

Quantitative reverse transcription-polymerase chain reaction (qRT-PCR). Tissues from different animals than those employed in the microarray screen were specifically chosen to increase overall confidence in both the confirmation and general reproducibility of expression differences identified in the microarray hybridization screen. Real time qRT-PCR was performed with the iCycler IQ Real Time PCR detection system (Bio-Rad Laboratories, Inc., Hercules, CA) using a one-step QuantiTect SYBR Green RT-PCR kit (Qiagen, Valencia, CA) on DNase-treated total RNA (Hashimoto *et al*, 2004). The qRT-PCR reactions were carried out in 25 μ l with 20 ng of total RNA. Relative expression of the RT-PCR product was determined using the comparative $\Delta\Delta C_t$ method, after normalizing expression to total RNA measured with RiboGreen (Molecular Probes, Eugene, OR, USA) (Hashimoto *et al*, 2004). Primers were designed based on the mRNA sequence by using Oligo v6.67 software (Oligo, Cascade, CO) and synthesized by Fisher Scientific (Pittsburg, PA), or were purchased pre-designed from Qiagen (Valencia, CA) or SuperArray (Frederick, MD). *Smad3* primers were designed based on the reference sequence NM_016769 (F-GCTTGTGCCTGGGCCTACTG; R-TCACTGAGGCACTCCGCAAAGA) and *Usp38* primers were designed based on the reference sequence NM_027554 (F-GTCGCCATCCTGGACTACATTC; R-GGCCTCTCGCAAACCAT). *Bclaf1*, *Cx3cl1*, *Diablo*, and *Mapk9* were ordered from Qiagen (catalog numbers QT00165396, QT00128345, QT00131677, QT00128737 respectively) and *Hbxip1* was ordered from SuperArray.

Real-time qRT-PCR efficiency was determined for each primer set using a five-fold dilution series of total RNA and did not differ significantly from 100%. The DNase-treated RNA showed that RNA was free of contaminates as indicated by UV 260/280

ratios of 2.0. Individual reaction kinetics were also analyzed to ensure each qRT-PCR did not differ significantly from 100%. Following PCR, specificity of the PCR reaction was confirmed with melt curve analysis to ensure that only the expected PCR product was amplified per reaction.

Assessment of EtOH induced brain damage. Male and female WSP and WSR mice (n = 8) were exposed to EtOH and withdrawn for 10 d. In addition to time to reach maximal neuronal damage following EtOH-induced excitotoxicity (Panegyres, 1998), this time course would also allow the changes in gene transcription observed during peak withdrawal to be translated in a biologically-relevant fashion. Mice were deeply anesthetized with mouse cocktail (ketamine 7.5mg/ml, xylazine 0.75mg/ml, acepromazine 0.15mg/ml; 0.1ml/10g mouse body weight) and perfused transcardially with cold 0.9% saline followed by 4% paraformaldehyde in 0.1M phosphate buffered saline (PBS). Brains were then isolated and fixed in 4% paraformaldehyde 0.1M PBS. Coronal blocks of each brain were processed by dehydration, paraffin infiltration, and embedding as previously described for other tissues (Wiren *et al*, 2004). Tissue sections (6 μ m) were cut with a microtome using coordinates from a standard mouse brain stereotaxic atlas (Franklin and Paxinos, 2001) and floated onto positively charged slides (Superfrost, Fisher Scientific). Sections were deparaffinized and hydrated through a xylene and a graded ethanol series. Brain slices chosen for characterization of cell death after withdrawal from chronic alcohol exposure included both the dorsal hippocampus (as a landmark) and the parietal cortex. For hematoxylin and eosin (H&E) staining, slides were placed in hematoxylin for 5 min, in 1% acid alcohol for a few

seconds, and in eosin for 5 min. A minimum of 3 sections were counted per brain resulting a minimum of 18 images analyzed. For each image, a 65 μm x 65 μm counting field was placed on the image, based on computer generated random, non-overlapping, coordinates. Only clearly identifiable neurons were counted.

References:

Franklin G, Paxinos K (2001): The mouse brain in stereotaxic coordinates. Academic Press: San Diego.

Hashimoto J, Beadles-Bohling A, Wiren K (2004). Comparison of RiboGreen and 18S rRNA quantitation for normalizing real-time RT-PCR expression analysis. *Biotechniques* **36**: 54-60.

Panegyres P (1998). The effects of excitotoxicity on the expression of the amyloid precursor protein gene in the brain and its modulation by neuroprotective agents. *J Neural Transm* **105**: 463-478.

Wiren K, Zhang X, Toombs A, Kasparcova V, Gentile M, Harada S, *et al* (2004). Targeted overexpression of androgen receptor in osteoblasts: unexpected complex bone phenotype in growing animals. *Endocrinology* **145**: 3507-3522.

Supplemental Figure 1 Schematic of the experimental approach for microarray analysis and array confirmation. A total of 32 arrays were analyzed to characterize expression profiles in male and female WSP and WSR mice during peak withdrawal from chronic EtOH withdrawal. Replicate lines (e.g., WSP-1 and WSP-2) were collapsed to identify selection phenotype relevant changes, reduce selection artifact and increase statistical power. Following background subtraction and z-score normalization, EtOH regulated genes were identified by *t*-test (see Supplemental Table 1 for top named genes; for full list see Supplemental Table 2 in supporting information online).

Supplemental Figure 2 Confirmation of selected EtOH regulated transcripts by qRT-PCR. *Bclaf*, *Cx3Cl1*, *Diablo*, *Hbxip*, *Mapk9*, *Smad3*, and *Usp38* for male and female WSP and male and female WSR are shown. See Supplemental methods for details. Microarray regulation (open bars) is plotted along with qRT-PCR results (hatched bars) for comparison. $n = 4$. Data are mean \pm SEM. *, $P < 0.05$.

Supplemental Figure 3 K-means clustering of EtOH regulated genes. Additional groups identified in cluster analysis not included in Figure 2 are presented here (clusters = 10, average linkage, Euclidian Distance).

Supplemental Table 1. All significantly EtOH regulated genes.

Array Acc	Accession #	Name	Symbol	EtOH Regulation
<i>Female WSP</i>				
AI324132	DV063122	Brain protein I3	Bri3	0.14
AI413285				0.38
AI413337	AK004398	ARV1 homolog (yeast)	Arv1	0.11
AI413884	BB546927	Transcribed locus		0.36
AI413964	AK036427	Coagulation factor II (thrombin) receptor-like 3	F2rl3	0.36
AI425962	BC039910	Galactosidase, beta 1-like	D1Ertd161e	0.68
AI426043	AK029840	MMS19 (MET18 <i>S. cerevisiae</i>)-like	Mms19l	-0.14
AI426196	AK157287	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	Adamts4	0.41
AI426210	NM_018856	Cyclin L2, transcript variant 2, mRNA (cDNA clone IMAGE:5353815)	Ccnl2	-0.34
AI426213	AK163183	Fibronectin type III domain containing 4	Fndc4	-0.68
AI426332				0.26
AI426426		Transcribed locus		0.35
AI427544	AK134712	Activin A receptor, type II-like 1	Acvr1l	-0.80

AI427986	NM_028108	Mak3 homolog (<i>S. cerevisiae</i>)	Mak3	0.37
AI428081	AK085036			0.33
AI428386	AK135797	Zinc finger, BED domain containing 3	Zbed3	0.44
AI428917	AK138077	CCR4-NOT transcription complex, subunit 2	Cnot2	0.73
AI447250	AK050546	Expressed sequence AI452372	AI452372	-0.49
AI447414	AK032754	DDHD domain containing 2	Ddhd2	0.55
AI447415	AK155063	Transcribed locus		0.41
AI447428	AI592054	Transcribed locus		0.47
AI447785	AK084373	RIKEN cDNA 2410002O22 gene	2410002O22Rik	0.33
AI447983	AK136931	Cleavage stimulation factor, 3' pre-RNA, subunit 3	Cstf3	0.52
AI448382	AK148847	RIKEN cDNA 2900070E19 gene	2900070E19Rik	0.25
AI448421				0.57
AI448487		Cytochrome c oxidase subunit VIb polypeptide 2	Cox6b2	0.25
AI448556	AK045683	RIKEN cDNA A630038E17 gene	A630038E17Rik	0.18
AI448691	AK037826	Receptor (calcitonin) activity modifying protein 1	Ramp1	0.33
AI449115	AI592536	Transcribed locus		0.48
AI449178	XM_204015	RIKEN cDNA E230012J19 gene	Rere	0.46
AI449308	AK147614	Adenosine deaminase, RNA-specific	Adar	0.27
AI449360	AK144663	Interferon activated gene 203	Ifi203	0.52
AI449420	BC024780	Diablo homolog (<i>Drosophila</i>)	Diablo	0.28

AI449524	AK147838	RNA binding motif, single stranded interacting protein 2	Rbms2	0.35
AI449659	XM_110503	Microtubule-actin crosslinking factor 1	Macf1	0.22
AI450087	BC082599	RIKEN cDNA 4930422G04 gene, mRNA (cDNA clone MGC:29401 IMAGE:5068638)	4930422G04Rik	0.65
AI450176	AK129060	Rho GTPase activating protein 4	Arhgap4	-0.16
AI450190	NM_001025394	BCL2-associated transcription factor 1	Bclaf1	0.46
AI450392	U39818	Tuberous sclerosis 2	Tsc2	0.46
AI451610		Transcribed locus		-0.29
AI451872	AK156231	RIKEN cDNA 5330421F07 gene	5330421F07Rik	0.36
AI451890				0.52
AI464342	BC056984	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	Ndufb7	0.59
AI464449	AK135612	REST corepressor 3	Rcor3	0.20
AI465143	CB319739	Lectin, galactose binding, soluble 1	Lgals1	0.26
AI465213	AK146093	WD repeat domain 55	2410080P20Rik	0.33
AI465217				0.76
AI465265		MutS homolog 5 (E. coli)	Msh5	0.24
AI661152	NM_029657	Mahogunin, ring finger 1	Mgrn1	0.21
AI661155	AK129140	Expressed sequence AW555814	AW555814	0.41
AI661200	AK015501	RIKEN cDNA 2900060B22 gene	2900060B22Rik	0.31
AI661287	AK135536	Transforming growth factor, beta induced	Tgfbi	0.58

AI661406				0.43
AI661477	AK154848	Suppressor of variegation 4-20 homolog 2 (Drosophila) (Suv420h2), mRNA	Suv420h2	-0.68
AI666546	AK166064	FIP1 like 1 (S. cerevisiae)	Fip111	0.18
AI666740				0.78
AI666741	AK008035	Phospholipase A2, group XIIB	Pla2g12b	0.52
AI666774	L36390	Internexin neuronal intermediate filament protein, alpha	Ina	0.25
AI893656	AK146128	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	Psmc7	0.30
<i>Female WSR</i>				
AI323295	AK136907	DNA-damage inducible transcript 3	Ddit3	-0.22
AI323923	BG296733	Similar to Carbonyl reductase (NADPH) 1 (NADPH-dependent carbonyl reductase 1)	Cbr1	0.44
AI325463	BU526252	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	Ndufb10	-0.32
AI326151	CB947099	Glycine N-methyltransferase	Gnmt	-0.28
AI326991	AK045451	Pleckstrin homology, Sec7 and coiled-coil domains 2	Pscd2	-0.57
AI413781				-0.33
AI413884	BB546927	Transcribed locus		-0.45
AI413927	AK158760	Neurexophilin 3	Nxph3	0.35
AI413955	NM_172746	Expressed sequence C86302	C86302	0.47

AI414205	AK082631	RIKEN cDNA C230071I02 gene	Nxn	-0.26
AI414311	AK145083	Mitogen activated protein kinase 9	Mapk9	0.34
AI414315	BC054784	Rhomboid, veinlet-like 4 (Drosophila)	Rhbdl4	0.35
AI414429	BC068283	UDP-glucose ceramide glucosyltransferase-like 1	Ugcgl1	0.41
AI414953	NM_018744	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	Sema6a	-0.36
AI415362	NM_178757	Interferon regulatory factor 2 binding protein 1	Irf2bp1	0.34
AI415416	BC094562	Solute carrier family 20, member 2	Slc20a2	0.48
AI415639	XM_620567	Gene model 166, (NCBI)	Gm166	0.25
AI425882				-0.43
AI425884				-0.42
AI425962	BC039910	Galactosidase, beta 1-like	D1Ertd161e	0.52
AI425994	BC085128	Replication initiator 1	Repin1	0.48
AI426244	U09383	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	Kcnma1	-0.23
AI426400	AK036940	Myocyte enhancer factor 2C, mRNA (cDNA clone MGC:46981 IMAGE:4500786)	Mef2c	-0.32
AI426949	BC103802	DNA segment, Chr 3, ERATO Doi 789, expressed	D3Ertd789e	0.32
AI426965	BC060191	RIKEN cDNA 2610300B10 gene	2610300B10Rik	0.35
AI427149	AK080889	RIKEN cDNA B430119L13 gene	B430119L13Rik	-0.47

AI427904	AK122561	WD repeat domain 22	Wdr22	-0.46
AI427986	NM_028108	Mak3 homolog (<i>S. cerevisiae</i>)	Mak3	-0.50
AI428081	AK085036			-0.39
AI428343	AB045324	Topoisomerase (DNA) III beta	Top3b	-0.26
AI428377	NM_181649	RIKEN cDNA 2310002B06 gene	2310002B06Rik	-0.39
AI428416				-0.44
AI428524				-0.31
AI428560	BC053753	Elastin microfibril interfacier 2	Emilin2	0.17
AI428578	AK051919	Sperm associated antigen 7	Spag7	-0.58
AI428777	NM_175523	Protein phosphatase 1K (PP2C domain containing)	A930026L03Rik	-0.32
AI428922	AI428922			0.40
AI429120	XM_485380			-0.32
AI429503	AK031312	Expressed sequence AI790326	AI790326	0.34
AI429518	AI429518	Transcribed locus		-0.30
AI429553	NM_018771	Regulator of G-protein signaling 19 interacting protein 1	Rgs19ip1	-0.37
AI430830	AK087815	PREDICTED: hypothetical protein LOC68621 (<i>Mus musculus</i>), mRNA sequence	1110019K23Rik	-0.31
AI430905	BI330372	RIKEN cDNA 6720485C15 gene	6720485C15Rik	-0.30
AI431020	AK079809			0.36
AI447219	BC094899	RIKEN cDNA A430102O06 gene	Trim12	0.54

AI447388	AK171779	Microtubule associated monooxygenase, calponin and LIM domain containing 1	Nical	-0.38
AI447515	AK134813	D-amino acid oxidase 1	Dao1	-0.22
AI447534				-0.47
AI447573	NM_175686	Paired related homeobox 1	Prrx1	-0.18
AI447659	AK139462	RWD domain containing 1 (Rwdd1), mRNA	Rwdd1	-0.39
AI447665				-0.27
AI447828	BC058195	Transmembrane channel-like gene family 6 (Tmc6), transcript variant 1, mRNA	Tmc6	0.43
AI447839	AK036401	RIKEN cDNA 0610013E23 gene Adult male aorta and vein cDNA, RIKEN full-length	0610013E23Rik	0.60
AI447882	AK138790	enriched library, clone:A530058D14 product:unknown EST, full insert sequence		-0.26
AI447887	AI447887	Transcribed locus		-0.20
AI447983	AK136931	Cleavage stimulation factor, 3' pre-RNA, subunit 3	Cstf3	0.17
AI448466	XM_133073	Nucleoporin 205	Nup205	-0.29
AI448474	AK147019			0.81
AI448497	AF116847			0.30
AI448603	AK129472	RIKEN cDNA 4930402E16 gene	4930402E16Rik	0.13
AI448657	BC057314	Splicing factor, arginine/serine-rich 8	Sfrs8	-0.20

AI448676	AI448676	Transcribed locus		0.20
AI448898	AK082145	RIKEN cDNA C230013L11 gene	C230013L11Rik	-0.31
AI449061	NM_145930	Expressed sequence AW549877	AW549877	0.32
AI449124	AK156059	CD3 antigen, zeta polypeptide	Cd3z	-0.38
AI449248				-0.21
AI449340		GLE1 RNA export mediator-like (yeast	Gle1l	-0.42
AI449360	AK144663	Interferon activated gene 203	Ifi203	0.49
AI449379	BC058761	UPF3 regulator of nonsense transcripts homolog B (yeast)	Upf3b	0.17
AI449453				-0.46
AI449581	AK156861	RIKEN cDNA 1700030G06 gene	6030443J06Rik	0.30
AI449678	BC050759	Fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	Fscn3	-0.19
AI449753	AK161464	X-ray radiation resistance associated 1	Xrra1	0.74
AI450079	AK087815	Transcribed locus		0.34
AI450225	BX529455	Transcribed locus		0.41
AI450246	BC059827	Poly (ADP-ribose) glycohydrolase	Parg	0.46
AI450282	AK164288	Follistatin (Fst), mRNA	Fst	0.34
AI450295	NM_178880	Son cell proliferation protein	Son	0.27
AI450320				-0.46
AI450987	AK142244	Ataxia telangiectasia and rad3 related	Atr	0.24

AI451068	AK004642	Transcribed locus, moderately similar to NP_766325.1 hypothetical protein D430041B17 (Mus musculus)		0.30
AI451097	AK038965	LPS-responsive beige-like anchor	Lrba	-0.37
AI451098				-0.35
AI451106	NM_015788	Sacsin (Sacs), mRNA	Sacs	-0.24
AI451110	AK034942	Acyl-CoA synthetase long-chain family member 5, mRNA (cDNA clone MGC:18968 IMAGE:3987201)		-0.57
AI451211	AK078573	Mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	Med6	-0.31
AI451434	AK049335	Diacylglycerol kinase, epsilon	Dgke	-0.21
AI451470				-0.38
AI451495	BC089370	RIKEN cDNA 4833428C12 gene	4833428C12Rik	0.43
AI451509	XM_126677	RIKEN cDNA 4933424M23 gene	4933424M23Rik	0.44
AI451576	XM_485838	Kelch domain containing 5	C230080I20Rik	0.37
AI451625	AK030827	Inducible T-cell co-stimulator	Icos	0.57
AI451660	AK086202	Aspartate-beta-hydroxylase	Asph	0.86
AI451891	BC028328	RIKEN cDNA 4833420G17 gene	4833420G17Rik	0.33
AI451930				-0.27
AI452009	XM_485667	Similar to dJ353E16.2 (meningioma (disrupted in balanced translocation) 1)	Mn1	0.39

AI452176	NM_025965	Signal sequence receptor, alpha	Ssr1	0.51
AI452228	AK138911	Adenylate cyclase 7	Adcy7	0.65
AI464505	AK147150	Lamin A	Lmna	0.26
AI464524				0.21
AI464551	AK079879	RIKEN cDNA 2810031P15 gene	Zfp618	-0.40
AI465262	BC051990	Four jointed box 1 (Drosophila)	Fjx1	-0.26
AI465313	NM_023672	Single-stranded DNA binding protein 3	Ssbp3	0.39
AI465410				0.47
AI465465	AB028272	DnaJ (Hsp40) homolog, subfamily B, member 1	Dnajb1	0.26
AI465481	BC061693	Zinc finger, A20 domain containing 2	Za20d2	0.51
AI465515				-0.21
AI528555	AK167271	RIKEN cDNA C130097A14 gene	Glb1	0.41
AI528630	AK138049	IL2-inducible T-cell kinase	Itk	-0.34
AI604771	AK156820	Myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	Mllt1	-0.32
AI608463	AK031836	RIKEN cDNA 1810063B07 gene	1810063B07Rik	-0.94
AI661477	AK154848	Suppressor of variegation 4-20 homolog 2 (Drosophila) (Suv420h2), mRNA	Suv420h2	-0.37
AI661836	U04710	Insulin-like growth factor 2 receptor	Igf2r	0.59
AI661939	CB575999	Fidgetin-like 1	Figl1	0.46

AI666307				-0.47
AI894147	AK154720	Sepiapterin reductase	Spr	0.38
AI894196	NM_027554	Ubiquitin specific protease 38	Usp38	0.39
<i>Male WSP</i>				
AI324173	AK138010	MAD homolog 3 (Drosophila)	Smad3	-0.22
AI325151	AK038702	Dystroglycan 1, mRNA (cDNA clone MGC:6651 IMAGE:3496914)	Dag1	-0.47
AI326151	CB947099	Glycine N-methyltransferase	Gnmt	-0.23
AI326801	BC010667	Adaptor-related protein complex 3, mu 1 subunit	Ap3m1	-0.36
AI413120	AK164474	Cadherin 5	Cdh5	-0.48
AI413869	BC054838	Chemokine (C-X3-C motif) ligand 1	Cx3cl1	-0.55
AI414397	NM_173749	RIKEN cDNA E430002G05 gene	E430002G05Rik	-0.52
AI414506	BC089604	Histone 1, H1c	Hist1h1c	-0.35
AI414514				-0.21
AI414560	AK080602			-0.36
AI414764	AK043832	Pre-B-cell leukemia transcription factor 4	Pbx4	-0.34
AI414773	BI658791	Membrane-associated ring finger (C3HC4) 6	F830029L24Rik	-0.39
AI414870	AK140195	Gene model 261, (NCBI)		0.54
AI415042	AK139193	Mitochondrial ribosomal protein S18C, mRNA (cDNA clone MGC:41331 IMAGE:1196057)	Mrps18c	-0.36

AI415232				-0.38
AI415704	AK155823	RIKEN cDNA 3110040N11 gene	3110040N11Rik	-0.31
AI425884				-0.34
AI426191	AK156339	RIKEN cDNA 1810013D10 gene	1810013D10Rik	-0.55
AI426244	U09383	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	Kcnma1	-0.21
AI427122	XM_110660	Expressed sequence AI427122, mRNA (cDNA clone IMAGE:4216549)	AI427122	-0.56
AI427428	AK133577	Xeroderma pigmentosum, complementation group A	Xpa	-0.40
AI429605	BC059072	RGM domain family, member A	Rgma	-0.38
AI430876	AI509087	Transcribed locus		-0.28
AI447436	AK047778	RIKEN cDNA 1700007D05 gene	1700007D05Rik	-0.94
AI447443	AK037659	SEC5-like 1 (<i>S. cerevisiae</i>)	Sec5l1	-0.41
AI447618	AK034724	RIKEN cDNA B230378P21 gene	B230378P21Rik	0.31
AI447731	BC031500	Cytidine monophospho-N-acetylneuraminic acid synthetase	Cmas	-0.46
AI447828	BC058195	Transmembrane channel-like gene family 6 (Tmc6), transcript variant 1, mRNA	Tmc6	0.28
AI448040	AK002289	Vesicle transport through interaction with t-SNAREs 1B homolog	Vti1b	-0.46

AI448307				-0.55
AI448593	AK042302	Beaded filament structural protein 2, phakinin	Bfsp2	-0.41
AI448817				-0.29
AI448871	CA492714	Hepatitis B virus x interacting protein	Hbxip	0.55
AI448906	BC057614	RIKEN cDNA 3000004C01 gene	3000004C01Rik	0.37
AI449094				0.37
AI449478	BC040390	Ras and Rab interactor 2 (Rin2), mRNA	Rin2	-0.48
AI449646	BC082564	Developmentally regulated GTP binding protein 2	Drg2	-0.26
AI450230				-0.22
AI450305	AK032489	Cathepsin W	Ctsw	-0.67
AI450557	AK156147	G protein-coupled receptor 114	Gpr114	-0.35
AI450779	AI450779	Transcribed locus		0.96
AI451224	DT912419	RIKEN cDNA 1700100M05 gene	1700100M05Rik	-0.88
AI451308	AI451308	Transcribed locus		-0.67
AI451434	AK049335	Diacylglycerol kinase, epsilon	Dgke	0.22
AI451701				-0.45
AI451962	NM_027769	Copine III	Cpne3	0.51
AI465402	L04289	Natural killer tumor recognition sequence	Nktr	0.55
AI465459	XM_197073	RIKEN cDNA 9330128J19 gene	9330128J19Rik	0.47
AI604771	AK156820	Myeloid/lymphoid or mixed lineage-leukemia translocation	Mllt1	-0.38

to 1 homolog (Drosophila)

AI661004	AK019872	Tafazzin	Taz	-0.67
AI662563	NM_011862	Protein kinase C and casein kinase substrate in neurons 2	Pacsin2	-0.39
AI666339	AK137625	Peptidyl arginine deiminase, type IV	Padi4	-0.30
AI666521	BB659805	Rac GTPase-activating protein 1	Racgap1	0.65
AI666741	AK008035	Phospholipase A2, group XIIB	Pla2g12b	-0.36
AI893653	NM_007626	Chromobox homolog 5 (Drosophila HP1a)	Cbx5	-0.41
<i>Male WSR</i>				
AI323626				-0.28
AI323755	AK149458	Aldo-keto reductase family 1, member C6	Akr1c6	0.34
AI324113	AK088985	Non-catalytic region of tyrosine kinase adaptor protein 2	Nck2	-0.66
AI324173	AK138010	MAD homolog 3 (Drosophila)	Smad3	0.48
AI325451	NM_011965	Proteasome (prosome, macropain) subunit, alpha type 1	Psma1	0.76
AI325957	AK133340	TDP-glucose 4,6-dehydratase	Tgds	-0.31
AI326773	AF132218	Histidine rich calcium binding protein	Hrc	-0.49
AI326815	XM_484402	Similar to Poly(A) binding protein, cytoplasmic 4, isoform 1		0.19
AI326913	AU051332	CDC28 protein kinase 1b	Cks1b	0.30
AI327085	BU516369	Heat shock protein 1 (chaperonin 10)	Hspe1	0.42
AI327321	AK122301	Ubiquitin specific protease 15	Usp15	-0.60
AI327338	CB321240	Acylphosphatase 2, muscle type	Acyp2	-0.33

AI327391	BC037131	Peptidylprolyl isomerase (cyclophilin)-like 1	Ppil1	0.34
AI327398				0.23
AI413315	NM_008131	RIKEN cDNA 5830403L16 gene	Glul	-0.71
AI413378	AK016704	RIKEN cDNA 4933406N12 gene	4933406N12Rik	0.35
AI413521	AK078481	RIKEN cDNA 2900016D05 gene, mRNA (cDNA clone MGC:36340 IMAGE:4952601) Adult male hypothalamus cDNA, RIKEN full-length	2900016D05Rik	0.63
AI413901	BX525839	enriched library, clone:A230064F10 product:unknown EST, full insert sequence		-0.39
AI413917	AK030810	Cyclin-dependent kinase 6	Cdk6	-0.51
AI413955	NM_172746	Expressed sequence C86302	C86302	-0.61
AI414231	AK077383	Villin 1	Vil1	0.57
AI414593				-0.41
AI415268	AK129415	RIKEN cDNA 1810041L15 gene	1810041L15Rik	-0.50
AI415417	AY570293	Submandibular gland protein C	Smgc	0.28
AI425892	BC059275	Protein phosphatase 1, regulatory (inhibitor) subunit 3F	Ppp1r3f	0.43
AI426146				0.37
AI426191	AK156339	RIKEN cDNA 1810013D10 gene	1810013D10Rik	0.19
AI426196	AK157287	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	Adamts4	0.40

AI426213	AK163183	Fibronectin type III domain containing 4	Fndc4	0.52
AI427022	BC066821	Bobby sox homolog (Drosophila)	Bbx	0.38
AI427082	AK032357	DNA segment, Chr 14, ERATO Doi 209, expressed	D14Ertd209e	0.49
AI427453	AF083929	Programmed cell death protein 7	Pdcd7	-0.50
AI428015	AF522069	Testis expressed gene 22 (Tex22), mRNA	1700028O09Rik	0.31
AI428254	AK133336	Sulfatase 2 (Sulf2), mRNA	Sulf2	0.24
AI428543	AF156605	Zinc finger protein 261	Zfp261	0.22
AI428788	AK136559	Serum/glucocorticoid regulated kinase 2	Sgk2	-0.57
AI428873	AK146474	RIKEN cDNA 1600014C10 gene	1600014C10Rik	-0.46
AI429120	XM_485380	PREDICTED: hypothetical protein LOC73398 (Mus musculus), mRNA sequence	1700054F22Rik	0.37
AI429495	BC052851	Torsin family 3, member A	Tor3a	0.27
AI429810	AY151252	RIKEN cDNA 1810044A24 gene	1810044A24Rik	0.35
AI430817	AK085022	RIKEN cDNA D430025H09 gene	D430025H09Rik	0.24
AI447379	BC085284	Similar to RIKEN cDNA 2210421G13		0.24
AI447414	AK032754	Phosphatidic acid phosphatase type 2 domain containing 1, mRNA (cDNA clone IMAGE:30252760)	Ppapdc1	-0.60
AI447510	AK082891	RIKEN cDNA A730042J05 gene	A730042J05Rik	-0.49
AI447560	CO042990	Transcribed locus		0.28
AI447571	BC058646	Retinoic acid induced 17	Rai17	0.24

AI447638	AK160791	SMT3 suppressor of mif two 3 homolog 2 (yeast) (Sumo2), mRNA	Sumo2	-0.81
AI447735	BC061488	Sh3 domain YSC-like 1	Sh3yl1	-0.45
AI447802	AK155065	Sprouty protein with EVH-1 domain 1, related sequence	Spred1	0.26
AI447952	AK122237	Transmembrane protein 24	Tmem24	-0.50
AI448242				0.43
AI448385	XM_355079	MKIAA4095 protein		0.18
AI448388	AK142463	Thyroid hormone receptor interactor 13	Trip13	0.18
AI448871	CA492714	Hepatitis B virus x interacting protein	Hbxip	0.37
AI448949	XM_620751	Iron responsive element binding protein 2	Ireb2	-0.45
AI449246	BC075698	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	Mpp5	-0.19
AI449247	AB183545	Ribosomal protein L23a, mRNA (cDNA clone MGC:36820 IMAGE:4163533)	Rpl23a	-0.23
AI449297	AK172680	Toll-like receptor 7	Tlr7	0.18
AI449339	BC043136	RIKEN cDNA 2610207F23 gene	2610207F23Rik	0.74
AI449373	AK144174	Adducin 3 (gamma)	Add3	-0.55
AI449488				-0.43
AI449745	AK053965	Pepsinogen 5, group I	Pga5	-0.10
AI450171	BC044740	PREDICTED: calreticulin 4 (Mus musculus), mRNA	4933403L16Rik	-0.36

		sequence		
AI450180	BC018481	RIKEN cDNA 4933428G09 gene (4933428G09Rik), mRNA	4933428G09Rik	-0.36
AI450282	AK164288	Follistatin (Fst), mRNA	Fst	0.39
AI450786	AK172251	Natural cytotoxicity triggering receptor 1	Ncr1	-0.63
AI450801	AI639766	Transcribed locus		-0.33
AI450901	AK147289	Oxoglutarate dehydrogenase (lipoamide)	Ogdh	0.20
AI451014	AK040980	Zinc finger protein 120, mRNA (cDNA clone MGC:19165 IMAGE:4222737)	Zfp120	-0.15
AI451111	AK038890	Asparagine-linked glycosylation 6 homolog (yeast, alpha- 1,3,-glucosyltransferase)	Alg6	1.00
AI451131	NM_027569	Sperm associated antigen 9	Spag9	-0.43
AI451186	U24703	Reelin	Reln	-0.23
AI451232	AK173010	DDHD domain containing 2	Ddhd2	-0.33
AI451247	AK043538	Ankyrin repeat domain 43 (Ankrd43), mRNA	A830006N08Rik	-0.37
AI451252	AK138718	RIKEN cDNA 2600011C06 gene	2600011C06Rik	-0.80
AI451411	BC050868	TRAF2 and NCK interacting kinase	Tnik	-0.18
AI451498				-0.45
AI451664	AA189972	Transcribed locus		-0.56
AI451679	XM_283719	Methyl-CpG binding domain protein 5	Mbd5	0.35
AI465247	AK129359	CDNA sequence BC003236	BC003236	0.36

AI465349	AK148224	RIKEN cDNA 2810421I24 gene	2810421I24Rik	0.34
AI465549		Expressed sequence AI646383	AI646383	0.30
AI661496	AK141032	Ubiquitin protein ligase E3A (Ube3a), transcript variant 2, mRNA	Ube3a	1.45
AI662051	NM_029432	RIKEN cDNA 4930402H24 gene, mRNA (cDNA clone IMAGE:5366525)	4930402H24Rik	-0.48
AI662162	AK152849	RIKEN cDNA 2410193C02 gene	2410193C02Rik	-0.79
AI666407	NM_009939	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	Cops2	-0.25
AI666521	BB659805	Rac GTPase-activating protein 1	Racgap1	-0.48
AI666774	L36390	Interneixin neuronal intermediate filament protein, alpha	Ina	-0.56
AI893623	X60367	Retinol binding protein 1, cellular	Rbp1	-0.26
AI894196	NM_027554	Ubiquitin specific protease 38	Usp38	-0.69

Supplemental Table 2. EtOH regulated gene categories.

Symbol	Name	Accession	EtOH Reg.	Sex	Line
<i>Apoptosis</i>					
Bclaf1	BCL2-associated transcription factor 1 (Bclaf1)	NM_001025394	0.46	Female	WSP
Ddit3	DNA-damage inducible transcript 3	AK136907	-0.22	Female	WSR
Diablo	Diablo homolog (Drosophila)	BC024780	0.28	Female	WSP
Pdcd7	Programmed cell death protein 7	AF083929	-0.50	Male	WSR
<i>Neurogenesis/Neural Migration</i>					
Ina	Internexin neuronal intermediate filament protein, alpha	L36390	0.25	Female	WSP
Ina	Internexin neuronal intermediate filament protein, alpha	L36390	-0.56	Male	WSR
Mef2c	Myocyte enhancer factor 2C	AK036940	-0.32	Female	WSR
Reln	Reelin	U24703	-0.23	Male	WSR
Sema6a	Semaphorin 6A	NM_018744	-0.36	Female	WSR
<i>Protein Catabolism/Protein Folding/Protein Biosynthesis</i>					
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	AB028272	0.26	Female	WSR
Hspe1	Heat shock protein 1 (chaperonin 10)	BU516369	0.42	Male	WSR
Mrps18c	Mitochondrial ribosomal protein S18C	AK139193	-0.36	Male	WSP

Nktr	Natural killer tumor recognition sequence	L04289	0.55	Male	WSP
Ppil1	Peptidylprolyl isomerase (cyclophilin)-like 1	BC037131	0.34	Male	WSR
Psm1	Proteasome (prosome, macropain) subunit, alpha type 1	NM_011965	0.76	Male	WSR
Rpl23a	Ribosomal protein L23a	AB183545	-0.23	Male	WSR
Sacs	Sacsin	NM_015788	-0.24	Female	WSR
Tor3a	Torsin family 3, member A	BC052851	0.27	Male	WSR
Ube3a	Ubiquitin protein ligase E3A (Ube3a)	AK141032	1.45	Male	WSR
Usp15	Ubiquitin specific peptidase 15	AK122301	-0.60	Male	WSR
Usp38	Ubiquitin specific peptidase 38	NM_027554	0.39	Female	WSR
Usp38	Ubiquitin specific peptidase 38	NM_027554	-0.69	Male	WSR

Cell Proliferation

Cdk6	Cyclin-dependent kinase 6	AK030810	-0.51	Male	WSR
Cops2	COP9 homolog, subunit 2 (Arabidopsis thaliana)	NM_009939	-0.25	Male	WSR
Mab21l2	MAB21L2	AK038965	-0.37	Female	WSR
Nck2	Non-catalytic region of tyrosine kinase adaptor protein 2	AK088985	-0.66	Male	WSR
Repin1	Replication initiator 1	BC085128	0.48	Female	WSR
Smad3	MAD homolog 3 (Drosophila)	AK138010	-0.22	Male	WSP
Smad3	MAD homolog 3 (Drosophila)	AK138010	0.48	Male	WSR
Son	Son cell proliferation protein	NM_178880	0.27	Female	WSR

Steroid/Hormone

Akr1c6	Aldo-keto reductase family 1, member C20	AK149458	0.34	Male	WSR
Trip13	Thyroid hormone receptor interactor 13	AK142463	0.18	Male	WSR

Transport

2410193C02Rik	RIKEN cDNA 2410193C02 gene	AK152849	-0.79	Male	WSR
4933402J24Rik	RIKEN cDNA 4933402J24 gene	AK086202	0.86	Female	WSR
Ap3m1	Adaptor-related protein complex 3, mu 1 subunit	BC010667	-0.36	Male	WSP
Cpne3	MKIAA0636 protein	NM_027769	0.51	Male	WSP
Dao1	D-amino acid oxidase 1	AK134813	-0.22	Female	WSR
Igf2r	Insulin-like growth factor 2 receptor	U04710	0.59	Female	WSR
Kcnma1	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	U09383	-0.23	Female	WSR
Kcnma1	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	U09383	-0.21	Male	WSP
Ndufb7	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	BC056984	0.59	Female	WSP
Nxn	Nucleoredoxin	AK082631	-0.26	Female	WSR
Ppil1	Peptidylprolyl isomerase (cyclophilin)-like 1	BC037131	0.34	Male	WSR
Psma1	Proteasome (prosome, macropain) subunit, alpha type 1	NM_011965	0.76	Male	WSR

Ramp1	RIKEN cDNA 9130218E19 gene	AK037826	0.33	Female	WSP
Rbp1	Retinol binding protein 1, cellular	X60367	-0.26	Male	WSR
Sec5l1	SEC5-like 1 (<i>S. cerevisiae</i>)	AK037659	-0.41	Male	WSP
Slc20a2	Type III sodium-dependent phosphate transporter	BC094562	0.48	Female	WSR
Tmc6	Transmembrane channel-like gene family 6	BC058195	0.43	Female	WSR
Tmc6	Transmembrane channel-like gene family 6	BC058195	0.28	Male	WSP
Vti1b	Vesicle transport through interaction with t-SNAREs 1B homolog	AK002289	-0.46	Male	WSP

Stress/Immune Response/DNA Repair

Cx3cl1	Chemokine (C-X3-C motif) ligand 1	BC054838	-0.55	Male	WSP
Ifi203	Interferon activated gene 203	AK144663	0.52	Female	WSP
Ifi203	Interferon activated gene 203	AK144663	0.49	Female	WSR
Repin1	Replication initiator 1	BC085128	0.48	Female	WSR
Tlr7	Toll-like receptor 7	AK172680	0.18	Male	WSR
Xpa	Xeroderma pigmentosum, complementation group A	AK133577	-0.40	Male	WSP

DNA binding

A830006N08Rik	Ankyrin repeat domain 43	AK043538	-0.37	Male	WSR
Adar	RNA adenosine deaminase 1	AK147614	0.27	Female	WSP

Arid3b	AT rich interactive domain 3B (Bright like)	AF116847	0.30	Female	WSR
Bbx	HMG-box transcription factor BBX	BC066821	0.38	Male	WSR
Bclaf1	BCL2-associated transcription factor 1	NM_001025394	0.46	Female	WSP
D1Ert161e	Galactosidase, beta 1-like	BC039910	0.68	Female	WSP
D1Ert161e	Galactosidase, beta 1-like	BC039910	0.52	Female	WSR
Ddit3	DNA-damage inducible transcript 3	AK136907	-0.22	Female	WSR
Hist1h1c	Histone 1, H1c	BC089604	-0.35	Male	WSP
Kcnma1	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	U09383	-0.23	Female	WSR
Kcnma1	Large conductance calcium activated potassium BK channel STREX-1 variant (Slo)	U09383	-0.21	Male	WSP
Mef2c	Myocyte enhancer factor 2C	AK036940	-0.32	Female	WSR
Mllt1	Myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	AK156820	-0.32	Female	WSR
Mllt1	Myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	AK156820	-0.38	Male	WSP
Pbx4	Pre-B-cell leukemia transcription factor 4	AK043832	-0.34	Male	WSP
Prrx1	Paired related homeobox 1, transcript variant 1	NM_175686	-0.18	Female	WSR
Smad3	MAD homolog 3 (Drosophila)	AK138010	-0.22	Male	WSP
Smad3	MAD homolog 3 (Drosophila)	AK138010	0.48	Male	WSR

Son	Son cell proliferation protein	NM_178880	0.27	Female	WSR
Ssbp3	Single-stranded DNA binding protein 3	NM_023672	0.39	Female	WSR
Top3b	Topoisomerase (DNA) III beta	AB045324	-0.26	Female	WSR
Xpa	Xeroderma pigmentosum, complementation group A	AK133577	-0.40	Male	WSP
Za20d2	Zinc finger, A20 domain containing 2	BC061693	0.51	Female	WSR
Zfp120	Zinc finger protein 120	AK040980	-0.15	Male	WSR

RNA binding

2600011C06Rik	RIKEN cDNA 2600011C06 gene	AK138718	-0.80	Male	WSR
Adar	RNA adenosine deaminase 1	AK147614	0.27	Female	WSP
Ireb2	Iron responsive element binding protein 2	XM_620751	-0.45	Male	WSR
Rbms2	RNA binding motif, single stranded interacting protein 2	AK147838	0.35	Female	WSP
Rpl23a	Ribosomal protein L23a	AB183545	-0.23	Male	WSR
Sfrs8	Splicing factor, arginine/serine-rich 8	BC057314	-0.20	Female	WSR
Son	Son cell proliferation protein	NM_178880	0.27	Female	WSR
Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	BC058761	0.17	Female	WSR

Supplemental Table 3. Significant EtOH-regulated genes represented in multiple comparisons.

Symbol	Name	Accession	Regulation*	Comparison†	
WSP vs WSR					
1810013D10Rik	RIKEN cDNA 1810013D10 gene	AK156339	-0.55	Male	WSP
1810013D10Rik	RIKEN cDNA 1810013D10 gene	AK156339	0.19	Male	WSR
Mak3	Mak3 homolog (S. cerevisiae)	NM_028108	0.37	Female	WSP
Mak3	Mak3 homolog (S. cerevisiae)	NM_028108	-0.50	Female	WSR
Mtx3	metaxin 3	AK085036	0.33	Female	WSP
Mtx3	metaxin 3	AK085036	-0.39	Female	WSR
Racgap1	Rac GTPase-activating protein 1	AK154929	0.65	Male	WSP
Racgap1	Rac GTPase-activating protein 1	AK154929	-0.48	Male	WSR
Smad3	MAD homolog 3 (Drosophila)	AK138010	-0.22	Male	WSP
Smad3	MAD homolog 3 (Drosophila)	AK138010	0.48	Male	WSR
Fst	folliculin	AK164288	0.34	Female	WSR
Fst	folliculin	AK164288	0.39	Male	WSR
Male vs Female					
C86302	Expressed sequence C86302	AI413955	0.47	Female	WSR
C86302	Expressed sequence C86302	AI413955	-0.61	Male	WSR
D1ErtD161e	Galactosidase, beta 1-like	BC039910	0.68	Female	WSP
D1ErtD161e	Galactosidase, beta 1-like	BC039910	0.52	Female	WSR
Cstf3	Cleavage stimulation factor, 3' pre-RNA, subunit 3	AK136931	0.52	Female	WSP
Cstf3	Cleavage stimulation factor, 3' pre-RNA, subunit 3	AK136931	0.17	Female	WSR
Hbxip	Hepatitis B virus x interacting protein	CA492714	0.55	Male	WSP
Hbxip	Hepatitis B virus x interacting protein	CA492714	0.37	Male	WSR
lfi203	Interferon activated gene 203	AK144663	0.52	Female	WSP
lfi203	Interferon activated gene 203	AK144663	0.49	Female	WSR
Suv420h2	suppressor of variegation 4-20 homolog 2 (Drosophila)	AK154848	-0.68	Female	WSP
Suv420h2	suppressor of variegation 4-20 homolog 2 (Drosophila)	AK154848	-0.37	Female	WSR
Pla2g12b	Phospholipase A2, group XIIB	AK008035	0.52	Female	WSP
Pla2g12b	Phospholipase A2, group XIIB	AK008035	-0.36	Male	WSP
Usp38	Ubiquitin specific protease 38	NM_027554	0.39	Female	WSR
Usp38	Ubiquitin specific protease 38	NM_027554	-0.69	Male	WSR
1700054F22Rik	RIKEN cDNA 1700054F22 gene	XM_485380	-0.32	Female	WSR
1700054F22Rik	RIKEN cDNA 1700054F22 gene	XM_485380	0.37	Male	WSR
Other					
Gnmt	Glycine N-methyltransferase	CB947099	-0.28	Female	WSR
Gnmt	Glycine N-methyltransferase	CB947099	-0.23	Male	WSP
Adamts4	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	AK157287	0.41	Female	WSP
Adamts4	A disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4	AK157287	0.40	Male	WSR
Fndc4	Fibronectin type III domain containing 4	AK163183	-0.68	Female	WSP
Fndc4	Fibronectin type III domain containing 4	AK163183	0.52	Male	WSR
Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	U09383	-0.23	Female	WSR
Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	U09383	-0.21	Male	WSP
Ddhd2	DDHD domain containing 2	AK173010	0.55	Female	WSP

Ddhd2	DDHD domain containing 2	AK173010	-0.60	Male	WSR
Tmc6	transmembrane channel-like gene family 6	BC058195	0.43	Female	WSR
Tmc6	transmembrane channel-like gene family 6	BC058195	0.28	Male	WSP
Dgke	Diacylglycerol kinase, epsilon	AK049335	-0.21	Female	WSR
Dgke	Diacylglycerol kinase, epsilon	AK049335	0.22	Male	WSP
Mllt1	Myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	AK156820	-0.32	Female	WSR
Mllt1	Myeloid/lymphoid or mixed lineage-leukemia translocation to 1 homolog (Drosophila)	AK156820	-0.38	Male	WSP
Ina	Internexin neuronal intermediate filament protein, alpha	L36390	0.25	Female	WSP
Ina	Internexin neuronal intermediate filament protein, alpha	L36390	-0.56	Male	WSR
Line & EtOH					
Akr1c6	Aldo-keto reductase family 1, member C6	AK149458	-0.56	Line Difference	
	Transcribed locus	AI413315	-0.49	Line Difference	
Arv1	ARV1 homolog (yeast)	AK004398	-0.62	Line Difference	
	Transcribed locus, weakly similar to XP_001069044.1 similar to polyA binding protein, cytoplasmic homolog (Rattus norvegicus)	BU518261	0.28	Line Difference	
	17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920067E03 product:weakly similar to Cytokine receptor-like molecule (Epstein-Barr virus induced gene 3) (Mus musculus), full insert sequence	AK146869	-0.55	Line Difference	
Cdk6	Cyclin-dependent kinase 6	AK030810	-0.51	Line Difference	
Usp37	Ubiquitin specific peptidase 37	AK077383	-0.61	Line Difference	
Ugcgl1	UDP-glucose ceramide glucosyltransferase-like 1	AK134231	-0.72	Line Difference	
Irf2bp1	Interferon regulatory factor 2 binding protein 1	NM_178757	-0.29	Line Difference	
Gm166	Gene model 166, (NCBI)	BC066021	-0.45	Line Difference	
D1ErtD161e	DNA segment, Chr 1, ERATO Doi 161, expressed	BC039910	-0.42	Line Difference	
Repin1	Replication initiator 1	AK048054	-0.64	Line Difference	
Mett11d1	Methyltransferase 11 domain containing 1	AK032357	-0.35	Line Difference	
Emilin2	Elastin microfibril interfacier 2	BC053753	-0.54	Line Difference	
Sgk2	Serum/glucocorticoid regulated kinase 2	AK136559	-0.65	Line Difference	
Cnot2	CCR4-NOT transcription complex, subunit 2	AK138077	-0.37	Line Difference	
	Transcribed locus	AI428922	-0.70	Line Difference	
Zc3h10	Zinc finger CCCH type containing 10	AK031312	-0.42	Line Difference	
	Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530094A21 product:unclassifiable, full insert sequence	AK035706	0.24	Line Difference	
Gipc1	GIPC PDZ domain containing family, member 1	NM_018771	-0.15	Line Difference	
Trim34	Tripartite motif protein 34	AK150759	-0.61	Line Difference	
Sh3yl1	Sh3 domain YSC-like 1	AK080739	-0.40	Line Difference	
Rps6kb1	Ribosomal protein S6 kinase, polypeptide 1	AK085687	-0.56	Line Difference	
	Transcribed locus	AI447887	-0.26	Line Difference	
Cstf3	Cleavage stimulation factor, 3' pre-RNA, subunit 3	AK164375	-0.46	Line Difference	
Cox6b2	Cytochrome c oxidase subunit VIb polypeptide 2	DV060583	-0.52	Line Difference	
Arid3b	AT rich interactive domain 3B (Bright like)	AF116847	-0.45	Line Difference	
4930402E16Rik	RIKEN cDNA 4930402E16 gene	AK160524	-0.42	Line Difference	
	Transcribed locus	AI448676	-0.45	Line Difference	
Ireb2	Iron responsive element binding protein 2	AK163808	-0.38	Line Difference	
Rere	Arginine glutamic acid dipeptide (RE) repeats	XM_204015	-0.66	Line Difference	

Mpp5	Membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)	BC075698	-0.33	Line Difference
lfi203	Interferon activated gene 203	AK143243	-0.54	Line Difference
Upf3b	UPF3 regulator of nonsense transcripts homolog B (yeast)	BC058761	-0.61	Line Difference
Diablo	Diablo homolog (Drosophila)	AK133194	-0.31	Line Difference
	Transcribed locus	AI449581	-0.72	Line Difference
Macf1	Microtubule-actin crosslinking factor 1	DQ067088	-0.29	Line Difference
Fscn3	Fascin homolog 3, actin-bundling protein, testicular (Strongylocentrotus purpuratus)	BC050759	-0.18	Line Difference
4930422G04Rik	RIKEN cDNA 4930422G04 gene	XM_001005249	-0.65	Line Difference
Calr4	Calreticulin 4	BC044740	-0.34	Line Difference
Parg	Poly (ADP-ribose) glycohydrolase	BC059827	-0.75	Line Difference
Son	Son cell proliferation protein	NM_178880	-0.67	Line Difference
Ncr1	Natural cytotoxicity triggering receptor 1	AK172251	-0.56	Line Difference
Atr	Ataxia telangiectasia and Rad3 related	AK142244	-0.71	Line Difference
	Transcribed locus	AI451097	-0.47	Line Difference
Med6	Mediator of RNA polymerase II transcription, subunit 6 homolog (yeast)	AK078573	-0.42	Line Difference
Ppapdc1	Phosphatidic acid phosphatase type 2 domain containing 1	XM_356065	-0.37	Line Difference
4833428C12Rik	RIKEN cDNA 4833428C12 gene	BC089370	-0.48	Line Difference
Icos	Inducible T-cell co-stimulator	AK030827	-0.54	Line Difference
Ccnt2	Cyclin T2	AK156231	-0.39	Line Difference
Mn1	Meningioma 1	NM_001081235	-0.57	Line Difference
Ssr1	Signal sequence receptor, alpha	NM_025965	-0.58	Line Difference
Rcor3	REST corepressor 3	AK135612	-0.77	Line Difference
Lmna	Lamin A	AK152728	-0.31	Line Difference
Zfp618	Zinc fingerprotein 618	BC059079	-0.35	Line Difference
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	AB028272	-0.44	Line Difference
Zfand5	Zinc finger, AN1-type domain 5	BC061693	-0.43	Line Difference
Glb1	Galactosidase, beta 1	AK171593	-0.70	Line Difference
Tgfb1	Transforming growth factor, beta induced	AK135536	-0.51	Line Difference
Igf2r	Insulin-like growth factor 2 receptor	U04710	-0.46	Line Difference
Figl1	Fidgetin-like 1	AK143850	-0.46	Line Difference
4930402H24Rik	RIKEN cDNA 4930402H24 gene	AK050350	-0.57	Line Difference
Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (Arabidopsis thaliana)	NM_009939	-0.53	Line Difference
	Transcribed locus	AI666521	-0.51	Line Difference
Usp38	Ubiquitin specific peptidase 38	NM_027554	-0.53	Line Difference
Sex & EtOH				
	Transcribed locus	AI414205	-0.32	Sex Difference
Tmc5	Transmembrane channel-like gene family 5	AK028404	-0.34	Sex Difference
Ccdc98	Coiled-coil domain containing 98	NM_172405	-0.25	Sex Difference
Zfp324	Zinc finger protein 324	AK052251	-0.27	Sex Difference
AI428898	Expressed sequence AI428898	AI428898	0.43	Sex Difference
Fndc4	Fibronectin type III domain containing 4	AK163183	0.61	Sex Difference
	Transcribed locus	AI427428	-0.19	Sex Difference
Flna	Filamin, alpha	NM_010227	0.29	Sex Difference
1600014C10Rik	RIKEN cDNA 1600014C10 gene	AK146474	-0.74	Sex Difference
	Transcribed locus	AA020017	-0.35	Sex Difference
Dcakd	Dephospho-CoA kinase domain containing	BI330372	-0.18	Sex Difference

Mical1	Microtubule associated monooxygenase, calponin and LIM domain containing 1	AK171779	-0.23	Sex Difference
Exoc2	Exocyst complex component 2	AK037659	-0.55	Sex Difference
Dao1	D-amino acid oxidase 1	NM_010018	-0.21	Sex Difference
Zmiz1	Zinc finger, MIZ-type containing 1	BC058646	0.32	Sex Difference
Prrx1	Paired related homeobox 1	NM_175686	-0.24	Sex Difference
Plxna4	Plexin A4	AB073228	-0.42	Sex Difference
	0 day neonate thymus cDNA, RIKEN full-length enriched library, clone:A430071M17 product:unclassifiable, full insert sequence	AK138790	-0.22	Sex Difference
Glrx5	Glutaredoxin 5 homolog (S. cerevisiae)	AK148847	-0.39	Sex Difference
AK220484	CDNA sequence AK220484	XM_977373	-0.60	Sex Difference
	Transcribed locus	AI645281	-0.40	Sex Difference
Sfrs8	Splicing factor, arginine/serine-rich 8	BC057314	-0.28	Sex Difference
	Transcribed locus	AI448676	-0.35	Sex Difference
Ramp1	Receptor (calcitonin) activity modifying protein 1	AK037826	-0.41	Sex Difference
3000004C01Rik	RIKEN cDNA 3000004C01 gene	BC057614	0.27	Sex Difference
Adar	Adenosine deaminase, RNA-specific	AK147614	-0.36	Sex Difference
Rbms2	RNA binding motif, single stranded interacting protein 2	NM_001039080	-0.24	Sex Difference
Drg2	Developmentally regulated GTP binding protein 2	BC082564	-0.40	Sex Difference
Pga5	Pepsinogen 5, group I	AK053965	0.47	Sex Difference
1110019K23Rik	RIKEN cDNA 1110019K23 gene	AK087815	-0.42	Sex Difference
4930422G04Rik	RIKEN cDNA 4930422G04 gene	XM_001005249	-0.52	Sex Difference
4933428G09Rik	RIKEN cDNA 4933428G09 gene	BC018481	-0.55	Sex Difference
	Transcribed locus	AI450779	1.03	Sex Difference
Alg6	Asparagine-linked glycosylation 6 homolog (yeast, alpha-1,3,-glucosyltransferase)	AK038890	0.71	Sex Difference
Spag9	Sperm associated antigen 9	NM_027569	-0.78	Sex Difference
Ankr43	Ankyrin repeat domain 43	NM_183173	-0.51	Sex Difference
Dgke	Diacylglycerol kinase, epsilon	AK049335	-0.19	Sex Difference
4833428C12Rik	RIKEN cDNA 4833428C12 gene	BC089370	-0.48	Sex Difference
Klhdc5	Kelch domain containing 5	NM_001081237	-0.41	Sex Difference
Icos	Inducible T-cell co-stimulator	AK030827	-0.55	Sex Difference
	Transcribed locus	AA189972	-0.75	Sex Difference
Lgals1	Lectin, galactose binding, soluble 1	CB319739	-0.36	Sex Difference
Wdr55	WD repeat domain 55	AK146093	-0.23	Sex Difference
Ctnbp2nl	CTTNBP2 N-terminal like	AK129359	0.38	Sex Difference
Fjx1	Four jointed box 1 (Drosophila)	BC051990	-0.27	Sex Difference
Dnajb1	DnaJ (Hsp40) homolog, subfamily B, member 1	AB028272	-0.55	Sex Difference
Hisppd1	Histidine acid phosphatase domain containing 1	AK129140	-0.66	Sex Difference
Suv420h2	Suppressor of variegation 4-20 homolog 2 (Drosophila)	AK154848	-0.50	Sex Difference
Pacsin2	Protein kinase C and casein kinase substrate in neurons 2	NM_011862	-0.51	Sex Difference

*Regulation is expressed as a log₂ ratio of EtOH vs. Air (positive number is up-regulated by EtOH) for the indicated sex and selected line, WSP Air exposed vs. WSR Air exposed (sexes collapsed based on selected line; positive numbers indicated WSP overexpression), or male vs. female (selected lines collapsed based on sex; positive numbers indicate female overexpression). † Comparison indicates the comparison where the gene was identified as significantly regulated.

Supplemental Table 4. Concordance of current expression analysis with EtOH relevant literature.

Current study				Reports from Literature						
Gene	EtOH Reg.	Sex	Line	Gene	Reg.	Sex	Species/Genetic Strain	Treatment	Brain Region	Citation
Acvr1	-0.8	Female	WSP	Acvr1	B6>BALB	Male	C57BL/6, BALB/cJ	basal comparison	striata	Saito <i>et al.</i> , 2004
Adar	0.27	Female	WSP	Adarb1	-2.07	Male	DBA/2J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Adcy7	0.65	Female	WSR	Adcy7	N/A	Male/Female	Transgenic/Heterozygous KO	basal comparison		Mattews <i>et al.</i> , 2005
Cdh5	-0.48	Male	WSP	CDH18	1.4, 1.7	Male	Human	chronic alcoholics	superior frontal cortex	Lewohl <i>et al.</i> , 2000
Cdh5	-0.48	Male	WSP	CDH18	down	Male/Female	Human	chronic alcoholics	prefrontal cortex	Iwamoto <i>et al.</i> , 2004
Cpne3	0.51	Male	WSP	Cpne6	1.4	Male	C57BL/6J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Ctsw	-0.67	Male	WSP	Ctsh	B6>BALB	Male	C57BL/6, BALB/cJ	basal comparison	striata	Saito <i>et al.</i> , 2004
Dnajb1	0.26	Female	WSR	Dnaja1	-1.35	Male	C57BL/6J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Fscn3	-0.19	Female	WSR	Fscn1	2.24	Male	DBA/2J	repeated ip EtOH	PFC	Kerns <i>et al.</i> ,

Gpr114	-0.35	Male	WSP	Gpr50	1.61	Male	DBA/2J	repeated ip EtOH	PFC	2005 Kerns <i>et al.</i> , 2005
Kcnma1	-0.23	Female	WSR	Kcnma1	1.88	Male	DBA/2J	repeated ip EtOH	NAC	2005 Kerns <i>et al.</i> , 2005
Kcnma1	-0.21	Male	WSP	Kcnma1	1.88	Male	DBA/2J	repeated ip EtOH	NAC	2005 Kerns <i>et al.</i> , 2005
Lgals1	0.26	Female	WSP	LGALS3	2.27	Male/Female	Human	chronic alcoholics	prefrontal cortex	2004 Iwamoto <i>et al.</i> , 2004
Mpp5	-0.19	Male	WSR	MPP5	3.01	Male/Female	Human	chronic alcoholics	prefrontal cortex	2004 Iwamoto <i>et al.</i> , 2004
Pbx4	-0.34	Male	WSP	Pbx3	-0.31	Male/Female	C57BL/6	EtOH	cortical neurons	2004 Gutala <i>et al.</i> , 2004
Pbx4	-0.34	Male	WSP	Pbx3	4.44	Male	DBA/2J	repeated ip EtOH	PFC	2005 Kerns <i>et al.</i> , 2005
Psma1	0.76	Male	WSR	Psma4	-1.61	Male	DBA/2J	repeated ip EtOH	VTA	2005 Kerns <i>et al.</i> , 2005
Psm7	0.3	Female	WSP	Psm7	-2.08	Male	C57BL/6J	repeated ip EtOH	NAC	2005 Kerns <i>et al.</i> , 2005
Psm7	0.3	Female	WSP	PSMD8	-2.01	Male/Female	Human	chronic alcoholics	PFC	2004 Iwamoto <i>et al.</i> , 2004
Rbp1	-0.26	Male	WSR	Rbp1	B6>BALB	Male	C57BL/6, BALB/cJ	oral self	striata	Saito <i>et al.</i> ,

								administration		2004
Rbp1	-0.26	Male	WSR	Rbp4	-1.79	Male	C57BL/6	repeated ip EtOH	VTA	Kerns <i>et al.</i> , 2005
Rpl23a	-0.23	Male	WSR	Rpl30	-1.66	Male	DBA/2J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Rpl23a	-0.23	Male	WSR	Rpl30	1.82	Male	C57BL/6J	repeated ip EtOH	VTA	Kerns <i>et al.</i> , 2005
Sema6a	-0.41	Female	WSR	Sema6b	2.65	Male	C57BL/6J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Sgk2	-0.57	Male	WSR	Sgk	2	Male	C57BL/6J, DB/2J	acute ip EtOH	whole brain	Treadwell and Singh, 2004
Sgk2	-0.57	Male	WSR	Sgk3	1.9	Male	C57BL/6J, DB/2J	acute ip EtOH	whole brain	Treadwell and Singh, 2004
Sgk2	-0.57	Male	WSR	Sgk	1.76	Male	C57BL/6J	repeated ip EtOH	NAC	Kerns <i>et al.</i> , 2005
Smad3	0.48	Male	WSR	Smad2	1.22	Male	AA, ANA	basal comparison	Hippocampus	Arlinde <i>et al.</i> , 2004
Smad3	-0.22	Male	WSP	Smad2	1.22	Male	AA, ANA	basal comparison	Hippocampus	Arlinde <i>et al.</i> , 2004
Tgfb1	0.58	Female	WSP	Tgfb14	B6>BALB	Male	C57BL/6, BALB/cJ	oral self administration	striata	Saito <i>et al.</i> , 2004

(NAC- nucleus accumbens, VTA- ventral tegmental area)

Citations:

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