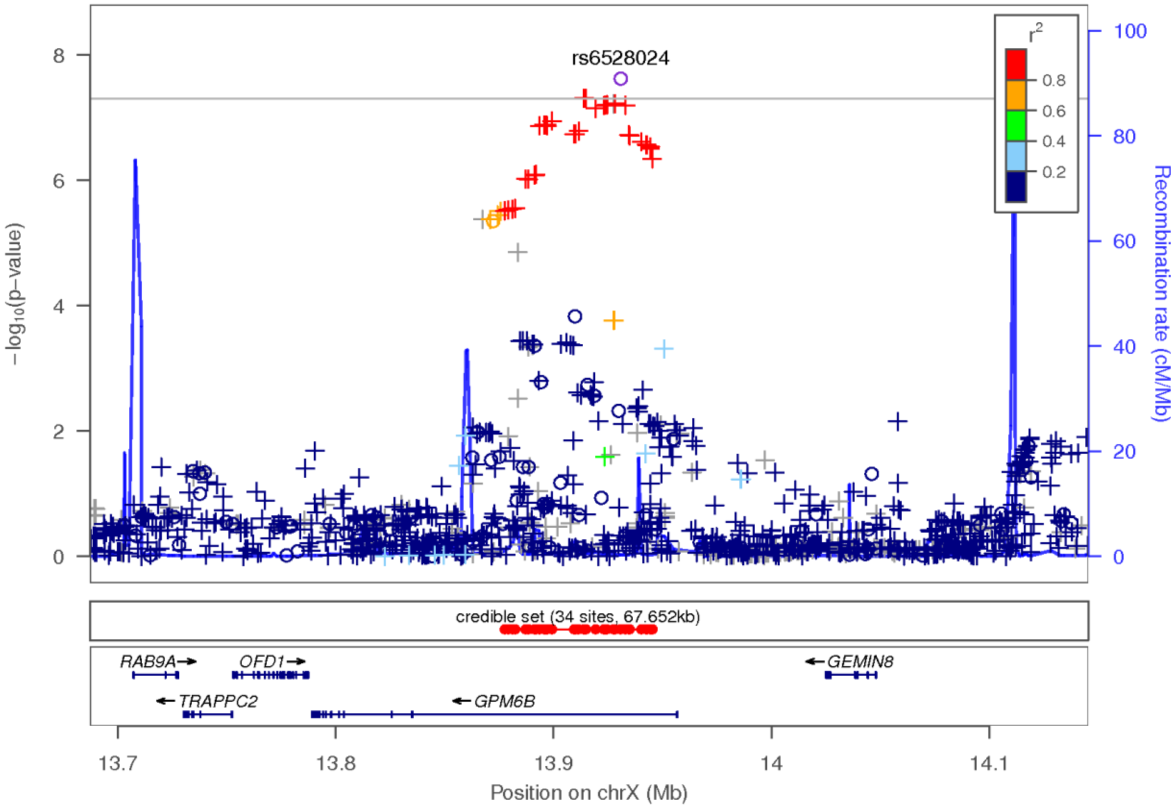
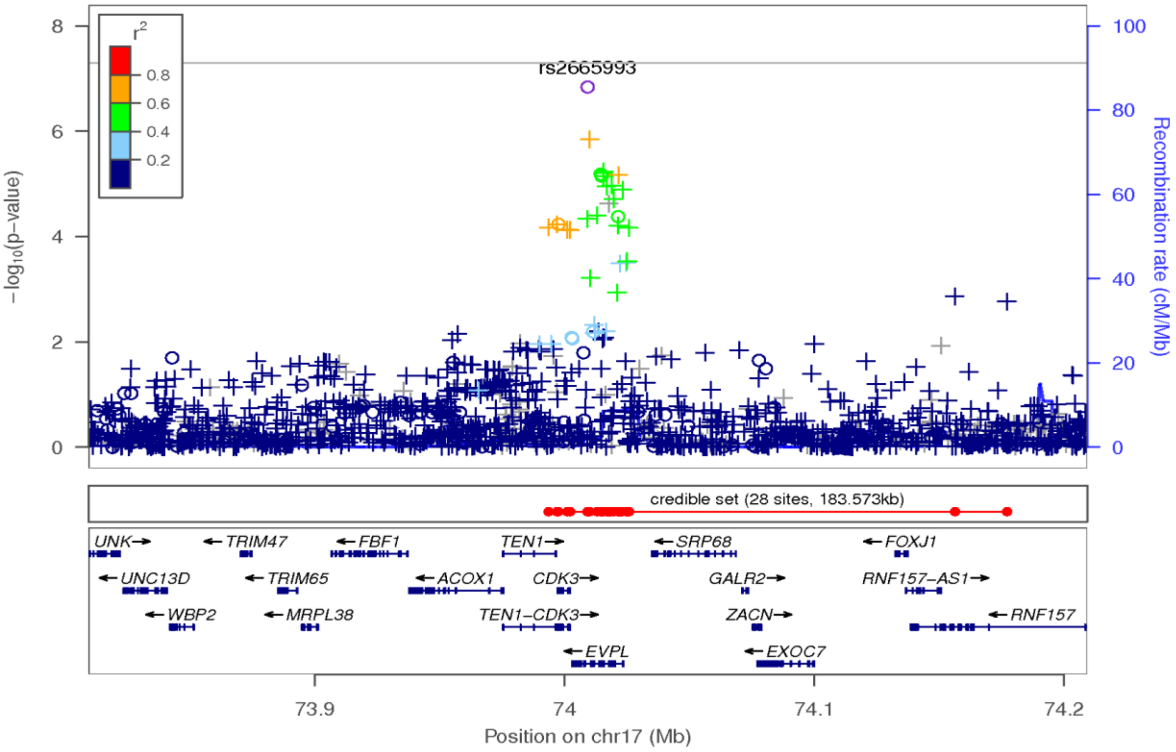


Supplementary Figure 1 Regional association plot focusing on top SNP rs6528025 at 3' of *GPM6B* gene on chromosome X at position 13.9 Mb. This plot was generated using LocusZoom[1]. The -log$_{10}$(*P* value) is shown on the left *y*-axis; position in Mb is on the *x*-axis. Recombination rates (expressed in centiMorgans cM per Mb; NCBI Build GRCh37; highlighted in blue) are shown on the right *y*-axis. Pairwise linkage disequilibrium (r^2) of each SNP with the top SNP in the region is indicated by its color. Crossed points represent imputed SNPs, circles represent directly genotyped SNPs. The statistical tests used were two-sided; sample size = 23,217.



Supplementary Figure 2 Regional association plot showing the second index SNP rs2665993, located in the *EVPL* gene on chromosome 17. This plot was generated using LocusZoom[1]. The -log$_{10}$(*P* value) is shown on the left *y*-axis; position in Mb is on the *x*-axis. Recombination rates (expressed in centiMorgans cM per Mb; NCBI Build GRCh37; highlighted in blue) are shown on the right *y*-axis. Pairwise linkage disequilibrium (r^2) of each SNP with the top SNP in the region is indicated by its color. Crossed points represent imputed SNPs, circles represent directly genotyped SNPs. The statistical tests used were two-sided; sample size = 23,217.

Supplementary Table 1

This table shows the number of SNPs after applying various quality control filters for genotyped and imputed dosage data, and association test results data, as described in the Online Methods.

	Genotyped	Imputed Dosage	Association Results
no filters	1,050,074	15,574,220	-
Hardy-Weinberg Equilibrium > 1e-20	954,373	-	-
genotype call rate > 90%	934,855	-	-
imputation quality	-	13,230,301	-
Minor Allele Frequency < 0.1% *	-	-	11,508,756

* = poor residual behavior

Supplementary Table 2

This table shows demographic characteristics of the 23andMe cohort.

	23andMe cohort *	Sample Size **
Demographics		
Age in years (mean, SD)	53.79 (16.08)	23,677
Age in years (range)	18-101	23,677
Female	55.30%	23,677
BMI (mean, S.D)	27.00 (5.79)	22,889
Years of education (mean, SD)	16.75 (2.62)	20,460
Household income (mean, SD)	6.07 (1.98)	17,919
Marital status (married vs. unmarried)	49.3%	21,862
Drug use [1]		
Drug exposure lifetime use	2.95 (2.04)	23,111
Alcohol use		
Alcohol lifetime use (*N*, never/ever)	1,376 / 23,108	24,484
Days of alcohol use (past 30 days)	8.78 (9.82)	21,727
Days of alcohol use (heaviest, lifetime, 30-day period)	13.78 (10.96)	21,229
Smoking [1]		
Smoking lifetime use (*N*, never/ever)	10,770 / 13,695	24,465
Number of cigarettes per day (past 30 days)	1.45 (5.69)	12,773
Number of cigarettes per day (heaviest, lifetime, 30-day period)	12.85 (14.93)	12,598
Days of tobacco use (past 30 days)	3.12 (8.65)	12,716
Days of tobacco use (heaviest, lifetime, 30-day period)	17.20 (13.23)	12,380
Cannabis Use [1]		
Cannabis lifetime use (*N*, never/ever)	10,514 / 13,864	24,378
Days of cannabis use (past 30 days)	1.75 (6.04)	13,067
Days of cannabis use (heaviest, lifetime, 30-day period)	7.08 (9.99)	12,805
Caffeine [1]		
Caffeine use (cups of coffee per day)	1.90 (2.12)	22,865
AUDIT [2]		
AUDIT total score (sample range 0-40)	3.84 (3.47)	20,754

* = European Ancestry only; ** = Prior to GWAS analysis (see Supplementary Table 3 for exclusion criteria; Final sample size = 23,127); *BMI* = Body Mass Index; *Household income* = 9 categories {$10K, $25K, $35K, $50K, $75K, $100K, $150K, $300K, $500K}; *Drug Use* = Lifetime drug use, one point was given for each drug the subjected endorsed having tried {Alcohol, Marijuana, Cocaine, Methamphetamines, LSD/Magic Mushrooms, Ecstasy, Prescription Stimulants (taken not as prescribed), Prescription Painkillers (taken not as prescribed), Heroin, Opium}; *AUDIT* = Alcohol Use Disorder Identification Test. Substance use was very low in this population, suggesting that DD was unlikely to be altered by substance use[3].

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Supplementary Table 3
Monetary Choice Questionnaire items.

Items	Would you rather have:	
1	$54 Today	$55 in 117 Days
2	$55 Today	$75 in 61 Days
3	$19 Today	$25 in 53 Days
4	$31 Today	$85 in 7 Days
5	$14 Today	$25 in 19 Days
6	$47 Today	$50 in 160 Days
7	$15 Today	$35 in 13 Days
8*	$55 Today	$85 Today
9	$25 Today	$60 in 14 Days
10	$78 Today	$80 in 162 Days
11	$40 Today	$55 in 62 Days
12	$11 Today	$30 in 7 Days
13	$67 Today	$75 in 119 Days
14	$34 Today	$35 in 186 Days
15	$27 Today	$50 in 21 Days
16	$69 Today	$85 in 91 Days
17*	$60 Today	$20 Today
18	$49 Today	$60 in 89 Days
19	$80 Today	$85 in 157 Days
20	$24 Today	$35 in 29 Days
21	$33 Today	$80 in 14 Days
22	$28 Today	$30 in 179 Days
23	$34 Today	$50 in 30 Days
24*	$15 Today	$35 Today
25	$25 Today	$30 in 80 Days
26	$41 Today	$75 in 20 Days
27	$54 Today	$60 in 111 Days
28	$54 Today	$80 in 30 Days
29	$22 Today	$25 in 136 Days
30	$20 Today	$55 in 7 Days

* These items are not part of the original questionnaire. We added them to identify individuals who responded carelessly. Participants choosing one or more lower monetary rewards for items 8, 17 or 24 were excluded from all analysis (because they were assumed to be responding carelessly). In addition, we excluded participants showing <80% of consistent preferences (i.e., the proportion of choices with which the *k* value is consistent). We excluded 550 subjects using these two criteria.

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Supplementary Table 4
Distribution (%) of DD scores expressed as $\log_{10}(k)$ from the Monetary Choice Questionnaire.

		Sex		Age			
$\log_{10}(k)$	Sample size	Male	Female	18-30	30-45	45-60	>60
-3.8,-2.67	6908	52.53%	47.47%	9.70%	23.60%	25.70%	41.10%
-2.67,-2.15	5607	44.75%	55.26%	9.30%	21.60%	25.90%	43.20%
-2.15,-1.73	5208	40.28%	59.72%	10.00%	22.40%	28.10%	39.50%
-1.73,-0.61	5404	39.80%	60.20%	10.20%	22.60%	27.30%	40.00%

Higher scores (more positive values) indicate higher rates of DD; meaning less value is placed on delayed rewards. Each row corresponds to a particular range.

Supplementary Table 5
Phenotypic correlations between DD and demographic, and drug (alcohol, tobacco, cannabis; current/heaviest use) and caffeine use traits.

Phenotype	Pearson *r*	t	*P* value	N**
Demographics				
Age in years	< 0.001	-0.02	0.99	23,664
Sex (male = 0, female = 1)*	0.11	16.56	< 0.0001	23,677
BMI *	0.11	17.14	< 0.0001	22,889
Household income *	-0.10	-13.48	< 0.0001	17,919
Marital status (0 = unmarried, 1 = married)	-0.01	-1.99	0.05	21,862
Years of education *	-0.17	-24.64	< 0.0001	20,460
Drug exposure lifetime *	0.05	8.29	< 0.0001	23,111
AUDIT total score	< 0.001	0.47	0.64	20,754
Alcohol use				
Days of alcohol use (past 30 days) *	-0.05	-7.33	< 0.0001	21,727
Days of alcohol use (heaviest, lifetime, 30-days period) *	-0.07	-9.85	< 0.0001	21,229
Smoking				
Number of cigarettes per day (lifetime, 30-days period) *	0.08	9.15	< 0.0001	12,773
Number of cigarettes per day (heaviest, lifetime, 30-days period)	0.04	4.18	< 0.0001	12,598
Days of tobacco use (past 30 days) *	0.09	10.19	< 0.0001	12,716
Days of tobacco use (heaviest, lifetime, 30-days period)	0.01	1.52	0.13	12,380
Cannabis use				
Days of cannabis use (past 30 days) *	0.05	6.16	< 0.0001	13,067
Days of cannabis use (heaviest, lifetime, 30-days period)	0.02	1.95	0.05	12,805
Caffeine use (cups of coffee per day)	0.01	1.81	0.07	22,865

All correlations are calculated using data from the 23andMe cohort. Pairwise phenotypic correlations (*r*); the statistical tests used were two-sided. *AUDIT* = Alcohol Use Disorder Identification Test; * = P < 0.001; ** = prior to GWAS analysis (see Supplementary Table 3 for exclusion criteria; Final sample size n= 23,127)

Supplementary Table 6
Null GWAS model with covariates

Covariates	Estimate	SE	t	Pr(>|t|)	Variance explained
Sex	0.15	0.01	16.00	2.10×10^{-57}	1.148 %
Age (inverse normalized)	0.01	0.01	1.20	0.21×10^{-1}	0.000 %
PC 0	0.00	0.01	0.60	5.30×10^{-1}	0.002 %
PC 1	0.00	0.01	0.10	9.40×10^{-1}	0.001 %
PC 2	0.04	0.01	7.30	3.60×10^{-13}	0.228 %
PC 3	−0.02	0.01	−3.20	1.20×10^{-3}	0.066 %
PC 4	0.02	0.01	4.80	1.40×10^{-6}	0.118 %
Platform v2	−0.02	0.03	−0.90	3.70×10^{-1}	0.071 %
Platform v3.1	0.06	0.02	3.50	4.00×10^{-4}	0.020 %
Platform v4	0.09	0.02	6.50	9.00×10^{-11}	0.184 %

Results of fitting a model for delay discounting based on covariates. Principal components (PC) computed from all SNP data from 23andMe research participants with European ancestry (n= 23,127). Effect sizes are in units of standard deviations.

Supplementary Table 7

Strongest associations ($P < 10^{-7}$) with DD in the 23andMe cohort

SNP id	chr	cytoband	bp	alleles	EAF	*P* value	β	SE	95% CI	R^2	*P* value batch effect	localization
rs6528024	X	Xp22.2	13930922	C/T	0.025	2.40×10^{-8}	−0.10	0.017	[-0.14,-0.07]	0.9990	0.0030	intron
rs2665993	17	17q25.1	74009211	A/G	0.376	1.40×10^{-7}	−0.04	0.007	[-0.05,-0.02]	0.9990	0.34	intron
rs146042968	18	18q12.1	25527620	G/T	0.987	3.00×10^{-7}	−0.17	0.031	[-0.23,-0.10]	0.8967	0.79	intron
rs192923788	2	2q11.2	102156781	A/G	0.003	3.90×10^{-7}	−0.39	0.077	[-0.55,-0.24]	0.6966	0.57	intergenic
rs455636	21	21q21.3	31351431	A/C	0.947	6.00×10^{-7}	0.08	0.015	[0.05,0.11]	0.9912	0.29	intergenic
rs187716580	18	18q12.3	40690093	C/T	0.003	8.00×10^{-7}	−0.40	0.081	[-0.56,-0.24]	0.5603	0.21	intron

SNP id = marker name; *chr* = chromosome; *bp* = position (HG37); *alleles* = Other Allele/Effect Allele; *EAF* = effect allele frequency; β = beta effect size; *CI* = confidence interval; R^2 = average score across imputation batches. The statistical tests used were two-sided; sample size = 23,217.

Supplementary Table 8

Associations (P < 0.05) between previous candidate genes and DD

										23andMe					
Chr	SNP id	Gene	Reference	EA	EAF	*p*	β	se	N	EA	EAF	*p*	β	se	N
3	rs3773678	*DRD3*	[1]	T	0.17	0.03	-0.19	NR	175 HA	G	0.87	0.20	-0.01	0.01	23127
	rs7638876			G	0.35	0.04	-0.14			T	0.67	0.41	-0.01	0.01	
5	rs464049	*SLC6A3*		G	0.45	0.02	-0.17			G	0.44	0.01	0.02	0.01	
	rs3756450			G	0.12	0.01	-0.29			G	0.12	0.25	0.01	0.01	
	rs12652860			A	0.27	0.01	0.01		174 HA	C	0.72	0.79	<0.01	0.01	
		DAT	[2]	ADHD x $\text{DAT}_{110/6}$	NR	<0.05	0.16*	0.00	36 ADHD, 32 HV	NR					
6	rs1360780	*FKBP5*	[3]	T	0.27	0.05	-0.67	0.29	84 HA	T	0.30	0.13	-0.01	0.01	
7	rs10249982	*DDC*	[1]	G	0.22	0.07	-0.02	NR	175 HA	G	0.24	0.70	<-0.01	0.01	
	rs10244632			T	0.25	0.01	-0.20			T	0.25	0.91	<0.01	0.01	
	rs1466163			A	0.11	0.05	-0.23			G	0.88	0.81	0.00	0.01	
	rs10499696			C	0.11	0.01	-0.28			C	0.10	0.97	<0.01	0.01	
10	rs363338	*SLC18A2*		G	0.30	0.01	-0.21			G	0.27	0.76	<0.01	0.01	
	rs1800544	*ADRA2A*	[4]	cocaine x G	0.30	<0.01	0.22*		215	T	0.69	0.76	<0.01	0.01	
11	rs1800497	*ANKK1*	[5]	G	0.22	0.01	0.02		713 DS	G	0.85	0.85	<0.01	0.01	
	rs6277	*DRD2*	[6]	G	0.05	0.04	1.41	0.577	90 HA	G	0.45	0.86	<0.01	0.01	
	VNTR	*DRD4*	[1]	7R+	0.14	0.05	-0.29	NR	175	NR					
22	rs4680	*COMT*	[7]	G	0.48	0.01	0.08*		10 HA, 9 AA	G	0.48	0.93	<-0.01	0.01	
			[2]	G	0.48	<0.05	0.10*	0.00	36 ADHD, 32 HV						
			[8]	age x G	0.48	0.01	0.07*		70 HA, 72 LA						
			[9]	G	0.54	<0.01	0.30	NR	73 HA						
			[5]	G	0.48	0.01	0.02		713 DS						

chr = chromosome; *SNP id* = marker name; *EA* = Effect Allele; *EAF* = effect allele frequency; β = beta effect size; * = eta squared or cohen's estimate of effect size; *NR* = not reported; *HA* = healthy adults; *DS* = daily smokers; *AA* = abstinent alcoholics; *LA* = late adolescents. Some of the reasons for discrepancies between candidate gene studies and our GWAS findings include small sample size of the candidate gene study, multiple testing within and between studies, publication bias, and an expectation that true allelic effect sizes are similar to those reported in GWAS[10].

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Supplementary Table 9

Top 10 entries for the gene-based association analysis using transcriptome data (S-PrediXcan)

gene name	*Z* score	effect size	*P* value	FDR < 0.05	gene expression variance	r^2 predicted performance	*P* predicted performance	*Q* predicted performance	SNPs used (N)	SNPs covariance (N)	SNPs model (N)	brain tissue
CDK3	5.18	0.09	2.19E-07	Yes	0.09	0.18	7.62E-05	5.40E-04	11	12	12	hippocampus
STRN4	-4.51	-0.08	6.45E-06	No	0.08	0.08	8.63E-03	2.05E-02	12	12	12	hypothalamus
TEN1	4.41	0.04	1.03E-05	No	0.37	0.50	7.02E-17	1.90E-15	22	23	23	cerebellum
PPP1R1C	-4.36	-0.06	1.33E-05	No	0.13	0.07	2.10E-02	3.40E-02	40	40	40	hippocampus
TEN1	4.32	0.09	1.54E-05	No	0.06	0.14	2.80E-04	9.15E-04	11	11	11	frontal cortex
CDK3	4.26	0.05	2.03E-05	No	0.20	0.35	4.12E-08	1.04E-06	9	9	9	anterior cingulate cortex
CDK3	4.16	0.07	3.18E-05	No	0.09	0.24	4.45E-06	5.41E-05	6	6	6	hypothalamus
TEN1	4.05	0.05	5.12E-05	No	0.20	0.25	2.03E-06	2.69E-05	16	16	16	hippocampus
CDK3	4.03	0.05	5.69E-05	No	0.14	0.32	6.17E-09	5.02E-08	4	4	4	cerebellar hemisphere
TEN1	4.00	0.06	6.30E-05	No	0.09	0.15	7.85E-05	2.89E-03	9	9	9	caudate basal ganglia

Gene name = as listed by the Transcriptome Model, generally extracted from Genquant (http://www.gencodegenes.org/); *Z score* = summary PrediXcan's association result for the gene; *effect size* = summary PrediXcan's association *effect size* for the gene; *P value* = P-value of the *effect size* statistic; *FDR* = False discovery rate < 5%; *gene expression variance* = variance of the gene expression, calculated as *W' * G * W* (where *W* is the vector of SNP weights in a gene's model, *W'* is its transpose, and *G* is the covariance matrix); r^2 *predicted performance* = prediction performance of tissue model's correlation to gene's measured transcriptome; *P predicted performance* = *P* value of tissue model's correlation to gene's measured transcriptome (prediction performance); *Q predicted performance* = *Q* value of tissue model's correlation to gene's measured transcriptome (prediction performance); *SNPs used (N)* = number of SNPs from GWAS used in Summary PrediXcan analysis; *SNPs covariance (N)* = number of SNPs in the covariance matrix; *SNPs model (N)* = number of SNPs in the model; *Brain tissue* gene expression models for different 10 brain tissues (anterior cingulate cortex, caudate basal ganglia, cerebellar hemisphere, cerebellum, cortex, frontal cortex, hippocampus, hypothalamus, nucleus accumbens basal ganglia, and putamen basal ganglia). Sample size = 23,217.

Supplementary Table 10

Genetic correlations between DD and other relevant traits using LD Regression Score (LDSC)

Phenotype	Sample Size	Reference	Genetic correlation (r_g)	Standard error	*P* value	FDR < 0.05
Years of Education	293,723	Okbay et al, 2016a	-0.67	0.09	7.97E-15	Yes
College attainment	95,427	Rietveld et al, 2013	-0.93	0.15	3.01E-10	Yes
Years of Education	101,069	Rietveld et al, 2013	-0.89	0.14	4.29E-10	Yes
Childhood IQ	12,441	Benyamin et al, 2014	-0.63	0.17	1.63E-04	Yes
ADHD	53,293	Demontis et al, 2017	0.37	0.11	7.76E-04	Yes
Schizophrenia PGC2	77,096	Ripke et al, 2014	-0.22	0.07	1.16E-03	Yes
Major Depressive Disorder	18,759	Ripke et al, 2013	0.47	0.17	6.87E-03	Yes
Smoking lifetime	74,035	Furberg et al, 2010	0.32	0.12	7.98E-03	Yes
Former smoker	70,675	Furberg et al, 2010	-0.41	0.16	8.89E-03	Yes
BMI	339,224	Locke et al, 2015	0.18	0.07	8.93E-03	Yes
Obesity class 1	98,697	Berndt et al, 2013	0.21	0.08	1.85E-02	Yes
Neuroticism	170,911	Okbay et al, 2016b	0.18	0.08	2.25E-02	Yes
Depressive Symptoms	161,460	Okbay et al, 2016b	0.24	0.11	3.17E-02	No
Daily cigarettes	68,028	Furberg et al, 2010	0.39	0.18	3.33E-02	No
Neuroticism	106,716	Smith et al, 2016	0.18	0.09	3.98E-02	No
Smoking Age onset	47,961	Furberg et al, 2010	-0.42	0.23	6.66E-02	No
Anorexia Nervosa	17,767	Boraska et al, 2014	-0.28	0.16	8.30E-02	No
Neo-openness to experience	17,375	Moor et al, 2012	-0.27	0.19	1.73E-01	No
Height	253,288	Wood et al, 2014	-0.08	0.06	1.77E-01	No
Bipolar disorder	16,731	Sklar et al, 2011	-0.17	0.13	2.19E-01	No
Subjective Wellbeing	298,420	Okbay et al, 2016b	0.12	0.11	3.00E-01	No
Extraversion	63,030	van den Berg et al, 2016	0.16	0.15	3.08E-01	No
Caudate	13,171	Hibar et al, 2015	-0.14	0.15	3.31E-01	No
Hippocampus	13,171	Hibar et al, 2015	0.19	0.21	3.41E-01	No
Childhood obesity	13,848	Bradfield et al, 2012	0.09	0.11	3.84E-01	No
Cannabis lifetime use	32,330	Stringer et al, 2016	-0.05	0.15	7.49E-01	No
Intracranial Brain Volume	13,171	Hibar et al, 2015	-0.05	0.18	8.00E-01	No
Nucleus Accumbens	13,171	Hibar *et al*, 2015	-0.03	0.25	9.09E-01	No

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LDSC: https://github.com/bulik/ldsc

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