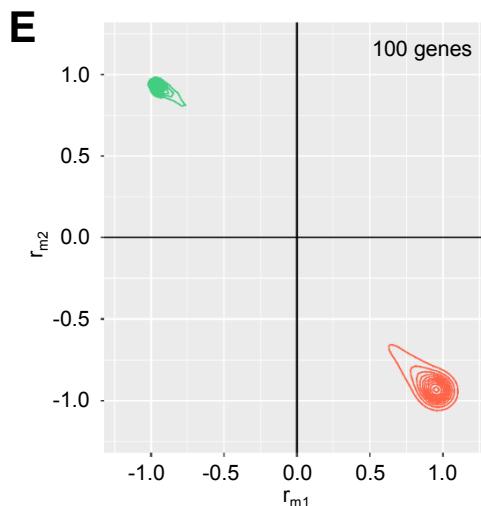
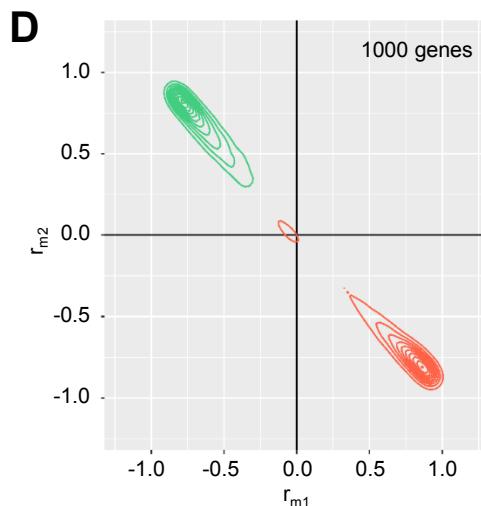
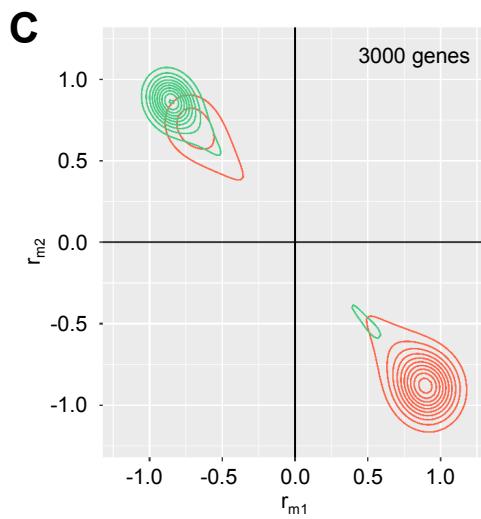
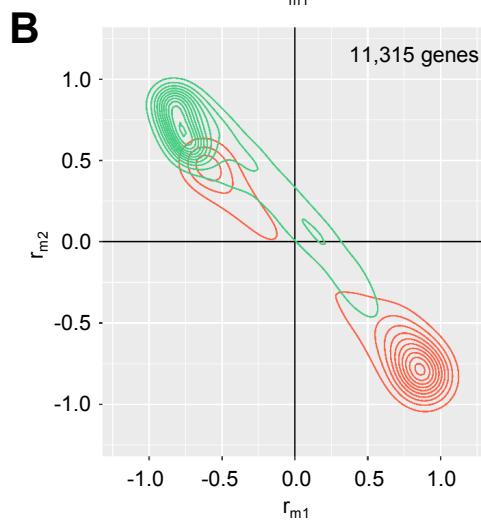
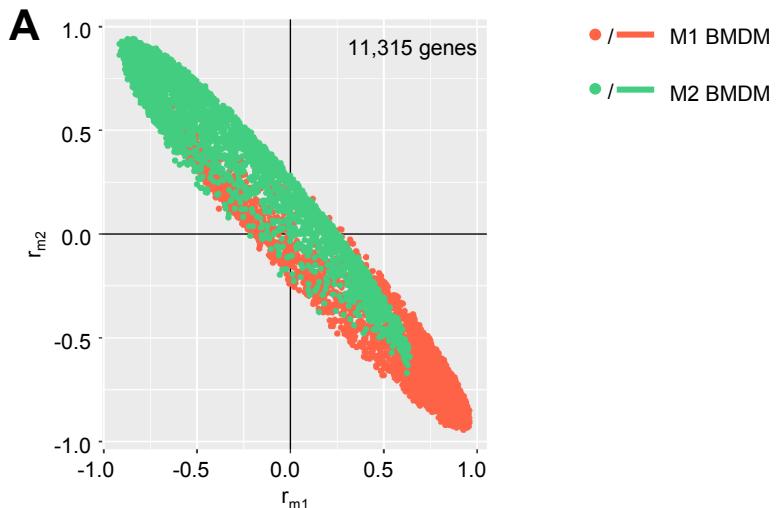


Supplemental Figure s1. scRNA-seq of BMDMs and ATMs. (A) Venn Diagram (non-proportional) of genes expressed in >1% of M0, M1, or M2 BMDMs and lean or obese ATMs. (B) t-SNE clustering of scRNA-seq from 1710 lean and 1758 obese ATMs.

(C) Expression of classic M1 and M2 markers in ATMs by t-SNE plots. (D) t-SNE dimensional reduction of ATMs by cluster (left) and percentage (right); color bars representing log2 transformed expression levels.

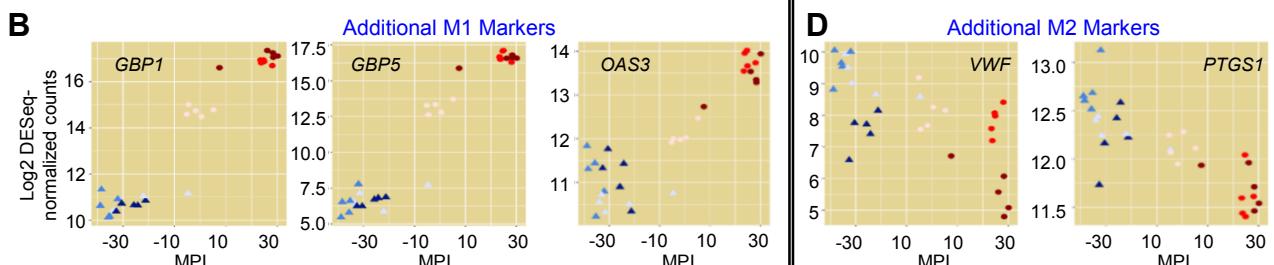
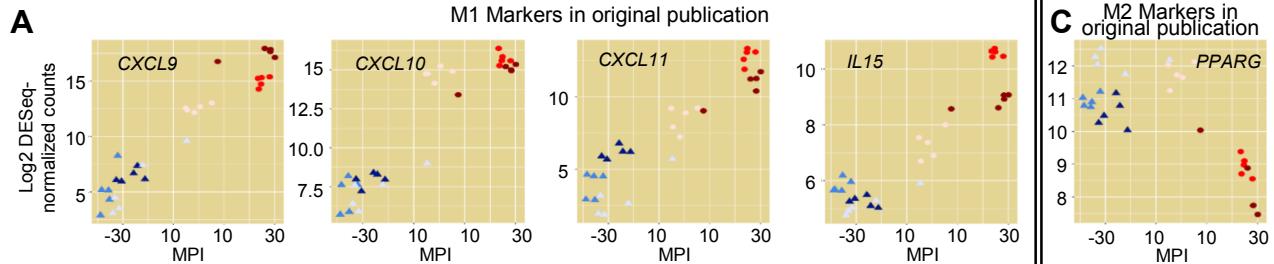


Supplemental Figure s2. Identification of gene sets allows efficient separation of BMDM M1 and M2 activation states. (A) r_{m1} vs. r_{m2} dot plot of M1 and M2 BMDMs including 11,315 genes expressed in >1% of M1 and/or M2 BMDMs. (B) r_{m1} vs. r_{m2} contour plot of M1 and M2 BMDMs including 11,315 genes expressed in

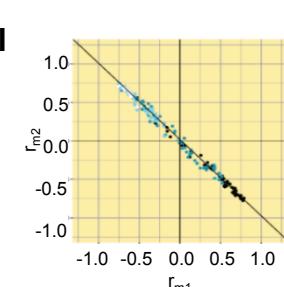
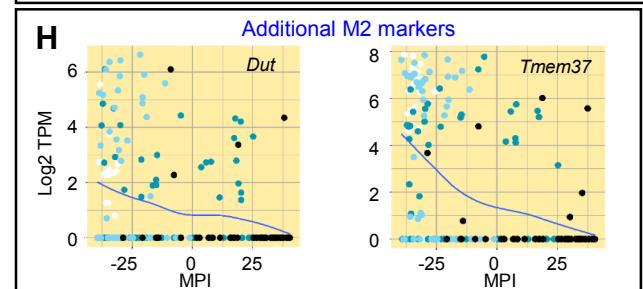
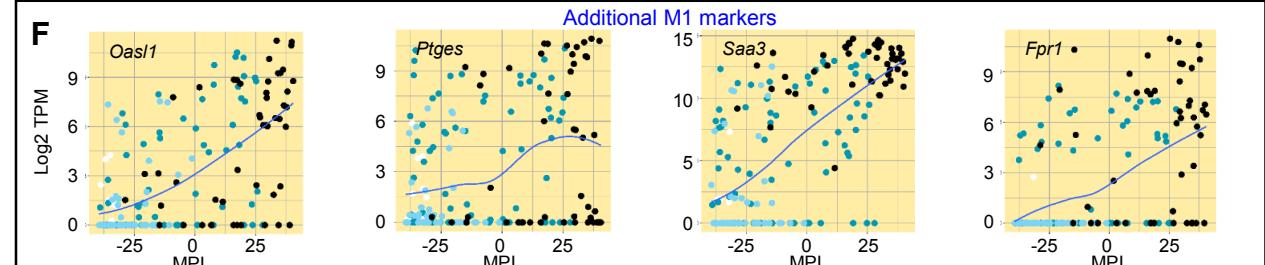
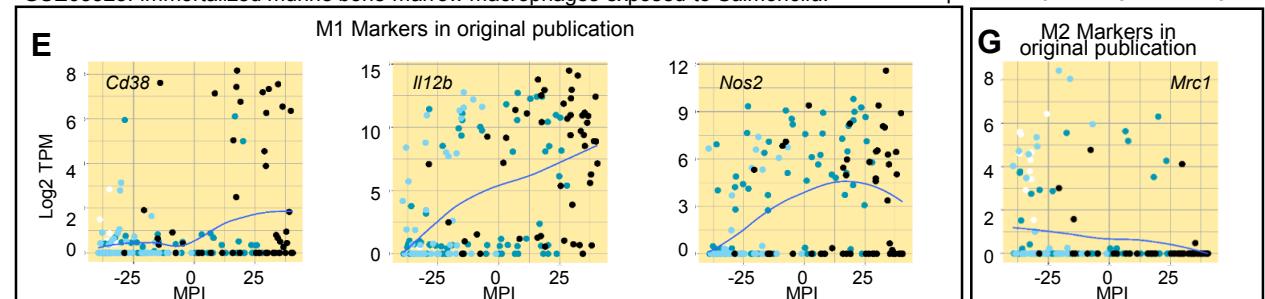
>1% of M1 and/or M2 BMDMs. (C-E) r_{m1} vs. r_{m2} contour plots of M1 and M2 BMDMs using the top 3000, 1000, and 100 most differentially expressed (absolute fold change) and significantly changed genes (FDR-adjusted $p < 10^{-10}$).

GSE82227: human PBMC-derived macrophages treated with IFNy

IFNy
Media
2h ○
6h ●
24h ▲

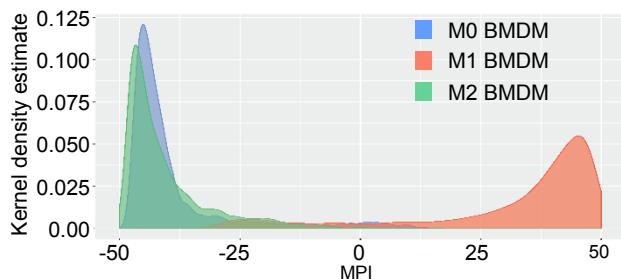
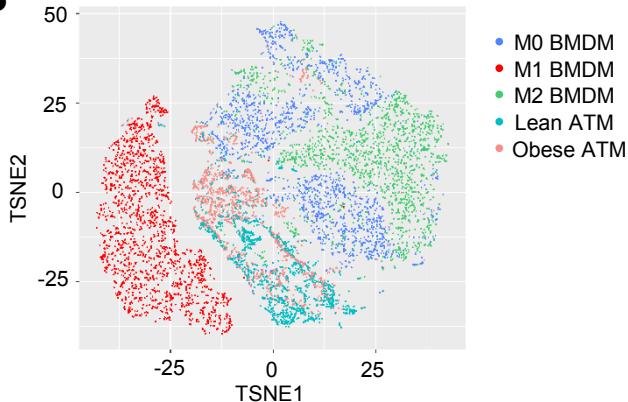
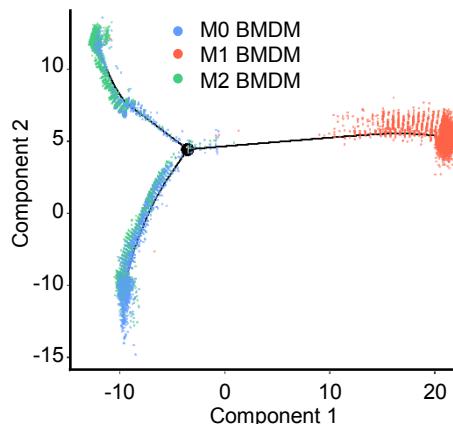
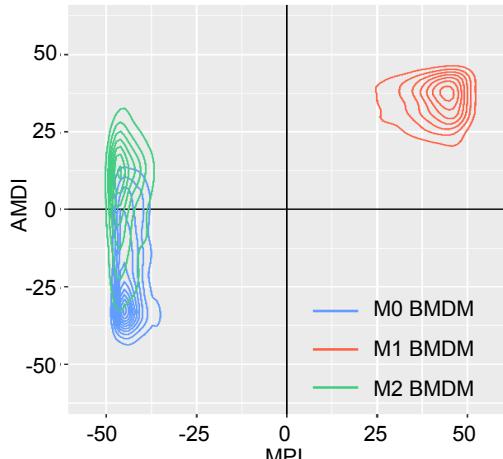
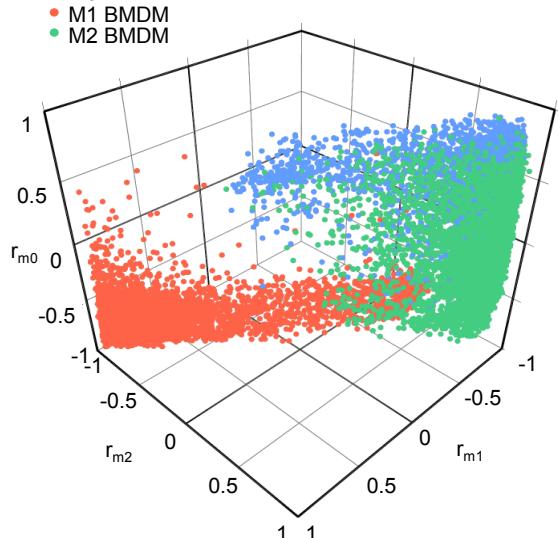
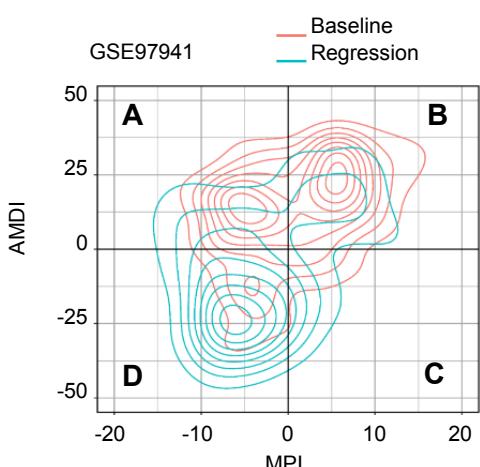
GSE65528: immortalized murine bone marrow macrophages exposed to *Salmonella*.

Time after exposure: ○ 0 h, ● 2.5 h, □ 4 h, ■ 8 h



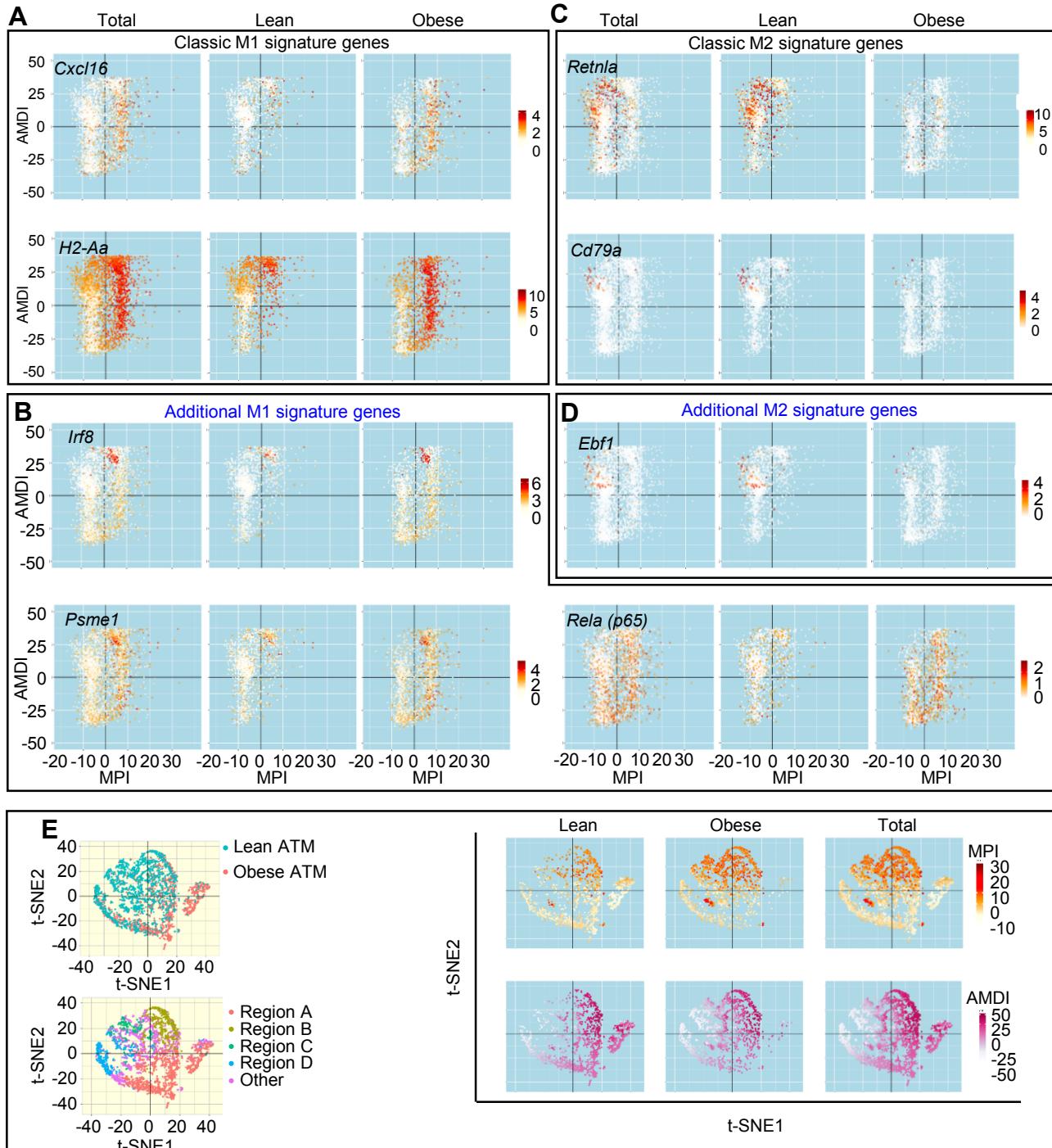
Supplemental Figure s3. Application of MPI to characterize expression patterns of signature genes from IFNy-stimulated (GSE82227) and *Salmonella*-stimulated (GSE65528) macrophages. (A-D) Gene-specific expression by MPI plots of human PBMC-derived macrophages stimulated with IFNy for 2, 6, and 24 hours; M1 (A) and M2 (C) activation genes reported in the original publication and additional M1 (B) and M2 (D) signature genes identified by MPI application; expression levels are

$\log_2(\text{DESeq-normalized counts}+1)$. (E-H), Gene-specific expression by MPI plots of immortalized murine BMDMs 0, 2.5, 4, and 8 hours after *Salmonella* exposure; M1 (E) and M2 (G) activation genes reported in the original publication and additional M1 (F) and M2 (H) signature genes identified in the present study; expression levels are $\log_2(\text{TPM}+1)$; Blue curves are loess smoothing lines. (I) r_{m1} vs. r_{m2} dot plot of the entire dataset.

A**B****C****D****E****F**

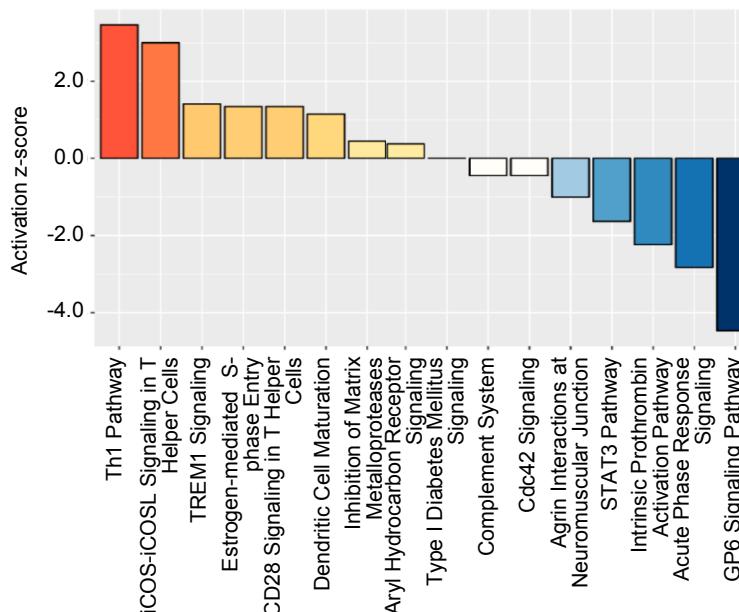
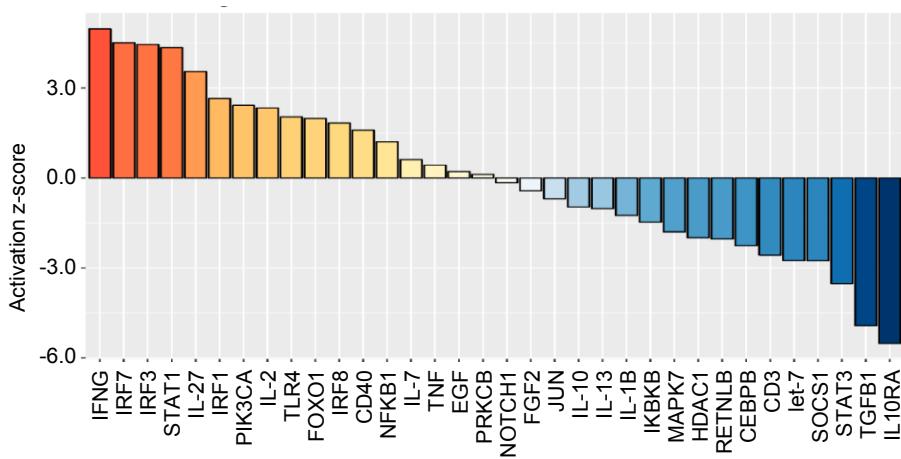
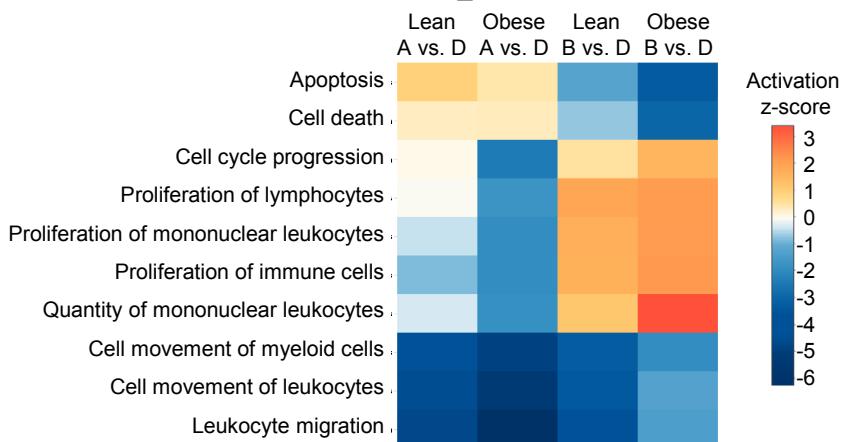
Supplemental Figure s4. Successful separation of BMDMs with various activation states using PSGs and AMDSGs. (A) Macrophage distributions along the MPI scale. (B) t-SNE analyses of BMDM M0/M1/M2 and ATM transcriptomes with PSGs and AMDSGs. Single-cell transcriptome profiles of M0, M1, M2 BMDMs (4736 cells from each sample) were analyzed using cell trajectory algorithms (30) with the whole transcriptome (C) that displayed overlapping of M0 and M2 populations. (D) M0,

M1, and M2 BMDM separation by MacSpectrum. (E) 3D plot of r_{m1}, r_{m2}, and r_{m0} (see Methods for calculation details) values from single-cell transcriptome profiles of M0, M1, and M2 populations. (F) Murine aortic macrophages during atherosclerosis progression (baseline) and regression (GSE97941) depicted by MacSpectrum (31), with the four regions (A,B,C, and D) labelled.



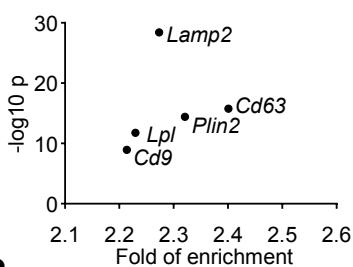
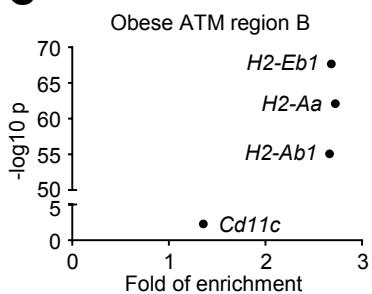
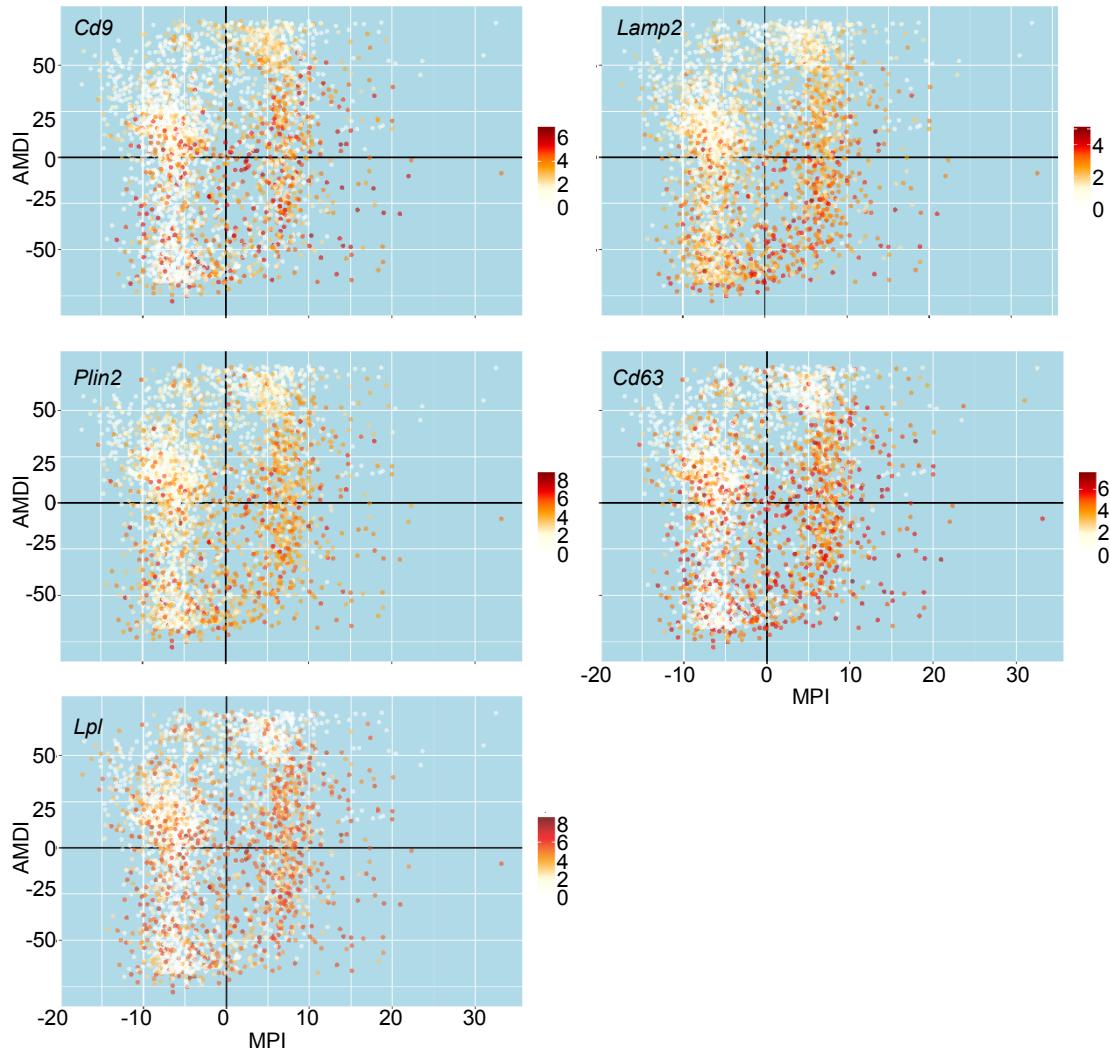
Supplemental Figure s5. MacSpectrum analysis of ATMs in obesity. (A-D) Expression of known classic M1 (A) and M2 genes (C), and additional M1 and M2 genes identified in this study (B, D)

by MacSpectrum plot of total, lean, and obese ATMs. Expression levels are $\log_2(\text{UMI counts}+1)$. (E) t-SNE dimensional reduction of ATMs using PSGs and AMDSGs.

A**B****C**

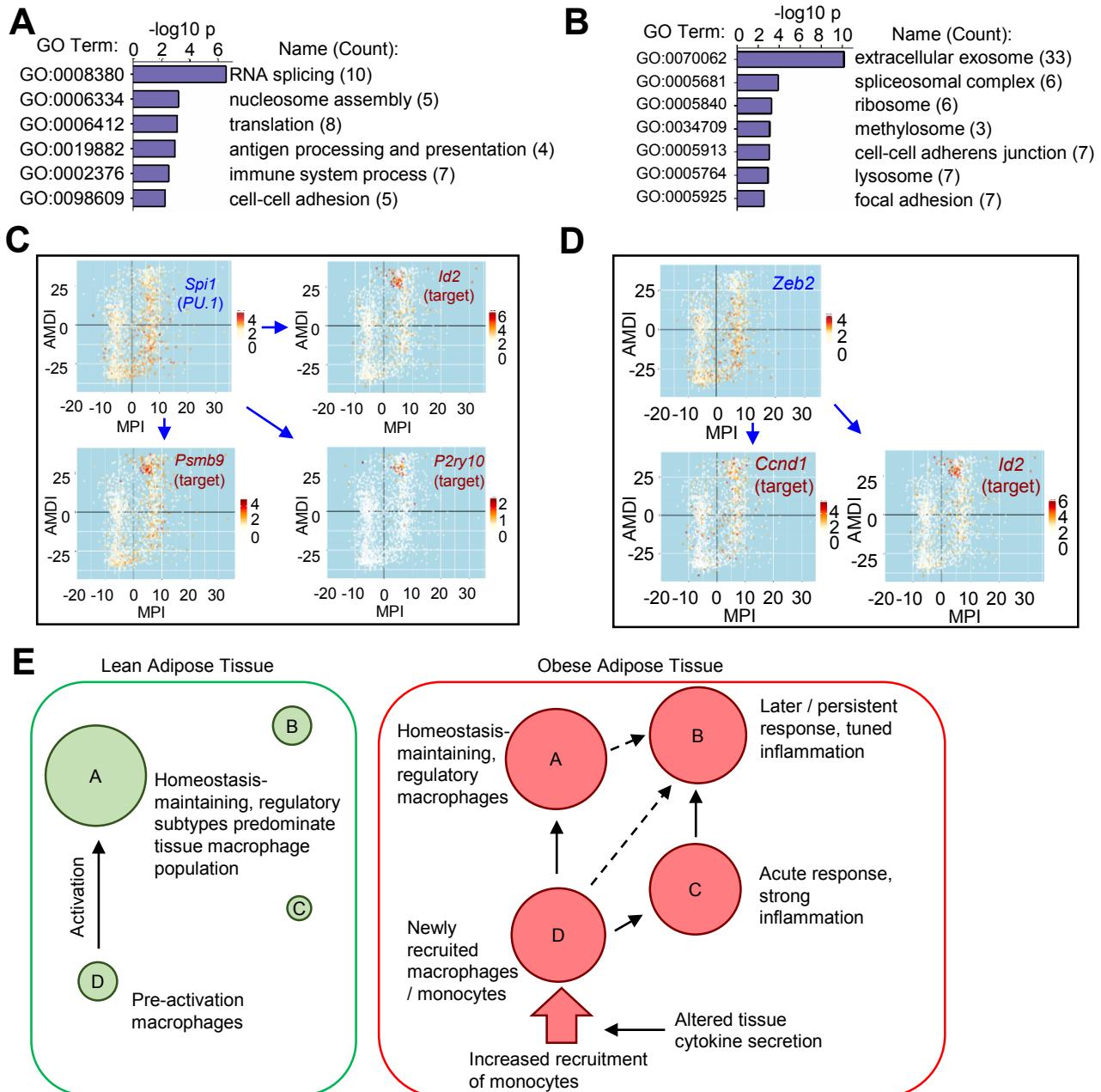
Supplemental Figure s6. Signaling pathway and regulator analysis of ATM subsets identified by the MacSpectrum. (A) Enriched pathways (A) and upstream regulators (B) in region B vs. A ATMs identified by IPA; positive and negative z-scores indicate estimated activation or inhibition, respectively; all pathways and regulators displayed are significantly different at $p < 0.05$.

(C) Most enriched biological functions in lean and obese ATMs in regions A and B compared to total (lean+obese) cells in region D identified by IPA; functions listed were significantly enriched ($p < 10^{-30}$) in at least one of the four comparisons (columns); positive and negative z-scores indicate estimated activation or inhibition, respectively.

A**C****B**

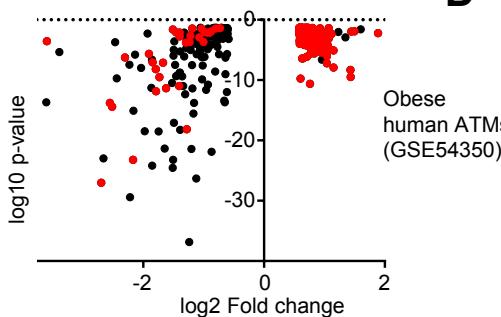
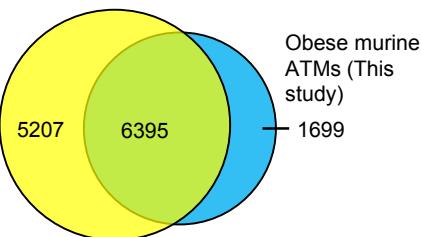
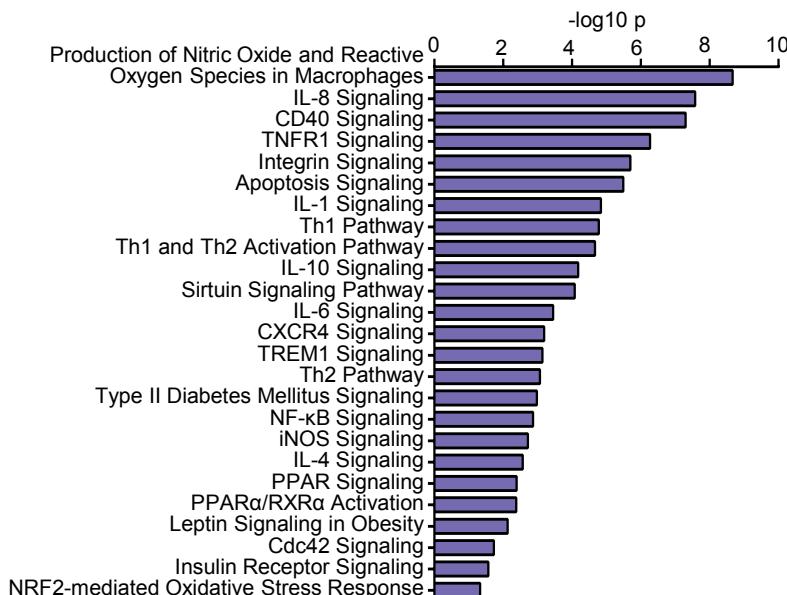
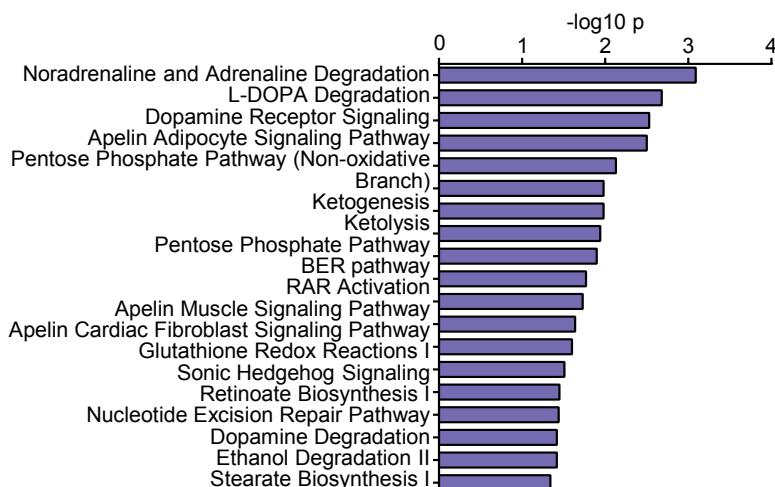
Supplemental Figure s7. MacSpectrum consistently identified reported features of murine ATMs. (A), (B) Enrichment of reported Cd9⁺ ATM signature genes in region C of obese ATMs. (C) Enrichment of dendritic cell signature genes in region B of

obese ATMs. p-values in (A), (C) were determined by 2-tailed Welch's t-test, color bars in (B) represented $\log_2(\text{UMI counts} + 1)$ of the genes.



Supplemental Figure s8. MacSpectrum revealed dynamic changes of ATM subsets in obesity. Obese or lean ATMs in regions A and B were analyzed using NIH-DAVID Bioinformatics Resources for gene function (A) and subcellular location (B). (C) Enrichment of transcription factor *Spi1* (*PU.1*) in region C, and its targets *Id2*, *Psmb9*, and *P2ry10* in region B of the obese ATMs. (D) Enrichment of transcription factor *Zeb2* in region C, and its targets *Ccnd1* and *Id2* in region B of the obese ATMs. (E) Schematic of ATM subpopulation changes during development of obesity. Under lean condition, a small quantity of less mature/ pre-activation (region D) reside in visceral adipose tissue; a dominant macrophage subset displays an “M2-like” phenotype (region A). Under an obese condition, recruitment of peripheral monocytes (region D) into adipose tissue is enhanced, which could replenish a tissue-maintenance “M2-like” subset (region A); more

importantly, a large portion of them gave rise to an immature but highly inflammatory subpopulation (C) as an initial response to the pro-inflammatory micro-environment in the tissue. Continuous exposure to the pro-inflammatory cues further developed the region C cells into a subpopulation (B) bearing a mature and tuned pro-inflammatory profile; and those cells accounted for the later/more-persistent responses to obesity stress. Targets of regulators in C, D were identified using IPA; expression levels in C, D are log₂(UMI counts+1).

A**D****B****C**

Supplemental Figure s9. Profiles of disease-associated gene sets identified by MacSpectrum. (A) Log₂ fold changes and log₁₀ p-values of the 603 genes that showed significant differential expression in obese vs lean monocyte-like cells. The 385 genes that consistently displayed polarization-associated expression are colored red, p-values were determined by 2-tailed Welch's t-test. (B) Pathways significantly enriched in the 436 genes that were expressed with distinct macrophage polarization pattern in murine ATMs

and displayed significant differential expression ($p < 0.05$) in CD14 $^{+}$ cells isolated from obese human subjects with or without diabetes (GSE54350). (C) Pathways significantly enriched in the 23 gene candidates identified using MacSpectrum in blood monocytes of obese patients. (D) Venn Diagram of the top 50% most abundant genes (average expressions) in obese human (GSE54350) and murine ATMs.

Ctsl	35.9107	38.91845	56.12828	82.46907	86.18031	84.22595	100	87.44422	68.23097	36.89708	38.38207	7.103265	1.164016	0	1.712462	2.284427	2.239502	2.201698	3.363393	4.643172
Clec10a	39.38382	53.30095	73.75852	100	89.72166	77.93102	82.0075	73.34033	81.71186	34.88266	25.88792	4.282356	9.403591	5.725874	0	0.239078	0.738501	1.119524	0.842824	1.030639
Clec4b1	31.00715	52.54836	68.65082	77.19093	74.42458	82.29034	95.14863	99.39302	100	41.41563	34.83962	11.47524	0	0	0.674818	0.948775	1.461214	0.978352	1.525124	1.411228
Cd124	16.31671	32.8038	49.98641	80.63613	83.11925	48.76949	52.48613	100	61.24346	6.055731	83.03153	2.633312	0	11.92573	2.370243	3.848157	5.370018	1.920308	2.468051	3.646472
Chil3	27.67546	36.55518	57.81724	90.83648	45.08028	67.81744	92.12922	100	78.02991	23.27723	5.849022	1.870193	0.124408	0	0	0.087313	0.080922	0.028505	0.017572	
Rbp4	24.33482	37.70836	52.25588	64.61264	45.18004	58.5903	78.76445	100	25.085	4.061426	4.014358	0	0.360871	0.574868	0	0	0	0	0	
Ear2	23.4678	53.03291	66.38726	100	79.2865	59.13267	99.93973	98.32461	33.73076	5.544365	8.052427	0	0	0	0	0	0	0.208048	0	

Supplemental Table s2. Gene ontology of BMDMs and ATMs.

Protein class

M0 BMDM	1008	nucleic acid binding (PC00171)
M1 BMDM	974	hydrolase (PC00121)
M2 BMDM	999	transcription factor (PC00218)
lean ATM	1003	transferase (PC00220)
obese ATM	1010	enzyme modulator (PC00095)
		transporter (PC00227)
		cytoskeletal protein (PC00085)
		oxidoreductase (PC00176)
		signaling molecule (PC00207)
		receptor (PC00197)
		ligase (PC00142)
		membrane traffic protein (PC00150)
		transfer/carrier protein (PC00219)
		calcium-binding protein (PC00060)
		defense/immunity protein (PC00090)
		chaperone (PC00072)
		lyase (PC00144)
		cell adhesion molecule (PC00069)
		extracellular matrix protein (PC00102)
		isomerase (PC00135)
		regulatory/adaptor protein (PC00226)
		cell junction protein (PC00070)
		structural protein (PC00211)
		viral protein (PC00237)
		storage protein (PC00210)
		surfactant (PC00212)

Gene type

	protein_coding	antisense_RNA	bidirectional_promoter_-lncRNA	A	lncRNA	processed_pseudogene	Other
M0 BMDM	10555	177		205	24	19	
M1 BMDM	10072	165	13	181	20	19	
M2 BMDM	10465	170	14	186	23	18	
lean ATM	10655	109	7	137	18	15	
obese ATM	10614	130	11	163	21	20	

Cellular component														
M0 BMDM			M1 BMDM			M2 BMDM			lean ATM			obese ATM		
GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value
GO:0005739	mitochondrion	-126.991	GO:0005739	mitochondrion	-125.6576	GO:0005739	mitochondrion	-130.1169	GO:0005739	mitochondrion	-116.0782	GO:0005739	mitochondrion	-123.818
GO:1902494	catalytic complex	-104.658	GO:1902494	catalytic complex	-104.5784	GO:1902494	catalytic complex	-105.433	GO:0005730	nucleolus	-90.7167	GO:1902494	catalytic complex	-90.0711
GO:0005730	nucleolus	-91.0159	GO:0005730	nucleolus	-87.466	GO:0005730	nucleolus	-90.7167	GO:1902494	transferase	-87.6594	GO:0005730	nucleolus	-91.2741
GO:1990234	complex	-82.5331	GO:1990904	n complex	-84.2596	GO:0044429	part	-80.3605	GO:1990234	complex	-72.8058	GO:1990234	complex	-77.3197
GO:0044429	mitochondrial part	-79.1772	GO:1990234	complex	-80.9136	GO:1990234	ribonucleoprotei	-80.3316	GO:0044429	mitochondrial part	-71.6211	GO:0044429	mitochondrial part	-76.7696
GO:1990904	ribonucleoprotei	-73.3958	GO:0044429	mitochondrial part	-80.1101	GO:1990904	n complex	-74.8665	GO:0031967	organelle envelope	-71.6176	GO:0031967	organelle envelope	-74.7167
GO:0031967	organelle envelope	-70.9666	GO:0031967	envelope	-70.7033	GO:0031967	envelope	-72.3215	GO:0031975	envelope	-71.4966	GO:0031975	envelope	-74.6003
GO:0031975	envelope	-70.8729	GO:0031975	envelope	-70.6757	GO:0031975	envelope	-72.2321	GO:1990904	ribonucleoprotei	-70.8642	GO:1990904	ribonucleoprotei	-73.9318
GO:0005694	chromosome	-59.1124	GO:0005694	chromosome	-40.9355	GO:0015630	microtubule cytoskeleton	-54.4597	GO:0005694	chromosome	-45.7162	GO:0005694	chromosome	-58.0835
GO:0015630	microtubule cytoskeleton	-54.6421	GO:0005773	vacuole	-40.8665	GO:0005694	chromosome	-51.6716	GO:0005773	vacuole	-43.997	GO:0015630	microtubule cytoskeleton	-52.1337
GO:0044427	chromosomal part	-51.1612	GO:0015630	cytoskeleton	-38.9957	GO:0044427	vacuolar membrane	-44.2277	GO:0015630	chromosomal part	-41.8955	GO:0044427	chromosomal part	-50.8153
GO:0005774	vacuolar membrane	-36.0004	GO:0005774	chromosomal part	-38.1772	GO:0005774	vacuole transferase complex, transferring phosphorus-containing groups	-40.0269	GO:0044427	vacuolar membrane	-39.3902	GO:0005774	vacuole vacuolar membrane	-36.2924
GO:0005773	vacuole transferase complex, transferring phosphorus-containing groups	-35.6655	GO:0044427	vacuole transferase complex, transferring phosphorus-containing groups	-35.4711	GO:0005773	vacuole transferase complex, transferring phosphorus-containing groups	-38.767	GO:0005774	vacuole transferase complex, transferring phosphorus-containing groups	-37.5678	GO:0005774	vacuole transferase complex, transferring phosphorus-containing groups	-35.5544
GO:0061695	transferring phosphorus-containing groups	-35.5331	GO:0061695	transferring phosphorus-containing groups	-35.2314	GO:0061695	transferring phosphorus-containing groups	-34.3507	GO:0005925	focal adhesion	-34.9469	GO:0061695	focal adhesion	-34.9626
GO:0005768	endosome	-25.8539	GO:0005768	endosome	-29.9469	GO:0005768	endosome	-27.857	GO:0061695	transferase complex, transferring phosphorus-containing groups	-33.1984	GO:0005768	endosome	-25.9281
GO:0005840	ribosome	-23.4815	GO:0005840	ribosome	-27.5575	GO:0005925	focal adhesion	-24.4547	GO:0005794	spliceosomal complex	-31.54	GO:0005925	focal adhesion	-25.2269
GO:0005925	focal adhesion	-22.3979	GO:0005681	spliceosomal complex	-24.0482	GO:0005840	spliceosomal complex	-23.9355	GO:0005768	ribosome	-28.2532	GO:0005794	spliceosomal complex	-24.2314
GO:0005681	endoplasmic reticulum membrane	-21.3478	GO:0005925	focal adhesion	-22.8297	GO:0005789	endoplasmic reticulum membrane	-22.4976	GO:0005840	endosome	-23.6156	GO:0005840	endoplasmic reticulum membrane	-23.0186
GO:0005789	reticulum membrane	-21.2652	GO:0005794	ribosome	-21.4202	GO:0005681	reticulum membrane	-21.7144	GO:0005794	ribosome	-20.9706	GO:0005794	ribosome	-20.9706

Molecular function														
M0 BMDM			M1 BMDM			M2 BMDM			lean ATM			obese ATM		
GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value	GO term	Name	log10 p-value
GO:0003723	RNA binding	-145.6944	GO:0003723	RNA binding	-157.8908	GO:0003723	RNA binding	-145.7404	GO:0003723	RNA binding	-135.1858	GO:0003723	RNA binding	-148.9788
GO:0019899	enzyme binding purine ribonucleoside triphosphate	-77.845	GO:0019899	enzyme binding purine ribonucleoside triphosphate	-72.9259	GO:0019899	enzyme binding purine ribonucleoside triphosphate	-79.7361	GO:0019899	enzyme binding purine ribonucleoside triphosphate	-80.8268	GO:0019899	enzyme binding purine ribonucleoside triphosphate	-73.5467
GO:0035639	binding purine ribonucleoside	-49.5889	GO:0035639	binding purine ribonucleoside	-41.3838	GO:0035639	binding purine ribonucleoside	-46.7433	GO:0035639	binding purine ribonucleoside	-47.8356	GO:0035639	binding purine ribonucleoside	-52.8894
GO:0032550	binding	-48.34	GO:0032550	binding	-40.6807	GO:0032550	binding	-45.5607	GO:0032550	binding	-47.2197	GO:0032550	binding	-51.5638
GO:0044877	macromolecular complex binding hydrolase activity, acting on acid anhydrides	-29.5432	GO:0016874	ligase activity ubiquitin-like protein transferase activity	-25.7627	GO:0016874	ligase activity	-29.3978	GO:0044877	macromolecular complex binding hydrolase activity, acting on acid anhydrides	-41.2733	GO:0044877	macromolecular complex binding hydrolase activity, acting on acid anhydrides	-31.7905
GO:0016817	anhydrides	-29.2262	GO:0019787	activity	-25.6317	GO:0044877	macromolecular complex binding	-28.9431	GO:0016817	anhydrides	-26.3809	GO:0016817	anhydrides	-30.041

GO:0016874	ligase activity ubiquitin-like protein transferase activity	-28.6813	GO:0043021	ribonucleoprotein complex binding	-25.5196	GO:0016817	hydrolase activity, acting on acid anhydrides	-27.7093	GO:0016772	transferase activity, transferring phosphorus-containing groups	-25.6038
GO:0019787	ubiquitin-protein transferase activity	-27.0813	GO:0004842	ubiquitin-protein transferase activity hydrolase	-25.0897	GO:0019787	activity, acting on acid anhydrides	-25.8139	GO:0004842	ubiquitin-protein transferase activity ubiquitin-like protein transferase	-24.266
GO:0004842	activity transferase activity, transferring phosphorus-containing groups	-26.9151	GO:0016817	anhydrides	-24.9393	GO:0004842	activity transferase activity, transferring phosphorus-containing groups	-25.5575	GO:0019787	activity	-23.9318
GO:0016772	ligase activity, forming carbon-nitrogen bonds	-26.3833	GO:0044877	macromolecular complex binding	-24.7249	GO:0016772	transferase activity, transferring phosphorus-containing groups	-24.9792	GO:0016874	ligase activity	-21.5884
GO:0016879	helicase activity ribonucleoprotein complex binding UDP-N-acetylglucosaminyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	-24.451	GO:0016772	ribonucleoprotein complex binding	-21.9987	GO:0043021	ligase activity, forming carbon-nitrogen bonds	-24.7471	GO:0004386	helicase activity	-20.0227
GO:0004386	GO:0004386	helicase activity ligase activity, forming carbon-nitrogen bonds	-21.2846	GO:0016879	GO:0004386	helicase activity	-23.218	GO:0003712	transcription cofactor activity transcription factor activity, protein binding	-19.9355	GO:0016879
GO:0043021	structural constituent of ribosome	-23.988	GO:0016879	transcription cofactor activity	-20.2323	GO:0003712	transcription cofactor activity	-22.1012	GO:0000988	ligase activity, forming carbon-nitrogen bonds	-19.4935
GO:0008766	protein-glycine ligase activity	-20.5535	GO:0003735	transcription factor activity, protein binding	-20.1481	GO:0003712	transcription factor activity, protein binding UDP-N-acetylglucosaminyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	-20.8908	GO:0016879	protein serine/threonine kinase activity	-18.2388
GO:0070735	tubulin-glycine ligase activity	-20.5535	GO:0003712	structural constituent of ribosome	-18.8908	GO:0000988	transcription factor activity, protein binding UDP-N-acetylglucosaminyl-D-glutamyl-2,6-diaminopimelate-D-alanyl-D-alanine ligase activity	-19.9154	GO:0004674	chromatin binding	-17.51
GO:0070738	coenzyme F420-2 alpha-glutamyl ligase activity	-20.5535	GO:0000988	protein-glycine ligase activity	-18.7474	GO:0008766	structural constituent of ribosome	-19.225	GO:0003682	coenzyme F420-2 alpha-glutamyl ligase activity	-16.6676
GO:0043774	ribosomal S6-glutamic acid ligase activity	-20.5535	GO:0032182	tubulin-glutamic acid ligase activity	-18.4179	GO:0070735	tubulin-glycine ligase activity	-19.225	GO:0003735	structural constituent of ribosome	-16.382
GO:0018169	transcription cofactor activity	-20.5535	GO:0070740	coenzyme F420-2 alpha-glutamyl ligase activity	-17.3854	GO:0070738	tubulin-glycine ligase activity	-19.225	GO:0070740	tubulin-glutamic acid ligase activity	-15.6162
GO:0003712	protein serine/threonine kinase activity	-19.0907	GO:0008766	protein-glycine ligase activity	-17.3402	GO:0043774	coenzyme F420-2 alpha-glutamyl ligase activity	-19.225	GO:0008766	coenzyme F420-2 alpha-glutamyl ligase activity	-15.6126
GO:0004674	transcription factor activity, protein binding	-18.9642	GO:0070738	ribosomal S6-glutamic acid ligase activity	-17.3402	GO:0018169	coenzyme F420-2 alpha-glutamyl ligase activity	-19.225	GO:0070738	protein serine/threonine kinase activity	-15.6126
GO:0000988	structural constituent of ribosome	-18.1774	GO:0043774	coenzyme F420-2 alpha-glutamyl ligase activity	-17.3402	GO:0004674	coenzyme F420-2 alpha-glutamyl ligase activity	-17.9884	GO:0043774	structural constituent of ribosome	-16.3665

GO:0032182	ubiquitin-like protein binding	-18.0397	GO:0070735	protein-glycine ligase activity	-17.3402	GO:0032182	ubiquitin-like protein binding structural constituent of ribosome	-17.4878	GO:0070735	protein-glycine ligase activity	-15.6126	GO:0032182	ubiquitin-like protein binding	-16.0996
GO:0043130	ubiquitin binding	-17.137	GO:0043130	ubiquitin binding	-17.1444	GO:0003735		-17.1374						

Supplemental Table s3. The heatmap of normalized gene expression levels ATM (B vs. A).

MPI:	32.5~40	40~42.5	42.5~45	45~47.5	47.5~50	50~52.5	52.5~55	55~57.5	57.5~60	60~83
Pdpn	100	82.18489	69.92856	36.67234	10.33509	35.98128	36.94823	63.80928	15.23747	0
Csf1	100	98.26826	52.41418	20.76507	15.14034	15.72593	0	90.91489	11.80287	41.93971
Nr2f2	82.32451	100	58.6066	42.56	0	0	0	0	0	0
Lgi2	100	92.16979	77.74644	35.86968	0	0	0	0	0	0
Il1r1	100	88.15483	71.3827	36.44962	0	0	0	0	0	0
Ndn	99.15665	100	67.16744	40.22888	0	12.26452	14.27172	9.906146	0	0
Hspb8	100	90.8058	64.22557	36.48295	0	13.81475	22.76638	0	0	0
Arhgap20	100	96.62504	56.32374	32.49827	0	19.84062	12.45301	0	0	0
S100a16	100	83.99566	51.44082	53.5079	7.29212	0	9.708708	6.920095	1.871644	4.473604
Meis2	100	84.57644	64.65139	51.02467	0	0	0	0	0	0
Tshz2	92.27399	100	83.19274	47.03949	0	24.58928	0	13.265	14.53736	0
Amotl1	86.44672	100	57.7261	57.31075	0	37.35328	0	0	0	0
Pxdn	96.40134	100	62.44321	84.78579	0	0	22.10541	0	0	35.99992
Adm	100	98.03677	87.10264	64.62442	15.39381	0	10.90221	32.00673	6.824056	22.44591
Fermt2	100	83.06135	63.67709	73.20026	11.15417	0	7.088534	17.56324	0	0
Adamts1	92.63805	100	67.32889	77.77511	27.60758	8.271097	0	12.71534	11.79856	0
Dlc1	95.39878	100	68.30329	71.4936	16.50616	0	0	13.91386	12.92003	0
Col4a2	88.24182	100	64.07992	63.92142	26.17418	15.67358	32.04632	14.26026	0	2.502032
Col4a1	93.74039	100	65.63146	48.63124	12.78937	9.141556	5.550563	22.83299	0	0
Igfbp7	91.60287	100	79.75644	53.44863	13.68751	1.469975	17.24918	18.36268	0	2.432609
Fndc1	100	58.9155	31.07607	10.66162	11.17264	29.0896	0	0	0	0
Prss23	100	54.14909	39.21762	14.59283	0	0	3.846607	1.324112	2.414724	0
Fbn1	100	57.6243	17.65126	9.272451	0	3.917668	2.352933	6.076422	0	0
Mfap5	100	64.64512	27.43699	11.60307	3.464319	0.242885	11.02619	0	0.782063	1.547368
Col5a2	100	72.17159	41.70873	9.940327	0	0	20.43438	12.66161	4.209864	0
Lhfp	100	77.98157	43.42333	0	0	10.77274	17.87539	12.60285	0	0
Ptgis	100	68.72311	54.41082	4.78235	0	10.01498	21.30213	11.7293	0	0
Sema3c	100	83.86259	37.99404	31.71377	0	0	8.511467	0	0	0
Efemp1	100	79.91932	48.36045	13.89364	0	0	10.17827	4.782822	2.255129	0
Islr	100	81.68001	55.96753	18.28579	0	0	5.334956	0	0	0
Ntn1	100	83.86415	52.04226	18.71857	0	0	12.81443	0	0	0
Ebf2	100	75.73721	38.46316	5.627289	0	0	13.55211	0	0	12.3392
Dpt	100	85.46229	36.92046	8.375153	0	8.363049	11.52602	7.987428	2.575852	3.709239

Col1a2	100	77.36432	39.26587	7.32022	0.706245	2.390425	10.77673	4.836665	1.527212	0
Pcolce2	100	82.4146	30.84865	10.23096	0	4.731947	8.126972	1.926038	0	0
Adgrd1	100	73.98662	26.12934	20.51254	0	12.22377	0	5.188188	0	0
Fstl1	100	69.61792	32.8046	16.00119	1.75836	5.317432	6.22958	12.4648	0	0
Col1a1	100	71.32234	33.40723	10.71687	0	5.228007	3.151636	5.677367	0.995348	1.441631
Dact1	100	77.47466	35.05719	13.79032	0	0	0	6.445683	0	0
Igfbp6	100	74.5315	41.37901	14.03399	2.983209	14.4818	8.585658	6.733865	0.438993	0
Dclk1	100	79.06067	41.51777	20.55537	11.74346	12.19494	7.518545	0	0	0
Meg3	100	84.93824	41.3339	14.80793	3.828103	3.986081	0	7.649352	2.942031	0
Loxl1	100	80.76085	37.52107	19.44508	9.940966	0	9.246349	8.343099	0	0
Akap12	100	95.66322	37.87584	30.04743	27.6765	0	12.85347	8.906885	8.254235	11.67893
Ackr3	100	92.43251	48.57431	24.76888	9.888728	0	9.1935	2.181237	0	5.681511
Lama4	100	86.79102	50.92272	24.91603	14.36898	0	9.244696	12.11395	0	15.75032
Prkcdbp	100	73.85919	47.48782	36.29551	17.99341	0	17.49734	3.605006	17.68695	14.66999
Sparc	100	73.62884	37.93381	33.68353	8.317068	0	10.91258	12.47932	0.183549	0.591278
Ebf1	100	70.88405	39.48625	44.16492	10.44835	2.3405	19.06008	4.552401	5.015652	0
Ptrf	100	61.31298	45.27882	51.61858	23.10666	18.94093	2.061962	1.799573	0.999143	0
Fbln5	100	85.06775	38.05445	38.38902	52.48468	7.260433	12.359	13.67962	5.388183	0
Cyr61	100	76.05	72.6661	40.41478	38.54662	0.883284	16.86148	25.20517	0	1.090802
Smoc2	94.34707	100	93.84815	14.89683	0	0	10.0258	29.11059	0	0
Figf	97.63445	100	84.74953	20.02771	0	0	0	12.35291	0	0
Snhg18	100	96.0958	67.03919	10.8716	0	11.84871	19.72826	4.959166	23.65264	0
Tcf21	99.14113	100	77.96168	6.334702	0	0	0	0	0	0
C1qtnf2	100	99.86012	77.86943	0	0	0	0	0	0	0
Steap4	75.05914	100	85.16673	0	0	8.476443	5.141244	44.87464	6.304784	8.980212
Gpc3	68.38196	100	66.09071	16.62543	9.344685	9.712349	5.93352	11.38556	0	0
Tril	61.08668	100	76.36992	11.54644	0	0	0	10.1843	0	0
Svep1	57.92408	100	64.40148	29.78538	0	0	9.349303	12.22699	11.36089	0
Abca8a	62.51421	100	65.1126	9.720672	0	0	17.61475	4.438691	14.89831	11.20464
Sod3	76.73282	100	57.83471	0.549062	5.079877	20.70675	6.985079	0	9.306631	21.98949
Eya2	70.73538	100	46.53141	0	0	0	0	15.50822	0	0
Dnm1	100	88.35566	50.08058	12.73643	0	43.30254	0	0	19.38041	26.56166
Camk2n1	95.99967	100	57.3202	28.19409	14.59155	33.14659	17.59238	15.03736	0	49.66815
Gprc5b	100	99.82206	66.68645	35.06891	37.02418	38.64346	20.99648	0	9.555384	18.13396
Lrrc17	91.60896	100	42.71966	11.94779	12.52195	0	21.41105	5.50026	0	0

Fxyd1	100	93.24363	65.22798	14.0415	4.56208	13.29902	17.68757	7.378357	0	0
Adamts5	100	83.36695	53.12973	10.17116	3.775434	14.3543	8.899925	8.955877	0	0
Clec3b	100	91.3817	51.53346	14.98702	1.666176	6.18512	12.0984	14.18898	0	0.261083
Tnxb	100	97.92123	49.79456	9.965651	4.390883	16.59101	25.1159	11.95975	3.375233	0
Ltbp1	91.46472	100	48.64408	7.16892	0	14.7455	9.147939	6.292572	0	0
Tmem100	97.49138	100	56.31016	19.81181	0	0	0	0	0	0
Gpr153	94.51976	100	47.76656	17.57119	0	0	0	0	0	0
Scara5	97.79921	100	58.57013	18.9884	0	0	11.26052	10.16774	4.891758	0
Medag	92.95058	100	54.23296	17.88758	0	0	8.384269	15.85516	10.21807	0
Pla1a	100	84.85882	50.30566	20.89847	0	4.791504	10.76694	17.1075	10.05397	9.772677
Cd248	100	84.86002	43.57475	21.64265	0	8.879022	7.93534	7.150319	6.622126	4.889179
Nid1	100	88.13278	44.59761	22.84009	0	11.1164	11.46129	14.93048	4.307294	0
Col6a1	100	91.18045	45.95406	1.245714	0	0	11.80783	17.02901	0	5.607552
Col6a2	100	91.38342	47.32335	9.472085	0	3.138958	8.830861	9.433929	4.536182	0
Ccdc80	100	87.94408	45.12995	9.741988	3.609915	0	4.417332	11.17305	5.418741	0
Lum	100	94.64343	47.10432	7.704539	1.977383	2.163803	2.984119	7.309163	0.930989	0
Col6a3	100	93.24074	52.11992	9.350866	0	0	0	13.1383	0	0
Mxra8	100	93.66239	62.20217	21.27056	7.177726	0	19.93859	14.0438	5.544671	0
Rarres2	99.69715	100	68.31822	17.3598	2.922097	3.044136	16.23794	19.16807	0	6.315389
Nbl1	100	96.26944	61.93682	17.85459	0	9.328174	20.21147	15.81203	3.567938	9.87877
Serpinh1	100	95.99558	67.50833	33.60816	1.892687	0	11.88331	23.77285	2.865168	8.013902
Prelp	95.00858	100	65.26962	31.63597	0	0	24.22608	25.70766	0	0
Dcn	80.79483	100	66.09718	8.43742	0.309053	1.590313	15.53214	18.57286	0	0.87604
Dpep1	81.52023	100	72.38698	11.3465	0	0	18.84931	14.05476	1.792934	5.077315
Cygb	86.18673	100	63.3002	12.84883	5.742338	5.976227	16.21207	13.3735	8.556011	0
Pdgfra	86.09764	100	61.13233	14.92077	8.30271	0	18.75121	18.86081	0	9.144657
Serpingle1	90.69063	100	60.25261	20.657	0.274125	4.952172	21.45752	19.32598	0	4.114498
C1s1	84.9894	100	56.43434	24.11886	3.761326	11.08244	18.47255	22.61341	0	8.056465
Serpine2	88.90904	100	60.4986	14.68515	18.05645	18.72496	15.18665	15.2782	0	7.284065
Egfr	86.00332	100	56.66237	12.43144	13.0285	13.52845	22.26836	15.79281	0	0
C3	98.13612	100	46.7928	19.67578	8.451296	0	1.122103	11.99747	14.73952	37.84358
Gpx8	92.41848	100	60.62493	14.26665	0	0	12.51879	23.13606	8.026754	29.45001
Sdc2	100	98.43079	64.51472	8.689006	0	0	0	11.1363	0	33.23728
Npdc1	100	74.56493	56.11501	23.16774	0	0	15.98835	28.82218	10.37172	26.33175
Itih5	100	79.06766	36.75278	29.26546	0	0	13.50394	11.53124	4.523635	17.57339

Bmp1	100	86.91612	40.31165	17.44399	0	0	21.78529	0	0	25.32478
Col15a1	76.26153	100	88.3637	18.26349	19.10942	10.64039	22.86267	22.99379	0	0
Ltbp4	84.75067	100	71.69256	38.81063	23.12403	23.9573	20.37447	24.58463	0	0
Rbp1	72.8299	100	68.14256	29.01486	13.86852	14.39861	29.90225	11.67764	10.83891	0
Tgfb3	100	95.9951	59.24948	44.32128	20.48289	0	6.987173	17.35197	22.98143	12.10489
Arhgap24	88.82245	100	75.0443	26.39403	27.54737	0	0	23.52109	21.95209	0
Fkbp9	100	77.46718	49.98195	28.99844	9.035544	32.19843	13.54256	32.67229	0	5.606752
Hspg2	100	75.37001	59.61541	32.81259	0	0	21.40995	27.29467	0	0
Cd34	100	79.01395	45.81423	47.20733	0	17.81648	24.8175	22.62468	2.461242	6.908329
Pcolce	99.02495	100	60.64351	19.744	33.31603	26.51637	9.744867	38.95253	8.535747	0
Rnase4	93.34075	100	43.85577	11.13054	16.57721	34.05724	5.652221	27.41054	17.67235	0
Ddr2	100	92.17391	44.55857	12.53363	0	7.198953	15.81951	24.60263	5.346194	0
Gpm6b	88.83999	100	40.02577	5.279528	10.62365	11.03806	6.766391	29.68746	0	0
Gfpt2	100	82.06172	37.16526	9.665433	0	19.4566	0	33.80816	0	7.660821
Plat	100	90.67435	48.74403	19.66045	0	14.98651	0	19.93506	5.916314	0
Loxl2	100	85.37036	52.85997	23.12262	0	17.7413	0	26.15286	0	0
Ppic	100	86.85206	52.40447	30.60304	26.65365	8.082781	9.448919	33.75041	0	0
Fbln2	100	91.5173	52.56562	22.65968	18.04988	0	8.9951	20.16422	0	0
Lamc1	100	97.58061	55.1414	22.23202	30.11033	11.74263	8.084033	16.97452	7.076134	0
Rbms3	100	85.90988	68.36223	15.19668	15.9119	16.50988	0	19.20781	0	0
Ogn	100	92.68441	72.34098	15.63705	0	7.335215	14.35364	26.25465	2.778634	0
Htra1	100	92.27386	63.60663	23.71457	0	6.648431	4.011548	23.07698	13.77467	0
Retnla	77.36195	77.97646	54.1286	72.65691	100	49.521	34.52105	7.591049	8.550482	0
Ltc4s	70.56655	85.65243	26.94504	29.37367	100	27.9398	3.718859	0	17.61484	15.78434
Fn1	100	65.78052	22.49105	45.63887	52.23623	45.98917	40.78732	10.82254	12.79041	0
Lyve1	66.51593	100	43.31569	20.96575	43.65871	11.17239	15.83421	4.689976	4.336839	0
Fcna	81.89963	100	50.4942	15.00178	64.12288	54.62096	0	7.501926	5.934309	2.724707
Vasn	96.45153	100	45.71009	17.8846	56.37035	47.30358	12.09971	15.81527	26.8966	0
Sdpr	37.02844	47.77289	67.82265	100	48.93919	0	9.212111	6.335108	7.697976	0
Wwtr1	43.19082	100	66.71939	98.80738	0	0	16.26322	11.34113	0	0
Sparcl1	59.02069	100	81.10422	81.43226	24.91779	0	14.25527	18.53582	3.18797	4.590275
G0s2	49.13638	95.76244	100	76.8098	9.328728	10.45883	8.951875	23.45949	15.01205	0
Ehd2	99.70716	92.79785	87.35878	100	64.40544	30.94904	0	25.3776	0	32.59532
Thbd	64.85732	81.78354	89.61171	100	56.86729	9.870403	0	15.3278	33.98918	59.0139
Galnt15	94.43133	90.65191	100	68.95901	47.75589	28.20659	17.78164	32.63801	38.62102	0

Tim3	100	86.87479	82.84649	95.4088	36.7087	14.75922	11.84949	25.46439	0	0
Tek	100	77.68303	66.09857	94.93122	45.37301	0	0	0	20.70469	0
Ly6c1	99.5109	75.32526	76.08014	100	52.88826	0	5.317353	7.895367	3.333034	13.59331
Ramp2	96.15954	85.06722	62.58809	100	40.59966	0	19.37429	10.37242	0	9.337496
Osmr	75.72789	100	60.62344	78.0476	62.31283	0	0	18.09645	0	0
Ablim1	100	94.43657	58.54751	62.72084	43.20367	19.6999	0	0.096897	11.4863	10.77472
Nfib	88.56081	100	61.97441	70.15213	46.25175	8.047058	4.865463	6.456862	0	0
Arhgap29	100	86.11023	60.21279	73.629	50.66785	21.83699	13.68077	9.460541	0	0
Uaca	0	62.35102	64.48327	100	85.18568	0	0	32.09688	21.35127	50.06513
Ctla2a	0	59.01549	85.44494	99.09552	67.95425	16.58817	41.68213	3.56699	12.44922	100
Tgm3	0	43.16155	88.59755	98.66808	93.79593	66.29197	35.3027	32.16855	16.22957	100
S1pr5	0	11.63853	82.68864	100	76.84965	27.43692	36.25321	24.35482	34.97483	86.44472
Lims2	74.87007	58.73489	68.91339	84.08525	14.67276	100	0	12.92016	63.5949	84.19845
Ednrb	67.55694	100	46.19301	67.30076	59.30459	78.5804	30.5406	0	57.80437	43.25277
Hspb1	32.58289	32.18012	25.84352	35.73122	10.35402	1.451664	0.296183	1.979258	0	100
Ets1	100	38.36461	52.40264	74.0651	36.24646	42.63871	0	20.11886	36.93835	54.38868
Nckap1	100	66.74942	60.34652	47.26232	20.51091	21.26391	24.50787	17.37704	0	52.77086
Ly6a	100	75.28457	58.78796	49.24026	35.72648	0	12.95446	19.15932	22.18776	47.88121
H2-DMb2	79.60717	11.40729	0	23.30376	34.79888	32.81808	100	96.15112	67.70747	67.34005
Siglecg	97.54203	33.48774	8.773002	0	23.62507	56.04583	100	83.53116	40.55625	39.17087
Bub1b	82.12686	15.66523	1.47809	0	66.81171	32.29317	82.12686	100	78.73409	16.07477
Cks1b	66.06775	12.14044	0	20.14031	79.26453	82.74926	99.38741	100	41.6668	18.07952
Ero1lb	55.33594	8.478186	0	26.32085	55.54187	58.20386	88.27617	100	57.51682	54.18773
Tacc3	43.28645	25.02782	0	9.579881	52.99374	61.64437	77.61296	100	63.60735	34.61883
Smc4	44.94616	9.634048	0	25.1821	60.48766	70.47935	93.59745	100	62.21914	29.57171
Anp32e	34.87804	14.8894	0	13.2393	50.75228	65.64564	97.17843	100	70.56645	36.11449
Fcho1	53.14775	10.23177	0	25.87852	43.17975	54.49096	100	97.01732	71.25586	12.68491
Smc2	46.00545	0	2.648633	15.43342	47.94527	41.28914	85.03126	100	55.19923	34.69273
Map4k1	43.29362	2.490799	0	10.6323	48.20329	49.60716	91.14838	100	62.48038	19.72756
Mtmr4	4.708605	12.47931	10.971	22.35147	40.57207	0	100	66.00966	25.76444	33.78665
Cxcr3	0	12.34414	6.391244	6.111532	35.85231	54.00404	100	62.84716	6.520696	13.37804
Tlr3	3.348811	3.318615	0.982413	0	48.83555	58.19441	100	50.53051	4.697238	9.943416
SigIRR	0.108462	5.051949	0	1.664619	60.81614	34.17112	100	47.43005	3.911059	18.12323
Kctd14	13.91857	0	11.22164	5.26937	45.57149	35.09998	100	63.10743	15.44183	11.62766
Lsr	5.817738	8.528355	0	22.69745	50.25979	37.25026	100	65.58144	20.61018	21.26549

Btla	19.19979	1.759035	0	4.706269	23.68567	46.64837	100	61.13333	13.51681	9.711809
Pdia5	21.85485	0	7.038603	4.247833	26.59893	59.14652	100	76.09387	19.09192	29.81555
Clec9a	0	2.418785	4.386529	5.916695	40.08065	62.92658	100	62.30051	23.30302	18.76607
Naaa	5.899179	5.36927	0	7.121274	46.18372	64.68505	100	77.55647	35.00593	20.31448
Naga	8.57526	0	9.990025	7.276505	46.41191	68.83042	100	77.76842	31.94843	20.77051
Nup210	31.4449	8.463688	0	5.570209	49.67412	56.11309	100	58.29559	29.33637	32.20301
6-Sep	20.50726	6.836624	0	5.140088	39.69692	56.57474	100	67.2764	25.68569	18.74518
Wdfy4	20.52111	0	0.892067	13.8613	52.68084	64.65925	100	58.97397	30.26222	12.54103
Kif23	28.22054	0	2.153718	17.19832	87.52528	69.83915	100	80.11189	34.00789	23.82619
Hmgb2	30.7815	0	4.206227	26.74986	69.07267	73.04096	100	92.1614	38.51527	33.68007
St3gal5	22.89343	0	7.964659	24.63258	61.87672	76.96809	100	64.29048	19.94467	12.56529
H2afx	17.173	0.857082	0	14.80407	53.70669	70.52099	100	90.40948	27.91874	30.19021
Tnni2	7.394872	10.57386	0	12.56614	64.36527	78.38875	100	74.15027	17.40607	24.32046
Unc119b	36.09915	29.52565	17.98355	0	66.12369	73.96958	100	83.92727	26.92471	11.14109
Racgap1	45.79793	18.18704	0	3.091541	57.30632	76.32421	96.522	100	31.05059	27.14321
Pkp3	38.97861	20.1113	2.750558	0	51.99748	67.65457	100	72.98188	40.83146	36.23452
Ap1s3	32.93385	0	1.592342	1.210218	56.25864	75.66002	100	88.67777	43.77619	22.29112
Itpr1	33.49376	1.880318	0	5.817879	48.15807	71.51432	100	80.98751	45.03868	19.71433
Mgl2	12.07258	15.81145	5.600157	16.38316	65.56278	56.91487	86.43484	100	26.22269	0
Klrb1b	20.52462	3.886649	7.174558	0	50.97321	40.28689	87.34763	100	34.3818	22.10808
Prss30	5.248936	0	24.36965	9.200177	66.73454	61.59552	76.89877	100	34.35306	25.35527
Aurkb	34.83817	0	6.837471	36.58941	40.2371	71.63024	100	94.45977	30.68216	32.53748
2810417H13Rik	24.63879	0	5.881184	42.69343	41.2012	52.62448	90.66541	100	38.75619	11.73228
Top2a	40.91713	1.118788	7.055011	28.31954	47.48939	61.67953	95.5457	100	37.71595	0
Spc24	48.05833	0	6.744371	21.1844	43.21174	50.2098	87.51242	100	36.44514	12.31972
Me2	28.13855	2.481448	0	25.72393	49.21628	68.37048	100	73.04386	46.60546	21.4599
Dctpp1	32.80445	6.110948	0	15.47989	45.60292	81.79144	100	79.60335	44.65955	24.40139
Cysltr1	18.96329	19.60041	0	18.06274	42.93617	72.73572	100	84.84197	56.45309	7.550011
Sesn2	15.92271	2.599561	0	2.760576	48.15622	65.59276	100	75.35092	47.50836	10.67565
Kmo	10.61301	0	11.4411	0.992155	44.06569	58.64706	98.74778	100	45.39622	12.14413
Cox6b2	17.74687	0	3.356199	2.747513	38.90357	72.30901	100	93.40089	32.55575	4.522661
Zbtb46	18.02173	14.98337	0	21.46861	38.02784	52.78103	100	89.26955	33.3646	7.33377
Olfm1	31.86405	13.46502	0	16.48999	45.73596	51.14475	100	89.94559	41.23505	20.78182
Gm2a	13.49852	0	1.734367	19.23434	33.71642	48.10159	100	85.63119	45.04452	24.16668
Itgb7	21.02376	0	15.35484	13.0054	32.85554	57.81745	100	81.34752	37.09612	14.6863

Impa2	24.52735	0	0.582039	15.70135	42.51268	64.04096	100	88.64862	34.02635	14.9631	
Sgsm3	0	11.49509	31.8388	35.42547	48.43098	80.2128	100	84.66598	31.61322	45.19113	
Gpr35	0	5.19889	28.8255	22.61809	56.90978	86.06485	93.96418	100	45.03377	60.64447	
Aldoc	24.60111	11.11225	8.281976	0	28.09706	97.007	98.37439	100	37.29919	18.32639	
Acss1	22.29472	2.530656	16.02806	38.05994	53.6408	88.63909	100	97.09742	45.62065	0	
Birc5	31.23071	0	3.252269	17.73307	61.39904	75.7346	82.74154	100	53.71684	32.55097	
Stmn1	28.6423	0	1.238555	24.03672	47.4433	75.98382	91.88352	100	47.62707	13.5025	
Nccrp1	0	0	11.56492	11.07616	45.98474	100	78.41427	50.29233	21.69643	16.48982	
A530099J19Rik	0	5.490499	5.209793	0	32.29607	83.38105	100	67.5447	0	8.76785	
Cxx1b	0.516731	0.443319	0.701821	0	43.96796	89.19655	100	71.44667	12.96389	0.033903	
Arsb	20.09313	5.384484	0	4.292625	54.06264	69.89139	100	79.96318	18.50135	2.044774	
Xcr1	4.219558	0	1.848032	3.894996	47.56245	70.58009	100	67.92132	14.88115	9.751551	
Amica1	3.17301	0	1.997632	0.34338	46.37997	76.52953	100	76.79447	24.14085	8.839979	
Mycl	2.795466	0	0.740571	11.95933	40.49225	65.02566	100	84.18298	3.474262	6.180346	
	3-Sep	8.322933	1.466484	8.701938	9.608524	48.39347	60.64669	100	66.27992	3.25898	0
Gcsam	0	7.391596	3.217534	0	56.84876	67.24126	100	73.621	0	8.042905	
Cd24a	48.89544	21.97533	14.57579	17.53342	48.62469	77.28832	100	55.24789	8.449698	0	
Fam149a	23.5552	25.9176	17.5184	0	43.92769	67.92952	100	65.24443	7.535984	19.86246	
Ifi205	22.88954	31.02235	15.36763	0	43.52501	53.98497	100	78.6423	7.765165	38.28657	
H2-Ob	46.79446	0.61702	0	5.153094	37.09588	51.50593	100	84.63082	25.50186	25.17473	
Hepacam2	33.25364	15.16978	9.988247	13.72219	46.7262	48.12192	100	75.32722	12.7008	0	
Ccdc69	46.11957	12.67602	11.24349	5.18961	37.38071	49.11321	100	91.03564	19.71886	0	
Oasl2	1.041064	5.499052	0	23.70939	60.61022	46.64951	28.63789	46.59546	100	94.14963	
Aif1	0	9.369559	4.39139	22.84239	47.52651	42.16726	52.97153	65.38274	100	90.37324	
Rtp4	0	12.23967	16.37027	38.85507	55.01678	46.41284	34.18303	54.68961	100	88.14229	
Ms4a6b	0	7.358298	21.10664	35.37216	54.91936	45.47413	46.62931	74.84539	100	79.51975	
Parp12	0	10.94079	9.112866	6.228937	38.70446	17.10265	44.76945	66.50827	100	80.7313	
Cxcl16	0	2.179617	1.080847	15.08381	22.85327	28.34371	45.04723	73.27736	92.30764	100	
Igtp	1.205599	0	10.80665	15.27563	38.84853	11.59768	42.4883	56.86491	81.06288	100	
Stat1	11.18246	0	15.75967	22.19197	37.50855	30.03926	43.50561	63.63856	91.71554	100	
Cd72	0	11.10392	6.900336	33.61333	20.22585	38.37501	20.33336	55.96884	100	97.28775	
Zbp1	4.545076	0	23.19656	40.11489	22.78124	19.95597	36.40649	63.09124	88.27134	100	
AW112010	0	5.38764	11.49805	21.84247	28.21996	39.02814	26.10122	28.60222	65.04073	100	
Ifi47	4.023177	0	7.137864	18.5002	22.20847	36.31305	29.44391	54.65555	75.28107	100	
Fam26f	0.619537	0	4.652167	24.26914	27.03445	25.77643	21.89738	49.16665	82.64113	100	

Relb	5.125278	0	6.310177	6.052259	21.18817	24.23662	33.89925	48.00084	61.17437	100
Cd40	18.22699	0	3.046442	5.053616	24.01958	21.77681	33.81875	45.58575	56.82083	100
Tbc1d4	12.52139	9.182747	0	3.308294	16.85122	30.05162	41.35858	39.48528	48.81779	100
Tmem123	20.21361	6.537935	0	3.629938	8.503719	25.712	31.70223	33.75815	52.83905	100
Il21r	13.1103	0	8.305561	9.545784	7.156672	42.00611	32.2642	58.33403	55.36116	100
Il4i1	0	12.84616	6.698482	8.799306	6.281698	22.08266	43.52603	53.27973	65.90921	100
Rogdi	5.261211	2.437322	0	8.181167	11.56258	26.70972	34.36057	53.16886	70.67965	100
Spint2	1.64184	0	10.33523	8.200539	20.11186	35.12858	59.80993	47.84617	45.46239	100
Cpne2	9.097849	0	1.451731	3.43121	24.3876	52.24029	59.48264	60.22645	49.44466	100
Irgm1	2.625258	0	10.04419	30.25656	21.80902	45.79291	48.92962	68.89772	56.17841	100
Lrrk1	0	1.600126	6.35075	14.92841	35.21512	35.41214	52.4875	65.9508	69.0954	100
Marcks1	6.281804	11.45019	0	9.003522	26.03601	37.58024	46.1378	58.99896	56.33111	100
Arhgap22	7.701469	6.078254	12.05796	0	30.34962	49.09508	69.02898	75.80077	71.77375	100
Traf1	1.914371	0	10.28109	16.57597	23.80686	43.48863	60.1485	75.64586	66.64241	100
Pyhin1	1.025964	0	6.272232	21.26058	31.71841	44.70663	74.40606	74.93569	66.79138	100
St8sia6	4.546927	14.93331	0	21.19276	25.9787	27.33528	73.09425	62.04509	69.05649	100
Fbrsl1	5.134999	18.22778	4.860532	0	17.61286	30.38854	67.86534	65.83403	60.32997	100
Ass1	43.72247	7.38274	0	33.53069	12.95019	26.1794	72.67043	50.46491	54.85345	100
Hmgm3	34.47767	7.972804	3.017859	0	11.91911	55.07544	60.79283	49.37429	32.88582	100
Pla2g16	13.07398	7.73044	0	11.54875	17.36288	65.07363	78.89182	51.71957	47.27881	100
Kynu	28.56319	0	26.92235	45.22091	28.08568	13.06922	67.90887	94.87295	100	45.27147
Tspan13	4.700598	0	37.65371	52.75164	57.10683	50.34582	100	98.16369	79.54315	71.0951
Mcemp1	0	12.03684	34.07773	49.79433	57.0829	59.53723	71.44236	100	91.84111	74.87432
Gpr18	17.67284	0	16.15857	37.52261	42.72154	23.67859	55.52252	95.82329	100	79.83356
9930111J21Rik2	25.87687	0	18.2951	38.76776	60.78842	35.11452	65.81528	100	96.05962	66.51703
Zbtb45	17.03772	0	13.81943	37.0729	36.68728	49.30486	73.73293	86.31547	100	80.2698
Cd180	7.332506	0	6.389206	33.37794	46.42487	57.54753	72.94947	92.41346	100	81.96931
H2-M3	0	21.72293	16.5656	33.52984	45.9682	38.30978	77.89234	94.44341	100	82.17999
Ms4a4c	0	2.002819	17.73899	38.05183	50.90073	41.27582	73.71225	100	99.33179	96.82658
Ms4a6c	0	5.301633	18.74627	36.05755	43.80718	49.3773	65.46038	95.70355	100	81.51029
Nmrnl1	17.03707	4.328068	0	10.0073	79.18795	30.225	100	87.46099	78.93612	65.79603
Vrk2	6.400652	3.558229	0	16.81666	65.99965	43.4565	100	78.57041	97.8611	94.82751
Taf6	0	21.32945	3.159313	11.69296	57.58097	35.06459	97.5713	100	92.5301	82.72864
Cenpl	26.20098	16.55925	0	12.68932	57.19958	19.83989	67.2537	100	47.2229	76.92685
Il18	35.40031	5.590375	0	23.53965	53.03824	21.90441	100	73.53965	66.52467	78.80457

Vrk3	24.24887	0	0.084355	8.463707	38.51812	23.93497	92.49008		100	79.76941	78.42339
Phf11a	0.018021	0	8.860584	16.6737	28.4679	31.36889		100	78.35788	53.08988	81.29694
Sass6	4.188697	0	32.08565	11.27953	47.06241	49.56874		100	88.59129	69.55956	84.76719
Selp1g	4.536112	0	1.521516	11.87736	50.99205	49.34091	85.47481		100	78.57418	87.38245
Phf11b	1.079955	0	9.176397	17.97586	46.38593	57.1929	87.58054	76.36021	72.86245		100
Tap1	4.577596	0	5.383085	12.00339	34.00132	44.39859	87.79911	81.5077	74.02673		100
Mnda	3.545145	0	3.333346	17.30108	46.99499	46.34042	88.88505	86.89089	62.73139		100
Pmaip1	20.92783	0	9.414419	22.4775	42.2507	72.64409		100	93.30203	58.42043	67.11036
Orai1	21.14774	0	6.381951	8.819606	36.38094	71.03414		100	92.79607	61.95146	73.03035
Tmpo	19.93968	0	11.18991	26.39843	39.4343	54.12679	90.68791		100	61.01608	70.36224
Lsp1	15.72662	0	5.907708	21.63447	44.56426	59.9852		100	90.60622	46.04743	56.30981
Def6	23.20706	0	2.796338	23.53564	44.32443	61.44259		100	85.68523	63.06629	62.15988
Rrad	20.19761	18.08567	6.180829	0	35.9157	38.15455		100	84.52792	74.80977	64.47038
Isyna1	19.18858	16.85937	0	1.235594	34.56566	64.92899		100	87.73111	69.96169	68.41614
2310040G24Rik	12.63312	10.61339	16.8701	0	44.49361	46.61161		100	81.77638	51.45303	69.76176
Parp8	0	9.081918	6.859909	9.219602	41.71037	44.27257		100	85.32072	65.8906	51.64627
Cntrl	14.81037	8.119131	0	21.58899	42.46869	45.2015		100	77.25255	62.99907	61.71243
Pold1	62.78539	0	15.39654	7.8882	12.90085	71.73742	95.0746	92.08531	85.65059		100
Mrps27	30.36794	13.73917	0	19.92386	15.49632	60.38778		100	86.01205	73.434	77.07974
Asnsd1	35.64993	12.64248	0	11.28106	29.1539	47.84465		100	92.1265	80.58135	85.90436
Eif2ak2	4.416953	7.751623	0	19.00387	57.33918	94.81344	60.62092	70.61796		100	78.72668
Fdps	5.548814	9.206666	0	16.40314	18.24333	65.72932	70.9974	55.86184		100	76.79394
Card11	34.42822	4.512322	0	11.24329	28.82315	60.48101	57.80706	84.3338		100	72.92494
Ccdc130	15.09154	10.0554	0	18.44676	30.09611	73.59598	43.18501	73.90274		100	73.12419
Tor3a	16.8934	0	4.426428	16.49776	38.78654	50.48015	38.56141	60.69518	81.37428		100
Icosl	9.019394	0	10.27186	9.319475	37.83979	72.70654	56.18015	74.04157	70.00237		100
Mx1	0	10.58793	11.7159	7.801379	33.87975	54.73326	60.04825	62.23548	79.5902		100
Psme2	9.953613	0.717917	0	13.59366	28.60065	50.65924	56.20914	60.37163	72.96221		100
Tmem176a	2.428434	5.899345	0	16.01871	46.19978	42.79	59.31602	87.56073		100	81.65474
Tmem176b	8.840061	6.646195	0	17.02848	48.4373	47.13783	54.54202	91.40145		100	73.26778
Slamf8	1.566115	1.511781	0	20.72963	29.26085	52.02856	61.76096	78.58861		100	92.46502
Tapbp	9.640463	0	4.295158	15.18832	36.73826	47.80735	64.31789	70.09216	81.53635		100
H2-T23	9.534794	0	0.02773	18.88954	42.3597	36.88875	66.93971	76.36417	86.4345		100
Slc31a2	1.075159	0	13.56334	4.34772	23.34442	57.02601		100	94.89857	99.746	98.04483
Slamf7	0	7.328077	10.73184	24.42006	44.13917	50.13248	92.73452	95.92241	87.53052		100

Ppil2	0	13.79603	12.9183	16.43609	34.85181	59.1273	92.54678	89.95468	89.69208	100
Traf2	0	17.12878	13.94911	15.64575	46.1892	58.16269	74.56492	80.74325	99.41446	100
Cd86	11.96363	0	7.983946	17.81032	48.41762	57.36789	75.52024	85.02189	90.53815	100
Coro1b	10.35659	0	7.122004	20.45753	39.41018	49.34659	71.01451	85.27568	95.39551	100
Tbc1d8	14.11703	0	29.06625	21.99272	39.48377	59.72246	85.9992	57.10423	66.17684	100
Apobec3	28.41637	0	10.62491	19.07624	31.84962	67.11152	73.8152	84.17402	69.31499	100
Mthfd2	26.2357	0	8.267914	12.72307	33.34072	86.96096	91.60405	83.46308	60.55714	100
Cadm1	0	0.306244	10.19583	31.36155	38.24588	81.71111	81.55158	95.58745	100	90.29238
Sp110	0.122302	0	13.48077	19.38617	43.95734	78.65314	80.73576	94.61346	90.84269	100
Scimp	0	15.37987	12.23165	44.73758	49.55651	71.78543	96.56717	95.73671	87.60601	100
Irf9	0	8.155543	10.12041	25.8367	57.35377	60.56003	94.22139	98.32231	99.20032	100
Psmb8	9.77463	0	6.383427	24.20775	46.44197	66.14421	94.11475	92.60936	88.20436	100
Mpeg1	4.75961	0	5.967132	24.92337	53.75067	72.28285	88.96767	95.3239	100	94.91089
Slc25a10	19.64989	15.18675	0	32.71703	50.75176	91.68019	85.32271	96.79274	98.61887	100
Eif2b2	22.13729	0	4.830625	15.46232	47.22937	96.33873	80.28449	92.18239	100	93.92913
Sh3bp1	20.1651	6.342668	0	10.80944	59.654	78.78	99.32436	100	94.98708	97.75667
Dapp1	26.35423	13.40757	0	16.2217	58.57022	77.97126	100	86.1769	92.05047	84.57074
Gltp	10.84845	6.448641	0	20.39708	49.98474	81.13614	86.79513	98.66136	100	82.80216
Sdf2l1	27.101	6.391686	0	28.93083	47.42496	78.81143	98.74854	100	97.87549	89.88061
Tmem150b	9.745417	0	11.10252	42.02258	33.99497	82.28955	98.18424	100	62.13425	86.58947
Slc46a3	0	6.820097	18.2326	29.77783	51.1563	70.13143	100	84.77539	78.65807	75.99525
Psmb9	9.060234	0	9.535961	27.94628	41.97609	68.65701	100	97.87487	72.90912	92.19195
Trpv2	1.059527	0	14.63472	29.97269	48.98104	76.49758	94.09886	95.30042	80.39303	100
Hn1l	29.29102	6.600509	0	16.96535	35.1041	78.33438	93.69327	100	76.91991	90.98276
Cnn2	16.51541	0	4.518006	10.9247	43.69846	76.12459	99.55618	100	69.37213	85.28483
Fuca2	21.392	0	2.084397	12.80695	33.22096	76.38881	100	86.35354	79.39622	88.22841
Gdi2	17.86918	0	0.583392	15.18279	38.73533	72.31896	100	93.5178	82.95369	77.62484
Cd83	9.411787	0	2.055582	14.24316	44.20766	66.02077	86.50189	100	90.78784	90.88314
Irf5	8.667492	1.345177	0	21.38307	37.91896	74.68013	89.42089	100	88.13962	95.68567
Syngr2	9.3547	2.624636	0	17.18655	31.29451	58.55842	89.42661	100	79.36565	88.82016
Ifi30	15.93555	3.461038	0	7.918327	33.68264	60.91463	84.42408	99.61018	85.72568	100
Fgl2	13.96589	7.342346	0	3.248234	40.09671	60.20417	100	99.93642	89.20379	90.20103
Avpi1	31.33226	0.158569	0	13.46472	46.31763	59.92266	96.18257	100	88.53144	96.5006
Tap2	14.77746	0	3.614682	18.19991	33.87966	67.70349	100	84.349	77.698	99.64764
Psme1	6.884772	0	0.318997	17.7913	44.11558	56.9068	100	87.09136	78.00664	95.21725

Hacd2	15.01148	0	0.65286	8.804477	41.77643	55.83016	100	87.16127	70.86921	85.99082
Tspan33	7.486746	0	2.453921	11.91725	50.89271	76.19167	100	85.12275	87.68683	79.89171
Ranbp3	14.14575	11.25588	0	5.561936	29.71684	75.0581	100	86.42433	91.53402	83.74111
Nudt14	32.76807	0	1.721646	22.70203	36.5179	46.2022	100	96.83422	95.90116	73.35654
Sp100	10.25807	0	7.988054	28.39325	44.11652	46.18487	97.84608	100	85.78481	70.03
Mboat7	20.29709	0	0.824416	40.60166	28.46196	49.70068	93.00369	100	86.27386	74.64848
Ciita	9.588059	0	6.690282	16.30864	39.75943	59.85738	80.55245	100	78.11738	55.05838
H2-Ab1	12.70613	4.919727	0	16.56794	49.89105	60.54376	91.49003	100	90.11931	64.26891
Cd74	12.63097	2.774782	0	20.06704	50.19527	63.21521	89.93415	100	92.17672	69.77967
H2-Aa	10.66548	3.293797	0	16.18351	48.93033	60.20428	86.85114	100	93.23483	72.55926
H2-Eb1	13.69382	4.565754	0	16.74382	49.03449	59.15048	86.55398	100	94.96454	69.34678
Ccnd1	0.630076	2.644584	0	18.67723	44.36999	47.60797	83.73379	100	92.62007	67.29947
Fam105a	0	1.05534	5.488224	21.04812	44.85996	50.51796	83.11599	100	92.48985	57.18082
Tmem173	0.088826	0	0.982488	29.02188	53.51517	62.61081	100	96.52273	90.38495	73.20446
Cd48	3.774913	0	3.418922	35.69291	55.22099	68.76145	90.34751	100	91.98785	70.00898
Abhd17a	21.9456	7.614105	0	14.48385	55.49272	53.76788	94.55225	100	81.41877	66.97006
H2-DMb1	16.34565	7.590319	0	17.25706	52.97669	66.34619	92.07809	100	86.81515	53.02142
H2-DMa	25.43825	9.606308	0	19.45458	56.13435	62.67882	96.26981	100	82.92407	54.18996
Polr1e	18.3826	1.449338	0	23.04806	45.55263	47.9265	89.93989	94.43425	93.1229	100
Sdccag8	18.83725	9.653735	0	29.32487	45.63382	40.97039	91.43655	100	96.50531	86.79933
Tifab	21.34048	0	18.58893	27.71755	54.04658	54.11603	82.53338	100	96.81205	88.40111
Trim12c	34.32335	0	6.623925	31.62236	72.15384	53.7977	91.11032	100	97.84974	87.26885
Coro2a	39.71505	0	3.899254	33.83397	57.75967	76.67403	88.86015	100	74.4367	85.24889
Ndufaf6	43.25339	0	9.101355	31.05025	57.24628	52.78051	94.93028	100	77.0102	92.18673
Nsmce1	24.19931	6.769607	0	14.62955	45.71279	59.86319	83.23074	100	77.63852	70.99529
Tubb5	36.59027	4.404767	0	19.30554	40.92371	62.16357	87.04396	100	72.5362	77.6843
Ptcd2	24.78538	0.774334	0	16.98349	47.67114	63.15115	79.41997	97.59127	100	77.63336
Rpa1	47.91936	5.821048	0	21.98968	45.62265	68.67539	84.0139	100	93.62149	73.59952
Mical1	0	7.797614	17.53481	21.18623	29.2734	45.7932	99.88424	100	52.44148	49.41383
Flt3	0	1.791663	1.312583	1.641646	29.71568	58.27185	93.9953	100	50.85296	50.65438
Klrd1	6.323829	0	5.318309	3.244922	15.55081	50.9642	84.25231	100	47.82449	43.64464
H2-Oa	8.520562	2.417463	0	11.61684	24.65971	40.78641	100	95.09138	61.74441	55.97542
Fh1	10.56114	8.463004	0	2.80486	21.13191	54.55984	85.72909	100	67.01216	58.49285
Aaas	0	13.52019	10.91718	8.928815	37.71274	61.77879	100	88.97474	60.27699	29.32472
Trappc5	2.19188	9.935544	0	14.37453	28.57785	59.76966	88.97196	100	64.03305	40.97369

Mcm7	7.469799	0	4.50275	30.40998	26.3833	66.68802	100	84.63606	73.94533	28.7527
Lig1	0	9.134068	0.735939	29.59771	21.15269	46.16542	100	91.71296	66.39464	26.95411
Mcm4	31.21671	20.92407	0	31.89984	25.32032	59.627	100	89.40218	51.61117	46.34492
Dnajc9	20.38024	6.047997	0	29.8827	28.39788	68.69978	100	99.74307	64.87351	32.15554
Mcm5	24.36147	5.135952	0	24.20741	11.69179	68.06752	100	95.77608	61.07547	23.84665
1700025G04Rik	14.8587	12.71343	0	11.70096	35.94396	50.27749	100	82.63074	45.65957	29.94118
Ccdc102a	15.99547	21.46244	0	11.92685	26.13	49.51401	100	73.23314	43.1313	31.06136
Dpp4	22.92439	0	3.39442	1.133476	19.62287	41.94482	100	76.17881	42.94417	39.19097
Bloc1s2	23.16505	0	4.989988	6.434679	30.5313	52.43427	100	75.46264	53.06292	42.15829
Prim2	27.14051	0	3.663528	11.72044	34.02152	50.44661	100	66.03229	58.42619	31.42987
Cd209a	5.011557	2.242881	0	1.646182	23.57906	34.94621	89.32585	100	46.74161	10.07726
Parvg	8.323313	0	3.071898	1.128424	12.31476	59.42462	100	97.04163	40.30466	21.40423
Trit1	0.312375	34.94467	21.00727	19.40867	0	47.11415	90.18222	100	88.27314	56.48907
Clec10a	7.278783	16.87378	0	7.096097	13.35356	58.58065	71.30928	100	70.94462	37.15915
6330416G13Rik	13.45249	24.99415	22.91997	25.12253	0	79.69388	70.36525	100	76.79051	31.4207
Ddr1	21.27783	8.209176	22.68308	0	13.32203	47.26878	57.75267	100	58.67334	60.55404
Bex6	31.3278	0	12.54123	1.988615	40.87275	47.84062	94.09414	100	80.68899	46.08574
Fgd2	23.9394	1.637272	0	5.668316	33.32727	62.45344	100	94.60027	71.74896	41.15863
Dynlt1f	25.37736	0.206666	0	3.168443	36.64456	65.92088	98.62667	100	73.24827	57.10421
Amz1	31.3369	0	11.81621	23.69471	38.51273	56.88157	71.48896	100	63.10197	40.97497
Incepnp	24.87585	0	6.632481	16.96716	40.08752	79.52671	76.19749	100	70.06729	53.54474
Rrm1	29.54154	11.75835	0	15.22762	42.45721	75.29483	77.26659	100	70.5529	36.10729
Timeless	31.44875	0	3.948561	17.28344	23.16517	74.56547	100	46.02679	67.98365	9.088718
Pnpo	18.34295	24.14482	0	0.230924	48.12679	51.22863	100	88.10984	85.24354	21.26759
Casp6	13.96858	29.9241	12.29873	0	38.32683	77.17606	100	90.92082	68.13246	29.41153
Atp6v0a2	29.56956	24.70189	0	8.137066	23.95358	68.54771	100	81.63661	69.74353	35.66493
Uhrf1	28.27943	8.020042	17.64337	32.58219	34.64347	55.08049	100	84.99966	81.12142	0
Tk1	12.0097	0	3.207433	15.58577	51.84985	34.40359	100	97.66661	63.35253	9.926088
Rnase6	11.18861	0	17.19464	30.33043	44.88357	64.72873	100	72.28609	37.07185	35.7297
Ppt1	0.187228	0	4.344565	8.929343	34.51222	59.06409	100	74.64348	40.79446	37.09585
Cst3	0.778619	0	4.410665	13.70842	43.00642	64.29748	100	73.26912	33.13058	35.5766
Ppm1m	15.51061	1.929966	0	17.25758	42.29536	62.15611	100	83.44987	40.60269	32.34188
Plbd1	2.645453	0	4.142935	14.4629	44.04024	67.00942	100	86.31011	42.15907	27.93753
Vrk1	7.607673	0	5.313163	13.99687	31.21611	70.07693	100	83.20828	38.19331	29.42067
Dynlt1a	0	2.23253	4.238432	19.35716	53.81412	80.23522	100	83.84403	52.61696	29.15469

Ffar4	10.06232	5.116613	0	16.84927	60.82256	77.10036	100	82.0864	43.48999	50.58827
Anxa6	19.98613	11.43516	0	15.71999	51.1648	73.81978	100	82.0299	48.75911	48.24919
BC035044	8.379845	0	2.388858	17.18677	54.30253	64.91662	100	75.10548	51.31699	39.4533
Cbfa2t3	16.8825	0	14.07993	22.01695	55.52964	60.8583	100	83.06999	47.06088	41.77217
Slc25a20	13.53097	0	3.323944	22.98414	38.4599	57.43343	100	50.21948	44.14149	44.25736
Irf8	1.039297	0	6.321221	10.11035	39.89419	70.52991	100	80.38549	41.47646	53.67481
Cldnd1	0	12.47546	0.008067	13.02745	36.49568	66.37204	100	75.21704	49.49869	65.35096
P2ry14	4.501528	0	13.7689	0.967989	30.27592	72.28124	100	49.73974	60.47441	68.99441
Rnaseh1	17.7522	13.35644	0	12.90347	36.24918	67.32683	100	67.87502	73.76077	49.17762
Slc25a38	26.52076	0	11.64491	3.978611	24.04467	64.21163	100	59.15413	76.0506	44.06889
Pafah1b3	41.83819	7.630652	0	1.328189	37.3298	81.32563	100	76.10091	40.53192	59.50617
Got2	35.753	0	0.887088	13.115	38.19484	82.26193	100	77.4936	55.76445	68.75758
Khk	26.69621	0	7.291138	15.09818	45.99311	59.53533	100	67.01426	61.80054	49.19998
Dock10	25.30019	0	6.848964	16.18842	50.69333	54.94972	100	79.07736	61.68909	52.42229
Pak1	12.53152	3.392721	0	1.968561	42.85853	59.12597	100	72.06872	64.30537	52.58474
Rab32	11.45304	0	4.487725	10.12517	39.12159	63.76622	100	77.42544	55.42288	56.92638
H2afy	14.4738	0.696192	0	12.54325	38.33773	66.51144	100	87.47966	57.23591	42.57713
Cnp	26.68884	2.220586	0	11.46006	46.30582	64.83939	100	83.98338	64.03992	35.85321
Ppp1r11	26.97742	14.31672	0	18.88192	50.10795	72.67254	100	85.85492	64.78182	56.82096
Dek	36.33526	3.579274	0	16.36671	36.43371	71.79367	100	88.7326	56.90412	52.78178
Napsa	15.72672	0	29.41463	40.24256	48.30879	48.27792	100	95.13341	52.51658	34.04272
Tyms	0	9.209071	9.964341	31.28264	47.82444	71.8267	100	99.22708	59.86	27.77284
St3gal4	6.84751	10.90044	0	35.49981	42.67109	59.50677	100	90.18322	61.02175	36.29135
Klhl6	30.55868	7.183939	0	33.58497	49.9283	71.34816	100	95.80505	54.45235	35.75349
Nrm	27.17901	3.022204	0	34.14165	48.86303	55.22484	98.16041	100	70.6615	35.1128
Camk1d	19.0894	0	0.94165	19.66985	56.32542	64.44231	100	97.94373	66.17392	33.47042
Ppfia4	0	1.408176	18.22705	25.9199	48.89355	69.26914	96.89133	100	84.1463	43.65802
Hfe	7.789749	0	22.60007	42.489	50.4424	59.59124	100	95.99959	67.55359	54.56941
B4galt4	0	20.52571	10.12732	49.52135	58.2191	60.29509	89.21143	100	62.07898	54.42398
Slc35c2	0	1.914535	1.565621	36.92299	55.34395	62.54795	97.32201	100	45.8901	49.6689
Cdca8	31.08539	11.021	0	13.4855	75.65782	51.74997	93.39266	100	48.68278	55.39171
Fnbp1	25.64276	12.59179	0	23.969	64.40751	57.70137	100	75.69881	37.64916	42.63355
Tbc1d9	9.34513	4.247378	0	16.36445	74.71834	61.8125	100	84.90766	38.39744	39.21417
Lmn nb1	25.34042	1.539133	0	9.504327	59.68211	56.77177	95.68318	100	43.66101	41.51553
Runx3	22.96571	2.220727	0	15.98125	50.08265	65.8567	80.74147	100	38.1418	53.92851

Mcm2	22.91027	0	4.216571	39.61966	51.94674	96.8632	100	83.66046	78.03085	50.37844
Sla	30.26685	0	6.932172	26.36803	49.73735	79.26934	100	94.23772	94.62222	39.76726
Tipin	32.11297	13.05414	0	28.72259	41.25142	88.85095	94.93463	100	83.9711	41.11541
Orc6	35.99553	1.900219	0	33.76528	33.80458	100	72.25301	99.19899	72.21301	37.01408
Pkmyt1	27.09996	20.27135	0	44.49488	49.79323	84.71765	87.63684	100	95.36362	30.61273
Prim1	12.50831	0.41707	0	43.11487	38.03213	84.82474	84.48858	100	79.33947	31.19383
Chaf1a	17.00451	13.71311	0	36.5835	38.9064	73.80065	84.54579	100	77.68801	26.34714
Fgfr1op	54.84267	19.74559	0	36.89482	21.73637	95.84144	100	91.37339	62.80717	49.51576
Gatm	31.86314	6.011883	0	37.99994	32.68265	74.64325	85.47472	100	59.93702	71.25537
Ppif	43.36986	11.03738	0	40.91629	31.70873	58.92838	80.60588	100	63.90298	63.53896
Syce2	28.83197	14.41107	0	43.01142	12.33237	76.29078	100	99.11824	72.91949	71.71692
Mcm6	51.15005	2.744583	0	31.86616	17.63	77.68278	100	97.77184	88.89207	77.98578

ENSMUSG00000027514	ENSMUSG00000031442	ENSMUSG00000027398	ENSMUSG00000030137	ENSMUSG00000025823
ENSMUSG00000021025	ENSMUSG00000033213	ENSMUSG00000043953	ENSMUSG00000041453	ENSMUSG00000070730
ENSMUSG00000029322	ENSMUSG00000050578	ENSMUSG00000022501	ENSMUSG00000090231	ENSMUSG00000015243
ENSMUSG00000044703	ENSMUSG00000037921	ENSMUSG00000022148	ENSMUSG00000041571	ENSMUSG0000008496
ENSMUSG00000073491	ENSMUSG0000004814	ENSMUSG00000066677	ENSMUSG00000078153	ENSMUSG00000039217
ENSMUSG00000032554	ENSMUSG00000021127	ENSMUSG00000037731	ENSMUSG00000020034	ENSMUSG00000059824
ENSMUSG00000046879	ENSMUSG00000035929	ENSMUSG00000025469	ENSMUSG00000027955	ENSMUSG0000008683
ENSMUSG00000019122	ENSMUSG00000034422	ENSMUSG00000079547	ENSMUSG00000029135	ENSMUSG00000026942
ENSMUSG00000037405	ENSMUSG00000027068	ENSMUSG00000064373	ENSMUSG00000032530	ENSMUSG00000057657
ENSMUSG00000026104	ENSMUSG00000029082	ENSMUSG00000028480	ENSMUSG00000059456	ENSMUSG00000032508
ENSMUSG00000030107	ENSMUSG00000027203	ENSMUSG00000050737	ENSMUSG00000087187	ENSMUSG00000021280
ENSMUSG00000018899	ENSMUSG00000039221	ENSMUSG00000024610	ENSMUSG00000027399	ENSMUSG00000022265
ENSMUSG00000053318	ENSMUSG00000034353	ENSMUSG00000012519	ENSMUSG00000030432	ENSMUSG00000021624
ENSMUSG00000060044	ENSMUSG00000024663	ENSMUSG00000035208	ENSMUSG00000039501	ENSMUSG00000025856
ENSMUSG00000020689	ENSMUSG0000003746	ENSMUSG00000036067	ENSMUSG00000040296	ENSMUSG0000000253
ENSMUSG00000026875	ENSMUSG00000073421	ENSMUSG00000030148	ENSMUSG00000039361	ENSMUSG00000022938
ENSMUSG00000015852	ENSMUSG00000026031	ENSMUSG00000034220	ENSMUSG00000024732	ENSMUSG00000022010
ENSMUSG00000047945	ENSMUSG0000001123	ENSMUSG00000037235	ENSMUSG00000024608	ENSMUSG00000066111
ENSMUSG00000010358	ENSMUSG00000063694	ENSMUSG00000057322	ENSMUSG00000019478	ENSMUSG00000013236
ENSMUSG00000025492	ENSMUSG00000035385	ENSMUSG00000056220	ENSMUSG00000072235	ENSMUSG00000038301

ENSMUSG00000031897	ENSMUSG00000048200	ENSMUSG0000007613	ENSMUSG0000003779
ENSMUSG00000053338	ENSMUSG00000032322	ENSMUSG00000030729	ENSMUSG00000026687
ENSMUSG00000022661	ENSMUSG00000069515	ENSMUSG00000042684	ENSMUSG00000019876
ENSMUSG00000055435	ENSMUSG00000032515	ENSMUSG00000027968	ENSMUSG00000037503
ENSMUSG00000031097	ENSMUSG00000031652	ENSMUSG00000075266	ENSMUSG00000022744
ENSMUSG00000049130	ENSMUSG00000042870	ENSMUSG00000027293	ENSMUSG00000004221
ENSMUSG00000020572	ENSMUSG00000068101	ENSMUSG0000003814	ENSMUSG00000022747
ENSMUSG00000049086	ENSMUSG00000018008	ENSMUSG00000048327	ENSMUSG00000029922
ENSMUSG00000026605	ENSMUSG00000034041	ENSMUSG00000028551	ENSMUSG00000047843
ENSMUSG00000071042	ENSMUSG00000035697	ENSMUSG00000052837	ENSMUSG00000036533
ENSMUSG00000024084	ENSMUSG00000017390	ENSMUSG00000032254	ENSMUSG0000001348
ENSMUSG00000032725	ENSMUSG00000026355	ENSMUSG00000030272	ENSMUSG00000026483
ENSMUSG00000072769	ENSMUSG00000027763	ENSMUSG00000007570	ENSMUSG00000029376
ENSMUSG0000002104	ENSMUSG00000038368	ENSMUSG00000021998	ENSMUSG00000031216
ENSMUSG00000063889	ENSMUSG00000025511	ENSMUSG00000026458	ENSMUSG00000031821
ENSMUSG00000064215	ENSMUSG00000024190	ENSMUSG00000029919	ENSMUSG00000032067
ENSMUSG00000020077	ENSMUSG00000026170	ENSMUSG0000004032	ENSMUSG00000010663
ENSMUSG0000004891	ENSMUSG00000024539	ENSMUSG00000044147	ENSMUSG00000040723
ENSMUSG00000025574	ENSMUSG00000049091	ENSMUSG00000076437	ENSMUSG00000024056
ENSMUSG00000032218	ENSMUSG00000031596	ENSMUSG00000070738	ENSMUSG00000039145
ENSMUSG00000018930	ENSMUSG00000041126	ENSMUSG00000029468	ENSMUSG00000025747
ENSMUSG00000060519	ENSMUSG000000055447	ENSMUSG00000033705	ENSMUSG00000030707
ENSMUSG00000035448	ENSMUSG00000025408	ENSMUSG00000028525	ENSMUSG00000027316
ENSMUSG00000047592	ENSMUSG00000021822	ENSMUSG00000030649	ENSMUSG00000107355
ENSMUSG00000026229	ENSMUSG00000027737	ENSMUSG00000028497	ENSMUSG00000003382
ENSMUSG00000094777	ENSMUSG00000045328	ENSMUSG00000054733	ENSMUSG00000036777
ENSMUSG00000026473	ENSMUSG00000026986	ENSMUSG00000026456	ENSMUSG00000038633
ENSMUSG00000033917	ENSMUSG00000021880	ENSMUSG00000038866	ENSMUSG00000029516
ENSMUSG00000018339	ENSMUSG00000042286	ENSMUSG00000038372	ENSMUSG00000026245
ENSMUSG00000032698	ENSMUSG00000024404	ENSMUSG00000018171	ENSMUSG00000073468
ENSMUSG00000024737	ENSMUSG00000060131	ENSMUSG00000024186	ENSMUSG00000022439
ENSMUSG00000026688	ENSMUSG00000024962	ENSMUSG0000001525	ENSMUSG00000026786

Supplemental Table s6. The 23 genes identified using MacSpectrum are significantly associated with obesity-induced phenotypes and diabetes.

Gene ID	Correlation r (GSE32575)		No Dia v.s. Dia (GSE54350)		Functions related to metabolism, inflammation, and macrophage/monocyte regulation
	BMI	IR	Plot	p-value	
<i>PRKAG2</i>	0.59	0.41		0.010	Protein kinase AMP-activated non-catalytic subunit gamma 2, involved in glycogen metabolism
<i>PNKP</i>	0.55	0.47		0.014	DNA repair in response to inflammation-associated oxidative damage
<i>ERCC1</i>	0.52	0.55		0.003	Nucleotide excision repair of DNA lesions; deletion of this gene caused autoinflammation and degeneration of adipose tissue
<i>CLIC1</i>	0.51	0.46		0.011	Regulating phagosomal acidification function of macrophages
<i>DAGLB</i>	0.50	0.36		0.008	Lipase catalyzing the hydrolysis of diacylglycerol (DAG) to 2-arachidonoyl-glycerol (2-AG)
<i>TKT</i>	0.43	0.35		0.024	A thiamine-dependent enzyme which plays a role in the channeling of excess sugar phosphates to glycolysis in the pentose phosphate pathway
<i>HPS1</i>	0.43	0.50		0.013	Involved in regulation of macrophage accumulation and inflammation
<i>RNASET2</i>	0.42	0.36		0.004	Extracellular ribonucleases; Inducing inflammation and macrophage polarization
<i>GPX1</i>	0.41	0.44		0.032	Glutathione peroxidase coping with reactive oxygen and nitrogen species; protection against type 2 diabetes in mice
<i>YIF1B</i>	0.37	0.58		0.025	Yip1 Interacting Factor Homolog B, Membrane Trafficking Protein
<i>COMT</i>	0.36	0.51		0.020	Involved in macrophage-mediated regulation of adipocyte lipolysis
<i>B3GNT8</i>	0.33	0.41		0.019	Protein glycosylation; involved in elongation of specific branch structures of multiantennary N-glycans
<i>GPC3</i>	-0.34	-0.41		0.028	macrophage/monocyte lineage differentiation and recruitment
<i>ADH1A</i>	-0.36	-0.46		0.034	Carbohydrate metabolism; catalyzing the oxidation of alcohols to aldehydes
<i>UACA</i>	-0.39	-0.39		0.043	Regulation of stress-induced apoptosis through apoptosome up-regulation, LGALS3/galectin-3 down-regulation and NF-kappa-B inactivation
<i>BDH2</i>	-0.40	-0.51		0.038	Ketone body metabolism, iron homeostasis and transport
<i>SLC9A3R2</i>	-0.41	-0.38		0.020	Glucose / energy metabolism
<i>RYK</i>	-0.44	-0.43		0.018	Coreceptor of Wnt proteins; involved in inflammatory Wnt5A signalling
<i>SPARC</i>	-0.46	-0.35		0.036	Promoting inflammation and macrophage M1 polarization
<i>PRRX1</i>	-0.47	-0.42		0.013	Regulation of cell growth and differentiation, including adipogenesis
<i>PPIC</i>	-0.47	-0.36		0.024	Regulation of immune response
<i>TRIM2</i>	-0.48	-0.44		0.039	Potential involvement in interferon γ signaling
<i>AMOTL2</i>	-0.64	-0.49		0.027	Regulation of cell proliferation and migration, involved in PPARγ signaling