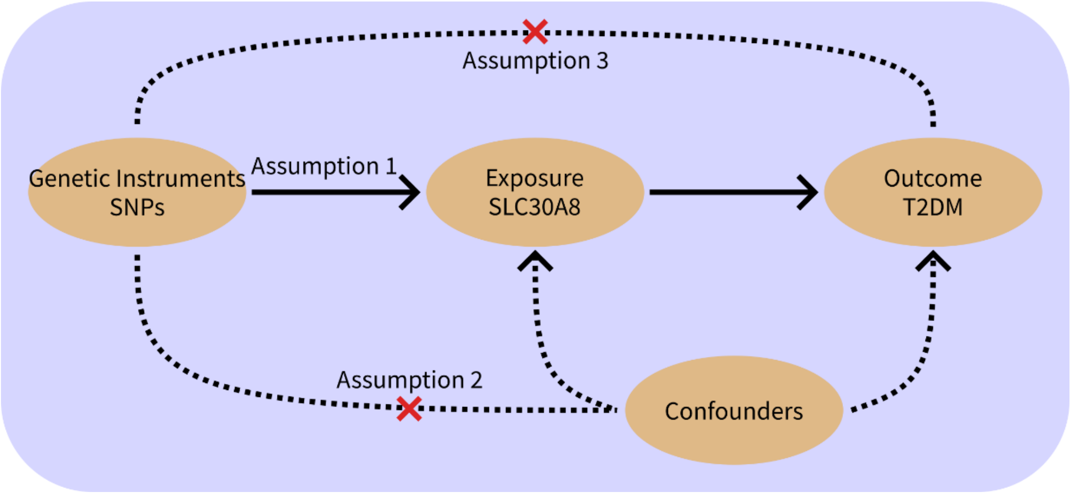

Supplementary Figure 1 depicts a flowchart of Mendelian Randomization analysis. MR analysis relies on three fundamental hypotheses:1) The instrumental variable hypothesis: the genetic variant selected as the instrumental variable (IV) is unintentionally related to the exposure of interest in a casual manner. 2) The used genetic variants should not be associated with potential confounding variables in the exposure–outcome relationship. 3) The pleiotropy hypothesis: the genetic variant used as the IV is associated solely with the outcome via its effect on the exposure and no other biological pathways.

Supplementary Table 1 Clinical Characters of SCA Patients with and without T2D

	SCA with T2D	**SCA without T2D**	***P* value**
N (women)	3 (3)	10 (6)	-
Age (years)	64.00±6.08	63.85±5.43	0.958
BG (mmol/L)	6.74±1.15	5.17±0.80	0.020
HbA1c (%)	7.57±1.67	5.65±0.49	0.005
/(mmo/mol)	/59.2±18.3	/38.3±5.3	
BMI (kg/m^2)	25.81±2.72	23.61±1.72	0.114
SBP (mmHg)	78.33±8.51	82.10±8.69	0.522
DBP (mmHg)	141.33±20.79	133.70±16.94	0.474

Data were the means ± SD. SCA: pancreatic serous cystadenoma; T2D: type 2 diabetes. Two newly diagnosed T2D, while one had diabetic duration for ≥10 years. BG, blood glucose; HbA1c, glycated hemoglobin; BMI, body mass index; SBP, systolic blood pressure; DBP, diastolic blood pressure; HbA1c values were converted with NGSP (National Glycohemoglobin Standardization Program) to IFCC (International Federation of Clinical Chemistry) unit: mmol/mol.

Supplementary Table 2 SNPs in the *SLC30A8* Gene for Mendelian Randomization Analysis

SNP	effect allele	other allele	eaf exposure	eaf outcome	beta exposure	beta outcome	F_stat	pval.outcome	pval.exposure	chr_name	chrom_start
rs2466293	G	A	0.41	0.60	0.29	-0.07	89.47	7.15E-24	3.11E-21	8	118185938
rs2466300	A	C	0.19	0.83	0.29	-0.08	55.59	1.29E-17	8.93E-14	8	118182924
rs57177943	C	G	0.08	0.05	-0.40	0.04	46.64	7.86E-03	8.52E-12	8	118153172

Additional Information and References Used in Mendelian Randomization Analysis

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