

Shared genetic architecture between obesity and psychiatric disorders reveals comorbid etiology and therapeutic targets

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Supplementary Methods

Pleiotropic analysis under composite null hypothesis (PLACO) and Bayesian colocalization test (COLOC) analysis

The PLACO approach uses Z-scores and P values to detect pleiotropic variants for two binary and/or continuous phenotypes, even if there are overlapping samples [1]. Data harmonization was applied to make sure each variant was in the same direction for both phenotypes. To avoid the false positive results caused by the variants with strong effects in one phenotype but not in another, all the variants with $Z\text{-score}^2 > 80$ were removed from the analysis.

The advantage of COLOC is using genome-wide association study (GWAS) summary statistics and the Bayes statistical method to estimate the associations for common or rare variants with two phenotypes [2]. Independent genetic variants ($r^2 < 0.001$ and window = 10,000 kb) that reached the genome-wide significance ($P < 5 \times 10^{-8}$ or $P < 5 \times 10^{-6}$, for the phenotypes that have two or fewer genetic variants) were extracted from the GWAS summary statistics as the leading single nucleotide polymorphism (SNP). All the SNPs located in the ± 500 kb window near the leading SNP were extracted from the pair of adiposity traits and psychiatric disorders for COLOC analysis. For the COLOC analysis, five hypotheses were tested, H_0 : no association for both phenotypes; H_1 : association with phenotype 1 only; H_2 : association with phenotype 2 only; H_3 : two independent SNPs associated with two phenotypes, respectively; H_4 : one SNP associated with both phenotypes. The summary posterior probability of hypothesis 4 ($PP.H4 > 0.8$) indicated that the region contains the shared causal variants for both phenotypes. Finally, the SNP with a highest $PP.H4$ was selected as the top significant variant.

Joint-tissue imputation (JTI) approach

To conduct the JTI transcriptome-wide association study (TWAS) analysis, we download the Genotype-Tissue Expression (GTEx) pre-trained prediction models from Zenodo (<https://doi.org/10.5281/zenodo.3842289>) [3]. Then we tested the associations between predicted gene expression and each trait in 26 tissues. After that, we compared candidate-shared genes (i.e., shared genes identified by PLACO and COLOC in the previous step; **Fig. 1A**) in each linkage pair to generate the final shared genes which are associated with both adiposity traits and psychiatric disorders in at least one tissue.

Gene-based integrative fine-mapping through conditional TWAS (GIFT) approach

We followed the two-stage version of GIFT using the GWAS summary statistics and pre-trained weights as input [4]. The detailed manual and example codes can be found on the github (yuanzhongshang.github.io/GIFT). We used the GTEx v8 multi-tissue expression weights from the FUSION approach [5]. Shared genes followed the similar criteria in the JTI analysis were finally retained as the causal shared genes.

Univariable two-sample Mendelian randomization (MR) analysis

The instrumental variants (IVs) used in all MR analyses satisfied three core assumptions: (1) the IVs must be vigorously associated with the exposure in univariable two-sample MR; (2) the IVs must not be associated with confounders of the associations between instruments of each exposure and each outcome; and (3) the effect of IVs on the outcome must go through the exposure. For the phenotypes that have two or fewer candidate IVs such as legs-leg fat ratio and trunk-trunk fat ratio in men, visceral adipose tissue and abdominal subcutaneous adipose tissue in men and women, and post-traumatic stress disorder, we used $P < 5 \times 10^{-6}$ as the threshold. We first utilized the `clump_data` function ($r^2 < 0.001$ and window=10,000 kb) in the `TwoSampleMR` R package to identify the representative genetic variants. Based on the European 1000 genomes reference panel, bi-allelic genetic variants with minor allele frequency > 0.01 would be retained for the following process. Each genetic variant was searched in the adiposity traits and psychiatric disorders GWAS summary statistics for the SNP-outcome associations. If a variant was absent from the outcome summary statistics, a high linkage disequilibrium (LD) proxy SNP (European descent, $r^2 > 0.8$, and window=500 kb) would be searched via the LDproxy tool (<https://ldlink.nci.nih.gov/?tab=ldproxy>) and replaced the original SNP for the outcome association. SNPs that were absent from the outcome GWAS summary statistics and did not have proxies were discarded from the MR analysis. After the multiple testing correction, an FDR-adjusted $P < 0.05$ was considered statistically significant.

The main MR results were tested via the inverse-variance weighted (IVW) method. The IVW method could generate precise MR estimations using multiple valid genetic variants from the GWAS data set [6]. A random-effects IVW method was

used when more than three IVs were available in the MR analysis [7]. Otherwise, a fixed-effect IVW method was used if there are only three or fewer IVs. An average F statistic was estimated for each exposure phenotype. Generally, F statistics greater than 10 supported the strong IVs and indicated that the MR estimates are unlikely to be influenced by weak instrument bias [8]. Furthermore, Cochran's Q test was used to assess the heterogeneity of causal effect estimates [9].

In the sensitivity MR analysis, several robust methods were employed, namely weighted median, weighted mode, MR-Egger, and MR pleiotropy residual sum and outlier (MR-PRESSO) [10-13]. The weighted median method could provide a consistent estimation even when the IV set contains less than 50% invalid genetic variants [10]. The weighted mode could provide a consistent causal estimate regardless of horizontal pleiotropy in the majority of IVs when the ZEROModal Pleiotropy Assumption is satisfied [11]. The MR-Egger regression could yield a consistent result even if all genetic variants are invalid under the Instrument Strength Independent of Direct Effect assumption [12]. The MR-PRESSO was used to obtain results when removing heterogeneous IVs [13].

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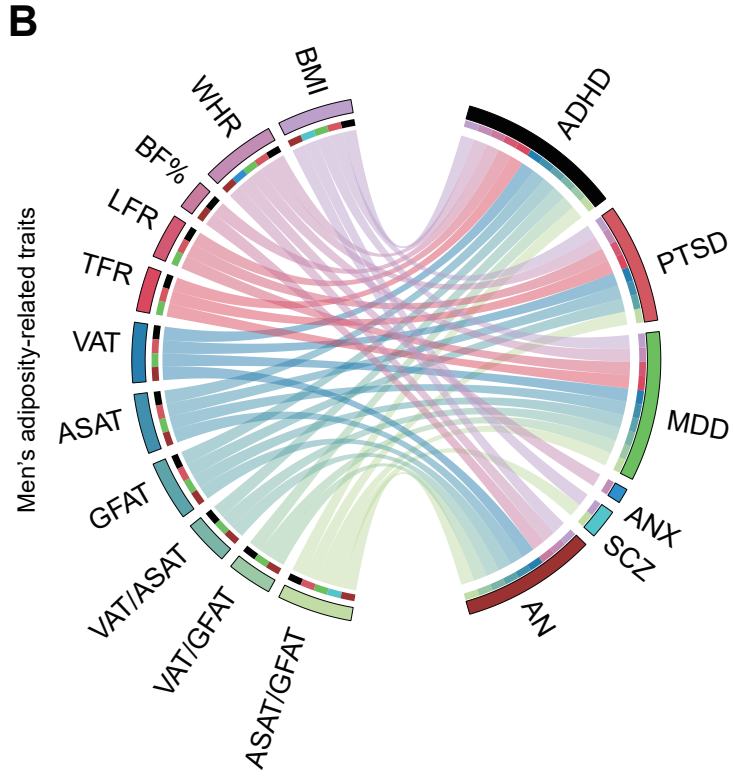
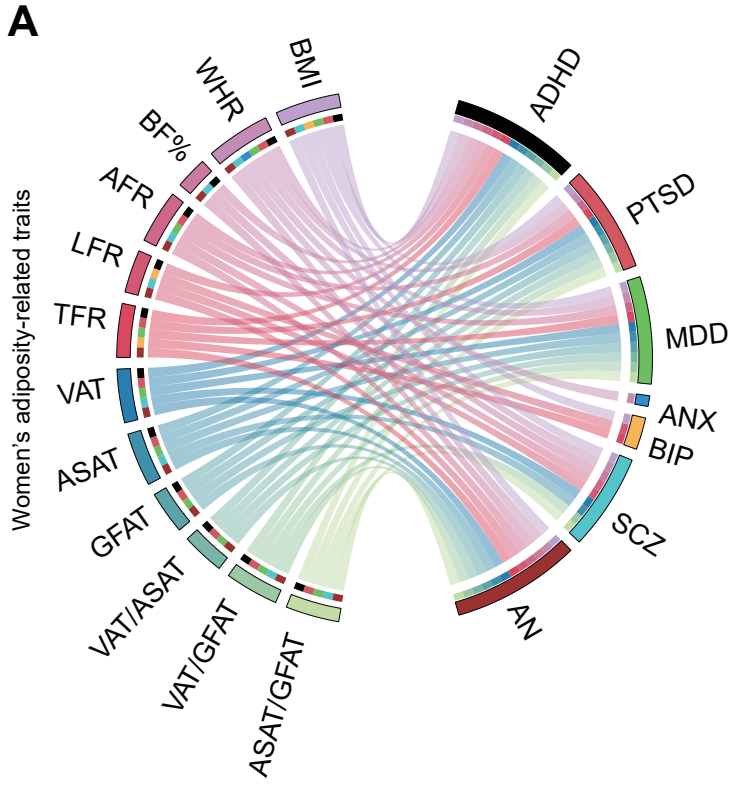
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Supplementary Figure 1. Linkage pairs between women's and men's adiposity traits and psychiatric disorders.

A. Pairs of women's adiposity traits and psychiatric disorders with significant genetic correlation in either LDSC or HDL. B. Pairs of men's adiposity traits and psychiatric disorders with significant genetic correlation in either LDSC or HDL.

Abbreviations: ADHD, attention deficit hyperactivity disorder; AFR, arms-arm fat ratio; AN, anorexia nervosa; ANX, anxiety; ASAT, abdominal subcutaneous adipose tissue; BF%, body fat percentage; BIP, bipolar disorder; BMI, body mass index; GFAT, gluteofemoral adipose tissue; HDL, high-definition likelihood; LDSC, linkage disequilibrium score regression; LFR, legs-leg fat ratio; MDD, major depressive disorder; PTSD, post-traumatic stress disorder; SCZ, schizophrenia; TFR, trunk-trunk fat ratio; VAT, visceral adipose tissue; WHR, waist-to-hip ratio.



Supplementary Figure 2. Shared genes between women's and men's adiposity traits and psychiatric disorders among linkage pairs.

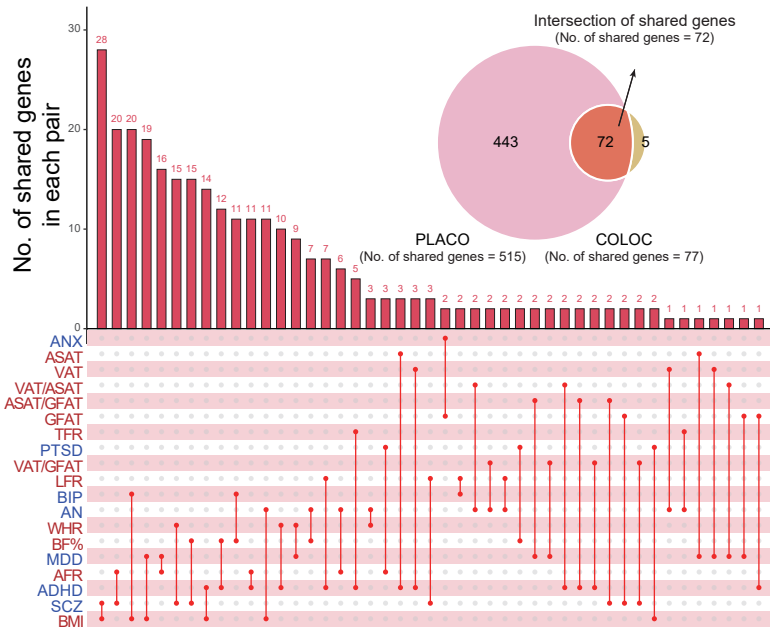
A. Shared genes for each linkage pair using women's adiposity traits and psychiatric disorders.

B. Shared genes for each linkage pair using men's adiposity traits and psychiatric disorders. The linked points in each column indicate the adiposity traits and psychiatric disorders for each linkage pair. The bar chart indicates the number of shared genes in the intersection of PLACO and COLOC analysis results. The abbreviations of adiposity traits are in red and the abbreviations of psychiatric disorders are in blue.

Abbreviations: ADHD, attention deficit hyperactivity disorder; AFR, arms-arm fat ratio; AN, anorexia nervosa; ANX, anxiety; ASAT, abdominal subcutaneous adipose tissue; BF%, body fat percentage; BIP, bipolar disorder; BMI, body mass index; COLOC, Bayesian colocalization test; GFAT, gluteofemoral adipose tissue; LFR, legs-leg fat ratio; MDD, major depressive disorder; PLACO, pleiotropic analysis under composite null hypothesis; PTSD, post-traumatic stress disorder; SCZ, schizophrenia; TFR, trunk-trunk fat ratio; VAT, visceral adipose tissue; WHR, waist-to-hip ratio.

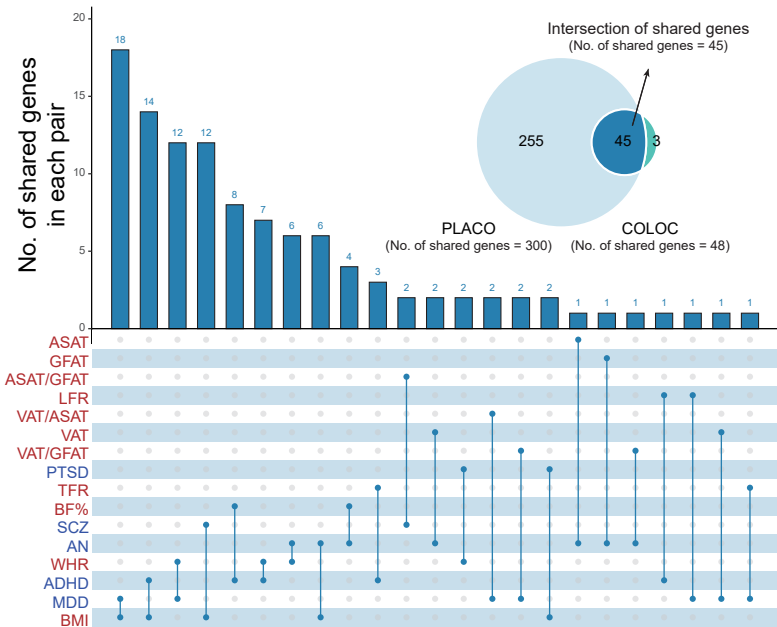
A

Shared genes between women's adiposity traits and psychiatric disorders



B

Shared genes between men's adiposity traits and psychiatric disorders



Supplementary Figure 3. Associations between genetically predicted expression of shared genes and adiposity traits and psychiatric disorders of general population in 26 tissues using JTI analysis.

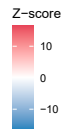
Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

	Adipose (Visceral Omentum) Adipose (Subcutaneous) Brain (Amygdala) Brain (Anterior Cingulate Cortex BA24) Brain (Caudate Basal Ganglia) Brain (Cerebellar Hemisphere) Brain (Cerebellum) Brain (Cortex) Brain (Frontal Cortex BA9) Brain (Hypothalamus) Brain (Hippocampus) Brain (Nucleus Accumbens Basal Ganglia) Brain (Putamen Basal Ganglia) Brain (Spinal Cord Cervical C-1) Colon (Transverse) Colon (Sigmoid) Small Intestine (Terminal Ileum) Stomach Liver Pancreas Pituitary Adrenal Gland Thyroid Muscle Skeletal Whole Blood																											
(1). BMAL1 (BMI)															0.94			6.43**								-7.35**		
(1). BMAL1 (WHR)															-0.47			2.15*								-5.94**		
(1). BMAL1 (BF%)															2.77*			5.79**								-5.89**		
(1). BMAL1 (AN)															1.27			-3.81*								4.63**		
(2). CCDC92 (WHR)	-17.26**	-14.85**			-13.12**	-13.44**	-13.36**			-13.36**			-11.17**	-13.25**		-10.13**	-8.63**	-13.93**	-12.1**	-14.23**	-9.99**	-8.78**	-14.15**	-10.98**	-9.96**	-9.06**		
(2). CCDC92 (GFAT)	8.44**	7.28**			6.99**	6.82**	6.78**			6.8**			6.17**	6.97**		5.01**	5.53**	6.81**	5.6**	6.98**	6.05**	5.85**	6.59**	6.2**	5.36**	3.89*		
(2). CCDC92 (VAT/GFAT)	-7.23**	-6.13**			-6.61**	-6.61**	-6.57**			-6.59**			-5.76**	-6.64**		-4.51**	-4.12**	-6.44**	-5.29**	-6.77**	-5.3**	-5.27**	-6.3**	-5.96**	-4.76**	-3.86*		
(2). CCDC92 (SCZ)	4.42*	4.14*			4.79*	4.55*	4.52*			4.54*			4.61**	4.82**		3.57*	2.33*	4.69**	4.54*	4.89**	3.53*	3.52*	4.66**	4.06*	3.85*	2.79*		
(3). CNNM2 (BMI)			6.06**	7.18**	7.82**	4.49**	5.86**	8.2**	7.92**	4.37*	5.52**	5.88**	6.73**			-4.82**							1.02			-0.45		
(3). CNNM2 (SCZ)			-6.76**	-7.46**	-8.53**	-5.8**	-6.89**	-7.73**	-7.59**	-0.46	-5.95**	-5.53**	-6.48**			1.8							-3.32*			4.42*		
(4). DENND1A (BMI)	4.72**	4.47*		1.64		1.46	1.65	1.54								2.9*		1.85	1.56		1.79	-0.38	-2.36*	1.94	2.63*	-3.82*		
(4). DENND1A (WHR)	5.27**	4.59*		3.78*		2.37*	3.66*	2.87*								2.37*		1.32	3.23*		3.85*	1.76	-3.64*	4.23**	4.65**	-1.97*		
(4). DENND1A (MDD)	4.42*	3.21*		4.57**		2.75*	4.53*	1.91								1.85		1.11	4.27*		4.56*	1.4	-3.76*	4.81**	4.54*	-1.4		
(5). FKBP2 (BMI)	-6.41**					-6.66**	-5.7**		-3.93*	2.31						-6.32**	-6.48**	-5.12**	-6.13**	-6.32**	-6.32**				-6.28**			
(5). FKBP2 (BF%)	-5.81**					-6.01**	-6.12**		-3.7*	3.27*						-6.01**	-5.9**	-5.15**	-5.64**	-5.76**	-5.75**				-5.84**			
(5). FKBP2 (BIP)	4.84**					4.86**	4.36*		3.32*	1.27						2.62**	4.84**	3.07*	4.49**	4.76**	4.67**				4.82**			
(6). HAPLN4 (BMI)	-3.93**	-3.98**	-5.36**	-4.05**	-4.99**	-4.23**	-4.09**	-6.17**	-4.56**	-6.33**	-4.27*	-4.46**	-3.96**			-4.97**	-4.12**		-4.04*				-3.85**	-3.99**	-3.86**			
(6). HAPLN4 (BIP)	3.07*	3.12*	3.66*	2.98*	3.7*	3.36*	3.23*	4.6**	3.19*	4.75**	3.28*	3.08*	3.12*			3.47*	3.11*		3.13*		2.84*	3.01*	3.42*					
(6). HAPLN4 (SCZ)	6.85**	6.93**	5.13**	6.99**	6.79**	6.54**	6.82**	5.29**	5.53**	5.01**	6.63**	5.49**	6.49**			7.2**	7.01**		6.91**		6.92**	6.95**	7.27**					
(7). MPHOSPH9 (WHR)	-8.3**	-8.53**				-4.21*					-8.15**	-8.26**	-4.87**				-8.42**	-6.51**	-8.47**	-8.48**			-5.74**	-7.77**	-8.21**	-8.06**	-8.49**	
(7). MPHOSPH9 (LFR)	-5.11**	-4.99**															-4.91**	-4.44**	-4.93**	-4.96**			-3.82**	-5.65**	-4.81**	-5.12**	-4.38**	
(7). MPHOSPH9 (TFR)	4.84**	4.69**			1						4.41*	4.5*	0.71				4.61*	4.36*	4.62**	4.65**			3.71*	5.14**	4.51**	4.84**	3.99*	
(7). MPHOSPH9 (ADHD)	-4.48**	-4.43**				-4.08**					-4.4*	-4.4*	-3.95**				-4.42**	-4.69**	-4.4*	-4.42**			-3.56**	-2.95**	-4.38**	-4.47**	-4.58**	
(7). MPHOSPH9 (SCZ)	6.28**	6.54**			4*			6.4**			6.36**	6.4**	4.28*				6.52**	5.31**	6.53**	6.53**			4.39*	5.02**	6.57**	6.22**	5.89**	
(8). NEGR1 (BMI)	-2.67*		11.79**		11.49**			11.79**		11.79**	13.63**	10.48**	11.63**	7.31**			11.72**											
(8). NEGR1 (MDD)	-3.2*		8.57**		8.59**			8.57**		8.57**	7.11**	8.21**	8.49**	3.66*			3.51*											
(9). NT5C2 (BMI)	3.58*	3.37*	1.06		1.15	-2.74*	0.99	0.76		0.82	1.18		1.63	0.84	2.68*	4.01*		1.96*				-0.95	0.36	5.63**			5.34**	
(9). NT5C2 (SCZ)	-2.73*	-1.93	-1.94		-1.4	2.2*	-1.29	-1.67		-1.67	-1.4		-4.32*	-1.81	-3.29*	-3.48*		-4.68**			2.49*	-0.93	-4.22*			-4.95**		
(10). RERE (BF%)	6.86**	6.8**	6.65**	6.54**	6.55**			6.54**	6.61**		6.6**	6.59**	6.5**						6.63**		6.67**	6.58**		6.34**	-3.64**	5.46**		
(10). RERE (MDD)	-4.82**	-4.64**	-4.78**	-4.59**	-4.6**			-4.6**	-5.16**		-5.17**	-4.25**	-4.4**						-4.89**		-4.75**	-5.21**		-5**	2.3*	-5.11**		
(10). RERE (SCZ)	5.93**	5.74**	5.94**	5.97**	5.98**			5.98**	6.13**		6.14**	5.79**	5.75**						5.92**		6.14**	6.13**		5.73**	-4.73**	5.69**		
(11). RTN4RL1 (BMI)	-5.36**	-5.79**				3.8*	3.66*						0.77				-5.47**	-5.5**	-5.04**	2.24*	-4.99**		-1.06	-5.19**	-5.59**			
(11). RTN4RL1 (BF%)	-5.56**	-6.12**				3.46*	3.26*						0.13				-5.72**	-5.69**	-4.84**	1.62	-4.93**		0.92	-4.44**	-5.78**			
(11). RTN4RL1 (BIP)	0.99	1.37				-5.66**	-5.66**						-2.1*				1.07	1.12	0.81		0.66		2.49*	0.88	1.17			
(12). SNX19 (BMI)	-5.98**	-5.93**	-7.14**	-7.24**	-7.33**	-6.16**	-5.43**	-7.37**	-7.4**	-7.42**	-6.98**	-6.83**	-7.34**	-7.02**	-7.02**	-5.36**	-5.57**	-4.43**	-5.96**	-5.32**	-5.89**	-3.97**	-5.99**	-5.04**	-6.45**	-4.23**		
(12). SNX19 (BF%)	-5.36**	-5.38**	-6.45**	-6.55**	-6.57**	-5.48**	-4.8**	-6.51**	-6.63**	-6.63**	-6.23**	-6.18**	-6.59**	-6.3**	-6.3**	-4.87**	-4.99**	-3.89**	-5.35**	-4.79**	-5.36**	-3.37**	-5.37**	-4.62**	-5.99**	-4.04**		
(12). SNX19 (SCZ)	6.27**	6.22**	6.02**	5.88**	6.09**	6.07**	5.71**	6.38**	6.17**	6.2**	6.53**	5.66**	6.11**	6.35**	6.34**	5.94**	6.14**	5.51**	6.29**	5.93**	6.21**	5.25**	6.29**	5.69**	4.66**	5.19**		
(13). SP4 (BMI)	3.34*	4.87**				5.65**		5.71**			5.85**	5.59**	5.89**			5.44**	3.99*	5.17**		-0.74	0.81		5.89**	4.31*	5.14**	5.43**	1.06	
(13). SP4 (BIP)	2.99*	5.15**				6.22**		6.19**			5.76**	6.22**	6.08**			6.19**	4.22**	5.35**		0.21	-1.24		6.05**	3.59**	5.18**	5.44**	1	
(13). SP4 (SCZ)	2.15*	3.53*				3.93*		4.12*			4.63**	3.82*	4.36*			3.65*	2.78*	3.68*		0.8	-1.79		4.39*	2.17*	3.56*	3.86*	0.69	
(14). TAOK2 (BMI)				-9.69**		-4.39*	-1.95						-11.53**					-2.88*					8.62**	-6.55**				
(14). TAOK2 (WHR)				-5.44**		-4.7**	-3.18*						-8.85**					-6.38**					3.63*	-6.27**				
(14). TAOK2 (BF%)				-5.71**		-4.76**	-3.18**						-6.54**					-2.4*					4.11*	-5.28**				
(14). TAOK2 (BIP)				2.43*		3.26*	2.14*						3.99*					3.56*					-0.73	4.89**				
(14). TAOK2 (SCZ)				5.91**		1.27	0.24						7.27**					2.85*					-3.44*	2.63*				
(15). TMEM106B (BMI)	3.04*	3.13*				3.71*	3.78*	3.39*	2.87*							3.1*	3.14*		4.85**		3.47*	4.37*	3.21*	1.45	2.8*	4.34*		
(15). TMEM106B (MDD)	6.22**	6.28**				6.36**	6.44**	6.31**	5.77**							6.55**	6.01**		7.11**		6.55**	6.97**	6.4**	1.09	5.38**	6.01**		
(16). TSNARE1 (BMI)	3.36*	3.23*	3.79*	4.12*	3.82*	3.9*	3.52*	3.37*	3.63*	3.77*	3.95*	3.7*	4.11*	4.64**	4.2*	3.15*	3.26*	0.67	3.15*	1.51	-0.75	3.55**	2.23*	3.26*	0.23	1.03		
(16). TSNARE1 (SCZ)	0.03	0.32	0.29	-0.57	0.67	0.46	0.19	0.37	0.1	-0.2	-0.11	0	0.2	-0.4	-0.07	0.26		1.38	0.25	0.75	5.28**	0.06	2.23*	0.23	3.39*	-0.83		
(17). YLPM1 (WHR)													5.41**	3.1*									-3.34*					
(17). YLPM1 (BF%)													6.91**	3.98*									-5.75**					
(17). YLPM1 (MDD)													5.55**	3.86*									-4.4*					
(18). ZNF664 (BMI)	5.73**	3.4*		-3.45**	-4.65**	-5.44**	-0.22	-2.8*	-3.2*				-3.07*					-0.61	-4.26**				-5.97**	-4.56**	-1.11	-5.51**	4.01*	-3.35
(18). ZNF664 (WHR)	-15.2**	-10.6**		5.04**	6.88**	8.05**	0.5	5.37**	6.02**				2.7*					-2.26*	8.54**			12.51**	7.12**	0.31	13.43**	-7.77**	8.4**	
(18). ZNF664 (BF%)	9.31**	6.01**		-3.64**	-5.31**	-6.51**	-0.58	-3.21*	-3.94**				-2.62*						-6.41**			-10.75**	-5.42**	-1.07	-10.27**	7.1**	-7.57**	
(18). ZNF664 (GFAT)	7.33**	5.06**		-3.52**	-3.81**	-4.73**	-1.6	-2.29*	-2.73**				-2.52*					1.2	-4.62**			-7.35**	-3.91**	-0.42	-6.56**	4.04*	-4.1*	
(18). ZNF664 (VAT/GFAT)	-5.62**	-3.87**		3.28**	3.96**	4.39**	1.45	2.78**	2.94**				2.71*					2.7*				6.74**	4.02**	1.24	6.93**	-4.33**	4.74**	
(18). ZNF664 (ASAT/GFAT)	-3.7*	-1.99*		2.78*	3.28**	3.81**	2.24*	2.09**	2.18**				2.24*					0.84	3.3*			4.35**	3.3**	1.48	5.61**	-3.22**	3.85**	
(18). ZNF664 (SCZ)	0.93	-0.42		-1.93	-3.07*	-3.35**	-2.16*	-2.08**	-2.14*				-1.51					-1.55	-0.52	</								

Supplementary Figure 4. Associations between genetically predicted expression of shared genes and women's adiposity traits and psychiatric disorders in 26 tissues using JTI analysis.

Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

	Adipose (Visceral Omentum)		Adipose (Subcutaneous)		Brain (Amygdala)		Brain (Anterior Cingulate Cortex BA24)		Brain (Caudate Basal Ganglia)		Brain (Cerebellar Hemisphere)		Brain (Cerebellum)		Brain (Cortex)		Brain (Frontal Cortex BA9)		Brain (Hypothalamus)		Brain (Hippocampus)		Brain (Nucleus Accumbens Basal Ganglia)		Brain (Putamen Basal Ganglia)		Brain (Spinal Cord Cervical C-1)		Colon (Substantia Nigra)		Colon (Transverse)		Small Intestine (Terminal Ileum)		Stomach		Liver		Pancreas		Pituitary		Adrenal Gland		Thyroid		Muscle Skeletal		Whole Blood	
(1). ARFGEF2 (AFR)	4.28 *	3.37 *			5.18 **	4.74 **		4.73 **	4.63 **								4.77 **	4.78 **	4.63 **	4.75 **	4.46 *	4.26 *	4.4 *		1.2	-0.31 *	-3.59 *	4.65 **					2.75 *	4.49 *	3.89 *															
(1). ARFGEF2 (PTSD)	-4.66 **	-4.47 *			-4.37 *	-4.31 *		-4.51 *	-4.32 *								-4.36 *	-4.45 *	-4.32 *	-4.47 *	-4.43 *	-4.46 *	-4.3 *		-0.88	-1.78	1.54	-4.14 *				0.14	-4.24 *	-1.35																
(2). BMAL1 (BMI)																						0.23				4.86 **																	-4.86 **							
(2). BMAL1 (AN)																						1.27				-3.81 *																	4.63 **							
(3). CTNNB1 (LFR)	-4.45 *	-6.86 **	-6.89 **	-1.33	-6.85 **		-6.29 **	-6.8 **	-6.91 **	-6.83 **	-6.55 **	-5.04 **	-6.4 **	-6.02 **	-6.77 **	-4.99 **	-6.83 **									-2.79 *						-0.37	-1.05	-6.6 **																
(3). CTNNB1 (TFR)	3.38 *	6.01 **	6.08 **	0.72	6.04 **		5.56 **	5.97 **	6.08 **	6.01 **	5.53 **	4.74 **	5.58 **	5.67 **	5.94 **	3.9 *	6.01 **									1.83						0.3	5.83 **																	
(3). CTNNB1 (AN)	-4.79 **	-4.85 **	-4.89 **	-3.61 *	-4.89 **		-4.61 **	-4.89 **	-4.82 **	-4.89 **	-4.72 **	-2.17 *	-4.54 **	-4.36 *	-4.89 **	-4.2 *	-4.77 **									-4.51 *						-0.73	-0.36	-4.59 **																
(4). DENND1B (BMI)	4.48 *	4.52 *			-3.79 *	-3.93 *	-2.03 *			-0.32	-3.43 *						4.09 *								4.45 *						4.58 **	4.28 *	1.36	-1.07																
(4). DENND1B (MDD)	-5.66 **	-5.74 **			5.09 **	5.23 **	2.33 *			0.84	3.38 *						-5.2 **								-5.8 **						-5.62 **	-5.13 **	-0.56	-0.16																
(5). FKBP2 (BMI)	-6.22 **				-6.36 **	-5.39 **		-2.77 *	2.54 *								-5.26 **	-6.28 **	-5.1 **	-5.76 **	-6.17 **	-6.12 **																							-5.99 **					
(5). FKBP2 (BF%)	-5.52 **				-5.66 **	-1.98 *		-0.81 *	3.58 *								-1	-5.25 **	-4.68 **	-4.77 **	-5.51 **	-5.18 **																							-3.51 *					
(5). FKBP2 (BIP)	4.84 **				4.86 **	4.36 *		3.32 *	1.27								2.62 *	4.84 **	3.07 *	4.49 *	4.76 **	4.67 **																								4.82 **				
(6). TAOK2 (BMI)				-8.05 **	-2.19 *												-8.4 **								-1.43						7.13 **	-4.33 *																		
(6). TAOK2 (WHR)				-3.78 *	-3.62 *	-2.1 *											-6.95 **								-5.87 **						2.49 *	-5.99 **																		
(6). TAOK2 (BF%)				5.18 **	-5.66 **	-4.98 **											-6.91 **								-1.19						-2.55 **	-5.17 **																		
(6). TAOK2 (AFR)				-5.12 **	-2.6 *	-1.86											-6.43 **								-2.38 *						5.75 **	-2.6 *																		
(6). TAOK2 (BIP)				2.43 *	3.26 *	2.14 *											3.99 *								3.56 *						-0.73	4.89 **																		
(6). TAOK2 (SCZ)				5.91 **	1.27	0.24											7.27 **								2.85 *						-3.44 *	2.63 *																		
(7). TMEM219 (BMI)			-8.12 **														-7.95 **	-7.85 **													-8.91 **	-8.74 **		-7.49 **																
(7). TMEM219 (WHR)			-4.5 **														-4.14 **	-4.35 **													-4.87 **	-5.73 **		-4.45 *																
(7). TMEM219 (SCZ)			6.54 **														6.3 **	6.41 **													5.79 **	5.33 **		6.87 **																
(8). ZNF664 (BMI)	5.14 **	3.2 *		-2.7 *	-3.36 *	-3.89 *	-0.07	-2.01 *	-2.38 *								-2.38 *								-0.15	-2.65 *					-4.9 **	-3.32 **	-0.67	-4.74 **	3.38 *	-3.27 *														
(8). ZNF664 (WHR)	-16.75 **	-10.84 **		6.29 **	9.31 **	10.86 **	1.17	6.17 **	7.05 **								3.87 *								-0.67	11.63 **	15.43 **	9.41 **	2.04 *	16.39 **	-9.29 **	10.23 **																		
(8). ZNF664 (BF%)	-3.73 *	-4.51 *		-0.63	-2.15 *	-1.36		-4.83 **	2.42 *	1.75							-1.16								-2.25 *	-4.94 **					-6.62 **	-1.74	-0.07	-4.91 **	1.8	-3.96 *														
(8). ZNF664 (LFR)	-6.99 **	-4.57 *		2.46 *	1.8	1.11	1.56	0.81	1.01								1.98 *								5.69 **						5.38 **	1.73	0.13	6.36 **	-1.5	3.65 *														
(8). ZNF664 (GFAT)	6.66 **	4.78 **		-2.17 *	-2.73 *	-3.82 *	-0.74	-1.67	-2.1 *								-0.94								1.84	-3.3 *					-6.05 **	-2.87 *	0.04	-5.68 **	4.89 **	-3.58 *														
(8). ZNF664 (VAT/GFAT)	-4.82 **	-2.87 *		3.59 *	4.63 **	5.09 **	2.71 *	3.34 *	3.57 *								3.13 *								0.78	2.04 *					7.49 **	4.65 **	2.38 *	7.84 **	-4.54 **	5.47 **														
(8). ZNF664 (ASAT/GFAT)	-4.15 *	-2.23 *		2.81 *	3.53 *	4.15 *	2.66 *	2.46 *	2.74 *								2.19 *								0.71	2.8 *					5.81 **	3.58 *	1.74	6.65 **	-3.6 *	4.63 **														
(8). ZNF664 (SCZ)	0.93	-0.42		-1.93	-3.07 *	-3.35 *	-2.16 *	-2.08 *	-2.14 *								-1.51								-1.55	-0.52					-2.89 *	-3 *	-2.51 *	-5.19 **	2.27 *	-4.03 *														



Supplementary Figure 5. Associations between genetically predicted expression of shared genes and men's adiposity traits and psychiatric disorders in 26 tissues using JTI analysis.

Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

	Adipose (Visceral Omentum)	Adipose (Subcutaneous)	Brain (Amygdala)	Brain (Anterior Cingulate Cortex BA24)	Brain (Caudate Basal Ganglia)	Brain (Cerebellar Hemisphere)	Brain (Cerebellum)	Brain (Cortex)	Brain (Frontal Cortex BA9)	Brain (Hypothalamus)	Brain (Hippocampus)	Brain (Nucleus Accumbens Basal Ganglia)	Brain (Putamen Basal Ganglia)	Brain (Spinal Cord Cervical C-1)	Colon (Substantia Nigra)	Colon (Transverse)	Colon (Sigmoid)	Small Intestine (Terminal Ileum)	Stomach	Liver	Pancreas	Pituitary	Adrenal Gland	Thyroid	Muscle	Skeletal	Whole Blood
(1). BMAL1 (BMI)															1.06			3.79 *								-5.41 **	
(1). BMAL1 (WHR)															1.18			1.7								-4.69 **	
(1). BMAL1 (AN)															1.27			-3.81 *								4.63 **	
(2). CNNM2 (BMI)			6.44 **	7.33 **	7.63 **	5.7 **	6.55 **	7.9 **	7.74 **	4.98 **	5.67 **	5.26 **	7.09 **		-3 *							1.01				-0.95	
(2). CNNM2 (WHR)			4.7 **	5.01 **	4.54 *	4.72 **	5.53 **	5.35 **	4.89 **	2.32 *	3.6 *	2.49 *	4.99 **		-0.77							2.52 *				1.64	
(2). CNNM2 (SCZ)			-6.76 **	-7.46 **	-8.53 **	-5.8 **	-6.89 **	-7.73 **	-7.59 **	-0.46	-5.95 **	-5.53 **	-6.48 **		1.8							-3.32 *				4.42 *	
(3). RERE (WHR)	4.75 **	4.2 *	4.41 *	4.34 *	4.37 *			4.37 *	4.9 **		4.91 **	4.03 *	4.05 *					4.75 **		5 **	4.95 **		4.82 **	-2.2 *	5.03 **		
(3). RERE (BF%)	-4.12 *	-5.04 **	-1.53	-0.59	-0.55			-0.54	-3.24 *		-3.11 *	-0.16	-1.19					-4.35 *		-3.49 *	-3.17 *		-3.3 *	2.35 *		-0.02	
(3). RERE (MDD)	-4.82 **	-4.64 **	-4.78 **	-4.59 **	-4.6 **			-4.6 **	-5.16 **		-5.17 **	-4.25 *	-4.4 *					-4.89 **		-4.75 **	-5.21 **		-5 **	2.3 *		-5.11 **	
(3). RERE (SCZ)	5.93 **	5.74 **	5.94 **	5.97 **	5.98 **			5.98 **	6.13 **		6.14 **	5.79 **	5.75 **					5.92 **		6.14 **	6.13 **		5.73 **	-4.73 **		5.69 **	
(4). SNX19 (BMI)	-4.12 *	-4.07 *	-4.27 *	-4.35 *	-4.58 **	-4.64 **	-4.42 *	-4.79 **	-4.66 **	-4.63 **	-4.63 **	-3.99 *	-4.59 **	-4.42 **	-4.41 *	-3.79 *	-3.78 *	-3.31 *	-4.09 *	-3.88 *	-4.07 *	-3.15 *	-4.12 *	-3.79 *	-3.26 *	-3.4 *	
(4). SNX19 (SCZ)	6.27 **	6.22 **	6.02 **	5.88 **	6.09 **	6.07 **	5.71 **	6.38 **	6.17 **	6.2 **	6.53 **	5.66 **	6.11 **	6.35 **	6.34 **	5.94 **	6.14 **	5.51 **	6.29 **	5.93 **	6.21 **	5.25 **	6.29 **	5.69 **	4.66 **	5.19 **	
(5). TMEM106B (BMI)	4.01 *	4.08 *				3.11 *	3.26 *	3.51 *	2.5 *						3.67 *	3.96 *		4.68 **		4.07 *	4.23 *	4.17 *	0.28	3.81 *	4.04 *		
(5). TMEM106B (MDD)	6.22 **	6.28 **				6.36 **	6.44 **	6.31 **	5.77 **						6.55 **	6.01 **		7.11 **		6.55 **	6.97 **	6.4 **	1.09	5.38 **	6.01 **		

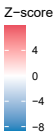
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Supplementary Figure 6. Associations between genetically predicted expression of shared genes and adiposity traits and psychiatric disorders of general population in 26 tissues using GIFT analysis.

Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

	Adipose (Visceral Omentum)		Adipose (Subcutaneous)		Brain (Amygdala)		Brain (Anterior Cingulate Cortex BA24)		Brain (Caudate Basal Ganglia)		Brain (Cerebellar Hemisphere)		Brain (Cerebellum)		Brain (Cortex)		Brain (Frontal Cortex BA9)		Brain (Hypothalamus)		Brain (Hippocampus)		Brain (Nucleus Accumbens Basal Ganglia)		Brain (Putamen Basal Ganglia)		Brain (Spinal Cord Cervical C-1)		Colon (Transverse)		Colon (Sigmoid)		Small Intestine (Terminal Ileum)		Stomach		Liver		Pancreas		Pituitary		Adrenal Gland		Thyroid		Muscle Skeletal		Whole Blood	
(1). BMAL1 (BMI)	13.97 **	-24.67 **	-33.92 **	23.14 **	-14.39 **	-30.18 **	-23.22 **	4.48 **	27.88 **	-27.67 **			-29.6 **	-18.87 **	15.2 **	-35.82 **			-36.46 **	20.22 **	22.87 **	17.36 **	-21.16 **	-29.58 **	9.23 **	-28.45 **	-32.26 **	-39.83 **																						
(1). BMAL1 (WHR)	13.97 **	-24.67 **	-33.92 **	23.14 **	-14.39 **	-30.18 **	-23.22 **	4.48 **	27.88 **	-27.67 **			-29.6 **	-18.87 **	15.2 **	-35.82 **			-36.46 **	20.22 **	22.87 **	17.36 **	-21.16 **	-29.58 **	9.23 **	-28.45 **	-32.26 **	-39.83 **																						
(1). BMAL1 (BF%)	4.29 **	-8.09 **	-7.42 **	6.15 **	-7.53 **	-7.67 **	-8.02 **		6.14 **	-8.08 **			-7.15 **	-5.64 **	4.44 **	-8.2 **			-8.4 **	7.37 **	6.66 **	7.63 **	-6.11 **	-7.05 **	3.66 *	-6.38 **	-7.03 **	-8.53 **																						
(1). BMAL1 (AN)	4.29 **	-5.88 **	-6.76 **	5.51 **	-2.23 **	-6.66 **	-6.73 **	3.99 **	6.36 **	-6.83 **			-6.15 **	-4.41 **	4.83 **	-7.03 **			-8.19 **	6.07 **	5.99 **	5.24 **	-5.02 **	-6.6 **	2.16 **	-6.32 **	-6.5 **																							
(2). CCDC92 (WHR)	-49.1 **	-48.02 **	-43.56 **	35.98 **	-48.1 **	-43.75 **	-48.62 **	44.88 **	48.14 **	-42.71 **			-26.2 **	-44.54 **	-49.23 **	-47.58 **	-49.12 **		-46.38 **	-49.12 **	-49.21 **	-46.65 **	-47.01 **	-48.91 **	-47.15 **	-49.29 **	-46.31 **	-47.88 **																						
(2). CCDC92 (GFAT)	4.55 **	1.67 *	1.3 *	-3.17 *	0.39 *	2.07 *	3.08 *	-0.2 *	-1.65 *	0.41 *			3.06 *	1.45 *	-0.11 *	2.18 *	0.58 *		1.76 *	0.57 *	1.52 *	2.83 *	-0.39 *	0.51 *	0.76 *	0.68 *	0.97 *	1.29 *																						
(2). CCDC92 (VAT/GFAT)		1.67 *	1.3 *	-3.17 *	0.39 *	2.07 *	3.08 *	-0.2 *	-1.65 *	0.41 *			3.06 *	1.45 *	-0.11 *	2.18 *	0.58 *		1.76 *	0.57 *	1.52 *	2.83 *	-0.39 *	0.51 *	0.76 *	0.68 *	0.97 *	1.29 *																						
(2). CCDC92 (SCZ)	4.55 **	2.41 *	2.45 *	-4.04 *	1.04 *	3.18 *	4.06 *	-1.22 *	-2.74 *	1.82 *			3.83 *	2.31 *	0.87 *	3.03 *	1.75 *		2.89 *	1.93 *	2.47 *	4.16 *	0.72 *	1.37 *	2.2 *	1.63 *	1.81 *	2.35 *																						
(3). CNNM2 (BMI)	-13.53 **	6.73 **	7.03 **	13.72 **	29.35 **	27.9 **	23.46 **	34.08 **	32.52 **	0.39 **	21.39 **	29.63 **	27.32 **	-7.17 **	21.87 **	-15.41 **	-4.57 **		-19 **	-17.47 **	29.16 **	14.64 **	-8.82 **	-0.74 **	10.1 **	-5.41 **	-16.28 **																							
(3). CNNM2 (SCZ)	-1.89 **	-4.68 **	-1.31 *	2.53 *	3.85 *	1.59 *	0.51 *	3.15 *		-5.33 **	-1.68 **	0.28 **		-4.1 **	1.14 **	-1.49 **	6.15 **		-3.1 **	-2.53 **	3.25 **	-0.84 **	-2.88 **	4 **	6.19 **	-3.04 **	-5.06 **																							
(4). DENND1A (BMI)	43.89 **	44.65 **	29.29 **	25.68 **	32.98 **	15.85 **	32.24 **	33.71 **	32.97 **	22.06 **	15.47 **	-36.25 **	38.78 **		24.12 **	39.55 **	42.99 **	9.24 **	45.41 **	-23.51 **	42.09 **	41.92 **	-32.78 **	32.42 **	29.18 **	-21.93 **																								
(4). DENND1A (WHR)	43.89 **	44.65 **	29.29 **	25.68 **	32.98 **	15.85 **	32.24 **	33.71 **	32.97 **	22.06 **	15.47 **	-36.25 **	38.78 **		24.12 **	39.55 **	42.99 **	9.24 **	45.41 **	-23.51 **	42.09 **	41.92 **	-32.78 **	32.42 **	29.18 **	-21.93 **																								
(4). DENND1A (MDD)	36.35 **	36.95 **	26.82 **	22.32 **	25.68 **	12.17 **	27.12 **	27.77 **	26.28 **	21.18 **	14 **	-29.19 **	32.38 **		24.25 **	33.46 **	36.52 **	10.5 **	37.61 **	-19.54 **	34.78 **	34.94 **	-26.86 **	28.15 **	23.98 **	-15.48 **																								
(5). MPHOSPH9 (WHR)	-32.63 **	-32 **	-34.92 **	-40.25 **	-29.01 **	33.82 **	-31.08 **	-20.56 **	-29.8 **	-36.97 **	-35.52 **	-28.61 **	-31.18 **	-39.76 **	-33.02 **	-36.04 **	-34.29 **	-36.47 **	-35.19 **	17.65 **	38.34 **	-27.16 **	-22.08 **	-34.99 **	-30.46 **	-36.87 **																								
(5). MPHOSPH9 (LFR)	-3.36 **	-4.65 **	-8.97 **	-14.49 **	-2.93 **	8.65 **	-3.67 **	0.73 **	-3.78 **	-8.73 **	-8.24 **	-4.24 **	-7.63 **	-13.59 **	-6.03 **	-11.76 **	-7.81 **	-11.22 **	-9.83 **	13.89 **	18.13 **	1.73 **	-3.7 **	-5.08 **	-9.69 **	-8.99 **																								
(5). MPHOSPH9 (TFR)	-3.36 *		-8.97 **	-14.49 **	-2.93 **	8.65 **	-3.67 **	0.73 **	-3.78 **	-8.73 **	-8.24 **	-4.24 **	-7.63 **	-13.59 **	-6.03 **	-11.76 **	-7.81 **			13.89 **	18.13 **	1.73 **	-3.7 **	-5.08 **		-8.99 **																								
(5). MPHOSPH9 (ADHD)	1.21 **	-0.67 **	-4.44 **	-4.16 **	-0.18 **	7.44 **	-1.04 **	8.03 **	6.31 **	-1.42 **	0.66 **	3.33 **	-0.72 **	0.06 **	-1.97 **	-1.35 **	-1.08 **	0.71 **	1.95 **	4.19 **	3.69 **	-0.05 **	1.1 **	0.1 **	1 **	-5.67 **																								
(5). MPHOSPH9 (SCZ)	1.04 **	-0.6 **	-3.89 **	-3.77 **	-0.55 **	7.3 **	-1.3 **	7.92 **	6.17 **	-2.11 **	1.01 **	2.98 **	-0.87 **	-0.06 **	-3.68 **	-1.22 **	-1.06 **	0.85 **	1.24 **	4.19 **	3.64 **	0.06 **	0.88 **	-0.02 **	1.24 **																									
(6). NEGR1 (BMI)	-32.47 **	-12.87 **	44.12 **	30.84 **	49.74 **	15.97 **	3.25 **	42.16 **	49.72 **	44.29 **	58.43 **	30.12 **	44.17 **	40.06 **	30.31 **	24.3 **	51.04 **	-23.65 **	-17.48 **		23.39 **	40.74 **	49.98 **	-1.8 **	-30.39 **																									
(6). NEGR1 (MDD)	-24.1 **	-9.1 **	37.82 **	24.14 **	41.39 **	9.87 **	0.07 **	33.49 **	39.64 **	37.51 **	50.04 **	26.38 **	34.1 **	35.51 **	25.65 **	24.93 **	45.13 **	-16.02 **	-13.59 **		17.05 **	34.5 **	45.13 **	-0.64 **	-22.89 **																									
(7). NT5C2 (BMI)	18.19 **	11.59 **	9.16 **	0.75 **	-3.23 **	0.03 **	-3.17 **	10.97 **	0.12 **	4.61 **	17.11 **	3.29 **	12.05 **	4.61 **	8.52 **	24.85 **	10.79 **	18.51 **	-3.88 **	1.61 **	-7.86 **	-1.3 **	25.29 **	-21.62 **	-10.03 **	22.78 **																								
(7). NT5C2 (SCZ)	3.82 *	5.44 **	3.17 *	-0.46 **	3.39 *	1.45 **	0.39 **	5.82 **	4.28 **	5.91 **	3.98 *	-0.26 **	-1.55 **	5.69 **	4.67 **	8.98 **	10.23 **		-3.74 **	3.89 **	0.15 **	-4.12 **	5.58 **	-3.58 **	-2.85 **																									
(8). RERE (BF%)	1.66 **	1.34 **	1.5 **	2.8 *	2.62 *	1.64 **	1.89 **	2.49 **	3.69 **	2.33 **	4.6 **	1.47 **	2.76 **	2.8 **	4.07 **	-3.21 **	3.95 **		4.25 **	0.96 **	2.6 **	2.51 **	-2.21 **	0.43 **	-2.87 **	1.6 **																								
(8). RERE (MDD)					5.43 **	5.5 **			3.15 **		5.97 **	6.03 **	5.08 **	4.2 **	0.81 **	5.12 **			5.16 **			-1.98 **		-5.27 **																										
(9). RTN4RL1 (BMI)	-14.11 **	-14.29 **		5.15 **	-3.52 **	6.21 **	4.49 **	-14.1 **		10.1 **	3.8 **	-10.28 **	-11.41 **	-6.5 **	-11.8 **	-14.97 **	-8.2 **	-16.4 **	-6.16 **	-14.6 **	-10.07 **	-12.32 **	-9.5 **	-12.64 **	-4.09 **	-7.05 **																								
(9). RTN4RL1 (BF%)	-7.24 **	-7 **		5.13 **	-2 **	4.68 **	4.66 **	-7 **		5.4 **	2.28 **	-7.31 **	-6.99 **	-2.6 **	-6.45 **	-8.16 **	-3.24 **	-10.44 **	-5.29 **	-8.64 **	-3.33 **	-8.93 **	-4.54 **	-6.61 **	-2.58 **	-5.5 **																								
(9). RTN4RL1 (BIP)	-4 **	-3.66 **		0.45 **	-1.79 **	-0.09 **	-1.46 **	-6.05 **		1.92 **	2.5 **	-2.93 **	-2.58 **	-4.08 **	-5.78 **	-3.95 **	-4.03 **	-3.89 **	0.05 **	-1.97 **	-4.35 **	-1.55 **	-3.96 **	-3.68 **	0.41 **	-2.54 **																								
(10). SP4 (BMI)	13.3 **	11.67 **	5.51 **	8.91 **	16.01 **	16.32 **	16.94 **	6.86 **	12.83 **	15.14 **	18.71 **	15.92 **	12.04 **	16.11 **	17.18 **	12.02 **	17.3 **	16 **	12.39 **	0.98 **	10.77 **	16.07 **	6.95 **	17.18 **	17.25 **	8.65 **																								
(10). SP4 (BIP)	3.33 *	4.8 **	0.63 **	2.19 **	5.02 **	5.3 **	4.92 **	1.05 **	3.72 **	4.28 **	5.74 **	4.66 **	3.34 **	4.87 **	5.66 **	3.15 **	5.87 **	4.56 **	3.05 **	1.4 **	4.65 **	4.98 **	2.44 **	4.8 **	5.75 **	2.9 **																								
(10). SP4 (SCZ)	3.33 **	4.8 **	0.63 **	2.19 **	5.02 **	5.3 **	4.92 **	1.05 **	3.72 **	4.28 **	5.74 **	4.66 **	3.34 **	4.87 **	5.66 **	3.15 **	5.87 **	4.56 **	3.05 **	1.4 **	4.65 **	4.98 **	2.44 **	4.8 **	5.75 **	2.9 **																								
(11). TAOK2 (BMI)	-30.87 **	-32.06 **	-29.89 **	-26.26 **	4.07 **	-34.85 **		26.73 **	-33.78 **	-35.14 **	-32.57 **	-19.16 **	-27.45 **	25.9 **	23.2 **	-34.56 **	-34.13 **	19.18 **	-30.54 **	-35.27 **	-19.9 **	-32.7 **	34.83 **	-11.03 **	-31.07 **	-32.88 **																								
(11). TAOK2 (WHR)	-30.87 **	-32.06 **	-29.89 **	-26.26 **	4.07 **	-34.85 **		26.73 **	-33.78 **	-35.14 **	-32.57 **	-19.16 **	-27.45 **	25.9 **	23.2 **	-34.56 **	-34.13 **		-30.54 **	-35.27 **	-19.9 **	-32.7 **	34.83 **	-11.03 **	-31.07 **	-32.88 **																								
(11). TAOK2 (BF%)	2.96 *	3.79 *	5.31 **		-3.94 **	4.03 **	4.92 **	-4.44 **	5.01 **	5.37 **	5.09 **	5 **		-5.17 **	-5.46 **	3.11 **	4.83 **	-4.95 **	4.6 **	4.51 **	4.64 **	4.56 **	-2.82 **	4.43 **	3.92 **	5.74 **																								
(11). TAOK2 (BIP)	-5.62 **	1.98 **	5.97 **		1.53 **	0.74 **	1.86 **	-6.07 **	-2.21 **	5.21 **	2.38 **	4.51 **	2.11 **	2.43 **	-6.66 **	1.58 **	-5.73 **	1.89 **	-3.45 **	-0.68 **	-2.73 **	-1.04 **	-3.84 **	1.87 **	-4.49 **	0.77 **																								
(11). TAOK2 (SCZ)	-5.62 **	1.98 **	5.97 **		1.53 **	0.74 **	1.86 **	-6.07 **	-2.21 **	5.21 **	2.38 **	4.51 **	2.11 **	2.43 **	-6.66 **	1.58 **	-5.73 **	1.89 **	-3.45 **	-0.68 **	-2.73 **	-1.04 **	-3.84 **	1.87 **	-4.49 **	0.77 **																								
(12). TMEM106B (BMI)	9.98 **	12.27 **	9.23 **	13.42 **		12.75 **	12.45 **	12.37 **	11.48 **	12.31 **	0.95 **	-13.36 **	5.98 **		-12.65 **	13.24 **	11.16 **	10.39 **	13.16 **	11.56 **	13.84 **	14.11 **	12.74 **	12.34 **	11.5 **	14.22 **																								
(12). TMEM106B (MDD)	8.37 **	11.32 **	8.11 **	11.74 **		11.68 **	10.82 **	10.75 **	9.82 **	10.24 **	-1.46 **	-11.53 **	4.99 **		-10.69 **	11.71 **	9.8 **	9.31 **	11.82 **	9.78 **	12.27 **	12.4 **	11.42 **	10.82 **	10.07 **	12.31 **																								
(13). TSNARE1 (BMI)	24.15 **	20.21 **	12.11 **	19.93 **	32.29 **	30.64 **	24.44 **	15.59 **																																										

Supplementary Figure 7. Associations between genetically predicted expression of shared genes and women's adiposity traits and psychiatric disorders in 26 tissues using GIFT analysis.

Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

	Adipose (Visceral Omentum) Adipose (Subcutaneous) Brain (Amygdala) Brain (Anterior Cingulate Cortex BA24) Brain (Caudate Basal Ganglia) Brain (Cerebellar Hemisphere) Brain (Cerebellum) Brain (Cortex) Brain (Frontal Cortex BA9) Brain (Hypothalamus) Brain (Hippocampus) Brain (Nucleus Accumbens Basal Ganglia) Brain (Putamen Basal Ganglia) Brain (Spinal Cord Cervical C-1) Colon (Substantia Nigra) Colon (Transverse) Colon (Sigmoid) Small Intestine (Terminal Ileum) Stomach Liver Pancreas Pituitary Adrenal Gland Thyroid Muscle Skeletal Whole Blood																									
(1). ARFGEF2 (AFR)	6.63 **	1.73	8.08 **	8.1 **	6.25 **	2.53 *	5.97 **	5.66 **	5.95 **	7.47 **	9.08 **	8.47 **	10.2 **	7.81 **	7.37 **	6.14 **	4.79 **	5.92 **	-7.17 **	6.41 **	-8.09 **	6.36 **	-4.33 **	8.27 **	8.08 **	7.84 **
(1). ARFGEF2 (PTSD)		-2.68 *	6.48 **	5.28 **	2.85 *	0.91	6.48 **	3.69 *	3.04 *	5.24 **	8.09 **	6.3 **	8.38 **	5.19 **	5.01 **	5.61 **	3.76 *	4.57 **	-5.17 **	6.28 **	-6.86 **	5.27 **	-3.85 *	7.44 **	5.72 **	6.54 **
(2). BMAL1 (BMI)	14.2 **	-15.6 **	-25.97 **	17.57 **	-6.08 **	-21.66 **	-13.86 **	6.45 **	21.23 **	-19 **		-24.09 **	-18.12 **	14.56 **	-25.5 **		-25.1 **	13.91 **	18.96 **	11.9 **	-19.17 **	-23.39 **	10.18 **	-23.28 **	-25.89 **	-28.73 **
(2). BMAL1 (AN)	4.34 **	-3.55 *	-5.39 **	3.91 **	-0.07	-5.03 **	-4.18 **	3.37 *	4.84 **	-4.63 **		-5.13 **	-4.73 **	4.74 **	-4.97 **		-5.71 **	4.14 **	4.98 **	3.19 *	-4.94 **	-5.24 **	2.77 *	-4.99 **	-5.31 **	
(3). CTNNB1 (LFR)	-8.85 **	-9.21 **	-8.29 **	-8.84 **	-9.19 **	-8.41 **	-8.42 **	-9.32 **	-9.01 **	-8.96 **	-9.06 **	-9.17 **	-8.96 **	-8.88 **	-9 **	-9.1 **	-9.1 **	-8.55 **	-8.03 **	-8.85 **	-7.24 **	-9.78 **	5.67 **	-4.52 **	-8.84 **	8.92 **
(3). CTNNB1 (TFR)	-8.85 **			-8.84 **		-8.41 **										-9.1 **		-8.55 **	-8.03 **	-8.85 **	-7.24 **	-9.78 **	5.67 **	-4.52 **		8.92 **
(3). CTNNB1 (AN)	-4.49 **	-4.49 **	-3.72 *	-4.46 **	-4.49 **	-4.45 **	-4.46 **	-4.47 **	-4.45 **	-4.4 **	-4.5 **	-4.45 **	-4.51 **	-4.45 **	-4.49 **	-4.43 **	-4.46 **	-4.57 **	-4.45 **	-4.5 **	-4.49 **	-4.5 **	-4.48 **	-4.47 **	-4.43 **	4.51 **
(4). DENND1B (BMI)	19.7 **	19.93 **	10.47 **		-16.54 **	-16.52 **	-20.93 **	3 *	14.78 **	-1.87	-18.47 **	-5.41 **			-4.44 **	5.36 **	14.48 **		22.03 **	16.62 **	8.31 **	2.82 *	17.56 **	17.01 **	-0.64	21.06 **
(4). DENND1B (MDD)			12.09 **		-16.84 **			2.74 *	14.69 **	-2.68 *	-18 **	-6.09 **			-5.28 **	6.34 **				16.07 **	8.57 **	1.92			0.27	20.74 **

Supplementary Figure 8. Associations between genetically predicted expression of shared genes and men's adiposity traits and psychiatric disorders in 26 tissues using GIFT analysis.

Grey blocks indicate the association was unavailable. Blocks with numbers only indicate the unadjusted $P \geq 0.05$. Blocks with numbers and “*” indicate the unadjusted $P < 0.05$. Blocks with numbers and “**” indicate the Bonferroni-adjusted $P < 0.05$.

		Adipose (Visceral Omentum)	Adipose (Subcutaneous)	Brain (Amygdala)	Brain (Anterior Cingulate Cortex BA24)	Brain (Caudate Basal Ganglia)	Brain (Cerebellar Hemisphere)	Brain (Cerebellum)	Brain (Cortex)	Brain (Frontal Cortex BA9)	Brain (Hypothalamus)	Brain (Hippocampus)	Brain (Nucleus Accumbens Basal Ganglia)	Brain (Putamen Basal Ganglia)	Brain (Spinal Cord Cervical C-1)	Brain (Substantia Nigra)	Colon (Transverse)	Colon (Sigmoid)	Small Intestine (Terminal Ileum)	Stomach	Liver	Pancreas	Pituitary	Adrenal Gland	Thyroid	Muscle Skeletal	Whole Blood
(1). BMAL1 (BMI)	3.82 **	-20.77 **	-22.66 **	15.24 **	-15.57 **	-22.87 **	-21.42 **	-0.32	18.5 **	-21 **		-17.45 **	-6.94 **	4.8 **	-26.65 **		-27.76 **	16.41 **	13.82 **	11.62 **	-9.93 **	-18.28 **	0.61	-16.96 **	-19.78 **	-28.52 **	
(1). BMAL1 (WHR)	3.82 **	-20.77 **	-22.66 **	15.24 **	-15.57 **	-22.87 **	-21.42 **	-0.32	18.5 **	-21 **		-17.45 **	-6.94 **	4.8 **	-26.65 **		-27.76 **	16.41 **	13.82 **	11.62 **	-9.93 **	-18.28 **	0.61	-16.96 **	-19.78 **	-28.52 **	
(1). BMAL1 (AN)	1.41	-5.2 **	-4.41 **	4.06 **	-3.55 *	-4.79 **	-6.09 **	2.44 *	4.34 **	-5.36 **		-3.68 *	-1.18	1.77	-5.34 **		-6.2 **	5.15 **	3.86 **	3.78 **	-2.09 *	-4.16 **	-0.45	-4.09 **	-3.95 **		
(2). CNM2 (BMI)	-11.6 **	6.13 **	7.08 **	13.27 **	26.72 **	26.62 **	22.52 **	31.58 **	28.84 **	0.82	19.51 **	27.09 **	26.21 **	-6.88 **	20.02 **	-13.59 **	-4.64 **	-15.88 **	-17.59 **	28.17 **	13.13 **	-8.18 **	0.47	8.95 **	-5.69 **	-14.94 **	
(2). CNM2 (WHR)	-11.6 **	6.13 **	7.08 **	13.27 **	26.72 **	26.62 **	22.52 **	31.58 **	28.84 **	0.82	19.51 **	27.09 **	26.21 **	-6.88 **	20.02 **	-13.59 **	-4.64 **	-15.88 **	-17.59 **	28.17 **	13.13 **	-8.18 **	0.47	8.95 **	-5.69 **	-14.94 **	
(2). CNM2 (SCZ)	-1.53	-2.16 *	-2.74 *	3.28 *	3.72 *	2.42 *	0.29	2.75 *		-3.2 *	-0.11	1.67		-4.32 **	1.39	-1.71	3.39 *	-0.74	-1.47	4.34 **	-1.36	-1.09	3.06 *	3.37 *	-2.2 *	-5.53 **	
(3). RERE (WHR)	33.93 **	29.26 **	39.67 **	37.3 **	31.41 **	35.09 **	32.14 **	32.08 **	24.94 **	-3.19 *	40 **	33.34 **	32.24 **	35.23 **	33.52 **	8.31 **	29.82 **		36.95 **	8.18 **	37.85 **	40.34 **	-22.11 **	35.82 **	-24.13 **	39.84 **	
(3). RERE (BF%)	16.23 **		19.07 **	17.71 **	15.27 **	16.8 **	15.05 **	15.63 **	10.96 **	-1.69	18.77 **	17.07 **	16.3 **	18.52 **	14.78 **	4.83 **	15.18 **		16.85 **	3.4 *	17.11 **	19.55 **	-10.8 **	17.85 **	-9.09 **	19.29 **	
(3). RERE (MDD)						28.6 **	25.6 **			-6.82 **		25.96 **	25.85 **	28.62 **	25.92 **	6.39 **	22.82 **			3.26 *			-21.26 **		-17.15 **		
(3). RERE (SCZ)	2.58 *	2.5 *	3.58 *	4.49 **	2.14 *	3.32 *	3.21 *	4.83 **	2.7 *	-0.91	4.63 **	2.63 *	3.43 *	4.5 **	5.28 **	-0.74	3.02 *		3.63 *	1.41	3.33 *	4.25 **	-4.73 **	3.05 *	-0.11	3.35 *	
(4). TMEM106B (BMI)	12.33 **	14.03 **	8.98 **	13.34 **		13.36 **	13.46 **	13.13 **	12.8 **	12.68 **	2.55 *	-13.81 **	7.59 **		-14.15 **	14.67 **	13.19 **	10.47 **	14.03 **	12.11 **	14.41 **	14.36 **	14.17 **	13.31 **	13.52 **	13.76 **	
(4). TMEM106B (MDD)	10.01 **	12.37 **	7.78 **	11.27 **		11.86 **	11.38 **	11.08 **	10.56 **	10.08 **	-0.37	-11.5 **	6.34 **		-11.44 **	12.48 **	11.25 **	9 **	12.21 **	10.01 **	12.33 **	12.14 **	12.24 **	11.27 **	11.45 **	11.44 **	

Z-score

40

20

0

-20

