Quantification of AMPK Knockout Blots

Katherine Kistler

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2 Experimental Details

Blotted liver lysates for AMPK and ACC

3 Raw Data

These data can be found in **/Users/davebrid/Documents/GitHub/TissueSpecificTscKnockouts/Mouse Data/Liver AMPK Ketogenic Diet/All Figures/Blots/Quantification** in files named **Male ACC.xls** and **Male pACC.xls**. This script was most recently updated on **Sun Aug 2 18:18:59 2020**.

4 Analysis

5 Lipogenic Proteins

5.1 Fatty Acid Synthase

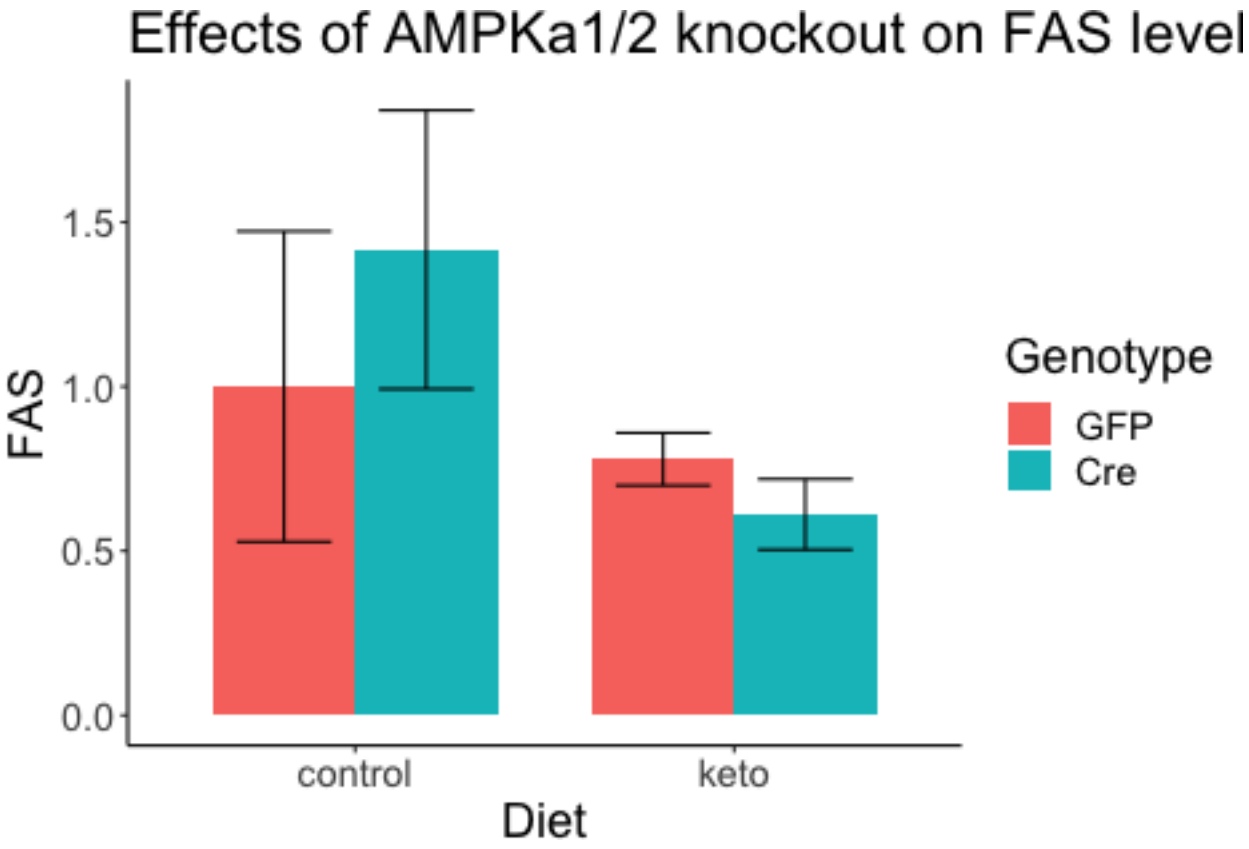

Table 1: ANOVA for FAS levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	3.109	0.108
Genotype	1	0	0	0.123	0.733
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	3.093	0.113
Genotype	1	0	0	0.122	0.734
Diet:Genotype	1	0	0	0.949	0.356
Residuals	9	0	0	NA	NA

5.2 Acetyl-CoA Carboxylase

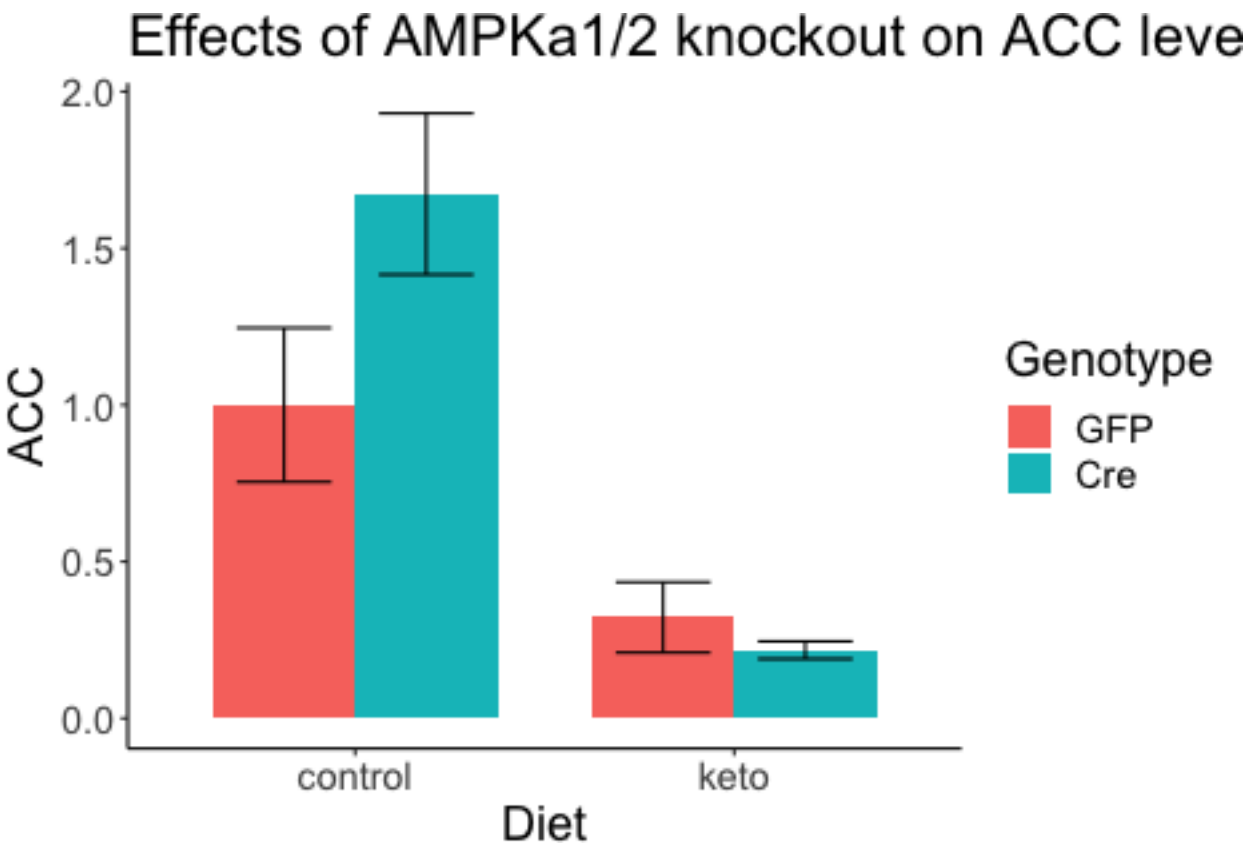

Table 3: ANOVA for ACC levels, no interaction

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

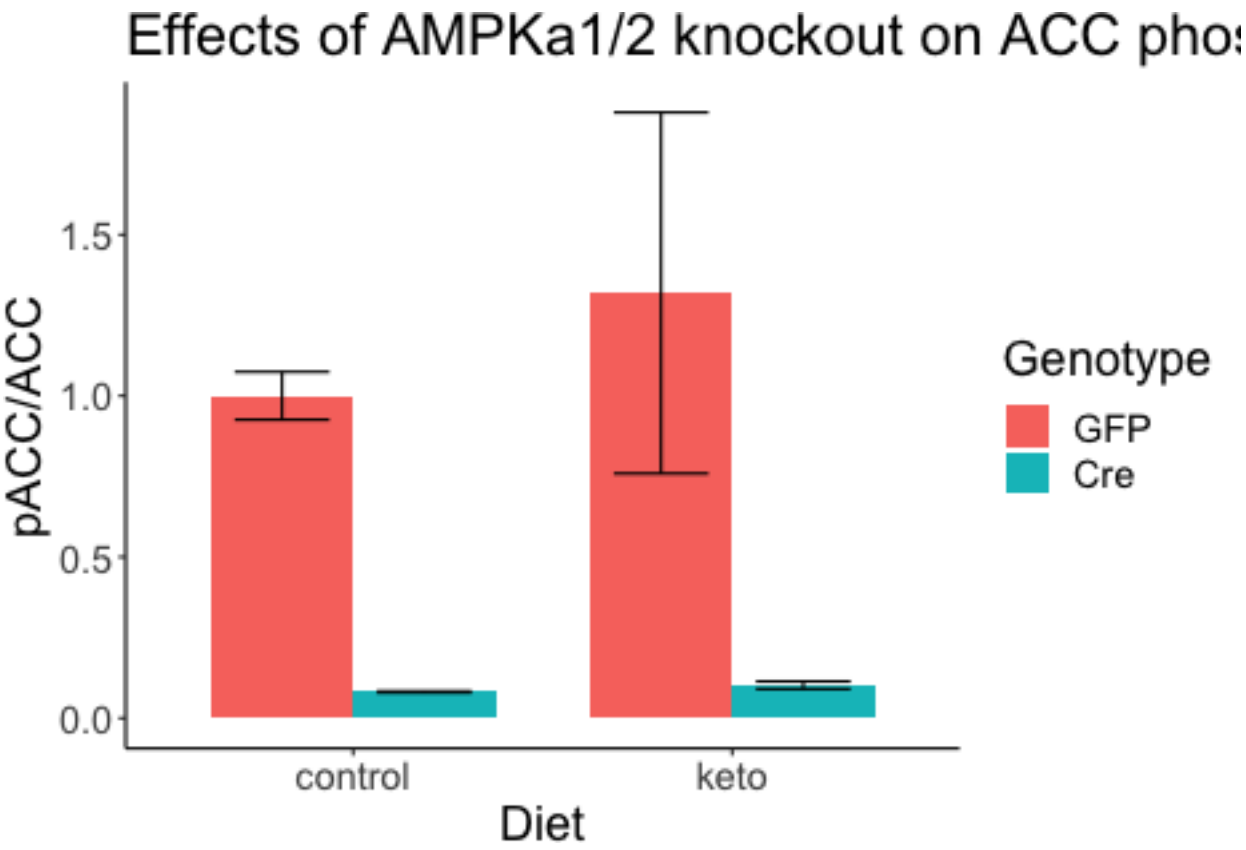

Table 5: ANOVA for ACC phosphorylation, no interaction

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

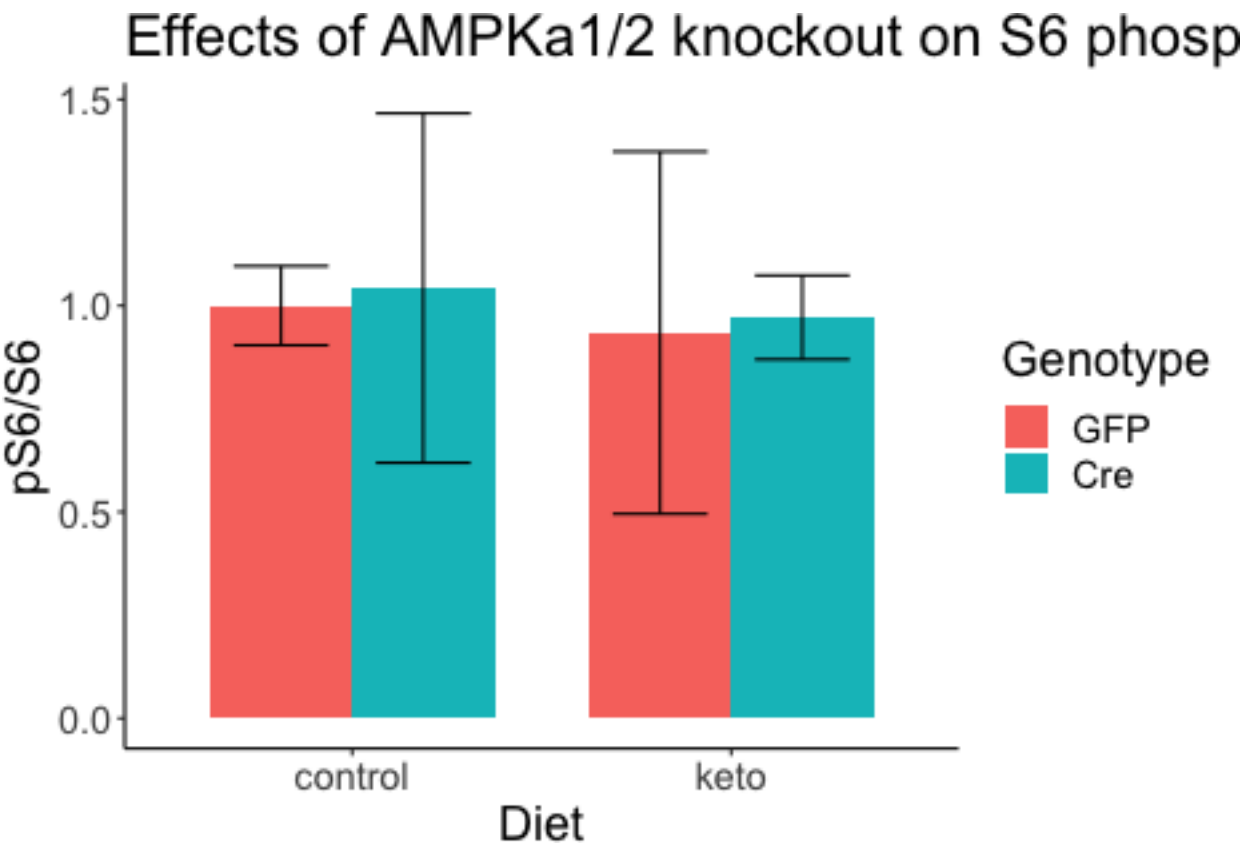

Table 7: ANOVA for S6 phosphorylation, no interaction

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

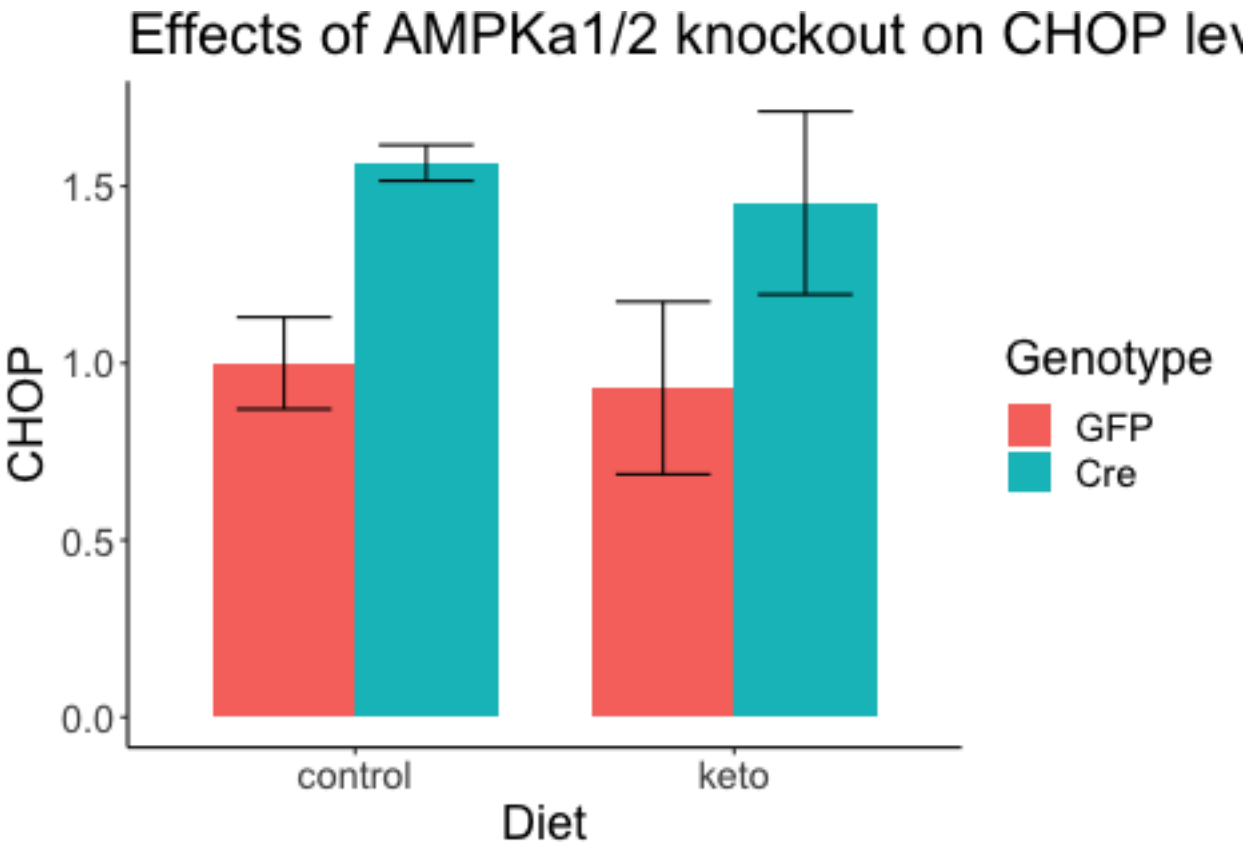

Table 9: ANOVA for CHOP levels, no interaction

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

6.1 AMP Activated Protein Kinase

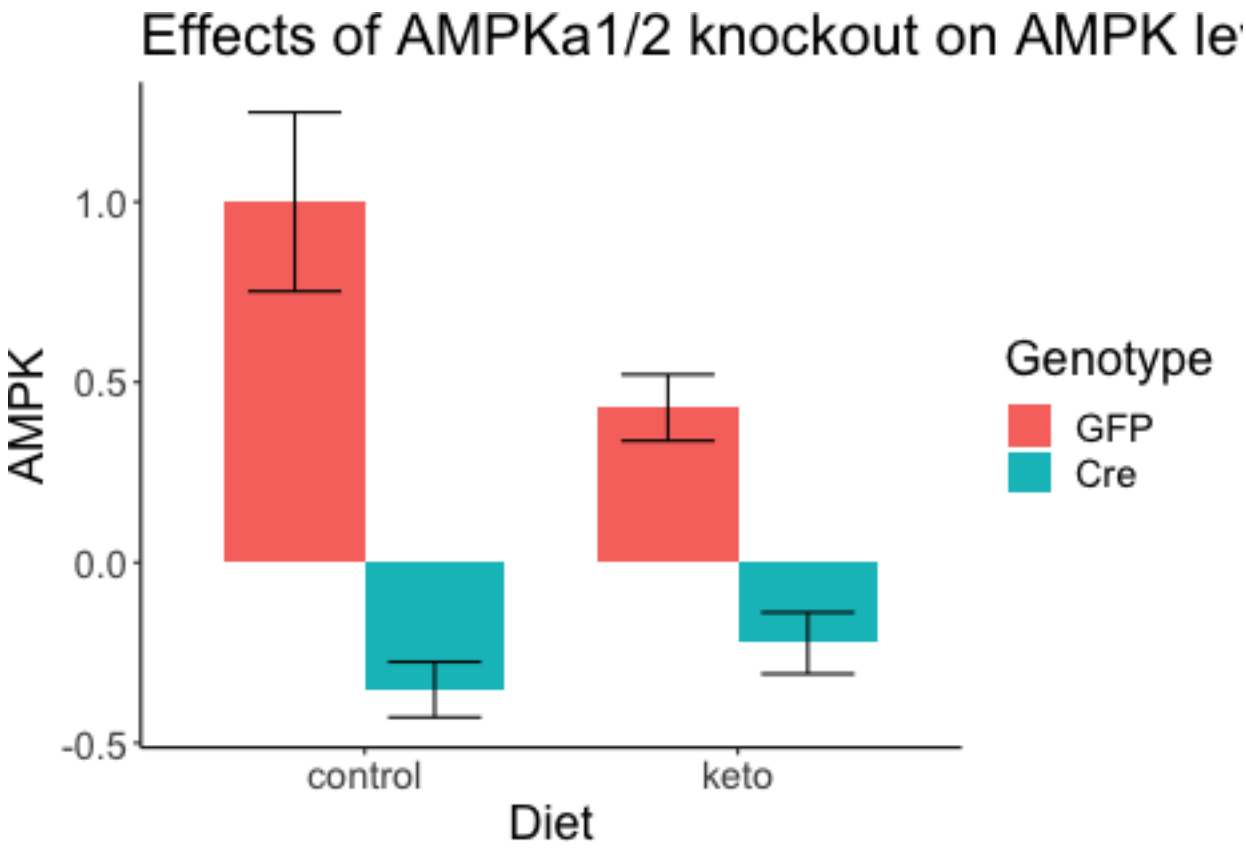

Table 11: ANOVA for AMPK levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	2.48	0.147
Genotype	1	0	0	32.99	0.000
Residuals	10	0	0	NA	NA

Table 12: ANOVA for AMPK levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	3.83	0.082
Genotype	1	0	0	51.11	0.000
Diet:Genotype	1	0	0	6.49	0.031
Residuals	9	0	0	NA	NA

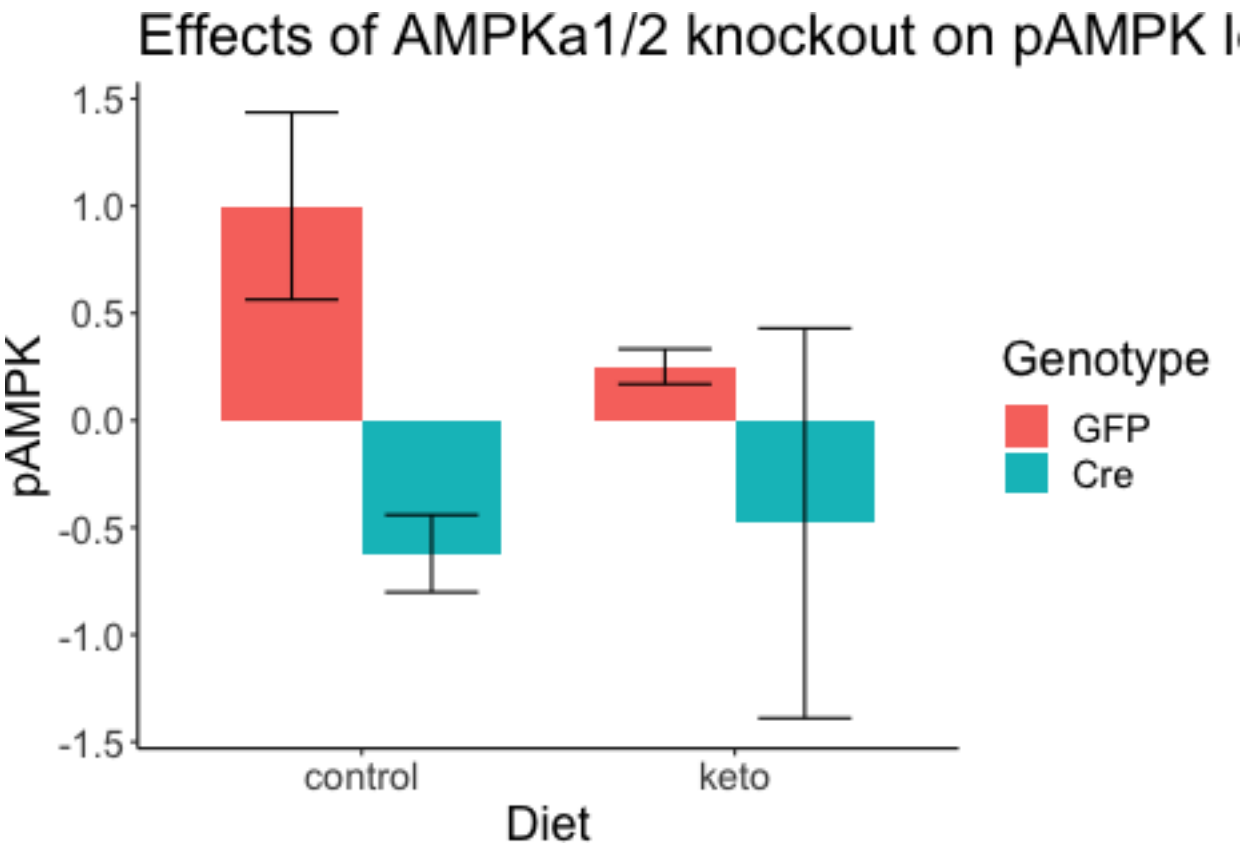

Table 13: ANOVA for pAMPK levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.179	0.179	0.343	0.571
Genotype	1	1.852	1.852	3.538	0.089
Residuals	10	5.235	0.524	NA	NA

Table 14: ANOVA for pAMPK levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0.179	0.179	0.326	0.582
Genotype	1	1.852	1.852	3.363	0.100
Diet:Genotype	1	0.278	0.278	0.505	0.496
Residuals	9	4.957	0.551	NA	NA

6.2 ATP citrate lyase

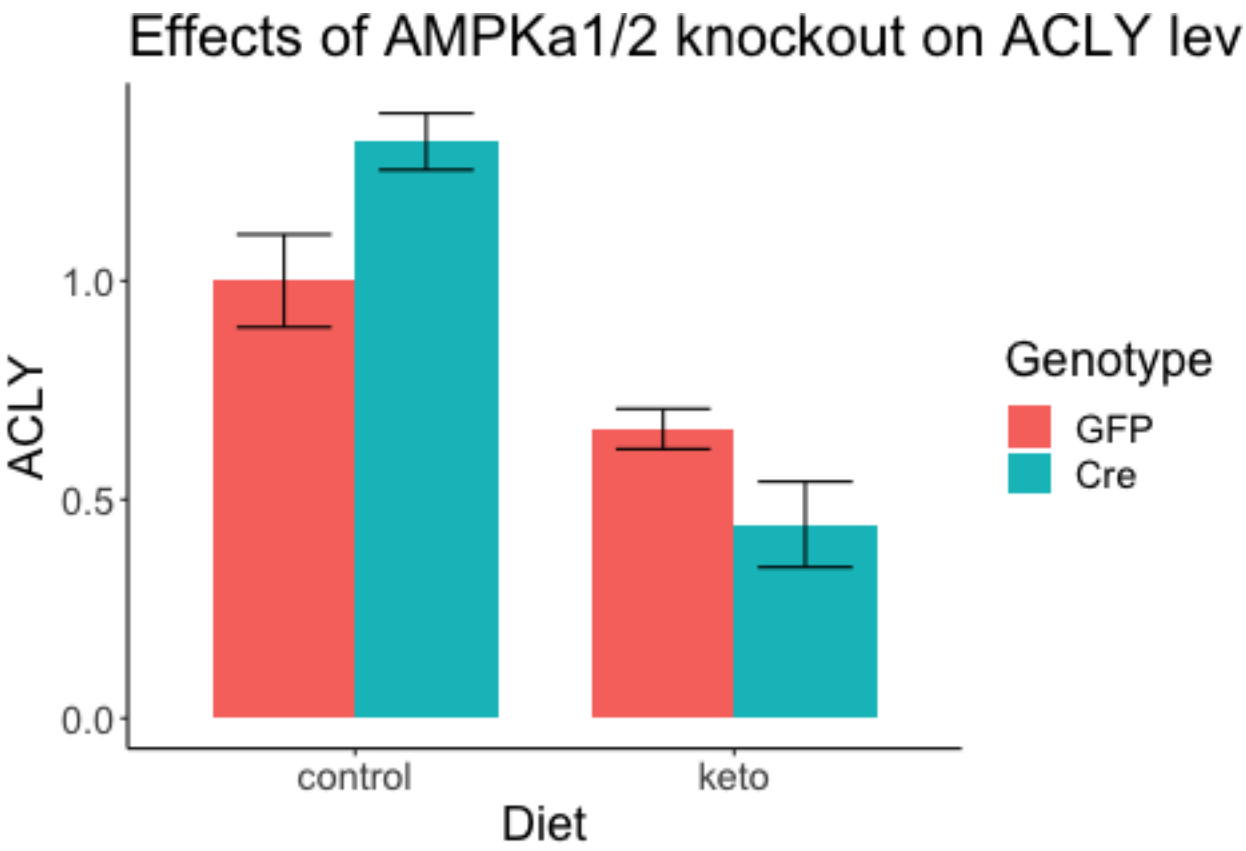

Table 15: ANOVA for ACLY levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	27.777	0.000
Genotype	1	0	0	0.073	0.792
Residuals	10	0	0	NA	NA

Table 16: ANOVA for ACLY levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	51.166	0.000
Genotype	1	0	0	0.135	0.722
Diet:Genotype	1	0	0	9.420	0.013
Residuals	9	0	0	NA	NA

6.3 Mitochondria Complexes Band 1

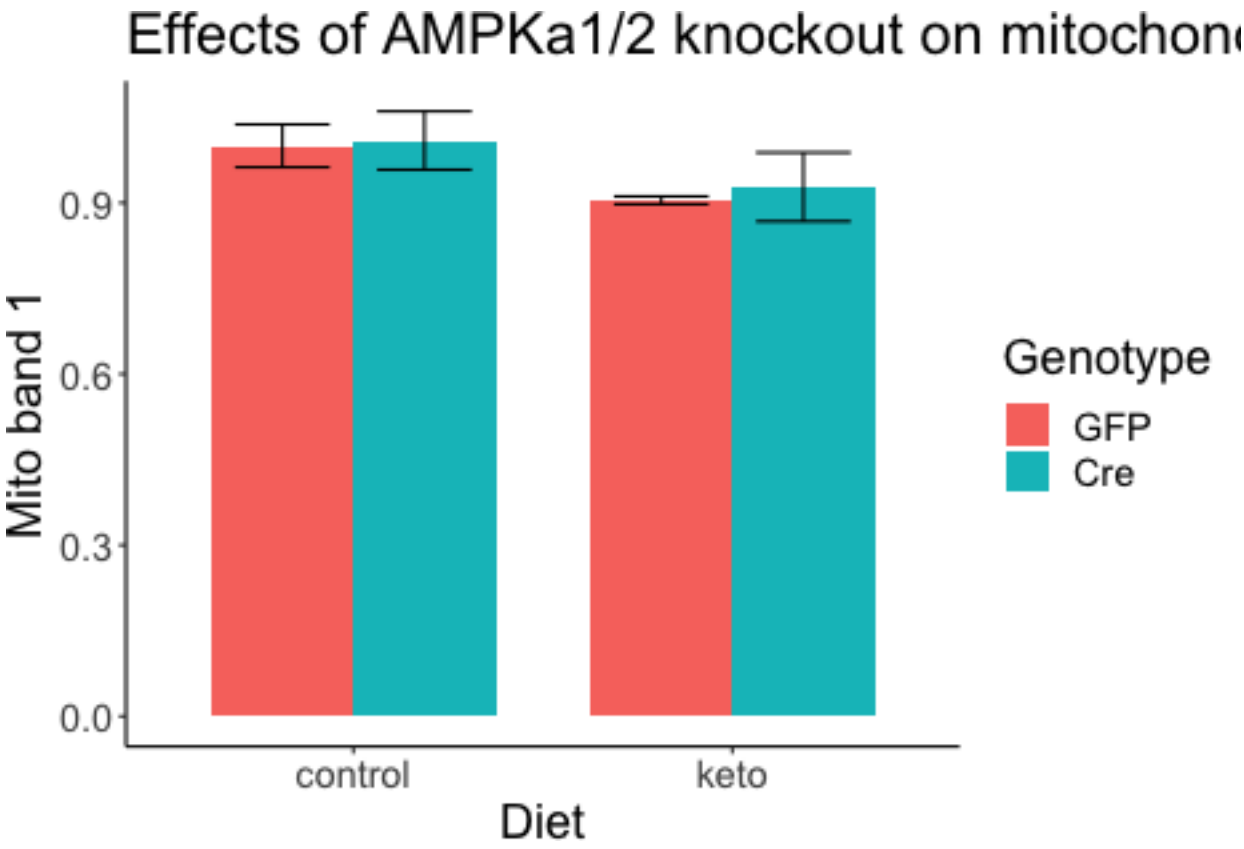

Table 17: ANOVA for mitochondira band 1 levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	3.563	0.088
Genotype	1	0	0	0.132	0.724
Residuals	10	0	0	NA	NA

Table 18: ANOVA for mitochondira band 1 levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	3.214	0.107
Genotype	1	0	0	0.119	0.738
Diet:Genotype	1	0	0	0.021	0.887
Residuals	9	0	0	NA	NA

6.4 Mitochondira Complexes band 2

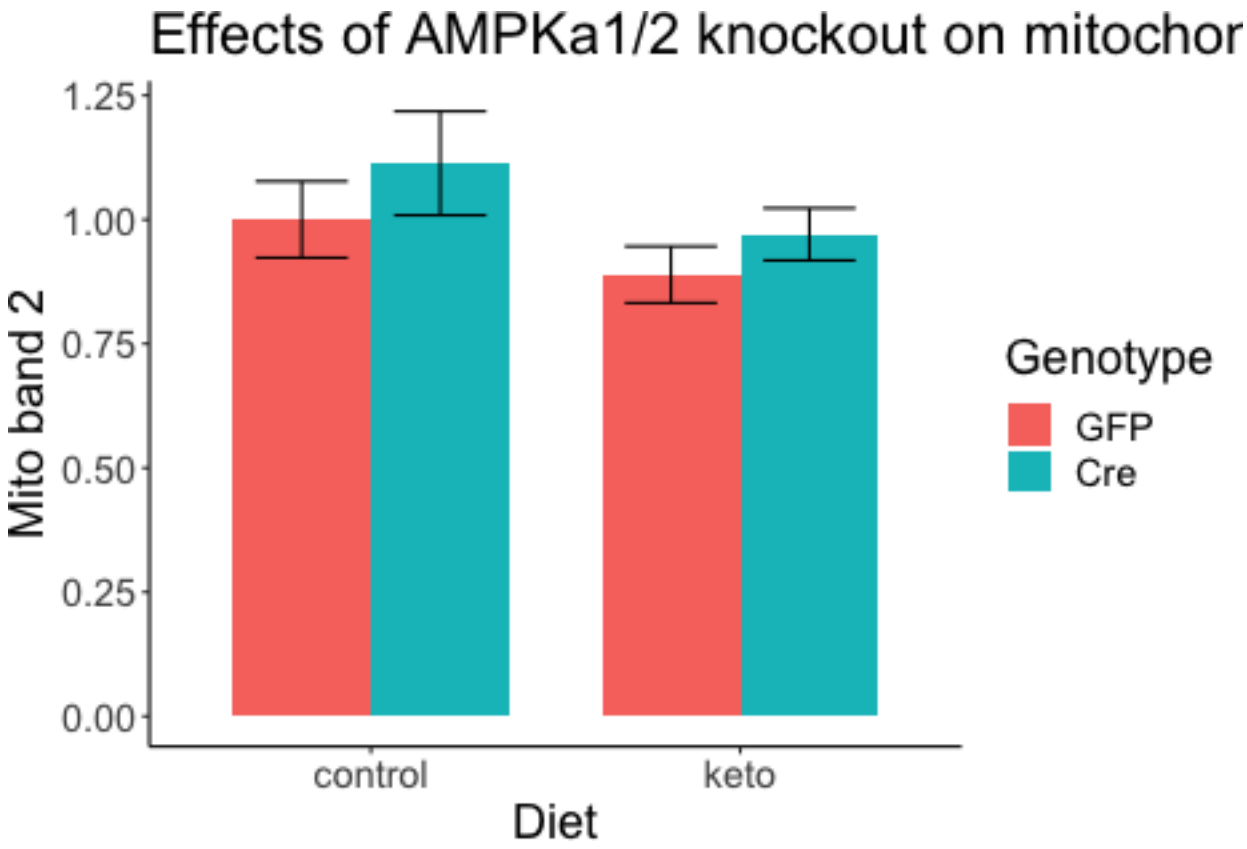

Table 19: ANOVA for mitochondira band 2 levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	3.07	0.110
Genotype	1	0	0	1.92	0.196
Residuals	10	0	0	NA	NA

Table 20: ANOVA for mitochondira band 2 levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	2.777	0.13
Genotype	1	0	0	1.741	0.22
Diet:Genotype	1	0	0	0.049	0.83
Residuals	9	0	0	NA	NA

6.5 Mitochondria Complexes Band 3

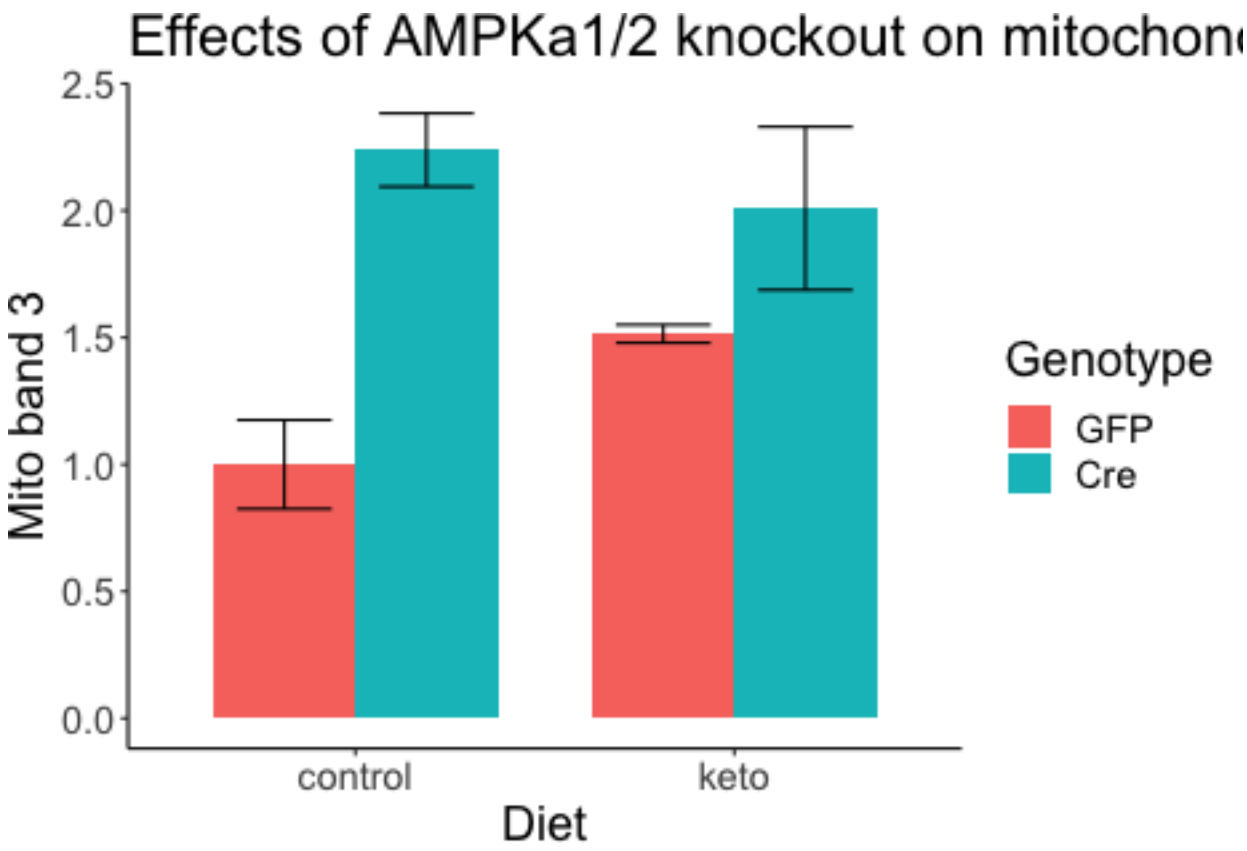

Table 21: ANOVA for mitochondira band 3 levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	0.509	0.492
Genotype	1	0	0	11.392	0.007
Residuals	10	0	0	NA	NA

Table 22: ANOVA for mitochondira band 3 levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	0.589	0.462
Genotype	1	0	0	13.175	0.005
Diet:Genotype	1	0	0	2.565	0.144
Residuals	9	0	0	NA	NA

6.6 Mitochondira Complexes Band 4

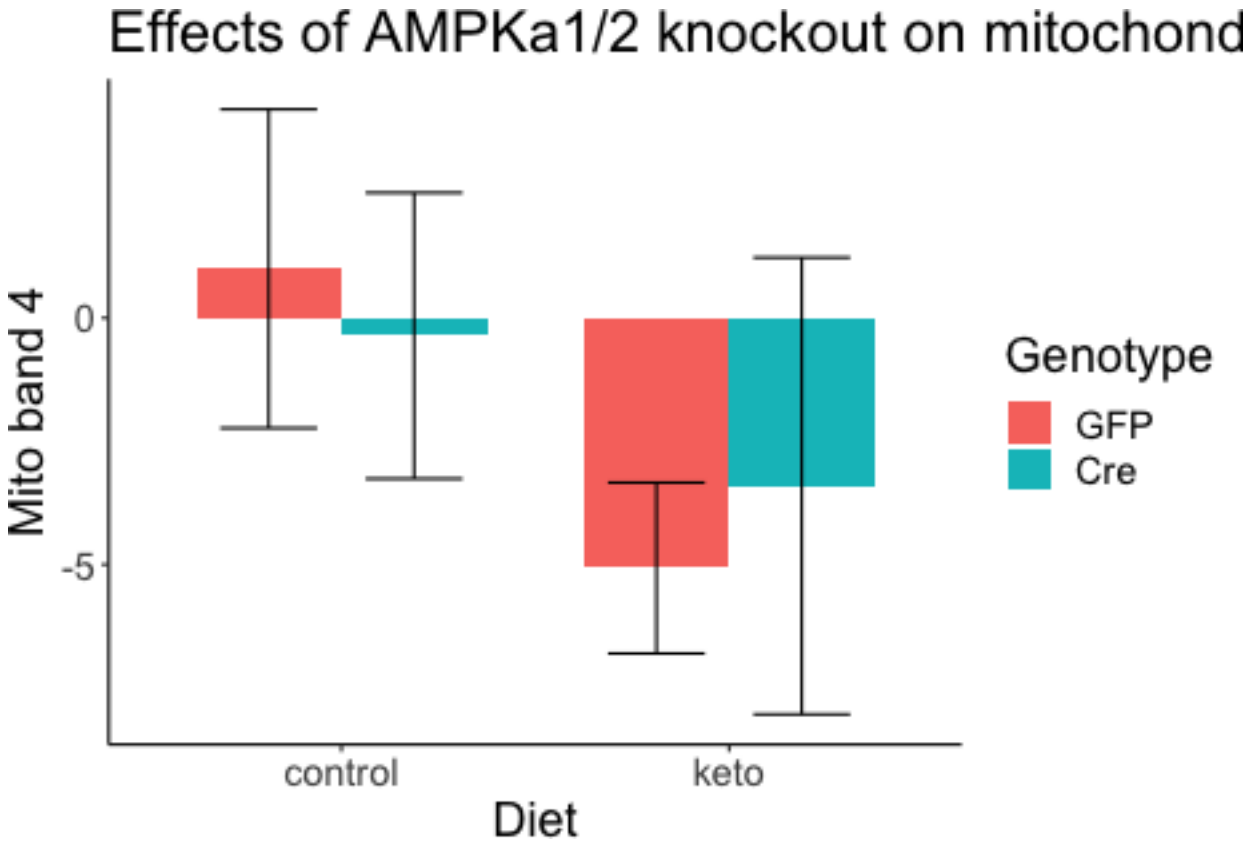

Table 23: ANOVA for mitochondira band 4 levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	1.608	0.233
Genotype	1	0	0	0.005	0.944
Residuals	10	0	0	NA	NA

Table 24: ANOVA for mitochondira band 4 levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	1.475	0.255
Genotype	1	0	0	0.005	0.946
Diet:Genotype	1	0	0	0.170	0.690
Residuals	9	0	0	NA	NA

6.7 Mitochondria Complexes Band 5

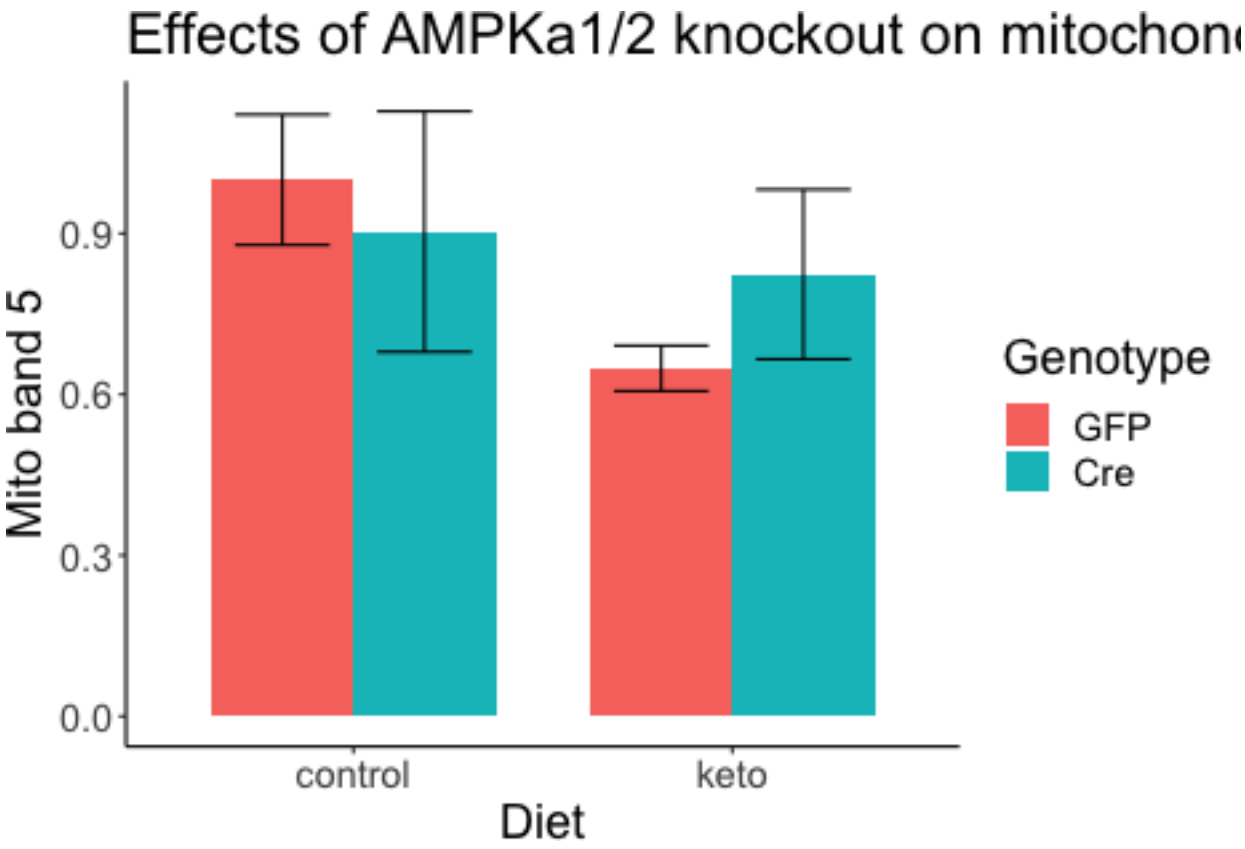

Table 25: ANOVA for mitochondira band 5 levels, no interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	1.751	0.215
Genotype	1	0	0	0.099	0.760
Residuals	10	0	0	NA	NA

Table 26: ANOVA for mitochondira band 5 levels, with interaction

term	df	sumsq	meansq	statistic	p.value
Diet	1	0	0	1.708	0.224
Genotype	1	0	0	0.096	0.763
Diet:Genotype	1	0	0	0.759	0.406
Residuals	9	0	0	NA	NA

7 Session Information

```
sessionInfo()
```

```
## R version 4.0.2 (2020-06-22)
```

```
## Platform: x86_64-apple-darwin17.0 (64-bit)
## Running under: macOS Catalina 10.15.6
##
## 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_0.7.0   ggplot2_3.3.2 readxl_1.3.1  dplyr_1.0.1   tidyr_1.1.1
## [6] knitr_1.29
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.5       magrittr_1.5     munsell_0.5.0    tidyselect_1.1.0
##  [5] colorspace_1.4-1 R6_2.4.1         rlang_0.4.7      highr_0.8
##  [9] stringr_1.4.0    tools_4.0.2      grid_4.0.2       gtable_0.3.0
## [13] xfun_0.16        withr_2.2.0      htmltools_0.5.0  ellipsis_0.3.1
## [17] yaml_2.2.1       digest_0.6.25    tibble_3.0.3     lifecycle_0.2.0
## [21] crayon_1.3.4     farver_2.0.3     purrr_0.3.4      vctrs_0.3.2
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## [29] stringi_1.4.6    compiler_4.0.2   pillar_1.4.6     cellranger_1.1.0
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