












## Summary

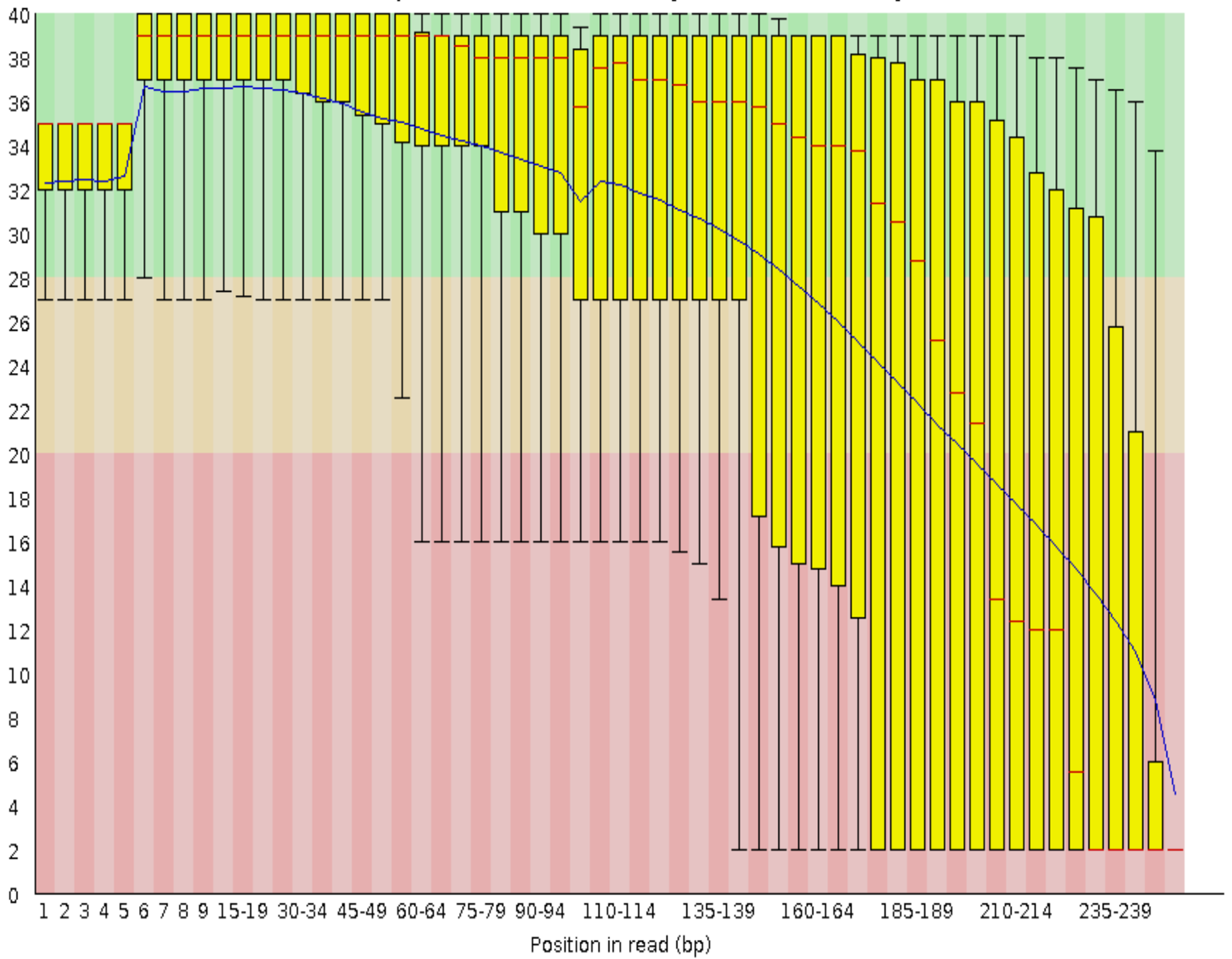
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## Basic Statistics

| Measure                           | Value                   |
|-----------------------------------|-------------------------|
| Filename                          | BS-MK_CATCCGG_R2.fastq  |
| File type                         | Conventional base calls |
| Encoding                          | Sanger / Illumina 1.9   |
| Total Sequences                   | 158447750               |
| Sequences flagged as poor quality | 0                       |
| Sequence length                   | 250                     |
| %GC                               | 42                      |

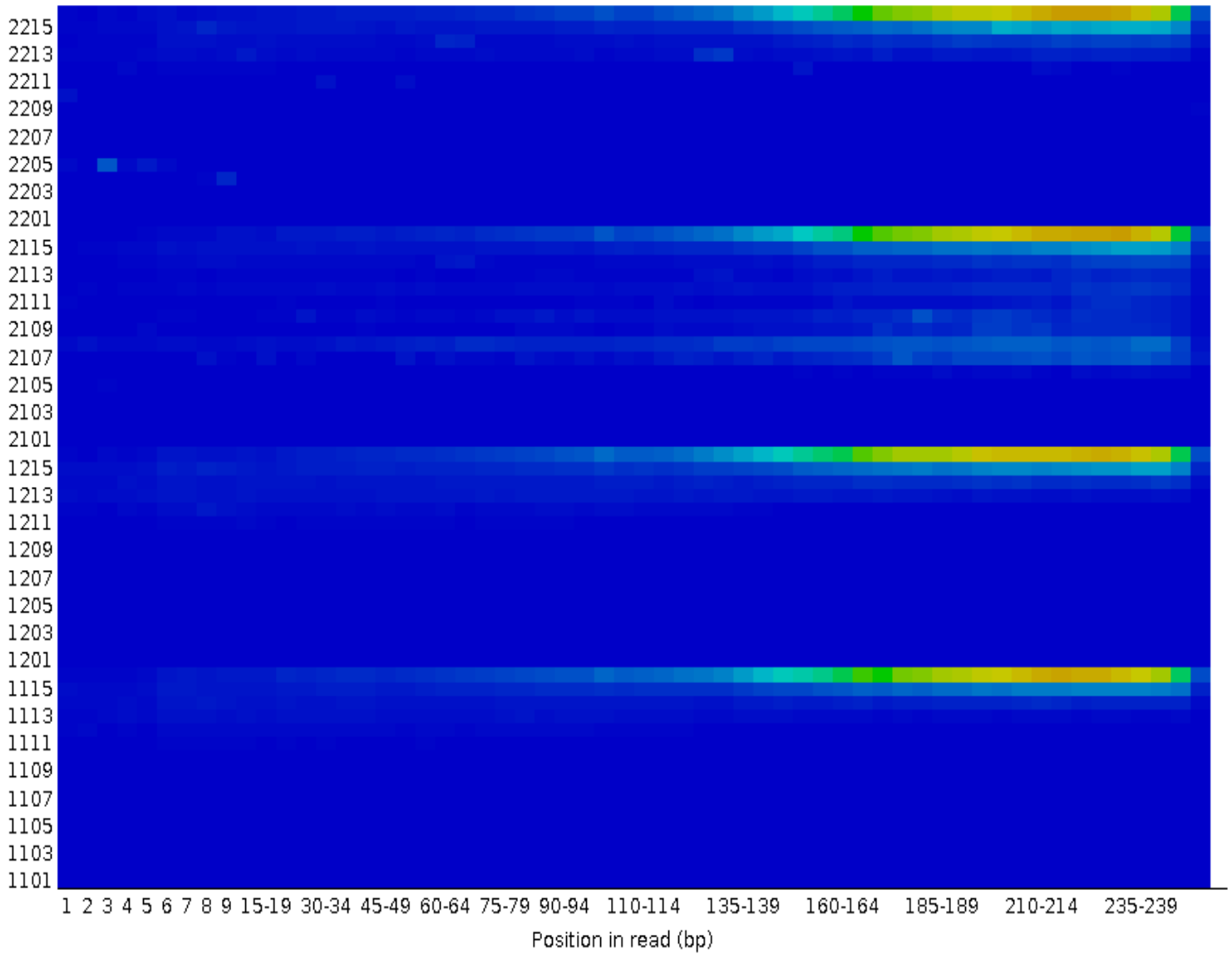
## Per base sequence quality

Quality scores across all bases (Sanger / Illumina 1.9 encoding)



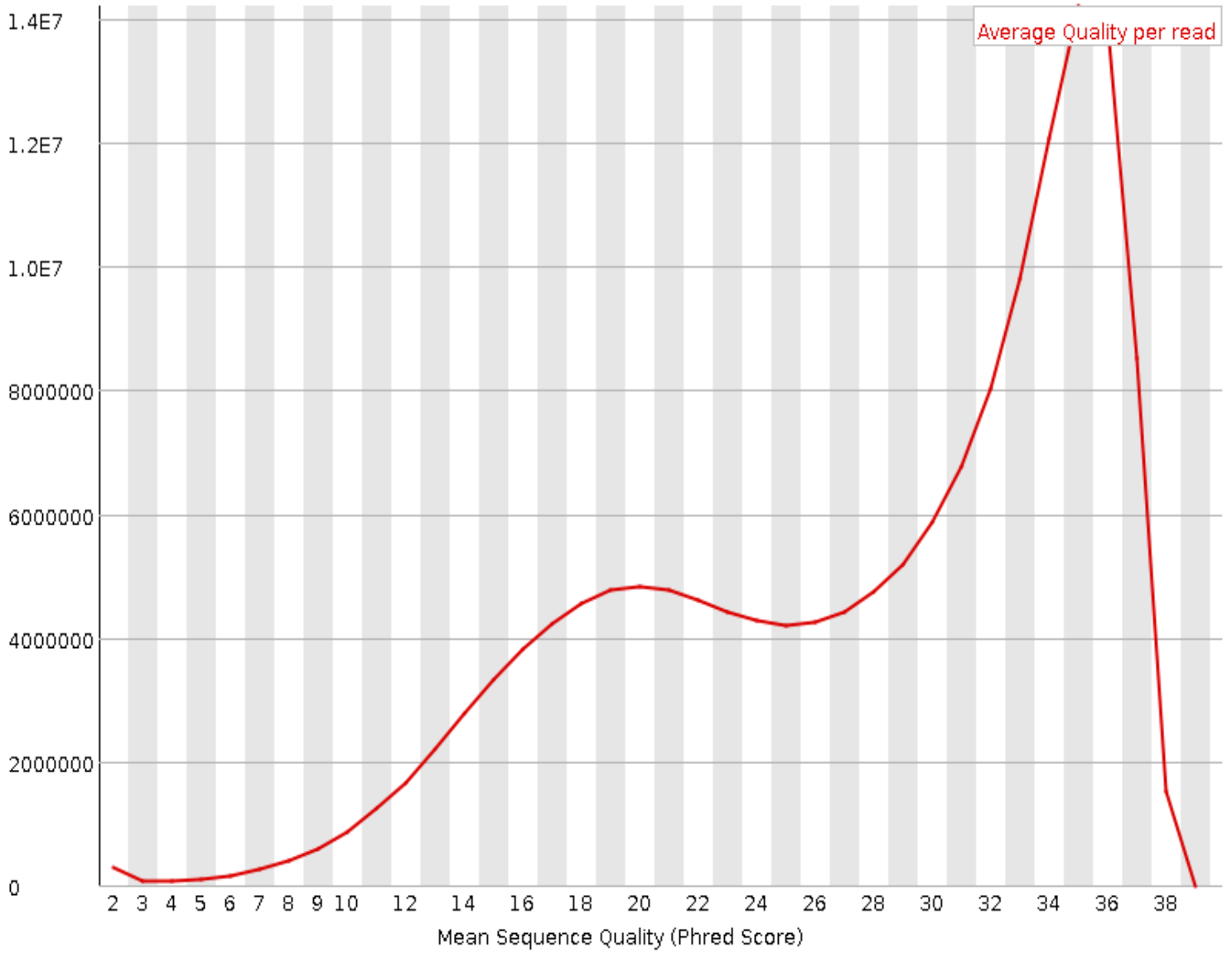
**! Per tile sequence quality**

Quality per tile



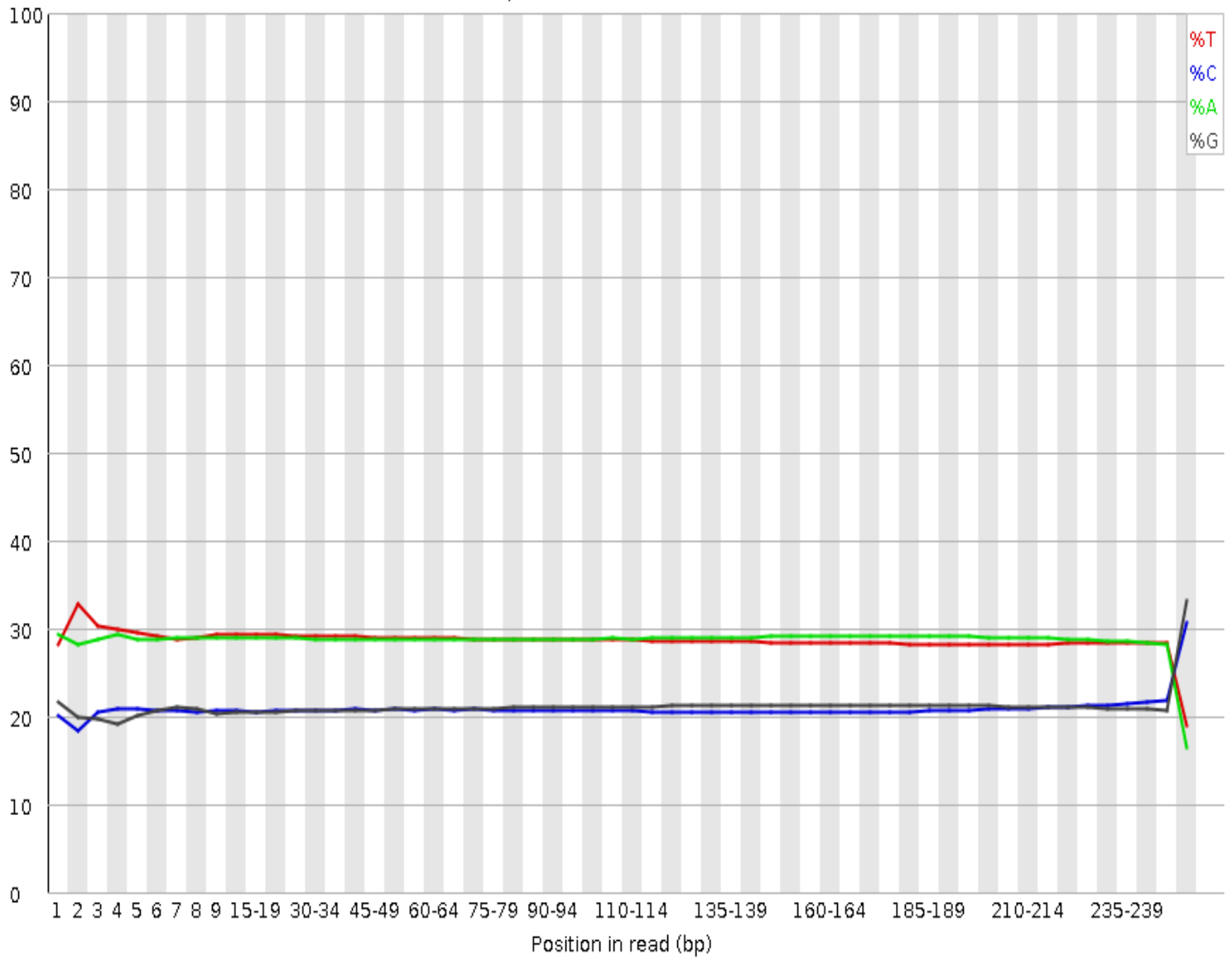
 **Per sequence quality scores**

Quality score distribution over all sequences



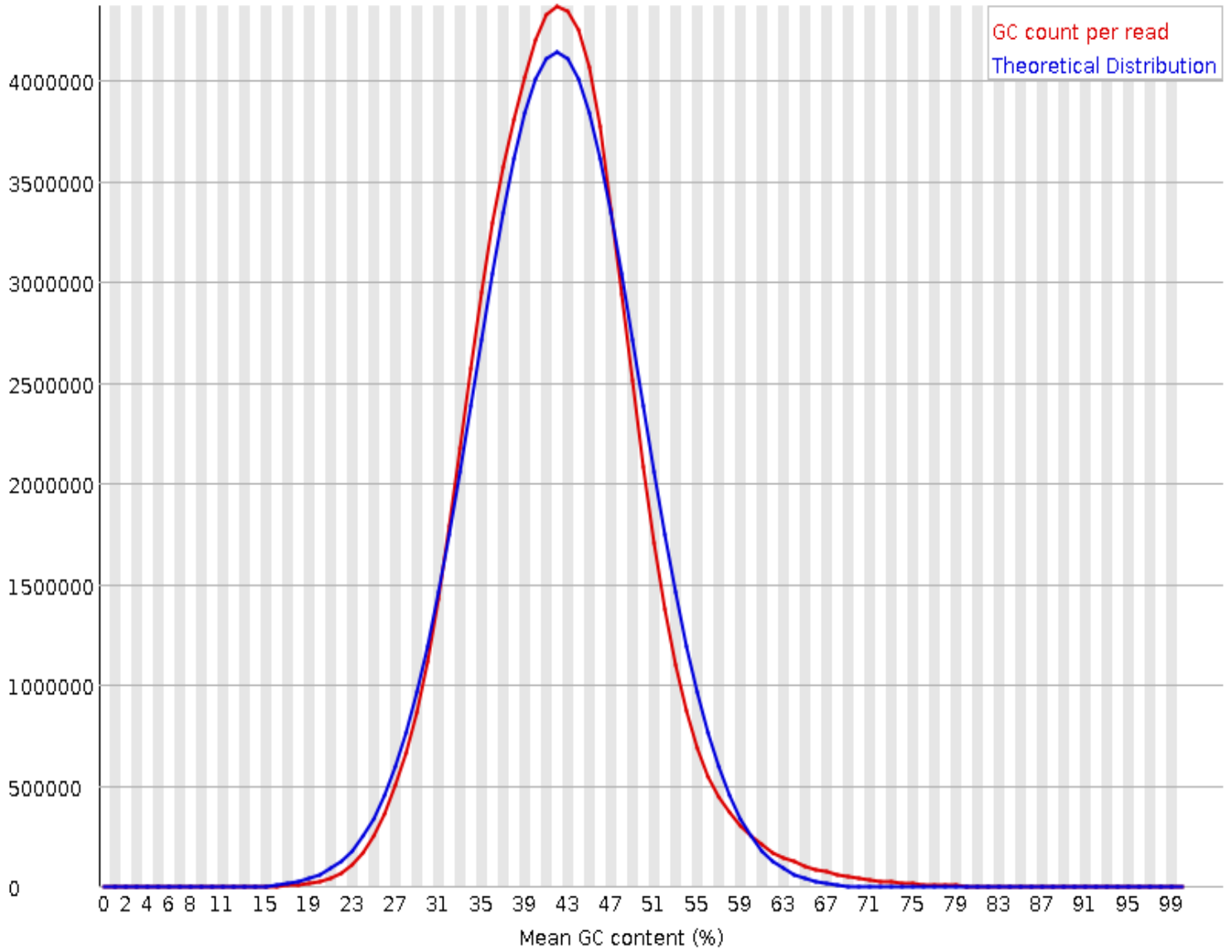
## ! Per base sequence content

Sequence content across all bases



 **Per sequence GC content**

GC distribution over all sequences



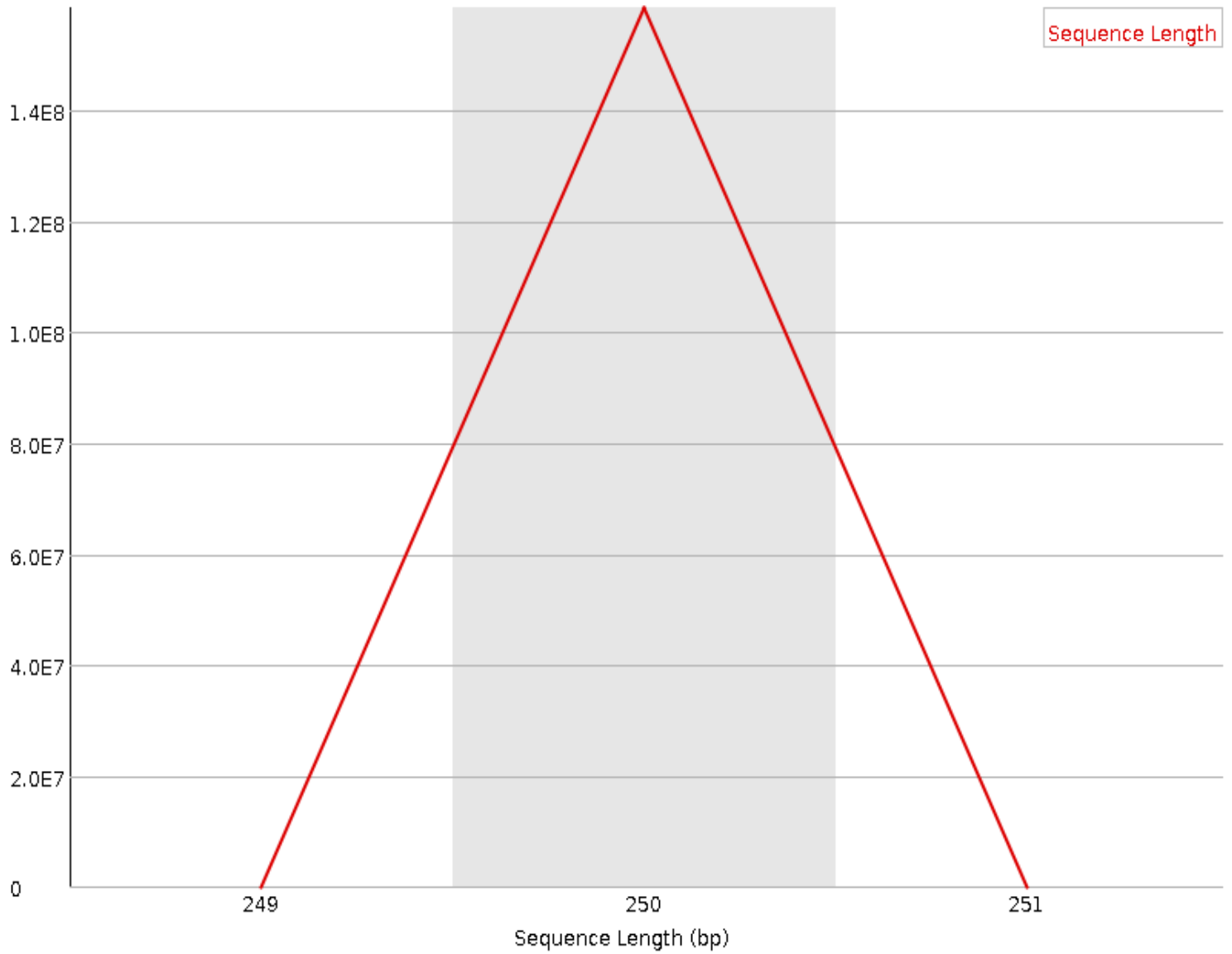
 **Per base N content**

N content across all bases



 **Sequence Length Distribution**

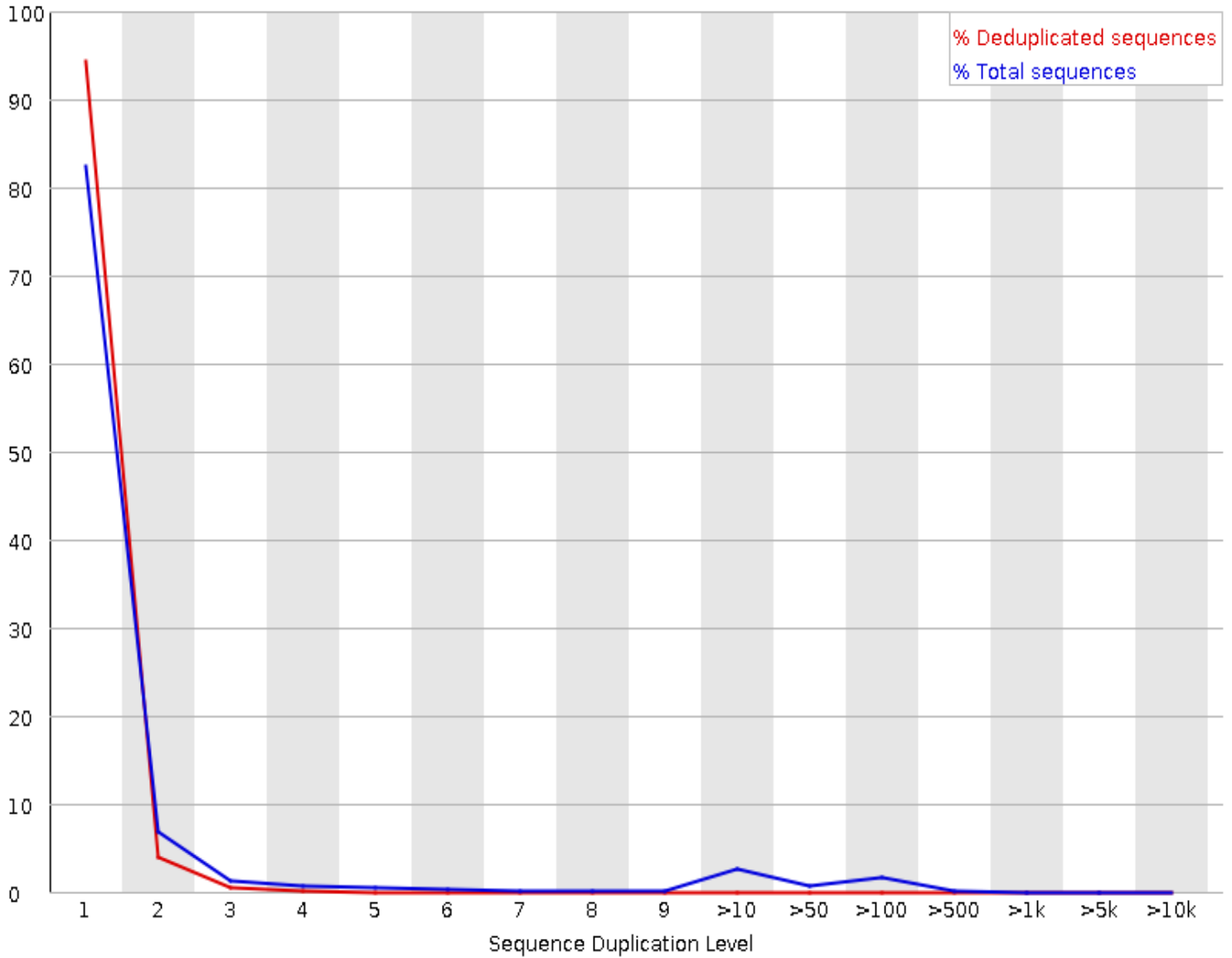
Distribution of sequence lengths over all sequences



## Sequence Duplication Levels



Percent of seqs remaining if deduplicated 87.25%

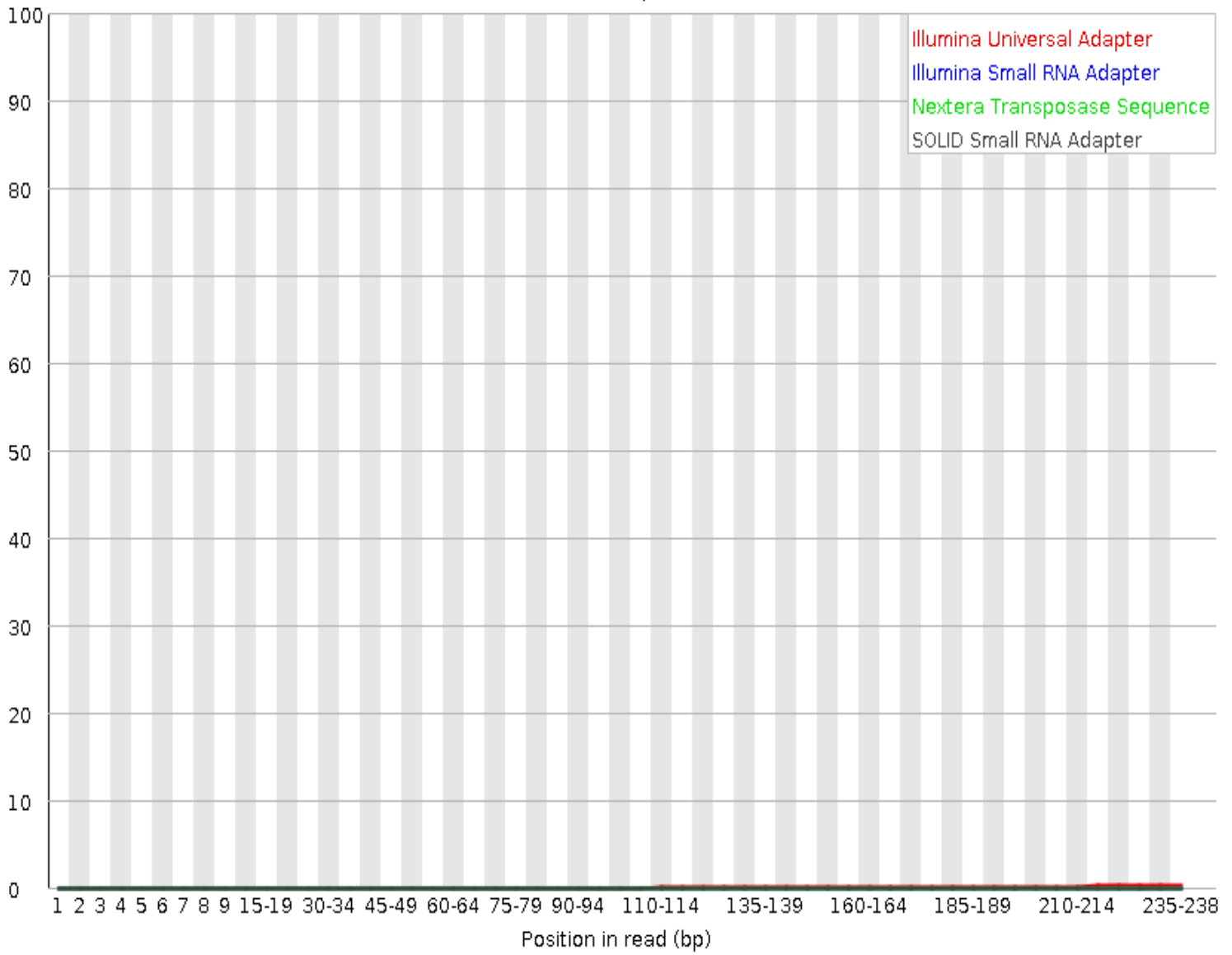


 **Overrepresented sequences**

No overrepresented sequences

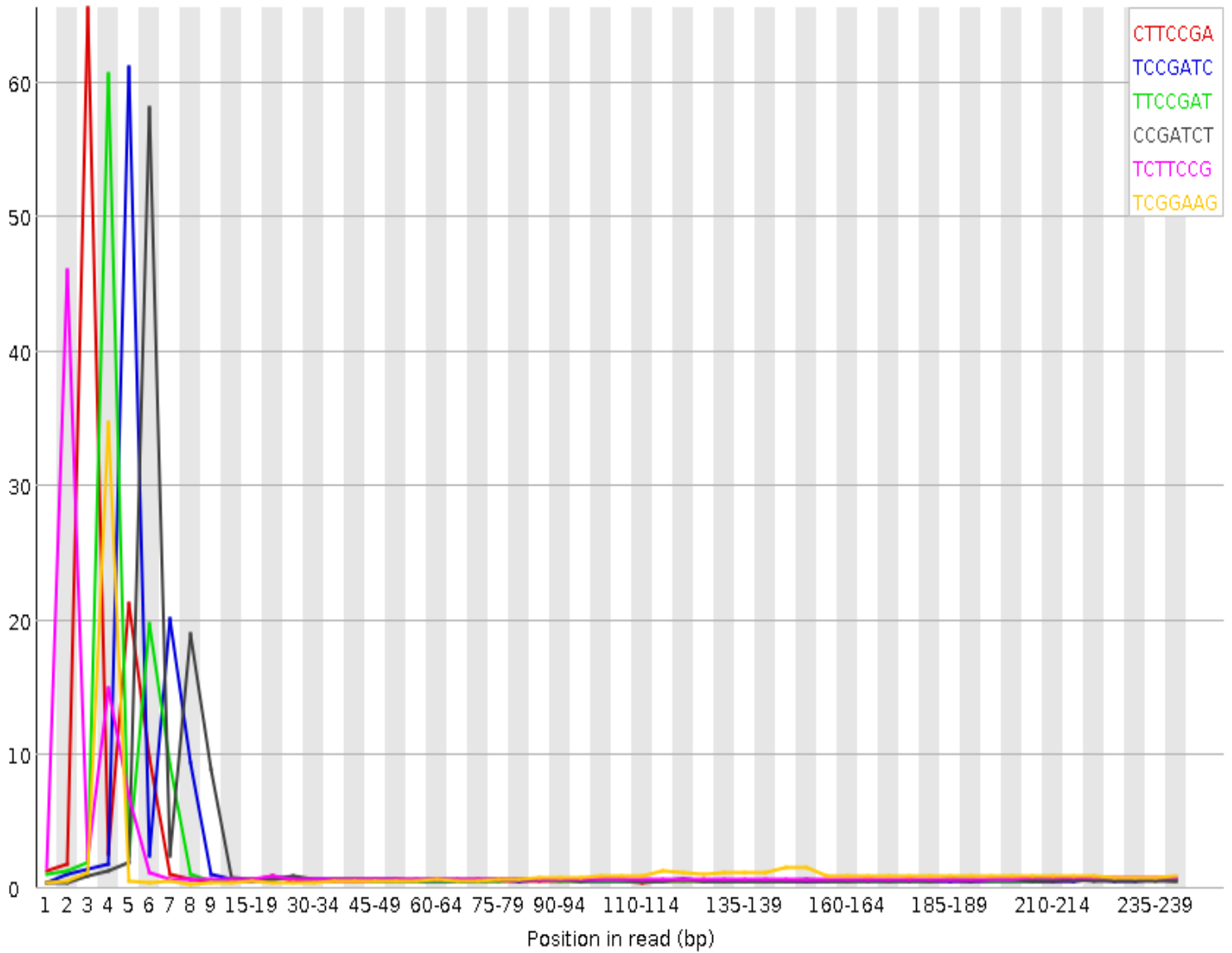
 **Adapter Content**

% Adapter



## Kmer Content

Log2 Obs/Exp



| Sequence | Count | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|-------|--------|-------------|----------------------|
|----------|-------|--------|-------------|----------------------|

|         |        |     |          |   |
|---------|--------|-----|----------|---|
| CTTCCGA | 145485 | 0.0 | 65.41115 | 3 |
|---------|--------|-----|----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| TCCGATC | 154605 | 0.0 | 61.056664 | 5 |
|---------|--------|-----|-----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| TTCCGAT | 156705 | 0.0 | 60.565445 | 4 |
|---------|--------|-----|-----------|---|

|         |        |     |          |   |
|---------|--------|-----|----------|---|
| CCGATCT | 162790 | 0.0 | 58.03173 | 6 |
|---------|--------|-----|----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| TCTTCCG | 209885 | 0.0 | 45.992474 | 2 |
|---------|--------|-----|-----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| TCGGAAG | 162065 | 0.0 | 34.652596 | 4 |
|---------|--------|-----|-----------|---|

|         |        |     |          |   |
|---------|--------|-----|----------|---|
| GATCGGA | 170045 | 0.0 | 33.12249 | 2 |
|---------|--------|-----|----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| ATCGGAA | 170730 | 0.0 | 32.900375 | 3 |
|---------|--------|-----|-----------|---|

|         |        |     |          |   |
|---------|--------|-----|----------|---|
| AGATCGG | 184190 | 0.0 | 30.81472 | 1 |
|---------|--------|-----|----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| CGATCTA | 104080 | 0.0 | 28.290354 | 7 |
|---------|--------|-----|-----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| CGGAAGA | 230210 | 0.0 | 24.755384 | 5 |
|---------|--------|-----|-----------|---|

|         |        |     |           |   |
|---------|--------|-----|-----------|---|
| CTCTTCC | 485115 | 0.0 | 20.53506  | 1 |
| CGATCTT | 135655 | 0.0 | 20.24767  | 7 |
| GAAGAGC | 317055 | 0.0 | 18.246536 | 7 |
| CAAGTCG | 111220 | 0.0 | 14.17306  | 5 |
| ACGCTCT | 99605  | 0.0 | 13.9517   | 1 |
| CGATCTC | 148585 | 0.0 | 13.71228  | 7 |
| AAGAGCG | 209410 | 0.0 | 13.560309 | 8 |
| AGAGCGT | 164215 | 0.0 | 13.121672 | 9 |
| GCTCTTC | 251080 | 0.0 | 12.671337 | 2 |

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