Supplementary Information

The distribution of BMI is presented in Figure S3 and shows the nonlinear relationship between BMI and progression to insulin requirement. Compared with those with a BMI of 21-23 kg/m² (the lowest risk group), participants with BMI<18.5 kg/m² had a hazard ratio (HR) of 1.4 (1.1-1.9), and those with a $31 \le BMI < 33$ kg/m² had a HR of 1.3 (1.1-1.7). Then we further divided BMI into four groups based on the World Health Organization definition for obesity in Asians: underweight (BMI<18.5 kg/m²), normal (18.5 $\le BMI < 23.0$ kg/m²), overweight (23.0 $\le BMI < 25.0$ kg/m²), and obese (25.0+ kg/m²) (1). Since the proportional hazard assumption for baseline HbA1c was not met, we stratified participants into three groups (HbA1c<7%, $\ge 7-9\%$ and $\ge 9\%$) to allow for a different hazard function in each group. Therefore, both BMI and baseline HbA1c categories were included as strata variables in Cox regression models, whereas the other covariates were considered to have the same effect across strata.

With regards to the effects of BMI, lower and higher BMI were both associated with increased risk of diabetes progression. With regards to the interaction effects of BMI on rLTL and diabetes progression, rLTL was significantly shorter in progressors from the normal/overweight/obese group, compared with non-progressors. However, the association between rLTL and diabetes progression in the normal BMI group and the obese group was attenuated after adjusting for confounders, while the significance in the overweight group remained unchanged after full adjustment. The significant association between rLTL and diabetes progression was only observed in the overweight group. (HR (95% CI): 1.157 (1.042-1.286), P=0.006). (Table S2)

The whole cohort was divided into three groups based on baseline HbA_{1c} (HbA_{1c} <7%, \geq 7-9% and \geq 9%), and there was a significant difference in mean rLTL between each group (4.67±1.18 vs. 4.51±1.20 vs. 4.38±1.18; P<0.001). The significant difference of rLTL between the three groups did not change after adjusting for age, sex, known diabetes duration and smoking status (P<0.001). Patients who progressed to insulin requirement had significantly shorter rLTL than those who did not in each group, after adjusting for age, sex, diabetes duration and smoking status (4.52±1.18 vs. 4.73±1.18; 4.44±1.15 vs. 4.61±1.26; 4.30±1.16 vs. 4.62±1.21; all P<0.05). We grouped subjects according to baseline HbA_{1c} and further examined the relationship between rLTL and glycaemic progression in three groups separately, we only observe significant associations between rLTL and glycaemic progression in patients with $HbA_{1c} \geq$ 9% (HR (95% CI): 1.122 (1.037-1.214), P=0.004), which was attenuated once risk factors considered. (Table S2).

The Kaplan-Meier analysis also shows that those from the tertile with the longest rLTL (≥5.092) had a decreased risk of progression to the requirement of insulin treatment (Figure 1). Compared with those with the longest tertile of rLTL, participants from the tertile with the shortest rLTL had a 1.269-fold higher risk of progression to insulin requirement.

Since HDL-Cholesterol was identified as an independent predictor for glycaemic deterioration in European patients, we included HDL-Cholesterol as a predictor with exclusion of TG and LDL-Cholesterol in multivariate Cox analysis. Shorter telomere length was still associated with a higher risk for requirement of insulin (HR (95% CI): 1.052 (1.008-1.098), P=0.021) in the fully adjusted model.

Besides, we compared the results of rLTL calculated based on NTC or QC reference sample. Like the results of rLTL based on NTC, subjects who progressed to requirement of insulin had significantly lower rLTL-QC (-0.21±1.02 vs. -0.03±1.02; P<0.001), compared with those remained on oral antidiabetic drugs during the follow-up period. Each unit decrease of rLTL based on QC materials was associated with a 1.113-times (95%CI: 1.065-1.164) higher risk of progression to insulin requirement. After adjusting for traditional risk factors, the association remained significant (HR (95% CI): 1.083 (1.031-1.139), P=0.002) (Table S7).

Table S1. Competing Risk Regression analysis showing subdistribution HRs of rLTL for glycaemic progression defined as need for insulin treatment.

Models	Unadjusted model		Fully adjusted model	
	HR (95% CI)	P value	HR (95% CI)	P value
rLTL in original model	1.098 (1.056-1.142)	<0.001	1.052 (1.007-1.100)	0.023
rLTL considering death	1.079 (1.037-1.072)	< 0.001	1.053 (1.005-0.736)	0.029
before DM progression				

sHR, subdistribution hazards ratio; rLTL, relative leukocyte telomere length calculated by water. Fully adjusted models included age at diagnosis, duration of diabetes, smoking, log(TG), LDL-C, log(ACR), eGFR, sensory neuropathy, retinopathy, use of lipid-lowering drugs, use of RAS inhibitors and use of oral glucose lowering drugs.

Table S2. Multivariate Cox proportional hazards models for the association between baseline telomere length (calculated using NTC) and incident diabetes progression defined as need for insulin use.

Diabetes progression	Events/Total (%)	Unadjusted model		Fully adjusted model	
		Hazard Ratio (95% CI)	P value	Hazard Ratio (95% CI)	P value
Overall	1803/3937	1.098 (1.056-1.142)	< 0.001	1.052 (1.007-1.100)	0.023
Women	964/2166	1.149 (1.089-1.212)	< 0.001	1.119 (1.054-1.187)	< 0.001
Men	839/1771	1.040 (0.982-1.102)	0.179	0.975 (0.912-1.042)	0.457
Young age at diagnos	is				
< 40 years	443/748	1.088 (1.041-1.138)	< 0.001	1.037 (0.987-1.090)	0.146
40+ years	1360/3188	1.156 (1.063-1.258)	0.001	1.146 (1.038-1.267)	0.007
BMI kg/m^2					
<18.5	46/95	1.212 (0.925-1.588)	0.164	1.130 (0.814-1.567)	0.466
18.5-23	478/1064	1.070 (0.992-1.153)	0.079	0.992 (0.912-1.078)	0.842
23-25	383/841	1.180 (1.088-1.281)	< 0.001	1.157 (1.042-1.286)	0.006
≥25	892/1917	1.071 (1.011-1.134)	0.020	1.042 (0.979-1.108)	0.195
HbA_{1C}					
< 7%	555/1904	1.062 (0.987-1.142)	0.107	1.020 (0.941-1.106)	0.624
≥7-9%	784/1412	1.038 (0.978-1.101)	0.219	1.052 (0.986-1.122)	0.127
≥9%	464/621	1.122 (1.037-1.214)	0.004	1.075 (0.982-1.178)	0.118

BMI and baseline HbA1c categories were included as strata variables. BMI was categorised as four groups (<18.5, 18.5-23, 23-25 and \geq 25 kg/m²) and baseline HbA1c was categorized as three groups (<7%, \geq 7-9% and \geq 9%). Fully adjusted models included age at diagnosis, duration of diabetes, smoking, log(TG), LDL-C, log(ACR), eGFR, sensory neuropathy, retinopathy, use of lipid-lowering drugs, use of RAS inhibitors and use of oral glucose-lowering drugs.

Table S3. Cox regression analysis for the association between baseline relative telomere length and glycaemic progression defined as actual use of insulin

Variables	Unadjusted model		Fully adjusted model	
variables	HR (95% CI) P valu		HR (95% CI)	P value
rLTL	1.121 (1.075-1.170)	< 0.001	1.065 (1.016-1.117)	0.009
Age at diagnosis (per 1 year)			0.967 (0.961-0.973)	< 0.001
Duration of diabetes (per 1 year)			1.023 (1.013-1.032)	< 0.001
Smoking				
Ex-smoker			1.213 (1.045-1.408)	0.011
Current smoker			1.097 (0.935-1.288)	0.256
log (triglyceride)			1.105 (0.853-1.431)	0.452
LDL-C			0.897 (0.845-0.952)	< 0.001
log urinary ACR			1.480 (1.351-1.622)	< 0.001
eGFR			0.988 (0.984-0.991)	< 0.001
Sensory neuropathy			1.245 (1.089-1.425)	0.001
Retinopathy			1.257 (1.100-1.437)	0.001
Use of oral glucose-lowering drugs			1.191 (1.050-1.352)	0.007
Use of lipid-lowering drugs			1.001 (0.844-1.188)	0.991
Use of RAS inhibitors			1.128 (0.969-1.313)	0.120

Table S4. The relationship between baseline relative telomere length and glycaemic exposure during follow-up.

Variables	Unadjusted model		Fully adjusted model	_
	Beta (95% CI)	P value	Beta (95% CI)	P value
(Intercept)	1.116 (1.054-1.179)	< 0.001	0.185 (0.365-0.004)	0.045
rLTL	-0.048 (-0.0610.035)	< 0.001	-0.018 (-0.0070.029)	0.001
Age at diagnosis (per 1 year)			0.000 (0.0010.001)	0.861
BMI (kg/m ²)			0.004 (0.007-0.001)	0.017
HbA1c (%)			0.017 (0.025-0.009)	< 0.001
Duration of diabetes (per 1 year)			-0.001 (0.0020.003)	0.676
Smoking				
Ex-smoker			0.018 (0.0520.015)	0.289
Current smoker			0.070 (0.106-0.033)	< 0.001
log (triglyceride)			-0.045 (0.0120.102)	0.126
LDL-C			-0.003 (0.0100.017)	0.615
log urinary ACR			0.006 (0.0290.017)	0.614
eGFR			0.001 (0.002-0.001)	< 0.001
Sensory neuropathy			-0.033 (0.0010.067)	0.057
Retinopathy			-0.025 (0.0060.057)	0.117
Use of oral glucose lowering drugs			-0.039 (-0.0100.067)	0.008
Use of lipid-lowering drugs			-0.069 (-0.0370.100)	< 0.001
Use of RAS inhibitors			-0.016 (0.0160.048)	0.327
Follow-up time (per 1 year)			0.053 (0.056-0.050)	<0.001

Table S5. Cox regression analysis for association between baseline absolute telomere length and glycaemic progression defined as need for insulin treatment.

Variables	Unadjusted model		Fully adjusted model	
	HR (95% CI)	P value	HR (95% CI)	P value
Absolute LTL (per kb)	1.688 (1.353-2.105)	< 0.001	1.332 (1.040-1.705)	0.023
Age at diagnosis (per 1 year)			0.971 (0.966-0.976)	< 0.001
Duration of diabetes (per 1 year)			1.020 (1.011-1.029)	< 0.001
Smoking				
Ex-smoker			1.248 (1.088-1.430)	0.002
Current smoker			1.158 (1.003-1.338)	0.045
log (triglyceride)			1.323 (1.044-1.675)	0.020
LDL-C			0.936 (0.886-0.987)	0.015
log urinary ACR			1.373 (1.262-1.495)	< 0.001
eGFR			0.991 (0.988-0.994)	< 0.001
Sensory neuropathy			1.268 (1.120-1.435)	< 0.001
Retinopathy			1.235 (1.092-1.396)	0.001
Use of oral glucose lowering drugs			1.284 (1.143-1.443)	< 0.001
Use of lipid-lowering drugs			1.049 (0.901-1.221)	0.542
Use of RAS inhibitors			1.147 (0.999-1.318)	0.052

Abbreviations: absolute LTL, absolute leukocyte telomere length estimated using telseq; LDL-C, low-density lipoprotein cholesterol; ACR, urinary albumin to creatinine ratio; eGFR, estimated glomerular filtration rate.

Table S6 The sensitivity analysis of association between shorter rLTL at baseline and diabetes progression, stratified by DM duration <5, 5-10, >10 years.

DM duration	Events/Total (%)	Unadjusted Model		Fully adjusted Model	
at baseline		HR (95% CI)	P value	HR (95% CI)	P value
≤5 years	919/2326	1.065 (1.006-1.127)	0.031	1.048 (0.985-1.115)	0.140
5-10 years	448/870	1.040 (0.962-1.123)	0.319	1.055 (0.966-1.152)	0.231
>10 years	436/740	1.116 (1.030-1.208)	0.007	1.024 (0.930-1.126)	0.633

HR, hazards ratio for each unit deceased in rLTL; rLTL, relative leukocyte telomere length calculated by water. Fully adjusted models included age at diagnosis, duration of diabetes, smoking, BMI, log(TG), LDL-C, log(ACR), eGFR, HbA1c, sensory neuropathy, retinopathy, use of lipid-lowering drugs, use of RAS inhibitors and use of oral glucose lowering drugs.

Table S7 Cox regression analysis for association between baseline relative telomere length and glycaemic progression defined as need for insulin treatment among 3868 subjects (after exclusion of subjects with GAD+)

Variables	Unadjusted model		Fully adjusted model	
	HR (95% CI)	P value	HR (95% CI)	P value
rLTL	1.099 (1.057-1.144)	< 0.001	1.052 (1.006-1.100)	0.026
Age at diagnosis (per 1 year)			0.971 (0.966-0.976)	< 0.001
Duration of diabetes (per 1 year)			1.021 (1.012-1.030)	< 0.001
Smoking				
Ex-smoker			1.244 (1.084-1.427)	0.002
Current smoker			1.150 (0.994-1.329)	0.060
log (triglyceride)			1.383 (1.088-1.756)	0.008
LDL-C			0.932 (0.883-0.985)	0.012
log urinary ACR			1.381 (1.268-1.504)	< 0.001
eGFR			0.991 (0.988-0.994)	< 0.001
Sensory neuropathy			1.275 (1.126-1.444)	< 0.001
Retinopathy			1.240 (1.096-1.404)	< 0.001
Use of oral glucose lowering drugs			1.268 (1.127-1.426)	< 0.001
Use of lipid-lowering drugs			1.057 (0.906-1.232)	0.482
Use of RAS inhibitors			1.155 (1.005-1.329)	0.043

Table S8. The genetic variants for Mendelian Randomization analysis of telomere length (exposure) and glyacemic progression (outcome)

SNP	Gene	Chr	Position	Effect Allele	Ref allele	Beta*	SE*	P value*	Beta#	SE#	P value#
rs10857352	NAF1	4	164101482	A	G	-0.031	0.027	2.45E-01	-0.064	0.011	4.85E-09
rs12415148	OBFC1	10	105680586	T	C	-0.050	0.048	2.98E-01	-0.204	0.020	2.78E-25
rs227080	ATM	11	108247888	G	A	-0.035	0.023	1.32E-01	-0.060	0.009	1.87E-10
rs2293607	TERC	3	169482335	C	T	-0.053	0.023	2.19E-02	-0.120	0.009	7.57E-39
rs28365964	TERF1	8	73920883	T	C	-0.239	0.109	2.85E-02	-0.270	0.035	6.96E-15
rs3219104	PARP1	1	226562621	A	C	-0.050	0.024	3.31E-02	-0.074	0.009	2.23E-16
rs41293836	TINF2	14	24721327	C	T	-0.216	0.040	9.11E-08	-0.233	0.017	2.47E-42
rs41309367	RTEL1	20	62309554	T	C	-0.016	0.026	5.24E-01	-0.058	0.010	1.16E-08
rs7705526	TERT	5	1285974	C	A	-0.023	0.023	3.22E-01	-0.118	0.009	2.61E-38
rs7776744	POT1	7	124599749	G	A	-0.001	0.023	9.70E-01	-0.058	0.009	2.51E-10

SNP, single nucleotide polymorphism; Chr, chromosome; Ref allele, reference allele; EAF, effect allele frequency; Beta, SE, P-value, assocation with telomere length in Singaporean GWAS study. *indicates analysis conducted in Hong Kong Diabetes Registry. #indicates the extracted data from original GWAS study.

Table S9 the relationship between genetically determined telomere length and glycaemic progression defiend as insulin requirement.

	Outcome	Exposure	Method	No of SNPs	OR (95%CI)*	P value
1	Insulin requirement	Telomere length	MR Egger	10	1.541 (0.804-2.954)	0.229
2	Insulin requirement	Telomere length	Maximum likelihood	10	1.382 (1.016-1.878)	0.039
3	Insulin requirement	Telomere length	Weighted median	10	1.351 (0.903-2.021)	0.144
4	Insulin requirement	Telomere length	Weighted mode	10	1.223 (0.721-2.074)	0.474
5	Insulin requirement	Telomere length	Inverse variance weighted (multiplicative random effects)	10	1.384 (1.124-1.704)	0.002
6	Insulin requirement	Telomere length	Inverse variance weighted (fixed effects)	10	1.384 (1.020-1.879)	0.037

^{*} indicates odds for glycaemic progression per 1-unit decreased in genetically determined telomere length. Glycaemic progression was defined as the need for insulin requirement.

Table S10 the relationship between genetically determined telomere length and glycaemic progression defiend as actual insulin use.

	Outcome	Exposure	Method	No of SNPs	OR (95%CI)*	P value
1	Insulin use	Telomere length	MR Egger	10	1.264 (0.651-2.452)	0.509
2	Insulin use	Telomere length	Maximum likelihood	10	1.367 (0.999-1.870)	0.051
3	Insulin use	Telomere length	Weighted median	10	1.393 (0.913-2.127)	0.124
4	Insulin use	Telomere length	Weighted mode	10	1.640 (0.863-3.113)	0.165
5	Insulin use	Telomere length	Inverse variance weighted (multiplicative random effects)	10	1.374 (1.038-1.818)	0.026
6	Insulin use	Telomere length	Inverse variance weighted (fixed effects)	10	1.374 (1.006-1.876)	0.046

^{*} indicates odds for glycaemic progression per 1-unit decreased in genetically determined telomere length. Glycaemic progression was defined as the need for actual insulin use.

Table S11 Cox regression showing the association between rLTL calculated based on QC materials and glycaemic progression.

Variables	Unadjusted model		Fully adjusted model	
variables	HR (95% CI) P value		HR (95% CI)	P value
rLTL based on QC	1.113 (1.065-1.164)	< 0.001	1.083 (1.031-1.139)	0.002
Age at diagnosis (per 1 year)			0.970 (0.965-0.976)	< 0.001
Duration of diabetes (per 1 year)			1.020 (1.011-1.029)	< 0.001
Smoking				
Ex-smoker			1.247 (1.088-1.430)	0.002
Current smoker			1.155 (1.000-1.334)	0.050
log (triglyceride)			1.331 (1.051-1.686)	0.018
LDL-C			0.933 (0.883-0.984)	0.011
log urinary ACR			1.370 (1.259-1.492)	< 0.001
eGFR			0.991 (0.988-0.994)	< 0.001
Sensory neuropathy			1.265 (1.118-1.432)	< 0.001
Retinopathy			1.237 (1.094-1.399)	0.001
Use of oral glucose-lowering drugs			1.289 (1.148-1.448)	< 0.001
Use of lipid-lowering drugs			1.049 (0.901-1.221)	0.539
Use of RAS inhibitors			1.144 (0.996-1.314)	0.057

Table S12. Hazard ratio (95% CI) for glycaemic progression according to tertiles of rLTL.

Variables	Unadjusted mo	del	Fully adjusted model	
	HR (95% CI)	P value	HR (95% CI)	P value
Tertile 1	1.269 (1.131-1.424)	<0.001	1.091 (0.963-1.236)	0.170
Tertile 2	1.155 (1.027-1.298)	0.016	1.071 (0.946-1.212)	0.277
Tertile 3	Reference			
Age at diagnosis (per 1 year)			0.971 (0.966-0.976)	<0.001
Duration of diabetes (per 1 year)			1.021 (1.012-1.030)	<0.001
Smoking				
Ex-smoker			1.249 (1.089-1.431)	0.001
Current smoker			1.161 (1.006-1.340)	0.042
log (triglyceride)			1.318 (1.041-1.670)	0.022
LDL-C			0.936 (0.887-0.988)	0.017
log urinary ACR			1.379 (1.267-1.502)	<0.001
eGFR			0.991 (0.988-0.994)	<0.001
Sensory neuropathy			1.267 (1.119-1.434)	<0.001
Retinopathy			1.235 (1.092-1.396)	0.001
Use of oral glucose-lowering drugs			1.282 (1.141-1.440)	<0.001
Use of lipid-lowering drugs			1.041 (0.894-1.212)	0.605
Use of RAS inhibitors			1.148 (0.999-1.318)	0.051

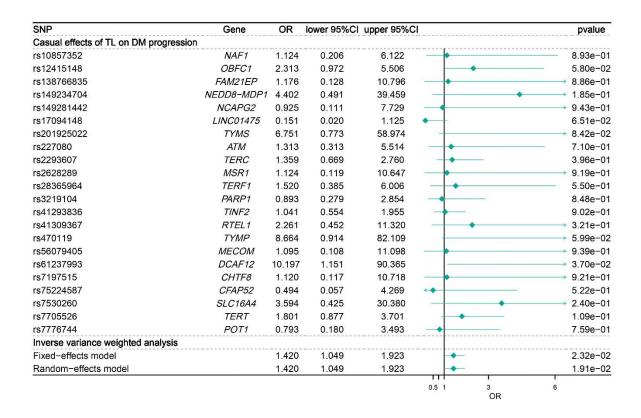


Figure S1. Odds ratio for glycaemic progression per 1-unit decreased in genetically determined relative leukocyte telomere length using 22 SNPs at significance <1*10⁻⁵.

SNP	Gene	OR	lower 95%CI	upper 95%C	1		pvalue
Leave-one-out for TL on DM pro	gression						
rs10857352	NAF1	1.394	1.022	1.902		*	3.62e-02
rs12415148	OBFC1	1.287	0.928	1.784	-	•	1.30e-01
rs227080	ATM	1.388	1.015	1.897		-	4.01e-02
rs2293607	TERC	1.390	0.991	1.950		•	5.68e-02
rs28365964	TERF1	1.377	1.007	1.884		-	4.53e-02
rs3219104	PARP1	1.430	1.042	1.963		-	2.69e-02
rs41293836	TINF2	1.511	1.065	2.142		-	2.06e-02
rs41309367	RTEL1	1.359	0.996	1.855		•	5.34e-02
rs7705526	TERT	1.306	0.932	1.831	-	•	1.21e-01
rs7776744	POT1	1.419	1.038	1.939		•	2.81e-02
ALL							
Fixed-effects model		1.384	1.020	1.879			3.71e-02
Random-effects model		1.384	1.124	1.704		-	2.21e-03
					05 075	1 15	1
					0.5 0.75	1 1.5 OR	2

Figure S2. Leave-one-out sensitivity analysis for the final instrument variable set. The solid lines represent 95% confidence intervals. Glycaemic progression was defined as need for insulin treatment.

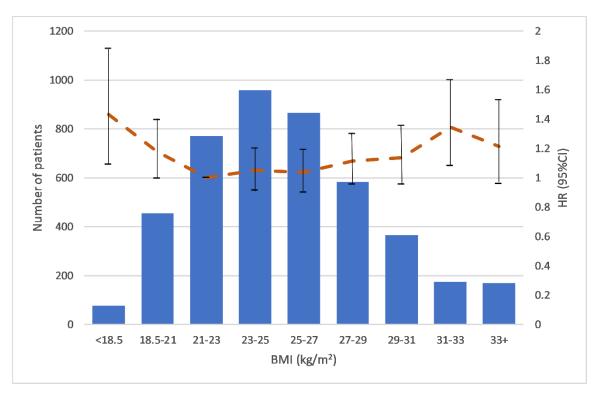


Figure S3 Association between BMI at baseline and progression to requirement of insulin treatment. Distribution of BMI and hazard ratios with BMI 21-23 kg/m² as the reference group.

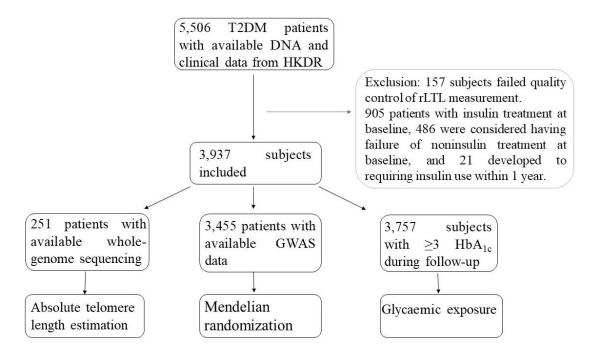


Figure S4. Flow diagram of patient selection

Abbreviation: T2DM, type 2 diabetes; HKDR, Hong Kong Diabetes Register; rLTL, relative leukocyte telomere length; GWAS, Genome-Wide Association Study.

Reference for supplementary

1. World Health Organization. The Asian-Pacific perspective: redefining obesity and its treatment, WHO Western Pacific Region, Geneva, Switzerland. 2000.