

**Supplemental Table S8.** Variant Analysis Results of Neurotransmitter, Forebrain Development and Collagen Genes.

| rsID        | Gene     | Type of Mutation | Ref Allele | Presumptive Risk Allele | Biological Impact of Variant   | Ref.      | FASD Cohort Risk Allele Count Frequency | Thousand Genomes Risk Allele Count (Frequency) | PolyPhen / Sift Prediction    | CADD PHRED Score | Statistic | p-Value                 | Passed Benjamini-Hochberg Threshold | Risk or Resilience |
|-------------|----------|------------------|------------|-------------------------|--|-----------|---|--|-------------------------------|------------------|-----------|-------------------------|-------------------------------------|--------------------|
| rs145379118 | ARNT2    | Missense         | G          | T                       | T allele has Probably damaging PolyPhen and damaging SIFT and CADD scores  | -         | 1/46 (0.02)                             | 14/10016 (1.4×10 <sup>-3</sup> )               | Probably Damaging /           | 23.3             | 325       | 2.67×10 <sup>-71</sup>  | Yes                                 | Risk               |
| rs1064583   | COL10A1* | Missense         | A          | G                       | G allele predicted to affect protein structure and splicing  | [121]     | 12/46 (0.26)                            | 44462/10016 (0.44)                             | Damaging Benign / Tolerated   | 12.91            | 6.34      | 4.00×10 <sup>-2</sup>   | No                                  | Resilience         |
| rs200235459 | COL10A1* | Missense         | C          | G                       | G allele has damaging PolyPhen and CADD predictions  | -         | 6/46 (0.13)                             | 2/10016 (2×10 <sup>-4</sup> )                  | Damaging / Tolerated          | 19.07            | 1426.96   | 1.38×10 <sup>-310</sup> | Yes                                 | Risk               |
| rs1635553   | COL2A1*  | Silent           | A          | G                       | G allele associated with hip osteoarthritis  | [122]     | 11/46 (0.24)                            | 4836/10016 (0.48)                              | NA / NA                       | 0.047            | 10.9      | 4.00×10 <sup>-3</sup>   | Yes                                 | Resilience         |
| rs2070739   | COL2A1*  | Missense         | C          | T                       | T allele associated with intervertebral disc degeneration and brain and eye congenital toxoplasmosis defects                           | [123,124] | 14/46 (0.30)                            | 1712/10016 (0.17)                              | Probably Damaging / Damaging  | 31               | 7.25      | 2.60×10 <sup>-2</sup>   | No                                  | Risk               |
| rs34392760  | COL2A1*  | Missense         | T          | A                       | A allele has a probably damaging PolyPhen and damaging CADD score  | -         | 1/46 (0.02)                             | 180/10016 (0.018)                              | Probably Damaging / Tolerated | 19.11            | 26.2      | 2.10×10 <sup>-6</sup>   | Yes                                 | Risk               |
| rs6271      | DBH*     | Missense         | C          | T                       | T allele is predicted to alter protein structure, synthensis and activity, and associated with bipolar disorder, schizophrenia and IBD | [125-129] | 1/46 (0.02)                             | 208/10016 (0.02)                               | Probably Damaging / Tolerated | 19.21            | 22.5      | 1.31×10 <sup>-5</sup>   | Yes                                 | Risk               |
| rs4531      | DBH*     | Missense         | G          | T                       | T allele associated with IBD and decreases in enzyme secretion and activity  | [126,127] | 2/46 (0.04)                             | 654/10016 (0.07)                               | Benign / Tolerated            | 1.27             | 6.55      | 4.00×10 <sup>-2</sup>   | No                                  | Resilience         |
| rs6275      | DRD2*    | Silent           | A          | A                       | A allele is associated with a reduction in DRD2 expression, alcohol use disorder and disk displacement                                 | [130-132] | 11/46 (0.24)                            | 4724/10016 (0.47)                              | NA / NA                       | 0.036            | 10.09     | 6.00×10 <sup>-3</sup>   | Yes                                 | Resilience         |
| rs936462    | DRD4     | Upstream         | G          | A                       | A allele is associated with heroin addiction   | [133]     | 20/46 (0.43)                            | 8906/10016 (0.88)                              | NA / NA                       | 2.94             | 97.33     | 7.32×10 <sup>-22</sup>  | Yes                                 | Resilience         |

|             |                |          |   |   |  |           |              |                                 |                      |       |        |                         |     |            |
|-------------|----------------|----------|---|---|--|-----------|--------------|---------------------------------|----------------------|-------|--------|-------------------------|-----|------------|
| rs747302    | <i>DRD4</i>    | Upstream | G | C | C allele is associated reduced expression, ADHD, schizophrenia and heroin/opiate dependence and addiction            | [134-138] | 1/46 (0.02)  | 4580/10016 (0.45)               | NA / NA              | 6.77  | 35.04  | $2.46 \times 10^{-8}$   | Yes | Resilience |
| rs199815231 | <i>DRD4</i>    | Missense | G | A | A allele has damaging PolyPhen, SIFT and CADD scores   | -         | 1/46 (0.02)  | 4/10016 ( $4 \times 10^{-4}$ )  | Damaging / Damaging  | 24.4  | 872.33 | $3.77 \times 10^{-190}$ | Yes | Risk       |
| rs1800044   | <i>HTR1A</i> * | Missense | C | A | A allele associated with loss of signal transduction, major depression and Tourette's Syndrome                       | [139-140] | 1/46 (0.02)  | 28/10016 ( $2 \times 10^{-3}$ ) | Damaging / Tolerated | 23.6  | 171.8  | $4.95 \times 10^{-38}$  | Yes | Risk       |
| rs6303      | <i>HTR1E</i>   | Missense | C | T | T allele has damaging PolyPhen and CADD score  | -         | 1/46 (0.02)  | 10/10016 ( $1 \times 10^{-3}$ ) | Damaging / Tolerated | 23.1  | 434.46 | $4.56 \times 10^{-95}$  | Yes | Risk       |
| rs3125      | <i>HTR2A</i>   | 3'UTR    | C | G | G allele associated with schizophrenia and depression  | [141-143] | 11/46 (0.24) | 1262/10016 (0.13)               | NA / NA              | 0.1   | 7.82   | $2.00 \times 10^{-2}$   | Yes | Risk       |
| rs6313      | <i>HTR2A</i>   | Silent   | G | G | G allele associated with reduced expression, poor mental health, OCD, schizophrenia, alcohol consumption and relapse | [144-148] | 41/46 (0.89) | 5596/10016 (0.56)               | NA / NA              | 6.52  | 20.59  | $3.38 \times 10^{-5}$   | Yes | Risk       |
| rs17116138  | <i>HTR3B</i> * | Missense | G | A | A allele results in less expression of HTR3B   | [149]     | 2/46 (0.04)  | 454/10016 (0.045)               | Benign / Tolerated   | 13.17 | 9.54   | $8.50 \times 10^{-3}$   | Yes | Resilience |
| rs73183412  | <i>HTR3D</i>   | Missense | C | G | G allele has damaging PolyPhen, SIFT and CADD scores   | -         | 5/46 (0.11)  | 614/10016 (0.0613)              | Damaging / Damaging  | 16.96 | 8.43   | $1.50 \times 10^{-2}$   | Yes | Risk       |
| rs1800883   | <i>HTR5A</i> * | 3' UTR   | G | G | G allele associated with bipolar disorder, depression, schizophrenia and borderline personality disorder             | [150-152] | 35/46 (0.76) | 5486/10016 (0.54)               | NA / NA              | 6.91  | 8.42   | $1.40 \times 10^{-2}$   | Yes | Risk       |

\*Directly regulated by retinoic acid