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	I
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	$381/\mathrm{wh}$	111	118	31.0	3294	127835	149024	
9	Wild-Type	9	$381/\mathrm{br}$	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

$\overline{ m WT}$	КО	Measurement	Difference	Pct.Difference
110.88	130.11	Basal.Glucose_mean	19.236	17.349
119.48	123.67	Clamp.Glucose_mean	4.188	3.505
28.10	24.26	Clamp.GIR_mean	-3.848	-13.694
3064.68	2633.34	$Clamp.AUC_mean$	-431.333	-14.074
192649.32	126094.59	Basal.SA_mean	-66554.729	-34.547
194547.40	141370.92	$Clamp.SA_mean$	-53176.476	-27.333
28.61	29.54	$Basal.Gtr_mean$	0.930	3.251
53.36	51.55	$Clamp.Gtr_mean$	-1.803	-3.378
28.61	29.54	Basal.HGP_mean	0.930	3.251
25.25	27.29	Clamp.HGP_mean	2.034	8.053
16.95	7.37	$Clamp.sHGP_mean$	-9.586	-56.542
16.49	16.35	$Clearance.Basal_mean$	-0.133	-0.805
33.34	27.32	Clearance.Clamp_mean	-6.029	-18.081
3.41	11.22	Insulin.Basal_mean	7.813	229.270
14.78	21.29	$Insulin.Clamp_mean$	6.513	44.078
13.08	13.03	$Gastroc_mean$	-0.051	-0.392
6.60	2.69	$V.fat_mean$	-3.912	-59.296
21.75	6.52	$S.fat_mean$	-15.228	-70.010
194.63	250.50	BAT_mean	55.867	28.704
341.70	445.18	Heart_mean	103.473	30.282

Table 3: T-Tests, Unadjusted

Clamp.GIR	Clamp.AUC	Basal.HGP	Clamp.HGP	sHGP	Clearance.Basal	Clearance.Clamp	Insulin	Gastroc
0.325	0.272	0.852	0.792	0.477	0.953	0.269	0.008	0.984

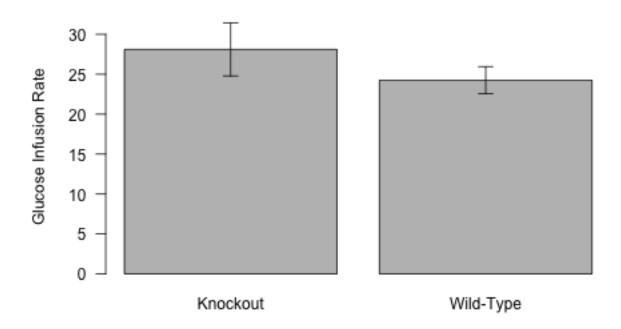
Table 4: Nominal and Benjamini-Hochberg Adjusted T-Tests

Clamp.GIR	Clamp.AUC	Basal.HGP	Clamp.HGP	sHGP	Clearance.Basal	Clearance.Clamp	Insulin	Gastroc
0.325	0.272	0.852	0.792	0.477	0.953	0.269	0.008	0.984
1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.090	1.000

2 Graphs

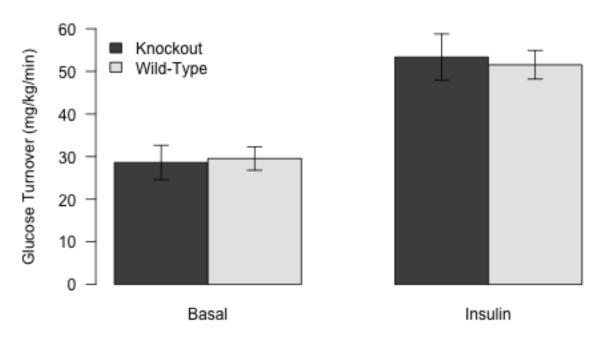
2.1 Glucose Infusion Rate

Clamp Glucose Infusion Rate



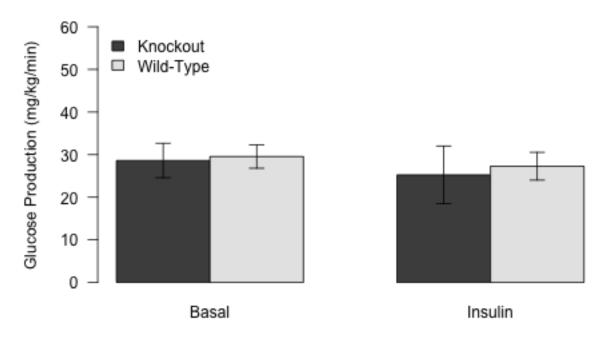
2.2 Glucose Turnover

Glucose Turnover Rate



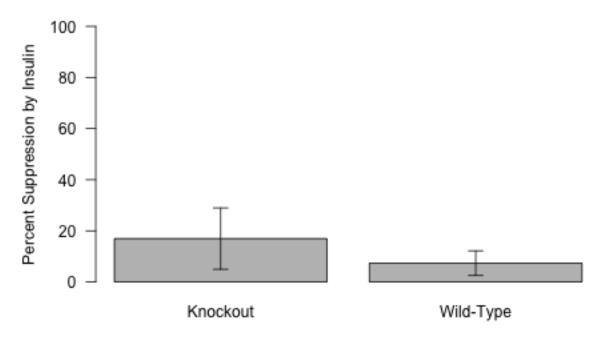
2.3 Endogenous Glucose Production

Endogenous Glucose Production



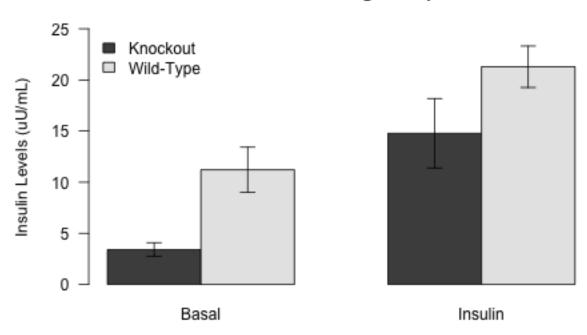
2.3.1 Suppression of Endogenous Glucose Production

Suppression of Endogenous Glucose Production



2.4 Insulin Levels

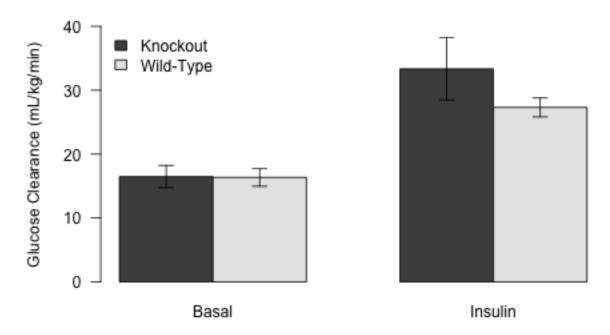
Insulin During Clamp



3 Glucose Clearance Rate

Blood glucose clearance

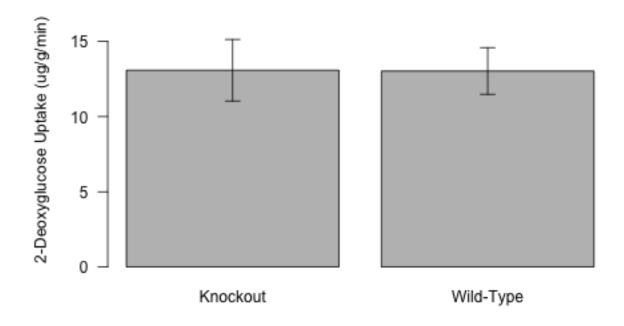
Glucose Clearance Rate



4 Tissue Glucose Clearance

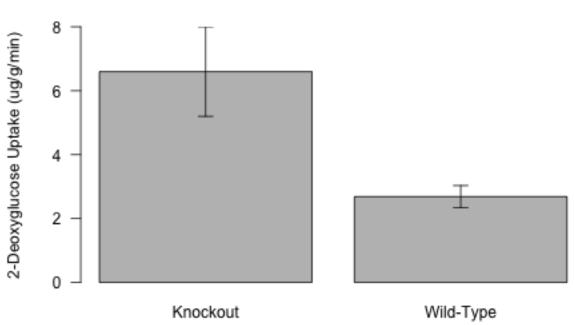
4.1 Gasctrocnemius Gluose Uptake During Clamp

Gastrocnemius



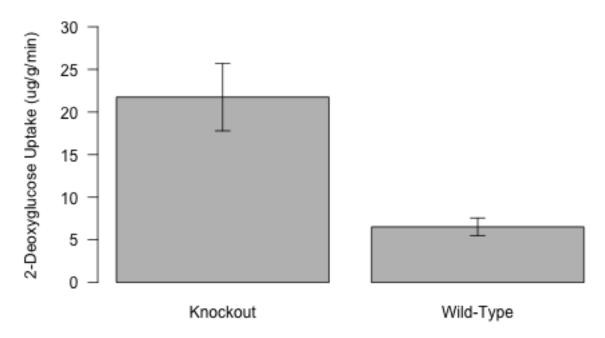
4.2 Visceral Fat Gluose Uptake During Clamp





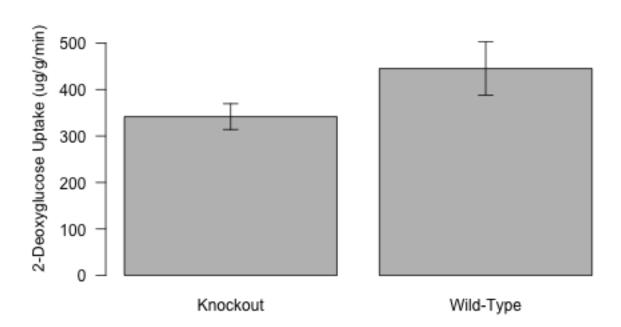
4.3 Subcutaneous Fat Gluose Uptake During Clamp

Subcutaneous Adipose



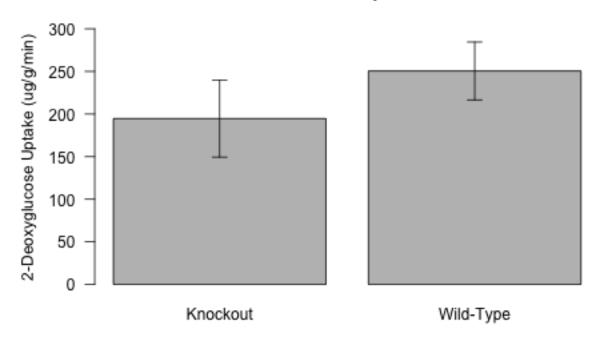
4.4 Heart Gluose Uptake During Clamp

Heart



4.5 Brown Adipose Tissue Gluose Uptake During Clamp





5 Session Information

```
sessionInfo()
```

```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
## Running under: macOS 10.14.5
##
## 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
##
## [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:
                 graphics grDevices utils
##
  [1] stats
                                               datasets methods
                                                                   base
##
## other attached packages:
                                 dplyr_0.8.1 tidyr_0.8.3 knitr_1.23
## [1] tibble_2.1.3 plyr_1.8.4
## loaded via a namespace (and not attached):
```

```
## [1] Rcpp_1.0.1
                                                         digest_0.6.19
                        assertthat_0.2.1 crayon_1.3.4
## [5] R6_2.4.0
                        magrittr_1.5
                                         evaluate_0.14
                                                         highr_0.8
## [9] pillar_1.4.1
                        rlang_0.3.4
                                         stringi_1.4.3
                                                         rmarkdown_1.13
## [13] tools_3.5.0
                        stringr_1.4.0
                                         glue_1.3.1
                                                         purrr_0.3.2
                                                         pkgconfig_2.0.2
## [17] xfun_0.7
                        yaml_2.2.0
                                         compiler_3.5.0
## [21] htmltools_0.3.6 tidyselect_0.2.5
```