

Supplementary Table S1. Specifically designed primers used in this study to measure human transcripts by quantitative PCR-based microfluidic assays, including 72 adipokines, 37 inflammasome components, and three internal reference-housekeeping genes (IRGs). Official name of the genes, primers sequences, sizes of the amplification products, and gene IDs are included.

Class	Gene	Sequence	Size (pb)	ID
ADIPOKINES	ACP5	CAGATCCTGGGTGCAGACTT GCGGTCAGAGAATACGTCCT	117	54
	ADIPOQ	AATCCAAGGCAGGAAAGGAG GTAAAGCGAATGGGCATGTT	111	9370
	ANGPTL2	AATGCGGGTGACTCCTTTAC GGTAGTGGGCACAGTTTCCT	94	23452
	ANGPTL4	AGGCTCAGAACAGCAGGATC AGTCTGGCTTTCAGATGCT	104	51129
	APLN	CCAGAGGGTCAAGGAATGGG TGGGTCCCTTATGGGAGAGG	90	8862
	AZGP1	GAATGGAGGATTGGAAGCAG GAGACCCGTTACTGTCGTTGT	108	563
	CCN4	AGGGAAGAAGTGTCTGGCTGT ACCTATTGTCCATGCAAACTCC	119	8840
	CFD	GGAAGGTGCAGGTTCTCCT TGTAGCAGCAGGAGGTCGT	136	1675
	CLU	ATGTTCCAGCCCTTCCTTG TCATCGTCGCCTTCTCGT	116	1191
	DPP4	TCCATATCCAAAGGCAGGAG AGAAGCAGGAGCAGTGATTG	115	1803
	FABP1	GCAGAGCCAGGAAAACCTTG CGTTGAGTTCGGTCACAGAC	290	2168
	FABP4	CAGGAAAGTCAAGAGCACCA TCCACCACAGTTTATCATCC	117	2167
	FABP5	CCCTGGGAGAGAAGTTGAAG CACTCCTGATGCTGAACCAA	97	2171
	FGF21	ATCGCTCCACTTGGACCTG GGGCTTCGGACTGGTAAACA	83	26291
	FNDG5	CAGGTGTCATTGCCCTCTTC GCTCTGGTGTGCTGGTTCT	108	252995
	ITLN1	CGGTGATCCTGTGGTCTAT GAACAAATCCCGCAGTGAAT	96	55600
	LCN2	CAGGACTTTTGTCCAGGTTG ATGCTGGTTGTAAGTTGGTGCT	115	3934
	LEP	GGAAGGAGTGGGAAAACCAAAG CCAAGCAATAAGATGGAAGAGG	126	3952
	MIF	AGAACCGCTCCTACAGCAAG CCGCGTTCATGTCGTAATAGT	99	4282
	NAMPT	TCTTTACATAGGACGCCAGCA TGTCACCTTGCCATTCTTGA	114	10135
	NGF	CAACAGGACTCACAGGAGCA GTCTGTGGCGGTGGTCTTAT	115	4803
	NUCB2	CAAGTGATTGATGTGCTGGAA CTTTGCTTAGCTCCCACTCT	94	4925
	RARRES2	ATGGGAGGAAACGGAAATG CCGCAGAACTTGGGTCTCTA	101	5919
	RBP4	TGAATAACTGGGACGTGTGC TGGAGAAAGGAGGCTACGC	103	5950
	RETN	TGCAGGATGAAAGCTCTCTG CCTCCTGGATCCTCTCATTG	109	56729
	SFRP5	TGCTCCAGTGACTTTGTGGT TTTTTCTGGGCTCCAATCAG	86	6425
	SPPI	TTTCGACAGCTGACATCC ATGGCCTTGTATGCACCATT	95	6696
	WNT5A	TCTTGGTGGTCGCTAGGTATG TGGCACAGTTTCTTCTGTCT	119	7474
	CCL2	CCCCAGTCACCTGCTGTTAT AGCTTCTTTGGGACACTTGCT	101	6347
	CCL3	TGCAACCAGTTCTCTGCATC GCTGCTCGTCTCAAAGTAGTCA	114	6348
	CCL5	TCGCCACATCAAGGAGTATT CCCGAACCATTCTTCTCT	116	6352
	CCL7	TCCCCGGGAAGCTGTAATCT GGGTTTCTTGTCAGGTGC	107	6354
	CCL8	ACACAAGAATCACCAACATCCA AATCCCTGACCCATCTCTCC	105	6355
	CCL11	TCAGCGACTAGAGAGCTACAGG TCCTGCACCACTTCTTGTT	120	6356
	CXCL1	CACCCCAAGAATCCAAAG GATGCAGGATTGAGGCAAG	113	2919
	CXCL2	TTGTCTCAACCCGCATC GCTTCTCTTCTTCTTGTT	92	2920

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<i>CXCL3</i>	AACCGAAGTCATAGCCACACTC GTGGTGCTCCCCTGTTC	109	2921
<i>CXCL5</i>	TCTGCAAGTGTTCGCCATAG TTTAGAAAAGGGGCTTCTGGA	105	6374
<i>CXCL8</i>	CTGTGTGAAGGTGCAGTTTTG GGTGGAAAGGTTGGAGTATGT	82	3576
<i>CXCL10</i>	GCTGTACCTGCATCAGCATTAG ACGTGGACAAAATTGGCTTC	92	3627
<i>CXCL12</i>	CCAACGTCAAGCATCTCAA CCACTTTAGCTTCGGGTCAA	110	6387
<i>CXCL16</i>	GCCCTTTCCTATGTGCTGTG CTTCCATTCTTGGCTCAGGT	119	58191
<i>IL1B</i>	TGGCAATGAGGATGACTTGTT TGGTGGTCGGAGATTTCGT	120	3553
<i>IL1R1</i>	CTGGAGGCTGATAAATGCAAG GGTTAAGAGGACAGGGACGA	91	3554
<i>IL3</i>	AACCTGGAGGCATTCAACAG CAGACATGGCAGGAGATTTT	87	3562
<i>IL4</i>	CAGACACACAGGCACCATCT TTCTCTCTGGGCTTTGTAGGC	80	3565
<i>IL6</i>	GGCAGAAAACAACCTGAACCT CTCAAACCTCCAAAAGACCAGTGA	115	3569
<i>IL10</i>	GTTTTCCCTGACCTCCCTCT GCTCCCTGGTTTCTCTTCCT	91	3586
<i>IL11</i>	AGCTGCAAGGTCAAGATGGT TGGCGTTCATCCACAGATG	115	3589
<i>IL12A</i>	CCTCTTTTATGATGGCCCTGT GCTTTGCATTCATGGTCTTG	87	3592
<i>IL15</i>	AGAAGCCAACCTGGGTGAATG TGCAACTGGGGTGAACATC	113	3600
<i>IL16</i>	CTGCTGAAACATCTGCCTTG CCCCATCATCGTCTTCCTT	102	3603
<i>IL17A</i>	GCAATGAGGACCCTGAGAGA GGGGACAGAGTTCATGTGGT	110	3605
<i>IL18</i>	CCAAGGAAATCGGCCTCT CCATACCTCTAGGCTGGCTATC	113	3606
<i>IL21</i>	TGGTCAGCTTTTCTCTGCTT GCATTTGTGGAAGGTGGTTT	119	59067
<i>IL22</i>	ATATCACCAACCGCACCTTC GCGCTCACTCATACTGACTCC	113	50616
<i>IL23A</i>	TTCTCTGCTCCCTGATAGCC GACTGAGGCTTGGAATCTGC	116	51561
<i>IL33</i>	GGTGACGGTGTGATGGTAA TGGCAGTGGTTTTTCACACT	120	90865
<i>LIF</i>	CCGCATAGTCGTGTACCTTG CGTTGAGCTTGCTGTGGA	98	3976
<i>OSM</i>	CAGGATTGGAGAGGTCTGG GGCCATGCAGTAGATGTTGTT	102	5008
<i>CCR1</i>	TGAGCAGAGCAGACATTTGG AGGCGTAGATCACTGGGTTG	89	1230
<i>CCR3</i>	TGTCTCGTTCTCCCTCTGCT CCGGATGGCCTTGACTTT	99	1232
<i>CCR5</i>	GATAGTCATCTTGGGGCTGGT CCTGTGCCTCTTCTTCTATT	106	1234
<i>CXCR1</i>	CTGGGAAATGACACAGCAA GGGTGAATCCATAGCAGAACA	106	3577
<i>CXCR2</i>	TGGGCAACAATACAGCAAAC GGGTGAATCCGTAGCAGAAC	105	3579
<i>IL1RN</i>	GGAAGATGTGCCTGTCTCTGT CGCTTGTCTGCTTCTGTT	103	3557
<i>IL4R</i>	TGTGTCCCCAGAGAAATGTG TGTGTCCCCAGAGAAATGTG	81	3566
<i>IL6R</i>	AAGGCTGTGCTCTTGGTGAG TGGGACTCCTGGGAATACTG	83	3570
<i>IL6ST</i>	ACAGATGAAGGTGGGAAGGA AAGCAAACAGGCACGACTATG	95	3572
<i>IL18R1</i>	CGACCTGAAAATGGAGAGGA ACAGCTCCTCCAGGCACTAC	119	8809
<i>LIFR</i>	CATCATCAGCGTAGTGGCTAAA CCTTTCCCATCCCAACAAC	116	3977
<i>OSMR</i>	GTGAGGCAAGTCAAGGAAATG TGAAGTCCTCGGTTTCACAA	108	9180
<i>TNF</i>	AGCCCATGTTGTAGCAAACC GCTGGTTATCTCTCAGCTCCAC	104	7124
<i>HMGB1</i>	GGCCTTCTTCTCTTCTGCT TTTCTTCGCAACATCACAA	85	3146
<i>S100A4</i>	AGCTTCTTGGGAAAAGGAC CTTCTGGGCTGCTTATCTG	171	6275
<i>S100A6</i>	AGCACACCCTGAGCAAGAAG AGTTCACCTCCTGGTCCTTGT	132	6277
<i>S100A8</i>	GTTGACCGAGCTGGAGAAAAG CCTGTAGACGGCATGGAAAT	91	6279

IRGs

<i>S100A9</i>	CAAAGAGCTGGTGCAGAAA GCTTGTCTGCATTGTGTCC	107	6280
<i>S100A10</i>	AAATTCGCTGGGATAAAGG CAGCCAGAGGGTCTTTTGA	103	6280
<i>CTSD</i>	CTGCACAAGTTCACGTCCAT GGGCGTCCATGTAGTTCTTG	157	1509
<i>CTSK</i>	AAGGTGGATGAAATCTCTCGGC CAGGTGGTTCATAGCCAGTTCA	117	1513
<i>CTSL</i>	AGCCCAACAAGAACCACACT AAAACCGTAAGCCCAGGAA	134	1514
<i>CTSS</i>	GCGTCATCCTTCTTTCTTCCT TCACCATAGCCAACCACAAG	99	1520
<i>CTSZ</i>	GGGAGAAGATGATGGCAGAA CATAGATGCCTCCGGTGTAGT	96	1522
<i>TNFRSF10D</i>	AGGGCAGAGCAGGTGTTTATC AGTCGGCAACCATTTACACA	96	8793
<i>P2RX7</i>	GACACCGCAGACTACACCTTC GTGGGATACTCGGGACACA	107	387298
<i>TLR1</i>	TGCCACCCTACTGTGAACCT GGTGTCTCAACCCAGAAAT	117	7096
<i>TLR2</i>	CTTCTGGAGCCCATTGAGAA CCAGGTAGGTCTTGGTGTTC	82	7097
<i>TLR4</i>	CCTTTCCAGCAACAAGATTCA AAGTTCATAGGGTTCAGGGACA	108	7099
<i>TLR8</i>	CCTGGCTCACCATTGTGTTT TTGGGATGTGGAAAGAGACC	94	51311
<i>TLR9</i>	TACCTTGCCTGCCTTCCTAC AAGTGGGGCACAGACTTCA	87	54106
<i>CHUK</i>	CTTGGAGAGATACAGCGAGCA CAACCTCAGCATAGTGGATGG	104	1147
<i>NFKB1</i>	CCTGTCTTTCTCATCCCATC TGCCAGAGTTTCGGTTCCT	85	373533
<i>MYD88</i>	CGCCTGTCTCTGTTCTTGA GTCCGCTTGTGTCTCCAGTT	114	17874
<i>CASP4</i>	GCAGGACAAATGCTTCTTCA GTGGTCCAGCCTCCATATTC	88	837
<i>AIM2</i>	AAAAGGTAAATGTCCCGCTGA ATTGTTCCAAGGGGCTGAGT	88	9447
<i>NAIP</i>	AGACCTTCAGAGCCGTGGT CTTCAACCTGTGCCATTCT	113	4671
<i>NLRC4</i>	GAGGTCCCACAACCTCGTCA GTTTTTCAGAGGGTTCTTTCCA	102	58484
<i>NLRP1</i>	CTTTGGGACTGACGATGAC GCCAGCTACAGGGAAGTGAA	104	22861
<i>NLRP2</i>	GAAGGAGGTGATGGCTCAGT TTGACGCAGAATGAAGATGG	81	55655
<i>NLRP3</i>	CTGAAACAGCAGATGGAGAGTG GCAGCAAACCTGGAAGGAAG	91	114548
<i>NLRP7</i>	TTCTGGTCAACACCTCCTCA CCTCCATCATCTCAGCCTTT	111	199713
<i>NLRP12</i>	ACCGACCTTIACCTGACCAA CCATCCCAAATAACCAGAGG	112	91662
<i>IFI16</i>	TCCGAGGTGATGCTGGTT TGATAGGGCTGGTCCTTTACTT	119	3428
<i>PYCARD</i>	GATGCTCTGTACGGGAAGGT GGCTGGTGTGAACTGAAGAG	105	28108
<i>CASP1</i>	TGTTCTGTGATGTGGAGGA TCTTTCAGTGGTGGGCATCT	90	834
<i>GSDMD</i>	GGTGCCTCCAACTTCCT TGTCAAAAGCTCCAGTTCC	117	69146
<i>IL1B</i>	TGGCAATGAGGATGACTTGTT TGGTGGTCGGAGATTCTGT	120	3553
<i>IL18</i>	CCAAGGAAATCGGCCTCT CCATACCTCTAGGCTGGCTATC	113	3606
<i>RPLP0</i>	AACTCTGCATTCTCGCTTCC GGACTCGTTTGTACCCGTTG	119	6175
<i>PGK1</i>	GGTGGAAATGGCTTTTACCTT ATCTTGGCTCCCTCTTCATC	83	5230
<i>LRP10</i>	GGCAACGTCAACATCACTT AATCTTGGCTGTAGGAGAGCA	82	26020