Supplementary Material

Supplementary Table 1. Quality control information for each subsample separately (QC 1) as well as for the combined sample (QC2). Table includes initial number of SNPs and individuals, SNPs not passing quality control for Hardy-Weinberg equilibrium (HWE), minor allele frequency (MAF) and SNP call rate, individuals not passing QC for overall call rate, and final number of SNPs and individuals.

Sample	Initial # of SNPs	HWE p<10-3	MAF <.01	SNP call rate <95%	final # of SNPs	Original # of individuals	Individual's call rate <95%	Final # of individuals	# of individuals related <.05
QC1									
YFS	546,677	1,207	327	100	545,050	1,382	0	1,382	1,277
HBCS	509,947	1,026	141	39	508,744	1,441	0	1,441	1,357
NFBC	347,622	1,316	15,487	0	330,849	4,506	0	4,506	3,175
QIMR	562,018*	242	2,645	-	559,131	5,530	-	5,530	2,853
QC2									
Combined samples	582,802	1,266	NA	312,600	269,616	12,859	NA	12,859	8,662

*number of SNPs ranged between individuals because they were genotyped on different platforms. This number represents the total number of different SNPs that were present in the QIMR subsample.

Supplementary Table 2. Additional removal of SNPs for Runs of Homozygosity analysis.

Initial # of SNPs	Removed due to MAF <.05	Light LD pruning	
		Removed	Retained
269,616	6,027	89,836	173,753

Light LD pruning: Removal of SNPs using PLINK with the following parameters: window size in SNPs = 50, number of SNPs to shift the window at each step = 5, VIF > 10 (r^2>0.9)

Supplementary Table 3. Parameters used for the PLINK -runs of homozygosity analysis based on recommendations from Howrigan et al. (2011).

ROH analysis, function parameters	**PLINK command**	**Value used**
- SNP threshold to call a ROH	--homozyg-snp	65 (after light pruning of SNPs)
- Sliding window size in SNPs	--homozyg-window-snp	65 (after light pruning of SNPs)
- Heterozygote allowance	--homozyg-window-het	0
- Missing SNP allowance	--homozyg-window-missing	3
- Window threshold to call a ROH	--homozyg-window-threshold	0.05% of SNP threshold
- Sliding window size in kb	--homozyg-window-kb	0 (unused)
- Kb threshold to call a ROH	--homozyg-kb	0 (unused)
- Minimum SNP density to call a ROH	--homozyg-density (kb)	5,000 (set high to ignore)
- Maximum gap before splitting ROH	--homozyg-gap (kb)	5,000 (set high to ignore)

Supplementary Table 4. Means (and standard deviations) of the four personality scales per subsample.

Subsample	Harm avoidance		Novelty seeking		Reward dependence		Persistence	
	Males	Females	Males	Females	Males	Females	Males	Females
YFS	6.8 (2.9)	6.9 (2.8)	8.9 (2.4)	9.0 (2.4)	6.9 (1.7)	7.0 (1.6)	2.7 (0.7)	2.7 (0.7)
HBCS	5.1 (4.1)	6.2 (4.3)	7.3 (3.6)	7.9 (3.8)	6.5 (2.6)	7.8 (2.4)	1.6 (1.2)	1.7 (1.3)
NFBC	6.0 (3.9)	6.9 (3.9)	8.8 (3.5)	9.4 (3.4)	6.0 (2.5)	7.7 (2.3)	2.9 (1.2)	2.7 (1.2)
QIMR	5.9 (4.2)	7.8 (4.4)	8.3 (3.9)	8.1 (3.7)	6.7 (2.7)	8.4 (2.4)	3.0 (1.5)	2.9 (1.5)

NB: Because the YFS subsample was assessed on items with a 5 point rating scale, their scale variances were lower than those for the other three samples. Because we standardised the results separately in each subsample this will not have influenced our results.

Supplementary Table 5. Phenotypic correlations between personality scales (N=12,749 - 12,776).

	Harm Avoidance	Novelty Seeking	Reward Dependence
Novelty Seeking	-.216**		
Reward Dependence	-.174**	.162**	
Persistence	-.114**	.011	.059**

** p<.001

Supplementary Table 6. Estimates of variance accounted for in each personality scale from a genetic similarity matrix based on all autosomal SNPs. Results from different models are presented.

Model	Harm Avoidance		Novelty Seeking		Reward Dependence		Persistence	
	N	h^2_{SNPs} (SE)	N	h^2_{SNPs} (SE)	N	h^2_{SNPs} (SE)	N	h^2_{SNPs} (SE)
Relatedness < 0.05, 20 PCs	8613	.066 (.037)	8620	.099 (.036)	8606	.042 (.036)	8618	.081 (.037)
Relatedness < .025, 20 PCs	4868	.009 (.066)	4874	.052 (.065)	4865	.057 (.066)	4874	.038 (.066)
Relatedness < .05, no PCs	8613	.104 (.035)	8620	.106 (.036)	8606	.035 (.035)	8616	.085 (.036)
Relatedness < .05, no PCs, 532,030 SNPs	8625	.075 (.037)	8632	.097 (.037)	8618	.046 (.037)	8630	.076 (.037)
Relatedness < .05, no PCs, adjusted for incomplete LD	8613	.070 (.039)	8620	.105 (.038)	8606	.044 (.038)	8618	.086 (.039)
Relatedness < .05, 20 PCs, males only	4198	.055 (.073)	-	-	4195	.045 (.074)	-	-
Relatedness < .05, 20 PCs, females only	5477	.048 (.058)	-	-	5473	.090 (.057)	-	-

h^2_{SNPs} = proportion of variance accounted for by all autosomal SNPs, SE=standard error of estimate

Relatedness <.05 or .025 means that one of each pair of individuals with an estimated genetic relationship of >.05 or >.025 is excluded from the analysis

PCs are the principal component estimates (eigenvectors) from the genetic relatedness matrix and represent dimensions of population structure

Adjustment for incomplete LD = variance estimate is corrected for incomplete LD of SNPs with causal variants of the same MAF as SNPs

Supplementary Table 7. Descriptive statistics for inbreeding coefficients (number of runs of homozygosity, proportion of genome in runs of homozygosity and $\hat{F}_{III}$).

Cohort*	Inbreeding measure	Minimum	Maximum	Mean	Median	SD
Overall sample (N=10,247)	Number of runs	0	52	9.82	10	6.34
	Proportion of genome in ROH	0	.14	.0079	.0065	.0076
	Number of runs, ROHs < 5Mb	0	41	9.13	9	5.707
	Proportion of genome in ROH < 5Mb	0	.03	.0056	.0053	.0039
	Number of runs, ROHs ≥ 5Mb	0	19	.69	0	1.241
	Proportion of genome in ROH ≥ 5Mb	0	.12	.0023	0	.0052
	$\hat{F}_{III}$	-.044	.168	.0057	.0047	.0085
CRYF (N=1382)	Number of runs	1	31	12.49	12	5.016
	Proportion of genome in ROH	0	.04	.0093	.0083	.0051
	$\hat{F}_{III}$	-.020	.034	.0053	.0045	.0066
HBCS (N=1440)	Number of runs	0	35	9.81	9	4.34
	Proportion of genome in ROH	0	.09	.0071	.0060	.0056
	$\hat{F}_{III}$	-.044	.090	.0032	.0025	.0079
NFBC (N=4490)	Number of runs	0	52	13.56	13	5.27
	Proportion of genome in ROH	0	.14	.0116	.0097	.0084
	$\hat{F}_{III}$	-.037	.168	.0064	.0049	.0102
QIMR (N=2935)	Number of runs	0	17	2.85	3	1.857
	Proportion of genome in ROH	0	.05	.0018	.0014	.0024
	$\hat{F}_{III}$	-.012	.088	.0059	.0055	.0060

*excluding closely related individuals (relatedness cut-off of 0.3)

ROH=runs of homozygosity

$\hat{F}_{III}$ is an inbreeding coefficient based on uniting gametes (Yang et al. 2011)

Supplementary Table 8. Correlations between inbreeding coefficients (runs of homozygosity and $\hat{F}_{III}$) and Cloninger's personality scales for overall sample and individual subsamples, as well as corresponding regression betas (personality standardised and inbreeding coefficient as a proportion between 0 and 1).

Cohort	**Personality scale**	**N**	**Total proportion of genome in ROH Light pruning - 65 SNPs cut-off**		$\hat{F}_{III}$	
			r	**Beta (SE)**	***r***	**Beta (SE)**
Overall sample	Harm Avoidance	10,197	.058**	7.65 (1.31)	.036**	4.26 (1.17)
	Novelty Seeking	10,202	-.052**	-6.81 (1.30)	-.038**	-4.43 (1.17)
	Reward Dependence	10,185	-.038**	-4.92 (1.30)	-.029**	-3.36 (1.16)
	Persistence	10,202	-.006	-0.76 (1.30)	-.024*	-2.79 (1.17)
Overall sample (outliers winsorised)	Harm Avoidance	10,197	.059**	9.25 (1.55)	.036**	5.03 (1.38)
	Novelty Seeking	10,202	-.054**	-8.43 (1.55)	-.043**	-5.98 (1.37)
	Reward Dependence	10,185	-.036**	-5.63 (1.54)	-.027**	-3.73 (1.37)
	Persistence	10,202	-.005	-0.78 (1.55)	-.026*	-3.53 (1.37)
NFBC	Harm Avoidance	4,479	.073**	8.63 (1.77)	.054**	5.27 (1.46)
	Novelty Seeking	4,479	-.070**	-8.30 (1.77)	-.047**	-4.53 (1.46)
	Reward Dependence	4,472	-.048**	-5.70 (1.77)	-.046**	-4.45 (1.46)
	Persistence	4,482	-.025	-2.97 (1.78)	-.031*	-3.05 (1.47)
QIMR	Harm Avoidance	2,923	.033	14.05 (7.91)	.030	5.12 (3.15)
	Novelty Seeking	2,913	-.063**	-26.45 (7.78)	-.048*	-7.95 (3.10)
	Reward Dependence	2,918	.008	3.46 (7.70)	-.024	-3.94 (3.07)
	Persistence	2,915	.013	5.43 (7.71)	.001	0.19 (3.07)

HBCS	Harm Avoidance	1,417	.017	2.97 (4.71)	-.036	-4.47 (3.35)
	Novelty Seeking	1,431	-.020	-3.55 (4.70)	-.005	-0.67 (3.35)
	Reward Dependence	1,415	-.024	-4.26 (4.69)	.001	1.33 (3.35)
	Persistence	1,423	-.032	-5.58 (4.71)	-.046	-5.73 (3.35)
YFS	Harm Avoidance	1,378	.075**	14.52 (5.19)	.071**	10.74 (4.06)
	Novelty Seeking	1,379	.017	3.23 (5.22)	-.030	-4.49 (4.08)
	Reward Dependence	1,380	.020	3.88 (5.23)	.000	-0.30 (4.08)
	Persistence	1,382	.019	3.58 (5.23)	-.016	-2.42 (4.07)
YFS, HBCS and QIMR subsamples combined†	Harm Avoidance	5,718	.044**	8.44 (2.53)	.015	2.26 (1.97)
	Novelty Seeking	5,723	-.031*	-5.90 (2.50)	-.027*	-4.03 (1.95)
	Reward Dependence	5,713	-.020	-3.71 (2.49)	-.007	-1.01 (1.95)
	Persistence	5,720	.006	1.22 (2.49)	-.018	-2.65 (1.94)

65 SNPs refers to the minimum number of SNPs to call a homozygous run

$\hat{F}_{III}$ is an inbreeding coefficient based on uniting gametes

*correlation is significant at .05 level

** correlation is significant at .01 level

†inbreeding results for three of the four subsamples to show that overall results are not only driven by the NFBC subsample (which has the most power due to having the largest N and highest variance in inbreeding