**Question 1**

**Run the Nanoplot command. What is the mean read length in your .txt file?**

7,039.6 (with margin: 1)

**Question 2**

**What is the total length of your Flye assembled sequence. This will appear at the bottom of the Flye code block where you ran your Flye command on the given sample**

187,760

**Question 3**

**Using the bandage tool, how many pieces did your chloroplast genome assembly come out in?**

**1**

**2**

**3**

**4**

**Question 4**

**How many overall chloroplast variants were observed?**

**5**

**7**

**12**

**37**