

Supplementary Information

A Common *CDH13* Variant is Associated with Low Agreeableness and Neural Responses to Working Memory Tasks in ADHD

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Cycling conditions

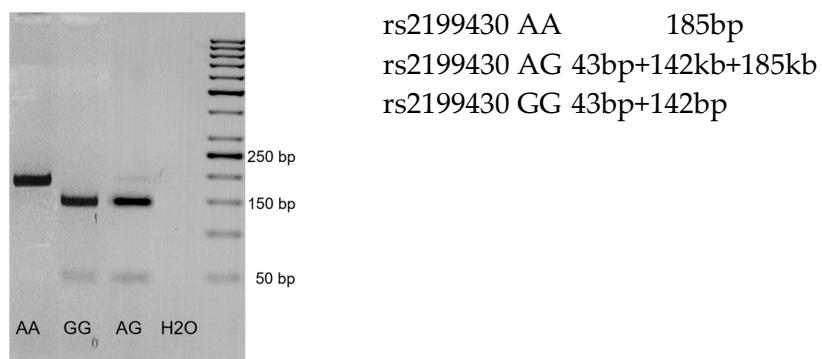
House-made Goldstar 10x Master Mix	2.5 µl
MgCl ₂ (25mM)	1.0 µl
2,5 mM Nucleotides each	1.0 µl
Primer-hu-Cdh13-F (10µM)	1.0 µl
Primer-hu-Cdh13-R (10µM)	1.0 µl
House-made Taq polymerase	0.3 µl
DNA-Template 1:10	1.0 µl
<u>ddH₂O</u>	<u>17.2 µl</u>
Endvolumen	25.0 µl

Rs2199430 primers

Hu-CDH13-rs2199430-F: 5'-AGACATCAGAGGCATTCCAGG-3'

Hu-CDH13-rs2199430-R: 5'-TCTCCACGTCTTGTGGTGC-3'

Digest with NEB BbsI-HF #R3539 leads to expected products of the following sizes:



Supplementary Table S1: Cycling conditions, primers, and agarose gel image depicting the expected band sizes of the digested PCR product for rs2199430 genotyping

	AA	AG	GG	sum
n controls	481	516	136	884
%	43.0	45.4	11.7	100
n aADHD	432	467	99	998
%	43.4	46.8	9.9	100

Supplementary Table S2: rs2199430 genotype distribution in the adult ADHD and control sample. A χ^2 -Test showed no significant association of rs2199430 genotype with disease category (aADHD vs. healthy controls, $p = 0.31$).

<i>NEO-PI-R</i>	<i>rs2199430 genotype</i>	<i>n</i>	<i>descriptives</i>	<i>F-statistics</i>	<i>p-value</i>
neuroticism	AA	378	M = 117.3 SD = 25.5	$F_{2,871} = 1.35$.260
	AG	410	M = 115.1 SD = 24.7		
	GG	88	M = 118.8 SD = 22.8		
extraversion	AA	378	M = 99.7 SD = 22.8	$F_{2,875} = 0.92$.398
	AG	410	M = 101.5 SD = 22.5		
	GG	89	M = 98.9 SD = 19.8		
openness	AA	382	M = 111.9 SD = 20.7	$F_{2,875} = 0.13$.879
	AG	409	M = 112.6 SD = 19.7		
	GG	89	M = 111.9 SD = 17.4		
conscientiousness	AA	381	M = 90.8 SD = 23.1	$F_{2,875} = 0.06$.942
	AG	410	M = 90.6 SD = 20.4		
	GG	89	M = 89.7 SD = 20.4		
agreeableness	AA	377	M = 112.8 SD = 16.5	$F_{2,871} = 5.04$.007
	AG	411	M = 112.3 SD = 16.7		
	GG	88	M = 107.4 SD = 16.8		

Supplementary Table S3: F-statistics for the *Big Five* personality traits with rs2199430 genotype as independent variable in the aADHD cohort revealing a significant association of

rs2199430 genotype with NEO-PI-R agreeableness scores while the other dimensions remained non-significant.