Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

eAppendix 1. MoBa genetic data generation and quality control

Genotyping in MoBa is ongoing. For the present study, we used approximately 17,000 trios from the Norwegian Mother, Father and Child cohort, genotyped in three batches. Genotypes were called using GenomeStudio (Illumina, San Diego, USA) and converted to PLINK format files. The first batch, comprising 20,664 individuals and 542,585 SNPs was genotyped at the NTNU Genomics Core Facility (Trondheim, Oslo) using the Illumina HumanCoreExome (Illumina, San Diego, USA) genotyping array, version 12 1.1. The second batch, comprising 12,874 individuals and 547,644 SNPs was genotyped at the NTNU Genomics Core Facility (Trondheim, Oslo) using the Illumina HumanCoreExome (Illumina, San Diego, USA) genotyping array, version24 1.0. The third batch, comprising 17,949 individuals and 692,367 SNPs, was genotyped at ERASMUS MC (the Netherlands) using the Illumina Global Screening Array (Illumina, San Diego, USA) version 24 1.

PLINK version 1.90 beta 3.36 (http://pngu.mgh.harvard.edu/purcell/plink/) was used to conduct the quality control, which has previously been described by Helgeland et al¹. Known problematic SNPs previously reported by the Cohorts for Heart and Aging Research in Genomic Epidemiology (CHARGE) consortium and Psychiatric Genomics Consortium (PGC) were excluded from each batch. Duplicate samples were removed, and each genotyping batch was split into parents and offspring. Quality control was then conducted by genotyping array in parents and offspring separately.

Individuals were excluded if they had a genotyping call rate below 95% or autosomal heterozygosity greater than four standard deviations from the sample mean. SNPs were excluded if they were ambiguous (A / T and C / G), had a genotyping call rate below 98%, minor allele frequency of less than 1%, or Hardy-Weinberg equilibrium P-value less than 1×10^{-6} . Population stratification was assessed, using the HapMap phase 3 release 3 as a reference, by principal component analysis using EIGENSTRAT version 6.1.4. Visual inspection identified a homogenous population of European ethnicity and individuals of non-European ethnicity were removed. Individuals with a genotyping call rate below 98% or autosomal heterozygosity greater than four standard deviations from the sample mean were then removed. A sex check was done by assessing the sex declared in the pedigree with the genetic sex, which was imputed based on the heterozygosity of chromosome X. When sex discrepancies were identified, the individual was flagged. Relatedness was assessed by flagging one individual from each pairwise comparison of identity-by-descent with a pi-hat greater than 0.1.

The parents and offspring datasets were then merged into one dataset per genotyping batch; keeping only the SNPs that passed quality control in both datasets. All individuals passing the genotyping call rate and autosomal heterozygosity measures were included in the merged datasets. Therefore, the merged datasets included individuals previously excluded or flagged as a duplicate, ethnic outlier, having a sex discrepancy, or high level of relatedness. Concordance checks were then conducted on validated duplicates. Duplicate, tri-allelic and discordant (any discordance between the validated duplicates) SNPs were excluded. Individuals and SNPs with a genotyping call rate below 98% in the merged datasets were excluded. The duplicate sample that was removed before the start of the quality control was then excluded. Mendelian errors identified by the assessment of duos and trios were then recoded to missing. Insertions and deletions were also excluded.

After QC the Human Core Exome 12 batch comprised 20,231 individuals and 384,855 SNPs, the Human Core Exome 24 batch comprised 12,757 individuals and 396,189 SNPs, and the Global Screening Array batch comprised 17,742 individuals and 568,275 SNPs. Phasing was conducted using Shapeit 2 release 837 and the duoHMM approach was used to account for the pedigree structure. Imputation was conducted using the Haplotype reference consortium (HRC) release 1-1 as the genetic reference panel. The Sanger Imputation Server was used to perform the imputation with the Positional Burrows-Wheeler Transform (PBWT). The phasing and imputation were conducted separately for each genotyping batch.

Post imputation quality control was performed by initially converting the dosages to best-guess genotypes. Individuals were removed if they had a genotyping call rate less than 99% or were of non-European ethnicity. SNPs with an imputation INFO quality score less than 0.8 (in any batch), genotyping call rate less than 98%, minor allele frequency less than 1%, or a Hardy-Weinberg equilibrium P-value less than 1×10^{-6} were removed. Mendelian errors were set to missing. Relatedness, which was accounted for within generation and genotyping batch during preimputation QC as described above, was assessed intergenerationally and across batches by flagging one individual from each pairwise comparison of identity-by-descent with a pi-hat greater than 0.15 (excepting known relationships, such as parent-offspring, full-sibling, half-sibling relationships). Individuals were flagged for removal only if the other member of their pair would otherwise be included in the same analysis. One individual from each pair was flagged at random, except when retaining one individual in a pair would keep more duo/trio data intact than the other, in which case the other member was dropped. After quality control, a core homogeneous sample of European ethnicity (based on PCA of markers overlapping with available HapMap markers) individuals across all batches and arrays were available for use in analysis (totals prior to analysis-specific exclusions for relatedness: Nchildren = 15,208; Nmothers = 14,804; Nfathers = 15,198). Additionally, participants were removed from our analysis if they had previously contributed genotype data to either the schizophrenia GWAS (as part of the TOP consortium) or ASD GWAS (as part of the BUPGen consortium).

eAppendix 2. Polygenic risk score thresholds

eTable 1a. Number of genetic variants (SNPs) included in the polygenic risk scores for attention deficit hyperactivity disorder (ADHD), autism and schizophrenia (SCZ) at specific p-value cut-offs.

eTable 1b. Correlation matrix of maternal and paternal polygenic risk scores for attention deficit hyperactivity disorder (ADHD), autism and schizophrenia (SCZ), where * = p<0.05.

eFigure 1. Histograms of maternal polygenic risk scores (n=13,898) for attention deficit hyperactivity disorder (ADHD), autism and schizophrenia (SCZ) at specific p-value thresholds as indicated on the top.

eFigure 2. Histograms of paternal polygenic risk scores (n=13,898) for attention deficit hyperactivity disorder (ADHD), autism and schizophrenia (SCZ) at specific p-value thresholds as indicated on the top.

eAppendix 3. Pregnancy-related factors

Prenatal factors were chosen after a literature review of potential adverse early life exposures that have previously been reported to be associated with neurodevelopmental conditions. We excluded all pregnancy-related factors with less than 100 cases, given that 100 cases (n_{total} =14,584 mothers) are needed to detect an odds ratio (OR) of 1.3 with 80% power and alpha 0.05. Where information on timing of the measure within pregnancy (trimester) was available, we combined them into one "during pregnancy" variable.

Phenotypes related to maternal behaviour and lifestyle during pregnancy included maternal age at delivery², cigarette smoking^{3,4}, alcohol consumption⁵, binge drinking⁶, coffee drinking and binge coffee drinking⁷, intake of nutritional supplements and intake of folate supplementation before⁸⁻¹⁰ and during pregnancy.

Phenotypes related to physical health during pregnancy included pre-pregnancy BMI and weight gain during pregnancy^{11,12}, type II diabetes (T2D) (incl. gestational diabetes)¹³, high blood pressure (incl. preeclampsia)^{13,14}, vaginal bleeding¹⁵⁻¹⁷, anaemia^{9,18}, fever¹⁹, upper and lower respiratory infections, urinary tract infections (UTI), any infection or inflammation^{20–22}, B12 insufficiency²³, type I diabetes (T1D), hypo-/hyperthyroidism⁵, asthma²⁰, psoriasis and other autoimmune diseases^{20,24–27}.

Self-reported indicators of maternal medication use during pregnancy included medication use for depression^{5,28}, depression or anxiety, epilepsy, pain (paracetamol and ibuprofen specifically), headache or migraine and fever^{5,29-33}.

A detailed list of sources for each pregnancy-related factor can be found below (Tables S2-S4). Unless otherwise specified, measures occurred during pregnancy. If the question was asked at multiple time points, then individuals were coded as 1 if they endorsed the measure at anytime point during pregnancy. For trimester specific factors we used the self-report from the respective questionnaires. Two time periods had information available in two consecutive questionnaires, which are i) "13+week" in questionnaire 1 and "13-16 week" in questionnaire 3 and ii) "29+ weeks" in questionnaire 3 and "last part of pregnancy" in questionnaire 4. To address this overlap, we collapsed both questions into one category and assigned them to the second and third trimester, respectively. Trimesters were defined as 0-12 weeks = first trimester, 13-28 weeks = second trimester and 29 + weeks = third trimester.

Information about pregnancy-related factors in mothers and fathers was obtained from selfreported questionnaire data and the Norwegian birth registry. For Tables S2-S4, self-report questionnaires are indicated as Q1, Q3, Q4 and QF. On average, mothers responded to Q1 at 15 weeks of gestation, Q3 at 30 weeks gestation and Q4 at 6 months after birth. Fathers responded to QF which was sent out alongside the 15-week questionnaire to mothers. Items from the Medical Birth Registry of Norway are indicated as MBRN.

eTable 3. Maternal variable definitions for secondary analysis: Timing during gestation

eTable 4. Paternal variable definitions

eAppendix 4. Principal Component Analysis (PCA)

A Bonferrroni correction for multiple testing would be too conservative for our analyses given the high correlation between variables, and would result in an overall alpha <5% and an inflated rate of false negative findings. Therefore, to correct for multiple testing of the 37 pregnancy-related factors, while accounting for the correlations between them, the number of independent tests was determined based on the number of principal components that explained more than 80% of covariance between the pregnancy-related factors in a principal component analysis (PCA). The 80% PCA approach was chosen to keep the overall alpha as close to 5% as possible.

An unrotated PCA was performed using the pca function in STATA 16.1 (see Table S2) and the number of PCs that explained 80% of covariance between the pregnancy-related factors was declared as independent tests. We concluded that 25 independent tests were performed in our main analysis, resulting in a multiple testing corrected p-value of p<0.002 (0.05/25). A conservative Bonferroni correction would yield a multiple testing corrected p-value of p<0.001 (0.05/37), assuming all tests to be independent.

eTable 5. Unrotated principal component analysis of 37 pregnancy related factors in 14,539 mothers of MoBa

eAppendix 5. Inverse Probability Weighting (IPW)

Genetic liability for ADHD and schizophrenia have been shown to be associated with attrition in other studies and genotyping in MoBa was originally performed on a selected subset of participants, for whom DNA samples of full mother, father, child trios was available. A comparison of the not genotyped and genotyped sample of MoBa suggested that the samples differed according to many analysed factors. Therefore, we performed IPW on missing maternal genetic data to adjust for this sampling bias (n = 80,922 missing genotype data, n = 12,564 complete genotype data). The prediction model for missingness was built using a logistic lasso approach (lassologit function from package lassopack^{1,2} in STATA 13), selecting the best fitting model (based on Bayesian Information Criterion (BIC)) from a set of 233 variables from birth registry data and MoBa questionnaire 1 at study recruitment. All prediction variables had less than 10% missing data. Weights were derived from the selected model including 32 variables (Table S3), which predicted missingness with a pseudo R^2 = 0.016. Weights ranged from 3.39 to 136.05. A sensitivity analysis using stabilised weights (and all weights greater than 10 set to 10) revealed no change to the pattern of results. Results of the IPW analysis are compared with the complete case results in Supplementary Figure S4.

Log(OR) SE p-value APGAR 5min -0.035 0.016 0.034 APGAR 1min \vert -0.037 \vert 0.012 \vert 0.002 Gestational length -0.051 | 0.007 \sim -0.001 Birthweight -0.0001 2E-05 <0.001 Paternal age at birth $\begin{array}{|c|c|c|c|c|c|c|c|c|} \hline 0.016 & 0.002 & <0.001 & \hline \end{array}$ Never been forced to have sexual intercourse \vert -0.655 \vert 0.043 \vert <0.001 Never having taken ecstasy \vert -0.061 | 0.031 | 0.051 Living with parents 1.1 and 1.272 0.099 0.006 Living with a spouse/partner -0.473 0.060 <0.001 Other long illnesses or health problems before pregnancy -0.104 0.041 0.012 Depression during pregnancy 0.174 0.073 0.018 Urinary tract infections before pregnancy -0.051 0.023 0.028 Kidney infection/ pyelonephritis before pregnancy -0.097 0.050 0.052 Other gastrointestinal problems before pregnancy \vert -0.141 \vert 0.045 \vert 0.002 Duodenal/stomach ulcer before pregnancy 0.310 0.134 0.020 Hypothyroidism or hyperthyroidism during pregnancy 0.168 0.076 0.028 Herpes (cold sores) before pregnancy \vert -0.077 | 0.029 | 0.008 Sugar in urine (weeks 9-12) 0.331 0.331 0.140 0.018 Fever with rash (weeks 0-4) 1.584 0.720 0.028 Oedema during pregnancy (weeks 13+) 0.158 | 0.054 0.004 Unusual tiredness/sleepiness (weeks 9-12) \vert -0.034 \vert 0.024 \vert 0.158 Unusual tiredness/sleepiness (weeks 5-8) \vert -0.070 \vert 0.024 \vert 0.004 Constipation during pregnancy (weeks 5-8) \vert -0.043 \vert 0.025 \vert 0.084 Itchy in pregnancy (weeks 0-4) 0.265 | 0.115 | 0.021 Nausea with vomiting (weeks 0-4) 0.091 0.039 0.018 Abdominal pain (weeks 5-8) -0.079 0.029 0.008 Pelvic pain (weeks 13+) 20080 0.034 0.019 Offspring congenital malformations $\begin{array}{|c|c|c|c|c|c|c|c|c|} \hline 0.149 & 0.049 & 0.002 \ \hline \end{array}$ Caesarean delivery $\begin{array}{|c|c|c|c|c|c|c|c|} \hline \text{Caes} & \text{O.055} & \text{$ Spontaneous delivery \vert -0.105 \vert 0.029 \vert <0.001

eTable 6. Model used to derive inverse probability weights for missingness of genotype of MoBa mothers to account for sampling bias (n=93,486, pseudo R^2 =0.016)

* Effect estimates for maternal age at birth, BMI and weight gain during pregnancy are shown as beta per 1 SD increase in PGS. Measures occurred during pregnancy unless otherwise specified. Multiple testing corrected p-value p<0.002.

eAppendix 6. Multiple Imputation (MI)

Since the pseudo r-squared of the IPW model was relatively low, we also performed chained equations multiple imputation using the *mi impute chained* command in STATA 16. We imputed all incomplete variables (n=14, see Table S8) to the total number of participants who responded at the first questionnaire (N = 86,076). One MI was conducted including all outcomes, exposures and auxiliary variables simultaneously (75 variables with n=100 iterations). As auxiliary variables, we included all variables identified to be predictive of missingness in the IPW model (n=32, Table S6) as well as all pregnancy related factors from the main analysis model. A summary of missing data which were imputed can be found in Table S8, and we assumed this data to be missing not at random. All variables were imputed in the same model using the *regress* command for continuous variables and *logit* command for binary variables. Truncated imputation was performed for gestational length (minimum 20 weeks), birthweight (minimum 500g), maternal age (minimum 16 years at childbirth), maternal ADHD symptoms (between 0 and 24), maternal BMI before pregnancy (minimum 12.5 kg/m^2) AGPAR scores (between 0 and 10). Results of the MI analysis are compared with the complete case results in Supplementary Figure S4.

eTable 9. The association between PGS for neurodevelopmental conditions and pregnancy-related factors after multiple imputation (N = 86,076)

Note. All measures occurred during pregnancy unless otherwise specified. * Effect estimates for maternal age at birth, BMI and weight gain during pregnancy are shown as beta per 1 SD increase in PGS. Multiple testing corrected p-value p<0.002.

eAppendix 7. ADHD symptom measures in adulthood in MoBa

Parental symptoms of ADHD were assessed as the sum of symptoms on the 6-item DSM-IV Adult ADHD Self-Report Scale (ASRS) at study recruitment (fathers) and at the year 3 follow-up (mothers). Of the 6 items, 4 capture inattention (e.g. "How often do you have problems remembering appointments or obligations?") and 2 capture hyperactivity (e.g. "How often do you feel overly active and compelled to do things, like you were driven by a motor?"). Responses were given on a 5-point likert scale (0 = never, 1 = rarely, 2=sometimes, 3 = often, 4 = very often), so summed scores ranged from 0-24. A cutoff of 14 can be used to suggest possible ADHD³⁴.

Statistical analysis

We regressed the standardised PGS (constructed at p-value threshold p<0.05) against ADHD symptoms in adulthood. The regression was run separately for males and females, and was adjusted for 10 principal components of population structure.

eAppendix 8. Paternal PGS sample overview and results

eTable 10. Sample overview of father pregnancy-related factors in MoBa (full cohort and genotyped cohort compared)

Note. All measures occurred during the partners pregnancy, unless otherwise specified. Multiple testing corrected p-value p<0.002.

eTable 11. Association of paternal polygenic risk scores (PGS) for attention deficit hyperactivity disorder (ADHD), autism and schizophrenia (SCZ) with pregnancy related factors measured in fathers.

Note. All measures occurred during the partners pregnancy, unless otherwise specified. * Effect estimates for paternal age at birth and BMI are shown as beta per 1 SD increase in PGS. Multiple testing corrected p-value p<0.002.

eAppendix 9. PGS associations at different p-value thresholds

eFigure 3a. Association of behaviour and lifestyle measures with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eFigure 3b. Association of metabolic conditions with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eFigure 3c. Association of autoimmune and infectious diseases with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eFigure 3d. Association of other physical health conditions with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eFigure 3e. Association of medication use (or health problems suggestive of possible medication use) with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eFigure 3f. Association of continuous measures with polygenic risk scores for ADHD, autism and schizophrenia across different p-value thresholds.

eAppendix 10. Comparison of complete case, inverse probability weighted and multiple imputation results

eFigure 4a. Associations between behaviour and lifestyle measures with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eFigure 4b. Associations between metabolic measures with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eFigure 4c. Associations between other physical health conditions with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eFigure 4d. Associations between autoimmune and infectious diseases with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eFigure 4e. Associations between indications for medication use with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eFigure 4f. Associations between continuous traits with polygenic risk scores for ADHD, autism and schizophrenia comparing results from complete case analysis, inverse probability weighting (IPW) and multiple imputation (MI).

eReferences

- 1. Helgeland Ø, Vaudel M, Juliusson PB, et al. Genome-wide association study reveals dynamic role of genetic variation in infant and early childhood growth. *Nat Commun*. 2019;10(1):4448. doi:10.1038/s41467-019-12308-0
- 2. Chang Z, Lichtenstein P, D'Onofrio BM, et al. Maternal age at childbirth and risk for ADHD in offspring: a population-based cohort study. *Int J Epidemiol*. 2014;43(6):1815-1824. doi:10.1093/ije/dyu204
- 3. Gustavson K, Ystrom E, Stoltenberg C, et al. Smoking in Pregnancy and Child ADHD. *Pediatrics*. 2017;139(2). doi:10.1542/peds.2016-2509
- 4. He Y, Chen J, Zhu L-H, Hua L-L, Ke F-F. Maternal Smoking During Pregnancy and ADHD: Results From a Systematic Review and Meta-Analysis of Prospective Cohort Studies. *J Atten Disord*. Published online March 1, 2017:1087054717696766. doi:10.1177/1087054717696766
- 5. Sciberras E, Mulraney M, Silva D, Coghill D. Prenatal Risk Factors and the Etiology of ADHD-Review of Existing Evidence. *Curr Psychiatry Rep*. 2017;19(1):1. doi:10.1007/s11920-017-0753- 2
- 6. Sayal K, Heron J, Draper E, et al. Prenatal exposure to binge pattern of alcohol consumption: mental health and learning outcomes at age 11. *Eur Child Adolesc Psychiatry*. 2014;23(10):891- 899. doi:10.1007/s00787-014-0599-7
- 7. Linnet KM, Wisborg K, Secher NJ, et al. Coffee consumption during pregnancy and the risk of hyperkinetic disorder and ADHD: a prospective cohort study. *Acta Paediatr Oslo Nor 1992*. 2009;98(1):173-179. doi:10.1111/j.1651-2227.2008.00980.x
- 8. Desai A, Sequeira JM, Quadros EV. The metabolic basis for developmental disorders due to defective folate transport. *Biochimie*. 2016;126:31-42. doi:10.1016/j.biochi.2016.02.012
- 9. Meli G, Ottl B, Paladini A, Cataldi L. Prenatal and perinatal risk factors of schizophrenia. *J Matern-Fetal Neonatal Med Off J Eur Assoc Perinat Med Fed Asia Ocean Perinat Soc Int Soc Perinat Obstet*. 2012;25(12):2559-2563. doi:10.3109/14767058.2012.699118
- 10. Surén P, Roth C, Bresnahan M, et al. Association between maternal use of folic acid supplements and risk of autism spectrum disorders in children. *JAMA*. 2013;309(6):570-577. doi:10.1001/jama.2012.155925
- 11. Martins-Silva T, Vaz JDS, Hutz MH, et al. Assessing causality in the association between attention-deficit/hyperactivity disorder and obesity: a Mendelian randomization study. *Int J Obes 2005*. 2019;43(12):2500-2508. doi:10.1038/s41366-019-0346-8
- 12. Van Lieshout RJ, Taylor VH, Boyle MH. Pre-pregnancy and pregnancy obesity and neurodevelopmental outcomes in offspring: a systematic review. *Obes Rev*. 2011;12(5):e548 e559. doi:10.1111/j.1467-789X.2010.00850.x
- 13. Wang C, Geng H, Liu W, Zhang G. Prenatal, perinatal, and postnatal factors associated with autism: A meta-analysis. *Medicine (Baltimore)*. 2017;96(18):e6696. doi:10.1097/MD.0000000000006696
- 14. Dachew BA, Scott JG, Mamun A, Alati R. Pre-eclampsia and the risk of attentiondeficit/hyperactivity disorder in offspring: Findings from the ALSPAC birth cohort study. *Psychiatry Res*. 2019;272:392-397. doi:10.1016/j.psychres.2018.12.123
- 15. Hoirisch-Clapauch S, Nardi AE. Autism spectrum disorders: let's talk about glucose? *Transl Psychiatry*. 2019;9(1):51. doi:10.1038/s41398-019-0370-4
- 16. Gardener H, Spiegelman D, Buka SL. Prenatal risk factors for autism: comprehensive metaanalysis. *Br J Psychiatry J Ment Sci*. 2009;195(1):7-14. doi:10.1192/bjp.bp.108.051672
- 17. Milberger S, Biederman J, Faraone SV, Guite J, Tsuang MT. Pregnancy, delivery and infancy complications and attention deficit hyperactivity disorder: issues of gene-environment interaction. *Biol Psychiatry*. 1997;41(1):65-75. doi:10.1016/0006-3223(95)00653-2
- 18. Wiegersma AM, Dalman C, Lee BK, Karlsson H, Gardner RM. Association of Prenatal Maternal Anemia With Neurodevelopmental Disorders. *JAMA Psychiatry*. Published online September 18, 2019:1-12. doi:10.1001/jamapsychiatry.2019.2309
- 19. Hornig M, Bresnahan MA, Che X, et al. Prenatal fever and autism risk. *Mol Psychiatry*. 2018;23(3):759-766. doi:10.1038/mp.2017.119
- 20. Instanes JT, Halmøy A, Engeland A, Haavik J, Furu K, Klungsøyr K. Attention-Deficit/Hyperactivity Disorder in Offspring of Mothers With Inflammatory and Immune System Diseases. *Biol Psychiatry*. 2017;81(5):452-459. doi:10.1016/j.biopsych.2015.11.024
- 21. Jiang H-Y, Xu L-L, Shao L, et al. Maternal infection during pregnancy and risk of autism spectrum disorders: A systematic review and meta-analysis. *Brain Behav Immun*. 2016;58:165- 172. doi:10.1016/j.bbi.2016.06.005
- 22. Werenberg Dreier J, Nybo Andersen A-M, Hvolby A, Garne E, Kragh Andersen P, Berg-Beckhoff G. Fever and infections in pregnancy and risk of attention deficit/hyperactivity disorder in the offspring. *J Child Psychol Psychiatry*. 2016;57(4):540-548. doi:10.1111/jcpp.12480
- 23. Dror DK, Allen LH. Interventions with vitamins B6, B12 and C in pregnancy. *Paediatr Perinat Epidemiol*. 2012;26 Suppl 1:55-74. doi:10.1111/j.1365-3016.2012.01277.x
- 24. Chen M-H, Su T-P, Chen Y-S, et al. Comorbidity of Allergic and Autoimmune Diseases Among Patients With ADHD: A Nationwide Population-Based Study. *J Atten Disord*. 2017;21(3):219- 227. doi:10.1177/1087054712474686
- 25. Chen S-W, Zhong X-S, Jiang L-N, et al. Maternal autoimmune diseases and the risk of autism spectrum disorders in offspring: A systematic review and meta-analysis. *Behav Brain Res*. 2016;296:61-69. doi:10.1016/j.bbr.2015.08.035
- 26. Rom AL, Wu CS, Olsen J, Jawaheer D, Hetland ML, Mørch LS. Parental Rheumatoid Arthritis and Autism Spectrum Disorders in Offspring: A Danish Nationwide Cohort Study. *J Am Acad Child Adolesc Psychiatry*. 2018;57(1):28-32.e1. doi:10.1016/j.jaac.2017.10.002
- 27. Wu S, Ding Y, Wu F, et al. Family history of autoimmune diseases is associated with an increased risk of autism in children: A systematic review and meta-analysis. *Neurosci Biobehav Rev*. 2015;55:322-332. doi:10.1016/j.neubiorev.2015.05.004
- 28. Clements CC, Castro VM, Blumenthal SR, et al. Prenatal antidepressant exposure is associated with risk for attention-deficit hyperactivity disorder but not autism spectrum disorder in a large health system. *Mol Psychiatry*. 2015;20(6):727-734. doi:10.1038/mp.2014.90
- 29. Bauer AZ, Kriebel D, Herbert MR, Bornehag C-G, Swan SH. Prenatal paracetamol exposure and child neurodevelopment: A review. *Horm Behav*. 2018;101:125-147. doi:10.1016/j.yhbeh.2018.01.003
- 30. Stergiakouli E, Thapar A, Davey Smith G. Association of Acetaminophen Use During Pregnancy With Behavioral Problems in Childhood: Evidence Against Confounding. *JAMA Pediatr*. 2016;170(10):964-970. doi:10.1001/jamapediatrics.2016.1775
- 31. Brandlistuen RE, Ystrom E, Nulman I, Koren G, Nordeng H. Prenatal paracetamol exposure and child neurodevelopment: a sibling-controlled cohort study. *Int J Epidemiol*. 2013;42(6):1702- 1713. doi:10.1093/ije/dyt183
- 32. Liew Z, Ritz B, Rebordosa C, Lee P-C, Olsen J. Acetaminophen use during pregnancy, behavioral problems, and hyperkinetic disorders. *JAMA Pediatr*. 2014;168(4):313-320. doi:10.1001/jamapediatrics.2013.4914
- 33. Gustavson K, Ystrom E, Ask H, et al. Acetaminophen use during pregnancy and offspring attention deficit hyperactivity disorder – a longitudinal sibling control study. *JCPP Adv*. 2021;1(2):e12020. doi:10.1002/jcv2.12020
- 34. Kessler RC, Adler L, Ames M, et al. The World Health Organization Adult ADHD Self-Report Scale (ASRS): a short screening scale for use in the general population. *Psychol Med*. 2005;35(2):245-256. doi:10.1017/s0033291704002892