

# Insulin Clamp Study on Mck-TSC1 Mice

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## 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

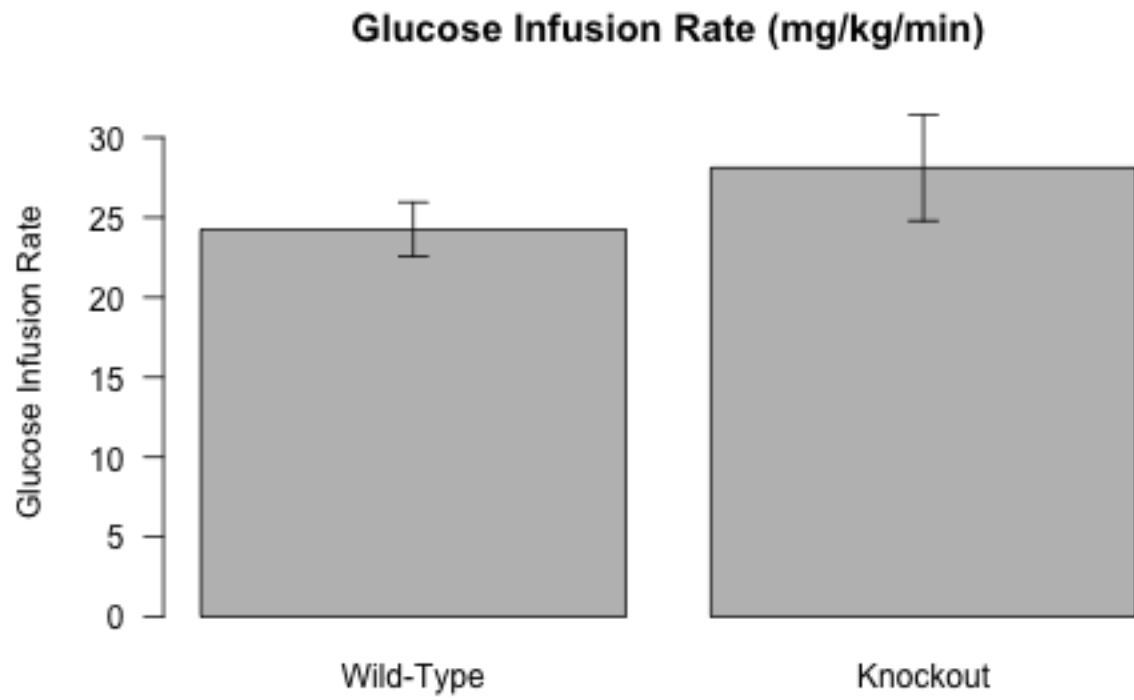
Clamp.GIR	0.325
Clamp.AUC	0.272
Basal.HGP	0.852
Clamp.HGP	0.792
sHGP	0.477
Clearance.Basal	0.953
Clearance.Clamp	0.269
Insulin	0.008
Gastroc	0.984
V.fat	0.027
S.fat	0.006
BAT	0.341
Heart.fit	0.131

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

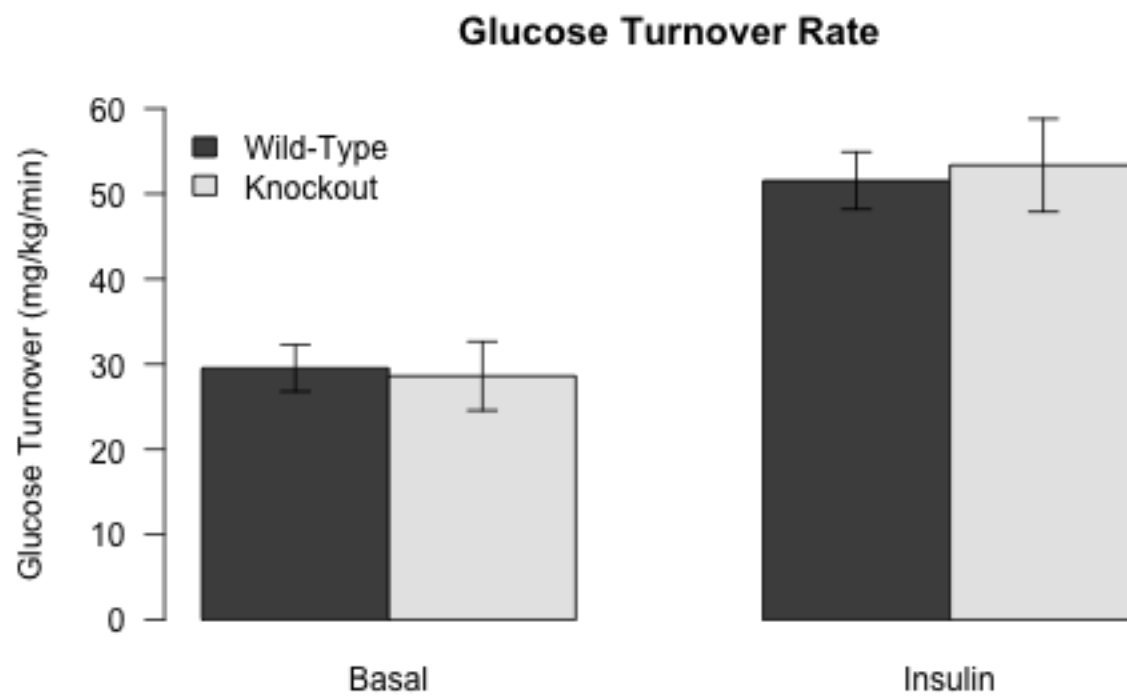
Clamp.GIR	Clamp.AUC	Basal.HGP	Clamp.HGP	sHGP	Clearance.Basal	Clearance.Clamp	Insulin	Gastroc
1	1	1	1	1	1	1	0.09	1

## 2 Graphs

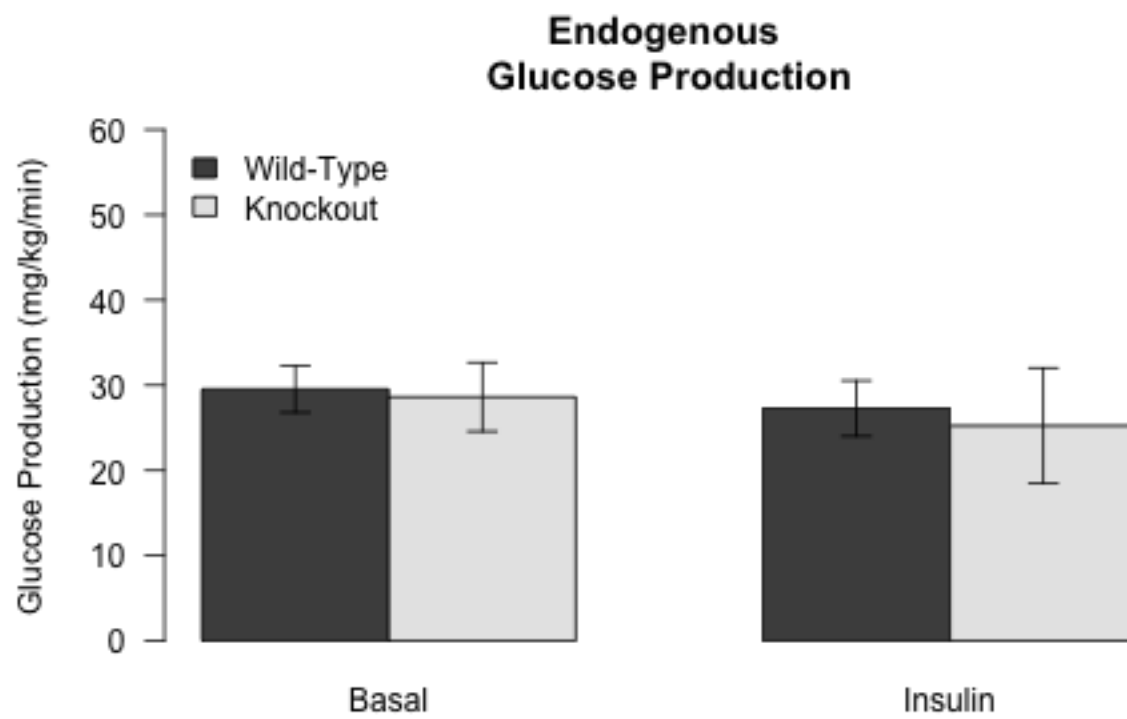
### 2.1 Glucose Infusion Rate



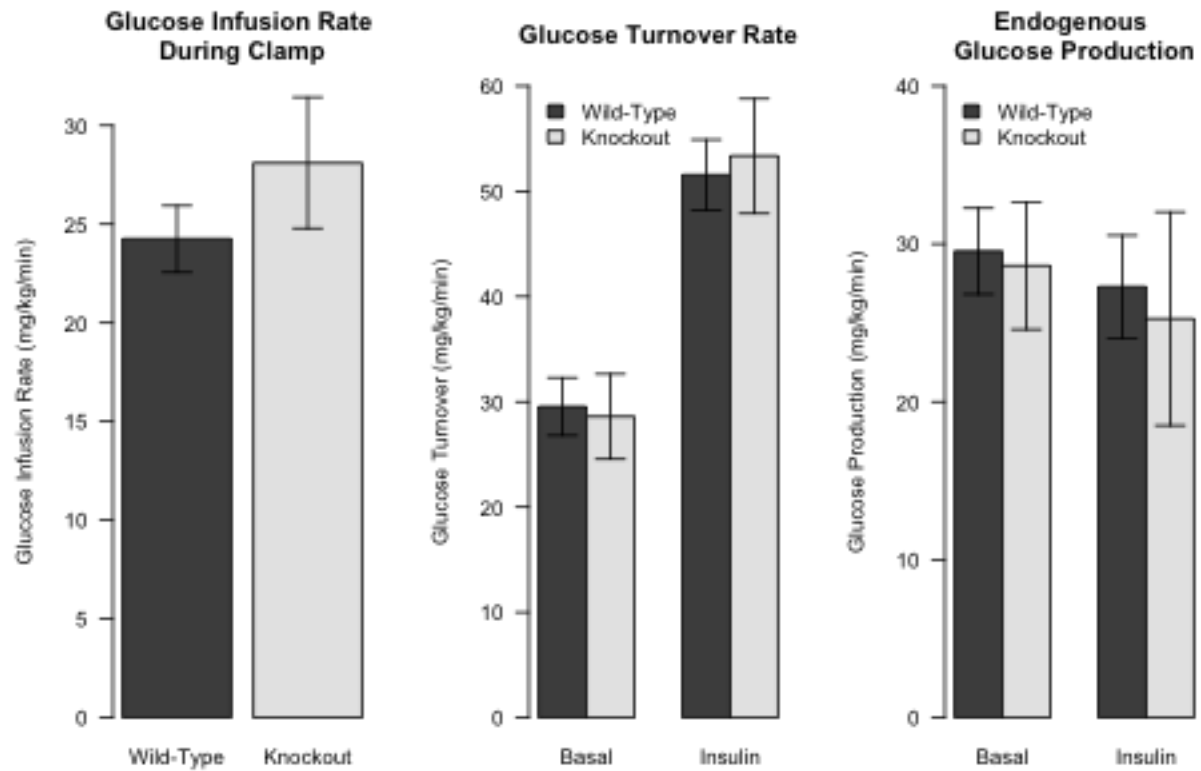
## 2.2 Glucose Turnover



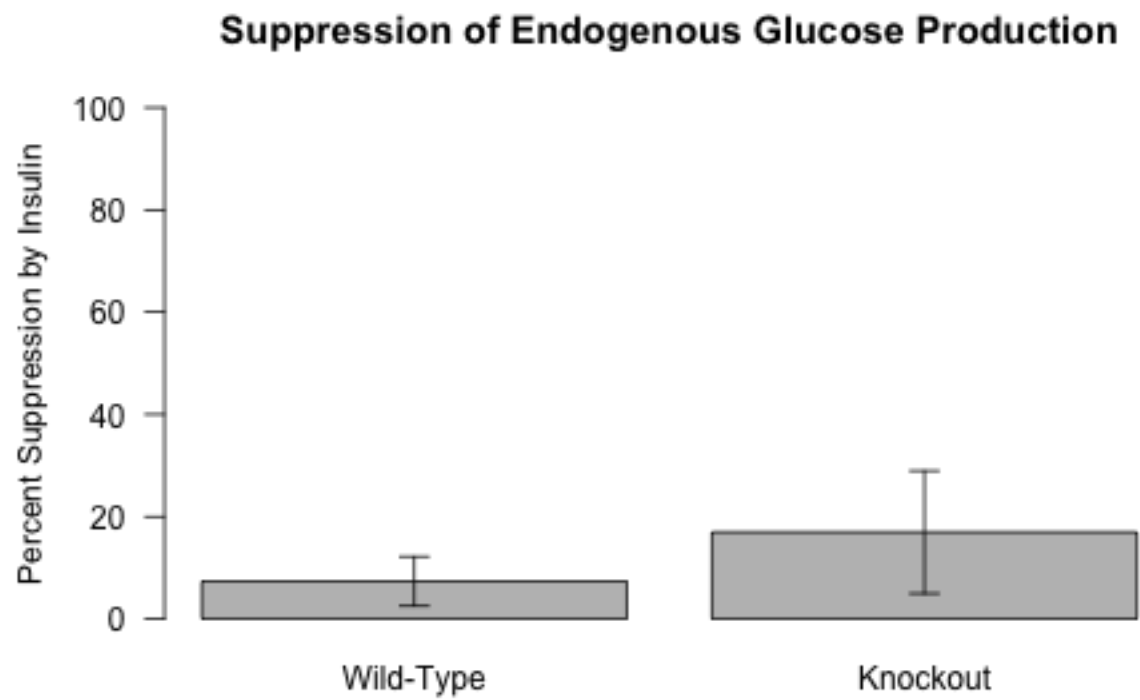
## 2.3 Endogenous Glucose Production



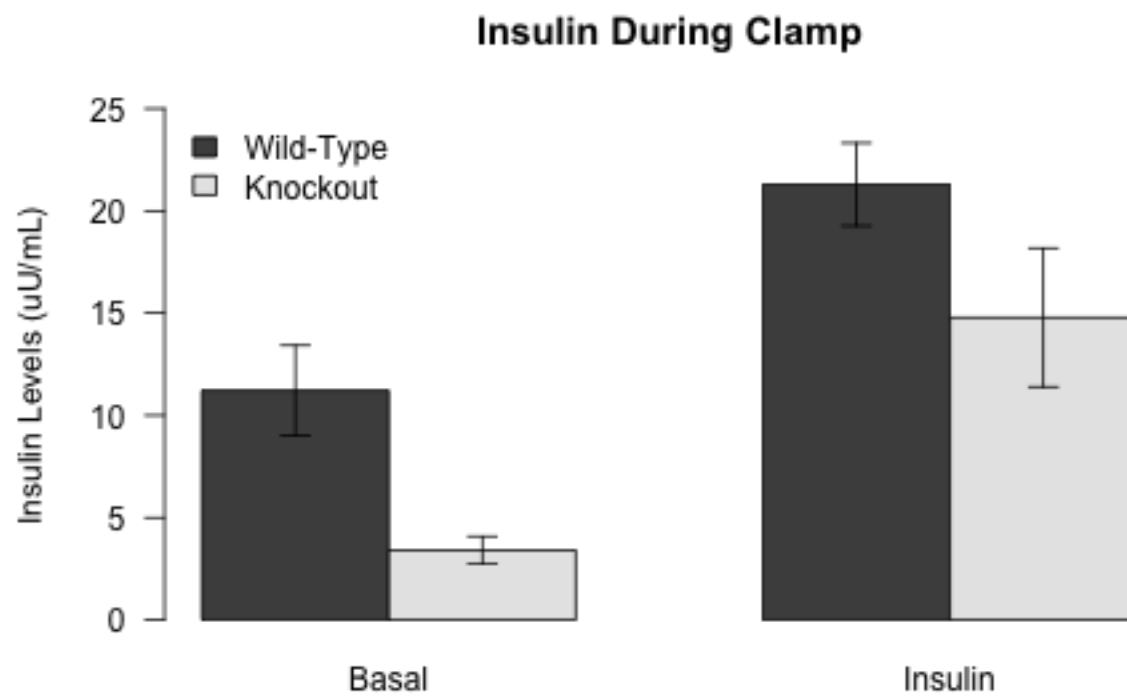
## 2.4 Clamp Summary



### 2.4.1 Suppression of Endogenous Glucose Production



## 2.5 Insulin Levels

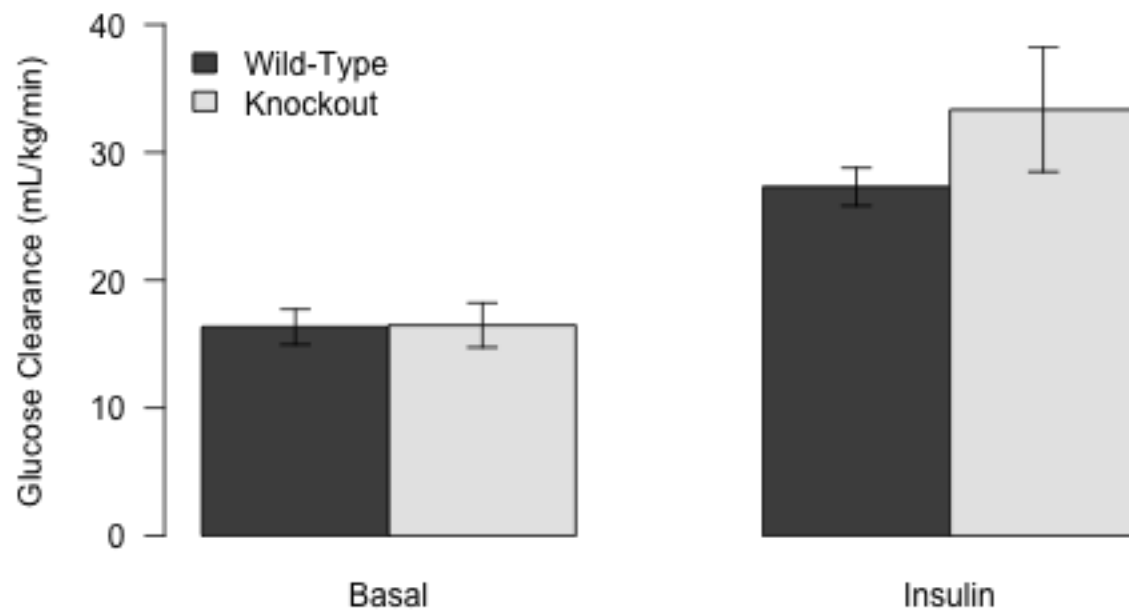


## 3 Glucose Clearance Rate

Blood glucose clearance

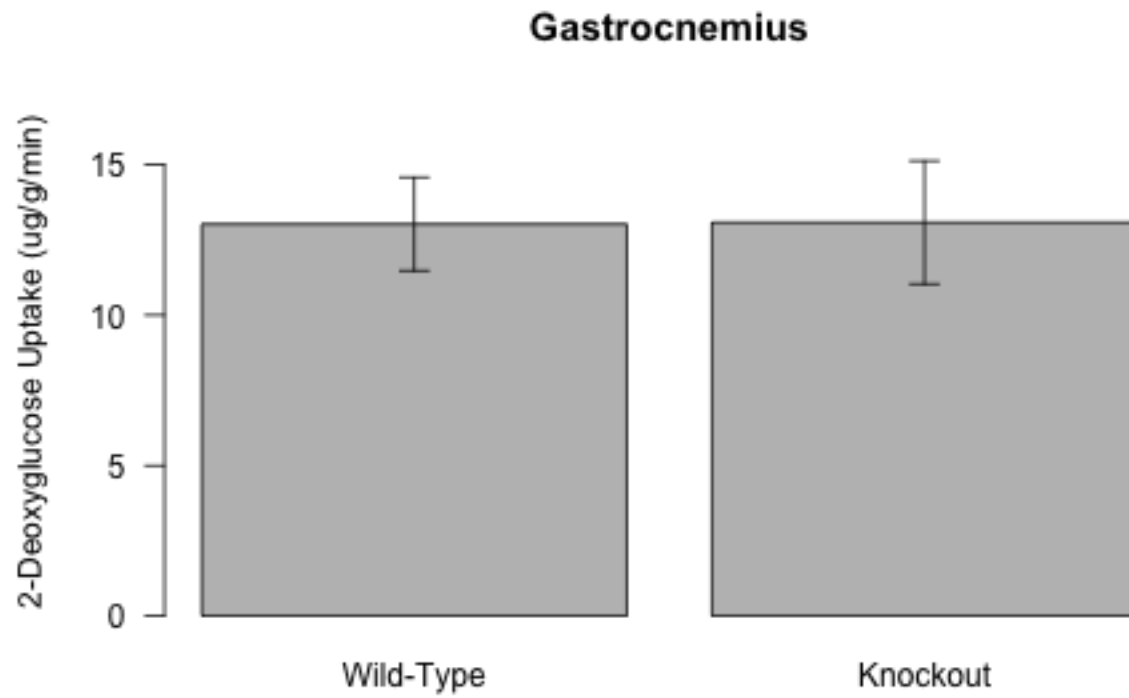


### Glucose Clearance Rate

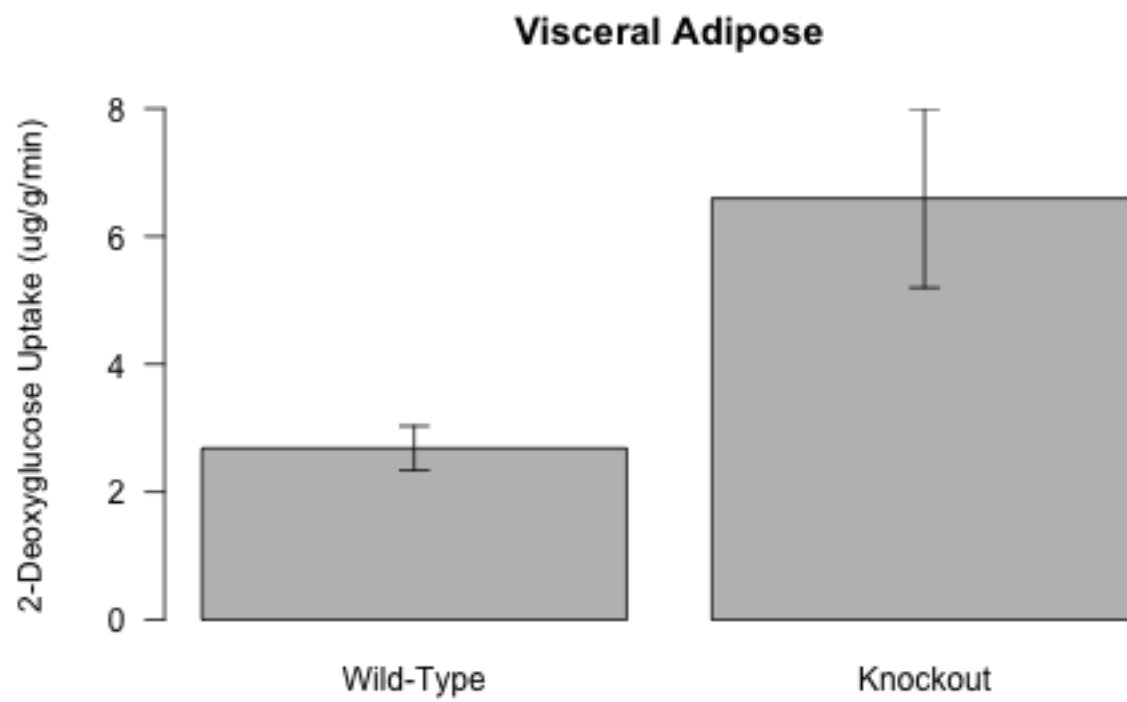


## 4 Tissue Glucose Clearance

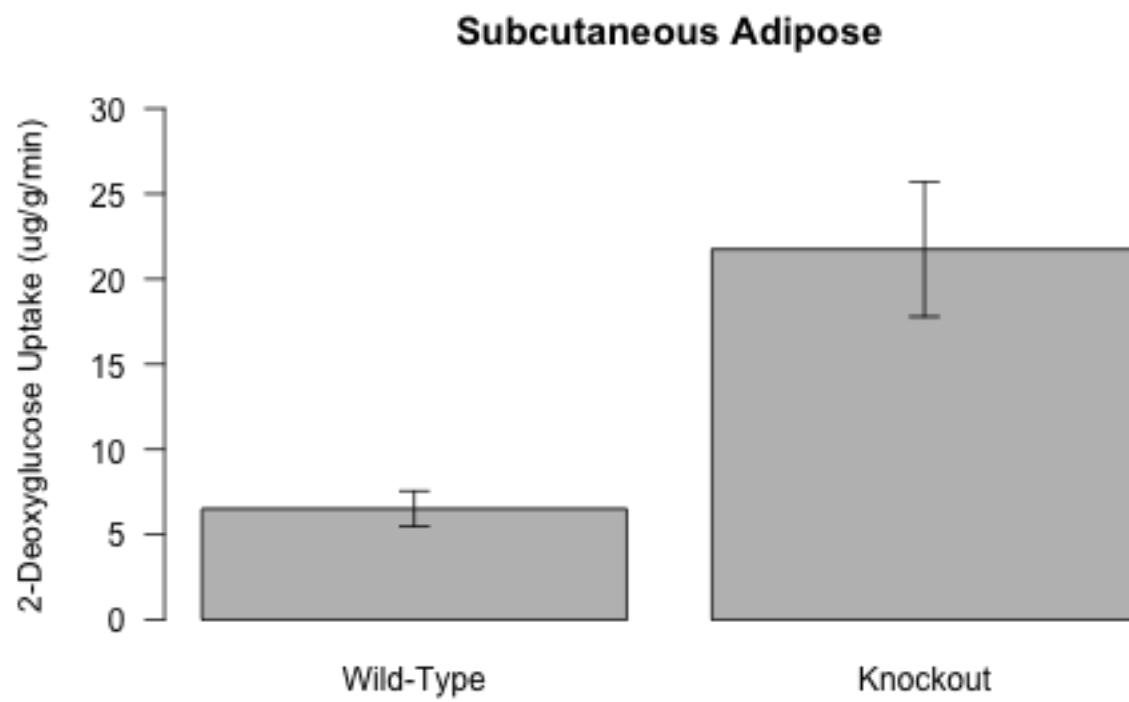
### 4.1 Gastrocnemius Glucose Uptake During Clamp



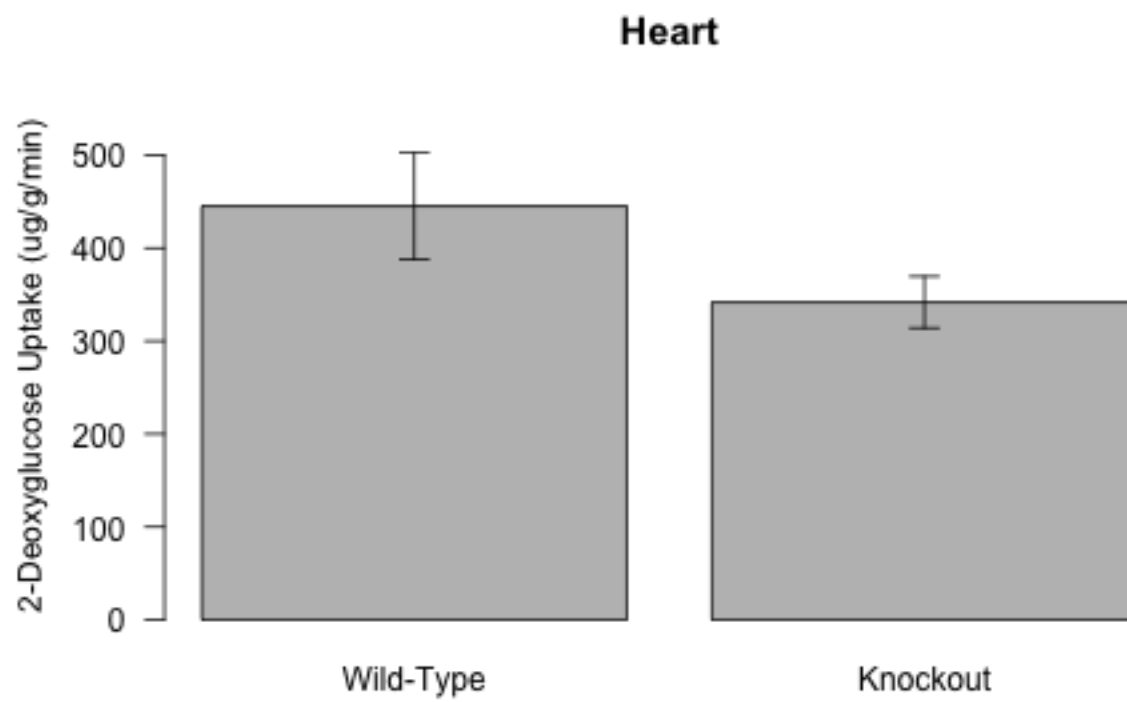
## 4.2 Visceral Fat Glucose Uptake During Clamp



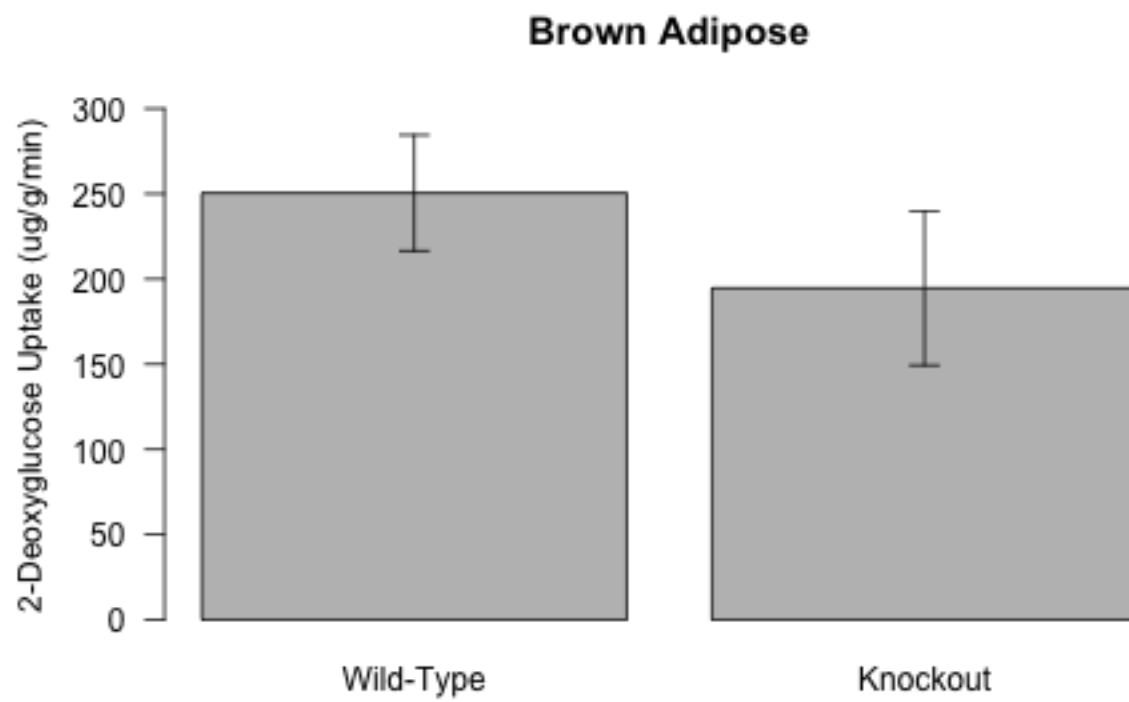
### 4.3 Subcutaneous Fat Glucose Uptake During Clamp



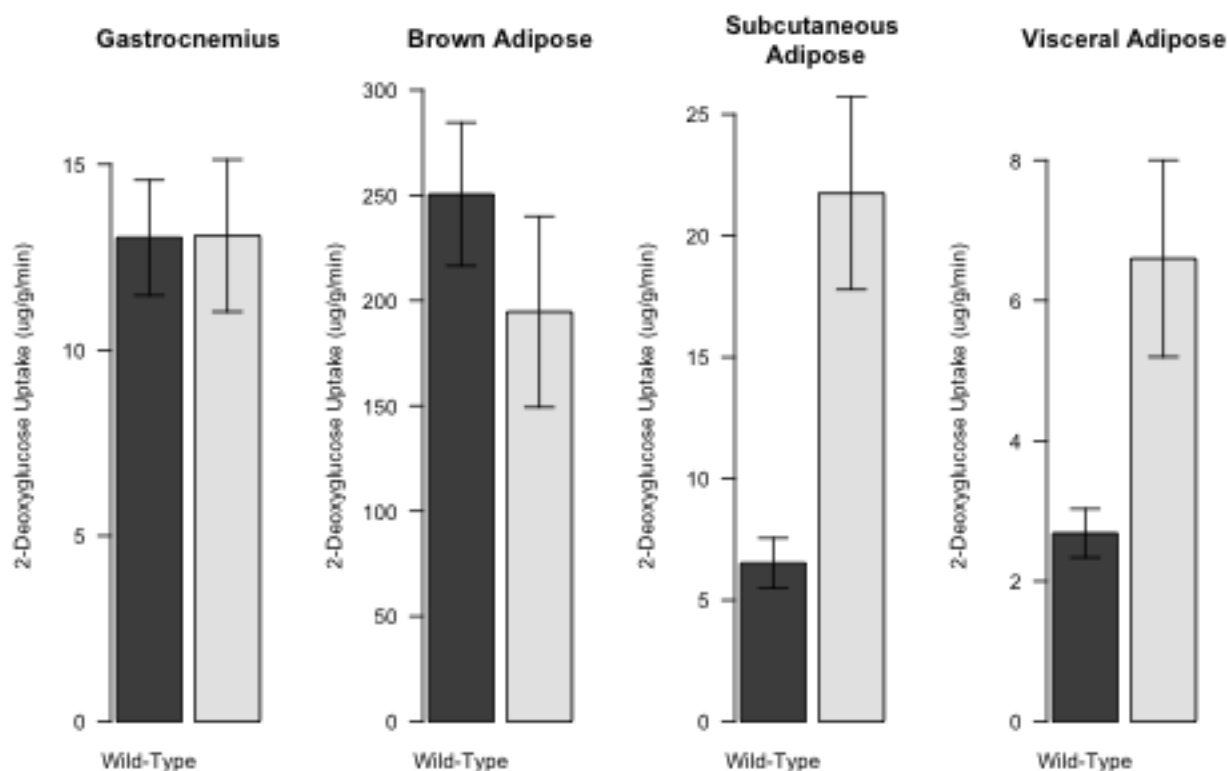
#### 4.4 Heart Glucose Uptake During Clamp



#### 4.5 Brown Adipose Tissue Glucose Uptake During Clamp



## 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
```