Figure 3e

```r
library(readxl)
library(lubridate)
```

```
##
## Attaching package: 'lubridate'
```

```
## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
```

```r
library(mgcv)
```

```
## Loading required package: nlme
```

```
## This is mgcv 1.8-34. For overview type 'help("mgcv-package")'.
```

```r
library(ggplot2)
library(ggsignif)
library(readr)
library(emmeans)
library(tidyr)
library(plyr)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:plyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize
```

```
## The following object is masked from 'package:nlme':
##
##     collapse
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
#load in raw data
dat <- data.frame(read_csv("3e_data.csv"))
```

```
##
## -- Column specification ---------------------------------------------------
## cols(
##   `Repeat(Date)` = col_character(),
##   Algae = col_character(),
```

```
##   Treatment = col_character(),
##   Well_ID = col_character(),
##   Larvae = col_double(),
##   Halo = col_double()
## )
```

```r
head(dat)
```

```
##   Repeat.Date. Algae Treatment Well_ID Larvae Halo
## 1            I SSB01      DMSO   S_D_I      1    0
## 2            I SSB01      DMSO   S_D_I      2    0
## 3            I SSB01      DMSO   S_D_I      3    1
## 4            I SSB01      DMSO   S_D_I      4    1
## 5            I SSB01      DMSO   S_D_I      5    1
## 6            I SSB01      DMSO   S_D_I      6    1
```

```r
#clean up raw data
dat$Algae <- factor(dat$Algae, levels= c("SSB01", "M. gaditana", "N. oculata", "C. velia"))
dat$Treatment <- factor(dat$Treatment)
dat$Repeat.Date. <- factor(as.character(dat$Repeat.Date.))
dat$Halo <- ifelse(dat$Halo>0,1,0)
dat$Well_ID <- factor(dat$Well_ID)
head(dat)
```

```
##   Repeat.Date. Algae Treatment Well_ID Larvae Halo
## 1            I SSB01      DMSO   S_D_I      1    0
## 2            I SSB01      DMSO   S_D_I      2    0
## 3            I SSB01      DMSO   S_D_I      3    1
## 4            I SSB01      DMSO   S_D_I      4    1
## 5            I SSB01      DMSO   S_D_I      5    1
## 6            I SSB01      DMSO   S_D_I      6    1
```

```r
#model data with generalised linear mixed modes
summary <- data.frame()

for(i in unique(dat$Algae))
{
#i <-  unique(dat$Algae)[1]
  Dat <- droplevels(dat[dat$Algae==i,])
  ##Regression model:
  mod <- gam(Halo ~ Treatment + s(Repeat.Date.,bs='re') + s(Well_ID,bs='re'),data=Dat,family=binomial())
  S <- summary(mod)$p.table
if(S[2,4]>0.1)
  {
    p <- ""
  }
if(S[2,4]<0.1)
  {
    p  <- ""
  }
if(S[2,4]<0.05)
  {
    p  <- "*"
  }
if(S[2,4]<0.01)
  {
```

```
    p <- "**"
  }
if(S[2,4]<0.001)
  {
    p <- "***"
  }
newline <- data.frame(Algae=i,outcome=S[1,1],SE=S[1,2],type="DMSO",p=NA,pvalue=NA)
  summary <- rbind(summary,newline)
newline <- data.frame(Algae=i,outcome=S[1,1] + S[2,1],SE=S[2,2],type="XMD17-109",p=p, pvalue=S[2,4])
  summary <- rbind(summary,newline)
}

summary$up <- plogis(summary$outcome + 1.96*summary$SE)
summary$down <- plogis(summary$outcome - 1.96*summary$SE)
summary$outcome <- plogis(summary$outcome)

summary
```

```
## Algae     outcome        SE      type   p      pvalue        up        down
## 1 SSB01 0.83931513 0.5440706     DMSO <NA>          NA 0.9381687 0.64262203
## 2 SSB01 0.09530589 0.8320048 XMD17-109  *** 2.707378e-06 0.3498324 0.02020854
```

```
write_csv(summary, "3e_summary.csv")
```

```
#Plot graph
P1 <- ggplot(data = summary,aes(x = Algae, y = outcome, group = type)) +
  geom_bar(stat = "identity", width = 0.75, size=1.5, position = "dodge", fill = c("#FF2500",alpha("#FF
  geom_errorbar(aes(ymin=down, ymax=up), width=.5, position =position_dodge(.75)) +
  geom_text(data = summary, aes(x=Algae,y=0.95),label=summary$p,size=6) +
  theme_classic() +
  labs(x = "", y = "LAMP-1 positive") +
  scale_y_continuous(expand = c(0, 0), limits = c(0,1), labels = scales::number_format(accuracy = 0.01)
plot(P1)
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```
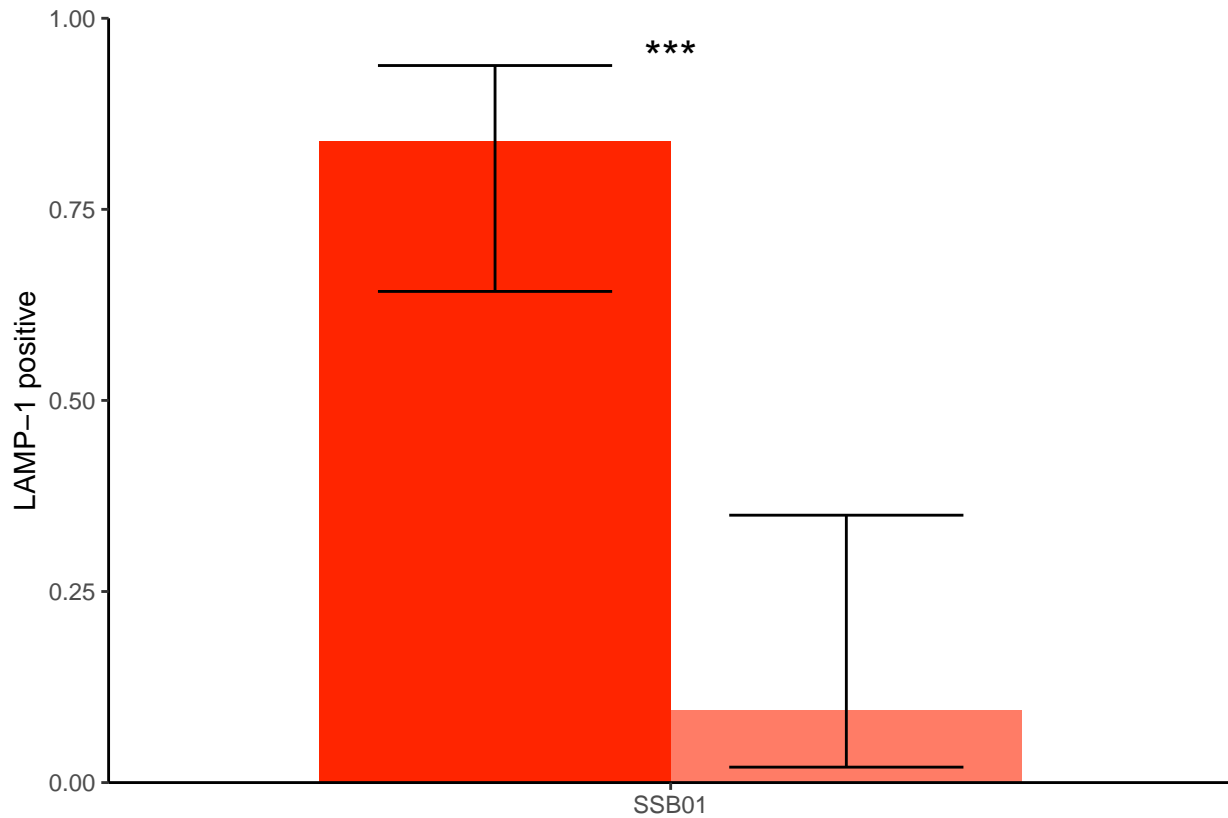
```
ggsave("Figure_3e.pdf",width=5.75,height=11,units="cm")
```

```
## Warning: Removed 1 rows containing missing values (geom_text).
```

```
# get n count per treatment
ndat <- ddply(dat, c("Algae", "Treatment", "Repeat.Date."), summarise,
              N    = length(Larvae))
n_Figure <-  ddply(ndat, c("Algae", "Treatment"), summarise,
              N    = length(Repeat.Date.))
n_Figure
```

```
##    Algae  Treatment N
## 1 SSB01       DMSO 3
## 2 SSB01 XMD-17-109 3
```

```
write_csv(n_Figure, "3e_n.csv")
```