

GENE SYMBOL	GO BIOLOGICAL PROCESS	GO CELLULAR COMPONENT	GO MOLECULAR FUNCTION	P-VALUE	FOLD-CHANGE
KIAA0125				5.81E-08	-5.72
C9orf89	negative regulation of I-kappaB kinase	nucleus	CARD domain binding	1.03E-06	-2.20
SASH3	positive regulation of immunoglobulin production	nucleus		1.71E-06	-2.53
CAT	response to reactive oxygen species	mitochondrion	aminoacylase activity	2.30E-06	-3.15
SEPT11	cell cycle	stress fiber	nucleotide binding	2.48E-06	2.34
SERPINB9	anti-apoptosis	cytoplasm	serine-type endopeptidase inhibitor activity	2.69E-06	3.53
STK32B	protein amino acid phosphorylation		nucleotide binding	3.14E-06	3.43
GFI1B	regulation of transcription during G1 phase of mitoti	intracellular	DNA binding	4.59E-06	-3.23
GABARAPL1		intracellular	protein binding	6.77E-06	-2.53
MED12L	transcription	nucleus	transcription regulator activity	8.66E-06	-4.39
ELF4	natural killer cell proliferation	nucleus	transcription factor activity	1.03E-05	-2.08
NFE2	nucleosome disassembly	nucleus	transcription factor activity	1.23E-05	-2.53
TM6SF1	biological_process	membrane	no biological data available	1.68E-05	3.53
TBXA2R	signal transduction	plasma membrane	receptor activity	2.22E-05	2.52
SDPR		cytoplasm	phosphatidylserine binding	3.32E-05	-3.09
HSPG2	cell adhesion	extracellular region	protein binding	3.40E-05	2.35
TPM1	positive regulation of heart rate by epinephrine i	stress fiber	actin binding	3.70E-05	-2.23
GATM	creatine biosynthetic process	cytoplasm	glycine amidinotransferase activity	4.18E-05	3.58
TBL1X	transcription	nucleus		5.34E-05	2.62
LASS4	regulation of transcription, DNA-dependent	nucleus	transcription factor activity	5.65E-05	2.32
BCAT1	G1	cytoplasm	branched-chain-amino-acid transaminase activity	6.87E-05	2.05
PDGFC	activation of transmembrane receptor protein tyrosine	extracellular region	platelet-derived growth factor receptor binding	7.67E-05	2.07
GBGT1	carbohydrate metabolic process	Golgi membrane	transferase activity, transferring hexosyl groups	8.19E-05	-2.44
NIPA1		membrane		9.20E-05	-2.54
LPXN	protein complex assembly	cytoplasm	zinc ion binding	0.000118028	-2.17
ADRA2C	activation of MAPK activity	endosome	receptor activity	0.000144705	2.40

CPEB2	regulation of translation	cytoplasm	nucleotide binding	0.000155393	-2.68
CD82		plasma membrane	protein binding	0.000180677	-2.16
CPNE7	lipid metabolic process		transporter activity	0.00019641	2.18
C6orf150				0.000204209	2.36
PXK	protein amino acid phosphorylation	cytoplasm	nucleotide binding	0.000204814	2.30
KCNH8	two-component signal transduction system (phosphorela	membrane	two-component sensor activity	0.000229385	2.35
MAP2K6	activation of MAPK activity		nucleotide binding	0.000262006	-2.01
HIST1H2BM	nucleosome assembly	nucleosome	DNA binding	0.000262673	4.05
MAP7	microtubule cytoskeleton organization	cytoplasm	structural molecule activity	0.000278934	-2.67
ATXN1	RNA processing	nucleus	RNA binding	0.000279414	-2.38
TPSD1	proteolysis	extracellular region	serine-type endopeptidase activity	0.000288331	2.44
HOXA3	blood vessel remodeling	nucleus	transcription factor activity	0.000329629	-3.17
LRP3	receptor-mediated endocytosis	coated pit	receptor activity	0.000342964	2.20
FUT7	protein amino acid glycosylation	Golgi apparatus	transferase activity, transferring glycosyl groups	0.00035261	-2.65
HOXA2	negative regulation of transcription from RNA polymer	nucleus	transcription factor activity	0.000389982	-3.28
UHRF1	DNA repair	nucleus	transcription factor activity	0.000391989	3.09
DNAH8	ciliary or flagellar motility	cytoplasm	nucleotide binding	0.000392471	2.67
GPR132	G1	plasma membrane	receptor activity	0.000408561	-2.17
PDGFD	cell proliferation	extracellular region	growth factor activity	0.000430734	-2.93
CXCL2	chemotaxis	extracellular region	chemokine activity	0.000444284	-3.14
HOXB3	regulation of transcription, DNA-dependent	nucleus	transcription factor activity	0.000461024	-4.93
NTNG2	multicellular organismal development	proteinaceous extracellular matrix	no biological data available	0.000469593	2.09
KIT	myeloid leukocyte differentiation	extracellular space	nucleotide binding	0.000507242	3.28
CYP7B1	lipid metabolic process	endoplasmic reticulum	monooxygenase activity	0.000607808	-3.09
TLR2	response to molecule of fungal origin	plasma membrane	lipopolysaccharide receptor activity	0.000747629	2.61
HOXB4	negative regulation of transcription from RNA polymer	nucleus	transcription factor activity	0.000791581	-2.53
HOXA4	regulation of transcription, DNA-dependent	nucleus	transcription factor activity	0.000801101	-3.41
PLCL1	lipid metabolic process	cytoplasm	phosphoinositide	0.000807905	-2.14

			phospholipase C activity		
CCL28	chemotaxis	extracellular region	chemokine activity	0.000835078	2.38
SYTL4	transport	plasma membrane	transporter activity	0.000904193	-2.11
ELL2	transcription	nucleus	RNA polymerase II transcription factor activity	0.000968956	-2.24
HOXB5	regulation of transcription, DNA-dependent	nucleus	transcription factor activity	0.00100033	-3.73
TRERF1	transcription	intracellular	transcription factor activity	0.00100373	2.40
C9orf95	pyridine nucleotide biosynthetic process		nucleotide binding	0.00103088	-2.04
HS3ST3B1	heparan sulfate proteoglycan biosynthetic process,	Golgi membrane	sulfotransferase activity	0.00105888	2.54
SERPINB10		nucleus	serine-type endopeptidase inhibitor activity	0.00108965	3.02
BST2	humoral immune response	Golgi apparatus	signal transducer activity	0.00109661	-2.68
HOXB8	regulation of transcription, DNA-dependent	nucleus	transcription factor activity	0.00118619	-3.78
FBLN5	cell adhesion	extracellular region	integrin binding	0.00123704	4.64

Table 13 List of 66 genes unique to the exon array analysis.