Supplementary Data Table of Contents

Supplementary Table 1. Characteristics of Included Genome-Wide Association Studies.

| Trait	Consortium and Data Download Web Address	Author	Number of individuals	Estimate of SNP-Based Heritability (where available) (%)	Quality Control
Type 2 Diabetes	DIAMANTE dbGaP - https://www.ncbi.nlm.nih.gov/gap/advanced_search/?TERM=phs001672.v3.p1 (data not available at time of writing but link identified in manuscript)	Vujkovic 2020	228,499 type 2 diabetes/1,178783 controls	19	HWE $<1 \times 10^{-10}$, call rate >0.975, MAD >0.1% (European), >1% (African American, Hispanic, Asian)
Type 2 Diabetes	DIAGRAM https://diagram-consortium.org/downloads.html; https://cnsgenomics.com/content/data	Mahajan 2018	74,124 type 2 diabetes cases/824,006 controls	18	DIAGRAM: Call rate ≥90%; HWE p value $< 1 \times 10^{-6}$, MAF≥ 1% UK Biobank data: excluded SNPs with minor allele count < 5%, Hardy-Weinberg equilibrium test p value $< 1 \times 10^{-6}$, missing genotype rate > 0.05, or imputation info score < 0.3.
Insulin Resistance	Fasting Insulin: MAGIC https://www.magicinvestigators.org/downloads/ Triglycerides/HLD-cholesterol: GLGC http://lipidgenetics.org/#data-downloads-title	Lotta 2017 Wang 2017	451,193	n/a	SNPs excluded if: MAF <1%; Hardy–Weinberg equilibrium p$< 1 \times 10^{-6}$; call rate <99%; showed differential missingness between cases and controls with p$< 1\times 10^{-6}$; differential genotyping between the CoreExome-24v1.0 and CoreExome-12v1.0 chips in a subset of 96 samples genotyped using both chips.
Fasting Glucose and Fasting Insulin	MAGIC https://www.magicinvestigators.org/downloads/	Scott 2012	133,010 (FG)	FG – 4.8 FI – 1.2	Call rate 95% and minor allele frequency (MAF) ≥ 1%.

			108,557 (FI)		Removed occurrences of sex discrepancies, ancestry outliers, heterozygosity, Hardy-Weinberg equilibrium p <1x10^{-4}, SNP effect estimate standard error ≥10 and SNP minor allele count <10.
Glycated Haemoglobin	MAGIC https://www.magicinvestigators.org/downloads/	Wheeler 2017	159,940	4-14	Cohorts were advised to keep SNPs with Hardy-Weinberg-disequilibrium p-value $\geq 1 \times 10^{-6}$, SNP genotyping call rate ≥ 95% and minor allele frequency (MAF) ≥ 1%
Heart Failure	HERMES https://www.hermesconsortium.org/	Shah 2020	47,309 cases/930,014 controls	8.8	Variants removed if imputation quality < 0.5, MAF < 1%, absolute betas and s.e.> 10. More stringent QC measures applied to studies where genotyping of cases and controls was performed on different platforms.
Coronary Heart Disease	CARDIOGRAMplusC4D http://www.cardiogramplusc4d.org/data-downloads/	Nelson 2017	10.801 cases/137,914controls	10.6	Call rate ≥90%; HWE p>1x10^{-9}; ethnic outliers
LDL-Cholesterol	GLGC http://lipidgenetics.org/#data-downloads-title	Willer 2013	188,578	14.6	Average standard errors for association statistics from each study were plotted against study sample size to identify outlier studies. Allele frequencies inspected for strand orientation. Genomic control values for study specific analyses were inspected, and all were <1.20. Variants for which the minor allele was observed <7 times excluded.
Body Mass Index	GIANT https://portals.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium_data_files	Locke 2015	339,224	2.7	Predominantly call rate ≥90%; HWE p>1x10^{-4}; MAF >1%
Systolic Blood Pressure	International Consortium of Blood Pressure Genome Wide Association Studies (ICBP)	Evangelou 2018 (also included data from UK BIOBANK)	1,006,863	5.7	MAF > 1%; HWE p >1x10-6; missingness < 0.015, imputation quality INFO >0.1

|	https://www.ebi.ac.uk/gwas/studies/GCST006624				

Supplementary Table 2. Baseline Characteristics of GoDARTS Patients.

|	Type 2 Diabetes (n=8,329)	No Type 2 Diabetes (n=4,590)	p value between groups
Age at recruitment (years)	65 ± 12	60 ± 12	<0.001
Male (%)	4267 (53.5)	2386 (52.0)	<0.001
Prior MI (%)	885 (11.1)	267 (5.8)	<0.001
Systolic BP (mmHg)	144 ± 4	143 ± 4	<0.001
Current/Past Smoker	3,827 (46.0)	455 (10.0)	<0.001
Body Mass Index (kg/m^2)	30.9 ± 5.8	29.9 ± 5.1	<0.001
Aspirin use	4,111 (49.4)	996 (21.7)	<0.001
Statin use	5,212 (62.6)	1,017 (22.2)	<0.001
Total cholesterol (mmol/l)	4.6 ± 0.6	4.9 ± 0.7	<0.001
HDL cholesterol (mmol/l)	1.3 ± 0.3	1.6 ± 0.4	<0.001
Serum creatinine (umol/l)	94 ± 30	96 ± 21	0.28
Glycated haemoglobin (%)	7.6 ± 1.3	6.1 ± 0.7	<0.001
Glycated haemoglobin (mmol/mol)	60 ± 14	43 ± 8	<0.001

Supplementary Figure 1. Example Power Calculations for Genetic Instruments Reflecting a Range of

Different Exposure Phenotypes and their associations with HF.
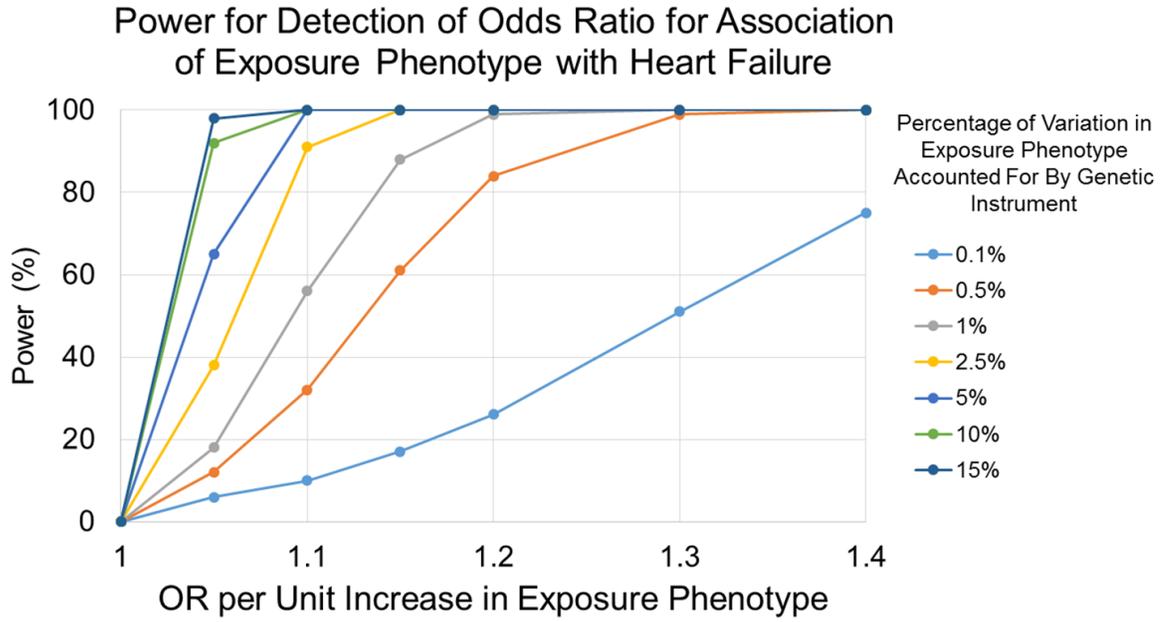
Supplementary Figure 2. MR Plot of Single Nucleotide Variants Associated with Type 2 Diabetes and their Association with Heart Failure.
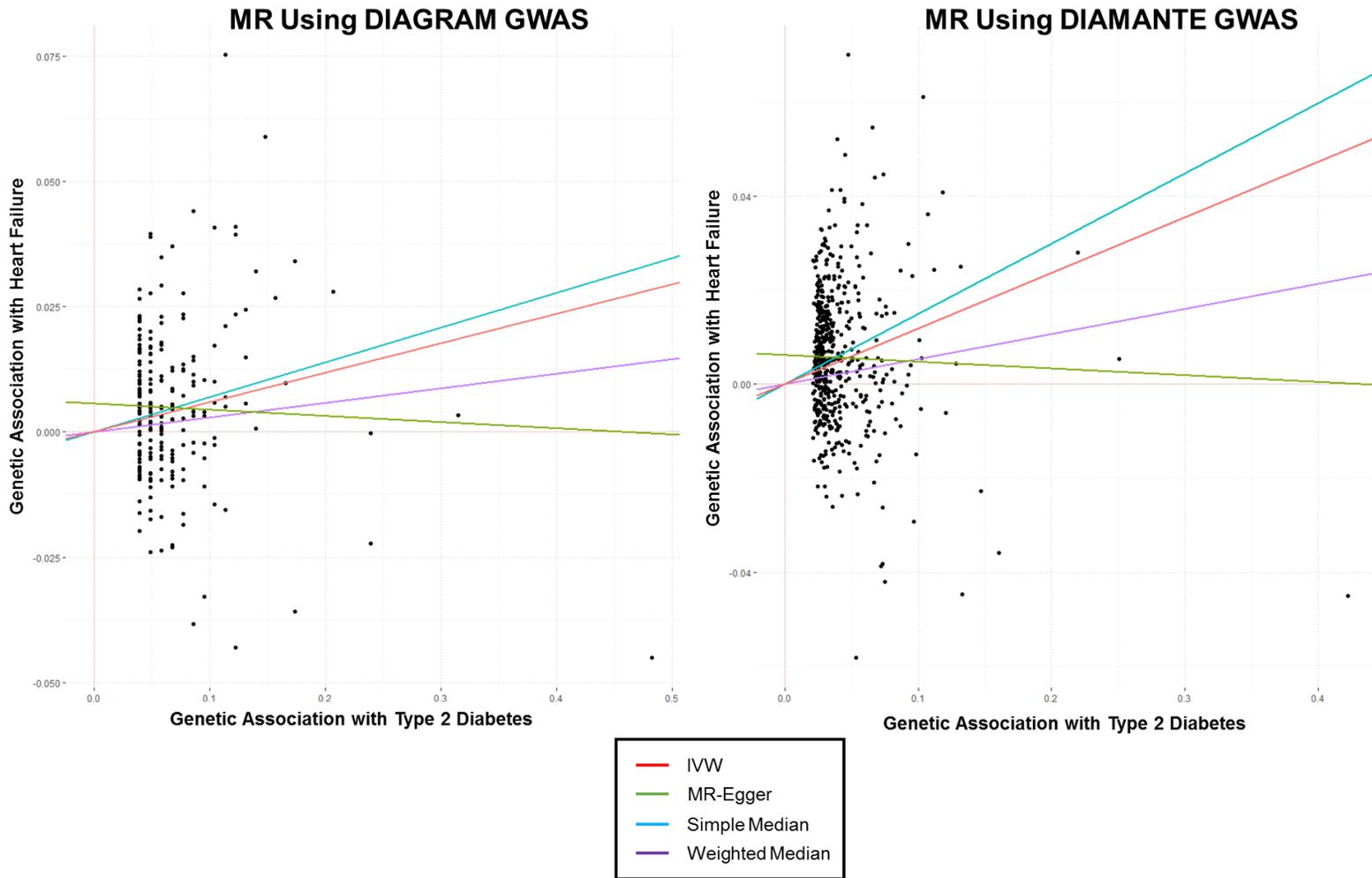
Supplementary Figure 3. MR Plot of Single Nucleotide Variants Associated with Insulin Resistance and their Association with Heart Failure.
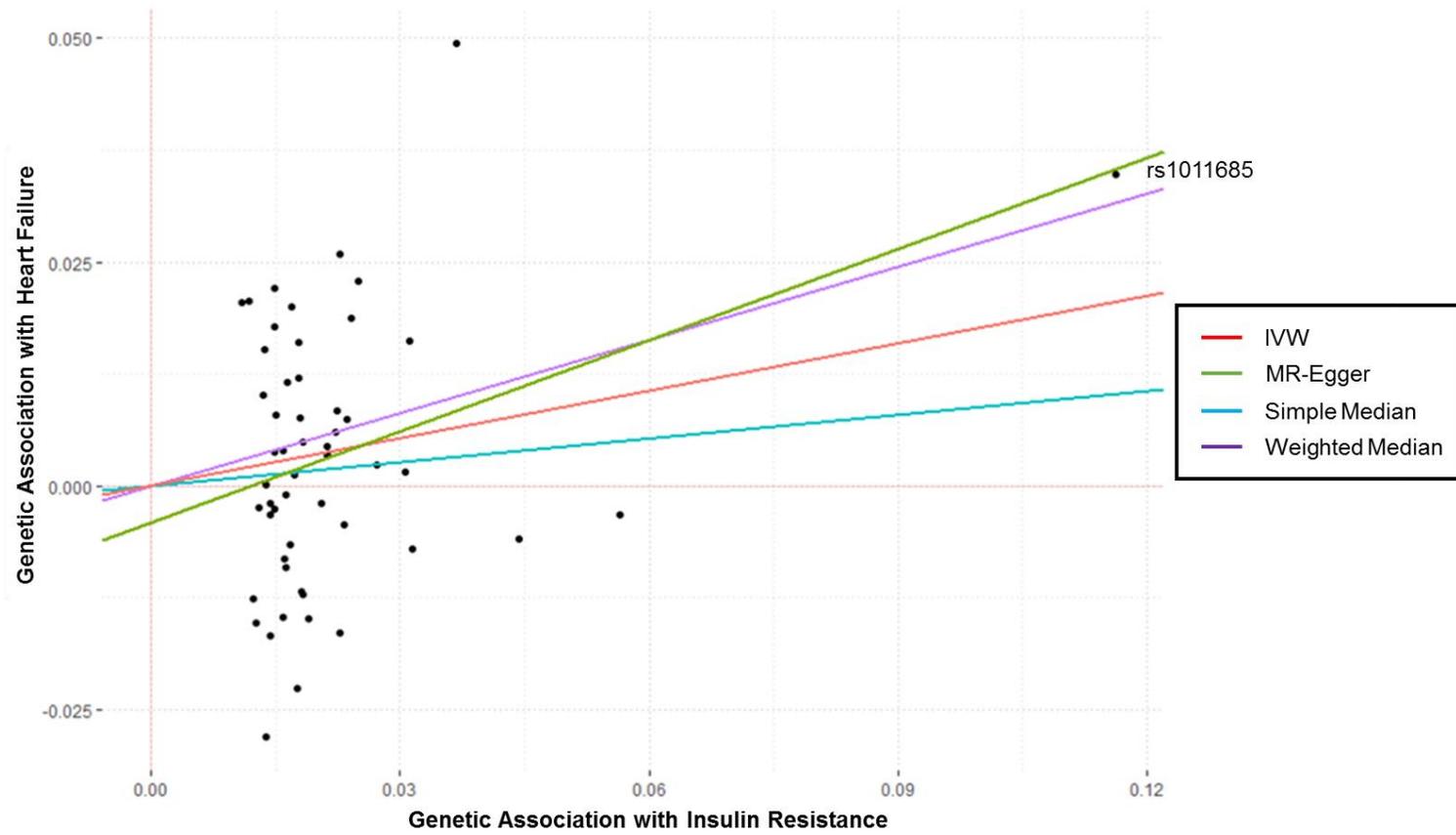
Supplementary Figure 4. MR Plot of Single Nucleotide Variants Associated with Heart Failure and their Association with Type 2 Diabetes.