Table S1. Genes showing significant 1.5-fold or greater changes in expression in both ethanol-treated and nicotine-treated animals compared with control animals

Biological process term	Probe set ID	Gene symbol	Gene title	Molecular function term	Cellular component term
Protein modification/ ubiquitination					
Protein modification process Ubiquitin cycle	Dr10525.1.S1_at	hectd1	HECT domain containing 1	Ubiquitin-protein ligase activity binding transferase activity ligase activity	Intracellular
Protein amino acid glycosylation	Dr11084.1.A1_at	zgc:76904	zgc:76904	Galactosyltransferase activity	Membrane
Ubiquitin cycle Zinc ion transport	Dr11667.1.S1_at	zgc:55389	zgc:55389	Protein binding zinc ion binding ligase activity metal ion binding	
Proteolysis	Dr12473.1.A1_at	npepps	aminopeptidase puromycin sensitive	Membrane alanyl aminopeptidase activity	
Ubiquitin-dependent protein catabolic process	Dr15777.1.A1_at	zgc:92791	zgc:92791	Endopeptidase activity threonine endopeptidase activity endopeptidase inhibitor activity peptidase activity hydrolase activity	Cytosol proteasome core complex (*sensu* Eukaryota) protein complex
Ubiquinone biosynthetic process protein metabolic process	Dr19634.1.S1_at	LOC559504	Hypothetical LOC559504	Oxidoreductase activity transition metal ion binding	
Proteolysis	Dr24341.1.S1_at	lgmn	legumain	Legumain activity cysteine-type endopeptidase activity	
Protein folding	Dr26406.1.S1_at	zgc:110686	zgc:110686	Protein binding unfolded protein binding	Prefoldin complex
Protein modification process Ubiquitin cycle	Dr2897.1.S1_at	LOC100001969 zgc:56340	zgc:56340 Hypothetical protein LOC100001969	Ubiquitin-protein ligase activity ligase activity small conjugating protein ligase activity	
Ubiquitin cycle Zinc ion transport	Dr3405.1.S1_at	syvn1	synovial apoptosis inhibitor 1, synoviolin	Protein binding zinc ion binding ligase activity metal ion binding	Endoplasmic reticulum membrane integral to membrane
Protein ubiquitination	Dr3564.1.S1_at	prp19	PRP19/PSO4 homolog (S. cerevisiae)	Ubiquitin-protein ligase activity	Ubiquitin ligase complex
Ubiquitin cycle	Dr8165.1.S1_at	fbxw4	F-box and WD-40 domain protein 4		Nucleus
Transcription/ translation					
mRNA processing RNA splicing	Dr1062.1.A1_at	ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	Nucleotide binding nucleic acid binding RNA binding Helicase activity ATP binding ATP-dependent helicase activity hydrolase activity	Nucleus
Regulation of transcription, DNA-dependent	Dr11222.1.A1_at	sox5	SRY-box containing gene 5	DNA binding	

Transcription RNA elongation regulation of transcription, DNA-dependent ATP synthesis coupled proton transport regulation of transcription	Dr11529.1.S1_at	tcea1	transcription elongation factor A (SII), 1	DNA binding RNA polymerase II transcription factor activity translation elongation factor activity zinc ion binding transcription regulator activity hydrogen ion transporting ATP synthase activity, rotational mechanism hydrogen ion transporting ATPase activity, rotational mechanism	Nucleus membrane proton-transporting two-sector ATPase complex
Regulation of transcription, DNA-dependent zinc ion transport	Dr1216.1.A1_at	atf7b	activating transcription factor 7b	Nucleic acid binding DNA binding transcription factor activity zinc ion binding sequence-specific DNA binding metal ion binding protein dimerization activity	Intracellular nucleus
Transcription transcription termination regulation of transcription, DNA-dependent transcription antitermination	Dr1403.1.S1_at	mef2d	myocyte enhancer factor 2d	DNA binding transcription factor activity sequence-specific DNA binding	Nucleus
DNA metabolic process chromosome organization and biogenesis	Dr1653.1.S1_at	smc4	structural maintenance of chromosomes 4	Protein binding ATP binding	Chromosome membrane
Regulation of transcription, DNA-dependent	Dr20806.1.S1_at	ing3	inhibitor of growth family, member 3	Protein binding zinc ion binding	
Transcription	Dr22506.1.A1_at	crsp7	cofactor required for Sp1 transcriptional activation, subunit 7		Nucleus
Translation	Dr284.3.S1_a_at	rpl6	ribosomal protein L6	Structural constituent of ribosome	Intracellular ribosome ribonucleoprotein complex
Translation translational initiation	Dr4943.1.S1_at	eif1b	eukaryotic translation initiation factor 1B	Translation initiation factor activity	
Translation	Dr8.2.S1_at	LOC798360 rpl5b	ribosomal protein L5b similar to ribosomal protein L5b	Structural constituent of ribosome 5S rRNA binding	Intracellular ribosome
Protein amino acid phosphorylation	Dr811.1.S1_at	rps6kal	ribosomal protein S6 kinase, like	Nucleotide binding magnesium ion binding protein kinase activity protein serine/threonine kinase activity serine-type endopeptidase Inhibitor activity ATP binding kinase activity transferase activity metal ion binding	
	Dr9079.1.S1_at	brd8	bromodomain containing 8		

Translation	Dr9746.3.S1_at	rpl19	ribosomal protein L19	Structural constituent of ribosome	Intracellular ribosome ribonucleoprotein complex
Neurotransmission/ synaptic plasticity					
Protein amino acid phosphorylation cell adhesion multicellular organismal development nervous system development cell differentiation	Dr12598.1.S1_at	ncam2	neural cell adhesion molecule 2	Vascular endothelial growth factor receptor activity protein binding ATP binding	Membrane attack complex membrane
	Dr12849.2.A1_a_at		Similar to NMDA receptor 1		
	Dr16098.1.S1_at	hcrtr2	hypocretin (orexin) receptor 2		
	Dr16352.1.A1_at	LOC562471	Similar to SLIT and NTRK-like family, member 5		
Protein amino acid phosphorylation transmembrane receptor protein tyrosine kinase signaling pathway	Dr17564.1.A1_at	epha4b	Eph receptor A4b	Nucleotide binding protein kinase activity protein-tyrosine kinase activity receptor activity ephrin receptor activity ATP binding kinase activity transferase activity	Membrane attack complex membrane integral to membrane
Ion transport	Dr18279.1.S1_at	gria2a	glutamate receptor, ionotropic, AMPA 2a	Receptor activity ionotropic glutamate receptor activity ion channel activity glutamate-gated ion channel activity	Membrane
Calcium ion transport homophilic cell adhesion	Dr21026.1.S1_at	pcdh10a	protocadherin 10a	Calcium channel activity calcium ion binding calcium channel inhibitor activity	Membrane
Catecholamine metabolic process lipid metabolic process xenobiotic metabolic process steroid metabolic process	Dr24258.1.S1_at	sult1st2	sulfotransferase family 1, cytosolic sulfotransferase 2	Sulfotransferase activity sulfotransferase activity transferase activity	Cytoplasm
	Dr3199.1.A1_at	LOC556181	Similar to solute carrier family 1 (glial high affinity glutamate transporter), member 3		
Gamma-aminobutyric acid metabolic process	Dr5312.1.S1_at	abat	4-Aminobutyrate aminotransferase	Catalytic activity 4-aminobutyrate transaminase activity transaminase activity transferase activity pyridoxal phosphate binding	
Transport cell cycle mitosis multicellular organismal development nervous system development cell differentiation cell division	Dr6616.1.S1_at	pafah1b1b	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit b (LIS-1A)		Cytoskeleton microtubule

Synaptic plasticity/ structural					
	Dr14127.1.S1_at	gfap	glial fibrillary acidic protein	Structural molecule activity	Cytoplasm intermediate filament type III intermediate filament
	Dr16118.1.A1_at	LOC567833	Similar to microtubule-associated protein tau		
Cell adhesion	Dr17585.1.S1_at	LOC569045	Similar to MGC115547 protein	Structural molecule activity	Actin cytoskeleton
Cell wall catabolic process	Dr19411.1.A1_at	zgc:86648	Zgc:86648	Tropomyosin binding	Cytoskeleton
Signal transduction					
Protein amino acid phosphorylation	Dr12674.1.S1_at	zgc:112307	zgc:112307	Protein kinase activity ATP binding	
Protein amino acid dephosphorylation	Dr15652.1.S1_at	pp2cb	protein phosphatase type 2C beta	Magnesium ion binding catalytic activity phosphoprotein phosphatase activity protein serine/threonine phosphatase activity protein phosphatase type 2C activity hydrolase activity metal ion binding	Protein serine/threonine phosphatase complex
Small GTPase mediated signal transduction	Dr16422.1.S1_at	diras1	DIRAS family, GTP-binding RAS-like 1	Nucleotide binding GTP binding	Membrane attack complex intracellular membrane
Protein transport regulation of GTPase activity	Dr18113.1.S1_at	gdi1 LOC554985	GDP dissociation inhibitor 1 similar to GDP dissociation inhibitor 1	Rab GDP-dissociation inhibitor activity	
Calcium ion transport	Dr19079.1.S1_at	zgc:92169	calcineurin B	Calcium channel activity calcium ion binding calcium channel inhibitor activity	
Protein amino acid phosphorylation	Dr19161.2.S1_at	zgc:153415	zgc:153415	Protein kinase activity protein serine/threonine kinase activity ATP binding	
Protein amino acid dephosphorylation	Dr20956.1.S1_at	pp2ca2	protein phosphatase type 2C alpha 2	Magnesium ion binding catalytic activity phosphoprotein phosphatase activity protein serine/threonine phosphatase activity protein phosphatase type 2C activity hydrolase activity metal ion binding	Protein serine/threonine phosphatase complex
Small GTPase mediated signal transduction	Dr23643.1.A1_s_at	arl11	ADP-ribosylation factor-like 11	Nucleotide binding GTP binding	Intracellular
Activation of MAPKKK activity central nervous system development neural crest cell development embryonic camera-type eye	Dr2414.1.S2_at	smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Nucleic acid binding DNA binding helicase activity ATP binding	

morphogenesis					
Negative regulation of signal transduction	Dr3391.1.A1_at	zgc:92099	zgc:92099		Membrane attack complex signal recognition particle, endoplasmic reticulum targeting membrane integral to membrane
	Dr7417.1.S1_at	sh3bp5	SH3-domain binding protein 5 (BTK-associated)		
Cell cycle/ apoptosis					
Regulation of progression through cell cycle	Dr17362.1.A1_at	zgc:153047	zgc:153047		
Cell cycle	Dr17497.1.A1_at	cul1a	Cullin 1a		
Regulation of progression through cell cycle regulation of cyclin-dependent protein kinase activity regulation of transcription	Dr18505.1.S1_at	wu:fi75b02	wu:fi75b02	Protein kinase binding	
Apoptosis	Dr2992.1.A1_at	opa1	optic atrophy 1 (human)	Nucleotide binding GTPase activity GTP binding	Membrane attack complex mitochondrion membrane integral to membrane
Apoptosis	Dr3900.1.A1_at	LOC100004578 tax1bp1	Tax1 (human T-cell leukemia virus type I) binding protein 1 similar to Tax1 (human T-cell leukemia virus type I) binding protein 1		
Negative regulation of apoptosis Double-strand break repair via non-homologous end joining DNA recombination response to ionizing radiation DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis.	Dr18239.2.A1_at	xrcc5	Double strand repair complementingdefective repair in Chinese hamster cells 5	DNA binding	Nucleus
Steroid/lipid transport					
Transport lipid transport steroid metabolic process	Dr11569.1.S1_at	osbpl2	oxysterol binding protein-like 2		
Lipid transport	Dr4188.2.S1_at	LOC791876 rtn1a	reticulon 1a Hypothetical protein LOC791876	Lipid transporter activity	Endoplasmic reticulum
	Dr6972.1.S1_at	lrpap1	low density lipoprotein receptor-related protein associated protein 1	Receptor activity heparin binding low-density lipoprotein receptor binding	Endoplasmic reticulum

Ion/protein transport					
Phosphate transport collagen catabolic process	Dr14041.1.S1_at	c1qc	complement component 1, q subcomponent, C chain		Cytoplasm
Zinc ion transport	Dr14198.1.S1_at	zgc:101840	zgc:101840	Zinc ion binding metal ion binding	
Transport iron ion transport iron ion homeostasis embryonic hemopoiesis erythrocyte maturation mitochondrial iron ion transport	Dr15077.2.A1_at	slc25a37	solute carrier family 25, member 37	Iron ion transporter activity binding iron ion binding	Membrane attack complex mitochondrion mitochondrion mitochondrial inner membrane membrane integral to membrane
Protein import into nucleus, docking intracellular protein transport	Dr19552.1.S1_at	zgc:76878	zgc:76878	Binding protein transporter activity	Nucleus nuclear pore cytoplasm
Transport cation transport calcium ion transport metabolic process	Dr3418.1.A1_at	si:dkey-18o7.1	si:dkey-18o7.1	Nucleotide binding magnesium ion binding catalytic activity calcium channel activity calcium-transporting ATPase activity calcium ion binding calmodulin binding ATP binding calcium ion transporter activity	Membrane attack complex membrane integral to membrane
	Dr10295.1.A1_at				
Metabolism					
Electron transport	Dr12134.3.S1_x_at	zgc:77225	zgc:77225	NADH dehydrogenase activity NADH dehydrogenase (ubiquinone) activity	Mitochondrion
Metabolic process	Dr15313.1.A1_at	zgc:85662	zgc:85662	Nucleotidyltransferase activity	
Metabolic process	Dr20398.2.A1_at	acsl1	acyl-CoA synthetase long-chain family member 1	Catalytic activity	
Metabolic process	Dr2430.1.S1_at	aldh7a1	aldehyde dehydrogenase 7 family, member A1	Oxidoreductase activity	
Aldehyde metabolic process metabolic process	Dr4751.1.S1_a_at	aldh2 aldh2l LOC100003829 LOC795450	aldehyde dehydrogenase 2, like aldehyde dehydrogenase 2 family (mitochondrial) Similar to mitochondrial aldehyde dehydrogenase 2 family	3-Chloroallyl aldehyde dehydrogenase activity oxidoreductase activity	
Biosynthetic process NAD biosynthetic process	Dr7457.1.A1_at	nmnat2	nicotinamide nucleotide adenylyltransferase 2	Transferase activity nucleotidyltransferase activity	
Metabolic process	Dr7774.1.S1_at	nat5	N-acetyltransferase 5	*N*-Acetyltransferase activity acyltransferase activity transferase activity	
Unknown					
	Dr10524.1.S1_at	zgc:85694	zgc:85694	Nucleotide binding nucleic acid binding	
	Dr10561.1.A1_at				
	Dr11083.1.S1_at	itm2b	integral membrane protein 2B		

Dr1116.1.S1_at	LOC100007066 si:dkey-78d16.1	si:dkey-78d16.1 Hypothetical protein LOC100007066	Calcium ion binding
Dr11200.1.S1_at	si:ch211-237l4.6	si:ch211-237l4.6	
Dr11208.1.A1_at		Transcribed locus	
Dr11248.1.A1_at			
Dr11640.1.S1_at		Transcribed locus	
Dr12482.2.A1_x_at		Transcribed locus	
Dr12816.1.A1_at		Transcribed locus	
Dr13060.1.S1_at	zgc:154072	zgc:154072	
Dr13437.1.A1_at		Transcribed locus	
Dr13462.1.A1_at		Transcribed locus	
Dr13756.1.S1_at		Transcribed locus	
Dr13817.1.A1_at	coro2b	Coronin, actin binding protein, 2B	
Dr13833.1.S1_at	LOC572069	Hypothetical LOC572069	
Dr13890.1.A1_at		Transcribed locus	
Dr14471.1.S1_at	zgc:100838	zgc:100838	
Dr15212.1.A1_at	zgc:92140	zgc:92140	
Dr15649.1.A1_at	LOC798982	Similar to ROD1 protein	
Dr15655.1.S1_at		Transcribed locus	
Dr15990.1.S1_at	LOC565937	Novel protein similar to vertebrate mitochondrial ribosomal protein S10 (MRSP10)	
Dr16158.1.A1_at		Transcribed locus	
Dr16406.1.A1_at	zgc:158299	Zgc:158299	
Dr16557.1.S1_at	LOC563634	Hypothetical LOC563634	
Dr17497.2.S1_at	zgc:110652	Zgc:110652	
Dr17592.1.A1_at	zgc:91819	zgc:91819	
Dr17958.2.A1_at	wu:fa04a07	Wu:fa04a07	
Dr18110.1.A1_at	LOC797948	Hypothetical protein LOC797948	
Dr18165.1.A1_at			
Dr18271.1.S1_at			
Dr18540.2.S1_a_at		Transcribed locus, weakly similar to XP_001344635.1 hypothetical protein [Danio rerio]	
Dr18540.3.A1_x_at	LOC799545	Hypothetical protein LOC799545	
Dr18766.1.A1_at			
Dr19097.1.A1_at	wu:fc57b04	wu:fc57b04	
Dr19215.1.S1_at	zgc:136828	zgc:136828	Sulfotransferase activity
Dr19228.1.A1_at			
Dr19364.1.S1_at	wu:fb96d05	wu:fb96d05	
Dr19468.1.A1_at	zgc:66100	Similar to AMMECR1	
Dr20716.1.A1_at	tpm1	tropomyosin 1 (alpha)	
Dr22471.1.A1_at	wu:fe38h02	wu:fe38h02	
Dr22737.1.A1_at	wu:fj47c02	wu:fj47c02	
Dr22745.1.A1_at	LOC100002604	Similar to Phosphodiesterase 5A	
Dr22801.1.A1_at	LOC567798	Similar to amylo-1, 6-glucosidase/4-alpha-glucancotransferase	

Dr23372.1.A1_at		Transcribed locus		
Dr23758.1.A1_at	wu:fa16a02	wu:fa16a02		
Dr24399.1.A1_at	zgc:55548	Zgc:55548		
Dr24527.1.S1_at				
Dr24664.1.S1_at		Transcribed locus		
Dr25022.1.A1_at	LOC792040	Hypothetical protein LOC792040		
Dr25444.1.A1_at		Transcribed locus		
Dr25559.1.S1_at	sb:cb166	sb:cb166		
Dr25648.1.S1_at				
Dr25880.1.A1_at		Transcribed locus		
Dr26095.1.A1_at		Transcribed locus		
Dr26303.1.A1_at	LOC100000869 LOC563456	Hypothetical LOC563456 Hypothetical protein LOC100000869		
Dr3198.1.S1_at	zgc:55768	zgc:55768	GTP binding	Intracellular
Dr3258.1.A1_at	wu:fc15h07	wu:fc15h07		
Dr374.1.S1_at	irf2bp2	interferon regulatory factor 2 binding protein 2		
Dr4033.1.A1_at	wu:fb72g11	wu:fb72g11		
Dr4676.1.A1_at		Transcribed locus		
Dr4736.1.A1_at	LOC563405	Hypothetical LOC563405		
Dr5133.1.S1_at	LOC569053	Hypothetical LOC569053		
Dr5162.1.A1_at	wu:fc17d03	wu:fc17d03		
Dr5293.1.S1_at	hn1l LOC798010 LOC798208	hematological and neurological expressed 1-like similar to HN1-like protein		
Dr5583.1.A1_at	LOC797252	Hypothetical protein LOC797252		
Dr5663.1.S1_at		Transcribed locus, strongly similar to XP_706968.1 hypothetical protein XP_701876 isoform 2 [Danio rerio]		
Dr5685.1.S1_at				
Dr6037.1.A1_at	zgc:91993	zgc:91993	Phospholipid binding	
Dr6517.2.S1_at	LOC796564	Hypothetical protein LOC796564		
Dr6752.1.A1_at				
Dr6837.1.S1_at	znf259	zinc finger protein 259	Protein binding zinc ion binding	
Dr7708.1.S1_at	lsm12	LSM12 homolog (S. cerevisiae)		
Dr891.1.S1_at	LOC797006	Hypothetical protein LOC797006		
Dr9070.1.A1_at	zgc:63770	zgc:63770	Nucleotide binding nucleic acid binding	
Dr9329.1.S1_at	LOC561168	Hypothetical LOC561168		
Dr9411.1.A1_a_at	zgc:158179	zgc:158179		
Dr9560.1.A1_at	LOC565706	Similar to cyclic AMP specific phosphodiesterase		
Dr97.1.A1_at	LOC100006553 LOC100006779 LOC571509	Hypothetical LOC571509 hypothetical protein LOC100006553 hypothetical protein LOC100006779		
Dr9711.2.A1_at	zgc:112466	zgc:112466		
Dr9746.7.A1_at	LOC560240	Hypothetical LOC560240		
Dr9888.1.A1_at				

Dr9954.1.A1_at	MGC162178	Hypothetical LOC564953

Gene names and roles are as assigned on the Affymetrix web site (http://www.affymetrix.com/analysis/index.affx).