Column Definition

Rank	Rank of the gene
Gene	Gene Id
FullName	Full Name of the gene
Pathway	Known Pathway Associated with the Gene
mRNA	Transcript ID
Chr	Chromosome
Score	VAAST score of the transcript
PValue	VAAST p-value of the transcript
LOD_Score	VAAST LOD score of the transcript
LOD_pValue	VAAST LOD score p-value of the transcript
Strand	Transcript Strand
#ofVar	Total number of variants in the transcript
VarType	Type of the variant. SNVs is labeled as either "TU" or "TR". If a target variant is observed in background genomes, it is labeled "TR" (for “target”); otherwise if a variant is only observed in target genomes, it is labeled "TU" (for “target unique”).
VarScore	Score of each variant, the sum roughly equals the transcript score ("Score") in column 8.
VarLODScore	VAAST LOD score of each variant
VarPosition	The chromosomal position of each variant
AlleleCount	Number of individuals in the background file containing a variant if the variant is not unique to the targets.
Ref	Reference nucelotide and amino-acid allele
GenoType	Individual genotypes following the VAAST output format. Please see the "VAAST Output" section of the VAAST users guide (http://www.yandell-lab.org/software/VAAST/VAAST_Users_Guide.pdf) for detailed description.

Commands

Command - dominant

```
 VAAST -gw 1e7 -m pvaast --indel --codon_bias --splice_site --fast_gp -pv_control TS0011_d.ctl -l phastcons-hg19-vertebrate.txt -o TS0011_d refGene_hg19.gff3 1kg-cgi-427_gene_only.cdr
```

Control File - dominant (TS0011_d.ctl)

```
#-------------------------   Basic options----------------------------

input_ped_cdr_files:                  TS0011.ped TS0011.cdr
pedigree_representatives:             3
unknown_representatives:              yes
additional_cases:
inheritance_model:                    dominant

#--------------------   Performance Tuning ----------------------------

informative_site_selection:           3
simulate_genotyping_error:            yes
genotyping_error_rate:                1.00E-04
penetrance_lower_bound:               0.6
penetrance_upper_bound:               1

#----------------   Gene and Variant Filtering ------------------------

max_prevalence_filter:                0.01
lod_score_filter:                     yes
clrt_score_filter:                    no
nocall_filter:                        yes
nocall_filter_cutoff:                 2
inheritance_error_filter:             yes
```

Command - recessive

```
 VAAST -gw 1e7 -m pvaast --indel --codon_bias --splice_site --fast_gp -pv_control TS0011_r.ctl -l phastcons-hg19-vertebrate.txt -o TS0011_r refGene_hg19.gff3 1kg-cgi-427_gene_only.cdr
```

Control File - recessive (TS0011_r.ctl)

```
#-------------------------   Basic options----------------------------

input_ped_cdr_files:                  TS0011.ped TS0011.cdr
pedigree_representatives:             3
unknown_representatives:              yes
additional_cases:
inheritance_model:                    recessive

#--------------------   Performance Tuning ----------------------------

informative_site_selection:           3
simulate_genotyping_error:            yes
genotyping_error_rate:                1.00E-04
penetrance_lower_bound:               0.6
penetrance_upper_bound:               1

#----------------   Gene and Variant Filtering ------------------------

max_prevalence_filter:                0.01
lod_score_filter:                     yes
clrt_score_filter:                    no
nocall_filter:                        yes
nocall_filter_cutoff:                 2
inheritance_error_filter:             yes
```

Dominant model

Rank	Gene	FullName	Pathway	mRNA	Chr	Score	PValue	Strand	#ofVar	VarType	VarScore	VarLODScore	VarPosition	AlleleCount	Ref	GenoType
1	ZNF557	Homo sapiens zinc finger protein 557 (ZNF557) transcript variant 1 mRNA.	Transcription Factor	NM_001044388	chr19	17.45	1.00E-04	+	1	SNP	11.96	0|1.19	7083322	NA	C|T	N|0,2-5|T:C|M:T
2	PNKD	Homo sapiens paroxysmal nonkinesigenic dyskinesia (PNKD) transcript variant 2 mRNA.		NM_015488	chr2	24.63	2.00E-04	+	1	SNP	19.14	0|1.19	219204814	NA	C|Q	N|0,2-5|T:C|*:Q
3	OR4C3	Homo sapiens olfactory receptor family 4 subfamily C member 3 (OR4C3) mRNA.		NM_001004702	chr11	14.1	3.00E-04	+	1	SNP	14.05	0|0.01	48346961	NA	A|N	N|0-5|A:T|N:Y
4	PRB1	Homo sapiens proline-rich protein BstNI subfamily 1 (PRB1) transcript variant 1 mRNA.		NM_005039	chr12	14.55	4.00E-04	-	1	SNP	9.06	0|1.19	11506669	NA	G|P	N|0,2-5|T:G|Q:P
5	ZNF560	Homo sapiens zinc finger protein 560 (ZNF560) mRNA.	Transcription Factor	NM_152476	chr19	19.2	4.00E-04	-	1	SNP	13.71	0|1.19	9578313	NA	C|C	N|0,2-5|T:C|Y:C
6	RFWD2	Homo sapiens ring finger and WD repeat domain 2 (RFWD2) transcript variant 1 mRNA.	Nervous System Development	NM_022457	chr1	16.88	5.00E-04	-	1	SNP	11.39	0|1.19	176118179	NA	A|M	N|0,2-5|A:G|M:T
7	GFM2	Homo sapiens G elongation factor mitochondrial 2 (GFM2) nuclear gene encoding mitochondrial protein transcript variant 3 mRNA.		NM_170681	chr5	15.78	5.00E-04	-	1	SNP	10.29	0|1.19	74034400	NA	G|L	N|0,2-5|C:G|V:L
8	IGSF3	Homo sapiens immunoglobulin superfamily member 3 (IGSF3) transcript variant 1 mRNA.		NM_001007237	chr1	19.19	6.00E-04	-	1	SNP	19.14	0|0.01	117142868	NA	C|W	N|0-5|T:C|*:W
9	CPN2	Homo sapiens carboxypeptidase N polypeptide 2 (CPN2) mRNA.	Neurological system process	NM_001080513	chr3	15.41	6.00E-04	-	1	SNP	15.36	0|0.01	194061907	NA	G|Q	N|2-3|A:A|*:*;N|0-1,4-5|A:G|*:Q
10	ZNF384	Homo sapiens zinc finger protein 384 (ZNF384) transcript variant 2 mRNA.	Transcription Factor	NM_001135734	chr12	13.52	6.00E-04	-	1	del	13.47	0|0.01	6777070	NA	TGC|QQ	0,2,4|-:-|-:-;1,3,5|-:TGC|-:QQ
11	KIRREL	Homo sapiens kin of IRRE like (Drosophila) (KIRREL) mRNA.		NM_018240	chr1	17.18	6.00E-04	+	1	SNP	11.69	0|1.19	158045965	NA	G|V	N|0,2-5|A:G|M:V
12	ZNF443	Homo sapiens zinc finger protein 443 (ZNF443) mRNA.	Transcription Factor	NM_005815	chr19	15.85	7.00E-04	-	1	SNP	10.36	0|1.19	12542654	NA	T|K	N|0,2-5|A:T|I:K
13	CBR4	Homo sapiens carbonyl reductase 4 (CBR4) mRNA.		NM_032783	chr4	16.43	7.00E-04	-	1	SNP	10.94	0|1.19	169928890	NA	T|S	N|0,2-5|A:T|C:S
14	MYEOV2	Homo sapiens myeloma overexpressed 2 (MYEOV2) transcript variant 2 mRNA.		NM_138336	chr2	14.78	7.00E-04	-	1	SNP	9.29	0|1.19	241075724	NA	C|S	N|0,2-5|A:C|I:S
15	ALS2CR8	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region candidate 8 (ALS2CR8) mRNA.		NM_024744	chr2	19.2	8.00E-04	+	1	SNP	13.71	0|1.19	203846831	NA	G|E	N|0,2-5|A:G|K:E
16	GOLGA6L6	Homo sapiens golgin A6 family-like 6 (GOLGA6L6) mRNA.		NM_001145004	chr15	19.18	8.00E-04	-	1	SNP	19.13	0|0.01	20740252	NA	C|E	N|0-5|A:C|*:E
17	SELE	Homo sapiens selectin E (SELE) mRNA.		NM_000450	chr1	14.5	9.00E-04	-	1	SNP	9.01	0|1.19	169701939	NA	C|V	N|0,2-5|T:C|M:V
18	RDH8	Homo sapiens retinol dehydrogenase 8 (all-trans) (RDH8) mRNA.	Neurological system process	NM_015725	chr19	13.41	9.00E-04	+	1	SNP	7.92	0|1.19	10132000	NA	G|M	N|0,2-5|A:G|I:M
19	CASP8	Homo sapiens caspase 8 apoptosis-related cysteine peptidase (CASP8) transcript variant C mRNA.	Huntington Disease;Neurodegenerative	NM_001228	chr2	10.53	9.00E-04	+	1	SNP	5.04	0|1.19	202134324	NA	A|I	N|0,2-5|A:G|I:V
20	CES1	Homo sapiens carboxylesterase 1 (CES1) transcript variant 3 mRNA.	Neurological system process;Nervous System Development	NM_001266	chr16	14.28	9.00E-04	-	1	SNP	14.23	0|0.01	55862883	NA	C|G	N|0-5|A:C|V:G
21	GPRIN1	Homo sapiens G protein regulated inducer of neurite outgrowth 1 (GPRIN1) mRNA.		NM_052899	chr5	17.41	1.00E-03	-	1	del	17.36	0|0.01	176026122	NA	CAAAGACCCAGGA|DPGSL	0-5|-:CAAAGACCCAGGA|-:DPGSL
22	PKD1L2	Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2) transcript variant 3 mRNA.	Ion channel activity	NM_001076780	chr16	22.85	1.00E-03	-	1	del	17.36	0|1.19	81242149	NA	TT|N	0|-:-|-:-;2-5|-:TT|-:N
23	ZNF717	Homo sapiens zinc finger protein 717 (ZNF717) mRNA.		NM_001128223	chr3	22.85	1.00E-03	-	1	del	17.36	0|1.19	75786895	NA	T|T	0,2-5|-:T|-:T
24	SERPINE2	Homo sapiens serpin peptidase inhibitor clade E (nexin plasminogen activator inhibitor type 1) member 2 (SERPINE2) transcript variant 4 mRNA.		NM_001136530	chr2	7.62	1.00E-03	-	1	SNP	7.57	0|0.01	224866427	2	A|M	B|0-4|A:G|M:T;N|5|G:G|T:T
25	KIAA0040	Homo sapiens KIAA0040 (KIAA0040) transcript variant 2 mRNA.		NM_001162893	chr1	19.63	1.00E-03	-	1	ins	14.14	0|1.19	175129924	NA	-|-	0,2-5|-:CTTCTT|-:KK
26	C5orf60	Homo sapiens chromosome 5 open reading frame 60 (C5orf60) mRNA.		NM_001142306	chr5	15.14	1.00E-03	-	1	del	9.65	0|1.19	179071810	NA	TCC|ED	0,2-5|-:TCC|-:ED
27	WWC1	Homo sapiens WW and C2 domain containing 1 (WWC1) transcript variant 3 mRNA.		NM_015238	chr5	16.26	1.00E-03	+	1	SNP	10.77	0|1.19	167858371	NA	G|M	N|2-5|T:G|I:M;N|0|T:T|I:I
28	TTYH3	Homo sapiens tweety homolog 3 (Drosophila) (TTYH3) mRNA.	Anion Channel;Ion channel activity	NM_025250	chr7	16.22	1.00E-03	+	1	SNP	10.73	0|1.19	2671862	1	T|W	N|0|G:G|G:G;B|2-5|T:G|W:G
29	ASPN	Homo sapiens asporin (ASPN) transcript variant 1 mRNA.		NM_017680	chr9	13.52	1.00E-03	-	1	del	13.47	0|0.01	95237025	NA	TCA|DE	1-3,5|-:-|-:-;0,4|-:TCA|-:DE
30	PDE11A	Homo sapiens phosphodiesterase 11A (PDE11A) transcript variant 2 mRNA.	Neurological system process	NM_001077358	chr2	12.18	1.00E-03	-	1	ins	12.13	0|0.01	178494173	NA	-|-	1-4|-:GGA|-:S;0,5|GGA:GGA|S:S
31	SCAF1	Homo sapiens SR-related CTD-associated factor 1 (SCAF1) mRNA.		NM_021228	chr19	19.01	1.00E-03	+	1	del	13.52	0|1.19	50155362	NA	CCGCTC|RRS	0|-:-|-:-;2-5|-:CCGCTC|-:RRS
32	GPATCH4	Homo sapiens G patch domain containing 4 (GPATCH4) transcript variant 2 mRNA.		NM_015590	chr1	17.41	2.00E-03	-	1	ins	17.36	0|0.01	156565049	NA	-|-	0-5|AC:AC|V:V
33	FRG2C_DUP_01	Homo sapiens FSHD region gene 2 family member C (FRG2C) mRNA.		NM_001124759	chr3	13.82	2.00E-03	+	1	SNP	8.33	0|1.19	75714337	NA	T|I	N|0,2-5|T:G|I:S
34	CDK11A	Homo sapiens cyclin-dependent kinase 11A (CDK11A) transcript variant 4 mRNA.		NM_033486	chr1	14.19	2.00E-03	-	1	ins	14.14	0|0.01	1647893	NA	-|-	0-5|-:TTTCTT|-:KK
35	LRRC14	Homo sapiens leucine rich repeat containing 14 (LRRC14) mRNA.		NM_014665	chr8	14.98	2.00E-03	+	1	SNP	9.49	0|1.19	145745196	NA	A|E	N|0,2-5|A:T|E:D
36	MT4	Homo sapiens metallothionein 4 (MT4) mRNA.		NM_032935	chr16	14.41	2.00E-03	+	1	SNP	14.36	0|0.01	56601720	NA	A|Y	N|0-5|G:G|C:C
37	TSTA3	Homo sapiens tissue specific transplantation antigen P35B (TSTA3) mRNA.		NM_003313	chr8	15.47	2.00E-03	-	1	SNP	9.98	0|1.19	144695921	NA	C|V	N|0,2-5|C:G|V:L
38	DLX6	Homo sapiens distal-less homeobox 6 (DLX6) mRNA.	Transcription Factor	NM_005222	chr7	12.18	2.00E-03	+	1	ins	12.13	0|0.01	96635420	NA	-|-	1-2,5|-:GCC|-:A;0,3-4|GCC:GCC|A:A
39	HYI	Homo sapiens hydroxypyruvate		NM_031207	chr1	5.7	2.00E-03	-	1	SNP	5.65	0|0.01	43919413	2	A|S	B|0,5|A:G|S:P;N|1-4|G:G|P:P

		isomerase (putative) (HYI) transcript variant 1 mRNA.															
40	LIX1L	Homo sapiens Lix1 homolog (mouse)-like (LIX1L) mRNA.		NM_153713	chr1	11.59	2.00E-03	+	1	SNP	6.1	0|1.19	145477223		4	G|R	B|0,2-5|A:G|Q:R
41	BCL6B	Homo sapiens B-cell CLL/lymphoma 6 member B (BCL6B) mRNA.	Transcription Factor	NM_181844	chr17	12.18	2.00E-03	+	1	ins	12.13	0|0.01	6928019	NA		-|-	0-2|-:CAG|-:Q;3-5|CAG:CAG|Q:Q
42	FMO2	Homo sapiens flavin containing monooxygenase 2 (non-functional) (FMO2) mRNA.		NM_001460	chr1	13.04	2.00E-03	+	1	SNP	12.99	0|0.01	171168584	NA		C|S	N|0-3,5|T:C|L:S;N|4|T:T|L:L
43	DCP1B	Homo sapiens DCP1 decapping enzyme homolog B (S. cerevisiae) (DCP1B) mRNA.	Transcription Factor;TGF-beta signaling pathway	NM_152640	chr12	12.18	2.00E-03	-	1	ins	12.13	0|0.01	2062323	NA		-|-	0,3-5|-:TGC|-:A;1-2|TGC:TGC|A:A
44	ACADL	Homo sapiens acyl-CoA dehydrogenase long chain (ACADL) nuclear gene encoding mitochondrial protein mRNA.		NM_001608	chr2	9.88	2.00E-03	-	1	SNP	4.39	0|1.19	211085491		7	G|T	B|0,2-5|A:G|I:T
45	KCNJ12	Homo sapiens potassium inwardly-rectifying channel subfamily J member 18 (KCNJ18) mRNA.	Potassium Channel;Neurological system process;Ion channel activity	NM_021012	chr17	9.07	2.00E-03	+	1	SNP	9.02	0|0.01	21319007	NA		G|R	N|0-5|A:G|Q:R
46	C4orf48	Homo sapiens chromosome 4 open reading frame 48 (C4orf48) transcript variant 2 mRNA.		NM_001141936	chr4	9.56	2.00E-03	+	1	SNP	9.51	0|0.01	2044128	NA		C|P	N|0-5|T:T|L:L
47	SELPLG	Homo sapiens selectin P ligand (SELPLG) transcript variant 1 mRNA.		NM_003006	chr12	13.52	2.00E-03	-	1	del	13.47	0|0.01	109017672	NA		GCA|VP	0,2-3|-:-|-:-;1,4-5|-:GCA|-:VP
48	IP6K3	Homo sapiens inositol hexakisphosphate kinase 3 (IP6K3) transcript variant 1 mRNA.		NM_001142883	chr6	12.84	2.00E-03	-	1	SNP	7.35	0|1.19	33690796	NA		C|V	N|2-5|T:C|I:V;N|0|T:T|I:I
49	FFAR3	Homo sapiens free fatty acid receptor 3 (FFAR3) mRNA.		NM_005304	chr19	4.24	2.00E-03	+	1	SNP	4.19	0|0.01	35849926		1	G|R	N|0|A:A|H:H;B|1-5|A:G|H:R
50	USP40	Homo sapiens ubiquitin specific peptidase 40 (USP40) mRNA.		NM_018218	chr2	17.62	3.00E-03	-	1	ins	12.13	0|1.19	234429739	NA		-|-	0,2-5|-:TTC|-:E
51	PSMG4	Homo sapiens proteasome (prosome macropain) assembly chaperone 4 (PSMG4) transcript variant 3 mRNA.		NM_001128592	chr6	7.66	3.00E-03	+	1	SNP	7.61	0|0.01	3264526	NA		C|L	N|1,3,5|T:C|F:L;N|0,2,4|T:T|F:F
52	MUC13	Homo sapiens mucin 13 cell surface associated (MUC13) mRNA.	Nervous System Development	NM_033049	chr3	12.18	3.00E-03	-	1	ins	12.13	0|0.01	124646705	NA		-|-	0-5|AAG:AAG|L:L
53	RESP18	Homo sapiens regulated endocrine-specific protein 18 homolog (rat) (RESP18) mRNA.		NM_001007089	chr2	7.2	3.00E-03	-	1	SNP	7.15	0|0.01	220197388	NA		C|E	N|3,5|A:A|D:D;N|0-2,4|A:C|D:E
54	CDC27	Homo sapiens cell division cycle 27 homolog (S. cerevisiae) (CDC27) transcript variant 2 mRNA.		NM_001256	chr17	15.38	3.00E-03	-	1	SNP	15.33	0|0.01	45234360		2	A|L	B|0-5|A:C|L:*
55	OR9G9	Homo sapiens olfactory receptor family 9 subfamily G member 9 (OR9G9) mRNA.		NM_001013358	chr11	9.56	3.00E-03	+	1	SNP	9.51	0|0.01	56468021	NA		G|C	N|0-5|A:G|Y:C
56	MUC1	Homo sapiens mucin 1 cell surface associated (MUC1) transcript variant 1 mRNA.		NM_001204285	chr1	9.73	3.00E-03	-	1	SNP	4.24	0|1.19	155160941		4	C|G	B|0,2-5|T:C|S:G
57	CCDC76	Homo sapiens coiled-coil domain containing 76 (CCDC76) mRNA.		NM_019083	chr1	10.55	3.00E-03	+	1	SNP	10.5	0|0.01	100598867	NA		C|A	N|0-5|T:T|V:V
58	SEPT9	Homo sapiens septin 9 (SEPT9) transcript variant 4 mRNA.		NM_001113496	chr17	6.22	3.00E-03	+	1	SNP	6.17	0|0.01	75494705	NA		A|M	N|0-5|G:G|V:V
59	TRIM50	Homo sapiens tripartite motif containing 50 (TRIM50) mRNA.	Neurontransmitter Secretion;Neurological system process	NM_178125	chr7	8.99	3.00E-03	-	1	SNP	8.94	0|0.01	72738763	NA		A|L	N|0-5|G:G|P:P
60	ATN1	Homo sapiens atrophin 1 (ATN1) transcript variant 2 mRNA.		NM_001007026	chr12	14.19	3.00E-03	+	1	ins	14.14	0|0.01	7045891	NA		-|-	0-5|-:CAGCAG|-:QQ
61	BST1	Homo sapiens bone marrow stromal cell antigen 1 (BST1) mRNA.		NM_004334	chr4	12.37	3.00E-03	+	1	SNP	6.88	0|1.19	15704779	NA		G|Q	N|0,2-5|C:G|H:Q
62	OR51M1	Homo sapiens olfactory receptor family 51 subfamily M member 1 (OR51M1) mRNA.		NM_001004756	chr11	7.4	4.00E-03	+	1	SNP	7.35	0|0.01	5411580	NA		T|F	N|0-5|C:C|L:L
63	PPM1E	Homo sapiens protein phosphatase Mg2+/Mn2+ dependent 1E (PPM1E) mRNA.	MAPKKK cascade	NM_014906	chr17	14.19	4.00E-03	+	1	ins	14.14	0|0.01	56833457	NA		-|-	0,4|GAACCC:-|EP:-;1-3,5|GAACCC:GAACCC|EP:EP
64	WDR66	Homo sapiens WD repeat domain 66 (WDR66) transcript variant 1 mRNA.		NM_001178003	chr12	14.07	4.00E-03	+	1	ins	14.02	0|0.01	122359397	NA		-|-	0-5|GAGGAGGAGGAGAAA:GAGGAGGAGGAGAAA|EEEEK:EEEEK
65	C1QTNF9	Homo sapiens C1q and tumor necrosis factor related protein 9 (C1QTNF9) mRNA.		NM_178540	chr13	9.52	4.00E-03	+	1	SNP	4.03	0|1.19	24895745		5	A|M	B|0,2-5|A:G|M:V
66	POU4F2	Homo sapiens POU class 4 homeobox 2 (POU4F2) mRNA.	Transcription Factor	NM_004575	chr4	12.18	4.00E-03	+	1	ins	12.13	0|0.01	147560457	NA		-|-	1-2,5|-:GGC|-:G;0,3-4|GGC:GGC|G:G
67	FLG	Homo sapiens filaggrin (FLG) mRNA.		NM_002016	chr1	18.08	4.00E-03	-	1	SNP	12.59	0|1.19	152277622		1	G|S	B|0,2-5|T:G|*:S
68	LSR	Homo sapiens lipolysis stimulated lipoprotein receptor (LSR) transcript variant 3 mRNA.		NM_015925	chr19	12.18	4.00E-03	+	1	ins	12.13	0|0.01	35758275	NA		-|-	0-5|GGA:GGA|G:G
69	ABP1	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1) mRNA.		NM_001091	chr7	12.8	4.00E-03	+	1	SNP	12.75	0|0.01	150556055	NA		C|T	N|0-5|G:G|R:R
70	IL12RB1	Homo sapiens interleukin 12 receptor beta 1 (IL12RB1) transcript variant 2 mRNA.		NM_005535	chr19	9.11	4.00E-03	-	1	SNP	3.62	0|1.19	18183095		5	C|R	B|0,2-5|T:C|Q:R
71	PRICKLE4	Homo sapiens prickle homolog 4 (Drosophila) (PRICKLE4) mRNA.		NM_013397	chr6	12.18	4.00E-03	+	1	ins	12.13	0|0.01	41754573	NA		-|-	0,2-3,5|-:CTT|-:L;1,4|CTT:CTT|L:L
72	ACOT12	Homo sapiens acyl-CoA thioesterase 12 (ACOT12) mRNA.		NM_130767	chr5	2.46	4.00E-03	-	1	SNP	0.53	0|0.42	80641789		10	C|V	B|0,2-5|T:C|I:V
73	ANKRD43	Homo sapiens sosondowah ankyrin repeat domain family member A (SOWAHA) mRNA.		NM_175873	chr5	16.25	4.00E-03	+	1	ins	16.2	0|0.01	132149322	NA		-|-	0,2-3|-:GCCGCCGCC|-:AAA;1,4-5|GCCGCCGCC:GCCGCCGCC|AAA:AAA
74	PHC3	Homo sapiens polyhomeotic homolog 3 (Drosophila) (PHC3) mRNA.	Transcription Factor;Nervous System Development	NM_024947	chr3	9.35	4.00E-03	-	1	SNP	3.86	0|1.19	169846735		2	T|I	B|0,2-5|T:C|I:V
75	PTH2R	Homo sapiens parathyroid hormone 2 receptor (PTH2R) mRNA.	G-protein coupled receptor;Neurological system process	NM_005048	chr2	12.15	5.00E-03	+	1	SNP	8.88	0|0.71	209302328		9	C|S	B|0,2-5|A:C|*:S
76	RBM23	Homo sapiens RNA binding motif protein 23 (RBM23) transcript variant 2 mRNA.	Neurological system process;Nervous System Development	NM_018107	chr14	12.18	5.00E-03	-	1	ins	12.13	0|0.01	23371255	NA		-|-	1-2|-:GGC|-:A;0,3-5|GGC:GGC|A:A
77	ZNF787	Homo sapiens zinc finger protein 787 (ZNF787) mRNA.	Transcription Factor	NM_001002836	chr19	13.52	5.00E-03	-	1	del	13.47	0|0.01	56599438	NA		TCG|DE	0-5|-:-|-:-
78	KLHL38	Homo sapiens kelch-like 38 (Drosophila) (KLHL38) mRNA.	Transcription Factor;Neurological system process	NM_001081675	chr8	6.58	5.00E-03	-	1	SNP	6.53	0|0.01	124664874	NA		T|H	N|0,2,4|C:C|R:R;N|1,3,5|T:C|H:R
79	PTGFRN	Homo sapiens prostaglandin F2 receptor negative regulator (PTGFRN) mRNA.		NM_020440	chr1	9	5.00E-03	+	1	SNP	8.95	0|0.01	117487711	NA		T|S	N|0-5|A:A|T:T
80	FARSA	Homo sapiens		NM_004461	chr19	2.05	5.00E-03	-	1	SNP	1.66	0|0.08	13035722		11	T|Q	B|0,2-5|T:C|Q:R

		phenylalanyl-tRNA synthetase alpha subunit (FARSA) mRNA.														
81	SLC29A3	Homo sapiens solute carrier family 29 (nucleoside transporters) member 3 (SLC29A3) transcript variant 1 mRNA.		NM_001174098	chr10	6.03	5.00E-03	+	1	SNP	5.98	0|0.01	73115942	NA	G|V	N|0-5|A:A|I:I
82	SDR39U1	Homo sapiens short chain dehydrogenase/reductase family 39U member 1 (SDR39U1) mRNA.		NM_020195	chr14	9.58	5.00E-03	-	1	SNP	9.53	0|0.01	24910973	NA	T|I	N|0-5|G:G|L:L
83	ARMC9	Homo sapiens armadillo repeat containing 9 (ARMC9) mRNA.		NM_025139	chr2	12.88	6.00E-03	+	1	SNP	12.83	0|0.01	232087475	NA	T|I	N|0-5|A:A|K:K
84	CACNA1C	Homo sapiens calcium channel voltage-dependent L type alpha 1C subunit (CACNA1C) transcript variant 1 mRNA.	Autism;Neurontransmitter Secretion;Neurological system process;Calcium Channel;Alzheimer Disease Amyloid Secretase Pathway;Ion channel activity	NM_001129830	chr12	9.6	6.00E-03	+	1	SNP	9.55	0|0.01	2791130	NA	C|P	N|0-5|T:T|L:L
85	KRTAP12-2	Homo sapiens keratin associated protein 12-2 (KRTAP12-2) mRNA.		NM_181684	chr21	8.2	6.00E-03	-	1	SNP	8.15	0|0.01	46086758	NA	C|A	N|0|T:C|T:A;N|1-5|T:T|T:T
86	ATXN3_DUP_01	Homo sapiens ataxin 3 (ATXN3) transcript variant h mRNA.		NM_001164778	chr14	4.8	6.00E-03	-	1	SNP	4.75	0|0.01	92537354	NA	C|G	N|0-5|G:G|R:R
87	TMCO4	Homo sapiens transmembrane and coiled-coil domains 4 (TMCO4) mRNA.		NM_181719	chr1	9.28	6.00E-03	-	1	SNP	9.23	0|0.01	20020994	NA	C|R	N|0,2-4|T:C|H:R;N|1,5|T:T|H:H
88	ECHS1	Homo sapiens enoyl CoA hydratase short chain 1 mitochondrial (ECHS1) nuclear gene encoding mitochondrial protein mRNA.		NM_004092	chr10	0.71	6.00E-03	-	1	SNP	0.66	0|0.01	135186806	1	A|V	B|1-5|A:G|V:A;N|0|G:G|A:A
89	ZNF844	Homo sapiens zinc finger protein 844 (ZNF844) mRNA.		NM_001136501	chr19	11.21	6.00E-03	+	1	SNP	5.72	0|1.19	12186921	NA	T|V	N|0,2-5|T:C|V:A
90	FZD5	Homo sapiens frizzled family receptor 5 (FZD5) mRNA.	Cadherin Signaling Pathway;Alzheimer Disease Presenilin Pathway;Wnt Signaling Pathway	NM_003468	chr2	7.7	6.00E-03	-	1	SNP	5.76	0|0.42	208632817	10	G|P	B|0,2-5|A:G|L:P
91	MUS81	Homo sapiens MUS81 endonuclease homolog (S. cerevisiae) (MUS81) mRNA.		NM_025128	chr11	10.08	6.00E-03	+	1	SNP	10.03	0|0.01	65629934	NA	G|R	N|1,3-5|C:C|P:P;N|0,2|C:G|P:R
92	MAP3K4	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4) transcript variant 2 mRNA.	PDGF Signaling Pathway;Imflammation mediated by chemokine and cytokine signaling;Oxidative stress response;FGF Signaling pathway;EGF receptor signaling pathway	NM_005922	chr6	13.52	6.00E-03	+	1	del	13.47	0|0.01	161519351	NA	CTG|PA	0-5|-:-|-:-
93	C9orf150	Homo sapiens chromosome 9 open reading frame 150 (C9orf150) mRNA.		NM_203403	chr9	12.4	6.00E-03	+	1	ins	12.34	0|0.01	12775861	NA	-|G	0-1,3-5|GGCGGCGGC:GGCGGCGGC|GGG:GGG;2|^:^|^:^
94	ZFAT	Homo sapiens zinc finger and AT hook domain containing (ZFAT) transcript variant 5 mRNA.	Transcription Factor	NM_020863	chr8	10.3	6.00E-03	-	1	SNP	4.81	0|1.19	135614326	7	G|R	B|0,2-5|A:G|W:R
95	F2RL3	Homo sapiens coagulation factor II (thrombin) receptor-like 3 (F2RL3) mRNA.	Neurological system process	NM_003950	chr19	9.81	6.00E-03	+	1	SNP	4.31	0|1.19	17001203	5	C|P	B|0,2-5|T:C|L:P
96	ZNF778	Homo sapiens zinc finger protein 778 (ZNF778) transcript variant 2 mRNA.	Transcription Factor	NM_001201407	chr16	17.41	6.00E-03	+	1	ins	17.36	0|0.01	89291210	NA	-|-	0-5|GTGA:GTGA|VM:VM
97	GAK	Homo sapiens cyclin G associated kinase (GAK) mRNA.		NM_005255	chr4	12.25	6.00E-03	-	1	SNP	6.76	0|1.19	862363	4	C|D	B|0,2-5|A:C|Y:D
98	BTNL2_DUP_07	Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2) mRNA.		NM_019602	chr6	10.69	6.00E-03	-	1	SNP	10.64	0|0.01	32362703	NA	G|P	N|0-1,3-5|T:G|Q:P;N|2|T:T|Q:Q
99	MPP2	Homo sapiens membrane protein palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2) mRNA.		NM_005374	chr17	10.01	6.00E-03	-	1	SNP	9.96	0|0.01	41960633	NA	C|V	N|0-5|G:G|L:L
100	MAFA	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian) (MAFA) mRNA.	Transcription Factor	NM_201589	chr8	7.76	6.00E-03	-	1	del	7.71	0|0.01	144511954	NA	TGG|HH	0-5|-:-|-:-
101	LSG1	Homo sapiens large subunit GTPase 1 homolog (S. cerevisiae) (LSG1) mRNA.		NM_018385	chr3	8.54	7.00E-03	-	1	SNP	8.49	0|0.01	194373832	NA	T|K	N|0-5|C:C|E:E
102	MCC	Homo sapiens mutated in colorectal cancers (MCC) transcript variant 2 mRNA.		NM_001085377	chr5	12.92	7.00E-03	-	1	ins	12.86	0|0.01	112824048	NA	-|S	0,2-3|-:GCC|-:G;1,4-5|GCC:GCC|G:G
103	DLC1	Homo sapiens deleted in liver cancer 1 (DLC1) transcript variant 3 mRNA.	PDGF Signaling Pathway	NM_024767	chr8	6.93	7.00E-03	-	1	SNP	6.88	0|0.01	13356819	NA	T|Q	N|0-5|G:G|H:H
104	MUC6	Homo sapiens mucin 6 oligomeric mucus/gel-forming (MUC6) mRNA.	Neurological system process	NM_005961	chr11	13.74	7.00E-03	-	1	SNP	8.25	0|1.19	1017691	NA	C|A	N|0,2-5|C:G|A:P
105	PCDHAC1	Homo sapiens protocadherin alpha subfamily C 2 (PCDHAC2) transcript variant 2 mRNA.		NM_014005	chr5	13.65	7.00E-03	+	1	SNP	8.16	0|1.19	140230371	NA	A|K	N|2-5|A:C|K:T;N|0|C:C|T:T
106	ISCU	Homo sapiens iron-sulfur cluster scaffold homolog (E. coli) (ISCU) nuclear gene encoding mitochondrial protein transcript variant 2 mRNA.		NM_213595	chr12	13.48	7.00E-03	+	1	SNP	13.43	0|0.01	108956418	NA	T|F	N|0-5|G:G|C:C
107	RNF169	Homo sapiens ring finger protein 169 (RNF169) mRNA.		NM_001098638	chr11	9.99	7.00E-03	+	1	SNP	4.5	0|1.19	74460148	8	C|P	B|2-5|T:C|S:P;N|0|T:T|S:S
108	FAM135B	Homo sapiens family with sequence similarity 135 member B (FAM135B) mRNA.		NM_015912	chr8	9.55	8.00E-03	-	1	SNP	9.5	0|0.01	139165273	NA	G|P	N|0,4|A:A|L:L;N|1-3,5|A:G|L:P
109	POTEF	Homo sapiens POTE ankyrin domain family member F (POTEF) mRNA.		NM_001099771	chr2	9.94	8.00E-03	-	1	SNP	9.89	0|0.01	130832292	NA	T|Y	N|1,3-5|A:A|F:F;N|0,2|A:T|F:Y
110	PCLO	Homo sapiens piccolo (presynaptic cytomatrix protein) (PCLO) transcript variant 2 mRNA.	Neurontransmitter Secretion;Neurological system process	NM_014510	chr7	17.41	9.00E-03	-	1	ins	17.36	0|0.01	82581488	NA	-|-	0-5|TCA:TCA|*:*
111	LAMA4	Homo sapiens laminin alpha 4 (LAMA4) transcript variant 5 mRNA.		NM_001105206	chr6	12.82	9.00E-03	-	1	SNP	12.77	0|0.01	112508770	NA	G|A	N|0-5|T:T|E:E
112	IRF2BPL	Homo sapiens interferon regulatory factor 2 binding protein-like (IRF2BPL) mRNA.		NM_024496	chr14	13.52	9.00E-03	-	1	del	13.47	0|0.01	77493792	NA	TGT|QQ	0-5|-:-|-:-
113	MICAL1	Homo sapiens microtubule associated monoxygenase calponin and LIM domain containing 1 (MICAL1) transcript variant 1 mRNA.	Neurological system process;Nervous System Development	NM_001159291	chr6	8.2	9.00E-03	-	1	SNP	8.15	0|0.01	109767931	NA	C|A	N|1-2,5|T:C|T:A;N|0,3-4|T:T|T:T
114	PIGQ	Homo sapiens phosphatidylinositol glycan anchor biosynthesis class Q (PIGQ) transcript variant 2 mRNA.		NM_148920	chr16	9.52	9.00E-03	+	1	SNP	9.47	0|0.01	633354	NA	G|C	N|2-4|A:A|Y:Y;N|0-1,5|A:G|Y:C

115	TMEM44	Homo sapiens transmembrane protein 44 (TMEM44) transcript variant 1 mRNA.		NM_001166305	chr3	7.06	9.00E-03	-	1	SNP	7.01	0|0.01	194338424	NA	G|R	N|2-3|C:C|G:G;N|0-1,4-5|C:G|G:R
116	CUL7	Homo sapiens cullin 7 (CUL7) transcript variant 2 mRNA.		NM_014780	chr6	8.57	9.00E-03	-	1	SNP	8.52	0|0.01	43014299	NA	T|Q	N|0-5|C:C|R:R
117	TMEM184A	Homo sapiens transmembrane protein 184A (TMEM184A) mRNA.		NM_001097620	chr7	12.18	1.00E-02	-	1	ins	12.13	0|0.01	1586653	NA	-|-	1-2,4|-:GCC|-:G;0,3,5|GCC:GCC|G:G
118	PCM1	Homo sapiens pericentriolar material 1 (PCM1) mRNA.		NM_006197	chr8	10.22	1.00E-02	+	1	SNP	10.17	0|0.01	17796382	NA	A|N	N|1-5|A:G|N:S;N|0|G:G|S:S
119	SPAG17	Homo sapiens sperm associated antigen 17 (SPAG17) mRNA.		NM_206996	chr1	12.06	1.00E-02	-	1	SNP	6.57	0|1.19	118644480	NA	G|P	N|0,2-5|C:G|A:P
120	KRTAP10-2	Homo sapiens keratin associated protein 10-2 (KRTAP10-2) mRNA.		NM_198693	chr21	14.62	1.00E-02	-	1	del	9.12	0|1.19	45970760	NA	CTTGCAGCAGACAGG|PVCCK	0,2-5|-:CTTGCAGCAGACAGG|-:PVCCK
121	CPS1	Homo sapiens carbamoyl-phosphate synthase 1 mitochondrial (CPS1) transcript variant 3 mRNA.		NM_001122633	chr2	7.76	1.00E-02	+	1	SNP	7.71	0|0.01	211456637	NA	A|T	N|1-5|A:G|T:A;N|0|G:G|A:A
122	RNF212	Homo sapiens ring finger protein 212 (RNF212) transcript variant 3 mRNA.		NM_001193318	chr4	17.41	1.00E-02	-	1	ins	17.36	0|0.01	1087327	NA	-|-	1|CTGCCCAGGCTAGAGCCAGCC:CTGCCCAGGCTAGAGCCAGCC|GWL*PGQ:GWL*PGQ;0,2-4|CTGCCCAGGCTGGAGCCAGCC:CTGCCCAGGCTGGAGCCAGCC|GWLQPGQ:GWLQPGQ;5|CTGTCCAGGCTGGAGCCAGCC:CTGTCCAGGCTGGAGCCAGCC|GWLQPGQ:GWLQPGQ
123	FMNL1	Homo sapiens formin-like 1 (FMNL1) mRNA.		NM_005892	chr17	6.63	1.00E-02	+	1	SNP	6.58	0|0.01	43318779	NA	C|P	N|0-5|G:G|A:A
124	TCF15	Homo sapiens transcription factor 15 (basic helix-loop-helix) (TCF15) mRNA.	Transcription Factor	NM_004609	chr20	10.03	1.00E-02	-	1	SNP	9.98	0|0.01	590542	NA	C|V	N|0-5|G:G|L:L
125	RAB11FIP1	Homo sapiens RAB11 family interacting protein 1 (class I) (RAB11FIP1) transcript variant 1 mRNA.		NM_025151	chr8	6.69	1.00E-02	-	1	SNP	6.64	0|0.01	37728017	3	A|M	B|0,3,5|A:G|M:T;B|1-2,4|G:G|T:T
126	MLL3	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 3 (MLL3) mRNA.		NM_170606	chr7	13.61	1.00E-02	-	1	ins	13.55	0|0.01	151945071	NA	-|Y	0-5|-:T|-:N
127	OAS3	Homo sapiens 2'-5'-oligoadenylate synthetase 3 100kDa (OAS3) mRNA.		NM_006187	chr12	3.87	1.00E-02	+	1	SNP	3.82	0|0.01	113388598	5	G|R	N|4|A:A|H:H;B|0-3,5|A:G|H:R
128	ZDBF2	Homo sapiens zinc finger DBF-type containing 2 (ZDBF2) mRNA.		NM_020923	chr2	7.91	1.00E-02	+	1	SNP	4.64	0|0.71	207173390	9	G|E	B|0,2-5|A:G|K:E
129	KRTAP9-1	Homo sapiens keratin associated protein 9-1 (KRTAP9-1) mRNA.		NM_001190460	chr17	13.52	1.00E-02	+	1	del	13.47	0|0.01	39346593	NA	CCT|TC	0-5|-:CCT|-:TC
130	NLRP6	Homo sapiens NLR family pyrin domain containing 6 (NLRP6) mRNA.		NM_138329	chr11	7.55	1.00E-02	+	1	SNP	7.5	0|0.01	280816	NA	A|Y	N|1|A:T|Y:F;N|0,2-5|T:T|F:F
131	FANCM	Homo sapiens Fanconi anemia complementation group M (FANCM) mRNA.		NM_020937	chr14	8.55	1.00E-02	+	1	SNP	3.06	0|1.19	45636328	7	A|N	B|0,2-5|A:G|N:S
132	TELO2	Homo sapiens TEL2 telomere maintenance 2 homolog (S. cerevisiae) (TELO2) mRNA.		NM_016111	chr16	7.42	2.00E-02	+	1	SNP	7.37	0|0.01	1544302	NA	A|E	N|0-4|A:G|E:G;N|5|G:G|G:G
133	NCOR2	Homo sapiens nuclear receptor corepressor 2 (NCOR2) transcript variant 1 mRNA.	Transcription Factor;Huntington Disease;Notch Signaling Pathway	NM_001206654	chr12	12.18	2.00E-02	-	1	ins	12.13	0|0.01	124887058	NA	-|-	0-5|GCT:GCT|S:S
134	PSD3	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3) transcript variant 2 mRNA.		NM_015310	chr8	9.53	2.00E-02	-	1	SNP	9.48	0|0.01	18729817	NA	G|T	N|0-5|A:A|M:M
135	COL24A1	Homo sapiens collagen type XXIV alpha 1 (COL24A1) mRNA.		NM_152890	chr1	3.86	3.00E-02	-	1	SNP	3.81	0|0.01	86591837	207	G|A	B|0,3,5|A:A|V:V;B|1-2,4|A:G|V:A
136	SCARF2	Homo sapiens scavenger receptor class F member 2 (SCARF2) transcript variant 2 mRNA.		NM_182895	chr22	10.03	3.00E-02	-	1	SNP	9.98	0|0.01	20779946	NA	C|V	N|0-5|G:G|L:L
137	DNAH17	Homo sapiens dynein axonemal heavy chain 17 (DNAH17) mRNA.	Huntington Disease	NM_173628	chr17	9.87	3.00E-02	-	1	SNP	9.82	0|0.01	76491127	NA	T|M	N|1,4|C:C|V:V;N|0,2-3,5|T:C|M:V
138	PLIN4	Homo sapiens perilipin 4 (PLIN4) mRNA.		NM_001080400	chr19	8.59	3.00E-02	-	1	SNP	8.54	0|0.01	4511453	NA	G|A	N|0-5|A:A|V:V
139	RNF213	Homo sapiens ring finger protein 213 (RNF213) transcript variant 2 mRNA.		NM_020914	chr17	2.76	3.00E-02	+	1	SNP	2.71	0|0.01	78346870	6	C|L	B|0-5|A:C|I:L
140	OBSCN	Homo sapiens obscurin cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN) transcript variant 1 mRNA.		NM_052843	chr1	10.77	3.00E-02	+	1	SNP	10.72	0|0.01	228412228	NA	G|A	N|4|A:A|T:T;N|0-3,5|A:G|T:A
141	KRTAP10-7	Homo sapiens keratin associated protein 10-7 (KRTAP10-7) mRNA.		NM_198689	chr21	0.47	4.00E-02	+	1	SNP	0.42	0|0.01	46020867	2	A|M	B|0-5|G:G|V:V
142	EPPK1	Homo sapiens epiplakin 1 (EPPK1) mRNA.		NM_031308	chr8	11.81	4.00E-02	-	1	SNP	6.3	0|1.19	144940779	2	G|R	B|0,2-5|A:G|C:R
143	MUC16	Homo sapiens mucin 16 cell surface associated (MUC16) mRNA.		NM_024690	chr19	6.77	5.00E-02	-	1	SNP	6.72	0|0.01	9001833	NA	A|M	N|0-5|G:G|T:T
144	HLA-DQB1_DUP_02	Homo sapiens major histocompatibility complex class II DQ beta 1 (HLA-DQB1) transcript variant 1 mRNA.		NM_002123	chr6	2.58	5.00E-02	-	1	SNP	2.53	0|0.01	32632745	4	G|A	B|0,2,4|A:A|V:V;B|1,3,5|A:G|V:A
145	DSP	Homo sapiens desmoplakin (DSP) transcript variant 1 mRNA.		NM_004415	chr6	0.28	1.00E+00	+	1	SNP	13.77	0|0.00	7582993	NA	A|E	N|1,3,5|A:T|E:V

Recessive model

Rank	Gene	FullName	Pathway	mRNA	Chr	Score	PValue	LOD_Score	LOD_PValue	Strand	#ofVar	VarType	VarScore	VarLODScore	VarPosition	AlleleCount	Ref	GenoType
1	C4orf48	Homo sapiens chromosome 4 open reading frame 48 (C4orf48) transcript variant 2 mRNA.		NM_001141936	chr4	32.38	9.00E-07	1.6	9.00E-07	+	1	SNP	25	0|1.60361112696843	2044128	NA	C|P	N|0-5|T:T|L:L
2	GPRIN1	Homo sapiens G protein regulated inducer of neurite outgrowth 1 (GPRIN1) mRNA.		NM_052899	chr5	44.11	2.00E-06	1.6	4.00E-04	-	2	del	19.37	0|1.60361112696843	176026136	NA	CCTCCTTCCTC|PRKED	0-5|-:CCTCCTTCCTC|-:PRKED
												del	19.37	0|1.60361112696843	176026122	NA	CAAAGACCCAGGA|DPGSL	0-5|-:CAAAGACCCAGGA|-:DPGSL
3	SEPT9	Homo sapiens septin 9 (SEPT9) transcript variant 4 mRNA.		NM_001113492	chr17	29.05	3.00E-06	1.6	3.00E-06	+	1	SNP	21.67	0|1.60361112696843	75494705	NA	A|M	N|0-5|G:G|V:V
4	KIAA0040	Homo sapiens KIAA0040 (KIAA0040) transcript variant 2 mRNA.		NM_001162893	chr1	49.5	3.00E-06	2.77	2.00E-05	-	2	del	19.37	0|2.78390360357584	175129948	NA	TCTTCTTG|NKKK	0-5|-:TCTTCTTG|-:NKKK
												del	19.37	0|2.78390360357584	175129946	NA	C|K	0-5|-:C|-:K
5	ATXN3_DUP_01	Homo sapiens ataxin 3 (ATXN3) transcript variant h mRNA.		NM_001164774	chr14	24.09	9.00E-06	1.6	1.00E-05	-	1	SNP	16.71	0|1.60361112696843	92537354	NA	C|G	N|0-5|G:G|R:R
6	SLC29A3	Homo sapiens solute carrier family 29 (nucleoside transporters) member 3 (SLC29A3) transcript variant 1 mRNA.		NM_001174098	chr10	28.85	1.00E-05	1.6	2.00E-05	+	1	SNP	21.47	0|1.60361112696843	73115942	NA	G|V	N|0-5|A:A|I:I
7	GPATCH4	Homo sapiens G patch domain containing 4 (GPATCH4) transcript variant 2 mRNA.		NM_182679	chr1	40.24	1.00E-05	1.6	2.00E-05	-	1	ins	32.86	0|1.60361112696843	156565049	NA	-|-	0-5|AC:AC|V:V
8	IRF2BPL	Homo sapiens interferon regulatory factor 2 binding protein-like (IRF2BPL) mRNA.		NM_024496	chr14	36.35	3.00E-05	1.6	4.00E-05	-	1	del	28.97	0|1.60361112696843	77493792	NA	TGT|QQ	0-5|-:-|-:-
9	PTGFRN	Homo sapiens prostaglandin F2 receptor negative regulator (PTGFRN) mRNA.		NM_020440	chr1	31.83	3.00E-05	1.6	9.00E-05	+	1	SNP	24.45	0|1.60361112696843	117487711	NA	T|S	N|0-5|A:A|T:T
10	ABP1	Homo sapiens amiloride binding protein 1 (amine oxidase (copper-containing)) (ABP1) mRNA.		NM_001091	chr7	35.63	3.00E-05	1.6	1.00E-04	+	1	SNP	28.25	0|1.60361112696843	150556055	NA	C|T	N|0-5|G:G|R:R
11	OR51M1	Homo sapiens olfactory receptor family 51 subfamily M member 1 (OR51M1) mRNA.		NM_001004756	chr11	30.23	6.00E-05	1.6	9.00E-04	+	1	SNP	22.85	0|1.60361112696843	5411580	NA	T|F	N|0-5|C:C|L:L
12	FMNL1	Homo sapiens formin-like 1 (FMNL1)		NM_005892	chr1	29.4	8.00E-	1.6	1.00E-04	+	1	SNP	22.08	0|1.603611126968	43318779	NA	C|P	N|0-5|G:G|A:A

		mRNA.			7	6	05							43				
13	LSG1	Homo sapiens large subunit GTPase 1 homolog (S. cerevisiae) (LSG1) mRNA.		NM_018385	chr3	31.36	1.00E-04	1.6	4.00E-04	-	1	SNP	23.98	0|1.60361112696843	194373832	NA	T|K	N|0-5|C:C|E:E
14	SDR39U1	Homo sapiens short chain dehydrogenase/reductase family 39U member 1 (SDR39U1) mRNA.		NM_020195	chr14	32.4	1.00E-04	1.6	4.00E-04	-	1	SNP	25.02	0|1.60361112696843	24910973	NA	T|I	N|0-5|G:G|L:L
15	KLF2	Homo sapiens Kruppel-like factor 2 (lung) (KLF2) mRNA.	Transcription Factor	NM_016270	chr19	21.82	1.00E-04	1.6	8.00E-05	+	1	SNP	14.44	0|1.60361112696843	16436262	5	T|L	B|0-5|C:C|P:P
16	LAMA4	Homo sapiens laminin alpha 4 (LAMA4) transcript variant 5 mRNA.		NM_001105206	chr6	35.65	1.00E-04	1.6	9.00E-04	-	1	SNP	28.27	0|1.60361112696843	112508770	NA	G|A	N|0-5|T:T|E:E
17	SOHLH1	Homo sapiens spermatogenesis and oogenesis specific basic helix-loop-helix 1 (SOHLH1) transcript variant 1 mRNA.		NM_001012415	chr9	27.15	1.00E-04	0.78	6.00E-05	-	1	SNP	23.56	0|0.779126465217891	138586966	NA	G|P	N|0,2-3,5|A:A|S:S;N|1|A:G|S:P
18	IGSF3	Homo sapiens immunoglobulin superfamily member 3 (IGSF3) transcript variant 1 mRNA.		NM_001007237	chr1	35.73	2.00E-04	1.58	2.00E-03	-	2	SNP	19.14	0|1.60361112696843	117142868	NA	C|W	N|0-5|T:C|*:W
												ins	12.13	0|1.60361112696843	117122285	NA	-|-	0-1,3,5|TCC:-|G:-;2,4|TCC:TCC|G:G
19	RBM23	Homo sapiens RNA binding motif protein 23 (RBM23) transcript variant 2 mRNA.	Neurological system process;Nervous System Development	NM_018107	chr14	31.22	2.00E-04	0.78	1.00E-04	-	1	ins	27.63	0|0.779126465217891	23371255	NA	-|-	1-2|-:GGC|-:A;0,3-5|GGC:GGC|A:A
20	MAP3K4	Homo sapiens mitogen-activated protein kinase kinase kinase 4 (MAP3K4) transcript variant 2 mRNA.	PDGF Signaling Pathway;Oxidative stress response;FGF Signaling pathway;EGF receptor signaling pathway;Imflammation mediated by chemokine and cytokine signaling	NM_005922	chr6	36.35	2.00E-04	1.6	4.00E-04	+	1	del	28.97	0|1.60361112696843	161519351	NA	CTG|PA	0-5|-:-|-:-
21	MPRIP	Homo sapiens myosin phosphatase Rho interacting protein (MPRIP) transcript variant 1 mRNA.		NM_015134	chr17	28.73	3.00E-04	0.78	2.00E-04	+	1	del	25.14	0|0.779126465217891	17039562	NA	CAG|TS	0,2-4|-:-|-:-;1|-:CAG|-:TS
22	MUC13	Homo sapiens mucin 13 cell surface associated (MUC13) mRNA.	Nervous System Development	NM_033049	chr3	35.01	3.00E-04	1.6	1.00E-03	-	1	ins	27.63	0|1.60361112696843	124646705	NA	-|-	0-5|AAG:AAG|L:L
23	PHLDA1	Homo sapiens pleckstrin homology-like domain family A member 1 (PHLDA1) mRNA.		NM_007350	chr12	23.95	3.00E-04	1.6	3.00E-04	-	1	del	16.56	0|1.60289380735475	76424938	NA	TGC|QQ	0-5|-:-|-:-
24	C19orf2	RecName: Full=Unconventional prefoldin RPB5 interactor; AltName: Full=Protein NNX3; AltName: Full=RNA polymerase II subunit 5-mediating protein; Short=RPB5-mediating protein;	Transcription Factor	NM_134447	chr19	15.75	3.00E-04	1.6	2.00E-04	+	1	del	8.36	0|1.60289380735475	30500119	NA	TGA|SD	0-5|-:-|-:-
25	WDR66	Homo sapiens WD repeat domain 66 (WDR66) transcript variant 1 mRNA.		NM_001178003	chr12	36.9	4.00E-04	1.6	5.00E-03	+	1	ins	29.52	0|1.60361112696843	122359397	NA	-|-	0-5|GAGGAGGAGGAGAAA:GAGGAGGAGGAGAAA|EEEEK:EEEEK
26	CES1	Homo sapiens carboxylesterase 1 (CES1) transcript variant 3 mRNA.	Neurological system process;Nervous System Development	NM_001025195	chr16	28.62	4.00E-04	1.37	2.00E-02	-	2	SNP	8.07	0|1.60361112696843	55862791	NA	T|I	N|0,3-5|T:C|I:V
												SNP	16.23	0|1.60361112696843	55862883	NA	C|G	N|0-5|A:C|V:G
27	CCDC102A	Homo sapiens coiled-coil domain containing 102A (CCDC102A) mRNA.		NM_033212	chr16	26.62	4.00E-04	1.6	5.00E-04	-	1	SNP	19.24	0|1.60361112696843	57562804	8	G|R	B|0-5|A:A|W:W
28	LSR	Homo sapiens lipolysis stimulated lipoprotein receptor (LSR) transcript variant 3 mRNA.		NM_205835	chr19	35.01	5.00E-04	1.6	3.00E-03	+	1	ins	27.63	0|1.60361112696843	35758275	NA	-|-	0-5|GGA:GGA|G:G
29	FMO2	Homo sapiens flavin containing monooxygenase 2 (non-functional) (FMO2) mRNA.		NM_001460	chr1	41.31	5.00E-04	2.78	1.00E-02	+	1	SNP	28.49	0|2.78390360357584	171168584	NA	C|S	N|0-3,5|T:C|L:S;N|4|T:T|L:L
30	NLRP6	Homo sapiens NLR family pyrin domain containing 6 (NLRP6) mRNA.		NM_138329	chr11	35.81	5.00E-04	2.78	8.00E-03	+	1	SNP	22.99	0|2.78390360357584	280816	NA	A|Y	N|1|A:T|Y:F;N|0,2-5|T:T|F:F
31	SCRT1	Homo sapiens scratch homolog 1 zinc finger protein (Drosophila) (SCRT1) mRNA.	Transcription Factor	NM_031309	chr8	13.65	6.00E-04	1.6	3.00E-04	-	1	SNP	6.26	0|1.60289380735475	145557497	18	A|S	B|0-5|C:C|A:A
32	KLHL38	Homo sapiens kelch-like 38 (Drosophila) (KLHL38) mRNA.	Transcription Factor;Neurological system process	NM_001081675	chr8	34.85	6.00E-04	2.78	3.00E-03	-	1	SNP	22.03	0|2.78390360357584	124664874	NA	T|H	N|0,2,4|C:C|R:R;N|1,3,5|T:C|H:R
33	ALS2CR8	Homo sapiens amyotrophic lateral sclerosis 2 (juvenile) chromosome region candidate 8 (ALS2CR8) mRNA.		NM_024744	chr2	26.53	7.00E-04	2.78	1.00E-03	+	1	SNP	13.71	0|2.78390360357584	203846831	NA	G|E	N|0,2-5|A:G|K:E
34	TGFB1	Homo sapiens transforming growth factor beta 1 (TGFB1) mRNA.	Neurodegenerative;TGF-beta signaling pathway	NM_000660	chr19	18.53	7.00E-04	1.6	8.00E-04	-	1	SNP	11.13	0|1.60289380735475	41858921	27	G|P	B|0-5|A:A|L:L
35	WWC1	Homo sapiens WW and C2 domain containing 1 (WWC1) transcript variant 3 mRNA.		NM_015238	chr5	39.09	7.00E-04	2.78	4.00E-03	+	1	SNP	26.27	0|2.78390360357584	167858371	NA	G|M	N|2-5|T:G|I:M;N|0|T:T|I:I
36	CUL7	Homo sapiens cullin 7 (CUL7) transcript variant 2 mRNA.		NM_014780	chr6	31.39	8.00E-04	1.6	2.00E-03	-	1	SNP	24.01	0|1.60361112696843	43014299	NA	T|Q	N|0-5|C:C|R:R
37	MAFA	Homo sapiens v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian) (MAFA) mRNA.	Transcription Factor	NM_201589	chr8	27.3	8.00E-04	1.6	2.00E-03	-	1	del	19.91	0|1.60361112696843	144511954	NA	TGG|HH	0-5|-:-|-:-
38	FAM171B	Homo sapiens family with sequence similarity 171 member B (FAM171B) mRNA.		NM_177454	chr2	19.94	8.00E-04	0.78	6.00E-04	+	1	ins	16.34	0|0.779130857883481	187559029	NA	-|Q	1|-:CAG|-:Q;2-5|CAG:CAG|Q:Q;0|^:^|^:^
39	ZNF778	Homo sapiens zinc finger protein 778 (ZNF778) transcript variant 2 mRNA.	Transcription Factor	NM_001201407	chr16	40.24	8.00E-04	1.6	5.00E-02	+	1	ins	32.86	0|1.60361112696843	89291210	NA	-|-	0-5|GTGA:GTGA|VM:VM
40	TCF15	Homo sapiens transcription factor 15 (basic helix-loop-helix) (TCF15) mRNA.	Transcription Factor	NM_004609	chr20	32.85	9.00E-04	1.6	2.00E-02	-	1	SNP	25.47	0|1.60361112696843	590542	NA	C|V	N|0-5|G:G|L:L
41	PGPEP1L	Homo sapiens pyroglutamyl-peptidase I-like (PGPEP1L) transcript variant 1 mRNA.		NM_001167902	chr15	11.54	9.00E-04	1.6	9.00E-04	-	1	SNP	4.23	0|1.60289380735475	99511873	105	G|A	B|0-5|A:A|V:V
42	SLC6A18	Homo sapiens solute carrier family 6 member 18 (SLC6A18) mRNA.	Neurological system process	NM_182632	chr5	20.82	1.00E-03	1.6	1.00E-03	+	1	SNP	13.44	0|1.60289380735475	1225687	13	C|T	B|0-5|T:T|I:I
43	SELPLG	Homo sapiens selectin P ligand (SELPLG) transcript variant 1 mRNA.		NM_001206609	chr12	36.35	1.00E-03	1.6	2.00E-02	-	1	del	28.97	0|1.60361112696843	109017672	NA	GCA|VP	0,2-3|-:-|-:-;1,4-5|-:GCA|-:VP
44	PCDHAC1	Homo sapiens protocadherin alpha subfamily C 2 (PCDHAC2) transcript variant 2 mRNA.		NM_031857	chr5	36.47	1.00E-03	2.78	6.00E-03	+	1	SNP	23.65	0|2.78390360357584	140230371	NA	A|K	N|2-5|A:C|K:T;N|0|C:C|T:T
45	TUBB1	Homo sapiens tubulin beta 1 class VI (TUBB1) mRNA.	Huntington Disease	NM_030773	chr20	19.94	1.00E-03	2.78	1.00E-03	+	2	SNP	6.45	0|2.78390360357584	57599303	6	C|T	B|0,4-5|T:C|M:T
												SNP	0.67	0|2.78390360357584	57599402	128	G|R	B|0,2-4|A:A|H:H;B|1,5|A:G|H:R
46	TARSL2	Homo sapiens threonyl-tRNA synthetase-like 2 (TARSL2) mRNA.		NM_152334	chr15	11.15	1.00E-03	1.6	9.00E-04	-	1	SNP	3.76	0|1.60289380735475	102264476	94	C|A	B|0-5|A:A|S:S
47	PIGQ	Homo sapiens phosphatidylinositol glycan anchor biosynthesis class Q (PIGQ) transcript variant 2 mRNA.		NM_148920	chr16	32.34	1.00E-03	1.6	2.00E-03	+	1	SNP	24.96	0|1.60361112696843	633354	NA	G|C	N|2-4|A:A|Y:Y;N|0-1,5|A:G|Y:C
48	ARMC9	Homo sapiens armadillo repeat containing 9 (ARMC9) mRNA.		NM_025139	chr2	35.7	1.00E-03	1.6	2.00E-03	+	1	SNP	28.32	0|0	232087475	NA	T|I	N|0-5|A:A|K:K
49	RNF212	Homo sapiens ring finger protein 212 (RNF212) transcript variant 3 mRNA.		NM_001193318	chr4	40.24	1.00E-03	1.6	4.00E-02	-	1	ins	32.86	0|1.60289380735475	1087327	NA	-|-	1|CTGCCCAGGCTAGAGCCAGCC:CTGCCCAGGCTAGAGCCAGCC|GWL*PGQ:GWL*PGQ;0,2-4|CTGCCCAGGCTGGAGCCAGCC:CTGCCCAGGCTGGAGCCAGCC|GWLQPGQ:GWLQPGQ;5|CTGTCCAGGCTGGAGCCAGCC:CTGTCCAGGCTGGAGCCAGCC|GWLQPGQ:GWLQPGQ
50	DLC1	Homo sapiens deleted in liver cancer 1 (DLC1) transcript variant 3 mRNA.	PDGF Signaling Pathway	NM_024767	chr8	29.76	1.00E-03	1.6	2.00E-02	-	1	SNP	22.38	0|0	13356819	NA	T|Q	N|0-5|G:G|H:H
51	BTNL2_DUP_07	Homo sapiens butyrophilin-like 2 (MHC class II associated) (BTNL2) mRNA.		NM_019602	chr6	33.51	1.00E-03	1.6	7.00E-03	-	1	SNP	26.13	0|1.60289380735475	32362703	NA	G|P	N|0-1,3-5|T:G|Q:P;N|2|T:T|Q:Q
52	MPP2	Homo sapiens membrane protein palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2) mRNA.		NM_005374	chr17	32.83	2.00E-03	1.6	2.00E-03	-	1	SNP	25.45	0|1.60361112696843	41960633	NA	C|V	N|0-5|G:G|L:L
53	CACNA1C	Homo sapiens calcium channel voltage-dependent L type alpha 1C subunit (CACNA1C) transcript variant 1 mRNA.	Calcium Channel;Neurological system process;Ion channel activity;Neurontransmitter Secretion;Autism;Alzheimer Disease Amyloid Secretase Pathway	NM_199460	chr12	32.42	2.00E-03	1.6	3.00E-03	+	1	SNP	25.04	0|1.60361112696843	2791130	NA	C|P	N|0-5|T:T|L:L
54	TRIM50	Homo sapiens tripartite motif containing 50 (TRIM50) mRNA.	Neurological system process;Neurontransmitter Secretion	NM_178125	chr7	31.81	2.00E-03	1.6	2.00E-03	-	1	SNP	24.43	0|0	72738763	NA	A|L	N|0-5|G:G|P:P
55	KRTAP4-7	Homo sapiens keratin associated protein 4-7 (KRTAP4-7) mRNA.		NM_033061	chr17	29.09	2.00E-03	1.6	3.00E-03	+	1	SNP	22.84	0|1.60289380735475	39240511	2	A|D	B|2,5|A:T|D:V;N|1,3-4|T:T|V:V
56	MT4	Homo sapiens metallothionein 4 (MT4) mRNA.		NM_032935	chr16	37.24	2.00E-03	1.6	2.00E-03	+	1	SNP	29.86	0|1.60361112696843	56601720	NA	A|Y	N|0-5|G:G|C:C
57	SRP14	Homo sapiens signal recognition particle 14kDa (homologous Alu RNA binding protein) (SRP14) mRNA.		NM_003134	chr15	10.75	2.00E-03	1.6	1.00E-03	-	1	SNP	3.43	0|1.60289380735475	40328575	34	G|P	B|0-5|C:C|A:A
58	CCDC76	Homo sapiens coiled-coil domain containing 76 (CCDC76) mRNA.		NM_019083	chr1	33.37	2.00E-03	1.6	2.00E-03	+	1	SNP	25.99	0|0	100598867	NA	C|A	N|0-5|T:T|V:V
59	ZNF787	Homo sapiens zinc finger protein 787 (ZNF787) mRNA.	Transcription Factor	NM_001002836	chr19	36.35	2.00E-03	1.6	2.00E-03	-	1	del	28.97	0|1.60361112696843	56599438	NA	TCG|DE	0-5|-:-|-:-
60	NKX1-2	Homo sapiens NK1 homeobox 2 (NKX1-2) mRNA.		NM_001146340	chr10	22.32	2.00E-03	2.78	2.00E-03	-	1	SNP	9.48	0|2.78390360357584	126136239	16	A|V	B|2-5|A:G|V:A;N|0|G:G|A:A
61	MKI67	Homo sapiens antigen identified by monoclonal antibody Ki-67 (MKI67) transcript variant 1 mRNA.		NM_002417	chr10	35.88	2.00E-03	2.78	8.00E-02	-	2	SNP	5.7	0|2.78390360357584	129905551	NA	A|V	N|0,3,5|A:G|V:A
												del	17.37	0|2.78390360357584	129913713	NA	C|G	0,3,5|-:C|-:G
62	FLT4	Homo sapiens fms-related tyrosine kinase 4 (FLT4) transcript variant 2 mRNA.	Stress Response;Nervous System Development	NM_002020	chr5	26.26	2.00E-03	2.78	4.00E-03	-	1	SNP	13.43	0|2.78390360357584	180039606	25	C|R	B|2-5|T:C|H:R;N|0|T:T|H:H
63	KLF14	Homo sapiens Kruppel-like factor 14 (KLF14) mRNA.	Transcription Factor	NM_138693	chr7	30.25	2.00E-03	1.6	1.00E-02	-	1	SNP	23.44	0|1.60361112696843	130418721	NA	T|H	N|0|G:G|P:P;N|2-3|T:G|H:P
64	MRC1	Homo sapiens mannose receptor C type 1 (MRC1) mRNA.		NM_002438	chr10	19.17	2.00E-03	1.6	2.00E-03	+	1	SNP	11.78	0|1.60361112696843	17891705	8	A|S	B|0-5|G:G|G:G

65	GAL3ST2	Homo sapiens galactose-3-O-sulfotransferase 2 (GAL3ST2) mRNA.		NM_022134	chr2	11.42	2.00E-03	0.18	4.00E-03	+	1	SNP	10.59	0|0.180112436754885	242743532	NA	T|L	N|0,3|T:C|L:P
66	PALM2	Homo sapiens A kinase (PRKA) anchor protein 2 (AKAP2) transcript variant 2 mRNA.		NM_007203	chr9	24.16	2.00E-03	1.6	2.00E-03	+	2	SNP	2.64	0|1.60361112696843	112899361	NA	A|K	N|0-5|C:C|Q:Q
												ins	14.14	0|1.60361112696843	112900341	NA	-|-	2-5|GAAGCT:-|EA:-;1|GAAGCT:GAAGCT|EA:EA
67	IRF2BP2	Homo sapiens interferon regulatory factor 2 binding protein 2 (IRF2BP2) transcript variant 1 mRNA.		NM_001077397	chr1	13.37	2.00E-03	1.6	1.00E-03	-	1	SNP	5.98	0|1.60289380735475	234745009	25	A|S	B|0-5|G:G|P:P
68	ISCU	Homo sapiens iron-sulfur cluster scaffold homolog (E. coli) (ISCU) nuclear gene encoding mitochondrial protein transcript variant 2 mRNA.		NM_213595	chr12	36.31	2.00E-03	1.6	3.00E-03	+	1	SNP	28.93	0|0	108956418	NA	T|F	N|0-5|G:G|C:C
69	PSD3	Homo sapiens pleckstrin and Sec7 domain containing 3 (PSD3) transcript variant 2 mRNA.		NM_015310	chr8	32.35	2.00E-03	1.6	1.00E-02	-	1	SNP	24.97	0|1.60289380735475	18729817	NA	G|T	N|0-5|A:A|M:M
70	OR9G9	Homo sapiens olfactory receptor family 9 subfamily G member 9 (OR9G9) mRNA.		NM_001013358	chr11	21.12	2.00E-03	1.6	6.00E-03	+	2	SNP	4.21	0|1.60361112696843	56468020	2	T|C	B|0-5|T:C|C:R
												SNP	9.79	0|1.60361112696843	56468021	NA	G|C	N|0-5|A:G|Y:C
71	TELO2	Homo sapiens TEL2 telomere maintenance 2 homolog (S. cerevisiae) (TELO2) mRNA.		NM_016111	chr16	30.24	2.00E-03	1.6	2.00E-02	+	1	SNP	22.86	0|1.60361112696843	1544302	NA	A|E	N|0-4|A:G|E:G;N|5|G:G|G:G
72	NEURL	Homo sapiens neuralized homolog (Drosophila) (NEURL) mRNA.	Notch Signaling Pathway;Nervous System Development	NM_004210	chr10	6.58	3.00E-03	0.18	2.00E-03	+	1	SNP	5.74	0|0.180112436754885	105344451	115	G|G	B|0,3-5|A:A|S:S;B|1-2|A:G|S:G
73	PTPLA	Homo sapiens protein tyrosine phosphatase-like (proline instead of catalytic arginine) member A (PTPLA) mRNA.		NM_014241	chr10	25.33	3.00E-03	1.6	4.00E-03	-	1	SNP	17.94	0|0	17659149	2	C|E	B|0-5|T:T|K:K
74	CDC42EP1	Homo sapiens CDC42 effector protein (Rho GTPase binding) 1 (CDC42EP1) mRNA.		NM_152243	chr22	18.7	3.00E-03	1.6	1.00E-03	+	1	del	11.31	0|1.60289380735475	37964409	NA	CAGCGCCTGCTGCAAACCCCT|PAPAANPS	0-5|-:-|-:-
75	EMR3	Homo sapiens egf-like module containing mucin-like hormone receptor-like 3 (EMR3) mRNA.	Neurological system process;Neurontransmitter Secretion	NM_032571	chr19	12.98	3.00E-03	1.6	2.00E-03	-	1	SNP	5.59	0|1.60289380735475	14769339	16	C|E	B|0-5|G:G|Q:Q
76	HOMEZ	Homo sapiens homeobox and leucine zipper encoding (HOMEZ) mRNA.	Transcription Factor	NM_020834	chr14	25.73	3.00E-03	2.77	3.00E-03	-	1	del	12.96	0|2.78390360357584	23744827	NA	TCC|EE	2|-:-|-:-;0-1,3-5|-:TCC|-:EE
77	TRNP1	Homo sapiens TMF1-regulated nuclear protein 1 (TRNP1) mRNA.		NM_001013642	chr1	10.7	3.00E-03	1.6	2.00E-03	+	1	SNP	3.3	0|1.60289380735475	27320356	27	T|W	B|0-5|C:C|R:R
78	SLC6A15	Homo sapiens solute carrier family 6 (neutral amino acid transporter) member 15 (SLC6A15) transcript variant 2 mRNA.	Neurological system process	NM_018057	chr12	16.59	3.00E-03	1.6	4.00E-03	-	1	SNP	9.2	0|1.60289380735475	85277561	70	T|D	B|0-5|A:A|V:V
79	SAMD11	Homo sapiens sterile alpha motif domain containing 11 (SAMD11) mRNA.		NM_152486	chr1	23.85	3.00E-03	1.6	5.00E-03	+	1	SNP	16.87	0|1.60361112696843	877831	4	T|W	B|0-5|C:C|R:R
80	COG3	Homo sapiens component of oligomeric golgi complex 3 (COG3) mRNA.		NM_031431	chr13	17.71	3.00E-03	1.6	3.00E-03	+	1	SNP	10.32	0|1.60289380735475	46108853	27	T|L	B|0-5|C:C|S:S
81	TNFRSF10C	Homo sapiens tumor necrosis factor receptor superfamily member 10c decoy without an intracellular domain (TNFRSF10C) mRNA.	MAPKKK cascade;Nervous System Development;NF-KappaB Cascade	NM_003841	chr8	13.97	3.00E-03	1.6	4.00E-03	+	1	SNP	6.58	0|1.60289380735475	22974450	62	T|I	B|0-5|C:C|T:T
82	NOL10	Homo sapiens nucleolar protein 10 (NOL10) mRNA.		NM_024894	chr2	9.86	4.00E-03	0.18	4.00E-03	-	1	SNP	9.02	0|0.180112436754885	10717806	81	C|D	B|1,5|T:C|N:D;B|0,2-4|T:T|N:N
83	RFX1	Homo sapiens regulatory factor X 1 (influences HLA class II expression) (RFX1) mRNA.	Transcription Factor	NM_002918	chr19	2.87	4.00E-03	0.18	4.00E-03	-	1	SNP	2.03	0|0.180112436754885	14083761	56	T|T	B|0,2-3,5|C:C|A:A;B|1,4|T:C|T:A
84	WWC2	Homo sapiens WW and C2 domain containing 2 (WWC2) mRNA.		NM_024949	chr4	16.3	4.00E-03	1.6	3.00E-03	+	1	SNP	8.91	0|1.60289380735475	184190233	49	G|A	B|2-5|T:G|S:A;B|0|T:T|S:S
85	MLLT6	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog Drosophila); translocated to 6 (MLLT6) mRNA.	Transcription Factor	NM_005937	chr17	16.68	4.00E-03	1.6	2.00E-03	+	1	SNP	9.44	0|1.60361112696843	36861983	6	T|V	B|0-5|C:C|A:A
86	PCLO	Homo sapiens piccolo (presynaptic cytomatrix protein) (PCLO) transcript variant 2 mRNA.	Neurological system process;Neurontransmitter Secretion	NM_033026	chr7	40.24	4.00E-03	1.6	1.00E-01	-	1	ins	32.86	0|1.60361112696843	82581488	NA	-|-	0-5|TCA:TCA|*:*
87	PARP9	Homo sapiens poly (ADP-ribose) polymerase family member 9 (PARP9) transcript variant 6 mRNA.		NM_031458	chr3	21.29	4.00E-03	2.78	6.00E-03	-	1	SNP	8.46	0|2.78390360357584	122277268	51	G|S	B|0|A:A|L:L;B|2-5|A:G|L:S
88	ZP3	Homo sapiens zona pellucida glycoprotein 3 (sperm receptor) (ZP3) transcript variant 1 mRNA.		NM_001110354	chr7	14.46	4.00E-03	1.6	5.00E-03	+	1	SNP	7.07	0|1.60289380735475	76054372	89	G|G	B|0-5|A:A|R:R
89	ZNF534	Homo sapiens zinc finger protein 534 (ZNF534) transcript variant 2 mRNA.	Transcription Factor	NM_001143939	chr19	20.61	4.00E-03	1.6	5.00E-03	+	1	SNP	13.22	0|1.60361112696843	52942445	10	C|H	B|0-5|T:T|Y:Y
90	SOBP	Homo sapiens sine oculis binding protein homolog (Drosophila) (SOBP) mRNA.		NM_018013	chr6	13.8	5.00E-03	1.6	3.00E-03	+	1	SNP	6.41	0|1.60289380735475	107956095	32	A|S	B|0-5|G:G|G:G
91	BCLAF1	Homo sapiens BCL2-associated transcription factor 1 (BCLAF1) transcript variant 1 mRNA.	Transcription Factor	NM_001077440	chr6	20.47	5.00E-03	1.6	7.00E-03	-	2	SNP	8.61	0|1.60289380735475	136590698	NA	C|R	N|0,4-5|T:C|H:R
												SNP	0.62	0|1.60289380735475	136597288	19	A|Y	B|0-5|A:C|Y:D
92	TXNDC2	Homo sapiens thioredoxin domain containing 2 (spermatozoa) (TXNDC2) transcript variant 1 mRNA.	Oxidative stress response;Stress Response	NM_001098529	chr18	18.54	5.00E-03	1.6	1.00E-02	+	1	SNP	11.15	0|1.60289380735475	9887497	6	G|E	B|0-5|A:A|K:K
93	AOX1	Homo sapiens aldehyde oxidase 1 (AOX1) mRNA.		NM_001159	chr2	11.89	5.00E-03	0.18	7.00E-03	+	1	SNP	11.06	0|0.180112436754885	201478598	NA	C|A	N|0,2-3|T:C|V:A
94	MEGF10	Homo sapiens multiple EGF-like-domains 10 (MEGF10) mRNA.	Nervous System Development	NM_032446	chr5	18.46	6.00E-03	2.78	6.00E-03	+	1	SNP	5.63	0|2.78390360357584	126791282	69	G|R	B|0|A:A|K:K;B|2-5|A:G|K:R
95	ARID3A	Homo sapiens AT rich interactive domain 3A (BRIGHT-like) (ARID3A) mRNA.	Transcription Factor	NM_005224	chr19	20.16	6.00E-03	1.6	6.00E-03	+	1	SNP	12.76	0|1.60361112696843	971949	NA	G|G	N|0-5|A:A|S:S
96	NCOR2	Homo sapiens nuclear receptor corepressor 2 (NCOR2) transcript variant 1 mRNA.	Transcription Factor;Notch Signaling Pathway;Huntington Disease	NM_001077261	chr12	35.01	6.00E-03	1.6	6.00E-02	-	1	ins	27.63	0|1.60361112696843	124887058	NA	-|-	0-5|GCT:GCT|S:S
97	MLL3	Homo sapiens myeloid/lymphoid or mixed-lineage leukemia 3 (MLL3) mRNA.		NM_170606	chr7	31.1	7.00E-03	1.6	3.00E-02	-	2	SNP	12.42	0|1.60361112696843	151945007	NA	C|G	N|1-2,5|T:C|S:G
												ins	13.55	0|1.60361112696843	151945071	NA	-|Y	0-5|-:T|-:N
98	ZNRF4	Homo sapiens zinc and ring finger 4 (ZNRF4) mRNA.		NM_181710	chr19	16.66	7.00E-03	2.78	7.00E-03	+	1	SNP	3.83	0|2.78390360357584	5455735	128	G|R	B|2,4|A:A|Q:Q;B|0-1,3,5|A:G|Q:R
99	PLIN4	Homo sapiens perilipin 4 (PLIN4) mRNA.		NM_001080400	chr19	31.42	7.00E-03	1.6	1.00E-01	-	1	SNP	24.04	0|1.60361112696843	4511453	NA	G|A	N|0-5|A:A|V:V
100	KIF27	Homo sapiens kinesin family member 27 (KIF27) mRNA.		NM_017576	chr9	18.42	8.00E-03	2.78	8.00E-03	-	1	SNP	5.59	0|2.78390360357584	86474115	96	T|N	B|0|C:C|D:D;B|2-5|T:C|N:D
101	GPR44	Homo sapiens prostaglandin D2 receptor 2 (PTGDR2) mRNA.	Neurological system process;G-protein coupled receptor	NM_004778	chr11	8.36	8.00E-03	1.6	6.00E-03	-	1	SNP	0.96	0|1.60289380735475	60620585	40	A|V	B|0-5|G:G|A:A
102	RIN3	Homo sapiens Ras and Rab interactor 3 (RIN3) mRNA.		NM_024832	chr14	19.51	8.00E-03	1.6	1.00E-02	+	1	SNP	12.12	0|1.60289380735475	93118229	44	C|R	B|0-5|T:T|C:C
103	ZMYM5	Homo sapiens zinc finger MYM-type 5 (ZMYM5) transcript variant 1 mRNA.	Transcription Factor	NM_001039649	chr13	17.93	9.00E-03	1.6	1.00E-02	-	1	SNP	10.54	0|1.60281654065169	20425911	72	C|C	N|4|A:A|F:F;B|0-3,5|A:C|F:C
104	BPIL1	Homo sapiens BPI fold containing family B member 2 (BPIFB2) mRNA.	Stress Response	NM_025227	chr20	5.11	1.00E-02	0.18	8.00E-03	+	1	SNP	4.31	0|0.180112436754885	31596472	97	A|K	B|1,5|A:T|K:M;B|0,2-4|T:T|M:M
105	CDC27	Homo sapiens cell division cycle 27 homolog (S. cerevisiae) (CDC27) transcript variant 2 mRNA.		NM_001114091	chr17	36.97	1.00E-02	1.58	5.00E-02	-	2	SNP	15.6	0|1.60361112696843	45234360	2	A|L	B|0-5|A:C|L:*
												SNP	14.63	0|1.60361112696843	45249316	NA	T|Y	N|0-5|T:C|Y:C
106	CDHR3	Homo sapiens cadherin-related family member 3 (CDHR3) mRNA.		NM_152750	chr7	15.96	1.00E-02	1.6	1.00E-02	+	1	SNP	8.57	0|1.60281654065169	105658451	126	G|C	B|0-5|A:A|Y:Y
107	PRIM2	Homo sapiens primase DNA polypeptide 2 (58kDa) (PRIM2) mRNA.		NM_000947	chr6	18.86	1.00E-02	1.6	1.00E-02	+	2	SNP	6.42	0|0	57398270	416	C|Q	B|0,2-5|T:C|*:Q
												ins	5.06	0|0	57398186	NA	-|E	0-5|A:-|K:-
108	SSC5D	Homo sapiens scavenger receptor cysteine rich domain containing (5 domains) (SSC5D) transcript variant 2 mRNA.		NM_001144950	chr19	31.22	1.00E-02	0.78	5.00E-02	+	1	ins	27.63	0|0.779126465217891	56029616	NA	-|-	0-1,4|-:CCA|-:P;2-3|CCA:CCA|P:P
109	C10orf92	Homo sapiens tetratricopeptide repeat domain 40 (TTC40) mRNA.		NM_001200049	chr10	23.97	1.00E-02	2.78	4.00E-02	-	2	SNP	1.91	0|2.78390360357584	134648279	38	C|E	B|0-1,3,5|T:C|K:E;B|2,4|T:T|K:K
												SNP	9.23	0|2.78390360357584	134660807	NA	C|G	N|0,3,5|T:C|S:G
110	C20orf151	Homo sapiens chromosome 20 open reading frame 151 (C20orf151) mRNA.	Transcription Factor	NM_080833	chr20	19.25	1.00E-02	1.6	2.00E-02	-	1	SNP	11.86	0|1.60289380735475	60987737	29	C|E	B|0-1,4-5|T:C|K:E;B|2-3|T:T|K:K
111	RP1L1	Homo sapiens retinitis pigmentosa 1-like 1 (RP1L1) mRNA.	Neurological system process	NM_178857	chr8	38.48	1.00E-02	1.58	1.00E-01	-	2	ins	19.36	0|1.60361112696843	10467685	NA	-|-	1-3,5|A:-|W:-
												ins	14.13	0|1.60361112696843	10467706	NA	-|-	2,4|-:CCC|-:G;0-1,3,5|-:CCG|-:R
112	AMH	Homo sapiens anti-Mullerian hormone (AMH) mRNA.		NM_000479	chr19	10.88	1.00E-02	1.6	9.00E-03	+	1	SNP	3.49	0|1.60361112696843	2251817	28	T|V	B|0-5|C:C|A:A
113	KCNH6	Homo sapiens potassium voltage-gated channel subfamily H (eag-related) member 6 (KCNH6) transcript variant 1 mRNA.	Seizure;Potassium Channel;Ligand-gated ion channel activity;Ion channel activity;Cyclic nucleotide-gated ion channel	NM_173092	chr17	5.97	1.00E-02	0.18	1.00E-02	+	1	SNP	5.13	0|0.180112436754885	61623052	104	C|T	B|1,3|T:C|M:T;B|0,2,4-5|T:T|M:M
114	OTOP1	Homo sapiens otopetrin 1 (OTOP1) mRNA.	Neurological system process	NM_177998	chr4	14.02	1.00E-02	1.6	1.00E-02	-	1	SNP	6.63	0|1.60289380735475	4199634	NA	A|D	N|0-5|T:T|E:E
116	GEN1	Homo sapiens Gen endonuclease homolog 1 (Drosophila) (GEN1)		NM_182625	chr2	8.56	2.00E-02	0.18	2.00E-02	+	1	SNP	7.73	0|0.180112436754885	17954397	7	G|E	B|0,2-3,5|A:G|K:E

		transcript variant 2 mRNA.																
117	ADRB1	Homo sapiens adrenergic beta-1-receptor (ADRB1) mRNA.	Neurological system process;G-protein coupled receptor;NF-KappaB Cascade;Calcium-mediated Signaling	NM_000684	chr10	18.67	2.00E-02	1.6	2.00E-02	+	1	SNP	11.34	0|1.60289380735475	115805056	54	G|G	B|0-5|C:C|R:R
118	OR2T27	Homo sapiens olfactory receptor family 2 subfamily T member 27 (OR2T27) mRNA.		NM_001001824	chr1	9.65	2.00E-02	1.6	1.00E-02	-	1	SNP	2.26	0|1.60289380735475	248814080	28	A|L	B|0-5|C:C|V:V
119	OBSCN	Homo sapiens obscurin cytoskeletal calmodulin and titin-interacting RhoGEF (OBSCN) transcript variant 1 mRNA.		NM_001098623	chr1	35.9	2.00E-02	2.65	8.00E-02	+	1	SNP	26.21	0|2.78390360357584	228412228	NA	G|A	N|4|A:A|T:T;N|0-3,5|A:G|T:A
120	ZNF681	Homo sapiens zinc finger protein 681 (ZNF681) mRNA.	Transcription Factor	NM_138286	chr19	17.37	2.00E-02	1.6	2.00E-02	-	1	SNP	9.99	0|1.60289380735475	23927555	NA	G|S	N|1,3|A:G|L:S
121	MAP3K6	Homo sapiens mitogen-activated protein kinase kinase kinase 6 (MAP3K6) mRNA.	FGF Signaling pathway	NM_004672	chr1	6.73	2.00E-02	0.18	2.00E-02	-	1	SNP	5.89	0|0.180112436754885	27687466	88	G|N	B|1-2|T:G|K:N;B|0,3-5|T:T|K:K
122	ZXDC	Homo sapiens ZXD family zinc finger C (ZXDC) transcript variant 2 mRNA.	Transcription Factor;Nervous System Development	NM_001040653	chr3	10.42	2.00E-02	1.6	1.00E-02	-	1	SNP	3.03	0|1.60289380735475	126194357	20	G|P	B|0-5|C:C|A:A
123	TMEM131	Homo sapiens transmembrane protein 131 (TMEM131) mRNA.		NM_015348	chr2	6.92	2.00E-02	0.18	2.00E-02	-	1	SNP	6.08	0|0.180112436754885	98409046	132	G|P	B|0,2-3,5|A:A|L:L;B|1,4|A:G|L:P
124	NCKAP5	Homo sapiens NCK-associated protein 5 (NCKAP5) transcript variant 2 mRNA.		NM_207363	chr2	19.33	2.00E-02	2.78	2.00E-02	-	1	SNP	8.34	0|2.78390360357584	133540605	94	G|P	B|2-5|T:G|Q:P;B|0|T:T|Q:Q
125	SENP6	Homo sapiens SUMO1/sentrin specific peptidase 6 (SENP6) transcript variant 1 mRNA.		NM_001100409	chr6	15.5	3.00E-02	1.6	3.00E-02	+	1	SNP	8.11	0|1.60289380735475	76344431	97	C|T	B|0-5|T:T|M:M
126	ADAM32	Homo sapiens ADAM metallopeptidase domain 32 (ADAM32) mRNA.	Neurological system process	NM_145004	chr8	7.91	3.00E-02	1.6	2.00E-02	+	1	SNP	0.52	0|1.60289380735475	39080632	56	C|T	B|0-5|G:G|S:S
127	ZNF837	Homo sapiens zinc finger protein 837 (ZNF837) transcript variant 2 mRNA.		NM_001129730	chr19	11.34	3.00E-02	1.6	2.00E-02	-	1	SNP	3.95	0|1.60289380735475	58879976	48	C|A	B|0-5|T:T|T:T
128	OR8U1	Homo sapiens olfactory receptor family 8 subfamily U member 8 (OR8U8) mRNA.		NM_001005204	chr11	15.58	3.00E-02	1.6	4.00E-02	+	2	SNP	6.54	0|1.60361112696843	56143158	NA	A|H	N|0,3-5|A:G|H:R
												SNP	1.66	0|1.60361112696843	56143977	10	A|Q	B|2-5|A:G|Q:R;N|1|G:G|R:R
129	COL5A3	Homo sapiens collagen type V alpha 3 (COL5A3) mRNA.		NM_015719	chr19	19.51	3.00E-02	2.78	3.00E-02	-	1	SNP	6.72	0|2.78390360357584	10085054	100	G|P	B|2,4|A:A|S:S;B|0-1,3,5|A:G|S:P
130	KLRC3	Homo sapiens killer cell lectin-like receptor subfamily C member 3 (KLRC3) transcript variant 2 mRNA.		NM_002261	chr12	9.77	3.00E-02	1.6	3.00E-02	-	1	SNP	2.38	0|1.60289380735475	10573095	119	A|W	B|0-5|G:G|R:R
131	COL6A3	Homo sapiens collagen type VI alpha 3 (COL6A3) transcript variant 3 mRNA.	Inflammation mediated by chemokine and cytokine signaling	NM_004369	chr2	18.09	3.00E-02	1.6	4.00E-02	-	2	SNP	5.27	0|1.60289380735475	238247734	24	C|D	B|0-1,5|C:G|D:H;N|2-4|G:G|H:H
												del	5.51	0|1.60289380735475	238244864	NA	GCA|AA	0-1,5|-:GCA|-:AA
132	MAML3	Homo sapiens mastermind-like 3 (Drosophila) (MAML3) mRNA.		NM_018717	chr4	16.29	4.00E-02	1.6	3.00E-02	-	1	del	8.9	0|1.60289380735475	140651585	NA	CTG|Q	0-5|-:-|-:-
133	IER5	Homo sapiens immediate early response 5 (IER5) mRNA.		NM_016545	chr1	11.92	4.00E-02	1.6	3.00E-02	+	1	SNP	4.6	0|1.60289380735475	181058618	42	C|R	B|0-3,5|C:G|R:G;B|4|G:G|G:G
134	SCARF2	Homo sapiens scavenger receptor class F member 2 (SCARF2) transcript variant 2 mRNA.		NM_182895	chr22	32.86	4.00E-02	1.6	1.00E-01	-	1	SNP	25.48	0|1.60361112696843	20779946	NA	C|V	N|0-5|G:G|L:L
135	KRTAP10-4	Homo sapiens keratin associated protein 10-4 (KRTAP10-4) mRNA.		NM_198687	chr21	17.86	4.00E-02	0.78	4.00E-02	+	1	SNP	14.26	0|0.779126465217891	45993819	9	C|R	B|1|T:C|C:R;N|0,2,4-5|T:T|C:C
136	KRTAP10-7	Homo sapiens keratin associated protein 10-7 (KRTAP10-7) mRNA.		NM_198689	chr21	20.27	4.00E-02	1.6	5.00E-02	+	1	SNP	12.88	0|1.60289380735475	46020867	2	A|M	B|0-5|G:G|V:V
137	PLEC	Homo sapiens plectin (PLEC) transcript variant 11 mRNA.		NM_201383	chr8	32.74	5.00E-02	2.78	8.00E-02	-	2	SNP	12.72	0|2.78390360357584	144998870	NA	C|A	N|1-3,5|T:C|T:A
												SNP	13.83	0|2.78390360357584	145009036	NA	C|R	N|1-3,5|T:C|Q:R
138	CTU2	Homo sapiens cytosolic thiouridylase subunit 2 homolog (S. pombe) (CTU2) transcript variant 2 mRNA.		NM_001012762	chr16	18.19	5.00E-02	0.18	8.00E-02	+	1	ins	17.36	0|0.180112436754885	88780635	NA	-|-	0,2-4|-:GTGT|-:VY
140	ACAN	Homo sapiens aggrecan (ACAN) transcript variant 2 mRNA.	Nervous System Development	NM_001135	chr15	15.81	5.00E-02	0.76	6.00E-02	+	1	SNP	14.47	0|1.60289380735475	89400023	2	A|T	B|5|A:G|T:A;N|0|G:G|A:A
141	AKAP9	Homo sapiens A kinase (PRKA) anchor protein (yotiao) 9 (AKAP9) transcript variant 3 mRNA.		NM_147185	chr7	13.39	6.00E-02	1.6	4.00E-02	+	1	SNP	6.01	0|1.60361112696843	91714911	34	C|P	B|0-5|T:T|S:S
142	KRTAP5-5	Homo sapiens keratin associated protein 5-5 (KRTAP5-5) mRNA.		NM_001001480	chr11	12.91	6.00E-02	1.6	4.00E-02	+	1	SNP	5.52	0|1.60361112696843	1651228	54	C|A	B|0-5|G:G|G:G
143	FAT1	Homo sapiens FAT tumor suppressor homolog 1 (Drosophila) (FAT1) mRNA.	Neurological system process;Wnt Signaling Pathway;Cadherin Signaling Pathway;Nervous System Development	NM_005245	chr4	16.32	8.00E-02	0.18	1.00E-01	-	2	SNP	8.79	0|0.180112436754885	187518041	4	T|D	B|0,3-5|T:C|D:G
												SNP	8.7	0|0.180112436754885	187630099	4	C|V	B|1,3-5|T:C|M:V
144	IMPG1	Homo sapiens interphotoreceptor matrix proteoglycan 1 (IMPG1) mRNA.	Neurological system process	NM_001563	chr6	2.65	8.00E-02	0.17	2.00E-02	-	1	SNP	1.98	0|0.180112436754885	76633385	95	C|S	B|1-2|T:C|N:S;B|0,3-5|T:T|N:N
145	RNF213	Homo sapiens ring finger protein 213 (RNF213) transcript variant 2 mRNA.		NM_020914	chr17	13.44	9.00E-02	1.6	9.00E-02	+	2	SNP	4.13	0|1.60289380735475	78346870	6	C|L	B|0-5|A:C|I:L
												SNP	3.34	0|1.60289380735475	78355494	25	C|L	B|0-5|C:G|L:V
146	FAM186A	Homo sapiens family with sequence similarity 186 member A (FAM186A) mRNA.		NM_001145475	chr12	14.9	1.00E-01	1.6	8.00E-02	-	1	SNP	7.52	0|1.60289380735475	50754642	NA	C|E	N|1-2,4-5|A:C|D:E
147	PKD1L2	Homo sapiens polycystic kidney disease 1-like 2 (PKD1L2) transcript variant 3 mRNA.	Ion channel activity	NM_001076780	chr16	38.88	1.00E-01	2.16	4.00E-02	-	1	del	32.86	0|2.78390360357584	81242149	NA	TT|N	0|-:-|-:-;2-5|-:TT|-:N
148	PDE4DIP	Homo sapiens phosphodiesterase 4D interacting protein (PDE4DIP) transcript variant 4 mRNA.	Nervous System Development	NM_001198834	chr1	18.09	1.00E-01	1.58	1.00E-01	-	2	SNP	5.71	0|1.60289380735475	144871782	15	A|L	B|0-5|A:G|L:P
												del	5.19	0|0	144873963	NA	T|Q	0,2-5|-:T|-:Q
149	MUC4	Homo sapiens mucin 4 cell surface associated (MUC4) transcript variant 5 mRNA.		NM_018406	chr3	29.43	1.00E-01	1.6	4.00E-01	-	1	SNP	22.05	0|1.60361112696843	195507107	NA	C|A	N|1,5|T:C|T:A;N|3|T:T|T:T
150	FSIP2	Homo sapiens fibrous sheath interacting protein 2 (FSIP2) mRNA.		NM_173651	chr2	4.22	1.00E-01	0.18	1.00E-01	+	2	SNP	3.38	0|0.180112436754885	186654867	117	G|D	B|0,2-5|C:G|H:D
												SNP	1.09	0|0.180112436754885	186659184	31	C|Q	B|0-4|A:C|K:Q
151	PRIC285	Homo sapiens peroxisomal proliferator-activated receptor A interacting complex 285 (PRIC285) transcript variant 2 mRNA.		NM_033405	chr20	8.76	2.00E-01	1.6	1.00E-01	-	1	SNP	1.37	0|1.60361112696843	62196807	67	T|H	B|0-5|C:C|R:R
152	HLA-DQA1	Homo sapiens major histocompatibility complex class II DQ alpha 1 (HLA-DQA1) mRNA.		NM_002122	chr6	9.79	2.00E-01	1.6	2.00E-01	+	1	SNP	2.4	0|1.60361112696843	32609173	95	C|Q	B|0-5|G:G|E:E
153	ZC3H3	Homo sapiens zinc finger CCCH-type containing 3 (ZC3H3) mRNA.		NM_015117	chr8	15.04	2.00E-01	0.14	5.00E-02	-	2	SNP	13.21	0|0.180112436754885	144522387	NA	G|S	N|0-3,5|T:G|*:S
												SNP	5.67	0|0.180112436754885	144522388	NA	A|S	N|0-3,5|A:T|S:T
154	ALPK3	Homo sapiens alpha-kinase 3 (ALPK3) mRNA.		NM_020778	chr15	20.45	3.00E-01	0.56	5.00E-02	+	2	SNP	8.73	0|1.60289380735475	85401193	NA	T|V	N|0,4-5|T:G|V:G
												SNP	5.17	0|1.60289380735475	85403105	7	C|A	B|1,4|A:C|D:A
155	SYNE1	Homo sapiens spectrin repeat containing nuclear envelope 1 (SYNE1) transcript variant 2 mRNA.	Neurological system process;Schizophrenia Associated;Nervous System Development	NM_033071	chr6	9.94	3.00E-01	0.18	3.00E-01	-	2	SNP	7.93	0|0.180112436754885	152679518	3	C|R	B|1-4|T:C|H:R
												SNP	1.03	0|0.180112436754885	152777095	33	A|L	B|0,3,5|A:C|L:V
156	KIR2DL1	Homo sapiens killer cell immunoglobulin-like receptor two domains long cytoplasmic tail 1 (KIR2DL1) mRNA.		NM_014218	chr19	17.87	4.00E-01	1.28	4.00E-02	+	2	SNP	3.59	0|2.78390360357584	55281315	58	G|V	B|0,2|T:G|F:V
												SNP	10.44	0|2.78390360357584	55286796	NA	G|D	N|0-5|A:G|N:D
157	KCNJ12	Homo sapiens potassium inwardly-rectifying channel subfamily J member 18 (KCNJ18) mRNA.	Neurological system process;Potassium Channel;Ion channel activity	NM_021012	chr17	12.52	4.00E-01	0.94	6.00E-02	+	2	SNP	9.02	0|1.60289380735475	21319007	NA	G|R	N|0-5|A:G|Q:R
												del	4.82	0|1.60289380735475	21319651	NA	GAG|E	0-5|-:GAG|-:E
158	DNAH7	Homo sapiens dynein axonemal heavy chain 7 (DNAH7) mRNA.	Huntington Disease	NM_018897	chr2	6.88	4.00E-01	0.31	1.00E-01	-	2	SNP	2.69	0|1.60289380735475	196673569	3	G|T	B|1,5|C:G|S:T
												SNP	0.03	0|1.60289380735475	196837129	56	G|S	B|0|C:C|C:C;B|2-5|C:G|C:S
159	HYDIN	Homo sapiens HYDIN axonemal central pair apparatus protein (HYDIN) transcript variant 4 mRNA.		NM_032821	chr16	10.51	5.00E-01	0.11	2.00E-01	-	2	SNP	11.21	0|0.180112436754885	70954571	NA	C|D	N|0-5|T:C|N:D
												del	4.64	0|0	70896016	NA	A|I	0-5|-:A|-:I
160	MUC6	Homo sapiens mucin 6 oligomeric mucus/gel-forming (MUC6) mRNA.	Neurological system process	NM_005961	chr11	13.43	6.00E-01	0.53	2.00E-01	-	2	del	15.47	0|1.60289380735475	1017496	NA	TGC|SI	0-4|-:TGC|-:SI
												del	15.47	0|1.60289380735475	1016989	NA	TGT|NI	0-4|-:TGT|-:NI
161	KRTAP12-2	Homo sapiens keratin associated protein 12-2 (KRTAP12-2) mRNA.		NM_181684	chr21	12.19	6.00E-01	0.62	1.00E-02	-	1	SNP	24.05	0|1.60361112696843	46086718	NA	G|S	N|3-4|C:C|C:C;N|0-2,5|C:G|C:S
162	OR4C3	Homo sapiens olfactory receptor family 4 subfamily C member 3 (OR4C3) mRNA.		NM_001004702	chr11	10.79	7.00E-01	0.51	4.00E-02	+	2	SNP	16.05	0|1.60289380735475	48346961	NA	A|N	N|0-5|A:T|N:Y
												SNP	12.28	0|1.602893807354	48346962	NA	A|N	N|0-5|A:G|N:S

														75				
163	ZNF217	Homo sapiens zinc finger protein 217 (ZNF217) mRNA.	Transcription Factor	NM_006526	chr20	5.86	8.00E-01	0.83	2.00E-02	-	1	SNP	2.76	0|0	52192595	10	C|R	B|0,2-3|T:C|Q:R
164	HLA-C_DUP_06	NA		NM_002117_DUP_03	chr6	3.49	8.00E-01	0.18	4.00E-01	-	1	SNP	23.81	0|1.60289380735475	31239776	1	A|C	B|0,2-3,5|A:C|C:G;N|1,4|C:C|G:G
165	SVEP1	Homo sapiens sushi von Willebrand factor type A EGF and pentraxin domain containing 1 (SVEP1) mRNA.		NM_153366	chr9	1.47	9.00E-01	0.14	1.00E-01	-	2	SNP	1.13	0|1.60289380735475	113166792	109	A|F	B|1,4-5|A:T|F:I
												SNP	0.4	0|1.60289380735475	113251951	20	T|I	B|0,2-3,5|T:C|I:V
166	MUC5B	Homo sapiens mucin 5B oligomeric mucus/gel-forming (MUC5B) mRNA.		NM_002458	chr11	3.34	9.00E-01	0.28	3.00E-01	+	1	SNP	20.56	0|2.78390360357584	1268608	NA	A|S	N|0|G:G|G:G
167	TTN	Homo sapiens titin (TTN) transcript variant novex-3 mRNA.		NM_133378	chr2	0.72	1.00E+00	0.05	3.00E-01	-	2	SNP	11.23	0|1.60289380735475	179400379	NA	A|F	N|0,2|A:G|F:L
												SNP	5.15	0|1.60289380735475	179444915	3	A|S	B|0,2|A:G|S:P
168	HLA-DQB1_DUP_02	Homo sapiens major histocompatibility complex class II DQ beta 1 (HLA-DQB1) transcript variant 1 mRNA.		NM_002123	chr6	0.65	1.00E+00	0.05	4.00E-01	-	1	SNP	14.44	0|1.60289380735475	32632745	4	G|A	B|0,2,4|A:A|V:V;B|1,3,5|A:G|V:A
169	HLA-A_DUP_07	NA		NM_002116_DUP_03	chr6	0.56	1.00E+00	0.03	3.00E-01	+	2	SNP	9.64	0|0	29911271	NA	G|E	N|1,3,5|C:G|D:E
												SNP	12.82	0|1.60281654065169	29911272	NA	T|W	N|1,5|T:G|W:G