

Characterization and Tissue Tropism of newly identified ifla-virus and negevirus in tsetse flies *Glossina morsitans morsitans*

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set up the working directory and load needed packages

```
library(ggplot2)
library(lattice)
library(gcookbook)
library(ggfortify)
library(datasets)
library(MASS)
library(survival)
library(rmarkdown)
library(knitr)
library(coxme)

## Loading required package: bdsmatrix

##
## Attaching package: 'bdsmatrix'

## The following object is masked from 'package:base':
##
##      backsolve

library(lme4)

## Loading required package: Matrix

library(nlme)

##
## Attaching package: 'nlme'

## The following object is masked from 'package:lme4':
##
##      lmList

library(tidyverse)

## -- Attaching packages -----
tidyverse 1.3.1 --
```

```

## v tibble 3.1.4      v dplyr 1.0.7
## v tidyr 1.1.3       v stringr 1.4.0
## v readr 2.0.1       v forcats 0.5.1
## v purrr 0.3.4

## -- Conflicts -----
tidyverse_conflicts() --
## x dplyr::collapse() masks nlme::collapse()
## x tidyr::expand()   masks Matrix::expand()
## x dplyr::filter()   masks stats::filter()
## x dplyr::lag()       masks stats::lag()
## x tidyr::pack()      masks Matrix::pack()
## x dplyr::select()    masks MASS::select()
## x tidyr::unpack()    masks Matrix::unpack()

library(gapminder)
library(rcompanion)
library(FSA)

## ## FSA v0.9.1. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related
## book.

library(stats)
library(RCA)

## Loading required package: igraph

##
## Attaching package: 'igraph'

## The following objects are masked from 'package:dplyr':
##
##   as_data_frame, groups, union

## The following objects are masked from 'package:purrr':
##
##   compose, simplify

## The following object is masked from 'package:tidyr':
##
##   crossing

## The following object is masked from 'package:tibble':
##
##   as_data_frame

## The following objects are masked from 'package:stats':
##
##   decompose, spectrum

```

```
## The following object is masked from 'package:base':
##
##      union

## Loading required package: gplots

## Registered S3 method overwritten by 'gplots':
##      method      from
##      reorder.factor DescTools

##
## Attaching package: 'gplots'

## The following object is masked from 'package:stats':
##
##      lowess

library(broom)
library(sp)
library(MuMIn)

## Registered S3 methods overwritten by 'MuMIn':
##      method      from
##      formula.coxme coxme
##      logLik.coxme  coxme
##      logLik.lmekin coxme

library(ggpubr)

## Registered S3 methods overwritten by 'car':
##      method      from
##      hist.boot    FSA
##      confint.boot FSA

library(AICcmodavg)

##
## Attaching package: 'AICcmodavg'

## The following objects are masked from 'package:MuMIn':
##
##      AICc, DIC, importance

## The following object is masked from 'package:lme4':
##
##      checkConv

library(car)

## Loading required package: carData

##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:FSA':
##
##      bootCase

## The following object is masked from 'package:dplyr':
##
##      recode

## The following object is masked from 'package:purrr':
##
##      some

library(ggthemes)
```

load the data and prepare it

```
#=====
#work with the average of the 3 technical reading
setwd("P:/Hannah/for_Review_meeting")

fig1 <- read.csv("organs_all_avg2.csv")

fig1
```

	Target	Sample	Tissue	Replicate	Virus
Normalized	Sex				
## 1	Nege	1A	Salivary_gland	2	Negevirus
77.402705950	Female				
## 2	Nege	7A	Fat_bodies	3	Negevirus
39.906292910	Male				
## 3	Nege	7A	Fat_bodies	1	Negevirus
39.349594060	Female				
## 4	Nege	1A	Salivary_gland	3	Negevirus
29.069334440	Female				
## 5	Nege	7A	Fat_bodies	1	Negevirus
20.357023310	Male				
## 6	Nege	7A	Fat_bodies	2	Negevirus
19.631228500	Female				
## 7	Nege	1A	Salivary_gland	2	Negevirus
18.722890740	Male				
## 8	Ifla	7A	Fat_bodies	1	Iflavirus
10.648584190	Female				
## 9	Ifla	7A	Fat_bodies	3	Iflavirus
9.314457044	Female				
## 10	Nege	3A	Malpighian_tubules	1	Negevirus
7.597307635	Female				
## 11	Ifla	7A	Fat_bodies	2	Iflavirus
5.013356605	Female				
## 12	Nege	1A	Salivary_gland	1	Negevirus
4.376742078	Male				
## 13	Ifla	3A	Malpighian_tubules	1	Iflavirus

3.923198149	Female			
## 14	Nege	7A	Fat_bodies	2 Negevirus
3.537905209	Male			
## 15	Nege	7A	Fat_bodies	3 Negevirus
3.331728226	Female			
## 16	Nege	1A	Salivary_gland	3 Negevirus
2.908747434	Male			
## 17	Ifla	4A	Mid_gut	3 Iflavirus
2.859857998	Male			
## 18	Ifla	8A	Brain	1 Iflavirus
2.764745961	Female			
## 19	Nege	8A	Brain	1 Negevirus
2.665310756	Female			
## 20	Ifla	1A	Salivary_gland	1 Iflavirus
1.918755308	Female			
## 21	Ifla	4A	Mid_gut	3 Iflavirus
1.825265012	Female			
## 22	Ifla	6A	Testes	3 Iflavirus
1.794807611	Male			
## 23	Ifla	8A	Brain	2 Iflavirus
1.786912992	Female			
## 24	Nege	8A	Brain	2 Negevirus
1.773831321	Female			
## 25	Ifla	6A	Testes	1 Iflavirus
1.697621456	Male			
## 26	Nege	9A	Milk_glands	2 Negevirus
1.412966980	Female			
## 27	Ifla	3A	Malpighian_tubules	3 Iflavirus
1.411609258	Female			
## 28	Ifla	9A	Milk_glands	2 Iflavirus
1.385602181	Female			
## 29	Ifla	6A	Testes	2 Iflavirus
1.320664580	Male			
## 30	Ifla	3A	Malpighian_tubules	2 Iflavirus
1.301843553	Male			
## 31	Ifla	7A	Fat_bodies	3 Iflavirus
1.269430000	Male			
## 32	Ifla	4A	Mid_gut	1 Iflavirus
1.211337107	Female			
## 33	Ifla	1A	Salivary_gland	3 Iflavirus
1.209748099	Male			
## 34	Ifla	8A	Brain	3 Iflavirus
1.207589381	Male			
## 35	Ifla	9A	Milk_glands	3 Iflavirus
1.178765779	Female			
## 36	Nege	5A	Front_gut	1 Negevirus
1.141186814	Female			
## 37	Nege	8A	Brain	1 Negevirus
1.060610153	Male			
## 38	Nege	6A	Testes	3 Negevirus

1.048261614	Male			
## 39	Ifla	8A	Brain	3 Iflavivirus
1.023812750	Female			
## 40	Ifla	9A	Milk_glands	1 Iflavivirus
1.021891196	Female			
## 41	Ifla	8A	Brain	1 Iflavivirus
1.021211123	Male			
## 42	Ifla	4A	Mid_gut	2 Iflavivirus
1.006193603	Male			
## 43	Nege	6A	Ovary	1 Negevirus
0.996945359	Female			
## 44	Nege	6A	Testes	1 Negevirus
0.981968623	Male			
## 45	Ifla	1A	Salivary_gland	3 Iflavivirus
0.967271882	Female			
## 46	Nege	4A	Mid_gut	3 Negevirus
0.944433541	Male			
## 47	Ifla	7A	Fat_bodies	2 Iflavivirus
0.930867859	Male			
## 48	Ifla	8A	Brain	2 Iflavivirus
0.864353004	Male			
## 49	Nege	5A	Front_gut	3 Negevirus
0.852571665	Male			
## 50	Ifla	1A	Salivary_gland	2 Iflavivirus
0.817396209	Female			
## 51	Ifla	5A	Front_gut	3 Iflavivirus
0.794423167	Male			
## 52	Ifla	3A	Malpighian_tubules	3 Iflavivirus
0.754561236	Male			
## 53	Nege	4A	Mid_gut	1 Negevirus
0.751201684	Female			
## 54	Ifla	4A	Mid_gut	2 Iflavivirus
0.719587999	Female			
## 55	Ifla	1A	Salivary_gland	2 Iflavivirus
0.659558977	Male			
## 56	Nege	2A	Hind_gut	1 Negevirus
0.596460970	Female			
## 57	Nege	9A	Milk_glands	1 Negevirus
0.579908913	Female			
## 58	Ifla	5A	Front_gut	2 Iflavivirus
0.489249866	Male			
## 59	Ifla	5A	Front_gut	3 Iflavivirus
0.474846292	Female			
## 60	Nege	8A	Brain	3 Negevirus
0.454187308	Male			
## 61	Ifla	5A	Front_gut	1 Iflavivirus
0.428891911	Female			
## 62	Nege	4A	Mid_gut	1 Negevirus
0.417650378	Male			
## 63	Ifla	7A	Fat_bodies	1 Iflavivirus

0.402634738	Male			
## 64	Ifla	3A	Malpighian_tubules	1 Iflavirus
0.371600886	Male			
## 65	Nege	9A	Milk_glands	3 Negevirus
0.371587771	Female			
## 66	Ifla	4A	Mid_gut	1 Iflavirus
0.365671927	Male			
## 67	Nege	1A	Salivary_gland	1 Negevirus
0.358316060	Female			
## 68	Ifla	2A	Hind_gut	1 Iflavirus
0.355361037	Female			
## 69	Ifla	3A	Malpighian_tubules	2 Iflavirus
0.354209947	Female			
## 70	Nege	6A	Testes	2 Negevirus
0.352838330	Male			
## 71	Nege	6A	Ovary	2 Negevirus
0.352644646	Female			
## 72	Nege	4A	Mid_gut	2 Negevirus
0.321005816	Female			
## 73	Ifla	2A	Hind_gut	1 Iflavirus
0.272778994	Male			
## 74	Nege	2A	Hind_gut	1 Negevirus
0.246349379	Male			
## 75	Nege	3A	Malpighian_tubules	3 Negevirus
0.225166941	Male			
## 76	Nege	5A	Front_gut	1 Negevirus
0.196212798	Male			
## 77	Nege	8A	Brain	2 Negevirus
0.179375639	Male			
## 78	Ifla	2A	Hind_gut	3 Iflavirus
0.170321852	Male			
## 79	Nege	3A	Malpighian_tubules	2 Negevirus
0.159920548	Female			
## 80	Ifla	2A	Hind_gut	2 Iflavirus
0.146907611	Female			
## 81	Ifla	2A	Hind_gut	3 Iflavirus
0.130858443	Female			
## 82	Ifla	1A	Salivary_gland	1 Iflavirus
0.117672441	Male			
## 83	Ifla	2A	Hind_gut	2 Iflavirus
0.109334722	Male			
## 84	Ifla	5A	Front_gut	1 Iflavirus
0.107608329	Male			
## 85	Nege	3A	Malpighian_tubules	1 Negevirus
0.103543820	Male			
## 86	Nege	5A	Front_gut	2 Negevirus
0.100733703	Female			
## 87	Ifla	5A	Front_gut	2 Iflavirus
0.099571356	Female			
## 88	Nege	4A	Mid_gut	3 Negevirus

```

0.094092464 Female
## 89 Nege 2A Hind_gut 2 Negevirus
0.089570912 Female
## 90 Nege 5A Front_gut 2 Negevirus
0.071801559 Male
## 91 Nege 8A Brain 3 Negevirus
0.057932219 Female
## 92 Nege 3A Malpighian_tubules 3 Negevirus
0.042103969 Female
## 93 Nege 5A Front_gut 3 Negevirus
0.039952549 Female
## 94 Nege 6A Ovary 3 Negevirus
0.032297897 Female
## 95 Nege 4A Mid_gut 2 Negevirus
0.028138818 Male
## 96 Nege 2A Hind_gut 3 Negevirus
0.023073452 Male
## 97 Ifla 6A Ovary 3 Iflavirus
0.021062121 Female
## 98 Ifla 6A Ovary 1 Iflavirus
0.017170381 Female
## 99 Nege 3A Malpighian_tubules 2 Negevirus
0.015372781 Male
## 100 Nege 2A Hind_gut 3 Negevirus
0.012167280 Female
## 101 Ifla 6A Ovary 2 Iflavirus
0.007298148 Female
## 102 Nege 2A Hind_gut 2 Negevirus
0.003874746 Male

str(fig1)

## 'data.frame': 102 obs. of 7 variables:
## $ Target : chr "Nege" "Nege" "Nege" "Nege" ...
## $ Sample : chr "1A" "7A" "7A" "1A" ...
## $ Tissue : chr "Salivary_gland" "Fat_bodies" "Fat_bodies"
"Salivary_gland" ...
## $ Replicate : int 2 3 1 3 1 2 2 1 3 1 ...
## $ Virus : chr "Negevirus" "Negevirus" "Negevirus" "Negevirus"
...
## $ Normalized: num 77.4 39.9 39.3 29.1 20.4 ...
## $ Sex : chr "Female" "Male" "Female" "Female" ...

#qpcr1$Normalized_Log_SQ<-as.numeric(qpcr1$Normalized_Log_SQ)
attach(fig1)
head(fig1)

## Target Sample Tissue Replicate Virus Normalized Sex
## 1 Nege 1A Salivary_gland 2 Negevirus 77.40271 Female
## 2 Nege 7A Fat_bodies 3 Negevirus 39.90629 Male
## 3 Nege 7A Fat_bodies 1 Negevirus 39.34959 Female

```



```
## 4   Nege      1A Salivary_gland      3 Negevirus  29.06933 Female
## 5   Nege      7A   Fat_bodies       1 Negevirus  20.35702   Male
## 6   Nege      7A   Fat_bodies       2 Negevirus  19.63123 Female
```

```
qpcr=na.omit(fig1)
```

Prepare fig 1 A and B

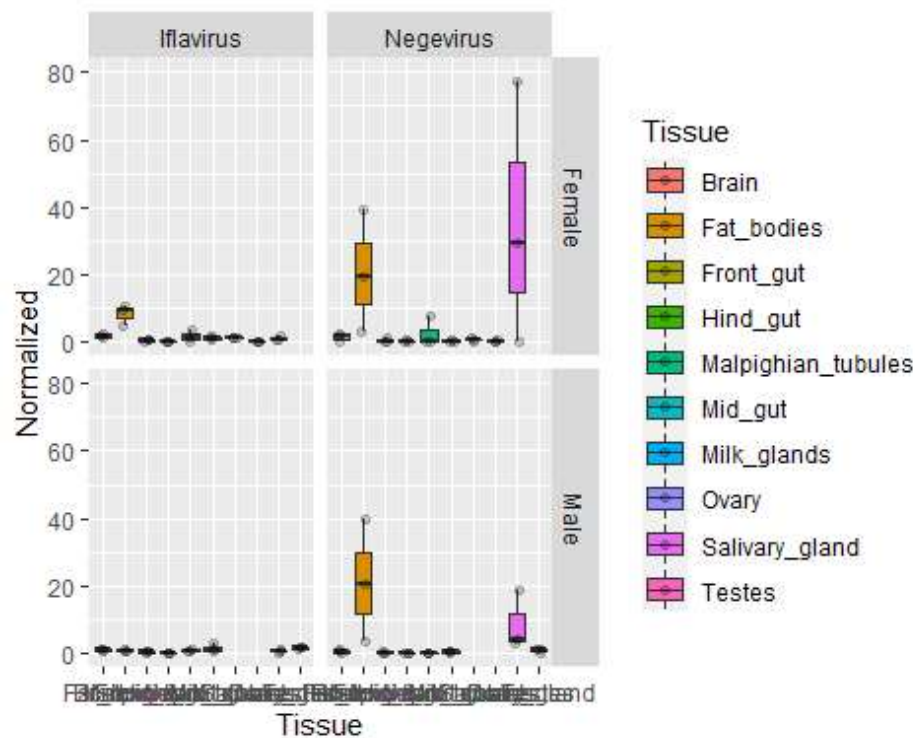
#produce figure

```
summary(fig1)
```

```
##      Target          Sample          Tissue
Replicate
## Length:102          Length:102          Length:102      Min.    :1
## Class :character    Class :character    Class :character    1st Qu.:1
## Mode  :character    Mode  :character    Mode  :character    Median :2
##                                     Mean   :2
##                                     3rd Qu.:3
##                                     Max.   :3
##      Virus          Normalized          Sex
## Length:102          Min.    : 0.00387    Length:102
## Class :character    1st Qu.: 0.18358    Class :character
## Mode  :character    Median : 0.77449    Mode  :character
##                                     Mean   : 3.48446
##                                     3rd Qu.: 1.41263
##                                     Max.   :77.40271
```

#to produce figure 6A

```
figs6avg<-ggplot(fig1,aes(x=Tissue,y=Normalized, fill=Tissue)) +
  geom_boxplot() + geom_jitter(width=0.1,alpha=0.2) +
  facet_grid(Sex~Virus) + ylim(0,80)
figs6avg
```



```
tiff("figs6avg1.tiff", width = 6, height = 6, units = 'in', res = 300)
plot(figs6avg+theme_tufte() + theme(axis.line = element_line(size = 1,
colour = "black"))) +
theme(axis.text.x=element_blank(),axis.ticks.x=element_blank()) +
theme(legend.title = element_text(face = "bold")) + theme(legend.text =
element_text(face = "italic")) + xlab(expression(bold("Tissues")))) +
ylab(expression (paste (bold("Normalized "), bold("density"))))
dev.off()
```

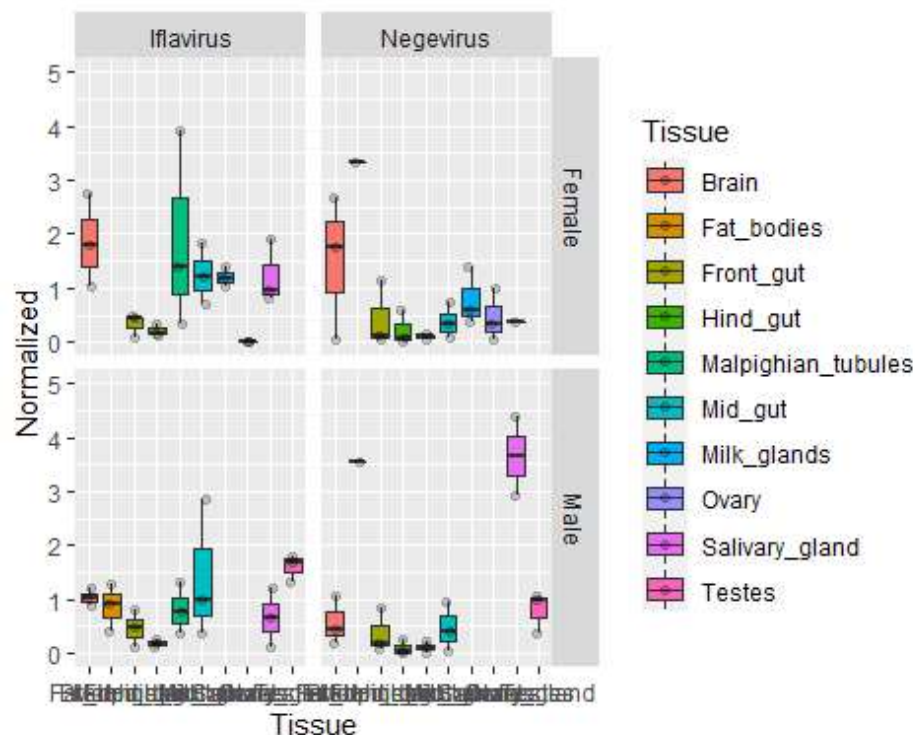
```
## png
## 2
```

#To produce the supplementary figure 6B

```
figs6avg<-ggplot(fig1,aes(x=Tissue,y=Normalized, fill=Tissue)) +
  geom_boxplot() + geom_jitter(width=0.1,alpha=0.2) +
  facet_grid(Sex~Virus) + ylim(0,5)
figs6avg
```

```
## Warning: Removed 11 rows containing non-finite values
(stat_boxplot).
```

```
## Warning: Removed 11 rows containing missing values (geom_point).
```



```
tiff("figs6avg1.tiff", width = 6, height = 6, units = 'in', res = 300)
plot(figs6avg+theme_tufte() + theme(axis.line = element_line(size = 1,
colour = "black")) +
theme(axis.text.x=element_blank(),axis.ticks.x=element_blank()) +
theme(legend.title = element_text(face = "bold")) + theme(legend.text =
element_text(face = "italic")))) + xlab(expression(bold("Tissues")))) +
ylab(expression (paste (bold("Normalized "), bold("density"))))
```

```
## Warning: Removed 11 rows containing non-finite values
(stat_boxplot).
```

```
## Warning: Removed 11 rows containing missing values (geom_point).
```

```
## Warning: Removed 11 rows containing non-finite values
(stat_boxplot).
```

```
## Warning: Removed 11 rows containing missing values (geom_point).
```

```
dev.off()
```

```
## png
## 2
```

```
#difference between tiussue regardsles the virus or the sex
model1<-glm(Normalized ~ Tissue, data = fig1)
summary(model1)
```

```
##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -12.405   -0.950   -0.177    0.184   65.859
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.23832     2.67881    0.462  0.64498
## TissueFat_bodies  11.56944     3.78841    3.054  0.00295 **
## TissueFront_gut   -0.83857     3.78841   -0.221  0.82531
## TissueHind_gut    -1.05857     3.78841   -0.279  0.78055
## TissueMalpighian_tubules 0.11671     3.78841    0.031  0.97549
## TissueMid_gut     -0.35962     3.78841   -0.095  0.92458
## TissueMilk_glands -0.24654     4.63983   -0.053  0.95774
## TissueOvary       -1.00042     4.63983   -0.216  0.82976
## TissueSalivary_gland 10.30577     3.78841    2.720  0.00780 **
## TissueTestes      -0.03896     4.63983   -0.008  0.99332
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 86.11222)
##
##      Null deviance: 10318.4  on 101  degrees of freedom
## Residual deviance:  7922.3  on  92  degrees of freedom
## AIC: 755.42
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  27.825  9   0.00102 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

statistical analysis for Iflavivirus

#work with iflavivirus alone

```
fig1ifla <- subset(fig1, Virus=="Iflavirus")
fig1ifla

##      Target Sample      Tissue Replicate      Virus
## Normalized Sex
## 8      Ifla      7A      Fat_bodies      1 Iflavivirus
```

10.648584190	Female			
## 9	Ifla	7A	Fat_bodies	3 Iflavivirus
9.314457044	Female			
## 11	Ifla	7A	Fat_bodies	2 Iflavivirus
5.013356605	Female			
## 13	Ifla	3A	Malpighian_tubules	1 Iflavivirus
3.923198149	Female			
## 17	Ifla	4A	Mid_gut	3 Iflavivirus
2.859857998	Male			
## 18	Ifla	8A	Brain	1 Iflavivirus
2.764745961	Female			
## 20	Ifla	1A	Salivary_gland	1 Iflavivirus
1.918755308	Female			
## 21	Ifla	4A	Mid_gut	3 Iflavivirus
1.825265012	Female			
## 22	Ifla	6A	Testes	3 Iflavivirus
1.794807611	Male			
## 23	Ifla	8A	Brain	2 Iflavivirus
1.786912992	Female			
## 25	Ifla	6A	Testes	1 Iflavivirus
1.697621456	Male			
## 27	Ifla	3A	Malpighian_tubules	3 Iflavivirus
1.411609258	Female			
## 28	Ifla	9A	Milk_glands	2 Iflavivirus
1.385602181	Female			
## 29	Ifla	6A	Testes	2 Iflavivirus
1.320664580	Male			
## 30	Ifla	3A	Malpighian_tubules	2 Iflavivirus
1.301843553	Male			
## 31	Ifla	7A	Fat_bodies	3 Iflavivirus
1.269430000	Male			
## 32	Ifla	4A	Mid_gut	1 Iflavivirus
1.211337107	Female			
## 33	Ifla	1A	Salivary_gland	3 Iflavivirus
1.209748099	Male			
## 34	Ifla	8A	Brain	3 Iflavivirus
1.207589381	Male			
## 35	Ifla	9A	Milk_glands	3 Iflavivirus
1.178765779	Female			
## 39	Ifla	8A	Brain	3 Iflavivirus
1.023812750	Female			
## 40	Ifla	9A	Milk_glands	1 Iflavivirus
1.021891196	Female			
## 41	Ifla	8A	Brain	1 Iflavivirus
1.021211123	Male			
## 42	Ifla	4A	Mid_gut	2 Iflavivirus
1.006193603	Male			
## 45	Ifla	1A	Salivary_gland	3 Iflavivirus
0.967271882	Female			
## 47	Ifla	7A	Fat_bodies	2 Iflavivirus

0.930867859	Male			
## 48	Ifla	8A	Brain	2 Iflavivirus
0.864353004	Male			
## 50	Ifla	1A	Salivary_gland	2 Iflavivirus
0.817396209	Female			
## 51	Ifla	5A	Front_gut	3 Iflavivirus
0.794423167	Male			
## 52	Ifla	3A	Malpighian_tubules	3 Iflavivirus
0.754561236	Male			
## 54	Ifla	4A	Mid_gut	2 Iflavivirus
0.719587999	Female			
## 55	Ifla	1A	Salivary_gland	2 Iflavivirus
0.659558977	Male			
## 58	Ifla	5A	Front_gut	2 Iflavivirus
0.489249866	Male			
## 59	Ifla	5A	Front_gut	3 Iflavivirus
0.474846292	Female			
## 61	Ifla	5A	Front_gut	1 Iflavivirus
0.428891911	Female			
## 63	Ifla	7A	Fat_bodies	1 Iflavivirus
0.402634738	Male			
## 64	Ifla	3A	Malpighian_tubules	1 Iflavivirus
0.371600886	Male			
## 66	Ifla	4A	Mid_gut	1 Iflavivirus
0.365671927	Male			
## 68	Ifla	2A	Hind_gut	1 Iflavivirus
0.355361037	Female			
## 69	Ifla	3A	Malpighian_tubules	2 Iflavivirus
0.354209947	Female			
## 73	Ifla	2A	Hind_gut	1 Iflavivirus
0.272778994	Male			
## 78	Ifla	2A	Hind_gut	3 Iflavivirus
0.170321852	Male			
## 80	Ifla	2A	Hind_gut	2 Iflavivirus
0.146907611	Female			
## 81	Ifla	2A	Hind_gut	3 Iflavivirus
0.130858443	Female			
## 82	Ifla	1A	Salivary_gland	1 Iflavivirus
0.117672441	Male			
## 83	Ifla	2A	Hind_gut	2 Iflavivirus
0.109334722	Male			
## 84	Ifla	5A	Front_gut	1 Iflavivirus
0.107608329	Male			
## 87	Ifla	5A	Front_gut	2 Iflavivirus
0.099571356	Female			
## 97	Ifla	6A	Ovary	3 Iflavivirus
0.021062121	Female			
## 98	Ifla	6A	Ovary	1 Iflavivirus
0.017170381	Female			

```
## 101 Ifla 6A Ovary 2 Iflavir
0.007298148 Female

#difference between tissue regardless the sex for iflavirus
model1<-glm(Normalized ~ Tissue, data = fig1ifla)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1ifla)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -4.1939  -0.3123  -0.0273   0.1740   6.0520
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.44477    0.69577    2.077  0.04416 *
## TissueFat_bodies      3.15178    0.98397    3.203  0.00263 **
## TissueFront_gut     -1.04567    0.98397   -1.063  0.29413
## TissueHind_gut      -1.24718    0.98397   -1.267  0.21213
## TissueMalpighian_tubules -0.09193    0.98397   -0.093  0.92602
## TissueMid_gut       -0.11345    0.98397   -0.115  0.90877
## TissueMilk_glands    -0.24935    1.20511   -0.207  0.83710
## TissueOvary         -1.42959    1.20511   -1.186  0.24234
## TissueSalivary_gland  -0.49637    0.98397   -0.504  0.61664
## TissueTestes         0.15959    1.20511    0.132  0.89529
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 2.904571)
##
##      Null deviance: 202.33  on 50  degrees of freedom
## Residual deviance: 119.09  on 41  degrees of freedom
## AIC: 209.98
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  28.658  9  0.0007399 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#difference between sex regardless the tissues for iflavirus
model1<-glm(Normalized ~ Sex, data = fig1ifla)
summary(model1)
```

```
##
## Call:
## glm(formula = Normalized ~ Sex, data = fig1ifla)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.8064  -0.8191  -0.4281   0.2353   8.8349
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.8137     0.3802   4.770 1.69e-05 ***
## SexMale      -0.9345     0.5542  -1.686  0.0981 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 3.902679)
##
##      Null deviance: 202.33  on 50  degrees of freedom
## Residual deviance: 191.23  on 49  degrees of freedom
## AIC: 218.14
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Sex    2.8432  1  0.09176 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#=====
#for male
fig1iflam <- subset(fig1ifla, Sex=="Male")
fig1iflam
```

##	Target	Sample	Tissue	Replicate	Virus	Normalized
## Sex						
## 17	Ifla	4A	Mid_gut	3	Iflavirus	2.8598580
## Male						
## 22	Ifla	6A	Testes	3	Iflavirus	1.7948076
## Male						
## 25	Ifla	6A	Testes	1	Iflavirus	1.6976215
## Male						
## 29	Ifla	6A	Testes	2	Iflavirus	1.3206646
## Male						
## 30	Ifla	3A	Malpighian_tubules	2	Iflavirus	1.3018436
## Male						
## 31	Ifla	7A	Fat_bodies	3	Iflavirus	1.2694300

Sex	Sample ID	Species	Strain	Tissue	Pathogen	Normalized Value
Male	## 33	Ifla	1A	Salivary_gland	3 Iflavivirus	1.2097481
Male	## 34	Ifla	8A	Brain	3 Iflavivirus	1.2075894
Male	## 41	Ifla	8A	Brain	1 Iflavivirus	1.0212111
Male	## 42	Ifla	4A	Mid_gut	2 Iflavivirus	1.0061936
Male	## 47	Ifla	7A	Fat_bodies	2 Iflavivirus	0.9308679
Male	## 48	Ifla	8A	Brain	2 Iflavivirus	0.8643530
Male	## 51	Ifla	5A	Front_gut	3 Iflavivirus	0.7944232
Male	## 52	Ifla	3A	Malpighian_tubules	3 Iflavivirus	0.7545612
Male	## 55	Ifla	1A	Salivary_gland	2 Iflavivirus	0.6595590
Male	## 58	Ifla	5A	Front_gut	2 Iflavivirus	0.4892499
Male	## 63	Ifla	7A	Fat_bodies	1 Iflavivirus	0.4026347
Male	## 64	Ifla	3A	Malpighian_tubules	1 Iflavivirus	0.3716009
Male	## 66	Ifla	4A	Mid_gut	1 Iflavivirus	0.3656719
Male	## 73	Ifla	2A	Hind_gut	1 Iflavivirus	0.2727790
Male	## 78	Ifla	2A	Hind_gut	3 Iflavivirus	0.1703219
Male	## 82	Ifla	1A	Salivary_gland	1 Iflavivirus	0.1176724
Male	## 83	Ifla	2A	Hind_gut	2 Iflavivirus	0.1093347
Male	## 84	Ifla	5A	Front_gut	1 Iflavivirus	0.1076083

```
fig1iflam$Tissue <- as.factor(fig1iflam$Tissue)
fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Brain")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)
```

```
##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.0311     0.3293   3.131  0.00645 **
## TissueFat_bodies -0.1634     0.4657  -0.351  0.73027
## TissueFront_gut  -0.5673     0.4657  -1.218  0.24087
## TissueHind_gut   -0.8469     0.4657  -1.818  0.08777 .
## TissueMalpighian_tubules -0.2217     0.4657  -0.476  0.64047
## TissueMid_gut     0.3795     0.4657   0.815  0.42710
## TissueSalivary_gland -0.3687     0.4657  -0.792  0.44012
## TissueTestes      0.5733     0.4657   1.231  0.23612
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##    Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Mid_gut")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.4106     0.3293   4.283  0.00057 ***
## TissueBrain      -0.3795     0.4657  -0.815  0.42710
## TissueFat_bodies -0.5429     0.4657  -1.166  0.26080
## TissueFront_gut  -0.9468     0.4657  -2.033  0.05900 .
## TissueHind_gut   -1.2264     0.4657  -2.633  0.01807 *
```

```

## TissueMalpighian_tubules -0.6012      0.4657 -1.291  0.21507
## TissueSalivary_gland    -0.7482      0.4657 -1.607  0.12770
## TissueTestes             0.1938      0.4657  0.416  0.68287
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
## Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Testes")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.6044     0.3293   4.872  0.00017 ***
## TissueMid_gut    -0.1938     0.4657  -0.416  0.68287
## TissueBrain      -0.5733     0.4657  -1.231  0.23612
## TissueFat_bodies -0.7367     0.4657  -1.582  0.13325
## TissueFront_gut  -1.1406     0.4657  -2.449  0.02622 *
## TissueHind_gut   -1.4202     0.4657  -3.049  0.00765 **
## TissueMalpighian_tubules -0.7950     0.4657  -1.707  0.10715
## TissueSalivary_gland -0.9420     0.4657  -2.023  0.06015 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##

```

```

##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Fat_bodies")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.86764    0.32933   2.635   0.018 *
## TissueTestes    0.73672    0.46574   1.582   0.133
## TissueMid_gut   0.54293    0.46574   1.166   0.261
## TissueBrain     0.16341    0.46574   0.351   0.730
## TissueFront_gut -0.40388    0.46574  -0.867   0.399
## TissueHind_gut  -0.68350    0.46574  -1.468   0.162
## TissueMalpighian_tubules -0.05831    0.46574  -0.125   0.902
## TissueSalivary_gland -0.20532    0.46574  -0.441   0.665
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Salivary_gland")
modell1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(modell1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.6623    0.3293   2.011  0.0615 .
## TissueFat_bodies  0.2053    0.4657   0.441  0.6652
## TissueTestes    0.9420    0.4657   2.023  0.0602 .
## TissueMid_gut    0.7482    0.4657   1.607  0.1277
## TissueBrain      0.3687    0.4657   0.792  0.4401
## TissueFront_gut  -0.1986    0.4657  -0.426  0.6755
## TissueHind_gut   -0.4782    0.4657  -1.027  0.3198
## TissueMalpighian_tubules 0.1470    0.4657   0.316  0.7564
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(modell1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Front_gut")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.4638     0.3293   1.408   0.1782
## TissueSalivary_gland  0.1986     0.4657   0.426   0.6755
## TissueFat_bodies     0.4039     0.4657   0.867   0.3987
## TissueTestes        1.1406     0.4657   2.449   0.0262 *
## TissueMid_gut        0.9468     0.4657   2.033   0.0590 .
## TissueBrain          0.5673     0.4657   1.218   0.2409
## TissueHind_gut      -0.2796     0.4657  -0.600   0.5567
## TissueMalpighian_tubules 0.3456     0.4657   0.742   0.4688
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref= "Hind_gut")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##

```

```
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.1841     0.3293   0.559  0.58380
## TissueFront_gut    0.2796     0.4657   0.600  0.55667
## TissueSalivary_gland 0.4782     0.4657   1.027  0.31983
## TissueFat_bodies   0.6835     0.4657   1.468  0.16161
## TissueTestes       1.4202     0.4657   3.049  0.00765 **
## TissueMid_gut      1.2264     0.4657   2.633  0.01807 *
## TissueBrain         0.8469     0.4657   1.818  0.08777 .
## TissueMalpighian_tubules 0.6252     0.4657   1.342  0.19822
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflam$Tissue <- relevel(fig1iflam$Tissue, ref=
"Malpighian_tubules")
model1<-glm(Normalized ~ Tissue, data = fig1iflam)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflam)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -1.0449  -0.3018  -0.0063   0.1800   1.4493
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.80934     0.32933   2.458  0.0258 *
```

```

## TissueHind_gut      -0.62519      0.46574     -1.342      0.1982
## TissueFront_gut     -0.34557      0.46574     -0.742      0.4688
## TissueSalivary_gland -0.14701      0.46574     -0.316      0.7564
## TissueFat_bodies     0.05831      0.46574      0.125      0.9019
## TissueTestes         0.79503      0.46574      1.707      0.1071
## TissueMid_gut        0.60124      0.46574      1.291      0.2151
## TissueBrain          0.22172      0.46574      0.476      0.6405
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 0.3253694)
##
##      Null deviance: 9.8230  on 23  degrees of freedom
## Residual deviance: 5.2059  on 16  degrees of freedom
## AIC: 49.431
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    14.19  7    0.0479 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#-----
#work with Iflavivirus females

fig1iflaf <- subset(fig1ifla, Sex=="Female")
fig1iflaf

##      Target Sample      Tissue Replicate      Virus
Normalized Sex
## 8      Ifla      7A      Fat_bodies      1 Iflavivirus
10.648584190 Female
## 9      Ifla      7A      Fat_bodies      3 Iflavivirus
9.314457044 Female
## 11     Ifla      7A      Fat_bodies      2 Iflavivirus
5.013356605 Female
## 13     Ifla      3A Malpighian_tubules      1 Iflavivirus
3.923198149 Female
## 18     Ifla      8A      Brain          1 Iflavivirus
2.764745961 Female
## 20     Ifla      1A      Salivary_gland      1 Iflavivirus
1.918755308 Female
## 21     Ifla      4A      Mid_gut          3 Iflavivirus
1.825265012 Female
## 23     Ifla      8A      Brain          2 Iflavivirus

```


1.786912992	Female			
## 27	Ifla	3A	Malpighian_tubules	3 Iflavivirus
1.411609258	Female			
## 28	Ifla	9A	Milk_glands	2 Iflavivirus
1.385602181	Female			
## 32	Ifla	4A	Mid_gut	1 Iflavivirus
1.211337107	Female			
## 35	Ifla	9A	Milk_glands	3 Iflavivirus
1.178765779	Female			
## 39	Ifla	8A	Brain	3 Iflavivirus
1.023812750	Female			
## 40	Ifla	9A	Milk_glands	1 Iflavivirus
1.021891196	Female			
## 45	Ifla	1A	Salivary_gland	3 Iflavivirus
0.967271882	Female			
## 50	Ifla	1A	Salivary_gland	2 Iflavivirus
0.817396209	Female			
## 54	Ifla	4A	Mid_gut	2 Iflavivirus
0.719587999	Female			
## 59	Ifla	5A	Front_gut	3 Iflavivirus
0.474846292	Female			
## 61	Ifla	5A	Front_gut	1 Iflavivirus
0.428891911	Female			
## 68	Ifla	2A	Hind_gut	1 Iflavivirus
0.355361037	Female			
## 69	Ifla	3A	Malpighian_tubules	2 Iflavivirus
0.354209947	Female			
## 80	Ifla	2A	Hind_gut	2 Iflavivirus
0.146907611	Female			
## 81	Ifla	2A	Hind_gut	3 Iflavivirus
0.130858443	Female			
## 87	Ifla	5A	Front_gut	2 Iflavivirus
0.099571356	Female			
## 97	Ifla	6A	Ovary	3 Iflavivirus
0.021062121	Female			
## 98	Ifla	6A	Ovary	1 Iflavivirus
0.017170381	Female			
## 101	Ifla	6A	Ovary	2 Iflavivirus
0.007298148	Female			

```
fig1iflaf$Tissue <- as.factor(fig1iflaf$Tissue)
fig1iflaf$Tissue <- relevel(fig1iflaf$Tissue, ref= "Brain")
model1<-glm(Normalized ~ Tissue, data = fig1iflaf)
summary(model1)
```

```
##
```

```
## Call:
```

```
## glm(formula = Normalized ~ Tissue, data = fig1iflaf)
```

```
##
```

```
## Deviance Residuals:
```

```
##      Min      1Q   Median      3Q      Max
## -3.3121 -0.2510 -0.0167  0.1673  2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.85849    0.70840   2.624  0.0172 *
## TissueFat_bodies      6.46698    1.00182   6.455 4.5e-06 ***
## TissueFront_gut     -1.52405    1.00182  -1.521  0.1456
## TissueHind_gut      -1.64745    1.00182  -1.644  0.1174
## TissueMalpighian_tubules 0.03785    1.00182   0.038  0.9703
## TissueMid_gut       -0.60643    1.00182  -0.605  0.5525
## TissueMilk_glands   -0.66307    1.00182  -0.662  0.5164
## TissueOvary        -1.84331    1.00182  -1.840  0.0823 .
## TissueSalivary_gland -0.62402    1.00182  -0.623  0.5412
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflaf$Tissue <- relevel(fig1iflaf$Tissue, ref= "Mid_gut")
model1<-glm(Normalized ~ Tissue, data = fig1iflaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflaf)
##
## Deviance Residuals:
##      Min      1Q   Median      3Q      Max
## -3.3121 -0.2510 -0.0167  0.1673  2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.25206    0.70840   1.767  0.0941 .
## TissueBrain      0.60643    1.00182   0.605  0.5525
```

```

## TissueFat_bodies      7.07340      1.00182      7.061 1.38e-06 ***
## TissueFront_gut      -0.91763      1.00182     -0.916  0.3718
## TissueHind_gut       -1.04102      1.00182     -1.039  0.3125
## TissueMalpighian_tubules 0.64428      1.00182      0.643  0.5283
## TissueMilk_glands    -0.05664      1.00182     -0.057  0.9555
## TissueOvary          -1.23689      1.00182     -1.235  0.2328
## TissueSalivary_gland -0.01759      1.00182     -0.018  0.9862
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1flaf$Tissue <- relevel(fig1flaf$Tissue, ref= "Ovary")
model1<-glm(Normalized ~ Tissue, data = fig1flaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1flaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.01518    0.70840   0.021  0.9831
## TissueMid_gut    1.23689    1.00182   1.235  0.2328
## TissueBrain      1.84331    1.00182   1.840  0.0823 .
## TissueFat_bodies  8.31029    1.00182   8.295 1.46e-07 ***
## TissueFront_gut  0.31926    1.00182   0.319  0.7536
## TissueHind_gut   0.19587    1.00182   0.196  0.8472
## TissueMalpighian_tubules 1.88116    1.00182   1.878  0.0767 .
## TissueMilk_glands 1.18024    1.00182   1.178  0.2541
## TissueSalivary_gland 1.21930    1.00182   1.217  0.2393

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflaf$Tissue <- relevel(fig1iflaf$Tissue, ref= "Fat_bodies")
model1<-glm(Normalized ~ Tissue, data = fig1iflaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.3255     0.7084  11.753 7.05e-10 ***
## TissueOvary      -8.3103     1.0018  -8.295 1.46e-07 ***
## TissueMid_gut    -7.0734     1.0018  -7.061 1.38e-06 ***
## TissueBrain      -6.4670     1.0018  -6.455 4.50e-06 ***
## TissueFront_gut  -7.9910     1.0018  -7.976 2.56e-07 ***
## TissueHind_gut   -8.1144     1.0018  -8.100 2.05e-07 ***
## TissueMalpighian_tubules -6.4291     1.0018  -6.417 4.85e-06 ***
## TissueMilk_glands -7.1300     1.0018  -7.117 1.24e-06 ***
## TissueSalivary_gland -7.0910     1.0018  -7.078 1.34e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
```

```

## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1lflaf$Tissue <- relevel(fig1lflaf$Tissue, ref= "Salivary_gland")
model1<-glm(Normalized ~ Tissue, data = fig1lflaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1lflaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    1.23447    0.70840   1.743  0.0985 .
## TissueFat_bodies    7.09099    1.00182   7.078 1.34e-06 ***
## TissueOvary       -1.21930    1.00182  -1.217  0.2393
## TissueMid_gut       0.01759    1.00182   0.018  0.9862
## TissueBrain         0.62402    1.00182   0.623  0.5412
## TissueFront_gut    -0.90004    1.00182  -0.898  0.3808
## TissueHind_gut     -1.02343    1.00182  -1.022  0.3205
## TissueMalpighian_tubules 0.66186    1.00182   0.661  0.5172
## TissueMilk_glands  -0.03905    1.00182  -0.039  0.9693
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1iflaf$Tissue <- relevel(fig1iflaf$Tissue, ref= "Front_gut")
model1<-glm(Normalized ~ Tissue, data = fig1iflaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1iflaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.3344     0.7084   0.472   0.643
## TissueSalivary_gland  0.9000     1.0018   0.898   0.381
## TissueFat_bodies     7.9910     1.0018   7.976 2.56e-07 ***
## TissueOvary         -0.3193     1.0018  -0.319   0.754
## TissueMid_gut        0.9176     1.0018   0.916   0.372
## TissueBrain         1.5241     1.0018   1.521   0.146
## TissueHind_gut      -0.1234     1.0018  -0.123   0.903
## TissueMalpighian_tubules 1.5619     1.0018   1.559   0.136
## TissueMilk_glands    0.8610     1.0018   0.859   0.401
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```

fig1flaf$Tissue <- relevel(fig1flaf$Tissue, ref= "Hind_gut")
model1<-glm(Normalized ~ Tissue, data = fig1flaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1flaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.2110     0.7084   0.298   0.769
## TissueFront_gut    0.1234     1.0018   0.123   0.903
## TissueSalivary_gland 1.0234     1.0018   1.022   0.321
## TissueFat_bodies    8.1144     1.0018   8.100 2.05e-07 ***
## TissueOvary        -0.1959     1.0018  -0.196   0.847
## TissueMid_gut       1.0410     1.0018   1.039   0.313
## TissueBrain         1.6474     1.0018   1.644   0.117
## TissueMalpighian_tubules 1.6853     1.0018   1.682   0.110
## TissueMilk_glands    0.9844     1.0018   0.983   0.339
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1flaf$Tissue <- relevel(fig1flaf$Tissue, ref= "Milk_glands")
model1<-glm(Normalized ~ Tissue, data = fig1flaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1flaf)

```

```
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.19542    0.70840   1.687   0.109
## TissueHind_gut    -0.98438    1.00182  -0.983   0.339
## TissueFront_gut   -0.86098    1.00182  -0.859   0.401
## TissueSalivary_gland  0.03905    1.00182   0.039   0.969
## TissueFat_bodies   7.13005    1.00182   7.117 1.24e-06 ***
## TissueOvary       -1.18024    1.00182  -1.178   0.254
## TissueMid_gut      0.05664    1.00182   0.057   0.956
## TissueBrain        0.66307    1.00182   0.662   0.516
## TissueMalpighian_tubules 0.70092    1.00182   0.700   0.493
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1flaf$Tissue <- relevel(fig1flaf$Tissue, ref=
"Malpighian_tubules")
model1<-glm(Normalized ~ Tissue, data = fig1flaf)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1flaf)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -3.3121  -0.2510  -0.0167   0.1673   2.3231
##
## Coefficients:
```



```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.89634    0.70840   2.677   0.0154 *
## TissueMilk_glands -0.70092    1.00182  -0.700   0.4931
## TissueHind_gut    -1.68530    1.00182  -1.682   0.1098
## TissueFront_gut   -1.56190    1.00182  -1.559   0.1364
## TissueSalivary_gland -0.66186    1.00182  -0.661   0.5172
## TissueFat_bodies    6.42913    1.00182   6.417 4.85e-06 ***
## TissueOvary        -1.88116    1.00182  -1.878   0.0767 .
## TissueMid_gut      -0.64428    1.00182  -0.643   0.5283
## TissueBrain        -0.03785    1.00182  -0.038   0.9703
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 1.505478)
##
##      Null deviance: 181.408  on 26  degrees of freedom
## Residual deviance:  27.099  on 18  degrees of freedom
## AIC: 96.721
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   102.5  8 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

statistical analysis for Negevirus

#work for Negevirus

```
fig1nege <- subset(fig1, Virus=="Negevirus")
fig1nege
```

	Target	Sample	Tissue	Replicate	Virus
	Normalized	Sex			
## 1	Nege	1A	Salivary_gland	2	Negevirus
	77.402705950	Female			
## 2	Nege	7A	Fat_bodies	3	Negevirus
	39.906292910	Male			
## 3	Nege	7A	Fat_bodies	1	Negevirus
	39.349594060	Female			
## 4	Nege	1A	Salivary_gland	3	Negevirus
	29.069334440	Female			
## 5	Nege	7A	Fat_bodies	1	Negevirus
	20.357023310	Male			
## 6	Nege	7A	Fat_bodies	2	Negevirus

19.631228500	Female			
## 7	Nege	1A	Salivary_gland	2 Negevirus
18.722890740	Male			
## 10	Nege	3A	Malpighian_tubules	1 Negevirus
7.597307635	Female			
## 12	Nege	1A	Salivary_gland	1 Negevirus
4.376742078	Male			
## 14	Nege	7A	Fat_bodies	2 Negevirus
3.537905209	Male			
## 15	Nege	7A	Fat_bodies	3 Negevirus
3.331728226	Female			
## 16	Nege	1A	Salivary_gland	3 Negevirus
2.908747434	Male			
## 19	Nege	8A	Brain	1 Negevirus
2.665310756	Female			
## 24	Nege	8A	Brain	2 Negevirus
1.773831321	Female			
## 26	Nege	9A	Milk_glands	2 Negevirus
1.412966980	Female			
## 36	Nege	5A	Front_gut	1 Negevirus
1.141186814	Female			
## 37	Nege	8A	Brain	1 Negevirus
1.060610153	Male			
## 38	Nege	6A	Testes	3 Negevirus
1.048261614	Male			
## 43	Nege	6A	Ovary	1 Negevirus
0.996945359	Female			
## 44	Nege	6A	Testes	1 Negevirus
0.981968623	Male			
## 46	Nege	4A	Mid_gut	3 Negevirus
0.944433541	Male			
## 49	Nege	5A	Front_gut	3 Negevirus
0.852571665	Male			
## 53	Nege	4A	Mid_gut	1 Negevirus
0.751201684	Female			
## 56	Nege	2A	Hind_gut	1 Negevirus
0.596460970	Female			
## 57	Nege	9A	Milk_glands	1 Negevirus
0.579908913	Female			
## 60	Nege	8A	Brain	3 Negevirus
0.454187308	Male			
## 62	Nege	4A	Mid_gut	1 Negevirus
0.417650378	Male			
## 65	Nege	9A	Milk_glands	3 Negevirus
0.371587771	Female			
## 67	Nege	1A	Salivary_gland	1 Negevirus
0.358316060	Female			
## 70	Nege	6A	Testes	2 Negevirus
0.352838330	Male			
## 71	Nege	6A	Ovary	2 Negevirus

0.352644646	Female				
## 72	Nege	4A	Mid_gut	2	Negevirus
0.321005816	Female				
## 74	Nege	2A	Hind_gut	1	Negevirus
0.246349379	Male				
## 75	Nege	3A	Malpighian_tubules	3	Negevirus
0.225166941	Male				
## 76	Nege	5A	Front_gut	1	Negevirus
0.196212798	Male				
## 77	Nege	8A	Brain	2	Negevirus
0.179375639	Male				
## 79	Nege	3A	Malpighian_tubules	2	Negevirus
0.159920548	Female				
## 85	Nege	3A	Malpighian_tubules	1	Negevirus
0.103543820	Male				
## 86	Nege	5A	Front_gut	2	Negevirus
0.100733703	Female				
## 88	Nege	4A	Mid_gut	3	Negevirus
0.094092464	Female				
## 89	Nege	2A	Hind_gut	2	Negevirus
0.089570912	Female				
## 90	Nege	5A	Front_gut	2	Negevirus
0.071801559	Male				
## 91	Nege	8A	Brain	3	Negevirus
0.057932219	Female				
## 92	Nege	3A	Malpighian_tubules	3	Negevirus
0.042103969	Female				
## 93	Nege	5A	Front_gut	3	Negevirus
0.039952549	Female				
## 94	Nege	6A	Ovary	3	Negevirus
0.032297897	Female				
## 95	Nege	4A	Mid_gut	2	Negevirus
0.028138818	Male				
## 96	Nege	2A	Hind_gut	3	Negevirus
0.023073452	Male				
## 99	Nege	3A	Malpighian_tubules	2	Negevirus
0.015372781	Male				
## 100	Nege	2A	Hind_gut	3	Negevirus
0.012167280	Female				
## 102	Nege	2A	Hind_gut	2	Negevirus
0.003874746	Male				

#difference between tissue regardless the sex for Negevirus

```
model1<-glm(Normalized ~ Tissue, data = fig1nege)
summary(model1)
```

```
##
```

```
## Call:
```

```
## glm(formula = Normalized ~ Tissue, data = fig1nege)
```

```
##
```

```
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -21.781   -0.913   -0.204    0.380   55.263
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      1.0319     4.7892   0.215  0.83048
## TissueFat_bodies    19.9871     6.7730   2.951  0.00522 **
## TissueFront_gut    -0.6315     6.7730  -0.093  0.92617
## TissueHind_gut     -0.8700     6.7730  -0.128  0.89842
## TissueMalpighian_tubules  0.3254     6.7730   0.048  0.96192
## TissueMid_gut     -0.6058     6.7730  -0.089  0.92917
## TissueMilk_glands  -0.2437     8.2952  -0.029  0.97670
## TissueOvary       -0.5712     8.2952  -0.069  0.94543
## TissueSalivary_gland  21.1079     6.7730   3.116  0.00334 **
## TissueTestes      -0.2375     8.2952  -0.029  0.97730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 137.62)
##
##      Null deviance: 9661.7  on 50  degrees of freedom
## Residual deviance: 5642.4  on 41  degrees of freedom
## AIC: 406.75
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  29.206  9  0.0005982 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#difference between sex regardless the tissues for Negevirus
model1<-glm(Normalized ~ Tissue, data = fig1nege)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1nege)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -21.781   -0.913   -0.204    0.380   55.263
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```

## (Intercept)          1.0319      4.7892    0.215    0.83048
## TissueFat_bodies     19.9871      6.7730    2.951    0.00522 **
## TissueFront_gut      -0.6315      6.7730   -0.093    0.92617
## TissueHind_gut       -0.8700      6.7730   -0.128    0.89842
## TissueMalpighian_tubules 0.3254      6.7730    0.048    0.96192
## TissueMid_gut        -0.6058      6.7730   -0.089    0.92917
## TissueMilk_glands    -0.2437      8.2952   -0.029    0.97670
## TissueOvary          -0.5712      8.2952   -0.069    0.94543
## TissueSalivary_gland  21.1079      6.7730    3.116    0.00334 **
## TissueTestes         -0.2375      8.2952   -0.029    0.97730
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 137.62)
##
##      Null deviance: 9661.7  on 50  degrees of freedom
## Residual deviance: 5642.4  on 41  degrees of freedom
## AIC: 406.75
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  29.206  9  0.0005982 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#for male
fig1negem <- subset(fig1negem, Sex=="Male")
fig1negem

##      Target Sample      Tissue Replicate      Virus
Normalized Sex
## 2      Nege      7A      Fat_bodies      3 Negevirus
39.906292910 Male
## 5      Nege      7A      Fat_bodies      1 Negevirus
20.357023310 Male
## 7      Nege      1A      Salivary_gland    2 Negevirus
18.722890740 Male
## 12     Nege      1A      Salivary_gland    1 Negevirus
4.376742078 Male
## 14     Nege      7A      Fat_bodies      2 Negevirus
3.537905209 Male
## 16     Nege      1A      Salivary_gland    3 Negevirus
2.908747434 Male
## 37     Nege      8A      Brain            1 Negevirus
1.060610153 Male

```

## 38	Nege	6A	Testes	3 Negevirus
1.048261614	Male			
## 44	Nege	6A	Testes	1 Negevirus
0.981968623	Male			
## 46	Nege	4A	Mid_gut	3 Negevirus
0.944433541	Male			
## 49	Nege	5A	Front_gut	3 Negevirus
0.852571665	Male			
## 60	Nege	8A	Brain	3 Negevirus
0.454187308	Male			
## 62	Nege	4A	Mid_gut	1 Negevirus
0.417650378	Male			
## 70	Nege	6A	Testes	2 Negevirus
0.352838330	Male			
## 74	Nege	2A	Hind_gut	1 Negevirus
0.246349379	Male			
## 75	Nege	3A	Malpighian_tubules	3 Negevirus
0.225166941	Male			
## 76	Nege	5A	Front_gut	1 Negevirus
0.196212798	Male			
## 77	Nege	8A	Brain	2 Negevirus
0.179375639	Male			
## 85	Nege	3A	Malpighian_tubules	1 Negevirus
0.103543820	Male			
## 90	Nege	5A	Front_gut	2 Negevirus
0.071801559	Male			
## 95	Nege	4A	Mid_gut	2 Negevirus
0.028138818	Male			
## 96	Nege	2A	Hind_gut	3 Negevirus
0.023073452	Male			
## 99	Nege	3A	Malpighian_tubules	2 Negevirus
0.015372781	Male			
## 102	Nege	2A	Hind_gut	2 Negevirus
0.003874746	Male			

```

fig1negem$Tissue <- as.factor(fig1negem$Tissue)
fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Brain")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)

```

```
## (Intercept)          0.5647      4.1251    0.137  0.89282
## TissueFat_bodies     20.7023      5.8338    3.549  0.00267 **
## TissueFront_gut      -0.1912      5.8338   -0.033  0.97426
## TissueHind_gut       -0.4736      5.8338   -0.081  0.93630
## TissueMalpighian_tubules -0.4500      5.8338   -0.077  0.93947
## TissueMid_gut        -0.1013      5.8338   -0.017  0.98636
## TissueSalivary_gland   8.1047      5.8338    1.389  0.18378
## TissueTestes         0.2296      5.8338    0.039  0.96909
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
## Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   23.392  7  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Mid_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.46341     4.12510    0.112  0.91195
## TissueBrain     0.10132     5.83378    0.017  0.98636
## TissueFat_bodies 20.80367     5.83378    3.566  0.00258 **
## TissueFront_gut -0.08988     5.83378   -0.015  0.98790
## TissueHind_gut  -0.37231     5.83378   -0.064  0.94990
## TissueMalpighian_tubules -0.34871     5.83378   -0.060  0.95308
## TissueSalivary_gland  8.20605     5.83378    1.407  0.17866
## TissueTestes    0.33095     5.83378    0.057  0.95546
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue    23.392  7   0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Testes")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.7944      4.1251   0.193  0.84972
## TissueMid_gut     -0.3309      5.8338  -0.057  0.95546
## TissueBrain       -0.2296      5.8338  -0.039  0.96909
## TissueFat_bodies  20.4727      5.8338   3.509  0.00291 **
## TissueFront_gut   -0.4208      5.8338  -0.072  0.94339
## TissueHind_gut    -0.7033      5.8338  -0.121  0.90555
## TissueMalpighian_tubules -0.6797      5.8338  -0.117  0.90870
## TissueSalivary_gland  7.8751      5.8338   1.350  0.19583
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
```



```
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  23.392  7  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Fat_bodies")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      21.267      4.125   5.156 9.58e-05 ***
## TissueTestes     -20.473      5.834  -3.509  0.00291 **
## TissueMid_gut     -20.804      5.834  -3.566  0.00258 **
## TissueBrain       -20.702      5.834  -3.549  0.00267 **
## TissueFront_gut   -20.894      5.834  -3.581  0.00249 **
## TissueHind_gut    -21.176      5.834  -3.630  0.00225 **
## TissueMalpighian_tubules -21.152      5.834  -3.626  0.00227 **
## TissueSalivary_gland -12.598      5.834  -2.159  0.04634 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
```

```

##          LR Chisq Df Pr(>Chisq)
## Tissue    23.392  7   0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Salivary_gland")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      8.669      4.125   2.102  0.0518 .
## TissueFat_bodies    12.598      5.834   2.159  0.0463 *
## TissueTestes       -7.875      5.834  -1.350  0.1958
## TissueMid_gut      -8.206      5.834  -1.407  0.1787
## TissueBrain        -8.105      5.834  -1.389  0.1838
## TissueFront_gut    -8.296      5.834  -1.422  0.1742
## TissueHind_gut     -8.578      5.834  -1.470  0.1608
## TissueMalpighian_tubules -8.555      5.834  -1.466  0.1619
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    23.392  7   0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Front_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

```

```
##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.37353     4.12510   0.091  0.92897
## TissueSalivary_gland  8.29593     5.83378   1.422  0.17421
## TissueFat_bodies    20.89355     5.83378   3.581  0.00249 **
## TissueTestes        0.42083     5.83378   0.072  0.94339
## TissueMid_gut       0.08988     5.83378   0.015  0.98790
## TissueBrain         0.19120     5.83378   0.033  0.97426
## TissueHind_gut     -0.28243     5.83378  -0.048  0.96199
## TissueMalpighian_tubules -0.25883     5.83378  -0.044  0.96516
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   23.392  7  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref= "Hind_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
```

```
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.0911      4.1251   0.022  0.98265
## TissueFront_gut    0.2824      5.8338   0.048  0.96199
## TissueSalivary_gland 8.5784      5.8338   1.470  0.16083
## TissueFat_bodies  21.1760      5.8338   3.630  0.00225 **
## TissueTestes       0.7033      5.8338   0.121  0.90555
## TissueMid_gut      0.3723      5.8338   0.064  0.94990
## TissueBrain        0.4736      5.8338   0.081  0.93630
## TissueMalpighian_tubules 0.0236      5.8338   0.004  0.99682
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##    Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    23.392  7  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negem$Tissue <- relevel(fig1negem$Tissue, ref=
"Malpighian_tubules")
model1<-glm(Normalized ~ Tissue, data = fig1negem)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negem)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -17.7292   -0.3978   -0.0776    0.2042   18.6392
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.1147      4.1251   0.028  0.97816
## TissueHind_gut   -0.0236      5.8338  -0.004  0.99682
## TissueFront_gut    0.2588      5.8338   0.044  0.96516
## TissueSalivary_gland 8.5548      5.8338   1.466  0.16191
## TissueFat_bodies  21.1524      5.8338   3.626  0.00227 **
```

```
## TissueTestes      0.6797      5.8338      0.117  0.90870
## TissueMid_gut     0.3487      5.8338      0.060  0.95308
## TissueBrain       0.4500      5.8338      0.077  0.93947
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 51.04947)
##
##      Null deviance: 2010.95  on 23  degrees of freedom
## Residual deviance:  816.79  on 16  degrees of freedom
## AIC: 170.76
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   23.392  7  0.001456 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#-----
#work with Iflavivirus females

fig1negef <- subset(fig1nege, Sex=="Female")
fig1negef
```

	Target	Sample	Tissue	Replicate	Virus	Normalized
## 1 Female	Nege	1A	Salivary_gland	2	Negevirus	77.40270595
## 3 Female	Nege	7A	Fat_bodies	1	Negevirus	39.34959406
## 4 Female	Nege	1A	Salivary_gland	3	Negevirus	29.06933444
## 6 Female	Nege	7A	Fat_bodies	2	Negevirus	19.63122850
## 10 Female	Nege	3A	Malpighian_tubules	1	Negevirus	7.59730763
## 15 Female	Nege	7A	Fat_bodies	3	Negevirus	3.33172823
## 19 Female	Nege	8A	Brain	1	Negevirus	2.66531076
## 24 Female	Nege	8A	Brain	2	Negevirus	1.77383132
## 26 Female	Nege	9A	Milk_glands	2	Negevirus	1.41296698
## 36	Nege	5A	Front_gut	1	Negevirus	1.14118681

Female					
## 43	Nege	6A	Ovary	1 Negevirus	0.99694536
Female					
## 53	Nege	4A	Mid_gut	1 Negevirus	0.75120168
Female					
## 56	Nege	2A	Hind_gut	1 Negevirus	0.59646097
Female					
## 57	Nege	9A	Milk_glands	1 Negevirus	0.57990891
Female					
## 65	Nege	9A	Milk_glands	3 Negevirus	0.37158777
Female					
## 67	Nege	1A	Salivary_gland	1 Negevirus	0.35831606
Female					
## 71	Nege	6A	Ovary	2 Negevirus	0.35264465
Female					
## 72	Nege	4A	Mid_gut	2 Negevirus	0.32100582
Female					
## 79	Nege	3A	Malpighian_tubules	2 Negevirus	0.15992055
Female					
## 86	Nege	5A	Front_gut	2 Negevirus	0.10073370
Female					
## 88	Nege	4A	Mid_gut	3 Negevirus	0.09409246
Female					
## 89	Nege	2A	Hind_gut	2 Negevirus	0.08957091
Female					
## 91	Nege	8A	Brain	3 Negevirus	0.05793222
Female					
## 92	Nege	3A	Malpighian_tubules	3 Negevirus	0.04210397
Female					
## 93	Nege	5A	Front_gut	3 Negevirus	0.03995255
Female					
## 94	Nege	6A	Ovary	3 Negevirus	0.03229790
Female					
## 100	Nege	2A	Hind_gut	3 Negevirus	0.01216728
Female					

```
fig1negef$Tissue <- as.factor(fig1negef$Tissue)
fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Brain")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)
```

```
##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784   -0.208    0.450   41.793
##
## Coefficients:
```

```
##
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.4990 8.3066 0.180 0.85881
## TissueFat_bodies 19.2718 11.7473 1.641 0.11825
## TissueFront_gut -1.0717 11.7473 -0.091 0.92832
## TissueHind_gut -1.2663 11.7473 -0.108 0.91535
## TissueMalpighian_tubules 1.1008 11.7473 0.094 0.92638
## TissueMid_gut -1.1103 11.7473 -0.095 0.92575
## TissueMilk_glands -0.7109 11.7473 -0.061 0.95241
## TissueOvary -1.0384 11.7473 -0.088 0.93054
## TissueSalivary_gland 34.1111 11.7473 2.904 0.00947 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
## Null deviance: 7541.5 on 26 degrees of freedom
## Residual deviance: 3725.9 on 18 degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
## LR Chisq Df Pr(>Chisq)
## Tissue 18.433 8 0.01821 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Mid_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -35.252 -0.784 -0.208 0.450 41.793
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.38877 8.30656 0.047 0.96319
## TissueBrain 1.11026 11.74726 0.095 0.92575
## TissueFat_bodies 20.38208 11.74726 1.735 0.09982 .
## TissueFront_gut 0.03852 11.74726 0.003 0.99742
## TissueHind_gut -0.15603 11.74726 -0.013 0.98955
## TissueMalpighian_tubules 2.21101 11.74726 0.188 0.85281
```

```

## TissueMilk_glands      0.39939    11.74726    0.034    0.97325
## TissueOvary            0.07186    11.74726    0.006    0.99519
## TissueSalivary_gland   35.22135    11.74726    2.998    0.00771 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##      Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   18.433  8   0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Ovary")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784   -0.208    0.450   41.793
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.46063     8.30656   0.055  0.95639
## TissueMid_gut  -0.07186    11.74726  -0.006  0.99519
## TissueBrain     1.03840    11.74726   0.088  0.93054
## TissueFat_bodies 20.31022    11.74726   1.729  0.10093
## TissueFront_gut -0.03334    11.74726  -0.003  0.99777
## TissueHind_gut  -0.22790    11.74726  -0.019  0.98474
## TissueMalpighian_tubules 2.13915    11.74726   0.182  0.85754
## TissueMilk_glands  0.32753    11.74726   0.028  0.97806
## TissueSalivary_gland 35.14949    11.74726   2.992  0.00782 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)

```



```
##
## Null deviance: 7541.5 on 26 degrees of freedom
## Residual deviance: 3725.9 on 18 degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
## LR Chisq Df Pr(>Chisq)
## Tissue 18.433 8 0.01821 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Fat_bodies")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
## Min 1Q Median 3Q Max
## -35.252 -0.784 -0.208 0.450 41.793
##
## Coefficients:
## Estimate Std. Error t value Pr(>|t|)
## (Intercept) 20.771 8.307 2.501 0.0223 *
## TissueOvary -20.310 11.747 -1.729 0.1009
## TissueMid_gut -20.382 11.747 -1.735 0.0998 .
## TissueBrain -19.272 11.747 -1.641 0.1183
## TissueFront_gut -20.344 11.747 -1.732 0.1004
## TissueHind_gut -20.538 11.747 -1.748 0.0974 .
## TissueMalpighian_tubules -18.171 11.747 -1.547 0.1393
## TissueMilk_glands -19.983 11.747 -1.701 0.1061
## TissueSalivary_gland 14.839 11.747 1.263 0.2226
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
## Null deviance: 7541.5 on 26 degrees of freedom
## Residual deviance: 3725.9 on 18 degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2
```

```

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    18.433  8    0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Salivary_gland")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784   -0.208    0.450   41.793
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      35.610      8.307   4.287 0.000444 ***
## TissueFat_bodies    -14.839     11.747  -1.263 0.222631
## TissueOvary         -35.149     11.747  -2.992 0.007818 **
## TissueMid_gut       -35.221     11.747  -2.998 0.007715 **
## TissueBrain         -34.111     11.747  -2.904 0.009468 **
## TissueFront_gut     -35.183     11.747  -2.995 0.007770 **
## TissueHind_gut      -35.377     11.747  -3.012 0.007495 **
## TissueMalpighian_tubules -33.010     11.747  -2.810 0.011585 *
## TissueMilk_glands   -34.822     11.747  -2.964 0.008306 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##      Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    18.433  8    0.01821 *

```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Front_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784   -0.208    0.450   41.793
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.42729      8.30656   0.051  0.95954
## TissueSalivary_gland 35.18283     11.74726   2.995  0.00777 **
## TissueFat_bodies    20.34356     11.74726   1.732  0.10042
## TissueOvary         0.03334     11.74726   0.003  0.99777
## TissueMid_gut      -0.03852     11.74726  -0.003  0.99742
## TissueBrain         1.07173     11.74726   0.091  0.92832
## TissueHind_gut     -0.19456     11.74726  -0.017  0.98697
## TissueMalpighian_tubules 2.17249     11.74726   0.185  0.85535
## TissueMilk_glands   0.36086     11.74726   0.031  0.97583
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##      Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  18.433  8   0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Hind_gut")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)
```

```
##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784  -0.208   0.450  41.793
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.2327     8.3066   0.028  0.97796
## TissueFront_gut    0.1946    11.7473   0.017  0.98697
## TissueSalivary_gland 35.3774    11.7473   3.012  0.00749 **
## TissueFat_bodies   20.5381    11.7473   1.748  0.09744 .
## TissueOvary        0.2279    11.7473   0.019  0.98474
## TissueMid_gut      0.1560    11.7473   0.013  0.98955
## TissueBrain        1.2663    11.7473   0.108  0.91535
## TissueMalpighian_tubules 2.3670    11.7473   0.201  0.84257
## TissueMilk_glands   0.5554    11.7473   0.047  0.96281
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##      Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue  18.433  8   0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref= "Milk_glands")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784  -0.208   0.450  41.793
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.7882      8.3066   0.095  0.92546
## TissueHind_gut    -0.5554     11.7473  -0.047  0.96281
## TissueFront_gut   -0.3609     11.7473  -0.031  0.97583
## TissueSalivary_gland 34.8220     11.7473   2.964  0.00831 **
## TissueFat_bodies   19.9827     11.7473   1.701  0.10614
## TissueOvary        -0.3275     11.7473  -0.028  0.97806
## TissueMid_gut      -0.3994     11.7473  -0.034  0.97325
## TissueBrain         0.7109     11.7473   0.061  0.95241
## TissueMalpighian_tubules 1.8116     11.7473   0.154  0.87915
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##    Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##          LR Chisq Df Pr(>Chisq)
## Tissue    18.433  8    0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

fig1negef$Tissue <- relevel(fig1negef$Tissue, ref=
"Malpighian_tubules")
model1<-glm(Normalized ~ Tissue, data = fig1negef)
summary(model1)

##
## Call:
## glm(formula = Normalized ~ Tissue, data = fig1negef)
##
## Deviance Residuals:
##      Min       1Q   Median       3Q      Max
## -35.252  -0.784   -0.208    0.450   41.793
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.600      8.307   0.313  0.7579
## TissueMilk_glands  -1.812     11.747  -0.154  0.8792
## TissueHind_gut     -2.367     11.747  -0.201  0.8426
```

```

## TissueFront_gut      -2.172      11.747  -0.185   0.8553
## TissueSalivary_gland 33.010      11.747   2.810   0.0116 *
## TissueFat_bodies     18.171      11.747   1.547   0.1393
## TissueOvary          -2.139      11.747  -0.182   0.8575
## TissueMid_gut        -2.211      11.747  -0.188   0.8528
## TissueBrain          -1.101      11.747  -0.094   0.9264
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for gaussian family taken to be 206.997)
##
##      Null deviance: 7541.5  on 26  degrees of freedom
## Residual deviance: 3725.9  on 18  degrees of freedom
## AIC: 229.66
##
## Number of Fisher Scoring iterations: 2

Anova(model1)

## Analysis of Deviance Table (Type II tests)
##
## Response: Normalized
##      LR Chisq Df Pr(>Chisq)
## Tissue   18.433  8   0.01821 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```