

# FastQC Report

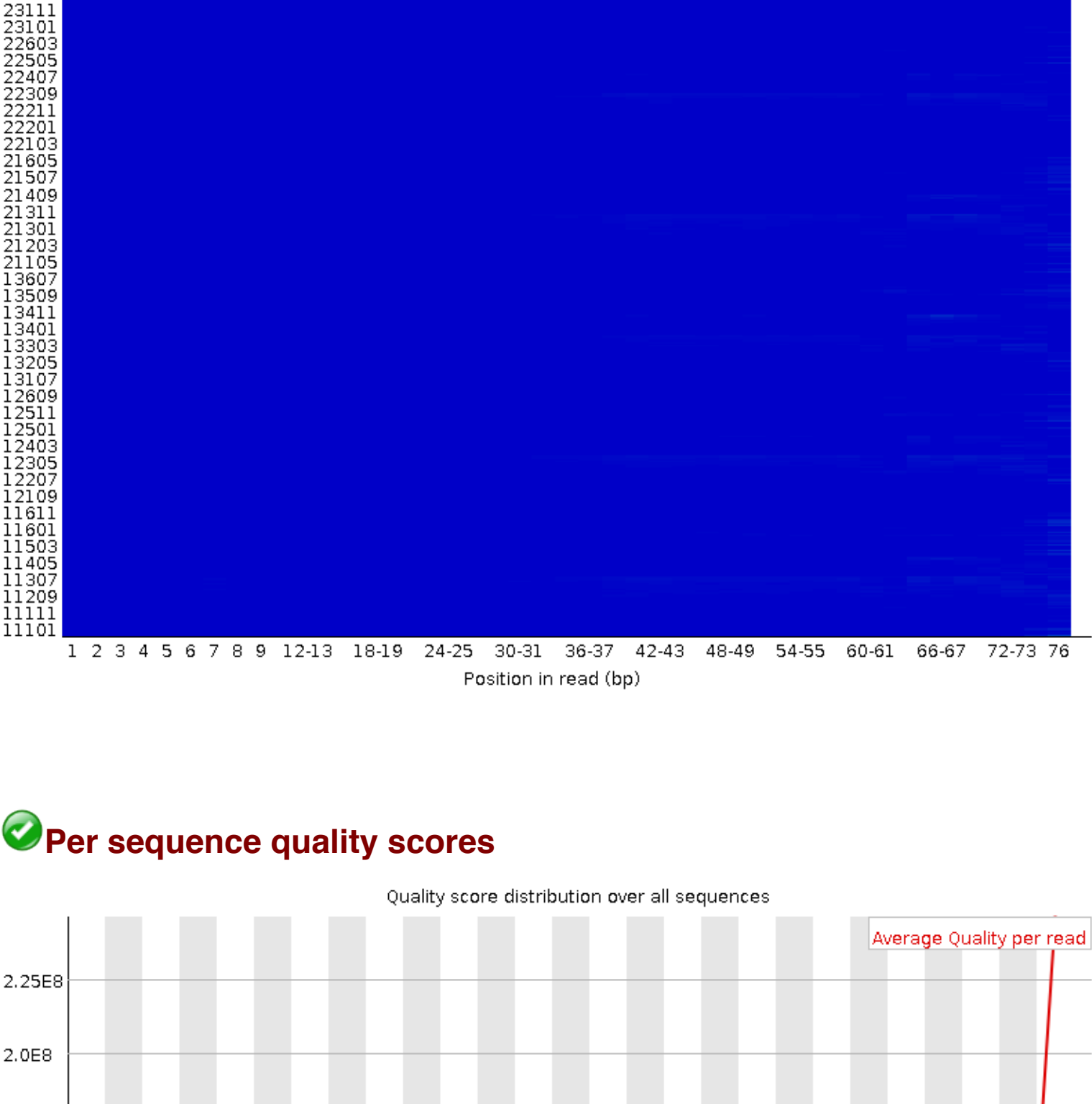
## Summary

- Basic Statistics
- Per base sequence quality
- Per tile 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
- Adapter Content
- Kmer Content

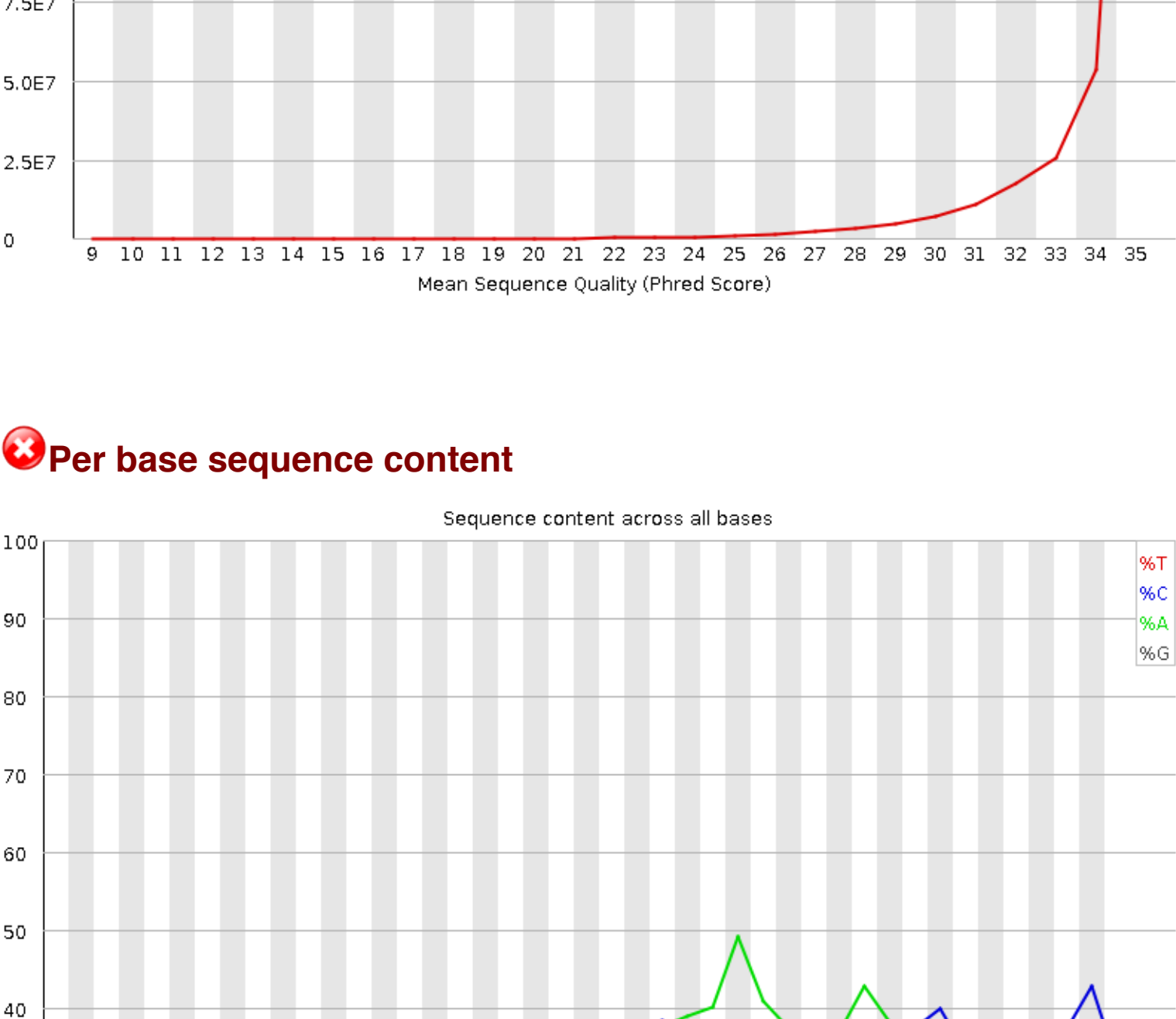
### Basic Statistics

| Measure                           | Value                   |
|-----------------------------------|-------------------------|
| Filename                          | jurkat_lm.fastq         |
| File type                         | Conventional base calls |
| Encoding                          | Sanger / Illumina 1.9   |
| Total Sequences                   | 378053973               |
| Sequences flagged as poor quality | 0                       |
| Sequence length                   | 76                      |
| GC                                | 52                      |

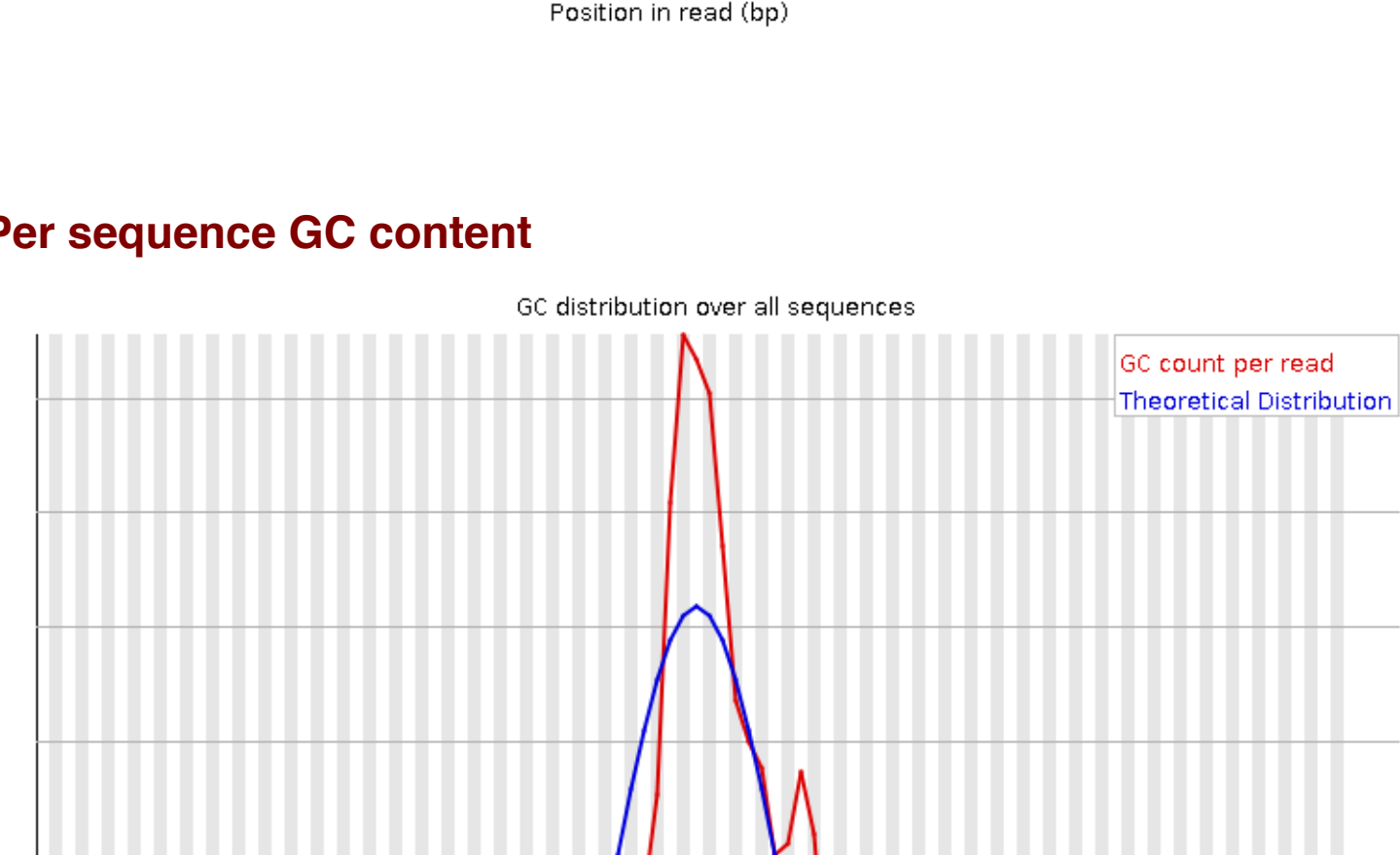
### Per base sequence quality



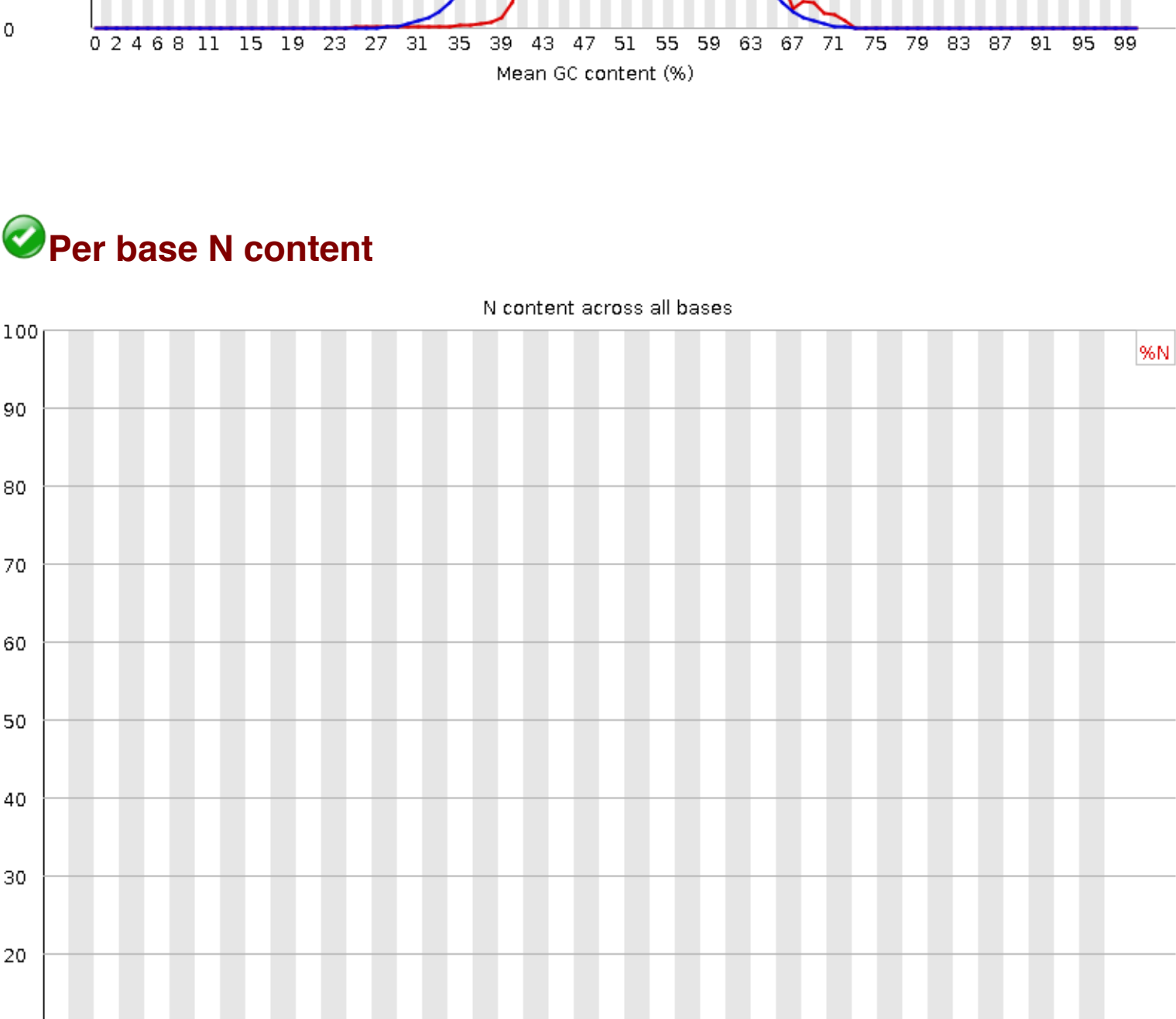
### Per tile sequence quality



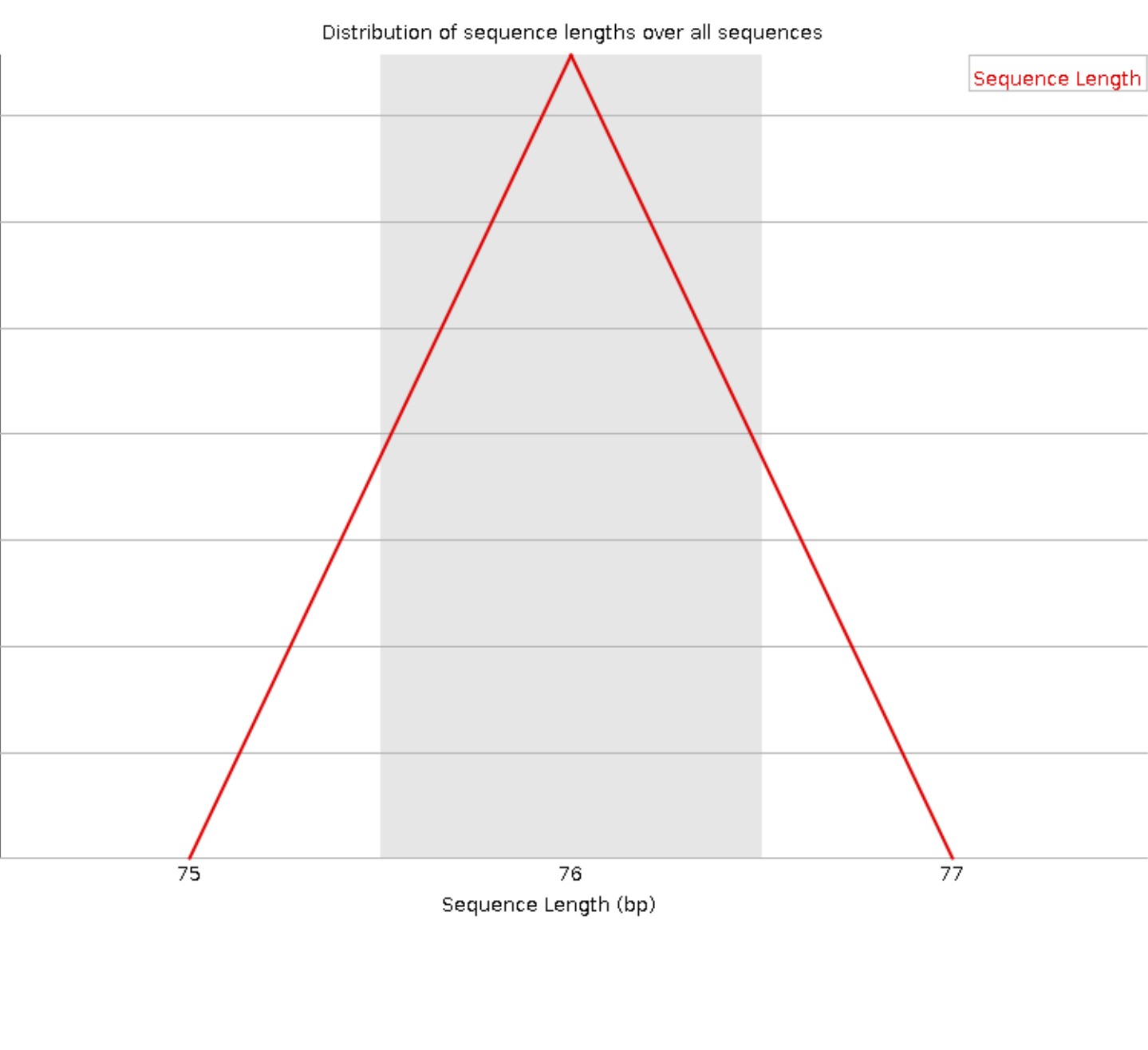
### Per sequence quality scores



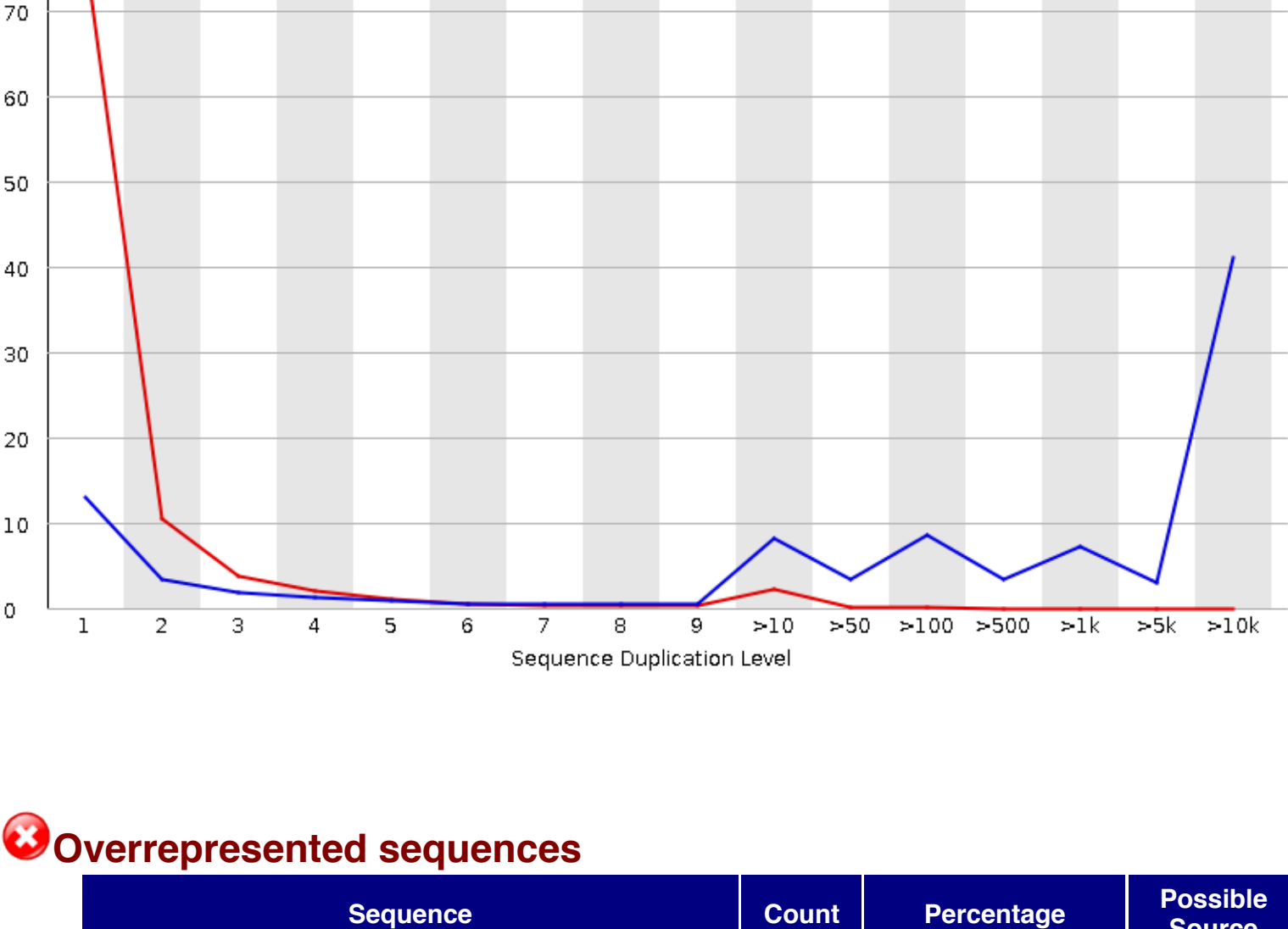
### Per base sequence content



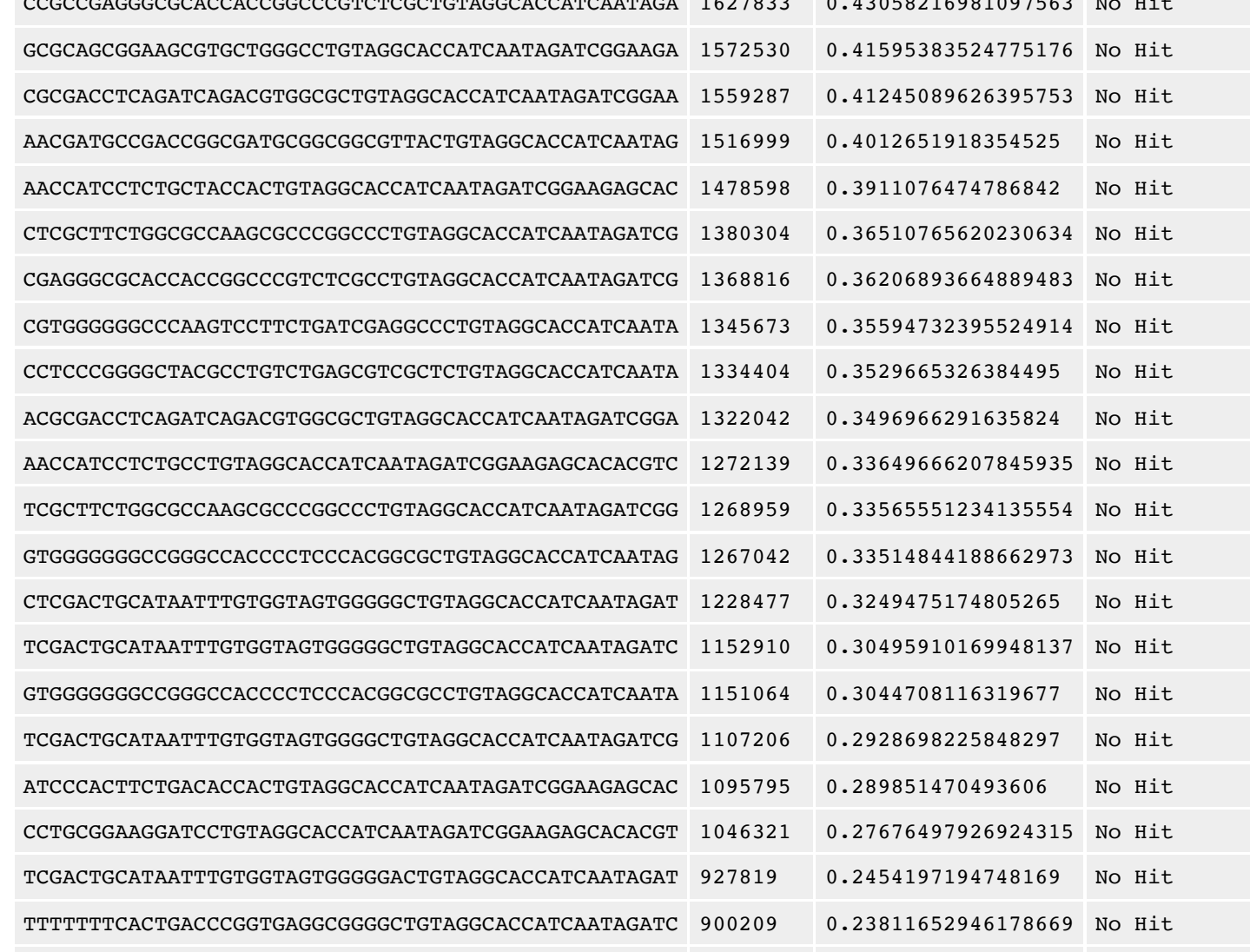
### Per sequence GC content



### Per base N content



### Sequence Length Distribution



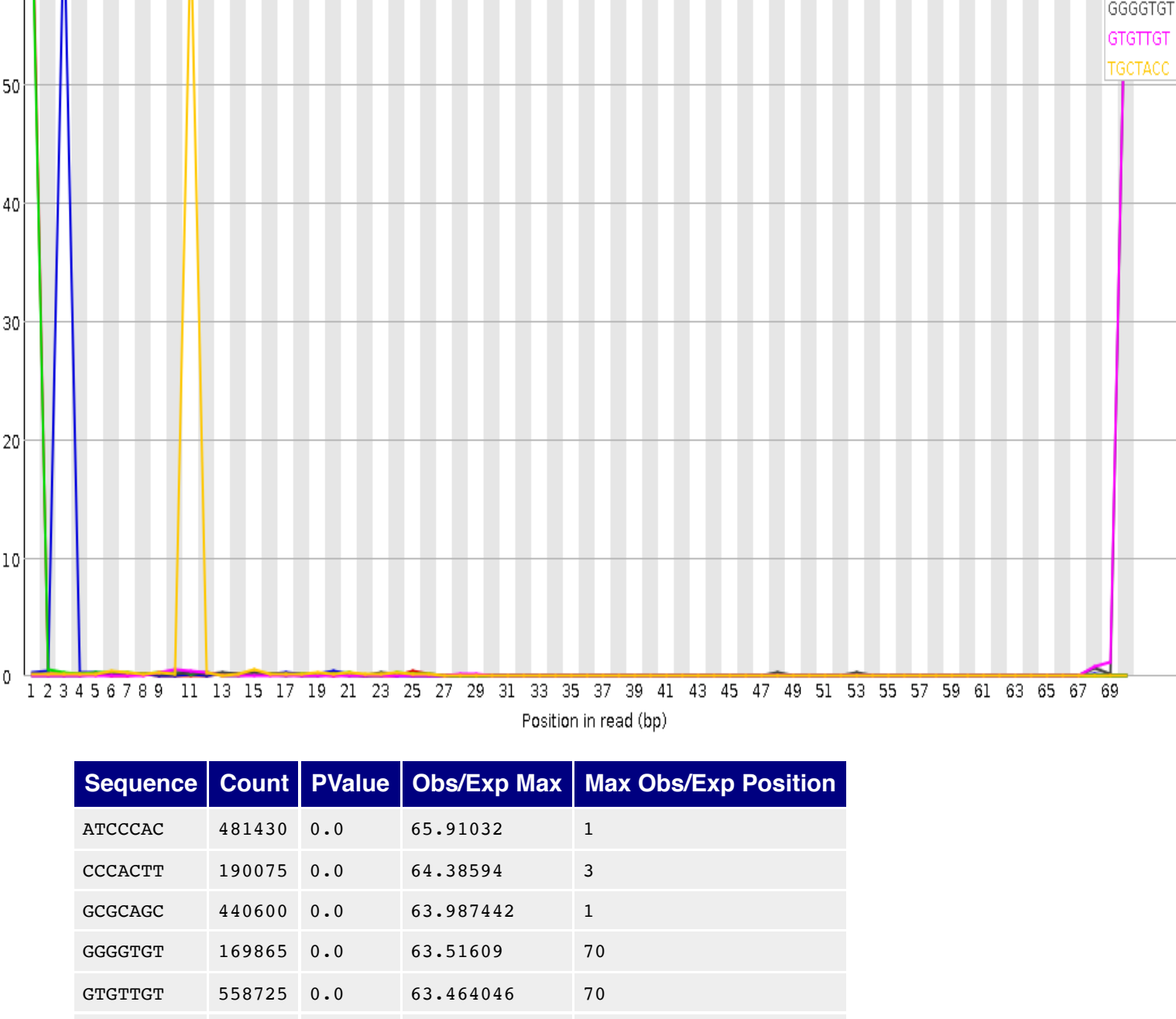
### Sequence Duplication Levels



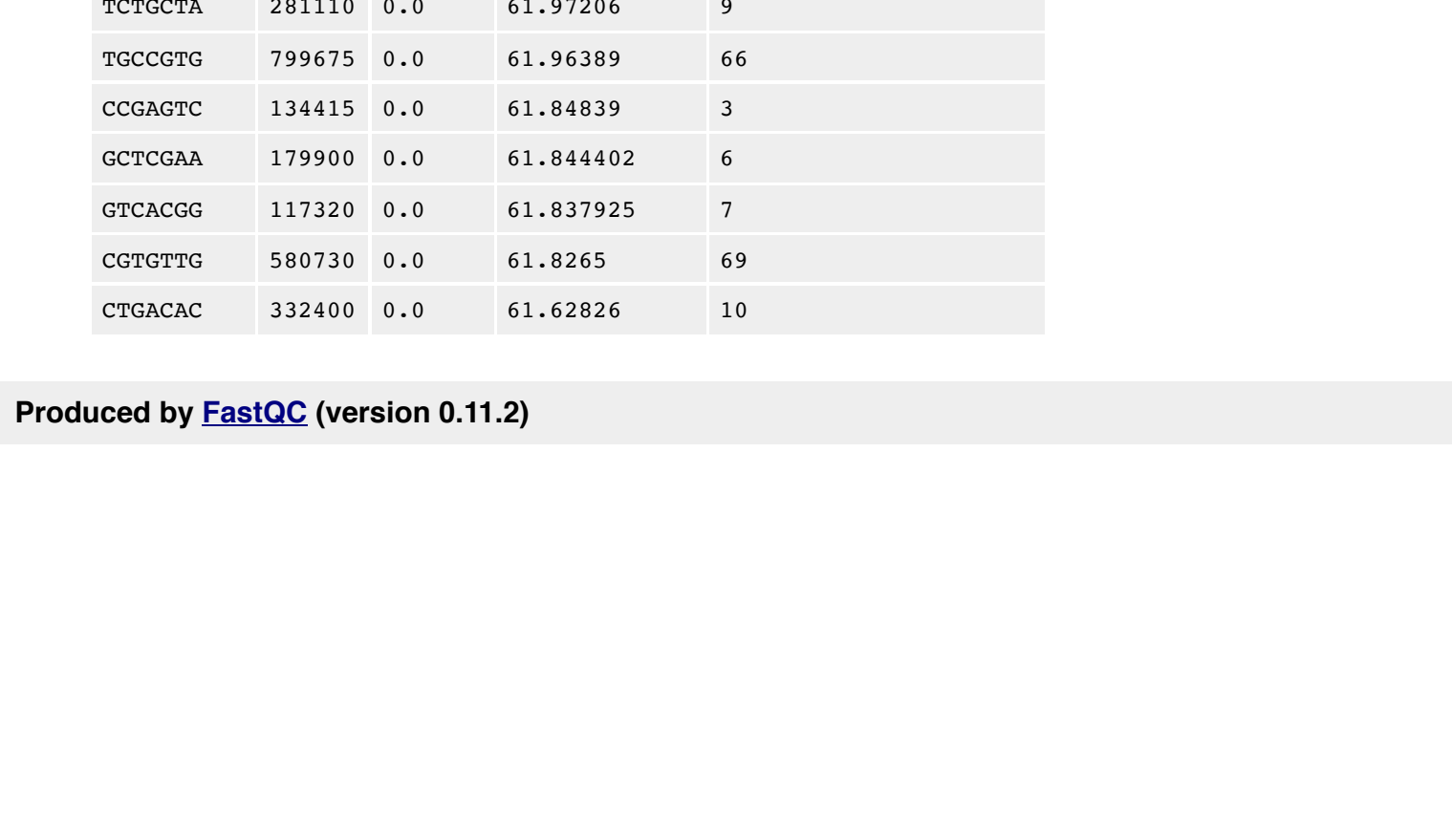
### Overrepresented sequences

| Sequence  | Count    | Percentage          | Possible Source  |
|---|----------|---------------------|--|
| CTGTAGGCACCATCAATAGATCGGAAGAGCACACGTCTGAACTCCAGTC   | 10588610 | 2.8008196596838832  | Illumina Multiplexing PCR Primer 2.01 (100% over 33bp) |
| CCGCCGAGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAG  | 7350290  | 1.944243553816587   | No Hit   |
| ACGATGCCGACCGCGGATGCGCGCGGCTTCTGTAGGCACCATCAATAGAT  | 2176818  | 0.5757955623971184  | No Hit   |
| AAGCATGCGGACCGGAGTGGGCGGCGTCTGTAGGCACCATCAATAGA     | 2097414  | 0.5547922121691339  | No Hit   |
| ACGATGCCGACCGCGGATGCGCGCGGCTTCTGTAGGCACCATCAATAGA   | 1842720  | 0.48742246652702154 | No Hit   |
| CCGCGGAGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAGA | 1627833  | 0.43058216981097563 | No Hit   |
| GGCCAGCGGAGGCGTGGTGGCGCTGTAGGCACCATCAATAGATCGAAGA   | 1572530  | 0.41595383524775176 | No Hit   |
| CGCGACTCATGATCAGGACGTCGGGCTGTAGGCACCATCAATAGATCGA   | 1559287  | 0.41245508962395753 | No Hit   |
| AAGCATGCGGACCGGATGCGCGCGGCTTCTGTAGGCACCATCAATAG     | 1516999  | 0.4012651918354525  | No Hit   |
| AACCATCTCTGTACTCACTGTAGGCACCATCAATAGATCGGAAGAGCAC   | 1478598  | 0.3911076474786842  | No Hit   |
| CTCGCTCTGGCCGAAAGCGCCGCTCTGTAGGCACCATCAATAGATCG     | 1380304  | 0.36510765620230634 | No Hit   |
| CGAGGGGCGCACCGCGGATGCGCGGCTTCTGTAGGCACCATCAATAG     | 1368816  | 0.36206893664889483 | No Hit   |
| CGAGGATCCCGACCAAGTCTCTGTAGGCACCATCAATAGATCGAAGA     | 1345673  | 0.35594732395524914 | No Hit   |
| CTCCCGGGGCTAGCCCTGTCTGTAGGCACCATCAATAGATCGAAGA      | 1334404  | 0.3529665326384495  | No Hit   |
| ACCGACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC     | 1227020  | 0.48742246652702154 | No Hit   |
| AACCATCTCTGTACTCACTGTAGGCACCATCAATAGATCGGAAGAGCAC   | 1272139  | 0.3364966207845935  | No Hit   |
| TGGCTCTGGCGCAAGCGGCGGCTGTAGGCACCATCAATAGATCG        | 1268959  | 0.3365551234135554  | No Hit   |
| GTGCACTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT    | 1228477  | 0.3249475174805265  | No Hit   |
| TGCACTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT     | 1107206  | 0.2928698225848627  | No Hit   |
| ATCCCACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC    | 1095795  | 0.289851470493606   | No Hit   |
| CCTGCGAAGGATCTCTGTAGGCACCATCAATAGATCGGAAGAGCAC      | 1046321  | 0.2767649792624315  | No Hit   |
| TGCATCTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT    | 927819   | 0.2451891973478169  | No Hit   |
| TTTTTCTCACTGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAG     | 900209   | 0.238116529474861   | No Hit   |
| ATCCCACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC    | 891082   | 0.235702239130036   | No Hit   |
| CCTGCGAAGGATCTCTGTAGGCACCATCAATAGATCGGAAGAGCAC      | 792728   | 0.20968646188516576 | No Hit   |
| GGCCAGCGGAGGCGTGGTGGCGCTGTAGGCACCATCAATAGATCGAAGA   | 746661   | 0.1975011647348623  | No Hit   |
| ATCCCACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC    | 734201   | 0.19350533903501655 | No Hit   |
| AAAGCATCCCGACCGGATGCGCGGCTTCTGTAGGCACCATCAATA       | 706115   | 0.18677624107391672 | No Hit   |
| CTCCCGGGGCTAGCCCTGTCTGTAGGCACCATCAATAGATCGAAGA      | 705618   | 0.18664477836343227 | No Hit   |
| CCTGCTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT     | 690417   | 0.1826292391257848  | No Hit   |
| CAGTCCGGGCGGACCATCTGTAGGCACCATCAATAGATCGGAAGAGCAC   | 687348   | 0.18181213506225453 | No Hit   |
| GTGCGGGGCCCAAGTCTCTGTAGGCACCATCAATAGATCGAAGA        | 657237   | 0.17384739929713686 | No Hit   |
| CTGCACTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT    | 645757   | 0.17081079584369294 | No Hit   |
| ATCCCACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC    | 631052   | 0.1669213959082766  | No Hit   |
| CCTGCGAAGGATCTCTGTAGGCACCATCAATAGATCGGAAGAGCAC      | 628544   | 0.16625774225099862 | No Hit   |
| CGATCCCGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT       | 616219   | 0.16299762573848153 | No Hit   |
| CGCGAGGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAG   | 610073   | 0.16137193193840604 | No Hit   |
| AAGCATGCGGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT     | 605418   | 0.16014062626978398 | No Hit   |
| ACCCCACTCTGACACCCTGTAGGCACCATCAATAGATCGGAAGAGCAC    | 584504   | 0.1570419274595874  | No Hit   |
| AAAGCATCCCGACCGGATGCGCGGCTTCTGTAGGCACCATCAATA       | 578863   | 0.1531164969399753  | No Hit   |
| AAATGATTTTTGAGCAGGACTGTAGGCACCATCAATAGATCGGAAGA     | 567595   | 0.1501359701356716  | No Hit   |
| ACGATGCCGACCGCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT    | 566094   | 0.14973893687925877 | No Hit   |
| CGATCCCGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT       | 552430   | 0.14612463813467186 | No Hit   |
| ATCCGATCCCGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT    | 525944   | 0.13911876016708336 | No Hit   |
| TTTTTCTCACTGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAG     | 521721   | 0.1380017238967093  | No Hit   |
| AACCATCTCTGTACTCACTGTAGGCACCATCAATAGATCGGAAGAGCAC   | 521229   | 0.1378715837487046  | No Hit   |
| TGCTCTGGCGCAAGCGGCGGCTGTAGGCACCATCAATAGATCG         | 519415   | 0.1378803297128688  | No Hit   |
| GFGGCGGGGCGGCGGACCCCTCAGCGGCCAGCCCTCTGTAGGCACCATCA  | 517471   | 0.1368775457889448  | No Hit   |
| TCCCGGAGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATA   | 513570   | 0.13584568254226492 | No Hit   |
| CCGAGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAGAT   | 497685   | 0.13164390154418507 | No Hit   |
| GGCCAGCGGAGGCGTGGGCGGCTGTAGGCACCATCAATAGATCGGAAGA   | 477025   | 0.12617907337796977 | No Hit   |
| AGGGGAGATCACCAGTACGGAAGGTGGTCTGTAGGCACCATCAATAGA    | 472218   | 0.1249075618099641  | No Hit   |
| CTGTAGGCACCATCAATAGATCGGAAGAGCACACGTCTGAACTCCAGTC   | 450815   | 0.11924620085926196 | Illumina Multiplexing PCR Primer 2.01 (96% over 33bp)  |
| GTGGGGGCGGCGGCGCCCTCAGCGGCGGCTTCTGTAGGCACCATCAATAG  | 448765   | 0.11870395024257555 | No Hit   |
| AACGATGCCGACCGCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT   | 443761   | 0.1173803297128688  | No Hit   |
| CTGCACTGCATAATTTGTGTAGTGCGGCTGTAGGCACCATCAATAGAT    | 431618   | 0.11416835447461361 | No Hit   |
| ATGTACACCGGATGCGCGGATGCGCGGCTTCTGTAGGCACCATCAATAG   | 407222   | 0.10771530762354929 | No Hit   |
| TGTAGGCACCATCAATAGATCGGAAGAGCACACGTCTGAACTCCAGTC    | 405476   | 0.10725346880563003 | Illumina Multiplexing PCR Primer 2.01 (100% over 34bp) |
| GAGGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAGATCGG | 400226   | 0.10586477820192092 | No Hit   |
| CTGTAGGCACCATCAATAGATCGGAAGAGCACACGTCTGAACTCCAGTC   | 392536   | 0.103830677108107   | Illumina Multiplexing PCR Primer 2.01 (100% over 33bp) |
| CGTFFTTTCACTGACCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT  | 390806   | 0.10337307049012284 | No Hit   |
| ATCCCGGGGCGCACCACCGGCCGCTCTCGCCTGTAGGCACCATCAATAGAT | 387449   | 0.10248510204123684 | No Hit   |
| CCTCTCCGACATCGGCCCTGTAGGCACCATCAATAGATCGGAAGAGCAC   | 384705   | 0.1024734643914153  | No Hit   |
| ATGTACACCGGATGCGCGGATGCGCGGCTTCTGTAGGCACCATCAATAGAT | 379647   | 0.10042137554787713 | No Hit   |

### Adapter Content



### Kmer Content



| Sequence | Count  | PValue | Obs/Exp Max | Max Obs/Exp Position |
|----------|--------|--------|-------------|----------------------|
| ATCCAC   | 481430 | 0.0    | 65.91032    | 1                    |
| CCCACT   | 190075 | 0.0    | 64.38594    | 3                    |
| GCCAGC   | 440600 | 0.0    | 63.987442   | 1                    |
| GGGGTG   | 169865 | 0.0    | 63.51609    | 70                   |
| GTTGTT   | 558725 | 0.0    | 63.464046   | 70                   |
| TGCTACC  | 261515 | 0.0    | 62.87718    | 11                   |
| TCTAGGG  | 99640  | 0.0    | 62.65088    | 2                    |
| TGACACC  | 313985 | 0.0    | 62.412216   | 11                   |
| TAGGGGT  | 100290 | 0.0    | 62.372917   | 4                    |
| ATCCTCT  | 578325 | 0.0    | 62.308665   | 5                    |
| CGGGTG   | 180950 | 0.0    | 62.220688   | 69                   |
| AGTCACG  | 129645 | 0.0    | 62.13122    | 6                    |
| TCCCACT  | 324980 | 0.0    | 62.004993   | 2                    |
| TCTGCTA  | 281110 | 0.0    | 61.97206    | 9                    |
| TGCCGTG  | 799675 | 0.0    | 61.96389    | 66                   |
| CCGATGC  | 134415 | 0.0    | 61.84839    | 3                    |
| GCTGAA   | 179900 | 0.0    | 61.844402   | 6                    |
| GTCACGG  | 117320 | 0.0    | 61.837925   | 7                    |
| CGTGTG   | 580730 | 0.0    | 61.8265     | 69                   |
| CTGCAC   | 332400 | 0.0    | 61.62826    | 10                   |