

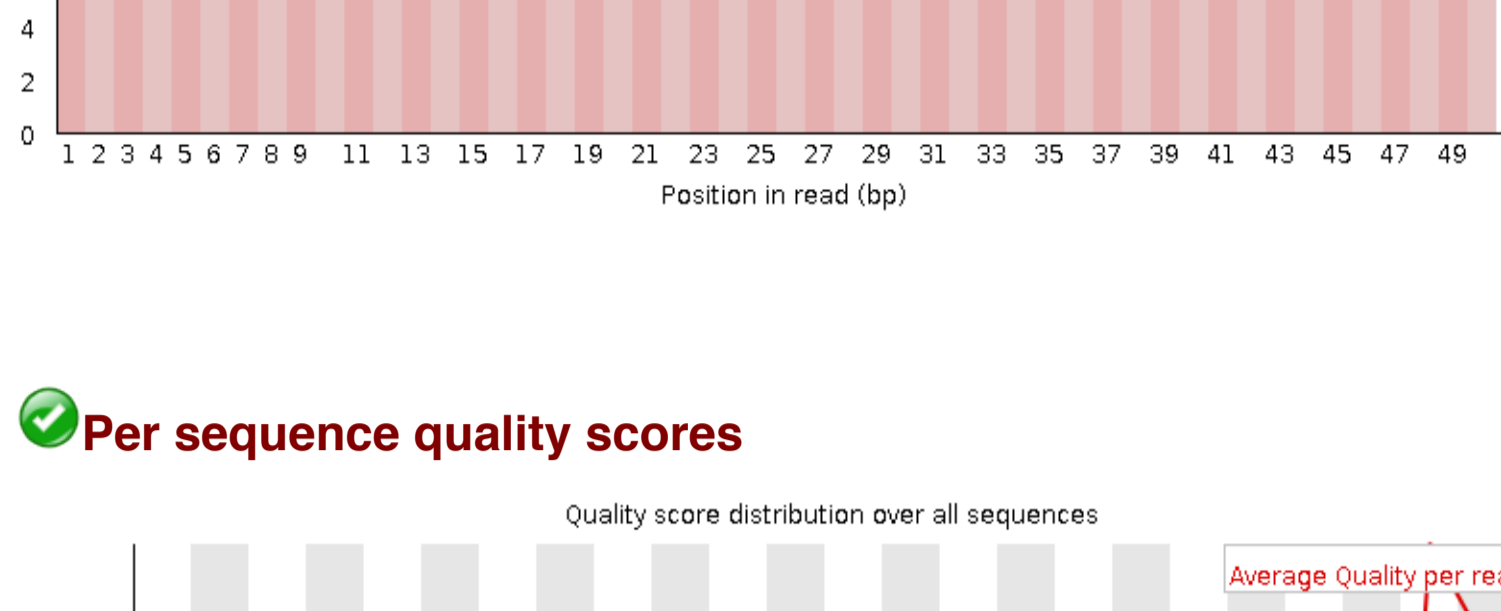
## Summary

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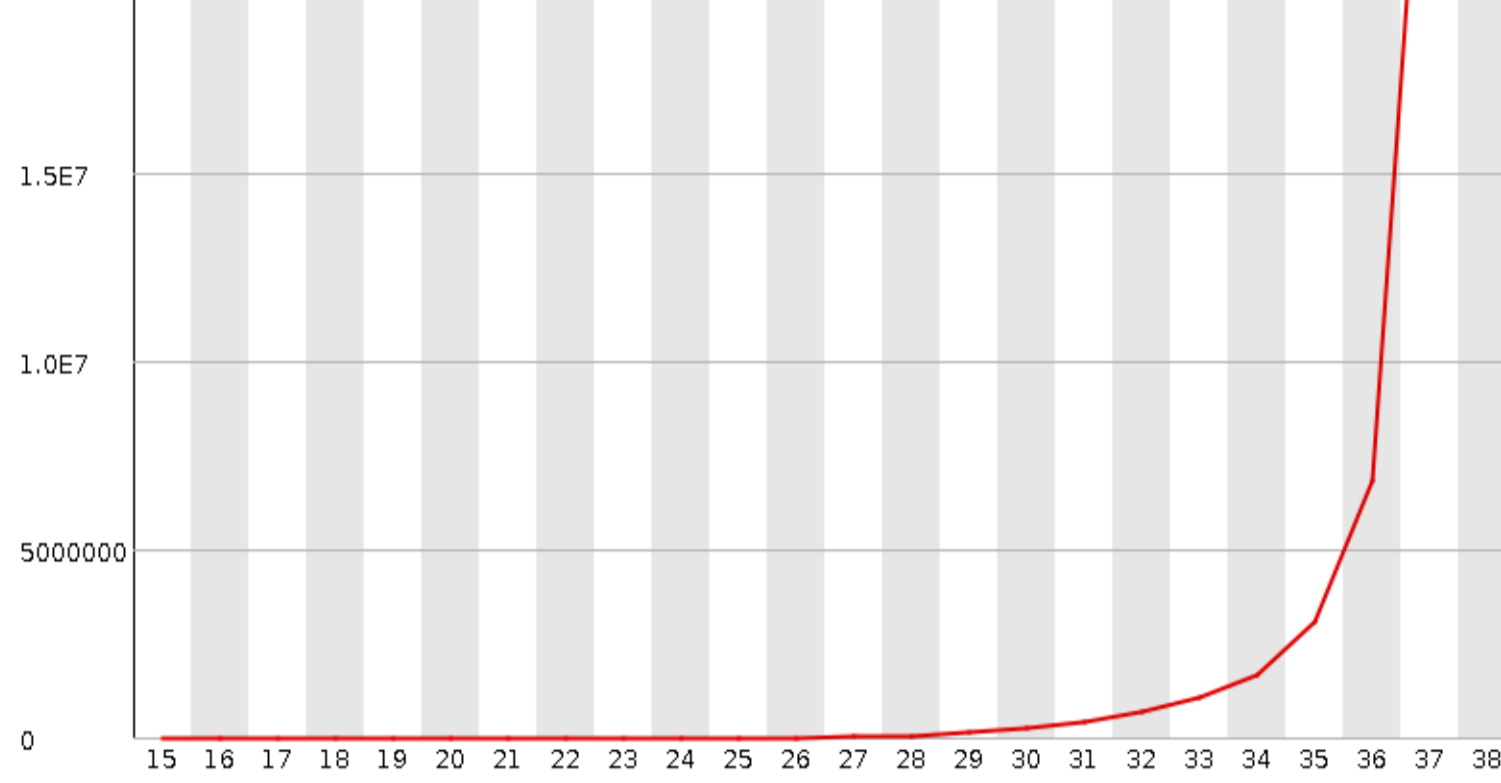
### Basic Statistics

Measure	Value
Filename	treat.sam
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	68465701
Sequences flagged as poor quality	0
Sequence length	20-50
%GC	51

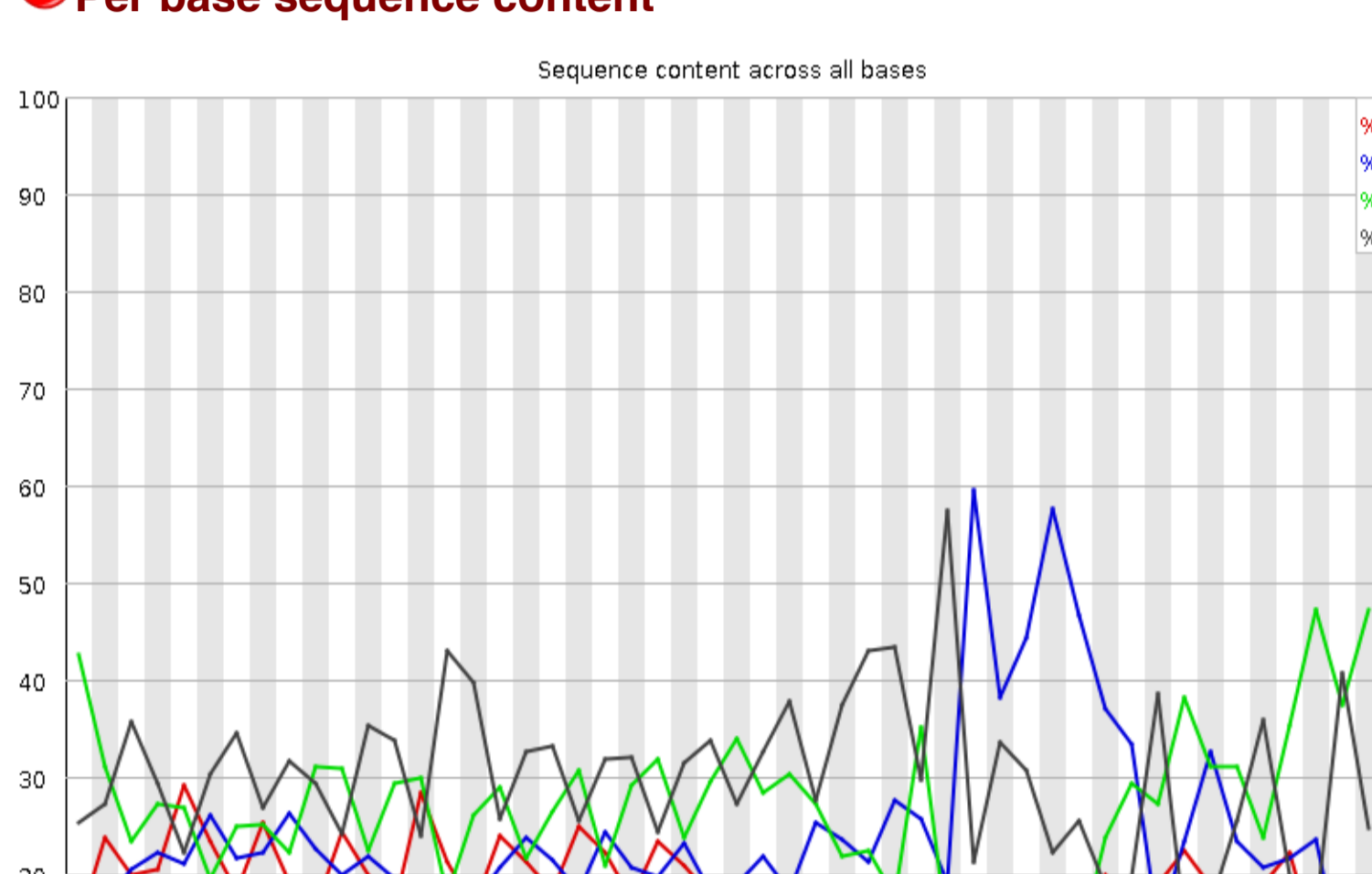
### Per base sequence quality



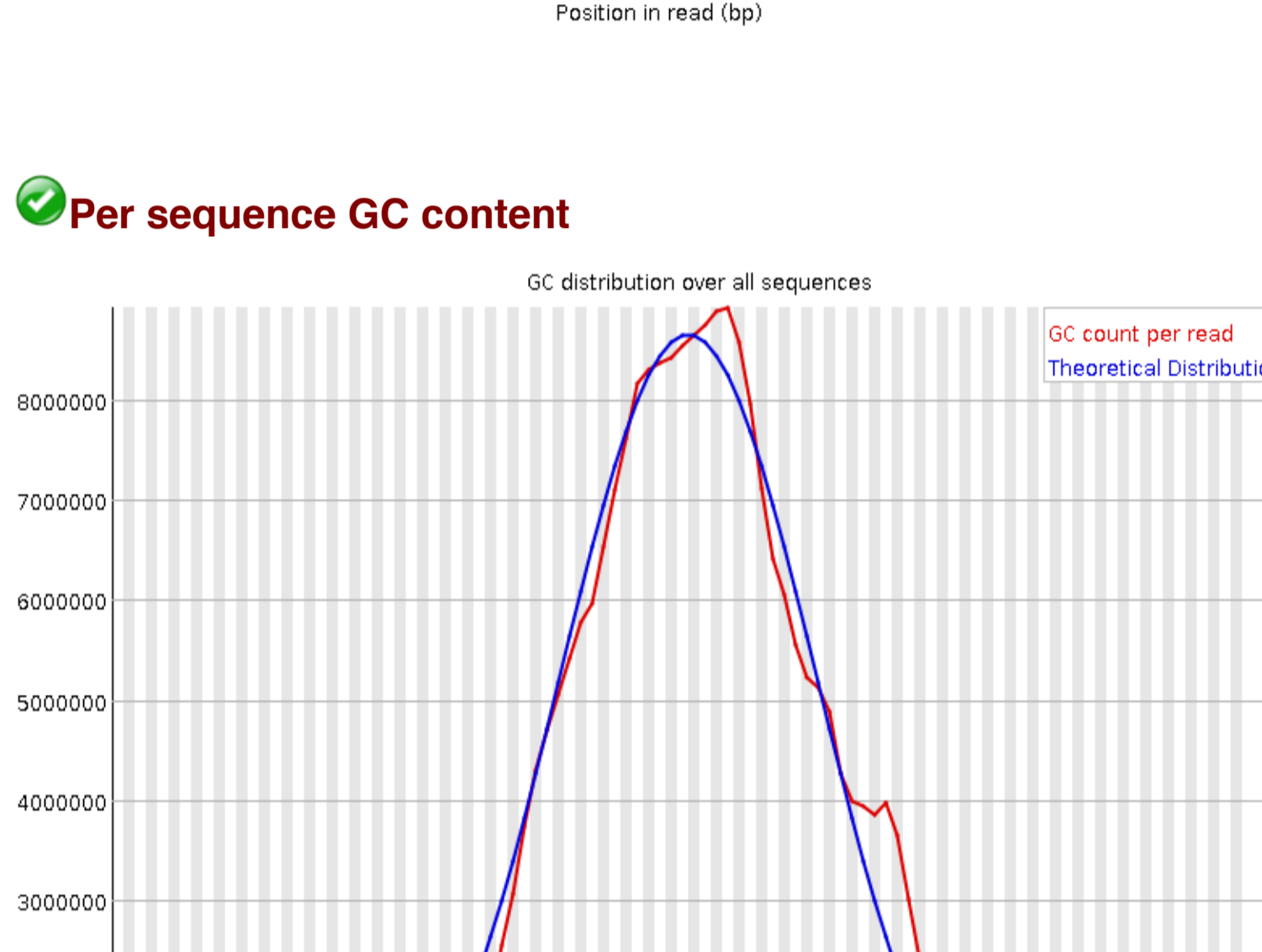
### Per sequence quality scores



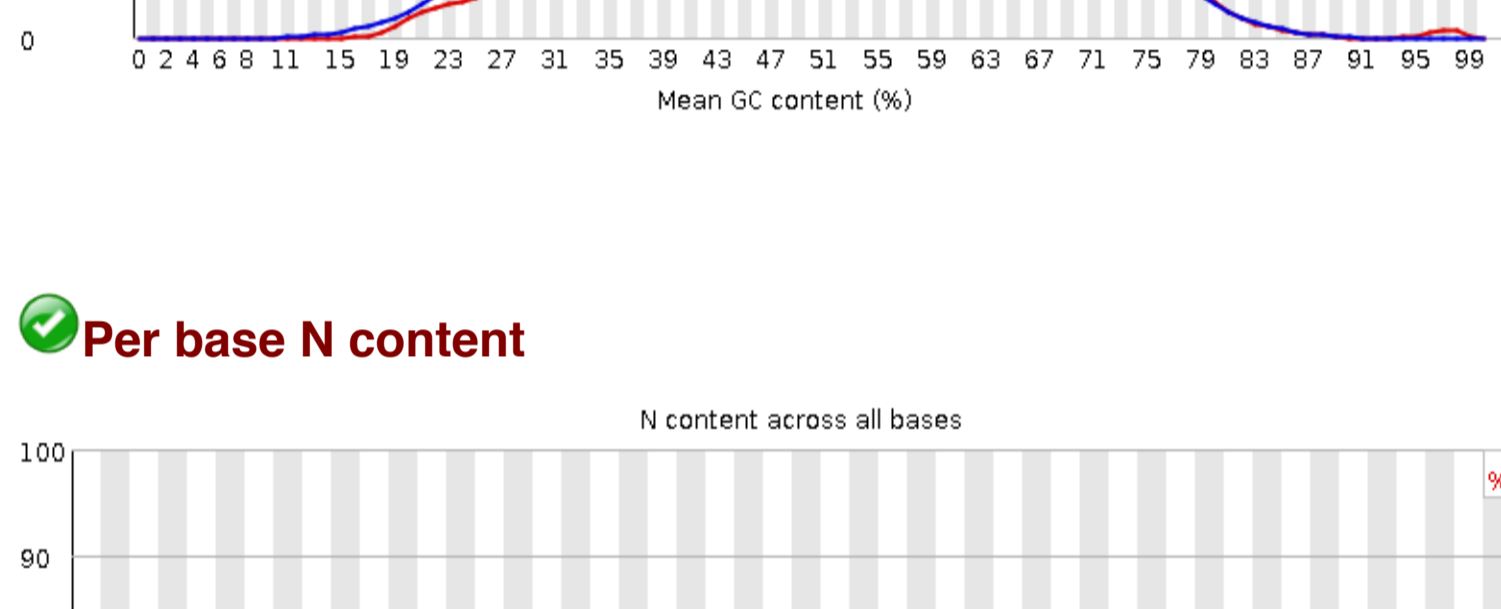
### Per base sequence content



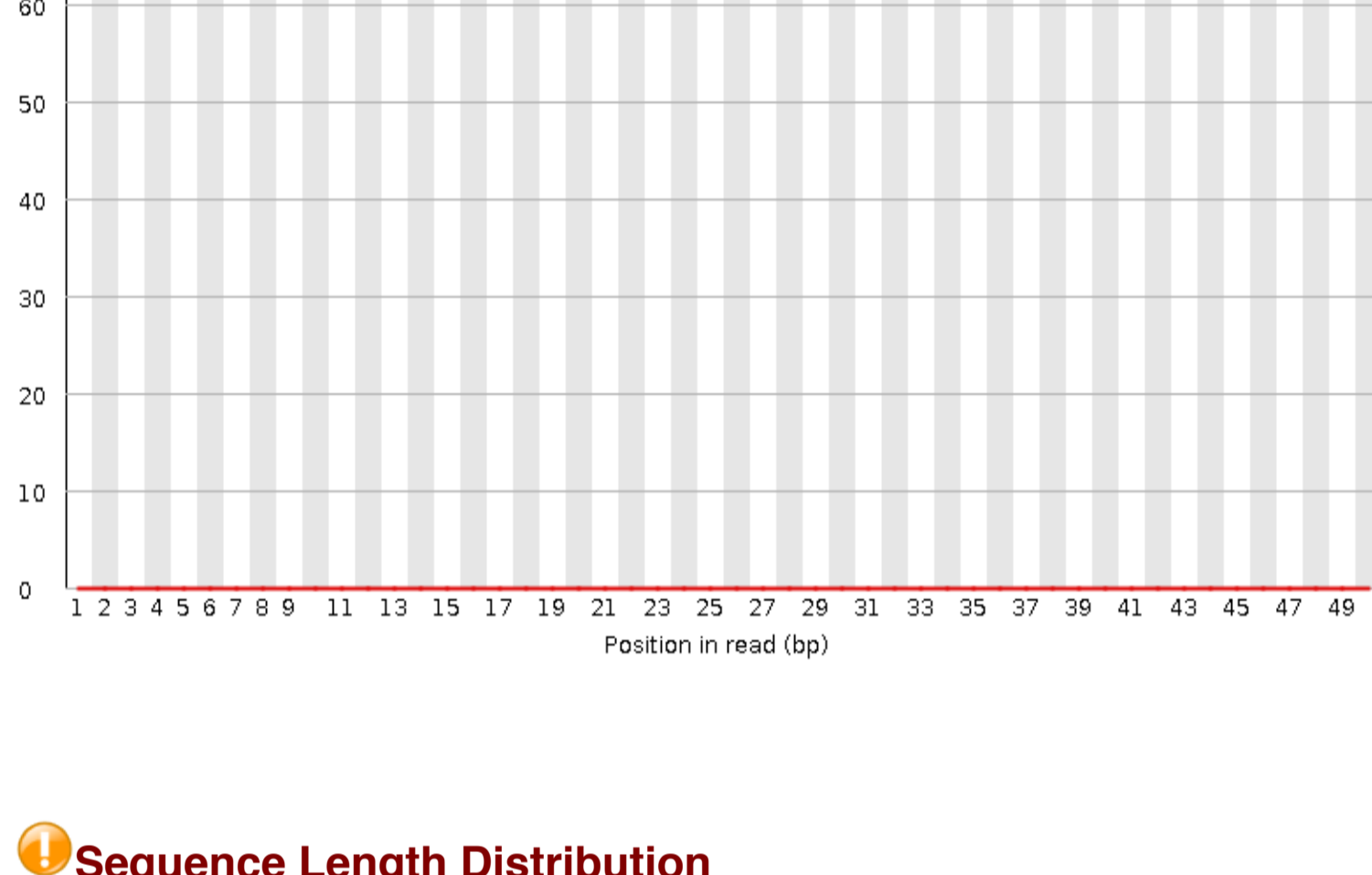
### Per sequence GC content



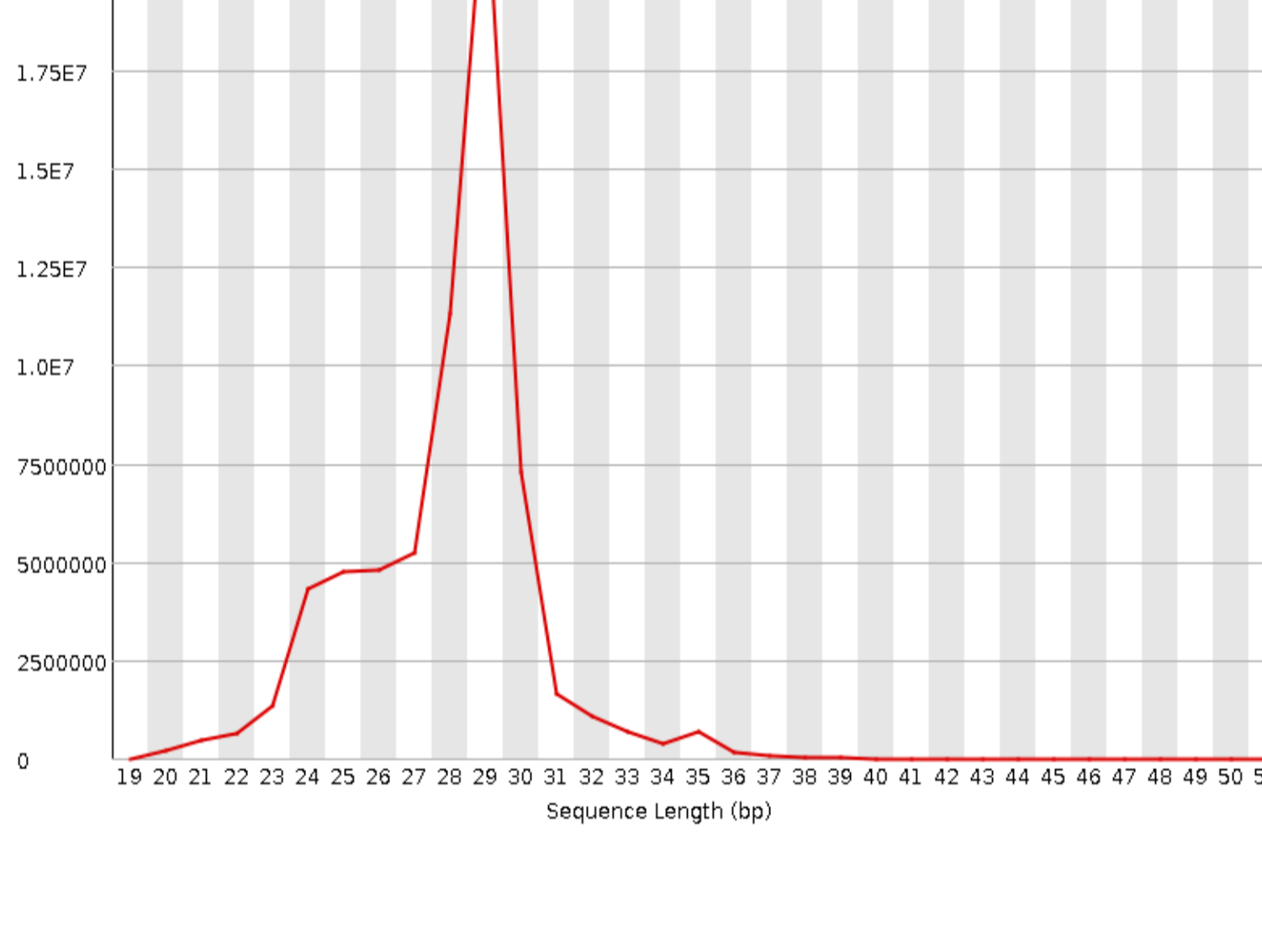
### Per base N content



### Sequence Length Distribution



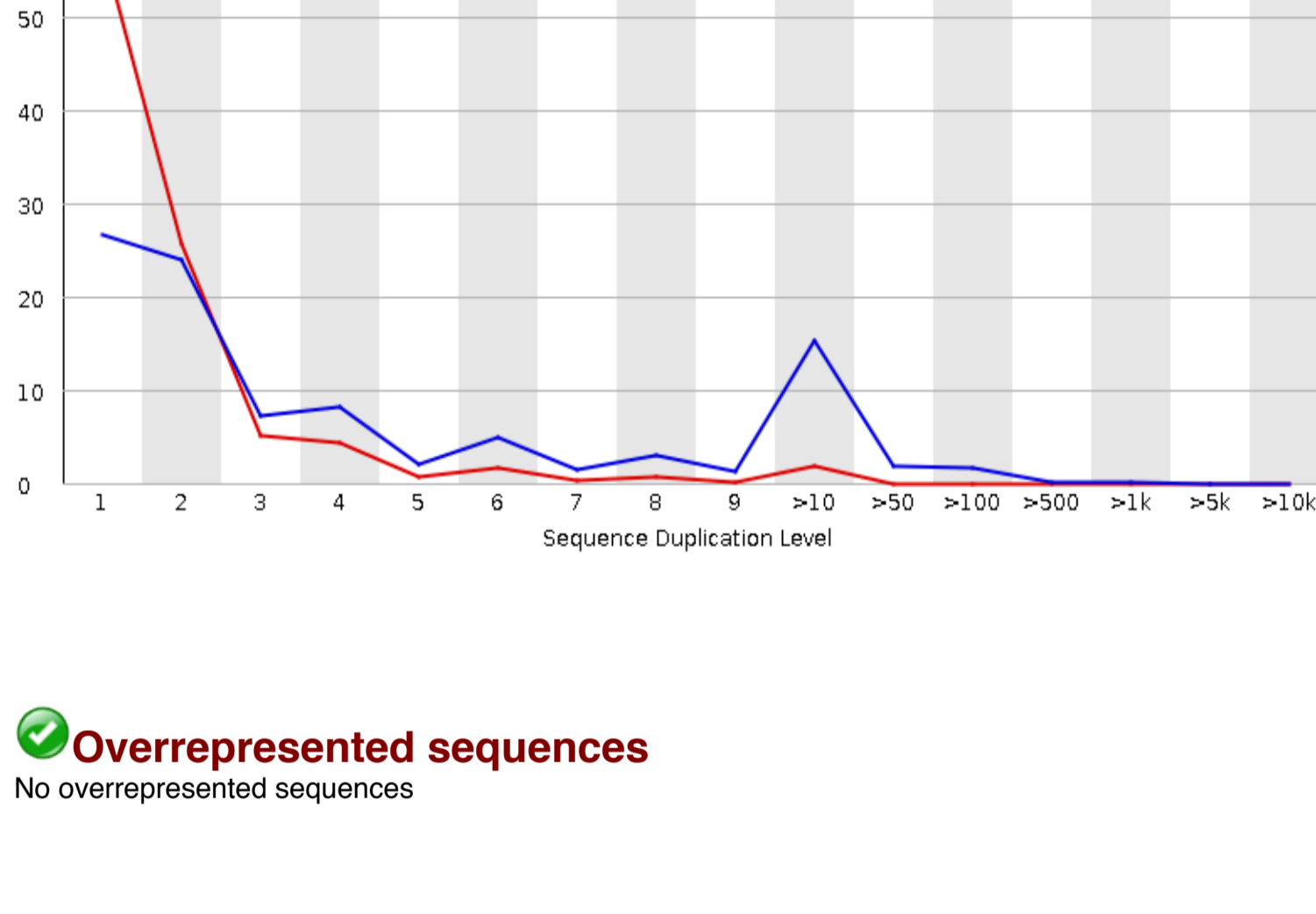
### Sequence Duplication Levels



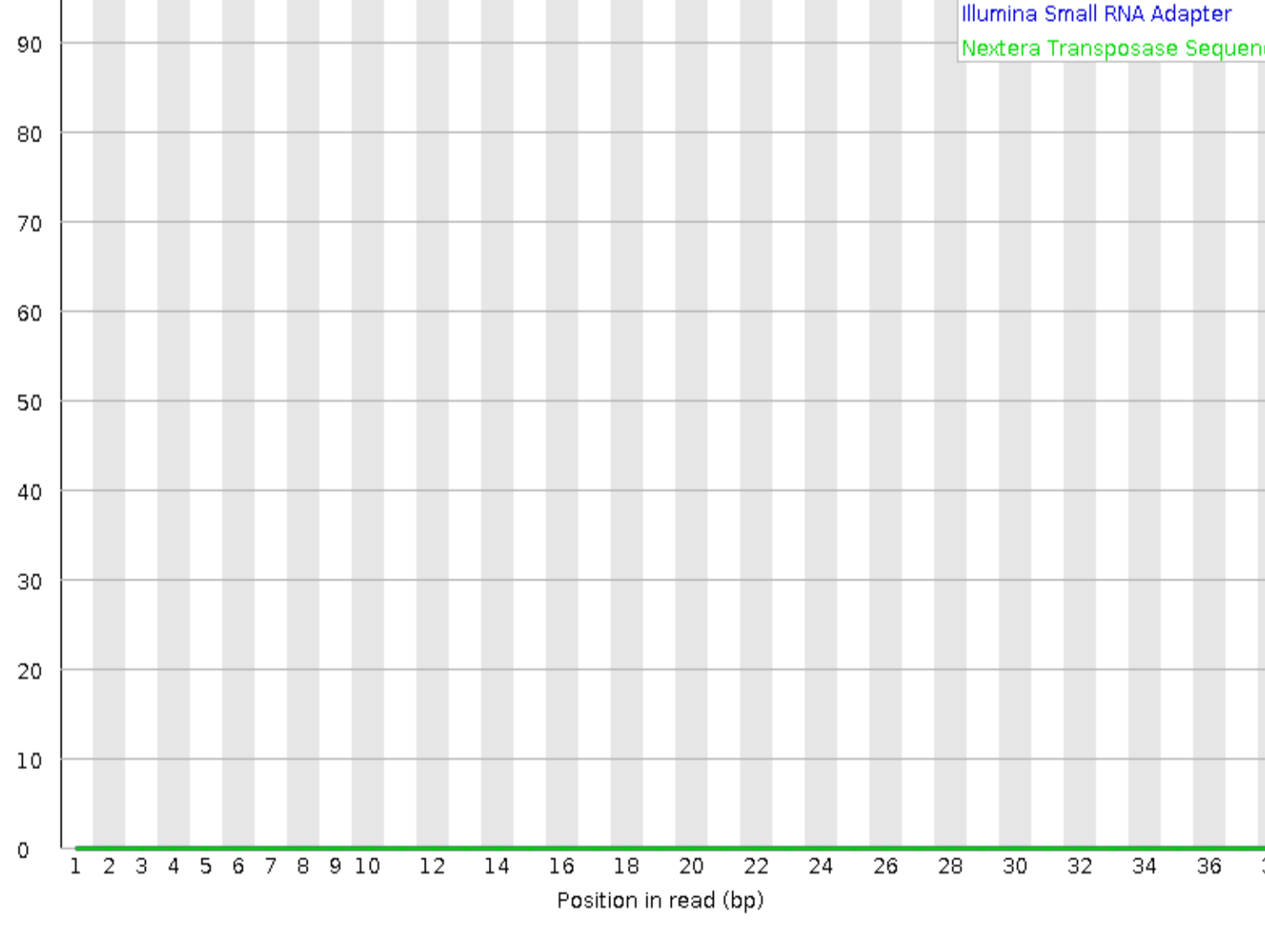
### Overrepresented sequences

No overrepresented sequences

### Adapter Content



### Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCCGGTA	1530	0.0	14317.783	42
CCGGTAG	2500	0.0	8762.485	43
CGGTAGA	2790	0.0	8147.978	44
GGCCGGT	2765	0.0	7512.886	41
CGCTAGC	590	2.1464075E-10	4641.1465	43
CACACGT	1615	0.0	3519.0188	44
AGGCCGG	6175	0.0	2748.1133	40
ACTCGAT	1045	0.0010867242	2719.2417	44
CGAAAAA	7275	0.0	2587.7183	39
TAACAAAT	2295	1.5200967E-6	2386.2976	42
AAATAAC	3760	9.094947E-12	2071.7883	41
AACAATA	2780	2.7014867E-6	1969.983	43
CCGCTAG	1480	0.0	1850.1869	42
GCTAGCA	1545	0.0023751701	1839.2281	44
CACGATC	1480	0.0026144295	1754.4874	44
ATAACAA	3100	4.405103E-6	1675.2526	41
TAGCCGG	1775	0.0	1636.1873	33
GCAACAG	3365	0.0	1627.5045	43
ACAATAG	1750	0.0030471492	1623.7758	44
ATTCAAT	1790	0.0031880108	1587.4902	44