```
```{r}
Fit model without exclusive
model.without.exclusive <- glm(online_only ~ limited_edition, family = binomial,</pre>
data = sephora)
sum model.without.exclusive <- summary(model.without.exclusive)</pre>
sum model.without.exclusive
٠.,
Call:
glm(formula = online only ~ limited edition, family = binomial,
 data = sephora)
Coefficients:
 Estimate Std. Error z value Pr(>|z|)
(Intercept)
 -1.25805 0.02667 -47.165 <2e-16 ***
limited_edition1 0.70269 0.07685 9.144 <2e-16 ***
Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
 Null deviance: 9791.0 on 8986 degrees of freedom
Residual deviance: 9712.2 on 8985 degrees of freedom
AIC: 9716.2
Number of Fisher Scoring iterations: 4
Likelihood ratio test without exclusive
```{r}
# residual deviance for model without exclusive
residual_deviance_without_exclusive <- round(model.without.exclusive$deviance,2)</pre>
G <- residual_deviance_without_exclusive - residual_deviance_full_model</pre>
```

Model without exclusive

```
p <- 1-pchisq(G, df = 1) ... H_0: eta_1=0 H_a: 	ext{at least one } eta \neq 0 G=9712.2-8649.08=1063.12 p=0
```

The "exclusive" variable is statistic significant because its p-value is close to zero

Percent change of beta

Although exclusive was droped of the model, the exclusive predictor is important confounder becouse it have percent changes more 15%