



Universiteit
Leiden
The Netherlands

Maternal sensitivity and child internalizing and externalizing behavior: a mediating role for glucocorticoid receptor gene (NR3C1) methylation?

Creasey, N.; Beijers, R.; O'Donnell, K.J.; de Weerth, C.; Tollenaar, M.S.

Citation


Creasey, N., Beijers, R., O'Donnell, K. J., De Weerth, C., & Tollenaar, M. S. (2023). Maternal sensitivity and child internalizing and externalizing behavior: a mediating role for glucocorticoid receptor gene (NR3C1) methylation? *Development And Psychopathology*, 1-12. doi:10.1017/S0954579423000226

Version: Publisher's Version
License: [Creative Commons CC BY 4.0 license](#)
Downloaded from: <https://hdl.handle.net/1887/3619799>

Note: To cite this publication please use the final published version (if applicable).

Regular Article

Maternal sensitivity and child internalizing and externalizing behavior: a mediating role for glucocorticoid receptor gene (*NR3C1*) methylation?

Nicole Creasey¹ , Roseriet Beijers², Kieran J. O'Donnell³, Carolina de Weerth⁴ and Marieke S. Tollenaar⁵

¹Preventive Youth Care, Research Institute of Child Development and Education, University of Amsterdam, the Netherlands, ²Department of Social Development, Behavioral Science Institute, Radboud University, the Netherlands, and Department of Cognitive Neuroscience, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center, the Netherlands, ³Ludmer Centre for Neuroinformatics and Mental Health, Douglas Hospital Research Centre, McGill University, QC, Canada; Canadian Institute for Advanced Research, Child and Brain Development Program, Canada; and Yale Child Study Center & Department of Obstetrics, Gynecology and Reproductive Sciences, Yale School of Medicine, USA, ⁴Department of Cognitive Neuroscience, Donders Institute for Brain, Cognition and Behaviour, Radboud University Medical Center, the Netherlands and ⁵Institute of Psychology and Leiden Institute for Brain and Cognition, Leiden University, the Netherlands

Abstract

The early caregiving environment can have lasting effects on child mental health. Animal models suggest that glucocorticoid receptor gene (*NR3C1*) DNA methylation plays a mediating role in linking more responsive caregiving to improved behavioral outcomes by its impact on the stress regulatory system. In this longitudinal study, we examined whether children's *NR3C1* methylation levels mediate an effect of maternal sensitivity in infancy on levels of child internalizing and externalizing behavior in a community sample. Maternal sensitivity of 145 mothers was rated at infant age 5 weeks, 12 months, and 30 months by observing mother–infant interactions. Buccal DNA methylation was assessed in the same children at age 6 years and maternal-reported internalizing and externalizing behavior was assessed at age 6 and 10 years. Higher sensitivity at age 5 weeks significantly predicted lower DNA methylation levels at two *NR3C1* CpG loci, although methylation levels at these loci did not mediate an effect of maternal sensitivity on levels of child internalizing and externalizing behavior. Overall, the study provides evidence that maternal sensitivity in early infancy is associated with DNA methylation levels at loci involved in stress regulation, but the significance of this finding for child mental health remains unclear.

Keywords: externalizing; internalizing; maternal sensitivity; methylation; *NR3C1*

(Received 16 May 2022; revised 18 October 2022; accepted 24 January 2023)

Introduction

Mental health problems are one of the main causes of disability worldwide and typically emerge before adulthood (Global Burden of Disease Study 2013 Collaborators 2015; Solmi et al., 2021; Whiteford et al., 2013). As such, it is crucial that we improve our understanding of early life factors that modify children's risk of developing mental health problems. One such factor is maternal sensitivity – the extent to which a mother is able to appropriately identify and respond to her infant's physical and emotional needs and signals (Ainsworth et al., 1974). Less sensitive caregiving during infancy is associated with higher levels of childhood internalizing behavior (i.e., anxiety, depression, and withdrawal; Kok et al., 2013) and externalizing behavior (i.e., aggression, defiance, and impulsivity; Wang et al., 2013; van der Voort et al., 2014). Child internalizing and externalizing behaviors are, in turn, major

predictors of later life psychopathology (Mathyssek et al., 2012; Reef et al., 2009). However, the pathways by which maternal sensitivity influences children's levels of internalizing and externalizing behavior are not yet fully understood and warrant further investigation in order to inform preventive interventions (Deans, 2020; Provenzi et al., 2019).

Maternal sensitivity may influence children's levels of internalizing and externalizing behavior through its effects on the developing stress regulatory system in early infancy. Specifically, sensitive caregiving provides infants with the external support they need to cope with emotional and physiological stress, and thus a model for infants to learn how to independently regulate stress (Bell & Ainsworth, 1972; Bowlby, 1980; Gianino & Tronick, 1988). On the other hand, insensitive caregiving – characterized by absent, noncontingent and/or intrusive responses to an infant's signals and behaviors – not only fails to provide infants with external regulation but may act as a source of stress in itself (Smeeckens et al., 2007; Tronick, 1989). As such, infants that receive insensitive caregiving may be at risk for long-term stress dysregulation (Laurent et al., 2016), which could contribute to higher levels of internalizing behavior and externalizing

Corresponding author: Nicole Creasey, email: n.l.creasey@uva.nl

Cite this article: Creasey, N., Beijers, R., O'Donnell, K. J., de Weerth, C., & Tollenaar, M. S. (2023). Maternal sensitivity and child internalizing and externalizing behavior: a mediating role for glucocorticoid receptor gene (*NR3C1*) methylation? *Development and Psychopathology*, 1–12, <https://doi.org/10.1017/S0954579423000226>

behavior (Ruttle et al., 2011). In this way, insensitive caregiving may act as a risk factor for later life psychopathology, while sensitive caregiving may act as a protective factor by ensuring that children are able to appropriately respond to the stressors that they will inevitably face in their daily environment. A potential biological pathway for this association is through epigenetic processes such as DNA methylation, a relatively stable modification to nuclear DNA that occurs most commonly at cytosine-guanine dinucleotide (CpG) sites and can functionally regulate gene expression (Aristizabal et al., 2020). Epigenetic changes in response to sensitive caregiving may alter the function of the hypothalamic pituitary adrenal axis to enhance recovery from stress and reduce stress-related behaviors such as internalizing and externalizing behaviors (Berretta et al., 2021). The current study tested the feasibility of this pathway in children by examining whether differential DNA methylation levels at the glucocorticoid receptor (GR) gene (*NR3C1*), a key regulator of the HPA axis, mediate an association between maternal sensitivity in infancy and later levels of internalizing and externalizing behavior.

Research in rodents has implicated DNA methylation changes at *NR3C1* as a mediator of the effects of maternal responsiveness on levels of stress-related behaviors, such as internalizing-like and externalizing-like behaviors. More sensitive caregiving behavior by rat dams (i.e., licking, grooming and arch-backed nursing) during the first week of life has been found to lead to long-term hypomethylation at exon 1₇ of the *NR3C1* promoter in the hippocampal tissues of their offspring (Weaver et al., 2004). In turn, *NR3C1* promoter hypomethylation is associated with increased hippocampal GR expression, and subsequently more modest HPA axis responses and less defensive, stress-related behaviors in adult rats (Weaver et al., 2004, 2005, 2006; van Hasselt et al., 2012). Given that higher maternal sensitivity has also been found to predict better HPA axis regulation in human infants (Albers et al., 2008; Blair et al., 2006), it is possible that a similar epigenetic pathway may link more sensitive caregiving with lower levels of child internalizing and externalizing behavior in humans.

To date, human studies have predominately focused on the effects of severely disrupted caregiving (i.e., child maltreatment) on DNA methylation and provide some preliminary evidence that *NR3C1* hypermethylation may link an adverse caregiving environment to later psychopathology (for a review see Wadji et al., 2021). However, relatively little attention has been given to typical variation in caregiving within community samples. To our knowledge, only two human studies have investigated the link between maternal sensitivity and *NR3C1* methylation, while no studies have considered the pathway from maternal sensitivity through *NR3C1* to subsequent stress-related behaviors. In one of the aforementioned studies, maternal insensitivity was associated cross-sectionally with higher methylation at the *NR3C1* 1f region in buccal-derived DNA of 5-month-old infants, although results differed based on infant sex and maternal depressive symptoms (Conradt et al., 2016, 2019). Notably, increased methylation at the 1f region – orthologous to the exon 1₇ in rodents – has been repeatedly linked to mental health problems in adult populations (for a review see Watkeys et al., 2018). In contrast, no association was found between maternal sensitivity at age 3–4 years and *NR3C1* methylation levels in whole blood DNA at age 6 in a prospective, longitudinal study (Dall'Aglio et al., 2020). The difference in findings between studies could be related to differences in methodology (e.g., rating scales for maternal sensitivity and methylation analysis method), but could also be related to a difference in the developmental timing of the

measurement of maternal sensitivity (i.e., 5 months vs. 3–4 years). Both rodent and human studies support the likelihood that there is a sensitive period in early infancy (i.e., before three years of age) during which the caregiving environment may have a more significant impact on children's DNA methylation (Curley & Champagne, 2016; Dunn et al., 2019). However, the timing of exposure to sensitive versus insensitive caregiving in relation to *NR3C1* methylation has not been considered in prior human studies. Moreover, it remains unclear from existing studies whether associations between maternal sensitivity and *NR3C1* methylation in early life persist into middle childhood and whether they mediate an effect of maternal sensitivity on children's behaviors.

Prior research has established associations of *NR3C1* methylation with child internalizing and externalizing behavior. A number of cross-sectional studies have demonstrated that higher parent-reported internalizing behavior associates with higher methylation levels at the *NR3C1* 1f exon in children aged 3–16 years (Dadds et al., 2015; Gardini et al., 2022; Parade et al., 2016), and at the *NR3C1* 1d exon in children aged 3–5 years (Parade et al., 2016). Furthermore, in a longitudinal study, higher *NR3C1* promoter methylation in adolescents aged 15–16 years predicted higher internalizing symptoms three years later (van der Knaap et al., 2015). Evidence for associations of *NR3C1* methylation with externalizing behavior is less consistent. In a study of children aged 4–16 years, higher parent-reported externalizing behavior was cross-sectionally associated with higher salivary *NR3C1* methylation levels at the 1f exon (Dadds et al., 2015). Likewise, positive associations were found between methylation levels at the 1f exon and parent-reported oppositional defiant problems in 3-year-olds (Gardini et al., 2022). In contrast, a cross-sectional study of children aged 3–5 years found no significant associations of parent-reported externalizing behavior with *NR3C1* promoter methylation (Parade et al., 2016), whereas a longitudinal study reported that lifetime externalizing disorder – based on parent reports from ages 3 to 19 years – predicted lower *NR3C1* 1f exon methylation at age 19 years (Heinrich et al., 2015). Together these findings lend some preliminary support for a pathway from *NR3C1* methylation to child behavior. However, there is a paucity of longitudinal studies during childhood that test said pathway. Furthermore, most studies to date have been limited in scope to the 1f exon of the *NR3C1* promoter and have relied solely on parental reports of child internalizing and externalizing behavior.

To address the gaps in prior research, the current study investigated whether *NR3C1* methylation mediates an effect of early maternal sensitivity on levels of internalizing and externalizing behaviors in later childhood. First, we examined whether maternal sensitivity at three time points in early infancy (5 weeks, 12 months, and 30 months) predicted children's *NR3C1* methylation levels at age six. Second, we examined whether children's *NR3C1* methylation levels at age 6 mediated an association of maternal sensitivity with children's levels of internalizing and externalizing behavior at ages 6 and 10 years. Based on earlier rodent models, we hypothesized that 1) more sensitive caregiving would be associated with lower levels of *NR3C1* methylation at age 6, and 2) CpG loci with lower levels of *NR3C1* methylation at age 6 would partially mediate a negative association of sensitive caregiving with children's levels of internalizing and externalizing behavior at ages 6 and 10 years. For the sake of completeness, we also explored whether there were associations between *NR3C1* methylation levels at age 6 on all 25 assessed CpG loci and child internalizing and externalizing behaviors at age 6 and 10 years.

Methods

Participant characteristics

Participants were mother–infant dyads recruited as part of an ongoing prospective study on the role of early environmental factors in infant and child development (BIBO project; Basal Influences on Child Development; see Beijers et al., 2010, 2011). Mothers were recruited during pregnancy in collaboration with midwife clinics located in or close to the cities of Nijmegen and Arnhem, The Netherlands. The project was approved by the Radboud University ethical committee of the social science faculty (ECG300107, SW2017-1303-49) and written informed consent was obtained from each participant on enrollment. The original maternal study sample reflected a healthy, nonclinical population of 193 mothers aged 21–42 years with the following inclusion criteria: a singleton uncomplicated pregnancy, no drug use, and no current physical or mental health problems. All infants had an uncomplicated birth and were born healthy with a 5-min APGAR score ≥ 7 . From the original study sample, 148 children provided buccal epithelial cells at age six for genetic and DNA methylation analyses with their mother's informed consent. All parents in the current study sample described their child's ethnic background as Caucasian. Chi-square and Mann–Whitney U tests revealed no significant differences between dyads with and without child buccal samples in terms of child sex, child birthweight, maternal age at childbirth, maternal sensitivity, and child behavioral outcomes.

Design

Maternal caregiving was observed at three time points: infant age 5 weeks (at home), 12 months (in the laboratory), and 30 months (at home). Buccal cell samples were collected for (epi)genetic analysis from the same children using buccal swabs when they were 6 years old. Mothers reported on the internalizing and externalizing behavior of their child via questionnaire when the same children were 6 years old and 10 years old. Children also reported on their own internalizing and externalizing behavior via questionnaire at age 10 years.

Measures

Maternal sensitivity

When the infants were five weeks old, mother–infant dyads were visited at home and mothers were videotaped while bathing their infant as they would normally (as described by Jansen et al., 2010, and Beijers et al., 2020). Two trained independent coders rated videotapes of the whole bathing routine for *sensitivity* – that is, the extent to which the mother timeously and adequately responds to the infant's needs and signals – on a 9-point rating scale using the Ainsworth Maternal Sensitivity Scale (Ainsworth et al., 1978). Interrater reliability was excellent (Cohen's kappa = .90). Higher scores represent mothers who displayed more appropriate responses to their child's needs and signals, that is, higher maternal sensitivity. Of the mothers, 24.3% received a rating of three or lower, reflecting low to inadequate care (Helmerhorst et al., 2017).

When the infants were 12 and 30 months old, mother–infant interactions were videotaped during a joint semi-structured play session (as described by Beijers et al., 2020). Specifically, at infant age 12 months, mothers were asked to play with their infants using four toys (e.g., puzzle, books, and hand puppets) for 3 minutes each during a lab visit. At infant age 30 months, mothers were asked to play with their children using three toys (e.g., puzzle and blocks)

for 4 minutes each during a home visit. The videotapes were rated by two independent observers using the Erickson scales (Erickson et al., 1985). For each mother–infant dyad a composite score for maternal sensitivity was computed by taking the mean of the seven-point subscales for *supportive presence* and *respect for autonomy* (Kok et al., 2013). *Supportive presence* refers to the extent a mother shows positive regard and emotional support to their infant, while *respect for autonomy* describes how far the mother refrains from interfering with the infant's desires, interests, or behavior during the task. The two measures were highly and positively correlated at age 12 months ($r = .62, p < .001$), and moderately and positively correlated at age 30 months ($r = .44, p < .001$). Interrater reliability was excellent for *supportive presence* at 12 months (intraclass coefficient [IC] = .95) and 30 months (IC = .91), and moderate for *respect for autonomy* at 12 months (IC = .70) and 30 months (IC = .70). Higher composite scores represent higher maternal sensitivity. Of the mothers, 22.9% received averaged ratings of three or lower when their infants were 12 months old, reflecting low to inadequate care, while all mothers scored above three when their infants were 30 months old, reflecting at least adequate care (Helmerhorst et al., 2017).

Internalizing and externalizing behavior

Child internalizing and externalizing behaviors were measured by maternal report at age six using the Dutch-version of the Child Behavior Checklist for ages 4–18 (CBCL/4-18; Achenbach, 2007). The CBCL/4-18 has good reliability in Dutch samples and is predictive of adult mental problems (Dekker et al., 2002; Roza et al., 2003). Items were rated from zero (not true as far as you know) to two (very true or often true), and included items such as, “Unhappy, sad, or depressed”. Ratings were used to form two broad-band scales: *internalizing* (anxiety-depression, somatic complaints, and withdrawal subscales) and *externalizing* (delinquent and aggressive subscales). Continuous raw scores, ranging 0–66 for both internalizing and externalizing, were used for each broad-band scale, with higher scores reflecting a higher frequency of child internalizing or externalizing behaviors.

Child internalizing and externalizing behaviors were also measured at age 10 years by child self-report with the Strengths and Difficulties questionnaire (SDQ; Mieloo et al., 2014), to confirm if study outcomes were consistent across informants and symptom checklists. An externalizing score ranging 0–20 was formed from the sum of the conduct and hyperactivity subscales, while an internalizing score ranging 0–20 was formed from the sum of the emotional and peer problems subscale (Goodman & Goodman, 2009).

NR3C1 DNA methylation

Genomic DNA was extracted from buccal epithelial cells with the QIAamp DNA Mini Kit (Qiagen, Germany) and quantified using a Nanodrop 2000 spectrometer (Thermo Fisher Scientific). The Zymo EZ DNA methylation kit (Zymo Research, Irvine, CA, USA) was then used to bisulfite convert 750 ng of gDNA, before genome-wide DNA methylation was described using the Infinium EPIC array (850k array; Illumina, San Diego CA, USA) in accordance with manufacturer's guidelines. Preprocessing was performed with the *meffil* package in R (Min et al., 2018). Probes failed quality control if for more than 10% of the samples they had either: a detection p -value $> .01$, and/or a bead count less than three. Moreover, samples were removed during quality control if either: the reported sex did not match the methylation-predicted sex, more than 10% of the sample's probes had a detection p -value $> .01$, and/or more than 10% of sample's

probes had a bead count less than three. Three samples failed quality control leaving a study sample of 145 children for the main analyses. Additionally, functional normalization (FN; Fortin *et al.*, 2014) was used to reduce non-biological differences between probes. Methylation was estimated based on the ratio of methylation signal to overall signal at each CpG and expressed as β -values ranging from 0 to 1. For our analyses, we extracted values for 25 CpG loci located within the CpG island in the 5' untranslated region of the *NR3C1* gene (GRCh37/hg19 chr5:142,782,071 to chr5:142,785,071; Palma-Gudiel *et al.*, 2015). Buccal epithelial cell content of the samples was estimated using the approach described by Smith and colleagues (Smith *et al.*, 2015) and included as a covariate in the main analyses to adjust for cell heterogeneity (Ong *et al.*, 2014).

Genetic covariates

The same buccal samples were genotyped using the Infinium Global Screening Array (Illumina, Inc.). During quality control, two participants were excluded due to missing single nucleotide polymorphism (SNP) rates higher than 5%. A principal component analysis-based approach was used to account for population stratification, which can confound the results of methylation analysis (Barfield *et al.*, 2014). The first two genetic principal components (PC1 and PC2), which best described the population structure of the sample, were included as covariates in the main analyses.

Maternal mental health

Mothers' scores on the State-Trait Anxiety Inventory (STAI; Spielberger *et al.*, 1983) and Edinburgh Postnatal Depression Scale (EPDS; Pop *et al.*, 1992) at 37 weeks gestational age, and at infant ages 3 months, 12 months, and 30 months, were used to control for maternal anxiety and depression in post hoc sensitivity analyses given potential confounding effects of maternal mental health on associations of maternal sensitivity with *NR3C1* methylation and child behavior.

Data analysis

Analyses were performed in IBM SPSS version 24 and an alpha level of 0.05 was used to assess statistical significance unless otherwise specified. To handle outliers and overcome violation of normality, child internalizing and externalizing scores were log-transformed during data preparation; as CBCL scores range from zero and log0 is undefined, we added a value of one to all scores before the log transformation, that is, transformed score = $\log(\text{original score} + 1)$. The missing data, which are described in Table 1, were missing completely at random (Little's test: $\chi^2(214) = 219.93$, $p = .376$) and thus handled using listwise deletion. Buccal cell count, genetic PC1 and PC2, child sex, child birthweight and maternal age at child birth (as a proxy for socioeconomic status) were selected *a priori* as covariates based on previous research and included in all statistical models (Barfield *et al.*, 2014; Liu *et al.*, 2010; McDade *et al.*, 2019; Mulligan *et al.*, 2012; Ong *et al.*, 2014; Yousefi *et al.*, 2015). In the preliminary analysis, Pearson's and biserial-point correlations were used to test associations between study variables (i.e., maternal sensitivity at three time points, internalizing and externalizing behavior at two time points, methylation at 25 CpG loci, and the preselected covariates).

In the first step of the main analyses, for each of the 25 CpG loci, a multiple regression analysis was performed to test maternal sensitivity scores at 5 weeks, 12 months, and 30 months as predictors

of methylation levels. Scores for maternal sensitivity at each time point were included as separate predictors within each model, thus allowing us to test the individual effect of maternal sensitivity at each time point on children's *NR3C1* methylation. Multiple regression is a suitable method for testing the association of repeatedly measured predictors on an outcome variable when the predictors are not highly correlated, that is, when statistical assumptions are not violated due to multicollinearity, and when data are missing completely at random (Ha *et al.*, 2007; Lubin *et al.*, 1997; Sánchez *et al.*, 2011). In our data, maternal sensitivity scores were not highly correlated between time points at the whole sample level (see Table 1 for Pearson's correlation coefficients) nor were maternal sensitivity scores highly correlated within subjects over time (intraclass correlation = 0.07, based on an unconditional means model run in R version 4.0.3). After running the multiple regression analyses for each CpG loci, a false-discovery rate (FDR) correction ($q = 0.05$) was applied to control for multiple comparisons (Benjamini & Hochberg, 1995). CpG loci whose methylation levels were significantly predicted by maternal caregiving at any time-point after correction were selected for the mediation analyses.

In the next step of the main analyses, methylation levels at CpG loci selected in the first step were tested as mediators of a possible relationship between maternal sensitivity and child internalizing and externalizing behavior. We performed a separate parallel mediation analysis for each outcome variable (i.e., internalizing behavior at age 6, internalizing behavior at age 10, externalizing behavior at age 6, and externalizing behavior at age 10) using multiple regression and bootstrapping procedures described by Hayes (2013). Each mediation analysis tested a total effect model of the relationship between maternal sensitivity scores and internalizing/externalizing behavior scores, and a direct effect model of the same relationship while additionally controlling for CpG loci methylation levels. Maternal sensitivity scores at all three time points and the preselected covariates were included as predictors in all models. Ninety-five percent bias-corrected confidence intervals and 1000 bootstrap resamples were then used to determine the significance of the indirect effect (i.e., the reduction in the effect of maternal sensitivity on internalizing/externalizing behavior when CpG loci methylation levels were included in the model). Confidence intervals that did not include zero were interpreted as statistically significant and indicative of partial mediation. As a sensitivity check, the mediation analyses were repeated with self-reported child internalizing and externalizing behavior scores at age 10 years as the dependent variable.

Additionally, Spearman's rank partial correlations were conducted to explore associations between methylation levels at individual CpG loci and child internalizing and externalizing behavior at both 6 and 10 years of age while controlling for the preselected covariates. Again, a false-discovery rate (FDR) correction ($q = 0.05$) was applied to control for multiple comparisons.

Finally, we conducted two post hoc analyses. First, in case of confounding between maternal mental health and maternal sensitivity, we reran the main regression analyses including both maternal anxiety symptoms (i.e., STAI) and depression symptoms (i.e., EPDS) as covariates, repeating the models for each time point that maternal mental health was measured (i.e., prenatal, 3 months, 12 months, and 30 months). Second, given prior research showing sex-specific effects of associations of maternal sensitivity with *NR3C1* 1f methylation (Conradt *et al.*, 2019), we repeated the main regression analyses including an interaction term for maternal sensitivity at each time point by child sex in separate models. We probed significant interactions by inspecting the sex-specific slopes

Table 1. Descriptive statistics

| | N | M | SD | Min–Max |
|--------------------------|-----|---------|--------|-------------|
| Child sex (% female) | 145 | 47.6% | | |
| Birthweight (g) | 145 | 3604.10 | 452.66 | 2670–4600 |
| Maternal age at delivery | 145 | 32.64 | 3.86 | 21.10–42.90 |
| Maternal sensitivity | 139 | | | |
| 5 weeks | | 5.31 | 2.31 | 1.00–9.00 |
| 12 months | | 4.31 | 1.29 | 1.00–7.00 |
| 30 months | | 5.30 | 0.70 | 3.25–6.50 |
| % Missing | | 4.3% | | |
| CBCL 6 years | | | | |
| Internalizing | 134 | 4.16 | 3.99 | 0.00–21.00 |
| Externalizing | | 6.44 | 5.29 | 0.00–26.00 |
| % Missing | | 7.6% | | |
| CBCL 10 years | 127 | | | |
| Internalizing | | 5.66 | 5.56 | 0.00–35.00 |
| Externalizing | | 6.32 | 6.00 | 0.00–30.00 |
| % Missing | | 12.4% | | |

Note. CBCL = Child Behavior Checklist.

and applied FDR correction to deal with multiple testing for the main effects.

Results

Preliminary analysis

Descriptive statistics for the sample characteristics, maternal sensitivity scores, and CBCL scores are shown in Table 1 and associations between these variables are reported in Table 2. Notably, across all time points, there were no significant associations of maternal sensitivity with child internalizing or externalizing behavior. However, we continued with the planned mediation analyses given that the absence of a direct association between the independent and dependent variables does not rule out the possibility of an indirect effect via a mediator (Hayes, 2013).

As for methylation levels, descriptive statistics are shown in Supplementary Table 1 and associations with the study covariates are reported in Supplementary Table 2. DNA methylation levels across the 25 CpG loci were consistent with hypomethylation of this promoter region (beta range: 0.01–0.12) with significant associations between methylation levels at several loci and the study covariates, with the exception of the two genetic PCs. Furthermore, methylation levels were significantly correlated between almost a third of CpG loci, as shown in Figure 1; these correlations were mostly positive, weak to moderate and did not show a pattern based on the spatial proximity of the loci.

Associations between maternal sensitivity and NR3C1 methylation

As shown in Table 3, maternal sensitivity at age five weeks was associated with methylation levels at two CpG loci after FDR correction for multiple testing. Specifically, higher maternal sensitivity scores were associated with significantly lower methylation levels at cg21702128 ($b = -0.002$, $p < .001$) and cg04111177 ($b = -0.001$, $p < .001$). In other words, each one unit increase

in maternal sensitivity at age five weeks was associated with a 0.2% decrease in methylation levels at cg21702128 and a 0.1% decrease in methylation levels at cg04111177. In contrast, there were no significant associations of maternal sensitivity at either 12 months or 30 months with children's methylation levels after correcting for multiple testing. As such, in the mediation analyses we tested possible indirect effects of maternal sensitivity at five weeks on child internalizing and externalizing behavior via methylation levels at cg21702128 and cg04111177.

Indirect effects of maternal sensitivity on child behaviors via NR3C1 methylation

The results of the mediation analyses are presented in Table 4. Maternal sensitivity at five weeks did not significantly predict child internalizing or externalizing behavior at age 6 or 10 years in the total and direct models. Moreover, there were no significant indirect effects, indicating that cg21702128 and cg04111177 methylation levels did not mediate an effect of maternal sensitivity at age five weeks on child internalizing or externalizing behavior at either age 6 or 10 years. Likewise, there were no significant indirect effects when child self-reported internalizing and externalizing behavior scores at age 10 years were used in the mediation analyses instead of maternal reports.

Exploratory analyses: associations between NR3C1 methylation and child behaviors

Coefficients and uncorrected p-values for the associations of methylation levels at individual CpG loci with child internalizing and externalizing behavior at ages 6 and 10 years are shown in Table 5. Partial correlations revealed a positive association of cg01967637 methylation levels with internalizing behavior at age 6 years, a negative association of cg00629244 methylation levels with internalizing behavior at age 6 years, and a positive association of cg19135245 methylation levels with internalizing at age 10 years. However, these associations did not remain significant after correction for multiple testing. No significant associations were found between methylation levels at any of the 25 CpG loci and children's externalizing behavior at ages six or 10 years. No significant associations were found after correction for multiple testing when including child self-reported internalizing and externalizing behavior scores at age 10 years either.

Post hoc analyses

Maternal mental health

Pearson's correlations revealed one significant association between maternal sensitivity and maternal mental health: specifically, a weak negative correlation between maternal sensitivity and maternal depression scores at infant age 30 weeks ($r = .20$, $p = .006$). Furthermore, there were no meaningful changes to the results for the associations of maternal sensitivity with NR3C1 methylation levels, or for the mediation analyses, when maternal anxiety and depression scores during pregnancy or at infant age 3 months, 12 months, or 30 months were included in the models.

Child sex

There were no moderating effects of child sex on the associations between maternal sensitivity at infant age 5 weeks or 12 months and NR3C1 methylation. However, child sex moderated the association between maternal sensitivity at age 30 months and cg21702128 methylation levels (interaction term: $b = 0.01$,

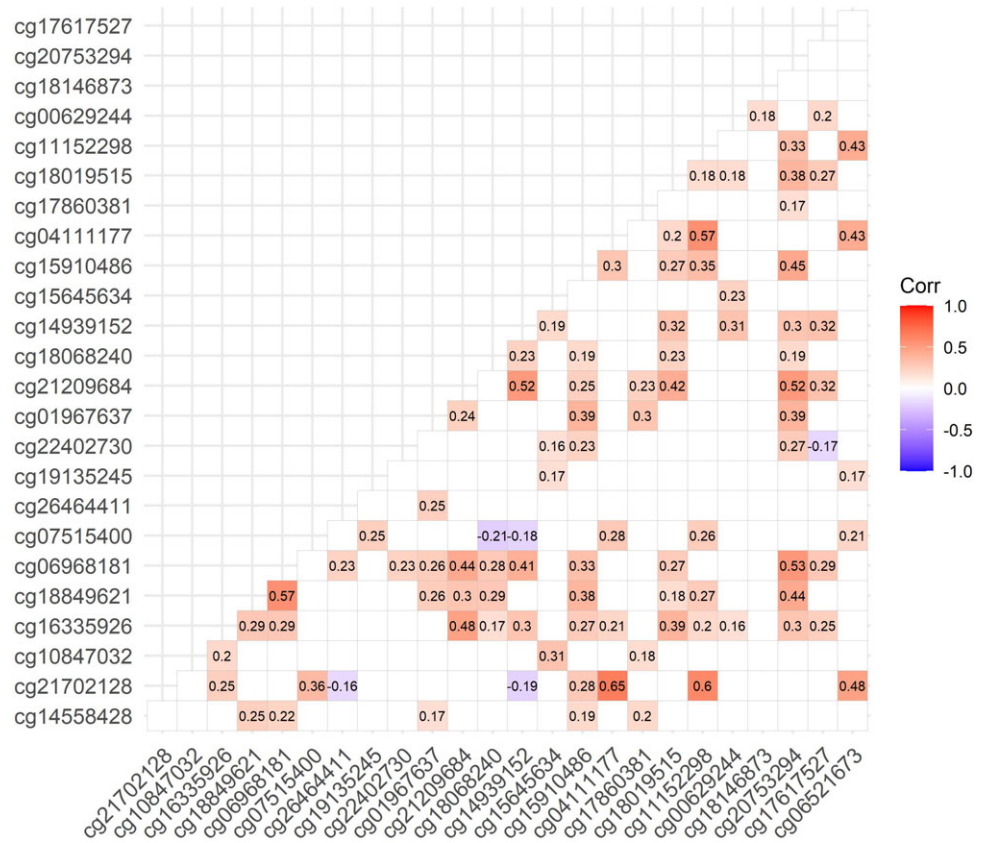
Table 2. Correlation coefficients for associations between study variables

| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|-----------------------------------|------|------|-------|------|------|------|-------|-------|-------|
| 1. Child sex | – | | | | | | | | |
| 2. Birthweight ^a | .20* | | | | | | | | |
| 3. Maternal age at delivery | .05 | .11 | | | | | | | |
| 4. Maternal sensitivity 5 weeks | .01 | .03 | –.06 | | | | | | |
| 5. Maternal sensitivity 12 months | –.16 | .00 | –.10 | .12 | | | | | |
| 6. Maternal sensitivity 30 months | –.01 | –.06 | –.13 | .03 | .03 | | | | |
| 7. Internalizing 6 years | .01 | –.07 | –.20* | –.10 | .05 | .04 | | | |
| 8. Externalizing 6 years | .03 | –.13 | –.08 | –.13 | –.08 | –.06 | .47** | | |
| 9. Internalizing 10 years | .06 | –.12 | –.04 | –.06 | –.15 | –.04 | .55** | .48** | |
| 10. Externalizing 10 years | .06 | –.08 | .03 | –.15 | –.13 | –.08 | .23** | .66** | .46** |

Note. Pearson's correlation coefficients are shown, except for child sex where the biserial-point correlation coefficient is reported.

^a $M_{boys} = 3689g$, $M_{girls} = 3510g$; * $p < .05$, ** $p < .01$

Figure 1. Heat map of significant correlations in methylation levels between 25 CpG Loci at the NR3C1 promoter region. Note. The figure shows the significant ($p < .05$) Pearson's correlation coefficients between methylation levels of the CpG loci at the NR3C1 promoter. The strength of the association is visualized on a color spectrum with red representing positive correlations and blue negative correlations as indicated in the key to the right of the heat map. The heat map includes, in chromosome location order, all CpG loci at the NR3C1 promoter region whose methylation levels are described by the EPIC array (GRCh37/hg19 chr5:142,782,071 to chr5:142,785,071).



$SE = .003$, $p = <.001$). Probing of the sex-specific slopes revealed a positive association between maternal sensitivity at 30 months and methylation levels cg21702128 in girls ($b = 0.005$, $SE = .003$, $p = .044$), whereas for boys the association was negative ($b = -0.007$, $SE = .002$, $p = .006$). However, neither association remained significant after FDR correction.

Discussion

The current study suggests that higher maternal sensitivity in the first weeks of infancy is associated with lower methylation levels at two loci at the NR3C1 promoter region in later childhood.

However, the study also highlights that the timing of caregiving quality may be particularly important given that maternal sensitivity later in infancy (i.e., 12 and 30 months) was not associated with children's NR3C1 methylation levels. Furthermore, contrary to our hypothesis, the study showed no associations between maternal sensitivity and child internalizing and externalizing behaviors at ages 6 or 10 years – neither directly nor indirectly via NR3C1 methylation.

In the current study, two CpG loci – cg21702128 and cg04111177 were significantly less methylated in 6-year-old children who had more sensitive mothers when they were 5 weeks old. These findings are in line with previous research that found

Table 3. Standardized regression coefficients for associations of CpG methylation levels at age 6 with maternal sensitivity at 5 weeks, 12 months, and 30 months of age

| CpG loci | Maternal sensitivity | | | | | |
|------------|----------------------|----------|-----------|----------|-----------|----------|
| | 5 weeks | | 12 months | | 30 months | |
| | β | <i>p</i> | β | <i>p</i> | β | <i>p</i> |
| cg14558428 | 0.04 | .658 | <0.01 | .960 | -0.05 | .603 |
| cg21702128 | -0.32* | <.001 | 0.10 | .242 | 0.02 | .785 |
| cg10847032 | -0.06 | .509 | <0.01 | .963 | 0.08 | .369 |
| cg16335926 | -0.10 | .253 | <0.01 | .960 | 0.02 | .837 |
| cg18849621 | -0.03 | .777 | 0.01 | .951 | 0.02 | .860 |
| cg06968181 | 0.02 | .814 | -0.06 | .515 | 0.06 | .461 |
| cg07515400 | -0.06 | .483 | -0.05 | .574 | 0.15 | .084 |
| cg26464411 | 0.19 | .027 | 0.16 | .060 | -0.05 | .515 |
| cg19135245 | 0.01 | .899 | 0.14 | .128 | 0.06 | .460 |
| cg22402730 | -0.04 | .661 | 0.05 | .566 | <-0.01 | .970 |
| cg01967637 | 0.22 | .012 | -0.10 | .272 | 0.02 | .835 |
| cg21209684 | 0.02 | .817 | -0.05 | .553 | 0.05 | .539 |
| cg18068240 | -0.12 | .172 | 0.11 | .227 | -0.02 | .792 |
| cg14939152 | 0.04 | .616 | -0.09 | .333 | 0.07 | .452 |
| cg15645634 | -0.09 | .290 | 0.04 | .636 | 0.03 | .756 |
| cg15910486 | 0.08 | .350 | -0.02 | .834 | <0.01 | .946 |
| cg04111177 | -0.32* | <.001 | 0.12 | .151 | 0.05 | .596 |
| cg17860381 | -0.01 | .930 | -0.04 | .589 | -0.04 | .584 |
| cg18019515 | -0.16 | .074 | 0.03 | .694 | 0.03 | .738 |
| cg11152298 | -0.23 | .009 | 0.16 | .074 | -0.05 | .562 |
| cg00629244 | -0.03 | .768 | 0.06 | .529 | -0.01 | .918 |
| cg18146873 | -0.02 | .820 | 0.09 | .300 | 0.01 | .906 |
| cg20753294 | 0.04 | .618 | 0.02 | .863 | 0.08 | .373 |
| cg17617527 | -0.04 | .674 | -0.13 | .146 | -0.03 | .761 |
| cg06521673 | -0.12 | .170 | 0.01 | .924 | 0.06 | .444 |

Note. *N* = 139, β = standardized regression coefficients, covariates: buccal cell count, genetic PC1 and PC2, maternal age, child birthweight, child sex.

*Significant after FDR correction for multiple testing.

significant associations of children's methylation levels at these two loci with severely disrupted caregiving (Weder et al., 2014). Furthermore, cg04111177 is located in the exon 1F region where methylation levels in 5-month-old infants were found to be cross-sectionally associated with maternal sensitivity in earlier studies using pyrosequencing (Conradt et al., 2016, 2019). Thus, the current study builds on previous findings by suggesting that links between maternal sensitivity and *NR3C1* methylation extend into childhood.

In relation to the functional relevance of cg21702128 and cg04111177, methylation at these sites has been linked to functioning of the HPA axis. Specifically, methylation at cg04111177 was found to predict morning cortisol values in school-aged children, although the direction of the effect was not reported (Weder et al., 2014). Meanwhile, higher methylation at cg21702128 – located in the exon 1D region – was found in patients with endogenous Cushing's syndromes, which is characterized by heightened cortisol levels (Glad et al., 2017). Therefore, differential methylation at

Table 4. Regression and bootstrapping results for testing effects of maternal sensitivity on child internalizing/externalizing behavior at age 6 and 10 as mediated by Cg21702128 and Cg04111177 methylation at age 6

| | Internalizing behavior | | Externalizing behavior | |
|---------------------------------|------------------------|---------------|------------------------|---------------|
| | 6 years | 10 years | 6 years | 10 years |
| | <i>B</i> (SE) | <i>B</i> (SE) | <i>B</i> (SE) | <i>B</i> (SE) |
| Total effect models | | | | |
| Maternal sensitivity at 5 weeks | -0.02 (0.01) | -0.01 (0.01) | -0.02 (0.01) | -0.02 (0.02) |
| Direct effect models | | | | |
| Maternal sensitivity at 5 weeks | -0.02 (0.01) | -0.01 (0.01) | -0.02 (0.01) | -0.02 (0.02) |
| cg21702128 methylation | -3.60 (2.82) | -0.48 (2.90) | 1.44 (2.77) | -0.15 (3.23) |
| cg04111177 methylation | 3.13 (3.92) | 0.61(4.09) | -5.05 (3.85) | 0.52 (4.56) |
| Indirect effects ^a | 0.02 (0.33) | <0.01 (0.04) | 0.03 (0.04) | <-0.01 (0.04) |
| CI | -0.05, 0.09 | -0.08, 0.10 | -0.05, 0.11 | -0.07, 0.08 |

Note. *N*_{6 years} = 134, *N*_{10 years} = 127, *B* = unstandardized regression coefficients, CI = 95% bias-corrected confidence interval for the significance of the indirect effects; all CIs cross zero indicating no significant effects. Covariates: maternal sensitivity at age 12 months and 30 months, buccal cell count, genetic PC1 and PC2, maternal age, child birthweight, child sex. ^aCompletely standardized indirect effects of maternal sensitivity at 5 weeks on the dependent variables.

**p* < .05

these two CpG loci may be related to regulation of the HPA axis. Yet, as in the current study, prior research has not established a link between methylation levels at either loci and internalizing or externalizing behavior (Cicchetti & Handley, 2017; Radtke et al., 2015; Weder et al., 2014).

As for the importance of developmental timing of sensitive caregiving, we found associations between children's *NR3C1* methylation levels at age 6 years and maternal sensitivity measured at age 5 weeks, but not at ages 12 and 30 months. These findings are partly in keeping with prior research and suggest a sensitive period for *NR3C1* methylation in response to maternal sensitivity before age 12 months (Conradt et al., 2016, 2019; Dall'Aglio et al., 2020; Dunn et al., 2019). However, it should be noted that there was a difference in the measurement of maternal sensitivity at age 5 weeks versus 12 and 30 months, which matches methodological differences between previous studies in younger versus older infants. As well as the use of different observational coding systems, maternal sensitivity was observed during a mild stressor at age 5 weeks (i.e., a bathing session) compared to a play task at later ages. Earlier research has indicated that maternal sensitivity ratings can differ in situations of infant distress versus non-distress and differentially predict child outcomes (Leerkes et al., 2012). That said, both measures used in the current study have been found to detect improvements in sensitivity following a parenting intervention to increase sensitivity, which supports the likelihood that they are measuring the same construct (Mesman & Emmen, 2013).

In terms of child behavioral outcomes, maternal sensitivity did not predict levels of child internalizing or externalizing behaviors at ages 6 or 10 years in the current sample, nor did we find indirect effects via *NR3C1* promoter methylation levels. A possible reason

Table 5. Spearman's rho coefficients and P-values for partial correlations of NR3C1 CpG loci methylation levels at age 6 with internalizing/externalizing behavior at age 6 and 10 years

| CpG loci | Internalizing | | | | Externalizing | | | |
|------------|---------------|------|----------|------|---------------|------|----------|------|
| | 6 years | | 10 years | | 6 years | | 10 years | |
| | r_s | p | r_s | p | r_s | p | r_s | p |
| cg14558428 | .04 | .614 | -.12 | .179 | -.13 | .131 | -.09 | .319 |
| cg21702128 | -.01 | .953 | .02 | .851 | .00 | .999 | .01 | .911 |
| cg10847032 | .07 | .405 | -.02 | .813 | .13 | .139 | .10 | .281 |
| cg16335926 | -.01 | .918 | -.02 | .786 | .01 | .949 | .00 | .964 |
| cg18849621 | -.06 | .477 | -.03 | .759 | -.05 | .585 | -.07 | .416 |
| cg06968181 | -.06 | .493 | .09 | .341 | .12 | .186 | .10 | .289 |
| cg07515400 | -.03 | .727 | -.03 | .729 | -.08 | .364 | -.09 | .297 |
| cg26464411 | .02 | .782 | -.03 | .743 | -.07 | .434 | -.10 | .270 |
| cg19135245 | -.17 | .051 | -.19 | .036 | -.12 | .155 | -.07 | .419 |
| cg22402730 | .06 | .504 | .12 | .195 | .12 | .168 | .13 | .159 |
| cg01967637 | .23 | .008 | .16 | .075 | .08 | .345 | .03 | .779 |
| cg21209684 | .03 | .760 | .11 | .226 | .02 | .820 | -.02 | .816 |
| cg18068240 | .10 | .239 | -.04 | .680 | .04 | .643 | .00 | .974 |
| cg14939152 | -.03 | .719 | .01 | .876 | .00 | .971 | .05 | .548 |
| cg15645634 | .14 | .100 | .08 | .357 | .07 | .394 | .01 | .880 |
| cg15910486 | .02 | .795 | -.06 | .543 | .06 | .494 | .03 | .703 |
| cg04111177 | .05 | .574 | .04 | .635 | -.06 | .520 | .06 | .535 |
| cg17860381 | -.01 | .906 | .05 | .563 | .09 | .321 | .01 | .900 |
| cg18019515 | -.03 | .739 | .13 | .163 | -.04 | .618 | .06 | .527 |
| cg11152298 | -.05 | .542 | -.04 | .675 | -.01 | .874 | .04 | .682 |
| cg00629244 | -.18 | .036 | -.11 | .244 | -.03 | .707 | .00 | .968 |
| cg18146873 | .02 | .838 | -.02 | .811 | .03 | .737 | .08 | .353 |
| cg20753294 | .10 | .250 | .12 | .189 | .00 | .992 | -.15 | .097 |
| cg17617527 | .03 | .742 | .03 | .764 | .03 | .744 | -.02 | .790 |
| cg06521673 | .08 | .340 | -.01 | .901 | -.03 | .693 | -.10 | .272 |

Note. $N_{6 \text{ years}} = 134$, $N_{10 \text{ years}} = 127$. covariates: buccal cell count, genetic PC1 and PC2, maternal age, child birthweight, and child sex.

might be the relatively long follow-up from the measurement of maternal sensitivity to child behavior, during which time other factors (e.g., parenting style, family support, and community social support) may have fostered resilience to internalizing and externalizing problems (Fritz et al., 2018). Such an explanation could also account for mixed evidence regarding the influence of maternal sensitivity on internalizing and externalizing behaviors in other community samples (Campbell et al., 2007; Kok et al., 2013; Propper et al., 2007). Moreover, most research that links higher NR3C1 methylation to increased psychopathology does so in the context of severe adversities (Palma-Gudiel et al., 2015; Parade et al., 2016; Tyrka et al., 2016; Watkeys et al., 2018). However, the current study sample comprised healthy mother–infant dyads of mainly higher socioeconomic status who were thus less likely to have been exposed to extreme stress (Turner & Avison, 2003) and were at lower risk for psychopathology (van Oort et al., 2011). This was reflected in low NR3C1 methylation levels and low child behavior scores across the current study sample; the lack of variation in the data hence potentially created difficulties for detecting associations. Future studies could recruit more heterogeneous

samples, for example including children with known risk factors for psychopathology, and consider the moderating effects of protective factors that may influence the potential pathway from caregiving to child behavior via DNA methylation. Also mentionable is that the small statistical effects of maternal sensitivity on children's methylation levels may not necessarily impact gene expression, and thus subsequent child behavior, which highlights a need for future studies that include measures of GR gene expression and HPA axis functioning to better assess the biological relevance of associations between caregiving and NR3C1 methylation.

This study is not without limitations. For example, the study was correlational and methylation was not measured prior to exposure to caregiving, which means that we cannot conclude that higher sensitivity causes a reduction in methylation levels at the NR3C1 promoter region. Additionally, the relatively small sample offered little power to fully evaluate the effects of possible moderators. Moreover, methylation levels were measured from buccal cells and thus the relationship with DNA methylation in brain regions implicated in stress physiology is unknown (Jones et al., 2018); although DNA methylation levels in buccal and brain

tissues have been found to be highly correlated at *NR3C1* ($r = .92$; Braun et al., 2019). On the other hand, in terms of strengths, the longitudinal design did allow us to measure mother–infant interactions by direct observation at multiple time points rather than relying on retrospective reports, as well as to assess longer-term associations of maternal sensitivity with children’s *NR3C1* methylation levels and stress-related behaviors. Furthermore, children’s internalizing and externalizing behaviors at age 10 years were also measured by child self-report rather than relying solely on parental reports. The next step would be to use intervention studies whereby methylation and behavioral data are collected before and after parental sensitivity training, thus providing causal evidence for epigenetic mechanisms that link caregiving to child behavioral outcomes (Montirosso et al., 2020; Overbeek et al., 2020). Moreover, future studies could include other caregivers, such as fathers, whose sensitivity may also be important for child development and compensate when maternal sensitivity is low (Malmberg et al., 2016).

To conclude, the current study aimed to improve our knowledge of the factors and mechanisms that protect children from the development of mental health problems in the context of universal prevention. In a community sample, we showed that typical variation in maternal sensitivity at infant age 5 weeks was associated with 6-year-old children’s methylation levels at *NR3C1* loci implicated in HPA axis regulation. However, the same results did not apply for maternal sensitivity measured at infant ages 12 and 30 months, suggesting a sensitive period for caregiving effects on *NR3C1* methylation within the first year of life. Moreover, we did not find evidence that differential *NR3C1* methylation mediates a pathway from sensitive caregiving to lower levels of child internalizing or externalizing behavior; this is potentially related to the influence of other protective factors and the low risk for psychopathology in our community sample. In the future, studies using parenting interventions in vulnerable (high stress) populations could expand our understanding of the biological mechanisms linking the early caregiving environment to child mental health and provide the causal evidence needed to inform universal prevention approaches.

Supplementary material. The supplementary material for this article can be found at <https://doi.org/10.1017/S0954579423000226>

Acknowledgements. This work was supported by the Dutch Research Council VENI grant 016.195.197 (RB), VIDI grant 575-25-009 (CdeW), and VICI grant 016.Vici.185.038 (CdeW), a Jacobs Foundation Advanced Research Fellowship (CdeW), and a Sara van Dam Project Grant of the Royal Netherlands Academy of Arts and Sciences (RB). KOD is a CIFAR Fellow in the Child and Brain Development Program and supported by the Brain and Behavior Research Foundation (Pfeil Fellow).

Conflict of Interest. None.

References

- Achenbach, T. M. (2007). Manual for the ASEBA school-age forms & profiles an integrated system of multi-informant assessment. *Research Center for Children*, 82, 60–90.
- Ainsworth, M. D. S., Bell, S. M., & Stayton, D. F. (1974). Infant–mother attachment and social development: Socialization as a product of reciprocal responsiveness to signals. In M. P. M. Richards (Eds.), *The integration of a child into a social world* (pp. 99–135). Cambridge University Press.
- Ainsworth, M. D. S., Blehar, M. C., Waters, E., & Wall, S. (1978). *Patterns of attachment: A psychological study of the strange situation*. Lawrence Erlbaum.
- Albers, E. M., Marianne Riksen-Walraven, J., Sweep, F. C. G. J., & Weerth, C. De (2008). Maternal behavior predicts infant cortisol recovery from a mild everyday stressor. *Journal of Child Psychology and Psychiatry*, 49(1), 97–103. <https://doi.org/10.1111/j.1469-7610.2007.01818.x>
- Aristizabal, M. J., Anreiter, I., Halldorsdottir, T., Odgers, C. L., McDade, T. W., Goldenberg, A., Mostafavi, S., Kobor, M. S., Binder, E. B., Sokolowski, M. B., O’Donnell, K. J. (2020). Biological embedding of experience: A primer on epigenetics. *Proceedings of the National Academy of Sciences of the United States of America*, 117(38), 23261–23269. <https://doi.org/10.1073/pnas.1820838116>
- Barfield, R. T., Almlil, L. M., Kilaru, V., Smith, A. K., Mercer, K. B., Duncan, R., Klengel, T., Mehta, D., Binder, E. B., Epstein, M. P., Ressler, K. J., Conneely, K. N. (2014). Accounting for population stratification in DNA methylation studies. *Genetic Epidemiology*, 38(3), 231–241. <https://doi.org/10.1002/gepi.21789>
- Beijers, R., Hartman, S., Shalev, I., Hastings, W., Mattern, B. C., de Weerth, C., & Belsky, J. (2020). Testing three hypotheses about effects of sensitive-insensitive parenting on telomeres. *Developmental Psychology*, 56(2), 237–250. <https://doi.org/10.1037/dev0000879>
- Beijers, R., Jansen, J., Riksen-Walraven, M., & de Weerth, C. (2010). Maternal prenatal anxiety and stress predict infant illnesses and health complaints. *Pediatrics*, 126(2), e401–e409. <https://doi.org/10.1542/peds.2009-3226>
- Beijers, R., Jansen, J., Riksen-Walraven, M., & de Weerth, C. (2011). Nonparental care and infant health: Do number of hours and number of concurrent arrangements matter? *Early Human Development*, 87(1), 9–15. <https://doi.org/10.1016/j.earlhumdev.2010.09.003>
- Bell, S. M., & Ainsworth, M. D. S. (1972). Infant crying and maternal responsiveness. *Child Development*, 43(4), 1171–1190. <https://doi.org/10.2307/1127388>
- Benjamini, Y., & Hochberg, Y. (1995). Controlling the false discovery rate: A practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society: Series B (Methodological)*, 57(1), 289–300. <https://doi.org/10.1111/j.2517-6161.1995.tb02031.x>
- Berretta, E., Guida, E., Forni, D., & Provenzi, L. (2021). Glucocorticoid receptor gene (*NR3C1*) methylation during the first thousand days: Environmental exposures and developmental outcomes. *Neuroscience and Biobehavioral Reviews*, 125, 493–502. <https://doi.org/10.1016/j.neubiorev.2021.03.003>
- Blair, C., Granger, D., Willoughby, M., & Kivlighan, K. (2006). Maternal sensitivity is related to hypothalamic–pituitary–adrenal axis stress reactivity and regulation in response to emotion challenge in 6-month-old infants. *Annals of the New York Academy of Sciences*, 1094(1), 263–267. <https://doi.org/10.1196/annals.1376.031>
- Bowlby, J. (1980). *Attachment and loss*. Basic Books.
- Braun, P. R., Han, S., Hing, B., Nagahama, Y., Gaul, L. N., Heinzman, J. T., Grossbach, A. J., Close, L., Dlouhy, B. J., Howard, M. A. 3rd, Kawasaki, H., Potash, J. B., & Shinozaki, G. (2019). Genome-wide DNA methylation comparison between live human brain and peripheral tissues within individuals. *Translational Psychiatry*, 9(1), 47. <https://doi.org/10.1038/s41398-019-0376-y>
- Campbell, S. B., Matestic, P., von Stauffenberg, C., Mohan, R., & Kirchner, T. (2007). Trajectories of maternal depressive symptoms, maternal sensitivity, and children’s functioning at school entry. *Developmental Psychology*, 43(5), 1202–1215. <https://doi.org/10.1037/0012-1649.43.5.1202>
- Cicchetti, D., & Handley, E. D. (2017). Methylation of the glucocorticoid receptor gene, nuclear receptor subfamily 3, group C, member 1 (*NR3C1*), in maltreated and nonmaltreated children: Associations with behavioral undercontrol, emotional lability/negativity, and externalizing and internalizing. *Development and Psychopathology*, 29(5), 1795–1806. <https://doi.org/10.1017/S0954579417001407>
- Conradt, E., Dylan Guerin, D. A., Marsit, C. J., Hawes, K., & Tronick, E. (2016). The contributions of maternal sensitivity and maternal depressive symptoms to epigenetic processes and neuroendocrine functioning. *Child Development*, 87(1), 73–85. <https://doi.org/10.1111/cdev.12483>
- Conradt, E., Ostlund, B., Guerin, D., Armstrong, D. A., Marsit, C. J., Tronick, E., LaGasse, L., & Lester, B. M. (2019). DNA methylation of *NR3c1* in infancy: Associations between maternal caregiving and infant

- sex. *Infant Mental Health Journal*, 40(4), 513–522. <https://doi.org/10.1002/imhj.21789>
- Curley, J. P., & Champagne, F. A. (2016). Influence of maternal care on the developing brain: Mechanisms, temporal dynamics and sensitive periods. *Frontiers in Neuroendocrinology*, 40, 52–66. <https://doi.org/10.1016/j.yfrne.2015.11.001>
- Dadds, M. R., Moul, C., Hawes, D. J., Mendoza Diaz, A., & Brennan, J. (2015). Individual differences in childhood behavior disorders associated with epigenetic modulation of the cortisol receptor gene. *Child Development*, 86(5), 1311–1320. <https://doi.org/10.1111/cdev.12391>
- Dall' Aglio, L., Rijlaarsdam, J., Mulder, R. H., Neumann, A., Felix, J. F., Kok, R., Bakermans-Kranenburg, M. J., van Ijzendoorn, M. H., Tiemeier, H., Cecil, C. A. M. (2020). Epigenome-wide associations between observed maternal sensitivity and offspring DNA methylation: A population-based prospective study in children. *Psychological Medicine*, 1-11(13), 2481–2491. <https://doi.org/10.1017/S0033291720004353>
- Deans, C. L. (2020). Maternal sensitivity, its relationship with child outcomes, and interventions that address it: A systematic literature review. *Early Child Development and Care*, 190(2), 252–275. <https://doi.org/10.1080/03004430.2018.1465415>
- Dekker, M. C., Koot, H. M., van der Ende, J., & Verhulst, F. C. (2002). Emotional and behavioral problems in children and adolescents with and without intellectual disability. *Journal of Child Psychology and Psychiatry, and Allied Disciplines*, 43(8), 1087–1098. <https://doi.org/10.1111/1469-7610.00235>
- Dunn, E. C., Soare, T. W., Zhu, Y., Simpkin, A. J., Suderman, M. J., Klengel, T., Smith, A. D. A. C., Ressler, K. J., & Relton, C. L. (2019). Sensitive periods for the effect of childhood adversity on DNA methylation: Results from a prospective, longitudinal study. *Biological Psychiatry*, 85(10), 838–849. <https://doi.org/10.1016/j.biopsych.2018.12.023>
- Erickson, M. F., Sroufe, L. A., & Egeland, B. (1985). The relationship between quality of attachment and behavior problems in preschool in a high-risk sample. *Monographs of the Society for Research in Child Development*, 50(1), 147–166.
- Fortin, J. P., Labbe, A., Lemire, M., Zanke, B. W., Hudson, T. J., Fertig, E. J., Greenwood, C. M., & Hansen, K. D. (2014). Functional normalization of 450k methylation array data improves replication in large cancer studies. *Genome Biology*, 15(11), 503. <https://doi.org/10.1186/s13059-014-0503-2>
- Fritz, J., de Graaff, A. M., Caisley, H., van Harmelen, A. L., & Wilkinson, P. O. (2018). A systematic review of amenable resilience factors that moderate and/or mediate the relationship between childhood adversity and mental health in young people. *Frontiers in Psychiatry*, 9, 230. <https://doi.org/10.3389/fpsy.2018.00230>
- Gardini, E. S., Schaub, S., Neuhauser, A., Ramseier, E., Villiger, A., Ehlert, U., Lanfranchi, A., & Turecki, G. (2022). Methylation of the glucocorticoid receptor promoter in children: Links with parents as teachers, early life stress, and behavior problems. *Development and Psychopathology*, 34(3), 810–822. <https://doi.org/10.1017/S0954579420001984>
- Gianino, A. F., & Tronick, E. Z. (1988). The mutual regulation model: The infant's self and interactive regulation and coping and defensive capacities. In T. M. Field, P. M. McCabe, & N. Schneiderman (Eds.), *Stress and coping across development* (pp. 47–68). Lawrence Erlbaum Associates, Inc.
- Glad, C. A. M., Andersson-Assarsson, J. C., Berglund, P., Berghthorsdottir, R., Ragnarsson, O., & Johannsson, G. (2017). Reduced DNA methylation and psychopathology following endogenous hypercortisolism – a genome-wide study. *Scientific Reports*, 7(1), 44445. <https://doi.org/10.1038/srep44445>
- Global Burden of Disease Study 2013 Collaborators (2015). Global, regional, and national incidence, prevalence, and years lived with disability for 301 acute and chronic diseases and injuries in 188 countries, 1990–2013: A systematic analysis for the Global Burden of Disease Study 2013. *The Lancet*, 386(9995), 743–800. [https://doi.org/10.1016/S0140-6736\(15\)60692-4](https://doi.org/10.1016/S0140-6736(15)60692-4)
- Goodman, A., & Goodman, R. (2009). Strengths and difficulties questionnaire as a dimensional measure of child mental health. *Journal of the American Academy of Child and Adolescent Psychiatry*, 48(4), 400–403. <https://doi.org/10.1097/CHI.0b013e3181985068>
- Ha, M., Mabuchi, K., Sigurdson, A. J., Freedman, D. M., Linet, M. S., Doody, M. M., & Hauptmann, M. (2007). Smoking cigarettes before first childbirth and risk of breast cancer. *American Journal of Epidemiology*, 166(1), 55–61. <https://doi.org/10.1093/aje/kwm045>
- Hayes, A. F. (2013). *Introduction to mediation, moderation, and conditional process analysis: A regression-based approach*. Guilford Press.
- Heinrich, A., Buchmann, A. F., Zohsel, K., Dukal, H., Frank, J., Treutlein, J., Nieratschker, V., Witt, S. H., Brandeis, D., Schmidt, M. H., Esser, G., Banaschewski, T., Laucht, M., Rietschel, M. (2015). Alterations of glucocorticoid receptor gene methylation in externalizing disorders during childhood and adolescence. *Behavior Genetics*, 45(5), 529–536. <https://doi.org/10.1007/s10519-015-9721-y>
- Helmerhorst, K., Riksen-Walraven, J., Fukkink, R. G., Tavecchio, L., & Gevers Deynoot-Schaub, M. (2017). Effects of the caregiver interaction profile training on caregiver-child interactions in Dutch child care centers: A randomized controlled trial. *Child & Youth Care Forum*, 46(3), 413–436. <https://doi.org/10.1007/s10566-016-9383-9>
- Jansen, J., Beijers, R., Riksen-Walraven, M., & de Weerth, C. (2010). Does maternal care-giving behavior modulate the cortisol response to an acute stressor in 5-week-old human infants? *Stress-the International Journal on The Biology of Stress*, 13(6), 491–497. <https://doi.org/10.3109/10253890.2010.483298>
- Jones, M., Moore, S., & Kobor, M. (2018). Principles and challenges of applying epigenetic epidemiology to psychology. *Annual Review of Psychology*, 69(459-485), 459–485. <https://doi.org/10.1146/annurev-psych-122414-033653>
- Kok, R., Linting, M., Bakermans-Kranenburg, M. J., van Ijzendoorn, M. H., Jaddoe, V. W. V., Hofman, A., Verhulst, F. C., & Tiemeier, H. (2013). Maternal sensitivity and internalizing problems: Evidence from two longitudinal studies in early childhood. *Child Psychiatry and Human Development*, 44(6), 751–765. <https://doi.org/10.1007/s10578-013-0369-7>
- Laurent, H. K., Harold, G. T., Leve, L., Shelton, K. H., & Van Goozen, S. H. M. (2016). Understanding the unfolding of stress regulation in infants. *Development and Psychopathology*, 28(4pt2), 1431–1440. <https://doi.org/10.1017/S0954579416000171>
- Leerkes, E. M., Weaver, J. M., & O'Brien, M. (2012). Differentiating maternal sensitivity to infant distress and non-distress. *Parenting, Science and Practice*, 12(2-3), 175–184. <https://doi.org/10.1080/15295192.2012.683353>
- Liu, J., Morgan, M., Hutchison, K., & Calhoun, V. D. (2010). A study of the influence of sex on genome wide methylation. *PLoS ONE*, 5(4), e10028. <https://doi.org/10.1371/journal.pone.0010028>
- Lubin, J. H., Tomásek, L., Edling, C., Hornung, R. W., Howe, G., Kunz, E., Kusiak, R. A., Morrison, H. I., Radford, E. P., Samet, J. M., Tirmarche, M., Woodward, A., Yao, S. X. (1997). Estimating lung cancer mortality from residential radon using data for low exposures of miners. *Radiation Research*, 147(2), 126–134. <https://doi.org/10.2307/3579412>
- Malmberg, L.-E., Lewis, S., West, A., Murray, E., Sylva, K., & Stein, A. (2016). The influence of mothers' and fathers' sensitivity in the first year of life on children's cognitive outcomes at 18 and 36 months. *Child: Care, Health and Development*, 42(1), 1–7. <https://doi.org/10.1111/cch.12294>
- Mathyssek, C. M., Olino, T. M., Verhulst, F. C., & van Oort, F. V. A. (2012). Childhood internalizing and externalizing problems predict the onset of clinical panic attacks over adolescence: The TRAILS study. *PLoS ONE*, 7(12), e51564. <https://doi.org/10.1371/journal.pone.0051564>
- McDade, T. W., Ryan, C. P., Jones, M. J., Hoke, M. K., Borja, J., Miller, G. E., Kuzawa, C. W., & Kobor, M. S. (2019). Genome-wide analysis of DNA methylation in relation to socioeconomic status during development and early adulthood. *American Journal of Physical Anthropology*, 169(1), 3–11. <https://doi.org/10.1002/ajpa.23800>
- Mesman, J., & Emmen, R. A. G. (2013). Mary Ainsworth's legacy: A systematic review of observational instruments measuring parental sensitivity. *Attachment and Human Development*, 15(5-6), 485–506. <https://doi.org/10.1080/14616734.2013.820900>
- Mieloo, C. L., Bevaart, F., Donker, M. C., van Oort, F. V., Raat, H., & Jansen, W. (2014). Validation of the SDQ in a multi-ethnic population of young children. *European Journal of Public Health*, 24(1), 26–32. <https://doi.org/10.1093/eurpub/ckt100>
- Min, J. L., Hemani, G., Davey Smith, G., Relton, C., & Suderman, M. (2018). Meffil: Efficient normalization and analysis of very large DNA methylation

- datasets. *Bioinformatics*, 34(23), 3983–3989. <https://doi.org/10.1093/bioinformatics/bty476>
- Montirosso, R., Rosa, E., Giorda, R., Fazzi, E., Orcesi, S., Cavallini, A., Provenzi, L., & Early Intervention Study Group (2020). Early Parenting Intervention - Biobehavioral Outcomes in infants with Neurodevelopmental Disabilities (EPI-BOND): Study protocol for an Italian multicentre randomised controlled trial. *BMJ Open*, 10(7), e035249. <https://doi.org/10.1136/bmjopen-2019-035249>,
- Mulligan, C. J., D'Errico, N. C., Stees, J., & Hughes, D. A. (2012). Methylation changes at NR3C1 in newborns associate with maternal prenatal stress exposure and newborn birth weight. *Epigenetics*, 7(8), 853–857. <https://doi.org/10.4161/epi.21180>
- Ong, M. L., Lin, X., & Holbrook, J. D. (2014). Measuring epigenetics as the mediator of gene/environment interactions in DOHAD. *Journal of Developmental Origins of Health and Disease*, 6(1), 10–16. <https://doi.org/10.1017/S2040174414000506>
- Overbeek, G., Creasey, N., Wesarg, C., Huijzer-Engbreghof, M., & Spencer, H. (2020). When mummy and daddy get under your skin: A new look at how parenting affects children's DNA methylation, stress reactivity, and disruptive behavior. *New Directions for Child and Adolescent Development*, 2020(172), 25–38. <https://doi.org/10.1002/cad.20362>
- Palma-Gudiel, H., Córdova-Palomera, A., Leza, J. C., & Fañanás, L. (2015). Glucocorticoid receptor gene (NR3C1) methylation processes as mediators of early adversity in stress-related disorders causality: A critical review. *Neuroscience and Biobehavioral Reviews*, 55, 520–535. <https://doi.org/10.1016/j.neubiorev.2015.05.016>
- Parade, S. H., Ridout, K. K., Seifer, R., Armstrong, D. A., Marsit, C. J., McWilliams, M. A., & Tyrka, A. R. (2016). Methylation of the glucocorticoid receptor gene promoter in preschoolers: Links with internalizing behavior problems. *Child Development*, 87(1), 86–97. <https://doi.org/10.1111/cdev.12484>
- Pop, V. J., Komproe, I. H., & van Son, M. J. (1992). Characteristics of the Edinburgh postnatal depression scale in The Netherlands. *Journal of Affective Disorders*, 26(2), 105–110.
- Propper, C., Willoughby, M., Halpern, C. T., Carbone, M. A., & Cox, M. (2007). Parenting quality, DRD4, and the prediction of externalizing and internalizing behaviors in early childhood. *Developmental Psychobiology*, 49(6), 619–632. <https://doi.org/10.1002/dev.20249>
- Provenzi, L., Brambilla, M., Scotto di Minico, G., Montirosso, R., & Borgatti, R. (2019). Maternal caregiving and DNA methylation in human infants and children: Systematic review. *Genes, Brain and Behavior*, 19(3), 1–11. <https://doi.org/10.1111/gbb.12616> September.
- Radtke, K. M., Schauer, M., Gunter, H. M., Ruf-Leuschner, M., Sill, J., Meyer, A., & Elbert, T. (2015). Epigenetic modifications of the glucocorticoid receptor gene are associated with the vulnerability to psychopathology in childhood maltreatment. *Translational Psychiatry*, 5(5), e571–e571. <https://doi.org/10.1038/tp.2015.63>
- Reef, J., Diamantopoulou, S., van Meurs, I., Verhulst, F., & van der Ende, J. (2009). Child to adult continuities of psychopathology: A 24-year follow-up. *Acta Psychiatrica Scandinavica*, 120(3), 230–238. <https://doi.org/10.1111/j.1600-0447.2009.01422.x>
- Roza, S. J., Hofstra, M. B., Van Der Ende, J., & Verhulst, F. C. (2003). Stable prediction of mood and anxiety disorders based on behavioral and emotional problems in childhood: A 14-year follow-up during childhood, adolescence, and young adulthood. *American Journal of Psychiatry*, 160(12), 2116–2121. <https://doi.org/10.1176/appi.ajp.160.12.2116>
- Ruttile, P. L., Shirliff, E. A., Serbin, L. A., Ben-Dat Fisher, D., Stack, D. M., & Schwartzman, A. E. (2011). Disentangling psychobiological mechanisms underlying internalizing and externalizing behaviors in youth: Longitudinal and concurrent associations with cortisol. *Hormones and Behavior*, 59(1), 123–132. <https://doi.org/10.1016/j.yhbeh.2010.10.015>
- Sánchez, B. N., Hu, H., Litman, H. J., & Téllez-rojo, M. M. (2011). Statistical methods to study timing of vulnerability with sparsely sampled data on environmental toxicants. *Environmental Health Perspectives*, 119(3), 409–415. <https://doi.org/10.1289/ehp.1002453>
- Smeekens, S., Marianne Riksen-Walraven, J., & van Bakel, H. J. A. (2007). Cortisol reactions in five-year-olds to parent-child interaction: The moderating role of ego-resiliency. *Journal of Child Psychology and Psychiatry*, 48(7), 649–656. <https://doi.org/10.1111/j.1469-7610.2007.01753.x>
- Smith, A. K., Kilaru, V., Klengel, T., Mercer, K. B., Bradley, B., Conneely, K. N., Ressler, K. J., & Binder, E. B. (2015). DNA extracted from saliva for methylation studies of psychiatric traits: Evidence tissue specificity and relatedness to brain. *American Journal of Medical Genetics, Part B: Neuropsychiatric Genetics*, 168(1), 36–44. <https://doi.org/10.1002/ajmg.b.32278>
- Solmi, M., Radua, J., Olivola, M., Croce, E., Soardo, L., Salazar de Pablo, G., Il Shin, J., Kirkbride, J. B., Jones, P., Kim, J. H., Kim, J. Y., Carvalho, A. F., Seeman, M. V., Correll, C. U., Fusar-Poli, P. (2021). Age at onset of mental disorders worldwide: Large-scale meta-analysis of 192 epidemiological studies. *Molecular Psychiatry*, 27(1), 281–295. <https://doi.org/10.1038/s41380-021-01161-7>
- Spielberger, C. D., Gorsuch, R. L., Lushene, P. R., Vagg, P. R., & Jacobs, G. A. (1983). *Manual for the state-trait anxiety inventory*. Palo Alto, CA: Consulting Psychologists Press.
- Tronick, E. Z. (1989). Emotions and emotional communication in infants. *American Psychologist*, 44(2), 112–119. <https://doi.org/10.1037/0003-066X.44.2.112>
- Turner, R. J., & Avison, W. R. (2003). Status variations in stress exposure: Implications for the interpretation of research on race. *Socioeconomic Status, and Gender. Journal of Health and Social Behavior*, 44(4), 488–505. <https://doi.org/10.2307/1519795>
- Tyrka, A. R., Ridout, K. K., & Parade, S. H. (2016). Childhood adversity and epigenetic regulation of glucocorticoid signaling genes: Associations in children and adults. *Development and Psychopathology*, 28(4pt2), 1319–1331. <https://doi.org/10.1017/S0954579416000870>
- van der Knaap, L. J., van Oort, F. V., Verhulst, F. C., Oldehinkel, A. J., & Riese, H. (2015). Methylation of NR3C1 and SLC6A4 and internalizing problems. *The TRAILS Study. Journal of Affective Disorders*, 180, 97–103. <https://doi.org/10.1016/j.jad.2015.03.056>
- van der Voort, A., Linting, M., Juffer, F., Bakermans-Kranenburg, M. J., Schoenmaker, C., & van IJzendoorn, M. H. (2014). The development of adolescents' internalizing behavior: Longitudinal effects of maternal sensitivity and child inhibition. *Journal of Youth and Adolescence*, 43(4), 528–540. <https://doi.org/10.1007/s10964-013-9976-7>
- van Hasselt, F. N., Cornelisse, S., Yuan Zhang, T., Meaney, M. J., Velzing, E. H., Krugers, H. J., & Joëls, M. (2012). Adult hippocampal glucocorticoid receptor expression and dentate synaptic plasticity correlate with maternal care received by individuals early in life. *Hippocampus*, 22(2), 255–266. <https://doi.org/10.1002/hipo.20892>
- van Oort, F. V., van der Ende, J., Wadsworth, M. E., Verhulst, F. C., & Achenbach, T. M. (2011). Cross-national comparison of the link between socioeconomic status and emotional and behavioral problems in youths. *Social Psychiatry and Psychiatric Epidemiology*, 46(2), 167–172. <https://doi.org/10.1007/s00127-010-0191-5>
- Wadji, D. L., Tandon, T., Ketcha Wanda, G. J. M., Wicky, C., Dentz, A., Hasler, G., Morina, N., & Martin-Soelch, C. (2021). Child maltreatment and NR3C1 exon 1F methylation, link with deregulated hypothalamus-pituitary-adrenal axis and psychopathology: A systematic review. *Child Abuse & Neglect*, 122(September), 105304. <https://doi.org/10.1016/j.chiabu.2021.105304>
- Wang, F., Christ, S. L., Mills-Koonce, W. R., Garrett-Peters, P., & Cox, M. J. (2013). Association between maternal sensitivity and externalizing behavior from preschool to preadolescence. *Journal of Applied Developmental Psychology*, 34(2), 89–100. <https://doi.org/10.1016/j.appdev.2012.11.003>
- Watkeys, O. J., Kremerskothen, K., Quidé, Y., Fullerton, J. M., & Green, M. J. (2018). Glucocorticoid receptor gene (NR3C1) DNA methylation in association with trauma, psychopathology, transcript expression, or genotypic variation: A systematic review. *Neuroscience & Biobehavioral Reviews*, 95(August), 85–122. <https://doi.org/10.1016/j.neubiorev.2018.08.017>
- Weaver, I. C. G., Cervoni, N., Champagne, F. A., D'Alessio, A. C., Sharma, S., Seckl, J. R., Dymov, S., Szyf, M., & Meaney, M. J. (2004). Epigenetic programming by maternal behavior. *Nature Neuroscience*, 7(8), 847–854. <https://doi.org/10.1038/nn1276>

- Weaver, I. C. G., Champagne, F. A., Brown, S. E., Dymov, S., Sharma, S., Meaney, M. J., & Szyf, M. (2005). Reversal of maternal programming of stress responses in adult offspring through methyl supplementation: Altering epigenetic marking later in life. *The Journal of Neuroscience: The Official Journal of the Society for Neuroscience*, 25(47), 11045–11054. <https://doi.org/10.1523/JNEUROSCI.3652-05.2005>
- Weaver, I. C. G., Meaney, M. J., & Szyf, M. (2006). Maternal care effects on the hippocampal transcriptome and anxiety-mediated behaviors in the offspring that are reversible in adulthood. *Proceedings of The National Academy of Sciences of The United States of America*, 103(9), 3480–3485. <https://doi.org/10.1073/pnas.0507526103>
- Weder, N., Zhang, H., Jensen, K., Yang, B. Z., Simen, A., Jackowski, A., Lipschitz, D., Douglas-Palumberi, H., Ge, M., Perepletchikova, F., O'Loughlin, K., Hudziak, J. J., Gelernter, J., Kaufman, J. (2014). Child abuse, depression, and methylation in genes involved with stress, neural plasticity, and brain circuitry. *Journal of the American Academy of Child and Adolescent Psychiatry*, 53(4), 417–424.e5. <https://doi.org/10.1016/j.jaac.2013.12.025>
- Whiteford, H. A., Degenhardt, L., Rehm, J., Baxter, A. J., Ferrari, A. J., Erskine, H. E., Charlson, F. J., Norman, R. E., Flaxman, A. D., Johns, N., Burstein, R., Murray, C. J., Vos, T. (2013). Global burden of disease attributable to mental and substance use disorders: Findings from the Global Burden of Disease Study 2010. *The Lancet*, 382(9904), 1575–1586. [https://doi.org/10.1016/S0140-6736\(13\)61611-6](https://doi.org/10.1016/S0140-6736(13)61611-6)
- Yousefi, P., Huen, K., Davé, V., Barcellos, L., Eskenazi, B., & Holland, N. (2015). Sex differences in DNA methylation assessed by 450 K BeadChip in newborns. *BMC Genomics*, 16(1), 911. <https://doi.org/10.1186/s12864-015-2034-y>