

Quantification of AMPK Knockout Blots

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Contents

1 Purpose	1
2 Experimental Details	1
3 Raw Data	1
4 Analysis	2
5 Lipogenic Proteins	2
5.1 Fatty Acid Synthase	2
5.2 Acetyl-CoA Carboxylase	3
5.3 S6 Phosphorylation	5
6 Integrated Stress Response	6
7 Session Information	6

1 Purpose

2 Experimental Details

Blotted liver lysates for AMPK and ACC

3 Raw Data

These data can be found in `/Volumes/BridgesLab/Kistler/AMPK KO/Blots/Katherine Blots July 2020/Quantification` in files named `Male ACC.xls` and `Male pACC.xls`. This script was most recently updated on **Thu Jul 16 14:09:00 2020**.

4 Analysis

5 Lipogenic Proteins

5.1 Fatty Acid Synthase

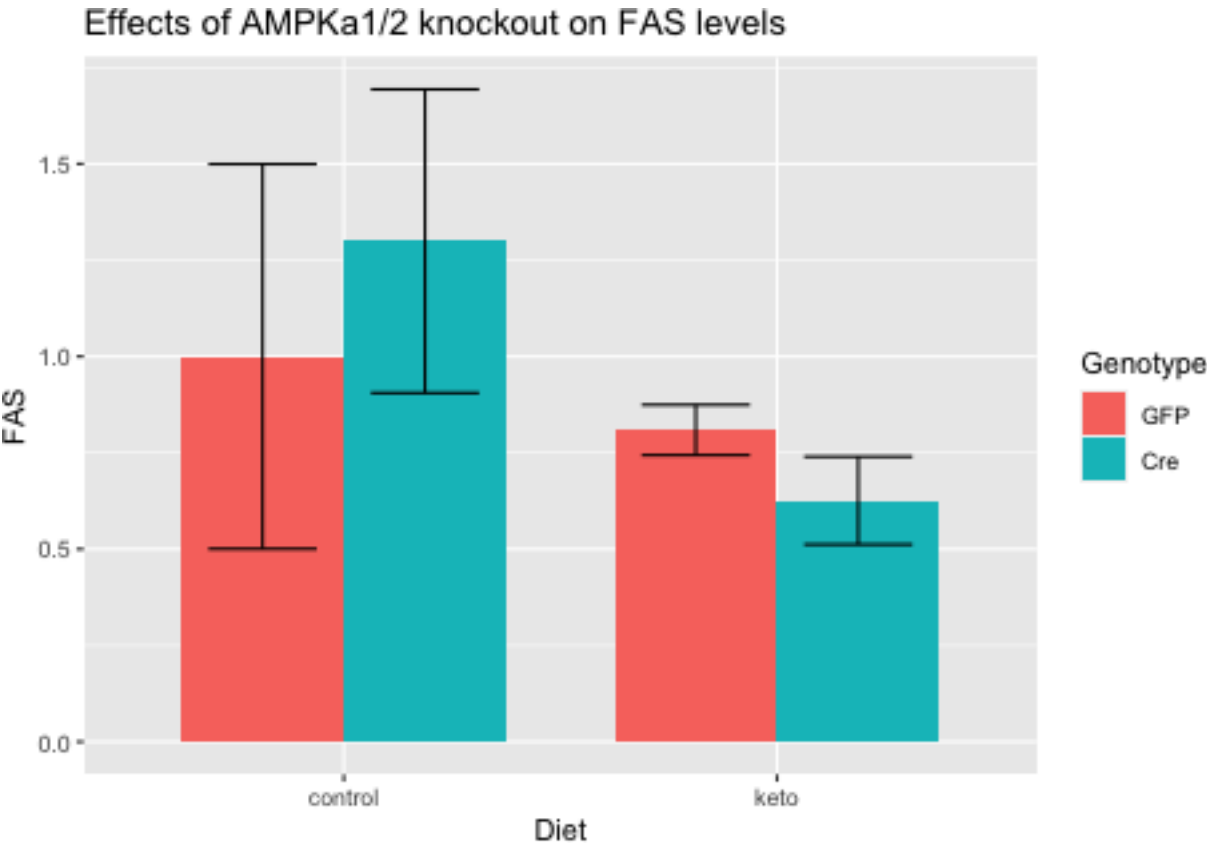


Table 1: ANOVA for FAS levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	2.29	0.161
Genotype	1	0	0	0.02	0.889
Residuals	10	0	0	NA	NA

Table 2: ANOVA for FAS levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	2.209	0.171
Genotype	1	0	0	0.020	0.892
Diet:Genotype	1	0	0	0.642	0.443
Residuals	9	0	0	NA	NA

5.2 Acetyl-CoA Carboxylase

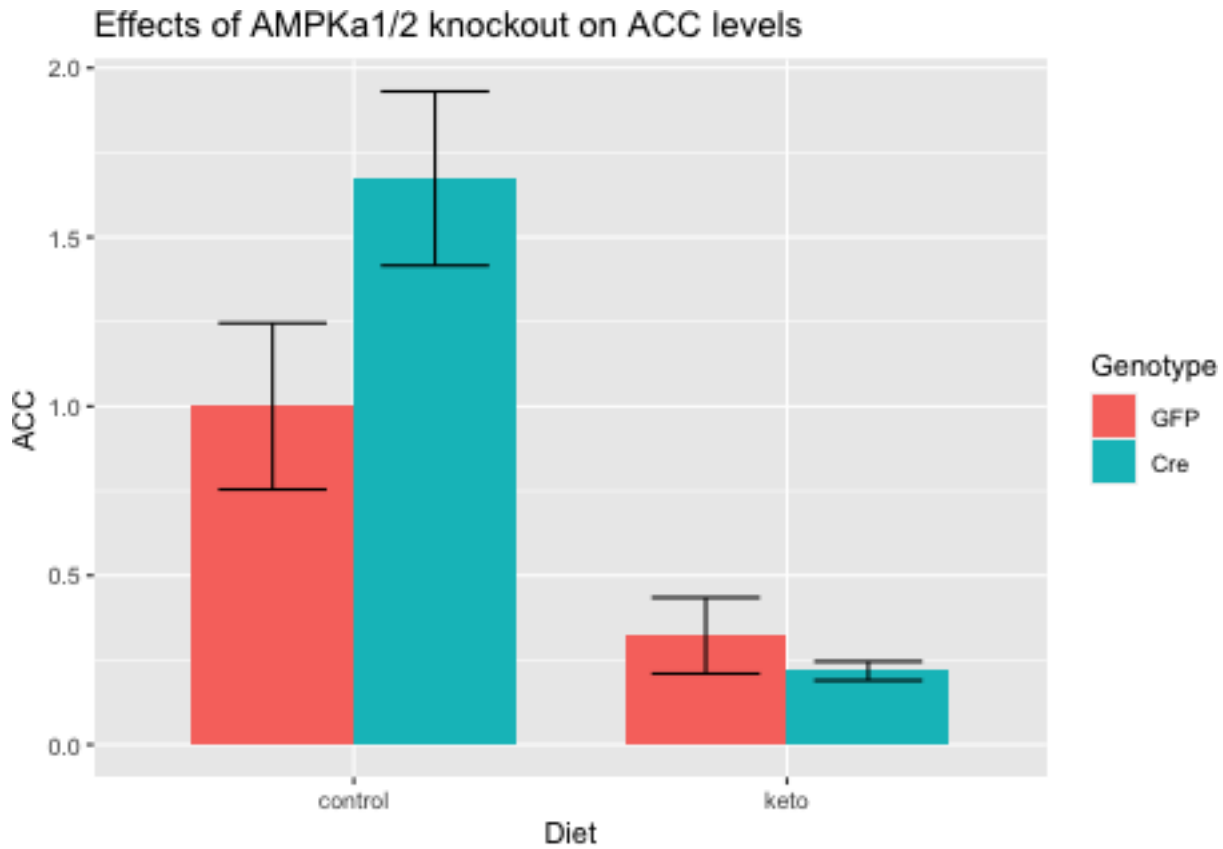


Table 3: ANOVA for ACC levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	28.05	0.000
Genotype	1	0	0	1.62	0.232
Residuals	10	0	0	NA	NA

Table 4: ANOVA for ACC levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	39.70	0.000
Genotype	1	0	0	2.29	0.165
Diet:Genotype	1	0	0	5.15	0.049
Residuals	9	0	0	NA	NA

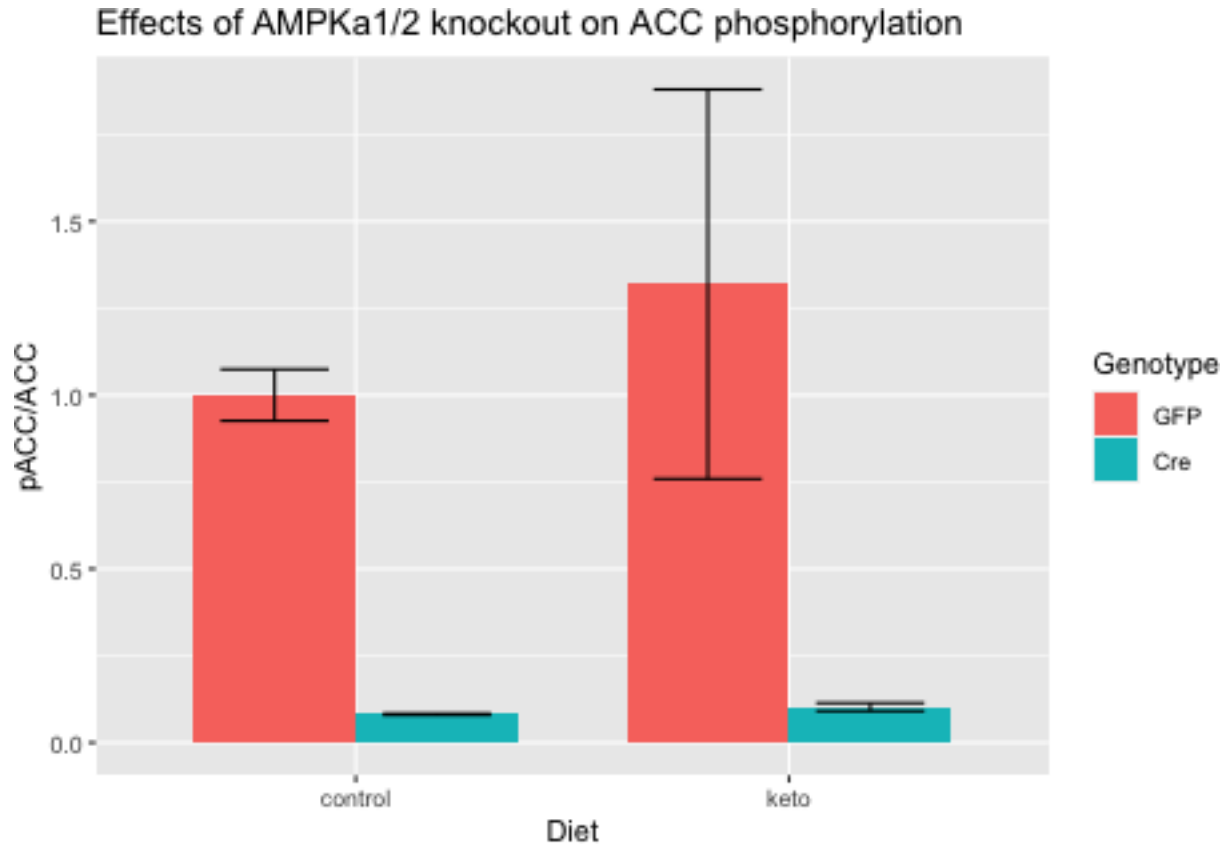


Table 5: ANOVA for ACC phosphorylation, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.305	0.305	0.112	0.744
Genotype	1	50.890	50.890	18.766	0.001
Residuals	10	27.118	2.712	NA	NA

Table 6: ANOVA for ACC phosphorylation, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.305	0.305	0.105	0.753
Genotype	1	50.890	50.890	17.515	0.002
Diet:Genotype	1	0.969	0.969	0.334	0.578
Residuals	9	26.149	2.905	NA	NA

5.3 S6 Phosphorylation

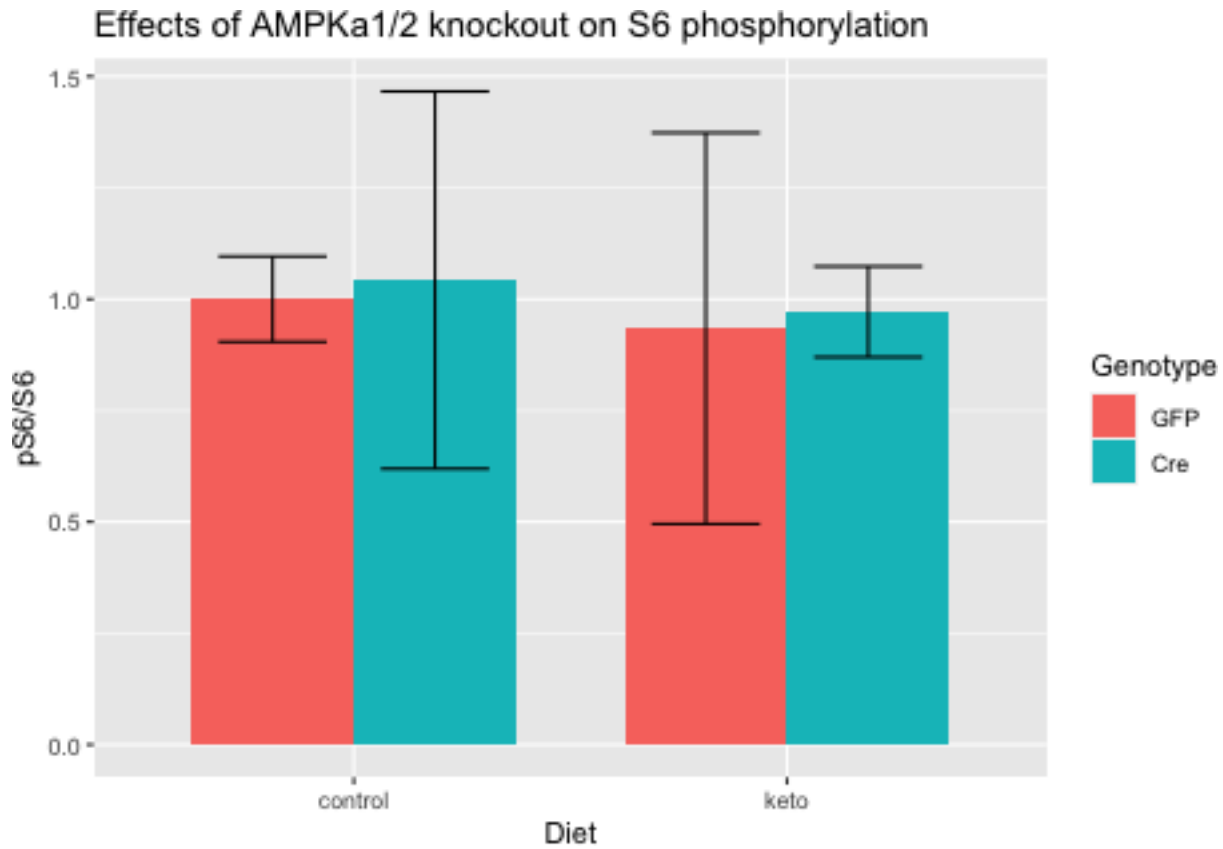


Table 7: ANOVA for S6 phosphorylation, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.726	0.726	0.058	0.815
Genotype	1	0.264	0.264	0.021	0.887
Residuals	10	125.354	12.535	NA	NA

Table 8: ANOVA for S6 phosphorylation, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.726	0.726	0.052	0.825
Genotype	1	0.264	0.264	0.019	0.893
Diet:Genotype	1	0.001	0.001	0.000	0.993
Residuals	9	125.353	13.928	NA	NA

6 Integrated Stress Response

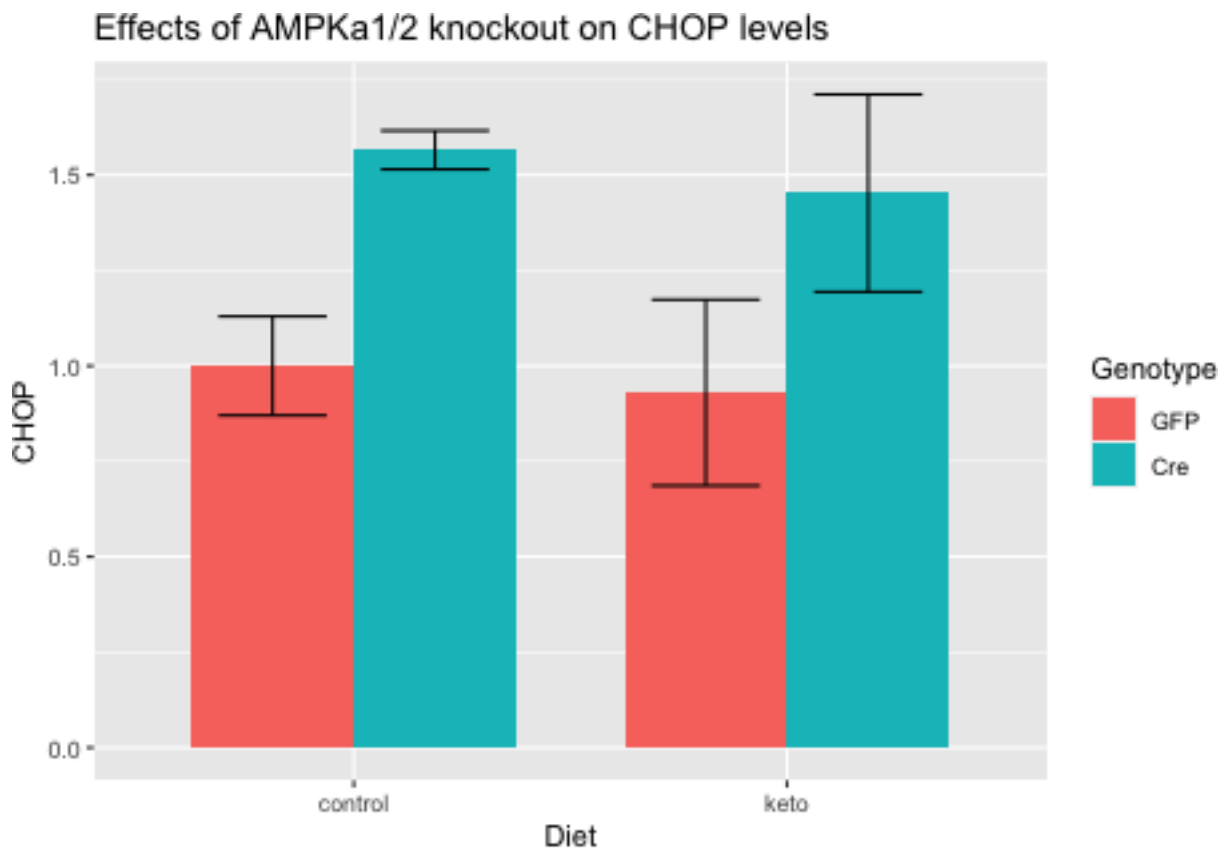


Table 9: ANOVA for CHOP levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	0.075	0.790
Genotype	1	0	0	7.416	0.021
Residuals	10	0	0	NA	NA

Table 10: ANOVA for CHOP levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	0.067	0.801
Genotype	1	0	0	6.682	0.029
Diet:Genotype	1	0	0	0.010	0.921
Residuals	9	0	0	NA	NA

7 Session Information

```
sessionInfo()
```

```
## R version 4.0.0 (2020-04-24)
```

```

## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.5
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRblas.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/4.0/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## other attached packages:
## [1] broom_0.5.6   ggplot2_3.3.0 readxl_1.3.1  dplyr_0.8.5   tidyr_1.0.3
## [6] knitr_1.28
##
## loaded via a namespace (and not attached):
## [1] Rcpp_1.0.4.6    highr_0.8      plyr_1.8.6     pillar_1.4.4
## [5] compiler_4.0.0  cellranger_1.1.0 tools_4.0.0     digest_0.6.25
## [9] evaluate_0.14   lifecycle_0.2.0 tibble_3.0.1    gtable_0.3.0
## [13] nlme_3.1-147    lattice_0.20-41 pkgconfig_2.0.3 rlang_0.4.6
## [17] magick_2.3      yaml_2.2.1     xfun_0.13      withr_2.2.0
## [21] stringr_1.4.0   generics_0.0.2 vctrs_0.2.4     grid_4.0.0
## [25] tidyselect_1.0.0 glue_1.4.0      R6_2.4.1        rmarkdown_2.1
## [29] purrr_0.3.4     farver_2.0.3   magrittr_1.5    backports_1.1.6
## [33] scales_1.1.0    ellipsis_0.3.0 htmltools_0.4.0 assertthat_0.2.1
## [37] colorspace_1.4-1 labeling_0.3     stringi_1.4.6   munsell_0.5.0
## [41] crayon_1.3.4

```