**Twin Research and Human Genetics**

**Supplementary material**

**Epigenome-wide association study of aggressive behavior**

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**Supplementary Figures and Tables**

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**Supplementary Figure S1:** Distribution of aggression scores in the EWAS.



**Supplementary Figure S2:** Scatterplots for the two top CpGs. Residual aggression scores are plotted against methylation level.

**Supplementary Table S1:** Sex and Age and Effects on Aggression

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | *N* | Intercept | Beta age (standardized beta)A | Robust *SE* age | *P* value age | Beta sex (standardized beta)B | Robust SE sex | *p* value sex |
| Survey 8 | 14,173 | 3.49 | -0.03 (0.01 SD) | 0.0017 | 4.19E-81 | 0.48 (0.15 SD) | 0.05 | 9.60E-19 |
| Survey 10 | 15,535 | 3.26 | -0.03 (0.01 SD) | 0.0017 | 2.37E-72 | 0.46 (0.15 SD) | 0.05 | 2.26E-20 |

Note: Estimates from a generalized estimation equation (GEE) model with ASR aggression score as outcome and age and sex as predictors. AChange in aggression score associated with a one year increase of age. The value between brackets (standardized beta) represents the effect expressed relative to the standard deviation of aggression score in the entire study sample. BDifference in aggression scores between the sexes (women minus men). The value between brackets (standardized beta) represents the effect expressed relative to the standard deviation of aggression score in the entire study sample.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|   | B | jack SE | jack T | jack P |
| (Intercept) | 1.020733 | 0.012342 | 82.70206 | 0 |
| Mean methylation level | -0.03733 | 0.010074 | -3.70617 | 0.00021 |
| *SD* methylation level | 0.546277 | 0.207655 | 2.6307 | 0.008521 |
| Downstream region | 0.009512 | 0.01956 | 0.486281 | 0.626768 |
| Gene body | 0.01138 | 0.007546 | 1.507976 | 0.131561 |
| Proximal promotor | 0.040094 | 0.008323 | 4.817295 | 1.46E-06 |
| Distal promotor | 0.006778 | 0.0132 | 0.513502 | 0.6076 |
| CpG island (CGI) | 0.004634 | 0.007114 | 0.651411 | 0.514781 |
| CGI shelf | -0.00259 | 0.008718 | -0.29693 | 0.766517 |
| CGI shore | -0.0047 | 0.006976 | -0.67422 | 0.500168 |
| DNase I hypersensitive site | 0.023931 | 0.005261 | 4.548676 | 5.40E-06 |
| Aggression loci | 0.036608 | 0.067437 | 0.542851 | 0.587232 |

**Supplementary Table S2:** Jackknife Estimates for the Regression of EWAS Test Statistics on Genomic Annotation Categories