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Note:Abbreviations: T2D = Type 2 diabetes; CMR = Cardiac magnetic resonance imaging

Detailed Information on Data Sources				
TRIT	PMID/Source	samplesize	case	control
Type 2 diabetes	35551307	933970	80154	853816
Cardiovascular magnetic resonance traits	37262162	40,000	NA	NA

Information of included CMR traits					
ID	Name	Repo	Full_Name	Category	Short
1	LVEDV	0.914449927	left ventricular end-diastolic volume	left ventricle	LV
2	LVESV	0.866983549	left ventricular end-systolic volume	left ventricle	LV
3	LVSV	0.788948849	left ventricular stroke volume	left ventricle	LV
4	LVEF	0.537392538	left ventricular ejection fraction	left ventricle	LV
5	LVCO	0.657578703	left ventricular cardiac output	left ventricle	LV
6	LVM	0.961838012	left ventricular myocardial mass	left ventricle	LV
7	RVEDV	0.923520852	right ventricular end-diastolic volume	right ventricle	RV
8	RVESV	0.914754907	right ventricular end-systolic volume	right ventricle	RV
9	RVSV	0.80431216	right ventricular stroke volume	right ventricle	RV
10	RVEF	0.63772661	right ventricular ejection fraction	right ventricle	RV
11	WT_AHA_1	0.662384028	regional myocardial-wall thickness at end-diastole	left ventricle	LV
12	WT_AHA_2	0.450696795	regional myocardial-wall thickness at end-diastole	left ventricle	LV
13	WT_AHA_3	0.507506553	regional myocardial-wall thickness at end-diastole	left ventricle	LV
14	WT_AHA_4	0.718285416	regional myocardial-wall thickness at end-diastole	left ventricle	LV
15	WT_AHA_5	0.82608823	regional myocardial-wall thickness at end-diastole	left ventricle	LV
16	WT_AHA_6	0.809221157	regional myocardial-wall thickness at end-diastole	left ventricle	LV
17	WT_AHA_7	0.838487955	regional myocardial-wall thickness at end-diastole	left ventricle	LV
18	WT_AHA_8	0.826576786	regional myocardial-wall thickness at end-diastole	left ventricle	LV
19	WT_AHA_9	0.864550376	regional myocardial-wall thickness at end-diastole	left ventricle	LV
20	WT_AHA_10	0.865374901	regional myocardial-wall thickness at end-diastole	left ventricle	LV
21	WT_AHA_11	0.864924386	regional myocardial-wall thickness at end-diastole	left ventricle	LV
22	WT_AHA_12	0.856077798	regional myocardial-wall thickness at end-diastole	left ventricle	LV
23	WT_AHA_13	0.711250973	regional myocardial-wall thickness at end-diastole	left ventricle	LV
24	WT_AHA_14	0.739935018	regional myocardial-wall thickness at end-diastole	left ventricle	LV
25	WT_AHA_15	0.71090078	regional myocardial-wall thickness at end-diastole	left ventricle	LV
26	WT_AHA_16	0.723329341	regional myocardial-wall thickness at end-diastole	left ventricle	LV
27	WT_global	0.907770368	global myocardial-wall thickness at end-diastole	left ventricle	LV

28	LAV_max	0.774006653	left atrium maximum volume	left atrium	LA
29	LAV_min	0.735361975	left atrium minimum volume	left atrium	LA
30	LASV	0.729844511	left atrium stroke volume	left atrium	LA
31	LAEF	0.590547005	left atrium ejection fraction	left atrium	LA
32	RAV_max	0.797313115	right atrium maximum volume	right atrium	RA
33	RAV_min	0.795500375	right atrium minimum volume	right atrium	RA
34	RASV	0.617412505	right atrium stroke volume	right atrium	RA
35	RAEF	0.527554879	right atrium ejection fraction	right atrium	RA
36	AAo_max_area	0.965016134	ascending aorta maximum area	ascending aorta	AAo
37	AAo_min_area	0.970004797	ascending aorta minimum area	ascending aorta	AAo
38	AAo_aortic_distensib	0.579325827	ascending aorta distensibility	ascending aorta	AAo
39	DAo_max_area	0.950356669	descending aorta maximum area	descending aorta	DAo
40	DAo_min_area	0.947103567	descending aorta minimum area	descending aorta	DAo
41	DAo_aortic_distensib	0.494833366	descending aorta distensibility	descending aorta	DAo
42	Ell_1	0.528900122	regional longitudinal strain	left ventricle	LV
43	Ell_2	0.516643988	regional longitudinal strain	left ventricle	LV
44	Ell_3	0.576433086	regional longitudinal strain	left ventricle	LV
45	Ell_4	0.534166006	regional longitudinal strain	left ventricle	LV
46	Ell_5	0.493779232	regional longitudinal strain	left ventricle	LV
47	Ell_6	0.53850742	regional longitudinal strain	left ventricle	LV
48	Ell_global	0.520800203	global longitudinal strain	left ventricle	LV
49	Ecc_AHA_1	0.513508628	regional peak circumferential strain	left ventricle	LV
50	Ecc_AHA_2	0.682417252	regional peak circumferential strain	left ventricle	LV
51	Ecc_AHA_3	0.508459789	regional peak circumferential strain	left ventricle	LV
52	Ecc_AHA_4	0.413383059	regional peak circumferential strain	left ventricle	LV
53	Ecc_AHA_5	0.506626398	regional peak circumferential strain	left ventricle	LV
54	Ecc_AHA_6	0.528917499	regional peak circumferential strain	left ventricle	LV
55	Ecc_AHA_7	0.614280288	regional peak circumferential strain	left ventricle	LV
56	Ecc_AHA_8	0.599704557	regional peak circumferential strain	left ventricle	LV

57	Ecc_AHA_9	0.595480332	regional peak circumferential strain	left ventricle	LV
58	Ecc_AHA_10	0.43734509	regional peak circumferential strain	left ventricle	LV
59	Ecc_AHA_11	0.54450754	regional peak circumferential strain	left ventricle	LV
60	Ecc_AHA_12	0.596206995	regional peak circumferential strain	left ventricle	LV
61	Ecc_AHA_13	0.652557382	regional peak circumferential strain	left ventricle	LV
62	Ecc_AHA_14	0.583013335	regional peak circumferential strain	left ventricle	LV
63	Ecc_AHA_15	0.610993498	regional peak circumferential strain	left ventricle	LV
64	Ecc_AHA_16	0.532973154	regional peak circumferential strain	left ventricle	LV
65	Ecc_global	0.742094745	global peak circumferential strain	left ventricle	LV
66	Err_AHA_1	0.479474006	regional radial strain	left ventricle	LV
67	Err_AHA_2	0.368929465	regional radial strain	left ventricle	LV
68	Err_AHA_3	0.496802977	regional radial strain	left ventricle	LV
69	Err_AHA_4	0.566715452	regional radial strain	left ventricle	LV
70	Err_AHA_5	0.622397597	regional radial strain	left ventricle	LV
71	Err_AHA_6	0.583605127	regional radial strain	left ventricle	LV
72	Err_AHA_7	0.447782961	regional radial strain	left ventricle	LV
73	Err_AHA_8	0.478995743	regional radial strain	left ventricle	LV
74	Err_AHA_9	0.508827191	regional radial strain	left ventricle	LV
75	Err_AHA_10	0.481198835	regional radial strain	left ventricle	LV
76	Err_AHA_11	0.545166144	regional radial strain	left ventricle	LV
77	Err_AHA_12	0.606392101	regional radial strain	left ventricle	LV
78	Err_AHA_13	0.494542274	regional radial strain	left ventricle	LV
79	Err_AHA_14	0.466407741	regional radial strain	left ventricle	LV
80	Err_AHA_15	0.447443218	regional radial strain	left ventricle	LV
81	Err_AHA_16	0.541549304	regional radial strain	left ventricle	LV
82	Err_global	0.610055136	global radial strain	left ventricle	LV

Overview of Cardiometabolic Disease GWAS Data								
No.	Disease	Abbreviation	Cases	Controls	Size effect	Database	PMID	Publication Year
1	Coronary artery calcification	CAC	35,776			CVDKP	37770635	2023
2	Coronary artery disease	CAD	210,842	1,167,328	897,943	Meta-analysis	36474045	2022
			51,098	402,635		FinnGen	36653562	2023
3	Coronary atherosclerosis	CA	56,685	378,019	434,704	FinnGen	36653562	2023
4	Heart failure	HF	47,309	930,014	304,096	CVDKP	31919418	2020
			33,250	420,483		FinnGen	36653562	2023
5	Stroke	Stroke	40,585	406,111	446,696	MEGASTROKE	29531354	2018
6	Ischemic stroke	I_stroke	34,217	406,111	440,328			
7	Myocardial infarction	MI	61,000	577,000	638,000	UK Biobank, CARDIoGRAMplusC4D	33532862	2021
8	Atrial fibrillation	AF	60,620	970,216	1,030,836	AFGen Consortium	30061737	2018
9	Transient ischemic attack	TIA	22,199	411,682	433,881	FinnGen	36653562	2023
10	Venous thromboembolism	VTE	12,240	472,358	484,598	UKBiobank	33959723	2021
11	Peripheral artery disease	PAD	11,226	649,565	660,791	UKBiobank, FinnGen, BioBank Japan	34594039	2021
12	Intracranial Aneurysm	IA	16,033	821,196	837,229	FinnGen	36653562	2023
13	Cardiomyopathy	CM	4,845	359,571	364,416	FinnGen	36653562	2023
14	Aortic aneurysm	AA	4,385	649,565	653,950	UKBiobank, FinnGen, BioBank Japan	34594039	2021

Meta-analyses of GWAS data

Trait	Sample size	lambda	Intercept	h2	P.h2
CAD	897942.977	1.2	1.0973 (0.0144)	0.0582 (0.0027)	1E-300
HF	304096.242	1.15	1.0719 (0.0091)	0.0476 (0.0029)	1E-300

Genetic Correlation Analysis Between T2D and CMR Traits Using LDSC			
Trait	rg	rg_se	rg_p
LVEDV	-0.045	0.033	1.69E-01
LVESV	-0.067	0.035	5.42E-02
LVSV	-0.016	0.045	7.28E-01
LVEF	0.060	0.051	2.34E-01
LVCO	0.014	0.050	7.84E-01
LVM	0.097	0.034	4.03E-03
RVEDV	-0.084	0.035	1.57E-02
RVESV	-0.106	0.038	6.02E-03
RVSV	-0.017	0.049	7.31E-01
RVEF	0.107	0.062	8.14E-02
WT_AHA_1	0.140	0.047	2.89E-03
WT_AHA_2	0.100	0.061	1.01E-01
WT_AHA_3	0.099	0.044	2.31E-02
WT_AHA_4	0.111	0.041	6.37E-03
WT_AHA_5	0.126	0.046	5.71E-03
WT_AHA_6	0.159	0.036	1.35E-05
WT_AHA_7	0.156	0.041	1.20E-04
WT_AHA_8	0.128	0.039	9.09E-04
WT_AHA_9	0.163	0.036	6.24E-06
WT_AHA_10	0.183	0.035	1.74E-07
WT_AHA_11	0.168	0.041	3.85E-05
WT_AHA_12	0.141	0.040	4.70E-04
WT_AHA_13	0.087	0.041	3.12E-02
WT_AHA_14	0.088	0.038	2.14E-02
WT_AHA_15	0.125	0.043	3.76E-03
WT_AHA_16	0.054	0.040	1.78E-01

WT_global	0.153	0.037	2.99E-05
LAV_max	0.024	0.048	6.26E-01
LAV_min	-0.003	0.044	9.47E-01
LASV	0.074	0.057	1.99E-01
LAEF	0.043	0.047	3.60E-01
RAV_max	-0.188	0.040	3.07E-06
RAV_min	-0.174	0.043	4.57E-05
RASV	-0.164	0.054	2.48E-03
RAEF	0.080	0.075	2.89E-01
AAo_max_area	-0.029	0.041	4.72E-01
AAo_min_area	-0.027	0.041	5.06E-01
AAo_aortic_distensibility	-0.120	0.049	1.45E-02
DAo_max_area	0.028	0.037	4.46E-01
DAo_min_area	0.037	0.038	3.28E-01
DAo_aortic_distensibility	-0.116	0.059	4.76E-02
Ell_1	-0.029	0.055	6.00E-01
Ell_2	-0.075	0.070	2.87E-01
Ell_3	-0.003	0.073	9.70E-01
Ell_4	-0.050	0.070	4.81E-01
Ell_5	0.050	0.070	4.77E-01
Ell_6	0.044	0.073	5.45E-01
Ell_global	-0.019	0.076	7.99E-01
Ecc_AHA_1	0.187	0.063	2.93E-03
Ecc_AHA_2	0.029	0.073	6.93E-01
Ecc_AHA_3	-0.011	0.049	8.15E-01
Ecc_AHA_4	0.125	0.094	1.87E-01
Ecc_AHA_5	0.083	0.058	1.57E-01
Ecc_AHA_6	0.002	0.046	9.62E-01

Ecc_AHA_7	0.021	0.087	8.11E-01
Ecc_AHA_8	-0.054	0.072	4.51E-01
Ecc_AHA_9	-0.072	0.038	6.29E-02
Ecc_AHA_10	-0.055	0.083	5.10E-01
Ecc_AHA_11	0.009	0.063	8.91E-01
Ecc_AHA_12	-0.047	0.047	3.23E-01
Ecc_AHA_13	-0.020	0.082	8.09E-01
Ecc_AHA_14	-0.016	0.054	7.64E-01
Ecc_AHA_15	0.022	0.055	6.87E-01
Ecc_AHA_16	-0.027	0.052	6.05E-01
Ecc_global	0.012	0.052	8.19E-01
Err_AHA_1	-0.030	0.074	6.89E-01
Err_AHA_2	-0.037	0.075	6.16E-01
Err_AHA_3	-0.070	0.056	2.10E-01
Err_AHA_4	0.014	0.067	8.40E-01
Err_AHA_5	0.044	0.055	4.26E-01
Err_AHA_6	-0.033	0.055	5.49E-01
Err_AHA_7	-0.003	0.069	9.60E-01
Err_AHA_8	0.080	0.059	1.78E-01
Err_AHA_9	0.151	0.063	1.60E-02
Err_AHA_10	0.074	0.085	3.87E-01
Err_AHA_11	-0.012	0.070	8.61E-01
Err_AHA_12	0.004	0.068	9.48E-01
Err_AHA_13	0.035	0.050	4.92E-01
Err_AHA_14	0.148	0.069	3.20E-02
Err_AHA_15	0.084	0.060	1.67E-01
Err_AHA_16	-0.027	0.057	6.29E-01
Err_global	0.034	0.058	5.56E-01

Note: LDSC:LD Score Regression

rg: Effect size, where a value greater than 0 indicates a positive correlation, and vice versa.

Genetic Correlation Analysis Between T2D and CMR Traits Using HDL			
Trait	rg	rg_se	P
LVEDV	-0.081	0.027	2.53E-03
LVESV	-0.073	0.027	6.34E-03
LVSV	-0.062	0.033	5.78E-02
LVEF	0.030	0.035	3.86E-01
LVCO	0.000	0.038	9.91E-01
LVM	0.088	0.026	6.15E-04
RVEDV	-0.127	0.027	3.05E-06
RVESV	-0.131	0.027	1.41E-06
RVSV	-0.060	0.030	4.45E-02
RVEF	0.093	0.035	7.41E-03
WT_AHA_1	0.137	0.033	4.06E-05
WT_AHA_2	0.068	0.032	3.69E-02
WT_AHA_3	0.081	0.034	1.71E-02
WT_AHA_4	0.098	0.029	6.40E-04
WT_AHA_5	0.145	0.029	6.29E-07
WT_AHA_6	0.176	0.031	1.39E-08
WT_AHA_7	0.160	0.034	2.71E-06
WT_AHA_8	0.131	0.033	6.12E-05
WT_AHA_9	0.185	0.034	6.35E-08
WT_AHA_10	0.202	0.032	1.82E-10
WT_AHA_11	0.187	0.027	8.06E-12
WT_AHA_12	0.146	0.028	1.75E-07
WT_AHA_13	0.090	0.037	1.61E-02
WT_AHA_14	0.132	0.040	8.58E-04
WT_AHA_15	0.146	0.039	2.06E-04
WT_AHA_16	0.078	0.035	2.59E-02
WT_global	0.163	0.027	1.38E-09

LAV_max	-0.015	0.033	6.53E-01
LAV_min	-0.024	0.033	4.61E-01
LASV	-0.013	0.036	7.14E-01
LAEF	0.025	0.036	4.82E-01
RAV_max	-0.166	0.032	2.35E-07
RAV_min	-0.128	0.036	4.24E-04
RASV	-0.171	0.035	1.38E-06
RAEF	-0.012	0.053	8.13E-01
AAo_max_area	-0.054	0.023	1.86E-02
AAo_min_area	-0.045	0.023	4.78E-02
AAo_aortic_distensibility	-0.133	0.045	2.98E-03
DAo_max_area	0.000	0.028	9.93E-01
DAo_min_area	0.009	0.028	7.39E-01
DAo_aortic_distensibility	-0.114	0.043	7.57E-03
Ell_1	0.047	0.046	3.05E-01
Ell_2	-0.107	0.053	4.40E-02
Ell_3	0.084	0.046	6.37E-02
Ell_4	-0.010	0.048	8.29E-01
Ell_5	0.142	0.056	1.17E-02
Ell_6	0.124	0.051	1.49E-02
Ell_global	0.064	0.050	2.00E-01
Ecc_AHA_1	0.150	0.069	2.97E-02
Ecc_AHA_2	0.043	0.040	2.86E-01
Ecc_AHA_3	-0.034	0.034	3.15E-01
Ecc_AHA_4	0.097	0.072	1.77E-01
Ecc_AHA_5	0.096	0.053	6.89E-02
Ecc_AHA_6	0.026	0.034	4.55E-01
Ecc_AHA_7	0.077	0.058	1.86E-01
Ecc_AHA_8	0.012	0.045	7.84E-01

Ecc_AHA_9	-0.075	0.024	2.07E-03
Ecc_AHA_10	-0.029	0.061	6.40E-01
Ecc_AHA_11	0.012	0.054	8.25E-01
Ecc_AHA_12	-0.069	0.037	5.94E-02
Ecc_AHA_13	0.014	0.048	7.76E-01
Ecc_AHA_14	0.003	0.040	9.38E-01
Ecc_AHA_15	0.020	0.034	5.64E-01
Ecc_AHA_16	-0.039	0.042	3.43E-01
Ecc_global	0.024	0.035	5.04E-01
Err_AHA_1	-0.070	0.050	1.56E-01
Err_AHA_2	-0.112	0.047	1.63E-02
Err_AHA_3	-0.138	0.039	4.45E-04
Err_AHA_4	-0.008	0.063	8.97E-01
Err_AHA_5	0.043	0.052	4.04E-01
Err_AHA_6	-0.045	0.039	2.50E-01
Err_AHA_7	0.028	0.049	5.74E-01
Err_AHA_8	0.063	0.059	2.87E-01
Err_AHA_9	0.125	0.064	5.18E-02
Err_AHA_10	-0.016	0.060	7.95E-01
Err_AHA_11	-0.018	0.051	7.28E-01
Err_AHA_12	-0.025	0.049	6.18E-01
Err_AHA_13	0.047	0.045	2.93E-01
Err_AHA_14	0.133	0.060	2.71E-02
Err_AHA_15	0.039	0.046	3.92E-01
Err_AHA_16	-0.035	0.045	4.37E-01
Err_global	-0.001	0.040	9.77E-01

Note: HDL:High-definition likelihood

rg: Effect size, where a value greater than 0 indicates a positive correlation, and vice versa.

Results of univariate MiXeR analyses												
name	pi (mean)	pi (std)	sig2_beta (mean)	sig2_beta (std)	sig2_zero	sig2_zero (std)	h2 (mean)	h2 (std)	nc@p9 (mean)	nc@p9 (std)	AIC	BIC
WT_AHA_6	9.28E-04	3.25E-19	1.01E-04	0.00E+00	1.020	0.000	0.194	2.78E-17	2958.460	0.000	23.706	14.159
WT_AHA_7	9.28E-04	3.25E-19	1.01E-04	0.00E+00	1.020	0.000	0.194	2.78E-17	2958.460	0.000	15.741	6.193
WT_AHA_9	9.28E-04	3.25E-19	1.01E-04	0.00E+00	1.020	0.000	0.194	2.78E-17	2958.460	0.000	14.237	4.689
WT_AHA_10	9.28E-04	3.25E-19	1.01E-04	0.00E+00	1.020	0.000	0.194	2.78E-17	2958.460	0.000	22.660	13.113
WT_AHA_11	9.28E-04	3.25E-19	1.01E-04	0.00E+00	1.020	0.000	0.194	2.78E-17	2958.460	0.000	34.653	25.105
WT_AHA_12	6.07E-04	6.35E-04	3.37E-04	1.85E-04	1.025	0.008	0.180	3.11E-02	1937.307	2025.032	21.285	11.738
WT_global	8.16E-04	2.71E-04	1.42E-04	1.13E-04	1.025	0.013	0.180	3.29E-02	2601.139	864.171	33.579	24.031
<i>RAV_min</i>	<i>1.97E-03</i>	<i>1.08E-03</i>	<i>4.19E-05</i>	<i>3.87E-05</i>	<i>1.030</i>	<i>0.013</i>	<i>0.092</i>	<i>1.82E-02</i>	<i>6297.169</i>	<i>3459.220</i>	<i>-2.720</i>	<i>-12.268</i>
<i>RAV_max</i>	<i>9.21E-04</i>	<i>5.92E-04</i>	<i>8.58E-05</i>	<i>5.05E-05</i>	<i>1.028</i>	<i>0.010</i>	<i>0.116</i>	<i>3.17E-02</i>	<i>2935.914</i>	<i>1888.451</i>	<i>-1.186</i>	<i>-10.733</i>
T2D	8.18E-04	8.59E-05	8.87E-05	7.57E-06	1.111	0.017	0.149	6.71E-03	2608.484	273.914	2432.398	2422.836

Note: AIC = Akaike Information Criterion, pi = polygenicity; sig2_beta = discoverability; h2 = heritability; nc@p9 = the number of variations affecting traits specific to each trait

Results of bivariate MiXeR analyses													
trait1	trait2	dice (mean)	dice (std)	pi1 (mean)	pi1 (std)	pi2 (mean)	pi2 (std)	pi12 (mean)	pi12 (std)	nc1@p9 (mean)	nc1@p9 (std)	nc2@p9 (mean)	nc2@p9 (std)
T2D	WT_AHA_6	0.344	0.130	5.16E-04	1.20E-04	6.26E-04	1.17E-04	3.02E-04	1.17E-04	1646.874	383.763	1996.850	373.602
T2D	WT_AHA_7	0.348	0.127	5.14E-04	1.24E-04	6.23E-04	1.16E-04	3.04E-04	1.16E-04	1637.778	394.854	1987.754	369.644
T2D	WT_AHA_9	0.268	0.083	5.83E-04	8.85E-05	6.93E-04	7.76E-05	2.35E-04	7.76E-05	1859.414	282.149	2209.390	247.484
T2D	WT_AHA_10	0.315	0.141	5.44E-04	1.59E-04	6.54E-04	1.17E-04	2.73E-04	1.17E-04	1734.877	507.011	2086.677	373.763
T2D	WT_AHA_11	0.457	0.144	4.19E-04	1.47E-04	5.29E-04	1.28E-04	3.99E-04	1.28E-04	1337.123	468.495	1687.098	408.770
T2D	WT_AHA_12	0.362	0.186	5.11E-04	2.64E-04	3.01E-04	3.92E-04	3.06E-04	2.89E-04	1631.132	841.282	959.955	1249.395
T2D	WT_global	0.463	0.178	4.31E-04	1.92E-04	4.29E-04	2.03E-04	3.87E-04	1.65E-04	1374.422	612.091	1367.077	648.551

trait1	trait2	rho_zero (mean)	rho_zero (std)	rho_beta (mean)	rho_beta (std)	rg (mean)	rg (std)	fraction_concordant_within_shared (mean)	fraction_concordant_within_shared (std)	best_vs_min_AIC	best_vs_min_BIC	best_vs_max_AIC	best_vs_max_BIC
T2D	WT_AHA_6	0.011	0.001	0.606	0.224	0.182	0.008	0.722	0.106	8.222	-1.288	27.784	18.274
T2D	WT_AHA_7	0.013	0.002	0.685	0.230	0.211	0.009	0.764	0.119	8.729	-0.782	20.333	10.823
T2D	WT_AHA_9	0.012	0.002	0.736	0.186	0.183	0.011	0.777	0.090	7.549	-1.961	26.504	16.993
T2D	WT_AHA_10	0.012	0.002	0.709	0.242	0.192	0.013	0.774	0.117	5.816	-3.695	26.598	17.088
T2D	WT_AHA_11	0.014	0.002	0.473	0.211	0.188	0.011	0.667	0.095	11.542	2.031	19.452	9.941
T2D	WT_AHA_12	0.012	0.002	0.535	0.279	0.181	0.025	0.702	0.134	9.391	-0.119	9.215	-0.295
T2D	WT_global	0.012	0.002	0.493	0.244	0.197	0.019	0.679	0.112	10.012	0.502	18.929	9.419

Note: “pi1,” “pi2,” and “pi12” represent the polygenicity of trait1-specific, trait2-specific, and shared components, respectively. “nc1@p9,” “nc2@p9,” and “nc12@p9” indicate the number of variants influencing each component. “rho_zero” reflects the correlation of z-scores due to potential sample overlap in GWAS studies, while “rho_beta” represents the correlation of effect sizes within the shared component. “fraction_concordant_within_shared” shows the proportion of shared variants with concordant effect directions in both traits. AIC: Akaike Information Criterion.

Distinct genomic loci associated with T2D at condFDR < 0.01 given association with CMR traits														
Trait1	Trait2	locus num	CHR	LEAD_SNP	LEAD_BP	FDR	nearestGene	func	CADD	RDB	PVAL_i n_Trait1	BETA_in_ Trait1	PVAL_i n_Trait2	BETA_in_ Trait2
T2D	WT_AHA_6	1	1	rs12759053	6709911	1.10E-03	DNAJC11	intronic	2.297	7	1.98E-07	0.035	8.31E-01	0.001
T2D	WT_AHA_6	2	1	rs10916785	20731117	2.86E-03	LINC01141	ncRNA_intronic	18.16	2b	7.62E-07	0.032	5.55E-01	-0.004
T2D	WT_AHA_6	3	1	rs3008226	26394997	2.75E-03	TRIM63	upstream	2.769	7	7.33E-07	0.042	5.15E-01	0.005
T2D	WT_AHA_6	4	1	rs4654365	29019724	4.60E-03	GMEB1	intronic	0.097	6	1.33E-06	-0.032	7.63E-01	-0.002
T2D	WT_AHA_6	5	1	rs6656963	31459054	5.38E-03	PUM1	intronic	0.289	7	1.67E-06	-0.032	7.26E-01	0.002
T2D	WT_AHA_6	6	1	rs3768321	40035928	1.30E-19	PABPC4:RP11-69E11.8	ncRNA_intronic	20.9	7	4.75E-26	0.084	4.58E-01	0.006
T2D	WT_AHA_6	7	1	rs58432198	51256091	9.08E-06	FAF1	intronic	2.611	7	5.71E-10	-0.064	4.71E-01	-0.007
T2D	WT_AHA_6	9	1	rs2269247	64107284	3.87E-03	PGM1	intronic	5.424	NA	1.59E-06	-0.040	1.37E-01	-0.012
T2D	WT_AHA_6	10	1	rs10889560	65989878	5.44E-03	LEPR	intronic	0.025	5	4.08E-06	0.052	2.98E-02	-0.026
T2D	WT_AHA_6	11	1	rs2815747	72821126	5.25E-04	RPL31P12	intergenic	1.058	NA	1.00E-07	0.044	3.01E-01	0.008
T2D	WT_AHA_6	12	1	rs12757137	85773321	8.26E-03	RP11-131L23.1	ncRNA_intronic	6.635	6	4.62E-06	-0.031	1.13E-01	-0.011
T2D	WT_AHA_6	13	1	rs35463305	111228243	9.52E-03	KCNA3	intergenic	1.4	7	3.68E-06	-0.038	6.55E-01	-0.004
T2D	WT_AHA_6	14	1	rs6687953	112293512	9.43E-04	FAM212B	intronic	1.083	7	1.92E-07	-0.034	4.33E-01	-0.005
T2D	WT_AHA_6	15	1	rs1127215	117532790	3.60E-09	PTGFRN	UTR3	2.461	5	3.92E-14	-0.049	8.43E-01	0.001
T2D	WT_AHA_6	16	1	rs320369	118143517	3.61E-04	AL157902.3	ncRNA_intronic	2.408	4	4.60E-08	0.037	8.88E-01	-0.001
T2D	WT_AHA_6	17	1	rs1493694	120526982	3.55E-10	NOTCH2	intronic	0.993	6	3.35E-15	0.080	3.49E-01	0.010
T2D	WT_AHA_6	18	1	rs145904381	151017991	3.14E-04	BNIP1	intronic	2.755	5	5.73E-08	0.172	2.02E-01	-0.039

T2D	WT_AHA_6	19	1	rs10913469	177913519	2.76E-07	SEC16B:RP4-798P15.3	ncRNA_intronic	0.216	5	1.16E-11	-0.055	2.03E-01	0.010
T2D	WT_AHA_6	20	1	rs567185	201763499	1.00E-03	NAV1:IPO9-AS1	ncRNA_intronic	2.815	NA	1.91E-07	0.035	6.03E-01	-0.003
T2D	WT_AHA_6	21	1	rs13303359	203518873	4.41E-03	OPTC	intergenic	1.894	6	1.00E-05	0.030	2.58E-03	0.020
T2D	WT_AHA_6	22	1	rs10157145	205261963	1.13E-04	NUAK2	intergenic	3.152	4	7.37E-08	-0.036	4.88E-03	-0.018
T2D	WT_AHA_6	23	1	rs9429893	206600992	1.14E-04	SRGAP2	intronic	6.107	5	5.54E-08	0.035	8.92E-03	-0.017
T2D	WT_AHA_6	24	1	rs4844949	210306846	9.53E-03	SYT14	intronic	0.638	7	4.30E-06	0.031	3.34E-01	0.006
T2D	WT_AHA_6	25	1	rs340874	214159256	1.66E-19	PROX1-AS1:PROX1	ncRNA_intronic	13.3	NA	1.56E-25	-0.068	7.94E-02	0.011
T2D	WT_AHA_6	26	1	rs4846567	219750717	4.08E-13	RP11-95P13.2	intergenic	14.9	5	3.62E-17	-0.059	2.91E-07	-0.036
T2D	WT_AHA_6	27	1	rs348330	229672955	8.65E-09	ABCB10	intronic	4.01	NA	2.10E-13	-0.049	1.23E-01	-0.010
T2D	WT_AHA_6	28	1	rs291367	235690800	3.25E-04	RP4-534P7.2	intergenic	0.005	5	6.06E-08	-0.038	1.95E-01	-0.009
T2D	WT_AHA_6	29	2	rs62107261	422144	5.58E-06	AC105393.2	ncRNA_exonic	4.222	5	2.62E-10	0.102	8.64E-01	-0.003
T2D	WT_AHA_6	30	2	rs34048824	25535543	1.46E-04	DNMT3A	intronic	5.037	5	2.06E-08	0.036	2.56E-01	-0.007
T2D	WT_AHA_6	31	2	rs1260326	27730940	2.01E-16	GCKR	exonic	13.22	5	1.62E-22	-0.064	8.64E-01	0.001
T2D	WT_AHA_6	32	2	rs28470852	43593000	9.61E-23	THADA	intronic	1.516	6	3.40E-28	0.122	3.21E-03	-0.032
T2D	WT_AHA_6	33	2	rs12464070	55247477	6.86E-03	RTN4	intronic	2.039	5	7.00E-06	0.029	1.81E-02	-0.015
T2D	WT_AHA_6	34	2	rs6545714	59307725	1.92E-04	LINC01122	intergenic	10.54	3a	2.25E-08	-0.036	6.40E-01	-0.003
T2D	WT_AHA_6	35	2	rs243019	60585806	1.33E-14	AC007381.2	downstream	12.31	NA	3.37E-20	-0.059	1.87E-01	-0.009
T2D	WT_AHA_6	36	2	rs2540945	65289825	2.81E-12	CEP68	intronic	2.927	NA	3.05E-16	0.054	5.89E-05	-0.027
T2D	WT_AHA_6	37	2	rs13004493	100598635	4.18E-03	AFF3	intronic	1.617	5	1.10E-06	-0.080	9.86E-01	0.000

T2D	WT_AHA_6	38	2	rs58584712	112249583	3.19E-03	MIR4435-1HG:AC017002.1:AC017002.2	ncRNA_exonic	3.451	5	1.17E-06	-0.040	1.64E-01	-0.011
T2D	WT_AHA_6	39	2	rs62157795	112827439	8.68E-03	TMEM87B	intronic	12.38	6	3.16E-06	-0.044	7.27E-01	0.003
T2D	WT_AHA_6	40	2	rs11688901	121318138	8.77E-07	AC073257.1	intergenic	3.27	5	4.88E-11	-0.059	1.66E-01	-0.012
T2D	WT_AHA_6	41	2	rs7559672	147855299	6.73E-04	AC062032.1	intergenic	3.26	6	1.69E-07	-0.047	1.32E-01	-0.014
T2D	WT_AHA_6	42	2	rs16841827	158329237	1.18E-05	CYTIP	intronic	1.931	6	6.34E-10	-0.082	9.68E-01	-0.001
T2D	WT_AHA_6	43	2	rs2193706	159309986	7.13E-03	CCDC148	intronic	4.759	7	6.28E-06	-0.045	2.58E-02	0.022
T2D	WT_AHA_6	44	2	rs7572970	161136656	1.08E-05	RBMS1	intronic	6.852	4	6.12E-10	-0.045	7.64E-01	-0.002
T2D	WT_AHA_6	45	2	rs1267073	162049999	4.97E-03	TANK	intronic	3.269	7	1.67E-06	-0.033	4.58E-01	-0.005
T2D	WT_AHA_6	46	2	rs12614955	163649480	4.60E-03	KCNH7:AC007740.1	ncRNA_intronic	5.048	7	1.93E-06	0.033	1.58E-01	0.010
T2D	WT_AHA_6	47	2	rs13389219	165528876	2.11E-15	COBLL1	intergenic	9.065	7	1.17E-20	-0.061	2.57E-02	-0.015
T2D	WT_AHA_6	48	2	rs2194754	166539042	1.45E-03	CSRNP3	UTR3	0.096	7	1.94E-06	0.030	3.57E-03	0.019
T2D	WT_AHA_6	49	2	rs6741930	172396366	6.07E-03	CYBRD1	intronic	3.039	6	2.89E-06	-0.034	1.38E-01	-0.011
T2D	WT_AHA_6	50	2	rs72917544	175241566	5.51E-04	CIR1	intronic	12.5	6	9.74E-08	-0.044	4.19E-01	-0.007
T2D	WT_AHA_6	51	2	rs9630985	181607676	3.14E-03	AC009478.1	intergenic	3.234	3a	8.45E-07	-0.033	5.94E-01	-0.004
T2D	WT_AHA_6	52	2	rs10932228	208919650	4.77E-04	RNA5SP116	upstream	12.96	7	6.98E-08	0.035	7.18E-01	-0.002
T2D	WT_AHA_6	53	2	rs11679164	213831335	3.51E-03	AC079610.1	ncRNA_intronic	0.677	7	1.00E-06	-0.034	5.52E-01	-0.004
T2D	WT_AHA_6	54	2	rs952227	227062080	1.61E-26	AC068138.1	intergenic	1.904	7	2.73E-34	-0.083	2.68E-01	-0.008
T2D	WT_AHA_6	55	2	rs28591249	228994006	7.68E-04	SPHKAP	intronic	5.053	6	1.85E-07	-0.033	1.76E-01	-0.009

Note: Distinct genomic loci associated with T2D at $\text{condFDR} < 0.05$ (based on CMR trait association).

ANNOVAR: Functional depletion score, where higher scores indicate greater deleterious effects. RegulomeDB score: Predicts the likelihood of regulatory functionality, with lower scores indicating higher likelihood.

Distinct genomic loci associated with CMR traits at condFDR < 0.01 given association with T2D														
Trait1	Trait2	locus num	CHR	LEAD_SN P	LEAD_BP	FDR	nearestGene	func	CADD	RDB	PVAL_in_Trait1	BETA_in_Trait1	PVAL_in_Trait2	BETA_in_Trait2
WT_AHA_6	T2D	1	1	rs7772278	214277163	8.33E-03	PROX1	intergenic	0.721	4	6.81E-05	-0.059	1.21E-05	0.061
WT_AHA_6	T2D	2	1	rs4846567	219750717	3.25E-04	RP11-95P13.2	intergenic	14.9	5	3.62E-17	-0.059	2.91E-07	-0.036
WT_AHA_6	T2D	3	2	rs2723063	65280185	7.75E-03	CEP68	intergenic	0.648	NA	8.23E-15	0.050	1.11E-05	-0.029
WT_AHA_6	T2D	4	3	rs6549252	69845515	6.28E-10	MITF	intronic	0.156	7	1.28E-03	-0.021	2.87E-13	-0.048
WT_AHA_6	T2D	5	3	rs4894803	171800256	1.59E-05	FNDC3B	intronic	21.6	4	3.27E-03	-0.019	5.25E-09	0.039
WT_AHA_6	T2D	6	4	rs2074974	17812615	1.58E-03	NCAPG	UTR5	8.05	NA	4.31E-08	-0.039	1.69E-06	0.034
WT_AHA_6	T2D	7	5	rs7710854	43824677	6.23E-03	RP11-8L21.1	intergenic	0.482	6	2.04E-01	0.013	2.86E-07	-0.052
WT_AHA_6	T2D	8	6	rs3176323	36646849	3.85E-06	CDKN1A	intronic	8.379	4	2.05E-03	0.021	1.56E-09	0.043
WT_AHA_6	T2D	9	9	rs9298763	16420174	3.28E-03	BNC2	intronic	4.329	7	1.19E-02	0.017	9.55E-07	0.033
WT_AHA_6	T2D	10	10	rs7099862	114448861	4.30E-03	VTI1A	intronic	0.79	6	4.49E-02	0.017	5.77E-07	-0.043
WT_AHA_6	T2D	11	10	rs7921252	127949632	5.39E-03	ADAM12	intronic	0.114	7	4.52E-01	0.005	1.22E-07	-0.034
WT_AHA_6	T2D	12	11	rs6189739	47381642	2.81E-05	SPI1	intronic	1.501	2b	9.46E-02	0.016	1.13E-09	0.059
WT_AHA_6	T2D	13	11	rs2306363	65405600	5.28E-03	SIPA1	UTR5	19.83	2b	1.10E-06	-0.040	6.99E-06	-0.036
WT_AHA_6	T2D	14	11	rs11603763	68789606	5.11E-03	RP11-554A11.6	intergenic	9.077	5	2.86E-05	-0.028	6.70E-06	-0.030
WT_AHA_6	T2D	15	12	rs1724975	90060586	4.67E-05	ATP2B1	intronic	1.939	6	2.95E-01	0.009	7.98E-10	-0.052
WT_AHA_6	T2D	16	15	rs2028762	67482003	9.53E-03	SMAD3	intronic	11.01	NA	2.39E-01	-0.009	4.26E-07	0.039
WT_AHA_6	T2D	17	15	rs1759998	85285536	9.71E-15	ZNF592	intergenic	12.12	6	6.18E-02	-0.013	2.33E-19	-0.065
WT_AHA_6	T2D	18	16	rs7203816	81597957	5.32E-03	CMIP	intronic	2.043	5	7.87E-04	-0.023	6.05E-06	-0.031
WT_AHA_6	T2D	19	19	rs1166800	57674644	3.71E-03	DUXA	intronic	5.029	5	8.55E-01	-0.001	4.45E-08	0.038
WT_AHA_7	T2D	1	1	rs6177541	26393505	3.76E-03	TRIM63	intronic	22.4	4	3.72E-06	-0.047	4.46E-06	0.043
WT_AHA_7	T2D	2	1	rs2494196	219762581	4.57E-04	ZC3H11B	intergenic	0.548	NA	3.29E-15	-0.056	4.04E-07	-0.034

WT_AHA_7	T2D	3	2	rs111692972	179669931	5.48E-04	TTN	intronic	1.587	7	1.35E-01	0.020	1.52E-08	-0.073
WT_AHA_7	T2D	4	3	rs6225600	53282990	4.26E-03	TKT	intronic	2.256	5	3.45E-01	0.009	7.72E-08	0.049
WT_AHA_7	T2D	5	3	rs1307170	69902514	4.42E-03	MITF	intronic	1.338	6	4.99E-04	-0.023	5.42E-06	-0.028
WT_AHA_7	T2D	6	3	rs6803608	158313583	3.35E-04	MLF1	intronic	0.808	5	2.51E-03	-0.019	1.28E-07	-0.032
WT_AHA_7	T2D	7	3	rs1773849	169117556	4.51E-03	MECOM	intronic	3.516	6	1.33E-03	0.024	3.54E-06	-0.033
WT_AHA_7	T2D	8	4	rs7700110	114439894	2.22E-04	CAMK2D	intronic	5.459	6	7.64E-02	0.013	8.63E-09	-0.039
WT_AHA_7	T2D	9	5	rs7280147	132444128	2.39E-04	HSPA4	intergenic	0.703	5	6.18E-03	-0.030	5.27E-08	-0.055
WT_AHA_7	T2D	10	6	rs3176326	36647289	4.62E-04	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	4.09E-07	0.039
WT_AHA_7	T2D	11	7	rs10264306	28239466	2.18E-03	JAZF1-AS1	ncRNA_intronic	0.365	6	1.41E-15	-0.063	2.34E-06	0.036
WT_AHA_7	T2D	12	7	rs4731701	130430930	2.14E-03	KLF14	intergenic	0.021	7	1.65E-13	-0.047	2.28E-06	-0.028
WT_AHA_7	T2D	13	10	rs7684306	75538382	6.36E-03	FUT11	intergenic	0.418	5	1.76E-01	-0.037	2.22E-07	0.133
WT_AHA_7	T2D	14	11	rs1160482	47725306	1.38E-06	AGBL2	intronic	3.446	7	1.27E-03	0.022	6.04E-10	-0.039
WT_AHA_7	T2D	15	11	rs1279869	69045735	3.94E-03	MYEOV	intergenic	11.21	4	7.53E-05	0.026	4.71E-06	-0.028
WT_AHA_7	T2D	16	15	rs5686428	85357649	1.63E-13	ALPK3	intergenic	0.529	7	8.61E-02	0.012	2.42E-18	-0.059
WT_AHA_7	T2D	17	15	rs1290622	99255960	7.32E-03	IGF1R	intronic	2.487	6	1.15E-01	0.010	3.69E-07	-0.031
WT_AHA_7	T2D	18	16	rs34829128	5843607	6.97E-03	RP11-420N3.2	ncRNA_intronic	0.457	5	9.23E-03	-0.020	2.03E-06	0.034
WT_AHA_7	T2D	19	17	rs8182252	37727950	8.14E-04	CDK12	intergenic	14.32	5	3.38E-05	-0.036	7.61E-07	-0.040
WT_AHA_7	T2D	20	17	rs55787734	43799052	1.89E-04	CRHR1:RP11-105N13.4	ncRNA_intronic	5.686	5	9.63E-03	-0.021	3.10E-08	0.040
WT_AHA_7	T2D	21	22	rs1004243	31497879	1.06E-03	SMTN	intronic	7.849	5	3.55E-01	0.006	1.46E-08	0.035
WT_AHA_9	T2D	1	1	rs4127549	11894133	2.06E-04	CLCN6	intronic	6.718	3a	2.28E-02	0.033	2.33E-08	-0.071
WT_AHA_9	T2D	2	1	rs1157896	116301670	1.69E-03	CASQ2	intronic	2.103	7	1.46E-01	-0.010	7.06E-08	0.033
WT_AHA_9	T2D	3	2	rs2163227	43549229	4.82E-05	THADA	intronic	2.536	7	1.92E-06	0.034	3.55E-08	-0.035

WT_AHA_9	T2D	4	3	rs34585560	169185399	1.47E-04	MECOM:RP11-641D5.2	ncRNA_intronic	20.3	6	6.02E-02	-0.012	8.23E-09	-0.034
WT_AHA_9	T2D	6	5	rs1174570	132444301	7.81E-06	HSPA4	intergenic	7.984	4	6.98E-02	0.013	2.28E-10	-0.042
WT_AHA_9	T2D	7	6	rs6676178	36636080	2.51E-03	Y_RNA	intergenic	12.7	2b	2.84E-03	0.023	1.00E-06	0.033
WT_AHA_9	T2D	8	6	rs9388519	127107228	5.55E-03	RPS4XP9	intergenic	8.719	6	1.90E-01	0.009	2.27E-07	0.030
WT_AHA_9	T2D	9	10	rs6187256	105345362	3.30E-04	NEURL1	intronic	0.807	6	4.38E-01	0.020	4.25E-09	0.140
WT_AHA_9	T2D	10	11	rs7928419	47392114	2.68E-05	SPI1	intronic	4.858	6	1.42E-04	-0.026	1.99E-08	-0.035
WT_AHA_9	T2D	11	11	rs12419237	65365077	6.31E-03	MAP3K11	downstream	1.679	5	9.58E-05	0.029	5.79E-06	-0.031
WT_AHA_9	T2D	12	12	rs76309861	26495668	4.72E-03	RP11-513G19.1:ITPR2	ncRNA_intronic	1.545	6	7.23E-03	0.018	1.29E-06	0.030
WT_AHA_9	T2D	13	15	rs3596080	85343980	2.48E-04	ZNF592	intronic	4.631	5	6.37E-02	-0.013	1.45E-08	-0.037
WT_AHA_9	T2D	14	15	rs1185831	99249029	1.06E-03	IGF1R	intronic	4.537	5	4.07E-02	-0.014	9.89E-08	-0.032
WT_AHA_9	T2D	16	22	rs133885	26159289	1.06E-03	MYO18B	exonic	17.86	4	4.50E-01	-0.005	1.76E-08	0.033
WT_AHA_10	T2D	1	1	rs1737632	11876662	2.28E-04	CLCN6	intronic	10.13	7	1.94E-02	-0.032	2.56E-08	-0.069
WT_AHA_10	T2D	2	2	rs2163227	43549229	2.39E-04	THADA	intronic	2.536	7	1.92E-06	0.034	2.23E-07	-0.032
WT_AHA_10	T2D	3	2	rs16866400	179448911	2.12E-04	TTN-AS1:TTN	ncRNA_intronic	0.409	7	5.68E-01	0.005	1.28E-09	-0.043
WT_AHA_10	T2D	4	3	rs2643826	27562988	2.13E-03	AC137675.1	intergenic	2.245	4	7.43E-02	0.011	1.51E-07	0.030
WT_AHA_10	T2D	5	3	rs6225317	69906486	4.35E-03	MITF	intronic	1.045	7	1.61E-02	-0.020	1.00E-06	0.036
WT_AHA_10	T2D	6	3	rs1205388	169157208	9.04E-03	MECOM	intronic	13.02	6	2.30E-02	0.017	1.93E-06	-0.031
WT_AHA_10	T2D	8	5	rs1174570	132444301	6.84E-04	HSPA4	intergenic	7.984	4	6.98E-02	0.013	3.65E-08	-0.036
WT_AHA_10	T2D	9	6	rs9462207	36627599	1.21E-05	Y_RNA	intergenic	2.056	5	2.38E-03	0.023	3.96E-09	0.039
WT_AHA_10	T2D	10	6	rs7499544	39294291	3.05E-03	KIF6	intergenic	6.817	5	1.71E-03	0.051	2.29E-06	0.067
WT_AHA_10	T2D	11	6	rs3566963	127188248	4.29E-05	RPS4XP9	intergenic	2.74	7	2.82E-01	-0.007	4.00E-10	0.036
WT_AHA_10	T2D	12	9	rs1081789	119245955	6.63E-03	ASTN2	intronic	0.596	5	6.91E-03	0.018	2.73E-06	0.028

WT_AHA_10	T2D	13	10	rs61870180	105438913	4.58E-03	SH3PXD2A	intronic	2.384	4	3.40E-01	0.024	1.16E-07	0.123
WT_AHA_10	T2D	14	11	rs1103933	47706141	1.16E-04	AGBL2	intronic	4.272	6	9.75E-07	-0.032	1.02E-07	0.030
WT_AHA_10	T2D	15	11	rs1089646	69073647	2.90E-03	MYEOV	intergenic	5.298	1f	5.36E-04	0.023	3.89E-06	-0.027
WT_AHA_10	T2D	16	12	rs1110536	90069276	1.83E-03	ATP2B1	intronic	7.273	5	2.95E-01	-0.009	3.66E-08	-0.041
WT_AHA_10	T2D	17	15	rs3803405	85383640	1.95E-06	ALPK3	exonic	10.99	5	2.58E-02	0.016	1.07E-10	-0.041
WT_AHA_10	T2D	18	15	rs1185831	99249029	7.02E-04	IGF1R	intronic	4.537	5	4.07E-02	-0.014	5.88E-08	-0.031
WT_AHA_10	T2D	19	17	rs12453217	37741982	1.71E-03	NEUROD2	intergenic	1.422	6	7.60E-05	0.032	2.11E-06	-0.034
WT_AHA_10	T2D	20	17	rs4630591	44192568	2.23E-05	KANSL1	intronic	0.795	6	6.77E-03	0.022	3.76E-09	0.042
WT_AHA_10	T2D	21	22	rs1004243	31497879	1.50E-03	SMTN	intronic	7.849	5	3.55E-01	0.006	2.29E-08	0.032
WT_AHA_11	T2D	1	1	rs6177541	26393505	9.65E-06	TRIM63	intronic	22.4	4	3.72E-06	-0.047	9.95E-09	0.052
WT_AHA_11	T2D	2	1	rs5761022	116304946	2.49E-03	CASQ2	intronic	13.09	7	2.10E-01	0.008	1.54E-07	-0.031
WT_AHA_11	T2D	3	2	rs2163227	43549229	3.84E-03	THADA	intronic	2.536	7	1.92E-06	0.034	7.53E-06	-0.029
WT_AHA_11	T2D	4	3	rs6225318	69907115	1.30E-07	MITF	intronic	0.004	7	1.51E-02	-0.020	1.53E-11	0.051
WT_AHA_11	T2D	5	3	rs5619527	169137301	7.35E-03	MECOM	intronic	1.232	6	1.35E-02	0.018	3.95E-06	-0.031
WT_AHA_11	T2D	6	4	rs6851635	186387444	4.08E-03	CCDC110	intronic	1.613	7	4.78E-03	-0.020	3.43E-06	-0.030
WT_AHA_11	T2D	7	6	rs3176326	36647289	2.30E-07	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.65E-10	0.047
WT_AHA_11	T2D	8	6	rs188181	118620094	8.62E-03	SLC35F1	intronic	0.18	NA	8.53E-04	0.021	1.54E-05	-0.025
WT_AHA_11	T2D	9	6	rs7753038	126077657	1.92E-05	HEY2	intronic	2.881	6	9.34E-08	0.034	2.20E-08	-0.033
WT_AHA_11	T2D	10	6	rs9388537	127198630	5.46E-03	RPS4XP9	intergenic	5.728	5	3.31E-01	0.006	2.52E-07	0.030
WT_AHA_11	T2D	11	7	rs117823438	52699269	8.96E-04	RP11-398K14.1	intergenic	0.082	6	1.07E-01	-0.020	8.75E-08	0.061
WT_AHA_11	T2D	13	10	rs1076265	76838306	6.38E-04	PPIAP13	intergenic	6.15	6	2.95E-03	0.019	5.74E-07	-0.030
WT_AHA_11	T2D	14	11	rs1103933	47706141	6.07E-05	AGBL2	intronic	4.272	6	9.75E-07	-0.032	8.28E-08	0.031
WT_AHA_11	T2D	15	11	rs1122837	68594174	1.95E-03	CPT1A	intronic	1.848	7	1.96E-03	-0.020	2.24E-06	-0.028
WT_AHA_11	T2D	16	11	rs1279869	69045735	5.83E-03	MYEOV	intergenic	11.21	4	7.53E-05	0.026	1.19E-05	-0.026
WT_AHA_11	T2D	17	15	rs3803405	85383640	3.71E-17	ALPK3	exonic	10.99	5	2.58E-02	0.016	1.16E-21	-0.063
WT_AHA_11	T2D	18	15	rs7166287	99273075	5.70E-05	IGF1R	intronic	3.33	4	1.92E-01	-0.009	2.02E-09	-0.037

WT_AHA_11	T2D	19	17	rs12453217	37741982	2.11E-08	NEUROD2	intergenic	1.422	6	7.60E-05	0.032	1.34E-11	-0.051
WT_AHA_11	T2D	20	17	rs2696532	44355602	1.30E-10	ARL17B	intronic	0.835	NA	9.10E-03	-0.021	1.30E-14	0.056
WT_AHA_11	T2D	21	18	rs2337143	46482070	4.53E-03	SMAD7	intergenic	6.132	2b	1.32E-01	-0.010	4.73E-07	0.031
WT_AHA_11	T2D	22	22	rs9608201	24166788	1.73E-05	SMARCB1	intronic	1.469	2b	7.63E-01	-0.002	1.39E-10	0.047
WT_AHA_11	T2D	23	22	rs1004243	31497879	2.31E-03	SMTN	intronic	7.849	5	3.55E-01	0.006	8.44E-08	0.032
WT_AHA_12	T2D	1	1	rs6177541	26393505	2.60E-06	TRIM63	intronic	22.4	4	3.72E-06	-0.047	1.99E-09	0.055
WT_AHA_12	T2D	2	1	rs6659025	116301019	4.11E-03	CASQ2	intronic	1.126	7	1.30E-01	-0.010	3.90E-07	0.032
WT_AHA_12	T2D	3	1	rs2494196	219762581	9.51E-03	ZC3H11B	intergenic	0.548	NA	3.29E-15	-0.056	2.09E-05	-0.028
WT_AHA_12	T2D	4	2	rs2075209	65246123	7.76E-03	SLC1A4	intronic	1.932	NA	3.91E-08	-0.047	1.63E-05	-0.034
WT_AHA_12	T2D	5	2	rs985092	155629561	5.14E-03	KCNJ3	intronic	1.502	6	2.24E-01	0.018	3.25E-07	0.071
WT_AHA_12	T2D	6	2	rs111692972	179669931	8.90E-03	TTN	intronic	1.587	7	1.35E-01	0.020	9.22E-07	-0.063
WT_AHA_12	T2D	7	3	rs6225318	69907115	4.95E-09	MITF	intronic	0.004	7	1.51E-02	-0.020	4.58E-13	0.055
WT_AHA_12	T2D	8	3	rs112781244	135685290	1.96E-03	PPP2R3A	intronic	12.95	4	1.36E-03	-0.022	1.95E-06	-0.030
WT_AHA_12	T2D	9	6	rs3176326	36647289	2.63E-09	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.71E-12	0.053
WT_AHA_12	T2D	10	6	rs2781564	73177863	4.50E-03	RP11-135M8__A.1	intergenic	5.866	7	1.09E-01	0.010	4.96E-07	0.030
WT_AHA_12	T2D	11	6	rs1159974	126090277	3.26E-03	HEY2	intergenic	3.681	5	6.60E-08	-0.035	5.55E-06	-0.027
WT_AHA_12	T2D	12	7	rs4731702	130433384	3.26E-03	KLF14	intergenic	0.116	7	1.47E-13	-0.047	5.54E-06	-0.027
WT_AHA_12	T2D	14	11	rs1160482	47725306	9.39E-05	AGBL2	intronic	3.446	7	1.27E-03	0.022	6.40E-08	-0.034
WT_AHA_12	T2D	15	11	rs11603763	68789606	5.41E-03	RP11-554A11.6	intergenic	9.077	5	2.86E-05	-0.028	1.05E-05	-0.027
WT_AHA_12	T2D	16	11	rs1279869	69045735	3.55E-03	MYEOV	intergenic	11.21	4	7.53E-05	0.026	6.18E-06	-0.027
WT_AHA_12	T2D	17	12	rs1110537	90088768	1.85E-03	ATP2B1	intronic	1.353	7	2.59E-01	0.010	8.81E-08	-0.042
WT_AHA_12	T2D	18	15	rs3803405	85383640	7.01E-25	ALPK3	exonic	10.99	5	2.58E-02	0.016	1.65E-29	-0.075

WT_AHA_12	T2D	19	15	rs7166287	99273075	1.23E-06	IGF1R	intronic	3.33	4	1.92E-01	-0.009	3.53E-11	-0.041
WT_AHA_12	T2D	20	16	rs74962019	66511905	6.66E-03	BEAN1:C TD- 2258A20.5 :RP11- 403P17.5	ncRNA_ex onic	2.208	3a	4.15E-01	-0.013	2.56E-07	0.080
WT_AHA_12	T2D	21	16	rs733324	85685120	6.89E-03	GSE1	intronic	0.281	4	8.10E-04	-0.025	1.18E-05	-0.030
WT_AHA_12	T2D	22	17	rs7994375	5917015	4.65E-03	WSCD1	intronic	5.205	7	1.60E-01	-0.052	3.80E-07	-0.162
WT_AHA_12	T2D	23	17	rs903503	37829571	1.44E-05	PGAP3	intronic	0.735	NA	1.50E-04	-0.026	1.19E-08	-0.036
WT_AHA_12	T2D	24	17	rs9303525	44187257	1.17E-08	KANSL1	intronic	2.711	1b	7.21E-03	-0.021	1.92E-12	0.049
WT_AHA_12	T2D	25	20	rs6220946	48375285	1.22E-03	SNRPFP1	intergenic	5.389	4	1.21E-01	-0.025	1.03E-07	-0.079
WT_AHA_12	T2D	26	22	rs1004243	31497879	2.35E-04	SMTN	intronic	7.849	5	3.55E-01	0.006	6.96E-09	0.035
WT_global	T2D	1	1	rs1737632	11876662	4.49E-03	CLCN6	intronic	10.13	7	1.94E-02	-0.032	1.84E-06	-0.058
WT_global	T2D	2	1	rs6659025	116301019	8.53E-03	CASQ2	intronic	1.126	7	1.30E-01	-0.010	1.14E-06	0.028
WT_global	T2D	3	1	rs2494196	219762581	9.02E-05	ZC3H11B	intergenic	0.548	NA	3.29E-15	-0.056	1.29E-07	-0.032
WT_global	T2D	4	2	rs2033834	42524781	5.65E-03	EML4	intronic	1.13	4	1.79E-02	0.041	2.50E-06	0.071
WT_global	T2D	5	2	rs2163227	43549229	3.02E-03	THADA	intronic	2.536	7	1.92E-06	0.034	5.35E-06	-0.028
WT_global	T2D	6	2	rs1009360	65276049	1.15E-03	CEP68	intergenic	1.02	NA	1.60E-13	0.048	1.86E-06	-0.027
WT_global	T2D	7	2	rs76948576	112423628	5.67E-03	AC093166 .1	intergenic	2.054	5	7.24E-03	-0.028	3.93E-06	-0.044
WT_global	T2D	8	2	rs355822	165703572	6.14E-03	AC019181 .2	ncRNA_int ronic	0.613	NA	3.41E-03	-0.019	5.94E-06	-0.025
WT_global	T2D	9	2	rs2618146	218302013	5.45E-03	DIRC3	intergenic	0.925	5	1.00E+00	0.000	1.41E-07	-0.031
WT_global	T2D	10	3	rs6225223	69893064	9.16E-08	MITF	intronic	0.655	7	1.59E-03	-0.021	5.47E-11	-0.037
WT_global	T2D	11	3	rs9637450	169148420	4.92E-03	MECOM	intronic	13.48	5	1.07E-02	0.019	2.78E-06	-0.030
WT_global	T2D	12	3	rs4894803	171800256	1.16E-04	FNDC3B	intronic	21.6	4	3.27E-03	-0.019	8.52E-08	0.031
WT_global	T2D	13	5	rs7710854	43824677	2.44E-04	RP11- 8L21.1	intergenic	0.482	6	2.04E-01	0.013	1.55E-08	-0.049
WT_global	T2D	14	5	rs7280147	132444128	3.44E-04	HSPA4	intergenic	0.703	5	6.18E-03	-0.030	2.04E-07	-0.049

WT_global	T2D	15	6	rs7774403	12950751	3.46E-03	PHACTR1	intronic	3.83	5	6.91E-02	0.012	6.38E-07	-0.028
WT_global	T2D	16	6	rs3176326	36647289	2.52E-11	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.53E-14	0.054
WT_global	T2D	17	6	rs1015150	41659304	5.98E-03	TFEB	intronic	0.494	5	1.77E-03	0.020	7.49E-06	-0.025
WT_global	T2D	18	6	rs1563666	77327285	5.58E-03	RP11-35J1.1	intergenic	2.59	7	3.05E-01	-0.009	3.82E-07	0.038
WT_global	T2D	19	6	rs1159974	126090277	2.62E-04	HEY2	intergenic	3.681	5	6.60E-08	-0.035	3.90E-07	-0.028
WT_global	T2D	20	6	rs9385410	127190027	1.87E-04	RPS4XP9	intergenic	2.453	7	3.23E-01	-0.006	7.84E-09	0.032
WT_global	T2D	21	7	rs4731701	130430930	5.02E-03	KLF14	intergenic	0.021	7	1.65E-13	-0.047	9.49E-06	-0.025
WT_global	T2D	22	8	rs306960	142005245	3.38E-03	PTK2	intronic	1.381	5	8.17E-01	-0.002	9.56E-08	0.030
WT_global	T2D	23	10	rs61870180	105438913	3.20E-03	SH3PXD2A	intronic	2.384	4	3.40E-01	0.024	1.86E-07	0.119
WT_global	T2D	24	11	rs621679	1902768	2.19E-03	LSP1	exonic	0.07	2a	5.09E-01	0.005	8.60E-08	0.031
WT_global	T2D	25	11	rs7506540	45864942	3.61E-04	CRY2	intergenic	8.161	4	1.02E-03	-0.051	4.35E-07	0.068
WT_global	T2D	26	11	rs1160482	47725306	1.72E-11	AGBL2	intronic	3.446	7	1.27E-03	0.022	6.15E-15	-0.045
WT_global	T2D	27	11	rs7117365	56738678	3.73E-03	OR5AK3P	ncRNA_exonic	5.445	6	1.99E-02	0.018	1.48E-06	-0.032
WT_global	T2D	28	11	rs2306363	65405600	3.44E-04	SIPA1	UTR5	19.83	2b	1.10E-06	-0.040	5.17E-07	-0.034
WT_global	T2D	29	11	rs1279869	69045735	4.90E-03	MYEOV	intergenic	11.21	4	7.53E-05	0.026	9.22E-06	-0.025
WT_global	T2D	30	12	rs1049376	26491475	5.44E-03	RP11-513G19.1:1TPR2	ncRNA_intronic	2.765	NA	1.03E-05	-0.031	1.05E-05	0.028
WT_global	T2D	31	12	rs2681492	90013089	2.13E-05	ATP2B1	intronic	0.451	NA	3.17E-01	-0.009	7.28E-10	-0.045
WT_global	T2D	32	15	rs3563068	85349231	6.87E-19	ZNF592	UTR3	11.99	7	7.91E-02	-0.013	8.83E-24	-0.063
WT_global	T2D	33	15	rs6202449	99276297	2.03E-05	IGF1R	intronic	0.398	6	6.19E-02	0.013	2.62E-09	-0.036
WT_global	T2D	34	17	rs3764351	37824339	4.65E-04	PNMT	intronic	5.182	NA	9.23E-05	-0.026	7.09E-07	-0.029
WT_global	T2D	36	18	rs497999	32672836	3.70E-05	MAPRE2	intronic	1.268	NA	5.92E-01	0.004	7.72E-10	-0.037
WT_global	T2D	37	22	rs2267039	24169751	1.07E-03	SMARCB1	intronic	6.324	5	7.34E-01	-0.003	2.71E-08	0.039
WT_global	T2D	38	22	rs4820654	26162902	5.17E-05	MYO18B	intronic	4.385	4	5.11E-01	0.004	1.28E-09	0.035

RAV_max	T2D	1	2	rs1218562	179680971	6.30E-03	TTN	intronic	3.074	5	9.67E-05	-0.030	7.18E-06	-0.039
RAV_max	T2D	2	5	rs2277923	172662024	8.83E-03	NKX2-5	exonic	18.15	NA	8.11E-01	-0.002	3.14E-08	0.044
RAV_max	T2D	3	6	rs937277	118673075	9.77E-05	SLC35F1	intergenic	3.662	5	1.21E-01	0.010	1.53E-09	-0.045
RAV_max	T2D	4	7	rs849138	28177338	3.65E-05	JAZF1	intronic	0.249	4	3.83E-41	-0.086	2.89E-08	-0.039
RAV_max	T2D	5	8	rs5623301	144981488	1.51E-03	PLEC	intergenic	1.569	6	4.04E-04	-0.060	1.39E-06	0.084
RAV_max	T2D	6	11	rs1123617	74341336	9.15E-04	POLD3	intronic	0.522	4	6.16E-01	0.003	3.86E-09	-0.042
RAV_max	T2D	7	19	rs915915	46274972	5.00E-03	AC074212 .6:DMPK	ncRNA_ex onic	9.474	NA	1.10E-04	0.025	5.45E-06	0.032
RAV_min	T2D	1	1	rs6177658	26438933	8.50E-04	PDIK1L	intronic	8.105	3a	1.35E-06	0.043	8.59E-07	-0.048
RAV_min	T2D	2	2	rs1218562	179680971	1.54E-04	TTN	intronic	3.074	5	9.67E-05	-0.030	1.30E-07	-0.045
RAV_min	T2D	3	3	rs5571689	71498561	5.33E-03	FOXP1	intronic	6.163	7	2.43E-05	0.027	7.78E-06	0.032
RAV_min	T2D	4	6	rs1221073	118653075	4.55E-04	SLC35F1	intergenic	3.445	7	7.09E-02	0.026	1.13E-08	-0.088
RAV_min	T2D	5	7	rs849138	28177338	8.33E-03	JAZF1	intronic	0.249	4	3.83E-41	-0.086	1.36E-05	-0.030
RAV_min	T2D	7	8	rs5623301	144981488	1.38E-04	PLEC	intergenic	1.569	6	4.04E-04	-0.060	1.16E-07	0.091
RAV_min	T2D	8	11	rs1021920	74324923	7.48E-04	POLD3	intronic	0.868	5	5.95E-01	0.003	3.20E-09	-0.041
RAV_min	T2D	9	12	rs7689596 3	4384844	3.95E-03	CCND2- AS1:CCN D2	ncRNA_int ronic	14	4	9.12E-69	0.483	5.33E-06	0.139
RAV_min	T2D	10	15	rs5925143 3	98272210	6.09E-04	LINC0092 3	intergenic	12.31	5	4.76E-01	0.005	3.13E-09	-0.042
RAV_min	T2D	11	19	rs5630903	46311420	5.88E-04	RSPH6A	intronic	3.054	7	3.13E-05	-0.028	5.66E-07	0.037

Note: Distinct genomic loci associated with CMR trait at condFDR < 0.05 (based on T2D association).

ANNOVAR: Functional depletion score, where higher scores indicate greater deleterious effects. RegulomeDB score: Predicts the likelihood of regulatory functionality, with lower scores indicating higher likelihood.

minChrState: Minimum chromatin state across 127 tissues where lower scores indicate more open chromatin commonChrState: Most common chromatin

Genomic loci shared between T2D and CMR phenotypic traits identified by conjunctonal FDR analyses

Conjunctonal FDR analysis							FUMA				Original GWAS summary sumstats				LAVA analysis	
Trait1	Trait2	locus num	CHR	LEAD_SN P	FDR q	ConcordEffect	nearestGene	func	CADD	RDB	PVAL_in_Trait1	BETA_in_Trait1	PVAL_in_Trait2	BETA_in_Trait2	rho	FDR q
T2D	RAV_max	1	2	rs12185628	1.87E-02	No	TTN	intronic	3.074	5	9.67E-05	-0.030	7.18E-06	-0.039	-1.000	3.76E-02
T2D	RAV_max	2	3	rs55716899	2.10E-02	No	FOXP1	intronic	6.163	7	2.43E-05	0.027	3.13E-05	0.030	-0.740	4.60E-02
T2D	RAV_max	3	7	rs849138	3.75E-05	No	JAZF1	intronic	0.249	4	3.83E-41	-0.086	2.89E-08	-0.039	-1.000	8.75E-08
T2D	RAV_max	4	8	rs11784619	4.72E-02	No	PLEC	intronic	15	2b	3.66E-04	-0.054	7.21E-06	0.070	-0.461	1.17E-01
T2D	RAV_max	5	9	rs550057	1.85E-02	Yes	ABO	ncRNA_intronic	1.329	6	6.16E-09	0.043	2.66E-05	0.034	0.699	6.14E-02
T2D	RAV_max	6	12	rs75616205	1.36E-02	No	CCND2-AS1	intergenic	0.28	6	1.47E-18	0.192	1.80E-05	0.107	-0.185	4.03E-01
T2D	RAV_max	7	12	rs7968682	4.14E-02	No	HMGA2	intergenic	13.76	6	3.65E-17	0.054	7.64E-05	0.028	NA	NA
T2D	RAV_max	8	15	rs11856538	1.80E-02	No	TSPAN3	intergenic	1.086	4	9.18E-05	0.026	1.79E-05	-0.031	-0.044	8.62E-01
T2D	RAV_max	9	19	rs16939	1.04E-02	No	DMPK	intronic	5.638	4	4.46E-05	-0.027	6.95E-06	0.032	-0.412	9.37E-02
T2D	RAV_min	1	1	rs61776586	8.33E-04	Yes	PDIK1L	intronic	8.105	3a	1.35E-06	0.043	8.59E-07	-0.048	1.000	2.51E-01
T2D	RAV_min	2	2	rs12185628	1.40E-02	No	TTN	intronic	3.074	5	9.67E-05	-0.030	1.30E-07	-0.045	-1.000	4.47E-02

T2D	RAV_mi_n	3	3	rs55716899	5.29E-03	No	FOXP1	intronic	6.163	7	2.43E-05	0.027	7.78E-06	0.032	-0.669	5.85E-02
T2D	RAV_mi_n	4	3	rs6798814	4.29E-02	No	RP11-132N15.3	ncRNA_intronic	0.878	5	3.42E-07	0.033	1.26E-04	-0.027	-1.000	3.31E-02
T2D	RAV_mi_n	5	6	rs62427982	1.55E-02	No	BEND3	upstream	17.12	4	1.29E-08	-0.039	3.12E-05	0.031	-0.858	4.47E-02
T2D	RAV_mi_n	6	6	rs72959041	4.88E-02	No	RSPO3	intronic	2.875	6	5.31E-04	0.050	1.50E-04	-0.063	-0.258	4.93E-01
T2D	RAV_mi_n	7	7	rs849138	8.22E-03	No	JAZF1	intronic	0.249	4	3.83E-41	-0.086	1.36E-05	-0.030	NA	NA
T2D	RAV_mi_n	9	8	rs12155647	2.24E-02	Yes	RP11-145O15.3	intergenic	1.264	7	1.82E-04	0.029	2.35E-05	0.037	NA	NA
T2D	RAV_mi_n	10	8	rs60394484	1.91E-02	No	OPLAH	intergenic	0.729	7	1.47E-04	-0.062	1.82E-05	0.068	-0.474	2.52E-01
T2D	RAV_mi_n	11	11	rs349080	4.18E-02	No	DLG2	intronic	1.902	5	3.17E-04	0.023	1.21E-04	-0.027	NA	NA
T2D	RAV_mi_n	12	12	rs76895963	3.91E-03	No	CCND2-AS1:CCND2	ncRNA_intronic	14	4	9.12E-69	0.483	5.33E-06	0.139	-0.395	1.16E-01
T2D	RAV_mi_n	13	12	rs10748028	3.74E-02	No	HMGA2	intergenic	1.037	7	3.67E-04	0.024	6.39E-05	-0.029	-0.804	6.79E-02
T2D	RAV_mi_n	14	15	rs2044453	1.76E-02	No	PEAK1	intronic	1.217	NA	9.72E-05	-0.025	3.72E-05	-0.030	-0.207	4.93E-01
T2D	RAV_mi_n	15	19	rs16980013	3.68E-03	No	AC074212.3	UTR3	4.294	4	1.72E-05	-0.030	3.72E-06	0.035	-0.476	6.14E-02
T2D	WT_AH_A_10	1	1	rs2820449	1.76E-02	Yes	RP11-95P13.2	intergenic	0.078	NA	9.57E-14	-0.050	3.47E-05	-0.025	NA	NA

T2D	WT_AH A_10	2	2	rs2163227	5.08E-04	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	2.23E-07	-0.032	0.801	3.77E-02
T2D	WT_AH A_10	3	2	rs2723086	2.32E-02	Yes	CEP68	intronic	11.02	4	2.10E-13	-0.049	4.93E-05	-0.024	NA	NA
T2D	WT_AH A_10	4	2	rs6436603	3.19E-02	Yes	AC06813 8.1	intergen ic	4.703	6	1.67E-05	0.029	7.53E-05	0.024	NA	NA
T2D	WT_AH A_10	5	3	rs3425560 0	4.85E-02	No	MITF	intronic	5.126	7	4.80E-04	-0.022	3.97E-05	-0.024	-0.109	8.15E-01
T2D	WT_AH A_10	6	4	rs1313509 2	3.62E-02	No	SLC39A8	intronic	10.31	6	3.29E-04	-0.046	5.30E-05	-0.043	-0.926	2.23E-01
T2D	WT_AH A_10	7	6	rs3176326	3.85E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	3.31E-08	0.040	-0.798	1.01E-01
T2D	WT_AH A_10	8	6	rs6938951	4.62E-02	Yes	RP11- 173D14.3	intergen ic	2.527	6	2.81E-04	-0.023	1.24E-04	-0.022	0.688	3.35E-01
T2D	WT_AH A_10	9	6	rs1155938	1.01E-02	Yes	RNU6- 200P	intergen ic	3.387	NA	5.03E-14	0.048	1.71E-05	0.024	0.068	7.19E-01
T2D	WT_AH A_10	10	6	rs622217	2.94E-02	Yes	SLC22A3	intergen ic	1.651	5	2.08E-08	0.036	6.75E-05	-0.023	0.596	1.80E-01
T2D	WT_AH A_10	11	7	rs3428290 4	1.10E-02	Yes	KLF14	intergen ic	1.608	7	1.86E-13	-0.047	1.90E-05	-0.024	0.459	1.68E-01
T2D	WT_AH A_10	12	11	rs1228672 1	2.46E-04	No	AGBL2	exonic	14.46	1f	8.14E-07	0.032	1.47E-07	0.030	-0.884	3.55E-02
T2D	WT_AH A_10	13	11	rs1279869 3	1.11E-02	Yes	MYEOV	intergen ic	11.21	4	7.53E-05	0.026	1.49E-05	-0.025	0.893	6.87E-02
T2D	WT_AH A_10	14	12	rs5627079 0	4.48E-02	Yes	RP11- 834C11.1 2:HOXC4 :RP11- 834C11.1 4	ncRNA _introni c	10.86	4	2.15E-04	-0.025	1.19E-04	-0.023	NA	NA

T2D	WT_AH A_10	15	12	rs7592961 6	4.31E-02	No	POC1B	intronic	5.876	3a	2.12E-04	-0.067	1.13E-04	-0.056	-0.470	3.03E-01
T2D	WT_AH A_10	16	17	rs8182252	6.16E-03	No	CDK12	intergenic	14.32	5	3.38E-05	-0.036	9.36E-06	-0.034	NA	NA
T2D	WT_AH A_11	1	1	rs6177541 8	8.50E-04	No	TRIM63	intronic	22.4	4	3.72E-06	-0.047	9.95E-09	0.052	-0.491	3.49E-01
T2D	WT_AH A_11	2	1	rs4617393	3.12E-02	Yes	MACF1	intronic	6.305	6	5.69E-18	-0.061	9.76E-05	0.025	NA	NA
T2D	WT_AH A_11	3	1	rs1213316 9	2.27E-02	Yes	ZC3H11B	intergenic	5.867	7	1.08E-08	-0.046	6.54E-05	-0.027	NA	NA
T2D	WT_AH A_11	4	2	rs2163227	3.55E-03	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	7.53E-06	-0.029	0.903	6.60E-02
T2D	WT_AH A_11	5	2	rs1009360	1.35E-02	Yes	CEP68	intergenic	1.02	NA	1.60E-13	0.048	3.46E-05	-0.024	NA	NA
T2D	WT_AH A_11	6	2	rs7834349 3	2.56E-02	No	COBL1	intergenic	2.318	6	2.34E-18	-0.085	7.57E-05	0.035	-0.284	2.52E-01
T2D	WT_AH A_11	7	3	rs3425560 0	4.27E-02	No	MITF	intronic	5.126	7	4.80E-04	-0.022	2.68E-08	-0.033	-0.572	1.36E-01
T2D	WT_AH A_11	8	6	rs3176326	3.37E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.65E-10	0.047	-0.858	6.14E-02
T2D	WT_AH A_11	9	6	rs1045746 9	3.02E-05	Yes	HEY2	intergenic	0.025	7	6.60E-08	0.035	2.90E-08	-0.032	NA	NA
T2D	WT_AH A_11	10	6	rs1015446	6.64E-03	Yes	RPS4XP9	intergenic	0.709	NA	4.03E-12	-0.044	1.52E-05	0.025	0.131	5.30E-01
T2D	WT_AH A_11	11	7	rs1197911 0	3.24E-02	Yes	KLF14	intergenic	0.059	7	5.28E-13	-0.046	1.03E-04	-0.023	0.230	4.21E-01
T2D	WT_AH A_11	13	10	rs921326	2.50E-02	No	DUPD1	intergenic	2.636	5	2.42E-04	0.025	4.92E-05	-0.025	-0.341	4.11E-01

T2D	WT_AH A_11	14	11	rs1382901 26	3.74E-02	No	WT1-AS	ncRNA _intronic	2.866	7	3.76E-06	-0.040	1.24E-04	-0.029	NA	NA
T2D	WT_AH A_11	15	11	rs1056387	1.80E-04	No	AGBL2	UTR3	1.579	NA	5.44E-07	0.032	1.75E-07	0.030	-0.729	3.65E-02
T2D	WT_AH A_11	16	11	rs1249580	3.76E-03	Yes	RP11- 554A11.4	downstr eam	3.991	NA	2.36E-05	-0.027	6.95E-06	-0.026	NA	NA
T2D	WT_AH A_11	17	11	rs1279869 3	9.71E-03	Yes	MYEOV	intergen ic	11.21	4	7.53E-05	0.026	1.19E-05	-0.026	1.000	5.85E-02
T2D	WT_AH A_11	18	12	rs1104847 0	1.57E-02	Yes	RP11- 283G6.4: RP11- 513G19.1	ncRNA _intronic	0.166	7	8.49E-06	0.032	4.16E-05	0.027	0.689	1.80E-01
T2D	WT_AH A_11	19	12	rs1104909 1	3.14E-02	Yes	PPFIBP1	intronic	0.88	6	9.38E-10	0.052	9.83E-05	-0.030	NA	NA
T2D	WT_AH A_11	20	12	rs1087576 2	4.18E-02	Yes	C12orf68	intergen ic	0.447	7	4.12E-06	-0.035	1.43E-04	0.026	0.836	2.52E-01
T2D	WT_AH A_11	21	15	rs881984	4.34E-03	No	ADAMTS L3	intronic	7.633	NA	2.82E-05	-0.029	1.47E-06	-0.030	NA	NA
T2D	WT_AH A_11	22	17	rs2100651	5.87E-04	No	RP11- 690G19.4	ncRNA _intronic	3.393	6	2.34E-06	-0.035	1.21E-07	-0.035	NA	NA
T2D	WT_AH A_11	23	20	rs6142109	4.20E-02	No	RPS2P1	intergen ic	0.135	7	1.67E-04	0.027	1.44E-04	0.025	-0.533	2.22E-01
T2D	WT_AH A_11	24	20	rs1303672 3	4.08E-02	Yes	NCOA3	intronic	4.03	6	8.22E-05	0.027	1.39E-04	-0.023	NA	NA
T2D	WT_AH A_12	1	1	rs6177541 8	1.01E-03	No	TRIM63	intronic	22.4	4	3.72E-06	-0.047	1.99E-09	0.055	-0.223	5.33E-01

T2D	WT_AH A_12	2	1	rs2494196	1.16E-02	Yes	ZC3H11B	intergenic	0.548	NA	3.29E-15	-0.056	2.09E-05	-0.028	1.000	3.66E-02
T2D	WT_AH A_12	3	2	rs2163227	2.23E-02	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	4.73E-05	-0.027	0.361	2.38E-01
T2D	WT_AH A_12	4	2	rs2075209	9.54E-03	Yes	SLC1A4	intronic	1.932	NA	3.91E-08	-0.047	1.63E-05	-0.034	1.000	9.41E-03
T2D	WT_AH A_12	5	3	rs3425560 0	4.26E-02	No	MITF	intronic	5.126	7	4.80E-04	-0.022	5.71E-10	-0.037	-0.356	2.94E-01
T2D	WT_AH A_12	6	3	rs1403769	2.66E-02	No	RP11- 305O4.1	intergenic	1.256	NA	2.42E-04	-0.025	3.45E-05	-0.026	-0.578	2.51E-01
T2D	WT_AH A_12	7	3	rs1499813	3.84E-02	Yes	FNDC3B	intronic	10.81	2b	4.12E-04	-0.023	7.35E-05	0.024	NA	NA
T2D	WT_AH A_12	8	6	rs3176326	3.47E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.71E-12	0.053	-1.000	3.66E-02
T2D	WT_AH A_12	9	6	rs1159974	4.05E-03	Yes	HEY2	intergenic	3.681	5	6.60E-08	-0.035	5.55E-06	-0.027	NA	NA
T2D	WT_AH A_12	10	7	rs4731702	4.05E-03	Yes	KLF14	intergenic	0.116	7	1.47E-13	-0.047	5.54E-06	-0.027	0.384	1.59E-01
T2D	WT_AH A_12	12	11	rs6485763	3.47E-03	No	Y_RNA	intergenic	1.615	1f	5.61E-06	-0.029	4.57E-06	0.027	-0.786	4.47E-02
T2D	WT_AH A_12	13	11	rs1160376 3	6.71E-03	Yes	RP11- 554A11.6	intergenic	9.077	5	2.86E-05	-0.028	1.05E-05	-0.027	0.754	8.84E-02
T2D	WT_AH A_12	14	15	rs881984	5.05E-03	No	ADAMTS L3	intronic	7.633	NA	2.82E-05	-0.029	2.65E-08	-0.035	NA	NA
T2D	WT_AH A_12	15	16	rs4843185	2.96E-02	Yes	GSE1	intronic	0.209	3a	2.08E-04	-0.027	6.81E-05	-0.027	0.253	5.82E-01
T2D	WT_AH A_12	16	17	rs6503513	3.11E-03	No	CTB- 131K11.1: MED1	ncRNA _intronic	20.4	7	1.55E-05	-0.036	2.08E-06	-0.036	NA	NA

T2D	WT_AH A_12	17	22	rs7292510	4.45E-02	Yes	RN7SL30 5P	intergen ic	0.107	7	6.66E-06	0.038	1.16E-04	-0.029	1.000	1.89E-02
T2D	WT_AH A_6	1	1	rs7413960 3	7.36E-03	No	PROX1	intergen ic	16.24	5	2.22E-05	0.064	1.27E-05	0.061	-0.939	4.47E-02
T2D	WT_AH A_6	2	1	rs4846567	2.70E-04	Yes	RP11- 95P13.2	intergen ic	14.9	5	3.62E-17	-0.059	2.91E-07	-0.036	NA	NA
T2D	WT_AH A_6	3	2	rs2163227	2.15E-02	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	4.64E-05	-0.029	0.717	4.47E-02
T2D	WT_AH A_6	4	2	rs2723063	6.56E-03	Yes	CEP68	intergen ic	0.648	NA	8.23E-15	0.050	1.11E-05	-0.029	NA	NA
T2D	WT_AH A_6	5	3	rs1499813	4.75E-02	Yes	FNDC3B	intronic	10.81	2b	4.12E-04	-0.023	3.46E-08	0.036	NA	NA
T2D	WT_AH A_6	6	4	rs2074974	1.31E-03	No	NCAPG	UTR5	8.05	NA	4.31E-08	-0.039	1.69E-06	0.034	NA	NA
T2D	WT_AH A_6	7	5	rs2914220	2.53E-02	Yes	RP11- 32D16.1	intergen ic	7.167	7	1.68E-04	0.026	2.07E-05	0.030	0.610	2.52E-01
T2D	WT_AH A_6	8	6	rs3176326	4.29E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.45E-08	0.046	-0.829	7.39E-02
T2D	WT_AH A_6	9	6	rs6902010	3.61E-02	Yes	RNU6- 1299P	intergen ic	1.789	2b	1.40E-05	0.028	8.92E-05	0.026	1.000	4.54E-02
T2D	WT_AH A_6	10	11	rs3527117 8	9.50E-03	Yes	KCNJ11	upstrea m	3.809	4	2.81E-18	-0.057	1.72E-05	0.028	0.984	1.31E-02
T2D	WT_AH A_6	11	11	rs1103933 6	5.51E-04	No	AGBL2	intronic	4.272	6	9.75E-07	-0.032	5.89E-07	0.032	-0.860	2.99E-02
T2D	WT_AH A_6	12	11	rs2306363	4.44E-03	Yes	SIPA1	UTR5	19.83	2b	1.10E-06	-0.040	6.99E-06	-0.036	0.737	3.77E-02
T2D	WT_AH A_6	13	11	rs1160376 3	7.00E-03	Yes	RP11- 554A11.6	intergen ic	9.077	5	2.86E-05	-0.028	6.70E-06	-0.030	0.322	5.23E-01

T2D	WT_AH A_6	14	15	rs881984	6.91E-03	No	ADAMTS L3	intronic	7.633	NA	2.82E-05	-0.029	2.81E-06	-0.032	NA	NA
T2D	WT_AH A_6	15	16	rs7189295	6.45E-03	Yes	CMIP	intronic	1.002	4	2.25E-06	0.031	1.09E-05	-0.029	NA	NA
T2D	WT_AH A_7	1	1	rs6177541 8	3.48E-03	No	TRIM63	intronic	22.4	4	3.72E-06	-0.047	4.46E-06	0.043	0.144	8.52E-01
T2D	WT_AH A_7	2	1	rs1015714 5	2.51E-02	Yes	NUAK2	intergen ic	3.152	4	7.37E-08	-0.036	5.04E-05	-0.025	1.000	6.14E-02
T2D	WT_AH A_7	3	1	rs2494196	4.20E-04	Yes	ZC3H11B	intergen ic	0.548	NA	3.29E-15	-0.056	4.04E-07	-0.034	0.977	9.41E-03
T2D	WT_AH A_7	4	2	rs2723063	1.69E-02	Yes	CEP68	intergen ic	0.648	NA	8.23E-15	0.050	3.06E-05	-0.025	NA	NA
T2D	WT_AH A_7	5	3	rs3425560 0	4.91E-02	No	MITF	intronic	5.126	7	4.80E-04	-0.022	6.67E-06	-0.027	-0.549	3.58E-01
T2D	WT_AH A_7	6	3	rs1714518	3.65E-02	Yes	RSRC1	intronic	4.819	5	1.94E-04	-0.024	8.22E-05	-0.023	0.533	2.52E-01
T2D	WT_AH A_7	7	6	rs3176326	3.93E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	4.09E-07	0.039	-0.792	1.16E-01
T2D	WT_AH A_7	8	6	rs1343116	2.29E-02	Yes	RP11- 624M8.1: HEY2	ncRNA _introni c	9.02	3a	6.00E-07	0.032	4.50E-05	-0.025	NA	NA
T2D	WT_AH A_7	9	6	rs1321204 4	2.52E-02	Yes	RPS4XP9	intergen ic	4.263	7	8.13E-06	-0.033	5.08E-05	-0.027	0.311	2.61E-01
T2D	WT_AH A_7	10	7	rs1026430 6	2.01E-03	Yes	JAZF1- AS1	ncRNA _introni c	0.365	6	1.41E-15	-0.063	2.34E-06	0.036	0.826	9.17E-04
T2D	WT_AH A_7	11	7	rs4731701	1.97E-03	Yes	KLF14	intergen ic	0.021	7	1.65E-13	-0.047	2.28E-06	-0.028	0.603	6.14E-02

T2D	WT_AH A_7	13	9	rs1011677 2	1.19E-02	No	GLIS3	intronic	16.71	4	1.09E-10	0.042	1.97E-05	-0.026	-0.502	1.10E-01
T2D	WT_AH A_7	14	11	rs2293578	9.67E-03	No	SLC39A1 3	UTR3	9.196	2b	6.04E-05	0.027	9.20E-09	-0.037	-0.324	3.03E-01
T2D	WT_AH A_7	15	11	rs1379302 59	4.43E-02	Yes	RP11- 707M1.1	ncRNA _intronic	0.06	5	6.46E-07	0.067	1.07E-04	0.046	0.849	4.77E-01
T2D	WT_AH A_7	16	11	rs2306363	9.85E-03	Yes	SIPA1	UTR5	19.83	2b	1.10E-06	-0.040	1.56E-05	-0.032	0.806	3.77E-02
T2D	WT_AH A_7	17	11	rs1279869 3	1.16E-02	Yes	MYEOV	intergenic	11.21	4	7.53E-05	0.026	4.71E-06	-0.028	0.888	6.14E-02
T2D	WT_AH A_7	18	12	rs723672	4.29E-02	Yes	CACNA1 C	intronic	17.27	4	3.32E-04	0.023	1.02E-04	0.024	NA	NA
T2D	WT_AH A_7	19	12	rs7133378	1.30E-02	Yes	DNAH10: CCDC92	intronic	0.707	7	3.43E-06	-0.032	2.20E-05	-0.027	NA	NA
T2D	WT_AH A_7	20	15	rs881984	5.11E-03	No	ADAMTS L3	intronic	7.633	NA	2.82E-05	-0.029	5.02E-07	-0.032	-0.653	1.43E-01
T2D	WT_AH A_7	21	17	rs8025120 1	3.89E-02	Yes	ATPAF2	intronic	14.04	5	1.47E-06	-0.048	8.95E-05	0.038	NA	NA
T2D	WT_AH A_7	22	17	rs6503513	3.08E-03	No	CTB- 131K11.1: MED1	ncRNA _intronic	20.4	7	1.55E-05	-0.036	2.21E-06	-0.036	NA	NA
T2D	WT_AH A_7	23	19	rs7562766 2	4.12E-02	Yes	APOE	downstream	4.8	2b	9.22E-10	-0.050	9.66E-05	-0.029	0.664	6.14E-02
T2D	WT_AH A_9	1	1	rs1213179 4	4.07E-02	Yes	ZC3H11B	intergenic	0.747	5	3.36E-14	-0.053	8.54E-05	-0.025	NA	NA
T2D	WT_AH A_9	2	2	rs2163227	4.20E-04	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	3.55E-08	-0.035	1.000	1.84E-02

T2D	WT_AH A_9	3	4	rs1313509 2	3.01E-02	No	SLC39A8	intronic	10.31	6	3.29E-04	-0.046	2.47E-05	-0.046	-0.564	3.51E-01
T2D	WT_AH A_9	4	5	rs26610	1.75E-02	Yes	ARL15	intronic	2.457	NA	2.05E-07	0.036	2.45E-05	-0.027	0.798	4.47E-02
T2D	WT_AH A_9	5	6	rs3176326	3.19E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	6.33E-06	0.033	-0.504	3.14E-01
T2D	WT_AH A_9	6	6	rs5621791 2	9.04E-03	Yes	RNU6- 200P	intergen ic	1.563	7	5.53E-06	-0.033	1.03E-05	-0.029	0.159	4.77E-01
T2D	WT_AH A_9	7	9	rs1011677 2	1.40E-02	No	GLIS3	intronic	16.71	4	1.09E-10	0.042	1.82E-05	-0.025	-0.593	8.84E-02
T2D	WT_AH A_9	8	11	rs3527117 8	4.74E-02	Yes	KCNJ11	upstrea m	3.809	4	2.81E-18	-0.057	1.09E-04	0.023	NA	NA
T2D	WT_AH A_9	9	11	rs7126378	4.62E-03	No	CELF1	intronic	0.938	5	2.98E-05	-0.027	4.53E-06	0.027	-0.709	3.66E-02
T2D	WT_AH A_9	10	11	rs3741378	7.63E-03	Yes	SIPA1	exonic	16.05	NA	5.24E-06	-0.043	8.33E-06	-0.037	1.000	9.17E-04
T2D	WT_AH A_9	11	11	rs1279869 3	4.25E-02	Yes	MYEOV	intergen ic	11.21	4	7.53E-05	0.026	9.15E-05	-0.023	NA	NA
T2D	WT_AH A_9	12	12	rs1084271 6	3.60E-02	Yes	RP11- 513G19.1: ITPR2	ncRNA _introni c	0.531	7	3.25E-04	-0.027	7.05E-05	0.028	0.777	1.61E-01
T2D	WT_AH A_9	13	12	rs1084299 4	3.46E-02	Yes	RN7SKP1 5	intergen ic	4.53	5	1.94E-20	-0.075	6.61E-05	-0.029	NA	NA
T2D	WT_AH A_9	14	17	rs2952151	3.91E-02	No	PGAP3	UTR3	3.808	2b	1.89E-04	0.026	8.00E-05	-0.025	NA	NA
T2D	WT_glo bal	1	1	rs7413960 3	3.18E-02	No	PROX1	intergen ic	16.24	5	2.22E-05	0.064	1.05E-04	0.047	-0.454	2.22E-01
T2D	WT_glo bal	2	1	rs2494196	1.09E-04	Yes	ZC3H11B	intergen ic	0.548	NA	3.29E-15	-0.056	1.29E-07	-0.032	1.000	2.69E-03

T2D	WT_glo bal	3	2	rs2163227	3.50E-03	Yes	THADA	intronic	2.536	7	1.92E-06	0.034	5.35E-06	-0.028	0.824	1.86E-02
T2D	WT_glo bal	4	2	rs1009360	1.37E-03	Yes	CEP68	intergen ic	1.02	NA	1.60E-13	0.048	1.86E-06	-0.027	NA	NA
T2D	WT_glo bal	5	3	rs3425560 0	3.57E-02	No	MITF	intronic	5.126	7	4.80E-04	-0.022	7.90E-10	-0.034	-0.498	1.96E-01
T2D	WT_glo bal	6	3	rs1403769	3.22E-02	No	RP11- 305O4.1	intergen ic	1.256	NA	2.42E-04	-0.025	1.07E-04	-0.023	-1.000	6.87E-02
T2D	WT_glo bal	7	3	rs1672928	4.70E-02	No	FAIM	intronic	10.52	NA	1.03E-04	-0.025	1.94E-04	-0.021	NA	NA
T2D	WT_glo bal	8	3	rs1499813	3.19E-02	Yes	FNDC3B	intronic	10.81	2b	4.12E-04	-0.023	5.03E-07	0.028	NA	NA
T2D	WT_glo bal	10	5	rs2454916	1.86E-02	Yes	ARL15	intronic	3.956	NA	5.76E-08	0.039	4.67E-05	-0.026	0.350	4.86E-01
T2D	WT_glo bal	11	5	rs2963478	2.47E-02	Yes	RP11- 32D16.1	intergen ic	2.048	NA	2.54E-04	0.025	7.13E-05	0.024	-0.836	5.85E-02
T2D	WT_glo bal	12	6	rs3176326	2.86E-02	No	CDKN1A	intronic	10.88	4	3.54E-04	-0.029	1.53E-14	0.054	-0.423	2.51E-01
T2D	WT_glo bal	13	6	rs4541741	4.37E-02	No	TFEB	intronic	1.394	6	6.42E-04	0.022	4.41E-05	-0.023	0.978	5.24E-02
T2D	WT_glo bal	14	6	rs1159974	3.18E-04	Yes	HEY2	intergen ic	3.681	5	6.60E-08	-0.035	3.90E-07	-0.028	0.248	2.30E-01
T2D	WT_glo bal	15	6	rs1321204 4	2.28E-03	Yes	RPS4XP9	intergen ic	4.263	7	8.13E-06	-0.033	3.27E-06	-0.029	0.637	1.17E-01
T2D	WT_glo bal	16	6	rs7295904 1	3.82E-02	Yes	RSPO3	intronic	2.875	6	5.31E-04	0.050	4.40E-05	0.053	0.823	1.23E-02
T2D	WT_glo bal	17	7	rs849335	3.28E-02	Yes	JAZF1- AS1	ncRNA _introni c	4.783	5	9.67E-30	0.076	1.10E-04	0.023	0.516	8.86E-02

T2D	WT_glo bal	18	7	rs4731701	5.64E-03	Yes	KLF14	intergen ic	0.021	7	1.65E-13	-0.047	9.49E-06	-0.025	0.386	3.08E-01
T2D	WT_glo bal	20	11	rs231362	1.98E-02	No	KCNQ1:K CNQ1OT 1	ncRNA _exonic	0.638	NA	5.84E-15	-0.052	5.16E-05	0.022	1.000	1.89E-02
T2D	WT_glo bal	21	11	rs3527117 8	4.66E-02	Yes	KCNJ11	upstrea m	3.809	4	2.81E-18	-0.057	1.92E-04	0.021	-0.694	1.89E-02
T2D	WT_glo bal	22	11	rs7124681	1.21E-05	No	CELF1	intronic	3.081	1f	2.45E-08	0.036	7.81E-11	-0.037	0.822	6.51E-03
T2D	WT_glo bal	23	11	rs2306363	4.17E-04	Yes	SIPA1	UTR5	19.83	2b	1.10E-06	-0.040	5.17E-07	-0.034	0.905	1.16E-01
T2D	WT_glo bal	24	11	rs1279869 3	8.81E-03	Yes	MYEOV	intergen ic	11.21	4	7.53E-05	0.026	9.22E-06	-0.025	0.534	2.61E-01
T2D	WT_glo bal	25	12	rs1049376	6.08E-03	Yes	RP11- 513G19.1: ITPR2	ncRNA _introni c	2.765	NA	1.03E-05	-0.031	1.05E-05	0.028	NA	NA
T2D	WT_glo bal	26	15	rs881984	4.03E-03	No	ADAMTS L3	intronic	7.633	NA	2.82E-05	-0.029	1.39E-07	-0.031	0.676	1.96E-01
T2D	WT_glo bal	27	17	rs6502764	3.17E-02	Yes	ZZEF1	intergen ic	3.038	6	3.83E-12	-0.046	1.04E-04	0.022	NA	NA
T2D	WT_glo bal	28	17	rs1877031	6.39E-03	No	STARD3	exonic	23.1	NA	5.00E-05	-0.028	1.92E-06	-0.028	0.961	5.59E-02
T2D	WT_glo bal	29	20	rs4809370	4.96E-02	Yes	AL158091 .1	intergen ic	0.196	5	8.16E-05	-0.026	2.13E-04	-0.021	NA	NA

Note:

Genes mapped by candidate SNPs with conjuncional FDR < 0.05 shared between T2D and CMR traits								
Trait	IndSigSNPs	symbol	pLI	ncRVIS	pos Ma pSN Ps	eqtlM apSN Ps	eqtlMapts	ciMapts
RAV_min	rs61776586	TMEM57	0.992504411290221	1.055454968	0	12	GTEX/v8/Esophagus_Gastroesophageal_Junction	NA
RAV_min	rs61776586	MTFR1L	0.431750877541367	0.035573706	0	140	GTEX/v8/Brain_Frontal_Cortex_BA9:GTEX/v8/Colon_Transverse:GTEX/v8/Esophagus_Gastroesophageal_Junction:GTEX/v8/Esophagus_Mucosa:GTEX/v8/Esophagus_Muscularis:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Heart_Left_Ventricle:GTEX/v8/Lung:GTEX/v8/Muscle_Skeletal:GTEX/v8/Skin_Sun_Exposed_Lower_leg:GTEX/v8/Stomach:GTEX/v8/Testis:GTEX/v8/Thyroid	NA
RAV_min	rs61776586	PAFAH2	2.68539651867445e-07	-0.682015872	0	140	GTEX/v8/Brain_Cerebellum:GTEX/v8/Muscle_Skeletal	NA
RAV_min	rs61776586	EXTL1	1.17897567862766e-12	-0.545045167	0	119	GTEX/v8/Brain_Cerebellar_Hemisphere:GTEX/v8/Brain_Cerebellum:GTEX/v8/Brain_Nucleus_accumbens_basal_ganglia:GTEX/v8/Brain_Putamen_basal_ganglia:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Muscle_Skeletal:GTEX/v8/Cells_Cultured_fibroblasts	NA
RAV_min	rs61776586	SLC30A2	0.708283236156756	NA	0	140	GTEX/v8/Heart_Left_Ventricle:GTEX/v8/Skin_Not_Sun_Exposed_Suprapubic:GTEX/v8/Skin_Sun_Exposed_Lower_leg	NA

RAV_min	rs61776586	TRIM63	4.71828632864004e-12	0.21677576	36	140	GTEX/v8/Cells_EBV-transformed_lymphocytes:GTEX/v8/Brain_Cerebellar_Hemisphere:GTEX/v8/Brain_Hypothalamus:GTEX/v8/Brain_Substantia_nigra:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Liver:GTEX/v8/Nerve_Tibial:GTEX/v8/Pancreas:GTEX/v8/Pituitary:GTEX/v8/Spleen:GTEX/v8/Testis:GTEX/v8/Thyroid:GTEX/v8/Uterus	NA
RAV_min	rs61776586	PDIK1L	0.381253877249055	-0.21720446	78	140	GTEX/v8/Brain_Anterior_cingulate_cortex_BA24:GTEX/v8/Brain_Cerebellar_Hemisphere:GTEX/v8/Brain_Cortex:GTEX/v8/Brain_Frontal_Cortex_BA9:GTEX/v8/Brain_Putamen_basal_ganglia:GTEX/v8/Esophagus_Mucosa:GTEX/v8/Cells_Cultured_fibroblasts:GTEX/v8/Skin_Not_Sun_Exposed_Suprapubic:GTEX/v8/Skin_Sun_Exposed_Lower_leg:GTEX/v8/Thyroid	NA
RAV_min	rs61776586	FAM110D	0.550404227081523	-0.050060073	10	0	NA	NA

RAV_min	rs61776586	CNKSRI	3.79048704121579e-16	-0.156165951	0	140	GTEX/v8/Adipose_Subcutaneous:GTEX/v8/Adipose_Visceral_Omentum:GTEX/v8/Artery_Aorta:GTEX/v8/Artery_Coronary:GTEX/v8/Artery_Tibial:GTEX/v8/Brain_Anterior_cingulate_cortex_BA24:GTEX/v8/Brain_Caudate_basal_ganglia:GTEX/v8/Brain_Cerebellar_Hemisphere:GTEX/v8/Brain_Cerebellum:GTEX/v8/Brain_Cortex:GTEX/v8/Brain_Hippocampus:GTEX/v8/Brain_Hypothalamus:GTEX/v8/Brain_Nucleus_accumbens_basal_ganglia:GTEX/v8/Brain_Putamen_basal_ganglia:GTEX/v8/Brain_Spinal_cord_cervical_c-1:GTEX/v8/Colon_Sigmoid:GTEX/v8/Esophagus_Gastroesophageal_Junction:GTEX/v8/Esophagus_Mucosa:GTEX/v8/Esophagus_Muscularis:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Heart_Left_Ventricle:GTEX/v8/Lung:GTEX/v8/Nerve_Tibial:GTEX/v8/Pituitary:GTEX/v8/Cells_Cultured_fibroblasts:GTEX/v8/Skin_Not_Sun_Exposed_Suprapubic:GTEX/v8/Skin_Sun_Exposed_Lower_leg:GTEX/v8/Testis:GTEX/v8/Thyroid	NA
RAV_min	rs61776586	CEP85	0.00585126875456993	-0.28245067	0	0	NA	Left_Ventricle
RAV_min	rs61776586	SH3BGRL3	0.795103829065415	-0.629466622	0	30	GTEX/v8/Heart_Atrial_Appendage	NA
RAV_min	rs61776586	CD52	0.530686211965741	0.099893421	0	97	GTEX/v8/Whole_Blood:GTEX/v8/Lung	NA
RAV_min	rs61776586	AIM1L	3.33461351873646e-07	NA	0	19	GTEX/v8/Lung	NA
RAV_min	rs61776586	RPS6KA1	0.725875552839744	0.354322377	0	1	GTEX/v8/Skin_Not_Sun_Exposed_Suprapubic	NA

RAV_min	rs12185628	PLEKHA3	0.0229786985598172	-0.310485926	0	1	GTEEx/v8/Cells_Cultured_fibroblasts	NA
RAV_min	rs12185628	TTN	1.21111377105808e-32	-0.562314594	8	7	GTEEx/v8/Pancreas	NA
RAV_min	rs12185628	CCDC141	1.4276211576785e-09	NA	5	7	GTEEx/v8/Pancreas	Left_Ventric le
RAV_min	rs55716899	FOXP1	0.999750735055125	-0.080650462	108	0	NA	NA
RAV_min	rs6798814	BCL6	0.982525139432015	-0.618718172	0	0	NA	Left_Ventric le
RAV_min	rs6798814	TPRG1	4.87825873738663e-05	-0.853843158	0	0	NA	Left_Ventric le:Right_Ve ntricle
RAV_min	rs62427982	BEND3	0.498328912747109	-0.809838595	19	0	NA	NA
RAV_min	rs62427982	PDSS2	1.89564464414184e-05	-0.637292192	0	10	GTEEx/v8/Lung	NA
RAV_min	rs62427982	SCML4	0.268213054620722	-0.122272059	0	0	NA	Left_Ventric le
RAV_min	rs72959041	TPD52L1	0.00842005639548042	0.000949749	0	0	NA	Left_Ventric le
RAV_min	rs72959041	RSPO3	0.043976319489366	NA	4	5	GTEEx/v8/Adipose_Subcutaneous	NA
RAV_min	rs849138	HOXA9	0.000100012594431347	-0.353761021	0	0	NA	Left_Ventric le
RAV_min	rs849138	RP1- 170O19.20	NA	NA	0	0	NA	Left_Ventric le
RAV_min	rs849138	HOXA10	0.678435260569461	-0.87103063	0	0	NA	Left_Ventric le
RAV_min	rs849138	HOXA11	0.863825169181447	0.401702198	0	0	NA	Left_Ventric le
RAV_min	rs849138	HOXA13	NA	-0.418411158	0	0	NA	Left_Ventric le
RAV_min	rs849138	TAX1BP1	2.99233082871036e-06	0.359414966	0	0	NA	Left_Ventric le

RAV_min	rs849138	JAZF1	0.958302381623798	-0.943258499	24	21	GTEX/v8/Adipose_Subcutaneous:GTEX/v8/Adipose_Visceral_Omentum:GTEX/v8/Artery_Aorta:GTEX/v8/Artery_Tibial:GTEX/v8/Colon_Sigmoid:GTEX/v8/Esophagus_Gastroesophageal_Junction:GTEX/v8/Esophagus_Muscularis:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Liver:GTEX/v8/Muscle_Skeletal:GTEX/v8/Nerve_Tibial:GTEX/v8/Pancreas:GTEX/v8/Cells_Cultured_fibroblasts:GTEX/v8/Spleen	NA
RAV_min	rs849138	GARS	0.788927209872354	0.029641868	0	0	NA	Left_Ventricle
RAV_min	rs12155647	C8orf48	NA	0.67185897	0	8	GTEX/v8/Thyroid	NA
RAV_min	rs60394484	TSTA3	0.0049919240345017	NA	0	3	GTEX/v8/Pancreas	NA
RAV_min	rs60394484	MAPK15	1.28603703609388e-16	NA	0	1	GTEX/v8/Skin_Not_Sun_Exposed_Suprapubic	NA
RAV_min	rs60394484	PLEC	0.024936270552365	-0.44044438	2	6	GTEX/v8/Adipose_Subcutaneous:GTEX/v8/Whole_Blood:GTEX/v8/Artery_Coronary:GTEX/v8/Artery_Tibial:GTEX/v8/Breast_Mammary_Tissue:GTEX/v8/Esophagus_Muscularis:GTEX/v8/Heart_Atrial_Appendage:GTEX/v8/Heart_Left_Ventricle:GTEX/v8/Lung:GTEX/v8/Muscle_Skeletal:GTEX/v8/Nerve_Tibial:GTEX/v8/Pancreas:GTEX/v8/Cells_Cultured_fibroblasts:GTEX/v8/Spleen:GTEX/v8/Testis:GTEX/v8/Thyroid	NA
RAV_min	rs60394484	PARP10	0.00291131564961967	-0.428650279	1	4	GTEX/v8/Whole_Blood:GTEX/v8/Thyroid	NA
RAV_min	rs60394484	SPATC1	3.5903133043143e-08	0.129497291	2	0	NA	NA
RAV_min	rs60394484	OPLAH	2.99003379437065e-11	NA	3	0	NA	NA

Multiple-trait mapping identified 1,184 genes, including 514 unique genes

TMEM57	C1orf143	WDR73	AL365202.1	SSPN	TMEM106C
MTFR1L	LYPLAL1	NMB	GLIS3	ITPR2	RP1-228P16.5
PAFAH2	SLC30A10	ZNF592	C11orf49	MRPS35	SENP1
EXTL1	THADA	ALPK3	ACP2	MANSC4	PFKM
SLC30A2	ZFP36L2	CTC-786C10.1	OR4B1	KLHL42	ASB8
TRIM63	PLEKHH2	RP11-680G10.1	OR4X2	PTHLH	C12orf68
PDIK1L	SLC3A1	GSE1	OR4X1	CCDC91	DKFZP779L1853
FAM110D	WDPCP	GINS2	OR4S1	OVCH1	OR10AD1
CNKSRI	UGP2	C16orf74	OR4C3	NEUROD2	H1FNT
CEP85	AFTPH	C17orf96	OR4C5	GRB7	ZNF641
SH3BGRL3	SLC1A4	STAC2	OR4A47	IKZF3	AC024257.1
CD52	CEP68	FBXL20	TRIM49B	GSDMA	ANP32D
AIM1L	RAB1A	MED1	TRIM64C	PSMD3	C12orf54
RPS6KA1	ACTR2	CDK12	FOLH1	CTD-2267D19.3	OR8S1
PLEKHA3	SPRED2	PPP1R1B	OR4C13	IRS1	LALBA
TTN	ETAA1	STARD3	OR4C12	RHBDD1	KANSL2
CCDC141	EOGT	TCAP	FAM89B	COL4A4	CCNT1
FOXP1	MITF	PNMT	EHBP1L1	COL4A3	DNAJC22
BCL6	EPHB1	PGAP3	KCNK7	IRAK1BP1	NECAB3
TPRG1	KY	ERBB2	RNASEH2C	PHIP	C20orf144
BEND3	PPP2R3A	MIEN1	AP5B1	HMGN3	ACTL10
PDSS2	MSL2	ZBPB2	SNX32	LCA5	E2F1
SCML4	PCCB	GSDMB	CTSW	SH3BGRL2	CHMP4B
TPD52L1	STAG1	ORMDL3	FIBP	TTK	RALY
RSPO3	IL20RB	CSF3	SF3B2	FAM46A	EIF2S2
HOXA9	PLD1	MED24	MYEOV	ACAT2	ASIP
RP1-170O19.2	PP13439	TOP2A	B4GALNT3	TCP1	AHCY
HOXA10	TMEM212	IGFBP4	ADIPOR2	MRPL18	ITCH
HOXA11	FNDC3B	CCR7	LRTM2	PNLDC1	DYNLRB1
HOXA13	AC092964.2	KCNH4	DCP1B	MAS1	MAP1LC3A
TAX1BP1	AC092964.1	HCRT	CACNA1C	SLC22A1	PIGU
JAZF1	GHSR	GHDC	FKBP4	SLC22A2	NCOA6
GARS	AC007919.2	STAT5B	DDX55	SLC22A3	TP53INP2
C8orf48	KCTD20	STAT5A	ATP6V0A2	LPA	GGT7
TSTA3	CDKN1A	C22orf24	DNAH10	TENC1	ACSS2
MAPK15	RAB44	YWHAH	CCDC92	RP11-834C11.12	GSS
PLEC	CPNE5	SLC5A1	DNAH10OS	HOXC6	MYH7B
PARP10	RNF217	SLC5A4	ZNF664	HOXC9	TRPC4AP
SPATC1	HDDC2	RFPL3	FAM101A	HOXC8	ZMYND8
OPLAH	HEY2	RTCB	UBC	HOXC4	NCOA3
EXOSC4	NCOA7	SYN3	TNFRSF13B	HOXC5	A4GNT
CYC1	HINT3	OBP2B	PLD6	SMUG1	NME9
SHARPIN	TRMT11	SURF1	COPS3	GTSF1	MRAS
MAF1	RNF146	MDM2	PEMT	KITLG	ESYT3

KIAA1875	STRIP2	EML2	RAI1	DUSP6	CEP70
DGAT1	TMEM209	PNMAL1	SREBF1	POC1B	FAIM
DLG2	SSMEM1	RPS6KC1	TOM1L2	GALNT4	PIK3CB
TMEM126A	CPA2	PROX1	LRRC48	POC1B-GALNT4	FOXL2
CCDC89	CPA4	PTPN14	ATPAF2	ATP2B1	C3orf72
SYTL2	CPA5	KCTD3	GID4	CCER1	PRR23C
PICALM	CEP41	FAM184B	DRG2	DCN	TFEB
PARP11	MEST	DCAF16	ALKBH5	RRAGC	AL035588.1
CCND2	KLF14	NCAPG	LLGL1	MYCBP	USP49
TBC1D30	ARHGAP1	LCORL	MIEF2	GJA9	CTSD
WIF1	CKAP5	EBF1	EVPLL	RHBDL2	KCNQ1
LEMD3	LRP4	UBLCP1	TOMM40	AKIRIN1	PAFAH1B1
HMGA2	PACSIN3	NUCB2	APOE	NDUFS5	TRPV3
AC090673.2	DDB2	NCR3LG1	APOC1	MACF1	P2RX1
CLK3	NR1H3	KCNJ11	APOC4-APOC2	KIAA0754	ATP2A3
SNUPN	MADD	ABCC8	APOC4	BMP8A	ZZEF1
FBXO22	MYBPC3	MAP3K11	APOC2	PABPC4	CYB5D2
SCAPER	SPI1	PCNXL3	CTB-129P6.11	HPCAL4	ANKFY1
PSTPIP1	SLC39A13	SIPA1	CLPTM1	OXCT2	UBE2G1
TSPAN3	PSMC3	CMIP	DDIT4L	RLF	SPNS3
PEAK1	RAPSN	KDM5B	EMCN	ZMPSTE24	TM4SF5
HMG20A	CELF1	RP11-480I12.4	BANK1	SLFNL1	MINK1
LINGO1	NDUFS3	PPP1R15B	SLC39A8	GRB14	SCIMP
ERCC1	PTPMT1	MDM4	UBE2D3	COBLL1	ZBTB46
FOSB	KBTBD4	NFASC	SLC9B1	SCN3A	AL158091.1
RTN2	FAM180B	CNTN2	FST	AP3M1	
PPM1N	C1QTNF4	TMEM81	NDUFS4	ADK	
SNRPD2	MTCH2	RBBP5	ARL15	KAT6B	
FBXO46	AGBL2	DSTYK	C11orf58	DUPD1	
AC074212.3	FNBP4	TMCC2	PIK3C2A	DUSP13	
SIX5	NUP160	NUAK2	KCNC1	SAMD8	
DMPK	PTPRJ	KLHDC8A	SAC3D1	VDAC2	
AC011530.4	LRP5	TIPARP	AP000769.1	WT1	
DMWD	MTL5	VEPH1	RELA	CHKA	
RSPH6A	CPT1A	C3orf55	KAT5	GAL	
SYMPK	MRPL21	SHOX2	OVOL1	TM7SF3	
FOXA3	IGHMBP2	RSRC1	CFL1	MED21	
CCDC8	MRGPRD	MLF1	EFEMP2	C12orf71	
STRN4	MRGPRF	GFM1	FOSL1	ARNTL2	
FKRP	TPCN2	LXN	DRAP1	PPFIBP1	
RHCE	BNC1	RARRES1	EIF1AD	REP15	
CATSPER4	ADAMTSL3	MFSD1	CST6	IPO8	
DHDDS	UBE2Q2L	CENPW	IFLTD1	RPAP3	
RRP15	GOLGA6L4	ECHDC1	RASSF8	ENDOU	
TGFB2	ZSCAN2	SOGA3	BHLHE41	VDR	

The S-PrediXcan blood single-tissue TWAS analysis identified significant associations with key CMR traits (adjusted P-value < 0.05, Benjamini-									
Trait	name	zscore	var_g	n_snps_used	n_snps_in_cov	n_snps_in_model	best_gwas_p	largest_weight	q
WT_AHA_6	BEND3	-3.634	0.004	1	1	1	0.000	0.093	6.23E-03
WT_AHA_6	HOXA10	3.472	0.040	2	2	2	0.002	0.212	1.03E-02
WT_AHA_6	TAX1BP1	-3.099	0.001	1	1	1	0.002	0.051	2.92E-02
WT_AHA_6	LEMD3	-3.063	0.001	2	2	2	0.005	0.054	3.17E-02
WT_AHA_6	CEP68	3.833	0.197	2	2	2	0.000	0.410	3.25E-03
WT_AHA_6	MITF	4.735	0.004	1	1	1	0.000	0.111	1.06E-04
WT_AHA_6	PPP2R3A	-3.315	0.006	1	1	1	0.001	0.128	1.67E-02
WT_AHA_6	MYBPC3	3.757	0.027	2	2	2	0.000	0.360	4.18E-03
WT_AHA_6	SLC39A13	-4.017	0.006	1	1	1	0.000	0.122	1.66E-03
WT_AHA_6	PSMC3	-5.181	0.003	2	2	2	0.000	0.057	1.72E-05
WT_AHA_6	C1QTNF4	5.019	0.105	1	2	2	0.000	0.518	3.07E-05
WT_AHA_6	FBNP4	-3.083	0.004	2	2	2	0.000	0.048	3.06E-02
WT_AHA_6	IGHMBP2	-4.186	0.547	2	3	3	0.000	1.045	9.08E-04
WT_AHA_6	ZSCAN2	-7.792	0.003	1	1	1	0.000	0.081	1.28E-12
WT_AHA_6	WDR73	8.388	0.010	2	2	2	0.000	0.159	1.34E-14
WT_AHA_6	NMB	8.317	0.015	1	1	1	0.000	0.196	2.24E-14
WT_AHA_6	ALPK3	-4.736	0.002	1	1	1	0.000	0.068	1.06E-04
WT_AHA_6	PPP1R1B	-3.625	0.003	2	2	2	0.000	0.103	6.39E-03
WT_AHA_6	PNMT	-3.510	0.014	1	1	1	0.000	0.170	9.22E-03
WT_AHA_6	PGAP3	-2.942	0.002	1	2	2	0.003	0.069	4.33E-02
WT_AHA_6	MIEN1	2.975	0.000	1	1	1	0.003	0.010	3.98E-02
WT_AHA_6	GSDMB	-2.893	0.098	3	3	3	0.004	0.339	4.75E-02
WT_AHA_6	DCAF16	4.675	0.008	3	3	3	0.000	0.105	1.40E-04
WT_AHA_6	KCNJ11	4.298	0.009	1	1	1	0.000	0.135	5.92E-04
WT_AHA_6	SIPA1	4.380	0.004	2	2	2	0.000	0.108	4.56E-04
WT_AHA_6	TIPARP	-2.978	0.002	2	2	2	0.034	0.095	3.98E-02

WT_AHA_6	CENPW	-3.224	0.005	1	1	1	0.001	0.101	2.11E-02
WT_AHA_6	KCNK7	3.174	0.020	2	2	2	0.000	0.126	2.40E-02
WT_AHA_6	ZNF664	2.960	0.004	1	1	1	0.003	0.089	4.12E-02
WT_AHA_6	IKZF3	3.077	0.003	1	1	1	0.002	0.074	3.09E-02
WT_AHA_7	TRIM63	-3.167	0.001	1	1	1	0.002	0.050	2.45E-02
WT_AHA_7	PDIK1L	-3.286	0.000	1	1	1	0.001	0.025	1.76E-02
WT_AHA_7	CNKSRI	-2.972	0.020	2	2	2	0.018	0.266	4.00E-02
WT_AHA_7	CEP68	2.975	0.197	2	2	2	0.000	0.410	3.98E-02
WT_AHA_7	PPP2R3A	-3.363	0.006	1	1	1	0.001	0.128	1.44E-02
WT_AHA_7	MYBPC3	4.108	0.027	2	2	2	0.000	0.360	1.20E-03
WT_AHA_7	SLC39A13	-3.927	0.006	1	1	1	0.000	0.122	2.29E-03
WT_AHA_7	PSMC3	-5.873	0.003	2	2	2	0.000	0.057	4.32E-07
WT_AHA_7	PTPMT1	2.935	0.002	2	2	2	0.002	0.123	4.40E-02
WT_AHA_7	C1QTNF4	5.682	0.105	1	2	2	0.000	0.518	1.25E-06
WT_AHA_7	NUP160	-3.512	0.003	1	1	1	0.000	0.096	9.22E-03
WT_AHA_7	PTPRJ	3.997	0.018	2	2	2	0.000	0.118	1.78E-03
WT_AHA_7	ZSCAN2	-7.153	0.003	1	1	1	0.000	0.081	1.36E-10
WT_AHA_7	WDR73	7.924	0.010	2	2	2	0.000	0.159	4.81E-13
WT_AHA_7	NMB	7.956	0.015	1	1	1	0.000	0.196	4.01E-13
WT_AHA_7	MED1	-3.439	0.001	2	2	2	0.000	0.039	1.13E-02
WT_AHA_7	PPP1R1B	-4.333	0.003	2	2	2	0.000	0.103	5.26E-04
WT_AHA_7	PNMT	-4.656	0.014	1	1	1	0.000	0.170	1.49E-04
WT_AHA_7	PGAP3	-4.132	0.002	1	2	2	0.000	0.069	1.11E-03
WT_AHA_7	ERBB2	-3.978	0.000	2	2	2	0.000	0.019	1.91E-03
WT_AHA_7	MIEN1	4.313	0.000	1	1	1	0.000	0.010	5.61E-04
WT_AHA_7	KCNJ11	3.345	0.009	1	1	1	0.001	0.135	1.51E-02
WT_AHA_7	SIPA1	4.315	0.004	2	2	2	0.000	0.108	5.61E-04
WT_AHA_7	MLF1	4.479	0.025	2	2	2	0.000	0.193	2.95E-04

WT_AHA_7	DNAH10OS	-3.658	0.002	1	1	1	0.000	0.071	5.75E-03
WT_AHA_7	ZNF664	3.721	0.004	1	1	1	0.000	0.089	4.57E-03
WT_AHA_7	SREBF1	-3.198	0.225	2	2	2	0.001	0.372	2.24E-02
WT_AHA_7	APOC1	3.490	0.001	1	1	1	0.000	0.055	9.81E-03
WT_AHA_7	IKZF3	3.471	0.003	1	1	1	0.001	0.074	1.03E-02
WT_AHA_9	CNKSRI	-3.070	0.020	2	2	2	0.017	0.266	3.13E-02
WT_AHA_9	PSTPIP1	3.398	0.002	3	3	3	0.001	0.097	1.30E-02
WT_AHA_9	CEP68	3.383	0.197	2	2	2	0.000	0.410	1.36E-02
WT_AHA_9	PPP2R3A	-3.216	0.006	1	1	1	0.001	0.128	2.14E-02
WT_AHA_9	MYBPC3	4.408	0.027	2	2	2	0.000	0.360	4.04E-04
WT_AHA_9	SLC39A13	-3.295	0.006	1	1	1	0.001	0.122	1.74E-02
WT_AHA_9	PSMC3	-5.131	0.003	2	2	2	0.000	0.057	1.96E-05
WT_AHA_9	C1QTNF4	5.038	0.105	1	2	2	0.000	0.518	2.91E-05
WT_AHA_9	FBNP4	-2.916	0.004	2	2	2	0.000	0.048	4.55E-02
WT_AHA_9	ZSCAN2	-5.148	0.003	1	1	1	0.000	0.081	1.88E-05
WT_AHA_9	WDR73	5.135	0.010	2	2	2	0.000	0.159	1.96E-05
WT_AHA_9	NMB	4.972	0.015	1	1	1	0.000	0.196	3.76E-05
WT_AHA_9	PPP1R1B	-4.041	0.003	2	2	2	0.000	0.103	1.54E-03
WT_AHA_9	PNMT	-3.783	0.014	1	1	1	0.000	0.170	3.83E-03
WT_AHA_9	PGAP3	-3.797	0.002	1	2	2	0.000	0.069	3.68E-03
WT_AHA_9	MIEN1	3.748	0.000	1	1	1	0.000	0.010	4.30E-03
WT_AHA_9	KCNJ11	3.869	0.009	1	1	1	0.000	0.135	2.86E-03
WT_AHA_9	SIPA1	4.616	0.004	2	2	2	0.000	0.108	1.78E-04
WT_AHA_9	KDM5B	-3.067	0.003	3	3	3	0.025	0.169	3.14E-02
WT_AHA_9	EHBP1L1	-4.242	0.004	1	1	1	0.000	0.113	7.45E-04
WT_AHA_9	KCNK7	3.017	0.020	2	2	2	0.000	0.126	3.56E-02
WT_AHA_9	SNX32	3.082	0.138	1	1	1	0.002	0.726	3.06E-02
WT_AHA_9	MRPS35	3.119	0.002	2	2	2	0.002	0.089	2.75E-02

WT_AHA_9	PHIP	2.920	0.002	1	1	1	0.004	0.072	4.51E-02
WT_AHA_9	TP53INP2	3.286	0.001	1	1	1	0.001	0.035	1.76E-02
WT_AHA_9	MYH7B	-3.567	0.018	2	2	2	0.000	0.241	7.74E-03
WT_AHA_9	TRPC4AP	3.154	0.025	3	3	3	0.000	0.417	2.52E-02
WT_AHA_10	PSTPIP1	2.903	0.002	3	3	3	0.002	0.097	4.65E-02
WT_AHA_10	CEP68	3.729	0.197	2	2	2	0.000	0.410	4.47E-03
WT_AHA_10	SPRED2	2.920	0.003	2	2	2	0.009	0.070	4.51E-02
WT_AHA_10	MITF	3.309	0.004	1	1	1	0.001	0.111	1.70E-02
WT_AHA_10	PPP2R3A	-3.515	0.006	1	1	1	0.000	0.128	9.19E-03
WT_AHA_10	MYBPC3	4.247	0.027	2	2	2	0.000	0.360	7.37E-04
WT_AHA_10	PSMC3	-4.230	0.003	2	2	2	0.000	0.057	7.76E-04
WT_AHA_10	C1QTNF4	4.809	0.105	1	2	2	0.000	0.518	7.89E-05
WT_AHA_10	FNBP4	-4.359	0.004	2	2	2	0.000	0.048	4.81E-04
WT_AHA_10	ZSCAN2	-6.243	0.003	1	1	1	0.000	0.081	6.15E-08
WT_AHA_10	WDR73	5.780	0.010	2	2	2	0.000	0.159	7.24E-07
WT_AHA_10	NMB	5.945	0.015	1	1	1	0.000	0.196	3.19E-07
WT_AHA_10	ALPK3	-3.504	0.002	1	1	1	0.000	0.068	9.38E-03
WT_AHA_10	MED1	-3.283	0.001	2	2	2	0.000	0.039	1.76E-02
WT_AHA_10	PPP1R1B	-4.800	0.003	2	2	2	0.000	0.103	8.15E-05
WT_AHA_10	PNMT	-4.482	0.014	1	1	1	0.000	0.170	2.95E-04
WT_AHA_10	PGAP3	-4.364	0.002	1	2	2	0.000	0.069	4.77E-04
WT_AHA_10	ERBB2	-3.946	0.000	2	2	2	0.000	0.019	2.14E-03
WT_AHA_10	MIEN1	4.221	0.000	1	1	1	0.000	0.010	7.96E-04
WT_AHA_10	KCNJ11	3.650	0.009	1	1	1	0.000	0.135	5.90E-03
WT_AHA_10	SIPA1	3.300	0.004	2	2	2	0.001	0.108	1.73E-02
WT_AHA_10	CENPW	-2.946	0.005	1	1	1	0.003	0.101	4.28E-02
WT_AHA_10	EHBP1L1	-2.901	0.004	1	1	1	0.004	0.113	4.66E-02
WT_AHA_10	PHIP	4.028	0.002	1	1	1	0.000	0.072	1.61E-03

WT_AHA_10	ASB8	3.020	0.004	2	2	2	0.003	0.083	3.56E-02
WT_AHA_11	TRIM63	-4.131	0.001	1	1	1	0.000	0.050	1.11E-03
WT_AHA_11	PDIK1L	-4.016	0.000	1	1	1	0.000	0.025	1.66E-03
WT_AHA_11	PSTPIP1	3.204	0.002	3	3	3	0.000	0.097	2.22E-02
WT_AHA_11	CEP68	3.571	0.197	2	2	2	0.000	0.410	7.67E-03
WT_AHA_11	MITF	5.266	0.004	1	1	1	0.000	0.111	1.15E-05
WT_AHA_11	PPP2R3A	-4.212	0.006	1	1	1	0.000	0.128	8.19E-04
WT_AHA_11	MYBPC3	3.970	0.027	2	2	2	0.000	0.360	1.95E-03
WT_AHA_11	SLC39A13	-3.035	0.006	1	1	1	0.002	0.122	3.40E-02
WT_AHA_11	PSMC3	-4.553	0.003	2	2	2	0.000	0.057	2.29E-04
WT_AHA_11	C1QTNF4	4.858	0.105	1	2	2	0.000	0.518	6.47E-05
WT_AHA_11	FNBP4	-3.860	0.004	2	2	2	0.000	0.048	2.93E-03
WT_AHA_11	IGHMBP2	-3.046	0.547	2	3	3	0.001	1.045	3.32E-02
WT_AHA_11	ZSCAN2	-9.356	0.003	1	1	1	0.000	0.081	5.60E-18
WT_AHA_11	WDR73	9.200	0.010	2	2	2	0.000	0.159	1.22E-17
WT_AHA_11	NMB	9.227	0.015	1	1	1	0.000	0.196	1.08E-17
WT_AHA_11	ALPK3	-5.072	0.002	1	1	1	0.000	0.068	2.50E-05
WT_AHA_11	MED1	-4.562	0.001	2	2	2	0.000	0.039	2.23E-04
WT_AHA_11	PPP1R1B	-6.153	0.003	2	2	2	0.000	0.103	9.41E-08
WT_AHA_11	PNMT	-6.180	0.014	1	1	1	0.000	0.170	8.30E-08
WT_AHA_11	PGAP3	-6.311	0.002	1	2	2	0.000	0.069	4.18E-08
WT_AHA_11	ERBB2	-5.940	0.000	2	2	2	0.000	0.019	3.19E-07
WT_AHA_11	MIEN1	6.212	0.000	1	1	1	0.000	0.010	7.13E-08
WT_AHA_11	GSDMB	-3.262	0.098	3	3	3	0.000	0.339	1.89E-02
WT_AHA_11	SIPA1	3.216	0.004	2	2	2	0.001	0.108	2.14E-02
WT_AHA_11	CENPW	-2.910	0.005	1	1	1	0.004	0.101	4.60E-02
WT_AHA_11	IKZF3	4.047	0.003	1	1	1	0.000	0.074	1.52E-03
WT_AHA_11	DUSP6	-2.905	0.000	2	2	2	0.006	0.059	4.65E-02

WT_AHA_11	GAL	3.244	0.122	1	1	1	0.001	0.786	1.99E-02
WT_AHA_11	ASB8	3.355	0.004	2	2	2	0.000	0.083	1.47E-02
WT_AHA_12	TRIM63	-4.544	0.001	1	1	1	0.000	0.050	2.33E-04
WT_AHA_12	PDIK1L	-4.535	0.000	1	1	1	0.000	0.025	2.37E-04
WT_AHA_12	CNKSR1	-2.921	0.020	2	2	2	0.011	0.266	4.51E-02
WT_AHA_12	TAX1BP1	-2.921	0.001	1	1	1	0.003	0.051	4.51E-02
WT_AHA_12	PSTPIP1	3.254	0.002	3	3	3	0.000	0.097	1.94E-02
WT_AHA_12	CEP68	3.536	0.197	2	2	2	0.000	0.410	8.55E-03
WT_AHA_12	MITF	5.934	0.004	1	1	1	0.000	0.111	3.19E-07
WT_AHA_12	PPP2R3A	-4.759	0.006	1	1	1	0.000	0.128	9.82E-05
WT_AHA_12	MSL2	-3.541	0.000	2	2	2	0.000	0.022	8.48E-03
WT_AHA_12	PCCB	3.195	0.013	1	2	2	0.001	0.166	2.25E-02
WT_AHA_12	MYBPC3	3.468	0.027	2	2	2	0.000	0.360	1.03E-02
WT_AHA_12	SLC39A13	-3.729	0.006	1	1	1	0.000	0.122	4.47E-03
WT_AHA_12	PSMC3	-5.031	0.003	2	2	2	0.000	0.057	2.95E-05
WT_AHA_12	C1QTNF4	4.973	0.105	1	2	2	0.000	0.518	3.76E-05
WT_AHA_12	FNBP4	-2.882	0.004	2	2	2	0.000	0.048	4.88E-02
WT_AHA_12	ZSCAN2	-9.518	0.003	1	1	1	0.000	0.081	1.59E-18
WT_AHA_12	WDR73	10.518	0.010	2	2	2	0.000	0.159	1.94E-22
WT_AHA_12	NMB	10.420	0.015	1	1	1	0.000	0.196	2.73E-22
WT_AHA_12	ALPK3	-3.763	0.002	1	1	1	0.000	0.068	4.11E-03
WT_AHA_12	MED1	-3.446	0.001	2	2	2	0.000	0.039	1.11E-02
WT_AHA_12	PPP1R1B	-4.832	0.003	2	2	2	0.000	0.103	7.19E-05
WT_AHA_12	PNMT	-5.230	0.014	1	1	1	0.000	0.170	1.36E-05
WT_AHA_12	PGAP3	-5.538	0.002	1	2	2	0.000	0.069	2.67E-06
WT_AHA_12	ERBB2	-5.349	0.000	2	2	2	0.000	0.019	7.52E-06
WT_AHA_12	MIEN1	5.607	0.000	1	1	1	0.000	0.010	1.87E-06
WT_AHA_12	DCAF16	2.963	0.008	3	3	3	0.007	0.105	4.09E-02

WT_AHA_12	SIPA1	3.595	0.004	2	2	2	0.000	0.108	7.10E-03
WT_AHA_12	DNAH10OS	-2.890	0.002	1	1	1	0.004	0.071	4.79E-02
WT_AHA_12	ZNF664	2.921	0.004	1	1	1	0.003	0.089	4.51E-02
WT_AHA_12	IKZF3	3.574	0.003	1	1	1	0.000	0.074	7.64E-03
WT_AHA_12	FAIM	3.017	0.008	1	1	1	0.003	0.125	3.56E-02
WT_global	BEND3	-3.148	0.004	1	1	1	0.002	0.093	2.55E-02
WT_global	TAX1BP1	-3.052	0.001	1	1	1	0.002	0.051	3.27E-02
WT_global	CEP68	3.795	0.197	2	2	2	0.000	0.410	3.69E-03
WT_global	MITF	5.105	0.004	1	1	1	0.000	0.111	2.19E-05
WT_global	PPP2R3A	-4.080	0.006	1	1	1	0.000	0.128	1.34E-03
WT_global	MYBPC3	5.929	0.027	2	2	2	0.000	0.360	3.19E-07
WT_global	SLC39A13	-5.164	0.006	1	1	1	0.000	0.122	1.83E-05
WT_global	PSMC3	-7.354	0.003	2	2	2	0.000	0.057	3.28E-11
WT_global	C1QTNF4	7.486	0.105	1	2	2	0.000	0.518	1.29E-11
WT_global	FNBP4	-4.369	0.004	2	2	2	0.000	0.048	4.72E-04
WT_global	ZSCAN2	-8.848	0.003	1	1	1	0.000	0.081	2.68E-16
WT_global	WDR73	9.251	0.010	2	2	2	0.000	0.159	1.01E-17
WT_global	NMB	9.303	0.015	1	1	1	0.000	0.196	7.39E-18
WT_global	ALPK3	-5.149	0.002	1	1	1	0.000	0.068	1.88E-05
WT_global	PPP1R1B	-4.663	0.003	2	2	2	0.000	0.103	1.46E-04
WT_global	PNMT	-4.959	0.014	1	1	1	0.000	0.170	3.93E-05
WT_global	PGAP3	-4.158	0.002	1	2	2	0.000	0.069	1.00E-03
WT_global	ERBB2	-3.912	0.000	2	2	2	0.000	0.019	2.41E-03
WT_global	MIEN1	4.079	0.000	1	1	1	0.000	0.010	1.34E-03
WT_global	DCAF16	3.298	0.008	3	3	3	0.003	0.105	1.73E-02
WT_global	KCNJ11	3.730	0.009	1	1	1	0.000	0.135	4.47E-03
WT_global	SIPA1	5.079	0.004	2	2	2	0.000	0.108	2.45E-05
WT_global	CENPW	-3.153	0.005	1	1	1	0.002	0.101	2.52E-02

WT_global	KCNK7	3.376	0.020	2	2	2	0.000	0.126	1.38E-02
WT_global	APOC1	3.105	0.001	1	1	1	0.002	0.055	2.87E-02
WT_global	KAT5	3.131	0.004	1	1	1	0.002	0.088	2.66E-02
WT_global	MRPS35	3.002	0.002	2	2	2	0.003	0.089	3.72E-02
WT_global	IKZF3	3.199	0.003	1	1	1	0.001	0.074	2.24E-02
WT_global	FAIM	3.377	0.008	1	1	1	0.001	0.125	1.38E-02
RAV_max	DMPK	4.542	0.017	2	2	2	0.000	0.180	2.33E-04
RAV_max	STRN4	-3.405	0.004	2	2	2	0.001	0.080	1.28E-02
RAV_max	FKRP	3.240	0.021	1	2	2	0.001	0.210	2.01E-02
RAV_max	FAM89B	-4.165	0.003	2	2	2	0.000	0.121	9.83E-04
RAV_max	FIBP	3.073	0.002	1	1	1	0.002	0.084	3.12E-02
RAV_max	GAL	-3.284	0.122	1	1	1	0.001	0.786	1.76E-02
RAV_max	MYH7B	-3.144	0.018	2	2	2	0.010	0.241	2.57E-02
RAV_min	TRIM63	4.524	0.001	1	1	1	0.000	0.050	2.47E-04
RAV_min	PDIK1L	4.573	0.000	1	1	1	0.000	0.025	2.14E-04
RAV_min	FBXO46	-3.042	0.002	1	1	1	0.002	0.074	3.35E-02
RAV_min	DMPK	4.355	0.017	2	2	2	0.000	0.180	4.82E-04
RAV_min	SYMPK	3.702	0.000	1	2	2	0.000	0.017	4.88E-03
RAV_min	STRN4	-3.740	0.004	2	2	2	0.000	0.080	4.39E-03
RAV_min	FKRP	3.810	0.021	1	2	2	0.000	0.210	3.54E-03
RAV_min	FAM89B	-2.999	0.003	2	2	2	0.000	0.121	3.74E-02
RAV_min	EHBP1L1	-3.484	0.004	1	1	1	0.000	0.113	9.96E-03
RAV_min	CCDC92	2.912	0.024	3	3	3	0.002	0.238	4.58E-02
RAV_min	DNAH10OS	3.136	0.002	1	1	1	0.002	0.071	2.63E-02
RAV_min	ZNF664	-3.154	0.004	1	1	1	0.002	0.089	2.52E-02
RAV_min	GAL	-3.305	0.122	1	1	1	0.001	0.786	1.71E-02

Note:zscore: Association result of the gene in S-PrediXcan;n_snps_used: Number of SNPs from GWAS used in the S-PrediXcan analysis;
n_snps_in_cov: Number of SNPs in the covariance matrix;n_snps_in_model: Number of SNPs in the model;var_g: Variance of gene expression;
best_gwas_p: Highest p-value among the GWAS SNPs used in this model;largest_weight: Largest (absolute) weight in this model;
q: P-value adjusted using the Benjamini-Hochberg correction.

The S-PrediXcan blood single-tissue TWAS analysis identified significant associations with T2D (adjusted P-value < 0.05, Benjamini-Hochberg)									
Trait	name	zscore	var_g	n_snps_used	n_snps_in	n_snps_in	best_gwas_p	largest_weight	q
T2D	PAFAH2	2.895	0.002	1	1	1	0.004	0.062	1.54E-02
T2D	TRIM63	4.952	0.001	1	1	1	0.000	0.050	1.00E-05
T2D	PDIK1L	4.575	0.000	1	1	1	0.000	0.025	5.73E-05
T2D	CD52	-3.381	0.219	4	4	4	0.001	0.430	3.97E-03
T2D	PLEKHA3	4.037	0.005	2	2	2	0.000	0.108	4.28E-04
T2D	BEND3	-4.134	0.004	1	1	1	0.000	0.093	2.90E-04
T2D	SCML4	-2.461	0.203	4	4	4	0.001	0.340	4.34E-02
T2D	TAX1BP1	-3.019	0.001	1	1	1	0.003	0.051	1.10E-02
T2D	TMEM126	-2.550	0.002	2	2	2	0.003	0.046	3.56E-02
T2D	CCND2	-7.210	0.008	1	1	1	0.000	0.154	1.87E-11
T2D	SNUPN	-6.354	0.076	3	3	3	0.000	0.235	4.84E-09
T2D	FBXO22	-3.311	0.008	1	1	1	0.001	0.388	4.74E-03
T2D	TSPAN3	3.647	0.067	3	3	3	0.005	0.377	1.78E-03
T2D	PEAK1	8.164	0.009	1	1	1	0.000	0.138	2.43E-14
T2D	HMG20A	7.171	0.002	2	2	2	0.000	0.067	2.24E-11
T2D	PPM1N	3.004	0.017	1	1	1	0.003	0.186	1.13E-02
T2D	SNRPD2	-5.750	0.002	1	1	1	0.000	0.067	1.79E-07
T2D	FBXO46	2.682	0.002	1	1	1	0.007	0.074	2.59E-02
T2D	DMPK	-3.987	0.017	2	2	2	0.000	0.180	4.90E-04
T2D	DMWD	-3.278	0.012	2	2	2	0.000	0.260	5.16E-03
T2D	THADA	4.996	0.003	1	1	1	0.000	0.091	8.40E-06
T2D	ZFP36L2	10.100	0.000	1	1	1	0.000	0.044	1.67E-21
T2D	PLEKHH2	3.842	0.036	2	2	2	0.002	0.227	8.36E-04
T2D	CEP68	7.989	0.197	2	2	2	0.000	0.410	8.22E-14
T2D	RAB1A	2.553	0.000	2	2	2	0.000	0.039	3.56E-02
T2D	ACTR2	-2.411	0.000	1	1	1	0.016	0.028	4.81E-02
T2D	SPRED2	7.936	0.003	2	2	2	0.000	0.070	1.05E-13

T2D	MITF	-3.349	0.004	1	1	1	0.001	0.111	4.28E-03
T2D	PPP2R3A	3.203	0.006	1	1	1	0.001	0.128	6.29E-03
T2D	MSL2	3.963	0.000	2	2	2	0.000	0.022	5.30E-04
T2D	IL20RB	3.492	0.021	1	1	1	0.000	0.218	2.94E-03
T2D	PLD1	2.749	0.026	2	2	2	0.018	0.175	2.17E-02
T2D	RNF146	-2.458	0.000	1	1	1	0.014	0.028	4.34E-02
T2D	PSMC3	3.209	0.003	2	2	2	0.000	0.057	6.27E-03
T2D	PTPMT1	4.702	0.002	2	2	2	0.000	0.123	3.37E-05
T2D	KBTBD4	-4.503	0.000	1	1	1	0.000	0.020	7.48E-05
T2D	C1QTNF4	-3.373	0.105	1	2	2	0.001	0.518	4.00E-03
T2D	FNBP4	4.373	0.004	2	2	2	0.000	0.048	1.15E-04
T2D	NUP160	-2.560	0.003	1	1	1	0.010	0.096	3.54E-02
T2D	PTPRJ	2.592	0.018	2	2	2	0.004	0.118	3.30E-02
T2D	MED1	4.341	0.001	2	2	2	0.000	0.039	1.25E-04
T2D	PPP1R1B	2.854	0.003	1	2	2	0.004	0.103	1.67E-02
T2D	PNMT	3.910	0.014	1	1	1	0.000	0.170	6.46E-04
T2D	PGAP3	3.380	0.002	1	2	2	0.001	0.069	3.97E-03
T2D	ERBB2	3.482	0.000	2	2	2	0.000	0.019	2.99E-03
T2D	MIEN1	-3.468	0.000	1	1	1	0.001	0.010	3.04E-03
T2D	RPS6KC1	-2.424	0.001	1	2	2	0.015	0.076	4.71E-02
T2D	DCAF16	-5.252	0.008	3	3	3	0.000	0.105	2.38E-06
T2D	LCORL	2.983	0.000	2	2	2	0.006	0.054	1.18E-02
T2D	NUCB2	-3.990	0.017	1	1	1	0.000	0.186	4.90E-04
T2D	NCR3LG1	-2.587	0.001	2	2	2	0.000	0.060	3.31E-02
T2D	KCNJ11	8.719	0.009	1	1	1	0.000	0.135	2.82E-16
T2D	SIPA1	5.075	0.004	2	2	2	0.000	0.108	5.84E-06
T2D	MDM4	3.399	0.012	2	2	2	0.002	0.171	3.85E-03
T2D	TMEM81	2.794	0.029	2	2	2	0.001	0.137	1.96E-02
T2D	RBBP5	3.474	0.003	2	2	2	0.000	0.103	3.03E-03

T2D	DSTYK	2.999	0.007	2	2	2	0.001	0.153	1.13E-02
T2D	TMCC2	2.608	0.007	2	2	2	0.001	0.084	3.19E-02
T2D	MLF1	3.096	0.025	2	2	2	0.003	0.193	8.82E-03
T2D	MFSD1	-2.882	0.004	2	2	2	0.004	0.230	1.59E-02
T2D	CENPW	-7.468	0.005	1	1	1	0.000	0.101	3.49E-12
T2D	ECHDC1	-3.620	0.004	1	2	2	0.000	0.084	1.93E-03
T2D	EHBP1L1	-7.366	0.004	1	1	1	0.000	0.113	6.63E-12
T2D	RNASEH2	-4.029	0.026	2	2	2	0.000	0.168	4.32E-04
T2D	SNX32	4.484	0.138	1	1	1	0.000	0.726	7.87E-05
T2D	CTSW	-3.574	0.057	2	2	2	0.000	0.460	2.25E-03
T2D	FIBP	4.441	0.002	1	1	1	0.000	0.084	9.31E-05
T2D	DNAH10	-2.410	0.016	2	2	2	0.009	0.197	4.81E-02
T2D	CCDC92	-2.489	0.024	3	3	3	0.009	0.238	4.06E-02
T2D	DNAH100	-4.379	0.002	1	1	1	0.000	0.071	1.15E-04
T2D	ZNF664	4.552	0.004	1	1	1	0.000	0.089	6.16E-05
T2D	SREBF1	-5.365	0.225	2	2	2	0.000	0.372	1.35E-06
T2D	TOM1L2	-3.016	0.007	2	2	2	0.000	0.171	1.10E-02
T2D	ATPAF2	3.229	0.019	2	2	2	0.000	0.405	6.03E-03
T2D	ALKBH5	-3.283	0.019	2	2	2	0.001	0.176	5.15E-03
T2D	LLGL1	3.545	0.002	2	2	2	0.000	0.072	2.46E-03
T2D	MIEF2	3.318	0.007	2	2	2	0.001	0.126	4.70E-03
T2D	APOC1	6.759	0.001	1	1	1	0.000	0.055	3.81E-10
T2D	UBE2D3	4.199	0.000	2	2	2	0.000	0.023	2.25E-04
T2D	KAT5	4.351	0.004	1	1	1	0.000	0.088	1.24E-04
T2D	MRPS35	6.540	0.002	2	2	2	0.000	0.089	1.54E-09
T2D	DUSP6	2.516	0.000	2	2	2	0.013	0.059	3.80E-02
T2D	PABPC4	-9.846	0.004	2	2	2	0.000	0.100	1.08E-20
T2D	COBLL1	-2.701	0.003	2	2	2	0.007	0.087	2.48E-02
T2D	VDAC2	-3.185	0.014	2	2	2	0.003	0.151	6.59E-03

T2D	TMEM106	-2.790	0.009	2	2	2	0.001	0.076	1.96E-02
T2D	SENP1	-2.860	0.003	1	1	1	0.004	0.081	1.67E-02
T2D	ASB8	4.267	0.004	2	2	2	0.000	0.083	1.71E-04
T2D	H1FNT	2.526	0.006	1	1	1	0.012	0.197	3.74E-02
T2D	CHMP4B	-4.430	0.027	2	2	2	0.000	0.197	9.46E-05
T2D	EIF2S2	6.245	0.000	1	1	1	0.000	0.023	9.12E-09
T2D	DYNLRB1	2.764	0.000	1	1	1	0.006	0.007	2.10E-02
T2D	PIGU	2.819	0.003	1	1	1	0.005	0.076	1.84E-02
T2D	TP53INP2	-3.059	0.001	1	1	1	0.002	0.035	9.82E-03
T2D	CEP70	-2.857	0.000	1	1	1	0.004	0.053	1.67E-02
T2D	FAIM	-3.220	0.008	1	1	1	0.001	0.125	6.13E-03
T2D	CTSD	-2.526	0.003	2	2	2	0.018	0.229	3.74E-02
T2D	ZZEF1	5.411	0.005	3	3	3	0.000	0.101	1.11E-06
T2D	ANKFY1	5.533	0.002	1	1	1	0.000	0.061	5.91E-07
T2D	UBE2G1	-4.584	0.000	1	1	1	0.000	0.022	5.71E-05

Note:zscore: Association result of the gene in S-PrediXcan;n_snps_used: Number of SNPs from GWAS used in the S-PrediXcan analysis;
n_snps_in_cov: Number of SNPs in the covariance matrix;n_snps_in_model: Number of SNPs in the model;var_g: Variance of gene expression;
best_gwas_p: Highest p-value among the GWAS SNPs used in this model;largest_weight: Largest (absolute) weight in this model;
q: P-value adjusted using the Benjamini-Hochberg correction.

The S-MulTiXcan cross-tissue TWAS analysis identified significant associations with key CMR traits (adjusted P-value < 0.05, Benjamini-Hochberg method)

Trait	name	n	n_in_dep	p_i_best	t_i_best	p_i_worst	t_i_worst	z_min	z_max	z_mean	z_sd	q
WT_AHA_6	RSPO3	44	4	0.000	Heart_Atrial_Appendage	0.974	Artery_Tibial	-1.053	4.221	2.617	1.706	3.58E-03
WT_AHA_6	MYBPC3	47	3	0.000	Adipose_Subcutaneous	0.682	Skin_Sun_Exposed_Lower_le	-4.675	4.700	1.011	2.357	9.30E-04
WT_AHA_6	MRGPRF	32	4	0.000	Heart_Atrial_Appendage	0.911	Whole_Blood	-4.686	4.110	-2.058	2.686	3.43E-03
WT_AHA_6	DCAF16	49	3	0.000	Adipose_Visceral_Ome	0.000	Brain_Cerebellar_Hemisphere	3.746	4.951	4.670	0.199	4.41E-04
WT_AHA_6	RBBP5	48	4	0.001	Heart_Atrial_Appendage	0.966	Esophagus_Muscularis	-3.416	2.268	-0.532	1.650	3.23E-02
WT_AHA_6	ACP2	49	3	0.000	Artery_Aorta	0.628	Cells_EBV-transformed_lymp	-4.138	-0.485	-2.925	0.984	1.12E-03
WT_AHA_6	IKZF3	23	3	0.002	Adipose_Visceral_Ome	0.205	Pancreas	1.268	3.077	2.975	0.388	3.07E-02
WT_AHA_6	ATP2B1	33	8	0.000	Adipose_Subcutaneous	0.816	Cells_Cultured_fibroblasts	-6.115	6.115	-0.308	3.257	1.96E-06
WT_AHA_7	TRIM63	33	3	0.000	Heart_Left_Ventricle	0.122	Testis	-4.589	3.331	0.510	3.047	6.55E-04
WT_AHA_7	CCDC141	34	8	0.008	Artery_Aorta	0.860	Heart_Atrial_Appendage	-2.647	2.647	-0.480	1.662	4.78E-03
WT_AHA_7	PSMC3	48	3	0.000	Artery_Aorta	0.000	Brain_Hypothalamus	-6.436	-4.179	-5.685	0.627	2.64E-07
WT_AHA_7	MTCH2	29	2	0.000	Adipose_Subcutaneous	0.733	Esophagus_Gastroesophageal	-5.926	-0.341	-5.093	1.572	2.40E-07
WT_AHA_7	ADAMTSL3	44	8	0.000	Artery_Aorta	0.946	Thyroid	-3.528	4.040	0.180	1.916	2.39E-02
WT_AHA_7	PGAP3	45	3	0.000	Heart_Atrial_Appendage	0.679	Liver	-4.561	0.976	-3.694	1.050	4.59E-03
WT_AHA_7	MIEN1	14	3	0.000	Whole_Blood	0.201	Brain_Cerebellum	-1.328	4.313	-0.348	1.728	3.67E-03
WT_AHA_7	RARRES1	46	3	0.000	Adipose_Subcutaneous	0.479	Esophagus_Gastroesophageal	-2.361	4.841	3.326	1.758	9.52E-04
WT_AHA_7	DNAH10OS	49	1	0.000	Adipose_Visceral_Ome	0.001	Brain_Cortex	-3.944	-3.286	-3.611	0.118	3.42E-03
WT_AHA_7	SREBF1	38	1	0.000	Heart_Atrial_Appendage	0.004	Artery_Tibial	-3.198	3.674	2.744	1.405	1.68E-02
WT_AHA_7	IKZF3	23	3	0.000	Artery_Coronary	0.209	Pancreas	1.255	3.483	3.358	0.473	8.53E-03
WT_AHA_7	ATP2B1	33	8	0.000	Artery_Tibial	0.924	Brain_Cerebellum	-4.855	4.108	-0.570	2.348	2.93E-03
WT_AHA_9	SLC30A2	26	2	0.000	Heart_Atrial_Appendage	0.565	Skin_Sun_Exposed_Lower_le	-4.383	4.383	2.099	3.228	6.17E-04
WT_AHA_9	CDKN1A	35	5	0.000	Heart_Left_Ventricle	0.424	Skin_Not_Sun_Exposed_Supr	-4.754	3.591	0.678	1.798	4.04E-03
WT_AHA_9	SLC39A13	47	3	0.000	Adipose_Visceral_Ome	0.109	Esophagus_Mucosa	-5.256	5.256	-4.145	2.229	1.64E-07
WT_AHA_9	PSMC3	48	3	0.000	Artery_Aorta	0.000	Adipose_Subcutaneous	-6.405	-3.536	-5.236	0.758	2.58E-07
WT_AHA_9	PPP1R1B	46	4	0.000	Whole_Blood	0.913	Brain_Putamen_basal_ganglia	-4.041	4.038	0.105	2.071	1.56E-02
WT_AHA_9	MIEN1	14	3	0.000	Whole_Blood	0.072	Artery_Aorta	-1.799	3.748	-0.541	2.094	8.73E-03

WT_AHA_9	EHP1L1	29	7	0.000	Whole_Blood	0.447	Artery_Tibial	-4.242	3.154	-0.451	1.982	1.32E-04
WT_AHA_9	DCP1B	45	5	0.000	Adipose_Visceral_Ome	0.908	Brain_Caudate_basal_ganglia	-3.639	3.718	0.699	1.852	4.44E-02
WT_AHA_9	OVOL1	40	6	0.001	Artery_Coronary	0.991	Thyroid	-2.964	3.480	0.963	2.031	2.40E-02
WT_AHA_9	IKZF3	23	3	0.000	Adipose_Subcutaneous	0.220	Cells_EBV-transformed_lymp	1.226	3.669	2.991	0.956	1.35E-02
WT_AHA_9	ATP2B1	33	8	0.000	Adipose_Subcutaneous	0.986	Colon_Sigmoid	-4.727	4.727	-0.282	2.556	9.75E-04
WT_AHA_9	REP15	21	5	0.001	Heart_Left_Ventricle	0.613	Spleen	-3.400	1.283	-1.308	0.947	1.08E-02
WT_AHA_10	CDKN1A	35	5	0.000	Heart_Left_Ventricle	0.597	Spleen	-5.886	3.505	0.377	1.945	1.16E-04
WT_AHA_10	PSMC3	48	3	0.000	Artery_Aorta	0.015	Testis	-5.597	-2.442	-4.375	0.846	1.07E-05
WT_AHA_10	MIEN1	14	3	0.000	Whole_Blood	0.095	Esophagus_Muscularis	-2.548	4.221	-1.147	2.350	1.35E-03
WT_AHA_10	CENPW	37	1	0.003	Adipose_Visceral_Ome	0.215	Ovary	-2.946	2.946	-2.421	1.640	2.86E-02
WT_AHA_10	IKZF3	23	3	0.000	Adipose_Subcutaneous	0.052	Cells_EBV-transformed_lymp	1.945	3.936	3.475	0.663	1.83E-03
WT_AHA_10	ATP2B1	33	8	0.000	Artery_Tibial	0.948	Stomach	-5.516	4.878	-0.185	2.727	3.13E-05
WT_AHA_11	TRIM63	33	3	0.000	Heart_Left_Ventricle	0.371	Minor_Salivary_Gland	-5.732	4.203	0.992	3.744	7.21E-06
WT_AHA_11	PEAK1	48	4	0.000	Adipose_Subcutaneous	0.628	Adrenal_Gland	-3.657	1.256	-2.282	1.290	4.25E-02
WT_AHA_11	RAB1A	46	3	0.001	Artery_Tibial	0.864	Pancreas	-3.417	3.449	-0.226	1.476	4.43E-02
WT_AHA_11	PSMC3	48	3	0.000	Artery_Aorta	0.003	Adipose_Subcutaneous	-6.160	-2.955	-4.798	0.861	4.03E-07
WT_AHA_11	CPT1A	16	5	0.000	Adipose_Subcutaneous	0.999	Artery_Tibial	-4.387	4.235	-2.335	2.549	2.98E-03
WT_AHA_11	IGHMBP2	48	3	0.000	Artery_Aorta	0.128	Brain_Hypothalamus	-4.371	1.998	-2.748	1.381	2.71E-03
WT_AHA_11	MRGPRF	32	4	0.000	Adipose_Visceral_Ome	0.860	Brain_Cerebellar_Hemisphere	-4.369	3.257	-1.767	2.152	2.67E-03
WT_AHA_11	TPCN2	40	9	0.001	Artery_Aorta	0.987	Artery_Coronary	-3.401	1.535	-0.838	1.327	4.04E-03
WT_AHA_11	PNMT	48	3	0.000	Heart_Left_Ventricle	0.796	Brain_Cortex	-6.457	6.180	-1.667	4.151	1.79E-07
WT_AHA_11	PGAP3	45	3	0.000	Heart_Atrial_Appendag	0.157	Liver	-6.611	1.485	-5.601	1.615	2.64E-07
WT_AHA_11	MIEN1	14	3	0.000	Whole_Blood	0.111	Brain_Cerebellum	-1.622	6.212	-0.118	2.583	6.54E-07
WT_AHA_11	CENPW	37	1	0.004	Adipose_Visceral_Ome	0.608	Ovary	-2.910	2.910	-2.373	1.639	3.22E-02
WT_AHA_11	ACP2	49	3	0.005	Artery_Tibial	0.869	Whole_Blood	-2.817	1.093	-1.033	0.945	3.29E-02
WT_AHA_11	IKZF3	23	3	0.000	Adipose_Subcutaneous	0.171	Pancreas	1.369	5.530	4.875	1.059	7.86E-06
WT_AHA_11	ATP2B1	33	8	0.000	Artery_Tibial	0.648	Brain_Substantia_nigra	-4.328	3.866	-0.551	2.176	4.33E-03
WT_AHA_11	GAL	29	4	0.001	Whole_Blood	0.978	Brain_Hypothalamus	-3.159	3.244	-0.069	1.020	4.78E-02
WT_AHA_12	TRIM63	33	3	0.000	Heart_Left_Ventricle	0.042	Adipose_Subcutaneous	-5.999	4.664	0.837	4.241	8.81E-07

WT_AHA_12	MSL2	46	4	0.000	Whole_Blood	0.813	Esophagus_Mucosa	-3.541	1.088	-0.991	1.215	4.89E-02
WT_AHA_12	CPT1A	16	5	0.001	Artery_Coronary	0.960	Cells_Cultured_fibroblasts	-3.294	3.294	-1.653	1.915	3.51E-02
WT_AHA_12	IGHMBP2	48	3	0.000	Adipose_Subcutaneous	0.431	Colon_Sigmoid	-3.783	1.999	-2.022	1.252	1.88E-02
WT_AHA_12	ADAMTSL3	44	8	0.000	Artery_Aorta	0.861	Pancreas	-3.697	5.372	0.783	2.273	7.93E-04
WT_AHA_12	PNMT	48	3	0.000	Heart_Left_Ventricle	0.996	Artery_Coronary	-5.601	5.233	-1.550	3.701	6.99E-05
WT_AHA_12	MIEN1	14	3	0.000	Whole_Blood	0.575	Brain_Cerebellum	-0.625	5.607	0.476	1.923	1.81E-05
WT_AHA_12	LXN	49	5	0.005	Heart_Left_Ventricle	0.822	Adipose_Visceral_Omentum	-1.546	2.790	1.719	0.683	4.31E-02
WT_AHA_12	ACP2	49	3	0.000	Artery_Aorta	0.931	Cells_EBV-transformed_lymph	-3.606	-0.087	-2.443	0.947	4.61E-03
WT_AHA_12	IKZF3	23	3	0.000	Artery_Coronary	0.555	Pancreas	0.590	4.647	4.131	0.932	4.54E-04
WT_AHA_12	ATP2B1	33	8	0.000	Artery_Tibial	0.832	Brain_Cerebellum	-5.320	4.379	-1.096	2.595	1.58E-04
WT_AHA_12	WT1	16	3	0.000	Heart_Left_Ventricle	0.064	Testis	-1.849	3.960	2.673	1.547	3.67E-03
WT_global	TRIM63	33	3	0.001	Heart_Left_Ventricle	0.115	Stomach	-3.449	2.510	0.306	2.429	2.66E-02
WT_global	RSPO3	44	4	0.000	Heart_Atrial_Appendage	0.959	Brain_Hippocampus	-0.863	4.321	2.712	1.824	2.97E-03
WT_global	FNDC3B	20	7	0.000	Artery_Tibial	0.912	Esophagus_Mucosa	-2.950	5.025	2.115	2.140	6.37E-03
WT_global	MYBPC3	47	3	0.000	Adipose_Subcutaneous	0.835	Testis	-7.269	7.360	1.541	3.668	8.12E-10
WT_global	PSMC3	48	3	0.000	Artery_Aorta	0.000	Brain_Hypothalamus	-9.017	-5.233	-7.472	1.007	1.58E-15
WT_global	MRGPRF	32	4	0.000	Heart_Atrial_Appendage	0.423	Whole_Blood	-3.991	3.638	-1.357	1.936	1.38E-02
WT_global	MIEN1	14	3	0.000	Whole_Blood	0.372	Prostate	-1.423	4.079	-0.529	1.645	6.68E-03
WT_global	RARRES1	46	3	0.000	Adipose_Subcutaneous	0.540	Esophagus_Gastroesophageal	-1.520	3.532	2.535	1.301	4.74E-02
WT_global	CENPW	37	1	0.002	Artery_Coronary	0.378	Ovary	-3.153	3.153	-2.579	1.766	1.71E-02
WT_global	DRG2	45	2	0.000	Heart_Atrial_Appendage	0.286	Heart_Left_Ventricle	-3.547	-1.067	-2.157	0.717	2.19E-02
WT_global	OVOL1	40	6	0.001	Artery_Coronary	0.964	Thyroid	-2.937	3.369	0.971	1.969	3.91E-02
WT_global	IKZF3	23	3	0.000	Adipose_Subcutaneous	0.112	Pancreas	1.588	3.715	3.438	0.508	6.45E-03
WT_global	ATP2B1	33	8	0.000	Artery_Tibial	0.595	Colon_Sigmoid	-6.160	5.564	-0.777	3.079	3.82E-06
WT_global	SCN3A	40	4	0.005	Adipose_Subcutaneous	0.951	Adipose_Visceral_Omentum	-2.533	2.794	0.004	0.968	1.56E-02
RAV_max	JAZF1	48	7	0.000	Adipose_Subcutaneous	0.980	Brain_Hypothalamus	-1.558	5.329	2.088	2.072	5.19E-05
RAV_max	HMG20A	42	7	0.006	Artery_Coronary	0.940	Skin_Sun_Exposed_Lower_leg	-2.489	2.737	1.107	1.338	1.71E-02
RAV_max	SIX5	21	2	0.000	Adipose_Visceral_Omentum	0.075	Colon_Transverse	-4.547	-1.780	-3.185	1.228	8.86E-04
RAV_max	DMPK	49	4	0.000	Whole_Blood	0.375	Brain_Hippocampus	0.887	4.542	2.964	1.179	2.75E-04

RAV_max	STRN4	42	3	0.000	Adipose_Subcutaneous	0.130	Brain_Anterior_cingulate_cor	-3.556	-1.515	-3.075	0.419	4.54E-02
RAV_min	JAZF1	48	7	0.000	Adipose_Subcutaneous	0.970	Pituitary	-1.061	4.194	1.500	1.593	2.02E-02
RAV_min	PLEC	45	1	0.000	Heart_Left_Ventricle	0.236	Brain_Cerebellar_Hemisphere	-4.752	-1.184	-2.585	0.590	3.81E-02
RAV_min	FBXO46	33	5	0.000	Artery_Tibial	0.043	Esophagus_Gastroesophageal	-4.691	4.164	-2.653	2.655	2.51E-05
RAV_min	SIX5	21	2	0.000	Artery_Tibial	0.050	Colon_Transverse	-4.349	-1.959	-3.150	1.045	1.82E-03
RAV_min	FKRP	49	2	0.000	Adipose_Subcutaneous	0.174	Cells_EBV-transformed_lymp	1.359	3.920	3.607	0.441	6.58E-03
RAV_min	GAL	29	4	0.001	Whole_Blood	0.696	Nerve_Tibial	-3.305	2.605	0.350	1.928	3.06E-02
RAV_min	VDR	46	7	0.002	Artery_Tibial	0.939	Adrenal_Gland	-3.136	2.233	0.108	1.338	1.38E-02

Note:n: Number of available "tissues" for the gene.

n_indep: Number of independent variation components retained in tissue prediction (synthesized independent tissues).

p_i_best: Best p-value from single-tissue S-PrediXcan association.

t_i_best: Name of the best single-tissue S-PrediXcan association.

p_i_worst: Worst p-value from single-tissue S-PrediXcan association.

t_i_worst: Name of the worst single-tissue S-PrediXcan association.

z_min: Minimum z-score in single-tissue S-PrediXcan associations.

z_max: Maximum z-score in single-tissue S-PrediXcan associations.

z_mean: Mean z-score in single-tissue S-PrediXcan associations.

z_sd: Standard deviation of the mean z-score in single-tissue S-PrediXcan associations.

q: P-value adjusted using the Benjamini-Hochberg correction.

The S-MulTiXcan cross-tissue TWAS analysis identified significant associations with T2D (adjusted P-value < 0.05, Benjamini-Hochberg method)												
Trait	name	n	n_in_dep	p_i_best	t_i_best	p_i_worst	t_i_worst	z_min	z_max	z_mean	z_sd	q
T2D	EXTL1	42	3	4.84E-06	Artery_Aor	9.15E-01	Colon_Sign	-4.318906077	4.571703538	2.955614649	2.382656796	3.12E-04
T2D	PLEKHA3	39	2	2.33E-05	Heart_Left	3.78E-01	Skin_Sun_I	-0.97049007	4.230922996	3.701523395	1.233219078	6.00E-04
T2D	JAZF1	48	7	5.35E-45	Adipose_Su	9.98E-01	Testis	-14.07580757	6.429825787	-6.463156616	5.339482673	1.45E-38
T2D	PARP10	44	3	2.69E-02	Whole_Blo	8.57E-01	Prostate	-1.048735261	2.212334405	0.906367982	0.773630362	4.91E-02
T2D	MAF1	48	2	1.18E-04	Heart_Left	3.16E-01	Nerve_Tibi	-1.685926318	3.850987968	1.873524798	1.019050248	6.98E-04
T2D	DLG2	44	5	7.41E-06	Heart_Atria	9.82E-01	Pituitary	-4.481527608	4.198021296	0.791878711	3.017680234	1.21E-03
T2D	TSPAN3	42	3	1.19E-08	Adipose_Su	2.95E-01	Brain_Sub	-1.046132207	5.701152802	2.791133884	2.452868826	1.13E-06
T2D	PEAK1	48	4	5.51E-31	Artery_Cor	6.81E-01	Brain_Putar	-11.57509518	11.57509518	1.892912842	5.12087661	2.53E-27
T2D	ERCC1	39	5	3.70E-03	Heart_Left	9.43E-01	Brain_Amy	-2.9030056	2.052293088	-1.080335581	1.260629634	3.43E-02
T2D	PPM1N	44	3	2.67E-03	Whole_Blo	6.52E-01	Skin_Sun_I	0.450724742	3.003948927	2.51096152	0.508523249	4.24E-02
T2D	THADA	32	6	1.41E-17	Adipose_V	9.06E-01	Minor_Sali	-4.684459209	8.534141541	3.628021425	3.979675151	8.74E-15
T2D	CEP68	49	5	1.81E-16	Adipose_Su	9.00E-02	Brain_Putar	-4.103030684	8.234077228	6.047155357	3.398288416	3.60E-12
T2D	SPRED2	26	4	9.64E-16	Artery_Cor	1.06E-02	Brain_Cere	-8.031297684	8.031297684	1.639563789	6.005336557	7.89E-14
T2D	CPA5	17	6	1.68E-03	Adipose_Su	3.81E-01	Whole_Blo	-3.141991979	1.661864281	-1.211259486	1.365901284	2.05E-02
T2D	MEST	43	5	5.59E-05	Adipose_V	7.32E-01	Brain_Cort	-4.029271603	1.98020947	-1.16054645	1.269542015	1.78E-03
T2D	KLF14	18	6	4.59E-16	Adipose_Su	6.11E-01	Breast_Mar	-8.121873519	7.358850956	0.70864311	3.294900599	9.97E-13
T2D	MYBPC3	47	3	1.53E-04	Adipose_Su	3.87E-01	Heart_Atria	-3.786908871	3.482421875	-0.621102608	1.870164053	2.27E-03
T2D	PTPMT1	49	3	7.34E-08	Adipose_Su	6.63E-01	Testis	-1.586021899	5.382673294	3.560487773	1.938373088	7.94E-05
T2D	IGHMBP2	48	3	1.61E-04	Adipose_Su	9.50E-01	Breast_Mar	-3.773303747	0.419295758	-2.350871973	1.111586136	6.69E-03
T2D	MRGPRF	32	4	8.12E-06	Heart_Atria	5.79E-01	Whole_Blo	-4.461887214	4.053433733	-1.953183045	2.542436073	1.15E-03
T2D	PGAP3	45	3	9.39E-06	Heart_Atria	1.51E-01	Liver	-1.924675226	4.430812386	3.128169852	0.915861812	6.46E-03
T2D	MIEN1	14	3	5.25E-04	Whole_Blo	9.49E-01	Artery_Aor	-3.467716932	0.064590558	-0.649266261	1.117980451	1.15E-02
T2D	RPS6KC1	22	3	1.53E-02	Whole_Blo	7.08E-01	Brain_Cere	-2.42401433	0.374274641	-1.999029601	0.53488432	4.91E-02
T2D	NUCB2	43	4	1.76E-09	Adipose_Su	9.11E-01	Testis	-6.01853221	3.482006716	-2.378320929	2.550134304	3.88E-07
T2D	CNTN2	30	9	3.19E-04	Artery_Aor	9.05E-01	Colon_Sign	-3.599279642	3.599279642	-1.031548845	2.266465359	2.69E-04
T2D	SHOX2	24	4	4.34E-06	Artery_Tibi	5.99E-01	Cells_EBV	-4.594259739	1.900099993	0.298098827	2.111961096	4.94E-04

T2D	RSRC1	47	7	1.91E-03	Artery_Tibi	8.23E-01	Brain_Spin	-3.103704432	2.276331602	-0.746757645	1.905829714	1.67E-03
T2D	CENPW	37	1	2.44E-14	Adipose_Su	3.40E-05	Ovary	-7.625071049	7.468474388	-6.171775564	4.143922494	2.10E-12
T2D	EHBP1L1	29	7	1.76E-13	Whole_Blo	9.93E-01	Adipose_V	-7.365647793	6.521883488	1.045953454	2.9655635	8.58E-11
T2D	CTSW	49	1	5.88E-06	Heart_Atria	1.67E-02	Brain_Fron	-4.530811995	-2.392441758	-3.786661565	0.416796791	4.17E-04
T2D	CACNA1C	13	7	2.17E-03	Artery_Aor	9.77E-01	Esophagus	-1.41096139	3.065508842	0.675435432	1.23420531	9.86E-03
T2D	CCDC92	43	5	3.02E-09	Adipose_V	7.30E-01	Testis	-5.930342984	3.792241163	-3.111005927	2.408574328	9.18E-05
T2D	SREBF1	38	1	1.51E-10	Heart_Atria	7.72E-07	Brain_Fron	-5.61316061	6.404689658	4.909849653	2.502555665	2.28E-07
T2D	GID4	31	1	2.97E-06	Adipose_V	2.97E-06	Brain_Ante	-4.672607422	4.672607422	-4.371148879	1.678450135	1.72E-05
T2D	PIK3C2A	16	4	3.17E-09	Adipose_V	7.03E-01	Thyroid	-4.869466305	5.922559738	2.27266461	3.644073546	4.15E-08
T2D	OVOL1	40	6	1.59E-04	Artery_Cor	9.76E-01	Cells_Cultu	-3.167630076	3.776888132	0.308524578	2.400338108	2.03E-04
T2D	EFEMP2	49	4	5.95E-03	Heart_Atria	9.77E-01	Colon_Tran	-2.750634432	0.910232306	0.107870331	0.744351416	3.86E-02
T2D	SSPN	29	3	1.78E-04	Heart_Left	3.05E-01	Thyroid	-2.801599264	3.749058008	1.454169313	2.049627474	7.62E-03
T2D	MRPS35	48	4	6.15E-11	Whole_Blo	9.37E-01	Heart_Left	-4.46397168	6.540099935	-0.523048526	2.561374016	4.61E-09
T2D	PTHLH	11	10	2.07E-11	Artery_Aor	7.97E-01	Brain_Nucl	-6.700998783	1.074496984	-0.994338403	2.084072636	2.67E-07
T2D	IKZF3	23	3	1.77E-03	Adipose_Su	6.50E-01	Pancreas	-3.12567091	-0.453901112	-2.565376989	0.820994391	3.68E-02
T2D	IRS1	47	6	9.11E-25	Adipose_V	9.81E-01	Nerve_Tibi	-10.27530299	1.930094011	-0.52636123	1.585770522	2.72E-19
T2D	TTK	40	6	3.78E-05	Artery_Cor	5.48E-01	Vagina	-4.017521113	4.120533812	-0.241389007	2.589229336	4.37E-03
T2D	MAS1	2	2	8.33E-03	Artery_Tibi	9.38E-02	Nerve_Tibi	1.675735593	2.638433695	2.157084644	0.680730356	2.56E-02
T2D	NDUFS5	49	2	1.20E-02	Artery_Tibi	8.35E-01	Testis	-2.01247406	2.510969877	0.615742093	0.57675654	3.67E-02
T2D	BMP8A	46	6	1.10E-20	Artery_Tibi	9.48E-01	Vagina	-2.178677926	9.326136589	4.649906145	3.801159004	1.28E-18
T2D	PPFIBP1	17	10	6.18E-07	Artery_Aor	9.44E-01	Adipose_Su	-0.940424204	4.9856208	1.02618903	1.453702828	3.40E-04
T2D	REP15	21	5	2.77E-10	Heart_Left	7.95E-01	Breast_Mar	-6.310853958	0.259304911	-2.424977667	1.725274864	1.94E-08
T2D	SENP1	24	4	3.61E-03	Artery_Aor	3.99E-01	Testis	-2.910717487	2.910717487	-1.603748007	2.227320887	7.86E-03
T2D	KANSL2	49	2	3.71E-03	Artery_Tibi	9.86E-01	Liver	-2.63219224	2.902077894	0.648077121	1.099837109	2.96E-02
T2D	NCOA3	47	3	1.38E-01	Adipose_Su	9.43E-01	Muscle_Ske	-1.37558123	1.484834968	0.519394122	0.713347272	4.24E-02
T2D	TFEB	33	6	7.84E-07	Adipose_V	2.63E-01	Adrenal_Gl	-4.939284643	3.104036093	-2.611443356	2.054656394	2.03E-04
T2D	ZZEF1	47	4	3.38E-14	Adipose_Su	7.70E-01	Esophagus	-3.117810249	7.582828999	4.240861544	3.235944196	1.84E-11
T2D	UBE2G1	15	6	1.18E-09	Heart_Atria	8.38E-01	Artery_Cor	-6.083176136	4.584442139	-1.309236787	3.967071644	2.78E-09

Note:n: Number of available "tissues" for the gene.

n_indep: Number of independent variation components retained in tissue prediction (synthesized independent tissues).

p_i_best: Best p-value from single-tissue S-PrediXcan association.

t_i_best: Name of the best single-tissue S-PrediXcan association.

p_i_worst: Worst p-value from single-tissue S-PrediXcan association.

t_i_worst: Name of the worst single-tissue S-PrediXcan association.

z_min: Minimum z-score in single-tissue S-PrediXcan associations.

z_max: Maximum z-score in single-tissue S-PrediXcan associations.

z_mean: Mean z-score in single-tissue S-PrediXcan associations.

z_sd: Standard deviation of the mean z-score in single-tissue S-PrediXcan associations.

q: P-value adjusted using the Benjamini-Hochberg correction.

SMR Analysis of Blood eQTLs in Relation to T2D and 14 Cardiometabolic Conditions(adjusted P-value < 0.05, Benjamini-Hochberg method)															
symbol	Trait	ProbeChr	topSNP	b_GWAS	se_GWAS	p_GWAS	b_eQTL	se_eQTL	p_eQTL	b_SMR	se_SMR	p_SMR	p_HEIDI	nsnp_HEIDI	BH_FDR
CEP68	T2D	2	rs1009358	-0.052	0.007	1.96E-15	-0.277	0.00877	#####	0.18915	0.02456	1.36E-14	0.071	20	2.65E-13
SPRED2	T2D	2	rs114625088	0.053	0.017	0.00145	0.4145	0.02121	4.51E-85	0.12787	0.04058	0.00163	0.13271	20	0.002758967
MITF	T2D	3	rs5638622	-0.024	0.008	0.00232	0.08618	0.00978	1.24E-18	-0.2738	0.0946	0.00379	0.49198	20	0.006165455
PPP2R3A	T2D	3	rs1269564	0.0303	0.007	2.08E-05	0.12225	0.00914	9.03E-41	0.24785	0.06096	4.79E-05	0.94151	20	0.000155753
FAIM	T2D	3	rs1672928	0.0248	0.006	0.0001	-0.2262	0.0083	#####	-0.1096	0.02858	0.00012	0.42703	20	0.000347744
MLF1	T2D	3	rs1093614	0.0199	0.009	0.02046	0.26809	0.01558	2.24E-66	0.07423	0.03237	0.02183	0.01021	20	0.028378714
DCAF16	T2D	4	rs7667864	-0.04	0.007	1.64E-08	0.16651	0.00876	1.23E-80	-0.2414	0.04449	5.75E-08	0.01867	20	3.20E-07
CENPW	T2D	6	rs1591805	-0.05	0.006	3.84E-15	0.0877	0.00871	7.42E-24	-0.5724	0.09249	6.08E-10	0.08796	20	4.74E-09
TAX1BP1	T2D	7	rs4722732	0.023	0.006	0.00032	-0.0854	0.00795	5.69E-27	-0.2692	0.07898	0.00065	0.38043	20	0.001341
KCNJ11	T2D	11	rs2074310	0.0684	0.007	3.41E-25	0.15719	0.01218	4.37E-38	0.43515	0.05386	6.49E-16	0.14449	20	2.53E-14
FNBP4	T2D	11	rs1103933	-0.03	0.006	3.58E-06	-0.1343	0.00799	2.49E-63	0.2204	0.04943	8.23E-06	0.11991	20	4.01E-05
EHBP1L1	T2D	11	rs1346	0.0601	0.008	1.85E-13	-0.16	0.01314	4.10E-34	-0.3757	0.05983	3.39E-10	0.01081	20	3.31E-09
FIBP	T2D	11	rs1204650	0.0369	0.008	8.15E-06	0.32562	0.01023	#####	0.11332	0.02574	1.07E-05	0.03775	20	4.16E-05
CCDC92	T2D	12	rs3768	-0.022	0.008	0.00902	0.27887	0.01025	#####	-0.0775	0.0299	0.00958	0.0321	20	0.013839774
ZNF664	T2D	12	rs7958691	-0.03	0.007	6.13E-06	-0.1766	0.00846	9.83E-97	0.17159	0.03882	9.88E-06	0.58622	20	4.16E-05
SREBF1	T2D	17	rs9891957	0.0388	0.007	4.05E-09	-0.3417	0.00789	0	-0.1136	0.01949	5.70E-09	0.03682	20	3.71E-08
MED1	T2D	17	rs1245055	0.0327	0.007	8.13E-06	0.16604	0.00915	1.55E-73	0.19695	0.04529	1.37E-05	0.43201	20	4.85E-05
PNMT	T2D	17	rs876493	0.0231	0.007	0.00046	0.06537	0.00831	3.62E-15	0.35336	0.1105	0.00138	0.12958	20	0.002651396
PGAP3	T2D	17	rs2952152	0.0257	0.007	0.00016	0.35496	0.00823	0	0.0724	0.01923	0.00017	0.03649	20	0.000405963
ERBB2	T2D	17	rs903506	0.0233	0.007	0.00062	0.06866	0.00843	3.68E-16	0.33933	0.10743	0.00159	0.05757	20	0.002758967
CEP68	AF	2	rs7418129	-0.068	0.009	3.21E-13	-0.2986	0.00944	#####	0.22609	0.03196	1.50E-12	0.22656	20	5.86E-11
MSL2	AF	3	rs834304	0.0354	0.007	1.57E-07	-0.0896	0.00889	6.53E-24	-0.395	0.08538	3.73E-06	0.57756	20	2.43E-05
CCDC92	AF	12	rs3768	-0.041	0.009	2.48E-06	0.27887	0.01025	#####	-0.1456	0.0313	3.30E-06	0.04601	20	2.43E-05
ZNF664	AF	12	rs7958691	-0.035	0.007	8.28E-07	-0.1766	0.00846	9.83E-97	0.19594	0.04074	1.51E-06	0.08846	20	1.96E-05

MED1	AF	17	rs1245055	0.036	0.008	2.46E-06	0.16604	0.00915	1.55E-73	0.21682	0.04731	4.58E-06	0.0752	20	2.55E-05
PNMT	AF	17	rs876493	0.0327	0.007	2.35E-06	0.06537	0.00831	3.62E-15	0.50021	0.12322	4.92E-05	0.07448	20	0.000239704
PGAP3	AF	17	rs2952152	0.0371	0.007	1.77E-07	0.35496	0.00823	0	0.10452	0.02015	2.13E-07	0.16948	20	4.16E-06
ERBB2	AF	17	rs903506	0.0409	0.007	9.52E-09	0.06866	0.00843	3.68E-16	0.59565	0.12663	2.55E-06	0.68737	20	2.43E-05
CEP68	CA	2	rs7418129	-0.032	0.008	3.27E-05	-0.2986	0.00944	#####	0.10767	0.02614	3.81E-05	0.06003	20	0.000495426
KAT5	CA	11	rs502468	0.029	0.007	9.38E-05	-0.056	0.00806	3.75E-12	-0.5184	0.15225	0.00066	0.0145	20	0.005166304
SREBF1	CA	17	rs9891957	0.0337	0.007	6.50E-06	-0.3417	0.00789	0	-0.0986	0.02198	7.29E-06	0.68572	20	0.000142156
CEP68	CAD	2	rs7418129	-0.015	0.004	0.00047	-0.2986	0.00944	#####	0.04991	0.01449	0.00057	0.19802	20	0.001716224
MLF1	CAD	3	rs1093614	0.0151	0.005	0.00462	0.26809	0.01558	2.24E-66	0.05632	0.02004	0.00494	0.23312	20	0.010707335
DCAF16	CAD	4	rs7667864	-0.017	0.005	0.00018	0.16651	0.00876	1.23E-80	-0.1015	0.02755	0.00023	0.32921	20	0.000894054
C1QTNF4	CAD	11	rs1317149	-0.015	0.004	0.00099	-0.4581	0.00884	0	0.03165	0.00962	0.00101	0.06826	20	0.002802757
ZNF664	CAD	12	rs4765541	-0.026	0.004	2.71E-09	-0.1763	0.00847	2.38E-96	0.14858	0.02595	1.03E-08	0.03649	20	1.01E-07
SREBF1	CAD	17	rs9891957	0.0292	0.004	7.09E-12	-0.3417	0.00789	0	-0.0855	0.01274	1.96E-11	0.25627	20	7.66E-10
MED1	CAD	17	rs1165401	0.0199	0.005	5.09E-05	0.1649	0.00915	1.27E-72	0.12068	0.03046	7.44E-05	0.09303	20	0.000400496
PPP1R1B	CAD	17	rs1165149	0.0187	0.005	0.00019	0.13035	0.00992	1.96E-39	0.14346	0.03988	0.00032	0.1329	20	0.001140792
PNMT	CAD	17	rs876493	0.0125	0.004	0.00354	0.06537	0.00831	3.62E-15	0.19121	0.07012	0.0064	0.04148	20	0.013127049
PGAP3	CAD	17	rs2941506	0.0174	0.004	8.02E-05	0.35502	0.00823	0	0.04901	0.01245	8.22E-05	0.2847	20	0.000400496
ERBB2	CAD	17	rs9747973	0.0098	0.004	0.01715	0.06281	0.00798	3.56E-15	0.15604	0.06823	0.02219	0.05195	20	0.043273737
KAT5	CM	11	rs502468	0.0931	0.021	9.37E-06	-0.056	0.00806	3.75E-12	-1.663	0.44516	0.00019	0.06448	20	0.007299618
MLF1	HF	3	rs1093614	0.0238	0.008	0.00142	0.26809	0.01558	2.24E-66	0.08878	0.02845	0.0018	0.0243	20	0.023452884
KCNJ11	HF	11	rs4148646	0.0166	0.006	0.00506	0.15432	0.01218	8.26E-37	0.10757	0.03916	0.00602	0.18845	20	0.039129942
KAT5	HF	11	rs502468	0.0195	0.006	0.00084	-0.056	0.00806	3.75E-12	-0.3482	0.11506	0.00248	0.46729	20	0.024143662
ZNF664	HF	12	rs4765541	-0.018	0.006	0.00456	-0.1763	0.00847	2.38E-96	0.10038	0.03549	0.00468	0.28085	20	0.03649003
SREBF1	HF	17	rs9891957	0.0208	0.006	0.00048	-0.3417	0.00789	0	-0.0609	0.01762	0.00055	0.14464	20	0.0107069
KCNJ11	I_stroke	11	rs2074310	0.0374	0.01	0.0003	0.15719	0.01218	4.37E-38	0.23793	0.06807	0.00047	0.96198	20	0.018468551
MITF	MI	3	rs5638622	-0.034	0.013	0.0074	0.08618	0.00978	1.24E-18	-0.3993	0.15569	0.01034	0.01449	20	0.040312389
PPP2R3A	MI	3	rs1269564	0.0337	0.012	0.0054	0.12225	0.00914	9.03E-41	0.27586	0.10122	0.00642	0.01474	20	0.031300449
FAIM	MI	3	rs1672928	0.0436	0.011	5.70E-05	-0.2262	0.0083	#####	-0.1928	0.04842	6.86E-05	0.36292	20	0.001337459

CENPW	MI	6	rs576049	-0.033	0.011	0.0023	-0.0955	0.00937	2.15E-24	0.346	0.11836	0.00346	0.48049	20	0.019291044
ZNF664	MI	12	rs7958691	-0.042	0.011	0.00025	-0.1766	0.00846	9.83E-97	0.23527	0.0653	0.00031	0.83247	20	0.002703223
SREBF1	MI	17	rs9891957	0.0405	0.011	0.00033	-0.3417	0.00789	0	-0.1186	0.03316	0.00035	0.5353	20	0.002703223
MED1	MI	17	rs1245055	0.0369	0.012	0.0029	0.16604	0.00915	1.55E-73	0.22217	0.07571	0.00334	0.06111	20	0.019291044
PGAP3	MI	17	rs2952152	0.0487	0.012	2.50E-05	0.35496	0.00823	0	0.13728	0.0327	2.70E-05	0.6035	20	0.001051326
ERBB2	MI	17	rs903506	0.0471	0.011	4.00E-05	0.06866	0.00843	3.68E-16	0.68637	0.18723	0.00025	0.01647	20	0.002703223
MITF	PAD	3	rs6084351	-0.054	0.017	0.00124	0.085	0.00981	4.68E-18	-0.6329	0.20962	0.00253	0.33115	20	0.049381703
SNX32	PAD	11	rs1122733	0.0647	0.021	0.0021	0.36919	0.0102	#####	0.17525	0.05709	0.00214	0.81798	20	0.049381703
KCNJ11	Stroke	11	rs2074310	0.0355	0.01	0.00024	0.15719	0.01218	4.37E-38	0.22584	0.06414	0.00043	0.98669	20	0.016774142

Detailed Information of 31 Single-cell eQTLs

SNP	exposure	gene.exposure	chr.e xposu re	pos.exposu re	othe r_all ele.e xposu re	effect _allele _exposu re	eaf.exposu re	pval.exposu re	beta.exposure	se.exposure
rs78846567	ENSG00000179195_CD8 ET	ENSG00000179195	12	124155733	C	A	0.06625	4.76E-06	-0.413406323	0.090356223
rs11039216	ENSG00000172247_CD4 NC	ENSG00000172247	11	47406592	C	T	0.55582	4.75E-05	0.184181519	0.045279808
rs773456	ENSG00000158234_CD4 NC	ENSG00000158234	3	138325495	T	C	0.57208	2.37E-08	0.252910525	0.045303039
rs1471712	ENSG00000109920_CD8 ET	ENSG00000109920	11	47912150	G	A	0.53143	1.46E-16	0.367552729	0.044499331
rs7933184	ENSG00000109920_CD8 NC	ENSG00000109920	11	47682402	C	T	0.47445	4.22E-13	-0.323603989	0.044646002
rs665306	ENSG00000172500_CD4 NC	ENSG00000172500	11	65624025	T	C	0.66078	1.74E-06	-0.22683918	0.04744434
rs9398804	ENSG00000203760_NK	ENSG00000203760	6	126703390	T	A	0.45428	1.20E-06	-0.219023188	0.045105281
rs12465024	ENSG00000011523_CD4 NC	ENSG00000011523	2	65345731	C	G	0.65023	2.23E-07	0.243673669	0.047053485
rs10838786	ENSG00000109920_B IN	ENSG00000109920	11	47904086	G	A	0.48955	3.15E-11	-0.296739962	0.044692957
rs10769288	ENSG00000109920_CD8 S100B	ENSG00000109920	11	47729180	G	A	0.42129	7.35E-07	-0.225287923	0.045495464
rs596002	ENSG00000172500_NK	ENSG00000172500	11	65645354	A	G	0.80452	2.34E-22	-0.540992647	0.055623898
rs12633687	ENSG00000178053_NK	ENSG00000178053	3	158338168	G	T	0.15086	1.89E-14	0.476275313	0.062192388
rs853981	ENSG00000203760_CD8 ET	ENSG00000203760	6	127045460	C	T	0.49989	2.70E-07	0.230834098	0.044883554
rs10838786	ENSG00000109920_CD4 ET	ENSG00000109920	11	47904086	G	A	0.48955	4.18E-09	-0.263284956	0.044801276
rs774015	ENSG00000158234_CD8 NC	ENSG00000158234	3	138170116	G	A	0.60353	2.15E-06	0.217605101	0.045924456
rs1602629	ENSG00000158234_CD8 NC	ENSG00000158234	3	139028722	T	C	0.80271	4.10E-05	-0.231880163	0.056531229
rs10936149	ENSG00000178053_CD8 ET	ENSG00000178053	3	158293893	T	G	0.15211	5.60E-14	0.466175568	0.062015491
rs844119	ENSG00000178053_CD4 NC	ENSG00000178053	3	158013223	C	T	0.43003	5.53E-05	0.183251188	0.045447243
rs9398804	ENSG00000203760_CD4 NC	ENSG00000203760	6	126703390	T	A	0.45428	2.21E-08	-0.251856657	0.045016879
rs34522617	ENSG00000073711_CD4 NC	ENSG00000073711	3	135724841	T	G	0.30878	3.98E-06	0.224353667	0.048640252
rs12303741	ENSG00000177981_CD4 NC	ENSG00000177981	12	48560820	G	A	0.34304	8.21E-09	0.272016538	0.047191985

rs12316865	ENSG00000177981_NK	ENSG00000177981	12	48654642	T	C	0.34582	7.38E-06	0.211832567	0.047259119
rs12453217	ENSG00000141744_CD8 ET	ENSG00000141744	17	37741982	T	C	0.79826	3.37E-30	0.622074384	0.054477923
rs7933184	ENSG00000109920_CD4 NC	ENSG00000109920	11	47682402	C	T	0.47445	4.19E-39	-0.566955031	0.043339722
rs61917746	ENSG00000177981_CD4 ET	ENSG00000177981	12	48403440	C	T	0.07327	9.05E-06	0.382936242	0.086270546
rs2126606	ENSG00000139318_CD4 NC	ENSG00000139318	12	89674799	T	C	0.38963	3.68E-05	-0.190359594	0.046129092
rs12576996	ENSG00000172500_CD8 S100B	ENSG00000172500	11	65580638	T	G	0.26308	7.52E-06	-0.228749056	0.051077378
rs1859445	ENSG00000177981_CD8 ET	ENSG00000177981	12	48518591	A	C	0.343	5.98E-07	0.236083104	0.047292952
rs11039332	ENSG00000109920_B Mem	ENSG00000109920	11	47695840	G	A	0.31328	5.87E-13	-0.346293237	0.048072823
rs588114	ENSG00000172500_CD8 ET	ENSG00000172500	11	65662752	G	A	0.19385	3.87E-10	0.354191608	0.056586552
rs28498823	ENSG00000109920_NK	ENSG00000109920	11	47914941	C	G	0.53125	7.08E-12	0.306722042	0.044737604

Detailed Information of SNPs Included in the Final Analysis After Exposure–Outcome Harmonization													
outcome	exposure	gene.exposure	SNP	beta.exposure	beta.outcome	eaf.exposure	eaf.outcome	se.outcome	pval.outcome	pval.exposure	se.exposure	F_statistics	steiger_pval
AF	ENSG00000011523_CD4 NC	ENSG00000011523	rs12465024	0.2437	0.059	0.65023	0.6669	0.007	5.48E-17	2.23E-07	0.04705	26.8184	1.01E-06
AF	ENSG00000141744_CD8 ET	ENSG00000141744	rs12453217	0.6221	-0.027	0.79826	0.7935	0.0086	0.00161	3.37E-30	0.05448	130.39	1.72E-28
CAD	ENSG00000158234_CD4 NC	ENSG00000158234	rs773456	0.2529	-0.023	0.57208	0.6088	0.0043	6.36E-08	2.37E-08	0.0453	31.1659	7.96E-08
CAD	ENSG00000073711_CD4 NC	ENSG00000073711	rs34522617	0.2244	0.0161	0.30878	0.3054	0.0045	0.00029	3.98E-06	0.04864	21.2753	7.71E-06
CAD	ENSG00000177981_NK	ENSG00000177981	rs12316865	0.2118	0.0156	0.34582	0.2681	0.0047	0.00086	7.38E-06	0.04726	20.0916	1.34E-05
CAD	ENSG00000178053_NK	ENSG00000178053	rs12633687	0.4763	0.0166	0.15086	0.1726	0.0054	0.00222	1.89E-14	0.06219	58.6464	7.76E-14
CAD	ENSG00000178053_CD8 ET	ENSG00000178053	rs10936149	0.4662	0.0151	0.15211	0.1802	0.0053	0.00462	5.60E-14	0.06202	56.5065	2.06E-13
CAD	ENSG00000177981_CD8 ET	ENSG00000177981	rs1859445	0.2361	0.0122	0.343	0.2783	0.0046	0.00791	5.98E-07	0.04729	24.9194	1.07E-06
CAD	ENSG00000177981_CD4 NC	ENSG00000177981	rs12303741	0.272	0.0117	0.34304	0.2779	0.0046	0.01094	8.21E-09	0.04719	33.2242	1.68E-08
CA	ENSG00000073711_CD4 NC	ENSG00000073711	rs34522617	0.2244	0.0293	0.30878	0.28702	0.00811	0.0003	3.98E-06	0.04864	21.2753	1.00E-05
CA	ENSG00000177981_NK	ENSG00000177981	rs12316865	0.2118	0.031	0.34582	0.21312	0.00893	0.00052	7.38E-06	0.04726	20.0916	1.74E-05
CA	ENSG00000177981_CD8 ET	ENSG00000177981	rs1859445	0.2361	0.0263	0.343	0.22164	0.00882	0.00285	5.98E-07	0.04729	24.9194	1.43E-06

CA	ENSG00000177981_CD4 NC	ENSG00000177981	rs12303741	0.272	0.026	0.34304	0.22174	0.00882	0.0032	8.21E-09	0.04719	33.2242	2.37E-08
CA	ENSG00000158234_CD4 NC	ENSG00000158234	rs773456	0.2529	-0.019	0.57208	0.69083	0.00793	0.01712	2.37E-08	0.0453	31.1659	5.59E-08
HF	ENSG00000178053_CD8 ET	ENSG00000178053	rs10936149	0.4662	0.0238	0.15211	0.1872	0.0075	0.00142	5.60E-14	0.06202	56.5065	4.13E-13
HF	ENSG00000178053_NK	ENSG00000178053	rs12633687	0.4763	0.0233	0.15086	0.1789	0.0076	0.00226	1.89E-14	0.06219	58.6464	1.42E-13
HF	ENSG00000178053_CD4 NC	ENSG00000178053	rs844119	0.1833	-0.015	0.43003	0.4548	0.0058	0.01001	5.53E-05	0.04545	16.2584	0.00011
I_stroke	ENSG00000109920_B Mem	ENSG00000109920	rs11039332	-0.346	-0.036	0.31328	0.2903	0.0111	0.0011	5.87E-13	0.04807	51.8906	3.02E-12
MI	ENSG00000158234_CD4 NC	ENSG00000158234	rs773456	0.2529	-0.038	0.57208	0.57147	0.01087	0.00046	2.37E-08	0.0453	31.1659	6.33E-08
MI	ENSG00000203760_CD8 ET	ENSG00000203760	rs853981	0.2308	0.0318	0.49989	0.50159	0.01084	0.0034	2.70E-07	0.04488	26.45	5.77E-07
MI	ENSG00000172500_CD4 NC	ENSG00000172500	rs665306	-0.227	-0.032	0.66078	0.65611	0.0114	0.0044	1.74E-06	0.04744	22.8595	3.40E-06
PAD	ENSG00000172500_NK	ENSG00000172500	rs596002	-0.541	-0.053	0.80452	0.7501	0.0164	0.00137	2.34E-22	0.05562	94.5932	3.70E-21
Stroke	ENSG00000109920_B Mem	ENSG00000109920	rs11039332	-0.346	-0.036	0.31328	0.2899	0.0102	0.00035	5.87E-13	0.04807	51.8906	3.33E-12
T2D	ENSG00000203760_CD8 ET	ENSG00000203760	rs853981	0.2308	-0.044	0.49989	0.5056	0.0064	4.03E-12	2.70E-07	0.04488	26.45	1.00E-06
T2D	ENSG00000011523_CD4 NC	ENSG00000011523	rs12465024	0.2437	0.041	0.65023	0.6691	0.0068	1.70E-09	2.23E-07	0.04705	26.8184	7.24E-07
T2D	ENSG00000109920_CD8 S100B	ENSG00000109920	rs10769288	-0.225	-0.031	0.42129	0.3881	0.0067	2.79E-06	7.35E-07	0.0455	24.5211	1.80E-06

T2D	ENSG00000109920_CD8 NC	ENSG00000109920	rs7933184	-0.324	-0.03	0.47445	0.4386	0.0064	3.32E-06	4.22E-13	0.04465	52.5367	2.10E-12
T2D	ENSG00000109920_CD4 NC	ENSG00000109920	rs7933184	-0.567	-0.03	0.47445	0.4386	0.0064	3.32E-06	4.19E-39	0.04334	171.13	3.30E-36
T2D	ENSG00000172500_CD8 ET	ENSG00000172500	rs588114	0.3542	0.0372	0.19385	0.1962	0.0081	3.95E-06	3.87E-10	0.05659	39.1787	1.33E-09
T2D	ENSG00000172500_NK	ENSG00000172500	rs596002	-0.541	-0.037	0.80452	0.8034	0.0081	5.97E-06	2.34E-22	0.05562	94.5932	4.50E-21
T2D	ENSG00000109920_CD8 ET	ENSG00000109920	rs1471712	0.3676	0.029	0.53143	0.5642	0.0065	7.92E-06	1.46E-16	0.0445	68.2232	1.11E-15
T2D	ENSG00000109920_B IN	ENSG00000109920	rs10838786	-0.297	-0.026	0.48955	0.4534	0.0064	3.57E-05	3.15E-11	0.04469	44.0833	1.12E-10
T2D	ENSG00000109920_CD4 ET	ENSG00000109920	rs10838786	-0.263	-0.026	0.48955	0.4534	0.0064	3.57E-05	4.18E-09	0.0448	34.5359	1.18E-08
T2D	ENSG00000141744_CD8 ET	ENSG00000141744	rs12453217	0.6221	-0.032	0.79826	0.8062	0.0081	7.60E-05	3.37E-30	0.05448	130.39	2.43E-28
T2D	ENSG00000109920_B Mem	ENSG00000109920	rs11039332	-0.346	-0.024	0.31328	0.2864	0.007	0.00069	5.87E-13	0.04807	51.8906	2.16E-12
T2D	ENSG00000178053_CD4 NC	ENSG00000178053	rs844119	0.1833	-0.022	0.43003	0.4209	0.0065	0.0007	5.53E-05	0.04545	16.2584	9.33E-05
T2D	ENSG00000158234_CD4 NC	ENSG00000158234	rs773456	0.2529	-0.021	0.57208	0.5735	0.0065	0.00151	2.37E-08	0.0453	31.1659	5.18E-08
T2D	ENSG00000073711_CD4 NC	ENSG00000073711	rs34522617	0.2244	0.0192	0.30878	0.3187	0.0068	0.00479	3.98E-06	0.04864	21.2753	6.80E-06
T2D	ENSG00000172247_CD4 NC	ENSG00000172247	rs11039216	0.1842	-0.018	0.55582	0.5226	0.0064	0.00586	4.75E-05	0.04528	16.5456	7.40E-05
T2D	ENSG00000172500_CD4 NC	ENSG00000172500	rs665306	-0.227	-0.018	0.66078	0.6701	0.0068	0.00686	1.74E-06	0.04744	22.8595	3.01E-06

T2D	ENSG00000178053_CD8 ET	ENSG00000178053	rs10936149	0.4662	0.0199	0.15211	0.1681	0.0086	0.02046	5.60E-14	0.06202	56.5065	1.78E-13
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Mendelian Randomization Results of Single-cell eQTLs for T2D and 14 Cardiometabolic Traits

outcome	exposure	symbol	celltype	method	nsnp	b	se	pval	FDR
AF	ENSG00000011523_CD4 NC	CEP68	CD4 NC	Wald ratio	1	0.242127105	0.028726945	3.50E-17	9.45E-16
AF	ENSG00000141744_CD8 ET	PNMT	CD8 ET	Wald ratio	1	-0.04340317	0.013824713	0.001692163	0.022844196
CAD	ENSG00000158234_CD4 NC	FAIM	CD4 NC	Wald ratio	1	-0.09252284	0.01700206	5.27E-08	7.38E-07
CAD	ENSG00000073711_CD4 NC	PPP2R3A	CD4 NC	Wald ratio	1	0.071761698	0.020057617	0.000346528	0.002425695
CAD	ENSG00000177981_NK	ASB8	NK	Wald ratio	1	0.073643067	0.022187334	0.000902923	0.004213639
CAD	ENSG00000178053_NK	MLF1	NK	Wald ratio	1	0.034853791	0.01133798	0.00211157	0.007390495
CAD	ENSG00000178053_CD8 ET	MLF1	CD8 ET	Wald ratio	1	0.03239123	0.011369107	0.004384908	0.012277742
CAD	ENSG00000177981_CD8 ET	ASB8	CD8 ET	Wald ratio	1	0.051676718	0.019484664	0.007997534	0.018660912
CAD	ENSG00000177981_CD4 NC	ASB8	CD4 NC	Wald ratio	1	0.043012091	0.016910736	0.010975489	0.021950977
CA	ENSG00000073711_CD4 NC	PPP2R3A	CD4 NC	Wald ratio	1	0.130644176	0.036128048	0.000299026	0.003674712
CA	ENSG00000177981_NK	ASB8	NK	Wald ratio	1	0.146141835	0.042143898	0.000524959	0.003674712
CA	ENSG00000177981_CD8 ET	ASB8	CD8 ET	Wald ratio	1	0.111409498	0.037341554	0.002849478	0.011183078
CA	ENSG00000177981_CD4 NC	ASB8	CD4 NC	Wald ratio	1	0.095571027	0.032415529	0.003195165	0.011183078
CA	ENSG00000158234_CD4 NC	FAIM	CD4 NC	Wald ratio	1	-0.074756873	0.031356939	0.017122739	0.047943669
HF	ENSG00000178053_CD8 ET	MLF1	CD8 ET	Wald ratio	1	0.051053727	0.016088359	0.001506994	0.015196728
HF	ENSG00000178053_NK	MLF1	NK	Wald ratio	1	0.048921284	0.015957157	0.002170961	0.015196728
HF	ENSG00000178053_CD4 NC	MLF1	CD4 NC	Wald ratio	1	-0.082400557	0.031650545	0.009229119	0.043069223
I_stroke	ENSG00000109920_B Mem	FNBP4	B Mem	Wald ratio	1	0.10424691	0.032053759	0.001144944	0.029768534
MI	ENSG00000158234_CD4 NC	FAIM	CD4 NC	Wald ratio	1	-0.150532158	0.042971201	0.000459887	0.012416952
MI	ENSG00000203760_CD8 ET	CENPW	CD8 ET	Wald ratio	1	0.137752974	0.046962294	0.003354147	0.039465544
MI	ENSG00000172500_CD4 NC	FIBP	CD4 NC	Wald ratio	1	0.143126383	0.050236608	0.00438506	0.039465544
PAD	ENSG00000172500_NK	FIBP	NK	Wald ratio	1	0.097043833	0.030314645	0.001368472	0.019158613
Stroke	ENSG00000109920_B Mem	FNBP4	B Mem	Wald ratio	1	0.105113228	0.029454806	0.000358856	0.009330263
T2D	ENSG00000203760_CD8 ET	CENPW	CD8 ET	Wald ratio	1	-0.191912722	0.02772554	4.46E-12	1.20E-10
T2D	ENSG00000011523_CD4 NC	CEP68	CD4 NC	Wald ratio	1	0.168257819	0.027906175	1.65E-09	2.22E-08
T2D	ENSG00000109920_CD8 S100B	FNBP4	CD8 S100B	Wald ratio	1	0.1393772	0.029739721	2.78E-06	1.88E-05
T2D	ENSG00000109920_CD8 NC	FNBP4	CD8 NC	Wald ratio	1	0.091778844	0.019777259	3.47E-06	1.88E-05

T2D	ENSG00000109920_CD4 NC	FNBP4	CD4 NC	Wald ratio	1	0.052385107	0.011288373	3.47E-06	1.88E-05
T2D	ENSG00000172500_CD8 ET	FIBP	CD8 ET	Wald ratio	1	0.105027898	0.022868978	4.38E-06	1.97E-05
T2D	ENSG00000172500_NK	FIBP	NK	Wald ratio	1	0.067468569	0.014972477	6.60E-06	2.55E-05
T2D	ENSG00000109920_CD8 ET	FNBP4	CD8 ET	Wald ratio	1	0.078900244	0.017684537	8.14E-06	2.75E-05
T2D	ENSG00000109920_B IN	FNBP4	B IN	Wald ratio	1	0.088966784	0.021567705	3.71E-05	0.000100098
T2D	ENSG00000109920_CD4 ET	FNBP4	CD4 ET	Wald ratio	1	0.100271586	0.024308263	3.71E-05	0.000100098
T2D	ENSG00000141744_CD8 ET	PNMT	CD8 ET	Wald ratio	1	-0.051280041	0.013020951	8.21E-05	0.000201446
T2D	ENSG00000109920_B Mem	FNBP4	B Mem	Wald ratio	1	0.06872788	0.020214082	0.000673859	0.00148039
T2D	ENSG00000178053_CD4 NC	MLF1	CD4 NC	Wald ratio	1	-0.120053792	0.035470439	0.000712781	0.00148039
T2D	ENSG00000158234_CD4 NC	FAIM	CD4 NC	Wald ratio	1	-0.081451731	0.025700789	0.00152843	0.002947686
T2D	ENSG00000073711_CD4 NC	PPP2R3A	CD4 NC	Wald ratio	1	0.085579167	0.030309288	0.004749807	0.008549652
T2D	ENSG00000172247_CD4 NC	C1QTNF4	CD4 NC	Wald ratio	1	-0.095557904	0.034748329	0.005959526	0.010056701
T2D	ENSG00000172500_CD4 NC	FIBP	CD4 NC	Wald ratio	1	0.081114735	0.029977185	0.006812318	0.010819563
T2D	ENSG00000178053_CD8 ET	MLF1	CD8 ET	Wald ratio	1	0.04268778	0.018447985	0.020670274	0.03100541