Characteristics of genome with extended alphabet

Biopython course project

Kolosov Nikita
Boris Shpak
Katerina Gibitova

2019

Task

- Given the assembled reads of unknown origin with unknown “nucleotides” extract some knowledge about what we are dealing with.

- Characterise sequence from standpoint of string sequence analysis.

After assembly: 3 “chromosomes”

1) 300454
2) 300454

1

3) 402937
4) 402937

2

5) 300001
6) 300001

3

Forward:

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 'T': 0.1778,
 'O': 0.1524,
 'I': 0.1611,
 'B': 0.1761,
 'N': 0.1778}
```

Reversed:

```
{'S': 0.1761,
 'T': 0.1778,
 'O': 0.1524,
 'I': 0.1778,
 'B': 0.1547,
 'N': 0.1611}
```

Forward:

```
{'S': 0.1547,
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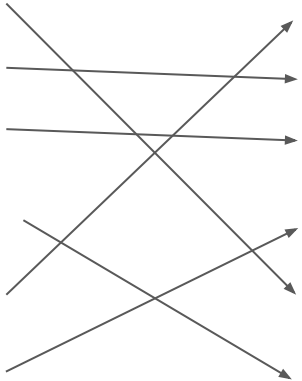
 'I': 0.1611,
 'B': 0.1761,
 'N': 0.1778}
```



Reversed:

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{'S': 0.1761,
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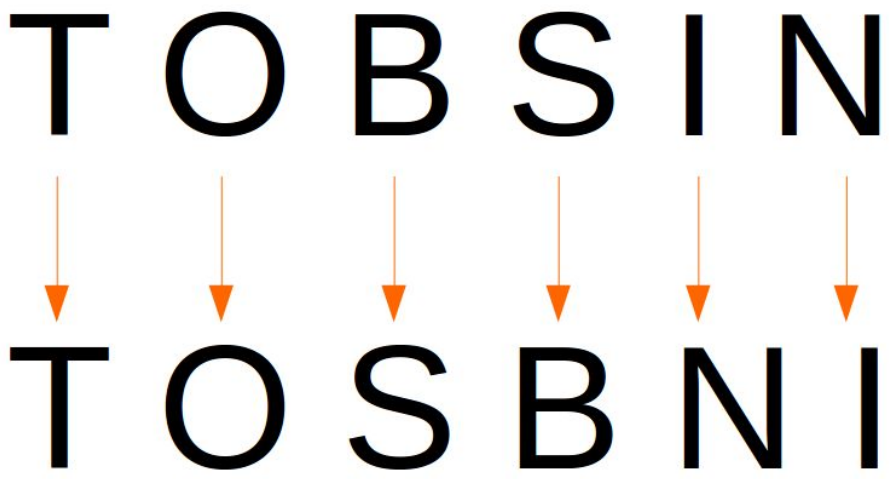
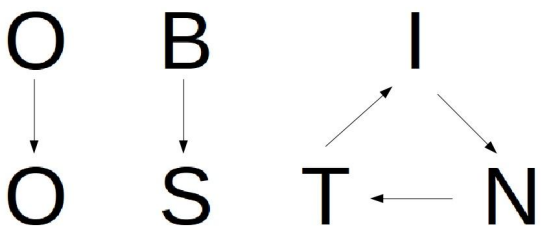
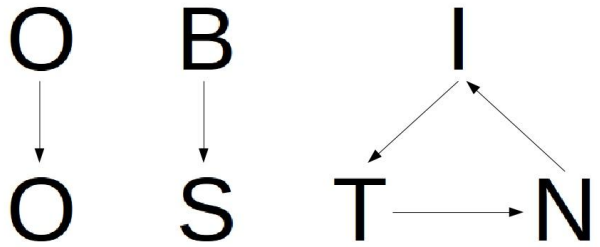

TOBSIN
TOSBNI

OR

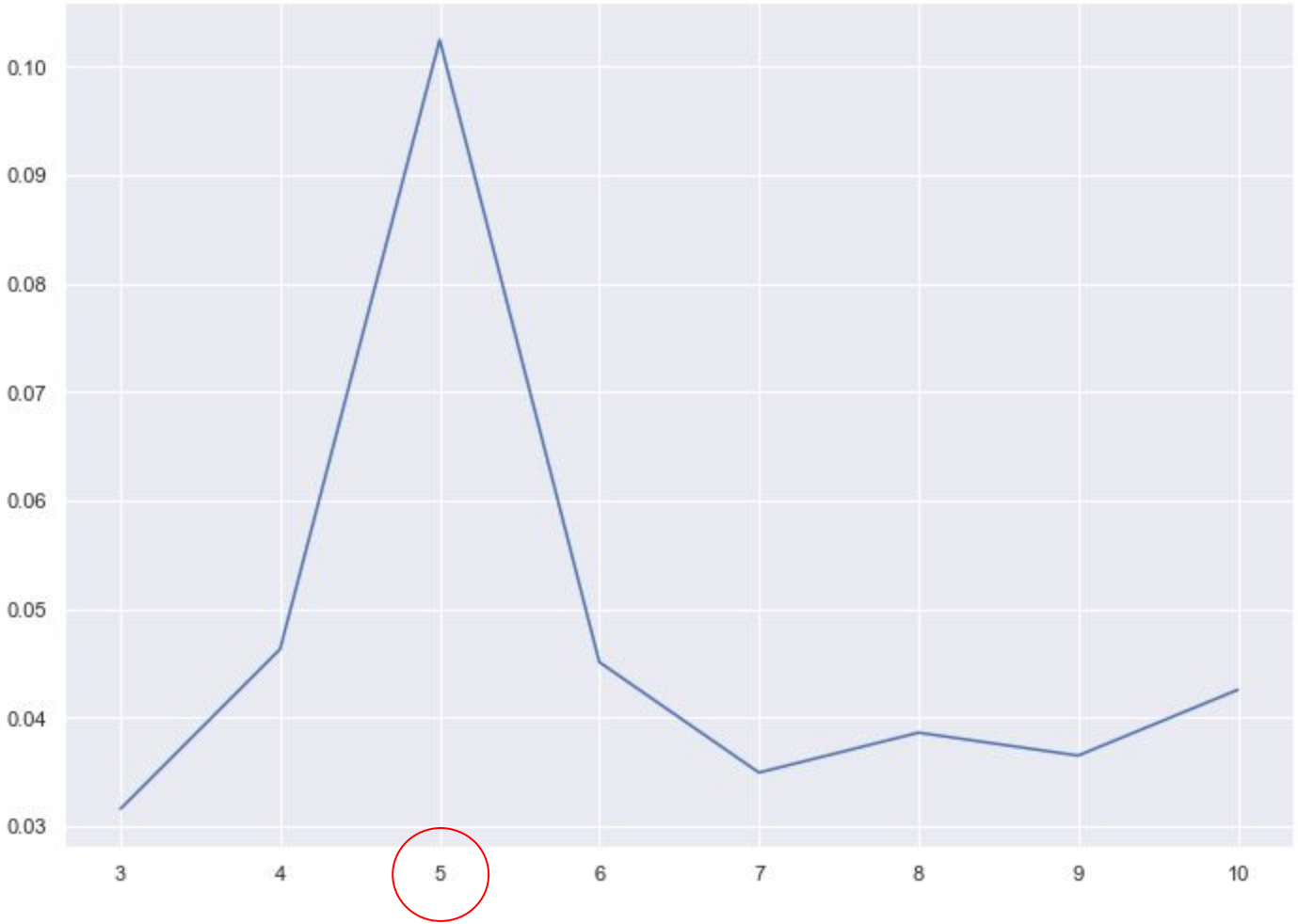
Forward



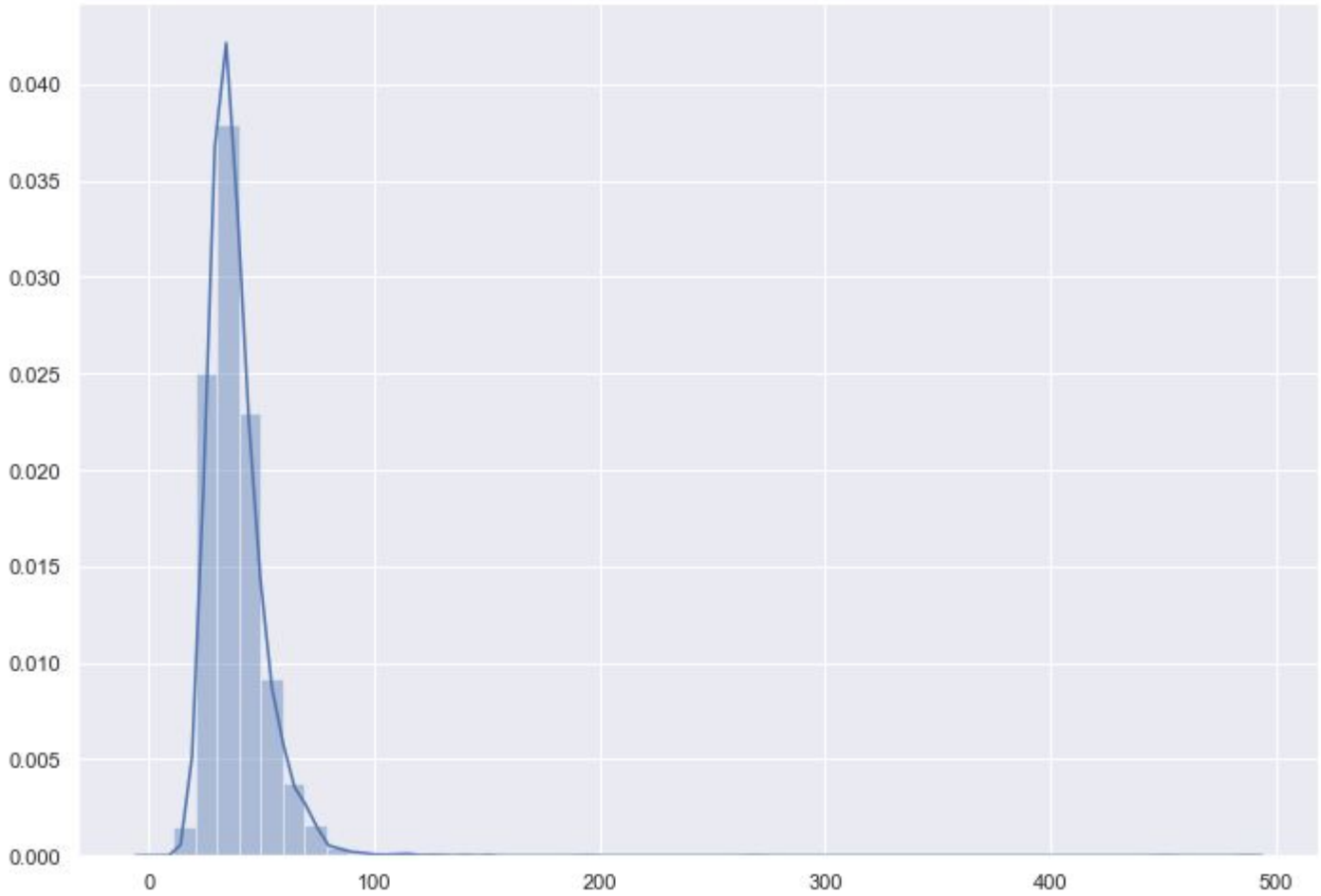
Reversed



Chromosome **1**



k = 5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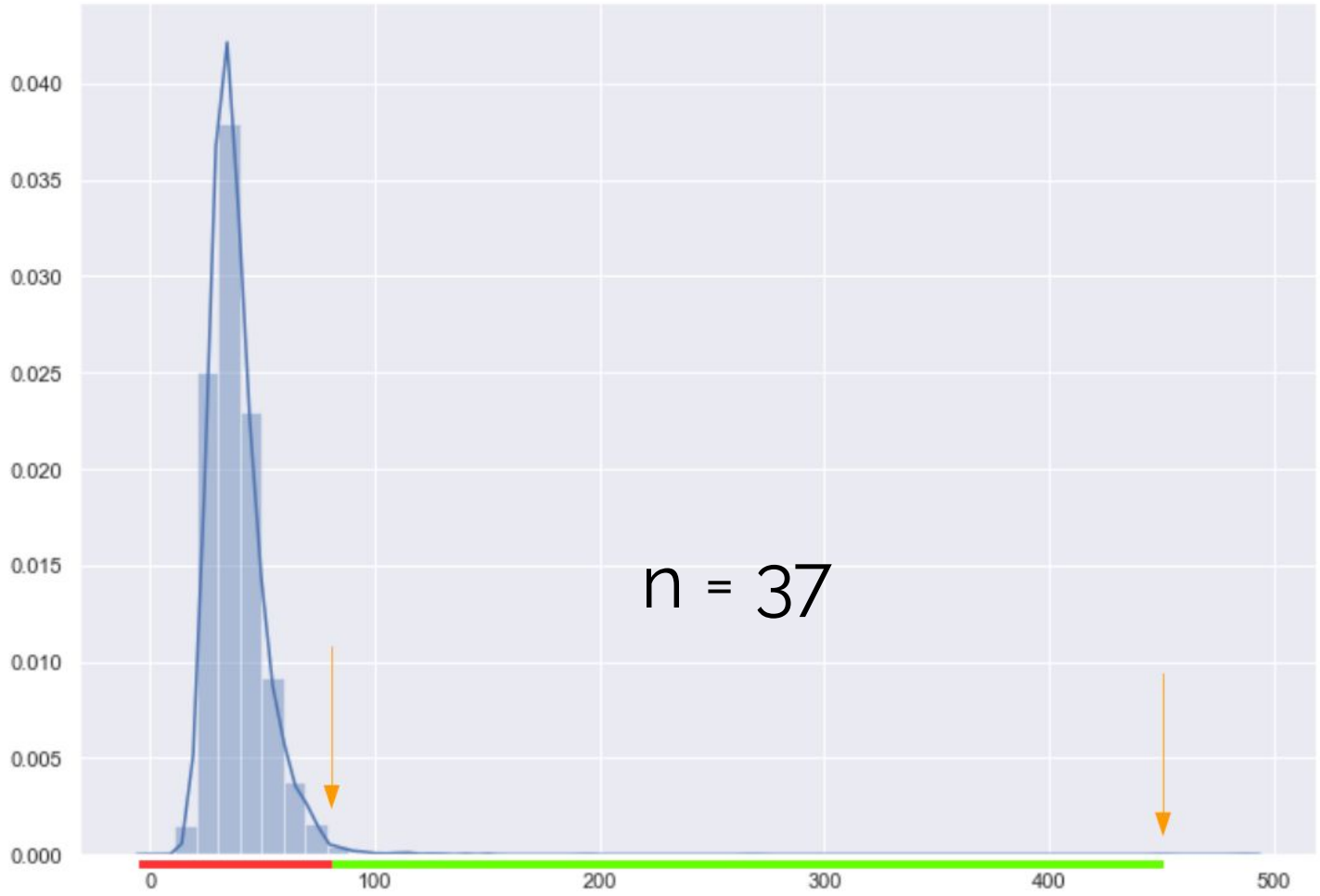
400
500

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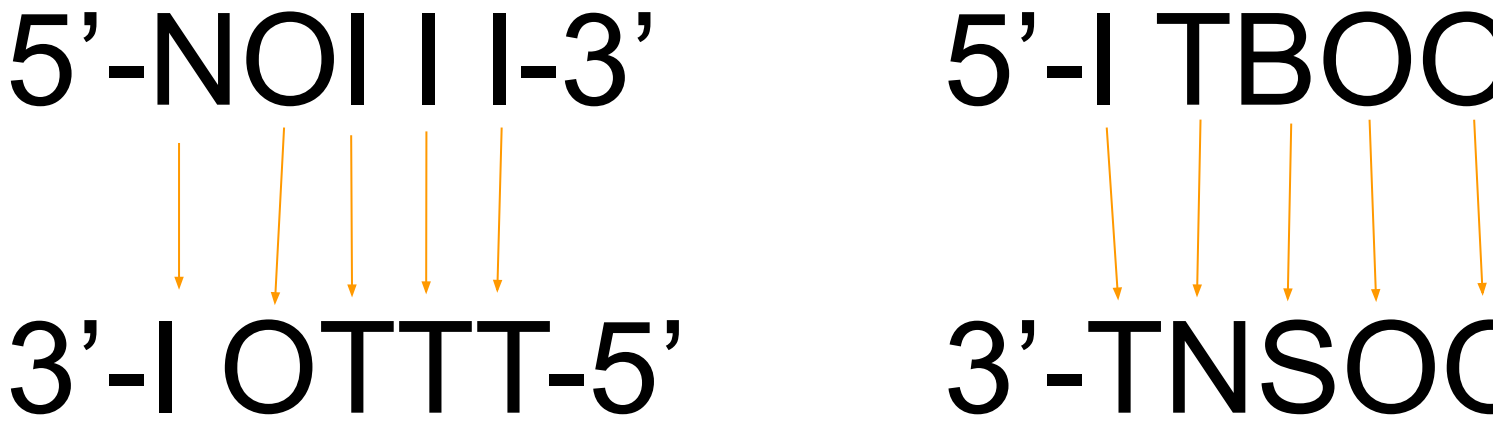
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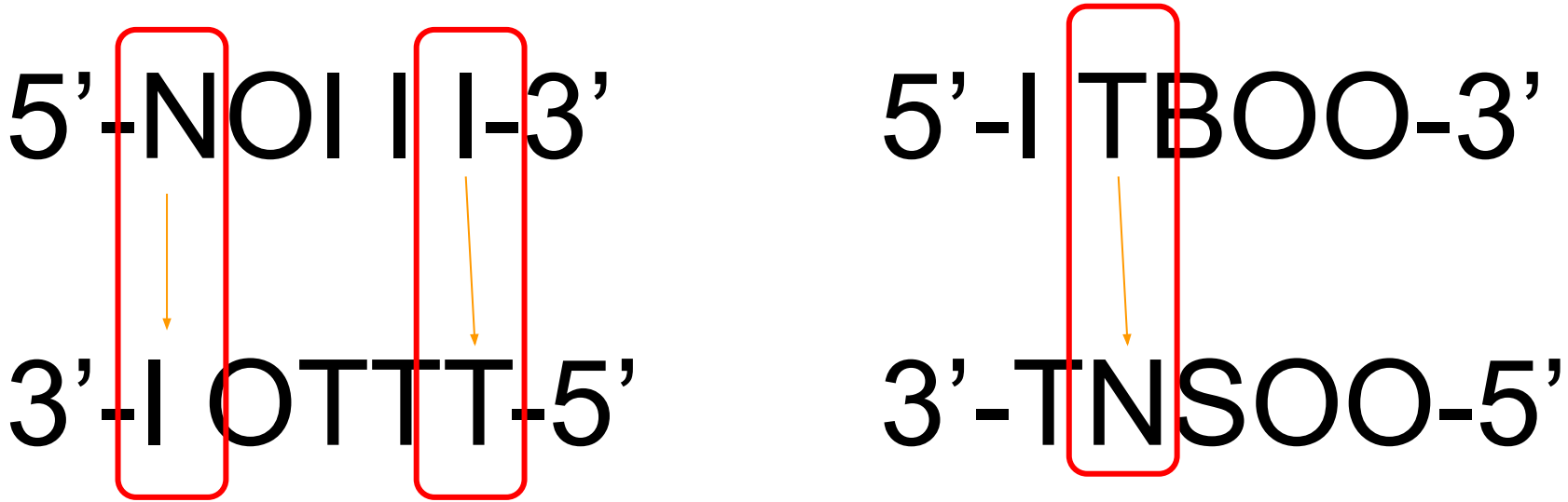
3’-I OTTT-5’
5’-I TBOO-3’
3’-TNSOO-5’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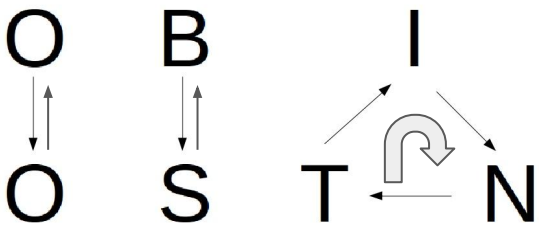
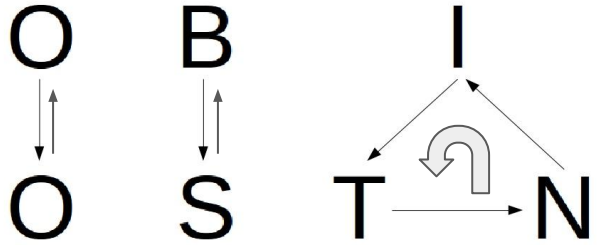
3’-I OTTT-5’
5’-I TBOO-3’
3’-TNSOO-5’

Forward

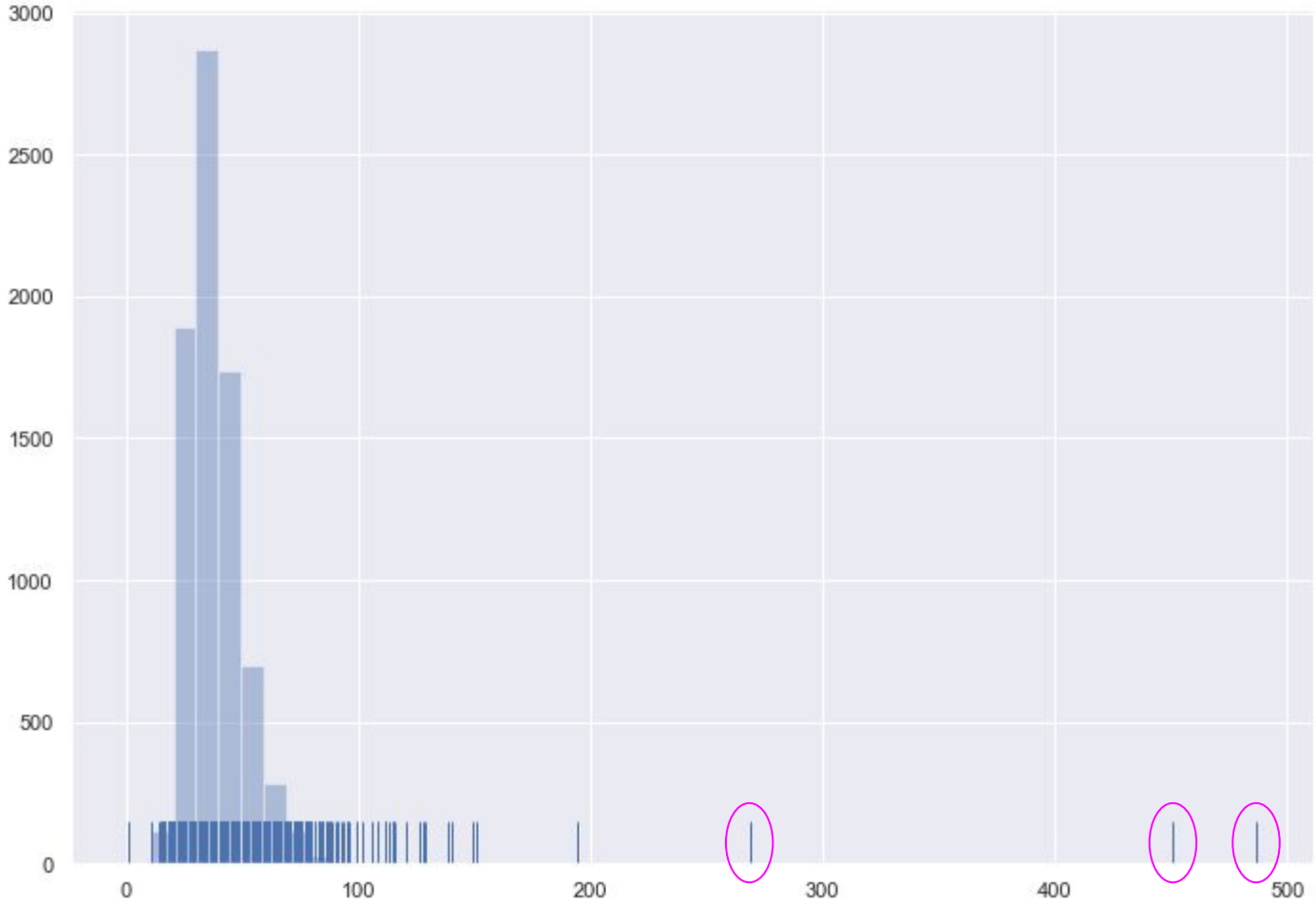


Reversed



Example: TTTOI BSNNITS

I I IONSBTTNIB

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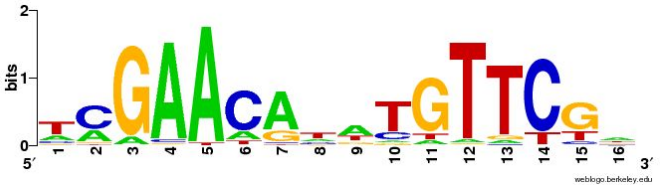
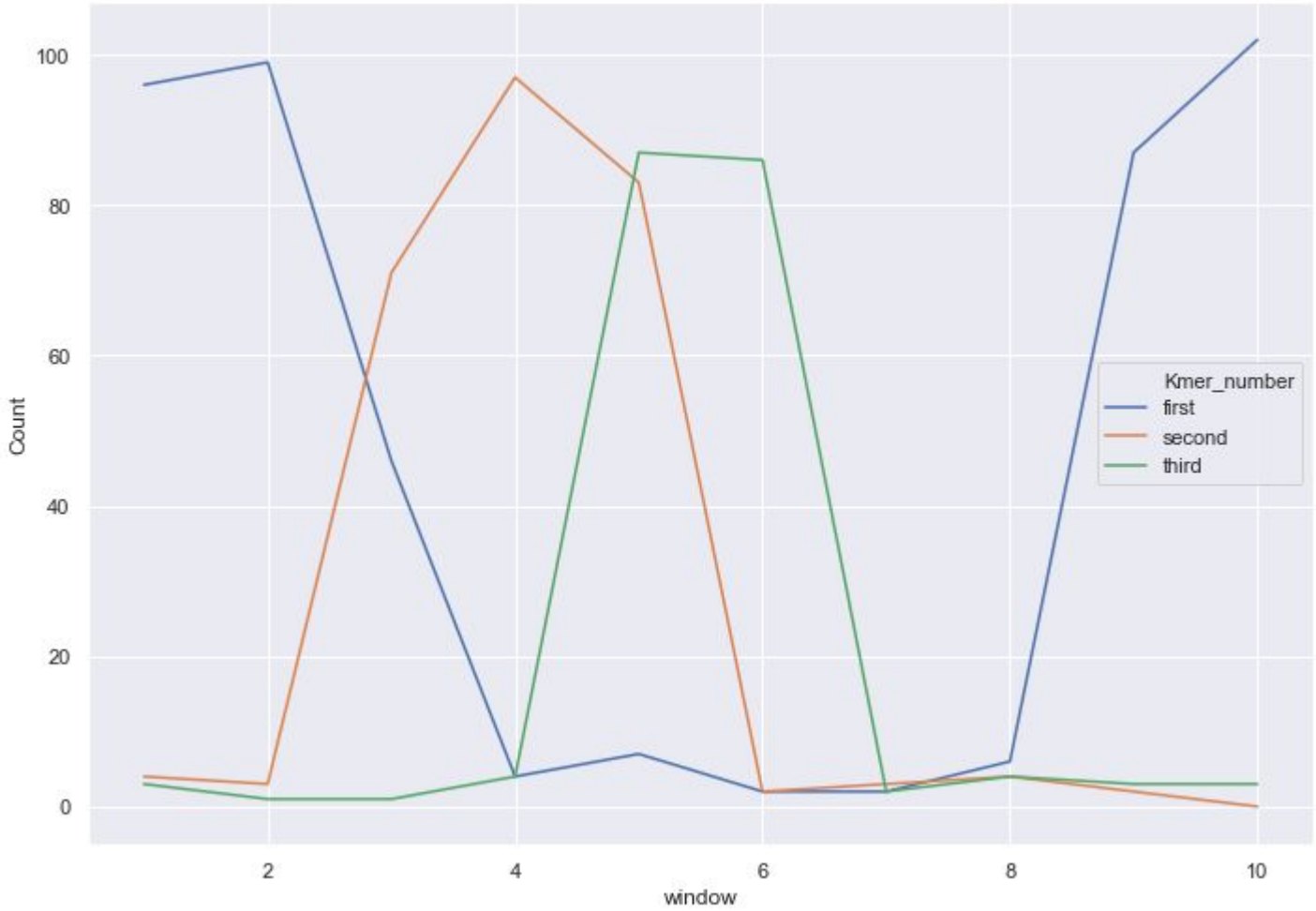
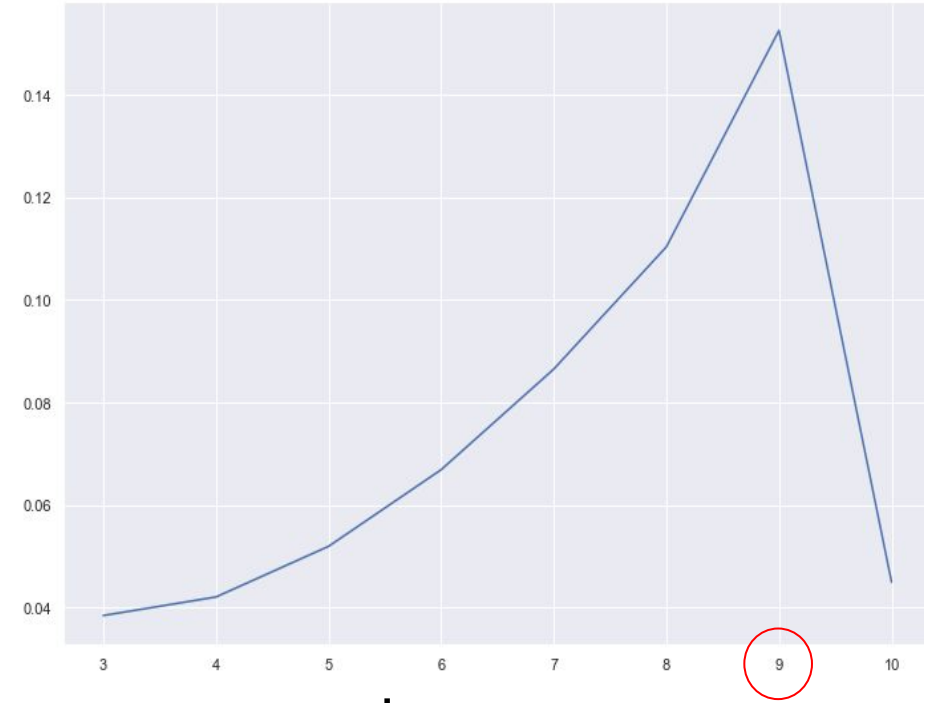
pLOGO for 'TTTOI':




100
80
60
40
20
0
Count
2
4
6
8
10
window
Kmer_number
first
second
third

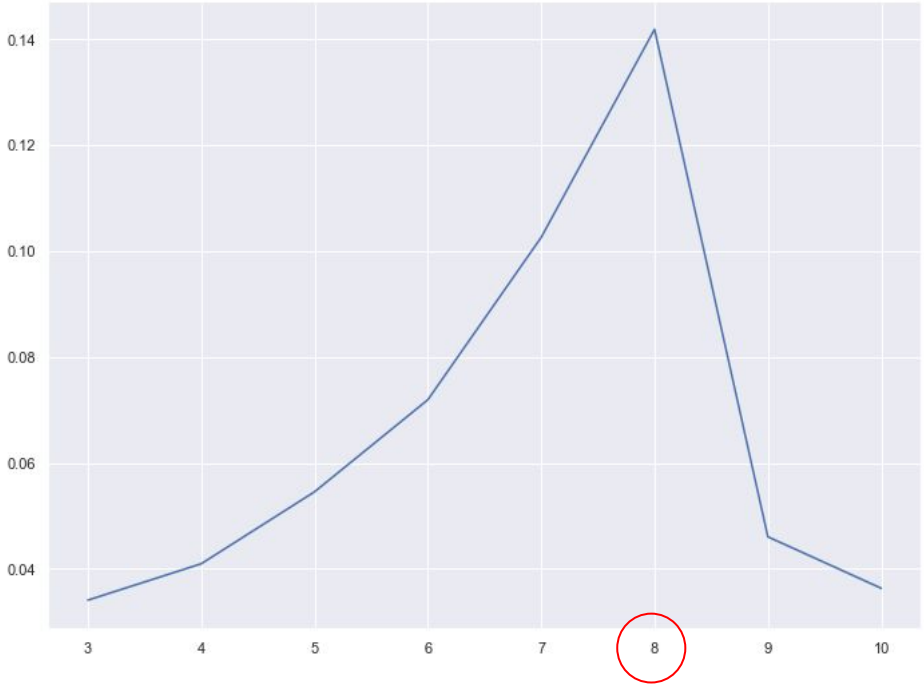
Chromosome **2** and **3**

2-nd chromosome



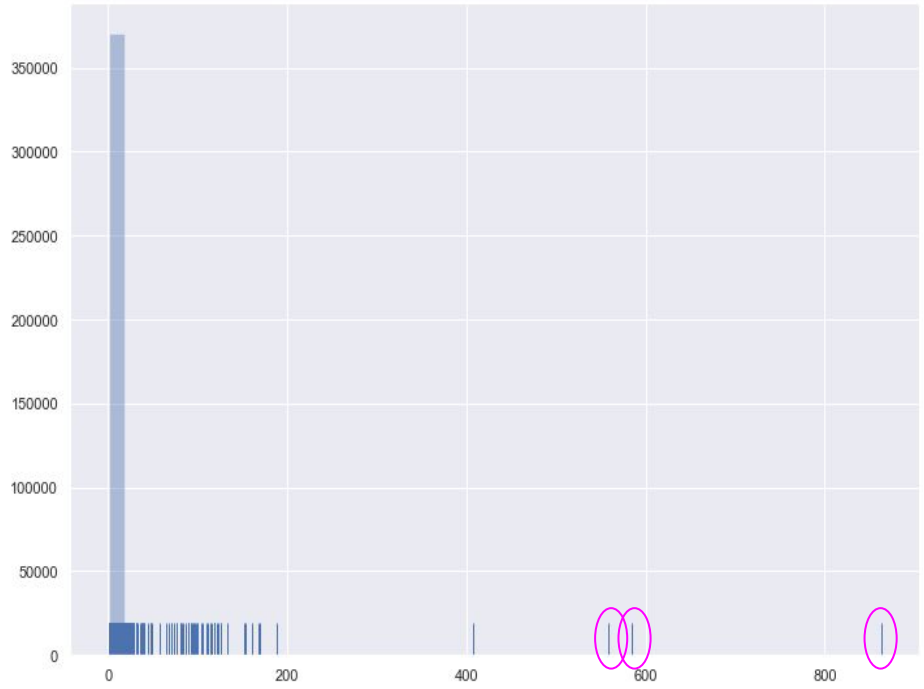
k = 9

3-d chromosome

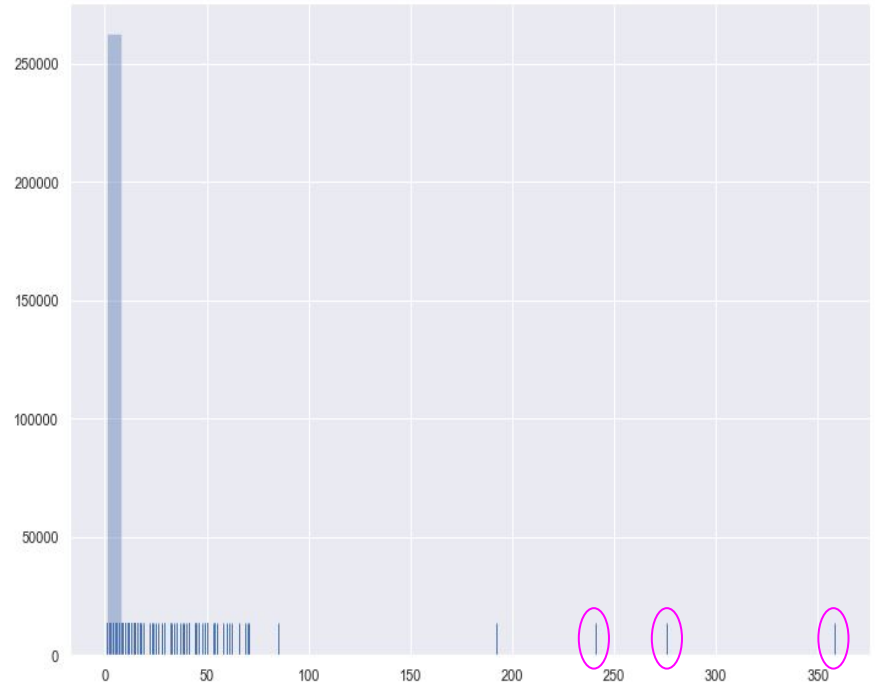


k = 8

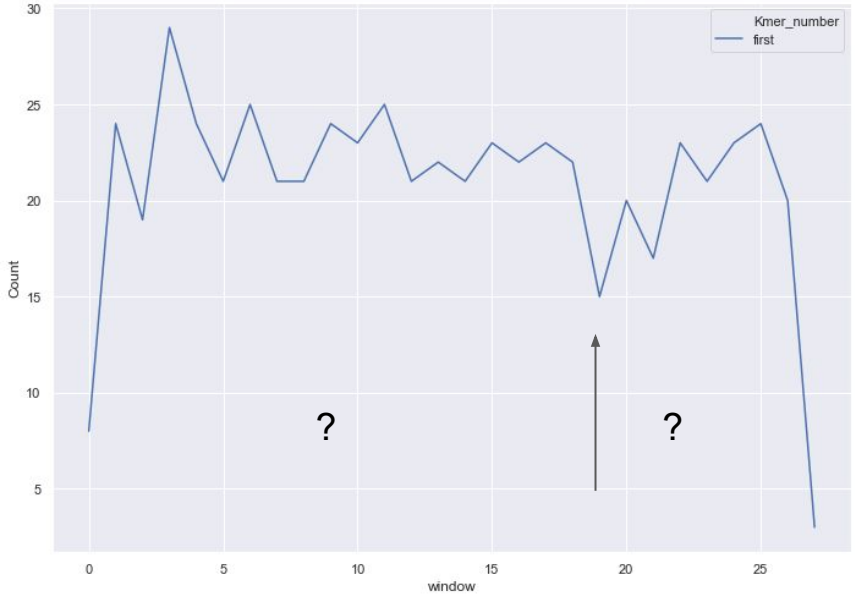
2-nd chromosome



3-d chromosome

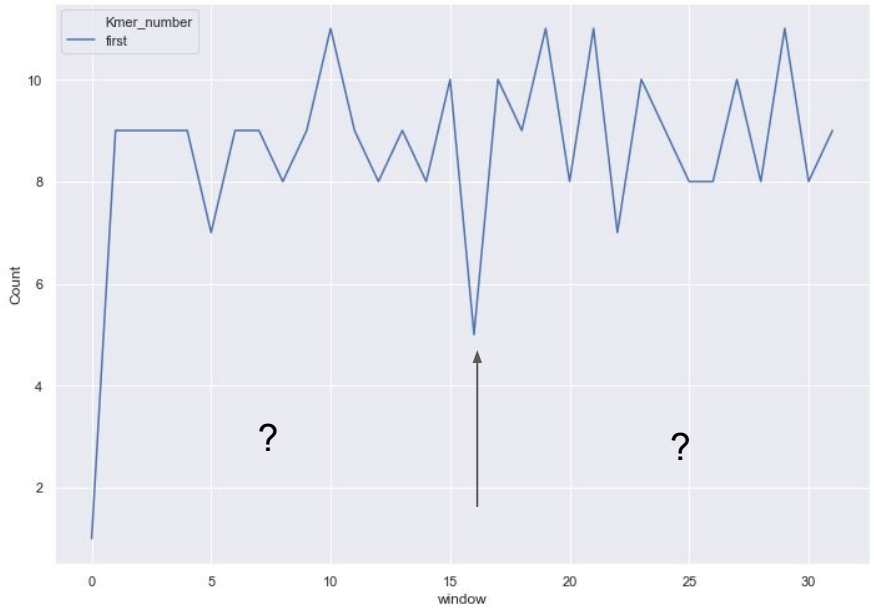


2-nd chromosome



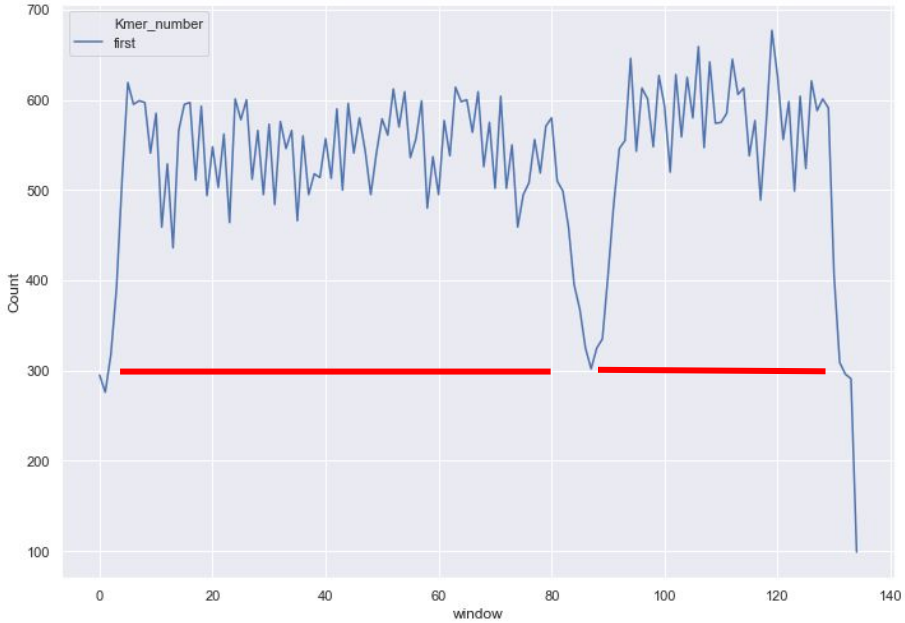
The most frequent kmer: 'OOOTIOOOI'

3-d chromosome



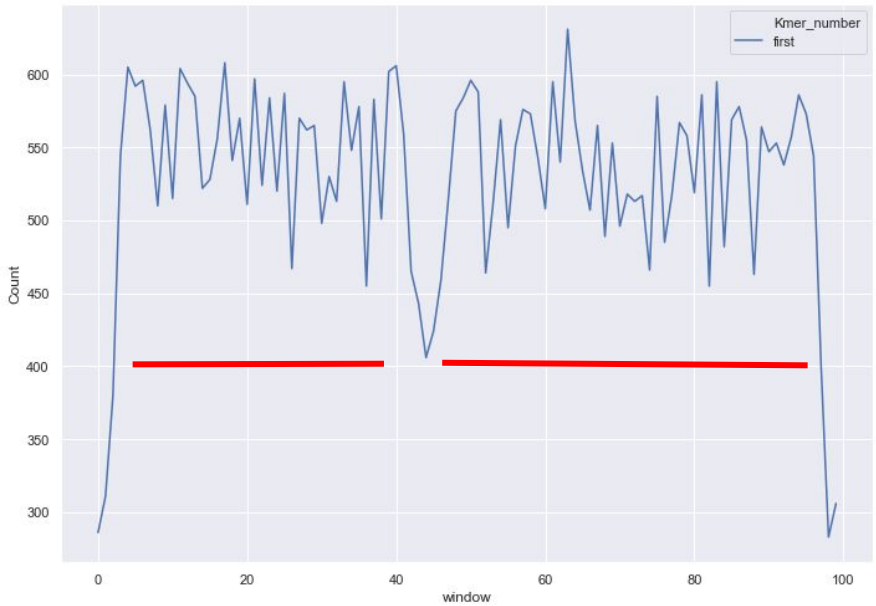
The most frequent kmer: 'OBITNNST'

2-nd chromosome



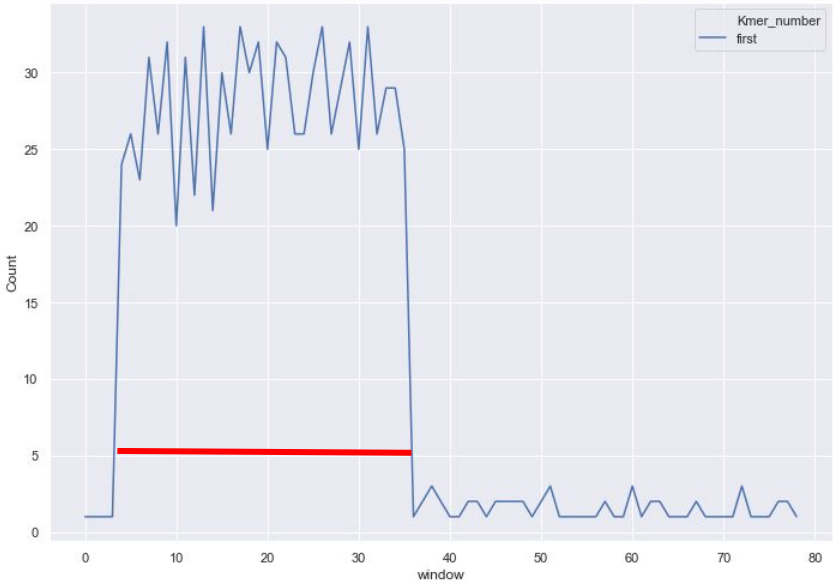
'TI'

3-d chromosome



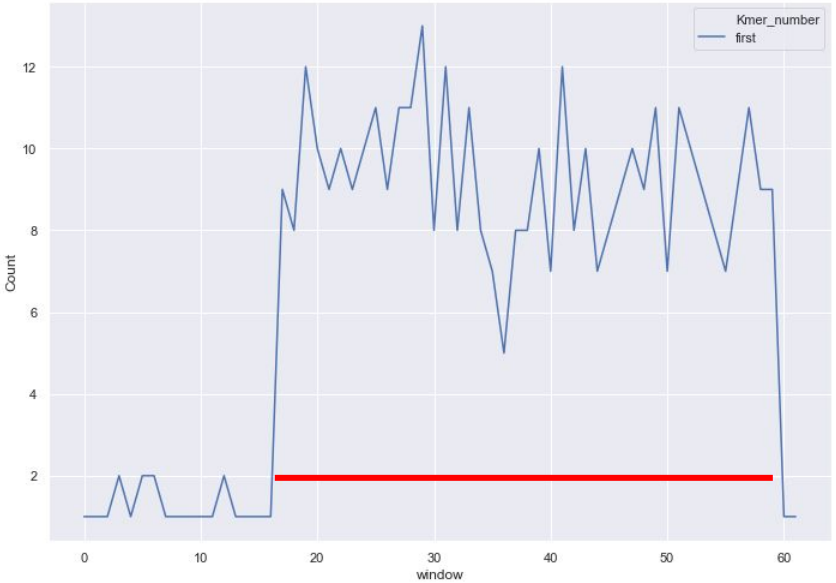
'T'

2-nd chromosome



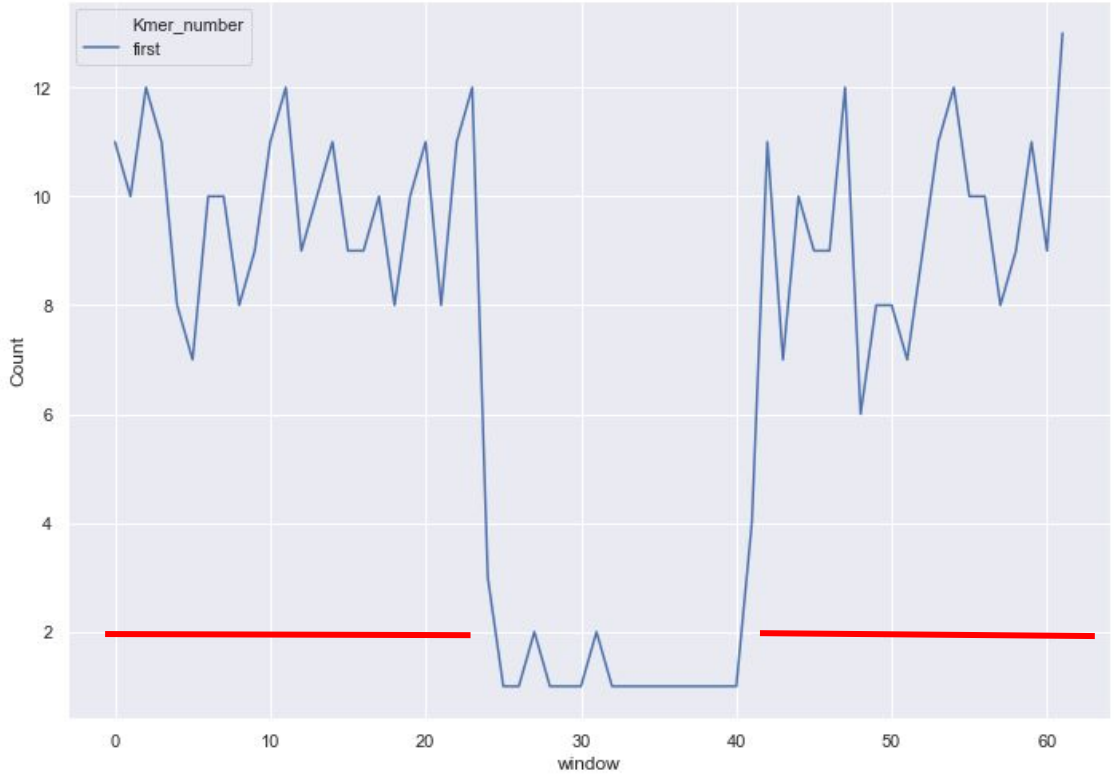
'TNNTN'

3-d chromosome



'NSTNS'

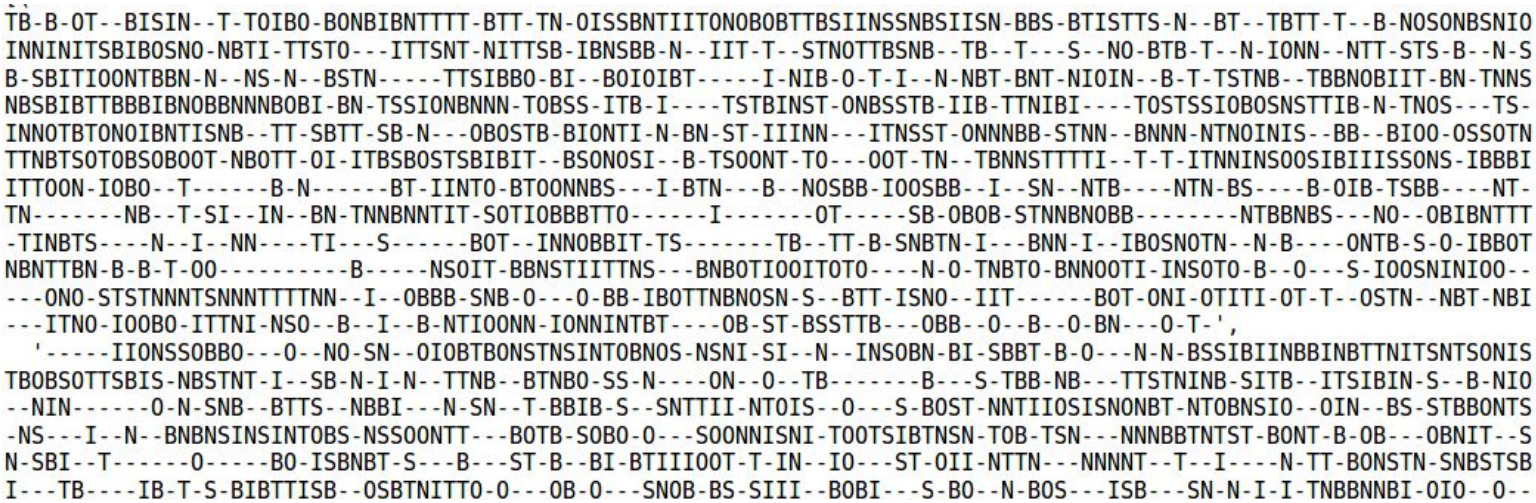
1-st chromosome



'TTTOI'

alignment?

- This fragments align better than random one # (527, 564)
- But I do not have stats...



diqqətinizə görə
təşəkkür edirik !