*Appendix A.* Summary of Subjects with Available Data used in Analyses.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Subject Grouping | | Total | 1 Sleep State Data Used in Analyses | 2 CSF *5-HIAA* Data Used in Analyses | 3Weight Data Used in Analyses | 4 *5HTT* Genotype Data Used in Analyses | | |
| Total | Homozygous *LL* | Heterozygous *Ls* |
| All Subjects | | 287 | 267 | 176 | 262 | 217 | 174 | 43 |
| Neglect Status | |  |  |  |  |  |  |  |
|  | Non-neglected Nursery-Reared | 271 | 255 | 165 | 251 | 209 | 168\* | 41\* |
|  | Neglected Nursery-Reared | 16 | 12 | 11 | 11 | 8 | 6\* | 2\* |
| *5HTT* Genotype | |  |  |  |  |  |  |  |
|  | Total | 217 | 203 | 130 | 200 | - | - | - |
|  | Homozygous *LL* | 174 | 162 | 103 | 160 | - | - | - |
|  | Heterozygous *Ls* | 43 | 41 | 27 | 40 | - | - | - |
| Subjects with no missing data | | 116 | 116 | 116 | 116 | 116 | 91 | 25 |

*Note:* The table summarizes the number of subjects that had available data for each variable used in analyses. There were 287 unique subjects that were included in at least one analysis. Sex and birthyear cohort are not shown on the table because no subjects were missing these data.

1Some sleep data are missing in a few subjects either because the subject had received anesthesia, technical staff were not available, or the subject was ill.

2A large number of the infants’ CSF data are missing, largely because of the small size of the entry point into the cistern. When CSF was collected, if the sample could not be safely obtained after two attempts, the protocol prevented further attempts. In other cases, the CSF obtained was contaminated by blood or the volume was too small to accurately measure CSF *5-HIAA* concentrations.

3Some subjects’ weight data were not obtained if the subject was ill, and in some cases the scales malfunctioned on the day of weighing. In a few cases, the weight recorded appeared to be an error, as indicated by extreme outliers in that subject’s measurements.

4Genotypes were only obtained if subjects remained in the laboratory past one year. In a few cases, technical difficulties prevented genotyping a subject.

\* The asterisks indicate a Pearson Chi Squared Test of Independence was performed for these cells. The analysis of *5HTT* genotype distribution showed that the frequency of genotypes were equally distributed between neglected and non-neglected nursery-reared subjects (χ2 = 0.14, *p* = .71).