

Supplementary Table S4

gene symbol	gene name	treated vs. untreated fold	treated vs. untreated FDR	P rat + ethanol	TPM GTEx brain	NHGRI GWAS	post- mortem AUD brain
TFCP2L1	transcription factor CP2 like 1	-2.6	7.06E-29	1	0.9		
RSAD2	radical S-adenosyl methionine domain containing 2	-1.7	4.51E-41	NA	5.1		
ACY3	aminoacylase 3	-1.7	1.37E-38	1	4.6		ACY3
BAG3	BCL2 associated athanogene 3	1.7	9.60E-12	1	91.6		BAG3
ANXA3	annexin A3	1.7	6.79E-09	2	11.4		
RNF130	ring finger protein 130	1.7	6.79E-08	NA	40.1		RNF130
CDHR1	cadherin related family member 1	1.6	2.04E-36	NA	23.1		
BCO1	beta-carotene oxygenase 1	-1.6	4.58E-15	NA	NA		
GPR153	G protein-coupled receptor 153	1.6	5.09E-15	NA	12.4		
BMP4	bone morphogenetic protein 4	1.6	1.26E-11	1	6.9		
SNX7	sorting nexin 7	1.6	1.10E-08	1	12.9		
DNAH14	dynein axonemal heavy chain 14	1.6	1.76E-05	NA	0.5		
OXTR	oxytocin receptor	1.5	3.91E-30	NA	6.6	OXTR	
IFI6	interferon alpha inducible protein 6	-1.5	1.05E-26	NA	191.5		
SPIRE1	spire type actin nucleation factor 1	1.5	6.69E-18	NA	28.1		SPIRE1
ISG15	ISG15 ubiquitin-like modifier	-1.5	1.30E-15	NA	50.6		
NPNT	nephronectin	1.5	3.78E-13	NA	7.4		
GIMAP1	GTPase, IMAP family member 1	-1.5	5.91E-11	NA	3		
ELOVL7	ELOVL fatty acid elongase 7	1.5	1.91E-09	2	18.5		ELOVL7
GSTM3	glutathione S-transferase mu 3	1.5	6.17E-08	1	43.3		
PRKCDBP	alias CAVIN3, Caveolae Associated Protein 3	1.5	1.27E-05	1	12.3		
IFIT1	interferon induced protein with tetratricopeptide repeats 1	-1.4	1.74E-29	NA	42.4		IFIT1
SOWAHC	soosondowah ankyrin repeat domain family member C	1.4	2.34E-14	NA	3.7		
SPR	sepiapterin reductase	1.4	9.99E-10	1	15.8		
RDH10	retinol dehydrogenase 10	1.4	1.95E-09	NA	5.7		
B3GLCT	beta 3-glucosyltransferase	1.4	1.69E-06	NA	NA		
SERPINA1	serpin family A member 1	-1.4	2.91E-06	4	3.1		
CHST3	carbohydrate sulfotransferase 3	1.4	4.62E-04	NA	8.7		CHST3
POMC	proopiomelanocortin	-1.4	3.85E-03	NA	7.9		
OAS3	2'-5'-oligoadenylate synthetase 3	-1.3	9.26E-20	NA	3.8	OAS3	
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6	-1.3	1.13E-16	NA	11.4		
IFI44L	interferon induced protein 44 like	-1.3	1.82E-15	NA	7.3		
F13A1	coagulation factor XIII A chain	1.3	9.44E-13	1	2		
PTGR1	prostaglandin reductase 1	1.3	3.52E-12	1	13.9		
C17orf100	chromosome 17 open reading frame 100	-1.3	8.45E-10	NA	1.2		
OAS1	2'-5'-oligoadenylate synthetase 1	-1.3	2.53E-08	1	3.1		OAS1
CRYBG3	crystallin beta-gamma domain containing 3	1.3	2.55E-07	NA	0.6		
GJC1	gap junction protein gamma 1	1.3	4.80E-07	NA	8.3		
TNFAIP2	TNF alpha induced protein 2	1.3	7.71E-07	1	15.8		
HELZ2	helicase with zinc finger 2	-1.3	1.10E-06	NA	1.7		
MED16	mediator complex subunit 16	-1.3	1.90E-06	NA	32.5		MED16
VASH2	vasohibin 2	1.3	2.01E-06	NA	1.2		
PTGES3L	prostaglandin E synthase 3 like	-1.3	4.56E-06	NA	4.7		
CABYR	calcium binding tyrosine phosphorylation regulated	1.3	7.20E-06	NA	4.4		
ZNF169	zinc finger protein 169	-1.3	8.20E-06	NA	5.8		
IRF7	interferon regulatory factor 7	-1.3	1.05E-05	3	14.3		IRF7
C10orf11		1.3	1.45E-04	NA	1.2		C10orf11
D2HGDH	D-2-hydroxyglutarate dehydrogenase	-1.3	2.07E-04	NA	16		
ZBED8	zinc finger BED-type containing 8	1.3	2.23E-04	NA	NA		

C17orf97	chromosome 17 open reading frame 97	1.3	2.42E-03	NA	7		
CSRP2	cysteine and glycine rich protein 2	1.3	5.89E-03	2	22.9		CSRP2
RPL28	ribosomal protein L28	-1.3	1.08E-02	3	80.8		RPL28
TRPC1	transient receptor potential cation channel subfamily C member 1	1.3	1.19E-02	NA	22.8		TRPC1
CASP7	caspase 7	-1.2	3.80E-17	NA	5.5		CASP7
EXT2	exostosin glycosyltransferase 2	1.2	4.09E-17	NA	22.9		EXT2
STAT2	signal transducer and activator of transcription 2	-1.2	3.98E-15	NA	84.7		
COMMD3-BMI1	COMMD3-BMI1 readthrough	1.2	6.33E-10	NA	NA		
LIN52	lin-52 DREAM MuvB core complex component	1.2	9.83E-10	NA	26.8		
HERC5	HECT and RLD domain containing E3 ubiquitin protein ligase 5	-1.2	5.32E-09	NA	3.3		
ARID5B	AT-rich interaction domain 5B	-1.2	5.80E-09	2	9.1		
GBP1	guanylate binding protein 1	-1.2	7.73E-09	NA	4.1		
SGCB	sarcoglycan beta	1.2	2.33E-08	NA	41.2		SGCB
TRAF3IP1	TRAF3 interacting protein 1	1.2	2.37E-08	1	13.4		
FMNL3	formin like 3	1.2	1.56E-07	NA	11.5		
DNAJB1	DnaJ heat shock protein family (Hsp40) member B1	1.2	1.93E-07	NA	74.6		DNAJB1
RRP36	ribosomal RNA processing 36	1.2	2.56E-07	NA	26.7		
SFT2D3	SFT2 domain containing 3	-1.2	4.80E-07	NA	NA		
ALDH3A2	aldehyde dehydrogenase 3 family member A2	1.2	1.69E-06	2	39.8		
NFE2L3	nuclear factor, erythroid 2 like 3	1.2	1.21E-05	NA	15.5		
KCTD21	potassium channel tetramerization domain containing 21	1.2	1.34E-05	NA	11.6		
BIRC3	baculoviral IAP repeat containing 3	1.2	1.88E-05	NA	1.3		
PCYOX1	prenylcysteine oxidase 1	1.2	3.34E-05	2	25.9		PCYOX1
NFKB2	nuclear factor kappa B subunit 2	1.2	3.54E-05	1	4.6		
RCN2	reticulocalbin 2	1.2	4.25E-05	3	71.9		RCN2
FPGT	fucose-1-phosphate guanylyltransferase	1.2	5.79E-05	1	3.6		
CHORDC1	cysteine and histidine rich domain containing 1	1.2	5.93E-05	1	11.3		CHORDC1
CXXC1	CXXC finger protein 1	-1.2	7.52E-05	NA	124		
PSRC1	proline and serine rich coiled-coil 1	-1.2	1.01E-04	NA	48		
ZDHHC13	zinc finger DHHC-type containing 13	1.2	1.28E-04	NA	17.9		ZDHHC13
TXNRD2	thioredoxin reductase 2	-1.2	1.31E-04	NA	36.4		
NUDT17	nudix hydrolase 17	-1.2	1.35E-04	NA	11		
CXXC4	CXXC finger protein 4	1.2	1.57E-04	1	8.8		
ZDHHC2	zinc finger DHHC-type containing 2	1.2	3.24E-04	NA	24.6		
C18orf54	chromosome 18 open reading frame 54	1.2	5.43E-04	NA	1.8		C18orf54
ZNF354A	zinc finger protein 354A	1.2	6.11E-04	NA	13.1		
KCTD11	potassium channel tetramerization domain containing 11	-1.2	7.03E-04	1	10.8		
P4HA2	prolyl 4-hydroxylase subunit alpha 2	1.2	7.03E-04	NA	3.6		
HACD1	3-hydroxyacyl-CoA dehydratase 1	1.2	9.27E-04	NA	NA		
NT5C3A	5'-nucleotidase, cytosolic IIIA	-1.2	1.15E-03	NA	21.3		
HILPDA	hypoxia inducible lipid droplet associated	-1.2	1.18E-03	NA	13.1		
DUSP23	dual specificity phosphatase 23	1.2	2.00E-03	NA	32.8		
CD302	CD302 molecule	1.2	2.10E-03	NA	5.4		
SAMD9L	sterile alpha motif domain containing 9 like	-1.2	2.18E-03	NA	2.9		
LOC100288637	OTU deubiquitinase 7A pseudogene	-1.2	2.43E-03	NA	NA		
MIS12	MIS12, kinetochore complex component	1.2	2.83E-03	NA	13.3		
SNHG5	small nucleolar RNA host gene 5	-1.2	3.03E-03	NA	44.8		
C10orf10		1.2	3.15E-03	NA	42.6		C10orf10
NADK2	NAD kinase 2, mitochondrial	1.2	3.99E-03	NA	22.4		
TOP1MT	DNA topoisomerase I mitochondrial	-1.2	5.11E-03	NA	2.7		

PTGS1	prostaglandin-endoperoxide synthase 1	-1.2	5.49E-03	1	3		
BBS5	Bardet-Biedl syndrome 5	1.2	6.35E-03	NA	17.7		
RPSAP58	ribosomal protein SA pseudogene 58	-1.2	7.41E-03	NA	6.5		
HMOX1	heme oxygenase 1	-1.2	1.01E-02	NA	16.5		HMOX1
TYMP	thymidine phosphorylase	-1.2	1.12E-02	2	19.7		
ACTA2	actin, alpha 2, smooth muscle, aorta	1.2	1.21E-02	NA	15.7		
PPDPF	pancreatic progenitor cell differentiation and proliferation factor	1.2	1.41E-02	NA	208.7		PPDPF
PLEKHA4	pleckstrin homology domain containing A4	-1.2	3.08E-02	NA	6.5		
FLVCR1-AS1	FLVCR1 antisense RNA 1	-1.2	3.51E-02	NA	1.5		
INTS1	integrator complex subunit 1	-1.2	3.83E-02	NA	75		
DHRS4L2	dehydrogenase/reductase 4 like 2	-1.2	3.96E-02	NA	6.2		
SLC39A4	solute carrier family 39 member 4	-1.2	4.74E-02	NA	7.2		
RAB31P	RAB3A interacting protein	1.1	3.37E-06	1	48.5		RAB31P
IFIT3	interferon induced protein with tetratricopeptide repeats 3	-1.1	7.01E-06	1	17.3		
SCIMP	SLP adaptor and CSK interacting membrane protein	-1.1	1.72E-05	NA	0.4		
ELL	elongation factor for RNA polymerase II	-1.1	3.09E-05	NA	22.8		
IL6R	interleukin 6 receptor	1.1	8.54E-05	1	5.2		
CDCA7L	cell division cycle associated 7 like	-1.1	1.25E-04	NA	2.7		
KMO	kynurenine 3-monooxygenase	-1.1	1.31E-04	NA	0.7		
ICAM2	intercellular adhesion molecule 2	-1.1	1.69E-04	2	12.2		
DUSP18	dual specificity phosphatase 18	1.1	1.97E-04	1	2.2		
TRIT1	tRNA isopentenyltransferase 1	-1.1	2.37E-04	NA	27.5		
MED17	mediator complex subunit 17	1.1	2.44E-04	NA	13.4		
ECHDC3	enoyl-CoA hydratase domain containing 3	1.1	2.44E-04	NA	4.5		
LGALS8	galectin 8	-1.1	2.95E-04	2	32.2		LGALS8
ZEB1-AS1	ZEB1 antisense RNA 1	-1.1	3.94E-04	NA	7.9		
ANKRD28	ankyrin repeat domain 28	-1.1	4.65E-04	NA	46.1		
NSUN4	NOP2/Sun RNA methyltransferase family member 4	-1.1	4.75E-04	NA	6		NSUN4
LMAN2L	lectin, mannose binding 2 like	1.1	5.78E-04	NA	19		
ZNF281	zinc finger protein 281	1.1	6.39E-04	NA	16.5		
BHLHE22	basic helix-loop-helix family member e22	-1.1	6.65E-04	2	35.3		
STEAP3	STEAP3 metalloredutase	1.1	9.49E-04	NA	9.9		
NXF1	nuclear RNA export factor 1	1.1	1.23E-03	1	90.6		
VILL	villin like	-1.1	1.30E-03	NA	10.1		
TRIP4	thyroid hormone receptor interactor 4	-1.1	1.71E-03	NA	14.8		
CLPP	caseinolytic mitochondrial matrix peptidase proteolytic subunit	-1.1	2.98E-03	1	62.9		CLPP
ZMYND8	zinc finger MYND-type containing 8	-1.1	3.30E-03	1	29.1		
NIT2	nitrilase family member 2	1.1	3.45E-03	NA	14.9		
ZNF16	zinc finger protein 16	-1.1	4.46E-03	NA	8.3		
ZNF788	Zinc Finger Family Member 788, Pseudogene	1.1	4.56E-03	NA	1.1		
USP21	ubiquitin specific peptidase 21	-1.1	4.63E-03	1	48.4		USP21
SAAL1	serum amyloid A like 1	1.1	5.25E-03	NA	9.9		
DDX42	DEAD-box helicase 42	-1.1	5.31E-03	NA	88.2		
DHRS4-AS1	DHRS4 antisense RNA 1	1.1	6.32E-03	NA	8.5		
BTN2A2	butyrophilin subfamily 2 member A2	1.1	7.05E-03	NA	17.8		
MGST1	microsomal glutathione S-transferase 1	1.1	7.07E-03	1	26		
AAED1	AhpC/TSA antioxidant enzyme domain containing 1	1.1	7.97E-03	NA	3.9		
QSOX2	quiescin sulfhydryl oxidase 2	-1.1	8.42E-03	2	69.1		
DDX51	DEAD-box helicase 51	-1.1	9.07E-03	NA	48.6		
KBTD7	kelch repeat and BTB domain containing 7	1.1	9.26E-03	NA	13.9		

ARSK	arylsulfatase family member K	1.1	1.04E-02	1	5.9		
RACGAP1	Rac GTPase activating protein 1	-1.1	1.05E-02	2	8.6		RACGAP1
SS18L1	SS18L1, nBAF chromatin remodeling complex subunit	-1.1	1.19E-02	NA	81.1		
ICAM1	intercellular adhesion molecule 1	1.1	1.21E-02	1	2.9		
DNAJC15	DnaJ heat shock protein family (Hsp40) member C15	-1.1	1.26E-02	NA	24.8		DNAJC15
ASNSD1	asparagine synthetase domain containing 1	1.1	1.33E-02	1	61.5		
EXOC2	exocyst complex component 2	1.1	1.33E-02	NA	18.1		EXOC2
SAMD9	sterile alpha motif domain containing 9	-1.1	1.37E-02	NA	0.8		
IRF9	interferon regulatory factor 9	-1.1	1.39E-02	NA	46.7		
EDEM3	ER degradation enhancing alpha-mannosidase like protein 3	1.1	1.40E-02	NA	18.7		
ZNF718	zinc finger protein 718	1.1	1.45E-02	NA	3.6		
GTF2H1	general transcription factor IIH subunit 1	1.1	1.50E-02	NA	22		
LY75	lymphocyte antigen 75	1.1	1.61E-02	NA	1		
MICU1	mitochondrial calcium uptake 1	-1.1	1.73E-02	NA	114.9		
RCAN1	regulator of calcineurin 1	1.1	1.87E-02	NA	33.9		
JMJD6	arginine demethylase and lysine hydroxylase	-1.1	1.89E-02	1	33.2		
SND1	staphylococcal nuclease and tudor domain containing 1	-1.1	2.19E-02	1	45.9		SND1
GATAD2A	GATA zinc finger domain containing 2A	-1.1	2.37E-02	NA	17.6		
PALD1	phosphatase domain containing, paladin 1	-1.1	2.73E-02	NA	21.7		
HEATR3	HEAT repeat containing 3	1.1	2.80E-02	NA	24.4		
IFT122	intraflagellar transport 122	-1.1	2.87E-02	NA	27.6		IFT122
CNOT10	CCR4-NOT transcription complex subunit 10	1.1	3.14E-02	1	13.6		CNOT10
XPR1	xenotropic and polytropic retrovirus receptor 1	1.1	3.19E-02	1	10.8		XPR1
IFT172	intraflagellar transport 172	-1.1	3.27E-02	NA	30.6		
PTBP2	polypyrimidine tract binding protein 2	1.1	3.27E-02	NA	11.6		PTBP2
IFIH1	interferon induced with helicase C domain 1	1.1	3.31E-02	NA	3.2		IFIH1
CYB5R3	cytochrome b5 reductase 3	-1.1	3.32E-02	1	85.4		CYB5R3
PLIN3	perilipin 3	-1.1	3.42E-02	NA	19.7		
POP5	POP5 homolog, ribonuclease P/MRP subunit	1.1	3.43E-02	NA	18.6		
SLC35A1	solute carrier family 35 member A1	1.1	3.47E-02	NA	59.9		SLC35A1
LARS2	leucyl-tRNA synthetase 2, mitochondrial	1.1	3.48E-02	NA	13.6		
FRA10AC1	FRA10A associated CGG repeat 1	1.1	3.50E-02	NA	13.2		
TRAPPC11	trafficking protein particle complex 11	1.1	3.57E-02	NA	32.2		
ACOT4	acyl-CoA thioesterase 4	1.1	3.67E-02	2	4		
TTF2	transcription termination factor 2	1.1	3.82E-02	NA	1.7		
EXOC6	exocyst complex component 6	1.1	3.83E-02	NA	8.6		EXOC6
TPST2	tyrosylprotein sulfotransferase 2	-1.1	3.88E-02	NA	13.4		
SMG6	SMG6, nonsense mediated mRNA decay factor	-1.1	3.92E-02	NA	25.7		
ZNF586	zinc finger protein 586	-1.1	4.06E-02	NA	5.3		
MCCC1	methylcrotonoyl-CoA carboxylase 1	-1.1	4.18E-02	NA	20.6		MCCC1
IL18BP	interleukin 18 binding protein	-1.1	4.31E-02	1	15.1		
C7orf13		-1.1	4.31E-02	NA	6.5		
SPECC1L	sperm antigen with calponin homology and coiled-coil domains 1 like	1.1	4.52E-02	NA	43.7		SPECC1L
S100A10	S100 calcium binding protein A10	1.1	4.61E-02	1	40.9		S100A10
GTF2F1	general transcription factor IIF subunit 1	-1.1	4.74E-02	NA	154.4		GTF2F1
FAM173B	family with sequence similarity 173 member B	1.1	4.89E-02	NA	14		FAM173B
CNOT4	CCR4-NOT transcription complex subunit 4	1.1	4.98E-02	NA	13.6		
ZSCAN29	zinc finger and SCAN domain containing 29	1	4.10E-02	NA	12.7		

Column **A-B**: Self-explanatory.

Column **C**: Fold change (FC) of expression in LCL treated with ethanol vs. untreated.

Column **D**: FDR of the change of expression.

Column **E**: Genes differentially expressed (DE) in drinking-preferring (P) rats vs. ctrl. Number of supporting studies (Total: analyses $\times$ brain regions = 20).

Column **F**: Largest mean TPM for all brain regions in GTEx. Expression cutoff is TPM > 2.

Column **G**: If gene appears here, it is reported or mapped closely to a variant with genome wide significance in NHGRI GWAS.

Column **H**: If gene appears here, it is DE in the AUD brain vs. ctrl.

The Venn diagram below highlights the intersections among the multiple categories of genes above. The intersection among n_1 , n_2 and n_3 has 20 genes, e.g., *ELOVL7*.

