Full article title:

Associations between childhood family emotional health, fronto-limbic grey matter volume, and saliva 5mC in young adulthood

Authors:

JR Pfeiffer[1,2], Angela C. Bustamante[3], Grace S. Kim[4], Don Armstrong[2], Annchen R. Knodt[5], Karestan C. Koenen[6], Ahmad R. Hariri[5,7], Monica Uddin[8]

Affiliations:

1. Department of Psychology, University of Illinois at Urbana-Champaign, Urbana, IL, USA;
2. Carl R. Woese Institute for Genomic Biology, Urbana, IL, USA;
3. Division of Pulmonary & Critical Care Medicine, Department of Internal Medicine, University of Michigan Medical School, Ann Arbor, MI, USA;
4. Medical Scholars Program, University of Illinois College of Medicine, Urbana, IL, USA;
5. Department of Psychology & Neuroscience, Duke University, Durham, NC, USA;
6. Department of Epidemiology, Harvard School of Public Health, Boston, MA, USA;
7. Laboratory of NeuroGenetics, Duke University, Durham, NC, USA;
8. University of South Florida, Genomics Program, College of Public Health, Tampa, FL, USA

Keywords:

Peripheral epigenetics, neuroimaging, family emotional health, adverse social environment, biological embedding, fronto-limbic.

Corresponding author:

Address correspondence to: Monica Uddin, PhD
Name: Monica Uddin, PhD
Address: University of South Florida, 3720 Spectrum Blvd., Suite 304
Phone: 813-974-9765
Email: monica43@usf.edu

Manuscript details:

Words in abstract (not including headers): 249
Words in text (not including headers): 4936
Number of references: 107
Number of figures: 3
Number of tables: 3

Abstract

Background Poor family emotional health (FEH) during childhood is prevalent and impactful, and likely confers similar neurodevelopmental risks as other adverse social environments. Pointed FEH study efforts are underdeveloped, and the mechanisms by which poor FEH are biologically embedded are unclear. The current exploratory study examined whether variability in DNA methylation (DNAm) and fronto-limbic grey matter volume may represent pathways through which FEH may become biologically embedded.

Results Self-reported childhood FEH was nominally associated with right hemisphere hippocampus (b=10.4, p=0.005), left hemisphere amygdala (b=5.3, p=0.009), and right hemisphere amygdala (b=5.8, p=0.016) volumes. Childhood FEH was also nominally associated with 49 DNAm MEs ($p_{range}=3x10^{-6}$ to 0.047). After limiting analyses to probes correlated between saliva and brain, saliva-derived DNAm MEs partially mediated the association between FEH and right hippocampal volume (Burlywood ME indirect effect b=-111, p=0.014), and fully mediated the FEH and right amygdala volume relationship (Pink4 ME indirect effect b=-48, p=0.026). Modules were enriched with probes falling in genes with immune, CNS, and metabolic functions.

Conclusions Findings extend work highlighting neurodevelopmental variability associated with adverse social environment exposure during childhood by specifically implicating poor FEH, while informing a mechanism of biological embedding. FEH-associated epigenetic signatures could function as proxies of altered fronto-limbic grey matter volume associated with poor childhood FEH and inform further investigation into primarily affected tissues such as endocrine, immune, and CNS cell types.

Background

Children can be exposed to an array of adverse social environments (ASEs) throughout their development. These include low socioeconomic status (SES), stressful life events (SLEs), trauma, and of particular interest, caregiver psychopathology. Caregiver psychopathology is prevalent in the United States; it is estimated that ~12.8 million parents suffer yearly from some form of mental illness (18.2%), and that ~2.7 million parents suffer yearly from a *serious* mental illness (3.8%)[1]. The psychological effects of living with mentally ill caregivers are notably deleterious. Children of caregivers with major depressive disorder (MDD), for example, experience more hostile, negative, and withdrawn parenting[2]. Estimates range from two to 13 times increased risk for children to develop either their caregiver's mental illness or a mental illness different from their caregiver's[3]. Children growing up in these conditions are also more likely to develop internalizing or externalizing behavioral problems, as well as social, cognitive, and academic difficulties[4, 5]. However, the mechanisms by which poor FEH are biologically embedded and produce these adverse outcomes are unclear.

The neuroimmune network hypothesis is one framework used to explain the physiological mechanisms via which ASEs and caregiver mental illness affect the mental health of offspring. The neuroimmune network hypothesis focuses on the integrated, bi-directional network of the central nervous system (CNS) and the immune system[6]. It posits that exposure to ASEs during childhood, an especially plastic window of development[7], impacts communication between peripheral inflammatory signals and brain regions responsible for threat, reward, executive control, memory, and adaptive behavioral/emotional responses (i.e. the fronto-limbic pathway), among others. Importantly, these functions are impaired in numerous mental illnesses, including but not limited to PTSD[8], MDD[9], anxiety disorders[10], bipolar disorder[11], and schizophrenia[11]. These inflammatory signals disrupt the inter-dependent functions of the front-limbic pathways, leading to altered behavioral states, and the pre-disposition to develop aberrant stress responses later in life[12]. These concepts are supported by a significant body of research that has shown immune system[13–15], hypothalamic-pituitary-adrenal (HPA)-axis[16, 17], and fronto-limbic pathway[17–21] associations with ASE exposure. More specifically, researchers have shown that childhood exposure to factors similar to poor FEH, such as maternal support and supportive/hostile parenting, are associated with lower hippocampus and amygdala grey matter volume later in life[22, 23]. Observed in association with ASE exposures,

the signatures of morphometric variability within the fronto-limbic pathway are regarded as neural correlates of these exposures[17–23], and as neural endophenotypes of psychiatric illness[24–26].

The molecular mechanisms by which ASEs, including caregiver mental illness, become biologically embedded in the CNS are currently under investigation[27], and research has pointed to the importance of epigenetics, particularly 5'-methyl-cytosine (5mC) levels, in this process[28, 29]. 5mC serves as a mediator of gene by environment interaction[30–33], but it remains challenging to measure epigenetics in the living human brain -- the primary etiologic tissue of interest in regards to mental health-related outcomes. This limitation has prompted investigation into epigenetic measures collected from peripheral tissue, such as saliva, which may serve as proxies for etiological tissue. Previous studies have provided a framework for the use of peripheral tissues in epigenome-wide association studies (EWAS) and support the potential use of peripheral 5mC as a proxy for etiological tissue 5mC[34]. Further bolstering the notion that peripheral 5mC is an efficacious proxy for etiological tissue 5mC, is research showing that peripheral epigenetic measures can index changes in the HPA-axis[35, 36], immune system[37, 38], and the CNS[39–41]. However, these relationships do not directly indicate association between peripheral epigenetic measures and CNS-relevant endophenotypes of psychopathology. On this note, studies have used human structural and functional neuroimaging data in tandem with epigenetic measures but have primarily utilized candidate gene approaches. Measuring peripheral 5mC of the *SLC6A4*[42–44], *NR3C1*[45, 46], *FKBP5*[47], and *SKA2*[48, 49] genes, these studies have investigated associations between peripheral 5mC and variability in the structure and function of the frontal cortex, hippocampus, and amygdala. Findings suggest that locus-specific peripheral 5mC can index CNS structural alterations[42–49], and may statistically mediate ASE-induced CNS structural alterations[49].

Despite the evidence that peripheral 5mC can index CNS-related phenotypes, to date few studies, to our knowledge, have examined these relations in a hemisphere-specific manner within the brain. Importantly, numerous aspects of human behavior and biology are subject to hemisphere-specific brain lateralization[50–52]. This, coupled with evidence of hemisphere-specific fronto-limbic variability in association with ASEs in humans[17–23], provide a solid framework to address the potential associations of poor FEH with *hemisphere-specific* volume measurements. Beyond the aforementioned reports, studies of poor FEH or caregiver mental illness on CNS structure are sparse and limited to biological offspring of parents with genetically heritable psychopathology, although they

do investigate associations of exposure with outcome on a hemisphere-specific basis[53, 54]. These types of ASEs are also associated with changes in cell type-specific and tissue-specific 5mC[55]. However, to our knowledge, investigations into the role of poor FEH in association with neural endophenotypes of psychopathology development have yet to be reported, and therefore, the magnitude of risk associated with poor childhood FEH has not been elucidated. In addition, investigations into the potential epigenetic mechanisms explaining the biological embedding of poor FEH have yet to be carried out.

To address these gaps in the field, and to improve understanding of poor FEH exposure risk, the current exploratory study applied genome-scale approaches to assess whether saliva-derived DNA methylation (DNAm) measurements might index CNS endophenotypes of psychopathology in a sample of 98 young adult volunteers. We were specifically interested whether saliva-derived DNAm module eigengenes (MEs) might statistically mediate the relationship between poor FEH and hemisphere-specific fronto-limbic grey matter volume, while controlling for age, sex, cellular heterogeneity, genomic ancestry, past year SLEs, and total brain volume (TBV). Such a result may serve as a peripheral proxy of such CNS variability, while informing a *potential* biological mechanism of physiological embedding. Based on previous work, we hypothesized that identified 5mC modules would be enriched with CpG probes falling in genes with HPA-axis, immune system, and CNS-relevant gene ontology (GO) functions.

Results

Study participants Descriptive statistics for demographic, psychosocial, and neuroimaging variables in study participants are shown in Table 1. FEH ranged from 34 to 70; the mean in the study sample was 60 (+/-8.5). [Insert Table 1 here].

Correlation analyses Pearson correlations between variables used in the current study were mapped (Figure 2). Of note, a strong negative association was observed between FEH and past year SLEs (Pearson's correlation: r=-0.44, p=7x10^{-6}).

FEH predicts hemisphere-specific BRV FEH was positively associated with right hippocampus (b=10.4, SE=3.6, t=2.9, p=0.005), left amygdala (b=5.3, SE=2.0, t=2.7, p=0.009), and right amygdala volumes (b=5.8, SE=2.3, t=2.4, p=0.016). These significant relationships were also observed in models without controlling for the covarying effect of TBV (right hippocampus p=0.015; left amygdala p=0.018; right amygdala p=0.023). FEH was not associated with left hippocampus (p=0.62), left dlPFC (p=0.10), right dlPFC (p=0.62), left mPFC (p=0.98), or right mPFC volume

(p=0.09). In controlling for seventy-two tests at FDR=0.10, all three brain regions with nominal p<0.05 were BH-significant (Table 2). [Insert Table 2 here].Regions associated with FEH were carried into following analyses.

FEH predicts ME values FEH was associated with 49 MEs (b_{min}=-0.006, b_{max}=0.006, p_{min}=3x10^{-6}, p_{max}=0.047). Twenty-nine out of 49 MEs achieved BH-significance, including the Burlywood and Pink4 MEs, taking 194 tests into account at FDR=0.10 (Supplementary Table 2).

ME values predict hemisphere-specific BRV Forty-nine MEs nominally associated with FEH were tested for association with right hippocampus, left amygdala, and right amygdala volumes (Supplementary Table 3). Seven MEs were nominally associated with right hippocampus volume, four of which were BH-significant: Burlywood (b=874.2, SE=252.1, t=3.5, p=8x10^{-4}) (Figure 3a), Darkolivegreen1 (b=770.0, SE=258.6, t=3.0, p=0.004), Thistle2 (b=728.1, SE=261.8, t=2.8, p=0.007), and Chocolate2 (b=-713.3, SE=259.3, t=-2.8, p=0.007). The Darkgray ME (b=-374.2, SE=140.1, t=-2.7, p=0.009) (Figure 3b) was negatively associated with left amygdala volume, in addition to the Darkolivegreen ME (b=-300.6, SE=142.2, t=-2.1, p=0.037). The Lavenderblush2 ME was positively associated with left amygdala volume (b=295.1, SE=144.5, t=2.0, p=0.044). Finally, the Pink4 ME (b=467.5, SE=165.8, t=2.8, p=0.006) (Figure 3c) was positively associated with right amygdala volume. In controlling for 49 tests within each of the three BRVs at FDR=0.10, only the aforementioned MEs associated with right hippocampus volume were BH-significant.

ME mediation Eleven MEs were tested for mediation between FEH and BRVs**.** The Burlywood ME was a partial *statistical* mediator between FEH and right hippocampus volume (b_{TE}=-366, p=8x10^{-4}; b_{IDE}=-111, p=0.014; b_{DE}=-254, p=0.037). The TE indicated that right hippocampal volume was 366 mm^3 less under poor FEH conditions compared to high FEH conditions, while the IDE of the Burlywood ME was accountable for 111 mm^3 (30%) of that effect. Without controlling for the covarying effect of TBV, the Burlywood ME was a full mediator (b_{TE}=-376, p=0.006; b_{IDE}=-114, p=0.031; b_{DE}=-261, p=0.071). The Darkolivegreen1 (b_{TE}=-369, p=0.001; b_{IDE}=-66, p=0.042; b_{DE}=-303, p=0.008) and Thistle2 (b_{TE}=-373, p=0.002; b_{IDE}=-64, p=0.025; b_{DE}=-309, p=0.010) MEs were also partial statistical mediators of the FEH and right hippocampus volume relationship. The Thistle ME was also a partial mediator in analyses without controlling for TBV (b_{TE}=-382, p=0.007; b_{IDE}=-85, p=0.017; b_{DE}=-297, p=0.042). On the other hand, the Chocolate2, Cornflowerblue, Aliceblue, and Yellow MEs were neither partial nor full mediators of the relationship (p_{TE}<0.05; p_{IDE} > 0.05; p_{DE}<0.05).

None of the Darkgray (b_{TE}=-183, p=0.014; b_{IDE}=-47, p=0.095; b_{DE}=-135, p=0.094), Darkolivegreen (b_{TE}=-185, p=0.013; b_{IDE}=-32, p=0.205; b_{DE}=-153, p=0.057), or Lavenderblush2 (b_{TE}=-187, p=0.011; b_{IDE}=-30, p=0.181; b_{DE}=-156, p=0.044) MEs were mediators of the relationship between FEH and left amygdala volume. However, the significant TE values indicated ~185 mm^3 lower left amygdala volume in poor FEH conditions. Regarding FEH and right amygdala volume, Pink4 ME value was a full statistical mediator of the relationship (b_{TE}=-204, p=0.017; b_{IDE}=-48, p=0.026; b_{DE}=-156, p=0.069), indicating that right amygdala volume was 204 mm^3 less in poor FEH conditions than in high FEH conditions. Results additionally indicate that Pink4 ME value accounted for 48 mm^3 (24%) of the aforementioned effect. Without controlling for the statistical effect of TBV, the Pink4 ME was again a full mediator of the FEH and right amygdala volume relationship (b_{TE}=-208, p=0.017; b_{IDE}=-52, p=0.025; b_{DE}=-157, p=0.087). In controlling for 33 tests at FDR=0.10, all nominally significant ME IDE's, DE's, and TE's were BH-significant (Table 3). Mediation analyses were then performed on individual probes from the Pink4 module in order to assess locus-specific effects. [Insert Table 3 here].

Probe-wise mediation Three out of 21 probes from the Pink4 module were full mediators between FEH and right amygdala volume: cg22325292 (b_{TE}=-204, p=0.013; b_{IDE}=-53, p=0.018; b_{DE}=-151, p=0.087), cg02398342 (b_{TE}=-204, p=0.014; b_{IDE}=-44, p=0.038; b_{DE}=-161, p=0.060), and cg00809820 (b_{TE}=-205, p=0.013; b_{IDE}=-48, p=0.049; b_{DE}=-157, p=0.064). These three probes also had extremely high Pearson correlation values with the Pink4 ME (r>0.93, $p<2x10^{-44}$), indicating that they are strong representatives of the Pink4 ME. In controlling for 63 tests at FDR=0.10, all nominally significant probe IDE's, DE's, and TE's were BH-significant (Supplementary Table 4).

Gene set enrichment analysis We performed GSEA using probe M-values as predictors of FEH and used resultant p-values to facilitate the testing of 3,186 GO-terms. After redundancy reduction, 45 BH-significant GO-terms remained for interpretation. CNS-related GO-terms included: beta-amyloid clearance (GO:0097242, $p=8x10^{-11}$, rank=2), filopodia assembly (GO:0046847, $p=2x10^{-8}$, rank=5), catecholamine metabolic process (GO:0006584, $p=4x10^{-5}$, rank=11), and positive regulation of neuron apoptotic process (GO:0043525, p=0.013, rank=25) among others. Although immune-related terms were limited, one was present in the top three: cytokine receptor activity (GO:0004896, $p=8x10^{-11}$, rank=3). Numerous metabolic functions were identified: negative regulation of stress-activated MAPK cascade (GO:0032873, $p=4x10^{-12}$, rank=1), NAD metabolic process (GO:0019674, $p=4x10^{-9}$, rank=4),

and TOR signaling (GO:0031929, $p=3x10^{-4}$, rank=12) among others. A complete list of BH-significant GO-terms can be found in Supplementary Table 5.

Discussion

The current exploratory study examined whether variability in DNAm and fronto-limbic grey matter volume represent pathways through which FEH becomes biologically embedded. Based on previous work, we hypothesized that 5mC modules would be enriched for immune system[13–15], HPA-axis[16, 17], and CNS-relevant[17–21] GO-terms. Our study findings indicated that exposure to poor FEH during childhood was associated with CNS endophenotypes of psychiatric illness, and that a subset of saliva-derived 5mC measurements *statistically* mediated this relationship. Additionally, we found the mediating 5mC modules were enriched with probes in genes with CNS-relevant and immune system GO-terms. Finally, we found that the underlying FEH-associated methylomic network was enriched with CNS-related, immune system, and metabolic gene sets. Overall, we posit that the FEH-associated epigenetic signatures could function as proxies of altered fronto-limbic grey matter volume associated with poor childhood FEH; peripheral epigenetic signatures indexing our relationships of interest may be explained by peripheral inflammation related to development of stress-related psychopathology, thereby supporting the neuroimmune network hypothesis[6].

The relationships observed between poor childhood FEH and left/right amygdala volume in the current study mirrored relationships observed throughout the literature regarding direction of effect and magnitude, but not hemisphere-specificity[17, 18]. Studies show hemisphere-specific effects of ASEs on amygdala volume, with stressors exerting notable statistical effects on left but not right amygdala volume. In one such prospective longitudinal study, SLEs negatively predicted left, but not right, amygdala volume in children with low to average polygenic risk scores. They showed that children exposed to the highest level of SLEs had ~9% less left amygdala volume than those exposed to the lowest levels of SLEs[17]. A more recent study showed lower left amygdala volumes in children who had experienced early neglect, low SES, or physical abuse compared to non-exposed controls[18]. Although we observed bilateral amygdala grey matter volume associations with poor childhood FEH exposure, our study did show a similar magnitude of effect; poor childhood FEH exposure was explanatory (DE) of -8.9% difference in left and -8.4% difference in right amygdala volume. The peripheral 5mC signature (Pink4 ME) mediating right amygdala volume and FEH accounted for -2.5% of additional volumetric difference (IDE).

Similar to our amygdala-related findings, the reported relationship between poor childhood FEH and low hippocampus volume supports previous findings from the field regarding direction and estimated magnitude of effect, but not hemisphere-specificity[22, 23]. In a prospective longitudinal study, researchers focused on childhood "maternal support" as their exposure of interest, finding that maternal support of children, three to five years old, was associated with increased hippocampal volume in both hemispheres later in childhood (seven to thirteen years old). Specifically, they found that children exposed to low maternal support during that time span had a difference in hippocampal volume of -7.1%[22]. This magnitude closely mirrors the findings of the current study, which show poor childhood FEH has a DE that explains -6.1% difference in right hippocampal volume, and peripheral 5mC signatures have an IDE responsible for an additional -1.7% of difference. A more recent study from the same group found that the positive association between SES and hippocampal volume was mediated by "supportive/hostile parenting" in both hemispheres, but only by SLEs in left hippocampus[23]. These studies identified significant associations of maternal support and supportive/hostile parenting in *both* hippocampal hemispheres, whereas the current study identified a significant association only in right hippocampus.

No salient effects of FEH were observed in dlPFC or mPFC, in either hemisphere. This finding does not support research showing deleterious effects of ASEs on frontal cortex morphometry[56–58]. Our findings across fronto-limbic brain regions imply that poor childhood FEH has specific morphometric associations with subcortical structures responsible for memory, avoidance, fear, stress, and negative valence, but not cortical structures managing those functions.

Beyond the observed associations between poor childhood FEH and fronto-limbic brain morphometry, we were interested in the peripheral epigenetic signatures that index the relationships, and that provide a potential mechanism of biological embedding of ASEs. The Pink4 module, which fully mediated the relationship between poor childhood FEH and right amygdala volume in both TBV-controlled and non TBV-controlled models, is composed of 21 probes mostly mapped to known genes (*SNORD123, TBCD, FN3K, NRXN3, GLB1L2, SBF2, PSMB1, SYT1, BEST2, TBATA,* and *GNA12*). GO-terms associated with mapped genes include GO:0048487 beta-tubulin binding, GO:0038023 signaling receptor activity, GO:0019905 syntaxin binding, and GO:0031683 G-protein beta/gamma-subunit complex binding. Three out of 21 probes from the Pink4 module were full mediators of FEH and right amygdala volume: cg22325292, cg02398342, and cg00809820. Probes cg22325292 and cg02398342 exist in the sixth

of six exons of the *FN3K* gene and fall in a putative CpG island and DNaseI hypersensitive region ~1,000 base pairs upstream of the *TBCD* transcription start site (TSS)[59, 60]. The main *TBCD* protein isomer plays a major role in the assembly of microtubules[61], the cell-cycle progression to mitosis[62], and neuronal morphogenesis[63]. Hypermethylation of the *TBCD* gene in CD4+ T-cells is also associated with rheumatoid arthritis[64], an autoimmune disorder associated with stress exposure[65]. Additionally, cg02398342 falls in the transcription factor binding site of the *EGR1* protein, which has integral, dynamic interactions with genes responsible for vesicular release and endocytosis, neurotransmitter metabolism and receptors, and actin cytoskeleton organization[66]. These interactions facilitate *EGR1*'s significant impact on synaptic and neuronal activation. Results suggest that the association of poor childhood FEH with right amygdala volume is indexed and *statistically* mediated by peripheral epigenetic signatures relevant to synapse development and cytoskeleton organization.

Three modules were partial mediators of the relationship between right hippocampus volume and poor childhood FEH: Burlywood, Darkolivegreen1, and Thistle2. The Burlywood module was a full mediator in the non TBV-controlled mediation model, implying that this peripheral epigenetic signature exerts more statistical effect on absolute right hippocampus volume, agnostic of TBV, through poor childhood FEH. Six of the 11 Burlywood probes are mapped to known genes (*MSH2, ATXN7L1, ODF2, SLC22A6, TGFB3,* and *DYX1C1*) with GO-terms including GO:0005245 voltage-gated calcium channel activity, GO:0002700 regulation of production of molecular mediator of immune response, and GO:0043524 negative regulation of neuron apoptotic process. GO-terms associated with probes from the Darkolivegreen1 and Thistle2 modules include GO:0001829 trophectodermal cell differentiation, GO:0045087 innate immune response, GO:0042552 myelination, and GO:0010506 regulation of autophagy, among others[59, 60]. Results imply that the associations of poor childhood FEH with right hippocampal volume are indexed by peripheral epigenetics signatures related to immune response and CNS cell development/lifecycle.

The top three GO-terms from our methylome network analysis were: 1. negative regulation of stress-activated MAPK cascade 2. beta-amyloid clearance 3. cytokine receptor activity. The MAPK cascade has long been established as a key driver of eukaryotic signal transduction, but more recently as an integral contributor to cell proliferation, differentiation, and inflammatory processes[67]. There is also a building body of evidence suggesting a significant role of the MAPK cascade in mental health outcomes. In a mouse model, modulation of the MAPK cascade in the forebrain is associated with both anxiety-like and depressive-like behaviors[68]. When p38 MAPK

protein is selectively knocked out (KO) of the dorsal raphe nucleus, rodents subjected to social defeat stress show significantly reduced social avoidance compared to wild-type animals[69]. Additionally, pro-inflammatory cytokine administration induces a state of increased serotonergic CNS activity (canonically thought to be depleted in MDD), and induction towards that state is blocked with p38 MAPK inhibition[70]. In humans, MDD is a common co-morbidity of rheumatoid arthritis (RA)[71]; peripheral inflammation is a hallmark of RA and is also observed in MDD patients[72]. Therefore, it is hypothesized that within the context of psychopathology development, environmental stressors induce peripheral cytokine signaling that communicates with fronto-limbic brain regions including the amygdala, hippocampus, and frontal cortex through mechanisms including the MAPK cascade[73]. To this end, numerous RA and anti-depressant drugs are observed to reduce canonical disease symptoms, while also reducing clinical inflammation markers and MAPK signaling[73].

It appears, then, that variability in peripheral DNAm and fronto-limbic grey matter volume represent pathways through which FEH becomes biologically embedded, with DNAm signatures that mediate the relation between FEH and grey matter volume being especially enriched with GO-terms related to the peripheral inflammatory sequela of stress-related psychopathology development. To our knowledge, the degree to which peripheral 5mC serves as a statistical mediator between poor childhood FEH (or ASEs in general) and variable fronto-limbic brain morphometry had not been previously elucidated. In addition, the observed GO-terms support potential mechanisms of biological embedding that are actively being considered in the field[68–70, 73, 74].

Dimension reduction techniques used throughout our research represent the foremost strengths of this study. These methods focus the analysis onto loci with greater prospect for proxy or surrogate status with etiologically relevant CNS tissue, and reduce the burden of multiple hypothesis testing. Clustering similarly methylated probes creates a relatively small number of modules which potentially contain probes from functionally related genes. On the other hand, limitations of the current study include relatively small sample size, lack of replication in an independent cohort, the balance of biological sex within the cohort, the potential cohort enrichment of higher SES participants, and the inability to correct for smoking-related effects. Additionally, in analyzing grey matter volume of fronto-limbic brain regions as outcomes of interest, we have omitted surface area- or cortical thickness-specific effects. The current study also falls short in establishing whether the mediation by peripheral 5mC modules is causal in nature. Longitudinal data could provide more precise insight into whether such relationships

exist. Future studies on this topic should capture longitudinal data from a diverse, increased sample size and could investigate genetic factors or tissues of etiological interest.

Conclusions

The current study showed that, in support of prior literature, exposure to poor childhood FEH is associated with low fronto-limbic BRV as measured in young adulthood. Newly reported here is the finding that saliva-derived 5mC modules mediate the FEH and BRV relationship and are enriched for immune system, CNS-related, and metabolic functions; with additional validation in independent cohorts, these 5mC modules could potentially be used as peripheral biomarkers of poor FEH exposure during childhood. Overall, the findings of the current study support the neuroimmune network hypothesis[6], extend the body of work highlighting neurodevelopmental variability associated with childhood ASE exposure, and inform a potential molecular mechanism of biologic embedding. Future research on these peripheral signatures could validate their use as proxies/biomarkers of perturbed underlying neurobiology in response to poor FEH exposure and could inform further investigation into primarily effected tissue such as endocrine, immune, and CNS cell types.

Materials and methods

Participants The current study draws on data from 98 university-age students (19.8±1.2 years old; 69% women; 49% white) who successfully completed the Duke Neurogenetics Study (DNS). The DNS aims to assess the associations among a wide range of behavioral, neural, and genetic variables in a large sample of young adults, with one of the core goals being to establish a link between these various phenotypes and psychopathology. This study was approved by the Duke University Medical Center Institutional Review Board, and all experiments were performed in accordance to its guidelines. Prior to the study, all participants provided informed consent. To be eligible for DNS, all participants were free of: 1) medical diagnoses of cancer, stroke, head injury with loss of consciousness, untreated migraine headaches, diabetes requiring insulin treatment, chronic kidney, or liver disease; 2) use of psychotropic, glucocorticoid, or hypolipidemic medication; and 3) conditions affecting cerebral blood flow and metabolism (e.g., hypertension)[75].

Family emotional health (FEH) Participants were asked to complete the Family History Questionnaire (FHQ), which produced the current study's measure of FEH. The FHQ is composed *fully* of questions from previously validated inventories [76–82]; fifty-five out of 70 questions were included from the Family History Screen (FHS)[76,

77]. The FHQ and FHS both capture family-wide psychiatric illness, but the FHQ is more encompassing of other ASEs, including cognitive decline of family members[78], externalizing behaviors[79], exposure to smoking[80], and drug/alcohol abuse treatment[81, 82]. The summed responses from 70 "yes/no" questions based on the aforementioned topics from the FHQ represent the current study's measure of FEH (Supplementary Table 1). Each "no" response corresponded to an additional score of one, with lower values representing poor FEH.

Cumulative perceived impact of past year stressful life events (past year SLEs) Participants were administered an inventory measuring the cumulative perceived impact of SLEs from the past year ("past year SLEs"). Prior research reported associations between stress exposure and significant variability in fronto-limbic brain region volumes (BRVs)[17–19]. Therefore, throughout the current study, we controlled for the effect of past years SLEs using a summation of 45 negatively valenced items[83, 84] from the Life Events Scale for Students[85].

Neuroimaging ASEs and exposures similar to poor FEH are known to impact fronto-limbic pathways in the human CNS[17–23]. In addition, a meta-analysis has shown that both the hippocampus and amygdala have hemisphere-specific volume differences in healthy adults[86], and ASEs are known to have hemisphere-specific effects on fronto-limbic brain regions[23, 87]. Therefore, hemisphere-specific amygdala, hippocampus dorso-lateral prefrontal cortex (dlPFC), and medial PFC (mPFC) volume measures were estimated. Volume measurements of dlPFC and mPFC were chosen as outcome variables from the frontal cortex due to the opposing nature of their afferent and efferent projections to hippocampus and amygdala, and their functional relationships with each region[88]. Participants were scanned on one of two identical research-dedicated GE MR750 3T scanners at the Duke-UNC Brain Imaging and Analysis Center, and measures were collected, pre-processed, and finalized in accordance with previously published methods[89]. Briefly, anatomical images for each subject were skull-stripped, intensity-normalized, and mapped to a study-specific average template. Region-specific border definitions were made using the Desikan-Killiany-Tourville scheme[90].

Molecular Saliva was collected from participants using the Oragene-DNA OG-500 kit (Oragene; Ottawa, Canada). DNA was extracted and cleaned using the DNA Genotek prepIT PT-L2P kit (DNA Genotek Inc; Ottawa, Canada) using manufacturer recommended methods. Purity of extracted DNA samples was assessed by absorbance using Nanodrop 1000 spectrophotometer (Thermo Fisher Scientific Inc; Waltham, Massachusetts). The quantity of double-stranded DNA was assessed using Quant-iT PicoGreen dsDNA kits with manufacturer recommended

protocols (Invitrogen; Carlsbad, California). A total of 500 ng of genomic DNA was bisulfite-converted (BSC) using manufacturer-recommended EZ DNAm kits (Zymo Research; Irvine, California). After conversion, BSC DNA was applied to the Infinium MethylationEPIC BeadChip (Illumina; San Diego, California) (850k) to measure 5mC at ~850k loci.

5mC pre-processing Beta-values measured from the 850k platform were background corrected in GenomeStudio, quality controlled, and filtered according to previously published methods[91]. All quality control and pre-processing was performed in R, version 3.6.1[92]. These steps removed low quality and potentially cross-hybridizing probes, quantile-normalized probe beta-values, and removed technical and batch effects[93–96]. 5mC beta-values were variance stabilized and logit-transformed into M-values[97]. X- and Y-chromosome-mapped probes were removed, along with *rs*-mapped probes. The remaining ~739k probes were then subset to include only those with observed nominally significant Pearson correlation ($p<0.05$) between saliva and brain tissue from the ImageCpG data repository[98]. This was done to focus the analysis on loci with greater prospect for proxy or surrogate status with etiologically relevant CNS tissue. Afterwards, 62,422 probes remained.

Cellular heterogeneity Cell heterogeneity was estimated using a reference-free deconvolution method[99, 100]. Briefly, the top 15k most variable CpG sites were selected from the pre-processed/quality controlled 850k data and used to estimate the number of cell types and generate a matrix containing the proportions. Based on these methods, the number of cell types was set at five. Estimated proportions were used as covariates in relevant analyses to account for cellular heterogeneity.

Genomic ancestry To avoid potential inaccuracies and confounding effects of self-reported race/ethnicity, genetic ancestry was modeled using multi-dimensional scaling (MDS) measures extracted from participant genomic data using PLINK[101]. Using previously collected GWAS data from the DNS, the first four MDS genetic ancestry measures were calculated and used as covariates across pertinent models based on visual inspection of scree plots. This methodology is in line with previous publications[75].

Probe clustering In order to remove non-desired effects, we fit linear models with age, validated biological sex, cellular heterogeneity, and genomic ancestry as predictors of probe-wise 5mC M-value. For each probe, residual values ("residualized M-values") were extracted for clustering. Taking the 62,422 residualized M-values, the "WGCNA" R package was used to build a co-methylation network[102]. First, scale-free topology model fit was

399 analyzed. As recommended, a soft-threshold value of four was chosen based on the lowest power at which adjusted
400 R^2>0.90. Adjacency and dissimilarity matrices were generated, and unsupervised hierarchical clustering was used to
401 generate a clustered, residual M-value network. Setting a minimum cluster size of 10 generated 194 modules,
402 identified by a unique color, for which module eigengenes (MEs) were calculated.

403 ***Statistical analyses*** In order to understand the relationships between variables, we computed Pearson
404 correlations and mapped their correlation coefficients. Based on these correlations, we conducted a set of analyses,
405 as shown in Figure 1. In Arm A analyses, FEH was used as a predictor of hemisphere-specific BRVs, while including
406 age, biological sex, four genomic ancestry MDS measures, past year SLEs, and TBV as covariates. In Arm B analyses,
407 FEH was used as a predictor of ME values, while including past year SLEs as a covariate. Age, sex, and genomic
408 ancestry effects were accounted for previously by using residualized M-values as input for clustering. In Arm C
409 analyses, ME values were used as individual predictors of BRV, while including the same covariates as in Arm A.
410 Throughout the current research, past year SLEs were included as a covariate because our FEH measure only
411 captures SLEs from childhood, and recent stress exposure is associated with variability in our outcome variables[17,
412 18, 23, 103]. TBV was included as a covariate but, where pertinent, non-TBV controlled model results are also
413 reported. Within each phase of the analyses, non-standardized continuous measures were used resulting in non-
414 standardized effect estimates. In addition, nominal p-values were corrected for multiple hypothesis testing by
415 controlling the false discovery rate (FDR=0.10) using the Benjamini Hochberg (BH) procedure[104]. Briefly, for each
416 nominal p-value, a BH critical value was calculated where nominal p-value's assigned rank over the number of tests
417 was multiplied by the accepted FDR. Nominal p-values less than this threshold were deemed BH-significant. Due to
418 the exploratory nature of the current work, both nominal and BH-significant terms were considered for
419 interpretation.

420 ***Mediation analyses*** To investigate whether the effect of poor FEH on hemisphere-specific BRV is
421 *statistically* mediated via peripheral 5mC signatures, MEs were tested for mediating status between FEH and
422 hemisphere-specific BRVs using the "mediation" package in R[105] (Figure 1). Importantly, only hemisphere-specific
423 BRVs associated with FEH (Figure 1, Arm A) were considered. Similarly, MEs tested for mediation included *only those*
424 associated with both FEH (Figure 1, Arm B) and hemisphere-specific BRV (Figure 1, Arm C). Mediation model inputs
425 were assembled per recommended "mediation" package protocol. Therefore, Arm A (plus ME as a covariate) and

Arm B models were used as inputs. For each ME, indirect effects (IDE), direct effects (DE), and total effects (TE) were calculated as a result of 10,000 non-parametric bootstrap simulations. Consistent with published methods[23], we considered an ME a full mediator if the DE=0 while the IDE and TE$\neq 0$, or a partial mediator if the DE, IDE, and TE$\neq 0$. Individual probes from full mediator modules were assessed for mediation status as well.

Gene set enrichment To assess the underlying methylomic network enrichment of the ~62,000 brain-saliva correlated probes, individual residualized probe M-values were used as predictors of FEH in Bayesian regression models. Age, sex, genomic ancestry measures, cell heterogeneity measures, and past year SLEs were included as covariates. From this analysis, BH-significant probe p-values were extracted and used as input to gene set enrichment analyses (GSEA) in the "methylGSA" package[106]. GO sets composed of 50 to 1,000 genes were allowed, which eliminated high-level GO-terms such as "biological process" and facilitated testing of 3,186 GO sets. To produce a condensed summary of non-redundant GO-terms, the web-based tool "Revigo" was used [107].

455 **Declarations:**

456 **Ethics approval and consent to participate**

457 This study was approved by the Duke University Medical Center Institutional Review Board, and all
458 experiments were performed in accordance to its guidelines.

459 **Consent for publication**

460 Not applicable.

461 **Availability of data and materials**

462 The ImageCpG dataset supporting the conclusions of this article is available at Gene Expression Omnibus
463 (GEO) Accession GSE111165; http://han-lab.org/methylation/default/imageCpG#. The DNS 850K datasets used
464 and/or analyzed during the current study are available from the corresponding author on reasonable request.

465 **Competing interests**

466 All listed authors declare no biomedical financial/non-financial interests, or potential conflicts of interest.

467 **Funding**

468 The Duke Neurogenetics Study received support from Duke University as well as the National Institute on
469 Drug Abuse under Grants R01DA033369 and R01DA031579. In addition, the Brain Imaging and Analysis Center
470 received support from the Office of the Director, National Institutes of Health under Award S10OD021480. This study
471 was also supported by the National Institute on Minority Health and Disparities grant R01MD011728.

472 **Authors' contributions**

473 JRP was a major contributor in study design, methodology, statistical analyses, and in writing the
474 manuscript. ACB was a major contributor in methodology and writing the manuscript. GSK was a major contributor
475 in methodology and writing the manuscript. DA was a major contributor in methodology and writing the manuscript.
476 ARK was a major contributor in writing the manuscript. KCK was a major contributor in writing the manuscript. ARH
477 was a major contributor in designing methodology and writing the manuscript. MU was a major contributor in study
478 design, methodology, and in writing the manuscript. All authors read and approved the final manuscript.

479 **Acknowledgements**

480 We thank the Duke Neurogenetics Study participants and the staff of the Laboratory of NeuroGenetics.

481

Figure titles and legends

Figure 1. Conceptual model testing module eigengenes (MEs) as mediators of the hypothesized association between family emotional health (FEH) and variability in hemisphere-specific brain region volume (BRV).

Arm A. FEH was used as a predictor of hemisphere-specific BRV, while including age, biological sex, four genomic ancestry MDS measures, past year SLEs, and total brain volume as covariates. **Arm B.** FEH was used as a predictor of ME value, while including past year SLEs as a covariate. The age, sex, and genomic ancestry effects on ME components were previously removed. **Arm C.** ME values were used as individual predictors of BRV, while including age, biological sex, four genomic ancestry MDS measures, past year SLEs, and total brain volume as covariates.

Figure 2. Pearson correlation heat map of variables used throughout the current analyses.

A. A strong negative relationship was observed between FEH and past year SLEs (Pearson's correlation: r=-0.44, p=7x10^{-6}). Strong positive relationships are also observed between hemisphere-specific brain regions (Pearson's correlation r range: 0.26 – 0.75).

Figure 3. ME values are associated with high right hippocampal, low left amygdala, and high right amygdala volume.

BRVs values shown are adjusted by covariates. Covariates across all models: age, sex, four genomic ancestry measures, past year SLEs, and total brain volume. The line of best fit (via least squares) is shown with a grey 95% SE confidence range. **A.** High Burlywood ME value is associated with high right hippocampal volume (b=874.2, SE=252.1, t=3.5, p=0.0008). **B.** High Darkgray ME value is associated with low left amygdala volume (b=- 374.2, SE=140.1, t=-2.7, p=0.009). **C.** High Pink4 ME value is associated with high right amygdala volume (b=467.5, SE=165.8, t=2.8, p=0.006).

509 **References**

510 1. Stambaugh LF, Forman-Hoffman V, Williams J, Pemberton MR, Ringeisen H, Hedden SL, et al. Prevalence of
511 serious mental illness among parents in the United States: results from the National Survey of Drug Use and
512 Health, 2008-2014. Ann Epidemiol. 2017;27:222–4.

513 2. National Research Council (US) and Institute of Medicine (US) Committee on Depression PP, England MJ, Sim LJ.
514 Associations Between Depression in Parents and Parenting, Child Health, and Child Psychological Functioning.
515 National Academies Press (US); 2009. https://www.ncbi.nlm.nih.gov/books/NBK215128/. Accessed 13 May 2020.

516 3. Dean K, Stevens H, Mortensen PB, Murray RM, Walsh E, Pedersen CB. Full Spectrum of Psychiatric Outcomes
517 Among Offspring With Parental History of Mental Disorder. Arch Gen Psychiatry. 2010;67:822–9.

518 4. Connell AM, Goodman SH. The association between psychopathology in fathers versus mothers and children's
519 internalizing and externalizing behavior problems: a meta-analysis. Psychol Bull. 2002;128:746–73.

520 5. Suveg C, Shaffer A, Morelen D, Thomassin K. Links Between Maternal and Child Psychopathology Symptoms:
521 Mediation Through Child Emotion Regulation and Moderation Through Maternal Behavior. Child Psychiatry Hum
522 Dev. 2011;42:507.

523 6. Nusslock R, Miller GE. Early-Life Adversity and Physical and Emotional Health Across the Lifespan: A
524 Neuroimmune Network Hypothesis. Biol Psychiatry. 2016;80:23–32.

525 7. Dunn EC, Soare TW, Zhu Y, Simpkin AJ, Suderman MJ, Klengel T, et al. Sensitive Periods for the Effect of
526 Childhood Adversity on DNA Methylation: Results From a Prospective, Longitudinal Study. Biol Psychiatry.
527 2019;85:838–49.

528 8. Walter KH, Palmieri PA, Gunstad J. More than symptom reduction: Changes in executive function over the
529 course of PTSD treatment. J Trauma Stress. 2010;23:292–5.

530 9. Misiak B, Beszłej JA, Kotowicz K, Szewczuk-Bogusławska M, Samochowiec J, Kucharska-Mazur J, et al. Cytokine
531 alterations and cognitive impairment in major depressive disorder: From putative mechanisms to novel treatment
532 targets. Prog Neuropsychopharmacol Biol Psychiatry. 2018;80:177–88.

533 10. Marganska A, Gallagher M, Miranda R. Adult attachment, emotion dysregulation, and symptoms of depression
534 and generalized anxiety disorder. Am J Orthopsychiatry. 2013;83:131–41.

535 11. Green MF. Cognitive impairment and functional outcome in schizophrenia and bipolar disorder. J Clin
536 Psychiatry. 2006;67:e12.

537 12. Anisman H. Cascading effects of stressors and inflammatory immune system activation: implications for major
538 depressive disorder. J Psychiatry Neurosci JPN. 2009;34:4–20.

539 13. Cohen S, Tyrrell DA, Smith AP. Negative life events, perceived stress, negative affect, and susceptibility to the
540 common cold. J Pers Soc Psychol. 1993;64:131–40.

541 14. Segerstrom SC, Miller GE. Psychological stress and the human immune system: a meta-analytic study of 30
542 years of inquiry. Psychol Bull. 2004;130:601–30.

543 15. Salleh MohdR. Life Event, Stress and Illness. Malays J Med Sci MJMS. 2008;15:9–18.

544 16. Lupien SJ, King S, Meaney MJ, McEwen BS. Child's stress hormone levels correlate with mother's
545 socioeconomic status and depressive state. Biol Psychiatry. 2000;48:976–80.

546 17. Pagliaccio D, Luby JL, Bogdan R, Agrawal A, Gaffrey MS, Belden AC, et al. Stress-System Genes and Life Stress
547 Predict Cortisol Levels and Amygdala and Hippocampal Volumes in Children. Neuropsychopharmacology.
548 2014;39:1245–53.

549 18. Hanson JL, Nacewicz BM, Sutterer MJ, Cayo AA, Schaefer SM, Rudolph KD, et al. Behavior Problems After Early
550 Life Stress: Contributions of the Hippocampus and Amygdala. Biol Psychiatry. 2015;77:314–23.

551 19. Kim P, Evans GW, Angstadt M, Ho SS, Sripada CS, Swain JE, et al. Effects of childhood poverty and chronic stress
552 on emotion regulatory brain function in adulthood. Proc Natl Acad Sci U S A. 2013;110:18442–7.

553 20. Swartz JR, Knodt AR, Radtke SR, Hariri AR. A Neural Biomarker of Psychological Vulnerability to Future Life
554 Stress. Neuron. 2015;85:505–11.

555 21. Swartz JR, Hariri AR, Williamson DE. An epigenetic mechanism links socioeconomic status to changes in
556 depression-related brain function in high-risk adolescents. Mol Psychiatry. 2017;22:209–14.

557 22. Luby JL, Barch DM, Belden A, Gaffrey MS, Tillman R, Babb C, et al. Maternal support in early childhood predicts
558 larger hippocampal volumes at school age. Proc Natl Acad Sci. 2012;109:2854–9.

559 23. Luby J, Belden A, Botteron K, Marrus N, Harms MP, Babb C, et al. The effects of poverty on childhood brain
560 development: the mediating effect of caregiving and stressful life events. JAMA Pediatr. 2013;167:1135–42.

561 24. Hasler G, Northoff G. Discovering imaging endophenotypes for major depression. Mol Psychiatry. 2011;16:604–
562 19.

563 25. Manoach DS, Agam Y. Neural markers of errors as endophenotypes in neuropsychiatric disorders. Front Hum
564 Neurosci. 2013;7. doi:10.3389/fnhum.2013.00350.

565 26. Matsubara T, Matsuo K, Harada K, Nakano M, Nakashima M, Watanuki T, et al. Distinct and Shared
566 Endophenotypes of Neural Substrates in Bipolar and Major Depressive Disorders. PLOS ONE. 2016;11:e0168493.

567 27. Toyokawa S, Uddin M, Koenen KC, Galea S. How does the social environment 'get into the mind'? Epigenetics
568 at the intersection of social and psychiatric epidemiology. Soc Sci Med 1982. 2012;74:67–74.

569 28. Klengel T, Mehta D, Anacker C, Rex-Haffner M, Pruessner JC, Pariante CM, et al. Allele-specific FKBP5 DNA
570 demethylation mediates gene–childhood trauma interactions. Nat Neurosci. 2013;16:33–41.

571 29. Weaver ICG. Integrating Early Life Experience, Gene Expression, Brain Development, and Emergent
572 Phenotypes. In: Advances in Genetics. Elsevier; 2014. p. 277–307. doi:10.1016/B978-0-12-800222-3.00011-5.

573 30. Jaenisch R, Bird A. Epigenetic regulation of gene expression: how the genome integrates intrinsic and
574 environmental signals. Nat Genet. 2003;33 Suppl:245–54.

575 31. Zilberman D, Gehring M, Tran RK, Ballinger T, Henikoff S. Genome-wide analysis of Arabidopsis thaliana DNA
576 methylation uncovers an interdependence between methylation and transcription. Nat Genet. 2007;39:61–9.

577 32. Talens RP, Boomsma DI, Tobi EW, Kremer D, Jukema JW, Willemsen G, et al. Variation, patterns, and temporal
578 stability of DNA methylation: considerations for epigenetic epidemiology. FASEB J Off Publ Fed Am Soc Exp Biol.
579 2010;24:3135–44.

580 33. Michaud EJ, van Vugt MJ, Bultman SJ, Sweet HO, Davisson MT, Woychik RP. Differential expression of a new
581 dominant agouti allele (Aiapy) is correlated with methylation state and is influenced by parental lineage. Genes
582 Dev. 1994;8:1463–72.

583 34. Smith AK, Kilaru V, Klengel T, Mercer KB, Bradley B, Conneely KN, et al. DNA extracted from saliva for
584 methylation studies of psychiatric traits: evidence tissue specificity and relatedness to brain. Am J Med Genet Part
585 B Neuropsychiatr Genet Off Publ Int Soc Psychiatr Genet. 2015;168B:36–44.

586 35. Perroud N, Paoloni-Giacobino A, Prada P, Olié E, Salzmann A, Nicastro R, et al. Increased methylation of
587 glucocorticoid receptor gene (NR3C1) in adults with a history of childhood maltreatment: a link with the severity
588 and type of trauma. Transl Psychiatry. 2011;1:e59.

589 36. Tyrka AR, Price LH, Marsit C, Walters OC, Carpenter LL. Childhood adversity and epigenetic modulation of the
590 leukocyte glucocorticoid receptor: preliminary findings in healthy adults. PloS One. 2012;7:e30148.

591 37. Uddin M, Aiello AE, Wildman DE, Koenen KC, Pawelec G, de los Santos R, et al. Epigenetic and immune function
592 profiles associated with posttraumatic stress disorder. Proc Natl Acad Sci U S A. 2010;107:9470–5.

593 38. Smith AK, Conneely KN, Kilaru V, Mercer KB, Weiss TE, Bradley B, et al. Differential immune system DNA
594 methylation and cytokine regulation in post-traumatic stress disorder. Am J Med Genet Part B Neuropsychiatr
595 Genet Off Publ Int Soc Psychiatr Genet. 2011;156B:700–8.

596 39. Davies MN, Volta M, Pidsley R, Lunnon K, Dixit A, Lovestone S, et al. Functional annotation of the human brain
597 methylome identifies tissue-specific epigenetic variation across brain and blood. Genome Biol. 2012;13:R43.

598 40. Hannon E, Lunnon K, Schalkwyk L, Mill J. Interindividual methylomic variation across blood, cortex, and
599 cerebellum: implications for epigenetic studies of neurological and neuropsychiatric phenotypes. Epigenetics.
600 2015;10:1024–32.

601 41. Yamamoto T, Toki S, Siegle GJ, Takamura M, Takaishi Y, Yoshimura S, et al. Increased amygdala reactivity
602 following early life stress: a potential resilience enhancer role. BMC Psychiatry. 2017;17. doi:10.1186/s12888-017-
603 1201-x.

604 42. Booij L, Szyf M, Carballedo A, Frey E-M, Morris D, Dymov S, et al. DNA methylation of the serotonin transporter
605 gene in peripheral cells and stress-related changes in hippocampal volume: a study in depressed patients and
606 healthy controls. PloS One. 2015;10:e0119061.

607 43. Frodl T, Szyf M, Carballedo A, Ly V, Dymov S, Vaisheva F, et al. DNA methylation of the serotonin transporter
608 gene (SLC6A4) is associated with brain function involved in processing emotional stimuli. J Psychiatry Neurosci JPN.
609 2015;40:296–305.

610 44. Ismaylova E, Lévesque ML, Pomares FB, Szyf M, Nemoda Z, Fahim C, et al. Serotonin transporter promoter
611 methylation in peripheral cells and neural responses to negative stimuli: A study of adolescent monozygotic twins.
612 Transl Psychiatry. 2018;8:1–9.

613 45. Vukojevic V, Kolassa I-T, Fastenrath M, Gschwind L, Spalek K, Milnik A, et al. Epigenetic modification of the
614 glucocorticoid receptor gene is linked to traumatic memory and post-traumatic stress disorder risk in genocide
615 survivors. J Neurosci Off J Soc Neurosci. 2014;34:10274–84.

616 46. Schechter DS, Moser DA, Paoloni-Giacobino A, Stenz L, Gex-Fabry M, Aue T, et al. Methylation of NR3C1 is
617 related to maternal PTSD, parenting stress and maternal medial prefrontal cortical activity in response to child
618 separation among mothers with histories of violence exposure. Front Psychol. 2015;6:690.

619 47. Tozzi L, Farrell C, Booij L, Doolin K, Nemoda Z, Szyf M, et al. Epigenetic Changes of FKBP5 as a Link Connecting
620 Genetic and Environmental Risk Factors with Structural and Functional Brain Changes in Major Depression.
621 Neuropsychopharmacol Off Publ Am Coll Neuropsychopharmacol. 2018;43:1138–45.

622 48. Sadeh N, Wolf EJ, Logue MW, Hayes JP, Stone A, Griffin LM, et al. EPIGENETIC VARIATION AT SKA2 PREDICTS
623 SUICIDE PHENOTYPES AND INTERNALIZING PSYCHOPATHOLOGY. Depress Anxiety. 2016;33:308–15.

624 49. Sadeh N, Spielberg JM, Logue MW, Wolf EJ, Smith AK, Lusk J, et al. SKA2 methylation is associated with
625 decreased prefrontal cortical thickness and greater PTSD severity among trauma-exposed veterans. Mol
626 Psychiatry. 2016;21:357–63.

627 50. Schaafsma S m, Riedstra B j, Pfannkuche K a, Bouma A, Groothuis T g. g. Epigenesis of behavioural lateralization
628 in humans and other animals. Philos Trans R Soc B Biol Sci. 2009;364:915–27.

629 51. Gotts SJ, Jo HJ, Wallace GL, Saad ZS, Cox RW, Martin A. Two distinct forms of functional lateralization in the
630 human brain. Proc Natl Acad Sci. 2013;110:E3435–44.

631 52. Francks C. Exploring human brain lateralization with molecular genetics and genomics. Ann N Y Acad Sci.
632 2015;1359:1–13.

633 53. Kim E, Garrett A, Boucher S, Park M-H, Howe M, Sanders E, et al. Inhibited Temperament and Hippocampal
634 Volume in Offspring of Parents with Bipolar Disorder. J Child Adolesc Psychopharmacol. 2016;27:258–65.

635 54. Haren NEM van, Setiaman N, Koevoets MGJC, Baalbergen H, Kahn RS, Hillegers MHJ. Brain structure, IQ, and
636 psychopathology in young offspring of patients with schizophrenia or bipolar disorder. Eur Psychiatry. 2020;63.
637 doi:10.1192/j.eurpsy.2019.19.

638 55. Klengel T, Pape J, Binder EB, Mehta D. The role of DNA methylation in stress-related psychiatric disorders.
639 Neuropharmacology. 2014;80:115–32.

640 56. Tomoda A, Suzuki H, Rabi K, Sheu Y-S, Polcari A, Teicher MH. Reduced Prefrontal Cortical Gray Matter Volume
641 in Young Adults Exposed to Harsh Corporal Punishment. NeuroImage. 2009;47 Suppl 2:T66–71.

642 57. Carrion VG, Weems CF, Richert K, Hoffman BC, Reiss AL. Decreased Prefrontal Cortical Volume Associated With
643 Increased Bedtime Cortisol in Traumatized Youth. Biol Psychiatry. 2010;68:491–3.

644 58. Corbo V, Salat DH, Amick MM, Leritz EC, Milberg WP, McGlinchey RE. Reduced cortical thickness in veterans
645 exposed to early life trauma. Psychiatry Res. 2014;223:53–60.

646 59. Kent WJ, Sugnet CW, Furey TS, Roskin KM, Pringle TH, Zahler AM, et al. The human genome browser at UCSC.
647 Genome Res. 2002;12:996–1006.

648 60. Rosenbloom KR, Sloan CA, Malladi VS, Dreszer TR, Learned K, Kirkup VM, et al. ENCODE Data in the UCSC
649 Genome Browser: year 5 update. Nucleic Acids Res. 2013;41:D56–63.

650 61. Tian G, Thomas S, Cowan NJ. Effect of TBCD and its regulatory interactor Arl2 on tubulin and microtubule
651 integrity. Cytoskelet Hoboken NJ. 2010;67:706–14.

652 62. Flex E, Niceta M, Cecchetti S, Thiffault I, Au MG, Capuano A, et al. Biallelic Mutations in TBCD, Encoding the
653 Tubulin Folding Cofactor D, Perturb Microtubule Dynamics and Cause Early-Onset Encephalopathy. Am J Hum
654 Genet. 2016;99:962–73.

655 63. Miyake N, Fukai R, Ohba C, Chihara T, Miura M, Shimizu H, et al. Biallelic TBCD Mutations Cause Early-Onset
656 Neurodegenerative Encephalopathy. Am J Hum Genet. 2016;99:950–61.

657 64. Guo S, Zhu Q, Jiang T, Wang R, Shen Y, Zhu X, et al. Genome-wide DNA methylation patterns in CD4+ T cells
658 from Chinese Han patients with rheumatoid arthritis. Mod Rheumatol. 2017;27:441–7.

659 65. Song H, Fang F, Tomasson G, Arnberg FK, Mataix-Cols D, Cruz LF de la, et al. Association of Stress-Related
660 Disorders With Subsequent Autoimmune Disease. JAMA. 2018;319:2388–400.

661 66. Duclot F, Kabbaj M. The Role of Early Growth Response 1 (EGR1) in Brain Plasticity and Neuropsychiatric
662 Disorders. Front Behav Neurosci. 2017;11. doi:10.3389/fnbeh.2017.00035.

663 67. Zhang W, Liu HT. MAPK signal pathways in the regulation of cell proliferation in mammalian cells. Cell Res.
664 2002;12:9–18.

665 68. Wefers B, Hitz C, Hölter SM, Trümbach D, Hansen J, Weber P, et al. MAPK Signaling Determines Anxiety in the
666 Juvenile Mouse Brain but Depression-Like Behavior in Adults. PLOS ONE. 2012;7:e35035.

667 69. Bruchas MR, Schindler AG, Shankar H, Messinger DI, Miyatake M, Land BB, et al. Selective p38α MAPK Deletion
668 in Serotonergic Neurons Produces Stress Resilience in Models of Depression and Addiction. Neuron. 2011;71:498–
669 511.

670 70. Zhu C-B, Lindler KM, Owens AW, Daws LC, Blakely RD, Hewlett WA. Interleukin-1 Receptor Activation by
671 Systemic Lipopolysaccharide Induces Behavioral Despair Linked to MAPK Regulation of CNS Serotonin
672 Transporters. Neuropsychopharmacology. 2010;35:2510–20.

673 71. Firestein GS. Immunologic mechanisms in the pathogenesis of rheumatoid arthritis. J Clin Rheumatol Pract Rep
674 Rheum Musculoskelet Dis. 2005;11 3 Suppl:S39-44.

675 72. Fifield J, Tennen H, Reisine S, McQuillan J. Depression and the long-term risk of pain, fatigue, and disability in
676 patients with rheumatoid arthritis. Arthritis Rheum. 1998;41:1851–7.

677 73. Malemud CJ, Miller AH. Pro-inflammatory cytokine-induced SAPK/MAPK and JAK/STAT in rheumatoid arthritis
678 and the new anti-depression drugs. Expert Opin Ther Targets. 2008;12:171–83.

679 74. Chan KL, Cathomas F, Russo SJ. Central and Peripheral Inflammation Link Metabolic Syndrome and Major
680 Depressive Disorder. Physiology. 2019;34:123–33.

681 75. Kim MJ, Avinun R, Knodt AR, Radtke SR, Hariri AR. Neurogenetic plasticity and sex influence the link between
682 corticolimbic structural connectivity and trait anxiety. Sci Rep. 2017;7:10959.

683 76. Weissman MM, Wickramaratne P, Adams P, Wolk S, Verdeli H, Olfson M. Brief screening for family psychiatric
684 history: the family history screen. Arch Gen Psychiatry. 2000;57:675–82.

685 77. Milne BJ, Caspi A, Crump R, Poulton R, Rutter M, Sears MR, et al. The Validity of the Family History Screen for
686 Assessing Family History of Mental Disorders. Am J Med Genet Part B Neuropsychiatr Genet Off Publ Int Soc
687 Psychiatr Genet. 2009;0:41–9.

688 78. Devi G, Marder K, Schofield PW, Tang MX, Stern Y, Mayeux R. Validity of family history for the diagnosis of
689 dementia among siblings of patients with late-onset Alzheimer's disease. Genet Epidemiol. 1998;15:215–23.

690 79. Bidaut-Russell M, Reich W, Cottler LB, Robins LN, Compton WM, Mattison RE. The Diagnostic Interview
691 Schedule for Children (PC-DISC v.3.0): parents and adolescents suggest reasons for expecting discrepant answers. J
692 Abnorm Child Psychol. 1995;23:641–59.

693 80. Williams RR, Hunt SC, Barlow GK, Chamberlain RM, Weinberg AD, Cooper HP, et al. Health family trees: a tool
694 for finding and helping young family members of coronary and cancer prone pedigrees in Texas and Utah. Am J
695 Public Health. 1988;78:1283–6.

696 81. Skinner HA. The drug abuse screening test. Addict Behav. 1982;7:363–71.

697 82. Selzer ML, Vinokur A, van Rooijen L. A self-administered Short Michigan Alcoholism Screening Test (SMAST). J
698 Stud Alcohol. 1975;36:117–26.

699 83. Avinun R, Nevo A, Knodt AR, Elliott ML, Radtke SR, Brigidi BD, et al. Reward-Related Ventral Striatum Activity
700 Buffers against the Experience of Depressive Symptoms Associated with Sleep Disturbances. J Neurosci Off J Soc
701 Neurosci. 2017;37:9724–9.

702 84. Nikolova YS, Bogdan R, Brigidi BD, Hariri AR. Ventral Striatum Reactivity to Reward and Recent Life Stress
703 Interact to Predict Positive Affect. Biol Psychiatry. 2012;72:157–63.

704 85. Clements K, Turpin G. The Life Events Scale for Students: Validation for use with British samples. Personal
705 Individ Differ. 1996;20:747–51.

706 86. Pedraza O, Bowers D, Gilmore R. Asymmetry of the hippocampus and amygdala in MRI volumetric
707 measurements of normal adults. J Int Neuropsychol Soc. 2004;10:664–78.

708 87. Lindauer RJL, Vlieger E-J, Jalink M, Olff M, Carlier IVE, Majoie CBLM, et al. Smaller hippocampal volume in Dutch
709 police officers with posttraumatic stress disorder. Biol Psychiatry. 2004;56:356–63.

710 88. Kovner R, Oler JA, Kalin NH. Cortico-Limbic Interactions Mediate Adaptive and Maladaptive Responses Relevant
711 to Psychopathology. Am J Psychiatry. 2019;176:987–99.

712 89. Elsayed NM, Kim MJ, Fields KM, Olvera RL, Hariri AR, Williamson DE. Trajectories of Alcohol Initiation and Use
713 During Adolescence: The Role of Stress and Amygdala Reactivity. J Am Acad Child Adolesc Psychiatry. 2018;57:550–
714 60.

715 90. Klein A, Tourville J. 101 Labeled Brain Images and a Consistent Human Cortical Labeling Protocol. Front
716 Neurosci. 2012;6. doi:10.3389/fnins.2012.00171.

717 91. Ratanatharathorn A, Boks MP, Maihofer AX, Aiello AE, Amstadter AB, Ashley-Koch AE, et al. Epigenome-wide
718 association of PTSD from heterogeneous cohorts with a common multi-site analysis pipeline. Am J Med Genet Part
719 B Neuropsychiatr Genet Off Publ Int Soc Psychiatr Genet. 2017;174:619–30.

720 92. R Core Team (2019). R: A language and environment for statistical computing. R Foundation for Statistical
721 Computing, Vienna, Austria. URL https://www.R-project.org/.

722 93. Barfield RT, Kilaru V, Smith AK, Conneely KN. CpGassoc: an R function for analysis of DNA methylation
723 microarray data. Bioinforma Oxf Engl. 2012;28:1280–1.

724 94. McCartney DL, Walker RM, Morris SW, McIntosh AM, Porteous DJ, Evans KL. Identification of polymorphic and
725 off-target probe binding sites on the Illumina Infinium MethylationEPIC BeadChip. Genomics Data. 2016;9:22–4.

726 95. Teschendorff AE, Marabita F, Lechner M, Bartlett T, Tegner J, Gomez-Cabrero D, et al. A beta-mixture quantile
727 normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data.
728 Bioinforma Oxf Engl. 2013;29:189–96.

729 96. Pidsley R, Y Wong CC, Volta M, Lunnon K, Mill J, Schalkwyk LC. A data-driven approach to preprocessing
730 Illumina 450K methylation array data. BMC Genomics. 2013;14:293.

731 97. Du P, Zhang X, Huang C-C, Jafari N, Kibbe WA, Hou L, et al. Comparison of Beta-value and M-value methods for
732 quantifying methylation levels by microarray analysis. BMC Bioinformatics. 2010;11:587.

733 98. Braun PR, Han S, Hing B, Nagahama Y, Gaul LN, Heinzman JT, et al. Genome-wide DNA methylation comparison
734 between live human brain and peripheral tissues within individuals. Transl Psychiatry. 2019;9:1–10.

735 99. Houseman EA, Molitor J, Marsit CJ. Reference-free cell mixture adjustments in analysis of DNA methylation
736 data. Bioinforma Oxf Engl. 2014;30:1431–9.

737 100. Houseman EA, Kile ML, Christiani DC, Ince TA, Kelsey KT, Marsit CJ. Reference-free deconvolution of DNA
738 methylation data and mediation by cell composition effects. BMC Bioinformatics. 2016;17:259.

739 101. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR, Bender D, et al. PLINK: a tool set for whole-
740 genome association and population-based linkage analyses. Am J Hum Genet. 2007;81:559–75.

741 102. Langfelder P, Horvath S. WGCNA: an R package for weighted correlation network analysis. BMC
742 Bioinformatics. 2008;9:559.

743 103. Unternaehrer E, Luers P, Mill J, Dempster E, Meyer AH, Staehli S, et al. Dynamic changes in DNA methylation
744 of stress-associated genes (OXTR, BDNF) after acute psychosocial stress. Transl Psychiatry. 2012;2:e150.

745 104. Benjamini Y, Hochberg Y. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple
746 Testing. J R Stat Soc Ser B Methodol. 1995;57:289–300.

747 105. Tingley D, Yamamoto T, Hirose K, Keele L, Imai K. mediation: R Package for Causal Mediation Analysis. J Stat
748 Softw. 2014;59. doi:10.18637/jss.v059.i05.

749 106. Ren X, Kuan PF. methylGSA: a Bioconductor package and Shiny app for DNA methylation data length bias
750 adjustment in gene set testing. Bioinforma Oxf Engl. 2019;35:1958–9.

751 107. Supek F, Bošnjak M, Škunca N, Šmuc T. REVIGO summarizes and visualizes long lists of gene ontology terms.
752 PloS One. 2011;6:e21800.

753

Tables

Table 1. Demographic, psychosocial, and neuroimaging summary stats for the current sample (n = 98)

Characteristic	Description	Value
Age	Mean [SD] (Range)	19.8 [1.2] (18 - 22)
Sex	Male	31%
	Female	69%
Self-reported race/ethnicity	Caucasian/White	49%
	African American/Black	6%
	Asian	22%
	American Indian	13%
	Bi- or multiracial	0%
	Other	9%
Cumulative perceived impact of past year SLEs	Mean [SD] (Range)	11 [7.6] (1 - 42)
Family emotional health (FEH)	Mean [SD] (Range)	60 [8.5] (34 - 70)
Left hippocampus volume (mm3)	Mean [SD] (Range)	4650 [446] (3267 - 5679)
Right hippocampus volume (mm3)	Mean [SD] (Range)	4741 [392] (3825 - 6031)
Left dlPFC volume (mm3)	Mean [SD] (Range)	11980 [1785] (7308 - 16007)
Right dlPFC volume (mm3)	Mean [SD] (Range)	10639 [1585] (7426 - 14819)
Left mPFC volume (mm3)	Mean [SD] (Range)	5745 [853] (3871 - 8686)
Right mPFC volume (mm3)	Mean [SD] (Range)	5790 [717] (4238 - 7442)
Left amygdala volume (mm3)	Mean [SD] (Range)	1655 [186] (1292 - 2157)
Right amygdala volume (mm3)	Mean [SD] (Range)	1859 [210] (1371 - 2417)
Total brain volume (mm3)	Mean [SD] (Range)	$1.2x10^6$ [$1.2x10^5$] ($9.0x10^5$-$1.5x10^{6)}$

Table 2. Family emotional health (FEH) predicts hemisphere-specific brain region volume (BRV)

L. hipp vol. (mm3)	**adj. R2**	**RSE**	**b**	**SE**	**R. hipp vol. (mm3)**	**adj. R2**	**RSE**	**b**	**SE**
Model	0.325***	369.2			Model	0.532***	255.9		
FEH			2.6	5.2	FEH			**10.4****	**3.6**
Sex (female)			-60.6	114.9	Sex (female)			-88.5	79.7
Age			-32.1	33.2	Age			-8.4	23.0
Cumulative impact of past year SLE			-2.5	5.9	Cumulative impact of past year SLE			4.1	4.1
Total brain volume (mm3)			**0.002*****	**0.0005**	Total brain volume (mm3)			**0.002*****	**0.0003**
L. dlPFC vol. (mm3)	**adj. R2**	**RSE**	**b**	**SE**	**R. dlPFC vol. (mm3)**	**adj. R2**	**RSE**	**b**	**SE**
Model	0.564***	1182.0			Model	0.344**	1254.0		
FEH			-27.9	16.7	FEH			-8.8	17.7
Sex (female)			366.8	367.9	Sex (female)			219.2	390.3
Age			-82.5	106.3	Age			**-323.2****	**112.8**
Cumulative impact of past year SLE			28.3	18.9	Cumulative impact of past year SLE			10.9	20.0
Total brain volume (mm3)			**0.013*****	**0.0015**	Total brain volume (mm3)			**0.008*****	**0.0016**
L. mPFC vol. (mm3)	**adj. R2**	**RSE**	**b**	**SE**	**R. mPFC vol. (mm3)**	**adj. R2**	**RSE**	**b**	**SE**
Model	0.559***	557.6			Model	0.539***	479.1		
FEH			0.2	7.9	FEH			-11.6	6.8
Sex (female)			159.9	173.6	Sex (female)			53.1	149.1
Age			-102.9*	50.2	Age			-11.6	43.1
Cumulative impact of past year SLE			4.8	8.9	Cumulative impact of past year SLE			5.7	7.7
Total brain volume (mm3)			**0.006*****	**0.0007**	Total brain volume (mm3)			**0.005*****	**0.0006**
L. amygdala vol. (mm3)	**adj. R2**	**RSE**	**b**	**SE**	**R. amygdala vol. (mm3)**	**adj. R2**	**RSE**	**b**	**SE**
Model	0.404***	139.2			Model	0.356***	166.2		
FEH			**5.2****	**2.0**	FEH			**5.8***	**2.3**
Sex (female)			-34.5	43.3	Sex (female)			-34.3	51.7
Age			-3.6	12.5	Age			-5.1	15.0
Cumulative impact of past year SLE			3.5	2.2	Cumulative impact of past year SLE			0.7	2.7
Total brain volume (mm3)			**0.001*****	**0.0002**	Total brain volume (mm3)			**0.001*****	**0.0002**

*** P < 0.001, ** P < 0.01, * P < 0.05, **P: BH-significant (bolded)**

Four genomic ancestry multi-dimensional scaling measures were included in each model, but are not shown here.

RSE: relative standard error, adj: adjusted, b: estimate, SE: standard error, L: left, R: right, hipp: hippocampus, vol: volume

Table 3. Module eigengenes (MEs) mediating observed family emotional health (FEH) and brain region volume (BRV) relationships

Burlywood: Right hippocampus	b	95% CI Lower	95% CI Upper
Average indirect effect (IDE)	**-111.2***	-255.5	-17.9
Average direct effect (DE)	**-254.4***	-528.2	-15.8
Average total effect (TE)	**-365.7*****	-641.0	-151.0
Darkolivegreen1: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	**-65.6***	-161.3	-1.6
Average direct effect (DE)	**-302.9****	-553.6	-84.3
Average total effect (TE)	**-368.5****	-623.6	-152.7
Thistle2: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	**-64.4***	-156.6	-5.6
Average direct effect (DE)	**-308.5***	-567.7	-79.2
Average total effect (TE)	**-372.9****	-640.1	-150.5
Chocolate2: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-82.8	-204.7	4.9
Average direct effect (DE)	**-281.5***	-585.5	-24.2
Average total effect (TE)	**-364.3****	-635.0	-144.5
Cornflowerblue: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-48.3	-132.5	14.3
Average direct effect (DE)	**-321.5****	-606.7	-96.5
Average total effect (TE)	**-369.8****	-641.6	-151.8
Aliceblue: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-53.4	-146.6	6.6
Average direct effect (DE)	**-317.6****	-591.1	-98.8
Average total effect (TE)	**-371.1*****	-642.8	-162.5
Yellow: Right hippocampus	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-39.7	-115.2	14.7
Average direct effect (DE)	**-332.2****	-610.1	-113.6
Average total effect (TE)	**-371.9****	-642.0	-158.7
Darkgray: Left amygdala	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-47.4	-115.8	8.9
Average direct effect (DE)	-135.2	-293.1	22.0
Average total effect (TE)	**-182.5***	-324.2	-38.6
Darkolivegreen: Left amygdala	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-32.1	-89.7	21.8
Average direct effect (DE)	-152.5	-310.8	4.6
Average total effect (TE)	**-184.6***	-323.9	-39.9
Lavenderblush2: Left amygdala	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	-30.4	-93.4	13.7
Average direct effect (DE)	**-156.4***	-301.0	-3.0
Average total effect (TE)	**-186.9***	-324.4	-44.0
Pink4: Right amygdala	**b**	**95% CI Lower**	**95% CI Upper**
Average indirect effect (IDE)	**-47.9***	-117.4	-3.7
Average direct effect (DE)	-156.1	-338.9	12.9
Average total effect (TE)	**-204.1***	-380.1	-44.2

*** P < 0.001, ** P < 0.01, * P < 0.05, **P: BH-significant (bolded)**

ME: module eigenvalue, b: estimate, CI: confidence interval