Insulin Clamp Study on Mck-TSC1 Mice

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March 21, 2012

Contents

1 Experiment Summary

	Genotype	X.	ID	Basal.Glucose	Clamp.Glucose	Clamp.GIR	Clamp.AUC	Basal.SA	Clamp.SA	B
8	Knockout	8	245	88	113	38.3	4303	166204	158722	
11	Knockout	1	266	107	125	40.4	4206	144050	157520	
12	Knockout	2	267	139	114	14.5	1760	95930	120125	
13	Knockout	3	323	139	112	15.8	1938	282602	261183	
14	Knockout	4	371	117	138	31.2	3515	360233	286396	
15	Knockout	5	197	89	117	31.0	3235	163434	212528	
16	Knockout	6	184	110	112	25.3	2594	164238	200053	
17	Knockout	7	230	98	124	28.3	2967	164504	159853	
1	Wild-Type	1	370	137	135	21.1	2336	176774	166972	
2	Wild-Type	2	186	130	115	16.4	1857	127462	164844	
3	Wild-Type	3	269	126	118	25.4	2651	156866	139891	
4	Wild-Type	4	268	138	134	22.7	2640	90144	106372	
5	Wild-Type	5	377	145	143	23.3	2468	84227	108108	
6	Wild-Type	6	378	152	120	25.2	2535	107524	112819	
7	Wild-Type	7	381/wh	111	118	31.0	3294	127835	149024	

	Genotype	X.	ID	Basal.Glucose	Clamp.Glucose	Clamp.GIR	Clamp.AUC	Basal.SA	Clamp.SA	B
9	Wild-Type	9	381/br	103	110	32.6	3461	112970	139744	
10	Wild-Type	10	262	129	120	20.7	2457	151048	184565	

1.1 Data Summary

The mean data is compiled with the standard errors

1.2 Statistics

Table 2: Summary statistics for each measurement

WT	KO	Measurement	Difference	Pct.Difference
130.11	110.88	Basal.Glucose_mean	-19.236	-14.784
123.67	119.48	Clamp.Glucose_mean	-4.188	-3.386
24.26	28.10	Clamp.GIR_mean	3.848	15.866
2633.34	3064.68	Clamp.AUC_mean	431.333	16.380
126094.59	192649.32	Basal.SA_mean	66554.729	52.782
141370.92	194547.40	Clamp.SA_mean	53176.476	37.615
29.54	28.61	Basal.Gtr_mean	-0.930	-3.149
51.55	53.36	Clamp.Gtr_mean	1.803	3.496
29.54	28.61	Basal.HGP_mean	-0.930	-3.149
27.29	25.25	Clamp.HGP_mean	-2.034	-7.453
7.37	16.95	Clamp.sHGP_mean	9.586	130.108
16.35	16.49	Clearance.Basal_mean	0.133	0.811
27.32	33.34	Clearance.Clamp_mean	6.029	22.072
11.22	3.41	Insulin.Basal_mean	-7.813	-69.630
21.29	14.78	Insulin.Clamp_mean	-6.513	-30.593
13.03	13.08	Gastroc_mean	0.051	0.394
2.69	6.60	V.fat_mean	3.912	145.674
6.52	21.75	S.fat_mean	15.228	233.446
250.50	194.63	BAT_mean	-55.867	-22.302
445.18	341.70	Heart_mean	-103.473	-23.243

Table 3: T-Tests, Unadjusted

Clamp.GIR	0.325
Clamp.AUC	0.272
Basal.HGP	0.852
Clamp.HGP	0.792
sHGP	0.477
Clearance.Basal	0.953
Clearance.Clamp	0.269
Insulin	0.008
Gastroc	0.984
V.fat	0.027
S.fat	0.006
BAT	0.341
Heart.fit	0.131

Table 4: Nominal and Benjamini-Hochberg Adjusted T-Tests

Clamp.GIR	Clamp.AUC	Basal.HGP	Clamp.HGP	sHGP	Clearance.Basal	Clearance.Clamp	Insulin	Gastroc
1	1	1	1	1	1	1	0.09	1

2 Graphs

2.1 Glucose Infusion Rate

Glucose Infusion Rate (mg/kg/min)
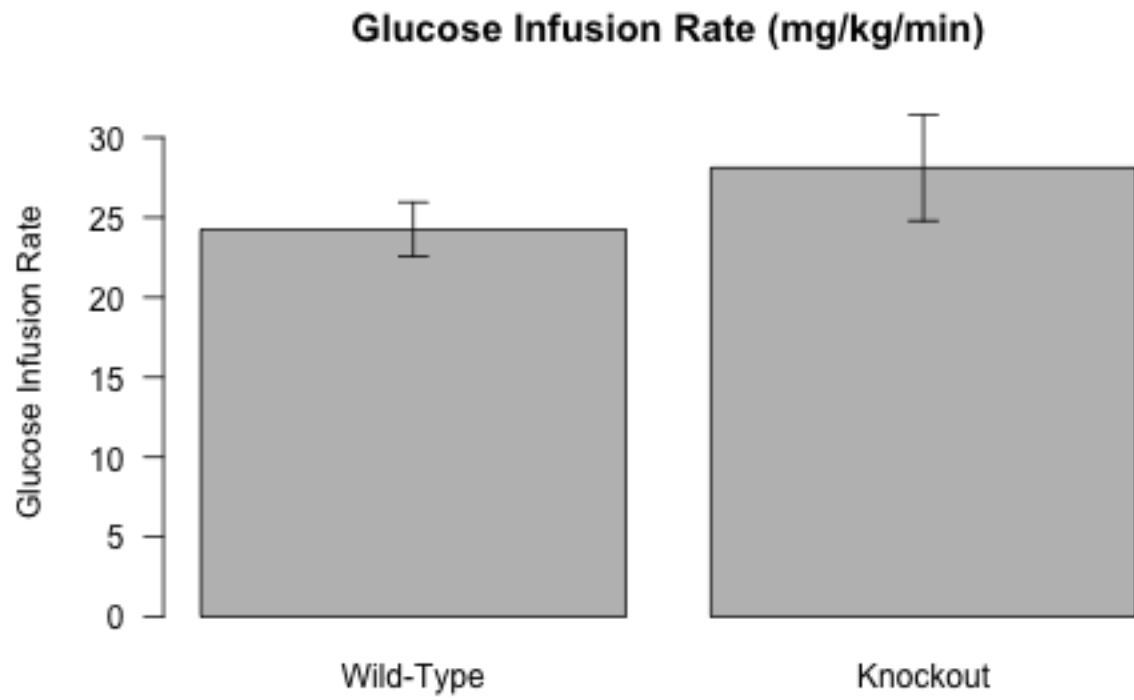
2.2 Glucose Turnover

Glucose Turnover Rate
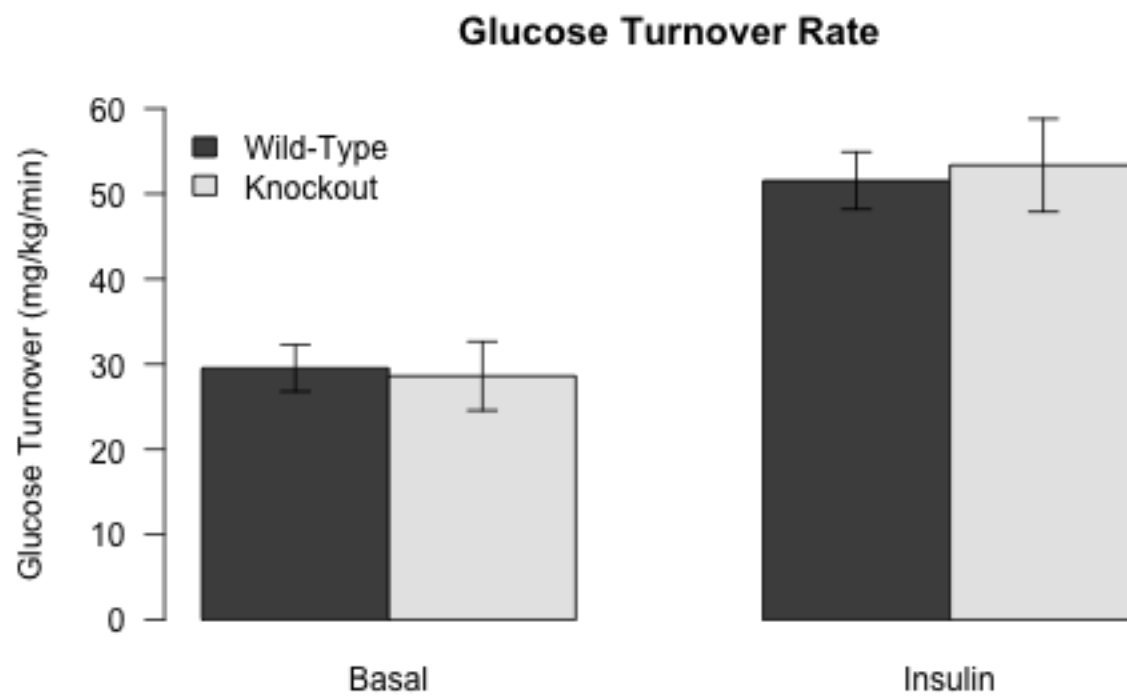
2.3 Endogenous Glucose Production

2.4   Clamp Summary

Glucose Infusion Rate During Clamp

Glucose Turnover Rate

Endogenous Glucose Production

2.4.1 Suppression of Endogenous Glucose Production
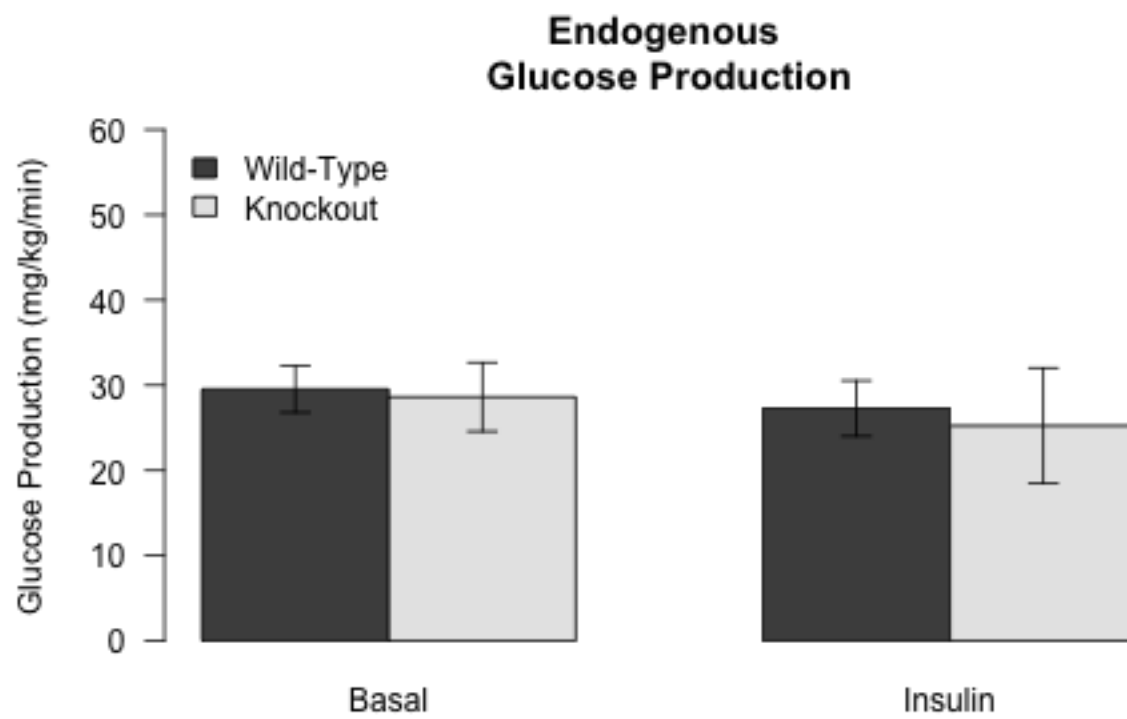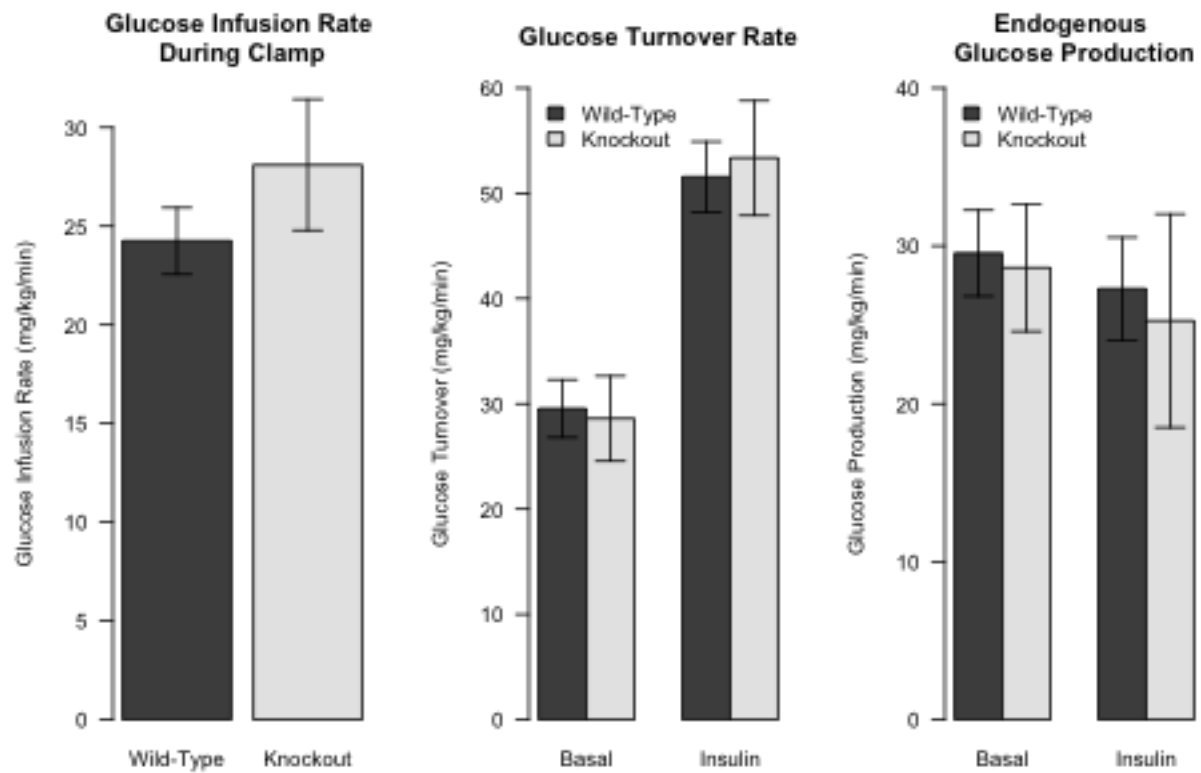
Suppression of Endogenous Glucose Production

2.5   Insulin Levels
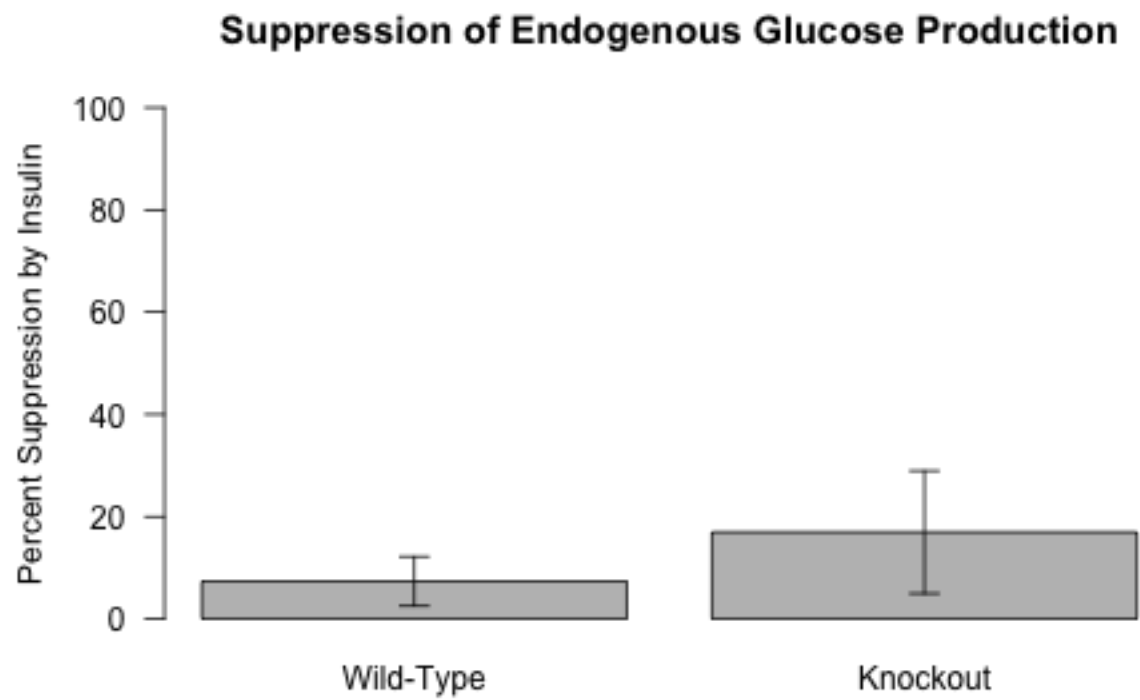
Insulin During Clamp
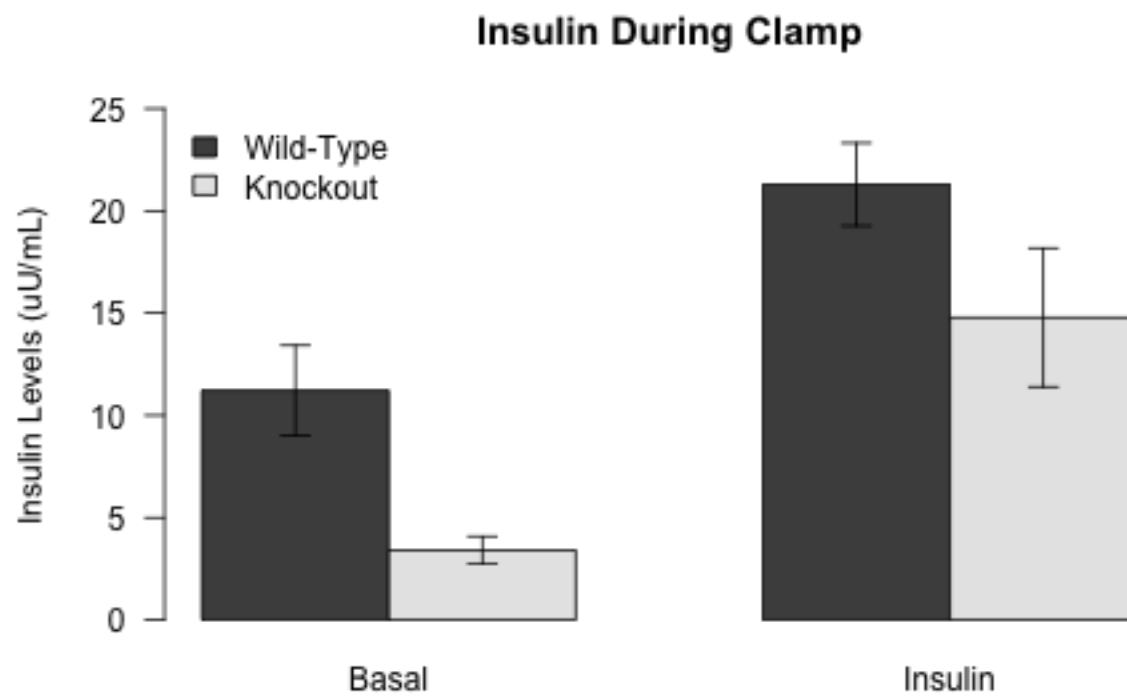
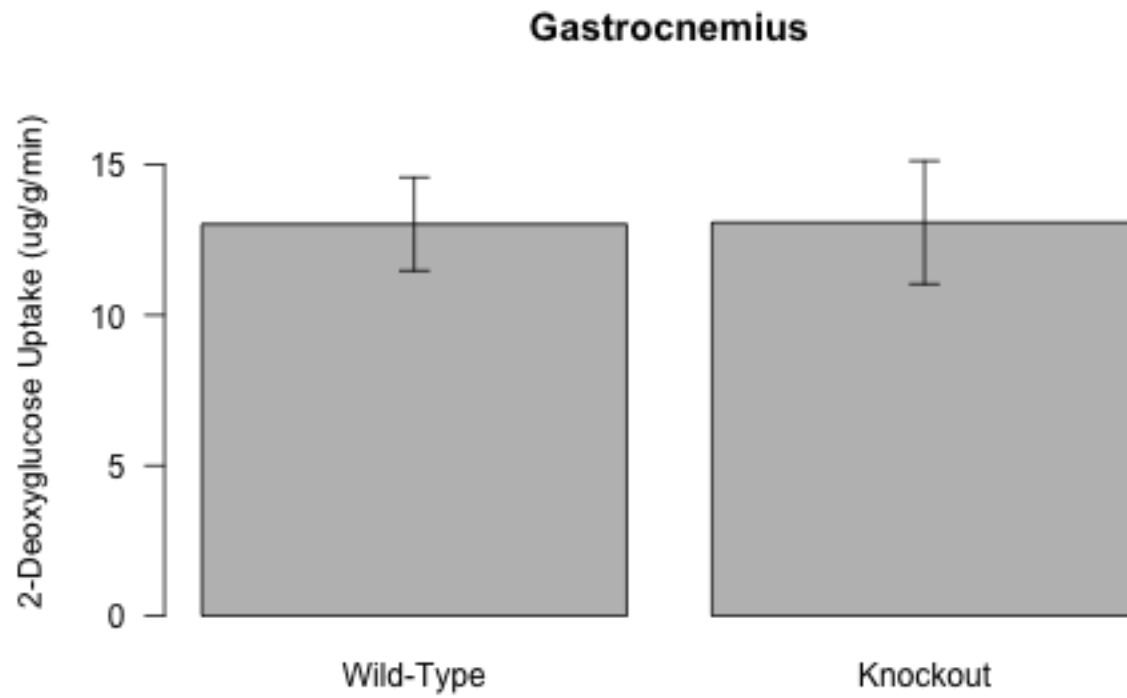# 3   Glucose Clearance Rate
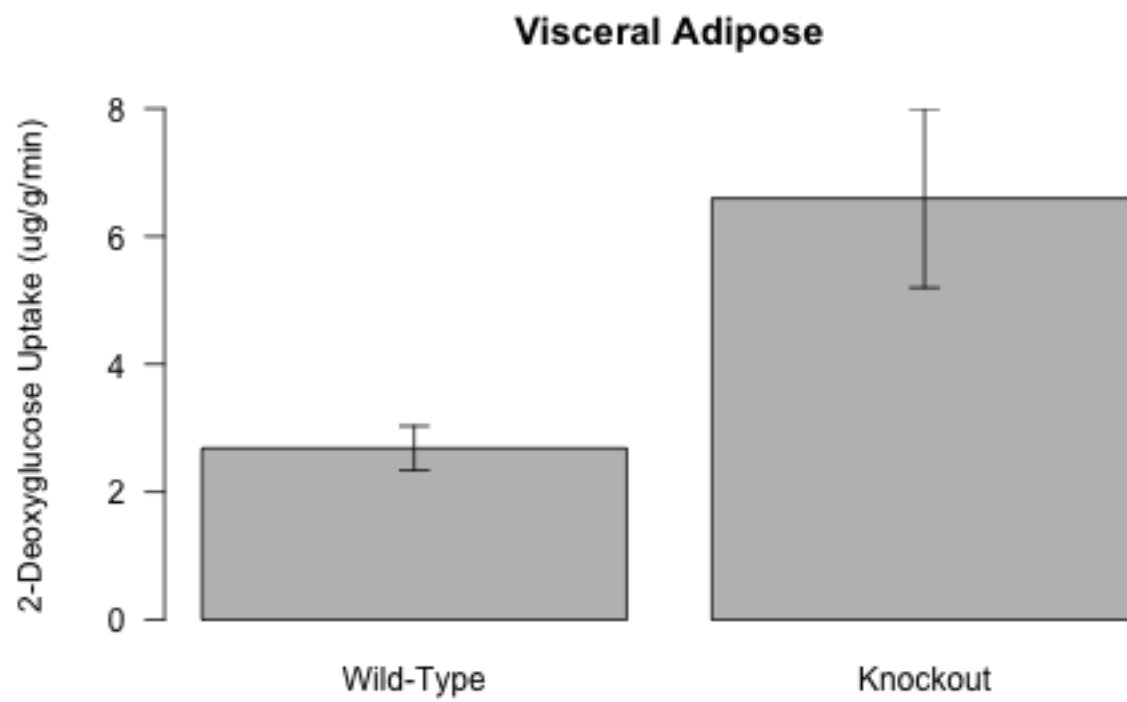
Blood glucose clearance

Glucose Clearance Rate
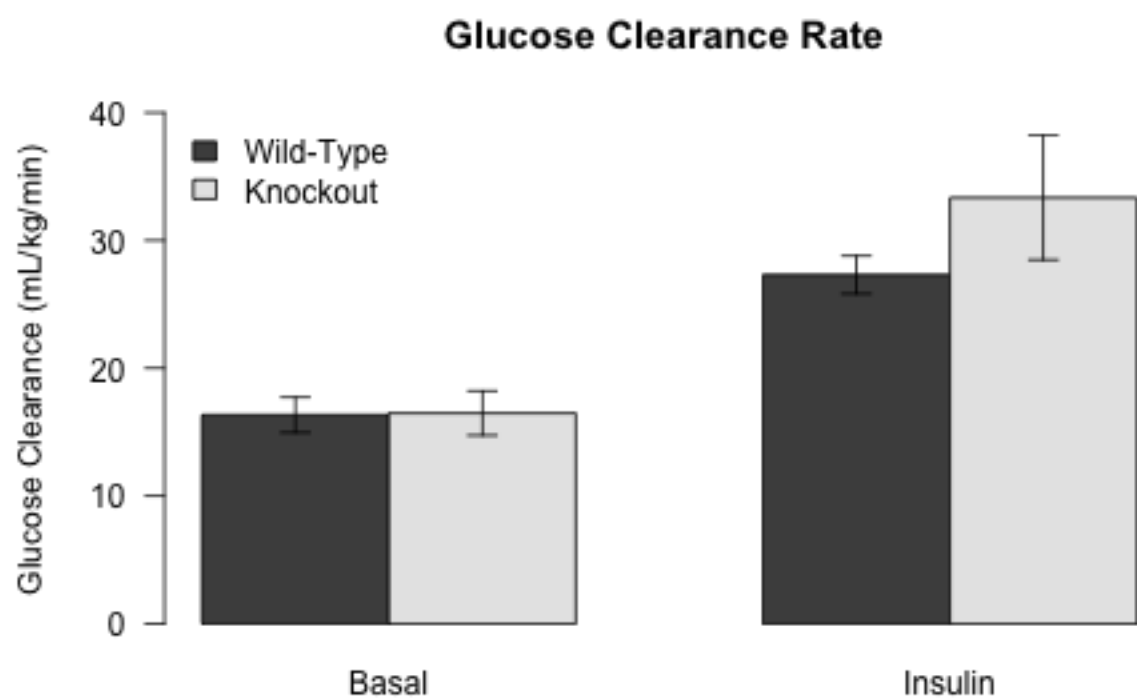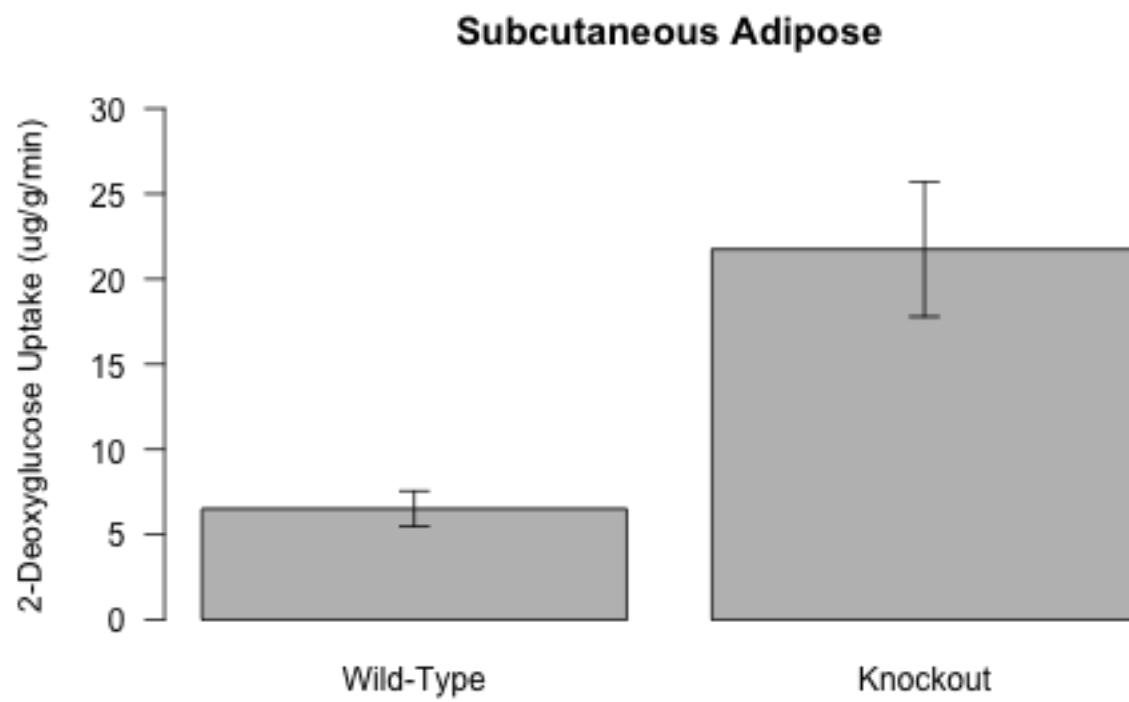
4   Tissue Glucose Clearance

4.1   Gasctrocnemius Gluose Uptake During Clamp
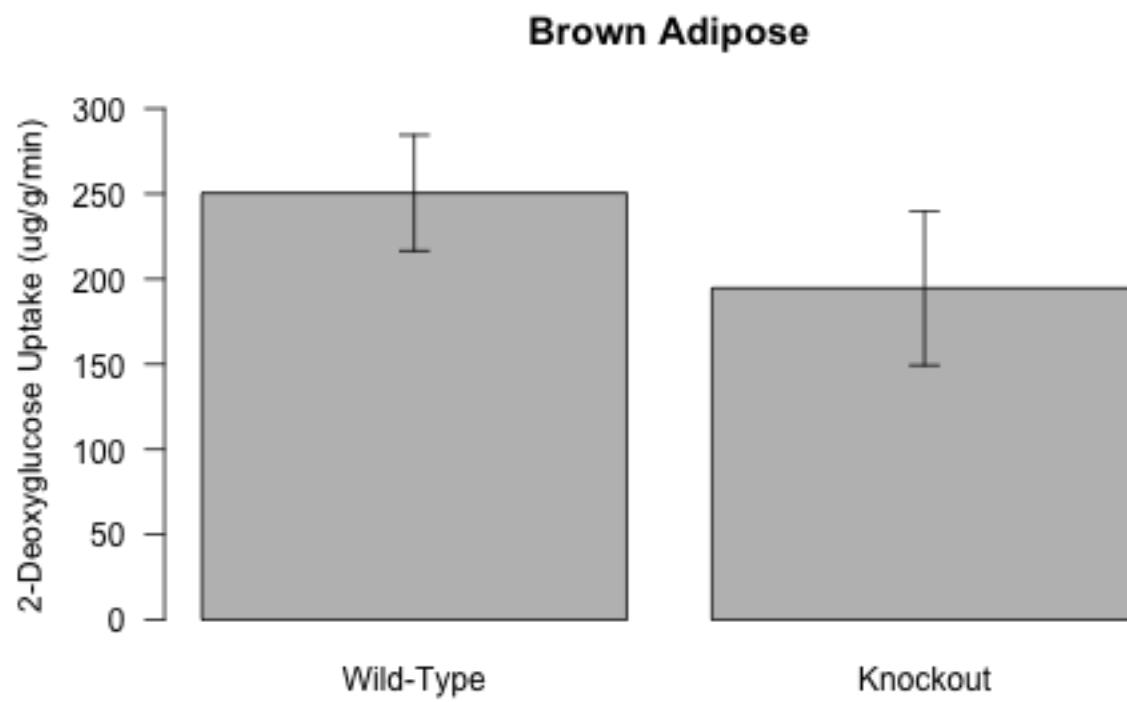
4.2 Visceral Fat Gluose Uptake During Clamp

Visceral Adipose

4.3 Subcutaneous Fat Gluose Uptake During Clamp

Subcutaneous Adipose

4.4   Heart Gluose Uptake During Clamp

Heart

Bar chart showing 2-Deoxyglucose Uptake (ug/g/min) for Wild-Type and Knockout groups. Wild-Type is approximately 445 and Knockout is approximately 345, each with error bars.
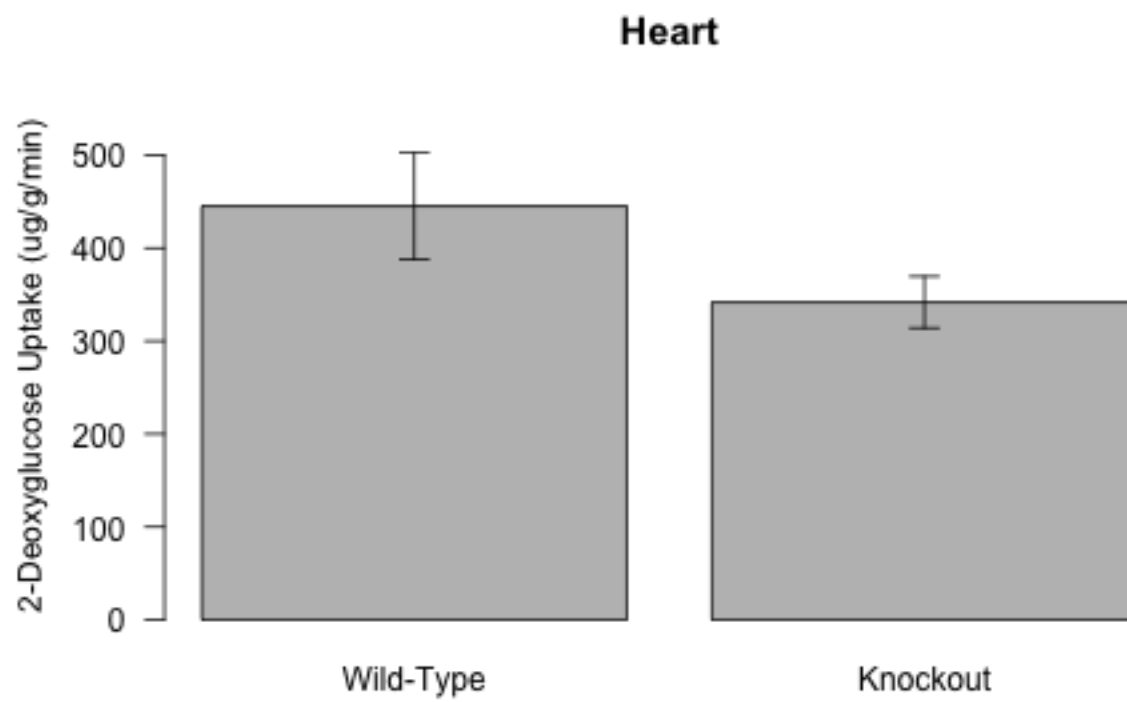
4.5   Brown Adipose Tissue Gluose Uptake During Clamp

Brown Adipose

4.6   Tissue Glucose Uptake Summary
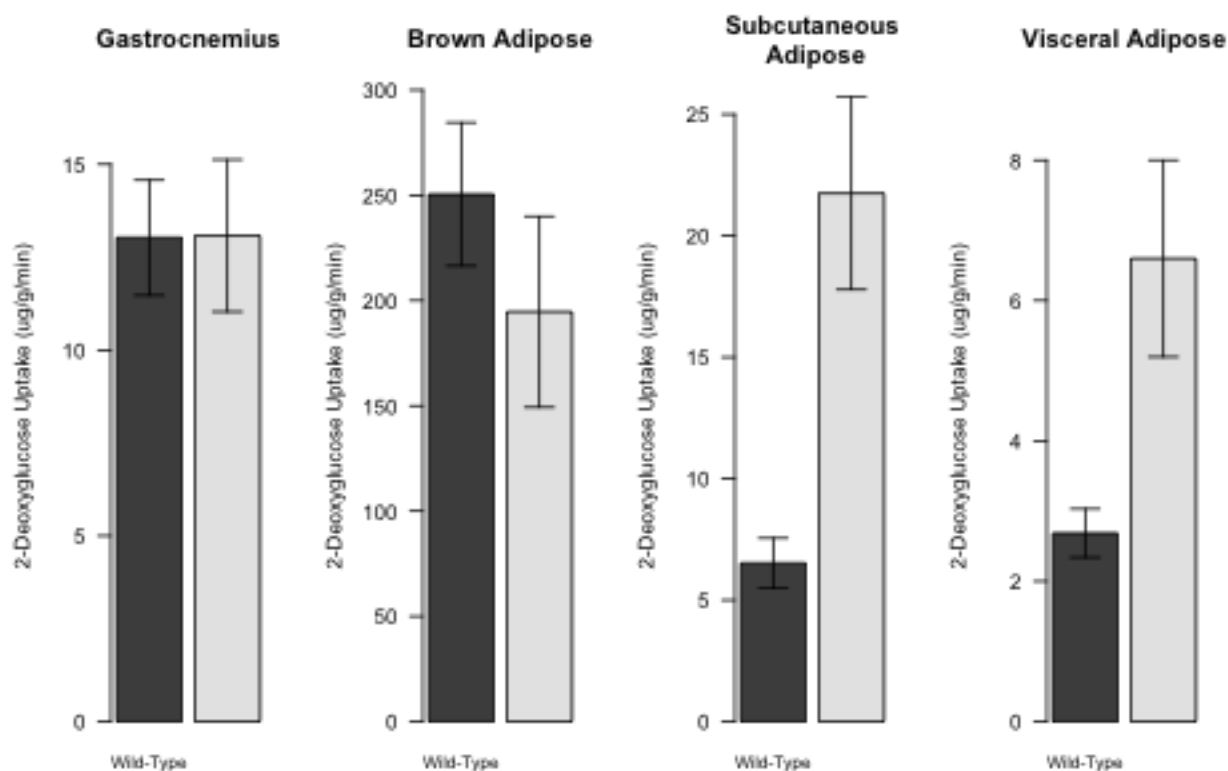
5   Session Information

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS  10.14.6
##
## 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
##
## 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] tibble_2.1.3     dplyr_0.8.3      tidyr_0.8.3.9000 knitr_1.23
##
## loaded via a namespace (and not attached):
```

```
##  [1] Rcpp_1.0.1       magrittr_1.5     tidyselect_0.2.5 R6_2.4.0
##  [5] rlang_0.4.0      stringr_1.4.0    highr_0.8         tools_3.5.0
##  [9] xfun_0.7         htmltools_0.3.6  yaml_2.2.0        digest_0.6.20
## [13] assertthat_0.2.1 crayon_1.3.4     purrr_0.3.2       vctrs_0.2.0
## [17] zeallot_0.1.0    glue_1.3.1       evaluate_0.14     rmarkdown_1.13
## [21] stringi_1.4.3    compiler_3.5.0   pillar_1.4.2      backports_1.1.4
## [25] pkgconfig_2.0.2
```