

1 **SUPPLEMENTARY MATERIALS**

2 ***SUPPLEMENTARY METHODS***

3 **Study design and population**

4 A case-control study was conducted from 2018 to 2022, in the Department of Internal Medicine from
5 Hospital Clínic of Barcelona (Barcelona, Spain), including 14 patients and 12 healthy volunteers. IBM
6 patients were diagnosed according to clinical and pathological tests performed in our hospital, after
7 fulfilling the criteria proposed by the European Neuromuscular Centre for IBM diagnosis[1]. Exclusion
8 criteria were: age < 40 years, family history of hereditary mitochondrial disease, comorbidities and
9 concomitant infections or drug abuse. Fourteen IBM patients decided to participate in the present
10 study and signed the informed consent previously approved by the Ethical Committee of our hospital
11 (code HCB/2015/0562). At the time of inclusion, the severity of disease was evaluated in IBM patients
12 according to the inclusion body myositis functional rating scale (IBMFRS), internationally validated to
13 functionally evaluate disease-specific disability. Epidemiological data (age, gender, and ethnicity) was
14 also compiled. Controls were collected from healthy volunteers, age and gender-paired to IBM
15 patients, after excluding any comorbidity or pathological process, and signed the corresponding
16 informed consent.

17 **Fibroblast culture**

18 Fibroblasts were obtained from a skin punch biopsy from cases and controls. Cells were grown in 25
19 mM glucose DMEM supplemented with 10% FBS and 1% penicillin-streptomycin, at 37 °C, in a
20 humidified 5% CO₂ air incubator (all from Gibco, Waltham, MA, USA). Cells were harvested and
21 collected by trypsin (Gibco, Waltham, MA, USA), at 80% of confluence, and phenotyped at passages 3
22 to 10. Transcriptomic and functional analyses were performed from these fibroblasts.

23 **RNA extraction and mRNA library preparation and sequencing**

24 Total RNA was isolated from cell lysates (2 million of cells) of 3 IBM and 3 CTL fibroblasts using RNeasy
25 Mini Kit (Qiagen, Hilden, Germany), according to the manufacturer's protocol. Total RNA content was
26 assessed through Quawell UV-Vis Spectrophotometer Q5000. Concentrations were adjusted to 100
27 ng/uL in RNase-free water. The quality control of the total RNA was done using the Qubit® RNA HS
28 Assay (Life Technologies) and RNA 6000 Nano Assay on a Bioanalyzer 2100 (Agilent, Santa Clara, CA,
29 USA). The RNASeq libraries were prepared using the TruSeq®Stranded mRNA LT Sample Prep Kit.
30 Briefly, total RNA (500ng) was enriched for the mRNA fraction and fragmented. Strand-specificity was
31 achieved by the second-strand cDNA incorporating dUTPs instead of dTTPs. The blunt-ended double
32 stranded cDNA was 3'adenylated and Illumina platform compatible adaptors with unique dual indexes
33 and unique molecular identifiers (Integrated DNA Technologies) were ligated. The ligation product
34 was enriched with 15 PCR cycles and the final library was validated on an Agilent 2100 Bioanalyzer
35 with the DNA 7500 assay. The libraries were sequenced on HiSeq 4000 (Illumina) with a read length
36 of 2x51bp using the HiSeq 4000 SBS kit (Illumina). Primary data analysis, image analysis, base calling
37 and quality scoring of the run were processed using the manufacturer's software Real Time Analysis
38 (RTA 2.7.7) followed by generation FASTQ sequence files.

39 **RNA-seq and pathway analysis**

40 RNA-seq reads were mapped against human reference genome (GRCh38) using STAR software version
41 2.5.3a[2]with ENCODE parameters. Annotated genes were quantified using human GENCODE

42 annotation file version 34 with RSEM v1.3.0 [3] and default parameters. Differential expression
43 analysis was performed with DESeq2 v1.26.0 R package [4] using a Wald test to compare affected and
44 control groups, adjusting for sex in the model. Genes were considered differentially expressed with
45 an adjusted p-value < 0.05 and absolute fold change |FC| > 1.5. A Gene Ontology enrichment analysis
46 was generated with the significant genes using gProfileR v.07.0 [5]. Additionally, a GSEA was
47 performed with a list of pre-ranked genes by the Wald statistic, using fgsea R package v1.12.0 [6] and
48 the Reactome pathways database. PCA plot was generated with regularized log transformed (rlog)
49 counts, considering only the top 500 most variable genes. Heatmap plot also represents rlog counts
50 to show scaled expression of the top 50 differentially expressed genes. These plots were generated
51 using ggplot2 v0.1.8 [7] and pheatmap R packages, respectively.

52 Moreover, pathway analysis was performed following the Core Analysis module of the IPA (QIAGEN
53 Redwood City, www.qiagen.com/ingenuity) to identify canonical pathways, upstream regulators and
54 top networks using a Fisher's exact test with a cut-off of p-value adj < 0.05. In addition, the Pathcards
55 database [8] was used to relate DEGs to the pathways of interest.

56 **Autophagy protein array**

57 Cell lysates were obtained from IBM and CTL fibroblasts with cell lysis buffer containing 1% protease
58 cocktail inhibitor (Thermo Scientific #78430, Massachusetts, USA). 250-500 ug of protein per sample
59 were loaded in the RayBio® C Series Human Autophagy Array 1 (Cat#: AAHATG-1-8, RayBiotech, Inc.,
60 Atlanta, GA, USA) and incubated overnight at 4°C in a pre-coated membrane, following the
61 manufacturer's protocol. The density of each spot pixel on the membrane was determined by
62 chemoluminescent signaling, using the Image Quant TL Software (GE Healthcare), and calculated by
63 AAH-ATG-1 analysis tools provided by RayBiotech, Inc. (Atlanta, USA).

64 **Autophagy time-course**

65 Autophagy flux in IBM vs. CTL fibroblasts was measured in a time-course manner in basal conditions
66 (0h time point), and after the addition of 4 and 8h of 0.1 µM bafilomycin A1 from *Streptomyces griseus*
67 (Sigma-Aldrich® #B1793 SIGMA, Missouri, USA), an inhibitor of the autophagic process aimed to block
68 autophagosome clearance. Afterward, fibroblasts were lysed with RIPA buffer (Sigma-Aldrich #R0278,
69 Missouri, USA) containing protease inhibitor cocktail (Thermo Scientific #78430, Massachusetts, USA)
70 and analyzed through western blot analysis. Blots were probed against the anti-SQSTM1/p62 (Abcam
71 #ab56416, Cambridge, UK) and anti-LC3B (Cell Signaling #2775S, Massachusetts, USA) antibodies.
72 LC3BII and p62 are considered autophagy markers and were normalized by total protein content
73 (measured with SYPRO Ruby Protein Blot Stain, Molecular Probes). The intensity of signals was
74 quantified by densitometric analysis of chemiluminescent signal (Image Quant TL Software, GE
75 Healthcare).

76 **Immunocytochemistry for autophagosome characterization**

77 Cells were seeded in a 16-well glass slide (Nunc™ #178599 Lab-Tek® Chamber Slide™, Austin, USA) at
78 37°C with 5% CO₂ for 24 h. They were fixed with 4% paraformaldehyde for 15 min and permeabilized
79 with 0.1% Triton X-100 in blocking solution (1% bovine serum albumin). Degradation of
80 autophagolysosomes was blocked by adding 100nM Bafilomycin A1 from *Streptomyces griseus*
81 (Sigma-Aldrich® #B1793 SIGMA, Missouri, USA) for 6 hours. Autophagosomes were stained by 1h
82 incubation with anti-LC3 pAB (MBL International® #PM036, Massachusetts, USA) and secondary
83 marked through the donkey anti-rabbit Alexa Fluor® 488 IgG antibody (Life Technologies Europe, NL).
84 Counterstain with DAPI was performed for nuclei staining (DAPI Fluoromount-G® #0100-20, Southern

85 Biotech, Alabama, USA). Images were obtained with a Zeiss LSM 880 laser scanning confocal system
86 using a 63X oil immersion objective.

87 **Mitochondrial Respiration**

88 Mitochondrial respiration was measured according to the oxygen consumption of the mitochondrial
89 respiratory chain (MRC). The oxygen consumption rate was detected with the XF Cell Mito Stress
90 Test™ (Seahorse-XF^e24-Analyzer, Agilent Technologies), according to the manufacturer's protocol.
91 Briefly, we seeded 40,000 fibroblasts per well in 24-well Seahorse culture plates and left them to
92 adhere overnight. Each cell line was seeded in quadruplicate per condition. Basal oxygen consumption
93 was measured before the addition of oligomycin (2μM, to measure MRC coupling), FCCP (1.4μM,
94 uncoupling agent, to measure maximal oxygen consumption capacity) and antimycin A and rotenone
95 addition (1μM each; to measure unspecific oxygen consumption of non-mitochondrial enzymes).
96 Results were expressed relative to total protein (BCA) and mitochondrial content (CS concentration)
97 as nmol/min/mg protein/CS.

98 **Oxidative stress**

99 Oxidative stress was measured through lipid peroxidation and total antioxidant capacity of the cell
100 (TAC). Briefly, lipid peroxidation was quantified by measuring malondialdehyde (MDA) and 4-
101 hydroxyalkenal (HAE) as indicators of ROS damage into cellular lipid compounds, using a BIOXYTECH®
102 LPO-586™ colorimetric assay (Oxys International Inc., CA, USA), as reported elsewhere [9]. The results
103 were normalized per mitochondrial content (μM MDA and HAE/mg protein/CS).

104 Concomitantly, TAC was quantified in cell culture supernatants using an OxiSelect™ Total Antioxidant
105 Capacity Assay kit (Cell Biolabs Inc., San Diego, CA, USA) by spectrophotometry (absorption maximum
106 at 490 nm), normalized by cell count and expressed as μM CRE (Copper Reducing Equivalent).

107 **Transmission Electron Microscopy**

108 Fibroblasts were washed in PBS and fixed for 1 h in 2.5% glutaraldehyde in 0.1 M phosphate buffer at
109 RT. Samples were gently scraped and pelleted in 1.5 ml tubes. Pellets were washed in PBS and
110 incubated with 1% OsO₄ for 90 min at 4 °C. Then samples were dehydrated, embedded in Spurr, and
111 sectioned using Leica ultramicrotome (Leica Microsystems). Ultrathin sections (50–70 nm) were
112 stained with 2% uranyl acetate for 10 min, a lead-staining solution for 5 min, and observed using a
113 TEM, JEOL JEM-1010 fitted with a Gatan Orius SC1000 (model 832) digital camera [10] to seek for
114 abnormal organelle structures.

115 **Metabolite quantification**

116 All fibroblasts' samples were quantified using a BCA protein assay (Thermo Scientific #23225,
117 Massachusetts, USA) and 5 mg/ml were resuspended in 200 μL of PBS, and centrifuged (1500× g; 10
118 min) to collect the supernatant, where aa and organic acids were quantified. Organic acids were
119 extracted in fibroblasts with ethyl acetate and diethyl ether and derivatized with bis(trimethylsilyl)
120 trifluoro-acetamide, as previously reported [11]. The trimethylsilyl derivatives obtained were
121 separated by gas chromatography (Agilent 7890A, Wilmington, DE, USA) and detected in a mass
122 spectrometer (Agilent 5975C, Wilmington, DE, USA). The results were expressed as nanomoles of
123 organic acid per milligram of protein (nmol/mg protein). Aa were quantified in fibroblasts by ultra-
124 performance liquid chromatography coupled to tandem mass spectrometry, as previously reported
125 [12]. Briefly, aa were separated in a Waters ACQUITY UPLC H-class chromatograph and quantified with
126 a Waters Xevo TQD triple-quadrupole mass spectrometer using positive electrospray ionization

127 conditions in the multiple reaction monitoring mode. The results were expressed as nanomoles of aa
128 per milligram of protein (nmol/mg protein).

129 **Supplementary References (from Supplementary Methods section)**

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160 **SUPPLEMENTARY TABLES**

161 **Supplementary Table 1.** Differentially expressed genes between IBM and CTL (778 genes with p-value adj
 162 (FDR) < 0.05, following alphabetical order)

GENE ID	GENE NAME	log2Fold change	p-value	p-value adj (FDR)
ABCC9	ATP binding cassette subfamily C member 9(ABCC9)	5.2418	0.0000	0.0001
ABHD12	abhydrolase domain containing 12(ABHD12)	-0.6465	0.0000	0.0000
ABI3BP	ABI family member 3 binding protein (ABI3BP)	-1.4671	0.0002	0.0092
ABLIM3	actin binding LIM protein family member 3(ABLIM3)	-0.8941	0.0003	0.0118
AC004556.3	unknown	24.8812	0.0000	0.0000
AC007405.4	unknown	3.7031	0.0007	0.0209
AC008764.4	unknown	6.7625	0.0000	0.0005
AC009779.4	unknown	-1.5096	0.0001	0.0052
AC010186.2	unknown	1.0420	0.0021	0.0464
AC011005.1	unknown	-2.9930	0.0022	0.0484
AC011484.1	unknown	1.5290	0.0009	0.0259
AC012531.1	unknown	3.4745	0.0018	0.0418
AC012651.1	unknown	-1.1590	0.0002	0.0091
AC016026.1	unknown	-0.8236	0.0001	0.0034
AC023055.1	unknown	-4.5706	0.0002	0.0085
AC027097.2	unknown	2.0449	0.0005	0.0159
AC034102.2	unknown	2.5011	0.0009	0.0247
AC067968.1	unknown	6.6426	0.0010	0.0270
AC078850.1	unknown	2.3634	0.0008	0.0229
AC104452.1	unknown	-0.8546	0.0002	0.0079
AC104461.1	unknown	4.9800	0.0004	0.0135
AC106782.1	unknown	-1.8723	0.0001	0.0063
AC106795.2	unknown	-2.7117	0.0001	0.0029
AC110079.1	unknown	1.5728	0.0002	0.0070
AC138894.1	unknown	-1.5118	0.0005	0.0168
AC138969.3	unknown	4.2973	0.0010	0.0274
AC243964.4	unknown	-1.5044	0.0004	0.0143
ACADM	acyl-CoA dehydrogenase, C-4 to C-12 straight chain (ACADM)	0.5216	0.0015	0.0369
ACAN	aggrecan (ACAN)	7.0350	0.0000	0.0002
ACKR4	atypical chemokine receptor 4(ACKR4)	-2.1493	0.0001	0.0029
ACSL5	acyl-CoA synthetase long-chain family member 5(ACSL5)	2.3992	0.0002	0.0068
ACTC1	actin, alpha, cardiac muscle 1(ACTC1)	2.3333	0.0000	0.0018
ADAM15	ADAM metallopeptidase domain 15(ADAM15)	-0.8433	0.0002	0.0078

ADAMTS14	ADAM metalloproteinase with thrombospondin type 1 motif 14(ADAMTS14)	-1.2174	0.0000	0.0009
ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif 8(ADAMTS8)	-2.4147	0.0005	0.0172
ADAMTSL4	ADAMTS like 4(ADAMTSL4)	-1.7184	0.0000	0.0001
ADAMTSL5	ADAMTS like 5(ADAMTSL5)	-0.9505	0.0000	0.0012
ADGRE5	adhesion G protein-coupled receptor E5(ADGRE5)	-0.7142	0.0002	0.0089
ADIRF	adipogenesis regulatory factor (ADIRF)	-1.1283	0.0006	0.0184
ADM2	adrenomedullin 2(ADM2)	0.7624	0.0000	0.0015
ADRA1D	adrenoceptor alpha 1D(ADRA1D)	-2.1892	0.0000	0.0000
ADRA2A	adrenoceptor alpha 2A(ADRA2A)	-1.8182	0.0005	0.0171
AFAP1	actin filament associated protein 1(AFAP1)	-0.8843	0.0012	0.0304
AGAP7P	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7, pseudogene (AGAP7P)	-4.8467	0.0000	0.0010
AGL	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase (AGL)	0.5079	0.0004	0.0132
AGPAT2	1-acylglycerol-3-phosphate O-acyltransferase 2(AGPAT2)	-0.4554	0.0002	0.0095
AGPS	alkylglycerone phosphate synthase (AGPS)	0.4610	0.0001	0.0031
AHNAK2	AHNAK nucleoprotein 2(AHNAK2)	-1.4524	0.0000	0.0000
AHSA2P	Activator Of HSP90 ATPase Homolog 2, Pseudogene	-0.5280	0.0011	0.0278
AKNA	AT-hook transcription factor (AKNA)	1.0736	0.0000	0.0001
AL049629.2	unknown	-1.0896	0.0000	0.0000
AL354740.1	unknown	-1.5696	0.0000	0.0024
AL365203.2	unknown	-0.9654	0.0011	0.0289
AL365205.1	unknown	-1.1985	0.0000	0.0001
AL627309.6	unknown	-2.3974	0.0001	0.0050
AL928654.3	unknown	-1.7488	0.0022	0.0480
ALDH18A1	aldehyde dehydrogenase 18 family member A1(ALDH18A1)	0.3572	0.0023	0.0498
ALDH1B1	aldehyde dehydrogenase 1 family member B1(ALDH1B1)	1.2248	0.0000	0.0011
ALDH1L2	aldehyde dehydrogenase 1 family member L2(ALDH1L2)	0.6341	0.0000	0.0018
ALDH3A1	aldehyde dehydrogenase 3 family member A1(ALDH3A1)	-2.5892	0.0001	0.0063
ALDH4A1	aldehyde dehydrogenase 4 family member A1(ALDH4A1)	-0.8059	0.0003	0.0104

ANK1	ankyrin 1(ANK1)	-3.0735	0.0000	0.0006
ANKRD13A	ankyrin repeat domain 13A(ANKRD13A)	-0.4556	0.0000	0.0012
ANKRD44	ankyrin repeat domain 44(ANKRD44)	0.8013	0.0009	0.0248
ANKRD50	ankyrin repeat domain 50(ANKRD50)	0.5588	0.0003	0.0117
ANKRD6	ankyrin repeat domain 6(ANKRD6)	2.5131	0.0000	0.0003
ANO4	anoctamin 4(ANO4)	-3.3334	0.0000	0.0000
ANPEP	alanyl aminopeptidase, membrane (ANPEP)	-0.6780	0.0000	0.0002
AP001273.2	unknown	7.6508	0.0000	0.0020
AP003071.4	unknown	-1.2800	0.0009	0.0254
APBB1	amyloid beta precursor protein binding family B member 1(APBB1)	-0.5300	0.0000	0.0010
APCDD1L	APC downregulated 1 like (APCDD1L)	-0.8223	0.0012	0.0296
APH1B	aph-1 homolog B, gamma- secretase subunit (APH1B)	-0.5951	0.0001	0.0029
APMAP	adipocyte plasma membrane associated protein (APMAP)	-0.6084	0.0015	0.0356
APOL1	apolipoprotein L1(APOL1)	-0.8892	0.0003	0.0112
AR	androgen receptor (AR)	3.7771	0.0000	0.0001
ARG2	arginase 2(ARG2)	0.9386	0.0002	0.0080
ARHGAP20	Rho GTPase activating protein 20(ARHGAP20)	1.9725	0.0008	0.0220
ARHGAP23	Rho GTPase activating protein 23(ARHGAP23)	-0.6173	0.0002	0.0092
ARHGAP27P1- BPTFP1- KPNA2P3	ARHGAP27P1-BPTFP1-KPNA2P3 Readthrough, Transcribed Pseudogene	-0.7563	0.0000	0.0004
ARHGEF2	Rho/Rac guanine nucleotide exchange factor 2(ARHGEF2)	0.4460	0.0010	0.0270
ARHGEF28	Rho guanine nucleotide exchange factor 28(ARHGEF28)	-1.0330	0.0018	0.0407
ARHGEF5	Rho guanine nucleotide exchange factor 5(ARHGEF5)	0.8280	0.0022	0.0484
ARID5A	AT-rich interaction domain 5A(ARID5A)	-1.1437	0.0004	0.0126
ARMH4	Armadillo Like Helical Domain Containing 4	-0.8213	0.0008	0.0221
ARMT1	acidic residue methyltransferase 1(ARMT1)	0.5181	0.0010	0.0275
ARPC1A	actin related protein 2/3 complex subunit 1A(ARPC1A)	-0.3344	0.0018	0.0417
ARRDC1	arrestin domain containing 1(ARRDC1)	-0.6306	0.0000	0.0007
ARSD	arylsulfatase D(ARSD)	-0.6414	0.0001	0.0046
ASNS	asparagine synthetase (glutamine-hydrolyzing) (ASNS)	1.1373	0.0000	0.0000

ATP13A3	ATPase 13A3(ATP13A3)	-0.6369	0.0001	0.0044
ATP1B3	ATPase Na ⁺ /K ⁺ transporting subunit beta 3(ATP1B3)	-0.5233	0.0011	0.0282
ATP2B4	ATPase plasma membrane Ca ²⁺ transporting 4(ATP2B4)	-1.0839	0.0000	0.0000
ATP2C1	ATPase secretory pathway Ca ²⁺ transporting 1(ATP2C1)	-0.3462	0.0014	0.0355
ATP6VOA1	ATPase H ⁺ transporting V0 subunit a1(ATP6VOA1)	-0.7267	0.0006	0.0191
ATP6VOE2	ATPase H ⁺ transporting V0 subunit e2(ATP6VOE2)	-0.8363	0.0008	0.0241
ATP6V1G1	ATPase H ⁺ transporting V1 subunit G1(ATP6V1G1)	0.5128	0.0000	0.0026
ATP8B1	ATPase phospholipid transporting 8B1(ATP8B1)	-1.2718	0.0000	0.0000
AUP1	ancient ubiquitous protein 1(AUP1)	-0.3966	0.0003	0.0104
B4GAT1	beta-1,4-glucuronyltransferase 1(B4GAT1)	-0.6639	0.0017	0.0403
BAIAP2	BAI1 associated protein 2(BAIAP2)	-0.6732	0.0010	0.0264
BANK1	B-cell scaffold protein with ankyrin repeats 1(BANK1)	2.9500	0.0000	0.0018
BCL11A	B-cell CLL/lymphoma 11A(BCL11A)	1.9714	0.0003	0.0114
BCL2L1	BCL2 like 1(BCL2L1)	-0.6640	0.0000	0.0000
BDKRB1	bradykinin receptor B1(BDKRB1)	-1.4603	0.0000	0.0001
BSCL2	BSCL2, seipin lipid droplet biogenesis associated (BSCL2)	-0.7716	0.0000	0.0002
BSG	basigin (Ok blood group) (BSG)	-0.6915	0.0002	0.0081
BTBD3	BTB domain containing 3(BTBD3)	-0.5217	0.0019	0.0438
BTF3L4	basic transcription factor 3 like 4(BTF3L4)	0.4380	0.0006	0.0195
BTF3L4P2	basic transcription factor 3 like 4 pseudogene 2(BTF3L4P2)	1.1680	0.0004	0.0126
BTN3A2	butyrophilin subfamily 3 member A2(BTN3A2)	-1.0128	0.0016	0.0378
BVES	blood vessel epicardial substance (BVES)	0.6310	0.0010	0.0271
C10orf105	chromosome 10 open reading frame 105(C10orf105)	-1.8647	0.0001	0.0063
C17orf107	chromosome 17 open reading frame 107(C17orf107)	0.9326	0.0020	0.0445
C17orf97	chromosome 17 open reading frame 97(C17orf97)	-1.4688	0.0000	0.0004
C1QTNF2	C1q and tumor necrosis factor related protein 2(C1QTNF2)	-1.3620	0.0019	0.0429

C2orf74	chromosome 2 open reading frame 74(C2orf74)	1.3086	0.0000	0.0027
C3orf18	chromosome 3 open reading frame 18(C3orf18)	-0.6791	0.0000	0.0000
C9orf64	chromosome 9 open reading frame 64(C9orf64)	0.6727	0.0000	0.0006
CA13	carbonic anhydrase 13(CA13)	1.6189	0.0012	0.0307
CADM3	cell adhesion molecule 3(CADM3)	5.0916	0.0000	0.0000
CADPS2	calcium dependent secretion activator 2(CADPS2)	1.8008	0.0012	0.0313
CAMKK1	calcium/calmodulin dependent protein kinase kinase 1 (CAMKK1)	-0.5466	0.0017	0.0405
CAPN3	calpain 3(CAPN3)	-0.8838	0.0010	0.0274
CARD10	caspase recruitment domain family member 10(CARD10)	-1.4910	0.0001	0.0052
CASC15	cancer susceptibility candidate 15 (non-protein coding) (CASC15)	3.1988	0.0001	0.0055
CASP4	caspase 4(CASP4)	0.3903	0.0008	0.0229
CATSPER1	cation channel sperm associated 1(CATSPER1)	-2.4289	0.0009	0.0249
CAV1	caveolin 1(CAV1)	-1.1562	0.0000	0.0008
CBR3	carbonyl reductase 3(CBR3)	-0.7673	0.0000	0.0007
CBWD4P	COBW domain containing 4 pseudogene (CBWD4P)	3.6966	0.0010	0.0274
CBX4	chromobox 4(CBX4)	0.6131	0.0004	0.0141
CCDC106	coiled-coil domain containing 106(CCDC106)	-0.4520	0.0009	0.0259
CCDC144A	coiled-coil domain containing 144A(CCDC144A)	7.7440	0.0000	0.0000
CCDC170	coiled-coil domain containing 170(CCDC170)	1.5433	0.0002	0.0092
CCDC84	coiled-coil domain containing 84(CCDC84)	-0.6570	0.0000	0.0009
CCN4	Cellular Communication Network Factor 4	1.3436	0.0000	0.0000
CCND1	cyclin D1(CCND1)	-1.5007	0.0000	0.0000
CCT2	chaperonin containing TCP1 subunit 2(CCT2)	0.3052	0.0010	0.0271
CD151	CD151 molecule (Raph blood group) (CD151)	-1.0611	0.0000	0.0006
CD163	CD163 molecule (CD163)	2.2650	0.0019	0.0437
CD248	CD248 molecule (CD248)	-0.5876	0.0010	0.0271
CD3EAP	CD3e molecule associated protein (CD3EAP)	0.9539	0.0007	0.0209
CD44	CD44 molecule (Indian blood group) (CD44)	-0.8714	0.0003	0.0104
CD47	CD47 molecule (CD47)	-0.5105	0.0000	0.0006
CD59	CD59 molecule (CD59)	-0.8524	0.0000	0.0000
CD63	CD63 molecule (CD63)	-0.8199	0.0000	0.0003
CD68	CD68 molecule (CD68)	-1.1347	0.0000	0.0018

CD81	CD81 molecule (CD81)	-0.6728	0.0000	0.0014
CD82	CD82 molecule (CD82)	-1.6099	0.0002	0.0067
CD9	CD9 molecule (CD9)	-2.3911	0.0000	0.0000
CD99	CD99 molecule (CD99)	-0.4673	0.0000	0.0002
CDC42EP2	CDC42 effector protein 2(CDC42EP2)	-0.8919	0.0004	0.0126
CDH18	cadherin 18(CDH18)	-5.0507	0.0000	0.0003
CDH6	cadherin 6(CDH6)	2.7957	0.0000	0.0001
CDHR3	cadherin related family member 3(CDHR3)	-1.0315	0.0001	0.0051
CDRT4	CMT1A duplicated region transcript 4(CDRT4)	-1.8932	0.0000	0.0001
CEBPG	CCAAT/enhancer binding protein gamma (CEBPG)	0.4814	0.0000	0.0018
CELSR1	cadherin EGF LAG seven-pass G-type receptor 1(CELSR1)	-2.9541	0.0003	0.0113
CERCAM	cerebral endothelial cell adhesion molecule (CERCAM)	-0.7539	0.0013	0.0335
CERS1	ceramide synthase 1(CERS1)	-1.2438	0.0005	0.0158
CFD	complement factor D(CFD)	1.6744	0.0000	0.0000
CHAC1	ChaC glutathione specific gamma-glutamylcyclotransferase 1(CHAC1)	1.7225	0.0003	0.0101
CHDH	choline dehydrogenase (CHDH)	-2.1142	0.0001	0.0062
CHN2	chimerin 2(CHN2)	5.1535	0.0001	0.0043
CHPF	chondroitin polymerizing factor (CHPF)	-0.9390	0.0017	0.0404
CHPT1	choline phosphotransferase 1(CHPT1)	-0.3680	0.0010	0.0262
CHST6	carbohydrate sulfotransferase 6(CHST6)	2.4710	0.0013	0.0321
CITED2	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2(CITED2)	-0.5678	0.0001	0.0062
CKB	creatine kinase B(CKB)	-1.6437	0.0000	0.0026
CLDN23	claudin 23(CLDN23)	1.2082	0.0017	0.0389
CLEC11A	C-type lectin domain family 11 member A(CLEC11A)	-0.9878	0.0000	0.0004
CLEC12A	C-type lectin domain family 12 member A(CLEC12A)	-4.2622	0.0000	0.0000
CLEC2A	C-type lectin domain family 2 member A(CLEC2A)	-7.3567	0.0000	0.0000
CLEC2B	C-type lectin domain family 2 member B(CLEC2B)	-1.7995	0.0000	0.0000
CLEC3B	C-type lectin domain family 3 member B(CLEC3B)	-3.2430	0.0000	0.0000
CLGN	calmegin (CLGN)	1.3861	0.0005	0.0168
CLIC2	chloride intracellular channel 2(CLIC2)	3.8043	0.0000	0.0002

CLIC6	chloride intracellular channel 6(CLIC6)	3.7952	0.0002	0.0065
CLMN	calmin (CLMN)	3.5275	0.0001	0.0062
CLTB	clathrin light chain B(CLTB)	-0.5051	0.0000	0.0013
CNN3	calponin 3(CNN3)	0.4807	0.0015	0.0369
COL10A1	collagen type X alpha 1 chain (COL10A1)	2.2962	0.0019	0.0432
COL13A1	collagen type XIII alpha 1 chain (COL13A1)	-1.1746	0.0000	0.0003
COL4A4	collagen type IV alpha 4 chain (COL4A4)	5.2061	0.0000	0.0024
COPB2	coatamer protein complex subunit beta 2(COPB2)	0.3450	0.0019	0.0432
COPZ2	coatamer protein complex subunit zeta 2(COPZ2)	-0.3562	0.0006	0.0191
CPB1	carboxypeptidase B1(CPB1)	4.0747	0.0008	0.0241
CPED1	cadherin like and PC-esterase domain containing 1(CPED1)	-1.2292	0.0010	0.0267
CPM	carboxypeptidase M(CPM)	3.3745	0.0000	0.0000
CRELD1	cysteine rich with EGF like domains 1(CRELD1)	-1.2557	0.0010	0.0267
CRIP1	cysteine rich protein 1(CRIP1)	-1.7549	0.0000	0.0000
CRIP2	cysteine rich protein 2(CRIP2)	-0.6618	0.0001	0.0034
CRTAP	cartilage associated protein (CRTAP)	-0.5255	0.0018	0.0417
CRYAB	crystallin alpha B(CRYAB)	-0.5729	0.0009	0.0242
CRYBG1	Crystallin Beta-Gamma Domain Containing 1	-1.4347	0.0000	0.0018
CST3	cystatin C(CST3)	-0.9566	0.0002	0.0073
CST6	cystatin E/M(CST6)	-2.5056	0.0001	0.0035
CSTF2T	cleavage stimulation factor subunit 2 tau variant (CSTF2T)	0.4714	0.0021	0.0461
CTDSPL	CTD small phosphatase like (CTDSPL)	-0.4733	0.0011	0.0282
CTH	cystathionine gamma-lyase (CTH)	0.9054	0.0007	0.0211
CTSB	cathepsin B(CTSB)	-0.7951	0.0000	0.0010
CTSC	cathepsin C(CTSC)	-1.9871	0.0000	0.0000
CTSZ	cathepsin Z(CTSZ)	-0.8578	0.0013	0.0318
CU633904.2	unknown	3.6259	0.0000	0.0000
CU634019.2	unknown	4.0153	0.0000	0.0005
CXCL14	C-X-C motif chemokine ligand 14(CXCL14)	2.2072	0.0018	0.0406
CYB5A	cytochrome b5 type A(CYB5A)	0.6328	0.0015	0.0360
CYB5D2	cytochrome b5 domain containing 2(CYB5D2)	-0.5325	0.0006	0.0178
CYB5R3	cytochrome b5 reductase 3(CYB5R3)	-0.5536	0.0021	0.0464
CYP2U1	cytochrome P450 family 2 subfamily U member 1(CYP2U1)	-1.1982	0.0000	0.0000

CYP4V2	cytochrome P450 family 4 subfamily V member 2(CYP4V2)	-0.6433	0.0007	0.0207
CYP7B1	cytochrome P450 family 7 subfamily B member 1(CYP7B1)	2.9934	0.0000	0.0000
DAB2	DAB2, clathrin adaptor protein (DAB2)	0.3330	0.0003	0.0104
DACT1	dishevelled binding antagonist of beta catenin 1(DACT1)	2.7342	0.0000	0.0000
DAG1	dystroglycan 1(DAG1)	-0.6364	0.0014	0.0352
DARS1	Aspartyl-TRNA Synthetase 1	0.4035	0.0004	0.0126
DDIT3	DNA damage inducible transcript 3(DDIT3)	0.4761	0.0001	0.0052
DDIT4	DNA damage inducible transcript 4(DDIT4)	1.3773	0.0001	0.0029
DDX18	DEAD-box helicase 18(DDX18)	0.4255	0.0002	0.0070
DENND3	DENN domain containing 3(DENND3)	-1.3941	0.0000	0.0000
DEPP1	DEPP1 Autophagy Regulator	2.0641	0.0001	0.0049
DEPTOR	DEP domain containing MTOR- interacting protein (DEPTOR)	1.3954	0.0000	0.0002
DGCR11	DiGeorge syndrome critical region gene 11 (non-protein coding) (DGCR11)	-1.2104	0.0002	0.0067
DGCR2	DiGeorge syndrome critical region gene 2(DGCR2)	-0.4936	0.0006	0.0175
DIAPH1	diaphanous related formin 1(DIAPH1)	-0.4682	0.0004	0.0149
DIO2	deiodinase, iodothyronine type II(DIO2)	2.8134	0.0001	0.0039
DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding) (DLEU2)	0.8991	0.0011	0.0278
DMKN	dermokine (DMKN)	2.2967	0.0000	0.0008
DMPK	dystrophia myotonica protein kinase (DMPK)	-0.8460	0.0000	0.0000
DNM3OS	DNM3 opposite strand/antisense RNA(DNM3OS)	0.9808	0.0008	0.0229
DPP7	dipeptidyl peptidase 7(DPP7)	-0.5894	0.0004	0.0138
DPT	dermatopontin (DPT)	1.3498	0.0002	0.0093
DSE	dermatan sulfate epimerase (DSE)	0.6231	0.0005	0.0157
DUOX1	dual oxidase 1(DUOX1)	-3.4372	0.0010	0.0264
ECHDC2	enoyl-CoA hydratase domain containing 2(ECHDC2)	-0.7406	0.0004	0.0126
EDNRB	endothelin receptor type B(EDNRB)	6.8732	0.0000	0.0008
EGFL6	EGF like domain multiple 6(EGFL6)	7.0166	0.0012	0.0314

EGFR	epidermal growth factor receptor (EGFR)	-0.5891	0.0006	0.0190
EHD1	EH domain containing 1(EHD1)	-0.9371	0.0000	0.0000
EHD3	EH domain containing 3(EHD3)	-0.9221	0.0013	0.0319
EIF4EBP1	eukaryotic translation initiation factor 4E binding protein 1(EIF4EBP1)	0.7723	0.0000	0.0018
ELFN1	extracellular leucine rich repeat and fibronectin type III domain containing 1(ELFN1)	-1.4073	0.0004	0.0141
EMCN	endomucin (EMCN)	2.9971	0.0010	0.0262
EMILIN2	elastin microfibril interfacier 2(EMILIN2)	-0.9512	0.0000	0.0018
EML5	echinoderm microtubule associated protein like 5(EML5)	5.8734	0.0000	0.0001
EMP1	epithelial membrane protein 1(EMP1)	-0.6413	0.0010	0.0262
EMP3	epithelial membrane protein 3(EMP3)	-0.6530	0.0000	0.0000
ENAH	enabled homolog (Drosophila)(ENAH)	0.3909	0.0000	0.0021
EPDR1	ependymin related 1(EPDR1)	-2.5181	0.0000	0.0000
EPRS1	Glutamyl-Prolyl-TRNA Synthetase 1	0.4312	0.0000	0.0009
ERGIC1	endoplasmic reticulum-golgi intermediate compartment 1(ERGIC1)	-0.5988	0.0001	0.0029
ERGIC2	ERGIC and golgi 2(ERGIC2)	-0.3696	0.0010	0.0274
ERICH2	glutamate rich 2(ERICH2)	4.9875	0.0013	0.0327
ERV3-1	endogenous retrovirus group 3 member 1(ERV3-1)	1.3180	0.0000	0.0000
ETHE1	ETHE1, persulfide dioxygenase (ETHE1)	-1.2257	0.0000	0.0007
ETS2	ETS proto-oncogene 2, transcription factor (ETS2)	-0.8156	0.0000	0.0000
EXOSC6	exosome component 6(EXOSC6)	0.5235	0.0001	0.0054
EXOSC8	exosome component 8(EXOSC8)	0.5764	0.0014	0.0344
EXOSC9	exosome component 9(EXOSC9)	0.6994	0.0001	0.0061
F11R	F11 receptor(F11R)	3.8174	0.0015	0.0363
FAM156B	family with sequence similarity 156 member B(FAM156B)	-0.8472	0.0017	0.0396
FAM174B	family with sequence similarity 174 member B(FAM174B)	2.1618	0.0004	0.0126
FAM180A	family with sequence similarity 180 member A(FAM180A)	-1.2671	0.0000	0.0000
FAM20C	FAM20C, golgi associated secretory pathway kinase (FAM20C)	-0.4772	0.0010	0.0262

FAM210B	family with sequence similarity 210 member B(FAM210B)	-0.5666	0.0000	0.0020
FAM66B	family with sequence similarity 66 member B(FAM66B)	1.5810	0.0000	0.0000
FAR2	fatty acyl-CoA reductase 2(FAR2)	3.0102	0.0000	0.0000
FARP1	FERM, ARH/RhoGEF and pleckstrin domain protein 1(FARP1)	-0.5316	0.0021	0.0459
FBXW5	F-box and WD repeat domain containing 5(FBXW5)	-0.3916	0.0000	0.0016
FCRLB	Fc receptor like B(FCRLB)	-1.2278	0.0007	0.0211
FITM2	fat storage inducing transmembrane protein 2(FITM2)	-0.5422	0.0004	0.0135
FKBP8	FK506 binding protein 8(FKBP8)	-0.2935	0.0012	0.0301
FLOT2	flotillin 2(FLOT2)	-0.5627	0.0000	0.0002
FMN1	formin 1(FMN1)	1.7393	0.0000	0.0001
FN3K	fructosamine 3 kinase (FN3K)	-0.8439	0.0003	0.0114
FNDC1	fibronectin type III domain containing 1(FNDC1)	2.6758	0.0000	0.0000
FNDC4	fibronectin type III domain containing 4(FNDC4)	-0.9180	0.0000	0.0017
FOLR3	folate receptor 3(FOLR3)	-2.3511	0.0000	0.0003
FOSL1	FOS like 1, AP-1 transcription factor subunit (FOSL1)	-0.4624	0.0000	0.0000
FOXC2	forkhead box C2(FOXC2)	-2.3388	0.0017	0.0393
FOXD1	forkhead box D1(FOXD1)	0.6955	0.0002	0.0085
FOXP1	forkhead box P1(FOXP1)	0.6402	0.0000	0.0002
FOXP4	forkhead box P4(FOXP4)	0.4798	0.0001	0.0054
FOXQ1	forkhead box Q1(FOXQ1)	-2.3371	0.0000	0.0005
FRMD8	FERM domain containing 8(FRMD8)	-0.5383	0.0018	0.0417
FRRS1	ferric chelate reductase 1(FRRS1)	1.6726	0.0002	0.0075
FST	follicle-stimulating hormone receptor type 1(FST)	-1.1043	0.0000	0.0000
FUCA2	fucosyltransferase 2, alpha-L- (FUCA2)	-0.8001	0.0000	0.0002
FZD1	frizzled class receptor 1(FZD1)	0.6714	0.0000	0.0006
GAB1	GRB2 associated binding protein 1(GAB1)	0.6600	0.0021	0.0464
GABRE	gamma-aminobutyric acid type A receptor epsilon subunit (GABRE)	0.8693	0.0000	0.0007
GALNT16	polypeptide N- acetylgalactosaminyltransferase 16(GALNT16)	-2.0373	0.0002	0.0077
GAMT	guanidinoacetate N- methyltransferase (GAMT)	-0.6399	0.0021	0.0457
GARS1	Glycyl-tRNA Synthetase 1	0.5152	0.0000	0.0000

GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase (GART)	0.5124	0.0000	0.0001
GAS5	growth arrest specific 5 (non-protein coding) (GAS5)	0.4187	0.0000	0.0021
GAS7	growth arrest specific 7(GAS7)	1.4805	0.0000	0.0004
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2(GCNT1)	-1.0822	0.0000	0.0004
GDF10	growth differentiation factor 10(GDF10)	4.2503	0.0000	0.0005
GDF5	growth differentiation factor 5(GDF5)	-2.3219	0.0004	0.0145
GLIPR1	GLI pathogenesis related 1(GLIPR1)	-1.0883	0.0014	0.0351
GLIS2	GLIS family zinc finger 2(GLIS2)	-0.5328	0.0001	0.0047
GLMP	glycosylated lysosomal membrane protein (GLMP)	-0.7173	0.0000	0.0000
GLS	glutaminase (GLS)	0.6049	0.0002	0.0073
GM2A	GM2 ganglioside activator (GM2A)	-0.6160	0.0003	0.0111
GNAI2	G protein subunit alpha i2(GNAI2)	-0.4145	0.0004	0.0142
GNB4	G protein subunit beta 4(GNB4)	0.3714	0.0020	0.0442
GOLGA8M	golgin A8 family member M(GOLGA8M)	2.9296	0.0009	0.0242
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial (GPAM)	1.1280	0.0000	0.0001
GPAT2	glycerol-3-phosphate acyltransferase 2, mitochondrial (GPAT2)	4.3310	0.0000	0.0000
GPC1	glypican 1(GPC1)	-1.1438	0.0000	0.0000
GPC4	glypican 4(GPC4)	1.9593	0.0005	0.0165
GPCPD1	glycerophosphocholine phosphodiesterase 1(GPCPD1)	0.5561	0.0000	0.0000
GPM6B	glycoprotein M6B(GPM6B)	4.2371	0.0022	0.0467
GPR176	G protein-coupled receptor 176(GPR176)	-0.5145	0.0003	0.0122
GPR183	G protein-coupled receptor 183(GPR183)	-2.2565	0.0006	0.0189
GPT2	glutamic--pyruvic transaminase 2(GPT2)	0.6465	0.0016	0.0384
GPX3	glutathione peroxidase 3(GPX3)	1.3889	0.0006	0.0186
GREM2	gremlin 2, DAN family BMP antagonist (GREM2)	-0.9529	0.0000	0.0000
GSC	gooseoid homeobox (GSC)	2.7325	0.0005	0.0171
GTF2E1	general transcription factor IIE subunit 1(GTF2E1)	0.8542	0.0007	0.0198
H2AC19	H2A Clustered Histone 19	-1.0675	0.0000	0.0002
H3-2	H3.2 Histone (Putative)	1.1051	0.0001	0.0058

HACD4	3-hydroxyacyl-CoA dehydratase 4(HACD4)	-0.7573	0.0000	0.0004
HDAC10	histone deacetylase 10(HDAC10)	-0.5418	0.0003	0.0102
HDAC5	histone deacetylase 5(HDAC5)	-0.5368	0.0000	0.0005
HIF1A	hypoxia inducible factor 1 alpha subunit (HIF1A)	0.7686	0.0003	0.0104
HIVEP1	human immunodeficiency virus type I enhancer binding protein 1(HIVEP1)	0.5699	0.0009	0.0248
HLA-B	major histocompatibility complex, class I, B(HLA-B)	-1.1355	0.0000	0.0001
HLA-C	major histocompatibility complex, class I, C(HLA-C)	-0.9217	0.0017	0.0390
HLA-E	major histocompatibility complex, class I, E(HLA-E)	-0.6173	0.0001	0.0028
HMGA1	high mobility group AT-hook 1(HMGA1)	-0.8551	0.0022	0.0471
HNMT	histamine N-methyltransferase (HNMT)	0.9497	0.0000	0.0000
HNRNPA0	heterogeneous nuclear ribonucleoprotein A0(HNRNPA0)	0.4307	0.0000	0.0004
HNRNPF	heterogeneous nuclear ribonucleoprotein F(HNRNPF)	0.3871	0.0015	0.0358
HOXD3	homeobox D3(HOXD3)	1.0292	0.0000	0.0012
HSBP1	heat shock factor binding protein 1(HSBP1)	-0.4605	0.0000	0.0009
HSD3B7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7(HSD3B7)	-0.9530	0.0007	0.0212
HSP90AA1	heat shock protein 90 alpha family class A member 1(HSP90AA1)	-0.2839	0.0019	0.0429
HSPA9	heat shock protein family A (Hsp70) member 9(HSPA9)	0.4581	0.0000	0.0000
HSPB2	heat shock protein family B (small) member 2(HSPB2)	-0.4951	0.0003	0.0100
HSPB3	heat shock protein family B (small) member 3(HSPB3)	-2.5316	0.0000	0.0001
HTR2A	5-hydroxytryptamine receptor 2A(HTR2A)	1.2348	0.0020	0.0450
HUNK	hormonally up-regulated Neu-associated kinase (HUNK)	1.5743	0.0021	0.0464
IARS1	Isoleucyl-TRNA Synthetase 1	0.5285	0.0000	0.0027
ICAM5	intercellular adhesion molecule 5(ICAM5)	-1.6126	0.0000	0.0026
ICMT	isoprenylcysteine carboxyl methyltransferase (ICMT)	-0.4293	0.0006	0.0189
IDS	iduronate 2-sulfatase (IDS)	-0.6541	0.0000	0.0023
IFFO1	intermediate filament family orphan 1(IFFO1)	-1.0338	0.0000	0.0002
IFI44L	interferon induced protein 44 like (IFI44L)	1.4548	0.0023	0.0490
IGF1	insulin like growth factor 1(IGF1)	5.0628	0.0000	0.0005

IGFBP6	insulin like growth factor binding protein 6(IGFBP6)	-1.1693	0.0001	0.0047
IGIP	IgA inducing protein (IGIP)	-0.6425	0.0004	0.0141
IL17RB	interleukin 17 receptor B(IL17RB)	-2.5456	0.0001	0.0055
IL20RB	interleukin 20 receptor subunit beta (IL20RB)	-0.7074	0.0002	0.0092
IL21R	interleukin 21 receptor (IL21R)	1.4041	0.0000	0.0002
IMPACT	impact RWD domain protein (IMPACT)	0.4420	0.0001	0.0038
INAFM2	InaF motif containing 2(INAFM2)	-0.7496	0.0001	0.0056
INHBE	inhibin beta E subunit (INHBE)	2.4445	0.0000	0.0000
IRS2	insulin receptor substrate 2(IRS2)	0.8275	0.0000	0.0009
ITGA3	integrin subunit alpha 3(ITGA3)	-1.2113	0.0000	0.0004
ITPKC	inositol-trisphosphate 3-kinase C(ITPKC)	-0.7535	0.0001	0.0036
ITPR3	inositol 1,4,5-trisphosphate receptor type 3(ITPR3)	-0.6587	0.0003	0.0103
JADE1	jade family PHD finger 1(JADE1)	0.6865	0.0001	0.0049
JMJD8	jumonji domain containing 8(JMJD8)	-0.4651	0.0021	0.0466
JUN	Jun proto-oncogene, AP-1 transcription factor subunit (JUN)	0.8012	0.0021	0.0461
KANK2	KN motif and ankyrin repeat domains 2(KANK2)	-0.3297	0.0009	0.0244
KCNA4	potassium voltage-gated channel subfamily A member 4(KCNA4)	4.5286	0.0010	0.0262
KCNB1	potassium voltage-gated channel subfamily B member 1(KCNB1)	-3.3101	0.0000	0.0002
KCNE3	potassium voltage-gated channel subfamily E regulatory subunit 3(KCNE3)	1.7444	0.0005	0.0166
KCNG1	potassium voltage-gated channel modifier subfamily G member 1(KCNG1)	1.1120	0.0001	0.0062
KCNIP3	potassium voltage-gated channel interacting protein 3(KCNIP3)	-0.9522	0.0002	0.0067
KCNJ8	potassium voltage-gated channel subfamily J member 8(KCNJ8)	2.6664	0.0000	0.0016
KCNS1	potassium voltage-gated channel modifier subfamily S member 1(KCNS1)	-2.1554	0.0001	0.0034
KIAA1324L	KIAA1324 like (KIAA1324L)	2.6763	0.0000	0.0008
KIAA1549	KIAA1549(KIAA1549)	-1.2872	0.0000	0.0000
KIAA1549L	KIAA1549 like (KIAA1549L)	-0.9136	0.0002	0.0077

KIF13A	kinesin family member 13A(KIF13A)	-0.5468	0.0000	0.0000
KIF1C	kinesin family member 1C(KIF1C)	-0.7860	0.0000	0.0000
KIF3B	kinesin family member 3B(KIF3B)	-0.4785	0.0011	0.0283
KIRREL3	kin of IRRE like 3 (Drosophila)(KIRREL3)	-1.6119	0.0000	0.0000
KLF14	Kruppel like factor 14(KLF14)	4.5977	0.0002	0.0082
KLF7	Kruppel like factor 7(KLF7)	0.5454	0.0003	0.0111
KLHDC7B	kelch domain containing 7B(KLHDC7B)	1.9449	0.0009	0.0252
KLHL8	kelch like family member 8(KLHL8)	0.6014	0.0007	0.0215
KRT15	keratin 15(KRT15)	-2.6166	0.0013	0.0315
KRT7	keratin 7(KRT7)	3.9203	0.0001	0.0042
KRTAP1-5	keratin associated protein 1-5(KRTAP1-5)	-2.2211	0.0000	0.0004
LAMA5	laminin subunit alpha 5(LAMA5)	-1.1729	0.0005	0.0161
LAMTOR4	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4(LAMTOR4)	-0.3282	0.0021	0.0460
LARS1	Leucyl-TRNA Synthetase 1	0.3803	0.0005	0.0161
LCTL	lactase like (LCTL)	2.4577	0.0001	0.0062
LDHB	lactate dehydrogenase B(LDHB)	0.4703	0.0001	0.0034
LDLRAP1	low density lipoprotein receptor adaptor protein 1(LDLRAP1)	-0.4097	0.0005	0.0164
LGR4	leucine rich repeat containing G protein-coupled receptor 4(LGR4)	1.2106	0.0014	0.0350
LIMD2	LIM domain containing 2(LIMD2)	0.7651	0.0001	0.0048
LINC00578	long intergenic non-protein coding RNA 578(LINC00578)	3.3227	0.0001	0.0029
LINC01085	long intergenic non-protein coding RNA 1085(LINC01085)	-4.9460	0.0000	0.0000
LINC01145	Long Intergenic Non-Protein Coding RNA 1145	1.3515	0.0000	0.0001
LINC01503	long intergenic non-protein coding RNA 1503(LINC01503)	1.4395	0.0001	0.0062
LINC01515	long intergenic non-protein coding RNA 1515(LINC01515)	-3.6335	0.0001	0.0057
LINC01638	Long Intergenic Non-Protein Coding RNA 1638	1.5917	0.0003	0.0102
LINC01936	Long Intergenic Non-Protein Coding RNA 1936	1.4080	0.0018	0.0420
LIPG	lipase G, endothelial type (LIPG)	2.4285	0.0017	0.0389
LMF1	lipase maturation factor 1(LMF1)	-0.5826	0.0004	0.0126
LMNA	lamin A/C(LMNA)	-0.4626	0.0012	0.0306

LMO4	LIM domain only 4(LMO4)	0.8049	0.0006	0.0188
LONP1	lon peptidase 1, mitochondrial (LONP1)	0.5523	0.0000	0.0027
LOXL1	lysyl oxidase like 1(LOXL1)	-0.6649	0.0000	0.0000
LOXL4	lysyl oxidase like 4(LOXL4)	-1.8183	0.0000	0.0011
LRMDA	Leucine Rich Melanocyte Differentiation Associated	1.1596	0.0010	0.0269
LRPAP1	LDL receptor related protein associated protein 1(LRPAP1)	-0.7858	0.0009	0.0260
LRRFIP2	LRR binding FLII interacting protein 2(LRRFIP2)	-0.7314	0.0009	0.0259
LRRN4CL	LRRN4 C-terminal like (LRRN4CL)	-1.2111	0.0000	0.0000
LY6E	lymphocyte antigen 6 complex, locus E(LY6E)	-1.0571	0.0005	0.0166
LYNX1	Ly6/neurotoxin 1(LYNX1)	-1.1334	0.0015	0.0365
LYPD3	LY6/PLAUR domain containing 3(LYPD3)	-2.6550	0.0000	0.0016
LYPD6	LY6/PLAUR domain containing 6(LYPD6)	-1.5093	0.0001	0.0043
LYPD6B	LY6/PLAUR domain containing 6B(LYPD6B)	-1.8648	0.0000	0.0001
LYPLA1	lysophospholipase I(LYPLA1)	0.5221	0.0022	0.0470
MALAT1	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding) (MALAT1)	-0.9479	0.0000	0.0000
MAP2K3	mitogen-activated protein kinase kinase 3(MAP2K3)	-0.5995	0.0000	0.0005
MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3(MAPKAPK3)	-0.4868	0.0003	0.0095
MARK1	microtubule affinity regulating kinase 1(MARK1)	3.5625	0.0009	0.0258
MARS1	Methionyl-TRNA Synthetase 1	0.5383	0.0000	0.0026
MATN2	matrilin 2(MATN2)	-0.9794	0.0000	0.0006
MBD4	methyl-CpG binding domain 4, DNA glycosylase (MBD4)	0.5041	0.0003	0.0111
MBNL1-AS1	MBNL1 antisense RNA 1(MBNL1-AS1)	-0.5080	0.0016	0.0378
MBOAT7	membrane bound O-acyltransferase domain containing 7(MBOAT7)	-0.6432	0.0003	0.0102
MDFI	MyoD family inhibitor (MDFI)	6.6073	0.0000	0.0001
MEF2A	myocyte enhancer factor 2A(MEF2A)	-0.5554	0.0001	0.0052
MFAP3L	microfibrillar associated protein 3 like (MFAP3L)	1.2370	0.0020	0.0439
MFAP4	microfibrillar associated protein 4(MFAP4)	0.9426	0.0002	0.0075
MFSD10	major facilitator superfamily domain containing 10(MFSD10)	-0.5952	0.0002	0.0091

MFSD12	major facilitator superfamily domain containing 12(MFSD12)	-0.5394	0.0014	0.0353
MFSD6	major facilitator superfamily domain containing 6(MFSD6)	-1.1723	0.0008	0.0233
MGARP	mitochondria localized glutamic acid rich protein (MGARP)	-0.7715	0.0005	0.0172
MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B(MGAT4B)	-0.5231	0.0001	0.0047
MIER3	MIER family member 3(MIER3)	0.5910	0.0007	0.0210
MIR503HG	MIR503 host gene (MIR503HG)	1.9294	0.0001	0.0034
MIR99AHG	mir-99a-let-7c cluster host gene (MIR99AHG)	1.3152	0.0000	0.0002
MME	membrane metalloendopeptidase (MME)	1.2066	0.0001	0.0029
MMP24OS	MMP24 Opposite Strand	-0.5785	0.0000	0.0001
MOK	MOK protein kinase (MOK)	-1.8993	0.0000	0.0000
MT-ATP6	Mitochondrially Encoded ATP Synthase Membrane Subunit 6	-0.6422	0.0002	0.0093
MTATP6P1	mitochondrially encoded ATP synthase 6 pseudogene 1(MTATP6P1)	-0.7252	0.0007	0.0207
MT-CO1	Mitochondrially Encoded Cytochrome C Oxidase I	-0.5153	0.0000	0.0022
MTCO1P12	mitochondrially encoded cytochrome c oxidase I pseudogene 12(MTCO1P12)	-0.5331	0.0014	0.0352
MT-CO2	Mitochondrially Encoded Cytochrome C Oxidase II	-0.8283	0.0002	0.0086
MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase (MTHFD2)	1.0596	0.0000	0.0000
MT-ND1	Mitochondrially Encoded NADH: Ubiquinone Oxidoreductase Core Subunit 1	-0.5235	0.0000	0.0023
MT-ND2	Mitochondrially Encoded NADH: Ubiquinone Oxidoreductase Core Subunit 2	-0.6281	0.0017	0.0393
MTND2P28	mitochondrially encoded NADH: ubiquinone oxidoreductase core subunit 2 pseudogene 28(MTND2P28)	-0.6876	0.0010	0.0264
MT-ND3	Mitochondrially Encoded NADH: Ubiquinone Oxidoreductase Core Subunit 3	-0.6251	0.0008	0.0219

MT-ND5	Mitochondrially Encoded NADH: Ubiquinone Oxidoreductase Core Subunit 5	-0.6271	0.0000	0.0015
MT-RNR1	Mitochondrially Encoded 12S RRNA	-1.1473	0.0000	0.0001
MT-RNR2	Mitochondrially Encoded 16S RRNA	-0.4799	0.0009	0.0259
MTSS1	MTSS1, I-BAR domain containing (MTSS1)	-1.2511	0.0008	0.0228
MUC20-OT1	MUC20 Overlapping Transcript	-0.6715	0.0002	0.0093
MXRA8	matrix remodeling associated 8(MXRA8)	-0.4727	0.0003	0.0102
MYBL1	MYB proto-oncogene like 1(MYBL1)	-1.5627	0.0000	0.0002
MYNN	myoneurin (MYNN)	0.4356	0.0020	0.0445
MYO18A	myosin XVIII A(MYO18A)	-0.4814	0.0016	0.0375
MYPN	myopalladin (MYPN)	-2.7570	0.0001	0.0056
NAALADL2	N-acetylated alpha-linked acidic dipeptidase like 2(NAALADL2)	-0.9212	0.0000	0.0012
NAGA	alpha-N- acetylgalactosaminidase (NAGA)	-0.4198	0.0018	0.0414
NARS1	Asparaginyl-TRNA Synthetase 1	0.3667	0.0016	0.0384
NBL1	neuroblastoma 1, DAN family BMP antagonist (NBL1)	-1.2085	0.0000	0.0000
NCEH1	neutral cholesterol ester hydrolase 1(NCEH1)	-1.3901	0.0000	0.0002
NCOA7	nuclear receptor coactivator 7(NCOA7)	0.5506	0.0023	0.0495
NCS1	neuronal calcium sensor 1(NCS1)	-0.5199	0.0000	0.0001
NEDD4	neural precursor cell expressed, developmentally down- regulated 4, E3 ubiquitin protein ligase (NEDD4)	0.4057	0.0023	0.0488
NEFL	neurofilament, light polypeptide (NEFL)	3.2710	0.0004	0.0126
NENF	neudesin neurotrophic factor (NENF)	-0.4056	0.0002	0.0067
NF2	neurofibromin 2(NF2)	-0.4780	0.0002	0.0073
NFASC	neurofascin (NFASC)	-0.6991	0.0000	0.0016
NFATC2	nuclear factor of activated T- cells 2(NFATC2)	-3.4974	0.0000	0.0000
NFKB2	nuclear factor kappa B subunit 2(NFKB2)	-0.4036	0.0020	0.0456
NGEF	neuronal guanine nucleotide exchange factor (NGEF)	-5.6823	0.0000	0.0001
NIN	ninein (NIN)	-0.4601	0.0008	0.0224
NIPAL2	NIPA like domain containing 2(NIPAL2)	-0.7043	0.0000	0.0010
NIPAL3	NIPA like domain containing 3(NIPAL3)	-1.2133	0.0000	0.0000

NLRP10	NLR family pyrin domain containing 10(NLRP10)	-2.2935	0.0000	0.0001
NOLC1	nucleolar and coiled-body phosphoprotein 1(NOLC1)	0.5939	0.0000	0.0016
NOS3	nitric oxide synthase 3(NOS3)	2.5281	0.0012	0.0303
NOTCH3	notch 3(NOTCH3)	-1.3878	0.0007	0.0205
NOX4	NADPH oxidase 4(NOX4)	1.5817	0.0003	0.0102
NPDC1	neural proliferation, differentiation, and control 1(NPDC1)	-0.8566	0.0010	0.0263
NPTX1	neuronal pentraxin 1(NPTX1)	-1.7373	0.0000	0.0003
NR2F1	nuclear receptor subfamily 2 group F member 1(NR2F1)	1.0049	0.0010	0.0271
NRN1	neuritin 1(NRN1)	-0.6493	0.0000	0.0002
NRP2	neuropilin 2(NRP2)	1.0733	0.0002	0.0078
NT5E	5'-nucleotidase ecto (NT5E)	-1.1556	0.0000	0.0003
NTRK3	neurotrophic receptor tyrosine kinase 3(NTRK3)	-3.3315	0.0001	0.0043
NUDT21	nudix hydrolase 21(NUDT21)	0.3692	0.0006	0.0185
NUMBL	NUMB like, endocytic adaptor protein (NUMBL)	-0.4174	0.0005	0.0173
NUP98	nucleoporin 98(NUP98)	0.3398	0.0016	0.0375
OIP5-AS1	OIP5 antisense RNA 1(OIP5-AS1)	0.5225	0.0000	0.0006
ORAI3	ORAI calcium release-activated calcium modulator 3(ORAI3)	-0.7194	0.0005	0.0156
OSBP2	oxysterol binding protein 2(OSBP2)	-2.3399	0.0000	0.0004
PAM	peptidylglycine alpha-amidating monooxygenase (PAM)	-0.9676	0.0005	0.0167
PARD3B	par-3 family cell polarity regulator beta (PARD3B)	-0.7846	0.0000	0.0001
PARP8	poly (ADP-ribose) polymerase family member 8(PARP8)	3.1539	0.0021	0.0464
PBX1	PBX homeobox 1(PBX1)	0.7722	0.0000	0.0023
PCDH9	protocadherin 9(PCDH9)	1.7627	0.0000	0.0000
PCDHGB6	protocadherin gamma subfamily B, 6(PCDHGB6)	1.4370	0.0002	0.0082
PCK2	phosphoenolpyruvate carboxykinase 2, mitochondrial (PCK2)	0.9622	0.0000	0.0000
PCSK1	proprotein convertase subtilisin/kexin type 1(PCSK1)	2.4307	0.0001	0.0064
PCSK5	proprotein convertase subtilisin/kexin type 5(PCSK5)	2.1519	0.0000	0.0000
PCYOX1	prenylcysteine oxidase 1(PCYOX1)	-0.7995	0.0002	0.0076
PDGFB	platelet derived growth factor subunit B(PDGFB)	5.2079	0.0007	0.0198

PDGFD	platelet derived growth factor D(PDGFD)	1.4314	0.0000	0.0000
PEX6	peroxisomal biogenesis factor 6(PEX6)	0.5051	0.0010	0.0262
PGAP6	Post-Glycosylphosphatidylinositol Attachment To Proteins 6	-0.4879	0.0002	0.0089
PHACTR3	phosphatase and actin regulator 3(PHACTR3)	4.1572	0.0003	0.0100
PHGDH	phosphoglycerate dehydrogenase (PHGDH)	0.6867	0.0001	0.0043
PI16	peptidase inhibitor 16(PI16)	3.4013	0.0018	0.0408
PI4KAP2	phosphatidylinositol 4-kinase alpha pseudogene 2(PI4KAP2)	-0.9526	0.0000	0.0004
PICRAR	P38 inhibited cutaneous squamous cell carcinoma associated lincRNA (PICRAR)	5.9841	0.0009	0.0259
PIK3R3	phosphoinositide-3-kinase regulatory subunit 3(PIK3R3)	-0.9867	0.0001	0.0064
PJA1	praja ring finger ubiquitin ligase 1(PJA1)	0.5068	0.0011	0.0279
PKD2	polycystin 2, transient receptor potential cation channel (PKD2)	-0.7511	0.0004	0.0141
PKIG	protein kinase (cAMP-dependent, catalytic) inhibitor gamma (PKIG)	-0.9822	0.0010	0.0263
PKN1	protein kinase N1(PKN1)	-0.3744	0.0012	0.0296
PLA2G15	phospholipase A2 group XV(PLA2G15)	-0.9474	0.0000	0.0000
PLA2R1	phospholipase A2 receptor 1(PLA2R1)	-0.6453	0.0015	0.0369
PLAC1	placenta specific 1(PLAC1)	4.3143	0.0012	0.0315
PLCD1	phospholipase C delta 1(PLCD1)	-0.7652	0.0000	0.0004
PLEC	plectin (PLEC)	-0.7812	0.0000	0.0011
PLP2	proteolipid protein 2(PLP2)	-0.6442	0.0016	0.0381
PLPP2	phospholipid phosphatase 2(PLPP2)	4.0119	0.0001	0.0046
PLPP4	phospholipid phosphatase 4(PLPP4)	1.0814	0.0000	0.0000
PLS3	plastin 3(PLS3)	0.5549	0.0001	0.0042
PLSCR1	phospholipid scramblase 1(PLSCR1)	0.7500	0.0000	0.0018
PLXDC2	plexin domain containing 2(PLXDC2)	4.2060	0.0007	0.0205
PNPLA6	patatin like phospholipase domain containing 6(PNPLA6)	-0.6430	0.0001	0.0028
PODN	podocan (PODN)	-0.9085	0.0001	0.0061
POLR2L	RNA polymerase II subunit L(POLR2L)	-0.6071	0.0000	0.0001

POMGNT1	protein O-linked mannose N-acetylglucosaminyltransferase 1 (beta 1,2-) (POMGNT1)	-0.6554	0.0008	0.0224
PPFIBP2	PPFIA binding protein 2(PPFIBP2)	0.7037	0.0000	0.0014
PPP1R12A	protein phosphatase 1 regulatory subunit 12A(PPP1R12A)	0.3686	0.0018	0.0417
PPP3CA	protein phosphatase 3 catalytic subunit alpha (PPP3CA)	0.4205	0.0004	0.0134
PRELP	proline and arginine rich end leucine rich repeat protein (PRELP)	-1.9811	0.0000	0.0020
PREX1	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 1(PREX1)	1.0772	0.0017	0.0390
PRICKLE1	prickle planar cell polarity protein 1(PRICKLE1)	2.2404	0.0017	0.0397
PRICKLE2	prickle planar cell polarity protein 2(PRICKLE2)	0.8628	0.0013	0.0323
PRIM2	primase (DNA) subunit 2(PRIM2)	-0.6940	0.0004	0.0135
PRKAB2	protein kinase AMP-activated non-catalytic subunit beta 2(PRKAB2)	0.5542	0.0000	0.0002
PRL	prolactin (PRL)	4.3352	0.0011	0.0279
PRNP	prion protein (PRNP)	-0.6324	0.0021	0.0467
PRPH2	peripherin 2(PRPH2)	-1.0871	0.0000	0.0026
PRPS1	phosphoribosyl pyrophosphate synthetase 1(PRPS1)	1.0850	0.0000	0.0014
PRR7	proline rich 7, synaptic (PRR7)	-0.7646	0.0010	0.0262
PRSS12	protease, serine 12(PRSS12)	-1.2755	0.0002	0.0082
PRXL2A	Peroxiredoxin Like 2A	4.6276	0.0008	0.0223
PSAT1	phosphoserine aminotransferase 1(PSAT1)	0.9058	0.0000	0.0000
PSEN2	presenilin 2(PSEN2)	-1.0165	0.0023	0.0488
PSG2	pregnancy specific beta-1-glycoprotein 2(PSG2)	-2.6682	0.0000	0.0000
PSG9	pregnancy specific beta-1-glycoprotein 9(PSG9)	-2.3971	0.0007	0.0198
PSMB2	proteasome subunit beta 2(PSMB2)	0.3780	0.0007	0.0198
PSPH	phosphoserine phosphatase (PSPH)	0.6097	0.0008	0.0228
PTGES	prostaglandin E synthase (PTGES)	-0.8495	0.0011	0.0279
PTPRU	protein tyrosine phosphatase, receptor type U(PTPRU)	-0.7977	0.0002	0.0092
PUM3	pumilio RNA binding family member 3(PUM3)	0.3802	0.0019	0.0438
RAB11FIP3	RAB11 family interacting protein 3(RAB11FIP3)	-0.5959	0.0000	0.0006

RAB15	RAB15, member RAS oncogene family (RAB15)	0.7355	0.0001	0.0054
RAB27B	RAB27B, member RAS oncogene family (RAB27B)	-2.0112	0.0001	0.0056
RABAC1	Rab acceptor 1(RABAC1)	-0.3043	0.0014	0.0348
RABGEF1	RAB guanine nucleotide exchange factor 1(RABGEF1)	-0.4452	0.0001	0.0051
RAD21	RAD21 cohesin complex component (RAD21)	0.3608	0.0003	0.0112
RAF1	Raf-1 proto-oncogene, serine/threonine kinase (RAF1)	-0.3560	0.0011	0.0278
RAI14	retinoic acid induced 14(RAI14)	0.4261	0.0007	0.0211
RAMP1	receptor activity modifying protein 1(RAMP1)	-2.1215	0.0000	0.0009
RANBP17	RAN binding protein 17(RANBP17)	3.3369	0.0022	0.0484
RAPGEF1	Rap guanine nucleotide exchange factor 1(RAPGEF1)	-0.5350	0.0003	0.0111
RASA2	RAS p21 protein activator 2(RASA2)	-0.6412	0.0000	0.0004
RASSF3	Ras association domain family member 3(RASSF3)	-0.4318	0.0008	0.0229
RASSF8-AS1	RASSF8 antisense RNA 1(RASSF8-AS1)	-0.5459	0.0007	0.0211
RBPM52	RNA binding protein with multiple splicing 2(RBPM52)	2.8402	0.0000	0.0004
RCOR2	REST corepressor 2(RCOR2)	1.5186	0.0006	0.0180
RDH5	retinol dehydrogenase 5(RDH5)	-2.2552	0.0000	0.0000
REC8	REC8 meiotic recombination protein (REC8)	-0.8628	0.0001	0.0061
REEP2	receptor accessory protein 2(REEP2)	-0.7837	0.0001	0.0048
REEP5	receptor accessory protein 5(REEP5)	-0.4489	0.0001	0.0043
REPS2	RALBP1 associated Eps domain containing 2(REPS2)	2.8756	0.0004	0.0126
RETSAT	retinol saturase (RETSAT)	-0.7231	0.0000	0.0002
RFX8	RFX family member 8, lacking RFX DNA binding domain (RFX8)	-1.4530	0.0001	0.0058
RGCC	regulator of cell cycle (RGCC)	-1.5791	0.0007	0.0210
RGMB	repulsive guidance molecule family member b(RGMB)	-1.3325	0.0000	0.0000
RGS20	regulator of G-protein signaling 20(RGS20)	-1.5956	0.0002	0.0082
RHOQ	ras homolog family member Q(RHOQ)	-0.3969	0.0021	0.0467
RIMKLB	ribosomal modification protein rimK like family member B(RIMKLB)	0.4632	0.0009	0.0242

RIN1	Ras and Rab interactor 1(RIN1)	-0.7982	0.0001	0.0061
RIPOR2	RHO Family Interacting Cell Polarization Regulator 2	-1.7306	0.0000	0.0000
RMI1	RecQ mediated genome instability 1(RMI1)	0.7358	0.0019	0.0425
RMND5A	required for meiotic nuclear division 5 homolog A(RMND5A)	0.6002	0.0001	0.0031
RNASE4	ribonuclease A family member 4(RNASE4)	-0.8012	0.0009	0.0244
RNASEK	ribonuclease K(RNASEK)	-0.3427	0.0013	0.0323
RNF150	ring finger protein 150(RNF150)	-0.6598	0.0001	0.0041
RNY3	RNA, Ro-associated Y3(RNY3)	-22.8998	0.0000	0.0000
RPL13P12	ribosomal protein L13 pseudogene 12(RPL13P12)	-2.6700	0.0000	0.0018
RPS10-NUDT3	RPS10-NUDT3 readthrough (RPS10-NUDT3)	0.5874	0.0005	0.0168
RRAD	RRAD, Ras related glycolysis inhibitor and calcium channel regulator (RRAD)	-1.1819	0.0005	0.0166
RRAS	related RAS viral (r-ras) oncogene homolog (RRAS)	-0.6678	0.0000	0.0000
RTN4	reticulon 4(RTN4)	-0.6114	0.0000	0.0018
S100A10	S100 calcium binding protein A10(S100A10)	-0.9511	0.0000	0.0000
S100A13	S100 calcium binding protein A13(S100A13)	-0.4506	0.0000	0.0003
S100A6	S100 calcium binding protein A6(S100A6)	-0.6903	0.0008	0.0240
S1PR3	sphingosine-1-phosphate receptor 3(S1PR3)	-1.1626	0.0000	0.0001
SAMD11	sterile alpha motif domain containing 11(SAMD11)	1.3825	0.0000	0.0005
SARS1	Seryl-TRNA Synthetase 1	0.3757	0.0000	0.0015
SAV1	salvador family WW domain containing protein 1(SAV1)	-0.6245	0.0001	0.0048
SCAMP5	secretory carrier membrane protein 5(SCAMP5)	1.6373	0.0000	0.0000
SCARB1	scavenger receptor class B member 1(SCARB1)	-0.6526	0.0001	0.0061
SCCPDH	saccharopine dehydrogenase (putative)(SCCPDH)	-0.3695	0.0001	0.0048
SDF4	stromal cell derived factor 4(SDF4)	-0.6114	0.0002	0.0078
SEC23IP	SEC23 interacting protein (SEC23IP)	0.3536	0.0020	0.0452
SELENOP	selenoprotein P(SELENOP)	1.4299	0.0000	0.0000
SEMA3B	semaphorin 3B(SEMA3B)	-1.5900	0.0000	0.0015
SEMA5A	semaphorin 5A(SEMA5A)	-0.8943	0.0004	0.0142
SEPHS2	selenophosphate synthetase 2(SEPHS2)	0.3465	0.0011	0.0292

SEPTIN9	Septin 9	-0.6340	0.0003	0.0103
SERAC1	serine active site containing 1(SERAC1)	0.8519	0.0001	0.0042
SERINC3	serine incorporator 3(SERINC3)	-0.5252	0.0016	0.0384
SESN2	sestrin 2(SESN2)	0.6681	0.0000	0.0001
SFRP4	secreted frizzled related protein 4(SFRP4)	-3.0215	0.0005	0.0171
SGMS2	sphingomyelin synthase 2(SGMS2)	-1.0588	0.0001	0.0034
SH2D5	SH2 domain containing 5(SH2D5)	-1.0802	0.0001	0.0039
SH3BGR13	SH3 domain binding glutamate rich protein like 3(SH3BGR13)	-0.5811	0.0002	0.0074
SH3RF1	SH3 domain containing ring finger 1(SH3RF1)	-0.8657	0.0000	0.0000
SHISA4	shisa family member 4(SHISA4)	-0.4384	0.0001	0.0031
SHMT2	serine hydroxymethyltransferase 2(SHMT2)	0.4713	0.0000	0.0010
SHPRH	SNF2 histone linker PHD RING helicase (SHPRH)	0.6954	0.0014	0.0343
SHROOM2	shroom family member 2(SHROOM2)	-3.0339	0.0003	0.0109
SIAH2	siah E3 ubiquitin protein ligase 2(SIAH2)	0.4481	0.0001	0.0043
SIGMAR1	sigma non-opioid intracellular receptor 1(SIGMAR1)	-0.3140	0.0016	0.0385
SLC13A4	solute carrier family 13 member 4(SLC13A4)	-1.3055	0.0016	0.0379
SLC16A4	solute carrier family 16 member 4(SLC16A4)	-0.9449	0.0016	0.0375
SLC18B1	solute carrier family 18 member B1(SLC18B1)	1.2289	0.0004	0.0140
SLC1A3	solute carrier family 1 member 3(SLC1A3)	0.6073	0.0001	0.0042
SLC20A2	solute carrier family 20 member 2(SLC20A2)	-1.0891	0.0000	0.0000
SLC2A11	solute carrier family 2 member 11(SLC2A11)	-0.8135	0.0000	0.0002
SLC35E2A	Solute Carrier Family 35 Member E2A	-0.8760	0.0011	0.0279
SLC35E4	solute carrier family 35 member E4(SLC35E4)	-1.0919	0.0000	0.0008
SLC39A8	solute carrier family 39 member 8(SLC39A8)	1.5875	0.0019	0.0423
SLC40A1	solute carrier family 40 member 1(SLC40A1)	1.7366	0.0019	0.0428
SLC4A11	solute carrier family 4 member 11(SLC4A11)	-1.3263	0.0000	0.0003
SLC4A4	solute carrier family 4 member 4(SLC4A4)	-1.0552	0.0001	0.0061
SLC6A9	solute carrier family 6 member 9(SLC6A9)	0.8106	0.0003	0.0100
SLC9A7	solute carrier family 9 member A7(SLC9A7)	-1.0647	0.0000	0.0019

SMG1P3	SMG1P3, nonsense mediated mRNA decay associated PI3K related kinase pseudogene 3(SMG1P3)	-0.9728	0.0001	0.0061
SMPD1	sphingomyelin phosphodiesterase 1(SMPD1)	-1.1262	0.0001	0.0063
SMURF2	SMAD specific E3 ubiquitin protein ligase 2(SMURF2)	-0.7436	0.0000	0.0014
SNORA73A	small nucleolar RNA, H/ACA box 73A(SNORA73A)	-4.9739	0.0006	0.0178
SNX21	sorting nexin family member 21(SNX21)	-0.5896	0.0001	0.0042
SORT1	sortilin 1(SORT1)	-1.1269	0.0001	0.0035
SOX4	SRY-box 4(SOX4)	1.1661	0.0000	0.0000
SPACA6	sperm acrosome associated 6(SPACA6)	-0.8253	0.0001	0.0042
SPART	Spartin	0.4609	0.0001	0.0049
SPON1	spondin 1(SPON1)	6.1499	0.0000	0.0000
SPTLC2	serine palmitoyltransferase long chain base subunit 2(SPTLC2)	-0.6049	0.0019	0.0438
SQOR	Sulfide Quinone Oxidoreductase	-0.7724	0.0007	0.0209
SRCAP	Snf2 related CREBBP activator protein (SRCAP)	0.4165	0.0023	0.0488
SRGAP2B	SLIT-ROBO Rho GTPase activating protein 2B(SRGAP2B)	0.4822	0.0013	0.0334
SRGAP2D	SLIT-ROBO Rho GTPase activating protein 2D (pseudogene)(SRGAP2D)	1.7082	0.0022	0.0467
SRP54	signal recognition particle 54(SRP54)	0.3824	0.0001	0.0056
ST6GALNAC5	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 5(ST6GALNAC5)	-0.9918	0.0011	0.0288
ST6GALNAC6	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 6(ST6GALNAC6)	-0.4336	0.0008	0.0224
STARD5	StAR related lipid transfer domain containing 5(STARD5)	-0.8347	0.0006	0.0176
STING1	Stimulator Of Interferon Response CGAMP Interactor 1	-0.5099	0.0000	0.0001
STK38L	serine/threonine kinase 38 like (STK38L)	0.6627	0.0003	0.0106
STMN2	stathmin 2(STMN2)	5.0619	0.0000	0.0015
STMN3	stathmin 3(STMN3)	-1.3951	0.0003	0.0097
STS	steroid sulfatase (microsomal), isozyme S(STS)	-0.9721	0.0000	0.0000

SYBU	syntabulin (SYBU)	2.7922	0.0000	0.0000
SYNE1	spectrin repeat containing nuclear envelope protein 1(SYNE1)	0.8581	0.0002	0.0067
SYNGR2	synaptogyrin 2(SYNGR2)	-1.3205	0.0000	0.0001
TACC2	transforming acidic coiled-coil containing protein 2(TACC2)	-0.8993	0.0000	0.0002
TAF5	TAF5 Chemokine Like Family Member 5	-1.2035	0.0000	0.0017
TANGO2	transport and golgi organization 2 homolog (TANGO2)	-0.4127	0.0006	0.0192
TAPBP	TAP binding protein (TAPBP)	-0.8226	0.0005	0.0157
TARS1	Threonyl-TRNA Synthetase 1	0.4725	0.0000	0.0007
TBC1D2	TBC1 domain family member 2(TBC1D2)	-1.0153	0.0000	0.0000
TBC1D3E	TBC1 domain family member 3E(TBC1D3E)	-21.7207	0.0000	0.0000
TBC1D3G	TBC1 domain family member 3G(TBC1D3G)	-22.0080	0.0000	0.0000
TBC1D3K	TBC1 domain family member 3K(TBC1D3K)	-21.9529	0.0000	0.0000
TBX2	T-box 2(TBX2)	-1.2766	0.0000	0.0012
TCEA1	transcription elongation factor A1(TCEA1)	0.6348	0.0000	0.0000
TCF7L2	transcription factor 7 like 2(TCF7L2)	0.6342	0.0006	0.0190
TCIM	Transcriptional And Immune Response Regulator	1.5278	0.0000	0.0004
TCP1	t-complex 1(TCP1)	0.2996	0.0016	0.0375
TCTA	T-cell leukemia translocation altered (TCTA)	-0.3387	0.0016	0.0385
TDRD9	tudor domain containing 9(TDRD9)	6.7596	0.0000	0.0027
TECR	trans-2,3-enoyl-CoA reductase (TECR)	-0.4494	0.0023	0.0494
TEDC1	Tubulin Epsilon and Delta Complex 1	-1.4449	0.0000	0.0000
TFPI	tissue factor pathway inhibitor (TFPI)	-0.9982	0.0000	0.0026
TGFB3	transforming growth factor beta 3(TGFB3)	0.7907	0.0001	0.0041
TGFBR3	transforming growth factor beta receptor 3(TGFBR3)	-1.2648	0.0002	0.0077
THSD1	thrombospondin type 1 domain containing 1(THSD1)	-1.7600	0.0000	0.0013
THY1	Thy-1 cell surface antigen (THY1)	-0.6983	0.0006	0.0192
TJP2	tight junction protein 2(TJP2)	-1.1266	0.0000	0.0006
TKT	transketolase (TKT)	-0.4637	0.0018	0.0411
TLE1	transducin like enhancer of split 1(TLE1)	-0.8108	0.0000	0.0000
TLX2	T-cell leukemia homeobox 2(TLX2)	-3.9318	0.0001	0.0052

TMBIM1	transmembrane BAX inhibitor motif containing 1(TMBIM1)	-0.8040	0.0000	0.0007
TMEM106C	transmembrane protein 106C(TMEM106C)	-0.4372	0.0002	0.0088
TMEM120A	transmembrane protein 120A(TMEM120A)	-0.4866	0.0007	0.0208
TMEM131L	Transmembrane 131 Like	-0.8242	0.0002	0.0085
TMEM132D	transmembrane protein 132D(TMEM132D)	-7.6383	0.0005	0.0157
TMEM155	transmembrane protein 155(TMEM155)	1.8723	0.0000	0.0000
TMEM176B	transmembrane protein 176B(TMEM176B)	3.7462	0.0006	0.0181
TMEM268	transmembrane protein 268(TMEM268)	0.5352	0.0004	0.0135
TMEM50A	transmembrane protein 50A(TMEM50A)	-0.4837	0.0016	0.0387
TMEM53	transmembrane protein 53(TMEM53)	-0.5830	0.0016	0.0384
TMEM8B	transmembrane protein 8B(TMEM8B)	-0.5112	0.0007	0.0210
TMTC2	transmembrane and tetratricopeptide repeat containing 2(TMTC2)	1.2282	0.0000	0.0000
TNC	tenascin C(TNC)	2.5881	0.0000	0.0000
TNFAIP3	TNF alpha induced protein 3(TNFAIP3)	-1.3651	0.0001	0.0035
TNFAIP6	TNF alpha induced protein 6(TNFAIP6)	1.9491	0.0000	0.0000
TNFRSF10C	TNF receptor superfamily member 10c(TNFRSF10C)	-2.3742	0.0017	0.0393
TNFRSF1B	TNF receptor superfamily member 1B(TNFRSF1B)	-1.7352	0.0006	0.0189
TNFRSF25	TNF receptor superfamily member 25(TNFRSF25)	-0.8975	0.0021	0.0466
TNIP1	TNFAIP3 interacting protein 1(TNIP1)	-0.3600	0.0011	0.0283
TPRG1L	tumor protein p63 regulated 1 like (TPRG1L)	-0.3398	0.0002	0.0081
TRAK1	trafficking kinesin protein 1(TRAK1)	-0.4590	0.0006	0.0189
TRAK2	trafficking kinesin protein 2(TRAK2)	-0.5974	0.0000	0.0001
TRH	thyrotropin releasing hormone (TRH)	-3.8444	0.0001	0.0063
TRIB3	tribbles pseudokinase 3(TRIB3)	1.3727	0.0000	0.0000
TRIL	TLR4 interactor with leucine rich repeats (TRIL)	3.4277	0.0000	0.0001
TRIM32	tripartite motif containing 32(TRIM32)	0.4071	0.0016	0.0383
TRIM47	tripartite motif containing 47(TRIM47)	-1.0113	0.0007	0.0215
TRPS1	transcriptional repressor GATA binding 1(TRPS1)	0.5034	0.0000	0.0024
TSFM	Ts translation elongation factor, mitochondrial (TSFM)	0.4978	0.0013	0.0318
TSHR	thyroid stimulating hormone receptor (TSHR)	4.4429	0.0003	0.0114

TSPAN18	tetraspanin 18(TSPAN18)	2.6062	0.0000	0.0000
TSPAN2	tetraspanin 2(TSPAN2)	1.8745	0.0007	0.0216
TSPAN4	tetraspanin 4(TSPAN4)	-0.7222	0.0021	0.0464
TTC39B	tetratricopeptide repeat domain 39B(TTC39B)	0.8691	0.0000	0.0001
TTI2	TELO2 interacting protein 2(TTI2)	0.5784	0.0011	0.0281
TTLL3	tubulin tyrosine ligase like 3(TTLL3)	-0.3926	0.0023	0.0490
TUBE1	tubulin epsilon 1(TUBE1)	0.7518	0.0000	0.0000
TYRO3	TYRO3 protein tyrosine kinase (TYRO3)	-0.5601	0.0007	0.0204
UBE2D4	ubiquitin conjugating enzyme E2 D4 (putative)(UBE2D4)	-0.4547	0.0015	0.0358
UBE2J1	ubiquitin conjugating enzyme E2 J1(UBE2J1)	0.2902	0.0012	0.0315
UGP2	UDP-glucose pyrophosphorylase 2(UGP2)	0.5577	0.0000	0.0027
UHRF1BP1	UHRF1 binding protein 1(UHRF1BP1)	0.6790	0.0021	0.0466
ULBP3	UL16 binding protein 3(ULBP3)	-0.8690	0.0000	0.0006
UQCC1	ubiquinol-cytochrome c reductase complex assembly factor 1(UQCC1)	-0.5303	0.0000	0.0019
USP32P1	ubiquitin specific peptidase 32 pseudogene 1(USP32P1)	5.1588	0.0000	0.0000
USP32P3	ubiquitin specific peptidase 32 pseudogene 3(USP32P3)	2.4374	0.0000	0.0007
VAMP1	vesicle associated membrane protein 1(VAMP1)	-1.0559	0.0014	0.0336
VAMP5	vesicle associated membrane protein 5(VAMP5)	-0.5569	0.0006	0.0176
VDR	vitamin D (1,25-dihydroxyvitamin D3) receptor (VDR)	0.7871	0.0005	0.0171
VEGFB	vascular endothelial growth factor B(VEGFB)	-0.6381	0.0000	0.0000
VHL	von Hippel-Lindau tumor suppressor (VHL)	0.4844	0.0000	0.0026
VIT	vitrin (VIT)	-2.1439	0.0000	0.0006
VPS9D1	VPS9 domain containing 1(VPS9D1)	-0.4514	0.0019	0.0431
WARS1	Tryptophanyl-TRNA Synthetase 1	0.7520	0.0000	0.0000
WNT5B	Wnt family member 5B(WNT5B)	-0.7916	0.0005	0.0151
WNT9A	Wnt family member 9A(WNT9A)	-0.9739	0.0015	0.0360
XG	Xg blood group (XG)	-1.1400	0.0000	0.0005
XKR8	XK related 8(XKR8)	-0.5845	0.0004	0.0133
XPOT	exportin for tRNA (XPOT)	0.5938	0.0000	0.0000
YARS1	Tyrosyl-TRNA Synthetase 1	0.3518	0.0010	0.0270

ZBTB47	zinc finger and BTB domain containing 47(ZBTB47)	-0.5276	0.0000	0.0003
ZDHH12	zinc finger DHH-type containing 12(ZDHH12)	-0.6469	0.0001	0.0039
ZDHH3	zinc finger DHH-type containing 3(ZDHH3)	-0.5707	0.0000	0.0014
ZFAND5	zinc finger AN1-type containing 5(ZFAND5)	-0.3712	0.0016	0.0375
ZFPM2	zinc finger protein, FOG family member 2(ZFPM2)	2.6636	0.0002	0.0078
ZFYVE16	zinc finger FYVE-type containing 16(ZFYVE16)	0.6565	0.0000	0.0014
ZNF22	zinc finger protein 22(ZNF22)	0.7277	0.0010	0.0275
ZNF334	zinc finger protein 334(ZNF334)	2.6140	0.0000	0.0000
ZNF385D	zinc finger protein 385D(ZNF385D)	-1.0770	0.0003	0.0110
ZNF624	zinc finger protein 624(ZNF624)	1.0290	0.0006	0.0192
ZNF704	zinc finger protein 704(ZNF704)	3.7128	0.0000	0.0000
ZNF770	zinc finger protein 770(ZNF770)	0.5909	0.0002	0.0075
ZSWIM4	zinc finger SWIM-type containing 4(ZSWIM4)	0.9554	0.0002	0.0083

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165 **Supplementary Table 2.** Lists of differentially expressed genes (DEGs) related to inflammation (62 DEGs),
 166 autophagy (37 DEGs) and mitochondria (42 DEGs)

Inflammation-related genes (62 DEGs)	Autophagy-related genes (37 DEGs)	Mitochondrial-related genes (42 DEGs)
LAMA5	FZD1	LONP1
TNFRSF1B	GAB1	ACADM
NFKB2	LMNA	HSPA9
STING1	RAF1	UQCC1
TRIM32	EIF4EBP1	TSFM
POLR2L	CCND1	ALDH4A1
ITPR3	IL20RB	ECHDC2
RAF1	RAB27B	ETHE1
PIK3R3	IL21R	MT-ATP6
EGFR	ITGA3	MT-CO2
MAP2K3	HSP90AA1	GLS
JUN	RAB15	SQOR
HTR2A	H2AC19	ALDH1B1
IGF1	HSBP1	CHDH
BDKRB1	LAMTOR4	SHMT2
RAPGEF1	PRKAB2	MTHFD2
CCND1	JUN	ALDH18A1
GNAI2	MAPKAPK3	LYPLA1
TCF7L2	VHL	ALDH1L2
NOTCH3	CITED2	GPT2
PPP3CA	NOX4	MT-CO1
HIF1A	CBX4	MT-ND2
HSP90AA1	GPX3	MT-ND5
NFATC2	HMGA1	PCK2
IL21R	NUP98	CHPT1
BCL2L1	MAP2K3	GARS1
TGFB3	ETS2	MT-ND3
<i>CD44</i>	HIF1A	ARG2
<i>CD81</i>	HSPA9	FAM210B
<i>CTSB</i>	PSMB2	CBR3
NEFL	IGF1	LDHB
PDGFB	IRS2	CYB5R3
IRS2	SESN2	FKBP8
NEDD4	PCK2	MT-ND1
PRL	CAMKK1	GPAM
PSMB2	PIK3R3	PRXL2A
NUP98	PPP1R12A	MGARP
IL20RB		SPTLC2
TNFRSF25		BCL2L1
RASA2		GPAT2
HLA-B		DMPK
IL17RB		SERAC1

HLA-C		
HLA-E		
CTSC		
TRIB3		
UBE2J1		
PJA1		
BTN3A2		
UBE2D4		
GAB1		
CLEC2B		
SIAH2		
SMURF2		
ICAM5		
ENAH		
ULBP3		
VHL		
TAPBP		
KIF3B		
FBXW5		
SH3RF1		

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169 **Supplementary Table 3.** Concentration of secreted inflammatory cytokines in IBM vs CTL supernatants. IBM
 170 fibroblasts revealed an increased expression of most of these cytokines.

CYTOKINE	CYTOKINE NAME	CTL (n=12)	IBM (n=13)	IBM/CTL	SEM IBM/MEAN CTL
GCSF	Granulocyte colony-stimulating factor	11.01 ± 9.45	146.42 ± 118.15	13.30	1,62
TNFα	Tumor necrosis factor α	0.33 ± 0.33	3.34 ± 1.51	10.12	0,40
GMCSF	Granulocyte-macrophage colony-stimulating factor	0.12 ± 0.12	0.62 ± 0.40	5.17	10,73
eotaxin*	C-C motif chemokine 11 (CCL11)	4.81 ± 4.10	20.18 ± 7.80	4.20	3,33
IL7	interleukin 7	0.55 ± 0.55	2.12 ± 1.04	3.85	0,44
MIP1a	C-C motif chemokine 3 (CCL3)	0.05 ± 0.03	0.15 ± 0.08	3.00	0,78
IL4	interleukin 4	0.31 ± 0.24	0.83 ± 0.25	2.68	0,46
IL8	interleukin 8	829.27 ± 325.46	2106.95 ± 746.50	2.54	0,81
IL13	interleukin 13	0.08 ± 0.06	0.20 ± 0.07	2.50	0,29
MCP1	Monocyte Chemoattractant Protein-1	162.62 ± 38.64	394.38 ± 100.04	2.43	1,89
RANTES	C-C motif chemokine 5 (CCL5)	5.14 ± 3.70	11.24 ± 6.98	2.19	0,90
IL17	interleukin 17	0.27 ± 0.27	0.55 ± 0.29	2.04	0,46
IL1β	Interleukin 1β	0.09 ± 0.09	0.18 ± 0.07	2.00	0,88
IL9	interleukin 9	7.85 ± 3.23	13.14 ± 3.63	1.67	1,07
MIP1b	C-C motif chemokine 4 (CCL4)	2.57 ± 1.36	4.02 ± 1.43	1.56	0,24
FGFbasic	Basic fibroblast growth factor	3.14 ± 1.49	3.84 ± 1.26	1.22	0,62
IL1ra	Interleukin-1 receptor antagonist protein	6.49 ± 6.27	7.89 ± 2.99	1.22	1,60
IFNγ	Interferon gamma	10.47 ± 8.04	11.50 ± 4.60	1.10	0,56
IL6	interleukin 6	778.34 ± 330.12	722.18 ± 224.65	0.93	1,36
VEGF	Vascular endothelial growth factor	67.93 ± 21.57	60.36 ± 21.65	0.89	4,58
IP10	C-X-C motif chemokine ligand 10 (CXCL10)	63.01 ± 51.9	39.60 ± 15.23	0.63	0,32

171 n=13 IBM vs 12 CTL; *p-value<0.05, Mann–Whitney U test; IBM: inclusion body myositis; CTL: controls. Color
 172 code for ratio IBM/CTL: <1 in blue (for decreased expression of cytokines in IBM); =1 in white (for equal
 173 expression between cohorts); and >1 in red (for higher expression in IBM). Mean fold change ratio (and deviation)
 174 of secreted cytokines in IBM patients vs. CTL fibroblasts, normalized by cell number, displayed in Fig 2B.

175 **Supplementary Table 4.** Expression of 20 autophagy proteins in IBM vs. CTL fibroblasts. Most of these proteins
 176 displayed a decreased expression in IBM, suggesting a reduced activity of the autophagy process.

Autophagy proteins	Autophagy protein name	CTL (n=8)	IBM (n=8)	IBM/CTL	SEM IBM/MEAN CTL
DDR2	Discoidin domain-containing receptor 2	1174.88 ± 187.39	1150.5 ± 215.46	0.98	0,18
BNIP3L	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3-like	2386.88 ± 374.14	2262 ± 349.84	0.95	0,15
ATG5	Autophagy related protein 5	1814.5 ± 327.55	1688.25 ± 398.4	0.93	0,22
ATG4A	Autophagy Related 4A Cysteine Peptidase	2707.38 ± 442.75	2454.38 ± 398.88	0.91	0,15
ATG3	Autophagy related protein 3	1889.88 ± 257.07	1682.13 ± 278.41	0.89	0,15
Rheb	Ras Homolog, MTORC1 Binding protein	1674.75 ± 224.93	1481.88 ± 301.1	0.88	0,18
ATG7	Autophagy related protein 7	2004.63 ± 307.41	1719.75 ± 291.61	0.86	0,15
ATG10	Autophagy related protein 10	2582.38 ± 351.96	2156.13 ± 314.94	0.83	0,12
ATG13	Autophagy related protein 13	2159.13 ± 303.39	1801.38 ± 204.21	0.83	0,09
Beclin	Beclin 1	1466.75 ± 243.15	1222.63 ± 170.38	0.83	0,12
ATG4B	Autophagy Related 4B Cysteine Peptidase	1411.88 ± 297.45	1149.5 ± 243.53	0.81	0,17
P62	Sequestosome 1 (SQSTM1)	17700.13 ± 2737.31	14212.38 ± 2118.71	0.8	0,12
LC3B	Microtubule-associated proteins 1A/1B light chain 3B	6540.13 ± 1259.3	5162.88 ± 679.67	0.79	0,10
GABARAP	Gamma-aminobutyric acid receptor-associated protein	1574.38 ± 199.19	1244.13 ± 165.29	0.79	0,10
LAMP1	Lysosome-associated membrane glycoprotein 1	2147 ± 320.11	1645.63 ± 208.2	0.77	0,10
Alpha-Synuclein	Alpha-Synuclein (SNCA gene)	1503.75 ± 144.86	1146.88 ± 149.84	0.76	0,10
LC3A	Microtubule-associated proteins 1A/1B light chain 3A	5914 ± 928.3	4432.13 ± 640.62	0.75	0,11
NBS1	Nibrin	5491.88 ± 1202	3654 ± 334.12	0.67	0,06
ATG12	Autophagy related protein 12	4844.13 ± 1173.43	3139 ± 399.84	0.65	0,08
MSK1	Ribosomal Protein S6 Kinase A5	485.13 ± 115.21	311.75 ± 44.59	0.64	0,09

177 Abbreviations: IBM: Inclusion Body Myositis; CTL: healthy control subjects. Concentration of each protein in the
 178 autophagy array presented as mean ± SEM or ratio IBM/CTL per each autophagic protein (n=8/group). Color
 179 code for ratio IBM/CTL: <1 in blue (for decreased expression of cytokines in IBM) and =1 in white (for equal
 180 expression between cohorts). Mean fold change ratio (and deviation) of autophagy proteins in IBM patients vs.
 181 CTL fibroblasts, normalized by protein content, displayed in Fig 3B.

182

183 **Supplementary Table 5.** Differentially expressed genes (DEGs) related to metabolite concentration in
 184 fibroblasts. The table depicts the relationship of 10 DEGs involved in metabolite metabolism with their
 185 respective alteration at amino acids and organic acids level, to relate expression vs. metabolism patterns in IBM
 186 vs. CTL fibroblasts.

Gene name	Description	Expression pattern	Metabolite pattern	Pathway
PSAT1	phosphoserine aminotransferase 1	upregulated	Increased serine and glycine	vitamin B6 pathway
ETHE1	ETHE1 persulfate dioxygenase	downregulated	Increase lactate, ethylmalonic and methyl succinic	Mitochondrial metabolism
MTND5	NADH dehydrogenase, subunit 5 (complex I)	downregulated	Increased lactate, alanine and TCA cycle	Mitochondrial metabolism
ARG2	arginase 2	upregulated	Reduced arginine	Mitochondrial metabolism
MTCO2	cytochrome c oxidase subunit II	downregulated	Increased lactate, alanine and TCA cycle	Mitochondrial metabolism
MTATP6	ATP synthase F0 subunit 6	downregulated	Increased lactate, alanine and TCA cycle	Mitochondrial metabolism
GPX3	glutathione peroxidase isoform 3	upregulated	Could be related to high pyroglutamic acid	glutathione metabolism
SQOR	sulphide quinone oxidoreductase	downregulated	Related to ETHE1	Mitochondrial metabolism
GPT2	glutamic--pyruvic transaminase 2	upregulated	Increased glutamate and alanine	Mitochondrial metabolism
SERAC1	serine active site containing 1	upregulated	Increased serine	Mitochondrial metabolism

187 Abbreviations: TCA: Tricarboxylic Acid Cycle.

188 **Supplementary Table 6.** Organic acids in IBM vs. CTL fibroblasts. Organic acids showed a general increase in IBM,
 189 suggesting a deregulation of intermediary metabolism related to mitochondrial function, as many organic acids
 190 are involved in tricarboxylic acid cycle (TCA) that further feeds the mitochondrial respiratory chain.

ORGANIC ACIDS (nmol/mg protein)	CTL (n=10)	IBM (n=11)	IBM/CTL	SEM IBM/MEAN CTL
2OHglutaric	0.33 ± 0.1	1.48 ± 0.62	4.48	1,88
2-hidroivaleric	0.3 ± 0.15	1.08 ± 0.38	3.60	1,27
a-ketoglutarate	3.9 ± 1.48	9.28 ± 3.86	2.38	0,99
succinic	0.07 ± 0.01	0.16 ± 0.06	2.29	0,86
lactic	0.26 ± 0.05	0.51 ± 0.06	1.96	0,23
citric	178.23 ± 56.65	322.66 ± 150.86	1.81	0,85
fumaric	0.68 ± 0.17	1.17 ± 0.18	1.72	0,26
sebacic	0.11 ± 0.01	0.18 ± 0.01	1.64	0,09
pyroglutamic	32.04 ± 2.6	44.71 ± 2.58	1.40	0,08
malic	0.9 ± 0.17	1.15 ± 0.2	1.28	0,22
glutaric	0.2 ± 0.02	0.25 ± 0.05	1.25	0,25
adipic	0.41 ± 0.03	0.48 ± 0.04	1.17	0,10
suberic	0.72 ± 0.07	0.79 ± 0.05	1.10	0,07
ethylmalonic	0.26 ± 0.01	0.26 ± 0.02	1.00	0,08
glycerol	5.09 ± 0.37	5.05 ± 0.61	0.99	0,12
3/OH/Sebacic	0.15 ± 0.03	0.14 ± 0.02	0.93	0,13
oxalate	36.33 ± 0.83	32.34 ± 2.03	0.89	0,06

191 Abbreviations: IBM: inclusion body myositis; CTL: healthy control subjects. N=11 IBM vs. 10 CTL; ***p-value<0.05**,
 192 Mann–Whitney U test. Color code for ratio IBM/CTL: <1 in blue (for decreased expression of metabolites in IBM);
 193 =1 in white (for equal expression between cohorts); and >1 in red (for higher expression in IBM). Concentration
 194 of each analyte presented as mean ± SEM and normalized by protein content. Mean fold change ratio (and
 195 deviation) of organic acids in IBM patients vs. CTL fibroblasts, normalized by protein content, displayed in Fig 6A.

196

197 **Supplementary Table 7.** Amino acids levels in fibroblasts of IBM patients vs. CTL fibroblasts.

Amino Acids (μmol/g)	CTL (n=10)	IBM (n=11)	IBM/CTL	SEM IBM/MEAN CTL
Ala	2.26 ± 0.16	2.63 ± 0.09	1.16	0,04
Asn	0.62 ± 0.04	0.72 ± 0.04	1.16	0,06
Ser	3.16 ± 0.13	3.52 ± 0.12	1.11	0,04
Arg	1.39 ± 0.1	1.52 ± 0.05	1.09	0,04
Tyr	1.21 ± 0.02	1.26 ± 0.02	1.04	0,02
Val	1.8 ± 0.04	1.84 ± 0.04	1.02	0,02
Lys	1.61 ± 0.05	1.63 ± 0.04	1.01	0,02
Trp	0.24 ± 0	0.24 ± 0.01	1.00	0,04
Leu	1.96 ± 0.04	1.95 ± 0.03	0.99	0,02
Ile	1.48 ± 0.04	1.47 ± 0.03	0.99	0,02
Gly	6.98 ± 0.36	6.88 ± 0.58	0.99	0,08
Pro	2.54 ± 0.22	2.46 ± 0.35	0.97	0,14
Met	0.58 ± 0.01	0.56 ± 0.01	0.97	0,02
Glu	21.51 ± 1.33	20.6 ± 1.54	0.96	0,07
Thr	3.46 ± 0.15	3.28 ± 0.11	0.95	0,03
Asp	3.47 ± 0.41	3.14 ± 0.41	0.90	0,12
Gln	3.81 ± 0.47	3.04 ± 0.43	0.80	0,11
Tau	2.91 ± 0.3	2.16 ± 0.42	0.74	0,14

198 Abbreviations: IBM: inclusion body myositis; CTL: healthy control subjects. N=11 IBM vs. 10 CTL. Color code for
 199 ratio IBM/CTL: <1 in blue (for decreased expression of metabolites in IBM); =1 in white (for equal expression
 200 between cohorts); and >1 in red (for higher expression in IBM). Concentration of each analyte presented as
 201 mean ± SEM and normalized by protein content and phenylalanine concentration. Mean fold change ratio (and
 202 deviation) of amino acids in IBM patients vs. CTL fibroblasts, normalized by protein content, displayed in Fig 6B.

203

204 **Supplementary Table 8.** Comparison of inflammatory, degenerative, and mitochondrial IBM hallmarks
 205 considering the evolution of IBM patients: stable vs progressive prognosis, compared to CTL fibroblasts.

TEST	CTL	IBM STB/CTL	IBM PROG/CTL	N (CTL-IBM STB-IBM PROG)
Secreted inflammatory cytokines	1.00	5.21	1.75	12-5-8
Autophagy proteins in basal conditions	1.00	0.91	0.72	8-4-4
Autophagy WB LC3BII	1.00	0.53	0.52	11-3-8
Autophagy WB p62	1.00	0.85	0.75	11-3-8
Mitochondrial respiration	1.00	0.85	0.83	10-3-7
COX/CS	1.00	0.60	0.52	10-3-7
Oxidative stress (by lipid peroxidation)	1.00	0.88	1.22	8-2-7
Total Antioxidant Capacity	1.00	1.68	2.73	4-4-7
Mitochondrial membrane potential	1.00	0.88	0.89	4-2-2
Organic acids	1.00	2.01	1.34	10-4-7
Amino acids	1.00	0.96	1.01	10-4-7

206 IBM: inclusion body myositis, separated in 2 groups: stable vs progressive prognosis; CTL: controls. Ratio of each
 207 parameter compared to CTL (ratio=1). Color code for ratio IBM/CTL: <1 in blue (for decreased expression in IBM);
 208 =1 in white (for equal expression in IBM and CTL); and >1 in red (for higher expression in IBM). The number of
 209 samples varies in each test, represented in N column.