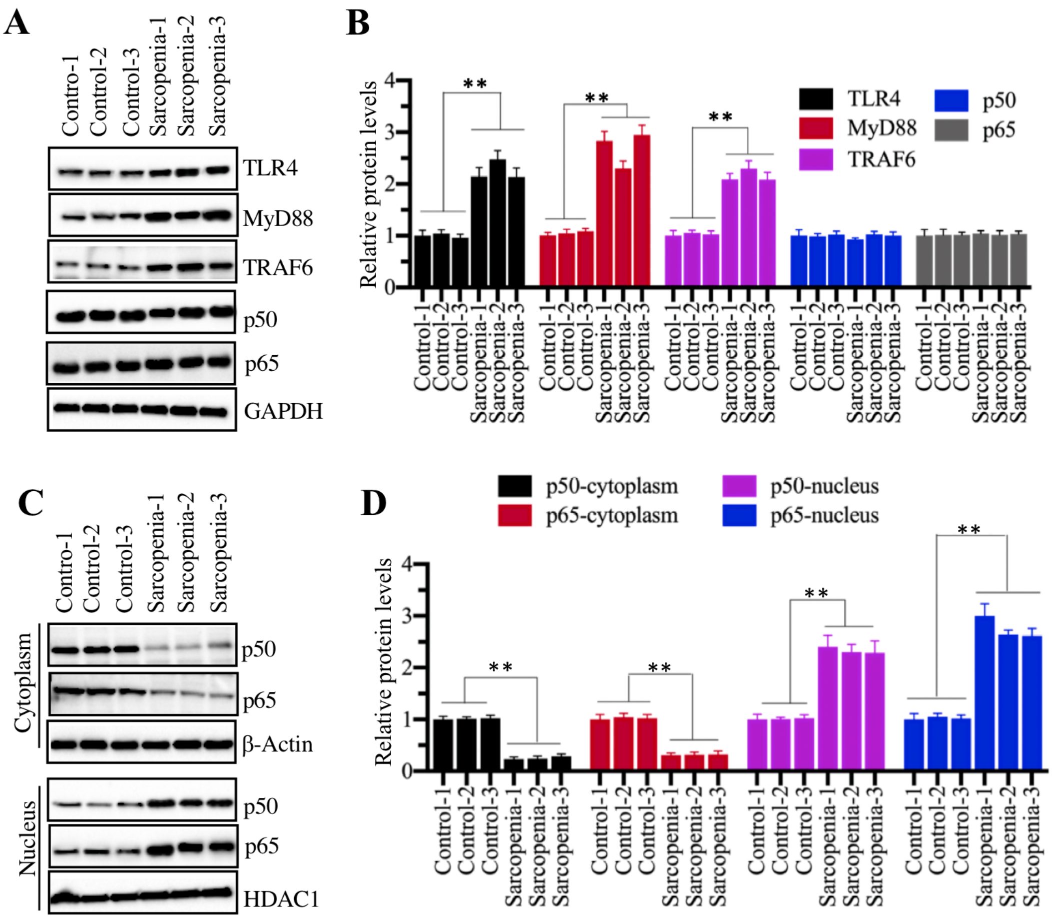
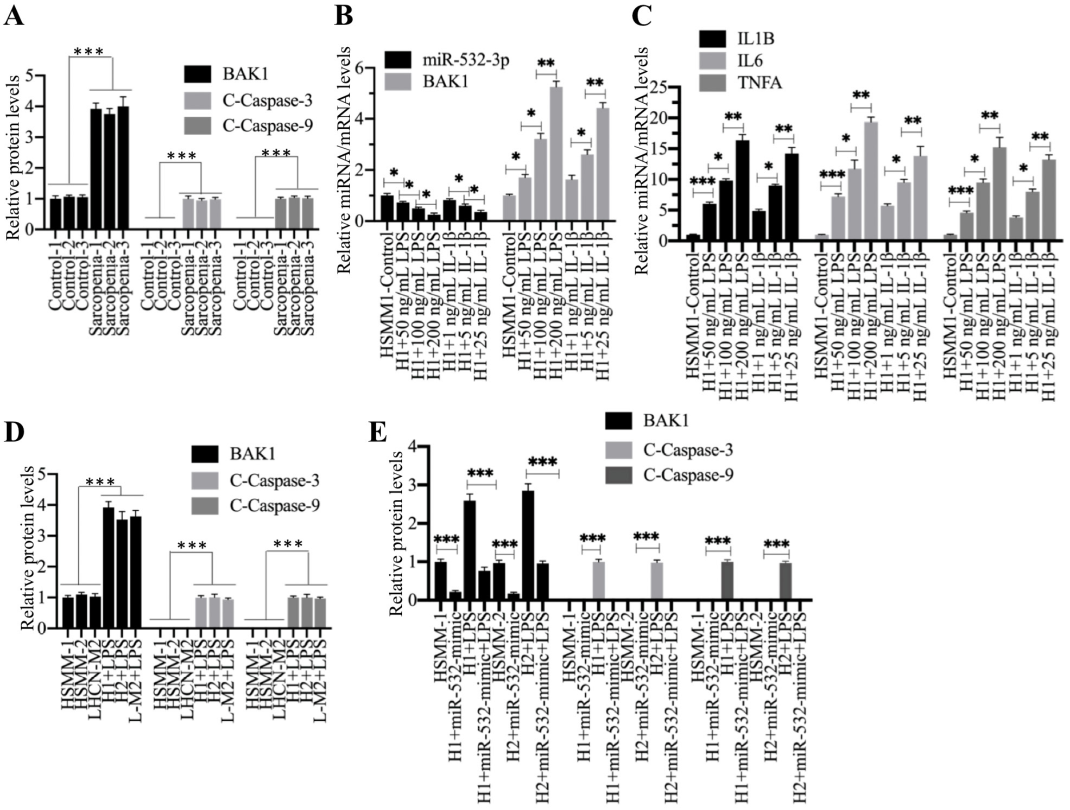


Supplementary Figure 1. The TLR4/NF-κB signalling axis was activated in sarcopenia patient samples

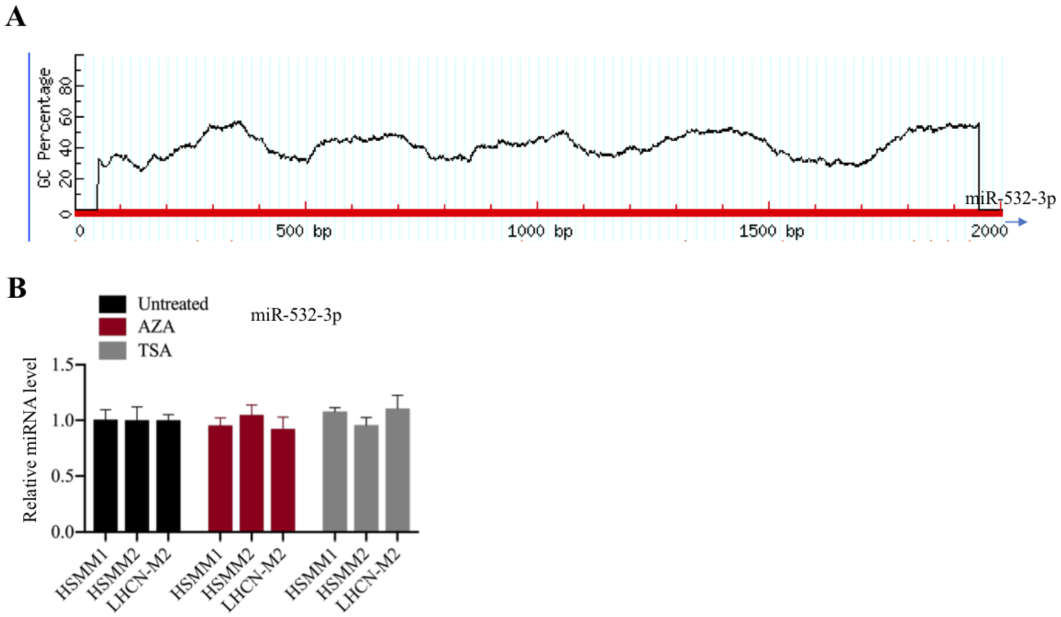
Three-paired muscle tissues from healthy controls and sarcopenia patients were subjected to total protein extraction and isolation of the cytoplasmic and nuclear protein fractions. **(A** and **B)** The protein levels of TLR4, MyD88, TRAF4, p50 and p65 in total cell extracts. Total cell extracts were subjected to immunoblot analyses to determine protein levels of TLR4, MyD88, TRAF4, p50 and p65. GAPDH was used as a loading control **(A)**. **(B)** The quantified protein levels in (A). ** $P < 0.01$. **(C** and **D)** The protein levels of p50 and p65 in the cytoplasmic and nuclear protein fractions. The purified cytoplasmic and nuclear fractions were subjected to immunoblot analyses to determine protein levels of p50 and p65. β-actin and HDAC1 were used as loading controls. **(D)** The quantified protein levels in (C). ** $P < 0.01$.



Supplementary Figure 2. The effects of LPS and IL-1β on miR-532-3p and its downstream molecules

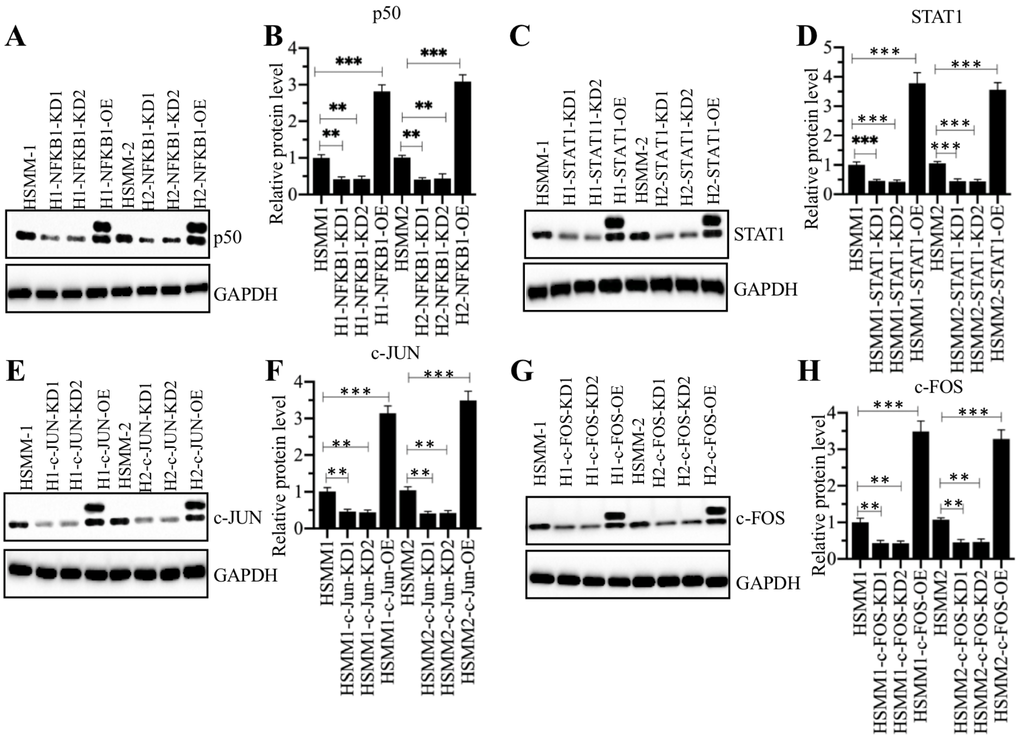
(A) The relative protein levels of BAK1 and Caspases in sarcopenia samples. The protein signals in Figure 5B were quantified using Image J software. The protein levels of BAK1 in Control-1 was defined as one-fold. The protein levels of C-Caspase3 and C-caspase-9 in sarcopenia-1 were defined as one-fold. *** $P < 0.001$. **(B)** The effects of different concentrations of LPS and IL-1β on the expression of miR-532-3p and *BAK1*. The HSMM-1 cells were treated with different concentrations of LPS (0, 50, 100 and 200 ng/mL) and IL-1β (0, 1, 5 and 25 ng/mL), followed by qRT-PCR analyses to examine the expression of miR-532-3p and *BAK1*. * $P < 0.05$ and ** $P < 0.01$. **(C)** The effects of different concentrations of LPS and IL-1β on the expression of NF-κB target genes. The cDNA samples used in (B) were subjected to measure the mRNA levels of

IL1B, *IL6* and *TNFA*. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$. **(D)** The relative protein levels of BAK1 protein level and Caspases in LPS-treated cells. The protein signals in Figure 5D were quantified using Image J software. The protein levels of BAK1 in HSMM-1 was defined as one-fold. The protein levels of C-Caspase3 and C-caspase-9 in LPS-treated HSMM-1 cells were defined as one-fold. *** $P < 0.001$. **(E)** The relative protein levels of BAK1 protein level and Caspases. The protein signals in Figure 5G were quantified using Image J software. The protein levels of BAK1 in HSMM-1 was defined as one-fold. The protein levels of C-Caspase3 and C-caspase-9 in LPS-treated HSMM-1 cells were defined as one-fold. *** $P < 0.001$.



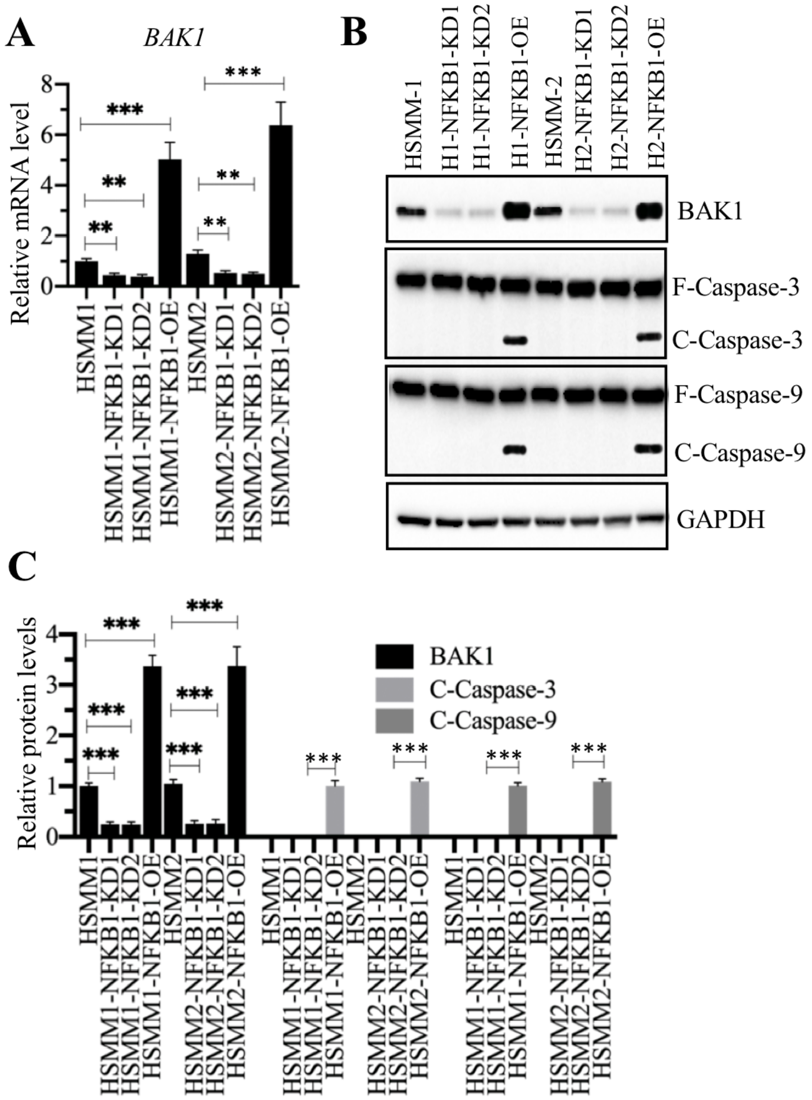
Supplementary Figure 3. Changes in epigenetic modification did not affect miR-532-3p expression

(A) The promoter region of miR-532-3p does not contain a CpG island. A 2000 bp-length promoter fragment from miR-532-3p was used to predict the presence of a CpG island. The position of miR-532-3p is indicated. **(B)** Treatment with the DNA methylation inhibitor AZA and the acetylation activator TSA did not change the miR-532-3p level. Three cell lines, HSMM-1, HSMM-2 and LHCN-M2, were treated with AZA and TSA, followed by qRT-PCR analyses to examine the expression of miR-532-3p.



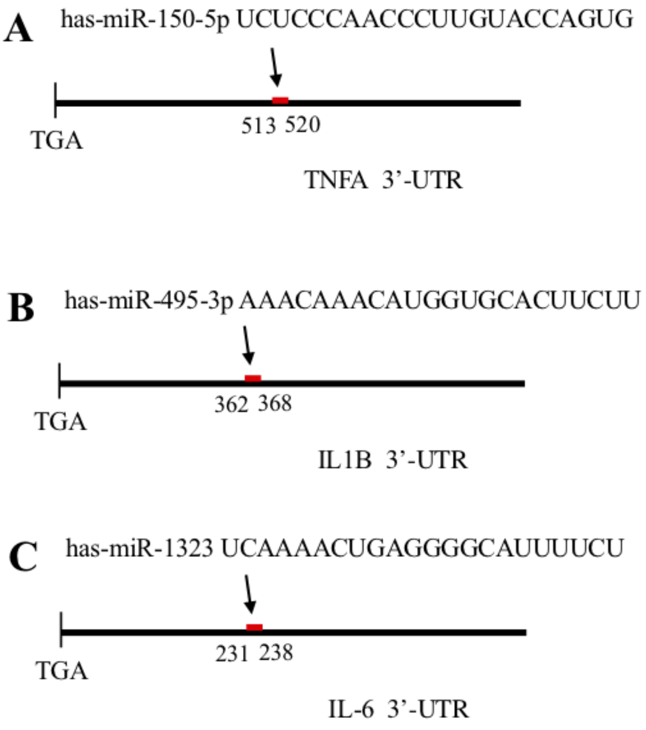
Supplementary Figure 4. The protein levels of transcription factors in their corresponding knockdown and overexpression cells

(A and **B)** The protein levels of p50. Total cell extracts from HSMM-1, HSMM1-NFKB1-KD1, HSMM1-NFKB1-KD2, HSMM1-NFKB1-OE, HSMM-2, HSMM2-NFKB1-KD1, HSMM2-NFKB1-KD2, and HSMM2-NFKB1-OE were subjected to immunoblots to examine the protein level of p50 **(A)**. GAPDH was used as a loading control. **(B)** The protein signals were quantified using Image J software. The protein levels of p50 in HSMM-1 was defined as one-fold. ** $P < 0.01$ and *** $P < 0.001$. **(C** and **D)** The protein levels of STAT1. Total cell extracts from HSMM-1, HSMM1-STAT1-KD1, HSMM1-STAT1-KD2, HSMM1-STAT1-OE, HSMM-2, HSMM2-STAT1-KD1, HSMM2-STAT1-KD2, and HSMM2-STAT1-OE were subjected to immunoblots to examine the protein level of STAT1 **(C)**. GAPDH was used as a loading control. **(D)** The protein signals were quantified using Image J software. The protein levels of STAT1 in HSMM-1 was defined as one-fold. *** $P <$ 0.001. **(E** and **F)** The protein levels of c-JUN. Total cell extracts from HSMM-1, HSMM1-c-JUN-KD1, HSMM1-c-JUN-KD2, HSMM1-c-JUN-OE, HSMM-2, HSMM2-c-JUN-KD1, HSMM2-c-JUN-KD2, and HSMM2-c-JUN-OE were subjected to immunoblots to examine the protein level of c-JUN **(E)**. GAPDH was used as a loading control. **(F)** The protein signals were quantified using Image J software. The protein levels of c-JUN in HSMM-1 was defined as one-fold. *** $P < 0.001$. **(G** and **H)** The protein levels of c-FOS. Total cell extracts from HSMM-1, HSMM1-c-FOS-KD1, HSMM1-c-FOS-KD2, HSMM1-c-FOS-OE, HSMM-2, HSMM2-c-FOS-KD1, HSMM2-c-FOS-KD2, and HSMM2-c-FOS-OE were subjected to immunoblots to examine the protein level of c-FOS **(G)**. GAPDH was used as a loading control. **(H)** The protein signals were quantified using Image J software. The protein levels of c-FOS in HSMM-1 was defined as one-fold. *** $P < 0.001$.



Supplementary Figure 5. Overexpression of *NFKB1* caused the activation of the downstream BAK1 signalling pathway

(A) Overexpression of *NFKB1* increased *BAK1* mRNA levels. The HSMM-1, HSMM1-NFKB1-KD1, HSMM1-NFKB1-KD2, HSMM1-NFKB1-OE, HSMM-2, HSMM2-NFKB1-KD1, HSMM2-NFKB1-KD2 and HSMM2-NFKB1-OE cells were used for RNA isolation, followed by qRT-PCR analyses to examine the expression of *BAK1*. *** $P < 0.001$. **(B** and **C)** Overexpression of *NFKB1* caused the activation of BAK1 downstream signalling pathway. The cells used in (A) were used for protein extraction. The protein was then used to detect the protein levels of BAK1, Caspase-3 and Caspase-9 **(B)**. GAPDH was used as a loading control. F: full length; C: cleaved length. The protein signals in (B) were quantified using Image J software **(C)**. *** $P < 0.001$.



Supplementary Figure 6. Several miRNAs have the potential to target proinflammatory cytokines

Three differentially expressed miRNAs, miR-150-5p, miR-495-3p and miR-1323, have the potential to target *TNFA*, *IL1B* and *IL6*, respectively. The putative binding sites are indicated with arrows.

Supplementary Table-1. Primers used for qRT-PCR analyses

Gene	Forward	Reverse
IL1B	5’-TGTACCTGTCCTGCGTGTT-3’	5’- CTCCCAGGAAGACGGGCATG-3’
BAK1	5’-TGGGCTTCGGCTACCGTCTGGC-3’	5’- GTTCAGGATGGGACCATTGC-3’
SOD1	5’-AGATGGTGTGGCCGATGTG-3’	5’TGTACTTTCTTCATTTCCA-3’
CDH1	5’-CACCACTGGGCTGGACCGAG-3’	5’-TGGGATTGAAGATCGGAGGA-3’
GNG11	5’-CGCTGCCAGAGCTAGCCCGAG-3’	5’- GATCCTCTCCAGAACGTTCTTC-3’
ZAP70	5’-GAGGTCATGGCCTTCATCGA-3’	5’- GCTCCACGGTCAGGAAGTCGG-3’
NFKB1	5’- TAGCTTCCCACACTATGGAT-3’	5’- ACAACCTTCAGGGTCCT-3’
STAT1	5’-TCCTGTCACAGCTGGATGA-3’	5’- CATAGACATCTGGATTG-3’
c-Jun	5’-GCCTTCGTTAACTGTGTAT-3’	5’- AACACTGGGCAGGATACCC-3’
c-FOS	5’-ACTCCAGGGCTGGCGTT-3’	5’-CTTGGAGTGTATCAGTCAGC-3’
β-Actin	5’-AGAGCTACGAGCTGCCTGAC-3	5’- AGCACTGTGTTGGCGTACAG -3’

Supplementary Table-2. Differentially expressed miRNAs in sarcopenia samples

miRNA	**Average fold change**	**P Value**	**Expression**
miR-17-3p	19.3	0.00036	Up
miR-873-5p	16.6	0.00097	Up
miR-1225	15.2	0.00044	Up
miR-192-3p	14.4	0.00067	Up
miR-2052	13.7	0.00024	Up
miR-590-5p	11.6	0.00045	Up
miR-30a-3p	11.2	0.00033	Up
miR-208a	10.9	0.00091	Up
miR-107	10.2	0.00027	Up
miR-361-5p	9.7	0.00046	Up
miR-33a-3p	9.3	0.00082	Up
miR-449c	8.9	0.00012	Up
miR-369	8.4	0.00044	Up
miR-559	7.8	0.00018	Up
miR-572	7.1	0.0024	Up
miR-675	5.9	0.00058	Up
miR-744	5.6	0.00052	Up
miR-1537	4.9	0.00011	Up
miR-1277	4.5	0.00046	Up
miR-382	4.1	0.00082	Up
miR-199a-1	3.4	0.00084	Up
miR-92a-1	2.5	0.00015	Up
miR-532-3p	-18.6	0.00065	Down
miR-4256	-18.1	0.00047	Down
miR-1291	-16.8	0.00024	Down
miR-34a-3p	-15.5	0.00083	Down
miR-663a	-14.3	0.00049	Down
miR-922	-13.2	0.00092	Down
miR-126-5p	-11.9	0.00018	Down
miR-328-3p	-10.6	0.00052	Down

miR-22-3p	-10.3	0.00035	Down
miR-370	-9.5	0.00057	Down
miR-23a	-7.3	0.00096	Down
miR-100	-7.1	0.00013	Down
miR-182	-6.9	0.00025	Down
miR-216a	-6.8	0.00029	Down
miR-150-5p	-6.6	0.00051	Down
miR-495-3p	-6.6	0.00037	Down
miR-1323	-6.4	0.00063	Down
miR-890	-6.2	0.00074	Down
miR-769	-6.1	0.00083	Down
miR-944	-5.8	0.0058	Down
miR-1469	-5.6	0.00052	Down
miR-630	-5.5	0.00064	Down
miR-544a	-5.2	0.00038	Down
miR-377	-5.0	0.00082	Down
miR-640	-4.8	0.00073	Down
miR-622	-4.7	0.00014	Down
miR-2110	-4.2	0.00017	Down
miR-1827	-3.9	0.00026	Down
miR-3168	-3.6	0.00057	Down
miR-4310	-3.3	0.00036	Down
miR-760	-2.6	0.00083	Down

Supplementary Table-3. The predicted targets of miR-532-3p

Target Rank	Target Score	Gene Symbol	Gene Description
1	99	MYB	MYB proto-oncogene, transcription factor
2	99	CYTH1	cytohesin 1
3	98	KLHL12	kelch like family member 12
4	98	ZFP90	ZFP90 zinc finger protein
5	96	DCAF6	DDB1 and CUL4 associated factor 6
6	96	FAM49A	family with sequence similarity 49 member A
7	95	HNRNPH3	heterogeneous nuclear ribonucleoprotein H3
8	95	BCL9	BCL9, transcription coactivator
9	95	ANKRD12	ankyrin repeat domain 12
10	94	C22orf46	chromosome 22 open reading frame 46
11	94	GALNT10	polypeptide N-acetylgalactosaminyltransferase 10
12	93	DDOST	dolichyl-diphosphooligosaccharide--protein glycosyltransferase non-catalytic subunit
13	93	CHD3	chromodomain helicase DNA binding protein 3
14	93	SZRD1	SUZ RNA binding domain containing 1
15	92	TNRC6B	trinucleotide repeat containing 6B
16	92	HNRNPH2	heterogeneous nuclear ribonucleoprotein H2
17	92	PRDM16	PR/SET domain 16
18	91	ZNF543	zinc finger protein 543
19	91	TET3	tet methylcytosine dioxygenase 3
20	91	WDR36	WD repeat domain 36
21	91	ZFP91	ZFP91 zinc finger protein
22	90	NIPBL	NIPBL, cohesin loading factor
23	90	ALCAM	activated leukocyte cell adhesion molecule
24	90	PAPPA	pappalysin 1
25	90	PRKCA	protein kinase C alpha
26	89	NFASC	Neurofascin
27	89	DTX4	deltex E3 ubiquitin ligase 4
28	89	GSPT1	G1 to S phase transition 1

29	89	QKI	QKI, KH domain containing RNA binding
30	89	GALNT6	polypeptide N-acetylgalactosaminyltransferase 6
31	88	GSG1L	GSG1 like
32	88	HMGA2	high mobility group AT-hook 2
33	88	TRABD2B	TraB domain containing 2B
34	87	RPL36A- HNRNPH2	RPL36A-HNRNPH2 readthrough
35	87	ZNF514	zinc finger protein 514
36	87	PHF20L1	PHD finger protein 20 like 1
37	87	ADCYAP1R1	ADCYAP receptor type I
38	87	RPRML	reprimo like
39	86	PRKAR2B	protein kinase cAMP-dependent type II regulatory subunit beta
40	86	IBA57	IBA57, iron-sulfur cluster assembly
41	86	CSF1	colony stimulating factor 1
42	85	SPCS2	signal peptidase complex subunit 2
43	85	TENT4B	terminal nucleotidyltransferase 4B
44	85	KPNA6	karyopherin subunit alpha 6
45	85	GUCY1A1	guanylate cyclase 1 soluble subunit alpha 1
46	85	RRM2	ribonucleotide reductase regulatory subunit M2
47	84	ZFX	zinc finger protein X-linked
48	84	C1orf21	chromosome 1 open reading frame 21
49	84	CLMP	CXADR like membrane protein
50	84	TMEM100	transmembrane protein 100
51	84	MRPL49	mitochondrial ribosomal protein L49
52	84	PEA15	proliferation and apoptosis adaptor protein 15
53	84	CHKA	choline kinase alpha
54	84	WDFY3	WD repeat and FYVE domain containing 3
55	84	FAM168A	family with sequence similarity 168 member A
56	84	MMP16	matrix metallopeptidase 16
57	84	LBH	limb bud and heart development
58	83	SUMO1	small ubiquitin-like modifier 1
59	83	KMT2A	lysine methyltransferase 2A

60	83	LDLRAD4	low density lipoprotein receptor class A domain containing 4
61	83	ELOVL3	ELOVL fatty acid elongase 3
62	83	EFNA5	ephrin A5
63	83	ATP1A2	ATPase Na+/K+ transporting subunit alpha 2
64	83	SLITRK2	SLIT and NTRK like family member 2
65	83	PSD	pleckstrin and Sec7 domain containing
66	82	TSPOAP1	TSPO associated protein 1
67	82	ELAVL4	ELAV like RNA binding protein 4
68	82	GLP1R	glucagon like peptide 1 receptor
69	82	CYB561D1	cytochrome b561 family member D1
70	81	NWD1	NACHT and WD repeat domain containing 1
71	81	ZGLP1	zinc finger, GATA-like protein 1
72	81	PTP4A1	protein tyrosine phosphatase type IVA, member 1
73	81	ZBTB10	zinc finger and BTB domain containing 10
74	81	TEAD3	TEA domain transcription factor 3
75	81	BET1	Bet1 golgi vesicular membrane trafficking protein
76	81	CDKL5	cyclin dependent kinase like 5
77	81	PDE7A	phosphodiesterase 7A
78	81	RBM7	RNA binding motif protein 7
79	81	EXOSC3	exosome component 3
80	81	CLSPN	Claspin
81	80	USP4	ubiquitin specific peptidase 4
82	80	PAX5	paired box 5
83	80	NDC1	NDC1 transmembrane nucleoporin
84	80	MTCH2	mitochondrial carrier 2
85	80	GPR182	G protein-coupled receptor 182
86	80	TMEM164	transmembrane protein 164
87	80	TRPV3	transient receptor potential cation channel subfamily V member 3
88	80	IQSEC2	IQ motif and Sec7 domain 2
89	80	NEK9	NIMA related kinase 9

90	80	TRIM13	tripartite motif containing 13
91	80	GOPC	golgi associated PDZ and coiled-coil motif containing
92	80	CSF3	colony stimulating factor 3
93	80	KDF1	keratinocyte differentiation factor 1
94	79	ADIPOR2	adiponectin receptor 2
95	79	ST6GALNAC2	ST6N-acetylgalactosaminidealpha-2,6-sialyltransferase 2
96	79	PPARGC1A	PPARG coactivator 1 alpha
97	79	PIK3CB	phosphatidylinositol-4,5-bisphosphate 3- kinase catalytic subunit beta
98	79	BBC3	BCL2 binding component 3
99	79	STARD7	StAR related lipid transfer domain containing 7
100	79	ZNF680	zinc finger protein 680
101	79	IGFL2	IGF like family member 2
102	79	PID1	phosphotyrosine interaction domain containing 1
103	79	FADS1	fatty acid desaturase 1
104	79	ANKRD33B	ankyrin repeat domain 33B
105	79	ZNF524	zinc finger protein 524
106	79	TARS	threonyl-tRNA synthetase
107	79	KIF13A	kinesin family member 13A
108	78	SYT2	synaptotagmin 2
109	78	TMEM127	transmembrane protein 127
110	78	RNF145	ring finger protein 145
111	78	B4GALT5	beta-1,4-galactosyltransferase 5
112	78	NPTN	Neuroplastin
113	78	CNTN5	contactin 5
114	78	SMARCD1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1
115	78	ZNF773	zinc finger protein 773
116	77	CHD2	chromodomain helicase DNA binding protein 2
117	77	UBE2L3	ubiquitin conjugating enzyme E2 L3
118	77	MLXIP	MLX interacting protein

119	77	PCBP4	poly(rC) binding protein 4
120	77	PISD	phosphatidylserine decarboxylase
121	77	MCAT	malonyl-CoA-acyl carrier protein transacylase
122	77	AMPD2	adenosine monophosphate deaminase 2
123	77	ZBTB21	zinc finger and BTB domain containing 21
124	77	RAB9A	RAB9A, member RAS oncogene family
125	77	ZEB1	zinc finger E-box binding homeobox 1
126	77	POLR2H	RNA polymerase II subunit H
127	77	MDM4	MDM4, p53 regulator
128	77	TRIM11	tripartite motif containing 11
129	76	TMEM92	transmembrane protein 92
130	76	PERP	PERP, TP53 apoptosis effector
131	76	NEDD8	neural precursor cell expressed, developmentally down-regulated 8
132	76	SLC30A7	solute carrier family 30 member 7
133	76	DAP	death associated protein
134	76	LMO7	LIM domain 7
135	76	SYT17	synaptotagmin 17
136	76	C6orf106	chromosome 6 open reading frame 106
137	76	LOC101927844	uncharacterized LOC101927844
138	76	STAT1	signal transducer and activator of transcription 1
139	76	ZNF718	zinc finger protein 718
140	76	OTUD7B	OTU deubiquitinase 7B
141	76	RIMKLB	ribosomal modification protein rimK like family member B
142	76	ETNK2	ethanolamine kinase 2
143	76	AEBP2	AE binding protein 2
144	75	TLK2	tousled like kinase 2
145	75	CNOT7	CCR4-NOT transcription complex subunit 7
146	75	TBC1D16	TBC1 domain family member 16
147	75	ZIC4	Zic family member 4
148	75	PTK6	protein tyrosine kinase 6

149	75	MAPKAPK3	mitogen-activated protein kinase-activated protein kinase 3
150	75	ETF1	eukaryotic translation termination factor 1
151	75	SMARCD2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
152	75	NR3C2	nuclear receptor subfamily 3 group C member 2
153	75	CBX1	chromobox 1
154	75	SNX30	sorting nexin family member 30
155	75	ZNF135	zinc finger protein 135
156	74	MBD1	methyl-CpG binding domain protein 1
157	74	ALPK3	alpha kinase 3
158	74	PCNX1	pecanex 1
159	74	ZBTB42	zinc finger and BTB domain containing 42
160	74	CFLAR	CASP8 and FADD like apoptosis regulator
161	74	EIF2B2	eukaryotic translation initiation factor 2B subunit beta
162	74	ZBTB7A	zinc finger and BTB domain containing7A
163	74	SPOPL	speckle type BTB/POZ protein like
164	74	RAPGEF6	Rap guanine nucleotide exchange factor 6
165	74	IRGQ	immunity related GTPase Q
166	74	SCUBE1	signal peptide, CUB domain and EGF like domain containing 1
167	74	GPR26	G protein-coupled receptor 26
168	74	CASTOR2	cytosolic arginine sensor for mTORC1 subunit 2
169	74	SLC17A4	solute carrier family 17 member 4
170	74	SAMD4A	sterile alpha motif domain containing 4A
171	73	EFNB1	ephrin B1
172	73	RNF141	ring finger protein 141
173	73	CALCR	calcitonin receptor
174	73	VOPP1	VOPP1, WBP1/VOPP1 family member
175	73	CD84	CD84 molecule
176	73	ARL6IP1	ADP ribosylation factor like GTPase 6 interacting protein 1

177	73	BORA	bora, aurora kinase A activator
178	73	PBX1	PBX homeobox 1
179	73	PADI1	peptidyl arginine deiminase 1
180	73	CNPPD1	cyclin Pas1/PHO80 domain containing 1
181	73	CXCL3	C-X-C motif chemokine ligand 3
182	73	METTL14	methyltransferase like 14
183	72	BAK1	BCL2 antagonist/killer 1
184	72	SRGAP3	SLIT-ROBO Rho GTPase activating protein 3
185	72	GOLGA8B	golgin A8 family member B
186	72	NTRK2	neurotrophic receptor tyrosine kinase 2
187	72	RPS6KA2	ribosomal protein S6 kinase A2
188	72	RYR3	ryanodine receptor 3
189	72	CYP4X1	cytochrome P450 family 4 subfamily X member 1
190	72	KIF1A	kinesin family member 1A
191	71	ZNF852	zinc finger protein 852
192	71	ZNF229	zinc finger protein 229
193	71	IPO11	importin 11
194	71	NSL1	NSL1, MIS12 kinetochore complex component
195	71	CCDC47	coiled-coil domain containing 47
196	71	CDK9	cyclin dependent kinase 9
197	71	TMEM245	transmembrane protein 245
198	71	SLC9B2	solute carrier family 9 member B2
199	71	TP53INP1	tumor protein p53 inducible nuclear protein 1
200	71	ARRB1	arrestin beta 1
201	71	HECTD1	HECT domain E3 ubiquitin protein ligase 1
202	71	TRIM47	tripartite motif containing 47
203	70	SMAP2	small ArfGAP2
204	70	NABP1	nucleic acid binding protein 1
205	70	C2orf72	chromosome 2 open reading frame 72
206	70	GART	phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase

207	70	GOLGA8N	golgin A8 family member N
208	70	RPRM	reprimo, TP53 dependent G2 arrest mediator homolog
209	70	CELF1	CUGBP Elav-like family member 1
210	70	ZKSCAN7	zinc finger with KRAB and SCAN domains 7
211	70	ZNF714	zinc finger protein 714
212	70	TP53INP2	tumor protein p53 inducible nuclear protein 2
213	69	LRFN2	leucine rich repeat and fibronectin type III domain containing 2
214	69	RTP1	receptor transporter protein 1
215	69	SOD2	superoxide dismutase 2
216	69	CCDC68	coiled-coil domain containing 68
217	69	ZNF592	zinc finger protein 592
218	69	MRPS18A	mitochondrial ribosomal protein S18A
219	69	SMC3	structural maintenance of chromosomes 3
220	69	CGNL1	cingulin like 1
221	69	CHMP2B	charged multivesicular body protein 2B
222	69	FAM210B	family with sequence similarity 210 member B
223	69	CNIH3	cornichon family AMPA receptor auxiliary protein 3
224	68	SYNJ2BP	synaptojanin 2 binding protein
225	68	DSG3	desmoglein 3
226	68	ZNF440	zinc finger protein 440
227	68	ATXN7	ataxin 7
228	68	HLA-DOA	major histocompatibility complex, class II, DO alpha
229	68	POM121	POM121 transmembrane nucleoporin
230	68	TCTEX1D1	Tctex1 domain containing 1
231	68	ANKRD63	ankyrin repeat domain 63
232	68	NDUFA8	NADH:ubiquinone oxidoreductase subunitA8
233	68	IFFO2	intermediate filament family orphan 2
234	67	VAV2	vav guanine nucleotide exchange factor 2
235	67	FRAT2	FRAT2, WNT signaling pathway regulator
236	67	ITGB3	integrin subunit beta 3
237	67	ZNF605	zinc finger protein 605

238	67	LRRN2	leucine rich repeat neuronal 2
239	67	PTBP3	polypyrimidine tract binding protein 3
240	67	SPOCK1	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 1
241	67	FAM171A1	family with sequence similarity 171 member A1
242	67	TRAPPC4	trafficking protein particle complex 4
243	67	RSU1	Ras suppressor protein 1
244	67	FAM160B1	family with sequence similarity 160 member B1
245	67	ORAI2	ORAI calcium release-activated calcium modulator 2
246	67	ATP2B1	ATPase plasma membrane Ca2+ transporting 1
247	66	SETD5	SET domain containing 5
248	66	WNT5B	Wnt family member 5B
249	66	MAVS	mitochondrial antiviral signaling protein
250	66	KLF15	Kruppel like factor 15
251	66	OPA3	OPA3, outer mitochondrial membrane lipid metabolism regulator
252	66	ARGFX	arginine-fifty homeobox
253	66	UBFD1	ubiquitin family domain containing 1
254	66	ATG4B	autophagy related 4B cysteine peptidase
255	66	DCUN1D5	defective in cullin neddylation 1 domain containing 5
256	65	INPP5A	inositol polyphosphate-5-phosphatase A
257	65	METTL7A	methyltransferase like 7A
258	65	C2orf68	chromosome 2 open reading frame 68
259	65	NIPAL3	NIPA like domain containing 3
260	65	DES	Desmin
261	65	CALHM5	calcium homeostasis modulator family
262	65	ODF2L	outer dense fiber of sperm tails 2 like
263	65	NLRP7	NLR family pyrin domain containing 7
264	65	CYP26B1	cytochrome P450 family 26 subfamily B member 1
265	65	PDIK1L	PDLIM1 interacting kinase 1 like
266	65	POU2F1	POU class 2 homeobox 1
267	64	LRPAP1	LDL receptor related protein associated protein 1

268	64	DNAL4	dynein axonemal light chain 4
269	64	TRHDE	thyrotropin releasing hormone degrading enzyme
270	64	DTX3L	deltex E3 ubiquitin ligase 3L
271	64	FRMD3	FERM domain containing 3
272	64	EIF4B	eukaryotic translation initiation factor 4B
273	64	TCTN1	tectonic family member 1
274	64	CALN1	calneuron 1
275	64	HAS3	hyaluronan synthase 3
276	64	C9orf152	chromosome 9 open reading frame 152
277	64	RFT1	RFT1 homolog
278	64	ZHX2	zinc fingers and homeoboxes 2
279	64	ASRGL1	asparaginase like 1
280	64	ATP8A2	ATPase phospholipid transporting 8A2
281	64	ICMT	isoprenylcysteine carboxyl methyltransferase
282	64	CEBPA	CCAAT enhancer binding protein alpha
283	64	RSRP1	arginine and serine rich protein 1
284	64	SEL1L	SEL1L, ERAD E3 ligase adaptor subunit
285	64	SMDT1	single-pass membrane protein with aspartate rich tail 1
286	64	DUSP13	dual specificity phosphatase 13
287	63	ADCY1	adenylate cyclase 1
288	63	H6PD	hexose-6-phosphate dehydrogenase/glucose 1-dehydrogenase
289	63	ACTRT1	actin related protein T1
290	63	TREM1	triggering receptor expressed on myeloid cells 1
291	63	FOXO4	forkhead box O4
292	63	EIF4G3	eukaryotic translation initiation factor 4 gamma 3
293	63	CARM1	coactivator associated arginine methyltransferase 1
294	63	TMEM250	transmembrane protein 250
295	62	TSEN15	tRNA splicing endonuclease subunit 15
296	62	PKP4	plakophilin 4
297	62	LEXM	lymphocyte expansion molecule
298	62	SNX11	sorting nexin 11

299	62	PITPNA	phosphatidylinositol transfer protein alpha
300	62	MBTD1	mbt domain containing 1
301	62	ATF2	activating transcription factor 2
302	62	KCNH8	potassium voltage-gated channel subfamily H member 8
303	62	TRAF2	TNF receptor associated factor 2
304	62	GNAL	G protein subunit alpha L
305	62	RNASEH2C	ribonuclease H2 subunit C
306	62	CBL	Cbl proto-oncogene
307	62	WSCD2	WSC domain containing 2
308	62	LPP	LIM domain containing preferred translocation partner in lipoma
309	62	A1CF	APOBEC1 complementation factor
310	62	VDR	vitamin D receptor
311	62	MYOM3	myomesin 3
312	62	UBE2W	ubiquitin conjugating enzyme E2 W
313	62	EZH1	enhancer of zeste 1 polycomb repressive complex 2 subunit
314	62	BTRC	beta-transducin repeat containing E3 ubiquitin protein ligase
315	61	STMN4	stathmin 4
316	61	ATP6V1H	ATPase H+ transporting V1 subunit H
317	61	MAPT	microtubule associated protein tau
318	61	PEG10	paternally expressed 10
319	61	CARHSP1	calcium regulated heat stable protein 1
320	61	MSTO1	misato mitochondrial distribution and morphology regulator 1
321	61	FAM133B	family with sequence similarity 133 member B
322	61	HNRNPR	heterogeneous nuclear ribonucleoprotein R
323	61	TRIL	TLR4 interactor with leucine rich repeats
324	61	CCNJ	cyclin J
325	61	CD36	CD36 molecule
326	61	SAMD14	sterile alpha motif domain containing 14

327	61	PPM1L	protein phosphatase, Mg2+/Mn2+ dependent 1L
328	61	USP7	ubiquitin specific peptidase 7
329	61	SLCO1A2	solute carrier organic anion transporter family member 1A2
330	61	UBE2O	ubiquitin conjugating enzyme E2 O
331	61	PIP5K1A	phosphatidylinositol-4-phosphate 5-kinase type 1 alpha
332	61	CNTD2	cyclin N-terminal domain containing 2
333	61	VHL	von Hippel-Lindau tumor suppressor
334	61	TRAFD1	TRAF-type zinc finger domain containing 1
335	60	PALD1	phosphatase domain containing paladin 1
336	60	UCP3	uncoupling protein 3
337	60	CALM3	calmodulin 3
338	60	ACOT11	acyl-CoA thioesterase 11
339	60	SMIM14	small integral membrane protein 14
340	60	CSRNP3	cysteine and serine rich nuclear protein 3
341	60	BARX2	BARX homeobox 2
342	60	PPP1R3F	protein phosphatase 1 regulatory subunit 3F
343	60	AGO1	argonaute RISC catalytic component 1
344	60	MAPK4	mitogen-activated protein kinase 4
345	60	DIPK2B	divergent protein kinase domain 2B
346	60	COL1A1	collagen type I alpha 1 chain
347	60	PRTG	Protogenin
348	60	SH3TC2	SH3 domain and tetratricopeptide repeats 2
349	60	SBNO1	strawberry notch homolog 1
350	60	ADPRH	ADP-ribosylarginine hydrolase
351	60	ZBTB20	zinc finger and BTB domain containing 20
352	60	GRAP2	GRB2 related adaptor protein 2
353	60	USH1G	USH1 protein network component sans
354	59	IST1	IST1, ESCRT-III associated factor
355	59	GIMAP6	GTPase, IMAP family member 6
356	59	SOCS7	suppressor of cytokine signaling 7
357	59	IGF2BP1	insulin like growth factor 2 mRNA binding protein 1

358	59	RNF135	ring finger protein 135
359	59	CMTM6	CKLF like MARVEL transmembrane domain containing 6
360	59	RAD54L	RAD54 like
361	59	MLPH	Melanophilin
362	59	AADACL3	arylacetamide deacetylase like 3
363	59	ADAM8	ADAM metallopeptidase domain 8
364	59	MOB1B	MOB kinase activator 1B
365	59	AXDND1	axonemal dynein light chain domain containing 1
366	59	CD99	CD99 molecule (Xg blood group)
367	59	PIK3R1	phosphoinositide-3-kinase regulatory subunit 1
368	59	NRXN3	neurexin 3
369	59	CIAO3	cytosolic iron-sulfur assembly component 3
370	59	HCN3	hyperpolarization activated cyclic nucleotide gated potassium channel 3
371	59	PERM1	PPARGC1 and ESRR induced regulator, muscle 1
372	59	DKC1	dyskerin pseudouridine synthase 1
373	59	ANKRD34A	ankyrin repeat domain 34A
374	59	ST6GAL1	ST6 beta-galactoside alpha-2,6- sialyltransferase 1
375	58	SLC35G3	solute carrier family 35 member G3
376	58	P2RX6	purinergic receptor P2X 6
377	58	ST7L	suppression of tumorigenicity 7 like
378	58	MYPOP	Myb related transcription factor, partner of profilin
379	58	ATPSCKMT	ATP synthase c subunit lysine N- methyltransferase
380	58	INO80D	INO80 complex subunit D
381	58	PPM1D	protein phosphatase, Mg2+/Mn2+ dependent 1D
382	58	JPH3	junctophilin 3
383	58	FOXR2	forkhead box R2
384	58	CTNNA3	catenin alpha 3
385	58	TNFRSF14	TNF receptor superfamily member 14
386	58	CYP3A4	cytochrome P450 family 3 subfamily A member 4
387	58	SLC25A42	solute carrier family 25 member 42

388	58	PIP4K2B	phosphatidylinositol-5-phosphate 4-kinase type 2 beta
389	58	GPATCH2L	G-patch domain containing 2 like
390	58	ASPN	Asporin
391	58	MGAT5	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase
392	58	RAD51	RAD51 recombinase
393	58	R3HCC1L	R3H domain and coiled-coil containing 1 like
394	58	GALNT1	polypeptide N-acetylgalactosaminyltransferase 1
395	58	PPP1R1A	protein phosphatase 1 regulatory inhibitor subunit 1A
396	58	ADORA1	adenosine A1 receptor
397	57	DDTL	D-dopachrome tautomerase like
398	57	TNS1	tensin 1
399	57	CD38	CD38 molecule
400	57	C6orf132	chromosome 6 open reading frame 132
401	57	SOGA3	SOGA family member 3
402	57	MYSM1	Myb like, SWIRM and MPN domains 1
403	57	HHIPL2	HHIP like 2
404	57	SLC1A3	solute carrier family 1 member 3
405	57	AMOTL2	angiomotin like 2
406	57	CPD	carboxypeptidase D
407	57	UNKL	unk like zinc finger
408	57	MAFK	MAF bZIP transcription factor K
409	57	PSAPL1	prosaposin like 1 (gene/pseudogene)
410	57	TMEM252	transmembrane protein 252
411	57	XRN1	5'-3' exoribonuclease 1
412	57	PTGER3	prostaglandin E receptor 3
413	57	TNC	tenascin C
414	57	HIPK2	homeodomain interacting protein kinase 2
415	57	SUPT3H	SPT3 homolog, SAGA and STAGA complex component
416	56	NR1D2	nuclear receptor subfamily 1 group D member 2
417	56	IPO9	importin 9

418	56	ZNF500	zinc finger protein 500
419	56	PLXNA4	plexin A4
420	56	PSD3	pleckstrin and Sec7 domain containing 3
421	56	TMEM229B	transmembrane protein 229B
422	56	SPTLC2	serine palmitoyltransferase long chain base subunit 2
423	56	RND2	Rho family GTPase 2
424	56	AMOTL1	angiomotin like 1
425	56	FOSL2	FOS like 2, AP-1 transcription factor subunit
426	56	TLE3	TLE family member 3, transcriptional corepressor
427	56	KCNIP1	potassium voltage-gated channel interacting protein 1
428	56	MEDAG	mesenteric estrogen dependent adipogenesis
429	56	TADA1	transcriptional adaptor 1
430	56	SKAP2	src kinase associated phosphoprotein 2
431	56	CACNG8	calcium voltage-gated channel auxiliary subunit gamma 8
432	56	THSD7A	thrombospondin type 1 domain containing 7A
433	56	NRBF2	nuclear receptor binding factor 2
434	56	SLC49A4	solute carrier family 49 member 4
435	56	GOLGA8A	golgin A8 family member A
436	56	MRPS25	mitochondrial ribosomal protein S25
437	56	SAP30BP	SAP30 binding protein
438	55	HSPB7	heat shock protein family B (small) member 7
439	55	NGB	Neuroglobin
440	55	GOLGA8J	golgin A8 family member J
441	55	ING4	inhibitor of growth family member 4
442	55	TMEM181	transmembrane protein 181
443	55	GOLGA8H	golgin A8 family member H
444	55	SREBF2	sterol regulatory element binding transcription factor 2
445	55	ZNF829	zinc finger protein 829
446	55	CNBP	CCHC-type zinc finger nucleic acid binding protein
447	55	GDAP2	ganglioside induced differentiation associated protein 2
448	55	ARHGEF10L	Rho guanine nucleotide exchange factor 10 like

449	55	ZNF74	zinc finger protein 74
450	55	PLXNA2	plexin A2
451	55	CELSR3	cadherin EGF LAG seven-pass G-type receptor 3
452	55	SP1	Sp1 transcription factor
453	55	GNL1	G protein nucleolar 1 (putative)
454	55	KSR2	kinase suppressor of ras 2
455	55	GOLGA8O	golgin A8 family member O
456	55	GOLGA8R	golgin A8 family member R
457	55	TBC1D2B	TBC1 domain family member 2B
458	55	NLK	nemo like kinase
459	55	ARFIP2	ADP ribosylation factor interacting protein 2
460	55	HCN4	hyperpolarization activated cyclic nucleotide gated potassium channel 4
461	55	MTMR12	myotubularin related protein 12
462	55	PPP1R13B	protein phosphatase 1 regulatory subunit 13B
463	55	NCR3	natural cytotoxicity triggering receptor 3
464	55	UBE2D3	ubiquitin conjugating enzyme E2 D3
465	55	GK	glycerol kinase
466	55	GOLGA8K	golgin A8 family member K
467	55	ZNF554	zinc finger protein 554
468	55	GRK6	G protein-coupled receptor kinase 6
469	55	RLF	rearranged L-myc fusion
470	54	PDE7B	phosphodiesterase 7B
471	54	WFDC1	WAP four-disulfide core domain 1
472	54	SHPK	sedoheptulokinase
473	54	HNF4A	hepatocyte nuclear factor 4 alpha
474	54	STARD9	StAR related lipid transfer domain containing 9
475	54	RASD2	RASD family member 2
476	54	THAP3	THAP domain containing 3
477	54	UBE2E1	ubiquitin conjugating enzyme E2 E1
478	54	KIAA1147	KIAA1147
479	54	CA8	carbonic anhydrase 8

480	54	RAB3B	RAB3B, member RAS oncogene family
481	54	KCNAB1	potassium voltage-gated channel subfamily A member regulatory beta subunit 1
482	54	DIRAS2	DIRAS family GTPase 2
483	54	TNFSF11	TNF superfamily member 11
484	54	MYORG	myogenesis regulating glycosidase (putative)
485	54	PSMB6	proteasome subunit beta 6
486	54	MGST2	microsomal glutathione S-transferase 2
487	54	NEURL1B	neuralized E3 ubiquitin protein ligase 1B
488	54	ZNF776	zinc finger protein 776
489	53	DNAJB5	DnaJ heat shock protein family (Hsp40) member B5
490	53	GOLGA6L9	golgin A6 family-like 9
491	53	DLG3	discs large MAGUK scaffold protein 3
492	53	GOLGA6L4	golgin A6 family-like 4
493	53	MGAT3	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase
494	53	LTN1	listerin E3 ubiquitin protein ligase 1
495	53	UBE2H	ubiquitin conjugating enzyme E2 H
496	53	ZNF736	zinc finger protein 736
497	53	CTIF	cap binding complex dependent translation initiation factor
498	53	PRR3	proline rich 3
499	53	ZNF775	zinc finger protein 775
500	53	GPRC5A	G protein-coupled receptor class C group 5 member A
501	53	TMEM101	transmembrane protein 101
502	53	APC2	APC2, WNT signaling pathway regulator
503	53	AMZ1	archaelysin family metallopeptidase 1
504	53	RRAD	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
505	53	RAB12	RAB12, member RAS oncogene family
506	53	RAB11FIP4	RAB11 family interacting protein 4
507	52	TEAD1	TEA domain transcription factor 1

508	52	OSCAR	osteoclast associated, immunoglobulin-like receptor
509	52	TRIM71	tripartite motif containing 71
510	52	SAMD12	sterile alpha motif domain containing 12
511	52	UBE2E3	ubiquitin conjugating enzyme E2 E3
512	52	NLN	Neurolysin
513	52	MEPCE	methylphosphate capping enzyme
514	52	UMPS	uridine monophosphate synthetase
515	52	BRF2	BRF2, RNA polymerase III transcription initiation factor subunit
516	52	BRF1	BRF1, RNA polymerase III transcription initiation factor subunit
517	52	SLC15A2	solute carrier family 15 member 2
518	52	GGNBP2	gametogenetin binding protein 2
519	52	NUP93	nucleoporin 93
520	52	PHKG1	phosphorylase kinase catalytic subunit gamma 1
521	52	LIMK2	LIM domain kinase 2
522	52	MEFV	MEFV, pyrin innate immunity regulator
523	52	RASSF2	Ras association domain family member 2
524	52	JCAD	junctional cadherin 5 associated
525	52	ZDHHC8	zinc finger DHHC-type containing 8
526	52	SLC38A3	solute carrier family 38 member 3
527	52	HOXA11	homeobox A11
528	52	PPP1R2	protein phosphatase 1 regulatory inhibitor subunit 2
529	52	NSUN4	NOP2/Sun RNA methyltransferase family member 4
530	51	NFAM1	NFAT activating protein with ITAM motif1
531	51	ACVRL1	activin A receptor like type 1
532	51	GRHL2	grainyhead like transcription factor 2
533	51	SHISAL1	shisa like 1
534	51	MCFD2	multiple coagulation factor deficiency 2
535	51	ADAM22	ADAM metallopeptidase domain 22
536	51	GATAD2B	GATA zinc finger domain containing 2B
537	51	TMEM199	transmembrane protein 199

538	51	PIRT	phosphoinositide interacting regulator of transient receptor potential channels
539	51	SLC25A30	solute carrier family 25 member 30
540	51	PRRT2	proline rich transmembrane protein 2
541	51	FAM76A	family with sequence similarity 76 member A
542	51	RAPGEF1	Rap guanine nucleotide exchange factor 1
543	51	CLDN2	claudin 2
544	51	TBC1D22B	TBC1 domain family member 22B
545	51	AZGP1	alpha-2-glycoprotein 1, zinc-binding
546	51	FOXK1	forkhead box K1
547	51	AGO4	argonaute RISC catalytic component 4
548	51	SH3PXD2A	SH3 and PX domains 2A
549	50	STYX	serine/threonine/tyrosine interacting protein
550	50	CDKN1B	cyclin dependent kinase inhibitor 1B
551	50	LMAN2L	lectin, mannose binding 2 like
552	50	CACNA2D4	calcium voltage-gated channel auxiliary subunit alpha2delta 4
553	50	ERMN	Ermin
554	50	FAM124A	family with sequence similarity 124 member A
555	50	THBS1	thrombospondin 1
556	50	CCSAP	centriole, cilia and spindle associated protein
557	50	C11orf71	chromosome 11 open reading frame 71
558	50	MTA3	metastasis associated 1 family member 3
559	50	OASL	2'-5'-oligoadenylate synthetase like
560	50	UNC119	unc-119 lipid binding chaperone
561	50	RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
562	50	FAM168B	family with sequence similarity 168 member B
563	50	SLC33A1	solute carrier family 33 member 1
564	50	UCP2	uncoupling protein 2
565	50	SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein

566	50	NYAP1	neuronal tyrosine phosphorylated phosphoinositide-3-kinase adaptor 1
567	50	TBC1D13	TBC1 domain family member 13
568	50	S100PBP	S100P binding protein

Supplementary Table-4. Differentially expressed genes in sarcopenia samples

Gene	Gene Description	Change fold	P Value	Expression
IL1B	Interleukin-1 beta	14.5	0.00032	Upregulation
S100A8	S100 calcium binding protein A8	13.4	0.00054	Upregulation
NFKB1	Nuclear factor Kappa B subunit 1	12.9	0.00067	Upregulation
IL6	Interleukin-6	12.2	0.00078	Upregulation
TNFA	Tumor necrosis factor alpha	11.9	0.00031	Upregulation
SOD1	Superoxide dismutase 1	11.5	0.00028	Upregulation
PTGS1	Prostaglandin-endoperoxide synthase 1	11.3	0.00065	Upregulation
BAK1	BCL2 antagonist/killer 1	10.9	0.00068	Upregulation
CD40	CD40 molecyle	10.8	0.00077	Upregulation
CXCL10	C-X-C motif chemokine ligand 10	10.7	0.00098	Upregulation
TGFB1	Transforming growth factor beta 1	10.5	0.00032	Upregulation
ICAM1	Intercellular adhesion molecule 1	10.3	0.00015	Upregulation
S100A9	S100 calcium binding protein A9	10.2	0.00035	Upregulation
VCAM1	Vascular cell adhesion molecule 1	9.9	0.00046	Upregulation
NLRP1	NLR family pyrin domain containing 1	9.5	0.00041	Upregulation
NLRP3	NLR family pyrin domain containing 3	9.2	0.00053	Upregulation
CASP1	Caspase 1	8.9	0.00064	Upregulation
CASP3	Caspase 3	8.5	0.00072	Upregulation
MDM2	MDM2 Proto-oncogene	8.3	0.00093	Upregulation
DUSP2	Dual specificity phosphatase 2	7.8	0.00065	Upregulation
CXCL2	C-X-C motif chemokine ligand 2	7.4	0.00035	Upregulation
SOD2	Superoxide dismutase 2	7.2	0.00064	Upregulation
PTGS2	Prostaglandin-endoperoxide synthase 2	7.2	0.00067	Upregulation
MMP13	Matrix metallopeptidase 13	7.1	0.00034	Upregulation
INFG	Interferon gamma	7.0	0.00065	Upregulation
TRAF6	TNF receptor associated factor 6	7.0	0.00011	Upregulation

BBC3	BCL2 binding component 3 MYC Proto-oncogene, BHLH transcription factor	6.9	0.00037	Upregulation
ZBTB9	Zinc finger and BTB Domain containing 9	6.7	0.00056	Upregulation
VPS52	Vacuolar protein sorting 52 homolog	6.5	0.00044	Upregulation
ZNF514	Zinc finger Protein 514	6.2	0.00036	Upregulation
SGK1	Serum/Glucocorticoid regulated kinase 1	5.9	0.00064	Upregulation
CAPN2	Calpain 2	5.7	0.00016	Upregulation
LTA	Lymphotoxin alpha	5.4	0.00053	Upregulation
GZMB	Granzyme B	5.3	0.00025	Upregulation
TRAF3	TNF receptor associated factor	5.1	0.00065	Upregulation
ITPR1	Inositol 1,4,5-Trisphosphate receptor type 1	5.1	0.00011	Upregulation
GRM4	Glutamate metabotropic receptor 4	4.9	0.00026	Upregulation
NUDT3	Nudix hydrolase 3	4.6	0.00092	Upregulation
CDC42	Cell division cycle 42	4.5	0.00079	Upregulation
PEA15‘	Proliferation and apoptosis adaptor protein 15	3.9	0.00084	Upregulation
NOL3	Nucleolar protein 3	3.7	0.00064	Upregulation
DDB2	Damage specific DNA binding protein 2	3.6	0.00028	Upregulation
CCND3	Cyclin D3	3.4	0.00017	Upregulation
MFN2	Mitofusin 2	3.3	0.00036	Upregulation
AXIN2	Axin 2	3.1	0.00034	Upregulation
DDB1	Damage specific DNA binding protein 2	2.9	0.00022	Upregulation
LEF1	Lymphoid enhancer binding factor 1	2.7	0.00012	Upregulation
PSEN2	Presenilin 2	2.5	0.00055	Upregulation
ANK1	Ankyrin 1	2.4	0.00017	Upregulation
CDH1	Cadherin 1	-15.1	0.0013	Downregulation

BDH1	3-Hydroxybutyrate dehydrogenase 1	-14.2	0.00018	Downregulation
PON1	Paraoxonase 1	-13.9	0.0091	Downregulation
BDH2	3-Hydroxybutyrate dehydrogenase 2	-13.4	0.00054	Downregulation
CD117	CD117 molecule	-12.7	0.0032	Downregulation
BMP4	Bone morphogenetic protein 4	-12.3	0.0065	Downregulation
GNG11	G Protein subunit gamma 11	-11.6	0.00043	Downregulation
NPTX1	Neuronal pentraxin 1	-11.2	0.00074	Downregulation
PTX3	Pentraxin 3	-10.3	0.00061	Downregulation
ZAP70	Zeta chain of T cell receptor associated protein kinase 70	-9.8	0.00093	Downregulation
SLA2	Src like adaptor 2	-8.2	0.0024	Downregulation
NR3C1	Nuclear receptor subfamily 3 group C member 1	-7.8	0.0018	Downregulation
CST3	Cystatin C	-7.4	0.00057	Downregulation
FGF9	Fibroblast growth factor 9	-7.1	0.00015	Downregulation
MFSD7	Major facilitator superfamily domain-containing protein 7	-6.7	0.00046	Downregulation
GLTPD	Glycolipid transfer protein domain containing 1	-6.4	0.0063	Downregulation
LRG1	Leucine-rich alpha-2-glycoprotein 1	-5.3	0.00074	Downregulation
ZFPM1	Zinc finger protein, FOG family member 1	-4.5	0.0084	Downregulation
KIF2A	Kinesin family member 2A	-4.2	0.00065	Downregulation
SORT1	Sortilin 1	-3.4	0.00043	Downregulation
INTS12	Integrator complex subunit 12	-2.5	0.00024	Downregulation