

Trait	Sample Size	Build	Frequency	Number of SNPs	Imputation score <0.9	Ambiguous markers	Indels	MAF<0.1	Final number of SNPs	below 10 ⁻⁵	Independent markers <10-5 selected after conditional regression	PMID
SCZ	82,315	hg19	Calculated from 1000 genomes EUR	9,444,231	2,254,640	1,024,909	543.413	2,109,325	3,511,943	18.755	409	25056061
Autism	15,954	hg19	Frequency of AI is provided	6,517,324	830.978	805.673	440.348	766.356	3,673,969	119	14	
BPD	51,710	hg19	Unaff_frq	13,414,632	5,976,560	1,061,507	530.623	2,385,153	3,460,789	3.665	135	31043756
MDD	18,759	hg18	CEU_frq	1,235,110	259.364	74.55	no data	168.062	733.133	16	5	22472876
Alzheimer	54,162	hg19	Calculated from 1000 genomes EUR	7,055,881	no data	1,051,453	no data	2,264,775	3,679,696	1.985	57	24162737
ADHD	55,374	hg19	Calculated from 1000 genomes EUR	8,047,420	691.02	1,029,646	5.727	2,725,753	3,595,274	1.929	77	29325848
Anorexia	14,477	hg19	Calculated from 1000 genomes EUR	13,694,841	6,129,145	1,077,505	538.548	2,230,624	3,508,450	170	10	24514567, 21079607
ICV	11,603	hg19	frq1 provided	8,700,908	no data	1,234,188	707.741	2,926,880	3,832,099	312	11	25607358
Hippocampus	11,603	hg19	frq1 provided	8,636,348	no data	1,222,741	717.675	2,846,989	3,848,943	89	10	25607358
Accumbes	11,603	hg19	frq1 provided	8,632,986	no data	1,222,296	717.334	2,842,016	3,851,340	17	8	25607358
Palladium	11,603	hg19	frq1 provided	8,630,495	no data	1,221,964	717.175	2,840,875	3,850,481	38	8	25607358
Amygdala	11,603	hg19	frq1 provided	8,612,778	no data	1,222,458	696.458	2,843,832	3,850,030	81	10	25607358
Putamen	11,603	hg19	frq1 provided	8,634,199	no data	1,222,436	717.435	2,844,739	3,849,589	837	18	25607358
Caudate	11,603	hg19	frq1 provided	8,636,889	no data	1,222,826	717.664	2,847,941	3,848,458	123	14	25607358
Thalamus	11,603	hg19	frq1 provided	8,641,328	no data	1,223,482	718.051	2,847,113	3,852,682	66	15	25607358
Anxiety	18,000	hg19	Freq_a1	6,330,995	no data	987.949	no data	1,295,732	4,047,314	76	13	26857599
Education	293,723	hg19	EAF from CEU, GBR and TSI	8,146,840	no data	1,254,949	no data	2,972,375	3,919,516	15.919	646	27225129
Subjective well-being	298,420	hg19	EAF	2,268,674	no data	350.114	no data	368.478	1,550,082	127	36	27089181
Depressive symptoms	161,460	hg19	EAF	6,524,474	no data	1,006,046	no data	1,635,133	3,883,295	470	64	27089181
Neuroticism	170,911	hg19	EAF	6,524,432	no data	1,006,044	no data	1,782,037	3,992,165	7.362	145	27089181
Extraversion	63,661	hg19	Maf from 1000 genomes, EUR ph1 v3	6,941,603	no data	1,080,685	no data	1,998,870	3,862,048	51	9	24828478
Openness	17,375	hg18	HapMap Maf	2,305,640	316.019	298.6	no data	301.157	1,367,494	25	8	21173776
Agreeableness	17,375	hg18	HapMap Maf	2,305,461	311.517	295.245	no data	299.274	1,378,560	9	3	21173776
Conscientiousness	17,375	hg18	HapMap Maf	2,305,682	308.209	292.906	no data	296.836	1,367,566	85	5	21173776
gF	282,014	hg19	Calculated from 1000 genomes EUR	12,871,897	no data	1,922,572	no data	4,788.896	3,581,785	22.672	474	29844566
Agression	18,988	hg18	Calculated from 1000 genomes EUR	2,188,528	no data	338.219	no data	270.294	1,555,097	17	4	26087016
Loneliness	10,760	hg19	EUR MAF provided	5,768,558	no data	872.296	no data	2,014,353	2,817,242	14	7	27629369
Total # of SNPs											2 215	
Unique SNPs											2 290	
SNPs not in genes											775	
Total genes											1 410	
Genes with one SNP per gene											1 168	
Genes with 2+ SNP per gene											242	
Blocks with unique combination of SNPs											1 161	
Blocks with one SNP											935	
Blocks with 2+ SNPs											226	

Columns: Trait – name of the trait; Sample Size – sample size of the study; Build – Genome build in downloaded data; Frequency – column name of the frequency in the original data, if frequency was provided. If frequency was not provided, it was calculated based on EUR sample from 1000 Genomes; Number of SNPs – number of SNPs in the original study; Imputation score <0.9 – number of SNPs that were filtered out based on imputation score, if imputation score is provided in the original data; Ambiguous markers – number of filtered ambiguous markers; Indels – number of filtered indels, if data is available; MAF<0.1 – number of SNPs filtered based on MAF 10%; Final number of SNPs – number of SNPs after filtering. Below 10⁻⁵ – Number of SNPs that passed threshold 10⁻⁵; Independent markers <10⁻⁵ selected after conditional