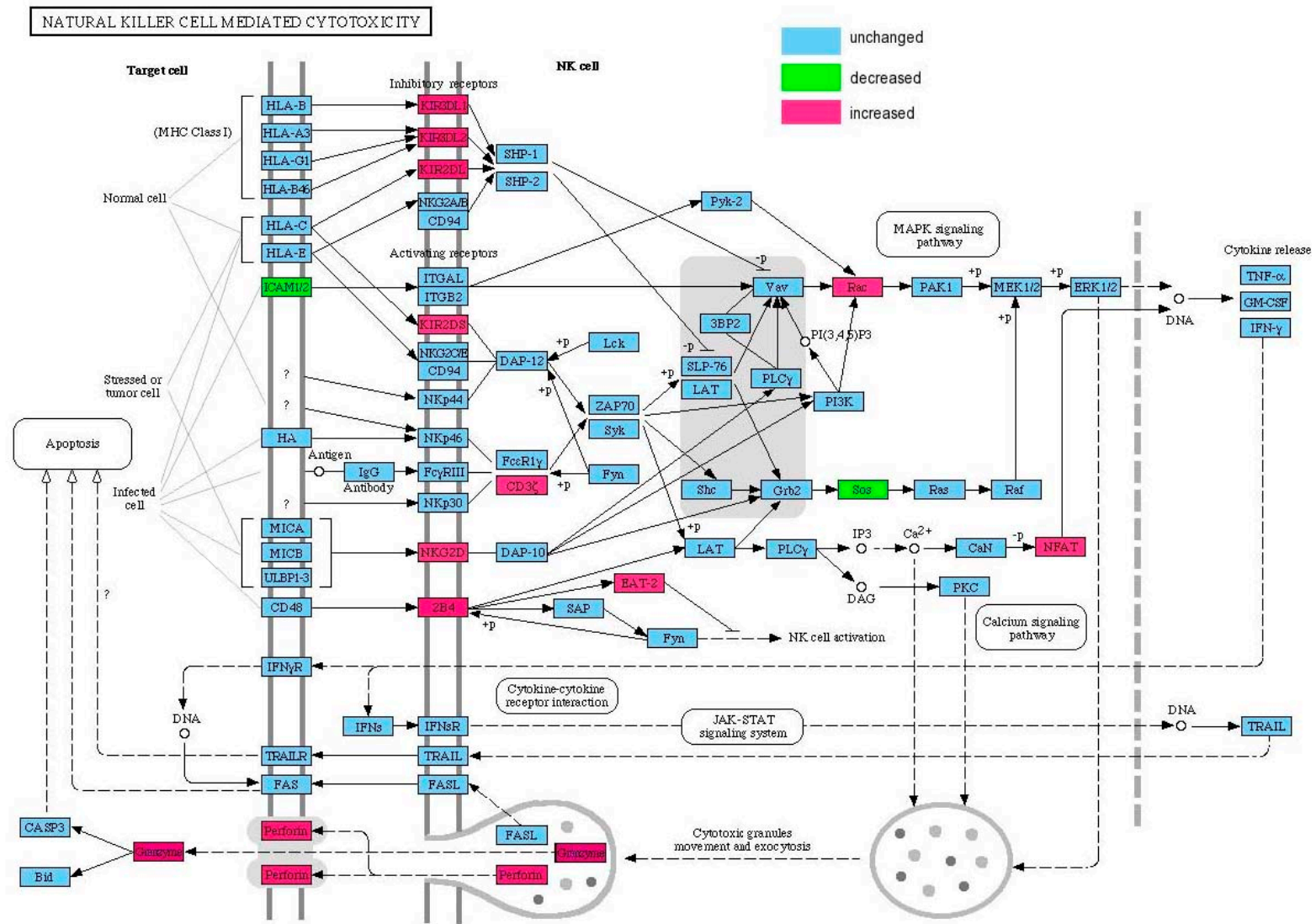


## Supplemental Material

**Figure 1.** Components of the KEGG Natural Killer Cell Mediated Cytotoxicity pathway modified by arsenic exposure. Genes with statistically significant expression differences were mapped to the KEGG pathway. Colored shapes show increased expression (pink), decreased expression (green), or no statistically significant expression change (blue).

**Table 1.** Listing of all SAM-selected probes.

**Table 2.** Listing of all urinary arsenic SAM-selected probes.



**Supplemental Material, Figure 1.** Components of the KEGG Natural Killer Cell Mediated Cytotoxicity pathway modified by arsenic exposure.

Supplemental Material, Table 1. All SAM-selected probes for high vs. low arsenic exposure.

Probe	Symbol	Description	Fold Change	Chromosome	Chromosome Location	GenBank	LocusLink	Cytoband	UniGene	PubMed	Gene Ontology	Pathway
<a href="#">203290_at</a>	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	3.38	6	32713160	<a href="#">NM_002122</a>	<a href="#">3117</a>	<a href="#">6p21.3</a>	<a href="#">Hs.387679</a>	<a href="#">70</a>	<a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">207314_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	2.25	19	60053740	<a href="#">NM_006737</a>	<a href="#">3812</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	<a href="#">19</a>	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">1553177_at</a>	SH2D1B	SH2 domain containing 1B	2.03	1	-160631679	<a href="#">BC022407</a>	<a href="#">117157</a>	<a href="#">1q21</a>	<a href="#">Hs.350581</a>	<a href="#">10</a>	<a href="#">biological process unknown</a> <a href="#">molecular function unknown</a> <a href="#">intracellular signaling cascade</a> <a href="#">cellular component unknown</a>	<a href="#">Natural killer cell mediated</a> <a href="#">cytotoxicity</a>
<a href="#">212509_s_at</a>	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	1.94	2	161873185	<a href="#">BF968134</a>	<a href="#">10213</a>	<a href="#">2q24.2</a>	<a href="#">Hs.567410</a>	<a href="#">3</a>	<a href="#">proteasome complex (sensu Eukaryota)</a> <a href="#">cytosol</a> <a href="#">ubiquitin-dependent protein catabolism</a>	<a href="#">Proteasome</a>
<a href="#">211389_x_at</a>	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	1.88	19	59989604	<a href="#">U73396</a>	<a href="#">3811</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a> <a href="#">Hs.643606</a>	<a href="#">32</a>	<a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">natural killer cell activation</a> <a href="#">negative regulation of natural killer cell activity</a> <a href="#">MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">208179_x_at</a>	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	1.82	19	59941785	<a href="#">AF022048</a>	<a href="#">3804</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	<a href="#">24</a>	<a href="#">biological process unknown</a> <a href="#">antigen binding</a> <a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">molecular function unknown</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">cellular component unknown</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
											<a href="#">regulation of progression through cell cycle</a>  <a href="#">nucleotide binding</a> <a href="#">protein-tyrosine kinase activity</a> <a href="#">protein-tyrosine kinase activity</a> <a href="#">protein binding</a>	<a href="#">Regulation of actin cytoskeleton</a> <a href="#">Epithelial cell signaling in</a> <a href="#">Helicobacter pylori infection</a>

<a href="#">206267_s_at</a>	MATK	megakaryocyte-associated tyrosine kinase	1.78	19	-3728967	<a href="#">NM_002378</a>	<a href="#">4145</a>	<a href="#">19p13.3</a>	<a href="#">Hs.631845</a>	<a href="#">28</a>	<a href="#">ATP binding</a> <a href="#">soluble fraction</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">intracellular signaling cascade</a> <a href="#">mesoderm development</a> <a href="#">cell proliferation</a> <a href="#">positive regulation of cell proliferation</a> <a href="#">transferase activity</a>	
<a href="#">210890_x_at</a>	KIR2DL1	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	1.78	19	59973076	<a href="#">U24078</a>	<a href="#">3802</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a> <a href="#">Hs.643606</a>	<a href="#">29</a>	<a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">negative regulation of natural killer cell activity</a> <a href="#">HLA-C specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">212843_at</a>	NCAM1	neural cell adhesion molecule 1	1.77	11	112337367	<a href="#">AA126505</a>	<a href="#">4684</a>	<a href="#">11q23.1</a>	<a href="#">Hs.503878</a>	<a href="#">65</a>	<a href="#">protein binding</a> <a href="#">plasma membrane</a> <a href="#">cell adhesion</a> <a href="#">cell adhesion</a> <a href="#">cell-cell signaling</a> <a href="#">synaptic transmission</a> <a href="#">nervous system development</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">cell differentiation</a> <a href="#">GPI anchor binding</a>	<a href="#">Cell adhesion molecules (CAMs)</a>
<a href="#">211688_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	1.75	19	60053740	<a href="#">AF263617</a>	<a href="#">3812</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	<a href="#">19</a>	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">211397_x_at</a>	KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	1.74	19	164614	<a href="#">L76669</a>	<a href="#">3803</a>	<a href="#">19q13.4</a>	<a href="#">Hs.643606</a>	<a href="#">18</a>	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">1553681_a_at</a>	PRF1	perforin 1 (pore forming protein)	1.74	10	-72027110	<a href="#">NM_005041</a>	<a href="#">5551</a>	<a href="#">10q22</a>	<a href="#">Hs.2200</a>	<a href="#">44</a>	<a href="#">calcium ion binding</a> <a href="#">cytosol</a> <a href="#">virus-infected cell apoptosis</a> <a href="#">transformed cell apoptosis</a> <a href="#">cellular defense response</a> <a href="#">pathogenesis</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">cytolysis</a> <a href="#">hemolysis of host red blood cells</a>	<a href="#">Natural killer cell mediated Type I diabetes mellitus</a>
<a href="#">212599_at</a>	AUTS2	autism susceptibility candidate 2	1.72	7	68702254	<a href="#">AK025298</a>	<a href="#">26053</a>	<a href="#">7q11.22</a>	<a href="#">Hs.21631</a>	<a href="#">5</a>	<a href="#">biological process unknown</a> <a href="#">serine-type endopeptidase inhibitor activity</a> <a href="#">molecular function unknown</a> <a href="#">cellular component unknown</a>	

<a href="#">216676_x_at</a>	KIR3DL3	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	1.68	19	59927795	<a href="#">AC006293</a>	115653	19q13.42	Hs.512572	4		<a href="#">Antigen processing and presentation</a>
<a href="#">216907_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	1.65	19	60053740	<a href="#">X93596</a>	3812	19q13.4	Hs.512572	19	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and presentation</a> <a href="#">Natural killer cell mediated</a>
<a href="#">205547_s_at</a>	TAGLN	transgelin	1.58	11	116575249	<a href="#">NM_003186</a>	6876	11q23.2	Hs.632099	18	<a href="#">actin binding</a> <a href="#">muscle development</a> <a href="#">muscle development</a>	
<a href="#">208203_x_at</a>	KIR2DS5	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5	1.57	19	240823	<a href="#">NM_014513</a>	3810	19q13.4	Hs.643606	6	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">HLA-C specific inhibitory MHC class I</a> <a href="#">receptor activity</a>	<a href="#">Antigen processing and presentation</a>
<a href="#">205291_at</a>	IL2RB	interleukin 2 receptor, beta	1.55	22	-35851827	<a href="#">NM_000878</a>	3560	22q13 22q13.1	Hs.474787	54	<a href="#">receptor activity</a> <a href="#">hematopoietin/interferon-class (D200-domain) cytokine receptor activity</a> <a href="#">interleukin-2 receptor activity</a> <a href="#">plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">protein complex assembly</a> <a href="#">signal transduction</a> <a href="#">external side of plasma membrane</a> <a href="#">cytokine and chemokine mediated signaling pathway</a> <a href="#">positive regulation of survival gene</a> <a href="#">product activity</a>	<a href="#">Cytokine-cytokine receptor</a> <a href="#">Jak-STAT signaling pathway</a>
<a href="#">207419_s_at</a>	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)	1.55	22	-35951257	<a href="#">NM_002872</a>	5880	22q13.1	Hs.517601	34	<a href="#">nucleotide binding</a> <a href="#">GTPase activity</a> <a href="#">protein binding</a> <a href="#">GTP binding</a> <a href="#">intracellular</a> <a href="#">signal transduction</a> <a href="#">small GTPase mediated signal transduction</a>	<a href="#">MAPK signaling pathway</a> <a href="#">Wnt signaling pathway</a> NA <a href="#">Axon guidance</a> <a href="#">Focal adhesion</a> <a href="#">Adherens junction</a> <a href="#">Natural killer cell mediated</a> <a href="#">cytotoxicity</a> <a href="#">B cell receptor signaling</a> <a href="#">Fc epsilon RI signaling pathway</a> <a href="#">Leukocyte transendothelial</a> <a href="#">Regulation of actin cytoskeleton</a> NA
<a href="#">214617_at</a>	PRF1	perforin 1 (pore forming protein)	1.53	10	-72027110	<a href="#">AI445650</a>	5551	10q22	Hs.2200	44	<a href="#">calcium ion binding</a> <a href="#">cytosol</a> <a href="#">virus-infected cell apoptosis</a> <a href="#">transformed cell apoptosis</a> <a href="#">cellular defense response</a> <a href="#">pathogenesis</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">cytolysis</a> <a href="#">hemolysis of host red blood cells</a>	<a href="#">Natural killer cell mediated</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">221267_s_at</a>	FAM108A1	family with sequence similarity 108, member A1	1.52	19	-1827975	<a href="#">NM_031213</a>	81926	19p13.3	Hs.465542 Hs.559579	3		
<a href="#">242644_at</a>	TMC8	transmembrane channel-like 8	1.51	17	73638463	<a href="#">BE676000</a>	147138	17q25.3	Hs.592102	3	<a href="#">endoplasmic reticulum</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	

<a href="#">228854_at</a>			1.49			<a href="#">AI492388</a>																				
<a href="#">226796_at</a>	LOC116236		1.49	17	-24912437	<a href="#">AI817418</a>	<a href="#">116236</a>	<a href="#">17q11.2</a>	<a href="#">Hs.106510</a>	<a href="#">3</a>																
<a href="#">211410_x_at</a>	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic	1.49	19	229379	<a href="#">AF217487</a>	<a href="#">57292</a>	<a href="#">19p13.3</a>	<a href="#">Hs.643606</a>	<a href="#">8</a>	<a href="#">receptor activity</a>	<a href="#">transmembrane receptor activity</a>	<a href="#">receptor signaling protein activity</a>	<a href="#">protein binding</a>	<a href="#">cytoplasm</a>	<a href="#">plasma membrane</a>	<a href="#">cell surface receptor linked signal transduction</a>	<a href="#">membrane</a>	<a href="#">integral to membrane</a>	<a href="#">T cell receptor complex</a>	<a href="#">protein homodimerization activity</a>	<a href="#">Antigen processing and presentation</a>	<a href="#">Natural killer cell mediated</a>	<a href="#">T cell receptor signaling</a>		
<a href="#">210031_at</a>	CD247	CD247 molecule	1.48	1	-165666507	<a href="#">J04132</a>	<a href="#">919</a>	<a href="#">1q22-q23</a>	<a href="#">Hs.156445</a>	<a href="#">95</a>																
<a href="#">208657_s_at</a>	9-Sep	septin 9	1.47	17	72827743	<a href="#">AF142408</a>	<a href="#">10801</a>	<a href="#">17q25</a>	<a href="#">Hs.440932</a>	<a href="#">21</a>																
<a href="#">221745_at</a>	WDR68	WD repeat domain 68	1.46	17	58981553	<a href="#">BE538424</a>	<a href="#">10238</a>	<a href="#">17q23.3</a>	<a href="#">Hs.410596</a>	<a href="#">7</a>	<a href="#">protein binding</a>	<a href="#">cytoplasm</a>														
<a href="#">207313_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	1.45	19	60053740	<a href="#">L76666</a>	<a href="#">3812</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	<a href="#">19</a>	<a href="#">receptor activity</a>	<a href="#">integral to plasma membrane</a>	<a href="#">cellular defense response</a>	<a href="#">membrane</a>	<a href="#">nucleotide binding</a>	<a href="#">protein serine/threonine kinase activity</a>	<a href="#">ATP binding</a>	<a href="#">intracellular</a>	<a href="#">protein amino acid phosphorylation</a>	<a href="#">intracellular signaling cascade</a>	<a href="#">zinc ion binding</a>	<a href="#">transferase activity</a>	<a href="#">diacylglycerol binding</a>	<a href="#">metal ion binding</a>	<a href="#">Antigen processing and presentation</a>	<a href="#">Natural killer cell mediated</a>
<a href="#">38269_at</a>	PRKD2	protein kinase D2	1.44	19	-51869413	<a href="#">AL050147</a>	<a href="#">25865</a>	<a href="#">19q13.3</a>	<a href="#">Hs.466987</a>	<a href="#">14</a>	<a href="#">protein binding</a>	<a href="#">nucleus</a>	<a href="#">transcription</a>	<a href="#">regulation of transcription, DNA-dependent</a>	<a href="#">development</a>	<a href="#">organ morphogenesis</a>	<a href="#">Wnt receptor signaling pathway</a>									
<a href="#">217729_s_at</a>	AES	amino-terminal enhancer of split	1.43	19	-3003907	<a href="#">NM_001130</a>	<a href="#">166</a>	<a href="#">19p13.3</a>	<a href="#">Hs.515053</a>	<a href="#">20</a>	<a href="#">sugar binding</a>	<a href="#">integral to plasma membrane</a>	<a href="#">cell surface receptor linked signal transduction</a>	<a href="#">membrane</a>	<a href="#">antimicrobial humoral response (sensu Vertebrata)</a>	<a href="#">MHC class I receptor activity</a>										
<a href="#">220646_s_at</a>	KLRF1	killer cell lectin-like receptor subfamily F, member 1	1.43	12	9871343	<a href="#">NM_016523</a>	<a href="#">51348</a>	<a href="#">12p12.3-13.2</a>	<a href="#">Hs.183125</a>	<a href="#">4</a>	<a href="#">nucleic acid binding</a>	<a href="#">transcription factor activity</a>	<a href="#">intracellular</a>	<a href="#">nucleus</a>	<a href="#">transcription</a>	<a href="#">regulation of transcription, DNA-dependent</a>	<a href="#">zinc ion binding</a>									

<a href="#">213639_s_at</a>	ZNF500	zinc finger protein 500	1.42	16	-4740815	<a href="#">AI871396</a>	<a href="#">26048</a>	<a href="#">16p13.3</a>	<a href="#">Hs.513316</a>	6	<a href="#">metal ion binding</a> <a href="#">nucleotide binding</a> <a href="#">GTPase activity</a> <a href="#">GTP binding</a> <a href="#">immune response</a> <a href="#">membrane</a>	
<a href="#">238581_at</a>	GBP5	guanylate binding protein 5	1.41	1	-89498852	<a href="#">BG271923</a>	<a href="#">115362</a>	<a href="#">1p22.2</a>	<a href="#">Hs.513726</a>	8	<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nuclear pore</a> <a href="#">mRNA processing</a> <a href="#">mRNA export from nucleus</a> <a href="#">protein targeting</a> <a href="#">protein transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">212316_at</a>	NUP210	nucleoporin 210kDa	1.40	3	-13332736	<a href="#">AA502912</a>	<a href="#">23225</a>	<a href="#">3p25.1</a>	<a href="#">Hs.475525</a>	19	<a href="#">biological process unknown</a> <a href="#">integral to membrane of membrane fraction</a> <a href="#">structural constituent of ribosome</a> <a href="#">ion channel activity</a> <a href="#">molecular function unknown</a> <a href="#">intracellular</a> <a href="#">ribosome</a> <a href="#">protein biosynthesis</a> <a href="#">ion transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">213395_at</a>	MLC1	megalencephalic leukoencephalopathy with subcortical cysts 1	1.40	22	-48839946	<a href="#">AL022327</a>	<a href="#">23209</a>	<a href="#">22q13.33</a>	<a href="#">Hs.517729</a>	26	<a href="#">biological process unknown</a> <a href="#">integral to membrane of membrane fraction</a> <a href="#">structural constituent of ribosome</a> <a href="#">ion channel activity</a> <a href="#">molecular function unknown</a> <a href="#">intracellular</a> <a href="#">ribosome</a> <a href="#">protein biosynthesis</a> <a href="#">ion transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">202481_at</a>	DHRS3	dehydrogenase/reductase (SDR family) member 3	1.40	1	-12550526	<a href="#">NM_004753</a>	<a href="#">9249</a>	<a href="#">1p36.1</a>	<a href="#">Hs.289347</a>	6	<a href="#">nucleotide binding</a> <a href="#">visual perception</a> <a href="#">metabolism</a> <a href="#">electron carrier activity</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">oxidoreductase activity</a> <a href="#">retinol metabolism</a>	<a href="#">gamma-Hexachlorocyclohexane degradation</a> <a href="#">Bisphenol A degradation</a> <a href="#">1- and 2-Methylnaphthalene</a> <a href="#">Benzoate degradation via CoA</a> <a href="#">Ethylbenzene degradation</a> <a href="#">Limonene and pinene</a>
<a href="#">225803_at</a>	FBXO32	F-box protein 32	1.39	8	-124584539	<a href="#">AW006123</a>	<a href="#">114907</a>	<a href="#">8q24.13</a>	<a href="#">Hs.403933</a>	8	<a href="#">ubiquitin cycle</a>	
<a href="#">225175_s_at</a>	SLC44A2	solute carrier family 44, member 2	1.39	19	10597228	<a href="#">AI569503</a>	<a href="#">57153</a>	<a href="#">19p13.1</a>	<a href="#">Hs.631631</a>	8	<a href="#">signal transducer activity</a> <a href="#">transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">positive regulation of I-kappaB kinase/NF-kappaB cascade</a>	
<a href="#">205821_at</a>	KLRK1	killer cell lectin-like receptor subfamily K,	1.38	12	-10416219	<a href="#">NM_007360</a>	<a href="#">22914</a>	<a href="#">12p13.2-p12.3</a>	<a href="#">Hs.387787</a>	47		<a href="#">Natural killer cell mediated cytotoxicity</a>
<a href="#">226401_at</a>	PARP10	poly (ADP-ribose) polymerase family, member 10	1.37	8	-145123315	<a href="#">AL040631</a>	<a href="#">84875</a>	<a href="#">8q24.3</a>	<a href="#">Hs.348609</a>	10	<a href="#">nucleotide binding</a> <a href="#">NAD+ ADP-ribosyltransferase activity</a> <a href="#">nucleus</a> <a href="#">protein amino acid ADP-ribosylation</a> <a href="#">transmembrane receptor activity</a> <a href="#">lipid transporter activity</a> <a href="#">integral to plasma membrane</a> <a href="#">lipid metabolism</a> <a href="#">lipid transport</a> <a href="#">intracellular protein transport</a> <a href="#">receptor mediated endocytosis</a> <a href="#">steroid metabolism</a>	

<a href="#">203509_at</a>	SORL1	sortilin-related receptor, L(DLR class) A repeats-containing	1.36	11	120828129	<a href="#">NM_003105</a>	6653	<a href="#">11q23.2-q24.2</a>	<a href="#">Hs.368592</a>	17	<a href="#">cholesterol metabolism</a> <a href="#">protein transporter activity</a> <a href="#">membrane</a>	
<a href="#">211242_x_at</a>	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	1.36	19	60006877, 199896	<a href="#">AF276292</a>	3805	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	30	<a href="#">receptor activity</a> <a href="#">transmembrane receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">signal transduction</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">1552667_a_at</a>	SH2D3C	SH2 domain containing 3C	1.35	9	-129540845, -129540418	<a href="#">NM_005489</a>	10044	<a href="#">9q34.11</a>	<a href="#">Hs.306412</a>	12	<a href="#">guanyl-nucleotide exchange factor</a> <a href="#">intracellular</a> <a href="#">intracellular signaling cascade</a> <a href="#">small GTPase mediated signal transduction</a>	
<a href="#">43511_s_at</a>			1.35			<a href="#">AI201594</a>						
<a href="#">213947_s_at</a>	NUP210	nucleoporin 210kDa	1.35	3	-13332736	<a href="#">AI867102</a>	23225	<a href="#">3p25.1</a>	<a href="#">Hs.475525</a>	19	<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nuclear pore</a> <a href="#">mRNA processing</a> <a href="#">mRNA export from nucleus</a> <a href="#">protein targeting</a> <a href="#">protein transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">221861_at</a>			1.35			<a href="#">AL157484</a>						
<a href="#">208198_x_at</a>	KIR2DS1	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	1.34	19	257787	<a href="#">NM_014512</a>	3806	<a href="#">19q13.4</a>	<a href="#">Hs.643606</a>	17	<a href="#">transmembrane receptor activity</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">212256_at</a>	GALNT10	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	1.33	5	153763529, 153550487	<a href="#">BE906572</a>	55568	<a href="#">5q33.2</a>	<a href="#">Hs.432818</a> <a href="#">Hs.631797</a>	7	<a href="#">polypeptide N-acetylgalactosaminyltransferase activity</a> <a href="#">calcium ion binding</a> <a href="#">sugar binding</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">transferase activity, transferring glycosyl groups</a> <a href="#">manganese ion binding</a>	<a href="#">O-Glycan biosynthesis</a> <a href="#">Glycan structures - biosynthesis</a>
<a href="#">212605_s_at</a>			1.33			<a href="#">AK025759</a>						
<a href="#">207416_s_at</a>	NFATC3	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3	1.33	16	66676875	<a href="#">NM_004555</a>	4775	<a href="#">16q22.2</a>	<a href="#">Hs.632209</a>	23	<a href="#">transcription factor activity</a> <a href="#">transcription coactivator activity</a> <a href="#">nucleus</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">regulation of transcription from RNA polymerase II promoter</a> <a href="#">inflammatory response</a>	<a href="#">Wnt signaling pathway</a> <a href="#">NA</a> <a href="#">Axon guidance</a> <a href="#">Natural killer cell mediated cytotoxicity</a> <a href="#">T cell receptor signaling pathway</a> <a href="#">B cell receptor signaling</a>
<a href="#">219566_at</a>	PLEKHF1	pleckstrin homology domain containing, family F (with FYVE domain)	1.32	19	34847802	<a href="#">NM_024310</a>	79156	<a href="#">19q12</a>	<a href="#">Hs.466383</a>	6		
<a href="#">221744_at</a>	WDR68	WD repeat domain 68	1.31	17	58981553	<a href="#">AK026008</a>	10238	<a href="#">17q23.3</a>	<a href="#">Hs.410596</a>	7	<a href="#">protein binding</a> <a href="#">cytoplasm</a> <a href="#">binding</a> <a href="#">nucleus</a> <a href="#">DNA repair</a> <a href="#">transcription</a>	



<a href="#">202167_s_at</a>	MMS19L	MMS19-like (MET18 homolog, <i>S. cerevisiae</i> )	1.30	10	-99208070	<a href="#">NM_022362</a>	<a href="#">64210</a>	<a href="#">10q24-q25</a>	<a href="#">Hs.500721</a>	10	<a href="#">regulation of transcription, DNA-dependent</a>	
<a href="#">226598_s_at</a>	GTPBP5	GTP binding protein 5 (putative)	1.30	20	60201647	<a href="#">AK001603</a>	<a href="#">26164</a>	<a href="#">20q13.33</a>	<a href="#">Hs.340636</a>	3	<a href="#">nucleotide binding</a> <a href="#">GTP binding</a> <a href="#">intracellular</a>	
<a href="#">222603_at</a>	KIAA1815	KIAA1815	1.30	9	-5774571	<a href="#">AL136980</a>	<a href="#">79956</a>	<a href="#">9p24</a>	<a href="#">Hs.591078</a>	4	<a href="#">proteolysis</a> <a href="#">peptidase activity</a>	
<a href="#">227065_at</a>	TRIAD3		1.30	7	-5626203	<a href="#">AA523105</a>	<a href="#">54476</a>	<a href="#">7p22.1</a>	<a href="#">Hs.487458</a>	14	<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">ubiquitin cycle</a> <a href="#">apoptosis</a> <a href="#">zinc ion binding</a> <a href="#">ATP synthesis coupled proton transport</a> <a href="#">proton-transporting two-sector ATPase</a> <a href="#">complex</a> <a href="#">ligase activity</a> <a href="#">metal ion binding</a> <a href="#">hydrogen-transporting ATP synthase activity, rotational mechanism</a> <a href="#">hydrogen-transporting ATPase activity, rotational mechanism</a>	
<a href="#">200695_at</a>	PPP2R1A	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	1.29	19	57385045	<a href="#">NM_014225</a>	<a href="#">5518</a>	<a href="#">19q13.33</a>	<a href="#">Hs.467192</a>	33	<a href="#">regulation of progression through cell cycle</a> <a href="#">protein phosphatase type 2A complex</a> <a href="#">inactivation of MAPK activity</a> <a href="#">antigen binding</a> <a href="#">binding</a> <a href="#">protein binding</a> <a href="#">soluble fraction</a> <a href="#">nucleus</a> <a href="#">mitochondrion</a> <a href="#">cytosol</a> <a href="#">regulation of DNA replication</a> <a href="#">regulation of translation</a> <a href="#">protein complex assembly</a> <a href="#">protein amino acid dephosphorylation</a> <a href="#">ceramide metabolism</a> <a href="#">induction of apoptosis</a> <a href="#">RNA splicing</a> <a href="#">protein phosphatase type 2A regulator activity</a> <a href="#">response to organic substance</a> <a href="#">microtubule cytoskeleton</a> <a href="#">membrane</a> <a href="#">second-messenger-mediated signaling</a> <a href="#">regulation of Wnt receptor signaling pathway</a> <a href="#">regulation of cell adhesion</a> <a href="#">negative regulation of cell growth</a> <a href="#">regulation of growth</a> <a href="#">negative regulation of tyrosine phosphorylation of Stat3 protein</a> <a href="#">regulation of transcription</a> <a href="#">regulation of cell differentiation</a> <a href="#">protein heterodimerization activity</a> <a href="#">biological process unknown</a> <a href="#">catalytic activity</a>	<a href="#">Wnt signaling pathway</a> <a href="#">Tight junction</a> <a href="#">Long-term depression</a>

<a href="#">211818_s_at</a>	PDE4C	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	1.29	19	-18181521	<a href="#">U88712</a>	<a href="#">5143</a>	<a href="#">19p13.11</a>	<a href="#">Hs.631628</a>	12	<a href="#">3',5'-cyclic-nucleotide phosphodiesterase activity</a> <a href="#">3',5'-cyclic-nucleotide phosphodiesterase activity</a> <a href="#">3',5'-cyclic-AMP phosphodiesterase activity</a> <a href="#">signal transduction</a> <a href="#">signal transduction</a> <a href="#">cellular component unknown</a> <a href="#">hydrolase activity</a>	<a href="#">Purine metabolism</a>
<a href="#">1553713_a_at</a>	RHEBL1	Ras homolog enriched in brain like 1	1.29	12	-47744734	<a href="#">NM_144593</a>	<a href="#">121268</a>	<a href="#">12q13.12</a>	<a href="#">Hs.159013</a>	7	<a href="#">nucleotide binding</a> <a href="#">GTP binding</a> <a href="#">intracellular</a> <a href="#">small GTPase mediated signal transduction</a> <a href="#">membrane</a>	
<a href="#">220142_at</a>	HAPLN2	hyaluronan and proteoglycan link protein 2	1.29	1	154855709	<a href="#">NM_021817</a>	<a href="#">60484</a>	<a href="#">1q23.1</a>	<a href="#">Hs.410719</a>	6	<a href="#">hyaluronic acid binding</a> <a href="#">extracellular matrix (sensu Metazoa)</a>	
<a href="#">213996_at</a>	YPEL1	yippee-like 1 (Drosophila)	1.29	22	-20381825	<a href="#">NM_013313</a>	<a href="#">29799</a>	<a href="#">22q11.2</a>	<a href="#">Hs.517436</a>	6	<a href="#">cell adhesion</a> <a href="#">nucleus</a>	
<a href="#">49111_at</a>			1.28			<a href="#">N80935</a>						
<a href="#">201349_at</a>	SLC9A3R1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1	1.28	17	70256378	<a href="#">NM_004252</a>	<a href="#">9368</a>	<a href="#">17q25.1</a>	<a href="#">Hs.396783</a>	56	<a href="#">protein binding</a> <a href="#">protein complex assembly</a> <a href="#">actin cytoskeleton</a> <a href="#">Wnt receptor signaling pathway</a> <a href="#">sodium:hydrogen antiporter regulator activity</a> <a href="#">beta-2 adrenergic receptor binding</a>	
<a href="#">227544_at</a>			1.28			<a href="#">H07095</a>	<a href="#">145225</a>					
<a href="#">239810_at</a>	VASH1	vasohibin 1	1.28	14	76298284	<a href="#">AU152507</a>	<a href="#">22846</a>	<a href="#">14q24.3</a>	<a href="#">Hs.525479</a>	5	<a href="#">cell cycle</a> <a href="#">cell cycle arrest</a>	
<a href="#">1555724_s_at</a>	TAGLN	transgelin	1.27	11	116575249	<a href="#">BC010946</a>	<a href="#">6876</a>	<a href="#">11q23.2</a>	<a href="#">Hs.632099</a>	18	<a href="#">actin binding</a> <a href="#">muscle development</a> <a href="#">muscle development</a>	
<a href="#">223438_s_at</a>	PPARA	peroxisome proliferative activated receptor, alpha	1.27	22	44925162, 44945846, 44945894, 44951326	<a href="#">BC004162</a>	<a href="#">5465</a>	<a href="#">22q12-q13.1</a> <a href="#">22q13.31</a>	<a href="#">Hs.103110</a>	124	<a href="#">transcription factor activity</a> <a href="#">steroid hormone receptor activity</a> <a href="#">receptor activity</a> <a href="#">ligand-dependent nuclear receptor</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">transcription from RNA polymerase II promoter</a> <a href="#">lipid metabolism</a> <a href="#">fatty acid metabolism</a> <a href="#">zinc ion binding</a> <a href="#">fatty acid transport</a> <a href="#">positive regulation of fatty acid beta-oxidation</a> <a href="#">sequence-specific DNA binding</a> <a href="#">metal ion binding</a>	<a href="#">NA</a> <a href="#">Adipocytokine signaling</a>
<a href="#">211976_at</a>			1.26			<a href="#">AK026168</a>						
<a href="#">228880_at</a>	LOC339984		1.26	4		<a href="#">AL041933</a>	<a href="#">339984</a>	<a href="#">4p16.3</a>	<a href="#">Hs.592482</a>		<a href="#">nucleic acid binding</a>	

<a href="#">201229_s_at</a>	ARH2	ariadne homolog 2 (Drosophila)	1.25	3	48931284	<a href="#">BC000422</a>	<a href="#">10425</a>	<a href="#">3p21.2-p21.3</a>	Hs.31387	<a href="#">13</a>	<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">ubiquitin cycle</a> <a href="#">development</a> <a href="#">zinc ion binding</a> <a href="#">metal ion binding</a>	
<a href="#">211245_x_at</a>	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	1.25	19	60006877, 199896	<a href="#">AF002256</a>	<a href="#">3805</a>	<a href="#">19q13.4</a>	Hs.512572	<a href="#">30</a>	<a href="#">receptor activity</a> <a href="#">transmembrane receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">signal transduction</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">206582_s_at</a>	GPR56	G protein-coupled receptor 56	1.25	16	56211458, 56220041, 56220022	<a href="#">NM_005682</a>	<a href="#">9289</a>	<a href="#">16q12.2-q21</a>	Hs.513633	<a href="#">10</a>	<a href="#">receptor activity</a> <a href="#">G-protein coupled receptor activity</a> <a href="#">G-protein coupled receptor activity</a> <a href="#">protein binding</a> <a href="#">integral to plasma membrane</a> <a href="#">cell adhesion</a> <a href="#">cell adhesion</a> <a href="#">signal transduction</a> <a href="#">neuropeptide signaling pathway</a> <a href="#">cell-cell signaling</a> <a href="#">brain development</a> <a href="#">membrane</a>	
<a href="#">205331_s_at</a>	REEP2	receptor accessory protein 2	1.25	5	137802674	<a href="#">NM_016606</a>	<a href="#">51308</a>	<a href="#">5q31</a>	Hs.416090	<a href="#">9</a>	<a href="#">integral to membrane</a>	
<a href="#">216232_s_at</a>	GCN1L1	GCN1 general control of amino-acid synthesis 1-	1.25	12	-119049398	<a href="#">AI697055</a>	<a href="#">10985</a>	<a href="#">12q24.2</a>	Hs.298716	<a href="#">6</a>	<a href="#">binding</a>	
<a href="#">212068_s_at</a>	KIAA0515	KIAA0515	1.25	9		<a href="#">AB011087</a>	<a href="#">84726</a>	<a href="#">9q34.13</a>	Hs.495349	<a href="#">4</a>	<a href="#">sugar porter activity</a> <a href="#">phosphoenolpyruvate-dependent sugar phosphotransferase system</a>	
<a href="#">206178_at</a>	PLA2G5	phospholipase A2, group V	1.25	1	20269424	<a href="#">NM_000929</a>	<a href="#">5322</a>	<a href="#">1p36-p34</a>	Hs.319438	<a href="#">25</a>	<a href="#">calcium ion binding</a> <a href="#">extracellular region</a> <a href="#">phospholipid metabolism</a> <a href="#">lipid catabolism</a> <a href="#">hydrolase activity</a> <a href="#">calcium-dependent phospholipase A2 activity</a>	<a href="#">Glycerophospholipid</a> <a href="#">Arachidonic acid metabolism</a> <a href="#">Linoleic acid metabolism</a> <a href="#">MAPK signaling pathway</a> NA <a href="#">Fc epsilon RI signaling pathway</a> <a href="#">Long-term depression</a> NA
<a href="#">207741_x_at</a>	TPSB2	tryptase beta 2	1.25	16	-1218337	<a href="#">NM_003293</a>	<a href="#">64499</a>	<a href="#">16p13.3</a>	Hs.405479 Hs.592982	<a href="#">12</a>	<a href="#">serine-type endopeptidase activity</a> <a href="#">extracellular region</a> <a href="#">proteolysis</a> <a href="#">tryptase activity</a>	
<a href="#">231194_at</a>	CFL1	cofilin 1 (non-muscle)	1.25	11	-65378862	<a href="#">AW340085</a>	<a href="#">1072</a>	<a href="#">11q13</a>	Hs.170622	<a href="#">60</a>	<a href="#">actin binding</a> <a href="#">protein binding</a> <a href="#">intracellular</a> <a href="#">nucleus</a> <a href="#">cytoplasm</a> <a href="#">cytoskeleton</a> <a href="#">anti-apoptosis</a> <a href="#">Rho protein signal transduction</a> <a href="#">actin cytoskeleton organization and biogenesis</a>	<a href="#">Axon guidance</a> <a href="#">Regulation of actin cytoskeleton</a>
<a href="#">223327_x_at</a>	FLJ22795		1.25	15	489917, -80937719, 80742015	<a href="#">AF316855</a>	<a href="#">80154</a>	<a href="#">15q25.2</a>	Hs.498322 Hs.546614	<a href="#">2</a>	<a href="#">biological process unknown</a> <a href="#">molecular function unknown</a> <a href="#">cellular component unknown</a>	

<a href="#">212135_s_at</a>	ATP2B4	ATPase, Ca <sup>++</sup> transporting, plasma membrane 4	1.24	1	201862550	<a href="#">AW517686</a>	493	<a href="#">1q32.1</a>	<a href="#">Hs.343522</a>	35	<a href="#">nucleotide binding</a> <a href="#">magnesium ion binding</a> <a href="#">calcium-transporting ATPase activity</a> <a href="#">calcium ion binding</a> <a href="#">calmodulin binding</a> <a href="#">ATP binding</a> <a href="#">plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">cation transport</a> <a href="#">calcium ion transport</a> <a href="#">metabolism</a> <a href="#">hydrolase activity</a> <a href="#">hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances</a>	<a href="#">Calcium signaling pathway</a>
<a href="#">207184_at</a>	SLC6A13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	1.24	12	-200051	<a href="#">NM_016615</a>	6540	<a href="#">12p13.3</a>	<a href="#">Hs.504398</a>	3	<a href="#">neurotransmitter:sodium symporter activity</a> <a href="#">gamma-aminobutyric acid:sodium symporter activity</a> <a href="#">integral to plasma membrane</a> <a href="#">neurotransmitter transport</a> <a href="#">symporter activity</a> <a href="#">membrane</a>	
<a href="#">208426_x_at</a>	KIR2DL4	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 4	1.24	19	60006877, 199896	<a href="#">NM_002255</a>	3805	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	30	<a href="#">receptor activity</a> <a href="#">transmembrane receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">signal transduction</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">218765_at</a>	SIDT2	SID1 transmembrane family, member 2	1.23	11	116555148	<a href="#">NM_015996</a>	51092	<a href="#">11q23.3</a>	<a href="#">Hs.410977</a>	5	<a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">227965_at</a>	APC2	adenomatosis polyposis coli 2	1.23	19	1401147	<a href="#">BE262551</a>	10297	<a href="#">19p13.3</a>	<a href="#">Hs.446376</a>	8	<a href="#">regulation of progression through cell cycle</a> <a href="#">protein complex assembly</a> <a href="#">signal transduction</a> <a href="#">beta-catenin binding</a> <a href="#">microtubule binding</a> <a href="#">Wnt receptor signaling pathway</a> <a href="#">catenin complex</a>	<a href="#">Wnt signaling pathway</a> <a href="#">Regulation of actin cytoskeleton</a> <a href="#">NA</a>
<a href="#">228917_at</a>			1.23			<a href="#">A1798769</a>						
<a href="#">229121_at</a>			1.23			<a href="#">BE857553</a>						
<a href="#">206873_at</a>	CA6	carbonic anhydrase VI	1.23	1	8928508	<a href="#">NM_001215</a>	765	<a href="#">1p36.2</a>	<a href="#">Hs.100322</a>	18	<a href="#">carbonate dehydratase activity</a> <a href="#">carbonate dehydratase activity</a> <a href="#">one-carbon compound metabolism</a> <a href="#">zinc ion binding</a> <a href="#">lyase activity</a> <a href="#">metal ion binding</a>	<a href="#">Nitrogen metabolism</a>
<a href="#">229154_at</a>	WNT10A	wingless-type MMTV integration site family, member 10A	1.23	2	219453498	<a href="#">AW873556</a>	80326	<a href="#">2q35</a>	<a href="#">Hs.121540</a>	3	<a href="#">signal transducer activity</a> <a href="#">extracellular region</a> <a href="#">frizzled-2 signaling pathway</a> <a href="#">development</a>	<a href="#">Wnt signaling pathway</a> <a href="#">Hedgehog signaling pathway</a>
<a href="#">224342_x_at</a>	IGLV1-44	immunoglobulin lambda variable 1-44	1.23	22		<a href="#">L14452</a>	28823	<a href="#">22q11.2</a>	<a href="#">Hs.449601</a>	3		
		eukaryotic translation									<a href="#">protein binding</a> <a href="#">regulation of translation</a> <a href="#">eukaryotic initiation factor 4E binding</a> <a href="#">negative regulation of protein</a>	

<a href="#">224645_at</a>	EIF4EBP2	initiation factor 4E binding protein 2	1.23	10	71833927	<a href="#">BG106477</a>	<a href="#">1979</a>	<a href="#">10q21-q22</a>	Hs.594234 Hs.621200	<a href="#">12</a>	<a href="#">negative regulation of translational initiation</a>	
<a href="#">208858_s_at</a>	FAM62A	family with sequence similarity 62 (C2 domain containing), member A	1.22	12	54808320	<a href="#">BC004998</a>	<a href="#">23344</a>	<a href="#">12q13.2</a>	<a href="#">Hs.632729</a>	<a href="#">5</a>	<a href="#">membrane integral to membrane</a>	
<a href="#">1559461_at</a>	CEP72	centrosomal protein 72kDa	1.22	5	665404	<a href="#">BE870585</a>	<a href="#">55722</a>	<a href="#">5p15.33</a>	<a href="#">Hs.591741</a>	<a href="#">4</a>		
<a href="#">241467_at</a>	OSBPL5	oxysterol binding protein-like 5	1.22	11	-3064921	<a href="#">AW204093</a>	<a href="#">114879</a>	<a href="#">11p15.4</a>	<a href="#">Hs.436166</a>	<a href="#">8</a>	<a href="#">cytosol lipid transport Golgi to plasma membrane transport oxysterol binding steroid metabolism cholesterol metabolism cholesterol transport</a>	
<a href="#">225185_at</a>	MRAS	muscle RAS oncogene homolog	1.22	3	139574396	<a href="#">BF343625</a>	<a href="#">22808</a>	<a href="#">3q22.3</a>	<a href="#">Hs.527021</a>	<a href="#">16</a>	<a href="#">nucleotide binding GTPase activity GTP binding intracellular plasma membrane Ras protein signal transduction development muscle development actin cytoskeleton organization and biogenesis GTP-dependent protein binding</a>	<a href="#">MAPK signaling pathway Axon guidance Tight junction Regulation of actin cytoskeleton</a>
<a href="#">219135_s_at</a>	LA16c-		1.22	16	-843638	<a href="#">AL515916</a>	<a href="#">64788</a>	<a href="#">16p13.3</a>	<a href="#">Hs.71912</a>	<a href="#">4</a>		
<a href="#">212123_at</a>	C10orf61	chromosome 10 open reading frame 61	1.22	10	-97413163	<a href="#">AL050022</a>	<a href="#">26123</a>	<a href="#">10q23.33</a>	<a href="#">Hs.438991</a>	<a href="#">4</a>	<a href="#">membrane integral to membrane</a>	
<a href="#">203683_s_at</a>	VEGFB	vascular endothelial growth factor B	1.22	11	63758841	<a href="#">NM_003377</a>	<a href="#">7423</a>	<a href="#">11q13</a>	<a href="#">Hs.78781</a>	<a href="#">14</a>	<a href="#">regulation of progression through cell cycle regulation of cell growth vascular endothelial growth factor receptor binding extracellular region signal transduction growth factor activity heparin binding cell proliferation positive regulation of cell proliferation membrane</a>	<a href="#">Cytokine-cytokine receptor interaction mTOR signaling pathway Focal adhesion</a>
<a href="#">220531_at</a>	FLJ14126		1.21	2		<a href="#">NM_024849</a>	<a href="#">79907</a>	<a href="#">2p24.1</a>	<a href="#">Hs.130593</a>	<a href="#">1</a>		
<a href="#">221752_at</a>	SSH1	slingshot homolog 1 (Drosophila)	1.21	12	-107705098	<a href="#">AL041728</a>	<a href="#">54434</a>	<a href="#">12q24.11</a>	<a href="#">Hs.199763</a>	<a href="#">16</a>	<a href="#">cellular morphogenesis actin binding protein tyrosine phosphatase activity cytoplasm cytoskeleton plasma membrane protein amino acid dephosphorylation protein tyrosine/serine/threonine phosphatase activity hydrolase activity actin cytoskeleton organization and biogenesis</a>	<a href="#">Regulation of actin cytoskeleton</a>
<a href="#">217044_s_at</a>	PLEKHG3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3	1.21	14	64240945	<a href="#">BC004298</a>	<a href="#">26030</a>	<a href="#">14q23.3</a>	<a href="#">Hs.509637</a>	<a href="#">2</a>	<a href="#">Rho guanyl-nucleotide exchange factor activity intracellular regulation of Rho protein signal transduction</a>	

<a href="#">210974_s_at</a>	AP3D1	adaptor-related protein complex 3, delta 1 subunit	1.21	19	-2051987	<a href="#">AF130042</a>	8943	<a href="#">19p13.3</a>	<a href="#">Hs.512815</a>	19	<a href="#">transporter activity</a> <a href="#">binding</a> <a href="#">Golgi apparatus</a> <a href="#">eye pigment biosynthesis</a> <a href="#">intracellular protein transport</a>	
<a href="#">1555062_s_at</a>	GTPBP3	GTP binding protein 3 (mitochondrial)	1.21	19	17309378, 17309363	<a href="#">AY078987</a>	84705	<a href="#">19p13.11</a>	<a href="#">Hs.334885</a>	11		
<a href="#">204821_at</a>	BTN3A3	butyrophilin, subfamily 3, member A3	1.21	6	26548741	<a href="#">NM_006994</a>	10384	<a href="#">6p21.3</a>	<a href="#">Hs.167741</a>	7	<a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">224893_at</a>	DKFZP564J0863		1.20	11	-63153012	<a href="#">AA775408</a>	25923	<a href="#">11q13.1</a>	<a href="#">Hs.356719</a>	3	<a href="#">GTPase activity</a> <a href="#">GTP binding</a> <a href="#">immune response</a>	
<a href="#">224049_at</a>	KCNK17	potassium channel, subfamily K, member 17	1.20	6	-39374755	<a href="#">AF339912</a>	89822	<a href="#">6p21.1</a>	<a href="#">Hs.162282</a>	5	<a href="#">voltage-gated ion channel activity</a> <a href="#">potassium channel activity</a> <a href="#">ion transport</a> <a href="#">potassium ion transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">potassium ion binding</a>	
<a href="#">1553970_s_at</a>	CEL	carboxyl ester lipase (bile salt-stimulated lipase)	1.20	9	134927185	<a href="#">BC042510</a>	1056	<a href="#">9q34.3</a>	<a href="#">Hs.533258</a>	42	<a href="#">serine esterase activity</a> <a href="#">serine esterase activity</a> <a href="#">sterol esterase activity</a> <a href="#">sterol esterase activity</a> <a href="#">triacylglycerol lipase activity</a> <a href="#">triacylglycerol lipase activity</a> <a href="#">cytoplasm</a> <a href="#">endoplasmic reticulum</a> <a href="#">lipid metabolism</a> <a href="#">triacylglycerol metabolism</a> <a href="#">triacylglycerol metabolism</a> <a href="#">cholesterol catabolism</a> <a href="#">cholesterol catabolism</a> <a href="#">cholesterol catabolism</a> <a href="#">heparin binding</a> <a href="#">heparin binding</a> <a href="#">fatty acid catabolism</a> <a href="#">fatty acid catabolism</a> <a href="#">lipid catabolism</a> <a href="#">hydrolase activity</a> <a href="#">hydrolase activity</a> <a href="#">protein amino acid esterification</a> <a href="#">protein amino acid esterification</a> <a href="#">pancreatic juice secretion</a> <a href="#">pancreatic juice secretion</a> <a href="#">cholesterol absorption</a> <a href="#">cholesterol absorption</a> <a href="#">intestinal lipid catabolism</a> <a href="#">intestinal lipid catabolism</a>	<a href="#">Bile acid biosynthesis</a> <a href="#">Glycerolipid metabolism</a>
<a href="#">221250_s_at</a>	MXD3	MAX dimerization protein 3	1.20	5	-176666818	<a href="#">NM_031300</a>	83463	<a href="#">5q35.3</a>	<a href="#">Hs.631950</a>	9	<a href="#">nucleus</a> <a href="#">transcription regulator activity</a> <a href="#">regulation of transcription</a>	
											<a href="#">receptor activity</a> <a href="#">calcium ion binding</a> <a href="#">protein binding</a> <a href="#">cell adhesion</a> <a href="#">homophilic cell adhesion</a> <a href="#">cell-matrix adhesion</a>	<a href="#">Focal adhesion</a> <a href="#">ECM-receptor interaction</a> <a href="#">Regulation of actin cytoskeleton</a>

											<a href="#">integrin-mediated signaling pathway</a> <a href="#">muscle development</a> <a href="#">integrin complex</a> <a href="#">regulation of cell shape</a> <a href="#">membrane</a>	
<a href="#">209663_s_at</a>	ITGA7	integrin, alpha 7	1.20	12	-54364622	<a href="#">AF072132</a>	<a href="#">3679</a>	<a href="#">12q13</a>	Hs.524484	<a href="#">25</a>		
<a href="#">240147_at</a>	MGC11257		1.20	7	-1003168	<a href="#">AA830578</a>	<a href="#">84310</a>	<a href="#">7p22.3</a>	Hs.639559	<a href="#">5</a>		
<a href="#">235663_at</a>			1.20			<a href="#">AI313160</a>						
											<a href="#">GTPase activity</a> <a href="#">protein binding</a> <a href="#">protein binding</a> <a href="#">GTP binding</a> <a href="#">soluble fraction</a> <a href="#">cytosol</a> <a href="#">electron transport</a> <a href="#">superoxide metabolism</a> <a href="#">cellular defense response</a> <a href="#">intracellular signaling cascade</a> <a href="#">electron carrier activity</a> <a href="#">phosphoinositide binding</a>	
<a href="#">225906_at</a>	NCF1	neutrophil cytosolic factor 1, (chronic granulomatous disease, autosomal 1)	1.20	7	-74210381	<a href="#">BG261385</a>	<a href="#">4687</a>	<a href="#">7q11.23</a>	Hs.520943	<a href="#">71</a>		<a href="#">Leukocyte transendothelial migration</a>
											<a href="#">chromatin</a> <a href="#">DNA binding</a> <a href="#">chromatin binding</a> <a href="#">transcription coactivator activity</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nucleoplasm</a> <a href="#">chromatin assembly or disassembly</a> <a href="#">chromatin remodeling</a> <a href="#">regulation of transcription from RNA polymerase II promoter</a> <a href="#">SWI/SNF complex</a> <a href="#">regulation of transcription</a> <a href="#">positive regulation of transcription, DNA-dependent</a>	
<a href="#">201072_s_at</a>	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	1.20	3	-47602390	<a href="#">AW152160</a>	<a href="#">6599</a>	<a href="#">3p23-p21</a>	Hs.476179	<a href="#">27</a>		
											<a href="#">nucleotide binding</a> <a href="#">magnesium ion binding</a> <a href="#">endonuclease activity</a> <a href="#">protein serine/threonine kinase activity</a> <a href="#">ATP binding</a> <a href="#">endoplasmic reticulum</a> <a href="#">electron transport</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">mRNA processing</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">apoptosis</a> <a href="#">induction of apoptosis</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">rRNA catabolism</a> <a href="#">negative regulation of transcription</a> <a href="#">transferase activity</a> <a href="#">hydrolase activity</a> <a href="#">endoribonuclease activity, producing 5'-phosphomonoesters</a>	
<a href="#">223910_at</a>	ERN2	endoplasmic reticulum to nucleus signalling 2	1.20	16	-23609197	<a href="#">AB047079</a>	<a href="#">10595</a>	<a href="#">16p12.2</a>	Hs.592041	<a href="#">3</a>		
											<a href="#">DNA binding</a>	

<a href="#">226788_at</a>	THAP11	THAP domain containing 11	1.19	16	66433713	<a href="#">AI436409</a>	<a href="#">57215</a>	<a href="#">16q22.1</a>	<a href="#">Hs.6322200</a>	<a href="#">3</a>	<a href="#">nucleus</a> <a href="#">zinc ion binding</a> <a href="#">metal ion binding</a>	
<a href="#">238333_s_at</a>	SPRN	shadow of prion protein homolog (zebrafish)	1.19	10	-135084068	<a href="#">AI355435</a>	<a href="#">503542</a>	<a href="#">10q26.3</a>	<a href="#">Hs.64968</a> <a href="#">Hs.501578</a>	<a href="#">5</a>		
<a href="#">207003_at</a>	GUCA1B	guanylate cyclase activator 1B (retina)	1.19	6	-42259000	<a href="#">NM_002098</a>	<a href="#">2979</a>	<a href="#">6p21.1</a>	<a href="#">Hs.446529</a>	<a href="#">7</a>	<a href="#">calcium ion binding</a> <a href="#">receptor guanylyl cyclase signaling pathway</a> <a href="#">cell-cell signaling</a> <a href="#">fluid secretion</a> <a href="#">visual perception</a> <a href="#">calcium sensitive guanylate cyclase activator activity</a> <a href="#">response to stimulus</a>	NA
<a href="#">39835_at</a>	SBF1	SET binding factor 1	1.19	22	-49232101	<a href="#">U93181</a>	<a href="#">6305</a>	<a href="#">22q13.33</a>	<a href="#">Hs.589924</a>	<a href="#">10</a>	<a href="#">inositol or phosphatidylinositol phosphatase activity</a> <a href="#">nucleus</a> <a href="#">protein amino acid dephosphorylation</a> <a href="#">protein tyrosine/serine/threonine phosphatase activity</a> <a href="#">integral to membrane</a> <a href="#">phospholipid dephosphorylation</a>	
<a href="#">216180_s_at</a>	SYNJ2	synaptojanin 2	1.19	6	158322906	<a href="#">AK026758</a>	<a href="#">8871</a>	<a href="#">6q25.3</a>	<a href="#">Hs.434494</a>	<a href="#">15</a>	<a href="#">nucleotide binding</a> <a href="#">RNA binding</a> <a href="#">phosphoinositide 5-phosphatase activity</a> <a href="#">hydrolase activity</a>	<a href="#">Inositol phosphate metabolism</a> <a href="#">Phosphatidylinositol signaling</a>
<a href="#">1553843_at</a>	C10orf67	chromosome 10 open reading frame 67	1.19	10	-23645526	<a href="#">NM_153714</a>	<a href="#">256815</a>	<a href="#">10p12.2</a>	<a href="#">Hs.522360</a>	<a href="#">1</a>		
<a href="#">1563903_x_at</a>	SPSB1	splA/ryanodine receptor domain and SOCS box containing 1	1.19	1	9275570	<a href="#">AK074468</a>	<a href="#">80176</a>	<a href="#">1p36.22</a>	<a href="#">Hs.8261</a> <a href="#">Hs.637089</a>	<a href="#">6</a>	<a href="#">intracellular signaling cascade</a>	
<a href="#">235160_at</a>			1.18			<a href="#">BG105181</a>						
<a href="#">229140_at</a>	ZNF579	zinc finger protein 579	1.18	19	-60780704	<a href="#">AI689676</a>	<a href="#">163033</a>	<a href="#">19q13.42</a>	<a href="#">Hs.112529</a>	<a href="#">3</a>	<a href="#">DNA binding</a> <a href="#">intracellular</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">zinc ion binding</a> <a href="#">metal ion binding</a>	
<a href="#">214667_s_at</a>	TP53I11	tumor protein p53 inducible protein 11	1.17	11	-44537174	<a href="#">AK026607</a>	<a href="#">9537</a>	<a href="#">11p11.2</a>	<a href="#">Hs.554791</a>	<a href="#">8</a>	<a href="#">response to stress</a> <a href="#">negative regulation of cell proliferation</a>	
											<a href="#">regulation of progression through cell cycle</a> <a href="#">rhodopsin-like receptor activity</a> <a href="#">receptor activity</a> <a href="#">receptor binding</a> <a href="#">Golgi apparatus</a> <a href="#">plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">apoptosis</a> <a href="#">caspase activation</a> <a href="#">cell motility</a> <a href="#">signal transduction</a> <a href="#">G-protein coupled receptor protein</a> <a href="#">signaling pathway</a> <a href="#">tyrosine phosphorylation of STAT</a>	<a href="#">Calcium signaling pathway</a> <a href="#">Neuroactive ligand-receptor</a> <a href="#">Complement and coagulation</a> <a href="#">Regulation of actin cytoskeleton</a>



											STAT protein nuclear translocation blood coagulation response to wounding morphogenesis thrombin receptor activity positive regulation of I-kappaB kinase/NF-kappaB cascade	
<a href="#">203989 x at</a>	F2R	coagulation factor II (thrombin) receptor	1.17	5	76047546	<a href="#">NM_001992</a>	2149	5q13	Hs.482562	102		
<a href="#">231708 at</a>	DKFZP586P0		1.17	11	-73423189	<a href="#">AI674774</a>	26005	11q13.4	Hs.557938	2		
<a href="#">1556249 a at</a>	FLJ33065		1.17	3		<a href="#">BC031275</a>	440952	3p22.1	Hs.585284	1		
											chromatin DNA binding protein binding nucleus chromosome DNA replication DNA repair transcription regulation of transcription, DNA- dependent	
<a href="#">200957 s at</a>	SSRP1	structure specific recognition protein 1	1.17	11	-56850035	<a href="#">NM_003146</a>	6749	11q12	Hs.523680	26		
<a href="#">1560874 at</a>	FLJ33046		1.17	12		<a href="#">AK057608</a>	440074	12p13.32	Hs.504534	1		
<a href="#">229786 at</a>			1.16			<a href="#">AI955001</a>						
											GTPase activator activity Ras GTPase activator activity intracellular signal transduction regulation of small GTPase mediated signal transduction	
<a href="#">234343 s at</a>	RASAL2	RAS protein activator like 2	1.16	1	176577228, 176330252	<a href="#">AK022662</a>	9462	1q24	Hs.167371	11		
											beta-amyloid binding beta-amyloid binding nucleus cell cycle arrest signal transduction signal transduction axonogenesis axonogenesis transcription factor binding lamellipodium lamellipodium actin filament-based movement negative regulation of cell growth growth cone growth cone histone acetyltransferase binding synapse synapse regulation of transcription negative regulation of S phase of mitotic cell cycle negative regulation of thymidylate synthase biosynthesis protein stabilization	
<a href="#">202652 at</a>	APBB1	amyloid beta (A4) precursor protein-binding, family B, member 1 (Fe65)	1.16	11	-6372930	<a href="#">NM_001164</a>	322	11p15	Hs.372840	44		Alzheimer's disease
											lysophingolipid and lysophosphatidic acid receptor activity receptor activity integral to plasma membrane immune response signal transduction	

<a href="#">206437_at</a>	EDG6	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 6	1.16	19	3129765	<a href="#">NM_003775</a>	8698	19p13.3	Hs.73797	15	<a href="#">G-protein coupled receptor protein signaling pathway</a> <a href="#">phospholipase C activation</a> <a href="#">elevation of cytosolic calcium ion concentration</a> <a href="#">lipid binding</a> <a href="#">membrane</a>	<a href="#">Neuroactive ligand-receptor interaction</a>
<a href="#">206517_at</a>	CDH16	cadherin 16, KSP-cadherin	1.16	16	-65499526	<a href="#">NM_004062</a>	1014	16q22.1	Hs.513660	13	<a href="#">calcium ion binding</a> <a href="#">protein binding</a> <a href="#">cell adhesion</a> <a href="#">homophilic cell adhesion</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">232813_s_at</a>	LOC653625		1.16	15		<a href="#">AI073403</a>	653625	15q24.1	Hs.458315			
<a href="#">207889_at</a>	SARDH	sarcosine dehydrogenase	1.16	9	-135518506	<a href="#">NM_007101</a>	1757	9q33-q34	Hs.198003	8	<a href="#">biological process unknown</a> <a href="#">aminomethyltransferase activity</a> <a href="#">cytoplasm</a> <a href="#">mitochondrion</a> <a href="#">mitochondrial matrix</a> <a href="#">electron transport</a> <a href="#">glycine catabolism</a> <a href="#">sarcosine dehydrogenase activity</a> <a href="#">sarcosine dehydrogenase activity</a> <a href="#">electron carrier activity</a> <a href="#">oxidoreductase activity</a>	<a href="#">Urea cycle and metabolism of amino groups</a> <a href="#">Glycine, serine and threonine</a>
<a href="#">219143_s_at</a>	RPP25	ribonuclease P 25kDa subunit	1.15	15	-73034495	<a href="#">NM_017793</a>	54913	15q24.1	Hs.8562	4	<a href="#">RNA binding</a> <a href="#">ribonuclease P activity</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">tRNA processing</a> <a href="#">hydrolase activity</a>	
<a href="#">238339_x_at</a>	LRIG1	leucine-rich repeats and immunoglobulin-like	1.15	3	-66511911	<a href="#">AI356774</a>	26018	3p14	Hs.518055	10	<a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">209976_s_at</a>	CYP2E1	cytochrome P450, family 2, subfamily E, polypeptide 1	1.15	10	135190856	<a href="#">AF182276</a>	1571	10q24.3-qter	Hs.12907	72	<a href="#">monooxygenase activity</a> <a href="#">iron ion binding</a>  <a href="#">endoplasmic reticulum</a> <a href="#">microsome</a> <a href="#">electron transport</a> <a href="#">membrane</a> <a href="#">oxygen binding</a> <a href="#">heme binding</a> <a href="#">metal ion binding</a> <a href="#">unspecific monooxygenase activity</a>	<a href="#">Arachidonic acid metabolism</a> <a href="#">Linoleic acid metabolism</a> <a href="#">Metabolism of xenobiotics by cytochrome P450</a>
<a href="#">232078_at</a>	TOMM40	translocase of outer mitochondrial membrane 40 homolog (yeast)	1.15	19	50086333	<a href="#">BE867789</a>	10452	19q13	Hs.110675	10	<a href="#">molecular function unknown</a> <a href="#">mitochondrion</a> <a href="#">mitochondrial outer membrane</a> <a href="#">protein targeting to mitochondrion</a> <a href="#">anion transport</a> <a href="#">mitochondrial transport</a> <a href="#">voltage-gated ion-selective channel activity</a> <a href="#">protein transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">outer membrane</a>	

<a href="#">1554110_at</a>	CDCP1	CUB domain containing protein 1	1.15	3	-45098773, -45126736	<a href="#">BC021099</a>	64866	<a href="#">3p21.31</a>	<a href="#">Hs.476093</a>	14	<a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">transcription factor activity</a> <a href="#">signal transducer activity</a> <a href="#">hematopoietin/interferon-class (D200-domain) cytokine receptor signal transducer activity</a> <a href="#">calcium ion binding</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription from RNA polymerase II promoter</a> <a href="#">intracellular signaling cascade</a> <a href="#">JAK-STAT cascade</a> <a href="#">response to virus</a>	
<a href="#">205170_at</a>	STAT2	signal transducer and activator of transcription 2, 113kDa	1.14	12	-55021650	<a href="#">NM_005419</a>	6773	<a href="#">12q13.2</a>	<a href="#">Hs.530595</a>	50	<a href="#">Jak-STAT signaling pathway</a>	
<a href="#">243776_at</a>			1.13			<a href="#">AW139582</a>						
<a href="#">214809_at</a>			1.12			<a href="#">AL050047</a>						
<a href="#">233113_at</a>			1.11			<a href="#">AU147726</a>						
<a href="#">1567681_at</a>	SNORA74A	small nucleolar RNA, H/ACA box 74A	1.10	5		<a href="#">X94290</a>	26821	<a href="#">5q31.2</a>	<a href="#">Hs.268939</a>	2		
<a href="#">244230_at</a>	MEF2C	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)	0.89	5	-88051921	<a href="#">AW263527</a>	4208	<a href="#">5q14</a>	<a href="#">Hs.444409</a>	41	<a href="#">transcription factor activity</a> <a href="#">RNA polymerase II transcription factor activity</a> <a href="#">transcription coactivator activity</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">transcription from RNA polymerase II promoter</a> <a href="#">nervous system development</a> <a href="#">muscle development</a> <a href="#">sequence-specific DNA binding</a> <a href="#">MAPK signaling pathway</a>	
<a href="#">215272_at</a>			0.88			<a href="#">R59977</a>						
<a href="#">207434_s_at</a>	FXSD2	FXSD domain containing ion transport regulator 2	0.88	11	-117195999	<a href="#">NM_021603</a>	486	<a href="#">11q23</a>	<a href="#">Hs.413137</a>	18	<a href="#">transporter activity</a> <a href="#">ion channel activity</a> <a href="#">ion channel activity</a> <a href="#">sodium:potassium-exchanging ATPase activity</a> <a href="#">sodium:potassium-exchanging ATPase complex</a> <a href="#">ion transport</a> <a href="#">ion transport</a> <a href="#">potassium ion transport</a> <a href="#">sodium ion transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">potassium ion binding</a> <a href="#">sodium ion binding</a>	
<a href="#">235099_at</a>	CMTM8	CKLF-like MARVEL transmembrane domain containing 8	0.87	3	32255174	<a href="#">AW080832</a>	152189	<a href="#">3p22.3</a>	<a href="#">Hs.154986</a>	3	<a href="#">cytokine activity</a> <a href="#">extracellular space</a> <a href="#">chemotaxis</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">238123_at</a>			0.86			<a href="#">W52448</a>					<a href="#">arachidonate 5-lipoxygenase activity</a> <a href="#">iron ion binding</a> <a href="#">Arachidonic acid metabolism</a> <a href="#">Linoleic acid metabolism</a>	

<a href="#">213952_s_at</a>	ALOX5	arachidonate 5-lipoxygenase	0.86	10	45189634	<a href="#">AI372974</a>	240	<a href="#">10q11.2</a>	Hs.89499	68	<a href="#">calcium ion binding</a> <a href="#">protein binding</a> <a href="#">electron transport</a> <a href="#">inflammatory response</a> <a href="#">lipoxygenase activity</a> <a href="#">oxidoreductase activity</a> <a href="#">leukotriene biosynthesis</a>
<a href="#">200690_at</a>	HSPA9B	heat shock 70kDa protein 9B (mortalin-2)	0.86	5	-137918923	<a href="#">AA927701</a>	3313	<a href="#">5q31.1</a>	Hs.184233	36	<a href="#">nucleotide binding</a> <a href="#">ATP binding</a> <a href="#">cytoplasm</a> <a href="#">mitochondrion</a> <a href="#">protein folding</a> <a href="#">anti-apoptosis</a> <a href="#">cell surface</a> <a href="#">unfolded protein binding</a> <a href="#">MAPK signaling pathway</a> <a href="#">Antigen processing and</a>
<a href="#">234125_at</a>	ERBB2IP	erbb2 interacting protein	0.86	5	65258139	<a href="#">AL137318</a>	55914	<a href="#">5q12.3</a>	Hs.591774	26	<a href="#">ErbB-2 class receptor binding</a> <a href="#">ErbB-2 class receptor binding</a> <a href="#">integrin binding</a> <a href="#">integrin binding</a> <a href="#">structural constituent of cytoskeleton</a> <a href="#">structural constituent of cytoskeleton</a> <a href="#">protein binding</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nucleus</a> <a href="#">cytoplasm</a> <a href="#">cytoplasm</a> <a href="#">cell cycle</a> <a href="#">cell cycle</a> <a href="#">cell adhesion</a> <a href="#">cell adhesion</a> <a href="#">epidermal growth factor receptor signaling pathway</a> <a href="#">epidermal growth factor receptor signaling pathway</a> <a href="#">integrin-mediated signaling pathway</a> <a href="#">integrin-mediated signaling pathway</a> <a href="#">cell growth</a> <a href="#">cell growth</a> <a href="#">hemidesmosome</a> <a href="#">hemidesmosome</a> <a href="#">intermediate filament cytoskeleton</a> <a href="#">organization and biogenesis</a> <a href="#">intermediate filament cytoskeleton</a> <a href="#">organization and biogenesis</a> <a href="#">basal protein localization</a> <a href="#">basal protein localization</a> <a href="#">establishment and/or maintenance of epithelial cell polarity</a> <a href="#">establishment and/or maintenance of epithelial cell polarity</a>
<a href="#">230246_at</a>	PLAC9	placenta-specific 9	0.86	10	81882237	<a href="#">AI275020</a>	219348	<a href="#">10q22.3</a>	Hs.204947	2	<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">proteolysis</a> <a href="#">peptidase activity</a> <a href="#">zinc ion binding</a>

<a href="#">239554_at</a>	RNF13	ring finger protein 13	0.85	3	151013193	<a href="#">AL634646</a>	<a href="#">11342</a>	<a href="#">3q25.1</a>	<a href="#">Hs.12333</a>	<a href="#">5</a>	<a href="#">metal ion binding</a>	
<a href="#">214766_s_at</a>	AHCTF1	AT hook containing transcription factor 1	0.85	1	-245069026	<a href="#">AL080144</a>	<a href="#">25909</a>	<a href="#">1q44</a>	Hs.300887 Hs.470435	<a href="#">3</a>		
<a href="#">219781_s_at</a>	ZNF771	zinc finger protein 771	0.85	16	30326977	<a href="#">AI992095</a>	<a href="#">51333</a>	<a href="#">16p11.2</a>	<a href="#">Hs.148584</a>	<a href="#">1</a>	<a href="#">nucleic acid binding</a> <a href="#">intracellular nucleus</a> <a href="#">zinc ion binding</a> <a href="#">metal ion binding</a>	
<a href="#">216547_at</a>	LOC127406		0.85	1		<a href="#">AL353681</a>	<a href="#">127406</a>	<a href="#">1p32.2</a>			<a href="#">structural constituent of ribosome</a> <a href="#">intracellular protein biosynthesis</a> <a href="#">small ribosomal subunit</a> <a href="#">zinc ion binding</a>	
<a href="#">223527_s_at</a>	CDADC1	cytidine and dCMP deaminase domain	0.84	13	48720103	<a href="#">AL138875</a>	<a href="#">81602</a>	<a href="#">13q14.2</a>	<a href="#">Hs.388220</a>	<a href="#">1</a>	<a href="#">hydrolase activity</a>	
<a href="#">240834_at</a>	FAM105B	family with sequence similarity 105, member B	0.84	5	14731835	<a href="#">AI813337</a>	<a href="#">90268</a>	<a href="#">5p15.2</a>	Hs.406335 Hs.591743	<a href="#">6</a>		
<a href="#">206611_at</a>	C2orf27	chromosome 2 open reading frame 27	0.84	2	132196533	<a href="#">NM_013310</a>	<a href="#">29798</a>	<a href="#">2q21.1-q21.2</a>	Hs.469971 Hs.635289	<a href="#">3</a>		
<a href="#">237287_at</a>	WDR34	WD repeat domain 34	0.83	9	-130435760	<a href="#">AW450386</a>	<a href="#">89891</a>	<a href="#">9q34.11</a>	<a href="#">Hs.495240</a>	<a href="#">1</a>		
<a href="#">216925_s_at</a>	TAL1	T-cell acute lymphocytic leukemia 1	0.83	1	-47454550	<a href="#">X51990</a>	<a href="#">6886</a>	<a href="#">1p32</a>	<a href="#">Hs.73828</a>	<a href="#">44</a>	<a href="#">DNA binding</a> <a href="#">nucleus</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">cell proliferation</a> <a href="#">cell differentiation</a> <a href="#">transcription regulator activity</a> <a href="#">regulation of transcription</a>	
<a href="#">212780_at</a>	SOS1	son of sevenless homolog 1 (Drosophila)	0.83	2	-39066469	<a href="#">AA700167</a>	<a href="#">6654</a>	<a href="#">2p22-p21</a>	<a href="#">Hs.278733</a>	<a href="#">58</a>	<a href="#">DNA binding</a> <a href="#">Ras guanyl-nucleotide exchange factor activity</a> <a href="#">Rho guanyl-nucleotide exchange factor activity</a> <a href="#">Rho GTPase activator activity</a> <a href="#">protein binding</a> <a href="#">intracellular signal transduction</a> <a href="#">Ras protein signal transduction</a> <a href="#">regulation of Rho protein signal transduction</a>	<a href="#">MAPK signaling pathway</a> <a href="#">Dorso-ventral axis formation</a> <a href="#">Focal adhesion</a> <a href="#">Gap junction</a> <a href="#">Jak-STAT signaling pathway</a> <a href="#">Natural killer cell mediated T cell receptor signaling</a> <a href="#">Fc epsilon RI signaling pathway</a> <a href="#">Regulation of actin cytoskeleton</a> <a href="#">Insulin signaling pathway</a> NA NA
											<a href="#">DNA strand annealing activity</a> <a href="#">transcription factor activity</a> <a href="#">transcription factor activity</a> <a href="#">nuclease activity</a> <a href="#">copper ion binding</a> <a href="#">protein binding</a> <a href="#">ATP binding</a> <a href="#">insoluble fraction</a> <a href="#">nucleus</a> <a href="#">nucleus</a> <a href="#">nucleoplasm</a> <a href="#">nucleolus</a> <a href="#">cytoplasm</a> <a href="#">mitochondrion</a> <a href="#">base-excision repair</a>	<a href="#">MAPK signaling pathway</a> <a href="#">Cell cycle</a> <a href="#">Apoptosis</a> <a href="#">Wnt signaling pathway</a> <a href="#">Amyotrophic lateral sclerosis</a> <a href="#">Huntington's disease</a> NA

<a href="#">224185_at</a>	I1tp53	mRNA of Intron 1 in gene of tp53	0.83	17	-7512464	<a href="#">U58658</a>	<a href="#">7157</a>	<a href="#">17p13.1</a>	<a href="#">Hs.408312</a>	<a href="#">1480</a>	<a href="#">nucleotide-excision repair</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">protein complex assembly</a> <a href="#">apoptosis</a> <a href="#">response to DNA damage stimulus</a> <a href="#">cell cycle</a> <a href="#">cell cycle arrest</a> <a href="#">cell aging</a> <a href="#">zinc ion binding</a> <a href="#">cell proliferation</a> <a href="#">caspase activation via cytochrome c</a> <a href="#">nuclear matrix</a> <a href="#">enzyme binding</a> <a href="#">cell differentiation</a> <a href="#">negative regulation of cell growth</a> <a href="#">DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis</a> <a href="#">metal ion binding</a> <a href="#">regulation of mitochondrial membrane permeability</a> <a href="#">protein heterodimerization activity</a> <a href="#">protein N-terminus binding</a> <a href="#">negative regulation of helicase activity</a> <a href="#">protein tetramerization</a>	
<a href="#">211200_s_at</a>	EFCAB2	EF-hand calcium binding domain 2	0.83	1	243200314	<a href="#">BC002836</a>	<a href="#">84288</a>	<a href="#">1q44</a>	<a href="#">Hs.134857</a>	<a href="#">2</a>	<a href="#">calcium ion binding</a>	
<a href="#">227991_x_at</a>			0.82			<a href="#">BF516567</a>						
<a href="#">242230_at</a>	ATXN1	ataxin 1	0.82	6	-16407322	<a href="#">BF438383</a>	<a href="#">6310</a>	<a href="#">6p23</a>	<a href="#">Hs.434961</a>	<a href="#">29</a>	<a href="#">RNA binding</a> <a href="#">nucleus</a> <a href="#">cytoplasm</a> <a href="#">identical protein binding</a>	
<a href="#">210017_at</a>	MALT1	mucosa associated lymphoid tissue lymphoma translocation gene 1	0.82	18	54489597	<a href="#">AF070528</a>	<a href="#">10892</a>	<a href="#">18q21</a>	<a href="#">Hs.180566</a>	<a href="#">34</a>	<a href="#">signal transducer activity</a> <a href="#">protein binding</a> <a href="#">intracellular</a> <a href="#">proteolysis</a> <a href="#">anti-apoptosis</a> <a href="#">defense response</a> <a href="#">activation of NF-kappaB-inducing</a> <a href="#">peptidase activity</a> <a href="#">caspase activity</a> <a href="#">regulation of apoptosis</a> <a href="#">positive regulation of I-kappaB kinase/NF-kappaB cascade</a>	<a href="#">T cell receptor signaling</a> <a href="#">B cell receptor signaling</a>
											<a href="#">nucleotide binding</a> <a href="#">magnesium ion binding</a> <a href="#">protein serine/threonine kinase activity</a> <a href="#">protein-tyrosine kinase activity</a> <a href="#">ATP binding</a> <a href="#">nucleus</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">apoptosis</a> <a href="#">intracellular signaling cascade</a>	

<a href="#">205486_at</a>	TESK2	testis-specific kinase 2	0.82	1	-45582141	<a href="#">NM_007170</a>	10420	1p32	<a href="#">Hs.591499</a>	6	<a href="#">spermatogenesis</a> <a href="#">transferase activity</a> <a href="#">actin cytoskeleton organization and biogenesis</a> <a href="#">manganese ion binding</a> <a href="#">focal adhesion formation</a>	
<a href="#">1553220_at</a>	ALS2CR13	amyotrophic lateral sclerosis 2 (juvenile) chromosome region,	0.82	2	203208455	<a href="#">NM_173511</a>	150864	2q33.1	<a href="#">Hs.471130</a>	3		
<a href="#">1554105_at</a>	FAM11A	family with sequence similarity 11, member A	0.81	X	-148486015	<a href="#">BC022405</a>	84548	Xq28	<a href="#">Hs.522172</a>	4	<a href="#">membrane</a> <a href="#">integral to membrane</a>	
<a href="#">1556721_at</a>	FLJ33706		0.81	20		<a href="#">AK091025</a>	284805	20q11.21	<a href="#">Hs.629708</a>	3		
<a href="#">208972_s_at</a>	ATP5G1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)	0.81	17	44325146	<a href="#">AL080089</a>	516	17q21.32	<a href="#">Hs.80986</a>	11	<a href="#">transporter activity</a> <a href="#">membrane fraction</a> <a href="#">mitochondrion</a> <a href="#">proton-transporting ATP synthase complex (sensu Eukaryota)</a> <a href="#">ion transport</a> <a href="#">lipid binding</a> <a href="#">ATP synthesis coupled proton transport</a> <a href="#">proton transport</a> <a href="#">membrane</a> <a href="#">proton-transporting two-sector ATPase complex</a> <a href="#">proton-transporting ATP synthase complex, coupling factor F(o)</a> <a href="#">hydrogen-transporting ATP synthase activity, rotational mechanism</a> <a href="#">hydrogen-transporting ATPase activity, rotational mechanism</a>	<a href="#">Oxidative phosphorylation</a> <a href="#">ATP synthesis</a>
<a href="#">229955_at</a>	FBXO3	F-box protein 3	0.81	11	-33719067, -33724868	<a href="#">AW772096</a>	26273	11p13	<a href="#">Hs.406787</a>	6	<a href="#">ubiquitin ligase complex</a> <a href="#">ubiquitin conjugating enzyme activity</a> <a href="#">ubiquitin-protein ligase activity</a> <a href="#">ubiquitin-protein ligase activity</a> <a href="#">proteolysis</a> <a href="#">ubiquitin cycle</a> <a href="#">protein ubiquitination</a>	
<a href="#">210427_x_at</a>	ANXA2	annexin A2	0.80	15	-58426643	<a href="#">BC001388</a>	302	15q21-q22	<a href="#">Hs.511605</a>	85	<a href="#">skeletal development</a> <a href="#">phospholipase inhibitor activity</a> <a href="#">phospholipase inhibitor activity</a> <a href="#">calcium ion binding</a> <a href="#">calcium-dependent phospholipid binding</a> <a href="#">soluble fraction</a> <a href="#">plasma membrane</a> <a href="#">cytoskeletal protein binding</a>	
<a href="#">232122_s_at</a>	VEPH1	ventricular zone expressed PH domain homolog 1	0.80	3	-158461391	<a href="#">AK022666</a>	79674	3q24-q25	<a href="#">Hs.127657</a>	7		
<a href="#">224898_at</a>	WDR26	WD repeat domain 26	0.80	1	-222639816	<a href="#">BG177759</a>	80232	1q42.11	<a href="#">Hs.497873</a>	3		
<a href="#">204929_s_at</a>	VAMP5	vesicle-associated membrane protein 5 (myobrevin)	0.80	2	85665041	<a href="#">NM_006634</a>	10791	2p11.2	<a href="#">Hs.172684</a>	5	<a href="#">plasma membrane</a> <a href="#">striated muscle development</a> <a href="#">integral to membrane</a> <a href="#">vesicle-mediated transport</a> <a href="#">cell differentiation</a>	<a href="#">SNARE interactions in vesicular transport</a>
<a href="#">222497_x_at</a>	NMD3	NMD3 homolog (S. chromosome 20 open reading frame 67)	0.79	3	162421792	<a href="#">AL520719</a>	51068	3q26.1	<a href="#">Hs.91384</a>	9		
<a href="#">89948_at</a>	C20orf67		0.79	20	43996723	<a href="#">AI743331</a>	63935	20q13.12	<a href="#">Hs.472856</a>	7	<a href="#">nucleus</a> <a href="#">transcription factor activity</a>	

												protein binding intracellular nucleus transcription regulation of transcription, DNA- dependent zinc ion binding metal ion binding
<a href="#">214482_at</a>	ZBTB25	zinc finger and BTB domain containing 25	0.78	14	-64023309	<a href="#">NM_006977</a>	7597	<a href="#">14q23-q24</a>	<a href="#">Hs.435974</a>	8		
<a href="#">229344_x_at</a>	FAM80B	family with sequence similarity 80, member B	0.78	12	8725553	<a href="#">AW135012</a>	57494	<a href="#">12p13.31</a>	<a href="#">Hs.504670</a>	2		
<a href="#">229602_at</a>			0.78			<a href="#">H97567</a>						
												taurine:sodium symporter activity taurine:sodium symporter activity integral to plasma membrane amino acid metabolism neurotransmitter transport symporter activity membrane
<a href="#">211030_s_at</a>	SLC6A6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0.77	3	14419109	<a href="#">BC006252</a>	6533	<a href="#">3p25-p24</a>	<a href="#">Hs.529488</a>	14		
												serine-type endopeptidase inhibitor activity nucleus transport porin activity integral to membrane outer membrane
<a href="#">204435_at</a>	NUPL1	nucleoporin like 1	0.77	13	24773665	<a href="#">NM_014778</a>	9818	<a href="#">13q12.13</a>	<a href="#">Hs.310453</a> <a href="#">Hs.507537</a>	10		
<a href="#">1553736_at</a>	PSRC2	proline/serine-rich coiled-coil 2	0.76	12	-70289650	<a href="#">NM_144982</a>	196441	<a href="#">12q21.1</a>	<a href="#">Hs.527874</a>	2		binding intracellular RNA processing
												cytosol protein folding apoptosis anti-apoptosis cellular component unknown Hsp70/Hsc70 protein regulator activity unfolded protein binding
<a href="#">217911_s_at</a>	BAG3	BCL2-associated athanogene 3	0.76	10	121400871	<a href="#">NM_004281</a>	9531	<a href="#">10q25.2-q26.2</a>	<a href="#">Hs.643507</a>	19		transporter activity iron ion transporter activity iron ion binding integral to plasma membrane ion transport iron ion transport membrane
<a href="#">203124_s_at</a>	SLC11A2	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	0.76	12	-49666043	<a href="#">NM_000617</a>	4891	<a href="#">12q13</a>	<a href="#">Hs.505545</a>	33		
<a href="#">235587_at</a>	LOC202781		0.76	7		<a href="#">BG400596</a>	202781	<a href="#">7q36.3</a>	<a href="#">Hs.193172</a>	1		biological process unknown chromosome_pericentric region DNA binding molecular function unknown nucleus cellular component unknown regulation of transcription
<a href="#">1553099_at</a>	TIGD1	tigger transposable element derived 1	0.76	2	-233121022	<a href="#">NM_145702</a>	200765	<a href="#">2q37.1</a>	<a href="#">Hs.211823</a>	4		
<a href="#">218023_s_at</a>	FAM53C	family with sequence similarity 53, member C	0.76	5	137701866	<a href="#">NM_016605</a>	51307	<a href="#">5q31</a>	<a href="#">Hs.54056</a>	5		
<a href="#">224831_at</a>	CPEB4	cytoplasmic polyadenylation element	0.75	5	173248794	<a href="#">BE620832</a>	80315	<a href="#">5q21</a>	<a href="#">Hs.127126</a>	3		nucleotide binding RNA binding regulation of progression through cell cycle nuclear mRNA splicing, via spliceosome





<a href="#">226350_at</a>	CHML	escort protein 2)	0.73	1	-239858790	<a href="#">AU155565</a>	<a href="#">1122</a>	<a href="#">1q42-qter</a>	<a href="#">Hs.534399</a>	<a href="#">12</a>	<a href="#">regulation of GTPase activity</a> <a href="#">regulation of progression through cell cycle</a> <a href="#">nuclear mRNA splicing, via spliceosome</a> <a href="#">RNA binding</a> <a href="#">nucleus</a> <a href="#">spliceosome complex</a> <a href="#">nucleolus</a>
<a href="#">201077_s_at</a>	NHP2L1	NHP2 non-histone chromosome protein 2-like 1 (S. cerevisiae)	0.73	22	-40399883	<a href="#">AF155235</a>	<a href="#">4809</a>	<a href="#">22q13.2-q13.31</a>	<a href="#">Hs.182255</a>	<a href="#">14</a>	<a href="#">ribosome biogenesis and assembly</a>
<a href="#">235982_at</a>	FCRL1	Fc receptor-like 1	0.72	1	-156031277	<a href="#">AA677057</a>	<a href="#">115350</a>	<a href="#">1q21-q22</a>	<a href="#">Hs.374126</a>	<a href="#">6</a>	<a href="#">receptor activity</a>
<a href="#">1568733_at</a>	C10orf76	chromosome 10 open reading frame 76	0.72	10	-103595345	<a href="#">BC032118</a>	<a href="#">79591</a>	<a href="#">10q24.32</a>	<a href="#">Hs.16004</a>	<a href="#">2</a>	
<a href="#">225478_at</a>			0.72			<a href="#">BE783723</a>					
<a href="#">210054_at</a>	C4orf15	chromosome 4 open reading frame 15	0.71	4	-2199893	<a href="#">BC003648</a>	<a href="#">79441</a>	<a href="#">4p16.3</a>	<a href="#">Hs.632582</a>	<a href="#">2</a>	
<a href="#">213019_at</a>	RANBP6	RAN binding protein 6	0.70	9	-6001019	<a href="#">AI123233</a>	<a href="#">26953</a>	<a href="#">9p24.1</a>	<a href="#">Hs.167496</a>	<a href="#">2</a>	<a href="#">binding</a> <a href="#">nucleus</a> <a href="#">protein transport</a>
<a href="#">244103_at</a>	C1orf55	chromosome 1 open reading frame 55	0.69	1	-224237030	<a href="#">AW963092</a>	<a href="#">163859</a>	<a href="#">1q42.12</a>	<a href="#">Hs.520192</a>	<a href="#">2</a>	
<a href="#">225265_at</a>	RBMS1	RNA binding motif, single stranded interacting protein 1	0.68	2	-160838760	<a href="#">AI580100</a>	<a href="#">5937</a>	<a href="#">2q24.2</a>	<a href="#">Hs.369265</a> <a href="#">Hs.470412</a>	<a href="#">10</a>	<a href="#">nucleotide binding</a> <a href="#">DNA binding</a> <a href="#">double-stranded DNA binding</a> <a href="#">double-stranded DNA binding</a> <a href="#">single-stranded DNA binding</a> <a href="#">single-stranded DNA binding</a> <a href="#">RNA binding</a> <a href="#">RNA binding</a> <a href="#">nucleus</a> <a href="#">nucleus</a> <a href="#">DNA replication</a> <a href="#">DNA replication</a> <a href="#">RNA processing</a> <a href="#">regulation of translation</a> <a href="#">cellular component unknown</a>
<a href="#">229157_at</a>	KCNH2	potassium voltage-gated channel, subfamily H (eag-related), member 2	0.67	7	-150272981, -150277447	<a href="#">AI949265</a>	<a href="#">3757</a>	<a href="#">7q35-q36</a>	<a href="#">Hs.438823</a>	<a href="#">100</a>	<a href="#">two-component sensor activity</a> <a href="#">two-component signal transduction system (phosphorelay)</a> <a href="#">delayed rectifier potassium channel activity</a> <a href="#">membrane fraction</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">ion transport</a> <a href="#">potassium ion transport</a> <a href="#">muscle contraction</a> <a href="#">sensory perception of sound</a> <a href="#">regulation of heart contraction</a> <a href="#">voltage-gated potassium channel</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">potassium ion binding</a>
<a href="#">239835_at</a>	KBTBD8	kelch repeat and BTB (POZ) domain containing	0.67	3	67132092	<a href="#">AA669114</a>	<a href="#">84541</a>	<a href="#">3p14</a>	<a href="#">Hs.116665</a>	<a href="#">3</a>	<a href="#">protein binding</a>
<a href="#">212723_at</a>	PTDSR	phosphatidylserine receptor	0.67	17	-72224004	<a href="#">AK021780</a>	<a href="#">23210</a>	<a href="#">17q25</a>	<a href="#">Hs.514505</a>	<a href="#">10</a>	<a href="#">nucleus</a> <a href="#">cell differentiation</a>
<a href="#">230304_at</a>			0.67			<a href="#">AW005298</a>					

<a href="#">240369_at</a>	TTC7A	tetratricopeptide repeat domain 7A	0.66	2	47021816	<a href="#">AW195569</a>	<a href="#">57217</a>	<a href="#">2p21</a>	<a href="#">Hs.370603</a>	<a href="#">3</a>	<a href="#">binding</a>	
<a href="#">203544_s_at</a>	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0.66	10	17726129	<a href="#">NM_003473</a>	<a href="#">8027</a>	<a href="#">10p14-p13</a>	<a href="#">Hs.441498</a>	<a href="#">24</a>	<a href="#">SH3/SH2 adaptor activity</a> <a href="#">intracellular protein transport</a> <a href="#">signal transduction</a>	<a href="#">Jak-STAT signaling pathway</a>
<a href="#">243797_at</a>	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	0.65	2	-196710102	<a href="#">AW070323</a>	<a href="#">9262</a>	<a href="#">2q32.3</a>	<a href="#">Hs.88297</a>	<a href="#">6</a>	<a href="#">nucleotide binding</a> <a href="#">protein serine/threonine kinase activity</a> <a href="#">ATP binding</a> <a href="#">nucleus</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">apoptosis</a> <a href="#">induction of apoptosis</a> <a href="#">protein kinase cascade</a> <a href="#">transferase activity</a>	
<a href="#">212681_at</a>	EPB41L3	erythrocyte membrane protein band 4.1-like 3	0.65	18	-5382387	<a href="#">AI770004</a>	<a href="#">23136</a>	<a href="#">18p11.32</a>	<a href="#">Hs.213394</a>	<a href="#">31</a>	<a href="#">biological process unknown</a> <a href="#">actin binding</a> <a href="#">structural molecule activity</a> <a href="#">binding</a> <a href="#">cytoplasm</a> <a href="#">cytoskeleton</a> <a href="#">plasma membrane</a> <a href="#">intercellular junction</a> <a href="#">cortical actin cytoskeleton organization</a> <a href="#">and biogenesis</a>	<a href="#">Tight junction</a>
<a href="#">235593_at</a>	ZFX1B	zinc finger homeobox 1b	0.64	2	-144862053	<a href="#">AL546529</a>	<a href="#">9839</a>	<a href="#">2q22</a>	<a href="#">Hs.34871</a>	<a href="#">28</a>	<a href="#">transcription factor activity</a> <a href="#">intracellular</a> <a href="#">nucleus</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">nervous system development</a> <a href="#">zinc ion binding</a> <a href="#">negative regulation of transcription</a> <a href="#">transcriptional repressor activity</a> <a href="#">phosphatase regulator activity</a> <a href="#">sequence-specific DNA binding</a> <a href="#">SMAD binding</a> <a href="#">metal ion binding</a>	
<a href="#">202988_s_at</a>	RGS1	regulator of G-protein signalling 1	0.64	1	190811479	<a href="#">NM_002922</a>	<a href="#">5996</a>	<a href="#">1q31</a>	<a href="#">Hs.75256</a>	<a href="#">17</a>	<a href="#">signal transducer activity</a> <a href="#">GTPase activator activity</a> <a href="#">calmodulin binding</a> <a href="#">plasma membrane</a> <a href="#">immune response</a> <a href="#">signal transduction</a> <a href="#">G-protein signaling, adenylate cyclase</a> <a href="#">inhibiting pathway</a> <a href="#">negative regulation of signal</a>	
<a href="#">209273_s_at</a>	HBLD2	HESB like domain containing 2	0.63	9	-88069283	<a href="#">BG387555</a>	<a href="#">81689</a>	<a href="#">9q21.33</a>	<a href="#">Hs.449291</a>	<a href="#">5</a>	<a href="#">iron ion binding</a> <a href="#">molecular function unknown</a> <a href="#">mitochondrion</a> <a href="#">metal ion binding</a> <a href="#">iron-sulfur cluster binding</a>	
<a href="#">227577_at</a>	EXOC8	exocyst complex component 8	0.63	1	-229535105	<a href="#">AI168350</a>	<a href="#">149371</a>	<a href="#">1q42.2</a>	<a href="#">Hs.356198</a>	<a href="#">12</a>	<a href="#">protein binding</a> <a href="#">exocytosis</a> <a href="#">protein transport</a> <a href="#">microtubule motor activity</a> <a href="#">protein binding</a> <a href="#">microtubule</a>	

<a href="#">229106_at</a>	DYNLL2	dynein, light chain, LC8-type 2	0.63	17	53515797	<a href="#">AA401429</a>	140735	17q22	Hs.591176	11	<a href="#">microtubule-based process</a> <a href="#">myosin</a> <a href="#">dynein complex</a> <a href="#">intracellular transport</a>	
<a href="#">202146_at</a>	IFRD1	interferon-related developmental regulator 1	0.62	7	111850461, 111877750	<a href="#">AA747426</a>	3475	7q22-q31	Hs.7879	12	<a href="#">binding</a> <a href="#">myoblast cell fate determination</a> <a href="#">cell differentiation</a>	
<a href="#">222309_at</a>	C6orf62	chromosome 6 open reading frame 62	0.62	6	-24813145	<a href="#">AW972292</a>	81688	6p22.2	Hs.519930	3	<a href="#">biological process unknown</a> <a href="#">molecular function unknown</a> <a href="#">cellular component unknown</a>	
<a href="#">219557_s_at</a>	NRIP3	nuclear receptor interacting protein 3	0.61	11	-8960968	<a href="#">NM_020645</a>	56675	11p15.3	Hs.523467	3		
<a href="#">1556874_a_at</a>	RKHD2	ring finger and KH domain containing 2	0.61	18	-46954919	<a href="#">BC032952</a>	51320	18q21.2	Hs.465144	2		
<a href="#">228702_at</a>	FLJ43663		0.61	7		<a href="#">AL569506</a>	378805	7q32.3	Hs.150556	2		
<a href="#">202558_s_at</a>	STCH	stress 70 protein chaperone, microsome-associated, 60kDa	0.60	21	-14665309	<a href="#">NM_006948</a>	6782	21q11.1 21q11	Hs.352341	12	<a href="#">nucleotide binding</a> <a href="#">ATP binding</a> <a href="#">endoplasmic reticulum</a> <a href="#">microsome</a>	
<a href="#">202637_s_at</a>	ICAM1	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor	0.60	19	10242778	<a href="#">AI608725</a>	3383	19p13.3- p13.2	Hs.643447	239	<a href="#">transmembrane receptor activity</a> <a href="#">protein binding</a> <a href="#">plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">cell-cell adhesion</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Natural killer cell mediated</a> <a href="#">Leukocyte transendothelial</a>
<a href="#">226650_at</a>	MGC11257		0.60	7	-1003168	<a href="#">AI984061</a>	84310	7p22.3	Hs.116567	5		
<a href="#">231863_at</a>	ING3	inhibitor of growth family, member 3	0.60	7	120378052	<a href="#">AF161419</a>	54556	7q31	Hs.489811	11	<a href="#">regulation of cell growth</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">zinc ion binding</a> <a href="#">chromatin modification</a> <a href="#">metal ion binding</a>	
<a href="#">228999_at</a>	CHD2	chromodomain helicase DNA binding protein 2	0.59	15	91244422	<a href="#">AW514564</a>	1106	15q26	Hs.220864	5	<a href="#">nucleotide binding</a> <a href="#">chromatin</a> <a href="#">DNA binding</a> <a href="#">chromatin binding</a> <a href="#">ATP-dependent DNA helicase activity</a> <a href="#">ATP binding</a> <a href="#">nucleus</a> <a href="#">chromatin assembly or disassembly</a> <a href="#">regulation of transcription from RNA polymerase II promoter</a> <a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a> <a href="#">hydrolase activity</a> <a href="#">regulation of transcription</a>	
<a href="#">206420_at</a>	IGSF6	immunoglobulin superfamily, member 6	0.58	16	-21560106	<a href="#">NM_005849</a>	10261	16p12-p13	Hs.530902	6	<a href="#">transmembrane receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">cell surface receptor linked signal transduction</a>	
											<a href="#">rhodopsin-like receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">signal transduction</a>	

<a href="#">205220_at</a>	GPR109B	G protein-coupled receptor 109B	0.58	12	-121765256	<a href="#">NM_006018</a>	8843	<a href="#">12q24.31</a>	<a href="#">Hs.458425</a>	6	<a href="#">G-protein coupled receptor protein signaling pathway</a> <a href="#">membrane</a> <a href="#">purinergic nucleotide receptor activity</a> <a href="#">G-protein coupled</a>
<a href="#">218936_s_at</a>	CCDC59	coiled-coil domain containing 59	0.58	12	-81270750	<a href="#">NM_014167</a>	29080	<a href="#">12q21.31</a>	<a href="#">Hs.582627</a>	3	
<a href="#">230048_at</a>	IFRD1	interferon-related developmental regulator 1	0.58	7	111850461, 111877750	<a href="#">BF061555</a>	3475	<a href="#">7q22-q31</a>	<a href="#">Hs.7879</a>	12	<a href="#">binding</a> <a href="#">myoblast cell fate determination</a> <a href="#">cell differentiation</a>
<a href="#">1568768_s_at</a>	BRE	brain and reproductive organ-expressed (TNFRSF1A modulator)	0.57	2	27967060, 27966985	<a href="#">AW080339</a>	9577	<a href="#">2p23.2</a>	<a href="#">Hs.11916</a> <a href="#">Hs.258314</a>	13	<a href="#">nuclear ubiquitin ligase complex</a> <a href="#">peroxisome targeting sequence binding</a> <a href="#">tumor necrosis factor receptor binding</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">cytoplasm</a> <a href="#">ubiquitin cycle</a> <a href="#">apoptosis</a> <a href="#">response to DNA damage stimulus</a> <a href="#">positive regulation of anti-apoptosis</a>
<a href="#">209795_at</a>	CD69	CD69 molecule	0.55	12	-9796352	<a href="#">L07555</a>	969	<a href="#">12p13-p12</a>	<a href="#">Hs.208854</a>	31	<a href="#">transmembrane receptor activity</a> <a href="#">sugar binding</a> <a href="#">integral to plasma membrane</a> <a href="#">defense response</a> <a href="#">cell surface receptor linked signal transduction</a> <a href="#">membrane</a>
<a href="#">212434_at</a>	GRPEL1	GrpE-like 1, mitochondrial (E. coli)	0.55	4	-7112680	<a href="#">AI984421</a>	80273	<a href="#">4p16</a>	<a href="#">Hs.443723</a>	5	<a href="#">adenyl-nucleotide exchange factor</a> <a href="#">mitochondrion</a> <a href="#">mitochondrial matrix</a> <a href="#">protein folding</a> <a href="#">protein import into mitochondrial matrix</a> <a href="#">protein homodimerization activity</a> <a href="#">unfolded protein binding</a> <a href="#">chaperone binding</a>
<a href="#">212998_x_at</a>	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.54	6	-3813334, - 4009260	<a href="#">AI583173</a>	3119	<a href="#">6p21.3</a>	<a href="#">Hs.409934</a> <a href="#">Hs.534322</a>	129	<a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>
											<a href="#">regulation of progression through cell cycle</a> <a href="#">nucleotide binding</a> <a href="#">regulation of cell growth</a> <a href="#">GTPase activity</a> <a href="#">protein binding</a> <a href="#">GTP binding</a> <a href="#">intracellular</a> <a href="#">cytoplasm</a> <a href="#">plasma membrane</a> <a href="#">cell cycle</a>
											<a href="#">MAPK signaling pathway</a> NA <a href="#">Axon guidance</a> <a href="#">Focal adhesion</a> <a href="#">Adherens junction</a> <a href="#">Tight junction</a> <a href="#">T cell receptor signaling</a> <a href="#">Leukocyte transendothelial</a> <a href="#">Regulation of actin cytoskeleton</a> NA

											establishment and/or maintenance of cell polarity small GTPase mediated signal transduction membrane actin cytoskeleton organization and biogenesis filopodium macrophage differentiation positive regulation of pseudopodium formation negative regulation of protein complex assembly cell division G1 phase	Epithelial cell signaling in Helicobacter pylori infection NA NA
<a href="#">214230_at</a>	CDC42	cell division cycle 42 (GTP binding protein, 25kDa)	0.53	1	22251706	<a href="#">R37664</a>	998	<a href="#">1p36.1</a>	<a href="#">Hs.597524</a>	171		
<a href="#">218723_s_at</a>	RGC32		0.53	13	40929711	<a href="#">NM_014059</a>	28984	<a href="#">13q14.11</a>	<a href="#">Hs.507866</a>	7		
<a href="#">227697_at</a>	SOCS3	suppressor of cytokine signaling 3	0.52	17	-73864458	<a href="#">AI244908</a>	9021	<a href="#">17q25.3</a>	<a href="#">Hs.527973</a>	64	regulation of cell growth protein kinase inhibitor activity anti-apoptosis intracellular signaling cascade JAK-STAT cascade negative regulation of signal	Jak-STAT signaling pathway Insulin signaling pathway Adipocytokine signaling Type II diabetes mellitus
<a href="#">211654_x_at</a>	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.51	6	-3813334, -4009260	<a href="#">M17565</a>	3119	<a href="#">6p21.3</a>	<a href="#">Hs.409934</a> <a href="#">Hs.534322</a>	129	immune response immune response membrane membrane integral to membrane antigen presentation, exogenous antigen processing, exogenous antigen via MHC class II MHC class II receptor activity MHC class II receptor activity	Cell adhesion molecules Antigen processing and Type I diabetes mellitus
<a href="#">213537_at</a>	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	0.49	6	-33140771, -4219191, -4413300	<a href="#">AI128225</a>	3113	<a href="#">6p21.3</a>	<a href="#">Hs.347270</a>	29	integral to plasma membrane immune response immune response membrane antigen presentation, exogenous antigen processing, exogenous antigen via MHC class II MHC class II receptor activity MHC class II receptor activity	Cell adhesion molecules Antigen processing and Type I diabetes mellitus
<a href="#">226370_at</a>	KLHL15	kelch-like 15 (Drosophila)	0.49	X	-23915883	<a href="#">BG149487</a>	80311	<a href="#">Xp22.1-p21</a>	<a href="#">Hs.495854</a>	3	protein binding	
<a href="#">216834_at</a>	RGS1	regulator of G-protein signalling 1	0.45	1	190811479	<a href="#">S59049</a>	5996	<a href="#">1q31</a>	<a href="#">Hs.75256</a>	17	signal transducer activity GTPase activator activity calmodulin binding plasma membrane immune response signal transduction G-protein signaling, adenylate cyclase inhibiting pathway negative regulation of signal	
											integral to plasma membrane immune response immune response membrane integral to membrane antigen presentation, exogenous	Cell adhesion molecules Antigen processing and Type I diabetes mellitus

<a href="#">236203_at</a>	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	0.38	6	32713160	<a href="#">AI377755</a>	<a href="#">3117</a>	<a href="#">6p21.3</a>	<a href="#">Hs.387679</a>	<a href="#">70</a>	<a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	
<a href="#">206157_at</a>	PTX3	pentraxin-related gene, rapidly induced by IL-1	0.35	3	158637300	<a href="#">NM_002852</a>	<a href="#">5806</a>	<a href="#">3q25</a>	<a href="#">Hs.591286</a>	<a href="#">28</a>	<a href="#">extracellular region</a> <a href="#">inflammatory response</a>	
<a href="#">212999_x_at</a>	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.35	6	-3813334, -4009260	<a href="#">AW276186</a>	<a href="#">3119</a>	<a href="#">6p21.3</a>	<a href="#">Hs.409934</a> <a href="#">Hs.534322</a>	<a href="#">129</a>	<a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">213831_at</a>	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	0.31	6	32713160	<a href="#">X00452</a>	<a href="#">3117</a>	<a href="#">6p21.3</a>	<a href="#">Hs.387679</a>	<a href="#">70</a>	<a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">209480_at</a>	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	0.28	6	-3813334, -4009260	<a href="#">M16276</a>	<a href="#">3119</a>	<a href="#">6p21.3</a>	<a href="#">Hs.409934</a> <a href="#">Hs.534322</a>	<a href="#">129</a>	<a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">238900_at</a>	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	0.22	6	-32654526	<a href="#">BE669692</a>	<a href="#">3123</a>	<a href="#">6p21.3</a>	<a href="#">Hs.534322</a>	<a href="#">213</a>	<a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Hematopoietic cell lineage</a> <a href="#">Type I diabetes mellitus</a>

Supplemental Material, Table 2. Listing of all urinary arsenic SAM-selected probes.

Probe	Symbol	Description	Chromosome	Chromosome Location	GenBank	LocusLink	Cytoband	UniGene	PubMed	Gene Ontology	Pathway
<a href="#">203290_at</a>	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	6	32713160	<a href="#">NM_002122</a>	<a href="#">3117</a>	6p21.3	<a href="#">Hs.387679</a>	70	<a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">antigen presentation, exogenous</a> <a href="#">antigen processing, exogenous</a> <a href="#">antigen via MHC class II</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a> <a href="#">MHC class II receptor activity</a>	<a href="#">Cell adhesion molecules</a> <a href="#">Antigen processing and</a> <a href="#">Type I diabetes mellitus</a>
<a href="#">207314_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	19	60053740	<a href="#">NM_006737</a>	<a href="#">3812</a>	19q13.4	<a href="#">Hs.512572</a>	19	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">211389_x_at</a>	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	19	59989604	<a href="#">U73396</a>	<a href="#">3811</a>	19q13.4	<a href="#">Hs.512572</a> <a href="#">Hs.643606</a>	32	<a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">natural killer cell activation</a> <a href="#">negative regulation of natural killer cell activity</a> <a href="#">MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">211688_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	19	60053740	<a href="#">AF263617</a>	<a href="#">3812</a>	19q13.4	<a href="#">Hs.512572</a>	19	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">216907_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	19	60053740	<a href="#">X93596</a>	<a href="#">3812</a>	19q13.4	<a href="#">Hs.512572</a>	19	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">216676_x_at</a>	KIR3DL3	receptor, three domains, long cytoplasmic tail, 3	19	59927795	<a href="#">AC006293</a>	<a href="#">115653</a>	19q13.42	<a href="#">Hs.512572</a>	4		<a href="#">Antigen processing and</a> <a href="#">presentation</a>
<a href="#">1553177_at</a>	SH2D1B	SH2 domain containing 1B	1	-160631679	<a href="#">BC022407</a>	<a href="#">117157</a>	1q21	<a href="#">Hs.350581</a>	10	<a href="#">biological process unknown</a> <a href="#">molecular function unknown</a> <a href="#">intracellular signaling cascade</a> <a href="#">cellular component unknown</a>	<a href="#">Natural killer cell mediated</a> <a href="#">cytotoxicity</a>
<a href="#">211397_x_at</a>	KIR2DL2	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	19	164614	<a href="#">L76669</a>	<a href="#">3803</a>	19q13.4	<a href="#">Hs.643606</a>	18	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and</a> <a href="#">Natural killer cell mediated</a>
<a href="#">218723_s_at</a>	RGC32		13	40929711	<a href="#">NM_014059</a>	<a href="#">28984</a>	13q14.11	<a href="#">Hs.507866</a>	7		
										<a href="#">calcium ion binding</a> <a href="#">cytosol</a> <a href="#">virus-infected cell apoptosis</a> <a href="#">transformed cell apoptosis</a>	<a href="#">Natural killer cell mediated</a> <a href="#">Type I diabetes mellitus</a>



<a href="#">1553681_a_at</a>	PRF1	perforin 1 (pore forming protein)	10	-72027110	<a href="#">NM_005041</a>	<a href="#">5551</a>	<a href="#">10q22</a>	<a href="#">Hs.2200</a>	<a href="#">44</a>	<a href="#">cellular defense response</a> <a href="#">pathogenesis</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">cytolysis</a> <a href="#">hemolysis of host red blood cells</a>	
<a href="#">212509_s_at</a>	PSMD14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	2	161873185	<a href="#">BF968134</a>	<a href="#">10213</a>	<a href="#">2q24.2</a>	<a href="#">Hs.567410</a>	<a href="#">3</a>	<a href="#">proteasome complex (sensu cytosol)</a> <a href="#">catabolism</a>	<a href="#">Proteasome</a>
<a href="#">211687_x_at</a>	KIR3DL1	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	19	59989604	<a href="#">AF262973</a>	<a href="#">3811</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a> <a href="#">Hs.643606</a>	<a href="#">32</a>	<a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">natural killer cell activation</a> <a href="#">negative regulation of natural killer cell activity</a> <a href="#">MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a> <a href="#">HLA-B specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">210890_x_at</a>	KIR2DL1	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	19	59973076	<a href="#">U24078</a>	<a href="#">3802</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a> <a href="#">Hs.643606</a>	<a href="#">29</a>	<a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">negative regulation of natural killer cell activity</a> <a href="#">HLA-C specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">208203_x_at</a>	KIR2DS5	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5	19	240823	<a href="#">NM_014513</a>	<a href="#">3810</a>	<a href="#">19q13.4</a>	<a href="#">Hs.643606</a>	<a href="#">6</a>	<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">membrane</a> <a href="#">HLA-C specific inhibitory MHC class I receptor activity</a>	<a href="#">Antigen processing and presentation</a>
<a href="#">205547_s_at</a>	TAGLN	transgelin	11	116575249	<a href="#">NM_003186</a>	<a href="#">6876</a>	<a href="#">11q23.2</a>	<a href="#">Hs.632099</a>	<a href="#">18</a>	<a href="#">actin binding</a> <a href="#">muscle development</a> <a href="#">muscle development</a>	
<a href="#">203921_at</a>	CHST2	carbohydrate (N-acetylglucosamine-6-O) sulfotransferase 2	3	144321357	<a href="#">NM_004267</a>	<a href="#">9435</a>	<a href="#">3q24</a>	<a href="#">Hs.8786</a>	<a href="#">10</a>	<a href="#">N-acetylglucosamine 6-O-sulfotransferase activity</a> <a href="#">Golgi trans face</a> <a href="#">carbohydrate metabolism</a> <a href="#">N-acetylglucosamine metabolism</a> <a href="#">sulfur metabolism</a> <a href="#">inflammatory response</a> <a href="#">membrane</a> <a href="#">integral to membrane</a> <a href="#">transferase activity</a> <a href="#">intrinsic to Golgi membrane</a>	<a href="#">Keratan sulfate biosynthesis</a> <a href="#">Glycan structures -</a>
										<a href="#">microtubule motor activity</a> <a href="#">protein binding</a>	

										<a href="#">microtubule</a> <a href="#">microtubule-based process</a> <a href="#">myosin</a> <a href="#">dynein complex</a> <a href="#">intracellular transport</a>	
<a href="#">229106_at</a>	DYNLL2	dynein, light chain, LC8-type 2	17	53515797	<a href="#">AA401429</a>	<a href="#">140735</a>	<a href="#">17q22</a>	<a href="#">Hs.591176</a>	11		
										<a href="#">receptor activity</a> <a href="#">hematopoietin/interferon-class (D200-domain) cytokine receptor</a> <a href="#">interleukin-2 receptor activity</a> <a href="#">plasma membrane</a> <a href="#">integral to plasma membrane</a> <a href="#">protein complex assembly</a> <a href="#">signal transduction</a> <a href="#">external side of plasma membrane</a> <a href="#">cytokine and chemokine mediated signaling pathway</a> <a href="#">positive regulation of survival gene product activity</a>	<a href="#">Cytokine-cytokine Jak-STAT signaling pathway</a>
<a href="#">205291_at</a>	IL2RB	interleukin 2 receptor, beta	22	-35851827	<a href="#">NM_000878</a>	<a href="#">3560</a>	22q13 22q13.1	<a href="#">Hs.474787</a>	54		
										<a href="#">nucleotide binding</a> <a href="#">protein serine/threonine kinase</a> <a href="#">ATP binding</a> <a href="#">nucleus</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">apoptosis</a> <a href="#">induction of apoptosis</a> <a href="#">protein kinase cascade</a> <a href="#">transferase activity</a>	
<a href="#">243797_at</a>	STK17B	serine/threonine kinase 17b (apoptosis-inducing)	2	-196710102	<a href="#">AW070323</a>	<a href="#">9262</a>	<a href="#">2q32.3</a>	<a href="#">Hs.88297</a>	6		
										<a href="#">receptor activity</a> <a href="#">integral to plasma membrane</a> <a href="#">cellular defense response</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">207313_x_at</a>	KIR3DL2	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2	19	60053740	<a href="#">L76666</a>	<a href="#">3812</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	19		
										<a href="#">regulation of progression through cell cycle</a>  <a href="#">nucleotide binding</a> <a href="#">protein-tyrosine kinase activity</a> <a href="#">protein-tyrosine kinase activity</a> <a href="#">protein binding</a> <a href="#">ATP binding</a> <a href="#">soluble fraction</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">protein amino acid phosphorylation</a> <a href="#">intracellular signaling cascade</a> <a href="#">mesoderm development</a> <a href="#">cell proliferation</a> <a href="#">positive regulation of cell transferase activity</a>	<a href="#">Regulation of actin cytoskeleton</a> <a href="#">Epithelial cell signaling in Helicobacter pylori</a>
<a href="#">206267_s_at</a>	MATK	megakaryocyte-associated tyrosine kinase	19	-3728967	<a href="#">NM_002378</a>	<a href="#">4145</a>	<a href="#">19p13.3</a>	<a href="#">Hs.631845</a>	28		
<a href="#">236717_at</a>	LOC165186		2	29109800	<a href="#">AI632621</a>	<a href="#">165186</a>	<a href="#">2p23.2</a>	<a href="#">Hs.47647</a>			
										<a href="#">binding</a>	
										<a href="#">biological process unknown</a> <a href="#">antigen binding</a> <a href="#">receptor activity</a> <a href="#">receptor activity</a> <a href="#">molecular function unknown</a> <a href="#">integral to plasma membrane</a> <a href="#">immune response</a> <a href="#">cellular component unknown</a> <a href="#">membrane</a>	<a href="#">Antigen processing and Natural killer cell mediated</a>
<a href="#">208179_x_at</a>	KIR2DL3	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3	19	59941785	<a href="#">AF022048</a>	<a href="#">3804</a>	<a href="#">19q13.4</a>	<a href="#">Hs.512572</a>	24		

										calcium ion binding cytosol virus-infected cell apoptosis transformed cell apoptosis cellular defense response pathogenesis membrane integral to membrane cytolysis hemolysis of host red blood cells	Natural killer cell mediated Type I diabetes mellitus
<a href="#">214617_at</a>	PRF1	perforin 1 (pore forming protein)	10	-72027110	<a href="#">AI445650</a>	<a href="#">5551</a>	<a href="#">10q22</a>	<a href="#">Hs.2200</a>	<a href="#">44</a>		
<a href="#">211410_x_at</a>	KIR2DL5A	killer cell immunoglobulin-like receptor, two domains, long	19	229379	<a href="#">AF217487</a>	<a href="#">57292</a>	<a href="#">19p13.3</a>	<a href="#">Hs.643606</a>	<a href="#">8</a>	receptor activity	Antigen processing and cytotoxicity
										nucleic acid binding DNA binding protein binding intracellular nucleus transcription regulation of transcription, DNA-dependent zinc ion binding metal ion binding	
<a href="#">225884_s_at</a>	ZNF336	zinc finger protein 336	20	23293020	<a href="#">AL046381</a>	<a href="#">64412</a>	<a href="#">20p12.3- p11.21</a>	<a href="#">Hs.28921</a>	<a href="#">4</a>		
										immunological synapse serine-type endopeptidase activity granzyme B activity nucleus cytoplasm proteolysis apoptosis cleavage of lamin peptidase activity cytolysis	Natural killer cell mediated Type I diabetes mellitus
<a href="#">210164_at</a>	GZMB	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	14	-24170003	<a href="#">J03189</a>	<a href="#">3002</a>	<a href="#">14q11.2</a>	<a href="#">Hs.1051</a>	<a href="#">90</a>		
										protein binding nucleus nuclear pore mRNA processing mRNA export from nucleus protein targeting protein transport membrane integral to membrane	
<a href="#">212316_at</a>	NUP210	nucleoporin 210kDa	3	-13332736	<a href="#">AA502912</a>	<a href="#">23225</a>	<a href="#">3p25.1</a>	<a href="#">Hs.475525</a>	<a href="#">19</a>		
										transmembrane receptor activity receptor signaling protein activity protein binding cytoplasm plasma membrane cell surface receptor linked signal transduction membrane integral to membrane T cell receptor complex protein homodimerization activity	Natural killer cell mediated T cell receptor signaling
<a href="#">210031_at</a>	CD247	CD247 molecule	1	-165666507	<a href="#">J04132</a>	<a href="#">919</a>	<a href="#">1q22-q23</a>	<a href="#">Hs.156445</a>	<a href="#">95</a>		
		killer cell immunoglobulin-like receptor, two domains, long		60006877,						receptor activity transmembrane receptor activity integral to plasma membrane cellular defense response signal transduction	Antigen processing and Natural killer cell mediated

<a href="#">211245_x_at</a>	KIR2DL4	cytoplasmic tail, 4	19	199896	<a href="#">AF002256</a>	3805	19q13.4	<a href="#">Hs.512572</a>	30	<a href="#">membrane</a>
										<a href="#">nucleotide binding</a> <a href="#">chromatin</a> <a href="#">DNA binding</a> <a href="#">chromatin binding</a> <a href="#">ATP-dependent DNA helicase</a> <a href="#">ATP binding</a> <a href="#">nucleus</a> <a href="#">chromatin assembly or disassembly</a> <a href="#">regulation of transcription from RNA polymerase II promoter</a> <a href="#">chromosome organization and biogenesis (sensu Eukaryota)</a> <a href="#">hydrolase activity</a> <a href="#">regulation of transcription</a>
<a href="#">228999_at</a>	CHD2	chromodomain helicase DNA binding protein 2	15	91244422	<a href="#">AW514564</a>	1106	15q26	<a href="#">Hs.220864</a>	5	
<a href="#">228702_at</a>	FLJ43863		7		<a href="#">AL569506</a>	378805	7q32.3	<a href="#">Hs.150556</a>	2	
<a href="#">226650_at</a>	MGC11257		7	-1003168	<a href="#">AI984061</a>	84310	7p22.3	<a href="#">Hs.116567</a>	5	
										<a href="#">binding</a> <a href="#">cytoskeleton</a> <a href="#">phagocytosis</a> <a href="#">apoptosis</a> <a href="#">membrane</a>
<a href="#">221528_s_at</a>	ELMO2	engulfment and cell motility 2	20	-44428098	<a href="#">BC000143</a>	63916	20q13	<a href="#">Hs.210469</a>	7	
										<a href="#">biological process unknown</a> <a href="#">chromosome, pericentric region</a> <a href="#">DNA binding</a> <a href="#">molecular function unknown</a> <a href="#">nucleus</a> <a href="#">cellular component unknown</a> <a href="#">regulation of transcription</a>
<a href="#">1553099_at</a>	TIGD1	tigger transposable element derived 1	2	-233121022	<a href="#">NM_145702</a>	200765	2q37.1	<a href="#">Hs.211823</a>	4	
										<a href="#">regulation of cell growth</a> <a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">transcription</a> <a href="#">regulation of transcription, DNA-dependent</a> <a href="#">zinc ion binding</a> <a href="#">chromatin modification</a> <a href="#">metal ion binding</a>
<a href="#">231863_at</a>	ING3	inhibitor of growth family, member 3	7	120378052	<a href="#">AF161419</a>	54556	7q31	<a href="#">Hs.489811</a>	11	
										<a href="#">protein binding</a> <a href="#">nucleus</a> <a href="#">nuclear pore</a> <a href="#">mRNA processing</a> <a href="#">mRNA export from nucleus</a> <a href="#">protein targeting</a> <a href="#">protein transport</a> <a href="#">membrane</a> <a href="#">integral to membrane</a>
<a href="#">213947_s_at</a>	NUP210	nucleoporin 210kDa	3	-13332736	<a href="#">AI867102</a>	23225	3p25.1	<a href="#">Hs.475525</a>	19	
<a href="#">213069_at</a>	HEG1	HEG homolog 1 (zebrafish)	3		<a href="#">AI148659</a>	57493	3q21.2	<a href="#">Hs.477420</a>	4	

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