Supplementary Information

Heritable *GATA2* Mutations Associated with Familial Myelodysplastic Syndrome and Acute Myeloid Leukemia

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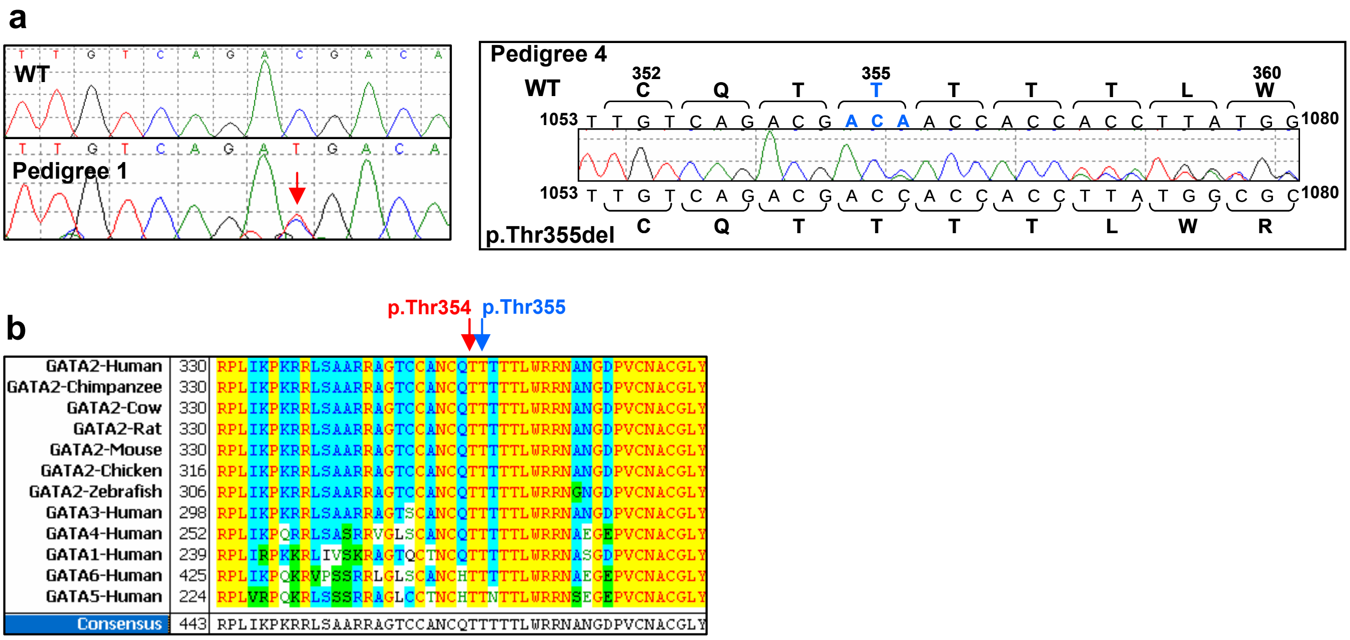
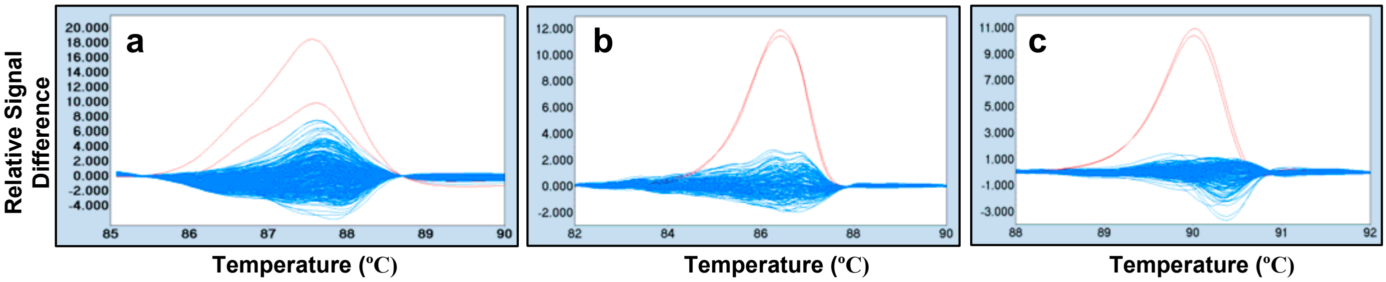
Supplementary Figure 1. Identification of novel germline p.Thr354Met and p.Thr355del variants in the highly conserved zinc finger 2 domain of GATA2 that is associated with MDS-AML. Sequence analysis was performed on representative AML or MDS affected individuals from the four pedigrees in **Fig. 1a**. **a.** p.Thr354Met and p.Thr355del germline sequence variants. A c.1061C>T heterozygous novel variation is seen in Pedigree 1, but not in wildtype (WT) sequence. An identical variation occurs in Pedigrees 2 and 3. A heterozygous c.1063-1065delACA occurs in Pedigree 4 (blue). **b.** p.Thr354 and p.Thr355 in GATA2 from different species and the corresponding Thr residues in other GATA proteins are highly conserved. These first 2 of 5 consecutive Thr residues within the zinc finger 2 domain are totally conserved in species from Human to Zebrafish and in all six GATA binding proteins.

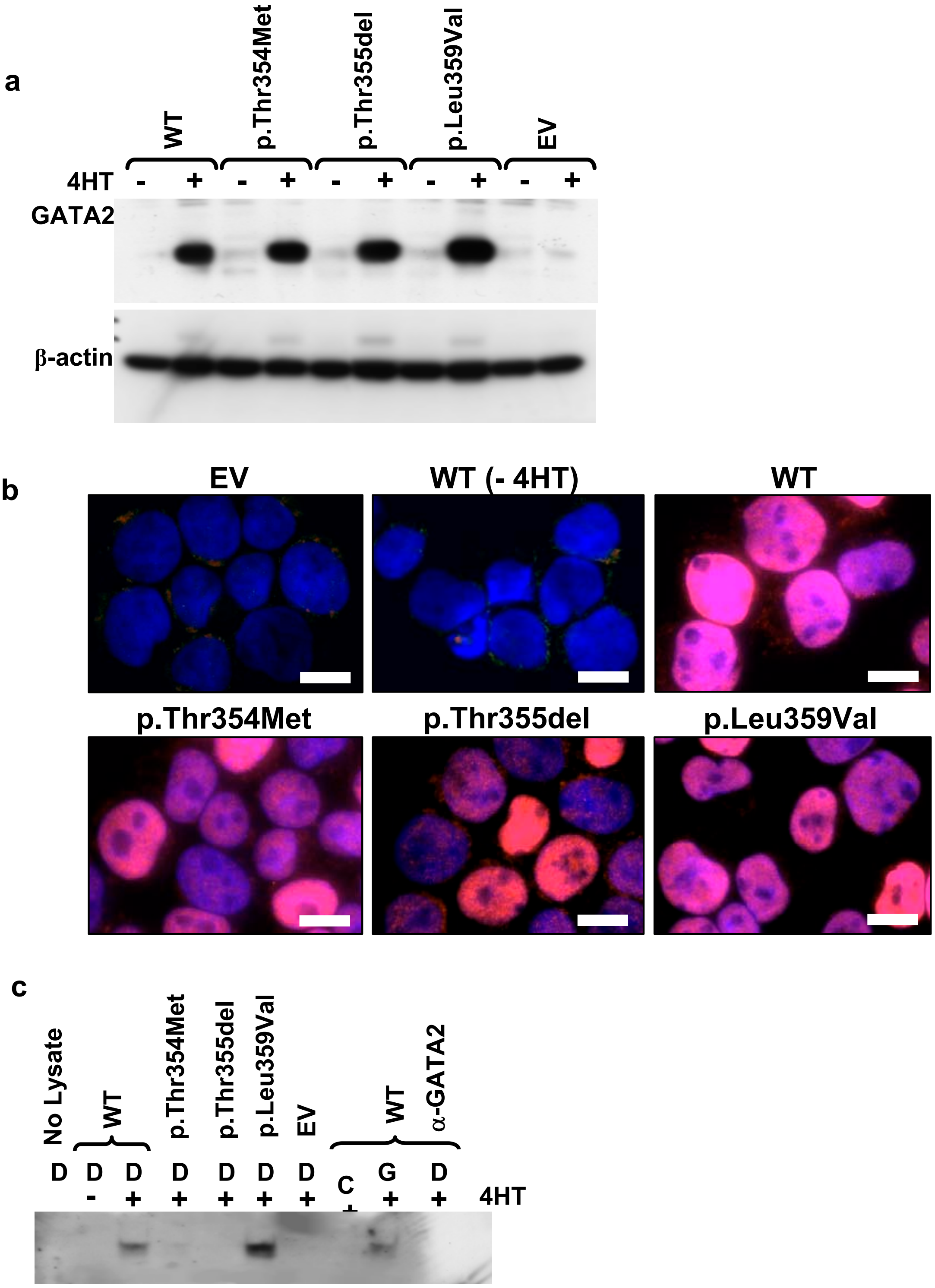


GATA2-Human	330	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Chimpanzee	330	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Cow	330	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Rat	330	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Mouse	330	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Chicken	316	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY
GATA2-Zebrafish	306	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNGNGDPVCNACGLY
GATA3-Human	298	RPLIKPKRRLSAARRAGTSCANCQTTTTTLWRRNANGDPVCNACGLY
GATA4-Human	252	RPLIKPQRRLSASRRVGLSCANCQTTTTTLWRRNAEGEPVCNACGLY
GATA1-Human	239	RPLIRPKKRLIVSKRAGTQCTNCQTTTTTLWRRNASGDPVCNACGLY
GATA6-Human	425	RPLIKPQKRVPSSRRLGLSCANCHTTTTTLWRRNAEGEPVCNACGLY
GATA5-Human	224	RPLVRPQKRLSSSRRAGLCCTNCHTTNTTLWRRNSEGEPVCNACGLY
Consensus	443	RPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGLY

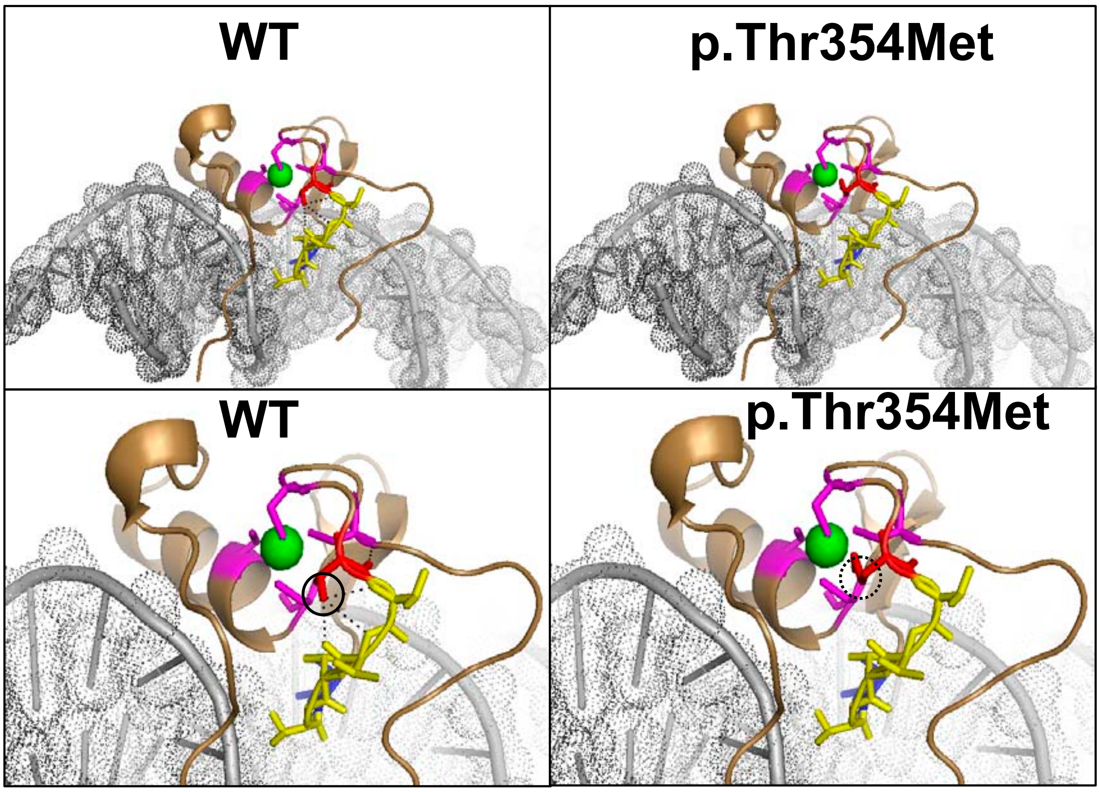
Supplementary Figure 2. Genetic analysis of *GATA2* gene variation in familial and sporadic samples. To screen for *GATA2* coding variants, high resolution melt across coding exons was performed on genomic DNA from human blood or bone marrow samples. **a.** Screen of *GATA2* exon 5 in 344 normal individuals; p.Thr354Met (red; Pedigree 2, III-4 and 3, IV-1) and wildtype p.Thr354 (blue). **b.** Screen of *GATA2* exon 5 in 268 AML patient samples; Pedigree 1, IV-1 with p.Thr354Met (red, duplicate) and wildtype p.Thr354 (blue). **c**. Screen of *GATA2* exon 2 in 268 AML patient samples; a unique variant c.182C>T (p.Ala61Val) was detected in one sample (red, duplicate).



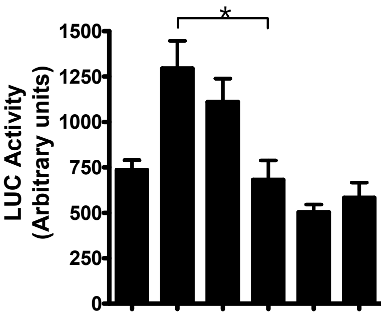
Supplementary Figure 3. Subcellular localisation and DNA binding properties of GATA2 WT and mutants in HL-60 cells. HL-60 cells carrying stably transduced 4HT-regulatable GATA2 (WT, p.Thr354Met and p.Leu359Val) or empty vector were treated with and without 4HT for 24 h. **a.** Western blot analysis of regulated GATA2 expression. Western blots of total cell lysate were probed for GATA2 and β-actin expression. **b.** Subcellular localisation of GATA2 WT and mutants. Cells from (**a**) were stained for GATA2 (red) and DAPI (blue). Scale bars, 10 µm. **c.** Electromobility shift assay (EMSA)-western blot of GATA2 WT and mutants. Nuclear lysates were prepared from cells in (**a**) and bound to GATA binding site oligonucleotides from the human TCRδ enhancer (**D**), GATA consensus (**C**) and GM-CSF promoter (**G**). The probes were visualised using chemiluminescence. A neutralizing α-GATA2 antibody in the far right lane specifically removes GATA2.



Supplementary Figure 4. Predicted structure of GATA2 zinc finger 2 binding to DNA. Human GATA2 ZF2 shares 97% sequence identity with human and mouse GATA3. We therefore used the known murine Gata3 ZF2 structure bound to DNA[20] to evaluate the effects of the observed mutations (**Supplementary Note**). The four zinc-coordinating cysteine residues are shown in purple with the zinc atom in green. Replacement of the threonine (red) at amino acid 354 in WT GATA2 with a methionine (red) disrupts interactions (circle and dotted lines) between adjacent threonines (yellow) and cysteine 349 (purple). This also introduces a bulky side-chain (dotted circle) that is predicted to alter the ZF structure or stability. Leucine 359 (blue; residue for p.Leu359Val mutation in CML BC) projects into the major groove and contacts DNA.

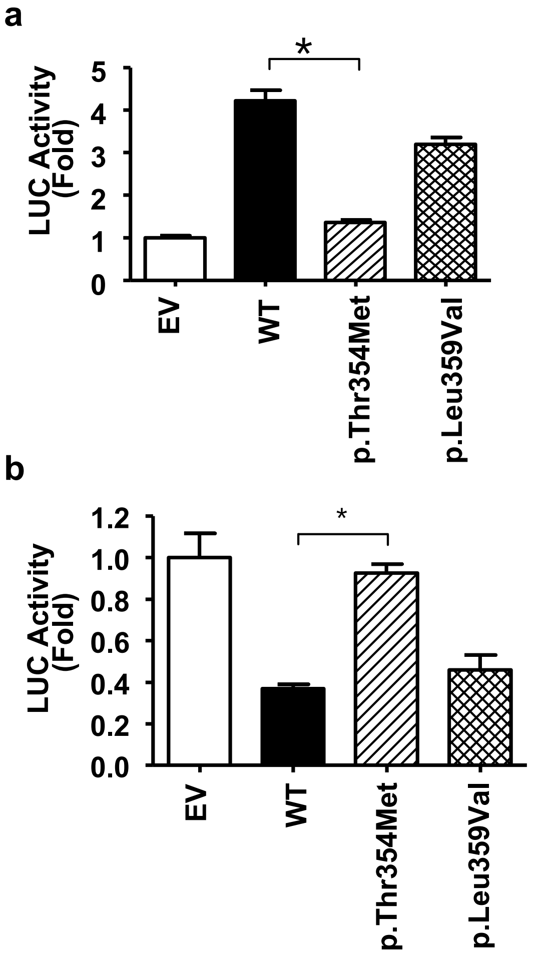


Supplementary Figure 5. p.Thr354Met acts as a dominant negative mutation over WT GATA2 on the *CD34* enhancer element. HEK293 cells were cotransfected with consistent amounts of 1) *CD34* enhancer-LUC reporter (100 ng) and 2) WT (300 ng), with increasing amounts of 3) p.Thr354Met (0 - 600 ng). EV was added appropriately to control for promoter squelching and transfection efficiency. After 20 h, cells were harvested and luciferase assays performed and plotted (mean ± s.e.m.) compared to EV control (*p<0.05; Student's t-test). A dominant negative activity of p.Thr354Met over WT became visible at a WT:p.Thr354Met mole ratio of 2:1, but became significant at and beyond a ratio of 1:1.



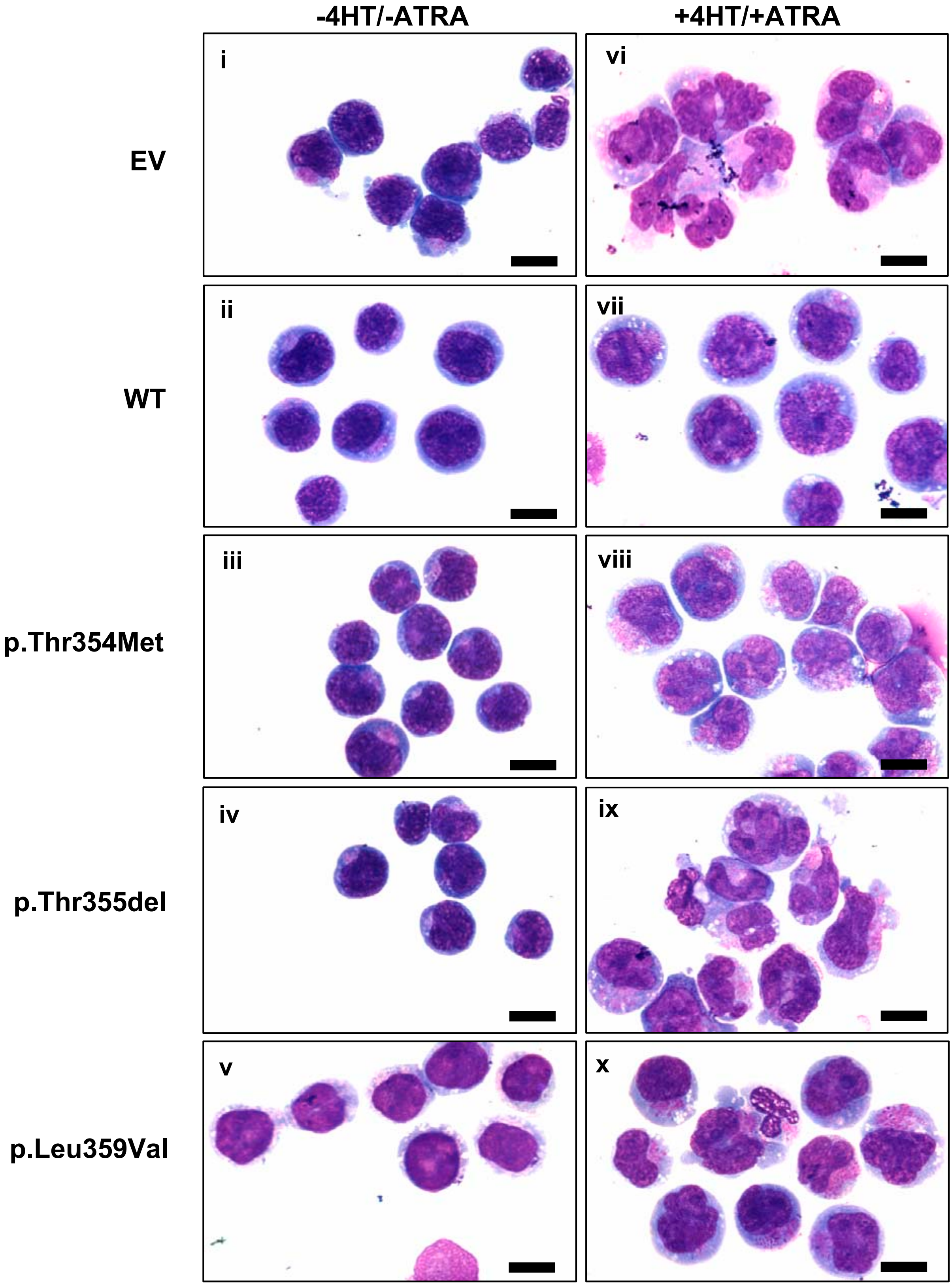
pGL3P-CD34	100	100	100	100	100	100
EV	0	600	450	300	150	0
WT	0	300	300	300	300	300
p.Thr354Met	0	0	150	300	450	600

Supplementary Figure 6. p.Thr354Met displays loss-of-function, despite opposite responses on *RUNX1* enhancer in different cell types. HEK293 and Cos-7 cells were transiently co-transfected with EV, WT, p.Thr354Met or p.Leu359Val and the *RUNX1* enhancer element linked to a LUC reporter. After 20 h, cells were harvested and luciferase assays performed and plotted as fold (mean ± s.e.m.) compared to EV control. p.Thr354Met displays loss-of-function compared to WT in both cell types (*p<0.05; Student's t-test).

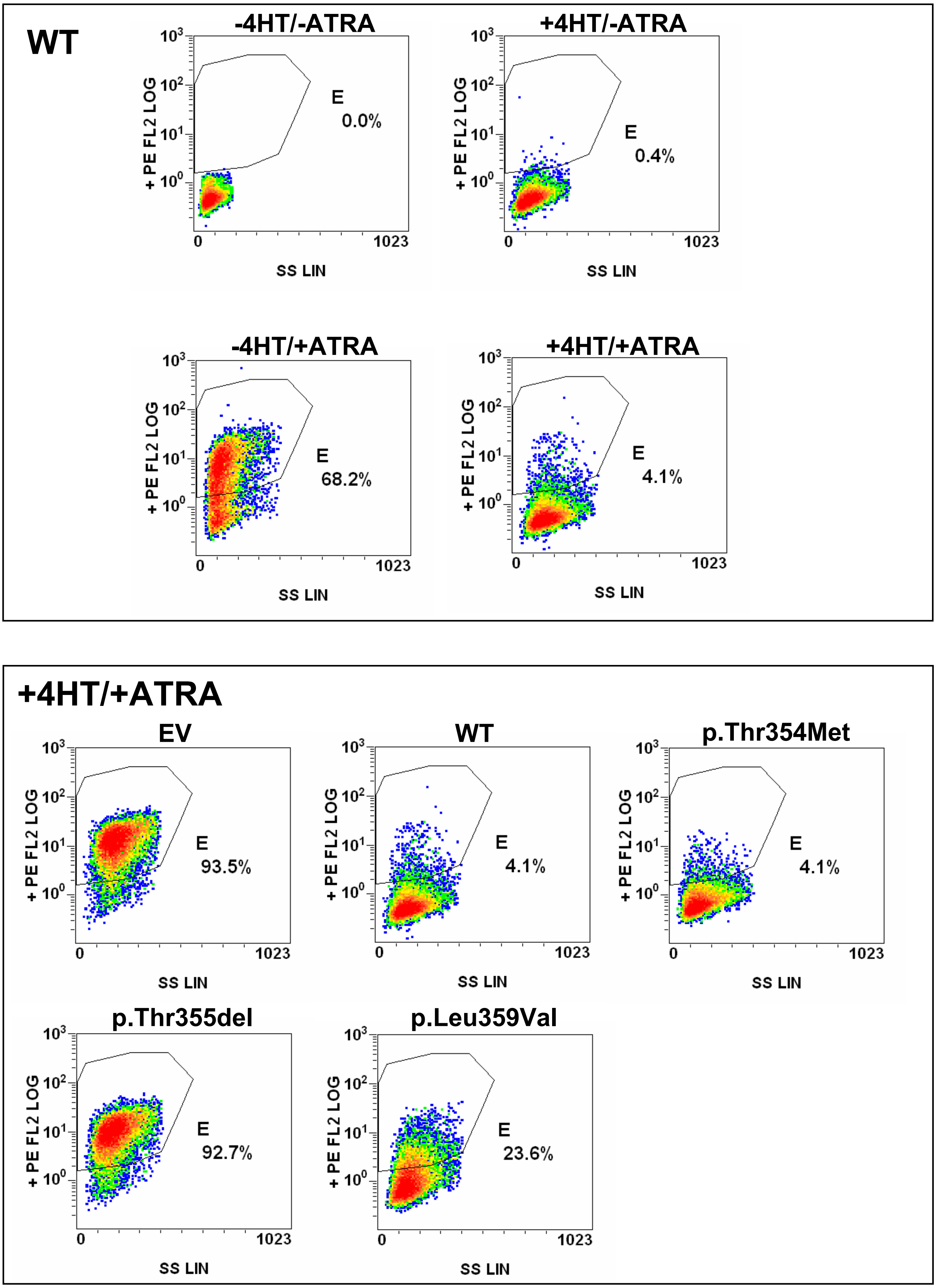


Supplementary Figure 7. p.Thr354Met inhibits ATRA-induced differentiation. HL-60 cells carrying stably transduced 4HT-regulatable GATA2 (WT, p.Thr354Met, p.Thr355del and p.Leu359Val) or EV were treated with or without 30 nM 4HT for 24 h and then with or without 2 μM ATRA for 6 days. **a.** Morphological differentiation of HL-60 cells into granulocytes. HL-60 cells were hematoxylin and eosin stained and photographs taken. Scale bars, 10 μm. **b.** CD11b expression following differentiation with ATRA. The level of surface CD11b expression was measured by FACS analysis using Phycoerythrin (PE) anti-CD11b. CD11b positive cells reside in region E. Indicative FACS plots relating to GATA2 WT (top panel – from **Figure 4a-d**) and +4HT/+ATRA (bottom panel from **Figure 4d**) are shown. **c.** Apoptosis following differentiation with ATRA. Cells were FACS analysed following staining with FITC anti-Annexin V and propidium iodide (PI). Indicative FACS plots of PI vs Annexin V relating to GATA2 WT (top panel – from **Figure 4i-m**) and +4HT/+ATRA (bottom panel from **Figure 4m**) are shown.

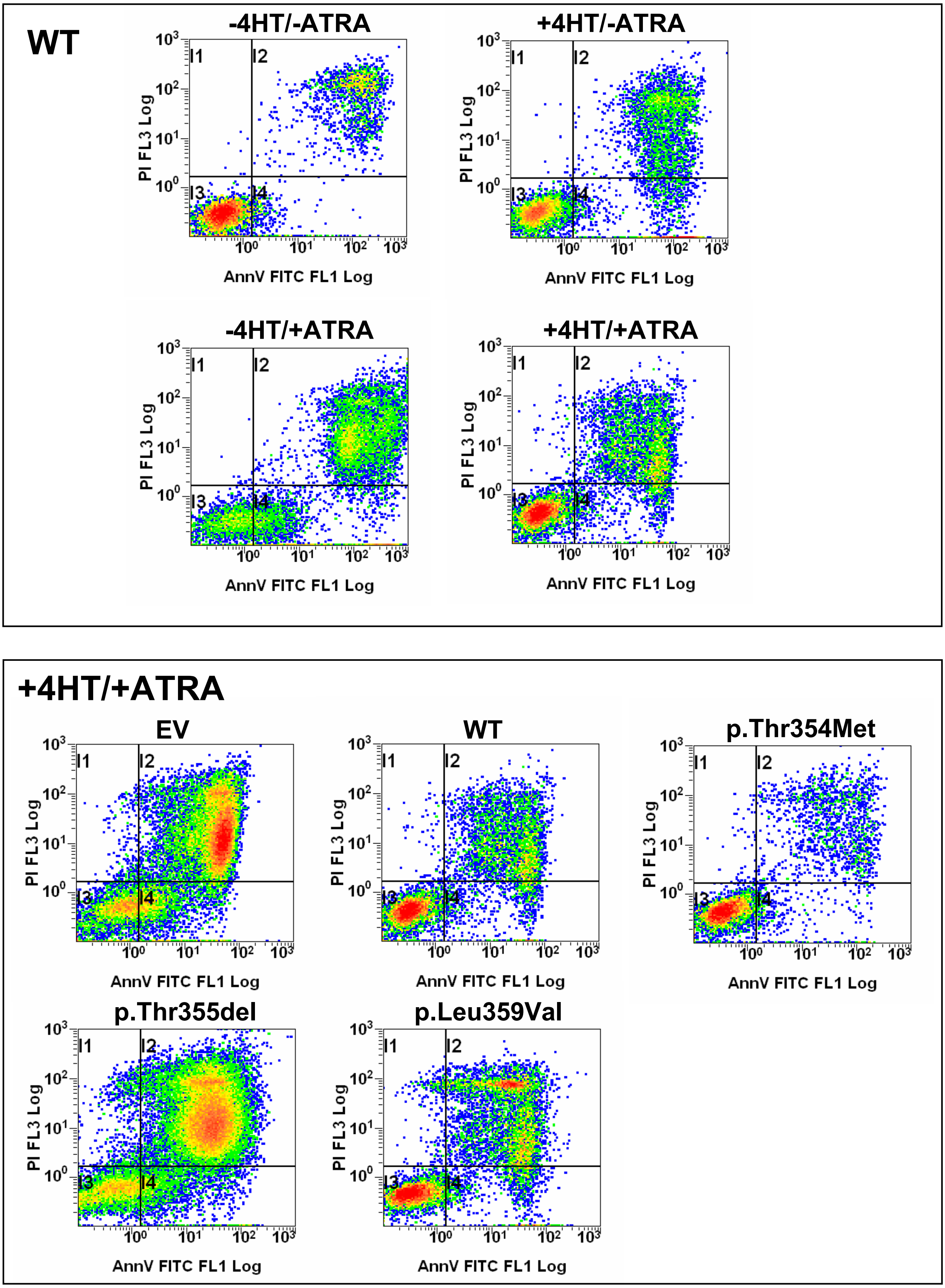
Supplementary Figure 7a. Morphological differentiation of HL-60 cells into granulocytes.



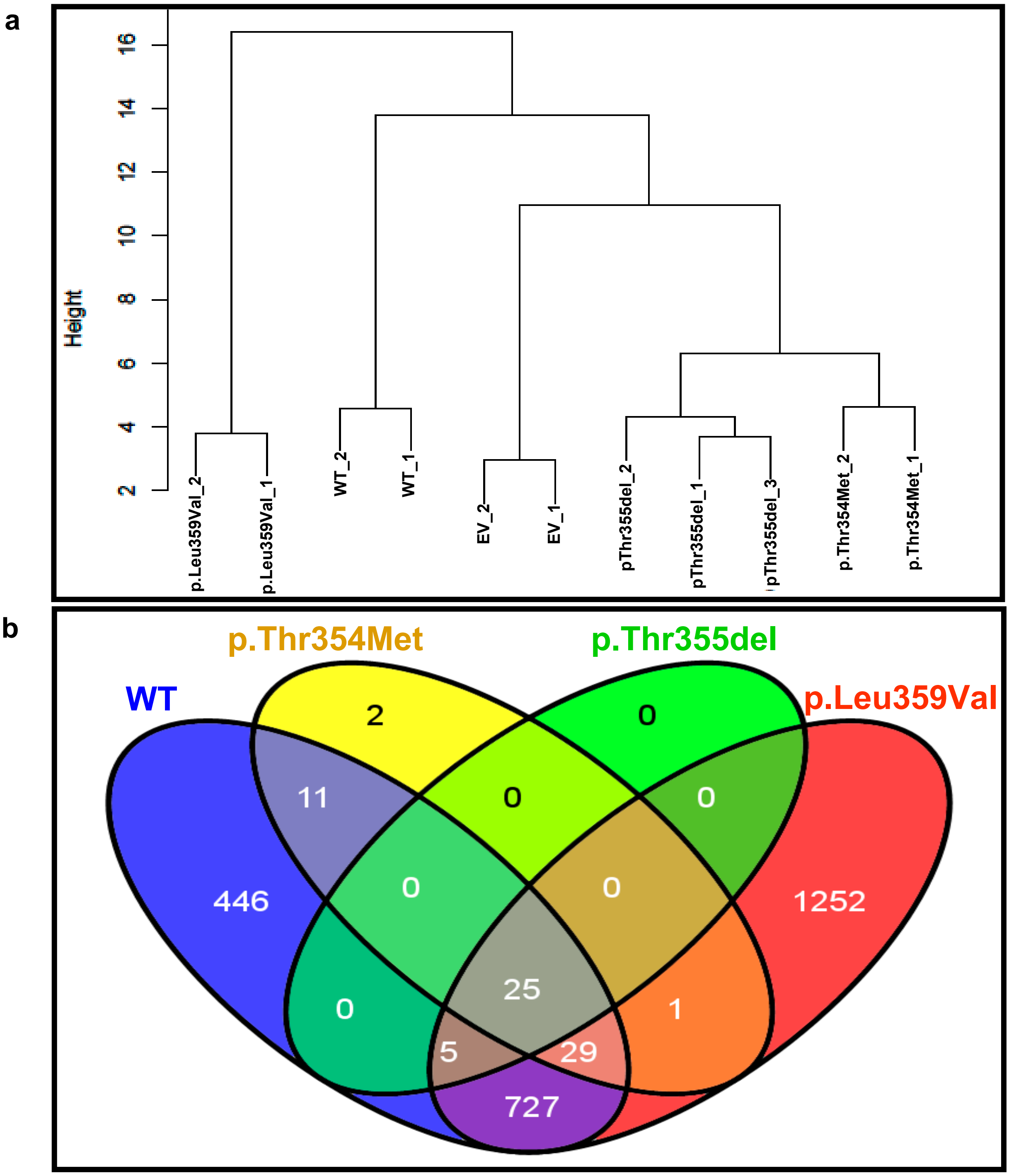
Supplementary Figure 7b. CD11b expression following differentiation with ATRA. Density plots – CD11b vs Side Scatter.



Supplementary Figure 7c. Apoptosis following differentiation with ATRA. Density plots – Propidium iodide vs Annexin V. Annexin V$^+$, PI$^-$ (region I4) (black) or Annexin V$^+$, PI$^+$ (region I2) (white).



Supplementary Figure 8. Differentially regulated genes upon expression of GATA2 WT and mutants in HL-60 cells. HL-60 cell lines were treated with 4HT to turn on GATA2 WT and mutant protein expression. After 24 h, gene expression levels were determined between EV and GATA2 expressing cell lines (see **Supplementary Table 6**). **a.** A cluster dendrogram shows GATA2 mutants p.Thr354Met and p.Thr355del being most similar to each other and most closely related to the EV suggesting loss-of-function (retaining only 65/1,243 and 30/1,243 genes that are differentially regulated, respectively) . It also shows that p.Leu359Val is quite different to these loss-of-function mutants demonstrating rather gain-of-function compared to WT. **b.** Differentially regulated genes are shown in a 4 Way Venn Diagram. **c.** The number of genes in common between any two GATA2 proteins is tabulated.



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	WT	p.Thr354Met	p.Thr355del	p.Leu359Val
WT	1,243	65	30	786
p.Thr354Met		68	25	55
p.Thr355del			30	30
p.Leu359Val				2,039

Supplementary Table 1. Panel of candidate oncogenic genes in AML. Primers were designed and generated to amplify all coding exons; some exons required multiple amplicons. Primer sequences are available upon request. The sequence of the resultant amplicons was determined by DNA sequencing and this was compared to the RefSeq database to identify variants/mutations. Genes were chosen on the basis of known or predicted role in the network of hematopoietic regulators based on the following criteria: known to be mutated in familial myeloid leukemia, displaying hematopoietic expression pattern(s), a known role in hematopoiesis, a candidate myeloid transcription factor[1], mutated in mouse models with hematopoietic defects, known somatic mutations in myeloid leukemia, *RUNX1* target genes or cofactors, common retroviral insertion sites, or members of the ETS transcription factor family.

Gene	Exons (coding)	Amplicons
ATM	63	72
BMI1	10 (9)	9
CALR	9	9
CCND3	5	5
CEBPA	1	4
CEBPB	1	3
CEBPD	2	4
CEBPE	1	3
KIT	21	21
CSF1R	22 (21)	22
CSF3R	17 (15)	16
ELF1	9 (8)	11
ELF2	9 (8)	9
ERG	11 (9)	12
ETS1	8	8
ETS2	10 (9)	9
ETV7	8	8
FIP1L1	18	18
FLI1	11 (10)	30
FLT3	24	24
ZFPM1	10	11
GATA2	6 (5)	7
GATA3	6 (5)	6
ID2	5 (2)	2
JAK2	25 (23)	23
JAK3	24 (23)	23
KLF3	6 (5)	6
KLF4	5 (4)	6
KLF5	4	7
KLF11	4	5
KRAS2	6 (4)	4
LEF1	12 (11)	11
MASTL	12	15
MEIS1	13 (12)	12
MLF1	7	7
MLL	36	48
MYB	15	14
NBN	16	16
NPM1	12 (11)	10
NRAS	7 (4)	4
PDGFRA	23 (22)	21
PIM1	6	6
PIM2	6	5
PTPN11	16 (15)	14
SPI1/PU1	5	5
RAPGEF1	24	27
RUNX1	11	11
SMAD3	9	9
SOX4	1	3
TAL1	4 (3)	3
Total Amplicons		638

Supplementary Table 2. Clinical details with genotype of individuals in four families harboring the MDS/AML-predisposing p.Thr354Met and p.Thr355del mutations. Asterisk - FAB classification of AML if known; Leukemia - refers to non-specific leukemia; unknown - disease status unknown, BMT – bone marrow transplant. FAB classification M2, M7; refractory anemia (RA); refractory cytopenia with multilineage dysplasia (RCMD); coronary artery disease (CAD); cardiovascular accident (CVA); Cytogenetically normal (CN).

Pedigree	Individual	Disease*	GATA2 Genotype	Age at diagnosis (years)	Age of Death (years)	Karyotype
1	I-1					
	I-2	**Leukemia**			42	
	II-1				alive	
	II-2	**MDS-AML**		36	40	
	II-3				41	
	II-4	**AML**			50	
	II-5	**AML** (and ALL)		10	10	
	II-6				68	
	II-7				62	
	II-8				78	
	II-9	**AML** (and CML?)		27	29	
	III-1		p.Thr354		alive	
	III-2	**MDS-AML**		16	34	1q abnormality (isochromosome)
	III-3		p.Thr354		alive	
	III-4	**MDS-AML**	**p.Thr354Met**		32	
	III-5		**p.Thr354Met**		alive	
	III-6				54	
	III-7		p.Thr354		alive	
	III-8		**p.Thr354Met**		alive	
	III-9	**MDS-AML**	**p.Thr354Met**		30	
	III-10	**AML M2**		13	14	
	III-11				alive	
	III-12	**AML M2**		19	19	
	III-13	**Leukemia (myeloid?)** , pancytopenia		18	19	
	IV-1	**MDS-AML** (received BMT)	**p.Thr354Met**	teenager	alive	-7, +21
	IV-2	**MDS-AML**	**p.Thr354Met**	15	15	
	IV-3		p.Thr354		alive	
	IV-4		p.Thr354		alive	
	IV-5				alive	
	IV-6				alive	
	IV-7				alive	
	IV-8				alive	
2	I-1				alive	
	I-2	**Acute Leukemia** , anemia, leukopenia, splenomegally			46	
	I-3	unknown			8 siblings	
	II-1				alive	
	II-2	**AML**			22	
	II-3				alive	
	II-4	**MDS;** received BMT	**p.Thr354Met**	45	alive	-7, +8
	II-5	**Atypical CML** (eosinophilia), pancytopenia			24	
	II-6		**p.Thr354Met**		alive	
	II-7				alive	
	III-1		p.Thr354		alive	
	III-2		p.Thr354		alive	
	III-3				alive	
	III-4	**MDS**	**p.Thr354Met**	20	alive	-7
	III-5		p.Thr354		alive	
	III-6				alive	
	IV-1				alive	

Pedigree	Individual	Disease*	GATA2 Genotype	Age at diagnosis (years)	Age of Death (years)	Karyotype
3	I-1	cerebral haemorrhage			49	
	I-2				85	
	II-1	pernicious anemia & congestive heart failure			72	
	II-2	**Leukemia** ?	**p.Thr354Met**		59	
	II-3	**AML M2**			41	
	II-4	macrocytic anemia & cerebral haemorrhage	**p.Thr354Met**		82	
	II-5				alive	
	II-6				alive	
	II-7	haemorrhagic stroke & breast			62	
	II-8	**Leukemia**		44	44	
	II-9	**AML M2**	**p.Thr354Met**	32	32	const. 9p21-22 variation
	III-1	**MDS-AML M2**	**p.Thr354Met**	38	42	CN
	III-2				alive (~74)	
	III-3				alive (~66)	
	III-4	**MDS-AML**	**p.Thr354Met**	23	28	
	III-5	unknown			2 siblings	
	III-6	**MDS(RA)-AML**	**p.Thr354Met**	35	40	
	III-7	unknown			2 siblings	
	III-8				alive	
	III-9	well	**p.Thr354Met**		alive (~61)	
	III-10	unknown			3 siblings	
	III-11	unknown			2 siblings	
	III-12				alive	
	III-13	haemorrhagic stroke			unknown	
	III-14	unknown			4 siblings	
	III-15	unknown			4 siblings	
	IV-1	**AML M7**; BMT at 21 years	**p.Thr354Met**	21	alive (~39)	-7, +8, t(1q:7p)
	IV-2	unknown			2 siblings	
	IV-3	Few abnormal BM cells (**MDS**?); BM donor for IV-1		16	alive (~33)	CN
	IV-4	well			alive	
	IV-5	**MDS**	**p.Thr354Met**	15	alive (32)	-7, const. 9p21-22 variation
	IV-6	well			alive	
	V-1	well			alive	
4	I-1	CAD; died CVA			unknown	
	I-2	died cirrhosis			unknown	
	II-2	**MDS** (RCMD); BMT at 53 years	**p.Thr355del**	53		+8 (2/20 cells)
	III-1	**MDS**; BMT at 15 years	**p.Thr355del**	13		-7

Supplementary Table 3. Clinical summary of affected individuals from Pedigree 1. Patient ID relates to Pedigree 1 (**Fig. 1a**). Age of death (Age) and diagnosis were verified with "Births, Deaths and Marriages Registries - Australia" or pathology reports. Asterisk – still alive.

Patient ID	Diagnosis	Age	Verification
I-2	Leukemia	42	Death certificate
II-2	Leukemia	40	Death certificate
II-4	AML	50	Death certificate
II-5	Acute lymphocytic leukemia	10	Death certificate
II-9	CML	29	Death certificate
III-2	MDS to AML	38	Pathology report
III-4	AML	32	Pathology report
III-9	MDS to AML	32	Pathology report
III-10	AML	14	Death certificate
III-12	AML	19	Death certificate
III-13	Pancytopenia	19	Death certificate
IV-1	MDS (BMT at 26 years in 2003)	33*	Pathology report
IV-2	MDS to AML	15	Pathology report

Supplementary Table 4. Cell lines screened for *GATA2* mutations.

Name	Origin	Cell Type
Ball1	B-ALL	B-Lymphoblastic
Daudi	Burkitt's Lymphoma	B-Lymphobalstic
HL-60	AML M2	Promyeloblastic
JURKAT	T-ALL	T-Lymphocytic
K562	CML BC	pre-Erythrocytic/Megakaryocytic blasts
KG-1a	AML	Promyeloblastic
KU812	CML BC	Basophilic blasts
REH	ALL (non-T; non-B)	pre-B-Lymphoblastic
U937	Histiocytic Lymphoma	Monoblastic
KCL-22	CML BC	Myeloblastic
KT-1	CML BC	Myeloblastic
KYO-1	CML BC	pre-Erythrocytic/Monocytic blasts
EM-2	CML BC	Myeloblastic
LAMA-84	CML BC	Erythrocytic/Megakaryocytic blasts
MEG-01	CML BC	Megakaryoblastic
HEK293T	Embryonic kidney	Fibroblastic

Supplementary Table 5. Haplotype analysis of p.Thr354Met mutation in three families. The haplotype of genomic DNA surrounding the p.Thr354Met mutation was determined by PCR sequencing of 9 selected amplicons containing a total of 50 SNPs. Shown is the name, position and genotype of 8 informative SNPs in each of the families that segregates with the c.1061C>T (p.Thr354Met) mutation. Pedigrees 1 and 2 contained a common haplotype (red) while Pedigree 3 differs (blue). ***a.*** Population Diversity; RefSeq SNP nucleotide and range of frequency in dbSNP in January, 2011. Asterisk; only p.Thr354Met carrying individuals in Pedigrees 1 and 2 contain these rare variations. A matched normal population screen showed 10/238 individuals heterozygous for a novel deletion of GTCT in the GATA2 promoter (-460), all of which were also heterozygous for the uncommon "T" variant of rs45463801 in the GATA2 3'UTR indicating possible linkage disequilibrium of this specific haplotype. Notably, none of these contained a p.Thr354Met mutation.

Variants	**Position**	**Population Diversity**[a]	**Pedigree 1**	**Pedigree 2**	**Pedigree 3**
rs7629791	-17,667	36-76% C	**T**	**C/T**	**C**
novel	-11,748 (-460 promoter)	100% GTCT	**GTCT/ΔGTCT***	**GTCT/ΔGTCT***	**GTCT**
p.Thr354Met	**+1 (Exon 5)**	**100% C**	**T**	**T**	**T**
rs45463801	+1,429 (Exon 6 - 3'UTR)	96-98% C	**C/T***	**C/T***	**C**
rs2713590	+7,949	76-86% T	**T**	**T**	**G**
rs10934854	+8,092	40-74% G	**G**	**G**	**T**
rs6808807	+8,969	75-86% G	**G**	**G**	**A**
rs2135644	+9,364	50-85% C	**C**	**C**	**T**
rs2135645	+9,375	69-88% C	**C**	**C**	**T**

Supplementary Table 6. Microarray analysis to identify differentially regulated genes following expression of GATA2 WT and mutants in HL-60 cells. HL-60 cell lines were treated with 100 nM 4HT to turn on GATA2 WT and mutant protein expression. After 24 h, gene expression levels were determined between EV and GATA2 WT and mutant expressing cell lines (see also **Supplementary Figure 8**).

Transcript Cluster ID	RefSeq Number	Symbol	Gene Name	Status	Fold WT	Fold L359V	Fold T354M	Fold delT355	FDR p value WT	FDR p value L359V	FDR p value T354M	FDR p value delT355
7922174	NM_000130	F5	coagulation factor V (proaccelerin, labile factor)	L359V only	1.25	6.10	1.23	1.50	1.76E-01	6.59E-06	6.92E-01	8.73E-02
7913655	NM_002167	ID3	inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	L359V only	2.25	4.33	1.58	1.63	1.50E-01	9.85E-03	8.36E-01	9.88E-01
8028963	NM_000767	CYP2B6	cytochrome P450, family 2, subfamily B, polypeptide 6	L359V only	1.19	4.18	0.96	1.33	3.90E-01	3.58E-05	9.65E-01	4.36E-01
8118734	NM_002224	ITPR3	inositol 1,4,5-triphosphate receptor, type 3	L359V only	1.33	3.54	1.03	1.29	1.09E-01	4.20E-05	9.76E-01	4.61E-01
8090823	NM_005630	SLCO2A1	solute carrier organic anion transporter family, member 2A1	L359V only	0.94	3.51	0.66	1.07	9.23E-01	4.05E-03	8.01E-01	1.00E+00
8081564	NM_198196	CD96	CD96 molecule	L359V only	0.84	3.47	0.83	1.22	6.38E-01	7.79E-04	8.76E-01	1.00E+00
8028955	NR_001278	CYP2B7P1	cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	L359V only	1.58	3.44	1.17	1.40	1.17E-01	7.77E-04	8.88E-01	7.16E-01
8041781	NM_001430	EPAS1	endothelial PAS domain protein 1	L359V only	1.57	3.02	1.07	1.32	1.04E-01	1.03E-03	9.55E-01	8.60E-01
8041447	NM_016441	CRIM1	cysteine rich transmembrane BMP regulator 1 (chordin-like)	L359V only	1.24	2.94	1.01	1.29	2.58E-01	1.34E-04	9.94E-01	5.52E-01
7900609	NM_001017922	ERMAP	erythroblast membrane-associated protein (Scianna blood group)	L359V only	1.39	2.75	1.07	1.35	6.88E-02	1.74E-04	9.22E-01	3.40E-01
8092578	NM_004454	ETV5	ets variant 5	L359V only	1.13	2.59	1.16	1.26	5.41E-01	1.96E-04	8.34E-01	5.78E-01
8091715	NM_020169	LXN	latexin	L359V only	1.25	2.52	1.09	1.32	2.36E-01	2.76E-04	9.01E-01	4.23E-01
8139128	---			L359V only	1.34	2.51	1.22	1.26	3.78E-01	4.67E-03	8.70E-01	1.00E+00
8122222	NM_018945	PDE7B	phosphodiesterase 7B	L359V only	1.19	2.39	1.11	1.27	1.69E-01	4.47E-05	8.25E-01	2.35E-01
8021301	NM_004163	RAB27B	RAB27B, member RAS oncogene family	L359V only	1.95	2.35	0.90	1.30	8.68E-02	2.34E-02	9.52E-01	1.00E+00
8058390	NM_213589	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	L359V only	1.39	2.32	1.25	1.32	7.10E-02	4.65E-04	7.28E-01	4.23E-01
8097801	NM_001109977	FAM160A1	family with sequence similarity 160, member A1	L359V only	1.69	2.31	1.23	1.40	1.26E-01	1.36E-02	8.76E-01	8.88E-01
8059387	NM_024785	FAM124B	family with sequence similarity 124B	L359V only	1.22	2.28	1.11	1.28	4.11E-01	1.74E-03	9.01E-01	7.70E-01
8168524	NM_014499	P2RY10	purinergic receptor P2Y, G-protein coupled, 10	L359V only	1.30	2.25	0.89	1.17	5.69E-01	3.05E-02	9.43E-01	1.00E+00
8123929	NM_207582	HERV-FRD	HERV-FRD provirus ancestral Env polyprotein	L359V only	1.51	2.24	1.45	1.41	1.98E-01	1.07E-02	7.38E-01	7.75E-01
7944335	NM_001716	CXCR5	chemokine (C-X-C motif) receptor 5	L359V only	1.34	2.24	1.01	1.24	2.19E-01	2.44E-03	9.97E-01	9.40E-01
8099721	NM_015187	KIAA0746	KIAA0746 protein	L359V only	0.96	2.20	0.83	1.17	9.20E-01	4.12E-03	8.51E-01	1.00E+00
8000869	NM_052838	SEPT1	septin 1	L359V only	1.47	2.20	1.27	1.36	1.24E-01	3.67E-03	8.11E-01	6.55E-01
8017547	NM_001099786	ICAM2	intercellular adhesion molecule 2	L359V only	1.31	2.20	1.24	1.31	1.45E-01	7.38E-04	7.50E-01	4.58E-01
8058498	NM_003468	FZD5	frizzled homolog 5 (Drosophila)	L359V only	1.07	2.15	0.92	1.14	6.61E-01	8.06E-05	8.70E-01	8.36E-01
8067869	NM_144770	RBM11	RNA binding motif protein 11	L359V only	1.71	2.13	1.00	1.36	1.33E-01	2.66E-02	9.99E-01	9.94E-01
7908388	NM_002922	RGS1	regulator of G-protein signaling 1	L359V only	1.09	2.06	1.17	1.21	6.23E-01	3.18E-04	7.79E-01	6.07E-01
8093294	NM_000647	CCR2	chemokine (C-C motif) receptor 2	L359V only	1.87	2.05	1.17	1.38	5.49E-02	2.23E-02	8.97E-01	8.84E-01
8079407	NM_003965	CCRL2	chemokine (C-C motif) receptor-like 2	L359V only	1.47	2.04	1.13	1.25	2.07E-01	1.62E-02	9.22E-01	1.00E+00
8093304	NM_003965	CCRL2	chemokine (C-C motif) receptor-like 2	L359V only	1.47	2.03	1.13	1.26	2.10E-01	1.63E-02	9.16E-01	1.00E+00
7973306	NM_022060	ABHD4	abhydrolase domain containing 4	L359V only	1.43	2.03	1.13	1.24	8.73E-02	2.58E-03	8.80E-01	8.38E-01
7992828	NM_001012631	IL32	interleukin 32	L359V only	1.22	2.02	1.22	1.24	2.01E-01	5.03E-04	6.71E-01	5.05E-01
8040340	NM_145693	LPIN1	lipin 1	L359V only	1.13	2.01	0.98	1.16	4.92E-01	4.92E-04	9.77E-01	8.93E-01
8079383	NM_001837	CCR3	chemokine (C-C motif) receptor 3	L359V only	0.99	2.00	0.96	1.14	9.49E-01	1.03E-04	9.22E-01	7.21E-01
8043498	---			L359V only	1.10	1.98	1.00	1.17	8.21E-01	2.26E-02	9.99E-01	1.00E+00
8038899	NM_002029	FPR1	formyl peptide receptor 1	L359V only	0.78	1.97	0.85	1.03	2.22E-01	2.77E-03	8.38E-01	1.00E+00
8121405	AK094715	FLJ37396	hypothetical protein FLJ37396	L359V only	1.08	1.97	1.29	1.20	8.37E-01	1.22E-02	8.13E-01	1.00E+00
8144802	NM_006207	PDGFRL	platelet-derived growth factor receptor-like	L359V only	0.97	1.96	1.03	1.16	9.32E-01	2.59E-03	9.77E-01	1.00E+00
7922219	NM_000655	SELL	selectin L	L359V only	1.59	1.95	1.47	1.29	1.40E-01	2.60E-02	7.23E-01	1.00E+00
8042468	NM_001153	ANXA4	annexin A4	L359V only	1.22	1.94	1.02	1.21	2.07E-01	7.05E-04	9.76E-01	6.61E-01
7999598	NM_173474	NTAN1	N-terminal asparagine amidase	L359V only	1.04	1.92	0.95	1.15	8.97E-01	2.15E-03	9.44E-01	1.00E+00
8062557	NM_015568	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	L359V only	1.42	1.91	1.17	1.26	1.99E-01	1.42E-02	8.77E-01	9.84E-01
8014706	NM_007144	PCGF2	polycomb group ring finger 2	L359V only	1.42	1.90	1.16	1.25	6.04E-02	2.49E-03	8.36E-01	6.95E-01
7931748	NM_033261	IDI2	isopentenyl-diphosphate delta isomerase 2	L359V only	0.91	1.90	0.96	1.12	7.82E-01	8.74E-03	9.76E-01	1.00E+00
8046380	NM_000210	ITGA6	integrin, alpha 6	L359V only	1.19	1.89	0.75	1.12	4.04E-01	2.63E-03	5.00E-01	1.00E+00
8142524	NM_012338	TSPAN12	tetraspanin 12	L359V only	1.06	1.87	1.22	1.25	8.08E-01	2.62E-03	7.93E-01	6.69E-01
8040587	NM_014971	EFR3B	EFR3 homolog B (S. cerevisiae)	L359V only	1.53	1.86	1.04	1.21	1.65E-01	3.11E-02	9.80E-01	1.00E+00
8167603	NM_001127899	CLCN5	chloride channel 5	L359V only	1.03	1.84	0.93	1.11	8.75E-01	2.02E-04	8.64E-01	9.16E-01
7955562	NM_000020	ACVRL1	activin A receptor type II-like 1	L359V only	1.69	1.83	1.41	1.34	6.13E-02	2.46E-02	7.24E-01	8.27E-01
8157905	NM_033446	FAM125B	family with sequence similarity 125, member B	L359V only	1.12	1.83	0.99	1.18	7.45E-01	1.85E-02	9.98E-01	1.00E+00
8143307	NM_022740	HIPK2	homeodomain interacting protein kinase 2	L359V only	1.23	1.81	1.05	1.11	9.59E-02	3.96E-04	9.30E-01	1.00E+00
8050427	NM_030797	FAM49A	family with sequence similarity 49, member A	L359V only	1.22	1.81	0.90	1.19	3.48E-01	5.48E-03	8.86E-01	9.92E-01
8071155	NM_017414	USP18	ubiquitin specific peptidase 18	L359V only	1.38	1.80	1.05	1.26	2.88E-01	3.34E-02	9.71E-01	1.00E+00
8139125	---			L359V only	1.55	1.79	1.07	1.17	1.46E-01	4.07E-02	9.60E-01	1.00E+00
8037374	NM_002659	PLAUR	plasminogen activator, urokinase receptor	L359V only	1.09	1.78	1.40	1.19	5.28E-01	3.55E-04	5.45E-02	4.73E-01
8143247	NM_020910	KIAA1549	KIAA1549	L359V only	1.32	1.78	1.27	1.24	1.10E-01	3.01E-03	6.39E-01	6.55E-01
8128247	NM_021813	BACH2	BTB and CNC homology 1, basic leucine zipper transcription factor 2	L359V only	1.05	1.77	0.88	1.06	8.64E-01	3.04E-03	8.43E-01	1.00E+00
7952451	BC040288	UNQ565	IGYY565	L359V only	1.79	1.76	1.14	1.28	5.56E-02	4.78E-02	9.15E-01	1.00E+00
8054712	NM_000575	IL1A	interleukin 1, alpha	L359V only	1.48	1.75	0.98	1.17	1.52E-01	3.12E-02	9.86E-01	1.00E+00
7898957	NM_013441	RCAN3	RCAN family member 3	L359V only	1.18	1.74	0.98	1.14	5.11E-01	1.23E-02	9.87E-01	1.00E+00
8079392	NM_000648	CCR2	chemokine (C-C motif) receptor 2	L359V only	1.61	1.73	1.10	1.25	6.80E-02	2.81E-02	9.27E-01	9.88E-01

8043443	ENST00000390266	LOC651751	similar to Ig kappa chain V-II region RPMI 6410 precursor	L359V only	1.17	1.73	1.19	1.16	5.74E-01	1.92E-02	8.52E-01	1.00E+00
7912347	NM_001079843	CASZ1	castor zinc finger 1	L359V only	1.56	1.73	1.06	1.20	9.61E-02	3.25E-02	9.59E-01	1.00E+00
7973618	NM_006084	IRF9	interferon regulatory factor 9	L359V only	1.54	1.72	1.15	1.23	5.93E-02	1.61E-02	8.75E-01	9.45E-01
8047459	---			L359V only	1.17	1.72	1.54	1.28	5.74E-01	2.05E-02	3.62E-01	8.36E-01
8043438	---			L359V only	1.07	1.71	1.18	1.16	8.35E-01	1.17E-02	8.41E-01	1.00E+00
8152821	BC070152	CCDC26	coiled-coil domain containing 26	L359V only	1.56	1.71	1.38	1.32	6.96E-02	2.30E-02	6.66E-01	7.32E-01
7906797	NM_001002901	FCRLB	Fc receptor-like B	L359V only	1.40	1.71	1.23	1.28	1.66E-01	2.17E-02	8.25E-01	8.38E-01
8133112	ENST00000304917	DKFZp434F142	hypothetical protein DKFZp434F142	L359V only	1.29	1.71	1.14	1.17	2.23E-01	9.91E-03	8.70E-01	1.00E+00
8014903	NM_001042471	GSDMB	gasdermin B	L359V only	1.26	1.70	1.04	1.18	2.32E-01	6.70E-03	9.57E-01	9.88E-01
8133540	NM_178831	tcag7.1177	opposite strand transcription unit to STAG3	L359V only	1.07	1.70	0.92	1.06	7.76E-01	3.86E-03	8.91E-01	1.00E+00
8140249	NM_178831	tcag7.1177	opposite strand transcription unit to STAG3	L359V only	1.07	1.70	0.92	1.06	7.76E-01	3.86E-03	8.91E-01	1.00E+00
8090503	---			L359V only	1.30	1.70	1.06	1.24	1.47E-01	5.13E-03	9.36E-01	6.56E-01
7947947	NM_024783	AGBL2	ATP/GTP binding protein-like 2	L359V only	1.26	1.70	1.04	1.13	3.32E-01	1.62E-02	9.71E-01	1.00E+00
8075310	NM_002309	LIF	leukemia inhibitory factor (cholinergic differentiation factor)	L359V only	1.49	1.69	1.10	1.23	8.37E-02	1.92E-02	9.22E-01	9.45E-01
7975459	NM_015556	SIPA1L1	signal-induced proliferation-associated 1 like 1	L359V only	1.17	1.69	0.93	1.10	3.84E-01	4.42E-03	9.10E-01	1.00E+00
8086607	NM_002343	LTF	lactotransferrin	L359V only	1.22	1.69	1.17	1.23	3.36E-01	9.22E-03	8.39E-01	8.36E-01
8050102	NM_207315	CMPK2	cytidine monophosphate (UMP-CMP) kinase 2, mitochondrial	L359V only	1.53	1.69	1.04	1.17	9.59E-02	3.07E-02	9.74E-01	1.00E+00
8120222	NM_018100	EFHC1	EF-hand domain (C-terminal) containing 1	L359V only	1.30	1.69	1.01	1.20	2.55E-01	1.87E-02	9.93E-01	1.00E+00
8171052	NR_024033	IL9R	interleukin 9 receptor	L359V only	1.23	1.68	1.31	1.16	5.89E-02	3.91E-04	1.07E-01	5.23E-01
8176972	NR_024033	IL9R	interleukin 9 receptor	L359V only	1.23	1.68	1.31	1.16	5.89E-02	3.91E-04	1.07E-01	5.23E-01
7960637	NM_020400	LPAR5	lysophosphatidic acid receptor 5	L359V only	1.27	1.68	1.23	1.12	1.25E-01	2.60E-03	6.35E-01	1.00E+00
8160260	NM_017637	BNC2	basonuclin 2	L359V only	1.14	1.68	0.96	1.10	4.87E-01	3.68E-03	9.54E-01	1.00E+00
8022378	---			L359V only	1.15	1.67	1.02	1.14	6.43E-01	2.64E-02	9.88E-01	1.00E+00
8137639	NM_018051	WDR60	WD repeat domain 60	L359V only	1.23	1.67	1.07	1.25	2.17E-01	3.84E-03	9.22E-01	5.69E-01
7951668	---			L359V only	0.96	1.67	1.13	1.15	8.96E-01	9.10E-03	8.76E-01	1.00E+00
8131600	NM_014399	TSPAN13	tetraspanin 13	L359V only	1.05	1.67	0.95	1.09	8.10E-01	2.76E-03	9.32E-01	1.00E+00
7989157	---			L359V only	1.13	1.67	1.27	1.25	6.01E-01	1.01E-02	7.28E-01	7.47E-01
8042283	NM_014181	HSPC159	galectin-related protein	L359V only	1.28	1.67	0.94	1.18	2.16E-01	9.46E-03	9.36E-01	1.00E+00
7965403	NM_002345	LUM	lumican	L359V only	1.54	1.67	1.20	1.26	1.22E-01	4.98E-02	8.69E-01	1.00E+00
7908351	NM_024420	PLA2G4A	phospholipase A2, group IVA (cytosolic, calcium-dependent)	L359V only	1.40	1.66	1.25	1.30	8.28E-02	9.15E-03	7.47E-01	5.44E-01
7983393	NM_003104	SORD	sorbitol dehydrogenase	L359V only	1.04	1.66	1.17	1.17	8.22E-01	1.28E-03	7.44E-01	6.86E-01
8136078	---			L359V only	1.54	1.66	1.49	1.35	5.42E-02	2.05E-02	3.84E-01	5.69E-01
7969640	NM_182848	CLDN10	claudin 10	L359V only	1.34	1.66	1.03	1.20	6.57E-02	3.68E-03	9.70E-01	7.09E-01
8053713	---			L359V only	1.02	1.65	1.12	1.10	9.64E-01	3.84E-02	9.12E-01	1.00E+00
7906764	NM_002155	HSPA6	heat shock 70kDa protein 6 (HSP70B')	L359V only	1.35	1.65	1.18	1.26	1.33E-01	1.15E-02	8.36E-01	7.02E-01
7903753	NM_000848	GSTM2	glutathione S-transferase mu 2 (muscle)	L359V only	1.36	1.65	1.10	1.19	1.05E-01	9.35E-03	8.99E-01	9.26E-01
7953532	NM_001975	ENO2	enolase 2 (gamma, neuronal)	L359V only	1.35	1.65	1.16	1.21	2.45E-01	3.64E-02	8.77E-01	1.00E+00
7928800	NM_018999	KIAA1128	KIAA1128	L359V only	1.20	1.64	1.04	1.07	3.28E-01	7.09E-03	9.60E-01	1.00E+00
7953409	NM_002824	PTMS	parathymosin	L359V only	1.34	1.64	1.13	1.11	6.09E-02	3.57E-03	8.38E-01	1.00E+00
8072302	NM_153050	MTMR3	myotubularin related protein 3	L359V only	1.27	1.63	1.07	1.16	5.95E-02	1.20E-03	8.90E-01	7.29E-01
8030277	NM_001774	CD37	CD37 molecule	L359V only	1.31	1.62	1.24	1.20	5.27E-02	2.05E-03	4.96E-01	5.78E-01
7979133	NM_007361	NID2	nidogen 2 (osteonidogen)	L359V only	1.30	1.62	1.31	1.21	5.44E-02	2.09E-03	2.64E-01	5.00E-01
8101449	NM_001098540	HPSE	heparanase	L359V only	1.18	1.61	0.98	1.10	5.31E-01	2.91E-02	9.89E-01	1.00E+00
8128818	NM_003931	WASF1	WAS protein family, member 1	L359V only	0.77	1.60	0.82	1.01	3.26E-01	4.32E-02	8.38E-01	1.00E+00
7921332	NM_005894	CD5L	CD5 molecule-like	L359V only	1.29	1.60	1.29	1.20	1.95E-01	1.37E-02	6.50E-01	9.09E-01
7959330	NM_144668	WDR66	WD repeat domain 66	L359V only	1.34	1.60	1.30	1.23	1.01E-01	9.90E-03	5.58E-01	7.32E-01
8114593	NM_133174	APBB3	amyloid beta (A4) precursor protein-binding, family B, member 3	L359V only	1.22	1.60	1.17	1.21	1.19E-01	1.57E-03	7.20E-01	4.46E-01
8014361	NM_005064	CCL23	chemokine (C-C motif) ligand 23	L359V only	1.07	1.60	0.99	1.13	8.25E-01	2.91E-02	9.95E-01	1.00E+00
8090018	NM_031458	PARP9	poly (ADP-ribose) polymerase family, member 9	L359V only	1.55	1.60	1.02	1.22	5.27E-02	2.92E-02	9.89E-01	9.88E-01
8042827	---			L359V only	1.22	1.60	1.12	1.15	3.79E-01	2.37E-02	8.86E-01	1.00E+00
8035278	NM_020959	ANO8	anoctamin 8	L359V only	1.25	1.59	1.09	1.15	2.51E-01	1.39E-02	9.07E-01	1.00E+00
8002571	NM_015020	PHLPPL	PH domain and leucine rich repeat protein phosphatase-like	L359V only	1.31	1.59	1.02	1.15	2.77E-01	4.30E-02	9.92E-01	1.00E+00
7899160	NM_001803	CD52	CD52 molecule	L359V only	1.16	1.59	1.24	1.13	3.90E-01	6.42E-03	6.71E-01	1.00E+00
8043433	ENST00000390266	LOC651751	similar to Ig kappa chain V-II region RPMI 6410 precursor	L359V only	1.09	1.59	1.20	1.15	7.70E-01	3.20E-02	8.38E-01	1.00E+00
8100426	---			L359V only	1.31	1.59	1.52	1.30	1.45E-01	1.16E-02	1.45E-01	4.78E-01
8155930	NM_001490	GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 (beta-1,6-N-acetylglucosaminyltransfer	L359V only	1.26	1.59	1.08	1.19	1.54E-01	6.15E-03	9.06E-01	8.17E-01
8096176	NM_080683	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1)	L359V only	1.20	1.59	1.08	1.19	2.91E-01	6.93E-03	9.02E-01	8.02E-01
8021768	NM_005786	TSHZ1	teashirt zinc finger homeobox 1	L359V only	0.91	1.58	1.04	1.06	6.40E-01	9.15E-03	9.60E-01	1.00E+00
7955142	NM_000725	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	L359V only	1.19	1.58	0.95	1.07	4.09E-01	1.62E-02	9.51E-01	1.00E+00
8003991	NM_153827	MINK1	misshapen-like kinase 1 (zebrafish)	L359V only	1.24	1.58	1.07	1.15	1.45E-01	3.88E-03	9.06E-01	9.04E-01
7935882	NM_022039	FBXW4	F-box and WD repeat domain containing 4	L359V only	1.23	1.58	1.06	1.18	1.79E-01	5.12E-03	9.17E-01	8.08E-01
7994981	NM_152288	ORAI3	ORAI calcium release-activated calcium modulator 3	L359V only	1.28	1.57	1.14	1.21	5.93E-02	2.45E-03	8.09E-01	4.69E-01
8048381	NM_015690	STK36	serine	L359V only	1.06	1.57	0.98	1.07	7.75E-01	4.31E-03	9.81E-01	1.00E+00
7996022	NM_002990	CCL22	chemokine (C-C motif) ligand 22	L359V only	1.00	1.57	1.06	1.02	9.98E-01	2.52E-02	9.52E-01	1.00E+00
7908597	NM_205860	NR5A2	nuclear receptor subfamily 5, group A, member 2	L359V only	0.88	1.57	1.02	1.05	5.81E-01	1.62E-02	9.82E-01	1.00E+00

8095422	NM_003154	STATH	statherin	L359V only	0.85	1.56	0.98	1.04	5.41E-01	3.77E-02	9.88E-01	1.00E+00
8008885	AY699265	MIR21	microRNA 21	L359V only	1.22	1.56	1.44	1.25	2.12E-01	6.60E-03	1.45E-01	4.97E-01
8048898	NM_007237	SP140	SP140 nuclear body protein	L359V only	1.49	1.56	1.15	1.24	5.51E-02	2.47E-02	8.64E-01	8.36E-01
8084742	NM_005578	LPP	LIM domain containing preferred translocation partner in lipoma	L359V only	1.26	1.56	0.96	1.11	7.02E-02	2.15E-03	9.32E-01	1.00E+00
8138084	---			L359V only	1.30	1.55	1.11	1.15	2.21E-01	2.69E-02	8.91E-01	1.00E+00
8002830	NM_153486	LDHD	lactate dehydrogenase D	L359V only	1.27	1.55	1.12	1.17	8.48E-02	3.43E-03	8.34E-01	7.05E-01
8142886	NM_003344	UBE2H	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast)	L359V only	1.37	1.55	1.11	1.18	5.32E-02	8.41E-03	8.75E-01	8.84E-01
7934459	NM_003635	NDST2	N-deacetylase	L359V only	1.28	1.55	1.06	1.13	7.87E-02	3.68E-03	9.25E-01	9.79E-01
8113666	NM_020796	SEMA6A	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin)	L359V only	0.95	1.55	0.85	1.02	8.46E-01	1.23E-02	8.19E-01	1.00E+00
8134122	NM_005751	AKAP9	A kinase (PRKA) anchor protein (yotiao) 9	L359V only	1.43	1.55	1.28	1.26	8.33E-02	2.64E-02	7.28E-01	7.46E-01
8013776	NM_018182	C17orf63	chromosome 17 open reading frame 63	L359V only	1.20	1.55	1.04	1.03	1.22E-01	1.52E-03	9.31E-01	1.00E+00
8028656	NM_022835	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	L359V only	1.31	1.55	1.00	1.09	1.21E-01	1.24E-02	9.99E-01	1.00E+00
8040725	NM_020134	DPYSL5	dihydropyrimidinase-like 5	L359V only	1.00	1.55	1.03	1.10	9.89E-01	1.74E-02	9.74E-01	1.00E+00
8046895	NM_177454	FAM171B	family with sequence similarity 171, member B	L359V only	1.12	1.55	1.01	1.16	6.00E-01	1.44E-02	9.93E-01	1.00E+00
8058415	NM_017759	INO80D	INO80 complex subunit D	L359V only	1.10	1.55	1.00	1.08	4.27E-01	1.18E-03	1.00E+00	1.00E+00
8087485	NM_003335	UBA7	ubiquitin-like modifier activating enzyme 7	L359V only	1.20	1.55	0.97	1.07	2.82E-01	9.15E-03	9.75E-01	1.00E+00
7909610	NM_001040619	ATF3	activating transcription factor 3	L359V only	1.09	1.54	1.11	1.18	6.71E-01	6.93E-03	8.68E-01	7.90E-01
7908161	NM_030806	C1orf21	chromosome 1 open reading frame 21	L359V only	1.08	1.54	0.96	1.12	6.04E-01	1.97E-03	9.27E-01	9.15E-01
7953626	NM_014718	CLSTN3	calsyntenin 3	L359V only	1.26	1.54	1.10	1.12	1.39E-01	7.40E-03	8.74E-01	1.00E+00
8103064	NM_031956	TTC29	tetratricopeptide repeat domain 29	L359V only	1.10	1.54	1.09	1.16	5.63E-01	4.94E-03	8.84E-01	8.44E-01
7961673	NM_021957	GYS2	glycogen synthase 2 (liver)	L359V only	0.94	1.54	0.99	1.06	8.11E-01	1.61E-02	9.94E-01	1.00E+00
7973629	NM_001048205	REC8	REC8 homolog (yeast)	L359V only	1.21	1.54	1.06	1.13	1.30E-01	2.63E-03	8.97E-01	9.01E-01
8096385	NM_014606	HERC3	hect domain and RLD 3	L359V only	1.20	1.54	0.99	1.13	2.51E-01	6.74E-03	9.90E-01	1.00E+00
8029219	NM_173633	TMEM145	transmembrane protein 145	L359V only	1.13	1.54	1.17	1.16	6.13E-01	2.24E-02	8.38E-01	1.00E+00
7897277	BC030279	C1orf211	chromosome 1 open reading frame 211	L359V only	1.40	1.54	1.12	1.25	9.07E-02	2.40E-02	8.85E-01	7.38E-01
7978760	NM_017658	KLHL28	kelch-like 28 (Drosophila)	L359V only	1.29	1.53	1.16	1.20	1.27E-01	1.11E-02	8.23E-01	8.01E-01
8111430	NM_014324	AMACR	alpha-methylacyl-CoA racemase	L359V only	1.14	1.53	1.01	1.14	3.96E-01	6.22E-03	9.94E-01	9.88E-01
8111524	NM_174914	UGT3A2	UDP glycosyltransferase 3 family, polypeptide A2	L359V only	0.97	1.53	1.02	1.09	9.24E-01	1.59E-02	9.85E-01	1.00E+00
8082314	NM_032242	PLXNA1	plexin A1	L359V only	1.14	1.52	1.13	1.16	2.45E-01	1.33E-03	7.74E-01	5.63E-01
8120043	NM_001024630	RUNX2	runt-related transcription factor 2	L359V only	1.36	1.52	1.27	1.18	5.11E-02	8.88E-03	5.20E-01	8.11E-01
8029701	NM_001080401	FLJ40125	hypothetical protein FLJ40125	L359V only	1.27	1.52	1.11	1.15	3.16E-01	4.76E-02	9.02E-01	1.00E+00
7977933	NM_012244	SLC7A8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	L359V only	0.76	1.52	0.73	0.89	5.43E-02	5.34E-03	1.72E-01	1.00E+00
7961215	NM_018423	STYK1	serine	L359V only	1.35	1.51	1.03	1.14	5.16E-02	7.85E-03	9.60E-01	9.81E-01
7952950	ENST00000318291	LOC100049716	hypothetical protein LOC100049716	L359V only	1.19	1.51	1.00	1.12	2.75E-01	9.46E-03	9.99E-01	1.00E+00
8042251	NM_014562	OTX1	orthodenticle homeobox 1	L359V only	1.10	1.51	1.16	1.10	6.23E-01	1.11E-02	8.14E-01	1.00E+00
7971602	NM_018191	RCBTB1	regulator of chromosome condensation (RCC1) and BTB (POZ) domain containing p	L359V only	1.27	1.51	1.05	1.21	7.29E-02	4.12E-03	9.29E-01	5.08E-01
8128939	NM_147686	TRAF3IP2	TRAF3 interacting protein 2	L359V only	1.16	1.51	1.08	1.13	4.47E-01	1.72E-02	9.15E-01	1.00E+00
8032509	NM_052847	GNG7	guanine nucleotide binding protein (G protein), gamma 7	L359V only	1.06	1.51	0.96	1.07	7.93E-01	8.37E-03	9.44E-01	1.00E+00
7941639	NM_024649	BBS1	Bardet-Biedl syndrome 1	L359V only	1.15	1.50	1.06	1.13	2.69E-01	3.33E-03	8.98E-01	8.95E-01
8054166	NM_025244	TSGA10	testis specific, 10	L359V only	1.35	1.50	1.11	1.19	6.28E-02	1.12E-02	8.68E-01	7.75E-01
7961595	NM_024730	RERGL	RERG	L359V only	1.06	1.50	1.08	1.13	8.19E-01	1.68E-02	9.14E-01	1.00E+00
7978331	NM_001039771	CBLN3	cerebellin 3 precursor	L359V only	0.99	1.50	0.98	1.07	9.84E-01	1.55E-02	9.77E-01	1.00E+00
7945550	NM_018494	LRDD	leucine-rich repeats and death domain containing	L359V only	1.20	1.50	1.05	1.10	1.27E-01	2.87E-03	9.12E-01	1.00E+00
7999468	NM_004862	LITAF	lipopolysaccharide-induced TNF factor	L359V only	0.97	1.49	1.10	1.10	8.66E-01	2.28E-03	8.35E-01	9.99E-01
7992518	NM_014353	RAB26	RAB26, member RAS oncogene family	L359V only	1.28	1.49	1.19	1.21	1.04E-01	8.80E-03	7.38E-01	6.27E-01
8011734	NM_000080	CHRNE	cholinergic receptor, nicotinic, epsilon	L359V only	1.08	1.49	1.12	1.15	7.27E-01	1.43E-02	8.58E-01	1.00E+00
8158317	NM_001130438	SPTAN1	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin)	L359V only	1.15	1.49	0.97	1.11	2.84E-01	3.67E-03	9.59E-01	1.00E+00
8138741	NM_024014	HOXA6	homeobox A6	L359V only	1.19	1.49	1.16	1.18	2.13E-01	5.91E-03	7.80E-01	6.73E-01
7906900	AY423733	DDR2	discoidin domain receptor tyrosine kinase 2	L359V only	1.01	1.49	1.16	1.15	9.69E-01	4.84E-02	8.64E-01	1.00E+00
8139873	NM_181722	LOC285908	hypothetical protein LOC285908	L359V only	1.14	1.49	1.00	1.09	5.76E-01	3.23E-02	1.00E+00	1.00E+00
8045604	NM_018328	MBD5	methyl-CpG binding domain protein 5	L359V only	1.26	1.48	1.01	1.09	1.31E-01	1.13E-02	9.87E-01	1.00E+00
8167287	NM_022825	PORCN	porcupine homolog (Drosophila)	L359V only	1.16	1.48	1.13	1.08	3.99E-01	1.51E-02	8.40E-01	1.00E+00
8097670	NM_172250	MMAA	methylmalonic aciduria (cobalamin deficiency) cblA type	L359V only	0.96	1.48	0.95	1.09	7.90E-01	3.67E-03	9.18E-01	1.00E+00
8026579	NM_024074	TMEM38A	transmembrane protein 38A	L359V only	1.18	1.48	1.16	1.17	2.48E-01	7.30E-03	7.97E-01	7.22E-01
8007228	NM_001130020	ATP6V0A1	ATPase, H+ transporting, lysosomal V0 subunit a1	L359V only	1.21	1.48	1.14	1.13	1.88E-01	8.55E-03	8.14E-01	1.00E+00
8140971	NM_152703	SAMD9L	sterile alpha motif domain containing 9-like	L359V only	1.31	1.47	0.94	1.05	1.10E-01	1.91E-02	9.27E-01	1.00E+00
8012376	NM_014232	VAMP2	vesicle-associated membrane protein 2 (synaptobrevin 2)	L359V only	1.22	1.47	1.16	1.08	2.61E-01	2.01E-02	8.25E-01	1.00E+00
8013159	NM_001082968	TOM1L2	target of myb1-like 2 (chicken)	L359V only	1.24	1.47	1.01	1.10	7.78E-02	3.68E-03	9.94E-01	1.00E+00
8155062	NM_006285	TESK1	testis-specific kinase 1	L359V only	1.19	1.47	1.00	1.06	1.97E-01	5.20E-03	9.99E-01	1.00E+00
8086600	NM_001295	CCR1	chemokine (C-C motif) receptor 1	L359V only	0.87	1.47	0.71	0.97	3.10E-01	5.62E-03	8.45E-02	1.00E+00
7954985	NM_032256	TMEM117	transmembrane protein 117	L359V only	1.03	1.47	0.64	0.98	9.40E-01	4.69E-02	2.00E-01	1.00E+00
7964631	NM_178539	FAM19A2	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	L359V only	1.41	1.47	1.22	1.25	8.69E-02	4.22E-02	8.06E-01	7.47E-01
8115464	NM_032782	HAVCR2	hepatitis A virus cellular receptor 2	L359V only	0.97	1.47	1.07	1.09	8.87E-01	1.18E-02	9.02E-01	1.00E+00
7953564	NM_138425	C12orf57	chromosome 12 open reading frame 57	L359V only	1.34	1.47	1.05	1.18	1.66E-01	4.77E-02	9.54E-01	1.00E+00
8022996	NM_020964	KIAA1632	KIAA1632	L359V only	1.28	1.47	1.11	1.16	5.27E-02	4.42E-03	8.34E-01	7.02E-01

8169995	AK295485	FAM122C	family with sequence similarity 122C	L359V only	1.16	1.47	0.88	1.08	5.20E-01	3.77E-02	8.69E-01	1.00E+00
8158380	NM_013355	PKN3	protein kinase N3	L359V only	1.18	1.47	1.17	1.15	3.98E-01	2.88E-02	8.25E-01	1.00E+00
8125007	NM_025262	LY6G5C	lymphocyte antigen 6 complex, locus G5C	L359V only	1.21	1.47	0.97	1.10	3.51E-01	3.85E-02	9.74E-01	1.00E+00
8124551	NR_002936	LOC222699	transducer of ERBB2, 2 pseudogene	L359V only	1.22	1.46	1.07	1.11	2.20E-01	1.43E-02	9.15E-01	1.00E+00
7951437	NM_000855	GUCY1A2	guanylate cyclase 1, soluble, alpha 2	L359V only	0.82	1.46	0.81	0.95	8.63E-02	3.42E-03	3.50E-01	1.00E+00
8133770	NM_020879	CCDC146	coiled-coil domain containing 146	L359V only	1.19	1.46	0.85	1.11	4.48E-01	4.69E-02	8.36E-01	1.00E+00
8034151	NM_020812	DOCK6	dedicator of cytokinesis 6	L359V only	1.24	1.46	1.28	1.21	1.28E-01	8.08E-03	3.90E-01	5.47E-01
8014916	NM_139280	ORMDL3	ORM1-like 3 (S. cerevisiae)	L359V only	1.17	1.46	1.11	1.13	3.72E-01	2.01E-02	8.74E-01	1.00E+00
7904812	NM_006099	PIAS3	protein inhibitor of activated STAT, 3	L359V only	1.26	1.46	1.05	1.06	1.32E-01	1.41E-02	9.44E-01	1.00E+00
8065612	NM_080616	C20orf112	chromosome 20 open reading frame 112	L359V only	1.17	1.45	0.92	1.03	4.20E-01	3.12E-02	8.98E-01	1.00E+00
8098121	NM_014247	RAPGEF2	Rap guanine nucleotide exchange factor (GEF) 2	L359V only	1.07	1.45	0.80	0.99	7.24E-01	1.09E-02	5.05E-01	1.00E+00
7977646	NM_016423	ZNF219	zinc finger protein 219	L359V only	1.18	1.45	1.02	1.14	2.66E-01	9.98E-03	9.75E-01	9.78E-01
8015511	NM_024119	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58	L359V only	1.26	1.45	1.10	1.15	1.49E-01	1.65E-02	8.76E-01	9.88E-01
7955589	NM_002135	NR4A1	nuclear receptor subfamily 4, group A, member 1	L359V only	1.21	1.45	1.21	1.16	1.75E-01	8.08E-03	5.84E-01	7.48E-01
8029136	NM_001783	CD79A	CD79a molecule, immunoglobulin-associated alpha	L359V only	1.19	1.45	1.08	1.06	1.40E-01	4.07E-03	8.64E-01	1.00E+00
8019912	NM_032048	EMILIN2	elastin microfibril interfacer 2	L359V only	0.97	1.45	1.09	1.12	9.23E-01	2.39E-02	8.97E-01	1.00E+00
7929719	NM_014472	C10orf28	chromosome 10 open reading frame 28	L359V only	1.24	1.45	0.99	1.15	2.23E-01	2.47E-02	9.91E-01	1.00E+00
8178554	NM_025262	LY6G5C	lymphocyte antigen 6 complex, locus G5C	L359V only	1.23	1.45	0.95	1.09	3.01E-01	4.00E-02	9.51E-01	1.00E+00
8151223	NM_030958	SLCO5A1	solute carrier organic anion transporter family, member 5A1	L359V only	1.04	1.45	1.11	1.15	8.54E-01	7.86E-03	8.41E-01	8.36E-01
8108579	NM_018502	TMCO6	transmembrane and coiled-coil domains 6	L359V only	1.14	1.45	1.12	1.16	2.13E-01	2.28E-03	7.94E-01	4.98E-01
8043835	BC021264	C2orf15	chromosome 2 open reading frame 15	L359V only	1.10	1.45	1.24	1.17	6.88E-01	4.34E-02	7.65E-01	1.00E+00
8171708	NM_198279	CXorf23	chromosome X open reading frame 23	L359V only	1.29	1.44	1.11	1.22	1.97E-01	4.48E-02	8.86E-01	8.45E-01
8156476	NM_005392	PHF2	PHD finger protein 2	L359V only	1.24	1.44	1.04	1.08	1.01E-01	6.94E-03	9.50E-01	1.00E+00
8098103	NM_020840	FNIP2	folliculin interacting protein 2	L359V only	1.13	1.44	0.91	1.06	4.15E-01	7.86E-03	8.56E-01	1.00E+00
7904050	NM_020963	MOV10	Mov10, Moloney leukemia virus 10, homolog (mouse)	L359V only	1.27	1.44	1.00	1.08	1.46E-01	2.00E-02	9.99E-01	1.00E+00
8006161	NM_015594	TBC1D29	TBC1 domain family, member 29	L359V only	1.07	1.44	1.01	1.07	7.48E-01	1.82E-02	9.90E-01	1.00E+00
7903334	NM_003672	CDC14A	CDC14 cell division cycle 14 homolog A (S. cerevisiae)	L359V only	1.10	1.44	0.97	1.08	6.26E-01	2.00E-02	9.73E-01	1.00E+00
7948493	NM_016582	SLC15A3	solute carrier family 15, member 3	L359V only	1.35	1.44	1.42	1.23	9.71E-02	3.37E-02	2.79E-01	7.38E-01
7958960	NM_017901	TPCN1	two pore segment channel 1	L359V only	1.25	1.44	1.16	1.12	7.34E-02	5.26E-03	7.28E-01	9.05E-01
7939738	NM_000107	DDB2	damage-specific DNA binding protein 2, 48kDa	L359V only	1.15	1.44	1.01	1.11	5.11E-01	3.41E-02	9.97E-01	1.00E+00
8173208	NM_001012968	SPIN4	spindlin family, member 4	L359V only	1.08	1.44	1.11	1.16	6.17E-01	5.91E-03	8.38E-01	6.73E-01
7969477	---			L359V only	1.16	1.44	1.40	1.20	4.97E-01	4.88E-02	4.09E-01	9.27E-01
8134117	NM_003505	FZD1	frizzled homolog 1 (Drosophila)	L359V only	1.30	1.43	1.08	1.16	1.22E-01	2.79E-02	9.06E-01	9.78E-01
8128894	NM_002912	REV3L	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)	L359V only	1.17	1.43	1.04	1.15	1.79E-01	3.67E-03	9.41E-01	6.27E-01
7899043	NM_020451	SEPN1	selenoprotein N, 1	L359V only	1.17	1.43	1.06	1.04	2.14E-01	6.93E-03	9.09E-01	1.00E+00
8079462	NM_015175	NBEAL2	neurobeachin-like 2	L359V only	1.15	1.43	1.03	1.07	2.25E-01	4.26E-03	9.47E-01	1.00E+00
7957806	NM_017988	SCYL2	SCY1-like 2 (S. cerevisiae)	L359V only	1.06	1.43	0.98	1.09	7.00E-01	4.99E-03	9.71E-01	1.00E+00
7912496	NM_005957	MTHFR	5,10-methylenetetrahydrofolate reductase (NADPH)	L359V only	0.99	1.43	0.95	1.00	9.31E-01	2.95E-03	8.98E-01	1.00E+00
7927091	AK128746	LOC399744	hypothetical LOC399744	L359V only	1.00	1.43	1.15	1.07	9.91E-01	1.44E-02	8.14E-01	1.00E+00
7930106	NM_024789	TMEM180	transmembrane protein 180	L359V only	1.20	1.43	1.03	1.06	1.45E-01	6.65E-03	9.55E-01	1.00E+00
8173340	NM_145119	PJA1	praja ring finger 1	L359V only	1.33	1.42	1.15	1.20	9.40E-02	3.10E-02	8.35E-01	8.01E-01
7902977	NM_015237	KIAA1107	KIAA1107	L359V only	1.41	1.42	1.10	1.21	7.29E-02	4.82E-02	8.98E-01	8.69E-01
7905974	NM_020897	HCN3	hyperpolarization activated cyclic nucleotide-gated potassium channel 3	L359V only	1.17	1.42	1.07	1.07	3.26E-01	1.72E-02	9.01E-01	1.00E+00
7946742	NM_024514	CYP2R1	cytochrome P450, family 2, subfamily R, polypeptide 1	L359V only	1.05	1.42	1.06	1.17	8.19E-01	2.46E-02	9.31E-01	8.94E-01
7912166	NM_012102	RERE	arginine-glutamic acid dipeptide (RE) repeats	L359V only	1.24	1.42	1.05	1.10	8.03E-02	6.23E-03	9.27E-01	1.00E+00
8034130	NM_015493	KANK2	KN motif and ankyrin repeat domains 2	L359V only	1.23	1.42	1.20	1.15	2.12E-01	2.51E-02	7.66E-01	1.00E+00
8028791	NM_012268	PLD3	phospholipase D family, member 3	L359V only	1.12	1.42	0.98	1.06	4.35E-01	7.43E-03	9.67E-01	1.00E+00
7920757	BC080538	C1orf104	chromosome 1 open reading frame 104	L359V only	1.25	1.42	1.03	1.11	7.75E-02	7.29E-03	9.64E-01	1.00E+00
7956842	NM_014319	LEMD3	LEM domain containing 3	L359V only	1.11	1.42	1.02	1.11	5.07E-01	9.26E-03	9.75E-01	1.00E+00
8042925	NM_004263	SEMA4F	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	L359V only	1.22	1.42	1.17	1.18	1.19E-01	7.86E-03	7.22E-01	6.19E-01
8003263	NM_015144	ZCCHC14	zinc finger, CCHC domain containing 14	L359V only	1.25	1.42	1.03	1.09	1.21E-01	1.36E-02	9.59E-01	1.00E+00
8073129	NM_002409	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	L359V only	0.99	1.42	1.03	1.08	9.83E-01	2.21E-02	9.65E-01	1.00E+00
8146285	NM_152419	HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase	L359V only	1.28	1.42	1.05	1.14	1.72E-01	3.90E-02	9.52E-01	1.00E+00
7918593	NM_175744	RHOC	ras homolog gene family, member C	L359V only	1.27	1.42	1.14	1.13	1.47E-01	2.65E-02	8.36E-01	1.00E+00
8050844	AF052121	LOC100131510	hypothetical LOC100131510	L359V only	1.10	1.42	0.87	1.06	6.40E-01	2.55E-02	8.36E-01	1.00E+00
7902660	NM_145172	WDR63	WD repeat domain 63	L359V only	1.00	1.42	0.97	1.07	9.89E-01	4.98E-02	9.75E-01	1.00E+00
7956242	NM_144576	COQ10A	coenzyme Q10 homolog A (S. cerevisiae)	L359V only	1.24	1.42	1.10	1.16	1.31E-01	1.40E-02	8.68E-01	8.36E-01
8114526	NM_152686	DNAJC18	DnaJ (Hsp40) homolog, subfamily C, member 18	L359V only	1.27	1.42	1.18	1.22	8.00E-02	1.11E-02	7.33E-01	4.76E-01
7956211	NM_021019	MYL6	myosin, light chain 6, alkali, smooth muscle and non-muscle	L359V only	1.27	1.42	1.04	1.07	1.42E-01	2.67E-02	9.52E-01	1.00E+00
8179238	NM_000247	MICA	MHC class I polypeptide-related sequence A	L359V only	1.37	1.41	1.13	1.19	5.87E-02	2.83E-02	8.51E-01	8.08E-01
7945344	AK294679	tcag7.907	hypothetical LOC402483	L359V only	1.12	1.41	1.19	1.14	5.81E-01	3.84E-02	8.01E-01	1.00E+00
8106354	NM_006633	IQGAP2	IQ motif containing GTPase activating protein 2	L359V only	1.26	1.41	1.07	1.15	5.91E-02	6.96E-03	8.85E-01	7.09E-01
8121095	NM_014942	ANKRD6	ankyrin repeat domain 6	L359V only	1.11	1.41	1.03	1.10	5.76E-01	2.17E-02	9.73E-01	1.00E+00
8172531	NM_007213	PRAF2	PRA1 domain family, member 2	L359V only	1.26	1.41	1.23	1.12	1.17E-01	1.64E-02	5.69E-01	1.00E+00
7924977	NM_024554	PGBD5	piggyBac transposable element derived 5	L359V only	0.85	1.41	0.85	0.97	2.25E-01	1.06E-02	7.38E-01	1.00E+00

8019347	---			L359V only	1.02	1.41	1.09	1.11	9.55E-01	4.98E-02	9.01E-01	1.00E+00
7947815	NM_001610	ACP2	acid phosphatase 2, lysosomal	L359V only	1.08	1.41	0.99	1.05	6.68E-01	1.62E-02	9.93E-01	1.00E+00
7987454	NM_001003940	BMF	Bcl2 modifying factor	L359V only	1.05	1.41	0.93	1.10	8.33E-01	2.85E-02	9.06E-01	1.00E+00
7961059	NM_002258	KLRB1	killer cell lectin-like receptor subfamily B, member 1	L359V only	1.10	1.41	1.19	1.19	6.47E-01	4.09E-02	8.03E-01	8.90E-01
8000910	NM_145271	ZNF688	zinc finger protein 688	L359V only	1.19	1.41	1.14	1.15	1.79E-01	9.58E-03	8.01E-01	7.75E-01
7941537	NM_018026	PACS1	phosphofurin acidic cluster sorting protein 1	L359V only	1.17	1.41	0.90	1.01	3.25E-01	1.99E-02	8.53E-01	1.00E+00
7960744	NM_001733	C1R	complement component 1, r subcomponent	L359V only	1.22	1.40	1.02	1.12	1.84E-01	1.75E-02	9.84E-01	1.00E+00
7904955	---			L359V only	1.24	1.40	1.04	1.15	1.30E-01	1.65E-02	9.43E-01	8.90E-01
8047565	NM_173511	FAM117B	family with sequence similarity 117, member B	L359V only	1.13	1.40	1.00	1.01	4.31E-01	1.79E-02	9.99E-01	1.00E+00
8010454	NM_020914	RNF213	ring finger protein 213	L359V only	1.24	1.40	0.98	1.04	8.00E-02	7.15E-02	9.81E-01	1.00E+00
8125687	NM_004761	RGL2	ral guanine nucleotide dissociation stimulator-like 2	L359V only	1.33	1.40	1.09	1.13	5.88E-02	2.09E-02	8.80E-01	1.00E+00
7966488	NM_001109662	C12orf51	chromosome 12 open reading frame 51	L359V only	1.16	1.40	0.98	1.04	2.85E-01	1.25E-02	9.76E-01	1.00E+00
7945462	NM_004031	IRF7	interferon regulatory factor 7	L359V only	1.18	1.40	1.05	1.11	2.07E-01	1.10E-02	9.22E-01	1.00E+00
8051928	NM_006036	PREPL	prolyl endopeptidase-like	L359V only	1.09	1.40	1.08	1.17	5.35E-01	7.80E-03	8.66E-01	6.07E-01
7995825	NM_005949	MT1F	metallothionein 1F	L359V only	1.18	1.40	1.11	1.09	2.67E-01	1.82E-02	8.46E-01	1.00E+00
7915468	NM_199342	CCDC23	coiled-coil domain containing 23	L359V only	1.08	1.40	0.97	1.09	7.56E-01	4.41E-02	9.68E-01	1.00E+00
8009844	NM_001031803	LLGL2	lethal giant larvae homolog 2 (Drosophila)	L359V only	1.17	1.40	0.96	1.08	4.31E-01	4.71E-02	9.59E-01	1.00E+00
8025672	NM_020428	SLC44A2	solute carrier family 44, member 2	L359V only	1.39	1.40	1.21	1.15	5.32E-02	3.62E-02	7.50E-01	1.00E+00
8131614	NM_001621	AHR	aryl hydrocarbon receptor	L359V only	1.16	1.40	0.75	0.99	4.23E-01	3.67E-02	3.90E-01	1.00E+00
7962375	NM_153026	PRICKLE1	prickle homolog 1 (Drosophila)	L359V only	0.87	1.39	0.92	1.02	4.43E-01	3.72E-02	8.94E-01	1.00E+00
7996954	NM_138714	NFAT5	nuclear factor of activated T-cells 5, tonicity-responsive	L359V only	1.26	1.39	0.97	1.07	5.89E-02	7.63E-03	9.59E-01	1.00E+00
8178955	NM_004761	RGL2	ral guanine nucleotide dissociation stimulator-like 2	L359V only	1.30	1.39	1.09	1.12	1.02E-01	2.91E-02	8.90E-01	1.00E+00
8180144	NM_004761	RGL2	ral guanine nucleotide dissociation stimulator-like 2	L359V only	1.30	1.39	1.09	1.12	1.02E-01	2.91E-02	8.90E-01	1.00E+00
8115623	NM_025153	ATP10B	ATPase, class V, type 10B	L359V only	1.07	1.39	1.05	1.08	7.27E-01	2.60E-02	9.36E-01	1.00E+00
8034762	NM_002730	PRKACA	protein kinase, cAMP-dependent, catalytic, alpha	L359V only	1.31	1.39	1.05	1.10	7.15E-02	2.30E-02	9.41E-01	1.00E+00
8004385	NM_020795	NLGN2	neuroligin 2	L359V only	1.18	1.39	1.22	1.18	2.52E-01	1.64E-02	5.66E-01	6.73E-01
7939723	NM_001003676	C11orf49	chromosome 11 open reading frame 49	L359V only	1.04	1.39	0.83	1.02	8.13E-01	4.13E-03	4.12E-01	1.00E+00
7907079	NM_052862	RCSD1	RCSD domain containing 1	L359V only	1.30	1.39	1.28	1.26	5.27E-02	1.36E-02	3.29E-01	3.17E-01
7969341	NM_030794	TDRD3	tudor domain containing 3	L359V only	1.24	1.39	1.06	1.15	1.34E-01	1.75E-02	9.13E-01	8.78E-01
7955535	NM_004302	ACVR1B	activin A receptor, type IB	L359V only	1.23	1.39	1.13	1.11	1.42E-01	1.76E-02	8.34E-01	1.00E+00
8113724	---			L359V only	1.11	1.39	1.17	1.13	6.12E-01	4.73E-02	8.16E-01	1.00E+00
7944463	NM_024618	NLRX1	NLR family member X1	L359V only	1.16	1.38	1.08	1.13	2.90E-01	1.55E-02	8.81E-01	9.88E-01
8117389	NM_003523	HIST1H2BE	histone cluster 1, H2be	L359V only	1.22	1.38	1.16	1.18	1.84E-01	2.47E-02	8.01E-01	7.47E-01
8030339	NM_001459	FLT3LG	fms-related tyrosine kinase 3 ligand	L359V only	1.15	1.38	1.04	1.07	2.15E-01	5.03E-03	9.31E-01	1.00E+00
7913001	NM_020765	UBR4	ubiquitin protein ligase E3 component n-recognin 4	L359V only	1.24	1.38	0.97	1.09	1.55E-01	2.69E-02	9.71E-01	1.00E+00
7984079	NM_000366	TPM1	tropomyosin 1 (alpha)	L359V only	1.27	1.38	1.06	1.14	7.02E-02	1.29E-02	9.07E-01	8.90E-01
7909529	NM_001136223	RCOR3	REST corepressor 3	L359V only	1.19	1.38	0.96	1.07	2.56E-01	2.69E-02	9.51E-01	1.00E+00
8049689	NM_018226	RNPEPL1	arginyl aminopeptidase (aminopeptidase B)-like 1	L359V only	1.26	1.38	1.21	1.15	5.04E-02	7.60E-03	4.49E-01	6.55E-01
8131067	NM_138445	GPR146	G protein-coupled receptor 146	L359V only	0.89	1.38	0.89	1.03	5.52E-01	4.85E-02	8.65E-01	1.00E+00
7974697	NM_014992	DAAM1	dishevelled associated activator of morphogenesis 1	L359V only	1.22	1.38	0.92	1.07	2.24E-01	3.28E-02	8.88E-01	1.00E+00
8149986	NM_018660	ZNF395	zinc finger protein 395	L359V only	1.08	1.38	1.00	1.06	6.59E-01	2.14E-02	9.99E-01	1.00E+00
7986049	NM_022769	CRTC3	CREB regulated transcription coactivator 3	L359V only	1.30	1.38	1.07	1.02	1.09E-01	4.01E-02	9.22E-01	1.00E+00
7911211	---			L359V only	0.95	1.38	1.03	1.03	8.02E-01	2.50E-02	9.64E-01	1.00E+00
8123936	NM_006403	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	L359V only	1.27	1.38	1.19	1.16	7.14E-02	1.42E-02	6.60E-01	7.38E-01
8170891	NM_001493	GDI1	GDP dissociation inhibitor 1	L359V only	1.29	1.38	1.06	1.08	6.99E-02	2.03E-02	9.21E-01	1.00E+00
8130032	NM_032145	FBXO30	F-box protein 30	L359V only	1.32	1.38	1.01	1.12	7.33E-02	3.08E-02	9.96E-01	1.00E+00
8073826	NM_005036	PPARA	peroxisome proliferator-activated receptor alpha	L359V only	1.25	1.38	0.99	1.06	1.10E-01	1.72E-02	9.86E-01	1.00E+00
7947110	NM_024680	E2F8	E2F transcription factor 8	L359V only	1.20	1.38	1.03	1.07	1.31E-01	1.01E-02	9.55E-01	1.00E+00
7955045	BC008360	FAM113B	family with sequence similarity 113, member B	L359V only	1.04	1.38	0.68	0.95	8.53E-01	2.95E-02	1.06E-01	1.00E+00
8112107	NM_003711	PPAP2A	phosphatidic acid phosphatase type 2A	L359V only	1.34	1.38	1.22	1.09	6.36E-02	3.41E-02	7.02E-01	1.00E+00
8033233	NM_006087	TUBB4	tubulin, beta 4	L359V only	1.23	1.37	1.07	1.15	1.37E-01	2.03E-02	8.94E-01	8.59E-01
7958620	NM_014055	IFT81	intraflagellar transport 81 homolog (Chlamydomonas)	L359V only	1.19	1.37	1.13	1.18	2.97E-01	3.75E-02	8.38E-01	8.60E-01
8141728	NM_022777	RABL5	RAB, member RAS oncogene family-like 5	L359V only	1.14	1.37	1.02	1.12	3.36E-01	1.35E-02	9.74E-01	9.88E-01
7967002	NM_001080855	PXN	paxillin	L359V only	1.10	1.37	1.08	1.10	6.05E-01	2.44E-02	8.94E-01	1.00E+00
7930074	NM_002502	NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49	L359V only	1.35	1.37	1.20	1.16	5.63E-02	3.15E-02	7.33E-01	8.97E-01
8155121	NM_003995	NPR2	natriuretic peptide receptor B guanylate cyclase B (atrionatriuretic peptide receptor	L359V only	1.07	1.37	1.03	1.08	6.53E-01	8.19E-03	9.43E-01	1.00E+00
8155110	NM_001080496	RGP1	RGP1 retrograde golgi transport homolog (S. cerevisiae)	L359V only	1.21	1.37	0.99	1.04	1.12E-01	9.58E-03	9.94E-01	1.00E+00
7964579	NM_005730	CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphata	L359V only	1.24	1.37	1.01	1.14	1.04E-01	1.64E-02	9.84E-01	8.90E-01
8024120	NM_019112	ABCA7	ATP-binding cassette, sub-family A (ABC1), member 7	L359V only	1.15	1.37	1.01	1.04	3.56E-01	2.41E-02	9.93E-01	1.00E+00
8150195	---			L359V only	1.12	1.37	1.25	1.17	5.06E-01	2.38E-02	4.96E-01	8.06E-01
8015133	NM_015515	KRT23	keratin 23 (histone deacetylase inducible)	L359V only	1.09	1.37	1.16	1.16	6.16E-01	2.69E-02	8.01E-01	8.90E-01
8003158	NM_020947	KIAA1609	KIAA1609	L359V only	1.34	1.37	1.17	1.21	6.14E-02	3.39E-02	8.02E-01	6.73E-01
7915882	NM_014774	KIAA0494	KIAA0494	L359V only	1.28	1.37	0.99	1.09	1.13E-01	3.41E-02	9.94E-01	1.00E+00
7960642	NM_032489	ACRBP	acrosin binding protein	L359V only	1.24	1.37	1.18	1.17	2.11E-01	4.95E-02	8.13E-01	9.49E-01
8150276	NM_001102559	PPAPDC1B	phosphatidic acid phosphatase type 2 domain containing 1B	L359V only	1.23	1.37	1.03	1.07	2.08E-01	3.76E-02	9.73E-01	1.00E+00

7960947	NM_000014	A2M	alpha-2-macroglobulin	L359V only	1.02	1.37	1.04	1.11	9.15E-01	1.54E-02	9.50E-01	1.00E+00
7997498	---			L359V only	1.08	1.37	1.19	1.15	7.03E-01	3.93E-02	7.79E-01	1.00E+00
7921179	NM_198236	ARHGEF11	Rho guanine nucleotide exchange factor (GEF) 11	L359V only	1.26	1.37	1.05	1.05	1.03E-01	2.21E-02	9.31E-01	1.00E+00
8012423	NM_025099	C17orf68	chromosome 17 open reading frame 68	L359V only	1.09	1.37	0.98	1.03	4.84E-01	7.89E-03	9.78E-01	1.00E+00
8073214	NM_001024843	TNRC6B	trinucleotide repeat containing 6B	L359V only	1.22	1.37	1.03	1.10	8.73E-02	8.79E-03	9.57E-01	1.00E+00
8099438	---			L359V only	0.91	1.37	0.94	1.01	5.97E-01	2.55E-02	9.22E-01	1.00E+00
8128716	NM_006016	CD164	CD164 molecule, sialomucin	L359V only	1.19	1.37	1.20	1.20	1.18E-01	6.74E-03	4.31E-01	3.37E-01
8064557	AK293638	FAM113A	family with sequence similarity 113, member A	L359V only	1.11	1.37	1.04	1.09	5.52E-01	2.96E-02	9.47E-01	1.00E+00
8075365	NM_001017981	RNF215	ring finger protein 215	L359V only	1.22	1.37	1.11	1.15	2.11E-01	3.74E-02	8.64E-01	9.69E-01
8016159	NM_024819	DCAKD	dephospho-CoA kinase domain containing	L359V only	1.10	1.37	1.05	1.03	4.66E-01	1.09E-02	9.27E-01	1.00E+00
7978066	NM_003917	AP1G2	adaptor-related protein complex 1, gamma 2 subunit	L359V only	1.14	1.36	1.04	1.03	2.84E-01	9.48E-03	9.43E-01	1.00E+00
7997662	NM_014732	KIAA0513	KIAA0513	L359V only	0.99	1.36	0.99	1.06	9.59E-01	3.36E-02	9.95E-01	1.00E+00
8155490	AK292642	LOC554249	hypothetical LOC554249	L359V only	1.17	1.36	1.11	1.12	2.93E-01	2.42E-02	8.45E-01	1.00E+00
8015635	NM_012232	PTRF	polymerase I and transcript release factor	L359V only	1.24	1.36	1.16	1.22	1.24E-01	2.32E-02	7.97E-01	5.00E-01
8121461	NM_015891	CDC40	cell division cycle 40 homolog (S. cerevisiae)	L359V only	0.95	1.36	0.93	1.06	7.70E-01	1.12E-02	8.76E-01	1.00E+00
8077123	NM_152247	CPT1B	carnitine palmitoyltransferase 1B (muscle)	L359V only	1.26	1.36	1.15	1.12	6.64E-02	1.33E-02	7.66E-01	9.88E-01
7917954	NM_001013660	FRRS1	ferric-chelate reductase 1	L359V only	1.22	1.36	1.04	1.14	1.28E-01	1.49E-02	9.46E-01	8.38E-01
8012539	NM_001010855	PIK3R6	phosphoinositide-3-kinase, regulatory subunit 6	L359V only	0.98	1.36	1.01	1.00	9.21E-01	8.26E-03	9.85E-01	1.00E+00
7915870	NM_022745	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	L359V only	1.24	1.36	1.07	1.16	1.66E-01	3.36E-02	9.02E-01	8.90E-01
8031992	AK294679	tcag7.907	hypothetical LOC402483	L359V only	1.02	1.36	1.11	1.06	9.34E-01	1.17E-02	8.30E-01	1.00E+00
8052024	NM_025133	FBXO11	F-box protein 11	L359V only	1.28	1.36	1.09	1.16	5.02E-02	1.37E-02	8.52E-01	6.98E-01
8140967	NM_017654	SAMD9	sterile alpha motif domain containing 9	L359V only	1.27	1.36	1.00	1.10	1.30E-01	4.07E-02	9.99E-01	1.00E+00
8012054	NM_001365	DLG4	discs, large homolog 4 (Drosophila)	L359V only	1.29	1.36	1.21	1.15	1.22E-01	4.72E-02	7.38E-01	9.88E-01
8083569	NM_015508	TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	L359V only	1.00	1.36	0.83	1.01	9.88E-01	2.30E-02	6.17E-01	1.00E+00
7963235	NM_030809	CSRNP2	cysteine-serine-rich nuclear protein 2	L359V only	1.23	1.36	1.10	1.07	1.15E-01	1.67E-02	8.53E-01	1.00E+00
7961381	NM_006143	GPR19	G protein-coupled receptor 19	L359V only	1.28	1.36	1.18	1.20	7.57E-02	2.42E-02	7.28E-01	6.19E-01
8165046	NM_015447	CAMSAP1	calmodulin regulated spectrin-associated protein 1	L359V only	1.01	1.36	0.99	1.06	9.81E-01	1.60E-02	9.83E-01	1.00E+00
7956470	NM_052897	MBD6	methyl-CpG binding domain protein 6	L359V only	1.16	1.36	1.15	1.09	3.22E-01	2.46E-02	8.01E-01	1.00E+00
8118100	NM_000247	MICA	MHC class I polypeptide-related sequence A	L359V only	1.27	1.35	1.10	1.15	1.51E-01	4.88E-02	8.78E-01	1.00E+00
8123006	NM_003898	SYNJ2	synaptojanin 2	L359V only	0.87	1.35	0.83	0.94	4.21E-01	4.55E-02	7.47E-01	1.00E+00
8083090	NM_001080412	ZBTB38	zinc finger and BTB domain containing 38	L359V only	1.08	1.35	0.94	1.09	7.13E-01	4.43E-02	9.28E-01	1.00E+00
7937438	NM_174940	TMEM80	transmembrane protein 80	L359V only	1.08	1.35	1.16	1.12	6.38E-01	2.19E-02	7.74E-01	9.88E-01
7947801	NM_016223	PACSIN3	protein kinase C and casein kinase substrate in neurons 3	L359V only	1.10	1.35	1.16	1.15	5.16E-01	2.05E-02	7.53E-01	8.06E-01
8064100	BC002531	C20orf149	chromosome 20 open reading frame 149	L359V only	1.05	1.35	1.06	0.98	8.12E-01	4.45E-02	9.33E-01	1.00E+00
8026250	NM_138353	LOC90379	hypothetical protein BC002926	L359V only	1.15	1.35	1.05	1.03	3.22E-01	2.05E-02	9.36E-01	1.00E+00
8028030	NM_052948	SNX26	sorting nexin 26	L359V only	1.21	1.35	1.12	1.11	1.83E-01	2.92E-02	8.38E-01	1.00E+00
8031516	NM_016202	ZNF580	zinc finger protein 580	L359V only	1.17	1.35	1.05	1.08	2.70E-01	2.51E-02	9.30E-01	1.00E+00
8145027	NM_022749	FAM160B2	family with sequence similarity 160, member B2	L359V only	1.26	1.35	1.13	1.11	7.08E-02	1.76E-02	8.13E-01	1.00E+00
8154563	NM_001010887	ACER2	alkaline ceramidase 2	L359V only	1.19	1.35	1.10	1.12	2.36E-01	2.84E-02	8.70E-01	1.00E+00
8092514	NM_022149	MAGEF1	melanoma antigen family F, 1	L359V only	1.21	1.35	1.15	1.15	1.17E-01	1.48E-02	7.52E-01	7.32E-01
8074106	NM_138433	KLHDC7B	kelch domain containing 7B	L359V only	1.11	1.35	1.23	1.17	4.91E-01	2.30E-02	5.20E-01	7.04E-01
8044563	NM_032556	IL1F10	interleukin 1 family, member 10 (theta)	L359V only	1.09	1.35	1.12	1.11	6.15E-01	2.85E-02	8.36E-01	1.00E+00
7912239	NM_024980	GPR157	G protein-coupled receptor 157	L359V only	1.21	1.34	1.12	1.16	2.20E-01	3.76E-02	8.43E-01	8.78E-01
7911591	NM_001110781	RP11-345P4.4	similar to solute carrier family 35, member E2	L359V only	1.16	1.34	1.07	1.11	1.93E-01	1.10E-02	8.83E-01	9.54E-01
7970441	NM_004004	GJB2	gap junction protein, beta 2, 26kDa	L359V only	1.34	1.34	1.41	1.22	5.44E-02	3.94E-02	1.57E-01	5.85E-01
7953622	AY358730	UNQ2963	hypothetical protein LOC283314	L359V only	1.21	1.34	1.01	1.09	2.42E-01	4.42E-02	9.87E-01	1.00E+00
7998434	NM_003294	TPSAB1	tryptase alpha	L359V only	1.06	1.34	1.06	1.08	8.06E-01	4.95E-02	9.26E-01	1.00E+00
8033956	NM_004230	S1PR2	sphingosine-1-phosphate receptor 2	L359V only	1.14	1.34	1.12	1.11	3.50E-01	2.12E-02	8.25E-01	1.00E+00
8075709	NM_030643	APOL4	apolipoprotein L, 4	L359V only	1.24	1.34	0.97	1.11	1.39E-01	3.25E-02	9.58E-01	1.00E+00
7984569	NM_017691	LRRC49	leucine rich repeat containing 49	L359V only	1.25	1.34	0.93	1.08	1.04E-01	2.74E-02	8.90E-01	1.00E+00
7980983	NM_022151	MOAP1	modulator of apoptosis 1	L359V only	1.24	1.34	1.13	1.16	6.71E-02	1.17E-02	7.79E-01	6.27E-01
8082100	NM_017554	PARP14	poly (ADP-ribose) polymerase family, member 14	L359V only	1.24	1.34	0.85	1.05	1.77E-01	4.96E-02	7.97E-01	1.00E+00
7973158	NM_018071	FLJ10357	hypothetical protein FLJ10357	L359V only	1.09	1.34	0.95	1.04	6.02E-01	2.46E-02	9.28E-01	1.00E+00
8172280	NM_032591	SLC9A7	solute carrier family 9 (sodium hydrogen exchanger), member 7	L359V only	1.14	1.34	1.08	1.11	4.45E-01	4.23E-02	8.94E-01	1.00E+00
8014871	NM_033419	PERLD1	per1-like domain containing 1	L359V only	1.28	1.34	1.01	1.12	1.06E-01	4.23E-02	9.86E-01	1.00E+00
8131709	NM_003112	SP4	Sp4 transcription factor	L359V only	1.16	1.34	1.02	1.06	2.26E-01	1.30E-02	9.72E-01	1.00E+00
7963721	NM_020898	CALCOCO1	calcium binding and coiled-coil domain 1	L359V only	1.25	1.34	1.13	1.14	1.39E-01	4.07E-02	8.36E-01	1.00E+00
8086706	NM_014159	SETD2	SET domain containing 2	L359V only	1.24	1.34	1.00	1.07	7.45E-02	1.61E-02	9.97E-01	1.00E+00
8174692	NM_145799	SEPT6	septin 6	L359V only	1.00	1.33	1.01	1.06	9.99E-01	2.06E-02	9.94E-01	1.00E+00
8168557	NM_003022	SH3BGRL	SH3 domain binding glutamic acid-rich protein like	L359V only	1.25	1.33	1.08	1.16	6.42E-02	1.47E-02	8.75E-01	6.28E-01
7939767	NM_003682	MADD	MAP-kinase activating death domain	L359V only	1.20	1.33	1.02	1.06	1.46E-01	1.91E-02	9.80E-01	1.00E+00
8154934	NM_147162	IL11RA	interleukin 11 receptor, alpha	L359V only	1.15	1.33	0.99	1.08	2.95E-01	2.09E-02	9.84E-01	1.00E+00
8155550	AK292642	LOC554249	hypothetical LOC554249	L359V only	1.28	1.33	1.12	1.16	9.21E-02	4.08E-02	8.41E-01	8.90E-01
8118915	NM_003427	ZNF76	zinc finger protein 76 (expressed in testis)	L359V only	1.12	1.33	1.02	1.08	5.03E-01	4.65E-02	9.78E-01	1.00E+00
7925851	NM_014023	WDR37	WD repeat domain 37	L359V only	0.96	1.33	0.95	1.03	8.21E-01	3.24E-02	9.29E-01	1.00E+00

8017186	NM_022070	HEATR6	HEAT repeat containing 6	L359V only	1.11	1.33	0.97	1.08	4.24E-01	1.59E-02	9.52E-01	1.00E+00
8150881	NM_002655	PLAG1	pleiomorphic adenoma gene 1	L359V only	1.14	1.33	1.10	1.15	3.96E-01	3.19E-02	8.59E-01	8.78E-01
7980338	NM_024496	C14orf4	chromosome 14 open reading frame 4	L359V only	1.06	1.33	0.99	1.04	7.54E-01	2.48E-02	9.84E-01	1.00E+00
8169920	NM_016024	RBMX2	RNA binding motif protein, X-linked 2	L359V only	1.01	1.33	1.05	1.08	9.72E-01	3.07E-02	9.27E-01	1.00E+00
7901479	NM_024646	ZYG11B	zyg-11 homolog B (C. elegans)	L359V only	1.26	1.33	1.04	1.12	1.25E-01	4.53E-02	9.55E-01	1.00E+00
7997247	NM_032268	ZNRF1	zinc and ring finger 1	L359V only	1.17	1.33	1.08	1.08	2.60E-01	2.55E-02	8.83E-01	1.00E+00
7970844	NM_001014380	KATNAL1	katanin p60 subunit A-like 1	L359V only	1.24	1.33	1.02	1.10	1.44E-01	4.07E-02	9.82E-01	1.00E+00
8029831	NM_005184	CALM3	calmodulin 3 (phosphorylase kinase, delta)	L359V only	1.19	1.33	1.09	1.07	9.51E-02	8.88E-03	8.36E-01	1.00E+00
7975889	NM_014909	VASH1	vasohibin 1	L359V only	1.04	1.33	0.98	1.05	8.33E-01	2.39E-02	9.73E-01	1.00E+00
8036956	NM_198476	C19orf54	chromosome 19 open reading frame 54	L359V only	1.16	1.33	1.07	1.02	1.88E-01	1.04E-02	8.77E-01	1.00E+00
7911754	NM_003820	TNFRSF14	tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator)	L359V only	1.06	1.33	0.99	1.02	6.94E-01	1.34E-02	9.91E-01	1.00E+00
7938364	BX641032	WEE1	WEE1 homolog (S. pombe)	L359V only	1.30	1.33	1.12	1.16	6.26E-02	3.25E-02	8.34E-01	7.91E-01
8017262	NM_032043	BRIP1	BRCA1 interacting protein C-terminal helicase 1	L359V only	1.22	1.33	0.99	1.14	1.17E-01	2.26E-02	9.92E-01	8.41E-01
8037621	NM_012155	EML2	echinoderm microtubule associated protein like 2	L359V only	1.24	1.32	1.15	1.12	7.84E-02	2.02E-02	7.46E-01	9.81E-01
7929288	NM_019053	EXOC6	exocyst complex component 6	L359V only	1.20	1.32	0.99	1.12	1.22E-01	1.62E-02	9.81E-01	8.90E-01
8047443	NM_018571	STRADB	STE20-related kinase adaptor beta	L359V only	1.19	1.32	1.00	1.11	2.33E-01	4.22E-02	9.99E-01	1.00E+00
8102862	NM_018717	MAML3	mastermind-like 3 (Drosophila)	L359V only	1.12	1.32	0.92	1.02	4.39E-01	2.55E-02	8.70E-01	1.00E+00
7989680	NM_025049	PIF1	PIF1 5'-to-3' DNA helicase homolog (S. cerevisiae)	L359V only	1.17	1.32	1.13	1.12	2.58E-01	2.69E-02	8.11E-01	1.00E+00
7998381	NM_022773	LMF1	lipase maturation factor 1	L359V only	1.16	1.32	1.13	1.12	2.67E-01	2.46E-02	8.14E-01	9.89E-01
7955195	NM_005480	TROAP	trophinin associated protein (tastin)	L359V only	1.23	1.32	1.16	1.09	9.34E-02	2.22E-02	7.36E-01	1.00E+00
8156116	NM_001001551	C9orf103	chromosome 9 open reading frame 103	L359V only	1.14	1.32	0.99	1.09	3.95E-01	4.16E-02	9.89E-01	1.00E+00
7957549	---			L359V only	1.19	1.32	1.11	1.06	1.93E-01	2.91E-02	8.38E-01	1.00E+00
8015946	NM_178542	C17orf65	chromosome 17 open reading frame 65	L359V only	1.24	1.32	1.10	1.10	1.15E-01	3.02E-02	8.61E-01	1.00E+00
8078898	NM_017875	SLC25A38	solute carrier family 25, member 38	L359V only	1.23	1.32	1.29	1.19	1.80E-01	4.98E-02	4.14E-01	7.37E-01
8081431	NM_001627	ALCAM	activated leukocyte cell adhesion molecule	L359V only	1.06	1.32	0.99	1.10	7.00E-01	1.84E-02	9.85E-01	1.00E+00
8060370	NM_031424	FAM110A	family with sequence similarity 110, member A	L359V only	1.28	1.32	1.24	1.18	8.37E-02	4.23E-02	5.21E-01	7.37E-01
8010050	BC035511	FAM100B	family with sequence similarity 100, member B	L359V only	1.24	1.32	1.22	1.16	9.33E-02	2.66E-02	5.08E-01	7.09E-01
7955168	---			L359V only	1.01	1.31	1.07	1.07	9.83E-01	4.60E-02	9.02E-01	1.00E+00
8036862	AY358191	UNQ6167	NINP6167	L359V only	0.98	1.31	1.04	1.04	9.23E-01	4.32E-02	9.54E-01	1.00E+00
8050894	NM_002254	KIF3C	kinesin family member 3C	L359V only	1.17	1.31	1.03	1.03	2.87E-01	4.29E-02	9.72E-01	1.00E+00
7940891	NM_005528	DNAJC4	DnaJ (Hsp40) homolog, subfamily C, member 4	L359V only	1.28	1.31	1.16	1.14	6.36E-02	2.91E-02	7.50E-01	8.90E-01
7944049	NM_001040455	SIDT2	SID1 transmembrane family, member 2	L359V only	1.26	1.31	1.13	1.14	8.32E-02	2.94E-02	8.19E-01	8.92E-01
8162177	---			L359V only	1.03	1.31	0.98	1.05	8.87E-01	1.74E-02	9.72E-01	1.00E+00
8008052	NM_003110	SP2	Sp2 transcription factor	L359V only	1.19	1.31	1.01	1.02	2.21E-01	3.59E-02	9.90E-01	1.00E+00
8091141	NM_019001	XRN1	5'-3' exoribonuclease 1	L359V only	1.31	1.31	1.00	1.11	6.04E-02	4.27E-02	9.97E-01	1.00E+00
7956978	NM_018656	SLC35E3	solute carrier family 35, member E3	L359V only	1.19	1.31	1.07	1.13	2.08E-01	3.60E-02	9.02E-01	9.81E-01
8085138	NM_000916	OXTR	oxytocin receptor	L359V only	1.16	1.31	1.21	1.13	3.08E-01	4.08E-02	6.28E-01	1.00E+00
8027128	NM_178526	SLC25A42	solute carrier family 25, member 42	L359V only	1.23	1.31	1.13	1.11	8.31E-02	2.14E-02	8.01E-01	9.81E-01
8139656	NM_001001555	GRB10	growth factor receptor-bound protein 10	L359V only	1.21	1.31	1.13	1.17	1.32E-01	2.53E-02	8.01E-01	6.47E-01
7976350	NM_020818	KIAA1409	KIAA1409	L359V only	1.13	1.31	1.10	1.12	3.96E-01	3.21E-02	8.49E-01	9.94E-01
8174207	NM_022052	NXF3	nuclear RNA export factor 3	L359V only	0.85	1.31	0.87	1.05	2.80E-01	4.22E-02	8.01E-01	1.00E+00
8165833	NM_001011719	ARSH	arylsulfatase family, member H	L359V only	1.05	1.31	1.08	1.11	8.00E-01	3.44E-02	8.80E-01	1.00E+00
7998233	NM_021259	TMEM8	transmembrane protein 8 (five membrane-spanning domains)	L359V only	1.12	1.31	1.02	0.97	4.32E-01	2.99E-02	9.76E-01	1.00E+00
8140129	NM_148912	ABHD11	abhydrolase domain containing 11	L359V only	1.13	1.31	1.03	1.06	4.09E-01	4.18E-02	9.62E-01	1.00E+00
8074286	NM_015241	MICAL3	microtubule associated monoxygenase, calponin and LIM domain containing 3	L359V only	1.16	1.31	0.98	1.06	3.18E-01	4.96E-02	9.78E-01	1.00E+00
8007730	NM_001135704	ACBD4	acyl-Coenzyme A binding domain containing 4	L359V only	1.21	1.31	1.03	1.10	8.89E-02	1.70E-02	9.59E-01	9.92E-01
8080714	NM_001457	FLNB	filamin B, beta (actin binding protein 278)	L359V only	1.13	1.31	1.06	1.07	3.31E-01	1.82E-02	8.93E-01	1.00E+00
7966517	NM_001109662	C12orf51	chromosome 12 open reading frame 51	L359V only	1.20	1.30	0.96	1.07	1.52E-01	2.64E-02	9.39E-01	1.00E+00
8177834	NM_024909	C6orf134	chromosome 6 open reading frame 134	L359V only	1.23	1.30	1.12	1.08	1.37E-01	4.22E-02	8.36E-01	1.00E+00
7931081	NM_021622	PLEKHA1	pleckstrin homology domain containing, family A (phosphoinositide binding specific)	L359V only	1.17	1.30	1.10	1.10	1.83E-01	2.17E-02	8.36E-01	1.00E+00
7950271	EF363480	FAM168A	family with sequence similarity 168, member A	L359V only	1.21	1.30	1.07	1.10	9.47E-02	1.96E-02	8.79E-01	1.00E+00
8043055	NM_001370	DNAH6	dynein, axonemal, heavy chain 6	L359V only	1.02	1.30	1.10	1.11	9.15E-01	4.77E-02	8.58E-01	1.00E+00
8085556	NM_004844	SH3BP5	SH3-domain binding protein 5 (BTK-associated)	L359V only	1.17	1.30	0.96	1.08	2.42E-01	3.46E-02	9.38E-01	1.00E+00
8015412	NM_002230	JUP	junction plakoglobin	L359V only	1.21	1.30	1.13	1.10	1.57E-01	3.33E-02	8.14E-01	1.00E+00
8043666	NM_017623	CNNM3	cyclin M3	L359V only	1.09	1.30	0.93	0.94	5.91E-01	3.98E-02	8.83E-01	1.00E+00
8125220	NM_005510	DOM3Z	dom-3 homolog Z (C. elegans)	L359V only	1.08	1.30	1.14	1.08	6.13E-01	3.56E-02	8.11E-01	1.00E+00
8178699	NM_005510	DOM3Z	dom-3 homolog Z (C. elegans)	L359V only	1.08	1.30	1.14	1.08	6.13E-01	3.56E-02	8.11E-01	1.00E+00
8172056	NM_000328	RPGR	retinitis pigmentosa GTPase regulator	L359V only	1.24	1.30	1.24	1.22	1.26E-01	4.43E-02	5.03E-01	5.05E-01
8050548	NM_014713	LAPTM4A	lysosomal protein transmembrane 4 alpha	L359V only	1.21	1.30	1.07	1.10	1.59E-01	3.70E-02	8.86E-01	1.00E+00
8173217	NM_015185	ARHGEF9	Cdc42 guanine nucleotide exchange factor (GEF) 9	L359V only	1.17	1.30	1.08	1.07	2.63E-01	4.08E-02	8.86E-01	1.00E+00
8179926	NM_005510	DOM3Z	dom-3 homolog Z (C. elegans)	L359V only	1.05	1.30	1.12	1.06	7.90E-01	4.93E-02	8.36E-01	1.00E+00
7940210	NM_173801	PLAC1L	placenta-specific 1-like	L359V only	0.91	1.30	0.99	1.01	5.19E-01	4.17E-02	9.95E-01	1.00E+00
7897561	NM_015074	KIF1B	kinesin family member 1B	L359V only	1.10	1.30	1.08	1.10	4.51E-01	1.94E-02	8.56E-01	1.00E+00
8009796	NM_014738	KIAA0195	KIAA0195	L359V only	1.12	1.30	1.03	1.06	2.90E-01	1.37E-02	9.41E-01	1.00E+00
8111271	NM_016279	CDH9	cadherin 9, type 2 (T1-cadherin)	L359V only	1.19	1.29	1.26	1.17	2.10E-01	4.26E-02	3.99E-01	7.32E-01

8107474	NM_005509	DMXL1	Dmx-like 1	L359V only	1.25	1.29	1.12	1.14	5.13E-02	2.10E-02	8.06E-01	7.47E-01
7902353	NM_001001933	LHX8	LIM homeobox 8	L359V only	1.06	1.29	1.03	1.08	7.31E-01	4.83E-02	9.64E-01	1.00E+00
8147221	NM_004337	OSGIN2	oxidative stress induced growth inhibitor family member 2	L359V only	1.28	1.29	1.01	1.09	6.36E-02	4.08E-02	9.93E-01	1.00E+00
8104590	AK129556	LOC100130744	hypothetical LOC100130744	L359V only	1.22	1.29	1.04	1.03	1.49E-01	4.37E-02	9.43E-01	1.00E+00
8117965	NM_024909	C6orf134	chromosome 6 open reading frame 134	L359V only	1.24	1.29	1.13	1.09	1.17E-01	4.58E-02	8.14E-01	1.00E+00
8179149	NM_024909	C6orf134	chromosome 6 open reading frame 134	L359V only	1.24	1.29	1.13	1.09	1.17E-01	4.58E-02	8.14E-01	1.00E+00
8159945	NM_016282	AK3	adenylate kinase 3	L359V only	1.21	1.29	1.14	1.16	1.20E-01	2.81E-02	7.79E-01	6.40E-01
8086961	NM_004567	PFKFB4	6-phosphofructo-2-kinase	L359V only	0.98	1.29	0.96	1.03	9.38E-01	3.09E-02	9.43E-01	1.00E+00
8178399	NM_007243	NRM	nurim (nuclear envelope membrane protein)	L359V only	1.12	1.29	1.02	1.05	4.58E-01	4.84E-02	9.77E-01	1.00E+00
8179683	NM_007243	NRM	nurim (nuclear envelope membrane protein)	L359V only	1.12	1.29	1.02	1.05	4.58E-01	4.84E-02	9.77E-01	1.00E+00
8037657	NM_004409	DMPK	dystrophia myotonica-protein kinase	L359V only	1.15	1.29	1.03	1.09	2.19E-01	2.09E-02	9.46E-01	1.00E+00
8128737	NM_022765	MICAL1	microtubule associated monoxygenase, calponin and LIM domain containing 1	L359V only	1.15	1.29	1.20	1.12	2.13E-01	2.08E-02	4.84E-01	8.90E-01
8035271	NM_024527	ABHD8	abhydrolase domain containing 8	L359V only	1.20	1.29	1.07	1.12	1.84E-01	4.82E-02	8.94E-01	1.00E+00
8093456	NM_052861	C4orf42	chromosome 4 open reading frame 42	L359V only	1.14	1.29	1.02	1.00	3.16E-01	2.85E-02	9.73E-01	1.00E+00
7974771	NM_022495	C14orf135	chromosome 14 open reading frame 135	L359V only	1.05	1.29	0.99	1.09	7.85E-01	3.45E-02	9.94E-01	1.00E+00
7991779	NM_032039	ITFG3	integrin alpha FG-GAP repeat containing 3	L359V only	1.11	1.29	1.08	1.08	4.35E-01	3.43E-02	8.73E-01	1.00E+00
8161114	NM_020944	GBA2	glucosidase, beta (bile acid) 2	L359V only	1.26	1.29	1.00	1.01	6.47E-02	3.39E-02	9.97E-01	1.00E+00
7900633	---			L359V only	1.01	1.29	1.23	1.11	9.76E-01	3.33E-02	4.49E-01	9.92E-01
7996012	NM_012106	ARL2BP	ADP-ribosylation factor-like 2 binding protein	L359V only	1.17	1.29	1.05	1.08	2.54E-01	4.86E-02	9.36E-01	1.00E+00
7935660	NM_015221	DNMBP	dynamin binding protein	L359V only	1.20	1.29	0.97	1.08	1.10E-01	2.09E-02	9.52E-01	1.00E+00
8101701	NM_152542	PPM1K	protein phosphatase 1K (PP2C domain containing)	L359V only	1.26	1.28	1.09	1.14	6.97E-02	3.67E-02	8.56E-01	8.61E-01
7956097	NM_000456	SUOX	sulfite oxidase	L359V only	1.29	1.28	1.17	1.07	5.54E-02	4.71E-02	7.38E-01	1.00E+00
8148270	NM_005005	NDUFB9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa	L359V only	1.16	1.28	1.01	1.08	2.07E-01	2.79E-02	9.92E-01	1.00E+00
7942697	NM_004055	CAPN5	calpain 5	L359V only	1.07	1.28	1.04	1.07	6.97E-01	4.85E-02	9.38E-01	1.00E+00
7936968	NM_003474	ADAM12	ADAM metallopeptidase domain 12	L359V only	1.14	1.28	1.15	1.12	2.90E-01	2.81E-02	7.40E-01	8.78E-01
7935780	NM_015490	SEC31B	SEC31 homolog B (S. cerevisiae)	L359V only	1.01	1.28	1.04	1.04	9.64E-01	4.84E-02	9.39E-01	1.00E+00
7919971	NM_000449	RFX5	regulatory factor X, 5 (influences HLA class II expression)	L359V only	1.25	1.28	1.08	1.15	7.93E-02	3.75E-02	8.70E-01	7.48E-01
8172088	NM_001123385	BCOR	BCL6 co-repressor	L359V only	1.28	1.28	1.06	1.07	5.02E-02	3.89E-02	9.07E-01	1.00E+00
8114083	NM_014423	AFF4	AF4	L359V only	1.24	1.28	1.02	1.10	6.28E-02	2.84E-02	9.76E-01	1.00E+00
8085000	NM_032773	LRCH3	leucine-rich repeats and calponin homology (CH) domain containing 3	L359V only	1.25	1.28	0.99	1.10	5.88E-02	2.99E-02	9.83E-01	1.00E+00
8141445	BC015722	C7orf43	chromosome 7 open reading frame 43	L359V only	1.06	1.28	1.04	1.02	7.16E-01	3.84E-02	9.39E-01	1.00E+00
7977841	BC001916	C14orf94	chromosome 14 open reading frame 94	L359V only	1.18	1.28	1.04	1.14	1.84E-01	3.62E-02	9.39E-01	8.21E-01
7975705	NM_194279	ISCA2	iron-sulfur cluster assembly 2 homolog (S. cerevisiae)	L359V only	1.14	1.28	1.05	1.08	3.05E-01	3.61E-02	9.29E-01	1.00E+00
8047839	NM_004379	CREB1	cAMP responsive element binding protein 1	L359V only	1.21	1.28	0.99	1.10	7.34E-02	1.81E-02	9.83E-01	9.81E-01
8044959	---			L359V only	1.05	1.28	1.06	1.09	7.34E-01	1.75E-02	8.80E-01	1.00E+00
8069399	NM_015151	DIP2A	DIP2 disco-interacting protein 2 homolog A (Drosophila)	L359V only	1.09	1.28	1.01	1.05	5.63E-01	3.37E-02	9.90E-01	1.00E+00
8029642	NM_031417	MARK4	MAP microtubule affinity-regulating kinase 4	L359V only	1.12	1.27	1.13	1.05	3.68E-01	3.03E-02	7.97E-01	1.00E+00
8130827	AB016899	C6orf54	chromosome 6 open reading frame 54	L359V only	1.22	1.27	1.03	1.09	1.19E-01	4.19E-02	9.51E-01	1.00E+00
8036938	NM_024876	ADCK4	aarF domain containing kinase 4	L359V only	1.23	1.27	1.16	1.13	7.63E-02	2.95E-02	6.86E-01	8.21E-01
7984203	NM_015042	ZNF609	zinc finger protein 609	L359V only	1.18	1.27	1.07	1.04	1.75E-01	3.23E-02	8.84E-01	1.00E+00
8022646	NM_001136205	KCTD1	potassium channel tetramerisation domain containing 1	L359V only	1.05	1.27	1.21	1.11	7.66E-01	4.61E-02	5.33E-01	1.00E+00
8065832	NM_015638	TRPC4AP	transient receptor potential cation channel, subfamily C, member 4 associated protei	L359V only	1.13	1.27	1.09	1.13	4.00E-01	4.90E-02	8.63E-01	9.05E-01
8018449	NM_199242	UNC13D	unc-13 homolog D (C. elegans)	L359V only	1.03	1.27	1.03	1.00	8.96E-01	3.56E-02	9.55E-01	1.00E+00
8009443	NM_014960	ARSG	arylsulfatase G	L359V only	1.22	1.27	1.11	1.12	8.21E-02	2.84E-02	8.23E-01	8.78E-01
7946180	NM_006458	TRIM3	tripartite motif-containing 3	L359V only	1.14	1.27	1.21	1.15	3.09E-01	4.23E-02	5.00E-01	7.32E-01
7955078	NM_000289	PFKM	phosphofructokinase, muscle	L359V only	1.07	1.27	1.04	1.07	6.71E-01	4.93E-02	9.43E-01	1.00E+00
8171024	AK127459	LOC401622	similar to LINE-1 reverse transcriptase homolog	L359V only	1.13	1.27	0.94	1.05	3.14E-01	3.74E-02	8.92E-01	1.00E+00
7994889	NM_006662	SRCAP	Snf2-related CREBBP activator protein	L359V only	1.08	1.27	1.00	0.97	6.06E-01	4.83E-02	9.99E-01	1.00E+00
8158269	NM_002540	ODF2	outer dense fiber of sperm tails 2	L359V only	0.94	1.27	0.95	1.05	6.73E-01	2.87E-02	8.99E-01	1.00E+00
8028016	NM_001039887	C19orf55	chromosome 19 open reading frame 55	L359V only	1.03	1.26	1.08	1.03	8.53E-01	2.88E-02	8.60E-01	1.00E+00
7933509	NM_000124	ERCC6	excision repair cross-complementing rodent repair deficiency, complementation grou	L359V only	1.12	1.26	0.98	1.07	3.63E-01	4.22E-02	9.64E-01	1.00E+00
7994506	NM_032815	NFATC2IP	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting	L359V only	1.12	1.26	1.01	1.04	3.27E-01	2.85E-02	9.83E-01	1.00E+00
8071185	NR_002733	DGCR5	DiGeorge syndrome critical region gene 5 (non-protein coding)	L359V only	0.95	1.26	1.07	1.07	7.69E-01	4.61E-02	8.81E-01	1.00E+00
8007799	AK295559	CRHR1	corticotropin releasing hormone receptor 1	L359V only	1.21	1.26	1.08	1.13	1.05E-01	3.97E-02	8.76E-01	8.60E-01
7964203	NM_013449	BAZ2A	bromodomain adjacent to zinc finger domain, 2A	L359V only	1.09	1.26	1.04	0.99	4.71E-01	3.06E-02	9.37E-01	1.00E+00
8167334	NM_000377	WAS	Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	L359V only	1.10	1.26	1.07	0.97	4.57E-01	4.43E-02	8.83E-01	1.00E+00
7947652	NM_017749	AMBRA1	autophagy	L359V only	1.14	1.26	1.13	1.07	2.76E-01	3.46E-02	7.82E-01	1.00E+00
7979849	NM_003861	WDR22	WD repeat domain 22	L359V only	1.15	1.26	1.00	1.08	2.02E-01	3.14E-02	9.94E-01	1.00E+00
7971950	NM_080759	DACH1	dachshund homolog 1 (Drosophila)	L359V only	1.08	1.25	1.05	1.01	5.91E-01	3.43E-02	9.15E-01	1.00E+00
8172538	NM_007075	WDR45	WD repeat domain 45	L359V only	1.15	1.25	1.14	1.14	2.41E-01	3.47E-02	7.51E-01	6.95E-01
8096333	---			L359V only	0.98	1.25	1.01	1.03	9.09E-01	3.91E-02	9.85E-01	1.00E+00
7999319	NM_014316	CARHSP1	calcium regulated heat stable protein 1, 24kDa	L359V only	1.24	1.25	1.05	1.07	7.55E-02	4.81E-02	9.22E-01	1.00E+00
8025255	NM_006949	STXBP2	syntaxin binding protein 2	L359V only	1.05	1.25	1.01	1.03	7.66E-01	4.61E-02	9.92E-01	1.00E+00
7972297	NM_005845	ABCC4	ATP-binding cassette, sub-family C (CFTR MRP), member 4	L359V only	1.04	1.25	0.94	1.05	8.09E-01	3.84E-02	8.94E-01	1.00E+00
7916986	NM_173808	NEGR1	neuronal growth regulator 1	L359V only	1.09	1.25	1.12	1.12	5.36E-01	3.89E-02	8.01E-01	8.47E-01

8081362	NM_024548	CEP97	centrosomal protein 97kDa	L359V only	1.26	1.25	1.04	1.11	5.03E-02	4.54E-02	9.44E-01	9.88E-01
7981046	NM_032036	IFI27L2	interferon, alpha-inducible protein 27-like 2	L359V only	1.19	1.25	1.10	1.08	1.47E-01	4.56E-02	8.38E-01	1.00E+00
7958202	NM_018413	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	L359V only	1.22	1.25	1.13	1.14	8.48E-02	4.39E-02	7.94E-01	7.89E-01
8000811	NM_001040056	MAPK3	mitogen-activated protein kinase 3	L359V only	1.12	1.25	1.09	1.06	3.59E-01	4.90E-02	8.59E-01	1.00E+00
8161618	NM_001163	APBA1	amyloid beta (A4) precursor protein-binding, family A, member 1	L359V only	1.14	1.24	1.21	1.15	2.46E-01	4.37E-02	4.33E-01	6.69E-01
8125360	NM_002586	PBX2	pre-B-cell leukemia homeobox 2	L359V only	1.23	1.24	1.05	1.06	5.89E-02	3.53E-02	9.12E-01	1.00E+00
8172119	NM_004229	MED14	mediator complex subunit 14	L359V only	1.13	1.24	1.04	1.04	2.89E-01	4.45E-02	9.39E-01	1.00E+00
7940824	NM_024771	NAT11	N-acetyltransferase 11 (GCN5-related, putative)	L359V only	1.07	1.24	1.02	1.00	6.36E-01	4.60E-02	9.71E-01	1.00E+00
8125713	NM_172208	TAPBP	TAP binding protein (tapasin)	L359V only	1.10	1.24	1.02	1.03	4.04E-01	3.58E-02	9.73E-01	1.00E+00
8009164	NM_005828	WDR68	WD repeat domain 68	L359V only	1.11	1.23	1.03	1.04	3.65E-01	3.77E-02	9.43E-01	1.00E+00
8048304	NM_021198	CTDSP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatas	L359V only	1.10	1.23	1.03	1.03	4.23E-01	4.96E-02	9.54E-01	1.00E+00
8129706	NM_006620	HBS1L	HBS1-like (S. cerevisiae)	L359V only	1.07	1.23	1.03	1.08	5.93E-01	4.02E-02	9.56E-01	1.00E+00
8179564	NM_002263	KIFC1	kinesin family member C1	L359V only	1.14	1.22	0.98	1.06	2.30E-01	4.64E-02	9.74E-01	1.00E+00
7952145	NM_006389	HYOU1	hypoxia up-regulated 1	L359V only	0.93	0.83	0.98	0.91	5.03E-01	4.84E-02	9.73E-01	9.88E-01
8145691	NM_005671	UBXN8	UBX domain protein 8	L359V only	0.92	0.82	0.86	0.93	4.93E-01	4.61E-02	5.99E-01	1.00E+00
7959070	NM_002567	PEBP1	phosphatidylethanolamine binding protein 1	L359V only	0.83	0.82	0.96	0.94	7.60E-02	4.23E-02	9.30E-01	1.00E+00
8156718	NM_002486	NCBP1	nuclear cap binding protein subunit 1, 80kDa	L359V only	0.89	0.81	0.92	0.93	2.76E-01	3.85E-02	8.38E-01	1.00E+00
8167797	NM_019067	GNL3L	guanine nucleotide binding protein-like 3 (nucleolar)-like	L359V only	0.81	0.81	0.90	0.92	5.21E-02	4.71E-02	8.02E-01	1.00E+00
7940781	NM_201428	RTN3	reticulon 3	L359V only	0.92	0.81	0.87	0.89	5.13E-01	4.85E-02	7.01E-01	8.12E-01
8128111	NM_016021	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	L359V only	0.88	0.81	0.92	0.92	2.80E-01	4.77E-02	8.52E-01	1.00E+00
8125941	NM_003137	SRPK1	SFRS protein kinase 1	L359V only	0.86	0.81	0.93	0.93	1.61E-01	4.31E-02	8.75E-01	1.00E+00
7971513	NM_001984	ESD	esterase D	L359V only	0.99	0.81	0.97	0.99	9.36E-01	3.88E-02	9.41E-01	1.00E+00
7962427	NM_031292	PUS7L	pseudouridylate synthase 7 homolog (S. cerevisiae)-like	L359V only	0.88	0.81	0.84	0.89	2.84E-01	4.16E-02	4.74E-01	8.60E-01
8105229	NM_015946	PELO	pelota homolog (Drosophila)	L359V only	0.86	0.81	0.92	0.88	1.99E-01	4.64E-02	8.53E-01	7.60E-01
8127824	NM_198920	UBE2CBP	ubiquitin-conjugating enzyme E2C binding protein	L359V only	0.96	0.81	0.93	0.94	7.98E-01	4.31E-02	8.76E-01	1.00E+00
8113689	---			L359V only	0.90	0.81	0.91	0.92	3.77E-01	4.58E-02	8.31E-01	1.00E+00
8046086	NM_203463	LASS6	LAG1 homolog, ceramide synthase 6	L359V only	0.81	0.81	0.87	0.90	6.67E-02	4.69E-02	7.38E-01	9.45E-01
8006123	NM_001304	CPD	carboxypeptidase D	L359V only	0.80	0.81	0.89	0.89	5.87E-02	4.57E-02	8.01E-01	8.78E-01
8071332	NM_002882	RANBP1	RAN binding protein 1	L359V only	0.83	0.80	0.92	0.91	1.00E-01	3.98E-02	8.38E-01	1.00E+00
8004497	NM_001416	EIF4A1	eukaryotic translation initiation factor 4A, isoform 1	L359V only	0.92	0.80	0.96	0.96	5.38E-01	3.80E-02	9.16E-01	1.00E+00
8059689	NM_005381	NCL	nucleolin	L359V only	0.89	0.80	0.95	0.95	2.92E-01	3.77E-02	9.01E-01	1.00E+00
7899134	NM_022778	CCDC21	coiled-coil domain containing 21	L359V only	0.90	0.80	0.94	0.93	4.01E-01	4.07E-02	8.92E-01	1.00E+00
7983350	NM_003758	EIF3J	eukaryotic translation initiation factor 3, subunit J	L359V only	0.89	0.80	0.91	0.91	3.10E-01	4.13E-02	8.36E-01	1.00E+00
8164665	NM_005312	RAPGEF1	Rap guanine nucleotide exchange factor (GEF) 1	L359V only	0.82	0.80	0.87	0.87	7.57E-02	3.93E-02	6.89E-01	6.27E-01
7989013	NM_016304	C15orf15	chromosome 15 open reading frame 15	L359V only	1.02	0.80	1.02	1.04	9.14E-01	4.84E-02	9.81E-01	1.00E+00
7985268	NM_000137	FAH	fumarylacetoacetate hydrolase (fumarylacetoacetase)	L359V only	0.84	0.80	0.85	0.88	1.18E-01	3.64E-02	6.04E-01	7.02E-01
8105191	NM_024615	PARP8	poly (ADP-ribose) polymerase family, member 8	L359V only	0.85	0.80	0.92	0.93	1.12E-01	2.45E-02	8.36E-01	1.00E+00
7975521	NM_021239	RBM25	RNA binding motif protein 25	L359V only	1.05	0.80	0.94	0.99	7.54E-01	3.20E-02	8.89E-01	1.00E+00
8019250	NM_000918	P4HB	prolyl 4-hydroxylase, beta polypeptide	L359V only	0.89	0.80	0.95	0.92	2.96E-01	2.64E-02	8.91E-01	1.00E+00
8098328	NM_017423	GALNT7	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferas	L359V only	0.89	0.80	0.89	0.89	3.54E-01	4.69E-02	8.13E-01	8.90E-01
8084951	NM_198565	LRRC33	leucine rich repeat containing 33	L359V only	0.86	0.80	0.91	0.86	2.07E-01	4.10E-02	8.38E-01	6.04E-01
8119993	NM_007355	HSP90AB1	heat shock protein 90kDa alpha (cytosolic), class B member 1	L359V only	0.85	0.80	0.90	0.91	1.44E-01	2.83E-02	8.13E-01	9.45E-01
7989023	NM_004580	RAB27A	RAB27A, member RAS oncogene family	L359V only	0.91	0.80	0.98	0.98	4.60E-01	3.97E-02	9.65E-01	1.00E+00
7935462	NM_016046	EXOSC1	exosome component 1	L359V only	0.92	0.80	0.93	0.94	5.85E-01	4.61E-02	8.76E-01	1.00E+00
8046848	NM_018471	ZC3H15	zinc finger CCCH-type containing 15	L359V only	0.87	0.80	0.93	0.96	1.95E-01	2.88E-02	8.64E-01	1.00E+00
8171747	NM_001412	EIF1AX	eukaryotic translation initiation factor 1A, X-linked	L359V only	0.89	0.80	0.94	0.92	2.69E-01	2.24E-02	8.70E-01	1.00E+00
8050695	NM_016047	SF3B14	splicing factor 3B, 14 kDa subunit	L359V only	0.95	0.80	0.97	0.94	6.86E-01	2.19E-02	9.40E-01	1.00E+00
8147483	NM_178812	MTDH	metadherin	L359V only	0.93	0.80	0.92	0.95	5.78E-01	3.72E-02	8.64E-01	1.00E+00
8094070	BC035655	C4orf23	chromosome 4 open reading frame 23	L359V only	0.86	0.79	0.90	0.89	2.28E-01	4.28E-02	8.25E-01	8.78E-01
8104760	NM_152295	TARS	threonyl-tRNA synthetase	L359V only	0.92	0.79	1.03	1.00	5.23E-01	4.03E-02	9.59E-01	1.00E+00
7924823	NM_023007	JMJD4	jumonji domain containing 4	L359V only	0.86	0.79	0.93	0.88	2.24E-01	4.34E-02	8.79E-01	8.36E-01
7916282	NM_004631	LRP8	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor	L359V only	0.80	0.79	0.90	0.87	6.80E-02	4.62E-02	8.36E-01	7.02E-01
8079140	NM_017719	SNRK	SNF related kinase	L359V only	0.93	0.79	0.91	0.94	6.59E-01	4.65E-02	8.41E-01	1.00E+00
8149673	NM_025232	REEP4	receptor accessory protein 4	L359V only	0.88	0.79	0.96	0.91	3.10E-01	4.31E-02	9.31E-01	1.00E+00
8026541	AF151902	FAM32A	family with sequence similarity 32, member A	L359V only	0.87	0.79	0.89	0.91	2.75E-01	4.44E-02	8.14E-01	1.00E+00
8151074	NM_002603	PDE7A	phosphodiesterase 7A	L359V only	1.09	0.79	0.98	0.98	5.43E-01	3.84E-02	9.76E-01	1.00E+00
7914750	BC034598	C1orf212	chromosome 1 open reading frame 212	L359V only	0.91	0.79	0.90	0.91	4.72E-01	3.46E-02	8.20E-01	1.00E+00
7983206	NM_014444	TUBGCP4	tubulin, gamma complex associated protein 4	L359V only	0.84	0.79	0.90	0.90	1.05E-01	2.57E-02	8.01E-01	8.65E-01
8128650	NM_007214	SEC63	SEC63 homolog (S. cerevisiae)	L359V only	0.90	0.79	0.94	0.96	3.98E-01	3.76E-02	8.93E-01	1.00E+00
7912670	NM_006004	UQCRH	ubiquinol-cytochrome c reductase hinge protein	L359V only	1.03	0.79	1.00	1.01	8.67E-01	3.56E-02	9.99E-01	1.00E+00
8052562	NM_006430	CCT4	chaperonin containing TCP1, subunit 4 (delta)	L359V only	0.89	0.79	0.95	0.93	2.95E-01	2.69E-02	8.93E-01	1.00E+00
7912198	NM_001428	ENO1	enolase 1, (alpha)	L359V only	0.81	0.79	0.92	0.88	8.84E-02	4.11E-02	8.64E-01	8.77E-01
8118661	NM_014260	PFDN6	prefoldin subunit 6	L359V only	0.85	0.79	0.93	0.89	2.11E-01	4.61E-02	8.77E-01	9.45E-01
8178270	NM_014260	PFDN6	prefoldin subunit 6	L359V only	0.85	0.79	0.93	0.89	2.11E-01	4.61E-02	8.77E-01	9.45E-01
8179559	NM_014260	PFDN6	prefoldin subunit 6	L359V only	0.85	0.79	0.93	0.89	2.11E-01	4.61E-02	8.77E-01	9.45E-01

8045946	NM_005805	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	L359V only	0.89	0.79	0.94	0.92	3.67E-01	4.12E-02	8.97E-01	1.00E+00
8046975	NM_032168	WDR75	WD repeat domain 75	L359V only	1.02	0.79	1.01	1.00	9.22E-01	2.91E-02	9.85E-01	1.00E+00
8089128	NM_014820	TOMM70A	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	L359V only	0.94	0.79	0.99	0.98	6.83E-01	3.14E-02	9.94E-01	1.00E+00
8134079	NM_033107	GTPBP10	GTP-binding protein 10 (putative)	L359V only	0.88	0.79	0.92	0.95	3.46E-01	4.38E-02	8.59E-01	1.00E+00
7950142	NM_030813	CLPB	ClpB caseinolytic peptidase B homolog (E. coli)	L359V only	0.86	0.79	0.95	0.89	2.21E-01	3.84E-02	9.09E-01	8.90E-01
7927536	NM_005437	NCOA4	nuclear receptor coactivator 4	L359V only	1.17	0.79	1.19	1.07	1.51E-01	2.48E-02	4.87E-01	1.00E+00
8177635	NM_003187	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	L359V only	0.88	0.79	0.96	0.93	3.08E-01	4.13E-02	9.45E-01	1.00E+00
7919226	NM_006468	POLR3C	polymerase (RNA) III (DNA directed) polypeptide C (62kD)	L359V only	0.86	0.79	0.90	0.93	2.07E-01	2.85E-02	8.19E-01	1.00E+00
8130567	NM_030752	TCP1	t-complex 1	L359V only	0.84	0.79	0.88	0.89	1.39E-01	3.63E-02	8.01E-01	8.90E-01
7927964	NM_002727	SRGN	serglycin	L359V only	0.94	0.79	1.07	0.95	7.04E-01	3.53E-02	8.80E-01	1.00E+00
7908022	NM_001357	DHX9	DEAH (Asp-Glu-Ala-His) box polypeptide 9	L359V only	0.93	0.79	0.90	0.90	5.86E-01	3.01E-02	8.23E-01	9.84E-01
8015460	NM_001096	ACLY	ATP citrate lyase	L359V only	0.88	0.79	0.99	0.89	3.06E-01	3.28E-02	9.87E-01	9.11E-01
8158930	NM_018956	C9orf9	chromosome 9 open reading frame 9	L359V only	0.82	0.79	0.96	0.89	1.22E-01	4.24E-02	9.41E-01	9.41E-01
8070194	NM_001001890	RUNX1	runt-related transcription factor 1	L359V only	1.04	0.79	1.02	0.92	8.03E-01	3.84E-02	9.75E-01	1.00E+00
7899462	NM_001048194	RCC1	regulator of chromosome condensation 1	L359V only	0.84	0.79	1.00	0.94	1.64E-01	4.33E-02	9.95E-01	1.00E+00
7933582	NM_006327	TIMM23	translocase of inner mitochondrial membrane 23 homolog (yeast)	L359V only	0.83	0.79	0.90	0.89	1.33E-01	3.84E-02	8.23E-01	9.35E-01
7977105	NM_152307	TRMT61A	tRNA methyltransferase 61 homolog A (S. cerevisiae)	L359V only	0.79	0.79	0.95	0.87	6.51E-02	4.71E-02	9.22E-01	8.38E-01
8048980	NM_016289	CAB39	calcium binding protein 39	L359V only	0.97	0.78	0.99	0.98	8.61E-01	2.30E-02	9.86E-01	1.00E+00
7936578	NM_022063	C10orf84	chromosome 10 open reading frame 84	L359V only	0.87	0.78	0.92	0.96	2.61E-01	3.00E-02	8.64E-01	1.00E+00
8134415	NM_020186	ACN9	ACN9 homolog (S. cerevisiae)	L359V only	0.91	0.78	0.94	0.94	4.91E-01	2.74E-02	8.94E-01	1.00E+00
7975416	NM_014982	PCNX	pecanex homolog (Drosophila)	L359V only	0.94	0.78	0.91	0.93	6.28E-01	2.13E-02	8.36E-01	1.00E+00
7962203	NM_001040436	YARS2	tyrosyl-tRNA synthetase 2, mitochondrial	L359V only	0.99	0.78	0.97	0.99	9.64E-01	3.35E-02	9.59E-01	1.00E+00
7989596	NM_014326	DAPK2	death-associated protein kinase 2	L359V only	1.10	0.78	1.04	0.98	4.77E-01	3.22E-02	9.31E-01	1.00E+00
8061542	NM_178580	HM13	histocompatibility (minor) 13	L359V only	0.79	0.78	0.85	0.85	8.00E-02	4.96E-02	7.14E-01	6.66E-01
8105612	NM_005869	SDCCAG10	serologically defined colon cancer antigen 10	L359V only	0.91	0.78	0.86	0.94	5.28E-01	4.13E-02	7.28E-01	1.00E+00
7970989	BC037403	SOHLH2	spermatogenesis and oogenesis specific basic helix-loop-helix 2	L359V only	0.95	0.78	1.03	1.02	7.63E-01	4.69E-02	9.62E-01	1.00E+00
8083826	NM_003262	SEC62	SEC62 homolog (S. cerevisiae)	L359V only	0.93	0.78	0.93	0.95	6.25E-01	2.94E-02	8.76E-01	1.00E+00
8060484	NM_006392	NOP56	NOP56 ribonucleoprotein homolog (yeast)	L359V only	0.83	0.78	0.88	0.91	1.02E-01	2.79E-02	7.79E-01	1.00E+00
8121300	NM_018292	QRSL1	glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1	L359V only	0.82	0.78	0.90	0.92	1.25E-01	4.67E-02	8.38E-01	1.00E+00
8155327	NM_000692	ALDH1B1	aldehyde dehydrogenase 1 family, member B1	L359V only	0.78	0.78	0.93	0.86	5.87E-02	4.70E-02	8.80E-01	7.09E-01
8069998	AF282851	C21orf59	chromosome 21 open reading frame 59	L359V only	0.87	0.78	0.91	0.93	3.25E-01	4.65E-02	8.58E-01	1.00E+00
7954631	NM_018099	FAR2	fatty acyl CoA reductase 2	L359V only	0.85	0.78	0.91	0.92	2.35E-01	4.65E-02	8.62E-01	1.00E+00
8159111	NM_017588	WDR5	WD repeat domain 5	L359V only	0.87	0.78	0.91	0.89	2.48E-01	2.91E-02	8.38E-01	8.97E-01
8096718	NM_004757	SCYE1	small inducible cytokine subfamily E, member 1 (endothelial monocyte-activating)	L359V only	0.93	0.78	0.93	0.93	6.12E-01	3.53E-02	8.85E-01	1.00E+00
8060599	NM_030811	MRPS26	mitochondrial ribosomal protein S26	L359V only	0.79	0.78	0.94	0.92	5.15E-02	3.20E-02	8.88E-01	1.00E+00
7925978	NM_017782	C10orf18	chromosome 10 open reading frame 18	L359V only	0.79	0.78	0.90	0.88	8.00E-02	4.86E-02	8.38E-01	8.86E-01
8047518	NM_015934	NOP5	NOP58	L359V only	0.89	0.78	0.90	0.92	3.80E-01	3.72E-02	8.25E-01	1.00E+00
7923007	NM_015984	UCHL5	ubiquitin carboxyl-terminal hydrolase L5	L359V only	0.91	0.78	0.96	0.96	4.58E-01	2.41E-02	9.28E-01	1.00E+00
7956785	NM_007235	XPOT	exportin, tRNA (nuclear export receptor for tRNAs)	L359V only	1.00	0.78	1.03	1.01	9.86E-01	2.00E-02	9.52E-01	1.00E+00
7997520	NM_001537	HSBP1	heat shock factor binding protein 1	L359V only	0.91	0.78	0.91	0.93	4.69E-01	3.37E-02	8.41E-01	1.00E+00
8135568	NM_199072	MDFIC	MyoD family inhibitor domain containing	L359V only	0.85	0.78	1.01	0.93	1.93E-01	3.76E-02	9.90E-01	1.00E+00
8113542	NM_005669	REEP5	receptor accessory protein 5	L359V only	0.85	0.78	0.87	0.88	1.79E-01	3.26E-02	7.65E-01	8.22E-01
7938777	NM_005566	LDHA	lactate dehydrogenase A	L359V only	0.83	0.78	0.98	0.90	1.10E-01	2.50E-02	9.72E-01	9.81E-01
7915995	NM_007051	FAF1	Fas (TNFRSF6) associated factor 1	L359V only	0.91	0.78	0.90	0.93	5.35E-01	4.59E-02	8.41E-01	1.00E+00
7896961	NM_031921	ATAD3B	ATPase family, AAA domain containing 3B	L359V only	0.77	0.78	0.90	0.86	5.13E-02	4.65E-02	8.41E-01	7.82E-01
8125091	NM_006295	VARS	valyl-tRNA synthetase	L359V only	0.85	0.78	0.99	0.87	2.03E-01	3.16E-02	9.85E-01	7.47E-01
8178609	NM_006295	VARS	valyl-tRNA synthetase	L359V only	0.85	0.78	0.99	0.87	2.03E-01	3.16E-02	9.85E-01	7.47E-01
8030908	NM_144684	ZNF480	zinc finger protein 480	L359V only	0.84	0.78	0.90	0.87	1.12E-01	1.92E-02	8.09E-01	6.07E-01
7991587	NM_203472	SELS	selenoprotein S	L359V only	0.97	0.78	0.92	0.89	8.51E-01	2.46E-02	8.55E-01	8.36E-01
8076586	NM_173050	SCUBE1	signal peptide, CUB domain, EGF-like 1	L359V only	1.14	0.78	1.25	0.98	3.09E-01	3.71E-02	3.90E-01	1.00E+00
8019807	NM_005151	USP14	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	L359V only	0.91	0.78	0.88	0.90	5.05E-01	4.19E-02	8.09E-01	1.00E+00
8016708	NM_018509	LRRC59	leucine rich repeat containing 59	L359V only	0.89	0.78	0.93	0.90	4.11E-01	4.85E-02	8.85E-01	1.00E+00
7902883	NM_001134479	LRRC8D	leucine rich repeat containing 8 family, member D	L359V only	0.79	0.78	0.89	0.93	5.76E-02	3.16E-02	8.13E-01	1.00E+00
7972810	NM_024537	CARS2	cysteinyl-tRNA synthetase 2, mitochondrial (putative)	L359V only	0.84	0.78	0.88	0.94	9.87E-02	1.73E-02	7.50E-01	1.00E+00
7928630	NM_001099692	EIF5AL1	eukaryotic translation initiation factor 5A-like 1	L359V only	0.93	0.78	0.97	0.92	6.55E-01	4.64E-02	9.54E-01	1.00E+00
8048120	NM_004044	ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase	L359V only	0.80	0.78	0.95	0.92	5.88E-02	2.41E-02	9.04E-01	1.00E+00
8038954	NM_178523	ZNF616	zinc finger protein 616	L359V only	0.95	0.78	0.86	0.92	7.40E-01	3.32E-02	7.38E-01	1.00E+00
8135514	NM_001550	IFRD1	interferon-related developmental regulator 1	L359V only	0.95	0.78	0.93	0.98	7.47E-01	3.70E-02	8.76E-01	1.00E+00
7981481	NM_004894	C14orf2	chromosome 14 open reading frame 2	L359V only	0.96	0.78	0.94	0.93	7.96E-01	3.15E-02	8.96E-01	1.00E+00
8056977	NM_006164	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	L359V only	0.98	0.78	1.00	0.97	9.24E-01	2.30E-02	9.98E-01	1.00E+00
8016832	NM_012329	MMD	monocyte to macrophage differentiation-associated	L359V only	0.85	0.78	0.96	0.91	2.59E-01	4.95E-02	9.36E-01	1.00E+00
7974352	NM_016039	C14orf166	chromosome 14 open reading frame 166	L359V only	0.98	0.78	0.95	0.94	9.07E-01	4.07E-02	9.30E-01	1.00E+00
8009685	NM_004252	SLC9A3R1	solute carrier family 9 (sodium	L359V only	0.79	0.78	0.84	0.82	5.18E-02	2.88E-02	5.58E-01	3.28E-01
7964250	NM_006601	PTGES3	prostaglandin E synthase 3 (cytosolic)	L359V only	0.92	0.78	0.94	0.97	5.89E-01	3.53E-02	8.88E-01	1.00E+00
8132943	NM_001762	CCT6A	chaperonin containing TCP1, subunit 6A (zeta 1)	L359V only	0.87	0.78	0.90	0.89	3.08E-01	4.62E-02	8.43E-01	1.00E+00

8007757	NM_005892	FMNL1	formin-like 1	L359V only	0.77	0.78	0.90	0.87	5.88E-02	4.69E-02	8.38E-01	8.80E-01
7958749	NM_005475	SH2B3	SH2B adaptor protein 3	L359V only	0.86	0.78	1.02	0.88	2.55E-01	3.60E-02	9.76E-01	8.84E-01
8141898	NM_014377	DNAJC2	DnaJ (Hsp40) homolog, subfamily C, member 2	L359V only	0.95	0.78	0.91	0.94	7.83E-01	3.53E-02	8.38E-01	1.00E+00
8166335	NM_000284	PDHA1	pyruvate dehydrogenase (lipoamide) alpha 1	L359V only	0.90	0.77	0.96	0.93	4.92E-01	4.75E-02	9.48E-01	1.00E+00
7936242	NM_033397	ITPRIP	inositol 1,4,5-triphosphate receptor interacting protein	L359V only	0.83	0.77	0.94	0.89	1.47E-01	3.20E-02	8.99E-01	8.92E-01
8117194	NM_020662	MRS2	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	L359V only	0.83	0.77	0.89	0.90	1.73E-01	4.48E-02	8.34E-01	1.00E+00
7979196	NM_198066	GNPNAT1	glucosamine-phosphate N-acetyltransferase 1	L359V only	0.86	0.77	0.98	0.91	2.63E-01	3.93E-02	9.72E-01	1.00E+00
8066247	NR_015366	LOC388796	hypothetical LOC388796	L359V only	0.77	0.77	0.95	0.88	6.02E-02	4.64E-02	9.31E-01	8.92E-01
7911559	NM_017971	MRPL20	mitochondrial ribosomal protein L20	L359V only	0.83	0.77	0.92	0.89	9.71E-02	1.74E-02	8.41E-01	8.38E-01
8039939	NM_017971	MRPL20	mitochondrial ribosomal protein L20	L359V only	0.83	0.77	0.92	0.89	9.71E-02	1.74E-02	8.41E-01	8.38E-01
7917331	NR_024113	C1orf52	chromosome 1 open reading frame 52	L359V only	0.83	0.77	0.84	0.85	1.50E-01	3.78E-02	6.39E-01	6.19E-01
8137584	NM_138400	NOM1	nucleolar protein with MIF4G domain 1	L359V only	0.84	0.77	0.89	0.89	1.76E-01	3.78E-02	8.14E-01	9.72E-01
7915091	NM_005955	MTF1	metal-regulatory transcription factor 1	L359V only	0.83	0.77	0.85	0.82	1.53E-01	3.56E-02	7.12E-01	4.16E-01
8023708	---			L359V only	0.87	0.77	0.89	0.88	3.32E-01	4.62E-02	8.28E-01	9.06E-01
8085531	NM_022497	MRPS25	mitochondrial ribosomal protein S25	L359V only	0.83	0.77	0.99	0.93	1.91E-01	4.82E-02	9.84E-01	1.00E+00
8046333	NM_024843	CYBRD1	cytochrome b reductase 1	L359V only	0.85	0.77	0.86	0.91	2.10E-01	2.92E-02	7.38E-01	1.00E+00
7930870	CR456475	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	L359V only	0.88	0.77	0.93	0.90	3.04E-01	2.34E-02	8.77E-01	9.35E-01
8150908	NM_017813	IMPAD1	inositol monophosphatase domain containing 1	L359V only	0.90	0.77	0.94	0.93	3.97E-01	2.47E-02	8.85E-01	1.00E+00
7956443	NM_004990	MARS	methionyl-tRNA synthetase	L359V only	0.89	0.77	1.07	0.99	3.79E-01	3.14E-02	8.89E-01	1.00E+00
8051528	NM_005760	CEBPZ	CCAAT	L359V only	0.96	0.77	0.93	0.95	8.48E-01	4.96E-02	8.86E-01	1.00E+00
8144557	NM_012331	MSRA	methionine sulfoxide reductase A	L359V only	0.82	0.77	0.83	0.85	1.10E-01	2.92E-02	5.48E-01	6.19E-01
8047243	NM_138395	MARS2	methionyl-tRNA synthetase 2, mitochondrial	L359V only	0.81	0.77	0.98	0.89	1.14E-01	3.70E-02	9.72E-01	1.00E+00
8162850	NM_017746	TEX10	testis expressed 10	L359V only	0.86	0.77	0.92	0.93	2.78E-01	3.96E-02	8.77E-01	1.00E+00
8114861	NM_020117	LARS	leucyl-tRNA synthetase	L359V only	0.94	0.77	1.07	1.04	6.92E-01	2.67E-02	8.88E-01	1.00E+00
7914563	NM_003680	YARS	tyrosyl-tRNA synthetase	L359V only	0.98	0.77	1.01	0.99	8.96E-01	2.19E-02	9.81E-01	1.00E+00
8138489	NM_018719	CDCA7L	cell division cycle associated 7-like	L359V only	0.95	0.77	1.00	1.02	7.85E-01	3.84E-02	9.99E-01	1.00E+00
8017421	NM_020198	CCDC47	coiled-coil domain containing 47	L359V only	0.90	0.77	0.92	0.94	4.00E-01	2.24E-02	8.47E-01	1.00E+00
8148293	NM_173685	NSMCE2	non-SMC element 2, MMS21 homolog (S. cerevisiae)	L359V only	0.94	0.77	0.90	0.97	7.25E-01	3.16E-02	8.34E-01	1.00E+00
7971967	NM_014953	DIS3	DIS3 mitotic control homolog (S. cerevisiae)	L359V only	0.98	0.77	0.96	0.94	9.13E-01	2.66E-02	9.29E-01	1.00E+00
7982753	NM_152260	RPUSD2	RNA pseudouridylate synthase domain containing 2	L359V only	0.82	0.77	0.91	0.87	1.39E-01	4.11E-02	8.48E-01	8.36E-01
7950473	NM_004041	ARRB1	arrestin, beta 1	L359V only	0.94	0.77	0.98	0.95	7.10E-01	3.72E-02	9.80E-01	1.00E+00
8072488	NM_004147	DRG1	developmentally regulated GTP binding protein 1	L359V only	0.97	0.77	0.95	1.00	8.96E-01	2.97E-02	9.16E-01	1.00E+00
7968670	NM_016617	UFM1	ubiquitin-fold modifier 1	L359V only	0.83	0.77	0.91	0.92	1.37E-01	2.55E-02	8.38E-01	1.00E+00
7934753	NM_001099692	EIF5AL1	eukaryotic translation initiation factor 5A-like 1	L359V only	0.92	0.77	0.95	0.91	5.81E-01	3.38E-02	9.28E-01	1.00E+00
8097543	NM_014487	ZNF330	zinc finger protein 330	L359V only	0.82	0.77	0.80	0.87	1.39E-01	3.53E-02	4.12E-01	8.08E-01
8175755	NM_004344	CETN2	centrin, EF-hand protein, 2	L359V only	0.87	0.77	0.95	0.90	2.87E-01	2.63E-02	9.18E-01	1.00E+00
8112728	NM_001089704	hCG_1757335	hCG1757335	L359V only	0.94	0.77	0.95	0.95	7.27E-01	2.67E-02	9.11E-01	1.00E+00
8022393	NM_002828	PTPN2	protein tyrosine phosphatase, non-receptor type 2	L359V only	0.82	0.77	0.87	0.91	1.40E-01	3.45E-02	7.99E-01	1.00E+00
8014487	NM_198839	ACACA	acetyl-Coenzyme A carboxylase alpha	L359V only	0.85	0.77	0.89	0.88	2.50E-01	4.16E-02	8.36E-01	9.35E-01
7958174	NM_003330	TXNRD1	thioredoxin reductase 1	L359V only	0.85	0.77	0.95	0.92	1.97E-01	2.37E-02	9.18E-01	1.00E+00
8035566	NM_004838	HOMER3	homer homolog 3 (Drosophila)	L359V only	0.79	0.77	1.00	0.93	1.04E-01	4.98E-02	9.99E-01	1.00E+00
7934278	NM_000917	P4HA1	prolyl 4-hydroxylase, alpha polypeptide I	L359V only	1.02	0.77	1.04	0.98	9.23E-01	4.26E-02	9.40E-01	1.00E+00
7963054	NM_006009	TUBA1A	tubulin, alpha 1a	L359V only	0.85	0.77	0.91	0.88	1.78E-01	2.05E-02	8.36E-01	8.17E-01
8107814	NM_016048	ISOC1	isochorismatase domain containing 1	L359V only	0.82	0.77	0.92	0.90	1.18E-01	2.52E-02	8.70E-01	9.96E-01
8071920	NM_004175	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	L359V only	0.86	0.77	0.90	0.91	2.42E-01	2.91E-02	8.25E-01	1.00E+00
8089527	NM_022488	ATG3	ATG3 autophagy related 3 homolog (S. cerevisiae)	L359V only	0.90	0.77	0.86	0.91	4.66E-01	3.22E-02	7.50E-01	1.00E+00
8012581	NM_004853	STX8	syntaxin 8	L359V only	0.82	0.77	0.87	0.90	1.20E-01	2.79E-02	7.84E-01	1.00E+00
7995843	NM_014669	NUP93	nucleoporin 93kDa	L359V only	0.83	0.77	0.95	0.91	2.07E-01	4.96E-02	9.30E-01	1.00E+00
7994280	NM_000418	IL4R	interleukin 4 receptor	L359V only	0.94	0.77	0.97	0.90	6.91E-01	1.72E-02	9.43E-01	9.45E-01
8003217	NM_006067	COX4NB	COX4 neighbor	L359V only	0.85	0.77	0.98	0.91	2.33E-01	3.37E-02	9.80E-01	1.00E+00
7979516	NM_020810	TRMT5	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	L359V only	0.78	0.77	0.83	0.87	5.55E-02	3.19E-02	6.08E-01	8.39E-01
7912852	BC110421	EIF1AP1	eukaryotic translation initiation factor 1A pseudogene 1	L359V only	0.94	0.77	0.95	0.94	6.90E-01	2.17E-02	9.09E-01	1.00E+00
8110894	NM_017755	NSUN2	NOL1	L359V only	0.84	0.77	0.94	0.92	1.60E-01	2.40E-02	9.01E-01	1.00E+00
8071649	BX641141	LOC96610	hypothetical gene LOC96610	L359V only	0.80	0.77	0.85	0.86	6.81E-02	2.62E-02	7.12E-01	6.68E-01
7954173	NM_007178	STRAP	serine threonine kinase receptor associated protein	L359V only	0.86	0.76	0.95	0.91	2.52E-01	2.52E-02	9.13E-01	1.00E+00
7958800	NM_003668	MAPKAPK5	mitogen-activated protein kinase-activated protein kinase 5	L359V only	0.88	0.76	0.90	0.92	4.13E-01	4.84E-02	8.53E-01	1.00E+00
8146448	NM_014175	MRPL15	mitochondrial ribosomal protein L15	L359V only	0.84	0.76	0.92	0.93	1.85E-01	2.84E-02	8.76E-01	1.00E+00
7925229	NM_152490	B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2	L359V only	0.85	0.76	0.89	0.90	1.79E-01	2.33E-02	8.15E-01	9.92E-01
7922051	NM_003851	CREG1	cellular repressor of E1A-stimulated genes 1	L359V only	0.97	0.76	1.07	0.98	8.61E-01	2.36E-02	8.88E-01	1.00E+00
8073032	NM_020243	TOMM22	translocase of outer mitochondrial membrane 22 homolog (yeast)	L359V only	0.81	0.76	0.93	0.88	8.00E-02	2.30E-02	8.76E-01	8.38E-01
8113504	NM_004772	C5orf13	chromosome 5 open reading frame 13	L359V only	0.95	0.76	0.93	0.94	7.48E-01	2.64E-02	8.86E-01	1.00E+00
8018169	NM_174892	CD300LB	CD300 molecule-like family member b	L359V only	0.80	0.76	0.96	0.87	1.03E-01	4.02E-02	9.41E-01	8.78E-01
8102162	NM_020395	INTS12	integrator complex subunit 12	L359V only	0.93	0.76	0.98	0.94	6.95E-01	4.24E-02	9.83E-01	1.00E+00
8056220	NM_015446	AHCTF1	AT hook containing transcription factor 1	L359V only	0.89	0.76	0.92	0.90	3.84E-01	2.71E-02	8.68E-01	1.00E+00
8040618	NM_016131	RAB10	RAB10, member RAS oncogene family	L359V only	0.91	0.76	0.93	0.94	4.10E-01	1.12E-02	8.69E-01	1.00E+00

8009351	---			L359V only	0.99	0.76	0.97	1.00	9.64E-01	3.60E-02	9.54E-01	1.00E+00
7904082	XM_001716411	LOC128322	hypothetical LOC128322	L359V only	0.86	0.76	0.87	0.89	2.22E-01	2.30E-02	7.50E-01	9.43E-01
8127977	NM_006372	SYNCRIP	synaptotagmin binding, cytoplasmic RNA interacting protein	L359V only	0.81	0.76	0.88	0.89	1.19E-01	3.23E-02	8.13E-01	9.47E-01
8032484	NM_012458	TIMM13	translocase of inner mitochondrial membrane 13 homolog (yeast)	L359V only	0.78	0.76	0.90	0.89	5.88E-02	2.66E-02	8.38E-01	9.65E-01
7906863	NM_003115	UAP1	UDP-N-acteylglucosamine pyrophosphorylase 1	L359V only	0.83	0.76	0.95	0.92	1.71E-01	3.14E-02	9.22E-01	1.00E+00
8024898	NM_018708	FEM1A	fem-1 homolog a (C. elegans)	L359V only	0.79	0.76	0.89	0.85	6.89E-02	2.47E-02	8.20E-01	6.27E-01
8126058	NM_016059	PPIL1	peptidylprolyl isomerase (cyclophilin)-like 1	L359V only	0.81	0.76	0.84	0.85	6.49E-02	1.64E-02	5.20E-01	5.28E-01
8131975	NM_006024	TAX1BP1	Tax1 (human T-cell leukemia virus type I) binding protein 1	L359V only	1.16	0.76	1.10	1.04	2.66E-01	2.66E-02	8.41E-01	1.00E+00
7925500	NM_001821	CHML	choroideremia-like (Rab escort protein 2)	L359V only	0.95	0.76	0.92	0.95	8.13E-01	4.22E-02	8.77E-01	1.00E+00
8131143	NM_001040167	LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	L359V only	0.78	0.76	0.87	0.85	9.09E-02	4.67E-02	8.09E-01	7.29E-01
7975224	NM_004094	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	L359V only	0.80	0.76	0.84	0.87	1.19E-01	4.62E-02	7.38E-01	9.26E-01
8114455	NM_004134	HSPA9	heat shock 70kDa protein 9 (mortalin)	L359V only	0.81	0.76	0.90	0.93	6.50E-02	1.60E-02	8.25E-01	1.00E+00
8162313	NM_013417	IARS	isoleucyl-tRNA synthetase	L359V only	0.83	0.76	0.99	0.95	1.35E-01	2.48E-02	9.85E-01	1.00E+00
8108015	NM_002154	HSPA4	heat shock 70kDa protein 4	L359V only	0.85	0.76	0.92	0.89	1.28E-01	9.41E-03	8.36E-01	8.07E-01
8165107	NM_052813	CARD9	caspase recruitment domain family, member 9	L359V only	0.85	0.76	0.90	0.89	2.11E-01	2.46E-02	8.36E-01	9.45E-01
8002919	NM_001130089	KARS	lysyl-tRNA synthetase	L359V only	0.85	0.76	0.92	0.92	1.31E-01	1.07E-02	8.36E-01	1.00E+00
7897620	NM_002631	PGD	phosphogluconate dehydrogenase	L359V only	0.89	0.76	0.99	0.95	4.04E-01	2.14E-02	9.90E-01	1.00E+00
7907690	NM_022371	TOR3A	torsin family 3, member A	L359V only	0.87	0.76	0.90	0.91	3.14E-01	3.34E-02	8.48E-01	1.00E+00
8090030	NM_024610	HSPBAP1	HSPB (heat shock 27kDa) associated protein 1	L359V only	0.87	0.76	0.88	0.92	3.96E-01	4.79E-02	8.25E-01	1.00E+00
7939902	ENST00000399175	LOC646813	hypothetical LOC646813	L359V only	1.03	0.76	0.96	0.95	9.13E-01	4.59E-02	9.54E-01	1.00E+00
7972867	NM_018386	PCID2	PCI domain containing 2	L359V only	0.85	0.76	0.91	0.93	2.04E-01	2.64E-02	8.52E-01	1.00E+00
8009693	NM_017728	TMEM104	transmembrane protein 104	L359V only	0.82	0.76	0.98	0.85	8.47E-02	1.42E-02	9.60E-01	4.98E-01
8114225	NM_004893	H2AFY	H2A histone family, member Y	L359V only	0.81	0.76	0.81	0.85	1.48E-01	4.67E-02	5.68E-01	7.88E-01
7915130	NM_006802	SF3A3	splicing factor 3a, subunit 3, 60kDa	L359V only	0.91	0.76	0.93	0.95	5.29E-01	2.59E-02	8.81E-01	1.00E+00
8056716	NM_014168	METTL5	methyltransferase like 5	L359V only	0.97	0.76	0.95	0.95	9.09E-01	4.64E-02	9.27E-01	1.00E+00
7935230	NM_002860	ALDH18A1	aldehyde dehydrogenase 18 family, member A1	L359V only	0.90	0.76	1.01	0.96	5.41E-01	4.22E-02	9.96E-01	1.00E+00
8031260	NM_153443	KIR3DL3	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3	L359V only	0.75	0.76	0.86	0.85	5.13E-02	3.89E-02	8.01E-01	7.18E-01
8173615	NM_183353	RNF12	ring finger protein 12	L359V only	0.92	0.76	0.94	0.96	5.83E-01	2.61E-02	8.98E-01	1.00E+00
8130185	NM_020861	ZBTB2	zinc finger and BTB domain containing 2	L359V only	0.84	0.76	0.89	0.87	1.19E-01	1.39E-02	8.01E-01	6.62E-01
8177046	---			L359V only	1.01	0.76	0.95	1.00	9.76E-01	2.55E-02	9.28E-01	1.00E+00
7925174	NM_014765	TOMM20	translocase of outer mitochondrial membrane 20 homolog (yeast)	L359V only	0.89	0.76	0.90	0.94	3.56E-01	1.31E-02	8.13E-01	1.00E+00
8085914	NM_003615	SLC4A7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	L359V only	1.00	0.76	0.93	0.96	9.91E-01	1.63E-02	8.74E-01	1.00E+00
7992414	NM_006453	TBL3	transducin (beta)-like 3	L359V only	0.80	0.76	0.91	0.86	1.33E-01	4.56E-02	8.70E-01	8.38E-01
8112458	NM_003187	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	L359V only	0.85	0.75	0.95	0.91	1.80E-01	1.69E-02	9.04E-01	1.00E+00
8031223	NM_006669	LILRB1	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), m	L359V only	0.84	0.75	0.84	0.84	2.63E-01	4.13E-02	7.34E-01	7.09E-01
7956937	NM_015646	RAP1B	RAP1B, member of RAS oncogene family	L359V only	0.95	0.75	0.94	0.95	7.76E-01	3.84E-02	9.12E-01	1.00E+00
7977058	NM_001969	EIF5	eukaryotic translation initiation factor 5	L359V only	0.91	0.75	0.87	0.88	4.32E-01	1.34E-02	7.44E-01	7.88E-01
8130952	NM_002793	PSMB1	proteasome (prosome, macropain) subunit, beta type, 1	L359V only	0.86	0.75	0.87	0.91	3.10E-01	3.21E-02	8.01E-01	1.00E+00
7917771	NM_014597	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	L359V only	0.87	0.75	0.88	0.89	3.64E-01	3.20E-02	8.23E-01	1.00E+00
8144894	NM_018142	INTS10	integrator complex subunit 10	L359V only	0.79	0.75	0.92	0.89	8.93E-02	3.14E-02	8.80E-01	1.00E+00
8073875	NM_018006	TRMU	tRNA 5-methylaminomethyl-2-thiouridylate methyltransferase	L359V only	0.88	0.75	0.89	0.88	3.52E-01	2.30E-02	8.25E-01	8.78E-01
7918345	NM_002790	PSMA5	proteasome (prosome, macropain) subunit, alpha type, 5	L359V only	0.84	0.75	0.87	0.87	2.60E-01	4.67E-02	8.23E-01	9.55E-01
8019762	NM_000918	P4HB	prolyl 4-hydroxylase, beta polypeptide	L359V only	0.87	0.75	0.92	0.90	2.45E-01	1.66E-02	8.56E-01	9.45E-01
7904000	NM_007204	DDX20	DEAD (Asp-Glu-Ala-Asp) box polypeptide 20	L359V only	0.86	0.75	0.78	0.87	3.32E-01	4.63E-02	4.65E-01	9.24E-01
8016578	NM_005827	SLC35B1	solute carrier family 35, member B1	L359V only	0.83	0.75	0.88	0.85	9.71E-02	1.07E-02	7.44E-01	4.98E-01
8151401	NM_001001481	UBE2W	ubiquitin-conjugating enzyme E2W (putative)	L359V only	0.94	0.75	0.97	0.97	7.28E-01	1.90E-02	9.55E-01	1.00E+00
8169365	NM_032227	TMEM164	transmembrane protein 164	L359V only	1.10	0.75	0.96	0.92	5.74E-01	3.46E-02	9.42E-01	1.00E+00
8049544	NM_001137550	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	L359V only	0.94	0.75	0.85	0.90	7.37E-01	3.98E-02	7.74E-01	1.00E+00
7924526	NM_005426	TP53BP2	tumor protein p53 binding protein, 2	L359V only	0.88	0.75	0.87	0.88	3.73E-01	2.21E-02	7.81E-01	8.99E-01
8057045	NM_181342	FKBP7	FK506 binding protein 7	L359V only	0.95	0.75	0.98	0.93	8.12E-01	3.41E-02	9.80E-01	1.00E+00
8050507	NM_001006657	WDR35	WD repeat domain 35	L359V only	0.76	0.75	0.87	0.89	8.53E-02	4.93E-02	8.23E-01	1.00E+00
7940857	NM_006819	STIP1	stress-induced-phosphoprotein 1	L359V only	0.80	0.75	0.89	0.87	1.15E-01	3.62E-02	8.36E-01	9.32E-01
8087596	NM_003549	HYAL3	hyaluronoglucosaminidase 3	L359V only	1.00	0.75	1.09	0.92	9.88E-01	1.92E-02	8.53E-01	1.00E+00
8070102	NM_000819	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetas	L359V only	0.85	0.75	0.98	0.94	1.63E-01	1.25E-02	9.76E-01	1.00E+00
7945740	NM_016093	RPL26L1	ribosomal protein L26-like 1	L359V only	0.82	0.75	0.91	0.86	1.75E-01	3.28E-02	8.58E-01	8.38E-01
7956949	NM_020401	NUP107	nucleoporin 107kDa	L359V only	0.84	0.75	0.88	0.89	1.74E-01	2.06E-02	8.05E-01	9.15E-01
8014081	NM_018428	UTP6	UTP6, small subunit (SSU) processome component, homolog (yeast)	L359V only	0.85	0.75	0.91	0.91	2.04E-01	1.62E-02	8.42E-01	1.00E+00
8031346	NM_002255	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	L359V only	0.74	0.75	0.82	0.82	5.44E-02	4.69E-02	6.90E-01	6.27E-01
7990700	NM_025234	WDR61	WD repeat domain 61	L359V only	0.82	0.75	0.88	0.87	1.97E-01	4.23E-02	8.25E-01	9.40E-01
8120402	NM_004282	BAG2	BCL2-associated athanogene 2	L359V only	0.76	0.75	0.90	0.87	5.11E-02	3.27E-02	8.50E-01	9.21E-01
8123148	NM_014161	MRPL18	mitochondrial ribosomal protein L18	L359V only	0.84	0.75	0.91	0.88	1.93E-01	2.27E-02	8.42E-01	9.04E-01
8167305	NM_006579	EBP	emopamil binding protein (sterol isomerase)	L359V only	0.85	0.75	0.93	0.87	3.14E-01	4.07E-02	8.98E-01	9.55E-01
8062326	NM_018840	C20orf24	chromosome 20 open reading frame 24	L359V only	0.81	0.75	0.83	0.84	1.14E-01	2.19E-02	5.88E-01	5.69E-01
8098150	NM_018352	C4orf43	chromosome 4 open reading frame 43	L359V only	0.93	0.75	0.96	0.95	6.19E-01	1.93E-02	9.47E-01	1.00E+00
8164883	NM_033161	SURF4	surfeit 4	L359V only	0.88	0.75	0.96	0.90	2.37E-01	7.01E-03	9.22E-01	8.60E-01

8096081	NM_021204	ENOPH1	enolase-phosphatase 1	L359V only	0.78	0.75	0.87	0.87	9.78E-02	3.96E-02	8.09E-01	9.13E-01
8043861	NM_015904	EIF5B	eukaryotic translation initiation factor 5B	L359V only	0.83	0.75	0.91	0.91	7.83E-02	8.79E-03	8.36E-01	9.89E-01
7913110	BC034589	KIAA0090	KIAA0090	L359V only	0.83	0.75	0.94	0.90	1.46E-01	1.66E-02	8.95E-01	1.00E+00
8021716	NM_014177	C18orf55	chromosome 18 open reading frame 55	L359V only	0.86	0.75	0.91	0.89	2.27E-01	1.56E-02	8.47E-01	9.45E-01
8097480	NM_057175	NARG1	NMDA receptor regulated 1	L359V only	0.86	0.75	0.93	0.91	1.48E-01	6.70E-03	8.41E-01	8.95E-01
7924388	NM_006085	BPNT1	3'(2'), 5'-bisphosphate nucleotidase 1	L359V only	1.00	0.75	0.92	0.90	9.95E-01	2.81E-02	8.80E-01	1.00E+00
7934870	NM_032810	ATAD1	ATPase family, AAA domain containing 1	L359V only	0.91	0.75	0.92	0.97	5.76E-01	2.64E-02	8.80E-01	1.00E+00
7926807	NM_014317	PDSS1	prenyl (decaprenyl) diphosphate synthase, subunit 1	L359V only	0.80	0.75	0.88	0.88	7.37E-02	1.88E-02	7.98E-01	8.38E-01
7957052	NM_006431	CCT2	chaperonin containing TCP1, subunit 2 (beta)	L359V only	0.84	0.75	0.88	0.87	1.77E-01	1.98E-02	8.01E-01	8.17E-01
8119898	NM_001025366	VEGFA	vascular endothelial growth factor A	L359V only	0.81	0.75	1.13	1.01	1.95E-01	4.64E-02	8.38E-01	1.00E+00
8059413	NM_014689	DOCK10	dedicator of cytokinesis 10	L359V only	1.16	0.75	0.98	0.93	3.09E-01	2.98E-02	9.76E-01	1.00E+00
7985240	NM_007364	TMED3	transmembrane emp24 protein transport domain containing 3	L359V only	0.90	0.75	1.07	0.92	5.32E-01	4.26E-02	9.01E-01	1.00E+00
7927267	NM_019054	FAM35A	family with sequence similarity 35, member A	L359V only	0.91	0.75	0.95	0.93	6.16E-01	4.77E-02	9.39E-01	1.00E+00
8092251	NM_021629	GNB4	guanine nucleotide binding protein (G protein), beta polypeptide 4	L359V only	0.92	0.75	0.96	0.94	6.07E-01	2.84E-02	9.52E-01	1.00E+00
7935054	---			L359V only	0.90	0.75	0.83	0.94	5.74E-01	4.13E-02	7.23E-01	1.00E+00
7959298	NM_001080825	TMEM120B	transmembrane protein 120B	L359V only	0.84	0.75	1.01	0.91	2.21E-01	2.91E-02	9.94E-01	1.00E+00
8174684	NM_017544	NKRF	NFKB repressing factor	L359V only	0.79	0.74	0.90	0.86	1.10E-01	3.26E-02	8.41E-01	8.36E-01
8152255	NM_030780	SLC25A32	solute carrier family 25, member 32	L359V only	0.79	0.74	0.96	0.90	5.49E-02	1.45E-02	9.36E-01	9.78E-01
7903119	NM_002858	ABCD3	ATP-binding cassette, sub-family D (ALD), member 3	L359V only	0.91	0.74	0.79	0.86	5.03E-01	1.39E-02	2.51E-01	6.27E-01
7927108	NM_014753	BMS1	BMS1 homolog, ribosome assembly protein (yeast)	L359V only	0.81	0.74	0.86	0.86	1.74E-01	4.13E-02	8.06E-01	8.85E-01
8001197	NM_018092	NETO2	neuropilin (NRP) and tolloid (TLL)-like 2	L359V only	0.94	0.74	0.94	0.94	7.48E-01	3.24E-02	9.11E-01	1.00E+00
7979416	NM_012460	TIMM9	translocase of inner mitochondrial membrane 9 homolog (yeast)	L359V only	0.85	0.74	0.92	0.93	2.77E-01	3.28E-02	8.81E-01	1.00E+00
8069003	NM_005049	PWP2	PWP2 periodic tryptophan protein homolog (yeast)	L359V only	0.74	0.74	0.88	0.86	5.15E-02	3.84E-02	8.34E-01	8.88E-01
8058552	NM_005896	IDH1	isocitrate dehydrogenase 1 (NADP+), soluble	L359V only	1.11	0.74	1.07	1.01	4.85E-01	2.39E-02	8.98E-01	1.00E+00
8147864	NM_014673	TTC35	tetratricopeptide repeat domain 35	L359V only	0.82	0.74	0.82	0.87	1.21E-01	1.86E-02	5.05E-01	8.14E-01
8175369	NM_024597	MAP7D3	MAP7 domain containing 3	L359V only	0.82	0.74	0.86	0.90	1.52E-01	2.50E-02	7.65E-01	1.00E+00
7987165	NM_020371	AVEN	apoptosis, caspase activation inhibitor	L359V only	0.89	0.74	0.88	0.91	5.12E-01	4.00E-02	8.30E-01	1.00E+00
8028186	NM_007145	ZNF146	zinc finger protein 146	L359V only	0.86	0.74	1.00	0.94	3.56E-01	4.35E-02	9.99E-01	1.00E+00
7916219	BC015313	C1orf163	chromosome 1 open reading frame 163	L359V only	0.77	0.74	0.93	0.89	6.23E-02	2.49E-02	8.93E-01	9.88E-01
7939265	NM_024662	NAT10	N-acetyltransferase 10 (GCN5-related)	L359V only	0.80	0.74	0.95	0.93	6.36E-02	1.19E-02	9.15E-01	1.00E+00
7964832	---			L359V only	1.00	0.74	0.85	0.94	9.98E-01	4.85E-02	8.01E-01	1.00E+00
8003425	NM_005187	CBFA2T3	core-binding factor, runt domain, alpha subunit 2; translocated to, 3	L359V only	0.80	0.74	0.85	0.83	6.48E-02	1.35E-02	6.65E-01	4.02E-01
8031277	NM_015868	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	L359V only	0.73	0.74	0.86	0.82	5.00E-02	4.76E-02	8.09E-01	6.34E-01
7931268	NM_016567	BCCIP	BRCA2 and CDKN1A interacting protein	L359V only	0.82	0.74	0.90	0.88	1.49E-01	2.15E-02	8.38E-01	9.27E-01
7910030	NM_144989	C1orf67	chromosome 1 open reading frame 67	L359V only	1.00	0.74	1.01	1.00	9.87E-01	4.84E-02	9.94E-01	1.00E+00
8167270	NM_177439	FTSJ1	FtsJ homolog 1 (E. coli)	L359V only	0.82	0.74	0.92	0.87	1.75E-01	3.39E-02	8.81E-01	9.45E-01
7912112	NM_018198	DNAJC11	DnaJ (Hsp40) homolog, subfamily C, member 11	L359V only	0.84	0.74	0.92	0.88	1.63E-01	1.42E-02	8.68E-01	8.44E-01
7919800	NM_004079	CTSS	cathepsin S	L359V only	1.13	0.74	1.09	1.02	4.61E-01	3.01E-02	8.81E-01	1.00E+00
8007397	NM_176863	PSME3	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	L359V only	0.83	0.74	0.91	0.87	1.85E-01	2.63E-02	8.59E-01	8.92E-01
7965436	NM_003566	EEA1	early endosome antigen 1	L359V only	0.95	0.74	0.98	0.96	7.89E-01	1.76E-02	9.73E-01	1.00E+00
8010078	NR_004397	SNORD1C	small nucleolar RNA, C	L359V only	0.80	0.74	1.08	0.92	1.26E-01	2.65E-02	8.86E-01	1.00E+00
8118314	NM_005346	HSPA1B	heat shock 70kDa protein 1B	L359V only	0.80	0.74	0.83	0.82	1.79E-01	4.88E-02	7.46E-01	6.34E-01
8123362	BX647686	CCR6	chemokine (C-C motif) receptor 6	L359V only	0.89	0.74	0.80	0.85	5.29E-01	4.96E-02	6.65E-01	8.78E-01
8050079	NM_002936	RNASEH1	ribonuclease H1	L359V only	0.88	0.74	1.00	0.94	3.19E-01	1.39E-02	9.98E-01	1.00E+00
8163185	NM_003329	TXN	thioredoxin	L359V only	0.90	0.74	0.98	0.94	5.37E-01	2.91E-02	9.81E-01	1.00E+00
8113602	NM_152549	CCDC112	coiled-coil domain containing 112	L359V only	0.88	0.74	0.82	0.92	4.46E-01	3.17E-02	6.50E-01	1.00E+00
8073242	NM_000026	ADSL	adenylosuccinate lyase	L359V only	0.82	0.74	0.90	0.90	8.62E-02	1.06E-02	8.17E-01	9.71E-01
7951034	NR_002920	SNORA8	small nucleolar RNA, H	L359V only	0.90	0.74	0.93	0.96	5.05E-01	2.46E-02	8.86E-01	1.00E+00
8116086	NM_024872	DOK3	docking protein 3	L359V only	0.77	0.74	0.94	0.88	5.40E-02	2.17E-02	9.08E-01	9.17E-01
7957467	NM_001009894	C12orf29	chromosome 12 open reading frame 29	L359V only	0.76	0.74	0.94	0.90	7.41E-02	3.36E-02	9.22E-01	1.00E+00
8092409	NM_018622	PARL	presenilin associated, rhomboid-like	L359V only	0.94	0.74	0.88	0.90	7.03E-01	1.74E-02	8.01E-01	1.00E+00
7942409	NM_176796	P2RY6	pyrimidinergic receptor P2Y, G-protein coupled, 6	L359V only	0.75	0.74	0.86	0.84	8.65E-02	4.88E-02	8.20E-01	8.21E-01
7961964	NM_018164	C12orf11	chromosome 12 open reading frame 11	L359V only	0.92	0.74	1.04	0.98	4.65E-01	6.59E-03	9.36E-01	1.00E+00
8104825	NM_018321	BXDC2	brix domain containing 2	L359V only	0.94	0.74	0.92	0.91	6.81E-01	8.65E-03	8.38E-01	1.00E+00
7922807	NM_015101	GLT25D2	glycosyltransferase 25 domain containing 2	L359V only	0.99	0.74	0.96	0.96	9.80E-01	3.39E-02	9.48E-01	1.00E+00
8045247	NM_017958	PLEKHB2	pleckstrin homology domain containing, family B (evectins) member 2	L359V only	0.80	0.74	0.90	0.89	6.76E-02	1.16E-02	8.21E-01	8.90E-01
8084035	NM_016331	ZNF639	zinc finger protein 639	L359V only	0.98	0.74	0.91	0.95	9.47E-01	3.99E-02	8.81E-01	1.00E+00
8023195	NM_005901	SMAD2	SMAD family member 2	L359V only	0.82	0.74	0.80	0.86	1.70E-01	2.82E-02	5.08E-01	8.36E-01
7920984	NM_005998	CCT3	chaperonin containing TCP1, subunit 3 (gamma)	L359V only	0.79	0.74	0.94	0.88	5.28E-02	1.29E-02	8.93E-01	8.60E-01
7966638	NM_016196	RBM19	RNA binding motif protein 19	L359V only	0.77	0.74	0.87	0.87	5.89E-02	2.14E-02	7.98E-01	8.38E-01
8095539	NM_020368	UTP3	UTP3, small subunit (SSU) processome component, homolog (S. cerevisiae)	L359V only	0.79	0.74	0.81	0.86	1.17E-01	3.00E-02	5.62E-01	8.49E-01
7917088	NM_005482	PIGK	phosphatidylinositol glycan anchor biosynthesis, class K	L359V only	0.89	0.73	0.90	0.94	3.26E-01	6.59E-03	8.09E-01	1.00E+00
8178086	NM_005346	HSPA1B	heat shock 70kDa protein 1B	L359V only	0.80	0.73	0.82	0.81	1.74E-01	4.63E-02	7.38E-01	6.27E-01
8179324	NM_005346	HSPA1B	heat shock 70kDa protein 1B	L359V only	0.80	0.73	0.82	0.81	1.74E-01	4.63E-02	7.38E-01	6.27E-01
8043349	NM_022662	ANAPC1	anaphase promoting complex subunit 1	L359V only	0.85	0.73	0.87	0.88	2.56E-01	2.16E-02	8.09E-01	9.45E-01

8030437	NM_198319	PRMT1	protein arginine methyltransferase 1	L359V only	0.77	0.73	0.95	0.85	7.87E-02	2.83E-02	9.27E-01	7.60E-01
8142019	NM_002553	ORC5L	origin recognition complex, subunit 5-like (yeast)	L359V only	0.84	0.73	0.91	0.94	2.08E-01	1.74E-02	8.52E-01	1.00E+00
8168357	NR_002309	RPS26L1	ribosomal protein S26-like 1	L359V only	0.82	0.73	0.92	0.85	7.57E-02	7.67E-03	8.41E-01	5.20E-01
8110803	NM_030782	CLPTM1L	CLPTM1-like	L359V only	0.80	0.73	0.89	0.86	8.19E-02	1.51E-02	8.14E-01	6.66E-01
7929779	NM_000392	ABCC2	ATP-binding cassette, sub-family C (CFTR	L359V only	0.93	0.73	0.96	0.90	7.45E-01	3.78E-02	9.58E-01	1.00E+00
7904314	NM_003594	TTF2	transcription termination factor, RNA polymerase II	L359V only	0.80	0.73	0.90	0.87	5.02E-02	7.29E-03	8.09E-01	6.15E-01
8011832	NM_002532	NUP88	nucleoporin 88kDa	L359V only	0.78	0.73	0.86	0.88	7.10E-02	2.03E-02	7.79E-01	9.69E-01
8117081	NM_153042	AOF1	amine oxidase (flavin containing) domain 1	L359V only	0.85	0.73	0.90	0.88	3.35E-01	3.81E-02	8.70E-01	1.00E+00
8133976	NM_006716	DBF4	DBF4 homolog (S. cerevisiae)	L359V only	1.00	0.73	0.94	0.95	9.95E-01	4.33E-02	9.22E-01	1.00E+00
8147447	NM_014754	PTDSS1	phosphatidylserine synthase 1	L359V only	0.82	0.73	0.89	0.90	8.65E-02	9.41E-03	8.11E-01	9.59E-01
8075106	NM_003595	TPST2	tyrosylprotein sulfotransferase 2	L359V only	0.88	0.73	0.91	0.90	5.11E-01	4.78E-02	8.83E-01	1.00E+00
8102342	NM_024090	ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1	L359V only	0.83	0.73	0.88	0.92	2.15E-01	2.48E-02	8.16E-01	1.00E+00
7969428	NM_006002	UCHL3	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	L359V only	0.84	0.73	0.93	0.92	3.30E-01	4.48E-02	9.01E-01	1.00E+00
8132070	NM_002047	GARS	glycyl-tRNA synthetase	L359V only	0.90	0.73	1.05	0.98	5.25E-01	2.88E-02	9.37E-01	1.00E+00
8054930	NM_032390	MKI67IP	MKI67 (FHA domain) interacting nucleolar phosphoprotein	L359V only	0.76	0.73	0.90	0.86	6.53E-02	2.66E-02	8.58E-01	8.36E-01
7912928	NM_003000	SDHB	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	L359V only	0.86	0.73	0.94	0.92	3.48E-01	3.63E-02	9.15E-01	1.00E+00
8041360	NM_017735	TTC27	tetratricopeptide repeat domain 27	L359V only	1.19	0.73	0.92	0.95	2.63E-01	3.20E-02	8.86E-01	1.00E+00
8084634	NM_016306	DNAJB11	DnaJ (Hsp40) homolog, subfamily B, member 11	L359V only	0.88	0.73	0.87	0.90	3.21E-01	1.15E-02	7.45E-01	9.81E-01
7969166	NM_173605	KCNRG	potassium channel regulator	L359V only	0.85	0.73	0.97	0.90	3.06E-01	3.28E-02	9.59E-01	1.00E+00
8098177	NM_007246	KLHL2	kelch-like 2, Mayven (Drosophila)	L359V only	0.92	0.73	0.89	0.90	6.08E-01	1.38E-02	8.14E-01	1.00E+00
8053036	NM_016058	TPRKB	TP53RK binding protein	L359V only	1.01	0.73	0.97	0.95	9.67E-01	1.63E-02	9.65E-01	1.00E+00
8080911	NM_032505	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	L359V only	0.81	0.73	0.85	0.88	1.26E-01	1.92E-02	7.28E-01	8.95E-01
7939477	NM_139178	ALKBH3	alkB, alkylation repair homolog 3 (E. coli)	L359V only	0.78	0.73	0.84	0.89	1.19E-01	3.37E-02	7.50E-01	1.00E+00
8019796	NM_002359	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	L359V only	0.88	0.73	0.81	0.82	3.87E-01	2.05E-02	5.20E-01	4.88E-01
7999025	NM_016292	TRAP1	TNF receptor-associated protein 1	L359V only	0.76	0.73	0.96	0.92	6.04E-02	2.64E-02	9.42E-01	1.00E+00
8000413	NM_145080	NSMCE1	non-SMC element 1 homolog (S. cerevisiae)	L359V only	0.96	0.73	0.99	0.96	8.31E-01	8.82E-03	9.89E-01	1.00E+00
7948900	NR_002561	SNORD30	small nucleolar RNA, C	L359V only	0.84	0.73	1.00	0.91	2.81E-01	3.01E-02	9.99E-01	1.00E+00
8142774	NM_018077	RBM28	RNA binding motif protein 28	L359V only	0.84	0.73	0.90	0.90	1.61E-01	1.24E-02	8.36E-01	1.00E+00
8018196	NM_139018	CD300LF	CD300 molecule-like family member f	L359V only	0.92	0.73	0.95	0.91	5.57E-01	1.26E-02	9.21E-01	1.00E+00
8101992	NM_022154	SLC39A8	solute carrier family 39 (zinc transporter), member 8	L359V only	0.80	0.73	0.92	0.88	5.18E-02	7.84E-03	8.53E-01	7.47E-01
7939465	NM_016142	HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12	L359V only	0.93	0.73	0.92	0.97	6.21E-01	1.11E-02	8.70E-01	1.00E+00
7926207	NM_006023	CDC123	cell division cycle 123 homolog (S. cerevisiae)	L359V only	0.83	0.73	0.89	0.88	1.38E-01	1.33E-02	8.14E-01	8.51E-01
8136631	NM_003143	SSBP1	single-stranded DNA binding protein 1	L359V only	0.91	0.73	0.97	0.94	5.99E-01	2.41E-02	9.65E-01	1.00E+00
8158224	NM_005094	SLC27A4	solute carrier family 27 (fatty acid transporter), member 4	L359V only	0.85	0.73	1.00	0.90	1.90E-01	1.04E-02	9.96E-01	9.84E-01
8085300	NM_183352	SEC13	SEC13 homolog (S. cerevisiae)	L359V only	0.90	0.73	0.94	0.89	5.57E-01	3.78E-02	9.16E-01	1.00E+00
7924351	NM_004446	EPRS	glutamyl-prolyl-tRNA synthetase	L359V only	0.84	0.73	0.96	0.95	1.77E-01	1.18E-02	9.36E-01	1.00E+00
7917674	AK300794	SET	SET nuclear oncogene	L359V only	0.88	0.73	0.87	0.90	2.88E-01	8.89E-03	7.38E-01	9.45E-01
8147548	NM_015029	POP1	processing of precursor 1, ribonuclease P	L359V only	0.80	0.73	0.83	0.82	7.90E-02	1.40E-02	6.11E-01	4.41E-01
8026520	NM_005370	RAB8A	RAB8A, member RAS oncogene family	L359V only	0.83	0.73	0.85	0.85	1.81E-01	1.93E-02	7.44E-01	7.35E-01
7932311	NM_012425	RSU1	Ras suppressor protein 1	L359V only	0.80	0.73	0.87	0.86	1.47E-01	2.88E-02	8.15E-01	9.07E-01
8115664	ENST00000393959	GABRB2	gamma-aminobutyric acid (GABA) A receptor, beta 2	L359V only	0.79	0.73	0.83	0.84	1.04E-01	2.26E-02	6.65E-01	6.66E-01
7986110	NM_002005	FES	feline sarcoma oncogene	L359V only	0.77	0.73	0.94	0.85	6.39E-02	2.08E-02	9.01E-01	7.21E-01
7995697	NM_017839	LPCAT2	lysophosphatidylcholine acyltransferase 2	L359V only	1.11	0.73	1.11	0.98	4.23E-01	8.88E-03	8.23E-01	1.00E+00
8128138	NM_014611	MDN1	MDN1, midasin homolog (yeast)	L359V only	0.79	0.73	0.83	0.86	1.51E-01	4.31E-02	7.66E-01	9.45E-01
8103437	NM_005038	PPID	peptidylprolyl isomerase D	L359V only	0.90	0.73	0.86	0.88	6.12E-01	4.85E-02	8.23E-01	1.00E+00
8160647	NM_004323	BAG1	BCL2-associated athanogene	L359V only	0.78	0.73	0.87	0.85	6.87E-02	1.75E-02	8.01E-01	7.18E-01
8051547	NM_005813	PRKD3	protein kinase D3	L359V only	0.83	0.73	0.88	0.88	2.73E-01	4.56E-02	8.42E-01	1.00E+00
8145889	NM_004095	EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1	L359V only	0.88	0.73	1.11	0.98	4.92E-01	4.19E-02	8.76E-01	1.00E+00
8112331	NM_030940	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	L359V only	0.87	0.72	0.94	0.94	3.25E-01	1.64E-02	9.06E-01	1.00E+00
7970737	NM_004119	FLT3	fms-related tyrosine kinase 3	L359V only	0.96	0.72	0.81	0.96	8.79E-01	4.82E-02	7.33E-01	1.00E+00
7979473	NM_016029	DHRS7	dehydrogenase	L359V only	0.91	0.72	0.92	0.91	6.00E-01	2.96E-02	8.93E-01	1.00E+00
8072004	NM_001013618	IGLL3	immunoglobulin lambda-like polypeptide 3	L359V only	0.82	0.72	1.07	0.94	1.70E-01	1.94E-02	8.97E-01	1.00E+00
8014787	---			L359V only	0.80	0.72	0.79	0.85	2.17E-01	4.98E-02	6.66E-01	9.18E-01
8044263	NM_006267	RANBP2	RAN binding protein 2	L359V only	0.89	0.72	0.89	0.92	3.63E-01	8.01E-03	8.03E-01	1.00E+00
8077858	NM_001136031	ATG7	ATG7 autophagy related 7 homolog (S. cerevisiae)	L359V only	0.86	0.72	0.92	0.88	2.46E-01	1.12E-02	8.76E-01	8.65E-01
7989915	NM_017858	TIPIN	TIMELESS interacting protein	L359V only	0.85	0.72	0.80	0.88	3.52E-01	4.23E-02	6.50E-01	1.00E+00
7930882	NM_207009	FAM45A	family with sequence similarity 45, member A	L359V only	0.91	0.72	1.04	0.92	4.89E-01	6.74E-03	9.33E-01	1.00E+00
8030364	NR_000019	SNORD34	small nucleolar RNA, C	L359V only	0.81	0.72	1.00	0.93	1.84E-01	2.84E-02	9.99E-01	1.00E+00
8032863	NM_019107	C19orf10	chromosome 19 open reading frame 10	L359V only	0.82	0.72	0.93	0.87	7.11E-02	5.36E-03	8.76E-01	6.27E-01
8039859	NM_002255	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	L359V only	0.74	0.72	0.81	0.81	7.09E-02	3.85E-02	7.01E-01	6.27E-01
7942879	NM_018480	TMEM126B	transmembrane protein 126B	L359V only	0.79	0.72	0.89	0.86	1.49E-01	3.46E-02	8.48E-01	9.11E-01
8138640	NM_018947	CYCS	cytochrome c, somatic	L359V only	0.89	0.72	0.93	0.91	4.81E-01	2.14E-02	8.94E-01	1.00E+00
7908639	BC106877	C1orf106	chromosome 1 open reading frame 106	L359V only	0.80	0.72	0.89	0.84	7.09E-02	8.26E-03	8.09E-01	4.98E-01
8166230	NM_018360	CXorf15	chromosome X open reading frame 15	L359V only	0.82	0.72	1.01	0.93	1.04E-01	8.37E-03	9.91E-01	1.00E+00
8162086	NM_015239	AGTPBP1	ATP	L359V only	0.87	0.72	0.88	0.91	2.11E-01	4.26E-03	7.14E-01	1.00E+00

8100495	NM_002703	PPAT	phosphoribosyl pyrophosphate amidotransferase	L359V only	0.83	0.72	0.91	0.91	2.35E-01	2.85E-02	8.77E-01	1.00E+00
7926875	NM_012342	BAMBI	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	L359V only	0.73	0.72	0.90	0.93	7.10E-02	4.61E-02	8.80E-01	1.00E+00
8044919	NM_002881	RALB	v-ral simian leukemia viral oncogene homolog B (ras related; GTP binding protein)	L359V only	1.15	0.72	1.06	0.99	4.22E-01	3.03E-02	9.22E-01	1.00E+00
8064790	NM_014737	RASSF2	Ras association (RalGDS	L359V only	0.89	0.72	0.96	0.90	4.14E-01	1.01E-02	9.29E-01	1.00E+00
8088092	NM_052859	RFT1	RFT1 homolog (S. cerevisiae)	L359V only	0.78	0.72	0.92	0.89	5.58E-02	1.17E-02	8.64E-01	9.32E-01
8081853	NM_152305	KTELC1	KTEL (Lys-Tyr-Glu-Leu) containing 1	L359V only	0.82	0.72	0.89	0.91	1.07E-01	9.08E-03	8.09E-01	1.00E+00
8168416	BC072683	USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	L359V only	0.88	0.72	0.90	0.89	5.25E-01	4.65E-02	8.82E-01	1.00E+00
7933933	NM_021800	DNAJC12	DnaJ (Hsp40) homolog, subfamily C, member 12	L359V only	0.79	0.72	0.92	0.90	1.85E-01	4.33E-02	9.01E-01	1.00E+00
8096296	AY956764	HSP90AB3P	heat shock protein 90kDa alpha (cytosolic), class B member 3 (pseudogene)	L359V only	1.00	0.72	0.95	0.99	9.92E-01	7.96E-03	9.02E-01	1.00E+00
8003068	NM_005792	MPHOSPH6	M-phase phosphoprotein 6	L359V only	0.97	0.72	0.90	0.94	9.02E-01	1.45E-02	8.41E-01	1.00E+00
7981290	NM_004184	WARS	tryptophanyl-tRNA synthetase	L359V only	0.85	0.72	1.06	0.98	2.81E-01	2.05E-02	9.13E-01	1.00E+00
8075529	NM_014338	PISD	phosphatidylserine decarboxylase	L359V only	0.80	0.72	0.91	0.86	6.87E-02	7.85E-03	8.36E-01	6.34E-01
7953594	NM_006331	EMG1	EMG1 nucleolar protein homolog (S. cerevisiae)	L359V only	0.86	0.72	0.86	0.88	2.78E-01	1.25E-02	7.50E-01	9.02E-01
8009366	NM_015462	NOL11	nucleolar protein 11	L359V only	0.90	0.72	0.92	0.93	4.92E-01	1.35E-02	8.77E-01	1.00E+00
8148476	NM_014957	DENND3	DENN	L359V only	0.77	0.72	0.98	0.92	6.52E-02	1.51E-02	9.72E-01	1.00E+00
7908766	NM_006335	TIMM17A	translocase of inner mitochondrial membrane 17 homolog A (yeast)	L359V only	0.82	0.72	0.85	0.84	2.37E-01	3.59E-02	8.03E-01	8.01E-01
7959294	NM_032790	ORAI1	ORAI calcium release-activated calcium modulator 1	L359V only	0.73	0.72	0.88	0.81	5.67E-02	3.46E-02	8.38E-01	6.07E-01
8157582	NM_000177	GSN	gelsolin (amyloidosis, Finnish type)	L359V only	0.80	0.72	0.82	0.85	1.49E-01	2.26E-02	6.76E-01	8.13E-01
7918284	NM_005645	TAF13	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kD	L359V only	0.98	0.72	0.93	0.87	9.44E-01	4.67E-02	9.25E-01	1.00E+00
8056753	NM_024770	METTL8	methyltransferase like 8	L359V only	0.86	0.72	0.86	0.88	2.52E-01	9.28E-03	7.23E-01	8.36E-01
8044965	NM_004622	TSN	translin	L359V only	0.79	0.72	0.92	0.91	1.08E-01	1.71E-02	8.76E-01	1.00E+00
8078405	NM_138410	CMTM7	CKLF-like MARVEL transmembrane domain containing 7	L359V only	0.81	0.72	0.99	0.87	1.30E-01	1.42E-02	9.86E-01	8.84E-01
8060839	NM_019095	CRLS1	cardiolipin synthase 1	L359V only	0.84	0.72	0.92	0.89	3.28E-01	3.29E-02	8.89E-01	1.00E+00
8109802	NM_002887	RARS	arginyl-tRNA synthetase	L359V only	0.82	0.72	0.83	0.86	1.35E-01	1.16E-02	5.96E-01	7.16E-01
7950683	NM_024678	NARS2	asparaginyl-tRNA synthetase 2, mitochondrial (putative)	L359V only	0.84	0.72	0.91	0.93	3.12E-01	3.29E-02	8.86E-01	1.00E+00
7995258	NM_003414	ZNF267	zinc finger protein 267	L359V only	0.90	0.72	0.87	0.90	5.53E-01	2.85E-02	8.20E-01	1.00E+00
8169868	NM_006649	UTP14A	UTP14, U3 small nucleolar ribonucleoprotein, homolog A (yeast)	L359V only	0.82	0.72	0.89	0.90	1.00E-01	7.21E-03	8.06E-01	9.62E-01
7944656	NM_006918	SC5DL	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	L359V only	0.98	0.72	0.97	0.91	9.40E-01	2.08E-02	9.59E-01	1.00E+00
7900201	NM_016037	UTP11L	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	L359V only	0.83	0.72	0.91	0.91	9.95E-02	4.42E-03	8.20E-01	1.00E+00
8141150	NM_133436	ASNS	asparagine synthetase	L359V only	0.82	0.72	0.99	1.01	2.52E-01	3.32E-02	9.94E-01	1.00E+00
8157283	NM_004697	PRPF4	PRP4 pre-mRNA processing factor 4 homolog (yeast)	L359V only	0.78	0.71	0.90	0.89	8.91E-02	2.06E-02	8.64E-01	1.00E+00
8084982	NR_024388	LOC152217	hypothetical LOC152217	L359V only	0.89	0.71	0.94	0.91	3.94E-01	8.26E-03	8.98E-01	1.00E+00
8049317	NM_152879	DGKD	diacylglycerol kinase, delta 130kDa	L359V only	0.84	0.71	0.92	0.90	1.98E-01	1.07E-02	8.75E-01	1.00E+00
8131860	BC012331	C7orf30	chromosome 7 open reading frame 30	L359V only	0.79	0.71	0.86	0.86	1.39E-01	2.94E-02	8.09E-01	9.58E-01
7935730	NM_018294	CWF19L1	CWF19-like 1, cell cycle control (S. pombe)	L359V only	0.81	0.71	0.87	0.87	1.63E-01	2.01E-02	8.19E-01	9.13E-01
8125919	NM_004117	FKBP5	FK506 binding protein 5	L359V only	0.82	0.71	0.87	0.85	1.85E-01	2.16E-02	8.23E-01	8.38E-01
8126153	NM_003740	KCNK5	potassium channel, subfamily K, member 5	L359V only	0.79	0.71	0.84	0.85	1.04E-01	1.65E-02	7.28E-01	7.48E-01
8086201	NM_001607	ACAA1	acetyl-Coenzyme A acyltransferase 1	L359V only	0.93	0.71	0.86	0.89	6.65E-01	1.52E-02	8.01E-01	1.00E+00
8080419	NM_206825	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	L359V only	0.79	0.71	0.87	0.88	1.32E-01	2.45E-02	8.16E-01	1.00E+00
8146717	NM_013257	SGK3	serum	L359V only	0.79	0.71	0.85	0.85	1.00E-01	1.51E-02	7.68E-01	6.95E-01
8150364	NM_031940	TM2D2	TM2 domain containing 2	L359V only	0.82	0.71	0.87	0.84	2.67E-01	3.41E-02	8.34E-01	8.60E-01
7936091	NM_032747	USMG5	up-regulated during skeletal muscle growth 5 homolog (mouse)	L359V only	0.76	0.71	0.89	0.83	5.43E-02	1.40E-02	8.25E-01	5.96E-01
8066117	NM_015474	SAMHD1	SAM domain and HD domain 1	L359V only	0.82	0.71	0.74	0.84	1.79E-01	1.82E-02	2.51E-01	6.61E-01
8150592	NM_005195	CEBPD	CCAAT	L359V only	0.74	0.71	0.82	0.86	7.86E-02	3.25E-02	7.49E-01	9.78E-01
8140420	NR_003262	FDPSL2A	MGC44478	L359V only	0.89	0.71	1.02	0.92	4.38E-01	9.62E-03	9.81E-01	1.00E+00
8119661	BC011933	C6orf153	chromosome 6 open reading frame 153	L359V only	0.86	0.71	0.88	0.87	3.63E-01	2.26E-02	8.34E-01	9.59E-01
8175924	NM_003491	ARD1A	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)	L359V only	0.82	0.71	0.92	0.84	1.22E-01	8.99E-03	8.73E-01	5.52E-01
8001876	NM_001018159	NAE1	NEDD8 activating enzyme E1 subunit 1	L359V only	0.81	0.71	0.88	0.94	1.46E-01	1.79E-02	8.34E-01	1.00E+00
7900922	NM_004047	ATP6V0B	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b	L359V only	0.75	0.71	0.93	0.84	7.27E-02	2.47E-02	9.09E-01	7.46E-01
8144669	NM_004462	FDFT1	farnesyl-diphosphate farnesyltransferase 1	L359V only	0.87	0.71	1.00	0.91	2.19E-01	4.39E-03	9.97E-01	9.88E-01
8018082	NM_139177	SLC39A11	solute carrier family 39 (metal ion transporter), member 11	L359V only	1.00	0.71	0.99	0.91	9.97E-01	2.17E-02	9.90E-01	1.00E+00
8173755	NM_004867	ITM2A	integral membrane protein 2A	L359V only	1.07	0.71	1.12	0.96	7.38E-01	2.64E-02	8.53E-01	1.00E+00
7958375	---			L359V only	0.86	0.71	0.91	0.92	3.58E-01	2.30E-02	8.77E-01	1.00E+00
8085660	NM_206831	DPH3	DPH3, KTI11 homolog (S. cerevisiae)	L359V only	0.84	0.71	0.90	0.87	2.35E-01	1.34E-02	8.52E-01	8.96E-01
8035905	NM_032139	ANKRD27	ankyrin repeat domain 27 (VPS9 domain)	L359V only	0.98	0.71	1.04	0.95	9.13E-01	9.05E-03	9.52E-01	1.00E+00
8114778	NM_004483	GCSH	glycine cleavage system protein H (aminomethyl carrier)	L359V only	0.87	0.71	0.97	0.95	3.35E-01	1.19E-02	9.67E-01	1.00E+00
8140443	NR_003262	FDPSL2A	MGC44478	L359V only	0.90	0.71	0.98	0.91	5.14E-01	1.34E-02	9.80E-01	1.00E+00
8026915	NM_015683	ARRDC2	arrestin domain containing 2	L359V only	0.88	0.71	0.94	0.86	5.22E-01	3.43E-02	9.31E-01	1.00E+00
8074399	NM_007098	CLTCL1	clathrin, heavy chain-like 1	L359V only	0.76	0.70	0.89	0.86	6.78E-02	1.72E-02	8.38E-01	8.90E-01
7938890	NM_005788	PRMT3	protein arginine methyltransferase 3	L359V only	0.86	0.70	0.91	0.93	2.73E-01	9.01E-03	8.60E-01	1.00E+00
8098195	NM_006745	SC4MOL	sterol-C4-methyl oxidase-like	L359V only	0.88	0.70	1.01	0.91	5.11E-01	3.71E-02	9.94E-01	1.00E+00
8092265	NM_020409	MRPL47	mitochondrial ribosomal protein L47	L359V only	0.81	0.70	0.92	0.91	1.77E-01	2.10E-02	8.86E-01	1.00E+00
8130732	NM_016098	BRP44L	brain protein 44-like	L359V only	0.78	0.70	0.84	0.85	7.09E-02	9.86E-03	6.82E-01	7.09E-01
8044278	NM_144978	CCDC138	coiled-coil domain containing 138	L359V only	0.91	0.70	0.90	0.92	6.67E-01	3.04E-02	8.78E-01	1.00E+00
8046604	NM_003659	AGPS	alkylglycerone phosphate synthase	L359V only	0.96	0.70	0.87	0.93	8.21E-01	4.31E-03	7.33E-01	1.00E+00

8017437	NM_017647	FTSJ3	FtsJ homolog 3 (E. coli)	L359V only	0.76	0.70	0.85	0.85	9.36E-02	2.60E-02	8.09E-01	8.99E-01
8099073	NM_002337	LRPAP1	low density lipoprotein receptor-related protein associated protein 1	L359V only	0.80	0.70	0.95	0.91	9.82E-02	1.10E-02	9.34E-01	1.00E+00
8085665	NM_015150	RFTN1	raftlin, lipid raft linker 1	L359V only	0.84	0.70	0.98	0.92	3.20E-01	2.64E-02	9.81E-01	1.00E+00
7922343	NM_003326	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	L359V only	0.82	0.70	1.01	0.85	3.10E-01	4.75E-02	9.90E-01	1.00E+00
7940717	NM_001012661	SLC3A2	solute carrier family 3 (activators of dibasic and neutral amino acid transport), memb	L359V only	0.88	0.70	1.09	0.98	4.70E-01	2.56E-02	8.90E-01	1.00E+00
8031825	U71363	ZNF587	zinc finger protein 587	L359V only	0.77	0.70	1.01	0.91	1.47E-01	4.13E-02	9.91E-01	1.00E+00
8020411	NM_006938	SNRPD1	small nuclear ribonucleoprotein D1 polypeptide 16kDa	L359V only	0.80	0.70	0.82	0.87	1.64E-01	2.05E-02	7.17E-01	9.47E-01
7923978	NM_001773	CD34	CD34 molecule	L359V only	0.86	0.70	1.13	0.90	3.27E-01	1.23E-02	8.23E-01	1.00E+00
7939376	NM_174902	LDLRAD3	low density lipoprotein receptor class A domain containing 3	L359V only	0.90	0.70	0.88	0.85	4.87E-01	1.13E-02	8.14E-01	7.42E-01
8029521	NM_001128917	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	L359V only	0.73	0.70	0.87	0.83	5.16E-02	2.05E-02	8.23E-01	7.09E-01
8080184	NM_000688	ALAS1	aminolevulinate, delta-, synthase 1	L359V only	0.80	0.70	0.99	0.89	1.84E-01	2.37E-02	9.92E-01	1.00E+00
8110920	NM_024091	FASTKD3	FAST kinase domains 3	L359V only	0.86	0.70	0.89	0.88	1.94E-01	4.26E-03	8.01E-01	7.60E-01
8169603	NM_001031855	LONRF3	LON peptidase N-terminal domain and ring finger 3	L359V only	0.83	0.70	1.10	0.95	1.81E-01	9.90E-03	8.54E-01	1.00E+00
8078173	NM_138381	OXNAD1	oxidoreductase NAD-binding domain containing 1	L359V only	0.81	0.70	0.83	0.88	1.08E-01	8.88E-03	6.04E-01	8.98E-01
7932160	BC072452	FAM107B	family with sequence similarity 107, member B	L359V only	0.82	0.70	0.98	0.96	1.84E-01	1.47E-02	9.81E-01	1.00E+00
8042588	NM_005791	MPHOSPH10	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	L359V only	0.86	0.70	0.82	0.87	4.56E-01	3.84E-02	7.79E-01	1.00E+00
7938592	NM_032228	FAR1	fatty acyl CoA reductase 1	L359V only	0.84	0.70	0.91	0.91	1.18E-01	3.65E-03	8.36E-01	1.00E+00
8075182	NM_005080	XBP1	X-box binding protein 1	L359V only	0.90	0.70	1.02	0.94	4.26E-01	6.74E-03	9.81E-01	1.00E+00
8089988	NM_001017928	CCDC58	coiled-coil domain containing 58	L359V only	0.83	0.70	0.95	0.93	2.51E-01	2.21E-02	9.42E-01	1.00E+00
7910014	NM_014184	CNIH4	cornichon homolog 4 (Drosophila)	L359V only	0.76	0.70	1.20	0.95	6.03E-02	1.29E-02	7.20E-01	1.00E+00
7937735	NM_002339	LSP1	lymphocyte-specific protein 1	L359V only	0.76	0.70	0.87	0.82	5.49E-02	1.25E-02	8.14E-01	5.55E-01
8047223	NM_002157	HSPE1	heat shock 10kDa protein 1 (chaperonin 10)	L359V only	0.75	0.70	0.87	0.83	7.09E-02	1.96E-02	8.25E-01	6.73E-01
7954591	NM_021821	MRPS35	mitochondrial ribosomal protein S35	L359V only	0.85	0.70	0.91	0.93	2.07E-01	7.15E-03	8.55E-01	1.00E+00
8112220	NM_001104631	PDE4D	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Dros	L359V only	0.84	0.70	0.95	0.90	3.70E-01	4.08E-02	9.52E-01	1.00E+00
8005839	NM_014573	TMEM97	transmembrane protein 97	L359V only	0.80	0.70	0.93	0.87	1.82E-01	2.23E-02	9.12E-01	1.00E+00
8171879	XM_942610	LOC389842	similar to RanBP1	L359V only	0.85	0.70	0.92	0.90	2.58E-01	9.85E-03	8.80E-01	1.00E+00
8121489	NM_001634	AMD1	adenosylmethionine decarboxylase 1	L359V only	0.86	0.70	0.94	0.91	2.55E-01	7.80E-03	9.07E-01	1.00E+00
8139203	NM_138701	C7orf11	chromosome 7 open reading frame 11	L359V only	0.94	0.70	0.96	0.95	7.83E-01	2.02E-02	9.53E-01	1.00E+00
7965200	NM_014167	CCDC59	coiled-coil domain containing 59	L359V only	1.00	0.70	0.94	0.99	9.92E-01	2.94E-02	9.34E-01	1.00E+00
7936641	NM_213649	SFXN4	sideroflexin 4	L359V only	0.83	0.70	0.96	0.92	9.08E-02	3.28E-03	9.36E-01	1.00E+00
8135638	NM_018412	ST7	suppression of tumorigenicity 7	L359V only	1.09	0.69	1.05	0.96	6.81E-01	2.85E-02	9.43E-01	1.00E+00
8071069	NM_014339	IL17RA	interleukin 17 receptor A	L359V only	0.80	0.69	0.89	0.85	5.15E-02	3.53E-03	8.06E-01	5.23E-01
7953697	---			L359V only	0.86	0.69	0.90	0.96	4.55E-01	2.85E-02	8.81E-01	1.00E+00
7907859	XR_038100	LOC100130511	hypothetical LOC100130511	L359V only	0.91	0.69	0.90	0.95	7.00E-01	3.47E-02	8.81E-01	1.00E+00
8103011	NM_199324	OTUD4	OTU domain containing 4	L359V only	0.98	0.69	0.94	0.95	9.23E-01	5.91E-03	8.89E-01	1.00E+00
8000323	NM_005003	NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha	L359V only	0.80	0.69	0.88	0.85	1.28E-01	9.98E-03	8.23E-01	7.16E-01
7948904	NR_002562	SNORD28	small nucleolar RNA, C	L359V only	1.03	0.69	1.02	1.04	9.19E-01	1.56E-02	9.83E-01	1.00E+00
7928471	NM_006721	ADK	adenosine kinase	L359V only	0.92	0.69	0.90	0.92	4.76E-01	2.15E-03	7.99E-01	1.00E+00
7987027	NR_024074	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	L359V only	0.80	0.69	0.85	0.86	9.52E-02	7.47E-03	7.28E-01	7.33E-01
8110392	NM_017510	TMED9	transmembrane emp24 protein transport domain containing 9	L359V only	0.96	0.69	0.96	0.89	8.28E-01	8.27E-03	9.52E-01	9.89E-01
7915015	NM_013285	GNL2	guanine nucleotide binding protein-like 2 (nucleolar)	L359V only	0.80	0.69	0.90	0.89	1.72E-01	1.75E-02	8.68E-01	1.00E+00
8088895	NR_024241	FAM86D	family with sequence similarity 86, member D	L359V only	0.81	0.69	0.91	0.85	1.65E-01	1.17E-02	8.64E-01	7.85E-01
8076455	NM_015703	RRP7A	ribosomal RNA processing 7 homolog A (S. cerevisiae)	L359V only	0.79	0.69	0.80	0.85	1.08E-01	1.10E-02	5.21E-01	7.38E-01
8082003	NM_018456	EAF2	ELL associated factor 2	L359V only	0.73	0.69	0.94	0.87	9.47E-02	3.94E-02	9.36E-01	1.00E+00
8005953	NR_000010	SNORD4A	small nucleolar RNA, C	L359V only	0.80	0.69	0.87	0.89	5.40E-02	3.64E-03	7.33E-01	9.07E-01
8057554	AF057356	CACYBP	calcyclin binding protein	L359V only	0.91	0.69	0.87	0.92	4.50E-01	3.02E-03	7.35E-01	1.00E+00
8063386	NM_005194	CEBPB	CCAAT	L359V only	1.07	0.69	1.02	0.91	7.35E-01	1.48E-02	9.82E-01	1.00E+00
8170590	NM_015922	NSDHL	NAD(P) dependent steroid dehydrogenase-like	L359V only	0.84	0.69	0.97	0.84	1.29E-01	2.61E-03	9.52E-01	4.11E-01
8089040	NM_001042533	MINA	MYC induced nuclear antigen	L359V only	0.77	0.69	0.91	0.88	1.98E-01	4.41E-02	8.98E-01	1.00E+00
8013015	NM_181716	CENPV	centromere protein V	L359V only	0.82	0.69	0.94	0.90	1.98E-01	1.32E-02	9.22E-01	1.00E+00
8022488	NM_138340	ABHD3	abhydrolase domain containing 3	L359V only	0.82	0.69	0.83	0.84	3.11E-01	3.14E-02	8.03E-01	9.26E-01
8061668	NM_002110	HCK	hemopoietic cell kinase	L359V only	0.78	0.69	0.92	0.87	2.28E-01	4.91E-02	9.15E-01	1.00E+00
8101099	NM_018115	SDAD1	SDA1 domain containing 1	L359V only	0.81	0.69	0.93	0.91	9.61E-02	5.39E-03	8.81E-01	1.00E+00
8008627	NM_005450	NOG	noggin	L359V only	0.76	0.69	1.05	0.88	8.65E-02	1.71E-02	9.40E-01	1.00E+00
8159854	NM_014878	KIAA0020	KIAA0020	L359V only	0.89	0.69	0.94	0.90	3.72E-01	4.53E-03	8.86E-01	1.00E+00
8052932	---			L359V only	0.75	0.68	1.04	0.82	1.22E-01	3.24E-02	9.65E-01	8.38E-01
8017143	NM_016077	PTRH2	peptidyl-tRNA hydrolase 2	L359V only	0.80	0.68	0.90	0.88	2.24E-01	2.90E-02	8.85E-01	1.00E+00
8083656	NM_022736	MFSD1	major facilitator superfamily domain containing 1	L359V only	0.80	0.68	0.98	0.91	7.60E-02	4.94E-03	9.71E-01	1.00E+00
8119974	NM_001078175	SLC29A1	solute carrier family 29 (nucleoside transporters), member 1	L359V only	0.80	0.68	0.95	0.85	7.57E-02	4.91E-03	9.13E-01	6.34E-01
8169984	NM_000194	HPRT1	hypoxanthine phosphoribosyltransferase 1	L359V only	0.86	0.68	0.91	0.90	3.39E-01	1.32E-02	8.76E-01	1.00E+00
7935692	NM_001100626	ERLIN1	ER lipid raft associated 1	L359V only	0.81	0.68	0.92	0.92	1.22E-01	6.23E-03	8.79E-01	1.00E+00
7965918	NM_016575	NT5DC3	5'-nucleotidase domain containing 3	L359V only	0.76	0.68	0.86	0.87	8.93E-02	1.68E-02	8.23E-01	9.89E-01
8069332	NR_002776	MCM3APAS	MCM3AP antisense RNA (non-protein coding)	L359V only	0.80	0.68	0.89	0.89	1.96E-01	2.04E-02	8.63E-01	1.00E+00
7916570	NM_145243	OMA1	OMA1 homolog, zinc metallopeptidase (S. cerevisiae)	L359V only	1.04	0.68	0.96	0.95	8.08E-01	3.16E-03	9.24E-01	1.00E+00
7958211	NM_152318	C12orf45	chromosome 12 open reading frame 45	L359V only	0.78	0.68	0.86	0.89	1.45E-01	2.23E-02	8.25E-01	1.00E+00

8082133	NM_006810	PDIA5	protein disulfide isomerase family A, member 5	L359V only	0.98	0.68	1.01	0.96	9.27E-01	9.85E-03	9.88E-01	1.00E+00
8162744	NM_003389	CORO2A	coronin, actin binding protein, 2A	L359V only	1.04	0.68	1.15	0.93	7.97E-01	3.68E-03	7.52E-01	1.00E+00
8123819	NM_004280	EEF1E1	eukaryotic translation elongation factor 1 epsilon 1	L359V only	0.82	0.68	0.91	0.89	1.74E-01	9.23E-03	8.70E-01	1.00E+00
8047815	NM_001136194	FASTKD2	FAST kinase domains 2	L359V only	0.80	0.68	0.81	0.83	1.01E-01	7.45E-03	5.02E-01	6.04E-01
8011245	NM_018128	TSR1	TSR1, 20S rRNA accumulation, homolog (S. cerevisiae)	L359V only	0.72	0.68	0.85	0.85	5.73E-02	1.93E-02	8.11E-01	9.23E-01
7967212	NM_002150	HPD	4-hydroxyphenylpyruvate dioxygenase	L359V only	0.69	0.68	0.84	0.79	5.15E-02	2.91E-02	8.14E-01	6.43E-01
8150217	NR_003671	hCG_1640171	hCG1640171	L359V only	0.95	0.68	0.74	0.87	8.53E-01	3.53E-02	5.00E-01	1.00E+00
7982935	---			L359V only	0.90	0.68	0.97	0.88	6.18E-01	2.36E-02	9.76E-01	1.00E+00
8112807	NM_000046	ARSB	arylsulfatase B	L359V only	1.07	0.68	1.05	0.94	6.33E-01	2.40E-03	9.09E-01	1.00E+00
8131583	NM_014038	BZW2	basic leucine zipper and W2 domains 2	L359V only	0.81	0.68	0.91	0.89	1.30E-01	7.29E-03	8.63E-01	1.00E+00
7934185	NM_022153	C10orf54	chromosome 10 open reading frame 54	L359V only	0.74	0.68	0.93	0.83	5.05E-02	1.16E-02	9.09E-01	6.73E-01
8097011	---			L359V only	0.75	0.68	0.96	0.90	1.34E-01	3.29E-02	9.60E-01	1.00E+00
7977786	NM_003982	SLC7A7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	L359V only	1.11	0.68	1.05	0.94	6.45E-01	2.75E-02	9.49E-01	1.00E+00
8095894	NM_020236	MRPL1	mitochondrial ribosomal protein L1	L359V only	0.74	0.68	0.76	0.81	5.23E-02	1.09E-02	3.29E-01	5.49E-01
7944530	NM_178507	OAF	OAF homolog (Drosophila)	L359V only	0.84	0.68	1.00	0.86	3.11E-01	1.64E-02	9.99E-01	9.56E-01
8014066	NM_001003927	EVI2A	ecotropic viral integration site 2A	L359V only	0.75	0.68	0.97	0.95	1.08E-01	2.26E-02	9.70E-01	1.00E+00
7902104	NM_002600	PDE4B	phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 dunce homolog, Dros	L359V only	0.79	0.67	0.94	0.87	1.44E-01	1.49E-02	9.27E-01	1.00E+00
7904967	---			L359V only	0.83	0.67	1.09	0.91	3.73E-01	2.98E-02	9.09E-01	1.00E+00
7945875	NM_001099653	FAM86C	family with sequence similarity 86, member C	L359V only	0.75	0.67	0.93	0.85	1.04E-01	2.04E-02	9.16E-01	9.32E-01
7967456	NM_145058	RILPL2	Rab interacting lysosomal protein-like 2	L359V only	0.81	0.67	0.88	0.88	2.76E-01	2.93E-02	8.66E-01	1.00E+00
8096109	NM_016067	MRPS18C	mitochondrial ribosomal protein S18C	L359V only	1.02	0.67	0.85	0.93	9.39E-01	2.34E-02	8.23E-01	1.00E+00
8106820	NM_006467	POLR3G	polymerase (RNA) III (DNA directed) polypeptide G (32kD)	L359V only	0.92	0.67	0.97	0.91	6.17E-01	7.02E-03	9.67E-01	1.00E+00
8000236	NM_001802	CDR2	cerebellar degeneration-related protein 2, 62kDa	L359V only	1.01	0.67	0.99	0.94	9.42E-01	3.16E-03	9.94E-01	1.00E+00
8084794	NM_002182	IL1RAP	interleukin 1 receptor accessory protein	L359V only	1.15	0.67	1.07	0.97	4.33E-01	1.48E-02	9.15E-01	1.00E+00
8100231	NM_003215	TEC	tec protein tyrosine kinase	L359V only	1.11	0.67	0.90	0.89	4.73E-01	3.67E-03	8.34E-01	9.45E-01
7909866	NM_017898	MOSC2	MOCO sulphurase C-terminal domain containing 2	L359V only	0.71	0.67	0.79	0.90	1.18E-01	4.89E-02	7.66E-01	1.00E+00
8065855	NM_018217	EDEM2	ER degradation enhancer, mannosidase alpha-like 2	L359V only	0.83	0.67	0.96	0.87	2.68E-01	1.49E-02	9.56E-01	1.00E+00
8081953	NM_005513	GTF2E1	general transcription factor IIE, polypeptide 1, alpha 56kDa	L359V only	0.77	0.67	0.85	0.85	2.25E-01	4.75E-02	8.41E-01	1.00E+00
7931873	NM_001494	GDI2	GDP dissociation inhibitor 2	L359V only	0.93	0.67	0.96	0.92	6.85E-01	7.53E-03	9.43E-01	1.00E+00
7934553	NM_032772	ZNF503	zinc finger protein 503	L359V only	0.73	0.67	0.80	0.72	1.26E-01	3.88E-02	7.66E-01	3.63E-01
8081786	NM_024638	QTRTD1	queuine tRNA-ribosyltransferase domain containing 1	L359V only	0.80	0.67	0.91	0.86	1.35E-01	8.43E-03	8.76E-01	8.60E-01
7943984	NM_006006	ZBTB16	zinc finger and BTB domain containing 16	L359V only	0.91	0.67	1.13	0.93	6.96E-01	2.52E-02	8.70E-01	1.00E+00
7951036	NR_003033	SNORD5	small nucleolar RNA, C	L359V only	0.83	0.67	1.01	0.93	3.64E-01	3.32E-02	9.90E-01	1.00E+00
8149296	NM_017884	PINX1	PIN2-interacting protein 1	L359V only	0.74	0.67	0.83	0.85	9.34E-02	2.33E-02	8.05E-01	9.78E-01
8042391	NM_002664	PLEK	pleckstrin	L359V only	1.09	0.67	1.16	1.06	6.23E-01	5.91E-03	7.77E-01	1.00E+00
8048703	XM_938653	LOC646644	similar to Chromosome 12 open reading frame 31	L359V only	0.89	0.67	1.02	0.91	4.31E-01	4.23E-03	9.74E-01	1.00E+00
7922104	NM_004483	GCSH	glycine cleavage system protein H (aminomethyl carrier)	L359V only	0.84	0.67	0.99	0.93	2.23E-01	7.08E-03	9.84E-01	1.00E+00
7950983	NM_012124	CHORDC1	cysteine and histidine-rich domain (CHORD)-containing 1	L359V only	0.89	0.67	0.88	0.84	5.69E-01	1.93E-02	8.42E-01	8.90E-01
7961891	NM_030762	BHLHE41	basic helix-loop-helix family, member e41	L359V only	0.74	0.67	0.99	0.85	1.22E-01	2.92E-02	9.93E-01	1.00E+00
8046003	NM_012198	GCA	grancalcin, EF-hand calcium binding protein	L359V only	0.91	0.67	0.86	0.90	5.61E-01	5.62E-03	7.92E-01	1.00E+00
8168644	---			L359V only	0.78	0.67	0.87	0.87	1.40E-01	1.42E-02	8.33E-01	1.00E+00
8159337	NM_015160	PMPCA	peptidase (mitochondrial processing) alpha	L359V only	0.81	0.67	0.80	0.84	1.71E-01	8.59E-03	5.45E-01	7.44E-01
8002999	NM_004483	GCSH	glycine cleavage system protein H (aminomethyl carrier)	L359V only	0.84	0.67	0.99	0.93	2.52E-01	7.51E-03	9.91E-01	1.00E+00
8092596	NM_001346	DGKG	diacylglycerol kinase, gamma 90kDa	L359V only	0.74	0.67	0.95	0.85	6.78E-02	1.32E-02	9.36E-01	8.84E-01
8128383	NM_017421	COQ3	coenzyme Q3 homolog, methyltransferase (S. cerevisiae)	L359V only	0.83	0.67	0.82	0.89	3.60E-01	2.51E-02	8.01E-01	1.00E+00
7956639	NM_005726	TSFM	Ts translation elongation factor, mitochondrial	L359V only	0.79	0.67	0.81	0.85	1.12E-01	8.32E-03	5.97E-01	8.36E-01
7922846	NM_052966	FAM129A	family with sequence similarity 129, member A	L359V only	0.81	0.67	0.90	0.89	1.39E-01	6.31E-03	8.43E-01	1.00E+00
7991485	NM_001040655	TTC23	tetratricopeptide repeat domain 23	L359V only	0.81	0.67	0.85	0.85	2.80E-01	2.60E-02	8.34E-01	9.87E-01
7973936	NM_002791	PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6	L359V only	0.85	0.66	0.90	0.92	4.24E-01	2.30E-02	8.82E-01	1.00E+00
7965681	NM_153687	IKIP	IKK interacting protein	L359V only	0.81	0.66	0.90	0.87	5.27E-02	1.57E-03	8.03E-01	6.07E-01
8085263	NM_018447	TMEM111	transmembrane protein 111	L359V only	0.79	0.66	0.84	0.86	1.21E-01	8.77E-03	7.38E-01	8.98E-01
7954196	NM_145792	MGST1	microsomal glutathione S-transferase 1	L359V only	0.84	0.66	0.91	0.86	1.46E-01	2.15E-03	8.36E-01	6.27E-01
8019243	NM_001007533	DYSFIP1	dysferlin interacting protein 1	L359V only	0.69	0.66	1.17	0.82	5.19E-02	2.69E-02	8.36E-01	8.46E-01
7909782	NM_016052	RRP15	ribosomal RNA processing 15 homolog (S. cerevisiae)	L359V only	0.84	0.66	0.87	0.88	3.06E-01	1.27E-02	8.36E-01	1.00E+00
7971388	NM_001010875	SLC25A30	solute carrier family 25, member 30	L359V only	0.80	0.66	0.89	0.90	1.45E-01	7.74E-03	8.36E-01	1.00E+00
7918517	NM_024102	WDR77	WD repeat domain 77	L359V only	0.75	0.66	0.83	0.80	9.61E-02	1.42E-02	7.86E-01	6.04E-01
8032682	NM_139355	MATK	megakaryocyte-associated tyrosine kinase	L359V only	0.77	0.66	0.94	0.89	6.59E-02	6.35E-03	9.15E-01	1.00E+00
8094068	---			L359V only	0.89	0.66	0.81	0.84	5.98E-01	1.65E-02	7.33E-01	8.95E-01
7902861	NM_001134476	LRRC8B	leucine rich repeat containing 8 family, member B	L359V only	0.77	0.66	0.89	0.84	5.27E-02	4.26E-03	8.30E-01	6.27E-01
8097461	NM_012118	CCRN4L	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	L359V only	0.77	0.66	0.95	0.89	8.93E-02	9.04E-03	9.38E-01	1.00E+00
7927786	NM_001001330	REEP3	receptor accessory protein 3	L359V only	0.83	0.66	0.83	0.87	1.64E-01	3.56E-03	6.08E-01	7.89E-01
8109194	NM_000112	SLC26A2	solute carrier family 26 (sulfate transporter), member 2	L359V only	0.94	0.66	1.01	0.91	6.64E-01	2.16E-03	9.94E-01	1.00E+00
7899192	NM_002953	RPS6KA1	ribosomal protein S6 kinase, 90kDa, polypeptide 1	L359V only	0.77	0.66	0.88	0.83	6.61E-02	6.06E-03	8.23E-01	6.04E-01
7932069	NM_014142	NUDT5	nudix (nucleoside diphosphate linked moiety X)-type motif 5	L359V only	0.86	0.66	0.90	0.86	2.16E-01	2.31E-03	8.20E-01	6.43E-01
8159815	NM_018491	CBWD1	COBW domain containing 1	L359V only	0.85	0.66	0.94	0.92	3.61E-01	1.19E-02	9.28E-01	1.00E+00

8041255	---			L359V only	0.93	0.66	0.81	0.84	6.75E-01	5.46E-03	5.21E-01	6.45E-01
8130495	---			L359V only	0.90	0.66	0.97	0.94	6.38E-01	2.09E-02	9.76E-01	1.00E+00
7912224	NM_003039	SLC2A5	solute carrier family 2 (facilitated glucose	L359V only	0.75	0.66	0.83	0.84	5.88E-02	7.29E-03	7.24E-01	7.16E-01
8044613	NM_172003	CBWD2	COBW domain containing 2	L359V only	0.85	0.66	0.93	0.91	2.99E-01	6.82E-03	9.01E-01	1.00E+00
8162260	---			L359V only	0.78	0.66	0.84	0.84	2.21E-01	2.75E-02	8.25E-01	9.92E-01
8096635	NM_003998	NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	L359V only	0.95	0.66	0.92	0.92	8.11E-01	8.65E-03	8.85E-01	1.00E+00
8025076	NM_005428	VAV1	vav 1 guanine nucleotide exchange factor	L359V only	0.79	0.65	0.82	0.85	8.20E-02	4.12E-03	5.47E-01	7.02E-01
8058295	NM_020919	ALS2	amyotrophic lateral sclerosis 2 (juvenile)	L359V only	1.07	0.65	1.21	0.98	7.76E-01	1.41E-02	7.74E-01	1.00E+00
8038885	NM_001098612	SIGLEC14	sialic acid binding Ig-like lectin 14	L359V only	0.74	0.65	0.84	0.75	7.33E-02	1.10E-02	7.83E-01	3.17E-01
8099807	AF220235	GAFA3	FGF-2 activity-associated protein 3	L359V only	0.81	0.65	0.85	0.80	1.98E-01	9.06E-03	7.97E-01	5.05E-01
8140814	NM_018843	SLC25A40	solute carrier family 25, member 40	L359V only	0.85	0.65	0.83	0.87	1.29E-01	1.11E-03	3.97E-01	5.89E-01
7907368	---			L359V only	0.84	0.65	0.98	0.89	4.07E-01	2.26E-02	9.85E-01	1.00E+00
7922414	NR_003942	SNORD76	small nucleolar RNA, C	L359V only	0.82	0.65	0.99	0.93	2.59E-01	1.16E-02	9.89E-01	1.00E+00
8096617	NM_017935	BANK1	B-cell scaffold protein with ankyrin repeats 1	L359V only	1.11	0.65	0.97	0.95	6.53E-01	2.08E-02	9.71E-01	1.00E+00
8164907	NM_020385	REXO4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	L359V only	0.83	0.65	0.99	0.90	4.50E-01	4.60E-02	9.92E-01	1.00E+00
8165156	NM_001039707	SDCCAG3	serologically defined colon cancer antigen 3	L359V only	0.75	0.65	0.79	0.83	8.27E-02	9.06E-03	5.57E-01	7.44E-01
7918157	NM_006113	VAV3	vav 3 guanine nucleotide exchange factor	L359V only	1.15	0.65	1.03	0.97	2.05E-01	1.20E-03	9.44E-01	1.00E+00
8161537	NM_201453	CBWD3	COBW domain containing 3	L359V only	0.84	0.65	0.96	0.91	2.92E-01	7.60E-03	9.48E-01	1.00E+00
7921667	NM_001778	CD48	CD48 molecule	L359V only	0.86	0.65	0.95	0.92	4.73E-01	1.73E-02	9.45E-01	1.00E+00
8157153	NM_007203	PALM2-AKAP2	PALM2-AKAP2 readthrough transcript	L359V only	1.02	0.65	0.91	0.87	9.28E-01	1.93E-03	8.40E-01	7.02E-01
8161587	NM_201453	CBWD3	COBW domain containing 3	L359V only	0.83	0.65	0.95	0.91	2.74E-01	1.08E-02	9.45E-01	1.00E+00
8103005	NM_014885	ANAPC10	anaphase promoting complex subunit 10	L359V only	0.80	0.65	0.86	0.84	2.80E-01	2.34E-02	8.41E-01	9.88E-01
7921076	NM_182679	GPATCH4	G patch domain containing 4	L359V only	0.76	0.65	0.86	0.85	9.13E-02	8.88E-03	8.20E-01	8.73E-01
7982350	NR_024074	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	L359V only	0.78	0.65	0.79	0.84	6.04E-02	3.26E-03	3.90E-01	6.07E-01
7987139	NR_024074	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	L359V only	0.78	0.65	0.79	0.84	6.04E-02	3.26E-03	3.90E-01	6.07E-01
8039692	AK022663	LOC730051	similar to hCG2044798	L359V only	1.10	0.65	0.97	1.01	7.69E-01	4.59E-02	9.77E-01	1.00E+00
8064003	XR_039224	LOC100132911	similar to DPH3 homolog B (CSL-type zinc finger-containing protein 1)	L359V only	0.84	0.65	0.84	0.86	3.25E-01	9.36E-03	7.98E-01	9.41E-01
7968126	NM_002339	LSP1	lymphocyte-specific protein 1	L359V only	0.73	0.65	0.82	0.79	9.50E-02	1.85E-02	7.85E-01	6.64E-01
8128322	NM_014165	C6orf66	chromosome 6 open reading frame 66	L359V only	0.75	0.65	0.88	0.84	1.47E-01	2.19E-02	8.66E-01	9.81E-01
8155636	NM_201453	CBWD3	COBW domain containing 3	L359V only	0.83	0.64	0.95	0.91	2.71E-01	7.86E-03	9.36E-01	1.00E+00
7915640	NM_020365	EIF2B3	eukaryotic translation initiation factor 2B, subunit 3 gamma, 58kDa	L359V only	0.82	0.64	0.88	0.87	1.93E-01	6.69E-03	8.35E-01	9.32E-01
7951325	NM_032299	DCUN1D5	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	L359V only	0.76	0.64	0.87	0.91	2.37E-01	4.33E-02	8.80E-01	1.00E+00
7922400	---			L359V only	0.79	0.64	1.11	0.92	2.65E-01	2.32E-02	8.93E-01	1.00E+00
8132503	NM_004760	STK17A	serine	L359V only	0.85	0.64	0.71	0.82	3.47E-01	7.08E-03	1.72E-01	6.26E-01
7938687	NM_005013	NUCB2	nucleobindin 2	L359V only	0.83	0.64	0.97	0.91	3.51E-01	1.46E-02	9.71E-01	1.00E+00
8164596	NM_016520	C9orf78	chromosome 9 open reading frame 78	L359V only	0.74	0.64	0.89	0.85	5.50E-02	6.37E-03	8.52E-01	8.14E-01
7927799	BC018658	REEP3	receptor accessory protein 3	L359V only	0.88	0.64	0.83	0.85	5.52E-01	1.39E-02	7.90E-01	9.88E-01
7954382	NM_024854	PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1	L359V only	0.99	0.64	1.00	1.01	9.78E-01	2.13E-02	9.99E-01	1.00E+00
8089568	NM_138806	CD200R1	CD200 receptor 1	L359V only	1.25	0.64	0.71	0.84	1.81E-01	8.39E-03	2.03E-01	8.36E-01
8166730	NM_000397	CYBB	cytochrome b-245, beta polypeptide	L359V only	0.81	0.64	0.88	0.87	5.27E-02	1.03E-03	7.28E-01	5.91E-01
8063345	NR_002433	SNORD12C	small nucleolar RNA, C	L359V only	0.80	0.64	0.91	0.86	1.65E-01	6.85E-03	8.82E-01	8.88E-01
7970864	NM_006644	HSPH1	heat shock 105kDa	L359V only	0.76	0.64	0.83	0.79	6.07E-02	4.04E-03	6.64E-01	3.35E-01
7925257	NM_000081	LYST	lysosomal trafficking regulator	L359V only	0.83	0.64	0.76	0.85	1.70E-01	3.16E-03	2.51E-01	7.02E-01
8038877	NM_003830	SIGLEC5	sialic acid binding Ig-like lectin 5	L359V only	1.01	0.64	1.07	0.85	9.76E-01	1.30E-02	9.31E-01	9.51E-01
8097903	NM_003264	TLR2	toll-like receptor 2	L359V only	0.85	0.63	1.06	0.94	4.56E-01	2.09E-02	9.44E-01	1.00E+00
8016870	NM_016070	MRPS23	mitochondrial ribosomal protein S23	L359V only	0.77	0.63	0.94	0.87	9.06E-02	5.35E-03	9.17E-01	9.45E-01
7983734	NM_014548	TMOD2	tropomodulin 2 (neuronal)	L359V only	0.78	0.63	0.78	0.85	1.82E-01	1.39E-02	6.39E-01	9.79E-01
7982256	NR_024074	GOLGA9P	golgi autoantigen, golgin subfamily a, 9 pseudogene	L359V only	0.78	0.63	0.81	0.85	1.01E-01	3.98E-03	5.76E-01	7.88E-01
8051396	NM_021209	NLRC4	NLR family, CARD domain containing 4	L359V only	0.75	0.63	0.93	0.83	1.48E-01	1.70E-02	9.30E-01	8.92E-01
8084955	NM_017861	PIGX	phosphatidylinositol glycan anchor biosynthesis, class X	L359V only	0.82	0.63	0.84	0.86	1.59E-01	2.96E-03	6.97E-01	8.35E-01
8155422	BC043420	CBWD5	COBW domain containing 5	L359V only	0.81	0.63	0.95	0.90	2.92E-01	1.45E-02	9.54E-01	1.00E+00
8116848	NM_017906	PAK1IP1	PAK1 interacting protein 1	L359V only	0.87	0.63	1.01	0.88	3.57E-01	3.58E-03	9.85E-01	1.00E+00
7942832	NM_145018	C11orf82	chromosome 11 open reading frame 82	L359V only	0.76	0.63	0.86	0.84	5.75E-02	2.96E-03	7.73E-01	6.45E-01
8051413	NM_015475	FAM98A	family with sequence similarity 98, member A	L359V only	0.78	0.63	0.90	0.83	1.51E-01	8.19E-03	8.73E-01	7.48E-01
7954729	NM_139241	FGD4	FYVE, RhoGEF and PH domain containing 4	L359V only	0.86	0.63	0.84	0.84	5.72E-01	2.67E-02	8.38E-01	1.00E+00
7951654	NM_138378	FDXACB1	ferredoxin-fold anticodon binding domain containing 1	L359V only	0.73	0.63	0.97	0.85	1.32E-01	2.16E-02	9.81E-01	1.00E+00
8097335	NM_014278	HSPA4L	heat shock 70kDa protein 4-like	L359V only	0.76	0.63	0.91	0.86	9.34E-02	6.70E-03	8.77E-01	9.35E-01
8115164	---			L359V only	0.78	0.63	0.88	0.84	1.92E-01	1.10E-02	8.64E-01	9.20E-01
8150877	NR_002437	SNORD54	small nucleolar RNA, C	L359V only	1.06	0.62	1.01	1.01	8.10E-01	9.66E-03	9.93E-01	1.00E+00
8106280	NM_000859	HMGCR	3-hydroxy-3-methylglutaryl-Coenzyme A reductase	L359V only	0.81	0.62	0.95	0.87	2.55E-01	1.04E-02	9.44E-01	1.00E+00
8070961	NM_002340	LSS	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	L359V only	0.79	0.62	0.95	0.83	1.92E-01	8.55E-03	9.43E-01	7.97E-01
8123137	NM_005891	ACAT2	acetyl-Coenzyme A acetyltransferase 2	L359V only	0.75	0.62	0.92	0.81	1.08E-01	9.58E-03	9.02E-01	7.09E-01
8153002	NM_001135242	NDRG1	N-myc downstream regulated 1	L359V only	1.14	0.62	1.25	0.93	3.11E-01	1.55E-03	3.74E-01	1.00E+00
8147262	NM_016023	OTUD6B	OTU domain containing 6B	L359V only	0.78	0.62	0.81	0.84	1.20E-01	5.23E-03	6.66E-01	7.88E-01
7948906	NR_002563	SNORD27	small nucleolar RNA, C	L359V only	1.00	0.62	0.87	0.96	9.91E-01	3.32E-02	8.81E-01	1.00E+00

8111153	NM_012334	MYO10	myosin X	L359V only	0.93	0.62	0.94	0.90	6.85E-01	2.83E-03	9.08E-01	1.00E+00
8062211	ENST00000368864	BXDC1	brix domain containing 1	L359V only	0.77	0.62	0.88	0.87	7.37E-02	3.37E-03	8.25E-01	8.99E-01
7913705	NM_001841	CNR2	cannabinoid receptor 2 (macrophage)	L359V only	0.85	0.62	0.92	0.80	2.96E-01	3.67E-03	8.85E-01	4.78E-01
8161575	BC043420	CBWD5	COBW domain containing 5	L359V only	0.79	0.62	0.95	0.87	3.81E-01	4.65E-02	9.70E-01	1.00E+00
8002760	ENST00000406997	LOC100132346	similar to chaperonin 10	L359V only	0.85	0.62	0.87	0.84	5.11E-01	2.08E-02	8.74E-01	1.00E+00
8122440	NM_032860	LTV1	LTV1 homolog (S. cerevisiae)	L359V only	0.79	0.62	0.86	0.83	1.92E-01	9.44E-03	8.34E-01	8.72E-01
7973110	NM_002934	RNASE2	ribonuclease, RNase A family, 2 (liver, eosinophil-derived neurotoxin)	L359V only	0.76	0.62	1.15	0.88	2.51E-01	3.21E-02	8.80E-01	1.00E+00
7990657	NM_144572	TBC1D2B	TBC1 domain family, member 2B	L359V only	0.79	0.62	0.90	0.87	1.30E-01	3.91E-03	8.66E-01	9.62E-01
8082673	NM_001099	ACPP	acid phosphatase, prostate	L359V only	0.77	0.62	1.06	0.88	6.42E-02	2.42E-03	9.15E-01	9.41E-01
7950990	NM_152313	SLC36A4	solute carrier family 36 (proton	L359V only	0.86	0.62	0.94	0.87	4.03E-01	6.17E-03	9.27E-01	1.00E+00
7979085	NM_002863	PYGL	phosphorylase, glycogen, liver	L359V only	0.92	0.61	1.03	0.91	5.48E-01	1.03E-03	9.59E-01	1.00E+00
8166455	NM_006406	PRDX4	peroxiredoxin 4	L359V only	0.79	0.61	0.96	0.86	1.06E-01	2.61E-03	9.54E-01	8.61E-01
8048864	NM_004591	CCL20	chemokine (C-C motif) ligand 20	L359V only	0.86	0.61	0.90	0.81	3.86E-01	5.10E-03	8.65E-01	6.26E-01
8123985	---			L359V only	0.78	0.61	0.73	0.85	2.87E-01	2.52E-02	6.30E-01	1.00E+00
8055465	NM_001008540	CXCR4	chemokine (C-X-C motif) receptor 4	L359V only	1.30	0.61	1.08	1.02	2.61E-01	2.32E-02	9.38E-01	1.00E+00
8114733	NM_022481	ARAP3	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	L359V only	0.83	0.61	0.87	0.80	1.57E-01	1.62E-03	8.01E-01	3.35E-01
8152606	NM_021021	SNTB1	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	L359V only	0.92	0.61	0.92	0.90	5.36E-01	7.94E-04	8.64E-01	9.35E-01
8046408	NM_002610	PDK1	pyruvate dehydrogenase kinase, isozyme 1	L359V only	0.81	0.61	0.99	0.90	1.66E-01	3.02E-03	9.94E-01	1.00E+00
7943605	NM_000019	ACAT1	acetyl-Coenzyme A acetyltransferase 1	L359V only	0.72	0.61	0.84	0.89	1.26E-01	1.76E-02	8.36E-01	1.00E+00
7901052	NR_001457	SNORD38B	small nucleolar RNA, C	L359V only	0.86	0.60	0.89	0.85	5.10E-01	1.39E-02	8.85E-01	1.00E+00
8113214	NM_002064	GLRX	glutaredoxin (thioltransferase)	L359V only	0.75	0.60	0.78	0.77	5.05E-02	2.45E-03	4.33E-01	2.81E-01
7909801	NM_138794	LYPLAL1	lysophospholipase-like 1	L359V only	0.93	0.60	0.90	0.89	8.04E-01	1.49E-02	8.90E-01	1.00E+00
8057561	---			L359V only	0.77	0.60	0.77	0.85	1.72E-01	7.53E-03	6.11E-01	9.93E-01
8156043	NM_058179	PSAT1	phosphoserine aminotransferase 1	L359V only	0.81	0.60	1.22	1.04	4.03E-01	2.52E-02	8.33E-01	1.00E+00
7923582	XM_001719378	LOC100132728	similar to cpn10 protein	L359V only	0.87	0.59	0.91	0.86	6.45E-01	2.34E-02	9.26E-01	1.00E+00
8150253	NM_000349	STAR	steroidogenic acute regulatory protein	L359V only	0.95	0.59	1.13	1.00	8.36E-01	3.25E-03	8.41E-01	1.00E+00
7945110	NM_006278	ST3GAL4	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	L359V only	0.81	0.59	0.95	0.86	1.73E-01	2.44E-03	9.36E-01	9.20E-01
8042381	NM_020143	PNO1	partner of NOB1 homolog (S. cerevisiae)	L359V only	0.77	0.59	0.80	0.83	1.87E-01	7.75E-03	7.52E-01	9.19E-01
8003861	NM_182538	SPNS3	spinster homolog 3 (Drosophila)	L359V only	0.68	0.59	0.95	0.81	5.58E-02	8.41E-03	9.47E-01	8.36E-01
8064451	NM_001122962	SIRPB2	signal-regulatory protein beta 2	L359V only	0.76	0.59	1.00	0.82	2.08E-01	1.39E-02	9.99E-01	9.32E-01
8119096	AK125083	FLJ43093	FLJ43093 protein	L359V only	1.04	0.58	1.10	0.89	8.31E-01	8.75E-04	8.41E-01	9.89E-01
7904414	M27137	HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	L359V only	0.87	0.58	1.10	0.90	6.26E-01	1.73E-02	9.21E-01	1.00E+00
8168470	NM_001866	COX7B	cytochrome c oxidase subunit VIIb	L359V only	0.84	0.58	0.77	0.84	3.61E-01	3.89E-03	5.43E-01	8.90E-01
8083850	---			L359V only	0.85	0.58	0.86	0.87	5.04E-01	1.24E-02	8.59E-01	1.00E+00
8020110	NM_006868	RAB31	RAB31, member RAS oncogene family	L359V only	0.91	0.58	0.77	0.81	7.59E-01	1.25E-02	7.28E-01	8.88E-01
7985224	BC141940	LOC646938	similar to TBC1 domain family, member 2B	L359V only	0.76	0.57	0.86	0.81	1.12E-01	3.19E-03	8.19E-01	6.23E-01
8056102	NM_014880	CD302	CD302 molecule	L359V only	1.02	0.57	1.00	0.92	9.46E-01	1.27E-03	9.99E-01	1.00E+00
8127989	NR_003044	SNORD50B	small nucleolar RNA	L359V only	0.89	0.57	0.86	0.86	7.17E-01	2.19E-02	8.77E-01	1.00E+00
8024062	NM_001928	CFD	complement factor D (adipsin)	L359V only	0.69	0.57	0.78	0.78	5.58E-02	6.17E-03	6.73E-01	6.01E-01
8152092	---			L359V only	0.95	0.57	0.63	0.76	8.78E-01	6.49E-03	1.44E-01	5.55E-01
8122554	NM_006834	RAB32	RAB32, member RAS oncogene family	L359V only	0.95	0.57	0.88	0.84	8.06E-01	1.49E-03	8.36E-01	7.47E-01
8174076	NM_000169	GLA	galactosidase, alpha	L359V only	0.85	0.56	0.89	0.87	2.70E-01	9.17E-04	8.33E-01	8.42E-01
8096459	---			L359V only	0.75	0.56	0.81	0.75	1.79E-01	8.06E-03	8.09E-01	5.70E-01
8095744	NM_001657	AREG	amphiregulin	L359V only	0.73	0.56	0.72	0.82	3.45E-01	4.98E-02	7.98E-01	1.00E+00
8114787	NM_005471	GNPDA1	glucosamine-6-phosphate deaminase 1	L359V only	0.69	0.56	0.80	0.81	2.07E-01	3.53E-02	8.41E-01	1.00E+00
8139456	NR_002952	SNORA9	small nucleolar RNA, H	L359V only	0.66	0.56	0.79	0.85	1.34E-01	2.83E-02	8.25E-01	1.00E+00
8119102	ENST00000229824	RAB44	RAB44, member RAS oncogene family	L359V only	0.90	0.55	1.04	0.83	5.17E-01	7.04E-04	9.40E-01	5.31E-01
8023259	NR_002571	SNORD58A	small nucleolar RNA, C	L359V only	0.80	0.55	1.15	0.95	1.29E-01	8.70E-04	8.09E-01	1.00E+00
8122265	NM_006290	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	L359V only	1.24	0.55	1.03	0.93	4.25E-01	1.32E-02	9.82E-01	1.00E+00
8107326	NR_002922	SNORA13	small nucleolar RNA, H	L359V only	0.69	0.55	0.89	0.79	7.12E-02	4.84E-03	8.81E-01	7.02E-01
7942400	NM_176072	P2RY2	purinergic receptor P2Y, G-protein coupled, 2	L359V only	0.92	0.54	1.22	0.89	7.63E-01	3.96E-03	8.01E-01	1.00E+00
7917779	NM_002061	GCLM	glutamate-cysteine ligase, modifier subunit	L359V only	0.64	0.54	0.84	0.77	5.58E-02	8.99E-03	8.38E-01	7.44E-01
7953901	NM_138337	CLEC12A	C-type lectin domain family 12, member A	L359V only	1.43	0.54	1.26	1.04	1.05E-01	7.26E-03	7.98E-01	1.00E+00
7951077	NM_144665	SESN3	sestrin 3	L359V only	0.92	0.54	0.79	0.78	6.71E-01	1.03E-03	5.38E-01	3.88E-01
8103951	NM_001995	ACSL1	acyl-CoA synthetase long-chain family member 1	L359V only	0.81	0.54	1.03	0.87	6.96E-02	2.24E-04	9.48E-01	6.93E-01
7943240	NM_152431	PIWIL4	piwi-like 4 (Drosophila)	L359V only	0.79	0.54	0.86	0.80	1.06E-01	7.97E-04	8.01E-01	4.56E-01
8041642	---			L359V only	0.71	0.53	0.78	0.75	3.10E-01	3.75E-02	8.38E-01	9.56E-01
7922416	NR_003941	SNORD75	small nucleolar RNA, C	L359V only	0.79	0.53	0.89	0.84	1.33E-01	1.09E-03	8.58E-01	7.47E-01
8023646	NM_000633	BCL2	B-cell CLL	L359V only	0.82	0.53	1.03	0.86	2.54E-01	1.20E-03	9.66E-01	9.41E-01
8121510	NM_032194	BXDC1	brix domain containing 1	L359V only	0.82	0.52	0.92	0.89	1.70E-01	5.62E-04	8.80E-01	1.00E+00
8056766	NM_003705	SLC25A12	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	L359V only	0.79	0.52	0.98	0.86	5.72E-02	2.70E-04	9.80E-01	6.58E-01
8086344	NM_001337	CX3CR1	chemokine (C-X3-C motif) receptor 1	L359V only	1.11	0.52	0.86	0.81	7.35E-01	6.67E-03	8.64E-01	9.62E-01
8029098	NM_002483	CEACAM6	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross react	L359V only	0.59	0.52	0.65	0.66	5.36E-02	1.57E-02	4.96E-01	4.46E-01
7957023	NM_000239	LYZ	lysozyme (renal amyloidosis)	L359V only	0.72	0.52	0.77	0.77	1.30E-01	4.06E-03	7.29E-01	6.55E-01
8147049	NM_001444	FABP5	fatty acid binding protein 5 (psoriasis-associated)	L359V only	0.72	0.52	0.94	0.81	7.55E-02	1.97E-03	9.30E-01	7.47E-01

8014316	NM_002985	CCL5	chemokine (C-C motif) ligand 5	L359V only	0.78	0.52	1.22	0.85	1.18E-01	7.97E-04	6.83E-01	8.17E-01
7948420	NM_001444	FABP5	fatty acid binding protein 5 (psoriasis-associated)	L359V only	0.72	0.51	0.93	0.81	6.62E-02	1.68E-03	9.27E-01	7.13E-01
7906377	NM_002432	MNDA	myeloid cell nuclear differentiation antigen	L359V only	0.70	0.51	0.87	0.76	9.84E-02	4.04E-03	8.66E-01	6.27E-01
7992861	---			L359V only	0.60	0.51	0.97	0.69	9.11E-02	2.29E-02	9.82E-01	6.77E-01
8123407	NM_001040001	MLLT4	myeloid lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translo	L359V only	0.96	0.49	1.02	0.86	7.71E-01	8.05E-05	9.62E-01	5.95E-01
7914950	NM_156039	CSF3R	colony stimulating factor 3 receptor (granulocyte)	L359V only	1.31	0.49	1.14	0.89	1.15E-01	8.25E-04	8.43E-01	1.00E+00
8170364	NM_002025	AFF2	AF4	L359V only	0.95	0.46	1.02	0.82	7.56E-01	1.28E-04	9.81E-01	4.61E-01
8010915	NM_182705	FAM101B	family with sequence similarity 101, member B	L359V only	1.12	0.46	1.24	0.88	4.97E-01	2.72E-04	5.83E-01	1.00E+00
7953749	NM_080387	CLEC4D	C-type lectin domain family 4, member D	L359V only	0.64	0.46	0.77	0.70	7.63E-02	3.97E-03	8.01E-01	5.23E-01
8045499	NM_006895	HNMT	histamine N-methyltransferase	L359V only	0.65	0.45	0.76	0.76	8.93E-02	3.35E-03	7.85E-01	7.47E-01
8127778	NM_017633	FAM46A	family with sequence similarity 46, member A	L359V only	0.87	0.44	1.05	0.86	4.26E-01	2.73E-04	9.36E-01	9.13E-01
8021645	NM_005024	SERPINB10	serpin peptidase inhibitor, clade B (ovalbumin), member 10	L359V only	0.69	0.44	1.37	0.85	3.80E-01	2.69E-02	8.36E-01	1.00E+00
7908376	NM_130782	RGS18	regulator of G-protein signaling 18	L359V only	0.86	0.43	0.82	0.75	4.00E-01	2.61E-04	7.35E-01	3.05E-01
8102800	NM_014331	SLC7A11	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	L359V only	1.24	0.43	1.50	1.12	4.92E-01	3.98E-03	5.43E-01	1.00E+00
8158684	---			L359V only	0.46	0.42	1.04	0.87	6.84E-02	3.15E-02	9.85E-01	1.00E+00
8139100	M30894	TARP	TCR gamma alternate reading frame protein	L359V only	0.89	0.42	1.00	0.83	4.87E-01	1.53E-04	9.99E-01	6.57E-01
8101788	NM_003728	UNC5C	unc-5 homolog C (C. elegans)	L359V only	1.03	0.41	0.95	0.84	9.32E-01	5.10E-04	9.54E-01	9.88E-01
7905060	NM_000566	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	L359V only	0.82	0.41	1.46	0.93	3.52E-01	6.09E-04	3.25E-01	1.00E+00
7919133	NM_000566	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	L359V only	0.82	0.40	1.46	0.93	3.23E-01	4.51E-04	2.75E-01	1.00E+00
7905047	NM_000566	FCGR1A	Fc fragment of IgG, high affinity Ia, receptor (CD64)	L359V only	0.81	0.38	1.45	0.92	4.06E-01	8.40E-04	4.52E-01	1.00E+00
7997188	NM_005143	HP	haptoglobin	L359V only	0.64	0.36	0.52	0.56	2.43E-01	7.63E-03	3.74E-01	3.86E-01
8131479	NM_019005	FLJ20323	hypothetical protein FLJ20323	T354M and L359V	0.94	0.65	0.65	0.86	7.16E-01	3.77E-03	3.18E-02	8.21E-01
7950578	NM_001128620	PAK1	p21 protein (Cdc42	T354M only	0.86	1.07	0.66	0.88	2.40E-01	6.19E-01	2.62E-02	8.38E-01
8012841	---	PIRT prom/enh	promoter-enhancer region	T354M only	0.72	0.59	0.36	0.60	3.72E-01	9.42E-02	4.10E-02	4.46E-01
8117034	NM_006877	GMPR	guanosine monophosphate reductase	WT and L359V	2.36	8.70	1.50	1.90	1.30E-02	5.75E-05	7.04E-01	1.98E-01
8171105	NM_022148	CRLF2	cytokine receptor-like factor 2	WT and L359V	2.38	5.47	1.63	1.98	5.31E-03	8.17E-05	3.65E-01	8.32E-02
8103769	NM_000860	HPGD	hydroxyprostaglandin dehydrogenase 15-(NAD)	WT and L359V	6.04	5.14	1.93	2.26	3.14E-04	3.91E-04	2.90E-01	1.05E-01
8006531	NM_144975	SLFN5	schlafen family member 5	WT and L359V	5.52	5.13	1.71	2.26	3.09E-04	2.78E-04	4.36E-01	7.78E-02
8044021	NM_016232	IL1RL1	interleukin 1 receptor-like 1	WT and L359V	3.92	4.73	2.24	2.03	1.08E-03	3.55E-04	9.60E-02	1.36E-01
7911199	AK124520	C1orf150	chromosome 1 open reading frame 150	WT and L359V	2.71	4.18	2.28	1.81	1.38E-02	1.42E-03	1.86E-01	3.99E-01
7906777	NM_004001	FCGR2B	Fc fragment of IgG, low affinity IIb, receptor (CD32)	WT and L359V	2.89	3.53	1.47	1.72	9.43E-03	2.63E-03	7.98E-01	4.76E-01
7906443	NM_002001	FCER1A	Fc fragment of IgE, high affinity I, receptor for; alpha polypeptide	WT and L359V	3.74	3.19	1.90	1.86	1.69E-03	2.33E-03	2.90E-01	2.63E-01
7926368	NM_003380	VIM	vimentin	WT and L359V	2.03	2.83	1.48	1.61	2.17E-03	1.85E-04	2.13E-01	7.78E-02
7961365	NM_018050	MANSC1	MANSC domain containing 1	WT and L359V	2.57	2.80	1.18	1.57	5.80E-04	2.73E-04	8.36E-01	1.32E-01
8034851	NM_032571	EMR3	egf-like module containing, mucin-like, hormone receptor-like 3	WT and L359V	2.57	2.77	1.17	1.52	1.87E-03	8.40E-04	8.75E-01	3.09E-01
8023043	NM_024430	PSTPIP2	proline-serine-threonine phosphatase interacting protein 2	WT and L359V	2.74	2.73	1.88	1.70	1.69E-03	1.11E-03	1.07E-01	1.74E-01
8047926	NM_002374	MAP2	microtubule-associated protein 2	WT and L359V	2.86	2.70	1.74	1.59	3.53E-04	3.55E-04	6.76E-02	1.25E-01
8112274	NM_024930	ELOVL7	ELOVL family member 7, elongation of long chain fatty acids (yeast)	WT and L359V	1.84	2.62	1.32	1.48	1.93E-02	1.20E-03	7.65E-01	3.85E-01
8047248	NM_001114661	PLCL1	phospholipase C-like 1	WT and L359V	1.94	2.59	1.18	1.45	5.50E-03	5.28E-04	8.36E-01	3.05E-01
7927732	NM_032199	ARID5B	AT rich interactive domain 5B (MRF1-like)	WT and L359V	1.44	2.52	1.17	1.34	2.07E-02	9.38E-05	8.01E-01	2.29E-01
8101131	NM_005409	CXCL11	chemokine (C-X-C motif) ligand 11	WT and L359V	1.94	2.52	1.41	1.61	3.00E-02	4.12E-03	7.50E-01	3.68E-01
8145293	NM_014265	ADAM28	ADAM metallopeptidase domain 28	WT and L359V	1.89	2.48	1.28	1.40	1.56E-02	1.73E-03	8.02E-01	5.52E-01
8029914	NM_018485	GPR77	G protein-coupled receptor 77	WT and L359V	2.74	2.33	1.71	1.70	2.96E-03	4.99E-03	3.02E-01	2.61E-01
7979269	NM_000161	GCH1	GTP cyclohydrolase 1	WT and L359V	1.63	2.30	1.06	1.31	2.68E-02	1.16E-03	9.52E-01	6.27E-01
8151512	NM_018440	PAG1	phosphoprotein associated with glycosphingolipid microdomains 1	WT and L359V	1.55	2.29	1.22	1.38	3.50E-03	6.68E-05	4.96E-01	7.78E-02
7942204	NM_005231	CTTN	cortactin	WT and L359V	2.00	2.28	1.18	1.44	9.05E-03	2.55E-03	8.61E-01	4.42E-01
8098611	NM_003265	TLR3	toll-like receptor 3	WT and L359V	2.03	2.27	1.34	1.44	1.87E-02	6.48E-03	8.01E-01	6.27E-01
7933228	NM_001002265	MARCH8	membrane-associated ring finger (C3HC4) 8	WT and L359V	2.74	2.25	1.51	1.62	1.61E-04	4.07E-04	1.24E-01	5.67E-02
8118945	NM_006238	PPARD	peroxisome proliferator-activated receptor delta	WT and L359V	1.75	2.24	0.97	1.31	3.06E-03	2.76E-04	9.72E-01	3.28E-01
8124828	NM_005803	FLOT1	flotillin 1	WT and L359V	2.02	2.22	1.29	1.40	5.06E-03	1.74E-03	7.46E-01	4.11E-01
8178419	NM_005803	FLOT1	flotillin 1	WT and L359V	2.02	2.22	1.29	1.40	5.06E-03	1.74E-03	7.46E-01	4.11E-01
8179688	NM_005803	FLOT1	flotillin 1	WT and L359V	2.02	2.22	1.29	1.40	5.06E-03	1.74E-03	7.46E-01	4.11E-01
8156848	NM_173198	NR4A3	nuclear receptor subfamily 4, group A, member 3	WT and L359V	2.03	2.21	1.55	1.49	2.51E-03	8.70E-04	1.53E-01	1.74E-01
8129573	NM_015529	MOXD1	monooxygenase, DBH-like 1	WT and L359V	1.77	2.21	1.21	1.35	9.83E-03	1.11E-03	8.13E-01	4.43E-01
8040365	NM_021643	TRIB2	tribbles homolog 2 (Drosophila)	WT and L359V	2.31	2.19	1.35	1.41	3.09E-04	3.12E-04	2.93E-01	1.46E-01
7899821	NM_020888	KIAA1522	KIAA1522	WT and L359V	1.88	2.16	1.32	1.41	5.56E-03	1.27E-03	6.27E-01	3.19E-01
8164833	NM_021996	GBGT1	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1	WT and L359V	2.03	2.16	1.36	1.45	4.00E-03	1.68E-03	5.51E-01	3.05E-01
8022728	NM_024421	DSC1	desmocollin 1	WT and L359V	2.82	2.16	1.10	1.47	1.08E-03	3.62E-03	9.22E-01	3.64E-01
7944803	NM_001130142	VWA5A	von Willebrand factor A domain containing 5A	WT and L359V	1.88	2.14	0.83	1.26	1.50E-02	4.06E-03	8.44E-01	9.32E-01
7903092	NM_001024948	FNBP1L	formin binding protein 1-like	WT and L359V	1.83	2.13	1.38	1.42	1.52E-03	2.89E-04	1.86E-01	1.11E-01
8099912	BC008502	C4orf34	chromosome 4 open reading frame 34	WT and L359V	2.31	2.12	1.32	1.51	8.12E-04	9.66E-04	5.21E-01	1.42E-01
8068788	NM_018961	UBASH3A	ubiquitin associated and SH3 domain containing, A	WT and L359V	1.45	2.11	1.08	1.32	4.98E-02	1.11E-03	9.13E-01	4.56E-01
8095854	NM_018243	SEPT11	septin 11	WT and L359V	1.39	2.10	1.05	1.32	3.72E-02	3.91E-04	9.40E-01	2.78E-01
8060461	NM_080751	TMC2	transmembrane channel-like 2	WT and L359V	1.47	2.09	1.03	1.28	9.39E-03	1.96E-04	9.55E-01	2.78E-01
8043945	NM_145686	MAP4K4	mitogen-activated protein kinase kinase kinase kinase 4	WT and L359V	1.50	2.09	1.11	1.27	9.57E-03	2.73E-04	8.56E-01	3.37E-01

7969256	NR_002793	LOC220115	TPTE pseudogene	WT and L359V	1.74	2.08	1.00	1.31	7.41E-03	1.12E-03	1.00E+00	4.91E-01
7922474	BC111699	KIAA0040	KIAA0040	WT and L359V	4.68	2.08	1.85	1.78	7.07E-04	2.45E-02	3.41E-01	3.10E-01
7996908	NM_006750	SNTB2	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	WT and L359V	2.13	2.07	1.38	1.42	1.81E-03	1.49E-03	4.33E-01	2.78E-01
8109908	AK093725	LOC257358	hypothetical protein LOC257358	WT and L359V	1.96	2.07	1.57	1.50	3.64E-03	1.61E-03	1.51E-01	1.79E-01
7915682	NM_020883	ZSWIM5	zinc finger, SWIM-type containing 5	WT and L359V	1.75	2.06	1.35	1.42	3.50E-03	5.59E-04	3.41E-01	1.52E-01
7966829	NM_018639	WSB2	WD repeat and SOCS box-containing 2	WT and L359V	2.06	2.06	1.22	1.38	1.33E-02	8.90E-03	8.48E-01	6.95E-01
7928671	BC022252	C10orf57	chromosome 10 open reading frame 57	WT and L359V	1.72	2.06	1.12	1.33	2.39E-03	3.55E-04	8.41E-01	2.18E-01
8114050	NM_015146	SEPT8	septin 8	WT and L359V	2.42	2.04	1.41	1.52	2.54E-04	5.59E-04	2.00E-01	7.35E-02
8133167	NM_153033	KCTD7	potassium channel tetramerisation domain containing 7	WT and L359V	2.03	2.03	1.32	1.37	1.69E-03	1.15E-03	5.07E-01	3.05E-01
8106978	NM_001131065	RFESD	Rieske (Fe-S) domain containing	WT and L359V	1.67	2.03	1.48	1.39	1.37E-02	1.74E-03	2.35E-01	3.17E-01
7929072	NM_012420	IFIT5	interferon-induced protein with tetratricopeptide repeats 5	WT and L359V	1.91	2.02	0.93	1.29	2.63E-02	1.25E-02	9.51E-01	9.45E-01
8136115	NM_020704	FAM40B	family with sequence similarity 40, member B	WT and L359V	1.58	2.01	1.07	1.28	3.33E-02	2.95E-03	9.37E-01	7.02E-01
7904907	NM_004326	BCL9	B-cell CLL	WT and L359V	1.75	2.01	1.29	1.30	2.96E-03	5.62E-04	4.49E-01	3.37E-01
7955441	NM_014033	METTL7A	methyltransferase like 7A	WT and L359V	2.32	2.01	1.61	1.60	4.21E-04	8.19E-04	5.45E-02	5.50E-02
8012464	XM_001724933	LOC100128288	hypothetical protein LOC100128288	WT and L359V	1.53	2.00	1.12	1.26	2.86E-02	1.72E-03	8.77E-01	6.53E-01
8059350	NM_001039569	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	WT and L359V	2.88	1.96	1.09	1.42	3.49E-03	2.26E-02	9.49E-01	7.37E-01
7897441	NM_004285	H6PD	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	WT and L359V	1.95	1.96	1.47	1.45	1.77E-03	1.12E-03	1.65E-01	1.52E-01
8170921	NM_017514	PLXNA3	plexin A3	WT and L359V	1.52	1.96	1.18	1.28	4.58E-02	3.33E-03	8.38E-01	6.81E-01
7968015	NM_148957	TNFRSF19	tumor necrosis factor receptor superfamily, member 19	WT and L359V	1.80	1.95	1.08	1.33	1.26E-02	4.33E-03	9.28E-01	5.96E-01
7906767	NM_201563	FCGR2C	Fc fragment of IgG, low affinity IIc, receptor for (CD32)	WT and L359V	1.84	1.95	1.33	1.35	8.03E-03	3.37E-03	6.32E-01	4.73E-01
8019954	NR_024101	FLJ35776	hypothetical LOC649446	WT and L359V	1.60	1.95	1.32	1.36	1.42E-02	1.55E-03	4.96E-01	3.17E-01
8143327	NM_022750	PARP12	poly (ADP-ribose) polymerase family, member 12	WT and L359V	1.70	1.94	1.21	1.33	1.41E-02	3.19E-03	8.16E-01	5.10E-01
7950501	NM_030792	GDPD5	glycerophosphodiester phosphodiesterase domain containing 5	WT and L359V	1.77	1.90	1.58	1.41	6.27E-03	2.42E-03	1.07E-01	2.70E-01
7899870	NM_152493	ZNF362	zinc finger protein 362	WT and L359V	1.80	1.90	1.20	1.34	6.24E-03	2.70E-03	8.13E-01	4.03E-01
8122660	NM_005715	UST	uronyl-2-sulfotransferase	WT and L359V	1.47	1.88	1.10	1.25	3.38E-02	2.05E-03	8.86E-01	6.27E-01
8102513	---			WT and L359V	2.44	1.88	1.33	1.48	5.54E-03	2.15E-02	8.02E-01	5.33E-01
7932214	NM_001039844	ACBD7	acyl-Coenzyme A binding domain containing 7	WT and L359V	2.05	1.88	1.47	1.50	3.91E-03	4.99E-03	3.52E-01	2.43E-01
8002618	NM_017530	ZNF821	zinc finger protein 821	WT and L359V	1.76	1.88	1.24	1.37	9.30E-03	3.64E-03	7.86E-01	3.85E-01
7932227	NM_004808	NMT2	N-myristoyltransferase 2	WT and L359V	1.64	1.87	1.26	1.33	6.59E-03	1.20E-03	5.76E-01	3.05E-01
8170119	NM_001449	FHL1	four and a half LIM domains 1	WT and L359V	2.26	1.87	1.59	1.51	7.19E-03	1.87E-02	4.14E-01	4.27E-01
8154962	NM_001135004	DNAJB5	DnaJ (Hsp40) homolog, subfamily B, member 5	WT and L359V	1.53	1.86	1.31	1.26	7.25E-03	6.50E-04	2.90E-01	3.40E-01
8138977	NM_015283	DPY19L1	dpy-19-like 1 (C. elegans)	WT and L359V	1.52	1.84	1.14	1.29	4.09E-03	3.55E-04	7.84E-01	1.94E-01
8139121	Y00790	TARP	TCR gamma alternate reading frame protein	WT and L359V	1.69	1.84	1.17	1.21	2.17E-02	7.51E-03	8.48E-01	9.88E-01
8058570	NM_152519	C2orf67	chromosome 2 open reading frame 67	WT and L359V	1.87	1.84	1.28	1.37	9.32E-04	7.33E-04	3.90E-01	1.36E-01
8036503	NM_170604	RASGRP4	RAS guanyl releasing protein 4	WT and L359V	1.75	1.83	1.18	1.19	1.54E-02	7.43E-03	8.40E-01	1.00E+00
7910694	NM_080738	EDARADD	EDAR-associated death domain	WT and L359V	1.59	1.83	1.05	1.27	2.57E-02	5.11E-03	9.57E-01	7.06E-01
8095343	NM_012108	STAP1	signal transducing adaptor family member 1	WT and L359V	2.16	1.82	1.26	1.41	4.79E-04	1.38E-03	5.44E-01	1.52E-01
8047078	NM_017694	MFSD6	major facilitator superfamily domain containing 6	WT and L359V	1.68	1.82	1.14	1.33	3.88E-02	1.48E-02	8.90E-01	7.09E-01
7960757	NM_016546	C1RL	complement component 1, r subcomponent-like	WT and L359V	1.71	1.81	1.27	1.31	7.40E-03	3.02E-03	6.52E-01	4.40E-01
7915775	NM_005897	IPP	intracisternal A particle-promoted polypeptide	WT and L359V	1.98	1.79	1.11	1.31	1.23E-02	1.84E-02	9.15E-01	8.14E-01
8032576	NM_198969	AES	amino-terminal enhancer of split	WT and L359V	1.49	1.79	1.28	1.29	3.70E-02	4.08E-03	6.75E-01	5.41E-01
8092358	NM_015078	MCF2L2	MCF.2 cell line derived transforming sequence-like 2	WT and L359V	1.33	1.79	1.17	1.26	4.49E-02	8.36E-04	7.46E-01	3.25E-01
8062623	NM_002660	PLCG1	phospholipase C, gamma 1	WT and L359V	1.57	1.78	1.10	1.23	1.81E-03	3.11E-04	8.26E-01	2.78E-01
8074780	NM_013313	YPEL1	yippee-like 1 (Drosophila)	WT and L359V	1.55	1.78	1.25	1.35	4.81E-02	9.86E-03	8.01E-01	5.54E-01
7928999	NM_001102469	LIPN	lipase, family member N	WT and L359V	1.56	1.78	1.26	1.40	3.18E-02	6.88E-03	7.53E-01	3.37E-01
7908917	NM_006763	BTG2	BTG family, member 2	WT and L359V	1.45	1.77	1.02	1.15	2.02E-02	1.57E-03	9.84E-01	9.78E-01
7952305	XR_018777	LOC283155	hypothetical LOC283155	WT and L359V	1.86	1.76	1.28	1.34	7.28E-03	8.02E-03	7.40E-01	4.98E-01
8083166	NM_003304	TRPC1	transient receptor potential cation channel, subfamily C, member 1	WT and L359V	1.81	1.76	1.24	1.37	4.79E-04	4.56E-04	3.88E-01	7.78E-02
8089261	NM_170662	CBLB	Cas-Br-M (murine) ecotropic retroviral transforming sequence b	WT and L359V	1.36	1.76	1.12	1.22	4.26E-02	1.40E-03	8.38E-01	5.88E-01
8123080	NM_001009991	SYTL3	synaptotagmin-like 3	WT and L359V	1.62	1.75	1.19	1.35	4.02E-02	1.47E-02	8.41E-01	6.04E-01
8023926	NM_032510	PARD6G	par-6 partitioning defective 6 homolog gamma (C. elegans)	WT and L359V	1.64	1.74	1.07	1.25	8.77E-03	3.28E-03	9.19E-01	5.96E-01
8162216	NM_016848	SHC3	SHC (Src homology 2 domain containing) transforming protein 3	WT and L359V	1.39	1.74	1.07	1.18	2.23E-02	9.66E-04	9.05E-01	6.57E-01
7987385	NM_172316	MEIS2	Meis homeobox 2	WT and L359V	2.00	1.73	1.37	1.34	4.30E-04	1.06E-03	1.57E-01	1.57E-01
7909954	NM_032890	DISP1	dispatched homolog 1 (Drosophila)	WT and L359V	1.38	1.73	1.16	1.21	2.53E-02	1.08E-03	7.73E-01	5.09E-01
8164464	NM_006336	ZER1	zer-1 homolog (C. elegans)	WT and L359V	1.26	1.73	1.03	1.15	4.11E-02	3.69E-04	9.48E-01	6.57E-01
8073072	NM_152426	APOBEC3D	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3D	WT and L359V	1.77	1.73	1.19	1.31	4.60E-04	4.00E-04	5.20E-01	1.10E-01
8150036	NM_015254	KIF13B	kinesin family member 13B	WT and L359V	1.38	1.72	1.14	1.22	3.53E-02	1.89E-03	8.31E-01	5.72E-01
8083876	NM_005414	SKIL	SKI-like oncogene	WT and L359V	1.83	1.72	1.18	1.37	7.02E-03	8.41E-03	8.34E-01	4.02E-01
8014248	NM_144682	SLFN13	schlafen family member 13	WT and L359V	1.46	1.72	1.12	1.27	1.52E-02	1.71E-03	8.41E-01	3.49E-01
8127051	NM_012288	TRAM2	translocation associated membrane protein 2	WT and L359V	1.31	1.72	1.16	1.18	3.29E-02	7.04E-04	7.40E-01	5.57E-01
8095870	NM_004354	CCNG2	cyclin G2	WT and L359V	1.60	1.71	1.24	1.32	4.18E-03	1.32E-03	5.30E-01	2.11E-01
8097288	NM_024582	FAT4	FAT tumor suppressor homolog 4 (Drosophila)	WT and L359V	1.54	1.71	1.11	1.26	3.49E-03	7.05E-04	8.31E-01	2.63E-01
7963670	NM_006301	MAP3K12	mitogen-activated protein kinase kinase kinase 12	WT and L359V	1.46	1.71	1.18	1.19	3.87E-02	5.12E-03	8.20E-01	8.90E-01
8079117	NM_001296	CCBP2	chemokine binding protein 2	WT and L359V	1.42	1.70	1.09	1.19	3.29E-02	3.05E-03	8.85E-01	8.13E-01
7902282	NM_001036645	HHLA3	HERV-H LTR-associating 3	WT and L359V	1.51	1.70	1.13	1.21	4.29E-02	9.35E-03	8.76E-01	9.23E-01

8107270	NM_033035	TSLP	thymic stromal lymphopoietin	WT and L359V	1.59	1.70	1.29	1.33	1.07E-02	3.66E-03	5.15E-01	3.13E-01
8167322	NM_017883	WDR13	WD repeat domain 13	WT and L359V	1.38	1.69	1.14	1.21	4.11E-02	2.76E-03	8.36E-01	6.69E-01
8073081	NM_145298	APOBEC3F	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	WT and L359V	1.65	1.69	1.16	1.23	3.06E-03	1.59E-03	7.92E-01	4.58E-01
7927876	NM_030625	TET1	tet oncogene 1	WT and L359V	1.56	1.69	1.35	1.32	6.93E-03	2.10E-03	2.37E-01	2.54E-01
7961767	AK295862	KIAA0528	KIAA0528	WT and L359V	1.83	1.68	0.82	1.20	2.08E-03	3.34E-03	7.23E-01	7.15E-01
7928855	NM_004329	BMPR1A	bone morphogenetic protein receptor, type IA	WT and L359V	1.80	1.68	1.24	1.32	6.62E-03	8.57E-03	7.67E-01	4.73E-01
7975203	NM_022474	MPP5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	WT and L359V	1.50	1.68	1.01	1.22	2.74E-02	6.17E-03	9.95E-01	7.45E-01
7915718	NM_007170	TESK2	testis-specific kinase 2	WT and L359V	1.49	1.67	1.24	1.33	2.68E-02	5.35E-03	7.19E-01	3.58E-01
7943413	NM_001165	BIRC3	baculoviral IAP repeat-containing 3	WT and L359V	1.58	1.67	1.35	1.33	1.66E-02	6.89E-03	4.46E-01	4.03E-01
8003962	NM_002663	PLD2	phospholipase D2	WT and L359V	1.71	1.67	1.38	1.32	1.91E-02	1.68E-02	5.47E-01	6.27E-01
7905909	NM_005227	EFNA4	ephrin-A4	WT and L359V	1.79	1.67	1.43	1.34	7.93E-03	1.01E-02	3.63E-01	4.56E-01
8106602	NM_014733	ZFYVE16	zinc finger, FYVE domain containing 16	WT and L359V	1.79	1.67	1.21	1.32	8.82E-03	1.13E-02	8.13E-01	5.28E-01
7953547	NM_001007026	ATN1	atrophin 1	WT and L359V	1.32	1.66	1.09	1.16	2.40E-02	7.04E-04	8.52E-01	6.27E-01
8020684	NM_021624	HRH4	histamine receptor H4	WT and L359V	1.88	1.66	1.41	1.31	1.51E-02	3.01E-02	6.04E-01	7.88E-01
8114030	NM_007054	KIF3A	kinesin family member 3A	WT and L359V	2.60	1.66	1.32	1.51	5.80E-04	1.23E-02	6.12E-01	1.85E-01
7951408	NM_052889	CARD16	caspase recruitment domain family, member 16	WT and L359V	2.22	1.66	1.10	1.34	8.31E-03	4.95E-02	9.29E-01	8.13E-01
7910706	NM_006499	LGALS8	lectin, galactoside-binding, soluble, 8	WT and L359V	1.46	1.66	1.19	1.26	2.86E-02	4.99E-03	7.99E-01	5.54E-01
8047187	NM_001080539	CCDC150	coiled-coil domain containing 150	WT and L359V	1.58	1.65	0.86	1.23	3.53E-02	1.71E-02	8.58E-01	9.07E-01
8142270	NM_001037132	NRCAM	neuronal cell adhesion molecule	WT and L359V	1.62	1.65	1.07	1.25	8.03E-03	4.44E-03	9.17E-01	5.69E-01
8021635	NM_002575	SERPINB2	serpin peptidase inhibitor, clade B (ovalbumin), member 2	WT and L359V	1.57	1.65	1.72	1.27	2.64E-02	1.16E-02	6.76E-02	6.64E-01
8025612	NM_022377	ICAM4	intercellular adhesion molecule 4 (Landsteiner-Wiener blood group)	WT and L359V	1.63	1.65	1.25	1.30	2.67E-02	1.71E-02	7.91E-01	6.55E-01
7959657	NM_012463	ATP6V0A2	ATPase, H+ transporting, lysosomal V0 subunit a2	WT and L359V	1.83	1.65	1.19	1.29	4.77E-04	9.66E-04	5.66E-01	1.85E-01
8009243	NM_001085423	C17orf60	chromosome 17 open reading frame 60	WT and L359V	2.17	1.65	1.27	1.38	6.40E-03	3.62E-02	8.09E-01	6.07E-01
8024566	---			WT and L359V	1.40	1.65	1.18	1.23	2.66E-02	2.58E-03	7.47E-01	4.88E-01
8179595	NM_001470	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	WT and L359V	1.52	1.65	1.25	1.30	1.71E-02	4.99E-03	6.65E-01	4.07E-01
7972177	NM_006237	POU4F1	POU class 4 homeobox 1	WT and L359V	1.50	1.64	1.09	1.28	8.11E-03	1.89E-03	8.76E-01	2.81E-01
8133155	NM_003596	TPST1	tyrosylprotein sulfotransferase 1	WT and L359V	1.68	1.64	1.15	1.25	3.79E-03	3.22E-03	8.14E-01	4.78E-01
8178298	NM_001470	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	WT and L359V	1.47	1.64	1.26	1.29	1.73E-02	3.40E-03	5.36E-01	3.32E-01
8057377	NM_173648	CCDC141	coiled-coil domain containing 141	WT and L359V	1.63	1.64	1.35	1.32	1.61E-02	1.12E-02	5.08E-01	4.98E-01
8171901	NM_152787	MAP3K7IP3	mitogen-activated protein kinase kinase kinase 7 interacting protein 3	WT and L359V	1.42	1.63	1.03	1.17	5.06E-03	5.28E-04	9.43E-01	4.93E-01
8058670	NM_016260	IKZF2	IKAROS family zinc finger 2 (Helios)	WT and L359V	1.78	1.63	1.74	1.33	1.51E-02	2.46E-02	1.09E-01	6.27E-01
8030128	NM_014330	PPP1R15A	protein phosphatase 1, regulatory (inhibitor) subunit 15A	WT and L359V	1.52	1.63	1.26	1.26	9.97E-03	3.22E-03	5.15E-01	4.23E-01
7935011	NM_014912	CPEB3	cytoplasmic polyadenylation element binding protein 3	WT and L359V	1.36	1.62	1.10	1.20	3.79E-02	2.87E-03	8.64E-01	6.53E-01
8116831	AK092393	LOC100130275	hypothetical protein LOC100130275	WT and L359V	1.73	1.62	1.28	1.32	1.53E-03	2.03E-03	3.44E-01	1.74E-01
7984124	NM_031301	APH1B	anterior pharynx defective 1 homolog B (C. elegans)	WT and L359V	1.65	1.61	1.26	1.35	7.96E-03	7.02E-03	6.44E-01	3.05E-01
7898677	NM_004807	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	WT and L359V	1.43	1.61	1.38	1.23	1.27E-02	2.05E-03	1.23E-01	4.19E-01
8161044	NM_003289	TPM2	tropomyosin 2 (beta)	WT and L359V	1.44	1.61	1.30	1.25	1.89E-02	3.56E-03	3.90E-01	4.28E-01
8139118	---			WT and L359V	1.66	1.60	1.08	1.11	1.13E-02	1.10E-02	9.15E-01	1.00E+00
8159876	NM_134428	RFX3	regulatory factor X, 3 (influences HLA class II expression)	WT and L359V	1.44	1.60	1.14	1.30	1.54E-02	2.87E-03	8.20E-01	2.71E-01
8124654	NM_001470	GABBR1	gamma-aminobutyric acid (GABA) B receptor, 1	WT and L359V	1.38	1.60	1.25	1.27	2.29E-02	2.49E-03	4.39E-01	3.05E-01
7913357	NM_001397	ECE1	endothelin converting enzyme 1	WT and L359V	1.53	1.60	1.27	1.31	2.67E-03	1.03E-03	2.17E-01	1.19E-01
8040552	NM_147223	NCOA1	nuclear receptor coactivator 1	WT and L359V	1.50	1.59	1.02	1.14	1.64E-02	5.91E-03	9.84E-01	1.00E+00
8142136	NM_175884	FLJ36031	hypothetical protein FLJ36031	WT and L359V	1.34	1.59	1.03	1.17	2.10E-02	1.44E-03	9.57E-01	6.39E-01
7979223	NM_030637	DDHD1	DDHD domain containing 1	WT and L359V	1.27	1.59	0.97	1.17	4.73E-02	1.20E-03	9.58E-01	5.75E-01
8092392	NM_130446	KLHL6	kelch-like 6 (Drosophila)	WT and L359V	1.66	1.58	1.18	1.25	8.92E-03	9.66E-03	8.14E-01	6.27E-01
8027604	NM_014686	KIAA0355	KIAA0355	WT and L359V	1.43	1.58	1.12	1.21	3.18E-02	6.74E-03	8.59E-01	6.95E-01
7937852	NM_002555	SLC22A18	solute carrier family 22, member 18	WT and L359V	1.39	1.58	1.14	1.20	2.09E-02	2.89E-03	8.09E-01	5.70E-01
7990033	NM_005078	TLE3	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	WT and L359V	1.52	1.58	1.31	1.21	7.02E-03	3.19E-03	2.93E-01	5.69E-01
8162533	NM_001083603	PTCH1	patched homolog 1 (Drosophila)	WT and L359V	1.42	1.58	1.07	1.21	2.03E-02	3.86E-03	8.97E-01	5.91E-01
8056005	NM_001105	ACVR1	activin A receptor, type I	WT and L359V	1.59	1.58	1.06	1.22	2.26E-02	1.71E-02	9.40E-01	8.46E-01
8065798	NM_178026	GGT7	gamma-glutamyltransferase 7	WT and L359V	1.67	1.57	1.33	1.31	1.02E-02	1.25E-02	4.97E-01	4.46E-01
8099696	NM_153825	SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	WT and L359V	1.49	1.57	1.15	1.29	1.24E-02	4.61E-03	8.13E-01	3.28E-01
8135224	NM_001085386	NF-E4	transcription factor NF-E4	WT and L359V	1.37	1.57	1.23	1.25	1.98E-02	2.28E-03	4.52E-01	3.05E-01
7929047	NM_001547	IFIT2	interferon-induced protein with tetratricopeptide repeats 2	WT and L359V	1.65	1.56	1.15	1.23	2.63E-02	3.15E-02	8.66E-01	9.11E-01
8066303	NM_032221	CHD6	chromodomain helicase DNA binding protein 6	WT and L359V	1.39	1.56	1.05	1.18	1.41E-02	1.96E-03	9.22E-01	6.03E-01
8078227	NM_003884	KAT2B	K(lysine) acetyltransferase 2B	WT and L359V	1.56	1.56	0.90	1.14	3.82E-02	2.85E-02	8.94E-01	1.00E+00
8047538	NM_001204	BMPR2	bone morphogenetic protein receptor, type II (serine	WT and L359V	1.66	1.56	1.02	1.14	2.14E-02	2.85E-02	9.85E-01	1.00E+00
7955469	NM_001039960	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8	WT and L359V	2.00	1.56	1.34	1.25	4.00E-04	3.22E-03	2.00E-01	3.40E-01
8045398	NM_012233	RAB3GAP1	RAB3 GTPase activating protein subunit 1 (catalytic)	WT and L359V	1.40	1.56	1.23	1.32	2.24E-02	3.68E-03	5.61E-01	2.17E-01
8090277	NM_022776	OSBPL11	oxysterol binding protein-like 11	WT and L359V	1.70	1.55	1.03	1.18	2.03E-02	3.41E-02	9.80E-01	1.00E+00
8005785	NM_014238	KSR1	kinase suppressor of ras 1	WT and L359V	1.45	1.55	1.32	1.15	2.02E-02	6.60E-03	3.74E-01	9.33E-01
8072279	NM_153050	MTMR3	myotubularin related protein 3	WT and L359V	1.50	1.55	1.11	1.19	1.85E-03	8.04E-04	8.01E-01	3.36E-01
7940191	NM_004177	STX3	syntaxin 3	WT and L359V	1.37	1.55	0.85	1.09	3.18E-02	4.57E-03	7.44E-01	1.00E+00
7969438	NM_005358	LMO7	LIM domain 7	WT and L359V	1.71	1.54	1.27	1.31	1.22E-02	2.41E-02	7.38E-01	5.52E-01
8009476	NM_002758	MAP2K6	mitogen-activated protein kinase kinase 6	WT and L359V	1.52	1.54	1.13	1.19	1.54E-02	9.43E-03	8.53E-01	8.30E-01

8119034	NM_015695	BRPF3	bromodomain and PHD finger containing, 3	WT and L359V	1.41	1.54	1.16	1.13	1.09E-02	2.38E-03	7.26E-01	8.99E-01
7952445	NM_024631	C11orf61	chromosome 11 open reading frame 61	WT and L359V	1.38	1.54	1.10	1.15	3.95E-02	7.47E-03	8.79E-01	9.41E-01
7902594	NM_182948	PRKACB	protein kinase, cAMP-dependent, catalytic, beta	WT and L359V	1.35	1.53	1.16	1.24	1.29E-02	1.31E-03	6.65E-01	2.44E-01
7948470	NM_004778	GPR44	G protein-coupled receptor 44	WT and L359V	1.97	1.53	1.55	1.36	4.77E-03	3.05E-02	2.00E-01	4.56E-01
7949400	NM_182556	SLC25A45	solute carrier family 25, member 45	WT and L359V	1.46	1.53	1.15	1.19	1.39E-02	4.99E-03	8.11E-01	6.47E-01
8032249	NM_213604	ADAMTSL5	ADAMTS-like 5	WT and L359V	1.42	1.53	1.15	1.19	3.72E-02	1.07E-02	8.25E-01	8.36E-01
8055130	NM_004807	HS6ST1	heparan sulfate 6-O-sulfotransferase 1	WT and L359V	1.37	1.53	1.33	1.19	1.38E-02	2.10E-03	1.39E-01	4.97E-01
8105681	NM_018695	ERBB2IP	erbb2 interacting protein	WT and L359V	1.68	1.53	1.21	1.30	1.69E-03	3.16E-03	5.43E-01	1.94E-01
8116992	---			WT and L359V	1.38	1.53	1.16	1.20	2.82E-02	5.27E-03	7.99E-01	6.27E-01
7959039	NM_153348	FBXW8	F-box and WD repeat domain containing 8	WT and L359V	1.38	1.53	1.24	1.24	1.76E-02	2.97E-03	4.37E-01	3.42E-01
7906061	NM_152280	SYT11	synaptotagmin XI	WT and L359V	1.59	1.52	1.27	1.23	3.95E-02	4.41E-02	7.79E-01	9.27E-01
7937823	NM_000218	KCNQ1	potassium voltage-gated channel, KQT-like subfamily, member 1	WT and L359V	1.35	1.52	1.15	1.20	3.95E-02	5.70E-03	8.01E-01	6.04E-01
7907893	NM_001531	MR1	major histocompatibility complex, class I-related	WT and L359V	1.51	1.52	1.08	1.23	1.43E-02	9.65E-03	8.97E-01	6.07E-01
8167125	NM_004651	USP11	ubiquitin specific peptidase 11	WT and L359V	1.34	1.52	1.14	1.15	2.83E-02	3.67E-03	8.01E-01	7.89E-01
8010426	NM_020954	KIAA1618	KIAA1618	WT and L359V	1.41	1.51	1.08	1.13	2.31E-02	6.74E-03	8.86E-01	1.00E+00
7959786	NM_023928	AACS	acetoacetyl-CoA synthetase	WT and L359V	1.39	1.51	1.24	1.23	2.31E-02	5.03E-03	5.15E-01	4.41E-01
8043377	NM_012477	WBP1	WW domain binding protein 1	WT and L359V	1.34	1.51	1.17	1.13	1.81E-02	2.15E-03	6.27E-01	8.63E-01
8055711	NM_004543	NEB	nebulin	WT and L359V	1.41	1.51	1.41	1.26	1.62E-02	4.46E-03	9.54E-02	3.05E-01
7909332	NM_001114752	CD55	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	WT and L359V	1.68	1.51	1.31	1.33	6.54E-03	1.40E-02	4.65E-01	3.25E-01
7924760	NM_002221	ITPKB	inositol 1,4,5-trisphosphate 3-kinase B	WT and L359V	1.69	1.51	1.20	1.25	5.30E-03	1.28E-02	7.65E-01	5.44E-01
8131013	NM_001130965	UNC84A	unc-84 homolog A (C. elegans)	WT and L359V	1.54	1.51	1.28	1.31	4.80E-03	3.98E-03	3.29E-01	1.74E-01
8138613	NM_015550	OSBPL3	oxysterol binding protein-like 3	WT and L359V	1.58	1.51	1.14	1.22	5.06E-03	6.17E-03	8.14E-01	5.28E-01
8052742	NM_001024680	FBXO48	F-box protein 48	WT and L359V	1.79	1.51	1.18	1.36	1.13E-02	3.97E-02	8.41E-01	4.56E-01
8117447	NM_006995	BTN2A2	butyrophilin, subfamily 2, member A2	WT and L359V	1.30	1.50	1.11	1.19	3.10E-02	2.57E-03	8.21E-01	4.76E-01
8116983	NM_004233	CD83	CD83 molecule	WT and L359V	1.31	1.50	1.16	1.20	4.09E-02	3.86E-03	7.65E-01	5.27E-01
8053599	NM_012477	WBP1	WW domain binding protein 1	WT and L359V	1.34	1.50	1.16	1.12	1.92E-02	2.69E-03	7.22E-01	8.93E-01
8108378	NM_001903	CTNNA1	catenin (cadherin-associated protein), alpha 1, 102kDa	WT and L359V	1.69	1.50	1.11	1.29	3.41E-03	8.81E-03	8.64E-01	3.24E-01
8080938	NM_198159	MITF	microphthalmia-associated transcription factor	WT and L359V	1.95	1.50	0.85	1.19	4.43E-04	4.61E-03	7.12E-01	6.13E-01
8008566	NM_178509	STXBP4	syntaxin binding protein 4	WT and L359V	1.46	1.50	0.95	1.15	8.03E-03	3.84E-03	9.27E-01	7.88E-01
8106962	NM_198150	ARSK	arylsulfatase family, member K	WT and L359V	1.65	1.50	1.14	1.22	1.69E-03	3.65E-03	7.94E-01	4.02E-01
7957551	NM_003877	SOCS2	suppressor of cytokine signaling 2	WT and L359V	1.49	1.49	1.26	1.28	2.64E-03	1.72E-03	2.00E-01	1.30E-01
7978492	NM_015473	HEATR5A	HEAT repeat containing 5A	WT and L359V	1.51	1.49	1.27	1.20	1.23E-02	9.86E-03	4.85E-01	6.58E-01
8149330	NM_147780	CTSB	cathepsin B	WT and L359V	1.55	1.49	1.15	1.21	1.55E-02	1.85E-02	8.36E-01	7.88E-01
7965652	NM_002595	PCTK2	PCTAIRE protein kinase 2	WT and L359V	1.40	1.49	1.13	1.25	1.38E-02	4.04E-03	8.13E-01	3.10E-01
7914184	NM_000952	PTAFR	platelet-activating factor receptor	WT and L359V	1.93	1.49	1.06	1.18	5.66E-04	6.22E-03	9.22E-01	6.55E-01
8029728	NM_000164	GIPR	gastric inhibitory polypeptide receptor	WT and L359V	1.32	1.49	1.13	1.19	2.53E-02	2.97E-03	8.01E-01	4.56E-01
7941714	NM_024650	C11orf80	chromosome 11 open reading frame 80	WT and L359V	1.41	1.49	1.16	1.22	1.38E-02	4.42E-03	7.62E-01	4.39E-01
8120927	NM_033411	RWDD2A	RWD domain containing 2A	WT and L359V	1.90	1.48	1.25	1.35	2.39E-03	2.04E-02	6.90E-01	3.10E-01
8049657	NM_001040445	ASB1	ankyrin repeat and SOCS box-containing 1	WT and L359V	1.54	1.48	1.31	1.26	1.85E-03	2.15E-03	1.17E-01	1.73E-01
8050702	NM_004881	TP53I3	tumor protein p53 inducible protein 3	WT and L359V	1.52	1.48	1.05	1.17	2.22E-02	2.22E-02	9.52E-01	9.45E-01
7910198	BC007286	MGC15634	hypothetical protein MGC15634	WT and L359V	1.41	1.48	1.06	1.18	4.90E-02	2.06E-02	9.40E-01	8.92E-01
7963313	NM_007210	GALNT6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferas	WT and L359V	1.56	1.47	1.22	1.19	4.81E-03	6.74E-03	5.72E-01	6.07E-01
8042867	NM_012477	WBP1	WW domain binding protein 1	WT and L359V	1.30	1.47	1.16	1.13	2.56E-02	2.77E-03	6.71E-01	8.44E-01
7967117	NM_003733	OASL	2'-5'-oligoadenylate synthetase-like	WT and L359V	1.42	1.46	1.08	1.16	4.54E-02	2.30E-02	9.12E-01	1.00E+00
7909011	NM_002393	MDM4	Mdm4 p53 binding protein homolog (mouse)	WT and L359V	1.77	1.46	1.42	1.43	4.95E-03	2.48E-02	2.46E-01	1.82E-01
8109576	NM_017872	THG1L	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	WT and L359V	1.51	1.46	1.13	1.28	4.95E-03	5.10E-03	8.11E-01	2.23E-01
8087985	NM_001010983	GLT8D1	glycosyltransferase 8 domain containing 1	WT and L359V	1.54	1.46	1.27	1.28	1.64E-02	2.23E-02	6.11E-01	4.81E-01
7980005	NM_001005743	NUMB	numb homolog (Drosophila)	WT and L359V	1.36	1.46	1.04	1.12	4.83E-02	1.32E-02	9.51E-01	1.00E+00
8143188	NM_194071	CREB3L2	cAMP responsive element binding protein 3-like 2	WT and L359V	1.45	1.45	1.16	1.10	1.23E-02	7.86E-03	7.65E-01	1.00E+00
8151308	---			WT and L359V	1.83	1.45	1.38	1.31	2.00E-03	1.73E-02	2.40E-01	3.09E-01
7929132	NM_032373	PCGF5	polycomb group ring finger 5	WT and L359V	1.60	1.44	1.24	1.23	1.56E-02	3.60E-02	7.38E-01	7.34E-01
7974533	NM_021255	PELI2	pellino homolog 2 (Drosophila)	WT and L359V	1.39	1.44	1.18	1.22	2.29E-02	1.00E-02	7.45E-01	4.78E-01
8120883	NM_015018	DOPEY1	dopey family member 1	WT and L359V	1.65	1.44	1.15	1.25	9.46E-04	3.67E-03	7.28E-01	2.29E-01
7906757	NM_001136219	FCGR2A	Fc fragment of IgG, low affinity IIa, receptor (CD32)	WT and L359V	1.71	1.43	1.30	1.28	7.25E-03	3.35E-02	5.59E-01	5.17E-01
8134435	NM_014916	LMTK2	lemur tyrosine kinase 2	WT and L359V	1.49	1.43	1.02	1.15	1.23E-02	1.43E-02	9.85E-01	9.15E-01
7919580	AK125737	LOC440570	LOC440570	WT and L359V	1.52	1.43	1.57	1.26	1.79E-02	2.55E-02	7.35E-02	5.42E-01
7919596	AK125737	LOC440570	LOC440570	WT and L359V	1.52	1.43	1.57	1.26	1.79E-02	2.55E-02	7.35E-02	5.42E-01
7902789	NM_012262	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	WT and L359V	1.30	1.43	1.05	1.18	4.23E-02	7.30E-03	9.27E-01	6.27E-01
8154394	NM_001039697	SNAPC3	small nuclear RNA activating complex, polypeptide 3, 50kDa	WT and L359V	1.27	1.42	1.14	1.16	3.78E-02	3.68E-03	7.50E-01	5.78E-01
8030064	NM_017457	CYTH2	cytohesin 2	WT and L359V	1.31	1.42	1.10	1.16	3.18E-02	6.81E-03	8.38E-01	6.93E-01
7924636	NM_014698	TMEM63A	transmembrane protein 63A	WT and L359V	1.39	1.42	1.19	1.17	6.89E-03	3.22E-03	4.51E-01	4.46E-01
8133662	NM_001040457	RHBDD2	rhomboid domain containing 2	WT and L359V	1.50	1.42	1.27	1.19	1.56E-02	2.31E-02	5.24E-01	7.95E-01
7912646	NM_001229	CASP9	caspase 9, apoptosis-related cysteine peptidase	WT and L359V	1.32	1.41	1.13	1.15	3.79E-02	9.13E-03	8.20E-01	8.05E-01
7925342	NM_019891	ERO1LB	ERO1-like beta (S. cerevisiae)	WT and L359V	1.46	1.41	1.08	1.22	3.18E-02	3.64E-02	9.10E-01	7.16E-01
7953765	NM_020734	RIMKLB	ribosomal modification protein rimK-like family member B	WT and L359V	1.37	1.41	1.09	1.17	2.41E-02	1.04E-02	8.70E-01	6.77E-01

7928411	NM_015037	KIAA0913	KIAA0913	WT and L359V	1.28	1.41	1.02	1.05	3.41E-02	4.33E-03	9.77E-01	1.00E+00
7991234	NM_005928	MFGE8	milk fat globule-EGF factor 8 protein	WT and L359V	1.32	1.41	1.25	1.24	3.64E-02	8.90E-03	4.13E-01	3.47E-01
8057056	NM_133378	TTN	titin	WT and L359V	1.38	1.41	1.15	1.18	3.17E-02	1.86E-02	8.13E-01	7.53E-01
8009382	NM_004459	BPTF	bromodomain PHD finger transcription factor	WT and L359V	1.48	1.40	1.07	1.13	1.15E-02	1.66E-02	8.98E-01	1.00E+00
7984112	NM_016530	RAB8B	RAB8B, member RAS oncogene family	WT and L359V	1.62	1.40	1.28	1.26	1.69E-03	7.53E-03	2.50E-01	2.35E-01
8129953	NM_006734	HIVEP2	human immunodeficiency virus type I enhancer binding protein 2	WT and L359V	0.74	1.40	0.94	1.03	1.91E-02	7.95E-03	8.98E-01	1.00E+00
8152703	NM_058229	FBXO32	F-box protein 32	WT and L359V	1.46	1.40	1.17	1.25	8.36E-03	1.05E-02	7.19E-01	3.05E-01
8007637	NM_001466	FZD2	frizzled homolog 2 (Drosophila)	WT and L359V	1.45	1.40	1.25	1.21	4.00E-02	4.81E-02	7.19E-01	8.29E-01
8082827	NM_025180	CEP63	centrosomal protein 63kDa	WT and L359V	1.42	1.39	1.11	1.19	1.38E-02	1.29E-02	8.36E-01	6.04E-01
8040698	NM_017877	C2orf18	chromosome 2 open reading frame 18	WT and L359V	1.24	1.39	1.18	1.14	4.73E-02	4.27E-03	5.36E-01	6.71E-01
8102720	NM_020337	ANKRD50	ankyrin repeat domain 50	WT and L359V	1.48	1.39	1.01	1.13	7.02E-03	1.10E-02	9.94E-01	8.99E-01
7999044	NM_004380	CREBBP	CREB binding protein	WT and L359V	1.27	1.39	1.01	1.04	4.01E-02	5.91E-03	9.83E-01	1.00E+00
8173732	NM_015975	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kD	WT and L359V	1.29	1.39	1.03	1.16	2.88E-02	5.62E-03	9.43E-01	5.69E-01
8176263	NM_015975	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kD	WT and L359V	1.29	1.39	1.03	1.16	2.88E-02	5.62E-03	9.43E-01	5.69E-01
7902592	NM_006465	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	WT and L359V	1.56	1.39	1.15	1.18	6.90E-03	2.01E-02	8.09E-01	7.16E-01
8061986	NM_031483	ITCH	itchy E3 ubiquitin protein ligase homolog (mouse)	WT and L359V	1.40	1.39	1.13	1.20	1.55E-02	1.19E-02	8.16E-01	5.05E-01
8006237	BC062632	LOC400590	hypothetical LOC400590	WT and L359V	1.38	1.39	1.20	1.16	4.24E-02	2.67E-02	7.47E-01	8.90E-01
8031526	NM_013301	CCDC106	coiled-coil domain containing 106	WT and L359V	1.27	1.39	1.17	1.18	4.70E-02	7.15E-03	6.50E-01	4.97E-01
7962112	NM_001002259	CAPRIN2	caprin family member 2	WT and L359V	1.42	1.39	0.99	1.15	4.31E-02	4.12E-02	9.93E-01	1.00E+00
7954419	NM_018638	ETNK1	ethanolamine kinase 1	WT and L359V	1.51	1.39	0.82	1.13	2.03E-02	4.07E-02	7.50E-01	1.00E+00
8036525	NM_001042600	MAP4K1	mitogen-activated protein kinase kinase kinase kinase 1	WT and L359V	1.30	1.39	1.22	1.17	3.92E-02	1.09E-02	5.08E-01	6.34E-01
8140170	NM_173537	GTF2IRD2	GTF2I repeat domain containing 2	WT and L359V	1.36	1.38	1.00	1.15	1.55E-02	7.89E-03	9.95E-01	6.67E-01
8127425	NM_018368	LMBRD1	LMBR1 domain containing 1	WT and L359V	1.59	1.38	1.04	1.22	9.57E-03	3.72E-02	9.61E-01	6.53E-01
8042843	NM_032118	WDR54	WD repeat domain 54	WT and L359V	1.28	1.38	1.12	1.18	4.00E-02	7.86E-03	8.14E-01	4.98E-01
8168359	NM_001013627	NHSL2	NHS-like 2	WT and L359V	1.82	1.38	1.19	1.23	1.59E-03	2.55E-02	7.50E-01	5.28E-01
8133549	NM_001003795	GTF2IRD2B	GTF2I repeat domain containing 2B	WT and L359V	1.38	1.38	0.98	1.15	1.35E-02	9.10E-03	9.70E-01	7.03E-01
8081171	NM_153605	CRYBG3	beta-gamma crystallin domain containing 3	WT and L359V	1.45	1.38	0.97	1.16	7.40E-03	1.08E-02	9.54E-01	7.15E-01
8117435	NM_007047	BTN3A2	butyrophilin, subfamily 3, member A2	WT and L359V	1.56	1.38	1.10	1.22	7.47E-03	2.48E-02	8.64E-01	5.87E-01
8052845	NM_022173	TIA1	TIA1 cytotoxic granule-associated RNA binding protein	WT and L359V	1.42	1.38	1.06	1.22	1.20E-02	1.29E-02	9.10E-01	4.02E-01
8069178	NM_001033049	ADARB1	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	WT and L359V	1.36	1.38	1.22	1.22	2.36E-02	1.37E-02	5.21E-01	4.28E-01
8158939	NM_004188	GFI1B	growth factor independent 1B transcription repressor	WT and L359V	1.85	1.37	1.48	1.33	2.60E-03	4.65E-02	1.45E-01	3.31E-01
7986250	NM_001271	CHD2	chromodomain helicase DNA binding protein 2	WT and L359V	1.49	1.37	1.14	1.25	2.39E-03	5.62E-03	7.26E-01	1.74E-01
8056060	NM_013450	BAZ2B	bromodomain adjacent to zinc finger domain, 2B	WT and L359V	1.63	1.37	1.17	1.23	1.85E-03	1.25E-02	7.26E-01	3.35E-01
8080511	NM_000720	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	WT and L359V	1.54	1.37	1.13	1.20	1.60E-02	4.95E-02	8.45E-01	7.82E-01
8110437	NM_022762	RMND5B	required for meiotic nuclear division 5 homolog B (S. cerevisiae)	WT and L359V	1.33	1.37	1.09	1.12	2.58E-02	1.28E-02	8.62E-01	9.32E-01
7954104	NM_018179	ATF7IP	activating transcription factor 7 interacting protein	WT and L359V	1.27	1.37	1.08	1.16	2.91E-02	5.60E-03	8.41E-01	4.98E-01
8161026	NM_032818	C9orf100	chromosome 9 open reading frame 100	WT and L359V	1.33	1.36	1.14	1.16	1.82E-02	8.56E-03	7.50E-01	6.27E-01
7966878	NM_007174	CIT	citron (rho-interacting, serine	WT and L359V	1.39	1.36	1.01	1.15	9.39E-03	8.88E-03	9.87E-01	6.86E-01
7903404	AK289844	RNPC3	RNA-binding region (RNP1, RRM) containing 3	WT and L359V	1.35	1.36	1.19	1.23	2.23E-02	1.41E-02	6.12E-01	3.50E-01
7917359	NM_017953	ZNHIT6	zinc finger, HIT type 6	WT and L359V	1.58	1.36	1.34	1.30	5.06E-03	2.47E-02	2.23E-01	2.70E-01
8117071	NM_016255	FAM8A1	family with sequence similarity 8, member A1	WT and L359V	1.29	1.35	1.14	1.16	4.68E-02	1.61E-02	8.01E-01	7.02E-01
7964119	NM_005419	STAT2	signal transducer and activator of transcription 2, 113kDa	WT and L359V	1.44	1.35	1.07	1.17	1.54E-02	2.64E-02	9.01E-01	7.44E-01
8172158	NM_003688	CASK	calcium	WT and L359V	1.55	1.35	1.05	1.15	1.06E-02	4.26E-02	9.45E-01	9.45E-01
8112260	NM_018369	DEPDC1B	DEP domain containing 1B	WT and L359V	1.35	1.35	1.18	1.17	3.00E-02	2.21E-02	7.28E-01	7.44E-01
8084323	NM_004423	DVL3	dishevelled, dsh homolog 3 (Drosophila)	WT and L359V	1.32	1.35	1.06	1.04	3.70E-02	1.88E-02	9.05E-01	1.00E+00
7956009	NM_152637	METTL7B	methyltransferase like 7B	WT and L359V	1.97	1.35	1.54	1.33	1.25E-03	4.81E-02	7.81E-02	3.05E-01
8149955	NM_018492	PBK	PDZ binding kinase	WT and L359V	1.51	1.35	1.23	1.23	1.48E-02	4.41E-02	6.65E-01	5.75E-01
8142036	NM_182691	SRPK2	SFRS protein kinase 2	WT and L359V	1.49	1.35	1.27	1.24	9.36E-03	2.63E-02	4.22E-01	4.17E-01
7971692	NM_012141	INTS6	integrator complex subunit 6	WT and L359V	1.37	1.35	1.27	1.22	1.03E-02	9.15E-03	2.11E-01	3.05E-01
8107005	NM_001750	CAST	calpastatin	WT and L359V	1.34	1.35	1.06	1.16	1.67E-02	1.07E-02	8.86E-01	6.27E-01
8154178	NM_004972	JAK2	Janus kinase 2 (a protein tyrosine kinase)	WT and L359V	1.54	1.35	0.83	1.11	5.06E-03	2.33E-02	6.28E-01	1.00E+00
7904726	NM_006472	TXNIP	thioredoxin interacting protein	WT and L359V	1.52	1.35	1.32	1.42	1.37E-02	4.63E-02	3.90E-01	1.46E-01
8098576	NM_001151	SLC25A4	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), mem	WT and L359V	1.46	1.34	1.27	1.27	6.93E-03	1.59E-02	2.79E-01	2.43E-01
8070097	NM_017833	DNAJC28	DnaJ (Hsp40) homolog, subfamily C, member 28	WT and L359V	1.46	1.34	0.98	1.10	1.15E-02	2.64E-02	9.75E-01	1.00E+00
8105436	NM_005921	MAP3K1	mitogen-activated protein kinase kinase kinase 1	WT and L359V	1.33	1.34	1.11	1.15	2.58E-02	1.61E-02	8.36E-01	7.32E-01
8029773	NM_001002915	IGFL2	IGF-like family member 2	WT and L359V	1.53	1.34	1.16	1.21	8.49E-03	3.55E-02	7.99E-01	6.07E-01
7978932	NM_006939	SOS2	son of sevenless homolog 2 (Drosophila)	WT and L359V	1.37	1.33	1.05	1.13	2.39E-02	2.71E-02	9.22E-01	9.45E-01
8067113	NM_006526	ZNF217	zinc finger protein 217	WT and L359V	1.30	1.33	1.04	1.14	2.79E-02	1.49E-02	9.31E-01	7.29E-01
8098995	NM_006454	MXD4	MAX dimerization protein 4	WT and L359V	1.42	1.33	1.05	1.13	2.20E-02	4.31E-02	9.31E-01	1.00E+00
8124088	NM_022113	KIF13A	kinesin family member 13A	WT and L359V	1.85	1.32	1.14	1.27	9.37E-04	3.41E-02	8.18E-01	3.05E-01
7932285	NM_024948	C10orf97	chromosome 10 open reading frame 97	WT and L359V	1.36	1.32	1.05	1.14	3.16E-02	3.67E-02	9.27E-01	9.12E-01
8155946	NM_033305	VPS13A	vacuolar protein sorting 13 homolog A (S. cerevisiae)	WT and L359V	1.45	1.32	1.11	1.22	1.83E-02	4.98E-02	8.62E-01	6.01E-01
7969129	NM_001040443	PHF11	PHD finger protein 11	WT and L359V	1.37	1.31	1.07	1.20	1.23E-02	1.73E-02	8.86E-01	4.13E-01
8095187	NM_025009	CEP135	centrosomal protein 135kDa	WT and L359V	1.34	1.31	1.05	1.17	3.49E-02	3.78E-02	9.35E-01	7.09E-01
7936419	NM_018017	C10orf118	chromosome 10 open reading frame 118	WT and L359V	1.48	1.31	1.10	1.18	8.82E-03	3.68E-02	8.55E-01	6.67E-01

7952069	BC022856	C11orf60	chromosome 11 open reading frame 60	WT and L359V	1.36	1.31	1.00	1.17	3.77E-02	4.82E-02	9.99E-01	8.00E-01
8048523	NM_006736	DNAJB2	DnaJ (Hsp40) homolog, subfamily B, member 2	WT and L359V	1.31	1.31	1.05	1.13	3.10E-02	2.23E-02	9.12E-01	8.76E-01
7965094	NM_203394	E2F7	E2F transcription factor 7	WT and L359V	1.31	1.30	0.97	1.03	4.79E-02	4.07E-02	9.52E-01	1.00E+00
8084173	NM_014616	ATP11B	ATPase, class VI, type 11B	WT and L359V	1.84	1.30	1.22	1.28	1.75E-04	1.33E-02	3.10E-01	1.19E-01
8058159	---			WT and L359V	1.34	1.29	1.19	1.18	2.71E-02	3.38E-02	6.39E-01	5.96E-01
8042195	NM_152392	AHSA2	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	WT and L359V	1.33	1.29	1.05	1.16	3.45E-02	4.41E-02	9.33E-01	7.48E-01
8047577	NM_024744	ALS2CR8	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 8	WT and L359V	1.47	1.28	1.04	1.19	8.51E-03	4.75E-02	9.47E-01	5.66E-01
7912257	NM_001009566	CLSTN1	calsyntenin 1	WT and L359V	1.33	1.28	1.05	1.11	1.59E-02	2.29E-02	9.01E-01	9.32E-01
7999642	NM_014647	KIAA0430	KIAA0430	WT and L359V	1.26	1.28	1.05	1.10	4.79E-02	2.91E-02	9.20E-01	1.00E+00
7969204	NM_052950	WDFY2	WD repeat and FYVE domain containing 2	WT and L359V	1.41	1.28	1.28	1.21	9.42E-03	3.36E-02	2.27E-01	3.70E-01
8089000	NM_001008390	CGGBP1	CGG triplet repeat binding protein 1	WT and L359V	1.32	1.26	1.21	1.20	2.41E-02	3.59E-02	4.70E-01	4.24E-01
7969017	NM_000321	RB1	retinoblastoma 1	WT and L359V	1.33	1.26	1.10	1.15	1.92E-02	3.60E-02	8.38E-01	6.43E-01
8011499	NM_002558	P2RX1	purinergic receptor P2X, ligand-gated ion channel, 1	WT and L359V	1.31	1.26	1.25	1.16	2.67E-02	4.19E-02	3.06E-01	6.56E-01
8004699	NM_001005273	CHD3	chromodomain helicase DNA binding protein 3	WT and L359V	1.47	1.26	1.19	1.14	4.75E-03	4.13E-02	5.66E-01	7.99E-01
7907861	NM_004736	XPR1	xenotropic and polytropic retrovirus receptor	WT and L359V	1.25	1.25	1.04	1.09	4.35E-02	3.05E-02	9.27E-01	1.00E+00
7916185	NM_001009881	ZCCHC11	zinc finger, CCHC domain containing 11	WT and L359V	1.26	1.25	1.10	1.12	4.02E-02	3.48E-02	8.25E-01	8.60E-01
8080878	NM_001128149	ATXN7	ataxin 7	WT and L359V	1.28	1.24	1.13	1.10	2.54E-02	3.14E-02	7.36E-01	9.88E-01
8092095	NM_015028	TNIK	TRAF2 and NCK interacting kinase	WT and L359V	1.50	1.23	1.30	1.15	2.38E-03	4.33E-02	1.20E-01	6.16E-01
8083221	NM_002586	PBX2	pre-B-cell leukemia homeobox 2	WT and L359V	1.26	1.23	1.04	1.06	4.06E-02	4.62E-02	9.22E-01	1.00E+00
7907445	NM_014458	KLHL20	kelch-like 20 (Drosophila)	WT and L359V	1.30	1.23	1.01	1.11	2.22E-02	4.84E-02	9.93E-01	9.13E-01
8102410	NR_002225	RPS26L	40S ribosomal protein S26-like	WT and L359V	0.80	0.82	0.93	0.87	4.44E-02	4.65E-02	8.58E-01	5.93E-01
7967987	NM_024026	MRP63	mitochondrial ribosomal protein 63	WT and L359V	0.79	0.81	0.91	0.90	3.79E-02	4.26E-02	8.36E-01	8.78E-01
7947450	NM_005574	LMO2	LIM domain only 2 (rhombotin-like 1)	WT and L359V	0.72	0.81	0.92	0.89	8.29E-03	4.26E-02	8.38E-01	8.67E-01
8018937	NM_025090	USP36	ubiquitin specific peptidase 36	WT and L359V	0.75	0.81	0.93	0.87	1.45E-02	4.48E-02	8.76E-01	6.07E-01
8092457	NM_005787	ALG3	asparagine-linked glycosylation 3, alpha-1,3- mannosyltransferase homolog (S. cere	WT and L359V	0.76	0.81	0.94	0.85	1.90E-02	3.98E-02	8.86E-01	4.42E-01
8072883	NM_024313	NOL12	nucleolar protein 12	WT and L359V	0.78	0.81	0.87	0.86	2.04E-02	2.92E-02	6.50E-01	4.46E-01
7921014	NM_005920	MEF2D	myocyte enhancer factor 2D	WT and L359V	0.77	0.81	0.95	0.87	2.74E-02	4.76E-02	9.13E-01	6.34E-01
8007008	NM_003250	THRA	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene ho	WT and L359V	0.76	0.80	0.86	0.86	1.89E-02	3.46E-02	6.50E-01	5.28E-01
8089830	NM_001099678	LRRC58	leucine rich repeat containing 58	WT and L359V	0.81	0.80	0.90	0.90	5.00E-02	2.91E-02	8.09E-01	8.84E-01
7942439	NM_032871	RELT	RELT tumor necrosis factor receptor	WT and L359V	0.76	0.80	0.86	0.85	1.70E-02	3.14E-02	6.11E-01	4.62E-01
8093976	NM_020773	TBC1D14	TBC1 domain family, member 14	WT and L359V	0.71	0.80	0.84	0.87	7.03E-03	3.41E-02	4.70E-01	6.73E-01
7967202	NM_019034	RHOF	ras homolog gene family, member F (in filopodia)	WT and L359V	0.77	0.80	0.87	0.85	3.58E-02	4.88E-02	7.38E-01	5.83E-01
7900510	NM_001905	CTPS	CTP synthase	WT and L359V	0.72	0.80	0.87	0.85	1.09E-02	4.33E-02	7.52E-01	5.52E-01
8003410	NM_000512	GALNS	galactosamine (N-acetyl)-6-sulfate sulfatase	WT and L359V	0.76	0.80	0.87	0.85	1.90E-02	3.28E-02	7.14E-01	4.58E-01
8073135	NM_019008	SMCR7L	Smith-Magenis syndrome chromosome region, candidate 7-like	WT and L359V	0.80	0.80	0.88	0.88	3.73E-02	2.70E-02	7.34E-01	7.02E-01
7966213	NM_052845	MMAB	methylmalonic aciduria (cobalamin deficiency) cblB type	WT and L359V	0.77	0.79	0.90	0.86	3.41E-02	4.19E-02	8.34E-01	6.66E-01
8042942	NM_000189	HK2	hexokinase 2	WT and L359V	0.73	0.79	0.81	0.82	1.38E-02	4.08E-02	4.12E-01	3.47E-01
8010271	NM_024419	PGS1	phosphatidylglycerophosphate synthase 1	WT and L359V	0.77	0.79	0.81	0.84	2.27E-02	2.85E-02	3.16E-01	3.70E-01
8063739	NM_080672	PHACTR3	phosphatase and actin regulator 3	WT and L359V	0.75	0.79	0.88	0.90	2.24E-02	3.72E-02	7.65E-01	9.89E-01
7934789	NM_017551	GRID1	glutamate receptor, ionotropic, delta 1	WT and L359V	0.66	0.79	0.78	0.82	4.16E-03	4.44E-02	2.80E-01	4.11E-01
8105481	NM_152687	GAPT	GRB2-binding adaptor protein, transmembrane	WT and L359V	1.29	0.79	1.06	1.03	2.36E-02	2.50E-02	8.90E-01	1.00E+00
7945579	NM_023947	CHID1	chitinase domain containing 1	WT and L359V	0.77	0.79	0.92	0.86	2.11E-02	2.08E-02	8.41E-01	4.98E-01
8162729	NM_014788	TRIM14	tripartite motif-containing 14	WT and L359V	0.73	0.79	0.89	0.83	1.47E-02	3.78E-02	8.19E-01	4.26E-01
8039413	NM_014931	SAPS1	SAPS domain family, member 1	WT and L359V	0.76	0.78	0.88	0.84	2.39E-02	2.87E-02	7.50E-01	4.02E-01
7921110	NM_030980	ISG20L2	interferon stimulated exonuclease gene 20kDa-like 2	WT and L359V	0.76	0.78	0.88	0.83	1.61E-02	1.99E-02	7.20E-01	3.05E-01
7927425	NM_020945	WDFY4	WDFY family member 4	WT and L359V	0.65	0.78	0.74	0.78	2.23E-03	2.87E-02	9.26E-02	1.69E-01
8159692	NM_152285	ARRDC1	arrestin domain containing 1	WT and L359V	0.79	0.78	0.89	0.86	2.74E-02	1.56E-02	7.82E-01	5.10E-01
7911359	NM_015658	NOC2L	nucleolar complex associated 2 homolog (S. cerevisiae)	WT and L359V	0.70	0.78	0.87	0.83	1.00E-02	3.84E-02	7.74E-01	4.61E-01
7974471	---			WT and L359V	1.29	0.78	1.05	1.05	3.07E-02	2.45E-02	9.09E-01	1.00E+00
8140020	NM_018044	NSUN5	NOL1	WT and L359V	0.76	0.78	0.84	0.88	3.82E-02	4.15E-02	6.30E-01	9.13E-01
7999102	NM_003223	TFAP4	transcription factor AP-4 (activating enhancer binding protein 4)	WT and L359V	0.76	0.78	0.94	0.87	3.73E-02	4.23E-02	9.09E-01	8.05E-01
8024584	NM_020170	NCLN	nicalin homolog (zebrafish)	WT and L359V	0.73	0.78	0.93	0.86	1.93E-02	3.93E-02	8.79E-01	6.91E-01
7956114	NM_001029	RPS26	ribosomal protein S26	WT and L359V	0.77	0.77	0.91	0.84	1.90E-02	1.61E-02	8.23E-01	3.69E-01
8087739	NM_013324	CISH	cytokine inducible SH2-containing protein	WT and L359V	0.76	0.77	0.95	0.87	2.88E-02	2.75E-02	9.22E-01	7.29E-01
8021884	NM_004715	CTDP1	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, su	WT and L359V	0.80	0.77	0.93	0.88	4.46E-02	1.64E-02	8.64E-01	7.01E-01
8063078	NM_001127695	CTSA	cathepsin A	WT and L359V	0.76	0.77	0.90	0.86	2.88E-02	2.64E-02	8.23E-01	6.27E-01
7981157	BC008299	C14orf139	chromosome 14 open reading frame 139	WT and L359V	0.69	0.77	0.84	0.83	7.35E-03	2.86E-02	6.11E-01	4.58E-01
8049799	NM_001001891	ANO7	anoctamin 7	WT and L359V	0.75	0.77	0.87	0.87	3.49E-02	4.08E-02	7.85E-01	8.59E-01
7997852	NM_016209	TRAPPC2L	trafficking protein particle complex 2-like	WT and L359V	0.76	0.77	0.92	0.84	1.53E-02	1.44E-02	8.47E-01	3.55E-01
8005089	NM_001303	COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransfera	WT and L359V	0.78	0.77	0.84	0.86	3.29E-02	1.76E-02	5.03E-01	5.23E-01
8025563	NM_001040664	PPAN-P2RY11	PPAN-P2RY11 readthrough transcript	WT and L359V	0.72	0.77	0.91	0.86	8.36E-03	1.66E-02	8.36E-01	5.65E-01
8024078	NM_005224	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	WT and L359V	0.79	0.77	0.91	0.85	2.80E-02	1.19E-02	8.25E-01	3.70E-01
8073612	NM_000714	TSPO	translocator protein (18kDa)	WT and L359V	0.71	0.77	0.90	0.84	1.73E-02	3.79E-02	8.37E-01	6.07E-01
7905881	NM_207196	ADAM15	ADAM metallopeptidase domain 15	WT and L359V	0.76	0.77	0.95	0.87	3.77E-02	2.82E-02	9.15E-01	7.93E-01
7967127	NM_006549	CAMKK2	calcium	WT and L359V	0.75	0.77	0.90	0.87	1.48E-02	1.42E-02	8.14E-01	6.34E-01

8134965	NM_020246	SLC12A9	solute carrier family 12 (potassium	WT and L359V	0.63	0.76	0.79	0.80	1.59E-03	1.80E-02	2.36E-01	2.12E-01
8065868	NM_002212	EIF6	eukaryotic translation initiation factor 6	WT and L359V	0.75	0.76	0.94	0.83	2.41E-02	2.42E-02	8.98E-01	4.56E-01
7897482	NM_005026	PIK3CD	phosphoinositide-3-kinase, catalytic, delta polypeptide	WT and L359V	0.67	0.76	0.81	0.81	6.14E-03	2.83E-02	4.42E-01	3.56E-01
8044793	NM_182915	STEAP3	STEAP family member 3	WT and L359V	0.70	0.76	0.88	0.82	5.75E-03	1.52E-02	7.38E-01	3.05E-01
8033789	NM_001008727	ZNF121	zinc finger protein 121	WT and L359V	0.72	0.76	0.87	0.88	2.28E-02	4.11E-02	8.05E-01	9.45E-01
8043197	NM_003761	VAMP8	vesicle-associated membrane protein 8 (endobrevin)	WT and L359V	0.77	0.76	0.92	0.86	4.24E-02	2.49E-02	8.58E-01	6.34E-01
8152750	NM_194291	TMEM65	transmembrane protein 65	WT and L359V	0.56	0.76	0.93	0.83	5.27E-04	2.15E-02	8.76E-01	4.39E-01
8025586	NM_146388	MRPL4	mitochondrial ribosomal protein L4	WT and L359V	0.75	0.76	0.95	0.87	1.45E-02	1.35E-02	9.02E-01	5.96E-01
7977820	NM_001039619	PRMT5	protein arginine methyltransferase 5	WT and L359V	0.74	0.76	0.90	0.86	1.38E-02	1.74E-02	8.20E-01	6.19E-01
7950906	NM_001814	CTSC	cathepsin C	WT and L359V	0.75	0.76	0.93	0.90	1.48E-02	1.45E-02	8.59E-01	9.45E-01
8037495	NM_145288	ZNF296	zinc finger protein 296	WT and L359V	0.67	0.76	0.87	0.82	9.53E-03	4.31E-02	8.07E-01	4.97E-01
7958379	NM_007062	PWP1	PWP1 homolog (S. cerevisiae)	WT and L359V	0.77	0.76	0.84	0.87	2.91E-02	1.60E-02	5.15E-01	6.87E-01
8063893	NM_007002	ADRM1	adhesion regulating molecule 1	WT and L359V	0.75	0.76	0.85	0.83	3.01E-02	2.69E-02	6.79E-01	4.56E-01
8138091	NM_139179	DAGLB	diacylglycerol lipase, beta	WT and L359V	0.75	0.76	0.91	0.88	2.42E-02	2.03E-02	8.37E-01	8.38E-01
8070799	NM_182688	UBE2G2	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)	WT and L359V	0.72	0.76	0.88	0.87	7.26E-03	1.17E-02	7.40E-01	5.79E-01
8077370	NM_006515	SETMAR	SET domain and mariner transposase fusion gene	WT and L359V	0.70	0.76	0.80	0.83	1.43E-02	3.37E-02	4.37E-01	5.23E-01
8087576	NM_006764	IFRD2	interferon-related developmental regulator 2	WT and L359V	0.77	0.76	0.93	0.87	4.52E-02	2.88E-02	8.80E-01	8.38E-01
8034615	NM_001136035	TRMT1	TRM1 tRNA methyltransferase 1 homolog (S. cerevisiae)	WT and L359V	0.75	0.76	0.88	0.87	4.83E-02	3.93E-02	8.15E-01	9.05E-01
8160036	AK292632	C9orf123	chromosome 9 open reading frame 123	WT and L359V	0.72	0.76	0.87	0.87	1.23E-02	1.94E-02	7.69E-01	7.09E-01
8040843	NM_004341	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	WT and L359V	0.76	0.76	0.90	0.82	2.56E-02	1.63E-02	8.23E-01	3.40E-01
8163569	NM_030767	AKNA	AT-hook transcription factor	WT and L359V	0.70	0.76	0.86	0.82	2.07E-02	4.82E-02	8.01E-01	5.93E-01
8020254	NM_031216	SEH1L	SEH1-like (S. cerevisiae)	WT and L359V	0.76	0.76	0.87	0.86	1.59E-02	1.10E-02	6.65E-01	4.98E-01
7927071	NM_001007094	ZNF37A	zinc finger protein 37A	WT and L359V	0.78	0.76	0.88	0.89	3.59E-02	1.44E-02	7.71E-01	8.85E-01
8119842	NM_203290	POLR1C	polymerase (RNA) I polypeptide C, 30kDa	WT and L359V	0.73	0.76	0.89	0.88	3.18E-02	3.80E-02	8.28E-01	9.40E-01
8034589	NM_004461	FARSA	phenylalanyl-tRNA synthetase, alpha subunit	WT and L359V	0.77	0.76	0.95	0.89	4.00E-02	1.94E-02	9.15E-01	8.97E-01
8002121	NM_001907	CTRL	chymotrypsin-like	WT and L359V	0.71	0.75	0.83	0.82	2.36E-02	3.84E-02	6.75E-01	5.65E-01
7966600	NM_024959	SLC24A6	solute carrier family 24 (sodium	WT and L359V	0.68	0.75	0.86	0.83	4.77E-03	1.45E-02	7.20E-01	3.56E-01
7997179	NM_001361	DHODH	dihydroorotate dehydrogenase	WT and L359V	0.74	0.75	0.85	0.87	4.59E-02	4.48E-02	7.91E-01	9.27E-01
8076344	NM_001018050	POLR3H	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)	WT and L359V	0.75	0.75	0.89	0.85	1.61E-02	1.31E-02	8.06E-01	5.05E-01
8075924	NM_002405	MFNG	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	WT and L359V	0.71	0.75	0.99	0.87	3.16E-02	4.93E-02	9.88E-01	9.81E-01
7912374	NM_003132	SRM	spermidine synthase	WT and L359V	0.71	0.75	0.94	0.82	5.06E-03	8.88E-03	8.80E-01	2.74E-01
8159249	NM_016034	MRPS2	mitochondrial ribosomal protein S2	WT and L359V	0.76	0.75	0.90	0.89	4.74E-02	2.69E-02	8.38E-01	9.94E-01
8126588	NM_020750	XPO5	exportin 5	WT and L359V	0.78	0.75	0.90	0.89	3.32E-02	1.10E-02	8.23E-01	7.89E-01
7956152	NM_006191	PA2G4	proliferation-associated 2G4, 38kDa	WT and L359V	0.78	0.75	0.88	0.86	3.21E-02	1.16E-02	7.65E-01	5.78E-01
7950119	BC001706	C11orf59	chromosome 11 open reading frame 59	WT and L359V	0.75	0.75	0.86	0.83	2.91E-02	2.25E-02	7.62E-01	4.97E-01
7964548	NM_005371	METTL1	methyltransferase like 1	WT and L359V	0.75	0.75	0.86	0.86	1.71E-02	1.23E-02	6.39E-01	6.04E-01
8131111	NM_001037283	EIF3B	eukaryotic translation initiation factor 3, subunit B	WT and L359V	0.78	0.75	0.90	0.87	3.70E-02	1.29E-02	8.25E-01	6.53E-01
8173269	NM_031206	LAS1L	LAS1-like (S. cerevisiae)	WT and L359V	0.79	0.75	0.92	0.92	4.74E-02	1.23E-02	8.41E-01	1.00E+00
8008664	NM_003488	AKAP1	A kinase (PRKA) anchor protein 1	WT and L359V	0.77	0.75	0.91	0.85	2.30E-02	8.80E-03	8.16E-01	4.67E-01
7962516	NM_030674	SLC38A1	solute carrier family 38, member 1	WT and L359V	0.74	0.74	0.90	0.91	3.33E-02	2.69E-02	8.48E-01	1.00E+00
7950294	NM_016565	CHCHD8	coiled-coil-helix-coiled-coil-helix domain containing 8	WT and L359V	0.74	0.74	0.86	0.84	3.49E-02	2.81E-02	7.72E-01	6.27E-01
8161229	NM_012166	FBXO10	F-box protein 10	WT and L359V	0.77	0.74	0.89	0.86	3.17E-02	1.36E-02	8.14E-01	6.66E-01
8122773	NM_015440	MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	WT and L359V	0.64	0.74	0.90	0.88	9.39E-03	4.43E-02	8.70E-01	1.00E+00
8112159	NM_024669	ANKRD55	ankyrin repeat domain 55	WT and L359V	0.61	0.74	0.87	0.84	5.48E-03	4.13E-02	8.16E-01	7.09E-01
8026806	NM_024656	GLT25D1	glycosyltransferase 25 domain containing 1	WT and L359V	0.79	0.74	0.93	0.88	3.18E-02	8.43E-03	8.62E-01	7.04E-01
7941822	NM_207354	ANKRD13D	ankyrin repeat domain 13 family, member D	WT and L359V	0.76	0.74	0.83	0.81	3.58E-02	1.66E-02	5.45E-01	3.50E-01
7929990	NM_015062	PPRC1	peroxisome proliferator-activated receptor gamma, coactivator-related 1	WT and L359V	0.78	0.74	0.92	0.83	4.23E-02	1.28E-02	8.56E-01	4.26E-01
8023191	NM_005901	SMAD2	SMAD family member 2	WT and L359V	0.77	0.74	0.73	0.80	4.96E-02	2.04E-02	1.24E-01	3.31E-01
8165552	NM_001130969	NELF	nasal embryonic LHRH factor	WT and L359V	0.72	0.74	0.81	0.80	1.90E-02	2.17E-02	5.05E-01	3.45E-01
7970473	NM_022459	XPO4	exportin 4	WT and L359V	0.78	0.74	0.88	0.87	3.15E-02	7.89E-03	7.69E-01	6.60E-01
8141688	NM_001084	PLOD3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	WT and L359V	0.78	0.74	1.01	0.85	4.17E-02	1.10E-02	9.94E-01	5.00E-01
8027100	NM_019070	DDX49	DEAD (Asp-Glu-Ala-Asp) box polypeptide 49	WT and L359V	0.72	0.74	0.86	0.83	1.51E-02	1.51E-02	7.26E-01	4.62E-01
7915472	NM_006516	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	WT and L359V	0.67	0.74	0.86	0.83	6.78E-03	1.97E-02	7.50E-01	5.23E-01
8076374	NM_005008	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	WT and L359V	0.72	0.74	0.88	0.86	1.93E-02	1.87E-02	8.13E-01	7.09E-01
7910416	NM_014777	URB2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae)	WT and L359V	0.69	0.74	0.84	0.78	4.95E-03	9.20E-03	4.99E-01	1.62E-01
8060854	NM_182734	PLCB1	phospholipase C, beta 1 (phosphoinositide-specific)	WT and L359V	0.63	0.74	0.67	0.79	9.52E-03	4.65E-02	1.15E-01	4.71E-01
8076569	NM_015140	TTLL12	tubulin tyrosine ligase-like family, member 12	WT and L359V	0.72	0.74	0.91	0.84	2.78E-02	3.05E-02	8.67E-01	6.95E-01
8008185	NM_016428	ABI3	ABI family, member 3	WT and L359V	0.65	0.74	0.70	0.74	3.19E-03	1.35E-02	6.04E-02	9.67E-02
8000884	NM_024096	DCTPP1	dCTP pyrophosphatase 1	WT and L359V	0.76	0.74	0.88	0.81	2.84E-02	1.25E-02	7.92E-01	3.25E-01
7903719	NM_004037	AMPD2	adenosine monophosphate deaminase 2 (isoform L)	WT and L359V	0.69	0.74	0.84	0.83	9.40E-03	1.68E-02	6.65E-01	4.61E-01
8011850	NM_001212	C1QBP	complement component 1, q subcomponent binding protein	WT and L359V	0.77	0.73	0.92	0.88	2.68E-02	9.58E-03	8.52E-01	8.13E-01
8131000	NM_017802	HEATR2	HEAT repeat containing 2	WT and L359V	0.70	0.73	0.90	0.82	6.93E-03	1.02E-02	8.20E-01	3.50E-01
8004510	NM_001251	CD68	CD68 molecule	WT and L359V	0.70	0.73	0.90	0.81	1.23E-02	1.72E-02	8.38E-01	4.02E-01
8149365	NR_003494	FAM86B1	family with sequence similarity 86, member B1	WT and L359V	0.79	0.73	0.93	0.86	4.65E-02	8.80E-03	8.64E-01	6.27E-01
8149389	NR_024241	FAM86D	family with sequence similarity 86, member D	WT and L359V	0.76	0.73	0.89	0.86	2.79E-02	1.14E-02	8.16E-01	6.55E-01

7963774	NM_015481	ZNF385A	zinc finger protein 385A	WT and L359V	0.63	0.73	0.81	0.75	4.98E-03	2.25E-02	5.47E-01	1.74E-01
7915084	NM_024640	YRDC	yrdC domain containing (E. coli)	WT and L359V	0.76	0.73	0.89	0.85	4.63E-02	1.75E-02	8.34E-01	6.96E-01
7899273	NM_006600	NUDC	nuclear distribution gene C homolog (A. nidulans)	WT and L359V	0.72	0.73	0.83	0.83	1.48E-02	1.30E-02	5.45E-01	4.73E-01
8119492	NM_004053	BYSL	bystin-like	WT and L359V	0.71	0.73	0.85	0.83	1.54E-02	1.55E-02	7.12E-01	4.78E-01
8008517	NM_198175	NME1	non-metastatic cells 1, protein (NM23A) expressed in	WT and L359V	0.76	0.73	0.96	0.87	3.29E-02	1.10E-02	9.29E-01	7.47E-01
8053496	NM_015425	POLR1A	polymerase (RNA) I polypeptide A, 194kDa	WT and L359V	0.72	0.73	0.83	0.82	2.21E-02	2.03E-02	6.69E-01	4.98E-01
8011861	NM_020162	DHX33	DEAH (Asp-Glu-Ala-His) box polypeptide 33	WT and L359V	0.71	0.73	0.90	0.85	6.90E-03	7.22E-03	8.23E-01	5.09E-01
8020495	NM_138375	CABLES1	Cdk5 and Abl enzyme substrate 1	WT and L359V	0.62	0.73	0.76	0.78	6.65E-03	3.04E-02	3.90E-01	3.86E-01
8164269	NM_000118	ENG	endoglin	WT and L359V	0.60	0.73	0.75	0.73	1.09E-03	9.01E-03	1.20E-01	7.68E-02
8126288	NM_024807	TREML2	triggering receptor expressed on myeloid cells-like 2	WT and L359V	0.71	0.73	0.78	0.78	1.92E-02	1.89E-02	3.63E-01	3.05E-01
8165011	NM_002003	FCN1	ficolin (collagen	WT and L359V	0.68	0.73	0.78	0.79	1.38E-02	2.55E-02	4.37E-01	3.70E-01
7922717	NM_002928	RGS16	regulator of G-protein signaling 16	WT and L359V	0.78	0.73	0.97	0.92	2.85E-02	6.70E-03	9.44E-01	1.00E+00
8073743	NM_006953	UPK3A	uroplakin 3A	WT and L359V	0.73	0.73	0.83	0.84	2.70E-02	1.61E-02	6.29E-01	6.00E-01
8113790	NM_178450	MARCH3	membrane-associated ring finger (C3HC4) 3	WT and L359V	0.73	0.72	0.96	0.88	1.46E-02	9.06E-03	9.29E-01	7.90E-01
8157761	NM_014397	NEK6	NIMA (never in mitosis gene a)-related kinase 6	WT and L359V	0.72	0.72	0.85	0.86	1.66E-02	1.19E-02	7.12E-01	6.82E-01
7960575	NM_001033714	NOP2	NOP2 nucleolar protein homolog (yeast)	WT and L359V	0.74	0.72	0.88	0.84	1.43E-02	7.09E-03	7.79E-01	4.46E-01
8012856	NM_018127	ELAC2	elaC homolog 2 (E. coli)	WT and L359V	0.77	0.72	0.83	0.85	3.00E-02	6.81E-03	4.46E-01	5.05E-01
8087852	NM_017442	TLR9	toll-like receptor 9	WT and L359V	0.58	0.72	0.87	0.75	8.39E-04	9.22E-03	7.67E-01	1.19E-01
7949577	NM_020470	YIF1A	Yip1 interacting factor homolog A (S. cerevisiae)	WT and L359V	0.71	0.72	0.86	0.83	1.14E-02	9.36E-03	7.24E-01	4.41E-01
8084397	NM_014693	ECE2	endothelin converting enzyme 2	WT and L359V	0.71	0.72	0.87	0.83	4.58E-03	4.05E-03	6.75E-01	3.05E-01
7967624	NM_145648	SLC15A4	solute carrier family 15, member 4	WT and L359V	0.69	0.72	0.83	0.81	1.31E-02	1.55E-02	6.50E-01	4.41E-01
7962183	NM_001005353	AK3L1	adenylate kinase 3-like 1	WT and L359V	0.67	0.72	0.92	0.87	2.45E-02	4.34E-02	8.93E-01	1.00E+00
8019392	NM_004104	FASN	fatty acid synthase	WT and L359V	0.70	0.72	0.80	0.64	3.92E-02	3.77E-02	6.46E-01	6.58E-02
8057887	NM_004226	STK17B	serine	WT and L359V	0.78	0.72	0.92	0.92	3.31E-02	6.21E-03	8.48E-01	1.00E+00
7985767	NM_022767	AEN	apoptosis enhancing nuclease	WT and L359V	0.73	0.72	0.88	0.82	1.54E-02	8.69E-03	8.01E-01	3.81E-01
8054344	AK298610	FLJ42986	FLJ42986 protein	WT and L359V	0.66	0.72	0.92	0.86	2.55E-02	4.67E-02	9.07E-01	1.00E+00
8175023	NM_016032	ZDHHC9	zinc finger, DHHC-type containing 9	WT and L359V	0.69	0.72	0.89	0.85	7.48E-03	8.30E-03	8.13E-01	5.62E-01
8069859	NM_181619	KRTAP21-1	keratin associated protein 21-1	WT and L359V	0.66	0.71	0.85	0.79	7.28E-03	1.53E-02	7.62E-01	3.40E-01
8044745	NM_006773	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	WT and L359V	0.79	0.71	0.89	0.88	3.18E-02	3.73E-03	7.93E-01	7.02E-01
8171136	NM_178129	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	WT and L359V	0.68	0.71	0.99	0.82	2.54E-02	3.16E-02	9.94E-01	6.69E-01
8177026	NM_178129	P2RY8	purinergic receptor P2Y, G-protein coupled, 8	WT and L359V	0.68	0.71	0.99	0.82	2.54E-02	3.16E-02	9.94E-01	6.69E-01
8032608	NM_174983	C19orf28	chromosome 19 open reading frame 28	WT and L359V	0.49	0.71	0.66	0.67	7.72E-04	2.55E-02	8.69E-02	7.78E-02
8099037	NM_001120	MFSD10	major facilitator superfamily domain containing 10	WT and L359V	0.76	0.71	1.00	0.84	3.95E-02	1.14E-02	9.99E-01	6.27E-01
8064766	NM_001134338	RNF24	ring finger protein 24	WT and L359V	0.72	0.71	1.00	0.88	1.40E-02	7.85E-03	9.98E-01	8.14E-01
7963174	NM_147190	LASS5	LAG1 homolog, ceramide synthase 5	WT and L359V	0.70	0.71	0.84	0.86	1.48E-02	1.19E-02	6.67E-01	7.89E-01
7906107	NM_022367	SEMA4A	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	WT and L359V	0.71	0.71	0.84	0.82	1.81E-02	1.32E-02	6.75E-01	5.09E-01
8070330	NM_003720	PSMG1	proteasome (prosome, macropain) assembly chaperone 1	WT and L359V	0.76	0.71	0.94	0.91	2.29E-02	4.99E-03	8.86E-01	1.00E+00
8073752	NM_001104595	FAM118A	family with sequence similarity 118, member A	WT and L359V	0.75	0.71	0.87	0.85	3.97E-02	1.17E-02	8.01E-01	7.03E-01
8037408	NM_002250	KCNN4	potassium intermediate	WT and L359V	0.56	0.71	0.79	0.80	1.55E-03	1.61E-02	4.37E-01	4.14E-01
8048370	NM_004328	BCS1L	BCS1-like (yeast)	WT and L359V	0.74	0.71	0.88	0.86	2.41E-02	9.15E-03	8.09E-01	6.77E-01
8090678	NM_007208	MRPL3	mitochondrial ribosomal protein L3	WT and L359V	0.80	0.71	0.90	0.90	3.18E-02	2.75E-03	8.01E-01	8.28E-01
7948267	NM_012456	TIMM10	translocase of inner mitochondrial membrane 10 homolog (yeast)	WT and L359V	0.73	0.71	0.90	0.83	3.15E-02	1.44E-02	8.41E-01	5.88E-01
7961230	NM_003651	CSDA	cold shock domain protein A	WT and L359V	0.66	0.71	0.91	0.85	1.02E-02	1.68E-02	8.66E-01	7.47E-01
8104422	NM_002454	MTRR	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	WT and L359V	0.79	0.71	0.91	0.86	4.63E-02	4.44E-03	8.34E-01	5.96E-01
8170971	NM_001363	DKC1	dyskeratosis congenita 1, dyskerin	WT and L359V	0.75	0.71	0.88	0.87	2.53E-02	6.97E-03	8.01E-01	7.44E-01
8156404	NM_032310	C9orf89	chromosome 9 open reading frame 89	WT and L359V	0.62	0.71	0.69	0.73	9.15E-03	2.89E-02	1.70E-01	2.61E-01
8045171	NM_033416	IMP4	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)	WT and L359V	0.69	0.71	0.90	0.86	1.14E-02	1.13E-02	8.40E-01	7.38E-01
8153664	AK293719	BOP1	block of proliferation 1	WT and L359V	0.56	0.71	0.79	0.73	7.03E-04	7.53E-03	3.41E-01	7.78E-02
8169657	NM_001105576	ANKRD58	ankyrin repeat domain 58	WT and L359V	0.70	0.71	0.88	0.88	3.89E-02	3.10E-02	8.41E-01	1.00E+00
7971361	NM_012345	NUFIP1	nuclear fragile X mental retardation protein interacting protein 1	WT and L359V	0.68	0.71	0.79	0.81	5.89E-03	6.42E-03	2.90E-01	3.05E-01
8143905	NM_007189	ABCF2	ATP-binding cassette, sub-family F (GCN20), member 2	WT and L359V	0.71	0.71	0.90	0.86	7.02E-03	4.57E-03	8.20E-01	5.55E-01
7951838	NM_003904	ZNF259	zinc finger protein 259	WT and L359V	0.74	0.71	0.82	0.86	2.36E-02	7.53E-03	5.15E-01	6.45E-01
7956878	NM_007199	IRAK3	interleukin-1 receptor-associated kinase 3	WT and L359V	0.68	0.70	0.78	0.80	3.84E-03	4.06E-03	1.86E-01	2.17E-01
8137526	NM_198336	INSIG1	insulin induced gene 1	WT and L359V	0.74	0.70	0.86	0.76	4.68E-02	1.47E-02	8.01E-01	2.55E-01
7928429	NM_002658	PLAU	plasminogen activator, urokinase	WT and L359V	0.63	0.70	0.84	0.81	5.75E-03	1.56E-02	7.28E-01	5.05E-01
8014956	NM_021724	NR1D1	nuclear receptor subfamily 1, group D, member 1	WT and L359V	0.60	0.70	0.91	0.76	1.47E-03	6.65E-03	8.45E-01	1.48E-01
8063942	NM_002531	NTSR1	neurotensin receptor 1 (high affinity)	WT and L359V	0.67	0.70	0.68	0.77	3.58E-02	4.43E-02	2.08E-01	4.98E-01
8075406	NM_014303	PES1	pescadillo homolog 1, containing BRCT domain (zebrafish)	WT and L359V	0.64	0.70	0.88	0.80	3.09E-03	6.66E-03	8.01E-01	3.05E-01
8120654	NM_019842	KCNQ5	potassium voltage-gated channel, KQT-like subfamily, member 5	WT and L359V	0.73	0.70	0.89	0.85	2.74E-02	1.04E-02	8.23E-01	7.02E-01
8069943	NM_014825	URB1	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	WT and L359V	0.67	0.70	0.89	0.82	4.85E-03	5.65E-03	8.01E-01	3.31E-01
7967544	NM_005505	SCARB1	scavenger receptor class B, member 1	WT and L359V	0.66	0.70	0.92	0.79	5.06E-03	7.43E-03	8.70E-01	2.74E-01
7901102	NM_015506	MMACHC	methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria	WT and L359V	0.68	0.70	0.90	0.82	2.39E-03	2.76E-03	8.05E-01	2.63E-01
7957890	NM_014503	UTP20	UTP20, small subunit (SSU) processome component, homolog (yeast)	WT and L359V	0.72	0.70	0.81	0.81	3.18E-02	1.61E-02	6.30E-01	5.44E-01
8112803	NM_005779	LHFPL2	lipoma HMGIC fusion partner-like 2	WT and L359V	0.76	0.70	0.83	0.82	2.33E-02	3.88E-03	4.37E-01	3.13E-01
8080013	NM_004635	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3	WT and L359V	0.75	0.70	0.90	0.85	2.37E-02	5.79E-03	8.29E-01	6.15E-01

7993167	NM_024997	ATF7IP2	activating transcription factor 7 interacting protein 2	WT and L359V	0.66	0.70	0.76	0.83	1.91E-02	2.56E-02	4.70E-01	7.47E-01
7959986	NM_025215	PUS1	pseudouridylate synthase 1	WT and L359V	0.73	0.70	0.94	0.90	2.57E-02	9.15E-03	8.99E-01	1.00E+00
8051030	NM_021095	SLC5A6	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	WT and L359V	0.72	0.70	0.89	0.82	7.35E-03	3.30E-03	7.97E-01	2.74E-01
8048227	NM_001557	IL8RB	interleukin 8 receptor, beta	WT and L359V	0.67	0.70	0.77	0.79	4.15E-02	4.53E-02	6.34E-01	6.27E-01
7930226	NM_014976	PDCD11	programmed cell death 11	WT and L359V	0.74	0.70	0.90	0.84	1.10E-02	2.87E-03	8.13E-01	4.02E-01
7937878	NR_002720	TRPC2	transient receptor potential cation channel, subfamily C, member 2 (pseudogene)	WT and L359V	0.62	0.70	0.64	0.72	1.48E-02	3.93E-02	1.23E-01	3.05E-01
8130003	NM_031287	SF3B5	splicing factor 3b, subunit 5, 10kDa	WT and L359V	0.66	0.69	0.87	0.79	1.57E-02	2.19E-02	8.34E-01	4.56E-01
8161829	BC034033	C9orf41	chromosome 9 open reading frame 41	WT and L359V	0.74	0.69	0.81	0.85	3.53E-02	9.41E-03	5.21E-01	7.09E-01
8070912	NM_194255	SLC19A1	solute carrier family 19 (folate transporter), member 1	WT and L359V	0.67	0.69	0.88	0.79	2.82E-03	3.26E-03	7.50E-01	1.81E-01
8156278	NM_005226	S1PR3	sphingosine-1-phosphate receptor 3	WT and L359V	0.62	0.69	0.90	0.83	4.98E-03	1.32E-02	8.58E-01	6.29E-01
7968242	NM_002097	GTF3A	general transcription factor IIIA	WT and L359V	0.74	0.69	0.91	0.87	4.57E-02	1.35E-02	8.76E-01	8.99E-01
7906904	NM_016371	HSD17B7	hydroxysteroid (17-beta) dehydrogenase 7	WT and L359V	0.74	0.69	0.88	0.83	4.44E-02	1.22E-02	8.34E-01	5.98E-01
8152988	NM_001045556	SLA	Src-like-adaptor	WT and L359V	0.74	0.69	0.78	0.83	2.56E-02	6.99E-03	2.79E-01	5.23E-01
8059319	NM_005687	FARSB	phenylalanyl-tRNA synthetase, beta subunit	WT and L359V	0.78	0.69	0.95	0.91	3.26E-02	3.40E-03	8.98E-01	1.00E+00
7898655	NM_001785	CDA	cytidine deaminase	WT and L359V	0.68	0.69	0.93	0.82	2.09E-02	1.97E-02	9.02E-01	6.27E-01
8003332	NM_002461	MVD	mevalonate (diphospho) decarboxylase	WT and L359V	0.73	0.69	0.88	0.80	3.87E-02	1.42E-02	8.36E-01	4.61E-01
8070615	NM_018669	WDR4	WD repeat domain 4	WT and L359V	0.71	0.69	0.86	0.86	3.90E-02	2.09E-02	8.16E-01	9.62E-01
8005475	NM_001037330	TRIM16L	tripartite motif-containing 16-like	WT and L359V	0.73	0.69	0.86	0.85	1.45E-02	4.39E-03	6.89E-01	5.78E-01
8174779	NM_013995	LAMP2	lysosomal-associated membrane protein 2	WT and L359V	0.60	0.69	0.78	0.81	1.08E-03	3.84E-03	2.00E-01	3.05E-01
8165094	NM_181701	QSOX2	quiescin Q6 sulfhydryl oxidase 2	WT and L359V	0.74	0.69	0.87	0.85	2.03E-02	4.27E-03	7.36E-01	5.96E-01
7975506	NM_015604	WDR21A	WD repeat domain 21A	WT and L359V	0.68	0.69	0.85	0.84	1.09E-02	7.89E-03	7.28E-01	6.17E-01
8044473	NM_019014	POLR1B	polymerase (RNA) I polypeptide B, 128kDa	WT and L359V	0.64	0.68	0.84	0.82	1.25E-03	2.10E-03	4.49E-01	2.74E-01
7929012	NM_020799	STAMBPL1	STAM binding protein-like 1	WT and L359V	0.56	0.68	0.79	0.76	2.94E-03	1.57E-02	5.66E-01	3.05E-01
8108447	NM_016463	CXXC5	CXXC finger 5	WT and L359V	0.64	0.68	0.85	0.82	1.14E-02	1.55E-02	8.01E-01	6.53E-01
8126296	AF534825	TREML3	triggering receptor expressed on myeloid cells-like 3	WT and L359V	0.56	0.68	0.82	0.77	4.81E-03	2.46E-02	7.65E-01	4.44E-01
8003773	NM_015085	GARNL4	GTPase activating Rap	WT and L359V	0.69	0.68	0.75	0.80	1.39E-02	7.76E-03	2.48E-01	3.56E-01
8078252	NM_152653	UBE2E2	ubiquitin-conjugating enzyme E2E 2 (UBC4	WT and L359V	0.66	0.68	0.87	0.81	8.36E-03	8.80E-03	8.11E-01	4.61E-01
7949995	NM_181515	MRPL21	mitochondrial ribosomal protein L21	WT and L359V	0.74	0.68	0.93	0.84	2.54E-02	5.74E-03	8.85E-01	6.07E-01
8149387	ENST00000307435	FAM90A1	family with sequence similarity 90, member A1	WT and L359V	0.78	0.68	0.92	0.82	4.31E-02	3.64E-03	8.64E-01	3.70E-01
8110755	NM_006598	SLC12A7	solute carrier family 12 (potassium	WT and L359V	0.66	0.68	0.87	0.81	1.25E-02	1.16E-02	8.16E-01	5.52E-01
7953914	NM_205852	CLEC12B	C-type lectin domain family 12, member B	WT and L359V	1.46	0.68	1.15	1.04	3.95E-02	2.57E-02	8.38E-01	1.00E+00
7897236	NM_003636	KCNAB2	potassium voltage-gated channel, shaker-related subfamily, beta member 2	WT and L359V	0.70	0.68	0.88	0.83	4.91E-03	1.97E-03	7.52E-01	3.31E-01
8030113	NM_006666	RUVBL2	RuvB-like 2 (E. coli)	WT and L359V	0.72	0.68	0.93	0.84	2.55E-02	7.15E-03	8.86E-01	6.43E-01
8090448	NM_003707	RUVBL1	RuvB-like 1 (E. coli)	WT and L359V	0.72	0.68	0.93	0.85	1.69E-02	4.42E-03	8.80E-01	6.43E-01
7921121	NM_145729	MRPL24	mitochondrial ribosomal protein L24	WT and L359V	0.70	0.67	0.93	0.85	1.76E-02	7.93E-03	8.86E-01	7.15E-01
8027876	NM_032635	TMEM147	transmembrane protein 147	WT and L359V	0.66	0.67	0.91	0.84	2.08E-03	1.83E-03	8.20E-01	3.47E-01
8050255	NM_024894	NOL10	nucleolar protein 10	WT and L359V	0.75	0.67	0.86	0.85	1.92E-02	2.58E-03	6.53E-01	5.52E-01
7949904	NM_030930	UNC93B1	unc-93 homolog B1 (C. elegans)	WT and L359V	0.76	0.67	0.92	0.85	2.91E-02	3.61E-03	8.55E-01	6.27E-01
7978132	NM_024658	IPO4	importin 4	WT and L359V	0.67	0.67	0.90	0.81	4.34E-03	3.16E-03	8.32E-01	3.25E-01
8056408	NM_004482	GALNT3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferas	WT and L359V	0.72	0.67	0.96	0.87	1.43E-02	3.73E-03	9.34E-01	7.35E-01
8009568	NM_032646	TTYH2	tweety homolog 2 (Drosophila)	WT and L359V	0.73	0.67	0.89	0.85	3.89E-02	8.65E-03	8.41E-01	7.67E-01
8175835	NM_005745	BCAP31	B-cell receptor-associated protein 31	WT and L359V	0.67	0.67	0.75	0.76	2.62E-02	1.88E-02	4.46E-01	4.02E-01
8114900	NM_004576	PPP2R2B	protein phosphatase 2 (formerly 2A), regulatory subunit B, beta isoform	WT and L359V	0.62	0.67	0.68	0.76	1.10E-02	1.74E-02	1.72E-01	3.56E-01
7981161	NM_152592	C14orf49	chromosome 14 open reading frame 49	WT and L359V	0.56	0.67	0.71	0.74	8.78E-04	4.42E-03	8.10E-02	1.32E-01
8103485	NM_138386	NAF1	nuclear assembly factor 1 homolog (S. cerevisiae)	WT and L359V	0.71	0.67	0.83	0.80	2.39E-02	7.09E-03	6.71E-01	3.99E-01
8077914	NM_025265	TSEN2	tRNA splicing endonuclease 2 homolog (S. cerevisiae)	WT and L359V	0.69	0.67	0.84	0.87	9.21E-03	3.91E-03	6.10E-01	8.17E-01
8148955	NM_023080	C8orf33	chromosome 8 open reading frame 33	WT and L359V	0.67	0.67	0.83	0.82	7.35E-03	4.50E-03	6.07E-01	4.41E-01
8026533	NM_032855	HSH2D	hematopoietic SH2 domain containing	WT and L359V	0.67	0.66	0.94	0.89	9.21E-03	5.91E-03	9.21E-01	1.00E+00
7950067	NM_001360	DHCR7	7-dehydrocholesterol reductase	WT and L359V	0.72	0.66	0.97	0.81	2.58E-02	6.70E-03	9.65E-01	4.56E-01
8041149	NM_015131	WDR43	WD repeat domain 43	WT and L359V	0.71	0.66	0.89	0.87	7.35E-03	1.94E-03	7.97E-01	6.43E-01
8154012	NM_153186	KANK1	KN motif and ankyrin repeat domains 1	WT and L359V	0.63	0.66	0.81	0.78	1.93E-02	2.64E-02	7.58E-01	6.18E-01
7999304	NM_201400	FAM86A	family with sequence similarity 86, member A	WT and L359V	0.72	0.66	0.88	0.83	3.07E-02	8.33E-03	8.36E-01	6.73E-01
7995926	NM_032206	NLRC5	NLR family, CARD domain containing 5	WT and L359V	0.71	0.66	0.82	0.80	1.72E-02	5.14E-03	5.61E-01	3.63E-01
8067040	NM_012340	NFATC2	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2	WT and L359V	0.63	0.66	0.81	0.77	6.12E-03	7.29E-03	5.66E-01	2.83E-01
8093950	NM_005980	S100P	S100 calcium binding protein P	WT and L359V	0.49	0.66	0.95	0.84	1.82E-03	2.03E-02	9.43E-01	8.90E-01
8028563	NM_021107	MRPS12	mitochondrial ribosomal protein S12	WT and L359V	0.68	0.66	0.89	0.78	9.03E-03	4.42E-03	8.25E-01	2.70E-01
8171876	NM_023033	METTL1	methyltransferase like 1	WT and L359V	0.61	0.66	0.85	0.79	4.18E-03	6.59E-03	7.50E-01	3.67E-01
7930008	NM_004741	NOLC1	nucleolar and coiled-body phosphoprotein 1	WT and L359V	0.76	0.66	0.92	0.87	2.86E-02	2.60E-03	8.66E-01	6.91E-01
8080487	NM_006254	PRKCD	protein kinase C, delta	WT and L359V	0.72	0.66	0.80	0.80	4.09E-02	9.62E-03	6.26E-01	5.23E-01
7996934	NM_016101	NIP7	nuclear import 7 homolog (S. cerevisiae)	WT and L359V	0.70	0.66	0.89	0.82	3.07E-02	1.16E-02	8.51E-01	6.46E-01
7917752	---			WT and L359V	0.70	0.66	0.99	0.80	1.17E-02	3.83E-03	9.93E-01	3.17E-01
8030721	NM_002975	CLEC11A	C-type lectin domain family 11, member A	WT and L359V	0.65	0.66	0.88	0.77	1.82E-02	1.58E-02	8.41E-01	4.69E-01
8176026	NM_001456	FLNA	filamin A, alpha (actin binding protein 280)	WT and L359V	0.73	0.66	0.90	0.80	2.42E-02	3.98E-03	8.36E-01	3.31E-01
7996341	NM_020786	PDP2	pyruvate dehydrogenase phosphatase isoenzyme 2	WT and L359V	0.75	0.66	0.90	0.83	3.77E-02	4.39E-03	8.38E-01	5.69E-01
7935903	NM_006993	NPM3	nucleophosmin	WT and L359V	0.70	0.66	0.92	0.83	4.57E-02	1.47E-02	9.01E-01	7.99E-01

7998637	NM_016332	SEPX1	selenoprotein X, 1	WT and L359V	0.69	0.65	0.77	0.76	9.04E-03	3.30E-03	2.50E-01	1.66E-01
8082816	NM_021203	SRPRB	signal recognition particle receptor, B subunit	WT and L359V	0.68	0.65	0.83	0.85	4.32E-02	1.97E-02	8.06E-01	9.56E-01
8145782	NM_032509	MAK16	MAK16 homolog (S. cerevisiae)	WT and L359V	0.77	0.65	0.90	0.87	2.62E-02	1.71E-03	8.13E-01	7.02E-01
8112176	NR_023344	RNU6ATAC	RNA, U6atac small nuclear (U12-dependent splicing)	WT and L359V	0.64	0.65	0.86	0.78	5.06E-03	4.33E-03	7.65E-01	3.05E-01
8082066	NM_014367	FAM162A	family with sequence similarity 162, member A	WT and L359V	0.67	0.65	0.83	0.86	5.06E-03	2.49E-03	5.24E-01	6.27E-01
7990757	NM_004390	CTSH	cathepsin H	WT and L359V	0.64	0.65	0.73	0.80	3.91E-03	3.00E-03	1.15E-01	3.12E-01
7900911	NM_001384	DPH2	DPH2 homolog (S. cerevisiae)	WT and L359V	0.62	0.65	0.81	0.75	1.11E-03	1.27E-03	3.22E-01	7.78E-02
8160682	NM_022917	NOL6	nucleolar protein family 6 (RNA-associated)	WT and L359V	0.65	0.65	0.84	0.75	1.59E-03	1.08E-03	4.84E-01	6.58E-02
7898549	NM_016183	MRTO4	mRNA turnover 4 homolog (S. cerevisiae)	WT and L359V	0.65	0.65	0.86	0.81	2.64E-03	1.67E-03	7.09E-01	2.74E-01
8173232	NM_152424	FAM123B	family with sequence similarity 123B	WT and L359V	0.72	0.65	0.91	0.82	1.92E-02	3.65E-03	8.68E-01	4.56E-01
7943690	NM_004398	DDX10	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	WT and L359V	0.72	0.64	0.87	0.85	9.91E-03	1.49E-03	7.50E-01	5.04E-01
8041961	NM_001008708	CHAC2	ChaC, cation transport regulator homolog 2 (E. coli)	WT and L359V	0.72	0.64	0.86	0.82	2.41E-02	4.12E-03	7.94E-01	5.28E-01
7949971	NM_001876	CPT1A	carnitine palmitoyltransferase 1A (liver)	WT and L359V	0.76	0.64	0.93	0.87	3.77E-02	2.76E-03	8.81E-01	8.38E-01
7929243	AF401219	NHP2	NHP2 ribonucleoprotein homolog (yeast)	WT and L359V	0.75	0.64	0.89	0.82	1.32E-02	9.58E-04	7.85E-01	2.61E-01
8040655	NM_033505	SELI	selenoprotein I	WT and L359V	0.76	0.64	0.90	0.88	2.67E-02	1.86E-03	8.25E-01	8.17E-01
7900365	NM_001136493	MFSD2	major facilitator superfamily domain containing 2	WT and L359V	0.73	0.64	0.82	0.80	2.02E-02	2.28E-03	5.05E-01	3.17E-01
7914112	NM_005248	FGR	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	WT and L359V	0.59	0.64	0.79	0.74	4.76E-03	7.29E-03	5.76E-01	2.58E-01
8052399	NM_022893	BCL11A	B-cell CLL	WT and L359V	0.68	0.64	0.92	0.87	1.48E-02	5.10E-03	8.82E-01	9.45E-01
7909188	NM_014002	IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon	WT and L359V	0.61	0.64	0.79	0.75	7.00E-03	7.40E-03	5.69E-01	3.05E-01
8003875	NM_001124758	SPNS2	spinster homolog 2 (Drosophila)	WT and L359V	0.59	0.63	0.81	0.76	2.23E-03	3.57E-03	5.66E-01	2.54E-01
8088830	NM_018130	SHQ1	SHQ1 homolog (S. cerevisiae)	WT and L359V	0.72	0.63	0.84	0.82	1.93E-02	2.38E-03	6.44E-01	4.61E-01
8058373	NM_018256	WDR12	WD repeat domain 12	WT and L359V	0.72	0.63	0.92	0.86	4.61E-02	7.53E-03	9.01E-01	9.63E-01
7928589	NM_005729	PPIF	peptidylprolyl isomerase F	WT and L359V	0.70	0.63	0.85	0.80	1.37E-02	2.42E-03	7.19E-01	3.40E-01
8105663	NM_020726	NLN	neurolysin (metallopeptidase M3 family)	WT and L359V	0.73	0.63	0.92	0.86	1.37E-02	1.12E-03	8.46E-01	6.13E-01
8011293	NM_015229	KIAA0664	KIAA0664	WT and L359V	0.69	0.63	0.89	0.79	4.62E-03	8.46E-04	8.01E-01	1.49E-01
8060940	NM_012261	C20orf103	chromosome 20 open reading frame 103	WT and L359V	0.59	0.63	0.81	0.81	1.25E-03	1.89E-03	4.37E-01	3.47E-01
8069085	NM_003307	TRPM2	transient receptor potential cation channel, subfamily M, member 2	WT and L359V	0.61	0.63	0.90	0.79	4.08E-03	3.61E-03	8.41E-01	3.50E-01
7973067	NM_000270	NP	nucleoside phosphorylase	WT and L359V	0.66	0.63	0.80	0.79	5.75E-03	2.31E-03	4.37E-01	3.05E-01
8156321	NM_003177	SYK	spleen tyrosine kinase	WT and L359V	0.68	0.63	0.79	0.80	4.82E-03	1.23E-03	2.85E-01	2.71E-01
8106193	NM_032175	UTP15	UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. cerevisiae)	WT and L359V	0.75	0.63	0.84	0.84	4.99E-02	3.62E-03	7.38E-01	6.56E-01
7897877	NM_001066	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B	WT and L359V	0.55	0.63	0.79	0.75	1.08E-03	2.61E-03	3.90E-01	1.67E-01
8066939	NM_004776	B4GALT5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	WT and L359V	0.71	0.63	0.77	0.78	1.48E-02	2.38E-03	3.02E-01	2.63E-01
8136918	NM_003461	ZYX	zyxin	WT and L359V	0.65	0.63	0.75	0.74	4.85E-03	2.04E-03	1.72E-01	1.26E-01
7947861	NM_001080547	SPI1	spleen focus forming virus (SFFV) proviral integration oncogene spi1	WT and L359V	0.64	0.63	0.89	0.76	5.50E-03	2.76E-03	8.36E-01	2.29E-01
8022118	NM_012307	EPB41L3	erythrocyte membrane protein band 4.1-like 3	WT and L359V	0.62	0.63	0.70	0.78	4.98E-03	3.68E-03	1.17E-01	3.37E-01
7950731	NM_199418	PRCP	prolylcarboxypeptidase (angiotensinase C)	WT and L359V	0.73	0.63	0.85	0.86	2.40E-02	2.09E-03	7.38E-01	7.44E-01
8043621	NM_212481	ARID5A	AT rich interactive domain 5A (MRF1-like)	WT and L359V	0.71	0.63	0.82	0.79	2.26E-02	3.40E-03	6.52E-01	3.70E-01
7975787	NM_001135049	JDP2	Jun dimerization protein 2	WT and L359V	0.73	0.62	0.95	0.86	4.30E-02	4.79E-03	9.31E-01	9.32E-01
7937039	NM_001005463	EBF3	early B-cell factor 3	WT and L359V	0.54	0.62	0.84	0.78	2.57E-03	7.53E-03	7.97E-01	4.46E-01
8143575	NM_005232	EPHA1	EPH receptor A1	WT and L359V	0.55	0.62	0.66	0.72	2.64E-03	5.65E-03	9.60E-02	1.89E-01
8097647	NM_002940	ABCE1	ATP-binding cassette, sub-family E (OABP), member 1	WT and L359V	0.76	0.62	0.87	0.86	2.50E-02	1.06E-03	7.50E-01	6.27E-01
7962689	NM_001017535	VDR	vitamin D (1,25- dihydroxyvitamin D3) receptor	WT and L359V	0.59	0.62	0.65	0.71	1.91E-02	2.33E-02	2.51E-01	3.85E-01
8011640	NM_014520	MYBBP1A	MYB binding protein (P160) 1a	WT and L359V	0.66	0.62	0.86	0.79	3.09E-03	1.03E-03	7.13E-01	2.24E-01
7944667	NM_003105	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	WT and L359V	0.63	0.62	0.78	0.78	4.00E-03	2.10E-03	3.69E-01	2.78E-01
7953321	NM_002342	LTBR	lymphotoxin beta receptor (TNFR superfamily, member 3)	WT and L359V	0.66	0.62	0.79	0.81	7.41E-03	2.49E-03	4.22E-01	4.23E-01
7951485	NM_017515	SLC35F2	solute carrier family 35, member F2	WT and L359V	0.77	0.62	1.04	0.88	3.70E-02	1.03E-03	9.44E-01	8.35E-01
8126839	NM_014452	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	WT and L359V	0.71	0.62	0.89	0.78	2.89E-02	3.86E-03	8.41E-01	3.70E-01
8068231	NM_005806	OLIG2	oligodendrocyte lineage transcription factor 2	WT and L359V	0.72	0.62	1.01	0.83	2.78E-02	2.82E-03	9.90E-01	6.27E-01
8087790	NM_004704	RRP9	ribosomal RNA processing 9, small subunit (SSU) processome component, homolog	WT and L359V	0.64	0.61	0.82	0.77	1.03E-02	4.26E-03	6.79E-01	3.56E-01
8064014	NM_022082	C20orf59	chromosome 20 open reading frame 59	WT and L359V	0.62	0.61	0.90	0.77	3.09E-03	1.89E-03	8.36E-01	2.15E-01
7949104	NM_001098671	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	WT and L359V	0.71	0.61	0.91	0.81	1.39E-02	1.51E-03	8.41E-01	3.47E-01
8157843	NM_005833	RABEPK	Rab9 effector protein with kelch motifs	WT and L359V	0.67	0.61	0.81	0.78	2.29E-02	5.34E-03	6.89E-01	4.71E-01
8063923	NM_016354	SLCO4A1	solute carrier organic anion transporter family, member 4A1	WT and L359V	0.51	0.61	0.72	0.72	3.09E-04	1.21E-03	9.54E-02	7.24E-02
8099107	NM_017816	LYAR	Ly1 antibody reactive homolog (mouse)	WT and L359V	0.68	0.61	0.85	0.83	1.22E-02	2.19E-03	7.44E-01	5.78E-01
8115907	NM_016391	NOP16	NOP16 nucleolar protein homolog (yeast)	WT and L359V	0.69	0.61	0.86	0.81	1.56E-02	2.75E-03	7.99E-01	4.75E-01
7927936	NM_004728	DDX21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	WT and L359V	0.74	0.61	0.96	0.87	1.33E-02	6.95E-04	9.22E-01	6.27E-01
7935146	NM_022451	NOC3L	nucleolar complex associated 3 homolog (S. cerevisiae)	WT and L359V	0.73	0.61	0.88	0.84	1.20E-02	6.95E-04	7.46E-01	4.56E-01
7899096	NM_015871	ZNF593	zinc finger protein 593	WT and L359V	0.66	0.61	0.84	0.78	5.89E-03	1.41E-03	6.28E-01	2.35E-01
8005097	NM_006041	HS3ST3B1	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	WT and L359V	0.64	0.61	0.82	0.83	2.02E-02	7.93E-03	7.90E-01	8.42E-01
8052331	NM_033109	PNPT1	polyribonucleotide nucleotidyltransferase 1	WT and L359V	0.76	0.61	0.87	0.84	1.52E-02	3.96E-04	6.28E-01	3.40E-01
8066038	NM_032214	SLA2	Src-like-adaptor 2	WT and L359V	0.54	0.61	0.67	0.68	3.25E-03	6.44E-03	1.55E-01	1.49E-01
8056113	NM_002349	LY75	lymphocyte antigen 75	WT and L359V	0.67	0.61	0.78	0.78	2.06E-02	4.79E-03	5.15E-01	4.46E-01
8099797	NM_001085399	RELL1	RELT-like 1	WT and L359V	0.69	0.61	0.86	0.84	5.15E-03	6.63E-04	6.65E-01	4.04E-01
8071036	NM_006272	S100B	S100 calcium binding protein B	WT and L359V	0.55	0.61	0.73	0.71	5.66E-04	1.08E-03	9.60E-02	5.73E-02
7944769	NM_020716	GRAMD1B	GRAM domain containing 1B	WT and L359V	0.57	0.61	0.84	0.79	2.78E-02	3.14E-02	8.56E-01	8.85E-01

8113039	NM_002397	MEF2C	myocyte enhancer factor 2C	WT and L359V	0.61	0.60	0.74	0.74	3.56E-02	2.30E-02	6.73E-01	6.13E-01
8068422	NM_005128	DOPEY2	dopey family member 2	WT and L359V	0.76	0.60	0.81	0.82	3.27E-02	8.70E-04	4.13E-01	3.63E-01
7935425	NM_015179	RRP12	ribosomal RNA processing 12 homolog (S. cerevisiae)	WT and L359V	0.59	0.60	0.82	0.76	5.66E-04	4.72E-04	3.95E-01	9.04E-02
8159127	NM_002957	RXRA	retinoid X receptor, alpha	WT and L359V	0.68	0.59	0.84	0.73	3.50E-03	4.56E-04	4.84E-01	5.73E-02
8081241	BC006512	C3orf26	chromosome 3 open reading frame 26	WT and L359V	0.66	0.59	0.89	0.82	4.62E-03	8.34E-04	8.13E-01	3.50E-01
8020702	NM_005640	TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105k	WT and L359V	0.71	0.59	1.04	0.89	3.23E-02	2.95E-03	9.52E-01	1.00E+00
7953100	NM_002014	FKBP4	FK506 binding protein 4, 59kDa	WT and L359V	0.64	0.59	0.86	0.77	2.58E-03	6.80E-04	6.79E-01	1.49E-01
7963614	NM_000889	ITGB7	integrin, beta 7	WT and L359V	0.49	0.59	0.63	0.63	1.21E-03	3.97E-03	7.35E-02	5.73E-02
8115410	NM_015465	GEMIN5	gem (nuclear organelle) associated protein 5	WT and L359V	0.63	0.59	0.81	0.78	2.08E-03	6.95E-04	4.23E-01	1.94E-01
8033587	NM_032152	PRAM1	PML-RARA regulated adaptor molecule 1	WT and L359V	0.45	0.59	0.60	0.67	1.25E-03	7.53E-03	8.10E-02	1.68E-01
7986214	NM_013272	SLCO3A1	solute carrier organic anion transporter family, member 3A1	WT and L359V	0.63	0.59	0.75	0.74	1.30E-03	3.96E-04	9.07E-02	6.10E-02
8136662	NM_004668	MGAM	maltase-glucoamylase (alpha-glucosidase)	WT and L359V	0.61	0.59	0.69	0.69	2.50E-02	1.34E-02	4.12E-01	3.05E-01
8018352	NM_001126121	SLC25A19	solute carrier family 25 (mitochondrial thiamine pyrophosphate carrier), member 19	WT and L359V	0.63	0.59	0.83	0.77	5.38E-03	1.57E-03	6.83E-01	2.78E-01
8099246	NM_025196	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	WT and L359V	0.72	0.58	0.86	0.83	2.41E-02	1.20E-03	7.79E-01	5.95E-01
8158568	NM_006676	USP20	ubiquitin specific peptidase 20	WT and L359V	0.65	0.58	0.88	0.77	4.76E-03	8.51E-04	8.01E-01	1.94E-01
7972557	NM_004951	GPR183	G protein-coupled receptor 183	WT and L359V	0.50	0.58	0.58	0.66	3.06E-03	6.97E-03	6.69E-02	1.74E-01
8066431	NM_000022	ADA	adenosine deaminase	WT and L359V	0.60	0.57	0.81	0.83	1.22E-02	5.21E-03	7.51E-01	8.84E-01
8146685	NM_015169	RRS1	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	WT and L359V	0.64	0.57	0.77	0.79	2.04E-02	4.78E-03	6.04E-01	6.19E-01
8003298	NM_003486	SLC7A5	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	WT and L359V	0.62	0.57	0.97	0.82	5.05E-03	1.33E-03	9.69E-01	5.52E-01
7911178	NM_004895	NLRP3	NLR family, pyrin domain containing 3	WT and L359V	0.66	0.57	0.89	0.78	1.96E-02	2.67E-03	8.59E-01	4.46E-01
7940762	NM_033101	LGALS12	lectin, galactoside-binding, soluble, 12	WT and L359V	0.66	0.57	0.82	0.74	2.88E-02	4.05E-03	7.92E-01	3.31E-01
8132347	NM_181791	GPR141	G protein-coupled receptor 141	WT and L359V	0.70	0.57	0.74	0.75	4.58E-02	3.65E-03	4.36E-01	3.70E-01
8142061	NM_019042	PUS7	pseudouridylate synthase 7 homolog (S. cerevisiae)	WT and L359V	0.68	0.56	0.82	0.80	1.19E-02	8.96E-04	6.12E-01	4.03E-01
7915485	NM_006824	EBNA1BP2	EBNA1 binding protein 2	WT and L359V	0.65	0.56	0.80	0.80	3.13E-02	5.62E-03	7.46E-01	7.13E-01
8163149	NM_002829	PTPN3	protein tyrosine phosphatase, non-receptor type 3	WT and L359V	0.48	0.56	0.66	0.71	1.31E-03	3.54E-03	1.45E-01	2.25E-01
7996064	NM_153837	GPR114	G protein-coupled receptor 114	WT and L359V	0.69	0.56	0.81	0.72	1.25E-02	7.94E-04	4.84E-01	9.67E-02
8138487	XR_018343	LOC340274	argininosuccinate synthase-like	WT and L359V	0.56	0.56	0.76	0.90	2.78E-02	1.93E-02	7.74E-01	1.00E+00
8083839	NM_014373	GPR160	G protein-coupled receptor 160	WT and L359V	0.69	0.56	0.87	0.85	3.09E-02	2.42E-03	8.34E-01	8.84E-01
7929901	NM_021830	C10orf2	chromosome 10 open reading frame 2	WT and L359V	0.71	0.56	0.77	0.80	1.54E-02	6.55E-04	2.80E-01	3.24E-01
7975976	NM_012111	AHSA1	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)	WT and L359V	0.73	0.56	0.81	0.75	2.74E-02	8.47E-04	5.47E-01	1.94E-01
8085206	NM_003656	CAMK1	calcium	WT and L359V	0.71	0.56	0.87	0.79	1.38E-02	5.35E-04	7.79E-01	2.74E-01
8165398	NM_004479	FUT7	fucosyltransferase 7 (alpha (1,3) fucosyltransferase)	WT and L359V	0.60	0.56	0.71	0.73	2.88E-03	9.59E-04	1.23E-01	1.52E-01
8061416	NM_003650	CST7	cystatin F (leukocystatin)	WT and L359V	0.44	0.55	0.92	0.76	1.37E-02	4.31E-02	9.52E-01	9.72E-01
8082058	NM_005213	CSTA	cystatin A (stefin A)	WT and L359V	0.65	0.55	0.71	0.74	1.55E-02	2.38E-03	2.50E-01	3.05E-01
8013068	NM_178836	PLD6	phospholipase D family, member 6	WT and L359V	0.57	0.55	0.79	0.76	1.49E-03	7.77E-04	4.14E-01	2.15E-01
7985099	NM_003978	PSTPIP1	proline-serine-threonine phosphatase interacting protein 1	WT and L359V	0.51	0.55	0.68	0.72	9.37E-04	1.20E-03	9.97E-02	1.49E-01
8148304	NM_025195	TRIB1	tribbles homolog 1 (Drosophila)	WT and L359V	0.58	0.55	0.79	0.75	2.36E-03	8.80E-04	4.49E-01	2.18E-01
7966749	NM_017899	TESC	tescalcin	WT and L359V	0.52	0.55	0.70	0.69	1.59E-03	1.57E-03	1.88E-01	1.26E-01
7954864	AK093065	MUC19	mucin 19, oligomeric	WT and L359V	0.56	0.55	0.73	0.75	1.83E-03	1.03E-03	2.10E-01	2.24E-01
8172425	NM_033518	SLC38A5	solute carrier family 38, member 5	WT and L359V	0.59	0.54	0.85	0.76	1.69E-03	5.01E-04	7.26E-01	1.86E-01
8024048	NM_002777	PRTN3	proteinase 3	WT and L359V	0.58	0.54	0.80	0.74	3.09E-03	1.11E-03	5.47E-01	2.25E-01
8064978	NM_000214	JAG1	jagged 1 (Alagille syndrome)	WT and L359V	0.66	0.54	0.81	0.83	1.90E-03	1.74E-04	2.93E-01	3.10E-01
8027556	NM_002333	LRP3	low density lipoprotein receptor-related protein 3	WT and L359V	0.52	0.54	0.78	0.70	4.43E-04	4.04E-04	2.98E-01	5.73E-02
8032623	NM_001060	TBXA2R	thromboxane A2 receptor	WT and L359V	0.49	0.54	0.68	0.72	1.90E-03	2.76E-03	2.00E-01	2.81E-01
8148317	NM_002467	MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	WT and L359V	0.60	0.54	0.95	0.80	4.98E-03	1.20E-03	9.34E-01	5.28E-01
7899394	NM_001105556	C1orf38	chromosome 1 open reading frame 38	WT and L359V	0.67	0.54	0.85	0.77	1.03E-02	6.95E-04	7.50E-01	2.63E-01
7952335	NR_003125	LOC85391	RNA, small nucleolar	WT and L359V	0.51	0.54	0.89	0.73	2.10E-03	2.10E-03	8.59E-01	2.81E-01
8130539	NM_054114	TAGAP	T-cell activation RhoGTPase activating protein	WT and L359V	0.60	0.53	0.83	0.76	6.10E-03	1.21E-03	7.42E-01	3.31E-01
8073890	NM_015124	GRAMD4	GRAM domain containing 4	WT and L359V	0.64	0.53	0.85	0.80	1.09E-02	1.03E-03	8.01E-01	5.10E-01
8021653	NM_002640	SERPINB8	serpin peptidase inhibitor, clade B (ovalbumin), member 8	WT and L359V	0.60	0.52	0.92	0.74	6.62E-03	1.20E-03	8.88E-01	2.70E-01
7905028	ENST00000271699	LOC645166	similar to lymphocyte-specific protein 1	WT and L359V	0.68	0.52	0.81	0.74	1.92E-02	8.25E-04	6.12E-01	2.14E-01
8129848	NM_052962	IL22RA2	interleukin 22 receptor, alpha 2	WT and L359V	0.57	0.52	0.67	0.67	7.18E-03	2.38E-03	2.00E-01	1.66E-01
8000184	NM_005849	IGSF6	immunoglobulin superfamily, member 6	WT and L359V	0.52	0.52	0.60	0.63	5.21E-03	3.32E-03	9.60E-02	1.25E-01
7956856	NM_001031679	MSRB3	methionine sulfoxide reductase B3	WT and L359V	0.60	0.52	0.80	0.77	1.10E-02	1.89E-03	7.28E-01	4.78E-01
7960518	NM_001065	TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A	WT and L359V	0.50	0.51	0.73	0.70	3.06E-03	2.44E-03	4.60E-01	2.78E-01
8063497	NM_020356	CASS4	Cas scaffolding protein family member 4	WT and L359V	0.50	0.51	0.53	0.61	2.78E-02	2.59E-02	2.40E-01	3.97E-01
7940349	NM_024098	CCDC86	coiled-coil domain containing 86	WT and L359V	0.73	0.51	0.95	0.79	7.93E-03	8.06E-05	9.08E-01	1.49E-01
8024038	NM_001700	AZU1	azurocidin 1	WT and L359V	0.60	0.51	0.81	0.73	2.39E-03	3.55E-04	4.96E-01	1.25E-01
8062444	NM_001725	BPI	bactericidal	WT and L359V	0.56	0.51	0.75	0.74	1.25E-02	3.90E-03	6.39E-01	5.14E-01
7906386	NM_152501	PYHIN1	pyrin and HIN domain family, member 1	WT and L359V	0.57	0.51	0.82	0.73	3.38E-02	9.72E-03	8.40E-01	6.73E-01
8041061	NM_153021	PLB1	phospholipase B1	WT and L359V	0.57	0.51	0.78	0.71	4.10E-03	8.80E-04	5.29E-01	1.73E-01
7904364	NM_006784	WDR3	WD repeat domain 3	WT and L359V	0.63	0.51	0.83	0.78	2.14E-02	2.10E-03	8.14E-01	5.88E-01
7927186	NM_032023	RASSF4	Ras association (RalGDS	WT and L359V	0.45	0.51	0.66	0.69	4.00E-04	6.32E-04	8.10E-02	9.67E-02
8127854	NM_002395	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	WT and L359V	0.56	0.50	0.83	0.73	9.37E-04	2.73E-04	6.00E-01	1.22E-01
8127549	NM_012434	SLC17A5	solute carrier family 17 (anion	WT and L359V	0.59	0.50	0.72	0.65	7.66E-03	1.18E-03	3.14E-01	9.04E-02

8102950	NM_003866	INPP4B	inositol polyphosphate-4-phosphatase, type II, 105kDa	WT and L359V	0.68	0.50	0.69	0.74	1.14E-02	3.55E-04	8.10E-02	1.73E-01
8133442	NM_032464	LAT2	linker for activation of T cells family, member 2	WT and L359V	0.54	0.49	0.76	0.79	9.31E-04	2.76E-04	2.79E-01	3.05E-01
7998927	---			WT and L359V	0.46	0.48	0.71	0.56	2.40E-02	2.47E-02	8.01E-01	3.05E-01
8158671	NM_000050	ASS1	argininosuccinate synthetase 1	WT and L359V	0.46	0.48	0.78	0.81	1.02E-02	9.41E-03	8.23E-01	1.00E+00
8113800	NM_001999	FBN2	fibrillin 2	WT and L359V	0.67	0.48	0.85	0.78	7.96E-03	1.89E-04	7.41E-01	2.70E-01
8100541	NM_001553	IGFBP7	insulin-like growth factor binding protein 7	WT and L359V	0.64	0.47	0.74	0.75	1.24E-02	4.56E-04	3.30E-01	3.05E-01
8131927	NM_016447	MPP6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)	WT and L359V	0.68	0.47	0.84	0.81	2.06E-02	3.91E-04	7.74E-01	5.83E-01
7991335	NM_001150	ANPEP	alanyl (membrane) aminopeptidase	WT and L359V	0.57	0.47	0.79	0.69	1.25E-03	1.85E-04	4.14E-01	5.73E-02
8126303	NM_018643	TREM1	triggering receptor expressed on myeloid cells 1	WT and L359V	0.57	0.46	0.82	0.66	3.12E-02	4.57E-03	8.38E-01	3.63E-01
8041422	NM_170672	RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	WT and L359V	0.50	0.46	0.73	0.65	1.30E-03	4.51E-04	3.19E-01	7.78E-02
7952274	NM_002855	PVRL1	poliovirus receptor-related 1 (herpesvirus entry mediator C)	WT and L359V	0.61	0.46	0.91	0.72	4.58E-03	2.73E-04	8.77E-01	1.57E-01
8171896	BC020611	CXorf21	chromosome X open reading frame 21	WT and L359V	0.56	0.46	0.75	0.75	1.79E-02	2.76E-03	7.15E-01	6.53E-01
7921677	NM_016382	CD244	CD244 molecule, natural killer cell receptor 2B4	WT and L359V	0.50	0.45	0.67	0.68	8.36E-04	2.75E-04	8.10E-02	8.32E-02
8080781	NM_017771	PXK	PX domain containing serine	WT and L359V	0.50	0.45	0.85	0.74	7.03E-04	2.54E-04	7.97E-01	2.15E-01
8038861	NM_001245	SIGLEC6	sialic acid binding Ig-like lectin 6	WT and L359V	0.47	0.45	0.66	0.55	1.45E-02	7.42E-03	5.66E-01	1.69E-01
8142452	NM_012252	TFEC	transcription factor EC	WT and L359V	0.63	0.45	0.78	0.73	1.03E-02	3.73E-04	5.21E-01	2.24E-01
7965565	NM_032147	USP44	ubiquitin specific peptidase 44	WT and L359V	0.56	0.42	0.92	0.77	2.12E-03	1.85E-04	8.87E-01	3.37E-01
8094240	NM_001775	CD38	CD38 molecule	WT and L359V	0.62	0.42	0.96	0.79	1.32E-02	3.66E-04	9.59E-01	6.15E-01
8076894	NM_015166	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	WT and L359V	0.50	0.42	0.80	0.69	5.75E-03	1.12E-03	8.01E-01	3.40E-01
7973108	ENST00000258817	LOC643332	similar to Nonsecretory ribonuclease precursor (Ribonuclease US) (Eosinophil-deriv	WT and L359V	0.47	0.41	0.93	0.66	4.37E-03	1.20E-03	9.38E-01	2.74E-01
8025103	NM_001974	EMR1	egf-like module containing, mucin-like, hormone receptor-like 1	WT and L359V	0.51	0.41	0.68	0.65	3.42E-03	4.51E-04	2.44E-01	1.26E-01
8121277	NM_001624	AIM1	absent in melanoma 1	WT and L359V	0.59	0.41	0.75	0.71	2.36E-02	1.07E-03	6.76E-01	4.40E-01
7903980	BC017973	C1orf162	chromosome 1 open reading frame 162	WT and L359V	0.68	0.39	0.72	0.69	7.56E-03	4.20E-05	9.72E-02	5.50E-02
8080964	BC127733	GLT8D4	glycosyltransferase 8 domain containing 4	WT and L359V	0.55	0.39	0.84	0.70	2.19E-03	1.04E-04	7.79E-01	1.25E-01
8107909	NM_003059	SLC22A4	solute carrier family 22 (organic cation	WT and L359V	0.40	0.38	0.54	0.56	2.38E-03	1.25E-03	1.06E-01	1.24E-01
8140468	NM_017439	PION	pigeon homolog (Drosophila)	WT and L359V	0.37	0.36	0.49	0.56	5.68E-03	3.37E-03	1.52E-01	2.63E-01
7904303	NM_004258	IGSF2	immunoglobulin superfamily, member 2	WT and L359V	0.45	0.36	0.64	0.60	1.22E-02	2.57E-03	5.30E-01	3.05E-01
8001007	NM_002773	PRSS8	protease, serine, 8	WT and L359V	0.43	0.36	0.66	0.61	4.46E-02	1.33E-02	8.01E-01	6.93E-01
8036004	NM_004364	CEBPA	CCAAT	WT and L359V	0.54	0.36	0.82	0.64	5.06E-03	1.96E-04	7.97E-01	1.17E-01
8031293	NM_014511	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	WT and L359V	0.39	0.35	0.58	0.52	1.31E-02	4.91E-03	5.02E-01	2.70E-01
8143471	NM_013252	CLEC5A	C-type lectin domain family 5, member A	WT and L359V	0.34	0.32	0.53	0.53	1.37E-02	7.30E-03	4.95E-01	4.02E-01
7968637	NM_003914	CCNA1	cyclin A1	WT and L359V	0.43	0.32	0.56	0.52	3.46E-03	3.96E-04	1.21E-01	6.59E-02
7978351	NM_001911	CTSG	cathepsin G	WT and L359V	0.45	0.29	0.71	0.66	3.73E-03	2.64E-04	5.47E-01	3.05E-01
8112428	NM_005582	CD180	CD180 molecule	WT and L359V	0.32	0.29	0.43	0.54	2.08E-03	8.42E-04	6.16E-02	1.74E-01
8016932	NM_000250	MPO	myeloperoxidase	WT and L359V	0.52	0.28	0.85	0.67	4.20E-03	6.68E-05	8.25E-01	1.73E-01
7934898	NM_144590	ANKRD22	ankyrin repeat domain 22	WT and L359V	0.43	0.19	0.66	0.55	1.38E-02	2.63E-04	6.69E-01	2.61E-01
8081537	NM_016388	TRAT1	T cell receptor associated transmembrane adaptor 1	WT and T354M	8.54	1.41	5.44	2.52	6.34E-05	2.72E-01	1.85E-03	5.50E-02
7902808	ENST00000370548	HS2ST1	heparan sulfate 2-O-sulfotransferase 1	WT and T354M	3.73	1.28	2.38	1.57	4.11E-04	3.32E-01	2.36E-02	3.05E-01
8163000	---			WT and T354M	3.89	1.19	2.82	1.72	9.46E-04	6.08E-01	2.36E-02	3.05E-01
8005814	NM_016231	NLK	nemo-like kinase	WT and T354M	1.85	1.16	1.39	1.20	2.79E-04	1.69E-01	4.79E-02	3.67E-01
8167360	NM_002049	GATA1	GATA binding protein 1 (globin transcription factor 1)	WT and T354M	3.30	1.11	1.77	1.48	3.30E-05	5.19E-01	1.25E-02	7.01E-02
7948455	NM_152852	MS4A6A	membrane-spanning 4-domains, subfamily A, member 6A	WT and T354M	1.83	0.95	2.04	1.33	4.47E-03	8.27E-01	1.24E-02	4.04E-01
7922689	NM_002065	GLUL	glutamate-ammonia ligase (glutamine synthetase)	WT and T354M	1.58	0.94	1.45	1.20	1.32E-03	5.78E-01	2.36E-02	3.40E-01
7994826	NM_002209	ITGAL	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1;	WT and T354M	1.67	0.86	1.44	1.17	8.36E-04	1.53E-01	3.17E-02	5.05E-01
7976080	NM_003608	GPR65	G protein-coupled receptor 65	WT and T354M	2.59	0.85	2.15	1.41	4.79E-04	4.17E-01	1.24E-02	3.05E-01
8107044	NM_022350	ERAP2	endoplasmic reticulum aminopeptidase 2	WT and T354M	0.63	0.79	0.57	0.77	5.75E-03	8.44E-02	1.25E-02	2.83E-01
7988050	NM_201631	TGM5	transglutaminase 5	WT and T354M	0.46	0.72	0.54	0.69	1.99E-03	8.86E-02	4.10E-02	2.70E-01
7908409	NM_002923	RGS2	regulator of G-protein signaling 2, 24kDa	WT only	2.52	2.23	1.36	1.42	4.23E-02	5.68E-02	8.64E-01	1.00E+00
7954293	NM_000921	PDE3A	phosphodiesterase 3A, cGMP-inhibited	WT only	2.13	1.75	1.01	1.26	4.98E-02	1.15E-01	9.97E-01	1.00E+00
8029907	NM_001736	C5AR1	complement component 5a receptor 1	WT only	2.19	1.68	1.94	1.69	1.74E-02	7.63E-02	2.01E-01	3.31E-01
7933237	NM_174890	ANUBL1	AN1, ubiquitin-like, homolog (Xenopus laevis)	WT only	2.68	1.58	1.93	1.55	5.49E-03	1.14E-01	2.08E-01	5.00E-01
8069582	NM_002772	PRSS7	protease, serine, 7 (enterokinase)	WT only	1.85	1.53	1.11	1.26	2.03E-02	7.05E-02	9.13E-01	9.45E-01
7908459	NM_000186	CFH	complement factor H	WT only	2.15	1.50	1.39	1.36	2.56E-02	1.99E-01	8.04E-01	9.35E-01
8168531	NM_032553	GPR174	G protein-coupled receptor 174	WT only	2.21	1.48	1.08	1.30	1.43E-02	1.70E-01	9.53E-01	1.00E+00
7980720	NM_001010854	TTC7B	tetratricopeptide repeat domain 7B	WT only	2.58	1.48	1.34	1.38	2.39E-03	1.04E-01	7.50E-01	6.34E-01
7988838	NM_138792	LEO1	Leo1, Paf1	WT only	1.56	1.46	1.30	1.29	3.79E-02	5.39E-02	7.09E-01	6.82E-01
8083737	---			WT only	1.71	1.45	1.14	1.32	3.18E-02	9.99E-02	8.88E-01	7.32E-01
8123739	NM_016588	NRN1	neuritin 1	WT only	1.54	1.44	1.26	1.29	4.45E-02	6.46E-02	7.79E-01	6.88E-01
7951397	NM_033292	CASP1	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)	WT only	2.42	1.44	1.27	1.34	2.08E-03	9.57E-02	8.01E-01	6.27E-01
7930894	NM_005308	GRK5	G protein-coupled receptor kinase 5	WT only	3.24	1.43	1.60	1.51	3.53E-04	9.21E-02	2.13E-01	2.74E-01
7976333	NM_015676	C14orf109	chromosome 14 open reading frame 109	WT only	1.51	1.40	1.31	1.21	2.88E-02	5.01E-02	5.47E-01	8.17E-01
8048976	---			WT only	1.52	1.40	1.05	1.19	3.18E-02	6.21E-02	9.51E-01	9.56E-01
8067305	NM_014258	SYCP2	synaptonemal complex protein 2	WT only	2.05	1.40	1.15	1.25	1.96E-03	5.77E-02	8.41E-01	6.73E-01
7967210	NR_002809	LOC338799	hypothetical locus LOC338799	WT only	1.65	1.39	1.26	1.23	4.33E-02	1.48E-01	8.13E-01	1.00E+00
8169519	NM_019045	WDR44	WD repeat domain 44	WT only	1.55	1.38	0.96	1.15	2.62E-02	6.72E-02	9.63E-01	1.00E+00

8103226	NM_152680	TMEM154	transmembrane protein 154	WT only	1.73	1.38	1.40	1.41	9.70E-03	7.74E-02	3.90E-01	3.05E-01
8127360	---			WT only	1.50	1.37	1.25	1.23	3.12E-02	6.75E-02	7.24E-01	7.57E-01
8051501	NM_002759	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	WT only	1.42	1.37	0.98	1.15	4.93E-02	6.04E-02	9.81E-01	1.00E+00
8132013	NM_004067	CHN2	chimerin (chimaerin) 2	WT only	1.76	1.35	1.46	1.28	1.94E-02	1.64E-01	4.54E-01	8.13E-01
8107518	---			WT only	1.78	1.35	1.29	1.38	3.22E-02	2.36E-01	8.13E-01	6.73E-01
8142307	NM_015723	PNPLA8	patatin-like phospholipase domain containing 8	WT only	1.52	1.34	1.22	1.23	1.89E-02	6.26E-02	7.38E-01	6.57E-01
8160559	NM_014314	DDX58	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	WT only	1.62	1.34	1.13	1.20	1.23E-02	7.50E-02	8.64E-01	8.67E-01
8050238	---			WT only	1.44	1.34	1.00	1.10	2.62E-02	5.02E-02	9.97E-01	1.00E+00
8089701	NM_015642	ZBTB20	zinc finger and BTB domain containing 20	WT only	1.53	1.33	1.19	1.24	1.43E-02	5.91E-02	7.97E-01	5.96E-01
7980998	NM_001002860	BTBD7	BTB (POZ) domain containing 7	WT only	1.45	1.33	1.11	1.13	3.64E-02	7.97E-02	8.76E-01	1.00E+00
8075332	NM_031937	TBC1D10A	TBC1 domain family, member 10A	WT only	1.59	1.32	1.23	1.21	4.09E-02	1.82E-01	8.19E-01	9.89E-01
8123893	NM_005906	MAK	male germ cell-associated kinase	WT only	1.65	1.32	1.09	1.17	3.29E-02	2.03E-01	9.29E-01	1.00E+00
7946275	NR_003945	GVIN1	GTPase, very large interferon inducible 1	WT only	1.78	1.31	1.15	1.24	5.38E-03	1.05E-01	8.38E-01	7.02E-01
8091260	NM_173653	SLC9A9	solute carrier family 9 (sodium	WT only	1.51	1.31	1.15	1.21	2.42E-02	1.04E-01	8.38E-01	8.29E-01
7969693	NM_021033	RAP2A	RAP2A, member of RAS oncogene family	WT only	1.72	1.30	1.05	1.24	1.18E-02	1.53E-01	9.59E-01	7.99E-01
8019622	NM_145041	TMEM106A	transmembrane protein 106A	WT only	1.39	1.30	1.16	1.14	3.88E-02	6.82E-02	8.13E-01	1.00E+00
8078147	NM_000060	BTD	biotinidase	WT only	1.63	1.30	1.11	1.22	5.06E-03	6.26E-02	8.56E-01	6.10E-01
7916898	NM_001114120	DEPDC1	DEP domain containing 1	WT only	1.47	1.30	1.18	1.27	4.09E-02	1.29E-01	8.23E-01	6.07E-01
8103563	NM_017631	DDX60	DEAD (Asp-Glu-Ala-Asp) box polypeptide 60	WT only	1.47	1.30	1.04	1.14	2.30E-02	8.70E-02	9.54E-01	1.00E+00
8089203	NM_020654	SENP7	SUMO1	WT only	1.47	1.29	1.09	1.22	1.30E-02	5.55E-02	8.80E-01	5.52E-01
8094476	NM_018317	TBC1D19	TBC1 domain family, member 19	WT only	1.41	1.29	1.14	1.25	2.39E-02	6.41E-02	8.24E-01	4.28E-01
8122365	NM_020455	GPR126	G protein-coupled receptor 126	WT only	1.63	1.29	1.23	1.22	2.36E-02	1.94E-01	8.09E-01	8.94E-01
8007483	NM_145041	TMEM106A	transmembrane protein 106A	WT only	1.36	1.28	1.17	1.13	4.98E-02	7.92E-02	8.01E-01	1.00E+00
8094719	NM_018177	N4BP2	NEDD4 binding protein 2	WT only	1.46	1.28	0.96	1.14	1.48E-02	6.78E-02	9.41E-01	9.42E-01
7980098	NM_005589	ALDH6A1	aldehyde dehydrogenase 6 family, member A1	WT only	1.43	1.28	0.98	1.11	2.52E-02	8.57E-02	9.79E-01	1.00E+00
8097435	NM_173487	C4orf33	chromosome 4 open reading frame 33	WT only	1.52	1.28	1.10	1.17	1.49E-02	1.03E-01	8.77E-01	9.13E-01
8126018	NM_007271	STK38	serine	WT only	1.35	1.28	1.01	1.14	3.10E-02	5.65E-02	9.87E-01	8.90E-01
8113103	AB020632	KIAA0825	KIAA0825 protein	WT only	1.53	1.28	0.95	1.09	3.09E-02	1.76E-01	9.46E-01	1.00E+00
8143209	NM_174959	SVOPL	SVOP-like	WT only	1.40	1.27	1.07	1.10	3.79E-02	1.02E-01	9.09E-01	1.00E+00
8010092	NM_024311	MFSD11	major facilitator superfamily domain containing 11	WT only	1.34	1.27	1.05	1.18	4.44E-02	7.19E-02	9.29E-01	7.29E-01
8075322	NM_001037666	LOC652968	hypothetical protein LOC652968	WT only	1.48	1.27	1.39	1.22	2.41E-02	1.28E-01	2.64E-01	7.01E-01
7903407	NM_020978	AMY2B	amylase, alpha 2B (pancreatic)	WT only	1.34	1.27	0.99	1.12	2.74E-02	5.05E-02	9.93E-01	9.68E-01
8135969	NM_022742	CCDC136	coiled-coil domain containing 136	WT only	1.51	1.27	1.05	1.19	3.09E-02	1.80E-01	9.54E-01	9.16E-01
8020090	NM_020648	TWSG1	twisted gastrulation homolog 1 (Drosophila)	WT only	1.41	1.26	1.07	1.14	3.41E-02	1.19E-01	9.19E-01	1.00E+00
8138596	NR_002711	CLK2P	CDC-like kinase 2, pseudogene	WT only	1.42	1.26	1.16	1.19	1.25E-02	6.01E-02	7.50E-01	6.00E-01
7957260	NM_006851	GLIPR1	GLI pathogenesis-related 1	WT only	0.51	1.26	0.65	0.82	4.17E-02	4.95E-01	6.65E-01	1.00E+00
7975066	NM_004857	AKAP5	A kinase (PRKA) anchor protein 5	WT only	1.95	1.26	1.12	1.23	4.30E-04	6.48E-02	8.25E-01	3.85E-01
7943424	NM_001166	BIRC2	baculoviral IAP repeat-containing 2	WT only	1.45	1.26	1.10	1.12	9.76E-03	6.24E-02	8.59E-01	9.77E-01
8009457	NM_212472	PRKAR1A	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguish	WT only	1.33	1.26	1.20	1.17	4.09E-02	7.83E-02	6.65E-01	7.18E-01
8085754	NM_001012410	SGOL1	shugoshin-like 1 (S. pombe)	WT only	1.33	1.25	1.01	1.12	2.56E-02	5.26E-02	9.93E-01	9.79E-01
7906400	NM_005531	IFI16	interferon, gamma-inducible protein 16	WT only	0.51	1.25	0.60	0.84	1.35E-02	3.63E-01	2.49E-01	1.00E+00
8096489	NM_006457	PDLIM5	PDZ and LIM domain 5	WT only	1.56	1.25	1.08	1.15	7.25E-03	1.03E-01	8.86E-01	9.32E-01
8167815	NM_014599	MAGED2	melanoma antigen family D, 2	WT only	1.41	1.25	1.09	1.07	4.06E-02	1.47E-01	8.92E-01	1.00E+00
8070010	NM_003895	SYNJ1	synaptojanin 1	WT only	1.39	1.25	1.01	1.09	2.06E-02	8.20E-02	9.93E-01	1.00E+00
7908397	NM_002927	RGS13	regulator of G-protein signaling 13	WT only	2.67	1.25	1.04	1.27	1.47E-04	1.55E-01	9.59E-01	4.81E-01
7980096	---			WT only	1.44	1.25	0.99	1.16	1.24E-02	8.24E-02	9.90E-01	8.13E-01
8101260	NM_058172	ANTXR2	anthrax toxin receptor 2	WT only	1.69	1.24	1.41	1.23	4.04E-03	1.34E-01	1.72E-01	5.78E-01
8110032	NM_153607	C5orf41	chromosome 5 open reading frame 41	WT only	1.35	1.24	1.04	1.14	2.25E-02	6.31E-02	9.36E-01	8.08E-01
8093258	NM_032263	IQCG	IQ motif containing G	WT only	1.35	1.24	1.01	1.13	3.54E-02	9.99E-02	9.93E-01	9.92E-01
8168472	NM_000052	ATP7A	ATPase, Cu++ transporting, alpha polypeptide	WT only	2.39	1.24	1.19	1.30	2.54E-04	1.47E-01	7.71E-01	3.40E-01
8098326	---			WT only	1.45	1.24	1.25	1.13	2.88E-02	1.69E-01	6.56E-01	1.00E+00
8149749	NM_003840	TNFRSF10D	tumor necrosis factor receptor superfamily, member 10d, decoy with truncated death	WT only	1.47	1.24	1.24	1.17	4.74E-02	2.37E-01	7.50E-01	1.00E+00
7923086	NM_018136	ASPM	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	WT only	1.44	1.24	1.14	1.19	8.64E-03	6.98E-02	8.01E-01	5.65E-01
7990511	NM_002833	PTPN9	protein tyrosine phosphatase, non-receptor type 9	WT only	1.52	1.24	1.11	1.16	4.52E-03	6.95E-02	8.34E-01	7.22E-01
8042144	NM_002908	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	WT only	1.35	1.24	1.09	1.10	1.45E-02	5.19E-02	8.44E-01	1.00E+00
7927955	NM_015634	KIAA1279	KIAA1279	WT only	1.35	1.23	1.01	1.12	3.41E-02	1.07E-01	9.93E-01	1.00E+00
8113064	NM_198273	LYSMD3	LysM, putative peptidoglycan-binding, domain containing 3	WT only	1.54	1.23	1.14	1.21	6.89E-03	1.13E-01	8.21E-01	5.87E-01
7972055	NM_138444	KCTD12	potassium channel tetramerisation domain containing 12	WT only	0.72	1.23	0.81	0.87	3.13E-02	1.33E-01	6.12E-01	9.05E-01
8111533	NM_001007527	LMBRD2	LMBR1 domain containing 2	WT only	1.37	1.23	1.03	1.18	1.90E-02	8.86E-02	9.52E-01	5.96E-01
7992865	NR_002169	OR1F2P	olfactory receptor, family 1, subfamily F, member 2	WT only	1.61	1.22	1.35	1.25	1.23E-02	2.26E-01	4.22E-01	6.27E-01
8128394	NM_032870	SFRS18	splicing factor, arginine	WT only	1.33	1.22	1.11	1.22	2.52E-02	8.22E-02	8.34E-01	3.63E-01
8143341	NM_030647	JHDM1D	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	WT only	1.30	1.22	1.11	1.14	4.83E-02	1.04E-01	8.36E-01	8.88E-01
8015759	NM_006373	VAT1	vesicle amine transport protein 1 homolog (T. californica)	WT only	1.31	1.22	1.32	1.16	2.91E-02	7.77E-02	1.53E-01	6.86E-01
7901788	NM_001134673	NFIA	nuclear factor I	WT only	1.86	1.22	1.52	1.33	1.23E-02	3.80E-01	3.50E-01	6.40E-01
8101411	NM_194282	LIN54	lin-54 homolog (C. elegans)	WT only	1.26	1.22	1.07	1.11	4.99E-02	7.10E-02	8.85E-01	9.63E-01

8090133	NM_022757	CCDC14	coiled-coil domain containing 14	WT only	1.35	1.22	1.05	1.17	2.54E-02	1.04E-01	9.22E-01	6.61E-01
8117476	NM_006994	BTN3A3	butyrophilin, subfamily 3, member A3	WT only	1.66	1.22	1.15	1.19	3.06E-03	1.38E-01	8.06E-01	6.55E-01
7938485	NM_014632	MICAL2	microtubule associated monoxygenase, calponin and LIM domain containing 2	WT only	0.71	1.22	1.04	0.93	1.27E-02	9.62E-02	9.44E-01	1.00E+00
7926609	NM_005180	BMI1	BMI1 polycomb ring finger oncogene	WT only	1.30	1.22	0.99	1.13	2.52E-02	6.72E-02	9.94E-01	8.36E-01
7909455	NM_025228	TRAF3IP3	TRAF3 interacting protein 3	WT only	1.55	1.21	1.25	1.23	3.62E-03	1.01E-01	3.78E-01	3.56E-01
8154333	NM_015061	JMJD2C	jumonji domain containing 2C	WT only	1.26	1.21	1.02	1.13	3.80E-02	6.23E-02	9.71E-01	7.53E-01
8127903	NM_014895	KIAA1009	KIAA1009	WT only	1.60	1.21	1.12	1.24	1.70E-02	2.78E-01	8.74E-01	7.09E-01
8093130	NM_152617	RNF168	ring finger protein 168	WT only	1.43	1.21	1.14	1.20	3.41E-02	2.22E-01	8.38E-01	8.10E-01
7983111	NM_003825	SNAP23	synaptosomal-associated protein, 23kDa	WT only	1.37	1.21	1.10	1.15	1.41E-02	9.11E-02	8.41E-01	7.02E-01
8157890	NM_006195	PBX3	pre-B-cell leukemia homeobox 3	WT only	1.27	1.21	0.97	1.05	4.74E-02	8.52E-02	9.55E-01	1.00E+00
7909371	NM_000573	CR1	complement component (3b	WT only	1.87	1.21	1.36	1.22	2.78E-03	2.49E-01	3.86E-01	7.47E-01
7978114	BC002491	FAM158A	family with sequence similarity 158, member A	WT only	1.28	1.21	1.10	1.11	4.98E-02	1.04E-01	8.45E-01	1.00E+00
8122464	NM_007124	UTRN	utrophin	WT only	1.37	1.21	1.09	1.14	6.93E-03	5.24E-02	8.36E-01	6.27E-01
8098556	NM_152683	CCDC111	coiled-coil domain containing 111	WT only	1.48	1.21	1.10	1.20	9.53E-03	1.49E-01	8.55E-01	5.86E-01
8147439	NM_024613	PLEKHF2	pleckstrin homology domain containing, family F (with FYVE domain) member 2	WT only	1.48	1.20	1.24	1.19	1.67E-02	2.00E-01	5.91E-01	7.44E-01
8147580	NM_017890	VPS13B	vacuolar protein sorting 13 homolog B (yeast)	WT only	1.39	1.20	1.07	1.13	1.14E-02	9.60E-02	8.77E-01	8.84E-01
7927215	NM_000698	ALOX5	arachidonate 5-lipoxygenase	WT only	1.86	1.20	1.20	1.17	1.02E-02	4.08E-01	8.35E-01	1.00E+00
8053484	NM_003896	ST3GAL5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	WT only	1.69	1.20	1.04	1.18	5.75E-03	2.47E-01	9.52E-01	8.90E-01
8166784	NM_004615	TSPAN7	tetraspanin 7	WT only	2.44	1.20	1.38	1.35	4.79E-04	2.99E-01	3.90E-01	3.47E-01
8046792	NM_080876	DUSP19	dual specificity phosphatase 19	WT only	1.57	1.20	1.20	1.24	4.16E-02	4.01E-01	8.36E-01	8.76E-01
7947248	NM_031217	KIF18A	kinesin family member 18A	WT only	1.35	1.20	1.06	1.18	2.29E-02	1.21E-01	8.95E-01	5.97E-01
8047403	NM_032977	CASP10	caspase 10, apoptosis-related cysteine peptidase	WT only	1.47	1.20	1.06	1.16	6.62E-03	1.20E-01	8.96E-01	7.09E-01
8096314	NM_000297	PKD2	polycystic kidney disease 2 (autosomal dominant)	WT only	1.53	1.20	1.38	1.29	1.75E-02	2.67E-01	2.99E-01	4.41E-01
8164343	NM_001035254	FAM102A	family with sequence similarity 102, member A	WT only	1.43	1.20	1.14	1.10	1.09E-02	1.31E-01	7.97E-01	1.00E+00
8086125	NM_014831	LBA1	lupus brain antigen 1	WT only	1.67	1.20	1.09	1.16	5.75E-03	2.51E-01	8.94E-01	9.55E-01
7930380	NM_016824	ADD3	adducin 3 (gamma)	WT only	1.43	1.19	1.09	1.18	1.14E-02	1.41E-01	8.58E-01	6.19E-01
8084912	NR_003265	SDHALP2	succinate dehydrogenase complex, subunit A, flavoprotein pseudogene 2	WT only	1.28	1.19	1.07	1.11	4.64E-02	1.25E-01	8.85E-01	1.00E+00
7941179	NM_005186	CAPN1	calpain 1, (mu	WT only	1.30	1.19	1.10	1.04	3.70E-02	1.33E-01	8.43E-01	1.00E+00
7958466	NM_001093	ACACB	acetyl-Coenzyme A carboxylase beta	WT only	1.46	1.19	1.16	1.23	1.55E-02	2.07E-01	8.01E-01	5.14E-01
7982757	NM_170589	CASC5	cancer susceptibility candidate 5	WT only	1.30	1.19	1.03	1.12	2.74E-02	1.05E-01	9.58E-01	8.88E-01
8041617	NM_020744	MTA3	metastasis associated 1 family, member 3	WT only	1.37	1.19	1.17	1.16	3.64E-02	2.15E-01	7.90E-01	8.90E-01
8097811	AL137273	DKFZP434I0714	hypothetical protein DKFZP434I0714	WT only	1.43	1.19	1.10	1.21	1.56E-02	1.91E-01	8.64E-01	5.75E-01
8027377	---			WT only	1.54	1.19	1.42	1.23	1.90E-02	3.06E-01	2.50E-01	7.02E-01
8082940	NM_015396	ARMC8	armadillo repeat containing 8	WT only	1.50	1.19	1.27	1.21	2.07E-02	2.92E-01	6.11E-01	7.55E-01
8129458	NM_033515	ARHGAP18	Rho GTPase activating protein 18	WT only	1.74	1.19	1.10	1.18	2.23E-03	2.19E-01	8.64E-01	7.45E-01
7963289	NM_016293	BIN2	bridging integrator 2	WT only	1.64	1.19	1.04	1.20	1.03E-02	3.20E-01	9.62E-01	8.45E-01
8157524	NR_024168	TLR4	toll-like receptor 4	WT only	1.50	1.18	1.31	1.16	2.24E-02	3.01E-01	4.88E-01	9.81E-01
8036954	---			WT only	1.34	1.18	1.06	1.16	2.26E-02	1.51E-01	9.11E-01	6.57E-01
8138922	NM_015483	KBTBD2	kelch repeat and BTB (POZ) domain containing 2	WT only	1.37	1.18	1.04	1.17	4.02E-02	2.46E-01	9.54E-01	8.54E-01
7951372	NM_033306	CASP4	caspase 4, apoptosis-related cysteine peptidase	WT only	1.28	1.18	0.97	1.09	3.72E-02	1.38E-01	9.43E-01	1.00E+00
7904695	NM_004892	SEC22B	SEC22 vesicle trafficking protein homolog B (S. cerevisiae)	WT only	1.43	1.18	1.08	1.17	1.48E-02	2.06E-01	8.80E-01	7.38E-01
7972062	NM_012158	FBXL3	F-box and leucine-rich repeat protein 3	WT only	1.32	1.18	1.06	1.13	4.18E-02	2.04E-01	9.18E-01	9.35E-01
7980080	NM_001249	ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5	WT only	1.42	1.18	1.19	1.18	3.16E-02	2.93E-01	7.85E-01	8.17E-01
7900009	NM_017629	EIF2C4	eukaryotic translation initiation factor 2C, 4	WT only	1.35	1.17	1.20	1.21	4.70E-02	2.58E-01	7.13E-01	5.97E-01
8073062	NM_004900	APOBEC3B	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	WT only	1.37	1.17	1.04	1.14	4.83E-02	2.88E-01	9.55E-01	1.00E+00
8063211	NM_181659	NCOA3	nuclear receptor coactivator 3	WT only	1.35	1.17	1.14	1.13	1.34E-02	1.29E-01	7.51E-01	8.11E-01
7902166	NM_020948	MIER1	mesoderm induction early response 1 homolog (Xenopus laevis)	WT only	1.43	1.17	1.07	1.16	1.31E-02	2.07E-01	8.88E-01	7.48E-01
8085081	NM_016302	CRBN	cereblon	WT only	1.37	1.17	0.97	1.14	1.09E-02	1.42E-01	9.54E-01	7.40E-01
8089112	NM_182909	FILIP1L	filamin A interacting protein 1-like	WT only	1.67	1.17	1.11	1.18	2.16E-02	4.83E-01	8.93E-01	1.00E+00
7940153	NM_022074	FAM111A	family with sequence similarity 111, member A	WT only	1.38	1.17	1.03	1.14	7.41E-03	1.26E-01	9.46E-01	6.96E-01
8056572	NM_020675	SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	WT only	1.32	1.16	1.13	1.12	1.68E-02	1.43E-01	7.74E-01	8.45E-01
8107532	NM_000414	HSD17B4	hydroxysteroid (17-beta) dehydrogenase 4	WT only	1.45	1.16	1.08	1.14	8.71E-03	2.14E-01	8.80E-01	8.78E-01
7898556	NM_001040125	PQLC2	PQ loop repeat containing 2	WT only	0.75	1.16	0.88	0.93	4.95E-02	2.78E-01	8.25E-01	1.00E+00
8173766	NM_153252	BRWD3	bromodomain and WD repeat domain containing 3	WT only	1.31	1.16	1.06	1.07	1.81E-02	1.41E-01	8.86E-01	1.00E+00
8175177	NM_018388	MBNL3	muscleblind-like 3 (Drosophila)	WT only	1.34	1.16	1.03	1.08	2.23E-02	2.00E-01	9.58E-01	1.00E+00
8017704	AK056627	FLJ32065	hypothetical protein FLJ32065	WT only	1.66	1.16	1.24	1.25	2.88E-02	5.33E-01	8.13E-01	8.78E-01
7988753	NM_032802	SPPL2A	signal peptide peptidase-like 2A	WT only	1.38	1.16	1.02	1.12	1.64E-02	2.32E-01	9.82E-01	1.00E+00
8135422	NM_001008407	BCAP29	B-cell receptor-associated protein 29	WT only	1.36	1.15	0.98	1.11	2.58E-02	2.72E-01	9.76E-01	1.00E+00
8116874	NM_001040274	SYCP2L	synaptonemal complex protein 2-like	WT only	1.54	1.15	1.32	1.28	3.10E-03	2.36E-01	1.70E-01	2.05E-01
7963212	NM_000617	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	WT only	1.57	1.15	1.29	1.19	1.54E-02	4.43E-01	5.72E-01	8.90E-01
8094251	AK096972	FLJ39653	hypothetical FLJ39653	WT only	1.30	1.14	1.05	1.10	2.88E-02	2.27E-01	9.26E-01	1.00E+00
8072757	NM_000395	CSF2RB	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	WT only	1.61	1.14	1.36	1.10	7.96E-03	4.25E-01	2.98E-01	1.00E+00
7917707	NM_005665	EVI5	ecotropic viral integration site 5	WT only	1.84	1.14	1.40	1.26	1.82E-03	4.04E-01	1.92E-01	4.56E-01
8059111	NM_005689	ABCB6	ATP-binding cassette, sub-family B (MDR	WT only	1.35	1.14	1.25	1.18	2.52E-02	2.97E-01	4.14E-01	6.27E-01
8052269	NM_001135597	CCDC88A	coiled-coil domain containing 88A	WT only	1.48	1.14	1.24	1.23	2.76E-02	4.57E-01	7.21E-01	6.73E-01

8093643	NM_176801	ADD1	adducin 1 (alpha)	WT only	1.29	1.14	1.10	1.09	4.95E-02	2.86E-01	8.39E-01	1.00E+00
8156688	NM_014290	TDRD7	tudor domain containing 7	WT only	1.30	1.14	0.94	1.07	4.18E-02	2.80E-01	9.00E-01	1.00E+00
8119052	NM_173676	PNPLA1	patatin-like phospholipase domain containing 1	WT only	1.87	1.14	1.47	1.24	1.49E-03	3.99E-01	9.66E-02	4.98E-01
8150714	NM_052937	PCMTD1	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1	WT only	1.39	1.14	1.13	1.27	2.62E-02	3.56E-01	8.27E-01	3.35E-01
8102076	NM_001813	CENPE	centromere protein E, 312kDa	WT only	1.42	1.14	1.14	1.22	7.26E-03	2.52E-01	7.77E-01	3.07E-01
7984276	NM_004727	SLC24A1	solute carrier family 24 (sodium	WT only	1.85	1.13	1.24	1.19	5.06E-03	5.25E-01	7.51E-01	9.45E-01
7922353	NM_178527	SLC9A11	solute carrier family 9, member 11	WT only	1.54	1.13	1.17	1.14	1.73E-02	4.70E-01	8.20E-01	1.00E+00
8083709	NM_005496	SMC4	structural maintenance of chromosomes 4	WT only	1.29	1.13	1.10	1.16	2.62E-02	2.46E-01	8.30E-01	5.81E-01
7908978	NM_014827	ZC3H11A	zinc finger CCCH-type containing 11A	WT only	1.52	1.13	1.14	1.25	9.91E-03	4.13E-01	8.23E-01	4.39E-01
8083214	NM_004267	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	WT only	1.37	1.13	1.24	1.15	2.64E-02	3.71E-01	4.88E-01	8.38E-01
8106784	NM_002890	RASA1	RAS p21 protein activator (GTPase activating protein) 1	WT only	1.32	1.13	1.07	1.16	1.82E-02	2.62E-01	8.77E-01	6.07E-01
8089082	NM_080927	DCBLD2	discoidin, CUB and LCCL domain containing 2	WT only	1.51	1.13	1.14	1.11	1.23E-02	4.43E-01	8.23E-01	1.00E+00
8156706	NM_003275	TMOD1	tropomodulin 1	WT only	1.35	1.12	1.15	1.15	3.49E-02	3.94E-01	8.06E-01	8.90E-01
8145624	NM_001440	EXTL3	exostoses (multiple)-like 3	WT only	1.40	1.12	1.03	1.08	1.75E-02	3.84E-01	9.67E-01	1.00E+00
7908178	NM_017673	C1orf26	chromosome 1 open reading frame 26	WT only	1.57	1.12	1.22	1.19	4.09E-02	6.26E-01	8.20E-01	1.00E+00
8057954	AY358249	C2orf66	chromosome 2 open reading frame 66	WT only	2.11	1.12	0.97	1.18	5.95E-03	6.66E-01	9.81E-01	1.00E+00
7955217	NM_023071	SPATS2	spermatogenesis associated, serine-rich 2	WT only	1.52	1.12	1.04	1.12	1.22E-02	4.65E-01	9.55E-01	1.00E+00
8109697	NM_004060	CCNG1	cyclin G1	WT only	1.31	1.12	1.14	1.17	2.58E-02	3.05E-01	7.50E-01	5.88E-01
8175420	NM_002139	RBMX	RNA binding motif protein, X-linked	WT only	1.29	1.12	1.12	1.16	3.22E-02	3.07E-01	8.13E-01	6.17E-01
8108861	NM_030571	NDFIP1	Nedd4 family interacting protein 1	WT only	1.57	1.12	1.30	1.21	9.14E-03	5.01E-01	4.33E-01	6.55E-01
8145636	NM_024567	HMBOX1	homeobox containing 1	WT only	1.38	1.12	1.08	1.11	2.42E-02	4.39E-01	8.86E-01	1.00E+00
7984517	NM_015554	GLCE	glucuronic acid epimerase	WT only	1.32	1.11	0.99	1.12	4.23E-02	4.29E-01	9.91E-01	9.88E-01
8105487	NM_138453	RAB3C	RAB3C, member RAS oncogene family	WT only	1.79	1.11	1.31	1.22	3.05E-02	7.21E-01	7.98E-01	1.00E+00
8161774	NM_017662	TRPM6	transient receptor potential cation channel, subfamily M, member 6	WT only	1.78	1.11	1.40	1.23	1.24E-02	6.52E-01	4.84E-01	8.84E-01
8127109	NM_016513	ICK	intestinal cell (MAK-like) kinase	WT only	1.70	1.11	1.23	1.23	7.35E-03	5.85E-01	7.38E-01	6.95E-01
7928019	NM_033500	HK1	hexokinase 1	WT only	1.91	1.11	1.22	1.22	1.24E-02	7.08E-01	8.36E-01	1.00E+00
7979307	NM_014750	DLGAP5	discs, large (Drosophila) homolog-associated protein 5	WT only	1.35	1.10	1.10	1.14	1.48E-02	3.82E-01	8.36E-01	7.36E-01
7944991	NM_152713	STT3A	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)	WT only	1.27	1.10	1.14	1.10	3.21E-02	3.56E-01	7.38E-01	9.89E-01
7976336	NM_175748	UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative)	WT only	1.35	1.10	1.02	1.11	3.56E-02	4.91E-01	9.81E-01	1.00E+00
8088745	NM_015123	FRMD4B	FERM domain containing 4B	WT only	1.51	1.10	0.92	1.13	3.56E-02	6.39E-01	9.16E-01	1.00E+00
8108127	NM_001745	CAMLG	calcium modulating ligand	WT only	1.48	1.10	1.25	1.27	3.94E-02	6.26E-01	7.38E-01	6.27E-01
8083941	NM_018098	ECT2	epithelial cell transforming sequence 2 oncogene	WT only	1.30	1.10	1.05	1.12	2.91E-02	4.07E-01	9.06E-01	8.90E-01
8058614	NM_006055	LANCL1	LanC lantibiotic synthetase component C-like 1 (bacterial)	WT only	1.37	1.10	1.02	1.13	1.88E-02	4.56E-01	9.78E-01	9.16E-01
8089478	NM_001008756	GCET2	germinal center expressed transcript 2	WT only	2.37	1.10	1.20	1.26	6.18E-04	6.33E-01	8.06E-01	6.27E-01
7969003	NM_021999	ITM2B	integral membrane protein 2B	WT only	1.29	1.10	1.13	1.14	2.06E-02	3.68E-01	7.52E-01	6.32E-01
8097282	NM_005841	SPRY1	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	WT only	0.75	1.10	0.87	0.94	3.77E-02	5.05E-01	8.01E-01	1.00E+00
8131539	NM_018374	TMEM106B	transmembrane protein 106B	WT only	1.36	1.10	1.12	1.15	2.54E-02	4.90E-01	8.23E-01	8.29E-01
7898663	NM_032409	PINK1	PTEN induced putative kinase 1	WT only	1.31	1.10	0.95	1.07	5.00E-02	5.11E-01	9.29E-01	1.00E+00
8057990	NM_153697	ANKRD44	ankyrin repeat domain 44	WT only	1.28	1.10	1.04	1.12	4.98E-02	4.63E-01	9.31E-01	9.26E-01
7923119	NM_194314	ZBTB41	zinc finger and BTB domain containing 41	WT only	1.30	1.10	1.06	1.05	2.39E-02	4.22E-01	8.86E-01	1.00E+00
8178552	NM_021184	C6orf47	chromosome 6 open reading frame 47	WT only	1.39	1.09	1.04	1.15	1.40E-02	4.83E-01	9.34E-01	7.29E-01
8179808	NM_021184	C6orf47	chromosome 6 open reading frame 47	WT only	1.39	1.09	1.04	1.15	1.40E-02	4.83E-01	9.34E-01	7.29E-01
8174051	NM_000061	BTK	Bruton agammaglobulinemia tyrosine kinase	WT only	1.85	1.09	1.08	1.24	9.67E-04	5.46E-01	8.85E-01	4.46E-01
7946446	NM_020645	NRIP3	nuclear receptor interacting protein 3	WT only	1.48	1.09	0.89	1.07	3.29E-02	6.52E-01	8.75E-01	1.00E+00
8174474	NM_022977	ACSL4	acyl-CoA synthetase long-chain family member 4	WT only	1.29	1.09	1.07	1.10	5.00E-02	5.31E-01	8.88E-01	1.00E+00
8040173	NM_005680	TAF1B	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	WT only	1.47	1.09	1.06	1.15	2.91E-02	6.61E-01	9.36E-01	1.00E+00
8165911	NM_005647	TBL1X	transducin (beta)-like 1X-linked	WT only	1.49	1.09	1.09	1.16	3.41E-02	6.89E-01	9.09E-01	1.00E+00
8009014	NM_006852	TLK2	tousled-like kinase 2	WT only	1.23	1.09	1.03	1.08	4.47E-02	4.31E-01	9.55E-01	1.00E+00
8082688	NM_015268	DNAJC13	DnaJ (Hsp40) homolog, subfamily C, member 13	WT only	1.28	1.08	0.96	1.09	4.90E-02	5.28E-01	9.43E-01	1.00E+00
8116372	NM_018434	RNF130	ring finger protein 130	WT only	1.78	1.08	1.37	1.27	1.59E-03	6.10E-01	1.91E-01	3.55E-01
8124994	NM_021184	C6orf47	chromosome 6 open reading frame 47	WT only	1.40	1.08	1.05	1.15	1.54E-02	5.61E-01	9.17E-01	7.60E-01
7954777	NM_032834	ALG10	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog (S. pomb	WT only	1.30	1.08	1.07	1.11	3.73E-02	5.41E-01	8.81E-01	1.00E+00
8136869	NM_032982	CASP2	caspase 2, apoptosis-related cysteine peptidase	WT only	1.29	1.08	1.01	1.04	2.48E-02	4.91E-01	9.86E-01	1.00E+00
7899018	NM_018202	TMEM57	transmembrane protein 57	WT only	1.33	1.08	1.18	1.16	3.74E-02	6.00E-01	7.26E-01	8.17E-01
7962312	NM_005164	ABCD2	ATP-binding cassette, sub-family D (ALD), member 2	WT only	1.90	1.08	1.53	1.32	9.91E-03	7.84E-01	3.12E-01	6.66E-01
7906244	NM_001007792	NTRK1	neurotrophic tyrosine kinase, receptor, type 1	WT only	1.77	1.08	1.31	1.22	4.48E-03	7.07E-01	4.87E-01	7.29E-01
8096079	---			WT only	1.53	1.08	0.99	1.14	5.31E-03	6.15E-01	9.84E-01	8.90E-01
7969677	NM_144778	MBNL2	muscleblind-like 2 (Drosophila)	WT only	1.54	1.07	1.33	1.18	1.47E-03	5.13E-01	7.35E-02	4.16E-01
7954711	NM_018169	C12orf35	chromosome 12 open reading frame 35	WT only	1.46	1.07	1.04	1.12	6.13E-03	5.85E-01	9.36E-01	9.26E-01
8130142	NM_032832	LRP11	low density lipoprotein receptor-related protein 11	WT only	0.70	1.07	0.83	0.91	1.75E-02	6.53E-01	6.50E-01	1.00E+00
8031566	XM_001726429	LOC100132178	similar to hCG2008275	WT only	1.35	1.07	1.22	1.16	2.38E-02	6.16E-01	5.03E-01	7.09E-01
8120961	NM_138409	MRAP2	melanocortin 2 receptor accessory protein 2	WT only	1.57	1.07	1.16	1.14	2.04E-02	7.53E-01	8.36E-01	1.00E+00
8157233	NM_032303	HSDL2	hydroxysteroid dehydrogenase like 2	WT only	1.39	1.07	1.02	1.11	1.61E-02	6.29E-01	9.82E-01	1.00E+00
8124166	NM_001080480	MBOAT1	membrane bound O-acyltransferase domain containing 1	WT only	1.39	1.07	1.07	1.09	1.38E-02	6.22E-01	8.85E-01	1.00E+00
7954789	NM_001013620	ALG10B	asparagine-linked glycosylation 10, alpha-1,2-glucosyltransferase homolog B (yeast)	WT only	1.27	1.07	1.08	1.10	4.41E-02	5.87E-01	8.72E-01	1.00E+00

8132913	---			WT only	1.30	1.07	1.20	1.14	4.26E-02	6.49E-01	5.76E-01	8.38E-01
8092134	NM_002662	PLD1	phospholipase D1, phosphatidylcholine-specific	WT only	1.56	1.07	1.29	1.27	1.48E-02	7.46E-01	5.42E-01	5.31E-01
8155849	NM_000700	ANXA1	annexin A1	WT only	1.46	1.07	1.24	1.10	1.19E-02	6.78E-01	5.15E-01	1.00E+00
8012397	NM_017622	C17orf59	chromosome 17 open reading frame 59	WT only	1.23	1.06	1.04	1.09	4.39E-02	5.72E-01	9.15E-01	1.00E+00
8056545	NM_013233	STK39	serine threonine kinase 39 (STE20	WT only	1.33	1.06	1.17	1.14	1.97E-02	6.31E-01	6.50E-01	7.37E-01
8155707	NM_004817	TJP2	tight junction protein 2 (zona occludens 2)	WT only	0.66	1.06	0.89	0.88	2.79E-02	7.86E-01	8.77E-01	1.00E+00
8127841	NM_015599	PGM3	phosphoglucomutase 3	WT only	1.68	1.06	1.29	1.21	6.26E-03	7.69E-01	5.15E-01	7.46E-01
8010918	NM_001128159	VPS53	vacuolar protein sorting 53 homolog (S. cerevisiae)	WT only	0.80	1.06	0.84	0.88	4.09E-02	6.36E-01	4.70E-01	6.43E-01
7984540	NM_138555	KIF23	kinesin family member 23	WT only	1.30	1.06	1.04	1.10	1.81E-02	6.37E-01	9.18E-01	9.71E-01
8055624	NM_014795	ZEB2	zinc finger E-box binding homeobox 2	WT only	1.36	1.06	1.18	1.17	1.35E-02	6.75E-01	6.08E-01	5.69E-01
8146171	NM_001556	IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta	WT only	1.31	1.05	1.11	1.10	3.32E-02	7.04E-01	8.25E-01	1.00E+00
8161727	NM_016014	FAM108B1	family with sequence similarity 108, member B1	WT only	1.29	1.05	1.11	1.11	4.07E-02	7.09E-01	8.36E-01	9.98E-01
8091120	NM_001039547	GK5	glycerol kinase 5 (putative)	WT only	1.36	1.05	1.14	1.10	2.73E-02	7.52E-01	8.14E-01	1.00E+00
8170360	AY258285	FTH1	ferritin, heavy polypeptide 1	WT only	1.26	1.05	1.06	1.11	4.90E-02	7.11E-01	8.98E-01	9.32E-01
8108301	NM_005733	KIF20A	kinesin family member 20A	WT only	1.26	1.05	1.06	1.08	4.69E-02	7.07E-01	8.92E-01	1.00E+00
8162236	NM_006378	SEMA4D	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short	WT only	1.34	1.05	1.25	1.11	1.14E-02	6.94E-01	2.09E-01	8.97E-01
7961900	NM_002223	ITPR2	inositol 1,4,5-triphosphate receptor, type 2	WT only	1.50	1.05	1.32	1.20	2.71E-02	8.35E-01	5.02E-01	8.62E-01
7903541	NM_007269	STXBP3	syntaxin binding protein 3	WT only	1.26	1.05	1.03	1.06	2.91E-02	7.05E-01	9.54E-01	1.00E+00
8083447	NM_002563	P2RY1	purinergic receptor P2Y, G-protein coupled, 1	WT only	1.61	1.04	1.29	1.17	1.81E-02	8.65E-01	6.65E-01	1.00E+00
7980580	NM_000153	GALC	galactosylceramidase	WT only	2.16	1.04	1.65	1.30	7.35E-03	9.06E-01	2.79E-01	8.44E-01
8145454	NM_004331	BNIP3L	BCL2	WT only	1.39	1.04	1.36	1.16	2.73E-02	8.19E-01	2.09E-01	8.84E-01
7902799	AK123670	LOC339524	hypothetical protein LOC339524	WT only	1.95	1.04	1.40	1.22	5.66E-04	8.16E-01	1.24E-01	5.16E-01
7926385	NM_003473	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	WT only	1.41	1.04	1.12	1.08	3.16E-02	8.45E-01	8.58E-01	1.00E+00
7905949	XM_001716780	LOC648822	similar to hCG2040565	WT only	1.37	1.03	1.14	1.12	1.89E-02	8.35E-01	7.97E-01	9.45E-01
8116835	NM_145649	GCNT2	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme (I blood group)	WT only	1.45	1.03	1.34	1.12	2.41E-02	8.71E-01	3.34E-01	1.00E+00
7993776	NM_030941	LOC81691	exonuclease NEF-sp	WT only	1.43	1.03	1.22	1.20	2.29E-02	8.65E-01	6.73E-01	6.73E-01
7932420	NM_014241	PTPLA	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A	WT only	1.35	1.03	1.30	1.14	1.59E-02	8.29E-01	1.79E-01	7.48E-01
8063755	AK304220	C20orf177	chromosome 20 open reading frame 177	WT only	1.62	1.03	1.05	1.11	1.74E-03	8.69E-01	9.29E-01	9.94E-01
8024754	NM_032607	CREB3L3	cAMP responsive element binding protein 3-like 3	WT only	0.80	1.03	0.94	0.95	3.00E-02	8.47E-01	8.83E-01	1.00E+00
8016044	NM_000419	ITGA2B	integrin, alpha 2b (platelet glycoprotein IIb of IIb	WT only	1.54	1.02	1.16	1.10	2.68E-03	8.77E-01	6.98E-01	1.00E+00
8129783	NM_003980	MAP7	microtubule-associated protein 7	WT only	0.71	1.02	0.88	0.91	3.18E-02	9.18E-01	8.37E-01	1.00E+00
8008802	NM_182569	GDPD1	glycerophosphodiester phosphodiesterase domain containing 1	WT only	1.39	1.02	1.04	1.08	1.82E-02	9.31E-01	9.43E-01	1.00E+00
8111210	---			WT only	1.58	1.01	1.10	1.22	4.75E-03	9.48E-01	8.60E-01	5.09E-01
8162142	NM_030940	ISCA1	iron-sulfur cluster assembly 1 homolog (S. cerevisiae)	WT only	0.70	1.01	0.91	0.91	1.50E-02	9.50E-01	8.60E-01	1.00E+00
7932867	NM_182755	ZNF438	zinc finger protein 438	WT only	1.59	1.01	1.38	1.14	1.23E-02	9.61E-01	3.07E-01	1.00E+00
7970949	NM_005584	MAB21L1	mab-21-like 1 (C. elegans)	WT only	1.48	1.01	1.29	1.16	1.48E-02	9.67E-01	4.37E-01	8.78E-01
8106418	NM_001882	CRHBP	corticotropin releasing hormone binding protein	WT only	0.77	1.01	0.84	0.93	3.23E-02	9.68E-01	5.66E-01	1.00E+00
8104570	BC011524	FAM105A	family with sequence similarity 105, member A	WT only	1.42	1.01	1.22	1.14	2.03E-02	9.75E-01	6.50E-01	9.42E-01
7974473	NM_017943	FBXO34	F-box protein 34	WT only	1.48	1.01	1.08	1.15	5.06E-03	9.73E-01	8.76E-01	7.53E-01
8120943	NM_016230	CYB5R4	cytochrome b5 reductase 4	WT only	1.25	1.00	1.05	1.08	4.94E-02	9.98E-01	9.06E-01	1.00E+00
7916808	NM_015139	SLC35D1	solute carrier family 35 (UDP-glucuronic acid	WT only	1.78	1.00	1.34	1.23	1.04E-02	9.97E-01	5.97E-01	8.85E-01
7988789	NM_015263	DMXL2	Dmx-like 2	WT only	1.29	1.00	1.21	1.10	3.09E-02	9.81E-01	4.49E-01	9.92E-01
8078497	NM_016300	ARPP-21	cyclic AMP-regulated phosphoprotein, 21 kD	WT only	1.38	1.00	1.27	1.14	1.72E-02	9.81E-01	3.12E-01	8.51E-01
8017599	NM_000442	PECAM1	platelet	WT only	1.45	0.99	1.35	1.13	3.14E-02	9.82E-01	3.65E-01	1.00E+00
8001410	NM_001012398	AKTIP	AKT interacting protein	WT only	1.46	0.99	1.00	1.11	4.14E-02	9.83E-01	9.99E-01	1.00E+00
8108873	NM_015071	ARHGAP26	Rho GTPase activating protein 26	WT only	0.75	0.99	0.84	0.88	1.73E-02	9.69E-01	5.02E-01	8.06E-01
7979328	BC109089	KIAA0831	KIAA0831	WT only	1.68	0.99	1.01	1.15	1.38E-02	9.76E-01	9.94E-01	1.00E+00
7950671	NM_080491	GAB2	GRB2-associated binding protein 2	WT only	1.56	0.99	1.23	1.18	1.79E-02	9.57E-01	7.38E-01	9.45E-01
7925525	NM_014812	CEP170	centrosomal protein 170kDa	WT only	1.38	0.98	1.12	1.13	9.85E-03	8.80E-01	8.09E-01	8.36E-01
8094911	NM_020453	ATP10D	ATPase, class V, type 10D	WT only	1.80	0.98	1.19	1.08	6.59E-03	9.36E-01	8.16E-01	1.00E+00
8102214	NM_005443	PAPSS1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	WT only	1.25	0.98	1.14	1.07	4.08E-02	8.71E-01	7.24E-01	1.00E+00
8096004	NM_198892	BMP2K	BMP2 inducible kinase	WT only	1.45	0.98	0.95	1.06	4.17E-03	8.74E-01	8.94E-01	1.00E+00
7909661	NM_012424	RPS6KC1	ribosomal protein S6 kinase, 52kDa, polypeptide 1	WT only	1.35	0.97	1.19	1.10	4.74E-02	8.94E-01	7.40E-01	1.00E+00
8095773	NM_003715	USO1	USO1 homolog, vesicle docking protein (yeast)	WT only	1.24	0.97	1.03	1.04	4.56E-02	7.95E-01	9.48E-01	1.00E+00
7985364	NM_172217	IL16	interleukin 16 (lymphocyte chemoattractant factor)	WT only	0.75	0.97	0.94	0.91	2.39E-02	8.17E-01	8.88E-01	1.00E+00
7985695	NM_006738	AKAP13	A kinase (PRKA) anchor protein 13	WT only	1.31	0.97	0.96	1.00	3.08E-02	8.17E-01	9.28E-01	1.00E+00
7938063	ENST00000316698	OR52E5	olfactory receptor, family 52, subfamily E, member 5	WT only	0.76	0.97	0.84	0.87	2.47E-02	8.06E-01	5.21E-01	6.66E-01
8133902	---			WT only	1.55	0.96	1.09	1.25	2.06E-02	8.70E-01	8.97E-01	6.43E-01
7964701	NM_002076	GNS	glucosamine (N-acetyl)-6-sulfatase	WT only	1.70	0.96	1.16	1.15	4.10E-03	8.41E-01	8.11E-01	9.45E-01
8164918	NM_017585	SLC2A6	solute carrier family 2 (facilitated glucose transporter), member 6	WT only	1.38	0.96	1.11	0.97	2.91E-02	8.03E-01	8.45E-01	1.00E+00
7995631	NM_005611	RBL2	retinoblastoma-like 2 (p130)	WT only	1.29	0.96	1.05	1.10	4.51E-02	7.56E-01	9.30E-01	1.00E+00
7965322	NM_000899	KITLG	KIT ligand	WT only	1.60	0.95	1.54	1.27	1.99E-02	8.48E-01	1.70E-01	6.27E-01
7983779	NM_001080534	UNC13C	unc-13 homolog C (C. elegans)	WT only	0.74	0.95	0.87	0.85	3.35E-02	7.69E-01	8.01E-01	7.18E-01
8077171	NM_001130921	RABL2B	RAB, member of RAS oncogene family-like 2B	WT only	0.78	0.95	0.89	0.90	4.41E-02	7.27E-01	8.06E-01	9.45E-01
8037123	NM_002698	POU2F2	POU class 2 homeobox 2	WT only	1.44	0.95	0.98	1.07	4.64E-03	6.72E-01	9.72E-01	1.00E+00

8044669	NM_013412	RABL2A	RAB, member of RAS oncogene family-like 2A	WT only	0.77	0.95	0.89	0.89	3.29E-02	6.84E-01	8.09E-01	9.17E-01
8130422	NM_173515	CNKSR3	CNKSR family member 3	WT only	1.54	0.94	1.28	1.12	6.71E-03	7.11E-01	3.85E-01	1.00E+00
8139033	NM_001637	AOAH	acyloxyacyl hydrolase (neutrophil)	WT only	0.73	0.94	1.02	0.94	1.40E-02	6.42E-01	9.81E-01	1.00E+00
8070720	NM_015259	ICOSLG	inducible T-cell co-stimulator ligand	WT only	0.59	0.94	0.78	0.82	1.89E-03	6.91E-01	3.70E-01	4.76E-01
8134981	NM_003302	TRIP6	thyroid hormone receptor interactor 6	WT only	0.69	0.94	0.91	0.89	1.90E-02	7.04E-01	8.75E-01	1.00E+00
7906433	---			WT only	0.70	0.94	0.77	0.83	3.22E-02	7.25E-01	4.70E-01	7.09E-01
8007561	NM_138387	G6PC3	glucose 6 phosphatase, catalytic, 3	WT only	0.79	0.93	0.98	0.88	4.69E-02	5.71E-01	9.75E-01	8.21E-01
8036840	NM_001626	AKT2	v-akt murine thymoma viral oncogene homolog 2	WT only	0.78	0.93	0.90	0.86	3.67E-02	5.59E-01	8.16E-01	5.65E-01
7959249	---			WT only	0.69	0.93	0.88	0.88	5.06E-03	5.43E-01	7.66E-01	7.46E-01
7954604	NM_020782	KLHDC5	kelch domain containing 5	WT only	0.74	0.92	0.91	0.87	2.86E-02	5.66E-01	8.44E-01	8.36E-01
8152522	NM_006209	ENPP2	ectonucleotide pyrophosphatase	WT only	1.45	0.92	1.01	1.04	2.41E-02	6.36E-01	9.86E-01	1.00E+00
8000890	NM_012248	SEPHS2	selenophosphate synthetase 2	WT only	1.38	0.92	1.32	1.15	9.28E-03	4.62E-01	1.15E-01	6.27E-01
8163775	NM_001080497	MEGF9	multiple EGF-like-domains 9	WT only	1.40	0.92	1.08	1.02	3.70E-02	6.17E-01	8.94E-01	1.00E+00
7907680	NM_014864	FAM20B	family with sequence similarity 20, member B	WT only	1.33	0.92	1.06	1.05	4.39E-02	5.49E-01	9.13E-01	1.00E+00
8150962	NM_014729	TOX	thymocyte selection-associated high mobility group box	WT only	2.20	0.92	1.66	1.31	1.12E-03	6.68E-01	6.76E-02	4.61E-01
8171762	NM_004586	RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	WT only	1.38	0.92	1.27	1.12	1.64E-02	4.97E-01	3.26E-01	9.92E-01
7999433	---			WT only	0.71	0.91	0.89	0.88	2.16E-02	5.63E-01	8.36E-01	9.63E-01
8135955	NM_001219	CALU	calumenin	WT only	1.28	0.91	1.04	1.06	2.79E-02	4.18E-01	9.27E-01	1.00E+00
7994292	NM_181078	IL21R	interleukin 21 receptor	WT only	0.75	0.91	0.92	0.90	3.73E-02	5.13E-01	8.74E-01	1.00E+00
7929511	NM_001776	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	WT only	1.53	0.91	1.49	1.17	1.92E-02	6.17E-01	1.44E-01	9.63E-01
8010673	NM_012140	SLC25A10	solute carrier family 25 (mitochondrial carrier; dicarboxylate transporter), member 10	WT only	0.74	0.91	0.88	0.86	1.90E-02	4.49E-01	7.93E-01	6.34E-01
8154951	AY513283	GLUL	glutamate-ammonia ligase (glutamine synthetase)	WT only	1.44	0.91	1.27	1.11	7.56E-03	4.44E-01	2.79E-01	9.84E-01
7958216	NM_015275	KIAA1033	KIAA1033	WT only	0.65	0.91	0.75	0.87	5.75E-03	4.91E-01	2.09E-01	8.67E-01
7921637	NM_003874	CD84	CD84 molecule	WT only	1.30	0.91	1.04	1.01	3.59E-02	4.29E-01	9.32E-01	1.00E+00
8039096	NM_144687	NLRP12	NLR family, pyrin domain containing 12	WT only	1.83	0.91	1.54	1.29	2.16E-02	7.35E-01	4.18E-01	8.61E-01
8113664	---			WT only	1.50	0.90	0.87	1.04	1.06E-02	5.04E-01	8.11E-01	1.00E+00
7929344	NM_181745	GPR120	G protein-coupled receptor 120	WT only	0.32	0.90	0.40	0.59	1.24E-02	8.53E-01	2.00E-01	6.28E-01
8038809	NM_005601	NKG7	natural killer cell group 7 sequence	WT only	0.64	0.90	0.95	0.81	5.49E-03	4.81E-01	9.22E-01	4.28E-01
8087833	NM_001947	DUSP7	dual specificity phosphatase 7	WT only	0.73	0.90	0.85	0.84	9.91E-03	3.44E-01	5.45E-01	3.85E-01
7897849	NM_021933	RP5-1077B9.4	invasion inhibitory protein 45	WT only	0.71	0.90	0.94	0.85	1.31E-02	4.24E-01	9.11E-01	6.66E-01
8015526	NM_021078	KAT2A	K(lysine) acetyltransferase 2A	WT only	0.78	0.90	0.93	0.86	4.54E-02	3.60E-01	8.75E-01	6.27E-01
7984317	---			WT only	0.79	0.90	0.87	0.88	4.29E-02	3.38E-01	7.41E-01	7.60E-01
8017210	AK299921	AP1S2	adaptor-related protein complex 1, sigma 2 subunit	WT only	1.55	0.90	1.38	1.19	3.50E-03	3.88E-01	9.60E-02	5.69E-01
8146934	NM_015364	LY96	lymphocyte antigen 96	WT only	1.64	0.90	1.34	1.19	4.09E-02	6.79E-01	7.26E-01	1.00E+00
8058973	NM_005081	ZNF142	zinc finger protein 142	WT only	0.77	0.89	0.88	0.87	1.94E-02	2.59E-01	7.26E-01	5.77E-01
8079294	NM_015004	EXOSC7	exosome component 7	WT only	0.78	0.89	0.95	0.95	4.90E-02	3.31E-01	9.27E-01	1.00E+00
8162194	NM_178432	CCRK	cell cycle related kinase	WT only	0.80	0.89	0.93	0.89	4.98E-02	2.48E-01	8.59E-01	8.65E-01
8157534	NM_007018	CEP110	centrosomal protein 110kDa	WT only	1.43	0.89	1.13	1.15	1.40E-02	3.64E-01	8.24E-01	8.60E-01
7899990	NM_014284	NCDN	neurochondrin	WT only	0.73	0.88	0.85	0.82	9.83E-03	2.41E-01	5.15E-01	2.70E-01
8047467	NM_139158	PFTK2	PFTAIRE protein kinase 2	WT only	4.33	0.88	1.71	1.43	4.17E-05	5.26E-01	7.43E-02	2.81E-01
7996677	NM_005796	NUTF2	nuclear transport factor 2	WT only	0.80	0.88	0.95	0.91	4.74E-02	2.07E-01	9.09E-01	9.85E-01
7931951	NM_001029880	SFMBT2	Scm-like with four mbt domains 2	WT only	0.76	0.87	0.82	0.89	3.13E-02	2.48E-01	4.84E-01	8.98E-01
8024089	NM_024100	WDR18	WD repeat domain 18	WT only	0.75	0.87	0.93	0.89	3.06E-02	2.57E-01	8.81E-01	9.32E-01
8048257	NM_015488	PNKD	paroxysmal nonkinesigenic dyskinesia	WT only	0.75	0.87	0.90	0.86	1.02E-02	1.54E-01	8.02E-01	4.46E-01
8135149	NM_020979	SH2B2	SH2B adaptor protein 2	WT only	0.75	0.87	0.82	0.86	4.11E-02	3.09E-01	6.04E-01	8.38E-01
7907970	XM_001131332	LOC730144	similar to translation initiation factor Eif1	WT only	1.33	0.87	1.11	1.15	4.41E-02	2.74E-01	8.41E-01	8.60E-01
8116096	NM_016222	DDX41	DEAD (Asp-Glu-Ala-Asp) box polypeptide 41	WT only	0.77	0.87	0.89	0.84	4.17E-02	2.21E-01	8.09E-01	5.54E-01
8175438	---			WT only	0.73	0.86	0.94	0.88	4.36E-02	3.32E-01	9.28E-01	1.00E+00
8137517	NM_024012	HTR5A	5-hydroxytryptamine (serotonin) receptor 5A	WT only	0.77	0.86	0.91	0.87	5.00E-02	2.46E-01	8.58E-01	8.63E-01
8146533	NM_147189	FAM110B	family with sequence similarity 110, member B	WT only	1.31	0.86	1.25	1.07	4.49E-02	2.33E-01	4.37E-01	1.00E+00
7934783	NM_015613	LRIT1	leucine-rich repeat, immunoglobulin-like and transmembrane domains 1	WT only	0.76	0.86	0.88	0.86	3.27E-02	2.13E-01	8.01E-01	6.60E-01
7920912	NM_020131	UBQLN4	ubiquilin 4	WT only	0.80	0.86	0.87	0.84	3.00E-02	1.06E-01	6.62E-01	3.05E-01
7999112	NM_016069	Magmas	mitochondria-associated protein involved in granulocyte-macrophage colony-stimula	WT only	0.74	0.86	0.96	0.85	3.29E-02	2.46E-01	9.47E-01	7.45E-01
7922162	NM_006996	SLC19A2	solute carrier family 19 (thiamine transporter), member 2	WT only	0.69	0.86	0.91	0.90	9.21E-03	1.94E-01	8.38E-01	9.98E-01
8012896	NM_000304	PMP22	peripheral myelin protein 22	WT only	1.81	0.86	1.29	1.17	6.90E-03	4.33E-01	6.65E-01	1.00E+00
7927120	NM_020975	RET	ret proto-oncogene	WT only	0.71	0.86	0.87	0.86	2.52E-02	2.70E-01	8.09E-01	8.78E-01
7928558	NM_020338	ZMIZ1	zinc finger, MIZ-type containing 1	WT only	0.77	0.85	0.80	0.80	1.55E-02	1.04E-01	1.83E-01	1.62E-01
7939590	NM_018389	SLC35C1	solute carrier family 35, member C1	WT only	0.73	0.85	0.80	0.80	1.38E-02	1.59E-01	3.07E-01	2.26E-01
7984008	---			WT only	1.48	0.85	1.12	1.21	4.39E-02	4.18E-01	8.80E-01	8.93E-01
8076563	NM_173467	MCAT	malonyl CoA:ACP acyltransferase (mitochondrial)	WT only	0.77	0.85	0.92	0.91	4.19E-02	1.76E-01	8.63E-01	1.00E+00
7945620	NM_019009	TOLLIP	toll interacting protein	WT only	0.78	0.85	0.86	0.87	4.46E-02	1.55E-01	7.26E-01	7.54E-01
8086505	NM_016598	ZDHHC3	zinc finger, DHHC-type containing 3	WT only	0.80	0.85	0.91	0.87	4.16E-02	1.15E-01	8.23E-01	6.27E-01
8160857	NM_005866	SIGMAR1	sigma non-opioid intracellular receptor 1	WT only	0.78	0.85	0.94	0.88	3.10E-02	1.20E-01	8.89E-01	7.57E-01
8020183	NM_014214	IMPA2	inositol(myo)-1(or 4)-monophosphatase 2	WT only	0.75	0.85	0.85	0.89	4.41E-02	2.14E-01	7.40E-01	1.00E+00
8165217	NM_017617	NOTCH1	Notch homolog 1, translocation-associated (Drosophila)	WT only	0.75	0.85	0.78	0.80	2.35E-02	1.52E-01	2.13E-01	2.81E-01

7904211	NM_138959	VANGL1	vang-like 1 (van gogh, Drosophila)	WT only	0.74	0.85	0.85	0.86	2.52E-02	1.76E-01	6.96E-01	7.16E-01
7897685	NM_013319	UBIAD1	UbiA prenyltransferase domain containing 1	WT only	0.76	0.85	0.89	0.86	3.22E-02	1.50E-01	8.16E-01	6.47E-01
8077595	NM_001003694	BRPF1	bromodomain and PHD finger containing, 1	WT only	0.80	0.85	0.85	0.84	3.91E-02	9.50E-02	4.95E-01	3.68E-01
7976726	NM_016337	EVL	Enah	WT only	0.76	0.85	0.92	0.88	4.93E-02	2.05E-01	8.82E-01	9.39E-01
8162455	NM_004148	NINJ1	ninjurin 1	WT only	0.70	0.84	0.87	0.87	2.50E-02	2.36E-01	8.14E-01	9.79E-01
8032871	NM_139159	DPP9	dipeptidyl-peptidase 9	WT only	0.77	0.84	0.82	0.82	2.86E-02	1.14E-01	4.13E-01	3.10E-01
8026895	NM_138442	CCDC124	coiled-coil domain containing 124	WT only	0.80	0.84	0.89	0.85	4.35E-02	9.11E-02	7.90E-01	4.61E-01
7902874	NM_032270	LRRC8C	leucine rich repeat containing 8 family, member C	WT only	0.75	0.84	0.81	0.86	3.59E-02	1.66E-01	4.95E-01	7.09E-01
7949619	NM_001532	SLC29A2	solute carrier family 29 (nucleoside transporters), member 2	WT only	0.69	0.84	0.94	0.83	1.35E-02	1.97E-01	9.17E-01	5.96E-01
7937977	---			WT only	0.77	0.84	0.84	0.86	3.09E-02	1.21E-01	5.70E-01	6.15E-01
7945666	NM_001909	CTSD	cathepsin D	WT only	0.77	0.84	0.86	0.84	3.92E-02	1.24E-01	7.28E-01	5.23E-01
8109283	NM_001543	NDST1	N-deacetylase	WT only	0.73	0.84	0.94	0.85	1.13E-02	9.33E-02	8.81E-01	4.56E-01
7921133	NM_004494	HDGF	hepatoma-derived growth factor (high-mobility group protein 1-like)	WT only	0.80	0.84	0.89	0.87	4.82E-02	7.87E-02	7.97E-01	5.90E-01
8110106	NM_001131055	HRH2	histamine receptor H2	WT only	0.61	0.83	0.71	0.76	2.83E-03	1.55E-01	1.01E-01	2.06E-01
8029437	NM_006505	PVR	poliovirus receptor	WT only	0.78	0.83	0.89	0.90	4.73E-02	1.18E-01	8.14E-01	9.88E-01
7999120	NM_024535	CORO7	coronin 7	WT only	0.80	0.83	0.90	0.85	4.78E-02	7.41E-02	8.01E-01	4.76E-01
8041995	NM_003128	SPTBN1	spectrin, beta, non-erythrocytic 1	WT only	1.27	0.83	1.11	1.07	4.69E-02	9.46E-02	8.23E-01	1.00E+00
8032480	NM_016199	LSM7	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)	WT only	0.72	0.83	0.87	0.78	4.26E-02	2.09E-01	8.23E-01	3.68E-01
7969986	NM_006573	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b	WT only	0.58	0.83	0.73	0.85	3.16E-03	2.04E-01	2.36E-01	8.55E-01
8131374	NM_006303	JTV1	JTV1 gene	WT only	0.76	0.83	0.89	0.86	4.07E-02	1.23E-01	8.16E-01	7.09E-01
8032365	NM_031918	KLF16	Kruppel-like factor 16	WT only	0.72	0.83	0.84	0.80	1.38E-02	1.04E-01	6.29E-01	3.05E-01
7950307	NM_003355	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)	WT only	0.76	0.83	0.98	0.90	1.78E-02	7.49E-02	9.71E-01	8.99E-01
7926037	NM_004566	PFKFB3	6-phosphofructo-2-kinase	WT only	0.78	0.83	0.84	0.87	2.91E-02	7.65E-02	5.15E-01	6.73E-01
8072160	NM_032173	ZNRF3	zinc and ring finger 3	WT only	0.71	0.83	0.89	0.87	6.62E-03	6.94E-02	8.01E-01	5.99E-01
8098877	AK091779	LOC100130872	hypothetical LOC100130872	WT only	0.73	0.83	0.95	0.86	4.19E-02	2.00E-01	9.31E-01	9.05E-01
7954717	NM_001714	BICD1	bicaudal D homolog 1 (Drosophila)	WT only	0.68	0.83	0.85	0.85	4.85E-03	8.59E-02	6.03E-01	5.25E-01
8155699	NM_000144	FXN	frataxin	WT only	0.64	0.83	0.86	0.85	7.96E-03	1.92E-01	8.03E-01	8.13E-01
8072979	NM_021974	POLR2F	polymerase (RNA) II (DNA directed) polypeptide F	WT only	0.76	0.83	0.88	0.83	4.02E-02	1.20E-01	8.13E-01	5.16E-01
8139891	NM_016038	SBDS	Shwachman-Bodian-Diamond syndrome	WT only	0.77	0.83	0.90	0.91	3.78E-02	9.56E-02	8.36E-01	1.00E+00
7900931	NM_003780	B4GALT2	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	WT only	0.77	0.83	0.92	0.86	4.93E-02	1.15E-01	8.71E-01	7.29E-01
8069644	NM_000484	APP	amyloid beta (A4) precursor protein	WT only	0.74	0.83	0.93	0.92	2.68E-02	1.18E-01	8.81E-01	1.00E+00
8128620	NM_001080450	BEND3	BEN domain containing 3	WT only	0.74	0.83	0.89	0.86	4.31E-02	1.59E-01	8.36E-01	8.29E-01
8116532	NR_002591	SNORD95	small nucleolar RNA, C	WT only	0.79	0.83	1.03	0.92	3.95E-02	6.89E-02	9.52E-01	1.00E+00
7982326	NM_015995	KLF13	Kruppel-like factor 13	WT only	0.74	0.82	0.81	0.84	2.42E-02	1.09E-01	4.50E-01	5.42E-01
8149592	NM_001135691	SLC18A1	solute carrier family 18 (vesicular monoamine), member 1	WT only	0.78	0.82	0.93	0.87	4.00E-02	8.63E-02	8.82E-01	7.09E-01
8007084	NM_000964	RARA	retinoic acid receptor, alpha	WT only	0.76	0.82	0.96	0.85	2.70E-02	8.22E-02	9.33E-01	5.83E-01
8107591	NM_207317	ZNF474	zinc finger protein 474	WT only	0.75	0.82	0.94	0.89	4.11E-02	1.39E-01	9.12E-01	9.90E-01
7905349	NM_024575	TNFAIP8L2	tumor necrosis factor, alpha-induced protein 8-like 2	WT only	0.73	0.82	0.77	0.80	3.07E-02	1.44E-01	3.70E-01	4.23E-01
7924853	NM_181462	MRPL55	mitochondrial ribosomal protein L55	WT only	0.75	0.82	0.95	0.88	1.40E-02	5.22E-02	9.06E-01	7.09E-01
8073682	NM_022141	PARVG	parvin, gamma	WT only	0.75	0.82	0.89	0.86	2.51E-02	8.53E-02	8.09E-01	6.92E-01
8135172	NM_001126340	ORAI2	ORAI calcium release-activated calcium modulator 2	WT only	0.65	0.82	0.88	0.82	4.37E-03	9.75E-02	8.01E-01	4.02E-01
7998251	NM_032366	C16orf13	chromosome 16 open reading frame 13	WT only	0.75	0.82	0.93	0.86	3.74E-02	1.11E-01	8.86E-01	7.88E-01
8013120	NM_148172	PEMT	phosphatidylethanolamine N-methyltransferase	WT only	0.74	0.82	1.00	0.88	1.88E-02	7.43E-02	9.99E-01	8.56E-01
8070297	NM_001136154	ERG	v-ets erythroblastosis virus E26 oncogene homolog (avian)	WT only	0.72	0.81	0.92	0.90	3.99E-02	1.52E-01	8.86E-01	1.00E+00
8090591	NM_015103	PLXND1	plexin D1	WT only	0.72	0.81	0.89	0.84	1.48E-02	7.41E-02	8.13E-01	5.28E-01
8030860	NM_001462	FPR2	formyl peptide receptor 2	WT only	0.61	0.81	0.61	0.74	4.70E-02	3.89E-01	2.42E-01	6.43E-01
7941976	NM_002496	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q redu	WT only	0.72	0.81	0.87	0.85	2.79E-02	1.16E-01	8.13E-01	7.29E-01
7988921	NM_000259	MYO5A	myosin VA (heavy chain 12, myoxin)	WT only	0.72	0.81	0.85	0.85	1.54E-02	6.92E-02	6.89E-01	5.88E-01
8029688	NM_012099	CD3EAP	CD3e molecule, epsilon associated protein	WT only	0.74	0.80	0.98	0.88	2.18E-02	6.88E-02	9.72E-01	8.90E-01
7939657	NM_001105540	DGKZ	diacylglycerol kinase, zeta 104kDa	WT only	0.68	0.80	0.97	0.87	3.39E-02	2.00E-01	9.68E-01	1.00E+00
7921319	NM_052938	FCRL1	Fc receptor-like 1	WT only	1.35	0.80	1.45	1.03	2.58E-02	7.36E-02	5.99E-02	1.00E+00
8033332	NR_024075	EMR4P	egf-like module containing, mucin-like, hormone receptor-like 4 pseudogene	WT only	1.44	0.80	0.98	0.97	3.00E-02	1.53E-01	9.82E-01	1.00E+00
8072798	NM_013385	CYTH4	cytohesin 4	WT only	0.70	0.80	0.82	0.87	2.78E-02	1.31E-01	6.88E-01	9.72E-01
8044844	NM_001105198	TMEM177	transmembrane protein 177	WT only	0.75	0.80	0.92	0.86	2.42E-02	5.49E-02	8.63E-01	6.34E-01
8003210	NM_206967	C16orf74	chromosome 16 open reading frame 74	WT only	0.69	0.80	0.88	0.87	4.73E-02	2.00E-01	8.56E-01	1.00E+00
8109350	NM_078483	SLC36A1	solute carrier family 36 (proton	WT only	0.74	0.80	0.73	0.78	3.70E-02	8.38E-02	1.79E-01	2.78E-01
8087210	NM_004157	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	WT only	0.74	0.80	0.87	0.85	3.70E-02	9.11E-02	8.14E-01	7.42E-01
8153424	NM_001100878	C8orf73	chromosome 8 open reading frame 73	WT only	0.64	0.80	0.86	0.82	3.00E-03	5.58E-02	7.36E-01	4.28E-01
8028705	NM_001001563	TIMM50	translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae)	WT only	0.76	0.80	0.91	0.86	3.12E-02	5.44E-02	8.38E-01	6.91E-01
8012349	NM_002616	PER1	period homolog 1 (Drosophila)	WT only	0.75	0.79	0.83	0.79	4.54E-02	8.45E-02	7.12E-01	3.70E-01
8066776	NM_033550	TP53RK	TP53 regulating kinase	WT only	1.61	0.79	1.03	1.06	5.49E-03	9.49E-02	9.72E-01	1.00E+00
8072847	NM_018957	SH3BP1	SH3-domain binding protein 1	WT only	0.72	0.79	0.78	0.80	2.68E-02	7.64E-02	3.97E-01	3.69E-01
8004804	NM_012393	PFAS	phosphoribosylformylglycinamidine synthase	WT only	0.74	0.79	0.89	0.85	4.03E-02	8.52E-02	8.38E-01	7.83E-01
7968890	NM_003646	DGKZ	diacylglycerol kinase, zeta 104kDa	WT only	0.75	0.79	0.84	0.82	4.36E-02	6.83E-02	7.14E-01	5.28E-01
8088958	NM_000158	GBE1	glucan (1,4-alpha-), branching enzyme 1	WT only	0.67	0.79	0.76	0.79	1.92E-02	1.09E-01	4.08E-01	4.78E-01

7927405	NM_020945	WDFY4	WDFY family member 4	WT only	0.64	0.79	0.78	0.80	5.56E-03	7.36E-02	4.13E-01	4.23E-01
8032094	NM_024888	PRG2	plasticity-related gene 2	WT only	0.73	0.79	0.85	0.84	2.45E-02	5.74E-02	7.29E-01	5.96E-01
7940473	NM_016464	TMEM138	transmembrane protein 138	WT only	0.76	0.78	0.94	0.85	4.16E-02	5.01E-02	8.94E-01	6.43E-01
8026982	NM_032683	FKSG24	hypothetical protein MGC12972	WT only	0.72	0.78	0.86	0.78	3.02E-02	7.63E-02	8.01E-01	3.28E-01
8063115	NM_004994	MMP9	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagena	WT only	0.66	0.78	0.74	0.78	3.35E-02	1.70E-01	5.03E-01	6.15E-01
8104180	NM_020731	AHRR	aryl-hydrocarbon receptor repressor	WT only	0.71	0.78	0.73	0.81	2.36E-02	7.44E-02	2.09E-01	5.01E-01
8024572	NM_002068	GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	WT only	0.72	0.78	1.02	0.89	2.36E-02	5.50E-02	9.82E-01	9.88E-01
8132980	---			WT only	0.76	0.78	0.81	0.78	4.83E-02	5.79E-02	5.15E-01	2.74E-01
7901087	NM_032756	HPDL	4-hydroxyphenylpyruvate dioxygenase-like	WT only	0.70	0.78	0.94	0.84	1.33E-02	5.01E-02	9.15E-01	6.27E-01
8071899	NM_000675	ADORA2A	adenosine A2a receptor	WT only	0.73	0.78	0.77	0.84	4.45E-02	7.49E-02	4.14E-01	7.29E-01
7927981	NM_003171	SUPV3L1	suppressor of var1, 3-like 1 (S. cerevisiae)	WT only	0.72	0.78	0.88	0.89	2.78E-02	6.52E-02	8.23E-01	1.00E+00
8004694	NM_144607	CYB5D1	cytochrome b5 domain containing 1	WT only	0.75	0.77	0.89	0.86	3.95E-02	5.01E-02	8.25E-01	8.17E-01
7997059	NM_018332	DDX19A	DEAD (Asp-Glu-Ala-As) box polypeptide 19A	WT only	0.74	0.77	0.88	0.85	4.93E-02	6.58E-02	8.34E-01	7.48E-01
8066697	NM_173179	SLC35C2	solute carrier family 35, member C2	WT only	0.75	0.77	0.87	0.86	4.74E-02	5.30E-02	8.13E-01	7.91E-01
8068833	NM_002606	PDE9A	phosphodiesterase 9A	WT only	0.62	0.77	0.72	0.80	6.81E-03	7.50E-02	2.08E-01	5.28E-01
8115144	NM_001012301	ARSI	arylsulfatase family, member I	WT only	0.73	0.77	0.88	0.83	4.28E-02	6.78E-02	8.32E-01	6.95E-01
8049722	NM_005301	GPR35	G protein-coupled receptor 35	WT only	0.63	0.76	0.85	0.82	1.74E-02	1.04E-01	8.16E-01	7.53E-01
8132305	NM_030636	EEPD1	endonuclease	WT only	0.61	0.76	0.73	0.75	4.95E-03	5.01E-02	2.13E-01	2.30E-01
8143825	NM_000238	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	WT only	1.78	0.76	1.71	1.19	6.90E-03	1.18E-01	5.99E-02	9.72E-01
8153678	NM_015201	BOP1	block of proliferation 1	WT only	0.72	0.75	0.83	0.83	3.56E-02	5.09E-02	7.26E-01	6.60E-01
8066848	NM_020820	PREX1	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 1	WT only	0.67	0.74	0.81	0.80	2.23E-02	6.30E-02	7.24E-01	5.88E-01
8095110	NM_000222	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	WT only	0.58	0.74	0.70	0.77	3.07E-02	2.01E-01	5.43E-01	7.99E-01
8068593	NM_005239	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	WT only	0.61	0.74	0.87	0.85	7.48E-03	5.49E-02	8.36E-01	9.05E-01
8031297	NM_014218	KIR2DL1	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	WT only	0.70	0.74	0.83	0.81	4.17E-02	6.83E-02	7.71E-01	6.86E-01
8041170	---			WT only	0.58	0.74	0.93	0.81	2.31E-02	1.61E-01	9.43E-01	9.45E-01
8084891	NM_153690	FAM43A	family with sequence similarity 43, member A	WT only	0.66	0.74	0.72	0.77	2.40E-02	6.91E-02	3.50E-01	4.56E-01
8022404	NM_001098801	C18orf19	chromosome 18 open reading frame 19	WT only	0.69	0.73	0.80	0.87	4.07E-02	6.00E-02	7.24E-01	1.00E+00
8039842	NM_012312	KIR2DS2	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2	WT only	0.69	0.73	0.82	0.80	3.70E-02	5.10E-02	7.50E-01	6.13E-01
8039829	NM_014219	KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	WT only	0.70	0.73	0.83	0.81	4.39E-02	5.82E-02	7.86E-01	6.96E-01
7928126	NM_014431	KIAA1274	KIAA1274	WT only	0.62	0.72	0.76	0.79	1.45E-02	5.55E-02	5.36E-01	6.08E-01
8166906	NM_001097579	GPR34	G protein-coupled receptor 34	WT only	2.61	0.71	1.37	1.17	5.75E-03	2.38E-01	8.01E-01	1.00E+00
8082035	NM_175862	CD86	CD86 molecule	WT only	0.56	0.69	0.80	0.77	4.06E-02	1.65E-01	8.38E-01	9.39E-01
7953211	NM_020375	C12orf5	chromosome 12 open reading frame 5	WT only	0.54	0.69	0.73	0.76	2.94E-02	1.45E-01	7.52E-01	8.78E-01
8149485	NM_004686	MTMR7	myotubularin related protein 7	WT only	0.64	0.68	0.85	0.82	4.93E-02	6.43E-02	8.55E-01	9.59E-01
8072108	NM_020437	ASPHD2	aspartate beta-hydroxylase domain containing 2	WT only	0.63	0.68	0.86	0.83	4.32E-02	6.76E-02	8.59E-01	1.00E+00
8095626	---			WT only	0.55	0.67	0.61	0.69	2.39E-02	9.10E-02	2.75E-01	4.56E-01
8168517	NM_005296	LPAR4	lysophosphatidic acid receptor 4	WT only	0.61	0.65	0.81	0.80	3.79E-02	5.23E-02	8.23E-01	8.98E-01
8006433	NM_002982	CCL2	chemokine (C-C motif) ligand 2	WT only	0.27	0.44	0.42	0.51	1.16E-02	6.07E-02	3.57E-01	5.00E-01
8136709	NR_003715	LOC93432	maltase-glucoamylase-like pseudogene	WT, delT355, L359V	3.29	3.49	1.45	1.75	3.42E-05	2.95E-05	1.23E-01	1.28E-02
7930454	NM_145341	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	WT, delT355, L359V	1.86	2.09	1.28	1.52	4.30E-04	1.11E-04	2.47E-01	2.05E-02
8012558	NM_014308	PIK3R5	phosphoinositide-3-kinase, regulatory subunit 5	WT, delT355, L359V	0.58	0.66	0.74	0.70	4.79E-04	1.61E-03	8.10E-02	2.91E-02
7906486	NM_020125	SLAMF8	SLAM family member 8	WT, delT355, L359V	0.51	0.47	0.64	0.63	1.11E-03	4.03E-04	5.85E-02	4.44E-02
7905789	NM_000565	IL6R	interleukin 6 receptor	WT, delT355, L359V	0.46	0.34	0.67	0.59	3.09E-04	4.20E-05	6.16E-02	1.27E-02
8151310	NM_000503	EYA1	eyes absent homolog 1 (Drosophila)	WT, T354M and L359V	2.35	3.68	1.90	1.82	1.56E-03	9.38E-05	4.13E-02	5.73E-02
7936050	NM_000102	CYP17A1	cytochrome P450, family 17, subfamily A, polypeptide 1	WT, T354M and L359V	2.93	3.38	2.95	1.99	2.08E-03	7.06E-04	1.25E-02	9.67E-02
8078888	NM_005201	CCR8	chemokine (C-C motif) receptor 8	WT, T354M and L359V	1.94	2.73	1.89	1.64	5.94E-03	4.20E-04	4.30E-02	1.19E-01
7923792	NM_033102	SLC45A3	solute carrier family 45, member 3	WT, T354M and L359V	2.31	2.67	1.71	1.52	2.54E-04	6.68E-05	1.76E-02	5.73E-02
7898407	AK125737	LOC440570	LOC440570	WT, T354M and L359V	3.00	2.63	2.16	1.74	3.09E-04	4.48E-04	1.40E-02	6.58E-02
8014891	NM_012481	IKZF3	IKAROS family zinc finger 3 (Aiolos)	WT, T354M and L359V	3.36	1.95	2.29	1.60	1.41E-04	2.96E-03	1.01E-02	1.17E-01
7969050	NM_020377	CYSLTR2	cysteinyl leukotriene receptor 2	WT, T354M and L359V	3.02	1.95	2.40	1.65	1.52E-03	1.39E-02	3.15E-02	2.70E-01
8024557	NM_002067	GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class)	WT, T354M and L359V	1.57	1.94	1.46	1.45	3.18E-03	2.75E-04	4.79E-02	5.40E-02
8059139	NM_001077198	ATG9A	ATG9 autophagy related 9 homolog A (S. cerevisiae)	WT, T354M and L359V	1.62	1.85	1.44	1.32	1.83E-03	3.35E-04	4.79E-02	1.26E-01
8010778	---			WT, T354M and L359V	1.45	1.78	1.74	1.31	4.68E-02	3.82E-03	4.13E-02	4.71E-01
8138789	NM_175061	JAZF1	JAZF zinc finger 1	WT, T354M and L359V	1.73	1.74	1.50	1.31	1.32E-03	8.19E-04	4.10E-02	1.94E-01
7902810	NM_006769	LMO4	LIM domain only 4	WT, T354M and L359V	2.21	1.46	1.56	1.42	1.17E-04	5.15E-03	1.80E-02	5.73E-02
8002729	NM_012201	GLG1	golgi apparatus protein 1	WT, T354M and L359V	0.74	0.78	0.66	0.84	1.25E-02	2.06E-02	1.64E-02	4.14E-01
7908968	NM_017773	LAX1	lymphocyte transmembrane adaptor 1	WT, T354M and L359V	2.88	0.70	1.72	1.28	5.02E-05	1.65E-02	1.74E-02	3.50E-01
8008646	NM_021626	SCPEP1	serine carboxypeptidase 1	WT, T354M and L359V	0.51	0.65	0.50	0.71	3.96E-03	2.40E-02	1.94E-02	3.05E-01
8106411	NM_130772	S100Z	S100 calcium binding protein Z	WT, T354M and L359V	0.42	0.64	0.51	0.67	3.09E-04	8.41E-03	1.01E-02	9.40E-02
8026456	NM_000896	CYP4F3	cytochrome P450, family 4, subfamily F, polypeptide 3	WT, T354M and L359V	0.63	0.64	0.59	0.68	1.17E-02	8.54E-03	3.17E-02	1.11E-01
8085293	NR_024138	GHRL	ghrelin	WT, T354M and L359V	0.65	0.63	0.66	0.75	7.25E-03	3.40E-03	4.79E-02	2.12E-01
7905571	NM_002965	S100A9	S100 calcium binding protein A9	WT, T354M and L359V	0.57	0.62	0.61	0.69	3.10E-03	4.87E-03	3.85E-02	1.05E-01
8094228	NM_004334	BST1	bone marrow stromal cell antigen 1	WT, T354M and L359V	0.66	0.62	0.65	0.75	2.96E-03	1.01E-03	1.71E-02	8.55E-02
8099760	NM_015230	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2	WT, T354M and L359V	0.47	0.59	0.57	0.70	1.59E-03	6.70E-03	4.13E-02	2.29E-01
7935058	NM_013451	MYOF	myoferlin	WT, T354M and L359V	0.58	0.58	0.59	0.70	1.30E-03	8.25E-04	1.14E-02	5.73E-02

8041467	NM_053276	VIT	vitrin	WT, T354M and L359V	0.58	0.57	0.62	0.72	2.91E-03	1.71E-03	3.14E-02	1.62E-01
7986195	NM_014848	SV2B	synaptic vesicle glycoprotein 2B	WT, T354M and L359V	0.56	0.55	0.56	0.68	8.03E-03	4.43E-03	4.79E-02	2.18E-01
7910387	NM_021205	RHOU	ras homolog gene family, member U	WT, T354M and L359V	0.59	0.51	0.67	0.73	6.07E-04	1.24E-04	1.80E-02	5.73E-02
8051583	NM_000104	CYP1B1	cytochrome P450, family 1, subfamily B, polypeptide 1	WT, T354M and L359V	0.42	0.51	0.37	0.55	5.42E-03	1.35E-02	1.76E-02	1.49E-01
8104492	NM_031916	ROPN1L	ropporin 1-like	WT, T354M and L359V	0.32	0.29	0.43	0.50	1.22E-03	5.59E-04	4.10E-02	8.32E-02
8014160	NM_002981	CCL1	chemokine (C-C motif) ligand 1	WT, T354M and L359V	0.18	0.28	0.27	0.37	1.59E-03	5.33E-03	4.10E-02	1.22E-01
7960900	NM_014358	CLEC4E	C-type lectin domain family 4, member E	WT, T354M and L359V	0.27	0.23	0.41	0.44	8.71E-04	3.10E-04	4.10E-02	5.50E-02
8101780	NM_014485	PGDS	prostaglandin D2 synthase, hematopoietic	WT, T354M, delT355, L359V	13.61	15.38	3.44	3.77	2.32E-05	2.16E-05	9.09E-03	5.30E-03
7995096	NM_000632	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)	WT, T354M, delT355, L359V	3.11	4.13	1.85	1.83	5.02E-05	2.37E-05	1.25E-02	1.22E-02
8085062	NM_000564	IL5RA	interleukin 5 receptor, alpha	WT, T354M, delT355, L359V	5.55	3.98	2.16	2.24	4.90E-05	1.41E-04	3.14E-02	2.12E-02
8083260	NM_001870	CPA3	carboxypeptidase A3 (mast cell)	WT, T354M, delT355, L359V	9.11	3.79	4.37	2.53	3.30E-05	3.55E-04	1.55E-03	2.05E-02
7912802	AK125737	LOC440570	LOC440570	WT, T354M, delT355, L359V	4.35	3.77	2.83	2.09	3.30E-05	4.20E-05	1.54E-03	9.03E-03
7988672	NM_002112	HDC	histidine decarboxylase	WT, T354M, delT355, L359V	3.67	3.61	1.96	1.91	3.83E-05	4.20E-05	1.25E-02	1.22E-02
8022356	NM_001128626	SPIRE1	spire homolog 1 (Drosophila)	WT, T354M, delT355, L359V	2.22	3.30	1.86	1.70	4.79E-04	4.20E-05	1.25E-02	2.45E-02
7963851	NM_001098815	KIAA0748	KIAA0748	WT, T354M, delT355, L359V	2.54	3.19	1.99	1.78	1.17E-04	3.58E-05	4.83E-03	1.07E-02
8097098	NM_019050	USP53	ubiquitin specific peptidase 53	WT, T354M, delT355, L359V	3.12	3.11	1.78	1.82	3.42E-05	3.58E-05	1.25E-02	8.90E-03
7903507	NM_001010883	FAM102B	family with sequence similarity 102, member B	WT, T354M, delT355, L359V	3.31	2.73	1.89	1.78	1.54E-05	2.37E-05	1.55E-03	5.30E-03
8090469	NM_032638	GATA2	GATA binding protein 2	WT, T354M, delT355, L359V	2.81	2.73	2.46	1.88	5.21E-05	5.88E-05	1.23E-03	8.17E-03
7969544	NM_019080	NDFIP2	Nedd4 family interacting protein 2	WT, T354M, delT355, L359V	2.79	2.61	2.01	1.81	6.25E-05	8.06E-05	4.83E-03	9.99E-03
8114536	NM_198282	TMEM173	transmembrane protein 173	WT, T354M, delT355, L359V	2.05	2.41	1.61	1.53	3.09E-04	6.68E-05	1.80E-02	2.91E-02
7983650	NM_003645	SLC27A2	solute carrier family 27 (fatty acid transporter), member 2	WT, T354M, delT355, L359V	3.01	2.23	2.23	1.74	2.32E-05	6.68E-05	7.55E-04	5.30E-03
8037679	NM_004943	DMWD	dystrophia myotonica, WD repeat containing	WT, T354M, delT355, L359V	1.92	2.13	1.38	1.46	1.17E-04	4.20E-05	4.10E-02	1.53E-02
7923131	NM_144977	DENND1B	DENN	WT, T354M, delT355, L359V	2.18	1.70	1.52	1.43	6.55E-05	5.73E-04	1.80E-02	3.96E-02
7923141	NM_144977	DENND1B	DENN	WT, T354M, delT355, L359V	2.07	1.60	1.49	1.41	5.21E-05	5.59E-04	1.25E-02	2.45E-02
7948667	NM_001620	AHNAK	AHNAK nucleoprotein	WT, T354M, delT355, L359V	3.14	1.55	1.69	1.65	3.45E-05	5.88E-03	1.80E-02	2.26E-02
8002403	NM_138383	MTSS1L	metastasis suppressor 1-like	WT, T354M, delT355, L359V	0.43	0.62	0.61	0.65	3.30E-05	5.28E-04	4.39E-03	8.90E-03
8031328	NM_006737	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	WT, T354M, delT355, L359V	0.50	0.55	0.63	0.66	2.93E-04	4.56E-04	1.76E-02	2.65E-02
7932985	NM_003873	NRP1	neuropilin 1	WT, T354M, delT355, L359V	0.46	0.47	0.41	0.57	1.02E-03	8.42E-04	2.74E-03	3.28E-02
8076690	NM_001009880	C22orf9	chromosome 22 open reading frame 9	WT, T354M, delT355, L359V	0.48	0.45	0.65	0.65	2.54E-04	1.03E-04	2.62E-02	2.44E-02
8031374	NM_002000	FCAR	Fc fragment of IgA, receptor for	WT, T354M, delT355, L359V	0.37	0.35	0.52	0.54	6.34E-05	4.97E-05	8.03E-03	8.90E-03
7923547	NM_001276	CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)	WT, T354M, delT355, L359V	0.30	0.30	0.32	0.44	4.90E-05	4.20E-05	7.55E-04	5.30E-03
7920244	NM_002964	S100A8	S100 calcium binding protein A8	WT, T354M, delT355, L359V	0.24	0.17	0.29	0.37	6.25E-05	2.95E-05	1.29E-03	5.30E-03

Supplementary Table 7. GATA2 and other hematopoietic factors: interactions and targets.

GATA2 interacting partners	**Supplementary Reference**
GATA1	3
SPI1 (PU.1)	4
ZFPM1 (FOG1)	5
ZFPM2 (FOG2)	6
LMO2	7
PML	8
ZBTB16 (PLZF)	9
RARA (RARα)	10
FLI1	11
TAL1	7,11
GATA2 target genes	
GATA1	12
RUNX1	13
CEBPA	14,15
FLI1	11
TAL1	11
SPI1 (PU.1)	15,16
Regulators of GATA2 transcription	
GATA1	17
FLI1	11
TAL1	11
CEBPA	14,18
HOXA9	19
EVI1	20
NOTCH1	21

Supplementary Table 8. Primer sequences for HRM analysis of *GATA2* coding exons. Primer sequences were designed using Primer3[2] to span all coding exons and splice junctions. The optimal PCR amplification conditions including $MgCl_2$ concentration and touchdown PCR annealing temperatures are given. Touchdown was performed at 1ºC/cycle until the lower target temperature was achieved, and subsequent annealing was performed at this temperature to a total of 50 cycles.

Primer Name	**Primer Sequence**	**$MgCl_2$ (mM)**	**Touchdown PCR**
GATA2Ex2a(f)	ACCTCGTGGTGGGACTTTGG	2.0	68ºC → 65ºC
GATA2Ex2a(r)	ACCTCGTCTGGAGGCAGCAG		
GATA2Ex2b(f)	CACCCGGCCGTGCTGAAT	2.0	68ºC → 65ºC
GATA2Ex2b(r)	CGCCTGGGTTCTCATCACCA		
GATA2Ex3a(f)	TGATCTTTCTGCCCACCCTGAT	2.0	68ºC → 65ºC
GATA2Ex3a(r)	TACACAGAGAGTGGGCCTCCAG		
GATA2Ex3b(f)	GTGAGCCCCTTCTCCAAGACG	2.0	68ºC → 65ºC
GATA2Ex3b(r)	CGGAAGATGAGGCTGGAGACG		
GATA2Ex3c(f)	CCACCCAAAGAAGTGTCTCCTGA	3.5	68ºC → 63ºC
GATA2Ex3c(r)	GCCGGCACATAGGAGGGGTAG		
GATA2Ex3d(f)	CTGCGCCCAGGCCTAGCTACTAT	3.5	68ºC → 63ºC
GATA2Ex3d(r)	AAAAACGCAAATGCTCCCCTCTT		
GATA2Ex4(f)	GTTAAGCAGGCCCCCGTGT	2.5	68ºC → 63ºC
GATA2Ex4(r)	CCTGTAATTAACCGCCAGCTCCT		
GATA2Exon5(f)	CCTGCTGACGCTGCCTTG	2.5	68ºC → 62ºC
GATA2Exon5(r)	GGTCCCCGTTGGCGTTTC		
GATA2Ex5(f)	TTTAGCCCTCCTTGACTGAGC	2.0	68ºC → 60ºC
GATA2Ex5(r)	CAAGCCAAGCTGGATATTGTG		
GATA2Ex6a(f)	AGGAAGGAACTGGCCCTCTGA	2.0	68ºC → 62ºC
GATA2Ex6a(r)	TGTCCGGAGTGGCTGAAGG		
GATA2Ex6b(f)	GGAGAAGTCATCCCCCTTCAGTG	2.0	68ºC → 61ºC
GATA2Ex6b(r)	CGGTCCTCGACGTCCATCTGTT		
GATA2ΔGTCT(f)	GGCCATGTGTGTCGGTGT	2.0	68ºC → 60ºC
GATA2ΔGTCT(r)	TTCCAGGAGTGCTCACACG		

Supplementary Table 9. Primers for GATA2-responsive promoter or enhancer-luciferase constructs. Underlined are the *Kpn*I, *Bgl*II and *Sfi*I restriction endonuclease sites used for cloning.

Primer Name	Primer Sequence
RUNX1enh-F	GGGGTACCCAGTTTCATGTGGGGGTAGG
RUNX1enh-R	GAAGATCTCTCGTAAATTTTGGCCTCCT
FLI1enh-F	GGGGTACCTCCTCCTCGAAATCTTGCTC
FLI1enh-R	GAAGATCTTAGCTCATCGACCCCTGGTA
LYL1prom-F	CTCTGGCCTAACTGGCCTATGTGATCCTGTAGCCAAGAG
LYL1prom-R	CTCTGGCCGCCGAGGCCCCCAGCACTGTTCTTGCAGCCT
CSF1Rprom-F	CTCTGGCCTAACTGGCCAGATATGCATTACTTTGGAGATTCCAAGG
CSF1Rprom-R	CTCTGGCCGCCGAGGCCCCTCGGTGGGGAAGTGGCA

Supplementary Table 10. Haplotype mapping primers pairs. Primer pairs were designed to amplify regions flanking the site of the GATA2 p.Thr354Met variant. Following PCR amplification, these amplicons were DNA sequenced and the SNPs identified for haplotype analysis.

Primer Name	**5’ Primer Sequence**	**3’ Primer Sequence**
GATA2-SNP1	TGGTTTACAGTACCTGGAAGGAGAAAG	TCCTGGAAGAGGAGCTGTGTGAC
GATA2-SNP3	AAACACAACGTAGGGTGGGCACT	AATGCATCATTTACCACCGCAGAT
GATA2-SNP5	TTGGAGAAAGACCTATGGACAGCAG	TCAGAAAGCTTGGGACACGTCTTTA
GATA2-SNP7	TTAGGTTACAAAGGGAGGGCAAACT	CACCATTTGACCTGGGTGCTTC
GATA2-Exon5	CCTGCTGACGCTGCCTTG	GGTCCCCGTTGGCGTTTC
GATA2-SNP13	ACAGACGAAGGCAACCATTTTTAGA	GCTCCTGTGGCTACGTACAATCAAC
GATA2-SNP15	CTGATCACCAATATTTCATCCATGC	GCAGAGACTTTGAAGACGATTCAGC
GATA2-SNP17	CTGGAGTGCAGACGTGCTATCAT	GGCCACAAAATTCAAACTGTTTACC
GATA2-SNP18	GTCGGCCTTCTTCCCTCTGTTT	AAATAATAGGGTCTGTTGCGGGTTT
GATA2-SNP19	ACAAAAACCTGTCTTCTCTGCCTTG	CTTCTAAGATTGGAGGTGGGTTTGG
GATA2-SNP20	CTCTCCTTTGTGCCAGCCTCCT	CTCTCCTAACTCCTGGAGCTTGTGC

Supplementary Table 11. Primers for GATA2 mutagenesis. Nucleotide changes leading to p.Thr354Met and p.Leu359Val mutations (bold underlined). We also introduced a single silent change (underlined) that generated a *Mfe*I site in p.Thr354Met clones and destroyed a *Nar*I site in p.Leu359Val clones.

Primer Name	Primer Sequence
T354M-F	GCACCTGTTGTGCCAATTGTCAGA**T**GACAACCACCACCTT
T354M-R	AAGGTGGTGGTTGTC**A**TCTGACAATTGGCACAACAGGTGC
L359V-F	ATTGTCAGACGACAACCACCACC**G**TATGGCGACGAAACGCCAACGGGGACCCTGTCT
L359V-R	AGACAGGGTCCCCGTTGGCGTTTCGTCGCCATA**C**GGTGGTGGTTGTCGTCTGACAAT
355delT-F	ATTGTCAGACG|ACCACCACCTTATGGCGCCGAAACGCCAACGGGG
355delT-R	CCCCGTTGGCGTTTCGGCGCCATAAGGTGGTGGT|CGTCTGACAAT

Supplementary Table 12. Primers for generation of *GATA2* and *GATA2*-FLAG tagged cDNAs. Underlined are the *Xba*I restriction endonuclease sites used for cloning.

Primer Name	**Primer Sequence**
KOZAK-GATA2-F	GTTCTAGAGCCACCATGGAGGTGGCGCCGGA
GATA2-FLAG-R	GTTCTAGACTACTTGTCATCGTCGTCCTTGTAGTCGCCCATGGCGGTCACCATGC
GATA2-R	GTTCTAGACTAGCCCATGGCGGTCACCATGC

Supplementary Table 13. Primers for electromobility shift assay (EMSA). GATA binding sites (underlined).

Primer Name	**Primer Sequence**
Human TCRδ enhancer-F	CACTTGATAACAGAAAGTGATAACTCT
Human TCRδ enhancer-R	AGAGTTATCACTTTCTGTTATCAAGTG
GATA Consensus-F	CAGGGACATGATAAGGGAGCCAA
GATA Consensus-R	TTGGCTCCCTTATCATGTCCCTG
Human GM-CSF-153 promoter-F	TCTCTCGTGATAAGGATCCTGGA
Human GM-CSF-153 promoter-R	TCCAGGATCCTTATCACGAGAGA

SUPPLEMENTARY NOTE

a. Clinical information

Pedigree 1. Pedigree 1 with MDS transforming to AML was described in 1983[22]. In 1983 there were six individuals who had been diagnosed with leukemia (one with a prior MDS phase) and three with MDS only. A total of 13 family members have now been diagnosed with leukaemia or related disorders (**Fig. 1a**). The diagnoses are summarized in **Supplementary Table 2** and **3**.

The proband (case 18[22]; III-2) had an underlying psoriasis that began at age 18 years. He also presented in 1978 with a five month history of suppurating lesions consisting of 1 cm diameter ulcers with a purulent discharge. These ulcers were responsive to treatment with prednisolone and were most likely due to a neutrophilic dermatosis such as Sweet's syndrome or Pyroderma gangrenosum, which are often associated with an underlying MDS or AML. Blood and bone marrow analyses at the time confirmed an MDS phenotype that later transformed into AML.

His sister (III-4) also had psoriasis and a six year history of raised erythematous lesions prior to a marrow biopsy in 1979 which revealed moderate hypocellularity and dysplastic myeloid and erythroid cells. In 1982, she presented with ulcerating lesions and her bone marrow was hypoplastic and dysplastic, suggestive of MDS. She later developed AML (after publication[22]). Neither psoriasis nor these ulcerating lesions have been documented for other family members suggesting that they may not be linked to the AML predisposition. The psoriasis may be linked to the chromosome 1q variation identified in case 18 (III-2), as this chromosome has been previously linked to this condition[23]. The ulcerating lesions are likely to be due to a neutrophilic dermatosis associated with the MDS in these two individuals, but not linked to the underlying genetic mutation responsible for the AML predisposition.

Recent analysis of the family indicates that both the son and daughter (IV-1 and IV-2) of the proband developed MDS. IV-1 underwent a bone marrow examination which identified refractory cytopenia with multi-lineage dysplasia. His bone marrow was hypocellular with active erythropoiesis and granulopoiesis, moderate dysplasia with macronormoblastic maturation and inadequate hemoglobinization. Cell counts revealed $3.3x10^9$ cells/l white cells, $121x10^9$ cells/l platelets, scanty neutrophils and less than 5% blasts. One paratrabecular focus of mononuclear cells, which may represent myeloblasts, was identified. Karyotyping revealed monosomy 7 in all cells and trisomy 21 in a small percentage of cells. He underwent a bone marrow transplantation in 2003 at age 26 years and is currently doing well.

The mother of the proband (II-2) also developed MDS-AML, as did her nephew (III-9). Her three sisters (II-4, II-5 and II-9) all developed AML while her mother (I-2) died of unspecified leukemia. Two of the proband’s cousins (III-10 and III-12) died of AML while another cousin (III-13) died of unspecified leukemia.

Pedigree 2. This previously undescribed pedigree consists of five affected individuals over three generations (**Fig. 1a**). Individual I-2 suffered of acute leukemia, II-2 of a not further characterized AML, II-4 and III-4 of MDS with monosomy 7 with II-4 having in addition a trisomy 8.

Individual II-5 was a previously well 24 year old man who presented with pancytopenia, peripheral eosinophilia, and recurrent pneumonia in the year preceding his death in 1971. Two separate bone marrow biopsies were notable for hypercellularity with eosinophilia. Karyotype was not performed. Skin biopsy of the scalp showed evidence of hyperkeratosis, papillomatosis, and inflammation. On his final hospital admission, left lung infiltrates were associated with progressive respiratory compromise and lung biopsy revealed chronic interstitial pneumonitis and fibrosis. A diagnosis of “Atypical CML” was made, in part, on the basis of eosinophilic lung infiltrates. The patient was treated with prednisone for a period before his respiratory status worsened and he developed hepatosplenomegaly. The patient eventually succumbed to an acute hypotensive episode leading to cardiopulmonary arrest.

Pedigree 3. This extensively described pedigree has eleven affected individuals over three generations (**Fig. 1a**)[24]. Individual IV-1 had acute megakaryoblastic leukemia (FAB M7) and was transplanted with his brother's (IV-3) bone marrow when 21 years of age and is still alive 18 years later. IV-3 and IV-5 had MDS, III-1, III-4 and III-6 all had MDS evolving into AML, II-3, II-9 had AML, and II-8 died of a not further specified leukemia. Karyotyped individuals IV-1 and IV-5 showed monosomy 7 in the affected cells with IV-1 also displaying trisomy 8 and t(1q:7p).

Pedigree 4. This previously undescribed pedigree consists of a father and son with MDS. As both father and son had undergone allogeneic bone marrow transplantation (**Supplementary Table 2**), DNA for the sequence analysis was obtained from buccal cells, confirming that the mutation was constitutional.

With the exception of the p.Thr354Met and p.Thr355del mutations, no other sequence changes in the coding region of *GATA2* were found in the families that we screened. Further, in all disease samples tested, p.Thr354Met and p.Thr355del remained heterozygous. Unfortunately, leukaemia-derived material for genetic analysis from the *GATA2* patients studied here was simply unavailable (most patients died within 2 years of diagnosis), thereby prohibiting unequivocal determination of the existence of somatic mutations in the unaffected allele. Also of note, the FLT3-ITD status of p.Thr354Met family members (Pedigree 1, III-13, IV-2; Pedigree 2, III-4; Pedigree 3, III-6; IV-1) was negative.

b. High resolution melt mutation screening. High resolution melt (HRM) analysis on the LC480 Lightcycler (Roche) using a LightCycler® 480 High Resolution Melting Master (Roche) according to the manufacturer's protocol was performed to develop a sensitive screen for mutation detection. Primer pairs were designed across each exon (multiple primer sets were used to span large exons) such that amplicons were no larger than 250 bp (**Supplementary Table 8**). All positive samples containing putative variants were confirmed by DNA sequencing. As a confirmation of the assay for detection of p.Thr354Met mutations, in comparison with DNA sequencing, the HRM assay produced 4% false positives and 0% false negatives (data not shown). All positives were checked by PCR sequencing.

c. Modeling of GATA structure. The human GATA2 C-terminal zinc finger protein sequence was uploaded to Swiss Model (an automated comparative protein modeling server). This generated a GATA2 ZF model based on PDB code:3dfx (mouse Gata3[25]; 97% sequence identity, Fig. 1E; E-value 8.6×10^{-21}). We used the PyMol program to visualise and predict the effects of the p.Thr354Met mutation[26]. The PDB file is available upon request.

d. Determination of genes differentially expressed in the presence of GATA2 mutants. HL-60 cell lines were treated with 100 nM 4HT to turn on GATA2 WT and mutant protein expression. After 24 h, gene expression levels were determined by microarray. Total RNA was purified using the RNeasy protocol (Qiagen) and converted to biotinylated sense DNA as per the Affymetrix Genechip Whole Transcript (WT) Sense Target Labeling Assay manual. Genechips were hybridized overnight at 45ºC for 17 h in an Affymetrix Hybridization oven, washed and scanned using the Affymetrix GSC3000 scanner.

Raw microarray data were normalized with robust multichip average (RMA) methods[27] using aroma.affymetrix analysis[28]. Quality control was assessed using normalized unscaled standard error

(NUSE) plot as implemented in aroma.affymetrix analysis. Batch effect was removed using ComBat analysis[29]. The differential gene expression was determined with the Empirical Bayes and moderated t-statistic using linear model for microarray analysis (LIMMA)[30]. Differential gene expression was adjusted for multiple testing to control the false discovery rate (FDR) using Benjamini-Hochberg method[31]. Genes with FDR $p<0.05$ were considered statistical significant. All statistical analyses were performed using R statistical software.

A number of analyses including ChIP Enrichment Analysis, Motif Activity Response Analysis and Gene Set Enrichment Analysis (see URLs) were performed on these array data. Among the patterns revealed were targets of the MYC oncogene such as numerous ribosomal proteins as a predominant feature for GATA2 WT, but not for p.Thr354Met or p.Thr355del. Indeed, MYC expression in our arrays is down regulated by GATA2 WT, but not by p.Thr354Met or p.Thr355del (**Supplementary Table 6**) consistent with repression of *MYC* by GATA2 WT being abrogated in p.Thr354Met and p.Thr355del.

URLs: ChIP Enrichment Analysis, http://amp.pharm.mssm.edu/lib/chea.jsp; Motif Activity Response Analysis, http://test.swissregulon.unibas.ch/cgi-bin/mara; Gene Set Enrichment Analysis, http://www.broadinstitute.org/gsea/index.jsp.

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