

Supplementary Table S1. Definition of Cardiovascular-kidney-metabolic risk factors at baseline

| Cardio-metabolic risk factors | Definition |
|--------------------------------------|---|
| Overweight | Body mass index ≥ 23 kg/m ² |
| General obesity | Body mass index ≥ 27.5 kg/m ² |
| Central obesity | Waist circumference ≥ 90 cm for male and ≥ 80 cm for female |
| Hypertension | Systolic BP ≥ 140 mmHg or diastolic BP ≥ 90 mmHg and/or baseline use of blood pressure-lowering drugs |
| Dyslipidaemia | Total cholesterol ≥ 6.20 mmol/L (240 mg/dL), or LDL cholesterol > 4.13 mmol/L (160 mg/dL), or triglycerides > 2.25 mmol/L (200mg/dL) or HDL cholesterol < 1.03 mmol/L (40 mg/dL), and/or baseline use of lipid-regulating agents |
| Microalbuminuria | Urine albumin-to-creatinine ratio 3- < 30 mg/mmol |
| Macroalbuminuria | Urine albumin-to-creatinine ratio ≥ 30 mg/mmol |

Supplementary Table S2: List of monogenic diabetes genes sequenced

| Gene | Mode of inheritance | Subtypes | GenBank Reference Sequence | References |
|---------------|----------------------------|---------------------|-----------------------------------|-------------------|
| <i>ABCC8</i> | Dominant, recessive | NDM, MODY | NM_000352 | (1-5) |
| <i>AKT2</i> | Dominant | IR | NM_001626 | (6-7) |
| <i>APPL1</i> | Dominant | MODY | NM_012096 | (8) |
| <i>CEL*</i> | Dominant | MODY, Syndrome | NM_001807 | (9-11) |
| <i>CISD2</i> | Recessive | NDM, Syndrome | NM_001008388 | (12) |
| <i>DCAF17</i> | Recessive | Syndrome | NM_025000 | (13) |
| <i>DNAJC3</i> | Recessive | Syndrome | NM_006260 | (14) |
| <i>DYRK1B</i> | Dominant | Syndrome | NM_004714 | (15) |
| <i>GATA4*</i> | Dominant | NDM, Syndrome | NM_002052 | (16) |
| <i>GATA6</i> | Dominant | NDM, Syndrome | NM_005257 | (17-18) |
| <i>GCK</i> | Dominant, recessive | NDM, MODY | NM_000162 | (19-23) |
| <i>HNF1A</i> | Dominant | MODY | NM_000545 | (24-26) |
| <i>HNF1B</i> | Dominant | NDM, MODY, Syndrome | NM_000458 | (27-29) |
| <i>HNF4A</i> | Dominant | MODY | NM_175914 | (26,30-31) |
| <i>INS</i> | Dominant, recessive | NDM, MODY | NM_001291897 | (32-35) |

| | | | | |
|-----------------|---------------------|---------------|--------------|---------|
| <i>INSR</i> | Dominant | NDM, IR | NM_000208 | (36) |
| <i>KCNJ11*</i> | Dominant | NDM, MODY | NM_000525 | (37-41) |
| <i>LMNA</i> | Dominant | IR | NM_170707 | (42-44) |
| <i>NEUROD1*</i> | Dominant, recessive | NDM, MODY | NM_002500 | (45-46) |
| <i>PAX4</i> | Dominant | MODY | NM_001366110 | (47-51) |
| <i>PAX6</i> | Dominant | Syndrome | NM_000280 | (52-54) |
| <i>PCBD1</i> | Recessive | Syndrome | NM_000281 | (55-56) |
| <i>PDX1*</i> | Dominant, recessive | NDM, MODY | NM_000209 | (57-60) |
| <i>PIK3R1</i> | Dominant | Syndrome | NM_181523 | (61) |
| <i>PLIN1</i> | Dominant | IR | NM_002666 | (62) |
| <i>POLD1*</i> | Dominant | IR | NM_001256849 | (63) |
| <i>PPARG</i> | Dominant | IR | NM_015869 | (64-65) |
| <i>PPP1R15B</i> | Recessive | Syndrome | NM_032833 | (66) |
| <i>RFX6</i> | Recessive | NDM, MODY | NM_173560 | (67) |
| <i>SLC29A3</i> | Recessive | NDM, Syndrome | NM_018344 | (68-69) |
| <i>TRMT10A</i> | Recessive | Syndrome | NM_001134665 | (70) |
| <i>WFS1</i> | Recessive | NDM, Syndrome | NM_006005 | (71-72) |
| <i>ZBTB20</i> | Dominant | Syndrome | NM_001348803 | (73) |

| | | | | |
|--|-----------|-----|--------------|------|
| ZFP57 | Recessive | NDM | NM_001109809 | (74) |
| <p>* Due to technical limitations of designing target-specific primers for certain sequences, the coverage of the coding and flanking regions of the genes are as follows: CEL (87.3%), GATA4 (95.2%), KCNJ11 (90.1%), NEUROD1 (96.3%), PDX1 (94.0%) and POLD1 (96.4%)</p> <p>Abbreviations:</p> <p>IR, insulin resistance; MODY, maturity-onset diabetes of the young; NDM, neonatal diabetes mellitus.</p> <p><i>ATP Binding Cassette Subfamily C Member 8, ABCC8</i></p> <p><i>AKT Serine/Threonine Kinase 2, AKT2</i></p> <p><i>Adaptor Protein, Phosphotyrosine Interacting With PH Domain And Leucine Zipper 1, APPL1</i></p> <p><i>Carboxyl Ester Lipase, CEL</i></p> <p><i>CDGSH Iron Sulfur Domain 2, CISD2</i></p> <p><i>DDB1 And CUL4 Associated Factor 17, DCAF17</i></p> <p><i>DnaJ Heat Shock Protein Family (Hsp40) Member C3, DNAJC3</i></p> <p><i>Dual Specificity Tyrosine Phosphorylation Regulated Kinase 1B, DYRK1B</i></p> <p><i>GATA Binding Protein 4, GATA4</i></p> <p><i>GATA Binding Protein 6, GATA6</i></p> <p><i>Glucokinase, GCK</i></p> <p><i>hepatocyte nuclear factor-1 alpha, HNF1A</i></p> <p><i>hepatocyte nuclear factor-1 beta, HNF1B</i></p> <p><i>hepatocyte nuclear factor 4 alpha, HNF4A</i></p> <p><i>Insulin, INS</i></p> <p><i>Insulin Receptor, INSR</i></p> <p><i>Potassium Inwardly Rectifying Channel Subfamily J Member 11, KCNJ11*</i></p> <p><i>Lamin A/C, LMNA</i></p> <p><i>Neurogenic differentiation 1, NEUROD1*</i></p> <p><i>Paired Box 4, PAX4</i></p> <p><i>Paired Box 6, PAX6</i></p> <p><i>Pterin-4 Alpha-Carbinolamine Dehydratase 1, PCBD1</i></p> <p><i>pancreatic and duodenal homeobox 1, PDX1*</i></p> <p><i>Phosphoinositide-3-Kinase Regulatory Subunit 1, PIK3R1</i></p> | | | | |

Perilipin 1, PLIN1

*DNA polymerase delta 1, POLD1**

Peroxisome proliferator activated receptor gamma, PPARG

Protein phosphatase 1 regulatory subunit 15B, PPP1R15B

Regulatory Factor X6, RFX6

Solute Carrier Family 29 Member 3, SLC29A3

TRNA Methyltransferase 10A, TRMT10A

Wolfram ER Transmembrane Glycoprotein, WFS1

Zinc Finger And BTB Domain Containing 20, ZBTB20

Zinc finger protein 57 homolog, ZFP57

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Supplementary Table S3. Genes used to construct polygenic risk scores for risk prediction of young-onset type 2 diabetes, diabetic complications and insulin requirement based on discoveries or verification in our cohort with supporting literature in other groups.

| Polygenic risk score (PRS) | Genes involved in construction of PRS |
|---|--|
| PRS for young-onset type 2 diabetes | POU2F, WFS1, CPE, PAX4, IDE, DACH1 |
| PRS for diabetic complications | AGT, AGTR1, NOS3, APOB, APOC3, APOE4, LPL, LPC, PRKAG2, GNB3, PRKCB, GABRR1, TNF, AKR1B1, TNF, AKR1B1, UMOD |
| PRS for insulin requirement | AGT, AGTR1, NOS3, APOB, APOC3, APOE4, LPL, LPC, PRKAG2, GNB3, PRKCB, GABRR1, TNF, AKR1B1, UMOD, PROX1-AS1, TMEM18, GCKR, COBLL1, UBE2E2, PTH1R, ADAMTS9-AS2, ST6GAL1, WFS1, C5orf67, POC5, CDKAL1, NFKBIL1, HLA-DOB, SLC22A3, DGKB, ANK1, TP53INP1, SLC30A8, GLIS3, CDKN2B-AS1/CKDN2B, CDKN28-AS1, TLE1, ABO, CDC123, CHUK, TCF7L2, KCNQ1, KCNJ11, ARAP1, MTNR1B, CCND2, KLHL42, RPSAP52, SOCS2, ZNF664-FAM101A, KL, SPRY2, C2CD4A, FTO, CMIP, ZZEF1, HNF1B, MC4R, SUGP1, GIPR, HNF4A, SLC22A1, SLC22A2, SLC47A1, C11orf65, SLC2A2, NBEA, CAPN10, CYP2C9, CYP2C19, IRS1, SLCO1B1, PPARG, ADIPOQ-AS1, |
| <p><u>Reference:</u></p> <p>Discovery or validation of genetic markers for diabetes and its complications in Chinese patients with type 2 diabetes:</p> <ol style="list-style-type: none"> 1. Young RP, Chan JCN, Poon E, Critchley JAJH, Cockram CS. Associations between albuminuria and angiotensinogen T235 and angiotensin converting enzyme insertion/deletion polymorphisms in Chinese NIDDM patients. <i>Diabetes care</i> 1997; 21: 431-7. 2. Ng MCY, Yeung VTF, Chow CC, et al. Mitochondrial DNA A3243G mutation in patients with early | |

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Supplementary Table S4. Methods of laboratory assays

1. Conventional biochemical parameters

Entities of blood and urine tests (fasting blood samples for HbA1c, plasma glucose, lipid, renal function, liver function, complete blood count and spot urine albumin-to-creatinine ratio (ACR) included as a part of complication screening program guided by JADE protocol was assayed in the Department of Chemical Pathology and Hematology Laboratory of the Department of Anatomical and Cellular Pathology at the Prince of Wales Hospital. The laboratory services were both accredited by the Accreditation Canada (AC) Diagnostics. HbA1c was measured by immunoassay; glucose, lipid, urea, creatinine and liver enzymes by spectrophotometry; sodium and potassium by ion selective electrode method; urine albumin and creatinine by immunoassay and spectrophotometry respectively; complete blood count by automated hematology analyser.

2. Fasting C-peptide and glutamic acid decarboxylase antibodies (GADA)

Assays of serum fasting C-peptide and GADA were performed in the CUHK Diabetes and Obesity Laboratory, Li Ka Shing Institute of Health Sciences at the PWH. Serum C-peptide was measured by Mercodia® C-peptide ELISA kit with a detection limit of 103 pmol/L. The intra-assay and inter-assay coefficients of variation (CV) were less than 6.8% and 4.8%, respectively. GADA was measured using the GAD Autoantibody ELISA kit (RSR Limited) with detection limit of 0.57 units/mL. A GADA titre of ≥ 5.0 U/mL was considered as GADA positivity in this study. The respective intra-assay and inter-assay CVs were 3.5–7.3% and 5.2–6.4% for a GADA range of 5.7–97 units/mL.

3. Quantitative polymerase-chain reaction (qPCR), genotyping and next generation sequencing (NGS)

We extracted DNA from blood samples to conduct genotyping, and targeted gene sequencing and qPCR.

We performed genotyping using Infinium® Asian Screening Array. The standard quality control

(QC) procedures were applied on the genome-wide SNP array data. The per-individual QC of genotype data consists of four steps: (1) sex checking based on the genotype call from chromosome X; (2) detection of low-quality samples based on outlying missing genotype and heterozygosity rate; (3) identification of possibly-related individuals or duplicated samples by estimates of identity-by-descent (IBD); (4) detection of population stratification by performing principal component analysis (PCA). Candidate variants and their risk alleles associated with type 2 diabetes, cardiovascular-kidney complications, or glycaemic deterioration were identified from published literatures (Supplementary table S4). Candidate variants with missing genotypes were replaced by proxy SNPs which were in linkage disequilibrium ($r^2 \geq 0.9$) with the original SNPs or the most common genotype in East Asians from 1000 Genomes Project. Genetic risk scores were calculated by summing up the number of risk alleles for each variant without weighting.

Targeted sequencing was used to identify variants for monogenic diabetes. The panel utilized in this study encompassed 34 genes known to be linked with neonatal diabetes, MODY, syndromic diabetes, and monogenic diabetes associated with severe insulin resistance (Supplementary Table S3). The sequencing regions covered exons and flanking regions located within 25 base pairs (bp) upstream and downstream of each exon. DNA libraries were prepared according to the workflow of AmpliSeq for Illumina Custom Panels (Illumina). Pooled libraries were loaded onto the Illumina MiSeq system and subjected to paired-end sequencing with a read length of 151 cycles. The quality assessment of raw sequencing data was performed using FastQC (Babraham Institute). Reads alignment and variant calling were conducted using the Local Run Manager in DNA Amplicon analysis module (Illumina).

The hotspot variant - A3243G mutation of mitochondrial DNA (mtA3243G) for monogenic

diabetes, were detected by qPCR using KAPA Probe Master Mix on Roche LightCycler 480 Instrument.

The interpretation of variants followed the guidelines developed by the American College of Medical Genetics and Genomics (ACMG). Variants were classified as “pathogenic” (P), “likely pathogenic” (LP), “variants of uncertain significance” (VUS), “likely benign” and “benign” based on the combined scored evidence criteria outlined in the ACMG guidelines. In this study, patients were considered to have monogenic diabetes if they were heterozygous or homozygous carriers of P/LP variants in autosomal dominant inheritance, or, homozygous or compound heterozygous carriers of P/LP variants in autosomal recessive inheritance.

Supplementary Table S5 Definition of selected primary and secondary outcomes

| Clinical outcomes | Definition |
|---|---|
| Coronary heart disease | ICD-9 Diagnosis Codes 410-414 |
| Congestive heart failure | ICD-9 Diagnosis Codes 428 |
| Stroke | ICD-9 Diagnosis Codes 430-438 |
| Peripheral artery disease | ICD-9 Diagnosis Codes 250.7, 443.81, 443.9, 785.4, 895-897 ICD-9 Procedure Codes 39.29, 39.90, 84.1 |
| Cardiovascular disease | A composite of coronary heart disease, congestive heart failure, stroke, and peripheral artery disease |
| Chronic kidney disease | Estimated glomerular filtration rate [eGFR] <60 ml/min/1.73m ² on 2 occasions at least 3 months apart, need for dialysis or kidney replacement therapy |
| Progression of chronic kidney disease | A change in stage of chronic kidney disease from stage G3 (estimated GFR 30-59 ml/min/1.73m ²) to stage G4 (estimated GFR 15-29 ml/min/1.73m ²) or G5 (estimated GFR <15 ml/min/1.73m ²), or from stage G4 to stage G5 |
| Progression of albuminuria | Change from microalbuminuria (urine ACR 3.0-<30 mg/mmol) to macroalbuminuria (urine ACR ≥30 mg/mmol) |
| Diabetic retinopathy (DR) | Mild non-proliferative DR: microaneurysms, retinal haemorrhages and hard exudates Moderate non-proliferative DR: mild non-proliferative DR plus cotton-wool spots and/or intra-retinal microvascular abnormality (IRMA) Severe non-proliferative DR: any of the followings (4-2-1 rule): <ul style="list-style-type: none"> ○ Microaneurysms in four quadrants ○ Marked venous beading in two or more quadrants ○ Moderate IRMA in one or more quadrant Proliferative: Presence of new vessels and/ or fibrous proliferations; or pre-retinal and/ or vitreous haemorrhage |
| Incident and/or progression of diabetic retinopathy | Worsening of diabetic retinopathy in either eye from mild to moderate, or moderate to severe non-proliferative, or non-proliferative to proliferative, incident vitreous |

| | |
|----------------------|---|
| | haemorrhage, photocoagulation, vitrectomy |
| Visual impairment | Visual acuity (VA) < 20/200 in either eye, or new operation for cataract or glaucoma |
| Sensory neuropathy | At least 2 out of 3 of the following in one of the lower limbs: <ul style="list-style-type: none">• reduced sensation to monofilament,• reduced vibration sense, or• self-reported abnormal sensation |
| Severe hypoglycaemia | ICD-9 Diagnosis Codes 251.2 |

Supplementary Table S6. Baseline characteristics of participants with young-onset diabetes based on JADE-guided assessments in the JADE-only group and JADE-PRISM group.

| Characteristics | JADE-only Group (n = 443) | | JADE-PRISM Group (n = 441) | | Total (n = 884) | | P value |
|---|---------------------------|--------------|----------------------------|--------------|--------------------|--------------|---------|
| | Number of patients | Observations | Number of patients | Observations | Number of patients | Observations | |
| <i>Demographics, socio-economic status and social habits</i> | | | | | | | |
| Age | 443 | 40.47 ± 6.55 | 441 | 40.89 ± 6.53 | 884 | 40.68 ± 6.54 | 0.343 |
| Men, n (%) | 443 | 241 (54.4) | 441 | 259 (58.7) | 884 | 500 (56.6) | 0.219 |
| Employed (full-time or part-time), n (%) | 441 | 370 (83.9) | 438 | 360 (82.2) | 879 | 730 (83.0) | 0.558 |
| Manual worker among those employed, n (%) | 433 | 91 (21.0) | 426 | 99 (23.2) | 859 | 190 (22.1) | 0.482 |
| High school or above education attained, n (%) | 442 | 208 (47.1) | 441 | 200 (45.4) | 883 | 408 (46.2) | 0.659 |
| Current or former tobacco use, n (%) | 443 | 141 (31.8) | 435 | 144 (33.1) | 878 | 285 (32.5) | 0.740 |
| Regular or occasional alcohol use, n (%) | 443 | 164 (37.0) | 435 | 157 (36.1) | 878 | 321 (36.6) | 0.829 |
| <i>Family history and growth experience</i> | | | | | | | |
| Family history of diabetes, n (%) | 433 | 330 (76.2) | 438 | 321 (73.3) | 871 | 651 (74.7) | 0.360 |
| History of diabetes of father, n (%) | 433 | 188 (43.4) | 439 | 203 (46.2) | 872 | 391 (44.8) | 0.441 |
| History of diabetes of mother, n (%) | 433 | 211 (48.7) | 440 | 198 (45.0) | 873 | 409 (46.8) | 0.300 |
| History of diabetes of both parents, n (%) | 433 | 82 (18.9) | 440 | 90 (20.5) | 873 | 172 (19.7) | 0.632 |
| History of diabetes of siblings, n (%) | 433 | 90 (20.8) | 438 | 77 (17.6) | 871 | 167 (19.2) | 0.265 |
| <i>Diabetes-related history and comorbidities</i> | | | | | | | |
| Age of diagnosis | 443 | 34 [29, 38] | 441 | 34 [29, 38] | 884 | 34 [29, 38] | 0.685 |
| Duration of diabetes (years) | 443 | 7 [3, 11] | 441 | 7 [3, 12] | 884 | 7 [3, 12] | 0.425 |
| History of diabetes ketoacidosis | 0 | NA | 420 | 10 (2.4) | 420 | 10 (2.4) | NA |
| Cardiovascular disease | 443 | 23 (5.2) | 441 | 23 (5.2) | 884 | 46 (5.2) | 1 |
| Coronary artery disease | 443 | 14 (3.2) | 441 | 16 (3.6) | 884 | 30 (3.4) | 0.843 |
| Stroke | 443 | 6 (1.4) | 441 | 5 (1.1) | 884 | 11 (1.2) | 1 |

| | | | | | | | |
|---|-----|--------------------|-----|--------------------|-----|--------------------|-------|
| Peripheral artery disease | 443 | 4 (0.9) | 441 | 2 (0.5) | 884 | 6 (0.7) | 0.686 |
| Congestive heart failure | 443 | 5 (1.1) | 441 | 2 (0.5) | 884 | 7 (0.8) | 0.451 |
| Chronic kidney disease | 443 | 26 (5.9) | 441 | 9 (2.0) | 884 | 35 (4.0) | 0.006 |
| End-stage kidney disease – non dialysis | 443 | 3 (0.7) | 441 | 1 (0.2) | 884 | 4 (0.5) | 0.619 |
| Cardiovascular and/or chronic kidney disease | 443 | 45 (10.2) | 441 | 31 (7.0) | 884 | 76 (8.6) | 0.124 |
| History of all-site cancer | 443 | 6 (1.4) | 441 | 21 (4.8) | 884 | 27 (3.1) | 0.006 |
| Sensory neuropathy | 443 | 2 (0.5) | 435 | 1 (0.2) | 878 | 3 (0.3) | 1 |
| Retinopathy | 443 | 58 (13.1) | 436 | 63 (14.4) | 879 | 121 (13.8) | 0.627 |
| <i>Diabetes education, self-management and hypoglycemia</i> | | | | | | | |
| Self-reported hypoglycemia in last three months | 441 | 132 (29.9) | 434 | 100 (23.0) | 875 | 232 (26.5) | 0.026 |
| Self-monitoring of blood glucose per week, n (%) | 437 | 193 (44.2) | 429 | 180 (42.0) | 866 | 373 (43.1) | 0.557 |
| Physical activity ≥ 3 times per week, n (%) | 441 | 71 (16.1) | 434 | 86 (19.8) | 875 | 157 (17.9) | 0.179 |
| Good adherence to balanced diet, n (%) | 441 | 148 (33.6) | 431 | 159 (36.9) | 872 | 307 (35.2) | 0.338 |
| Education by dietitian, n (%) | 441 | 352 (79.8) | 434 | 340 (78.3) | 875 | 692 (79.1) | 0.650 |
| Education by podiatrist, n (%) | 442 | 80 (18.1) | 434 | 85 (19.6) | 876 | 165 (18.8) | 0.634 |
| Education by diabetes nurse, n (%) | 441 | 372 (84.4) | 434 | 379 (87.3) | 875 | 751 (85.8) | 0.244 |
| <i>Physical measurements and cardio-metabolic risk factors</i> | | | | | | | |
| Body mass index (kg/m ²) | 443 | 28.65 \pm 5.79 | 441 | 28.15 \pm 5.75 | 884 | 28.40 \pm 5.77 | 0.197 |
| Waist circumference, male (cm) | 241 | 100.35 \pm 14.16 | 254 | 99.22 \pm 13.82 | 495 | 99.77 \pm 13.99 | 0.367 |
| Waist circumference, female (cm) | 201 | 95.06 \pm 13.60 | 180 | 92.63 \pm 13.98 | 381 | 93.91 \pm 13.82 | 0.086 |
| Systolic blood pressure (mmHg) | 443 | 128.65 \pm 16.98 | 441 | 128.89 \pm 16.52 | 884 | 128.77 \pm 16.74 | 0.830 |
| Diastolic blood pressure (mmHg) | 442 | 80.13 \pm 11.39 | 441 | 80.04 \pm 11.60 | 883 | 80.08 \pm 11.49 | 0.912 |
| Overweight, n (%) | 443 | 378 (85.3) | 441 | 363 (82.3) | 884 | 741 (83.8) | 0.260 |
| General obesity, n (%) | 443 | 238 (53.7) | 441 | 216 (49.0) | 884 | 454 (51.4) | 0.179 |
| Central obesity, n (%) | 442 | 358 (81.0) | 434 | 336 (77.4) | 876 | 694 (79.2) | 0.222 |
| Hypertension, n (%) | 442 | 311 (70.4) | 441 | 278 (63.0) | 883 | 589 (66.7) | 0.025 |
| Dyslipidemia, n (%) | 440 | 332 (75.5) | 436 | 337 (77.3) | 876 | 669 (76.4) | 0.575 |
| Albuminuria, n (%) | 443 | 161 (36.3) | 435 | 150 (34.5) | 878 | 311 (35.4) | 0.613 |

| | | | | | | | |
|---|-----|---------------------------|-----|---------------------------|-----|---------------------------|-------|
| Microalbuminuria, n (%) | 443 | 108 (24.4) | 435 | 102 (23.4) | 878 | 210 (23.9) | 0.807 |
| Macroalbuminuria, n (%) | 443 | 53 (12.0) | 435 | 48 (11.0) | 878 | 101 (11.5) | 0.745 |
| Laboratory investigations | | | | | | | |
| Fasting plasma glucose (mmol/L) | 443 | 7.94 ± 2.99 | 441 | 8.00 ± 2.73 | 884 | 7.97 ± 2.86 | 0.746 |
| HbA1c (%) | 443 | 7.48 ± 1.70 | 441 | 7.56 ± 1.62 | 884 | 7.52 ± 1.66 | 0.502 |
| Range of HbA1c, n (%) | 443 | | 441 | | 884 | | 0.519 |
| HbA1c <6.0% | | 48 (10.8) | | 35 (7.9) | | 83 (9.4) | |
| HbA1c 6.0-<7.0% | | 154 (34.8) | | 148 (33.6) | | 302 (34.2) | |
| HbA1c 7.0-<8.0% | | 123 (27.8) | | 134 (30.4) | | 257 (29.1) | |
| HbA1c 8.0-<9.0% | | 51 (11.5) | | 59 (13.4) | | 110 (12.4) | |
| HbA1c ≥9.0% | | 67 (15.1) | | 65 (14.7) | | 132 (14.9) | |
| Total cholesterol (mmol/L) | 422 | 4.34 ± 0.91 | 417 | 4.35 ± 0.90 | 839 | 4.34 ± 0.90 | 0.860 |
| HDL cholesterol (mmol/L) | 439 | 1.18 ± 0.31 | 435 | 1.21 ± 0.31 | 874 | 1.19 ± 0.31 | 0.136 |
| LDL cholesterol (mmol/L) | 424 | 2.27 ± 0.76 | 419 | 2.26 ± 0.76 | 843 | 2.26 ± 0.76 | 0.787 |
| Triglycerides (mmol/L) | 443 | 1.40 [1.00, 2.20] | 435 | 1.40 [1.00, 2.20] | 878 | 1.40 [1.00, 2.20] | 0.865 |
| Urine albumin-to-creatinine ratio (mg/mmol) | 443 | 1.60 [0.70, 6.40] | 435 | 1.40 [0.70, 7.10] | 878 | 1.48 [0.70, 6.68] | 0.635 |
| Estimated GFR (mL/min/1.73m ²) | 443 | 106.67 [92.37, 115.07] | 441 | 107.72 [95.78, 114.99] | 884 | 107.21 [94.17, 115.04] | 0.239 |
| CKD grade, n (%) | 443 | | 441 | | 884 | | 0.074 |
| CKD grade 1 (eGFR ≥90 mL/min/1.73m ²) | | 346 (78.1) | | 361 (81.9) | | 707 (80.0) | |
| CKD grade 2 (eGFR 60-89 mL/min/1.73m ²) | | 73 (16.5) | | 71 (16.1) | | 144 (16.3) | |
| CKD grade 3 (eGFR 30-59 mL/min/1.73m ²) | | 20 (4.5) | | 9 (2.0) | | 29 (3.3) | |
| CKD grade 4 (eGFR 15-29 mL/min/1.73m ²) | | 3 (0.7) | | 0 (0.0) | | 3 (0.3) | |
| CKD grade 5 (eGFR <15 mL/min/1.73m ²) | | 1 (0.2) | | 0 (0.0) | | 1 (0.1) | |
| Alkaline phosphatase, ALP (IU/L) | 443 | 64.00 [53.00, 77.50] | 435 | 65.00 [55.00, 76.00] | 878 | 64.00 [54.00, 77.00] | 0.501 |
| Alanine transaminase, ALT (IU/L) | 443 | 26.00 [18.00, 42.00] | 435 | 28.00 [20.00, 41.00] | 878 | 27.00 [19.00, 41.75] | 0.213 |

| | | | | | | | |
|---|-----|------------|-----|------------|-----|------------|-------|
| ALT \geq 47 IU/L, n (%) | 443 | 98 (22.1) | 435 | 91 (20.9) | 878 | 189 (21.5) | 0.725 |
| Medications at enrolment, n (%) | | | 441 | | | | |
| Glucose-lowering drugs | 438 | 424 (96.8) | 439 | 420 (95.7) | 877 | 844 (96.2) | 0.482 |
| Insulin | 443 | 124 (28.0) | 441 | 121 (27.4) | 884 | 245 (27.7) | 0.913 |
| Glucagon-like peptide-1 receptor agonist | 443 | 26 (5.9) | 441 | 22 (5.0) | 884 | 48 (5.4) | 0.668 |
| Oral glucose-lowering drugs | 443 | 416 (93.9) | 439 | 411 (93.2) | 884 | 827 (93.6) | 0.771 |
| Dipeptidyl peptidase-4 inhibitor | 438 | 198 (45.2) | 439 | 189 (43.1) | 877 | 387 (44.1) | 0.566 |
| Metformin | 438 | 400 (91.3) | 439 | 392 (89.3) | 877 | 792 (90.3) | 0.367 |
| Sodium–glucose cotransporter 2 inhibitor | 438 | 130 (29.7) | 439 | 125 (28.5) | 877 | 255 (29.1) | 0.750 |
| Sulphonylurea | 438 | 145 (33.1) | 439 | 171 (39.0) | 877 | 316 (36.0) | 0.083 |
| Thiazolidinedione | 438 | 65 (14.8) | 439 | 65 (14.8) | 877 | 130 (14.8) | 1 |
| Number of glucose-lowering drugs used | 438 | | 439 | | 877 | | 0.689 |
| \leq 2 | | 221 (50.5) | | 229 (52.2) | | 450 (51.3) | |
| 3-4 | | 190 (43.4) | | 179 (40.8) | | 369 (42.1) | |
| \geq 5 | | 27 (6.2) | | 31 (7.1) | | 58 (6.6) | |
| Blood pressure-lowering drugs | 443 | 282 (63.7) | 441 | 246 (55.8) | 884 | 528 (59.7) | 0.020 |
| Renin–angiotensin system inhibitor | 438 | 219 (50.0) | 438 | 207 (47.3) | 876 | 426 (48.6) | 0.457 |
| ACE inhibitors | 438 | 108 (24.7) | 438 | 111 (25.3) | 876 | 219 (25.0) | 0.876 |
| Angiotensin II receptor blockers | 438 | 111 (25.3) | 438 | 96 (21.9) | 876 | 207 (23.6) | 0.266 |
| Lipid-regulating drugs | 443 | 261 (58.9) | 441 | 265 (60.1) | 884 | 526 (59.5) | 0.774 |
| Statin | 438 | 238 (54.3) | 436 | 239 (54.8) | 874 | 477 (54.6) | 0.941 |
| Aspirin | 443 | 35 (7.9) | 441 | 24 (5.4) | 884 | 59 (6.7) | 0.184 |
| Treatment target attainment, n (%) | | | | | | | |
| Conventional targets | | | | | | | |
| HbA1c <7.0% | 443 | 202 (45.6) | 441 | 183 (41.5) | 884 | 385 (43.6) | 0.245 |
| Blood pressure <130/80 mmHg | 443 | 183 (41.3) | 441 | 185 (42.0) | 884 | 368 (41.6) | 0.900 |
| LDL cholesterol <2.6mmol/L (or <1.8 mmol/L in presence of cardiovascular disease) | 424 | 280 (66.0) | 419 | 284 (67.8) | 843 | 564 (66.9) | 0.642 |

| | | | | | | | |
|---|-----|--------------------|-----|--------------------|-----|--------------------|-------|
| All three targets above | 441 | 65 (14.7) | 438 | 61 (13.9) | 879 | 126 (14.3) | 0.805 |
| Strict targets | | | | | | | |
| HbA1c <6.2% | 443 | 84 (19.0) | 441 | 54 (12.2) | 884 | 138 (15.6) | 0.008 |
| Blood pressure <120/80 mmHg | 443 | 123 (27.8) | 441 | 118 (26.8) | 884 | 241 (27.3) | 0.794 |
| LDL cholesterol <1.8 mmol/L | 424 | 97 (22.9) | 419 | 110 (26.3) | 843 | 207 (24.6) | 0.290 |
| Triglycerides <1.2 mmol/L | 443 | 152 (34.3) | 435 | 151 (34.7) | 878 | 303 (34.5) | 0.957 |
| Waist circumference <80 cm in female and <85cm in male | 442 | 56 (12.7) | 434 | 62 (14.3) | 876 | 118 (13.5) | 0.548 |
| Attainment of 3 or more targets | 423 | 55 (13.0) | 418 | 60 (14.4) | 841 | 115 (13.7) | 0.638 |
| <i>Patient reported outcomes and psychological-behavioral parameters using structured questionnaires</i> | | | | | | | |
| EQ-5D index value (quality of life) | 430 | 0.88 [0.87, 0.96] | 426 | 0.88 [0.87, 0.96] | 856 | 0.88 [0.87, 0.96] | 0.663 |
| DASS-21 (negative emotions), total score | 429 | 9.00 [3.00, 17.00] | 423 | 8.00 [3.00, 17.00] | 852 | 9.00 [3.00, 17.00] | 0.420 |
| DASS-21 score ≥ 17 , n (%) | 429 | 114 (26.6) | 423 | 110 (26.0) | 852 | 224 (26.3) | 0.912 |
| PHQ-9 (depression), total score | 426 | 4.00 [2.00, 8.00] | 426 | 4.00 [1.00, 7.00] | 852 | 4.00 [1.00, 7.00] | 0.270 |
| PHQ-9 score ≥ 7 , n (%) | 426 | 132 (31.0) | 426 | 129 (30.3) | 852 | 261 (30.6) | 0.882 |
| CDDS-15 (diabetes distress), total score | 418 | 41.34 \pm 12.90 | 422 | 40.57 \pm 12.16 | 840 | 40.95 \pm 12.53 | 0.370 |
| CDDS-15 score ≥ 45 , n (%) | 418 | 161 (38.5) | 422 | 155 (36.7) | 840 | 316 (37.6) | 0.643 |
| DES-20 (self-efficacy), total score | 431 | 55.07 \pm 10.38 | 425 | 56.10 \pm 10.35 | 856 | 55.58 \pm 10.37 | 0.144 |
| SDSCA-15 (self-care), mean score | | | | | | | |
| Diet | 433 | 3.75 [2.75, 4.50] | 426 | 3.75 [2.75, 4.50] | 859 | 3.75 [2.75, 4.50] | 0.817 |
| Exercise | 431 | 2.00 [1.00, 3.00] | 428 | 2.00 [1.00, 3.00] | 859 | 2.00 [1.00, 3.00] | 0.684 |
| Blood glucose monitoring | 421 | 1.00 [0.00, 3.00] | 425 | 1.00 [0.00, 2.00] | 846 | 1.00 [0.00, 2.00] | 0.071 |
| Foot care | 428 | 3.00 [2.33, 4.33] | 428 | 3.00 [2.33, 4.67] | 856 | 3.00 [2.33, 4.67] | 0.729 |
| Medication | 215 | 3.67 [2.33, 4.67] | 183 | 4.33 [2.33, 4.67] | 398 | 4.00 [2.33, 4.67] | 0.798 |
| CQ-4 (medication adherence), total score | 431 | 4.00 [3.00, 4.00] | 421 | 4.00 [3.00, 4.00] | 852 | 4.00 [3.00, 4.00] | 0.560 |
| Medication adherence, n (%) | 431 | | 421 | | 852 | | 0.828 |
| High adherence | | 241 (55.9) | | 243 (57.7) | | 484 (56.8) | |
| Intermediate adherence | | 154 (35.7) | | 142 (33.7) | | 296 (34.7) | |

| | | | |
|---------------|----------|----------|----------|
| Low adherence | 36 (8.4) | 36 (8.6) | 72 (8.5) |
|---------------|----------|----------|----------|

Glycated haemoglobin, HbA1c; high-density lipoprotein cholesterol, HDL cholesterol; low-density lipoprotein cholesterol, LDL cholesterol; glomerular filtration rate, GFR; chronic kidney disease, CKD; 21-item Depression, Anxiety and Stress Scale, DASS-21; Patient Health Questionnaire-9, PHQ-9; 15-item Chinese Diabetes Distress Scale, CDDS-15; 20-item Diabetes Empowerment Scale, DES-20; 14-item Summary of Diabetes Self Care Activities Assessment, SDSCA-14; 4-item Compliance Questionnaire (CQ-4)

EQ-5D: score ranges from 0 to 1, where 1 represents full health and 0 represents a health state equivalent to death ; DASS-21: score ranges from 0 to 63, a higher score indicates a higher severity/ frequency of negative emotion states of depression/anxiety/stress; PHQ-9: score ranges from 0 to 27, a higher score indicates a higher severity of depression; CDDS-15: score ranges from 0 to 90, a higher score indicates a high level of diabetes distress; DES-20 : score ranges from 0 to 80; a higher score indicates a higher level of patient empowerment; SDSCA-14: score for each domain of diabetes self-care activities shown ranges from 0 to 7 days/week practising appropriate corresponding diabetes self-care activities; CQ-4 : score ranges from 0 to 4, a higher score indicates a lower level of medication adherence.