

# aTSC Lipidomics

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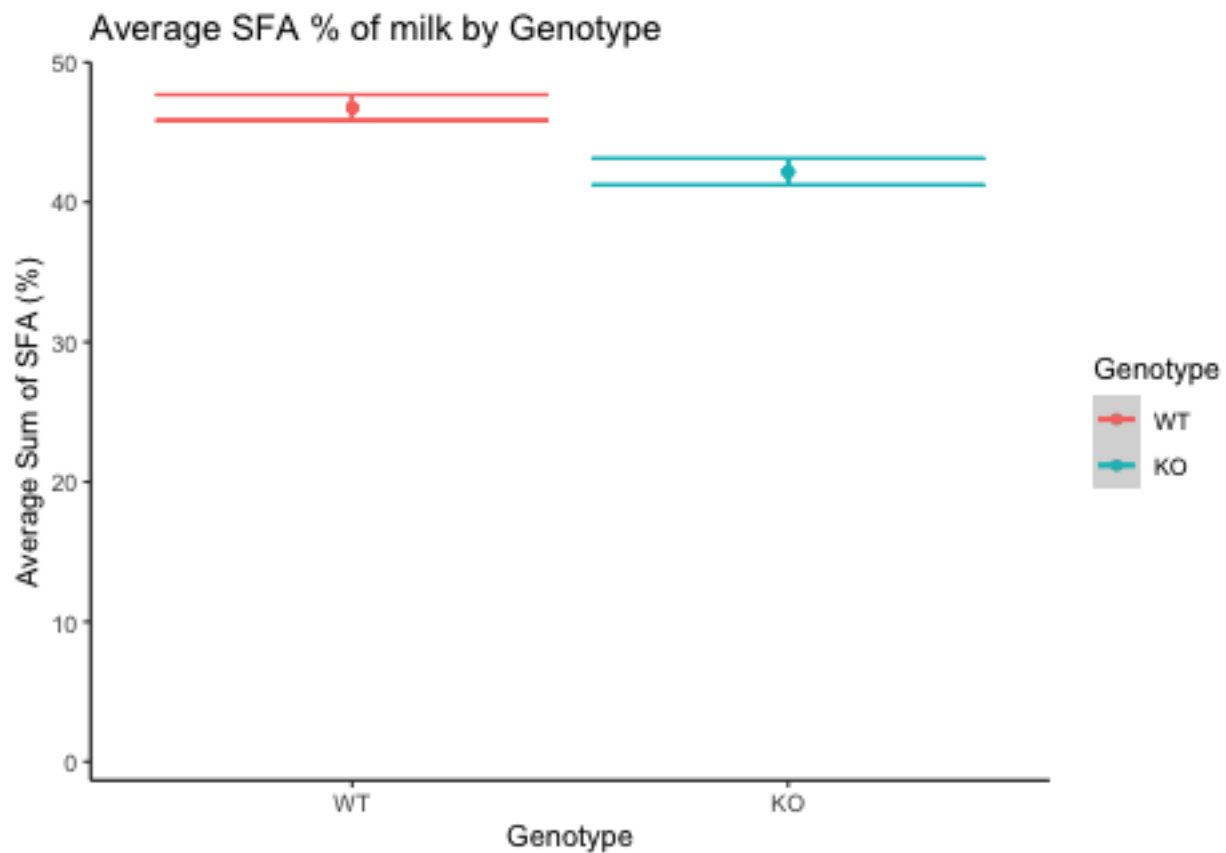
12/14/2020

## R Markdown

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When you click the **Knit** button a document will be generated that includes both content as well as the output of any embedded R code chunks within the document. You can embed an R code chunk like this:

```
## [1] 42.2 42.2 42.2 42.2 42.2 46.8 46.8 46.8 46.8 46.8
```



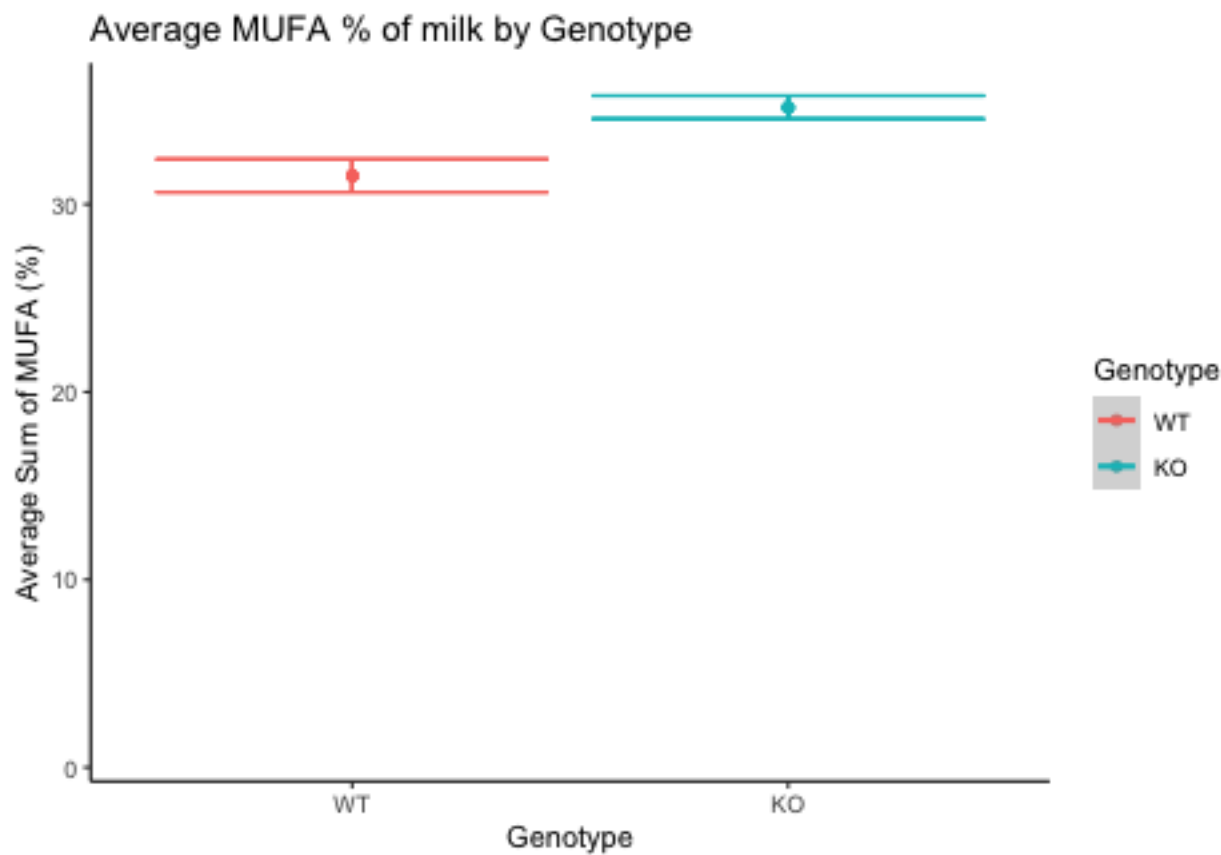
```
##  
## Shapiro-Wilk normality test  
##  
## data: filter(lipidomics.data, Genotype == "KO")$`%SFA`  
## W = 1, p-value = 0.8
```

```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%SFA`
## W = 0.9, p-value = 0.7
```

Table 1: Student’s t-test for %SFA by maternal genotype

term	df	statistic	p.value
group	1	0.017	0.899
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
4.6	46.8	42.2	3.47	0.008	8	1.54	7.65	Two Sample t-test	two.sided



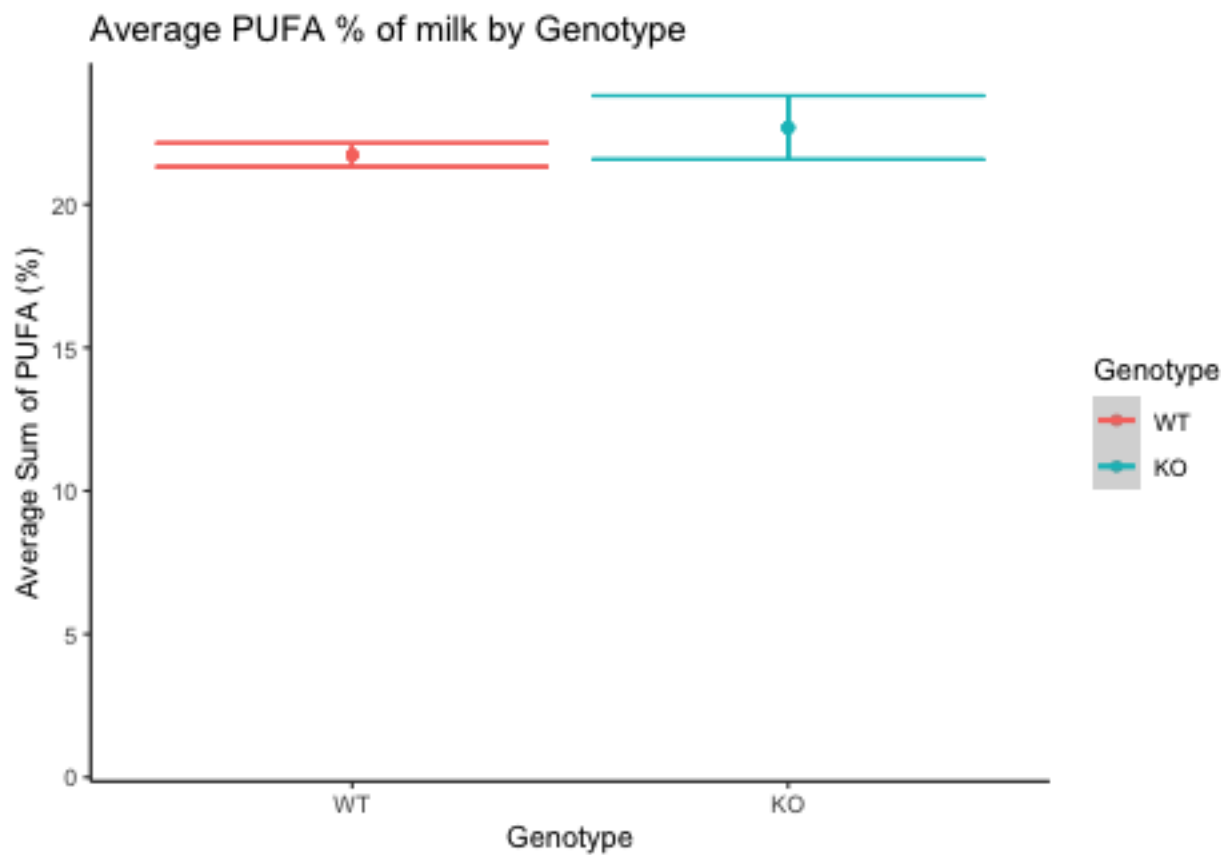
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%MUFA`
## W = 1, p-value = 1
##
## Shapiro-Wilk normality test
```

```
##
## data: filter(lipidomics.data, Genotype == "WT")$`%MUFA`
## W = 0.9, p-value = 0.6
```

Table 3: Student’s t-test for %MUFA by maternal genotype

term	df	statistic	p.value
group	1	0.108	0.751
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-3.64	31.5	35.2	-3.41	0.009	8	-6.1	-1.18	Two Sample t-test	two.sided



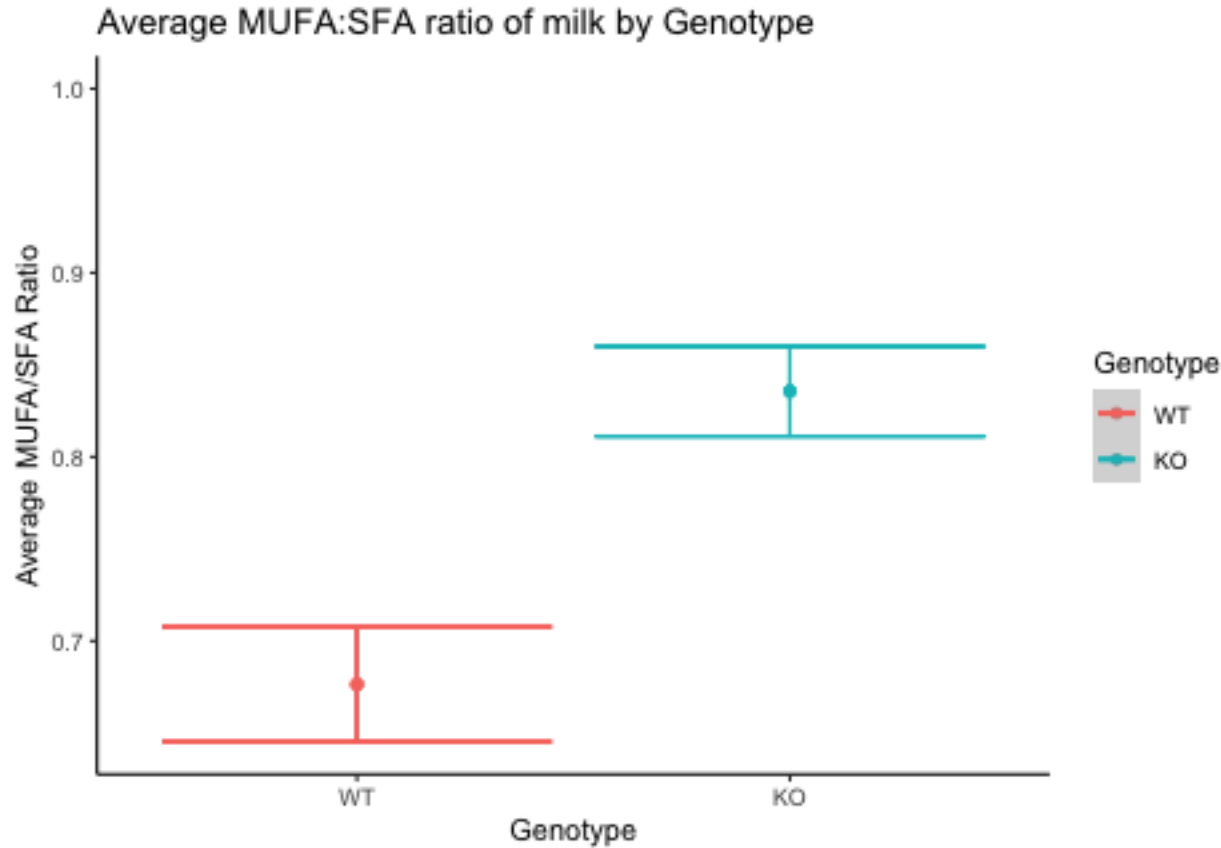
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%PUFA`
## W = 0.8, p-value = 0.07
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%PUFA`
```

## W = 0.8, p-value = 0.04

Table 5: Student’s t-test for %MUFA by maternal genotype

statistic	p.value	method	alternative
10	0.69	Wilcoxon rank sum exact test	two.sided

## [1] 0.836 0.836 0.836 0.836 0.836 0.676 0.676 0.676 0.676 0.676

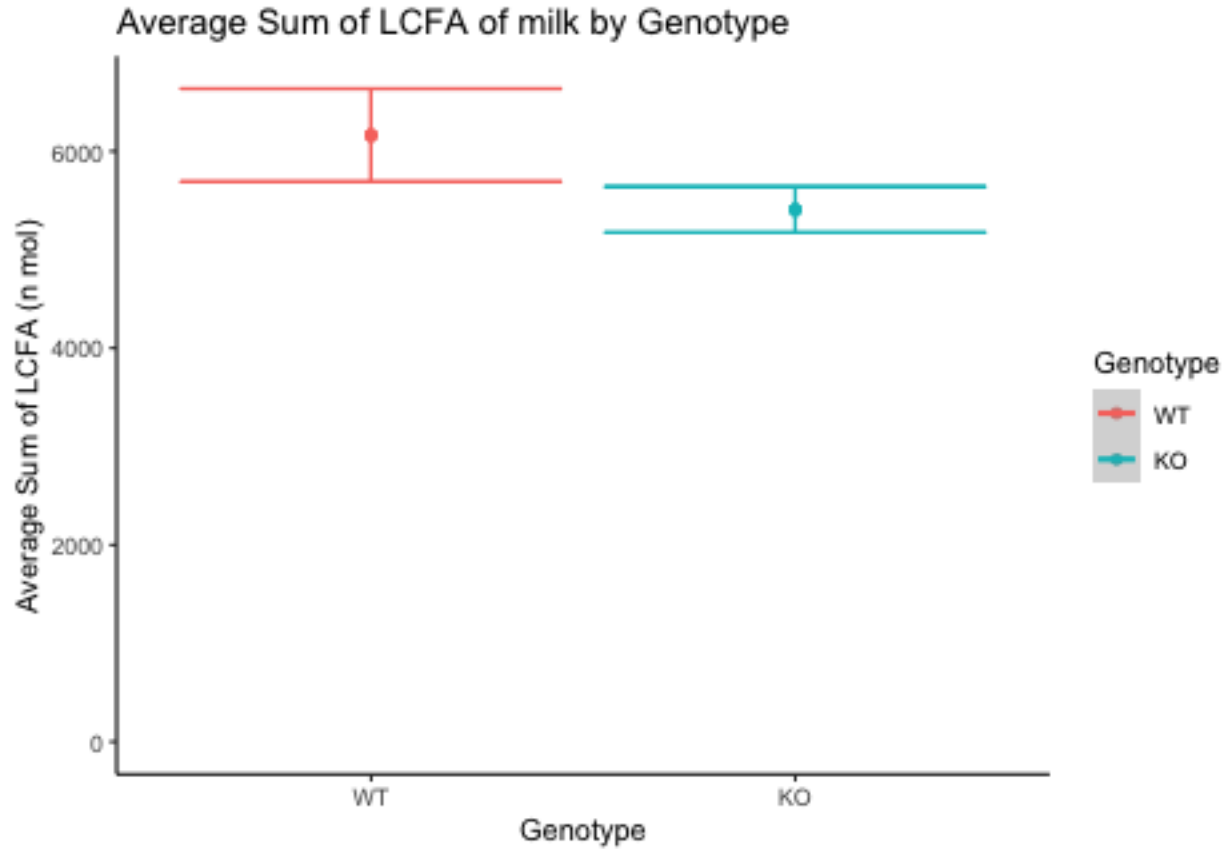


```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`MUFA/SFA`
## W = 0.9, p-value = 0.4
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`MUFA/SFA`
## W = 1, p-value = 0.9
```

Table 6: Student’s t-test for MUFA/SFA ratio by maternal genotype

term	df	statistic	p.value
group	1	0.058	0.815
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.159	0.676	0.836	-4.03	0.004	8	-0.25	-0.068	Two Sample t-test	two.sided



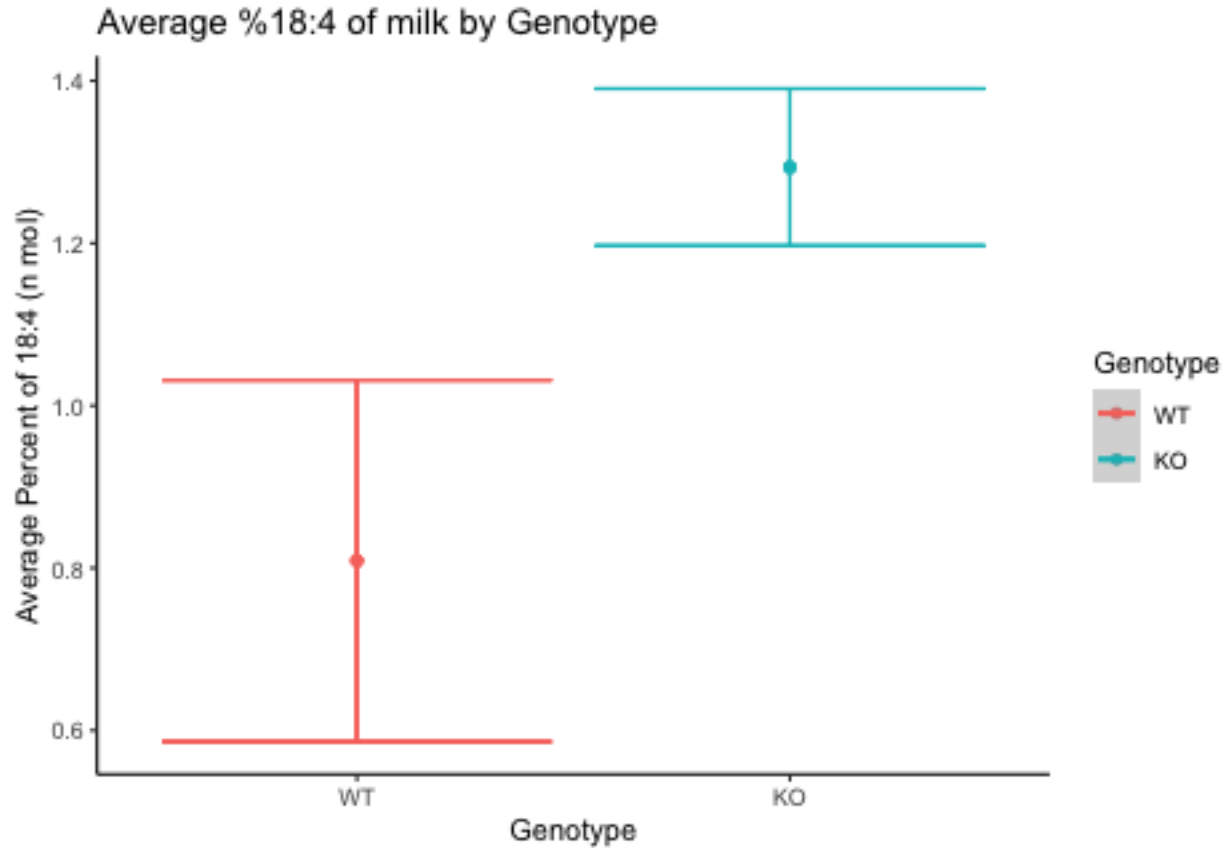
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`Sum (n mol)`
## W = 0.9, p-value = 0.4
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`Sum (n mol)`
## W = 0.9, p-value = 0.4
```

Table 8: Student's t-test for LCFA sum by maternal genotype

term	df	statistic	p.value
group	1	1.44	0.264
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
757	6162	5405	1.44	0.189	8	-459	1974	Two Sample t-test	two.sided

```
## [1] 1.293 1.293 1.293 1.293 1.293 0.809 0.809 0.809 0.809 0.809
```



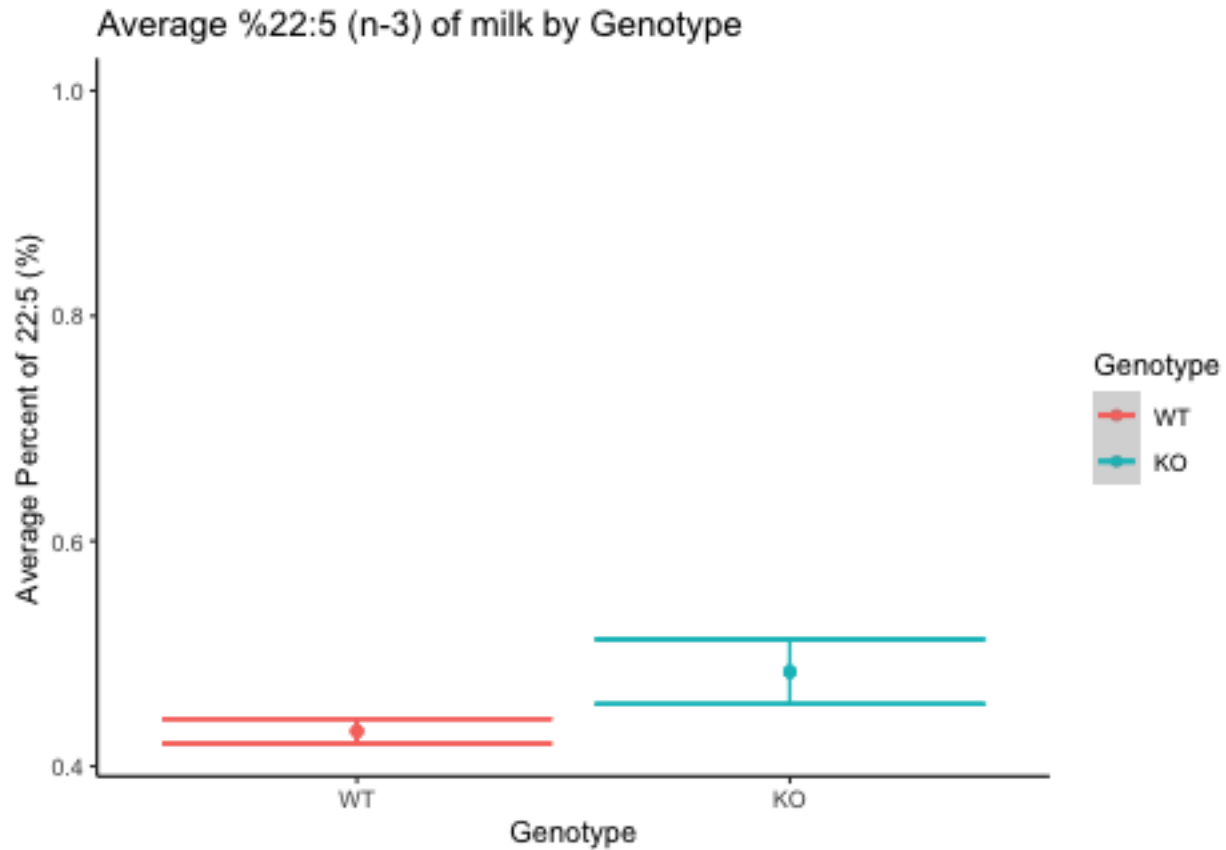
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%18:4 (n-3)`
## W = 0.9, p-value = 0.7
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%18:4 (n-3)`
## W = 0.9, p-value = 0.4
```

Table 10: Student's t-test for '%18:4 (n-3) by maternal genotype

term	df	statistic	p.value
group	1	1.64	0.236
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.485	0.809	1.29	-2	0.081	8	-1.04	0.075	Two Sample t-test	two.sided

```
## [1] 0.484 0.484 0.484 0.484 0.484 0.431 0.431 0.431 0.431 0.431
```

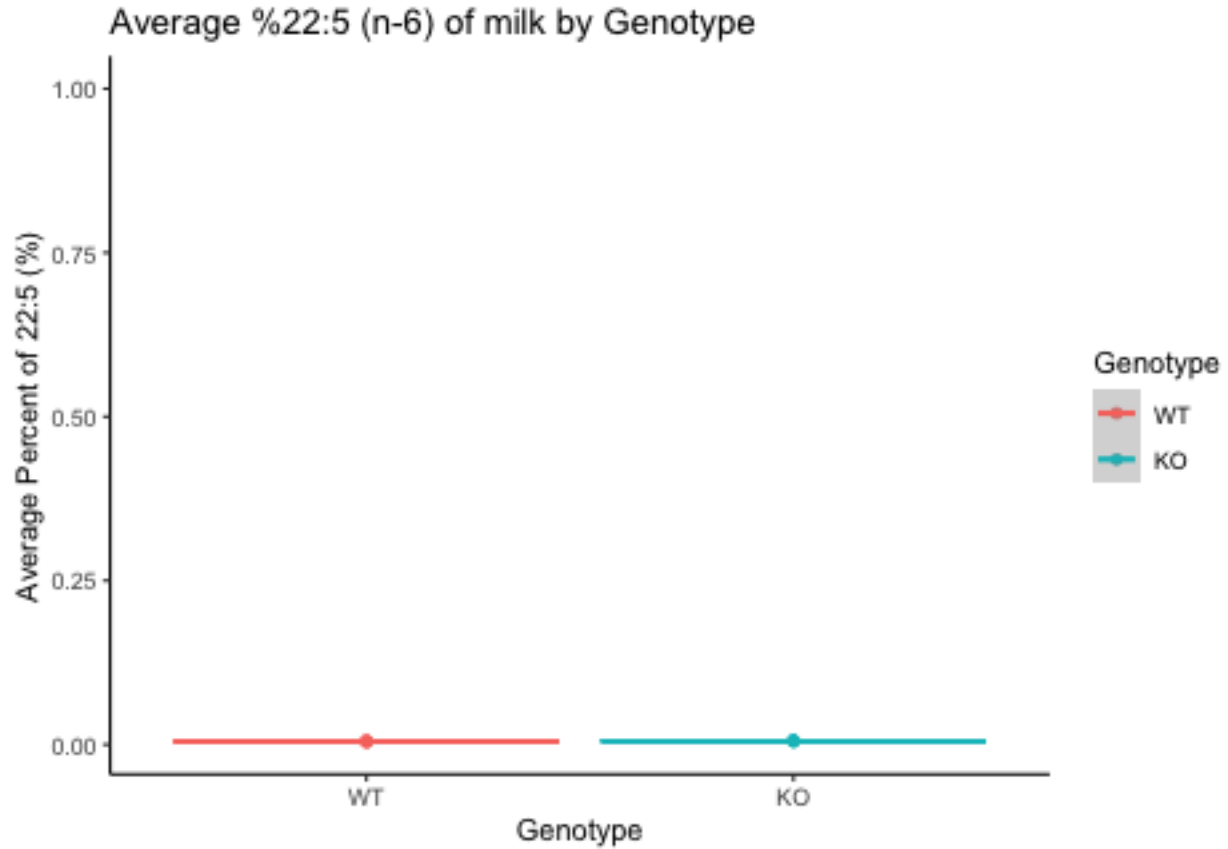


```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%22:5 (n-3)`
## W = 0.9, p-value = 0.7
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%22:5 (n-3)`
## W = 0.8, p-value = 0.1
```

Table 12: Student's t-test for %22:5 (n-3) by maternal genotype

term	df	statistic	p.value
group	1	2.68	0.14
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.053	0.431	0.484	-1.72	0.124	8	-0.124	0.018	Two Sample t-test	two.sided



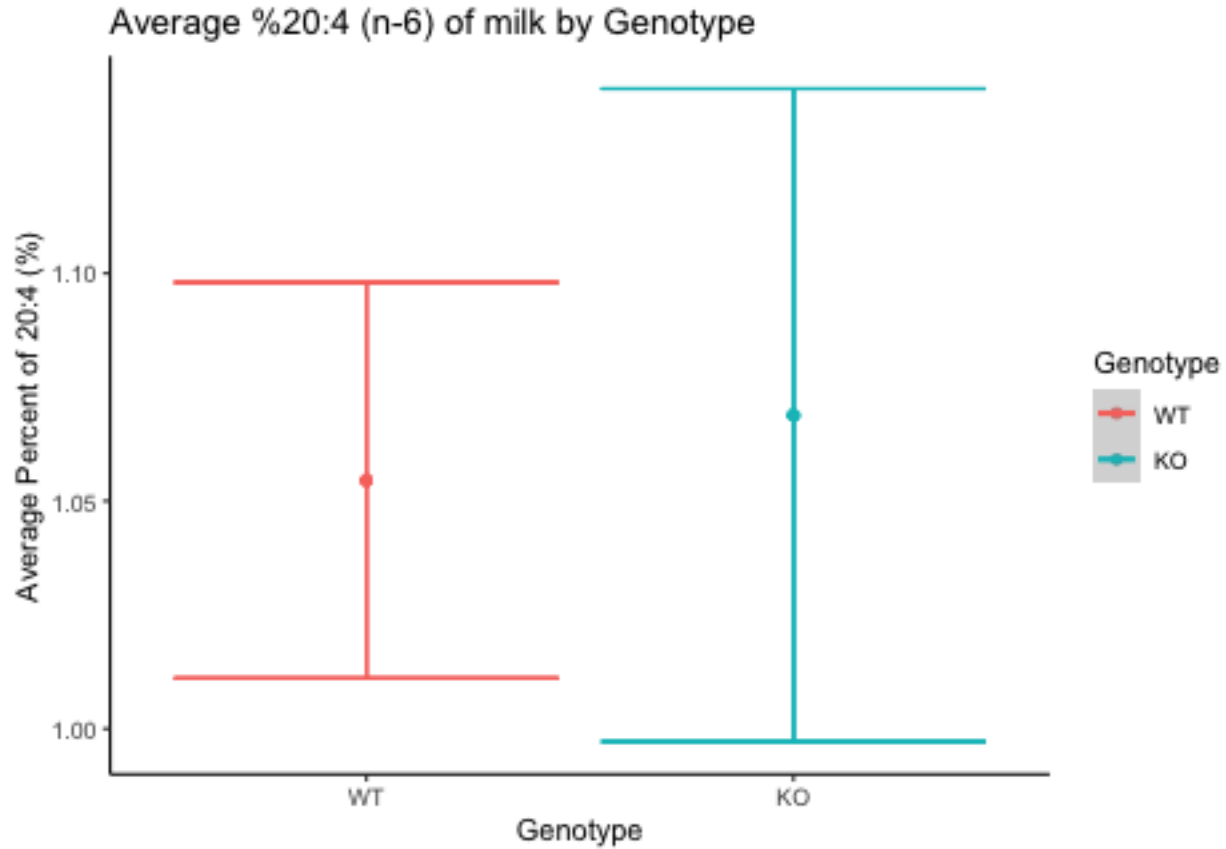
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%22:5 (n-6)`
## W = 0.8, p-value = 0.2
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%22:5 (n-6)`
## W = 0.8, p-value = 0.1
```

Table 14: Student's t-test for %22:5 (n-6) by maternal genotype

term	df	statistic	p.value
group	1	0.307	0.595
	8	NA	NA



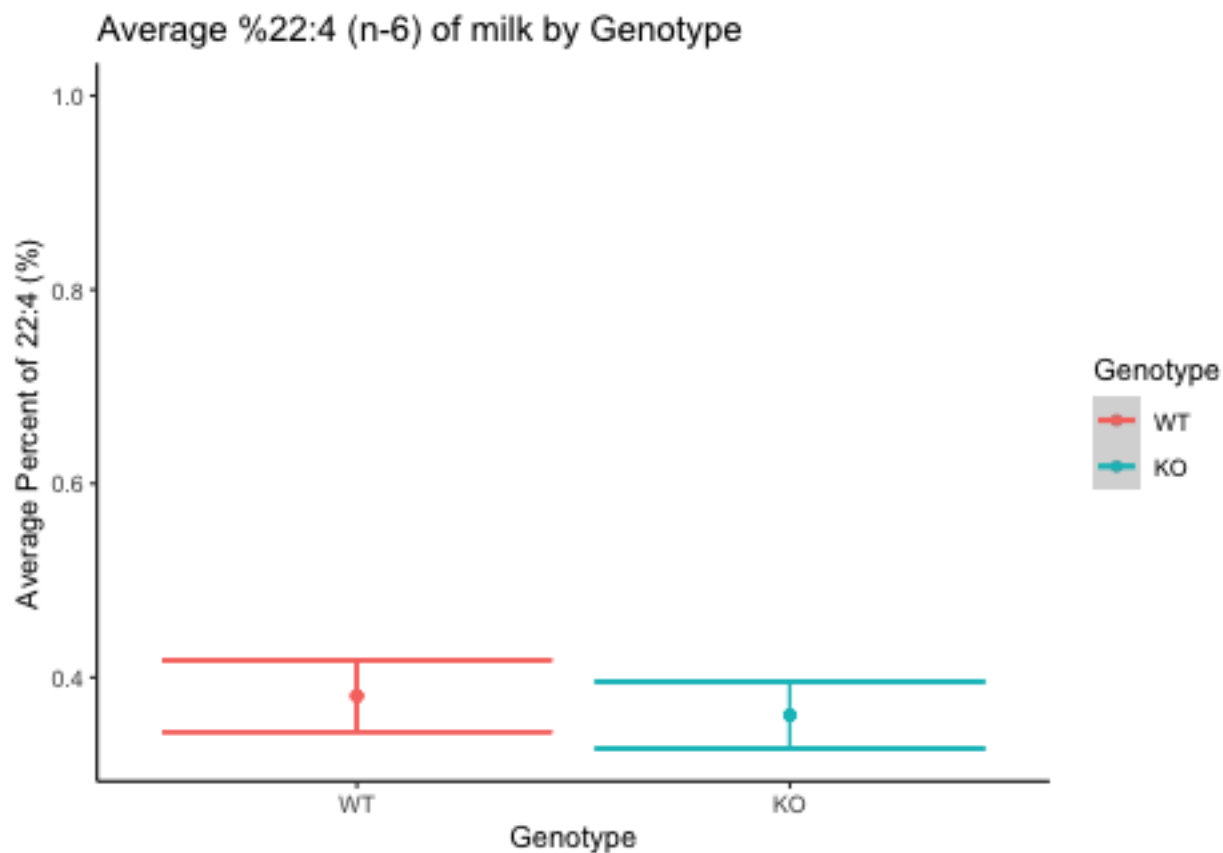
estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.001	0.005	0.006	-0.959	0.366	8	-0.003	0.001	Two Sample t-test	two.sided



```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%20:4 (n-6)`
## W = 0.9, p-value = 0.4
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%20:4 (n-6)`
## W = 0.8, p-value = 0.05
```

Table 16: Student's t-test for %20:4 (n-6) by maternal genotype

statistic	p.value	method	alternative
9	0.548	Wilcoxon rank sum exact test	two.sided

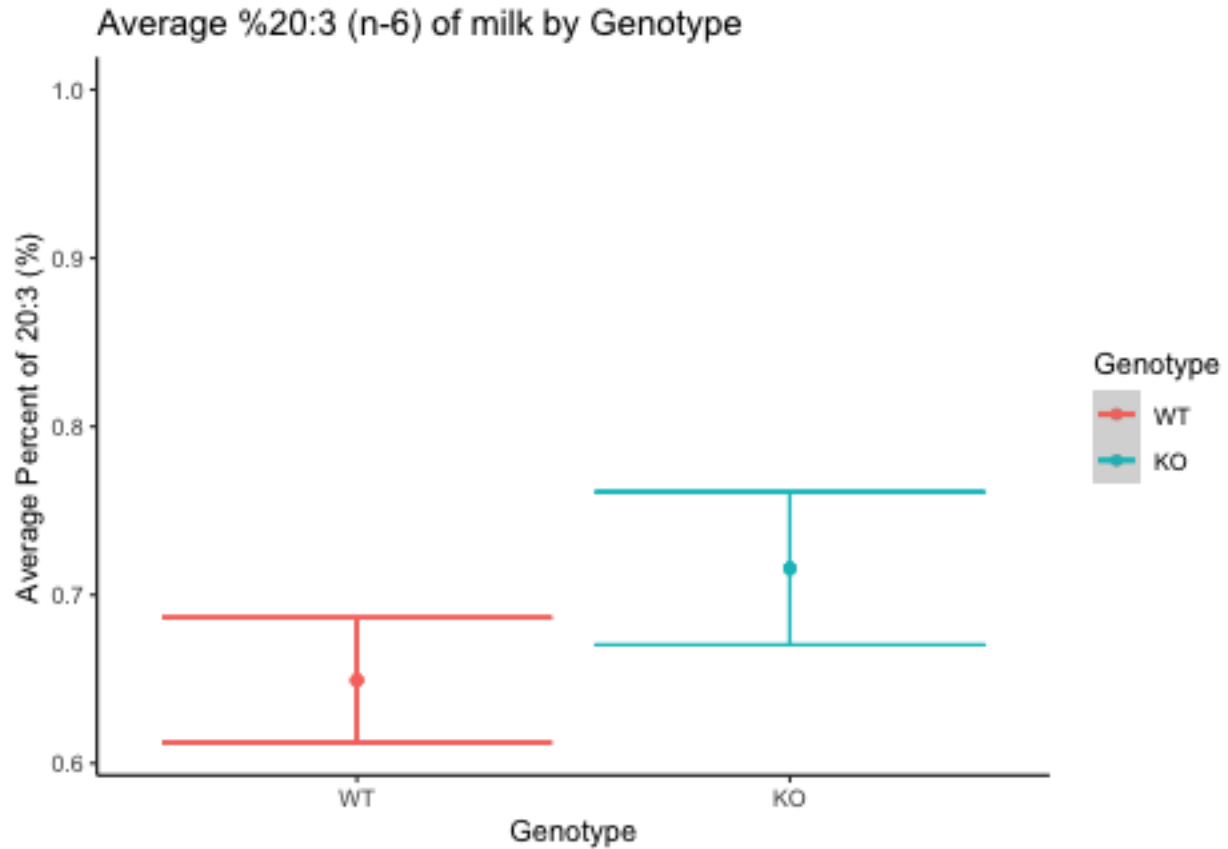


```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%22:4 (n-6)`
## W = 1, p-value = 0.8

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%22:4 (n-6)`
## W = 0.8, p-value = 0.05
```

Table 17: Student's t-test for %22:5 (n-6) by maternal genotype

statistic	p.value	method	alternative
14	0.841	Wilcoxon rank sum exact test	two.sided



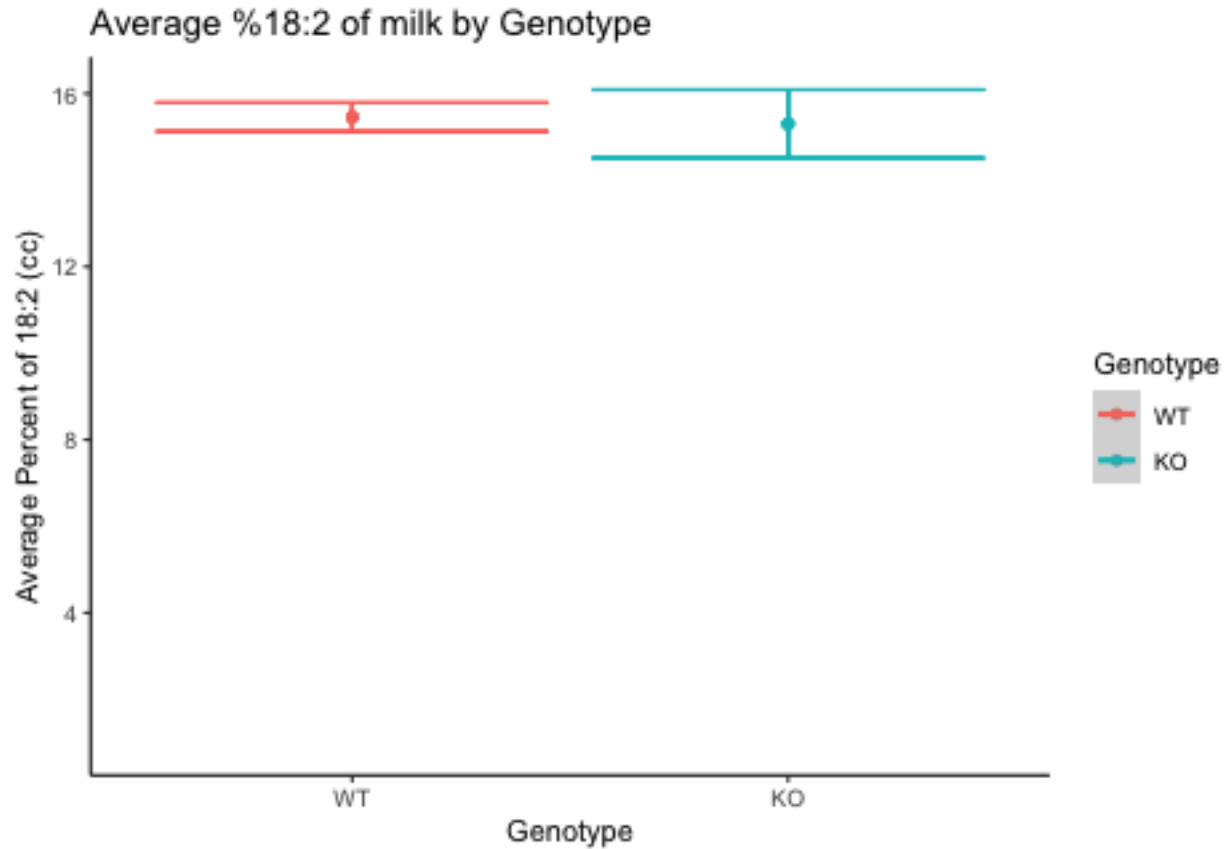
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%20:3 (n-6)`
## W = 1, p-value = 0.9

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%20:3 (n-6)`
## W = 1, p-value = 0.9
```

Table 18: Student's t-test for %20:3 (n-6) by maternal genotype

term	df	statistic	p.value
group	1	0.123	0.735
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.066	0.649	0.716	-1.13	0.292	8	-0.201	0.069	Two Sample t-test	two.sided



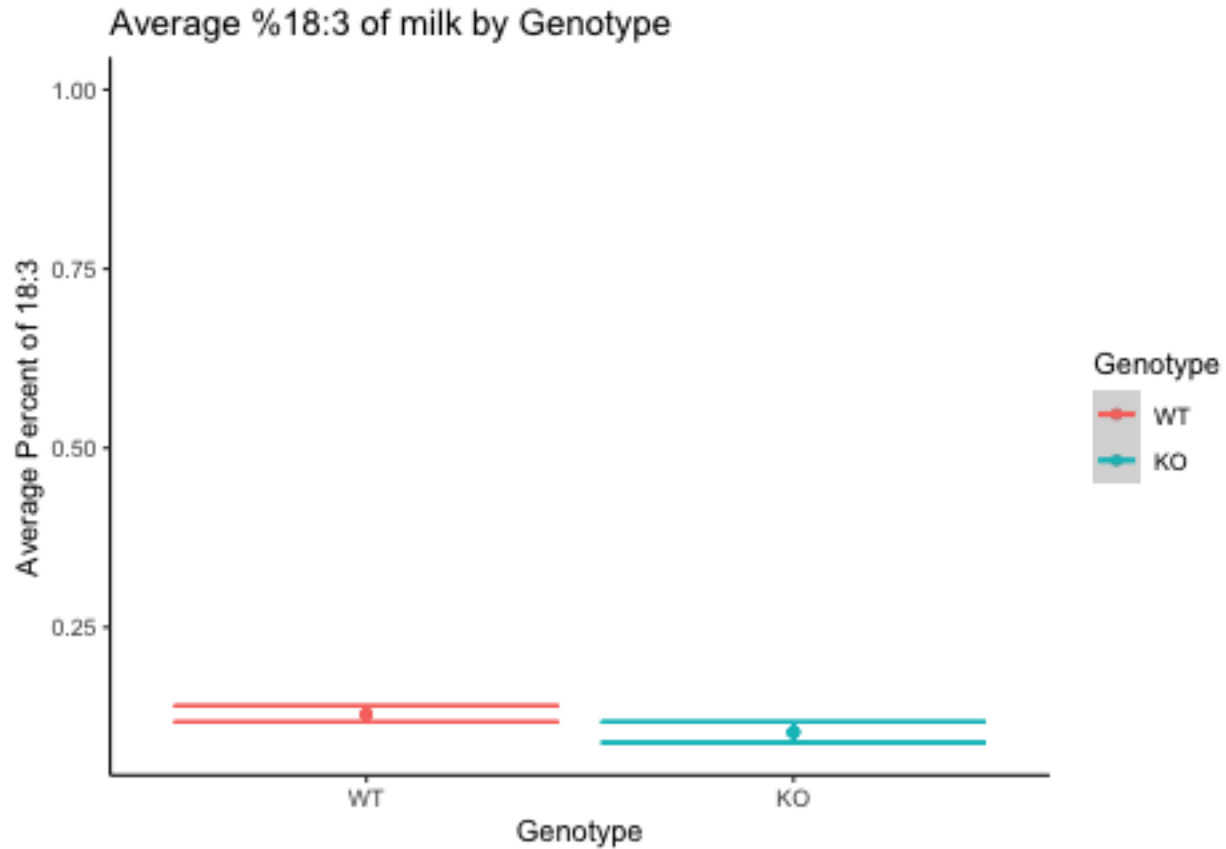
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%18:2 (n-6)cc`
## W = 0.9, p-value = 0.4

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%18:2 (n-6)cc`
## W = 1, p-value = 0.8
```

Table 20: Student's t-test for %18:2 (n-6)cc by maternal genotype

term	df	statistic	p.value
group	1	2.14	0.182
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
0.156	15.5	15.3	0.182	0.86	8	-1.82	2.13	Two Sample t-test	two.sided



```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%18:3` (n=6)
## W = 0.9, p-value = 0.2

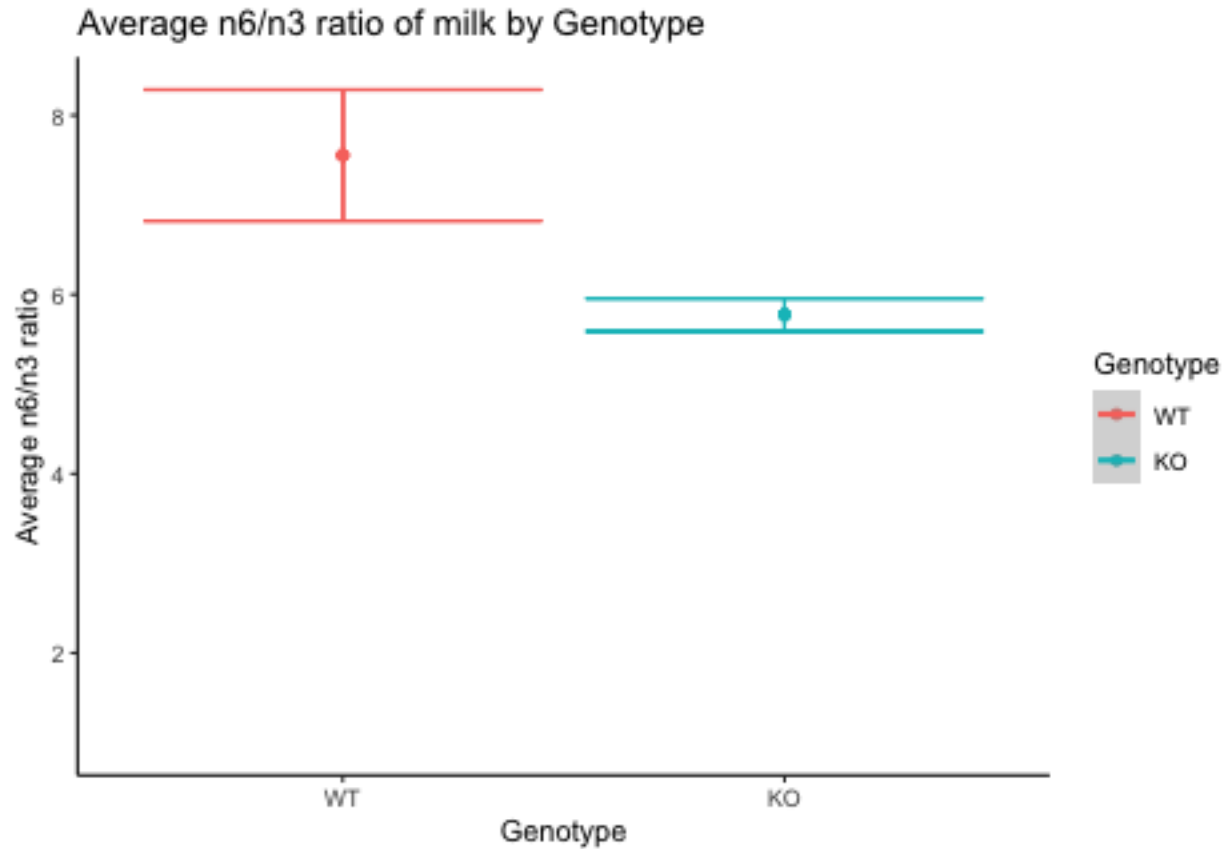
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%18:3` (n=6)
## W = 0.8, p-value = 0.08
```

Table 22: Student's t-test for %18:3 (n=6) by maternal genotype

term	df	statistic	p.value
group	1	0.213	0.657
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
0.025	0.129	0.103	1.39	0.201	8	-0.017	0.068	Two Sample t-test	two.sided

```
## [1] 5.77 5.77 5.77 5.77 5.77 7.55 7.55 7.55 7.55 7.55
```



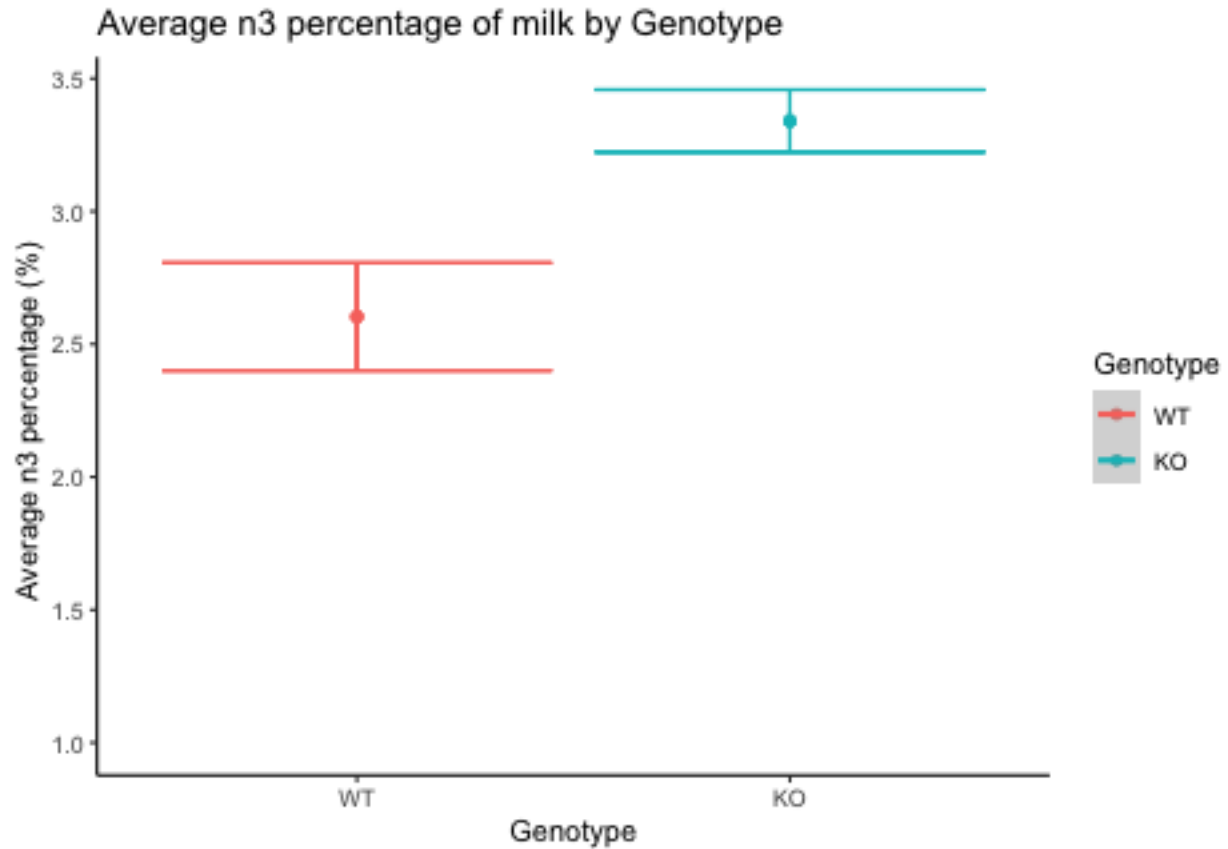
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`Ratio n6/n3`
## W = 0.9, p-value = 0.5

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`Ratio n6/n3`
## W = 0.8, p-value = 0.05
```

Table 24: Student's t-test for Ratio n6/n3 by maternal genotype

statistic	p.value	method	alternative
25	0.008	Wilcoxon rank sum exact test	two.sided

```
## [1] 3.34 3.34 3.34 3.34 3.34 2.60 2.60 2.60 2.60 2.60
```



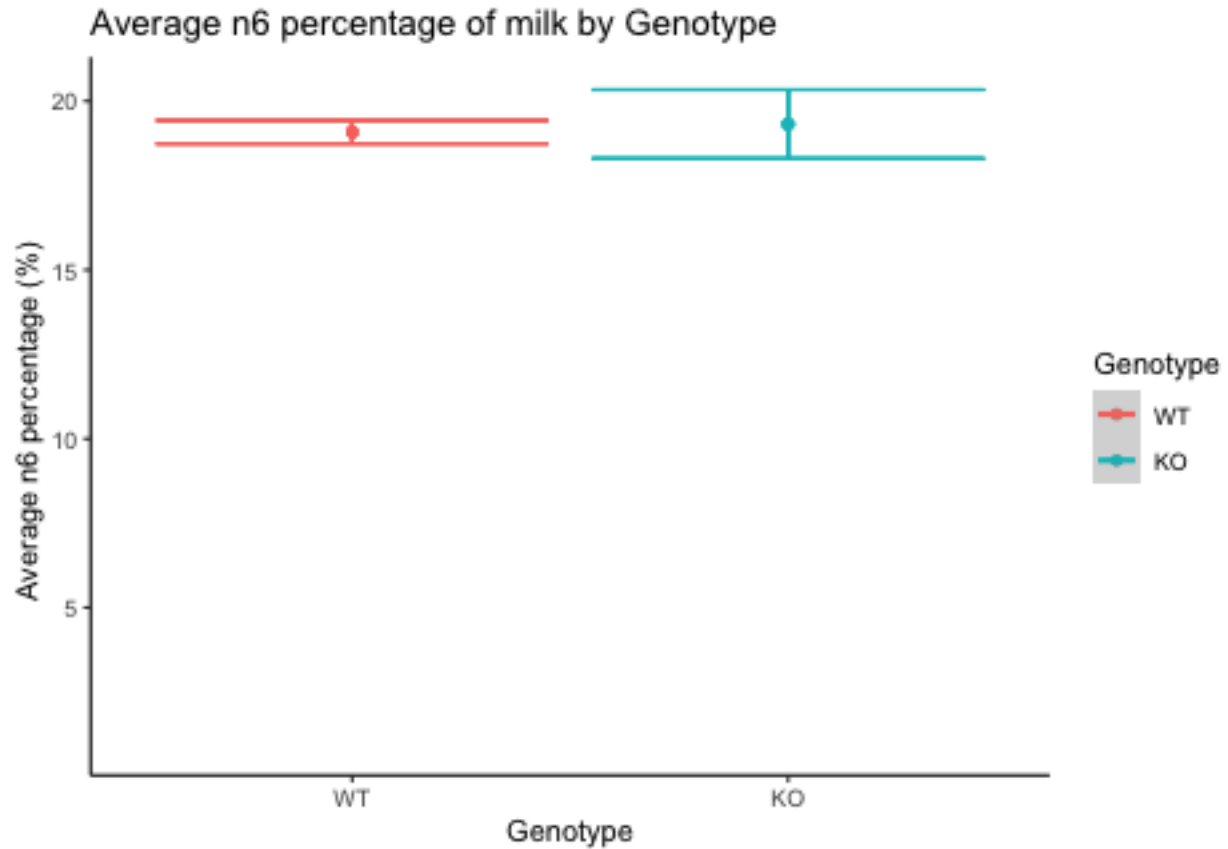
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%n3`
## W = 0.9, p-value = 0.4

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%n3`
## W = 0.8, p-value = 0.08
```

Table 25: Student's t-test for %n3 by maternal genotype

term	df	statistic	p.value
group	1	0.494	0.502
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.737	2.6	3.34	-3.16	0.013	8	-1.28	-0.199	Two Sample t-test	two.sided



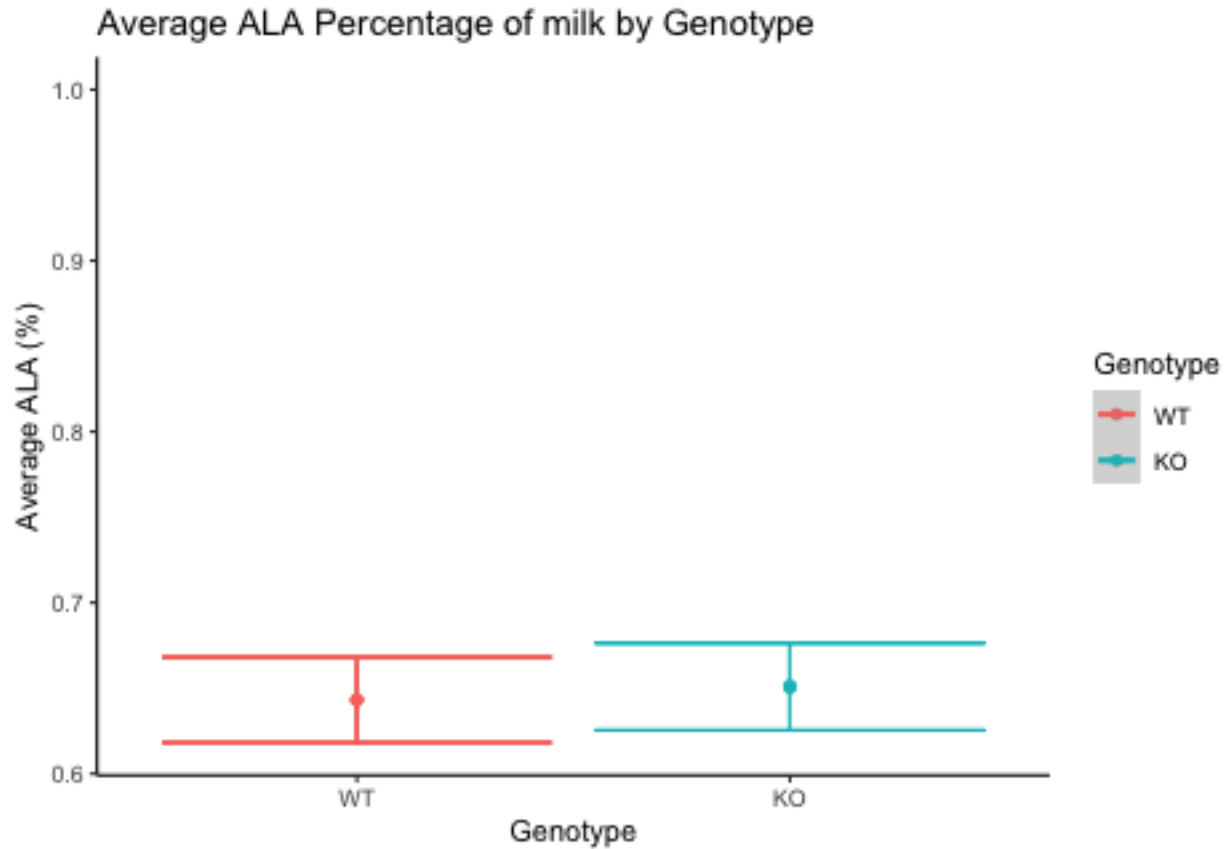
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%n6`
## W = 0.8, p-value = 0.04

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%n6`
## W = 0.9, p-value = 0.3
```

Table 27: Student's t-test for %n6 by maternal genotype

statistic	p.value	method	alternative
10	0.69	Wilcoxon rank sum exact test	two.sided





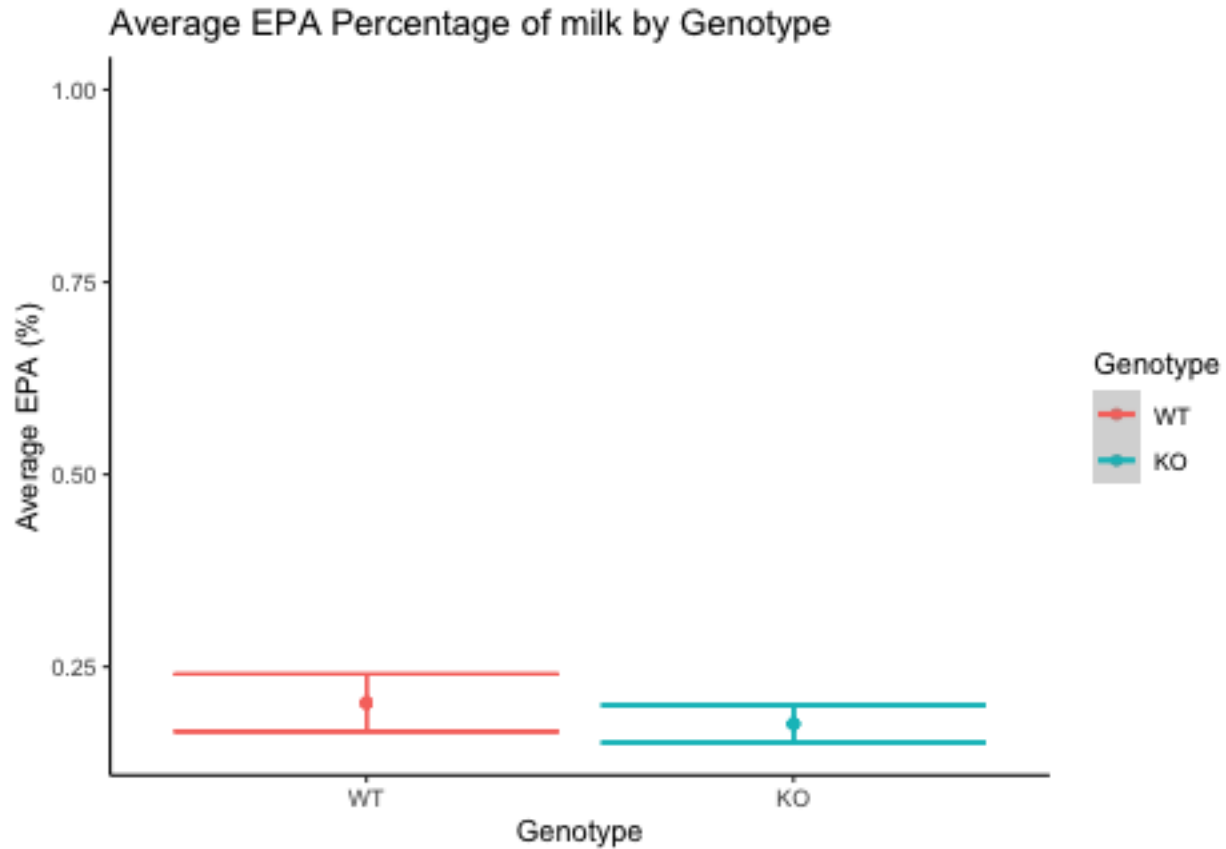
```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%18:3 (n-3)`
## W = 0.9, p-value = 0.5

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%18:3 (n-3)`
## W = 0.9, p-value = 0.4
```

Table 28: Student's t-test for %18:3 (n-3) by maternal genotype

term	df	statistic	p.value
group	1	0.016	0.901
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.008	0.643	0.651	-0.217	0.833	8	-0.09	0.075	Two Sample t-test	two.sided



```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%20:5 (n-3)`
## W = 0.9, p-value = 0.5

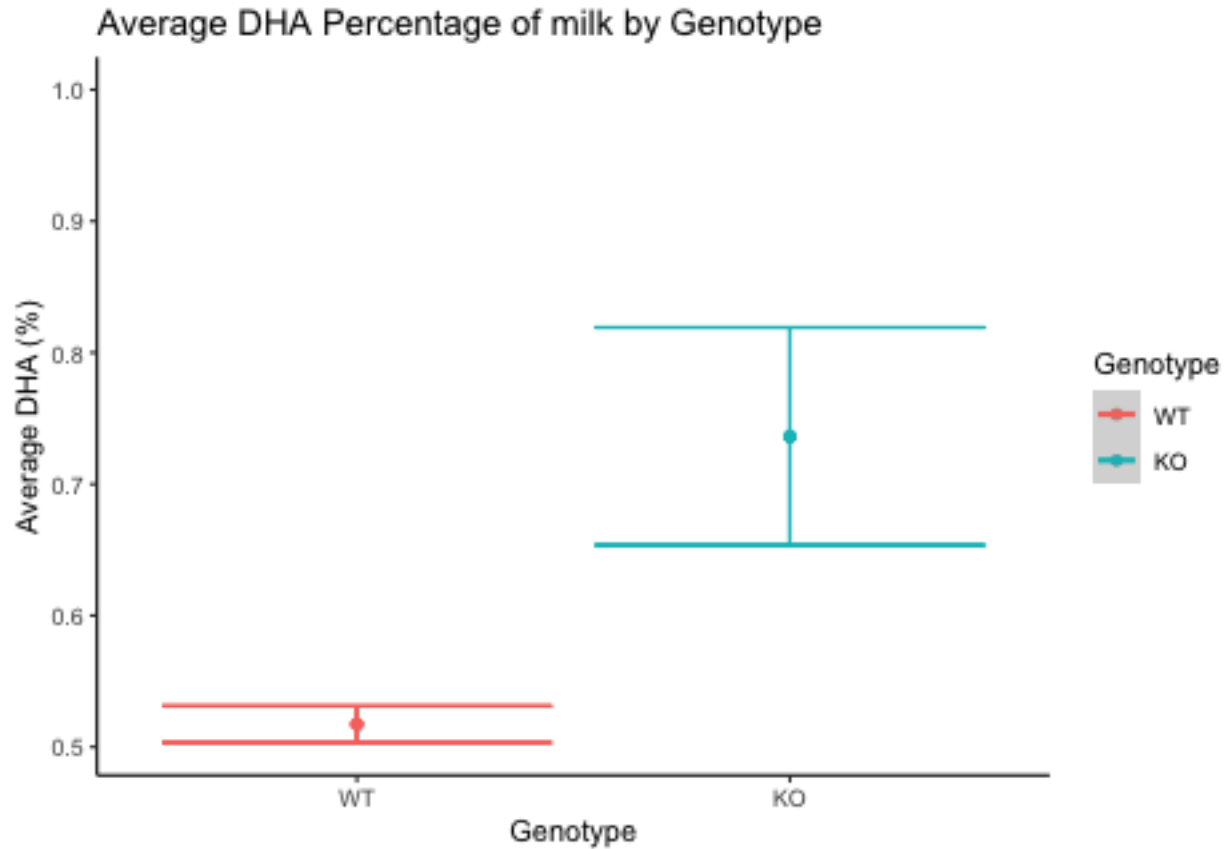
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%20:5 (n-3)`
## W = 0.9, p-value = 0.4
```

Table 30: Student's t-test for %18:3 (n-3) by maternal genotype

term	df	statistic	p.value
group	1	1.13	0.319
	8	NA	NA

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
0.027	0.203	0.176	0.615	0.556	8	-0.075	0.13	Two Sample t-test	two.sided

```
## [1] 0.736 0.736 0.736 0.736 0.736 0.517 0.517 0.517 0.517 0.517
```



```
##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "KO")$`%22:6 (n-3)`
## W = 0.9, p-value = 0.5

##
## Shapiro-Wilk normality test
##
## data: filter(lipidomics.data, Genotype == "WT")$`%22:6 (n-3)`
## W = 0.9, p-value = 0.5
```

Table 32: Student's t-test for %22:6 (n-3) by maternal genotype

term	df	statistic	p.value
group	1	3.68	0.091
	8	NA	NA

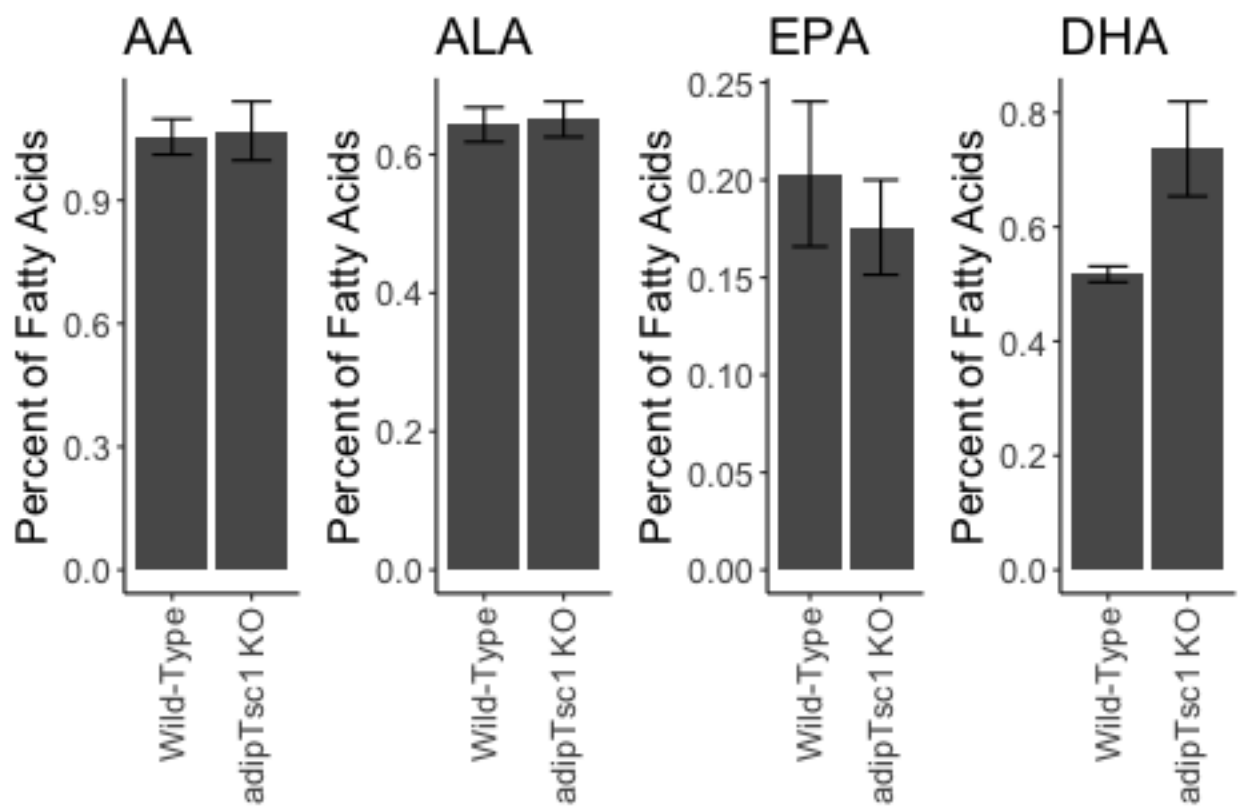
estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
-0.219	0.517	0.736	-2.61	0.031	8	-0.413	-0.025	Two Sample t-test	two.sided

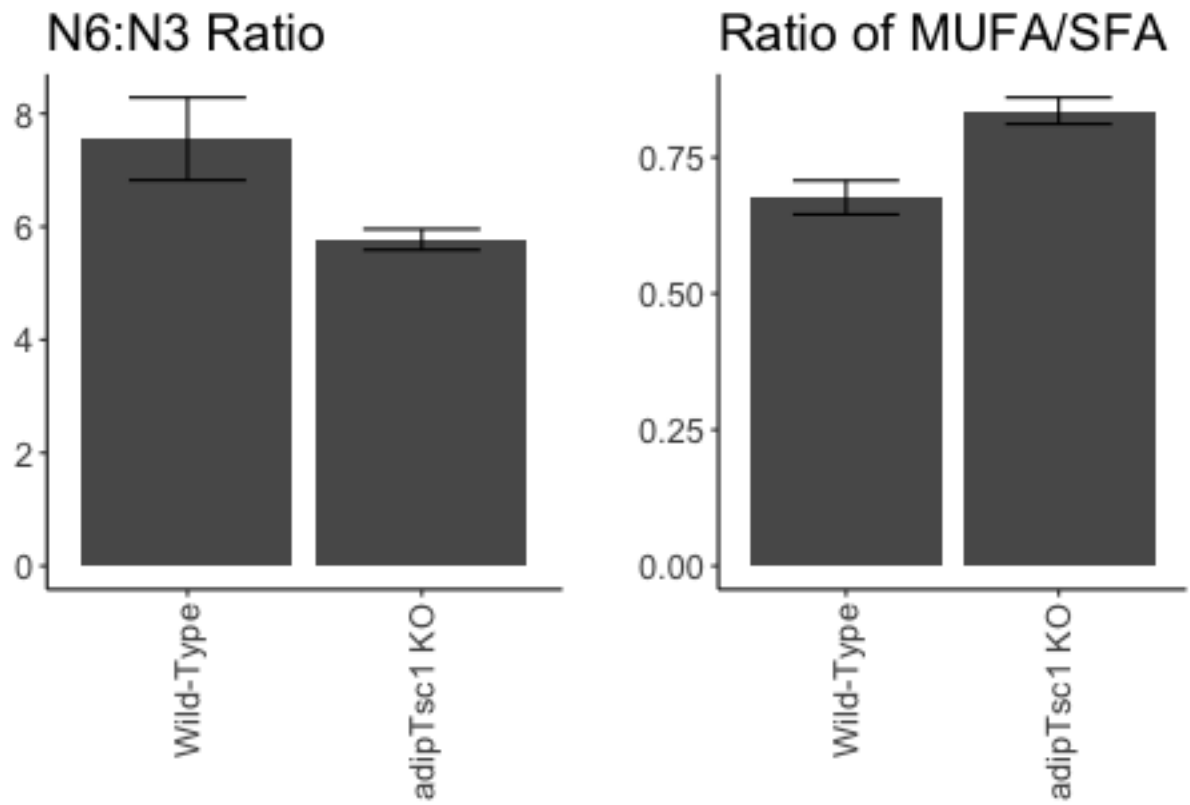
## Lipid Summary

Table 34: Changes in lipids (percent)

Lipid	WT	KO	Percent.Change	Test	P.Value	Sig
%14:0	12.681	11.154	88.0	Student	0.210	
%14:1 (n-5)	0.064	0.078	122.6	Student	0.645	
%15:0	0.138	0.152	110.1	Mann Whitney	0.421	
%16:0	28.811	25.789	89.5	Student	0.008	**
%16:1 (n-7)c	2.373	2.385	100.5	Student	0.941	
%16:1 (n-7)t	0.241	0.221	91.8	Student	0.649	
%18:0	4.847	4.778	98.6	Student	0.846	
%18:1(n-7)	5.022	6.054	120.5	Student	0.015	*
%18:1(n-9)	23.336	26.117	111.9	Student	0.026	*
%18:2 (n-6)cc	15.455	15.299	99.0	Student	0.860	
%18:2 (n-6)tt	0.033	0.123	374.8	Student	0.038	*
%18:2 (n-7,9) Conju	0.033	0.025	73.7	Student	0.273	
%18:3 (n-3)	0.643	0.651	101.2	Student	0.833	
%18:3 (n-6)	0.129	0.103	80.3	Student	0.201	
%18:4 (n-3)	0.809	1.293	159.9	Student	0.081	.
%19:0	0.062	0.071	114.4	Mann Whitney	0.690	
%20:0	0.084	0.070	82.6	Student	0.315	
%20:1	0.263	0.051	19.4	Mann Whitney	0.690	
%20:2 (n-6)	1.255	1.470	117.2	Student	0.207	
%20:3 (n-6)	0.649	0.716	110.2	Student	0.292	
%20:4 (n-6)	1.055	1.069	101.4	Student	0.869	
%20:5 (n-3)	0.203	0.176	86.5	Student	0.556	
%20:5 (n-6)	0.079	0.089	112.1	Student	0.705	
%21:0	0.048	0.044	92.0	Student	0.708	
%22:0	0.034	0.032	95.9	Student	0.835	
%22:1	0.120	0.137	114.1	Student	0.254	
%22:2 (n-6)	0.046	0.080	175.8	Student	0.259	
%22:4 (n-6)	0.381	0.361	94.8	Mann Whitney	0.841	
%22:5 (n-3)	0.431	0.484	112.3	Student	0.124	
%22:5 (n-6)	0.005	0.006	115.3	Student	0.366	
%22:6 (n-3)	0.517	0.736	142.4	Student	0.031	*
%24:0	0.054	0.071	133.0	Student	0.447	
%24:1	0.101	0.114	112.8	Student	0.409	
%SFA	46.758	42.161	90.2	Student	0.008	**
%MUFA	31.519	35.158	111.5	Student	0.009	**
%PUFA	21.722	22.681	104.4	Mann Whitney	0.690	
%n3	2.603	3.340	128.3	Student	0.013	*
%n6	19.086	19.316	101.2	Mann Whitney	0.690	
MUFA/SFA	0.676	0.836	123.5	Student	0.004	**
Ratio n6/n3	7.554	5.774	76.4	Student	0.046	*

## [1] 27.5





Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.