

Supplementary materials

Exercise Protocol. Patients in the transcutaneous neuromuscular electrical stimulation group (NMES; n = 13) performed a NMES protocol delivered using a hand-held, battery powered device (Empi 300PV, Minnesota, USA) linked to two skin surface gel electrodes (7 x 4 cm). The negative electrode was positioned proximal to the patella so as to cover the motor points of the vastus lateralis and vastus medialis muscles with the positive electrode placed longitudinally over the rectus femoris motor point. The 30 min stimulation protocol consisted of repetitions of 15 s stimulation (including 2 s ramp-up and 2 s ramp-down of current) and 5 s rest. Stimulation was a biphasic pulse at 50 Hz with a pulse duration of 300 μ s. During stimulation patients were seated with knees extended and supported on a physiotherapists couch.

RNA Extraction. Previously frozen muscle samples were homogenised in TRI Reagent Solution (Applied Biosystems / Life Technologies, Paisley, UK). Chloroform was used to separate the homogenate into aqueous-, inter- and organic-phases. RNA was precipitated from the aqueous phase with isopropanol, the resulting pellet washed in ethanol and then re-suspended in nuclease free water.

Extracted RNA was quantified according to its absorbance of 260nm light (Nanodrop 2000 Spectrophotometer, Thermoscientific, Waltham, MA, USA) before reverse transcription to cDNA. One micro-gram of RNA per sample was incubated with random hexamer primers, dNTPs (deoxynucleotide triphosphates) and reverse transcriptase (SuperScript III, Life Technologies / Invitrogen) in order to synthesise complimentary DNA.

Change in abundance of mRNA is expressed using the widely accepted $\Delta\Delta$ CT method (Livak & Schmittgen, Methods; 2001). In this term, the first Δ refers to the relative difference between target and housekeeping gene within a sample (Δ CT), the second Δ refers to the relative difference between Δ CT in the baseline and 24 hr samples. The value of $\Delta\Delta$ CT equates to fold change from baseline in the target gene.

Table S1. Transcript name abbreviations

Abbreviation	Transcript name
AQP4	aquaporin 4
ASPA	aspartoacylase
ATP2B2	ATPase, Ca ⁺⁺ transporting, plasma membrane 2
ATP5G3	ATP synthase, H ⁺ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)
BCHE	butyrylcholinesterase
CCL19	chemokine (C-C motif) ligand 19
CCNG1	cyclin G1
CCNG2	cyclin G2
CD38	CD38 molecule
CDK2	cyclin-dependent kinase 2
CDKN2C	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
CES2	carboxylesterase 2
CHI3L1	chitinase 3-like 1 (cartilage glycoprotein-39)
CLCN1	chloride channel, voltage-sensitive 1
CSDE1	cold shock domain containing E1, RNA-binding
CTSL	cathepsin L
CYBA	cytochrome b-245, alpha polypeptide
DYSF	dysferlin
EIF2B4	eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa
EIF4H	eukaryotic translation initiation factor 4H
ETFB	electron-transfer-flavoprotein, beta polypeptide
FADS3	fatty acid desaturase 3
FANCA	Fanconi anemia, complementation group A
FOS	FBJ murine osteosarcoma viral oncogene homolog
GLRX2	glutaredoxin 2
HSPA5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
IL10	interleukin 10
IL6	interleukin 6
IRS1	insulin receptor substrate 1
ITGB6	integrin, beta 6
JUN	jun proto-oncogene
LTC4S	leukotriene C4 synthase
MDH1	malate dehydrogenase 1, NAD (soluble)
MFAP4	microfibrillar-associated protein 4
MGST2	microsomal glutathione S-transferase 2
MN1	meningioma (disrupted in balanced translocation) 1
MSTN	myostatin
MYC	v-myc avian myelocytomatosis viral oncogene homolog
MYLPF	myosin light chain, phosphorylatable, fast skeletal muscle

NDUFS3	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
NPY6R	neuropeptide Y receptor Y6 (pseudogene)
OSTM1	osteopetrosis associated transmembrane protein 1
P2RX5	purinergic receptor P2X, ligand gated ion channel, 5
PCCB	propionyl CoA carboxylase, beta polypeptide
PLA2G4C	phospholipase A2, group IVC (cytosolic, calcium-independent)
PPARD	peroxisome proliferator-activated receptor delta
PPIA	peptidylprolyl isomerase A (cyclophilin A)
PXMP4	peroxisomal membrane protein 4, 24kDa
RASGRP3	RAS guanyl releasing protein 3 (calcium and DAG-regulated)
RELA	v-rel avian reticuloendotheliosis viral oncogene homolog A
RELB	v-rel avian reticuloendotheliosis viral oncogene homolog B
RRAD	Ras-related associated with diabetes
RUNX1	runt related transcription factor 1
SERPINB1	serpin peptidase inhibitor, clade B (ovalbumin), member 1
SIRT2	sirtuin 2
SLC25A11	solute carrier family 25 (mitochondrial carrier; oxoglutarate carrier), member 11
SLC25A12	solute carrier family 25 (aspartate/glutamate carrier), member 12
SLC25A36	solute carrier family 25 (pyrimidine nucleotide carrier), member 36
SOAT1	sterol O-acyltransferase 1
SOD2	superoxide dismutase 2, mitochondrial
SORCS1	sortilin-related VPS10 domain containing receptor 1
SPAG7	sperm associated antigen 7
TIMP1	TIMP metalloproteinase inhibitor 1
TNFRSF11A	tumor necrosis factor receptor superfamily, member 11a, NFkB activator
TP53	tumor protein p53
TPM1	tropomyosin 1 (alpha)
UCRC	ubiquinol-cytochrome c reductase, complex III subunit X
UQCRC1	ubiquinol-cytochrome c reductase core protein I
UQCRCF1	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
VDAC3	voltage-dependent anion channel 3
YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta

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28 Results.

29 In order to further investigate the function of the 14 genes commonly regulated by both RE and
30 NMES, targets and expression values were interrogated using Ingenuity Pathway Analysis (IPA;
31 QIAGEN Redwood City, USA www.qiagen.com/ingenuity).

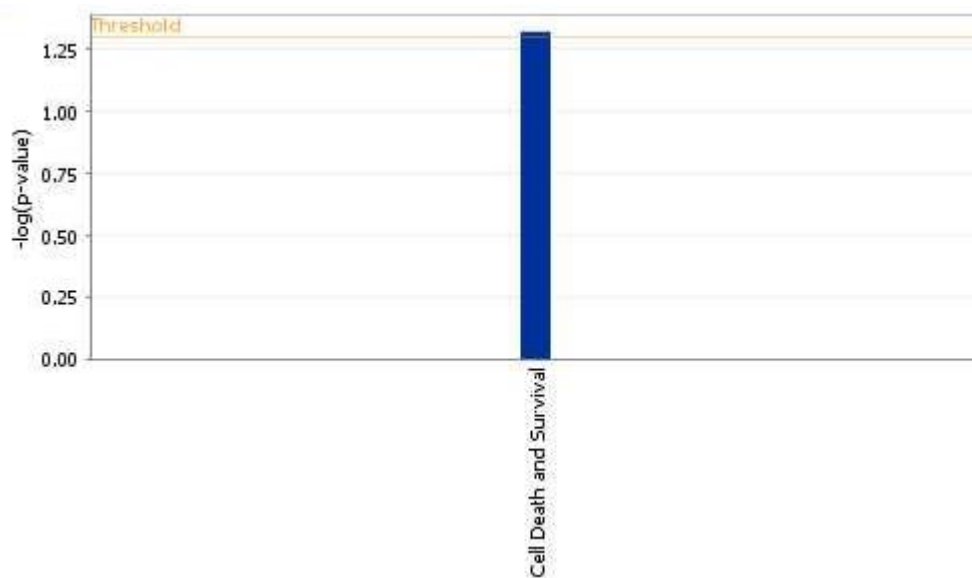


Figure S1. Probability of influence on the cellular function (*Cell Death and Survival*) identified by IPA.

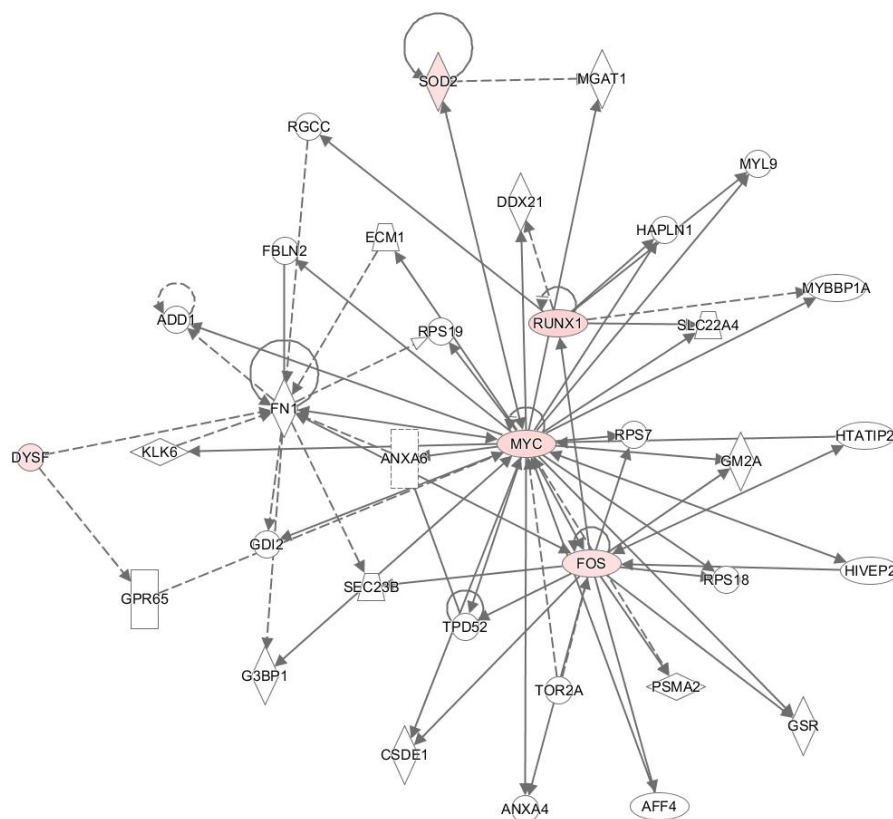


Figure S2. Network of gene interactions within the *Cell Death and Survival* function. Targets coloured pink were significantly changed in abundance following both RE and NMES.

Table S2. Mean Fold Change ($2^{-\Delta\Delta Ct}$) between baseline and sample obtained 24 h after either resistance exercise (RE) or transcutaneous neuromuscular electrical stimulation (NMES).

RE	
Gene	Mean $2^{-\Delta\Delta Ct}$
NFKBIA	0.97
RELA	1.95
TP53	2.40
MYC	11.55
CFLAR	0.68
E2F1	1.57
ACTN3	6.16
SLC25A4	0.71
DAXX	1.55
DECR1	0.76
FLNC	1.76
HSPB2	1.31
IL18	0.81
ACAA1	0.83
APOA2	Undetected
APOC1	1.38
BPGM	1.09
CAST	1.72
DCI	1.11
FLII	0.93
GLP1R	0.09
GOT1	0.89
GPX4	0.89
KCNN3	2.44
KCNN4	6.13
LAMB1	1.43
MN1	0.58
MYOD1	1.53
NDUFB5	0.79
NDUFC1	0.70
NDUFS8	0.88
PGM1	0.51
PSMB10	1.43
PSMD3	1.06
PTPN3	0.98
ST3GAL1	0.81
SOAT1	2.51
TFR2	1.45

UQCRC1	0.69
ASPA	0.51
GAMT	0.62
NCF1C;NCF1;NCF1B	2.51
PGAM2	0.65
TPM1	0.66
PCCB	0.69
RYR1	0.66
SOD2	3.62
ACACA	2.06
HPGD	1.34
ITGB6	0.55
LTC4S	0.59
INSR	0.79
CDH13	0.76
DPT	0.72
FOS	8.72
CCL22	4.71
CCNG1	0.70
CCNG2	0.58
CCL19	21.65
TIMP1	11.17
MRAS	1.97
MGMT	0.90
ENDOG	0.84
BRCA1	1.07
ANKRD1	8.77
IL10	17.10
IL1A	1.00
TNF	4.43
IL6	51.26
ITGA7	0.79
NFKB2	2.11
AK1	0.75
CDKN2C	0.65
CKMT2	0.97
PDK2	0.67
PDK4	2.73
PI4KAP2;PI4KA;PI4KAP1	1.08
MAP2K3	1.40
SQSTM1	1.07
AKT1	1.45
IRS1	0.51
MAP3K12	1.32
FASTK	11.90
CHRNE	1.88

FASLG	1.90
CHRNA1	0.75
CHRNA2	2.71
MGST2	0.72
SRF	1.04
ATP5D	0.85
IRF7	0.16
MFAP5	1.00
ACOX2	1.26
SLC25A11	0.65
SLC25A12	0.65
TNFRSF11A	5.01
CES2	2.47
MYOM2	0.75
EIF2S1	1.65
RRAD	11.29
SDHA	0.67
BAD	38.13
CLCN2	1.72
CHKB;CPT1B	0.63
CTSH	0.96
FHL3	0.57
NDUFA10	0.83
NDUFS3	0.84
POLR1C	2.18
SPAG7	0.75
MYBPH	5.29
NDUFS1	0.75
RPL3L	0.55
GNG7	0.67
COX6A2	0.66
MSTN	0.39
GRB10	1.44
MAF	0.67
PDLIM7	0.78
ARPC4	1.81
PPIF	1.67
FARP1	1.68
MDH1	0.67
S100A13	1.05
CCT3	1.50
AKR1A1	1.47
PECI	0.72
GMPR	0.66
UPK3A	0.54
ADRM1	1.13

RPP14	1.83
NDUFV1	0.79
CSDE1	0.74
ADAT1	1.28
CA14	1.05
GRHPR	0.77
MORF4L2	1.96
ICMT	3.17
MYLPF	0.57
UCRC	0.75
OSTM1	1.59
BZW2	1.06
PKD2L2	Undetected
ZNF330	1.07
CDC42BPA	1.20
RASGRP3	0.61
NPDC1	1.34
GSTK1	0.87
CYLD	1.53
MRPS33	0.81
BRP44L	1.63
PPME1	0.92
HP1BP3	0.93
SLC25A36	0.62
ZC3H15	1.37
ZMAT5	0.71
TNXB	Undetected
NT5M	1.28
ANK1	2.37
NDUFV2	0.87
XRCC5	1.23
RRAGD	0.90
FADS3	3.36
SIGIRR	1.55
UCP1	Undetected
TSPYL2	2.34
GNB1L	1.08
UBE2Z	1.75
PSTPIP2	1.22
CARS2	1.23
VCPIP1	1.06
SERPINB1	13.35
MRPS15	0.82
RUNX1	12.59
LMO1	0.91
MEF2C	0.64

MYOG	0.92
SMARCA4	1.76
CNBP	0.80
RUNX3	2.39
CREB1	1.09
PPARA	0.71
RELB	4.36
IL12B	Undetected
PLA2G4C	0.59
MMP2	1.02
DAPK1	3.52
FRAP1	1.01
YWHAZ	3.01
ACTN1	2.33
ANXA6	1.04
AQP4	0.42
CBFB	2.60
MRPL12	1.11
DYSF	4.18
ACCN3	0.81
NDUFA9	0.70
NPY6R	0.50
SIRT2	0.67
TOR1B	1.60
EIF2B4	1.74
ABR	2.87
EIF4H	3.14
GNRHR2;RBM8A	1.03
OLFM1	1.56
FARS2	1.11
RABL2A;RABL2B	2.00
WBP11	1.10
NDUFS7	1.36
SLC37A4	1.27
TRIM63	2.56
MYL3	0.64
DNAJA1	1.53
ATP5G3	0.79
COX6B1	0.81
PRKAR1A	1.50
SMARCC1	1.74
TBCC	0.98
TNNI2	0.75
PKP4	1.25
IDH1	0.74
PRMT5	1.56

CCT4	1.26
MRCL3	0.89
ATP5I	1.16
DNAJB5	Undetected
RPS27L	2.04
TPRKB	1.10
GSK3B	1.19
SIVA1	0.79
CCND1	1.12
CD38	0.61
JUN	0.64
C22orf9	1.26
LGALS1	1.08
INS	Undetected
ALDH2	0.72
SFN	Undetected
HSPB1	0.89
CYC1	0.73
FNTA	1.39
NOL3	0.81
SLC16A3	1.02
DEXI	0.88
SORCS1	0.51
MYL1	0.66
TCAP	0.60
VDAC3	0.69
ARS2	1.66
PACSIN3	0.74
FBXO32	1.05
COX7B	0.79
GLRX2	1.47
SYNGR1	0.78
CTSL1	5.35
TBC1D22A	1.19
KIAA0368	0.95
DYNC1H1	0.87
CTNNA3	0.80
PREPL	1.77
OSBP	0.88
PSME1	1.07
LRP4	1.28
CCPG1	1.09
IKBKB	1.36
LIAS	0.91
MFAP4	0.53
AKR1C2;AKR1C1	1.03

CDC2L1;CDC2L2	1.02
CALCOCO2	1.22
ADK	1.00
CLIP1	0.66
ACO2	0.94
CTSL2	Undetected
ATP5O	0.75
COX5B	0.75
PSMB1	1.13
PSMD7	1.18
SFRS2	6.11
FBP2	0.74
NDUFB8	0.84
RTN3	12.97
MAN2C1	1.06
TXN2	0.83
ARTS	1.52
P2RX5	4.20
MARS2	1.48
FADD	2.59
CAPN3	0.77
ACTA1	0.75
ANXA7	1.00
UQCRB	0.75
CHAF1B	0.67
PRDX1	1.09
PPARD	2.48
PPP2R4	1.25
GPSN2	0.73
ALDOA	0.78
RPL38	0.92
EIF4EBP1	1.02
CDK2	3.08
CYBA	2.06
HMBS	1.00
CHI3L1	59.28
AARS	1.04
KALRN	1.37
DLG5	2.32
MLL	0.96
UQCRFS1	0.71
TOX4	1.18
CCR10	1.06
CDK2AP2	2.26
ANP32B	1.35
NAP1L1	1.20

PRPS1	1.29
MYH4	3.60
PKM2	1.06
NFKB1	1.62
EIF3K	0.87
FOXO3	0.87
NSFL1C	1.02
ZFAND5	1.79
ATP5G1	1.02
EIF2S2	Undetected
PLA2G12A	2.15
MKRN1	1.09
SYNGR2	1.82
LDHA	1.51
POLRMT	2.90
GPC1	0.88
CLCN1	0.50
LARGE	2.04
GBP2	1.89
DLAT	0.75
MAPT	0.81
ATF4	1.30
SOCS2	2.44
SVIL	0.61
MDH2	2.05
CTSB	2.14
ADARB1	0.76
REL	1.13
DUSP13	0.71
ATP5B	0.80
COX4I1	0.81
GPI	1.01
AMPD3	2.92
PYGM	0.66
BCHE	0.45
UQCRC2	0.76
VCP	1.13
COL4A1	2.47
PMVK	2.33
CASP10	1.19
KCNN2	1.67
HSPA1B	1.63
FOXO1	0.80
IKBKE	3.82
RXRA	0.84
HRASLS	0.82

ETFB	0.69
ATP2B2	0.38
RUVBL2	1.09
ATP2A1	0.53
RFX2	2.13
DGKD	2.69
FANCA	5.81
TRIB2	1.44
PSAP	1.01
DBI	1.02
PXMP4	0.74
TPI1	0.83
COX7C	1.68
LOC654007;EEF1G	0.79
PSME2	1.94
CDC2L2	2.15
HSPA5	3.17
PPIA	3.87
HPRT1	1.80
TGFB1	1.76

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NMES

Detector	Mean Fold Change (2 ^{ΔΔCt})
NFKBIA	1.09
RELA	3.13
TP53	4.42
MYC	10.35
CFLAR	0.77
E2F1	1.11
ACTN3	0.94
SLC25A4	0.62
DAXX	1.75
DECR1	0.79
18S	0.75
18S	0.79
FLNC	2.65
HSPB2	0.74
IL18	0.75
ACAA1	0.80
APOA2	Undetected
APOC1	1.39
BPGM	1.07

CAST		1.99
ECI1		0.98
FLII		1.23
GLP1R	Undetected	
GOT1		0.79
GPX4		0.87
KCNN3		4.83
KCNN4		4.00
LAMB1		1.30
MN1		0.43
MYOD1		1.36
NDUFB5		0.75
NDUFC1		0.74
NDUFS8		0.94
PGM1		0.74
18S		0.84
18S		0.83
PSMB10		0.91
PSMD3		1.53
PTPN3		1.38
ST3GAL1		0.89
SOAT1		3.05
TFR2		1.00
UQCRC1		0.62
ASPA		0.64
GAMT		0.70
NCF1C;NCF1B;NCF1		1.81
PGAM2		0.73
TPM1		0.61
PCCB		0.72
RYR1		0.94
SERPINE1		15.74
SOD2		3.64
ACACA		2.55
HPGD		1.21
ITGB6		0.69
LTC4S		0.46
INSR		1.20
CDH13		1.09
DPT		0.53
FOS		17.63
CCL22		12.94
CCNG1		0.88
CCNG2		0.53
CCL19		9.76
TIMP1		16.67

MRAS	2.60
MGMT	0.84
ENDOG	0.83
BRCA1	0.78
ANKRD1	7.22
IL10	5.20
IL1A	2.03
TNF	3.01
IL6	25.79
ITGA7	0.89
NFKB2	2.54
AK1	0.76
CDKN2C	0.77
CKMT2	0.92
PDK2	0.84
PDK4	3.12
PI4KA;PI4KAP1;PI4KAP2	1.40
MAP2K3	1.37
SQSTM1	1.29
AKT1	1.42
IRS1	0.63
MAP3K12	1.18
FASTK	1.27
CHRNE	1.09
FASLG	2.29
CHRNA1	0.98
CHRNA2	4.13
MGST2	0.82
SRF	1.42
ATP5D	0.68
IRF7	2.09
MFAP5	0.75
ACOX2	0.63
SLC25A11	0.71
SLC25A12	0.74
TNFRSF11A	5.92
CES2	4.91
MYOM2	0.88
EIF2S1	1.77
RRAD	10.29
SDHA	0.82
BAD	1.08
CLCN2	0.83
CPT1B;CHKB	0.80
CTSH	1.08
FHL3	0.84

NDUFA10	0.76
NDUFS3	0.64
POLR1C	2.70
SPAG7	0.96
MYBPH	10.83
NDUFS1	0.82
RPL3L	0.71
GNG7	0.75
COX6A2	0.92
MSTN	0.53
GRB10	1.73
MAF	0.79
PDLIM7	0.98
ARPC4	1.85
PPIF	1.76
FARP1	2.10
MDH1	0.87
S100A13	1.53
CCT3	1.74
AKR1A1	1.30
ECI2	0.93
GMPR	0.78
UPK3A	0.78
ADRM1	1.19
RPP14	1.51
NDUFV1	0.79
CSDE1	1.06
ADAT1	1.49
CA14	0.58
GRHPR	0.71
MORF4L2	3.97
ICMT	3.36
MYLPF	0.62
UQCR10	0.86
OSTM1	1.41
BZW2	1.41
PKD2L2	Undetected
ZNF330	1.57
CDC42BPA	1.06
RASGRP3	0.62
NPDC1	4.29
GSTK1	0.85
CYLD	1.54
MRPS33	0.68
MPC1	1.11
PPME1	1.07

HP1BP3		1.05
SLC25A36		0.85
ZC3H15		1.90
ZMAT5		0.86
	Undetected	
NT5M		1.08
ANK1		2.84
NDUFV2		1.14
XRCC5		1.37
RRAGD		1.41
FADS3		3.68
SIGIRR		1.04
UCP1	Undetected	
TSPYL2		1.00
GNB1L		1.44
UBE2Z		1.72
PSTPIP2		1.26
CARS2		1.03
VCPIP1		2.20
MRPS15		0.89
RUNX1		15.74
LMO1		1.37
MEF2C		0.85
MYOG		1.66
SMARCA4		2.21
CNBP		1.01
RUNX3		3.49
CREB1		1.11
PPARA		0.73
RELB		5.84
IL12B	Undetected	
PLA2G4C		0.65
MMP2		0.99
DAPK1		1.51
MTOR		1.21
YWHAZ		5.03
ACTN1		1.70
ANXA6		1.05
AQP4		0.42
CBFB		2.77
MRPL12		1.26
DYSF		6.19
ASIC3		1.06
NDUFA9		1.02
NPY6R		0.67
SIRT2		2.89

TOR1B		1.83
EIF2B4		2.10
ABR		1.48
EIF4H		3.21
GNRHR2;RBM8A		1.03
OLFM1		1.37
FARS2		0.99
RABL2B;RABL2A		2.04
WBP11		1.43
NDUFS7		0.73
SLC37A4		0.63
TRIM63		2.88
MYL3		1.55
DNAJA1		1.53
ATP5G3		0.64
COX6B1		1.02
PRKAR1A		1.64
SMARCC1		1.76
TBCC		0.87
TNNI2		0.91
PKP4		1.33
IDH1		0.83
PRMT5		1.88
CCT4		1.57
MYL12A		1.28
ATP5I		0.75
DNAJB5		4.09
TPRKB		1.17
GSK3B		1.25
SIVA1		1.00
CCND1		1.25
CD38		0.62
JUN		1.07
KIAA0930		1.31
LGALS1		0.90
INS	Undetected	
ALDH2		0.68
	Undetected	
HSPB1		1.22
CYC1		0.86
FNTA		2.10
NOL3		0.83
SLC16A3		0.72
DEXI		1.02
SORCS1		0.85
MYL1		0.84

TCAP	1.01
VDAC3	1.18
SRRT	2.22
PACSIN3	0.80
FBXO32	0.87
COX7B	1.20
GLRX2	1.38
SYNGR1	0.79
CTSL	5.23
TBC1D22A	1.32
KIAA0368	1.10
DYNC1H1	0.88
CTNNA3	0.62
PREPL	1.73
OSBP	1.08
PSME1	1.41
LRP4	0.79
DYX1C1	1.14
IKBKB	1.64
LIAS	0.86
MFAP4	0.59
AKR1C2;AKR1C1	1.15
CDK11B;CDK11A	1.17
CALCOCO2	0.80
ADK	1.39
CLIP1	0.99
ACO2	0.84
CTSV	Undetected
ATP5O	0.85
COX5B	0.90
PSMB1	1.48
PSMD7	1.28
SRSF2	2.27
FBP2	0.59
NDUFB8	0.81
RTN3	1.14
MAN2C1	1.13
TXN2	0.79
ERAP1	1.16
P2RX5;P2RX5	4.94
MARS2	1.82
FADD	1.81
CAPN3	1.09
ACTA1	1.11
ANXA7	1.20
UQCRB	0.85

CHAF1B	0.96
PRDX1	1.29
PPARD	2.29
PPP2R4	1.19
TECR	0.73
ALDOA	0.79
RPL38	1.06
EIF4EBP1	1.06
CDK2	3.19
CYBA	1.51
HMBS	1.00
CHI3L1	84.44
AARS	1.13
KALRN	1.60
DLG5	2.65
KMT2A	1.26
UQCRCF1	0.67
TOX4	1.33
CCR10	1.52
CDK2AP2	2.71
ANP32B	1.81
NAP1L1	1.51
PRPS1	1.84
MYH4	0.69
PKM	1.06
NFKB1	1.79
EIF3K	1.35
FOXO3	1.18
NSFL1C	1.13
ZFAND5	2.24
ATP5G1	0.89
EIF2S2	Undetected
PLA2G12A	0.76
MKRN1	1.35
SYNGR2	1.77
LDHA	1.66
POLRMT	1.07
GPC1	1.12
CLCN1	0.62
LARGE	1.31
GBP2	1.91
DLAT	0.93
MAPT	0.80
ATF4	1.49
SOCS2	2.15
SVIL	0.73

MDH2	1.34
CTSB	3.26
ADARB1	0.70
REL	2.07
DUSP13	0.80
ATP5B	1.35
COX4I1	0.93
GPI	1.02
AMPD3	5.57
PYGM	0.64
BCHE	0.69
UQCRC2	0.83
VCP	1.40
COL4A1	2.41
PMVK	0.75
CASP10	1.11
KCNN2	0.71
HSPA1B	2.33
FOXO1	0.79
IKBKE	2.08
RXRA	0.78
HRASLS	0.83
ETFB	0.72
ATP2B2	0.37
RUVBL2	1.57
ATP2A1	0.51
RFX2	1.28
DGKD	3.06
FANCA	3.49
TRIB2	1.32
PSAP	1.03
DBI	1.37
PXMP4	0.75
TPI1	0.84
COX7C	0.99
RPL12	1.27
EEF1G	0.92
PSME2	1.34
CDK11B;CDK11A	1.39
HSPA5	3.72
PPIA	4.11
HPRT1	2.62
TGFB1	2.59