Supplementary Table 1. Differentially expressed genes (FDR < 0.05)

FC - fold change, FDR - false discovery rate

RPKM - average reads per kilobase per million mapped reads, for control and alcohol exposed animals

Other studies - number of other studies in which this gene was found significant. P-drinking - studies with P animals exposed to ethanol, Pvs. NP naïve - studies comparing gene expression in P to NP animals, GWAS - human genome wide association studies, GE in PM - Studies of post mortem human tissue

Other brain regions - fold change for genes called significant in Accumbens shell, Central nucleus of the Amygdala and Dorsal Raphe Nucleus in the same animals

	PAG					Other studies				Other brain regions							
gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Alb	-173.07	0.00E+00	0.00E+00	493.5	2.9	1	2					-3.85	albumin	1.98E-58	Y		
Apob	-222.02	1.03E-285	6.24E-282	14.6	0.1							-7.11	apolipoprotein B (including Ag(x) antigen)	1.81E-74	Y		
Serpina1	-70.69	2.66E-201	1.07E-197	69.6	1.0	2						-4.00	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, an	8.02E-33	Y		
Cps1	-73.96	8.11E-157	2.46E-153	13.0	0.2							-2.25	carbamoyl-phosphate synthase 1, mitochondrial	2.33E-08	Y		
Hpx	-42.36	3.75E-141	9.09E-138	38.2	0.9							-3.35	hemopexin	1.06E-17	Y		
Hp	-37.71	1.51E-140	3.05E-137	48.8	1.3		1					-3.61	haptoglobin	7.46E-17	Y		
C3	-7.97	2.26E-88	3.91E-85	23.3	2.9	1	2					-1.42	complement component 3	1.12E-03	Y		
Itih4	-11.71	4.89E-75	7.41E-72	11.8	1.0							-1.86	inter-alpha-trypsin inhibitor heavy chain family, member 4	7.94E-06	Y		
Baat	-13.14	8.14E-63	1.10E-59	13.0	1.0							-2.62	bile acid CoA: amino acid N-acyltransferase (glycine N-choloyltrans	2.03E-07	Y		
Cyp2c11	-11.40	4.34E-60	5.26E-57	12.3	1.1							-2.41	cytochrome P450, subfamily IIC (mephenytoin 4-hydroxylase), polypeptide 11	1.56E-07	Y		
Hpd	-11.19	1.29E-37	1.42E-34	8.6	0.8							-2.20	4-hydroxyphenylpyruvate dioxygenase	1.12E-04	Y		
Nr4a1	3.63	2.12E-37	2.14E-34	8.6	31.1	1			1			6.56	nuclear receptor subfamily 4, group A, member 1	3.86E-83	Y		
Fos	3.10	5.76E-33	5.37E-30	25.4	78.7	4				1.68		3.12	FBJ murine osteosarcoma viral oncogene homolog	4.28E-41	Y	Y	
Pah	-7.97	8.57E-33	7.42E-30	5.5	0.7	1						-2.22	phenylalanine hydroxylase	1.08E-07	Y		
Npas4	3.76	1.83E-30	1.48E-27	3.4	12.8							4.81	neuronal PAS domain protein 4	2.21E-38	Y		
Pcp2	2.85	1.39E-28	1.05E-25	88.0	251.0							3.65	Purkinje cell protein 2	2.50E-51	Y		
Igfbp4	-6.67	1.55E-28	1.11E-25	4.8	0.7		1					-1.47	insulin-like growth factor binding protein 4	4.05E-02	Y		
Car3	-3.21	4.13E-27	2.78E-24	51.2	15.9								carbonic anhydrase 3	9.89E-01	N		
Cth	-3.46	2.07E-23	1.32E-20	12.6	3.7			1				-1.65	cystathionase (cystathionine gamma-lyase)	1.76E-04	Y		
F2	-3.92	9.05E-23	5.49E-20	8.3	2.1								coagulation factor II (thrombin)	9.26E-01	N		
Apoc1	-3.71	1.47E-22	8.49E-20	36.5	9.9		2					-1.62	apolipoprotein C-I	7.32E-04	Y		
Pvalb	2.33	4.69E-21	2.58E-18	185.2	431.5	1	1		1			3.34	parvalbumin	3.00E-51	Y		
Rbp4	-2.72	1.45E-20	7.64E-18	44.2	16.2		2						retinol binding protein 4, plasma	9.05E-01	N		
Zic1	2.29	2.17E-20	1.10E-17	74.3	170.1							4.27	Zic family member 1	1.31E-68	Y		
Homer3	2.35	5.12E-20	2.48E-17	39.6	92.9	1					-1.15	3.75	homer homolog 3 (Drosophila)	1.49E-52	Y		N
Tf	-2.17	2.10E-19	9.79E-17	384.1	176.9		2		4			-1.24	transferrin	1.13E-02	Y		
Atp2a3	2.23	2.32E-19	1.04E-16	24.0	53.6							4.38	ATPase, Ca++ transporting, ubiquitous	1.26E-72	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Car8	2.19	2.44E-19	1.06E-16	220.0	481.8							4.06	carbonic anhydrase 8	6.46E-73	Y		
Serpinf2	-4.24	5.55E-19	2.32E-16	4.3	1.0								serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigme	8.47E-01	N		
Gdf10	2.25	6.40E-18	2.59E-15	18.7	42.1							3.68	growth differentiation factor 10	2.62E-48	Y		
Dusp1	2.24	1.46E-17	5.71E-15	22.2	49.7	5	1			1.88	1.57	2.04	dual specificity phosphatase 1	4.34E-17	Y	Y	Y
Hes3	2.55	3.89E-17	1.47E-14	11.8	30.1							4.16	hairy and enhancer of split 3 (Drosophila)	1.53E-34	Y		
Spp1	-3.25	6.00E-17	2.20E-14	21.5	6.6		1		1			-1.49	secreted phosphoprotein 1	1.13E-02	Y		
Akr1c14	-3.26	7.95E-17	2.83E-14	5.7	1.8								aldo-keto reductase family 1, member C14	2.84E-01	N		
Cbln3	2.06	1.81E-16	6.27E-14	106.2	219.0							5.22	cerebellin 3 precursor	3.51E-90	Y		
RGD1310507	-4.13	3.97E-16	1.34E-13	5.5	1.3									5.44E-01	N		
Nr4a2	2.11	1.48E-15	4.85E-13	17.6	37.1		1		1			3.85	nuclear receptor subfamily 4, group A, member 2	4.77E-50	Y		
Impg1	2.36	1.76E-15	5.61E-13	4.7	11.2							3.80	interphotoreceptor matrix proteoglycan 1	8.01E-40	Y		
Tnnt1	2.26	2.24E-15	6.96E-13	20.4	46.2		1					2.48	troponin T type 1 (skeletal, slow)	7.27E-22	Y		
Neurod2	2.32	2.40E-15	7.27E-13	8.2	19.0				1			4.75	neuronal differentiation 2	9.51E-39	Y		
Slc1a6	2.06	2.72E-15	8.04E-13	31.3	64.6				1			2.79	solute carrier family 1 (high affinity aspartate/glutamate transpor	1.83E-33	Y		
Prkcg	1.99	5.55E-15	1.60E-12	58.3	115.9		1					2.85	protein kinase C, gamma	6.58E-41	Y		
Gabrd	1.99	1.11E-14	3.13E-12	59.8	119.0		2					4.34	gamma-aminobutyric acid (GABA) A receptor, delta	1.68E-68	Y		
Sgk1	-1.97	1.95E-14	5.37E-12	84.8	43.1	3	3				-1.46	-1.63	serum/glucocorticoid regulated kinase 1	7.81E-10	Y		Y
Dpys	-8.36	3.33E-14	8.88E-12	1.5	0.2								dihydropyrimidinase	0.00E+00	N		
Acan	-2.36	3.37E-14	8.88E-12	3.6	1.5		1					-1.64	aggrecan	1.02E-04	Y		
Scn4b	-1.97	5.01E-14	1.29E-11	35.7	18.1		1					1.90	sodium channel, voltage-gated, type IV, beta subunit	3.34E-13	N		
Btg2	2.32	7.44E-14	1.88E-11	4.8	11.1	2	2			2.07		1.70	BTG family, member 2	2.79E-07	Y	Y	
Asah2	-2.24	8.45E-14	2.09E-11	13.7	6.1							-1.57	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2	5.05E-05	Y		
Slc27a5	-3.58	1.06E-13	2.54E-11	3.2	0.9								solute carrier family 27 (fatty acid transporter), member 5	7.00E-01	N		
Ccl9	-4.72	1.07E-13	2.54E-11	3.9	0.8								chemokine (C-C motif) ligand 9	0.00E+00	N		
Sepp1	-1.89	1.23E-13	2.87E-11	377.0	199.5				4				selenoprotein P, plasma, 1	2.61E-01	N		
Cbln1	1.91	1.26E-13	2.88E-11	82.7	158.3							2.90	cerebellin 1 precursor	7.88E-42	Y		
Rgl3	1.96	1.32E-13	2.96E-11	28.3	55.3							4.19	ral guanine nucleotide dissociation stimulator-like 3	5.28E-59	Y		
Sbk1	1.94	1.64E-13	3.61E-11	21.0	40.8				1			2.49	SH3-binding domain kinase 1	2.88E-29	Y		
Tle2	2.02	1.95E-13	4.22E-11	15.5	31.2							1.87	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila) //	4.62E-12	Y		
Igf1	-2.41	2.00E-13	4.25E-11	10.6	4.4		1					1.31	insulin-like growth factor 1 (somatomedin C)	4.97E-02	N		
Slc17a7	1.88	3.72E-13	7.78E-11	165.8	311.3							5.06	solute carrier family 17 (sodium-dependent inorganic phosphate c	2.46E-91	Y		
Adcy1	1.87	4.77E-13	9.80E-11	185.7	346.4				1			3.21	adenylate cyclase 1 (brain)	1.65E-52	Y		
Dmgdh	-5.69	7.55E-13	1.53E-10	1.3	0.2								dimethylglycine dehydrogenase	0.00E+00	N		
Itpr1	1.85	8.04E-13	1.60E-10	142.2	263.0		1					3.52	inositol 1,4,5-trisphosphate receptor, type 1	1.05E-61	Y		
Nefm	-1.86	1.05E-12	2.05E-10	100.4	53.9		1						neurofilament, medium polypeptide	3.62E-01	N		
Plp1	-1.82	1.43E-12	2.75E-10	2382.8	1306.7				3			-1.56	proteolipid protein 1	1.04E-08	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Fat2	1.82	2.69E-12	5.10E-10	99.2	180.8							4.88	FAT tumor suppressor homolog 2 (Drosophila)	3.18E-93	Y		
Cfb	-2.20	3.23E-12	6.02E-10	10.7	4.8		1	1	1				complement factor B	4.37E-01	N		
Ndst4	-2.20	3.99E-12	7.33E-10	9.3	4.2								N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4	1.43E-01	N		
Neurod1	1.83	4.14E-12	7.49E-10	139.7	255.4	1						4.33	neuronal differentiation 1	1.63E-75	Y		
Htr2c	-1.83	4.76E-12	8.49E-10	79.6	43.6							-1.70	5-hydroxytryptamine (serotonin) receptor 2C, G protein-coupled	9.23E-12	Y		
Ywhab	-1.82	6.48E-12	1.14E-09	126.0	69.2				1			-1.21	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pro	3.69E-02	Y		
Sema3g	1.91	7.91E-12	1.37E-09	11.1	21.2							2.34	sema domain, immunoglobulin domain (Ig), short basic domain, secr	1.30E-20	Y		
Mrf	-1.84	8.93E-12	1.52E-09	30.9	16.8							-1.36		4.10E-04	Y		
Slc17a6	-1.80	1.07E-11	1.80E-09	125.3	69.7		1					-1.82	solute carrier family 17 (sodium-dependent inorganic phosphate c	6.77E-13	Y		
F5	-3.88	1.11E-11	1.84E-09	0.8	0.2							1.81	coagulation factor V (proaccelerin, labile factor)	4.71E-02	N		
Tmem195	-2.85	1.26E-11	2.06E-09	4.2	1.5				1			-1.58	transmembrane protein 195	1.20E-03	Y		
Cbln2	-1.97	1.69E-11	2.73E-09	20.5	10.4		1					-2.12	cerebellin 2 precursor	1.91E-19	Y		
Kcns1	-3.98	1.90E-11	3.03E-09	0.0	0.0								potassium voltage-gated channel, delayed-rectifier, subfamily S, m	0.00E+00	N		
Dlk1	-1.99	1.94E-11	3.05E-09	30.9	15.5							-1.76	delta-like 1 homolog (Drosophila)	3.44E-11	Y		
Glra1	-1.88	2.42E-11	3.76E-09	35.2	18.7				1			-1.75	glycine receptor, alpha 1	1.05E-11	Y		
Col23a1	2.06	2.79E-11	4.28E-09	5.1	10.4			1				2.43	collagen, type XXIII, alpha 1	2.00E-17	Y		
F12	-4.35	3.80E-11	5.69E-09	2.0	0.5		1					-1.96	coagulation factor XII (Hageman factor)	5.45E-03	Y		
Slc27a2	-2.03	3.80E-11	5.69E-09	11.5	5.7		1					-1.42	solute carrier family 27 (fatty acid transporter), member 2	1.12E-03	Y		
St14	2.23	6.03E-11	8.91E-09	2.5	5.6							2.87	suppression of tumorigenicity 14 (colon carcinoma)	1.44E-13	Y		
Slc38a4	-3.70	6.11E-11	8.92E-09	2.5	0.7				1			-1.71	solute carrier family 38, member 4	5.26E-07	Y		
Kcnh3	1.83	7.40E-11	1.07E-08	12.9	23.6	1	1					4.54	potassium voltage-gated channel, subfamily H (eag-related), member	7.23E-58	Y		
Nr4a3	1.82	8.95E-11	1.28E-08	13.0	23.6	3	1		1			3.01	nuclear receptor subfamily 4, group A, member 3	7.45E-37	Y		
Pon3	-3.62	9.26E-11	1.31E-08	3.4	0.9								paraoxonase 3	5.75E-02	N		
Ugt8	-1.76	1.03E-10	1.44E-08	96.8	55.2	1			3			-1.51	UDP glycosyltransferase 8	2.88E-07	Y		
Scg2	-1.75	1.16E-10	1.60E-08	153.4	87.6	1			1			-1.84	secretogranin II	1.32E-15	Y		
Cdc42bpg	1.90	1.19E-10	1.62E-08	4.2	7.9							2.40	CDC42 binding protein kinase gamma (DMPK-like)	4.71E-20	Y		
Junb	2.28	1.30E-10	1.75E-08	3.7	8.5	1	1		1			1.78	jun B proto-oncogene	3.36E-06	Y		
Elavl2	-1.77	1.57E-10	2.09E-08	44.4	25.1	1	1					-1.81	ELAV (embryonic lethal, abnormal vision, Drosophila)-like	1.26E-14	Y		
Itga7	1.77	1.74E-10	2.29E-08	27.9	49.3							2.59	integrin, alpha 7	3.56E-31	Y		
Plac9	2.86	1.99E-10	2.59E-08	6.1	17.4							3.26	placenta-specific 9	5.71E-14	Y		
Uncx	2.10	2.10E-10	2.71E-08	4.0	8.3							3.21	UNC homeobox	1.40E-20	Y		
Col27a1	1.81	2.32E-10	2.96E-08	8.2	14.8			1				2.36	collagen, type XXVII, alpha 1	2.34E-21	Y		
Rgs8	1.73	2.60E-10	3.28E-08	100.9	174.3	1						2.48	regulator of G-protein signaling 8	1.24E-32	Y		
Barhl2	1.94	3.20E-10	4.00E-08	10.9	21.1			1				4.06	BarH-like homeobox 2	1.93E-30	Y		
Pde5a	1.75	3.26E-10	4.03E-08	32.1	56.2				1			3.22	phosphodiesterase 5A, cGMP-specific	4.00E-47	Y		
Tmem212	1.89	3.29E-10	4.03E-08	17.1	32.3							2.48	transmembrane protein 212	1.74E-23	Y		

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Il16	1.73	3.72E-10	4.51E-08	46.5	80.3	1						4.02	interleukin 16	4.70E-68	Y		
Nos1	1.75	4.80E-10	5.76E-08	25.0	43.9								nitric oxide synthase 1 (neuronal)	7.10E-02	N		
Selm	1.75	5.39E-10	6.41E-08	132.4	231.3		1		1			1.67	selenoprotein M	4.75E-10	Y		
Ccdc153	1.82	5.63E-10	6.57E-08	24.4	44.5		1					2.18	coiled-coil domain containing 153	8.11E-20	Y		
Gas7	1.70	5.64E-10	6.57E-08	86.4	147.3				1			3.25	growth arrest-specific 7	4.95E-53	Y		
Mrgprf	1.84	5.85E-10	6.75E-08	12.7	23.4							4.72	MAS-related GPR, member F	2.24E-48	Y		
Kctd4	-2.01	6.56E-10	7.50E-08	7.8	3.9		1					-1.61	potassium channel tetramerisation domain containing 4	1.03E-05	Y		
Jup	1.74	7.23E-10	8.19E-08	26.2	45.6							1.96	junction plakoglobin	1.94E-16	Y		
Eps8l2	1.94	7.68E-10	8.62E-08	4.7	9.1		1		1			2.96	EPS8-like 2	2.25E-24	Y		
Tspan2	-1.70	7.75E-10	8.62E-08	108.3	63.6	1	1					-1.53	tetraspanin 2	8.95E-08	Y		
Papss2	-1.92	8.80E-10	9.70E-08	9.0	4.7							-1.36	3'-phosphoadenosine 5'-phosphosulfate synthase 2	7.18E-03	Y		
Hhip	-1.86	9.11E-10	9.95E-08	16.8	9.0	1	2					-1.52	hedgehog interacting protein	1.21E-05	Y		
Scd1	-1.82	9.21E-10	9.97E-08	13.1	7.2	1							stearoyl-CoA desaturase (delta-9-desaturase) (rat/rodent, human SCD)	1.73E-01	N		
Zic2	1.73	9.31E-10	9.99E-08	31.5	54.5		1					3.80	Zic family member 2	1.89E-56	Y		
Ugt1a1	-2.34	1.02E-09	1.08E-07	4.9	2.1									4.89E-01	N		
Btbd4	1.78	1.02E-09	1.08E-07	14.0	24.9							2.24	BTB (POZ) domain containing 4	2.32E-19	Y		
Trim36	-1.94	1.03E-09	1.08E-07	12.7	6.5							-1.69	tripartite motif containing 36	3.26E-08	Y		
Sdc1	1.78	1.10E-09	1.14E-07	13.2	23.6	1						5.13	syndecan 1	2.36E-62	Y		
Fam107a	1.71	1.11E-09	1.14E-07	54.1	92.5				2			2.86	family with sequence similarity 107, member A	1.56E-39	Y		
Pcp4l1	-1.92	1.14E-09	1.16E-07	20.4	10.6		1					-1.63	Purkinje cell protein 4 like 1	4.17E-06	Y		
Cyr61	3.18	1.15E-09	1.16E-07	0.8	2.7	2				3.83	1.56	3.60	cysteine-rich, angiogenic inducer, 61	3.60E-14	Y	Y	Y
RGD1309873	-1.79	1.16E-09	1.16E-07	53.6	30.1							-1.69		1.13E-09	Y		
Mobp	-1.68	1.35E-09	1.34E-07	216.3	128.6	1	1		2			-1.54	myelin-associated oligodendrocyte basic protein	3.64E-08	Y		
Slco2a1	-3.34	1.47E-09	1.45E-07	1.7	0.5				1			-1.61	solute carrier organic anion transporter family, member 2A1	3.84E-02	Y		
Inpp5a	1.71	1.48E-09	1.45E-07	48.5	82.8							2.01	inositol polyphosphate-5-phosphatase, 40kDa	9.75E-19	Y		
Tjp3	2.07	1.82E-09	1.76E-07	2.8	5.9							2.41	tight junction protein 3 (zona occludens 3)	2.66E-15	Y		
Timp4	1.73	1.83E-09	1.76E-07	43.8	75.6		1		1			1.86	TIMP metallopeptidase inhibitor 4	6.70E-14	Y		
Hrnbp3	1.73	1.91E-09	1.82E-07	63.9	110.6		1					2.15		2.69E-19	Y		
RGD1305592	1.72	1.98E-09	1.88E-07	47.6	82.0							1.90		5.55E-14	Y		
Kitlg	1.72	2.04E-09	1.92E-07	15.1	26.0		1					2.13	KIT ligand	8.00E-21	Y		
Plk5	1.76	2.06E-09	1.92E-07	20.6	36.2		1					4.59	polo-like kinase 5	2.21E-52	Y		
Arhgap10	1.77	2.16E-09	1.99E-07	13.8	24.6							2.86	Rho GTPase activating protein 10	1.67E-30	Y		
Vim	1.70	2.17E-09	1.99E-07	82.3	139.6	1			1		-1.59	2.03	vimentin	1.27E-19	Y		N
Wdr63	1.82	2.22E-09	2.02E-07	9.4	17.1							1.96	WD repeat domain 63	8.72E-15	Y		
Grid2ip	1.85	2.26E-09	2.04E-07	6.2	11.4							3.49		6.93E-34	Y		
Cyp4f1	-2.27	2.31E-09	2.07E-07	5.6	2.5								cytochrome P450, family 4, subfamily f, polypeptide 1	3.36E-01	N		
Trpc3	1.71	2.33E-09	2.07E-07	25.2	43.2			1				2.13	transient receptor potential cation channel, subfamily C, member 3	7.13E-21	Y		
Pip5k1b	1.72	2.34E-09	2.07E-07	24.6	42.3		1					1.83	phosphatidylinositol-4-phosphate 5-kinase, type I, beta	6.18E-13	Y		
Cabp7	-1.85	2.71E-09	2.38E-07	12.9	7.0								calcium binding protein 7	3.31E-01	N		
Gsbs	1.70	2.76E-09	2.41E-07	67.3	114.0							3.57		4.24E-56	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Reln	1.67	2.83E-09	2.45E-07	65.2	108.6	1	1					2.96	reelin	4.71E-46	Y		
Diras2	1.69	2.85E-09	2.45E-07	110.2	186.5							2.31	DIRAS family, GTP-binding RAS-like 2	1.66E-25	Y		
Npy5r	-2.45	3.21E-09	2.74E-07	3.6	1.5	2	2			1.23	1.36	-1.61	neuropeptide Y receptor Y5	7.37E-04	Y	N	N
Kcnj12	1.72	3.37E-09	2.86E-07	27.3	47.0							2.64	potassium inwardly-rectifying channel, subfamily J, member 12	1.84E-29	Y		
Shroom2	-1.68	3.46E-09	2.91E-07	31.5	18.7							-1.57	shroom family member 2	1.48E-08	Y		
Iyd	-11.07	3.63E-09	3.03E-07	1.2	0.1								iodotyrosine deiodinase	0.00E+00	N		
Neto1	-1.91	3.68E-09	3.06E-07	7.7	4.0		1						neuropilin (NRP) and tolloid (TLL)-like 1	7.50E-01	N		
Lgi2	-1.73	4.26E-09	3.51E-07	50.0	29.0							-1.24	leucine-rich repeat LGI family, member 2	2.22E-02	Y		
Fgf1	-2.03	4.44E-09	3.64E-07	14.8	7.3		1		2				fibroblast growth factor 1 (acidic)	9.51E-01	N		
Odf3b	2.12	4.54E-09	3.69E-07	6.9	14.7							2.70	outer dense fiber of sperm tails 3B	7.87E-16	Y		
Grid2	1.66	5.06E-09	4.09E-07	63.4	105.3							2.31	glutamate receptor, ionotropic, delta 2	1.53E-27	Y		
Tcf7l2	-1.68	5.42E-09	4.35E-07	51.2	30.5				2				transcription factor 7-like 2 (T-cell specific, HMG-box) /	4.88E-01	N		
Cited4	2.18	6.56E-09	5.23E-07	6.0	13.1							4.05	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-te	2.75E-20	Y		
Chn2	1.67	7.31E-09	5.79E-07	109.5	183.0			1	1			1.98	chimerin (chimaerin) 2	4.67E-17	Y		
Fndc7	1.84	7.42E-09	5.84E-07	4.9	9.0							2.40	fibronectin type III domain containing 7	1.95E-17	Y		
Hpcal1	1.65	7.50E-09	5.87E-07	173.3	286.1				1			1.48	hippocalcin-like 1	1.34E-06	Y		
Mbp	-1.63	7.95E-09	6.18E-07	1805.2	1107.2				1			-1.45	myelin basic protein	2.78E-06	Y		
Entpd3	-1.87	8.10E-09	6.25E-07	9.2	4.9		1						ectonucleoside triphosphate diphosphohydrolase 3	9.09E-02	N		
Atp1a1	1.64	9.73E-09	7.47E-07	276.5	452.3							2.10	ATPase, Na+/K+ transporting, alpha 1 polypeptide	1.86E-22	Y		
Nefh	-1.63	1.13E-08	8.62E-07	144.8	88.6		2		3				neurofilament, heavy polypeptide	8.39E-01	N		
Vtn	-1.76	1.14E-08	8.64E-07	32.8	18.6								vitronectin	4.92E-01	N		
Fam107b	1.68	1.15E-08	8.66E-07	25.5	42.7		1		1			2.22	family with sequence similarity 107, member B	4.00E-22	Y		
Chrna7	-1.88	1.19E-08	8.91E-07	17.3	9.2	2		1				-1.37	cholinergic receptor, nicotinic, alpha 7 (neuronal)	4.01E-04	Y		
Opalin	-1.68	1.21E-08	9.00E-07	44.8	26.7							-1.62	oligodendrocytic myelin paranodal and inner loop protein /	6.58E-09	Y		
Slitrk6	-1.82	1.26E-08	9.31E-07	7.5	4.1							-1.52	SLIT and NTRK-like family, member 6	4.22E-05	Y		
Grin2c	1.65	1.30E-08	9.55E-07	37.7	62.1			1				2.61	glutamate receptor, ionotropic, N-methyl D-aspartate 2C	5.29E-33	Y		
Gprc5c	1.75	1.32E-08	9.64E-07	15.2	26.7							3.38	G protein-coupled receptor, family C, group 5, member C	4.97E-32	Y		
Ak7	1.70	1.43E-08	1.04E-06	17.5	29.8							2.09	adenylate kinase 7	8.37E-19	Y		
Sec14l4	-3.98	1.49E-08	1.08E-06	1.0	0.3				1				SEC14-like 4 (S. cerevisiae)	0.00E+00	N		
Kit	1.65	1.54E-08	1.10E-06	32.8	54.1								v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	1.37E-01	N		
Nab2	1.75	1.55E-08	1.11E-06	8.0	13.9		1					2.57	NGFI-A binding protein 2 (EGR1 binding protein 2)	2.07E-20	Y		
Adprhl1	1.93	1.59E-08	1.13E-06	6.5	12.6							3.63	ADP-ribosylhydrolase like 1	4.61E-25	Y		
Oprm1	-1.83	1.62E-08	1.14E-06	9.7	5.3							-1.64		1.44E-07	Y		
Ftcd	-4.88	1.76E-08	1.23E-06	0.0	0.0		1						formiminotransferase cyclodeaminase	0.00E+00	N		
Itpka	1.73	1.97E-08	1.37E-06	20.3	35.0	1	1		1			2.15	inositol-trisphosphate 3-kinase A	2.24E-17	Y		
Ankrd34c	-1.94	2.02E-08	1.40E-06	7.4	3.8							-1.57	ankyrin repeat domain 34C	1.91E-03	Y		
Npy1r	-2.00	2.10E-08	1.43E-06	6.1	3.1		2					-1.57	neuropeptide Y receptor Y1	2.96E-05	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Bhlhe22	1.75	2.10E-08	1.43E-06	8.9	15.5							1.82	basic helix-loop-helix family, member e22	4.26E-11	Y		
Prkcd	1.72	2.10E-08	1.43E-06	12.6	21.6	1			1			2.40	protein kinase C, delta	1.17E-22	Y		
Tmem88b	-1.78	2.12E-08	1.44E-06	19.8	11.1							-1.54	transmembrane protein 88b	1.26E-05	Y		
Gabra6	1.62	2.18E-08	1.47E-06	322.9	523.0							4.53	gamma-aminobutyric acid (GABA) A receptor, alpha 6	2.13E-82	Y		
Zmynd10	1.71	2.19E-08	1.47E-06	22.2	37.9							1.93	zinc finger, MYND-type containing 10	3.68E-14	Y		
Rgn	-2.99	2.35E-08	1.57E-06	2.9	1.0	1							regucalcin (senescence marker protein-30)	4.41E-01	N		
Jph1	1.74	2.49E-08	1.65E-06	10.6	18.4							3.10	junctophilin 1	4.47E-29	Y		
RGD1562658	1.96	2.62E-08	1.72E-06	7.9	15.5							2.43		2.36E-15	Y		
Tll1	1.71	2.64E-08	1.72E-06	7.4	12.6							3.11	tolloid-like 1	1.03E-32	Y		
Ermn	-1.66	2.64E-08	1.72E-06	62.5	37.6		2					-1.57	ermin, ERM-like protein	7.07E-08	Y		
Wipf3	-2.05	2.67E-08	1.73E-06	3.1	1.5		1						WAS/WASL interacting protein family, member 3	8.36E-02	N		
Enc1	-1.64	2.70E-08	1.74E-06	45.2	27.6	1	1		1			-1.53	ectodermal-neural cortex 1 (with BTB-like domain)	1.46E-07	Y		
Kcnk16	1.96	2.85E-08	1.83E-06	3.7	7.3							2.64	potassium channel, subfamily K, member 16	9.25E-17	Y		
Ehhadh	-2.09	2.88E-08	1.84E-06	4.0	1.9								enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase	2.38E-01	N		
LOC691995	-1.61	3.20E-08	2.03E-06	325.3	202.0							-1.79		2.72E-14	Y		
Cnksr3	1.65	3.26E-08	2.06E-06	23.0	37.9							2.13	CNKSR family member 3	2.55E-19	Y		
Dnah1	1.63	3.50E-08	2.20E-06	10.8	17.6							2.10	dynein, axonemal, heavy chain 1	4.03E-21	Y		
Ccdc120	1.76	3.75E-08	2.34E-06	9.8	17.3							1.98	coiled-coil domain containing 120	1.40E-10	Y		
Icmt	1.64	4.10E-08	2.55E-06	52.3	85.6	1						2.38	isoprenylcysteine carboxyl methyltransferase	1.81E-26	Y		
Rcan2	-1.61	4.12E-08	2.55E-06	103.8	64.5		1					-1.72	regulator of calcineurin 2	1.62E-12	Y		
Ccdc135	1.77	4.14E-08	2.55E-06	7.0	12.4							2.20	coiled-coil domain containing 135	7.44E-17	Y		
Cd83	-1.66	4.17E-08	2.55E-06	45.4	27.4		1					-1.74	CD83 molecule	9.45E-11	Y		
Tcfap2d	-2.41	4.20E-08	2.55E-06	6.0	2.5									0.00E+00	N		
Apln	-1.75	4.21E-08	2.55E-06	12.8	7.3	2						-1.31	apelin	1.05E-02	Y		
B3galt5	-1.66	4.26E-08	2.57E-06	17.3	10.4							-1.38	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	2.91E-04	Y		
Apoa5	-2.36	4.29E-08	2.57E-06	4.2	1.8								apolipoprotein A-V	5.80E-02	N		
Dusp5	1.70	4.32E-08	2.58E-06	13.7	23.2							3.36	dual specificity phosphatase 5	8.31E-35	Y		
Qdpr	-1.62	4.49E-08	2.67E-06	165.5	102.1		2		2			-1.56	quinoid dihydropteridine reductase	2.22E-08	Y		
Ttpa	-1.84	4.52E-08	2.67E-06	11.9	6.5								tocopherol (alpha) transfer protein	5.14E-01	N		
Ebf3	-1.64	4.84E-08	2.85E-06	27.0	16.5			1				-1.30	early B-cell factor 3	7.42E-03	Y		
Mapk15	1.84	4.99E-08	2.92E-06	6.8	12.5							2.18	mitogen-activated protein kinase 15	2.57E-14	Y		
Vwa3a	1.66	5.23E-08	3.05E-06	13.0	21.5							1.87	von Willebrand factor A domain containing 3A	5.96E-14	Y		
Tspan9	1.60	5.73E-08	3.32E-06	51.7	82.9							2.77	tetraspanin 9	1.07E-38	Y		
Col1a2	1.65	5.75E-08	3.32E-06	13.6	22.4		1					2.18	collagen, type I, alpha 2	4.84E-21	Y		
Leprel2	1.62	5.77E-08	3.32E-06	49.1	79.8							1.58	leprecan-like 2	3.46E-08	Y		
Lhb	3.81	6.02E-08	3.44E-06	1.4	5.2							2.25	luteinizing hormone beta polypeptide	5.23E-04	Y		
Inpp5j	1.63	6.23E-08	3.55E-06	24.1	39.3							2.18	inositol polyphosphate-5-phosphatase J	1.31E-20	Y		
Gas2l2	1.87	6.26E-08	3.55E-06	3.5	6.6							2.19	growth arrest-specific 2 like 2	2.13E-13	Y		
Dgkz	1.59	6.97E-08	3.93E-06	108.1	172.2							2.00	diacylglycerol kinase, zeta	2.89E-19	Y		
Iqcg	1.91	7.05E-08	3.96E-06	5.4	10.4							2.06	IQ motif containing G	3.42E-11	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Gfap	1.59	7.29E-08	4.07E-06	245.0	388.9		2		2			1.81	glial fibrillary acidic protein	9.02E-15	Y		
Cxcr4	1.95	7.44E-08	4.14E-06	4.7	9.1	1	1		1			1.45	chemokine (C-X-C motif) receptor 4	6.75E-04	Y		
Col3a1	1.66	7.61E-08	4.21E-06	10.1	16.7	1						1.85	collagen, type III, alpha 1	3.10E-13	Y		
Pex5l	-1.62	7.81E-08	4.30E-06	72.0	44.4	1	1		1		-1.2	-1.46	peroxisomal biogenesis factor 5-like	6.84E-06	Y		Y
Ppp1r1b	1.62	8.17E-08	4.48E-06	50.5	82.0		1					2.21	protein phosphatase 1, regulatory (inhibitor) subunit 1B	4.55E-22	Y		
Myo7a	1.71	8.22E-08	4.49E-06	3.9	6.6				1			2.30	myosin VIIA	4.29E-19	Y		
Rps6ka1	1.62	8.86E-08	4.82E-06	38.1	62.0		1		2			2.66	ribosomal protein S6 kinase, 90kDa, polypeptide 1	3.61E-30	Y		
St8sia5	1.66	8.99E-08	4.86E-06	35.3	58.7		1					3.03	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5	3.66E-33	Y		
Gabrg3	-1.82	9.02E-08	4.86E-06	14.3	7.9							-1.42	gamma-aminobutyric acid (GABA) A receptor, gamma 3	7.34E-04	Y		
Lingo3	1.79	9.33E-08	5.00E-06	7.5	13.4							2.93	leucine rich repeat and Ig domain containing 3	3.23E-21	Y		
Vwc2	-1.83	9.75E-08	5.21E-06	6.5	3.5		1					-1.78	von Willebrand factor C domain containing 2	4.76E-09	Y		
Hs6st2	-1.72	9.85E-08	5.24E-06	17.1	9.9							-1.66	heparan sulfate 6-O-sulfotransferase 2	1.75E-09	Y		
Dpf3	1.68	1.01E-07	5.35E-06	26.7	44.7							3.00		7.62E-30	Y		
Ctxn3	1.67	1.08E-07	5.69E-06	22.5	37.6							2.35	cortexin 3	9.77E-22	Y		
Trerf1	-1.78	1.10E-07	5.77E-06	7.0	3.9		1		1			-1.46	transcriptional regulating factor 1	1.39E-04	Y		
Arg1	-1.92	1.15E-07	5.98E-06	10.9	5.7		1					-1.42	arginase, liver	1.08E-02	Y		
Oplah	1.61	1.15E-07	5.98E-06	22.8	36.8							2.21	5-oxoprolinase (ATP-hydrolysing)	1.22E-21	Y		
Neurod6	1.88	1.16E-07	6.01E-06	4.7	8.8							2.79	neuronal differentiation 6	3.87E-18	Y		
Calb1	1.58	1.18E-07	6.09E-06	201.2	318.0		1					3.04	calbindin 1, 28kDa	3.68E-47	Y		
Camkk2	1.60	1.21E-07	6.22E-06	51.7	82.9		3					1.97	calcium/calmodulin-dependent protein kinase kinase 2, beta	1.92E-16	Y		
Ifi27l2b	-3.30	1.25E-07	6.39E-06	7.5	2.3		2					-1.58		4.22E-02	Y		
Scn7a	-1.88	1.28E-07	6.49E-06	2.9	1.6								sodium channel, voltage-gated, type VII, alpha subunit	3.43E-01	N		
Cck	-1.88	1.28E-07	6.49E-06	25.2	13.4								cholecystokinin	7.53E-02	N		
Rtn4r	1.73	1.41E-07	7.12E-06	13.7	23.7							2.28	reticulon 4 receptor	9.80E-14	Y		
RGD1310269	-1.59	1.48E-07	7.44E-06	76.8	48.2							-1.73		2.02E-12	Y		
Cldn11	-1.58	1.55E-07	7.76E-06	190.1	120.6	1	1		1			-1.42	claudin 11	2.05E-05	Y		
Gja1	-1.58	1.59E-07	7.93E-06	110.4	70.0	1			2				gap junction protein, alpha 1, 43kDa	8.94E-01	N		
Casq2	1.77	1.60E-07	7.95E-06	5.9	10.5							2.70	calsequestrin 2 (cardiac muscle)	2.16E-20	Y		
Slit1	-1.64	1.73E-07	8.54E-06	15.5	9.4		4	1				-1.64	slit homolog 1 (Drosophila)	4.59E-09	Y		
Clic6	1.81	1.74E-07	8.54E-06	5.1	9.3							2.93	chloride intracellular channel 6	4.67E-17	Y		
Rps6ka6	-1.76	1.74E-07	8.54E-06	10.5	5.9							-1.78	ribosomal protein S6 kinase, 90kDa, polypeptide 6	1.04E-10	Y		
LOC690333	-1.76	1.83E-07	8.95E-06	9.0	5.1							-1.75		8.03E-11	Y		
Iiig9	1.65	2.11E-07	1.03E-05	23.6	39.0							2.18		3.07E-19	Y		
Efhb	1.85	2.14E-07	1.04E-05	3.7	6.8							2.25	EF-hand domain family, member B	7.08E-14	Y		
Elfn1	-1.82	2.15E-07	1.04E-05	4.8	2.6							-1.34	extracellular leucine-rich repeat and fibronectin type III	1.54E-02	Y		
Rbm11	-2.10	2.25E-07	1.08E-05	3.8	1.8							-1.52	RNA binding motif protein 11	9.37E-04	Y		
Tekt1	1.81	2.27E-07	1.09E-05	8.3	15.1		2					1.68	tektin 1	4.31E-07	Y		
Usp29	-1.56	2.44E-07	1.16E-05	59.6	38.2							-1.73	ubiquitin specific peptidase 29	1.01E-12	Y		
Sytl1	2.09	2.53E-07	1.20E-05	2.1	4.5							4.26	synaptotagmin-like 1	2.04E-13	Y		
Tacr1	-1.75	2.60E-07	1.23E-05	7.8	4.5		1					-1.82	tachykinin receptor 1	3.77E-08	Y		

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Syt12	1.60	2.66E-07	1.25E-05	33.1	53.0				1			1.95	synaptotagmin XII	3.29E-15	Y		
Pik3r3	1.59	2.67E-07	1.25E-05	61.6	98.0	1						1.80	phosphoinositide-3-kinase, regulatory subunit 3 (gamma)	1.66E-12	Y		
Zmat4	-1.70	2.75E-07	1.29E-05	9.2	5.4		1					-1.49	zinc finger, matrin-type 4	8.36E-05	Y		
Acsl1	-1.59	2.80E-07	1.31E-05	36.3	22.8	1	1					-1.20	acyl-CoA synthetase long-chain family member 1	5.00E-02	Y		
Ncald	-1.57	2.84E-07	1.32E-05	86.9	55.5							-1.74	neurocalcin delta	4.65E-13	Y		
Sla	1.80	3.01E-07	1.39E-05	6.7	12.2							2.72	Src-like-adaptor	2.56E-20	Y		
Gabra5	-1.65	3.11E-07	1.43E-05	19.4	11.7		1		1			-1.80	gamma-aminobutyric acid (GABA) A receptor, alpha 5	2.17E-11	Y		
Fmo3	-3.62	3.14E-07	1.44E-05	1.4	0.4							-2.02	flavin containing monooxygenase 3	3.53E-03	Y		
Gabra2	-1.58	3.24E-07	1.48E-05	66.8	42.3		2		3			-1.62	gamma-aminobutyric acid (GABA) A receptor, alpha 2	1.32E-09	Y		
Stac3	-4.47	3.37E-07	1.54E-05	1.4	0.3								SH3 and cysteine rich domain 3	0.00E+00	N		
Hist2h4	1.73	3.45E-07	1.56E-05	40.9	70.7							1.92		5.47E-11	Y		
RGD1560691	-1.61	3.45E-07	1.56E-05	19.9	12.4									6.76E-01	N		
Cbln4	-1.80	3.52E-07	1.59E-05	7.0	3.9							-1.83	cerebellin 4 precursor	7.38E-14	Y		
Meis1	1.58	3.64E-07	1.63E-05	35.9	56.6			1				2.16	Meis homeobox 1	1.13E-20	Y		
Rtkn2	-2.63	3.75E-07	1.68E-05	1.1	0.4								rhotekin 2	2.76E-01	N		
Ralyl	-1.64	3.77E-07	1.68E-05	35.5	21.6			1				-1.71	RALY RNA binding protein-like	1.35E-10	Y		
Gpr165	-1.56	3.84E-07	1.71E-05	69.1	44.2							-1.72		3.20E-12	Y		
Tmem132a	1.56	3.89E-07	1.72E-05	75.5	117.3		1					1.91	transmembrane protein 132A	2.54E-16	Y		
Egr4	2.19	3.99E-07	1.76E-05	1.7	3.7		1					7.48	early growth response 4	3.91E-19	Y		
Nap1l5	-1.54	4.04E-07	1.77E-05	537.1	348.4		1					-1.80	nucleosome assembly protein 1-like 5	7.55E-15	Y		
Pak3	-1.59	4.05E-07	1.77E-05	49.8	31.3				2			-1.78	p21 protein (Cdc42/Rac)-activated kinase 3	2.10E-13	Y		
Hebp2	-1.97	4.15E-07	1.81E-05	5.2	2.6		1		1			-1.72	heme binding protein 2	5.60E-08	Y		
Ppp1r3b	-2.24	4.46E-07	1.94E-05	1.6	0.7							-1.47	protein phosphatase 1, regulatory subunit 3B	2.45E-02	Y		
Tnfaip2	-2.13	4.49E-07	1.94E-05	2.1	1.0		1						tumor necrosis factor, alpha-induced protein 2	9.94E-01	N		
Cfh	-1.64	4.61E-07	1.99E-05	12.5	7.6	1	1						complement factor H	4.41E-01	N		
Amy1a	-2.61	4.75E-07	2.04E-05	2.8	1.1								amylase, alpha 1A (salivary)	6.63E-02	N		
Grm1	1.55	4.98E-07	2.13E-05	29.9	46.4	1	1					2.06	glutamate receptor, metabotropic 1	2.42E-20	Y		
Dpysl4	1.56	5.01E-07	2.14E-05	45.5	71.1							1.48	dihydropyrimidinase-like 4	2.32E-06	Y		
Nrsn2	-1.57	5.27E-07	2.24E-05	108.8	69.5							-1.63	neurensin 2	8.41E-10	Y		
Zfyve28	1.56	5.43E-07	2.30E-05	26.6	41.6		1					2.13	zinc finger, FYVE domain containing 28	3.53E-20	Y		
Ddah1	-1.62	5.60E-07	2.37E-05	24.6	15.1		1	1	1			-1.38	dimethylarginine dimethylaminohydrolase 1	1.78E-04	Y		
Ano4	-1.59	5.67E-07	2.39E-05	21.9	13.7				1			-1.33	anoctamin 4	1.79E-03	Y		
Kcns3	-2.00	5.72E-07	2.40E-05	4.5	2.2		1					-1.47	potassium voltage-gated channel, delayed-rectifier, subfamily S, m	4.20E-03	Y		
Gpc3	-1.92	5.94E-07	2.48E-05	5.8	3.0		1					-1.55	glypican 3	3.95E-06	Y		
Dgkg	1.56	6.05E-07	2.52E-05	35.9	55.8	1						2.16	diacylglycerol kinase, gamma 90kDa	1.26E-21	Y		
Rnf19b	1.62	6.14E-07	2.55E-05	26.3	42.6							1.71	ring finger protein 19B	6.01E-09	Y		
Epha8	1.67	6.20E-07	2.56E-05	7.1	11.9							2.51	EPH receptor A8	3.74E-17	Y		
Crtam	1.74	6.21E-07	2.56E-05	7.4	12.8							4.87	cytotoxic and regulatory T cell molecule	6.93E-31	Y		
Myo5b	-1.69	6.28E-07	2.58E-05	5.3	3.2		1		1			-1.71	myosin VB	4.41E-10	Y		
Evi2a	-1.63	6.35E-07	2.60E-05	36.9	22.7							-1.68	ecotropic viral integration site 2A	3.54E-09	Y		
RGD1312005	-1.56	6.43E-07	2.62E-05	75.6	48.4							-1.59		7.44E-09	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Odz2	-1.56	6.48E-07	2.64E-05	19.6	12.6	1							odz, odd Oz/ten-m homolog 2 (Drosophila)	4.41E-01	N		
Ptprr	1.56	6.56E-07	2.65E-05	26.1	40.7							1.82	protein tyrosine phosphatase, receptor type, R	1.86E-13	Y		
Zdhhc14	1.70	6.57E-07	2.65E-05	12.1	20.6		1					1.68	zinc finger, DHHC-type containing 14	1.05E-06	Y		
Baiap2	1.60	6.74E-07	2.71E-05	26.2	41.9	1	1		1			1.98	BAI1-associated protein 2	7.14E-14	Y		
Col18a1	1.59	7.06E-07	2.83E-05	11.0	17.4							2.66	collagen, type XVIII, alpha 1	2.01E-28	Y		
Dcaf12l1	-1.56	7.20E-07	2.88E-05	39.3	25.2							-1.58	DDB1 and CUL4 associated factor 12-like 1	1.99E-08	Y		
Prrxl1	-5.00	7.25E-07	2.89E-05	0.7	0.1									0.00E+00	N		
Mgst1	-1.66	7.48E-07	2.97E-05	42.9	25.8								microsomal glutathione S-transferase 1	5.90E-01	N		
LOC688553	1.93	7.67E-07	3.04E-05	4.2	8.1							2.02		2.20E-08	Y		
Uchl1	-1.53	7.84E-07	3.10E-05	704.5	461.7	1						-1.73	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	4.92E-13	Y		
Nrip3	-1.57	8.00E-07	3.15E-05	26.4	16.8		1					-1.61	nuclear receptor interacting protein 3	2.38E-09	Y		
Slc22a18	-3.22	8.27E-07	3.24E-05	2.0	0.6			1					solute carrier family 22, member 18	5.49E-01	N		
Vamp1	-1.52	8.37E-07	3.27E-05	377.0	247.7	1	1						vesicle-associated membrane protein 1 (synaptobrevin 1)	1.69E-01	N		
Bmp1	1.57	8.40E-07	3.27E-05	19.2	30.1							1.75	bone morphogenetic protein 1	1.02E-10	Y		
Plcl1	-1.56	8.57E-07	3.33E-05	22.9	14.7			1				-1.61	phospholipase C-like 1	1.68E-09	Y		
Scn1b	1.53	8.81E-07	3.41E-05	163.5	250.5		1		1			2.08	sodium channel, voltage-gated, type I, beta subunit	7.02E-21	Y		
Oprl1	-1.61	8.84E-07	3.41E-05	18.6	11.5							-1.52	opiate receptor-like 1	2.73E-06	Y		
Mog	-1.55	8.95E-07	3.44E-05	98.9	63.8	2			1			-1.51	myelin oligodendrocyte glycoprotein	5.58E-07	Y		
Rab9b	-1.56	9.10E-07	3.48E-05	49.8	32.0							-1.62	RAB9B, member RAS oncogene family	2.82E-09	Y		
Cxcr5	5.69	9.11E-07	3.48E-05	0.3	1.5								chemokine (C-X-C motif) receptor 5	0.00E+00	N		
Slitrk3	-1.60	9.18E-07	3.50E-05	20.1	12.6							-1.35	SLIT and NTRK-like family, member 3	1.12E-03	Y		
Grem2	-1.60	9.47E-07	3.60E-05	16.9	10.5		1					-1.75	gremlin 2	9.87E-12	Y		
Pold2	1.74	9.68E-07	3.67E-05	7.7	13.4	1	1		1			1.27	polymerase (DNA directed), delta 2, accessory subunit	4.97E-02	Y		
Tox2	-1.69	9.91E-07	3.74E-05	14.4	8.5			1				-1.59	TOX high mobility group box family member 2	9.75E-07	Y		
RGD1305627	2.10	1.00E-06	3.75E-05	2.9	6.2							3.20		3.73E-13	Y		
Iqsec3	-1.53	1.00E-06	3.75E-05	35.9	23.4		1					-1.23	IQ motif and Sec7 domain 3	1.92E-02	Y		
Gjc2	-1.61	1.01E-06	3.78E-05	25.5	15.9				1			-1.34	gap junction protein, gamma 2, 47kDa	2.89E-03	Y		
Pgbd5	1.55	1.02E-06	3.80E-05	42.6	66.2		1					2.17	piggyBac transposable element derived 5	4.08E-21	Y		
Dlgap2	-1.65	1.03E-06	3.81E-05	9.5	5.7	2	2	1				-1.30	discs, large (Drosophila) homolog-associated protein 2	1.67E-02	Y		
Fa2h	-1.58	1.03E-06	3.81E-05	31.6	20.0	1			1			-1.42	fatty acid 2-hydroxylase	8.27E-05	Y		
Lpar1	-1.55	1.03E-06	3.81E-05	49.3	31.9							-1.39	lysophosphatidic acid receptor 1	8.02E-05	Y		
Sstr1	-1.66	1.08E-06	3.98E-05	8.7	5.2	1	1		2			-1.55	somatostatin receptor 1	1.13E-06	Y		
Zfhx4	-1.53	1.10E-06	4.04E-05	20.1	13.2	1				-1.21		-1.57	zinc finger homeobox 4	1.49E-08	Y	Y	
Nsdhl	-1.60	1.14E-06	4.16E-05	34.6	21.6	1						-1.43	NAD(P) dependent steroid dehydrogenase-like	6.67E-05	Y		
Mical2	1.53	1.14E-06	4.16E-05	72.6	110.9			1				2.20	microtubule associated monoxygenase, calponin and LIM domain cont	1.74E-23	Y		
Abcc6	-1.89	1.15E-06	4.17E-05	2.1	1.1								ATP-binding cassette, sub-family C (CFTR/MRP), member 6	9.32E-01	N		
RGD1559613	-1.70	1.15E-06	4.17E-05	37.1	21.8							-1.66		1.74E-08	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Msx1	1.77	1.17E-06	4.22E-05	5.9	10.4							2.44	msh homeobox 1	3.28E-15	Y		
Prr18	-1.64	1.17E-06	4.22E-05	40.9	24.9							-1.34	proline rich 18	6.34E-03	Y		
St8sia6	-2.62	1.22E-06	4.38E-05	3.4	1.3							-1.57	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6	5.62E-04	Y		
Dnali1	1.64	1.22E-06	4.38E-05	10.4	17.1							2.13	dynein, axonemal, light intermediate chain 1	3.44E-16	Y		
Synpr	-1.60	1.23E-06	4.40E-05	35.5	22.2		1					-1.71	synaptoporin	9.90E-10	Y		
Cntnap5b	-1.63	1.24E-06	4.42E-05	10.3	6.3							-1.65	contactin associated protein-like 5B	2.20E-08	Y		
Kcnt2	-1.68	1.25E-06	4.44E-05	8.6	5.1							-1.61	potassium channel, subfamily T, member 2	1.63E-06	Y		
RGD1307443	-1.55	1.29E-06	4.57E-05	30.4	19.6							-1.55		6.04E-08	Y		
Gfra1	-1.56	1.30E-06	4.59E-05	27.6	17.7		1		1			-1.56	GDNF family receptor alpha 1	3.34E-08	Y		
Pxn	1.57	1.32E-06	4.65E-05	14.5	22.8				1			1.74	paxillin	8.17E-10	Y		
Itgb4	1.73	1.36E-06	4.77E-05	2.1	3.6				1			2.22	integrin, beta 4	7.55E-12	Y		
Enpp4	-1.54	1.36E-06	4.77E-05	29.1	18.9				1			-1.41	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	4.06E-05	Y		
Dao	1.63	1.41E-06	4.93E-05	14.0	22.9		1					1.86	D-amino-acid oxidase	2.36E-11	Y		
RGD1305679	-2.52	1.43E-06	4.97E-05	4.1	1.6									1.92E-01	N		
Gnas	-1.61	1.43E-06	4.97E-05	42.8	26.5		2		1			-2.03	GNAS complex locus	8.86E-16	Y		
Tiam1	1.52	1.44E-06	4.97E-05	38.8	59.0	1	1	1	2			2.37	T-cell lymphoma invasion and metastasis 1	2.22E-28	Y		
Slc1a3	1.51	1.44E-06	4.97E-05	250.9	379.0		1		3			1.70	solute carrier family 1 (glial high affinity glutamate transporte	5.65E-12	Y		
Bnc2	-1.64	1.46E-06	5.03E-05	8.9	5.5				1				basonuclin 2	7.08E-01	N		
Grm4	1.53	1.49E-06	5.12E-05	45.7	69.9		1					2.98	glutamate receptor, metabotropic 4	1.24E-40	Y		
Kctd16	-1.66	1.53E-06	5.22E-05	22.5	13.6							-1.41	potassium channel tetramerisation domain containing 16	2.29E-03	Y		
Dynlrb2	1.64	1.53E-06	5.22E-05	40.7	66.9				1			1.90	dynein, light chain, roadblock-type 2	1.05E-12	Y		
Kcng4	1.54	1.68E-06	5.72E-05	21.5	33.1							2.15	potassium voltage-gated channel, subfamily G, member 4	1.33E-21	Y		
Aspa	-1.63	1.69E-06	5.74E-05	25.2	15.4	2	1					-1.54	aspartoacylase	5.46E-06	Y		
Fam5c	-1.58	1.75E-06	5.93E-05	21.3	13.5				1			-1.36	family with sequence similarity 5, member C	6.14E-04	Y		
Gp1bb	1.75	1.77E-06	5.98E-05	11.1	19.4							1.49	glycoprotein Ib (platelet), beta polypeptide	9.41E-04	Y		
Camkv	-1.53	1.78E-06	5.99E-05	47.4	31.0	1	1		1			-1.48	CaM kinase-like vesicle-associated	4.63E-06	Y		
Ubqln2	-1.53	1.79E-06	6.01E-05	48.5	31.7								ubiquilin 2	2.43E-01	N		
Lrfn5	-1.56	1.80E-06	6.03E-05	5.8	3.7							-1.51	leucine rich repeat and fibronectin type III domain containing 5 /	5.67E-05	Y		
Ankrd33b	2.22	1.81E-06	6.04E-05	1.5	3.4		1					3.99	ankyrin repeat domain 33B	1.53E-15	Y		
Erbb3	-1.57	1.82E-06	6.06E-05	15.5	9.8							-1.30	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) //	5.72E-03	Y		
Adamts4	-1.65	1.84E-06	6.09E-05	11.0	6.7		1		1			-1.39	ADAM metallopeptidase with thrombospondin type 1 motif, 4	1.45E-03	Y		
Gcnt1	1.54	1.84E-06	6.09E-05	14.6	22.4	1						3.21	glucosaminyl (N-acetyl) transferase 1, core 2	1.40E-41	Y		
Prkg2	-1.76	1.85E-06	6.11E-05	5.7	3.2							-1.51	protein kinase, cGMP-dependent, type II	5.70E-05	Y		
Isoc1	-1.53	1.91E-06	6.29E-05	46.7	30.5		1		1			-1.29	isochorismatase domain containing 1	2.89E-03	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Mx1	2.96	2.07E-06	6.80E-05	0.0	0.0				1				myxovirus (influenza virus) resistance 1, interferon-inducible prote	0.00E+00	N		
Rsph10b	1.61	2.16E-06	7.08E-05	10.3	16.6							1.77		2.27E-10	Y		
P2rx5	-2.08	2.19E-06	7.12E-05	3.1	1.5								purinergic receptor P2X, ligand-gated ion channel, 5	1.61E-01	N		
Car7	1.73	2.19E-06	7.12E-05	7.0	12.2		1					3.05	carbonic anhydrase 7	3.06E-19	Y		
Dlgap1	1.51	2.19E-06	7.12E-05	44.2	66.9							1.87	discs, large (Drosophila) homolog-associated protein 1	3.63E-15	Y		
Lrrc7	-1.55	2.20E-06	7.13E-05	17.4	11.2	1	1					-1.41	leucine rich repeat containing 7	9.68E-05	Y		
Sc4mol	-1.52	2.24E-06	7.24E-05	120.6	79.5	1	1		1			-1.49		7.54E-07	Y		
Lin7a	1.57	2.25E-06	7.25E-05	59.3	92.8	1						2.46	lin-7 homolog A (C. elegans)	1.26E-21	Y		
RGD1310641	1.67	2.26E-06	7.27E-05	7.0	11.7							2.29		2.40E-18	Y		
Oxsm	-1.83	2.32E-06	7.44E-05	4.8	2.6								3-oxoacyl-ACP synthase, mitochondrial	8.83E-01	N		
Ptpro	-1.56	2.34E-06	7.48E-05	16.1	10.4							-1.68	protein tyrosine phosphatase, receptor type, O	1.35E-10	Y		
Nap1l3	-1.54	2.41E-06	7.69E-05	34.5	22.3	1	1					-1.33	nucleosome assembly protein 1-like 3	1.14E-03	Y		
Fam70a	-1.52	2.42E-06	7.70E-05	76.6	50.4							-1.85	family with sequence similarity 70, member A	2.22E-15	Y		
Pid1	-1.71	2.47E-06	7.84E-05	25.9	15.1								phosphotyrosine interaction domain containing 1	7.53E-01	N		
Nefl	-1.50	2.48E-06	7.85E-05	257.8	172.0	1			1				neurofilament, light polypeptide	5.10E-02	N		
Mal	-1.50	2.54E-06	8.02E-05	184.7	123.1	2	1	1	1			-1.44	mal, T-cell differentiation protein	6.95E-06	Y		
Cd164	-1.51	2.59E-06	8.13E-05	77.1	51.0		1					-1.25	CD164 molecule, sialomucin	1.22E-02	Y		
Rnf112	1.50	2.59E-06	8.13E-05	89.8	135.1		1					1.39	ring finger protein 112	8.03E-05	Y		
Nat8l	-1.50	2.64E-06	8.27E-05	123.3	82.2		1						N-acetyltransferase 8-like (GCN5-related, putative)	4.79E-01	N		
Cdh13	-1.52	2.68E-06	8.37E-05	43.2	28.4		1	2				-1.61	cadherin 13, H-cadherin (heart)	1.84E-09	Y		
Lrrc56	1.68	2.69E-06	8.38E-05	6.9	11.5		1					2.26		2.11E-15	Y		
Amigo2	-1.63	2.71E-06	8.42E-05	11.0	6.8		1					-1.65	adhesion molecule with Ig-like domain 2	3.60E-09	Y		
Vstm2b	-1.67	2.73E-06	8.46E-05	12.9	7.8		1					-1.56	V-set and transmembrane domain containing 2B	7.30E-06	Y		
Krt8	1.69	2.77E-06	8.57E-05	8.0	13.6							2.21	keratin 8	4.46E-13	Y		
Acpl2	1.58	2.84E-06	8.76E-05	11.5	18.1		1					1.41	acid phosphatase-like 2	4.85E-04	Y		
Plekhf1	1.63	2.88E-06	8.86E-05	13.2	21.6	2	2				-1.44	1.69	pleckstrin homology domain containing, family F (with FYVE domai	5.75E-07	Y		N
Hrh3	-1.65	2.89E-06	8.87E-05	10.7	6.5	1	1				1.17	-1.41	histamine receptor H3	7.40E-04	Y		N
Cdh19	-1.80	3.30E-06	1.01E-04	5.7	3.2				1			-1.67	cadherin 19, type 2	8.23E-06	Y		
MGC94915	1.58	3.31E-06	1.01E-04	12.2	19.2							1.82		1.85E-11	Y		
Gng13	1.70	3.37E-06	1.02E-04	33.2	56.6							1.62	guanine nucleotide binding protein (G protein), gamma 13	5.85E-05	Y		
Sv2c	-1.52	3.37E-06	1.02E-04	42.9	28.1		1						synaptic vesicle glycoprotein 2C	5.74E-01	N		
Spag8	1.63	3.41E-06	1.03E-04	12.7	20.6							2.13	sperm associated antigen 8	6.05E-15	Y		
RGD1308626	-1.55	3.43E-06	1.04E-04	34.7	22.4							-1.38		3.82E-04	Y		
Gnb3	1.72	3.52E-06	1.06E-04	6.7	11.5							1.81	guanine nucleotide binding protein (G protein), beta polypeptide 3	2.67E-06	Y		
Kcnd1	-1.77	3.54E-06	1.06E-04	4.1	2.3								potassium voltage-gated channel, Shal-related subfamily, member 1	8.88E-01	N		
Sema5a	-1.50	3.63E-06	1.09E-04	30.3	20.3		1	1				-1.62	sema domain, seven thrombospondin repeats (type 1 and type 1-like),	7.77E-10	Y		
A2m	1.53	3.71E-06	1.11E-04	13.7	21.0	1						1.78	alpha-2-macroglobulin	6.73E-12	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Enpp2	-1.49	3.71E-06	1.11E-04	120.5	80.7				2			-1.24	ectonucleotide pyrophosphatase/phosphodiesterase 2	1.50E-02	Y		
Cmip	-1.51	3.73E-06	1.11E-04	73.9	49.1	1						-1.38	c-Maf inducing protein	1.23E-04	Y		
Cntnap5a	-1.56	3.74E-06	1.11E-04	15.8	10.1							-1.56	contactin associated protein-like 5A; similar to contactin associated protein-like 5 isoform 1	2.82E-07	Y		
Fxyd1	1.67	3.76E-06	1.11E-04	26.5	44.4		1					1.84	FXYD domain containing ion transport regulator 1	1.30E-08	Y		
Chrm2	-1.59	3.76E-06	1.11E-04	16.6	10.4							-1.41	cholinergic receptor, muscarinic 2	1.95E-04	Y		
Slc8a2	1.50	3.81E-06	1.12E-04	60.2	90.2	1						2.04	solute carrier family 8 (sodium/calcium exchanger), member 2	6.19E-19	Y		
Kcnh5	-1.54	3.86E-06	1.14E-04	20.9	13.5							-1.40	potassium voltage-gated channel, subfamily H (eag-related), member	2.92E-04	Y		
Lrrc23	1.54	3.96E-06	1.16E-04	30.7	47.3	1	2					1.82	leucine rich repeat containing 23	1.80E-11	Y		
RGD1309453	1.61	4.01E-06	1.17E-04	5.1	8.1							2.34		2.50E-19	Y		
RGD1559747	-1.58	4.02E-06	1.17E-04	14.2	9.0							-1.28		1.30E-02	Y		
Ipcef1	1.65	4.03E-06	1.17E-04	10.0	16.5							2.19	interaction protein for cytohesin exchange factors 1	4.43E-11	Y		
Tmem229a	-1.50	4.07E-06	1.18E-04	46.1	30.7		1					-1.27	transmembrane protein 229A	7.03E-03	Y		
Tsnaxip1	1.73	4.19E-06	1.22E-04	3.8	6.6							2.21	translin-associated factor X interacting protein 1	3.97E-13	Y		
Doc2a	-1.56	4.23E-06	1.22E-04	38.3	24.6							-1.72	double C2-like domains, alpha	3.28E-09	Y		
Npas1	-1.78	4.25E-06	1.22E-04	6.9	3.9							-1.57	neuronal PAS domain protein 1	1.54E-05	Y		
Slc12a4	1.53	4.25E-06	1.22E-04	15.4	23.6							1.75	solute carrier family 12 (potassium/chloride transporters), memb	5.96E-11	Y		
Dab2ip	1.49	4.30E-06	1.24E-04	48.2	71.7							1.62	DAB2 interacting protein	1.27E-09	Y		
Zfp365	-1.54	4.34E-06	1.24E-04	27.7	18.0	2	1					-1.24		2.52E-02	Y		
Pdgfd	1.95	4.35E-06	1.24E-04	6.5	12.7							1.72	platelet derived growth factor D	8.72E-05	Y		
Adamts18	1.59	4.36E-06	1.24E-04	6.1	9.8			1	1			3.70	ADAM metallopeptidase with thrombospondin type 1 motif, 18	2.28E-33	Y		
Nptx1	1.48	4.37E-06	1.24E-04	113.6	168.5		1					2.48	neuronal pentraxin I	3.16E-32	Y		
Dcc	-1.57	4.42E-06	1.25E-04	9.7	6.2	1				1.23		-1.36	deleted in colorectal carcinoma	6.66E-04	Y	N	
B3gnt5	1.66	4.49E-06	1.27E-04	3.2	5.4							1.76	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	1.08E-07	Y		
RGD1560028	-1.96	4.51E-06	1.27E-04	2.6	1.3									3.22E-01	N		
Ust	1.63	4.72E-06	1.33E-04	10.3	16.8			1	1			2.06	uronyl-2-sulfotransferase	1.80E-12	Y		
Chrna4	-1.56	4.73E-06	1.33E-04	25.9	16.6							-1.48	cholinergic receptor, nicotinic, alpha 4 (neuronal)	9.18E-06	Y		
Usp14	-1.49	4.78E-06	1.34E-04	138.9	93.2							-1.44	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase) //	6.53E-06	Y		
Ccdc19	1.72	4.80E-06	1.34E-04	5.8	10.0							2.09	coiled-coil domain containing 19	5.85E-12	Y		
Ly6g6e	1.63	5.02E-06	1.40E-04	18.0	29.2							2.79		6.11E-19	Y		
Lhx1	1.63	5.04E-06	1.40E-04	8.4	13.7							2.95	LIM homeobox 1	3.05E-23	Y		
Samd5	-1.62	5.25E-06	1.46E-04	11.9	7.3							-1.44	sterile alpha motif domain containing 5	1.50E-04	Y		
Mal2	-1.52	5.28E-06	1.46E-04	36.5	24.1							-1.84	mal, T-cell differentiation protein 2 (gene/pseudogene)	4.92E-15	Y		
Bcat1	-1.47	5.37E-06	1.49E-04	806.0	547.8							-1.47	branched chain amino-acid transaminase 1, cytosolic	7.09E-07	Y		
Dleu7	-1.71	5.48E-06	1.51E-04	10.4	6.1							-1.94	deleted in lymphocytic leukemia, 7	6.04E-12	Y		
Hopx	1.72	5.49E-06	1.51E-04	9.4	16.2		1					1.75	HOP homeobox	6.04E-06	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Cdh15	1.58	5.53E-06	1.52E-04	9.6	15.1							2.54	cadherin 15, type 1, M-cadherin (myotubule)	7.51E-20	Y		
Ccdc40	1.55	5.55E-06	1.52E-04	7.8	12.1							2.08	coiled-coil domain containing 40	4.94E-17	Y		
Pde8a	-1.63	5.59E-06	1.53E-04	10.8	6.6				1			-1.60	phosphodiesterase 8A	1.89E-06	Y		
Slc7a3	-1.55	5.60E-06	1.53E-04	27.4	17.7		1					-1.64	solute carrier family 7 (cationic amino acid transporter, y+ syst	1.21E-08	Y		
Adam11	1.49	5.61E-06	1.53E-04	59.7	89.0		1					1.66	ADAM metallopeptidase domain 11	3.36E-10	Y		
Odz4	-1.49	5.68E-06	1.54E-04	23.2	15.5								odz, odd Oz/ten-m homolog 4 (Drosophila)	6.33E-01	N		
RGD1563714	1.94	5.92E-06	1.60E-04	2.4	4.6							2.14		1.67E-08	Y		
Suox	1.58	5.92E-06	1.60E-04	11.2	17.7		1						sulfite oxidase	7.77E-01	N		
Nyx	1.77	6.13E-06	1.66E-04	3.6	6.3							2.20	nyctalopin	4.14E-08	Y		
Calml4	2.04	6.15E-06	1.66E-04	3.8	7.7							2.51	calmodulin-like 4	6.36E-11	Y		
Ndst3	1.49	6.37E-06	1.71E-04	50.2	74.7							2.91	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	1.13E-39	Y		
Timp2	-1.48	6.38E-06	1.71E-04	195.0	131.8	1			3			-1.43	TIMP metallopeptidase inhibitor 2	8.17E-06	Y		
Enpp6	-1.76	6.45E-06	1.73E-04	7.8	4.4			2				-1.41	ectonucleotide pyrophosphatase/phosphodiesterase 6	4.86E-03	Y		
RGD1304810	1.51	6.49E-06	1.73E-04	26.9	40.7							2.51		8.06E-27	Y		
Ier2	1.76	6.54E-06	1.74E-04	5.3	9.3	4	1			1.70	1.26	2.92	immediate early response 2	9.21E-18	Y	Y	Y
Cep76	1.50	6.59E-06	1.75E-04	31.5	47.3							2.65	centrosomal protein 76kDa	8.02E-33	Y		
Cacna1g	1.48	6.89E-06	1.83E-04	35.7	52.8							1.76	calcium channel, voltage-dependent, T type, alpha 1G subunit	6.24E-13	Y		
Kcnk12	1.64	6.93E-06	1.83E-04	7.4	12.2							3.06	potassium channel, subfamily K, member 12	2.47E-18	Y		
Klhl14	-1.83	6.95E-06	1.84E-04	2.7	1.5							-1.71	kelch-like 14 (Drosophila)	2.25E-04	Y		
Oprk1	-1.77	7.41E-06	1.95E-04	9.6	5.4	2	1					-1.38	opioid receptor, kappa 1	1.33E-02	Y		
Ttll9	1.60	7.59E-06	1.99E-04	11.4	18.2							1.77	tubulin tyrosine ligase-like family, member 9	3.03E-09	Y		
Scn3b	-1.48	7.59E-06	1.99E-04	63.7	43.1		3					-1.63	sodium channel, voltage-gated, type III, beta subunit	3.19E-10	Y		
Zic3	2.08	7.69E-06	2.01E-04	1.4	2.9		2					3.16	Zic family member 3	2.11E-09	Y		
RGD1565512	1.58	7.78E-06	2.03E-04	7.5	11.9							2.13		3.88E-16	Y		
Fbxo23	-1.63	7.86E-06	2.05E-04	15.5	9.5		1					-1.50		1.72E-05	Y		
Syt17	-1.58	7.89E-06	2.05E-04	13.8	8.8		1					-1.35	synaptotagmin XVII	1.22E-03	Y		
Olig1	-1.50	8.05E-06	2.09E-04	55.0	36.7	2						-1.30	oligodendrocyte transcription factor 1	3.54E-03	Y		
Pygl	-1.88	8.26E-06	2.14E-04	3.4	1.8		3						phosphorylase, glycogen, liver	2.15E-01	N		
Lhfp	1.49	8.27E-06	2.14E-04	49.1	73.1	1	1				-1.16	1.84	lipoma HMGIC fusion partner	7.80E-14	Y		N
Plekhh3	1.59	8.35E-06	2.15E-04	6.7	10.6							1.97	pleckstrin homology domain containing, family H (with MyTH4 doma	3.48E-10	Y		
Fank1	1.83	8.42E-06	2.17E-04	4.4	8.1			1				1.97	fibronectin type III and ankyrin repeat domains 1	7.82E-08	Y		
RGD1308226	1.63	8.46E-06	2.17E-04	5.0	8.1							1.88		5.47E-11	Y		
Slc9a3	1.62	8.64E-06	2.21E-04	2.9	4.7	1						3.80	solute carrier family 9, subfamily A (NHE3, cation proton antiporte	2.22E-28	Y		
Ptpn5	-1.49	8.78E-06	2.25E-04	44.9	30.1	1	1					-1.32	protein tyrosine phosphatase, non-receptor type 5 (striatum-enrich	1.55E-03	Y		
Dpyd	-1.61	9.04E-06	2.30E-04	6.8	4.2		2		1			-1.41	dihydropyrimidine dehydrogenase	5.72E-04	Y		
Camkk1	-1.48	9.04E-06	2.30E-04	48.5	32.7							-1.47	calcium/calmodulin-dependent protein kinase kinase 1, alpha	4.10E-06	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
RGD1561849	-1.52	9.15E-06	2.33E-04	20.9	13.8							-1.28		6.38E-03	Y		
Htr2a	-1.86	9.27E-06	2.35E-04	6.2	3.3	1	1					-1.40	5-hydroxytryptamine (serotonin) receptor 2A, G protein-coupled	5.20E-03	Y		
Usp43	1.57	9.29E-06	2.35E-04	1.3	2.1			1				2.16	ubiquitin specific peptidase 43	1.59E-03	Y		
Ccdc114	1.58	9.31E-06	2.35E-04	8.2	13.0							2.07	coiled-coil domain containing 114	5.51E-15	Y		
Zfp219	1.51	9.37E-06	2.36E-04	18.5	28.0							1.58		2.33E-07	Y		
Kif15	2.49	9.53E-06	2.39E-04	0.4	0.9	2	2			1.39	1.45	1.63	kinesin family member 15	2.68E-02	Y	Y	Y
Wfdc1	1.56	9.53E-06	2.39E-04	24.5	38.3	1		1				1.83	WAP four-disulfide core domain 1	1.55E-10	Y		
Pou3f3	-1.52	9.57E-06	2.40E-04	24.8	16.3							-1.34	POU class 3 homeobox 3	1.40E-03	Y		
Col6a2	1.65	9.66E-06	2.41E-04	3.5	5.8							1.48	collagen, type VI, alpha 2	3.69E-04	Y		
Dok6	-1.54	9.81E-06	2.45E-04	36.0	23.4							-1.35	docking protein 6	1.01E-03	Y		
Spata18	1.54	9.92E-06	2.47E-04	16.4	25.2							2.13	spermatogenesis associated 18	2.35E-17	Y		
Ptpn22	1.89	9.93E-06	2.47E-04	1.7	3.1							3.62	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	3.00E-11	Y		
Ap1s2	-1.50	1.04E-05	2.57E-04	58.0	38.8							-1.41	adaptor-related protein complex 1, sigma 2 subunit	4.57E-05	Y		
Scoc	-1.47	1.04E-05	2.57E-04	164.1	111.7							-1.36	short coiled-coil protein	1.57E-04	Y		
Pde1b	-1.48	1.05E-05	2.59E-04	75.1	50.6							-1.23	phosphodiesterase 1B, calmodulin-dependent	2.45E-02	Y		
LOC499980	1.62	1.06E-05	2.61E-04	5.1	8.3							1.96		4.73E-12	Y		
Pltp	1.47	1.06E-05	2.61E-04	73.0	107.7							1.71	phospholipid transfer protein	1.51E-11	Y		
Adcy7	-1.54	1.07E-05	2.63E-04	12.6	8.2				1			-1.70	adenylate cyclase 7	5.19E-10	Y		
LOC681766	2.37	1.08E-05	2.65E-04	2.9	6.9							1.90		2.44E-03	Y		
Tekt4	1.68	1.09E-05	2.66E-04	6.6	11.0	1						2.02	tektin 4	7.29E-11	Y		
Pik3c2g	1.57	1.13E-05	2.76E-04	3.8	5.9							1.78	phosphoinositide-3-kinase, class 2, gamma polypeptide	2.12E-07	Y		
Dcun1d4	-1.47	1.16E-05	2.82E-04	57.7	39.3		3					-1.32	DCN1, defective in cullin neddylation 1, domain containing 4 (S.	9.91E-04	Y		
Il22ra2	-1.76	1.17E-05	2.84E-04	5.0	2.8		2					-1.34	interleukin 22 receptor, alpha 2	1.97E-02	Y		
Cdon	1.48	1.18E-05	2.86E-04	22.3	32.9				1			2.22	Cdon homolog (mouse)	3.75E-22	Y		
Stac2	-1.58	1.23E-05	2.98E-04	11.2	7.1								SH3 and cysteine rich domain 2	7.40E-01	N		
Wnt16	1.99	1.24E-05	2.99E-04	2.0	4.0							2.33	wingless-type MMTV integration site family, member 16	9.47E-05	Y		
Brpf1	1.48	1.25E-05	3.01E-04	23.0	34.0							1.78	bromodomain and PHD finger containing, 1	2.28E-12	Y		
Slc13a4	1.62	1.26E-05	3.03E-04	7.0	11.4							2.27	solute carrier family 13 (sodium/sulfate symporters), member 4 /	6.17E-17	Y		
Arl4d	1.87	1.28E-05	3.07E-04	3.3	6.3		1					1.58	ADP-ribosylation factor-like 4D	5.08E-03	Y		
Eno4	1.65	1.28E-05	3.07E-04	4.9	8.1							1.63	enolase family member 4	3.95E-06	Y		
Pdyn	-1.64	1.29E-05	3.08E-04	8.4	5.1		1		1			-1.54	prodynorphin	2.98E-04	Y		
Zic5	1.62	1.29E-05	3.08E-04	6.9	11.1							3.19	Zic family member 5	9.67E-23	Y		
Spata2	1.49	1.34E-05	3.19E-04	26.5	39.5							1.52	spermatogenesis associated 2	1.82E-06	Y		
Adhfe1	-1.54	1.35E-05	3.20E-04	23.9	15.5				1			-1.42	alcohol dehydrogenase, iron containing, 1	1.47E-04	Y		
Kcnh7	-1.51	1.35E-05	3.20E-04	19.4	12.9								potassium voltage-gated channel, subfamily H (eag-related), member	6.20E-01	N		
Cnksr2	1.46	1.36E-05	3.22E-04	37.9	55.5		1		1			2.04	connector enhancer of kinase suppressor of Ras 2	2.94E-19	Y		
Stk17b	1.54	1.39E-05	3.28E-04	12.5	19.2							1.92	serine/threonine kinase 17b	7.55E-12	Y		
Slit2	-1.52	1.39E-05	3.28E-04	8.5	5.6		2		2			-1.35	slit homolog 2 (Drosophila)	4.43E-04	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Tmeff1	-1.50	1.44E-05	3.39E-04	32.8	21.9	1			1			-1.73	transmembrane protein with EGF-like and two follistatin-like doma	2.11E-11	Y		
Xrcc1	1.51	1.48E-05	3.47E-04	19.6	29.6							1.41	X-ray repair complementing defective repair in Chinese hamster cells	3.14E-04	Y		
Wbscr17	1.48	1.48E-05	3.47E-04	43.9	65.1							1.46	Williams-Beuren syndrome chromosome region 17	1.57E-05	Y		
Shank3	1.46	1.49E-05	3.49E-04	30.8	44.9		1					1.82	SH3 and multiple ankyrin repeat domains 3	4.34E-14	Y		
Hmgcs1	-1.45	1.51E-05	3.53E-04	154.6	106.6	1						-1.54	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble)	3.95E-08	Y		
LOC100158225	1.79	1.52E-05	3.54E-04	2.9	5.2							1.83		2.90E-05	Y		
Dcx	-1.49	1.58E-05	3.68E-04	9.4	6.3	1	1					-1.50	doublecortin	1.21E-06	Y		
LOC654482	1.61	1.63E-05	3.79E-04	11.2	18.0							1.64		8.07E-07	Y		
Mras	-1.47	1.64E-05	3.80E-04	46.5	31.7		2					-1.31	muscle RAS oncogene homolog	1.97E-03	Y		
T	2.14	1.65E-05	3.82E-04	1.2	2.6							1.85	T, brachyury homolog (mouse)	7.32E-04	Y		
Acat3	-1.53	1.68E-05	3.88E-04	22.9	15.0							-1.44		3.84E-05	Y		
Slc7a8	1.48	1.71E-05	3.94E-04	17.4	25.7								solute carrier family 7 (amino acid transporter light chain, L sy	4.67E-01	N		
Gpd1	-1.45	1.72E-05	3.96E-04	94.1	64.7	4	2					-1.22	glycerol-3-phosphate dehydrogenase 1 (soluble)	2.64E-02	Y		
Vkorc1l1	-1.57	1.74E-05	3.99E-04	30.8	19.7	1						-1.37	vitamin K epoxide reductase complex, subunit 1-like 1	9.00E-04	Y		
Pcdh7	-1.46	1.74E-05	3.99E-04	43.9	30.0							-1.37	protocadherin 7	2.30E-04	Y		
Cpne4	-1.64	1.75E-05	4.00E-04	4.7	2.9							-1.55	copine IV	7.23E-06	Y		
Pnma3	-1.50	1.75E-05	4.00E-04	24.4	16.3							-1.63	paraneoplastic Ma antigen 3	4.56E-09	Y		
Ppm1j	1.80	1.82E-05	4.15E-04	3.2	5.8							2.14	protein phosphatase, Mg2+/Mn2+ dependent, 1J	3.77E-07	Y		
Eif5a2	-1.46	1.84E-05	4.19E-04	44.2	30.3		1					-1.26	eukaryotic translation initiation factor 5A2	6.82E-03	Y		
Per1	1.46	1.86E-05	4.22E-04	39.4	57.4		2					1.51	period homolog 1 (Drosophila)	4.99E-07	Y		
Rgs17	-1.47	1.88E-05	4.25E-04	51.6	35.2		3					-1.62	regulator of G-protein signaling 17	3.58E-09	Y		
Cx3cl1	-1.46	1.88E-05	4.25E-04	71.2	48.9		1					-1.33	chemokine (C-X3-C motif) ligand 1	8.26E-04	Y		
Wnk3	-1.50	1.91E-05	4.31E-04	13.7	9.2							-1.48	WNK lysine deficient protein kinase 3	4.41E-06	Y		
Mns1	1.60	1.97E-05	4.44E-04	8.1	13.0							1.96	meiosis-specific nuclear structural 1	4.25E-12	Y		
Mag	-1.44	2.03E-05	4.57E-04	169.9	117.7	1	1	1				-1.35	myelin associated glycoprotein	3.14E-04	Y		
Olfm2	-1.48	2.09E-05	4.68E-04	45.4	30.7							-1.59	olfactomedin 2	1.53E-08	Y		
Camk4	1.46	2.09E-05	4.68E-04	74.6	108.8	2	1					3.00	calcium/calmodulin-dependent protein kinase IV	2.66E-41	Y		
Hmgcr	-1.47	2.14E-05	4.79E-04	28.2	19.2	2	1		2			-1.21	3-hydroxy-3-methylglutaryl-CoA reductase	3.75E-02	Y		
Cerk	1.45	2.21E-05	4.93E-04	39.4	57.2		2					2.20	ceramide kinase	3.14E-23	Y		
Arnt2	-1.45	2.22E-05	4.95E-04	48.7	33.7							-1.30	aryl-hydrocarbon receptor nuclear translocator 2	2.15E-03	Y		
Hspa2	1.58	2.23E-05	4.96E-04	6.7	10.6		2		1				heat shock 70kDa protein 2	9.35E-02	N		
Phka2	1.54	2.25E-05	5.00E-04	6.5	10.0							1.59	phosphorylase kinase, alpha 2 (liver)	1.18E-06	Y		
Rin1	1.72	2.29E-05	5.07E-04	2.9	4.9				1			2.17	Ras and Rab interactor 1	2.95E-09	Y		
Pnma2	-1.46	2.29E-05	5.07E-04	39.4	26.9							-1.65	paraneoplastic Ma antigen 2	4.60E-10	Y		
Akt2	1.47	2.34E-05	5.17E-04	34.4	50.6							1.75	v-akt murine thymoma viral oncogene homolog 2	4.48E-11	Y		
Sstr3	1.51	2.37E-05	5.22E-04	8.8	13.2							3.18	somatostatin receptor 3	1.96E-30	Y		
Plxdc1	1.54	2.42E-05	5.32E-04	7.9	12.2				1			2.22	plexin domain containing 1	8.00E-16	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Tpd52l1	1.50	2.45E-05	5.38E-04	28.2	42.5		1	1				1.38	tumor protein D52-like 1	1.06E-03	Y		
Cadm3	1.44	2.52E-05	5.52E-04	212.8	306.7							1.25	cell adhesion molecule 3	1.22E-02	Y		
Cryab	-1.50	2.54E-05	5.56E-04	88.5	59.1		2		3				crystallin, alpha B	2.44E-01	N		
Bmp6	1.58	2.66E-05	5.81E-04	11.6	18.3							2.21	bone morphogenetic protein 6	1.53E-15	Y		
Ugt1a5	-1.80	2.70E-05	5.89E-04	4.1	2.3									4.50E-01	N		
RGD1310371	1.60	2.75E-05	5.99E-04	9.8	15.6							2.12		5.36E-14	Y		
Wisp1	2.91	2.81E-05	6.09E-04	0.4	1.3								WNT1 inducible signaling pathway protein 1	0.00E+00	N		
Rimbp2	-1.47	2.81E-05	6.09E-04	13.3	9.0							-1.71	RIMS binding protein 2	1.16E-11	Y		
Aurkb	1.74	2.86E-05	6.19E-04	3.6	6.2							1.73	aurora kinase B	1.41E-05	Y		
Pip5k1c	1.44	2.88E-05	6.22E-04	58.2	83.7							1.38	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	1.01E-04	Y		
Ugt1a3	-1.81	2.96E-05	6.39E-04	4.0	2.2									4.94E-01	N		
Mep1a	3.09	3.00E-05	6.46E-04	0.2	0.7							3.24	meprin A, alpha (PABA peptide hydrolase)	4.69E-05	Y		
Cplx2	1.44	3.07E-05	6.60E-04	153.1	221.2								complexin 2	8.35E-01	N		
Hist3h2ba	1.58	3.15E-05	6.76E-04	23.1	36.5								histone cluster 3, H2ba, pseudogene	7.52E-02	N		
Reep6	-2.06	3.17E-05	6.79E-04	2.5	1.2								receptor accessory protein 6	1.07E-01	N		
Ldb2	-1.53	3.18E-05	6.80E-04	18.6	12.2		1						LIM domain binding 2	5.42E-02	N		
Tmem63a	-1.54	3.23E-05	6.88E-04	9.7	6.3		1					-1.35	transmembrane protein 63A	4.94E-03	Y		
Cbfb	-1.52	3.23E-05	6.88E-04	13.4	8.8								core-binding factor, beta subunit	6.40E-02	N		
Sod2	-1.43	3.30E-05	7.02E-04	142.4	99.2	1	1		1			-1.38	superoxide dismutase 2, mitochondrial	7.17E-05	Y		
Rasgrf1	-1.43	3.32E-05	7.05E-04	134.2	94.1							-1.37	Ras protein-specific guanine nucleotide-releasing factor 1	1.07E-04	Y		
Sfmbt2	-1.82	3.35E-05	7.10E-04	3.2	1.8							-1.55	Scm-like with four mbt domains 2	1.15E-03	Y		
C4bpb	-2.36	3.38E-05	7.14E-04	3.2	1.4				2				complement component 4 binding protein, beta	3.30E-01	N		
Nipa1	-1.47	3.38E-05	7.14E-04	51.0	34.8				1			-1.43	non imprinted in Prader-Willi/Angelman syndrome 1	2.64E-05	Y		
Pip4k2a	-1.46	3.45E-05	7.27E-04	38.3	26.3		1		2				phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	5.90E-02	N		
LOC363267	1.66	3.51E-05	7.39E-04	5.2	8.7							2.09		5.63E-12	Y		
Lats2	1.45	3.53E-05	7.42E-04	19.7	28.6		1					1.58	LATS, large tumor suppressor, homolog 2 (Drosophila)	3.53E-08	Y		
Ghr	-1.58	3.56E-05	7.47E-04	7.8	4.9								growth hormone receptor	9.34E-01	N		
Tgfa	-1.52	3.62E-05	7.58E-04	8.8	5.8	2						-1.31	transforming growth factor, alpha	7.24E-03	Y		
Bcas1	-1.44	3.63E-05	7.59E-04	85.8	59.8		2					-1.36	breast carcinoma amplified sequence 1	1.93E-04	Y		
Sptb	1.43	3.65E-05	7.62E-04	56.5	80.7							2.05	spectrin, beta, erythrocytic	2.50E-20	Y		
Slc22a6	1.73	3.67E-05	7.63E-04	3.1	5.4							1.98	solute carrier family 22 (organic anion transporter), member 6 /	1.85E-08	Y		
T2	1.65	3.67E-05	7.63E-04	6.3	10.5							1.99		1.55E-09	Y		
Plekho1	1.45	3.68E-05	7.64E-04	52.8	76.8		1		2			1.94	pleckstrin homology domain containing, family O member 1	5.63E-15	Y		
Lipa	-1.46	3.71E-05	7.69E-04	31.3	21.5				1			-1.51		5.69E-07	Y		
Slc6a20	1.52	3.73E-05	7.72E-04	12.8	19.4		1					2.23	solute carrier family 6 (proline IMINO transporter), member 20	1.78E-18	Y		
Hdc	1.96	3.80E-05	7.85E-04	1.3	2.6							1.74	histidine decarboxylase	8.94E-04	Y		
Slc16a11	1.61	3.83E-05	7.88E-04	6.4	10.3							1.85	solute carrier family 16, member 11 (monocarboxylic acid transp	1.36E-06	Y		
Rnf148	1.59	3.83E-05	7.88E-04	11.7	18.5							2.86	ring finger protein 148	4.95E-16	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Epha4	-1.45	3.95E-05	8.12E-04	18.5	12.8		1						EPH receptor A4	4.52E-01	N		
Slc6a11	-1.42	3.98E-05	8.16E-04	260.4	183.0			1					solute carrier family 6 (neurotransmitter transporter, GA	5.28E-02	N		
P2rx2	-2.09	3.99E-05	8.17E-04	2.6	1.3							-1.85	purinergic receptor P2X, ligand-gated ion channel, 2	3.05E-07	Y		
Shisa7	-1.47	4.01E-05	8.20E-04	12.0	8.2		1					-1.45	shisa homolog 7 (Xenopus laevis)	1.92E-05	Y		
Egln3	-1.56	4.02E-05	8.20E-04	9.4	6.0	1	1		1			-1.38	egl nine homolog 3 (C. elegans)	2.51E-03	Y		
Shisa6	1.53	4.04E-05	8.23E-04	13.9	21.2							1.80	shisa homolog 6 (Xenopus laevis)	3.86E-09	Y		
Sgcz	-1.79	4.09E-05	8.32E-04	7.7	4.3							-1.49	sarcoglycan, zeta	4.40E-03	Y		
Zic4	1.61	4.10E-05	8.32E-04	5.6	8.9		1					2.61	Zic family member 4	2.49E-13	Y		
Sh3kbp1	-1.49	4.11E-05	8.32E-04	15.8	10.6	1			1			-1.53	SH3-domain kinase binding protein 1	9.37E-07	Y		
Mpped1	-1.47	4.11E-05	8.32E-04	21.3	14.5							-1.62	metallophosphoesterase domain containing 1	5.60E-08	Y		
Cobl	-1.49	4.17E-05	8.42E-04	10.9	7.3		1					-1.69	cordon-bleu homolog (mouse)	3.58E-10	Y		
Pax6	1.47	4.18E-05	8.42E-04	22.5	33.2							2.19	paired box 6	8.56E-18	Y		
Gabra3	-1.53	4.19E-05	8.42E-04	25.8	16.9							-1.69	gamma-aminobutyric acid (GABA) A receptor, alpha 3	3.65E-09	Y		
Osbp2	1.45	4.19E-05	8.42E-04	19.5	28.3							1.81	oxysterol binding protein 2	2.30E-12	Y		
Nrsn1	-1.45	4.23E-05	8.49E-04	83.4	57.5							-1.39	neurensin 1	9.45E-05	Y		
Ppfia4	1.43	4.24E-05	8.50E-04	42.8	61.0							1.56	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF	3.74E-08	Y		
RGD1562284	-1.61	4.28E-05	8.56E-04	19.5	12.1							-1.77		3.12E-09	Y		
Vwa5b2	-1.46	4.33E-05	8.63E-04	20.5	14.1							-1.21	von Willebrand factor A domain containing 5B2	4.72E-02	Y		
Cd99l2	-1.43	4.33E-05	8.63E-04	58.4	40.8				1			-1.45	CD99 molecule-like 2	3.91E-06	Y		
Sptbn2	1.42	4.39E-05	8.74E-04	80.5	114.3		1		2			1.71	spectrin, beta, non-erythrocytic 2	3.33E-12	Y		
Wdr86	4.04	4.42E-05	8.78E-04	0.2	0.9							2.46	WD repeat domain 86	1.17E-03	Y		
Rnd2	-1.43	4.45E-05	8.83E-04	134.2	93.5				1				Rho family GTPase 2	6.09E-02	N		
Slc9a3r1	1.49	4.50E-05	8.91E-04	23.1	34.4	1	2					2.08	solute carrier family 9, subfamily A (NHE3, cation proton antip	3.66E-15	Y		
Bcar1	1.44	4.53E-05	8.96E-04	32.3	46.4							1.67	breast cancer anti-estrogen resistance 1	3.48E-10	Y		
Neurl	1.50	4.54E-05	8.96E-04	33.3	50.1							1.43	neuralized homolog (Drosophila)	3.60E-04	Y		
Stk10	1.54	4.62E-05	9.11E-04	3.7	5.7							1.59	serine/threonine kinase 10	9.63E-06	Y		
Pih1d2	1.61	4.64E-05	9.13E-04	8.7	13.9							1.90	PIH1 domain containing 2	2.92E-10	Y		
Ppp2r2b	-1.45	4.71E-05	9.25E-04	41.0	28.3			1				-1.47	protein phosphatase 2, regulatory subunit B, beta	2.88E-06	Y		
Tnni3	1.81	4.80E-05	9.42E-04	5.6	10.2							2.20	troponin I type 3 (cardiac)	2.91E-08	Y		
Slc26a3	2.89	4.81E-05	9.42E-04	0.3	0.8			1				1.79	solute carrier family 26, member 3	2.44E-02	Y		
Chst7	1.55	4.93E-05	9.64E-04	6.9	10.7							2.39	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	3.74E-14	Y		
Slc2a10	1.58	5.01E-05	9.78E-04	3.6	5.7							1.70	solute carrier family 2 (facilitated glucose transporter), membe	7.27E-07	Y		
Ugt1a8	-1.76	5.03E-05	9.80E-04	4.2	2.4									3.81E-01	N		
Tagln	1.60	5.09E-05	9.90E-04	11.0	17.5		3					1.28	transgelin	3.58E-02	Y		
Rab26	-1.49	5.18E-05	1.01E-03	43.1	28.9							-1.57	RAB26, member RAS oncogene family	4.27E-07	Y		
Lrrc50	1.60	5.22E-05	1.01E-03	5.0	8.0							2.23		1.93E-13	Y		
Dhcr7	-1.49	5.24E-05	1.01E-03	18.6	12.5	1						-1.39	7-dehydrocholesterol reductase	4.07E-04	Y		
Hs3st2	-1.71	5.28E-05	1.02E-03	4.8	2.8	1						-1.79	heparan sulfate (glucosamine) 3-O-sulfotransferase 2	1.25E-08	Y		
Slc35f1	-1.45	5.31E-05	1.03E-03	23.8	16.5							-1.47	solute carrier family 35, member F1	4.52E-06	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Nfix	1.45	5.37E-05	1.03E-03	45.0	65.3		1					2.33	nuclear factor I/X (CCAAT-binding transcription factor)	5.78E-23	Y		
Slc5a11	-1.56	5.46E-05	1.05E-03	11.4	7.3		1					-1.29	solute carrier family 5 (sodium/glucose cotransporter), member 1	2.51E-02	Y		
Gpr63	1.50	5.47E-05	1.05E-03	11.4	17.0							2.67	G protein-coupled receptor 63	1.30E-23	Y		
Stk35	1.48	5.50E-05	1.06E-03	10.3	15.2							1.31	serine/threonine kinase 35	6.92E-03	Y		
Mlf1	1.51	5.55E-05	1.06E-03	21.6	32.5							1.69	myeloid leukemia factor 1	4.97E-09	Y		
Cacna1h	-1.46	5.55E-05	1.06E-03	9.1	6.2	1						-1.39	calcium channel, voltage-dependent, T type, alpha 1H subu	2.46E-04	Y		
Rora	1.44	5.56E-05	1.06E-03	50.1	72.1							1.89	RAR-related orphan receptor A	2.50E-14	Y		
Sh3bgrl	-1.43	5.67E-05	1.08E-03	53.4	37.3							-1.26	SH3 domain binding glutamic acid-rich protein like	7.88E-03	Y		
Snrnp70	1.42	5.71E-05	1.09E-03	171.0	242.7							1.33	small nuclear ribonucleoprotein 70kDa (U1)	8.19E-04	Y		
Pld5	1.49	5.77E-05	1.09E-03	17.6	26.1							1.84	phospholipase D family, member 5	9.38E-11	Y		
Cntnap5	-1.46	5.77E-05	1.09E-03	17.1	11.7							-1.47	contactin associated protein-like 5	6.61E-06	Y		
Tmem109	1.45	5.78E-05	1.09E-03	32.2	46.7				1			1.58	transmembrane protein 109	2.39E-07	Y		
Nrep	1.42	5.81E-05	1.10E-03	366.8	522.0		1					2.99	neuronal regeneration related protein homolog (rat)	1.54E-42	Y		
Krt1	-2.47	5.86E-05	1.11E-03	1.2	0.5			1				-2.52	keratin 1	9.12E-04	Y		
Cckbr	-1.77	5.88E-05	1.11E-03	4.2	2.4							-1.88	cholecystokinin B receptor	2.83E-05	Y		
Mir124-1	1.51	5.96E-05	1.12E-03	238.1	360.5							2.08	microRNA 124-1	5.27E-12	Y		
Glra3	-1.61	6.00E-05	1.13E-03	4.1	2.6							-1.56	glycine receptor, alpha 3	4.53E-03	Y		
Nr5a2	-3.28	6.07E-05	1.14E-03	0.9	0.3				1				nuclear receptor subfamily 5, group A, member 2	0.00E+00	N		
Plekhh1	-1.42	6.07E-05	1.14E-03	32.3	22.7							-1.37	pleckstrin homology domain containing, family H (with MyTH4 doma	1.88E-04	Y		
Spata2L	1.50	6.22E-05	1.16E-03	8.7	13.0		1					1.42	spermatogenesis associated 2-like	6.47E-04	Y		
Lcat	1.48	6.25E-05	1.17E-03	25.2	37.2							2.37	lecithin-cholesterol acyltransferase	2.00E-22	Y		
Ccng2	1.43	6.26E-05	1.17E-03	40.8	58.4							2.58	cyclin G2	8.20E-30	Y		
Emid1	1.57	6.34E-05	1.18E-03	7.8	12.2		1					2.46	EMI domain containing 1	6.07E-15	Y		
Exoc3l	1.59	6.35E-05	1.18E-03	4.5	7.2							2.06	exocyst complex component 3-like	5.85E-09	Y		
Galnt9	1.43	6.43E-05	1.19E-03	27.6	39.6							1.62	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosam	2.35E-08	Y		
Zdhhc20	-1.43	6.47E-05	1.20E-03	64.4	44.9				1			-1.43	zinc finger, DHHC-type containing 20	1.95E-05	Y		
Nsun7	-1.90	6.50E-05	1.20E-03	4.4	2.3							-1.45	NOP2/Sun domain family, member 7	1.77E-02	Y		
Als2	1.41	6.66E-05	1.23E-03	73.8	104.1							1.87	amyotrophic lateral sclerosis 2 (juvenile)	1.05E-15	Y		
Phf21b	1.64	6.68E-05	1.23E-03	4.1	6.7							3.15	PHD finger protein 21B	2.70E-16	Y		
Pkp1	-2.09	6.77E-05	1.25E-03	1.0	0.5								plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	9.77E-01	N		
Pqcp	1.47	6.84E-05	1.26E-03	14.9	21.9							1.27		1.61E-02	Y		
Hspa12a	-1.41	6.86E-05	1.26E-03	56.5	40.0	1		1			1.12	-1.22	heat shock 70kDa protein 12A	2.33E-02	Y		N
Vwc2l	-1.64	6.87E-05	1.26E-03	10.0	6.1							-1.88	von Willebrand factor C domain containing protein 2-like	2.84E-09	Y		
Aebp1	1.49	6.87E-05	1.26E-03	6.6	9.9							2.23	AE binding protein 1	1.86E-18	Y		
Nrgn	-1.47	6.90E-05	1.26E-03	42.5	28.9	1	1		1				neurogranin (protein kinase C substrate, RC3)	5.71E-01	N		
Sh3bgrl3	-1.51	6.94E-05	1.27E-03	44.7	29.7		1					-1.57	SH3 domain binding glutamic acid-rich protein like 3	1.52E-07	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Agtr1a	-2.62	7.11E-05	1.30E-03	1.2	0.4	1						-1.81	angiotensin II receptor, type 1a	3.26E-03	Y		
Ldlr	-1.45	7.12E-05	1.30E-03	25.2	17.4							-1.44	low density lipoprotein receptor	2.37E-05	Y		
Cpt1b	1.53	7.20E-05	1.31E-03	6.2	9.4				1			2.14	carnitine palmitoyltransferase 1b, muscle	4.07E-12	Y		
Dpy19l1	-1.42	7.22E-05	1.31E-03	38.5	27.1								dpy-19-like 1 (C. elegans)	7.56E-02	N		
Serinc5	-1.41	7.23E-05	1.31E-03	47.2	33.4								serine incorporator 5	4.88E-01	N		
Gpr37	-1.41	7.27E-05	1.32E-03	84.6	59.9		1		1			-1.31	G protein-coupled receptor 37 (endothelin receptor type B-like) //	1.36E-03	Y		
Csad	1.46	7.28E-05	1.32E-03	18.8	27.5		1					1.54	cysteine sulfinic acid decarboxylase	4.30E-06	Y		
Glra2	-1.45	7.33E-05	1.32E-03	21.9	15.0		1					-2.02	glycine receptor, alpha 2	4.03E-19	Y		
Cp	-1.49	7.35E-05	1.32E-03	10.4	7.0	2	1				-1.32	1.50	ceruloplasmin (ferroxidase)	1.74E-05	N		N
Loxl3	1.69	7.39E-05	1.33E-03	2.4	4.0							1.79	lysyl oxidase-like 3	9.00E-06	Y		
Flna	1.42	7.41E-05	1.33E-03	17.3	24.5							1.38	filamin A, alpha	1.49E-04	Y		
Grm5	-1.43	7.51E-05	1.35E-03	30.4	21.3		1	1					glutamate receptor, metabotropic 5	7.27E-02	N		
Zbtb16	-1.48	7.54E-05	1.35E-03	19.4	13.2				1			-1.36	zinc finger and BTB domain containing 16	1.10E-03	Y		
Plekhg1	-1.48	7.61E-05	1.36E-03	10.2	6.9			1				-1.31	pleckstrin homology domain containing, family G (with Rho	4.44E-03	Y		
Aadat	-1.96	7.78E-05	1.39E-03	3.0	1.5	1	1						aminoadipate aminotransferase	9.64E-01	N		
Capsl	1.67	7.80E-05	1.39E-03	7.4	12.4							2.06	calcyphosine-like	2.82E-10	Y		
Klk6	-1.50	7.95E-05	1.42E-03	29.8	19.8	1	1		3			-1.35	kallikrein-related peptidase 6	3.29E-03	Y		
Prc1	1.57	8.02E-05	1.43E-03	4.2	6.6							1.95	protein regulator of cytokinesis 1	2.63E-09	Y		
Hcrt	1.77	8.03E-05	1.43E-03	8.5	15.0							3.28	hypocretin (orexin) neuropeptide precursor	5.89E-11	Y		
Galntl1	-1.42	8.10E-05	1.44E-03	39.3	27.6							-1.22	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	3.49E-02	Y		
Robo2	-1.42	8.46E-05	1.50E-03	17.2	12.1		1					-1.40	roundabout, axon guidance receptor, homolog 2 (Drosophila)	5.24E-05	Y		
Igsf1	-1.43	8.52E-05	1.51E-03	27.2	19.1		1					-1.42	immunoglobulin superfamily, member 1	2.58E-05	Y		
Serpinf1	-1.72	8.58E-05	1.51E-03	7.7	4.5				1				serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigme	9.22E-01	N		
Fah	-1.51	8.58E-05	1.51E-03	21.4	14.2							-1.34	fumarylacetoacetate hydrolase (fumarylacetoacetase)	5.53E-03	Y		
Rtn4rl1	1.44	8.61E-05	1.51E-03	16.3	23.5		2					2.55	reticulon 4 receptor-like 1	5.69E-25	Y		
Adam32	-2.32	8.71E-05	1.53E-03	1.4	0.6								ADAM metallopeptidase domain 32	5.66E-02	N		
Hsd17b11	-1.50	8.80E-05	1.54E-03	21.1	14.1				1				hydroxysteroid (17-beta) dehydrogenase 11	3.42E-01	N		
Pfn2	-1.40	8.83E-05	1.55E-03	298.7	213.5							-1.41	profilin 2	1.99E-05	Y		
Zfp385b	1.42	8.92E-05	1.56E-03	26.4	37.5							1.96		2.79E-16	Y		
Unc5d	-1.45	8.93E-05	1.56E-03	21.6	14.9							-1.47	unc-5 homolog D (C. elegans)	1.62E-05	Y		
Itga11	1.46	8.95E-05	1.56E-03	6.9	10.1							4.30	integrin, alpha 11	7.12E-44	Y		
Kcnj9	1.50	8.97E-05	1.56E-03	9.8	14.8	1							potassium inwardly-rectifying channel, subfamily J, member 9	1.89E-01	N		
Txnrd3	-1.62	8.99E-05	1.56E-03	5.0	3.1		2					-1.31	thioredoxin reductase 3	2.62E-02	Y		
Robo1	-1.43	9.03E-05	1.57E-03	21.6	15.2							-1.28	roundabout, axon guidance receptor, homolog 1 (Drosophila)	5.67E-03	Y		
Smyd2	-1.44	9.09E-05	1.58E-03	49.9	34.7		1					-1.50	SET and MYND domain containing 2	1.98E-06	Y		
Cldn10	-1.66	9.10E-05	1.58E-03	9.2	5.5							-1.34	claudin 10	3.49E-02	Y		
RGD1310773	-1.58	9.21E-05	1.59E-03	6.1	3.9							-1.44		1.36E-03	Y		
Tymp	1.51	9.23E-05	1.59E-03	7.9	11.9							1.44	thymidine phosphorylase	4.21E-04	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Ppp1r14a	-1.69	9.39E-05	1.62E-03	19.9	11.7		1		1			-1.53	protein phosphatase 1, regulatory (inhibitor) subunit 14A	4.11E-03	Y		
Kcnj3	1.41	9.46E-05	1.63E-03	74.5	105.3							1.70	potassium inwardly-rectifying channel, subfamily J, member 3	8.67E-11	Y		
LOC501110	-2.02	9.68E-05	1.66E-03	2.3	1.1							-1.60		1.23E-02	Y		
Trpm2	-1.49	9.69E-05	1.66E-03	8.1	5.4							-1.24	transient receptor potential cation channel, subfamily M, member 2	3.88E-02	Y		
Abcc8	1.42	9.71E-05	1.66E-03	18.1	25.8							1.51	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	1.95E-06	Y		
RGD1564149	1.60	1.03E-04	1.76E-03	6.7	10.7							2.12		1.25E-11	Y		
Pnpla1	-1.81	1.03E-04	1.76E-03	3.9	2.2							-1.83	patatin-like phospholipase domain containing 1	2.22E-04	Y		
Syt9	1.46	1.04E-04	1.77E-03	22.8	33.2							1.37	synaptotagmin IX	1.71E-03	Y		
Pctk3	-1.49	1.04E-04	1.77E-03	22.9	15.4				1			-1.29		2.01E-02	Y		
Capn1	1.45	1.05E-04	1.78E-03	12.6	18.4				1			1.77	calpain 1, (mu/I) large subunit	2.08E-09	Y		
Npas2	-1.53	1.07E-04	1.82E-03	5.6	3.7		2		1				neuronal PAS domain protein 2	2.20E-01	N		
LOC360919	-2.82	1.10E-04	1.86E-03	1.4	0.5							-1.87		6.31E-03	Y		
Gata2	-1.76	1.12E-04	1.89E-03	2.3	1.3							-1.57	GATA binding protein 2	2.31E-06	Y		
Tmem178	1.43	1.12E-04	1.90E-03	35.7	51.0		1					2.10		2.23E-17	Y		
Rph3al	1.59	1.13E-04	1.91E-03	5.2	8.3							1.81	rabphilin 3A-like (without C2 domains)	6.51E-07	Y		
Ugt1a2	-1.73	1.17E-04	1.97E-03	3.9	2.2									5.33E-01	N		
Lox	1.79	1.17E-04	1.97E-03	2.3	4.1		1					2.34	lysyl oxidase	3.59E-08	Y		
Ddo	1.81	1.19E-04	2.00E-03	3.7	6.6							1.86	D-aspartate oxidase	6.80E-06	Y		
Dhcr24	-1.40	1.20E-04	2.02E-03	125.3	89.3							-1.43	24-dehydrocholesterol reductase	1.30E-05	Y		
Ptk2b	-1.45	1.20E-04	2.02E-03	13.2	9.1		1						PTK2B protein tyrosine kinase 2 beta	8.60E-01	N		
Pacrg	1.54	1.21E-04	2.02E-03	11.6	17.9							1.63	PARK2 co-regulated	1.81E-06	Y		
Myo1d	-1.44	1.23E-04	2.05E-03	11.0	7.6		1		1			-1.38	myosin ID	4.29E-04	Y		
Ccdc22	1.45	1.24E-04	2.08E-03	13.2	19.2								coiled-coil domain containing 22	5.42E-02	N		
Kcnh1	1.41	1.25E-04	2.09E-03	20.0	28.2	1	1					2.24	potassium voltage-gated channel, subfamily H (eag-related), member	2.03E-21	Y		
Galntl6	-1.60	1.29E-04	2.15E-03	7.3	4.6							-1.83	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosa	9.74E-11	Y		
Bmper	-1.60	1.30E-04	2.17E-03	5.3	3.3								BMP binding endothelial regulator	3.94E-01	N		
Plagl1	-1.48	1.30E-04	2.17E-03	7.7	5.2	2	1						pleiomorphic adenoma gene-like 1	3.23E-01	N		
LOC100302465	-1.70	1.32E-04	2.18E-03	3.2	1.9							-1.91		5.36E-07	Y		
Cd24	1.45	1.32E-04	2.18E-03	19.6	28.3	1	3					1.54	CD24 molecule	1.23E-06	Y		
Mmel1	-1.68	1.32E-04	2.19E-03	3.7	2.2							-1.73	membrane metallo-endopeptidase-like 1	1.90E-05	Y		
Dnajb13	1.72	1.33E-04	2.21E-03	2.2	3.8							2.12	DnaJ (Hsp40) homolog, subfamily B, member 13	1.06E-08	Y		
Slit3	1.42	1.34E-04	2.21E-03	13.6	19.3		1					1.76	slit homolog 3 (Drosophila)	3.60E-11	Y		
Ptpn14	1.62	1.35E-04	2.23E-03	1.9	3.1							2.10	protein tyrosine phosphatase, non-receptor type 14	1.14E-10	Y		
Tmem14a	-1.45	1.35E-04	2.23E-03	42.3	29.1		3					-1.52	transmembrane protein 14A	2.30E-06	Y		
Tmem90a	-1.59	1.37E-04	2.25E-03	8.5	5.4							-1.52		5.04E-04	Y		
Syt7	1.41	1.38E-04	2.27E-03	58.0	81.8							1.66	synaptotagmin VII	1.80E-09	Y		
Ccdc33	1.76	1.40E-04	2.29E-03	1.5	2.6							2.06	coiled-coil domain containing 33	4.06E-07	Y		
Xkr7	1.46	1.42E-04	2.32E-03	10.4	15.1							2.42	XK, Kell blood group complex subunit-related family, member 7	8.54E-18	Y		
Tspan4	1.43	1.43E-04	2.34E-03	31.1	44.5		1	1				1.71	tetraspanin 4	9.79E-09	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Gria4	1.38	1.45E-04	2.37E-03	129.1	178.8		1	1				1.31	glutamate receptor, ionotropic, AMPA 4	1.10E-03	Y		
Rasa3	1.41	1.47E-04	2.39E-03	30.1	42.5							1.64	RAS p21 protein activator 3	7.73E-09	Y		
Grin3a	-1.42	1.48E-04	2.41E-03	19.7	13.9	1						-1.39	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	1.75E-04	Y		
Adora1	1.40	1.48E-04	2.41E-03	95.2	133.7				1			1.68	adenosine A1 receptor	5.51E-10	Y		
St18	1.40	1.49E-04	2.42E-03	33.4	46.7			1	2			2.27	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger pr	3.89E-24	Y		
Ncam2	-1.39	1.51E-04	2.44E-03	79.7	57.3	1		2	1			-1.39	neural cell adhesion molecule 2	5.23E-05	Y		
Grin2b	-1.41	1.51E-04	2.45E-03	21.7	15.4				1			-1.56	glutamate receptor, ionotropic, N-methyl D-aspartate 2B //	6.62E-08	Y		
Lrrtm4	-1.44	1.55E-04	2.50E-03	19.0	13.1							-1.47	leucine rich repeat transmembrane neuronal 4	1.32E-05	Y		
Btg1	1.39	1.56E-04	2.53E-03	119.3	166.1	1	1					2.06	B-cell translocation gene 1, anti-proliferative	8.29E-20	Y		
Pgrmc1	-1.40	1.57E-04	2.53E-03	96.0	68.7							-1.67	progesterone receptor membrane component 1	5.89E-11	Y		
LOC502684	1.55	1.61E-04	2.59E-03	9.1	14.0							1.56		8.69E-05	Y		
Tagln3	1.39	1.61E-04	2.60E-03	163.1	226.8		1					1.43	transgelin 3	1.73E-05	Y		
Hs3st5	-1.55	1.62E-04	2.60E-03	6.0	3.9			1	1			-1.74	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	3.35E-08	Y		
Insc	-1.65	1.62E-04	2.61E-03	4.7	2.9								inscuteable homolog (Drosophila)	1.20E-01	N		
Iqgap3	-1.77	1.64E-04	2.62E-03	1.2	0.7		1					-1.76	IQ motif containing GTPase activating protein 3	4.09E-06	Y		
Fat3	-1.39	1.67E-04	2.67E-03	23.3	16.8							-1.42	FAT tumor suppressor homolog 3 (Drosophila)	1.66E-05	Y		
Sema3d	-1.47	1.68E-04	2.68E-03	7.1	4.9				1			-1.24	sema domain, immunoglobulin domain (Ig), short basic domain, secr	4.64E-02	Y		
RGD1309079	1.39	1.70E-04	2.71E-03	44.6	62.0							1.77		8.03E-13	Y		
Zfp238	1.40	1.71E-04	2.73E-03	59.8	83.8							3.16		1.45E-42	Y		
Mctp2	-1.80	1.72E-04	2.74E-03	2.5	1.4								multiple C2 domains, transmembrane 2	9.04E-01	N		
LOC690276	1.67	1.75E-04	2.78E-03	6.5	10.9							2.05		9.30E-08	Y		
Msx2	1.73	1.76E-04	2.79E-03	2.3	4.0							3.46	msh homeobox 2	8.63E-13	Y		
Hdac11	-1.38	1.77E-04	2.81E-03	130.6	94.4							-1.39	histone deacetylase 11	4.78E-05	Y		
Pcdh20	-1.42	1.78E-04	2.82E-03	12.9	9.0	1	2						protocadherin 20	5.11E-02	N		
Aloxe3	1.42	1.82E-04	2.88E-03	20.7	29.4		2					1.64	arachidonate lipoxygenase 3	5.60E-08	Y		
Ndrg1	-1.39	1.83E-04	2.88E-03	70.3	50.6		1					-1.35	N-myc downstream regulated 1	3.82E-04	Y		
Dnaja1	-1.40	1.83E-04	2.89E-03	78.6	56.1				1				DnaJ (Hsp40) homolog, subfamily A, member 1	1.36E-01	N		
Mchr1	-1.91	1.83E-04	2.89E-03	4.1	2.2							-1.50	melanin-concentrating hormone receptor 1	2.98E-03	Y		
Hs3st1	1.43	1.84E-04	2.90E-03	46.2	65.9		2		2			1.55	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	2.44E-06	Y		
Rab11a	-1.38	1.85E-04	2.90E-03	119.2	86.1							-1.44	RAB11A, member RAS oncogene family	5.86E-06	Y		
Car2	-1.39	1.85E-04	2.90E-03	152.9	110.2							-1.33	carbonic anhydrase II	8.87E-04	Y		
Fbxl22	1.91	1.85E-04	2.90E-03	0.6	1.1							2.82	F-box and leucine-rich repeat protein 22	2.13E-05	Y		
Tmprss5	-1.57	1.87E-04	2.93E-03	6.4	4.1							-1.42	transmembrane protease, serine 5	2.68E-03	Y		
Gas2	-1.61	1.87E-04	2.93E-03	6.0	3.7							-1.59	growth arrest-specific 2	9.56E-05	Y		
Rnf39	1.65	1.90E-04	2.96E-03	3.1	5.0		1					2.30	ring finger protein 39	3.62E-06	Y		
Lcp1	-1.50	1.92E-04	3.00E-03	7.1	4.7				1			-1.29	lymphocyte cytosolic protein 1 (L-plastin)	1.33E-02	Y		
Etv1	1.38	1.96E-04	3.05E-03	75.7	104.2	1	3		1	-1.14		3.33	ets variant 1	8.43E-55	Y	N	

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Ptms	1.39	1.98E-04	3.07E-03	120.5	167.6								parathymosin	5.33E-02	N		
Tac1	-1.42	1.98E-04	3.08E-03	69.7	49.2		1						tachykinin, precursor 1	3.71E-01	N		
Plvap	1.59	2.00E-04	3.11E-03	4.3	6.9		1					1.93	plasmalemma vesicle associated protein	5.30E-06	Y		
Mylk3	-4.62	2.04E-04	3.16E-03	0.4	0.1								myosin light chain kinase 3	0.00E+00	N		
Fam161a	1.56	2.04E-04	3.16E-03	5.1	8.0							1.72	family with sequence similarity 161, member A	1.95E-06	Y		
Insig1	-1.41	2.05E-04	3.16E-03	31.6	22.4		1		1			-1.46	insulin induced gene 1	9.84E-06	Y		
LOC100125362	-1.39	2.05E-04	3.16E-03	28.8	20.7							-1.24		1.41E-02	Y		
Plat	1.39	2.05E-04	3.16E-03	55.9	77.6	1					-1.32	1.50	plasminogen activator, tissue	5.13E-07	Y		N
Sorl1	1.37	2.06E-04	3.16E-03	90.3	124.0							1.87	sortilin-related receptor, L(DLR class) A repeats containing	2.94E-16	Y		
Dock11	-1.41	2.06E-04	3.16E-03	12.3	8.7		1					-1.36	dedicator of cytokinesis 11	3.89E-04	Y		
Mcrs1	1.40	2.06E-04	3.16E-03	35.8	50.3							1.30	microspherule protein 1	3.76E-03	Y		
Asap1	-1.40	2.07E-04	3.17E-03	37.0	26.5			1				-1.27	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	5.79E-03	Y		
Pdk2	1.38	2.07E-04	3.17E-03	79.6	110.1				1			1.65	pyruvate dehydrogenase kinase, isozyme 2	5.82E-10	Y		
Azi1	1.42	2.09E-04	3.20E-03	13.3	18.9							1.36	5-azacytidine induced 1	9.78E-04	Y		
Cpm	-1.46	2.11E-04	3.22E-03	6.2	4.2		1	1				-1.32	carboxypeptidase M	7.78E-03	Y		
Sox10	-1.42	2.12E-04	3.24E-03	20.3	14.2		1						SRY (sex determining region Y)-box 10	8.41E-02	N		
Lrfn5	-1.54	2.13E-04	3.24E-03	5.8	3.8							-1.54	leucine rich repeat and fibronectin type III domain containing 5 /	5.67E-05	Y		
Ppp1r15a	1.46	2.16E-04	3.30E-03	12.2	17.8								protein phosphatase 1, regulatory subunit 15A	2.75E-01	N		
Mab21l1	1.43	2.17E-04	3.31E-03	16.3	23.2							2.76	mab-21-like 1 (C. elegans)	9.16E-25	Y		
Kcnip3	1.44	2.19E-04	3.33E-03	34.3	49.5				1			1.71	Kv channel interacting protein 3, calsenilin	4.25E-08	Y		
Kcnb2	-1.43	2.20E-04	3.33E-03	15.3	10.7								potassium voltage-gated channel, Shab-related subfamily, member 2	6.34E-01	N		
Cdyl	1.40	2.20E-04	3.33E-03	39.1	54.6							1.67	chromodomain protein, Y-like	5.88E-10	Y		
LOC314655	1.47	2.24E-04	3.39E-03	10.2	15.0							1.75		3.56E-08	Y		
Eif1a	-1.44	2.25E-04	3.39E-03	26.1	18.2							-1.31	eukaryotic translation initiation factor 1A, Y-linked; eukaryotic translation initiation factor 1A	3.40E-03	Y		
Penk	-1.39	2.25E-04	3.40E-03	99.0	71.2		1						proenkephalin	9.12E-01	N		
Dhx16	1.40	2.27E-04	3.42E-03	28.9	40.3							1.53	DEAH (Asp-Glu-Ala-His) box polypeptide 16	7.75E-07	Y		
Hspa1a	1.56	2.28E-04	3.43E-03	4.0	6.2				1			1.48	heat shock 70kDa protein 1A	4.00E-04	Y		
Dqx1	1.56	2.28E-04	3.43E-03	3.7	5.8							1.64	DEAQ box RNA-dependent ATPase 1	7.04E-05	Y		
Clip4	-1.45	2.29E-04	3.43E-03	19.6	13.6							-1.30	CAP-GLY domain containing linker protein family, member 4	8.89E-03	Y		
Usp3	1.42	2.30E-04	3.45E-03	22.0	31.1							2.30	ubiquitin specific peptidase 3	4.83E-20	Y		
Il1rapl2	-1.76	2.32E-04	3.48E-03	2.1	1.2							-1.58	interleukin 1 receptor accessory protein-like 2	1.83E-03	Y		
S100a4	3.00	2.35E-04	3.52E-03	1.2	3.5		1					3.15	S100 calcium binding protein A4	3.07E-05	Y		
Rapgef5	-1.39	2.35E-04	3.52E-03	21.2	15.2			1	1			-1.51	Rap guanine nucleotide exchange factor (GEF) 5	6.45E-07	Y		
Cyth3	1.40	2.36E-04	3.52E-03	20.0	28.0							1.41	cytohesin 3	8.31E-05	Y		
Ptgds	1.38	2.36E-04	3.52E-03	308.5	424.8				1			1.63	prostaglandin D2 synthase 21kDa (brain)	4.63E-10	Y		
Mxd4	1.43	2.37E-04	3.53E-03	28.1	40.2							1.69	MAX dimerization protein 4	4.07E-08	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Solh	1.39	2.38E-04	3.54E-03	19.4	26.9							1.57	small optic lobes homolog (Drosophila)	8.20E-08	Y		
Snx2	-1.41	2.38E-04	3.54E-03	36.5	25.9								sorting nexin 2	3.34E-01	N		
Olfml1	-1.42	2.39E-04	3.54E-03	22.3	15.7		1					-1.31	olfactomedin-like 1	3.25E-03	Y		
Nhs	-1.48	2.39E-04	3.55E-03	4.9	3.3							-1.44	Nance-Horan syndrome (congenital cataracts and dental anomalies)	3.05E-04	Y		
Zfp653	1.45	2.42E-04	3.57E-03	11.5	16.7							1.64		7.44E-07	Y		
Ntsr1	-1.81	2.42E-04	3.57E-03	1.6	0.9		1					-1.43	neurotensin receptor 1 (high affinity)	8.65E-03	Y		
Elovl7	-1.52	2.44E-04	3.60E-03	17.4	11.5				1			-1.35	ELOVL fatty acid elongase 7	9.80E-03	Y		
Atpaf1	-1.40	2.47E-04	3.64E-03	26.4	18.8								ATP synthase mitochondrial F1 complex assembly factor 1 //	1.53E-01	N		
Scn1a	-1.37	2.48E-04	3.65E-03	85.6	62.6		1						sodium channel, voltage-gated, type I, alpha subunit	1.01E-01	N		
Gldc	1.45	2.49E-04	3.66E-03	6.9	10.1		1					1.81	glycine dehydrogenase (decarboxylating)	1.20E-09	Y		
Nek7	-1.42	2.49E-04	3.66E-03	68.4	48.3							-1.39	NIMA (never in mitosis gene a)-related kinase 7	3.35E-04	Y		
Ugt1a6	-1.64	2.50E-04	3.67E-03	4.2	2.6									3.62E-01	N		
Septin5	1.38	2.50E-04	3.67E-03	#N/A	#N/A				1			1.17		#N/A	Y		
Chrm3	-1.41	2.52E-04	3.69E-03	16.9	12.0		1						cholinergic receptor, muscarinic 3	7.20E-02	N		
RGD1566112	1.41	2.53E-04	3.69E-03	14.4	20.3							1.81		1.61E-11	Y		
C8g	-1.67	2.56E-04	3.74E-03	12.3	7.4								complement component 8, gamma polypeptide	9.79E-01	N		
Pnck	-1.41	2.57E-04	3.75E-03	43.8	31.1							-1.60	pregnancy up-regulated non-ubiquitously expressed CaM kinase	6.62E-08	Y		
Pcdh19	-1.38	2.58E-04	3.75E-03	37.1	26.8							-1.37	protocadherin 19	2.40E-04	Y		
Aox3	-1.69	2.58E-04	3.75E-03	1.8	1.1								aldehyde oxidase 3	2.17E-01	N		
Sfxn5	1.39	2.59E-04	3.77E-03	99.1	137.9							1.50	sideroflexin 5	1.89E-06	Y		
Lrrn1	-1.40	2.60E-04	3.77E-03	28.8	20.6								leucine rich repeat neuronal 1	5.89E-01	N		
Als2cr12	1.54	2.60E-04	3.77E-03	6.1	9.4			1				2.17	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, c	1.86E-12	Y		
Rabl4	1.49	2.61E-04	3.77E-03	16.0	23.8							1.62		7.12E-06	Y		
Serinc2	1.73	2.61E-04	3.78E-03	2.3	4.0			1	1			2.92	serine incorporator 2	3.73E-12	Y		
Sncg	-1.51	2.63E-04	3.79E-03	29.1	19.3		1					-1.75	synuclein, gamma (breast cancer-specific protein 1)	1.43E-11	Y		
Hapln2	-1.52	2.65E-04	3.83E-03	13.9	9.2		1					-1.42	hyaluronan and proteoglycan link protein 2	2.70E-03	Y		
Katnal1	-1.41	2.67E-04	3.85E-03	41.4	29.4								katanin p60 subunit A-like 1	6.32E-02	N		
March1	-1.62	2.67E-04	3.85E-03	12.1	7.5			1				-1.40		1.60E-02	Y		
Cd22	-3.28	2.71E-04	3.89E-03	0.4	0.1			1	2				CD22 molecule	0.00E+00	N		
Snrk	1.38	2.73E-04	3.92E-03	57.3	79.0							1.74	SNF related kinase	9.84E-06	Y		
Lrsam1	-1.39	2.74E-04	3.93E-03	20.9	15.0		1					-1.31	leucine rich repeat and sterile alpha motif containing 1	2.38E-03	Y		
Thsd7b	-1.45	2.78E-04	3.97E-03	6.5	4.5		2	2				-1.41	thrombospondin, type I, domain containing 7B	1.21E-04	Y		
Ptprk	-1.43	2.78E-04	3.97E-03	21.0	14.7	1		1	1				protein tyrosine phosphatase, receptor type, K	8.19E-01	N		
Mgll	1.42	2.78E-04	3.97E-03	31.2	44.3	2	2					1.39	monoglyceride lipase	4.90E-04	Y		
Pdzd2	-1.47	2.78E-04	3.97E-03	3.4	2.3			1					PDZ domain containing 2	1.00E+00	N		
St6gal1	-1.43	2.79E-04	3.97E-03	12.0	8.4	1	1					-1.29	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	9.06E-03	Y		
Rtn4	-1.36	2.82E-04	4.02E-03	221.3	162.4				1			-1.40	reticulon 4	2.86E-05	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Tanc2	-1.37	2.84E-04	4.04E-03	48.9	35.8							-1.34	tetratricopeptide repeat, ankyrin repeat and coiled-coil co	4.91E-04	Y		
Rsph1	1.60	2.84E-04	4.04E-03	7.5	11.9							2.40	radial spoke head 1 homolog (Chlamydomonas)	9.66E-14	Y		
Tmtc2	1.39	2.86E-04	4.06E-03	29.1	40.4			1				1.58	transmembrane and tetratricopeptide repeat containing 2	7.76E-08	Y		
Ifitm3	1.55	2.87E-04	4.06E-03	16.5	25.5	1	2		1			1.83	interferon induced transmembrane protein 3	1.37E-07	Y		
Phlda3	-1.43	2.87E-04	4.06E-03	32.1	22.5		1					-1.42	pleckstrin homology-like domain, family A, member 3	1.45E-04	Y		
Zbtb17	1.44	2.87E-04	4.06E-03	9.7	14.0							1.30	zinc finger and BTB domain containing 17	1.39E-02	Y		
Zhx3	1.37	2.89E-04	4.09E-03	50.9	69.8							1.38	zinc fingers and homeoboxes 3	1.10E-04	Y		
LOC361016	-1.59	2.92E-04	4.12E-03	6.0	3.8									6.88E-01	N		
Gjb1	-1.50	2.93E-04	4.13E-03	13.7	9.1		1		2			-1.30	gap junction protein, beta 1, 32kDa	3.30E-02	Y		
Apbb1ip	-1.83	2.95E-04	4.14E-03	2.2	1.2								amyloid beta (A4) precursor protein-binding, family B, member 1	6.98E-01	N		
Fam101b	1.56	2.95E-04	4.14E-03	6.5	10.1		3					1.38	family with sequence similarity 101, member B	1.33E-02	Y		
Depdc7	-1.60	3.01E-04	4.23E-03	7.3	4.5								DEP domain containing 7	5.22E-01	N		
Elovl6	-1.40	3.04E-04	4.27E-03	35.6	25.5	2	1			-1.13		-1.37	ELOVL fatty acid elongase 6	2.97E-04	Y	Y	
Ass1	-1.43	3.05E-04	4.28E-03	35.3	24.7		1					-1.53	argininosuccinate synthase 1	9.98E-07	Y		
Masp1	-1.47	3.06E-04	4.28E-03	5.1	3.4	1	1						mannan-binding lectin serine peptidase 1 (C4/C2 activating	5.11E-01	N		
MGC114440	1.50	3.09E-04	4.33E-03	6.4	9.5							1.94		1.17E-10	Y		
Rassf2	1.39	3.13E-04	4.37E-03	24.7	34.2				1			1.63	Ras association (RalGDS/AF-6) domain family member 2	3.65E-09	Y		
Aifm3	1.37	3.14E-04	4.38E-03	53.6	73.6	1						1.65	apoptosis-inducing factor, mitochondrion-associated, 3	8.11E-10	Y		
Acyp2	-1.47	3.16E-04	4.40E-03	19.3	13.1	1	1			-1.37		-1.23	acylphosphatase 2, muscle type	1.68E-02	Y	Y	
Akna	1.42	3.24E-04	4.51E-03	6.1	8.6							1.65	AT-hook transcription factor	4.70E-08	Y		
Mum1l1	-1.49	3.25E-04	4.52E-03	5.9	4.0							-1.77	melanoma associated antigen (mutated) 1-like 1	6.39E-10	Y		
Spag6	1.41	3.29E-04	4.57E-03	19.9	28.0							1.87	sperm associated antigen 6	2.21E-13	Y		
Rps6	-1.36	3.30E-04	4.57E-03	444.3	325.8							-1.52	ribosomal protein S6	9.00E-08	Y		
Hcn2	-1.37	3.30E-04	4.58E-03	63.2	46.0								hyperpolarization activated cyclic nucleotide-gated potassium chann	7.51E-01	N		
Rpe65	-1.48	3.33E-04	4.60E-03	12.9	8.7	1	1					-1.35	retinal pigment epithelium-specific protein 65kDa	3.80E-03	Y		
Meis2	-1.42	3.33E-04	4.60E-03	18.5	13.0		1						Meis homeobox 2	8.28E-01	N		
Sycp2	-1.59	3.34E-04	4.61E-03	2.4	1.5								synaptonemal complex protein 2	1.29E-01	N		
Sult1d1	-1.55	3.36E-04	4.63E-03	7.0	4.5		1					-1.55		1.99E-04	Y		
Bmp7	1.91	3.41E-04	4.70E-03	1.0	1.8				1			1.88	bone morphogenetic protein 7	6.14E-05	Y		
Hspb6	1.41	3.42E-04	4.70E-03	32.7	46.0							1.67	heat shock protein, alpha-crystallin-related, B6	2.73E-08	Y		
Rad54l	1.59	3.43E-04	4.71E-03	2.6	4.2							2.09	RAD54-like (S. cerevisiae)	1.20E-07	Y		
Alk	-1.41	3.44E-04	4.71E-03	8.3	5.8	1	1					-1.65	anaplastic lymphoma receptor tyrosine kinase	3.50E-08	Y		
Pcsk1	-1.40	3.44E-04	4.71E-03	12.2	8.7	1	1					-1.52	proprotein convertase subtilisin/kexin type 1	1.99E-06	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Ugt1a9	-1.66	3.44E-04	4.71E-03	3.9	2.4									6.32E-01	N		
Kif26b	-1.44	3.44E-04	4.71E-03	4.7	3.3			1				-1.25	kinesin family member 26B	2.88E-02	Y		
Dusp26	-1.41	3.46E-04	4.73E-03	35.2	25.0		1		1			-1.41	dual specificity phosphatase 26 (putative)	1.01E-04	Y		
Pcdh17	-1.36	3.48E-04	4.75E-03	63.5	46.5							-1.33	protocadherin 17	8.18E-04	Y		
Mall	2.25	3.48E-04	4.75E-03	0.7	1.6							2.58	mal, T-cell differentiation protein-like	5.95E-05	Y		
Cdkn2c	1.64	3.50E-04	4.76E-03	3.8	6.3				1			3.63	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)	1.44E-12	Y		
RGD1564620	-2.31	3.51E-04	4.78E-03	2.7	1.2									4.70E-01	N		
Chmp1b	-1.42	3.52E-04	4.79E-03	18.7	13.2	1	3						charged multivesicular body protein 1B	2.39E-01	N		
Trim67	1.51	3.54E-04	4.80E-03	4.1	6.2							1.94	tripartite motif containing 67	5.24E-08	Y		
Dnai1	1.44	3.54E-04	4.80E-03	10.0	14.4							1.96	dynein, axonemal, intermediate chain 1	1.51E-13	Y		
Mir3541	2.40	3.57E-04	4.84E-03	9.7	23.1								miRNA 3541	3.71E-01	N		
Tmem100	-1.44	3.65E-04	4.94E-03	24.3	16.9		2					-1.35	transmembrane protein 100	3.14E-03	Y		
Cd200	-1.36	3.72E-04	5.03E-03	120.6	88.5				1			-1.67	CD200 molecule	4.04E-11	Y		
E2f1	1.54	3.81E-04	5.14E-03	3.5	5.4							1.88	E2F transcription factor 1	1.79E-06	Y		
Ehd1	1.37	3.83E-04	5.16E-03	33.8	46.3		1						EH-domain containing 1	7.80E-02	N		
Osgin1	-2.28	3.84E-04	5.18E-03	1.1	0.5			1					oxidative stress induced growth inhibitor 1	0.00E+00	N		
Scx	1.81	3.88E-04	5.22E-03	2.7	4.8		1							1.69E-01	N		
RGD1563888	-1.47	3.90E-04	5.25E-03	26.7	18.1									1.18E-01	N		
Pde9a	1.41	3.91E-04	5.25E-03	17.8	25.1							1.70	phosphodiesterase 9A	8.55E-09	Y		
LRRTM1	-1.44	3.96E-04	5.31E-03	11.3	7.8		1					-1.45	leucine rich repeat transmembrane neuronal 1	6.79E-05	Y		
Gstm1	1.36	3.97E-04	5.31E-03	159.9	218.3							1.36	glutathione S-transferase mu 1	2.03E-04	Y		
Akap14	1.68	4.00E-04	5.36E-03	2.5	4.2							2.18	A kinase (PRKA) anchor protein 14	2.52E-08	Y		
Hist1h1d	-1.63	4.06E-04	5.42E-03	85.2	52.2								histone cluster 1, H1d	9.91E-01	N		
Pde11a	-1.54	4.11E-04	5.48E-03	3.2	2.1								phosphodiesterase 11A	6.73E-01	N		
Rims1	1.36	4.13E-04	5.51E-03	70.3	95.3	1						1.51	regulating synaptic membrane exocytosis 1	2.36E-07	Y		
Sfrp2	-1.88	4.14E-04	5.52E-03	2.3	1.2								secreted frizzled-related protein 2	9.45E-01	N		
Mfsd4	1.40	4.15E-04	5.52E-03	11.5	16.2							2.31	major facilitator superfamily domain containing 4	3.42E-18	Y		
Arhgap24	-1.48	4.15E-04	5.52E-03	7.6	5.1		2	1				-1.53	Rho GTPase activating protein 24	1.05E-06	Y		
Pnkd	-1.36	4.21E-04	5.58E-03	66.7	49.0		1		1				paroxysmal nonkinesigenic dyskinesia	5.59E-02	N		
Pcsk6	1.39	4.21E-04	5.58E-03	14.1	19.7				1			2.14	proprotein convertase subtilisin/kexin type 6	2.40E-18	Y		
Grb10	-1.36	4.25E-04	5.63E-03	41.5	30.4	1		2		-1.19		-1.66	growth factor receptor-bound protein 10	9.14E-11	Y	Y	
Tmx4	-1.35	4.29E-04	5.68E-03	187.4	138.8							-1.43	thioredoxin-related transmembrane protein 4	6.77E-06	Y		
Wipf1	-1.41	4.35E-04	5.75E-03	13.1	9.3								WAS/WASL interacting protein family, member 1	1.40E-01	N		
Map1lc3b	-1.36	4.41E-04	5.82E-03	124.7	91.6	1						-1.25	microtubule-associated protein 1 light chain 3 beta	1.01E-02	Y		
Mthfd1l	1.37	4.43E-04	5.85E-03	25.1	34.4	1	1					1.38	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	2.28E-04	Y		
Dusp14	1.50	4.45E-04	5.87E-03	19.8	29.6		1					1.94	dual specificity phosphatase 14	2.52E-08	Y		
Dusp3	-1.36	4.48E-04	5.89E-03	74.2	54.8		1					-1.25	dual specificity phosphatase 3	9.42E-03	Y		
Tmem130	-1.35	4.52E-04	5.94E-03	392.3	291.1							-1.57	transmembrane protein 130	6.05E-09	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Cfp	1.44	4.56E-04	5.99E-03	13.3	19.2				1			1.26	complement factor properdin	4.44E-02	Y		
Galr1	-1.63	4.58E-04	6.01E-03	4.1	2.5							-1.97	galanin receptor 1	4.53E-06	Y		
Theg	1.88	4.59E-04	6.01E-03	2.0	3.8							1.95	theg spermatid protein	4.68E-04	Y		
Nov	1.51	4.59E-04	6.01E-03	7.0	10.5							1.50	nephroblastoma overexpressed	3.49E-04	Y		
Olr59	-2.01	4.59E-04	6.01E-03	1.2	0.6									2.59E-01	N		
Lbx1	2.96	4.66E-04	6.09E-03	0.5	1.3								ladybird homeobox 1	0.00E+00	N		
Armcx2	-1.36	4.76E-04	6.21E-03	53.8	39.5							-1.77	armadillo repeat containing, X-linked 2	2.29E-13	Y		
Slc30a3	-1.49	4.76E-04	6.21E-03	11.5	7.7								solute carrier family 30 (zinc transporter), member 3	1.07E-01	N		
Sgcg	1.63	4.80E-04	6.25E-03	3.7	6.0							2.13	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	3.56E-09	Y		
Rp1	1.48	4.85E-04	6.30E-03	2.0	2.9							1.86		1.03E-10	Y		
Grin2d	-1.42	4.86E-04	6.31E-03	8.2	5.8							-1.40	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	3.86E-04	Y		
LOC686506	-1.48	4.87E-04	6.32E-03	12.1	8.2									3.82E-01	N		
Ndn	-1.35	4.89E-04	6.34E-03	205.6	152.1							-1.52	necdin homolog (mouse)	8.83E-08	Y		
Ttll10	1.58	4.90E-04	6.35E-03	2.9	4.6							2.12	tubulin tyrosine ligase-like family, member 10	1.16E-08	Y		
Capn2	-1.38	4.93E-04	6.38E-03	24.3	17.6								calpain 2, (m/II) large subunit	7.03E-01	N		
RT1-T24-3	1.84	4.95E-04	6.40E-03	1.8	3.3							1.55		1.10E-02	Y		
Glrb	-1.35	4.99E-04	6.45E-03	169.6	125.2				1			-1.24	glycine receptor, beta	1.48E-02	Y		
RGD1565496	-1.35	5.05E-04	6.51E-03	143.3	106.1							-1.40		2.76E-05	Y		
Sytl5	-1.50	5.06E-04	6.51E-03	7.3	4.9							-1.44	synaptotagmin-like 5	5.28E-04	Y		
Efcab1	1.45	5.06E-04	6.52E-03	16.3	23.7							1.66	EF-hand calcium binding domain 1	4.63E-08	Y		
Casp4	1.48	5.10E-04	6.56E-03	11.3	16.6		1					1.82	caspase 4, apoptosis-related cysteine peptidase	2.27E-08	Y		
Ston1	1.41	5.14E-04	6.60E-03	9.2	13.0							2.00		3.00E-15	Y		
Cacng3	-1.58	5.17E-04	6.63E-03	11.8	7.5		1					-1.78	calcium channel, voltage-dependent, gamma subunit 3	1.03E-09	Y		
Porcn	1.37	5.18E-04	6.64E-03	38.3	52.6							1.46	porcupine homolog (Drosophila)	1.57E-05	Y		
Slc44a1	-1.35	5.19E-04	6.65E-03	53.8	39.8		2		1			-1.20	solute carrier family 44, member 1	4.72E-02	Y		
Zfp385d	1.41	5.29E-04	6.77E-03	17.1	24.1							1.43		3.01E-04	Y		
Vps37b	1.42	5.31E-04	6.79E-03	10.1	14.4							1.56	vacuolar protein sorting 37 homolog B (S. cerevisiae)	7.77E-06	Y		
RGD1565611	1.56	5.35E-04	6.82E-03	8.8	13.7							2.69		4.51E-16	Y		
Plxnb2	1.35	5.37E-04	6.84E-03	36.2	48.9							1.69	plexin B2	5.01E-11	Y		
Rtn3	-1.34	5.38E-04	6.85E-03	422.8	315.2		1					-1.45	reticulon 3	2.05E-06	Y		
Cd38	-1.39	5.39E-04	6.86E-03	27.8	20.0		1					-1.36	CD38 molecule	5.78E-04	Y		
Cyp26b1	1.37	5.41E-04	6.88E-03	19.4	26.5							1.25	cytochrome P450, family 26, subfamily B, polypeptide 1	1.50E-02	Y		
Ubxd3	1.47	5.45E-04	6.91E-03	8.8	12.9							1.44		6.66E-04	Y		
Pdzrn4	-1.59	5.46E-04	6.92E-03	3.0	1.9							-1.42	PDZ domain containing ring finger 4	3.06E-03	Y		
Rasgrp2	-1.42	5.46E-04	6.92E-03	16.9	11.9		2					-1.50	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	1.10E-05	Y		
Gsta3	-1.41	5.51E-04	6.97E-03	36.3	25.8		2					-1.35	glutathione S-transferase alpha 3	1.46E-03	Y		
Trim3	1.36	5.56E-04	7.02E-03	44.9	60.9							1.26	tripartite motif containing 3	9.75E-03	Y		
Slc22a23	-1.35	5.56E-04	7.02E-03	38.6	28.5	1		1					solute carrier family 22, member 23	2.16E-01	N		
Cited2	1.37	5.57E-04	7.02E-03	35.7	48.9				1			1.87	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-te	1.25E-13	Y		
Rnf133	1.47	5.58E-04	7.03E-03	10.2	15.0							3.50	ring finger protein 133	2.71E-23	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Fign	-1.49	5.58E-04	7.03E-03	5.8	3.9								fidgetin	9.66E-01	N		
Ccdc134	1.49	5.61E-04	7.06E-03	7.4	11.0							1.93	coiled-coil domain containing 134	2.38E-09	Y		
Rassf4	-1.41	5.63E-04	7.07E-03	15.7	11.1	2	1		1				Ras association (RalGDS/AF-6) domain family member 4	8.20E-01	N		
RGD1565819	1.55	5.65E-04	7.09E-03	1.6	2.5							1.71		3.16E-05	Y		
RragB	-1.35	5.66E-04	7.10E-03	100.4	74.3		1		1			-1.35	Ras-related GTP binding B	3.28E-04	Y		
Rasgrf2	-1.44	5.73E-04	7.17E-03	7.7	5.4			1				-1.60	Ras protein-specific guanine nucleotide-releasing factor 2	1.14E-07	Y		
Slc43a2	1.35	5.77E-04	7.21E-03	39.2	53.0		2	1				1.46	solute carrier family 43, member 2	5.64E-06	Y		
Enkur	1.44	5.77E-04	7.21E-03	15.2	21.9							1.98	enkurin, TRPC channel interacting protein	3.94E-13	Y		
C1qtnf9	-3.52	5.78E-04	7.21E-03	1.0	0.3								C1q and tumor necrosis factor related protein 9	0.00E+00	N		
Plcd4	-1.39	5.81E-04	7.24E-03	20.5	14.7	1	1		1				phospholipase C, delta 4	1.93E-01	N		
Cytl1	2.67	5.81E-04	7.24E-03	0.4	0.9								cytokine-like 1	6.86E-01	N		
Atp13a4	-1.42	5.82E-04	7.24E-03	8.3	5.8							-1.32	ATPase type 13A4	4.97E-03	Y		
Pftk1	-1.35	5.83E-04	7.25E-03	55.6	41.2		1	1				-1.46		2.58E-06	Y		
Ubash3b	1.37	5.84E-04	7.25E-03	25.4	34.8		3	1				1.55	ubiquitin associated and SH3 domain containing B	5.85E-07	Y		
Notch2	1.36	5.84E-04	7.25E-03	13.6	18.4							1.67	notch 2	4.63E-10	Y		
Limk1	-1.36	5.87E-04	7.28E-03	39.5	29.0		1					-1.28	LIM domain kinase 1	5.06E-03	Y		
En2	1.37	5.99E-04	7.42E-03	23.2	31.7				1			1.64	engrailed homeobox 2	1.59E-08	Y		
Mcm7	1.45	6.01E-04	7.44E-03	7.4	10.7								minichromosome maintenance complex component 7	4.47E-01	N		
Ppfia1	1.35	6.02E-04	7.44E-03	35.4	47.8							1.47	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF	2.60E-06	Y		
Prelp	1.47	6.13E-04	7.56E-03	10.1	14.9							2.05	proline/arginine-rich end leucine-rich repeat protein	4.16E-12	Y		
Kcnk2	-1.39	6.16E-04	7.59E-03	16.0	11.5		1					-1.51	potassium channel, subfamily K, member 2	5.57E-06	Y		
Sephs2	-1.37	6.16E-04	7.59E-03	34.3	25.0	1	4					-1.25	selenophosphate synthetase 2	1.52E-02	Y		
Sh3gl3	-1.40	6.17E-04	7.59E-03	31.4	22.4		1	1				-1.47	SH3-domain GRB2-like 3	2.29E-05	Y		
Chrm2	-1.70	6.18E-04	7.59E-03	17.1	10.0							-1.28	cholinergic receptor, muscarinic 2	1.95E-04	Y		
P2rx4	1.38	6.19E-04	7.60E-03	25.5	35.2		1					1.56	purinergic receptor P2X, ligand-gated ion channel, 4	4.41E-07	Y		
Grap	2.40	6.22E-04	7.63E-03	0.6	1.4								GRB2-related adaptor protein	4.06E-01	N		
Adat3	1.59	6.23E-04	7.63E-03	4.4	6.9							1.50	adenosine deaminase, tRNA-specific 3	7.83E-03	Y		
Syt6	-1.44	6.28E-04	7.68E-03	16.5	11.5	1	1					-1.30	synaptotagmin VI	2.92E-02	Y		
Aplp1	-1.34	6.33E-04	7.74E-03	548.5	410.2							-1.36	amyloid beta (A4) precursor-like protein 1	1.29E-04	Y		
Lrrc43	1.66	6.36E-04	7.78E-03	2.2	3.6							2.18	leucine rich repeat containing 43	1.35E-07	Y		
B3gnt4	1.60	6.39E-04	7.81E-03	4.0	6.5							2.94	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	1.62E-12	Y		
Gfra2	-1.38	6.42E-04	7.83E-03	22.4	16.2		1					-1.33	GDNF family receptor alpha 2	2.10E-03	Y		
Olig2	-1.40	6.52E-04	7.94E-03	16.1	11.5							-1.29	oligodendrocyte lineage transcription factor 2	1.21E-02	Y		
C1r	1.40	6.52E-04	7.94E-03	11.7	16.4	1	3		1		-1.44	1.90	complement component 1, r subcomponent	3.34E-12	Y		N
Gad2	-1.35	6.61E-04	8.04E-03	129.6	96.3	2			1				glutamate decarboxylase 2 (pancreatic islets and brain, 65kDa)	6.37E-01	N		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Zcchc12	-1.34	6.78E-04	8.23E-03	191.2	142.6							-1.51	zinc finger, CCHC domain containing 12	1.48E-07	Y		
Timm13	1.46	6.78E-04	8.23E-03	17.9	26.1	1							translocase of inner mitochondrial membrane 13 homolog (yeast) //	6.00E-01	N		
Kcna6	-1.34	6.79E-04	8.23E-03	47.2	35.2		1					-1.35	potassium voltage-gated channel, shaker-related subfamily, member	2.36E-04	Y		
Slc2a5	-1.59	6.80E-04	8.24E-03	4.3	2.7	1					-1.22		solute carrier family 2 (facilitated glucose/fructose transporter),	6.23E-02	N		Y
Tmem38a	1.37	6.82E-04	8.25E-03	42.7	58.5	1					1.12		transmembrane protein 38A	2.02E-01	N		Y
Akap8l	1.36	6.83E-04	8.26E-03	49.2	66.6	3	1		1				A kinase (PRKA) anchor protein 8-like	5.25E-02	N		
Tmeff2	-1.36	6.86E-04	8.28E-03	37.5	27.6							-1.31	transmembrane protein with EGF-like and two follistatin-like doma	1.79E-03	Y		
Dos	-1.34	6.92E-04	8.34E-03	115.7	86.3							-1.31	downstream of Stk11	1.42E-03	Y		
Igfbp5	1.36	6.96E-04	8.38E-03	53.0	72.0	1					-1.26	2.50	insulin-like growth factor binding protein 5	6.92E-26	Y		N
P2rx6	1.37	6.97E-04	8.40E-03	23.5	32.3							1.86	purinergic receptor P2X, ligand-gated ion channel, 6	4.94E-13	Y		
LOC688452	1.39	7.00E-04	8.42E-03	29.2	40.7							1.42		3.71E-04	Y		
Hcn4	-1.55	7.04E-04	8.46E-03	2.9	1.9								hyperpolarization activated cyclic nucleotide-gated potassiu	7.00E-01	N		
Rnf190	1.79	7.09E-04	8.51E-03	1.0	1.7							2.09		1.15E-05	Y		
Bcl6	1.36	7.13E-04	8.55E-03	24.7	33.5		1		1			1.87	B-cell CLL/lymphoma 6	5.43E-14	Y		
Pitpnm1	1.34	7.19E-04	8.62E-03	101.4	135.6	1			1			1.26	phosphatidylinositol transfer protein, membrane-associated 1	6.47E-03	Y		
Kcnab2	-1.35	7.24E-04	8.66E-03	79.9	59.0								potassium voltage-gated channel, shaker-related subfamily, beta m	9.29E-02	N		
Rps6kb2	1.40	7.38E-04	8.83E-03	16.4	23.0				1				ribosomal protein S6 kinase, 70kDa, polypeptide 2	6.15E-02	N		
Mmd2	-1.35	7.45E-04	8.90E-03	82.0	60.9								monocyte to macrophage differentiation-associated 2	2.69E-01	N		
Kctd9	-1.37	7.50E-04	8.95E-03	24.5	17.9		1					-1.39	potassium channel tetramerisation domain containing 9	1.20E-04	Y		
Btbd3	1.34	7.54E-04	8.98E-03	109.0	146.0		1					2.09	BTB (POZ) domain containing 3	6.05E-21	Y		
Spata24	1.72	7.56E-04	9.00E-03	5.2	9.0							1.42	spermatogenesis associated 24	1.97E-02	Y		
C6	-2.35	7.63E-04	9.07E-03	0.0	0.0								complement component 6	0.00E+00	N		
Lpp	1.39	7.68E-04	9.12E-03	15.2	21.2							1.68	LIM domain containing preferred translocation partner in lipoma	1.14E-07	Y		
LOC683626	-1.37	7.68E-04	9.12E-03	31.8	23.2							-1.37		2.88E-04	Y		
Cib2	-1.41	7.70E-04	9.13E-03	25.2	17.9		1					-1.29	calcium and integrin binding family member 2	9.03E-03	Y		
Dhdpsl	-1.68	7.71E-04	9.13E-03	3.7	2.2									5.47E-01	N		
Tob1	1.35	7.72E-04	9.14E-03	43.2	58.5							1.71	transducer of ERBB2, 1	1.03E-10	Y		
Erc1	1.34	7.76E-04	9.18E-03	54.4	72.9							1.43	ELKS/RAB6-interacting/CAST family member 1	1.34E-05	Y		
Hhex	-2.00	7.81E-04	9.23E-03	2.0	1.0	3	1			1.27			hematopoietically expressed homeobox	3.05E-01	N	N	
Kcnip4	1.38	7.85E-04	9.26E-03	32.1	44.3	1	1	1				1.62	Kv channel interacting protein 4	1.57E-07	Y		
Epdr1	-1.35	7.87E-04	9.28E-03	71.5	53.0							-1.39	ependymin related protein 1 (zebrafish)	7.37E-05	Y		
Pcdh18	-1.39	7.88E-04	9.28E-03	9.1	6.5		1					-1.27	protocadherin 18	1.74E-02	Y		
Ddr2	1.51	7.90E-04	9.29E-03	2.7	4.1		1					1.65	discoidin domain receptor tyrosine kinase 2	1.84E-05	Y		
Mir29b-1	-3.59	8.00E-04	9.41E-03	13.1	3.6								microRNA 29b-1	0.00E+00	N		

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Pex11a	-1.39	8.05E-04	9.46E-03	18.8	13.5	1	1					-1.35	peroxisomal biogenesis factor 11 alpha	1.76E-03	Y		
Kcnd2	1.33	8.10E-04	9.50E-03	112.6	150.2	1		1				1.63	potassium voltage-gated channel, Shal-related subfamily, member 2	5.15E-10	Y		
Dysf	-1.52	8.10E-04	9.50E-03	2.1	1.4							-1.75	dysferlin, limb girdle muscular dystrophy 2B (autosomal rece	8.00E-10	Y		
Nrg2	1.41	8.12E-04	9.51E-03	7.2	10.2							1.88	neuregulin 2	7.31E-10	Y		
Phyhipl	-1.34	8.16E-04	9.54E-03	118.6	88.3								phytanoyl-CoA 2-hydroxylase interacting protein-like	1.57E-01	N		
Prdx3	-1.37	8.19E-04	9.57E-03	49.8	36.4	1						-1.33	peroxiredoxin 3	1.14E-03	Y		
Ppapdc1a	-1.47	8.31E-04	9.71E-03	14.4	9.8		1					-1.54	phosphatidic acid phosphatase type 2 domain containing 1A	5.05E-05	Y		
Slc1a2	-1.33	8.33E-04	9.72E-03	338.6	254.6				2				solute carrier family 1 (glial high affinity glutamate tra	1.37E-01	N		
Tmem51	1.44	8.36E-04	9.75E-03	8.0	11.6							1.71	transmembrane protein 51	1.51E-06	Y		
Ctxn2	-1.51	8.42E-04	9.80E-03	30.4	20.1	1	1			-1.12		-1.91		8.11E-10	Y	Y	
Irf7	1.55	8.45E-04	9.83E-03	3.6	5.5		1					1.32	interferon regulatory factor 7	3.07E-02	Y		
Smarcd2	1.36	8.51E-04	9.89E-03	22.3	30.3	1						1.63	SWI/SNF related, matrix associated, actin dependent regulator of	2.65E-08	Y		
Tcte1	1.43	8.54E-04	9.92E-03	6.4	9.2							1.64	t-complex-associated-testis-expressed 1	1.61E-06	Y		
RGD1561039	-2.44	8.59E-04	9.97E-03	3.2	1.3									7.07E-01	N		
Ankrd34b	-1.40	8.62E-04	1.00E-02	11.3	8.0	1				-1.15		-1.28	ankyrin repeat domain 34B	7.76E-03	Y	Y	
Jun	1.36	8.71E-04	1.01E-02	20.8	28.2	2				1.2		1.33	jun proto-oncogene	1.40E-03	Y	Y	
Agpat9	-1.55	8.83E-04	1.02E-02	5.4	3.5								1-acylglycerol-3-phosphate O-acyltransferase 9	7.19E-02	N		
Sh3bp5	1.36	8.84E-04	1.02E-02	23.2	31.6			2				1.22	SH3-domain binding protein 5 (BTK-associated)	4.07E-02	Y		
Snrk	1.34	8.86E-04	1.02E-02	58.3	78.0							1.44	SNF related kinase	9.84E-06	Y		
Folr1	1.58	8.86E-04	1.02E-02	6.5	10.2							3.37	folate receptor 1 (adult)	3.87E-19	Y		
Tcp11	4.31	8.90E-04	1.03E-02	0.0	0.0								t-complex 11 homolog (mouse)	0.00E+00	N		
Rassf5	-1.36	8.95E-04	1.03E-02	21.2	15.5		1						Ras association (RalGDS/AF-6) domain family member 5	2.67E-01	N		
Trim59	-1.44	9.04E-04	1.04E-02	8.3	5.7		1		1			-1.45	tripartite motif containing 59	3.87E-04	Y		
Otud7b	-1.34	9.11E-04	1.05E-02	33.0	24.6								OTU domain containing 7B	5.37E-02	N		
RGD1359156	-2.24	9.13E-04	1.05E-02	2.0	0.9									7.81E-01	N		
Pde1a	-1.41	9.13E-04	1.05E-02	17.1	12.1							-1.66	phosphodiesterase 1A, calmodulin-dependent	1.47E-09	Y		
Chi3l1	-1.38	9.14E-04	1.05E-02	28.4	20.5	1							chitinase 3-like 1 (cartilage glycoprotein-39)	2.18E-01	N		
Ppp2r3a	-1.35	9.31E-04	1.07E-02	18.2	13.5			1				-1.27	protein phosphatase 2, regulatory subunit B", alpha	8.30E-03	Y		
Hr	1.35	9.39E-04	1.07E-02	14.9	20.1							1.62	hairless homolog (mouse)	1.90E-08	Y		
Fnta	-1.35	9.40E-04	1.07E-02	56.4	41.7		1		1				farnesyltransferase, CAAX box, alpha	6.78E-02	N		
Srd5a1	-1.39	9.46E-04	1.08E-02	16.2	11.6								steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-ste	8.95E-02	N		
Prlr	-1.53	9.49E-04	1.08E-02	4.7	3.1							-1.43	prolactin receptor	2.88E-02	Y		
Atp2b3	1.33	9.52E-04	1.09E-02	92.4	122.8							1.54	ATPase, Ca++ transporting, plasma membrane 3	4.68E-08	Y		
Ypel5	-1.34	9.54E-04	1.09E-02	96.8	72.4							-1.30	yippee-like 5 (Drosophila)	2.02E-03	Y		
Crb2	1.40	9.58E-04	1.09E-02	8.1	11.4							1.66	crumbs homolog 2 (Drosophila)	2.54E-07	Y		

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Npr3	-1.94	9.71E-04	1.10E-02	2.0	1.0								natriuretic peptide receptor C/guanylate cyclase C (atrionatriureti	0.00E+00	N		
Map1a	-1.32	9.85E-04	1.12E-02	286.2	216.5								microtubule-associated protein 1A	8.50E-02	N		
Egfl8	1.61	9.88E-04	1.12E-02	3.7	5.9							2.45	EGF-like-domain, multiple 8	1.70E-08	Y		
Syn1	-1.34	9.89E-04	1.12E-02	58.6	43.9		1					-1.25	synapsin I	1.28E-02	Y		
Maf	1.43	9.92E-04	1.12E-02	8.4	12.0							2.08	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	4.12E-11	Y		
Sgms2	-1.58	9.96E-04	1.13E-02	4.8	3.0								sphingomyelin synthase 2	7.79E-02	N		
Nppc	1.78	1.00E-03	1.13E-02	2.6	4.6							1.67	natriuretic peptide C	9.39E-03	Y		
Trhr	-1.52	1.01E-03	1.14E-02	3.5	2.3		1					-1.63	thyrotropin-releasing hormone receptor	1.76E-03	Y		
Kcnc2	-1.34	1.01E-03	1.14E-02	50.1	37.5	1	1	1				-1.24	potassium voltage-gated channel, Shaw-related subfamily, member 2	1.77E-02	Y		
Abr	-1.32	1.01E-03	1.14E-02	128.3	96.9		1					-1.29	active BCR-related	2.33E-03	Y		
Mir770	-1.38	1.02E-03	1.15E-02	556.4	402.1									6.32E-02	N		
Prph	-1.44	1.03E-03	1.15E-02	11.7	8.1								peripherin	5.03E-01	N		
Tmem90b	1.35	1.03E-03	1.16E-02	39.5	53.2		1		1			1.84		7.39E-13	Y		
Epb49	-1.34	1.03E-03	1.16E-02	57.8	43.2							-1.21	erythrocyte membrane protein band 4.9 (dematin)	4.03E-02	Y		
Dgkb	-1.34	1.04E-03	1.16E-02	24.2	18.1		2	1				-1.42	diacylglycerol kinase, beta 90kDa	1.93E-05	Y		
Tal1	-1.40	1.05E-03	1.17E-02	7.7	5.5							-1.30	T-cell acute lymphocytic leukemia 1	1.06E-02	Y		
Slc44a4	1.44	1.05E-03	1.18E-02	6.7	9.7							2.31	solute carrier family 44, member 4	3.34E-16	Y		
Cys1	-1.46	1.06E-03	1.18E-02	5.9	4.1		1					-1.28	cystin 1	3.83E-02	Y		
Ugt1a7c	-1.54	1.07E-03	1.19E-02	4.7	3.0									6.52E-01	N		
Scn5a	-1.64	1.08E-03	1.21E-02	0.8	0.5							-1.63	sodium channel, voltage-gated, type V, alpha subunit	7.56E-03	Y		
Mpp5	-1.36	1.08E-03	1.21E-02	23.2	17.0							-1.27	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5) //	9.87E-03	Y		
Adfp	-1.41	1.09E-03	1.21E-02	14.5	10.2		1					-1.48	adipose differentiation related protein	4.43E-05	Y		
Tomm20	-1.34	1.10E-03	1.23E-02	118.3	88.1	1						-1.41	translocase of outer mitochondrial membrane 20 homolog (yeast)	3.57E-05	Y		
Tll2	2.43	1.11E-03	1.24E-02	0.3	0.6								tolloid-like 2	7.43E-01	N		
Ctbp2	1.34	1.12E-03	1.24E-02	25.7	34.5		1	1				1.41	C-terminal binding protein 2	5.13E-05	Y		
Kcnq3	-1.34	1.12E-03	1.24E-02	19.1	14.2	2						-1.39	potassium voltage-gated channel, KQT-like subfamily, member 3	8.61E-05	Y		
Znf521	1.33	1.12E-03	1.24E-02	41.2	54.9			1				2.09	zinc finger protein 521	3.34E-20	Y		
Rnf182	1.38	1.13E-03	1.25E-02	24.2	33.4		1		1			2.77	ring finger protein 182	1.53E-25	Y		
Sp110	1.58	1.14E-03	1.26E-02	3.0	4.8	1							SP110 nuclear body protein	3.71E-01	N		
Prtfdc1	-1.38	1.14E-03	1.26E-02	39.9	29.0			1						1.66E-01	N		
Rnf40	1.34	1.14E-03	1.26E-02	21.4	28.8							1.22	ring finger protein 40, E3 ubiquitin protein ligase	3.72E-02	Y		
Canx	-1.32	1.14E-03	1.26E-02	211.2	160.1	1			1			-1.33	calnexin	4.07E-04	Y		
Atp5g3	-1.33	1.15E-03	1.27E-02	274.0	205.7								ATP synthase, H+ transporting, mitochondrial Fo complex, subunit	9.88E-01	N		
Trank1	-1.33	1.15E-03	1.27E-02	33.2	25.1							-1.49	tetratricopeptide repeat and ankyrin repeat containing 1 /	5.68E-07	Y		
Cat	-1.33	1.16E-03	1.28E-02	75.2	56.4		3	1					catalase	2.72E-01	N		
Omg	-1.34	1.16E-03	1.28E-02	80.8	60.5	1	1		1			-1.36	oligodendrocyte myelin glycoprotein	2.37E-04	Y		
RGD1565675	-1.37	1.16E-03	1.28E-02	86.8	63.3							-1.40		1.75E-04	Y		
Prosc	-1.35	1.16E-03	1.28E-02	65.4	48.4		1					-1.42	proline synthetase co-transcribed homolog (bacterial)	5.00E-05	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Slc25a46	-1.34	1.17E-03	1.28E-02	51.9	38.8							-1.35	solute carrier family 25, member 46	3.11E-04	Y		
Gng7	-1.42	1.17E-03	1.28E-02	8.5	6.0	1	1					-1.55	guanine nucleotide binding protein (G protein), gamma 7	7.96E-06	Y		
RGD1562373	-1.53	1.17E-03	1.28E-02	7.9	5.2									2.99E-01	N		
Ssbp4	1.35	1.19E-03	1.30E-02	37.6	50.9								single stranded DNA binding protein 4	6.20E-01	N		
Ypel3	1.34	1.19E-03	1.30E-02	95.5	127.9								yippee-like 3 (Drosophila)	1.17E-01	N		
Slc35d3	-2.05	1.20E-03	1.31E-02	1.0	0.5		2						solute carrier family 35, member D3	7.07E-01	N		
Sfrs8	1.35	1.21E-03	1.32E-02	21.0	28.3			1	1			1.32		2.88E-03	Y		
Atp2b4	-1.33	1.21E-03	1.32E-02	43.2	32.5	1						-1.21	ATPase, Ca++ transporting, plasma membrane 4	3.76E-02	Y		
Arhgap22	-1.58	1.21E-03	1.32E-02	3.9	2.5								Rho GTPase activating protein 22	2.38E-01	N		
Ttc7	1.37	1.21E-03	1.32E-02	7.4	10.2	1						1.64		2.04E-07	Y		
Drd5	-1.72	1.21E-03	1.32E-02	3.6	2.1			1					dopamine receptor D5	0.00E+00	N		
Myh11	1.35	1.21E-03	1.32E-02	8.3	11.2		1						myosin, heavy chain 11, smooth muscle	9.33E-02	N		
Heyl	-1.36	1.23E-03	1.33E-02	13.8	10.2		1		1				hairy/enhancer-of-split related with YRPW motif-like	1.72E-01	N		
Otx2	-1.46	1.23E-03	1.33E-02	7.0	4.8								orthodenticle homeobox 2	2.85E-01	N		
Pank1	-1.35	1.23E-03	1.33E-02	31.4	23.3		1						pantothenate kinase 1	4.88E-01	N		
Hspa1b	1.45	1.23E-03	1.33E-02	2.2	3.2	1			1			1.43	heat shock 70kDa protein 1B	9.93E-04	Y		
Tm4sf1	-1.55	1.24E-03	1.34E-02	5.0	3.3		1						transmembrane 4 L six family member 1	1.76E-01	N		
Layn	1.64	1.24E-03	1.34E-02	3.5	5.8							1.44	layilin	9.63E-03	Y		
Fgr	1.75	1.25E-03	1.34E-02	1.1	1.9							1.75	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog	1.28E-02	Y		
Fam13b1	-1.32	1.25E-03	1.34E-02	67.6	51.1		2						family with sequence similarity 13, member B1	5.37E-02	N		
RT1-N3	2.00	1.25E-03	1.35E-02	0.8	1.6							1.66		1.66E-02	Y		
Scnm1	1.45	1.26E-03	1.36E-02	11.7	17.0								sodium channel modifier 1	8.98E-01	N		
Ak3l1	1.36	1.28E-03	1.37E-02	56.4	76.9	1	1					1.39	adenylate kinase 3-like 1	7.02E-04	Y		
Mmp17	-1.40	1.29E-03	1.38E-02	8.6	6.2		1					-1.56	matrix metallopeptidase 17 (membrane-inserted)	3.95E-07	Y		
Acly	-1.32	1.29E-03	1.39E-02	72.3	54.7	2	1					-1.30	ATP citrate lyase	1.62E-03	Y		
Klc4	1.36	1.30E-03	1.39E-02	16.2	22.0		1		1			1.29	kinesin light chain 4	8.15E-03	Y		
Map3k6	1.65	1.30E-03	1.39E-02	0.9	1.4				1			2.12	mitogen-activated protein kinase kinase kinase 6	6.61E-05	Y		
Nfib	1.33	1.30E-03	1.39E-02	56.6	75.2	2		1	1			1.70	nuclear factor I/B	8.63E-11	Y		
RGD1565972	-2.92	1.30E-03	1.39E-02	0.3	0.1									0.00E+00	N		
Disp2	-1.31	1.30E-03	1.39E-02	196.6	149.6		1					-1.44	dispatched homolog 2 (Drosophila)	4.11E-06	Y		
Grb14	-1.39	1.33E-03	1.42E-02	17.7	12.7		4					-1.34	growth factor receptor-bound protein 14	5.18E-03	Y		
Dpysl5	-1.34	1.34E-03	1.43E-02	22.3	16.7	1			1			-1.44	dihydropyrimidinase-like 5	1.02E-05	Y		
Gpatch4	-1.42	1.35E-03	1.44E-02	12.5	8.8	2	1				-1.23	-1.53	G patch domain containing 4	4.73E-05	Y		Y
Fdps	-1.34	1.35E-03	1.44E-02	94.8	70.8	1						-1.53	farnesyl diphosphate synthase	1.82E-07	Y		
Rpp25	-1.51	1.36E-03	1.45E-02	8.2	5.4							-1.57	ribonuclease P/MRP 25kDa subunit	8.93E-05	Y		
Gpr64	-1.45	1.36E-03	1.45E-02	4.1	2.8		1					-1.30	G protein-coupled receptor 64	1.46E-02	Y		
Sec31b	-1.55	1.37E-03	1.46E-02	2.5	1.6								SEC31 homolog B (S. cerevisiae)	7.24E-01	N		
RGD1560471	1.36	1.39E-03	1.47E-02	7.9	10.8							2.34		2.00E-19	Y		
Wdr93	1.47	1.39E-03	1.48E-02	5.0	7.3							1.51	WD repeat domain 93	3.73E-04	Y		
Qsox2	1.34	1.39E-03	1.48E-02	16.0	21.5							1.39	quiescin Q6 sulfhydryl oxidase 2	2.22E-04	Y		
Lrrc48	1.40	1.40E-03	1.48E-02	11.7	16.3							1.57	leucine rich repeat containing 48	2.66E-06	Y		
Trappc2	-1.35	1.40E-03	1.48E-02	54.8	40.7		1					-1.35	trafficking protein particle complex 2	6.85E-04	Y		
Speg	1.33	1.40E-03	1.48E-02	11.3	15.0		1					1.37	SPEG complex locus	2.34E-04	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Slc27a3	1.37	1.40E-03	1.48E-02	13.4	18.3		1		1			1.27	solute carrier family 27 (fatty acid transporter), member 3	1.97E-02	Y		
Racgap1	1.43	1.41E-03	1.49E-02	5.8	8.2				1			1.80	Rac GTPase activating protein 1	5.60E-08	Y		
Pnlip	-1.65	1.41E-03	1.49E-02	4.3	2.6	2							pancreatic lipase	9.17E-02	N		
Mtus1	1.32	1.42E-03	1.49E-02	109.5	144.1	1	2		1			2.15	microtubule associated tumor suppressor 1	2.74E-23	Y		
Lppr5	-1.39	1.42E-03	1.49E-02	11.4	8.2	1						-1.60	lipid phosphate phosphatase-related protein type 5	1.08E-07	Y		
Baalc	-1.33	1.42E-03	1.50E-02	51.8	38.9							-1.24	brain and acute leukemia, cytoplasmic	1.97E-02	Y		
Tcp11l2	1.34	1.44E-03	1.51E-02	28.1	37.7	1	1					1.46	t-complex 11 (mouse)-like 2	1.74E-05	Y		
RGD1310429	-1.34	1.44E-03	1.51E-02	35.5	26.4							-1.28		7.63E-03	Y		
Lingo4	-1.44	1.44E-03	1.51E-02	2.9	2.0							1.45	leucine rich repeat and Ig domain containing 4	7.62E-03	N		
LOC685045	-1.65	1.45E-03	1.52E-02	9.0	5.5							-1.36		4.76E-02	Y		
Spag16	1.85	1.45E-03	1.52E-02	1.8	3.3							2.23	sperm associated antigen 16	2.37E-05	Y		
Epha7	1.37	1.46E-03	1.52E-02	9.2	12.6		1	1				1.22	EPH receptor A7	4.90E-02	Y		
Rxrg	-1.50	1.46E-03	1.52E-02	6.0	4.0		1		1			-1.67	retinoid X receptor, gamma	2.68E-03	Y		
Kif13a	1.32	1.46E-03	1.52E-02	24.3	32.2		1					1.75	kinesin family member 13A	5.06E-12	Y		
P4ha3	1.84	1.47E-03	1.53E-02	1.2	2.2							1.99	prolyl 4-hydroxylase, alpha polypeptide III	1.38E-03	Y		
Ip6k2	1.34	1.47E-03	1.53E-02	38.0	50.9		3						inositol hexakisphosphate kinase 2	3.98E-01	N		
Lmod1	-1.40	1.48E-03	1.54E-02	6.7	4.8							-1.32	leiomodin 1 (smooth muscle)	1.63E-02	Y		
Mcam	-1.35	1.48E-03	1.54E-02	23.0	17.0							-1.32	melanoma cell adhesion molecule	1.89E-03	Y		
Adam1a	1.44	1.48E-03	1.54E-02	3.2	4.6								a disintegrin and metallopeptidase domain 1a	1.23E-01	N		
Kctd8	1.35	1.48E-03	1.54E-02	15.6	21.1								potassium channel tetramerisation domain containing 8	2.39E-01	N		
Reep1	-1.32	1.48E-03	1.54E-02	58.6	44.3		1					-1.52	receptor accessory protein 1	1.29E-07	Y		
Aldh1a2	1.53	1.48E-03	1.54E-02	2.9	4.5							1.43	aldehyde dehydrogenase 1 family, member A2	4.96E-03	Y		
Sphkap	1.31	1.49E-03	1.54E-02	101.5	133.2		1					2.32	SPHK1 interactor, AKAP domain containing	5.74E-28	Y		
Fgf11	1.50	1.49E-03	1.54E-02	11.3	17.0							1.58	fibroblast growth factor 11	5.74E-04	Y		
Lrrc10b	1.64	1.49E-03	1.54E-02	3.2	5.2							1.49		1.49E-02	Y		
Lass2	-1.35	1.49E-03	1.54E-02	32.5	24.0									1.33E-01	N		
Cecr2	1.36	1.49E-03	1.54E-02	8.2	11.2							1.76	cat eye syndrome chromosome region, candidate 2	2.61E-09	Y		
Cdo1	-1.35	1.50E-03	1.54E-02	41.8	30.9				1				cysteine dioxygenase, type I	2.63E-01	N		
Pctk1	1.32	1.50E-03	1.54E-02	108.6	142.9	1						1.31		1.41E-03	Y		
Stk36	1.36	1.50E-03	1.54E-02	7.4	10.0							1.65	serine/threonine kinase 36	5.87E-08	Y		
Cacna1a	1.31	1.52E-03	1.57E-02	55.8	73.3							1.53	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit /	6.73E-08	Y		
Kcnmb4	1.46	1.54E-03	1.58E-02	10.4	15.2							1.44	potassium large conductance calcium-activated channel, subfamily	4.39E-03	Y		
Bcl7b	1.38	1.54E-03	1.58E-02	18.6	25.7								B-cell CLL/lymphoma 7B	2.33E-01	N		
Scn2b	1.32	1.54E-03	1.58E-02	180.6	238.5	1	3						sodium channel, voltage-gated, type II, beta subunit	4.10E-01	N		
Grip2	-1.34	1.55E-03	1.58E-02	17.6	13.2		1					-1.58	glutamate receptor interacting protein 2	1.51E-08	Y		
Dnajb9	-1.36	1.55E-03	1.58E-02	28.5	21.1		1						DnaJ (Hsp40) homolog, subfamily B, member 9	1.17E-01	N		
Gstt3	-1.37	1.55E-03	1.59E-02	23.2	16.9		1					-1.29		1.21E-02	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Dlgap3	1.34	1.57E-03	1.61E-02	15.5	20.8	1	1				1.15	1.34	discs, large (Drosophila) homolog-associated protein 3	1.75E-03	Y		Y
Serping1	-1.41	1.57E-03	1.61E-02	14.3	10.1		1		1			1.34	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 //	1.28E-02	N		
Tarsl2	-1.50	1.58E-03	1.61E-02	6.0	4.0								threonyl-tRNA synthetase-like 2	2.20E-01	N		
Fam69a	-1.34	1.58E-03	1.62E-02	34.0	25.4								family with sequence similarity 69, member A	7.75E-02	N		
Prr16	-1.40	1.60E-03	1.63E-02	8.5	6.1			1					proline rich 16	5.86E-01	N		
MGC114520	1.70	1.60E-03	1.63E-02	1.9	3.3							1.98		3.25E-05	Y		
Enah	-1.33	1.61E-03	1.64E-02	52.2	39.2	1							enabled homolog (Drosophila)	2.58E-01	N		
LOC500413	-1.45	1.62E-03	1.65E-02	10.6	7.3							-1.50		1.21E-04	Y		
Znf598	1.33	1.62E-03	1.65E-02	28.0	37.2							1.24	zinc finger protein 598	1.99E-02	Y		
Mir349	1.65	1.63E-03	1.66E-02	36.7	60.7									7.61E-02	N		
Htr4	-1.48	1.63E-03	1.66E-02	10.9	7.4	1	1					-1.80	5-hydroxytryptamine (serotonin) receptor 4, G protein-coupled	2.48E-05	Y		
Rps6ka2	-1.34	1.64E-03	1.66E-02	13.4	10.0	2		2				-1.36	ribosomal protein S6 kinase, 90kDa, polypeptide 2	4.50E-04	Y		
Asmt	2.55	1.64E-03	1.66E-02	0.4	1.0							2.01	acetylserotonin O-methyltransferase	3.94E-02	Y		
Cdh10	-1.35	1.64E-03	1.66E-02	19.7	14.6							-1.29	cadherin 10, type 2 (T2-cadherin)	5.50E-03	Y		
Fhdc1	-1.38	1.67E-03	1.69E-02	8.3	6.0							-1.26	FH2 domain containing 1	3.34E-02	Y		
Rnase4	-1.35	1.67E-03	1.69E-02	42.6	31.6									9.50E-01	N		
Olfm1	1.31	1.68E-03	1.70E-02	85.8	112.7		1		2			1.46	olfactomedin 1	3.70E-06	Y		
Pam	-1.31	1.69E-03	1.70E-02	71.4	54.3	1	1					-1.42	peptidylglycine alpha-amidating monooxygenase	1.71E-05	Y		
Angpt2	1.67	1.69E-03	1.71E-02	1.5	2.5							1.45	angiopoietin 2	1.41E-02	Y		
Lgi3	-1.31	1.70E-03	1.71E-02	105.1	80.2		1		1			-1.22	leucine-rich repeat LGI family, member 3	2.58E-02	Y		
Pllp	-1.35	1.71E-03	1.72E-02	37.6	27.8	1			1			-1.24	plasmolipin	3.69E-02	Y		
Fam18b2	-1.46	1.74E-03	1.75E-02	8.6	5.9							-1.22	family with sequence similarity 18, member B2	1.93E-02	Y		
Glrx1	-1.38	1.75E-03	1.76E-02	27.7	20.1									1.31E-01	N		
Cherp	1.35	1.75E-03	1.76E-02	11.4	15.4							1.33	calcium homeostasis endoplasmic reticulum protein	3.35E-03	Y		
Zdhhc22	-1.44	1.76E-03	1.76E-02	15.3	10.6	1						-1.43	zinc finger, DHHC-type containing 22	4.68E-04	Y		
Fam117a	1.44	1.76E-03	1.76E-02	4.9	7.0							2.20	family with sequence similarity 117, member A	3.68E-11	Y		
Acot7	-1.31	1.76E-03	1.76E-02	155.8	118.6				1			-1.42	acyl-CoA thioesterase 7	1.22E-05	Y		
Fundc1	-1.35	1.76E-03	1.76E-02	30.1	22.3							-1.37	FUN14 domain containing 1	4.50E-04	Y		
Bat5	1.32	1.77E-03	1.77E-02	58.6	77.4	2						1.42	HLA-B associated transcript 5	3.04E-05	Y		
Znf524	1.66	1.78E-03	1.78E-02	3.4	5.6	1					-1.12		zinc finger protein 524	6.17E-01	N		Y
Abca7	1.33	1.79E-03	1.78E-02	12.1	16.1		1						ATP-binding cassette, sub-family A (ABC1), member 7	1.47E-01	N		
Pcbd1	-1.42	1.81E-03	1.80E-02	26.2	18.4		1					-1.68	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of	3.98E-08	Y		
RGD1561852	-1.46	1.83E-03	1.82E-02	12.1	8.3									8.22E-01	N		
Prima1	-1.42	1.85E-03	1.84E-02	6.0	4.3								proline rich membrane anchor 1	2.21E-01	N		
Stk11	1.33	1.85E-03	1.84E-02	20.5	27.2							1.26	serine/threonine kinase 11	1.40E-02	Y		
Cdkl2	-1.38	1.85E-03	1.84E-02	15.2	11.0							-1.47	cyclin-dependent kinase-like 2 (CDC2-related kinase)	5.68E-05	Y		
Pcdh8	-1.38	1.87E-03	1.86E-02	11.3	8.2							-1.44	protocadherin 8	1.03E-04	Y		
Klhl25	1.37	1.87E-03	1.86E-02	7.5	10.3							1.31	kelch-like 25 (Drosophila)	8.70E-03	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Mfsd2	-1.36	1.87E-03	1.86E-02	20.0	14.7	1								1.11E-01	N		
Nap1l2	-1.32	1.88E-03	1.86E-02	74.5	56.6	1						-1.27	nucleosome assembly protein 1-like 2	6.13E-03	Y		
Pold1	1.52	1.88E-03	1.86E-02	1.9	3.0	1						2.03	polymerase (DNA directed), delta 1, catalytic subunit	5.74E-07	Y		
Chst1	-1.32	1.88E-03	1.86E-02	66.2	50.2	1	1					-1.34	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	5.69E-04	Y		
Zfp395	1.34	1.88E-03	1.86E-02	13.6	18.2		1					1.35		1.37E-03	Y		
Cdc42ep4	1.37	1.88E-03	1.86E-02	8.9	12.1							1.70	CDC42 effector protein (Rho GTPase binding) 4	3.92E-08	Y		
Pgr15l	-1.55	1.89E-03	1.86E-02	5.3	3.4									4.63E-01	N		
Tpm2	1.65	1.90E-03	1.87E-02	3.4	5.6		1						tropomyosin 2 (beta)	7.48E-01	N		
RGD1565283	1.82	1.91E-03	1.88E-02	2.6	4.7							2.09		2.22E-04	Y		
Anxa11	1.34	1.91E-03	1.88E-02	24.2	32.3		3					1.75	annexin A11	1.00E-10	Y		
B3galt6	-1.40	1.94E-03	1.91E-02	11.1	7.9								UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptid	5.03E-02	N		
Cblb	1.33	1.95E-03	1.91E-02	19.3	25.7							1.41	Cbl proto-oncogene, E3 ubiquitin protein ligase B	1.10E-04	Y		
Stox2	-1.31	1.96E-03	1.92E-02	45.5	34.7							-1.20	storkhead box 2	4.04E-02	Y		
Ttc25	1.49	1.96E-03	1.93E-02	3.4	5.1				1			2.15	tetratricopeptide repeat domain 25	3.75E-10	Y		
Spsb4	-1.60	1.97E-03	1.93E-02	2.4	1.5		1						splA/ryanodine receptor domain and SOCS box containing 4	1.12E-01	N		
Atf7	1.33	1.97E-03	1.93E-02	30.4	40.4							1.65	activating transcription factor 7	6.41E-09	Y		
Ubr7	-1.34	1.98E-03	1.94E-02	16.9	12.6								ubiquitin protein ligase E3 component n-recognin 7 (putative)	8.20E-01	N		
RGD1563349	-1.34	1.99E-03	1.94E-02	12.9	9.6							-1.43		2.92E-05	Y		
MGC114464	-1.37	2.01E-03	1.96E-02	22.9	16.7							-1.42		2.08E-04	Y		
Kcnt1	1.31	2.02E-03	1.97E-02	63.6	83.2	2	1				1.18	1.74	potassium channel, subfamily T, member 1	5.11E-12	Y		Y
RGD1359634	1.41	2.02E-03	1.97E-02	10.6	15.0									6.78E-02	N		
Thrsp	-1.34	2.02E-03	1.97E-02	44.8	33.4		3						thyroid hormone responsive	5.24E-01	N		
RGD1309537	1.38	2.04E-03	1.98E-02	20.6	28.6									8.51E-02	N		
Myl9	1.44	2.05E-03	1.99E-02	10.5	15.2							1.43	myosin, light chain 9, regulatory	1.86E-03	Y		
St8sia4	-1.46	2.05E-03	1.99E-02	5.7	3.9			1				-1.27	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	2.16E-02	Y		
St3gal2	1.31	2.05E-03	2.00E-02	53.3	69.8		1					1.40	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	6.18E-05	Y		
Ppl	1.46	2.06E-03	2.00E-02	1.5	2.1							2.17	periplakin	2.27E-10	Y		
Tacr3	1.36	2.07E-03	2.01E-02	12.2	16.7	1						1.34	tachykinin receptor 3	5.33E-03	Y		
Scml4	-1.38	2.08E-03	2.01E-02	6.3	4.6							-1.33	sex comb on midleg-like 4 (Drosophila)	1.23E-02	Y		
Znf286a	-1.44	2.09E-03	2.02E-02	5.2	3.6							-1.33	zinc finger protein 286A	1.62E-02	Y		
Rhobtb3	-1.36	2.10E-03	2.03E-02	8.0	5.9	1			1				Rho-related BTB domain containing 3	4.50E-01	N		
Zmat3	-1.30	2.11E-03	2.04E-02	267.6	205.1		1		1			-1.29	zinc finger, matrin-type 3	2.53E-03	Y		
Rab11fip1	1.45	2.11E-03	2.04E-02	1.3	1.9							1.90	RAB11 family interacting protein 1 (class I)	1.73E-08	Y		
Ube2ql1	-1.32	2.13E-03	2.05E-02	43.7	33.1		1					-1.24		1.73E-02	Y		
Hsd17b14	2.25	2.13E-03	2.05E-02	1.1	2.4								hydroxysteroid (17-beta) dehydrogenase 14	4.39E-01	N		
Cdh6	-1.37	2.13E-03	2.05E-02	9.6	7.0							-1.40	cadherin 6, type 2, K-cadherin (fetal kidney)	2.40E-04	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Id3	1.48	2.13E-03	2.05E-02	8.4	12.4								inhibitor of DNA binding 3, dominant negative helix-loop-helix prote	6.35E-02	N		
RGD1304952	-1.32	2.15E-03	2.07E-02	49.2	37.3							-1.31		2.29E-03	Y		
Col9a2	1.37	2.15E-03	2.07E-02	8.0	11.0							1.72	collagen, type IX, alpha 2	2.92E-06	Y		
Atf3	2.24	2.17E-03	2.09E-02	0.5	1.0	2			1	1.79		2.96	activating transcription factor 3	3.21E-05	Y	Y	
Rasgrp3	-1.37	2.17E-03	2.09E-02	8.0	5.9				1				RAS guanyl releasing protein 3 (calcium and DAG-regulated)	1.61E-01	N		
Rhoq	-1.34	2.18E-03	2.09E-02	13.5	10.0		1					-1.24	ras homolog family member Q	2.41E-02	Y		
Rhov	-1.39	2.18E-03	2.09E-02	15.9	11.5		1					-1.31	ras homolog family member V	8.52E-03	Y		
Cyp2s1	-1.64	2.19E-03	2.09E-02	2.2	1.3								cytochrome P450, family 2, subfamily S, polypeptide 1	5.75E-02	N		
Cacng8	-1.44	2.19E-03	2.10E-02	11.6	8.0							-1.39	calcium channel, voltage-dependent, gamma subunit 8	4.29E-03	Y		
Nrbp2	1.30	2.20E-03	2.10E-02	139.5	181.6		1					1.20	nuclear receptor binding protein 2	3.68E-02	Y		
Metrn	1.33	2.20E-03	2.10E-02	63.9	84.9							1.58	meteorin, glial cell differentiation regulator	1.21E-07	Y		
Adamts1	1.44	2.20E-03	2.10E-02	2.5	3.6	1	1					1.66	ADAM metallopeptidase with thrombospondin type 1 motif, 1	6.19E-06	Y		
Caln1	1.33	2.21E-03	2.11E-02	73.6	97.7							2.33	calneuron 1	2.74E-20	Y		
Sccpdh	-1.32	2.21E-03	2.11E-02	76.7	58.2							-1.34	saccharopine dehydrogenase (putative)	7.33E-04	Y		
Mgat3	1.31	2.24E-03	2.13E-02	63.7	83.3							1.25	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltrans	1.37E-02	Y		
Tmed7	-1.31	2.24E-03	2.13E-02	69.8	53.4	1						-1.20		4.48E-02	Y		
Doc2g	1.69	2.24E-03	2.13E-02	1.9	3.3								double C2, gamma	5.03E-02	N		
Tyro3	1.30	2.26E-03	2.14E-02	68.4	89.1		1					1.47	TYRO3 protein tyrosine kinase	2.90E-06	Y		
Epn3	1.38	2.26E-03	2.14E-02	5.3	7.3							2.36	epsin 3	3.21E-14	Y		
Gfod1	1.34	2.29E-03	2.18E-02	32.7	43.6							1.89	glucose-fructose oxidoreductase domain containing 1	6.50E-13	Y		
Elk1	1.33	2.30E-03	2.18E-02	16.7	22.3							1.46	ELK1, member of ETS oncogene family	6.22E-05	Y		
Myom2	1.62	2.30E-03	2.18E-02	0.8	1.3							2.15	myomesin (M-protein) 2, 165kDa	4.42E-05	Y		
Ndfip1	-1.30	2.30E-03	2.18E-02	395.8	305.0							-1.36	Nedd4 family interacting protein 1	1.27E-04	Y		
Nr1h3	1.43	2.30E-03	2.18E-02	7.6	10.9	1						1.61	nuclear receptor subfamily 1, group H, member 3	8.92E-05	Y		
Tox3	-1.43	2.31E-03	2.18E-02	5.9	4.1							-1.51	TOX high mobility group box family member 3	8.00E-05	Y		
Rilpl2	1.41	2.31E-03	2.18E-02	10.2	14.5							1.33	Rab interacting lysosomal protein-like 2	1.22E-02	Y		
Sv2b	1.30	2.32E-03	2.19E-02	61.8	80.4		1					1.28	synaptic vesicle glycoprotein 2B	3.81E-03	Y		
Clk2	1.34	2.32E-03	2.19E-02	23.4	31.4				1			1.37	CDC-like kinase 2	1.15E-03	Y		
Ckb	1.30	2.32E-03	2.19E-02	721.6	935.6	3						1.37	creatine kinase, brain	9.61E-05	Y		
Polh	1.38	2.33E-03	2.19E-02	6.0	8.2							1.27	polymerase (DNA directed), eta	3.77E-02	Y		
Rem2	1.57	2.35E-03	2.21E-02	2.7	4.2	1	1					1.81	RAS (RAD and GEM)-like GTP binding 2	1.20E-03	Y		
Nol3	-1.42	2.36E-03	2.22E-02	11.4	8.0	1	1		1			-1.47	nucleolar protein 3 (apoptosis repressor with CARD domain)	1.57E-04	Y		
Gal3st3	1.36	2.37E-03	2.23E-02	12.7	17.2							1.58	galactose-3-O-sulfotransferase 3	3.01E-06	Y		
Eif2c1	-1.32	2.39E-03	2.24E-02	22.2	16.8								eukaryotic translation initiation factor 2C, 1	3.94E-01	N		
Cdig2	-1.31	2.39E-03	2.24E-02	36.9	28.2								Cdig2 protein	1.34E-01	N		
Cmas	-1.32	2.39E-03	2.24E-02	54.3	41.2							-1.41	cytidine monophosphate N-acetylneuraminic acid synthetase	5.50E-05	Y		
Tdrd5	-1.69	2.40E-03	2.24E-02	1.4	0.8							-1.45	tudor domain containing 5	1.66E-02	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Tect2	1.36	2.41E-03	2.25E-02	10.8	14.7							1.39		8.61E-04	Y		
Tarbp2	1.38	2.41E-03	2.25E-02	24.7	34.2								TAR (HIV-1) RNA binding protein 2	3.34E-01	N		
Eln	1.44	2.42E-03	2.26E-02	2.8	4.0							1.42	elastin	1.25E-02	Y		
RGD1309139	1.55	2.43E-03	2.27E-02	2.1	3.3							1.83		3.45E-05	Y		
Cnp	-1.30	2.44E-03	2.27E-02	282.8	218.3				2			-1.25	2',3'-cyclic nucleotide 3' phosphodiesterase	9.57E-03	Y		
Sema3c	-1.37	2.44E-03	2.27E-02	6.1	4.4		1	1				-1.29	sema domain, immunoglobulin domain (Ig), short basic domain, secr	7.78E-03	Y		
Capza1	-1.31	2.45E-03	2.28E-02	54.5	41.7		1					-1.43	capping protein (actin filament) muscle Z-line, alpha 1	1.06E-05	Y		
Clip3	1.30	2.45E-03	2.28E-02	214.8	278.6							1.28	CAP-GLY domain containing linker protein 3	3.50E-03	Y		
Sult1a1	-1.42	2.47E-03	2.29E-02	13.9	9.8		1						sulfotransferase family, cytosolic, 1A, phenol-preferring	9.81E-01	N		
Ubxn11	1.38	2.47E-03	2.29E-02	11.6	16.0		1					1.58	UBX domain protein 11	5.88E-06	Y		
Ccdc8	1.44	2.47E-03	2.30E-02	3.1	4.4							1.56	coiled-coil domain containing 8	3.24E-04	Y		
Gpr139	-1.73	2.48E-03	2.30E-02	4.1	2.4								G protein-coupled receptor 139	2.04E-01	N		
Nkiras1	-1.31	2.49E-03	2.31E-02	46.1	35.2	1	1				1.16		NFKB inhibitor interacting Ras-like 1	7.63E-01	N		Y
Nr1d1	1.32	2.50E-03	2.32E-02	30.1	39.7	1						1.83	nuclear receptor subfamily 1, group D, member 1	4.13E-12	Y		
Grm7	-1.32	2.51E-03	2.32E-02	4.4	3.3	1	1	2			1.37		glutamate receptor, metabotropic 7	1.21E-01	N		N
Polr2i	1.71	2.52E-03	2.33E-02	3.3	5.7		1					1.65	polymerase (RNA) II (DNA directed) polypeptide I, 14.5kDa	1.64E-02	Y		
Ruvbl2	1.34	2.53E-03	2.34E-02	23.3	31.2				1				RuvB-like 2 (E. coli)	6.95E-02	N		
Mapk9	-1.30	2.54E-03	2.34E-02	76.3	58.7							-1.22	mitogen-activated protein kinase 9	2.78E-02	Y		
Selo	1.32	2.54E-03	2.34E-02	27.1	35.7							1.48	selenoprotein O	1.01E-05	Y		
Itfg1	-1.30	2.58E-03	2.38E-02	139.6	107.7							-1.23	integrin alpha FG-GAP repeat containing 1	1.96E-02	Y		
Tm4sf19	-1.97	2.58E-03	2.38E-02	3.4	1.7							-2.02	transmembrane 4 L six family member 19	2.55E-04	Y		
Cdgap	1.32	2.59E-03	2.38E-02	11.6	15.4		1					1.47	Cdc42 GTPase-activating protein	2.24E-05	Y		
Fdft1	-1.30	2.60E-03	2.40E-02	66.8	51.3		1					-1.47	farnesyl-diphosphate farnesyltransferase 1	1.54E-06	Y		
Col1a1	1.34	2.62E-03	2.41E-02	6.3	8.4	1						2.09	collagen, type I, alpha 1	2.65E-16	Y		
Ppm1d	1.32	2.63E-03	2.41E-02	19.0	25.1							1.82	protein phosphatase, Mg2+/Mn2+ dependent, 1D	1.65E-11	Y		
Jakmip1	-1.33	2.65E-03	2.43E-02	28.0	21.1		1	1				-1.53	janus kinase and microtubule interacting protein 1	3.55E-07	Y		
Tspo	1.59	2.66E-03	2.44E-02	4.8	7.7							1.76	translocator protein (18kDa)	3.16E-04	Y		
Ptger4	1.73	2.66E-03	2.44E-02	1.6	2.8				1				prostaglandin E receptor 4 (subtype EP4)	1.73E-01	N		
Ankrd54	1.36	2.66E-03	2.44E-02	13.4	18.1							1.26	ankyrin repeat domain 54	3.62E-02	Y		
Slc26a1	-1.69	2.67E-03	2.45E-02	1.4	0.8								solute carrier family 26 (sulfate transporter), member 1	3.75E-01	N		
Tcfe2a	1.39	2.68E-03	2.45E-02	5.4	7.6							1.40		3.90E-03	Y		
Orai3	1.37	2.68E-03	2.45E-02	11.9	16.2		1					1.63	ORAI calcium release-activated calcium modulator 3	8.18E-07	Y		
Itpripl1	1.97	2.69E-03	2.46E-02	0.7	1.4								inositol 1,4,5-trisphosphate receptor interacting protein-like	4.16E-01	N		
Gpc5	-1.33	2.70E-03	2.46E-02	21.4	16.1			1				-1.36	glypican 5	6.12E-04	Y		

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Crhr1	1.36	2.70E-03	2.46E-02	19.2	26.1		1		1			3.00	corticotropin releasing hormone receptor 1	1.94E-23	Y		
Tmem150c	-1.32	2.72E-03	2.47E-02	24.6	18.6							-1.60		1.10E-08	Y		
LOC679651	-1.29	2.72E-03	2.48E-02	38.6	29.8							-1.39		4.50E-05	Y		
Kremen1	1.48	2.73E-03	2.48E-02	3.7	5.5							1.53	kringle containing transmembrane protein 1	1.87E-03	Y		
Tob2	1.35	2.75E-03	2.50E-02	13.0	17.5							1.79	transducer of ERBB2, 2	2.61E-09	Y		
Vcan	1.30	2.77E-03	2.51E-02	12.7	16.5		2					1.50	versican	7.96E-07	Y		
H6pd	1.32	2.77E-03	2.51E-02	11.4	15.1							1.71	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	3.57E-09	Y		
Nrg1	-1.38	2.80E-03	2.54E-02	4.0	2.9	1	1	1		-1.24		-1.26	neuregulin 1	2.47E-02	Y	Y	
Hcrtr2	-1.53	2.80E-03	2.54E-02	2.8	1.8		1					-2.09	hypocretin (orexin) receptor 2	7.42E-16	Y		
Car14	-1.43	2.81E-03	2.54E-02	14.5	10.2		1						carbonic anhydrase 14	1.63E-01	N		
Kcnj2	-1.52	2.81E-03	2.54E-02	6.4	4.2				1				potassium inwardly-rectifying channel, subfamily J, member 2	1.37E-01	N		
Tmem116	2.24	2.82E-03	2.55E-02	0.6	1.4								transmembrane protein 116	6.78E-02	N		
Pkp3	1.84	2.83E-03	2.55E-02	0.6	1.1							3.89	plakophilin 3	8.90E-09	Y		
Pnkp	1.37	2.83E-03	2.56E-02	11.2	15.4	1							polynucleotide kinase 3'-phosphatase	2.91E-01	N		
Npepl1	1.44	2.85E-03	2.57E-02	5.2	7.4				2			1.30	aminopeptidase-like 1	3.84E-02	Y		
Map3k12	1.30	2.85E-03	2.57E-02	67.7	87.7							1.28	mitogen-activated protein kinase kinase kinase 12	4.87E-03	Y		
Alkbh4	1.44	2.85E-03	2.57E-02	5.1	7.4								alkB, alkylation repair homolog 4 (E. coli)	1.20E-01	N		
Mir384	-1.40	2.87E-03	2.58E-02	222.7	158.7									3.82E-01	N		
Pdk4	-1.40	2.87E-03	2.58E-02	14.0	10.0				2				pyruvate dehydrogenase kinase, isozyme 4	1.42E-01	N		
Reep5	-1.29	2.87E-03	2.58E-02	200.5	155.3		1					-1.40	receptor accessory protein 5	2.22E-05	Y		
Spag4	-1.53	2.87E-03	2.58E-02	5.4	3.5		2						sperm associated antigen 4	6.90E-02	N		
Map1b	-1.29	2.89E-03	2.59E-02	381.6	296.6	2	1		1			-1.28	microtubule-associated protein 1B	2.47E-03	Y		
Klhl4	-1.38	2.90E-03	2.60E-02	7.1	5.2				1				kelch-like 4 (Drosophila)	7.33E-02	N		
Rab5a	-1.36	2.90E-03	2.60E-02	44.7	32.9		1					-1.24	RAB5A, member RAS oncogene family	4.51E-02	Y		
Lrfn4	1.36	2.91E-03	2.60E-02	9.7	13.2							1.32	leucine rich repeat and fibronectin type III domain containing 4 /	9.00E-03	Y		
Naprt1	1.41	2.93E-03	2.62E-02	6.9	9.7							1.34	nicotinate phosphoribosyltransferase domain containing 1	1.75E-02	Y		
Serpine2	-1.30	2.94E-03	2.63E-02	107.4	82.8								serpin peptidase inhibitor, clade E (nexin, plasminogen activat	2.10E-01	N		
Unc13c	1.29	2.94E-03	2.63E-02	47.8	61.8	1		1				2.33	unc-13 homolog C (C. elegans)	2.09E-27	Y		
Mr1	1.39	2.94E-03	2.63E-02	10.7	14.8							1.99	major histocompatibility complex, class I-related	6.10E-11	Y		
Nus1	-1.31	2.96E-03	2.64E-02	32.0	24.5		2					-1.30		2.57E-03	Y		
Efcab10	1.82	2.96E-03	2.64E-02	2.2	3.9							1.94	EF-hand calcium binding domain 10	3.32E-04	Y		
Zcchc8	1.33	2.96E-03	2.64E-02	14.9	19.8								zinc finger, CCHC domain containing 8	1.38E-01	N		
Pacsin3	1.32	2.98E-03	2.65E-02	30.7	40.5							1.54	protein kinase C and casein kinase substrate in neurons 3	2.60E-06	Y		
Camk2d	1.29	2.99E-03	2.66E-02	107.6	139.2	1	1	1					calcium/calmodulin-dependent protein kinase II delta	8.00E-02	N		
Chkb	1.33	3.00E-03	2.67E-02	26.7	35.4		1					1.36	choline kinase beta	1.09E-03	Y		
Cdh11	-1.32	3.02E-03	2.68E-02	14.8	11.2	2						-1.30	cadherin 11, type 2, OB-cadherin (osteoblast)	3.30E-03	Y		
Afap1l1	-1.54	3.04E-03	2.70E-02	2.2	1.4								actin filament associated protein 1-like 1	8.26E-01	N		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
LOC499240	1.55	3.08E-03	2.73E-02	3.7	5.8							2.00		2.26E-06	Y		
Hpse	-2.15	3.08E-03	2.73E-02	0.9	0.4								heparanase	8.76E-02	N		
Efhc1	1.38	3.09E-03	2.74E-02	7.9	10.9							1.51	EF-hand domain (C-terminal) containing 1	4.38E-05	Y		
Il11	1.84	3.09E-03	2.74E-02	1.4	2.6							1.66	interleukin 11	3.66E-02	Y		
RGD1307461	1.36	3.09E-03	2.74E-02	8.4	11.4							1.57		2.71E-05	Y		
Mfsd6	-1.29	3.11E-03	2.74E-02	62.5	48.4		1					-1.35	major facilitator superfamily domain containing 6	2.82E-04	Y		
Mir495	-2.50	3.11E-03	2.74E-02	17.5	7.0								microRNA 495	5.44E-01	N		
Adcy10	-1.63	3.12E-03	2.75E-02	1.0	0.6								adenylate cyclase 10 (soluble)	1.53E-01	N		
Tmed3	-1.37	3.12E-03	2.75E-02	20.1	14.7	1	1					-1.34	transmembrane emp24 protein transport domain containing 3	3.01E-03	Y		
Traf2	1.35	3.13E-03	2.75E-02	12.7	17.2								TNF receptor-associated factor 2	7.36E-02	N		
Ube2v2	-1.31	3.15E-03	2.77E-02	29.0	22.1				2			-1.37	ubiquitin-conjugating enzyme E2 variant 2	2.19E-04	Y		
Atp2a2	1.29	3.16E-03	2.77E-02	303.6	390.3		3		1			1.37	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	8.82E-05	Y		
Samd4a	-1.31	3.16E-03	2.77E-02	28.7	21.9		1	1				-1.29	sterile alpha motif domain containing 4A	3.76E-03	Y		
Htr3a	-1.61	3.16E-03	2.77E-02	2.8	1.7		1					-1.58	5-hydroxytryptamine (serotonin) receptor 3A, ionotropic	2.81E-03	Y		
Casq1	1.71	3.17E-03	2.78E-02	1.3	2.3								calsequestrin 1 (fast-twitch, skeletal muscle)	8.14E-02	N		
Epha10	-1.35	3.18E-03	2.79E-02	13.0	9.7							-1.47	EPH receptor A10	2.82E-05	Y		
Impad1	-1.29	3.18E-03	2.79E-02	78.1	60.7							-1.23	inositol monophosphatase domain containing 1	1.52E-02	Y		
Fam21c	1.29	3.21E-03	2.81E-02	81.7	105.3		1					1.35	family with sequence similarity 21, member C	2.35E-04	Y		
Tanc1	1.30	3.21E-03	2.81E-02	21.8	28.3							1.69	tetratricopeptide repeat, ankyrin repeat and coiled-coil containin	2.28E-10	Y		
Caps2	1.61	3.22E-03	2.82E-02	1.8	2.9							1.82	calcyphosine 2	4.23E-05	Y		
Acsm5	-2.01	3.23E-03	2.83E-02	1.0	0.5							1.96	acyl-CoA synthetase medium-chain family member 5	3.47E-02	N		
Corin	-3.06	3.24E-03	2.83E-02	0.3	0.1								corin, serine peptidase	0.00E+00	N		
Neu4	-1.42	3.30E-03	2.87E-02	6.1	4.3							-1.31	sialidase 4	2.85E-02	Y		
Htr1a	-1.48	3.30E-03	2.87E-02	7.9	5.3			1				-1.60	5-hydroxytryptamine (serotonin) receptor 1A, G protein-coupled	1.48E-07	Y		
Nutf2	-1.33	3.30E-03	2.88E-02	26.3	19.8							-1.26	nuclear transport factor 2	1.66E-02	Y		
Ttc29	1.44	3.31E-03	2.88E-02	5.0	7.3			1				2.09	tetratricopeptide repeat domain 29	2.26E-11	Y		
Evx1	-2.05	3.34E-03	2.91E-02	0.9	0.5								even-skipped homeobox 1	0.00E+00	N		
Herv-frd	-1.61	3.35E-03	2.91E-02	3.0	1.9									2.64E-01	N		
Cyp2j10	-1.46	3.35E-03	2.91E-02	5.8	3.9		1					-1.76	cytochrome P450, family 2, subfamily j, polypeptide 13; cytochrome P450, family 2, subfamily j, polypeptide 10	3.42E-06	Y		
Nfatc2	-1.37	3.36E-03	2.91E-02	6.6	4.8							-1.33	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dep	9.08E-03	Y		
Nedd4l	1.29	3.36E-03	2.91E-02	51.0	65.8		1	1	1			1.63	neural precursor cell expressed, developmentally down-regulated 4	1.48E-09	Y		
Gabre	-1.79	3.36E-03	2.91E-02	1.2	0.6							-2.27	gamma-aminobutyric acid (GABA) A receptor, epsilon	2.82E-15	Y		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Hcn1	1.31	3.37E-03	2.92E-02	26.3	34.4	2						1.72	hyperpolarization activated cyclic nucleotide-gated potassium chann	1.20E-10	Y		
Lypd1	-1.33	3.38E-03	2.93E-02	23.7	17.8							-1.76	LY6/PLAUR domain containing 1	2.05E-12	Y		
Ifitm2	1.57	3.40E-03	2.94E-02	6.4	10.1				2			2.00	interferon induced transmembrane protein 2	2.95E-06	Y		
Stk32a	1.37	3.40E-03	2.94E-02	11.7	16.1			1				1.46	serine/threonine kinase 32A	2.62E-04	Y		
Ptafr	-1.45	3.42E-03	2.95E-02	3.7	2.5								platelet-activating factor receptor	7.00E-01	N		
Pcdhb6	-1.54	3.44E-03	2.97E-02	2.2	1.4								protocadherin beta 6	4.26E-01	N		
Znf483	-1.29	3.44E-03	2.97E-02	68.8	53.2							-1.40	zinc finger protein 483	4.41E-05	Y		
Slc28a3	1.74	3.47E-03	2.99E-02	1.1	1.8							1.64	solute carrier family 28 (sodium-coupled nucleoside transporter)	3.35E-02	Y		
Mir764	-2.02	3.47E-03	2.99E-02	20.7	10.2								miRNA 764	2.05E-01	N		
Ube2d2	-1.31	3.49E-03	3.00E-02	119.1	91.1	3						-1.23	ubiquitin-conjugating enzyme E2D 2	2.60E-02	Y		
Slc6a5	-1.33	3.49E-03	3.00E-02	7.5	5.7			1					solute carrier family 6 (neurotransmitter transporter, glycine),	7.69E-01	N		
Wwtr1	1.41	3.50E-03	3.01E-02	7.3	10.3			1	1			1.35	WW domain containing transcription regulator 1	1.47E-02	Y		
Lgi4	1.30	3.51E-03	3.01E-02	50.0	64.7							1.64	leucine-rich repeat LGI family, member 4	1.46E-09	Y		
Idua	1.30	3.51E-03	3.01E-02	34.9	45.4		1						iduronidase, alpha-L-	8.79E-01	N		
Plxnb3	-1.30	3.51E-03	3.01E-02	23.2	17.9								plexin B3	4.17E-01	N		
Uhmk1	-1.31	3.51E-03	3.01E-02	25.3	19.4	1						-1.46	U2AF homology motif (UHM) kinase 1	5.06E-06	Y		
RGD1306739	1.35	3.53E-03	3.02E-02	20.6	27.8							1.65		8.81E-08	Y		
Ophn1	1.45	3.53E-03	3.02E-02	14.3	20.8		1					1.37	oligophrenin 1	1.33E-02	Y		
Calhm2	1.50	3.53E-03	3.02E-02	3.1	4.6							3.06	calcium homeostasis modulator 2	1.16E-11	Y		
Syncrip	-1.41	3.55E-03	3.03E-02	9.7	6.9	1						1.41	synaptotagmin binding, cytoplasmic RNA interacting protein	7.16E-03	N		
Tubb3	-1.28	3.56E-03	3.04E-02	284.3	221.4		1					-1.41	tubulin, beta 3 class III	1.52E-05	Y		
Pcif1	1.31	3.56E-03	3.04E-02	14.2	18.6							1.59	PDX1 C-terminal inhibiting factor 1	1.95E-07	Y		
Ncan	-1.29	3.57E-03	3.05E-02	41.0	31.8							-1.21	neurocan	3.98E-02	Y		
RGD1562136	-1.33	3.58E-03	3.05E-02	16.0	12.0									1.22E-01	N		
LOC100125384	1.39	3.59E-03	3.05E-02	9.0	12.5									5.19E-02	N		
Tomm34	-1.30	3.59E-03	3.06E-02	52.1	40.0							-1.23	translocase of outer mitochondrial membrane 34	2.86E-02	Y		
Adpgk	-1.31	3.62E-03	3.07E-02	27.2	20.7		1					-1.31	ADP-dependent glucokinase	2.76E-03	Y		
LOC501194	-1.34	3.62E-03	3.07E-02	25.5	19.0									1.56E-01	N		
Trim65	1.36	3.62E-03	3.07E-02	9.8	13.3							1.26	tripartite motif containing 65	4.04E-02	Y		
RGD1564257	-1.59	3.63E-03	3.08E-02	13.0	8.2									5.99E-01	N		
Foxb1	-1.91	3.65E-03	3.10E-02	1.6	0.8								forkhead box B1	4.97E-01	N		
Rwdd2a	-1.60	3.68E-03	3.12E-02	3.6	2.3		1						RWD domain containing 2A	1.43E-01	N		
Stxbp6	-1.38	3.68E-03	3.12E-02	16.9	12.3			1				-1.32	syntaxin binding protein 6 (amisyn)	1.10E-02	Y		
Slc25a22	1.29	3.69E-03	3.12E-02	87.6	112.9	1		1	2			1.30	solute carrier family 25 (mitochondrial carrier: glutamate), me	2.25E-03	Y		
Golim4	-1.33	3.69E-03	3.12E-02	13.3	10.0				1				golgi integral membrane protein 4	5.33E-01	N		
RGD1305733	-1.29	3.70E-03	3.12E-02	111.9	86.7							-1.55		2.91E-08	Y		
Sec14l1	1.29	3.70E-03	3.13E-02	42.5	54.9		1		1			1.52	SEC14-like 1 (S. cerevisiae)	3.92E-07	Y		
Znf474	1.51	3.70E-03	3.13E-02	2.5	3.7							1.98	zinc finger protein 474	4.45E-08	Y		
Arse	1.47	3.71E-03	3.13E-02	3.7	5.5		1					1.45	arylsulfatase E (chondrodysplasia punctata 1)	7.23E-03	Y		
Sqle	-1.30	3.72E-03	3.13E-02	59.0	45.5	1			1			-1.47	squalene epoxidase	3.08E-06	Y		
Ar	-1.38	3.72E-03	3.13E-02	5.3	3.8		2					-1.64	androgen receptor	5.29E-06	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Lrrc34	1.35	3.73E-03	3.13E-02	11.9	16.0							2.10	leucine rich repeat containing 34	3.66E-16	Y		
Iqub	1.35	3.73E-03	3.13E-02	8.1	10.9		1					1.60	IQ motif and ubiquitin domain containing	1.23E-06	Y		
RGD1311358	1.48	3.73E-03	3.13E-02	4.5	6.7							1.37		2.94E-02	Y		
Ret	1.30	3.74E-03	3.14E-02	15.2	19.7		1						ret proto-oncogene	7.15E-02	N		
Clic1	1.42	3.75E-03	3.15E-02	8.4	12.0							1.61	chloride intracellular channel 1	1.82E-05	Y		
Grik4	-1.33	3.76E-03	3.15E-02	13.6	10.2								glutamate receptor, ionotropic, kainate 4	5.19E-02	N		
Neu2	-1.94	3.76E-03	3.15E-02	1.5	0.8		1						sialidase 2 (cytosolic sialidase)	5.20E-01	N		
Fads6	1.31	3.76E-03	3.15E-02	28.5	37.4			1				1.49	fatty acid desaturase domain family, member 6	1.03E-05	Y		
Synj2	-1.32	3.77E-03	3.15E-02	10.0	7.6								synaptojanin 2	7.85E-01	N		
Kcnf1	-1.51	3.77E-03	3.16E-02	3.0	2.0								potassium voltage-gated channel, subfamily F, member 1	6.16E-01	N		
Gsk3b	-1.30	3.77E-03	3.16E-02	86.8	67.0	1			1				glycogen synthase kinase 3 beta	1.54E-01	N		
Grm8	-1.31	3.78E-03	3.16E-02	25.2	19.2		2						glutamate receptor, metabotropic 8	6.35E-01	N		
Ccdc85a	-1.34	3.78E-03	3.16E-02	20.2	15.0							-1.55	coiled-coil domain containing 85A	6.45E-07	Y		
Rap1a	-1.30	3.79E-03	3.16E-02	35.1	26.9		1						RAP1A, member of RAS oncogene family	2.10E-01	N		
LOC500227	1.44	3.79E-03	3.16E-02	4.5	6.5							1.62		8.72E-05	Y		
Lgals3	1.71	3.79E-03	3.16E-02	2.5	4.3							1.80	lectin, galactoside-binding, soluble, 3	2.98E-04	Y		
Nog	1.45	3.80E-03	3.16E-02	4.7	6.8							1.91	noggin	3.87E-06	Y		
Hrasls	-1.40	3.80E-03	3.16E-02	5.6	4.0		3		1			-1.36	HRAS-like suppressor	9.63E-03	Y		
Gpr143	-1.56	3.82E-03	3.17E-02	3.9	2.5								G protein-coupled receptor 143	1.90E-01	N		
Slitrk2	-1.33	3.83E-03	3.18E-02	15.2	11.4								SLIT and NTRK-like family, member 2	6.61E-01	N		
Zgpat	1.30	3.83E-03	3.18E-02	37.3	48.6				1			1.23	zinc finger, CCCH-type with G patch domain	3.32E-02	Y		
Trhde	1.30	3.87E-03	3.21E-02	9.9	12.9							1.35	thyrotropin-releasing hormone degrading enzyme	9.53E-04	Y		
Raf1	1.29	3.87E-03	3.21E-02	46.8	60.4							1.24	v-raf-1 murine leukemia viral oncogene homolog 1	1.97E-02	Y		
Asgr2	-1.97	3.88E-03	3.22E-02	1.7	0.9								asialoglycoprotein receptor 2	7.81E-01	N		
Slc2a13	-1.32	3.91E-03	3.23E-02	8.8	6.7		1					-1.57	solute carrier family 2 (facilitated glucose transporter), membe	1.26E-07	Y		
Per3	1.29	3.92E-03	3.24E-02	32.3	41.8		1					1.44	period homolog 3 (Drosophila)	1.79E-05	Y		
Nxph3	1.54	3.92E-03	3.24E-02	4.1	6.4	1	1		1			-1.38	neurexophilin 3	6.83E-03	N		
Kif21b	-1.30	3.93E-03	3.25E-02	16.4	12.6								kinesin family member 21B	6.92E-02	N		
Epor	1.59	3.94E-03	3.25E-02	2.0	3.1				1			5.45	erythropoietin receptor	1.75E-10	Y		
Slc22a2	1.99	3.97E-03	3.28E-02	0.5	1.1							2.08	solute carrier family 22 (organic cation transporter), member 2	2.10E-03	Y		
Stx4	1.32	3.97E-03	3.28E-02	40.8	53.8				1				syntaxin 4	6.50E-01	N		
Marcksl1	-1.30	4.01E-03	3.30E-02	66.4	51.1		1					-1.33	MARCKS-like 1	1.26E-03	Y		
Shc2	-1.32	4.01E-03	3.30E-02	12.9	9.8							-1.34	SHC (Src homology 2 domain containing) transforming protein 2	1.57E-03	Y		
Ttc9b	1.32	4.03E-03	3.32E-02	42.4	56.2							1.50	tetratricopeptide repeat domain 9B	2.61E-05	Y		
RGD1560608	-1.47	4.03E-03	3.32E-02	13.8	9.4									9.48E-02	N		
Ptgs2	1.57	4.05E-03	3.32E-02	2.1	3.3		1	1				3.24	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase	3.85E-12	Y		
Rgs7bp	1.31	4.05E-03	3.32E-02	34.9	45.8		2					1.61	regulator of G-protein signaling 7 binding protein	1.02E-07	Y		
Spef2	1.34	4.05E-03	3.33E-02	4.8	6.5							1.91	sperm flagellar 2	1.01E-12	Y		

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Dlgap4	1.29	4.06E-03	3.33E-02	42.1	54.3							1.25	discs, large (Drosophila) homolog-associated protein 4	1.11E-02	Y		
Nrp2	-1.31	4.08E-03	3.34E-02	17.2	13.1			1					neuropilin 2	1.08E-01	N		
Car12	-1.62	4.09E-03	3.35E-02	4.6	2.8		1						carbonic anyhydrase 12	6.68E-01	N		
Yaf2	-1.30	4.10E-03	3.35E-02	49.7	38.1							-1.33	YY1 associated factor 2	1.16E-03	Y		
Rps29	-1.31	4.11E-03	3.36E-02	231.0	176.8	1			1				ribosomal protein S29	2.02E-01	N		
Pex6	1.31	4.12E-03	3.37E-02	3.7	4.8								peroxisomal biogenesis factor 6	7.29E-01	N		
RGD1304879	1.34	4.13E-03	3.37E-02	13.7	18.4									1.90E-01	N		
Fzd1	1.30	4.13E-03	3.37E-02	20.3	26.3		1					2.15	frizzled family receptor 1	6.64E-19	Y		
LOC297756	1.59	4.14E-03	3.38E-02	5.0	8.0									5.40E-01	N		
Fmnl1	1.30	4.20E-03	3.43E-02	21.4	27.8		1					1.59	formin-like 1	5.84E-08	Y		
RGD1565236	-1.66	4.21E-03	3.43E-02	7.6	4.6							-1.71		4.88E-03	Y		
Grm3	-1.29	4.22E-03	3.43E-02	38.1	29.5		2		1				glutamate receptor, metabotropic 3	9.46E-01	N		
Gps2	1.35	4.22E-03	3.43E-02	14.2	19.2								G protein pathway suppressor 2	2.07E-01	N		
Accn4	-1.35	4.23E-03	3.44E-02	10.3	7.6		1					-1.46	amiloride-sensitive cation channel 4, pituitary	4.59E-04	Y		
MGC95152	-1.31	4.23E-03	3.44E-02	36.4	27.7									7.65E-02	N		
Tmem132b	-1.40	4.25E-03	3.45E-02	15.2	10.9								transmembrane protein 132B	5.35E-01	N		
Sh3bgr	1.39	4.25E-03	3.45E-02	11.0	15.3		1		1			2.90	SH3 domain binding glutamic acid-rich protein	2.41E-15	Y		
Tmem196	-1.39	4.26E-03	3.46E-02	10.3	7.4								transmembrane protein 196	4.15E-01	N		
Anxa1	1.54	4.28E-03	3.47E-02	3.2	4.9							1.87	annexin A1	8.57E-08	Y		
Onecut1	-1.59	4.29E-03	3.47E-02	2.3	1.5								one cut homeobox 1	2.86E-01	N		
Cyp4b1	-1.77	4.30E-03	3.48E-02	1.7	1.0								cytochrome P450, family 4, subfamily B, polypeptide 1	8.70E-01	N		
Sema3a	1.38	4.34E-03	3.51E-02	5.9	8.2							2.00	sema domain, immunoglobulin domain (Ig), short basic domain, secr	1.71E-10	Y		
Gpr34	-1.44	4.37E-03	3.53E-02	8.7	6.1	1						-1.47	G protein-coupled receptor 34	1.51E-03	Y		
Alg11	-1.30	4.38E-03	3.54E-02	48.9	37.7							-1.32	asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase	1.84E-03	Y		
Ubc	-1.28	4.38E-03	3.54E-02	314.3	246.5				1			-1.33	ubiquitin C	5.30E-04	Y		
Trabd	1.33	4.41E-03	3.55E-02	11.6	15.4		1					1.27	TraB domain containing	2.43E-02	Y		
Apba3	1.35	4.44E-03	3.58E-02	10.5	14.2	1						1.32	amyloid beta (A4) precursor protein-binding, family A, member 3 //	1.09E-02	Y		
Irak3	-1.58	4.46E-03	3.59E-02	1.9	1.2								interleukin-1 receptor-associated kinase 3	1.67E-01	N		
Folh1	-1.30	4.49E-03	3.61E-02	31.1	24.0		2						folate hydrolase (prostate-specific membrane antigen) 1	9.49E-02	N		
Vof16	-1.31	4.49E-03	3.61E-02	26.2	19.9	2	3			-1.23		-1.36	ischemia related factor vof-16	9.49E-04	Y	Y	
Met	-1.69	4.49E-03	3.61E-02	1.0	0.6							-1.55	met proto-oncogene (hepatocyte growth factor receptor)	6.97E-05	Y		
Itgb5	1.29	4.49E-03	3.61E-02	27.0	34.9		1					1.59	integrin, beta 5	5.78E-08	Y		
Igsf10	1.35	4.53E-03	3.64E-02	2.3	3.1							1.66	immunoglobulin superfamily, member 10	2.38E-07	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Abcg3l1	-1.53	4.53E-03	3.64E-02	3.6	2.4		1						similar to ATP-binding cassette sub-family G member 3; similar to ATP-binding cassette, sub-family G (WHITE), member 3; ATP-binding cassette, sub-family G (WHITE), member 3-like 1; ATP-binding cassette, sub-family G (WHITE), member 3; ATP-binding cassette, sub-family G (WHITE), member 3-like 2	6.58E-01	N		
Chrnb3	-1.51	4.54E-03	3.64E-02	2.9	1.9			1				-2.44	cholinergic receptor, nicotinic, beta 3 (neuronal)	1.23E-03	Y		
Slc25a29	1.39	4.56E-03	3.66E-02	6.2	8.6								solute carrier family 25 (mitochondrial carnitine/acylcarnitine	4.21E-01	N		
Aig1	1.29	4.57E-03	3.66E-02	66.1	85.3								androgen-induced 1	8.52E-02	N		
Pik3r2	1.29	4.59E-03	3.67E-02	29.4	37.9				1				phosphoinositide-3-kinase, regulatory subunit 2 (beta)	6.23E-02	N		
Slc6a13	1.37	4.60E-03	3.68E-02	7.2	9.9							1.80	solute carrier family 6 (neurotransmitter transporter, GABA), me	7.00E-09	Y		
Prkar2b	-1.31	4.61E-03	3.68E-02	16.3	12.4		1					-1.57	protein kinase, cAMP-dependent, regulatory, type II, beta	9.43E-08	Y		
Gabrg1	-1.29	4.62E-03	3.69E-02	65.8	50.9	1						-1.22	gamma-aminobutyric acid (GABA) A receptor, gamma 1	3.47E-02	Y		
Mrpl13	-1.37	4.63E-03	3.70E-02	25.5	18.6								mitochondrial ribosomal protein L13	3.18E-01	N		
Fbln1	1.36	4.64E-03	3.70E-02	5.8	7.9		1		1			1.48	fibulin 1	2.35E-04	Y		
Ncln	1.29	4.65E-03	3.70E-02	25.4	32.9								nicalin	3.76E-01	N		
Rhebl1	1.55	4.66E-03	3.71E-02	3.4	5.2								Ras homolog enriched in brain like 1	8.39E-01	N		
Sema7a	1.28	4.70E-03	3.74E-02	93.1	119.0				1			2.19	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group	1.16E-23	Y		
Cabp1	1.32	4.70E-03	3.74E-02	22.3	29.3							1.61	calcium binding protein 1	6.36E-07	Y		
Tm7sf2	-1.37	4.71E-03	3.74E-02	13.1	9.5	1							transmembrane 7 superfamily member 2	2.59E-01	N		
Cry1	1.30	4.71E-03	3.74E-02	19.9	25.8		2					1.76	cryptochrome 1 (photolyase-like)	1.04E-10	Y		
Myo7b	-2.64	4.72E-03	3.75E-02	0.2	0.1								myosin VIIB	0.00E+00	N		
Per2	1.28	4.73E-03	3.75E-02	22.4	28.8	1	1					1.59	period homolog 2 (Drosophila)	2.36E-08	Y		
RGD1309735	1.34	4.76E-03	3.77E-02	35.8	48.0							1.28		2.05E-02	Y		
Nipal4	-1.39	4.76E-03	3.77E-02	4.9	3.5							-1.52	NIPA-like domain containing 4	1.77E-04	Y		
Msrb2	-1.41	4.76E-03	3.77E-02	12.4	8.8				1			-1.33	methionine sulfoxide reductase B2	1.13E-02	Y		
Ccdc113	1.41	4.76E-03	3.77E-02	8.4	11.8							1.60	coiled-coil domain containing 113	2.07E-05	Y		
Sumo2	1.32	4.77E-03	3.77E-02	29.0	38.3								SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae)	8.19E-01	N		
Pafah1b1	-1.27	4.78E-03	3.78E-02	241.6	189.9	1			2			-1.23	platelet-activating factor acetylhydrolase 1b, regulator	1.88E-02	Y		
Fxyd7	1.31	4.80E-03	3.79E-02	66.2	86.5							1.30	FXYD domain containing ion transport regulator 7	7.88E-03	Y		
Smtn	1.45	4.80E-03	3.79E-02	2.2	3.2		1					1.60	smoothelin	3.49E-03	Y		
Elovl1	-1.32	4.83E-03	3.81E-02	41.5	31.3								ELOVL fatty acid elongase 1	6.34E-01	N		
Fbxl4	-1.34	4.83E-03	3.81E-02	11.7	8.7				1			-1.26	F-box and leucine-rich repeat protein 4	2.83E-02	Y		
Ccdc126	-1.34	4.83E-03	3.81E-02	12.3	9.2								coiled-coil domain containing 126	9.04E-01	N		
Cxxc5	1.29	4.88E-03	3.84E-02	32.3	41.8		2					1.50	CXXC finger protein 5	2.91E-06	Y		
Dpp4	-1.55	4.88E-03	3.84E-02	1.5	0.9			1	1				dipeptidyl-peptidase 4	2.97E-01	N		
Prss23	1.47	4.89E-03	3.84E-02	3.3	4.9	1	1						protease, serine, 23	7.40E-02	N		

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Aifm2	-1.33	4.90E-03	3.85E-02	10.4	7.9							-1.24	apoptosis-inducing factor, mitochondrion-associated, 2	3.95E-02	Y		
Pan2	1.29	4.90E-03	3.85E-02	19.5	25.3							1.45	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	3.25E-05	Y		
Pmfbp1	-1.63	4.93E-03	3.87E-02	1.4	0.9							-1.70	polyamine modulated factor 1 binding protein 1	3.43E-02	Y		
Ccdc88b	1.30	4.93E-03	3.87E-02	15.3	19.9		1					1.25	coiled-coil domain containing 88B	2.55E-02	Y		
Ahi1	-1.27	4.94E-03	3.87E-02	200.6	157.7	2	2		1	-1.37		-1.40	Abelson helper integration site 1	3.00E-05	Y	Y	
Sbno2	1.34	4.95E-03	3.88E-02	4.8	6.5							1.37	strawberry notch homolog 2 (Drosophila)	2.89E-03	Y		
Man1c1	1.32	4.97E-03	3.89E-02	8.8	11.6		1					1.74	mannosidase, alpha, class 1C, member 1	4.76E-09	Y		
Atp5f1	-1.28	4.98E-03	3.89E-02	228.0	178.6		1					-1.25	ATP synthase, H+ transporting, mitochondrial Fo complex, s	9.05E-03	Y		
Rangrf	1.40	4.98E-03	3.89E-02	12.8	17.9		1						RAN guanine nucleotide release factor	7.80E-02	N		
Asns	-1.30	4.98E-03	3.89E-02	38.9	30.0		2					-1.40	asparagine synthetase (glutamine-hydrolyzing)	1.03E-04	Y		
Fbxw4	1.30	5.00E-03	3.90E-02	28.6	37.2							1.33	F-box and WD repeat domain containing 4	1.98E-03	Y		
Rasd2	-1.31	5.01E-03	3.91E-02	17.3	13.3	1	2						RASD family, member 2	6.80E-01	N		
Pth2r	-1.98	5.02E-03	3.91E-02	0.0	0.0								parathyroid hormone 2 receptor	0.00E+00	N		
Lgals8	-1.29	5.02E-03	3.91E-02	38.4	29.7		1		1			-1.24	lectin, galactoside-binding, soluble, 8	1.67E-02	Y		
RGD1310572	-2.33	5.03E-03	3.91E-02	1.1	0.5							-1.66		1.22E-03	Y		
Scn9a	-1.30	5.04E-03	3.92E-02	6.6	5.0			1				-1.91	sodium channel, voltage-gated, type IX, alpha subunit	7.89E-17	Y		
Aqp11	-1.40	5.06E-03	3.94E-02	11.5	8.2		2					-1.52	aquaporin 11	9.68E-05	Y		
Fat1	1.27	5.07E-03	3.94E-02	67.2	85.4		2					2.05	FAT tumor suppressor homolog 1 (Drosophila)	4.19E-21	Y		
Ppp1cc	1.27	5.07E-03	3.94E-02	137.5	175.2							1.30	protein phosphatase 1, catalytic subunit, gamma isozyme	2.03E-03	Y		
RGD1560888	-1.42	5.08E-03	3.94E-02	25.5	18.0									9.21E-01	N		
Cry2	1.28	5.12E-03	3.97E-02	67.2	86.1		1					1.25	cryptochrome 2 (photolyase-like)	1.37E-02	Y		
Snhg4	-1.52	5.13E-03	3.98E-02	29.3	19.3							-1.75		3.78E-07	Y		
Tmx1	-1.28	5.19E-03	4.02E-02	132.7	104.0							-1.49	thioredoxin-related transmembrane protein 1	6.59E-07	Y		
LOC296884	1.30	5.21E-03	4.03E-02	23.3	30.2							1.36		7.37E-04	Y		
Cpeb1	-1.31	5.22E-03	4.04E-02	17.6	13.4		1					-1.32	cytoplasmic polyadenylation element binding protein 1	2.40E-03	Y		
Bcl2l11	1.75	5.22E-03	4.04E-02	3.2	5.6								BCL2-like 11 (apoptosis facilitator)	9.83E-02	N		
Mapk6	-1.28	5.23E-03	4.04E-02	39.9	31.2		1		1				mitogen-activated protein kinase 6	5.13E-01	N		
Tp73	1.36	5.23E-03	4.04E-02	3.2	4.4							2.31	tumor protein p73	1.97E-15	Y		
Gpr182	1.58	5.28E-03	4.07E-02	1.8	2.8							2.48	G protein-coupled receptor 182	3.24E-12	Y		
Gna12	-1.29	5.29E-03	4.08E-02	28.6	22.2								guanine nucleotide binding protein (G protein) alpha 12	8.87E-01	N		
Cdc42ep1	1.31	5.31E-03	4.09E-02	18.3	23.9		1					1.50	CDC42 effector protein (Rho GTPase binding) 1	1.66E-05	Y		
Phyhip	1.27	5.31E-03	4.09E-02	104.7	133.3		1					1.74	phytanoyl-CoA 2-hydroxylase interacting protein	2.28E-12	Y		
Ccdc65	1.33	5.32E-03	4.10E-02	14.4	19.0							1.35	coiled-coil domain containing 65	2.15E-03	Y		
Yod1	1.37	5.33E-03	4.10E-02	15.5	21.2							1.30	YOD1 OTU deubiquinating enzyme 1 homolog (S. cerevisiae)	3.59E-02	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
Ggps1	-1.29	5.33E-03	4.10E-02	33.5	25.9	1			1			-1.24	geranylgeranyl diphosphate synthase 1	2.15E-02	Y		
Gdi2	-1.27	5.34E-03	4.10E-02	179.0	140.8							-1.21	GDP dissociation inhibitor 2	3.27E-02	Y		
Trappc1	-1.37	5.34E-03	4.10E-02	35.0	25.6								trafficking protein particle complex 1	9.22E-01	N		
Scnn1a	-1.61	5.36E-03	4.11E-02	1.4	0.9							-1.45	sodium channel, non-voltage-gated 1 alpha subunit	3.73E-02	Y		
Dydc2	1.73	5.37E-03	4.12E-02	2.3	4.0							1.89	DPY30 domain containing 2	1.07E-03	Y		
Wnt3	1.53	5.40E-03	4.14E-02	1.4	2.2							1.50	wingless-type MMTV integration site family, member 3	2.73E-02	Y		
Zfp469	1.28	5.41E-03	4.14E-02	17.2	22.0							1.29		3.47E-03	Y		
Tbc1d2	1.46	5.41E-03	4.14E-02	1.6	2.3			1					TBC1 domain family, member 2	7.89E-02	N		
Bles03	1.30	5.46E-03	4.17E-02	29.5	38.3								basophilic leukemia expressed protein BLES03	3.78E-01	N		
Vegfb	-1.32	5.46E-03	4.17E-02	20.5	15.5		2		1				vascular endothelial growth factor B	3.78E-01	N		
C1ql3	-1.59	5.48E-03	4.19E-02	6.7	4.2				1				complement component 1, q subcomponent-like 3	1.41E-01	N		
Atp6v1d	-1.28	5.51E-03	4.21E-02	114.6	89.5							-1.26	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	7.83E-03	Y		
Epha5	-1.28	5.53E-03	4.22E-02	13.9	10.8		1	1				-1.51	EPH receptor A5	2.12E-07	Y		
Nkain4	1.34	5.54E-03	4.22E-02	30.2	40.4		1	1				1.45	Na+/K+ transporting ATPase interacting 4	4.59E-04	Y		
Galr2	-1.48	5.54E-03	4.22E-02	6.9	4.7		2					-1.76	galanin receptor 2	1.51E-05	Y		
Kcng2	-1.78	5.57E-03	4.24E-02	1.7	0.9								potassium voltage-gated channel, subfamily G, member 2	2.77E-01	N		
Tgfb1i1	-1.56	5.59E-03	4.25E-02	2.9	1.8		1						transforming growth factor beta 1 induced transcript 1	7.01E-02	N		
Mef2d	1.29	5.64E-03	4.29E-02	36.7	47.2							1.33	myocyte enhancer factor 2D	1.80E-03	Y		
Mpst	1.37	5.67E-03	4.31E-02	12.3	16.8								mercaptopyruvate sulfurtransferase	8.67E-02	N		
RGD1560455	-2.26	5.68E-03	4.31E-02	0.0	0.0									0.00E+00	N		
Bag2	1.33	5.68E-03	4.31E-02	15.2	20.3		1					1.25	BCL2-associated athanogene 2	4.79E-02	Y		
Cdc20	2.05	5.72E-03	4.34E-02	0.0	0.0								cell division cycle 20 homolog (S. cerevisiae)	0.00E+00	N		
Vps4b	-1.28	5.76E-03	4.37E-02	37.1	28.9							-1.28	vacuolar protein sorting 4 homolog B (S. cerevisiae)	5.93E-03	Y		
Trpc4ap	-1.28	5.79E-03	4.39E-02	55.2	43.3								transient receptor potential cation channel, subfamily C, member	5.68E-01	N		
Mmp15	-1.31	5.80E-03	4.39E-02	11.3	8.6		1						matrix metallopeptidase 15 (membrane-inserted)	7.04E-01	N		
Prickle2	-1.27	5.81E-03	4.39E-02	25.8	20.3		1		1			-1.36	prickle homolog 2 (Drosophila)	1.92E-04	Y		
Shox2	-1.35	5.81E-03	4.39E-02	14.4	10.7				1			-1.45	short stature homeobox 2	7.13E-03	Y		
Trhr2	-1.43	5.83E-03	4.40E-02	10.4	7.3									5.57E-01	N		
Strada	1.31	5.83E-03	4.40E-02	17.1	22.4								STE20-related kinase adaptor alpha	1.13E-01	N		
Lrrc32	1.51	5.83E-03	4.40E-02	1.1	1.7							1.43	leucine rich repeat containing 32	4.05E-02	Y		
Toe1	1.40	5.83E-03	4.40E-02	6.8	9.5								target of EGR1, member 1 (nuclear)	1.57E-01	N		
Ntrk3	1.27	5.84E-03	4.41E-02	83.6	106.2	1							neurotrophic tyrosine kinase, receptor, type 3	1.11E-01	N		
Mvp	1.31	5.85E-03	4.41E-02	12.4	16.2								major vault protein	9.27E-02	N		
Lmcd1	1.45	5.85E-03	4.41E-02	3.9	5.7		1					1.64	LIM and cysteine-rich domains 1	4.60E-04	Y		
Slc2a4	1.46	5.85E-03	4.41E-02	2.4	3.5							1.95	solute carrier family 2 (facilitated glucose transporter), member 4	3.59E-06	Y		
Ispd	-1.34	5.87E-03	4.42E-02	9.4	7.0							-1.31		1.37E-02	Y		

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gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
RGD1560672	1.41	5.88E-03	4.42E-02	5.2	7.4							2.45		6.60E-13	Y		
Dagla	1.28	5.91E-03	4.44E-02	19.1	24.4				1			1.76	diacylglycerol lipase, alpha	1.03E-11	Y		
Sumo1	-1.28	5.92E-03	4.44E-02	91.6	71.4								SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)	1.27E-01	N		
Adra1a	-1.41	5.94E-03	4.45E-02	8.5	6.0			1	1				adrenergic, alpha-1A-, receptor	1.40E-01	N		
Slc4a7	-1.32	5.96E-03	4.46E-02	10.2	7.7	1							solute carrier family 4, sodium bicarbonate cotransporter, member	2.78E-01	N		
Adrbk2	1.29	5.96E-03	4.47E-02	27.1	35.1				1			1.57	adrenergic, beta, receptor kinase 2	4.59E-07	Y		
Pros1	-1.39	5.97E-03	4.47E-02	4.6	3.3								protein S (alpha)	6.79E-01	N		
Slc6a7	-1.30	5.98E-03	4.48E-02	22.9	17.6		1					-1.24	solute carrier family 6 (neurotransmitter transporter, L-proline	2.25E-02	Y		
Tcerg1l	1.32	6.00E-03	4.49E-02	13.1	17.3							1.72	transcription elongation regulator 1-like	2.73E-07	Y		
Drd2	-1.33	6.01E-03	4.49E-02	11.3	8.5		1						dopamine receptor D2	5.23E-01	N		
Hunk	1.38	6.01E-03	4.49E-02	5.6	7.7							1.50	hormonally up-regulated Neu-associated kinase	2.03E-04	Y		
Sema3f	-1.31	6.08E-03	4.54E-02	13.5	10.3								sema domain, immunoglobulin domain (Ig), short basic domain, secr	2.46E-01	N		
Pld3	-1.27	6.11E-03	4.56E-02	184.0	145.2		2					-1.48	phospholipase D family, member 3	6.02E-07	Y		
Ak2	1.36	6.12E-03	4.57E-02	7.2	9.8							1.38	adenylate kinase 2	7.24E-03	Y		
Furin	1.28	6.13E-03	4.57E-02	17.9	22.9							1.41	furin (paired basic amino acid cleaving enzyme)	1.04E-04	Y		
Psma3l	-1.33	6.14E-03	4.57E-02	31.5	23.7									1.13E-01	N		
Mir410	-1.94	6.15E-03	4.58E-02	28.1	14.5							-1.78	microRNA 410	2.05E-02	Y		
Ppp1r14b	1.51	6.22E-03	4.63E-02	6.1	9.3	1							protein phosphatase 1, regulatory (inhibitor) subunit 14B	9.12E-01	N		
Ogfod1	-1.29	6.25E-03	4.65E-02	52.0	40.4							-1.46	2-oxoglutarate and iron-dependent oxygenase domain containing 1 /	7.18E-06	Y		
Tox	-1.35	6.26E-03	4.65E-02	7.1	5.3							-1.49	thymocyte selection-associated high mobility group box	4.22E-05	Y		
Ssr1	-1.27	6.26E-03	4.65E-02	93.8	73.8		1						signal sequence receptor, alpha	8.22E-02	N		
Dbp	1.28	6.28E-03	4.66E-02	47.7	61.1	1	1		1		1.16	1.50	D site of albumin promoter (albumin D-box) binding protein	2.46E-06	Y		Y
Maz	1.30	6.30E-03	4.67E-02	30.4	39.4							1.28	MYC-associated zinc finger protein (purine-binding transcript	1.07E-02	Y		
Pcsk2	-1.27	6.33E-03	4.69E-02	69.1	54.3		2	1	1				proprotein convertase subtilisin/kexin type 2	3.49E-01	N		
Ntm	1.27	6.33E-03	4.69E-02	61.2	77.9							1.25	neurotrimin	1.39E-02	Y		
Mthfd2	-1.44	6.34E-03	4.69E-02	4.6	3.2		1		1				methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, meth	1.32E-01	N		
Sppl2b	1.28	6.41E-03	4.74E-02	34.5	44.0							1.42	signal peptide peptidase like 2B	4.94E-05	Y		
Znf511	1.39	6.44E-03	4.76E-02	8.7	12.0							1.32	zinc finger protein 511	3.48E-02	Y		
Mir376a	-2.32	6.44E-03	4.76E-02	16.6	7.2								miRNA 376a	6.38E-01	N		
Mcm2	1.37	6.44E-03	4.76E-02	3.9	5.3				1				minichromosome maintenance complex component 2	3.45E-01	N		
Cbx2	1.42	6.51E-03	4.80E-02	2.0	2.9		1					1.42	chromobox homolog 2	3.55E-02	Y		
LOC100125385	1.29	6.51E-03	4.80E-02	30.5	39.5									2.53E-01	N		
Tcp11l1	-1.28	6.52E-03	4.80E-02	40.3	31.6							-1.26	t-complex 11 (mouse)-like 1	1.01E-02	Y		
Fgf14	1.30	6.54E-03	4.81E-02	55.3	71.8		1					1.26	fibroblast growth factor 14	2.05E-02	Y		
Unc119	-1.32	6.54E-03	4.82E-02	24.6	18.6	1	1					-1.27	unc-119 homolog (C. elegans)	1.83E-02	Y		

Supplementary Table 1

gene	FC	Pvalue	FDR	control RPKM	alcohol RPKM	P drinking	P vs. NP naïve	GWAS	GE in PM	AcbSh	CeA	DRN	gene title	DRN FDR	same dir	PAG+ ACB	PAG+ CeA
RGD1308059	-1.37	6.56E-03	4.83E-02	14.7	10.8									9.37E-01	N		
Lrrc9	1.34	6.57E-03	4.83E-02	5.6	7.5							1.39	leucine rich repeat containing 9	9.55E-04	Y		
Rhob	-1.27	6.61E-03	4.85E-02	122.3	96.5				2				ras homolog family member B	2.47E-01	N		
Anp32a	1.27	6.61E-03	4.85E-02	101.3	129.2	1						1.33	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	1.28E-03	Y		
Cd59	-1.27	6.62E-03	4.86E-02	114.3	89.8		1		1			-1.27	CD59 molecule, complement regulatory protein	7.01E-03	Y		
Wfikkn1	1.57	6.64E-03	4.87E-02	2.0	3.1							1.60	WAP, follistatin/kazal, immunoglobulin, kunitz and netrin domain	2.44E-02	Y		
Efna5	-1.40	6.68E-03	4.90E-02	16.6	11.8			1					ephrin-A5	5.14E-01	N		
Rnf165	-1.31	6.69E-03	4.90E-02	6.2	4.8		1					-1.28	ring finger protein 165	1.42E-02	Y		
Smpdl3b	1.44	6.71E-03	4.91E-02	3.5	5.0							1.77	sphingomyelin phosphodiesterase, acid-like 3B	5.45E-05	Y		
Bcl7c	1.40	6.71E-03	4.91E-02	9.0	12.6							1.46	B-cell CLL/lymphoma 7C	2.49E-03	Y		
RGD1308117	-1.57	6.73E-03	4.92E-02	2.6	1.7									6.93E-02	N		
Egfr	-1.34	6.74E-03	4.92E-02	5.8	4.4	1							epidermal growth factor receptor	8.63E-01	N		
Fgf13	-1.29	6.75E-03	4.93E-02	32.0	24.7		1					-1.49	fibroblast growth factor 13	2.88E-06	Y		
Rassf8	1.32	6.75E-03	4.93E-02	17.0	22.5							1.39	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	9.35E-04	Y		
Ehd3	-1.28	6.76E-03	4.93E-02	47.8	37.4				1			-1.27	EH-domain containing 3	9.12E-03	Y		
Cd55	-1.62	6.77E-03	4.93E-02	2.4	1.5		1					-1.61	CD55 molecule, decay accelerating factor for complement (Cromer blo	7.73E-05	Y		
Prr3	-1.31	6.77E-03	4.94E-02	22.0	16.7								proline rich 3	2.51E-01	N		
Slc19a3	-1.45	6.81E-03	4.96E-02	5.2	3.6								solute carrier family 19, member 3	1.42E-01	N		
Wif1	1.42	6.81E-03	4.96E-02	3.5	5.0		1					1.43	WNT inhibitory factor 1	1.93E-02	Y		
Itgb8	-1.28	6.83E-03	4.97E-02	35.8	28.0							-1.24	integrin, beta 8	1.68E-02	Y		
Ranbp1	-1.32	6.86E-03	4.98E-02	26.7	20.2							-1.29	RAN binding protein 1	1.18E-02	Y		
Hadh	-1.34	6.87E-03	4.99E-02	14.4	10.7								hydroxyacyl-CoA dehydrogenase	7.14E-01	N		
Th	1.61	6.88E-03	4.99E-02	1.6	2.5			1					tyrosine hydroxylase	1.58E-01	N		