Western Blot Quantification from Muscle Tsc1 Knockout Quadriceps

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Data Entry and Calculations

These data are found in /Users/davebrid/Documents/GitHub/TissueSpecificTscKnockouts/Mouse Data/Muscle Tsc1 Knockout/NCD/Protein Blots and were most recently updated on Mon Mar 4 14:29:14 2019. It reads from the input quantification file named Quantification.csv.

Table 1: Raw Quantification Data

Genotype	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Knockout	Knockout	Knockout	K
Sample	811	867	1251	1260	1550	869	1264	1265	12
4F2hc	11400	15600	17700	-3770	10500	18800	24700	18600	33
Actin	296000	201000	321000	405000	317000	451000	493000	617000	52
CD36	501000	68100	465000	686000	397000	619000	833000	1160000	14
CI-NDUF88	67800	72400	80900	74300	47600	60100	53500	68300	72
CII-SDHB	174000	186000	269000	168000	118000	166000	157000	127000	17
CIII-UQCRC2	400000	444000	465000	468000	325000	487000	440000	255000	24
CIV-MTCO1	6180	77100	17800	2350	15900	45100	30900	25300	25
CV-ATP5A	218000	223000	344000	283000	224000	469000	301000	198000	21

Table 2: Summarized Ratios

Sample	811	867	1251	1260	1550	869	1264	1265	
Genotype	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Knockout	Knockout	Knockout	
pS6K.Ratio	0.0261	0.0228	0.0269	0.0219	0.0315	0.1212	0.1084	0.0801	
pS6.Ratio	1.40	1.13	11.04	1.12	17.75	21.41	32.75	28.34	
pJNK.Ratio	0.641	0.580	0.588	0.708	0.671	2.039	0.946	0.897	
LC3.Ratio	2.056	2.033	1.302	1.672	1.103	0.158	0.259	0.168	
CD36.Ratio	0.477	0.049	0.388	0.597	0.320	0.534	0.817	0.829	
NDUF88.Ratio	0.0646	0.0521	0.0674	0.0646	0.0384	0.0518	0.0525	0.0488	
SDHB.Ratio	0.1657	0.1338	0.2242	0.1461	0.0952	0.1431	0.1539	0.0907	
UQCRC2.Ratio	0.381	0.319	0.388	0.407	0.262	0.420	0.431	0.182	
MTCO1.Ratio	0.00589	0.05547	0.01483	0.00204	0.01282	0.03888	0.03029	0.01807	
ATP5A.Ratio	0.208	0.160	0.287	0.246	0.181	0.404	0.295	0.141	
LAT1.Ratio	0.00821	0.01453	0.01475	0.01339	0.00903	0.01164	0.01245	0.00921	
Sarcolipin.Ratio	0.1038	0.1345	0.1333	0.0254	0.1532	0.4284	0.4892	0.4921	
4F2hc.Ratio	0.01086	0.01122	0.01475	-0.00328	0.00847	0.01621	0.02422	0.01329	

Table 3: Summarized Normalized Ratios

Sample	811	867	1251	1260	1550	869	1264	1265	
Genotype	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Wild-Type	Knockout	Knockout	Knockout	
pS6K.norm	1.011	0.882	1.041	0.846	1.220	4.689	4.197	3.098	4

pS6.norm	0.216	0.175	1.702	0.172	2.735	3.300	5.048	4.369	3
pJNK.norm	1.005	0.910	0.922	1.110	1.053	3.197	1.484	1.407	1
LC3.norm	2.056	2.033	1.302	1.672	1.103	0.158	0.259	0.168	(
CD36.norm	1.303	0.134	1.059	1.630	0.875	1.458	2.231	2.263	2
NDUF88.norm	1.125	0.907	1.174	1.125	0.669	0.902	0.914	0.850	(
SDHB.norm	1.083	0.875	1.465	0.955	0.622	0.935	1.006	0.593	(
UQCRC2.norm	1.084	0.909	1.103	1.158	0.746	1.195	1.228	0.518	(
MTCO1.norm	0.3232	3.0459	0.8145	0.1122	0.7041	2.1350	1.6635	0.9924	(
ATP5A.norm	0.960	0.742	1.325	1.138	0.835	1.869	1.364	0.654	(
LAT1.norm	0.685	1.213	1.231	1.118	0.754	0.971	1.039	0.769	1
4F2hc.norm	1.29	1.34	1.76	-0.39	1.01	1.93	2.88	1.58	2
Sarcolipin.norm	0.943	1.222	1.211	0.231	1.392	3.893	4.445	4.472	3

Table 4: Summarized Values

| Genotype	Wild-Type	Knockout
pS6K.norm_mean	1.0	3.8
pS6.norm_mean	1.00	3.79
pJNK.norm_mean	1.00	1.67
LC3.norm_mean	1.63	0.22
CD36.norm_mean	1.00	2.45
NDUF88.norm_mean	1.00	1.08
SDHB.norm_mean	1.000	0.951
UQCRC2.norm_mean	1.000	0.851
MTCO1.norm_mean	1.00	1.15
ATP5A.norm_mean	1.0	1.1
LAT1.norm_mean	1.00	1.02
4F2hc.norm_mean	1.00	2.16
Sarcolipin.norm_mean	1.0	4.1
pS6K.norm_se	0.0663	0.3368
pS6.norm_se	0.524	0.391
pJNK.norm_se	0.0381	0.4093
LC3.norm_se	0.1912	0.0277
CD36.norm_se	0.251	0.383
NDUF88.norm_se	0.0949	0.2126
SDHB.norm_se	0.139	0.155
UQCRC2.norm_se	0.076	0.165
MTCO1.norm_se	0.527	0.353
ATP5A.norm_se	0.105	0.235
LAT1.norm_se	0.1167	0.0809
4F2hc.norm_se	0.367	0.243
Sarcolipin.norm_se	0.205	0.197

S6K Phosphorylation
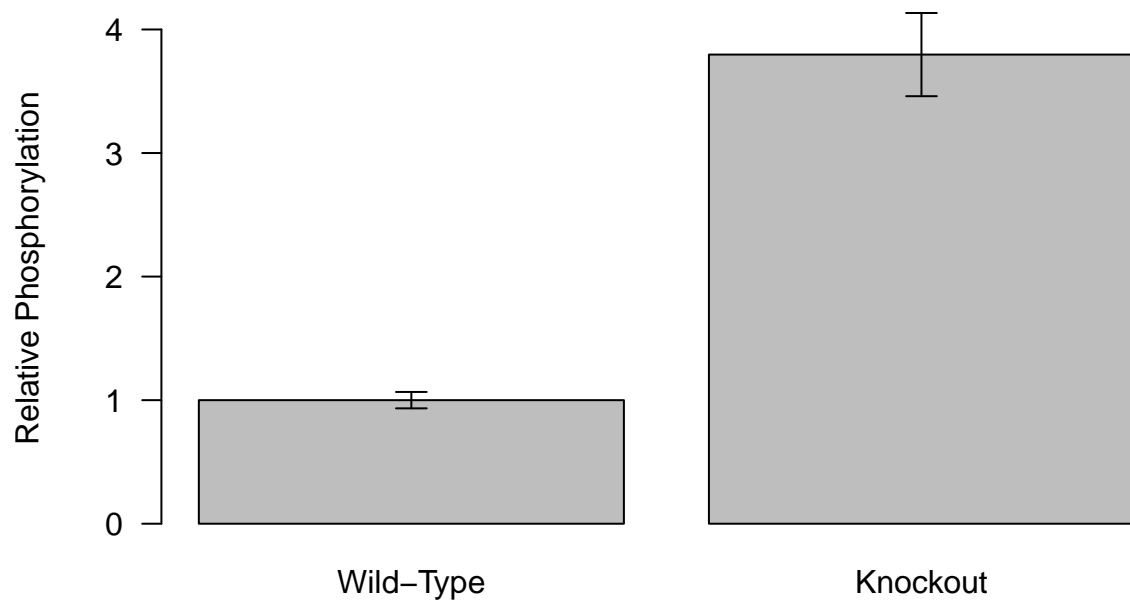
Figure 1: Normalized mTORC1 Activity in Quadriceps
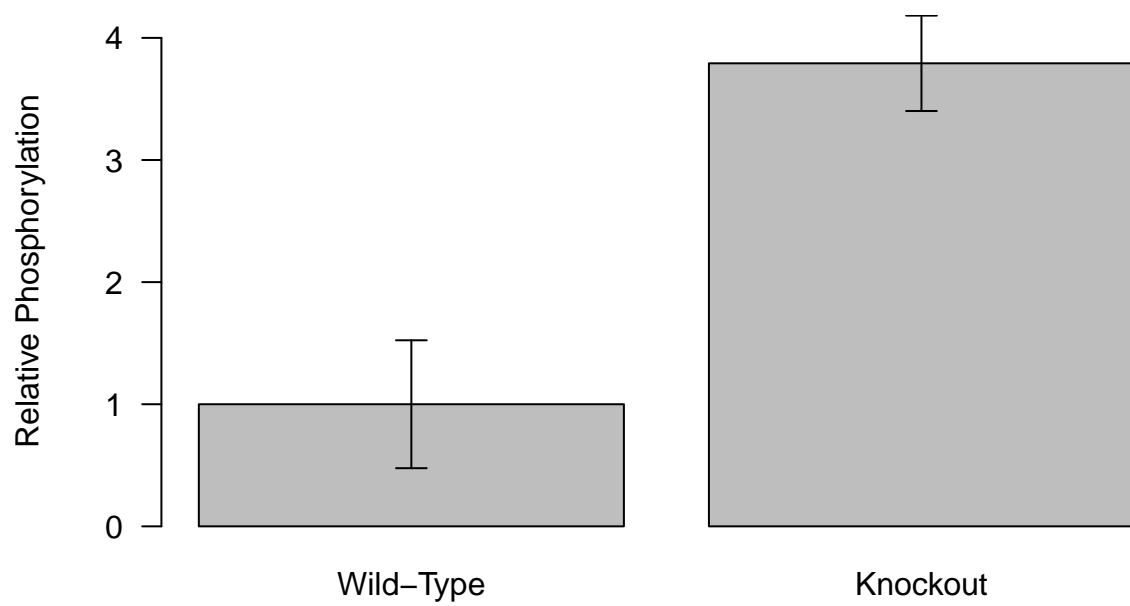
S6 Phosphorylation
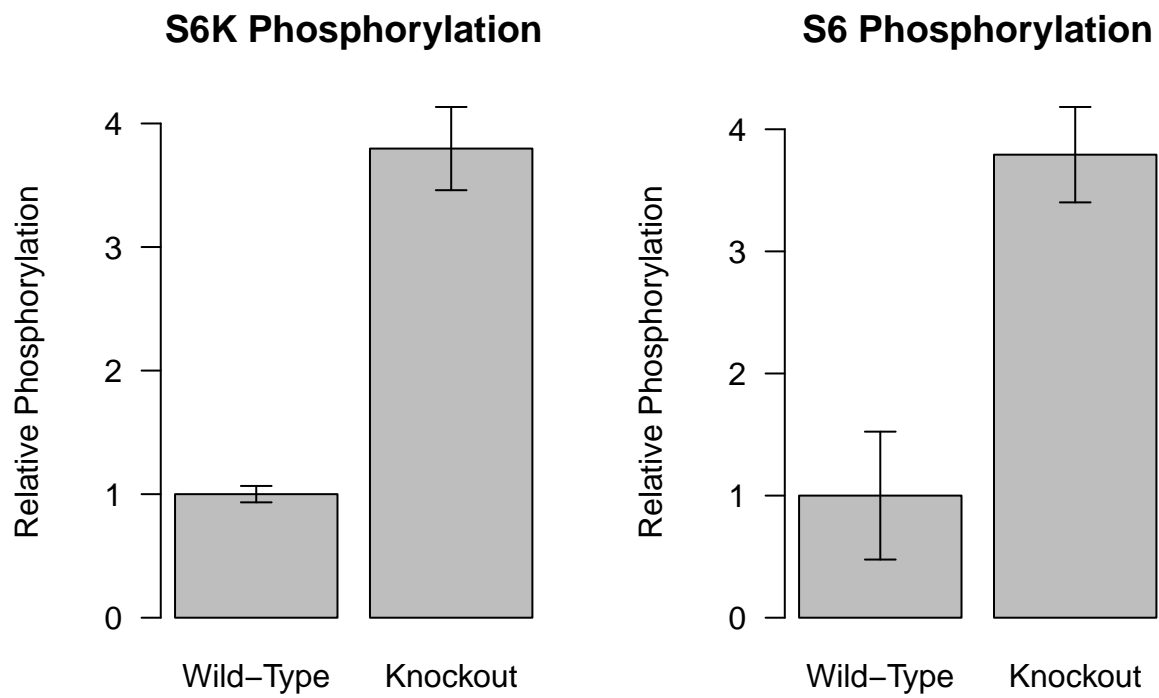

Figure 2: Normalized S6K Activity in Quadriceps

S6K Phosphorylation

S6 Phosphorylation

Figure 3: Normalized mTORC1 Activity in Quadriceps
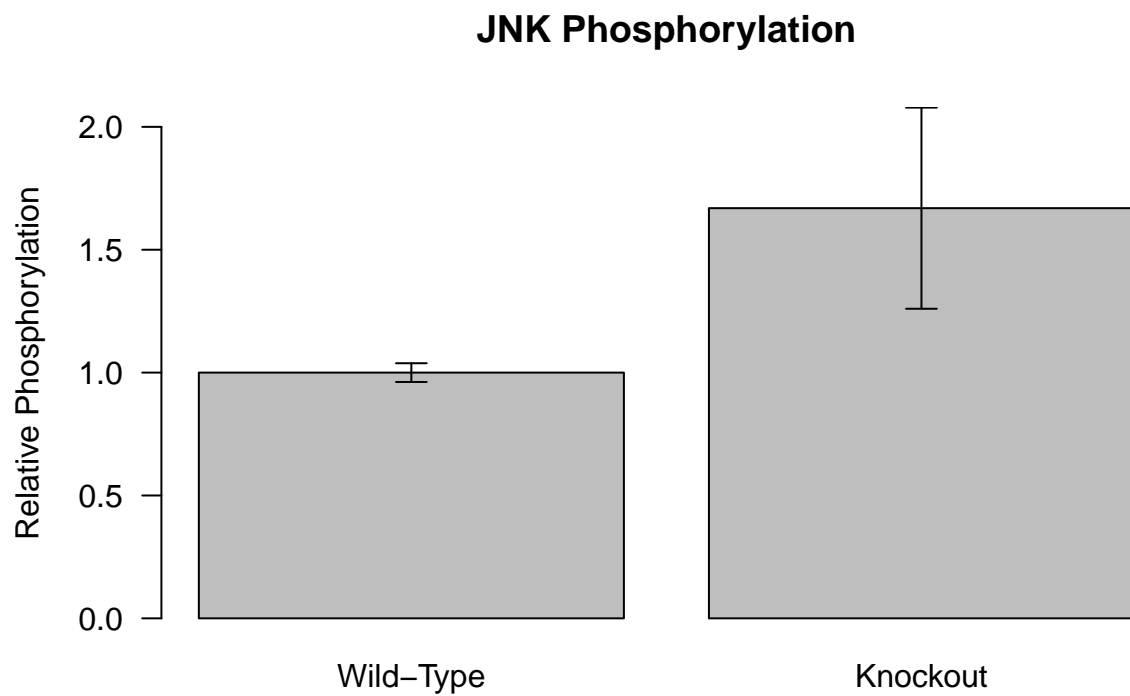
JNK Phosphorylation
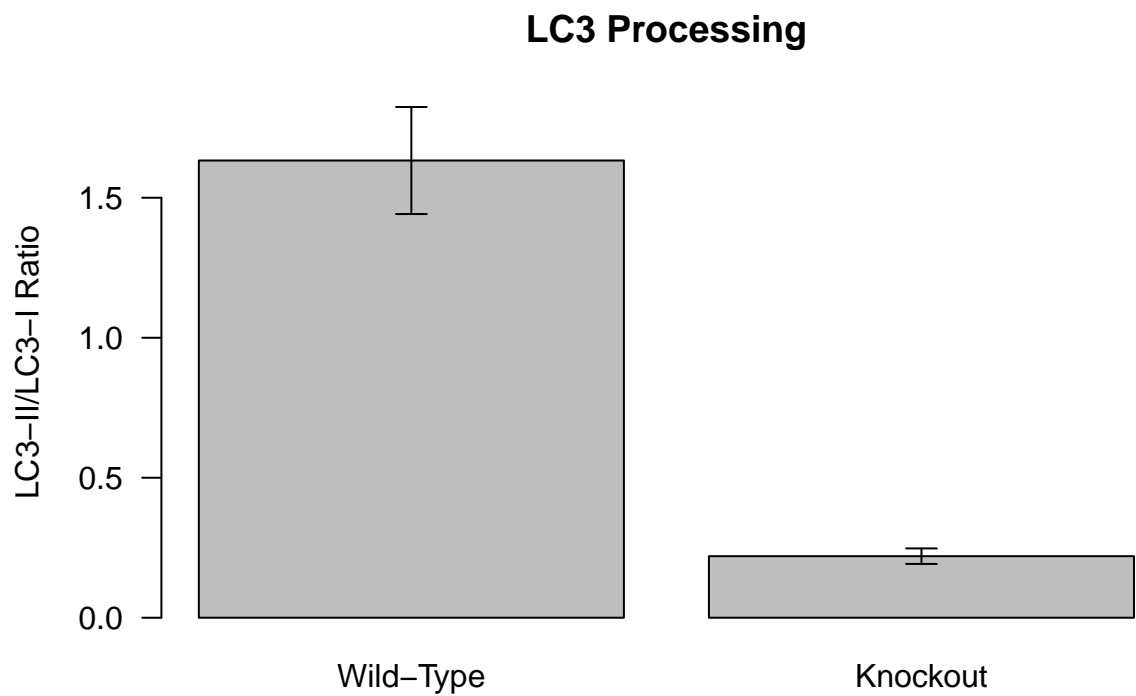
Figure 4: Normalized JNK Phosphorylation in Quadriceps

LC3 Processing

Figure 5: Normalized LC3 Processing in Quadriceps
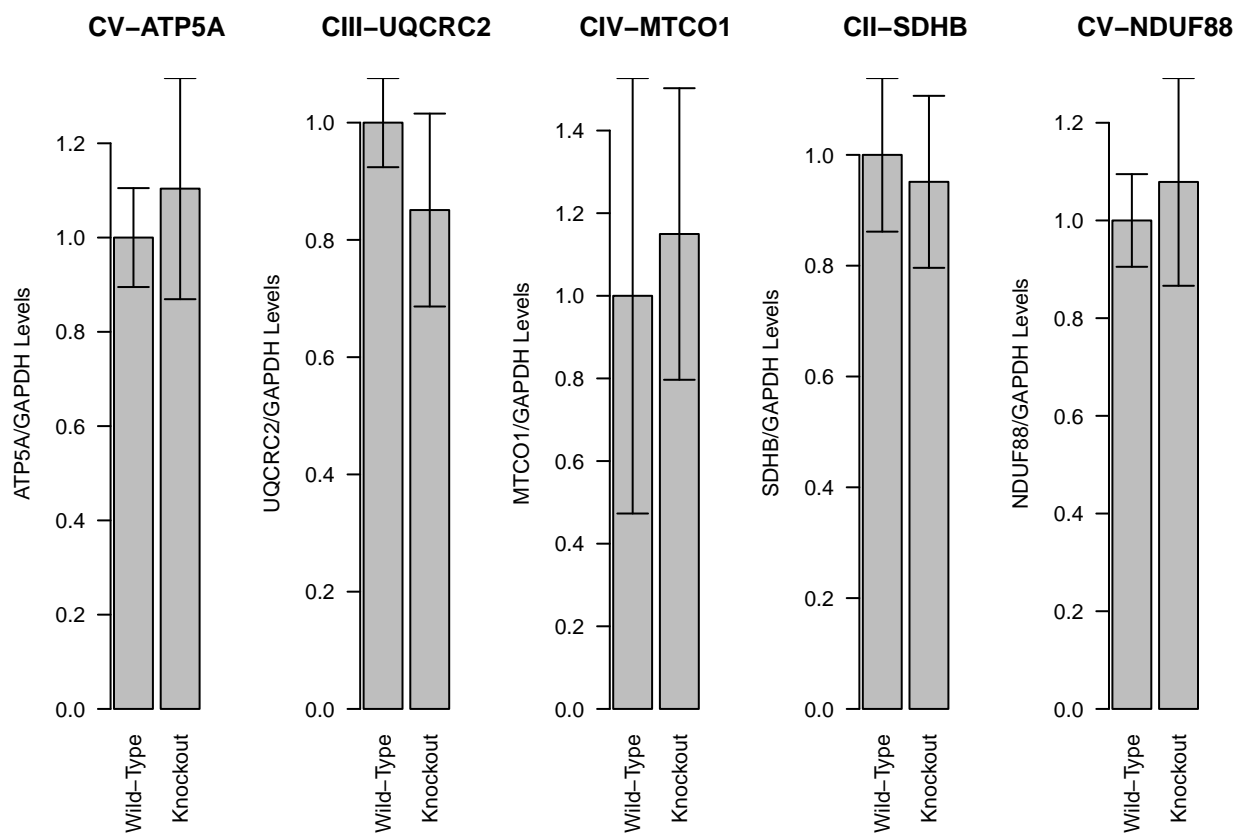
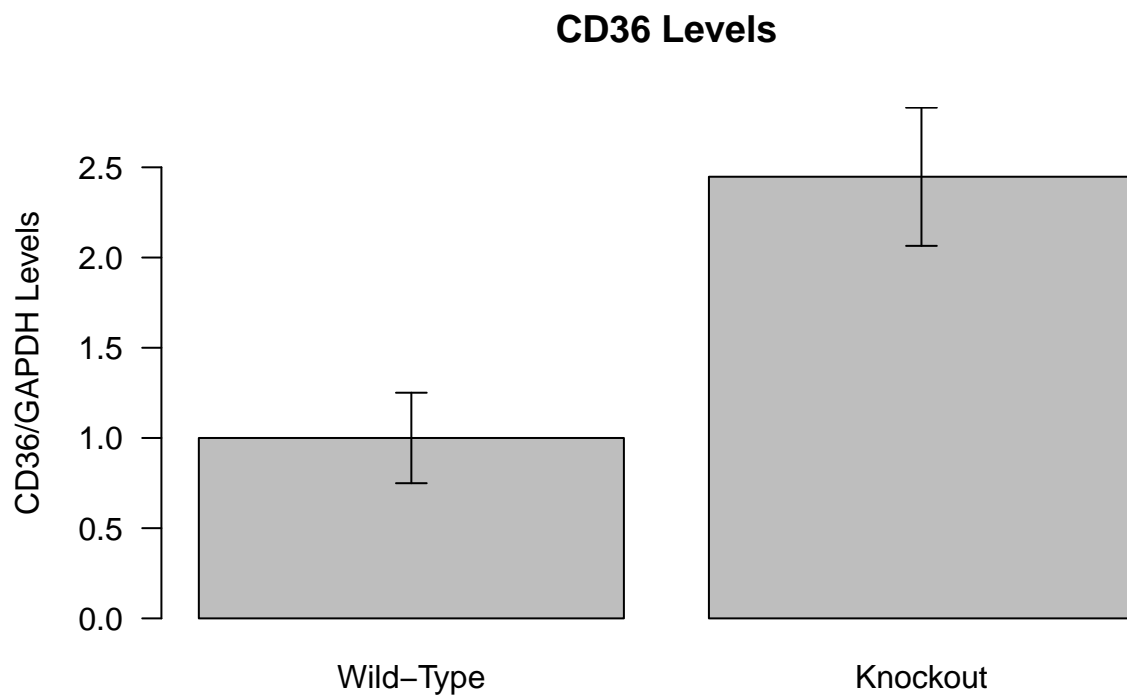Figure 6: Normalized Mitochondrial Protein Levels in Quadriceps

CD36 Levels

Figure 7: Normalized CD36 Levels in Quadriceps
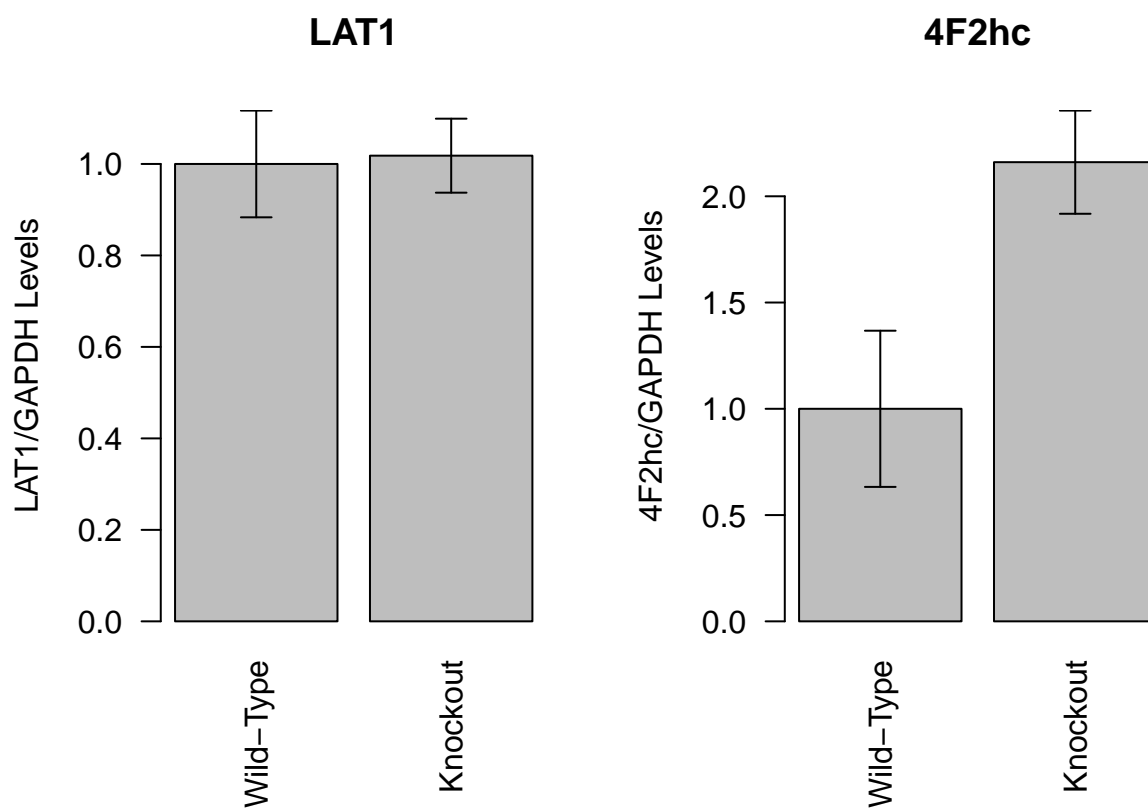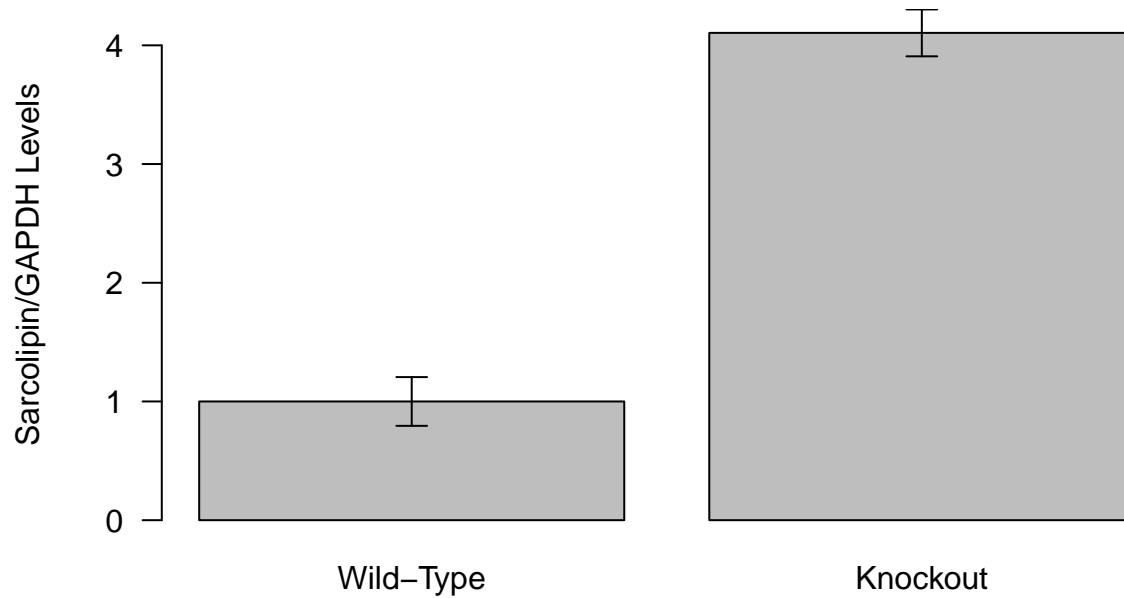
LAT1

4F2hc

Figure 8: Normalized LAT1 Protein Levels in Quadriceps

Sarcolipin

Statistics

Table 5: Statistical Summary

	Shapiro-WT	Shapiro-KO	Wilcoxon	Levene	Welch	Student
pS6K	0.648	0.446	0.008	0.076	0.001	0.000
pS6	0.058	0.133	0.008	0.772	0.003	0.003
pJNK	0.603	0.158	0.151	0.206	0.178	0.142
LC3	0.395	0.605	0.008	0.015	0.002	0.000
ATP5A	0.838	0.493	1.000	0.187	0.701	0.697
UQCRC2	0.361	0.281	0.841	0.118	0.444	0.435
MTCO1	0.045	0.911	0.548	0.815	0.820	0.819
SDHB	0.885	0.596	0.841	0.849	0.821	0.821
NDUF88	0.163	0.002	0.690	0.679	0.747	0.743
Sarcolipin	0.153	0.272	0.008	0.900	0.000	0.000
CD36	0.793	0.412	0.016	0.701	0.016	0.013

Sarcolipin is upregulated 4.105 fold, p=0 from a Student's t-test.

Session Information

- R version 3.5.0 (2018-04-23), `x86_64-apple-darwin15.6.0`

- Locale: `en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8`

- Running under: `macOS  10.14.2`

- Matrix products: default

- BLAS: `/Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib`

- LAPACK: `/Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib`

- Base packages: base, datasets, graphics, grDevices, methods, stats, utils

- Other packages: bindrcpp 0.2.2, car 3.0-2, carData 3.0-2, dplyr 0.7.8, knitr 1.21, tidyr 0.8.2

- Loaded via a namespace (and not attached): abind 1.4-5, assertthat 0.2.0, bindr 0.1.1, cellranger 1.1.0, compiler 3.5.0, crayon 1.3.4, curl 3.2, data.table 1.11.8, digest 0.6.18, evaluate 0.12, forcats 0.3.0, foreign 0.8-71, glue 1.3.0, haven 2.0.0, highr 0.7, hms 0.4.2, htmltools 0.3.6, magrittr 1.5, openxlsx 4.1.0, pillar 1.3.1, pkgconfig 2.0.2, purrr 0.2.5, R6 2.3.0, Rcpp 1.0.0, readxl 1.2.0, rio 0.5.16, rlang 0.3.1, rmarkdown 1.11, stringi 1.2.4, stringr 1.3.1, tibble 2.0.0, tidyselect 0.2.5, tools 3.5.0, xfun 0.4, yaml 2.2.0, zip 1.0.0