Online Methods, Tables, and Figures

Online Methods

Meta-analysis of three omics based on their *P* values

The meta-analysis Z-scores (Z_{meta}) and *P* values (P_{meta}) for each gene were computed as $Z_{meta} = \frac{\sum w_i Z_i}{\sqrt{\sum w_i^2}}$ and $P_{meta} = \Phi(Z_{meta})$, in which $Z_i = \Phi^{-1}(P_i)$ are the z-scores for each omics data, computed from the gene-based association *P* values. The weights w_i were assigned based on the number of AF cases in each omics data set: $w_i = N_{case_i}^{1/j}$, in which *i* was the type of data (*i*= GWAS, EWAS, or TWAS), N_{case_i} was the number of AF cases for each omics data, and *j* was set equal across the three types of data. As the GWAS sample size dominates the other two data sets, we used *j* to up-weight the EWAS and TWAS data compared to the GWAS data. As *j* increases, the weights for each data set became more similar. We first considered integer values *j*=1, 2, 3,…, 1000; we also considered values ranging from 2 to 10 by 0.2 increments, for more weights compositions if needed. We also investigated two extreme scenarios: 1) 100% weight for GWAS while no weights for EWAS and TWAS, and 2) equal weights for all three omics data. Bonferroni correction was used to account for multiple testing, and genes with P_{meta}<0.05/M, in which M=14,364 is the number of tested genes that were considered as significant AF-related genes. The relative weight of GWAS was annotated as *w_g*:

$$w\_g = \frac{\sqrt[j]{N_{case_{GWAS}}}}{(\sqrt[j]{N_{case_{GWAS}}} + \sqrt[j]{N_{case_{EWAS}}} + \sqrt[j]{N_{case_{TWAS}}})}$$

Network-wide Association Study (NetWAS)

NetWAS [1] is a machine learning-based method that combines gene-level association results with tissue-specific interaction network. The network was built from over 14,000 publications and low-throughput tissue-specific expression data. The list of datasets used to build the network is shown in https://hb.flatironinstitute.org/data. A specific network is built for each tissue type (e.g., heart, blood, and brain), which may be used for downstream analyses. The tissue-specific networks were downloaded from https://hb.flatironinstitute.org/download.

NetWAS trained a support vector machine classifier using nominally significant (e.g., $P < 0.01$) genes as "pre-positive" examples and non-significant (e.g., $P \geq 0.01$) genes as "pre-negatives". The classifier was constructed using a tissue network relevant to a disease (e.g., general heart tissue for AF), where the classifier or hyperplane could maximally distinguished pre-positive and pre-negative genes in the network. Genes were re-ranked using their distance from the hyperplane, which represented as the NetWAS score. If a "pre-positive" gene was predicted positive (i.e., NetWAS score > 0, or referred as "post-positive"), the gene was considered as a disease related genes. The implementation of NetWAS has been described in the previous publication.[1] Detailed steps of how to use the NetWAS online tool (https://hb.flatironinstitute.org/netwas) are shown in **Online Figure XI** with the summary statistics from meta-analysis for the tissue-specific analysis.

Description of gene expression sequencing data

- The Genotype-Tissue Expression (GTEx) project

The gene expression data in GTEx project was from 53 types of normal, non-diseased tissues across nearly 1,000 donors. We downloaded the raw RNA sequencing (RNA-Seq) data (reads per kilobase of transcript, RPKM) by genes from the GTEx V6 analysis freeze (dbGaP Accession phs000424.v6.p1): https://storage.googleapis.com/gtex_analysis_v6/rna_seq_data/GTEx_Analysis_v6_RNA-seq_RNA-SeQCv1.1.8_gene_rpkm.gct.gz.

- Gene expression in left atrium

  There were 101 non-structural heart disease samples obtained from Myocardial Applied Genomics Network (MAGNet) repository. RNA-Seq was performed on the Illumina HiSeq 4000 platform at Broad Institute Genomic Services by standard procedures. Gene expression levels were also defined as RPKM values.

Gene expression levels across multiple heart tissues

As genes could have varied expression levels across different samples, we converted the raw expression levels (RPKM values) into percentiles. An illustration is shown in **Online Figure VIII**. Assuming a specific tissue has *m* samples, each with *n* genes, the expression level of gene i across all genes in sample j is represented as a percentile $R_{i,j}$. The representative gene expression level for gene *i* is defined as the median ranking of gene *i* across all *m* samples for the tissue. Independent AF-related genes were defined as those AF-related genes with Spearman's r^2 <0.25. Similarly, independent non-AF-related genes were defined as those non-AF-related genes with pairwise Spearman's r^2 <0.25. There were 1,057 (left atria, LA) and 773 (right atrial appendage, RA) independent genes in AF-related gene set, while 5,030 (LA) and 3,901 (RA) in non-AF-related gene set. Two-sample Kolmogorov-Smirnov test was then used to compare two independent gene sets.

Tissue-specific expression analysis

The tissue-specific expression analysis (TSEA)[2] was calculated by two steps: the first is an algorithm to define sets of genes with enriched or specific expression in each tissue, and the second is to identify and display significant overlaps between tissue-enriched gene sets and lists of candidate genes. Mathematically, for any gene *i* in a tissue *t*, tissue enrichment is defined as $SI_{i,t} = \frac{\sum_{k \neq t}^{m} \left(rank \left(\frac{RPKM_{i,t}}{RPKM_{i,k}} \right) \right)}{m-1}$, where *m* represents the number of tissues, RPKM represents the expression level. In order to account for different number of expressed genes in different tissues, *pSI* is calculated as $pSI_{i,t} = Probability(SI_{i,t} | Data\ of\ tissue\ t)$, which represents the probability of the rankings of one transcript expression level in a specific tissue (t) comparing to other tissues. For each tissue, genes with *pSI* <0.05 are considered as significantly enriched in the tissue. Then we can calculate the significance of the overlap between the candidate genes and the genes enriched in each tissue using the Fisher's Exact test.

Heritability estimation from summary statistics (HESS)

Before the heritability estimation, HESS [3] (http://bogdan.bioinformatics.ucla.edu/software/hess/) needed to set up the parameters to get a more accurate estimates: 1) Adjust the heritability by the genomic control factor, because the GWAS summary statistics in our analysis were all accounting for population stratification to some degree, we should adjust the heritability estimates by the genomic control factors estimated by HESS (the genomic control factor in

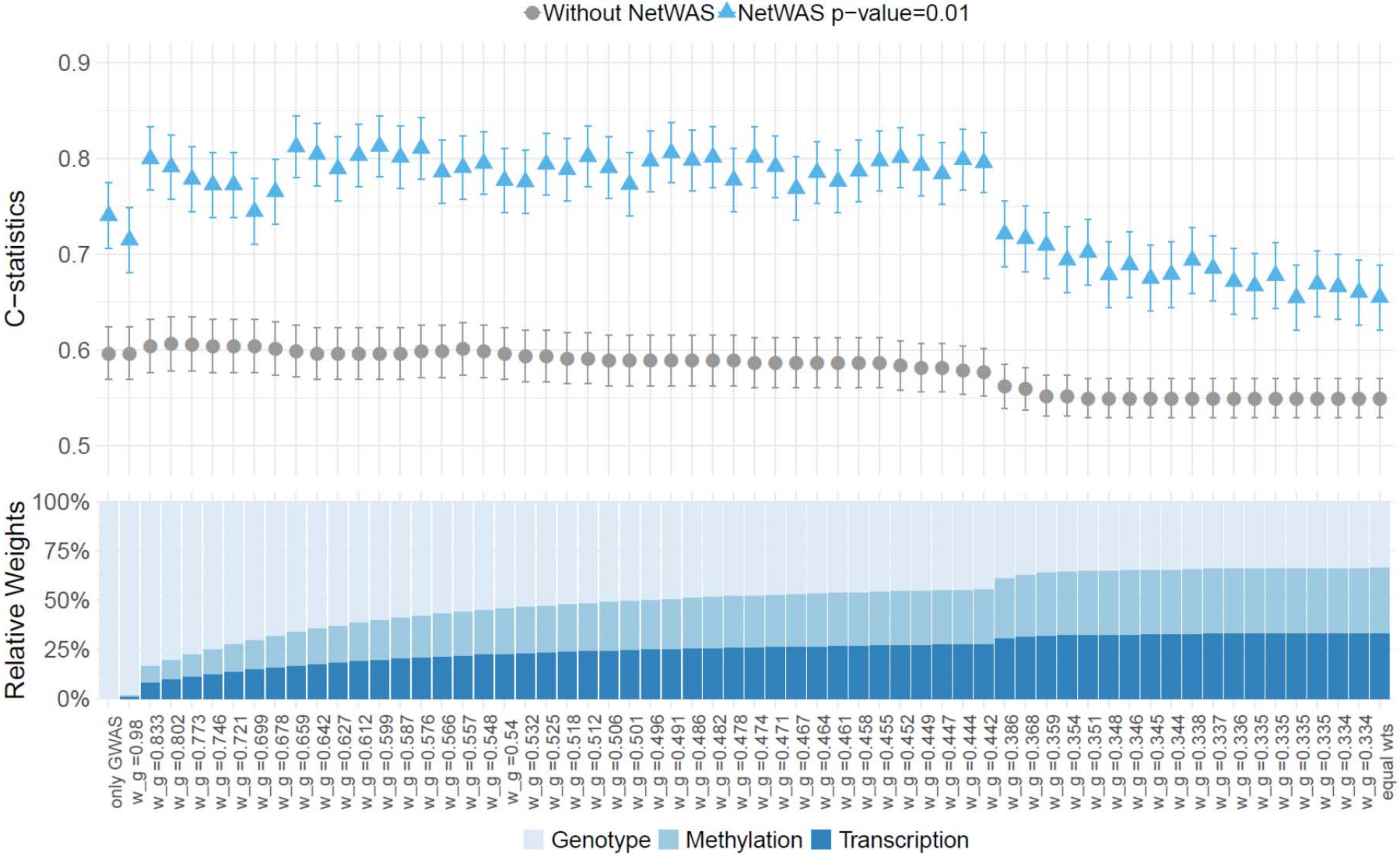
AFGen 2018 Europeans [4] was 1.194, and in UKBB Europeans [5] was 1.246). 2) The number of eigenvectors of the truncated-SVD regularization of LD matrices which should be chosen based on the GWAS sample size, the default number of eigenvectors in HESS was 50 which was based on the simulations of 50,000 individuals, but the total sample size in AFGen 2018 or UKBB Europeans were much larger (both above 300,000 individuals). Because a GWAS with large sample size should use a large number of eigenvectors, we increased the number of eigenvectors until we could get a stable heritability estimation (**Online Figure IX** and **Online Figure X**). In our situation, we chose 200 as the number of eigenvectors.

Evaluation of type 1 error for multi-omic meta-analysis with or without NetWAS

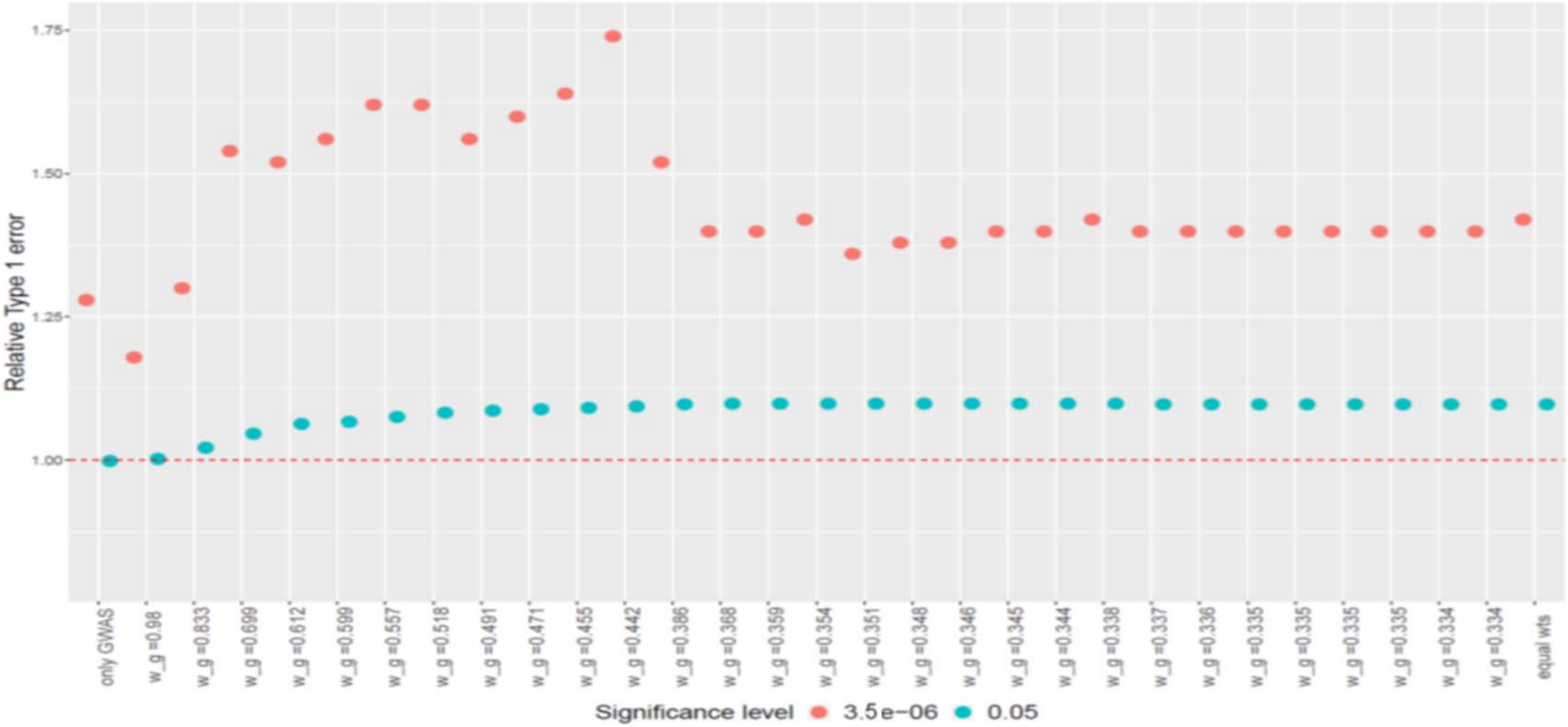
We estimated the type 1 error without NetWAS. Because we could simulate the gene-level summary statistics for the meta-analysis (without NetWAS) appropriately, but it was difficult for us to simulate the gene-gene interaction networks which were behind the summary statistics for NetWAS.

We simulated the z-scores for three types of omics of 15,000 genes, following a multivariate normal distribution with each mean of zero, and the covariance matrix as estimated from AFGen 2017 GWAS, EWAS, and TWAS (see partial table from **Online Table I**). The correlations between GWAS-EWAS, GWAS-TWAS, and EWAS-TWAS were 0.06, 0.005, and 0.022 respectively. One thousand replicates were simulated. Then, we used meta-analysis to combine those z-scores by different weights irrespective of the association directions. We calculated the relative type 1 error assuming the significance level (α) of 0.05, and 3.3e-06 (0.05/15,000). Relative type 1 error equaled the total number of genes with *P* value less than α across 1,000 replicates, divided by the expected number of false positives ($\alpha \times 15,000 \times 1,000$). The results for relative type 1 error was in **Online Figure II**.

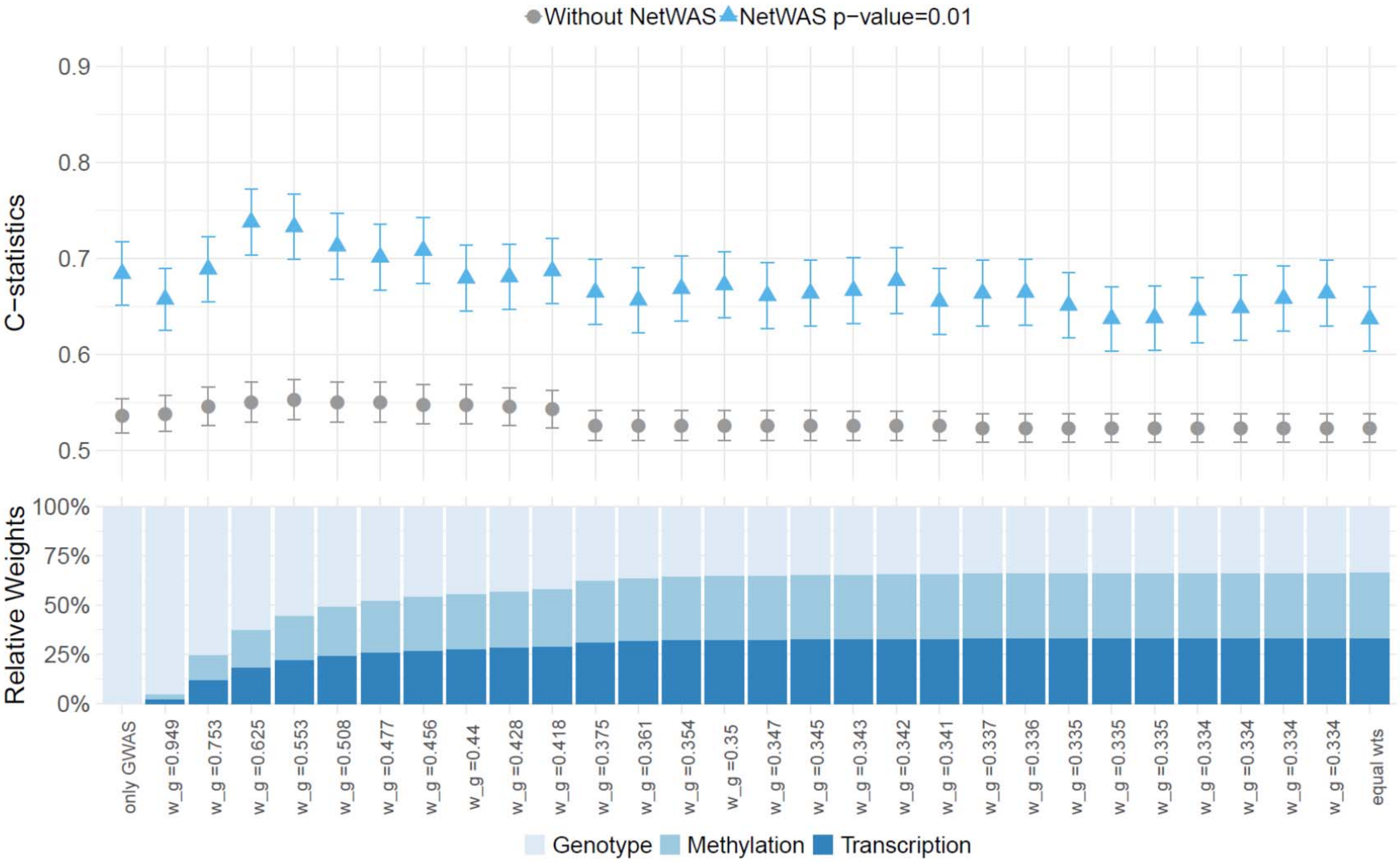
Online Figure I. C-statistics for multi-omics integration approach across different weights compositions of AFGen 2017 GWAS, methylation, and transcription. w_g is the relative weight of genotype data. NetWAS *P* value is the cutoff for defining "pre-positive" genes.



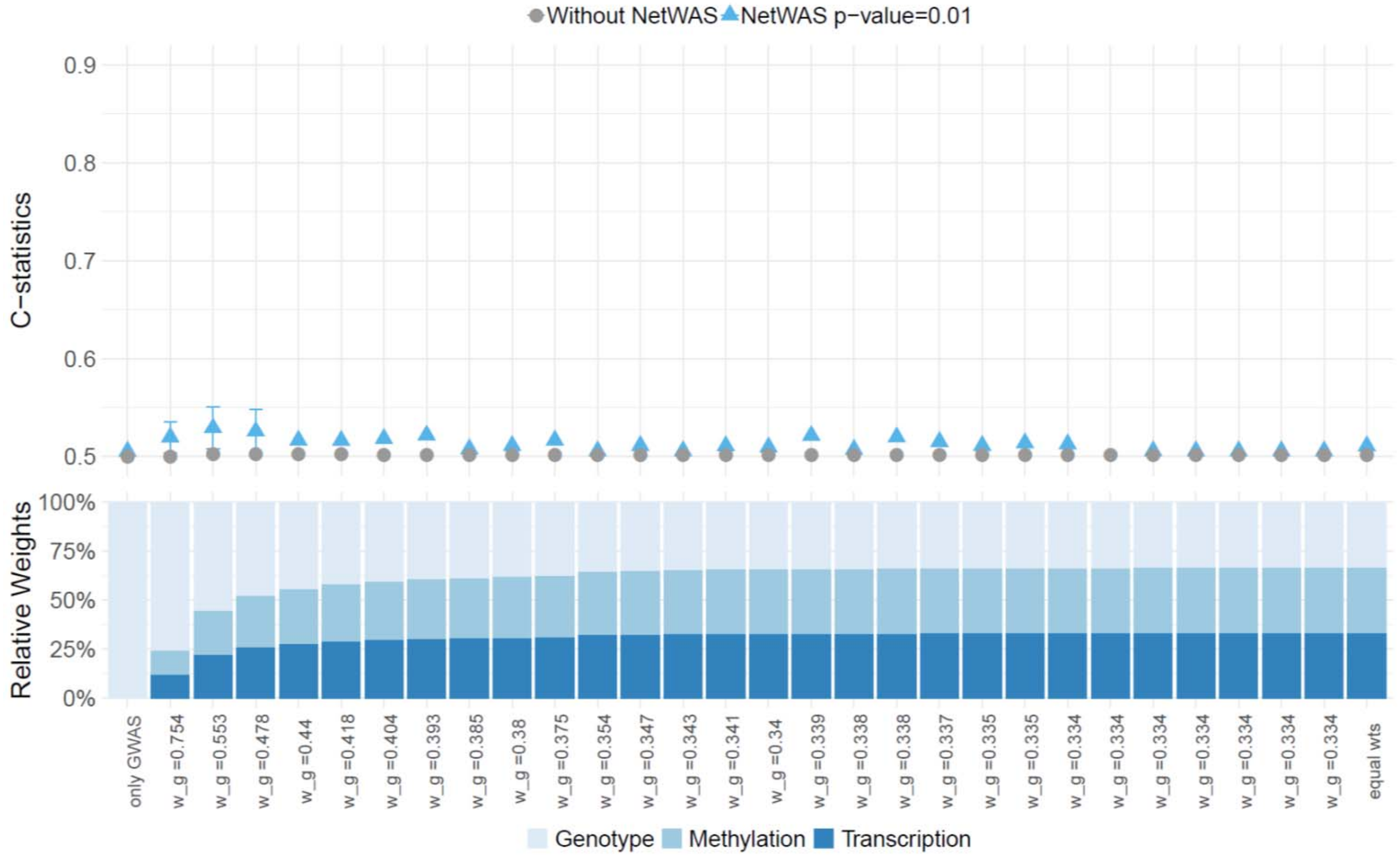
Online Figure II. Relative type 1 error for multi-omics integration approach across different weights compositions of AFGen 2017 GWAS, methylation, and transcription in heart tissues. w_g is the relative weight of genotype data.



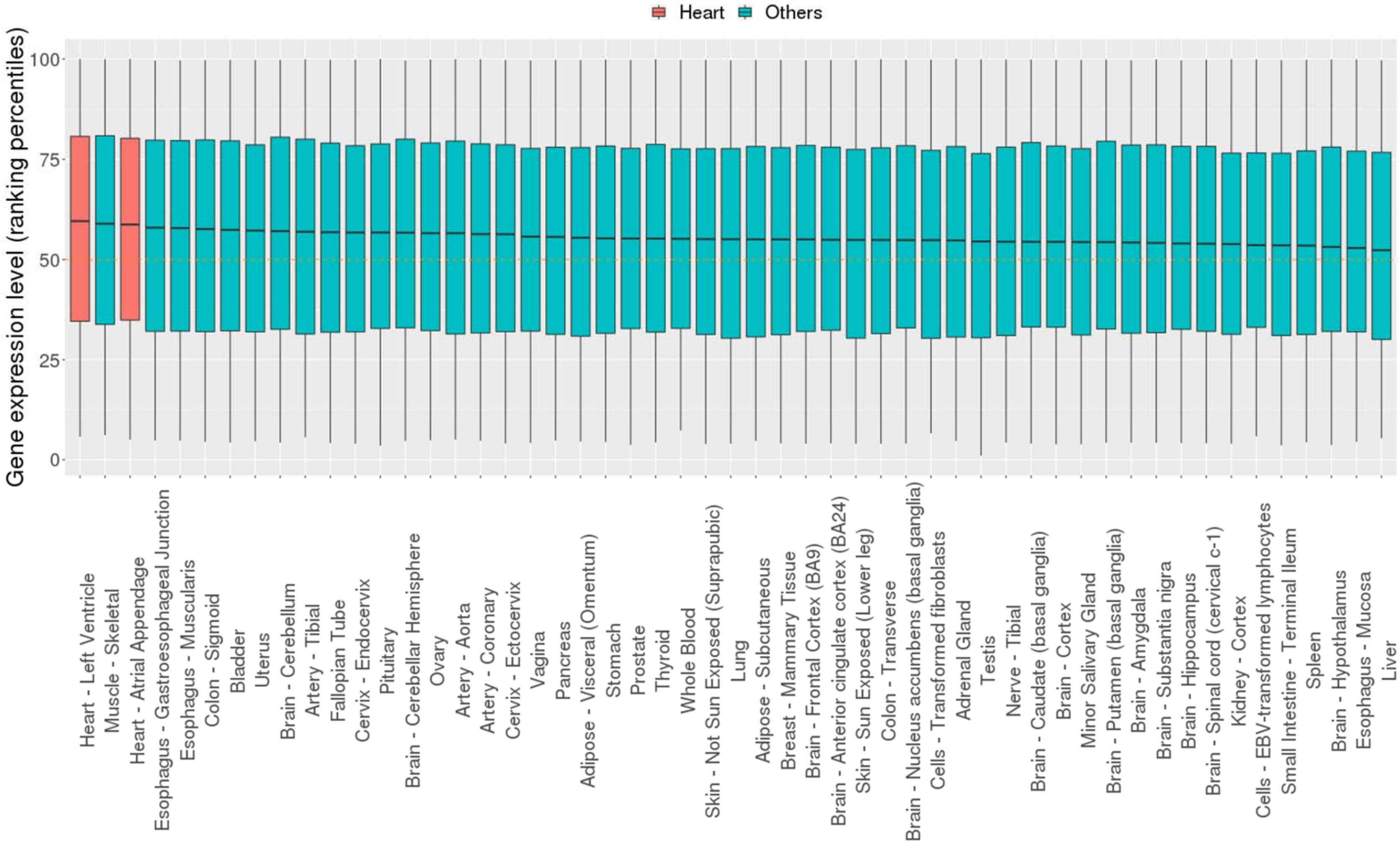
Online Figure III. C-statistics for multi-omics integration approach across different weights compositions of AFGen 2012 GWAS, methylation, and transcription in heart tissues. w_g is the relative weight of genotype data. NetWAS *P* value is the cutoff for defining “pre-positive” genes.



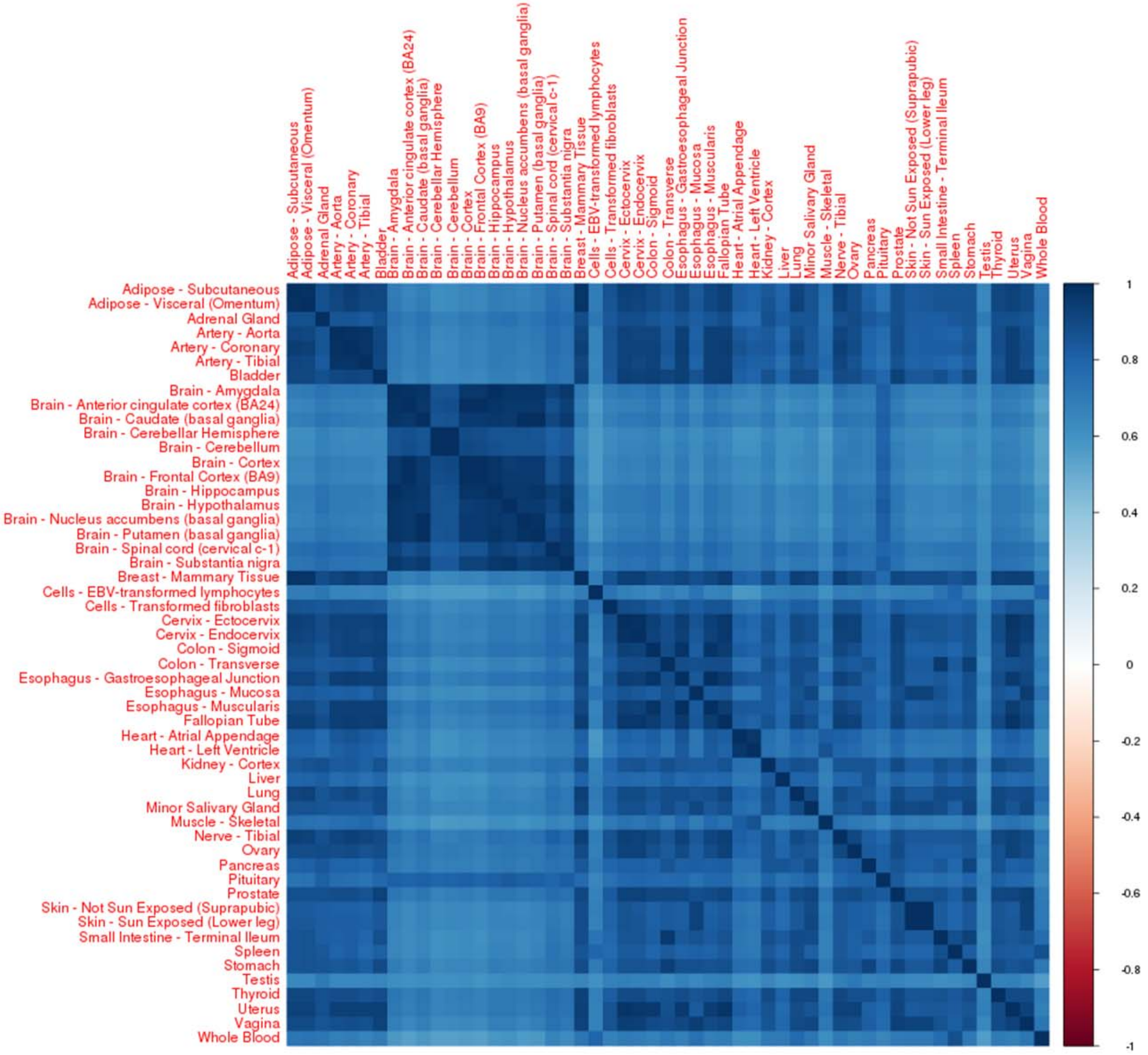
Online Figure IV. C-statistics for multi-omics integration approach across different weights compositions of FHS AF GWAS, methylation, and transcription by in heart tissues. w_g is the relative weight of genotype data. NetWAS *P* value is the cutoff for defining "pre-positive" genes.



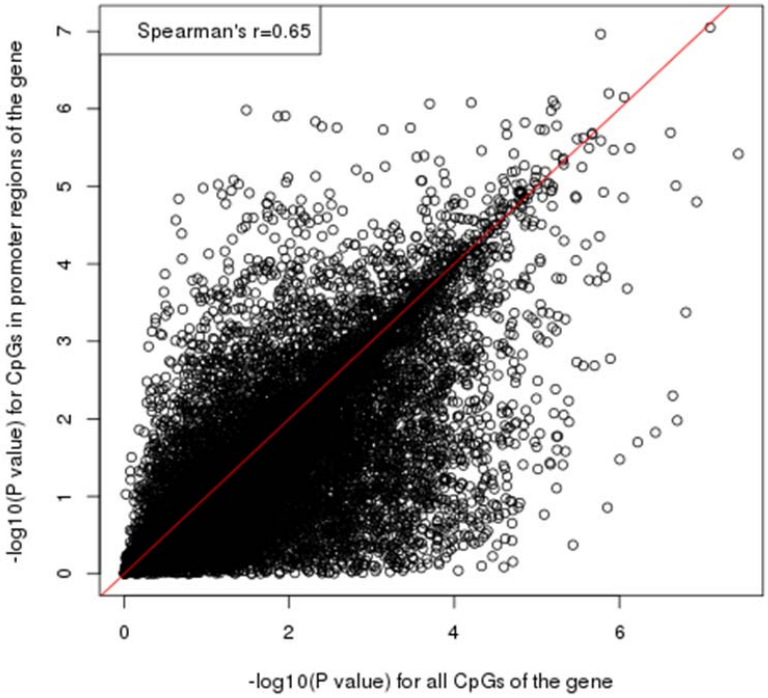
Online Figure V. The expression of AF-related genes by multi-omics integration across different tissues in GTEx.



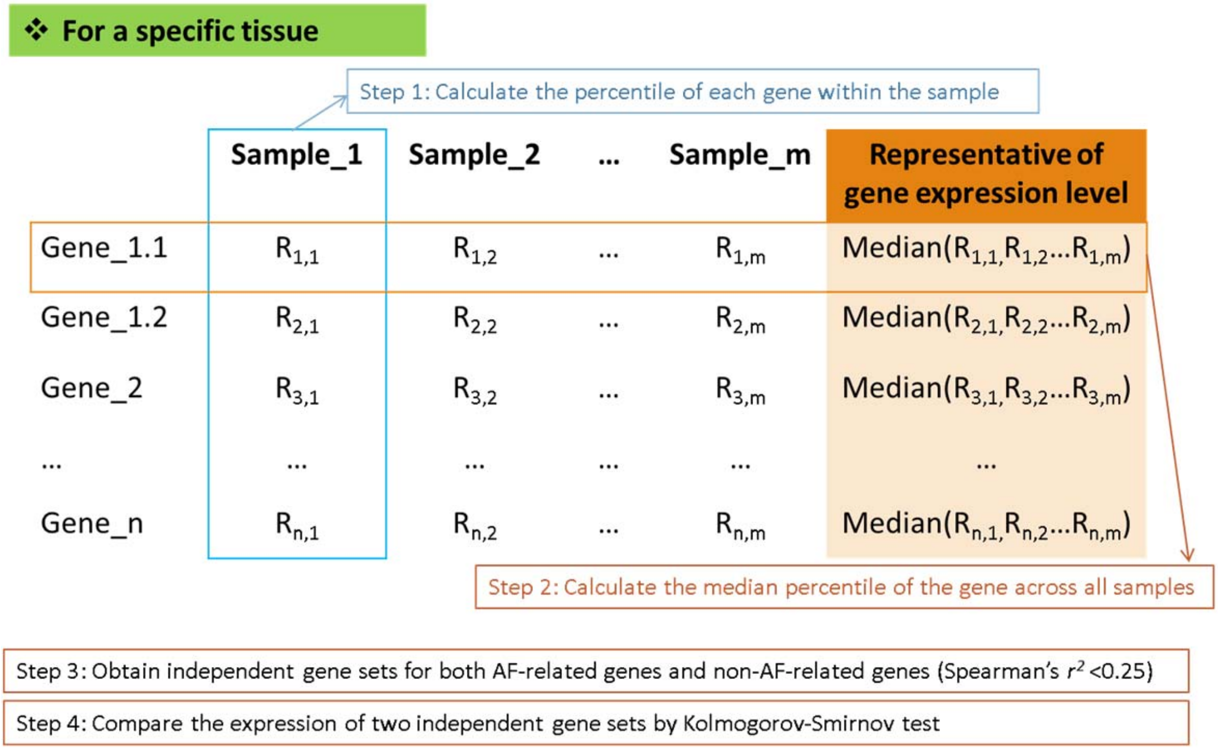
Online Figure VI. Spearman's correlations of gene expression levels (in ranking percentiles) for the AF-related genes by multi-omics integration across different tissues in GTEx.



Online Figure VII. Spearman's correlation of -log10(*P* values) in association analysis of combing all CpGs versus CpGs in promoter region (annotated as "TSS1500", "TS200" and "5'UTR") of the gene.



Online Figure VIII. Analysis flowchart of gene expression levels across multiple heart tissues.



❖ For a specific tissue

Step 1: Calculate the percentile of each gene within the sample

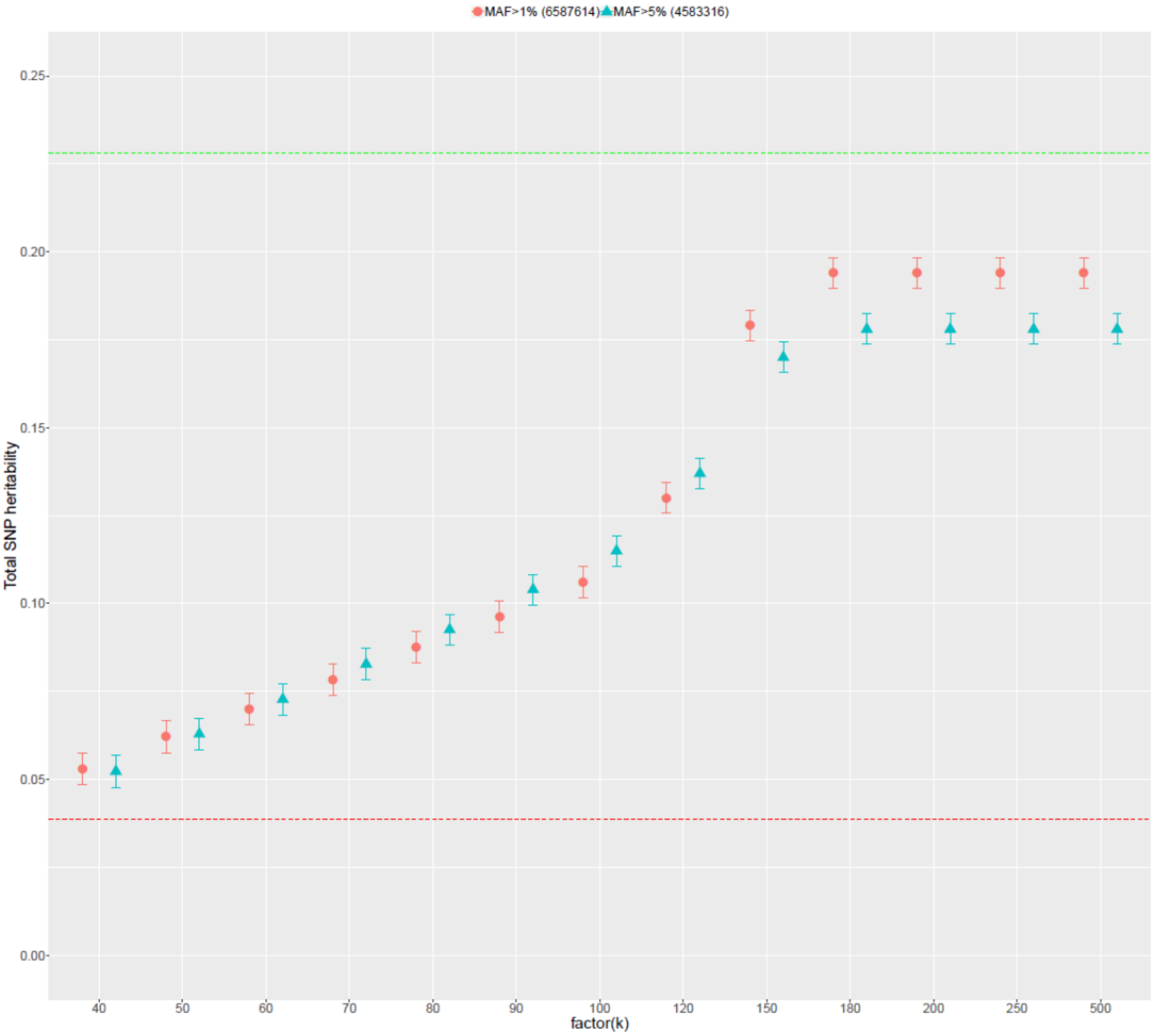
	Sample_1	Sample_2	...	Sample_m	Representative of gene expression level
Gene_1.1	$R_{1,1}$	$R_{1,2}$	...	$R_{1,m}$	Median($R_{1,1,}R_{1,2}...R_{1,m}$)
Gene_1.2	$R_{2,1}$	$R_{2,2}$	...	$R_{2,m}$	Median($R_{2,1,}R_{2,2}...R_{2,m}$)
Gene_2	$R_{3,1}$	$R_{3,2}$	...	$R_{3,m}$	Median($R_{3,1,}R_{3,2}...R_{3,m}$)
...	...	...	...	...	...
Gene_n	$R_{n,1}$	$R_{n,2}$	...	$R_{n,m}$	Median($R_{n,1,}R_{n,2}...R_{n,m}$)

Step 2: Calculate the median percentile of the gene across all samples

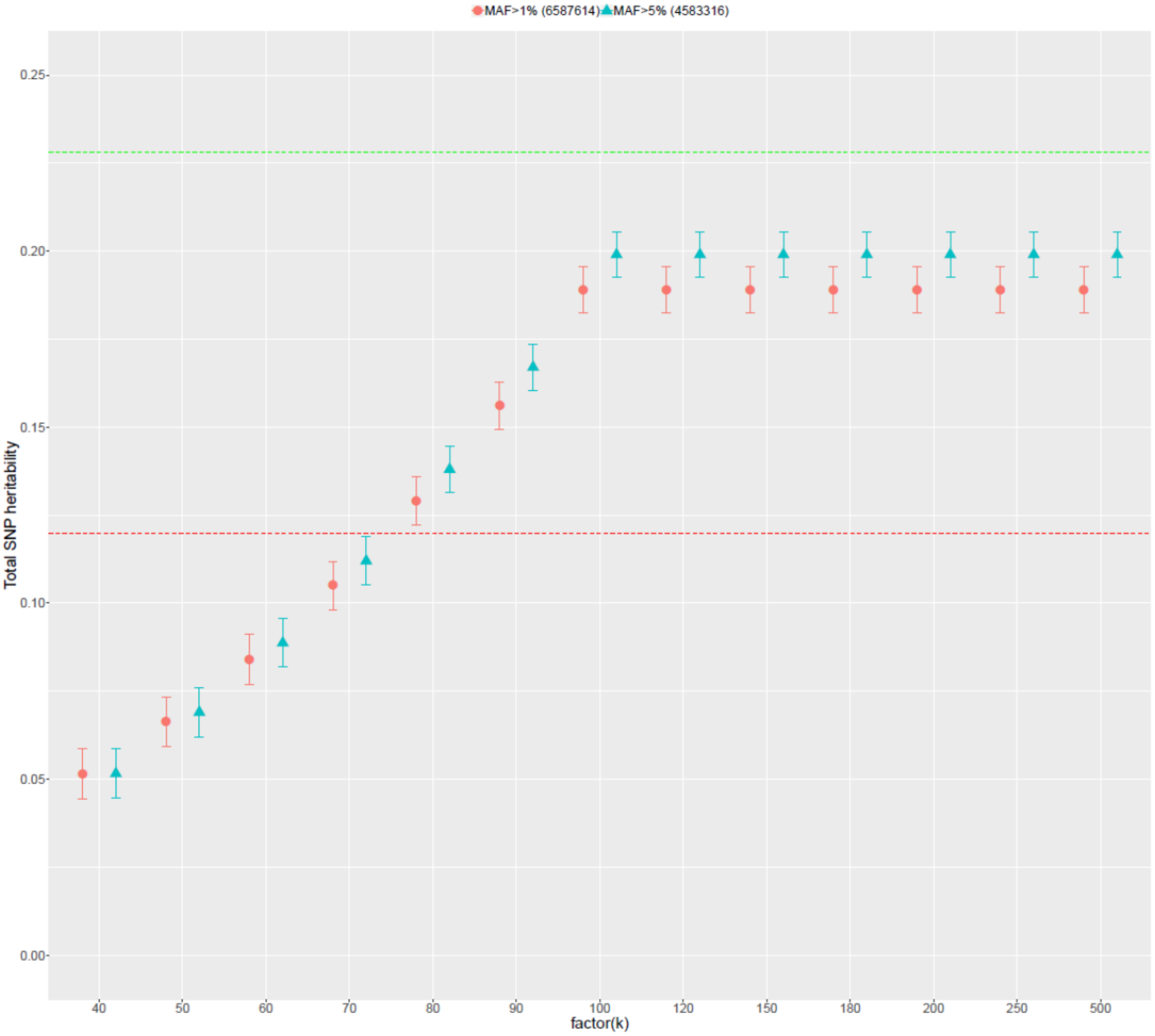
Step 3: Obtain independent gene sets for both AF-related genes and non-AF-related genes (Spearman's r^2 <0.25)

Step 4: Compare the expression of two independent gene sets by Kolmogorov-Smirnov test

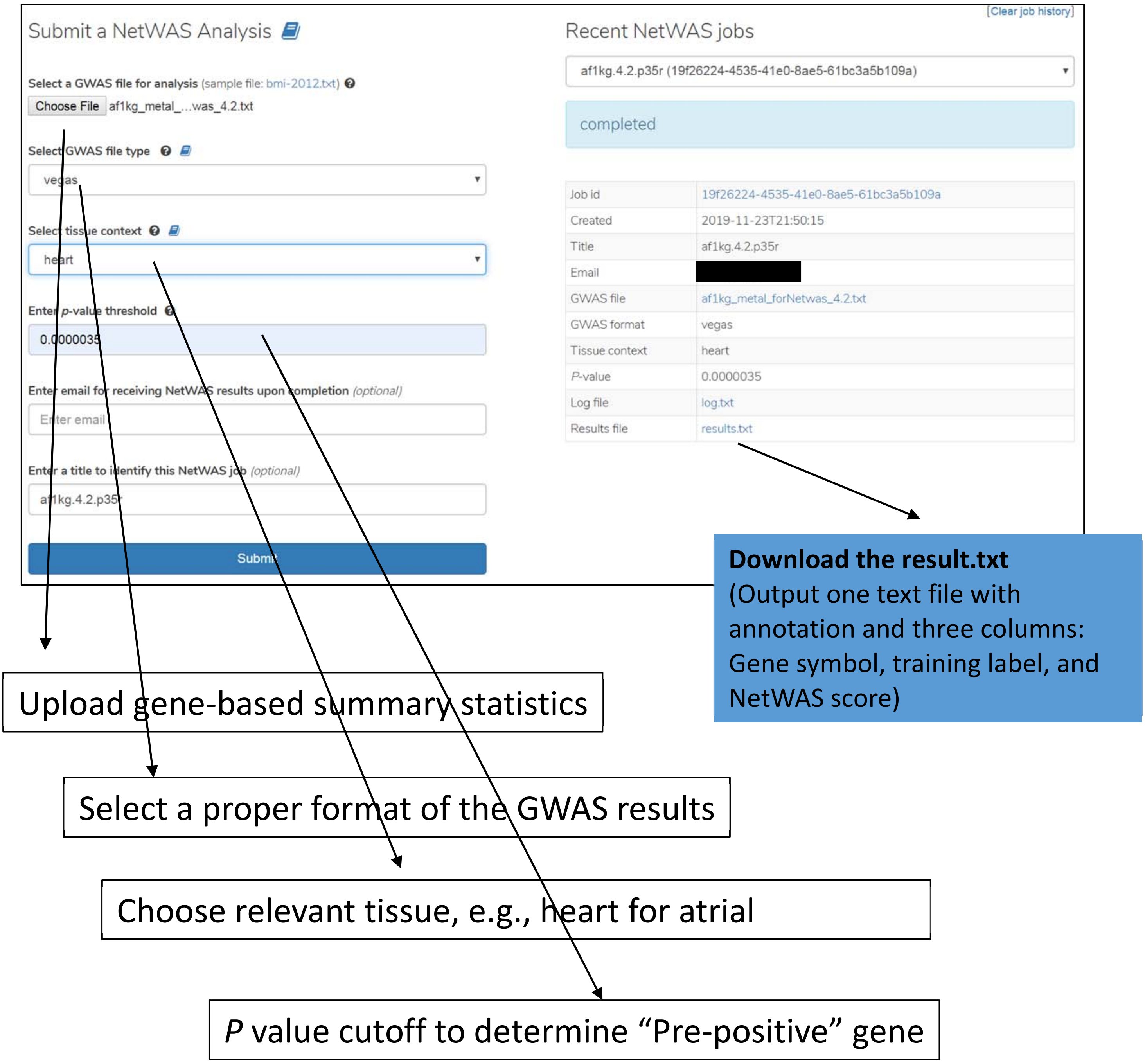
Online Figure IX. Total heritability estimates by HESS across different number of eigenvectors of the LD matrices for AFGen 2018 Europeans. The x-axis is the number of eigenvectors (k), while the y-axis is the total heritability, red dots are the variants with minor allele frequency (MAF) >1% while green dots are MAF>5%, and the number in the parenthesis are the total number of variants. Red dash line is the heritability estimates by LDSC regression as 0.0388 (SE=0.0041), and the green dash line is the heritability estimates by individual level data as 0.228 (SE=0.0454).



Online Figure X. Total heritability estimates by HESS across different number of eigenvectors of the LD matrices for UKBB European participants. The x-axis is the number of eigenvectors (k), while the y-axis is the total heritability, red dots are the variants with minor allele frequency (MAF) >1% while green dots are MAF>5%, and the number in the parenthesis are the total number of variants. Red dash line is the heritability estimates by LDSC regression as 0.1197 (SE=0.0344), and the green dash line is the heritability estimates by individual level data as 0.228 (SE=0.0454).



Online Figure XI. Screenshots of how to use the NetWAS online tool to run the analysis.



Submit a NetWAS Analysis

Select a GWAS file for analysis (sample file: bmi-2012.txt)
Choose File af1kg_metal_...was_4.2.txt

Select GWAS file type: vegas

Select tissue context: heart

Enter *p*-value threshold: 0.0000035

Enter email for receiving NetWAS results upon completion *(optional)*: Enter email

Enter a title to identify this NetWAS job *(optional)*: af1kg.4.2.p35r

Submit

Recent NetWAS jobs

[Clear job history]

af1kg.4.2.p35r (19f26224-4535-41e0-8ae5-61bc3a5b109a)

completed

Job id	19f26224-4535-41e0-8ae5-61bc3a5b109a
Created	2019-11-23T21:50:15
Title	af1kg.4.2.p35r
Email	[redacted]
GWAS file	af1kg_metal_forNetwas_4.2.txt
GWAS format	vegas
Tissue context	heart
P-value	0.0000035
Log file	log.txt
Results file	results.txt

Download the result.txt
(Output one text file with annotation and three columns: Gene symbol, training label, and NetWAS score)

Upload gene-based summary statistics

Select a proper format of the GWAS results

Choose relevant tissue, e.g., heart for atrial

P value cutoff to determine “Pre-positive” gene

The summary statistics from meta-analysis can be downloaded from https://drive.google.com/file/d/1X0GmYv8MYHO9RXioaihCSWOKCTFgNMjZ/view?usp=sharing.

Online Table I. Correlations of genotype, methylation, and transcription calculated by their gene-based association *P* values with atrial fibrillation.

Data	FHS GWAS	AFGen 2012 GWAS	AFGen 2017 GWAS	AFGen 2018 GWAS	FHS EWAS	FHS TWAS
FHS GWAS	1	0.094	0.043	0.015	-0.009	0.01
AFGen 2012 GWAS	0.094	1	0.269	0.117	0.056	0.026
AFGen 2017 GWAS	0.043	0.269	1	0.339	0.06	0.005
AFGen 2018 GWAS	0.015	0.117	0.339	1	0.065	-0.008
FHS EWAS	-0.009	0.056	0.06	0.065	1	0.022
FHS TWAS	0.01	0.026	0.005	-0.008	0.022	1

The cells with yellow high-lighted background are the correlation coefficients across different types of omics data by their Z statistics from association *P* values (e.g., GWAS-EWAS, GWAS-TWAS, and EWAS-TWAS). FHS: Framingham Heart Study.

Online Table II. Twenty-five tissue groups for tissue-specific enrichment analysis from GTEx.

Tissue	**Tissue group**
Adipose Subcutaneous	Adipose Tissue
Adipose Visceral Omentum	Adipose Tissue
Adrenal Gland	Adrenal Gland
Artery Aorta	Blood Vessel
Artery Coronary	Blood Vessel
Artery Tibial	Blood Vessel
Brain Amygdala	Brain
Brain Anterior cingulate cortex BA24	Brain
Brain Caudate basal ganglia	Brain
Brain Cerebellar Hemisphere	Brain
Brain Cerebellum	Brain
Brain Cortex	Brain
Brain Frontal Cortex BA9	Brain
Brain Hippocampus	Brain
Brain Hypothalamus	Brain
Brain Nucleus accumbens basal ganglia	Brain
Brain Putamen basal ganglia	Brain
Brain Spinal cord cervical	Brain
Brain Substantia nigra	Brain
Breast Mammary Tissue	Breast
Cells EBV transformed lymphocytes	Not consider
Cells Transformed fibroblasts	Not consider
Colon Transverse	Colon
Esophagus Mucosa	Esophagus
Esophagus Muscularis	Esophagus
Fallopian Tube	Fallopian Tube
Heart Atrial Appendage	Heart
Heart Left Ventricle	Heart
Kidney Cortex	Kidney
Liver	Liver
Lung	Lung
Muscle Skeletal	Muscle
Nerve Tibial	Nerve
Ovary	Ovary
Pancreas	Pancreas
Pituitary	Pituitary
Prostate	Prostate
Skin Not Sun Exposed Suprapubic	Skin
Skin Sun Exposed Lower leg	Skin
Stomach	Stomach
Testis	Testis
Thyroid	Thyroid

Tissue	Tissue group
Uterus	Uterus
Vagina	Vagina
Whole Blood	Whole Blood

Online Table III. Comparisons of performances of multi-omics integration approach by to the single GWAS analysis from AFGen 2017.

Weights composition	With NetWAS					Without NetWAS				
	Nf	Nv	Sensitivity	Specificity	Delta C-stats	Nf	Nv	Sensitivity	Specificity	Delta C-stats
GWAS only (w_g=1)	378	103	0.500	0.981	Ref	44	40	0.194	1.000	Ref
j=1 (w_g=0.98)	333	92	0.447	0.983	-0.025	44	40	0.194	1.000	0.000
j=2 (w_g=0.833)	583	130	0.631	0.968	0.059	48	43	0.209	1.000	0.007
j=2.2 (w_g=0.802)	615	127	0.617	0.965	0.051	49	44	0.214	1.000	0.010
j=2.4 (w_g=0.773)	628	122	0.592	0.964	0.038	50	44	0.214	1.000	0.010
j=2.6 (w_g=0.746)	654	120	0.583	0.962	0.032	49	43	0.209	1.000	0.007
j=2.8 (w_g=0.721)	654	120	0.583	0.962	0.032	49	43	0.209	1.000	0.007
j=3 (w_g=0.699)	677	109	0.529	0.960	0.004	49	43	0.209	1.000	0.007
j=3.2 (w_g=0.678)	720	118	0.573	0.957	0.025	49	42	0.204	1.000	0.005
j=3.4 (w_g=0.659)	860	139	0.675	0.949	0.072	49	41	0.199	0.999	0.002
j=3.6 (w_g=0.642)	873	136	0.660	0.948	0.064	49	40	0.194	0.999	0.000
j=3.8 (w_g=0.627)	880	130	0.631	0.947	0.049	50	40	0.194	0.999	0.000
j=4 (w_g=0.612)	900	136	0.660	0.946	0.063	50	40	0.194	0.999	0.000
j=4.2 (w_g=0.599)	978	141	0.684	0.941	0.072	50	40	0.194	0.999	0.000
j=4.4 (w_g=0.587)	954	136	0.660	0.942	0.061	50	40	0.194	0.999	0.000
j=4.6 (w_g=0.576)	1041	141	0.684	0.936	0.070	52	41	0.199	0.999	0.002
j=4.8 (w_g=0.566)	1039	131	0.636	0.936	0.046	52	41	0.199	0.999	0.002
j=5 (w_g=0.557)	980	132	0.641	0.940	0.050	54	42	0.204	0.999	0.005
j=5.2 (w_g=0.548)	1135	136	0.660	0.929	0.054	54	41	0.199	0.999	0.002
j=5.4 (w_g=0.54)	1153	129	0.626	0.928	0.037	54	40	0.194	0.999	0.000
j=5.6 (w_g=0.532)	1195	129	0.626	0.925	0.035	53	39	0.189	0.999	-0.003
j=5.8 (w_g=0.525)	1230	137	0.665	0.923	0.054	54	39	0.189	0.999	-0.003
j=6 (w_g=0.518)	1323	136	0.660	0.916	0.048	53	38	0.184	0.999	-0.005
j=6.2 (w_g=0.512)	1355	142	0.689	0.914	0.061	53	38	0.184	0.999	-0.005
j=6.4 (w_g=0.506)	1334	137	0.665	0.915	0.050	52	37	0.180	0.999	-0.008
j=6.6 (w_g=0.501)	1339	130	0.631	0.914	0.033	52	37	0.180	0.999	-0.008
j=6.8 (w_g=0.496)	1418	141	0.684	0.910	0.057	52	37	0.180	0.999	-0.008
j=7 (w_g=0.491)	1452	145	0.704	0.908	0.065	51	37	0.180	0.999	-0.008
j=7.2 (w_g=0.486)	1462	142	0.689	0.907	0.058	51	37	0.180	0.999	-0.008
j=7.4 (w_g=0.482)	1506	144	0.699	0.904	0.061	52	37	0.180	0.999	-0.008
j=7.6 (w_g=0.478)	1427	133	0.646	0.908	0.037	53	37	0.180	0.999	-0.008
j=7.8 (w_g=0.474)	1512	144	0.699	0.903	0.061	52	36	0.175	0.999	-0.010
j=8 (w_g=0.471)	1506	140	0.680	0.903	0.051	52	36	0.175	0.999	-0.010
j=8.2 (w_g=0.467)	1459	130	0.631	0.906	0.028	52	36	0.175	0.999	-0.010
j=8.4 (w_g=0.464)	1475	137	0.665	0.905	0.045	52	36	0.175	0.999	-0.010
j=8.6 (w_g=0.461)	1524	134	0.650	0.902	0.036	52	36	0.175	0.999	-0.010
j=8.8 (w_g=0.458)	1504	138	0.670	0.903	0.046	52	36	0.175	0.999	-0.010
j=9 (w_g=0.455)	1619	144	0.699	0.896	0.057	53	36	0.175	0.999	-0.010
j=9.2 (w_g=0.452)	1591	145	0.704	0.898	0.061	52	35	0.170	0.999	-0.013
j=9.4 (w_g=0.449)	1614	142	0.689	0.896	0.052	51	34	0.165	0.999	-0.015
j=9.6 (w_g=0.447)	1651	139	0.675	0.893	0.044	51	34	0.165	0.999	-0.015
j=9.8 (w_g=0.444)	1654	145	0.704	0.893	0.058	50	33	0.160	0.999	-0.017

Weights composition	With NetWAS					Without NetWAS				
	Nf	Nv	Sensitivity	Specificity	Delta C-stats	Nf	Nv	Sensitivity	Specificity	Delta C-stats
j=10 (w_g=0.442)	1673	144	0.699	0.892	0.055	47	32	0.155	0.999	-0.020
j=20 (w_g=0.386)	1613	113	0.549	0.894	-0.019	45	26	0.126	0.999	-0.035
j=30 (w_g=0.368)	1681	112	0.544	0.889	-0.024	46	25	0.121	0.999	-0.037
j=40 (w_g=0.359)	1667	109	0.529	0.890	-0.031	45	22	0.107	0.998	-0.044
j=50 (w_g=0.354)	1758	104	0.505	0.883	-0.046	46	22	0.107	0.998	-0.044
j=60 (w_g=0.351)	1740	107	0.519	0.885	-0.038	45	21	0.102	0.998	-0.047
j=70 (w_g=0.348)	1635	96	0.466	0.891	-0.062	45	21	0.102	0.998	-0.047
j=80 (w_g=0.346)	1686	101	0.490	0.888	-0.051	45	21	0.102	0.998	-0.047
j=90 (w_g=0.345)	1739	96	0.466	0.884	-0.065	45	21	0.102	0.998	-0.047
j=100 (w_g=0.344)	1691	97	0.471	0.887	-0.061	45	21	0.102	0.998	-0.047
j=200 (w_g=0.338)	1695	103	0.500	0.887	-0.047	47	21	0.102	0.998	-0.047
j=300 (w_g=0.337)	1656	99	0.481	0.890	-0.055	47	21	0.102	0.998	-0.047
j=400 (w_g=0.336)	1556	92	0.447	0.896	-0.069	47	21	0.102	0.998	-0.047
j=500 (w_g=0.335)	1475	89	0.432	0.902	-0.073	47	21	0.102	0.998	-0.047
j=600 (w_g=0.335)	1512	94	0.456	0.900	-0.062	47	21	0.102	0.998	-0.047
j=700 (w_g=0.335)	1477	84	0.408	0.901	-0.086	46	21	0.102	0.998	-0.047
j=800 (w_g=0.335)	1486	90	0.437	0.901	-0.071	46	21	0.102	0.998	-0.047
j=900 (w_g=0.334)	1495	89	0.432	0.901	-0.074	46	21	0.102	0.998	-0.047
j=1000 (w_g=0.334)	1526	87	0.422	0.898	-0.080	46	21	0.102	0.998	-0.047
Equal weights (w_g=0.333)	1535	85	0.413	0.897	-0.085	46	21	0.102	0.998	-0.047

The j is the parameter as the weights function of number of AF cases during association studies, $w_i = N_{case_i}^{1/j}$, where *w* is the weight for specific omics data, *N* is the number of AF cases (the number of AF cases are 17,931, 183, and 177 for genotype, methylation, and transcription respectively), *j* is a squence of numbers, and *i* is the type of data (*i*= GWAS, EWAS, or TWAS), w_g is the relative weight of GWAS,

$$w\_g = \frac{\sqrt[j]{N_{case_{GWAS}}}}{(\sqrt[j]{N_{case_{GWAS}}} + \sqrt[j]{N_{case_{EWAS}}} + \sqrt[j]{N_{case_{TWAS}}})}$$

Nf is the total number of genes found by the integration approach, Nv is the number of genes validated by the reference gene set (AFGen 2018 GWAS), Delta C-stats is the difference of C-stats of C-stats (with omics integration) minus the reference C-stats (only GWAS).

The optimal weights are the weights compositions when we have a maxium postive delta C-statistics comparing to Only GWAS. The optimal weights with NetWAS is j=4.2 (w_g=0.599, Delta C-stats = 0.07236).

Online Table IV. Number of AF-related genes by GWAS only versus by multi-omics when reached the optimal C-statistics.

Parameters	Number of AF-related genes (by 2017 GWAS only)	Number of AF-related genes (by 2017 GWAS + EWAS + TWAS)
Without NetWAS	44	49
NetWAS Heart (P=3.5×10^{-6})	10	15
NetWAS Heart (P=0.0001)	26	69
NetWAS Heart (P=0.01)	378	978
NetWAS Heart (P=0.1)	1,700	2,627
NetWAS Whole blood (P=0.01)	276	630

Online Table V. Comparisons of AF-associated genes by our multi-omics approach with other GWAS studies, GWAS catalog, Open Targets Platform, OMIM.

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
A1CF	0	0	0	0	0	1	0
A2M	0	0	0	0	0	1	0
A4GALT	1	0	0	0	0	0	0
AAGAB	1	0	0	0	0	0	0
AAK1	1	0	0	0	0	0	0
AAT8	0	0	0	0	0	0	1
AAT9	0	0	0	0	0	0	1
ABCA1	1	0	0	0	0	1	0
ABCA12	0	0	0	0	1	1	0
ABCA3	1	0	0	0	0	0	0
ABCB1	0	0	0	0	0	1	0
ABCB4	0	0	0	0	0	1	0
ABCB8	1	0	0	0	0	0	0
ABCB9	1	0	0	0	0	0	0
ABCC9	0	0	0	0	0	0	1
ABCD2	0	0	0	0	0	1	0
ABCD3	0	0	0	0	0	1	0
ABCD4	1	0	0	0	0	0	0
ABCG2	0	0	0	0	0	1	0
ABHD10	0	0	1	0	0	0	0
ABHD17C	0	0	0	1	1	0	0
ABHD6	1	0	0	0	0	0	0
ABI1	1	0	0	0	0	1	0
ABL1	0	0	0	0	0	1	0
ABL2	1	0	0	0	0	0	0
ABLIM1	1	0	0	0	0	0	0
ABO	0	0	0	0	0	1	0
ABS2	0	0	0	0	0	0	1
ACAA1	1	0	0	0	0	0	0
ACACA	1	0	0	0	0	0	0
ACAD8	1	0	0	0	0	0	0
ACADS	0	0	0	0	0	1	0
ACAP1	1	0	0	0	0	0	0
ACBD4	1	0	0	0	0	0	0
ACDMPV	0	0	0	0	0	0	1
ACE	0	0	0	0	0	1	0
ACE2	0	0	0	0	0	1	0
ACG2	0	0	0	0	0	0	1
ACHE	0	0	0	0	0	1	0
ACP5	0	0	0	0	0	1	0
ACP6	1	0	0	0	0	0	0
ACR	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ACSL1	0	0	0	0	0	1	0
ACSL6	1	0	0	0	0	0	0
ACSM3	0	0	0	0	0	1	0
ACTB	0	0	0	0	0	1	0
ACTC1	1	0	0	0	0	0	1
ACTN2	0	0	0	0	0	1	1
ACTN4	1	0	0	0	0	0	0
ACTR1A	1	0	0	0	0	0	0
ACTR2	1	0	0	0	0	0	0
ACTR8	1	0	0	0	0	0	0
ACVR1B	0	0	0	0	0	1	0
ACVR2A	1	0	1	0	0	0	0
ACVR2B	0	0	0	0	0	0	1
ACVRL1	0	0	0	0	0	0	1
ADA	0	0	0	0	0	1	0
ADAM15	1	0	1	0	0	0	0
ADAM17	1	0	0	0	0	0	0
ADAM32	1	0	0	0	0	0	0
ADAMTS13	0	0	0	0	0	1	0
ADAMTS14	1	0	0	0	0	0	0
ADAP1	1	0	1	0	0	0	0
ADAP2	0	0	0	0	0	0	1
ADAT2	1	0	0	0	0	0	0
ADCY10	0	0	0	0	0	1	0
ADCY3	1	0	0	0	0	0	0
ADCY4	1	0	0	0	0	0	0
ADCY6	1	0	0	0	0	0	0
ADCYAP1	0	0	0	0	0	1	0
ADGB	0	0	0	0	0	1	0
ADGRD1	0	0	0	0	0	1	0
ADH1B	0	0	0	0	0	1	0
ADIPOR1	1	0	0	0	0	0	0
ADK	0	0	0	0	0	1	0
ADM	0	0	0	0	0	1	0
ADM2	0	0	0	0	0	1	0
ADORA1	1	0	0	0	0	1	0
ADORA2A	0	0	0	0	0	1	0
ADORA2B	0	0	0	0	0	1	1
ADORA3	0	0	0	0	0	1	1
ADPGK	1	0	0	0	0	0	0
ADRA1A	0	0	0	0	0	1	0
ADRA1B	0	0	0	0	0	1	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ADRA1D	1	0	0	0	0	1	0
ADRB1	0	0	0	0	0	1	0
ADRB2	1	0	0	0	0	1	0
ADRB3	0	0	0	0	0	1	0
ADSS	1	0	0	0	0	0	0
AEBP1	1	0	0	0	0	0	0
AFAP1	0	0	0	0	0	1	0
AFDN	0	0	0	0	0	1	0
AGBL4	0	0	0	1	1	0	0
AGER	0	0	0	0	0	1	0
AGOTC	0	0	0	0	0	0	1
AGPAT1	1	0	0	0	0	0	0
AGPAT3	1	0	0	0	0	0	0
AGR2	1	0	0	0	0	0	0
AGR3	1	0	0	0	0	0	0
AGT	0	0	0	0	0	1	1
AGTR1	0	0	0	0	0	1	1
AGXT	0	0	0	0	0	1	0
AHRR	1	0	0	0	0	0	0
AHSP	0	0	0	0	0	1	0
AIF1	1	0	0	0	0	0	0
AIRE	1	0	0	0	0	0	0
AK1	0	0	0	0	0	1	0
AKAP10	0	0	0	0	0	1	0
AKAP5	1	0	0	0	0	0	0
AKAP6	1	0	1	1	1	1	0
AKIRIN2	1	0	0	0	0	0	0
AKR1B1P6	0	0	0	0	1	0	0
AKT2	1	0	0	0	0	0	0
AL132671.2	0	0	0	0	0	1	0
ALB	0	0	0	0	0	1	0
ALDH1A3	0	0	0	0	0	0	1
ALDH2	1	0	0	0	0	1	0
ALDH3A1	1	0	0	0	0	0	0
ALDH6A1	1	0	0	0	0	0	0
ALDOA	1	0	0	0	0	0	0
ALG10	1	0	0	0	0	0	0
ALGS1	0	0	0	0	0	0	1
ALGS2	0	0	0	0	0	0	1
ALK	0	0	0	0	0	1	0
ALKAS	0	0	0	0	0	0	1
ALMS1	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ALOX15	1	0	0	0	0	0	0
ALPK1	0	0	0	1	1	0	0
ALS2CL	1	0	0	0	0	0	0
ALS5	0	0	0	0	0	0	1
ALX1	0	0	0	0	0	0	1
AMD1	0	0	0	0	0	1	0
AMER1	0	0	0	0	0	0	1
AMFR	1	0	0	0	0	0	0
AMH	0	0	0	0	0	1	0
ANAPC2	1	0	0	0	0	0	0
ANG	0	0	0	0	0	1	0
ANGPT4	1	0	0	0	0	0	0
ANK2	0	0	0	0	0	1	1
ANK3	0	0	0	0	0	1	0
ANKH	1	0	0	0	0	0	0
ANKHD1-EIF4EBP3	1	0	0	0	0	0	0
ANKK1	1	0	0	0	0	0	0
ANKRD1	1	0	0	0	0	0	1
ANKRD16	1	0	0	0	0	0	0
ANKRD26	0	0	0	0	1	0	0
ANKRD29	1	0	0	0	0	0	0
ANKRD31	0	0	0	0	1	0	0
ANKRD44	1	0	0	0	0	0	0
ANKRD50	1	0	0	0	0	0	0
ANKRD52	1	0	0	0	0	0	0
ANKRD6	0	0	0	0	0	1	0
ANKS1A	1	0	0	0	0	0	0
ANKS3	0	0	0	0	0	0	1
ANO5	1	0	0	0	0	0	0
ANP32E	1	0	0	0	0	0	0
ANPEP	0	0	0	0	0	1	0
ANXA13	1	0	0	0	0	0	0
ANXA2	1	0	0	0	0	0	0
ANXA4	1	1	1	0	1	1	0
ANXA5	1	0	0	0	0	1	0
ANXA6	0	0	0	0	0	1	0
ANXA7	1	0	0	0	0	1	0
ANXA9	0	0	0	0	0	1	0
AOC2	0	0	0	0	0	1	0
AOS1	0	0	0	0	0	0	1
AOS4	0	0	0	0	0	0	1
AOS5	0	0	0	0	0	0	1
AP1AR	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
AP3B1	1	0	0	0	0	0	0
APBB3	1	0	0	0	0	0	0
APC	1	0	0	0	0	0	0
APEX1	0	0	0	0	0	1	0
APH1A	1	0	0	0	0	0	0
APLN	0	0	0	0	0	1	0
APLNR	0	0	0	0	0	1	0
APOA1	0	0	0	0	0	1	0
APOB	0	0	0	0	1	1	0
APOBEC2	1	0	0	0	0	0	0
APOC1	0	0	0	0	1	1	0
APOC1P1	0	0	0	0	1	0	0
APOE	0	0	0	0	0	1	0
APOLD1	1	0	0	0	0	0	0
APP	1	0	0	0	0	1	0
APPL1	1	0	0	0	0	0	0
APUG	0	0	0	0	0	0	1
AQP2	0	0	0	0	0	0	1
AQP4	0	0	0	0	0	1	0
AQP5	1	0	0	0	0	0	0
ARCL2C	0	0	0	0	0	0	1
ARCL2D	0	0	0	0	0	0	1
ARCL3A	0	0	0	0	0	0	1
ARCS1	0	0	0	0	0	0	1
ARCS2	0	0	0	0	0	0	1
ARF1	1	0	0	0	0	0	0
ARF4	1	0	0	0	0	0	0
ARFIP1	1	0	0	0	0	0	0
ARHGAP10	1	0	1	1	1	1	0
ARHGAP12	1	0	0	0	0	0	0
ARHGAP19	1	0	0	0	0	0	0
ARHGAP22	0	0	0	0	0	1	0
ARHGAP24	1	0	0	0	0	0	0
ARHGAP26	1	0	0	0	1	0	0
ARHGAP31	0	0	0	0	0	0	1
ARHGEF2	1	0	0	0	0	0	0
ARL10	1	0	0	0	0	0	0
ARL5B	0	0	0	0	1	1	0
ARL6IP1	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ARL6IP5	1	0	0	0	0	0	0
ARMH3	0	0	0	0	0	1	0
ARNT2	1	0	0	1	1	1	0
ARNTL	1	0	0	0	0	0	0
ARNTL2	1	0	0	0	0	0	0
ARRB2	1	0	0	0	0	0	0
ARRDC1	1	0	0	0	0	0	0
ARRDC4	1	0	0	0	0	0	0
ARS	0	0	0	0	0	0	1
ARSA	0	0	0	0	0	1	0
ART3	1	0	0	0	0	0	0
ARVD1	0	0	0	0	0	0	1
ARVD8	0	0	0	0	0	0	1
AS3MT	1	0	0	0	0	0	0
ASAH1	1	0	1	1	1	1	0
ASAP1	1	0	0	0	0	0	0
ASB8	1	0	0	0	0	0	0
ASCL2	1	0	0	0	0	0	0
ASD1	0	0	0	0	0	0	1
ASD2	0	0	0	0	0	0	1
ASD3	0	0	0	0	0	0	1
ASD4	0	0	0	0	0	0	1
ASD5	0	0	0	0	0	0	1
ASD6	0	0	0	0	0	0	1
ASD7	0	0	0	0	0	0	1
ASD8	0	0	0	0	0	0	1
ASD9	0	0	0	0	0	0	1
ASGR1	0	0	0	0	0	1	0
ASGR2	1	0	0	0	0	0	0
ASH1L	1	0	0	0	0	0	0
ASPH	1	0	0	0	0	0	0
ASPRV1	1	1	1	0	0	0	0
ASTN2	0	0	0	0	0	1	0
ASXL2	1	0	0	0	0	0	0
ATAD2	1	0	0	0	0	0	0
ATE1	0	0	0	0	0	0	1
ATF3	0	0	0	0	0	1	0
ATF4	0	0	0	0	0	1	0
ATFB1	0	0	0	0	0	0	1
ATFB10	0	0	0	0	0	0	1
ATFB11	0	0	0	0	0	0	1
ATFB12	0	0	0	0	0	0	1
ATFB13	0	0	0	0	0	0	1
ATFB14	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ATFB15	0	0	0	0	0	0	1
ATFB18	0	0	0	0	0	0	1
ATFB2	0	0	0	0	0	0	1
ATFB3	0	0	0	0	0	0	1
ATFB4	0	0	0	0	0	0	1
ATFB5	0	0	0	0	0	0	1
ATFB6	0	0	0	0	0	0	1
ATFB7	0	0	0	0	0	0	1
ATFB8	0	0	0	0	0	0	1
ATFB9	0	0	0	0	0	0	1
ATG5	0	0	0	0	0	1	0
ATG9B	1	0	0	0	0	0	0
ATL3	1	0	0	0	0	0	0
ATM	0	0	0	0	0	1	0
ATP13A2	0	0	0	0	0	1	0
ATP13A5	1	0	0	0	0	0	0
ATP1A1	0	0	0	0	0	1	0
ATP1A2	0	0	0	0	0	1	0
ATP1A3	1	0	0	0	0	1	0
ATP1A4	0	0	0	0	0	1	0
ATP1B1	0	0	0	0	0	1	0
ATP1B2	1	0	0	0	0	1	0
ATP1B3	0	0	0	0	0	1	0
ATP1B4	0	0	0	0	0	1	0
ATP2A2	0	0	0	0	0	1	0
ATP2B1	1	0	0	0	1	1	0
ATP2B2	0	0	0	0	0	0	1
ATP4A	0	0	0	0	0	1	0
ATP4B	0	0	0	0	0	1	0
ATP6AP2	0	0	0	0	0	1	0
ATP6V0A1	1	0	0	0	0	0	0
ATP6V1F	1	0	0	0	0	0	0
ATP7A	0	0	0	0	0	1	0
ATP7B	0	0	0	0	0	1	0
ATRST1	0	0	0	0	0	0	1
ATRST2	0	0	0	0	0	0	1
ATXN1	1	0	1	1	1	1	0
ATXN3	1	0	0	0	0	0	0
AVSD	0	0	0	0	0	0	1
AVSD3	0	0	0	0	0	0	1
AVSD4	0	0	0	0	0	0	1
AVSD5	0	0	0	0	0	0	1
AXIN1	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
AZI2	1	0	0	0	0	0	0
B2M	0	0	0	0	0	1	0
B3GNT2	1	0	0	0	0	0	0
B3GNT8	1	0	0	0	0	0	0
B3GNT9	1	0	0	0	0	0	0
B3GNTL1	1	0	0	0	0	0	0
B9D2	1	0	0	0	0	0	0
BAK1	0	0	0	0	0	1	0
BAMBI	1	0	0	0	0	0	0
BANF1	0	0	0	0	0	1	0
BANK1	0	0	0	0	0	1	0
BARTS3	0	0	0	0	0	0	1
BARX2	1	0	0	0	0	0	0
BAX	0	0	0	0	0	1	0
BAZ1A	1	0	1	0	0	0	0
BAZ1B	0	0	0	0	1	0	0
BAZ2A	1	0	1	0	0	0	0
BBC3	1	0	0	0	0	0	0
BBIS	0	0	0	0	0	0	1
BBS2	0	0	0	0	0	0	1
BBS7	1	0	0	0	0	0	0
BBS9	1	0	0	0	0	0	0
BCAP29	1	0	1	0	0	0	0
BCAT1	1	0	0	0	0	0	0
BCC1	0	0	0	0	0	0	1
BCHE	1	0	0	0	0	1	0
BCL11A	1	0	0	0	0	0	0
BCL2	1	0	0	0	0	1	0
BCL2A1	0	0	0	0	0	1	0
BCL2L11	1	0	0	0	0	0	0
BCL2L2	1	0	0	0	0	0	0
BCL3	0	0	0	0	1	1	0
BCL9	1	0	0	0	0	0	0
BCO1	0	0	0	0	0	1	0
BCO2	1	0	0	0	0	0	0
BCOR	0	0	0	0	0	0	1
BDH2	1	0	0	0	0	0	0
BDNF	0	0	0	0	0	1	0
BEND7	1	0	0	0	0	0	0
BEST3	0	0	1	1	1	1	0
BGLAP	0	0	0	0	0	1	0
BHLHE41	1	0	0	0	0	0	0
BID	0	0	0	0	0	1	0
BLK	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
BLOC1S2	1	0	0	0	0	1	0
BMKS	0	0	0	0	0	0	1
BMP10	0	0	0	0	0	1	1
BMP2	0	0	0	1	0	1	1
BMP7	0	0	0	0	0	1	0
BMP8A	1	0	0	0	0	0	0
BMPR1B	1	0	0	0	0	0	0
BNC2	1	0	0	0	0	0	0
BNIP1	1	0	1	0	0	0	0
BOLA1	1	0	0	0	0	0	0
BOLL	1	0	0	0	0	0	0
BOPS	0	0	0	0	0	0	1
BOR1	0	0	0	0	0	0	1
BRAP	0	0	0	0	0	1	0
BRD1	0	0	0	0	0	1	0
BRD3	1	0	0	0	0	0	0
BRD8	1	0	1	0	0	0	0
BRD9	1	0	0	0	0	0	0
BRGDA1	0	0	0	0	0	0	1
BRGDA2	0	0	0	0	0	0	1
BRGDA3	0	0	0	0	0	0	1
BRGDA4	0	0	0	0	0	0	1
BRGDA5	0	0	0	0	0	0	1
BRGDA7	0	0	0	0	0	0	1
BRGDA8	0	0	0	0	0	0	1
BRINP3	0	0	0	0	0	1	0
BRMS1L	1	0	0	0	0	0	0
BRWD1	1	0	0	0	0	0	0
BRWS1	0	0	0	0	0	0	1
BSG	0	0	0	0	0	1	0
BSPRY	1	0	0	0	0	0	0
BSX	0	0	0	0	1	1	0
BTC	1	0	0	0	0	0	0
BTG1	1	0	0	0	0	0	0
BTK	0	0	0	0	0	1	0
BTRC	1	0	0	0	0	0	0
BVVLS1	0	0	0	0	0	0	1
BVVLS2	0	0	0	0	0	0	1
C10orf11	0	0	0	1	1	0	0
C10orf55	1	0	1	0	0	0	0
C10orf71	1	0	0	0	0	0	0
C10orf76	0	0	0	0	1	0	0
C10orf95	1	0	0	0	0	0	0
C11orf21	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
C11orf45	1	0	1	0	0	0	0
C11orf52	1	0	0	0	0	0	0
C12orf76	1	0	0	0	0	0	0
C17orf99	1	0	0	0	0	0	0
C19orf18	1	0	0	0	0	0	0
C19orf54	1	0	0	0	0	0	0
C1orf116	1	0	0	0	0	0	0
C1orf185	0	0	0	0	1	1	0
C1orf61	1	0	0	0	0	0	0
C1QTNF7	0	0	0	0	0	1	0
C2	1	0	0	0	0	0	0
C21orf2	1	0	0	0	0	0	0
C21orf62	1	0	0	0	0	0	0
C22orf15	1	0	0	0	0	0	0
C2CD4A	1	0	0	0	0	0	0
C2orf40	1	0	0	0	0	0	0
C2orf42	1	0	0	0	0	0	0
C2orf69	1	0	1	0	0	0	0
C2orf88	1	0	0	0	0	0	0
C3orf52	1	0	1	0	0	0	0
C4B	1	0	0	0	0	0	0
C4BPA	1	0	0	0	0	0	0
C5orf24	1	0	0	0	0	0	0
C5orf30	1	0	0	0	0	0	0
C5orf47	0	0	0	0	1	0	0
C6orf106	1	0	0	0	0	0	0
C6orf15	1	0	0	0	0	0	0
C6orf48	1	0	0	0	0	0	0
C7orf31	1	0	0	0	0	0	0
C7orf50	1	0	0	0	0	0	0
C7orf61	1	0	0	0	0	0	0
C8orf44	1	0	0	0	0	0	0
C9orf3	1	0	1	1	1	1	0
C9orf40	1	0	0	0	0	0	0
C9orf72	0	0	0	0	0	1	0
C9orf84	1	0	0	0	0	0	0
CA1	0	0	0	0	0	1	0
CA12	1	0	0	0	0	0	0
CA14	1	0	0	0	0	0	0
CAAP1	0	0	0	0	0	1	0
CAB39	1	0	0	0	0	0	0
CABIN1	0	0	0	0	0	1	0
CACNA1C	1	0	0	0	0	1	1
CACNA1	1	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
D							
CACNA1F	0	0	0	0	0	1	0
CACNA1S	0	0	0	0	0	1	0
CACNB1	1	0	0	0	0	0	0
CACNB2	0	0	0	0	0	1	0
CACNB3	1	0	0	0	0	0	0
CADM1	0	0	0	0	0	1	0
CAGE1	1	0	0	0	0	0	0
CAID	0	0	0	0	0	0	1
CALCR	0	0	0	0	0	1	0
CALD1	1	0	0	0	0	0	0
CALHM1	1	0	0	0	0	0	0
CALHM2	1	0	0	0	0	0	0
CALHM3	1	0	1	0	0	0	0
CALM1	0	0	0	0	0	0	1
CALM2	0	0	0	0	0	0	1
CALM2P1	0	0	0	0	1	0	0
CALN1	1	0	0	0	0	0	0
CALR	1	0	0	0	0	1	0
CALU	1	0	0	0	0	0	0
CAMK2A	1	0	0	0	0	0	0
CAMK2D	1	0	0	1	1	1	0
CAMK2G	1	0	1	0	0	0	0
CAND2	0	0	0	1	1	1	0
CAP2	0	0	0	0	0	1	0
CAPN12	1	0	0	0	0	0	0
CAPNS1	1	0	0	0	0	0	0
CAPRIN2	1	0	0	0	0	0	0
CAPZB	1	0	0	0	0	0	0
CARD9	1	0	0	0	0	0	0
CARF	0	0	0	0	0	1	0
CASC15	0	0	0	0	0	1	0
CASC20	0	0	0	1	1	0	0
CASKIN1	1	0	0	0	0	0	0
CASP3	0	0	0	0	0	1	0
CASP4	1	0	0	0	0	0	0
CASP8	0	0	0	0	0	1	0
CASP9	0	0	0	0	0	1	0
CASQ2	1	0	1	1	1	1	0
CASR	1	0	0	0	0	0	0
CAST	0	0	0	0	0	1	0
CASZ1	1	0	0	1	1	1	0
CAT	0	0	0	0	0	1	0
CAV1	1	1	1	1	1	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CAV2	1	1	1	0	1	1	0
CAV3	0	0	0	0	0	1	0
CAVIN1	0	0	0	0	0	0	1
CAVIN4	0	0	0	0	0	1	1
CBFA2T3	1	0	0	0	0	0	0
CBS	0	0	0	0	0	1	0
CBX5	0	0	0	0	0	1	0
CBY1	0	0	0	0	0	1	0
CCDC105	1	0	0	0	0	0	0
CCDC117	1	0	0	0	0	0	0
CCDC12	1	0	0	0	0	0	0
CCDC127	1	0	0	0	0	0	0
CCDC136	1	0	0	0	0	0	0
CCDC146	1	0	0	0	0	0	0
CCDC15	1	0	0	0	0	0	0
CCDC151	1	0	0	0	0	0	0
CCDC158	1	0	0	0	0	0	0
CCDC170	0	0	0	0	0	1	0
CCDC60	1	0	0	0	0	0	0
CCDC62	1	0	0	0	0	0	0
CCDC77	1	0	0	0	0	0	0
CCDC78	1	0	0	0	0	0	0
CCDC8	1	0	0	0	0	0	0
CCDC92	1	0	1	1	1	0	0
CCDD	0	0	0	0	0	0	1
CCHCR1	1	0	0	0	0	0	0
CCK	1	0	0	0	0	0	0
CCL1	1	0	0	0	0	0	0
CCL11	0	0	0	0	0	1	0
CCL16	0	0	0	0	0	1	0
CCL2	0	0	0	0	0	1	0
CCL21	0	0	0	0	0	1	0
CCL4	0	0	0	0	0	1	0
CCL5	0	0	0	0	0	1	0
CCMS	0	0	0	0	0	0	1
CCN1	0	0	0	0	0	1	0
CCN2	0	0	0	0	0	1	0
CCND1	1	0	0	0	0	0	0
CCR2	0	0	0	0	0	1	0
CCR4	1	0	0	0	0	0	0
CCRL2	1	0	0	0	0	0	0
CCS	1	0	0	0	0	1	0
CCT2	0	0	1	0	0	0	0
CD14	1	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CD163	0	0	0	0	0	1	0
CD180	1	0	0	0	0	0	0
CD19	1	0	0	0	0	0	0
CD274	0	0	0	0	0	1	0
CD28	0	0	0	0	0	1	0
CD34	1	0	0	0	0	1	0
CD36	1	0	0	0	0	1	0
CD3G	1	0	0	0	0	0	0
CD4	0	0	0	0	0	1	0
CD40	1	0	0	0	0	1	0
CD40LG	0	0	0	0	0	1	0
CD6	0	0	0	0	0	1	0
CD63	0	0	0	0	0	1	0
CD68	1	0	1	0	0	1	0
CD82	1	0	0	0	0	0	0
CD8A	1	0	0	0	0	0	0
CDA	1	0	0	0	0	0	0
CDC14B	1	0	1	0	0	0	0
CDC23	1	0	1	0	0	0	0
CDC25C	0	0	1	0	0	0	0
CDC27	1	0	0	0	0	0	0
CDC42BPA	1	0	0	0	0	0	0
CDC42BPB	1	0	0	0	0	0	0
CDC45	0	0	0	0	0	0	1
CDCA2	1	0	0	0	0	0	0
CDG1L	0	0	0	0	0	0	1
CDG2G	0	0	0	0	0	0	1
CDGF	0	0	0	0	0	0	1
CDH2	0	0	0	0	0	1	0
CDK12	1	0	0	0	0	0	0
CDK6	1	0	0	1	1	1	0
CDKAL1	1	0	0	0	0	0	0
CDKL2	1	0	0	0	0	0	0
CDKN1A	1	0	0	1	1	1	0
CDKN1B	1	0	0	0	0	0	0
CDKN2B	0	0	0	0	0	1	0
CDKN2B-AS1	0	0	0	0	1	1	0
CDKN2C	1	0	0	0	0	0	0
CDLS1	0	0	0	0	0	0	1
CDRT4	0	0	0	0	0	1	0
CDS1	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CEACAM5	0	0	0	0	0	1	0
CEBPA	1	0	0	0	0	0	0
CEBPB	1	0	0	0	0	0	0
CEBPZ	0	0	0	0	0	1	0
CECR1	0	0	0	0	0	0	1
CED2	0	0	0	0	0	0	1
CELA3B	0	0	0	0	1	0	0
CELSR2	0	0	0	0	1	1	0
CENPJ	0	0	0	0	0	1	0
CENPO	1	0	0	0	0	0	0
CENPV	1	0	0	0	0	0	0
CEP250	1	0	0	0	0	0	0
CEP41	0	0	0	0	0	0	1
CEP57	0	0	0	0	0	0	1
CEP68	0	1	1	1	1	1	0
CEP85L	0	0	0	0	1	1	0
CETP	0	0	0	0	1	1	0
CFB	1	0	0	0	0	0	0
CFC1	0	0	0	0	0	0	1
CFC2	0	0	0	0	0	0	1
CFI	0	0	0	0	0	1	0
CFL2	1	0	1	1	1	1	0
CFSMR	0	0	0	0	0	0	1
CFTD	0	0	0	0	0	0	1
CFZS	0	0	0	0	0	0	1
CGA	1	0	1	1	1	0	0
CGL4	0	0	0	0	0	0	1
CGN	1	0	0	0	0	0	0
CGNL1	0	0	0	0	1	1	0
CHAF1A	0	0	0	0	0	1	0
CHAPLE	0	0	0	0	0	0	1
CHCHD1	1	1	1	0	0	0	0
CHCHD10	1	0	0	0	0	0	0
CHD6	1	0	0	0	0	0	0
CHD7	0	0	0	0	0	0	1
CHDFIDD	0	0	0	0	0	0	1
CHDSKM	0	0	0	0	0	0	1
CHDTHP	0	0	0	0	0	0	1
CHEK1	1	0	0	0	0	0	0
CHEK2	0	0	0	0	0	1	0
CHGA	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CHGB	0	0	0	0	0	1	0
CHI3L1	1	0	0	0	0	1	0
CHID1	1	0	0	0	0	0	0
CHIT1	1	0	0	0	0	0	0
CHN1	0	0	0	0	0	0	1
CHN3	0	0	0	0	0	0	1
CHRNA1	1	0	0	0	0	0	0
CHRNB1	1	0	1	0	0	0	0
CHRNB2	1	0	0	0	0	0	0
CHRNB4	1	0	0	0	0	0	0
CHTD2	0	0	0	0	0	0	1
CHTD3	0	0	0	0	0	0	1
CHTD5	0	0	0	0	0	0	1
CHTD6	0	0	0	0	0	0	1
CIART	0	0	0	0	0	1	0
CIB1	0	0	0	0	0	1	0
CIC	1	0	0	0	0	0	0
CILD25	0	0	0	0	0	0	1
CILP	1	0	0	0	0	0	0
CISD2	0	0	1	0	0	0	0
CITED2	0	0	0	0	0	0	1
CKAP5	1	0	0	0	0	0	0
CLASP2	1	0	0	0	0	0	0
CLCN6	1	0	0	0	0	0	0
CLDN19	0	0	0	0	0	1	0
CLDN7	1	0	0	0	0	0	0
CLDND1	1	0	0	0	0	0	0
CLEC5A	1	0	0	0	0	0	0
CLIC1	1	0	0	0	0	0	0
CLIC2	0	0	0	0	0	1	0
CLIC6	1	0	0	0	0	1	0
CLIP1	0	0	0	0	0	1	0
CLIP2	1	0	0	0	0	0	0
CLK2	1	0	0	0	0	0	0
CLPX	1	0	0	0	0	0	0
CLSTN3	0	0	0	0	0	1	0
CLTB	1	0	0	0	0	0	0
CLU	0	0	0	0	0	1	0
CMA1	0	0	0	0	0	1	0
CMAS	1	0	0	0	0	0	0
CMBL	1	0	0	0	0	0	0
CMD1A	0	0	0	0	0	0	1
CMD1AA	0	0	0	0	0	0	1
CMD1D	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CMD1E	0	0	0	0	0	0	1
CMD1I	0	0	0	0	0	0	1
CMD1KK	0	0	0	0	0	0	1
CMD1P	0	0	0	0	0	0	1
CMD1R	0	0	0	0	0	0	1
CMD1S	0	0	0	0	0	0	1
CMD1Y	0	0	0	0	0	0	1
CMD2B	0	0	0	0	0	0	1
CMH1	0	0	0	0	0	0	1
CMH10	0	0	0	0	0	0	1
CMH11	0	0	0	0	0	0	1
CMH12	0	0	0	0	0	0	1
CMH13	0	0	0	0	0	0	1
CMH16	0	0	0	0	0	0	1
CMH18	0	0	0	0	0	0	1
CMH2	0	0	0	0	0	0	1
CMH20	0	0	0	0	0	0	1
CMH26	0	0	0	0	0	0	1
CMH4	0	0	0	0	0	0	1
CMH6	0	0	0	0	0	0	1
CMH7	0	0	0	0	0	0	1
CMH8	0	0	0	0	0	0	1
CMT2D	0	0	0	0	0	0	1
CMT2L	0	0	0	0	0	0	1
CMTM5	1	0	1	0	0	0	0
CNC1	0	0	0	0	0	0	1
CNC2	0	0	0	0	0	0	1
CNGA1	1	0	0	0	0	0	0
CNM2	0	0	0	0	0	0	1
CNNM2	1	0	0	0	0	0	0
CNR1	0	0	0	0	0	1	0
CNR2	1	0	0	0	0	1	0
CNTD1	1	0	0	0	0	0	0
CNTN5	0	0	0	0	1	1	0
COG5	1	0	0	0	1	1	0
COG8	1	0	0	0	0	0	0
COGIS	0	0	0	0	0	0	1
COL15A1	1	0	0	0	0	0	0
COL1A2	0	0	0	0	0	0	1
COL21A1	0	0	0	0	0	0	1
COL25A1	1	0	0	0	0	0	0
COL4A3BP	0	0	0	0	1	1	0
COMMD4	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
COMP	0	0	0	0	0	1	0
COPA	1	0	0	0	0	0	0
COPB1	1	0	0	0	0	0	0
COPS4	1	1	0	0	0	0	0
COQ10A	1	0	0	0	0	0	0
COQ10B	1	0	0	0	0	0	0
CORIN	1	0	0	0	0	1	1
CORO1A	1	0	0	0	0	0	0
COX15	1	0	0	0	0	0	0
COX7B	0	0	0	0	0	0	1
CP	0	0	0	0	0	1	0
CPB1	0	0	0	0	0	1	0
CPCMR	0	0	0	0	0	0	1
CPEB4	1	0	0	1	1	1	0
CPNE1	1	0	0	0	0	0	0
CPNE7	1	0	0	0	0	0	0
CPNE8	1	0	0	0	0	0	0
CPOX	1	0	0	0	0	1	0
CPSF3	1	0	0	0	0	0	0
CPVT1	0	0	0	0	0	0	1
CPVT3	0	0	0	0	0	0	1
CPVT4	0	0	0	0	0	0	1
CRADD	1	0	0	0	0	0	0
CRAMP1	0	0	0	1	0	0	0
CRAMP1L	0	0	0	0	1	0	0
CRAT	1	0	0	0	0	0	0
CREB1	1	0	0	0	0	0	0
CREB3L2	1	0	0	0	0	0	0
CREB3L4	1	0	0	0	0	0	0
CREB5	1	0	1	1	1	1	0
CRELD1	0	0	0	0	0	0	1
CREM	1	0	0	0	0	1	0
CRHR1	1	0	0	0	0	0	0
CRIM1	1	0	0	0	0	0	0
CRK	1	0	1	1	1	0	0
CRLS1	0	0	0	0	0	1	0
CRP	0	0	0	0	0	1	0
CRPT1	0	0	0	0	0	0	1
CRPT2	0	0	0	0	0	0	1
CRTAP	1	0	0	0	0	0	0
CRYGC	0	0	0	0	0	1	0
CS	1	0	0	0	0	0	0
CSF2	1	0	0	0	0	1	0
CSF3	1	1	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CSMD1	0	0	0	0	0	1	0
CSN1S1	0	0	0	0	0	1	0
CSNK1G2	1	0	0	0	0	0	0
CSNK1G3	0	0	0	0	0	1	0
CSNK2B	1	0	0	0	0	0	0
CSPG4	1	0	0	0	0	0	0
CSPG5	0	0	0	0	0	1	0
CSRP3	1	0	0	0	0	0	0
CSS1	0	0	0	0	0	0	1
CSS5	0	0	0	0	0	0	1
CSS6	0	0	0	0	0	0	1
CST3	0	0	0	0	0	1	0
CST7	1	0	0	0	0	0	0
CSTA	1	0	0	0	0	0	0
CSTLO	0	0	0	0	0	0	1
CTBP1	1	0	0	0	0	0	0
CTCF	0	0	0	0	0	0	1
CTDSPL	1	0	0	0	0	0	0
CTF1	0	0	0	0	0	1	0
CTHM	0	0	0	0	0	0	1
CTNNA2	1	0	0	0	0	0	0
CTNNAL1	1	0	0	0	0	0	0
CTSA	0	0	0	0	0	1	0
CTSB	1	0	0	0	0	0	0
CTSF	1	0	0	0	0	0	0
CTSK	1	0	0	0	0	1	0
CTSL	0	0	0	0	0	0	1
CTSV	0	0	0	0	0	1	0
CTSZ	0	0	0	0	0	1	0
CTTN	1	0	0	0	0	0	0
CUEDC2	1	0	0	0	0	0	0
CUL4A	1	0	0	1	1	0	0
CUTC	1	0	0	0	0	0	0
CUX2	0	0	0	0	1	1	0
CVDD	0	0	0	0	0	0	1
CWF19L1	1	0	0	0	0	0	0
CWS1	0	0	0	0	0	0	1
CX3CL1	0	0	0	0	0	1	0
CX3CR1	1	0	0	0	0	0	0
CXCL10	0	0	0	0	0	1	0
CXCL12	0	0	0	0	0	1	0
CXCL8	0	0	0	0	0	1	0
CXCR4	0	0	0	0	0	1	0
CYB5A	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
CYB5R1	1	0	0	0	0	0	0
CYB5R3	1	0	0	0	0	0	0
CYBB	0	0	0	0	0	1	0
CYBRD1	0	0	0	0	0	1	0
CYCS	0	0	0	0	0	1	0
CYP11A1	0	0	0	0	0	0	1
CYP11B1	0	0	0	0	0	0	1
CYP11B2	0	0	0	0	0	1	0
CYP17A1	1	0	0	0	0	0	1
CYP1A1	0	0	0	0	0	1	0
CYP1A2	0	0	0	0	0	1	0
CYP20A1	0	0	0	0	0	1	0
CYP21A2	1	0	0	0	1	1	1
CYP26B1	1	0	0	0	0	0	0
CYP2C19	0	0	0	0	0	1	0
CYP2C9	0	0	0	0	0	1	0
CYP2D6	0	0	0	0	0	1	0
CYP2J2	0	0	0	0	0	1	0
CYP39A1	1	0	0	0	0	0	0
CYP3A4	0	0	0	0	0	1	0
CYP3A5	0	0	0	0	0	1	0
CYP4F2	0	0	0	0	0	1	0
CYTH1	0	0	0	1	1	0	0
DA9	0	0	0	0	0	0	1
DAP3	1	0	0	0	0	0	0
DAPK2	1	0	0	0	0	0	0
DBA1	0	0	0	0	0	0	1
DBA16	0	0	0	0	0	0	1
DBA4	0	0	0	0	0	0	1
DBA6	0	0	0	0	0	0	1
DBA7	0	0	0	0	0	0	1
DBN1	0	0	0	0	0	1	0
DBT	0	0	0	0	0	1	0
DCAF12	1	0	0	0	0	0	0
DCAF4	1	0	1	0	0	0	0
DCAF5	1	0	0	0	0	0	0
DCAF8	1	0	0	0	0	0	0
DCAKD	1	0	0	0	0	0	0
DCBLD1	1	0	0	0	1	1	0
DCC	0	0	0	0	0	1	0
DCK	1	0	0	0	0	0	0
DCN	0	0	0	0	0	1	0
DCST1	1	1	1	0	0	0	0
DCST2	1	1	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
DCT	0	0	0	0	0	1	0
DCTN2	0	0	0	0	0	1	0
DCUN1D2	1	0	0	0	0	0	0
DDAH2	1	0	0	0	0	0	0
DDOST	1	0	0	0	0	0	0
DDR2	0	0	0	0	0	1	0
DDRGK1	0	0	0	0	0	1	0
DDT	0	0	0	0	0	1	0
DDX25	1	0	0	0	0	0	0
DDX39AP1	0	0	0	0	1	0	0
DDX54	1	0	0	0	0	0	0
DDX59	1	0	0	0	0	0	0
DEDD2	1	0	0	0	0	0	0
DEFB129	1	0	0	0	0	0	0
DEFB132	1	0	0	0	0	0	0
DEK	0	0	1	0	0	0	0
DENND4A	1	0	0	0	0	0	0
DENR	1	0	0	0	0	0	0
DERL3	1	0	0	0	0	0	0
DES	0	0	0	0	0	1	0
DFFA	0	0	0	0	0	1	0
DGKB	1	0	0	1	1	1	0
DGKZ	0	0	0	0	0	1	0
DGS	0	0	0	0	0	0	1
DHPS	1	0	0	0	0	0	0
DHRS1	1	0	0	0	0	0	0
DHRS9	0	0	0	0	0	1	0
DHX35	1	0	0	0	0	0	0
DHX36	0	0	0	0	0	1	0
DIAR10	0	0	0	0	0	0	1
DICER1	0	0	0	0	0	1	1
DIH2	0	0	0	0	0	0	1
DIRAS2	1	0	0	0	0	0	0
DIRAS3	0	0	0	0	0	1	0
DIS3L2	1	0	0	0	0	0	0
DKKL1	0	0	0	0	0	1	0
DLC1	1	0	0	0	0	0	0
DLEC1	1	0	0	0	0	0	0
DLG1	0	0	0	0	0	1	0
DLG5	0	0	0	0	0	1	0
DLK2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
DLL1	0	0	0	0	0	1	0
DLX1	1	0	0	0	0	0	0
DLX5	1	0	0	0	0	0	0
DLX6	1	0	0	0	0	0	0
DM1	0	0	0	0	0	0	1
DMC1	1	0	0	0	0	0	0
DMD	0	0	0	0	0	1	0
DMPK	1	0	0	0	0	1	0
DMRT3	1	0	0	0	0	0	0
DMRTA1	0	0	0	0	1	0	0
DMWD	1	0	0	0	0	0	0
DNAH10	0	0	0	0	1	0	0
DNAH11	0	0	0	0	0	1	0
DNAH12	1	0	0	0	0	0	0
DNAH2	1	0	0	0	1	1	0
DNAJA4	1	0	0	0	0	0	0
DNAJB2	1	0	0	0	0	0	0
DNAJB6	0	0	0	0	0	1	0
DNAJC1	1	0	0	0	0	0	0
DNAJC12	1	0	0	0	0	0	0
DNAJC5	0	0	0	0	0	1	0
DNAJC5B	0	0	0	0	0	1	0
DNAJC9	1	0	0	0	0	0	0
DNAL4	1	0	0	0	0	0	0
DNASE1L2	1	0	0	0	0	0	0
DND1	1	0	0	0	0	0	0
DNER	0	0	0	0	0	1	0
DNM3	1	0	0	0	0	0	0
DNMT3A	1	0	0	0	0	0	0
DNMT3B	1	0	0	0	0	0	0
DOCK11	0	0	0	0	0	1	0
DOCK7	1	0	0	0	0	0	0
DOCK9	1	0	0	0	0	0	0
DOK2	1	0	1	0	0	0	0
DPF3	1	0	1	1	1	1	0
DPP4	0	0	0	0	0	1	0
DPP6	0	0	0	0	0	0	1
DPT	0	0	0	0	0	1	0
DPYS	0	0	0	0	0	1	0
DPYSL4	0	0	0	0	0	1	0
DRRS	0	0	0	0	0	0	1
DSC1	1	0	0	0	0	0	0
DSC2	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
DSC3	1	0	0	0	0	0	0
DSE	0	0	0	0	0	1	0
DSG3	0	0	0	0	0	1	0
DSMA5	0	0	0	0	0	0	1
DST	1	0	0	0	0	1	0
DSTYK	1	0	0	0	0	0	0
DTGA1	0	0	0	0	0	0	1
DTNA	1	0	0	0	0	0	0
DTNB	1	0	0	0	0	0	0
DUS4L	1	0	1	0	0	0	0
DUSP11	1	0	0	0	0	0	0
DUSP13	1	0	0	0	0	0	0
DYSF	1	0	0	0	0	0	0
E4F1	1	0	0	0	1	0	0
EBF1	1	0	0	0	0	0	1
EBPL	1	0	0	0	0	0	0
ECCL	0	0	0	0	0	0	1
ECE1	1	0	0	0	0	0	0
ECE2	1	0	0	0	0	0	0
ECSIT	1	0	0	0	0	0	0
ECT2	1	0	0	0	0	0	0
EDMD1	0	0	0	0	0	0	1
EDMD2	0	0	0	0	0	0	1
EDMD3	0	0	0	0	0	0	1
EDMD7	0	0	0	0	0	0	1
EDN1	0	0	0	0	0	1	0
EDN2	0	0	0	0	0	1	0
EDNRA	0	0	0	0	0	1	0
EDSCV	0	0	0	0	0	0	1
EDSMC1	0	0	0	0	0	0	1
EEF1A1	1	0	0	0	0	0	0
EEF2	0	0	0	0	0	1	0
EEFSEC	1	0	0	0	0	0	0
EFCAB2	1	0	0	0	0	0	0
EFHC1	1	0	0	0	0	0	0
EFNA1	1	0	0	0	0	0	0
EFNA3	1	0	1	0	0	0	0
EFNA4	1	0	1	0	0	0	0
EFNA5	1	0	0	0	0	1	0
EFNB3	1	0	0	0	0	0	0
EFR3B	1	0	0	0	0	0	0
EFS	0	0	1	0	0	0	0
EFTUD2	1	0	0	0	0	0	0
EGR1	1	0	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
EGR3	1	0	0	0	0	0	0
EHD4	1	0	0	0	0	0	0
EHF	0	0	0	0	0	1	0
EHMT2	1	0	0	0	0	0	0
EIF1B	1	0	0	0	0	0	0
EIF2AK2	1	0	0	0	0	0	0
EIF3A	1	0	0	0	0	0	0
EIF4A1	1	0	1	0	0	0	0
EIF5A	1	0	0	0	0	0	0
ELAC1	1	0	0	0	0	0	0
ELAVL3	1	0	0	0	0	0	0
ELN	1	0	0	0	0	1	0
ELOVL3	1	0	1	0	1	1	0
EMB	0	0	0	0	0	1	0
EMD	0	0	0	0	0	1	1
EMP1	0	0	0	0	0	1	0
EMP2	1	0	0	0	0	0	0
ENG	1	0	0	0	0	1	0
ENHO	0	0	0	0	0	1	0
ENO2	0	0	0	0	0	1	0
ENO3	0	0	0	0	0	1	0
ENPEP	1	1	1	0	1	1	0
ENPP2	1	0	0	0	0	0	0
ENTPD5	1	0	0	0	0	0	0
EOGT	0	0	0	0	0	0	1
EPAS1	0	0	0	1	0	0	0
EPHA3	1	0	1	1	1	1	0
EPHB2	0	0	0	0	0	1	0
EPHB4	0	0	0	0	0	0	1
EPHX2	0	0	0	0	0	1	0
EPM2A	1	0	0	0	0	0	0
EPO	1	0	0	0	0	1	0
EPS15	1	0	1	0	0	0	0
ERAP2	1	0	0	0	0	0	0
ERAS	0	0	0	0	0	1	0
ERBB2	0	0	1	0	0	1	0
ERBB4	1	0	0	1	1	1	0
ERC2	1	0	0	0	0	0	0
ERCC4	1	0	0	0	0	0	0
ERCC6	0	0	0	0	0	1	0
ERCC8	0	0	0	0	0	1	0
ERF	1	0	0	0	0	0	0
ERGIC1	1	0	0	0	0	0	0
ERI2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ERLIN2	1	0	0	0	0	0	0
ERP44	1	0	0	0	0	0	0
ESD	0	0	0	0	0	1	0
ESPN	1	0	0	0	0	0	0
ESPNL	1	0	1	0	0	0	0
ESR1	0	0	0	0	0	1	0
ESR2	1	1	1	0	0	1	0
ESRRG	0	0	0	0	0	1	0
ETAA1	1	0	0	0	0	0	0
ETV3	0	0	0	0	0	1	0
ETV3L	1	0	0	0	0	0	0
EVC	0	0	0	0	0	0	1
EVC	0	0	0	0	0	0	1
EVC2	1	0	0	0	0	0	1
EVPLS	0	0	0	0	0	0	1
EVX1	1	0	0	0	0	0	0
EXD2	1	0	0	0	0	0	0
EXOSC3	0	0	0	0	0	1	0
EXT1	0	0	0	1	0	0	0
EYA4	1	0	0	0	1	1	0
EZH2	1	0	0	0	0	0	0
F10	1	0	0	0	0	1	0
F11	0	0	0	0	0	1	0
F11R	0	0	0	0	0	1	0
F2	0	0	0	0	0	1	0
F2R	0	0	0	0	0	1	0
F3	0	0	0	0	0	1	0
F8	0	0	0	0	0	1	0
FABP3	0	0	0	0	0	1	0
FABP4	1	0	0	0	0	0	0
FABP7	1	0	0	0	0	0	0
FADS1	0	0	0	0	1	1	0
FADS2	0	0	0	0	0	1	0
FAF1	1	0	0	0	1	1	0
FAHD1	1	0	0	0	0	0	0
FAM110A	1	0	0	0	0	0	0
FAM114A1	1	0	0	0	0	0	0
FAM129A	1	0	0	0	0	0	0
FAM129B	0	0	0	0	0	1	0
FAM131A	1	0	0	0	0	0	0
FAM136A	1	0	0	0	0	0	0
FAM13B	1	1	1	0	1	1	0
FAM149B	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
1							
FAM160B1	1	0	0	0	0	0	0
FAM160B2	1	0	0	0	0	0	0
FAM162A	1	0	0	0	0	0	0
FAM173A	1	0	0	0	0	0	0
FAM173B	1	0	0	0	0	0	0
FAM186B	1	0	0	0	0	0	0
FAM187B	1	0	0	0	0	0	0
FAM189B	1	0	0	0	0	0	0
FAM43A	1	0	0	0	0	0	0
FAM47E	1	0	0	0	0	0	0
FAM49B	1	0	0	0	0	0	0
FAM53C	1	0	1	0	0	0	0
FAM83A	1	0	0	0	0	0	0
FAM83C	1	0	0	0	0	0	0
FAM89B	1	0	0	0	0	0	0
FANCC	1	0	1	0	0	1	0
FANCE	1	0	0	0	0	0	0
FANCI	0	0	0	0	0	0	1
FANCN	0	0	0	0	0	0	1
FARS2	1	0	0	0	0	0	0
FASLG	0	0	0	0	0	1	0
FBLN1	0	0	0	0	0	1	0
FBN1	0	0	0	0	0	1	0
FBN2	1	0	0	0	0	0	1
FBP1	1	0	0	0	0	0	0
FBP2	1	0	0	0	0	0	0
FBRSL1	1	0	0	1	1	0	0
FBXL16	1	0	0	0	0	0	0
FBXL2	1	0	0	0	0	0	0
FBXL20	1	0	0	0	0	0	0
FBXL22	1	0	0	0	0	0	0
FBXO11	1	0	0	0	0	0	0
FBXO16	1	0	0	0	0	0	0
FBXO30	1	0	0	0	0	0	0
FBXO32	1	1	1	1	1	1	0
FBXO9	1	0	0	0	0	0	0
FBXW11	0	0	0	0	0	1	0
FBXW4	1	0	1	0	0	0	0
FCAMR	1	0	0	0	0	0	0
FCGR1A	1	0	0	0	0	0	0
FCRLB	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
FDFT1	1	0	0	0	0	0	0
FDPS	1	0	0	0	0	0	0
FER	1	0	0	0	0	0	0
FER1L4	0	0	0	0	0	1	0
FERD3L	0	0	0	0	1	1	0
FES	1	0	0	0	0	0	0
FEV	0	0	0	0	0	1	0
FGD5	1	0	0	0	0	0	0
FGF11	1	0	1	0	0	0	0
FGF16	0	0	0	0	0	1	0
FGF17	1	0	0	0	0	0	0
FGF18	1	0	0	0	0	0	0
FGF2	0	0	0	0	0	1	0
FGF21	0	0	0	0	0	1	0
FGF23	0	0	0	0	0	1	0
FGF3	1	0	0	0	0	0	0
FGF4	1	0	0	0	0	0	0
FGF5	1	0	0	1	1	1	0
FGF7	1	0	0	0	0	0	0
FGF8	1	0	0	0	0	0	0
FGF9	1	0	0	0	0	0	0
FGFR4	0	0	0	0	0	1	0
FGFRL1	1	0	0	0	0	0	0
FGL1	1	0	1	0	0	0	0
FHL1	0	0	0	0	0	1	1
FHL2	1	0	0	0	0	0	0
FIG4	1	0	0	0	0	0	0
FIGN	1	0	0	0	0	0	0
FILIP1	1	0	0	1	0	0	0
FITM2	1	0	0	0	0	0	0
FKBP1B	0	0	0	0	0	1	0
FKBP7	1	0	1	0	0	0	0
FKBP9	1	0	0	0	0	0	0
FKBPL	1	0	0	0	0	0	0
FLAD1	1	1	1	0	0	0	0
FLHS	0	0	0	0	0	0	1
FLI1	1	0	0	0	0	0	0
FLNA	0	0	0	0	0	0	1
FLNB	1	0	0	0	0	0	0
FLNC	1	0	0	0	0	0	1
FLOT2	0	0	0	0	0	1	0
FLPIS	0	0	0	0	0	0	1
FLT1	1	0	0	0	0	0	0
FN1	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
FN3KRP	1	0	0	0	0	0	0
FND1	0	0	0	0	0	0	1
FNDC3B	1	0	0	0	0	0	0
FOXA3	1	0	0	0	0	0	0
FOXC1	1	0	0	0	0	0	1
FOXE1	1	0	0	0	0	1	0
FOXF2	0	0	0	0	0	1	0
FOXO3	0	0	0	0	0	1	0
FOXP4	1	0	0	0	0	0	0
FPGS	1	0	0	0	0	0	0
FPS	0	0	0	0	0	0	1
FRAT1	1	0	0	0	0	0	0
FRAT2	1	0	0	0	0	0	0
FRMD4A	1	0	0	0	0	0	0
FRMD4B	0	0	0	1	1	0	0
FRMD6	1	0	0	0	0	0	0
FRMD8	1	0	0	0	0	0	0
FRNS	0	0	0	0	0	0	1
FRS2	1	0	1	0	0	0	0
FSHD1	0	0	0	0	0	0	1
FTDALS3	0	0	0	0	0	0	1
FTDALS4	0	0	0	0	0	0	1
FTO	1	0	0	0	1	1	0
FUCA1	1	0	0	0	0	0	0
FURIN	1	0	0	0	0	0	0
FUT8	1	0	0	0	0	0	0
FXN	1	0	0	0	0	0	0
FXR2	1	0	1	0	0	0	0
FXYD2	0	0	0	0	0	1	0
FXYD4	1	0	0	0	0	0	0
FXYD5	1	0	0	0	0	0	0
FZD2	0	0	0	0	0	0	1
G3BP2	1	0	0	0	0	0	0
G6PC3	0	0	0	0	0	0	1
GAB2	1	0	0	0	0	0	0
GABPA	1	0	0	0	0	0	0
GABPB1	1	0	0	0	0	0	0
GABRA5	1	0	0	0	0	0	0
GABRA6	1	0	0	0	0	0	0
GABRG3	1	0	0	0	0	0	0
GADD45GIP1	1	0	0	0	0	0	0
GAL	0	0	0	0	0	1	0
GALE	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
GALK2	1	0	0	0	0	0	0
GALNT12	1	0	0	0	0	0	0
GAP43	0	0	0	0	0	1	0
GAPDH	0	0	0	0	0	1	0
GATA4	1	0	0	1	0	1	1
GATA5	1	0	0	0	0	1	1
GATA6	0	0	0	0	0	1	1
GBA	1	0	0	0	0	0	0
GBBB2	0	0	0	0	0	0	1
GBF1	1	0	1	0	0	0	0
GCAT	1	0	0	0	0	0	0
GCKR	0	0	0	0	1	1	0
GCLC	1	0	0	0	0	0	0
GCOM1	0	0	0	1	1	0	0
GCSH	0	0	0	0	0	1	0
GDF1	0	0	0	0	0	0	1
GDF15	0	0	0	0	0	1	0
GDF5	1	0	0	0	0	0	0
GDF6	1	0	0	0	0	0	1
GDI2	1	0	0	0	0	0	0
GDPD3	1	0	0	0	0	0	0
GET4	0	0	0	0	0	1	0
GFAP	1	0	0	0	0	0	0
GFER	1	0	0	0	0	0	0
GFRA3	1	0	1	0	0	0	0
GGCX	0	0	0	0	0	1	0
GHR	1	0	0	0	0	1	0
GIGYF1	1	0	0	0	0	0	0
GIGYF2	1	0	0	0	0	0	0
GIMAP1	1	0	0	0	0	0	0
GIMAP2	1	0	0	0	0	0	0
GIMAP6	1	0	0	0	0	0	0
GIMAP7	1	0	0	0	0	0	0
GIPC1	1	0	0	0	0	0	0
GIPR	1	0	0	0	0	0	0
GIT2	1	0	0	0	0	0	0
GJA1	1	0	0	0	0	1	0
GJA4	0	0	0	0	0	1	0
GJA5	1	0	1	1	1	1	1
GJB7	0	0	1	0	0	0	0
GJC1	0	0	0	0	0	1	0
GJC2	1	0	0	0	0	0	0
GJC3	0	0	0	0	0	1	0
GJD2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
GJD3	0	0	0	0	0	0	1
GLA	0	0	0	0	0	0	1
GLB1	1	0	0	0	0	1	0
GLB1L3	1	0	0	0	0	0	0
GLC1A	0	0	0	0	0	0	1
GLCE	1	0	0	0	0	0	0
GLP1R	0	0	0	0	0	1	0
GLTSCR1	0	0	0	1	0	0	0
GLUL	1	0	0	0	0	0	0
GMCL1	0	1	1	1	1	1	0
GMPR	1	0	0	0	0	0	0
GNA12	1	0	0	0	0	0	1
GNA13	0	0	0	0	0	0	1
GNAO1	0	0	0	0	0	0	1
GNAS	1	0	0	0	0	0	0
GNB1	1	0	0	0	0	0	0
GNB2	1	0	0	0	0	0	0
GNB3	0	0	0	0	0	1	0
GNB4	1	0	0	1	1	1	0
GNPNAT1	1	0	0	0	0	0	0
GOLT1A	1	0	0	0	0	0	0
GON4L	1	0	0	0	0	0	0
GOPC	1	0	0	0	0	0	0
GORAB	0	0	1	0	1	0	0
GOSR2	0	0	0	0	1	1	0
GOT2	0	0	0	0	0	1	0
GP6	0	0	0	0	0	1	0
GPD1L	0	0	0	0	0	1	0
GPD2	0	0	0	0	0	1	0
GPI	0	0	0	0	0	1	0
GPR14	0	0	0	0	0	0	1
GPR15	1	0	0	0	0	0	0
GPR153	1	0	0	0	0	0	0
GPR155	1	0	1	0	0	0	0
GPR180	0	0	0	0	0	1	0
GPR19	1	0	0	0	0	0	0
GPR21	1	0	0	0	0	0	0
GPR22	0	0	0	0	0	1	0
GPR27	1	0	0	0	0	0	0
GPR65	0	0	0	0	0	1	0
GPRC5C	1	0	0	0	0	0	0
GPSM1	1	0	0	0	0	0	0
GPX3	0	0	0	0	0	1	0
GPX4	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
GRASP	1	0	0	0	0	0	0
GREM1	1	0	0	0	0	0	0
GREM2	0	0	0	0	0	1	0
GRHL1	0	0	0	0	1	1	0
GRHL3	1	0	0	0	0	0	0
GRIK5	1	0	0	0	0	0	0
GRIN1	1	0	0	0	0	0	0
GRIN2D	1	0	0	0	0	0	0
GRINA	1	0	0	0	0	0	0
GRK5	1	0	0	0	0	1	0
GRM1	1	0	0	0	0	0	0
GSD0B	0	0	0	0	0	0	1
GSD15	0	0	0	0	0	0	1
GSD3	0	0	0	0	0	0	1
GSDMC	1	0	0	0	0	0	0
GSK3A	1	0	0	0	0	0	0
GSN	0	0	0	0	0	1	0
GSTA1	0	0	0	0	0	1	0
GTF2I	1	0	1	1	1	1	0
GTF2IRD1	1	0	0	0	0	0	0
GTF2IRD2	1	0	0	0	0	0	0
GTPTS	0	0	0	0	0	0	1
GUCA2B	0	0	0	0	0	0	1
GUCY2C	1	0	0	0	0	0	0
GUCY2EP	0	0	0	0	0	0	1
GUK1	1	0	0	0	0	0	0
GUSB	0	0	0	0	0	1	0
GYG1	1	0	0	0	0	0	0
GYPB	1	0	0	0	0	0	0
GYPC	1	0	0	1	1	1	0
GZF1	1	0	0	0	0	0	0
H19	0	0	0	0	0	1	0
H1F0	1	0	0	0	0	0	0
H1FNT	1	0	0	0	0	0	0
H1FOO	1	0	0	0	0	0	0
H3F3AP4	0	0	0	0	1	0	0
HABP2	1	0	0	0	0	1	0
HABP4	1	0	0	0	0	0	0
HADH	1	0	0	0	0	0	0
HAGH	1	0	0	0	0	0	0
HAGHL	1	0	0	0	0	0	0
HAMP	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
HAND1	0	0	0	0	0	0	1
HAND2	1	0	1	1	1	1	1
HAND2AS1	0	0	0	0	0	0	1
HAND2-AS1	0	0	0	1	0	0	0
HARS	1	0	0	0	0	0	0
HARS2	1	0	0	0	0	0	0
HBEGF	1	0	0	1	1	1	0
HBM	1	0	0	0	0	0	0
HBP1	1	0	0	1	0	0	0
HBQ1	1	0	0	0	0	0	0
HCAD	0	0	0	0	0	0	1
HCFC2	1	0	0	0	0	0	0
HCG9	0	0	0	0	0	1	0
HCN2	0	0	0	0	0	1	0
HCN3	1	0	0	0	0	1	0
HCN4	1	1	1	1	1	1	1
HDAC10	1	0	0	0	0	0	0
HDAC3	1	0	0	0	0	0	0
HDAC4	1	0	0	0	0	0	0
HDAC6	0	0	0	0	0	1	0
HDAC7	1	0	0	0	0	0	0
HDAC8	0	0	0	0	0	0	1
HDAC9	0	0	0	0	0	1	0
HDCA	0	0	0	0	0	0	1
HDGFL1	1	0	0	0	0	0	0
HDHD3	1	0	0	0	0	0	0
HEG1	0	0	0	0	0	0	1
HERC1	1	0	0	1	1	0	0
HERC4	1	0	0	0	0	0	0
HERPUD1	0	0	0	0	1	0	0
HES4	1	0	0	0	0	0	0
HES6	1	0	0	0	0	0	0
HEXIM1	1	0	0	0	0	0	0
HEXIM2	1	0	0	0	0	0	0
HEY2	1	0	0	0	0	0	1
HEYL	1	0	0	0	0	0	0
HFASD	0	0	0	0	0	0	1
HFE2A	0	0	0	0	0	0	1
HFM	0	0	0	0	0	0	1
HGF	0	0	0	0	0	1	0
HHLA2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
HIBADH	1	0	0	0	0	0	0
HIF3A	1	0	0	0	0	0	0
HIGD1B	1	0	0	0	0	0	0
HIGD2A	1	0	0	0	0	0	0
HIP1	1	0	0	0	0	0	0
HIP1R	1	0	0	1	1	1	0
HIRIP3	1	0	0	0	0	0	0
HIST1H1D	1	0	0	0	0	0	0
HIST1H1E	1	0	0	0	0	0	0
HIST1H2AE	1	0	0	0	0	0	0
HIST1H2BD	1	0	0	0	0	0	0
HIST1H2BF	1	0	0	0	0	0	0
HIST1H2BI	1	0	0	0	0	0	0
HIST1H3D	1	0	0	0	0	0	0
HIST1H3E	1	0	0	0	0	0	0
HIST1H3G	1	0	0	0	0	0	0
HIST1H4D	1	0	0	0	0	0	0
HIST1H4E	1	0	0	0	0	0	0
HIST1H4F	1	0	0	0	0	0	0
HIST1H4G	1	0	0	0	0	0	0
HIST1H4H	1	0	0	0	0	0	0
HIST2H2AB	1	0	0	0	0	0	0
HIST2H2BE	1	0	0	0	0	0	0
HIST2H2BF	1	0	0	0	0	0	0
HJCYS	0	0	0	0	0	0	1
HJV	0	0	0	0	0	0	1
HK3	1	0	0	0	0	0	0
HKLLS1	0	0	0	0	0	0	1
HLA-B	0	0	0	1	0	1	0
HLA-DQA2	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
HLA-DQB1	0	0	0	0	0	1	0
HLA-DRB1	0	0	0	0	0	1	0
HLHS1	0	0	0	0	0	0	1
HLHS2	0	0	0	0	0	0	1
HLTF	1	0	0	0	0	0	0
HMBS	1	0	0	0	0	1	0
HMGA1	1	0	0	0	0	0	0
HMGA2	0	0	0	0	0	1	0
HMGB1	0	0	0	0	0	1	0
HMGCL	1	0	0	0	0	0	0
HMGCR	0	0	0	0	1	1	0
HMGCS1	1	0	0	0	0	0	0
HMMS	0	0	0	0	0	0	1
HMN2D	0	0	0	0	0	0	1
HMOX1	0	0	0	0	0	1	0
HMSNO	0	0	0	0	0	0	1
HNF4G	1	0	0	0	0	0	0
HNRNPA0	1	1	1	0	0	0	0
HNRNPF	1	0	0	0	0	0	0
HNRNPR	1	0	0	0	0	0	0
HOMER2	1	0	0	0	0	0	0
HOPX	0	0	0	0	0	1	0
HOS	0	0	0	0	0	0	1
HOXA10	1	0	0	0	0	0	0
HOXA13	1	0	0	0	0	0	0
HOXA9	1	0	0	0	0	0	0
HOXD1	1	0	0	0	0	0	0
HOXD11	1	0	0	0	0	0	0
HOXD8	1	0	0	0	0	0	0
HOXD9	1	0	0	0	0	0	0
HPCAL4	1	0	0	0	0	0	0
HPGDS	1	0	0	0	0	1	0
HPMRS1	0	0	0	0	0	0	1
HPMRS2	0	0	0	0	0	0	1
HPMRS3	0	0	0	0	0	0	1
HPN	0	0	0	0	0	1	0
HPR	0	0	0	0	0	1	0
HPRT1	0	0	0	0	0	1	0
HPS3	1	0	0	0	0	0	0
HPS6	1	0	0	0	0	0	0
HRAS	0	0	0	0	0	0	1
HRASLS	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
HRASLS2	1	0	0	0	0	0	0
HRH1	0	0	0	0	0	1	0
HRH2	0	0	0	0	0	1	0
HRH3	1	0	0	0	0	0	0
HSD11B2	0	0	0	0	0	1	0
HSD17B14	1	0	0	0	0	0	0
HSD17B3	1	0	0	0	0	0	0
HSD17B6	1	0	1	0	0	1	0
HSD17B7	0	0	0	0	0	0	1
HSF1	0	0	0	0	0	1	0
HSF2	1	0	1	1	0	1	0
HSF4	1	0	0	0	0	0	0
HSP90B1	1	0	0	0	0	1	0
HSPA13	1	0	0	0	0	0	0
HSPA14	0	0	0	0	0	1	0
HSPA1A	1	0	0	0	0	0	0
HSPA1L	1	0	0	0	0	0	0
HSPA5	1	0	0	0	0	0	0
HSPA9	0	0	0	0	0	1	0
HSPB1	0	0	0	0	0	1	0
HSPD1	1	0	0	0	0	1	0
HSPG2	1	0	0	1	1	0	0
HTR3C	1	0	0	0	0	0	0
HTR4	0	0	0	0	0	1	1
HTRA2	0	0	0	0	0	1	0
HTX1	0	0	0	0	0	0	1
HTX3	0	0	0	0	0	0	1
HTX4	0	0	0	0	0	0	1
HTX5	0	0	0	0	0	0	1
HTX6	0	0	0	0	0	0	1
HTX7	0	0	0	0	0	0	1
HTX8	0	0	0	0	0	0	1
HYAL1	1	0	0	0	0	0	0
HYAL2	1	0	0	0	0	0	0
HYC2	0	0	0	0	0	0	1
HYLS1	1	0	0	0	0	0	0
IAH1	0	0	0	0	0	1	0
IAPP	1	0	0	0	0	1	0
IBTK	0	0	0	0	0	1	0
ICAM1	1	0	0	0	0	1	0
ICAM3	1	0	0	0	0	0	0
ICAM4	1	0	0	0	0	0	0
ICAM5	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
IDH1	0	0	0	0	0	1	0
IDS	0	0	0	0	0	1	0
IDUA	1	0	0	0	0	0	0
IER2	1	0	0	0	0	0	0
IER5L	1	0	0	0	0	0	0
IFNG	0	0	0	0	0	1	0
IFNGR2	0	0	0	0	0	1	0
IFRD1	1	0	0	0	0	0	0
IFT140	1	0	0	0	0	0	0
IGDCC3	1	0	0	0	0	0	0
IGF1	0	0	0	0	0	1	0
IGF1R	1	0	1	1	1	1	0
IGF1RES	0	0	0	0	0	0	1
IGF2	0	0	0	0	0	1	0
IGF2BP2	1	0	0	0	0	0	0
IGFALS	1	0	0	0	0	0	0
IGFBP2	0	0	0	0	0	1	0
IGFBP3	0	0	0	0	0	1	0
IGFBP7	1	0	0	0	0	1	0
IGHMBP2	0	0	0	0	0	0	1
IHH	1	0	0	0	0	0	0
IK	0	0	0	0	0	1	0
IKZF3	1	0	0	0	0	0	0
IL10	0	0	0	0	0	1	0
IL11	0	0	0	0	0	1	0
IL15	0	0	0	0	0	1	0
IL17A	0	0	0	0	0	1	0
IL17D	0	0	0	0	0	1	0
IL18	1	0	0	0	0	1	0
IL18R1	0	0	0	0	0	1	0
IL1B	0	0	0	0	0	1	0
IL1RN	0	0	0	0	0	1	0
IL2	0	0	0	0	0	1	0
IL20RB	1	0	0	0	0	0	0
IL25	1	0	1	0	0	0	0
IL3	1	0	0	0	0	0	0
IL31RA	0	0	0	0	0	1	0
IL33	0	0	0	0	0	1	0
IL37	0	0	0	0	0	1	0
IL4	0	0	0	0	0	1	0
IL4I1	0	0	0	0	0	1	0
IL6	0	0	0	0	0	1	0
IL6R	1	0	0	1	1	1	0
IL9	1	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ILDR2	1	0	0	0	0	0	0
ILF2	1	0	0	0	0	0	0
ILK	0	0	0	0	0	0	1
IMDDHH	0	0	0	0	0	0	1
IMF1	0	0	0	0	0	0	1
IMMT	1	0	0	0	0	0	0
INA	1	0	0	0	0	0	0
ING1	1	0	0	0	0	0	0
INHA	1	0	0	0	0	0	0
INHBA	0	0	0	0	0	1	0
INO80E	1	0	0	0	0	0	0
INPP5K	1	0	0	0	0	0	0
INS	0	0	0	0	0	1	0
INSM2	1	0	0	0	0	0	0
INSRR	0	0	0	0	0	1	0
INTS3	1	0	0	0	0	0	0
INTS4	1	0	0	0	0	0	0
INVS	1	0	0	0	0	0	0
IPMK	1	0	0	0	0	0	0
IPO8	0	0	0	0	0	1	0
IQCD	1	0	0	0	0	0	0
IQCH	1	0	0	0	0	0	0
IQGAP3	1	0	0	0	0	0	0
IQSEC1	1	0	0	0	0	0	0
IRF2BP1	1	0	0	0	0	0	0
IRF2BPL	0	0	0	1	0	1	0
IRF5	1	0	0	0	0	0	0
IRF6	0	0	0	0	0	1	0
ISCA1	1	0	0	0	0	0	0
ISL1	0	0	0	0	0	0	1
ISL2	1	0	0	0	0	0	0
ISOC2	1	0	0	0	0	0	0
ITGA5	0	0	0	0	0	1	0
ITGA9	1	0	0	0	0	0	0
ITGB1	1	0	0	0	0	0	0
ITGB2	0	0	0	0	0	1	0
ITGB3	0	0	0	0	0	1	0
ITLN1	0	0	0	0	0	1	0
ITPK1	1	0	0	0	1	1	0
ITPRIP	1	0	0	0	0	0	0
IVD	0	0	0	0	0	1	0
JAM3	0	0	0	0	0	0	1
JARID2	1	0	0	0	0	0	0
JAZF1	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
JBS	0	0	0	0	0	0	1
JBS	0	0	0	0	0	0	1
JDSCD	0	0	0	0	0	0	1
JLNS1	0	0	0	0	0	0	1
JMJD1C	1	0	1	0	0	0	0
JMJD8	1	0	0	0	0	0	0
JOSD1	1	0	0	0	0	0	0
JPH2	1	0	0	0	0	1	0
JSRP1	1	0	0	0	0	0	0
KABUK1	0	0	0	0	0	0	1
KABUK2	0	0	0	0	0	0	1
KANK4	0	0	0	0	0	0	1
KBTBD11	1	0	0	0	0	0	0
KCNA1	0	0	0	0	0	1	0
KCNA10	0	0	0	0	0	1	0
KCNA2	0	0	0	0	0	1	0
KCNA3	0	0	0	0	0	1	0
KCNA4	1	0	0	0	0	1	1
KCNA5	0	0	0	0	0	1	1
KCNA6	0	0	0	0	0	1	0
KCNA7	0	0	0	0	0	1	0
KCNB1	1	0	0	0	0	1	0
KCNB2	0	0	0	0	0	1	0
KCNC1	0	0	0	0	0	1	0
KCNC2	0	0	0	0	0	1	0
KCNC3	0	0	0	0	0	1	0
KCNC4	0	0	0	0	0	1	0
KCND1	0	0	0	0	0	1	0
KCND2	0	0	0	0	0	1	0
KCND3	1	0	1	1	1	1	1
KCNE1	1	0	0	0	0	1	0
KCNE1B	0	0	0	0	0	1	0
KCNE2	1	0	0	0	0	1	1
KCNE3	0	0	0	0	0	1	1
KCNE4	0	0	0	0	0	1	0
KCNE5	0	0	0	0	0	1	0
KCNF1	0	0	0	0	0	1	0
KCNG1	0	0	0	0	0	1	0
KCNG2	0	0	0	0	0	1	0
KCNG3	0	0	0	0	0	1	0
KCNG4	0	0	0	0	0	1	0
KCNH1	0	0	0	0	0	1	0
KCNH2	1	0	1	1	1	1	1
KCNH3	1	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
KCNH4	0	0	0	0	0	1	0
KCNH5	0	0	0	0	0	1	0
KCNH6	0	0	0	0	0	1	0
KCNH7	0	0	0	0	0	1	0
KCNH8	0	0	0	0	0	1	0
KCNIP1	0	0	0	0	0	1	0
KCNIP2	1	0	1	0	0	1	0
KCNJ1	1	0	1	0	0	0	0
KCNJ12	0	0	0	0	0	0	1
KCNJ2	1	0	0	0	0	1	1
KCNJ3	0	0	0	0	0	1	1
KCNJ5	1	0	1	1	1	1	1
KCNJ6	1	0	0	0	0	0	0
KCNJ8	0	0	0	0	0	1	1
KCNK1	0	0	0	0	0	1	0
KCNK15	1	0	0	0	0	0	0
KCNK17	0	0	0	0	0	1	1
KCNK3	0	0	0	0	0	1	0
KCNK7	1	0	0	0	0	0	0
KCNK9	0	0	0	0	0	1	0
KCNN2	1	0	1	1	1	1	0
KCNN3	1	1	1	1	1	1	1
KCNQ1	0	0	0	0	0	1	1
KCNQ2	0	0	0	0	0	1	0
KCNQ3	0	0	0	0	0	1	0
KCNQ4	1	0	0	0	0	1	0
KCNQ5	0	0	0	0	0	1	0
KCNRG	1	0	0	0	0	0	0
KCNS1	1	0	0	0	0	1	0
KCNS2	1	0	0	0	0	1	0
KCNS3	0	0	0	0	0	1	0
KCNV1	0	0	0	0	0	1	0
KCNV2	0	0	0	0	0	1	0
KCP	1	0	0	0	0	0	0
KCTD10	1	0	0	0	0	0	0
KCTD11	1	0	0	0	0	0	0
KCTD20	1	0	0	0	0	0	0
KCTD7	1	0	0	0	0	0	0
KDM1B	0	0	0	1	1	1	0
KDM3A	1	0	1	0	1	0	0
KDM3B	1	0	1	0	0	0	0
KDM4B	1	0	0	0	0	0	0
KDM6A	0	0	0	0	0	0	1
KDM6B	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
KDVS	0	0	0	0	0	0	1
KEL	1	0	0	0	0	0	0
KFS4	0	0	0	0	0	0	1
KIAA0040	1	0	0	0	0	0	0
KIAA0232	1	0	0	0	0	0	0
KIAA0442	0	0	0	0	0	0	1
KIAA1109	0	0	0	0	0	1	0
KIAA1147	1	0	0	0	0	0	0
KIAA1191	1	0	0	0	0	0	0
KIAA1841	1	0	0	0	0	0	0
KIF11	0	0	0	0	0	0	1
KIF14	1	0	0	0	0	0	0
KIF17	1	0	0	0	0	0	0
KIF20A	1	0	1	0	0	0	0
KIF3C	1	0	1	1	1	1	0
KIF5B	1	0	0	0	0	0	0
KIF7	1	0	0	0	0	0	0
KIFAP3	1	0	0	0	0	0	0
KL	0	0	0	0	0	1	0
KLC3	1	0	0	0	0	0	0
KLEFS1	0	0	0	0	0	0	1
KLF11	1	0	0	0	0	0	0
KLF12	1	0	0	0	0	0	0
KLF7	1	0	0	0	0	0	0
KLHDC10	1	0	0	0	0	0	0
KLHL14	1	0	0	0	0	0	0
KLHL17	1	0	0	0	0	0	0
KLHL21	1	0	0	0	0	0	0
KLHL3	1	0	1	0	0	0	0
KLHL30	0	0	1	0	0	0	0
KLHL38	0	0	0	1	1	1	0
KLK3	0	0	0	0	0	1	0
KLKB1	1	0	0	0	0	0	0
KLRG1	1	0	0	0	0	0	0
KMT2D	0	0	0	0	0	0	1
KOS	0	0	0	0	0	0	1
KPNA1	1	0	0	0	0	0	0
KRAS	0	0	0	0	0	0	1
KRT76	0	0	0	0	0	1	0
KRT78	0	0	0	0	0	1	0
KRTCAP2	1	0	0	0	0	0	0
KY	1	0	0	0	0	0	0
L2HGA	0	0	0	0	0	0	1
LACHT	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
LAMP1	1	0	0	0	0	0	0
LAP3	0	0	0	0	0	1	0
LAPTM4A	0	0	0	0	0	1	0
LAPTM4B	1	0	0	0	0	0	0
LARP4B	1	0	0	0	0	0	0
LAT	0	0	0	0	0	1	0
LAT2	1	0	0	0	0	0	0
LBR	1	0	0	0	0	0	0
LCA5L	1	0	0	0	0	0	0
LCN2	0	0	0	0	0	1	0
LDB1	1	0	0	0	0	0	0
LDB3	0	0	0	0	0	0	1
LDLR	0	0	0	0	0	1	0
LDS1	0	0	0	0	0	0	1
LDS2	0	0	0	0	0	0	1
LDS3	0	0	0	0	0	0	1
LDS5	0	0	0	0	0	0	1
LECT1	0	0	0	0	0	0	1
LEF1	1	0	0	0	0	0	0
LEKR1	1	0	0	0	0	0	0
LENEP	1	1	1	0	0	0	0
LEP	0	0	0	0	0	1	0
LEPR	1	0	0	0	0	0	0
LFNG	1	0	0	0	0	0	0
LGALS1	0	0	0	0	0	1	0
LGALS3	0	0	0	0	0	1	0
LGALS4	1	0	0	0	0	0	0
LGALS8	1	0	0	0	0	0	0
LGI3	1	0	0	0	0	0	0
LHFPL2	1	0	0	0	0	0	0
LHFPL3	1	0	0	0	0	0	0
LHPP	1	0	0	0	0	0	0
LHX3	1	0	0	1	1	0	0
LIMCH1	1	0	0	0	0	0	0
LIN54	1	1	1	1	0	0	0
LINC00477	0	0	0	1	0	0	0
LINC00540	0	0	0	1	0	0	0
LINC00621	0	0	0	1	0	0	0
LINC00702	0	0	0	0	0	1	0
LINC00844	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
LINC00964	0	0	0	1	0	0	0
LINC01142	0	0	0	1	0	0	0
LINC01426	0	0	0	1	1	0	0
LINC01681	0	0	0	1	0	0	0
LIPC	0	0	0	0	1	0	0
LIPE	1	0	0	0	0	0	0
LMAN1	1	0	0	0	0	0	0
LMAN1L	0	0	0	0	0	0	1
LMNA	0	0	0	0	0	1	1
LMO1	1	0	0	0	0	0	0
LMO2	1	0	0	0	0	0	0
LMOD2	0	0	0	0	0	1	0
LMOD3	1	0	0	0	0	0	0
LMPH3	0	0	0	0	0	0	1
LMTK2	0	0	0	0	0	1	0
LNPEP	1	0	0	0	0	1	0
LNX2	1	0	0	0	0	0	0
LOC100128711	0	0	0	0	1	0	0
LOC100130936	0	0	0	0	1	0	0
LOC100422418	0	0	0	0	1	0	0
LOC101926943	0	0	0	0	1	0	0
LOC101928002	0	0	0	0	1	0	0
LOC101928277	0	0	0	1	0	0	0
LOC101928409	0	0	0	0	1	0	0
LOC101928478	0	0	0	0	1	0	0
LOC101928694	0	0	0	0	1	0	0
LOC101929560	0	0	0	0	1	0	0
LOC102467213	0	0	0	1	1	0	0
LOC102723321	0	0	0	0	1	0	0
LOC102723694	0	0	0	1	1	0	0
LOC1027	0	0	0	0	1	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
24233							
LOC102725112	0	0	0	0	1	0	0
LOC105369439	0	0	0	1	0	0	0
LOC105369698	0	0	0	0	1	0	0
LOC105369823	0	0	0	0	1	0	0
LOC105369846	0	0	0	0	1	0	0
LOC105370578	0	0	0	0	1	0	0
LOC105371449	0	0	0	0	1	0	0
LOC105371609	0	0	0	0	1	0	0
LOC105371610	0	0	0	1	1	0	0
LOC105371884	0	0	0	0	1	0	0
LOC105372516	0	0	0	0	1	0	0
LOC105373666	0	0	0	0	1	0	0
LOC105373673	0	0	0	0	1	0	0
LOC105374040	0	0	0	0	1	0	0
LOC105374317	0	0	0	0	1	0	0
LOC105374478	0	0	0	0	1	0	0
LOC105374778	0	0	0	0	1	0	0
LOC105375743	0	0	0	0	1	0	0
LOC105375746	0	0	0	0	1	0	0
LOC105376270	0	0	0	0	1	0	0
LOC105376440	0	0	0	0	1	0	0
LOC105377362	0	0	0	1	1	0	0
LOC105377363	0	0	0	0	1	0	0
LOC105377364	0	0	0	1	1	0	0
LOC1053	0	0	0	0	1	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
77366							
LOC105377367	0	0	0	1	1	0	0
LOC105377621	0	0	0	0	1	0	0
LOC105377731	0	0	0	0	1	0	0
LOC105377979	0	0	0	1	1	0	0
LOC105378208	0	0	0	0	1	0	0
LOC105378360	0	0	0	0	1	0	0
LOC105379168	0	0	0	0	1	0	0
LOC105379242	0	0	0	0	1	0	0
LOC105379311	0	0	0	0	1	0	0
LOC107984029	0	0	0	0	1	0	0
LOC107984402	0	0	0	0	1	0	0
LOC107984628	0	0	0	0	1	0	0
LOC107984728	0	0	0	0	1	0	0
LOC107984734	0	0	0	0	1	0	0
LOC107984788	0	0	0	0	1	0	0
LOC107985401	0	0	0	0	1	0	0
LOC107986203	0	0	0	0	1	0	0
LOC107986773	0	0	0	0	1	0	0
LOC341056	0	0	0	0	1	0	0
LOC729200	0	0	0	0	1	0	0
LOR	0	0	0	0	0	1	0
LOX	0	0	0	0	0	1	0
LPA	0	0	0	0	0	1	0
LPL	0	0	0	0	1	1	0
LPP	0	0	0	0	0	1	0
LPRD1	0	0	0	0	0	0	1
LQT1	0	0	0	0	0	0	1
LQT10	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
LQT12	0	0	0	0	0	0	1
LQT13	0	0	0	0	0	0	1
LQT14	0	0	0	0	0	0	1
LQT15	0	0	0	0	0	0	1
LQT2	0	0	0	0	0	0	1
LQT3	0	0	0	0	0	0	1
LQT5	0	0	0	0	0	0	1
LQT6	0	0	0	0	0	0	1
LRCH1	1	0	1	1	0	0	0
LRIG1	1	0	1	1	1	1	0
LRMDA	0	0	0	0	0	1	0
LRP12	1	0	0	0	0	0	0
LRP3	1	0	0	0	0	0	0
LRPAP1	0	0	0	0	0	1	0
LRRC1	1	0	0	0	0	0	0
LRRC10	0	0	1	1	1	0	0
LRRC3	1	0	0	0	0	0	0
LRRC45	1	0	0	0	0	0	0
LRRC63	0	0	0	0	1	1	0
LRRFIP1	1	0	0	0	0	0	0
LRRN2	1	0	0	0	0	0	0
LRRN4	0	0	0	0	0	1	0
LRS	0	0	0	0	0	0	1
LSDMCA1	0	0	0	0	0	0	1
LSDMCA2	0	0	0	0	0	0	1
LSDMCA3	0	0	0	0	0	0	1
LSG1	1	0	0	0	0	0	0
LSM14A	1	0	0	0	0	0	0
LSM2	1	0	0	0	0	0	0
LSM4	1	0	0	0	0	0	0
LSP1	1	0	0	0	0	0	0
LST1	1	0	0	0	0	0	0
LTA	1	0	0	0	0	0	0
LTB	1	0	0	0	0	0	0
LTBP3	1	0	0	0	0	0	0
LTBP4	0	0	0	0	0	0	1
LTF	1	0	0	0	0	0	0
LVNC1	0	0	0	0	0	0	1
LVNC8	0	0	0	0	0	0	1
LY6G5C	1	0	0	0	0	0	0
LY6G6C	1	0	0	0	0	0	0
LY6G6D	1	0	0	0	0	0	0
LY86	0	0	0	0	0	1	0
LY96	0	0	0	0	1	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
LYPLA2	1	0	0	0	0	0	0
LYSMD3	1	0	0	0	0	0	0
LYSMD4	1	0	0	0	0	0	0
LYST	0	0	0	0	0	1	0
LYVE1	0	0	0	0	0	1	0
MACF1	1	0	0	0	0	0	0
MACROD2	0	0	0	0	0	1	0
MAD2L1	1	0	0	0	0	0	0
MAF	0	0	0	0	0	1	0
MAFB	1	0	0	0	0	0	0
MAFG	1	0	0	0	0	0	0
MAG	0	0	0	0	0	1	0
MAHCJ	0	0	0	0	0	0	1
MAML3	0	0	0	0	1	1	0
MAN1A2	1	0	0	0	0	0	0
MAN2A1	1	0	0	0	0	0	0
MAN2A2	1	0	0	0	0	0	0
MAN2C1	1	0	0	0	0	0	0
MANBA	1	0	1	0	0	0	0
MAP1B	0	0	0	0	0	1	0
MAP2K4	0	0	0	0	0	1	0
MAP3K1	0	0	0	0	0	1	0
MAP3K11	1	0	0	0	0	0	0
MAP3K14	1	0	0	0	0	0	0
MAP3K20	0	0	0	0	0	1	0
MAP3K3	1	0	0	0	0	0	0
MAP4K4	1	0	0	0	0	0	0
MAP6	0	0	0	0	0	1	0
MAP9	0	0	0	0	0	1	0
MAPK1	0	0	0	0	0	1	0
MAPK11	1	0	0	0	0	0	0
MAPK12	1	0	0	0	0	0	0
MAPK13	1	0	0	0	0	0	0
MAPK14	1	0	0	0	0	0	0
MAPK3	0	0	0	0	0	1	0
MAPK8IP3	1	0	0	0	0	0	0
MAPK9	0	0	0	0	0	1	0
MAPRE2	1	0	0	0	0	0	0
MAPT	1	0	0	0	1	1	0
MARCH2	1	0	0	0	0	0	0
MARCH6	0	0	0	0	0	1	0
MARCH7	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
MARS2	1	0	0	0	0	0	0
MAS1L	1	0	0	0	0	0	0
MASP1	0	0	0	0	0	0	1
MATN1	0	0	0	0	0	1	0
MATN2	1	0	0	0	0	0	0
MAX	0	0	0	0	0	1	0
MB	0	0	0	0	0	1	0
MBD5	1	0	1	0	1	1	0
MBTD1	1	0	0	0	0	0	0
MBTPS2	0	0	0	0	0	0	1
MCAHS1	0	0	0	0	0	0	1
MCAHS2	0	0	0	0	0	0	1
MCAP	0	0	0	0	0	0	1
MCAT	0	0	0	0	0	1	0
MCIDAS	0	0	0	0	0	1	0
MCLDS	0	0	0	0	0	0	1
MCLMR	0	0	0	0	0	0	1
MCOLN1	0	0	0	0	0	1	0
MCOLN2	0	0	0	0	0	1	0
MCOLN3	0	0	0	0	0	1	0
MCOP8	0	0	0	0	0	0	1
MCOPCB10	0	0	0	0	0	0	1
MCOPS12	0	0	0	0	0	0	1
MCOPS2	0	0	0	0	0	0	1
MCOPS3	0	0	0	0	0	0	1
MCOPS9	0	0	0	0	0	0	1
MCRS1	1	0	0	0	0	0	0
MCT1D	0	0	0	0	0	0	1
MCTP2	1	0	0	0	0	0	0
MDCMC	0	0	0	0	0	0	1
MDDGA4	0	0	0	0	0	0	1
MDLS	0	0	0	0	0	0	1
MDM4	1	0	0	0	0	0	0
ME1	1	0	0	0	0	0	0
ME2	1	0	0	0	0	0	0
MECP2	0	0	0	0	0	1	0
MECRCN	0	0	0	0	0	0	1
MED1	1	0	0	0	0	0	0
MED13L	1	0	0	0	0	0	0
MED24	1	1	0	0	0	0	0
MEF2A	1	0	0	0	0	0	1
MEF2C	1	0	0	0	0	0	0
MEF2D	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
MEGF8	1	0	0	0	0	0	0
MEIS1	1	0	0	0	0	0	0
MEIS2	1	0	0	0	0	0	1
MELAS	0	0	0	0	0	0	1
MEPCE	1	0	0	0	0	0	0
METRN	1	0	0	0	0	0	0
METRNL	1	0	0	0	0	0	0
METTL11B	0	0	0	0	0	1	0
METTL7B	1	0	0	0	1	0	0
MEX3C	0	0	1	1	1	1	0
MFAP2	1	0	0	0	0	0	0
MFDGA	0	0	0	0	0	0	1
MFF	0	0	0	0	0	1	0
MFHAS1	1	0	0	0	0	0	0
MFM1	0	0	0	0	0	0	1
MFM4	0	0	0	0	0	0	1
MFN1	1	0	0	0	0	0	0
MFRG	0	0	0	0	0	0	1
MFSD2A	1	0	0	0	0	0	0
MGAT3	1	0	0	0	0	0	0
MGORS7	0	0	0	0	0	0	1
MHS1	0	0	0	0	0	0	1
MICAL3	0	0	0	0	0	1	0
MICALCL	1	0	0	0	0	0	0
MICB	1	0	0	0	0	1	0
MICCAP	0	0	0	0	0	0	1
MID1	0	0	0	0	0	0	1
MIF	0	0	0	0	0	1	0
MIR1-1HG	0	0	0	0	1	0	0
MIR1-2	0	0	0	0	0	0	1
MIR133A1	0	0	0	0	0	0	1
MIR133A2	0	0	0	0	0	0	1
MIR208A	0	0	0	0	0	0	1
MIR26A1	0	0	0	0	0	0	1
MIR297	0	0	0	0	1	1	0
MIR6500	0	0	0	1	1	0	0
MITF	1	0	0	0	0	0	0
MKI67	1	0	0	0	0	0	0
MKRN2	1	0	1	0	0	0	0
MLIP	0	0	0	0	0	0	1
MLLT3	0	0	0	0	0	1	0
MLRD	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
MLST8	1	0	0	0	0	0	0
MLXIP	1	0	0	0	0	0	0
MLXIPL	0	0	0	0	1	1	0
MMAB	1	0	0	0	0	0	0
MMD1	0	0	0	0	0	0	1
MME	0	0	0	0	0	1	1
MMP1	0	0	0	0	0	1	0
MMP11	1	0	0	0	0	0	0
MMP12	0	0	0	0	0	1	0
MMP13	0	0	0	0	0	1	0
MMP17	1	0	0	0	0	0	0
MMP19	0	0	0	0	0	1	0
MMP2	0	0	0	0	0	1	0
MMP21	0	0	0	0	0	0	1
MMP28	0	0	0	0	0	1	0
MMP3	0	0	0	0	0	1	0
MMP7	0	0	0	0	0	1	0
MMP9	0	0	0	0	0	1	0
MMRN1	0	0	0	0	0	1	0
MMUT	0	0	0	0	0	1	0
MNAT1	1	0	0	0	0	0	0
MNKES	0	0	0	0	0	0	1
MNS	0	0	0	0	0	0	1
MOB3B	0	0	0	0	0	1	0
MOGAT1	1	0	0	0	0	0	0
MOPD1	0	0	0	0	0	0	1
MORC3	1	0	0	0	0	0	0
MOWS	0	0	0	0	0	0	1
MPD1	0	0	0	0	0	0	1
MPDU1	1	0	1	0	0	0	0
MPI	0	0	0	0	0	1	0
MPL	0	0	0	0	0	1	0
MPO	1	0	0	0	0	1	1
MPP2	0	0	0	0	0	1	0
MPPED2	1	0	1	0	0	0	0
MPPH1	0	0	0	0	0	0	1
MPSPS	0	0	0	0	0	0	1
MRAP	0	0	0	0	0	1	0
MRC1	0	0	0	0	0	1	0
MRD21	0	0	0	0	0	0	1
MRD26	0	0	0	0	0	0	1
MRD32	0	0	0	0	0	0	1
MRPL14	1	0	0	0	0	0	0
MRPL23	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
MRPL4	1	0	0	0	0	0	0
MRPL44	1	0	0	0	0	0	0
MRPS16	1	0	0	0	0	0	0
MRPS24	1	0	0	0	0	0	0
MRPS27	1	0	0	0	0	0	0
MRPS34	1	0	0	0	0	0	0
MRSHSS	0	0	0	0	0	0	1
MRT65	0	0	0	0	0	0	1
MRVI1	1	0	0	0	0	0	0
MRXS32	0	0	0	0	0	0	1
MRXS34	0	0	0	0	0	0	1
MRXS99F	0	0	0	0	0	0	1
MS4A6A	1	0	0	0	0	0	0
MSE	0	0	0	0	0	0	1
MSH5	1	0	0	0	0	0	0
MSL2	1	0	0	0	0	0	0
MSMA	0	0	0	0	0	0	1
MSRB3	1	0	0	0	0	0	0
MSTN	0	0	0	0	0	1	0
MSTO1	1	0	0	0	0	0	0
MSX1	1	0	0	0	0	0	0
MSX2	0	0	0	0	0	0	1
MT1DP	0	0	0	0	0	1	0
MTCO3P6	0	0	0	0	1	0	0
MTCYBP4	0	0	0	0	1	0	0
MTHFD1	1	0	1	0	0	0	0
MTHFD2P7	0	0	0	0	1	0	0
MTHFR	1	0	0	0	1	1	0
MTMR11	1	0	0	0	0	0	0
MT-ND1	0	0	0	0	0	1	0
MT-ND2	0	0	0	0	0	1	0
MT-ND3	0	0	0	0	0	1	0
MT-ND4	0	0	0	0	0	1	0
MT-ND4L	0	0	0	0	0	1	0
MT-ND5	0	0	0	0	0	1	0
MT-ND6	0	0	0	0	0	1	0
MTO1	1	0	0	0	0	1	0
MTR	0	0	0	0	0	1	0
MTRR	0	0	0	0	0	1	0
MTSS1	0	0	0	1	0	1	0
MTTL1	0	0	0	0	0	0	1
MTUS1	1	0	0	0	0	0	0
MTX1	1	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
MUC1	1	0	0	0	0	1	0
MUC16	0	0	0	0	0	1	0
MUSTN1	1	0	0	0	0	0	0
MVA2	0	0	0	0	0	0	1
MVD	0	0	0	0	0	1	0
MVK	1	0	0	0	0	0	0
MVP	0	0	0	0	0	1	0
MVP1	0	0	0	0	0	0	1
MVP2	0	0	0	0	0	0	1
MX1	0	0	0	0	1	1	0
MXD1	1	1	1	0	0	0	0
MXI1	0	0	0	0	0	1	0
MYBPC3	0	0	0	0	0	1	1
MYBPH	1	0	0	0	0	0	0
MYEOV	1	0	0	0	0	0	0
MYH14	1	0	0	0	0	0	0
MYH6	1	0	1	1	1	0	1
MYH7	1	0	1	0	1	1	1
MYL1	0	0	0	0	0	0	1
MYL2	1	0	0	0	0	0	1
MYL3	1	0	0	0	0	1	1
MYL4	0	0	0	0	0	1	1
MYL7	0	0	0	0	0	0	1
MYLPF	1	0	0	0	0	0	0
MYO18B	1	0	0	1	1	1	1
MYO1C	1	0	0	1	0	0	0
MYO1H	1	0	0	0	0	0	0
MYO6	1	0	0	0	0	0	0
MYOCD	1	0	0	1	1	1	0
MYOG	1	0	1	0	0	0	0
MYOM3	1	0	0	0	0	0	0
MYOT	1	1	1	0	0	0	0
MYOZ1	1	0	1	0	0	1	0
MYPN	0	0	0	0	0	1	1
MYRIP	1	0	0	0	0	0	0
MYSM1	0	0	0	0	0	1	0
MYZAP	0	0	0	0	1	0	0
NAAA	0	0	0	0	0	1	0
NACA	1	0	1	1	1	1	0
NACC2	0	0	0	0	0	1	0
NAGLU	1	0	0	0	0	0	0
NAMPT	0	0	0	0	0	1	0
NANOS1	1	0	0	0	0	1	0
NAPA	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
NAPB	1	0	0	0	0	0	0
NAPRT	0	0	0	0	0	1	0
NAPSA	1	0	0	0	0	0	0
NARFL	1	0	0	0	0	0	0
NARS2	1	0	0	0	0	0	0
NAT14	1	0	0	0	0	0	0
NAT2	1	0	0	0	0	0	0
NAT8B	1	0	0	0	0	0	0
NAT9	0	0	0	0	0	1	0
NAV2	1	0	1	1	1	1	0
NCAPG2	1	0	0	0	0	0	0
NCEH1	1	0	0	0	0	0	0
NCF1	0	0	0	0	0	1	0
NCKAP1	1	0	0	0	0	0	0
NCKAP5	0	0	0	0	0	1	0
NCKAP5L	1	0	0	0	0	0	0
NCLN	1	0	0	0	0	0	0
NCOA2	1	0	0	0	0	0	0
NCOR2	1	0	0	0	0	0	0
NCR3	1	0	0	0	0	0	0
NCSTN	1	0	0	0	0	0	0
NDEL1	1	0	0	0	0	0	0
NDH	0	0	0	0	0	0	1
NDST2	1	1	1	0	0	0	0
NDUFA1	0	0	0	0	0	1	0
NDUFA10	0	0	0	0	0	1	0
NDUFA11	0	0	0	0	0	1	0
NDUFA12	0	0	0	0	0	1	0
NDUFA13	0	0	0	0	0	1	0
NDUFA2	0	0	0	0	0	1	0
NDUFA3	0	0	0	0	0	1	0
NDUFA4	0	0	0	0	0	1	0
NDUFA4L2	0	0	0	0	0	1	0
NDUFA5	0	0	0	0	0	1	0
NDUFA6	0	0	0	0	0	1	0
NDUFA7	0	0	0	0	0	1	0
NDUFA8	0	0	0	0	0	1	0
NDUFA9	0	0	0	0	0	1	0
NDUFAB1	0	0	0	0	0	1	0
NDUFAF1	0	0	0	0	0	1	0
NDUFAF2	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
NDUFAF3	0	0	0	0	0	1	0
NDUFAF4	0	0	0	0	0	1	0
NDUFB1	0	0	0	0	0	1	0
NDUFB10	1	0	1	0	1	1	0
NDUFB11	0	0	0	0	0	1	1
NDUFB2	0	0	0	0	0	1	0
NDUFB3	0	0	0	0	0	1	0
NDUFB4	0	0	0	0	0	1	0
NDUFB5	0	0	0	0	0	1	0
NDUFB6	0	0	0	0	0	1	0
NDUFB7	0	0	0	0	0	1	0
NDUFB8	0	0	0	0	0	1	0
NDUFB9	0	0	0	0	0	1	0
NDUFC1	0	0	0	0	0	1	0
NDUFC2	0	0	0	0	0	1	0
NDUFS1	0	0	0	0	0	1	0
NDUFS2	0	0	0	0	0	1	0
NDUFS3	0	0	0	0	0	1	0
NDUFS4	0	0	0	0	0	1	0
NDUFS5	0	0	0	0	0	1	0
NDUFS6	0	0	0	0	0	1	0
NDUFS7	0	0	0	0	0	1	0
NDUFS8	0	0	0	0	0	1	0
NDUFV1	0	0	0	0	0	1	0
NDUFV2	0	0	0	0	0	1	0
NDUFV3	0	0	0	0	0	1	0
NEAT1	0	0	0	0	0	1	0
NEB	0	0	0	0	0	1	0
NEBL	1	0	0	0	1	1	0
NEDD4L	1	0	0	0	0	0	0
NEGR1	0	0	0	0	0	1	0
NEIL1	1	0	0	0	0	0	0
NEIL2	1	0	0	0	0	0	0
NEIMY	0	0	0	0	0	0	1
NEK10	1	0	0	0	0	0	0
NEK8	0	0	0	0	0	0	1
NEO1	1	0	1	0	0	0	0
NEU1	1	0	0	0	0	0	0
NEURL1	0	0	0	1	1	1	0
NEURL4	1	0	0	0	0	0	0
NEUROD2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
NF1	0	0	0	0	0	1	1
NF1	0	0	0	0	0	1	1
NF2	0	0	0	0	0	1	0
NFAT5	0	0	0	0	0	1	0
NFATC1	0	0	0	0	0	1	0
NFATC2IP	1	0	0	0	0	0	0
NFATC3	0	0	0	0	0	1	0
NFATC4	1	0	0	0	0	1	0
NFE2	1	0	0	0	0	1	0
NFE2L2	1	0	0	0	0	0	0
NFIA	1	0	0	0	0	0	0
NFIX	1	0	0	0	0	0	0
NFKB1	1	0	0	0	0	1	0
NFKB2	1	0	1	0	0	0	0
NFKBIL1	1	0	0	0	0	0	0
NFKBIZ	0	0	0	0	0	1	0
NFNS	0	0	0	0	0	0	1
NFYB	1	0	0	0	0	0	0
NFYC	1	0	0	0	0	0	0
NGF	0	0	0	0	0	1	0
NGPS	0	0	0	0	0	0	1
NHLH1	1	0	0	0	0	0	0
NHLH2	1	0	0	0	0	0	0
NIN	1	0	0	0	0	0	0
NIP7	1	0	0	0	0	0	0
NISCH	0	0	0	0	0	1	0
NKD2	1	0	0	0	0	0	0
NKIRAS1	1	0	0	0	0	0	0
NKX2-1	0	0	0	0	0	1	0
NKX2-2	1	0	0	0	0	0	0
NKX2-3	1	0	0	0	0	0	0
NKX2-5	1	0	1	1	1	1	1
NKX6-2	1	0	0	0	0	0	0
NLGN2	1	0	1	0	0	0	0
NLRP3	0	0	0	0	0	1	0
NLS1	0	0	0	0	0	0	1
NMB	1	0	0	0	0	0	0
NME1	1	0	0	0	0	0	0
NME3	1	0	0	0	0	0	0
NME4	1	0	0	0	0	0	0
NME5	1	0	1	0	1	0	0
NME7	0	0	0	0	0	1	0
NMI	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
NNT	0	0	0	0	0	1	0
NOG	0	0	0	0	0	1	0
NOS1	0	0	0	0	0	1	0
NOS2	0	0	0	0	0	1	0
NOS3	1	0	1	0	0	1	0
NOSTRIN	1	0	0	0	0	0	0
NOTCH4	0	0	0	0	0	1	0
NOX4	0	0	0	0	0	1	0
NOXO1	1	0	0	0	0	0	0
NPAS1	1	0	0	0	0	0	0
NPC1	1	0	0	0	0	0	0
NPEPL1	1	0	0	0	0	0	0
NPHP3	0	0	0	0	0	0	1
NPM2	1	0	1	0	0	0	0
NPM3	0	0	1	0	0	0	0
NPPA	1	0	0	0	0	1	1
NPPB	1	0	0	0	0	1	1
NPPC	0	0	0	0	0	0	1
NPR1	1	0	0	0	0	0	1
NPR2	0	0	0	0	0	0	1
NPR3	1	0	0	0	0	1	1
NPS	0	0	0	0	0	1	0
NPTN	1	0	0	0	0	0	0
NPTXR	1	0	0	0	0	0	0
NPY4R	0	0	0	0	0	1	0
NQO1	0	0	0	0	0	1	0
NR1D2	0	0	0	0	0	1	0
NR2F2	0	0	0	0	0	0	1
NR3C1	1	0	1	1	1	1	1
NR3C2	1	0	1	0	0	1	0
NRAP	1	0	0	0	0	0	0
NRBF2	1	0	1	0	0	0	0
NRBP1	0	0	0	0	1	0	0
NREP	0	0	0	0	0	1	0
NRG1	1	0	0	0	0	1	0
NRG2	1	0	0	0	0	0	0
NRIP1	1	0	0	0	0	0	0
NRTN	0	0	0	0	0	1	0
NRXN2	1	0	0	0	0	0	0
NRXN3	0	0	0	0	0	1	0
NS1	0	0	0	0	0	0	1
NS3	0	0	0	0	0	0	1
NS4	0	0	0	0	0	0	1
NS7	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
NS8	0	0	0	0	0	0	1
NSD1	0	0	0	0	0	0	1
NSLH1	0	0	0	0	0	0	1
NSLH2	0	0	0	0	0	0	1
NSLL	0	0	0	0	0	0	1
NSUN6	1	0	0	0	0	0	0
NT5C1A	1	0	0	0	0	0	0
NT5C2	1	0	0	0	0	0	0
NT5C3A	0	0	0	0	0	1	0
NTF3	0	0	0	0	0	0	1
NTHL1	1	0	0	0	0	0	0
NTM	0	0	0	0	0	1	0
NTN3	1	0	0	0	0	0	0
NTRK2	1	0	0	0	0	1	0
NUBP2	1	0	0	0	0	0	0
NUCKS1	1	0	1	1	1	1	0
NUDT13	1	0	0	0	0	0	0
NUDT3	1	0	0	0	1	0	0
NUP155	0	0	0	0	0	1	1
NXD	0	0	0	0	0	0	1
NXPH3	1	0	0	0	0	0	0
OAZ3	1	0	0	0	0	0	0
OBSCN	1	0	0	0	0	0	0
ODDD	0	0	0	0	0	0	1
ODF3L1	1	0	0	0	0	0	0
OFD11	0	0	0	0	0	0	1
OGDNS	0	0	0	0	0	0	1
OLA1	1	0	0	0	0	0	0
OLFML2B	1	0	0	0	0	0	0
OMOD1	0	0	0	0	0	0	1
OPA3	1	0	0	0	0	0	0
OPN1SW	1	0	0	1	1	1	0
OPN4	1	0	0	0	0	0	0
OR10AE3P	0	0	0	1	0	0	0
OR1G1	1	0	0	0	0	0	0
OR7C2	1	0	0	0	0	0	0
OR8B4	1	0	0	0	0	0	0
ORMDL3	1	0	0	0	0	0	0
OSBP2	1	0	0	0	0	0	0
OSBPL10	1	0	0	0	0	0	0
OSBPL1A	0	0	0	0	0	1	0
OSBPL6	1	0	0	0	0	0	0
OSCAR	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
OSCS	0	0	0	0	0	0	1
OSM	1	0	0	0	0	1	0
OSTF1P1	0	0	0	0	1	0	0
OTC	0	0	0	0	0	1	0
OTUD6B	1	0	0	0	0	0	0
OTUD7B	1	0	0	0	0	0	0
P2RY12	1	0	0	0	0	1	0
P4HA1	1	0	0	0	0	0	0
P4HB	0	0	0	0	0	1	0
PABPC4	1	0	0	0	0	0	0
PACA	0	0	0	0	0	0	1
PACSIN1	1	0	0	0	0	0	0
PADI2	1	0	0	0	0	0	0
PAFAH1B2	1	0	0	0	0	0	0
PAK2	1	0	1	0	1	1	0
PAK4	1	0	0	0	0	0	0
PAM	0	0	0	0	0	1	0
PANCR	0	0	0	1	0	0	1
PANX1	0	0	0	0	0	1	0
PAPA8	0	0	0	0	0	0	1
PAPLN	1	0	0	0	0	0	0
PAPOLG	1	0	0	0	0	0	0
PAQR3	1	0	0	0	0	0	0
PAQR5	1	0	0	0	0	0	0
PAQR6	1	0	0	0	0	0	0
PAQR7	1	0	0	0	0	0	0
PAQR8	1	0	0	0	0	0	0
PAQR9	1	0	0	0	0	0	0
PARM1	1	0	0	0	0	0	0
PARP16	1	0	0	0	0	0	0
PAX6	0	0	0	0	0	1	0
PAXIP1	1	0	0	0	0	0	0
PBD10A	0	0	0	0	0	0	1
PBD12A	0	0	0	0	0	0	1
PBX2	1	0	0	0	0	0	0
PBXIP1	1	1	1	0	0	0	0
PC	1	0	0	0	0	0	0
PCAT29	0	0	0	0	1	0	0
PCBP1	1	0	0	0	0	0	0
PCCB	1	0	0	0	0	0	0
PCDH18	0	0	0	0	0	1	0
PCDH8	1	0	0	0	0	0	0
PCGF6	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
PCID2	1	0	0	0	0	0	0
PCM1	1	0	1	0	0	0	0
PCMT1	1	0	0	0	0	0	0
PCNA	0	0	0	0	0	1	0
PCNX1	0	0	0	0	0	1	0
PCSK7	1	0	0	0	0	0	0
PCSK9	0	0	0	0	0	1	0
PCYOX1	1	0	0	0	0	0	0
PCYT1A	0	0	0	0	0	1	0
PDC	0	0	0	0	0	1	0
PDCD11	1	0	0	0	0	0	0
PDE3B	1	0	0	0	0	0	0
PDE4B	1	0	0	0	0	0	0
PDE4D	0	0	0	0	0	1	0
PDE8B	1	0	0	0	0	0	0
PDGFRA	0	0	0	0	0	1	0
PDGFRB	0	0	0	0	0	1	0
PDHB	1	0	0	0	0	0	0
PDLIM2	1	0	0	0	0	0	0
PDLIM5	1	0	0	0	0	0	0
PDPK1	0	0	0	0	0	0	1
PDPN	0	0	0	0	0	0	1
PDRG1	1	0	0	0	0	0	0
PDS5B	1	0	0	0	0	0	0
PEA15	0	0	0	0	0	1	0
PEAMO	0	0	0	0	0	0	1
PEE5	0	0	0	0	0	0	1
PELP1	1	0	0	0	0	0	0
PENK	1	0	0	0	0	0	0
PEOA3	0	0	0	0	0	0	1
PEOB1	0	0	0	0	0	0	1
PEPD	0	0	0	0	0	1	0
PER2	1	0	0	0	0	0	0
PEX13	1	0	0	0	0	0	0
PEX14	1	0	0	0	0	0	0
PEX19	1	0	0	0	0	0	0
PEX26	1	0	0	0	0	0	0
PEX3	1	0	0	0	0	0	0
PEX5L	1	0	0	0	0	0	0
PEX6	0	0	0	0	0	1	0
PF4	0	0	0	0	0	1	0
PFDN1	1	0	0	0	0	0	0
PFHB1A	0	0	0	0	0	0	1
PFHB2	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
PFKFB2	1	0	0	0	0	0	0
PGAP2	1	0	0	0	0	0	0
PGAP3	1	0	0	0	0	0	0
PGD	1	0	0	0	0	0	0
PGK1	0	0	0	0	0	1	0
PGP	0	0	0	1	1	1	0
PGS1	1	0	0	0	0	0	0
PHA2A	0	0	0	0	0	0	1
PHACTR2	1	0	0	0	0	1	0
PHC2	1	0	0	0	0	0	0
PHF1	1	0	0	0	0	0	0
PHF13	1	0	0	0	0	0	0
PHF19	1	0	0	0	0	1	0
PHLDA1	0	0	0	1	0	1	0
PHLDB2	1	0	1	1	1	1	0
PHOX2A	1	0	0	0	0	0	0
PHTF2	1	0	1	0	0	0	0
PHYHIP	0	0	0	0	0	0	1
PIGL	1	0	0	0	0	0	0
PIGQ	1	0	0	0	0	0	0
PIGX	0	0	1	0	0	0	0
PIK3C2B	1	0	0	0	0	0	0
PIK3CA	0	0	0	0	0	1	0
PIK3R1	0	0	0	0	0	1	0
PIK3R3	1	0	0	0	0	0	0
PILRA	1	0	0	0	0	0	0
PIM1	1	0	0	0	0	0	0
PINK1	1	0	0	0	0	0	0
PIP4K2A	1	0	0	0	0	0	0
PIP5K1B	1	0	0	0	0	0	0
PITPNA	1	0	0	0	0	0	0
PITPNC1	1	0	0	0	0	0	0
PITX2	1	1	1	1	1	1	1
PITX3	1	0	1	0	1	1	0
PKD1	1	0	0	0	0	0	0
PKD2L1	1	0	0	0	0	0	0
PKD2L2	1	1	1	0	1	1	0
PKD4	0	0	0	0	0	0	1
PKHD1L1	0	0	0	0	0	1	0
PKLR	1	0	0	0	0	0	0
PKN2	0	0	0	0	0	1	0
PKP2	1	0	1	1	1	1	0
PKS	0	0	0	0	0	0	1
PLA2G12	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
B							
PLA2G1B	0	0	0	0	0	1	0
PLA2G4A	1	0	0	0	0	0	0
PLA2G4E	1	0	0	0	0	0	0
PLA2G7	1	0	0	0	0	1	0
PLAC8	1	0	0	0	0	0	0
PLAT	0	0	0	0	0	1	1
PLAU	0	0	1	0	0	1	0
PLBD2	1	0	0	0	0	0	0
PLCD1	1	0	0	0	0	0	0
PLCD3	1	0	0	0	0	0	0
PLCG1	0	0	0	0	1	1	0
PLCL1	1	0	0	0	0	0	0
PLCXD2	1	0	1	0	1	0	0
PLCXD3	0	0	0	0	0	0	1
PLD1	0	0	0	0	0	0	1
PLD3	1	0	0	0	0	0	0
PLEC	0	0	0	0	0	1	0
PLEKHA3	1	1	1	0	0	0	0
PLEKHG4B	1	0	0	0	0	0	0
PLEKHM2	1	0	0	0	0	0	0
PLG	1	0	0	0	0	1	0
PLIN1	1	0	1	0	0	0	0
PLN	1	0	0	0	0	1	1
PLSCR3	1	0	0	0	0	0	0
PLXNC1	1	0	0	0	0	0	0
PLXND1	1	0	0	0	0	0	0
PMCH	1	0	0	0	0	0	0
PMP2	1	0	0	0	0	0	0
PMSE	0	0	0	0	0	0	1
PMVK	1	1	1	0	0	0	0
PNKD	0	0	0	0	0	1	0
PNMT	1	0	0	0	0	0	0
PNOC	1	0	0	0	0	0	0
PNPLA3	1	0	0	0	0	0	0
POC5	0	0	0	0	1	1	0
POFUT2	1	0	0	0	0	0	0
POLDIP3	1	0	0	0	0	0	0
POLK	0	0	0	0	1	1	0
POLL	1	0	0	0	0	0	0
POLR1A	1	0	0	0	0	0	0
POLR1B	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
POLR2A	0	0	1	0	1	1	0
POLR2B	1	0	0	0	0	0	0
POLR2E	1	0	0	0	0	0	0
POLR3B	1	0	0	0	0	0	0
POLR3G	1	0	0	0	0	1	0
POMC	1	0	0	0	0	1	0
PON1	0	0	0	0	0	1	0
POP7	1	0	0	0	0	0	0
POR	0	0	0	0	0	1	0
POSTN	0	0	0	0	0	1	0
POU2F2	1	0	0	0	0	0	0
POU5F1	0	0	0	0	0	1	0
PPARA	0	0	0	0	0	1	0
PPARD	0	0	0	0	0	1	0
PPARG	1	0	0	0	0	1	0
PPARGC1A	0	0	0	0	0	1	0
PPB	0	0	0	0	0	0	1
PPFIA4	0	0	0	1	1	1	0
PPFIBP1	1	0	0	0	0	0	0
PPH1	0	0	0	0	0	0	1
PPIA	1	0	0	0	0	1	0
PPIE	1	0	0	0	0	0	0
PPIL4	1	0	0	0	0	0	0
PPL	1	0	0	0	0	0	0
PPM1G	0	0	0	0	1	1	0
PPOX	0	0	0	0	0	1	0
PPP1CB	0	0	0	0	0	0	1
PPP1R12A	0	0	0	0	0	1	0
PPP1R15B	1	0	0	0	0	0	0
PPP1R16B	1	0	0	0	0	0	0
PPP1R1B	1	0	0	0	0	0	0
PPP1R3E	1	0	0	0	0	0	0
PPP1R9B	0	0	0	0	0	1	0
PPP2R2B	1	0	0	0	0	0	0
PPP2R3A	1	0	0	1	1	0	0
PPP2R5C	1	0	0	0	0	0	0
PPP3CB	1	0	0	0	0	0	0
PPP4R1	0	0	0	0	0	1	0
PPP5C	1	0	0	0	0	0	0
PPRC1	0	0	0	0	0	1	0
PPT2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
PQBP1	0	0	0	0	0	0	1
PRAM1	1	0	0	0	0	0	0
PRDM16	1	0	0	0	0	0	1
PRDM8	0	0	0	0	1	0	0
PRDX2	0	0	0	0	0	1	0
PREP	1	0	0	0	0	0	0
PREX1	0	0	0	0	0	1	0
PRF1	1	0	0	0	0	0	0
PRH1	0	0	0	0	0	1	0
PRIM1	1	0	1	0	0	0	0
PRKAG2	0	0	0	0	0	1	1
PRKAR2B	1	0	0	0	0	0	0
PRKCD	1	0	0	0	0	0	0
PRKCE	1	0	0	0	0	0	0
PRKD1	0	0	0	0	0	1	0
PRKD2	0	0	0	0	0	1	0
PRKD3	1	0	0	0	0	0	0
PRKG2	1	0	0	0	0	0	0
PRKN	0	0	0	0	0	1	0
PRKRA	1	0	1	0	0	0	0
PRL	1	0	0	0	0	1	0
PRMT2	1	0	0	0	0	0	0
PROK2	1	0	0	0	0	0	0
PROS1	1	0	0	0	0	0	0
PROX1	1	0	0	0	0	1	0
PROZ	1	0	0	0	0	0	0
PRPF40B	1	0	0	0	0	0	0
PRR19	1	0	0	0	0	0	0
PRRT1	1	0	0	0	0	0	0
PRRX1	1	1	1	0	1	1	0
PRSS27	0	0	0	0	0	1	0
PRSS48	1	0	0	0	0	0	0
PSD	1	0	1	0	0	0	0
PSD2	1	0	0	0	0	0	0
PSD4	0	0	0	0	0	1	0
PSEN1	1	0	0	0	0	0	0
PSG7	1	0	0	0	0	0	0
PSMA1	1	0	0	0	0	0	0
PSMB10	0	0	0	0	0	1	0
PSMB3P	0	0	0	0	1	0	0
PSMB7	0	0	1	1	1	1	0
PSMC1P5	0	0	0	0	1	0	0
PSMD2	1	0	0	0	0	0	0
PSMD3	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
PSME4	1	0	0	0	0	0	0
PSMF1	0	0	0	0	0	1	0
PSMG1	1	0	0	0	0	1	0
PSORS1C1	1	0	0	0	0	1	0
PSPH	1	0	0	0	0	0	0
PSRC1	0	0	0	0	0	1	0
PTCD2	1	0	0	0	0	0	0
PTCD3	1	0	0	0	0	0	0
PTCH1	0	0	0	0	0	0	1
PTEN	0	0	0	0	0	0	1
PTER	0	0	0	0	0	1	0
PTGDS	0	0	0	0	0	1	0
PTGES3	0	0	0	0	1	0	0
PTGS1	0	0	0	0	0	1	0
PTGS2	0	0	0	0	0	1	0
PTH	0	0	0	0	0	1	0
PTH1R	1	0	0	0	0	0	0
PTK2	1	0	1	1	1	1	1
PTLS	0	0	0	0	0	0	1
PTP4A1	1	0	0	0	0	0	0
PTP4A2	1	0	0	0	0	0	0
PTPN11	0	0	0	0	0	1	1
PTPN12	1	0	0	0	0	0	0
PTPN22	1	0	0	0	0	0	0
PTPN9	1	0	0	0	0	0	0
PTPRA	1	0	0	0	0	0	0
PTPRC	0	0	0	0	0	1	0
PTPRG	0	0	0	0	0	1	0
PTPRN	1	0	0	0	0	0	0
PTPRU	1	0	0	0	0	1	0
PTPRZ1	1	0	0	0	0	0	0
PTRH1	1	0	0	0	0	0	0
PTS	0	0	0	0	0	1	0
PTX3	1	0	0	0	0	0	0
PUM2	1	0	0	0	0	0	0
PURA	1	0	0	0	0	0	0
PVALB	1	0	0	0	0	0	0
PVOD1	0	0	0	0	0	0	1
PVR	0	0	0	0	0	1	0
PXE	0	0	0	0	0	0	1
PXK	1	0	0	0	0	0	0
PXN	1	0	0	1	0	0	0
PYCR2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
PYGO2	1	1	1	0	0	0	0
QPCT	1	0	0	0	0	0	0
QSOX2	1	0	0	0	0	0	0
RAB10	1	0	0	0	0	0	0
RAB11B	1	0	0	0	0	0	0
RAB11FIP3	1	0	0	0	0	0	0
RAB12	0	0	0	0	0	1	0
RAB17	1	0	0	0	0	0	0
RAB1A	1	1	1	0	0	0	0
RAB25	1	0	0	0	0	0	0
RAB26	1	0	0	0	0	0	0
RAB40C	1	0	0	0	0	0	0
RAB8B	1	0	0	0	0	0	0
RABAC1	1	0	0	0	0	0	0
RABEP2	1	0	0	0	0	0	0
RABGEF1	1	0	0	0	0	0	0
RACGAP1	1	0	0	0	0	0	0
RAF1	1	0	1	0	0	0	1
RAI	0	0	0	0	0	0	1
RALA	1	0	0	0	0	0	0
RANP6	0	0	0	0	1	0	0
RAPGEF5	0	0	0	0	0	1	0
RARRES2	0	0	0	0	0	1	0
RARS2	1	0	0	0	0	0	0
RASA1	0	0	0	0	0	1	0
RASA2	1	0	0	0	0	0	0
RASAL1	1	0	0	0	0	0	0
RASGRP2	1	0	0	0	0	0	0
RASL10B	0	0	0	0	0	0	1
RASL12	0	0	0	0	0	1	0
RAVER1	1	0	0	0	0	0	0
RBBP5	1	0	0	0	0	0	0
RBM10	0	0	0	0	0	0	1
RBM20	0	0	0	1	1	1	0
RBM24	1	0	0	0	0	0	0
RBM25	1	0	0	0	0	0	0
RBM43	1	0	0	0	0	0	0
RBM4B	1	0	0	0	0	0	0
RBMS2	1	0	0	0	0	0	0
RBPMS	0	0	0	0	0	1	0
RBS	0	0	0	0	0	0	1
RCAN1	1	0	0	0	0	0	0
RCDP1	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
RCM1	0	0	0	0	0	0	1
RCM3	0	0	0	0	0	0	1
RCN1P1	0	0	0	0	1	0	0
RCN2	1	0	0	0	0	0	0
RDX	1	0	0	0	0	0	0
RECQL5	1	0	0	0	0	0	0
REEP1	1	0	0	1	1	1	0
REEP2	1	0	1	0	0	0	0
REEP3	0	0	1	1	1	1	0
REEP4	1	0	0	0	0	0	0
REEP5	1	0	0	0	0	0	0
REN	1	0	0	0	0	1	1
RENS1	0	0	0	0	0	0	1
RET	0	0	0	0	0	1	0
RETN	0	0	0	0	0	1	0
RFH1	0	0	0	0	0	0	1
RFMN	0	0	0	0	0	0	1
RFT1	1	0	0	0	0	0	0
RFTN1	0	0	0	0	0	1	0
RFTN2	1	0	0	0	0	0	0
RFX1	1	0	0	0	0	0	0
RFX4	1	0	0	0	0	0	0
RGS3	1	0	0	0	0	0	0
RGS4	0	0	0	0	0	1	0
RGS6	0	0	0	0	0	1	0
RHBDF2	1	0	0	0	0	0	0
RHBDL1	1	0	0	0	0	0	0
RHBDL2	1	0	0	0	0	0	0
RHBG	1	0	0	0	0	0	0
RHD	0	0	0	0	0	1	0
RHOA	0	0	0	0	0	1	0
RHOB	1	0	0	0	0	0	0
RHOBTB1	1	0	0	0	0	0	0
RHOD	1	0	0	0	0	0	0
RHOJ	0	0	0	0	0	1	0
RHOT2	1	0	0	0	0	0	0
RHPD1	0	0	0	0	0	0	1
RHPD2	0	0	0	0	0	0	1
RIC3	1	0	0	0	0	0	0
RIEG3	0	0	0	0	0	0	1
RIMKLB	1	0	0	0	0	0	0
RIMS3	1	0	0	0	0	0	0
RIN1	1	0	0	0	0	0	0
RIT1	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
RN7SKP155	0	0	0	0	1	0	0
RN7SL728P	0	0	0	0	1	0	0
RN7SL734P	0	0	0	0	1	0	0
RNASEH2B	1	0	0	0	0	0	0
RNF10	1	0	0	0	0	0	0
RNF103	1	0	0	0	0	0	0
RNF11	1	0	0	0	0	0	0
RNF144B	1	0	1	0	0	0	0
RNF212	1	0	0	0	0	0	0
RNF6	1	0	0	0	0	0	0
RNH1	0	0	0	0	0	1	0
RNLS	0	0	0	0	0	1	0
RNPEP	0	0	0	0	0	1	0
RNU1-18P	0	0	0	0	1	0	0
RNU6-1148P	0	0	0	0	1	0	0
RNU6-289P	0	0	0	1	1	0	0
RNU6-745P	0	0	0	1	1	0	0
RNU7-2P	0	0	0	0	1	0	0
ROBO1	1	0	0	0	0	0	0
ROCK1	0	0	0	0	0	1	0
ROCK2	0	0	0	0	0	1	0
RORC	1	0	0	0	0	0	0
ROS1	0	0	0	0	0	1	0
RP9	1	0	0	0	0	0	0
RPE	0	0	0	0	0	1	0
RPL12P6	0	0	0	0	1	0	0
RPL13AP24	0	0	0	0	1	0	0
RPL17	0	0	0	0	0	1	0
RPL35P2	0	0	0	0	1	0	0
RPL36AP23	0	0	0	1	1	0	0
RPL3L	1	0	0	1	1	1	0
RPL7AP73	0	0	0	0	1	0	0
RPLP0	0	0	0	0	0	1	0
RPLP1	0	0	0	0	0	1	0
RPRML	1	0	0	0	0	0	0
RPS15A	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
RPS17	0	0	0	0	0	0	1
RPS2	1	0	1	0	1	0	0
RRAD	0	0	0	0	0	1	0
RRAGC	1	0	0	0	0	0	0
RRBP1	0	0	0	0	0	1	0
RREB1	1	0	0	0	0	0	0
RRM1	1	0	0	0	0	1	0
RRM2	0	0	0	0	0	1	0
RRP12	1	0	0	0	0	0	0
RRS	0	0	0	0	0	0	1
RSBN1	0	0	0	0	0	1	0
RSBN1L	1	0	0	0	0	0	0
RSC1A1	1	0	0	0	0	0	0
RSPH6A	1	0	0	0	0	0	0
RSTS1	0	0	0	0	0	0	1
RTN3	1	0	0	0	0	0	0
RTSC1	0	0	0	0	0	0	1
RTSC2	0	0	0	0	0	0	1
RUNX1	1	0	0	0	0	0	0
RUNX3	1	0	0	0	0	0	0
RUSC1	1	0	0	0	0	0	0
RWDD3	0	0	0	0	0	1	0
RXFP4	1	0	0	0	0	0	0
RXRA	0	0	0	0	0	1	1
RYBP	1	0	0	0	0	0	0
RYR2	0	0	0	0	0	1	1
S100A13	1	0	0	0	0	0	0
S100A14	1	0	0	0	0	0	0
S100A16	1	0	0	0	0	0	0
S100B	0	0	0	0	0	1	0
S1PR2	1	0	0	0	0	0	1
S1PR3	0	0	0	0	0	0	1
SACS	1	0	0	0	0	0	0
SALL1	0	0	0	0	0	1	0
SALL4	0	0	0	0	0	1	0
SALMY	0	0	0	0	0	0	1
SAMD4A	1	0	0	0	0	0	0
SAMD8	1	0	0	0	0	0	0
SAMM50	1	0	0	0	0	0	0
SATB1	1	0	0	0	0	0	0
SATB2	1	0	0	0	0	1	0
SBNO1	0	0	0	0	0	1	0
SBNO2	1	0	0	0	0	0	0
SCA18	0	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SCAMP3	1	0	0	0	0	0	0
SCAMP4	1	0	0	0	0	0	0
SCAPER	1	0	0	0	0	0	0
SCARA3	0	0	0	0	0	1	0
SCARB1	0	0	0	0	0	1	0
SCD	0	0	0	0	0	1	0
SCD5	1	0	0	0	0	0	0
SCDO1	0	0	0	0	0	0	1
SCG5	1	0	0	0	0	0	0
SCGN	0	0	0	0	0	1	0
SCHIP1	1	0	0	0	0	0	0
SCKL9	0	0	0	0	0	0	1
SCLT1	0	0	0	0	0	0	1
SCLY	1	0	0	0	0	0	0
SCMH1	1	0	0	1	1	1	0
SCN10A	1	0	1	1	1	1	0
SCN11A	0	0	0	0	0	1	0
SCN1A	0	0	0	0	0	1	0
SCN1B	0	0	0	0	0	0	1
SCN2A	0	0	0	0	0	1	0
SCN2B	0	0	0	0	0	1	1
SCN3A	0	0	0	0	0	1	0
SCN3B	0	0	0	0	0	1	1
SCN4	0	0	0	0	0	0	1
SCN4A	0	0	0	0	0	1	0
SCN4B	0	0	0	0	0	1	1
SCN5A	1	0	1	1	1	1	1
SCN7A	0	0	0	0	0	1	0
SCN8A	0	0	0	0	0	1	0
SCN9A	0	0	0	0	0	1	0
SCRN3	1	0	0	0	0	0	0
SCT	0	0	0	0	0	1	0
SCUBE3	1	0	0	0	0	0	0
SCYL1	1	0	0	0	0	0	0
SCYL3	1	0	0	0	0	0	0
SDC1	0	0	0	0	0	1	0
SDC2	1	0	0	0	0	0	0
SDC4	0	0	0	0	0	1	0
SDCCAG8	1	0	0	0	0	0	0
SDDHD	0	0	0	0	0	0	1
SDK1	1	0	0	0	0	0	0
SEC14L2	1	0	0	0	0	0	0
SEC22B	1	0	0	0	0	0	0
SEC24C	0	1	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SEC31A	0	1	1	0	0	0	0
SEC61A1	1	0	0	0	0	0	0
SELE	1	0	0	0	0	1	0
SELENBP1	1	0	0	0	0	0	0
SELL	1	0	0	0	0	0	0
SELP	1	0	0	0	0	1	0
SEMA3A	0	0	0	0	0	0	1
SEMA4D	0	0	0	0	0	1	0
SEMA5B	0	0	0	0	1	1	0
SEMA6D	1	0	0	0	0	0	0
SEMDJL1	0	0	0	0	0	0	1
SEMDJL2	0	0	0	0	0	0	1
SEMDK	0	0	0	0	0	0	1
SENP2	0	0	0	0	0	1	0
SENP3	1	0	1	0	0	0	0
SEPT1	1	0	0	0	0	0	0
SEPT14	1	0	0	0	0	0	0
SEPT4	1	0	0	0	0	0	0
SEPT5	1	0	0	0	0	0	0
SERINC1	1	0	0	0	0	0	0
SERPINA2	0	0	0	0	0	1	0
SERPINA4	0	0	0	0	0	1	0
SERPINA5	1	0	0	0	0	1	0
SERPINB1	1	0	0	0	0	0	0
SERPINB10	1	0	0	0	0	0	0
SERPINB3	1	0	0	0	0	0	0
SERPINC1	0	0	0	0	0	1	0
SERPINE1	1	0	0	0	0	1	0
SERPINF2	1	0	0	0	0	1	0
SERTAD4	1	0	0	0	0	0	0
SESN3	1	0	0	0	0	0	0
SETD7	1	0	0	0	0	0	0
SF3B1	1	0	0	0	0	0	0
SFMBT1	1	0	0	0	0	0	0
SFRP5	0	0	0	0	0	1	0
SFXN2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SFXN4	1	0	0	0	0	0	0
SGCA	0	0	0	0	0	1	0
SGCG	0	0	0	1	0	1	0
SGMS1	1	0	0	0	0	0	0
SGOL1	0	0	0	0	0	0	1
SGPL1	1	0	0	0	0	0	0
SGS	0	0	0	0	0	0	1
SH2D3C	1	0	0	0	0	0	0
SH3BGR	1	0	0	0	0	0	0
SH3BP5	0	0	0	0	0	1	0
SH3PXD2A	1	1	1	1	1	1	0
SHAPNS	0	0	0	0	0	0	1
SHBG	1	0	0	0	0	1	0
SHC1	1	1	1	0	0	0	0
SHC4	1	0	0	0	0	0	0
SHD	0	0	0	0	0	1	0
SHDRA	0	0	0	0	0	0	1
SHLD1	0	0	0	0	0	1	0
SHOX2	0	0	0	0	0	1	0
SHROOM3	1	0	0	0	0	0	0
SIAH2	1	0	0	0	0	0	0
SIDT1	1	0	0	0	0	0	0
SIDT2	1	0	0	0	0	0	0
SIK1	1	0	0	0	0	0	0
SIK3	1	0	0	0	1	1	0
SIN3A	1	0	0	0	0	0	0
SIRT1	1	0	0	1	1	1	0
SIX4	1	0	0	0	0	0	0
SKAP2	0	0	0	0	0	1	0
SKS	0	0	0	0	0	0	1
SLC11A2	1	0	0	0	0	0	0
SLC12A2	1	0	0	0	0	0	0
SLC12A7	1	0	0	0	0	0	0
SLC12A8	1	0	0	0	0	0	0
SLC14A1	1	0	0	0	0	0	0
SLC16A1	0	0	0	0	0	0	1
SLC16A10	1	0	0	0	0	0	0
SLC17A5	1	0	0	0	0	1	0
SLC18A2	0	0	0	0	0	1	0
SLC19A1	0	0	0	0	0	1	0
SLC19A2	0	0	0	0	0	0	1
SLC1A2	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SLC1A4	1	0	1	0	0	0	0
SLC1A6	1	0	0	0	0	0	0
SLC22A12	1	0	0	0	0	0	0
SLC22A14	1	0	0	0	0	0	0
SLC22A17	0	0	1	0	0	0	0
SLC22A23	0	0	0	0	0	1	0
SLC22A25	0	0	0	0	0	1	0
SLC22A4	0	0	0	0	0	1	0
SLC24A2	0	0	0	0	1	0	0
SLC25A10	0	0	0	0	0	1	0
SLC25A15	1	0	0	0	0	0	0
SLC25A26	0	0	0	0	1	1	0
SLC25A34	1	0	0	0	0	0	0
SLC25A36	0	0	0	0	0	1	0
SLC25A37	1	0	0	0	0	0	0
SLC26A1	1	0	0	0	0	0	0
SLC26A4	1	0	0	0	0	0	0
SLC27A3	1	0	0	0	0	0	0
SLC27A6	1	0	0	1	0	1	0
SLC29A4	1	0	0	0	0	0	0
SLC2A11	1	0	0	0	0	0	1
SLC2A2	0	0	0	0	0	1	0
SLC2A4	1	0	0	0	0	0	1
SLC30A1	0	0	0	0	0	1	0
SLC30A3	0	0	0	0	1	1	0
SLC30A5	0	0	0	0	0	1	0
SLC33A1	0	0	0	0	0	1	0
SLC35A4	1	0	0	0	0	0	0
SLC35D2	1	0	0	0	0	0	0
SLC35F1	0	0	0	1	1	1	0
SLC41A1	1	0	0	0	0	0	0
SLC44A4	1	0	0	0	0	0	0
SLC44A5	1	0	0	0	0	0	0
SLC45A1	0	0	0	0	0	1	0
SLC45A3	1	0	0	0	0	0	0
SLC48A1	1	0	0	0	0	0	0
SLC4A1	1	0	0	0	0	0	0
SLC4A10	1	0	0	0	0	0	0
SLC4A3	0	0	0	0	0	1	0
SLC4A4	1	0	0	0	0	0	0
SLC4A7	1	0	0	0	0	1	0
SLC4A9	1	0	0	0	0	0	0
SLC6A1	0	0	0	0	0	1	0
SLC7A10	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SLC7A11	0	0	0	0	0	1	0
SLC8A1	0	0	0	0	0	0	1
SLC9A1	0	0	0	0	0	1	0
SLC9A3R2	1	0	0	0	0	0	0
SLC9B1	0	0	0	1	1	1	0
SLCO1B1	0	0	0	0	0	1	0
SLCO1B3	0	0	0	0	0	1	0
SLCO4A1	0	0	0	0	0	1	0
SLFNL1	1	0	0	0	0	0	0
SLIT3	1	0	0	1	1	0	0
SLK	1	0	0	0	0	0	0
SLMAP	1	0	0	0	0	0	0
SLN	0	0	0	0	0	1	0
SLOS	0	0	0	0	0	0	1
SLURP1	0	0	0	0	0	1	0
SMA1	0	0	0	0	0	0	1
SMA2	0	0	0	0	0	0	1
SMA3	0	0	0	0	0	0	1
SMABF1	0	0	0	0	0	0	1
SMAD1	0	0	0	0	0	1	0
SMAD2	0	0	0	0	0	1	1
SMAD3	1	0	0	0	0	1	0
SMAD4	0	0	0	0	1	0	0
SMAD6	1	0	0	0	0	0	0
SMAD7	1	0	0	1	1	1	0
SMARCA5	1	0	0	0	0	0	0
SMARCAD1	1	0	0	0	0	0	0
SMARCB1	1	0	0	0	0	0	0
SMAX1	0	0	0	0	0	0	1
SMC3	1	0	0	0	0	0	0
SMC5	1	0	0	0	0	0	0
SMDMDM	0	0	0	0	0	0	1
SMDP3	0	0	0	0	0	0	1
SMDS	0	0	0	0	0	0	1
SMG5	1	0	0	0	0	0	0
SMG6	1	0	0	0	0	0	0
SMG7	1	0	0	0	0	0	0
SMIM29	0	0	0	0	0	1	0
SMOX	1	0	0	0	0	0	0
SMPD2	1	0	0	0	0	0	0
SMPDL3A	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SMTN	1	0	0	0	0	0	0
SMTNL2	1	0	0	0	0	0	0
SNAP25	0	0	0	0	0	1	0
SNAPIN	1	0	0	0	0	0	0
SND1	1	0	0	0	0	0	0
SNRNP27	1	1	1	0	1	1	0
SNRPB	0	0	0	0	0	0	1
SNTA1	0	0	0	0	0	1	0
SNTB1	0	0	0	0	0	1	0
SNTB2	1	0	0	0	0	0	0
SNTG1	1	0	0	0	0	0	0
SNX19	1	0	0	0	0	0	0
SNX22	1	0	0	0	0	0	0
SNX27	1	0	0	0	0	0	0
SNX33	1	0	0	0	0	0	0
SOAT1	0	0	0	0	0	1	0
SOCS1	1	0	0	0	0	0	0
SOCS2	1	0	0	0	0	0	0
SOCS3	1	0	0	0	0	0	0
SOD1	0	0	0	0	0	1	0
SORBS2	0	0	0	0	0	1	0
SORL1	0	0	0	1	1	1	0
SOS	0	0	0	0	0	0	1
SOS1	0	0	0	0	0	0	1
SOTOS1	0	0	0	0	0	0	1
SOX1	1	0	0	0	0	0	0
SOX15	1	0	1	0	0	0	0
SOX5	1	0	1	1	1	1	0
SP4	0	0	0	0	0	1	0
SP8	1	0	0	0	0	0	0
SP9	1	0	0	0	0	0	0
SPAG4	1	0	0	0	0	0	0
SPARC	1	0	0	0	0	0	0
SPAST	1	0	0	0	0	0	0
SPATA16	1	0	0	0	0	0	0
SPATA17	1	0	0	0	0	0	0
SPATA5	1	0	0	0	0	1	0
SPATC1L	0	0	0	0	0	1	0
SPATS2L	0	0	1	1	1	1	0
SPEM1	0	0	1	0	0	0	0
SPEN	1	0	0	0	0	0	0
SPHK1	1	0	0	0	0	0	0
SPNS1	1	0	0	0	0	0	0
SPOCK1	1	0	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
SPON1	1	0	0	0	0	0	0
SPON2	1	0	0	0	0	0	0
SPP1	0	0	0	0	0	1	0
SPPL2A	0	0	0	0	0	1	0
SPRED2	1	0	0	0	0	0	0
SPRY1	1	0	0	0	0	0	0
SPSB3	1	0	0	0	0	0	0
SPTB	1	0	0	0	0	0	0
SPTBN2	1	0	0	0	0	0	0
SPTBN5	1	0	0	0	0	0	0
SQT1	0	0	0	0	0	0	1
SQT2	0	0	0	0	0	0	1
SQT3	0	0	0	0	0	0	1
SRF	0	0	0	0	0	0	1
SRFBP1	0	0	0	0	0	0	1
SRGAP1	1	0	0	0	0	0	0
SRI	0	0	0	0	0	1	0
SRL	1	0	0	0	0	0	0
SRM	0	0	0	0	0	1	0
SRR	1	0	0	0	0	0	0
SRSF10P1	0	0	0	0	1	0	0
SRTD14	0	0	0	0	0	0	1
SRTD6	0	0	0	0	0	0	1
SSPN	1	0	0	1	1	1	0
SSR2	1	0	0	0	0	0	0
SSS1	0	0	0	0	0	0	1
SSS2	0	0	0	0	0	0	1
SST	0	0	0	0	0	1	0
ST13	0	0	0	0	0	1	0
ST3GAL4	0	0	0	0	0	1	0
ST8SIA4	0	0	0	0	0	1	0
STAC2	1	0	0	0	0	0	0
STAG1	1	0	0	0	0	0	0
STAP2	0	0	0	0	0	1	0
STARD3	1	0	0	0	0	0	0
STAT1	0	0	0	0	0	1	0
STAT2	1	0	0	0	0	0	0
STAT3	0	0	0	0	0	1	0
STAT5A	1	0	0	0	0	0	0
STH	1	0	0	0	0	0	0
STIM1	1	0	0	0	0	0	0
STK11	1	0	0	0	0	1	0
STK16	1	0	0	0	0	0	0
STK19	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
STOM	1	0	0	0	0	0	0
STOX1	1	0	0	0	0	0	0
STRA6	0	0	0	0	0	0	1
STS	0	0	0	0	0	1	0
STUB1	1	0	0	0	0	0	0
STX17	1	0	0	0	0	0	0
STX19	1	0	0	0	0	0	0
STXBP4	1	0	0	0	0	0	0
STYX	1	0	0	0	0	0	0
SUFU	1	0	0	0	0	0	0
SUGP1	0	0	0	0	1	1	0
SULF2	0	0	0	0	0	1	0
SULT1E1	0	0	0	0	0	1	0
SUMF2	1	0	0	0	0	0	0
SUN1	0	0	0	1	1	1	0
SV2A	1	0	0	0	0	0	0
SYK	0	0	0	0	1	1	0
SYMPK	1	0	0	0	0	0	0
SYNE1	0	0	0	0	0	1	0
SYNE2	0	0	1	1	1	1	0
SYNGR1	1	0	0	0	0	0	0
SYNGR2	1	0	0	0	0	0	0
SYNGR3	1	0	0	0	0	0	0
SYNGR4	1	0	0	0	0	0	0
SYNPO2L	1	0	1	1	1	1	0
SYT12	1	0	0	0	0	0	0
TAB2	0	0	0	0	0	0	1
TAC1	0	0	0	0	0	1	0
TAF11	1	0	0	0	0	0	0
TAF5	1	0	0	0	0	0	0
TAGLN3	1	0	1	0	0	0	0
TAPVR1	0	0	0	0	0	0	1
TAR	0	0	0	0	0	0	1
TARPS	0	0	0	0	0	0	1
TARS2	1	0	0	0	0	0	0
TBC1D10A	1	0	0	0	0	0	0
TBC1D10B	1	0	0	0	0	0	0
TBC1D24	1	0	0	0	0	0	0
TBC1D32	0	0	0	0	0	0	1
TBCB	1	0	0	0	0	0	0
TBHS	0	0	0	0	0	0	1
TBL3	1	0	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TBP	0	0	0	0	0	1	0
TBPL1	1	0	0	0	0	0	0
TBRS	0	0	0	0	0	0	1
TBX1	0	0	0	0	0	0	1
TBX18	0	0	0	0	0	0	1
TBX20	1	0	0	0	0	0	1
TBX3	1	0	0	0	1	1	1
TBX5	1	1	1	1	1	1	1
TBX6	0	0	0	0	0	0	1
TCAP	1	0	0	0	0	0	0
TCEA3	1	0	0	0	0	0	0
TCF19	1	0	0	0	0	0	0
TCF21	1	0	0	0	0	0	0
TCF7L2	0	0	0	0	1	1	0
TCFL5	0	0	0	0	0	1	0
TCHHL1	0	0	0	0	0	1	0
TCN1	1	0	0	0	0	0	0
TCP1	0	0	0	0	0	1	0
TCP11L2	1	0	0	0	0	0	0
TDRD1	1	0	0	0	0	0	0
TDRD10	1	0	0	0	0	0	0
TDRD15	0	0	0	0	1	1	0
TDRD7	1	0	0	0	0	0	0
TDRKH	1	0	0	0	0	0	0
TEAD1	1	0	0	0	0	0	0
TEAD3	1	0	0	0	0	0	0
TEAD4	0	0	0	0	1	0	0
TEMTYS	0	0	0	0	0	0	1
TERF2	1	0	0	0	0	0	0
TES	1	0	0	0	0	0	0
TET1	0	0	0	0	0	1	0
TEX12	1	0	0	0	0	0	0
TEX41	0	0	0	1	1	0	0
TFAP2A	0	0	0	0	0	0	1
TFAP2C	1	0	0	0	0	0	0
TFAP4	1	0	0	0	0	0	0
TFDP1	1	0	0	0	0	0	0
TFEC	1	0	0	0	0	0	0
TFPI	0	0	0	0	0	1	0
TFRC	0	0	0	0	0	1	0
TG	0	0	0	0	0	1	0
TGFB1	1	0	0	0	0	1	0
TGFB3	0	0	0	0	0	0	1
TGFBR1	1	0	0	0	0	0	1

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TGFBR2	0	0	0	0	0	1	0
TGFBRAP1	1	0	0	0	0	0	0
TGM2	1	0	0	0	0	0	0
TH	0	0	0	0	0	1	0
THAP10	1	0	0	0	0	0	0
THAP3	1	0	0	0	0	0	0
THAP8	1	0	0	0	0	0	0
THAP9	1	1	1	0	0	0	0
THBD	0	0	0	0	0	1	0
THBS3	1	0	0	0	0	0	0
THEMIS3P	0	0	0	0	1	0	0
THRA	1	1	0	0	0	1	0
THRB	1	0	0	1	1	1	1
THYN1	1	0	0	0	0	0	0
TIA1	0	0	0	0	0	1	0
TIIAC	0	0	0	0	0	0	1
TIMM50	1	0	0	0	0	0	0
TIMP1	0	0	0	0	0	1	0
TIMP2	0	0	0	0	0	1	0
TIMP3	0	0	0	0	0	1	0
TIMP4	0	0	0	0	0	1	0
TIPARP	1	0	0	0	0	0	0
TJP2	1	0	0	0	0	0	0
TK2	0	0	0	0	0	0	1
TKTL1	0	0	0	0	0	1	0
TLE2	1	0	0	0	0	0	0
TLE3	1	0	0	0	0	1	0
TLE6	1	0	0	0	0	0	0
TLL1	0	0	0	0	0	0	1
TLR2	0	0	0	0	0	1	0
TLR4	0	0	0	0	0	1	0
TLR6	1	0	0	0	0	0	0
TLX1NB	0	0	0	0	0	1	0
TLX2	0	0	0	0	0	1	0
TMBIM6	1	0	0	0	0	0	0
TMC8	1	0	0	0	0	0	0
TMCC1	1	0	0	0	0	0	0
TMCC2	1	0	0	0	0	0	0
TMCO3	1	0	0	0	0	0	0
TMCO6	1	0	0	0	0	0	0
TMED6	1	0	0	0	0	0	0
TMEM102	1	0	1	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TMEM135	1	0	0	0	0	0	0
TMEM144	1	0	0	0	0	0	0
TMEM145	1	0	0	0	0	0	0
TMEM160	1	0	0	0	0	0	0
TMEM171	1	0	0	0	0	0	0
TMEM173	1	0	0	0	0	0	0
TMEM176B	1	0	0	0	0	0	0
TMEM18	1	0	0	0	0	0	0
TMEM183A	1	0	1	0	0	0	0
TMEM189	1	0	0	0	0	0	0
TMEM203	0	0	0	0	0	1	0
TMEM256	0	0	0	0	0	1	0
TMEM256-PLSCR3	0	0	0	0	0	1	0
TMEM40	1	0	1	0	0	0	0
TMEM43	0	0	0	0	0	0	1
TMEM44	1	0	0	0	0	0	0
TMEM60	1	0	1	0	0	0	0
TMEM65	0	0	0	0	0	0	1
TMEM79	1	0	0	0	0	0	0
TMEM87B	0	0	0	0	0	0	1
TMEM91	1	0	0	0	0	0	0
TMEM95	1	0	0	0	0	0	0
TMEM9B	1	0	0	0	0	0	0
TMF1	1	0	0	0	0	0	0
TMIE	1	0	0	0	0	0	0
TMPO	0	0	0	0	0	0	1
TMPRSS2	0	0	0	0	1	1	0
TMUB2	1	0	0	0	0	0	0
TNC	0	0	0	0	0	0	1
TNF	1	0	0	0	0	1	0
TNFRSF11B	0	0	0	0	0	1	0
TNFRSF12A	0	0	0	0	0	0	1
TNFRSF13B	0	0	0	0	0	1	0
TNFRSF1A	0	0	0	0	0	1	0
TNFRSF1B	0	0	0	0	0	1	0
TNFSF11	0	0	0	0	0	1	0
TNFSF12	0	0	0	1	1	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TNFSF12-TNFSF13	1	0	1	0	1	0	0
TNFSF13	0	0	0	0	0	1	0
TNIP1	1	0	0	0	0	0	0
TNK1	1	0	0	0	0	0	0
TNK2	1	0	0	0	0	0	0
TNNC1	0	0	0	0	0	0	1
TNNI1	0	0	0	0	0	1	0
TNNI2	0	0	0	0	0	0	1
TNNI3	0	0	0	0	0	1	1
TNNI3K	1	0	0	0	0	0	1
TNNT2	0	0	0	0	0	1	1
TNNT3	1	0	0	0	0	0	0
TNPO1	1	0	0	0	0	1	0
TNRC6C	1	0	0	0	0	0	0
TNXB	1	0	0	0	0	1	0
TOB1	0	0	0	0	0	1	0
TOF	0	0	0	0	0	0	1
TOP2B	1	0	0	0	0	0	0
TOPBP1	1	0	0	0	0	0	0
TOR3A	1	0	0	0	0	0	0
TOX2	1	0	0	0	0	0	0
TP53	1	0	0	0	0	0	0
TP53AIP1	1	0	1	0	0	0	0
TP63	0	0	0	0	0	1	0
TPCN1	1	0	0	0	0	0	0
TPCN2	1	0	0	0	0	0	0
TPR	0	0	0	0	0	1	0
TPRKB	1	0	0	0	0	0	0
TRADD	0	0	0	0	0	1	0
TRAF5	1	0	0	0	0	0	0
TRAF6	0	0	0	0	0	1	0
TRAF7	1	0	0	0	0	0	0
TRAK1	1	0	0	0	0	0	0
TRAK2	1	0	0	0	0	0	0
TRAM2	1	0	0	0	0	0	0
TRAPPC9	0	0	0	0	0	1	0
TRDN	0	0	0	0	0	0	1
TRH	1	0	0	0	0	1	0
TRIB1	0	0	0	0	1	1	0
TRIM13	1	0	0	0	0	0	0
TRIM27	1	0	0	0	0	0	0
TRIM35	1	0	0	0	0	0	0
TRIM37	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TRIM46	1	0	0	0	0	0	0
TRIM55	0	0	0	0	0	1	0
TRIM58	1	0	0	0	0	0	0
TRIM62	1	0	0	0	0	0	0
TRIM72	0	0	0	0	0	1	0
TRIM8	1	0	0	0	0	0	0
TRIML2	1	0	0	0	0	0	0
TRIP13	1	0	0	0	0	1	0
TRMA	0	0	0	0	0	0	1
TRMT5	1	0	0	0	0	0	0
TRPA1	0	0	0	0	0	1	0
TRP-AGG2-8	0	0	0	0	1	0	0
TRPC1	0	0	0	0	0	1	0
TRPC3	1	0	0	0	0	1	0
TRPC4	0	0	0	0	0	1	0
TRPC5	0	0	0	0	0	1	0
TRPC6	0	0	0	0	0	1	0
TRPM2	1	0	0	1	0	0	0
TRPM3	0	0	0	0	0	1	0
TRPM4	0	0	0	0	0	1	1
TRPM5	0	0	0	0	0	1	0
TRPM6	0	0	0	0	0	1	0
TRPM7	0	0	0	0	0	1	1
TRPM8	0	0	0	0	0	1	0
TRPV1	0	0	0	0	0	1	0
TRPV2	0	0	0	0	0	1	0
TRPV3	0	0	0	0	0	1	0
TRPV4	0	0	0	0	0	1	0
TRPV5	0	0	0	0	0	1	0
TRPV6	0	0	0	0	0	1	0
TS	0	0	0	0	0	0	1
TSBP1	0	0	0	0	0	1	0
TSC1	0	0	0	0	0	0	1
TSC2	1	0	1	0	0	0	0
TSC22D2	1	0	0	0	0	0	0
TSHR	0	0	0	0	0	1	0
TSNARE1	1	0	0	0	0	0	0
TSPAN10	0	0	0	0	0	1	0
TSPAN13	1	0	0	0	0	0	0
TSPAN2	0	0	0	0	0	1	0
TSPAN32	1	0	0	0	0	0	0
TSPAN9	1	0	0	0	0	1	0
TTC12	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
TTC27	1	0	0	0	0	0	0
TTC29	1	0	0	0	0	0	0
TTC3	0	0	0	0	0	1	0
TTC39A	1	0	0	0	0	0	0
TTC9B	1	0	0	0	0	0	0
TTLL7	0	0	0	0	0	1	0
TTN	1	0	1	1	1	1	1
TTN-AS1	0	0	0	0	1	0	0
TTR	0	0	0	0	0	1	1
TTYH3	1	0	0	0	0	0	0
TUB	1	0	0	0	0	0	0
TUBA1A	0	0	0	0	0	1	0
TUBA1B	0	0	0	0	0	1	0
TUBA1C	0	0	0	0	0	1	0
TUBA3D	0	0	0	0	0	1	0
TUBA3E	0	0	0	0	0	1	0
TUBA4A	0	0	0	0	0	1	0
TUBA8	1	0	0	1	1	0	0
TUBB	0	0	0	0	0	1	0
TUBB1	0	0	0	0	0	1	0
TUBB2A	0	0	0	0	0	1	0
TUBB2B	0	0	0	0	0	1	0
TUBB3	0	0	0	0	0	1	0
TUBB4A	0	0	0	0	0	1	0
TUBB4B	0	0	0	0	0	1	0
TUBB6	0	0	0	0	0	1	0
TUBB8	0	0	0	0	0	1	0
TUBGCP6	1	0	0	0	0	0	0
TUFM	1	0	0	0	0	0	0
TUFT1	1	0	0	0	0	0	0
TULP1	1	0	0	0	0	0	0
TUSC2	1	0	0	0	0	0	0
TWF1	1	0	0	0	0	0	0
TXNDC5	1	0	0	0	0	0	0
TXNIP	0	0	0	0	0	1	0
TXNRD1	1	0	0	0	0	0	0
TXNRD2	0	0	0	0	0	1	0
TYK2	1	0	0	0	0	0	0
TYRO3	0	0	0	0	0	1	0
UBAC1	1	0	0	0	0	0	0
UBB	1	0	0	0	0	0	0
UBC	0	0	0	0	0	1	0
UBE2D3	0	0	1	0	0	0	0
UBE2D4	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
UBE2E1	1	0	0	0	0	0	0
UBE2F	1	0	0	0	0	0	0
UBE2G1	0	0	0	0	0	1	0
UBE2H	1	0	0	0	0	0	0
UBE2O	1	0	0	0	0	0	0
UBE2Q1	1	0	0	0	0	0	0
UBE3B	1	0	0	0	0	0	0
UBE4B	0	0	0	0	1	0	0
UBP1	1	0	0	0	0	0	0
UBQLN4	1	0	0	0	0	0	0
UBQLN4P1	0	0	0	1	0	0	0
UBR1	0	0	0	0	0	0	1
UBR5	0	0	0	0	0	1	0
UBTD2	1	0	0	0	0	0	0
UCHL1	1	0	0	0	0	0	0
UCN	0	0	0	0	0	1	0
UCN3	0	0	0	0	0	1	0
UGCG	1	0	0	0	0	1	0
UGDH	0	0	0	0	0	0	1
UHRF1	1	0	0	0	0	0	0
UHRF1BP1	1	0	0	0	0	0	0
UNC5CL	1	0	0	0	0	0	0
UQCRB	1	0	0	0	0	0	0
URGCP	1	0	0	0	0	0	0
URI1	0	0	0	0	0	1	0
USF2	1	0	0	0	0	0	0
USO1	1	0	0	0	0	0	0
USP18	1	0	0	0	0	0	0
USP3	1	0	0	0	1	1	0
USP31	0	0	0	0	0	1	0
USP34	1	0	1	1	1	0	0
USP36	1	0	0	0	0	0	0
USP54	1	0	0	0	0	0	0
UST	1	0	1	1	1	1	0
UTS2	0	0	0	0	0	1	0
UXS1	1	0	0	0	0	0	0
VACTERLX	0	0	0	0	0	0	1
VAMP2	0	0	0	0	0	1	0
VANGL1	0	0	1	0	0	0	0
VARS	1	0	0	0	0	0	0
VASP	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
VCAM1	0	0	0	0	0	1	0
VCPIP1	1	0	0	0	0	0	0
VCRL1	0	0	0	0	0	0	1
VDAC2	1	0	0	0	0	0	0
VEGFA	1	0	0	0	0	1	0
VEGFB	0	0	0	0	0	1	0
VEPH1	1	0	0	0	0	0	0
VETD	0	0	0	0	0	0	1
VF1	0	0	0	0	0	0	1
VF2	0	0	0	0	0	0	1
VGLL2	1	0	0	0	0	0	0
VGLL3	0	0	0	0	0	1	0
VGLL4	1	0	0	0	0	0	0
VILL	1	0	0	0	0	0	0
VIP	0	0	0	0	0	1	0
VKORC1	0	0	0	0	0	1	0
VKORC1L1	1	0	0	0	0	0	0
VODI	0	0	0	0	0	0	1
VPREB3	1	0	0	0	0	0	0
VPS13C	1	0	0	0	0	0	0
VPS25	1	0	0	0	0	0	0
VPS26B	1	0	0	0	0	0	0
VPS37B	1	0	0	0	0	0	0
VPS37D	0	0	0	0	1	0	0
VPS39	0	0	0	0	0	1	0
VPS51	0	0	0	0	0	1	0
VPS54	0	0	0	0	0	0	1
VRJS	0	0	0	0	0	0	1
VSD1	0	0	0	0	0	0	1
VSD3	0	0	0	0	0	0	1
VSIG8	0	0	0	0	0	1	0
VSX2	1	0	0	0	0	0	0
VTI1A	1	0	0	0	0	0	0
VWA2	1	0	0	0	0	0	0
VWCE	1	0	0	0	0	0	0
VWF	0	0	0	0	0	1	0
WAC	1	0	0	0	0	0	0
WBS	0	0	0	0	0	0	1
WDFY1	1	0	0	0	0	0	0
WDR1	0	0	1	1	1	1	0
WDR24	1	0	0	0	0	0	0
WDR25	1	0	0	0	0	0	0
WDR26	1	0	0	0	0	0	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
WDR27	1	0	0	0	0	0	0
WDR41	1	0	0	0	0	0	0
WDR55	1	0	0	0	0	0	0
WDR5B	1	0	0	0	0	0	0
WDR6	0	0	0	0	0	0	1
WDR62	1	0	0	0	0	0	0
WDR72	0	0	0	0	0	1	0
WDR73	1	0	0	0	0	0	0
WDR81	1	0	0	0	0	0	0
WDR90	1	0	0	0	0	0	0
WDR93	1	0	0	0	0	0	0
WDYHV1	1	0	0	0	0	0	0
WHS	0	0	0	0	0	0	1
WIPF1	1	0	1	1	1	1	0
WNK1	1	0	0	0	0	0	0
WNT3	1	0	0	1	1	0	0
WNT5A	1	0	0	0	0	0	0
WNT8A	1	1	1	1	1	1	0
WNT9A	1	0	0	0	0	0	0
WRAP53	1	0	0	0	0	0	0
WRB	1	0	0	0	0	0	0
WRN	0	0	0	0	0	1	0
WS3	0	0	0	0	0	0	1
WSS	0	0	0	0	0	0	1
WT1	1	0	0	0	0	0	0
WTAP	0	0	0	0	0	1	0
XBP1	1	0	0	0	0	0	1
XIRP1	0	0	0	0	0	1	0
XKR6	1	0	0	0	0	0	0
XPO1	1	0	1	0	1	1	0
XPO7	1	0	1	1	1	1	0
XRN2	1	0	0	0	0	0	0
XXYLT1	0	0	0	1	1	1	0
XYLB	1	0	0	0	0	0	0
YAP1	1	0	0	0	0	0	0
YARS2	1	0	0	0	0	0	0
YBX2	1	0	0	0	0	0	0
YIPF4	1	0	0	0	0	0	0
YME1L1	1	0	0	0	0	0	0
YPEL3	1	0	0	0	0	0	0
YWHAE	1	0	1	1	1	0	0
YWHAG	1	0	0	0	0	0	0
YWHAZ	0	0	0	0	0	1	0
YY1	0	0	0	0	0	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
YY1AP1	1	0	0	0	0	0	0
ZAK	0	0	0	0	0	0	1
ZBED1P1	0	0	0	0	1	0	0
ZBTB1	1	0	0	0	0	0	0
ZBTB12	1	0	0	0	0	0	0
ZBTB20	0	0	0	0	0	1	0
ZBTB25	1	0	0	0	0	0	0
ZBTB3	1	0	0	0	0	0	0
ZBTB38	0	0	0	1	0	0	0
ZBTB4	1	0	1	0	0	0	0
ZBTB46	1	0	0	0	0	0	0
ZBTB48	1	0	0	0	0	0	0
ZBTB7B	1	1	1	0	0	0	0
ZC3H11A	1	0	0	0	0	0	0
ZC3HC1	0	0	0	0	0	1	0
ZCCHC24	1	0	0	0	0	0	0
ZCCHC3	1	0	0	0	0	0	0
ZCCHC8	0	0	0	0	1	1	0
ZDHHC11	1	0	0	0	0	0	0
ZEB2	1	0	0	0	0	1	1
ZFAND3	1	0	0	0	0	1	0
ZFAT	0	0	0	0	0	1	0
ZFHX3	1	1	1	1	1	1	1
ZFHX4	1	0	0	0	0	0	0
ZFP36L1	1	0	0	0	0	1	0
ZFP42	1	0	0	0	0	0	0
ZFPM2	1	0	0	0	0	0	1
ZFYVE1	1	0	0	0	0	0	0
ZGLP1	1	0	0	0	0	1	0
ZGPAT	0	0	0	0	0	1	0
ZHX3	1	0	0	0	1	1	0
ZIC3	0	0	0	0	0	0	1
ZLS1	0	0	0	0	0	0	1
ZMIZ1	1	0	0	0	0	0	0
ZNF12	1	0	0	0	0	0	0
ZNF124	1	0	0	0	0	0	0
ZNF143	0	0	0	0	0	1	0
ZNF169	1	0	0	0	0	0	0
ZNF20	1	0	0	0	0	0	0
ZNF212	1	0	0	0	0	0	0
ZNF256	1	0	0	0	0	0	0
ZNF280B	1	0	0	0	0	0	0
ZNF280D	1	0	0	0	0	0	0
ZNF292	0	0	0	0	1	1	0

Gene	Multi-omics integration	Gene-based result from AFGen 2017 GWAS	Gene-based result from AFGen 2018 GWAS	Meta-analysis of SNPs by two large AF GWAS in 2018	GWAS catalog	Open Targets Platform	OMIM
ZNF362	1	0	0	0	0	0	0
ZNF366	1	0	0	0	0	0	0
ZNF367	1	0	0	0	0	0	0
ZNF395	1	0	0	0	0	0	0
ZNF414	1	0	0	0	0	0	0
ZNF417	1	0	0	0	0	0	0
ZNF418	1	0	0	0	0	0	0
ZNF436	1	0	0	0	0	0	0
ZNF460	1	0	0	0	0	0	0
ZNF462	1	0	0	1	1	1	0
ZNF48	1	0	0	0	0	0	0
ZNF526	1	0	0	0	0	0	0
ZNF574	1	0	0	0	0	0	0
ZNF587	1	0	0	0	0	0	0
ZNF598	1	0	0	0	0	0	0
ZNF606	1	0	0	0	0	0	0
ZNF619	1	0	0	0	0	0	0
ZNF620	1	0	0	0	0	0	0
ZNF641	1	0	0	0	0	0	0
ZNF653	1	0	0	0	0	0	0
ZNF664	1	0	1	0	0	0	0
ZNF689	1	0	0	0	0	0	0
ZNF7	1	0	0	0	0	0	0
ZNF70	1	0	0	0	0	0	0
ZNF713	1	0	0	0	0	0	0
ZNF737	1	0	0	0	0	0	0
ZNF767P	0	0	0	0	0	1	0
ZNF771	1	0	0	0	0	0	0
ZNF787	1	0	0	0	0	0	0
ZP4	0	0	0	0	0	1	0
ZPBP2	1	0	0	1	1	1	0
ZPR1	0	0	0	0	1	1	0
ZSCAN1	1	0	0	0	0	0	0
ZSCAN2	1	0	0	0	0	0	0
ZSCAN20	1	0	0	0	0	0	0
ZZEF1	1	0	0	0	0	0	0

Online Table VI. AF pathogensis genes and their functions.

Gene	Functions
KCNQ1	Potassium channel mutations
KCNE1	Potassium channel mutations
KCNE2	Potassium channel mutations
KCNE3	Potassium channel mutations
KCNE4	Potassium channel mutations
KCNE5	Potassium channel mutations
KCNH2	Potassium channel mutations
KCND3	Potassium channel mutations
KCNJ2	Potassium channel mutations
KCNJ5	Potassium channel mutations
KNCJ8	Potassium channel mutations
ABCC9	Potassium channel mutations
KCNA5	Potassium channel mutations
HCN4	Potassium channel mutations
KCNN3	Potassium channel mutations
SCN5A	Sodium channel mutations
SCN1B	Sodium channel mutations
SCN2B	Sodium channel mutations
SCN3B	Sodium channel mutations
SCN4B	Sodium channel mutations
SCN1Bb	Sodium channel mutations
SCN10A	Sodium channel mutations
NUP155	Nuclear pore complex/reduction in nuclear membrane permeability
LMNA	Nuclear envelope structure
GJA1	Gap-junction protein/impaired intracellular transport and intercellular electrical coupling
GJA5	Gap-junction protein/impaired intracellular transport and intercellular electrical coupling
NPPA	Blood pressure regulation/elevated levels of mutant ANP
GATA4	Cardiogenesis
GATA5	Cardiogenesis
GATA6	Cardiogenesis
NKX2-5	Cardiogenesis
NKX2-6	Cardiogenesis
PITX2	Cardiogenesis
GREM2	Bone morphogenetic protein antagonist
JPH2	Calcium homeostasis
RYR2	Calcium homeostasis
AGT	Renin-angiotensin system
ACE	Renin-angiotensin system
GNB3	Signal integration
IL6	Cytokine
IL10	Cytokine
MMP2	Zinc-dependent enzyme
SLN	Sarcoplasmic reticulum calcium-ATPase
eNOS	Regulates L-type calcium channel
CETP	Transfer between lipoproteins

Gene	Functions
SYNE2	Cytoskeleton LINC complex
ZFHX3	Transcription factor
PRRX1	Establishment of diverse mesodermal muscle types
WNT8A	Development of early embryos as well as germ cell tumors
CAV1	Main component of the caveolae plasma membranes
C9orf3	Zinc-dependent metallopeptidase
SYNPO2L	Modulating actin-based shape
SYNE2	Maintenance of the structural integrity of the nucleus
CAND2	Probable assembly factor of SCF (SKP1-CUL1-F-box protein) E3 ubiquitin ligase complexes
NEURL	Hippocampal-dependent synaptic plasticity, learning and memory
TBX5	Transcription factors involved in the regulation of developmental processes, e.g., in heart development, specification of limb identity
CUX2	DNA-binding motifs
METTL11B	Methyltransferase activity and N-terminal protein N-methyltransferase activity
KIFAP3	Interaction of chromosomes with an ATPase motor protein.
ANXA4	Calcium-dependent phospholipid binding proteins
GMCL1	Nuclear envelope protein that appears to be involved in spermatogenesis
CEP68	Protein kinase binding and protein domain specific binding
TTN	Abundant protein of striated muscle
KCNN2	Voltage-independent calcium-activated channel with three other calmodulin-binding subunits
KLHL3	Actin bindingand structural molecule activity
FAM13B	GTPase activator activity
SLC35F1	Putative solute transporter
PLN	cAMP-dependent protein kinase in cardiac muscle
ASAH1	Acid ceramidase family of proteins
PCM1	Electron dense granules scattered around centrosomes
SH3PXD2A	Adhesion pathyways
SOX5	Transcription factors involved in the regulation of embryonic development and in the determination of the cell fate
IL6R	Cytokine receptor
CAV3	Component of the caveolae plasma membranes
ANK2	Targeting and stability of Na/Ca exchanger 1 in cardiomyocytes
MYOZ1	Tether calcineurin to the sarcomere of cardiac and skeletal muscle
NEURL1	Hippocampal-dependent synaptic plasticity, learning and memory

Online Table VII. Heritability estimation by the UKBB Europeans GWAS summary statistics.

Regions	Heritability, % (95% CI)
Genome-wide significant genes by GWAS alone	1.7 (1.6-1.9)
Top 1,931 genes identified by GWAS alone	5.5 (5.2-5.8)
The 1,931 genes identified by multi-omics approach	8.0 (7.6-8.4)
All genes across the whole genome	18.9 (18.2-19.5)

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