**Supplementary Materials**

**Statistics: Lifespan**

**Survival probability by genotype**

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | Mean | SD | n |
| QF2 | 45.7 | 22.2 | 120 |
| Aβ42 | 17.5 | 4.64 | 120 |
| QUAS | 52.3 | 20.9 | 120 |

**Table 1:** Output from Kaplan-Meier statistics. Mean and SD values of each genotype, with combined social treatments.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genotype** | **n** | **Events** | **Median Survival (days)** | **95%CI** |
| **QF2** | 120 | 80 | 60.0 | 54-63 |
| **Aβ42** | 120 | 99 | 18.0 | 17-19 |
| **QUAS** | 120 | 73 | 62.5 | 60-66 |

**Table 2:** Kaplan-Meir survival of each genotype, displaying median survival in days.

> cox in relation to QF2

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Genotype** | **Hazard Ratio, HR (Exp(coef))** | **Coefficient (β)** | **SE(coef)** | **z** | **p** |
| Aβ42 vs QF2 | 78.22 | 4.36 | 0.38 | 11.45 | <0.001\*\* |
| **QUAS vs QF2** | 0.69 | -0.37 | 0.16 | -2.31 | .0207 |
| Likelihood ratio test=321.8 on 2 df, p=< 2.2e-16  n= 360, number of events= 252 | | | | | |

**Table 3:** Cox proportional Hazards Model of survival by genotype, displaying hazard ratios of each genotype compared to QF2.

**Statistics: Lifespan**

**Survival probability of QF2 by social environment: Alone (A) or Group (G)**

summary\_lifespan

# A tibble: 2 × 4

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | Mean | SD | n |
| Isolated | 45.0 | 22.8 | 60 |
| Social | 46.4 | 21.7 | 60 |

**Table 1:** Output from Kaplan-Meier statistics. Mean and SD values of each social environment.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Treatment** | **n** | **Events** | **Median Survival (days)** | **95%CI** |
| **Isolated** | **60** | **38** | **60.0** | **52-66** |
| **Social** | **60** | **42** | **60.0** | **56-63** |

**Table 2:** Kaplan-Meir survival of each social environment, displaying median survival in days.

Call:

coxph(formula = Surv(Age\_days, Status) ~ Treatment, data = data)

Likelihood ratio test=0.25 on 1 df, p=0.6168

n= 120, number of events= 80

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | **Hazard Ratio, HR (Exp(coef))** | **95% CI for HR** | **Coefficient (β)** | **Se(coef)** | **z** | **P** |
| **Social** | **1.1187** | **0.72-1.73** | **0.1122** | **0.2243** | **0.5** | **0.617** |

**Table 3:** Cox proportional Hazards Model of survival by social environment, displaying hazard ratios of each genotype compared to isolated treatment.

**Statistics: Lifespan**

**Survival probability of QUAS by social environment: Alone (A) or Group (G)**

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | Mean | SD | n |
| Isolated | 52.8 | 21.4 | 60 |
| Social | 51.8 | 20.6 | 60 |

|  |
| --- |
| **Table 1:** Output from Kaplan-Meier statistics. Mean and SD values of each social environment. |
| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | |  |  |  |  |  | | --- | --- | --- | --- | --- | | **Treatment** | **n** | **Events** | **Median Survival (days)** | **95%CI** | | **Isolated** | **60** | **31** | **64.5** | **60-NA** | | **Social** | **60** | **42** | **62.0** | **60-66** | | |

**Table 2:** Kaplan-Meir survival of each social environment, displaying median survival in days.

> cox

Call:

coxph(formula = Surv(Age\_days, Status) ~ Treatment, data = data)

Likelihood ratio test=4.18 on 1 df, p=0.04093

n= 120, number of events= 73

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | **Hazard Ratio, HR (Exp(coef))** | **95% CI for HR** | **Coefficient (β)** | **Se(coef)** | **z** | **P** |
| **Social** | **1.6238** | **1.02-2.59** | **0.4848** | **0.2389** | **2.029** | **0.0425** |

**Table 3:** Cox proportional Hazards Model of survival by social environment, displaying hazard ratios of each genotype compared to isolated treatment.

**Statistics: Lifespan**

**Survival probability of Aβ42 by social environment: Alone (A) or Group (G)**

|  |  |  |  |
| --- | --- | --- | --- |
| Genotype | Mean | SD | n |
| Isolated | 45.0 | 22.8 | 60 |
| Social | 46.4 | 21.7 | 60 |

**Table 1:** Output from Kaplan-Meier statistics. Mean and SD values of each social treatment.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Treatment** | **n** | **Events** | **Median Survival (days)** | **95%CI** |
| **Isolated** | **60** | **50** | **19.0** | **17-20** |
| **Social** | **60** | **49** | **17.0** | **17-19** |

**Table 2:** Kaplan-Meir survival of each social environment, displaying median survival in days.

Call:

coxph(formula = Surv(Age\_days, Status) ~ Treatment, data = data)

Likelihood ratio test=2.5 on 1 df, p=0.1141

n= 120, number of events= 99

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | **Hazard Ratio, HR (Exp(coef))** | **95% CI for HR** | **Coefficient (β)** | **Se(coef)** | **z** | **P** |
| **Social** | **1.3838** | **0.93 – 2.07** | **0.3248** | **0.2053** | **1.582** | **0.114** |

**Table 3:** Cox proportional Hazards Model of survival by social environment, displaying hazard ratios of each genotype compared to isolated treatment.

**Statistics: Climbing**

**Number that climbed**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| genotype | yes | no | total | % |
| QF2 | 23 | 7 | 30 | 76.6 |
| QUAS | 22 | 8 | 30 | 73.33333 |
| QQ | 11 | 19 | 30 | 36.66667 |

**Figure 1:** Raw data of number of flies that did (yes) or did not (no) climb within each genotype in week 1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | yes | no | Total | % |
| QF2-control Isolated | 13 | 2 | 15 | 86.66667 |
| QF2-control Social | 10 | 5 | 15 | 66.66667 |
| QUAS-control Isolated | 9 | 6 | 15 | 60 |
| QUAS-control Social | 13 | 2 | 15 | 86.66667 |
| Aβ42 Isolated | 9 | 6 | 15 | 60 |
| Aβ42 Social | 2 | 13 | 15 | 13.33333 |

**Figure 2:** Raw data of number of flies that did (yes) or did not (no) climb within each treatment in week 1.

**Weeks 1-2 (GLLM with binomial distribution)**

|  |
| --- |
| summary(model\_interact)  Generalized linear mixed model fit by maximum likelihood  (Laplace Approximation) ['glmerMod']  Family: binomial ( logit )  Formula: Climbed ~ Genotype \* Treatment + Week + (1 | Vial\_ID)  Data: long\_data  AIC BIC logLik -2\*log(L) df.resid  183.3 208.8 -83.7 167.3 170  Scaled residuals:  Min 1Q Median 3Q Max  -3.1376 -0.2832 0.4027 0.5061 3.7605  Random effects:  Groups Name Variance Std.Dev.  Vial\_ID (Intercept) 0.1854 0.4306  Number of obs: 178, groups: Vial\_ID, 89  Fixed effects:  Estimate Std. Error z value Pr(>|z|)  (Intercept) 1.8189 0.8664 2.100 0.03577 \*  GenotypeQQ -2.1385 0.7715 -2.772 0.00557 \*\*  GenotypeQUAS -0.8311 0.7875 -1.055 0.29126  TreatmentG -1.0347 0.7755 -1.334 0.18209  Week 0.3069 0.3942 0.779 0.43621  GenotypeQQ:TreatmentG -1.7586 1.1618 -1.514 0.13011  GenotypeQUAS:TreatmentG 1.0359 1.0283 1.007 0.31376  ---  Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1  Correlation of Fixed Effects:  (Intr) GntyQQ GnQUAS TrtmnG Week GQQ:TG  GenotypeQQ -0.633  GenotypQUAS -0.583 0.664  TreatmentG -0.597 0.682 0.645  Week -0.632 -0.052 -0.014 -0.019  GntypQQ:TrG 0.355 -0.552 -0.411 -0.641 -0.031  GntyQUAS:TG 0.452 -0.516 -0.768 -0.755 0.015 0.482  > exp(fixef(model\_interact))  (Intercept) GenotypeQQ GenotypeQUAS TreatmentG  6.1651917 0.1178280 0.4355626 0.3553256  Week GenotypeQQ:TreatmentG GenotypeQUAS:TreatmentG  1.3592079 0.1722923 2.8175631 |
|  |
| |  | | --- | |  | |

**Weeks 1-6 (GLLM with binomial distribution)**

model\_interact <- glmer(Climbed ~ Genotype \* Treatment + Week +

+ (1 | Vial\_ID),

+ family = binomial,

+ data = long\_data)

> summary(model\_interact)

Generalized linear mixed model fit by maximum likelihood

(Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: Climbed ~ Genotype \* Treatment + Week + (1 | Vial\_ID)

Data: long\_data

AIC BIC logLik -2\*log(L) df.resid

183.3 208.8 -83.7 167.3 170

Scaled residuals:

Min 1Q Median 3Q Max

-3.1376 -0.2832 0.4027 0.5061 3.7604

Random effects:

Groups Name Variance Std.Dev.

Vial\_ID (Intercept) 0.1854 0.4306

Number of obs: 178, groups: Vial\_ID, 89

Fixed effects:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 2.1258 0.6887 3.087 0.00203 \*\*

GenotypeQQ -2.1385 0.7715 -2.772 0.00557 \*\*

GenotypeQUAS -0.8311 0.7875 -1.055 0.29127

TreatmentG -1.0347 0.7755 -1.334 0.18209

WeekWeek\_2 0.3069 0.3942 0.779 0.43622

GenotypeQQ:TreatmentG -1.7585 1.1618 -1.514 0.13014

GenotypeQUAS:TreatmentG 1.0359 1.0283 1.007 0.31377

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) GntyQQ GnQUAS TrtmnG WkWk\_2 GQQ:TG

GenotypeQQ -0.826

GenotypQUAS -0.742 0.664

TreatmentG -0.762 0.682 0.645

WeekWeek\_2 -0.223 -0.052 -0.014 -0.019

GntypQQ:TrG 0.429 -0.552 -0.411 -0.641 -0.031

GntyQUAS:TG 0.577 -0.516 -0.768 -0.755 0.015 0.482

> #odds ratio

> exp(fixef(model\_simple))

(Intercept) GenotypeQUAS TreatmentG Week

18.1742525 1.9472320 0.9533797 0.6432382

> exp(fixef(model\_interact))

(Intercept) GenotypeQQ GenotypeQUAS TreatmentG

8.3798975 0.1178257 0.4355672 0.3553152

WeekWeek\_2 GenotypeQQ:TreatmentG GenotypeQUAS:TreatmentG

1.3592026 0.1723022 2.8175131

> summary(model\_week\_factor)

(nb. used week as a factor)

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: Climbed ~ Genotype \* Treatment + Week + (1 | Vial\_ID)

Data: long\_data

AIC BIC logLik -2\*log(L) df.resid

311.3 349.8 -145.6 291.3 338

Scaled residuals:

Min 1Q Median 3Q Max

-4.6030 0.1939 0.3199 0.4403 1.6809

Random effects:

Groups Name Variance Std.Dev.

Vial\_ID (Intercept) 0.06736 0.2595

Number of obs: 348, groups: Vial\_ID, 60

Fixed effects:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 1.0343 0.4040 2.560 0.010468 \*

GenotypeQUAS 0.2734 0.4317 0.633 0.526551

TreatmentG -0.4819 0.4134 -1.165 0.243830

WeekWeek\_2 0.9598 0.5108 1.879 0.060237 .

WeekWeek\_3 1.5874 0.6072 2.614 0.008945 \*\*

WeekWeek\_4 1.3112 0.5642 2.324 0.020130 \*

WeekWeek\_5 0.3208 0.4587 0.699 0.484342

WeekWeek\_6 -1.7075 0.4457 -3.831 0.000128 \*\*\*

GenotypeQUAS:TreatmentG 0.9234 0.6196 1.490 0.136115

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) GnQUAS TrtmnG WkWk\_2 WkWk\_3 WkWk\_4 WkWk\_5 WkWk\_6

GenotypQUAS -0.501

TreatmentG -0.550 0.501

WeekWeek\_2 -0.438 0.011 -0.021

WeekWeek\_3 -0.364 0.013 -0.026 0.309

WeekWeek\_4 -0.397 0.013 -0.016 0.330 0.280

WeekWeek\_5 -0.498 -0.004 0.001 0.399 0.336 0.362

WeekWeek\_6 -0.541 -0.069 0.051 0.382 0.313 0.343 0.450

GntyQUAS:TG 0.373 -0.683 -0.670 0.021 0.024 0.018 0.003 -0.064

> exp(fixef(model\_week\_factor))

(Intercept) GenotypeQUAS TreatmentG WeekWeek\_2 WeekWeek\_3 WeekWeek\_4 WeekWeek\_5 WeekWeek\_6 GenotypeQUAS:TreatmentG

2.8130897 1.3144443 0.6176332 2.6111623 4.8908870 3.7105625 1.3782022 0.1813244 2.5178851

**Statistics: Climbing**

**Time of those that climbed**

**Week 1 using Kruskal-Wallis and Wilcoxon rank sum test**

**Kruskal-Wallis test: Effect of genotype**

> kruskal.test(Week\_1 ~ Genotype, data = my\_data)

data: Week\_1 by Genotype

Kruskal-Wallis chi-squared = 3.2156, df = 2, p-value = 0.2003

> pairwise.wilcox.test(my\_data$Week\_1, my\_data$Genotype,

+ p.adjust.method = "bonferroni")

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: my\_data$Week\_1 and my\_data$Genotype

QF2 QQ

QQ 0.21 -

QUAS 1.00 0.85

**Wilcoxon rank sum test with continuity correction: Effect of social environment**

**QF2**

data: Week\_1 by Treatment

W = 38.5, p-value = 0.1057

alternative hypothesis: true location shift is not equal to 0

**QUAS**

data: Week\_1 by Treatment

W = 27, p-value = 0.03817

alternative hypothesis: true location shift is not equal to 0

**Aβ42**

data: Week\_1 by Treatment

W = 2, p-value = 0.1455

alternative hypothesis: true location shift is not equal to 0

**Week 1-6 using separate ANOVA**

> res.aov <- anova\_test(

+ data = long\_data, dv = Climbed, wid =Vial.ID,

+ between = c(Genotype), within = Week)

> res.aov

ANOVA Table (type III tests)

Effect DFn DFd F p p<.05 ges

1 Genotype 1 2 189.062 0.005 \* 0.041

2 Week 6 12 0.346 0.899 0.147

3 Genotype:Week 6 12 0.253 0.949 0.112

> res.aov <- anova\_test(

+ data = long\_data, dv = Climbed, wid =Vial.ID,

+ between = c(Genotype, Treatment), within = Week)

> res.aov

ANOVA Table (type III tests)

Effect DFn DFd F p p<.05 ges

1 Treatment 1 2 1.526 0.342 0.028

2 Week 6 12 1.018 0.458 0.329

3 Treatment:Week 6 12 1.595 0.231 0.434

**Week 1-6 with linear mixed-effects model**

> model\_2 <- lmer(Climbed ~ Genotype \* Treatment \* Week +

+ (1 | Vial.ID),

+ data = long\_data)

fixed-effect model matrix is rank deficient so dropping 10 columns / coefficients

> summary(model\_2)

Linear mixed model fit by REML. t-tests use Satterthwaite's method ['lmerModLmerTest']

Formula: Climbed ~ Genotype \* Treatment \* Week + (1 | Vial.ID)

Data: long\_data

REML criterion at convergence: 2127.9

Scaled residuals:

Min 1Q Median 3Q Max

-2.4814 -0.5518 -0.2218 0.3253 3.7515

Random effects:

Groups Name Variance Std.Dev.

Vial.ID (Intercept) 9.454 3.075

Residual 125.925 11.222

Number of obs: 299, groups: Vial.ID, 73

Fixed effects:

Estimate Std. Error df t value Pr(>|t|)

(Intercept) 14.1676 3.2234 263.7154 4.395

1.61e-05 \*\*\*

GenotypeQQ 5.8767 5.0424 262.4890 1.165 0.2449

GenotypeQUAS -3.0117 5.0331 265.9898 -0.598 0.5501

TreatmentG 3.8181 4.8857 264.9506 0.781 0.4352

WeekWeek\_2 -4.0598 4.3363 201.2486 -0.936 0.3503

WeekWeek\_3 -5.9695 4.4225 206.6707 -1.350 0.1786

WeekWeek\_4 -3.1233 4.4225 206.6707 -0.706 0.4808

WeekWeek\_5 6.7196 4.7635 219.7215 1.411 0.1598

WeekWeek\_6 12.1559 6.5330 241.1691 1.861 0.0640 .

WeekWeek\_7 9.0958 11.9053 246.5256 0.764 0.4456

GenotypeQQ:TreatmentG 7.6376 10.3245 262.0073 0.740 0.4601

GenotypeQUAS:TreatmentG 6.9042 7.0144 265.5300 0.984 0.3259

GenotypeQQ:WeekWeek\_2 5.6255 7.1659 215.0859 0.785 0.4333

GenotypeQUAS:WeekWeek\_2 1.4372 6.4428 207.2241 0.223 0.8237

GenotypeQQ:WeekWeek\_3 15.9252 13.0374 265.5661 1.222 0.2230

GenotypeQUAS:WeekWeek\_3 4.3438 6.5538 212.6553 0.663 0.5082

GenotypeQUAS:WeekWeek\_4 2.7403 6.5534 212.2738 0.418 0.6763

GenotypeQUAS:WeekWeek\_5 -0.9882 6.7886 218.6474 -0.146 0.8844

GenotypeQUAS:WeekWeek\_6 10.5185 8.8957 244.1248 1.182 0.2382

GenotypeQUAS:WeekWeek\_7 -9.2667 16.9567 244.8978 -0.546 0.5852

TreatmentG:WeekWeek\_2 -3.0521 6.4424 212.1723 -0.474 0.6362

TreatmentG:WeekWeek\_3 -1.7556 6.4316 207.0596 -0.273 0.7852

TreatmentG:WeekWeek\_4 1.4569 6.4314 206.8306 0.227 0.8210

TreatmentG:WeekWeek\_5 -3.4806 7.3509 225.0872 -0.473 0.6363

TreatmentG:WeekWeek\_6 8.6043 13.6905 246.6859 0.628 0.5303

TreatmentG:WeekWeek\_7 -8.6665 16.9925 257.4882 -0.510 0.6105

GenotypeQUAS:TreatmentG:WeekWeek\_2 -0.4692 9.2486 210.1820 -0.051 0.9596

GenotypeQUAS:TreatmentG:WeekWeek\_3 -10.8969 9.1058 207.9361 -1.197 0.2328

GenotypeQUAS:TreatmentG:WeekWeek\_4 -17.7292 9.1813 209.0609 -1.931 0.0548 .

GenotypeQUAS:TreatmentG:WeekWeek\_5 -15.9957 9.7767 218.1152 -1.636 0.1033

GenotypeQUAS:TreatmentG:WeekWeek\_6 -32.7900 15.7455 243.9682 -2.083 0.0383 \*

GenotypeQUAS:TreatmentG:WeekWeek\_7 7.7864 22.0970 252.2215 0.352 0.7249

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**Week 1-6 Estimated Marginal Means**

> emm\_genotype <- emmeans(model\_2, ~Genotype)

Genotype emmean SE df lower.CL upper.CL

QF2 17.7 1.77 169 14.2 21.2

QQ nonEst NA NA NA NA

QUAS 14.4 1.39 102 11.6 17.1

**Shapiro-Wilk normality test**

> shapiro.test(res)

data: res

W = 0.90754, p-value = 1.392e-12

**Statistics: Reproductive Output**

**Week 1 using Kruskal-Wallis and Wilcoxon rank sum test**

**Kruskal-Wallis : Effect of genotype**

> kruskal.test(Week\_1 ~ Genotype, data = my\_data)

Kruskal-Wallis rank sum test

data: Week\_1 by Genotype

Kruskal-Wallis chi-squared = 17.726, df = 2, p-value = 0.0001415

> pairwise.wilcox.test(my\_data$Week\_1, my\_data$Genotype,

+ p.adjust.method = "bonferroni")

Pairwise comparisons using Wilcoxon rank sum test with continuity correction

data: my\_data$Week\_1 and my\_data$Genotype

QF2 QQ

QQ 5.5e-06 -

QUAS 1.0 0.1

P value adjustment method: bonferroni

**Wilcoxon rank sum test on each genotype: Effect of social treatment**

> wilcox.test(Week\_1 ~ Treatment, data = my\_data)

**QF2**

Wilcoxon rank sum test with continuity correction

data: Week\_1 by Treatment

W = 148.5, p-value = 0.1405

alternative hypothesis: true location shift is not equal to 0

**QUAS**

Wilcoxon rank sum test with continuity correction

data: Week\_1 by Treatment

W = 216, p-value = 1.915e-05

alternative hypothesis: true location shift is not equal to 0

**Aβ42**

Wilcoxon rank sum test with continuity correction

data: Week\_1 by Treatment

W = 180, p-value = 0.005406

alternative hypothesis: true location shift is not equal to 0

**Statistics: Social Network Analysis**

**Strength**

**Effect of genotype:**

> kruskal.test(Strength ~ Genotype, data = my\_data)

Kruskal-Wallis rank sum test

data: Strength by Genotype

Kruskal-Wallis chi-squared = 3.395, df = 2, p-value = 0.1831

**Effect of social environment on each genotype:**

**QF2**

> wilcox.test(Strength ~ Treatment, data = my\_data)

Wilcoxon rank sum exact test

data: Strength by Treatment

W = 9, p-value = 0.8857

alternative hypothesis: true location shift is not equal to 0

**QUAS**

> wilcox.test(Strength ~ Treatment, data = my\_data)

Wilcoxon rank sum exact test

data: Strength by Treatment

W = 6, p-value = 0.6857

alternative hypothesis: true location shift is not equal to 0

**Aβ42**

> wilcox.test(Strength ~ Treatment, data = my\_data)

Wilcoxon rank sum exact test

data: Strength by Treatment

W = 3, p-value = 0.2

alternative hypothesis: true location shift is not equal to 0

**Statistics: Social Network Analysis**

**Clustering Coefficient**

**Effect of genotype:**

> kruskal.test(Clustering ~ Genotype, data = my\_data)

Kruskal-Wallis rank sum test

data: Clustering by Genotype

Kruskal-Wallis chi-squared = 1.5118, df = 2, p-value = 0.4696

**Effect of social environment on each genotype:**

**QF2**

> wilcox.test(Clustering ~ Treatment, data = my\_data)

Wilcoxon rank sum test with continuity correction

data: Clustering by Treatment

W = 14, p-value = 0.1038

alternative hypothesis: true location shift is not equal to 0

**QUAS**

> wilcox.test(Clustering ~ Treatment, data = my\_data)

Wilcoxon rank sum test with continuity correction

data: Clustering by Treatment

W = 3, p-value = 0.1913

alternative hypothesis: true location shift is not equal to 0

**Aβ42**

> wilcox.test(Clustering ~ Treatment, data = my\_data)

Wilcoxon rank sum exact test

data: Clustering by Treatment

W = 7, p-value = 0.8857

alternative hypothesis: true location shift is not equal to 0

**Statistics: Social Network Analysis**

**Density**

**Effect of genotype:**

> kruskal.test(Density ~ Genotype, data = my\_data)

Kruskal-Wallis rank sum test

data: Density by Genotype

Kruskal-Wallis chi-squared = 0.44935, df = 2, p-value = 0.7988

**Effect of social environment on each genotype:**

**QF2**

> wilcox.test(Density ~ Treatment, data = my\_data)

Wilcoxon rank sum test with continuity correction

data: Density by Treatment

W = 13, p-value = 0.1776

alternative hypothesis: true location shift is not equal to 0

**QUAS**

> wilcox.test(Density ~ Treatment, data = my\_data)

Wilcoxon rank sum test with continuity correction

data: Density by Treatment

W = 6, p-value = 0.64

alternative hypothesis: true location shift is not equal to 0

**Aβ42**

> wilcox.test(Density ~ Treatment, data = my\_data)

Wilcoxon rank sum test with continuity correction

data: Density by Treatment

W = 6, p-value = 0.6489

alternative hypothesis: true location shift is not equal to 0