Table A. Results from hierarchal regression (interaction) analyses including only participants who identified as Caucasian (n = 118).

Variable	*F*	(Δ)R^2	Beta	SE	*t*	P-value
Step 1	3.18	.029				.08
(Constant)			3.44	.29	11.95	.00
Age			-.02	.01	-1.78	.08
Step 2	1.45	.026				.24
5-HTTLPR			.21	.15	1.40	.16
BDNF			.17	.18	.96	.34
Step 3	2.27	.020				.14
5-HTTLPR x BDNF			.39	.26	1.51	.14
Step 2	1.31	.023				.27
5-HTTLPR			.23	.14	1.60	.11
COMT			-.03	.15	-.17	.86
Step 3	.04	.000				.84
5-HTTLPR x COMT			-.04	.21	-.21	.84
Step 2	.47	.009				.62
BDNF			.17	.18	.96	.34
COMT			-.03	.16	-.18	.86
Step 3	.02	.000				.88
BDNF x COMT			-.04	.28	-.15	.88

Notes. Betas presented above are unstandardized, and p-values are two-tailed. Since each regression analysis was intended to test a distinct hypothesis, these analyses were conducted separately to preserve degrees of freedom. However, the results from Step 1 are presented only once given that all of the predictors in this step were the same across all three of these analyses.

Table B. Contingency table showing combinations of 5-HTTLPR and *BDNF* genotypes.

	BDNF val-val	*BDNF* val-met	*BDNF* met-met
5-HTTLPR long-long	24	20	1
5-HTTLPR long-short	45	35	5
5-HTTLPR short-short	22	16	3

Notes. Given the relatively low number of *BDNF* met-met participants (which was expected), we also conducted exploratory analyses in which we combined the val-met and met-met participants into a single group, as has been done in some previous research on this polymorphism (e.g., Wells et al., 2010). The interaction results from these analyses were quite consistent with our main findings, but predictably not quite as strong ($B = .19$, $p = .07$).