

Table S2. Gene ontology using down-regulated genes in sarcopenia (cutoff: *P* value <0.05)

Category	Term	Count	%	<i>P</i> value	Genes
GOTERM_BP_FAT	GO:0019752~carboxylic acid metabolic process	18	13.8462	<0.001	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, DCXR, SORD, MIF, ACAT2, GSTZ1, ALDH1A3, PSAT1, EHHADH, PCCB, SMS, CRYL1, GNE, SNCA
GOTERM_BP_FAT	GO:0043436~oxoacid metabolic process	18	13.8462	<0.001	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, DCXR, SORD, MIF, ACAT2, GSTZ1, ALDH1A3, PSAT1, EHHADH, PCCB, SMS, CRYL1, GNE, SNCA
GOTERM_BP_FAT	GO:0032787~monocarboxylic acid metabolic process	14	10.7692	<0.001	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, DCXR, SORD, MIF, ACAT2, ALDH1A3, EHHADH, PCCB, CRYL1, SNCA
GOTERM_BP_FAT	GO:0006082~organic acid metabolic process	18	13.8462	<0.001	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, DCXR, SORD, MIF, ACAT2, GSTZ1, ALDH1A3, PSAT1, EHHADH, PCCB, SMS, CRYL1, GNE, SNCA
GOTERM_BP_FAT	GO:0060337~type I interferon signaling pathway	6	4.61538	<0.001	STAT1, OAS2, OAS3, IFI6, ISG15, IRF9
GOTERM_BP_FAT	GO:0071357~cellular response to type I interferon	6	4.61538	<0.001	STAT1, OAS2, OAS3, IFI6, ISG15, IRF9
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	11	8.46154	<0.001	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, EHHADH, PCCB, CRYL1, MIF, ACAT2, SNCA
GOTERM_BP_FAT	GO:0034340~response to type I interferon	6	4.61538	<0.001	STAT1, OAS2, OAS3, IFI6, ISG15, IRF9
GOTERM_BP_FAT	GO:0044283~small molecule biosynthetic process	12	9.23077	<0.001	SEC14L2, ALDH1A3, XBP1, PLA2G4F, PSAT1, ELOVL5, RFK, PCCB, SORD, DHCR7, MIF, SNCA
GOTERM_BP_FAT	GO:0051167~xylulose 5-phosphate metabolic process	3	2.30769	<0.001	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:1901159~xylulose 5-phosphate biosynthetic process	3	2.30769	<0.001	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:0019640~glucuronate catabolic process to xylulose 5-phosphate	3	2.30769	<0.001	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:0006064~glucuronate catabolic process	3	2.30769	<0.001	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:0072329~monocarboxylic acid catabolic process	6	4.61538	0.001	EHHADH, DCXR, PCCB, SORD, CRYL1, ACAT2
GOTERM_BP_FAT	GO:0036498~IRE1-mediated unfolded protein response	5	3.84615	0.001	XBP1, SERP1, DNAJB9, WIP1, PDIA5
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	7	5.38462	0.002	GSTZ1, EHHADH, DCXR, PCCB, SORD, CRYL1, ACAT2
GOTERM_BP_FAT	GO:0030968~endoplasmic reticulum unfolded protein response	6	4.61538	0.002	XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1
GOTERM_BP_FAT	GO:0034620~cellular response to unfolded protein	6	4.61538	0.002	XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1
GOTERM_BP_FAT	GO:0006629~lipid metabolic process	19	14.6154	0.002	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, MBOAT2, MIF, ACAT2, SULT2B1, SEC14L2, INPP4B, ALDH1A3, RDH11, EHHADH, PCCB, CRYL1, DHCR7, MPDU1, SNCA
GOTERM_BP_FAT	GO:0044255~cellular lipid metabolic process	16	12.3077	0.003	CYP2J2, LYPLA1, XBP1, PLA2G4F, ELOVL5, MBOAT2, MIF, ACAT2, INPP4B, ALDH1A3, RDH11, EHHADH, PCCB, CRYL1, MPDU1, SNCA
GOTERM_BP_FAT	GO:0044712~single-organism catabolic process	14	10.7692	0.003	XBP1, PLA2G4F, DCXR, SORD, ACAT2, HSP90B1, GSTZ1, EHHADH, PCCB, CRYL1, DNAJB9, ADPRM, CTBS, PDE9A
GOTERM_BP_FAT	GO:0035967~cellular response to topologically incorrect protein	6	4.61538	0.003	XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	7	5.38462	0.003	GSTZ1, EHHADH, DCXR, PCCB, SORD, CRYL1, ACAT2
GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	11	8.46154	0.004	MCUR1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	11	8.46154	0.005	MCUR1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0006986~response to unfolded protein	6	4.61538	0.005	XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1
GOTERM_BP_FAT	GO:0050801~ion homeostasis	12	9.23077	0.005	MCUR1, SCO1, IFI6, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	12	9.23077	0.006	XBP1, MCUR1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0044282~small molecule catabolic process	8	6.15385	0.006	GSTZ1, EHHADH, DCXR, PCCB, SORD, CRYL1, ADPRM, ACAT2
GOTERM_BP_FAT	GO:0044248~cellular catabolic process	20	15.3846	0.007	XBP1, PLA2G4F, DCXR, SORD, ISG15, ACAT2, HSP90B1, GSTZ1, HERC3, SCO1, OAS2, ANPEP, EHHADH, PCCB, CRYL1, DNAJB9, ADPRM, PDE9A, RNFI187, SNCA
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	7	5.38462	0.007	ALDH1A3, XBP1, PLA2G4F, PSAT1, ELOVL5, PCCB, MIF
GOTERM_BP_FAT	GO:0072330~monocarboxylic acid biosynthetic process	6	4.61538	0.007	ALDH1A3, XBP1, PLA2G4F, ELOVL5, PCCB, MIF
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	13	10	0.007	XBP1, MCUR1, GPR89B, PDIA5, HSP90B1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, SLC39A4, TRPM4, SNCA
GOTERM_BP_FAT	GO:0035966~response to topologically incorrect protein	6	4.61538	0.007	XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1
GOTERM_BP_FAT	GO:0055080~cation homeostasis	11	8.46154	0.008	MCUR1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	7	5.38462	0.009	ALDH1A3, XBP1, PLA2G4F, PSAT1, ELOVL5, PCCB, MIF
GOTERM_BP_FAT	GO:0006066~alcohol metabolic process	7	5.38462	0.010	SEC14L2, INPP4B, ALDH1A3, RDH11, SORD, DHCR7, SNCA
GOTERM_BP_FAT	GO:0098771~inorganic ion homeostasis	11	8.46154	0.010	MCUR1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, GPR89B, SLC39A4, HSP90B1, TRPM4, SNCA
GOTERM_BP_FAT	GO:0055114~oxidation-reduction process	14	10.7692	0.010	CYP2J2, ABCC4, SMOX, DCXR, SORD, ACAT2, PDIA5, C15ORF48, ALDH1A3, RDH11, EHHADH, CRYL1, DHCR7, SNCA
GOTERM_BP_FAT	GO:0071310~cellular response to organic substance	24	18.4615	0.011	SPON2, XBP1, PAQR6, PLA2G4F, GALNT3, STAT1, IFI6, ISG15, WIP1, MIF, FGFR1L, PDIA5, GNAI1, HIPK2, HSP90B1, KRT18, SERP1, OAS2, OAS3, DNAJB9, ATP6V0E2, IRF9, TRPM4, SNCA
GOTERM_BP_FAT	GO:0005975~carbohydrate metabolic process	12	9.23077	0.011	SERP1, GALNT3, OAS2, DCXR, RPN1, TFF3, SORD, CHP1, CTBS, GNE, MPDU1, SNCA
GOTERM_BP_FAT	GO:0006633~fatty acid biosynthetic process	5	3.84615	0.014	XBP1, PLA2G4F, ELOVL5, PCCB, MIF
GOTERM_BP_FAT	GO:0060333~interferon-gamma-mediated signaling pathway	4	3.07692	0.015	STAT1, OAS2, OAS3, IRF9
GOTERM_BP_FAT	GO:0019585~glucuronate metabolic process	3	2.30769	0.015	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:0006063~uronic acid metabolic process	3	2.30769	0.015	DCXR, SORD, CRYL1
GOTERM_BP_FAT	GO:0051607~defense response to virus	6	4.61538	0.016	SPON2, STAT1, OAS2, OAS3, ISG15, IRF9
GOTERM_BP_FAT	GO:1901615~organic hydroxy compound metabolic process	8	6.15385	0.017	SEC14L2, INPP4B, ALDH1A3, PSAT1, RDH11, SORD, DHCR7, SNCA
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	14	10.7692	0.017	XBP1, MCUR1, STAT1, IFI6, GPR89B, HSP90B1, SCO1, CHP1, TNNI3, TRPM8, ATP6V0E2, SLC39A4, TRPM4, SNCA
GOTERM_BP_FAT	GO:0042592~homeostatic process	19	14.6154	0.017	XBP1, MCUR1, STAT1, IFI6, ISG15, MIF, GPR89B, PDIA5, HIPK2, HSP90B1, SCO1, CHP1, TNNI3, POTEF, TRPM8, ATP6V0E2, SLC39A4, TRPM4, SNCA
GOTERM_BP_FAT	GO:0045087~innate immune response	12	9.23077	0.018	SPON2, RPS6KA3, STAT1, OAS2, OAS3, IFI6, RAB27A, ISG15, MIF, IRF9, HSP90B1, SNCA
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	10	7.69231	0.019	SEC14L2, INPP4B, ALDH1A3, XBP1, PLA2G4F, ELOVL5, PCCB, MBOAT2, DHCR7, MIF
GOTERM_BP_FAT	GO:1902930~regulation of alcohol biosynthetic process	3	2.30769	0.020	SEC14L2, DHCR7, SNCA
GOTERM_BP_FAT	GO:0034341~response to interferon-gamma	5	3.84615	0.020	STAT1, OAS2, OAS3, IRF9, SNCA
GOTERM_BP_FAT	GO:1901137~carbohydrate derivative biosynthetic process	11	8.46154	0.024	SERP1, GALNT3, OAS2, RFK, DCXR, RPN1, SORD, CRYL1, CHP1, GNE, MPDU1
GOTERM_BP_FAT	GO:0044723~single-organism carbohydrate metabolic process	10	7.69231	0.025	SERP1, GALNT3, OAS2, DCXR, RPN1, SORD, CHP1, CTBS, MPDU1, SNCA

GOTERM_BP_FAT	GO:0070887~cellular response to chemical stimulus	26	20	0.028	<i>SPON2, IFI6, FGFR1, GNAI1, HSP90B1, SERP1, DNAJB9, ATP6V0E2, TRPM4, SNCA, CYP2J2, XBP1, PAQR6, PLA2G4F, GALNT3, STAT1, WIP1, ISG15, MIF, PDIA5, HIPK2, KRT18, OAS2, OAS3, SAA2, IRF9</i>
GOTERM_BP_FAT	GO:1901135~carbohydrate derivative metabolic process	15	11.5385	0.029	<i>GALNT3, DCXR, RPN1, SORD, SULT2B1, SERP1, OAS2, RFK, CRYL1, CHP1, CTBS, PDE9A, GNE, MPDU1, SNCA</i>
GOTERM_BP_FAT	GO:0034976~response to endoplasmic reticulum stress	6	4.61538	0.030	<i>XBP1, SERP1, DNAJB9, WIP1, PDIA5, HSP90B1</i>
GOTERM_BP_FAT	GO:0090407~organophosphate biosynthetic process	9	6.92308	0.031	<i>INPP4B, XBP1, OAS2, RFK, DCXR, SORD, MBOAT2, CRYL1, SNCA</i>
GOTERM_BP_FAT	GO:0002700~regulation of production of molecular mediator of immune response	4	3.07692	0.032	<i>SPON2, XBP1, MIF, TRPM4</i>
GOTERM_BP_FAT	GO:0032309~icosanoid secretion	3	2.30769	0.032	<i>ABCC4, PLA2G4F, MIF</i>
GOTERM_BP_FAT	GO:0010033~response to organic substance	27	20.7692	0.033	<i>SPON2, IFI6, FGFR1, GNAI1, HSP90B1, RPS6KA3, SERP1, DNAJB9, ATP6V0E2, TRPM4, SNCA, ABCC4, XBP1, PAQR6, PLA2G4F, GALNT3, STAT1, SORD, WIP1, ISG15, MIF, PDIA5, HIPK2, KRT18, OAS2, OAS3, IRF9</i>
GOTERM_BP_FAT	GO:0033559~unsaturated fatty acid metabolic process	4	3.07692	0.038	<i>CYP2J2, PLA2G4F, ELOVL5, MIF</i>
GOTERM_BP_FAT	GO:0071715~icosanoid transport	3	2.30769	0.038	<i>ABCC4, PLA2G4F, MIF</i>
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	8	6.15385	0.039	<i>MCUR1, SLC39A4, SLC39A4, HSP90B1, TRPM4, SNCA</i>
GOTERM_BP_FAT	GO:0009605~response to external stimulus	21	16.1538	0.040	<i>SPON2, CNTNAP2, XBP1, STAT1, PLEKH81, SORD, ISG15, MIF, TTN, RPS6KA3, ALDH1A3, RELN, RDH11, OAS2, OAS3, SAA2, TRPM8, IRF9, SLC39A4, TRPM4, SNCA</i>
GOTERM_BP_FAT	GO:0009581~detection of external stimulus	4	3.07692	0.040	<i>RDH11, PLEKH81, TRPM8, TTN</i>
GOTERM_BP_FAT	GO:0009582~detection of abiotic stimulus	4	3.07692	0.043	<i>RDH11, PLEKH81, TRPM8, TTN</i>
GOTERM_BP_FAT	GO:0008215~spermine metabolic process	2	1.53846	0.044	<i>SMOX, SMS</i>
GOTERM_BP_FAT	GO:0002252~immune effector process	10	7.69231	0.049	<i>SPON2, XBP1, STAT1, OAS2, OAS3, RAB27A, ISG15, MIF, IRF9, TRPM4</i>