

## Supplementary files2

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**Table S4**

Source of multivariate MR data							
Trait	Data sources	PMID	Use	Number of cases	Number of controls	Ancestry	Download
RA	FinnGen	NA	Exposure	9,243	368,029	European	finngen_R9_RHE UMA_SEROPOS _WIDE
AF	Nielsen, et al.	3E+07	Outcome	60,620	970,216	European	ebi-a- GCST006414
Heart failure	HERMES Consortium	3.2E+07	Confounder	977,323	7,773,021	European	ebi-a- GCST009541
Type 2 diabetes	Xue, et al.	3E+07	Confounder	61,714	591,178	European	ebi-a- GCST006867

**Table S6**

Confounding factors were removed in PhenoScanner V2

snp	hg38_coordinates	trait
rs2476601	chr1:113834946	Medication for cholesterol, blood pressure or diabetes: insulin Coronary artery disease Coronary artery disease
rs2013002	chr12:111762346	Medication for cholesterol, blood pressure or diabetes: blood pressure medication Medication for cholesterol, blood pressure or diabetes: none of the above No treatment with medication for cholesterol, blood pressure, diabetes, or take exogenous hormones No treatment with medication for cholesterol, blood pressure, diabetes, or take exogenous hormones
rs2395269	chr6:32849997	hormones
rs7453967	chr6:31346466	Medication for cholesterol, blood pressure or diabetes: insulin Medication for cholesterol, blood pressure or diabetes: insulin
rs9268145	chr6:32289507	No treatment with medication for cholesterol, blood pressure, diabetes, or take exogenous hormones

[PhenoScanner V2:http://www.phenoscaner.medschl.cam.ac.uk/](http://www.phenoscaner.medschl.cam.ac.uk/)

**Table S7**

Mendelian randomization analysis											
exposure	outcome	method	nsnp	b	se	pval	or	or_lci95	or_uci95	Power	F-statistic
		Inverse variance									
RA	AF	weighted	24	0.00880176	0.01161607	0.448616915	1.00884061	0.98613134	1.03207285	0.21	389904.8
RA	AF	MR Egger	24	0.02232884	0.02124622	0.304686702	1.02257999	0.98087156	1.06606194	0.83	389904.8
		Weighted									
RA	AF	median	24	0.02190944	0.01659259	0.186689715	1.02215121	0.98944408	1.05593952	0.81	389904.8
RA	AF	Simple mode	24	0.02763104	0.02889898	0.348951562	1.02801632	0.97140583	1.08792589	0.95	389904.8
RA	AF	Weighted mode	24	0.02097	0.0184107	0.266423008	1.02119142	0.98499868	1.05871401	0.78	389904.8

Calculation of power:<https://shiny.cnsgenomics.com/mRnd/>

Sample size	1030836
$\alpha$	0.05
K	0.956125191
OR	Based on method
R2xz	0.274437173

**Table S8**

SNP	other_allele. exposure	effect_allele. exposure	Instrumental Variable information						
			pval. exposure	beta. exposure	se. exposure	eaf. exposure	R2	F	SD
rs78248443	C	T	3.82E-08	-0.163422	0.0297194	0.0752801	0.0037183	58.66429	18.25439
rs78782944	C	T	1.06E-10	0.15952	0.0247	0.0948137	0.0043679	68.958053	15.17135
rs10174238	G	A	3.20E-11	-0.115333	0.017377	0.764142	0.0047947	75.729263	10.673383
rs3087243	G	A	4.10E-16	-0.131586	0.0161742	0.330287	0.00766	121.33431	9.9345934
rs10517086	G	A	2.31E-11	0.10964	0.0164009	0.281956	0.0048674	76.883663	10.073838
rs66654254	G	A	9.91E-09	-0.0878528	0.015326	0.434795	0.0037934	59.854512	9.413608
rs7731626	G	A	2.81E-09	-0.100943	0.0169873	0.279038	0.0040998	64.707832	10.434019
rs13180950	T	C	2.27E-08	0.113664	0.0203339	0.155334	0.0033902	53.470816	12.489584
rs72849211	C	G	5.84E-22	0.204365	0.0212165	0.12978	0.0094337	149.69622	13.031699
rs144835716	A	T	3.56E-83	0.634386	0.0328337	0.0366511	0.0284189	459.77283	20.16727
rs28579922	G	A	2.41E-149	-0.67936	0.0261015	0.125317	0.1011791	1769.4243	16.032186
rs2144016	A	G	3.93E-79	-0.340349	0.0180705	0.250081	0.0434484	713.97034	11.099348
rs6456160	T	C	4.30E-14	-0.113708	0.0150578	0.557506	0.0063792	100.91666	9.2488729
rs60600003	T	G	4.07E-08	0.132171	0.0240846	0.102223	0.0032064	50.562526	14.793357
rs3757387	T	C	4.26E-12	0.104714	0.0151137	0.425307	0.0053602	84.708431	9.2832081
rs16903065	C	A	3.00E-09	-0.144104	0.024294	0.115459	0.0042416	66.955829	14.921975
rs3118470	T	C	4.05E-09	0.0886434	0.0150703	0.441338	0.0038747	61.142595	9.2565507
rs10995019	C	T	8.24E-10	0.0934553	0.0152203	0.424804	0.0042682	67.377437	9.3486844
rs9603597	C	T	2.06E-09	-0.102661	0.0171292	0.268948	0.0041444	65.414757	10.521178
rs3114891	A	G	9.60E-09	0.0870388	0.0151697	0.427948	0.0037092	58.520865	9.3176047
rs117753409	C	A	1.36E-08	0.146151	0.0257371	0.0853339	0.0033344	52.587538	15.808363
rs73510898	G	A	2.71E-08	-0.155807	0.0280265	0.0849334	0.0037734	59.537634	17.214569
rs34536443	G	C	4.36E-16	-0.401166	0.049355	0.0302719	0.0094486	149.93583	30.315061
rs6032664	A	T	3.37E-08	0.0942537	0.017071	0.727155	0.0035251	55.605531	10.48543

**Table S9**

Test of heterogeneity					
exposure	outcome	method	Q	Q_df	Q_pval
RA	AF	MR Egger	19.9867	22	0.583871
RA	AF	IVW	20.5649	23	0.607639

Test of pleiotropy				
exposure	outcome	egger_intercept	se	pval
RA	AF	-0.002545795	0.00335	0.5

**Table S10**

MVMR_IVW		Number of Variants : 122		
Exposure	Estimate	Std Error	95% CI	P-value
RA	0.018	0.025	-0.030, 0.067	0.465
Heart failure	-0.026	0.018	-0.062, 0.009	0.144
Type 2 diabetes	0.57	0.076	0.420, 0.719	0

Heterogeneity test statistic = 365.4039 on 119 degrees of freedom

MVMR_MR-Egger		Number of Variants : 122		
Exposure	Estimate	Std Error	95% CI	P-value
RA	0.038	0.028	-0.017, 0.092	0.179
Heart failure	-0.023	0.018	-0.059, 0.012	0.199
Type 2 diabetes	0.579	0.076	0.429, 0.728	0
(intercept)	-0.002	0.001	-0.005, 0.001	0.141

Heterogeneity test statistic = 358.7982 on 118 degrees of freedom