger protein 220	42 (0.00)	257 (0.51)	1.36
12-03	Gp4 Focus 1	g.chr6:19613423C>A	RNA	RP1-167F1.2			31 (0.00)	43 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr17:33900732C>A	lincRNA	RP11-1094M14.11			25 (0.00)	18 (0.33)	0.89
12-03	Gp4 Focus 1	g.chr12:112193492C>A	Missense Mutation	RP11-162P23.	p.P16Q		24 (0.00)	32 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr1:63166544G>T	RNA	RP11-230B22.1			20 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr17:29374256G>T	RNA	RP11-271K11.5			24 (0.00)	72 (0.46)	1.52
12-03	Gp4 Focus 1	g.chr1:208050348C>T	lincRNA	RP11-328D5.1			61 (0.00)	107 (0.20)	0.52
12-03	Gp4 Focus 1	g.chr16:69362952G>A	Missense Mutation	RP11-343C2.1	p.T161M		55 (0.00)	106 (0.42)	1.45
12-03	Gp4 Focus 1	g.chr12:25956393G>C	lincRNA	RP11-443N24.2			34 (0.00)	25 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr5:162843665C>T	RNA	RP11-541P9.3			53 (0.00)	20 (0.35)	0.93
12-03	Gp4 Focus 1	g.chr17:44999734G>A	lincRNA	RP11-63A1.1			15 (0.00)	34 (0.32)	1.17
12-03	Gp4 Focus 1	g.chr17:33734633C>A	RNA	RP11-686D22.8			91 (0.00)	78 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr12:53928314G>A	Nonsense Mutation	RP11-793H13.	p.Q178*		65 (0.00)	23 (0.52)	1.39
12-03	Gp4 Focus 1	g.chr17:43627128G>A	lincRNA	RP11-798G7.6			142 (0.00)	84 (0.13)	0.47

12-03	Gp4 Focus 1	g.chr14:21771516C>A	Missense Mutation	RPGRIP1	p.S205Y	retinitis pigmentosa GT	54 (0.00)	66 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr12:113325607C>T	Missense Mutation	RPH3A	p.S481F	rabphilin 3A	73 (0.00)	42 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr12:113325681C>A	Missense Mutation	RPH3A	p.P506T	rabphilin 3A	94 (0.01)	48 (0.46)	1.22
12-03	Gp4 Focus 1	g.chr8:74204608T>C	Silent	RPL7	p.E12E	ribosomal protein L7	45 (0.00)	103 (0.19)	0.52
12-03	Gp4 Focus 1	g.chr6:166914390G>A	Missense Mutation	RPS6KA2	p.H108Y	ribosomal protein S6 ki	55 (0.00)	122 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr1:213277836T>A	Nonsense Mutation	RPS6KC1	p.C89*	ribosomal protein S6 ki	135 (0.00)	71 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr1:213414501C>T	Missense Mutation	RPS6KC1	p.P549L	ribosomal protein S6 ki	27 (0.00)	24 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr15:41770789C>T	Missense Mutation	RTF1	p.T595I	Rtf1, Paf1/RNA polyme	136 (0.00)	69 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr2:74659599G>C	Missense Mutation	RTKN	p.S52R	rhotekin	20 (0.00)	249 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr3:72434375C>T	Intron	RYBP		RING1 and YY1 bindin	131 (0.00)	31 (0.29)	0.77
12-03	Gp4 Focus 1	g.chr3:72453168C>T	Intron	RYBP		RING1 and YY1 bindin	107 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 1	g.chr3:72455355C>T	Intron	RYBP		RING1 and YY1 bindin	48 (0.00)	18 (0.83)	2.22
12-03	Gp4 Focus 1	g.chr3:72455365A>G	Intron	RYBP		RING1 and YY1 bindin	50 (0.00)	19 (0.84)	2.25
12-03	Gp4 Focus 1	g.chr19:38939145C>A	Silent	RYR1	p.I317I	ryanodine receptor 1 (sk	40 (0.00)	259 (0.11)	0.39
12-03	Gp4 Focus 1	g.chr19:39070675C>T	Silent	RYR1	p.N4806N	ryanodine receptor 1 (sk	21 (0.00)	87 (0.20)	0.71
12-03	Gp4 Focus 1	g.chr15:33993194G>A	Silent	RYR3	p.R2132R	ryanodine receptor 3	51 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 1	g.chr11:18111040C>A	Missense Mutation	SAAL1	p.V203L	serum amyloid A-like 1	22 (0.00)	30 (0.23)	0.62
12-03	Gp4 Focus 1	g.chr13:23929005T>C	Silent	SACS	p.E582E	sacsin molecular chaper	20 (0.00)	78 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr19:5621407C>A	Splice Site	SAFB2	p.A63S	scaffold attachment fact	155 (0.00)	226 (0.16)	0.61
12-03	Gp4 Focus 1	g.chr20:50408754G>A	Missense Mutation	SALL4	p.H90Y	spalt-like transcription f	48 (0.00)	134 (0.28)	0.76
12-03	Gp4 Focus 1	g.chr11:65744512G>T	Missense Mutation	SART1	p.D629Y	squamous cell carcinom	18 (0.00)	156 (0.20)	0.69
12-03	Gp4 Focus 1	g.chr5:147261112G>A	Silent	SCGB3A2	p.L53L	secretoglobin, family 3	61 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr17:62020383C>A	Missense Mutation	SCN4A	p.C1364F	sodium channel, voltage	26 (0.00)	38 (0.79)	2.11
12-03	Gp4 Focus 1	g.chr11:118015813G>A	Missense Mutation	SCN4B	p.H65Y	sodium channel, voltage	84 (0.00)	223 (0.19)	0.51
12-03	Gp4 Focus 1	g.chr4:76878762G>T	Missense Mutation	SDAD1	p.R560S	SDA1 domain containin	114 (0.00)	114 (0.39)	1.03
12-03	Gp4 Focus 1	g.chr3:195690315G>A	RNA	SDHAP1		succinate dehydrogenas	107 (0.01)	12 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr7:4167045G>A	Missense Mutation	SDK1	p.E1286K	sidekick cell adhesion m	109 (0.00)	36 (0.17)	0.63
12-03	Gp4 Focus 1	g.chr17:71418491G>T	Silent	SDK2	p.S660S	sidekick cell adhesion m	17 (0.00)	86 (0.33)	0.87
12-03	Gp4 Focus 1	g.chr17:75208031G>A	Splice Site	SEC14L1		SEC14-like 1 (S. cerevis	24 (0.00)	79 (0.35)	1.24
12-03	Gp4 Focus 1	g.chr2:97530468G>A	Silent	SEMA4C	p.T312T	sema domain, immunog	28 (0.00)	404 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr5:115813763G>A	Silent	SEMA6A	p.T505T	sema domain, transmem	69 (0.00)	114 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr20:43836077C>A	Missense Mutation	SEMG1	p.H47N	semenogelin I	22 (0.00)	47 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr4:77926819C>A	Missense Mutation	SEPT11	p.P70T	septin 11	39 (0.00)	75 (0.47)	1.24
12-03	Gp4 Focus 1	g.chr7:55874853C>A	Nonsense Mutation	SEPT14	p.E306*	septin 14	19 (0.00)	62 (0.40)	1.08
12-03	Gp4 Focus 1	g.chr17:56598158G>A	Silent	SEPT4	p.V441V	septin 4	59 (0.00)	11 (0.73)	1.94

12-03	Gp4 Focus 1	g.chr6:158535948A>G	Silent	SERAC1	p.T519T	serine active site contair	64 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr6:2838147G>T	Silent	SERPINB1	p.T131T	serpin peptidase inhibitc	66 (0.00)	33 (0.76)	2.02
12-03	Gp4 Focus 1	g.chr6:2840702G>T	Missense Mutation	SERPINB1	p.A40D	serpin peptidase inhibitc	42 (0.00)	29 (0.52)	1.38
12-03	Gp4 Focus 1	g.chr12:132198708C>G	Missense Mutation	SFSWAP	p.A104G	splicing factor, suppress	28 (0.00)	19 (0.47)	1.26
12-03	Gp4 Focus 1	g.chr12:132250696C>A	Missense Mutation	SFSWAP	p.A662D	splicing factor, suppress	59 (0.00)	47 (0.28)	0.74
12-03	Gp4 Focus 1	g.chr10:81318721C>G	Silent	SFTPA2	p.G71G	surfactant protein A2	67 (0.00)	91 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr2:201399842T>A	Missense Mutation	SGOL2	p.V86E	shugoshin-like 2 (S. por	24 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr3:72808324A>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	46 (0.00)	14 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr5:132160315G>C	Silent	SHROOM1	p.P411P	shroom family member	23 (0.00)	156 (0.74)	1.97
12-03	Gp4 Focus 1	g.chr10:69672462C>A	Missense Mutation	SIRT1	p.T530K	sirtuin 1	19 (0.00)	15 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr16:67995559G>C	Silent	SLC12A4	p.V87V	solute carrier family 12	31 (0.00)	55 (0.18)	0.62
12-03	Gp4 Focus 1	g.chr17:6604348G>A	Missense Mutation	SLC13A5	p.L272F	solute carrier family 13	36 (0.00)	103 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr17:73102001C>A	Missense Mutation	SLC16A5	p.P464Q	solute carrier family 16	60 (0.00)	48 (0.40)	1.39
12-03	Gp4 Focus 1	g.chr2:113417313A>G	Silent	SLC20A1	p.S527S	solute carrier family 20	55 (0.00)	51 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr1:116577928C>T	Silent	SLC22A15	p.I355I	solute carrier family 22,	52 (0.00)	20 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr15:65945063C>A	Silent	SLC24A1	p.T959T	solute carrier family 24	37 (0.00)	47 (0.49)	1.30
12-03	Gp4 Focus 1	g.chr15:65946276G>A	Silent	SLC24A1	p.L1023L	solute carrier family 24	19 (0.00)	18 (0.56)	1.48
12-03	Gp4 Focus 1	g.chr2:172666785A>G	Splice Site	SLC25A12	p.G391G	solute carrier family 25	51 (0.00)	81 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr15:45567706G>T	Missense Mutation	SLC28A2	p.A658S	solute carrier family 28	134 (0.00)	279 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr12:8075534G>A	Silent	SLC2A3	p.P385P	solute carrier family 2 (	124 (0.00)	27 (0.78)	2.07
12-03	Gp4 Focus 1	g.chr17:70943976G>T	Missense Mutation	SLC39A11	p.N115K	solute carrier family 39,	17 (0.00)	56 (0.46)	1.24
12-03	Gp4 Focus 1	g.chr1:75805298C>G	Missense Mutation	SLC44A5	p.D24H	solute carrier family 44,	74 (0.00)	119 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr22:32630921G>C	Missense Mutation	SLC5A4	p.P275R	solute carrier family 5 (	17 (0.00)	17 (0.41)	1.10
12-03	Gp4 Focus 1	g.chr5:1235753C>T	Silent	SLC6A18	p.I199I	solute carrier family 6 (	45 (0.00)	134 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr2:40342737C>T	Missense Mutation	SLC8A1	p.D860N	solute carrier family 8 (	35 (0.00)	12 (0.67)	1.78
12-03	Gp4 Focus 1	g.chr10:105727599C>A	Missense Mutation	SLK	p.D32E	STE20-like kinase	29 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 1	g.chr16:3639022G>T	Silent	SLX4	p.P1539P	SLX4 structure-specific	28 (0.00)	200 (0.11)	0.38
12-03	Gp4 Focus 1	g.chr18:48557730G>A	Intron	SMAD4		SMAD family member	92 (0.00)	125 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr19:11114048A>G	Missense Mutation	SMARCA4	p.E659G	SWI/SNF related, matri	43 (0.00)	39 (0.33)	1.18
12-03	Gp4 Focus 1	g.chr11:93212347C>A	Missense Mutation	SMCO4	p.Q3H	single-pass membrane p	34 (0.00)	47 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr17:2203145G>A	Missense Mutation	SMG6	p.T301I	SMG6 nonsense mediat	25 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 1	g.chr1:183514254C>T	Missense Mutation	SMG7	p.P726L	SMG7 nonsense mediat	86 (0.00)	48 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr17:57288584C>T	Missense Mutation	SMG8	p.S391F	SMG8 nonsense mediat	43 (0.00)	62 (0.58)	2.07
12-03	Gp4 Focus 1	g.chr17:57290270G>A	Missense Mutation	SMG8	p.A696T	SMG8 nonsense mediat	77 (0.00)	79 (0.11)	0.41
12-03	Gp4 Focus 1	g.chr7:128845061C>A	Silent	SMO	p.I185I	smoothened, frizzled cla	32 (0.00)	84 (0.21)	0.57

12-03	Gp4 Focus 1	g.chr12:54576234C>A	Missense Mutation	SMUG1	p.E153D	single-strand-selective m	24 (0.00)	170 (0.55)	1.47
12-03	Gp4 Focus 1	g.chr17:62543863C>T	Silent	SMURF2	p.R642R	SMAD specific E3 ubiq	26 (0.00)	99 (0.27)	0.73
12-03	Gp4 Focus 1	g.chr1:151638475A>G	Missense Mutation	SNX27	p.S325G	sorting nexin family me	57 (0.00)	41 (0.63)	1.69
12-03	Gp4 Focus 1	g.chr10:108380308G>C	Missense Mutation	SORCS1	p.H892D	sortilin-related VPS10 d	25 (0.00)	12 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr15:45357535C>T	Silent	SORD	p.A164A	sorbitol dehydrogenase	18 (0.00)	23 (0.30)	0.81
12-03	Gp4 Focus 1	g.chr4:77816747T>C	Missense Mutation	SOWAHB	p.I752M	sosondowah ankyrin rep	44 (0.00)	64 (0.59)	1.58
12-03	Gp4 Focus 1	g.chr12:53777045C>T	Silent	SP1	p.L438L	Sp1 transcription factor	49 (0.00)	85 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr7:21469739C>T	Missense Mutation	SP4	p.S319F	Sp4 transcription factor	32 (0.00)	68 (0.16)	0.43
12-03	Gp4 Focus 1	g.chr2:214794752G>A	Missense Mutation	SPAG16	p.C428Y	sperm associated antiger	47 (0.00)	28 (0.39)	1.05
12-03	Gp4 Focus 1	g.chr1:84991757G>C	RNA	SPATA1		spermatogenesis associa	55 (0.00)	47 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr9:65506533C>A	Nonsense Mutation	SPATA31A7	p.E343*	SPATA31 subfamily A,	168 (0.00)	184 (0.55)	1.46
12-03	Gp4 Focus 1	g.chr3:113184499C>T	Splice Site	SPICE1		spindle and centriole ass	30 (0.00)	29 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr17:47707028G>A	Intron	SPOP		speckle-type POZ protei	42 (0.00)	34 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr2:54873334C>T	Missense Mutation	SPTBN1	p.L1530F	spectrin, beta, non-eryth	129 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr19:41040238C>A	Silent	SPTBN4	p.L1449L	spectrin, beta, non-eryth	24 (0.00)	144 (0.12)	0.46
12-03	Gp4 Focus 1	g.chr16:30733454G>T	Missense Mutation	SRCAP	p.V1185F	Snf2-related CREBBP a	47 (0.00)	42 (0.21)	0.74
12-03	Gp4 Focus 1	g.chr17:17723759T>A	Silent	SREBF1	p.A56A	sterol regulatory elemen	35 (0.00)	166 (0.71)	1.90
12-03	Gp4 Focus 1	g.chr1:24975467G>A	Missense Mutation	SRRM1	p.G118R	serine/arginine repetitiv	36 (0.00)	175 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr16:2812862G>C	Missense Mutation	SRRM2	p.S778T	serine/arginine repetitiv	31 (0.00)	48 (0.42)	1.45
12-03	Gp4 Focus 1	g.chr16:2817022C>T	Missense Mutation	SRRM2	p.P2165S	serine/arginine repetitiv	30 (0.00)	253 (0.13)	0.47
12-03	Gp4 Focus 1	g.chr7:100483543G>A	Nonsense Mutation	SRRT	p.W480*	serrate, RNA effector m	35 (0.00)	115 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr7:100485362T>A	Missense Mutation	SRRT	p.H736Q	serrate, RNA effector m	56 (0.00)	144 (0.22)	0.57
12-03	Gp4 Focus 1	g.chr7:149485096C>T	RNA	SSPO		SCO-spondin	17 (0.00)	69 (0.13)	0.49
12-03	Gp4 Focus 1	g.chrX:48054277A>T	Missense Mutation	SSX5	p.I69N	synovial sarcoma, X bre	60 (0.00)	41 (0.46)	0.59
12-03	Gp4 Focus 1	g.chr3:52556659G>A	Silent	STAB1	p.Q2233Q	stabilin 1	43 (0.00)	68 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr7:74303832G>T	RNA	STAG3L2		stromal antigen 3-like 2	133 (0.00)	59 (0.34)	0.90
12-03	Gp4 Focus 1	g.chr10:134039103C>G	Missense Mutation	STK32C	p.D117H	serine/threonine kinase	16 (0.00)	103 (0.43)	1.14
12-03	Gp4 Focus 1	g.chr9:136199408C>A	Missense Mutation	SURF6	p.E194D	surfeit 6	36 (0.00)	448 (0.14)	0.48
12-03	Gp4 Focus 1	g.chr9:113173964C>A	Missense Mutation	SVEP1	p.W1986C	sushi, von Willebrand fa	45 (0.00)	21 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr8:110587722C>T	Missense Mutation	SYBU	p.E468K	syntabulin (syntaxin-int	40 (0.00)	82 (0.20)	0.52
12-03	Gp4 Focus 1	g.chr1:85655811T>G	Missense Mutation	SYDE2	p.Q457P	synapse defective 1, Rh	64 (0.00)	56 (0.39)	1.05
12-03	Gp4 Focus 1	g.chr1:33160509G>A	Missense Mutation	SYNC	p.A397V	syncoilin, intermediate f	141 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr20:24524185A>G	Missense Mutation	SYNDIG1	p.E151G	synapse differentiation i	23 (0.00)	48 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr14:64449373G>A	Nonsense Mutation	SYNE2	p.W621*	spectrin repeat containir	58 (0.00)	30 (0.27)	0.71
12-03	Gp4 Focus 1	g.chr4:119951109G>A	Silent	SYNPO2	p.G393G	synaptopodin 2	178 (0.00)	116 (0.82)	2.18

12-03	Gp4 Focus 1	g.chr11:45274089C>A	Missense Mutation	SYT13	p.L243F	synaptotagmin XIII	19 (0.00)	55 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr11:61291355A>G	Missense Mutation	SYT7	p.I328T	synaptotagmin VII	41 (0.00)	33 (0.30)	0.64
12-03	Gp4 Focus 1	g.chr1:43908190G>T	Missense Mutation	SZT2	p.W2627C	seizure threshold 2 hom	33 (0.00)	128 (0.38)	1.02
12-03	Gp4 Focus 1	g.chr6:149699457G>A	Missense Mutation	TAB2	p.G136S	TGF-beta activated kina	24 (0.00)	22 (0.68)	1.82
12-03	Gp4 Focus 1	g.chr6:149730821G>A	Missense Mutation	TAB2	p.R683H	TGF-beta activated kina	77 (0.00)	15 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr10:123847395G>T	Missense Mutation	TACC2	p.V1794F	transforming, acidic coil	41 (0.00)	130 (0.15)	0.39
12-03	Gp4 Focus 1	g.chr8:120758947G>A	Missense Mutation	TAF2	p.P1036S	TAF2 RNA polymerase	27 (0.00)	10 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr17:61492963G>A	Silent	TANC2	p.E1281E	tetratricopeptide repeat,	85 (0.00)	30 (0.93)	2.49
12-03	Gp4 Focus 1	g.chr12:53897517C>T	Missense Mutation	TARBP2	p.S25F	TAR (HIV-1) RNA binc	15 (0.00)	48 (0.56)	1.50
12-03	Gp4 Focus 1	g.chr15:102261454G>A	Silent	TARSL2	p.L147L	threonyl-tRNA syntheta	27 (0.00)	23 (0.61)	1.62
12-03	Gp4 Focus 1	g.chr7:122635168T>C	Missense Mutation	TAS2R16	p.H174R	taste receptor, type 2, m	51 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr17:77925288C>A	Missense Mutation	TBC1D16	p.Q350H	TBC1 domain family, n	20 (0.00)	137 (0.14)	0.49
12-03	Gp4 Focus 1	g.chr17:34803411C>A	Missense Mutation	TBC1D3G	p.K136N	TBC1 domain family, n	46 (0.00)	28 (0.18)	0.62
12-03	Gp4 Focus 1	g.chr17:58085806C>G	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	99 (0.00)	104 (0.17)	0.62
12-03	Gp4 Focus 1	g.chr17:58090473G>A	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	50 (0.00)	12 (0.83)	2.97
12-03	Gp4 Focus 1	g.chr5:179315190C>T	Silent	TBC1D9B	p.R389R	TBC1 domain family, n	19 (0.00)	86 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr22:42610876G>A	Missense Mutation	TCF20	p.L146F	transcription factor 20 (	63 (0.00)	30 (0.23)	0.78
12-03	Gp4 Focus 1	g.chr1:152081943G>T	Missense Mutation	TCHH	p.F1250L	trichohyalin	38 (0.03)	63 (0.21)	0.55
12-03	Gp4 Focus 1	g.chr1:152085435G>T	Nonsense Mutation	TCHH	p.Y86*	trichohyalin	44 (0.00)	82 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr5:167674643C>T	Silent	TENM2	p.H1994H	teneurin transmembrane	24 (0.00)	15 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr11:78380192T>C	Missense Mutation	TENM4	p.I2400V	teneurin transmembrane	57 (0.00)	32 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr17:56638908A>G	Missense Mutation	TEX14	p.L1423P	testis expressed 14	73 (0.00)	109 (0.18)	0.49
12-03	Gp4 Focus 1	g.chr17:62271042G>T	Missense Mutation	TEX2	p.Q685K	testis expressed 2	54 (0.00)	37 (0.43)	1.15
12-03	Gp4 Focus 1	g.chr3:51733577G>T	Missense Mutation	TEX264	p.Q212H	testis expressed 264	49 (0.00)	46 (0.20)	0.52
12-03	Gp4 Focus 1	g.chr3:133475798C>T	Missense Mutation	TF	p.A272V	transferrin	47 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr22:26890138C>A	Missense Mutation	TFIP11	p.D709Y	tuftelin interacting prote	24 (0.00)	18 (0.44)	1.19
12-03	Gp4 Focus 1	g.chr8:134125688G>A	Missense Mutation	TG	p.R2532Q	thyroglobulin	22 (0.00)	20 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr15:39876578T>A	Missense Mutation	THBS1	p.N327K	thrombospondin 1	25 (0.00)	33 (0.45)	1.21
12-03	Gp4 Focus 1	g.chr2:88474204C>A	Silent	THNSL2	p.V58V	threonine synthase-like	23 (0.00)	75 (0.20)	0.39
12-03	Gp4 Focus 1	g.chr5:175387079G>A	Missense Mutation	THOC3	p.P317S	THO complex 3	65 (0.00)	41 (0.54)	1.43
12-03	Gp4 Focus 1	g.chr13:52952547C>A	Missense Mutation	THSD1	p.A520S	thrombospondin, type I,	39 (0.03)	222 (0.32)	0.41
12-03	Gp4 Focus 1	g.chr15:90168022C>A	Missense Mutation	TICRR	p.A1494E	TOPBP1-interacting che	31 (0.00)	27 (0.56)	1.48
12-03	Gp4 Focus 1	g.chr3:114026883C>A	Missense Mutation	TIGIT	p.Q214K	T cell immunoreceptor	147 (0.00)	49 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr12:56827594G>T	Missense Mutation	TIMELESS	p.H72N	timeless circadian clock	71 (0.00)	21 (0.48)	1.27
12-03	Gp4 Focus 1	g.chr19:39978833T>A	Missense Mutation	TIMM50	p.L277M	translocase of inner mit	25 (0.00)	141 (0.16)	0.57

12-03	Gp4 Focus 1	g.chr20:30730810T>C	Missense Mutation	TM9SF4	p.F185S	transmembrane 9 superf	18 (0.00)	62 (0.48)	1.29
12-03	Gp4 Focus 1	g.chr2:98409341C>A	Missense Mutation	TMEM131	p.V1218F	transmembrane protein	16 (0.00)	50 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr19:19243283C>T	Silent	TMEM161A	p.V107V	transmembrane protein	22 (0.00)	56 (0.20)	0.70
12-03	Gp4 Focus 1	g.chr7:150493453C>G	Splice Site	TMEM176B		transmembrane protein	25 (0.00)	19 (0.53)	1.96
12-03	Gp4 Focus 1	g.chr15:72699007C>A	Missense Mutation	TMEM202	p.A49D	transmembrane protein	32 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 1	g.chr3:190159235C>T	Nonsense Mutation	TMEM207	p.W50*	transmembrane protein	46 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr10:81850597T>A	Missense Mutation	TMEM254	p.L99Q	transmembrane protein	46 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr14:57114081T>A	Missense Mutation	TMEM260	p.L664I	transmembrane protein	17 (0.00)	33 (0.45)	1.21
12-03	Gp4 Focus 1	g.chr1:226048652G>T	Nonsense Mutation	TMEM63A	p.C377*	transmembrane protein	31 (0.00)	34 (0.29)	1.01
12-03	Gp4 Focus 1	g.chr12:98925568A>G	Missense Mutation	TMPO	p.R173G	thymopoietin	35 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr12:51281196A>T	Missense Mutation	TMPRSS12	p.H316L	transmembrane (C-term	21 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr18:66344203C>T	Silent	TMX3	p.E444E	thioredoxin-related trans	20 (0.00)	19 (0.74)	1.96
12-03	Gp4 Focus 1	g.chr17:17766072C>A	Missense Mutation	TOM1L2	p.G339V	target of myb1-like 2 (cl	19 (0.00)	25 (0.28)	0.75
12-03	Gp4 Focus 1	g.chr17:7575232G>A	Intron	TP53		tumor protein p53	36 (0.00)	35 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr17:7586095C>T	Intron	TP53		tumor protein p53	24 (0.00)	26 (0.77)	2.05
12-03	Gp4 Focus 1	g.chr17:27898642G>A	Missense Mutation	TP53I13	p.A73T	tumor protein p53 induc	56 (0.00)	186 (0.16)	0.53
12-03	Gp4 Focus 1	g.chr11:68840126G>C	Missense Mutation	TPCN2	p.V365L	two pore segment chann	23 (0.00)	88 (0.15)	0.51
12-03	Gp4 Focus 1	g.chr19:53945546G>A	RNA	TPM3P9		tropomyosin 3 pseudog	27 (0.00)	32 (0.78)	2.79
12-03	Gp4 Focus 1	g.chr14:21500193G>C	Missense Mutation	TPPP2	p.S157T	tubulin polymerization-	62 (0.00)	12 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr1:186301464G>C	Missense Mutation	TPR	p.P1823A	translocated promoter r	28 (0.00)	25 (0.76)	2.03
12-03	Gp4 Focus 1	g.chr3:127298662A>G	Missense Mutation	TPRA1	p.F60S	transmembrane protein,	50 (0.00)	98 (0.14)	0.38
12-03	Gp4 Focus 1	g.chr19:57876304C>T	Missense Mutation	TRAPPC2P1	p.R35C	trafficking protein parti	49 (0.00)	47 (0.17)	0.45
12-03	Gp4 Focus 1	g.chr14:22446991T>C	RNA	TRAV8-6		T cell receptor alpha va	64 (0.00)	17 (0.47)	0.91
12-03	Gp4 Focus 1	g.chr17:18638583C>T	Missense Mutation	TRIM16L	p.P286L	tripartite motif containi	16 (0.00)	17 (0.94)	2.51
12-03	Gp4 Focus 1	g.chr9:119461005C>A	Missense Mutation	TRIM32	p.S328R	tripartite motif containi	74 (0.01)	57 (0.26)	0.70
12-03	Gp4 Focus 1	g.chr16:2105473C>T	Silent	TSC2	p.V184V	tuberous sclerosis 2	20 (0.00)	261 (0.15)	0.51
12-03	Gp4 Focus 1	g.chr13:45149012G>A	Missense Mutation	TSC22D1	p.P400L	TSC22 domain family,	47 (0.00)	12 (0.92)	1.19
12-03	Gp4 Focus 1	g.chr13:45149601G>A	Missense Mutation	TSC22D1	p.L204F	TSC22 domain family,	29 (0.00)	15 (0.80)	1.04
12-03	Gp4 Focus 1	g.chr20:51871004C>A	Missense Mutation	TSHZ2	p.T336N	teashirt zinc finger hom	40 (0.00)	24 (0.38)	1.00
12-03	Gp4 Focus 1	g.chr19:31770056G>A	Missense Mutation	TSHZ3	p.R215C	teashirt zinc finger hom	155 (0.00)	90 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr16:67859142C>G	Missense Mutation	TSNAXIP1	p.Q207E	translin-associated facto	15 (0.00)	52 (0.56)	1.90
12-03	Gp4 Focus 1	g.chr1:231064814G>A	Silent	TTC13	p.H442H	tetratricopeptide repeat	52 (0.00)	29 (0.55)	1.47
12-03	Gp4 Focus 1	g.chr22:28504323C>G	Missense Mutation	TTC28	p.A504P	tetratricopeptide repeat	43 (0.00)	44 (0.52)	1.39
12-03	Gp4 Focus 1	g.chr2:178482400C>T	Missense Mutation	TTC30A	p.A344T	tetratricopeptide repeat	104 (0.00)	169 (0.27)	0.73
12-03	Gp4 Focus 1	g.chr5:94834186G>A	Missense Mutation	TTC37	p.H1151Y	tetratricopeptide repeat	47 (0.00)	55 (0.25)	0.68

12-03	Gp4 Focus 1	g.chr14:91211211G>T	Missense Mutation	TTC7B	p.D167E	tetratricopeptide repeat	65 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 1	g.chr22:43459846G>C	Silent	TTLL1	p.L240L	tubulin tyrosine ligase-li	32 (0.00)	41 (0.24)	0.82
12-03	Gp4 Focus 1	g.chr2:179410751C>A	Missense Mutation	TTN	p.A31738S	titin	69 (0.00)	71 (0.99)	2.63
12-03	Gp4 Focus 1	g.chr2:179425781C>A	Missense Mutation	TTN	p.D28360Y	titin	39 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 1	g.chr2:179439106G>A	Missense Mutation	TTN	p.P23918L	titin	106 (0.01)	139 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr2:179455080G>A	Missense Mutation	TTN	p.P20458S	titin	108 (0.00)	69 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr2:179485146C>T	Missense Mutation	TTN	p.E15368K	titin	71 (0.00)	24 (0.62)	1.67
12-03	Gp4 Focus 1	g.chr2:179582935A>T	Missense Mutation	TTN	p.F8266L	titin	69 (0.00)	31 (0.35)	0.95
12-03	Gp4 Focus 1	g.chr2:132237911C>G	Silent	TUBA3D	p.R215R	tubulin, alpha 3d	39 (0.00)	25 (0.60)	2.14
12-03	Gp4 Focus 1	g.chr20:57599599G>A	Missense Mutation	TUBB1	p.A373T	tubulin, beta 1 class VI	38 (0.00)	43 (0.21)	0.56
12-03	Gp4 Focus 1	g.chr15:43689510G>A	Missense Mutation	TUBGCP4	p.E424K	tubulin, gamma comple	15 (0.00)	68 (0.50)	1.33
12-03	Gp4 Focus 1	g.chr22:50682471C>T	Missense Mutation	TUBGCP6	p.G140R	tubulin, gamma comple	26 (0.00)	59 (0.14)	0.46
12-03	Gp4 Focus 1	g.chrX:16850824A>G	Missense Mutation	TXLNG	p.I315V	taxilin gamma	21 (0.00)	26 (0.38)	0.64
12-03	Gp4 Focus 1	g.chr18:9886243G>A	Silent	TXNDC2	p.L24L	thioredoxin domain con	15 (0.00)	20 (0.45)	1.20
12-03	Gp4 Focus 1	g.chr11:88924443G>A	Missense Mutation	TYR	p.R298Q	tyrosinase	42 (0.00)	17 (0.71)	1.88
12-03	Gp4 Focus 1	g.chr3:69127005T>C	Missense Mutation	UBA3	p.K43E	ubiquitin-like modifier	19 (0.00)	42 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr1:64669746G>A	Missense Mutation	UBE2U	p.A5T	ubiquitin-conjugating e	34 (0.00)	23 (0.70)	1.86
12-03	Gp4 Focus 1	g.chr7:157041189T>C	Missense Mutation	UBE3C	p.L870S	ubiquitin protein ligase	89 (0.00)	101 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr8:103359299C>A	Silent	UBR5	p.V136V	ubiquitin protein ligase	50 (0.00)	41 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr2:234627941G>A	Missense Mutation	UGT1A4	p.A159T	UDP glucuronosyltrans	74 (0.00)	36 (0.42)	1.11
12-03	Gp4 Focus 1	g.chr4:70361547C>T	Silent	UGT2B4	p.L11L	UDP glucuronosyltrans	44 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr19:18956803C>T	Silent	UPF1	p.G82G	UPF1 regulator of nons	30 (0.00)	110 (0.18)	0.64
12-03	Gp4 Focus 1	g.chr19:18974298C>G	Silent	UPF1	p.L884L	UPF1 regulator of nons	63 (0.00)	519 (0.16)	0.55
12-03	Gp4 Focus 1	g.chr19:18976259G>T	Splice Site	UPF1	p.G1007W	UPF1 regulator of nons	47 (0.00)	116 (0.11)	0.40
12-03	Gp4 Focus 1	g.chr11:17542528C>G	Missense Mutation	USH1C	p.E367Q	Usher syndrome 1C (au	43 (0.00)	42 (0.88)	2.35
12-03	Gp4 Focus 1	g.chr19:17370100G>T	Nonsense Mutation	USHBP1	p.Y348*	Usher syndrome 1C bin	15 (0.00)	35 (0.63)	2.23
12-03	Gp4 Focus 1	g.chr8:11996013C>A	Missense Mutation	USP17L2	p.G86V	ubiquitin specific peptid	344 (0.00)	293 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr3:49348071G>A	Silent	USP4	p.F312F	ubiquitin specific peptid	36 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 1	g.chr7:6189213G>A	Splice Site	USP42		ubiquitin specific peptid	20 (0.00)	38 (0.29)	0.77
12-03	Gp4 Focus 1	g.chr10:75258554C>A	Missense Mutation	USP54	p.G1630C	ubiquitin specific peptid	50 (0.00)	16 (0.81)	2.78
12-03	Gp4 Focus 1	g.chr10:11504511C>A	Missense Mutation	USP6NL	p.G806W	USP6 N-terminal like	41 (0.00)	58 (0.43)	1.15
12-03	Gp4 Focus 1	g.chr17:30200717T>C	Missense Mutation	UTP6	p.Q454R	UTP6, small subunit (S	145 (0.00)	38 (0.24)	0.63
12-03	Gp4 Focus 1	g.chr17:30200719G>T	Missense Mutation	UTP6	p.S453R	UTP6, small subunit (S	141 (0.00)	36 (0.25)	0.67
12-03	Gp4 Focus 1	g.chr6:144811323G>A	Missense Mutation	UTRN	p.M1417I	utrophin	23 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 1	g.chr8:67578136T>C	Missense Mutation	VCPIP1	p.N353S	valosin containing prote	51 (0.00)	48 (0.40)	1.06

12-03	Gp4 Focus 1	g.chr3:51454295C>A	Missense Mutation	VPRBP	p.E734D	Vpr (HIV-1) binding pr	48 (0.00)	42 (0.17)	0.44
12-03	Gp4 Focus 1	g.chr9:79933427C>T	Missense Mutation	VPS13A	p.L1745F	vacuolar protein sorting	25 (0.00)	14 (0.57)	1.52
12-03	Gp4 Focus 1	g.chr8:100403806C>A	Missense Mutation	VPS13B	p.L986I	vacuolar protein sorting	30 (0.00)	23 (0.78)	2.09
12-03	Gp4 Focus 1	g.chr8:100790994C>A	Missense Mutation	VPS13B	p.P2530Q	vacuolar protein sorting	51 (0.00)	85 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr6:142539739C>T	Silent	VTA1	p.L295L	vesicle (multivesicular	17 (0.00)	100 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr2:98887308G>A	Missense Mutation	VWA3B	p.A1003T	von Willebrand factor A	43 (0.00)	35 (0.40)	1.07
12-03	Gp4 Focus 1	g.chr9:137019599C>A	Missense Mutation	WDR5	p.P215T	WD repeat domain 5	37 (0.00)	188 (0.15)	0.51
12-03	Gp4 Focus 1	g.chr16:74943470G>A	Missense Mutation	WDR59	p.T524M	WD repeat domain 59	30 (0.00)	36 (0.64)	1.70
12-03	Gp4 Focus 1	g.chr1:43688629C>T	Silent	WDR65	p.N889N		15 (0.00)	35 (0.29)	0.94
12-03	Gp4 Focus 1	g.chr19:38379959T>C	Missense Mutation	WDR87	p.K1412R	WD repeat domain 87	45 (0.00)	92 (0.13)	0.48
12-03	Gp4 Focus 1	g.chr12:1003773C>T	Missense Mutation	WNK1	p.A1852V	WNK lysine deficient p	47 (0.00)	25 (0.64)	1.71
12-03	Gp4 Focus 1	g.chr3:55504271C>T	Missense Mutation	WNT5A	p.G331D	wingless-type MMTV i	22 (0.00)	47 (0.32)	0.85
12-03	Gp4 Focus 1	g.chr10:102240801C>A	Silent	WNT8B	p.V96V	wingless-type MMTV i	29 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 1	g.chr12:108634254G>C	Missense Mutation	WSCD2	p.M426I	WSC domain containin	108 (0.00)	238 (0.29)	0.77
12-03	Gp4 Focus 1	g.chr3:14209238C>T	Intron	XPC		xeroderma pigmentosun	107 (0.01)	53 (0.98)	1.13
12-03	Gp4 Focus 1	g.chr3:14217269T>A	Intron	XPC		xeroderma pigmentosun	113 (0.00)	39 (0.44)	0.50
12-03	Gp4 Focus 1	g.chr2:61721055G>A	Nonsense Mutation	XPO1	p.Q407*	exportin 1	16 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 1	g.chr2:216990707C>T	Silent	XRCC5	p.L251L	X-ray repair complemer	28 (0.00)	29 (0.24)	0.64
12-03	Gp4 Focus 1	g.chr12:69756642G>A	Silent	YEATS4	p.G42G	YEATS domain contain	41 (0.00)	37 (0.27)	0.72
12-03	Gp4 Focus 1	g.chr12:69756645C>T	Silent	YEATS4	p.H43H	YEATS domain contain	41 (0.00)	40 (0.15)	0.40
12-03	Gp4 Focus 1	g.chrX:21875362G>A	Missense Mutation	YY2	p.V254I	YY2 transcription facto	90 (0.00)	85 (0.76)	1.27
12-03	Gp4 Focus 1	g.chr22:50277386G>A	Missense Mutation	ZBED4	p.E26K	zinc finger, BED-type c	30 (0.00)	17 (0.29)	0.99
12-03	Gp4 Focus 1	g.chr20:56188259G>A	Silent	ZBP1	p.H210H	Z-DNA binding protein	19 (0.00)	33 (0.21)	0.57
12-03	Gp4 Focus 1	g.chr20:56190071G>C	Missense Mutation	ZBP1	p.A125G	Z-DNA binding protein	73 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr9:129594873C>T	Nonsense Mutation	ZBTB43	p.Q29*	zinc finger and BTB do	25 (0.00)	18 (0.94)	2.52
12-03	Gp4 Focus 1	g.chr1:203816625C>A	Missense Mutation	ZC3H11A	p.S452R	zinc finger CCCH-type	79 (0.00)	20 (0.65)	1.73
12-03	Gp4 Focus 1	g.chr7:129680936C>T	Silent	ZC3HC1	p.L88L	zinc finger, C3HC-type	55 (0.00)	81 (0.53)	1.42
12-03	Gp4 Focus 1	g.chr2:220072707G>A	Silent	ZFAND2B	p.R127R	zinc finger, AN1-type d	22 (0.00)	28 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr14:24003545G>C	Silent	ZFHX2	p.V330V	zinc finger homeobox 2	19 (0.00)	98 (0.28)	0.53
12-03	Gp4 Focus 1	g.chr16:72829578G>A	Silent	ZFHX3	p.L2335L	zinc finger homeobox 3	100 (0.00)	171 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr16:72991627G>T	Nonsense Mutation	ZFHX3	p.C806*	zinc finger homeobox 3	50 (0.00)	256 (0.20)	0.53
12-03	Gp4 Focus 1	g.chr19:36898794G>A	Missense Mutation	ZFP82	p.S44L	ZFP82 zinc finger prote	28 (0.00)	72 (0.32)	1.17
12-03	Gp4 Focus 1	g.chr16:68591943G>T	Nonsense Mutation	ZFP90	p.E26*	ZFP90 zinc finger prote	37 (0.00)	53 (0.30)	1.03
12-03	Gp4 Focus 1	g.chr16:25264294T>C	Silent	ZKSCAN2	p.T217T	zinc finger with KRAB	101 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr17:4645082G>T	Missense Mutation	ZMYND15	p.Q266H	zinc finger, MYND-typ	31 (0.00)	17 (0.29)	0.78

12-03	Gp4 Focus 1	g.chr16:3282449G>C	Missense Mutation	ZNF200	p.D146E	zinc finger protein 200	45 (0.02)	21 (0.43)	1.50
12-03	Gp4 Focus 1	g.chr11:7022224C>A	Missense Mutation	ZNF214	p.W230C	zinc finger protein 214	91 (0.00)	22 (0.77)	1.55
12-03	Gp4 Focus 1	g.chr19:44661933G>A	Silent	ZNF234	p.R588R	zinc finger protein 234	60 (0.00)	48 (0.31)	0.83
12-03	Gp4 Focus 1	g.chr6:43325190C>T	Missense Mutation	ZNF318	p.D288N	zinc finger protein 318	17 (0.00)	25 (0.52)	1.39
12-03	Gp4 Focus 1	g.chr6:26637735T>A	Silent	ZNF322	p.L349L	zinc finger protein 322	106 (0.00)	171 (0.23)	0.79
12-03	Gp4 Focus 1	g.chr19:37101581C>G	Missense Mutation	ZNF382	p.R57G	zinc finger protein 382	15 (0.00)	56 (0.68)	2.48
12-03	Gp4 Focus 1	g.chr18:72344148C>T	Silent	ZNF407	p.L391L	zinc finger protein 407	186 (0.00)	52 (0.27)	0.72
12-03	Gp4 Focus 1	g.chr16:49764776C>A	Missense Mutation	ZNF423	p.M61I	zinc finger protein 423	39 (0.00)	15 (0.60)	1.60
12-03	Gp4 Focus 1	g.chr1:23688682C>T	Missense Mutation	ZNF436	p.S398N	zinc finger protein 436	35 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 1	g.chr10:31133922C>A	Missense Mutation	ZNF438	p.V819L	zinc finger protein 438	30 (0.00)	33 (0.18)	0.48
12-03	Gp4 Focus 1	g.chr19:53345247C>T	Silent	ZNF468	p.Q100Q	zinc finger protein 468	57 (0.00)	21 (0.29)	1.02
12-03	Gp4 Focus 1	g.chr1:247492530C>T	Silent	ZNF496	p.V117V	zinc finger protein 496	23 (0.00)	111 (0.24)	0.65
12-03	Gp4 Focus 1	g.chr20:62598747A>G	Missense Mutation	ZNF512B	p.L84P	zinc finger protein 512	52 (0.00)	319 (0.20)	0.54
12-03	Gp4 Focus 1	g.chr19:2876134G>A	Silent	ZNF556	p.Q58Q	zinc finger protein 556	98 (0.00)	22 (0.41)	1.56
12-03	Gp4 Focus 1	g.chr15:64967936C>T	Silent	ZNF609	p.I961I	zinc finger protein 609	24 (0.00)	54 (0.19)	0.49
12-03	Gp4 Focus 1	g.chr19:53209750A>T	Missense Mutation	ZNF611	p.D186E	zinc finger protein 611	69 (0.00)	64 (0.28)	1.00
12-03	Gp4 Focus 1	g.chr9:116811943C>A	Silent	ZNF618	p.L787L	zinc finger protein 618	40 (0.00)	391 (0.19)	0.50
12-03	Gp4 Focus 1	g.chr17:16526115G>A	Silent	ZNF624	p.P695P	zinc finger protein 624	48 (0.00)	45 (0.22)	0.59
12-03	Gp4 Focus 1	g.chr19:22363491C>A	Missense Mutation	ZNF676	p.G343V	zinc finger protein 676	76 (0.00)	44 (0.27)	0.97
12-03	Gp4 Focus 1	g.chr19:12015617C>A	Silent	ZNF69	p.G135G	zinc finger protein 69	18 (0.00)	33 (0.21)	0.75
12-03	Gp4 Focus 1	g.chr15:90611556C>A	Missense Mutation	ZNF710	p.A396D	zinc finger protein 710	22 (0.00)	192 (0.23)	0.61
12-03	Gp4 Focus 1	g.chr15:90611719G>A	Silent	ZNF710	p.L450L	zinc finger protein 710	47 (0.00)	51 (0.35)	0.94
12-03	Gp4 Focus 1	g.chr7:149318081C>T	RNA	ZNF767			18 (0.00)	60 (0.12)	0.44
12-03	Gp4 Focus 1	g.chr7:148963789C>A	Missense Mutation	ZNF783	p.L130M	zinc finger family mem	40 (0.00)	312 (0.11)	0.39
12-03	Gp4 Focus 1	g.chr7:149557977G>T	Missense Mutation	ZNF862	p.E576D	zinc finger protein 862	83 (0.00)	152 (0.18)	0.66
12-03	Gp4 Focus 1	g.chr10:75558774G>A	Silent	ZSWIM8	p.L1392L	zinc finger, SWIM-type	26 (0.00)	81 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr4:170988511C>T	Nonsense Mutation	AADAT	p.W310*	aminoadipate aminotran	24 (0.00)	32 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr7:48545969G>A	Silent	ABCA13	p.L4443L	ATP-binding cassette, s	20 (0.00)	45 (0.31)	0.83
12-03	Gp4 Focus 2	g.chr17:66873758C>T	Silent	ABCA8	p.E1367E	ATP-binding cassette, s	23 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr2:169791882C>T	Silent	ABCB11	p.E956E	ATP-binding cassette, s	62 (0.00)	103 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr12:21998665C>A	Nonsense Mutation	ABCC9	p.G990*	ATP-binding cassette, s	34 (0.00)	35 (0.46)	1.22
12-03	Gp4 Focus 2	g.chr2:44078934C>T	Silent	ABCG8	p.T178T	ATP-binding cassette, s	55 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr2:233877953C>T	Silent	AC106876.2	p.F74F		53 (0.00)	23 (0.30)	0.81
12-03	Gp4 Focus 2	g.chr5:179078941C>A	Missense Mutation	AC136604.1	p.Q142K		22 (0.00)	15 (0.40)	1.07
12-03	Gp4 Focus 2	g.chr17:35454032G>A	Silent	ACACA	p.L2227L	acetyl-CoA carboxylase	35 (0.00)	25 (0.20)	0.53

12-03	Gp4 Focus 2	g.chr4:8398748G>T	Silent	ACOX3	p.A324A	acyl-CoA oxidase 3, pri	46 (0.00)	21 (0.33)	1.52
12-03	Gp4 Focus 2	g.chr7:149983558C>A	Missense Mutation	ACTR3C	p.W123C	ARP3 actin-related prot	49 (0.00)	41 (0.24)	0.65
12-03	Gp4 Focus 2	g.chrX:127185969G>A	Missense Mutation	ACTRT1	p.P73S	actin-related protein T1	51 (0.00)	43 (0.19)	0.42
12-03	Gp4 Focus 2	g.chr8:38880759G>A	Missense Mutation	ADAM9	p.A277T	ADAM metallopeptidas	17 (0.00)	42 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr1:167865842C>T	Missense Mutation	ADCY10	p.E244K	adenylate cyclase 10 (so	50 (0.00)	58 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr8:131792741G>A	Silent	ADCY8	p.N1217N	adenylate cyclase 8 (bra	38 (0.00)	39 (0.31)	0.82
12-03	Gp4 Focus 2	g.chr8:131792750C>A	Missense Mutation	ADCY8	p.E1214D	adenylate cyclase 8 (bra	37 (0.00)	30 (0.40)	1.07
12-03	Gp4 Focus 2	g.chr8:67357640C>T	Silent	ADHFE1	p.L181L	alcohol dehydrogenase,	35 (0.00)	64 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr4:7770701G>A	Missense Mutation	AFAP1	p.S679L	actin filament associate	20 (0.00)	17 (0.47)	2.14
12-03	Gp4 Focus 2	g.chr5:132232069C>A	Missense Mutation	AFF4	p.E751D	AF4/FMR2 family, men	42 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr6:151672374G>A	Missense Mutation	AKAP12	p.V950I	A kinase (PRKA) ancho	69 (0.00)	37 (0.16)	0.51
12-03	Gp4 Focus 2	g.chr19:15508426G>A	Missense Mutation	AKAP8L	p.T437I	A kinase (PRKA) ancho	23 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr10:82012502G>A	Missense Mutation	AL359195.1	p.G7D		35 (0.00)	23 (0.30)	0.81
12-03	Gp4 Focus 2	g.chr10:82013288C>T	Missense Mutation	AL359195.1	p.P269L		53 (0.00)	31 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr3:183967021A>G	Silent	ALG3	p.C15C	ALG3, alpha-1,3- mann	42 (0.00)	16 (0.44)	1.17
12-03	Gp4 Focus 2	g.chr11:46439466G>A	Missense Mutation	AMBRA1	p.P948L	autophagy/beclin-1 regu	100 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr12:53825000G>T	Missense Mutation	AMHR2	p.D394Y	anti-Mullerian hormone	45 (0.00)	58 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr16:89349555C>T	Missense Mutation	ANKRD11	p.G1132E	ankyrin repeat domain 1	45 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr10:37430813T>C	Missense Mutation	ANKRD30A	p.S274P	ankyrin repeat domain 3	15 (0.00)	47 (0.11)	0.44
12-03	Gp4 Focus 2	g.chr2:98206157G>A	RNA	ANKRD36B		ankyrin repeat domain 3	73 (0.00)	54 (0.70)	1.88
12-03	Gp4 Focus 2	g.chr17:41019553C>A	RNA	AOC4P		amine oxidase, copper c	47 (0.00)	35 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr19:16317154G>A	Missense Mutation	AP1M1	p.V68I	adaptor-related protein	22 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr12:99043335G>A	Silent	APAF1	p.V133V	apoptotic peptidase acti	27 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 2	g.chr14:20923852G>A	Silent	APEX1	p.E16E	APEX nuclease (multifu	20 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chrX:130217182G>A	Silent	ARHGAP36	p.L87L	Rho GTPase activating	24 (0.00)	15 (0.40)	0.67
12-03	Gp4 Focus 2	g.chr5:90669505G>A	Missense Mutation	ARRDC3	p.S395L	arrestin domain containi	47 (0.00)	54 (0.20)	0.79
12-03	Gp4 Focus 2	g.chr19:4902748G>A	Silent	ARRDC5	p.T44T	arrestin domain containi	42 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr2:9458726G>T	Splice Site	ASAP2	p.G140V	ArfGAP with SH3 dom	60 (0.00)	41 (0.20)	0.52
12-03	Gp4 Focus 2	g.chr6:101215115G>A	Missense Mutation	ASCC3	p.T501I	activating signal cointeg	52 (0.00)	47 (0.21)	0.57
12-03	Gp4 Focus 2	g.chr2:25966186A>T	Missense Mutation	ASXL2	p.V1007D	additional sex combs lik	41 (0.00)	57 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr2:25976410C>T	Missense Mutation	ASXL2	p.G379R	additional sex combs lik	69 (0.01)	142 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr22:39918005G>A	Missense Mutation	ATF4	p.D152N	activating transcription	20 (0.00)	75 (0.21)	0.57
12-03	Gp4 Focus 2	g.chr13:25255764G>A	Missense Mutation	ATP12A	p.G25E	ATPase, H+/K+ transpo	33 (0.00)	29 (0.21)	0.55
12-03	Gp4 Focus 2	g.chr16:84485531G>A	Silent	ATP2C2	p.L555L	ATPase, Ca++ transport	36 (0.00)	18 (0.28)	0.89
12-03	Gp4 Focus 2	g.chr3:48491453G>A	Silent	ATRIP	p.K86K	ATR interacting protein	75 (0.00)	88 (0.28)	0.76

12-03	Gp4 Focus 2	g.chr12:657251G>A	Missense Mutation	B4GALNT3	p.D257N	beta-1,4-N-acetyl-galact	15 (0.00)	26 (0.23)	0.62
12-03	Gp4 Focus 2	g.chr7:97939854G>A	Silent	BAIAP2L1	p.P286P	BAI1-associated protein	27 (0.00)	64 (0.09)	0.38
12-03	Gp4 Focus 2	g.chr2:160189186G>A	Silent	BAZ2B	p.I1936I	bromodomain adjacent t	49 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chrX:18221684G>A	Missense Mutation	BEND2	p.P282S	BEN domain containing	15 (0.00)	52 (0.63)	1.25
12-03	Gp4 Focus 2	g.chr3:5024690G>A	Silent	BHLHE40	p.Q184Q	basic helix-loop-helix fa	84 (0.00)	14 (0.43)	1.14
12-03	Gp4 Focus 2	g.chr2:32740724G>A	Missense Mutation	BIRC6	p.A3746T	baculoviral IAP repeat c	21 (0.00)	67 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr2:32774525C>T	Missense Mutation	BIRC6	p.S4374L	baculoviral IAP repeat c	56 (0.00)	76 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr15:91266271T>C	Intron	BLM		Bloom syndrome, RecQ	29 (0.00)	35 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr15:91266293A>G	Intron	BLM		Bloom syndrome, RecQ	29 (0.00)	40 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr15:91320111G>A	Intron	BLM		Bloom syndrome, RecQ	15 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr15:91320120G>A	Intron	BLM		Bloom syndrome, RecQ	18 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr15:91356957G>A	Intron	BLM		Bloom syndrome, RecQ	25 (0.00)	95 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr10:43292949C>T	Silent	BMS1	p.L689L	BMS1 ribosome biogen	36 (0.00)	36 (0.22)	0.76
12-03	Gp4 Focus 2	g.chr4:13603261C>T	Missense Mutation	BOD1L1	p.V1755I	biorientation of chromo	92 (0.00)	174 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr4:13606508G>A	Silent	BOD1L1	p.D672D	biorientation of chromo	90 (0.00)	112 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr1:220233124G>A	Silent	BPNT1	p.L228L	3'(2'), 5'-bisphosphate n	58 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr17:41203938C>T	Intron	BRCA1		breast cancer 1, early on	15 (0.00)	41 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr13:32956917G>A	Intron	BRCA2		breast cancer 2, early on	68 (0.00)	61 (0.30)	0.79
12-03	Gp4 Focus 2	g.chr11:8947589C>T	Missense Mutation	C11orf16	p.G209R	chromosome 11 open re	59 (0.00)	26 (0.42)	1.13
12-03	Gp4 Focus 2	g.chr14:23732136G>A	Splice Site	C14orf164			69 (0.00)	39 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr16:67180180G>A	Splice Site	C16orf70		chromosome 16 open re	28 (0.00)	54 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr16:9197090C>T	Missense Mutation	C16orf72	p.P186L	chromosome 16 open re	17 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr3:126915935C>G	Missense Mutation	C3orf56	p.P136R	chromosome 3 open rea	81 (0.00)	39 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr5:41917325G>A	Missense Mutation	C5orf51	p.G270E	chromosome 5 open rea	18 (0.00)	29 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr5:41153964G>A	Silent	C6	p.C746C	complement component	27 (0.00)	18 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr8:86250583G>A	Silent	CA1	p.L45L	carbonic anhydrase I	62 (0.00)	66 (0.38)	1.01
12-03	Gp4 Focus 2	g.chr1:181731730G>A	Nonsense Mutation	CACNA1E	p.W1542*	calcium channel, voltag	28 (0.00)	90 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr1:201020130G>A	Silent	CACNA1S	p.Y1365Y	calcium channel, voltag	29 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr3:85085740C>G	Intron	CADM2		cell adhesion molecule	33 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr3:85117158G>A	Intron	CADM2		cell adhesion molecule	43 (0.00)	39 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr3:85156162G>A	Intron	CADM2		cell adhesion molecule	16 (0.00)	46 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr3:85157248G>A	Intron	CADM2		cell adhesion molecule	55 (0.00)	39 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr3:85239009G>A	Intron	CADM2		cell adhesion molecule	54 (0.00)	59 (0.17)	0.45
12-03	Gp4 Focus 2	g.chr3:85412573G>C	Intron	CADM2		cell adhesion molecule	109 (0.00)	48 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr3:85579380C>G	Intron	CADM2		cell adhesion molecule	34 (0.00)	72 (0.17)	0.44

12-03	Gp4 Focus 2	g.chr3:85603518G>A	Intron	CADM2		cell adhesion molecule	19 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr3:85666403G>T	Intron	CADM2		cell adhesion molecule	57 (0.00)	22 (0.32)	0.85
12-03	Gp4 Focus 2	g.chr3:85800395G>A	Intron	CADM2		cell adhesion molecule	43 (0.00)	103 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr3:85856120G>A	Intron	CADM2		cell adhesion molecule	20 (0.00)	39 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr3:85869424G>A	Intron	CADM2		cell adhesion molecule	31 (0.00)	60 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr8:91094887G>A	Silent	CALB1	p.A13A	calbindin 1, 28kDa	46 (0.00)	32 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr15:42681196G>A	Missense Mutation	CAPN3	p.V235M	calpain 3, (p94)	65 (0.02)	28 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr11:76825414G>A	Silent	CAPN5	p.R251R	calpain 5	45 (0.00)	35 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr2:74418556G>A	Missense Mutation	CATX-2	p.G14R		16 (0.00)	27 (0.30)	0.79
12-03	Gp4 Focus 2	g.chr18:70205565G>A	Missense Mutation	CBLN2	p.A174V	cerebellin 2 precursor	39 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr10:70520911G>A	Missense Mutation	CCAR1	p.D690N	cell division cycle and a	40 (0.00)	62 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr2:55529097C>T	Missense Mutation	CCDC88A	p.G1500E	coiled-coil domain cont	43 (0.00)	24 (0.21)	0.45
12-03	Gp4 Focus 2	g.chr14:91779496C>T	Silent	CCDC88C	p.E888E	coiled-coil domain cont	35 (0.00)	48 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr10:42920824A>T	RNA	CCNYL2		cyclin Y-like 2	20 (0.00)	35 (0.74)	2.56
12-03	Gp4 Focus 2	g.chr10:73472429C>T	Silent	CDH23	p.G1081G	cadherin-related 23	30 (0.00)	21 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr12:123749797C>T	Missense Mutation	CDK2AP1	p.E48K	cyclin-dependent kinase	31 (0.00)	55 (0.53)	1.41
12-03	Gp4 Focus 2	g.chr19:43025647G>A	Missense Mutation	CEACAM1	p.P244S	carcinoembryonic antig	53 (0.00)	43 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr22:17662415C>T	Silent	CECR1	p.K498K	cat eye syndrome chron	131 (0.00)	63 (0.30)	0.80
12-03	Gp4 Focus 2	g.chr3:48699809C>G	Missense Mutation	CELSR3	p.G87R	cadherin, EGF LAG sev	16 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr3:101450768G>A	Missense Mutation	CEP97	p.A178T	centrosomal protein 97k	64 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr21:37775080G>A	Missense Mutation	CHAF1B	p.D230N	chromatin assembly fac	98 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr5:98259918G>A	Intron	CHD1		chromodomain helicase	25 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr12:6682247C>A	Silent	CHD4	p.L1875L	chromodomain helicase	19 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr20:40161867C>T	Missense Mutation	CHD6	p.E126K	chromodomain helicase	63 (0.00)	31 (0.16)	0.52
12-03	Gp4 Focus 2	g.chr14:21873998G>A	Missense Mutation	CHD8	p.T978I	chromodomain helicase	18 (0.00)	34 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr16:53276894G>A	Missense Mutation	CHD9	p.C1007Y	chromodomain helicase	44 (0.00)	84 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr16:53288454G>A	Silent	CHD9	p.L1322L	chromodomain helicase	102 (0.00)	163 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr1:86896578G>A	Missense Mutation	CLCA2	p.R170H	chloride channel access	114 (0.00)	49 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr14:38724346C>T	Silent	CLEC14A	p.P294P	C-type lectin domain fa	37 (0.00)	20 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr17:57733367T>C	Silent	CLTC	p.I316I	clathrin, heavy chain (H	16 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chrX:150911895G>A	Nonsense Mutation	CNGA2	p.W307*	cyclic nucleotide gated	34 (0.00)	22 (0.32)	0.53
12-03	Gp4 Focus 2	g.chr6:154771236C>T	De novo Start OutOf	CNKSR3		CNKSR family member	25 (0.00)	41 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr12:56705144C>T	Missense Mutation	CNPY2	p.D87N	canopy FGF signaling r	47 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr1:205033477C>T	Missense Mutation	CNTN2	p.P423L	contactin 2 (axonal)	53 (0.00)	45 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr2:125530513G>A	Missense Mutation	CNTNAP5	p.V890M	contactin associated pro	40 (0.00)	33 (0.39)	1.59

12-03	Gp4 Focus 2	g.chr9:123933708G>A	Missense Mutation	CNTRL	p.C2100Y	centriolin	53 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 2	g.chrX:107783035G>A	Splice Site	COL4A5	p.K47K	collagen, type IV, alpha	17 (0.00)	26 (0.27)	0.45
12-03	Gp4 Focus 2	g.chr11:61196698C>T	Missense Mutation	CPSF7	p.G4R	cleavage and polyadeny	28 (0.00)	50 (0.30)	0.80
12-03	Gp4 Focus 2	g.chr19:18864379C>T	Missense Mutation	CRTC1	p.A203V	CREB regulated transcr	129 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr3:39185882C>A	Missense Mutation	CSRNP1	p.D176Y	cysteine-serine-rich nuc	45 (0.00)	20 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr4:1244587G>A	RNA	CTBP1-AS2		CTBP1 antisense RNA	22 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr19:22868402C>T	RNA	CTC-457E21.9			27 (0.00)	42 (0.12)	0.46
12-03	Gp4 Focus 2	g.chr10:67862982G>A	Missense Mutation	CTNNA3	p.S637F	catenin (cadherin-associ	40 (0.00)	32 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr11:66334725G>A	Missense Mutation	CTSF	p.S200L	cathepsin F	41 (0.00)	34 (0.26)	0.71
12-03	Gp4 Focus 2	g.chr4:74863957C>T	Missense Mutation	CXCL5	p.A70T	chemokine (C-X-C moti	36 (0.00)	18 (0.39)	1.04
12-03	Gp4 Focus 2	g.chr1:47366047G>A	RNA	CYP4Z2P		cytochrome P450, famil	17 (0.00)	16 (0.31)	0.83
12-03	Gp4 Focus 2	g.chr9:124409606C>T	Intron	DAB2IP		DAB2 interacting protei	33 (0.00)	56 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr9:124442241G>A	Intron	DAB2IP		DAB2 interacting protei	67 (0.01)	16 (0.38)	1.00
12-03	Gp4 Focus 2	g.chr9:124452487C>T	Intron	DAB2IP		DAB2 interacting protei	45 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr11:6645078G>A	Missense Mutation	DCHS1	p.T2610I	dachsous cadherin-relat	46 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr13:114138273C>T	Silent	DCUN1D2	p.E34E	DCN1, defective in cull	67 (0.00)	27 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr12:124103357G>A	Missense Mutation	DDX55	p.E436K	DEAD (Asp-Glu-Ala-A	28 (0.00)	46 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr1:161092312G>A	Splice Site	DEDD	p.D194D	death effector domain c	27 (0.00)	32 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr20:210326G>T	Missense Mutation	DEFB129	p.A156S	defensin, beta 129	49 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr2:234377165C>T	Missense Mutation	DGKD	p.S1174F	diacylglycerol kinase, d	42 (0.00)	10 (0.70)	1.87
12-03	Gp4 Focus 2	g.chr4:24572332C>T	Missense Mutation	DHX15	p.E216K	DEAH (Asp-Glu-Ala-H	29 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr17:5353690C>A	Nonsense Mutation	DHX33	p.E297*	DEAH (Asp-Glu-Ala-H	83 (0.00)	51 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr5:140903731G>A	Missense Mutation	DIAPH1	p.R1211W	diaphanous-related form	27 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr14:95562950G>A	Missense Mutation	DICER1	p.A1436V	dicer 1, ribonuclease ty	23 (0.00)	39 (0.21)	0.55
12-03	Gp4 Focus 2	g.chr10:518472G>A	Missense Mutation	DIP2C	p.P59S	DIP2 disco-interacting	48 (0.00)	13 (0.54)	1.44
12-03	Gp4 Focus 2	g.chr15:41223819C>T	Silent	DLL4	p.Y171Y	delta-like 4 (Drosophila	70 (0.00)	19 (0.37)	0.98
12-03	Gp4 Focus 2	g.chr10:124339155G>A	Silent	DMBT1	p.V247V	deleted in malignant bra	237 (0.00)	67 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr10:70182126G>A	Silent	DNA2	p.D851D	DNA replication helicas	70 (0.00)	117 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr7:21775420C>T	Missense Mutation	DNAH11	p.R2535C	dynein, axonemal, heav	66 (0.00)	102 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr17:76420158G>A	Silent	DNAH17	p.I4401I	dynein, axonemal, heav	61 (0.00)	19 (0.42)	1.12
12-03	Gp4 Focus 2	g.chr17:11607546G>A	Nonsense Mutation	DNAH9	p.W1726*	dynein, axonemal, heav	61 (0.00)	42 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr3:186299241C>T	Silent	DNAJB11	p.L180L	DnaJ (Hsp40) homolog,	66 (0.00)	52 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr19:12987105C>T	Missense Mutation	DNASE2	p.G261D	deoxyribonuclease II, ly	34 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr11:6519942C>T	Missense Mutation	DNHD1	p.P166L	dynein heavy chain dom	101 (0.00)	32 (0.41)	1.08
12-03	Gp4 Focus 2	g.chr10:101668873G>A	Missense Mutation	DNMBP	p.S764L	dynamin binding protei	29 (0.00)	20 (0.25)	0.67

12-03	Gp4 Focus 2	g.chr19:10270547G>A	Missense Mutation	DNMT1	p.L365F	DNA (cytosine-5-)-met	37 (0.00)	38 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr6:7580848C>T	Silent	DSP	p.T1475T	desmoplakin	82 (0.00)	31 (0.23)	0.60
12-03	Gp4 Focus 2	g.chr1:221879483G>T	Missense Mutation	DUSP10	p.N379K	dual specificity phospha	146 (0.00)	37 (0.57)	1.51
12-03	Gp4 Focus 2	g.chr14:102452290G>A	Silent	DYNC1H1	p.K576K	dynein, cytoplasmic 1,	21 (0.00)	27 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr2:207530722C>A	Missense Mutation	DYTN	p.D338Y	dystrotelin	76 (0.00)	64 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr3:137802972C>T	Missense Mutation	DZIP1L	p.A396T	DAZ interacting zinc fi	21 (0.00)	35 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr5:158140069G>A	Silent	EBF1	p.N426N	early B-cell factor 1	62 (0.00)	30 (0.23)	0.62
12-03	Gp4 Focus 2	g.chr1:236557749G>A	Missense Mutation	EDARADD	p.G2D	EDAR-associated death	21 (0.00)	33 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr2:88874638C>T	Missense Mutation	EIF2AK3	p.C788Y	eukaryotic translation in	28 (0.00)	105 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr15:40259742C>T	Silent	EIF2AK4	p.Y405Y	eukaryotic translation in	18 (0.00)	34 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr17:12898306G>A	Silent	ELAC2	p.L628L	elaC ribonuclease Z 2	31 (0.00)	24 (0.50)	1.33
12-03	Gp4 Focus 2	g.chr13:41525490G>A	Silent	ELF1	p.G112G	E74-like factor 1 (ets do	37 (0.00)	32 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr4:111398170C>T	Silent	ENPEP	p.L200L	glutamyl aminopeptidas	27 (0.00)	31 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr22:40161500G>A	Missense Mutation	ENTHD1	p.P316L	ENTH domain containi	40 (0.00)	48 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr22:41521986A>T	Missense Mutation	EP300	p.N283I	E1A binding protein p3	19 (0.00)	44 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr22:41572259T>A	Missense Mutation	EP300	p.F1596L	E1A binding protein p3	26 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 2	g.chr22:41572260G>A	Missense Mutation	EP300	p.V1597M	E1A binding protein p3	26 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 2	g.chr12:132479425G>A	Silent	EP400	p.E917E	E1A binding protein p4	21 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr12:56489559G>T	Missense Mutation	ERBB3	p.R675M	v-erb-b2 avian erythrob	27 (0.00)	49 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr16:14022092G>A	Splice Site	ERCC4	p.K264K	excision repair cross-co	60 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr21:39803533C>T	Intron	ERG		v-ets avian erythroblast	60 (0.00)	46 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr21:39833410G>A	Intron	ERG		v-ets avian erythroblast	42 (0.00)	70 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr12:56537050G>A	Missense Mutation	ESYT1	p.R1063Q	extended synaptotagmin	21 (0.00)	49 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr1:11142912G>A	Silent	EXOSC10	p.D371D	exosome component 10	55 (0.00)	42 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr8:28574101G>C	Silent	EXTL3	p.R175R	exostosin-like glycosylt	82 (0.00)	18 (0.28)	0.74
12-03	Gp4 Focus 2	g.chrX:154176085G>A	Silent	F8	p.F667F	coagulation factor VIII,	29 (0.00)	12 (0.58)	0.97
12-03	Gp4 Focus 2	g.chr19:17653015G>A	Missense Mutation	FAM129C	p.S445N	family with sequence si	38 (0.00)	24 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr5:16474862C>A	Silent	FAM134B	p.L353L	family with sequence si	29 (0.00)	49 (0.20)	0.54
12-03	Gp4 Focus 2	g.chr5:137298122C>A	Missense Mutation	FAM13B	p.G406C	family with sequence si	47 (0.00)	34 (0.26)	0.71
12-03	Gp4 Focus 2	g.chr1:55077364C>T	Silent	FAM151A	p.L285L	family with sequence si	64 (0.00)	19 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr11:6235765C>T	Silent	FAM160A2	p.A825A	family with sequence si	88 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr14:45432442C>T	Missense Mutation	FAM179B	p.S273F	family with sequence si	41 (0.00)	63 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr15:31210489C>T	Missense Mutation	FAN1	p.P645L	FANCD2/FANCI-assoc	19 (0.00)	40 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr9:35078246C>A	Missense Mutation	FANCG	p.E134D	Fanconi anemia, compl	35 (0.03)	33 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr2:223504350C>G	Missense Mutation	FARSB	p.R135P	phenylalanyl-tRNA syn	18 (0.00)	57 (0.14)	0.45

12-03	Gp4 Focus 2	g.chr4:187510185G>A	Missense Mutation	FAT1	p.P4443L	FAT atypical cadherin 1	186 (0.00)	79 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr2:97364816C>T	RNA	FER1L5		fer-1-like family memb	22 (0.00)	28 (0.39)	1.05
12-03	Gp4 Focus 2	g.chr15:91437287G>A	Splice Site	FES	p.K775K	FES proto-oncogene, ty	84 (0.00)	48 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr11:65655091G>A	Missense Mutation	FIBP	p.L131F	fibroblast growth factor	103 (0.00)	29 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr6:76024295C>T	Missense Mutation	FILIP1	p.S418N	filamin A interacting pr	55 (0.00)	135 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr9:115973787G>A	Missense Mutation	FKBP15	p.P47S	FK506 binding protein	40 (0.00)	41 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr1:152281564C>T	Missense Mutation	FLG	p.R1933K	filaggrin	36 (0.00)	56 (0.14)	0.38
12-03	Gp4 Focus 2	g.chrX:153592436G>A	Missense Mutation	FLNA	p.A745V	filamin A, alpha	15 (0.00)	14 (0.71)	1.19
12-03	Gp4 Focus 2	g.chr5:180038347G>A	Missense Mutation	FLT4	p.H1224Y	fms-related tyrosine kin	15 (0.00)	17 (0.59)	1.57
12-03	Gp4 Focus 2	g.chr15:33180430G>A	Nonsense Mutation	FMN1	p.Q1260*	formin 1	82 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr16:15977957G>A	Missense Mutation	FOPNL	p.S45L	FGFR1OP N-terminal li	26 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr17:26856214C>G	Missense Mutation	FOXN1	p.L268V	forkhead box N1	22 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr9:14750188G>A	Missense Mutation	FREM1	p.P1832S	FRAS1 related extracell	54 (0.00)	59 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr17:61901527C>A	Missense Mutation	FTSJ3	p.K357N	FtsJ homolog 3 (E. coli)	43 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr3:97705698C>T	RNA	GABRR3		gamma-aminobutyric ac	24 (0.00)	45 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr12:51753019C>A	Missense Mutation	GALNT6	p.S422I	polypeptide N-acetylgal	62 (0.00)	36 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr4:174235285C>T	Silent	GALNT7	p.T522T	polypeptide N-acetylgal	25 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr9:128113092G>A	Silent	GAPVD1	p.V1149V	GTPase activating prote	23 (0.00)	34 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr17:34074279G>A	Missense Mutation	GAS2L2	p.P281S	growth arrest-specific 2	62 (0.00)	24 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr15:90784200C>T	Silent	GDPGP1	p.D20D	GDP-D-glucose phosph	72 (0.00)	46 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr7:150164198G>T	Missense Mutation	GIMAP8	p.D138Y	GTPase, IMAP family	24 (0.00)	28 (0.21)	0.57
12-03	Gp4 Focus 2	g.chr3:155624035C>T	Missense Mutation	GMPS	p.S170F	guanine monphosphate	87 (0.00)	66 (0.14)	0.52
12-03	Gp4 Focus 2	g.chr3:121410022T>C	Missense Mutation	GOLGB1	p.E2730G	golgin B1	72 (0.00)	108 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr10:101163297C>T	Nonsense Mutation	GOT1	p.W296*	glutamic-oxaloacetic tra	30 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr1:167023636C>T	Missense Mutation	GPA33	p.D299N	glycoprotein A33 (trans	42 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr1:156565880C>A	Missense Mutation	GPATCH4	p.A162S	G patch domain contain	93 (0.00)	30 (0.27)	0.71
12-03	Gp4 Focus 2	g.chr10:25886763C>T	Silent	GPR158	p.N736N	G protein-coupled recep	28 (0.00)	46 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr16:57689836G>A	Missense Mutation	GPR56	p.V317I	G protein-coupled recep	76 (0.00)	43 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr16:46952544C>A	Missense Mutation	GPT2	p.D304E	glutamic pyruvate trans	24 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 2	g.chr22:40351859C>A	Missense Mutation	GRAP2	p.L39I	GRB2-related adaptor p	22 (0.00)	21 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr17:37900461G>A	Splice Site	GRB7		growth factor receptor-	99 (0.00)	21 (0.57)	1.52
12-03	Gp4 Focus 2	g.chr16:10032177G>A	Nonsense Mutation	GRIN2A	p.Q216*	glutamate receptor, ion	30 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr7:74148315C>T	Missense Mutation	GTF2I	p.A452V	general transcription fac	19 (0.00)	51 (0.10)	0.42
12-03	Gp4 Focus 2	g.chr17:73774948G>A	Silent	H3F3B	p.I75I	H3 histone, family 3B (	40 (0.03)	13 (0.54)	1.44
12-03	Gp4 Focus 2	g.chr7:18572882C>A	Intron	HDAC9		histone deacetylase 9	32 (0.00)	44 (0.27)	0.73

12-03	Gp4 Focus 2	g.chr7:18603147C>T	Intron	HDAC9		histone deacetylase 9	39 (0.00)	54 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr7:18665634G>A	Intron	HDAC9		histone deacetylase 9	56 (0.00)	36 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr7:18701015T>C	Intron	HDAC9		histone deacetylase 9	56 (0.00)	99 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr7:18813137G>A	Intron	HDAC9		histone deacetylase 9	49 (0.00)	86 (0.26)	0.68
12-03	Gp4 Focus 2	g.chr12:112681724C>G	Missense Mutation	HECTD4	p.E1389Q	HECT domain containir	190 (0.00)	43 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr4:185941508C>T	Missense Mutation	HELT	p.T104M	helt bHLH transcription	26 (0.00)	23 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr2:75107481G>A	Missense Mutation	HK2	p.G424D	hexokinase 2	20 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr16:72110506C>G	Silent	HPR	p.L191L	haptoglobin-related prot	70 (0.00)	65 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr22:26861504G>A	Silent	HPS4	p.P240P	Hermansky-Pudlak sync	29 (0.00)	30 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr1:152192218G>A	Silent	HRNR	p.T629T	hornerin	116 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr1:152192634G>A	Missense Mutation	HRNR	p.H491Y	hornerin	83 (0.00)	40 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr16:22926459C>T	Missense Mutation	HS3ST2	p.T227I	heparan sulfate (glucosa	94 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr1:120056517G>A	Missense Mutation	HSD3B1	p.S124N	hydroxy-delta-5-steroid	118 (0.00)	84 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr9:95040546G>A	Silent	IARS	p.L256L	isoleucyl-tRNA synthet	80 (0.00)	40 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr3:107885714G>A	Missense Mutation	IFT57	p.A323V	intraflagellar transport 5	26 (0.04)	49 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr3:159819046G>A	RNA	IL12A-AS1		IL12A antisense RNA 1	39 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr1:67792495G>A	Missense Mutation	IL12RB2	p.G148R	interleukin 12 receptor,	58 (0.00)	98 (0.29)	0.76
12-03	Gp4 Focus 2	g.chrX:114242502G>T	Nonsense Mutation	IL13RA2	p.C330*	interleukin 13 receptor,	22 (0.00)	28 (0.18)	0.40
12-03	Gp4 Focus 2	g.chr15:81552182C>T	Missense Mutation	IL16	p.P128S	interleukin 16	68 (0.01)	42 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr22:17583188C>T	Missense Mutation	IL17RA	p.P253L	interleukin 17 receptor	49 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr1:62586932C>A	Missense Mutation	INADL	p.T1657K	InaD-like (Drosophila)	26 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr4:142993899T>A	Intron	INPP4B		inositol polyphosphate-	56 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr4:143000416C>T	Intron	INPP4B		inositol polyphosphate-	74 (0.00)	113 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr4:143190839C>T	Intron	INPP4B		inositol polyphosphate-	34 (0.00)	44 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr4:143519581G>A	Intron	INPP4B		inositol polyphosphate-	108 (0.00)	43 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr4:143598958C>A	Intron	INPP4B		inositol polyphosphate-	21 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr4:143683761T>C	Intron	INPP4B		inositol polyphosphate-	51 (0.00)	28 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr22:31529449G>A	Missense Mutation	INPP5J	p.V429M	inositol polyphosphate-	41 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr1:44422885G>A	Silent	IPO13	p.T430T	importin 13	85 (0.00)	40 (0.30)	0.80
12-03	Gp4 Focus 2	g.chr12:54793728C>T	Missense Mutation	ITGA5	p.D883N	integrin, alpha 5 (fibron	82 (0.00)	27 (0.30)	0.79
12-03	Gp4 Focus 2	g.chr9:5123117C>T	Missense Mutation	JAK2	p.P1058L	Janus kinase 2	26 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr3:124207129G>A	Missense Mutation	KALRN	p.A1453T	kalirin, RhoGEF kinase	27 (0.00)	31 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr2:210993868C>T	Missense Mutation	KANSL1L	p.V373I	KAT8 regulatory NSL c	19 (0.00)	61 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr10:76735529G>A	Silent	KAT6B	p.V478V	K(lysine) acetyltransfer	28 (0.00)	35 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr12:4920153G>T	Missense Mutation	KCNA6	p.V316L	potassium voltage-gated	22 (0.00)	13 (0.38)	1.03

12-03	Gp4 Focus 2	g.chr3:19575559G>A	Missense Mutation	KCNH8	p.E1098K	potassium voltage-gated	19 (0.00)	34 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr1:202724551G>A	Silent	KDM5B	p.N462N	lysine (K)-specific dem	36 (0.00)	48 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr13:46919720G>A	Silent	KIAA0226L	p.F392F	KIAA0226-like	42 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr4:154517429C>T	Missense Mutation	KIAA0922	p.S672F	KIAA0922	38 (0.03)	52 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr12:105535011G>A	Missense Mutation	KIAA1033	p.E592K	KIAA1033	31 (0.00)	34 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr4:123237970G>A	Silent	KIAA1109	p.V3541V	KIAA1109	25 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr4:37440446G>A	Missense Mutation	KIAA1239	p.A244T		46 (0.00)	46 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr1:10357269G>A	Missense Mutation	KIF1B	p.E694K	kinesin family member	75 (0.00)	98 (0.45)	1.20
12-03	Gp4 Focus 2	g.chr5:132046693C>T	Missense Mutation	KIF3A	p.G396S	kinesin family member	62 (0.00)	60 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr4:39436201G>A	Silent	KLB	p.A399A	klotho beta	28 (0.00)	25 (0.36)	0.96
12-03	Gp4 Focus 2	g.chr1:161069906C>A	Silent	KLHDC9	p.R314R	kelch domain containin	64 (0.00)	47 (0.28)	0.74
12-03	Gp4 Focus 2	g.chr4:39082739G>A	Missense Mutation	KLHL5	p.V180I	kelch-like family memb	22 (0.00)	38 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr7:149430301C>T	Missense Mutation	KRBA1	p.T692I	KRAB-A domain contai	61 (0.00)	19 (0.42)	1.12
12-03	Gp4 Focus 2	g.chr17:38978597C>T	Missense Mutation	KRT10	p.G81S	keratin 10	80 (0.00)	42 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr17:39553636G>A	Silent	KRT31	p.F52F	keratin 31	49 (0.00)	41 (0.51)	1.37
12-03	Gp4 Focus 2	g.chr17:39643968G>A	Nonsense Mutation	KRT36	p.Q241*	keratin 36	82 (0.00)	40 (0.23)	0.60
12-03	Gp4 Focus 2	g.chr21:46000130G>A	Missense Mutation	KRTAP10-5	p.S109L	keratin associated protei	20 (0.00)	16 (0.50)	1.33
12-03	Gp4 Focus 2	g.chr21:31869281G>A	Missense Mutation	KRTAP19-4	p.R50C	keratin associated protei	16 (0.00)	57 (0.32)	0.84
12-03	Gp4 Focus 2	g.chr11:71277119C>G	Missense Mutation	KRTAP5-10	p.C162W	keratin associated protei	20 (0.00)	27 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr11:71238802G>A	Silent	KRTAP5-7	p.Q152Q	keratin associated protei	36 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr1:183209483C>A	Silent	LAMC2	p.I1095I	laminin, gamma 2	50 (0.00)	63 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr3:182872149G>A	Missense Mutation	LAMP3	p.A3V	lysosomal-associated m	50 (0.00)	55 (0.47)	1.26
12-03	Gp4 Focus 2	g.chr4:113565862G>A	Missense Mutation	LARP7	p.E13K	La ribonucleoprotein do	17 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr20:36982694G>A	Missense Mutation	LBP	p.G127S	lipopolysaccharide bind	24 (0.00)	21 (0.38)	1.02
12-03	Gp4 Focus 2	g.chr1:152586534G>A	Missense Mutation	LCE3B	p.G83D	late cornified envelope	34 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr12:51446013C>A	Missense Mutation	LETMD1	p.P138Q	LETM1 domain contain	65 (0.00)	51 (0.37)	0.99
12-03	Gp4 Focus 2	g.chr6:63990210G>A	Missense Mutation	LGSN	p.P416S	lengsin, lens protein wit	25 (0.00)	24 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr12:8519315G>A	lincRNA	LINC00937		long intergenic non-prot	92 (0.00)	131 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr5:96314977G>C	Missense Mutation	LNPEP	p.R52P	leucyl/cystinyl aminope	35 (0.00)	61 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr4:62599259G>T	Silent	LPHN3	p.L394L	latrophilin 3	71 (0.00)	56 (0.18)	0.88
12-03	Gp4 Focus 2	g.chr1:54432007G>A	Silent	LRRC42	p.V322V	leucine rich repeat conta	23 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr13:36050069G>T	Silent	MAB21L1	p.I69I	mab-21-like 1 (C. elega	82 (0.00)	20 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr7:20193857C>T	Missense Mutation	MACC1	p.E769K	metastasis associated in	55 (0.00)	71 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr1:39750077G>A	Missense Mutation	MACF1	p.E375K	microtubule-actin crossl	39 (0.00)	35 (0.23)	0.61
12-03	Gp4 Focus 2	g.chrX:151092936C>T	Missense Mutation	MAGEA4	p.P267L	melanoma antigen famil	29 (0.00)	26 (0.46)	0.77

12-03	Gp4 Focus 2	g.chr7:77680222C>T	Intron	MAGI2		membrane associated gu	52 (0.00)	81 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr7:77702646G>A	Intron	MAGI2		membrane associated gu	27 (0.00)	88 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr7:77741090G>A	Intron	MAGI2		membrane associated gu	35 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr7:77811827C>T	Intron	MAGI2		membrane associated gu	26 (0.00)	101 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr7:77932238G>A	Intron	MAGI2		membrane associated gu	84 (0.00)	100 (0.33)	0.88
12-03	Gp4 Focus 2	g.chr7:77985586C>T	Intron	MAGI2		membrane associated gu	29 (0.00)	89 (0.30)	0.81
12-03	Gp4 Focus 2	g.chr7:77991771C>A	Intron	MAGI2		membrane associated gu	56 (0.00)	73 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr7:78004770C>T	Intron	MAGI2		membrane associated gu	38 (0.00)	51 (0.18)	0.47
12-03	Gp4 Focus 2	g.chr7:78244325C>T	Intron	MAGI2		membrane associated gu	24 (0.00)	58 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr7:78338672T>A	Intron	MAGI2		membrane associated gu	58 (0.00)	43 (0.37)	0.99
12-03	Gp4 Focus 2	g.chr7:78492563G>A	Intron	MAGI2		membrane associated gu	19 (0.00)	52 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr7:78497205G>A	Intron	MAGI2		membrane associated gu	49 (0.00)	100 (0.41)	1.09
12-03	Gp4 Focus 2	g.chr7:78615834C>T	Intron	MAGI2		membrane associated gu	25 (0.00)	53 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr7:78782008G>A	Intron	MAGI2		membrane associated gu	21 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr7:78876943C>G	Intron	MAGI2		membrane associated gu	31 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr6:10791973G>A	Silent	MAK	p.A417A	male germ cell-associat	17 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr1:220986672G>A	Missense Mutation	MARC1	p.G309E	mitochondrial amidoxin	73 (0.00)	19 (0.32)	0.84
12-03	Gp4 Focus 2	g.chr2:20200233G>A	Silent	MATN3	p.Y379Y	matrilin 3	61 (0.00)	52 (0.23)	0.62
12-03	Gp4 Focus 2	g.chr1:150550762G>A	Silent	MCL1	p.L298L	myeloid cell leukemia 1	29 (0.00)	100 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr20:5948189C>G	Missense Mutation	MCM8	p.T328R	minichromosome maint	24 (0.00)	48 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr2:32168432G>A	Silent	MEMO1	p.L28L	mediator of cell motility	38 (0.00)	61 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr3:15467828G>A	Missense Mutation	METTL6	p.T64I	methyltransferase like 6	69 (0.00)	65 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr1:12058852C>T	Silent	MFN2	p.L209L	mitofusin 2	43 (0.00)	42 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr17:74771093G>A	Missense Mutation	MFSD11	p.G297S	major facilitator superfa	61 (0.00)	96 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr7:141766376C>T	Nonsense Mutation	MGAM	p.Q1592*	maltase-glucoamylase (a	41 (0.00)	41 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr7:141766401C>T	Missense Mutation	MGAM	p.A1600V	maltase-glucoamylase (a	49 (0.00)	51 (0.25)	0.68
12-03	Gp4 Focus 2	g.chr14:50088371G>A	Missense Mutation	MGAT2	p.E129K	mannosyl (alpha-1,6-)-g	24 (0.00)	15 (0.40)	1.07
12-03	Gp4 Focus 2	g.chr1:236966801G>A	Silent	MTR	p.G36G	5-methyltetrahydrofolat	21 (0.00)	44 (0.45)	1.21
12-03	Gp4 Focus 2	g.chr7:100638730G>A	Missense Mutation	MUC12	p.G1772D	mucin 12, cell surface a	218 (0.00)	97 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr7:100638847G>A	Missense Mutation	MUC12	p.G1811E	mucin 12, cell surface a	243 (0.00)	44 (0.32)	0.85
12-03	Gp4 Focus 2	g.chr7:100646436C>T	Missense Mutation	MUC12	p.P4341S	mucin 12, cell surface a	52 (0.00)	29 (0.28)	0.74
12-03	Gp4 Focus 2	g.chr19:9018439G>A	Silent	MUC16	p.L12579L	mucin 16, cell surface a	28 (0.00)	29 (0.28)	0.74
12-03	Gp4 Focus 2	g.chr19:9061463G>A	Silent	MUC16	p.S8661S	mucin 16, cell surface a	84 (0.00)	90 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr19:9063153A>G	Missense Mutation	MUC16	p.V8098A	mucin 16, cell surface a	37 (0.00)	85 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr3:195487949T>C	Missense Mutation	MUC4	p.D649G	mucin 4, cell surface ass	59 (0.00)	20 (0.25)	0.67

12-03	Gp4 Focus 2	g.chr6:135515529G>A	Silent	MYB	p.K293K	v-myb avian myeloblast	20 (0.00)	59 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr17:10547729G>A	Missense Mutation	MYH3	p.T450M	myosin, heavy chain 3,	39 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr6:2685639C>T	Splice Site	MYLK4	p.E146K	myosin light chain kina	23 (0.00)	22 (0.36)	0.97
12-03	Gp4 Focus 2	g.chr17:18077135C>T	Missense Mutation	MYO15A	p.T728M	myosin XVA	40 (0.00)	22 (0.32)	0.85
12-03	Gp4 Focus 2	g.chr18:3126839C>A	Missense Mutation	MYOM1	p.V951F	myomesin 1	31 (0.00)	55 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr12:8051466C>T	RNA	NANOGP1		Nanog homeobox pseud	78 (0.01)	84 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr2:15674696G>A	Silent	NBAS	p.I239I	neuroblastoma amplifie	18 (0.00)	43 (0.26)	0.68
12-03	Gp4 Focus 2	g.chr2:232320281G>A	Silent	NCL	p.A629A	nucleolin	62 (0.00)	47 (0.17)	0.45
12-03	Gp4 Focus 2	g.chr11:74716721C>T	Silent	NEU3	p.A190A	sialidase 3 (membrane s	43 (0.00)	70 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr6:41048637G>A	Splice Site	NFYA		nuclear transcription fac	38 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr5:175815471G>A	Missense Mutation	NOP16	p.R24W	NOP16 nucleolar protei	33 (0.00)	32 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr14:24773417C>A	Silent	NOP9	p.L527L	NOP9 nucleolar protein	66 (0.00)	34 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr7:75044572G>A	RNA	NSUN5P1		NOP2/Sun domain fami	78 (0.00)	50 (0.12)	0.52
12-03	Gp4 Focus 2	g.chr4:123838689G>A	Missense Mutation	NUDT6	p.P137S	nudix (nucleoside dipho	30 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr4:123838694C>G	Missense Mutation	NUDT6	p.R135T	nudix (nucleoside dipho	30 (0.00)	60 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr11:71726835C>T	Missense Mutation	NUMA1	p.E572K	nuclear mitotic apparatu	35 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr5:37351425C>T	Missense Mutation	NUP155	p.G197E	nucleoporin 155kDa	37 (0.00)	53 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr9:131757697C>T	Silent	NUP188	p.H1085H	nucleoporin 188kDa	78 (0.00)	42 (0.40)	1.08
12-03	Gp4 Focus 2	g.chr11:3724014G>A	Missense Mutation	NUP98	p.S1064F	nucleoporin 98kDa	44 (0.00)	33 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr1:228432225G>A	Missense Mutation	OBSCN	p.S1237N	obscurin, cytoskeletal c	15 (0.00)	42 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr9:138011913C>A	Silent	OLFM1	p.I422I	olfactomedin 1	74 (0.00)	32 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr13:53603053C>T	Missense Mutation	OLFM4	p.P28S	olfactomedin 4	41 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr7:128415694G>A	Missense Mutation	OPN1SW	p.L51F	opsin 1 (cone pigments)	105 (0.00)	25 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr1:248084523C>T	Silent	OR2T8	p.D68D	olfactory receptor, famil	86 (0.00)	35 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr19:14991426C>T	Missense Mutation	OR7A17	p.V248I	olfactory receptor, famil	20 (0.00)	38 (0.18)	0.49
12-03	Gp4 Focus 2	g.chr8:101718917G>A	Nonsense Mutation	PABPC1	p.Q522*	poly(A) binding protein,	82 (0.00)	46 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr1:176525598G>A	Missense Mutation	PAPPA2	p.G47E	pappalysin 2	68 (0.00)	29 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr1:55223584G>A	Silent	PARS2	p.T417T	prolyl-tRNA synthetase	32 (0.00)	50 (0.32)	0.85
12-03	Gp4 Focus 2	g.chr2:242066724C>G	Missense Mutation	PASK	p.E536Q	PAS domain containing	79 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr7:154790482G>A	Missense Mutation	PAXIP1	p.L32F	PAX interacting (with t	120 (0.00)	33 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr1:154918714C>T	Nonsense Mutation	PBXIP1	p.W479*	pre-B-cell leukemia ho	55 (0.00)	34 (0.26)	0.71
12-03	Gp4 Focus 2	g.chr5:140210033C>A	Missense Mutation	PCDHA6	p.A786E	protocadherin alpha 6	20 (0.00)	32 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr5:140710633G>A	Missense Mutation	PCDHGA1	p.D128N	protocadherin gamma s	85 (0.00)	62 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr5:140811927C>T	Missense Mutation	PCDHGA12	p.A534V	protocadherin gamma s	61 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 2	g.chr5:140811937C>T	Silent	PCDHGA12	p.N537N	protocadherin gamma s	64 (0.00)	22 (0.27)	0.73

12-03	Gp4 Focus 2	g.chr5:140811964G>A	Silent	PCDHGA12	p.V546V	protocadherin gamma su	64 (0.00)	23 (0.52)	1.39
12-03	Gp4 Focus 2	g.chr5:140725013C>T	Silent	PCDHGA3	p.I471I	protocadherin gamma su	29 (0.00)	60 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr5:140740027G>A	Missense Mutation	PCDHGB2	p.V109I	protocadherin gamma su	54 (0.00)	37 (0.32)	0.86
12-03	Gp4 Focus 2	g.chr5:140752018C>T	Missense Mutation	PCDHGB3	p.A686V	protocadherin gamma su	79 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr5:140865182C>T	Missense Mutation	PCDHGC4	p.P148S	protocadherin gamma su	64 (0.00)	46 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr17:53848466G>A	Splice Site	PCTP		phosphatidylcholine tra	31 (0.00)	71 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr5:31983679G>A	Missense Mutation	PDZD2	p.A299T	PDZ domain containing	64 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr12:41967091C>T	Missense Mutation	PDZRN4	p.S837L	PDZ domain containing	77 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr19:57325276C>A	Nonsense Mutation	PEG3	p.E1512*	paternally expressed 3	90 (0.00)	40 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr19:57328102C>T	Missense Mutation	PEG3	p.E570K	paternally expressed 3	16 (0.00)	45 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr4:152622557G>A	Missense Mutation	PET112	p.P333L		48 (0.00)	36 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr12:7360356G>A	Silent	PEX5	p.L356L	peroxisomal biogenesis	28 (0.00)	31 (0.19)	0.52
12-03	Gp4 Focus 2	g.chr10:6265923G>A	Missense Mutation	PFKFB3	p.E406K	6-phosphofructo-2-kina	59 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr6:28269429C>T	Missense Mutation	PGBD1	p.L600F	piggyBac transposable e	62 (0.00)	67 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr1:249212344G>A	Missense Mutation	PGBD2	p.A521T	piggyBac transposable e	43 (0.00)	33 (0.55)	1.45
12-03	Gp4 Focus 2	g.chr1:33833011G>A	Nonsense Mutation	PHC2	p.R228*	polyhomeotic homolog	27 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr18:60413497C>T	Intron	PHLPP1		PH domain and leucine	16 (0.00)	21 (0.29)	0.76
12-03	Gp4 Focus 2	g.chr18:60451520G>A	Intron	PHLPP1		PH domain and leucine	56 (0.00)	50 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr18:60485157G>A	Intron	PHLPP1		PH domain and leucine	28 (0.00)	35 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr18:60553324C>T	Intron	PHLPP1		PH domain and leucine	56 (0.00)	62 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr18:60632645G>T	Intron	PHLPP1		PH domain and leucine	28 (0.00)	52 (0.46)	1.23
12-03	Gp4 Focus 2	g.chr18:60642970G>A	Intron	PHLPP1		PH domain and leucine	57 (0.00)	59 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr9:131689403G>A	Silent	PHYHD1	p.V40V	phytanoyl-CoA dioxyge	18 (0.00)	37 (0.27)	0.72
12-03	Gp4 Focus 2	g.chr6:36931116C>A	Missense Mutation	PI16	p.P333Q	peptidase inhibitor 16	27 (0.00)	23 (0.30)	0.81
12-03	Gp4 Focus 2	g.chr1:145584280C>G	Silent	PIAS3	p.A477A	protein inhibitor of activ	30 (0.00)	33 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr3:178942525C>T	Missense Mutation	PIK3CA	p.P778S	phosphatidylinositol-4,5	54 (0.00)	27 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr16:81241222G>A	RNA	PKD1L2		polycystic kidney diseas	45 (0.00)	37 (0.16)	0.52
12-03	Gp4 Focus 2	g.chr5:137226244T>C	Missense Mutation	PKD2L2	p.F36L	polycystic kidney diseas	56 (0.00)	56 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr8:110474026C>T	Silent	PKHD1L1	p.L2424L	polycystic kidney and h	44 (0.00)	30 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr14:65208571C>T	Missense Mutation	PLEKHG3	p.S779F	pleckstrin homology do	38 (0.00)	29 (0.24)	0.64
12-03	Gp4 Focus 2	g.chrX:114874721A>G	Splice Site	PLS3	p.D298G	plastin 3	15 (0.00)	29 (0.31)	0.70
12-03	Gp4 Focus 2	g.chr6:160237620G>A	Missense Mutation	PNLDC1	p.C369Y	poly(A)-specific ribonu	88 (0.00)	23 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr7:108154721C>T	Missense Mutation	PNPLA8	p.S258N	patatin-like phospholipa	51 (0.00)	57 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr3:119190190G>T	Missense Mutation	POGLUT1	p.G71C	protein O-glucosyltrans	19 (0.00)	53 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr17:7412292G>A	Silent	POLR2A	p.T1165T	polymerase (RNA) II (D	31 (0.00)	53 (0.15)	0.40

12-03	Gp4 Focus 2	g.chr17:7417193C>T	Silent	POLR2A	p.T1870T	polymerase (RNA) II (D	41 (0.00)	67 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr4:57897145G>A	Missense Mutation	POLR2B	p.M1172I	polymerase (RNA) II (D	61 (0.00)	38 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr7:44054385G>A	RNA	POLR2J4		polymerase (RNA) II (D	74 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr7:75052255G>A	Missense Mutation	POM121C	p.A427V	POM121 transmembran	45 (0.00)	25 (0.44)	1.91
12-03	Gp4 Focus 2	g.chr9:134382876G>A	Missense Mutation	POMT1	p.M134I	protein-O-mannosyltran	37 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr3:87313505C>T	Missense Mutation	POU1F1	p.M124I	POU class 1 homeobox	35 (0.00)	43 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr11:70194509C>G	Missense Mutation	PPFIA1	p.L716V	protein tyrosine phospha	46 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr4:159631922G>T	Missense Mutation	PPID	p.Q325K	peptidylprolyl isomerase	34 (0.00)	43 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr1:40209591C>T	Nonsense Mutation	PPIE	p.Q127*	peptidylprolyl isomerase	47 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr7:113519955C>T	Missense Mutation	PPP1R3A	p.D398N	protein phosphatase 1, r	36 (0.00)	60 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr1:12954673G>T	Missense Mutation	PRAMEF10	p.P204T	PRAME family member	40 (0.00)	43 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr1:186277096C>T	Missense Mutation	PRG4	p.P749S	proteoglycan 4	63 (0.00)	28 (0.21)	0.57
12-03	Gp4 Focus 2	g.chr16:24196821C>T	Missense Mutation	PRKCB	p.S552F	protein kinase C, beta	41 (0.00)	34 (0.21)	0.55
12-03	Gp4 Focus 2	g.chr3:53220653G>A	Missense Mutation	PRKCD	p.G432R	protein kinase C, delta	22 (0.00)	22 (0.36)	0.97
12-03	Gp4 Focus 2	g.chr7:18067122G>A	Missense Mutation	PRPS1L1	p.A95V	phosphoribosyl pyropho	88 (0.00)	96 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr17:46030542G>A	Missense Mutation	PRR15L	p.P20L	proline rich 15-like	27 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr19:40478145C>T	Silent	PSMC4	p.R43R	proteasome (prosome, m	37 (0.00)	30 (0.23)	0.62
12-03	Gp4 Focus 2	g.chr14:53178219G>A	Missense Mutation	PSMC6	p.E154K	proteasome (prosome, m	117 (0.00)	101 (0.46)	1.21
12-03	Gp4 Focus 2	g.chr2:232030664G>A	Missense Mutation	PSMD1	p.R883Q	proteasome (prosome, m	22 (0.00)	31 (0.23)	0.60
12-03	Gp4 Focus 2	g.chr10:89714051G>A	Intron	PTEN		phosphatase and tensin h	149 (0.00)	61 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr8:27255086G>A	De novo Start InFram	PTK2B		protein tyrosine kinase 2	48 (0.00)	21 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr9:8449726C>T	Splice Site	PTPRD	p.P1329P	protein tyrosine phospha	25 (0.00)	80 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr2:61175181C>T	Missense Mutation	PUS10	p.G483D	pseudouridylate synthas	51 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr3:12626089G>A	Missense Mutation	RAF1	p.S624F	Raf-1 proto-oncogene, s	50 (0.00)	24 (0.42)	1.11
12-03	Gp4 Focus 2	g.chr3:12626372T>C	Missense Mutation	RAF1	p.K593E	Raf-1 proto-oncogene, s	105 (0.00)	44 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr13:48977620G>A	Intron	RB1		retinoblastoma 1	26 (0.00)	32 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr13:48999709C>T	Intron	RB1		retinoblastoma 1	17 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 2	g.chrX:106310817G>A	Silent	RBM41	p.L394L	RNA binding motif prot	28 (0.00)	53 (0.17)	0.38
12-03	Gp4 Focus 2	g.chr11:66444439C>T	Missense Mutation	RBM4B	p.G38S	RNA binding motif prot	92 (0.00)	37 (0.22)	0.58
12-03	Gp4 Focus 2	g.chr7:103236996C>T	Missense Mutation	RELN	p.R1149K	reelin	24 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr4:57797262G>A	Silent	REST	p.Q746Q	RE1-silencing transcript	152 (0.00)	66 (0.35)	0.93
12-03	Gp4 Focus 2	g.chr9:136277502T>A	Missense Mutation	REXO4	p.Y276F	REX4, RNA exonucleas	77 (0.00)	20 (0.30)	0.80
12-03	Gp4 Focus 2	g.chr3:16535350C>T	Silent	RFTN1	p.E9E	raftlin, lipid raft linker 1	94 (0.00)	39 (0.67)	1.78
12-03	Gp4 Focus 2	g.chr2:107040786G>A	Nonsense Mutation	RGPD3	p.Q1213*	RANBP2-like and GRII	107 (0.01)	139 (0.17)	0.64
12-03	Gp4 Focus 2	g.chr2:108496546C>T	Missense Mutation	RGPD4	p.L1683F	RANBP2-like and GRII	122 (0.00)	97 (0.10)	0.38

12-03	Gp4 Focus 2	g.chr18:13731535G>A	Missense Mutation	RNMT	p.A7T	RNA (guanine-7-) meth	19 (0.00)	40 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr11:124765442C>T	Missense Mutation	ROBO4	p.G316D	roundabout, axon guida	26 (0.00)	14 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr16:12021549G>A	Missense Mutation	RP11-166B2.1	p.S292L		181 (0.00)	63 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr16:12021561G>A	Missense Mutation	RP11-166B2.1	p.P288L		182 (0.00)	58 (0.16)	0.41
12-03	Gp4 Focus 2	g.chr1:155141989G>A	Missense Mutation	RP11-201K10.	p.P217S		22 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr3:187433497G>A	Missense Mutation	RP11-211G3.3	p.G33D		38 (0.00)	57 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr3:187433524G>A	Missense Mutation	RP11-211G3.3	p.S42N		29 (0.00)	65 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr10:42831772G>A	RNA	RP11-313J2.1			37 (0.00)	64 (0.11)	0.38
12-03	Gp4 Focus 2	g.chr7:63353853G>A	lincRNA	RP11-340I6.7			84 (0.00)	34 (0.18)	0.76
12-03	Gp4 Focus 2	g.chr14:24600988C>T	Missense Mutation	RP11-468E2.6	p.P260S		26 (0.00)	15 (0.47)	1.24
12-03	Gp4 Focus 2	g.chr17:3214154C>T	RNA	RP11-64J4.2			46 (0.00)	23 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr15:41829170C>A	Missense Mutation	RPAP1	p.D52Y	RNA polymerase II assc	94 (0.00)	33 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr17:37357546C>T	Missense Mutation	RPL19	p.T27I	ribosomal protein L19	37 (0.00)	47 (0.17)	0.45
12-03	Gp4 Focus 2	g.chr15:40863926C>T	Missense Mutation	RPUSD2	p.H183Y	RNA pseudouridylate sy	52 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr1:218475661C>T	Silent	RRP15	p.H55H	ribosomal RNA process	45 (0.00)	47 (0.26)	0.68
12-03	Gp4 Focus 2	g.chr9:35546526G>A	Missense Mutation	RUSC2	p.S3N	RUN and SH3 domain c	18 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr3:72474666G>A	Intron	RYBP		RING1 and YY1 bindin	60 (0.00)	40 (0.40)	1.07
12-03	Gp4 Focus 2	g.chr12:46318555G>A	Nonsense Mutation	SCAF11	p.Q1288*	SR-related CTD-associa	17 (0.00)	22 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr7:29980461C>T	Silent	SCRN1	p.S192S	secernin 1	17 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr7:83614762G>T	Missense Mutation	SEMA3A	p.S495Y	sema domain, immunog	18 (0.00)	47 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr3:50219769C>A	Silent	SEMA3F	p.A232A	sema domain, immunog	27 (0.00)	40 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr10:102740587C>T	Silent	SEMA4G	p.L492L	sema domain, immunog	17 (0.00)	25 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr18:61647065C>T	Missense Mutation	SERPINB8	p.H67Y	serpin peptidase inhibitc	51 (0.00)	93 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr1:173878928G>T	Silent	SERPINC1	p.P305P	serpin peptidase inhibitc	62 (0.00)	41 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr1:154938476C>T	Missense Mutation	SHC1	p.G445R	SHC (Src homology 2 d	19 (0.00)	24 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr9:91657089G>A	Silent	SHC3	p.D404D	SHC (Src homology 2 d	32 (0.00)	41 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr3:72864821G>A	Intron	SHQ1		SHQ1, H/ACA ribonucl	40 (0.00)	31 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr3:72875098C>T	Intron	SHQ1		SHQ1, H/ACA ribonucl	42 (0.00)	92 (0.20)	0.52
12-03	Gp4 Focus 2	g.chr11:111594380C>A	Missense Mutation	SIK2	p.L770M	salt-inducible kinase 2	62 (0.00)	44 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr10:61414159C>A	Missense Mutation	SLC16A9	p.D209Y	solute carrier family 16,	51 (0.00)	59 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr6:133110931C>A	Missense Mutation	SLC18B1	p.V109F	solute carrier family 18,	33 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr11:124949021G>A	Missense Mutation	SLC37A2	p.E110K	solute carrier family 37	76 (0.00)	29 (0.21)	0.55
12-03	Gp4 Focus 2	g.chr3:50255357C>T	RNA	SLC38A3		solute carrier family 38,	58 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr9:108145534C>T	Missense Mutation	SLC44A1	p.S588F	solute carrier family 44	52 (0.00)	93 (0.29)	0.77
12-03	Gp4 Focus 2	g.chr2:27423947G>A	Silent	SLC5A6	p.T561T	solute carrier family 5 (s	27 (0.00)	23 (0.48)	1.28

12-03	Gp4 Focus 2	g.chr3:170198160G>A	Silent	SLC7A14	p.A637A	solute carrier family 7,	28 (0.00)	42 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr1:27480616C>A	Missense Mutation	SLC9A1	p.E70D	solute carrier family 9,	26 (0.00)	24 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr12:21377702G>A	Silent	SLCO1B1	p.T598T	solute carrier organic an	28 (0.00)	45 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr10:98762722G>A	Missense Mutation	SLIT1	p.A1298V	slit homolog 1 (Drosop	55 (0.02)	25 (0.28)	0.75
12-03	Gp4 Focus 2	g.chr15:59172239C>A	Nonsense Mutation	SLTM	p.G1022*	SAFB-like, transcriptio	35 (0.00)	33 (0.48)	1.29
12-03	Gp4 Focus 2	g.chr18:48582726G>A	Intron	SMAD4		SMAD family member	72 (0.00)	54 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr14:91927762G>A	Missense Mutation	SMEK1	p.P772L	SMEK homolog 1, supp	110 (0.01)	108 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr16:18896889G>A	Missense Mutation	SMG1	p.P308S	SMG1 phosphatidylinos	55 (0.00)	90 (0.23)	1.07
12-03	Gp4 Focus 2	g.chr8:42407725G>A	Missense Mutation	SMIM19	p.D100N	small integral membran	28 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr9:139275843C>T	Splice Site	SNAPC4	p.A773A	small nuclear RNA acti	32 (0.00)	26 (0.19)	0.51
12-03	Gp4 Focus 2	g.chr15:25463809C>T	RNA	SNHG14		small nucleolar RNA ho	70 (0.00)	40 (0.17)	0.47
12-03	Gp4 Focus 2	g.chr3:43389856G>A	Missense Mutation	SNRK	p.G702D	SNF related kinase	94 (0.00)	59 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr17:46189435C>T	Silent	SNX11	p.N10N	sorting nexin 11	24 (0.00)	33 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr2:27598426C>T	Silent	SNX17	p.A276A	sorting nexin 17	56 (0.00)	34 (0.50)	1.33
12-03	Gp4 Focus 2	g.chr9:35811780G>A	Missense Mutation	SPAG8	p.S88F	sperm associated antige	23 (0.00)	13 (0.38)	1.03
12-03	Gp4 Focus 2	g.chr17:47727835G>A	Intron	SPOP		speckle-type POZ protei	15 (0.00)	27 (0.30)	0.79
12-03	Gp4 Focus 2	g.chr17:47737996C>T	Intron	SPOP		speckle-type POZ protei	56 (0.00)	29 (0.21)	0.55
12-03	Gp4 Focus 2	g.chr1:153004948C>A	Missense Mutation	SPRR1B	p.P43T	small proline-rich protei	32 (0.00)	21 (0.48)	1.27
12-03	Gp4 Focus 2	g.chr1:24995670C>A	Missense Mutation	SRRM1	p.P599Q	serine/arginine repetitiv	32 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr15:42927060C>T	Nonsense Mutation	STARD9	p.Q81*	StAR-related lipid trans	20 (0.00)	44 (0.23)	0.61
12-03	Gp4 Focus 2	g.chr19:19119180C>T	Missense Mutation	SUGP2	p.G799E	SURP and G patch dom	103 (0.00)	119 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr8:70551002C>T	Silent	SULF1	p.G820G	sulfatase 1	28 (0.00)	41 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr2:108872087G>A	Silent	SULT1C3	p.R153R	sulfotransferase family,	16 (0.00)	28 (0.18)	0.66
12-03	Gp4 Focus 2	g.chr7:883146G>A	Missense Mutation	SUN1	p.R216K	Sad1 and UNC84 domai	55 (0.00)	48 (0.17)	0.65
12-03	Gp4 Focus 2	g.chr9:136220643C>T	Missense Mutation	SURF1	p.G159E	surfeit 1	50 (0.00)	52 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr10:29821708G>A	Missense Mutation	SVIL	p.P530S	supervillin	65 (0.00)	48 (0.46)	1.22
12-03	Gp4 Focus 2	g.chr14:64599079G>T	Missense Mutation	SYNE2	p.A4730S	spectrin repeat containi	49 (0.00)	29 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr14:64681041C>T	Silent	SYNE2	p.L6338L	spectrin repeat containi	32 (0.00)	42 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr17:76166897G>A	Splice Site	SYNGR2		synaptogyrin 2	58 (0.00)	55 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr6:149699671G>A	Missense Mutation	TAB2	p.S207N	TGF-beta activated kina	20 (0.00)	56 (0.21)	0.68
12-03	Gp4 Focus 2	g.chr17:58094857C>T	lincRNA	TBC1D3P1-DHX40P1		TBC1D3P1-DHX40P1	134 (0.01)	85 (0.39)	1.04
12-03	Gp4 Focus 2	g.chr17:60342444A>G	RNA	TBC1D3P2		TBC1 domain family,	67 (0.00)	24 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr17:80842040G>A	Missense Mutation	TBCD	p.V499M	tubulin folding cofactor	161 (0.00)	31 (0.42)	1.12
12-03	Gp4 Focus 2	g.chr17:80858545T>C	Silent	TBCD	p.F556F	tubulin folding cofactor	28 (0.00)	32 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr19:33292756G>A	Missense Mutation	TDRD12	p.S725N	tudor domain containing	20 (0.00)	48 (0.19)	0.50

12-03	Gp4 Focus 2	g.chr17:15234625C>T	Missense Mutation	TEKT3	p.R93K	tektin 3	39 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr15:30003155G>A	Missense Mutation	TJP1	p.R1342C	tight junction protein 1	35 (0.00)	79 (0.11)	0.46
12-03	Gp4 Focus 2	g.chr15:30010244G>A	Missense Mutation	TJP1	p.H1243Y	tight junction protein 1	72 (0.00)	56 (0.14)	0.58
12-03	Gp4 Focus 2	g.chr3:52257086C>A	Missense Mutation	TLR9	p.W569L	toll-like receptor 9	23 (0.00)	28 (0.18)	0.48
12-03	Gp4 Focus 2	g.chr17:41365203G>A	Missense Mutation	TMEM106A	p.C48Y	transmembrane protein	26 (0.00)	30 (0.17)	0.44
12-03	Gp4 Focus 2	g.chr12:130185004G>A	Missense Mutation	TMEM132D	p.P107S	transmembrane protein	20 (0.00)	24 (0.25)	1.01
12-03	Gp4 Focus 2	g.chr1:202992083G>A	Missense Mutation	TMEM183A	p.G349D	transmembrane protein	183 (0.00)	25 (0.24)	0.64
12-03	Gp4 Focus 2	g.chr1:46159154C>T	Silent	TMEM69	p.P107P	transmembrane protein	64 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr9:100353666C>A	Missense Mutation	TMOD1	p.Q322K	tropomodulin 1	20 (0.00)	48 (0.15)	0.39
12-03	Gp4 Focus 2	g.chr12:83250808C>T	Nonsense Mutation	TMTC2	p.Q35*	transmembrane and tetr	20 (0.00)	50 (0.38)	1.60
12-03	Gp4 Focus 2	g.chr9:117852978G>A	Missense Mutation	TNC	p.P107L	tenascin C	97 (0.00)	41 (0.20)	0.52
12-03	Gp4 Focus 2	g.chr1:201332489C>A	Nonsense Mutation	TNNT2	p.E169*	troponin T type 2 (cardi	43 (0.00)	64 (0.16)	0.42
12-03	Gp4 Focus 2	g.chr16:24788264G>T	Missense Mutation	TNRC6A	p.Q58H	trinucleotide repeat cont	182 (0.00)	45 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr22:40711390C>T	Silent	TNRC6B	p.N790N	trinucleotide repeat cont	31 (0.00)	34 (0.24)	0.63
12-03	Gp4 Focus 2	g.chr17:76063993G>A	Missense Mutation	TNRC6C	p.G920R	trinucleotide repeat cont	41 (0.00)	54 (0.20)	0.54
12-03	Gp4 Focus 2	g.chr2:12863524A>G	Missense Mutation	TRIB2	p.M137V	tribbles pseudokinase 2	54 (0.00)	23 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr4:154217169C>T	Silent	TRIM2	p.D470D	tripartite motif containi	41 (0.00)	37 (0.24)	0.65
12-03	Gp4 Focus 2	g.chr5:180651803G>A	Silent	TRIM41	p.Q268Q	tripartite motif containi	48 (0.00)	20 (0.40)	1.07
12-03	Gp4 Focus 2	g.chr11:5631433T>A	Missense Mutation	TRIM6	p.F103I	tripartite motif containi	38 (0.00)	38 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr1:26392814G>A	Nonsense Mutation	TRIM63	p.Q93*	tripartite motif containi	24 (0.00)	17 (0.29)	0.78
12-03	Gp4 Focus 2	g.chr21:38567975G>A	Splice Site	TTC3		tetratricopeptide repeat	20 (0.00)	35 (0.17)	0.46
12-03	Gp4 Focus 2	g.chr2:179397070G>A	Missense Mutation	TTN	p.P34758S	titin	126 (0.00)	99 (0.15)	0.40
12-03	Gp4 Focus 2	g.chr2:179417150G>A	Silent	TTN	p.P30159P	titin	18 (0.00)	105 (0.67)	1.78
12-03	Gp4 Focus 2	g.chr2:179629254C>T	Splice Site	TTN	p.V3330I	titin	91 (0.00)	60 (0.33)	0.89
12-03	Gp4 Focus 2	g.chr2:179629262G>C	Nonsense Mutation	TTN	p.S3327*	titin	100 (0.01)	61 (0.34)	0.92
12-03	Gp4 Focus 2	g.chr13:19748059C>T	Missense Mutation	TUBA3C	p.E433K	tubulin, alpha 3c	36 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr20:57599157C>G	Silent	TUBB1	p.L225L	tubulin, beta 1 class VI	73 (0.00)	27 (0.67)	1.78
12-03	Gp4 Focus 2	g.chr7:66703393C>T	Silent	TYW1	p.S692S	tRNA-yW synthesizing	84 (0.00)	52 (0.23)	1.00
12-03	Gp4 Focus 2	g.chr2:234669144G>A	Missense Mutation	UGT1A8	p.G71R	UDP glucuronosyltrans	21 (0.00)	45 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr15:54305873C>T	Missense Mutation	UNC13C	p.T258I	unc-13 homolog C (C. e	24 (0.00)	37 (0.19)	0.50
12-03	Gp4 Focus 2	g.chr15:91479619G>A	Missense Mutation	UNC45A	p.V119M	unc-45 homolog A (C. e	19 (0.00)	12 (0.50)	1.33
12-03	Gp4 Focus 2	g.chr17:58332538G>A	Nonsense Mutation	USP32	p.Q358*	ubiquitin specific peptid	47 (0.00)	37 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr2:219330847G>A	Silent	USP37	p.N690N	ubiquitin specific peptid	26 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr19:54545441G>A	Missense Mutation	VSTM1	p.S166F	V-set and transmembra	18 (0.00)	43 (0.26)	0.68
12-03	Gp4 Focus 2	g.chr10:50256581G>A	Silent	VSTM4	p.P239P	V-set and transmembra	56 (0.02)	33 (0.30)	0.81

12-03	Gp4 Focus 2	g.chr10:122618179C>T	Missense Mutation	WDR11	p.H75Y	WD repeat domain 11	15 (0.00)	27 (0.19)	0.49
12-03	Gp4 Focus 2	g.chr1:85587443G>A	Missense Mutation	WDR63	p.V643M	WD repeat domain 63	46 (0.00)	28 (0.36)	0.95
12-03	Gp4 Focus 2	g.chr1:27622882C>A	Missense Mutation	WDTC1	p.H313Q	WD and tetratricopeptid	73 (0.00)	45 (0.22)	0.59
12-03	Gp4 Focus 2	g.chr4:6302761C>T	Silent	WFS1	p.F413F	Wolfram syndrome 1 (w	38 (0.00)	19 (0.26)	0.70
12-03	Gp4 Focus 2	g.chr7:5257582C>T	Silent	WIPI2	p.D184D	WD repeat domain, pho	39 (0.00)	31 (0.19)	0.76
12-03	Gp4 Focus 2	g.chr3:39229551C>A	Silent	XIRP1	p.G462G	xin actin-binding repeat	45 (0.00)	36 (0.36)	0.96
12-03	Gp4 Focus 2	g.chr22:42059771G>A	Silent	XRCC6	p.L594L	X-ray repair complemer	47 (0.00)	24 (0.21)	0.56
12-03	Gp4 Focus 2	g.chr7:100373152C>T	RNA	ZAN		zonadhesin (gene/pseud	36 (0.00)	20 (0.25)	0.67
12-03	Gp4 Focus 2	g.chr22:50277537C>T	Missense Mutation	ZBED4	p.S76F	zinc finger, BED-type c	28 (0.00)	74 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr11:62519590A>G	Missense Mutation	ZBTB3	p.F566S	zinc finger and BTB do	45 (0.00)	32 (0.41)	1.08
12-03	Gp4 Focus 2	g.chr1:22817964G>A	Missense Mutation	ZBTB40	p.V257I	zinc finger and BTB do	84 (0.00)	32 (0.31)	0.83
12-03	Gp4 Focus 2	g.chr1:52941017C>T	Silent	ZCCHC11	p.S738S	zinc finger, CCHC dom	100 (0.00)	69 (0.14)	0.39
12-03	Gp4 Focus 2	g.chr19:44662041C>T	Silent	ZNF234	p.Y624Y	zinc finger protein 234	40 (0.00)	101 (0.35)	0.92
12-03	Gp4 Focus 2	g.chr19:21719827G>A	Silent	ZNF429	p.R324R	zinc finger protein 429	21 (0.00)	23 (0.30)	0.81
12-03	Gp4 Focus 2	g.chr19:21606879C>A	Missense Mutation	ZNF493	p.S473Y	zinc finger protein 493	15 (0.00)	43 (0.16)	0.43
12-03	Gp4 Focus 2	g.chr19:37441970G>A	Missense Mutation	ZNF568	p.E639K	zinc finger protein 568	21 (0.00)	35 (0.14)	0.38
12-03	Gp4 Focus 2	g.chr19:42585365G>A	Silent	ZNF574	p.E869E	zinc finger protein 574	26 (0.00)	22 (0.27)	0.73
12-03	Gp4 Focus 2	g.chr7:57522288C>T	Silent	ZNF716	p.S54S	zinc finger protein 716	44 (0.00)	88 (0.14)	0.60
12-03	Gp4 Focus 2	g.chr19:22498639G>A	Nonsense Mutation	ZNF729	p.W807*	zinc finger protein 729	28 (0.00)	39 (0.15)	0.41
12-03	Gp4 Focus 2	g.chr14:102802148G>T	Missense Mutation	ZNF839	p.Q544H	zinc finger protein 839	66 (0.00)	71 (0.20)	0.53
12-03	Gp4 Focus 2	g.chr20:47870345G>A	Missense Mutation	ZNFX1	p.A988V	zinc finger, NFX1-type	49 (0.00)	79 (0.16)	0.44
12-03	Gp4 Focus 2	g.chr19:56758152C>G	Silent	ZSCAN5D	p.V260V		21 (0.00)	31 (0.26)	0.69
12-03	Gp4 Focus 2	g.chr1:45553773G>A	Silent	ZSWIM5	p.Y244Y	zinc finger, SWIM-type	20 (0.00)	64 (0.27)	0.71