

# TSAR: Clinical EDA

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## Scan for Missing Data

```
sum(is.na(train_symptom_df)) #0
```

```
[1] 0
```

```
sum(is.na(train_clinic1_df)) #4318
```

```
[1] 4318
```

```
sum(is.na(phas1_clinic1_df)) #60
```

```
[1] 60
```

```
sum(is.na(phas2_clinic1_df)) #88
```

```
[1] 88
```

```
sum(is.na(phas3_clinic1_df)) #62
```

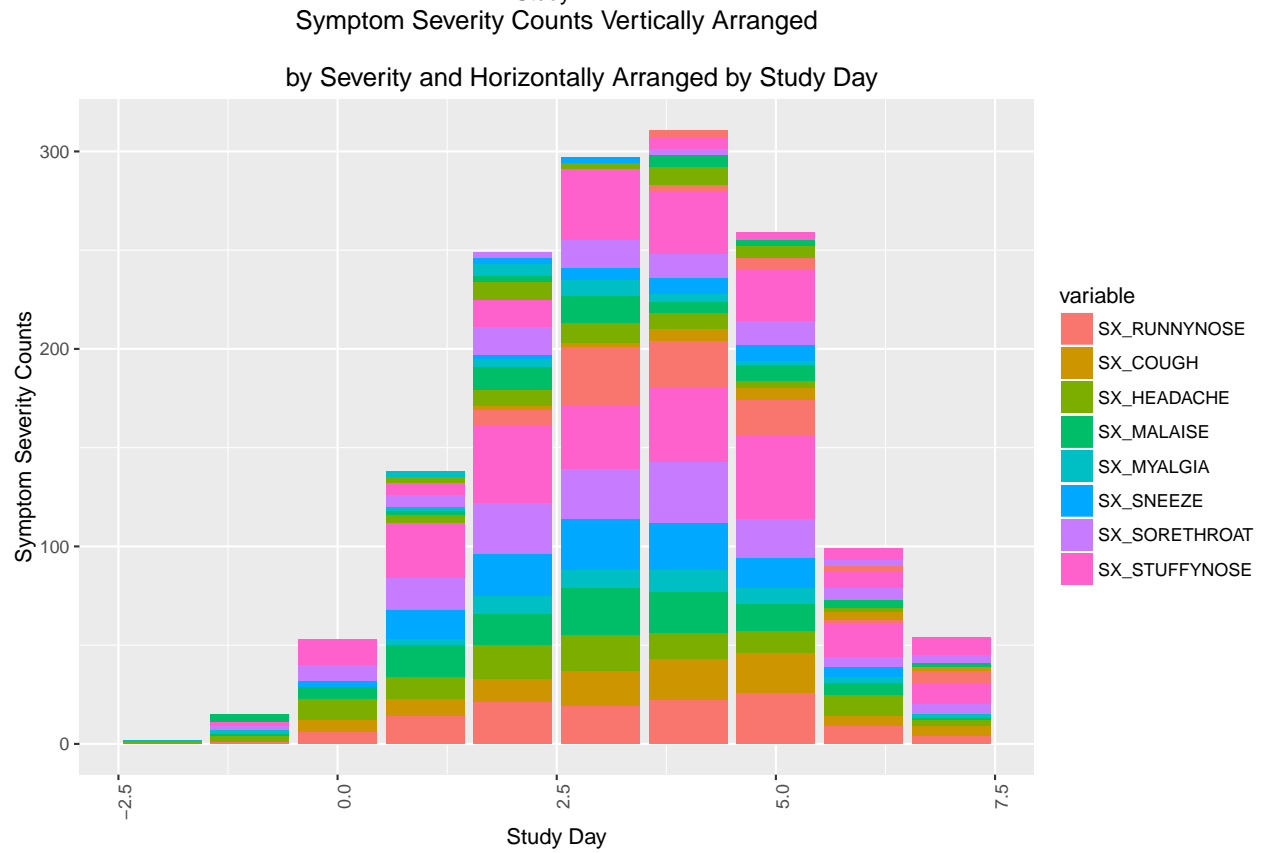
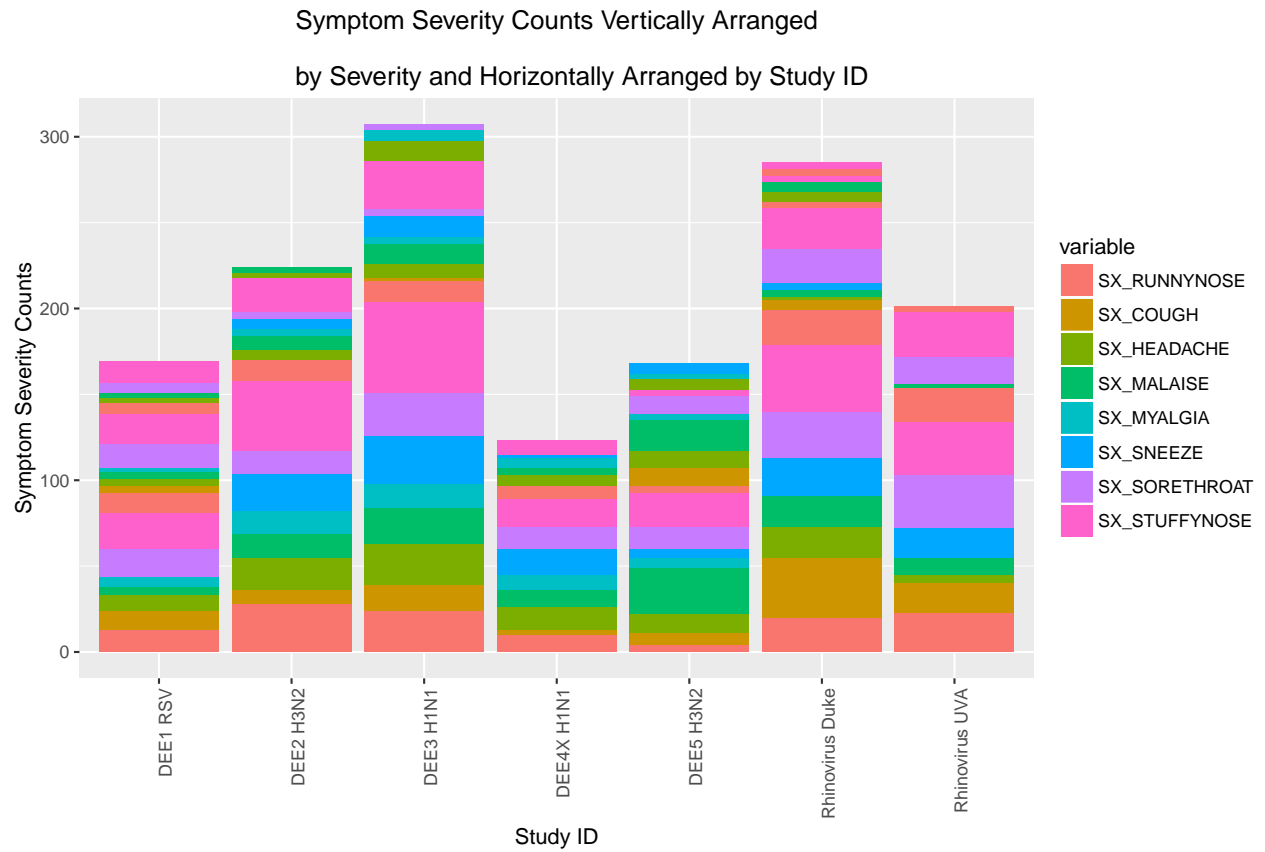
```
[1] 62
```

## Fix Missing Data

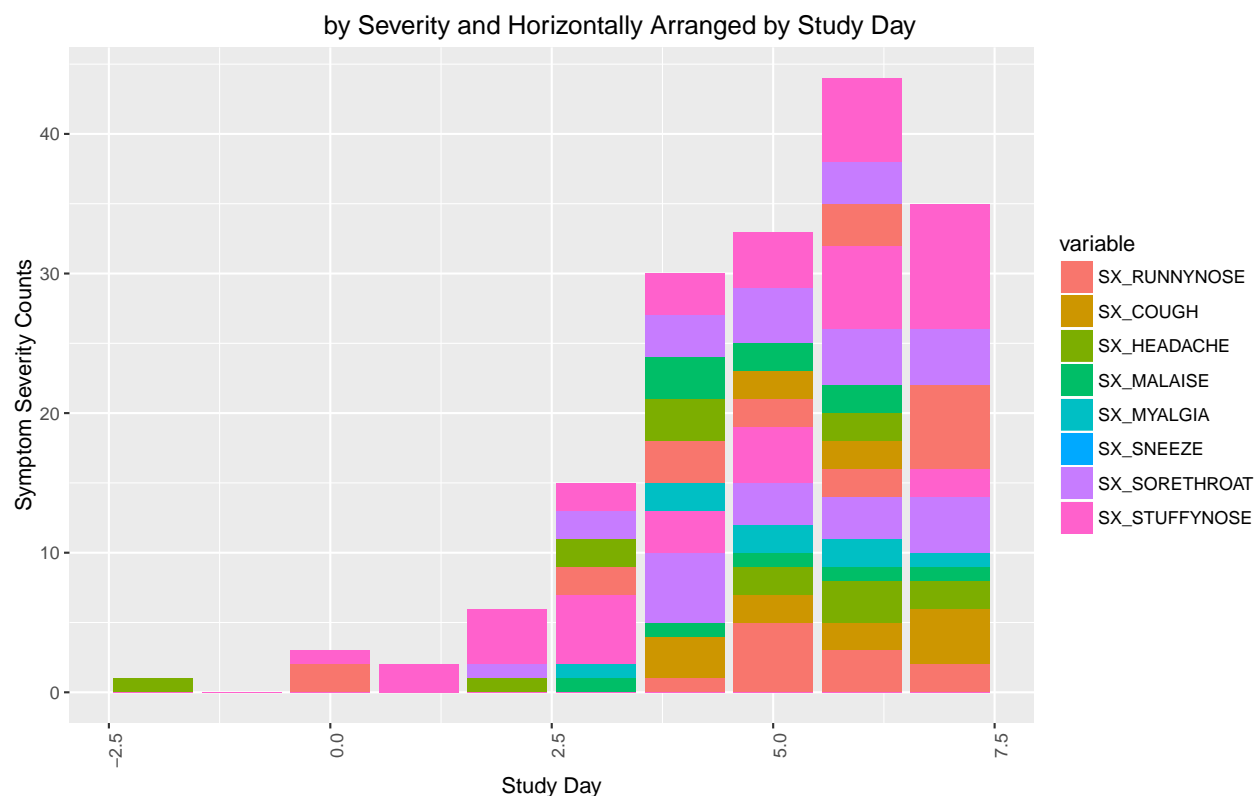
All NA's are found in EARLYTX and SHAM. Change those columns to binary values.

## Checking Distributions

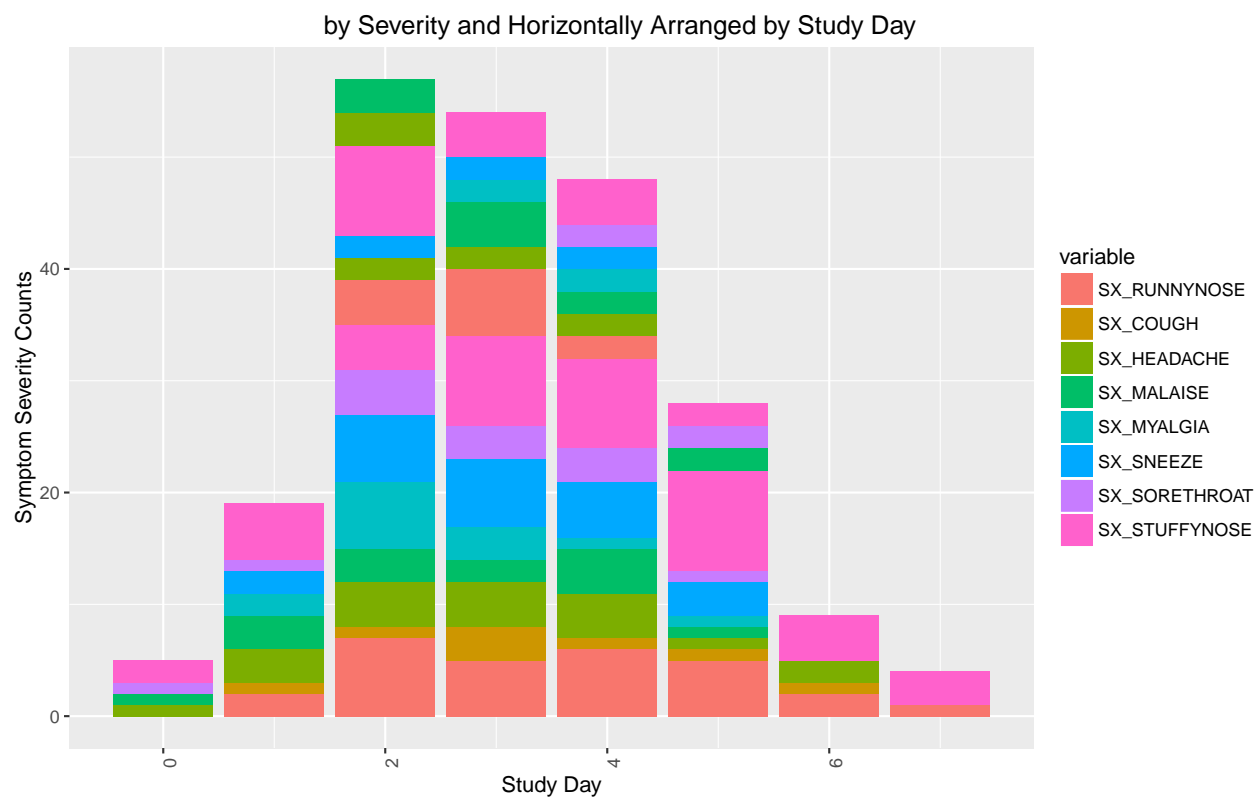
### Symptoms



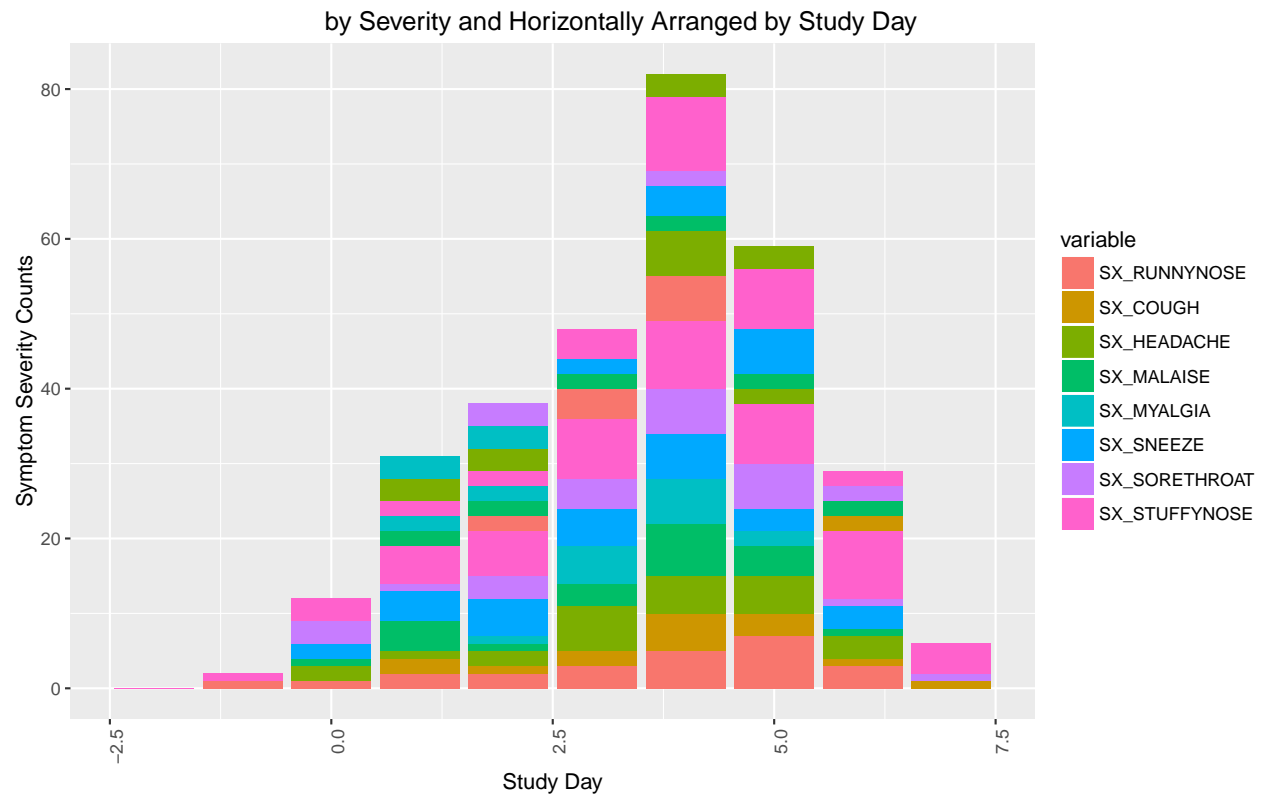
DEE1 RSV: Symptom Severity Counts Vertically Arranged



DEE2 H3N2: Symptom Severity Counts Vertically Arranged



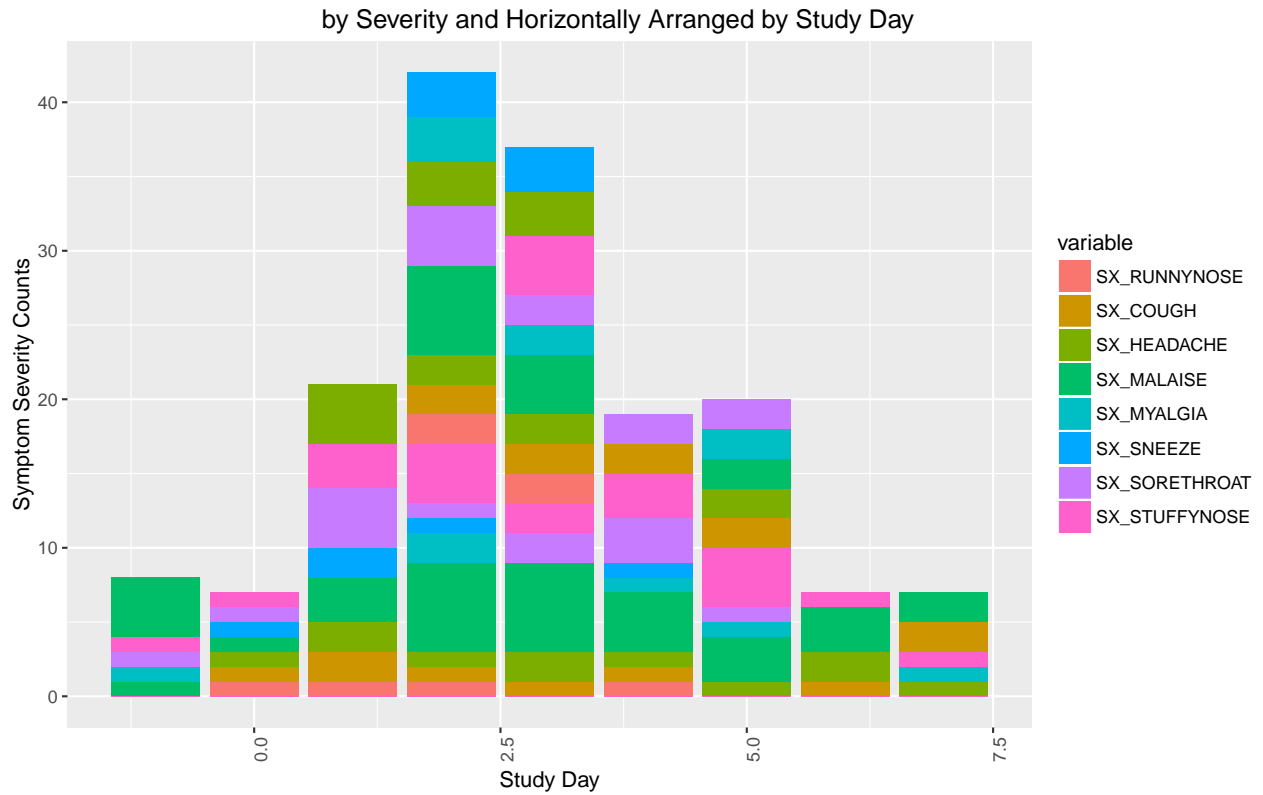
DEE3 H1N1: Symptom Severity Counts Vertically Arranged



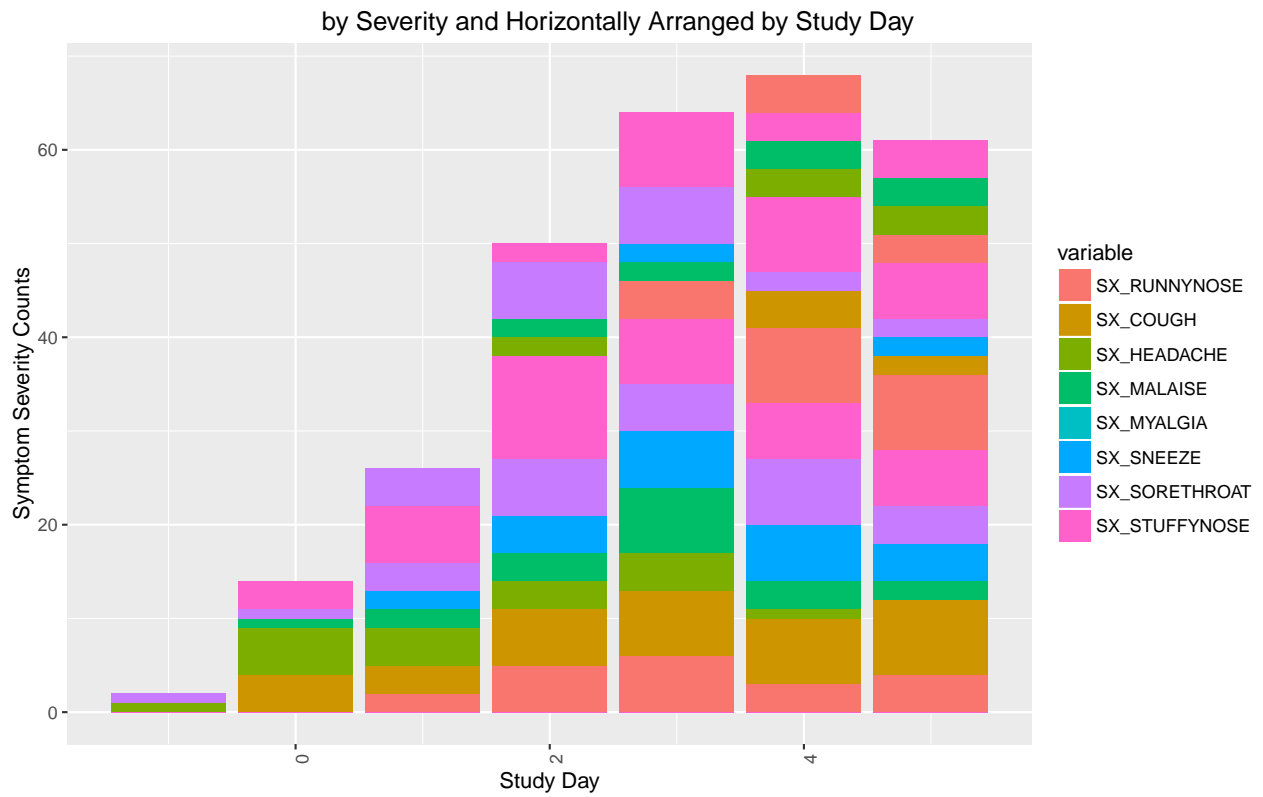
DEE4X H1N1: Symptom Severity Counts Vertically Arranged



DEE5 H3N2: Symptom Severity Counts Vertically Arranged

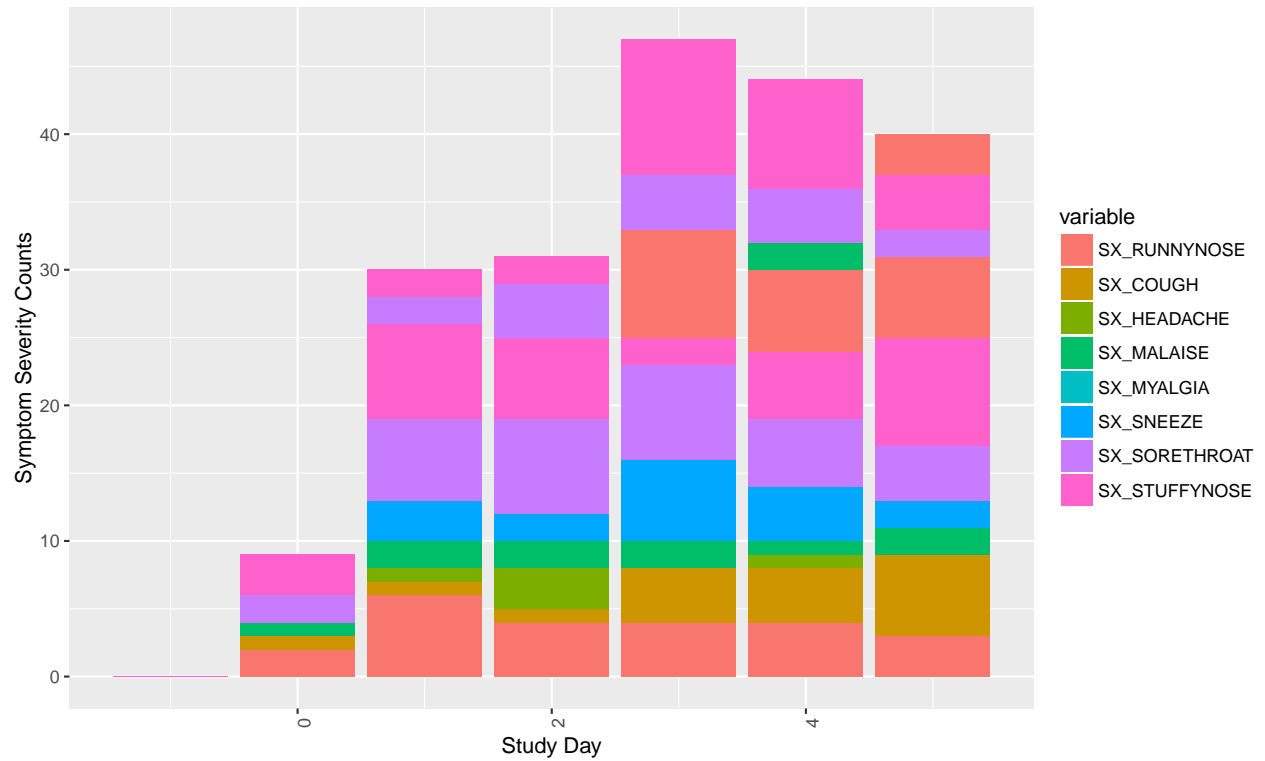


Rhinovirus Duke: Symptom Severity Counts Vertically Arranged



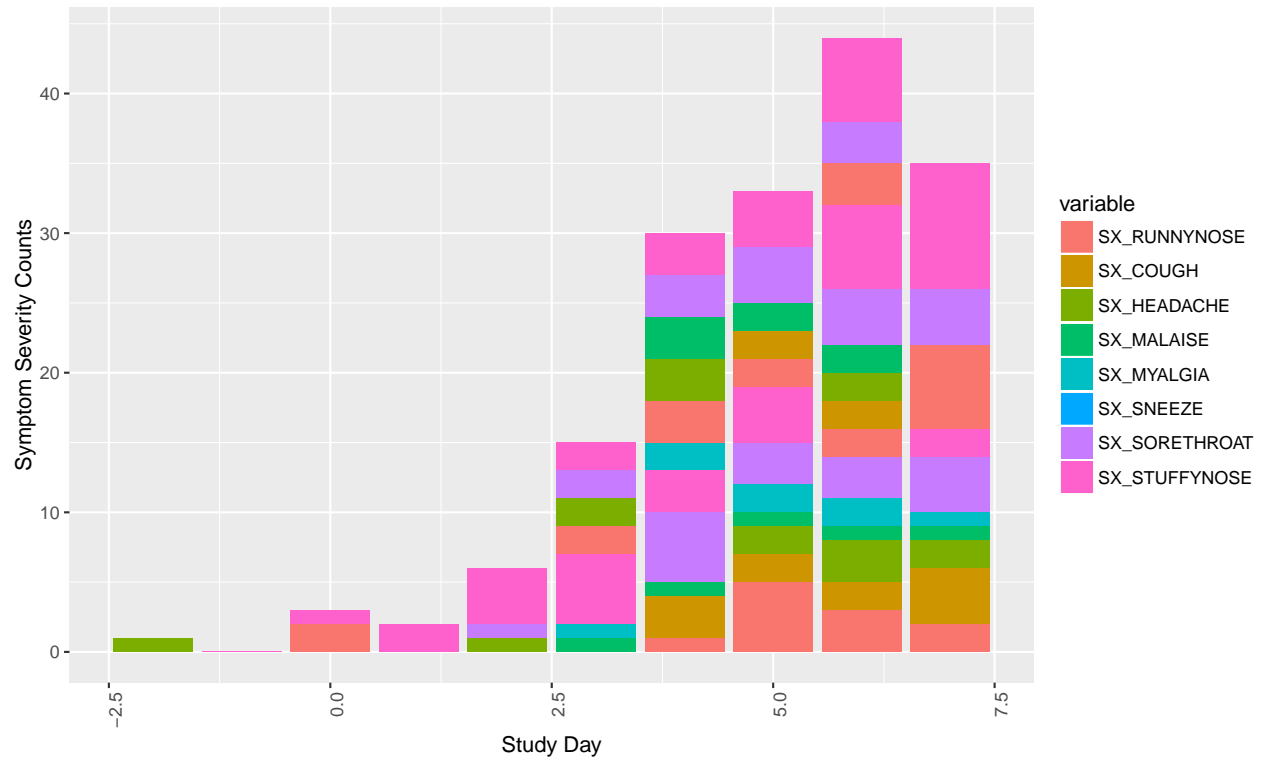
# Rhinovirus UVA: Symptom Severity Counts Vertically Arranged

by Severity and Horizontally Arranged by Study Day



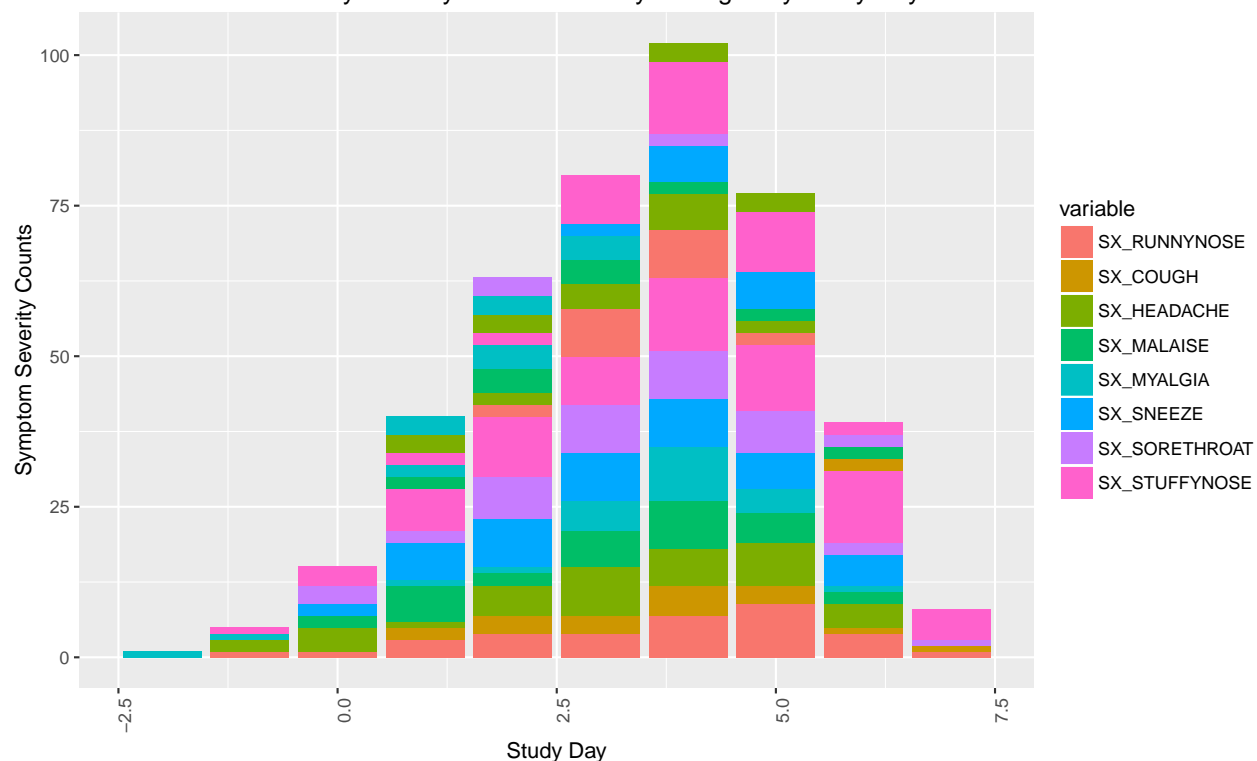
RSV: Symptom Severity Counts Vertically Arranged

by Severity and Horizontally Arranged by Study Day



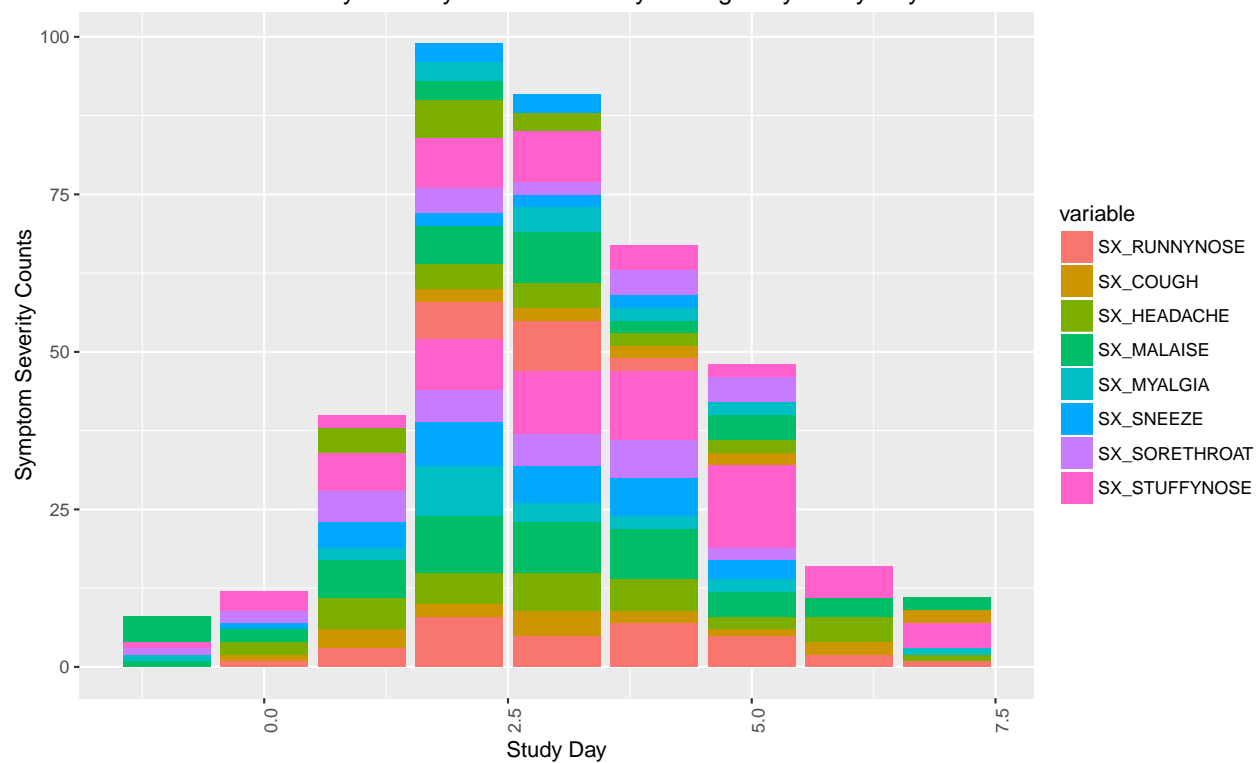
H1N1: Symptom Severity Counts Vertically Arranged

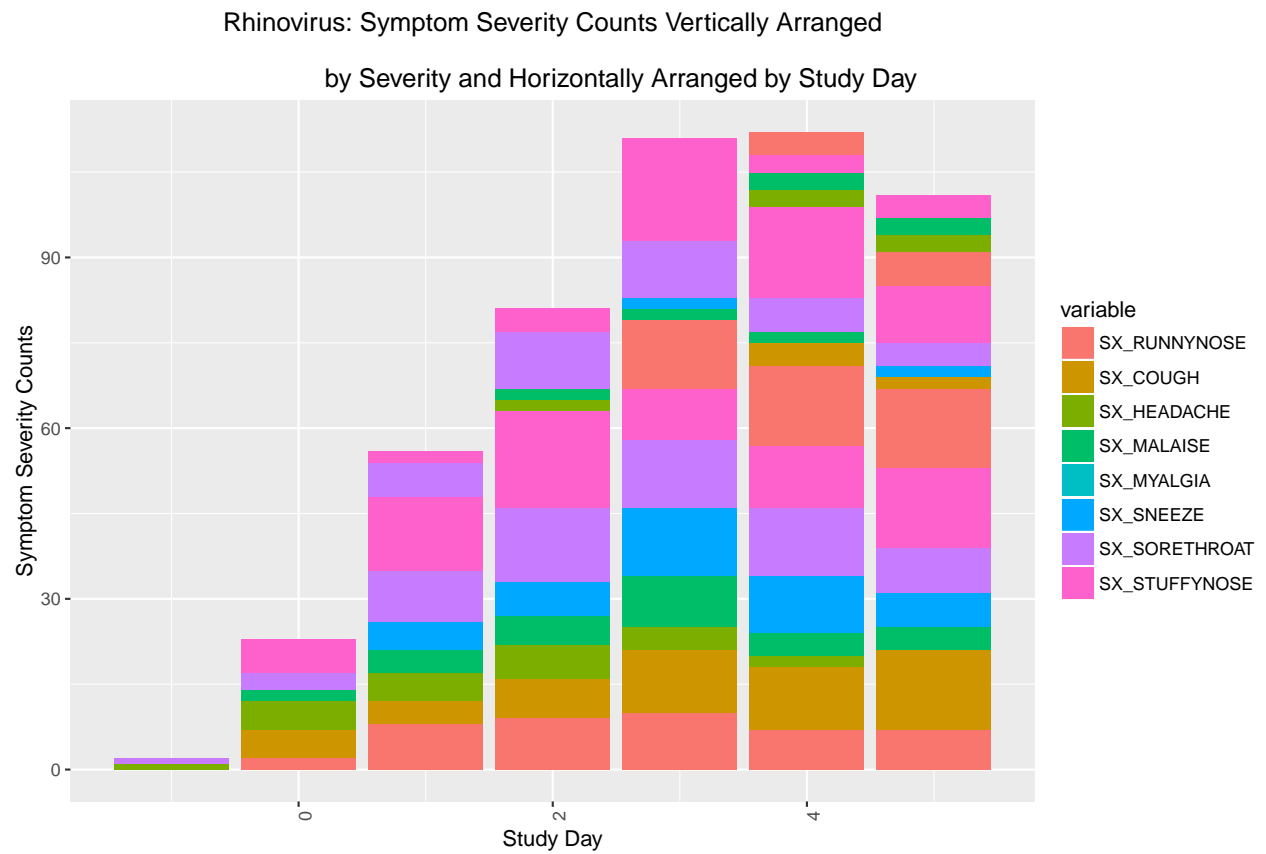
by Severity and Horizontally Arranged by Study Day



H3N2: Symptom Severity Counts Vertically Arranged

by Severity and Horizontally Arranged by Study Day

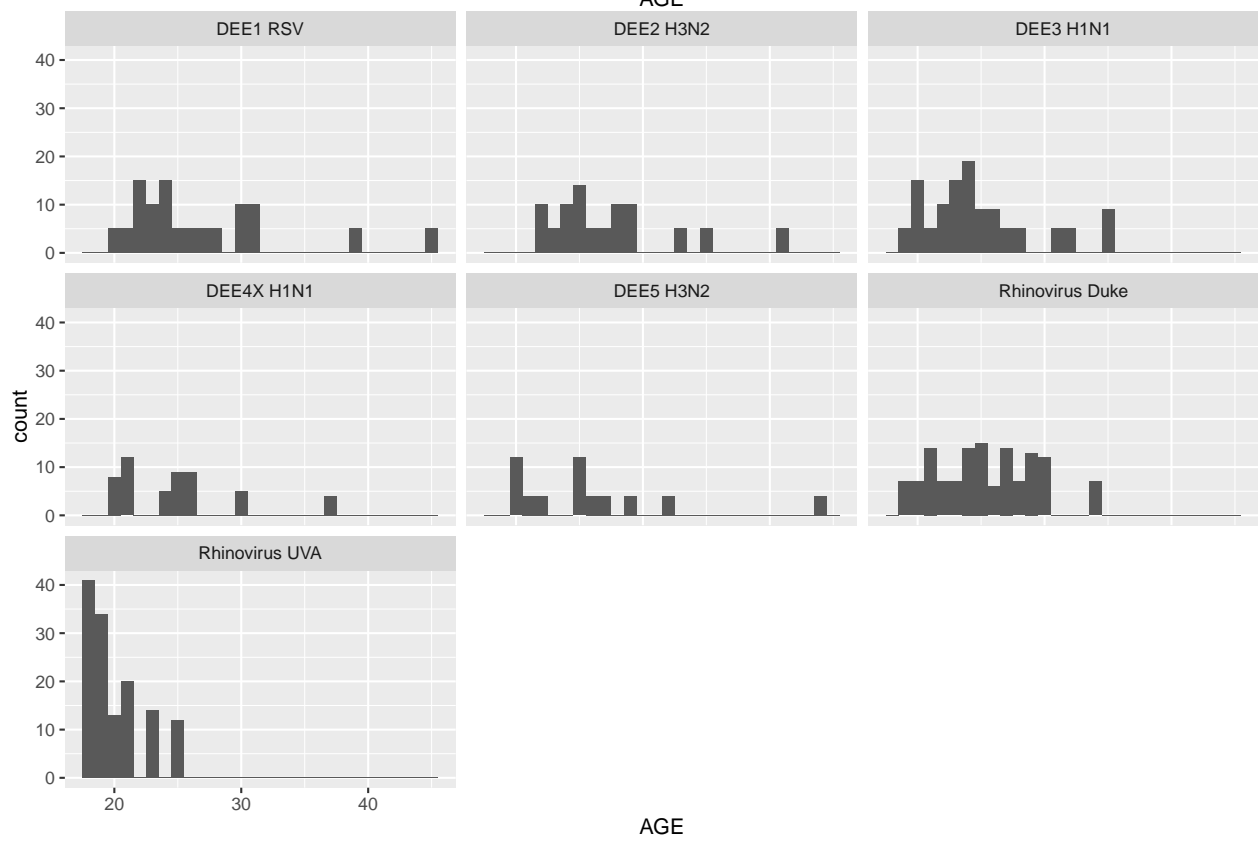
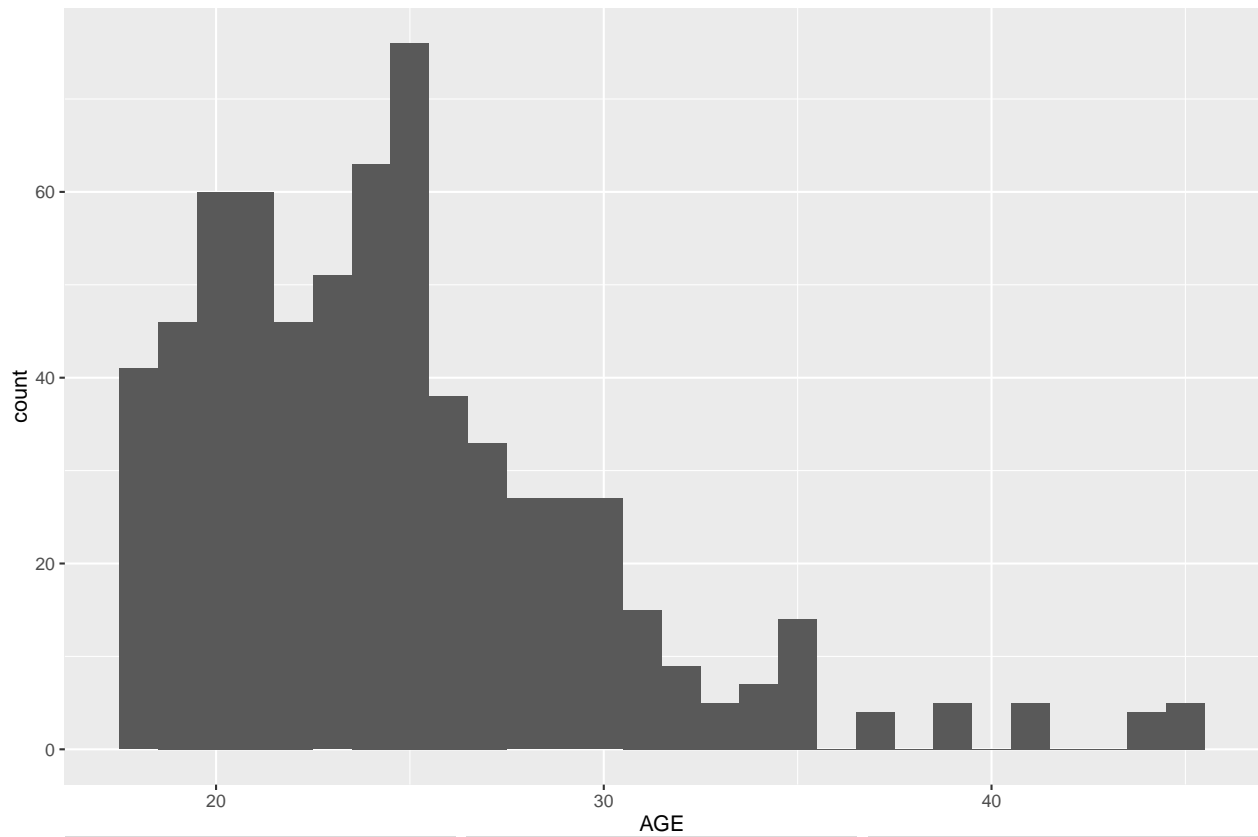


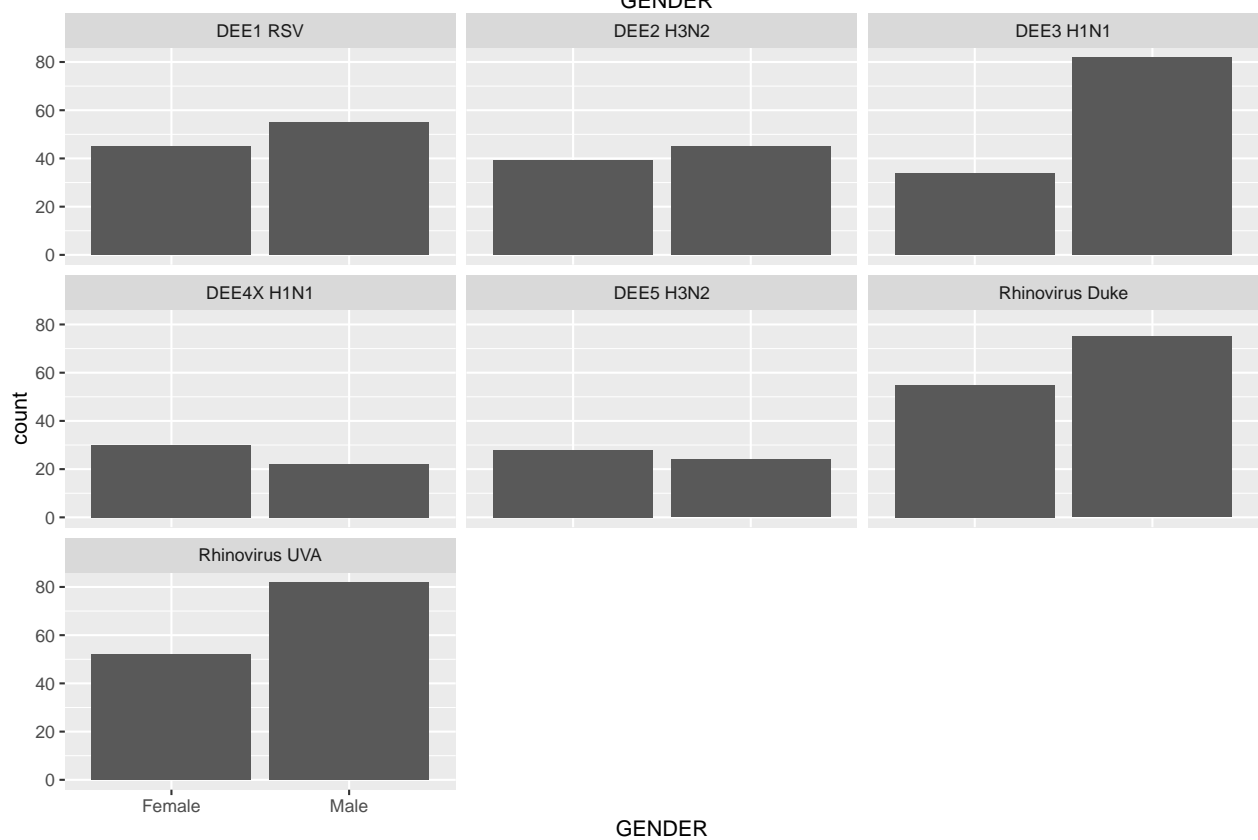
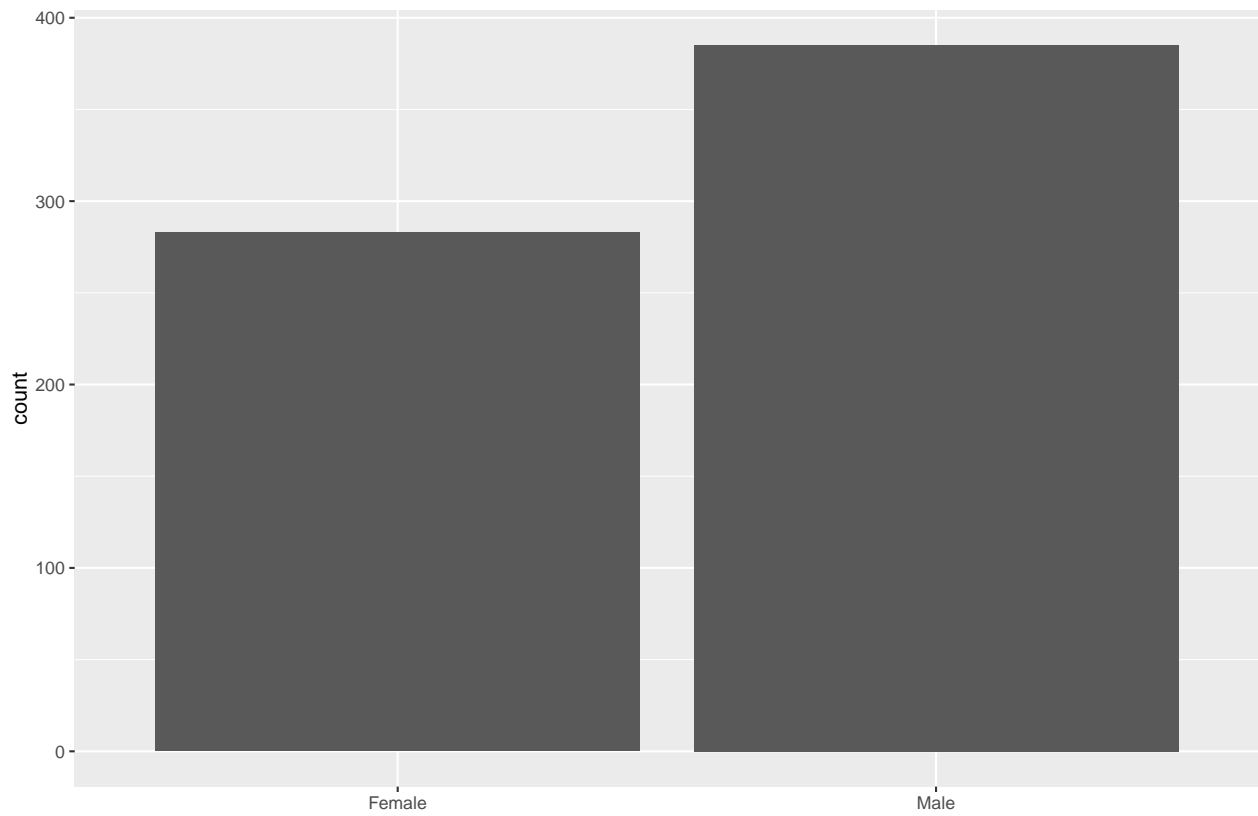


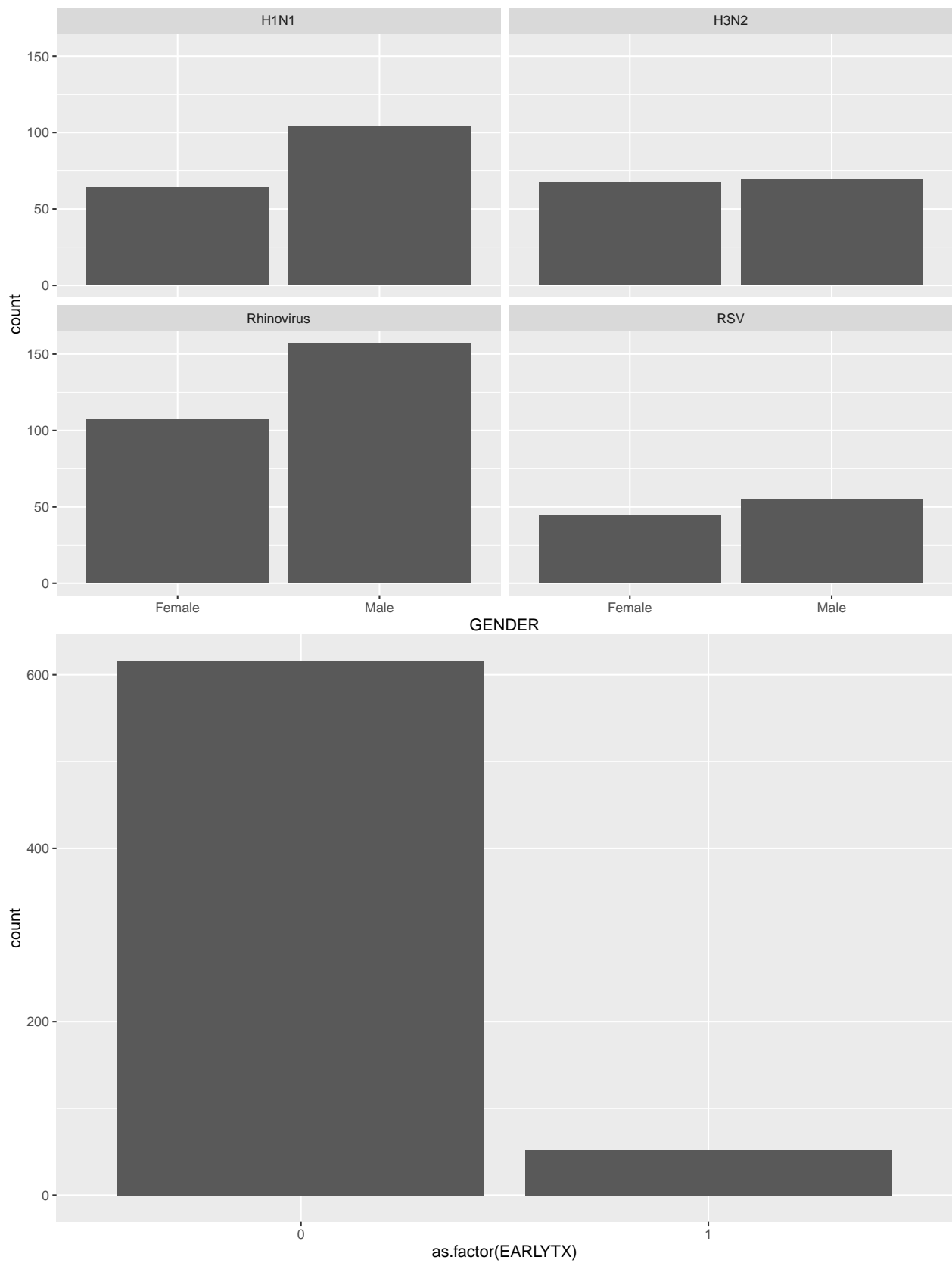
## Clinical Features

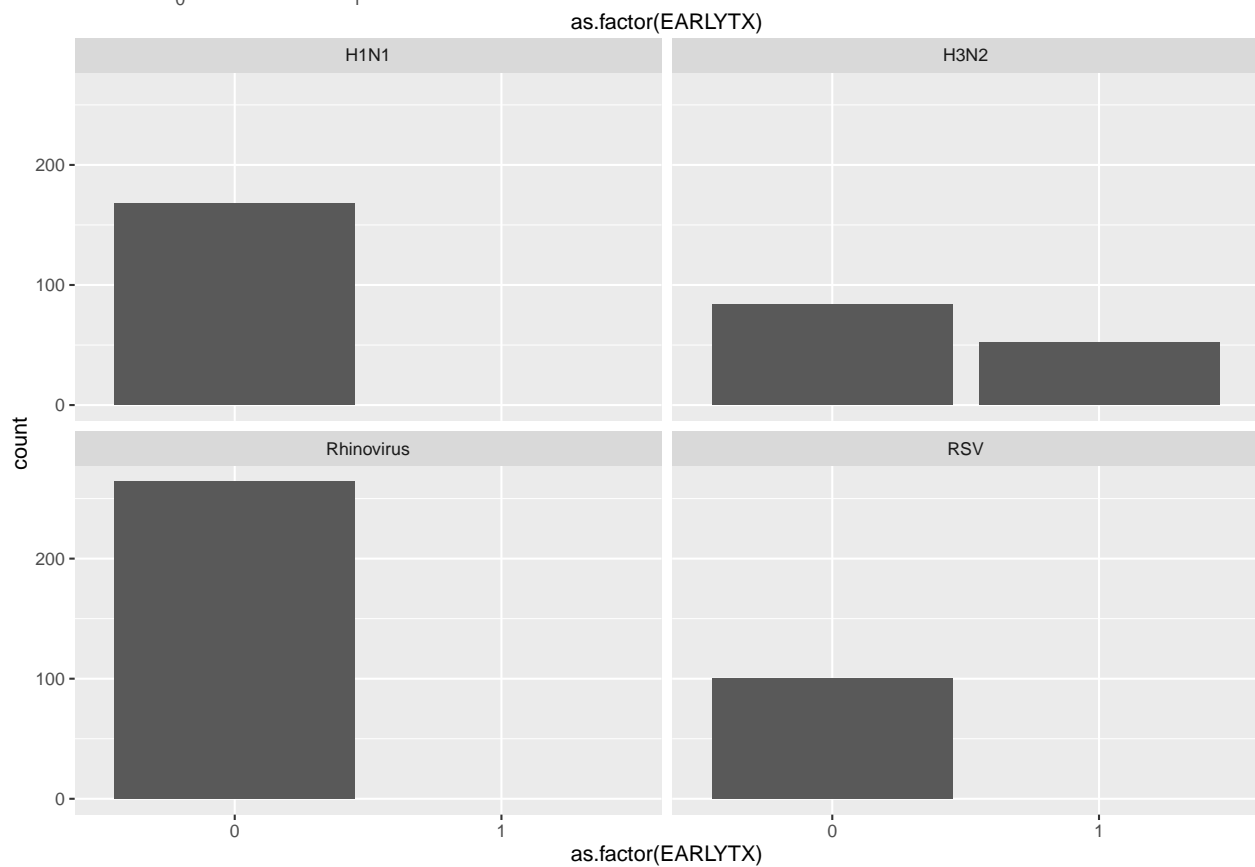
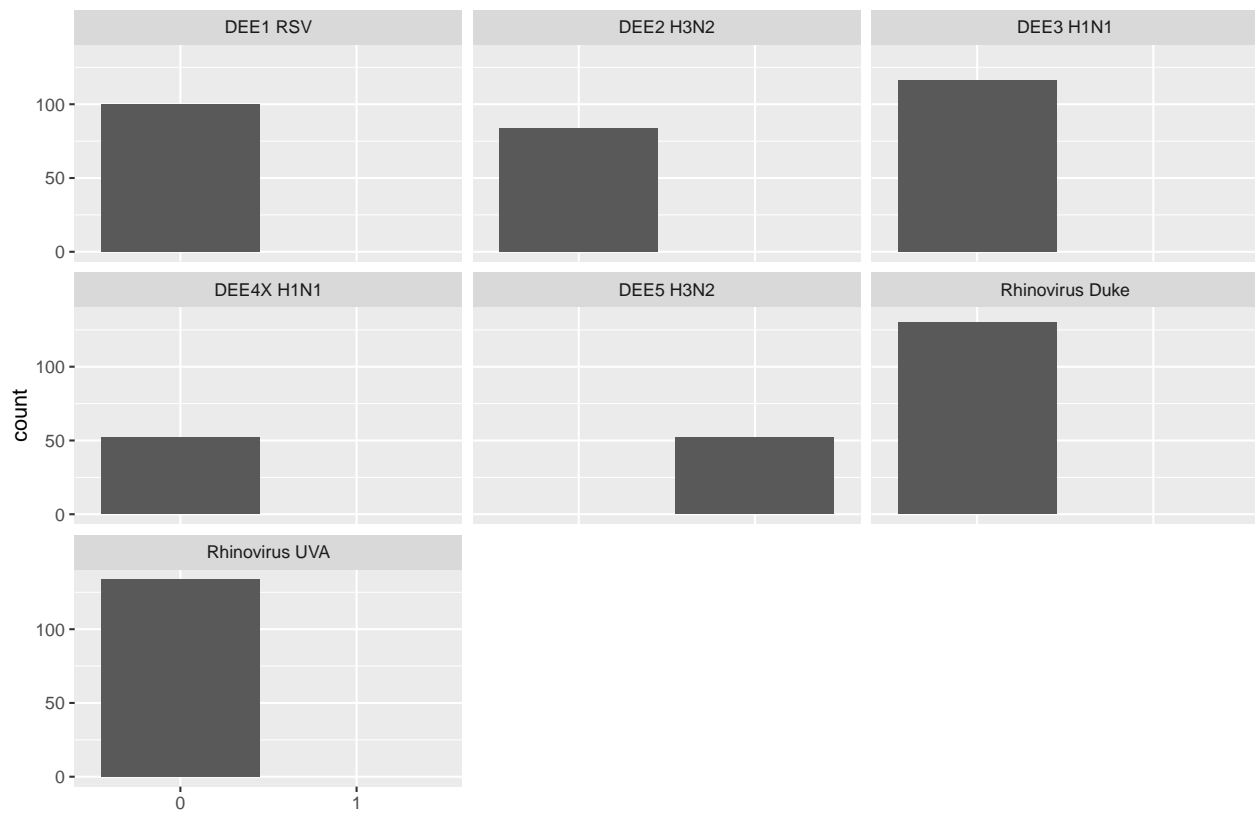
Timepoints are available in this file post-24h following viral challenge. Remove them prior to studying other clinical distributions.

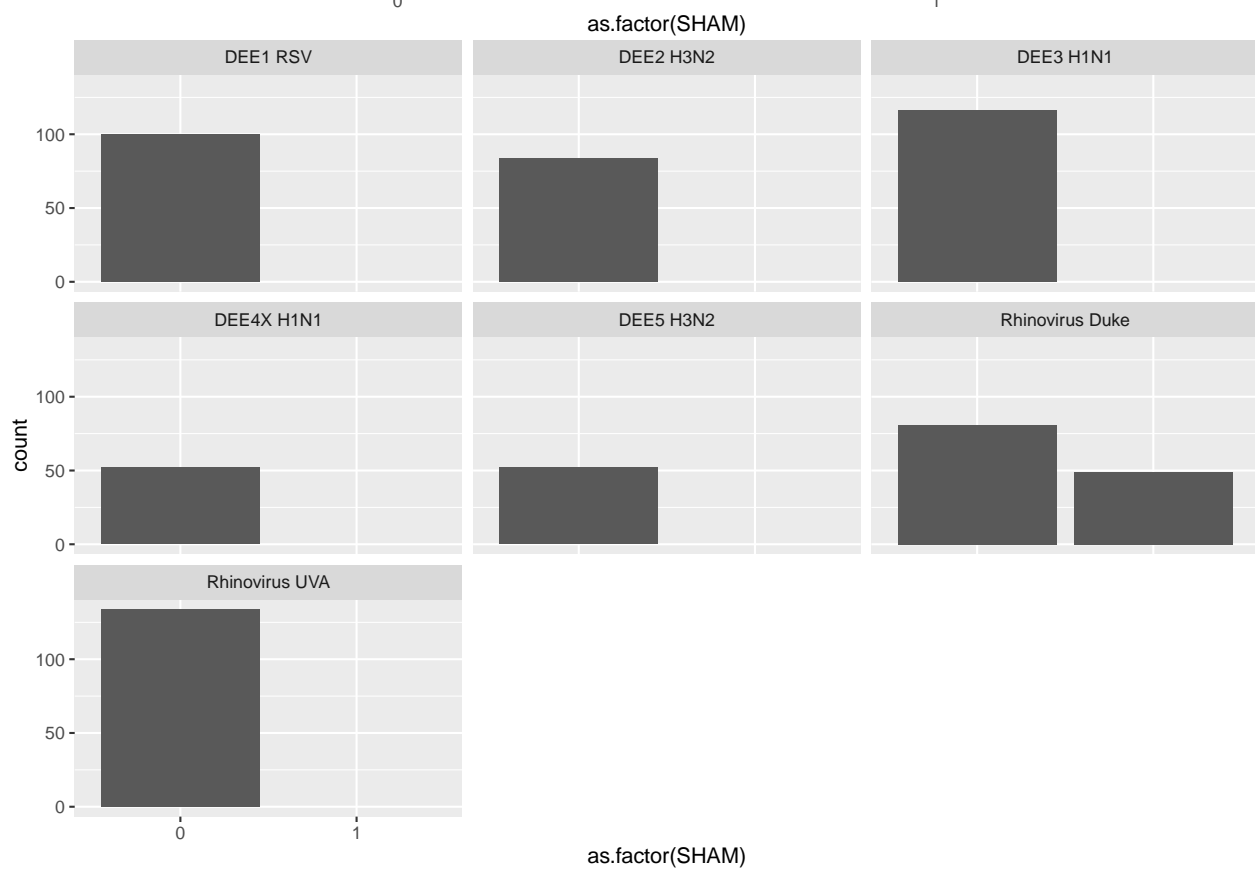
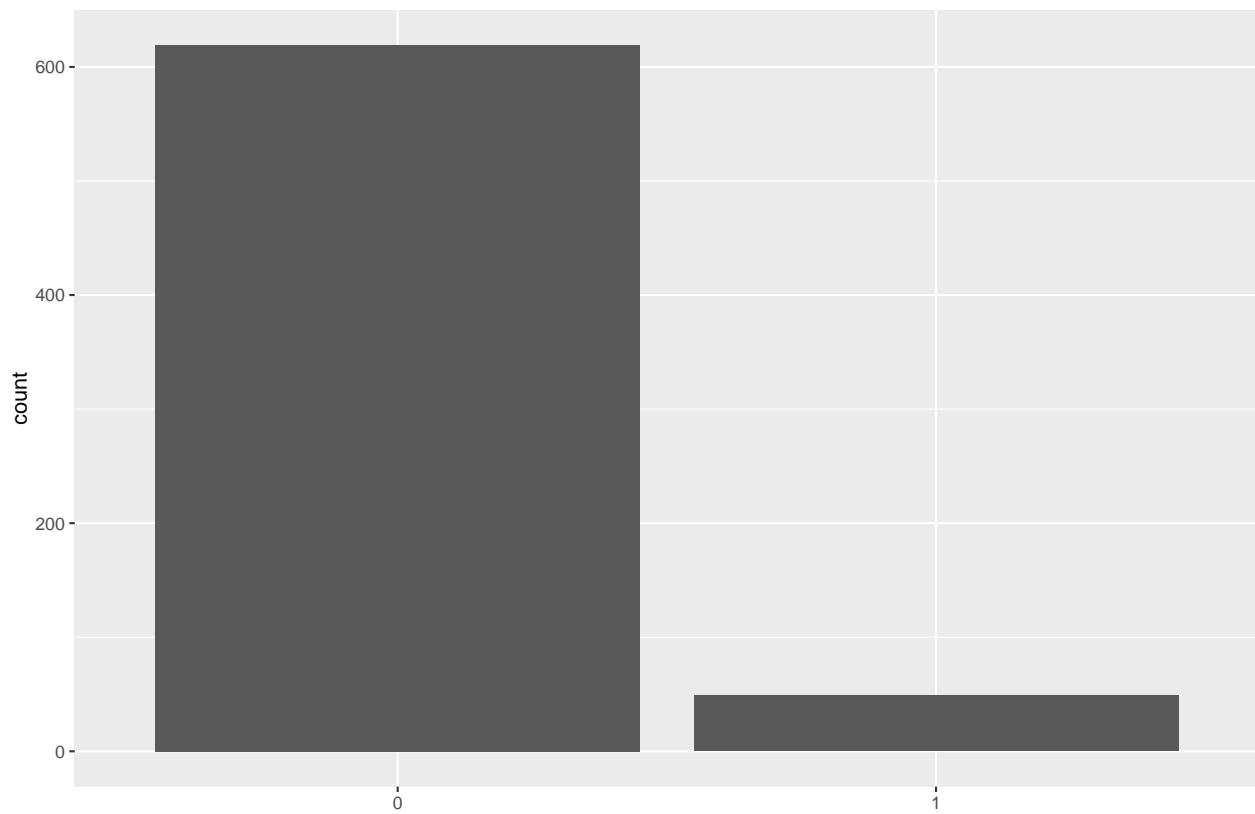


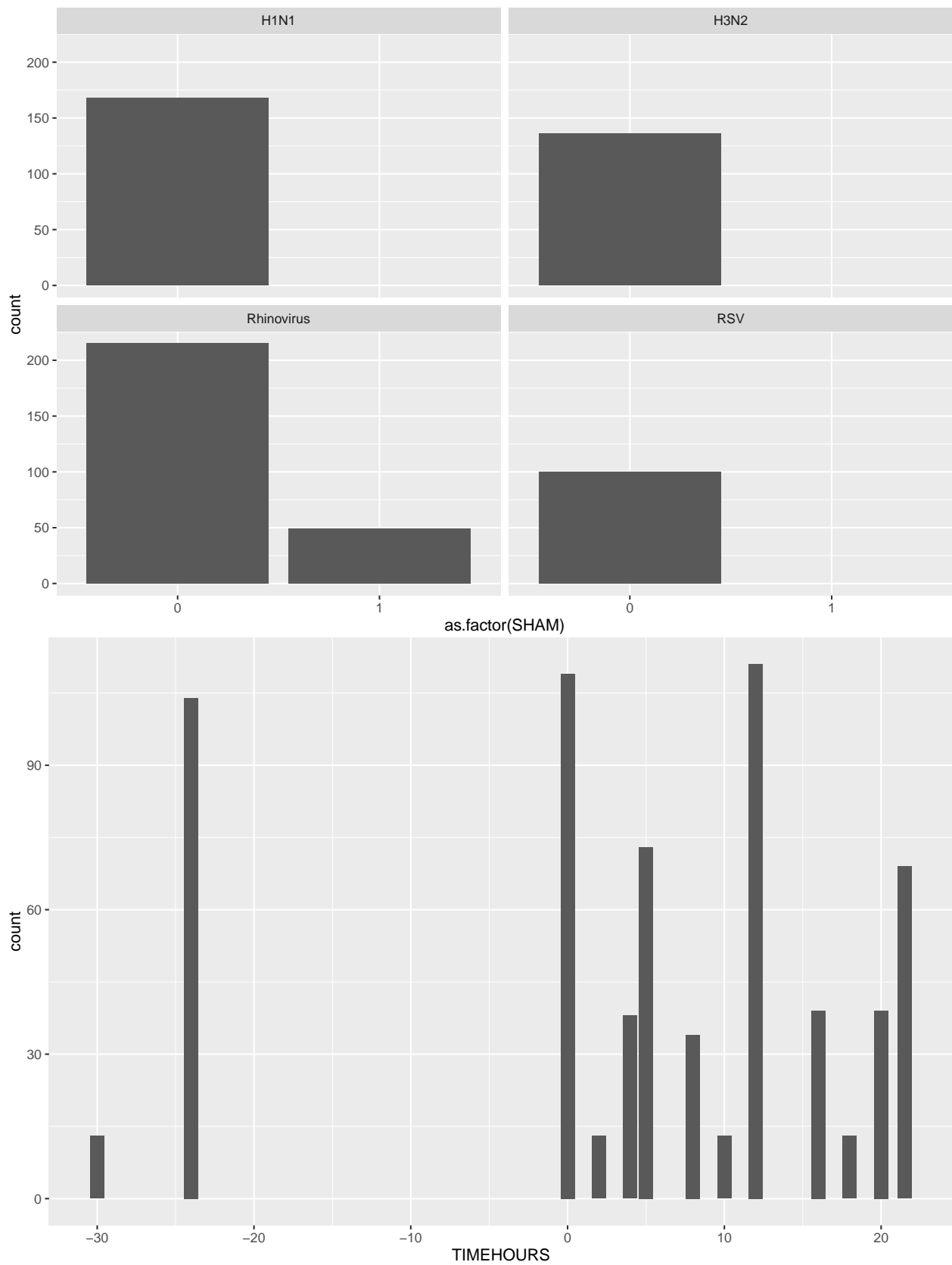


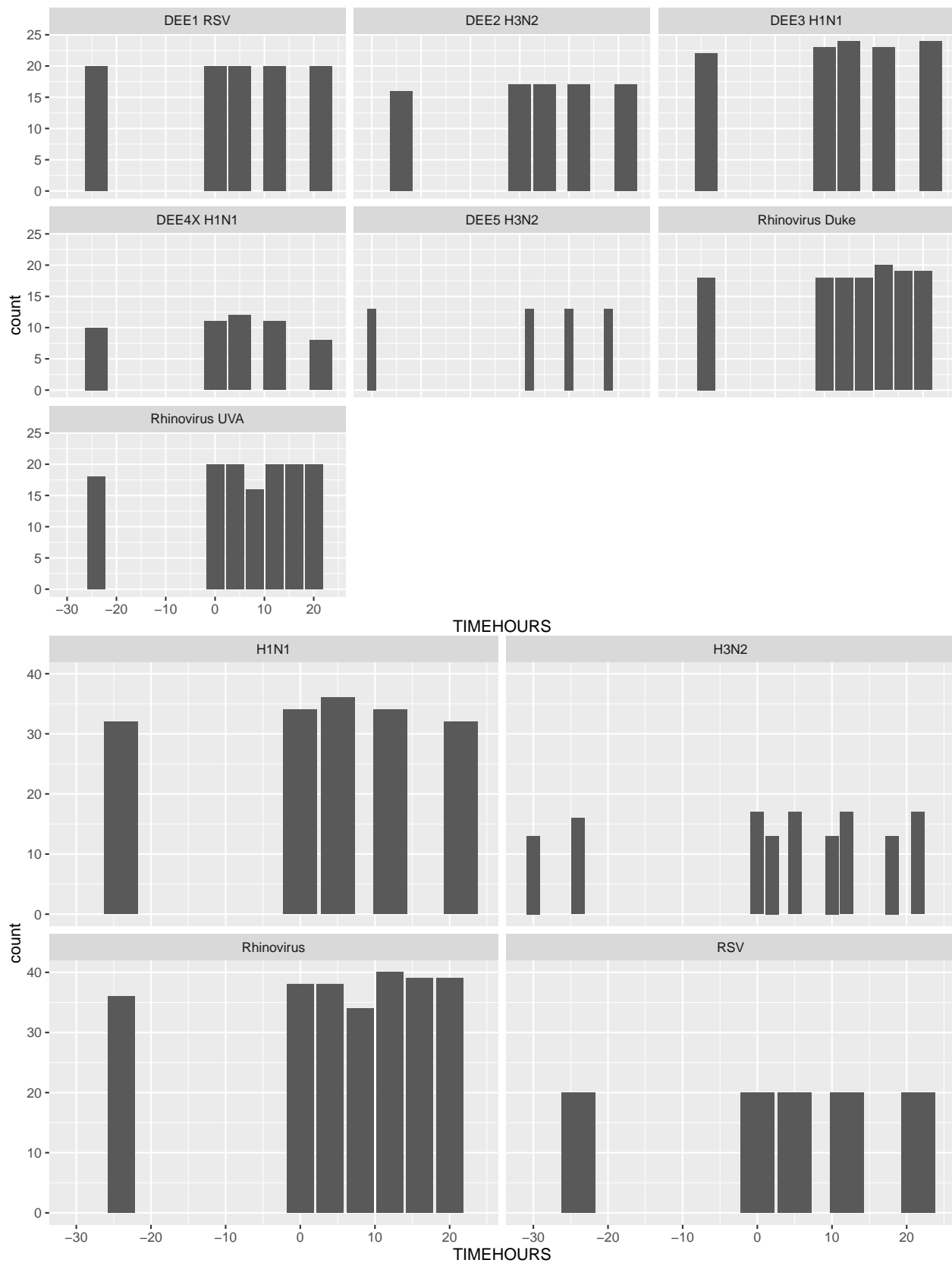




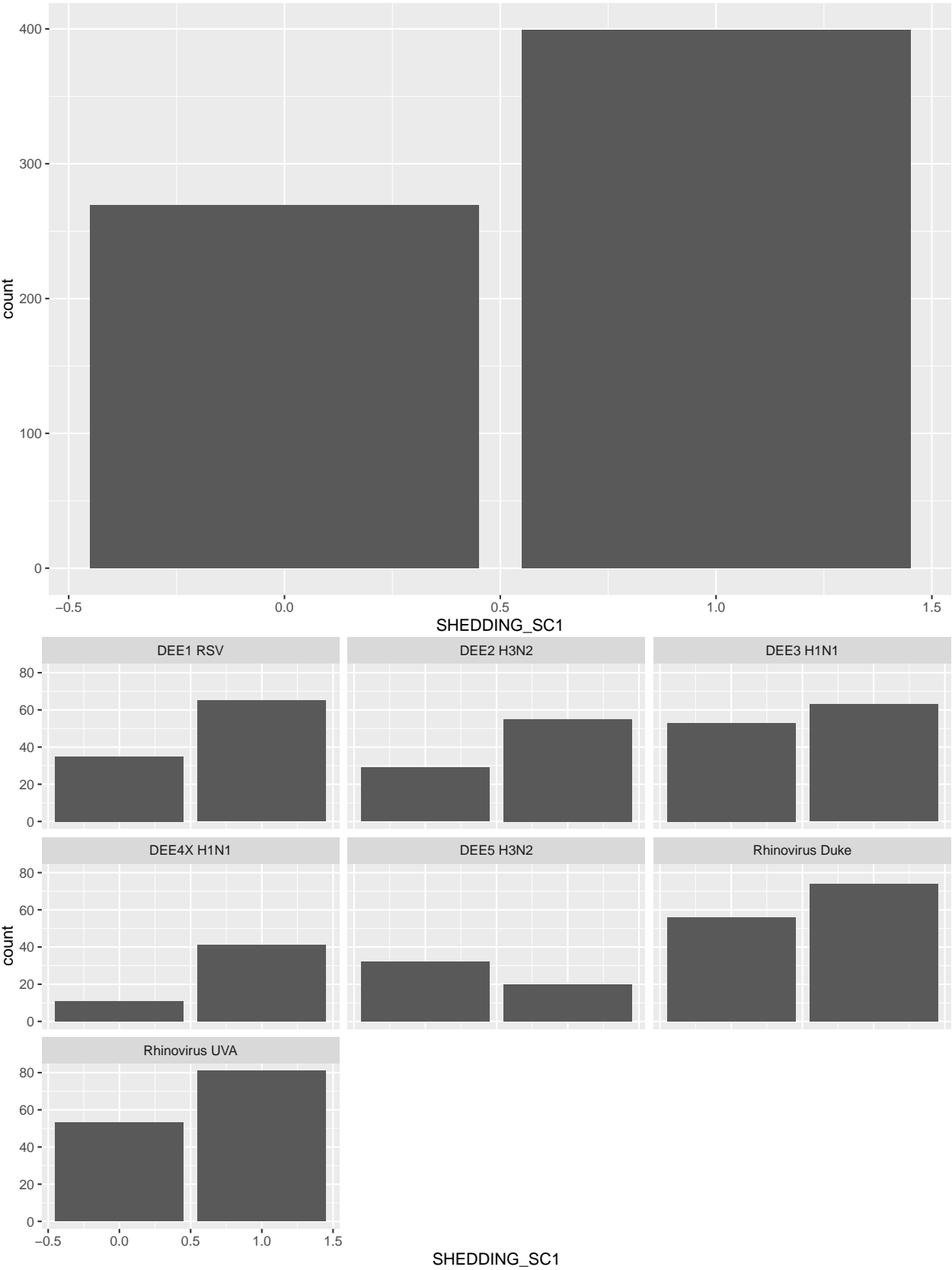




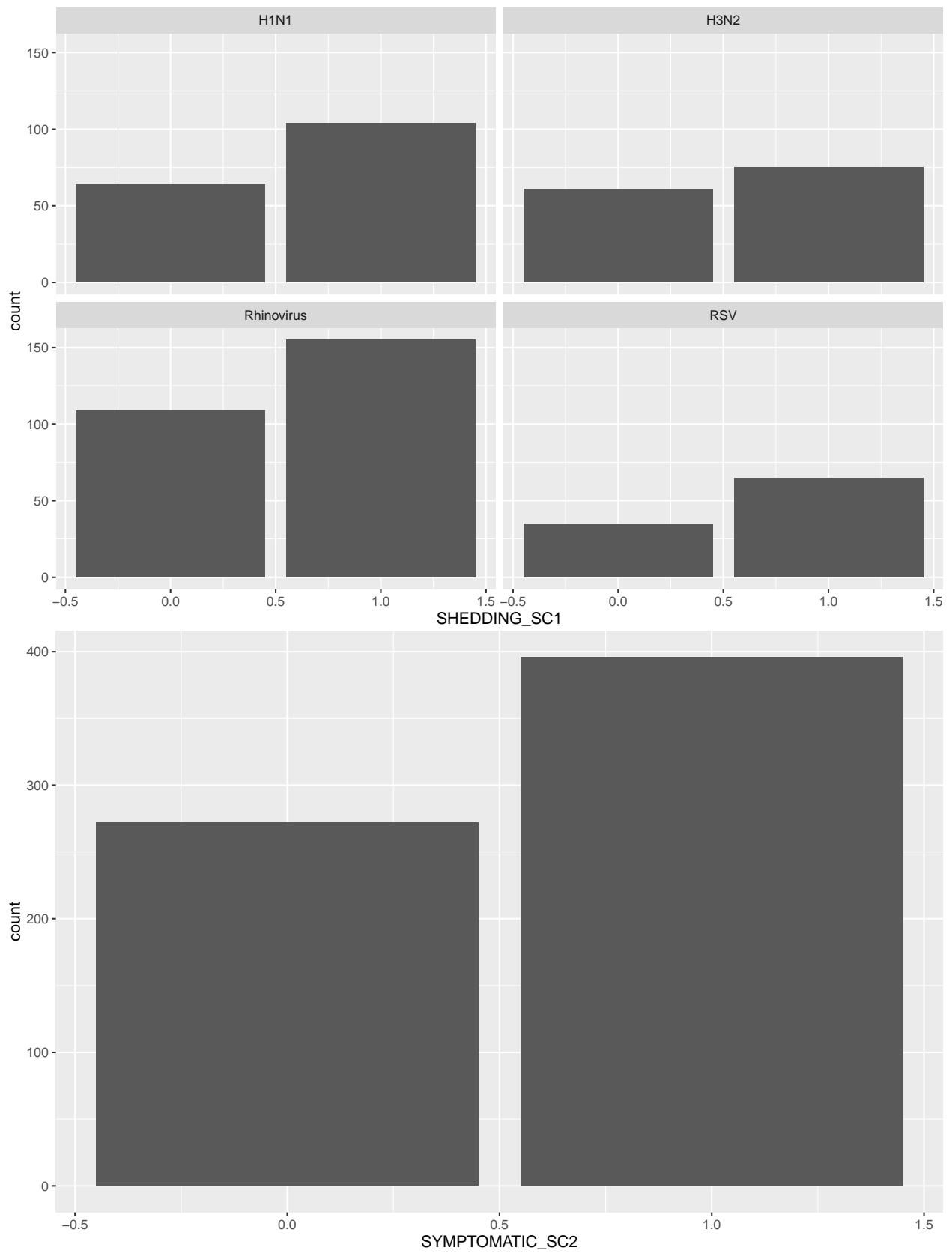


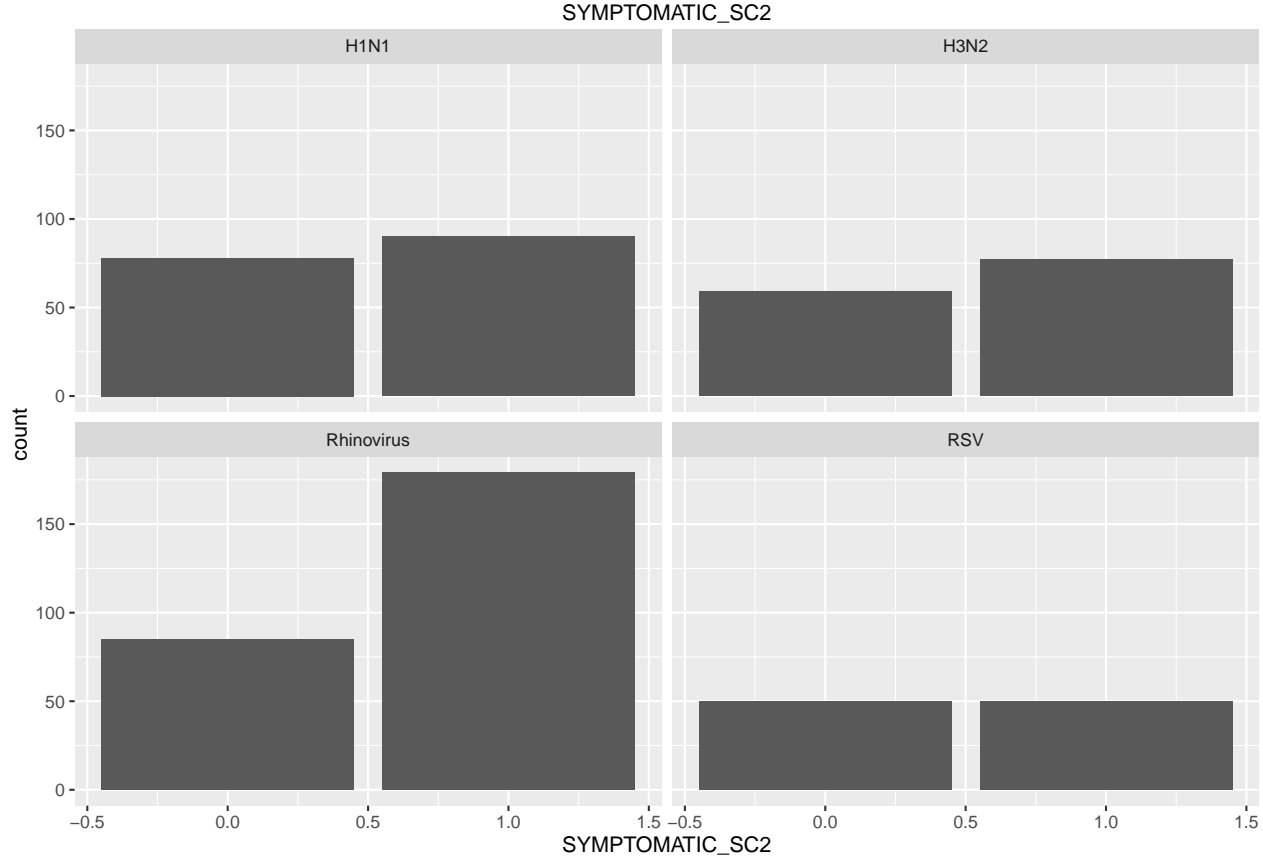
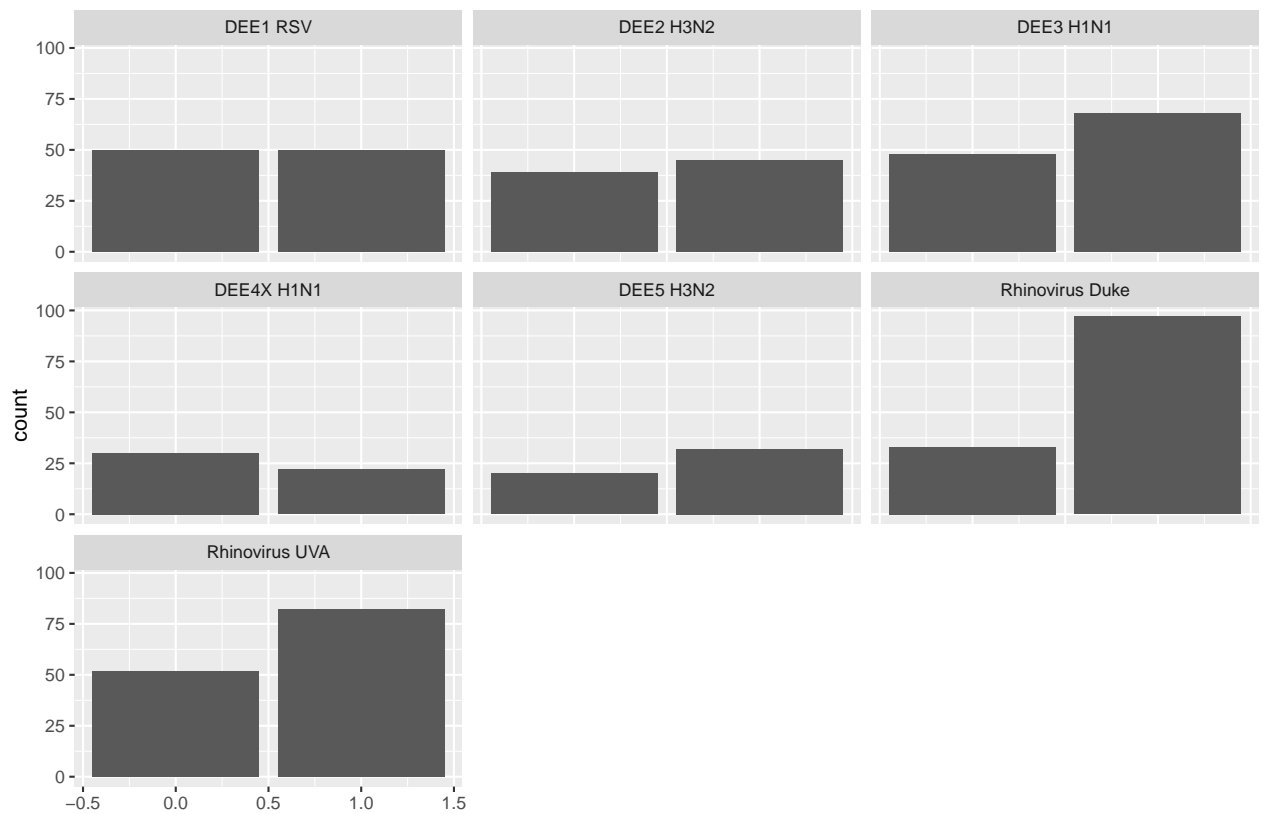


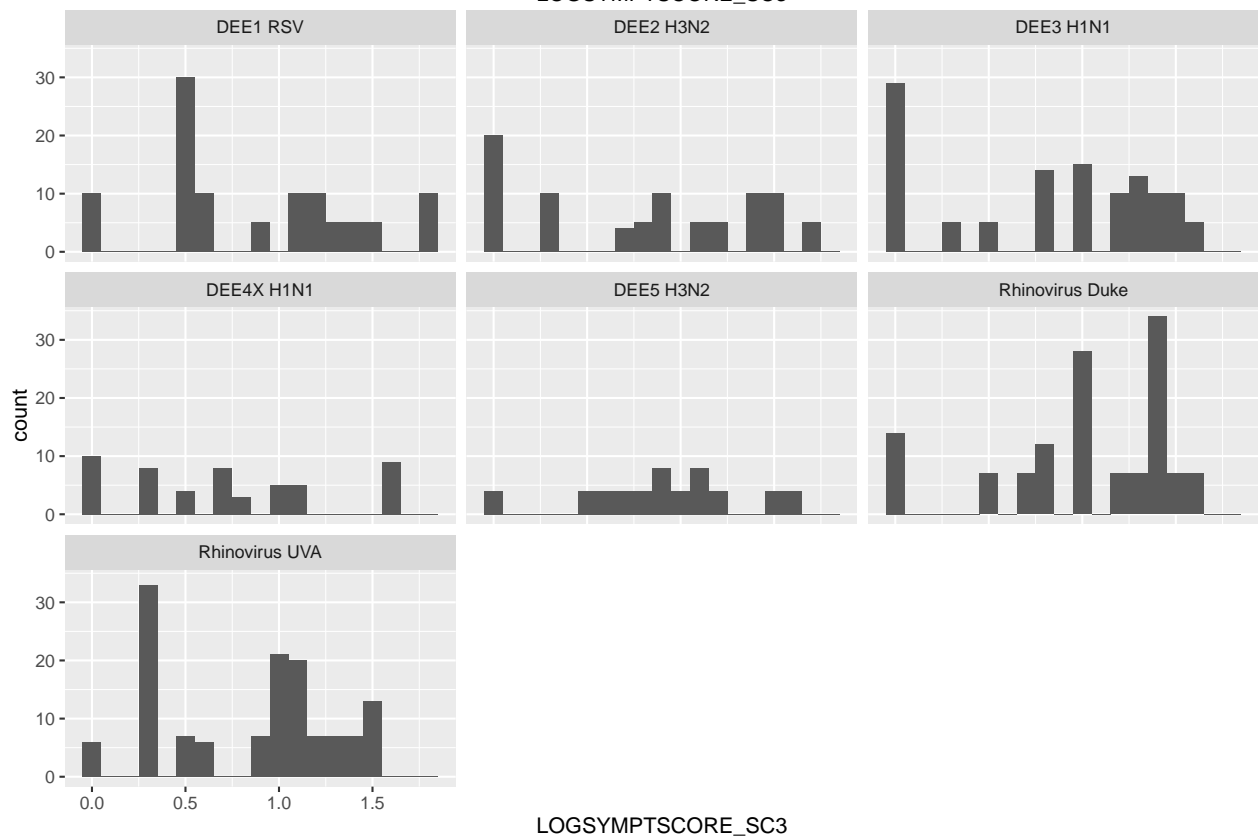
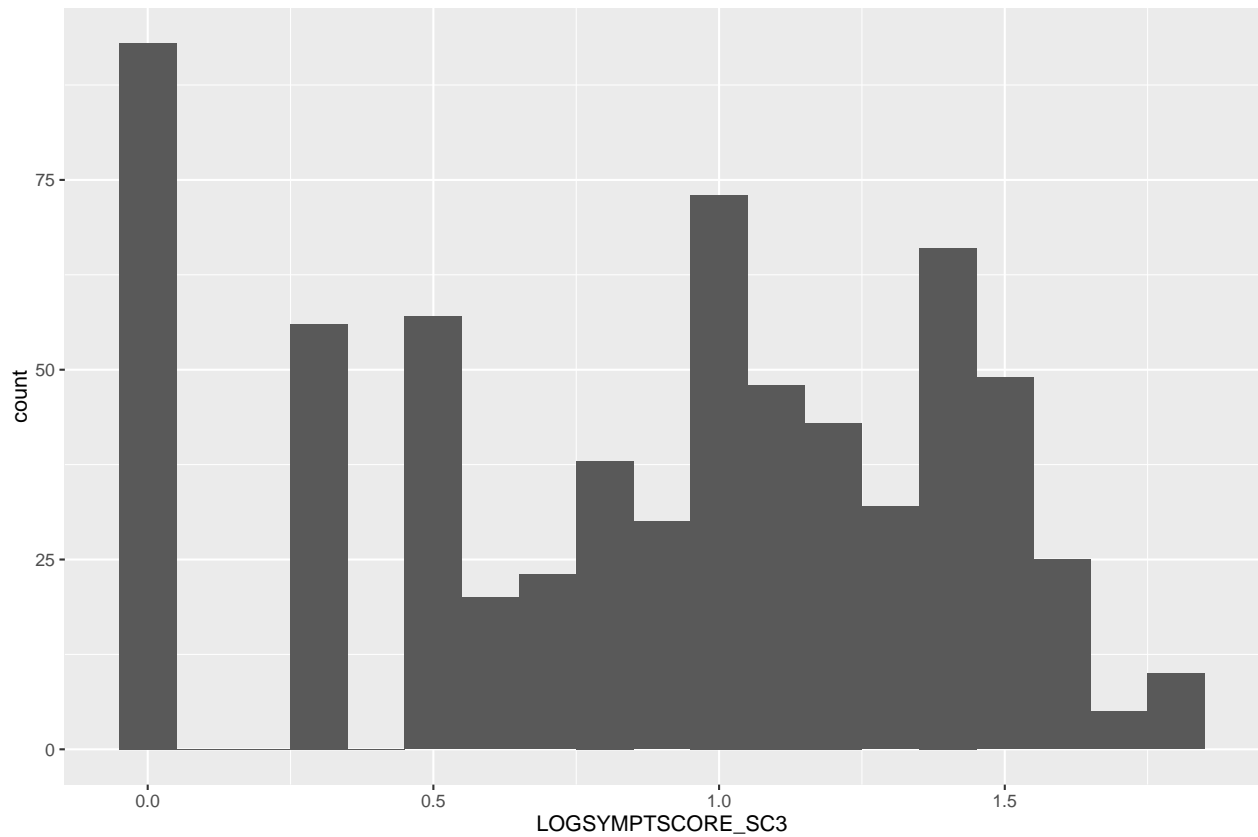
Clinical Outcomes

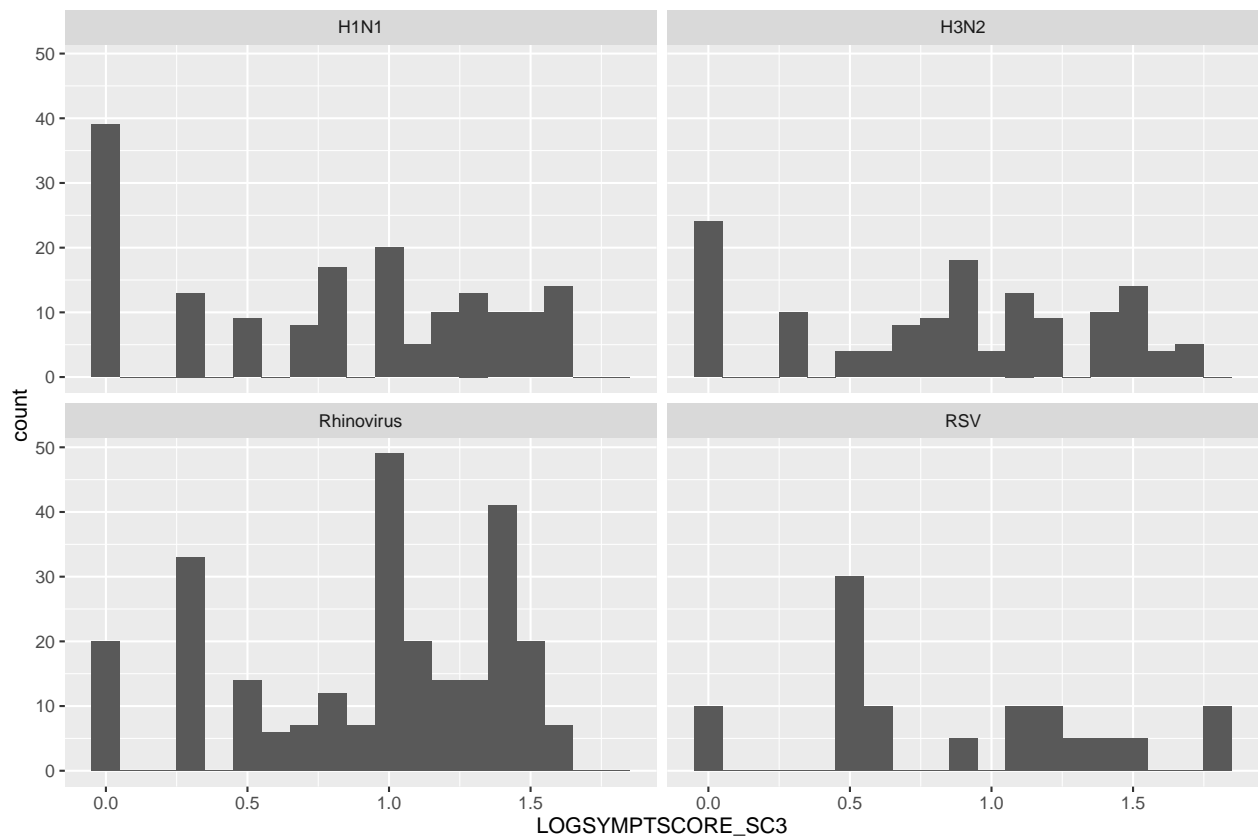












## Features vs Outcomes

