

Data supplement

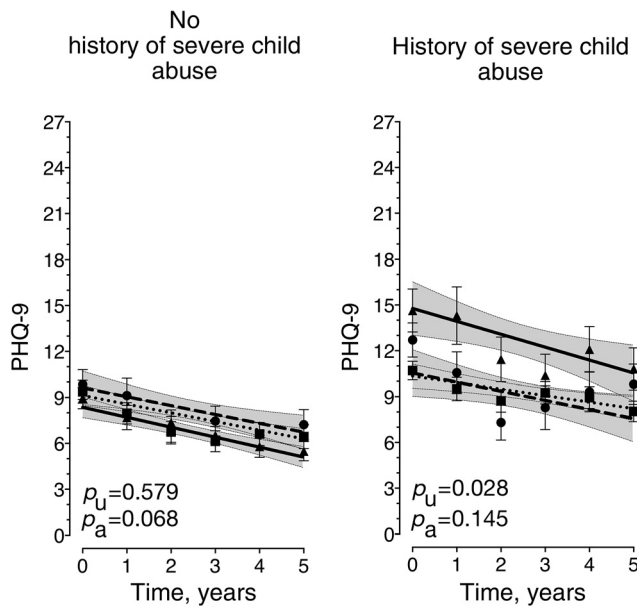
Table DS1 Ancestry informative markers by HapMap population		
CEU	CHB	YRI
rs1402851	rs10488619	rs1368928
rs16877243	rs11098964	rs1446959
rs1698042	rs11184898	rs1494962
rs2930125	rs11203006	rs1563382
rs2934193	rs1347201	rs2388511
rs3912537	rs1488299	rs4241398
rs4484738	rs1519260	rs7158302
rs4653130	rs1538956	rs10933921
rs4721415	rs315280	rs1444893
rs6510332	rs36110	rs1716167
rs1001484	rs5753625	rs1811510
rs6552216	rs6595142	rs1823778
rs1002587	rs12595448	rs1827950
rs10879311	rs12644851	rs1894450
rs1227647	rs2416504	rs2220128
rs12678324	rs2486448	rs2416791
rs1986420	rs2927385	rs2948905
rs2759281	rs4240793	rs4737761
rs326626	rs4265409	rs6785846
rs6141319	rs590614	rs692713

CEU, Northern and Western European in Utah; CHB, Han Chinese in Beijing; YRI, Yoruba in Ibadan, Nigeria.

Table DS2 Parameter estimates for terms included in the unadjusted linear mixed model		
Parameter	F	P
Intercept	710.41	<0.001
Time	53.57	<0.001
Severe childhood abuse	10.40	<0.001
Genotype	2.73	0.067
Genotype × severe childhood abuse	3.28	0.039
Severe childhood abuse × time	0.13	0.909
Genotype × time	1.21	0.299
Genotype × severe childhood abuse × time	0.31	0.734

Table DS3 Parameter estimates for terms included in the final covariate adjusted linear mixed model		
Parameter	F	P
Intercept	252.00	<0.001
Time	30.30	<0.001
Severe childhood abuse	1.40	0.237
Genotype	2.90	0.090
Genotype × severe childhood abuse	3.10	0.047
Severe childhood abuse × time	1.80	0.167
Genotype × time	0.01	0.929
Genotype × severe childhood abuse × time	0.55	0.578
Gender	9.20	0.003
Gender × genotype	4.80	0.009
Sedative use	0.24	0.628
Sedative use × genotype	2.90	0.054
Self-rated health	30.70	<0.001
Self-rated health × time	6.50	0.011
Substance abuse (other than alcohol)	5.90	0.015
WHOQOL-BREF social	167.50	<0.001
WHOQOL-BREF social × genotype	3.20	0.041

WHOQOL-BREF, World Health Organization Quality of Life and Functioning.



**Fig. DS1** Longitudinal measurements of depressive symptoms over 5 years by history of severe child abuse and 5HTTLPR.

Points are observed mean PHQ-9 scores with standard error bars. Lines are predicted values with 95% confidence intervals shaded based on linear mixed model analysis. Solid line/triangles, s/s genotype; dotted line/squares, s/l genotype; dashed line/circles, l/l genotype; PHQ-9, Primary Care Evaluation of Mental Disorders Patient Health Questionnaire-9;  $p_U$ , covariate-unadjusted P-value;  $p_a$ , covariate-adjusted P-value. P-values based on estimated marginal means