# **Supplemental Online Content**

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## **eFigure 1. Pipeline of the**

**study.**



### **eFigure 2.**

**The analytic framework of the study.**



### **eFigure 3.**

## **Heatmaps demonstrating the overall correlations of GCIPLT and metabolites.**



### **eFigure 4.**

### **Associations of GCIPLT metabolic profiles and risk of morbidity of common**

### **diseases and mortality.**



## **eFigure 5.**





## **eFigure 6.**

**Predictive power of GCIPLT metabolic profiles and clinical indicators for common diseases and mortality.** 



## **eFigure 7**

Receiver operating characteristic curves of clinical indicators-based models, GCIPLT metabolic state models, and combined models for

**predicting common diseases and mortality.**



## **eFigure 8**



**Calibration plotsillustrating predicted and observed probabilities for common diseases and mortality.**

## **eFigure 9**

**Net benefit curves of clinical utility for common diseases and mortality.**



**List summarizing all metabolic markers quantifying using 1H-NMR profiling.**























## **Metabolic markers used in models discriminating common diseases and mortality.**











## **Baseline characteristics of the study population from the UKB cohort.**







§ Bold indicates statistically significant.

† Comparison of characteristics between population-I and population-II.

‡ Comparison of characteristics between discovery set and validation set in population-II.

## **Baseline characteristics of the study population from the GDES cohort.**



§ Bold indicates statistically significant.

## **Significant metabolites associated with GCIPLT.**





§Adjusted for sex, age, race, education, Townsend deprivation index, household income, body mass index, smoking, alcohol, lipid-lowering medication, spherical equivalent, and intraocular pressure.

†Benjamini-Hochberg corrected P value.

GCIPLT = ganglion cell-inner plexiform layer thickness; HDL = high-density lipoprotein;

LDL = low-density lipoprotein; VLDL = very low-density lipoprotein; CI = confidence interval.





T2D = type 2 diabetes; MI = myocardial infarction; HF = heart failure; OSAHS =

obstructive sleep apnea/hypopnea syndrome; CVD = cardiovascular disease.

**Discriminative power of clinical indicators and GCIPLT metabolic profiles for predicting mortality and common diseases.** 



\*Clinical indicators-based model for predicting T2D includes age,sex, Townsend deprivation index,smoking, drinking, ethnicity, BMI, WHR, blood pressure-lowering medication, and family history of diabetes. Clinical indicators-based model for predicting MI includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, diabetes, total cholesterol, and LDL-c. Clinical indicators-based model for predicting HF includes age, sex, ethnicity, smoking, drinking, BMI, ACR, HbA1c, hemoglobin, cardiovascular diseases, and family history of CVD. Clinical indicators-based model for predicting stroke includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, family history of stroke, total cholesterol, and SBP. Clinical indicators-based model for predicting mortality includes age, sex, Townsend deprivation index, smoking, drinking, BMI, physical activity, lipid-lowering medication, SBP, diabetes, and total cholesterol. Clinical indicators-based model for predicting dementia includes age, sex, ethnicity, smoking, drinking, education, BMI, stroke, family history of dementia, and apoE4 allele. Clinical indicators-based model for predicting OSAHS includes age, sex, smoking, drinking, ethnicity, BMI, WHR, hypertension, and diabetes.

†GCIPLT metabolic state models based on GCIPLT-related metabolites.

‡Combined models based on clinical indicators and GCIPLT-related metabolites.

§Compared between model 3 and model 1.

T2D = type 2 diabetes; MI = myocardial infarction; HF = heart failure; OSAHS = obstructive sleep apnea/hypopnea syndrome; CVD = cardiovascular disease; BMI = body mass index; WHR = waist-to-hip ratio; ACR = microalbumin/creatinine ratio; HbA1c = glycosylated hemoglobin A1c; SBP = systolic blood pressure; apoE4 = apolipoprotein E4.

**NRIs improvements of incorporating GCIPLT metabolic profilesfor mortality** 



**and morbidity of common diseases.** 

NRI = net reclassification index; GCIPLT = ganglion cell-inner plexiform layer thickness;

T2D = type 2 diabetes; MI = myocardial infarction; HF = heart failure; OSAHS =

obstructive sleep apnea/hypopnea syndrome; CVD = cardiovascular disease; CI =

confidential interval.

**†** CIs were estimated using bootstrap.

## **List summarizing metabolic profiles identified in the GDES cohort using LC/MS profiling.**





### **Sensitivity analysis of excluding all missing values.**



\*Clinical indicators-based model for predicting T2D includes age,sex, Townsend deprivation index,smoking, drinking, ethnicity, BMI, WHR, blood pressure-lowering medication, and family history of diabetes. Clinical indicators-based model for predicting MI includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, diabetes, total cholesterol, and LDL-c. Clinical indicators-based model for predicting HF includes age, sex, ethnicity, smoking, drinking, BMI, ACR, HbA1c, hemoglobin, cardiovascular diseases, and family history of CVD. Clinical indicators-based model for predicting stroke includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, family history of stroke, total cholesterol, and SBP. Clinical indicators-based model for predicting mortality includes age, sex, Townsend deprivation index, smoking, drinking, BMI, physical activity, lipid-lowering medication, SBP, diabetes, and total cholesterol. Clinical indicators-based model for predicting dementia includes age, sex, ethnicity, smoking, drinking, education, BMI, stroke, family history of dementia, and apoE4 allele. Clinical indicators-based model for predicting OSAHS includes age, sex, smoking, drinking, ethnicity, BMI, WHR, hypertension, and diabetes.

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#### **eMethods**

#### **Eligibility criteria**

A total of 93,838 participants from the UKB cohort were included for final analysis in this study, which comprised 7,824 for phase-I analysis and 86,014 for phase-II analysis. Phase-I analysis included participants who underwent both eligible retinal OCT measurements and metabolomic profiling at baseline assessment. Details were as follows. In accordance with established quality control standards, we excluded eyes with missing thickness values (1,350 right eyes and 1,791 left eyes), low signal strength (Q<45) (6,105 right eyes and 5,149 left eyes), poor centration or segmentation (poorest 20% indicators) (19,780 right eyes and 20,022 left eyes) from a total of 67,135 participants underwent OCT scanning at baseline. To minimize the impact of other ocular parameters, we also excluded eyes with high refractive error (spherical equivalent [SE] >6 or <-6 diopters [D]) (1,633 right eyes and 1,833 left eyes), visual impairment (> 0.1 logarithm of the minimum angle of resolution [logMAR]) (9,345 right eyes and 8,863 left eyes), or abnormal intraocular pressure (IOP) ( $\geq$  22 or  $\leq$  5 mmHg) (3,148 right eyes and 3,551 left eyes). Additionally, we excluded patients with glaucoma (400 participants), other retinal disorders (703 participants), and neurodegenerative diseases (111 participants) due to the potential secondary RNFL destruction. Finally, participants without metabolomics profiling were further excluded. This resulted in a total of 7,824 participants for phase-I analysis. The medical history of participants was obtained through questionnaires, interviews, and inpatient diagnoses prior to baseline. Participants who did not complete metabolomic profiling were further excluded.

Phase-II analysisincluded 110,730 participants who complete metabolomic profiling at baseline assessment, with the exclusion of participants who lack hospital records (18,032 participants). Meanwhile, those who already included in phase-I analysis (6,684 participants) were further excluded. Thus, the participants for phase-II analysis and those for phase-I analysis are two separate subsets that do not overlap with each other. This resulted in a total of 86,014 participants for phase-II analysis.

Participants with previous diagnosis were further excluded for each analysis (e.g., in the case of T2D endpoint analysis, participants diagnosed with T2D at baseline were excluded).

### **Profiling details and quality control processes of 1H-NMR profiling**

Details about the metabolomic profiling protocol have been described elsewhere.<sup>1</sup> Sample collection was undertaken at baseline in 22 local assessment centers across the UK between 2007 and 2010. The blood sample handling and storage protocol has been previously described.<sup>2</sup> The metabolomic profiling took place in Finland between 2019 and 2020 using six NMR spectrometers. Accredited quality control was done during the whole process to eliminate systemic and technical variance, and only samples and biomarkers that underwent the quality control process were stored in the UK Biobank dataset and used in our present study.

EDTA plasma samples from aliquot 3 were prepared in 96-well plates by UK Biobank laboratory (Stockport, UK). TECAN freedom EVO 150 robotic liquid handlers were used for aliquoting plasma samples. The plasma samples were shipped in batches to Nightingale Health laboratories in Finland on dry ice. Before preparation, frozen samples were thawed slowly, mixed gently and centrifuged. Aliquots of each sample were mixed with a phosphate buffer and subjected to measurement using six 500 MHz NMR spectrometers. Nightingale Health's proprietary software (quantification library 2020) was used to quantify the biomarkers.

Each 96-well plate included two internal control samples provided by Nightingale Health to track consistency across multiple spectrometers. Four sets of internal control samples with different biomarker concentration span were used across 1,352 96-well plates and interleaved between NMR instruments for extended periods. Blind duplicate samples from UK Biobank were included on each 96-well plate, with position revealed only after results delivery. The coefficient of variation (CV) distributions for the blinded replicates and Nightingale Health'sinternal control samples were typically below 5%. These results met pre-specified CV targets for each set of approximately 20,000 consecutively measured samples.

The NMR biomarker data in the UK Biobank can generally be used for epidemiological analyses without any preprocessing and can in principle be analyzed in the same manner as the clinical chemistry data available in UKB. Biomarker values substantially affected by interfering substances have been removed during the quality control procedures.

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### **Quality control of SD-OCT imaging in the UKB cohort**

Quality control measures for scanning included the image quality score, ILM indicator, validity count, and motion indicators. The IQS measures the signal strength, while the ILM indicator identifies blinks and segmentation errors. The validity count identifies significant clipping in the OCT scan's z-axis dimension. The motion indicators use Pearson correlations and absolute differences of the nerve fiber layer and full retinal thicknesses from each set of consecutive B-scans to identify blinks, eye-motion artifacts, and segmentation failures.

#### **Assessments of covariates in the UKB cohort**

At baseline (2006–2010), physical measurements, face-to-face interviews, and detailed self-administered touchscreen questionnaires were conducted on all participants. The questionnaires included demographic and socioeconomic factors (age, sex, race, education level, Townsend deprivation index, and income), lifestyle factors (smoking and drinking status, and physical activity time per week), family history, and medical history, including the use of insulin, lipid-lowering medications, antihypertensive drugs, and disease diagnosis. Baseline diseases were defined using questionnaires, interviews, and inpatient data based on the ICD-10 codes. Physical measurements including baseline body mass index (BMI), waist-to-hip ratio, blood pressure, visual acuity, refractive error, spherical equivalent, intraocular pressure (IOP), total cholesterol, low-density lipoprotein cholesterol, high-density lipoprotein cholesterol levels, glycosylated hemoglobin A1c, urine microalbumin, and creatinine were obtained. The presence of apolipoprotein E (apoE) ε4 allele was defined using the apoE  $\varepsilon$ 4+ dominant model of  $\varepsilon$ 3/ $\varepsilon$ 4 and  $\varepsilon$ 4/ $\varepsilon$ 4. Detailed information is as followed.

In brief, age at baseline assessment were divided into five categories, including < 50 years, 50~54 years, 55~59 years, 60~64 years, and > 64 years. Townsend deprivation index (TDI) were assigned according to participants' postal codes, which reflected the proportions of unemployment, crowding household, non-car ownership, and homelessness in corresponding output areas. Four quantiles were categorized in the ascending order for TDI ( $\leq$  -3.6, 3.6 $\sim$ -2.1, -2.1 $\sim$ 0.6, > 0.6, and missing). Body mass index (BMI) were constructed from height and weight, which were measured by Seca 240cm height measure and Tanita BC418MA body composition analyzer at baseline respectively, and was divided into four categories, including < 25, 25~29.9, ≥30.0, and missing. In the touchscreen questionnaire, UK Biobank participants were asked about their ethnic group, including White, Mixed, Asian, Black, Chinese, and missing. Due to the small number of participants, the last five alternatives were

assembled into others. The average total household income before tax were directly derived from questionnaires, including < £18,000, £18,000 to £30,999, £31,000 to £51,999, £52,000 to £100,000, > £100,000, and missing. Educational qualifications reflected the highest diploma achieved which were divided into three categories including O levels or equivalent, A levels or equivalent, college or university degree, and missing. Time spent on moderate to vigorous activity (MVPA) was categorized into four quantiles based on adapted questions from the short International Physical Activity Questionnaire. Weighted by expended energy, MVPA time were transformed into metabolic Equivalent Task (MET) minutes/week and categorized into four quantiles and missing. For smoking status, previous smokers and current smokers were distinguished from those who never smoked tobacco. Similarly, previous and current drinkers were also separated from those who never drank alcohol. Sensitivity analyses were also conducted by excluding all missing values. The study results can be found in *Supplementary eTable S9*.

Blood biochemistry assessments: Analysis of serum biomarkers utilized 10 immunoassay analyzers (6x DiaSorin Liaison XL & 4x Beckman Coulter DXI 800 and 4 clinical chemistry analyzers (2x Beckman Coulter AU5800 & 2x Siemens Advia 1800).

HbA1c assessment: The HbA1c assay was performed using five Bio-Rad Variant II Turbo analyzers. The five analyzers underwent a rigorous validation protocol including matrix validation for the use of PRBC an atypical matrix for this CE marked assay, to ensure they were all compliant with ISO 17025:2005 standards before analysis commenced. The validation study also included a multi-instrument comparison to ensure five instruments were all in agreement. The Bio-Rad Variant II Turbo Hemoglobin Testing System uses HPLC to determine the relative concentration of HbA1c in PRBCs.

Urine assays: All tests were carried out on a single Beckman Coulter AU5400 clinical chemistry analyzer using the manufacturer's reagents and calibrators except urinary microalbumin which used reagents and calibratorssourced from Randox Bioscience, UK. The Beckman Coulter AU5400 series clinical chemistry analyzer uses a photometric measurement for the determination of creatinine and microalbumin concentration and a potentiometric measurement for the determination of sodium and potassium concentration.

apoE ε4 allele assessment: Genotyping was conducted by Affymetrix using a bespoke BiLEVE Axiom array or the UK Biobank Axiom array.<sup>1</sup> All genetic data were quality controlled and imputed by UK Biobank. apoE genotype was directly genotyped based on two SNPs (rs7412 and rs429358). apoE ε4+ dominant model of ε3/e4 and ε4/ε4 was used to define the presence of apoE  $\varepsilon$ 4.<sup>2</sup>

### **Reference**

- 1. Bycroft, C., Freeman, C., Petkova, D., Band, G., Elliott, L. T., Sharp, K., Motyer, A., Vukcevic, D., Delaneau, O., O'Connell, J., Cortes, A., Welsh, S., Young, A., Effingham, M., McVean, G., Leslie, S., Allen, N., Donnelly, P., & Marchini, J. (2018). The UK Biobank resource with deep phenotyping and genomic data. Nature, 562(7726), 203–209.
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## **SS-OCT imaging protocols and quality control processes in the GDES cohort**

After dilatation, structural images of the macula were obtained using a commercially available SS-OCT device (DRI OCT Triton; Topcon, Japan). The instrument has an axial and lateral resolution of 8 and 20 μm, respectively, and uses a wavelength of 1050 nm with a scan speed of 100,000 A-scans per second. This

instrument is characterized by high scanning speed and deep penetration, which is especially suitable for imaging of deep structures. Each OCT scan is performed through an internal fixator, and the fixation is monitored by the instrument's built-in fundus camera. Within 1.3 seconds, the retina was imaged using a 3D Macula Cube 7×7 mm scan mode centered on the fovea with a scan density of 512 A-scans × 512 B-scans.

The SS-OCT software automatically segments each layer of the retina and automatically measures the thickness of GCIPL. All OCT scans are performed by a trained technician who is unaware of the patient's diagnosis. Previous studies have demonstrated excellent reliability and reproducibility of both retinal and choroidal thickness measurements by SS-OCT. The results of the automated segmentation were evaluated by an image expert (WW), and the participants' data were masked during processing. If segmentation errors existed, manual adjustments were performed. Only high-quality scanned images were used for analysis, and images with (1) image quality scores <60, (2) defocus, (3) motion artifacts or blink artifacts, (4) out of center, (5) images with poor contrast due to refractive media opacity (local signal missing, blurred images, masking), and (6) unable-correctable segmentation errors were excluded.

#### **Profiling details and quality control processes of LC/MS profiling**

The sample stored at -80 °C refrigerator was thawed on ice and vortexed for 10 s. 50 μL of sample and 300 μL of extraction solution (ACN : Methanol = 1:4, V/V) containing internal standards were added into a 2 mL microcentrifuge tube. The sample was vortexed for 3 min and then centrifuged at 12000 rpm for 10 min (4 °C). 200 μL of the supernatant was collected and placed in -20 °C for 30 min, and then centrifuged at 12000 rpm for 3 min (4 °C). A 180 μL aliquots of supernatant were transferred for LC-MS analysis.

The sample extracts were analyzed using an LC-ESI-MS/MS system (UPLC, ExionLC

AD, https://sciex.com.cn/; MS, QTRAP® System, https://sciex.com/). The analytical conditions were as follows, UPLC: column, Waters ACQUITY UPLC HSS T3 C18 (1.8 µm, 2.1 mm\*100 mm); column temperature, 40 °C; flow rate, 0.4 mL/min; injection volume, 2μL; solvent system, water (0.1% formic acid): acetonitrile (0.1% formic acid); gradient program, 95:5 V/V at 0 min, 10:90 V/V at 11.0 min, 10:90 V/V at 12.0 min, 95:5 V/V at 12.1 min, 95:5 V/V at 14.0 min.

LIT and triple quadrupole (QQQ) scans were acquired on a triple quadrupole-linear ion trap mass spectrometer (QTRAP), QTRAP® LC-MS/MS System, equipped with an ESI Turbo Ion-Spray interface, operating in positive and negative ion mode, and controlled by Analyst 1.6.3 software (Sciex). The ESI source operation parameters were as follows: source temperature 500 °C; ion spray voltage (IS) 5500 V (positive), -4500 V (negative); ion source gas I (GSI), gas II (GSII), curtain gas (CUR) were set at 55, 60, and 25.0 psi, respectively; the collision gas (CAD) was high. Instrument tuning and mass calibration were performed with 10 and 100 μmol/L polypropylene glycol solutions in QQQ and LIT modes, respectively. A specific set of MRM transitions were monitored for each period according to the metabolites eluted within this period.

Quality control samples (QC) were prepared by mixing sample extracts to analyze the reproducibility of the samples under the same processing method. During the instrument analysis process, one QC sample was inserted every ten analytical samples to monitor the reproducibility of the analysis process. Overlapping analysis of the total ion chromatogram (TIC) of different QC samples were used to evaluate the reproducibility of metabolite extraction and detection, i.e., technical reproducibility. The high stability of the instrument providesimportant guarantees for the reproducibility and reliability of the data.

To monitor the presence of any residual substances during the detection process, blank samples were included at various stages of the experiment. The appearance

of peaks in these samples could indicate cross-contamination between samples or the presence of unwanted substances.

In addition, to ensure the reliability and accuracy of the experimental results, internal standards with known concentrations were added to the quality control process. The response of the internal standards was used as an indicator of the stability of the detection process, with smaller variation in response indicating higher data quality. The CVs for all internal standards in the current profiling were all below 0.01.

### **Reference**

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- 3. Viant M R, Kurland I J, Jones M R, et al. How close are we to complete annotation of metabolomes? Current opinion in chemical biology, 2017, 36: 64-69.

### **Testing of the PH assumption and managing potential violations**

First, the cumulative risk graph shows that all curves are roughly in line with proportional risk, except for other mortality. Then, the PH assumption was tested using the Schoenfeld residual method. Assuming risk varies over time, the function of the hazard ratio over time for any variable is expressed as follows:  $\exp(\beta_i + \pi_i)$  $\beta_{k+i} \times \phi(t)$ ). Thus, the expectation of the scaled Schoenfeld residuals for this variable at time point m is expressed as:  $E(r * sch,m) = \beta_{k+i} \times \varphi(t)$ . Therefore, to

test the PH hypothesis is equivalent to determining whether  $\beta_{k+i}$  is equal to zero. In the construction of the CPH models, interaction terms with time were introduced for variables that did not satisfy the PH assumption. If this variable was removed from subsequent stepwise regressions, the time interaction term for this variable was also removed along with it.

### **Details of the model development in the UKB cohort**

We developed three models to discriminate each health outcome in the discovery set, namely a clinical indicators-based model, a GCIPLT metabolic state model, and a combined model. Feature selection was performed using LASSO, which achieves sparsity of model parameters by adding an L1 regularization term to the optimization objective function to reduce model complexity and the risk of overfitting. This approach is very effective when dealing with high-dimensional data, such as omics data. The selected variables were used to construct CPH models. After the Schoefeld residual method test described above, the necessary time interaction terms were added to the models. Stepwise regression was used to select models with the best performance, with Akaike information as the selection criterion and the direction of stepwise regression set to 'both'.

Details of the GCIPLT metabolic state models for each outcome are available in Supplementary eTable S2. The clinical indicators used for each outcome are as follows. The clinical indicators-based model for predicting T2D includes age, sex, Townsend deprivation index, smoking, drinking, ethnicity, BMI, WHR, blood pressure-lowering medication, and family history of diabetes. The clinical indicators-based model for predicting MI includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, diabetes, total cholesterol, and LDL-c. The clinical indicators-based model for predicting HF includes age, sex, ethnicity, smoking, drinking, BMI, ACR, HbA1c, hemoglobin, cardiovascular diseases, and family history of CVD. The clinical indicators-based model for predicting stroke includes age, sex, ethnicity, smoking, drinking, BMI, hypertension, family history of stroke, total

cholesterol, and SBP. The clinical indicators-based model for predicting dementia includes age, sex, ethnicity, smoking, drinking, education, BMI, stroke, family history of dementia, and apoE4 allele. The clinical indicators-based model for predicting OSAHS includes age, sex, smoking, drinking, ethnicity, BMI, WHR, hypertension, and diabetes. The clinical indicators-based model for predicting mortality includes age, sex, Townsend deprivation index, smoking, drinking, BMI, physical activity, lipid-lowering medication, SBP, diabetes, and total cholesterol.

### **Methodsfor assessing predictive performance and clinical utility**

Several metrics for assessing model performance were used in the current study. The C-statistic, also referred to as the concordance statistic, is a widely used statistical measure in medical research to evaluate the performance of predictive models. It assesses the ability of a diagnostic test or predictive model to distinguish between individuals with and without a specific outcome, such as a diseases or mortality. It ranges from 0.5 to 1.0, where a value of 0.5 indicates that the model has no discriminatory power and is no better than random guessing, while a value of 1.0 indicates perfect discrimination, meaning the model can correctly predict all cases. Typically, a C-statistic of 0.7 or higher is considered to indicate good performance.

The net reclassification index (NRI) is a statistical measure commonly used in medical research to assess the improvement in risk prediction models when new biomarkers or variables are added. The NRI evaluates the ability of a new model to correctly reclassify individuals into higher or lower risk categories compared to the original model. The NRI is calculated as the sum of two components: the proportion of individuals who are correctly reclassified into a higher risk category (NRI+) minus the proportion of individuals who are incorrectly reclassified into a lower risk category (NRI-), with a positive value indicating an improvement in risk prediction and a negative value indicating a worsening of risk prediction. Unlike other measures of model performance, such as the area under the receiver operating

characteristic curve (AUC), the NRI provides information on the direction and magnitude of reclassification, enabling direct comparison of the performance of two models, even when their AUCs are similar.

The calibration plot is a graphical tool that compares the predicted probabilities of a statistical model with the actual observed probabilities. It is commonly used in binary classification problems where the goal is to predict the probability of an event occurring or not occurring. The x-axis of the plot represents the predicted probabilities, while the y-axis represents the observed probabilities of the event occurring. The primary objective of a calibration plot is to assess the accuracy and reliability of a predictive model. Ideally, a well-calibrated model should have predicted probabilities that match the observed probabilities, resulting in a diagonal line with a slope of 1.0. Any deviation from this diagonal line indicates that the model is either overestimating or underestimating the probability of the event occurring. In practice, it is rare to achieve perfect calibration, and therefore the goal is to create a model that is as calibrated as possible. The calibration plot can be used to compare the calibration of different models by plotting their calibration curves on the same graph. The model with the closest fit to the diagonal line is considered as the most calibrated.

The decision curve analysis (DCA) is a statistical method that evaluates the clinical usefulness of predictive models and diagnostic tests. It was developed as an extension of the traditional ROC curve and net benefit analysis. DCA helps to determine whether a predictive model or diagnostic test has clinical value by assessing the net benefit of using the model or test compared to other available strategies for making decisions. The DCA method involves plotting the net benefit of a model or test against the threshold probability for making the decision. The threshold probability representsthe probability of an event occurring at which the clinician would be willing to make a particular decision. The DCA plot displays the net benefit curves for the model or test being evaluated and for two other

reference strategies: a treat-all strategy and a treat-none strategy. The treat-all strategy assumes that all patients have the disease or outcome of interest and are treated, while the treat-none strategy assumes that no patients have the disease or outcome and do not receive treatment.

#### **eAppendix**

### **Extended discussion on T2D**

GCIPLT metabolomic fingerprints provided an impressive value in the prediction of T2D. This study implicates decreased HDL cholesterol, and changes in its multiple components as factors that confer an increased risk of T2D, consistent with the complex shifts in lipid metabolism that occur in T2D. Precisely, the synthesis and release of triglyceride (TG)-rich very low-density lipoprotein (VLDL) in the liver drives the exchange of TG and cholesterol esters between VLDL and HDL, leading to a decrease in HDL cholesterol in T2D. $<sup>1</sup>$  In addition, unstable TG-rich HDL particles</sup> are considered more susceptible to clearance, $2$  explaining the negative association between HDL and apoA1 levels and the risk of developing T2D in this study. Since HDL particles are primarily responsible for reverse transport of cellular cholesterol, their reduction or inactivity can cause lipid accumulation in pancreatic β-cells, causing inflammation and impaired β-cell function.<sup>3-6</sup> This cholesterol transport activity and antioxidant capacity of HDL were also reported to be associated with its surface lipid components, which determines the protein's mobility<sup>7-9</sup>; hence, decreased ratios of unsaturated FAsto saturated FAs, phospholipids, and free cholesterol observed in the present study impair antioxidant capacity, which predispose an individual to T2D.

### **Extended discussion on dementia**

While there was no significant improvement in the C-index, the GCIPLT metabolic fingerprints showed a significant increase in both the net reclassification power and clinical utility for dementia prediction. ApoA1, HDL particle concentration and multiple components within HDL were found to be independently associated with decreased risk of dementia. Debate about the prospective relationship between plasma HDL levels and dementia is ongoing,<sup>10</sup> and it was recently demonstrated that plasma apoA1-HDL crossed the blood–brain barrier through scavenger receptors, inferring it could participate in brain lipid metabolism.<sup>11</sup> Extracellular deposition of amyloid  $\beta$  (A $\beta$ ) is thought to be the initiating event for dementia,<sup>12</sup>

and *in vitro* studies show that apoA1 binds to Aβ to interfere with Aβ monomer assembly, preventing neurotoxicity.<sup>13, 14</sup> In addition,  $\Delta \beta$ -bound HDL was reported to promote *in situ* degradation of Aβ by binding to scavenger receptors on glial cells,<sup>15</sup> explaining why plasma apoA1 and HDL were protective against dementia in this study. These consolidate the current literature and provide further insight into the pathophysiology of dementia.

### **Extended discussion on OSAHS**

OSAHS is a common sleep disorder and airway disease characterized by sleep apnea, causing subsequent chronic hypoxia.<sup>16</sup> Elevated levels of free FAs (FFAs) are common in mice exposed to intermittent hypoxia (IH) and in OSAHS patients,  $17-21$ likely from IH-associated activation of the sympathetic system that triggers the release of FFAs from adipose tissue.<sup>22</sup> Similar to T2D, FFAs are sent to the liver to synthesize TG-rich VLDL, which ultimately decreases HDL cholesterol and clearance of unstable HDL particles, $2$  as supported by our results. IH is also thought to impair the sensitivity of adipose tissue to insulin, which further leads to increased FFAs release and decreased HDL cholesterol and HDL particles.<sup>23</sup> In addition, patients with OSAHS have been reported to undergo lipid peroxidation more frequently,<sup>24</sup> hence higher levels of HDL particles with higher phospholipid and free cholesterol content that are associated with good antioxidant capacity were deemed protective against OSAHS in the present study. $8, 9$ 

### **Extended discussion on metrics used for model assessment**

To ensure a further comprehensive evaluation of model performance and effectiveness in future real world-setting studies, it is essential to consider multiple indicators beyond the metrics used in the current study. Factors such as interpretability, robustness, and generalizability may also play a critical role in evaluating the model's quality. For instance, model interpretability refers to the ability to understand and explain the model's decision-making process, which can facilitate its adoption and implementation in real-world settings. Robustness, on the other hand, refers to the model's ability to perform well even when the data is noisy or incomplete. Generalizability refers to the model's ability to perform well on data that it has not been trained on. By considering these factors, a more comprehensive and accurate assessment of the model's quality can be achieved.

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