Table S1. Characteristics of the ED cohort and the three trajectories probability classes.

	Total	Chronic	Remitting	Resilient
Number of Subjects (%)	377	41 (10.9%)	124 (32.9%)	212 (56.2%)
Sex (% Females)	47.0%	61.0%	56.1%	39.10%
Age (SD)	36.0 (12.8)	34.1 (11.0)	36.9 (13.5)	35.9 (12.8)
Race				
African ancestry	75.5%	80.5%	82.9%	70.3%
European ancestry	16.5%	9.8%	11.4%	20.7%
Other	8.0%	9.8%	5.7%	9.0%
Trauma				
No Sexual Assault	6.9%	4.9%	11.3%	4.7%
Sexual Assault	6.1%	17.1%	7.3%	3.3%
Road Accidents[a]	70.3%	56.1%	66.9%	75.0%
Gun Accidents	4.5%	9.8%	3.2%	4.2%
Stabbing	2.4%	2.4%	3.2%	1.9%
Animal Bites	1.1%	2.4%	0.8%	0.9%
Other	8.8%	7.3%	7.3%	9.9%
Education				
Some HS or less	13.6%	19.5%	13.8%	12.3%
HS graduate	27.1%	31.7%	28.5%	25.5%
AA/some college	40.2%	39.0%	42.3%	39.2%
BS/BA	14.1%	7.3%	9.8%	17.9%
Master/PhD	5.0%	2.4%	5.7%	5.2%
Baseline PTSD symptoms (SD)	9.3 (9.9)	17.9 (12.1)	12.2 (9.6)	6.1 (7.9)

[a]Road Accidents includes motor vehicles crashes, and pedestrians and bike accidents.

Table S2. Low expression in *GRIN3B* and *AMOLT1* genes predicts resilience during a 12-month period.

GENE	logFC	AveExpr	t	P-Value	FDR
GRIN3B	-0.75	1.12	-5.30	4.50×10^{-7}	0.0063
AMOTL1	-0.78	0.57	-4.83	3.63×10^{-6}	0.0253

FC: Fold Change
AveExp: average expression
FDR: adjusted P-values using False Discovery Rate

Table S4. *GRIN3B* expression levels associate with PSS symptoms over a 12-month period.

PSS	Estimate	SE	t-value	Pr(>|t|)
Baseline	-0.0008	0.0027	-0.3	0.7647
1-month	0.0049	0.0025	1.985	0.0486
3-month	0.0085	0.0028	3.071	0.0025
6-month	0.0112	0.0027	4.119	$6.3x10^{-5}$
12-month	0.0095	0.0032	2.998	0.0033

SE Standard Error

Table S5. WGCNA Modules association in resilience vs chronic class-trajectory

module	logFC	AveExpr	t	P.Value	adj.P.Val
ME26	-0.0257	0.0003	-1.8462	0.0670	0.7191
ME15	-0.0209	0.0016	-1.7024	0.0909	0.7191
ME32	0.0184	0.0069	1.4864	0.1394	0.7191
ME22	-0.0211	0.0030	-1.4840	0.1401	0.7191
ME23	0.0115	0.0026	1.3835	0.1687	0.7191
ME9	-0.0165	0.0039	-1.3682	0.1734	0.7191
ME30	0.0186	0.0001	1.3437	0.1812	0.7191
ME3	-0.0172	-0.0060	-1.3287	0.1861	0.7191
ME8	-0.0183	-0.0022	-1.2772	0.2037	0.7191
ME33	-0.0163	-0.0019	-1.2700	0.2062	0.7191
ME4	-0.0171	-0.0020	-1.2435	0.2158	0.7191
ME5	0.0106	0.0039	1.2286	0.2213	0.7191
ME13	-0.0127	-0.0024	-1.1739	0.2424	0.7273
ME7	-0.0176	-0.0005	-1.1142	0.2671	0.7378
ME19	0.0154	0.0019	0.9844	0.3266	0.7378
ME27	-0.0104	0.0082	-0.9813	0.3281	0.7378
ME20	0.0080	0.0047	0.9594	0.3390	0.7378
ME24	0.0135	-0.0023	0.9564	0.3405	0.7378
ME12	0.0114	0.0012	0.8766	0.3822	0.7554
ME21	0.0097	0.0028	0.8385	0.4032	0.7554
ME18	0.0087	0.0032	0.7715	0.4417	0.7554
ME25	0.0077	-0.0005	0.7600	0.4485	0.7554
ME35	-0.0089	0.0029	-0.7436	0.4584	0.7554
ME2	-0.0058	0.0035	-0.6991	0.4857	0.7554
ME10	-0.0082	0.0032	-0.6915	0.4904	0.7554
ME1	0.0041	-0.0059	0.6342	0.5270	0.7554
ME34	-0.0103	-0.0001	-0.5973	0.5513	0.7554
ME11	0.0051	0.0075	0.5823	0.5613	0.7554
ME14	0.0040	0.0000	0.5817	0.5617	0.7554
ME38	0.0062	0.0024	0.3537	0.7241	0.9193
ME17	0.0042	-0.0050	0.3448	0.7307	0.9193
ME36	-0.0046	0.0002	-0.2741	0.7844	0.9201
ME31	0.0029	-0.0033	0.2424	0.8088	0.9201
ME6	0.0019	-0.0035	0.1977	0.8436	0.9201
ME28	-0.0020	-0.0023	-0.1903	0.8494	0.9201
ME29	-0.0014	-0.0044	-0.0788	0.9373	0.9748
ME37	0.0009	0.0023	0.0631	0.9498	0.9748
ME16	-0.0004	0.0023	-0.0303	0.9759	0.9759

Table S6. Characteristics of the Grady Trauma Project Cohort.

Characteristics	Total	PSS ≤ 7	PSS ≥ 19
Number of Subjects (%)	5248	2186	1335
Sex (% Females)	75.2%	72.9%%	76.5%%
Mean PSS-Symptoms (SD)	12.5 (12.1)	2.4 (2.4)	29.2(7.5)
Age	39.9 (13.9)	40.2(14.7)	40.3(12.3)

All individuals were of African ancestry
Total Median was 9 (minimum 0 and maximum 51)

Table S7. Genetic association analyses for five[a] *GRIN3B* variants and PTSD in the GTP dataset.

Variants	MAF	(A1/A2)[b]	N	OR	SE	P
rs10401454	**0.235**	**G/C**	**3521**	**1.13**	**0.059**	**0.0359**
rs10666583	**0.113**	**GCGTT/G[c]**	**3490**	**0.86**	**0.076**	**0.0442**
rs2240158	0.484	C/T	3521	1.05	0.049	0.3505
rs4806908	0.311	A/G	3488	0.96	0.053	0.4935
rs8109756	0.475	T/C	3521	0.10	0.049	0.9741

PTSD cases had PSS >19; controls had PSS <7
[a]Four of these variants (rs10401454, rs2240158, rs4806908, rs8109756) are blood eQTL in our study; rs10666583 is a stop mutation previously associated with SCZ in previous studies.
[b] A1/A2 indicate the two different alleles; A1 is the reference minor allele.
[c]4 bases insertion.

Table S8. Association between *GRIN3B* eQTLs and symptom trajectories in the ED cohort.

SNP	A1	MAF	N	BETA	SE	P
Chronic-PTSD vs. Remitting vs. Resilient						
rs2240158	**T**	**0.442**	**269**	**-0.154**	**0.0643**	**0.017**
rs4806908	**A**	**0.262**	**113**	**-0.254**	**0.1113**	**0.024**
rs8109756	T	0.395	269	-0.056	0.0653	0.393
rs10401454	G	0.267	269	0.045	0.0709	0.527
rs10666583*	INDEL	0.117	228	0.050	0.1188	0.674
Chronic-PTSD vs. Resilient						
rs4806908	A	**0.442**	84	-0.885	0.4862	0.069
rs2240158	T	**0.262**	181	-0.377	0.3122	0.227
rs10401454	G	0.395	181	0.309	0.3571	0.387
rs8109756	T	0.267	181	-0.249	0.3053	0.415
rs10666583*	INDEL	0.117	160	0.476	0.6561	0.468

Note: ODD-RATIOS were changed to beta for logistic regression to compare directions among different phenotypes.

***This null variant was associated with SCZ in two previous studies.**

Figure S1. Trajectories of PTSD symptoms across one year after trauma exposure. Trajectories of PTSD severity symptoms (y-axis) are plotted across baseline, 1, 3, 6, and 12 months after trauma exposure. Trajectories were calculated using a latent growth mixture modeling, excluding baseline. Colors define the different trajectories classes, with red indicating chronicity (10.9%), green remittance (32.9%), and blue resilience (56.2%). Means and SDs of the severity symptoms at each data point are displayed.

Figure S2. Box and Whiskers plots of blood mRNA expressions level for *GRIN3B* and *AMOLT1* comparing three different categories (chronic, recovery, and resilience). Y-axis shows gene expression values. A. *GRIN3B* expression levels gradually decrease from chronic to recovery to resilience, mimicking a dose-effect response ($p=1.04x10^{-5}$; t= -4.5). B. *AMOLR1* expression levels in the three-class trajectory (t=2.7 p=0.0083) does not show a comparable dose-effect response.

Figure S3. Plots representing brain expression level from brain regions derived from public databases. A-B BrainCloud. Rs10401454 associates with expression values from dorsolateral prefrontal cortices (DLPFCs) from 412 subjects (175 patients with schizophrenia) (A) and control only B. C-D GTEx. Plot representing brain cortex and frontal cortex expression levels changing with rs10401454 different genotypes (from GTEx portal) for Brain Cortex (C) and Frontal Cortex (D)**.**

Figure S4. *GRIN3B* rs10401454 eQTL for 49 tissues, including brain and whole blood from GTEx. NES indicates the normalized effect size; p is the eQTL p-value for each tissue. **M-value** indicates the posterior probability that an eQTL effect exists in each tissue tested in the cross-tissue meta-analysis; m-values range between 0 and 1, with 0 predicting not having an effect, and 1 predicting having an effect (2)

1. Hinrichs R, van Rooij SJ, Michopoulos V, Schultebraucks K, Winters S, Maples-Keller J, Rothbaum AO, Stevens JS, Galatzer-Levy I, Rothbaum BO, Ressler KJ, Jovanovic T. Increased Skin Conductance Response in the Immediate Aftermath of Trauma Predicts PTSD Risk. Chronic Stress (Thousand Oaks). 2019;3. Epub 2019/06/11. doi: 10.1177/2470547019844441. PubMed PMID: 31179413; PMCID: PMC6553652.
2. Han B, Eskin E. Interpreting meta-analyses of genome-wide association studies. PLoS Genet. 2012;8(3):e1002555. Epub 2012/03/08. doi: 10.1371/journal.pgen.1002555. PubMed PMID: 22396665; PMCID: PMC3291559.

Figure S1. Trajectories of symptoms of PTSD across one year after trauma.

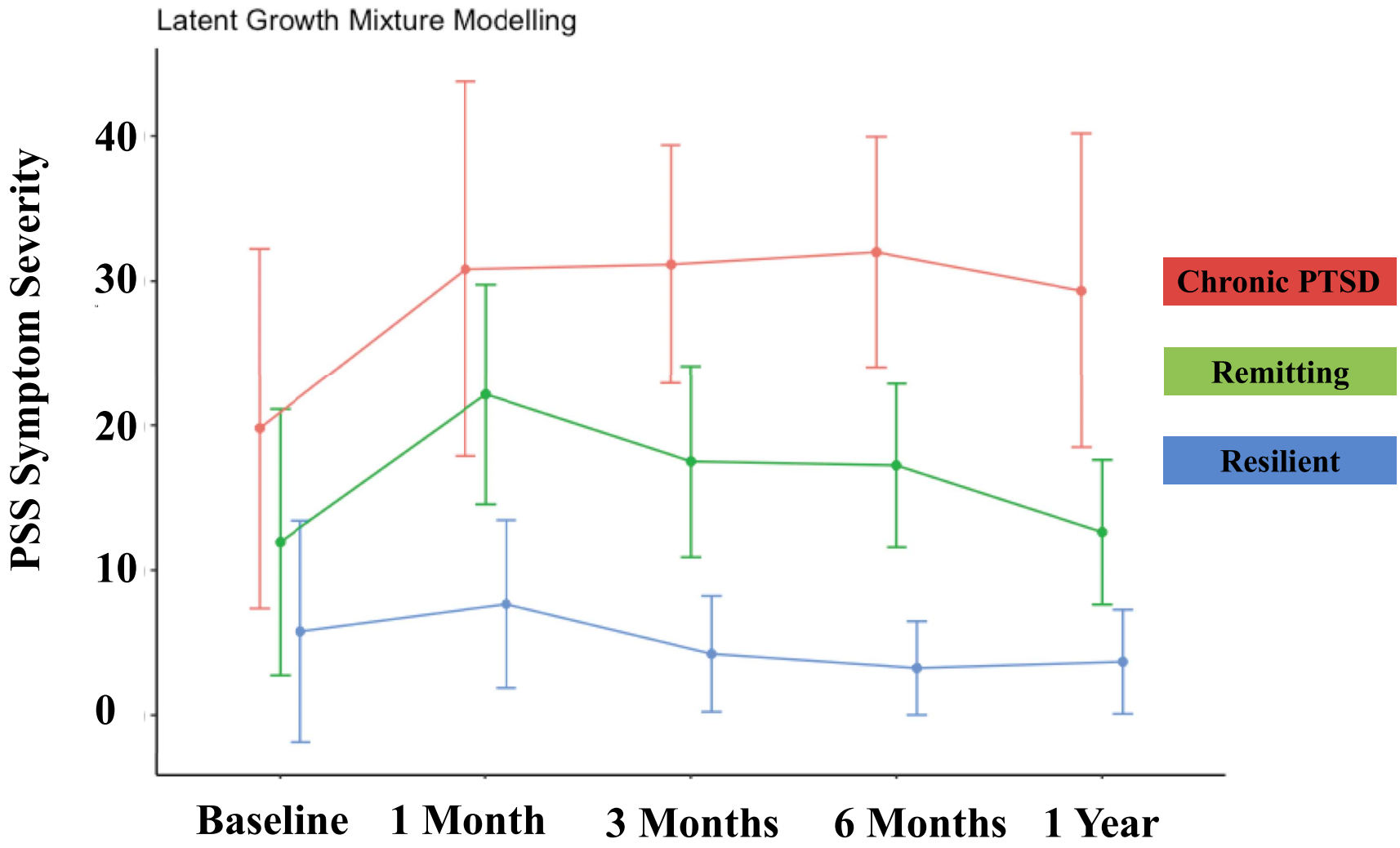

Figure S2. *GRIN3B* and *AMOLT1* expression profiles of the three class trajectories

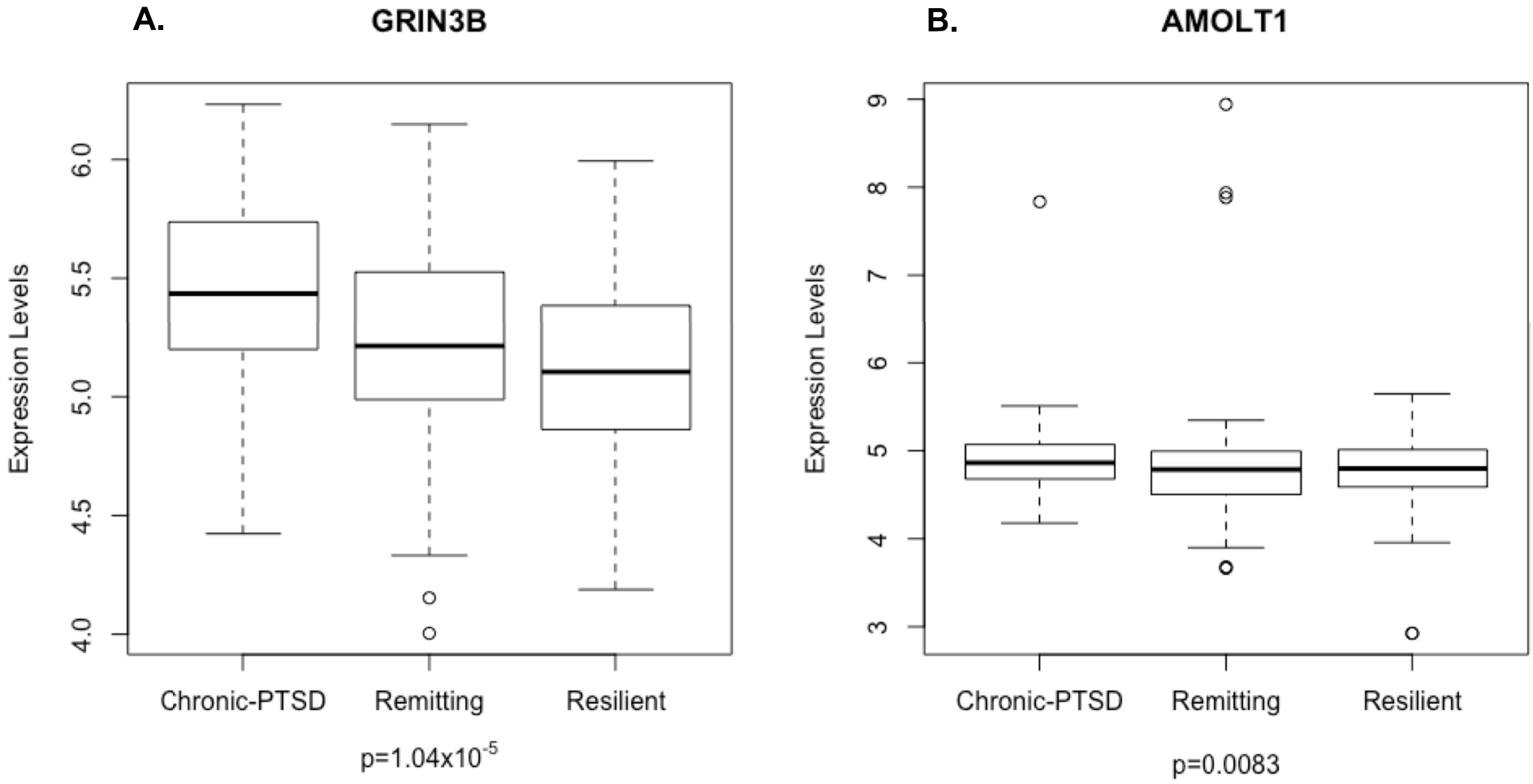

Figure S3. Brain eQTL for rs10401454 from Brain Cloud and GTEx

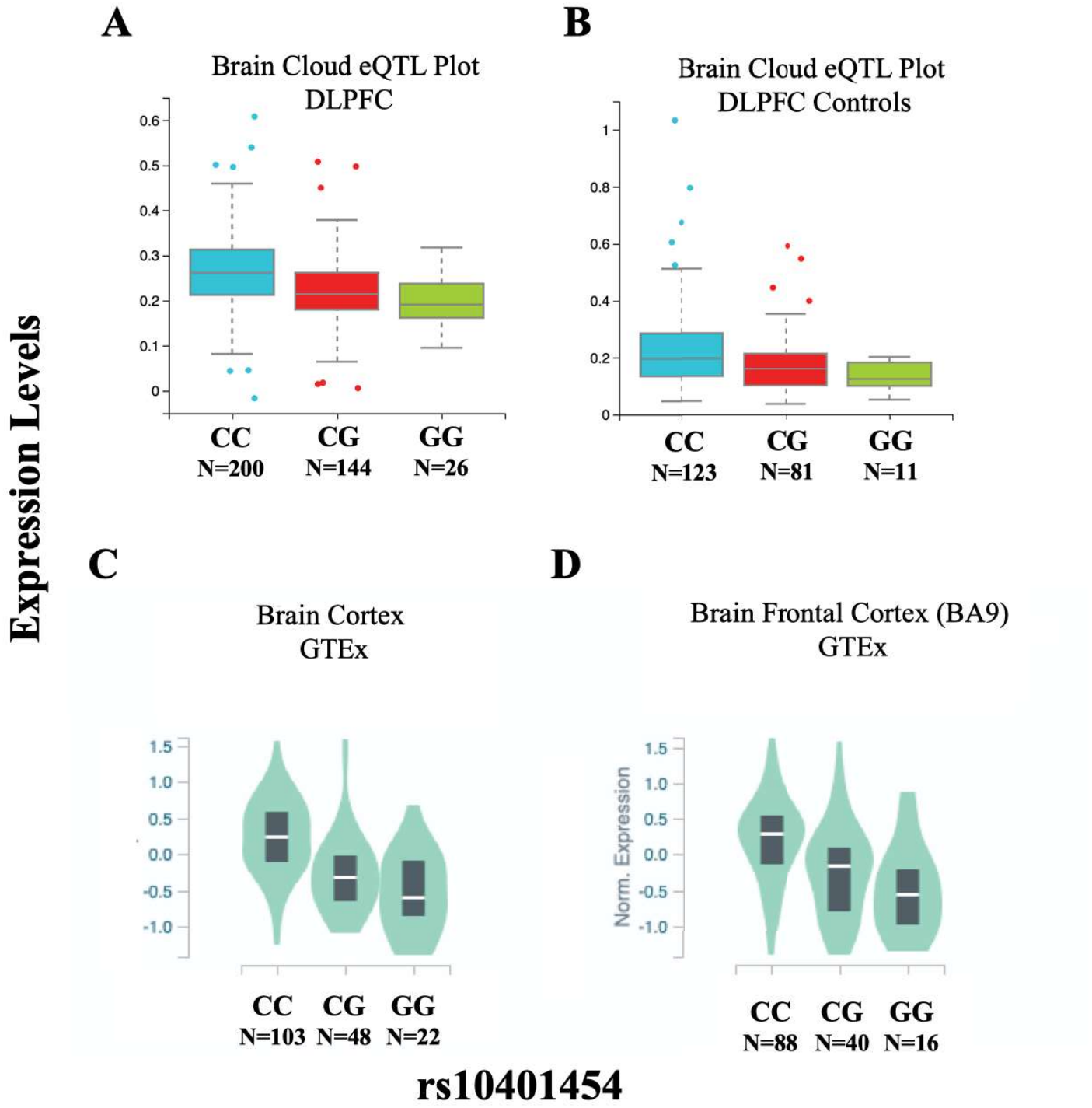

Figure S4. *GRIN3B* rs10401454 RNA regulation of multi tissues (GTEx)

Tissue	Samples	NES	p-value	m-value
Testis	322	0.263	9.9e-4	0.00
Kidney - Cortex	73	0.0955	0.6	0.0340
Cells - Cultured fibroblasts	483	-0.0741	0.02	0.00
Brain - Caudate (basal ganglia)	194	-0.0818	0.2	0.00
Brain - Substantia nigra	114	-0.0979	0.4	0.00300
Brain - Hippocampus	165	-0.122	0.06	0.00
Lung	515	-0.150	5.8e-11	0.00
Brain - Anterior cingulate cortex (BA24)	147	-0.175	0.06	0.0990
Brain - Spinal cord (cervical c-1)	126	-0.195	0.1	0.680
Brain - Amygdala	129	-0.221	0.01	0.641
Brain - Hypothalamus	170	-0.253	1.7e-4	0.987
Whole Blood	670	-0.277	1.2e-10	1.00
Heart - Left Ventricle	386	-0.307	2.9e-9	1.00
Ovary	167	-0.355	4.0e-4	1.00
Brain - Putamen (basal ganglia)	170	-0.372	3.0e-5	1.00
Uterus	129	-0.382	3.0e-5	1.00
Brain - Nucleus accumbens (basal ganglia)	202	-0.387	9.0e-9	1.00
Vagina	141	-0.392	2.8e-4	1.00
Muscle - Skeletal	706	-0.394	3.2e-26	1.00
Cells - EBV-transformed lymphocytes	147	-0.400	2.6e-4	1.00
Adrenal Gland	233	-0.409	1.9e-7	1.00
Pancreas	305	-0.412	1.3e-9	1.00
Brain - Cerebellum	209	-0.430	3.9e-8	1.00
Artery - Aorta	387	-0.434	4.3e-17	1.00
Brain - Cerebellar Hemisphere	175	-0.435	1.3e-7	1.00
Brain - Frontal Cortex (BA9)	175	-0.435	6.2e-6	1.00
Colon - Sigmoid	318	-0.438	1.7e-13	1.00
Brain - Cortex	205	-0.446	2.0e-10	1.00
Prostate	221	-0.452	2.0e-9	1.00
Artery - Coronary	213	-0.455	6.7e-9	1.00
Artery - Tibial	584	-0.471	3.6e-29	1.00
Liver	208	-0.473	4.6e-8	1.00
Heart - Atrial Appendage	372	-0.480	3.4e-17	1.00
Esophagus - Muscularis	465	-0.488	3.1e-28	1.00
Esophagus - Gastroesophageal Junction	330	-0.493	1.2e-16	1.00
Esophagus - Mucosa	497	-0.496	2.6e-26	1.00
Adipose - Visceral (Omentum)	469	-0.496	8.2e-19	1.00
Skin - Not Sun Exposed (Suprapubic)	517	-0.518	6.5e-36	1.00
Skin - Sun Exposed (Lower leg)	605	-0.520	3.5e-41	1.00
Colon - Transverse	368	-0.523	2.6e-18	1.00
Nerve - Tibial	532	-0.524	4.9e-39	1.00
Stomach	324	-0.530	2.5e-13	1.00
Spleen	227	-0.534	2.0e-14	1.00
Adipose - Subcutaneous	581	-0.539	4.6e-35	1.00
Breast - Mammary Tissue	396	-0.547	1.1e-30	1.00
Pituitary	237	-0.548	1.2e-14	1.00
Small Intestine - Terminal Ileum	174	-0.559	2.2e-8	1.00
Thyroid	574	-0.572	2.2e-54	1.00
Minor Salivary Gland	144	-0.728	4.1e-14	1.00