Preliminary Analysis - Negative Strand

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Set up the Data Sets:

```
## 'data.frame':    77 obs. of  5 variables:
##  $ Well  : chr  "A01" "A02" "A03" "A04" ...
##  $ Target: chr  "BQCV-F" "BQCV-F" "BQCV-F" "BQCV-F" ...
##  $ Sample: int  47 50 51 76 78 88 120 124 125 149 ...
##  $ Melt  : num  79 NA NA 79 79 79 NA 79 79 NA ...
##  $ Cq    : num  33.1 41.7 35.5 40.4 38.4 ...
```

Clean the Data set:

```r
DatClean <- Dat
#DatClean <- DatClean[!(DatClean$Cq>33),]
#DatClean <- DatClean[!(DatClean$Melt<78),]
DatClean$Binary <- ifelse(DatClean$Melt > 0, 1, 0)
DatClean$Binary[is.na(DatClean$Binary)] <- 0
```

```r
#ddply summarize:
plotdat <- ddply(DatClean, c("Target", "apiary_near_far"), summarise,
                      n = length(Binary),
                      mean = mean(Binary, na.rm=TRUE),
                      sd = sqrt(((mean(Binary))*(1-mean(Binary)))/n))

plotdat$apiary_near_far <- ifelse(plotdat$apiary_near_far==0, "No Apiary", "Apiary")
plotdat <- plotdat[-1,]

plot1 <- ggplot(plotdat, aes(x=apiary_near_far, y=mean, fill=Target)) +
  geom_bar(stat="identity", color="black",
          position=position_dodge()) + labs(y="Prevalence", x="Site Type") + geom_errorbar(aes(ymin = 

plot1 + theme_minimal(base_size = 18) + coord_cartesian(ylim = c(0, 1)) + scale_y_continuous(labels = s
```
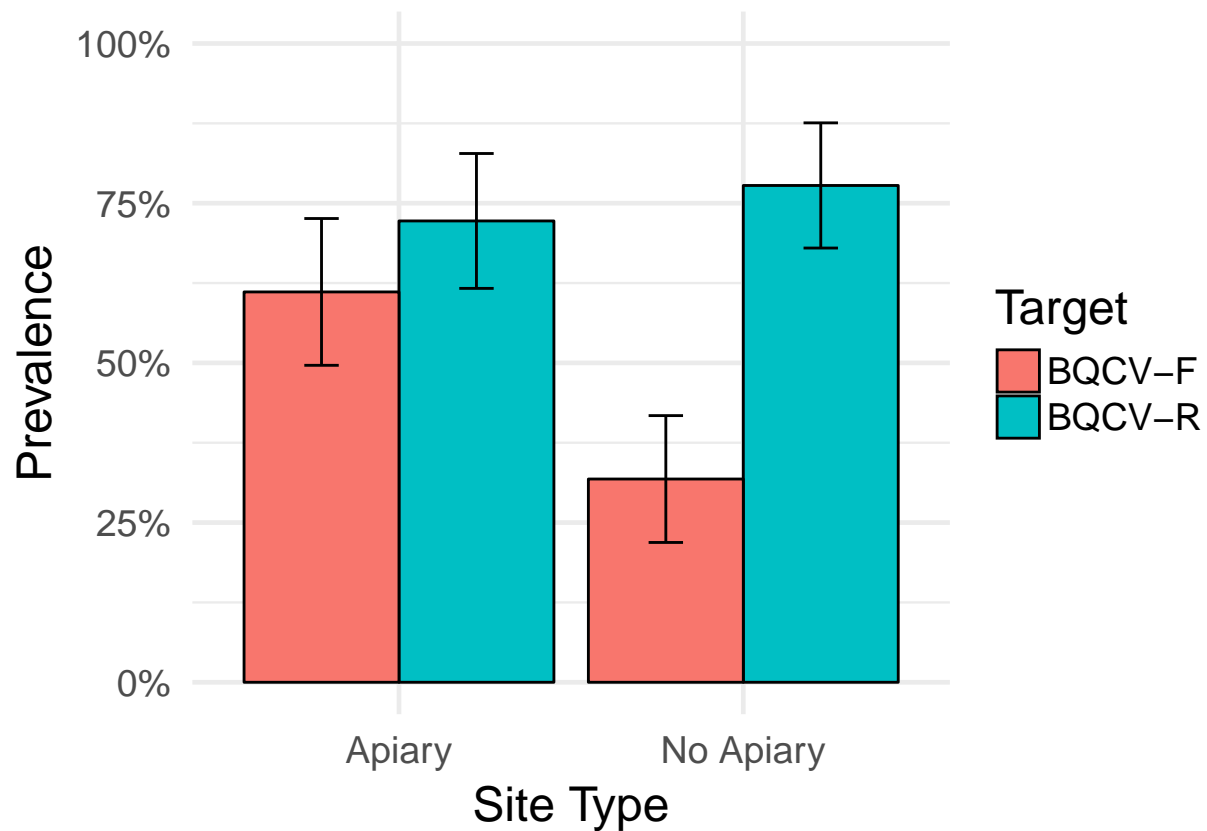
Is there a relationship between Neg Strand and Apiary vs no Apiary (p=0.1)

```
DatCleanNeg <- DatClean[DatClean$Target=="BQCV-F",]

fisher.test(DatCleanNeg$Binary, DatCleanNeg$apiary_near_far)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  DatCleanNeg$Binary and DatCleanNeg$apiary_near_far
## p-value = 0.1098
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##   0.7684977 15.1840339
## sample estimates:
## odds ratio
##   3.259978
```