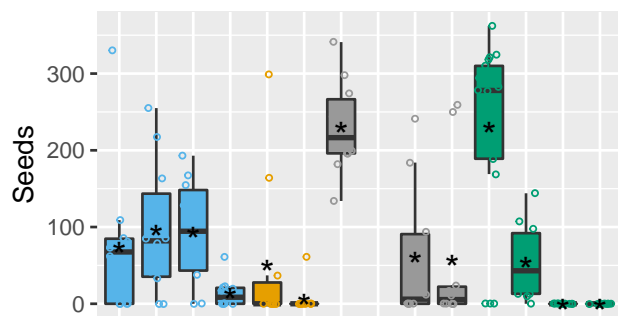


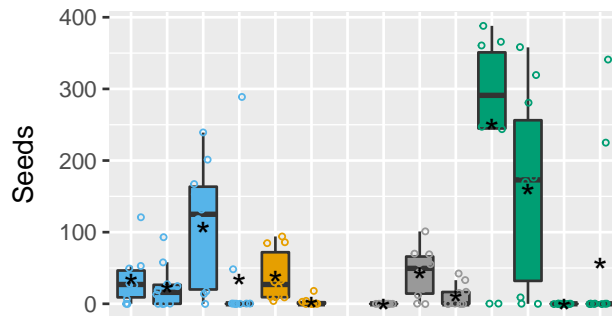
Data_visualization

Solanaceae Focal Species

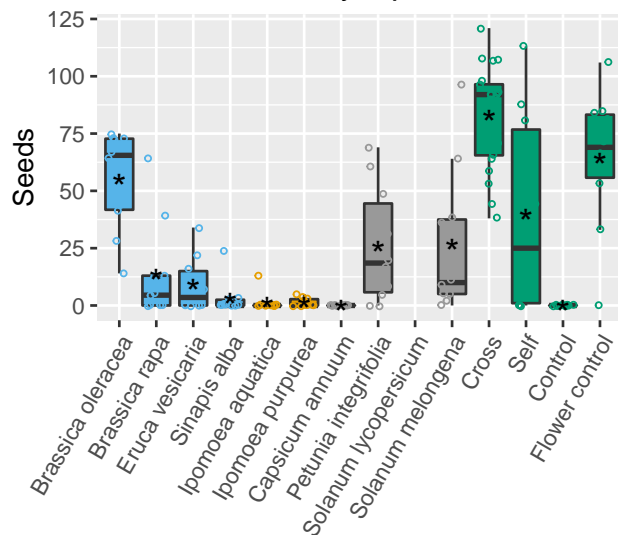
Petunia integrifolia



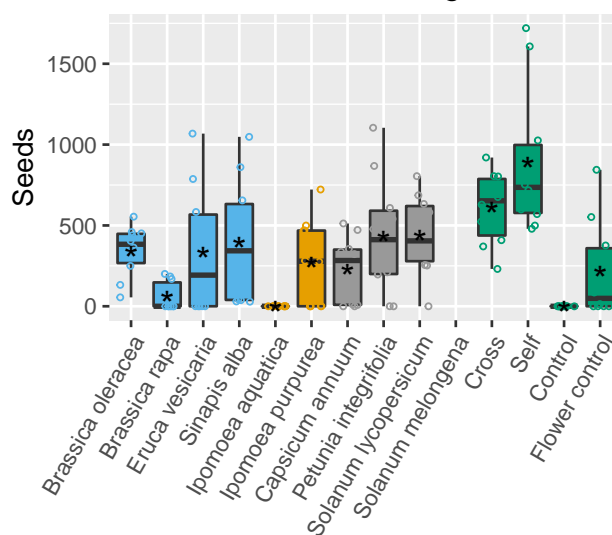
Capsicum annuum



Solanum lycopersicum

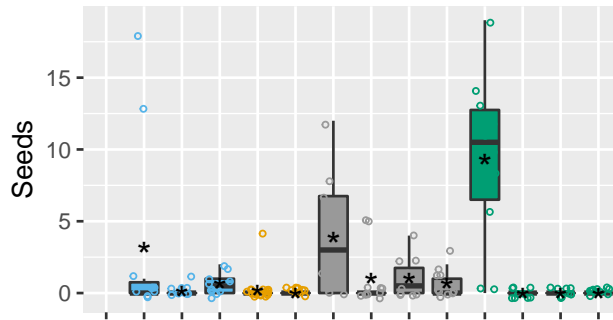


Solanum melongena

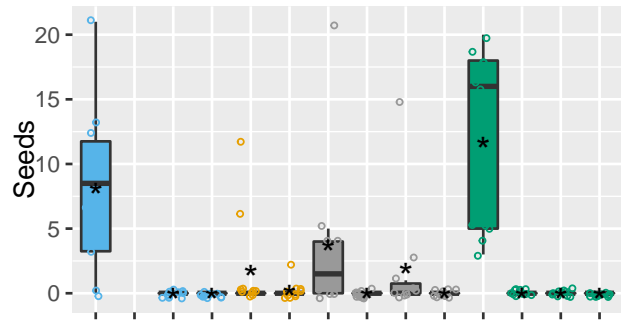


Brassicaceae Focal species

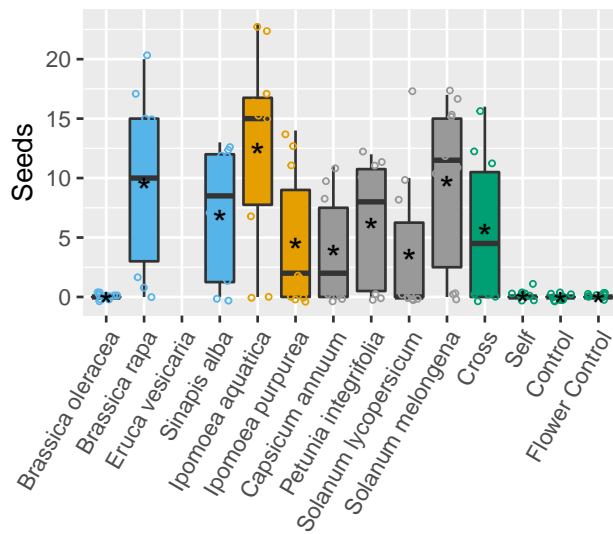
Brassica oleracea



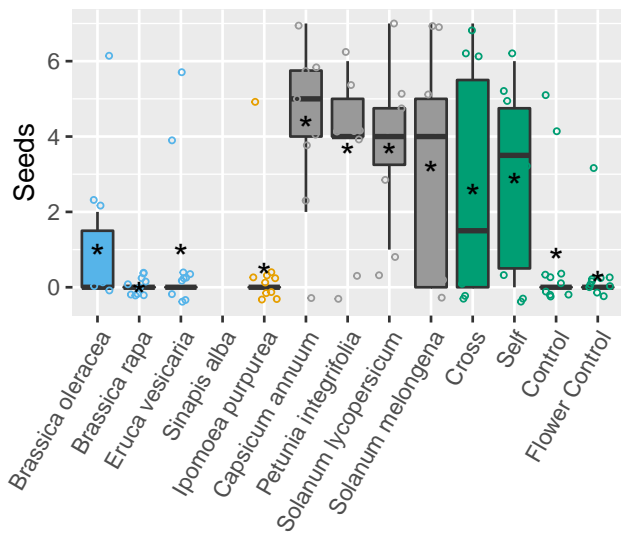
Brassica rapa



Eruca vesicaria

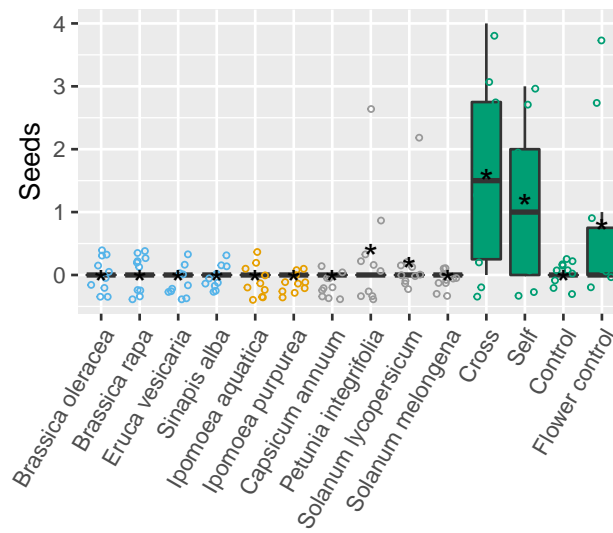


Sinapis alba

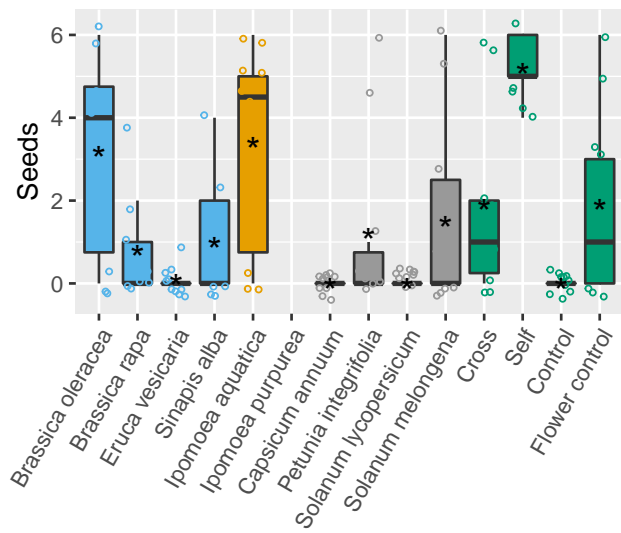


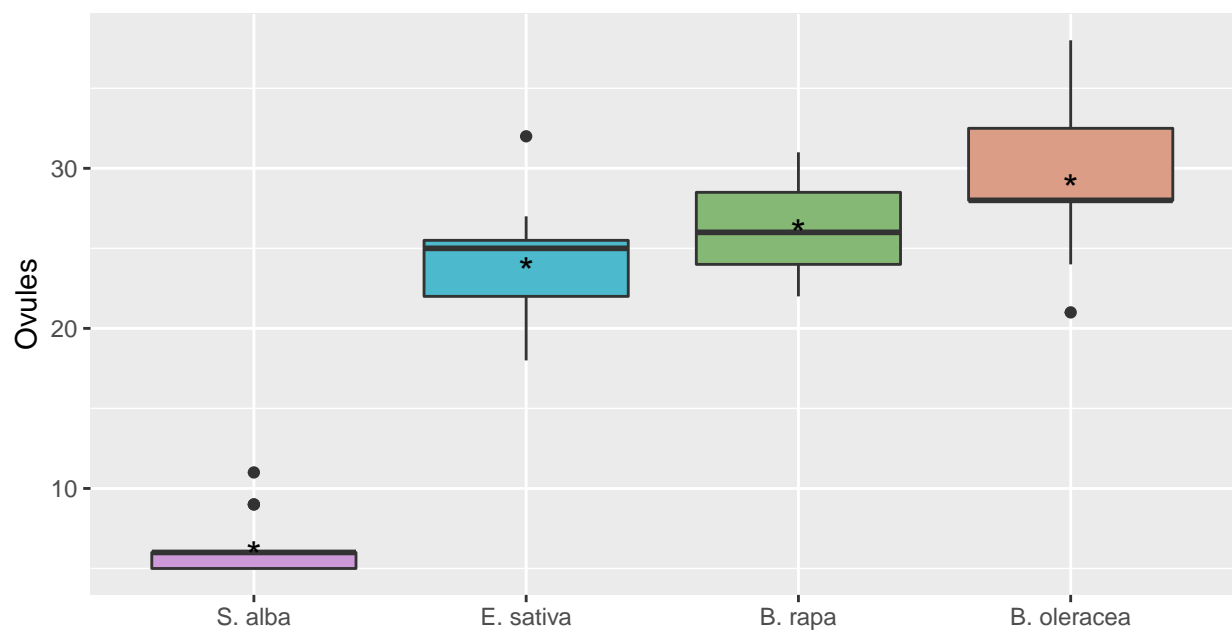
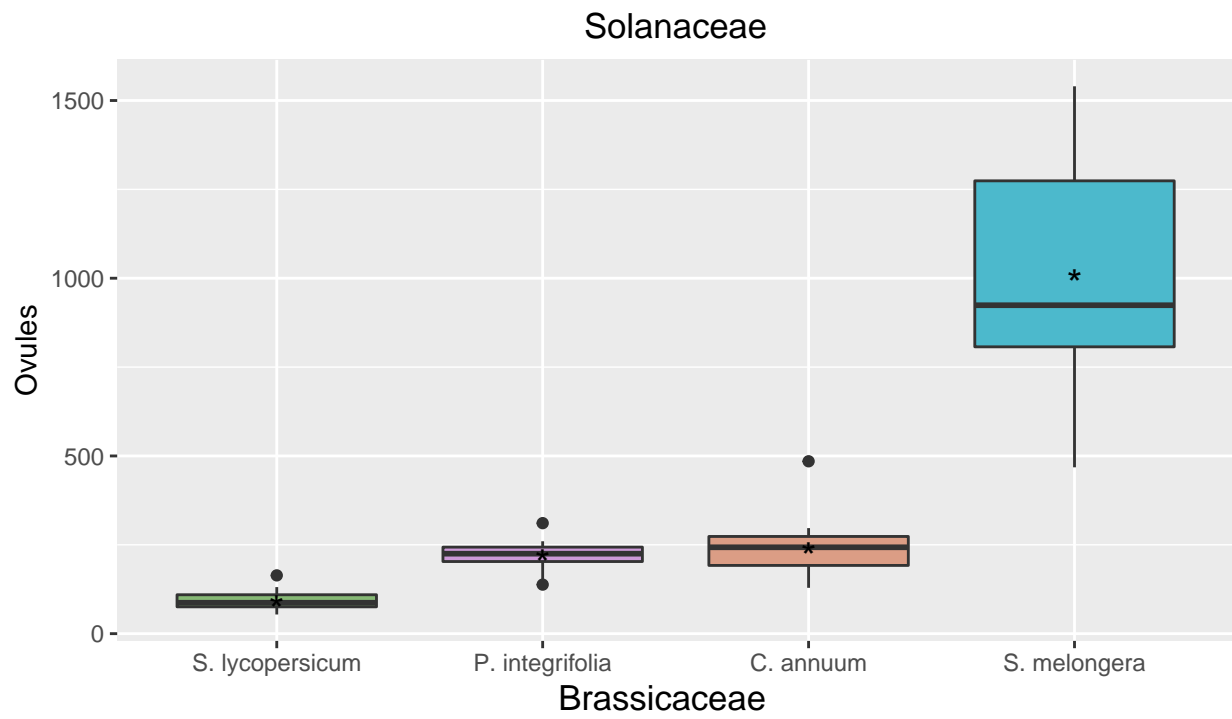
Convolvulaceae

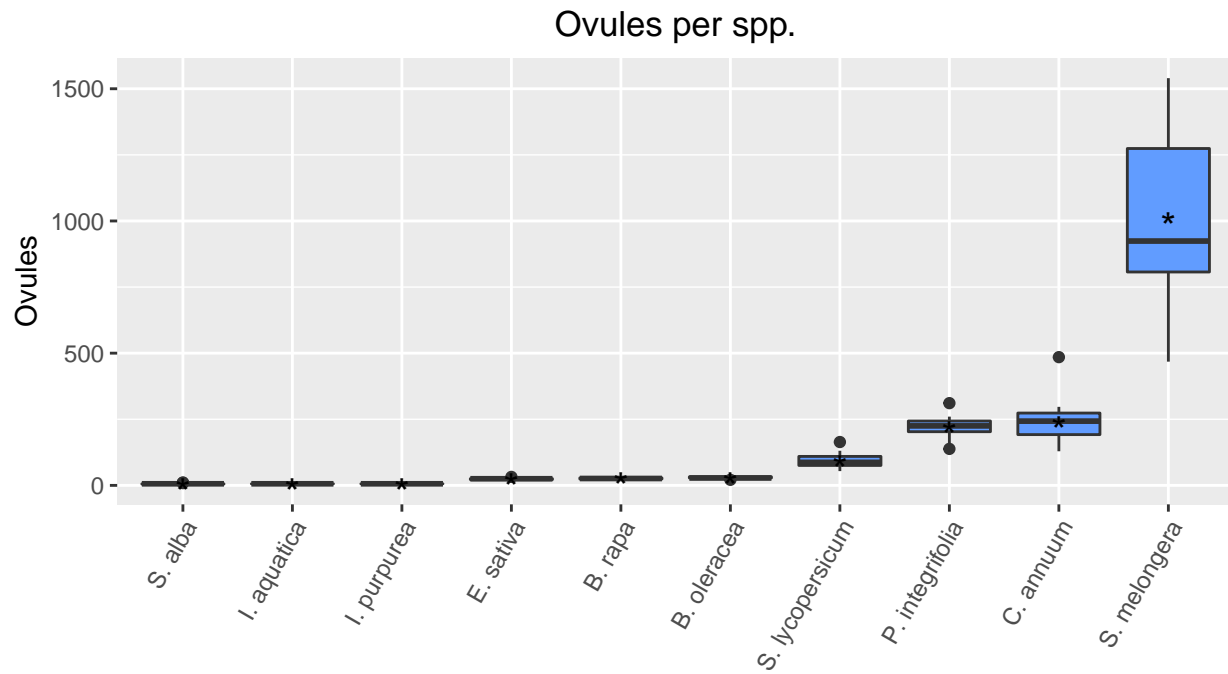
Ipomoea aquatica



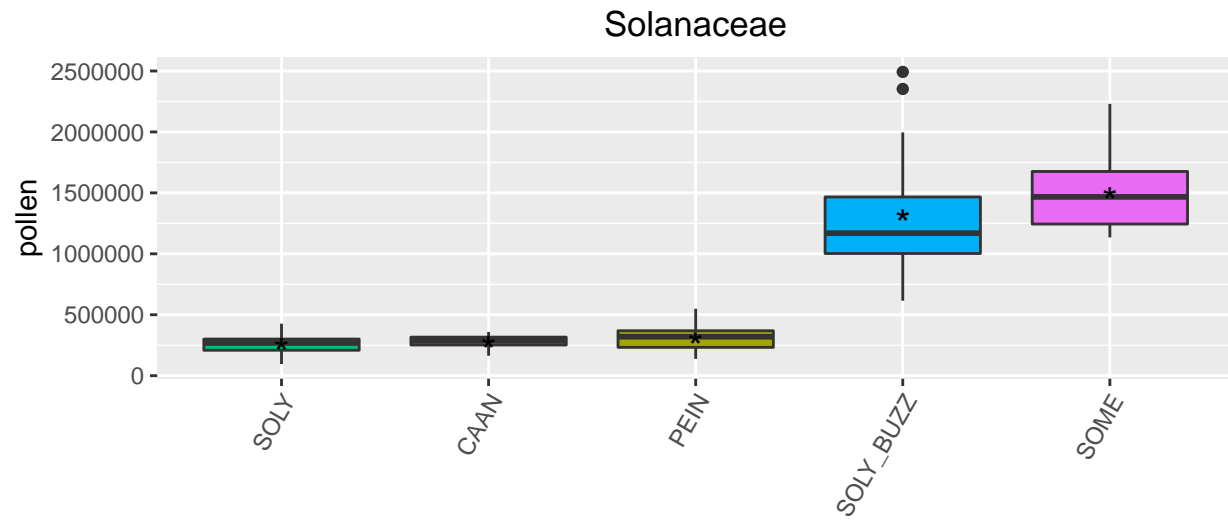
Ipomoea purpurea

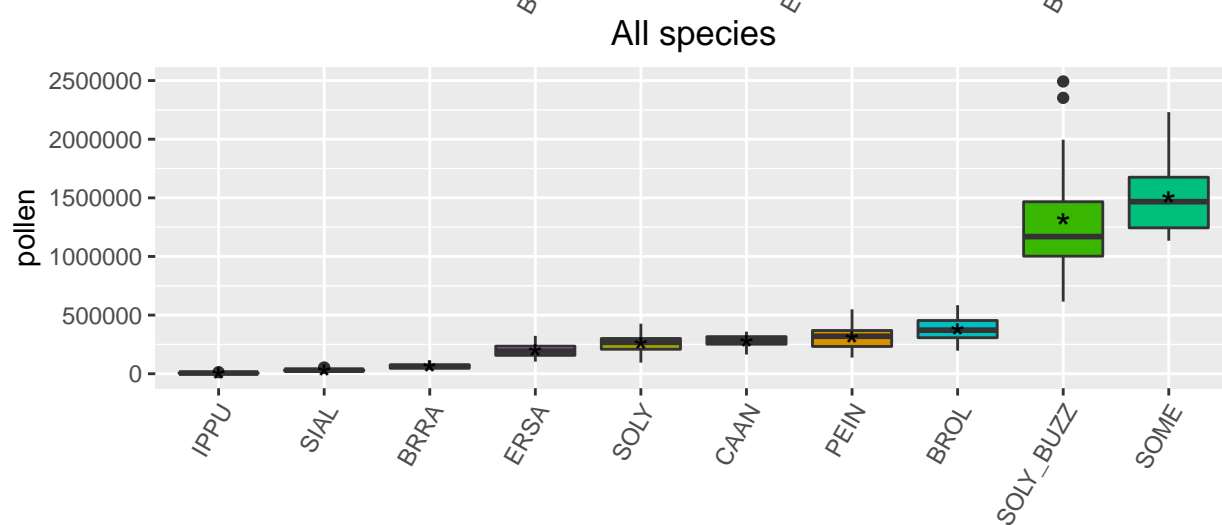
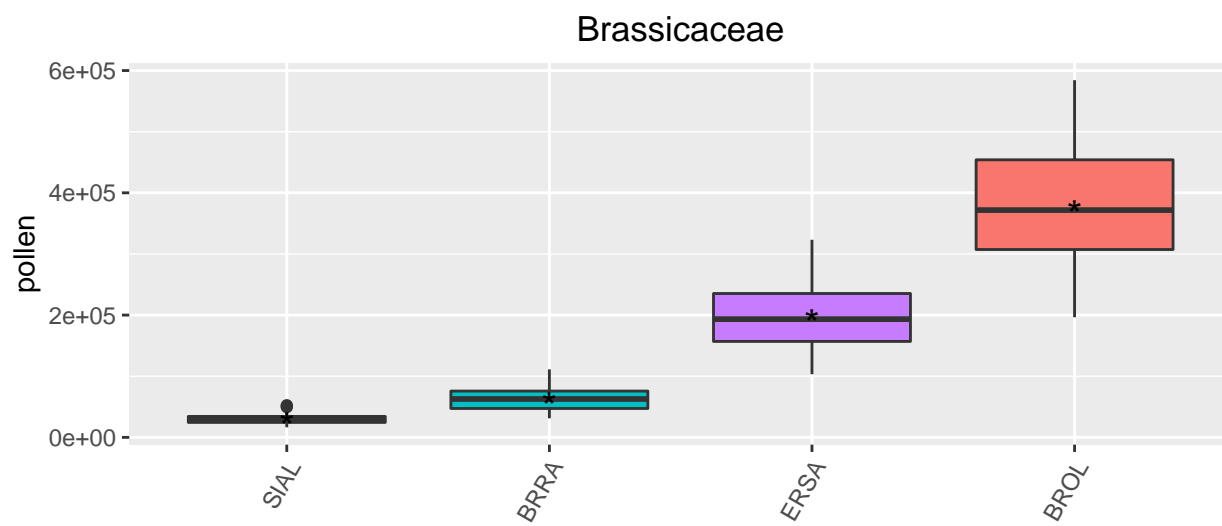


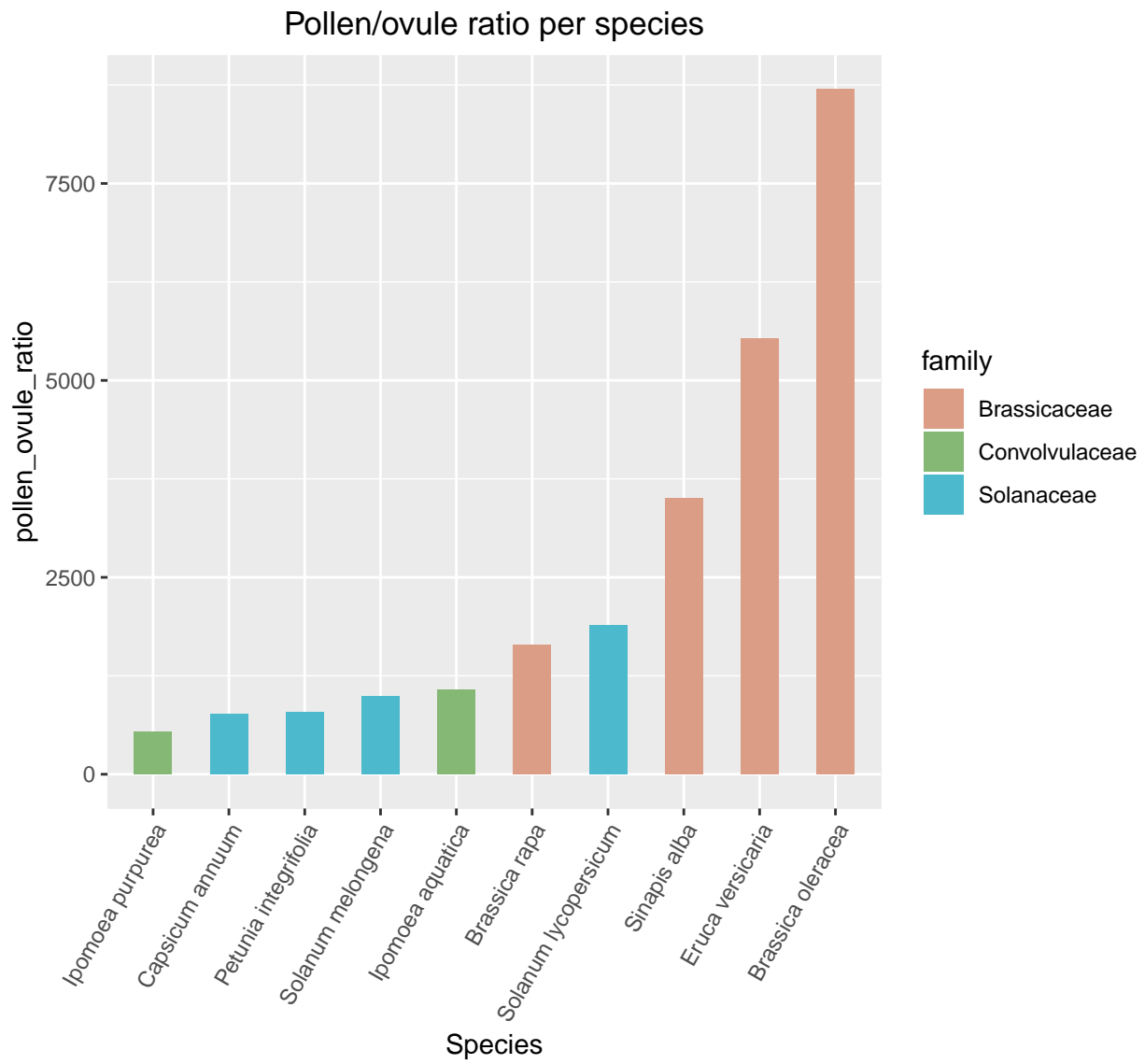


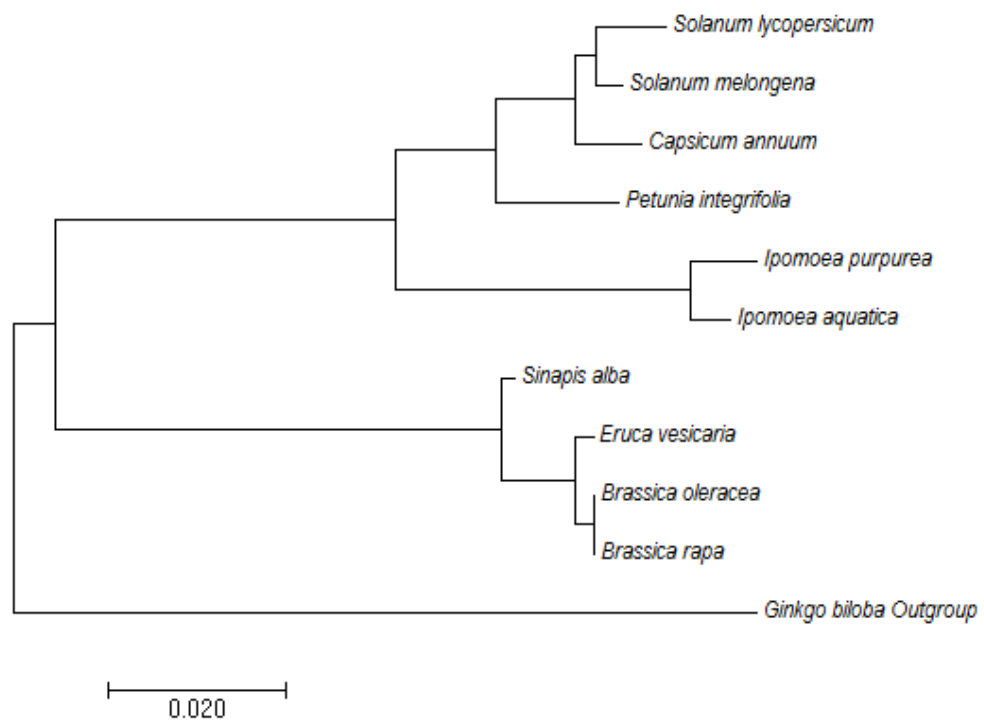


Pollen per anther, just one Convolvulaceae at the moment



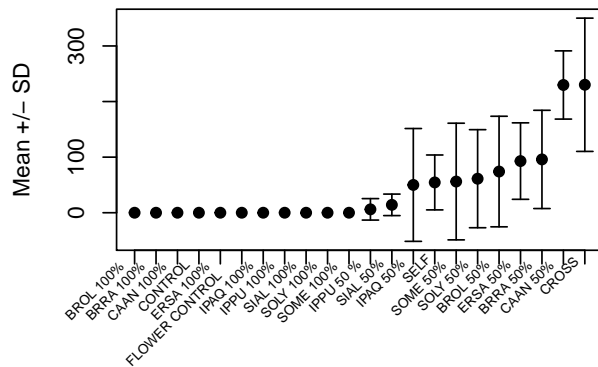




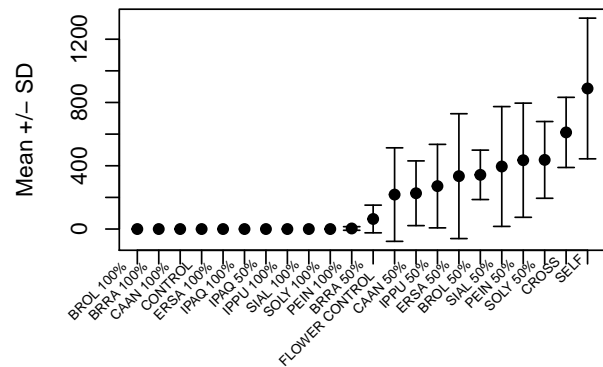


```
## 'data.frame': 22 obs. of 3 variables:
## $ Treatment: chr "BROL 100%" "BROL 50%" "BRRA 100%" "BRRA 50%" ...
## $ avg : num 0 74.1 0 95.9 0 ...
## $ sdev : num 0 99.4 0 88.4 0 ...
```

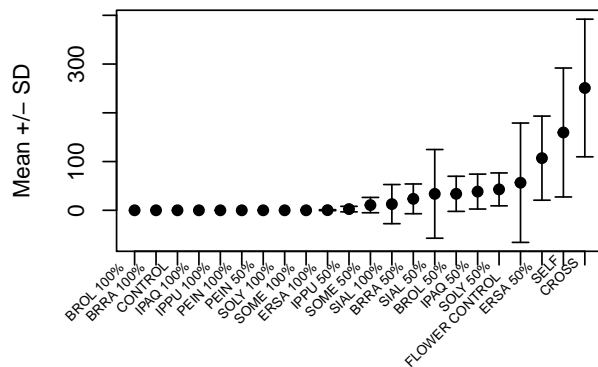
Petunia integrifolia



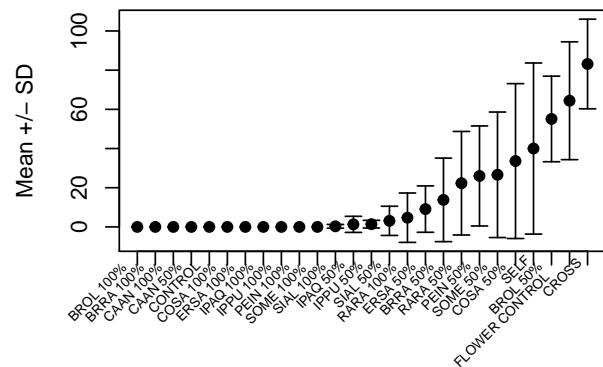
Solanum melongena

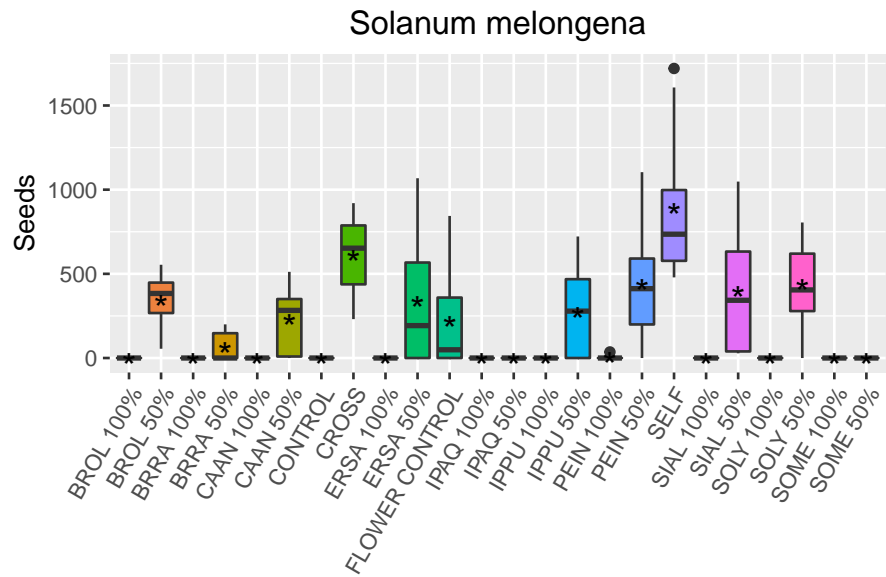
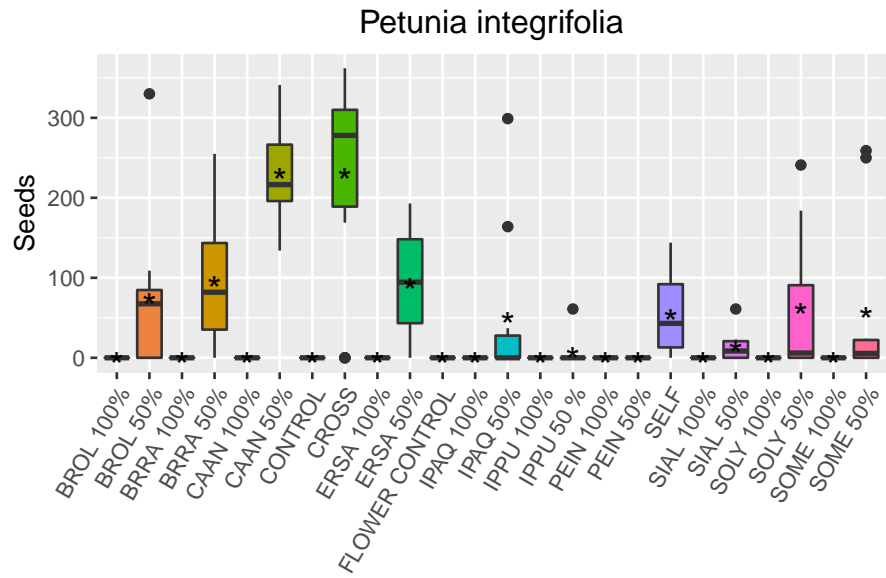


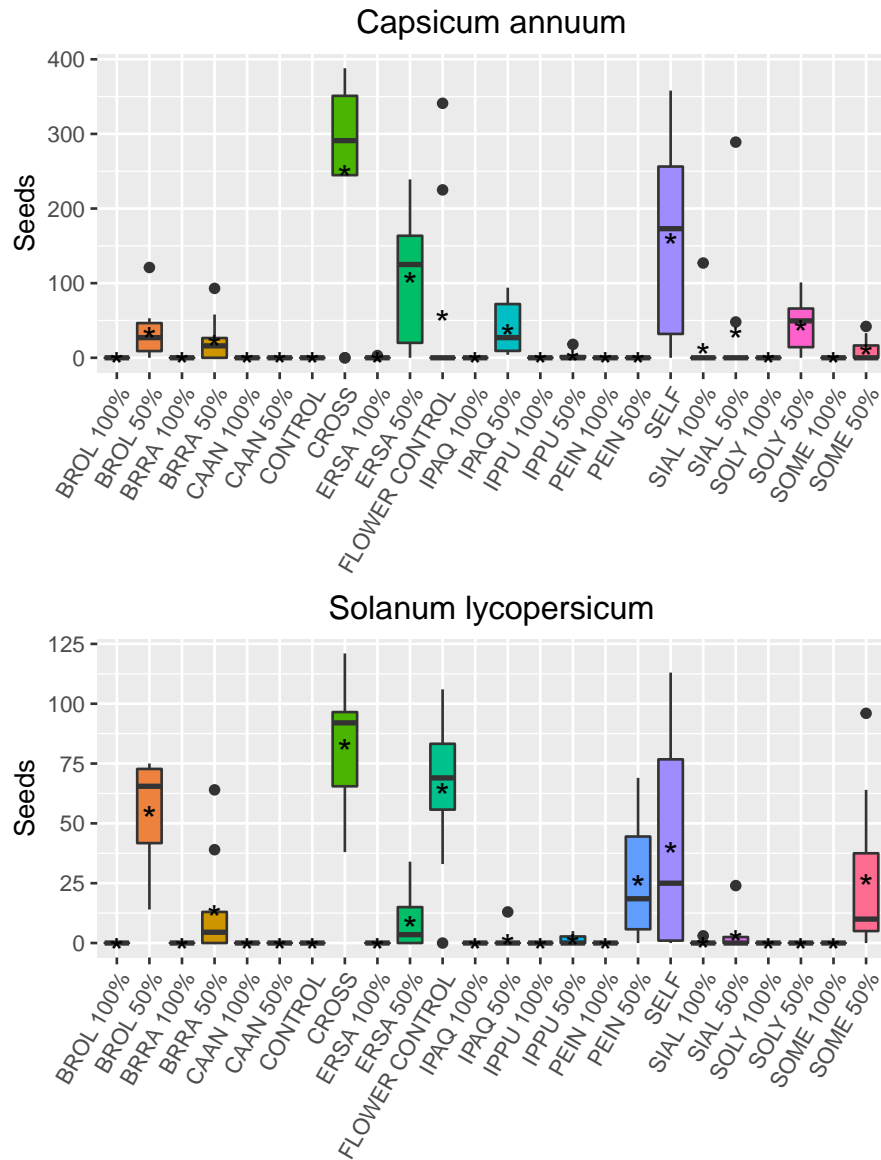
Capsicum annum



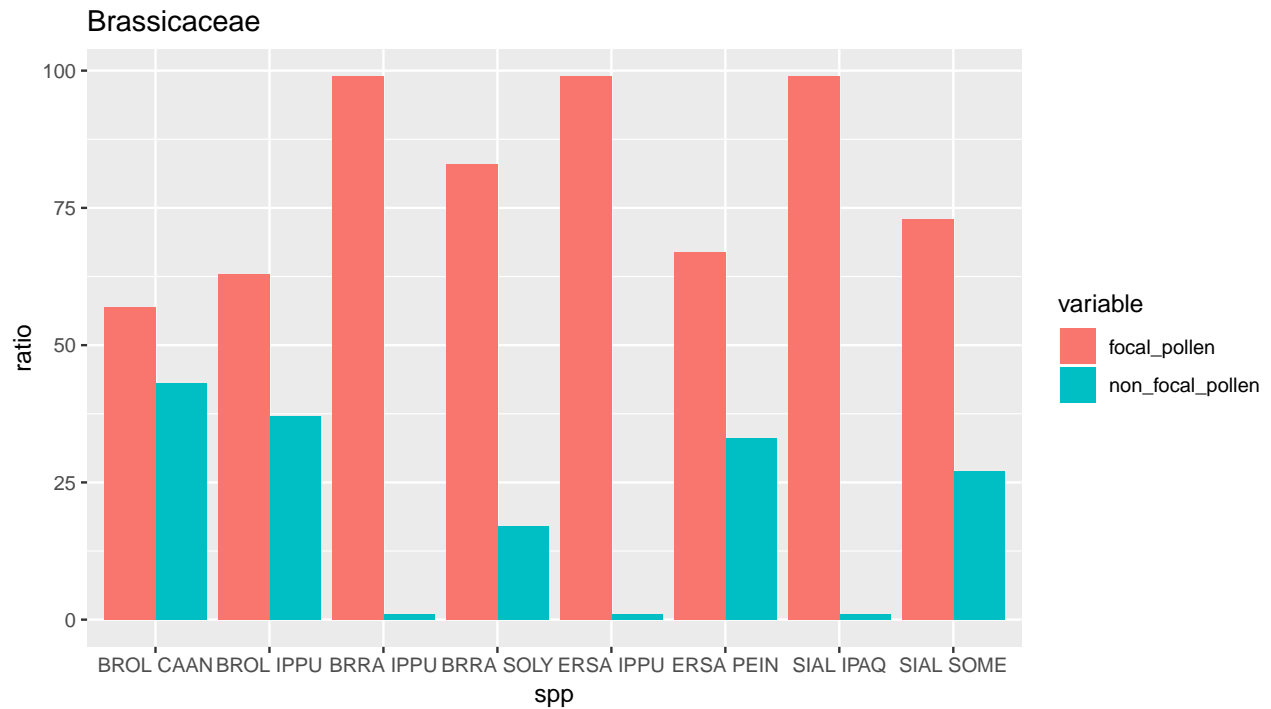
Solanum lycopersicum



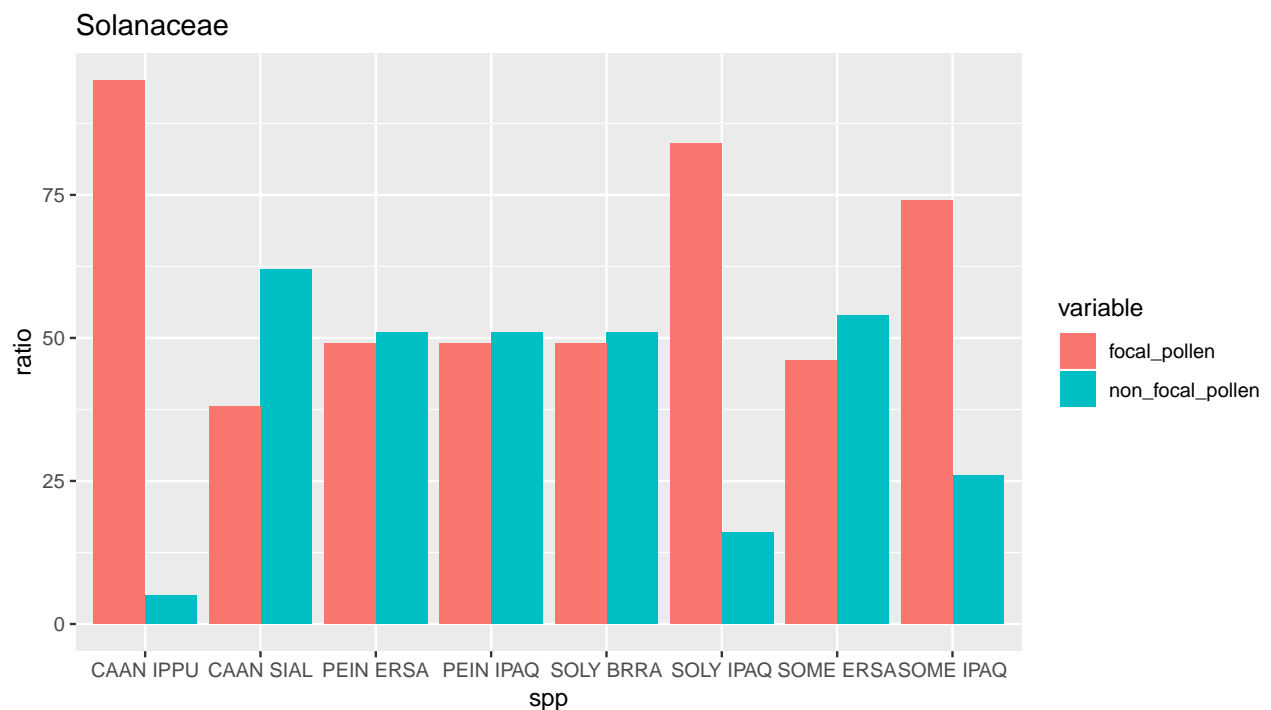




```
pollen_ratios_brassicaceae <- read.csv("Data/pollen_ratios_brassicaceae.csv", header = T)
ggplot(pollen_ratios_brassicaceae, aes(x=spp, y=ratio, fill=variable)) +
  geom_bar(stat='identity', position='dodge') + labs(title="Brassicaceae")
```



```
pollen_ratios_solanaceae <- read.csv("Data/pollen_ratios_solanaceae.csv", header = T)
ggplot(pollen_ratios_solanaceae, aes(x=spp, y=ratio, fill=variable)) +
  geom_bar(stat='identity', position='dodge') + labs(title="Solanaceae")
```



```
pollen_ratios_convolvulaceae <- read.csv("Data/pollen_ratios_convolvulaceae.csv", header = T)
ggplot(pollen_ratios_convolvulaceae, aes(x=spp, y=ratio, fill=variable)) +
  geom_bar(stat='identity', position='dodge') + labs(title="Convolvulaceae")
```

