Supplemental Information

Supplemental Methods

10-fraction LC/LC-MS/MS sample preparation. Three WT and 3 KO 4-week-old quadriceps samples were used. To each sample, 8M urea in 50 mM ammonium bicarbonate, pH 8.0 was added at a constant 10 uL per mg of tissue. Samples were then subjected to mechanical disruption using a Tissue Tearer followed by 2 rounds of probe sonication on ice at 30% power. Samples were spun to remove insoluble material and 4 uL was removed and subjected to a Bradford assay to determine total protein quantity. Protein concentrations ranged from 8.4 mg/ml to 11.7 mg/ml corresponding to between 8.4% and 11.7% solubilization rate. This range is within other experiments from muscle tissue. From each sample, 100 ug of total protein was removed and concentrations were normalized. Samples were then diluted 1.6M urea with 50 mM ammonium bicarbonate. All samples were then reduced for 20 min at 80C with 10 mM dithiolthreitol and alkylated for 40 min at room temperature with 25 mM iodoacetamide. Trypsin was added to a 1:50 ratio (enzyme to total protein) and allowed to proceed for 18 hr at 37C. Samples were then acidified with 0.2% TFA (pH 2.5) and subjected to C18 SPE cleanup (Sep-Pak, 50 mg bed). Following elution, all samples were then frozen and then lyophilized to dryness.

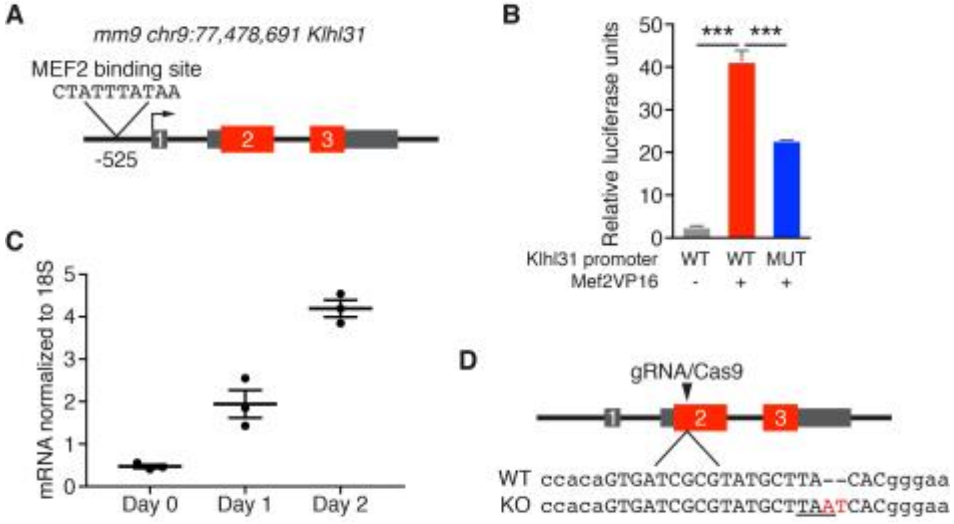
TMT Labeling Procedure. Each sample was resuspended in 100 µL 200 mM triethylammonium bicarbonate, pH 8.0 (TEAB). Fresh TMT reagents (0.8 mg for each 6-plex reagent) was resuspended in 100 µL 100% acetonitrile (ACN). 50 uL of each TMT tag was added to a specific sample (126-128 to KO samples, 129-131 to WT samples) and were incubated for 4 hours at RT (at 2 hour time point, spin down and vortex manually before replacing on auto-vortex tube holder for another 2 hours at a low setting). After 4 hour reaction, 8 μL 5% hydroxylamine was added to quench the reaction. 20% of each sample (31.6 uL) were combined at a 1:1:1:1:1:1 ratio and was then lyophilized to dryness prior to LC- MS/MS analysis. The remaining portion of each sample was stored in -80C.

Quantitative Analysis, Methods. Quantitative two-dimensional liquid chromatography – tandem mass spectrometry (LC/LC-MS/MS) was performed on approximately 7.5 μg of protein digest per sample. The method uses two-dimensional liquid chromatography in a high-low pH reversed phase/reversed phase configuration on a nanoAcquity UPLC system (Waters Corp) coupled to a Thermo QExactive Plus high resolution accurate mass tandem mass spectrometer with nanoelectrospray ionization. Peptides were first trapped at 2 μl/min at 97/3 v/v water/MeCN in 20 mM ammonium formate (pH 10) on a 5 μm XBridge BEH130 C18 300 um × 50 mm column (Waters). A series of step-elutions of MeCN at 2 μl/min was used to elute peptides from the 1st dimension column. Ten steps of 14.0%, 16.0%, 17.3%, 18.5%, 20.3%, 22.0%, 23.5%, 25.0%, 30.0%, and 50.0% MeCN were utilized for the analyses; these percentages were optimized for delivery of an approximately equal load to the 2nd dimension column for each fraction. For 2nd dimension separation, the eluent from the 1st dimension was first diluted 10-fold online with 99.8/0.1/0.1 v/v/v water/MeCN/formic acid and trapped on a 5 μm Symmetry C18 180 μm × 20 mm trapping column (Waters). The 2nd dimension separations were performed using a 1.7 um Acquity BEH130 C18 75 mm × 250 mm column (Waters Corp.) using a 90-min gradient of 3 to 25% acetonitrile with 0.1% formic acid at a flow rate of 400 nanoliters/minute (nL/min) with a column temperature of 55C. Data collection on the QExactive Plus mass spectrometer was performed in a data-dependent acquisition (DDA) mode of acquisition with a r=70,000 (@ m/z 200) full MS scan from m/z 375 – 1600 with a target AGC value of 1e6 ions followed by 20 MS/MS scans at r-17,500 (@ m/z 200) at a target AGC value of 5e4 ions. A 30s dynamic exclusion was employed to increase depth of coverage. The total analysis cycle time for each sample injection was approximately 2-hours.

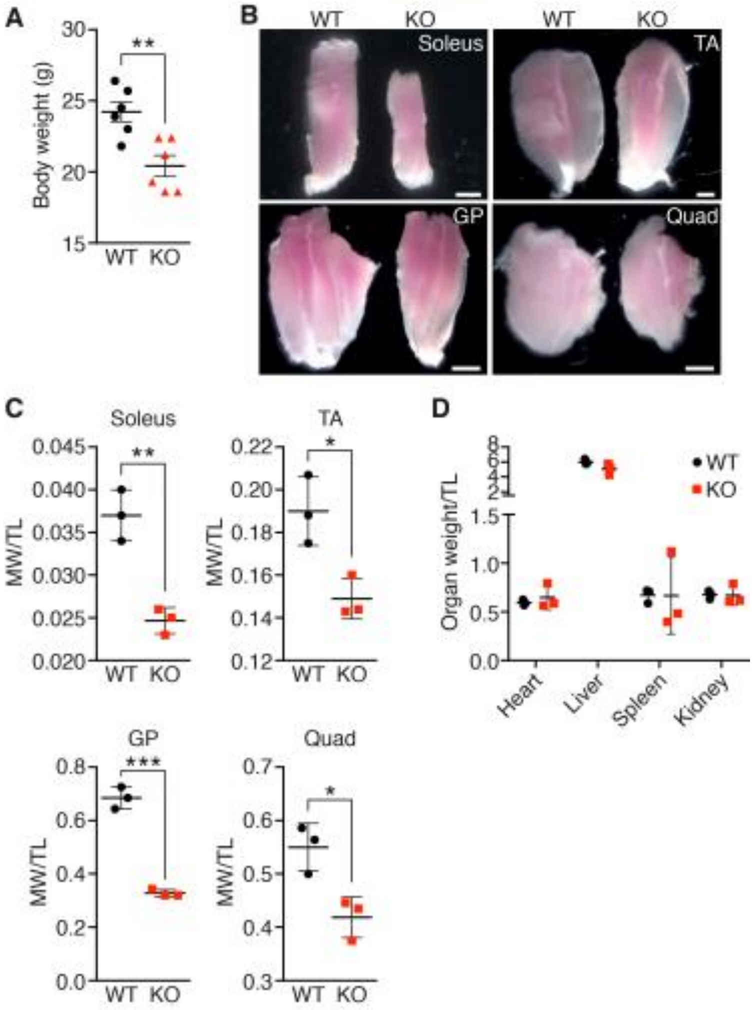
Following the 10 LC-MS/MS analyses, raw data were processed by Protein Discoverer to create .MGF files. This MS/MS data was searched against a SwissProt_Mouse database within Mascot Server (Matrix Science) which also contained a reversed-sequence “decoy” entry for each protein for false positive rate determination. Searching allowed variable M (oxidation, +15.995 Da) and TMT modifications on Lys and peptide N-termini (+229.163 Da) as well as static carboxyamidomethylated Cys residues (from Cys alkylations). Search tolerances were 5 ppm precursor and 0.02 Da product ions with full trypsin protease rules and up to two missed cleavages. Search results were imported to Scaffold Q+S v4.4.6 (Proteome Software) and data was annotated at a Protein False Discovery Rate of 1.0%. The overall dataset yielded 28,538 total identified MS/MS spectra acquired over the ten fractions - including redundant identifications. These 28,538 peptides corresponded to 2,106 TMT labeled proteins. To perform quantitative analysis on these 28,538 TMT labeled peptides, only peptides uniquely identified to a protein were considered. To normalize the six different channels to account of differences in labeling efficiencies and mixing percentages, we calculated the summed intensity for each channel. Each channel was then normalized to the average of all 6 channels. Following this peptide level normalization, protein level intensities were generated by summing all of the unique peptide intensities to that protein.

Data QC and Outlier Screening. To assess processing vs biological variability, the intensity-scaled expression data was used to calculate coefficient of variations for each protein across processing replicates (channel 126-128 and 129-131) and across all replicates (channel 126-131). For this particular replicate, the average CV of protein expression within the KO group was 14.1%, within the WT group was 13.0%, and across both KO and WT was 23.0%. As expected, the variation across both WT and KO groups was the highest because of the additional biological variation imparted by the *Klhl31* KO. To group the samples within an LC-MS/MS analysis based on protein expression, we performed 2D Principle Component Analysis on Log2 transformed protein expression values. Initial Statistical Processing. To identify differences between WT and *Klhl31* KO animals, a two-tailed ttest was performed on log2 protein intensity. Fold changes were calculated for the same comparisons by diving the average intensity of the KO animals by the WT animals. We then calculated the negative in KO relative to WT it would have a negative direction. To consider something differentially expressed between the groups, we required a p-value < 0.05 and a fold-change of 50%. This fold-change was chosen based on the average processing variation (i.e. average CV of the WT or KO group) and a statistical power calculator (https://www.dssresearch.com/KnowledgeCenter/toolkitcalculators/statisticalpowercalculators.aspx) set to an alpha value of 5%.

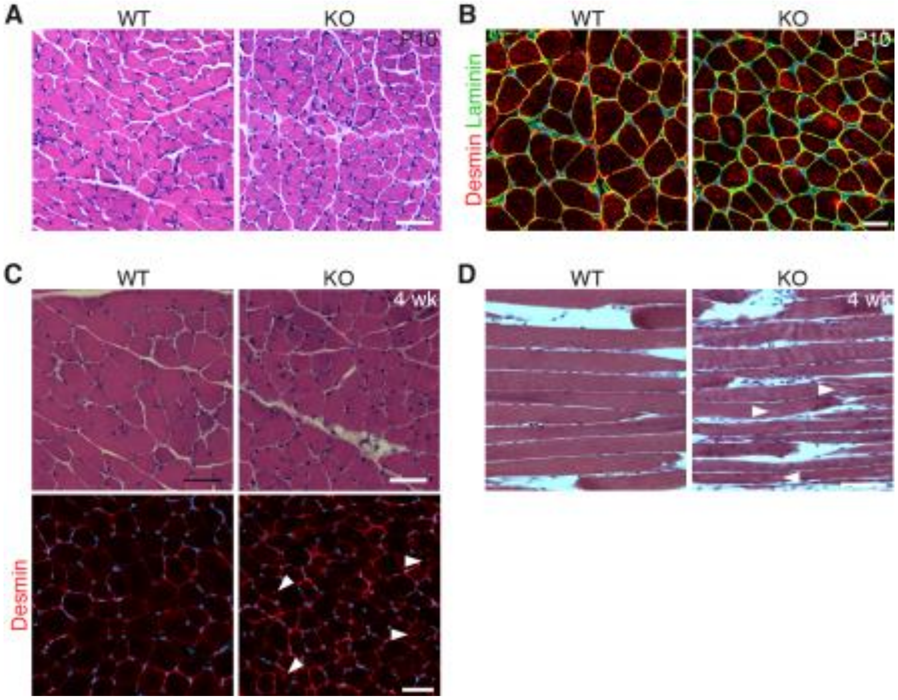
Supplemental Figures



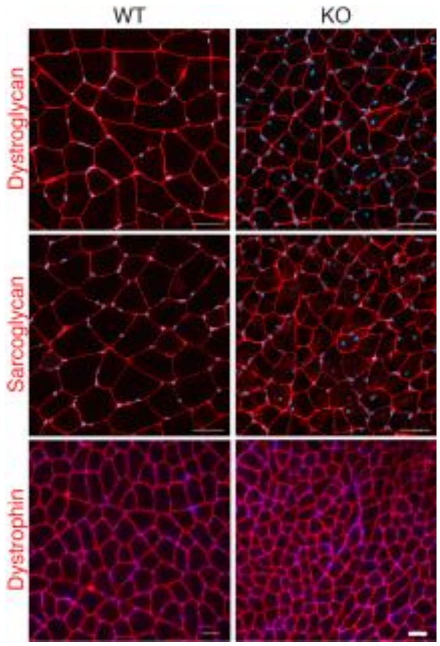
Supplemental Figure 1. *Klhl31* is a MEF2 responsive gene. (**A**) Schematic of the *Klhl31* gene structure highlighting the conserved MEF2 binding site. (**B**) A 2 kb fragment of the *Klhl31* promoter cloned into the pGL3b vector has no activation alone (grey bar). When MEF2-VP16 is co-transfected with the *Klhl31* promoter, we observed about a 40-fold induction of luciferase activity (red bar). A 50% decrease in luciferase activity was observed when the MEF2 consensus sequence is mutated (blue bar). (n = 3). *** $P < 0.001$. Data are represented as mean ± SEM. (**C**) *Klhl31* expression in differentiating C2C12 myoblasts. Day 0 is the day prior to the addition of serum-free differentiation media. Each dot represents the mean of one experiment. (n = 3). (**D**) Schematic of CRISPR-Cas9 gene targeting. A single gRNA was designed (crispr.mit.edu) to target the second exon. The uppercase font represents the gRNA. The red font in the KO sequence represents the 2 bp insertion, and the underlined text represents the TAA stop codon. Statistical analyses were performed using an unpaired two-tailed Student's t-test.



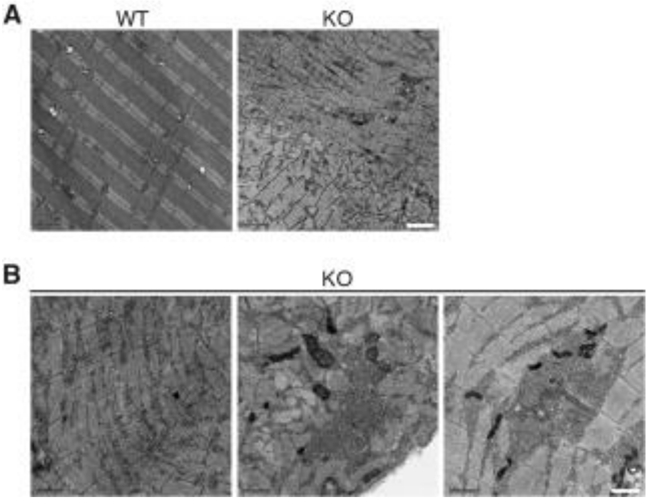
Supplemental Figure 2. Decreased body weight in *Klhl31* KO mice can be attributed to a decrease in muscle weight. (**A**) Body weight of WT and *Klhl31* KO mice at 6-weeks of age. (*n* = 6 for both genotypes). ** *P* < 0.01. Data are represented as mean ± SEM. (**B**) Representative images of different hindlimb muscle groups from 6-week-old WT and *Klhl31* KO mice. Scale bar for soleus and TA: 1 mm. Scale bar for GP and quad: 2 mm. (**C**) Muscle weight of WT and *Klhl31* KO mice normalized to tibia length. (*n* = 3 for both genotypes). * *P* < 0.05, ** *P* < 0.01, *** *P* < 0.001. Data are represented as mean ± SD. (**D**) Organ weight of WT and *Klhl31* KO mice at 6-weeks of age normalized to tibia length (*n* = 3 for both genotypes). Data are represented as mean ± SD. Statistical analyses were performed using an unpaired two-tailed Student's *t*-test.



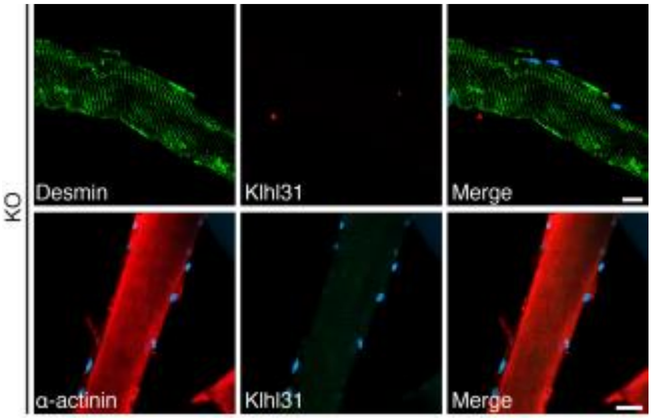
Supplemental Figure 3. Skeletal muscle pathology in *Klhl31* KO mice. (**A**) H&E staining of WT and *Klhl31* KO quadriceps at P10. Scale bar: 50 µm. (**B**) Immunohistochemistry of WT and *Klhl31* KO muscle at P10 using desmin (red) and laminin (green) antibody. Nuclei are correctly positioned and there is little evidence of desmin aggregation. Scale bar: 20 µm. (**C**) H&E staining (top panels) and immunohistochemistry (bottom panels) of WT and *Klhl31* KO mice at 4 weeks of age. Desmin aggregation (arrowheads) are seen in Klhl31 KO mice. Scale bar: 50 µm. (**D**) H&E stain of longitudinal quadriceps of WT and *Klhl31* KO mice at 4-weeks of age. Smaller myofibers and paucity of sarcomere proteins (arrowheads) is seen in KO muscle (*n* = 3 for both genotypes).



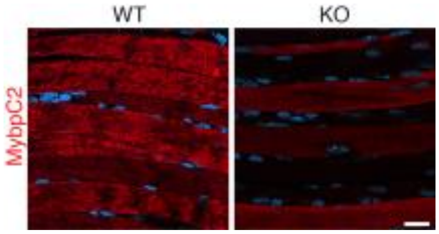
Supplemental Figure 4. Normal membrane protein expression in *Klhl31* KO mice. Representative images of immunohistochemistry of WT and *Klhl31* KO quadriceps at 12-weeks of age. Myonuclear internalization and normal expression of the sarcolemmal-associated proteins dystroglycan (top panel), sarcoglycan (middle panel), and dystrophin (bottom panel) is seen. Scale bars: 50 µm. (*n* = 3 for both genotypes).



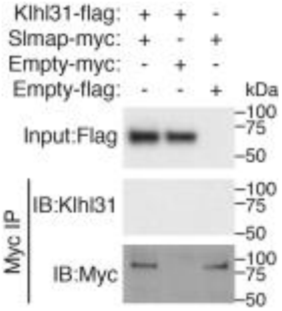
Supplemental Figure 5. Sarcomeric disarray and sarcotubular expansion and dilation in 7-month old *Klhl31* KO mice. Transmission electron microscopic images showing (**A**) sarcomeric disarray, loss of contractile elements, Z-line discontinuity, and SR expansion in KO muscle. Scale bar: 1 µm (**B**) Representative images of the dilated and rearranged SR network in KO mice. Scale bar: 2 µm.



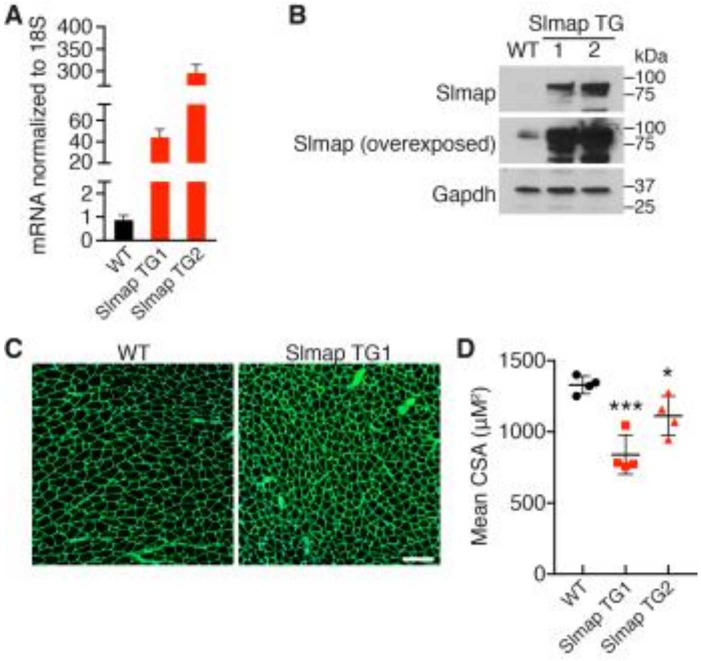
Supplemental Figure 6. Immunohistochemistry of *Klhl31* KO muscle. (**A**) Isolated myofibers from *Klhl31* KO quadriceps co-stained with desmin and *Klhl31* (top) or α-actinin and Klhl31 (bottom) show no reactivity to the Klhl31 antibody, in contrast to the WT mice in Figure 4A and B. Scale bar: 20 µm.



Supplemental Figure 7. MybpC2 is down-regulated in *Klhl31* KO mice. Immunohistochemistry of WT and *Klhl31* KO quadriceps at 4-weeks of age demonstrates reduction of MybpC2 (red) in KO. MybpC2 is the only protein identified by proteomics as being significantly down-regulated in *Klhl31* KO muscle. Scale bar: 50 µm.



Supplemental Figure 8. Klhl31 does not bind to Slmap. Binding of Slmap and Klhl31 was not detected by co-immunoprecipitation assay in transfected COS-7 cells.



Supplemental Figure 9. Skeletal muscle-specific over-expression of *Slmap* causes stunted postnatal skeletal muscle growth. (**A**) *Slmap* transcript levels in F1 2-week-old quadriceps from WT and Slmap transgenic mouse lines TG1 and TG2. (**B**) Representative western blot analysis of WT and transgenic lines TG1 and TG2 from quadriceps. The middle panel is a longer exposure to show WT expression. (**C**) Representative immunohistochemistry of laminin staining to highlight the smaller muscle fibers in the quadriceps of Slmap TG mice. Scale bar: 100 µm. (**D**) Quantification of the mean cross sectional area in WT and Slmap transgenic lines TG1 and TG2. (*n* = 4 for all genotypes for all experiments). * $P < 0.05$, *** $P < 0.001$. Data are presented as mean ± SEM. Statistical analyses were performed using an unpaired two-tailed Student's *t*-test.

Supplemental Table 1. Differentially expressed proteins identified in the Klhl31 KO mice by proteomics.

Protein Name	Unique Peptides	ttest	fold change in KO
Sarcolemmal membrane-associated protein OS=Mus musculus GN=Slmap PE=1 SV=2	6	0.008	3.28
Smoothelin-like protein 1 OS=Mus musculus GN=Smtnl1 PE=1 SV=1	2	0.034	3.11
KAT8 regulatory NSL complex subunit 1 OS=Mus musculus GN=Kansl1 PE=1 SV=1	1	0.009	3.01
Death-associated protein kinase 2 OS=Mus musculus GN=Dapk2 PE=1 SV=1	1	0.005	2.97
SAFB-like transcription modulator OS=Mus musculus GN=Sltm PE=1 SV=1	1	0.045	2.88
Myomesin-3 OS=Mus musculus GN=Myom3 PE=1 SV=1	17	0.005	2.85
Beta-synuclein OS=Mus musculus GN=Sncb PE=1 SV=1	1	0.010	2.65
Musculoskeletal embryonic nuclear protein 1 OS=Mus musculus GN=Mustn1 PE=1 SV=1	2	0.000	2.58
Myozenin-2 OS=Mus musculus GN=Myoz2 PE=1 SV=1	1	0.046	2.51
Leukocyte elastase inhibitor A OS=Mus musculus GN=Serpinb1a PE=1 SV=1	9	0.008	2.50
Non-histone chromosomal protein HMG-17 OS=Mus musculus GN=Hmgn2 PE=1 SV=2	3	0.014	2.49
Sorbin and SH3 domain-containing protein 1 OS=Mus musculus GN=Sorbs1 PE=1 SV=2	2	0.047	2.46
Cell cycle exit and neuronal differentiation protein 1 OS=Mus musculus GN=Cend1 PE=1 SV=1	1	0.040	2.43
Histone H3.3 OS=Mus musculus GN=H3f3a PE=1 SV=2	1	0.031	2.41
Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	38	0.037	2.31
Coronin-1A OS=Mus musculus GN=Coro1a PE=1 SV=5	1	0.025	2.29
Chromobox protein homolog 1 OS=Mus musculus GN=Cbx1 PE=1 SV=1	1	0.027	2.28
Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=1 SV=2	2	0.030	2.25
Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Mus musculus GN=Uchl1 PE=1 SV=1	1	0.046	2.24
Polypyrimidine tract-binding protein 3 OS=Mus musculus GN=Ptbp3 PE=1 SV=1	1	0.032	2.21
Coactosin-like protein OS=Mus musculus GN=Cotl1 PE=1 SV=3	1	0.011	2.14
Tropomodulin-2 OS=Mus musculus GN=Tmod2 PE=1 SV=2	1	0.030	2.14
4-trimethylaminobutyraldehyde dehydrogenase OS=Mus musculus GN=Aldh9a1 PE=1 SV=1	1	0.033	2.13
Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus GN=Lrrfip1 PE=1 SV=2	1	0.010	2.13
U1 small nuclear ribonucleoprotein A OS=Mus musculus GN=Snrpa PE=1 SV=3	1	0.010	2.13
LIM and cysteine-rich domains protein 1 OS=Mus musculus GN=Lmcd1 PE=1 SV=1	11	0.015	2.10
Heat shock protein beta-7 OS=Mus musculus GN=Hspb7 PE=1 SV=3	4	0.033	2.09
Clathrin light chain A OS=Mus musculus GN=Clta PE=1 SV=2	3	0.014	2.08
Transcription elongation factor A protein-like 5 OS=Mus musculus GN=Tceal5 PE=1 SV=1	6	0.006	2.08
5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Mus musculus GN=Prkaa1 PE=1 SV=2	1	0.015	2.08
Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1	2	0.008	2.06
Non-histone chromosomal protein HMG-14 OS=Mus musculus GN=Hmgn1 PE=1 SV=2	1	0.009	2.05
Histone H2A type 2-A OS=Mus musculus GN=Hist2h2aa1 PE=1 SV=3	2	0.019	2.05
Cleavage and polyadenylation specificity factor subunit 6 OS=Mus musculus GN=Cpsf6 PE=1 SV=1	1	0.034	2.03
Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	46	0.045	2.01
Unconventional myosin-XVIIIa OS=Mus musculus GN=Myo18a PE=1 SV=2	15	0.030	2.00
Beta-parvin OS=Mus musculus GN=Parvb PE=1 SV=1	2	0.002	1.98
Protein-arginine deiminase type-2 OS=Mus musculus GN=Padi2 PE=1 SV=2	16	0.004	1.98
Drebrin-like protein OS=Mus musculus GN=Dbnl PE=1 SV=2	2	0.025	1.97

Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	1	0.014	1.97
Myelin basic protein OS=Mus musculus GN=Mbp PE=1 SV=2	7	0.045	1.97
Histone deacetylase complex subunit SAP18 OS=Mus musculus GN=Sap18 PE=1 SV=1	2	0.019	1.96
Histone H2A.V OS=Mus musculus GN=H2afv PE=1 SV=3	2	0.015	1.95
Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	9	0.019	1.94
Acetyl-coenzyme A synthetase, cytoplasmic OS=Mus musculus GN=Acss2 PE=1 SV=2	2	0.023	1.94
Nuclear factor 1 X-type OS=Mus musculus GN=Nfix PE=1 SV=2	3	0.017	1.94
60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=1 SV=3	3	0.050	1.93
Protein S100-A13 OS=Mus musculus GN=S100a13 PE=1 SV=1	2	0.004	1.93
Prothymosin alpha OS=Mus musculus GN=Ptma PE=1 SV=2	4	0.043	1.93
Phosphoglucomutase-2 OS=Mus musculus GN=Pgm2 PE=1 SV=1	1	0.045	1.93
SH3 domain-binding glutamic acid-rich-like protein 3 OS=Mus musculus GN=Sh3bgrl3 PE=1 SV=1	2	0.027	1.92
Tetraspanin-8 OS=Mus musculus GN=Tspan8 PE=1 SV=1	2	0.021	1.91
Phospholemman OS=Mus musculus GN=Fxyd1 PE=1 SV=1	1	0.000	1.90
Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	2	0.040	1.90
Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=1 SV=2	10	0.047	1.90
V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	4	0.023	1.89
Rab GTPase-activating protein 1 OS=Mus musculus GN=Rabgap1 PE=1 SV=1	1	0.012	1.89
Lupus La protein homolog OS=Mus musculus GN=Ssb PE=1 SV=1	2	0.025	1.89
Collagen alpha-1(XIV) chain OS=Mus musculus GN=Col14a1 PE=1 SV=2	21	0.010	1.89
Transketolase OS=Mus musculus GN=Tkt PE=1 SV=1	9	0.022	1.88
DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2	1	0.030	1.87
Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	6	0.007	1.86
Manganese-transporting ATPase 13A1 OS=Mus musculus GN=Atp13a1 PE=1 SV=2	1	0.010	1.85
Lamin-B2 OS=Mus musculus GN=Lmnb2 PE=1 SV=2	12	0.013	1.84
Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	4	0.022	1.83
Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	8	0.023	1.83
Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Mus musculus GN=Camk2d PE=1 SV=1	4	0.009	1.83
Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	3	0.031	1.82
Ran-binding protein 3 OS=Mus musculus GN=Ranbp3 PE=1 SV=2	1	0.002	1.82
Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE=1 SV=1	2	0.014	1.82
Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	40	0.021	1.81
ADP-ribosylation factor 6 OS=Mus musculus GN=Arf6 PE=1 SV=2	1	0.011	1.81
Multiple coagulation factor deficiency protein 2 homolog OS=Mus musculus GN=Mcfd2 PE=1 SV=1	1	0.016	1.81
Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	12	0.019	1.80
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	8	0.043	1.80
Lysosome-associated membrane glycoprotein 1 OS=Mus musculus GN=Lamp1 PE=1 SV=2	1	0.007	1.80
N-alpha-acetyltransferase 50 OS=Mus musculus GN=Naa50 PE=1 SV=1	1	0.003	1.80
Calsequestrin-2 OS=Mus musculus GN=Casq2 PE=1 SV=3	10	0.046	1.80
Prostaglandin E synthase 3 OS=Mus musculus GN=Ptges3 PE=1 SV=1	2	0.007	1.79
Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	10	0.036	1.79

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Lysosome membrane protein 2 OS=Mus musculus GN=Scarb2 PE=1 SV=3	3	0.021	1.79
Cytochrome c oxidase assembly protein COX14 OS=Mus musculus GN=Cox14 PE=3 SV=1	1	0.046	1.79
Charged multivesicular body protein 1a OS=Mus musculus GN=Chmp1a PE=1 SV=1	1	0.014	1.79
Sorting nexin-6 OS=Mus musculus GN=Snx6 PE=1 SV=2	3	0.046	1.79
Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	4	0.045	1.79
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform OS=Mus musculus GN=Ppp2r5a PE=1 SV=1	3	0.004	1.79
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Alpha-1-acid glycoprotein 1 OS=Mus musculus GN=Orm1 PE=1 SV=1	3	0.001	1.77
Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	1	0.000	1.77
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TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	3	0.028	1.76
Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=1 SV=1	5	0.007	1.76
Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=2	3	0.005	1.76
Phosphatidylserine synthase 1 OS=Mus musculus GN=Ptdss1 PE=1 SV=1	2	0.037	1.76
Serine/arginine-rich splicing factor 10 OS=Mus musculus GN=Srsf10 PE=1 SV=2	2	0.017	1.75
LIM and senescent cell antigen-like-containing domain protein 1 OS=Mus musculus GN=Lims1 PE=1 SV=3	2	0.003	1.75
Ferritin heavy chain OS=Mus musculus GN=Fth1 PE=1 SV=2	2	0.011	1.75
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Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=3	1	0.018	1.74
Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	6	0.008	1.74
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Src substrate cortactin OS=Mus musculus GN=Cttn PE=1 SV=2	3	0.015	1.74
Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2	3	0.016	1.74
Microtubule-associated protein 1B OS=Mus musculus GN=Map1b PE=1 SV=2	4	0.030	1.73
Alpha-2-HS-glycoprotein OS=Mus musculus GN=Ahsg PE=1 SV=1	7	0.039	1.73
Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1	2	0.026	1.73
Protein S100-A10 OS=Mus musculus GN=S100a10 PE=1 SV=2	1	0.009	1.73
IgG receptor FcRn large subunit p51 OS=Mus musculus GN=Fcgrt PE=1 SV=1	1	0.009	1.73
Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	2	0.017	1.73
39S ribosomal protein L54, mitochondrial OS=Mus musculus GN=Mrpl54 PE=1 SV=1	1	0.039	1.73
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Mus musculus GN=Nsdhl PE=1 SV=1	1	0.011	1.72
Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	5	0.018	1.72
Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Mus musculus GN=Fkbp9 PE=1 SV=1	3	0.050	1.72
Vesicular integral-membrane protein VIP36 OS=Mus musculus GN=Lman2 PE=1 SV=2	2	0.002	1.72

Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	2	0.002	1.72
Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=1 SV=3	1	0.050	1.72
Putative RNA-binding protein Luc7-like 2 OS=Mus musculus GN=Luc7l2 PE=1 SV=1	2	0.016	1.71
Protein transport protein Sec31A OS=Mus musculus GN=Sec31a PE=1 SV=2	4	0.050	1.71
RNA binding motif protein, X-linked-like-1 OS=Mus musculus GN=Rbmxl1 PE=2 SV=1	4	0.013	1.71
C-terminal-binding protein 2 OS=Mus musculus GN=Ctbp2 PE=1 SV=2	1	0.023	1.71
Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Mus musculus GN=Ergic1 PE=1 SV=1	1	0.044	1.71
Beta-sarcoglycan OS=Mus musculus GN=Sgcb PE=1 SV=1	3	0.007	1.71
Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	9	0.042	1.71
Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1	8	0.006	1.71
Programmed cell death protein 10 OS=Mus musculus GN=Pdcd10 PE=1 SV=1	1	0.026	1.70
Actin-like protein 6A OS=Mus musculus GN=Actl6a PE=1 SV=2	1	0.044	1.70
Transducin beta-like protein 2 OS=Mus musculus GN=Tbl2 PE=1 SV=2	1	0.025	1.70
14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	6	0.011	1.70
Tubulin-specific chaperone A OS=Mus musculus GN=Tbca PE=1 SV=3	2	0.011	1.70
DnaJ homolog subfamily B member 6 OS=Mus musculus GN=Dnajb6 PE=1 SV=4	1	0.006	1.70
Glutathione S-transferase kappa 1 OS=Mus musculus GN=Gstk1 PE=1 SV=3	4	0.003	1.70
60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=1 SV=3	5	0.042	1.69
Rho-related GTP-binding protein RhoG OS=Mus musculus GN=Rhog PE=1 SV=1	2	0.003	1.69
Protein FAM162A OS=Mus musculus GN=Fam162a PE=1 SV=1	1	0.038	1.69
Translocon-associated protein subunit gamma OS=Mus musculus GN=Ssr3 PE=1 SV=1	1	0.002	1.69
Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	47	0.009	1.69
Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	12	0.048	1.69
Heat shock protein beta-8 OS=Mus musculus GN=Hspb8 PE=1 SV=1	5	0.023	1.69
Xin actin-binding repeat-containing protein 2 OS=Mus musculus GN=Xirp2 PE=1 SV=1	23	0.033	1.69
Protein LSM14 homolog A OS=Mus musculus GN=Lsm14a PE=1 SV=1	1	0.003	1.69
Alpha-synuclein OS=Mus musculus GN=Snca PE=1 SV=2	1	0.014	1.69
Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	1	0.031	1.68
Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=1 SV=2	19	0.050	1.68
Choline transporter-like protein 2 OS=Mus musculus GN=Slc44a2 PE=1 SV=2	2	0.003	1.68
Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=1 SV=2	6	0.021	1.68
Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=1 SV=1	2	0.015	1.68
Sacsin OS=Mus musculus GN=Sacs PE=1 SV=2	2	0.048	1.68
Lamin-B1 OS=Mus musculus GN=Lmnb1 PE=1 SV=3	19	0.014	1.68
DnaJ homolog subfamily C member 8 OS=Mus musculus GN=Dnajc8 PE=1 SV=2	2	0.035	1.68
Ataxin-2-like protein OS=Mus musculus GN=Atxn2l PE=1 SV=1	2	0.019	1.68
SH3 domain-binding glutamic acid-rich-like protein OS=Mus musculus GN=Sh3bgrl PE=1 SV=1	3	0.040	1.68
PRA1 family protein 3 OS=Mus musculus GN=Arl6ip5 PE=1 SV=2	2	0.003	1.68
Hsp90 co-chaperone Cdc37 OS=Mus musculus GN=Cdc37 PE=1 SV=1	2	0.028	1.68
Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	5	0.013	1.68
39S ribosomal protein L43, mitochondrial OS=Mus musculus GN=Mrpl43 PE=1 SV=1	2	0.049	1.68

Heterochromatin protein 1-binding protein 3 OS=Mus musculus GN=Hp1bp3 PE=1 SV=1	1	0.015	1.68
Thioredoxin-related transmembrane protein 1 OS=Mus musculus GN=Tmx1 PE=1 SV=1	2	0.001	1.68
Sodium/potassium-transporting ATPase subunit beta-1 OS=Mus musculus GN=Atp1b1 PE=1 SV=1	5	0.020	1.67
Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrnpc PE=1 SV=1	6	0.027	1.67
Methyl-CpG-binding protein 2 OS=Mus musculus GN=Mecp2 PE=1 SV=1	3	0.031	1.67
Wolframin OS=Mus musculus GN=Wfs1 PE=1 SV=1	5	0.021	1.67
AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=3	1	0.025	1.67
Cytochrome b5 OS=Mus musculus GN=Cyb5a PE=1 SV=2	3	0.009	1.67
Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Mus musculus GN=Gnai1 PE=1 SV=1	1	0.005	1.67
Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh4a1 PE=1 SV=3	11	0.046	1.66
Hematopoietic progenitor cell antigen CD34 OS=Mus musculus GN=Cd34 PE=1 SV=1	3	0.021	1.66
von Willebrand factor A domain-containing protein 5A OS=Mus musculus GN=Vwa5a PE=1 SV=2	6	0.016	1.66
Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=2	6	0.029	1.66
6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=1 SV=3	6	0.015	1.65
Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=1 SV=3	2	0.011	1.65
Alpha-adducin OS=Mus musculus GN=Add1 PE=1 SV=2	2	0.008	1.65
Gamma-adducin OS=Mus musculus GN=Add3 PE=1 SV=2	2	0.015	1.65
Heat shock 70 kDa protein 12A OS=Mus musculus GN=Hspa12a PE=1 SV=1	3	0.012	1.65
Leucine-rich repeat flightless-interacting protein 2 OS=Mus musculus GN=Lrrfip2 PE=1 SV=1	1	0.049	1.65
Syncoilin OS=Mus musculus GN=Sync PE=1 SV=1	3	0.018	1.65
Branched-chain-amino-acid aminotransferase, mitochondrial OS=Mus musculus GN=Bcat2 PE=1 SV=2	3	0.032	1.65
Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2	2	0.029	1.65
PEST proteolytic signal-containing nuclear protein OS=Mus musculus GN=Pcnp PE=1 SV=1	2	0.020	1.65
Protein S100-A6 OS=Mus musculus GN=S100a6 PE=1 SV=3	3	0.012	1.64
Muscular LMNA-interacting protein OS=Mus musculus GN=Mlip PE=1 SV=1	2	0.004	1.64
GrpE protein homolog 1, mitochondrial OS=Mus musculus GN=Grpel1 PE=1 SV=1	4	0.037	1.64
Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	3	0.011	1.64
Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	6	0.010	1.64
Hepatoma-derived growth factor OS=Mus musculus GN=Hdgf PE=1 SV=2	5	0.002	1.64
ADP-ribosylation factor 5 OS=Mus musculus GN=Arf5 PE=1 SV=2	2	0.016	1.64
Cytochrome c oxidase assembly factor 6 homolog OS=Mus musculus GN=Coa6 PE=1 SV=1	1	0.021	1.64
Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=2	5	0.011	1.63
DnaJ homolog subfamily B member 4 OS=Mus musculus GN=Dnajb4 PE=1 SV=1	5	0.014	1.63
Phosphatidylglycerophosphatase and protein-tyrosine phosphatase 1 OS=Mus musculus GN=Ptpmt1 PE=1 SV=1	1	0.025	1.63
ADP-ribosylation factor GTPase-activating protein 2 OS=Mus musculus GN=Arfgap2 PE=1 SV=1	3	0.008	1.63
Aspartyl/asparaginyl beta-hydroxylase OS=Mus musculus GN=Asph PE=1 SV=1	3	0.011	1.63
D-dopachrome decarboxylase OS=Mus musculus GN=Ddt PE=1 SV=3	3	0.018	1.63
Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	3	0.042	1.63
Flotillin-2 OS=Mus musculus GN=Flot2 PE=1 SV=2	1	0.008	1.63
Astrocytic phosphoprotein PEA-15 OS=Mus musculus GN=Pea15 PE=1 SV=1	2	0.047	1.63
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Mus musculus GN=Dad1 PE=1 SV=3	2	0.021	1.63

Translocation protein SEC62 OS=Mus musculus GN=Sec62 PE=1 SV=1	2	0.030	1.62
Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1	2	0.013	1.62
Protein FAM210A OS=Mus musculus GN=Fam210a PE=1 SV=1	1	0.018	1.62
Cytosolic purine 5'-nucleotidase OS=Mus musculus GN=Nt5c2 PE=1 SV=2	1	0.039	1.62
Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	9	0.043	1.62
Calcyclin-binding protein OS=Mus musculus GN=Cacybp PE=1 SV=1	2	0.011	1.62
Complement factor I OS=Mus musculus GN=Cfi PE=1 SV=3	4	0.005	1.62
SEC23-interacting protein OS=Mus musculus GN=Sec23ip PE=1 SV=2	2	0.027	1.62
Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	34	0.001	1.62
Myeloid-derived growth factor OS=Mus musculus GN=Mydgf PE=1 SV=1	3	0.048	1.62
RNA-binding protein EWS OS=Mus musculus GN=Ewsr1 PE=1 SV=2	1	0.046	1.62
Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	3	0.010	1.62
CCA tRNA nucleotidyltransferase 1, mitochondrial OS=Mus musculus GN=Trnt1 PE=1 SV=1	1	0.009	1.61
Sorting nexin-1 OS=Mus musculus GN=Snx1 PE=1 SV=1	1	0.030	1.61
LEM domain-containing protein 2 OS=Mus musculus GN=Lemd2 PE=1 SV=1	2	0.002	1.61
60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=1 SV=2	1	0.037	1.61
Barrier-to-autointegration factor OS=Mus musculus GN=Banf1 PE=1 SV=1	2	0.040	1.61
Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	28	0.021	1.61
Translin-associated protein X OS=Mus musculus GN=Tsnax PE=1 SV=1	2	0.018	1.61
Parathymosin OS=Mus musculus GN=Ptms PE=1 SV=3	1	0.035	1.61
Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	6	0.029	1.61
Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1	5	0.046	1.61
Migration and invasion enhancer 1 OS=Mus musculus GN=Mien1 PE=1 SV=1	2	0.013	1.61
Actin-binding Rho-activating protein OS=Mus musculus GN=Abra PE=1 SV=1	3	0.029	1.61
Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Mus musculus GN=Gng5 PE=1 SV=2	1	0.027	1.61
Kinesin light chain 1 OS=Mus musculus GN=Klc1 PE=1 SV=3	3	0.041	1.61
Vesicle-associated membrane protein 2 OS=Mus musculus GN=Vamp2 PE=1 SV=2	1	0.023	1.61
Coatomer subunit gamma-1 OS=Mus musculus GN=Copg1 PE=1 SV=1	5	0.034	1.60
SUMO-activating enzyme subunit 2 OS=Mus musculus GN=Uba2 PE=1 SV=1	3	0.044	1.60
Chloride intracellular channel protein 4 OS=Mus musculus GN=Clic4 PE=1 SV=3	1	0.034	1.60
39S ribosomal protein L9, mitochondrial OS=Mus musculus GN=Mrpl9 PE=1 SV=2	1	0.014	1.60
Dehydrogenase/reductase SDR family member 7 OS=Mus musculus GN=Dhrs7 PE=1 SV=2	2	0.050	1.60
A-kinase anchor protein 12 OS=Mus musculus GN=Akap12 PE=1 SV=1	6	0.044	1.60
Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=4	6	0.026	1.60
Phosphatidylinositol 3,4,5-trisphosphate 5-phosphatase 2 OS=Mus musculus GN=Inppl1 PE=1 SV=1	2	0.013	1.60
Flotillin-1 OS=Mus musculus GN=Flot1 PE=1 SV=1	4	0.012	1.60
Sorting nexin-2 OS=Mus musculus GN=Snx2 PE=1 SV=2	2	0.018	1.60
ATP synthase-coupling factor 6, mitochondrial OS=Mus musculus GN=Atp5j PE=1 SV=1	5	0.041	1.60
14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	5	0.013	1.59
KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Mus musculus GN=Khdrbs1 PE=1 SV=2	3	0.037	1.59
Ankyrin-2 OS=Mus musculus GN=Ank2 PE=1 SV=2	1	0.019	1.59

Cytochrome c oxidase subunit 7C, mitochondrial OS=Mus musculus GN=Cox7c PE=1 SV=1	2	0.033	1.59
Isoleucine--tRNA ligase, mitochondrial OS=Mus musculus GN=Iars2 PE=1 SV=1	3	0.017	1.59
Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Mus musculus GN=Nudt4 PE=1 SV=1	1	0.012	1.59
BAG family molecular chaperone regulator 3 OS=Mus musculus GN=Bag3 PE=1 SV=2	17	0.013	1.59
Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3	5	0.049	1.59
V-type proton ATPase subunit E 1 OS=Mus musculus GN=Atp6v1e1 PE=1 SV=2	4	0.050	1.59
Cytoplasmic dynein 1 intermediate chain 2 OS=Mus musculus GN=Dync1i2 PE=1 SV=1	4	0.050	1.59
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Mus musculus GN=Gspt1 PE=1 SV=2	3	0.014	1.59
N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Mus musculus GN=Naa15 PE=1 SV=1	3	0.028	1.59
Transmembrane emp24 domain-containing protein 2 OS=Mus musculus GN=Tmed2 PE=1 SV=1	2	0.006	1.59
AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1 SV=1	3	0.033	1.59
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dbt PE=1 SV=2	5	0.002	1.59
Annexin A4 OS=Mus musculus GN=Anxa4 PE=1 SV=4	6	0.026	1.59
Solute carrier family 12 member 2 OS=Mus musculus GN=Slc12a2 PE=1 SV=2	6	0.014	1.59
Decorin OS=Mus musculus GN=Dcn PE=1 SV=1	11	0.004	1.59
Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Mus musculus GN=Nucks1 PE=1 SV=1	1	0.010	1.58
AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=2	1	0.027	1.58
Heterogeneous nuclear ribonucleoprotein D0 OS=Mus musculus GN=Hnrnpd PE=1 SV=2	6	0.046	1.58
Carbonyl reductase [NADPH] 2 OS=Mus musculus GN=Cbr2 PE=1 SV=1	1	0.018	1.58
60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	23	0.025	1.58
Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3	2	0.016	1.58
UBX domain-containing protein 1 OS=Mus musculus GN=Ubxn1 PE=1 SV=1	4	0.000	1.58
Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4	2	0.020	1.58
ADP-ribosylation factor 3 OS=Mus musculus GN=Arf3 PE=2 SV=2	3	0.008	1.58
Acyl-coenzyme A thioesterase 9, mitochondrial OS=Mus musculus GN=Acot9 PE=1 SV=1	5	0.001	1.58
Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2	3	0.011	1.58
Lumican OS=Mus musculus GN=Lum PE=1 SV=2	10	0.009	1.57
Cystatin-C OS=Mus musculus GN=Cst3 PE=1 SV=2	4	0.014	1.57
Supervillin OS=Mus musculus GN=Svil PE=1 SV=1	12	0.015	1.57
Armadillo repeat-containing protein 1 OS=Mus musculus GN=Armc1 PE=1 SV=1	1	0.022	1.57
DnaJ homolog subfamily A member 4 OS=Mus musculus GN=Dnaja4 PE=1 SV=1	4	0.037	1.57
Tumor protein D54 OS=Mus musculus GN=Tpd52l2 PE=1 SV=1	2	0.038	1.57
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 5, mitochondrial OS=Mus musculus GN=Ndufb5 PE=1 SV=1	5	0.021	1.57
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Mccc2 PE=1 SV=1	4	0.013	1.57
Inter-alpha-trypsin inhibitor heavy chain H1 OS=Mus musculus GN=Itih1 PE=1 SV=2	2	0.015	1.57
Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	70	0.034	1.57
Emerin OS=Mus musculus GN=Emd PE=1 SV=1	2	0.005	1.57
Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Mus musculus GN=Hnrnpul1 PE=1 SV=1	4	0.014	1.57
Uroporphyrinogen decarboxylase OS=Mus musculus GN=Urod PE=1 SV=2	1	0.015	1.57
Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3	6	0.007	1.57
Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=3	13	0.006	1.57

Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	2	0.013	1.57
FUN14 domain-containing protein 2 OS=Mus musculus GN=Fundc2 PE=1 SV=1	2	0.001	1.57
Glutathione S-transferase theta-1 OS=Mus musculus GN=Gstt1 PE=1 SV=4	1	0.018	1.56
Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Mus musculus GN=Fkbp4 PE=1 SV=5	4	0.029	1.56
Alanine aminotransferase 1 OS=Mus musculus GN=Gpt PE=1 SV=3	4	0.009	1.56
Mitochondrial fission 1 protein OS=Mus musculus GN=Fis1 PE=1 SV=1	1	0.033	1.56
Protein RER1 OS=Mus musculus GN=Rer1 PE=1 SV=1	1	0.024	1.56
General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=2	5	0.006	1.56
Nardilysin OS=Mus musculus GN=Nrdc PE=1 SV=1	2	0.030	1.56
Cystatin-B OS=Mus musculus GN=Cstb PE=1 SV=1	1	0.006	1.56
Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=3	2	0.038	1.56
Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	5	0.007	1.56
ATPase family AAA domain-containing protein 3 OS=Mus musculus GN=Atad3 PE=1 SV=1	3	0.016	1.56
Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	17	0.025	1.56
Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=1 SV=2	2	0.023	1.56
BolA-like protein 2 OS=Mus musculus GN=Bola2 PE=1 SV=1	2	0.032	1.56
Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	5	0.005	1.56
NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial OS=Mus musculus GN=Ndufs4 PE=1 SV=3	3	0.024	1.56
Peroxiredoxin-6 OS=Mus musculus GN=Prdx6 PE=1 SV=3	9	0.015	1.56
Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	14	0.025	1.55
E3 ubiquitin-protein ligase TRIP12 OS=Mus musculus GN=Trip12 PE=1 SV=1	1	0.003	1.55
Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	5	0.004	1.55
Transaldolase OS=Mus musculus GN=Taldo1 PE=1 SV=2	12	0.031	1.55
Monoacylglycerol lipase ABHD12 OS=Mus musculus GN=Abhd12 PE=1 SV=2	1	0.040	1.55
Ubiquitin domain-containing protein UBFD1 OS=Mus musculus GN=Ubfd1 PE=1 SV=2	1	0.031	1.55
Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	4	0.016	1.55
Cleft lip and palate transmembrane protein 1 homolog OS=Mus musculus GN=Clptm1 PE=1 SV=1	2	0.005	1.55
Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1	6	0.004	1.55
Voltage-dependent calcium channel gamma-1 subunit OS=Mus musculus GN=Cacng1 PE=2 SV=1	1	0.008	1.55
Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Mus musculus GN=Hmgcl PE=1 SV=2	4	0.019	1.55
Thioredoxin-like protein 1 OS=Mus musculus GN=Txnl1 PE=1 SV=3	2	0.012	1.55
MICOS complex subunit Mic27 OS=Mus musculus GN=Apool PE=1 SV=1	4	0.032	1.55
Clustered mitochondria protein homolog OS=Mus musculus GN=Cluh PE=1 SV=2	9	0.016	1.55
CDGSH iron-sulfur domain-containing protein 3, mitochondrial OS=Mus musculus GN=Cisd3 PE=1 SV=1	2	0.000	1.55
Eukaryotic initiation factor 4A-III OS=Mus musculus GN=Eif4a3 PE=1 SV=3	2	0.016	1.54
Epidermal growth factor receptor substrate 15 OS=Mus musculus GN=Eps15 PE=1 SV=1	2	0.011	1.54
Synaptopodin OS=Mus musculus GN=Synpo PE=1 SV=2	6	0.018	1.54
Secretory carrier-associated membrane protein 1 OS=Mus musculus GN=Scamp1 PE=1 SV=1	1	0.032	1.54
Kelch-like protein 41 OS=Mus musculus GN=Klhl41 PE=1 SV=1	27	0.014	1.54
Stomatin-like protein 2, mitochondrial OS=Mus musculus GN=Stoml2 PE=1 SV=1	2	0.023	1.54
Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	2	0.021	1.54

Annexin A3 OS=Mus musculus GN=Anxa3 PE=1 SV=4	3	0.047	1.54
B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=4	7	0.008	1.54
28S ribosomal protein S29, mitochondrial OS=Mus musculus GN=Dap3 PE=1 SV=1	2	0.042	1.54
Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	4	0.041	1.54
AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=2	1	0.009	1.54
Up-regulated during skeletal muscle growth protein 5 OS=Mus musculus GN=Usmg5 PE=1 SV=1	2	0.017	1.54
Complement C3 OS=Mus musculus GN=C3 PE=1 SV=3	22	0.020	1.53
Serine/arginine-rich splicing factor 1 OS=Mus musculus GN=Srsf1 PE=1 SV=3	4	0.046	1.53
Uncharacterized protein C6orf47 homolog OS=Mus musculus GN=D17h6s53e PE=1 SV=1	1	0.033	1.53
Alcohol dehydrogenase [NADP(+)] OS=Mus musculus GN=Akr1a1 PE=1 SV=3	5	0.010	1.53
Target of Myb protein 1 OS=Mus musculus GN=Tom1 PE=1 SV=1	3	0.014	1.53
Coatomer subunit delta OS=Mus musculus GN=Arcn1 PE=1 SV=2	2	0.031	1.53
Mitochondrial import inner membrane translocase subunit TIM44 OS=Mus musculus GN=Timm44 PE=1 SV=2	7	0.034	1.53
Protein phosphatase inhibitor 2 OS=Mus musculus GN=Ppp1r2 PE=1 SV=3	1	0.050	1.53
Phosphoglucomutase-like protein 5 OS=Mus musculus GN=Pgm5 PE=1 SV=2	1	0.029	1.53
Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=1 SV=3	17	0.005	1.53
Cdc42-interacting protein 4 OS=Mus musculus GN=Trip10 PE=1 SV=2	2	0.007	1.53
Uncharacterized protein C6orf203 homolog OS=Mus musculus PE=1 SV=1	1	0.009	1.53
Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Mus musculus GN=Ppp2ca PE=1 SV=1	2	0.004	1.53
Transcription factor BTF3 OS=Mus musculus GN=Btf3 PE=1 SV=3	3	0.046	1.53
78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	24	0.034	1.53
Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1	6	0.008	1.53
Cytoplasmic dynein 1 light intermediate chain 1 OS=Mus musculus GN=Dync1li1 PE=1 SV=1	3	0.021	1.52
14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	4	0.023	1.52
Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=2	4	0.041	1.52
Kinesin light chain 2 OS=Mus musculus GN=Klc2 PE=1 SV=1	2	0.009	1.52
26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1	5	0.018	1.52
Metaxin-1 OS=Mus musculus GN=Mtx1 PE=1 SV=1	3	0.035	1.52
Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus GN=Syncrip PE=1 SV=2	12	0.040	1.52
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	10	0.049	1.52
Nucleoprotein TPR OS=Mus musculus GN=Tpr PE=1 SV=1	3	0.023	1.52
Microtubule-associated protein 1S OS=Mus musculus GN=Map1s PE=1 SV=2	1	0.045	1.52
Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus GN=Sptan1 PE=1 SV=4	39	0.032	1.52
DnaJ homolog subfamily B member 2 OS=Mus musculus GN=Dnajb2 PE=1 SV=2	1	0.014	1.52
Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1	1	0.020	1.52
Protein arginine N-methyltransferase 1 OS=Mus musculus GN=Prmt1 PE=1 SV=1	8	0.043	1.52
Profilin-1 OS=Mus musculus GN=Pfn1 PE=1 SV=2	6	0.050	1.52
Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3	25	0.017	1.52
Thioredoxin OS=Mus musculus GN=Txn PE=1 SV=3	4	0.008	1.52
Ubiquitin-conjugating enzyme E2 D3 OS=Mus musculus GN=Ube2d3 PE=1 SV=1	2	0.007	1.52
Protein transport protein Sec61 subunit alpha isoform 2 OS=Mus musculus GN=Sec61a2 PE=2 SV=3	3	0.018	1.52

Transmembrane emp24 domain-containing protein 1 OS=Mus musculus GN=Tmed1 PE=1 SV=1	2	0.025	1.52
26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	7	0.005	1.51
60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	5	0.005	1.51
Glutathione S-transferase omega-1 OS=Mus musculus GN=Gsto1 PE=1 SV=2	2	0.041	1.51
Malectin OS=Mus musculus GN=Mlec PE=1 SV=2	5	0.000	1.51
E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3	6	0.020	1.51
N-alpha-acetyltransferase 25, NatB auxiliary subunit OS=Mus musculus GN=Naa25 PE=1 SV=1	2	0.040	1.51
AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	4	0.043	1.51
Corticosteroid-binding globulin OS=Mus musculus GN=Serpina6 PE=1 SV=1	2	0.025	1.51
Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	9	0.012	1.51
Synaptophysin-like protein 1 OS=Mus musculus GN=Sypl1 PE=1 SV=2	3	0.005	1.51
Receptor expression-enhancing protein 5 OS=Mus musculus GN=Reep5 PE=1 SV=1	3	0.036	1.51
Procollagen C-endopeptidase enhancer 1 OS=Mus musculus GN=Pcolce PE=1 SV=2	2	0.014	1.51
Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrnpm PE=1 SV=3	7	0.041	1.51
UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Uggt1 PE=1 SV=4	3	0.001	1.51
UPF0568 protein C14orf166 homolog OS=Mus musculus PE=1 SV=1	8	0.011	1.50
Oligosaccharyltransferase complex subunit OSTC OS=Mus musculus GN=Ostc PE=1 SV=1	1	0.018	1.50
Huntingtin-interacting protein K OS=Mus musculus GN=Hypk PE=1 SV=2	2	0.034	1.50
Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Mus musculus GN=Sgta PE=1 SV=2	5	0.038	1.50
Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	5	0.032	1.50
CLIP-associating protein 1 OS=Mus musculus GN=Clasp1 PE=1 SV=2	2	0.035	1.50
Cadherin-13 OS=Mus musculus GN=Cdh13 PE=1 SV=2	11	0.018	1.50
26S proteasome non-ATPase regulatory subunit 8 OS=Mus musculus GN=Psmd8 PE=1 SV=2	3	0.015	1.50
Mimecan OS=Mus musculus GN=Ogn PE=1 SV=1	10	0.008	1.50
Cytochrome b-c1 complex subunit 6, mitochondrial OS=Mus musculus GN=Uqcrh PE=1 SV=2	6	0.041	1.50
FH1/FH2 domain-containing protein 1 OS=Mus musculus GN=Fhod1 PE=1 SV=3	9	0.000	1.50
Alanyl-tRNA editing protein Aarsd1 OS=Mus musculus GN=Aarsd1 PE=1 SV=2	5	0.022	1.50
Proteasome subunit alpha type-1 OS=Mus musculus GN=Psma1 PE=1 SV=1	7	0.023	1.50
Myosin-binding protein C, fast-type OS=Mus musculus GN=Mybpc2 PE=1 SV=1	76	0.003	-1.63

Supplemental Table 2. Primer sequences

Sybr real-time primers:

Klhl31
F: CAGGTGGTGAGGACCAGAAT
R: CCCAAGTGAATCCAGGTGTT

Slmap
F: TCACCCAAGAGGCTTCAGAT
R: TGGCTGTGGTTTCATAGCTG

Ckap4
F: GCTCAACCGAATTAGCGAAG
R: GCTCCTCGACTGTGTTCTCC

Usmg5
F: AAAGTGATGGCCAATTCCAG
R: AGCAAAGCAATGCCTCCATA

FlnC
F: GGGCTTTGTCTGTCACCATT
R: CTTTGCTTTGAAGGGACTGC

Cloning primers:

Klhl31 promoter pGL3b
F: TAAGCAGGTACCTGGCCCTTTACCTGCATC – KpnI
R: TGCTTAGCTAGCCCTAGGATCCAGTCGGCA – NheI

Klhl31 site directed mutagenesis Mef2Δ
F: TCCTGTGAGGAGACTGGTTATCCCTAGACTGTTCTGTAGAGGAGG
R: CCTCCTCTACAGAACAGTCTAGGGATAACCAGTCTCCTCACAGGA

Klhl31 pcDNA3.1 C-terminal epitope tag
F: TAAGCAGGATCCCGCCACCATGGCACCCAAAAAGAAGACT – BamHI
R: TGCTTATCTAGAGATACTGACCGGCACGGA – XbaI

Usmg5 pcDNA3.1 C-terminal epitope tag
F: TAAGCAGGATCCCGCCACCATGGCTGGTGCAGAAAGTG – BamHI
R: TGCTTACTCGAGTGTTGCTTTCACAGCTGGAG – XhoI

Bag3 pcDNA3.1 C-terminal epitope tag
F: TAAGCAGGTACCCGCCACCATGAGCGCCGCCACCCAAT – KpnI
R: TGCTTACTCGAGGGGAGCCACCAGGTTGCCAG – XhoI

Slmap pcDNA3.1 C-terminal epitope tag
F: TAAGCAGAATTCCGCCACCATGCCGTCAGCCTTGG – EcoRI
R: TGCTTACTCGAGCCACAATGGACCGAAACAC – XhoI

Slmap SKA transgene
F: TAAGCAGCGGCCGCCGCCACCATGCCGTCAGCCTTGG – NotI
R: TGCTTAGCGGCCGCCTACCACAATGGACCGAAACA – NotI

Cul3 pcDNA3.1 C-terminal epitope tag
F: TAAGCAGGTACCCGCCACCATGTCGAATCTGAGCAAAGGC – KpnI
R: TGCTTACTCGAGTGCTACATATGTGTATACTTTGCGATC – XhoI

pRK5-HA-Ub-WT K48R
F: TCTTCCAGCTGTCTCCCAGCAAAGATCAACCTCT
R: AGAGGTTGATCTTTGCTGGGAGACAGCTGGAAGA

SKA-Slmap genotyping primers:
F: CGAGAGTAGCAGTTGTAGCTA
R: CCGATGTAAGGCCTCCTGTA