Table S1 (related to Figure 1D): List of cell surface markers highly expressed in Type III cell population (top 20).

	Gene Symbol	Description	Signal to Noise (Type III to rest)
1	*Cd63*	CD63 antigen	0.3695
2	*Cd81*	CD81 antigen	0.3528
3	*Ncam1*	neural cell adhesion molecule 1	0.3494
4	*Tnfrsf12a*	tumor necrosis factor receptor superfamily, member 12a	0.3245
5	*Psmb6*	proteasome (prosome, macropain) subunit, beta type 6	0.3115
6	*Itga5*	integrin alpha 5 (fibronectin receptor alpha)	0.28
7	*Ifitm1*	interferon induced transmembrane protein 1	0.2591
8	*Lamp2*	lysosomal-associated membrane protein 2	0.2534
9	*Bst2*	bone marrow stromal cell antigen 2	0.2195
10	*Rae1*	ribonucleic acid export 1	0.217
11	*Icosl*	icos ligand	0.2119
12	*Il15ra*	interleukin 15 receptor, alpha chain	0.1931
13	*Gstm7*	glutathione S-transferase, mu 7	0.1925
14	*Tnfsf8*	tumor necrosis factor (ligand) superfamily, member 8	0.1925
15	*Cxcr6*	chemokine (C-X-C motif) receptor 6	0.1925
16	*Mfi2*	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	0.1859
17	*Krt20*	keratin 20	0.183
18	*Abcg2*	ATP-binding cassette, sub-family G (WHITE), member 2	0.1781
19	*Pdgfra*	platelet derived growth factor receptor, alpha polypeptide	0.1742
20	*Cd59a*	CD59a antigen	0.1719

Table S2 (related to Table 1): Baseline characteristics of study participants (n=28).

Characteristic	Value
Age (years)	50 ± 11
Men	48 ± 12
Women	52 ± 10
Gender, n (%)	
Men	12 (43%)
Women	16 (57%)
Body mass index (kg/m^2)	36 ± 10
Fat mass (kg)	41 ± 13
Percentage body fat (%)	39 ± 7
Lean mass (kg)	55 ± 15
VAT mass (kg)	0.79 ± 0.39
%VAT/FM	2.1 (1.2 - 2.8)
Diabetes, n (%)	11 (39%)
Fasting glucose (mg/dL)[a]	129 ± 43
Fasting Insulin (mIU/L)[a]	27 ± 115
HOMA-IR[a]	10 ± 8
Triglycerides (mg/dL)	183 ± 226
Total cholesterol (mg/dL)	192 ± 52
LDL cholesterol (mg/dL)	105 ± 37
HDL cholesterol (mg/dL)	51 ± 14
DBP (mmHg)	84 ± 12
SBP (mmHg)	131 ± 11

Data are presented as mean ± SD or median (IQR).

[a] Insulin-treated patient (n = 1) was excluded from the analysis.

VAT: visceral adipose tissue; FM: fat mass; DBP: diastolic blood pressure; SBP: systolic blood pressure. HOMA-IR = Fasting insulin (mIU/L) x [fasting blood glucose (mg/dL)/405].

Table S3 (related to STAR methods): Primer sequences used for quantitative RT-PCR.

Gene	Forward	Reverse
Acta2	GTCCCAGACATCAGGGAGTAA	TCGGATACTTCAGCGTCAGGA
Adipoq	GCACTGGCAAGTTCTACTGCAA	GTAGGTGAAGAGAACGGCCTTGT
Adrb1	CCGAAAGCAGGTGAATGCAA	AGCCAGTAAGCCATACTAAGCCACA
Adrb2	CATTGATGTGTTGTGCGTCA	ACTCGGGCCTTATTCTTGGT
Adrb3	CCTTCCGTCGTCTTCTGTGT	AGCCATCAAACCTGTTGAGC
Cd11c (Itgax)	AAAATCTCCAACCCATGCTG	CACCACCAGGGTCTTCAAGT
Cd36	TGCATTTGCCAATGTCTAGC	CCCTCCAGAATCCAGACAAC
Cd81	TCTACGTGGGCATCTACATTCT	ATCCTTGGCGATCTGGTCTTT
Cd206 (Mrc1)	CAAGGAAGGTTGGCATTTGT	CCTTTCAGTCCTTTGCAAGC
Cidea	ATCACAACTGGCCTGGTTACG	TACTACCCGGTGTCCATTTCT
Col1a1	GCTCCTCTTAGGGGCCACT	CCACGTCTCACCATTGGGG
Col3a1	CTGTAACATGGAAACTGGGGAAA	CCATAGCTGAACTGAAAACCACC
Col6a1	CTGCTGCTACAAGCCTGCT	CCCCATAAGGTTTCAGCCTCA
Col6a3	GCTGCGGAATCACTTTGTGC	CACCTTGACACCTTTCTGGGT
Cox7a	CAGCGTCATGGTCAGTCTGT	AGAAAACCGTGTGGCAGAGA
Cox8b	GAACCATGAAGCCAACGACT	GCGAAGTTCACAGTGGTTCC
Dio2	CAGTGTGGTGCACGTCTCCAATC	TGAACCAAAGTTGACCACCAG
Elovl3	TCCGCGTTCTCATGTAGGTCT	GGACCTGATGCAACCCTATGA
F4/80 (Adgre1)	TTTCCTCGCCTGCTTCTTC	CCCCGTCTCTGTATTCAACC
Il6	CTGATGCTGGTGACAACCAC	TTTTCTGCAAGTGCATCATCGT
Itgb2	AGGAGCATCGCTAATCCTGAG	CCTGGTCGCAAGTAAAGTGTC
Kcnk3	ACGGAGGCAAGGTGTTCTG	ACGACACGAAACCGATGAGC
Loxl2	ATTAACCCCAACTATGAAGTGCC	CTGTCTCCTCACTGAAGGCTC
Mcp1 (Ccl2)	ATGCAGGTCCCTGTCATGCTT	GGCATCACAGTCCGAGTCACAC
Myh11	GAGCAAACTCAGGAGAGGAAAC	GTCCCGAGCGTCCATTTCTTC
Myl9	ACAGCGCCGAGGACTTTTC	AGACATTGGACGTAGCCCTCT
Pgc1a	AGCCGTGACCACTGACAACGAG	GCTGCATGGTTCTGAGTGCTAAG
Pparg	GCATGGTGCCTTCGCTGA	TGGCATCTCTGTGTCAACCATG
Prdm16	GGCGAGGAAGCTAGCCAAA	GGTCTCCTCCTCGGCACTCT
Sm22	CAACAAGGGTCCATCCTACGG	ATCTGGGCGGCCTACATCA
Tgfb1	CTCCCGTGGCTTCTAGTGC	GCCTTAGTTTGGACAGGATCTG
Tnfa	ACACTCAGATCATCTTCTCAAAATTCG	GTGTGGGTGAGGAGCACGTAGT
Ucp1	CACCTTCCCGCTGGACACT	CCCTAGGACACCTTTATACCTAATGG
Tbp	ACCCTTCACCAATGACTCCTATG	TGACTGCAGCAAATCGCTTGG
36B4	TCCAGGCTTTGGGCATCA	CTTTATCAGCTGCACATCACTCAGA
Hprt	TCAGTCAACGGGGGACATAAA	GGGGCTGTACTGCTTAACCAG