

Supplemental Table 1. Basic characteristics of type 2 diabetic obese patients and controls (mean±SD)

	Age	Gender (M/F)	Weight (kg)	Height (cm)	BMI (kg/m ²)	FPG (mmol/L)	HbA1C (%)
IS (n=5)	56±6.51	2/3	62.5±6.59	160.8±9.1	24.18±1.55	5.22±0.82	4.96±0.12
IRO (n=5)	34.4±11.31	3/2	110.34±22.21	165.6±5.3	40.24±8.18**	7.02±1.47	6.8±0.86**

FPG: fasting plasma glucose, Data represent mean ±SD. **P value<0.01 vs. control group.

Supplemental Table 2. Summary of primer sequences used for RT-qPCR

Gene (Mouse)	Sequence
36B4	Forward: 5' AAG CGC GTC CTG GCA TTG TCT 3' Reverse: 5' CCG CAG GGG CAG CAG TGG T 3'
TYROBP	Forward: 5' CCC AAG ATG CGA CTG TTC TTC 3' Reverse: 5' GTC CCT TGA CCT CGG GAG A 3'
CSF1R	Forward: 5' GAC CCT GAA TCT CCC GGA AG 3' Reverse: 5' GGT ACA ACG GTA GGT CCC AG 3'
C1QC	Forward: 5' GGA CGG GCA TGA TGG ACT C 3' Reverse: 5' TTC TGT TTG TAT CGG CCC TCC 3'

Gene (human)	Sequence
18srRNA	Forward: 5' GTA ACC CGT TGA ACC CCA TT 3' Reverse: 5' CCA TCC AAT CGG TAG TAG CG 3'
TYROBP	Forward: 5' ACT GAG ACC GAG TCG CCT TAT 3' Reverse: 5' ATA CGG CCT CTG TGT GTT GAG 3'
CSF1R	Forward: 5' GGG AAT CCC AGT GAT AGA GCC 3' Reverse: 5' TTG GAA GGT AGC GTT GTT GGT 3'
C1QC	Forward: 5' AGG ATG GGT ACG ACG GAC TG 3' Reverse: 5' GTA AGC CGG GTT CTC CCT TC 3'

Supplemental Table 3: 30 commonly expressed DEGs screened with the criterion of adjust P value < 0.05.

Dataset	GSE26637		GSE55200		GSE27951	
	adj.P.Val	logFC	adj.P.Val	logFC	adj.P.Val	logFC
AGPAT9	0.04519139	-1.9928709	0.00240209	-1.7607205	0.0078735	-2.59138
AZGP1	0.00472905	-2.6933204	0.000057	-1.2010294	0.0191697	-1.5627873
C1QC	0.00704368	1.68620184	0.00105074	1.30892911	0.00915404	1.34165792
CD14	0.02903238	1.4717209	0.00018284	1.2502385	0.00869382	1.60174306
CD163	0.0423012	1.55662533	0.00025533	1.92441829	0.00439782	1.5551218
CHI3L1	0.01728097	1.35174399	0.00175412	2.38142797	0.01040376	1.28393556
CPA3	0.00470132	2.8103774	0.00988517	1.09096226	0.0234259	1.24048682

CSF1R	0.04967523	1.22549938	0.00186747	1.06269301	0.00566927	1.19298158
CTSS	0.00868886	2.21366745	0.00073858	1.95602201	0.01062991	1.13945304
EGFL6	0.01797568	5.94188898	0.0000335	4.25984323	0.00135512	5.76999774
F13A1	0.00731403	1.92333973	0.00105466	1.58685523	0.00566927	1.94490756
GLIPR1	0.00806924	1.82056229	0.00011768	1.81202707	0.02374759	1.0217565
GPR137B	0.00039253	2.59188921	0.00063175	1.31125336	0.00642285	1.10709188
GPR183	0.0094948	1.99241317	0.00030686	1.59054317	0.01093567	1.1326671
HPGDS	0.02304208	1.65643333	0.0075545	1.39060375	0.00419154	1.11175674
LYZ	0.00256153	2.07844913	0.0000335	2.33646229	0.01975614	1.20754834
MMP9	0.00425476	3.60589158	0.00045118	2.78054382	0.0191697	1.04911908
MPEG1	0.01102319	2.09934075	0.00108424	1.28821919	0.00391054	1.601917
MRC1	0.04861885	1.6869311	0.00105245	1.4993624	0.00363163	1.78570942
MS4A4A	0.00459704	2.43189743	0.01654572	1.26916719	0.00536005	1.5622467
MS4A6A	0.00980783	1.68148543	0.00152616	1.35482459	0.00306827	1.27517444
NCF4	0.01890602	1.10276741	0.00069763	1.0431129	0.00364892	1.27080062
RASSF2	0.01042758	1.89963848	0.0000366	1.45417735	0.02702299	1.04251308
RNASE6	0.00301195	1.70196547	0.00272933	1.06711815	0.00364892	1.5035469
SFRP4	0.01697967	2.98620636	0.00066859	2.08400676	0.01040376	1.69665736
SIGLEC1	0.00961541	1.15186016	0.00062177	1.14549075	0.00364892	1.1222956
SLIT2	0.00384933	1.2495788	0.00000363	1.41701056	0.00569882	1.03757892
TNMD	0.00473808	2.16296092	0.00077847	1.82611576	0.02066304	1.30645022
TYROBP	0.00425476	2.25225615	0.00025359	1.96352148	0.01040376	1.52437288
VSIG4	0.01342969	2.50974512	0.00037849	1.77386698	0.00442355	1.70864357

Supplemental Table 4: The 15 top common expressed DEGs across three datasets measured by three degrees in Cytoscape.

Rank	Name	Degree Score	Closeness Score	MNC Score
1	TYROBP	17	17.5	17
2	CSF1R	16	15.5	13
2	C1QC	16	15	12
4	CD163	11	15	12
5	MS4A6A	10	14	10
5	VSIG4	10	14	10
7	CD14	9	13.5	9
7	MRC1	9	13.5	9
9	F13A1	8	13	8
9	MS4A4A	8	13	8
9	SIGLEC1	8	13	8
12	MMP9	7	12.5	7
12	LYZ	7	12.5	7
12	CTSS	7	12.5	7
15	RNASE6	5	11.5	5

Supplemental Table 5 Node genes measured in three indexes of genes in module A

Gene	Betweenness	Closeness	Degree
CSF1R	3.22857	9.5	12
TYROBP	2.37619	10	10
C1QC	2.37619	10	10
VSIG4	1.79048	9.5	10
CD14	1.55714	9.5	9
MRC1	1.30476	9	9
F13A1	0.98571	9	8
SIGLEC1	0.98571	9	8
MS4A6A	1.01905	8.5	8
CD163	1.10476	8.5	7
MS4A4A	1.27143	8.5	7

Supplemental Figure 1 :Downregulation of hub genes in IS improving weight-maintenance phase in GSE35411(*P value< 0.05).

