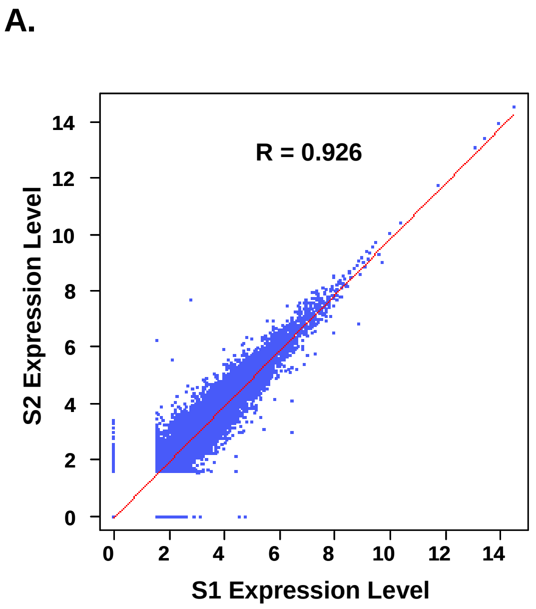
Supporting Information



B.

Number of Genes	Expression Level (average reads)	Fraction of transcripts
50	235-22476	26.6%
2000	23-235	34.5%
13958	1-23	38.9%

Figure S1. Genome-wide transcript levels in hippocampus detected by RNA-seq. *(A)*. Correlation of all 16,008 detected transcripts between two individual (drug-free control) samples. *(B)*. Signal distribution of all sequenced reads for all of the 16,008 expressed genes. The most highly expressed 50 genes account for 26.6% of all sequence reads. Vast majority of the genes (13,958) are expressed at relatively low level and account for 38.9% of the total signal.

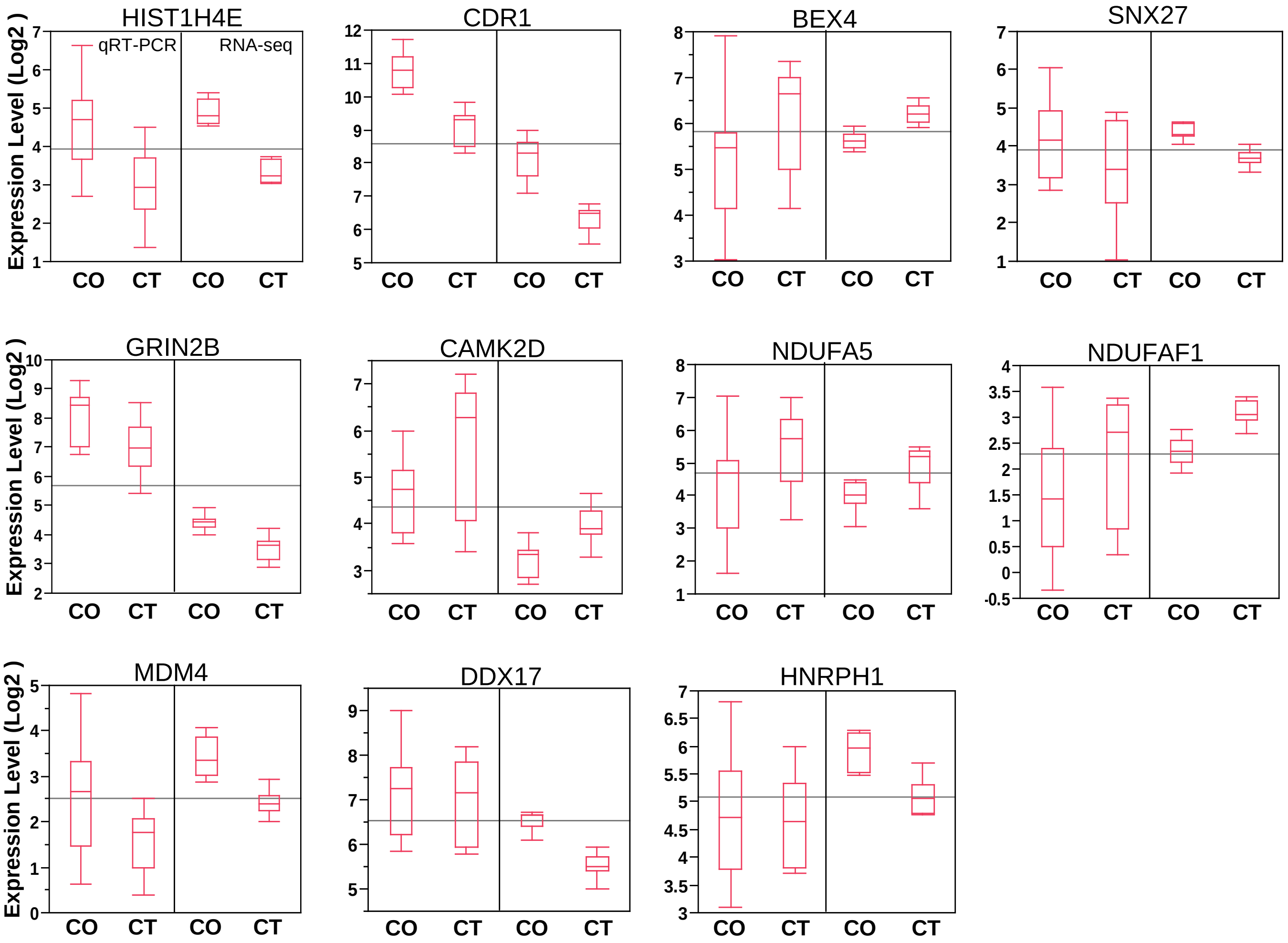


Figure S2. Box plots displaying expression changes of the 11 genes measured by both RNA-seq and quantitative RT-PCR. For both cocaine (CO) and control (CT) groups, the plots show the median, 75% percentile, minimum, and maximum expression levels measured by either qRT-PCR (left) and RNA-seq (right). Note that the expression levels are relative and not comparable between qRT-PCR and RNA-seq.

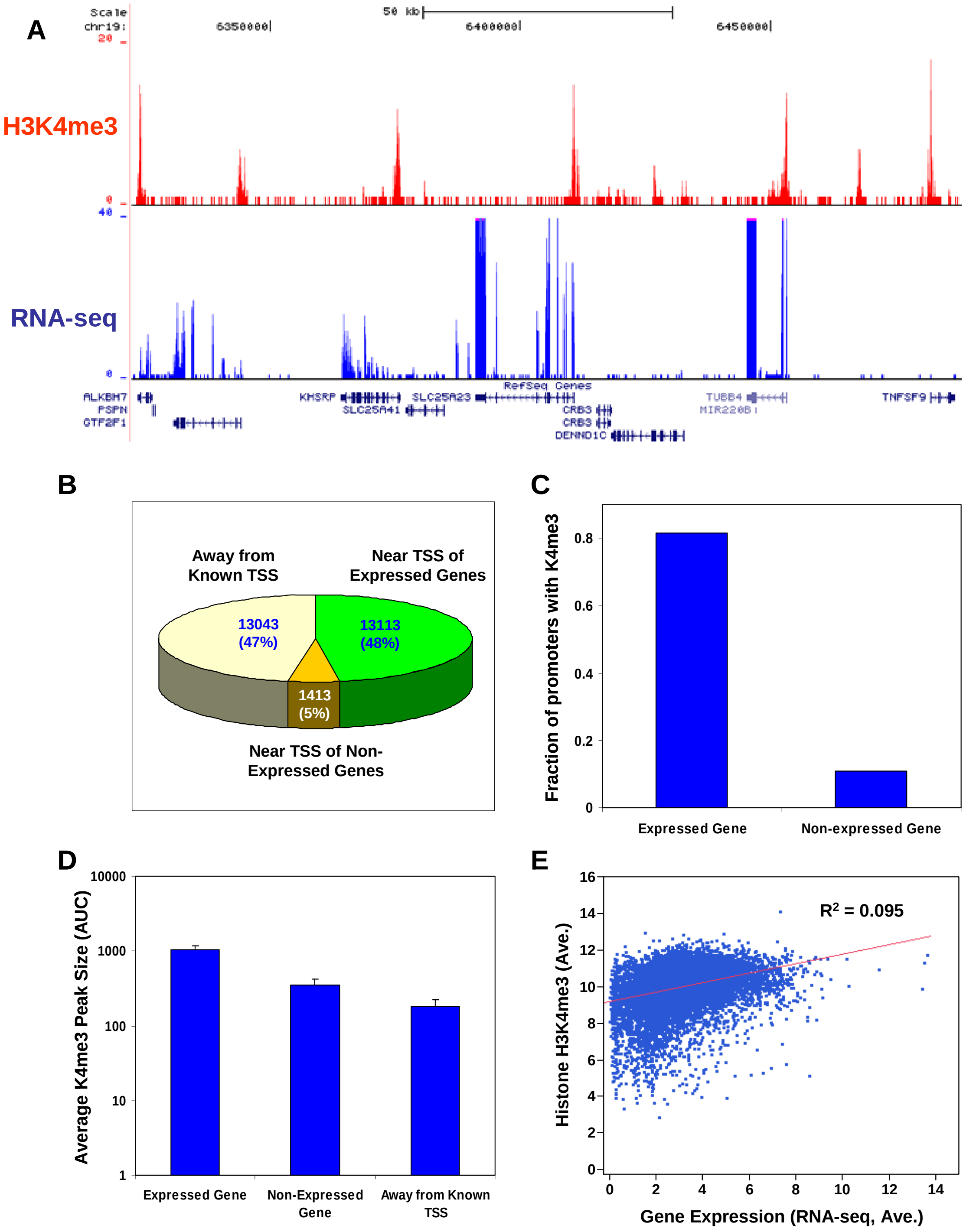


Figure S3. Genome-wide distribution of histone H3K4me3 signal and its correlation with gene expression. *(A)*. Co-localization of histone H3K4me3 ChIP-seq reads with RNA-seq reads in a 150 kb region of chromosome 19. Histone H3K4me3 signals (upper track, red) are mapped to the promoter regions of the annotated genes where mRNA sequencing reads (lower track, blue) are also aligned with exonic regions of the expressed genes. Note the presence of H3K4me3 in some gene loci where expression was not detected. *(B)*. Distribution of histon H3K4me3 peaks (27,569 in total genome-wide) in the promoters of expressed genes (13,113 peaks, 48%), non-expressed genes (1413 peaks, 5%), and away from known transcription start site (13043 peaks, 47%). *(C)*. Fractions of the promoters with histon H3K4Me3 in the expressed (82%) and non-expressed (11%) genes. *(D)*. Average signal levels (peak sizes) of histone H3K4me3 in the expressed genes, non-expressed genes, and non-genic regions. *(E)*. Global correlation of histone H3K4 me3 signal level with mRNA transcript level in 13,113 expressed genes in hippocampus.

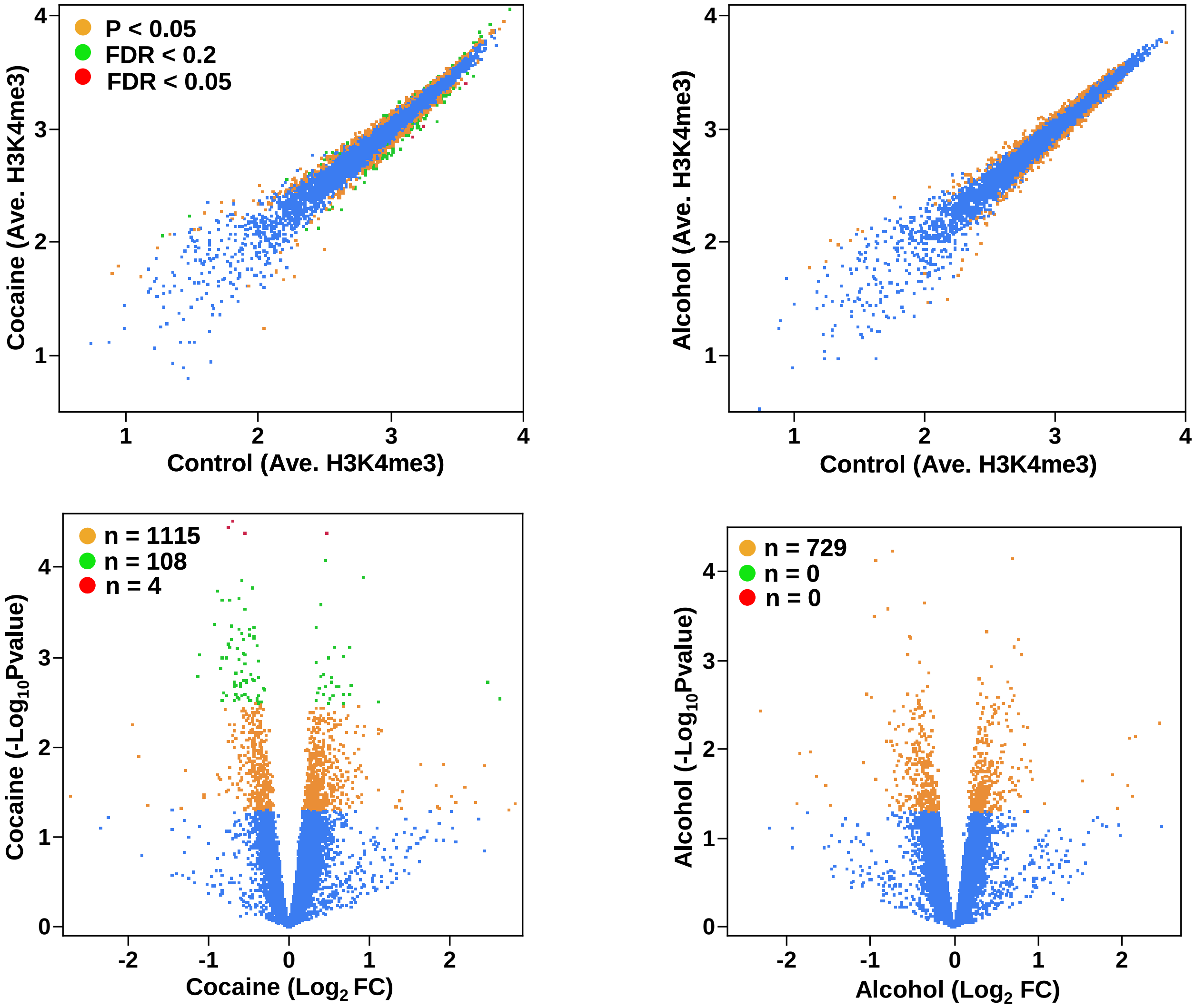


Figure S4. Profiles of histone H3K4me3 in the promoters of hippocampal expressed genes and their changes in chronically cocaine- or alcohol-addicted individuals. Upper panels display the scatter plots of the H3K4me3 levels in the promoters of13,113 expressed genes in control vs. cocaine- (left) or alcohol-addicted (right) individuals. Lower panels provide the *P* values and alteration of the signal, in terms of fold-change, for all 13,113 genes in cocaine- (left) and alcohol- addicted (right) individuals. H3K4me3 peaks that are altered at different levels: uncorrected $P < 0.05$, FDR <0.2, or FDR < 0.05 are indicated by the color coding.

Table S1. Study subject information

Sample ID	Race[1]	Age	Gender	PMI[2] (h)	Phenotype	Cause of Death	Cocaine (Blood) (mg/L)	BE[3] (Blood) (mg/L)	Cocaine (Brain) (mg/kg)	BE (Brain) (mg/kg)	ETOH (Blood) (%)
CT1	C	43	M	8	Control	Atherosclerotic heart disease					
CT2	C	30	M	16.8	Control	Ventricular arrhythmia				.	
CT3	C	36	M	22	Control	Atherosclerotic cardiovascular disease					
CT4	B	31	M	22	Control	Atherosclerotic and hypertensive heart disease					
CT5	C	50	M	11	Control	Acute myocardial infarction					
CT6	C/H	41	M	18.3	Control	Myocardial infarct					
CT7	B	46	M	16	Control	Gunshot wound to chest					
CT8	C/H	32	M	18	Control	Blunt force trauma					
CT9	C/H	41	M	16	Control	Atherosclerotic heart disease					
CO1	C/H	37	M	19	Cocaine abuse	Acute cocaine toxicity	6.0	5.40	3.1	0.28	
CO2	C	35	M	20	Cocaine abuse	Cocaine intoxication	14.8 *	NQ***	2.3	0.67	
CO3	B	41	M	18.5	Cocaine abuse	Cocaine toxicity	0.56 **	2.0	1.85	0.84	
CO4	C	32	M	22	Cocaine abuse	Acute cocaine intoxication	0.05	1.30	0.11	0.58	
CO5	B	38	M	20	Cocaine abuse	Cocaine intoxication	1.71	12.5	3.33	5.7	
CO6	B	45	M	12	Cocaine abuse	Cocaine/ETOH intoxication	0.33	0.97	0.27	0.40	0.11
CO7	C/H	49	M	19	Cocaine abuse	Acute cocaine intoxication	0.01	0.55	0.13	0.16	
CO8	C	39	M		Cocaine abuse	Cocaine intoxication	0.51	0.830	0.13	0.65	
CO9	C/H	35	M	15	Cocaine abuse	Cocaine toxicity	6.0	5.40	3.1	0.28	
ETOH 1	C	28	M	22	Alcohol abuse	Occlusive coronary arteriosclerosis					0.01
ETOH 2	C	33	M	15	Alcohol abuse	Multiple blunt impact injuries					0.02
ETOH 3	C/H	43	M	16	Alcohol abuse	Complications of chronic ethanolism					0.15
ETOH 4	B	48	M	13	Alcohol abuse	Gunshot wound					0.02
ETOH 5	C	25	M	13.5	Alcohol abuse	Stab wound to chest/homicide					0.18
ETOH 6	C/H	29	M	12.25	Alcohol abuse	Anoxic encephalopathy					0.06
ETOH 7	C	39	M		Alcohol abuse	Ischemic heart disease					0.05
ETOH 8	C/H	50	M	19	Alcohol abuse	Ischemic heart disease					0.01

[1] C: Caucasian, C/H: Caucasian/Hispanic, B: Black; [2] PMI: postmortem (death to freezing) interval; [3] Benzoylecgonine
* Postmortem heart blood; ** Aorta; *** NQ: not quantified

Table S2. Genes with significant differential expression (FDR < 0.2) observed in cocaine-addicted individuals

Gene Symbol	**Gene Name**	**Log FC**	***P* value**	**FDR**
HIST1H4E	Histone cluster 1, h4e	1.57	1.6E-10	0.000
RN7SK	RNA, 7SK small nuclear	2.42	5.3E-10	0.000
CDR1	Cerebellar degeneration-related protein 1, 34kda	1.81	5.2E-09	0.000
DDX17	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17	1.02	1.4E-08	0.000
SNORD89	Small nucleolar RNA, C/D box 89	1.53	5.6E-08	0.000
SNORA73A	Small nucleolar RNA, H/ACA box 73A	1.41	2.2E-07	0.001
MCCC1	Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-1.01	1.4E-06	0.003
SCARNA17	Small Cajal body-specific RNA 17	1.30	1.6E-06	0.004
AEBP2	AE binding protein 2	0.90	2.8E-06	0.004
MDM4	Mdm4 p53 binding protein homolog (mouse)	1.01	3.0E-06	0.004
SNX27	Sorting nexin family member 27	0.68	3.8E-06	0.004
RIN2	Ras and Rab interactor 2	0.65	3.9E-06	0.004
DPYSL2	Dihydropyrimidinase-like 2	0.93	3.9E-06	0.004
PAPD1	Mitochondrial poly(A) polymerase	0.95	4.1E-06	0.004
CACNB2	Calcium channel, voltage-dependent, beta 2 subunit	0.87	4.8E-06	0.005
IGF1R	Insulin-like growth factor 1 receptor	0.80	7.9E-06	0.008
MRPS17	Mitochondrial ribosomal protein S17	-0.80	8.5E-06	0.008
LRCH4	Leucine-rich repeats and calponin homology (CH) domain containing 4	0.80	8.8E-06	0.008
SNORD42A	Small nucleolar RNA, C/D box 42A	-1.47	1.2E-05	0.010
ZNF483	Zinc finger protein 483	1.14	1.3E-05	0.010
ZIM2	Zinc finger, imprinted 2	1.13	1.4E-05	0.010
SNORA47	Small nucleolar RNA, H/ACA box 47	1.82	1.5E-05	0.010
IRGQ	Immunity-related gtpase family, Q	0.76	1.6E-05	0.011
C3orf28	Family with sequence similarity 162, member A	-0.93	1.7E-05	0.011
SCARNA5	Small Cajal body-specific RNA 5	1.50	2.0E-05	0.012
LENG8	Leukocyte receptor cluster (LRC) member 8	0.77	2.3E-05	0.014
SNORA39	Small nucleolar RNA, H/ACA box 39	1.67	2.7E-05	0.015
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	0.86	2.8E-05	0.015
BEX4	Brain expressed, X-linked 4	-0.58	2.8E-05	0.015
FAM123A	Family with sequence similarity 123A	0.72	3.9E-05	0.019
HIVEP3	Human immunodeficiency virus type I enhancer binding protein 3	0.70	3.9E-05	0.019
GTF2A1	General transcription factor IIA, 1, 19/37kda	0.74	4.7E-05	0.023
KIAA0754	Kiaa0754	0.71	5.8E-05	0.026
TXLNA	Taxilin alpha	0.66	5.9E-05	0.026
ILF2	Interleukin enhancer binding factor 2, 45kda	-0.65	6.0E-05	0.026
LILRB1	Leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 1	-1.15	6.0E-05	0.026
C4orf12	Chromosome 4 open reading frame 12	0.78	6.3E-05	0.026

HNRPH1	Heterogeneous nuclear ribonucleoprotein H1	0.81	6.5E-05	0.026
RAP2B	RAP2B, member of RAS oncogene family	0.98	6.6E-05	0.026
NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-0.73	7.9E-05	0.030
CD36	CD36 molecule (thrombospondin receptor)	-1.43	8.3E-05	0.031
PPCS	Phosphopantothenoylcysteine synthetase	-0.80	9.0E-05	0.033
ZGPAT	Zinc finger, CCCH-type with G patch domain	0.55	9.2E-05	0.033
SLC8A1	Solute carrier family 8 (sodium/calcium exchanger), member 1	0.93	9.8E-05	0.033
C20orf112	Chromosome 20 open reading frame 112	0.82	9.8E-05	0.033
LENG9	Leukocyte receptor cluster (LRC) member 9	0.73	1.1E-04	0.035
STIM2	Stromal interaction molecule 2	0.75	1.1E-04	0.035
KLHL12	Kelch-like 12 (Drosophila)	-0.75	1.1E-04	0.035
BEX1	Brain expressed, X-linked 1	-0.66	1.1E-04	0.035
UQCRH	Ubiquinol-cytochrome c reductase hinge protein	-0.74	1.1E-04	0.035
PBXIP1	Pre-B-cell leukemia homeobox interacting protein 1	0.91	1.2E-04	0.035
SNORA74B	Small nucleolar RNA, H/ACA box 74B	1.60	1.2E-04	0.035
SLC24A4	Solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	0.89	1.2E-04	0.035
IGSF9B	Immunoglobulin superfamily, member 9B	1.05	1.3E-04	0.037
SNORA62	Small nucleolar RNA, H/ACA box 62	1.87	1.3E-04	0.038
FLJ23556	Flj23556	1.40	1.4E-04	0.038
MTA2	Metastasis associated 1 family, member 2	0.78	1.4E-04	0.038
SNORD76	Small nucleolar RNA, C/D box 76	1.21	1.6E-04	0.042
ELK4	ELK4, ETS-domain protein (SRF accessory protein 1)	0.60	1.7E-04	0.042
SCARNA7	Small Cajal body-specific RNA 7	1.53	1.7E-04	0.042
RNF41	Ring finger protein 41	-0.61	1.7E-04	0.042
PPP3CA	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	0.91	1.8E-04	0.042
HIST1H4H	Histone cluster 1, h4h	1.03	1.8E-04	0.042
LRRTM4	Leucine rich repeat transmembrane neuronal 4	0.77	1.8E-04	0.042
MGC22014	Tet oncogene family member 3p	0.82	1.8E-04	0.042
SNORD33	Small nucleolar RNA, C/D box 33	0.74	1.8E-04	0.042
RNF187	Ring finger protein 187	-0.60	1.9E-04	0.042
ZBTB44	Zinc finger and BTB domain containing 44	0.61	1.9E-04	0.043
LRCH3	Leucine-rich repeats and calponin homology (CH) domain containing 3	0.76	2.0E-04	0.043
SLC25A14	Solute carrier family 25 (mitochondrial carrier, brain), member 14	-0.78	2.0E-04	0.043
SNORD74	Small nucleolar RNA, C/D box 74	1.37	2.1E-04	0.044
IFITM1	Interferon induced transmembrane protein 1 (9-27)	1.36	2.1E-04	0.044
ERF	Ets2 repressor factor	0.65	2.2E-04	0.046
MRPL27	Mitochondrial ribosomal protein L27	-0.50	2.2E-04	0.046
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-0.61	2.3E-04	0.046
SIRPB1	Signal-regulatory protein beta 1	-1.60	2.3E-04	0.046

CAMK2D	Calcium/calmodulin-dependent protein kinase II delta	-0.72	2.3E-04	0.047
MRPS28	Mitochondrial ribosomal protein S28	-0.78	2.4E-04	0.049
RPSA	Ribosomal protein SA	1.56	2.5E-04	0.050
DNAJC19	Dnaj (Hsp40) homolog, subfamily C, member 19	-0.74	2.5E-04	0.050
BMF	Bcl2 modifying factor	-1.26	2.7E-04	0.051
MAMDC4	MAM domain containing 4	0.59	2.8E-04	0.053
FMN2	Formin 2	0.54	2.8E-04	0.053
HINT1	Histidine triad nucleotide binding protein 1	-0.75	2.9E-04	0.053
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast)	-1.27	2.9E-04	0.053
HMSD	Histocompatibility (minor) serpin domain containing	-1.06	2.9E-04	0.053
COL4A3BP	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0.83	2.9E-04	0.053
HNRNPU	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0.70	2.9E-04	0.053
SNORD116-29	Small nucleolar RNA, C/D box 116-29	-1.68	3.0E-04	0.053
MCM6	Minichromosome maintenance complex component 6	-0.58	3.0E-04	0.053
PSMG1	Proteasome (prosome, macropain) assembly chaperone 1	-0.74	3.1E-04	0.054
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kda	-0.91	3.1E-04	0.054
CCDC104	Coiled-coil domain containing 104	-0.72	3.1E-04	0.054
ALS2CR4	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4	-0.60	3.5E-04	0.059
SELT	Selenoprotein T	-0.81	3.6E-04	0.059
ZBTB7B	Zinc finger and BTB domain containing 7B	0.58	3.6E-04	0.059
MRPL15	Mitochondrial ribosomal protein L15	-0.60	3.6E-04	0.060
C9orf119	Chromosome 9 open reading frame 119	-0.61	3.8E-04	0.061
GSTA4	Glutathione S-transferase alpha 4	-0.64	3.8E-04	0.062
TMEM168	Transmembrane protein 168	-0.67	4.2E-04	0.067
ARID5B	AT rich interactive domain 5B (MRF1-like)	0.72	4.2E-04	0.067
MUPCDH	Mucin-like protocadherin	0.83	4.3E-04	0.067
C9orf139	Chromosome 9 open reading frame 139	0.90	4.4E-04	0.068
PLDN	Pallidin homolog (mouse)	-0.85	4.5E-04	0.069
SUMO1P3	SUMO1 pseudogene 3	-0.84	4.6E-04	0.069
PRPSAP2	Phosphoribosyl pyrophosphate synthetase-associated protein 2	-0.67	4.7E-04	0.070
MYO19	Myosin XIX	-0.79	4.8E-04	0.070
TMEM14B	Transmembrane protein 14B	-0.79	4.9E-04	0.072
PPP1R1B	Protein phosphatase 1, regulatory (inhibitor) subunit 1B	0.75	5.0E-04	0.073
PHACTR1	Phosphatase and actin regulator 1	0.73	5.4E-04	0.077
ZMAT2	Zinc finger, matrin type 2	-0.55	5.7E-04	0.080
TRO	Trophinin	-0.49	5.9E-04	0.081
ARV1	ARV1 homolog (S. Cerevisiae)	-0.63	5.9E-04	0.081
LMTK2	Lemur tyrosine kinase 2	0.61	5.9E-04	0.081

OTUD7A	OTU domain containing 7A	0.58	6.0E-04	0.081
SNORD22	Small nucleolar RNA, C/D box 22	1.17	6.1E-04	0.081
SYNPO2	Synaptopodin 2	0.61	6.1E-04	0.081
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.59	6.2E-04	0.081
C9orf3	Chromosome 9 open reading frame 3	0.70	6.5E-04	0.084
TSC22D2	TSC22 domain family, member 2	0.62	6.6E-04	0.085
XKR4	XK, Kell blood group complex subunit-related family, member 4	0.51	6.9E-04	0.088
THYN1	Thymocyte nuclear protein 1	-0.64	7.0E-04	0.088
HMBOX1	Homeobox containing 1	0.72	7.2E-04	0.090
TMSB4Y	Thymosin beta 4, Y-linked	-0.56	7.3E-04	0.090
AP3M2	Adaptor-related protein complex 3, mu 2 subunit	-0.70	7.3E-04	0.090
TMEM14A	Transmembrane protein 14A	-0.74	7.3E-04	0.090
PLXDC2	Plexin domain containing 2	0.66	7.3E-04	0.090
HSPG2	Heparan sulfate proteoglycan 2	0.67	7.5E-04	0.091
HDAC2	Histone deacetylase 2	-0.75	7.7E-04	0.094
NF2	Neurofibromin 2 (merlin)	0.74	7.8E-04	0.094
RANBP17	RAN binding protein 17	-1.36	8.2E-04	0.098
PCYOX1L	Prenylcysteine oxidase 1 like	-0.68	8.3E-04	0.098
TARS2	Threonyl-trna synthetase 2, mitochondrial (putative)	-0.53	8.4E-04	0.098
STX1B	Syntaxin 1B	0.69	8.4E-04	0.098
NUFIP2	Nuclear fragile X mental retardation protein interacting protein 2	0.72	8.5E-04	0.099
MICALL2	MICAL-like 2	0.55	8.8E-04	0.100
SLA2	Src-like-adaptor 2	1.25	9.0E-04	0.101
POLR2G	Polymerase (RNA) II (DNA directed) polypeptide G	-0.65	9.0E-04	0.101
POLR1D	Polymerase (RNA) I polypeptide D, 16kda	-0.68	9.1E-04	0.102
TNKS1BP1	Tankyrase 1 binding protein 1, 182kda	0.60	9.4E-04	0.102
PROK1	Prokineticin 1	0.79	9.4E-04	0.102
H2AFZ	H2A histone family, member Z	-0.62	9.5E-04	0.102
QSER1	Glutamine and serine rich 1	0.64	9.9E-04	0.103
SDHA	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-0.49	9.9E-04	0.103
RAB6A	RAB6A, member RAS oncogene family	-0.79	1.0E-03	0.103
LRP1B	Low density lipoprotein-related protein 1B (deleted in tumors)	0.52	1.0E-03	0.104
SFRS6	Splicing factor, arginine/serine-rich 6	0.67	1.0E-03	0.104
HYLS1	Hydrolethalus syndrome 1	-0.77	1.0E-03	0.106
MTCH2	Mitochondrial carrier homolog 2 (C. Elegans)	-0.50	1.0E-03	0.106
PPP1CB	Protein phosphatase 1, catalytic subunit, beta isoform	0.75	1.1E-03	0.106
ZDHHC11B	Zinc finger, DHHC-type containing 11B	1.00	1.1E-03	0.106
OLFML3	Olfactomedin-like 3	-0.69	1.1E-03	0.106
KCNA2	Potassium voltage-gated channel, shaker-related subfamily, member 2	0.67	1.1E-03	0.106

NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kda	-0.86	1.1E-03	0.106
P2RX5	Purinergic receptor P2X, ligand-gated ion channel, 5	-0.73	1.1E-03	0.106
TM2D3	TM2 domain containing 3	-0.62	1.1E-03	0.106
TNIK	TRAF2 and NCK interacting kinase	0.58	1.1E-03	0.106
AFF1	AF4/FMR2 family, member 1	0.47	1.1E-03	0.106
IGF2	Insulin-like growth factor 2 (somatomedin A)	1.30	1.1E-03	0.106
MAPK7	Mitogen-activated protein kinase 7	0.54	1.1E-03	0.107
ACRV1	Acrosomal vesicle protein 1	-1.19	1.1E-03	0.107
TFR2	Transferrin receptor 2	-0.65	1.1E-03	0.107
ARHGAP17	Rho gtpase activating protein 17	0.58	1.2E-03	0.108
DCXR	Dicarbonyl/L-xylulose reductase	0.53	1.2E-03	0.108
PRICKLE2	Prickle homolog 2 (Drosophila)	0.84	1.2E-03	0.108
CTDSP2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	0.49	1.2E-03	0.109
SCARNA6	Small Cajal body-specific RNA 6	1.03	1.2E-03	0.110
C7orf46	Chromosome 7 open reading frame 46	-0.62	1.2E-03	0.110
ZNF165	Zinc finger protein 165	-0.99	1.2E-03	0.114
ZSCAN5	Zinc finger and SCAN domain containing 5A	-0.62	1.3E-03	0.115
SHPRH	SNF2 histone linker PHD RING helicase	0.49	1.3E-03	0.115
TARBP1	TAR (HIV-1) RNA binding protein 1	-0.70	1.3E-03	0.115
GYS2	Glycogen synthase 2 (liver)	1.00	1.3E-03	0.118
DHX34	DEAH (Asp-Glu-Ala-His) box polypeptide 34	0.53	1.4E-03	0.121
ZBTB16	Zinc finger and BTB domain containing 16	0.57	1.4E-03	0.121
TTTY15	Testis-specific transcript, Y-linked 15 (non-protein coding)	0.68	1.4E-03	0.122
RMRP	RNA component of mitochondrial RNA processing endoribonuclease	0.82	1.4E-03	0.122
SIAE	Sialic acid acetylesterase	-0.51	1.4E-03	0.123
SCNN1A	Sodium channel, nonvoltage-gated 1 alpha	1.73	1.4E-03	0.123
EXOC6B	Exocyst complex component 6B	0.51	1.4E-03	0.124
PPP1R3B	Protein phosphatase 1, regulatory (inhibitor) subunit 3B	0.62	1.4E-03	0.124
C10orf93	Chromosome 10 open reading frame 93	0.82	1.5E-03	0.125
C1orf215	Chromosome 1 open reading frame 215	-1.03	1.5E-03	0.125
SLC41A3	Solute carrier family 41, member 3	-0.59	1.5E-03	0.126
HPS6	Hermansky-Pudlak syndrome 6	-0.63	1.6E-03	0.131
MDM2	Mdm2 p53 binding protein homolog (mouse)	0.51	1.6E-03	0.132
COPS4	COP9 constitutive photomorphogenic homolog subunit 4 (Arabidopsis)	-0.66	1.6E-03	0.133
SNORD4A	Small nucleolar RNA, C/D box 4A	-1.31	1.6E-03	0.133
PSMC2	Proteasome (prosome, macropain) 26S subunit, atpase, 2	-0.55	1.7E-03	0.136
MSI1	Musashi homolog 1 (Drosophila)	0.60	1.7E-03	0.137
MRPL45	Mitochondrial ribosomal protein L45	-0.72	1.7E-03	0.137
KIAA1199	Kiaa1199	0.70	1.7E-03	0.137

PTPRD	Protein tyrosine phosphatase, receptor type, D	-0.68	1.7E-03	0.137
C6orf98	Chromosome 6 open reading frame 98	-1.07	1.7E-03	0.138
LAMA5	Laminin, alpha 5	0.54	1.7E-03	0.138
RNASEN	Ribonuclease type III, nuclear	-0.57	1.7E-03	0.138
C9orf105	Chromosome 9 open reading frame 105	-0.65	1.7E-03	0.138
CENTB5	Arfgap with coiled-coil, ankyrin repeat and PH domains 3	0.54	1.8E-03	0.139
GRP	Gastrin-releasing peptide	-0.72	1.8E-03	0.139
LPHN1	Latrophilin 1	0.72	1.8E-03	0.139
TAOK2	TAO kinase 2	0.56	1.8E-03	0.139
LEF1	Lymphoid enhancer-binding factor 1	0.69	1.8E-03	0.139
ZNF518A	Zinc finger protein 518A	0.53	1.8E-03	0.139
ARIH1	Ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	0.66	1.8E-03	0.139
ZDHHC4	Zinc finger, DHHC-type containing 4	-0.67	1.8E-03	0.139
IRF3	Interferon regulatory factor 3	0.64	1.8E-03	0.140
UBE2V2	Ubiquitin-conjugating enzyme E2 variant 2	-0.77	1.9E-03	0.140
EVI5	Ecotropic viral integration site 5	0.64	1.9E-03	0.143
HERC1	Hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 1	0.44	1.9E-03	0.143
CHST3	Carbohydrate (chondroitin 6) sulfotransferase 3	0.51	1.9E-03	0.143
NRP1	Neuropilin 1	0.75	2.0E-03	0.145
TMEM14C	Transmembrane protein 14C	-0.62	2.0E-03	0.145
XYLT2	Xylosyltransferase II	0.63	2.0E-03	0.146
STX12	Syntaxin 12	-0.50	2.0E-03	0.146
NFIA	Nuclear factor I/A	0.72	2.0E-03	0.146
MLLT6	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	0.48	2.0E-03	0.146
GAS5	Growth arrest-specific 5 (non-protein coding)	1.01	2.0E-03	0.146
RNF8	Ring finger protein 8	-0.43	2.0E-03	0.146
TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kda	-0.72	2.0E-03	0.146
KLHL1	Kelch-like 1 (Drosophila)	-1.06	2.1E-03	0.147
HEATR1	HEAT repeat containing 1	-0.39	2.1E-03	0.147
TIMP2	TIMP metallopeptidase inhibitor 2	-0.63	2.1E-03	0.147
LGALS8	Lectin, galactoside-binding, soluble, 8	-0.39	2.1E-03	0.147
ABCG4	ATP-binding cassette, sub-family G (WHITE), member 4	-0.54	2.1E-03	0.149
HIST1H4C	Histone cluster 1, h4c	0.70	2.2E-03	0.152
FRG1B	FSHD region gene 1 family, member B	-0.57	2.2E-03	0.153
TLE3	Transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	0.52	2.2E-03	0.153
SLC25A5	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	-0.69	2.2E-03	0.153
NPM3	Nucleophosmin/nucleoplasmin 3	-0.97	2.3E-03	0.153

VISA	Mitochondrial antiviral signaling protein	0.44	2.3E-03	0.153
L3MBTL	L(3)mbt-like (Drosophila)	0.46	2.3E-03	0.153
WDR42C	DDB1 and CUL4 associated factor 8-like 2	-1.36	2.3E-03	0.154
DIPAS	PAPPA antisense RNA	1.21	2.3E-03	0.154
GPR75	G protein-coupled receptor 75	0.52	2.3E-03	0.154
ATF7IP	Activating transcription factor 7 interacting protein	0.47	2.3E-03	0.154
IFITM3	Interferon induced transmembrane protein 3 (1-8U)	1.16	2.4E-03	0.156
IQCH	IQ motif containing H	-1.11	2.4E-03	0.159
KIAA1305	NYN domain and retroviral integrase containing	0.44	2.5E-03	0.162
ZBTB20	Zinc finger and BTB domain containing 20	0.85	2.5E-03	0.162
FLJ21438	RAS protein activator like 3	-0.88	2.5E-03	0.162
ZNF469	Zinc finger protein 469	0.45	2.5E-03	0.162
LETMD1	LETM1 domain containing 1	-0.55	2.5E-03	0.162
PACRG	PARK2 co-regulated	-0.85	2.5E-03	0.163
ZMAT3	Zinc finger, matrin type 3	0.62	2.6E-03	0.163
CPO	Carboxypeptidase O	-1.11	2.6E-03	0.163
C11orf38	Prostate and testis expressed 2	-1.05	2.6E-03	0.163
ATP7B	Atpase, Cu++ transporting, beta polypeptide	0.43	2.6E-03	0.163
GPR132	G protein-coupled receptor 132	-1.06	2.6E-03	0.163
CRHBP	Corticotropin releasing hormone binding protein	-0.74	2.6E-03	0.163
PRR19	Proline rich 19	-1.04	2.6E-03	0.163
SBNO2	Strawberry notch homolog 2 (Drosophila)	0.66	2.7E-03	0.166
GTF2F2	General transcription factor IIF, polypeptide 2, 30kda	-0.52	2.7E-03	0.166
NDRG3	NDRG family member 3	-0.67	2.7E-03	0.167
BMP4	Bone morphogenetic protein 4	1.22	2.7E-03	0.168
TNRC6C	Trinucleotide repeat containing 6C	0.59	2.8E-03	0.170
SPATS2	Spermatogenesis associated, serine-rich 2	0.41	2.8E-03	0.171
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.73	2.8E-03	0.171
GAD1	Glutamate decarboxylase 1 (brain, 67kda)	-0.78	2.8E-03	0.171
PHF16	PHD finger protein 16	-0.45	2.9E-03	0.172
ECOP	EGFR-coamplified and overexpressed protein	-0.42	2.9E-03	0.172
KLF13	Kruppel-like factor 13	0.40	2.9E-03	0.172
CCNDBP1	Cyclin D-type binding-protein 1	-0.60	2.9E-03	0.173
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	0.65	2.9E-03	0.173
SFT2D2	SFT2 domain containing 2	0.81	2.9E-03	0.173
AS3MT	Arsenic (+3 oxidation state) methyltransferase	-0.50	2.9E-03	0.173
TXN	Thioredoxin	-0.65	3.0E-03	0.173
RFXAP	Regulatory factor X-associated protein	0.62	3.0E-03	0.173
CCDC115	Coiled-coil domain containing 115	-0.57	3.0E-03	0.175
CLASP2	Cytoplasmic linker associated protein 2	-0.44	3.0E-03	0.175
SLC30A9	Solute carrier family 30 (zinc transporter), member 9	-0.53	3.0E-03	0.176
PSMD4	Proteasome (prosome, macropain) 26S subunit, non-atpase, 4	-0.47	3.1E-03	0.176
KIAA1370	Kiaa1370	0.67	3.1E-03	0.177
RAD52	RAD52 homolog (S. Cerevisiae)	0.46	3.1E-03	0.177

C11orf47	Chromosome 11 open reading frame 47	0.52	3.1E-03	0.177
PHC3	Polyhomeotic homolog 3 (Drosophila)	0.40	3.1E-03	0.177
STMN1	Stathmin 1	-0.59	3.2E-03	0.178
C11orf1	Chromosome 11 open reading frame 1	-0.58	3.2E-03	0.178
SCGB1A1	Secretoglobin, family 1A, member 1 (uteroglobin)	0.81	3.2E-03	0.178
DYNLT3	Dynein, light chain, Tctex-type 3	-0.85	3.2E-03	0.178
C2orf28	Chromosome 2 open reading frame 28	-0.42	3.2E-03	0.178
MRPS9	Mitochondrial ribosomal protein S9	-0.53	3.2E-03	0.178
MLXIP	MLX interacting protein	0.37	3.2E-03	0.178
TMEM182	Transmembrane protein 182	-0.77	3.2E-03	0.178
SNHG1	Small nucleolar RNA host gene 1 (non-protein coding)	0.96	3.3E-03	0.179
CCDC61	Coiled-coil domain containing 61	0.59	3.3E-03	0.179
SENP5	SUMO1/sentrin specific peptidase 5	0.46	3.3E-03	0.179
MPP3	Membrane protein, palmitoylated 3 (MAGUK p55 subfamily member 3)	-0.46	3.3E-03	0.179
UBE2D2	Ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	-0.52	3.3E-03	0.179
TAC4	Tachykinin-4	0.95	3.4E-03	0.179
NAIP	NLR family, apoptosis inhibitory protein	-1.03	3.4E-03	0.179
PIP4K2A	Phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	0.76	3.4E-03	0.179
PCOLCE2	Procollagen C-endopeptidase enhancer 2	-0.76	3.4E-03	0.179
CAPN2	Calpain 2, (m/II) large subunit	0.42	3.4E-03	0.179
ANAPC13	Anaphase promoting complex subunit 13	-0.50	3.4E-03	0.179
LBX2	Ladybird homeobox 2	0.79	3.4E-03	0.179
SNORD59B	Small nucleolar RNA, C/D box 59B	1.51	3.4E-03	0.179
DKFZP564J0863	Atlastin gtpase 3	0.67	3.4E-03	0.179
COX5B	Cytochrome c oxidase subunit Vb	-0.37	3.4E-03	0.179
INE1	Inactivation escape 1 (non-protein coding)	0.57	3.4E-03	0.179
RUFY3	RUN and FYVE domain containing 3	0.54	3.4E-03	0.179
C3orf1	Chromosome 3 open reading frame 1	-0.56	3.5E-03	0.180
MSH4	Muts homolog 4 (E. Coli)	0.79	3.5E-03	0.180
MOXD1	Monooxygenase, DBH-like 1	-0.66	3.5E-03	0.180
KRTAP5-8	Keratin associated protein 5-8	0.87	3.5E-03	0.180
SLC25A20	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-0.53	3.5E-03	0.180
EXTL2	Exostoses (multiple)-like 2	-0.53	3.5E-03	0.180
BCL10	B-cell CLL/lymphoma 10	0.52	3.6E-03	0.180
CMAS	Cytidine monophosphate N-acetylneuraminic acid synthetase	-0.63	3.6E-03	0.180
MBD3	Methyl-cpg binding domain protein 3	0.51	3.6E-03	0.180
TMEM18	Transmembrane protein 18	-0.64	3.6E-03	0.180
EYA1	Eyes absent homolog 1 (Drosophila)	0.46	3.6E-03	0.180
KLF7	Kruppel-like factor 7 (ubiquitous)	0.52	3.6E-03	0.180

LARP4	La ribonucleoprotein domain family, member 4	0.55	3.6E-03	0.180
OTX2	Orthodenticle homeobox 2	1.51	3.6E-03	0.180
GSTZ1	Glutathione transferase zeta 1	-0.75	3.7E-03	0.181
BAHD1	Bromo adjacent homology domain containing 1	0.54	3.7E-03	0.181
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kda	-0.61	3.7E-03	0.181
MRPS23	Mitochondrial ribosomal protein S23	-0.63	3.7E-03	0.181
PDHB	Pyruvate dehydrogenase (lipoamide) beta	-0.52	3.7E-03	0.181
ATXN2L	Ataxin 2-like	0.42	3.7E-03	0.181
TIMM23	Translocase of inner mitochondrial membrane 23 homolog (yeast)	-0.65	3.7E-03	0.181
C17orf38	Phosphoinositide-3-kinase, regulatory subunit 6	-1.01	3.7E-03	0.181
SNORD83B	Small nucleolar RNA, C/D box 83B	0.88	3.8E-03	0.182
DYNC1I1	Dynein, cytoplasmic 1, intermediate chain 1	-0.69	3.8E-03	0.182
CD74	CD74 molecule, major histocompatibility complex, class II invariant chain	-1.10	3.8E-03	0.182
C11orf41	Chromosome 11 open reading frame 41	0.50	3.8E-03	0.182
ATP5H	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d	-0.45	3.8E-03	0.182
SCN4A	Sodium channel, voltage-gated, type IV, alpha subunit	0.79	3.8E-03	0.182
RNU4B2	RNA, U4 small nuclear 1	1.36	3.9E-03	0.184
ACTL6A	Actin-like 6A	-0.48	3.9E-03	0.184
HELZ	Helicase with zinc finger	0.51	3.9E-03	0.184
ACP2	Acid phosphatase 2, lysosomal	-0.55	3.9E-03	0.184
FLJ27365	Flj27365	0.63	3.9E-03	0.184
TOP2B	Topoisomerase (DNA) II beta 180kda	-0.39	3.9E-03	0.184
COL4A1	Collagen, type IV, alpha 1	0.68	3.9E-03	0.184
TADA1L	Transcriptional adaptor 1 (HFI1 homolog, yeast) like	-0.60	4.0E-03	0.184
TXNL4A	Thioredoxin-like 4A	-0.56	4.0E-03	0.184
EIF2C1	Eukaryotic translation initiation factor 2C, 1	0.51	4.0E-03	0.184
HSD17B6	Hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)	-0.55	4.0E-03	0.184
SPON2	Spondin 2, extracellular matrix protein	0.43	4.0E-03	0.184
CPOX	Coproporphyrinogen oxidase	0.68	4.0E-03	0.184
ACOT2	Acyl-coa thioesterase 2	-0.45	4.0E-03	0.184
PGLS	6-phosphogluconolactonase	-0.49	4.0E-03	0.185
ZNF32	Zinc finger protein 32	-0.48	4.0E-03	0.185
DNAJC10	Dnaj (Hsp40) homolog, subfamily C, member 10	-0.47	4.1E-03	0.186
LIN7C	Lin-7 homolog C (C. Elegans)	0.60	4.1E-03	0.188
LYRM5	LYR motif containing 5	-0.48	4.2E-03	0.189
HIPK1	Homeodomain interacting protein kinase 1	0.48	4.2E-03	0.189
C14orf24	Family with sequence similarity 177, member A1	-0.69	4.2E-03	0.189
PTPN14	Protein tyrosine phosphatase, non-receptor type 14	0.51	4.2E-03	0.189
ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 readthrough	0.97	4.2E-03	0.189
GPR6	G protein-coupled receptor 6	-1.03	4.2E-03	0.189

C16orf42	Chromosome 16 open reading frame 42	-0.54	4.2E-03	0.189
LRPAP1	Low density lipoprotein receptor-related protein associated protein 1	-0.36	4.2E-03	0.189
GFOD1	Glucose-fructose oxidoreductase domain containing 1	0.55	4.2E-03	0.189
SNX2	Sorting nexin 2	-0.55	4.3E-03	0.189
MFAP4	Microfibrillar-associated protein 4	0.65	4.3E-03	0.189
C16orf72	Chromosome 16 open reading frame 72	0.54	4.3E-03	0.189
DDB2	Damage-specific DNA binding protein 2, 48kda	-0.55	4.3E-03	0.189
HIPK3	Homeodomain interacting protein kinase 3	0.52	4.3E-03	0.189
NPY2R	Neuropeptide Y receptor Y2	-0.70	4.3E-03	0.189
DMN	Synemin, intermediate filament protein	0.60	4.3E-03	0.189
GPT	Glutamic-pyruvate transaminase (alanine aminotransferase)	0.46	4.4E-03	0.190
PEX19	Peroxisomal biogenesis factor 19	-0.57	4.4E-03	0.190
OR2L13	Olfactory receptor, family 2, subfamily L, member 13	-0.62	4.4E-03	0.190
BAIAP3	BAI1-associated protein 3	-0.58	4.4E-03	0.190
PRELP	Proline/arginine-rich end leucine-rich repeat protein	0.59	4.4E-03	0.190
BSG	Basigin (Ok blood group)	0.40	4.4E-03	0.191
PACS1	Phosphofurin acidic cluster sorting protein 1	-0.40	4.5E-03	0.192
ZNF462	Zinc finger protein 462	0.46	4.5E-03	0.192
COL10A1	Collagen, type X, alpha 1	0.85	4.5E-03	0.192
CRH	Corticotropin releasing hormone	-0.95	4.5E-03	0.192
FLCN	Folliculin	0.60	4.5E-03	0.192
C10orf68	Chromosome 10 open reading frame 68	0.59	4.5E-03	0.193
ZADH1	Prostaglandin reductase 2	-0.68	4.6E-03	0.193
MTERFD3	MTERF domain containing 3	-0.43	4.6E-03	0.193
FASTKD3	FAST kinase domains 3	-0.57	4.6E-03	0.193
C1orf128	Chromosome 1 open reading frame 128	-0.67	4.6E-03	0.193
TGFB3	Transforming growth factor, beta 3	0.69	4.6E-03	0.193
KIAA1546	Tet oncogene family member 2	0.60	4.6E-03	0.193
IL12RB1	Interleukin 12 receptor, beta 1	-0.99	4.6E-03	0.193
ZNF490	Zinc finger protein 490	0.51	4.6E-03	0.193
TTC19	Tetratricopeptide repeat domain 19	-0.40	4.6E-03	0.193
ACOT9	Acyl-coa thioesterase 9	-0.56	4.7E-03	0.193
ZNF815	Zinc finger protein 815	-0.56	4.7E-03	0.193
CCR5	Chemokine (C-C motif) receptor 5	-0.79	4.7E-03	0.194
C9orf102	Chromosome 9 open reading frame 102	0.51	4.7E-03	0.195
MARCH_6	Membrane-associated ring finger (C3HC4) 6	0.79	4.7E-03	0.195
RPA2	Replication protein A2, 32kda	-0.57	4.8E-03	0.196
WDR65	WD repeat domain 65	-0.86	4.8E-03	0.196
FXR1	Fragile X mental retardation, autosomal homolog 1	0.52	4.8E-03	0.196
HYAL2	Hyaluronoglucosaminidase 2	0.59	4.8E-03	0.196
NBR1	Neighbor of BRCA1 gene 1	-0.51	4.8E-03	0.196
PLAC9	Placenta-specific 9	0.66	4.9E-03	0.199

Table S3. Genes with differential expression (*P* < 0.01, FDR < 0.4) observed in alcoholic individuals

Gene Symbol	Gene Name	Log FC	P value	FDR
HIST1H4E	Histone cluster 1, h4e	1.70	2.5E-11	0.000
PAPD1	Mitochondrial poly(A) polymerase	1.17	1.1E-07	0.001
TMC3	Transmembrane channel-like 3	1.21	7.2E-07	0.004
FAM123A	Family with sequence similarity 123A	0.92	8.0E-07	0.004
SNORD89	Small nucleolar RNA, C/D box 89	1.30	1.1E-06	0.004
CDR1	Cerebellar degeneration-related protein 1, 34kda	1.36	1.1E-06	0.004
USP6	Ubiquitin specific peptidase 6 (Tre-2 oncogene)	-1.50	2.9E-06	0.008
ERF	Ets2 repressor factor	0.82	8.7E-06	0.018
SNORD42A	Small nucleolar RNA, C/D box 42A	-1.48	1.1E-05	0.018
SCARNA17	Small Cajal body-specific RNA 17	1.08	3.0E-05	0.042
RN7SK	RNA, 7SK small nuclear	1.31	3.6E-05	0.044
LENG8	Leukocyte receptor cluster (LRC) member 8	0.72	6.2E-05	0.066
CCR5	Chemokine (C-C motif) receptor 5	-1.19	7.4E-05	0.070
SNORD116-29	Small nucleolar RNA, C/D box 116-29	-1.82	1.2E-04	0.103
LTK	Leukocyte receptor tyrosine kinase	1.28	1.3E-04	0.104
LRCH4	Leucine-rich repeats and calponin homology (CH) domain containing 4	0.65	1.5E-04	0.112
CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	0.91	1.5E-04	0.112
TRIMP1	Tripartite motif-containing pseudogene 1	-1.39	1.8E-04	0.124
RNY5	RNA, Ro-associated Y5	-1.48	1.9E-04	0.129
SEL1L	Sel-1 suppressor of lin-12-like (C. Elegans)	0.63	2.1E-04	0.138
SNORA47	Small nucleolar RNA, H/ACA box 47	1.48	2.3E-04	0.140
TAOK2	TAO kinase 2	0.68	2.4E-04	0.141
POLR1B	Polymerase (RNA) I polypeptide B, 128kda	-0.60	2.7E-04	0.141
ZGPAT	Zinc finger, CCCH-type with G patch domain	0.51	2.7E-04	0.141
HNRPH1	Heterogeneous nuclear ribonucleoprotein H1	0.72	2.7E-04	0.141
HIVEP3	Human immunodeficiency virus type I enhancer binding protein 3	0.59	3.3E-04	0.163
KCNA2	Potassium voltage-gated channel, shaker-related subfamily, member 2	0.74	3.7E-04	0.171
RANBP3L	RAN binding protein 3-like	-0.79	3.9E-04	0.171
C9orf3	Aminopeptidase O	0.73	4.0E-04	0.171
SEMA7A	Semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	0.73	4.1E-04	0.171
MSH4	Muts homolog 4 (E. Coli)	0.99	4.2E-04	0.171
ABCA2	ATP-binding cassette, sub-family A (ABC1), member 2	0.73	4.2E-04	0.171
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	0.79	4.3E-04	0.171

SPCS3	Signal peptidase complex subunit 3 homolog (S. Cerevisiae)	0.84	4.4E-04	0.171
RAB11FIP4	RAB11 family interacting protein 4 (class II)	0.61	4.6E-04	0.171
FRMD5	FERM domain containing 5	0.78	4.6E-04	0.171
CENTB5	Arfgap with coiled-coil, ankyrin repeat and PH domains 3	0.61	4.7E-04	0.171
CACNB2	Calcium channel, voltage-dependent, beta 2 subunit	0.61	4.8E-04	0.171
MAOA	Monoamine oxidase A	-0.81	4.8E-04	0.171
CNOT6	CCR4-NOT transcription complex subunit 6	0.74	5.1E-04	0.176
C9orf139	Chromosome 9 open reading frame 139	0.89	5.2E-04	0.176
PACS2	Phosphofurin acidic cluster sorting protein 2	0.56	5.2E-04	0.176
RNU5B	U5B small nuclear 1	-1.55	5.4E-04	0.176
C16orf72	Chromosome 16 open reading frame 72	0.66	6.0E-04	0.186
EXOC6B	Exocyst complex component 6B	0.55	6.4E-04	0.190
RBM34	RNA binding motif protein 34	-0.75	6.4E-04	0.190
TNRC6C	Trinucleotide repeat containing 6C	0.69	6.5E-04	0.190
SNORA73A	Small nucleolar RNA, H/ACA box 73A	0.81	6.5E-04	0.190
ZCWPW1	*Zinc finger, CW type with PWWP domain 1*	*0.50*	*8.0E-04*	*0.218*
VPS53	*Vacuolar protein sorting 53 homolog (S. Cerevisiae)*	*0.73*	*8.8E-04*	*0.231*
DDX17	*DEAD (Asp-Glu-Ala-Asp) box polypeptide 17*	*0.49*	*9.1E-04*	*0.232*
NADSYN1	*NAD synthetase 1*	*0.60*	*9.3E-04*	*0.233*
PSMD12	*Proteasome (prosome, macropain) 26S subunit, non-atpase, 12*	*0.86*	*9.6E-04*	*0.237*
C4orf12	*Chromosome 4 open reading frame 12*	*0.62*	*9.6E-04*	*0.237*
CETN2	*Centrin, EF-hand protein, 2*	*-0.57*	*1.0E-03*	*0.237*
ZIM2	*Zinc finger, imprinted 2*	*0.79*	*1.0E-03*	*0.237*
TMEM165	*Transmembrane protein 165*	*0.62*	*1.1E-03*	*0.237*
IRGQ	*Immunity-related gtpase family, Q*	*0.53*	*1.1E-03*	*0.237*
ZDHHC11B	*Zinc finger, DHHC-type containing 11B*	*0.99*	*1.1E-03*	*0.237*
PPP1R16B	*Protein phosphatase 1, regulatory (inhibitor) subunit 16B*	*0.51*	*1.1E-03*	*0.237*
CREB5	*Camp responsive element binding protein 5*	*0.75*	*1.1E-03*	*0.237*
MORC1	*MORC family CW-type zinc finger 1*	*-1.19*	*1.2E-03*	*0.238*
NFKBIZ	*Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta*	*-0.71*	*1.2E-03*	*0.245*
DDX39	*DEAD (Asp-Glu-Ala-Asp) box polypeptide 39*	*0.60*	*1.2E-03*	*0.245*
GPD2	*Glycerol-3-phosphate dehydrogenase 2 (mitochondrial)*	*-0.49*	*1.2E-03*	*0.245*
SNORD21	*Small nucleolar RNA, C/D box 21*	*-0.80*	*1.3E-03*	*0.250*
FKBP7	*FK506-binding protein 7*	*-0.94*	*1.3E-03*	*0.250*
NXPH3	*Neurexophilin 3*	*0.77*	*1.3E-03*	*0.250*
PGRMC2	*Progesterone receptor membrane component 2*	*0.63*	*1.3E-03*	*0.250*
MID1IP1	*MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))*	*0.62*	*1.3E-03*	*0.250*
C1orf84	*Chromosome 1 open reading frame 84*	*0.86*	*1.3E-03*	*0.250*

GNL3L	Guanine nucleotide binding protein-like 3 (nucleolar)-like	-0.55	1.4E-03	0.250
MDM2	Mdm2 p53 binding protein homolog (mouse)	0.51	1.5E-03	0.259
C22orf9	Uncharacterized protein c22orf9	0.55	1.5E-03	0.268
ARHGEF18	Rho/Rac guanine nucleotide exchange factor (GEF) 18	0.41	1.6E-03	0.275
PPCS	Phosphopantothenoylcysteine synthetase	-0.61	1.7E-03	0.279
GPR62	G protein-coupled receptor 62	0.54	1.7E-03	0.281
FAM151A	Family with sequence similarity 151, member A	-0.64	1.7E-03	0.285
MAMDC4	MAM domain containing 4	0.49	1.8E-03	0.285
TCEA1	Transcription elongation factor A (SII), 1	-0.71	1.8E-03	0.285
COL10A1	Collagen, type X, alpha 1	0.94	1.9E-03	0.289
C1QL3	Complement c1q-like protein 3	-1.03	1.9E-03	0.297
TMEM168	Transmembrane protein 168	-0.57	2.0E-03	0.304
MBD3	Methyl-cpg-binding domain protein 3	0.55	2.0E-03	0.304
DKFZP434B0335	Tectonin beta-propeller repeat containing 1	0.48	2.1E-03	0.304
GJC2	Gap junction protein, gamma 2, 47kda	0.67	2.1E-03	0.304
CCDC137	Coiled-coil domain containing 137	0.61	2.1E-03	0.304
GSK3B	Glycogen synthase kinase 3 beta	-0.63	2.1E-03	0.304
C2orf62	Chromosome 2 open reading frame 62	-0.95	2.1E-03	0.304
HISPPD1	Histidine acid phosphatase domain containing 1	-0.50	2.2E-03	0.304
ELP3	Elongation protein 3 homolog (S. Cerevisiae)	0.53	2.2E-03	0.304
AGXT2L1	Alanine-glyoxylate aminotransferase 2-like 1	-0.80	2.2E-03	0.304
ADAMTS18	ADAM metallopeptidase with thrombospondin type 1 motif, 18	1.04	2.2E-03	0.304
CPOX	Coproporphyrinogen oxidase	0.73	2.3E-03	0.308
PWWP2B	PWWP domain containing 2B	0.60	2.3E-03	0.310
RAMP3	Receptor (G protein-coupled) activity modifying protein 3	0.66	2.4E-03	0.310
DDX24	DEAD (Asp-Glu-Ala-Asp) box polypeptide 24	-0.57	2.4E-03	0.310
DNAJA2	Dnaj (Hsp40) homolog, subfamily A, member 2	0.62	2.4E-03	0.315
CLDN11	Claudin 11	0.70	2.4E-03	0.316
CTDSPL2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	0.59	2.5E-03	0.320
ABCG1	ATP-binding cassette, sub-family G (WHITE), member 1	0.50	2.6E-03	0.323
CCDC148	Coiled-coil domain containing 148	-0.55	2.6E-03	0.323
EHBP1	EH domain binding protein 1	-0.51	2.6E-03	0.323
C10orf93	Chromosome 10 open reading frame 93	0.76	2.7E-03	0.323
L3MBTL	L(3)mbt-like (Drosophila)	0.45	2.7E-03	0.323
GNRHR2	Gonadotropin-releasing hormone (type 2) receptor 2	-0.52	2.8E-03	0.323
DOCK5	Dedicator of cytokinesis 5	0.56	2.8E-03	0.323
NTSR2	Neurotensin receptor 2	-0.69	2.8E-03	0.323
CDKL3	Cyclin-dependent kinase-like 3	-0.65	2.8E-03	0.323

WBP11P1	*WW domain binding protein 11 pseudogene 1*	*-0.61*	*2.8E-03*	*0.323*
PRAF2	*PRA1 domain family, member 2*	*-0.48*	*2.8E-03*	*0.323*
SNHG10	*Small nucleolar RNA host gene 10 (non-protein coding)*	*-0.80*	*2.8E-03*	*0.323*
GNA13	*Guanine nucleotide binding protein (G protein), alpha 13*	*-0.54*	*2.8E-03*	*0.323*
RAD21	*RAD21 homolog (S. Pombe)*	*-0.60*	*2.9E-03*	*0.323*
LMTK2	*Lemur tyrosine kinase 2*	*0.52*	*2.9E-03*	*0.323*
HIP1R	*Huntingtin interacting protein 1 related*	*0.53*	*2.9E-03*	*0.325*
TCF6L1	*Transcription factor 6-like 1 (mitochondrial transcription factor 1-like)*	*-1.07*	*3.1E-03*	*0.333*
ZNF497	*Zinc finger protein 497*	*0.45*	*3.1E-03*	*0.333*
RSPO3	*R-spondin 3 homolog (Xenopus laevis)*	*-0.85*	*3.1E-03*	*0.333*
RSRC1	*Arginine/serine-rich coiled-coil 1*	*-0.59*	*3.1E-03*	*0.333*
CDKN1B	*Cyclin-dependent kinase inhibitor 1B (p27, Kip1)*	*0.48*	*3.1E-03*	*0.333*
SNIP	*SRC kinase signaling inhibitor 1*	*0.62*	*3.1E-03*	*0.333*
IL17RD	*Interleukin 17 receptor D*	*-0.44*	*3.1E-03*	*0.333*
HTATSF1	*HIV-1 Tat specific factor 1*	*-0.48*	*3.2E-03*	*0.336*
CCDC91	*Coiled-coil domain containing 91*	*-0.72*	*3.2E-03*	*0.337*
LARP6	*La ribonucleoprotein domain family, member 6*	*0.45*	*3.3E-03*	*0.343*
MUTYH	*Muty homolog (E. Coli)*	*0.64*	*3.4E-03*	*0.346*
FAM131B	*Family with sequence similarity 131, member B*	*0.52*	*3.4E-03*	*0.346*
CTDSP2	*CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2*	*0.44*	*3.4E-03*	*0.346*
PIGG	*Phosphatidylinositol glycan anchor biosynthesis, class G*	*0.45*	*3.4E-03*	*0.346*
TTC7A	*Tetratricopeptide repeat domain 7A*	*0.37*	*3.4E-03*	*0.346*
LPO	*Lactoperoxidase*	*1.24*	*3.5E-03*	*0.347*
RUNX2	*Runt-related transcription factor 2*	*0.68*	*3.5E-03*	*0.347*
IGSF9B	*Immunoglobulin superfamily, member 9B*	*0.76*	*3.5E-03*	*0.347*
ARMC3	*Armadillo repeat containing 3*	*-0.84*	*3.5E-03*	*0.347*
ACTR3B	*ARP3 actin-related protein 3 homolog B (yeast)*	*0.54*	*3.5E-03*	*0.347*
SMARCA2	*SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2*	*-0.58*	*3.6E-03*	*0.349*
SMAD7	*SMAD family member 7*	*0.46*	*3.6E-03*	*0.349*
MYO1B	*Myosin IB*	*-0.61*	*3.6E-03*	*0.349*
DSCAML1	*Down syndrome cell adhesion molecule like 1*	*0.45*	*3.6E-03*	*0.349*
CXCL5	*Chemokine (C-X-C motif) ligand 5*	*-0.83*	*3.7E-03*	*0.351*
TFR2	*Transferrin receptor 2*	*-0.57*	*3.7E-03*	*0.351*
CCDC61	*Coiled-coil domain containing 61*	*0.58*	*3.7E-03*	*0.351*
POLR2A	*Polymerase (RNA) II (DNA directed) polypeptide A, 220kda*	*-0.51*	*3.7E-03*	*0.351*
PRKCA	*Protein kinase C, alpha*	*-0.51*	*3.8E-03*	*0.352*
PLDN	*Pallidin homolog (mouse)*	*-0.68*	*3.8E-03*	*0.352*
PCTK3	*PCTAIRE protein kinase 3*	*0.63*	*3.8E-03*	*0.352*

CYP4Z1	*Cytochrome P450, family 4, subfamily Z, polypeptide 1*	*-1.01*	*3.9E-03*	*0.352*
OSBPL8	*Oxysterol binding protein-like 8*	*-0.51*	*3.9E-03*	*0.352*
AJAP1	*Adherens junctions associated protein 1*	*-0.76*	*4.0E-03*	*0.352*
SHOX2	*Short stature homeobox 2*	*1.23*	*4.0E-03*	*0.352*
NR2E1	*Nuclear receptor subfamily 2, group E, member 1*	*-0.56*	*4.0E-03*	*0.352*
KIAA0329	*Tectonin beta-propeller repeat containing 2*	*0.74*	*4.0E-03*	*0.352*
NEBL	*Nebulette*	*-0.52*	*4.0E-03*	*0.352*
SFRS6	*Splicing factor, arginine/serine-rich 6*	*0.58*	*4.0E-03*	*0.352*
REM1	*RAS (RAD and GEM)-like GTP-binding 1*	*0.79*	*4.0E-03*	*0.352*
TTC21A	*Tetratricopeptide repeat domain 21A*	*0.48*	*4.0E-03*	*0.352*
ZNF248	*Zinc finger protein 248*	*0.48*	*4.0E-03*	*0.352*
ACBD7	*Acyl-Coenzyme A binding domain containing 7*	*-0.68*	*4.2E-03*	*0.352*
STX4	*Syntaxin 4*	*0.45*	*4.2E-03*	*0.352*
CDC40	*Cell division cycle 40 homolog (S. Cerevisiae)*	*-1.02*	*4.2E-03*	*0.352*
C18orf1	*Chromosome 18 open reading frame 1*	*0.45*	*4.2E-03*	*0.352*
PGM1	*Phosphoglucomutase 1*	*-0.40*	*4.2E-03*	*0.352*
DLEU2L	*Deleted in lymphocytic leukemia 2-like*	*-0.99*	*4.3E-03*	*0.353*
MUPCDH	*Mucin-like protocadherin*	*0.65*	*4.3E-03*	*0.353*
GSN	*Gelsolin (amyloidosis, Finnish type)*	*0.48*	*4.3E-03*	*0.353*
PSEN1	*Presenilin 1*	*0.54*	*4.3E-03*	*0.353*
FLJ23556	*Hypothetical protein FLJ23556*	*0.99*	*4.3E-03*	*0.353*
MIF	*Macrophage migration inhibitory factor (glycosylation-inhibiting factor)*	*0.52*	*4.4E-03*	*0.354*
PMS2L11	*Postmeiotic segregation increased 2-like protein 11*	*0.65*	*4.4E-03*	*0.354*
DHX34	*DEAH (Asp-Glu-Ala-His) box polypeptide 34*	*0.46*	*4.5E-03*	*0.354*
SLC1A3	*Solute carrier family 1 (glial high affinity glutamate transporter), member 3*	*-0.70*	*4.5E-03*	*0.354*
QDPR	*Quinoid dihydropteridine reductase*	*0.68*	*4.5E-03*	*0.354*
SLC25A36	*Solute carrier family 25, member 36*	*-0.43*	*4.6E-03*	*0.354*
DEGS2	*Degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)*	*0.53*	*4.6E-03*	*0.354*
PRKRIR	*Protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor)*	*-0.67*	*4.6E-03*	*0.354*
GTF2A1	*General transcription factor IIA, 1, 19/37kda*	*0.48*	*4.6E-03*	*0.354*
SNX27	*Sorting nexin family member 27*	*0.37*	*4.6E-03*	*0.354*
SYT1	*Synaptotagmin I*	*-0.57*	*4.7E-03*	*0.360*
MDM4	*Mdm4 p53 binding protein homolog (mouse)*	*0.54*	*4.7E-03*	*0.360*
SDCCAG10	*Serologically defined colon cancer antigen 10*	*-0.58*	*4.8E-03*	*0.360*
C6orf199	*Chromosome 6 open reading frame 199*	*-0.70*	*4.8E-03*	*0.362*
HNRNPL	*Heterogeneous nuclear ribonucleoprotein L*	*0.48*	*4.8E-03*	*0.362*
PAFAH1B2	*Platelet-activating factor acetylhydrolase, isoform Ib, subunit 2 (30kda)*	*0.51*	*4.9E-03*	*0.362*
HARS2	*Histidyl-trna synthetase 2, mitochondrial (putative)*	*0.72*	*4.9E-03*	*0.362*
BIN1	*Bridging integrator 1*	*0.48*	*4.9E-03*	*0.362*

HSP90AB2P	*Heat shock protein 90kda alpha (cytosolic), class B member 2 (pseudogene)*	*-1.39*	*4.9E-03*	*0.362*
CSNK1G2	*Casein kinase 1, gamma 2*	*0.46*	*5.0E-03*	*0.362*
PCBP4	*Poly(rc) binding protein 4*	*0.47*	*5.0E-03*	*0.362*
NOLA1	*GAR1 ribonucleoprotein homolog (yeast)*	*0.53*	*5.0E-03*	*0.362*
NUDT3	*Nudix (nucleoside diphosphate linked moiety X)-type motif 3*	*0.57*	*5.0E-03*	*0.362*
EAPP	*E2F-associated phosphoprotein*	*-0.66*	*5.0E-03*	*0.362*
CD99L2	*CD99 molecule-like 2*	*0.39*	*5.1E-03*	*0.362*
PPP1R14A	*Protein phosphatase 1 regulatory subunit 14A*	*0.76*	*5.1E-03*	*0.362*
KIAA1659	*KIAA1659 protein*	*0.99*	*5.1E-03*	*0.362*
PLXDC2	*Plexin domain containing 2*	*0.53*	*5.2E-03*	*0.362*
TINP1	*Ribosome biogenesis protein NSA2 homolog*	*-0.79*	*5.2E-03*	*0.362*
RGS12	*Regulator of G-protein signaling 12*	*0.64*	*5.2E-03*	*0.362*
RSL1D1	*Ribosomal L1 domain containing 1*	*-0.57*	*5.2E-03*	*0.362*
RHOT2	*Ras homolog gene family, member T2*	*0.40*	*5.3E-03*	*0.362*
ZNF589	*Zinc finger protein 589*	*0.36*	*5.3E-03*	*0.362*
RNF138P1	*Ring finger protein 138 pseudogene 1*	*0.66*	*5.3E-03*	*0.362*
POLR3G	*Polymerase (RNA) III (DNA directed) polypeptide G (32kd)*	*-0.65*	*5.3E-03*	*0.362*
TMEM135	*Transmembrane protein 135*	*-0.41*	*5.3E-03*	*0.362*
FLNC	*Filamin C, gamma*	*0.41*	*5.4E-03*	*0.362*
HP1BP3	*Heterochromatin protein 1, binding protein 3*	*-0.49*	*5.4E-03*	*0.363*
SH3GLB2	*SH3-domain GRB2-like endophilin B2*	*0.51*	*5.4E-03*	*0.363*
TRIB1	*Tribbles homolog 1 (Drosophila)*	*-0.55*	*5.5E-03*	*0.363*
CCDC60	*Coiled-coil domain containing 60*	*-1.03*	*5.5E-03*	*0.363*
ATP1B2	*Atpase, Na+/K+ transporting, beta 2 polypeptide*	*-0.81*	*5.5E-03*	*0.363*
ADC	*Arginine decarboxylase*	*0.61*	*5.5E-03*	*0.363*
PPIL5	*Peptidylprolyl isomerase (cyclophilin)-like 5*	*-0.99*	*5.6E-03*	*0.363*
DDAH1	*Dimethylarginine dimethylaminohydrolase 1*	*-0.57*	*5.6E-03*	*0.363*
MAP3K5	*Mitogen-activated protein kinase kinase kinase 5*	*-0.46*	*5.6E-03*	*0.364*
FAM3C	*Family with sequence similarity 3, member C*	*0.82*	*5.7E-03*	*0.364*
NUP188	*Nucleoporin 188kda*	*0.45*	*5.7E-03*	*0.364*
KIAA1370	*Kiaa1370*	*0.62*	*5.8E-03*	*0.364*
ATP1A2	*Atpase, Na+/K+ transporting, alpha 2 (+) polypeptide*	*-0.65*	*5.8E-03*	*0.364*
PDE10A	*Phosphodiesterase 10A*	*-0.51*	*5.8E-03*	*0.364*
TPM4	*Tropomyosin 4*	*0.43*	*5.9E-03*	*0.364*
NSFL1C	*NSFL1 (p97) cofactor (p47)*	*0.53*	*5.9E-03*	*0.364*
PAK3	*P21 protein (Cdc42/Rac)-activated kinase 3*	*-0.70*	*5.9E-03*	*0.364*
MORN3	*MORN repeat containing 3*	*-0.48*	*5.9E-03*	*0.364*
CHRNA2	*Cholinergic receptor, nicotinic, alpha 2 (neuronal)*	*0.92*	*5.9E-03*	*0.364*
ACOT9	*Acyl-coa thioesterase 9*	*-0.54*	*5.9E-03*	*0.364*
FLJ10357	*Rho guanine nucleotide exchange factor (GEF) 40*	*-0.48*	*6.0E-03*	*0.364*
NLK	*Nemo-like kinase*	*0.59*	*6.0E-03*	*0.364*
HIST1H2BD	*Histone cluster 1, h2bd*	*0.76*	*6.0E-03*	*0.364*

SNAPC3	*Small nuclear RNA activating complex, polypeptide 3, 50kda*	*0.58*	*6.0E-03*	*0.364*
INHA	*Inhibin, alpha*	*0.60*	*6.1E-03*	*0.364*
ILF2	*Interleukin enhancer binding factor 2, 45kda*	*-0.41*	*6.1E-03*	*0.364*
FLJ25006	*Uncharacterized serine/threonine-protein kinase sgk494*	*-0.47*	*6.3E-03*	*0.372*
BMP2K	*BMP2 inducible kinase*	*0.46*	*6.3E-03*	*0.372*
FLJ42258	*FLJ42258 protein*	*0.44*	*6.4E-03*	*0.374*
PAIP2	*Poly(A) binding protein interacting protein 2*	*0.68*	*6.5E-03*	*0.375*
SPG20	*Spastic paraplegia 20 (Troyer syndrome)*	*-0.73*	*6.5E-03*	*0.375*
KIAA0427	*Kiaa0427*	*0.41*	*6.5E-03*	*0.375*
YRDC	*Yrdc domain containing (E. Coli)*	*0.61*	*6.5E-03*	*0.375*
SIRPB1	*Signal-regulatory protein beta 1*	*-1.12*	*6.6E-03*	*0.375*
FAM20A	*Family with sequence similarity 20, member A*	*0.69*	*6.6E-03*	*0.375*
PSMC1	*Proteasome (prosome, macropain) 26S subunit, atpase, 1*	*-0.75*	*6.6E-03*	*0.375*
C2orf55	*Chromosome 2 open reading frame 55*	*-0.50*	*6.6E-03*	*0.375*
SLC31A2	*Solute carrier family 31 (copper transporters), member 2*	*0.70*	*6.6E-03*	*0.375*
GPLD1	*Glycosylphosphatidylinositol specific phospholipase D1*	*-0.52*	*6.7E-03*	*0.375*
RPL13	*Ribosomal protein L13*	*0.53*	*6.8E-03*	*0.375*
ZNF572	*Zinc finger protein 572*	*-0.99*	*6.8E-03*	*0.375*
NMD3	*NMD3 homolog (S. Cerevisiae)*	*-0.60*	*6.8E-03*	*0.376*
MESP2	*Mesoderm posterior 2 homolog (mouse)*	*-1.01*	*6.9E-03*	*0.376*
C20orf116	*DDRGK domain containing 1*	*0.46*	*6.9E-03*	*0.377*
C11orf37	*Non-protein coding RNA 167*	*0.80*	*6.9E-03*	*0.377*
C20orf112	*Chromosome 20 open reading frame 112*	*0.53*	*7.0E-03*	*0.380*
HDAC2	*Histone deacetylase 2*	*-0.58*	*7.1E-03*	*0.382*
TRIM8	*Tripartite motif-containing 8*	*-0.46*	*7.1E-03*	*0.382*
HEATR1	*HEAT repeat containing 1*	*-0.34*	*7.1E-03*	*0.382*
SCN1B	*Sodium channel, voltage-gated, type I, beta*	*0.81*	*7.1E-03*	*0.382*
DYNLRB2	*Dynein, light chain, roadblock-type 2*	*-0.63*	*7.2E-03*	*0.382*
SLC1A4	*Solute carrier family 1 (glutamate/neutral amino acid transporter), member 4*	*-0.59*	*7.2E-03*	*0.382*
CYBRD1	*Cytochrome b reductase 1*	*-0.48*	*7.2E-03*	*0.382*
TTC25	*Tetratricopeptide repeat domain 25*	*-0.50*	*7.2E-03*	*0.382*
FUT1	*Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)*	*0.69*	*7.3E-03*	*0.382*
POLR2F	*Polymerase (RNA) II (DNA directed) polypeptide F*	*0.55*	*7.4E-03*	*0.382*
NKX6-2	*NK6 homeobox 2*	*0.70*	*7.4E-03*	*0.382*
ACTN4	*Actinin, alpha 4*	*0.53*	*7.4E-03*	*0.382*
PIP4K2A	*Phosphatidylinositol-5-phosphate 4-kinase, type II, alpha*	*0.68*	*7.4E-03*	*0.382*
UBXD2	*UBX domain protein 4*	*-0.74*	*7.5E-03*	*0.382*
CPLX3	*Complexin 3*	*0.66*	*7.5E-03*	*0.382*

PGM2L1	*Phosphoglucomutase 2-like 1*	*-0.55*	*7.5E-03*	*0.382*
GABRA2	*Gamma-aminobutyric acid (GABA) A receptor, alpha 2*	*-0.52*	*7.5E-03*	*0.382*
SNORA2A	*Small nucleolar RNA, H/ACA box 2A*	*-1.14*	*7.5E-03*	*0.382*
RNF166	*Ring finger protein 166*	*0.47*	*7.6E-03*	*0.383*
SEMA4B	*Sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B*	*-0.49*	*7.6E-03*	*0.383*
C10orf68	*Chromosome 10 open reading frame 68*	*-0.55*	*7.7E-03*	*0.383*
GALNT13	*UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (galnac-T13)*	*-0.48*	*7.7E-03*	*0.383*
CTNNAL1	*Catenin (cadherin-associated protein), alpha-like 1*	*-0.59*	*7.7E-03*	*0.383*
C7orf10	*Chromosome 7 open reading frame 10*	*-0.68*	*7.7E-03*	*0.383*
UFM1	*Ubiquitin-fold modifier 1*	*-0.50*	*7.8E-03*	*0.383*
WASF2	*WAS protein family, member 2*	*0.66*	*7.8E-03*	*0.383*
XK	*X-linked Kx blood group (mcleod syndrome)*	*-0.52*	*7.8E-03*	*0.383*
CYorf15B	*Chromosome Y open reading frame 15B*	*-0.41*	*7.8E-03*	*0.383*
LGALS8	*Lectin, galactoside-binding, soluble, 8*	*-0.33*	*7.8E-03*	*0.383*
CNTN2	*Contactin 2 (axonal)*	*0.58*	*7.9E-03*	*0.383*
ZNF536	*Zinc finger protein 536*	*0.46*	*7.9E-03*	*0.383*
MYO9B	*Myosin IXB*	*0.47*	*7.9E-03*	*0.383*
PPP3CB	*Protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform*	*-0.57*	*7.9E-03*	*0.383*
RPL6	*Ribosomal protein L6*	*-0.67*	*7.9E-03*	*0.383*
MOXD1	*Monooxygenase, DBH-like 1*	*-0.59*	*7.9E-03*	*0.383*
ZNF469	*Zinc finger protein 469*	*0.39*	*8.0E-03*	*0.383*
PLSCR4	*Phospholipid scramblase 4*	*-0.51*	*8.1E-03*	*0.386*
DPY19L3	*Dpy-19-like 3 (C. Elegans)*	*-0.42*	*8.1E-03*	*0.386*
LGI3	*Leucine-rich repeat LGI family, member 3*	*0.48*	*8.1E-03*	*0.386*
RNF182	*Ring finger protein 182*	*-0.59*	*8.1E-03*	*0.386*
ZMPSTE24	*Zinc metallopeptidase (STE24 homolog, S. Cerevisiae)*	*-0.52*	*8.1E-03*	*0.386*
CCBL2	*Cysteine conjugate-beta lyase 2*	*-0.44*	*8.2E-03*	*0.386*
RPLP2	*Ribosomal protein, large, P2*	*0.54*	*8.2E-03*	*0.386*
TMTC3	*Transmembrane and tetratricopeptide repeat containing 3*	*-0.46*	*8.3E-03*	*0.386*
IQCK	*IQ motif containing K*	*0.50*	*8.3E-03*	*0.386*
ADAMTS15	*ADAM metallopeptidase with thrombospondin type 1 motif, 15*	*0.59*	*8.3E-03*	*0.386*
C9orf57	*Chromosome 9 open reading frame 57*	*0.59*	*8.3E-03*	*0.386*
HBE1	*Hemoglobin, epsilon 1*	*-0.59*	*8.3E-03*	*0.386*
HDGFRP3	*Hepatoma-derived growth factor-related protein 3*	*-0.74*	*8.3E-03*	*0.386*
SNORD74	*Small nucleolar RNA, C/D box 74*	*0.91*	*8.4E-03*	*0.386*
BMP2KL	*BMP2 inducible kinase-like*	*0.66*	*8.5E-03*	*0.386*
KIAA1430	*Kiaa1430*	*-0.47*	*8.5E-03*	*0.386*

LAMA3	Laminin, alpha 3	-0.50	8.5E-03	0.386
RPPH1	Ribonuclease P RNA component H1	-0.70	8.5E-03	0.386
CD82	CD82 molecule	0.49	8.6E-03	0.386
ZMAT3	Zinc finger, matrin type 3	0.53	8.6E-03	0.386
PGAM4	Phosphoglycerate mutase family member 4	-0.67	8.6E-03	0.386
RRAGB	Ras-related GTP binding B	-0.43	8.6E-03	0.386
KIF2C	Kinesin family member 2C	-0.99	8.6E-03	0.386
FOXK2	Forkhead box K2	0.33	8.7E-03	0.386
HMG2L1	HMG box domain containing 4	-0.56	8.7E-03	0.386
FLJ23356	Protein kinase-like protein sgk196	0.45	8.7E-03	0.386
CLDN20	Claudin 20	0.99	8.7E-03	0.386
WDR20	WD repeat domain 20	0.43	8.7E-03	0.386
SLCO5A1	Solute carrier organic anion transporter family, member 5A1	-1.07	8.8E-03	0.386
WDR82	WD repeat-containing protein 82	-0.32	8.8E-03	0.386
MAP7D2	MAP7 domain containing 2	-0.54	8.8E-03	0.386
FLJ44653	Shadow of prion protein homolog (zebrafish) pseudogene 1	0.52	8.8E-03	0.386
PCDHGB8P	Protocadherin gamma subfamily B, 8 pseudogene	0.99	8.8E-03	0.386
ITSN1	Intersectin 1 (SH3 domain protein)	-0.78	8.8E-03	0.386
COL4A3BP	Collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0.57	8.8E-03	0.386
DNAL1	Dynein, axonemal, light chain 1	-0.43	8.9E-03	0.386
CSN1S1	Casein alpha s1	0.79	8.9E-03	0.386
ARV1	ARV1 homolog (S. Cerevisiae)	-0.46	8.9E-03	0.387
C14orf38	Chromosome 14 open reading frame 38	-0.94	8.9E-03	0.387
ZNF33A	Zinc finger protein 33A	-0.45	9.0E-03	0.387
HNRNPR	Heterogeneous nuclear ribonucleoprotein R	-0.50	9.0E-03	0.387
EXOSC7	Exosome component 7	0.54	9.0E-03	0.387
ZDHHC8	Zinc finger, DHHC-type containing 8	0.37	9.1E-03	0.388
SPG11	Spatacsin	-0.66	9.1E-03	0.388
AEBP2	AE binding protein 2	0.44	9.2E-03	0.392
TOP1	Topoisomerase (DNA) I	-0.60	9.2E-03	0.392
TXLNA	Taxilin alpha	0.39	9.3E-03	0.392
FLJ35776	Hypothetical LOC649446	-0.64	9.3E-03	0.393
GPRC5B	G protein-coupled receptor, family C, group 5, member B	0.49	9.3E-03	0.393
COX4NB	COX4 neighbor	0.79	9.3E-03	0.393
BEX1	Protein BEX1	-0.41	9.4E-03	0.393
TNKS2	Tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	-0.40	9.4E-03	0.393
SURF1	Surfeit 1	-0.60	9.4E-03	0.394
VEGFB	Vascular endothelial growth factor B	-0.52	9.5E-03	0.394
SPOP	Speckle-type POZ protein	-0.41	9.5E-03	0.394
ARFRP1	ADP-ribosylation factor related protein 1	0.51	9.5E-03	0.394
LHX2	LIM homeobox 2	-0.49	9.6E-03	0.394

ZNF692	*Zinc finger protein 692*	*0.56*	*9.6E-03*	*0.394*
CCNYL1	*Cyclin Y-like 1*	*0.44*	*9.6E-03*	*0.394*
POLK	*Polymerase (DNA directed) kappa*	*-0.48*	*9.6E-03*	*0.394*
LENG9	*Leukocyte receptor cluster (LRC) member 9*	*0.45*	*9.6E-03*	*0.394*
C10orf39	*Janus kinase and microtubule interacting protein 3*	*0.54*	*9.6E-03*	*0.394*
RBM42	*RNA binding motif protein 42*	*0.54*	*9.7E-03*	*0.394*
TTC35	*Tetratricopeptide repeat domain 35*	*-0.39*	*9.8E-03*	*0.397*
TCEAL4	*Transcription elongation factor A (SII)-like 4*	*-0.54*	*9.8E-03*	*0.397*
DNAJC12	*Dnaj (Hsp40) homolog, subfamily C, member 12*	*-0.56*	*9.8E-03*	*0.397*
GRIN2B	*Glutamate receptor, ionotropic, N-methyl D-aspartate 2B*	*0.48*	*9.8E-03*	*0.397*
TTC8	*Tetratricopeptide repeat domain 8*	*-0.44*	*9.9E-03*	*0.398*
GJB6	*Gap junction protein, beta 6, 30kda*	*-0.60*	*9.9E-03*	*0.398*
LCTL	*Lactase-like*	*-0.86*	*1.0E-02*	*0.399*

Table S4. Differentially expressed genes (FDR < 0.2) involved in mitochondrial functions, oxidative phosphorylation, and neurodegenerative diseases in chronic cocaine-addicted individuals.

Gene Symbol	**Gene Name**	**Log FC**	***P* value**	**FDR**	**GO term or KEGG pathway***				
					GO: 0005743	**hsa 00190**	**hsa 05016**	**hsa 05012**	**hsa 05010**
ATP5H	ATP synthase subunit d, mitochondrial	-0.45	3.8E-03	0.182	x	x	x	x	x
ATP5O	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-0.61	2.3E-04	0.046	x	x	x	x	x
CAPN2	Calpain 2, (m/II) large subunit	0.42	3.4E-03	0.179					x
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	0.59	6.2E-04	0.081	x				
COX5B	Cytochrome c oxidase subunit Vb	-0.37	3.4E-03	0.179	x	x	x	x	x
DNAJC19	Dnaj (Hsp40) homolog, subfamily C, member 19	-0.74	2.5E-04	0.050	x				
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	0.86	2.8E-05	0.015			x		x
HDAC2	Histone deacetylase 2	-0.75	7.7E-04	0.094			x		
MCCC1	Methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	-1.01	1.4E-06	0.003	x				
MRPL45	Mitochondrial ribosomal protein L45	-0.72	1.7E-03	0.137	x				
MTCH2	Mitochondrial carrier homolog 2 (C. Elegans)	-0.50	1.0E-03	0.106	x				
NDUFA5	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kda	-0.91	3.1E-04	0.054	x	x	x	x	x
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kda	-0.86	1.1E-03	0.106	x	x	x	x	x
NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	-0.73	7.9E-05	0.030	x				
NDUFV3	NADH dehydrogenase (ubiquinone) flavoprotein 3, 10kda	-0.61	3.7E-03	0.181	x	x	x	x	x
POLR2G	Polymerase (RNA) II (DNA directed) polypeptide G	-0.65	9.0E-04	0.101			x		
PPP3CA	Protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform	0.91	1.8E-04	0.042					x
SDHA	Succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	-0.49	9.9E-04	0.103	x	x	x	x	x
SLC25A14	Solute carrier family 25 (mitochondrial carrier, brain), member 14	-0.78	2.0E-04	0.043	x				
SLC25A20	Solute carrier family 25 (carnitine/acylcarnitine translocase), member 20	-0.53	3.5E-03	0.180	x				
SLC25A5	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	-0.69	2.2E-03	0.153	x		x	x	
TAF4B	TAF4b RNA polymerase II, TATA box binding protein (TBP)-associated factor, 105kda	-0.72	2.0E-03	0.146			x		
TIMM23	Translocase of inner mitochondrial membrane 23 homolog (yeast)	-0.65	3.7E-03	0.181	x				
UQCRH	Ubiquinol-cytochrome c reductase hinge protein	-0.74	1.1E-04	0.035	x	x	x	x	x

* GO:0005743, Mitochondrial inner membrane; hsa00190, Oxidative phosphorylation; hsa05016, Huntington's disease; hsa05010, Alzheimer's disease; hsa05012, Parkinson's disease.

Table S5. Expression changes of the genes involved in the mitochrondrial oxidative phosphorylation reaction in chronic cocaine addicts

Gene Symbol	**Gene Name**	**Cocaine**		**Alcohol**	
		logFC	**P value**	**logFC**	**P value**
NDUFAF1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1, mitochondrial	-0.734	0.00008	0.032	0.84481
UQCRH	Cytochrome b-c1 complex subunit 6, mitochondrial	-0.742	0.00011	-0.234	0.17260
ATP5O	ATP synthase subunit O, mitochondrial	-0.613	0.00023	-0.230	0.12739
NDUFA5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	-0.914	0.00031	-0.485	0.03899
SDHA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	-0.486	0.00099	0.102	0.45036
NDUFAB1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, mitochondrial	-0.861	0.00110	-0.432	0.08012
COX5B	Cytochrome c oxidase subunit 5B, mitochondrial	-0.367	0.00343	0.011	0.92324
NDUFV3	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	-0.615	0.00369	-0.108	0.58458
ATP5H	ATP synthase subunit d, mitochondrial	-0.450	0.00381	-0.282	0.05834
NDUFA12L	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2 [	-0.527	0.00748	-0.231	0.21881
NDUFB10	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	-0.427	0.00799	-0.074	0.62841
NDUFS2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	-0.486	0.00875	0.029	0.87019
NDUFA1	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	-0.409	0.00875	-0.021	0.88639
UQCRQ	Cytochrome b-c1 complex subunit 8	-0.527	0.01076	-0.056	0.77296
ATP5I	ATP synthase subunit e, mitochondrial	-0.325	0.01145	-0.155	0.20842
COX6BP1	Cytochrome c oxidase subunit 6B1, pseudogene1	-1.146	0.01203	0.156	0.71863
NDUFS4	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	-0.528	0.01602	0.186	0.37632
UQCRB	Cytochrome b-c1 complex subunit 7	-0.438	0.01746	-0.218	0.21979
COX7A2	Cytochrome c oxidase polypeptide 7A2, mitochondrial	-0.524	0.01947	-0.286	0.18780
COX4I2	Cytochrome c oxidase subunit 4 isoform 2, mitochondrial	-0.859	0.02164	-0.162	0.65141
SDHB	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	-0.415	0.02876	0.069	0.70548
COX6C	Cytochrome c oxidase subunit 6C	-0.379	0.02942	-0.123	0.46575
NDUFB3	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	-0.529	0.03035	-0.156	0.50824

COX7B	Cytochrome c oxidase subunit 7B, mitochondrial	-0.444	0.03676	-0.008	0.96800
NDUFB6	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 6	-0.507	0.03719	0.201	0.39364
NDUFB9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	-0.351	0.03753	-0.007	0.96703
COX7A2L	Cytochrome c oxidase subunit 7A-related protein, mitochondrial	-0.326	0.03817	-0.148	0.33448
COX17	Cytochrome c oxidase copper chaperone	-0.540	0.03996	0.303	0.23756
ATP5E	ATP synthase subunit epsilon, mitochondrial	-0.397	0.04095	-0.423	0.03004
ATP5G1	ATP synthase lipid-binding protein, mitochondrial	-0.497	0.04331	-0.091	0.70086
NDUFB8	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	-0.348	0.04916	0.236	0.17506
NDUFB4	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	-0.334	0.59756	0.135	0.83018
NDUFA4	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	-0.411	0.05376	-0.046	0.82565
ATP5S	ATP synthase subunit s, mitochondrial	-0.086	0.64662	-0.062	0.74082
COX7C	Cytochrome c oxidase subunit 7C, mitochondrial	-0.322	0.05604	-0.109	0.50721
NDUFA8	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	-0.073	0.76353	0.659	0.01035
SDHD	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit, mitochondrial	-0.402	0.08343	-0.499	0.03399
UQCR	Cytochrome b-c1 complex subunit 10	0.133	0.47290	0.343	0.07036
NDUFS7	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	0.108	0.60445	0.368	0.08356
NDUFC2	NADH dehydrogenase [ubiquinone] 1 subunit C2	-0.350	0.09253	0.351	0.09180
NDUFA4L2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2	0.120	0.54278	-0.306	0.12676
COX5A	Cytochrome c oxidase subunit 5A, mitochondrial	-0.552	0.05723	0.410	0.15239
COX4I1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	-0.239	0.07837	0.187	0.16402
NDUFS6	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	0.222	0.13387	0.205	0.16431
COX15	Cytochrome c oxidase assembly protein COX15 homolog	0.092	0.55530	0.217	0.16845
NDUFA11	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	0.053	0.75122	0.230	0.17573
NDUFV1	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	0.053	0.70520	0.189	0.18413
NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	-0.304	0.06326	-0.214	0.18527

ATP5F1	ATP synthase subunit b, mitochondrial	-0.498	0.05545	-0.315	0.21711
COX19	Cytochrome c oxidase assembly protein COX19	0.057	0.69185	0.176	0.22449
COX7A1	Cytochrome c oxidase polypeptide 7A1, mitochondrial	-0.442	0.17380	0.393	0.22510
NDUFA13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	-0.071	0.52582	0.128	0.25357
COX6A2	Cytochrome c oxidase subunit 6A2, mitochondrial	-0.056	0.88862	-0.452	0.25955
COX8A	Cytochrome c oxidase subunit 8A, mitochondrial	-0.014	0.93629	0.202	0.26281
NDUFC1	NADH dehydrogenase [ubiquinone] 1 subunit C1, mitochondrial	-0.421	0.05932	0.236	0.28095
ATP5G2	ATP synthase lipid-binding protein, mitochondrial	-0.024	0.85861	0.141	0.29549
COX6A1	Cytochrome c oxidase subunit 6A1, mitochondrial	-0.174	0.25373	-0.159	0.29606
NDUFA2	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	-0.317	0.07220	0.177	0.30590
NDUFA7	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	0.174	0.47200	0.233	0.33700
NDUFB7	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	0.234	0.12842	0.129	0.39464
COX18	Cytochrome c oxidase assembly protein COX18	-0.197	0.25036	-0.143	0.40109
NDUFA9	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	-0.240	0.16040	0.140	0.40700
NDUFA12	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	-0.310	0.09756	-0.152	0.40792
ATP5G3	ATP synthase lipid-binding protein, mitochondrial	-0.324	0.33079	0.272	0.41279
COX6B1	Cytochrome c oxidase subunit 6B1	-0.181	0.20445	-0.108	0.44441
ATP5J2	ATP synthase subunit f, mitochondrial	-0.219	0.38826	0.185	0.46534
NDUFB5	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial	-0.302	0.29420	-0.200	0.48395
UQCRC1	Cytochrome b-c1 complex subunit 1, mitochondrial	0.075	0.67149	0.118	0.50171
ATP5J	ATP synthase-coupling factor 6, mitochondrial	-0.253	0.22833	-0.119	0.56810
NDUFS8	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	0.185	0.23248	0.086	0.57723
COX11P	Cytochrome c oxidase assembly protein COX11, pseudogene	-0.475	0.23354	0.217	0.58333
NDUFV2	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	-0.293	0.20037	0.118	0.60126
UQCRC2	Cytochrome b-c1 complex subunit 2, mitochondrial	-0.422	0.09911	0.126	0.61598

ATP5D	ATP synthase subunit delta, mitochondrial	-0.059	0.70701	0.073	0.64322
ATP5C1	ATP synthase subunit gamma, mitochondrial	-0.478	0.06127	-0.109	0.65986
NDUFB1	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	-0.411	0.13060	-0.106	0.69090
ATP5A1	ATP synthase subunit alpha, mitochondrial	-0.390	0.13379	0.094	0.71249
ATP5SL	ATP5S-like	-0.150	0.34837	0.054	0.73529
NDUFA3	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 3	0.049	0.77049	0.055	0.74359
SDHC	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial	0.072	0.63033	0.044	0.76889
NDUFA6	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	-0.187	0.31972	0.047	0.80213
NDUFB2	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial	-0.334	0.07081	0.037	0.83874
NDUFS5	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5, mitochondrial	-0.356	0.06243	-0.032	0.86336
NDUFB11	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial	-0.117	0.55453	0.026	0.89525
ATP5B	ATP synthase subunit beta, mitochondrial	-0.400	0.11475	-0.032	0.89828
COX11	Cytochrome c oxidase assembly protein COX11, mitochondrial	0.006	0.97229	0.019	0.91077
NDUFA10	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial	-0.220	0.29296	-0.019	0.92558
ATP5L	ATP synthase subunit g, mitochondrial	0.006	0.96350	0.012	0.93201
NDUFS1	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial	0.103	0.56139	-0.008	0.96187
UQCRFS1	Cytochrome b-c1 complex subunit Rieske, mitochondrial	-0.629	0.09330	0.002	0.99628

Table S6. Differentially expressed genes (FDR < 0.2) involved in negative regulation of gene expression, gene silencing, and covalent chromatin modification in chronic cocaine- and alcohol- addicted individuals

Gene Symbol	**Gene Name**	**Cocaine**			**Alcohol**			**Gene Ontology Term***		
		Log FC	***P* value**	**FDR**	**Log FC**	**P value**	**FDR**	**GO: 0010629**	**GO: 0016458**	**GO 0016569**
MDM4	Mdm4 p53 binding protein homolog (mouse)	1.01	3.0E-06	0.004	*0.54*	*4.7E-03*	*0.360*	x		
LRCH4	Leucine-rich repeats and calponin homology (CH) domain containing 4	0.80	8.8E-06	0.008	0.65	1.5E-04	0.112	x		
ZGPAT	Zinc finger, CCCH-type with G patch domain	0.55	9.2E-05	0.033	0.51	2.7E-04	0.141	x		
PBXIP1	Pre-B-cell leukemia homeobox interacting protein 1	0.91	1.2E-04	0.035	*-0.13*	*5.3E-01*	*0.917*	x		
MTA2	Metastasis associated 1 family, member 2	0.78	1.4E-04	0.038	*0.15*	*4.1E-01*	*0.884*	x		
ARID5B	AT rich interactive domain 5B (MRF1-like)	0.72	4.2E-04	0.067	*0.15*	*4.1E-01*	*0.882*	x		
SUMO1P3	SUMO1 pseudogene 3	-0.84	4.6E-04	0.069	*-0.58*	*1.1E-02*	*0.424*	x		
HDAC2	Histone deacetylase 2	-0.75	7.7E-04	0.094	*-0.58*	*7.1E-03*	*0.382*	x	x	x
SLA2	Src-like-adaptor 2	1.25	9.0E-04	0.101	*0.59*	*9.1E-02*	*0.673*	x		
ZBTB16	Zinc finger and BTB domain containing 16	0.57	1.4E-03	0.121	*0.19*	*2.4E-01*	*0.815*	x		
MDM2	Mdm2 p53 binding protein homolog (mouse)	0.51	1.6E-03	0.132	*0.51*	*1.5E-03*	*0.259*	x		
RNASEN	Ribonuclease type III, nuclear	-0.57	1.7E-03	0.138	*-0.39*	*2.5E-02*	*0.524*	x	x	
LEF1	Lymphoid enhancer-binding factor 1	0.69	1.8E-03	0.139	*0.30*	*1.5E-01*	*0.755*	x		
RNF8	E3 ubiquitin-protein ligase RNF8	-0.43	2.0E-03	0.146	*0.01*	*9.3E-01*	*1.000*			x
L3MBTL	L(3)mbt-like (Drosophila)	0.46	2.3E-03	0.153	*0.45*	*2.7E-03*	*0.323*	x		
ATF7IP	Activating transcription factor 7 interacting protein	0.47	2.3E-03	0.154	*0.23*	*1.1E-01*	*0.702*	x		
SBNO2	Strawberry notch homolog 2 (Drosophila)	0.66	2.7E-03	0.166	*0.38*	*6.4E-02*	*0.616*	x		
BMP4	Bone morphogenetic protein 4	1.22	2.7E-03	0.168	*0.49*	*2.0E-01*	*0.790*	x		
TNRC6C	Trinucleotide repeat containing 6C	0.59	2.8E-03	0.170	0.69	6.5E-04	0.190	x	x	
DNMT3A	DNA (cytosine-5-)-methyltransferase 3 alpha	0.73	2.8E-03	0.171	*0.30*	*1.9E-01*	*0.786*	x	x	x
PHF16	PHD finger protein 16	-0.45	2.9E-03	0.172	*0.00*	*9.7E-01*	*1.000*			x
SCGB1A1	Secretoglobin, family 1A, member 1 (uteroglobin)	0.81	3.2E-03	0.178	*-0.20*	*4.4E-01*	*0.893*	x		
MBD3	Methyl-CpG-binding domain protein 3	0.51	3.6E-03	0.180	*0.55*	*2.0E-03*	*0.304*	x	x	x
EYA1	Eyes absent homolog 1	0.46	3.6E-03	0.180	*-0.08*	*5.8E-01*	*0.925*			x
ACTL6A	Actin-like protein 6A	-0.48	3.9E-03	0.184	*-0.34*	*3.5E-02*	*0.546*			x
TADA1L	Transcriptional adapter 1-like protein	-0.60	4.0E-03	0.184	*0.18*	*3.6E-01*	*0.862*			x
EIF2C1	Eukaryotic translation initiation factor 2C, 1	0.51	4.0E-03	0.184	*0.38*	*2.8E-02*	*0.532*	x	x	

* GO:0010629, negative regulation of gene expression; GO:0016458, gene silencing; GO:0016569, covalent chromatin modification

Table S7. Differentially expressed RNA-binding genes (FDR < 0.2)

Gene Symbol	**Gene Name**	**Cocaine**			**Alcohol**		
		Log FC	***P* value**	**FDR**	**Log FC**	***P* value**	**FDR**
DDX17	Probable ATP-dependent RNA helicase DDX17	1.02	1.4E-08	0.0001	*0.49*	*9.1E-04*	*0.2321*
PAPD1	Mitochondrial poly(A) polymerase	0.95	4.1E-06	0.0045	1.17	1.1E-07	0.0011
MRPS17	28S ribosomal protein S17, mitochondrial	-0.80	8.5E-06	0.0079	*-0.17*	*2.8E-01*	*0.8292*
HNRPH1	Heterogeneous nuclear ribonucleoprotein H1	0.81	6.5E-05	0.0259	0.72	2.7E-04	0.1414
HNRNPU	Heterogeneous nuclear ribonucleoprotein U	0.70	2.9E-04	0.0525	*0.35*	*5.1E-02*	*0.5894*
NUFIP2	Nuclear fragile X mental retardation-interacting protein 2	0.72	8.5E-04	0.0992	*0.18*	*3.7E-01*	*0.8678*
POLR2G	DNA-directed RNA polymerase II subunit RPB7	-0.65	9.0E-04	0.1009	*-0.09*	*6.3E-01*	*0.9293*
SFRS6	Splicing factor, arginine/serine-rich 6	0.67	1.0E-03	0.1036	*0.58*	*4.0E-03*	*0.3518*
TARBP1	Probable methyltransferase TARBP1	-0.70	1.3E-03	0.1152	*-0.10*	*6.0E-01*	*0.9263*
DHX34	Probable ATP-dependent RNA helicase DHX34	0.53	1.4E-03	0.1210	*0.46*	*4.5E-03*	*0.3536*
MSI1	RNA-binding protein Musashi homolog 1	0.60	1.7E-03	0.1366	*0.21*	*2.4E-01*	*0.8157*
RNASEN	Ribonuclease 3	-0.57	1.7E-03	0.1383	*-0.39*	*2.5E-02*	*0.5237*
ZMAT3	Zinc finger matrin-type protein 3	0.62	2.6E-03	0.1633	*0.53*	*8.6E-03*	*0.3855*
TNRC6C	Trinucleotide repeat-containing gene 6C protein	0.59	2.8E-03	0.1699	0.69	6.5E-04	0.1898
LARP4	La ribonucleoprotein domain family, member 4	0.55	3.6E-03	0.1803	*0.29*	*1.1E-01*	*0.6999*
EIF2C1	Protein argonaute-1	0.51	4.0E-03	0.1841	*0.38*	*2.8E-02*	*0.5320*
ANKHD1-EIF4EBP3	ANKHD1-EIF4EBP3 readthrough	0.97	4.2E-03	0.1890	*0.49*	*1.2E-01*	*0.7145*
FXR1	Fragile X mental retardation syndrome-related protein 1	0.52	4.8E-03	0.1957	*0.34*	*5.4E-02*	*0.5984*
CNOT6	CCR4-NOT transcription complex subunit 6	*0.54*	*7.8E-03*	*0.2263*	0.74	5.1E-04	0.1758
RBM34	RNA-binding protein 34	*-0.23*	*2.4E-01*	*0.6598*	-0.75	6.4E-04	0.1898

Table S8. Differentially expressed snoRNA genes (FDR < 0.2) in chronic cocaine and alcohol addicted individuals

Gene Symbol	**Gene Name**	**Cocaine**			**Alcohol**		
		Log FC	***P* value**	**FDR**	**Log FC**	***P* value**	**FDR**
SNORD89	small nucleolar RNA, C/D box 89	1.53	5.6E-08	0.0002	1.30	1.1E-06	0.0036
SNORA73A	small nucleolar RNA, H/ACA box 73A	1.41	2.2E-07	0.0006	0.81	6.5E-04	0.1898
SNORD42A	small nucleolar RNA, C/D box 42A	-1.47	1.2E-05	0.0097	-1.48	1.1E-05	0.0176
SNORA47	small nucleolar RNA, H/ACA box 47	1.82	1.5E-05	0.0101	1.48	2.3E-04	0.1397
SNORA39	small nucleolar RNA, H/ACA box 39	1.67	2.7E-05	0.0153	*0.66*	*6.0E-02*	*0.6092*
SNORA74B	small nucleolar RNA, H/ACA box 74B	1.60	1.2E-04	0.0354	*0.35*	*3.4E-01*	*0.8548*
SNORA62	small nucleolar RNA, H/ACA box 62	1.87	1.3E-04	0.0376	*0.41*	*3.4E-01*	*0.8556*
SNORD76	small nucleolar RNA, C/D box 76	1.21	1.6E-04	0.0421	*0.61*	*3.8E-02*	*0.5556*
SNORD33	small nucleolar RNA, C/D box 33	0.74	1.8E-04	0.0421	*0.24*	*1.8E-01*	*0.7801*
SNORD74	small nucleolar RNA, C/D box 74	1.37	2.1E-04	0.0441	*0.91*	*8.4E-03*	*0.3855*
SNORD116-29	small nucleolar RNA, C/D box 116-29	-1.68	3.0E-04	0.0534	-1.82	1.2E-04	0.1029
SNORD22	small nucleolar RNA, C/D box 22	1.17	6.1E-04	0.0813	*0.28*	*3.7E-01*	*0.8662*
SNORD4A	small nucleolar RNA, C/D box 4A	-1.31	1.6E-03	0.1331	*-0.72*	*6.7E-02*	*0.6239*
SNORD59B	small nucleolar RNA, C/D box 59B	1.51	3.4E-03	0.1790	*1.27*	*1.2E-02*	*0.4309*
SNORD83B	small nucleolar RNA, C/D box 83B	0.88	3.8E-03	0.1818	*-0.18*	*5.3E-01*	*0.9183*

Table S9. Differentially expressed gene (FDR < 0.2) in the extra-cellular matrix part in chronic cocaine addicted individuals

Gene Symbol	**Gene name**	**Log FC**	***P* value**	**FDR**
COL4A1	Collagen, type IV, alpha 1	0.68	3.9E-03	0.184
COL10A1	Collagen, type X, alpha 1	0.85	4.5E-03	0.192
GRIN2B	Glutamate receptor, ionotropic, N-methyl D-aspartate 2B	0.86	2.8E-05	0.015
HSPG2	Heparan sulfate proteoglycan 2	0.67	7.5E-04	0.091
LAMA5	Laminin, alpha 5	0.54	1.7E-03	0.138
MFAP4	Microfibrillar-associated protein 4	0.65	4.3E-03	0.189
TIMP2	Metalloproteinase inhibitor 2	-0.63	2.1E-03	0.147

Table S10. Expression of Brain expressed, X-linked genes

Gene Symbol	Gene Name	Cocaine			Alcohol		
		Log FC	**P value**	**FDR**	**Log FC**	**P value**	**FDR**
BEX1	Brain expressed, X-linked 1	-0.66	1.1E-04	0.035	-0.41	9.4E-03	0.393
BEX2	Brain expressed, X-linked 2	-0.63	4.5E-02	0.385	0.02	9.5E-01	1.000
BEX3 (NGFRAP1)	Brain expressed, X-linked 3	-0.45	7.1E-03	0.220	-0.10	5.3E-01	0.919
BEX4	Brain expressed, X-linked 4	-0.58	2.8E-05	0.015	-0.13	2.8E-01	0.833
BEX5	Brain expressed, X-linked 5	-0.50	6.2E-03	0.213	-0.41	2.2E-02	0.515

Table S11. Expression changes of the genes involved in the long-term potentiation in chronic cocaine addicted individuals

Gene Symbol	**Gene Name**	**Log FC**	***P* value**	**FDR**
GRIN2B	Glutamate [NMDA] receptor subunit epsilon-2	0.860	0.00003	0.015
PPP3CA	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	0.912	0.00018	0.042
CAMK2D	Calcium/calmodulin-dependent protein kinase type II delta chain	-0.723	0.00023	0.047
PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0.747	0.00105	0.106
CALM2	Calmodulin 2	-0.765	0.01247	0.264
CREB1	Cyclic AMP-responsive element-binding protein 1	0.436	0.01257	0.710
ADCY1	Adenylate cyclase type 1	-0.434	0.01789	0.300
PPP1CC	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	0.511	0.02717	0.336
PRKCB1	protein kinase C, beta	0.550	0.02778	0.337
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog	0.412	0.04238	0.378

Table S12. Histone H3K4me3 changes (FDR < 0.2) at the promoters of expressed genes in chronic cocaine addicted individuals.

Gene Symbol	**Gene Name**	**H3K4me3**			**Gene Expression**			
		Log FC	***P* value**	**FDR**	**Log FC**	***P* value**	**FDR**	
NFASC	Neurofascin homolog (chicken)	-0.70	3.0E-05	0.040	0.04	7.5E-01	0.937	
MOG	Myelin oligodendrocyte glycoprotein	-0.75	3.5E-05	0.041	-0.26	6.5E-01	0.895	
CNP	2',3'-cyclic nucleotide 3' phosphodiesterase	-0.54	4.2E-05	0.041	0.45	3.9E-02	0.368	*
BAHCC1	BAH domain and coiled-coil containing 1	0.47	4.2E-05	0.041	0.22	1.5E-01	0.562	
BCL2L11	BCL2-like 11 (apoptosis facilitator)	0.46	8.4E-05	0.054	0.00	9.7E-01	1.000	
MYLK	Myosin light chain kinase	0.92	1.3E-04	0.062	0.25	2.7E-01	0.682	
NUDT5	Nudix (nucleoside diphosphate linked moiety X)-type motif 5	-0.57	1.4E-04	0.062	0.09	6.2E-01	0.878	
CDC123	Cell division cycle 123 homolog (S. Cerevisiae)	-0.57	1.4E-04	0.062	-0.48	1.9E-02	0.305	*
SCD	Stearoyl-coa desaturase (delta-9-desaturase)	-0.46	1.7E-04	0.062	-0.38	7.3E-02	0.450	
LAPTM5	Lysosomal protein transmembrane 5	-0.88	1.8E-04	0.062	-0.37	3.5E-01	0.737	
GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.87	1.8E-04	0.062	-0.45	3.7E-02	0.365	*
MAST3	Microtubule associated serine/threonine kinase 3	-0.61	2.2E-04	0.070	0.12	5.7E-01	0.862	
MAG	Myelin associated glycoprotein	-0.72	2.3E-04	0.071	-0.25	3.0E-01	0.701	
CMTM5	CKLF-like MARVEL transmembrane domain containing 5	-0.83	2.3E-04	0.071	-0.06	7.8E-01	0.944	
FZD8	Frizzled homolog 8 (Drosophila)	0.40	2.6E-04	0.077	0.00	9.9E-01	1.000	
ACP2	Acid phosphatase 2, lysosomal	-0.54	2.9E-04	0.078	-0.55	3.9E-03	0.184	**
PPYR1	Pancreatic polypeptide receptor 1	-0.92	4.4E-04	0.098	0.01	9.7E-01	1.000	
PLP1	Proteolipid protein 1	-0.72	4.6E-04	0.098	-0.29	2.1E-01	0.630	
DDR1	Discoidin domain receptor tyrosine kinase 1	-0.44	4.6E-04	0.098	0.15	8.3E-01	0.965	
SLC30A1	Solute carrier family 30 (zinc transporter), member 1	0.33	4.7E-04	0.098	0.22	3.2E-01	0.721	
KCNJ10	Potassium inwardly-rectifying channel, subfamily J, member 10	-0.62	4.8E-04	0.098	-0.34	1.1E-01	0.505	
ATM	Ataxia telangiectasia mutated	-0.49	4.8E-04	0.098	0.08	6.8E-01	0.908	
NPAT	Nuclear protein, ataxia-telangiectasia locus	-0.49	4.8E-04	0.098	0.33	3.2E-02	0.351	*
RND1	Rho family gtpase 1	-0.58	5.4E-04	0.104	0.34	1.8E-01	0.597	
DNAJB2	Dnaj (Hsp40) homolog, subfamily B, member 2	-0.48	5.6E-04	0.108	0.24	2.0E-01	0.617	
PI4KB	Phosphatidylinositol 4-kinase, catalytic, beta	-0.44	5.9E-04	0.110	-0.05	7.1E-01	0.920	
PSRC1	Proline/serine-rich coiled-coil 1	-0.43	6.1E-04	0.111	-0.16	4.2E-01	0.788	

UQCRC2	Ubiquinol-cytochrome c reductase core protein II	-0.56	6.3E-04	0.112	-0.42	9.9E-02	0.494	
OPCML	Opioid binding protein/cell adhesion molecule-like	-0.71	6.4E-04	0.113	-0.03	9.0E-01	0.988	
STMN4	Stathmin-like 4	-0.76	7.2E-04	0.116	-0.29	1.6E-01	0.571	
SLC6A1	Solute carrier family 6 (neurotransmitter transporter, GABA), member 1	-0.40	7.4E-04	0.117	-0.18	3.8E-01	0.762	
KLF13	Kruppel-like factor 13	0.57	7.6E-04	0.119	0.40	2.9E-03	0.172	**
C5orf4	Chromosome 5 open reading frame 4	-0.73	7.7E-04	0.119	-0.11	5.1E-01	0.837	
FAM18B2	Family with sequence similarity 18, member B2	0.75	7.8E-04	0.119	0.00	1.0E+00	1.000	
MYL6	Myosin, light chain 6, alkali, smooth muscle and non-muscle	-0.64	8.0E-04	0.121	-0.05	7.8E-01	0.945	
RNASE1	Ribonuclease, rnase A family, 1 (pancreatic)	-0.57	8.9E-04	0.127	-0.15	4.6E-01	0.813	
MYO1F	Myosin IF	-1.10	9.4E-04	0.129	-0.01	9.4E-01	1.000	
SOX10	SRY (sex determining region Y)-box 10	-0.54	9.4E-04	0.129	0.13	4.6E-01	0.813	
METTL2B	Methyltransferase like 2B	0.67	9.7E-04	0.129	-0.23	3.1E-01	0.708	
AMMECR1L	AMME chromosomal region gene 1-like	-0.82	1.0E-03	0.131	-0.26	1.1E-01	0.508	
SLCO2B1	Solute carrier organic anion transporter family, member 2B1	-0.77	1.0E-03	0.131	0.01	9.7E-01	1.000	
SH3BGRL2	SH3 domain binding glutamic acid-rich protein like 2	0.48	1.0E-03	0.131	0.33	7.4E-02	0.452	
TRIM2	Tripartite motif-containing 2	-0.62	1.1E-03	0.132	0.01	9.7E-01	1.000	
CALM2	Calmodulin 2 (phosphorylase kinase, delta)	-0.38	1.1E-03	0.133	-0.77	1.2E-02	0.264	*
FADS3	Fatty acid desaturase 3	0.35	1.1E-03	0.137	0.36	9.6E-02	0.489	
DKK2	Dickkopf homolog 2 (Xenopus laevis)	-0.54	1.2E-03	0.139	0.04	9.1E-01	0.995	
HAVCR2	Hepatitis A virus cellular receptor 2	-0.85	1.3E-03	0.151	-0.67	3.4E-02	0.356	*
PRIM2	Primase, DNA, polypeptide 2 (58kda)	-0.59	1.5E-03	0.159	0.17	5.9E-01	0.869	
LARP7	La ribonucleoprotein domain family, member 7	-0.66	1.5E-03	0.163	-0.27	3.2E-01	0.719	
C4orf21	Chromosome 4 open reading frame 21	-0.66	1.5E-03	0.163	-0.18	5.6E-01	0.857	
APOLD1	Apolipoprotein L domain containing 1	0.43	1.6E-03	0.164	0.23	5.2E-01	0.843	
LRFN3	Leucine rich repeat and fibronectin type III domain containing 3	-0.47	1.6E-03	0.164	-0.13	4.2E-01	0.788	
PCDHGA9	Protocadherin gamma subfamily A, 9	-1.13	1.6E-03	0.164	0.31	1.3E-01	0.543	
GPR176	G protein-coupled receptor 176	0.40	1.6E-03	0.164	-0.33	1.6E-01	0.574	
LACE1	Lactation elevated 1	-0.36	1.7E-03	0.164	0.13	5.0E-01	0.833	
CHAD	Chondroadherin	0.53	1.7E-03	0.164	-0.24	2.7E-01	0.682	
TF	Transferrin	-0.45	1.8E-03	0.164	-0.15	5.3E-01	0.846	
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2	-0.43	1.8E-03	0.164	0.07	6.4E-01	0.888	

TXNIP	Thioredoxin interacting protein	-0.57	1.8E-03	0.166	0.26	3.1E-01	0.709	
ADAMTS4	ADAM metallopeptidase with thrombospondin type 1 motif, 4	-0.53	1.9E-03	0.166	0.65	2.9E-03	0.173	**
NDUFS2	NADH dehydrogenase (ubiquinone) Fe-S protein 2, 49kda (NADH-coenzyme Q reductase)	-0.53	1.9E-03	0.166	-0.49	8.7E-03	0.232	*
HSD17B7	Hydroxysteroid (17-beta) dehydrogenase 7	2.47	1.9E-03	0.166	-0.18	5.3E-01	0.846	
ZNF595	Zinc finger protein 595	-0.52	1.9E-03	0.166	0.21	4.0E-01	0.778	
TOMM7	Translocase of outer mitochondrial membrane 7 homolog (yeast)	-0.67	1.9E-03	0.167	-0.24	1.5E-01	0.563	
IRS2	Insulin receptor substrate 2	0.53	1.9E-03	0.167	-0.02	9.5E-01	1.000	
ATG4C	ATG4 autophagy related 4 homolog C (S. Cerevisiae)	-0.60	2.0E-03	0.169	-0.34	1.0E-01	0.495	
ATP2C2	Atpase, Ca++ transporting, type 2C, member 2	0.78	2.0E-03	0.171	0.24	1.4E-01	0.550	
RG9MTD1	RNA (guanine-9-) methyltransferase domain containing 1	-0.66	2.1E-03	0.171	-0.26	2.1E-01	0.626	
GTPBP10	GTP-binding protein 10 (putative)	-0.68	2.1E-03	0.171	-0.24	1.7E-01	0.584	
SKI	V-ski sarcoma viral oncogene homolog (avian)	0.45	2.1E-03	0.171	0.30	5.9E-02	0.421	
NBPF1	Neuroblastoma breakpoint family, member 1	0.62	2.1E-03	0.171	0.64	5.6E-02	0.413	
EIF3E	Eukaryotic translation initiation factor 3, subunit E	-0.60	2.1E-03	0.171	0.10	6.8E-01	0.908	
TCERG1L	Transcription elongation regulator 1-like	0.59	2.1E-03	0.171	-0.18	3.0E-01	0.703	
UQCRB	Ubiquinol-cytochrome c reductase binding protein	-0.66	2.2E-03	0.172	-0.44	1.7E-02	0.298	*
WWC2	WW and C2 domain containing 2	0.38	2.2E-03	0.173	0.21	2.7E-01	0.679	
ZNF496	Zinc finger protein 496	0.39	2.2E-03	0.173	-0.05	6.9E-01	0.910	
ZNF462	Zinc finger protein 462	-0.32	2.2E-03	0.174	0.46	4.5E-03	0.192	**
TFEB	Transcription factor EB	-0.29	2.3E-03	0.175	0.14	4.7E-01	0.816	
PNOC	Prepronociceptin	-0.80	2.4E-03	0.183	-0.54	4.4E-02	0.383	*
SOCS2	Suppressor of cytokine signaling 2	0.35	2.5E-03	0.184	0.00	9.9E-01	1.000	
TUBGCP5	Tubulin, gamma complex associated protein 5	0.43	2.5E-03	0.186	-0.20	2.7E-01	0.682	
SH3TC2	SH3 domain and tetratricopeptide repeats 2	-0.65	2.5E-03	0.186	0.45	5.5E-02	0.411	
SLC1A3	Solute carrier family 1 (glial high affinity glutamate transporter), member 3	-0.54	2.6E-03	0.186	-0.17	4.6E-01	0.816	
CYYR1		0.76	2.6E-03	0.186	0.00	9.9E-01	1.000	
ASS1	Argininosuccinate synthetase 1	0.68	2.6E-03	0.187	-0.07	7.6E-01	0.938	
FBXL2	F-box and leucine-rich repeat protein 2	0.55	2.6E-03	0.188	-0.33	1.5E-01	0.561	
TMEM10	Oligodendrocytic myelin paranodal and inner loop protein	-0.77	2.7E-03	0.188	-0.36	2.5E-01	0.660	

SH3BP5L	SH3-binding domain protein 5-like	-0.58	2.7E-03	0.189	-0.03	8.8E-01	0.982	
MLL5	Myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	-0.38	2.7E-03	0.189	0.18	3.4E-01	0.730	
FGF12	Fibroblast growth factor 12	-0.63	2.8E-03	0.192	-0.12	5.5E-01	0.853	
CSDE1	Cold shock domain containing E1, RNA-binding	-0.50	2.8E-03	0.192	0.12	4.1E-01	0.784	
ZNF770	Zinc finger protein 770	-0.40	2.9E-03	0.192	-0.04	8.2E-01	0.964	
SBDS	Shwachman-Bodian-Diamond syndrome	0.50	2.9E-03	0.193	-0.36	6.5E-02	0.431	
PCDHA2	Protocadherin alpha 2	2.62	2.9E-03	0.193	-0.40	1.4E-01	0.545	
PTN	Pleiotrophin	-0.62	2.9E-03	0.193	0.09	6.3E-01	0.884	
EIF2B5	Eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kda	-0.47	3.0E-03	0.197	0.04	7.9E-01	0.951	
CDKN2AIP	CDKN2A interacting protein	0.35	3.0E-03	0.197	-0.21	2.5E-01	0.660	
CPEB4	Cytoplasmic polyadenylation element binding protein 4	-0.49	3.0E-03	0.197	0.37	2.0E-01	0.623	
CHRM1	Cholinergic receptor, muscarinic 1	-0.67	3.0E-03	0.197	-0.10	6.2E-01	0.878	
APOD	Apolipoprotein D	-0.82	3.1E-03	0.197	0.32	1.4E-01	0.549	
TLN1	Talin 1	-0.39	3.1E-03	0.197	0.07	6.4E-01	0.890	
CREB3	Camp responsive element binding protein 3	-0.39	3.1E-03	0.197	0.15	2.4E-01	0.654	
KCNN3	Potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	-0.33	3.1E-03	0.198	0.18	4.3E-01	0.792	
CTF1	Cardiotrophin 1	1.11	3.2E-03	0.199	0.10	5.3E-01	0.844	
SERF2	Small EDRK-rich factor 2	-0.35	3.2E-03	0.199	0.26	5.5E-02	0.411	
CXCL5	Chemokine (C-X-C motif) ligand 5	0.69	3.2E-03	0.199	-0.25	3.5E-01	0.743	
SPOCK3	Sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 3	-0.37	3.2E-03	0.199	-0.46	3.1E-02	0.349	*
RILPL2	Rab interacting lysosomal protein-like 2	0.49	3.2E-03	0.199	0.24	1.3E-01	0.543	

* Gene expression $P < 0.05$

** Gene expression FDR < 0.2

Table S13. Histone H3K4me3 changes ($P < 0.005$) at the promoters of expressed genes in chronic alcoholic individuals.

Gene Symbol	**Gene Name**	**H3K4me3**			**Gene Expression**			
		Log FC	**P value**	**FDR**	**Log FC**	**P value**	**FDR**	
NSUN6	NOL1/NOP2/Sun domain family, member 6	-0.74	5.9E-05	0.325	-0.20	2.0E-01	0.792	
ZNF675	Zinc finger protein 675	0.69	7.2E-05	0.325	0.08	6.4E-01	0.933	
GPD1	Glycerol-3-phosphate dehydrogenase 1 (soluble)	-0.94	7.6E-05	0.325	-0.06	7.7E-01	0.968	
ZNF740	Zinc finger protein 740	-0.35	2.3E-04	0.412	0.17	3.3E-01	0.855	
CSAD	Cysteine sulfinic acid decarboxylase	-0.35	2.3E-04	0.412	-0.02	8.8E-01	0.996	
NACA	Nascent polypeptide-associated complex alpha subunit	-0.79	2.6E-04	0.412	-0.11	5.4E-01	0.920	
PSCD4	Cytohesin 4	-0.94	3.2E-04	0.444	-0.15	4.3E-01	0.888	
D4S234E	DNA segment on chromosome 4 (unique) 234 expressed sequence	0.38	4.8E-04	0.525	0.10	6.9E-01	0.947	
CHD8	Chromodomain helicase DNA binding protein 8	-0.53	5.4E-04	0.531	-0.28	2.0E-01	0.792	
MED19	Mediator complex subunit 19	-0.52	5.6E-04	0.531	0.07	7.3E-01	0.959	
TXNDC14	Thioredoxin-related transmembrane protein 2	-0.52	5.6E-04	0.531	0.00	1.0E+00	1.000	
AIFM3	Apoptosis-inducing factor, mitochondrion-associated, 3	0.76	5.8E-04	0.534	-0.08	6.3E-01	0.930	
SQRDL	Sulfide quinone reductase-like (yeast)	0.72	7.0E-04	0.589	0.00	9.9E-01	1.000	
BAT2	HLA-B associated transcript 2	-0.55	8.6E-04	0.663	0.21	3.2E-01	0.855	
GPR78	G protein-coupled receptor 78	0.81	8.7E-04	0.663	0.45	2.1E-01	0.800	
C15orf23	Chromosome 15 open reading frame 23	-0.41	1.1E-03	0.663	-0.08	6.8E-01	0.943	
EXOSC10	Exosome component 10	0.45	1.2E-03	0.663	0.11	5.1E-01	0.912	
PODXL2	Podocalyxin-like 2	-0.29	1.4E-03	0.663	0.10	6.5E-01	0.935	
FAT	FAT tumor suppressor homolog 1 (Drosophila)	0.30	1.6E-03	0.663	0.00	1.0E+00	1.000	
METTL2B	Methyltransferase like 2B	0.63	1.7E-03	0.663	-0.31	1.7E-01	0.774	
AQP11	Aquaporin 11	0.34	1.8E-03	0.663	0.33	3.8E-02	0.558	*
EIF1AD	Eukaryotic translation initiation factor 1A domain containing	-0.32	2.0E-03	0.663	0.13	5.0E-01	0.912	
BANF1	Barrier to autointegration factor 1	-0.32	2.0E-03	0.663	-0.13	6.0E-01	0.927	
MSC	Musculin (activated B-cell factor-1)	0.67	2.1E-03	0.663	0.14	4.3E-01	0.889	
C1orf84	Chromosome 1 open reading frame 84	-0.37	2.2E-03	0.663	0.86	1.3E-03	0.250	*
MED8	Mediator complex subunit 8	-0.37	2.2E-03	0.663	-0.07	7.2E-01	0.955	
SMPD3	Sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)	0.32	2.4E-03	0.663	-0.08	7.6E-01	0.964	
CARS2	Cysteinyl-trna synthetase 2, mitochondrial (putative)	-0.56	2.4E-03	0.663	-0.10	6.1E-01	0.928	
IFI35	Interferon-induced protein 35	-1.04	2.4E-03	0.663	-0.03	8.8E-01	0.994	
APLN	Apelin	0.71	2.5E-03	0.663	-0.20	2.9E-01	0.838	

PRPF6	PRP6 pre-mrna processing factor 6 homolog (S. Cerevisiae)	-0.45	2.5E-03	0.663	-0.03	7.8E-01	0.970	
KLHL7	Kelch-like 7 (Drosophila)	0.40	2.6E-03	0.663	-0.02	9.2E-01	1.000	
SLITRK2	SLIT and NTRK-like family, member 2	0.52	2.6E-03	0.663	0.09	5.4E-01	0.920	
CCDC66	Coiled-coil domain containing 66	0.53	2.6E-03	0.663	-0.39	1.1E-01	0.700	
MYO1F	Myosin IF	-0.99	2.6E-03	0.663	-0.05	7.8E-01	0.970	
CXCL5	Chemokine (C-X-C motif) ligand 5	0.70	2.8E-03	0.663	-0.83	3.7E-03	0.351	*
C19orf47	Chromosome 19 open reading frame 47	-0.43	2.8E-03	0.663	0.18	2.8E-01	0.830	
PLD3	Phospholipase D family, member 3	-0.43	2.8E-03	0.663	0.09	7.4E-01	0.959	
PPP1R3F	Protein phosphatase 1, regulatory (inhibitor) subunit 3F	-0.41	2.8E-03	0.663	0.14	4.3E-01	0.891	
C12orf41	Chromosome 12 open reading frame 41	-0.43	3.0E-03	0.663	-0.04	8.4E-01	0.988	
ZNF385B	Zinc finger protein 385B	0.59	3.1E-03	0.663	0.22	2.7E-01	0.828	
TMEM65	Transmembrane protein 65	0.28	3.1E-03	0.663	-0.07	6.4E-01	0.931	
SCRN3	Secernin 3	-0.41	3.2E-03	0.663	-0.39	1.3E-02	0.449	*
CIR	Potassium inwardly-rectifying channel, subfamily J, member 5	-0.41	3.2E-03	0.663	-0.52	2.2E-02	0.515	*
POP5	Processing of precursor 5, ribonuclease P/MRP subunit (S. Cerevisiae)	0.48	3.2E-03	0.663	-0.02	8.8E-01	0.994	
PON3	Paraoxonase 3	0.65	3.2E-03	0.663	-0.68	3.8E-02	0.559	*
FGD1	FYVE, rhogef and PH domain containing 1	0.45	3.3E-03	0.663	-0.05	7.9E-01	0.974	
SPPL2A	Signal peptide peptidase-like 2A	-0.61	3.3E-03	0.663	-0.27	1.1E-01	0.693	
ABHD4	Abhydrolase domain containing 4	-0.43	3.4E-03	0.663	-0.10	5.1E-01	0.913	
C18orf32	Chromosome 18 open reading frame 32	-0.41	3.4E-03	0.663	-0.24	2.1E-01	0.797	
PGM3	Phosphoglucomutase 3	0.35	3.4E-03	0.663	-0.21	1.6E-01	0.767	
RWDD2A	RWD domain containing 2A	0.35	3.4E-03	0.663	-0.04	8.3E-01	0.986	
PGAP1	Post-GPI attachment to proteins 1	-0.40	3.4E-03	0.663	-0.02	9.3E-01	1.000	
ZNF643	Zinc finger protein 643	-0.43	3.4E-03	0.663	0.02	9.2E-01	1.000	
COPB2	Coatomer protein complex, subunit beta 2 (beta prime)	0.54	3.4E-03	0.663	-0.14	3.4E-01	0.857	
PRKCH	Protein kinase C, eta	0.48	3.5E-03	0.663	0.10	6.2E-01	0.928	
TSN	Translin	-0.45	3.5E-03	0.663	-0.27	9.4E-02	0.677	
ZSCAN16	Zinc finger and SCAN domain containing 16	-0.71	3.6E-03	0.663	0.21	1.5E-01	0.754	
FAM129B	Family with sequence similarity 129, member B	-2.30	3.7E-03	0.663	-0.02	9.2E-01	1.000	
SLC35E1	Solute carrier family 35, member E1	-0.28	3.7E-03	0.663	-0.08	5.3E-01	0.917	
PPP1R11	Protein phosphatase 1, regulatory (inhibitor) subunit 11	-0.51	3.7E-03	0.663	-0.10	8.1E-01	0.981	
C12orf39	Chromosome 12 open reading frame 39	0.50	3.8E-03	0.663	-0.40	1.9E-01	0.788	
CDKN2AIP	CDKN2A interacting protein	0.34	3.8E-03	0.663	-0.25	1.8E-01	0.781	
PI4KB	Phosphatidylinositol 4-kinase, catalytic, beta	-0.36	3.8E-03	0.663	-0.26	4.7E-02	0.581	*
ORC2L	Origin recognition complex, subunit 2-like (yeast)	0.50	3.9E-03	0.663	0.18	2.3E-01	0.802	
PHF21A	PHD finger protein 21A	-0.35	3.9E-03	0.663	-0.01	9.4E-01	1.000	

GNL3	Guanine nucleotide binding protein-like 3 (nucleolar)	-0.49	4.0E-03	0.663	-0.48	1.4E-02	0.452	*
PBRM1	Polybromo 1	-0.49	4.0E-03	0.663	-0.01	9.4E-01	1.000	
C14orf1	Chromosome 14 open reading frame 1	0.62	4.0E-03	0.663	-0.09	5.8E-01	0.925	
TTLL5	Tubulin tyrosine ligase-like family, member 5	0.62	4.0E-03	0.663	-0.07	6.7E-01	0.941	
LRRC20	Leucine rich repeat containing 20	0.48	4.0E-03	0.663	-0.02	9.2E-01	1.000	
SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	0.33	4.0E-03	0.663	-0.28	1.6E-01	0.761	
MTERFD3	MTERF domain containing 3	0.76	4.1E-03	0.663	-0.29	4.6E-02	0.580	*
MDN1	Midasin	-0.37	4.2E-03	0.668	-0.21	3.0E-01	0.843	
KLHL2	Kelch-like 2, Mayven (Drosophila)	-0.25	4.4E-03	0.668	0.21	4.4E-01	0.892	
ANKRD19	Ankyrin repeat domain 19 pseudogene	0.47	4.4E-03	0.668	0.19	4.5E-01	0.899	
PITPNA	Phosphatidylinositol transfer protein, alpha	-0.40	4.4E-03	0.668	0.20	3.5E-01	0.859	
WDFY2	WD repeat and FYVE domain containing 2	0.31	4.5E-03	0.668	0.20	1.9E-01	0.789	
GPM6A	Glycoprotein M6A	-0.48	4.5E-03	0.668	-0.14	4.1E-01	0.883	
C10orf4	Chromosome 10 open reading frame 4	-0.50	4.5E-03	0.668	-0.08	7.3E-01	0.958	
TMLHE	Trimethyllysine hydroxylase, epsilon	0.63	4.7E-03	0.678	-0.03	8.8E-01	0.995	
JUB	Jub, ajuba homolog (Xenopus laevis)	0.40	4.9E-03	0.693	-0.44	9.9E-02	0.682	

* Gene expression $P < 0.05$

Table S14. Genes with up- or down-regulation of both mRNA expression and histone H3K4me3 modification (uncorrected $P < 0.05$) in chronic cocaine addicted individuals

Gene Symbol	**Gene Name**	**Gene Expression**		**H3K4me3**	
		Log FC	***P* Value**	**Log FC**	***P* Value**
IGSF9B	Protein turtle homolog B	1.055	1.29E-04	0.310	3.65E-02
TRPV4	Transient receptor potential cation channel subfamily V member 4	0.948	3.28E-02	0.915	3.35E-02
SYPL2	Synaptophysin-like protein 2	0.897	5.78E-03	0.377	2.39E-02
IGF1R	Insulin-like growth factor 1 receptor	0.800	7.91E-06	0.318	1.85E-02
FAM20A	Protein FAM20A	0.676	7.78E-03	0.329	4.03E-02
MSI1	RNA-binding protein Musashi homolog 1	0.596	1.67E-03	0.262	4.61E-02
MICALL2	MICAL-like protein 2	0.550	8.78E-04	0.245	4.79E-02
MTERFD2	MTERF domain containing 2	0.536	1.05E-02	0.300	2.53E-02
SYTL4	Synaptotagmin-like protein 4	0.509	4.30E-02	0.715	3.43E-02
HELZ	Probable helicase with zinc finger domain	0.508	3.88E-03	0.339	5.39E-03
PGF	Placenta growth factor	0.476	4.20E-02	0.350	4.99E-02
SVIL	Supervillin	0.472	1.65E-02	0.271	8.87E-03
ATF7IP	Activating transcription factor 7-interacting protein 1	0.468	2.34E-03	0.787	2.90E-02
EYA1	Eyes absent homolog 1	0.456	3.61E-03	0.745	2.23E-02
ANXA3	Annexin A3	0.450	4.47E-02	0.580	2.12E-02
DDR2	Discoidin domain-containing receptor 2	0.448	3.43E-02	1.413	3.08E-02
COL6A2	Collagen alpha-2(VI) chain	0.428	4.58E-02	0.566	5.58E-03
TOP3B	DNA topoisomerase 3-beta-1	0.419	1.56E-02	0.417	1.96E-02
COL4A3	Collagen alpha-3(IV) chain	0.415	1.95E-02	0.250	3.36E-02
PPAN-P2RY11	PPAN-P2RY11 readthrough	0.397	2.28E-02	0.307	4.40E-02
KLF13	Krueppel-like factor 13	0.395	2.87E-03	0.571	7.62E-04
INSR	Insulin receptor	0.394	2.69E-02	0.251	1.65E-02
EP400	E1A-binding protein p400	0.391	1.12E-02	0.263	4.40E-02
SLITRK2	SLIT and NTRK-like protein 2	0.385	1.32E-02	0.331	4.41E-02
METRNL	Meteorin-like protein	0.380	4.53E-02	0.413	1.49E-02
C17orf76	Chromosome 17 open reading frame 76	0.365	2.18E-02	0.362	1.60E-02
PPAN	Suppressor of SWI4 1 homolog	0.354	2.43E-02	0.307	4.40E-02
RREB1	Ras-responsive element-binding protein 1	0.345	8.13E-03	0.293	1.72E-02
FOXO1	Forkhead box protein O1	0.340	4.89E-02	0.339	6.95E-03
TTC7A	Tetratricopeptide repeat protein 7A	0.328	7.93E-03	0.333	1.63E-02
CDC42EP3	Cdc42 effector protein 3	0.299	4.18E-02	0.289	1.86E-02
CALM2	Calmodulin 2	-0.765	1.25E-02	-0.381	1.09E-03
PRDM8	PR domain zinc finger protein 8	-0.675	2.65E-02	-0.333	3.19E-02

HAVCR2	Hepatitis A virus cellular receptor 2	-0.669	3.38E-02	-0.852	1.32E-03
CYB5B	Cytochrome b5 type B	-0.623	9.18E-03	-0.472	1.86E-02
HADHB	Trifunctional enzyme subunit beta, mitochondrial	-0.588	5.29E-03	-0.308	1.63E-02
ACP2	Lysosomal acid phosphatase	-0.552	3.89E-03	-0.543	2.89E-04
MRPS18C	Mitochondrial ribosomal protein S18C	-0.549	2.03E-02	-0.389	3.65E-02
PNOC	Nociceptin	-0.538	4.43E-02	-0.802	2.45E-03
EXTL2	Exostosin-like 2	-0.535	3.55E-03	-0.353	6.71E-03
RNF181	E3 ubiquitin-protein ligase RNF181	-0.529	2.36E-02	-0.311	4.59E-02
NDUFA12L	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2	-0.527	7.48E-03	-0.372	4.73E-02
SLC6A15	Orphan sodium- and chloride-dependent neurotransmitter transporter NTT73	-0.511	1.68E-02	-0.329	1.62E-02
KIAA0528	Uncharacterized protein KIAA0528	-0.510	5.95E-03	-0.263	3.54E-02
MRPS33	28S ribosomal protein S33, mitochondrial	-0.491	1.27E-02	-0.496	1.15E-02
TRO	Trophinin	-0.488	5.91E-04	-0.749	8.55E-03
NDUFS2	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	-0.486	8.75E-03	-0.531	1.85E-03
CDC123	Cell division cycle protein 123 homolog	-0.476	1.89E-02	-0.574	1.41E-04
ISCU	Iron-sulfur cluster assembly enzyme ISCU, mitochondrial	-0.473	2.85E-02	-0.324	3.80E-03
MED8	Mediator of RNA polymerase II transcription subunit 8	-0.460	2.21E-02	-0.283	1.52E-02
SPOCK3	Testican-3	-0.459	3.15E-02	-0.369	3.21E-03
GPD1	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic	-0.447	3.71E-02	-0.874	1.80E-04
UQCRB	Cytochrome b-c1 complex subunit 7	-0.438	1.75E-02	-0.665	2.16E-03
MRPL24	39S ribosomal protein L24, mitochondrial	-0.436	5.68E-03	-0.324	4.68E-02
C1orf19	chromosome 1 open reading frame 19	-0.414	1.25E-02	-0.256	4.65E-02
PIGS	GPI transamidase component PIG-S	-0.409	1.49E-02	-0.315	2.05E-02
MRPL2	39S ribosomal protein L2, mitochondrial	-0.397	1.81E-02	-0.333	8.17E-03
ZWILCH	Protein zwilch homolog	-0.396	1.05E-02	-0.460	1.44E-02
CCDC49	Coiled-coil domain containing 49	-0.395	3.86E-02	-0.489	1.81E-02
HEATR1	HEAT repeat-containing protein 1	-0.393	2.08E-03	-0.564	5.89E-03
FDPS	Farnesyl pyrophosphate synthetase	-0.378	3.23E-02	-0.337	3.38E-02
MBD6	Methyl-cpg-binding domain protein 6	-0.372	1.35E-02	-0.347	9.36E-03
TOMM40L	Mitochondrial import receptor subunit TOM40B	-0.370	1.48E-02	-0.505	2.43E-02

COX7A2L	Cytochrome c oxidase subunit 7A-related protein, mitochondrial	-0.326	3.82E-02	-0.346	2.00E-02
ZNF561	Zinc finger protein 561	-0.319	2.99E-02	-0.297	2.97E-02
ZFYVE20	Rabenosyn-5	-0.315	2.48E-02	-0.562	1.02E-02
PQBP1	Polyglutamine-binding protein 1	-0.282	4.57E-02	-0.556	4.49E-03

Table S15. Genes with up- or down-regulation of both mRNA expression and histone H3K4me3 modification (uncorrected *P* < 0.05) in chronic alcoholic individuals

Gene Symbol	**Gene Name**	**Gene Expression**		**H3K4me3**	
		Log FC	***P* Value**	**Log FC**	***P* Value**
REM1	GTP-binding protein REM 1	0.792	4.02E-03	0.912	1.79E-02
PCDHA7	Protocadherin alpha-7	0.701	3.82E-02	0.658	2.95E-02
ALG13	UDP-N-acetylglucosamine transferase subunit ALG13 homolog	0.648	1.83E-02	0.701	2.35E-02
TTC21A	Tetratricopeptide repeat protein 21A	0.478	4.04E-03	0.191	2.38E-02
TCERG1L	Transcription elongation regulator 1-like protein	0.440	1.43E-02	0.438	1.90E-02
FAM105B	Family with sequence similarity 105, member B	0.378	4.17E-02	0.213	3.86E-02
CHMP4B	Charged multivesicular body protein 4b	0.370	2.12E-02	0.368	7.00E-03
PSMG3	Proteasome (prosome, macropain) assembly chaperone 3	0.366	3.40E-02	0.405	9.08E-03
SNAPC4	Snrna-activating protein complex subunit 4	0.350	3.12E-02	0.377	1.27E-02
AQP11	Aquaporin-11	0.335	3.81E-02	0.336	1.83E-03
SPATA5L1	Spermatogenesis-associated protein 5-like protein 1	0.333	4.62E-02	0.242	1.20E-02
SEC14L1	Sec14l1	0.327	3.41E-02	0.276	1.83E-02
FMN2	Formin-2	0.327	1.81E-02	0.223	3.75E-02
ABL1	Proto-oncogene tyrosine-protein kinase ABL1	0.261	3.67E-02	0.317	3.65E-02
CDC40	Pre-mrna-processing factor 17	-1.020	4.16E-03	-0.234	2.90E-02
DKK2	Dickkopf-related protein 2	-0.849	3.39E-02	-0.333	3.43E-02
ITSN2	Intersectin-2	-0.677	1.75E-02	-0.266	4.73E-02
CDKL3	Cyclin-dependent kinase-like 3	-0.648	2.78E-03	-0.609	4.19E-02
NMD3	60S ribosomal export protein NMD3	-0.596	6.84E-03	-0.285	3.15E-02
SFPQ	Splicing factor, proline- and glutamine-rich	-0.524	1.85E-02	-0.275	1.56E-02
CIR	Potassium inwardly-rectifying channel, subfamily J, member 5	-0.517	2.18E-02	-0.407	3.20E-03
UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	-0.484	2.43E-02	-0.422	1.97E-02
GNL3	Guanine nucleotide-binding protein-like 3	-0.476	1.37E-02	-0.485	3.95E-03
SLC25A14	Brain mitochondrial carrier protein 1	-0.472	1.61E-02	-0.485	2.21E-02
EBAG9	Receptor-binding cancer antigen expressed on siso cells	-0.455	1.91E-02	-0.269	1.08E-02
CETN3	Centrin, EF-hand protein, 3	-0.444	3.53E-02	-0.405	4.11E-02
TAF10	Transcription initiation factor TFIID subunit 10	-0.419	4.47E-02	-0.301	4.01E-02

MRPS33	28S ribosomal protein S33, mitochondrial	-0.401	3.87E-02	-0.412	3.30E-02
SCRN3	Secernin 3	-0.391	1.34E-02	-0.407	3.20E-03
GTPBP10	GTP-binding protein 10	-0.386	2.96E-02	-0.528	1.38E-02
ZNF10	Zinc finger protein 10	-0.352	2.80E-02	-0.327	1.60E-02
USP37	Ubiquitin carboxyl-terminal hydrolase 37	-0.326	3.90E-02	-0.332	1.99E-02
C9orf119	chromosome 9 open reading frame 119	-0.323	4.09E-02	-0.373	3.02E-02
MED7	Mediator complex subunit 7	-0.320	3.08E-02	-0.328	4.75E-02
PI4KB	Phosphatidylinositol 4-kinase beta	-0.256	4.71E-02	-0.357	3.85E-03

Supplementary Materials and Methods:

Subjects:

Postmortem brain tissue was provided by the University of Miami Brain Bank. Subjects include nine chronic cocaine addicts and eight alcoholics. Specimens were obtained during routine autopsy from chronic cocaine and alcohol abusers and age-matched drug- and alcohol-free control subjects (Table S1) . Medicolegal investigations of the cause and manner of deaths were conducted by forensic pathologists (1, 2). The circumstances of death and toxicology data were reviewed carefully before classifying a cocaine intoxication case. The cocaine intoxication cases were evaluated for common drugs of abuse and alcohol and positive urine screens were confirmed by quantitative analysis of cocaine and benzoylecgonine in blood and brain. All subjects in the cocaine or alcohol groups met DSM-IV criteria for either abuse or dependence. Retrospective review demonstrated a regular pattern of current cocaine or alcohol use, including binge and/or daily use for years prior to death. None of the case histories revealed confirmation of neuropsychiatric disorders from all available sources of information, including medical examiner reports, next-of-kin informants, and medical and/or legal records. Drug-free age-matched nine control subjects were selected from accidental or cardiac sudden deaths with negative urine screens for all common drugs and there was no reported history of licit or illicit drug use prior to death. All subjects died suddenly without a prolonged agonal state. Brain pH measures were done as quality control for each case with values > 6.0. Due to the availability of high-quality RNA and immuno-precipitation enriched chromatin DNA, RNA-seq analysis included eight cocaine, eight alcoholic, and eight control individuals, and ChIP-seq analysis included eight cocaine, eight alcoholic, and nine controls. The research protocols for this study were approved by the University of Miami.

Construction of double-stranded cDNA library:

100 mg tissue of postmortem brain hippocampus (dentate gyrus and CA1 to CA4) was used for total RNA extraction. Tissue samples were submerged in Guanidinium thiocyanate and phenol-based RNA extraction solution STAT-60 (Friendswood, TX) and homogenized using a glass-Teflon homogenizer. Following mixing with chloroform and centrifugation, the aqueous phase of the solution was collected and isopropanol was added. RNA was purified onRNeasy spin columns (Qiagen, Valencia, CA). To eliminate residual genomic DNA contamination, RNA samples were incubated with DNase I (Qiagen) on column at room temperature for 15 min and washed several times before collection in elution buffer.

To isolate mRNA, 35 μg of total RNA was heated at 65 C for 2 minu, and then mixed with 0.5 mg of Dynabeads oligo $(dT)_{25}$ magnetic beads (Invitrogen) in the binding buffer (20 mM Tris-HCl, pH 7.5, 1.0 M LiCl, 2 mM EDTA). After incubation at room temperature for 5 min and several washes several times, mRNA was eluted from the beads by heating at 80 C for 2 min. The purified mRNA was fragmented to 150 – 500 base pair range by being mixed with 10 x fragmentation buffer (Ambion, Austin, TX) and heating at 70 C for 3 min. mRNA was then purified with RNeasy spin columns.

Two-hundred ng of fragmented mRNA was reverse transcribed to first strand cDNAs by random priming, using 3 μg of the random hexamer oligos and 200 units of Superscript II reverse transcriptase (Invitrogen). The reaction was carried out at 45 C for 1 hr in the presence of the

First Strand Buffer (Invitrogen), 10 mM DTT, and 0.5 mM dNTP mix. For second strand cDNA synthesis, 400 units of *E. Coli* DNA polymerase, 2 units of *E. Coli* RNase H, and 10 units of *E. Coli* DNA ligase were added, and reaction was carried out at 16 C for 2 hrs in the presence of Second Strand Buffer and 0.2 mM dNTP mix. 20 units of T4 DNA polymerase was added at the end of incubation for end repair. Synthesized double-stranded cDNA library were purified with QIAquick purification kits (Qiagen).

Chromatin Immunoprecipitation (ChIP):
Postmortem hippocampal tissue samples (50 mg) were cut into slices less than 1 mm in thickness, and fixed in 3 ml of 1% formaldehyde/PBS solution for 10 min at room temperature to cross-link chromatin DNA and proteins. After being washed with PBS, the tissue samples were homogenized in a glass-Teflon homogenizer. Following homogenization, chromatin was isolated using the Magna ChIP G kit (Millipore, Temecula, CA) according to the Millipore protocol. Briefly, cells were lysed in Cell Lysis Buffer in the presence of protease inhibitor cocktail. Nuclei were isolated from the lysed cells by centrifugation, and resuspended in Nuclear Lysis Buffer. The chromatin DNA was then fragmented into 150 – 500 base-pair range by sonication using a Branson Sonifer (Danbury, Connecticut).

To immuno-precipitate specific genomic regions of chromatin DNA, the isolated chromatin fragments were incubated with antibodies against histone H3 trimethylated at Lysine 4 (H3K4-me3, Abcam, Cambridge, MA) and magnetic protein G beads (Millipore) at 4 C for 2.5 hr. Following incubation, the beads were washed with low salt, high salt, LiCl salt, and TE buffers, and chromatin fragments were reverse cross-linked by proteinase K digestion at 62 C for 2 hr. The eluted DNA was purified after reverse cross-linking by column purification. The H3k4me3-specific enrichment was validated by PCR amplification of select positive and negative genomic regions and amplification signals were normalized to the input DNA samples which were extracted from the same pools of chromatin fragments without enrichment by immuno-precipitation.

High-throughput, massively parallel sequencing using an Illumina Genome Analyzer (GAIIx):
Sample preparation and sequencing on the Genome Analyzer (Illumina, San Diego, CA) were carried out according to the Illumina protocols with some modifications. Briefly, the double-stranded cDNA and ChIP-enriched genomic DNA were treated with T4 DNA polymerase and the Klenow fragment for end repair. The 5’ end of the DNA fragments were then phosphorylated by T4 polynucleotide kinase, and an adenosine base was added to the 3’ end of the fragments by Klenow (3’-5’ exo$^-$). A universal adaptor was then added to both ends of the DNA fragments by A-T ligation. Following 18 cycles of PCR with the Phusion DNA polymerase, the DNA library was then be purified on a 2% agarose gel, and fragments of 170 – 300 base-pair in size were recovered. Around 15 ng of the DNA library was then used for cluster generation on a grafted GAII Flow Cell, and

then sequenced on the Genome Analyzer for 36 cycles using the “Sequencing-by-synthesis” method.

Sequence base-calling, mapping to genome, data normalization and statistical analysis: Sequences were called from image files with the Illumina Genome Analyzer Pipeline (GApipeline) and aligned to the reference genome (UCSC hg18) using Extended Eland in the GApipeline. A total of 3,181,000 uniquely mapped RNA-seq reads and 3,269,000 uniquely mapped H3K4-me3 reads for each sample were retrieved from export.txt files (output of Extended Eland). Based on their mapping locations, these selected reads were parsed with in-house Perl scripts to generate base coverage in WIG file format. After moving average smoothing, the chromosome location s of enrichment peaks were identified from pooled WIG files using in-house Perl scripts. For peak identification from the pooled WIG files, the minimum of height, width and border distance between two peaks (two peaks were merged if they were within this distance) were 5, 30 bp and 50 bp respectively for RNA-seq and 15, 80bp, and 1000 bp respectively for H3K4-me3 ChIPseq. On average, 68% of RNA-seq reads and 21% of H3K4-me3 ChIPseq reads fell into the peaks. For RNA-seq data, the numbers of sequencing reads of the most abundantly covered 50 base pairs (bp) of the highest peak in an annotated RefSeq gene were counted for each sample. For histone H3K4me3 ChIP-seq data, the numbers of reads in the area under the curve of each individual peak were counted for each sample. The read counts were then log2 transformed and normalized using quantile normalization. The group comparisons between the drug-free individuals and the cocaine addicted or alcoholic individuals were performed using *t*-tests, FDR q value was calculated for each P value using the Benjamini-Hochberg method. For gene ontology and functional annotation analysis, lists of subsets of the genes that were significantly different in expression (FDR < 0.2) between the control and the cocaine, addicted , or alcohol group were analyzed with the Functional Annotation Tool of the DAVID Bioinformatics Resources 6.7, National Institute of Allergy and Infectious Diseases (NIAID), NIH (http://david.abcc.ncifcrf.gov/).

Quantitative RT-PCR:
mRNA (50 ng) was primed with 150 ng of random hexamer (Invitrogen) and reverse transcribed into first strand cDNA with Superscript RT II (Invitrogen) in the presence of the First Strand Buffer, 10 mM DTT, and 0.5 mM dNTPs at 45 C for 1 hr in a 20 μl reaction volume. For quantitative PCR, 0.5 μl of cDNA was mixed with gene-specific primers (0.25 μM final concentration), 2x SYBR Green master mix (Applied Biosystems) in a 10 μl volume. Reactions were carried out on the ABI 7900 real-time PCR system. Relative gene expression level for each sample was calculated using the ΔCT value (normalized detection threshold).

References:

1. Stephens BG, Jentzen JM, Karch S, Mash DC, Wetli CV (2004) Criteria for the interpretation of cocaine levels in human biological samples and their relation to the cause of death. *Am J Forensic Med Pathol* 25**:**1-10.
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