

Allelic Imbalance in SZ (Supplemental Material 1)

This is a document containing supplemental figures and tables for the “Comparison of Quantitative Trait Loci Methods: Total Expression and Allelic Imbalance Method in Brain RNA-seq” manuscript.

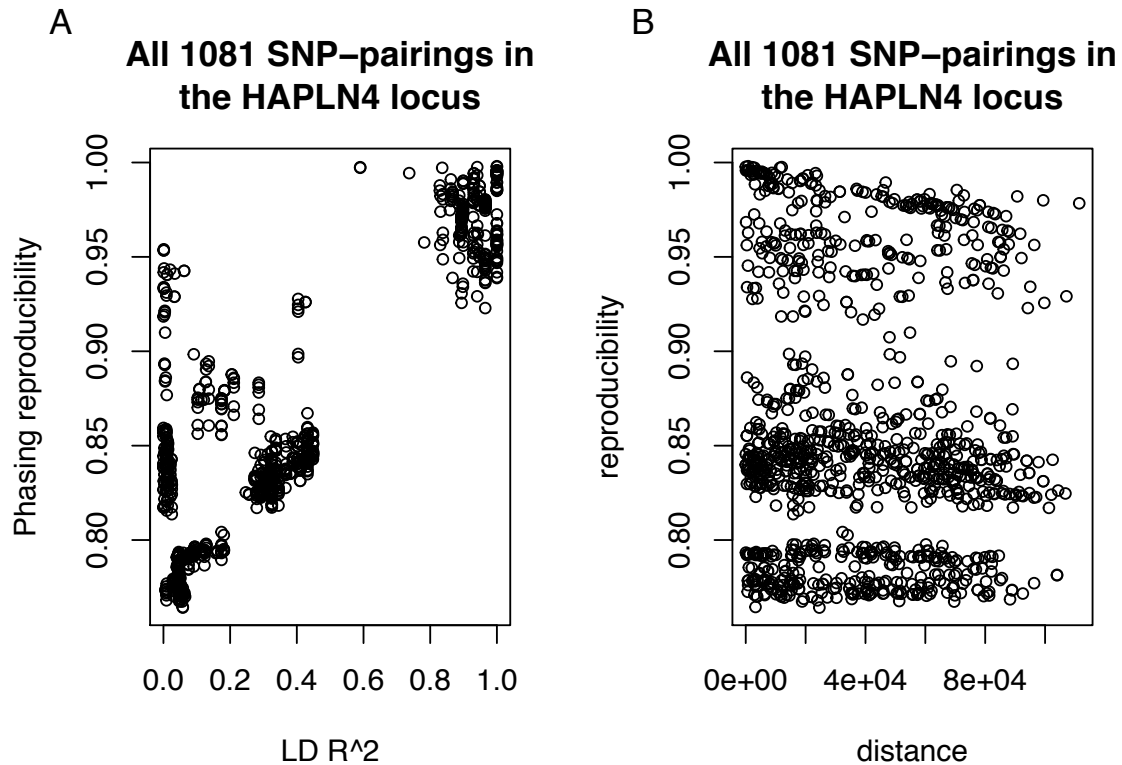


Fig S1-1: Illustration of the phasing quality of SNPs in the HAPLN4 region. All risk-SNP regions were phased using the Shapeit2 tool in order to link risk-SNPs with txSNPs. The fundamental mechanism of phasing is to determine likely parent of origin for all txSNPs that are heterozygous, by assigning alleles as being either of parent 1 (P1) origin or parent 2 (P2) origin. According to Shapeit2 notation, this is denoted with a vertical bar |, such that for example an A/G heterozygous SNP can be either A|G or G|A, meaning that the A-allele was inherited from the parent 1 or the parent 2, respectively.

A default execution of Shapeit2 provides one guess of likely haplotype, so the degree of probability is not directly available. However, as suggested by Shapeit2 authors a probability can be calculated by iterating through the same phasing using different random seeds. The phasing reproducibility between any two SNPs is then defined as the fraction of iterations where the two SNPs have the same results with different random seeds; a value of 1 indicates perfect reproducibility and 0.5 indicates random choice.

We used this approach to investigate the relation between reproducibility and linkage disequilibrium (LD) R², as well as between reproducibility and distance. This is illustrated here for all pairwise combinations of SNPs in the HAPLN4 region. For A) reproducibility and LD, we unsurprisingly found that all SNP-pairs in perfect LD (R²=1) achieve almost completely perfect phasing reproducibility. However, importantly SNP-pairs that are not in LD (R²=0) also can achieve reproducibility-values above 0.9. Moreover, in this region no SNP-pair had worse reproducibility than 0.78. For B) reproducibility and distance, we found that at the investigated distance (400KB) there was only a weak tendency towards diminished phasing reproducibility with distance.

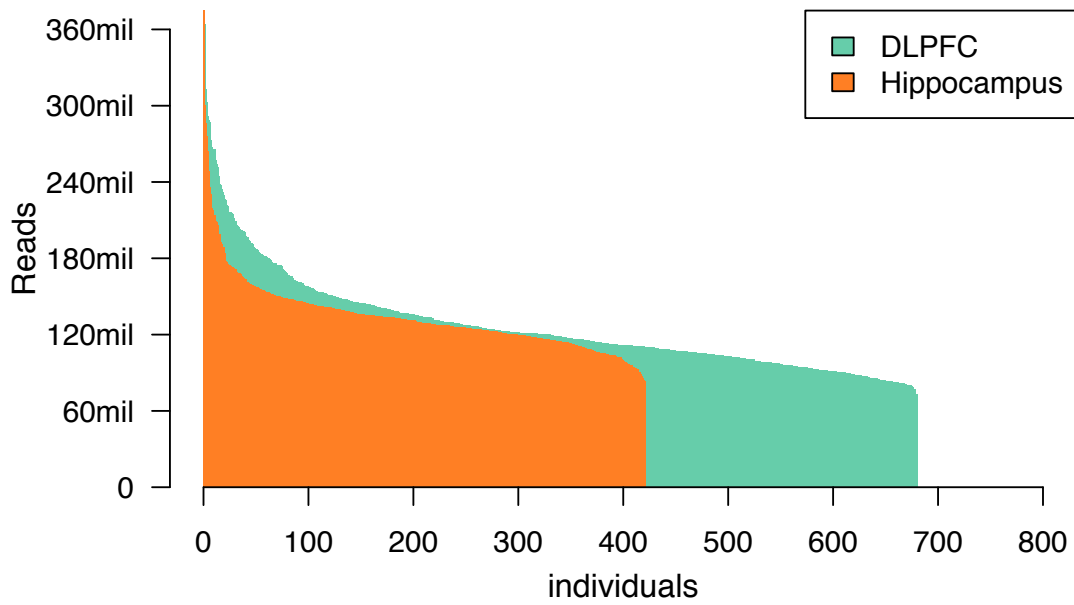


Fig S1-2: Pair-end reads in each fastq file for respective individual

	DLPFC	Hippocampus	Both
Mean	127133556	134174615	129825914
SD	39665006	30281344	36510189

Table S1-1: mean and standard deviation values for read counts in fastq files

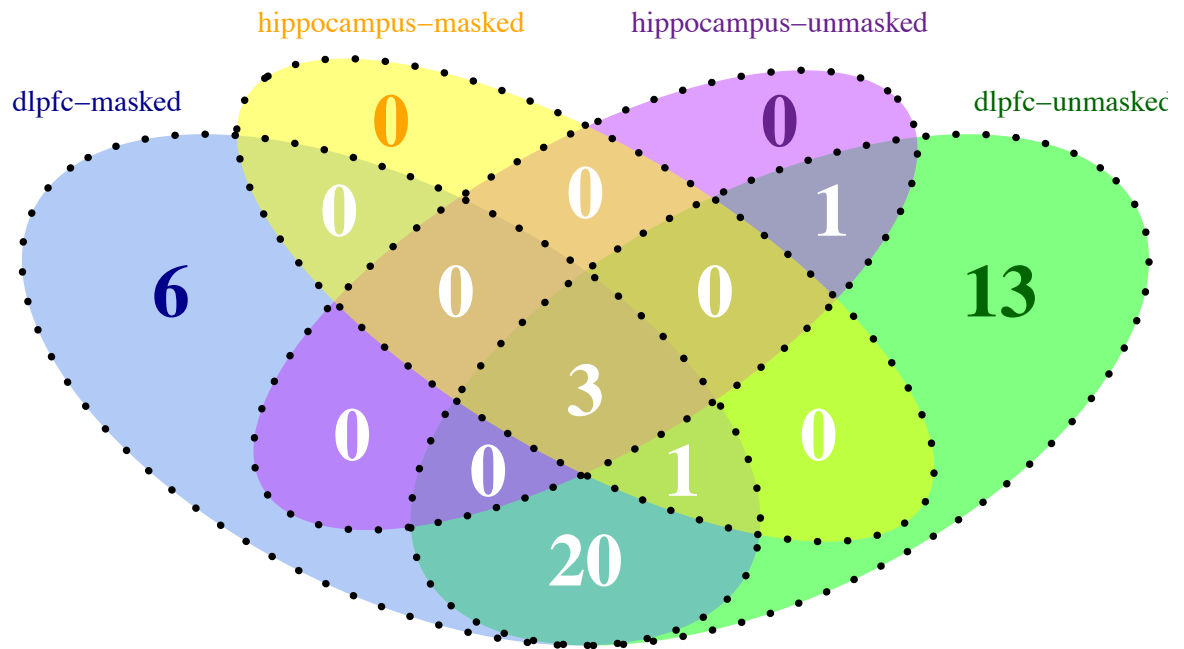


Fig S1-3: The number of aeQTLs found in respective tissue and alignment using significance thresholds set according to FDR5% as in main text table 1

	mean	sd	txSNPs
dlpfc.masked	0.506	0.127	247978
dlpfc.unmasked	0.517	0.125	239262
hippocampus.masked	0.505	0.161	137116
hippocampus.unmasked	0.513	0.160	135948

Table S1-2: A table of reference frequency and number of txSNPs in all genes and samples used for the calculation

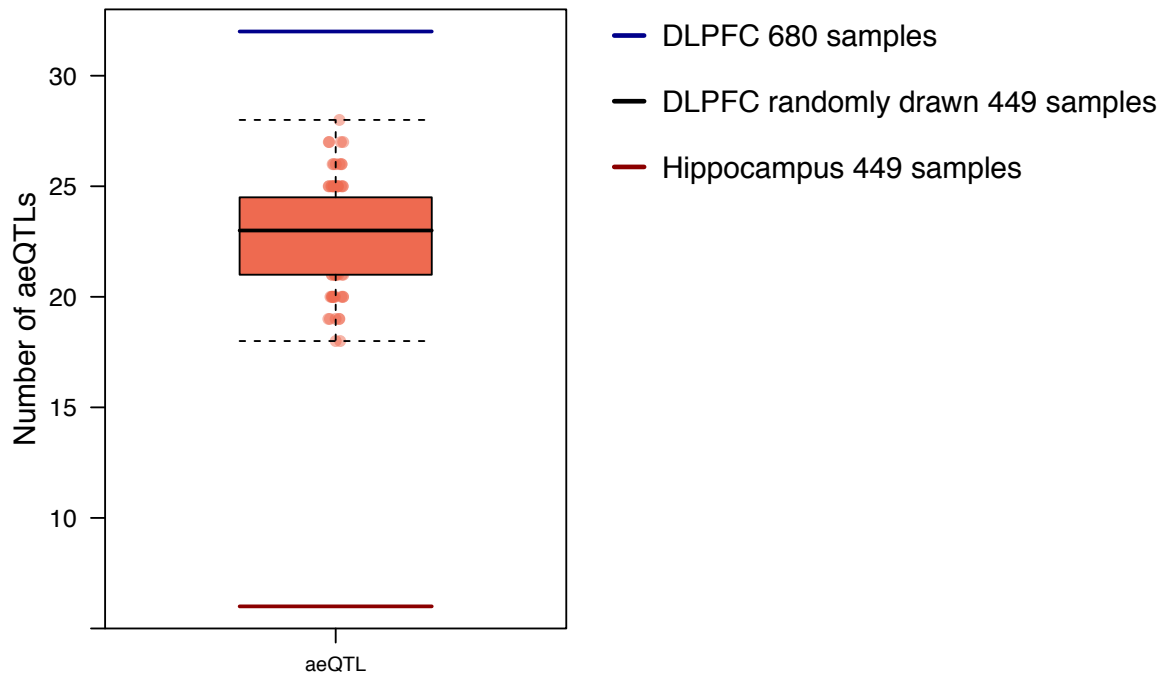


Fig S1-4: Figure demonstrating the amount of aeQTLs found for DLPFC(n=680) using the same sample size as Hippocampus(n=449). The DLPFC dataset was downsampled down to 449 and investigated for aeQTLs 100 times.

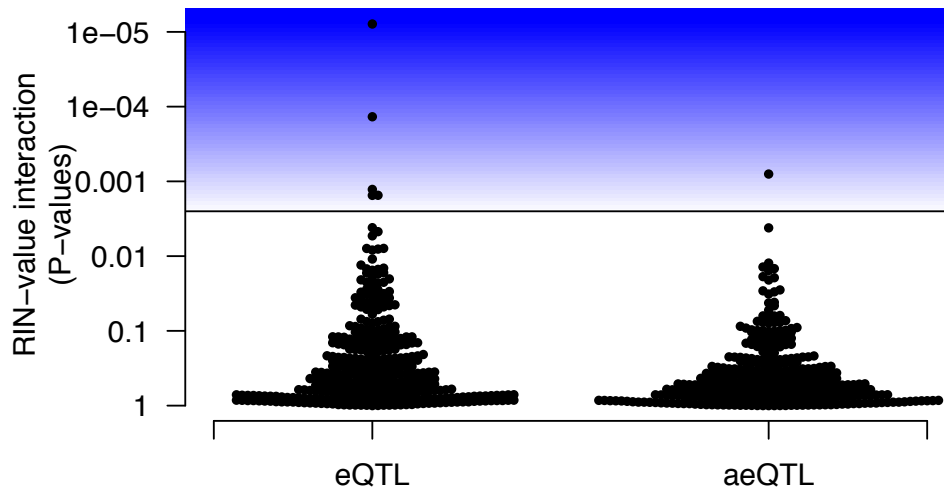


Fig S1-5: Calculation of RIN-interaction values for eQTL and aeQTL. Each dot shows the interaction P-value for all SNP-gene pairs. A binary RIN value cutoff was set at RIN 8. For the eQTL analysis 5 pairs were significant after multiple testing correction, in aeQTL analysis 1 pair was significant ($P < 0.0025$).

LRRN3 – rs13240464

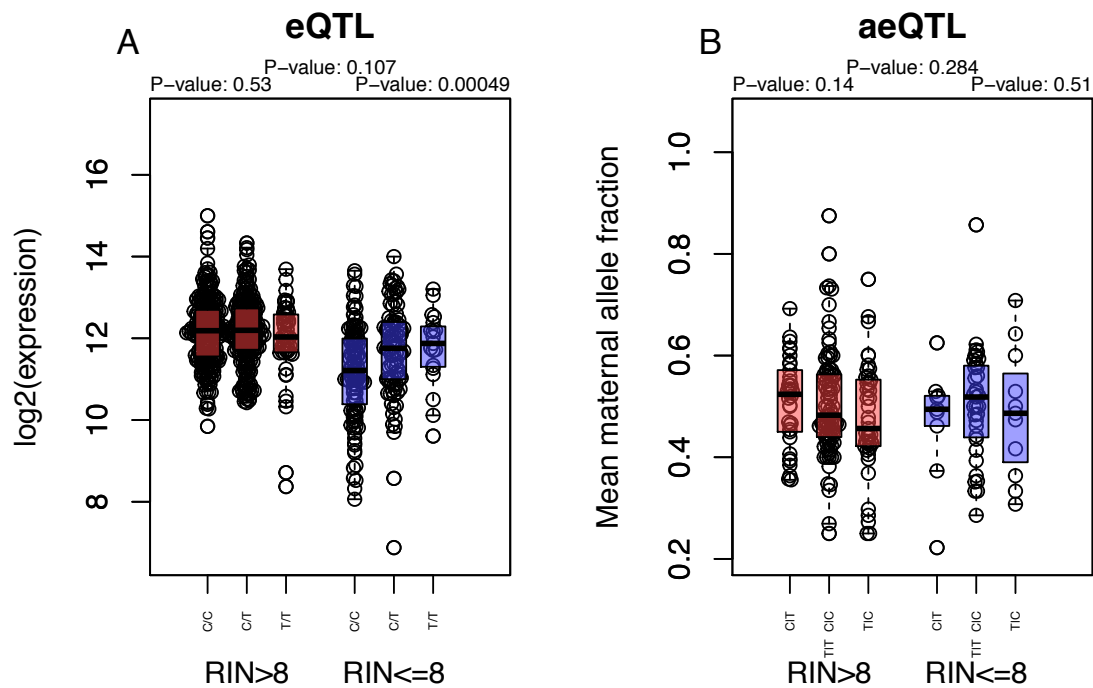


Fig S1-6: The eQTL for LRRN3 and risk-SNP rs13240464, stratified by RIN value. This plot illustrates an eQTL with potential interaction effects caused by RNA-degradation: when testing eQTL effect A), there was a significant interaction between RIN-value and risk-SNP genotype ($P_{\text{interaction}}=1.36e-04$), with lower RIN values giving rise to a stronger eQTL effect. B) This was not the case for aeQTL ($P_{\text{interaction}}=0.37$). Neither the non-stratified by RIN, but RIN-corrected eQTL ($P=0.107$) nor the aeQTL ($P=0.284$) for this gene-SNP pair were significant after multiple testing

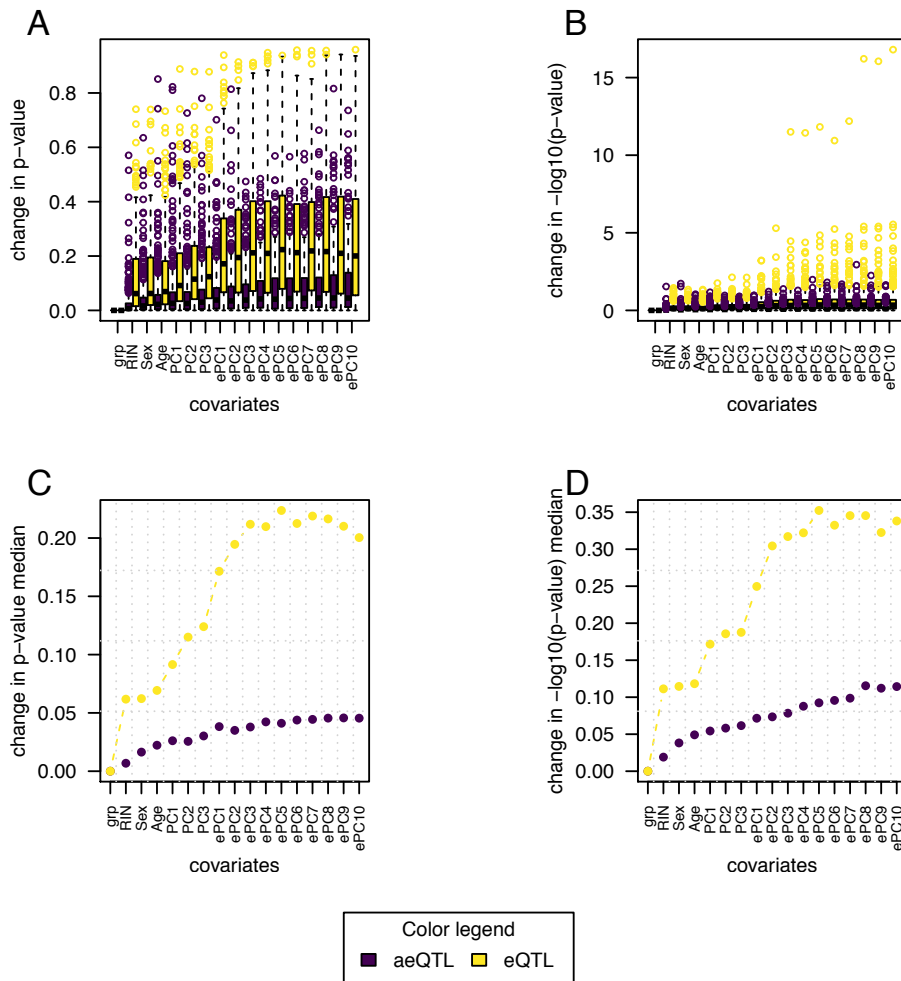


Fig S1-7: Covariates impact on p-values in aeQTL versus eQTL. All testable 371 gene-snp pairs in DLPFC have been included in this analysis, comparing the change of p-value distributions of aeQTL (purple) and eQTL (yellow). For each step to the right on the x-axis one more covariate is added, indicated as x-axis labels. For example, the third point's p-value was calculated using the formula $\text{expr} \sim \text{grp} + \text{RIN} + \text{Sex}$. A) Changes in raw p-value, calculated by $|\text{pvalue1} - \text{pvalue0}|$, giving more effect of p-values in the higher p-value range. B) Performing the same comparison, but starting with p-values which had been $-\log_{10}$ transformed, to give more effect on changes in the lower range of p-values. Taking the median from each p-value change using C) raw p-value and D) $-\log_{10}$ p-value, the pattern for both variants are very similar, indicating a similar effect of each additional covariate on the whole p-value range. In general, the aeQTL analysis shows little impact of covariate usage compared to eQTL analysis.

Gene	RiskSNP	Pos	Dist (Kb)	Ref/Alt	acQTL (est)	acQTL (pval)	acQTL (pval)	acQTL (pval)	acQTL (pval)	rsSNP	Reads	Genegroup
ALKBH5	rs8029200	chr17:18	-154	G/A	4.1e-05	-0.027	0.99	0.00998	0.00998	rs13284	110	57/116/54
ALKBH5	rs8029290	chr17:18	-153	G/A	4.1e-05	0.031	0.99	0.002	0.002	rs1565371	84	57/116/54
BAG5	rs7267548	chr20:48	-119	C/T	0.16	0.1	0.0076	0.0023	0.0023	rs75023	18	10/16/4
BAG5	rs12887734	chr14:104	23	C/T	0.029	0.046	0.0048	3.8e-07	3.8e-07	rs7695	110	50/158/49
CDIPT	rs12691307	chr16:30	66	A/G	-0.029	-0.039	0.027	5.9e-05	5.9e-05	rs115410970	19	10/20/14
CNNM2	rs11191419	chr10:105	-202	T/A	-0.0084	-0.036	0.26	5.0e-01	5.0e-01	rs2275271	87	112/55/114
CNNM2	rs9420	chr11:58	-75	A/G	-0.007	-0.024	0.13	3.9e-07	3.9e-07	rs708228	140	101/14/127
CNNM2	rs9420	chr11:58	-76	A/G	-0.007	-0.024	0.13	3.9e-07	3.9e-07	rs200470100	12	77/29/16
CNNM2	rs9420	chr11:58	-54	A/G	0.036	-0.032	0.13	0.0024	0.0024	rs10896644	34	62/115/68
CYP2D6	rs602055	chr22:43	78	C/T	0.036	0.13	0.035	0.00075	0.00075	rs28371704	34	22/25/16
DFA5	chr7_24747494_D	chr7:25	-11	I/D	-0.028	-0.058	0.0097	0.0027	0.0027	rs7891420	1900	50/206/21
DFA5	rs605094	chr20:37	-168	A/G	0.014	0.16	0.32	0.0013	0.0013	rs36053162	8.7	7/10/8
DFA5	rs6704768	chr2:234	-120	G/A	-0.015	-0.085	0.028	9.2e-08	9.2e-08	rs12328151	300	52/64/53
GIGYP2	rs12325245	chr16:59	-60	A/T	-0.036	-0.034	0.55	5.9e-06	5.9e-06	rs6993	310	45/221/44
HSPA9	rs3849046	chr5:138	-51	C/T	0.0087	0.018	0.72	7e-07	7e-07	rs1042665	4900	86/74/75
HSPA9	SNORD63	chr5:138	-40	C/T	0.0087	-0.043	0.72	2.5e-06	2.5e-06	rs11032	67	10/17/11
HSPA9	SNORD63	chr5:138	-190	C/T	0.005	0.017	0.85	0.00092	0.00092	rs1042665	4900	51/143/41
HSPA9	SNORD63	chr16:68	205	G/A	0.033	0.035	0.00039	0.026	0.026	rs11542821	18	34/41/40
HSPA9	SNORD63	chr16:68	212	G/A	0.033	0.036	0.00039	0.066	0.066	rs1109166	3.1	15/21/15
HSPA9	SNORD63	chr16:68	212	G/A	0.033	0.052	0.00039	0.3	0.3	rs11860141	2.9	8/7/13
HSPA9	SNORD63	chr16:68	210	G/A	0.033	-0.13	0.00039	0.42	0.42	rs11860115	1.3	7/5/8
HSPA9	SNORD63	chr16:68	210	G/A	0.033	-0.025	0.00039	0.59	0.59	rs17851876	8.2	5/38/4
HSPA9	SNORD63	chr16:68	208	G/A	0.033	-0.0011	0.00039	0.96	0.96	rs11860125	7.1	31/31/23
HSPA9	SNORD63	chr22:42	-14	T/C	-0.013	-0.076	0.082	1e-05	1e-05	rs62240997	120	49/151/46
LINC00634	rs1023500	chr22:42	-14	T/C	-0.013	-0.076	0.082	0.0021	0.0021	rs62240998	150	46/150/60
LINC00634	chr7_2025096_I	chr7:2	45	D/I	0.04	0.33	0.0011	0.0011	0.0011	rs10950456	41	96/22/92
LINC00634	chr7_2025096_I	chr7:2	45	D/I	-0.0071	-0.041	0.33	0.0025	0.0025	rs11557347	42	86/28/83
LINC00634	rs4702	chr15:91	-37	G/A	0.0045	0.017	0.3	0.0029	0.0029	rs4773	180	73/156/70
MA2	rs2905426	chr19:19	11	G/T	-0.0078	-0.037	0.078	0.0022	0.0022	rs756997	29	51/71/49
MA2	rs2905426	chr19:19	11	G/T	0.014	0.028	0.13	8.1e-05	8.1e-05	rs1064395	130	64/98/65
MA2	rs2905426	chr19:19	132	G/T	0.014	-0.05	0.13	2.5e-05	2.5e-05	rs2228600	88	16/59/21
MA2	rs2905426	chr19:19	132	G/T	0.014	-0.05	0.13	2.5e-05	2.5e-05	rs17821543	1800	23/7/36
MA2	rs2905426	chr22:43	122	C/T	-0.011	-0.031	0.0083	2.8e-07	2.8e-07	chr22_42481849	120	98/71/80
MA2	rs2905426	chr22:43	122	C/T	-0.011	-0.031	0.0083	2.4e-09	2.4e-09	rs709937	1500	95/46/120
MA2	rs2905426	chr22:43	122	C/T	-0.011	-0.031	0.0083	4e-05	4e-05	rs748002	1600	104/56/117
MA2	rs2905426	chr20:19	-90	T/G	-0.0059	-0.018	0.023	1.7e-05	1.7e-05	rs373525672	10	23/98/11
MA2	rs2905426	chr15:41	-16	G/A	0.048	0.11	0.0032	0.0027	0.0027	rs62021888	3	21/4/13
MA2	rs2905426	chr15:41	-16	G/A	-0.015	-0.11	0.34	0.00027	0.00027	rs21292804	23	30/14/25
MA2	rs2905426	chr14:104	-154	G/T	0.036	0.035	6e-04	0.58	0.58	rs10134157	40	8/48/6
MA2	rs2905426	chr14:104	-154	G/T	0.036	0.035	6e-04	0.58	0.58	rs45562136	31	11/27/8
MA2	rs2905426	chr20:37	-95	A/G	0.029	0.058	0.51	0.0013	0.0013	rs3743741	85	34/119/40
MA2	rs2905426	chr16:68	-156	G/A	-0.029	-0.072	0.00081	0.005	0.005	rs61733486	32	21/23/27
MA2	rs2905426	chr16:68	-156	G/A	-0.029	-0.072	0.00081	0.005	0.005	rs61746794	340	43/55/40
MA2	rs2905426	chr16:68	-198	G/A	-0.029	-0.021	0.00081	0.095	0.095	rs1131933	530	48/207/64
MA2	rs2905426	chr16:68	-200	G/A	-0.029	-0.0082	0.00081	0.38	0.38	rs1131933	530	48/207/64
MA2	rs2905426	chr16:68	-184	G/A	-0.029	-0.0065	0.00081	0.96	0.96	rs75567372	5.7	2/12/6
MA2	rs2905426	chr16:68	-184	G/A	-0.029	-0.0065	0.00081	NaN	NaN	rs138720818	2.9	3/5/5
MA2	rs2905426	chr16:30	114	A/G	-0.029	-0.087	0.3	0.00061	0.00061	rs14436390	31	7/7/6
MA2	rs2905426	chr12:57	-186	A/C	-0.01	0.1	0.11	0.0017	0.0017	rs77784795	56	7/13/8
MA2	rs2905426	chr19:50	45	T/G	-0.025	-0.075	0.088	1e-04	1e-04	rs3187346	50	40/49/34
MA2	rs2905426	chr5:138	-70	C/T	-0.00031	-0.0099	0.89	0.00086	0.00086	rs1046576	470	109/118/117
MA2	rs2905426	chr1_8424984_D	12	I/D	-0.0048	-0.04	0.15	2.9e-11	2.9e-11	rs1064826	250	74/28/107
MA2	rs2905426	chr1_8424984_D	12	I/D	-0.0048	-0.026	0.15	9.2e-08	9.2e-08	rs8627	420	79/136/99
MA2	rs2905426	chr1_8424984_D	6	I/D	-0.0048	0.026	0.15	8.1e-05	8.1e-05	rs11121172	240	87/22/121
MA2	rs2905426	chr1_8424984_D	6	I/D	-0.0048	0.021	0.15	0.0018	0.0018	rs1058766	240	86/19/121
MA2	rs2905426	chr1_8424984_D	6	I/D	-0.0048	-0.03	0.11	2.5e-05	2.5e-05	rs7582536	43	120/3/104
MA2	rs2905426	chr2:198	-132	G/A	-0.021	-0.051	0.07	0.0014	0.0014	rs1755056	26	30/56/55
MA2	rs2905426	chr19:50	92	T/G	-0.024	-0.071	0.7	0.0014	0.0014	rs10927011	26	64/136/48
MA2	rs2905426	chr1:244	-24	A/G	0.015	-0.059	0.033	5.3e-05	5.3e-05	rs10927011	160	67/148/74
MA2	rs2905426	rs12691307	29	A/G	0.015	-0.033	0.033	4e-04	4e-04	rs11344	160	64/136/48
MA2	rs2905426	rs4523957	23	G/T	0.026	0.037	0.62	5.3e-06	5.3e-06	rs749240	23	112/17/123
MA2	rs2905426	chr17:2	6	G/T	0.026	-0.042	0.62	0.0012	0.0012	rs1885987	27	53/82/68

Gene	RisksNP	Pos	Dist (Kb)	Ref/Alt	aeQTL (est)	aeQTL txSNP (est)	aeQTL (pval)	aeQTL txSNP (pval)	Reads	Genomgroup (ind)
SOX2, SOX2-OT	rs9831016	chr3:181	-291	T/A	-0.004	0.039	0.49	0.0017	610	39/188/49
STAT6	rs324017	chr12:57	-2	A/C	0.0074	0.11	0.25	8.8e-26	180	94/141/89
STAT6	rs324017	chr12:57	-2	A/C	0.0074	-0.055	0.25	1e-13	54	104/18/108
STAT6	rs324017	chr12:57	-2	A/C	0.0074	-0.032	0.25	0.00011	83	67/148/66
SUGP1	rs2905326	chr19:19	88	G/T	-0.00062	0.079	0.25	0.00011	35	18/60/16
TAOK2	rs12691307	chr16:30	-55	A/G	0.001	-0.03	0.81	0.00045	240	60/80/57
TCF20	rs6002655	chr22:43	-6	C/T	-0.012	-0.1	0.13	0.0011	280	95/56/112
TMEM110, TMEM110, TMEM110	rs2535627	chr3:33	-23	T/C	-0.012	0.11	0.05	0.0013	2.8	9/18/10
MUSTN1, TMEM110, MUSTN1	rs140505938	chr1:150	-8	C/T	0.056	0.062	0.0018	0.0037	5.2	18/39/21
VPS45	rs1191419	chr10:105	38	T/A	-0.002	-0.034	0.63	0.00019	46	103/110/105
WBP1L	chr5_140143664_1	chr5:140	95	D/U	-0.0094	-0.1	0.14	0.00019	9.6	31/26/11
WDR55										

Table S1-3: For DLPPC, similar to Table 1 in the main manuscript, but for individual txSNPs that were FDR5% signif cant

Gene	RisksNP	Pos	Dist (Kb)	Ref/Alt	aeQTL (est)	aeQTL txSNP (est)	aeQTL (pval)	aeQTL txSNP (pval)	Reads	Genomgroup (ind)
AS3MT, BORCS7	rs55833108	chr10:105	118	G/T	-0.032	-0.13	0.14	0.0027	35	10/95/9
ATXN7	rs832187	chr3:64	-155	C/T	-0.004	-0.082	0.69	0.00156	54	40/45/27
BAG5	rs12887734	chr14:104	23	G/T	0.013	0.077	0.3	0.0017	46	21/73/25
CTNND1, TMX2, C11orf31	rs9420	chr11:58	-19	A/G	0.0083	0.088	0.28	3e-04	210	29/64/19
DFNA5	chr7_24747494_D	chr7:25	9	I/D	-0.056	-0.089	0.029	0.0026	39	22/43/18
FAM53C	rs10043984	chr5:138	27	C/T	0.022	0.077	0.056	0.0014	37	27/74/21
HAPLN4	rs2905426	chr19:19	111	G/T	0.038	0.093	0.022	0.0021	39	20/45/24
HSPA9, SNORD63	rs10043984	chr5:138	-190	C/T	0.0047	0.042	0.42	2.9e-05	4800	33/88/29
HSPA9, SNORD63	rs3849046	chr5:138	-51	C/T	0.0022	0.031	0.68	0.0066	4800	48/55/47
HSPA9, SNORD63	rs12887734	chr14:104	-49	G/T	-0.0028	-0.022	0.68	0.0066	380	61/52/60
KLC1	rs12826178	chr12:58	33	G/T	0.02	0.17	0.22	0.0085	27	7/53/10
LRP1	rs11210892	chr1:44	13	G/A	0.011	-0.073	0.9	0.0016	110	5/180/5
PTRF	rs11210892	chr1:44	13	G/A	0.011	-0.073	0.9	0.0016	160	57/163/60
REFF	rs10803138	chr1:8	12	U/D	0.0049	-0.053	0.55	0.0012	68	42/21/55
SDCCAG8, MIR4677	rs10803138	chr1:244	61	A/G	-0.042	-0.11	0.0032	0.0071	760	24/30/26
SEPT3	rs1023500	chr22:42	-52	T/C	0.003	0.067	0.65	0.0027	190	7/51/10
SF3B1	rs6434928	chr2:198	47	G/A	-0.0083	-0.027	0.13	0.0015	170	71/1/70
SOX2, SOX2-OT	rs9841616	chr3:181	-291	T/A	-0.007	0.24	0.45	0.0012	89	5/12/7
SREBF2, MIR33A	rs1023500	chr22:42	64	T/C	-0.0057	-0.11	0.95	0.0038	2900	14/53/15
STAT6	rs324017	chr12:57	-2	A/C	-0.028	-0.055	0.038	0.0026	19	36/5/36
TMEM110, TMEM110, TMEM110	rs2535627	chr3:33	-27	T/C	-0.0055	-0.12	0.64	0.0016	13	14/27/19
MUSTN1, TMEM110, MUSTN1										
TOM1L2	rs8082590	chr17:18	210	G/A	-0.011	-0.043	0.026	0.0018	66	68/43/74

Table S1-4: For Hippocampus, similar to Table 1 in the main manuscript, but for individual txSNPs that were FDR5% signif cant

Gene	SNP	Pos	Dist (Kb)	Dist Rank	Ref/Alt	Direction	aeQTL p-value	txSNPReads	Individuals per group	Support
AS3MT, BORCS7	rs1191419	chr10:105	-2	1	T/A	up	3.1e-21	20	150	59/41/152 Ge, Ga, Re, Je, Js
PROPT1	rs12887734	chr14:104	58	1	C/T	down	4e-22	8	6300	129/64/16 Ge, Ga, Je, Js
ZMAT2	chr5_140143664_I	chr5:140	58	2	D/H	down	4e-22	9	230	162/36/143 Ga
HAPLN4	rs2905426	chr19:19	109	5	G/T	down	5.8e-19	12	230	103/163/106 Ga
BRINP2	rs723273	chr12:08	8	1	A/G	up	5.4e-17	9	230	147/21/126 Ge, Ga, Je, Js
NDUFA2	rs6070165	chr11:17	29	1	A/G	down	3e-12	4	1000	84/272/93 Ga, Js
TOM1L2	chr5_140143664_I	chr5:140	116	8	D/H	down	3e-12	2	77	134/85/107 Ga, Re
FURIN	rs8025390	chr17:18	186	8	G/A	down	5.3e-12	24	360	140/154/162 Ga, Js
ANP32E	rs14702	chr15:91	0	1	G/A	down	4.4e-10	8	680	142/226/144 Ga, Fe
SFC51	rs12887734	chr14:104	-160	8	C/T	down	7.7e-09	3	8900	70/268/71 Ga
SNX19	rs12887734	chr14:104	59	4	C/T	down	8e-09	3	240	120/135/104 Ga
PTPRF	rs2535627	chr5:53	103	6	T/C	down	1.6e-08	44	710	160/319/145 Ga, Je, Js
NEK4	rs10791097	chr11:131	-28	1	T/C	up	2.3e-07	17	1600	140/311/131 Ga
FAM57B	rs2535627	chr14:104	59	4	T/C	down	4.8e-07	9	44	140/170/141 Ga, Je, Js
LRP1	rs126913007	chr16:30	-96	12	A/G	down	6.6e-07	4	370	139/167/152 Ga, Js
HSPD1	rs12826178	chr12:58	16	4	G/T	down	5.9e-06	32	150	25/455/23 Ga
VPS45	rs6434928	chr2:198	-47	3	G/A	down	3.9e-05	9	51	127/149/119 Ga
PRMT7	rs140505938	chr1:150	-8	1	C/T	down	4e-05	5	120	20/90/24 Ga, Js
ZFYVE21	rs12887734	chr14:104	-146	7	G/T	down	0.00027	9	520	86/288/103 Ge, Ga, Re, Je, Js
FAM53C	rs10043984	chr5:138	27	2	C/T	down	0.00034	7	420	118/255/103 Ga
AS3MT, BORCS7	rs5833108	chr10:105	80	2	G/T	down	0.00035	9	100	104/260/89 Ga, Js
IK, MIR3635	chr5_140143664_I	chr5:140	102	7	D/H	down	6e-04	20	150	39/369/44 Ge, Ga
SNL3	rs2535627	chr5:53	117	8	T/C	down	0.00066	5	160	96/130/81 Ga
SNORD19, SNORD69, SNORD19B	rs12887734	chr14:104	-153	8	G/T	up	7e-04	9	410	153/167/144 Re
PPP1R13B	rs12887734	chr14:104	43	1	C/T	down	0.001	9	42	43/119/39 Ga
RIMS1	rs1339227	chr6:73	43	1	C/T	down	0.0012	21	420	130/365/108 Ga
DNAJC19	chr3_180594593_I	chr3:181	-107	2	D/H	up	0.0014	2	54	126/19/132 Ga
CDIPT	rs126913007	chr16:30	66	7	A/G	down	0.0016	3	31	27/63/24 Ga
GATA2A	rs2905426	chr19:19	-98	4	G/T	down	0.0016	15	85	135/162/144 Ga, Je, Js
CUL3	rs11685299	chr2:225	0	1	C/A	up	0.0018	24	820	96/217/96 Ga, Re
NSUN6	rs7893279	chr10:19	-90	2	T/G	up	0.0023	2	23	39/241/31 Ga, Js

Table S1-3: For DLFFC, similar to Table 1 in the main manuscript, but here all fetal samples were used

Gene	SNP	Pos	Dist (Kb)	Dist Rank	Ref/Alt	Direction	aeQTL p-value	txSNPReads	Individuals per group	Support
AS3MT, BORCS7	rs1191419	chr10:105	-2	1	T/A	up	2.2e-08	20	120	90/88/88 Ge, Ga, Re, Je, Js
ZMAT2	chr5_140143664_I	chr5:140	58	2	D/H	down	3.9e-09	2	180	97/34/78 Ga
SNX19	rs10791097	chr11:131	-28	1	T/G	up	2e-07	44	970	98/212/90 Ga, Je, Js
HSPD1	rs6434928	chr2:198	-47	3	G/A	down	6.3e-06	6	380	77/157/71 Ga, Js
DNAJC19	chr3_180594593_I	chr3:181	-107	2	D/H	up	0.0015	2	37	79/21/64 Ga
SDCCAG8	rs10803138	chr12:44	0	1	A/G	down	0.0022	4	730	54/148/54 Ga

Table S1-6: For Hippocampus, similar to Table 1 in the main manuscript, but here all fetal samples were used