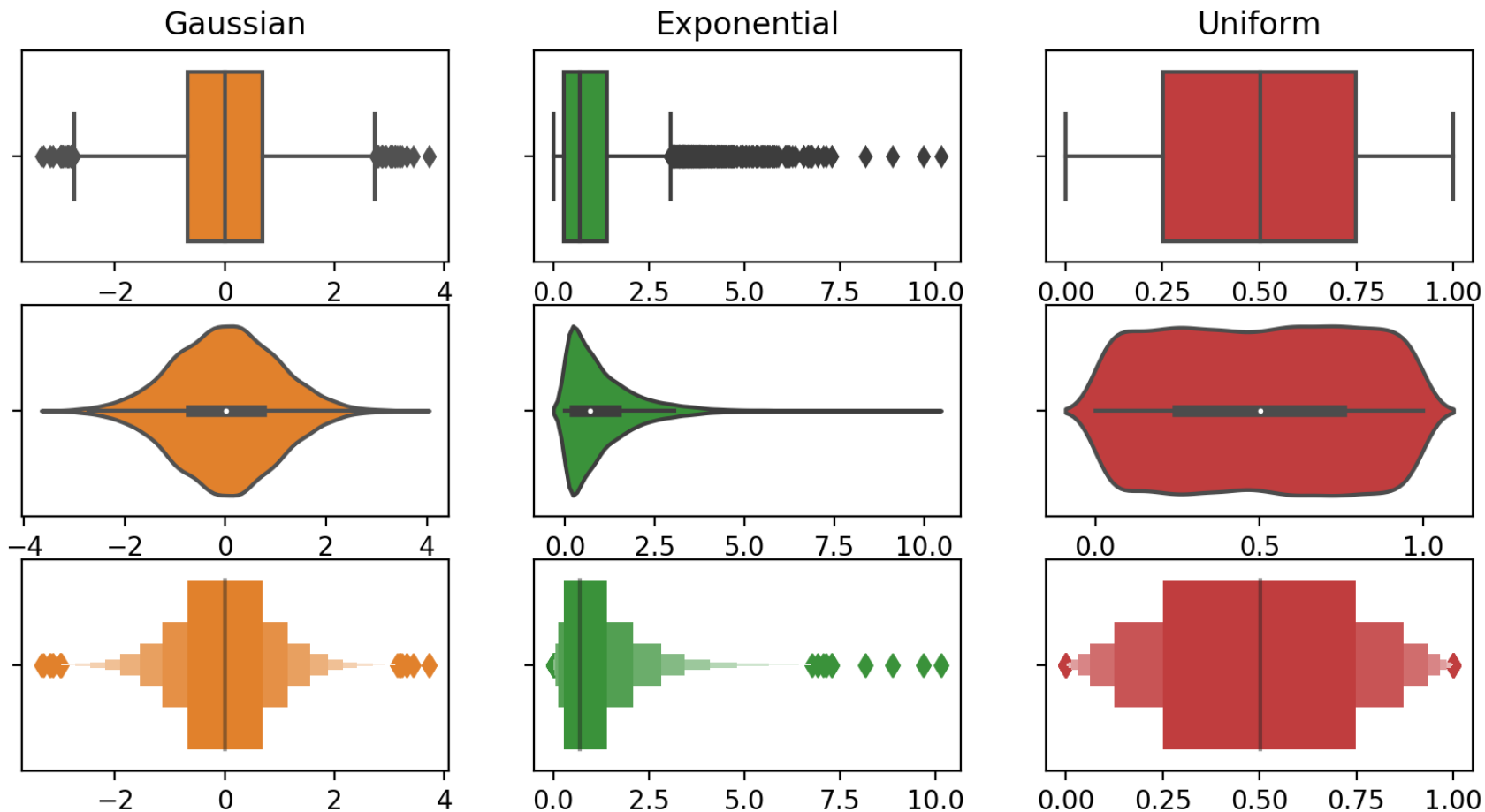
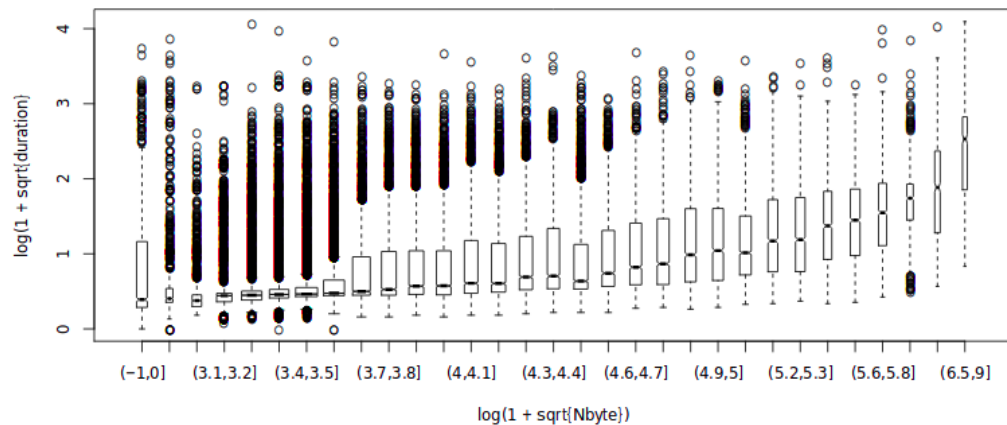
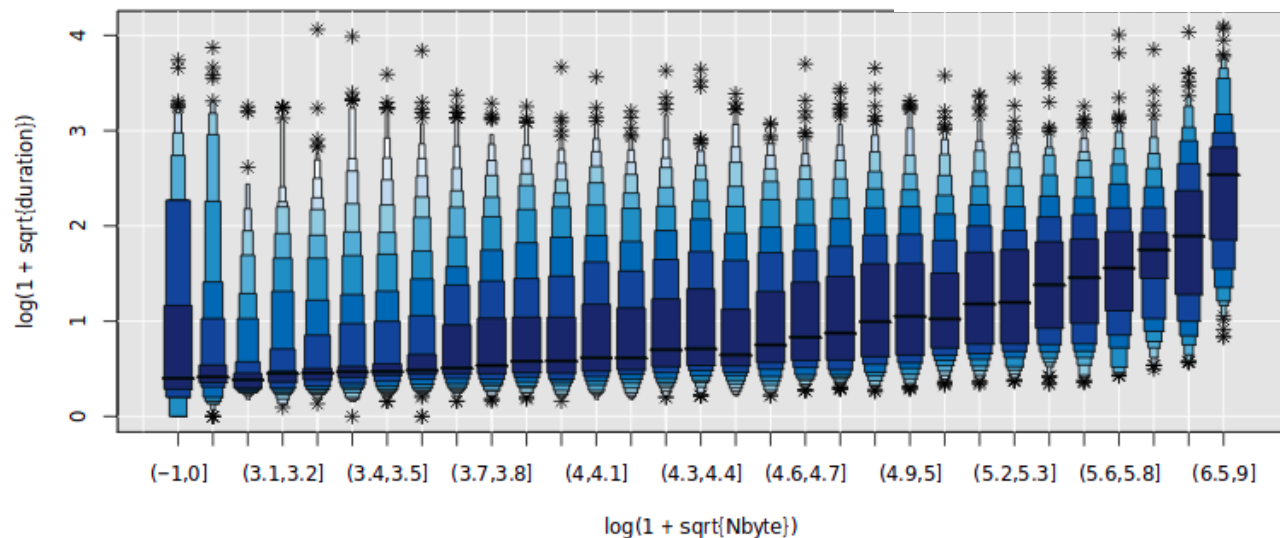


# Boxenplot



- Боксплоты для больших распределений, с выбросами

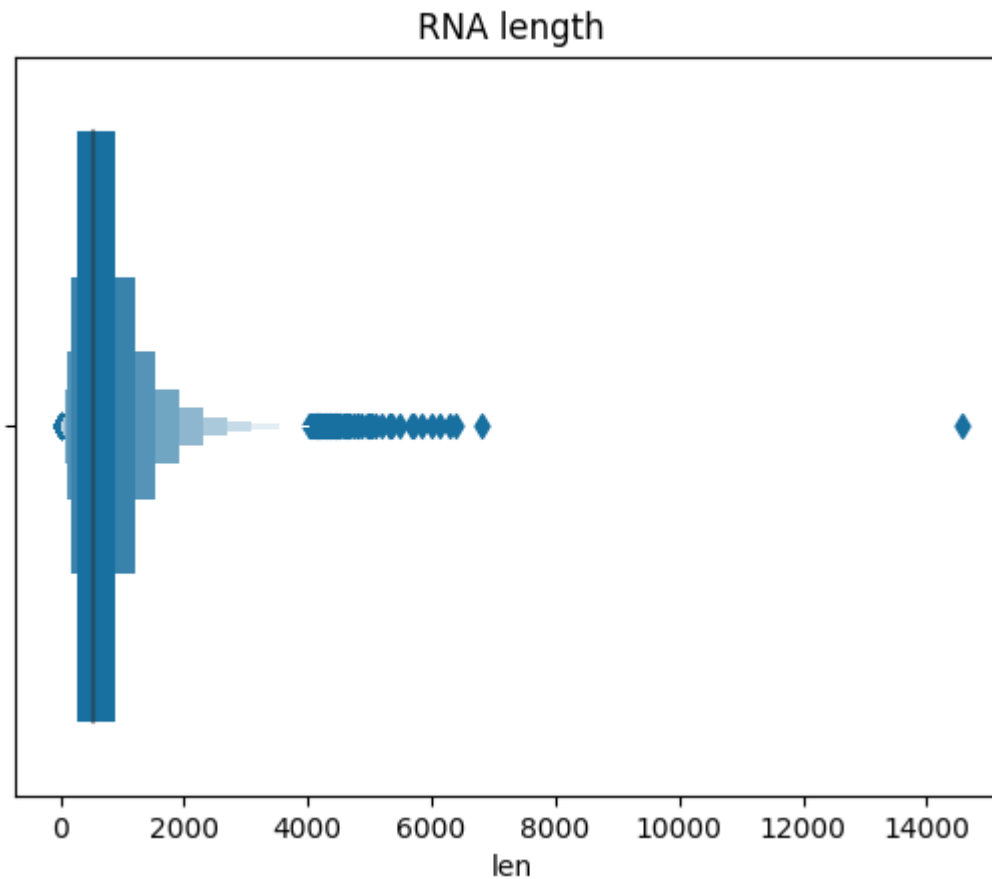


```
import seaborn as sns
import matplotlib.pyplot as plt
```

```
gr = sns.boxenplot(x=a)
```

```
# a — список или массив
```

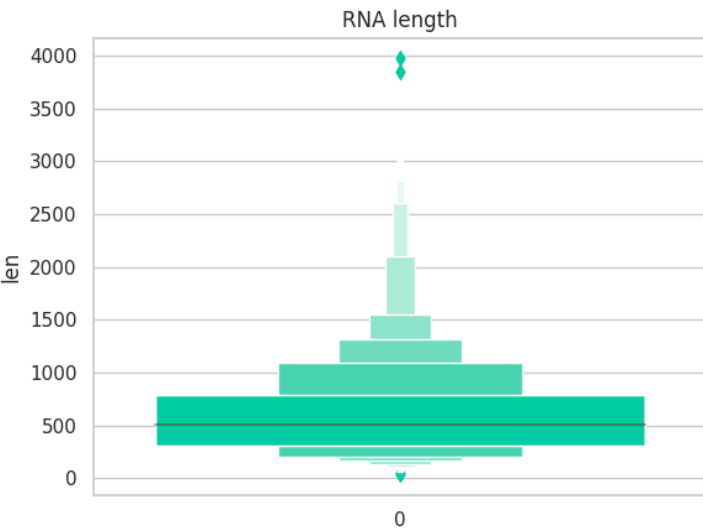
```
gr.set(xlabel = "len")
plt.title("RNA length")
plt.show()
```



```
gr = sns.boxenplot(data=a, orient="v", palette="Set2",
```

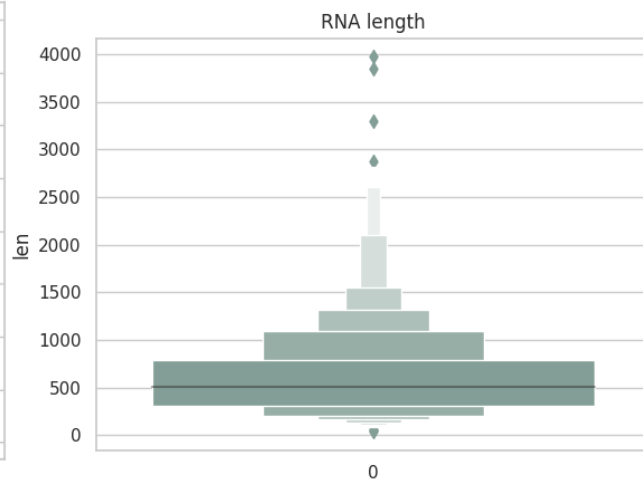
```
k_depth='trustworthy',
```

```
saturation=6)
```



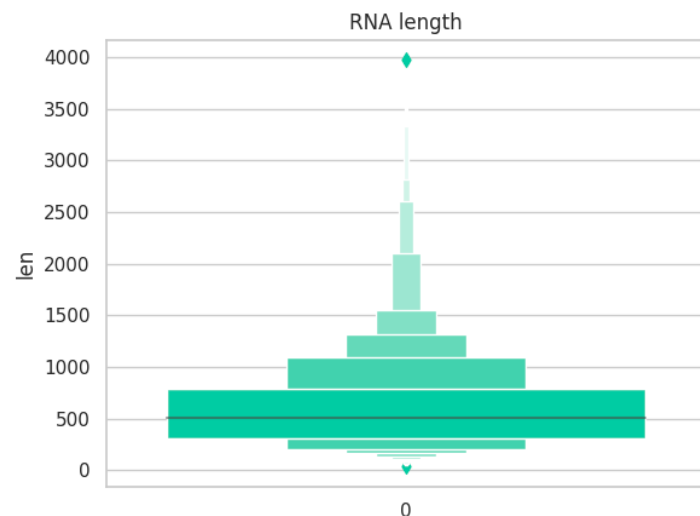
```
k_depth='tukey',
```

```
saturation=0.2)
```



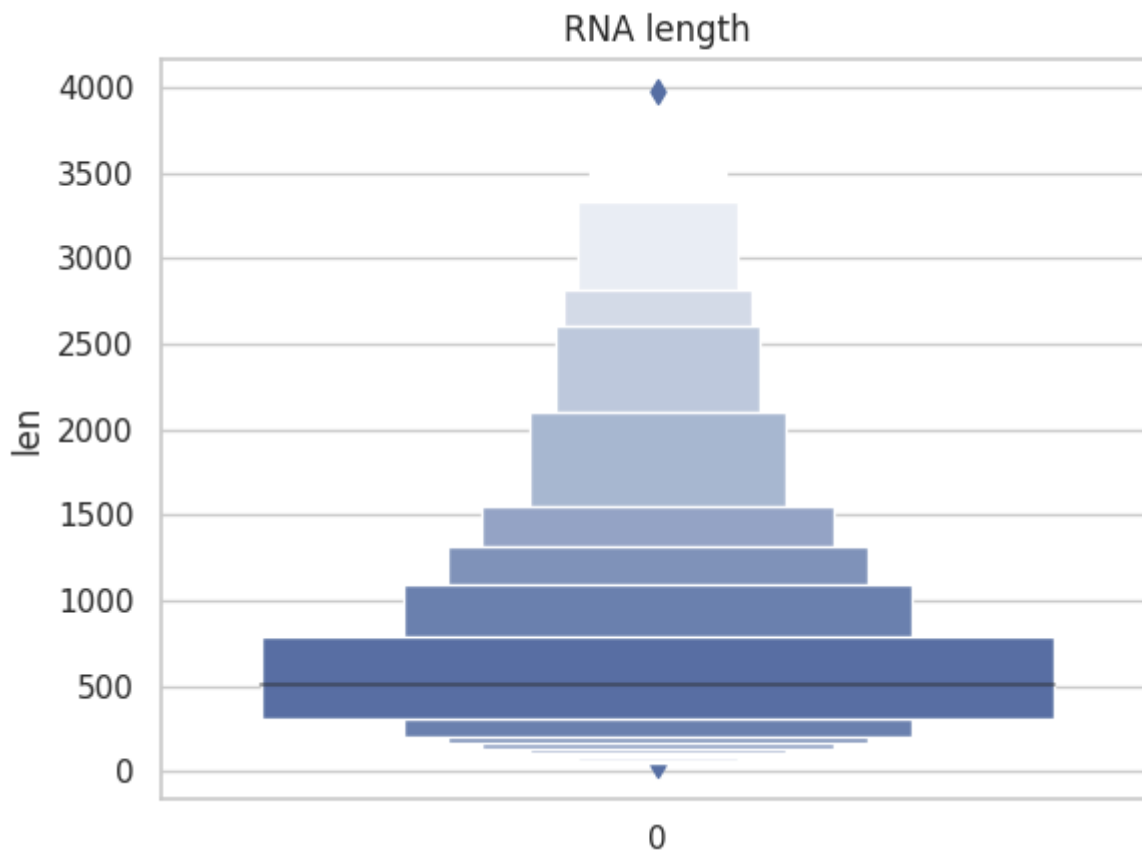
```
k_depth='proportion',
```

```
linewidth=4.5, saturation=20.2)
```



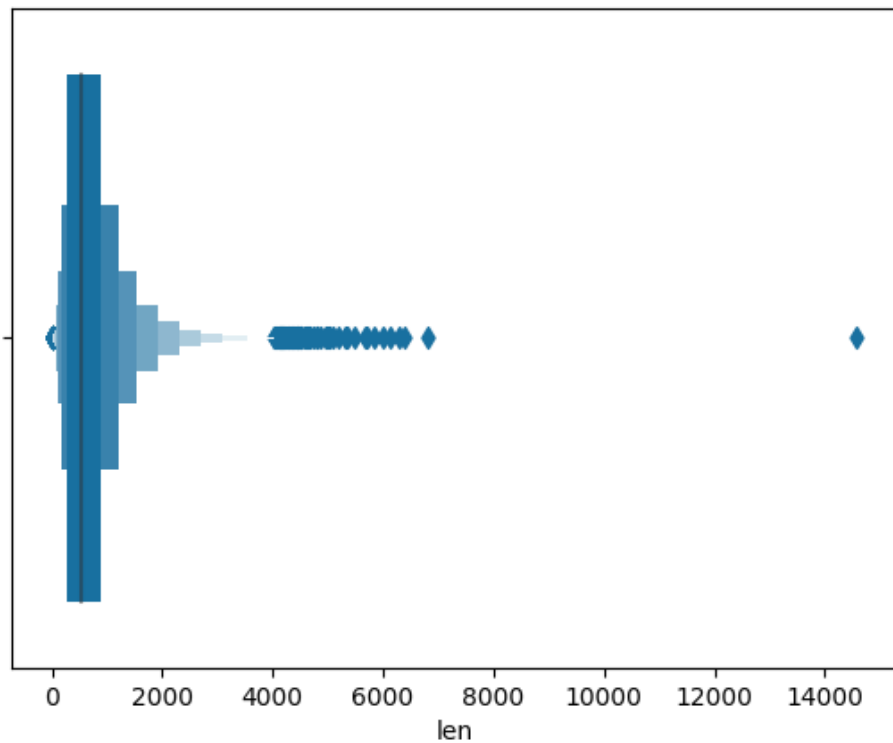
# scale="area"

- "linear"
- "exponential"

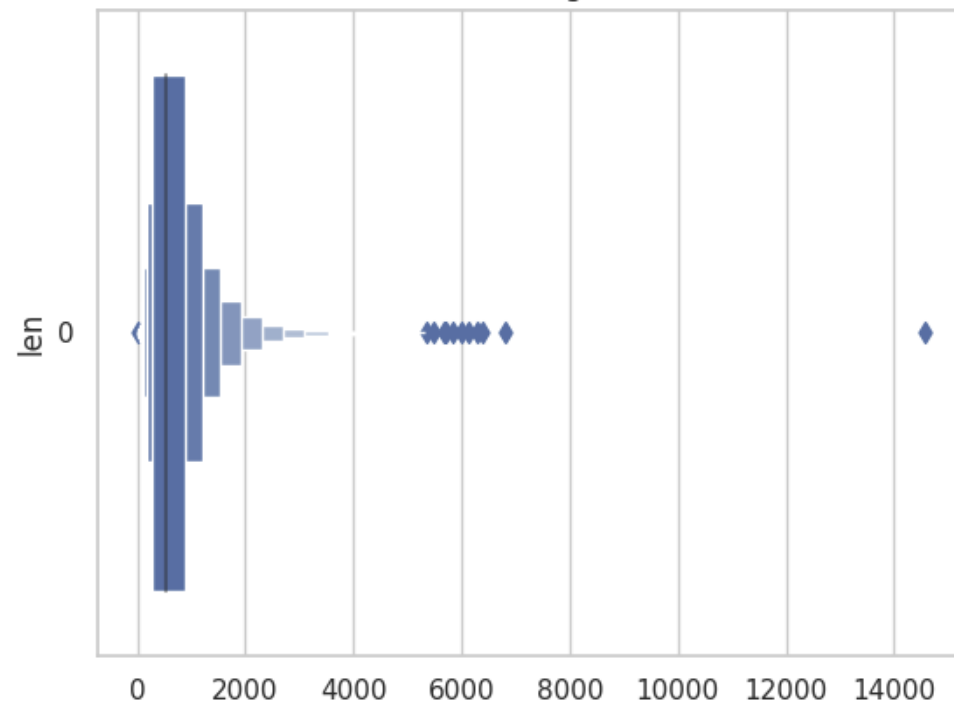


outlier\_prop=0.001

RNA length

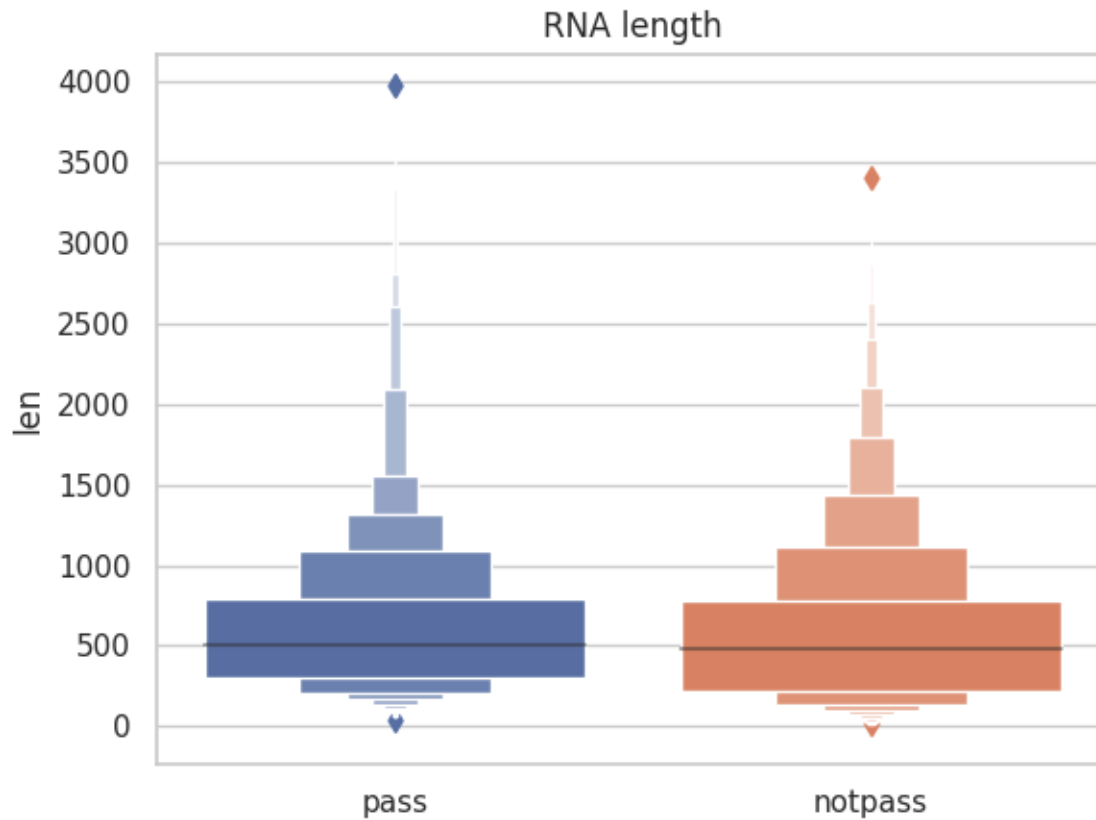


RNA length



```
da = np.array(a, dtype=[("vec", "int"), ("fac", "U10")])
```

```
gr = sns.boxenplot(x=da["fac"], y=da["vec"])
```



```
gr = sns.boxenplot(x=da["fac"], y=da["vec"], hue=da["fac2"], orient="v")
```

