Supplementary material

Individual quality control assessment

A genome-wide association study was undertaken in a sample of 799 children with ADHD and 6,000 individuals from the Wellcome Trust Case Control Consortium (WTCCC)-Phase 2. Individual and SNP quality control assessment was performed using PLINK version 1.07 (1). 800 control individuals were excluded according to WTCCC-Phase 2 recommendations. All samples with a call rate lower than 99% were removed (47 cases and 95 controls). Mean autosomal heterozygosity was examined to remove samples with extreme heterozygosity, as indicated by the F inbreeding coefficient. Samples with F<-0.02 or F>0.02 were removed (5 cases and 8 controls). In addition, individuals that passed the previous filters were assessed for possible genetic relatedness by calculating identity-by-descent (IBD) for all pairs of individuals and removing one individual from each pair with a proportion of IBD more than 0.06, which indicates that the pair could be half-first cousins or closer (8 cases and 16 controls).

Although participants were questioned on their origin, we performed analysis to detect any individuals with non-European ancestry. We obtained genotype information from the 518,511 SNPs that were common between cases and controls on 210 unrelated European (CEU), Asian (CHB and JPT) and Yoruban (YRI) samples from the HapMap project. The next step was to remove SNPs in regions of extensive LD (Chr 5: 44-51.5 Mb; Chr 6: 25-33.5 Mb; Chr 8: 8-12 Mb; Chr 11: 45-57 Mb) (2) and any SNP from a pair that had $r^2>0.2$ within a 50-SNP window. Individuals from Hapmap were then merged with cases and controls and principal component analysis was performed using EIGENSTRAT. After plotting the first two principal components, there were three clusters corresponding to European, Asian and Yoruban individuals. Twelve cases were subsequently excluded from analysis, since they did not appear to cluster with the European samples.

After these quality control filters had been applied, 727 cases and 5,081 controls were included in the study.

The Wellcome Trust Case Control Consortium (WTCCC)-Phase 2 controls were all of UK Caucasian ancestry. as were the ADHD cases. Cases of non-European ancestry, based on information collected at assessment (inclusion criterion=all parents and grandparents of UK or Irish ethnicity), were not included in analysis. The Wellcome Trust Case Control Consortium has previously shown that the control samples are suitable for GWAS of UK populations. Finally in our own analysis, 2 principal components were included as covariates to correct for any remaining subtle ancestral differences in individuals.

SNP quality control assessment

518,511 SNPs were common between the Illumina Human660W-Quad BeadChip and the Illumina Human 1.2M BeadChip. Only autosomal SNPs were included in this analysis due to genotype-calling issues with a proportion of SNPs on the sex chromosomes.

SNPs were excluded if they had minor allele frequency (MAF) < 0.01, Hardy-Weinberg $p< 1 \times 10^{-5}$or call rate <0.99 in either cases or controls. In addition, the genotypes of the same 1,074 control individuals genotyped on two different Illumina chip arrays (Illumina 550K and Illumina Human 1.2M BeadChip) were compared to identify SNPs that were not behaving in the same way between different Illumina arrays. 115 SNPs with more than 1% of discordant genotypes were excluded from further analysis.

After these quality control filters had been applied, 15,809 SNPs were excluded.

Testing overlap in signal between Cardiff GWAS and other studies

The top 100 SNPs from the present GWAS were tested for excess association signal in the ADHD genetics consortium meta-analysis (3) as follows:

First, the 100 SNPs were LD-pruned using PLINK version 1.07. For each pair of SNPs <1Mb apart with r^2>0.2, the SNP with the less-significant p-value in the present GWAS was removed. This left a total of 60 SNPs. Then, log odds ratios (with respect to the same allele as our GWAS) and their standard errors from each of the four individual samples comprising the ADHD genetics consortium meta-analysis (IMAGE1, IMAGE2, CHOP and PUWMA) were corrected for the genomic inflation present in that sample (by multiplying the standard error by the square root of lambda). There were 204 cases in common between the sample used in our study and the IMAGE2 sample, so the expected correlation in log odds ratios between the samples was calculated using the formula given in Lin & Sullivan (4). This correlation was then used to correct the log odds ratios from the IMAGE2 sample for dependence on our GWAS. Finally, a fixed-effects inverse-variance meta -analysis was performed on the four ADHD genetics consortium samples, giving an overall odds ratio and association p-value. The Simes test (5) and Fisher's method for combining p-values were applied to the set of (one-sided) p-values from this analysis to give a test of enrichment of signal (and thus replication) across the set of SNPs as a whole. The Simes and Fisher's analyses were applied to the deCODE sample (which had no overlap with our GWAS) and also to the results of a fixed-effects inverse-variance meta –analysis of the four ADHD genetics consortium samples with the deCODE sample. Results for individual SNPs are given in Table S2 (note that p-values are one-sided for being in the same direction as the Cardiff GWAS).

Finally, although not a measure of replication, a fixed-effects inverse-variance meta –analysis of the Cardiff GWAS, the four ADHD genetics consortium samples and the deCODE sample was carried out on the top 100 SNPs from the Cardiff GWAS (without pruning). Individual p-values for each SNP are given in Supplementary Table S3.

Table S1. Top 100 SNPs in the ADHD GWAS

SNP	Chr	Position	Closest gene	Location relative to gene	Minor allele	Other allele	MAF	P	OR
rs1744062	6	137350879	IL20RA	Within non-coding genes	G	A	0.43	4.16E-06	0.75 (0.67-0.85)
rs11079828	17	43964102	HOXB1	Upstream	T	C	0.47	6.54E-06	1.32 (1.17-1.49)
rs42259	5	14439655	TRIO	Intronic	T	C	0.17	6.76E-06	1.41 (1.22-1.64)
rs3779312	7	77549692	MAGI2	Intronic	T	C	0.21	8.38E-06	1.37 (1.19-1.57)
rs616668	12	110458663	ATXN2	Intronic	G	T	0.20	8.62E-06	1.38 (1.2-1.59)
rs11175219	12	62648986	SRGAP1	Intronic	T	C	0.12	1.06E-05	1.46 (1.23-1.73)
rs4238186	13	18588836	LOC100128765	Intergenic	A	G	0.18	1.11E-05	1.39 (1.2-1.61)
rs7746680	6	45885325	-	Intergenic	A	G	0.24	1.14E-05	1.35 (1.18-1.54)
rs11686538	2	225526808	DOCK10	Intronic	G	A	0.29	1.27E-05	0.74 (0.64-0.84)
rs1304358	2	198677828	PLCL1	Intronic	C	T	0.49	1.27E-05	1.3 (1.16-1.47)
rs406742	10	8885947	-	Intergenic	G	A	0.26	1.49E-05	1.33 (1.17-1.51)
rs790531	13	49623515	DLEU2	Intergenic	G	A	0.06	1.50E-05	1.62 (1.3-2.02)
rs6815704	4	93693589	GRID2	Intronic	A	G	0.15	2.09E-05	1.4 (1.2-1.64)
rs9842394	3	181095930	PEX5L	Intronic	T	C	0.47	2.68E-05	0.77 (0.69-0.87)
rs2636788	10	98866931	SLIT1	Intronic	G	A	0.17	2.74E-05	0.7 (0.59-0.83)
rs1490046	5	173888653	-	Intergenic	A	G	0.08	2.87E-05	1.56 (1.27-1.92)
rs1050567	2	61559167	XPO1	3' UTR	T	C	0.11	2.89E-05	1.44 (1.22-1.72)
rs9384245	6	155201820	TIAM2	Intronic	T	C	0.42	3.00E-05	0.77 (0.68-0.87)
rs1370072	13	54739939	-	Intergenic	T	C	0.45	3.28E-05	1.29 (1.14-1.45)
rs874836	22	15681843	XKR3	Intronic	A	G	0.13	3.32E-05	1.41 (1.2-1.67)
rs11698703	20	61149452	C20orf51	Intronic	G	A	0.13	3.76E-05	1.42 (1.2-1.67)
rs4862417	4	185927595	ACSL1	Intronic	G	A	0.24	3.76E-05	0.74 (0.64-0.85)
rs2348997	4	161041441	-	Intergenic	A	G	0.07	3.81E-05	1.56 (1.26-1.93)
rs4674953	2	225535055	DOCK10	Intronic	C	T	0.28	3.86E-05	1.31 (1.15-1.49)
rs11695623	2	218776360	ARPC2	Downstream	G	A	0.08	3.92E-05	0.59 (0.46-0.76)
rs12433945	14	32941853	NPAS3	Intronic	G	A	0.22	4.03E-05	0.73 (0.63-0.85)
rs6557383	6	155263292	LOC729436	Within non-coding genes	T	C	0.40	4.14E-05	1.28 (1.14-1.45)
rs6749316	2	137789970	THSD7B	Intronic	T	C	0.46	4.54E-05	0.78 (0.69-0.88)
rs1872492	7	68093828	-	Intergenic	T	C	0.13	4.78E-05	1.42 (1.2-1.69)
rs2421083	2	124962562	CNTNAP5	Intronic	A	G	0.33	4.92E-05	1.29 (1.14-1.46)

rs11846075	14	25712317	-	Intergenic	A	G	0.06	4.93E-05	1.57 (1.26-1.95)
rs7724098	5	176592176	NSD1	Intronic	G	A	0.24	5.20E-05	1.32 (1.15-1.5)
rs4977447	9	18796999	ADAMTSL1	Intronic	G	A	0.30	5.23E-05	1.3 (1.15-1.48)
rs2281855	1	65557960	Intergenic	Intronic	G	A	0.28	5.25E-05	0.75 (0.65-0.86)
rs7318072	13	39044225	LHFP	Intronic	G	A	0.47	5.65E-05	0.78 (0.69-0.88)
rs11252601	10	4617405	-	Intergenic	C	T	0.01	6.10E-05	2.29 (1.53-3.43)
rs16833765	2	192049165	-	Intergenic	G	A	0.24	6.38E-05	0.74 (0.64-0.86)
rs17097328	14	98104636	-	Intergenic	T	C	0.19	6.53E-05	1.35 (1.16-1.56)
rs11696842	20	1548794	SIRPB1	Upstream	T	C	0.22	6.54E-05	1.33 (1.16-1.53)
rs1009930	21	25041309	-	Intergenic	A	G	0.49	6.65E-05	1.28 (1.13-1.44)
rs7307884	12	30950091	-	Intergenic	C	T	0.24	6.83E-05	0.75 (0.64-0.86)
rs3918339	13	104778801	-	Intergenic	G	A	0.47	6.87E-05	0.78 (0.69-0.88)
rs2037358	3	45112091	CDCP1	Intronic	G	T	0.48	6.98E-05	1.28 (1.13-1.44)
rs11167915	5	145269194	-	Intergenic	C	T	0.24	7.11E-05	1.31 (1.15-1.49)
rs17567779	5	75961672	F2RL2	Intronic	A	G	0.06	7.94E-05	1.6 (1.27-2.01)
rs1146581	1	75985612	ACADM	Intronic	G	T	0.34	7.96E-05	0.77 (0.68-0.88)
rs660211	11	75497476	UVRAG	Intronic	G	A	0.10	8.09E-05	0.63 (0.5-0.79)
rs1359047	1	173849411	TNR	Intronic	C	T	0.10	8.12E-05	1.44 (1.2-1.73)
rs228285	17	34176036	PSMB3	3' UTR	A	G	0.22	8.17E-05	1.32 (1.15-1.52)
rs9964783	18	45619003	MYO5B	Intronic	A	C	0.37	8.18E-05	1.28 (1.13-1.44)
rs2225535	10	110344970	-	Intergenic	T	C	0.19	8.38E-05	1.34 (1.16-1.55)
rs2174546	3	72132778	-	Intergenic	A	G	0.34	8.43E-05	1.28 (1.13-1.44)
rs4868257	5	172682128	STC2	Intronic	C	T	0.50	8.48E-05	0.79 (0.7-0.89)
rs4812641	20	35023663	SAMHD1	Intergenic	A	C	0.35	8.63E-05	0.77 (0.68-0.88)
rs17243607	14	43680082	LOC645086	Intergenic	C	T	0.20	8.66E-05	0.73 (0.62-0.85)
rs12936559	17	57680004	-	Intergenic	A	G	0.10	9.13E-05	1.44 (1.2-1.72)
rs6671682	1	225946898	-	Intergenic	T	C	0.08	9.18E-05	1.49 (1.22-1.83)
rs2287652	14	77467201	ADCK1	Intronic	G	A	0.11	9.20E-05	1.42 (1.19-1.68)
rs4801083	18	52955230	-	Intergenic	C	A	0.32	9.27E-05	0.77 (0.67-0.88)
rs708414	10	36289489	-	Intergenic	A	G	0.16	9.32E-05	1.36 (1.16-1.58)
rs13145682	4	183741011	ODZ3	Intronic	T	C	0.39	9.46E-05	0.78 (0.69-0.88)
rs7512378	1	166091758	SAC	Intronic	G	A	0.29	9.60E-05	0.76 (0.67-0.87)
rs8078764	17	784925	NXN	Intronic	T	C	0.24	9.87E-05	1.3 (1.14-1.48)

rs7709243	5	67569795	PIK3R1	Intronic	C	T	0.49	9.95E-05	1.27 (1.12-1.42)
rs10956576	8	132233501	-	Intergenic	T	C	0.14	0.000102	1.36 (1.17-1.59)
rs768750	14	32017697	AKAP6	Intronic	G	A	0.45	0.000102	0.79 (0.7-0.89)
rs2292506	12	51224587	KRT71	Coding non-synonymous	T	C	0.06	0.000103	1.56 (1.25-1.95)
rs11591797	10	99760323	CRTAC1	Intronic	G	A	0.26	0.000108	0.76 (0.66-0.87)
rs2302862	3	10233493	IRAK2	Intronic	T	C	0.23	0.000112	0.75 (0.64-0.87)
rs11143600	9	75304877	-	Intergenic	T	C	0.19	0.000114	0.73 (0.62-0.85)
rs17620176	7	39498513	-	Intergenic	T	C	0.47	0.000117	0.79 (0.7-0.89)
rs233783	21	21805149	NCAM2	Intronic	C	A	0.11	0.000117	1.42 (1.19-1.69)
rs1457020	14	82809160	-	Intergenic	T	C	0.27	0.000118	1.28 (1.13-1.46)
rs2289705	7	121771079	CADPS2	Intronic	G	A	0.22	0.000119	1.31 (1.14-1.51)
rs3849537	3	21454458	ZNF385D	Intronic	T	C	0.19	0.000125	0.73 (0.62-0.86)
rs896381	8	70990827	-	Intergenic	G	A	0.22	0.00013	0.75 (0.64-0.87)
rs889704	16	69949563	CALB2	Upstream	A	C	0.14	0.000133	0.7 (0.59-0.84)
rs2170342	3	19957139	RAB5A	Intronic	T	C	0.14	0.000134	1.37 (1.16-1.6)
rs4425130	2	134231156	-	Intergenic	A	G	0.38	0.000135	0.79 (0.69-0.89)
rs2611605	15	30228925	CHRNA7	Intronic	T	C	0.21	0.000142	0.74 (0.63-0.86)
rs2991751	9	76126818	-	Intergenic	T	C	0.09	0.000142	0.63 (0.5-0.8)
rs5751346	22	21261688	IGLV2-33	Downstream	G	T	0.08	0.000142	0.61 (0.48-0.79)
rs2132683	6	99778735	-	Intergenic	C	T	0.34	0.000145	1.27 (1.12-1.44)
rs4712494	6	20516898	E2F3	Intronic	C	T	0.24	0.000152	0.75 (0.65-0.87)
rs740691	19	18095441	MAST3	Synonymous coding	C	T	0.47	0.000153	1.26 (1.12-1.41)
rs8102349	19	53524366	EMP3	Intronic	A	G	0.48	0.000153	1.26 (1.12-1.42)
rs7573893	2	137632795	THSD7B	Intronic	C	T	0.28	0.000154	1.28 (1.13-1.46)
rs8013122	14	35500214	-	Intergenic	C	T	0.12	0.000162	0.68 (0.56-0.83)
rs7667760	4	34408184	-	Intergenic	A	G	0.21	0.000165	0.75 (0.64-0.87)
rs4149497	16	70116471	CHST4	Upstream	A	G	0.13	0.000167	1.38 (1.17-1.64)
rs2541300	12	22366227	ST8SIA1	Intronic	T	G	0.41	0.000169	1.26 (1.12-1.42)
rs1956859	14	98094726	-	Intergenic	C	A	0.45	0.00017	0.79 (0.7-0.89)
rs1973077	2	138402683	-	Intergenic	G	A	0.20	0.000174	1.32 (1.14-1.52)
rs2192439	12	9765493	CLECL1	Downstream	A	G	0.08	0.000177	1.45 (1.2-1.77)
rs196051	6	22164110	-	Intergenic	G	A	0.39	0.000186	1.25 (1.11-1.41)
rs2205851	1	168006274	-	Intergenic	C	T	0.34	0.000186	1.26 (1.12-1.43)

rs11098119	4	112466012	-	Intergenic	A	G	0.28	0.000187	1.28 (1.12-1.45)
rs6946515	7	39369376	POU6F2	Intronic	C	T	0.22	0.000189	1.3 (1.13-1.5)
rs7692829	4	26431475	-	Intergenic	A	G	0.40	0.000189	1.26 (1.11-1.42)
rs916620	9	135586571	SARDH	Intronic	T	C	0.36	0.000191	0.78 (0.69-0.89)

Chr: Chromosome; MAF: Minor Allele Frequency; OR: Odds Ratio for minor allele; 95% CI: 95% Confidence Interval; UTR: Untranslated Region

Table S2. Replication p-values in ADHD GWAS consortium meta-analysis (ADHDCon) and deCODE sample for the 100 most significant SNPs in the present GWAS. Note: this list has been LD -pruned such that pairwise r^2 between SNPs is <0.2. Note also that p-values for ADHD GWAS consortium meta-analysis and deCODE are one-sided (testing for effects in same direction as the current GWAS)

SNP	OR (ADHD GWAS Cardiff)	p (ADHD GWAS Cardiff)	OR (ADHD Consortium)	p (ADHD Consortium)	OR (deCODE)	p (deCODE)	OR (ADHD Con+deCODE)	p (ADHD Con+deCODE)
rs1744062	0.75	4.16E-06	0.99	0.414	1.09	0.96	1.02	0.772
rs11079828	1.32	6.54E-06	1.04	0.172	1.00	0.51	1.03	0.176
rs42259	1.41	6.76E-06	1.02	0.361	0.91	0.92	0.98	0.660
rs3779312	1.37	8.38E-06	1.09	0.042	0.98	0.65	1.05	0.098
rs616668	1.38	8.62E-06	0.93	0.920	0.94	0.86	1.00	0.539
rs11175219	1.46	1.06E-05	0.81	0.903	0.93	0.75	0.88	0.904
rs4238186	1.39	1.11E-05	0.96	0.758	0.96	0.72	0.97	0.752
rs7746680	1.35	1.14E-05	0.99	0.608	1.03	0.32	1.01	0.384
rs11686538	0.74	1.27E-05	0.94	0.081	1.02	0.63	0.96	0.136
rs1304358	1.30	1.27E-05	1.11	0.006	1.04	0.19	1.09	0.004
rs406742	1.33	1.49E-05	1.04	0.201	1.11	0.06	1.07	0.033
rs790531	1.62	1.50E-05	0.98	0.572	1.02	0.44	1.02	0.412
rs6815704	1.40	2.09E-05	1.00	0.531	1.12	0.08	1.05	0.151
rs9842394	0.77	2.69E-05	0.91	0.016	1.03	0.73	0.96	0.074
rs2636788	0.70	2.74E-05	1.00	0.480	1.00	0.48	0.99	0.382
rs1490046	1.56	2.87E-05	1.09	0.192	0.93	0.77	1.02	0.393
rs1050567	1.44	2.89E-05	N/A	N/A	0.93	0.82	0.93	0.819
rs9384245	0.77	3.00E-05	1.06	0.923	0.96	0.20	1.01	0.637
rs1370072	1.29	3.29E-05	0.99	0.556	0.96	0.80	0.99	0.669
rs874836	1.41	3.32E-05	0.98	0.629	1.11	0.06	0.95	0.870
rs4862417	0.74	3.76E-05	1.07	0.923	1.05	0.83	1.06	0.932
rs11698703	1.42	3.76E-05	1.11	0.268	1.21	0.005	1.19	0.005
rs2348997	1.56	3.81E-05	0.99	0.541	0.78	0.98	0.92	0.873
rs4674953	1.31	3.86E-05	0.95	0.868	1.00	0.52	0.98	0.734
rs11695623	0.59	3.92E-05	0.93	0.209	0.99	0.45	0.94	0.184
rs12433945	0.73	4.03E-05	1.02	0.655	0.97	0.27	0.99	0.372
rs6749316	0.78	4.54E-05	0.96	0.166	0.99	0.42	0.97	0.147
rs1872492	1.42	4.78E-05	0.98	0.579	1.07	0.16	1.04	0.195
rs2421083	1.29	4.93E-05	1.00	0.498	1.04	0.24	1.02	0.247
rs11846075	1.57	4.93E-05	N/A	N/A	1.09	0.21	1.09	0.207
rs7724098	1.32	5.21E-05	1.03	0.262	0.92	0.94	0.99	0.628
rs4977447	1.30	5.23E-05	1.01	0.456	1.04	0.23	1.03	0.217
rs2281855	0.75	5.26E-05	0.99	0.402	1.02	0.68	1.00	0.459
rs7318072	0.78	5.65E-05	1.03	0.766	1.03	0.74	1.02	0.775
rs11252601	2.29	6.10E-05	0.76	0.947	0.75	0.87	0.78	0.957
rs16833765	0.74	6.38E-05	0.99	0.456	1.01	0.59	1.00	0.526
rs17097328	1.35	6.53E-05	0.97	0.735	0.96	0.72	0.97	0.734
rs11696842	1.33	6.54E-05	0.98	0.682	0.89	0.98	0.95	0.929
rs1009930	1.28	6.65E-05	0.98	0.671	1.08	0.07	1.03	0.195
rs7307884	0.75	6.83E-05	1.01	0.586	1.04	0.79	1.02	0.689
rs3918339	0.78	6.87E-05	1.04	0.818	1.06	0.87	1.05	0.925
rs2037358	1.28	6.98E-05	0.99	0.605	1.06	0.11	0.97	0.843
rs11167915	1.31	7.11E-05	0.95	0.856	1.00	0.51	0.98	0.727
rs17567779	1.60	7.94E-05	0.90	0.826	1.13	0.11	1.04	0.312

rs1146581	0.77	7.96E-05	N/A	N/A	1.11	0.98	1.11	0.982
rs660211	0.63	8.09E-05	0.93	0.215	0.96	0.33	0.95	0.195
rs1359047	1.44	8.12E-05	1.27	0.006	0.81	1.00	1.00	0.533
rs228285	1.32	8.17E-05	0.99	0.550	1.07	0.12	1.03	0.188
rs9964783	1.28	8.19E-05	1.06	0.098	1.09	0.05	1.08	0.013
rs2225535	1.34	8.38E-05	1.00	0.502	1.00	0.50	1.01	0.414
rs2174546	1.28	8.43E-05	1.00	0.457	1.02	0.39	1.00	0.453
rs4868257	0.79	8.48E-05	0.96	0.178	1.06	0.88	1.00	0.544
rs4812641	0.77	8.63E-05	1.02	0.660	0.96	0.21	0.99	0.342
rs17243607	0.73	8.66E-05	0.93	0.080	1.10	0.94	0.99	0.415
rs12936559	1.44	9.13E-05	1.11	0.234	0.99	0.53	1.04	0.332
rs6671682	1.49	9.18E-05	1.01	0.464	1.02	0.42	1.03	0.330
rs2287652	1.42	9.20E-05	1.07	0.222	1.01	0.45	1.05	0.206
rs4801083	0.77	9.27E-05	0.95	0.136	1.04	0.80	0.98	0.317
rs708414	1.36	9.32E-05	1.10	0.046	1.02	0.38	1.08	0.041
rs13145682	0.78	9.46E-05	1.05	0.873	0.98	0.31	1.01	0.628

Table S3. Fixed-effects inverse-variance meta-analysis of the top 100 Cardiff GWAS SNPs in Cardiff, ADHD GWAS consortium (ADHDCon) and deCODE samples. P-values are two sided

SNP	OR (ADHD GWAS Cardiff)	p (ADHD GWAS Cardiff)	OR (Cardiff+ADHDCon+ deCODE)	p (Cardiff+ADHDCon +deCODE)
rs1744062	0.75	4.16E-06	0.96	1.83E-01
rs11079828	1.32	6.54E-06	1.08	4.79E-03
rs42259	1.41	6.76E-06	1.07	8.57E-02
rs3779312	1.37	8.38E-06	1.12	1.31E-03
rs616668	1.38	8.62E-06	1.06	6.13E-02
rs739496	1.37	8.92E-06	1.02	4.96E-01
rs11175219	1.46	1.06E-05	1.15	2.62E-02
rs4238186	1.39	1.11E-05	1.05	1.58E-01
rs7746680	1.35	1.14E-05	1.07	2.54E-02
rs11686538	0.74	1.27E-05	0.91	3.74E-03
rs1304358	1.30	1.27E-05	1.13	1.45E-05
rs2301621	1.37	1.31E-05	1.02	5.94E-01
rs6490162	1.37	1.40E-05	1.02	6.03E-01
rs406742	1.33	1.49E-05	1.13	2.29E-04
rs790531	1.62	1.50E-05	1.16	1.55E-02
rs7091279	1.33	1.61E-05	1.13	2.34E-04
rs607316	1.36	1.63E-05	1.02	5.87E-01
rs16903338	1.38	1.68E-05	1.06	9.19E-02
rs706617	1.62	1.74E-05	1.15	2.00E-02
rs1475119	0.76	1.78E-05	0.96	1.92E-01
rs2490637	1.61	1.98E-05	1.17	9.73E-03
rs6815704	1.40	2.09E-05	1.12	3.67E-03
rs4749821	1.32	2.29E-05	1.13	1.45E-04
rs630512	1.36	2.34E-05	1.02	5.69E-01
rs979534	1.32	2.38E-05	1.13	1.67E-04
rs13024433	0.75	2.49E-05	0.92	5.82E-03
rs7328859	1.36	2.61E-05	1.05	1.49E-01
rs9842394	0.77	2.69E-05	0.92	1.71E-03
rs2636788	0.70	2.74E-05	0.93	4.27E-02
rs1490046	1.56	2.87E-05	1.15	1.79E-02
rs10774623	1.34	2.87E-05	1.02	5.32E-01
rs1050567	1.44	2.89E-05	1.14	3.49E-02
rs9384245	0.77	3.00E-05	0.96	1.31E-01
rs42204	1.37	3.08E-05	1.06	1.15E-01
rs1370072	1.29	3.29E-05	1.04	1.52E-01
rs42405	1.37	3.30E-05	1.06	1.05E-01
rs874836	1.41	3.32E-05	1.04	3.06E-01
rs11708154	0.76	3.33E-05	0.90	4.35E-04
rs17019538	1.39	3.41E-05	1.12	3.47E-03
rs4862417	0.74	3.76E-05	0.99	6.88E-01
rs11698703	1.42	3.76E-05	1.27	6.38E-06
rs7667109	1.39	3.81E-05	1.12	4.90E-03
rs2348997	1.56	3.81E-05	1.08	2.23E-01
rs4674953	1.31	3.86E-05	1.04	1.85E-01
rs11695623	0.59	3.92E-05	0.85	8.81E-03
rs12433945	0.73	4.03E-05	0.93	3.95E-02
rs6557383	1.28	4.14E-05	1.08	1.26E-02

rs706615	1.59	4.36E-05	1.15	1.53E-02
rs4690963	1.56	4.42E-05	1.08	1.96E-01
rs11255920	1.31	4.43E-05	1.13	2.58E-04
rs6749316	0.78	4.54E-05	0.92	5.72E-03
rs1872492	1.42	4.78E-05	1.13	6.80E-03
rs2421083	1.29	4.93E-05	1.08	1.51E-02
rs11846075	1.57	4.93E-05	1.28	1.20E-03
rs7724098	1.32	5.21E-05	1.05	1.31E-01
rs918459	1.32	5.22E-05	1.05	1.33E-01
rs7630877	0.76	5.22E-05	0.90	6.53E-04
rs4977447	1.30	5.23E-05	1.08	1.18E-02
rs3120890	1.28	5.25E-05	1.04	1.41E-01
rs2281855	0.75	5.26E-05	0.95	7.33E-02
rs2817708	0.76	5.38E-05	0.93	1.61E-02
rs7318072	0.78	5.65E-05	0.97	2.72E-01
rs7071899	1.30	5.74E-05	1.13	3.39E-04
rs11252601	2.29	6.10E-05	1.09	4.57E-01
rs7990319	1.28	6.11E-05	1.04	1.57E-01
rs16833765	0.74	6.38E-05	0.94	9.12E-02
rs4344605	1.28	6.45E-05	1.04	1.36E-01
rs17097328	1.35	6.53E-05	1.06	1.60E-01
rs11696842	1.33	6.54E-05	1.02	6.36E-01
rs6436025	0.59	6.59E-05	0.85	7.41E-03
rs1009930	1.28	6.65E-05	1.07	1.15E-02
rs9537011	1.28	6.70E-05	1.04	1.44E-01
rs7307884	0.75	6.83E-05	0.96	2.07E-01
rs3918339	0.78	6.87E-05	0.99	6.09E-01
rs2037358	1.28	6.98E-05	1.03	3.74E-01
rs11167915	1.31	7.11E-05	1.04	1.88E-01
rs653178	0.79	7.63E-05	0.94	3.64E-02
rs10853100	1.28	7.66E-05	1.07	1.93E-02
rs2575907	1.27	7.92E-05	1.04	1.54E-01
rs17567779	1.60	7.94E-05	1.17	1.55E-02
rs1146581	0.77	7.96E-05	0.97	4.99E-01
rs660211	0.63	8.09E-05	0.87	1.22E-02
rs1359047	1.44	8.12E-05	1.11	4.57E-02
rs12450225	1.27	8.14E-05	1.07	2.38E-02
rs228285	1.32	8.17E-05	1.09	1.07E-02
rs9964783	1.28	8.19E-05	1.11	1.87E-04
rs2225535	1.34	8.38E-05	1.08	3.83E-02
rs2174546	1.28	8.43E-05	1.06	6.17E-02
rs4868257	0.79	8.48E-05	0.95	9.19E-02
rs7996238	0.79	8.59E-05	0.97	2.96E-01
rs4812641	0.77	8.63E-05	0.94	3.83E-02
rs17243607	0.73	8.66E-05	0.93	6.23E-02
rs2325948	1.27	8.73E-05	1.07	2.17E-02
rs2209313	1.32	8.98E-05	1.02	6.42E-01
rs12936559	1.44	9.13E-05	1.23	2.39E-03
rs6671682	1.49	9.18E-05	1.14	1.93E-02
rs2287652	1.42	9.20E-05	1.15	5.78E-03
rs4801083	0.77	9.27E-05	0.94	3.62E-02
rs708414	1.36	9.32E-05	1.14	7.47E-04
rs13145682	0.78	9.46E-05	0.96	1.63E-01

Table S4. Enrichment p values for Pathway analysis of Cardiff GWAS SNP data. 315 pathways were nominally significant (top 100 are shown in the table)

Pathway number	Number of genes in pathway	Total number of significant genes	Number of expected significant genes	Pathway-specific p-value	Corrected p-value	Expected pathways/study	Function
GO:21561	3	2	0.03	0.0002	0.678	1.73	facial nerve development
GO:21783	3	2	0.03	0.0002	0.678	1.73	preganglionic parasympathetic nervous system development
MGI: 1694	8	3	0.18	0.0002	0.678	1.73	failure to form egg cylinders
GO:60123	6	3	0.25	0.0006	0.855	3.25	regulation of growth hormone secretion
PAN-F 211	42	7	2.11	0.0006	0.855	3.25	Kinase activator
GO:48483	13	4	0.64	0.0008	0.903	4.04	autonomic nervous system development
GO:32088	15	4	0.45	0.0010	0.936	4.83	negative regulation of NF-kappaB transcription factor activity
GO:30148	29	6	1.35	0.0010	0.936	4.83	sphingolipid biosynthetic process
GO: 9249	4	3	0.17	0.0010	0.936	4.83	protein lipoylation
GO:21781	5	3	0.36	0.0012	0.952	5.62	glial cell fate commitment
GO:48011	4	2	0.06	0.0012	0.952	5.62	nerve growth factor receptor signaling pathway
MGI: 6267	9	3	0.33	0.0012	0.952	5.62	abnormal intercalated disc morphology
GO: 5814	23	5	0.88	0.0014	0.968	6.4	centriole
GO:18065	7	3	0.24	0.0014	0.968	6.4	protein-cofactor linkage
GO:48486	4	2	0.06	0.0014	0.968	6.4	parasympathetic nervous system development
PAN-F 94	106	13	5.77	0.0014	0.968	6.4	Kinase modulator
GO: 7417	318	46	32.44	0.0016	0.975	7.23	central nervous system development
GO:32268	440	32	19.4	0.0016	0.975	7.23	regulation of cellular protein metabolic process
MGI: 5178	76	12	4.62	0.0016	0.975	7.23	increased circulating cholesterol level
GO:42771	13	4	0.68	0.0018	0.982	8.05	DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis
GO: 5227	17	6	1.8	0.0018	0.982	8.05	calcium activated cation channel activity

KEGG 4130	27	5	1.05	0.0018	0.982	8.05	SNARE interactions in vesicular transport
GO: 7586	62	8	2.76	0.0020	0.984	8.84	digestion
GO:19894	9	3	0.3	0.0020	0.984	8.84	kinesin binding
GO:16410	58	8	2.26	0.0022	0.988	9.64	N-acyltransferase activity
GO:10608	202	15	7.04	0.0022	0.988	9.64	posttranscriptional regulation of gene expression
GO:30330	21	5	1.08	0.0024	0.991	10.47	DNA damage response, signal transduction by p53 class mediator
GO:46513	16	4	0.7	0.0024	0.991	10.47	ceramide biosynthetic process
GO:10586	3	2	0.1	0.0024	0.991	10.47	miRNA metabolic process
GO:10587	3	2	0.1	0.0024	0.991	10.47	miRNA catabolic process
MGI: 3982	86	13	5.46	0.0026	0.992	11.21	increased cholesterol level
GO: 8415	138	13	5.46	0.0032	0.994	13.59	acyltransferase activity
GO:35308	3	2	0.11	0.0032	0.994	13.59	negative regulation of protein amino acid dephosphorylation
GO:35305	3	2	0.11	0.0032	0.994	13.59	negative regulation of dephosphorylation
GO:46467	32	6	1.52	0.0034	0.995	14.39	membrane lipid biosynthetic process
MGI: 4574	3	2	0.14	0.0034	0.995	14.39	broad limb buds
GO:16747	140	13	5.64	0.0038	0.997	15.99	transferase activity, transferring acyl groups other than amino-acyl groups
GO:51289	22	5	1.34	0.0038	0.997	15.99	protein homotetramerization
GO: 7062	12	3	0.32	0.0038	0.997	15.99	sister chromatid cohesion
GO:51259	152	18	9.73	0.0040	0.997	16.75	protein oligomerization
GO:16746	145	13	5.72	0.0042	0.998	17.58	transferase activity, transferring acyl groups
MGI: 794	18	7	2.56	0.0042	0.998	17.58	abnormal parietal lobe morphology
GO:55093	6	2	0.14	0.0048	0.999	20.01	response to hyperoxia
GO:46520	18	4	0.79	0.0048	0.999	20.01	sphingoid biosynthetic process
PAN-PR 34	207	15	7.42	0.0048	0.999	20.01	DNA metabolism
GO:42535	5	2	0.11	0.0050	0.999	20.85	positive regulation of tumor necrosis factor biosynthetic process
GO: 781	31	5	1.15	0.0052	1	21.7	chromosome, telomeric region

GO: 6498	3	2	0.12	0.0052	1	21.7	N-terminal protein lipidation
GO:48478	3	2	0.14	0.0054	1	22.5	replication fork protection
GO: 8502	3	2	0.17	0.0054	1	22.5	melatonin receptor activity
GO:31065	3	2	0.13	0.0054	1	22.5	positive regulation of histone deacetylation
GO:31063	3	2	0.13	0.0054	1	22.5	regulation of histone deacetylation
MGI: 3828	16	4	0.79	0.0054	1	22.5	pulmonary edema
PAN-F 180	74	15	8.45	0.0058	1	24.16	Extracellular matrix glycoprotein
GO:90312	4	2	0.13	0.0060	1	25.01	positive regulation of protein amino acid deacetylation
GO:90311	4	2	0.13	0.0060	1	25.01	regulation of protein amino acid deacetylation
PAN-PR 36	111	10	4.28	0.0060	1	25.01	DNA repair
GO: 6977	3	2	0.16	0.0062	1	25.8	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest
GO:35304	5	3	0.69	0.0064	1	26.64	regulation of protein amino acid dephosphorylation
GO:43274	7	3	0.7	0.0066	1	27.48	phospholipase binding
GO:15269	13	5	1.65	0.0068	1	28.38	calcium-activated potassium channel activity
GO:31399	273	23	14.1	0.0072	1	30	regulation of protein modification process
GO: 6643	69	8	2.9	0.0072	1	30	membrane lipid metabolic process
MGI: 3085	22	4	0.86	0.0072	1	30	abnormal egg cylinder morphology
GO:21675	21	5	1.46	0.0076	1	31.71	nerve development
MGI: 484	26	5	1.22	0.0076	1	31.71	abnormal pulmonary artery morphology
KEGG 601	19	4	0.94	0.0078	1	32.58	Glycosphingolipid biosynthesis - lacto and neolacto series
GO:46545	59	10	4.82	0.0080	1	33.45	development of primary female sexual characteristics
GO:46660	60	10	4.84	0.0082	1	34.31	female sex differentiation
GO:71158	4	2	0.18	0.0084	1	35.2	positive regulation of cell cycle arrest
GO:51260	81	11	5.2	0.0088	1	36.86	protein homooligomerization

GO:16363	51	6	1.92	0.0088	1	36.86	nuclear matrix
GO:19005	15	3	0.45	0.0088	1	36.86	SCF ubiquitin ligase complex
GO:60349	19	4	1	0.0090	1	37.67	bone morphogenesis
MGI: 1411	6	3	0.69	0.0090	1	37.67	spinning
GO: 19	4	2	0.15	0.0092	1	38.45	regulation of mitotic recombination
MGI: 162	20	4	0.94	0.0094	1	39.22	lordosis
PAN-PR 137	144	16	9.04	0.0094	1	39.22	Protein targeting and localization
GO:65003	461	33	22.41	0.0096	1	40.02	macromolecular complex assembly
GO:14049	5	3	0.77	0.0096	1	40.02	positive regulation of glutamate secretion
GO:42534	9	2	0.16	0.0100	1	41.62	regulation of tumor necrosis factor biosynthetic process
GO: 7173	22	5	1.45	0.0102	1	42.38	epidermal growth factor receptor signaling pathway
MGI: 9149	3	2	0.2	0.0104	1	43.19	decreased pancreatic acinar cell number
GO: 6364	65	4	0.89	0.0108	1	44.82	rRNA processing
GO: 6040	18	3	0.63	0.0108	1	44.82	amino sugar metabolic process
GO:51246	499	33	22.47	0.0110	1	45.63	regulation of protein metabolic process
GO:43900	32	4	0.9	0.0110	1	45.63	regulation of multi-organism process
MGI: 321	18	3	0.45	0.0110	1	45.63	increased bone marrow cell number
GO:30388	4	2	0.23	0.0112	1	46.38	fructose 1,6-bisphosphate metabolic process
GO:70061	4	2	0.23	0.0112	1	46.38	fructose binding
GO:31647	38	5	1.34	0.0112	1	46.38	regulation of protein stability
GO:10165	13	3	0.52	0.0114	1	47.23	response to X-ray
MGI: 4249	14	4	1.14	0.0114	1	47.23	abnormal crista ampullaris morphology
GO: 6461	377	30	20.13	0.0116	1	48.07	protein complex assembly
GO:70271	377	30	20.13	0.0116	1	48.07	protein complex biogenesis
GO:33574	11	3	0.53	0.0116	1	48.07	response to testosterone stimulus
MGI: 859	15	6	2.36	0.0118	1	48.91	abnormal somatosensory cortex morphology
PAN-F 286	154	11	5.37	0.0118	1	48.91	Other DNA-binding protein

GO:51592	47	9	4.21	0.0120	1	49.67	response to calcium ion
KEGG 3060	21	3	0.69	0.0120	1	49.67	Protein export

Table S5. CNVs in 727 cases with ADHD. Batch 1 consists of 318 cases and batch 2 consists of 409 cases with ADHD

1st CNV						**2nd CNV**					
Chr	**CNV start**	**CNV end**	**Batch**	**CNV type**	**CNV Size**	**Chr**	**CNV start**	**CNV end**	**Batch**	**CNV type**	**CNV Size**
1	245714416	246522135	1	Deletion	807720	11	5582423	7488751	1	Deletion	1906329
1	159732044	160485312	1	Deletion	753269						
1	235967993	237757467	1	Duplication	1789475						
2	32497032	33181898	1	Duplication	684867						
2	153846483	154652950	1	Duplication	806468						
3	849785	1451706	1	Duplication	601922						
3	3999657	4922174	1	Duplication	922518						
3	1166638	2183832	1	Duplication	1017195						
3	174547344	176016137	1	Duplication	1468794						
3	2969491	4461303	1	Deletion	1491813						
3	96242194	98639625	1	Duplication	2397432						
4	65791505	66605654	1	Deletion	814150	4	89231344	90528335	1	Duplication	1296992
4	75931128	77058132	1	Duplication	1127005						
4	26350218	27635050	1	Duplication	1284833						
4	23596065	27014659	1	Duplication	3418595						
7	122788319	123645842	1	Duplication	857524						
7	69777660	71572992	1	Duplication	1795333						
8	85438801	88424995	1	Deletion	2986195	17	31964475	33297438	1	Duplication	1332964
8	89227035	90419753	1	Duplication	1192719						
11	133553353	134382876	1	Duplication	829524						
11	67841909	69060612	1	Duplication	1218704						
13	63330923	63886321	1	Deletion	555399	20	12795614	14242196	1	Duplication	1446583
15	29734334	30302218	1	Duplication	567885						
15	29734334	30302218	1	Duplication	567885						
15	27000239	28153539	1	Duplication	1153301						
15	30688712	32587887	1	Duplication	1899176						

15	21016722	25902239	1	Duplication	4885518						
16	15408600	16190572	1	Duplication	781973						
16	21851681	22651534	1	Deletion	799854						
16	15387380	16190572	1	Duplication	803193						
16	29563594	30367556	1	Deletion	803963						
16	15387380	16197033	1	Duplication	809654						
16	15387380	16197033	1	Duplication	809654						
16	15398985	18174650	1	Duplication	2775666						
16	15156431	18174650	1	Duplication	3018220						
17	31979521	33318471	1	Deletion	1338951						
1	53772097	54338898	2	Duplication	566802						
1	144975398	146268315	2	Duplication	1292918						
1	5220394	5754188	2	Duplication	533795						
1	5198919	5747986	2	Duplication	549068						
2	32487194	33181898	2	Duplication	694705						
2	128985135	129881989	2	Deletion	896855						
2	106690781	108292465	2	Duplication	1601685						
2	107907419	109818614	2	Deletion	1911196						
3	193473269	194025326	2	Duplication	552058						
3	32039611	33903472	2	Duplication	1863862						
4	184952586	185493309	2	Duplication	540724						
4	71457385	72257388	2	Duplication	800004						
4	18233904	19901337	2	Duplication	1667434						
4	189649974	190598641	2	Deletion	948668						
6	122085305	122622855	2	Duplication	537551						
7	17811400	18312755	2	Duplication	501356	16	15032942	16197033	2	Duplication	1164092
8	9082416	9659969	2	Duplication	577554						
8	5374826	6304573	2	Deletion	929748						
8	43143782	43910848	2	Duplication	767067						

8	18578565	19386565	2	Duplication	808001						
10	47920669	50764666	2	Deletion	2843998						
11	102605727	106728114	2	Deletion	4122388						
11	59437619	60222063	2	Deletion	784445						
12	34122001	34711193	2	Duplication	589193						
12	28812958	29402567	2	Duplication	589610						
12	33175713	33809963	2	Deletion	634251						
13	22494127	23860983	2	Duplication	1366857						
14	92009962	92767834	2	Duplication	757873						
15	29722573	30302218	2	Duplication	579646						
15	29722573	30302218	2	Duplication	579646						
15	29722573	30302218	2	Duplication	579646						
15	30713368	32447708	2	Deletion	1734341						
15	29722573	30302218	2	Duplication	579646						
15	31406234	31913133	2	Duplication	506900						
15	82183518	82749322	2	Duplication	565805	16	26396505	27321840	2	Duplication	925336
16	15032942	16197033	2	Duplication	1164092						
16	45096893	48052382	2	Duplication	2955490						
16	85987740	86536663	2	Deletion	548924						
17	31889664	33319881	2	Duplication	1430218						
17	51088	583572	2	Duplication	532485						
19	32615675	33220146	2	Deletion	604472						
19	23164768	23816927	2	Duplication	652160						
22	17257787	19792353	2	Duplication	2534567						

1. Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MA, Bender D, Maller J, Sklar P, de Bakker PI, Daly MJ, Sham PC. PLINK: a tool set for whole-genome association and population-based linkage analyses. Am J Hum Genet. 2007 Sep;81(3):559-75.
2. Price AL, Weale ME, Patterson N, Myers SR, Need AC, Shianna KV, Ge D, Rotter JI, Torres E, Taylor KD, Goldstein DB, Reich D. Long-range LD can confound genome scans in admixed populations. Am J Hum Genet. 2008 Jul;83(1):132-5; author reply 5-9.
3. Neale BM, Medland SE, Ripke S, Asherson P, Franke B, Lesch KP, Faraone SV, Nguyen TT, Schafer H, Holmans P, Daly M, Steinhausen HC, Freitag C, Reif A, Renner TJ, Romanos M, Romanos J, Walitza S, Warnke A, Meyer J, Palmason H, Buitelaar J, Vasquez AA, Lambregts-Rommelse N, Gill M, Anney RJ, Langely K, O'Donovan M, Williams N, Owen M, Thapar A, Kent L, Sergeant J, Roeyers H, Mick E, Biederman J, Doyle A, Smalley S, Loo S, Hakonarson H, Elia J, Todorov A, Miranda A, Mulas F, Ebstein RP, Rothenberger A, Banaschewski T, Oades RD, Sonuga-Barke E, McGough J, Nisenbaum L, Middleton F, Hu X, Nelson S. Meta-analysis of genome-wide association studies of attention-deficit/hyperactivity disorder. J Am Acad Child Adolesc Psychiatry. 2010 Sep;49(9):884-97.
4. Lin DY, Sullivan PF. Meta-analysis of genome-wide association studies with overlapping subjects. Am J Hum Genet. 2009 Dec;85(6):862-72.
5. Simes RJ. An improved Bonferroni procedure for multiple tests of significance. Biometrika. 1986;73:751-4.