DSDR | DATA SHARING FOR DEMOGRAPHIC RESEARCH

ICPSR 27031

National Longitudinal Study of Adolescent Health (Add Health), 1994-2008: Wave III DNA [Restricted Use]

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Codebook

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Variable Description and Frequencies

Note: Frequencies displayed for the variables are not weighted. They are purely descriptive and may not be representative of the study population. Please review any sampling or weighting information available with the study.

Summary statistics (minimum, maximum, mean, median, and standard deviation) may not be available for every variable in the codebook. Conversely, a listing of frequencies in table format may not be present for every variable in the codebook either. However, all variables in the dataset are present and display sufficient information about each variable. These decisions are made intentionally and are at the discretion of the archive producing this codebook.

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AID — RESPONDENT IDENTIFIER

Location: 1-8 (width: 8; decimal: 0)

Variable Type: character

Based upon 2574 valid cases out of 2574 total cases.

DAT1A — DOPAMINE TRANSPORTER-DAT1-ALLELE A

Location: 9-12 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	12	0.5 %
10R	1555	60.4 %
6R	1	0.0 %
7R	13	0.5 %
8R	20	0.8 %
9R	973	37.8 %

Based upon 2574 valid cases out of 2574 total cases.

DAT1B — DOPAMINE TRANSPORTER-DAT1-ALLELE B

Location: 13-16 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	12	0.5 %
10R	2386	92.7 %
11R	45	1.7 %
8R	5	0.2 %
9R	126	4.9 %

Based upon 2574 valid cases out of 2574 total cases.

DRD4A — DOPAMINE RECEPTOR-DRD4-ALLELE A

Location: 17-20 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	15	0.6 %
2R	412	16.0 %
3R	136	5.3 %

Value	*Unweighted Frequency*	*%*
4R	1865	72.5 %
5R	15	0.6 %
6R	5	0.2 %
7R	126	4.9 %

Based upon 2574 valid cases out of 2574 total cases.

DRD4B **DOPAMINE RECEPTOR-DRD4-ALLELE B**

Location: 21-24 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	15	0.6 %
10R	8	0.3 %
2R	31	1.2 %
3R	16	0.6 %
4R	1449	56.3 %
5R	56	2.2 %
6R	34	1.3 %
7R	914	35.5 %
8R	48	1.9 %
9R	3	0.1 %

Based upon 2574 valid cases out of 2574 total cases.

HTTLPRA **SEROTONIN TRANSPORTER-5HTTLPR-ALLELE A**

Location: 25-25 (width: 1; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	16	0.6 %
L	862	33.5 %
S	1696	65.9 %

Based upon 2574 valid cases out of 2574 total cases.

HTTLPRB **SEROTONIN TRANSPORTER-5HTTLPR-ALLELE B**

Location: 26-26 (width: 1; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	16	0.6 %
L	2049	79.6 %
S	509	19.8 %

Based upon 2574 valid cases out of 2574 total cases.

MAOA_VA **MONOAMINE OXIDASE A-uVNTR-ALLELE A**

Location: 27-30 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	35	1.4 %
2R	45	1.7 %
3.5R	28	1.1 %
3R	1283	49.8 %
4R	1167	45.3 %
5R	16	0.6 %

Based upon 2574 valid cases out of 2574 total cases.

MAOA_VB **MONOAMINE OXIDASE A-uVNTR-ALLELE B**

Location: 31-34 (width: 4; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	35	1.4 %
2R	14	0.5 %
3.5R	17	0.7 %
3R	733	28.5 %
4R	1730	67.2 %
5R	45	1.7 %

Based upon 2574 valid cases out of 2574 total cases.

CYP2A6A **CYTOCHROME P450 2A6-ALLELE A**

Location: 35-35 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	2555	99.3 %
. (M)	19	0.7 %

Based upon 2555 valid cases out of 2574 total cases.

- Mean: 1.00
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 1.00
- Standard Deviation: 0.00

CYP2A6B **CYTOCHROME P450 2A6-ALLELE B**

Location: 36-36 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	2437	94.7 %
2	118	4.6 %
. (M)	19	0.7 %

Based upon 2555 valid cases out of 2574 total cases.

- Mean: 1.05
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 2.00
- Standard Deviation: 0.21

DRD2A **DOPAMINE D2 RECEPTOR-TAQIA-ALLELE A**

Location: 37-38 (width: 2; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	17	0.7 %
A1	201	7.8 %
A2	2356	91.5 %

Based upon 2574 valid cases out of 2574 total cases.

DRD2B **DOPAMINE D2 RECEPTOR-TAQIA-ALLELE B**

Location: 39-40 (width: 2; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	17	0.7 %

Value	*Unweighted Frequency*	*%*
A1	1162	45.1 %
A2	1395	54.2 %

Based upon 2574 valid cases out of 2574 total cases.

S000001A **rs2304297 - ALLELE A**

Location: 41-41 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
2	2017	78.4 %
3	351	13.6 %
. (M)	206	8.0 %

Based upon 2368 valid cases out of 2574 total cases.

- Mean: 2.15
- Median: 2.00
- Mode: 2.00
- Minimum: 2.00
- Maximum: 3.00
- Standard Deviation: 0.36

S000001B **rs2304297 - ALLELE B**

Location: 42-42 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
2	1087	42.2 %
3	1281	49.8 %
. (M)	206	8.0 %

Based upon 2368 valid cases out of 2574 total cases.

- Mean: 2.54
- Median: 3.00
- Mode: 3.00
- Minimum: 2.00
- Maximum: 3.00
- Standard Deviation: 0.50

S000002A **rs892413 - ALLELE A**

Location: 43-43 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	2127	82.6 %
2	319	12.4 %
. (M)	128	5.0 %

Based upon 2446 valid cases out of 2574 total cases.

- Mean: 1.13
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 2.00
- Standard Deviation: 0.34

S000002B **rs892413 - ALLELE B**

Location: 44-44 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	1218	47.3 %
2	1228	47.7 %
. (M)	128	5.0 %

Based upon 2446 valid cases out of 2574 total cases.

- Mean: 1.50
- Median: 2.00
- Mode: 2.00
- Minimum: 1.00
- Maximum: 2.00
- Standard Deviation: 0.50

S000003A **rs4950 - ALLELE A**

Location: 45-45 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	1172	45.5 %
3	1245	48.4 %
. (M)	157	6.1 %

Based upon 2417 valid cases out of 2574 total cases.

- Mean: 2.03
- Median: 3.00
- Mode: 3.00
- Minimum: 1.00
- Maximum: 3.00
- Standard Deviation: 1.00

S000003B **rs4950 - ALLELE B**

Location: 46-46 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	2088	81.1 %
3	329	12.8 %
. (M)	157	6.1 %

Based upon 2417 valid cases out of 2574 total cases.

- Mean: 1.27
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 3.00
- Standard Deviation: 0.69

S000004A **rs13280604 - ALLELE A**

Location: 47-47 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	1119	43.5 %
3	1179	45.8 %
. (M)	276	10.7 %

Based upon 2298 valid cases out of 2574 total cases.

- Mean: 2.03
- Median: 3.00
- Mode: 3.00
- Minimum: 1.00
- Maximum: 3.00
- Standard Deviation: 1.00

S000004B **rs13280604 - ALLELE B**

Location: 48-48 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	1942	75.4 %
3	356	13.8 %
. (M)	276	10.7 %

Based upon 2298 valid cases out of 2574 total cases.

- Mean: 1.31
- Median: 1.00
- Mode: 1.00
- Minimum: 1.00
- Maximum: 3.00
- Standard Deviation: 0.72

DNA2 **DNA BASED ZYGOSITY**

Location: 49-49 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
1	308	12.0 %
2	412	16.0 %
. (M)	1854	72.0 %

Based upon 720 valid cases out of 2574 total cases.

- Mean: 1.57
- Median: 2.00
- Mode: 2.00
- Minimum: 1.00
- Maximum: 2.00
- Standard Deviation: 0.50

CONCORD **CONCORDANCE OF 12 ZYGOSITY MARKERS**

Location: 50-56 (width: 7; decimal: 0)

Variable Type: character

Value	*Unweighted Frequency*	*%*
	1854	72.0 %
0/12	2	0.1 %
1/12	14	0.5 %
11/11	38	1.5 %

Value	*Unweighted Frequency*	*%*
11/12	2	0.1 %
12/12	268	10.4 %
2/11	2	0.1 %
2/12	36	1.4 %
2/8	2	0.1 %
3/11	6	0.2 %
3/12	62	2.4 %
3/8	6	0.2 %
4/11	8	0.3 %
4/12	78	3.0 %
5/12	78	3.0 %
6/12	66	2.6 %
7/11	4	0.2 %
7/12	36	1.4 %
8/12	12	0.5 %

Based upon 2574 valid cases out of 2574 total cases.

ZYGCHG **ZYGOSITY CHANGED-BASED ON SALIVA TEST**

Location: 57-57 (width: 1; decimal: 0)

Variable Type: numeric

Value	*Unweighted Frequency*	*%*
0	654	25.4 %
1	66	2.6 %
. (M)	1854	72.0 %

Based upon 720 valid cases out of 2574 total cases.

- Mean: 0.09
- Median: 0.00
- Mode: 0.00
- Minimum: 0.00
- Maximum: 1.00
- Standard Deviation: 0.29