

Supplementary Table S1. Clinical characteristics of the exploratory and validation cohorts.

	Exploratory cohort	Validation cohort	p	Pooled cohort
N	75	39		114
Females (%)	58(77)	33(85)	0.127	91(80)
Age	50.42 ± 10.10	51.82 ± 11.39	0.509	50.53 ± 10.65
BMI	43.43 (41.02, 47.91)	45.97 (40.35, 48.41)	0.565	43.49 (41.01, 48.18)
T2D (%)	21(28)	17(44)	0.155	38(33)
Type of surgery				
SG (%)	27(36)	15(39)	>0.999	42(37)
RYGB (%)	45(60)	24(61)		69(60)
TBWL (%)	31.98 ± 7.97	29.15 ± 6.35	0.043	31.25 ± 7.72

Data are presented as the mean ± SD, median (95%CI) or number (%). BMI, body mass index; T2D, type 2 diabetes; SG, sleeve gastrectomy; RYGB, Roux-en-Y Gastric Bypass; TBWL, total body weight loss.

Supplementary Table S2. Clinical characteristics of non-obese and ex-obese subjects.

	non-Ob (n=17)	ex-Ob (n=18)
Sex (Female)	13 (62%)	16 (89%)
Age	60.81 ± 9.35	49.94 ± 11.87
Weight	73.87 ± 12.16	71.13 ± 7.84
Height	1.65 ± 0.11	1.64 ± 2.12
BMI	27.12 ± 2.55	26.37 ± 2.12
FPG	93 (84, 98)	81.19 ± 8.68
Hypertension	4 (19%)	0 (0%)
Total cholesterol	196.6 ± 35.88	169.0 ± 24.55
HDL	60.05 (55, 84)	55.88 ± 11.57
LDL	104.5 ± 33.53	97.25 ± 17.94
TG	98.23 ± 37.93	79.19 ± 22.07
AST	20.56 ± 6.74	20 (17, 29)
ALT	18 (14, 36)	21 (10, 38)
GGT	32.3 ± 14.21	10.5 (8, 27)

Data are presented as the mean ± SD, median (95%CI) or number (%). BMI, body mass index; FPG, fasting plasma glucose; HDL, serum high-density lipoprotein cholesterol; LDL, serum low-density lipoprotein cholesterol; TG, serum triglycerides; AST, serum aspartate aminotransferase; ALT, serum alanine aminotransferase; GGT, gamma-glutamyl transferase.

Supplementary Table S3. List of primers used in the study.

GENE	SEQUENCE	(5'-3')
ABCA1	F	GGAGGCCAGAATGACATCTTAG
ABCA1	R	TTTCCAGCCCCATTAACTCC
PLIN2	F	AGTATCCCTACCTGAAGTCTGTG
PLIN2	R	CCCCTTACAGGCATAGGTATTG
ADIPOQ	F	ACAATGACTCCACCTTCACAG
ADIPOQ	R	TTCTAACCCTACTGAAAGCC
ADIPOR1	F	TCATCTACCTCTCCATCGTCTG
ADIPOR1	R	CACTCAAGCCAAGTCCCAG
ADIPOR2	F	CAGCCATTATAGTCTCCAGTG
ADIPOR2	R	CCGAGATGACATAGTGCAAGG
ANGPT1	F	TTAAAGGACTTACAGGGACAGC
ANGPT1	R	GACCACATGCATCAAAACAC
ANGPT2	F	CCACGAGACTTGAACCTTCAGC
ANGPT2	R	TGTGCTTGTCTTCCATAGCTAG
ATG12	F	AATCAGTCTTTTGTCTCTCC
ATG12	R	GCAAGTTGATTTTCTTTGTGTTTC
ATG5	F	AGCAACTCTGGATGGGATTG
ATG5	R	AGGTCTTTCAGTCGTTGTCTG
ATG7	F	TTTTGCTACTCTGCCCTCTG
ATG7	R	GCTGTGACTCTTCTGTTGAC
ATGL	F	CACTTCACTCCAAGGACGAG
ATGL	R	CTCATAGAGTGGCAGGTTGTC
BGN	F	TGGAGAACAGTGGCTTTGAAC
BGN	R	GTTGTGGTCTAGGTGGAGTTTC
CD14	F	CAGAGGTTTCGGAAGACTTATCG
CD14	R	TTCCGAGAAAGTTGCAGACG
CD206 / MRC1	F	GCAAAGTGGATTACGTGTCTTG
CD206 / MRC1	R	CTGTTATGTCGCTGGCAAAATG
CD68	F	ATGGCGGTGGAGTACAATG
CD68	R	TGGACAGCTGGTGAAGAATG
COL1A1	F	CCCTCGGAAGAATGGAGATG
COL1A1	R	CATCCAAACCACTGAAACCTC
COL3A1	F	ATGGTGCTCTGGTAAGAATG
COL3A1	R	GGTCTGTGCTCTCTTTGTC
COL4A1	F	TGTGGATCGGCTACTCTTTTG
COL4A1	R	TAGTAATTGCAGGTCCCACG
COL5A1	F	TCGCTTACAGAGTCAACAAAG
COL5A1	R	GTTGTAGATGGAGACCAGGAAG
COL6A1	F	AGGAGTCAAGAGAGCAAAAGG
COL6A1	R	GCATTACAGCAAGAGCAC
COL6A3	F	AACCATTGGCTCTCACTGAAACA
COL6A3	R	GCACAGCTTTTGGTGTGGGA
DGAT2	F	TCCGAATGCCTGTGTTGAG
DGAT2	R	CAATAGTCTATGGTGTCCCGG
ELN	F	CCTGGCTTCGGATTGTCTC
ELN	R	CAAAGGGTTTACATTCTCCACC
F13A1	F	ATCCCATCAAAGTCAGCCG
F13A1	R	ATGTCAACGCTTCCAGTCC
FABP4	F	CATGTGCAGAAATGGGATGG
FABP4	R	AACCTCAGTCCAGGTCAACG
FASN	F	CAGAGTCGGAGAACTTGCAG
FASN	R	GGAGGCATCAAACCTAGACAG
FN1	F	GTGGCAGAAGGAATATCTCGG
FN1	R	GAGAATACTGGTTGTAGGACTGG
HAS1	F	CTTGTACAGCTACTTCCACTG
HAS1	R	CGGTCAATCCCAAAGTACAG
HAS2	F	CTCAATTTTGGAAACTGCCCG
HAS2	R	CTCAGGATACATAGAAACCTCTCAC
HIF1A	F	AAGAACTTTTAGGCCGCTCA
HIF1A	R	CAACCCAGACATATCCACCTC
HSL / LIPE	F	TCATCTCCATCGACTACTCCC
HSL / LIPE	R	AGATTGCTTCCCTGTTGAG
HYAL1	F	GATGGCTGTGGAGTTCAAATG
HYAL1	R	CCCAGAGTGCATTAGGTTCTC
HYAL2	F	TGTGAGCTTCCGTGTTGAG
HYAL2	R	CTCGCAATGGTATGAGATGAG
IL1B	F	GGTACATCAGCACCTCTCAAG
IL1B	R	CACATTCAGCACAGGACTCTC
IL6	F	CAACCTGAACCTTCAAAGATG
IL6	R	ACCTCAAACCTCAAAGACACAG
IRS1	F	TCTGCTCAGCGTTGGTG
IRS1	R	GTGCATGCTCTTGGGTTTG
ITGB2	F	CCCCAAGTTTGCTGAGAGTTAG
ITGB2	R	TGAGGGCGGAAAATAACTGG
KLB	F	CATGGGTATGGGACAGGTATG
KLB	R	TCTGATGTGGGCGGAAATG
LEP	F	GCTTCAGGCTACTCCACAG
LEP	R	CCTTCCCTTAACTAGTCTCTG
LEPR	F	TCAACCACTACAATCCAGTCAC
LEPR	R	TTTGGGCTCAGATATGGGATG

GENE	SEQUENCE	(5'-3')
LOX	F	ACATTGCTACACAGGACATC
LOX	R	TTCCCACTTCAGAACACCCAG
LOXL2	F	GTGCAGCGACAAAAGGATTG
LOXL2	R	GCGGTAGGTTGAGAGGATG
LOXL4	F	GTGGCAGAGTCAGATTCTCC
LOXL4	R	TTGTTCTGAGACGCTGTTTC
LPL	F	GGACTGAGAGTGAAACCCATAC
LPL	R	GGAAGGAGTAGGTCTTATTTGTGG
MCP1 / CCL2	F	CCTCCAGCATGAAAGTCTCTG
MCP1 / CCL2	R	TCTGCACTGAGATCTTCTATTG
MMP13	F	GGAATTGGTGATAAAGTAGATGCTG
MMP13	R	ACGCGAACAATACGGTTACTC
MMP14	F	GGATGGACACGGAGAATTITG
MMP14	R	TTTATCAGGAACAGAAGGCCG
MMP15	F	CCCAAGCCCATCAGGTTC
MMP15	R	CGCTCATTTGCGAATTTCCAG
MMP2	F	ACCCATTACACCTACACCAAG
MMP2	R	TGTTTGAGATCTCAGGAGTG
MMP9	F	CGAATTTGACAGCGACAAG
MMP9	R	CACTGAGGAATGATCTAAGCCC
MOGAT1	F	GAAAGCCATCCACACTGTTG
MOGAT1	R	GCCATACTTTCTTTGTGTTCC
MSR1	F	ATCTGTGAAATTTGATGCTCGC
MSR1	R	CCAATGAGAGGGATGAGAACTG
NPY1R	F	GATCTGAGCAGGAGAAATACCAG
NPY1R	R	CTGAATTTCTTCACTTGAAGTG
p16 / CDKN2A	F	GATGTCGACGGTACTCTG
p16 / CDKN2A	R	TCTCTGGTTCTTTCAATCGGG
P21 / CDKN1A	F	GAACCTCGACTTTGTCAACCGAGAC
P21 / CDKN1A	R	TGGAGTGGTAGAAATCTGTCATGCT
p53 / TP53	F	CAGCAGATGACGGAGGTTGT
p53 / TP53	R	TCATCCAAATCTCCACACGC
PAI-1 / SERPINE1	F	GTGGACTTTTCAGAGGTGGAG
PAI-1 / SERPINE1	R	GAAGTAGAGGGCATTACCCAG
PDGFRA	F	TTCTCTGCTGACATTGAC
PDGFRA	R	GTCTTCAATGGTCTCGTCTC
PDGFRB	F	ATGTGACGGAGAGTGTGAATG
PDGFRB	R	GCAGCTCAGCAAATGTAGTG
PLIN1	F	CATTGAGAAGGTGGTGGAGTAC
PLIN1	R	GTGTATCGAGAGAGGGTGTG
PLIN2	F	AGTATCCCTACCTGAAGTCTGTG
PLIN2	R	CCCCTTACAGGCATAGGTTATTG
PPARG	F	GTCCGTTTCAGAAATGCCTTG
PPARG	R	GCTGGTCGATCACTGGAG
PPARGC1A / PGC1A	F	CAGGCAGTAGATCTCTTCAAG
PPARGC1A / PGC1A	R	TCCTCGTAGCTGTACATCTG
RPL6 F	F	CTTAAATCTCTTCCCATCTTGC
RPL6 R	R	TTCTTGGCTTCGGGTTTCTT
SLC2A1 / GLUT1	F	TCATCGTGGCTGAATCTTC
SLC2A1 / GLUT1	R	GATGAAGACGTAGGGACACC
SLC2A4 / GLUT4	F	ACTGGACGAGCAACTTCATC
SLC2A4 / GLUT4	R	GAGGACCGCAAATAGAAGGAA
SREBF1	F	TTCTGACAGCCATGAAGACAG
SREBF1	R	CCGCATCTACGAACTG
TCF21	F	ATACGAGAACGGGTACATTAC
TCF21	R	CTCGCTCCAGGTACCAAC
TGFB1	F	ITGATGTCACCGGAGTTGTG
TGFB1	R	GTAGTGAACCCGTTGATGTC
TIMP1	F	CCCCTAGCGTGGACATTTATC
TIMP1	R	AACAGGATGCCAGAAGCC
TIMP2	F	CCCTCTGTGACTTCACTCGT
TIMP2	R	GAGATGTAGCAGCGGATCATG
TIMP3	F	CCTTCTGCAACTCCGACATC
TIMP3	R	GCCTCGGTACATCTTCATCTG
TNFA	F	AGGTCTACTTTGGGATCATTGC
TNFA	R	GAAGAGGTTGAGGGTGTCTG
UCP1	F	GGACTACTCCCAATCTGATGAG
UCP1	R	AAATCCAGCGATAAGAGCCG
UCP2	F	TCCTGAAAGCCAACTCATG
UCP2	R	GGCAGAGTTCACTGTATCTGTC
UCP3	F	AGAAAATACAGCGGGACTATGG
UCP3	R	CTTGAGGATGTCGTAGGTCAC
VEGFA	F	AGTCCAACATCACCATGCAG
VEGFA	R	TTCCCTTTCTCGAACTGATT
VEGFB	F	CTTAGAGCTCAACCCAGACAC
VEGFB	R	ACCTGCTGAGTCTGAAAAG
VEGFR1	F	TCCTCAACCTACAATCAAGTG
VEGFR1	R	GCTCTCAATTTCTTTCCCATG
VEGFR2	F	CATTTCAAAGGAGAAGCAGAGC
VEGFR2	R	GAGGAATGGCATAGACCGTAC

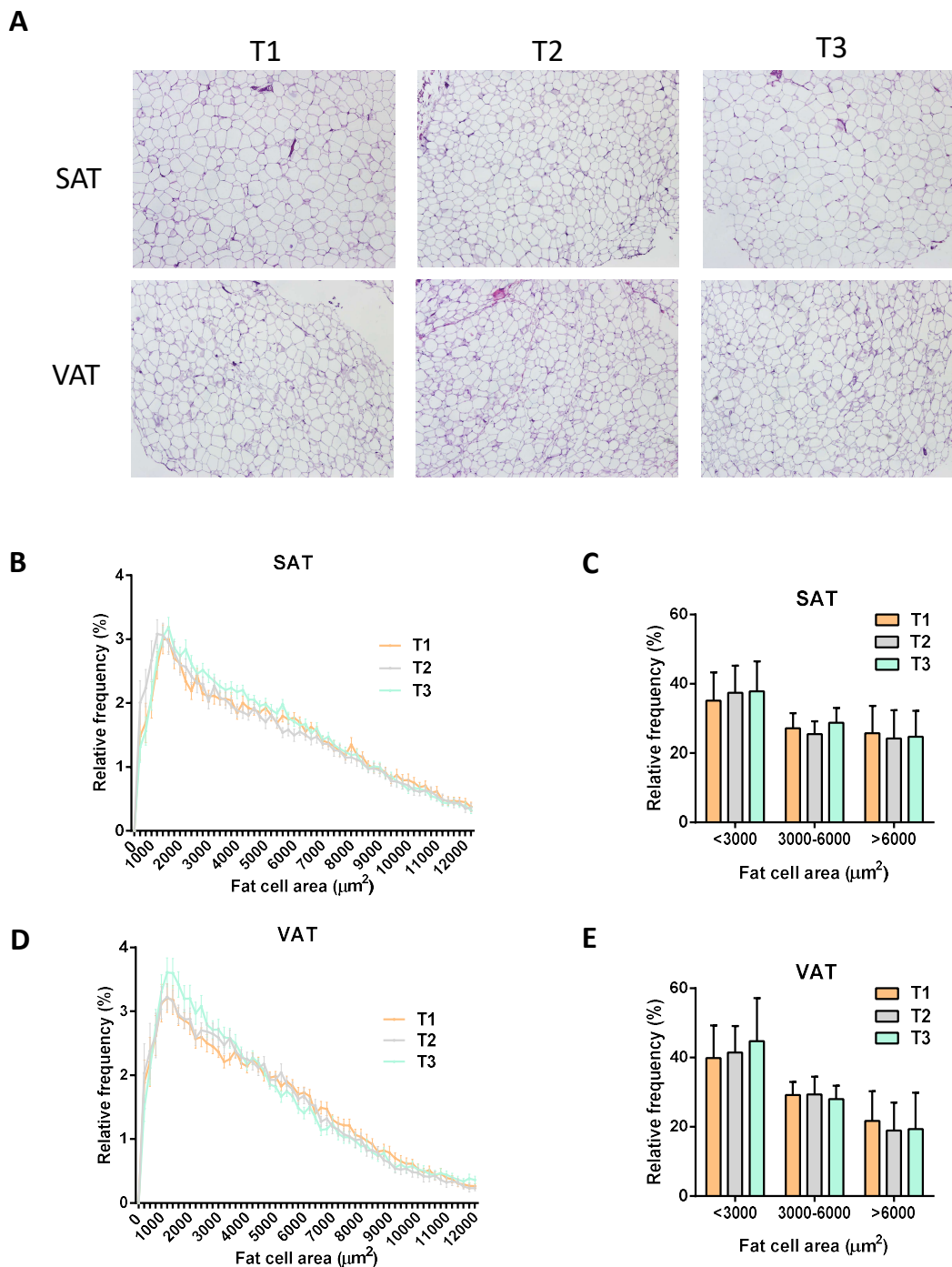
F, forward; R, reverse.

Supplementary Table S4. Summary of multivariate regression models predicting TBWL.

Model	Predictor	β	SE	95% CI	p	Adjusted R ²	p
1	Constant	29.394	1.539	(26.35, 32.44)	<0.001	0.134	<0.001
	Type of BS	4.387	1.365	(1.69, 7.09)	0.002		
	Age	-0.128	0.061	(-0.25, -0.01)	0.038		
	Sex	-0.045	1.369	(-2.75, 2.66)	0.974		
	BMI	0.079	0.125	(-0.17, 0.33)	0.529		
	T2D	-2.543	1.347	(-5.21, 0.12)	0.061		
2	Constant	25.888	2.085	(21.75, 30.03)	<0.001	0.228	<0.001
	Type of BS	6.689	1.749	(3.21, 10.17)	<0.001		
	Age	-0.192	0.075	(-0.34, -0.04)	0.012		
	Sex	1.595	1.619	(-1.62, 4.81)	0.327		
	BMI	0.06	0.153	(-0.25, 0.37)	0.697		
	T2D	-1.614	1.567	(-4.73, 1.5)	0.306		
	COL1A1	-5.501	1.909	(-9.3, -1.71)	0.005		
3	Constant	26.41	2.048	(22.33, 30.49)	<0.001	0.306	<0.001
	Type of BS	5.424	1.827	(1.79, 9.06)	0.004		
	Age	-0.146	0.076	(-0.3, 0.01)	0.059		
	Sex	2.293	1.593	(-0.88, 5.47)	0.154		
	BMI	0.145	0.155	(-0.16, 0.45)	0.353		
	T2D	-1.659	1.542	(-4.73, 1.41)	0.286		
	COL5A1	-24.732	5.58	(-35.84, -13.62)	<0.001		
4	Constant	27.128	1.791	(23.57, 30.69)	<0.001	0.301	<0.001
	Type of BS	6.015	1.603	(2.83, 9.2)	<0.001		
	Age	-0.167	0.069	(-0.3, -0.03)	0.018		
	Sex	1.434	1.48	(-1.51, 4.38)	0.335		
	BMI	0.095	0.142	(-0.19, 0.38)	0.503		
	T2D	-2.301	1.437	(-5.16, 0.56)	0.113		
	COL6A3	-12.712	2.741	(-18.16, -7.26)	<0.001		

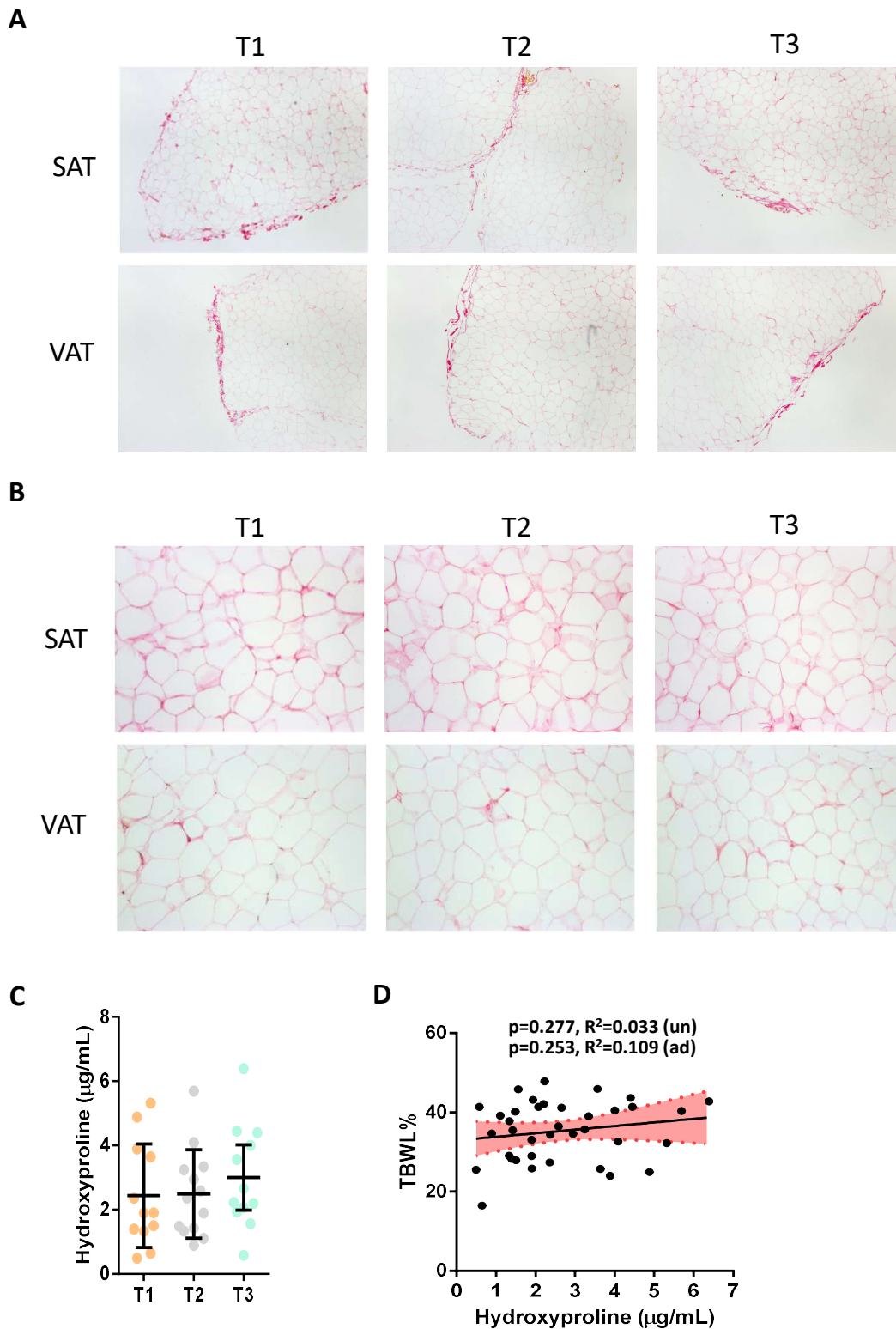
Type of BS: 0-SG, 1-GBP; sex: 0-male; 1-female; T2D: 0-no; 1-yes. β : Beta coefficient; SE: standard error; CI: confidence interval.

Supplementary Figure S1. Adipocyte size distribution across weight loss tertiles.



A: Representative images of hematoxylin and eosin staining of SAT and VAT samples among TBWL tertile groups. B, C: Frequency distribution analysis of fat cell areas divided by size into bin intervals of 200 μm^2 (B) and three representative sizes in SAT (C). D, E: Frequency distribution analysis of fat cell areas divided by size into bin intervals of 200 μm^2 (D) and three representative sizes in VAT (E). Data are presented as the mean \pm SD.

Supplementary Figure S2. Adipose tissue fibrosis across weight loss tertiles.



A, B: Representative images of Sirius red staining showing total (A) and pericellular fibrosis (B) in SAT and VAT samples among TBWL tertile groups. C: Determination of SAT hydroxyproline residues in TBWL tertiles. Data are presented as the mean \pm SD. D: Regression analysis between hydroxyproline concentration in SAT and TBWL%. Simple linear regression (solid line) and 95% confidence interval (dashed lines) are shown. P-values are unadjusted (un) or adjusted for sex, age, baseline BMI, T2D and type of surgery (ad).