

# FastQC Report

## Summary

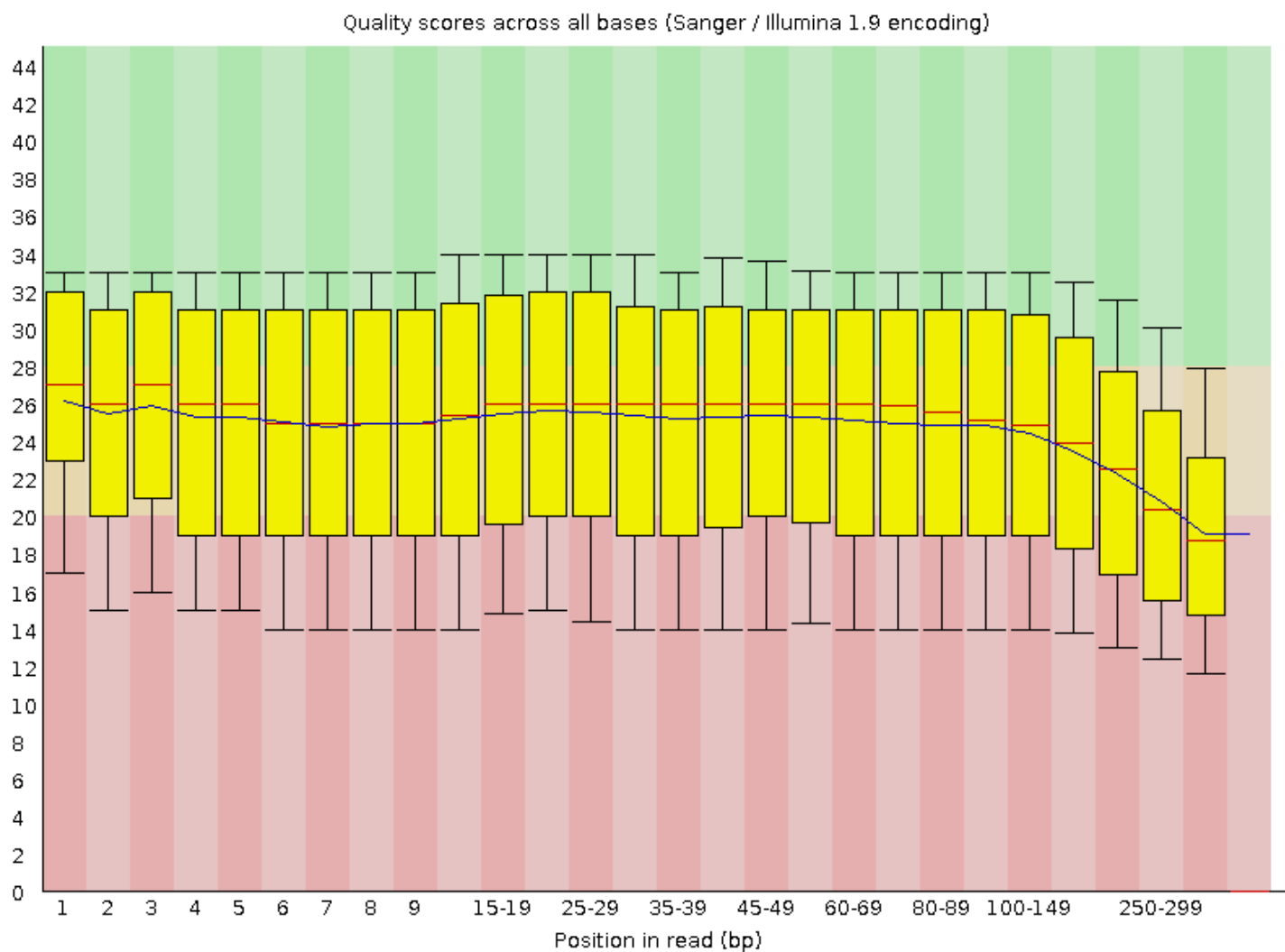
Thu 4 Jul 2013  
rawlib.basecaller.bam

-  [Basic Statistics](#)
-  [Per base sequence quality](#)
-  [Per sequence quality scores](#)
-  [Per base sequence content](#)
-  [Per base GC content](#)
-  [Per sequence GC content](#)
-  [Per base N content](#)
-  [Sequence Length Distribution](#)
-  [Sequence Duplication Levels](#)
-  [Overrepresented sequences](#)
-  [Kmer Content](#)

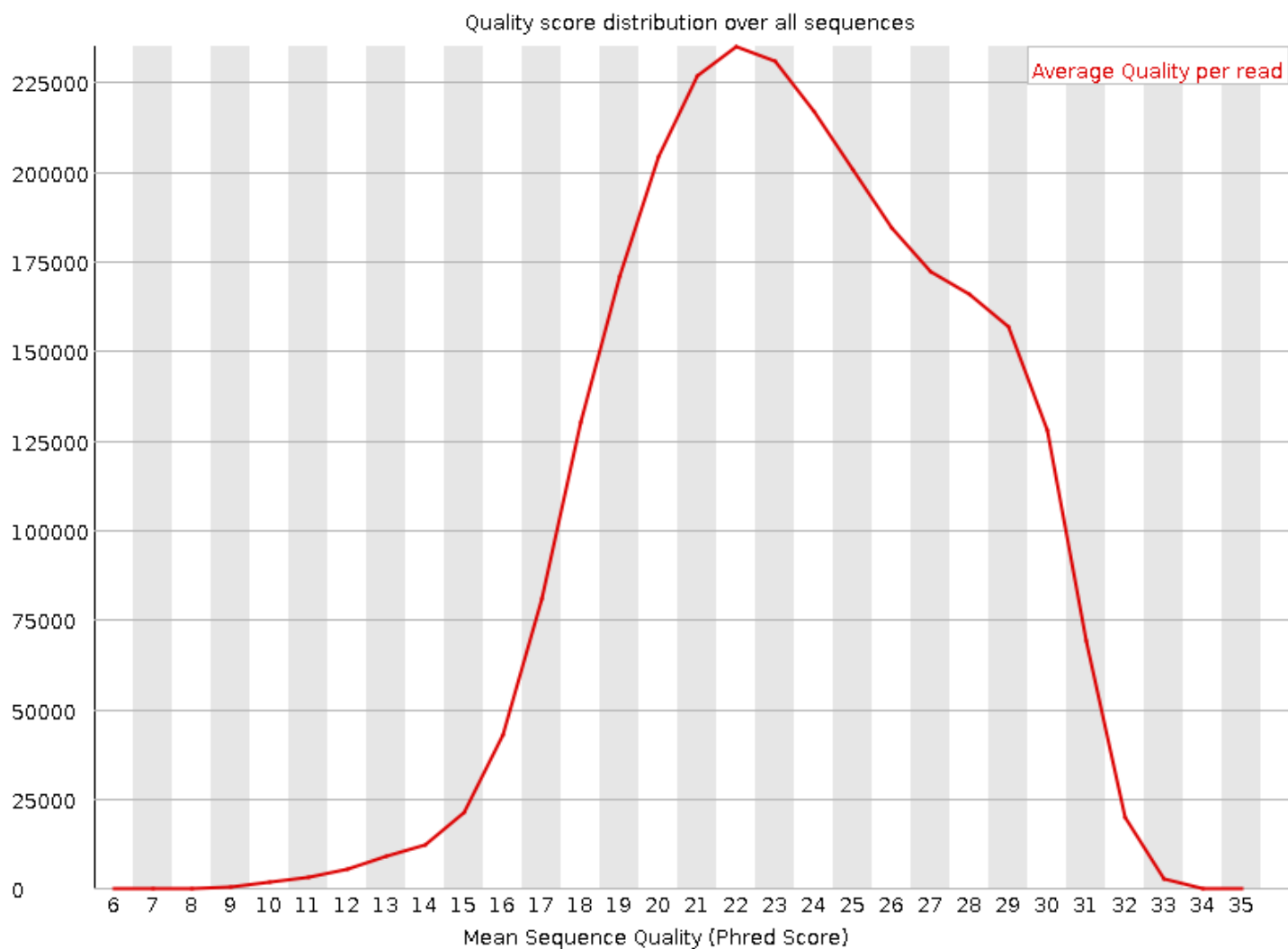
### Basic Statistics

| Measure            | Value                   |
|--------------------|-------------------------|
| Filename           | rawlib.basecaller.bam   |
| File type          | Conventional base calls |
| Encoding           | Sanger / Illumina 1.9   |
| Total Sequences    | 2695575                 |
| Filtered Sequences | 0                       |
| Sequence length    | 8-359                   |
| %GC                | 48                      |

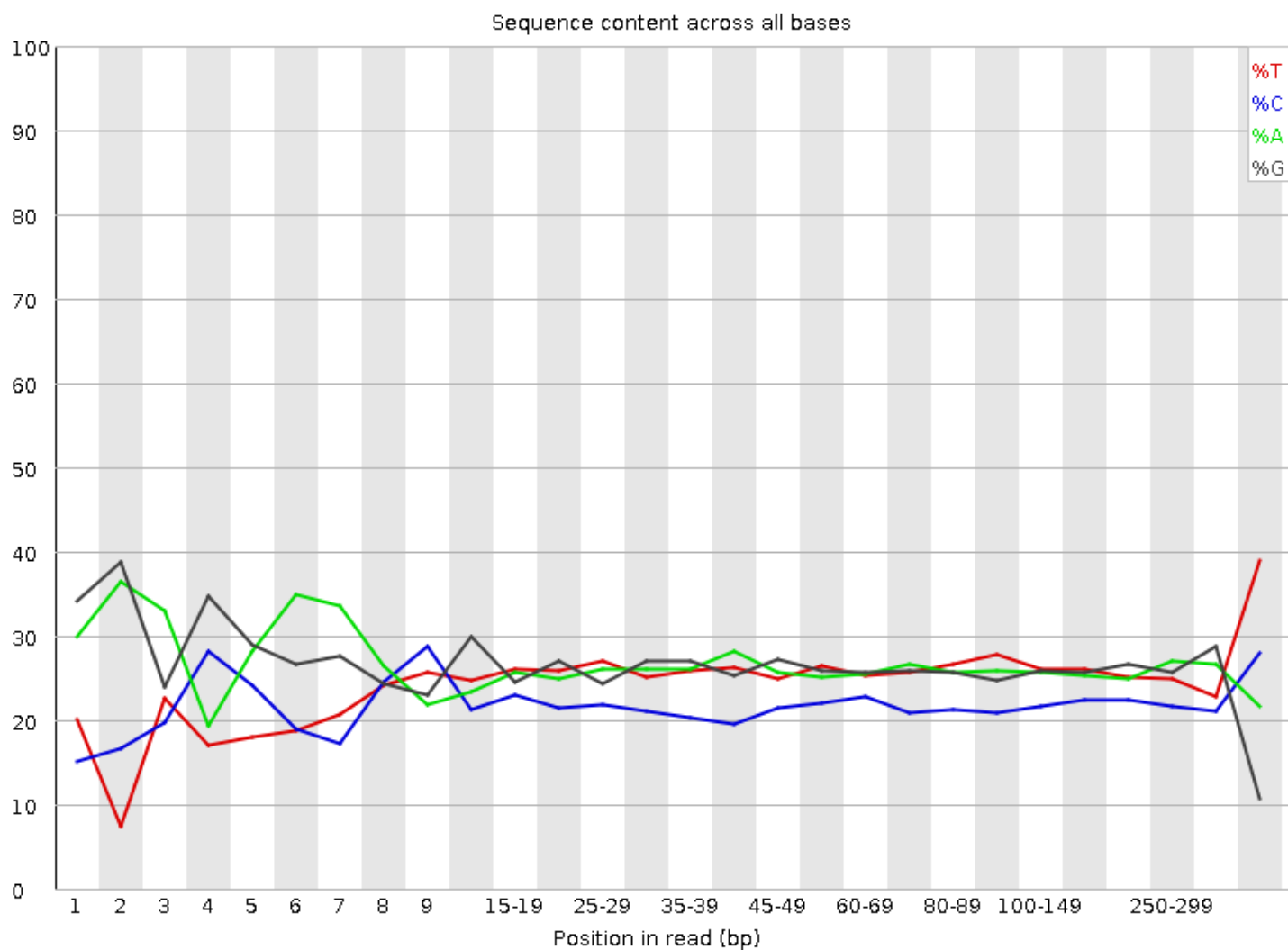
### Per base sequence quality



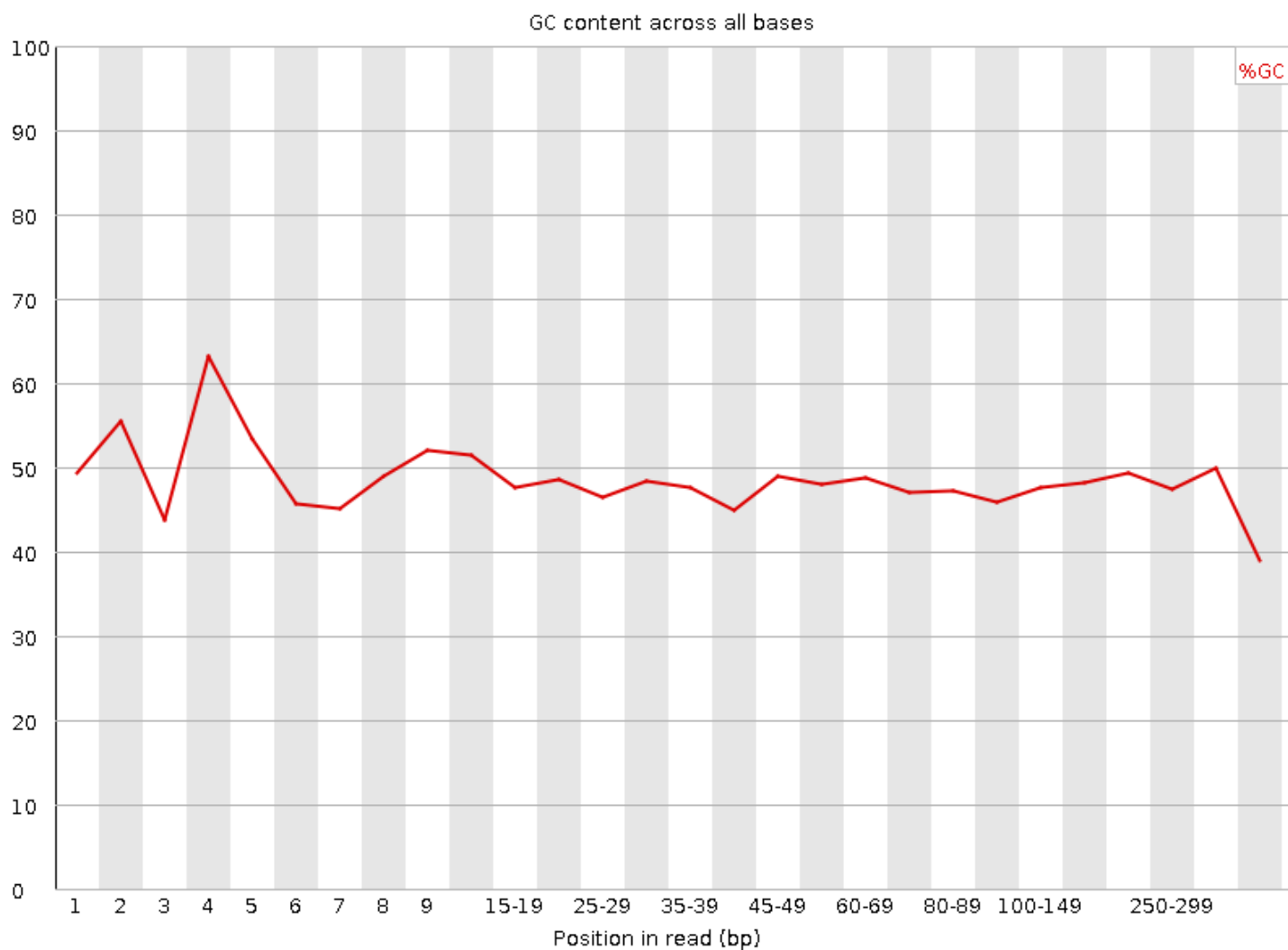
## Per sequence quality scores



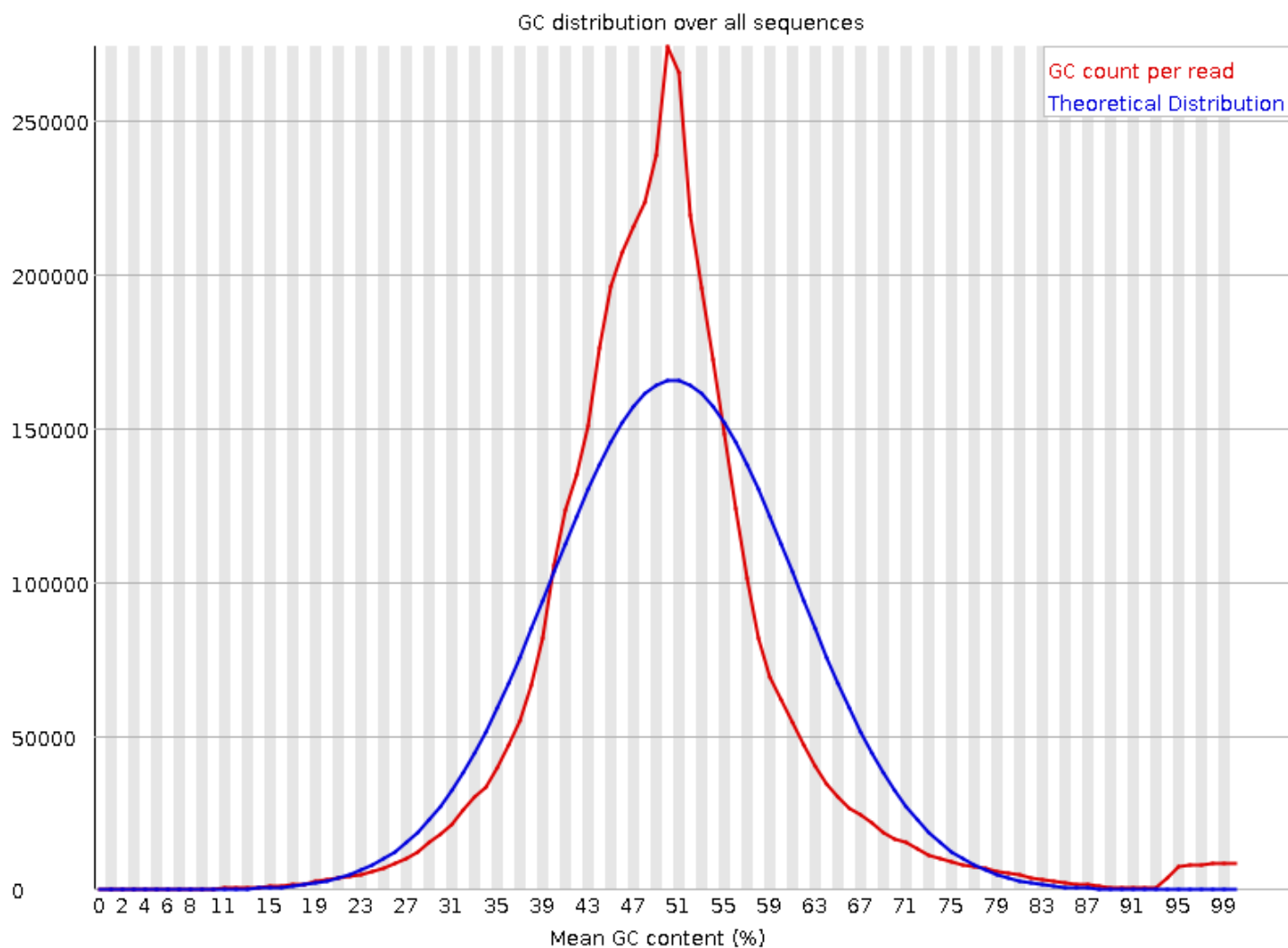
## Per base sequence content



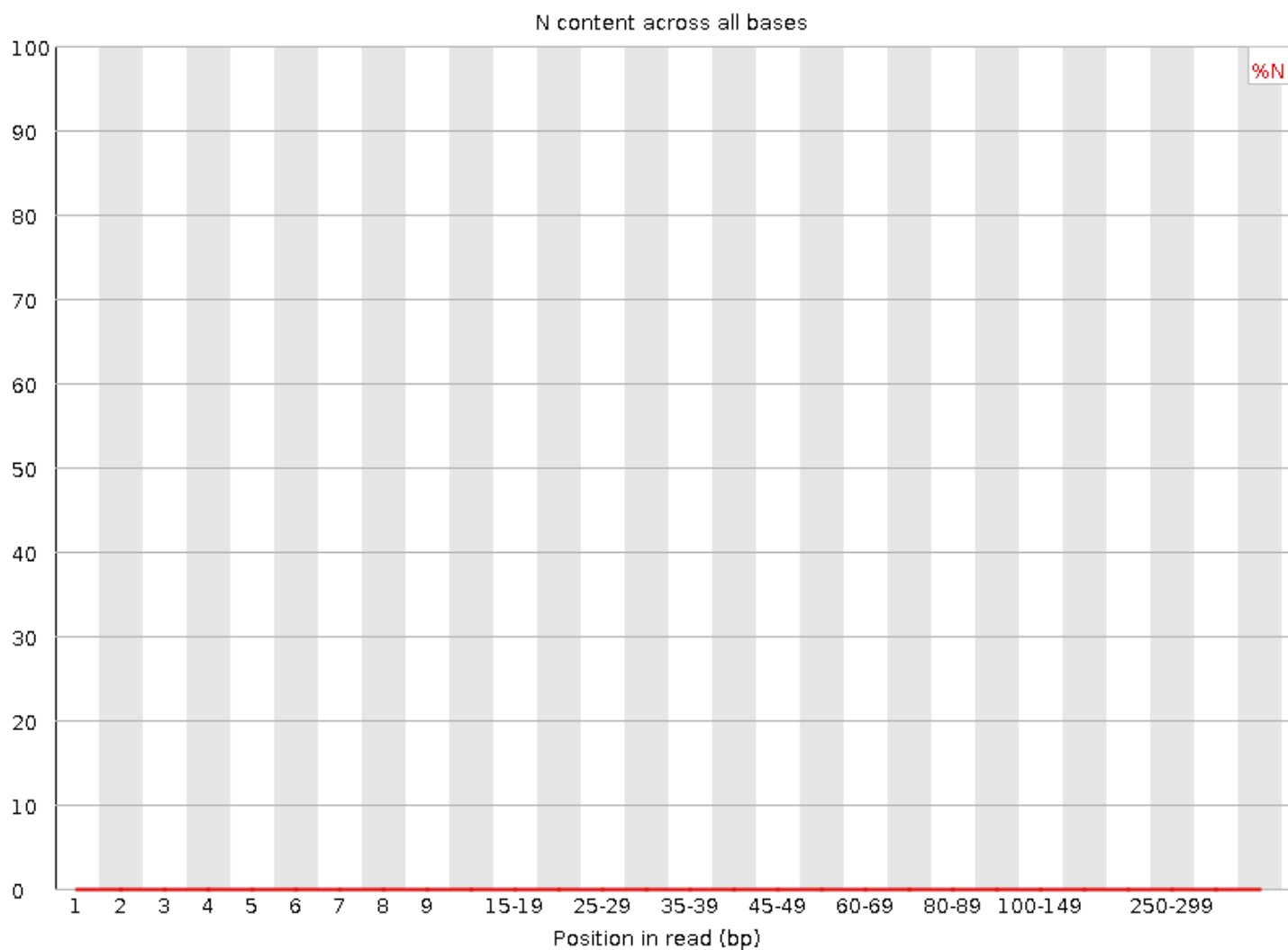
**Per base GC content**



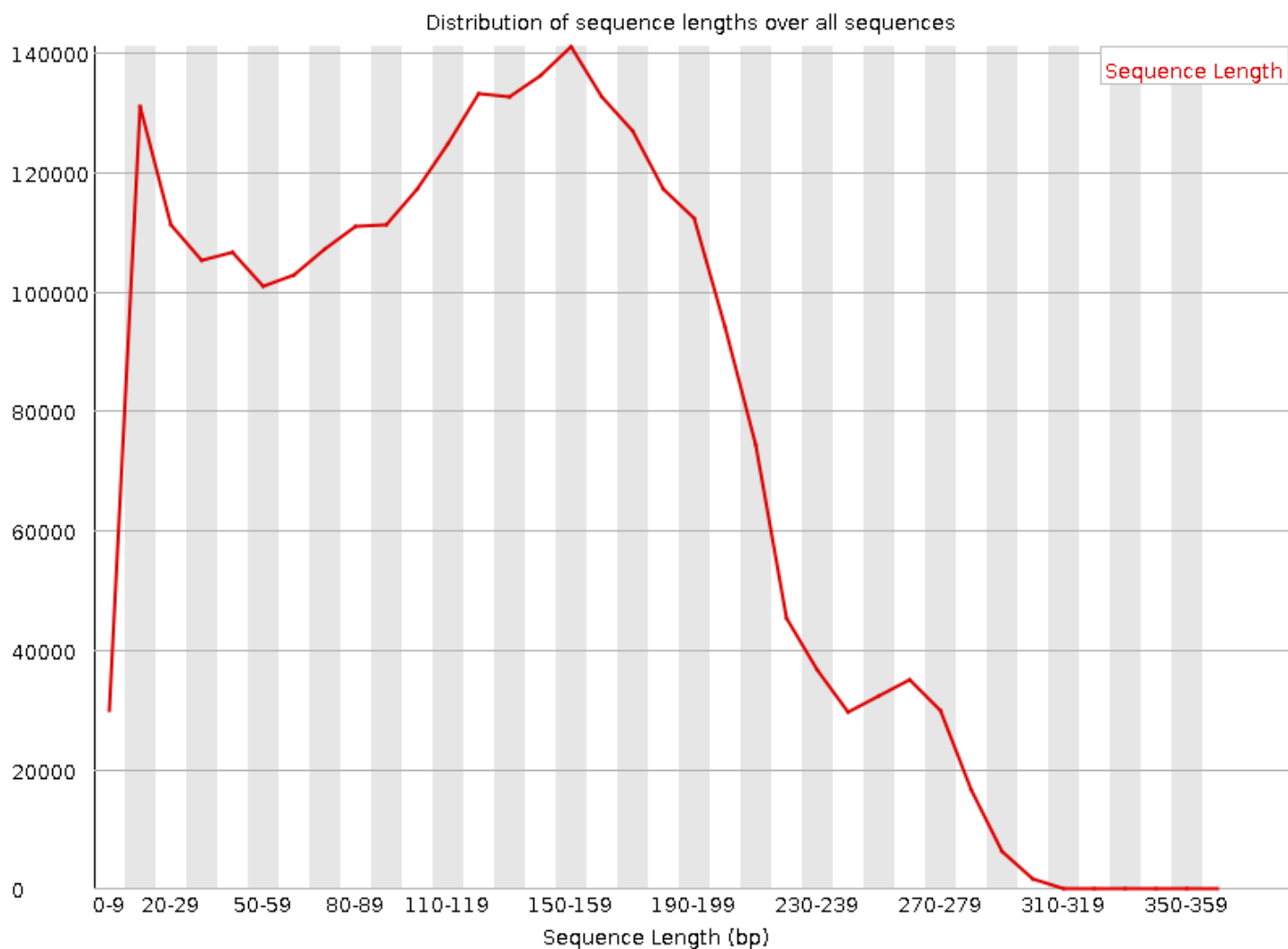
Per sequence GC content



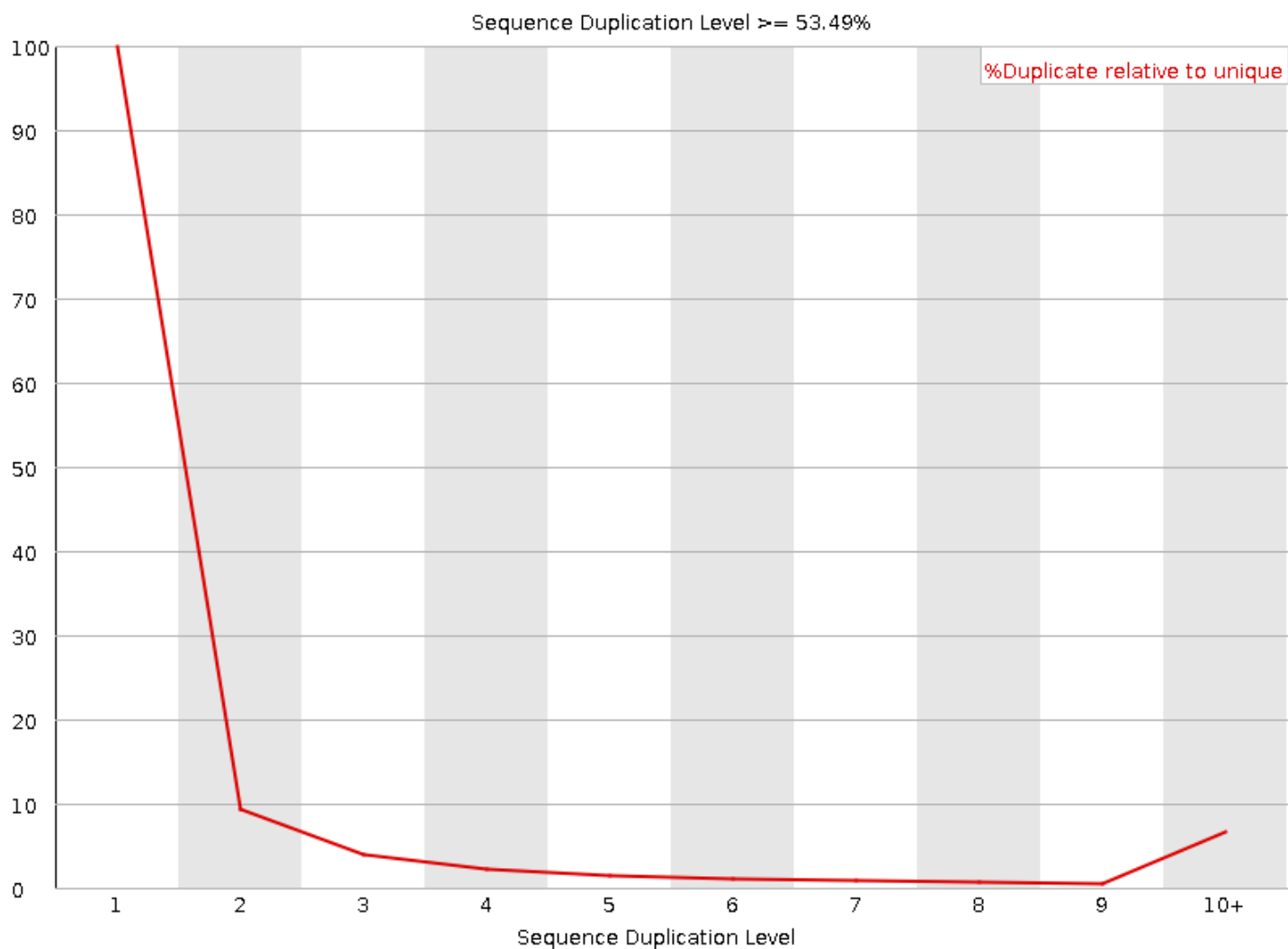
**Per base N content**



## Sequence Length Distribution



## Sequence Duplication Levels

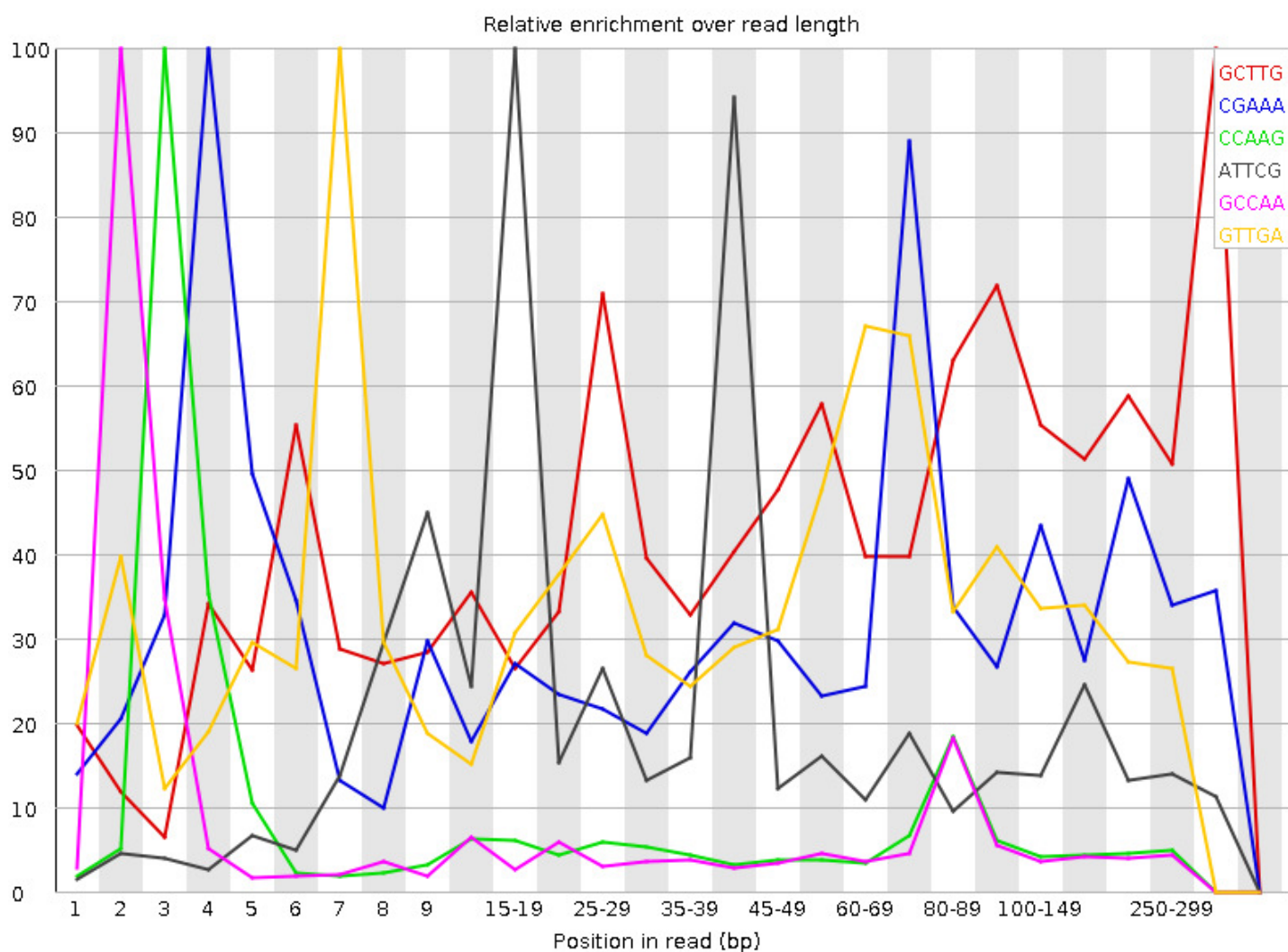


## Overrepresented sequences

| Sequence                                            | Count | Percentage          | Possible Source |
|-----------------------------------------------------|-------|---------------------|-----------------|
| GGACAAACCGGGGGCATTTCGTATCATTACGCGAGAGGTGAAATTCGTGGA | 57954 | 2.1499680031162183  | No Hit          |
| CATGCAACTATACCCCAACGCAAGGCGGGGTGCAATTATTAGAACAGACC  | 24455 | 0.9072275859510494  | No Hit          |
| TACCTGATTGATTCTGTCAGCGGATATGCTCAAGTAAAAGATTAAGCCA   | 20678 | 0.7671090583641709  | No Hit          |
| GAAAGCGTGGCCTATCGATCCTTTTAATCCTGATTGTTTCAGGTAAGAGG  | 14630 | 0.5427413446110756  | No Hit          |
| GATGAACCAAACGTGGAGTTAAGGTGCCTAACTTCTCGCTCATGAGACCC  | 10790 | 0.400285653339269   | No Hit          |
| GGTACGGACTCAGGGAATCCGACTGTCTAATTAACAGAGGTGACAGAT    | 10457 | 0.387932073861792   | No Hit          |
| TAAACCGTTGAAATTCTTCCATGTCCGGGATAGGGTATTGTAATTATTGC  | 9944  | 0.3689008838559491  | No Hit          |
| TAACGAGTAGGAAGGTCGTGGCGGTTGCGTTGAAGGCTATGAGCGTAGGC  | 9006  | 0.33410311343590887 | No Hit          |
| AAGTGGGCCATTTTTGTTAAGCAGAACTGGCGCTGTGGGATGAACCAAAC  | 8285  | 0.3073555734861764  | No Hit          |
| CAGCCAAGCGTCCATAGCGACGTTGCTTTTGTATCCTTCGATGTCGCTCT  | 7908  | 0.29336968921287665 | No Hit          |

|                                                      |      |                     |        |
|------------------------------------------------------|------|---------------------|--------|
| GGACAACCGGGGGGCATTTCGTATCATTACGCGAGAGGTGAAATTCGTGGAC | 7795 | 0.2891776337145136  | No Hit |
| TAGTGTATCTCGTTATTGCTGCGGTTAAAAAGCTCGTAGTTGGATCTAGG   | 7436 | 0.27585951049405044 | No Hit |
| TCAGGATAGCTGGATCTCAGGCAGTTATATTCGGTAAAGCTAATGATTAG   | 7258 | 0.2692560956382219  | No Hit |
| GACTCAGGGAATCCGACTGTCTAATTAACAGAGGTGACAGATGGTCCT     | 7200 | 0.26710442113463734 | No Hit |
| AGAGCTTATGCCCTATGTATGGCCTTGGCGTCGTAGTGAATTCTGCGACG   | 6434 | 0.23868747855281341 | No Hit |
| TCTCAACCTGAACTCAGTCGTGATTACCCGCTGAACTTAAGCATATCATT   | 6365 | 0.23612772785027314 | No Hit |
| AGTGGTTGGAACGGTTGGCCAGTTGGTTGATGCTTGTCGGCGCAGTTCT    | 6289 | 0.23330829229385197 | No Hit |
| AGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCAGCTCTCCTAGTG    | 6017 | 0.22321768082876567 | No Hit |
| GGTTGGAACGGTTGGCCAGTTGGTTGATGCTTGTCGGCGCAGTTCTGTC    | 5302 | 0.19669272789664544 | No Hit |
| ACCCGAAAGATGGTGAACATATGCCTGAGCAGGATGAAGCCAGAGGAACT   | 5216 | 0.19350231397753725 | No Hit |
| ACAGGGATAACTGGCTTGTGGCAGCCAAGCGTCCATAGCGACGTTGCTTT   | 5212 | 0.19335392263246245 | No Hit |
| TGGTTGTTACGGGTAACGGAGAATAAGGGTTCGACTCCGGAGAGGGAGCC   | 5193 | 0.19264906374335716 | No Hit |
| GAAGCAGAATTCGCCAAGCGTTGGATTGTTACCCACTAATAGGGAACGT    | 5106 | 0.1894215519879803  | No Hit |
| TGGCAACACGAGAGCTTATGCCCTATGTATGGCCTTGGCGTCGTAGTGAA   | 5093 | 0.1889392801164872  | No Hit |
| CAAACGTGGAGTTAAGGTGCCTAACTTCTCGCTCATGAGACCCCATAAAA   | 4698 | 0.17428563479035086 | No Hit |
| ACTGACAGATTGAAAGCTCTTTCTCGATTGTTGGTGGTTGGTGGTGCATGGC | 4679 | 0.17358077590124554 | No Hit |
| ACTGGCGCTGTGGGATGAACCAAACGTGGAGTTAAGGTGCCTAACTTCTC   | 4515 | 0.16749673075317884 | No Hit |
| GTTGGAACGGTTGGCCAGTTGGTTGATGCTTGTCGGCGCAGTTCTGTCT    | 4336 | 0.16085621806108158 | No Hit |
| AGTGGAACCGGAGACAGTTGATGTTGCTTGGAGACAAGCTTGGTGACTGG   | 4185 | 0.15525444478450795 | No Hit |
| GATCTGTGTTCTTCGGAGTGACGCGACCCACGGCCCTGTGCGTGTCACTT   | 4108 | 0.15239791139181807 | No Hit |
| ATAGCTGGATCTCAGGCAGTTATATTCGGTAAAGCTAATGATTAGAGGCC   | 4103 | 0.15221242221047457 | No Hit |
| TAGAGGGATAAGCGGTGTTTAGCCGCACGAGATTGAGCGATAACAGGTCT   | 4078 | 0.1512849763037571  | No Hit |
| CGGGTGTCGTTTCCTATGCTACGCCGACGGCGTTGGCTGCTCGTTCTAGC   | 3924 | 0.14557190951837734 | No Hit |
| GCTGTGGGATGAACCAAACGTGGAGTTAAGGTGCCTAACTTCTCGCTCAT   | 3866 | 0.14342023501479276 | No Hit |
| TCAGGCAGTTATATTCGGTAAAGCTAATGATTAGAGGCCTTGGGGACGTA   | 3853 | 0.14293796314329968 | No Hit |
| CAGCCAAGCGTCCATAGCGACGTTGCTTTTTGATCCTTCGATGTCGGCTC   | 3820 | 0.14171373454643257 | No Hit |
| GAAGCATTAAGCGGAGCCATTTTATGGCACCGTGACTCTCCTCGAAGACA   | 3658 | 0.13570388507090325 | No Hit |
| GGAGTTTGACTGGGGCGGTACATCTATCAAATCGTAACGTAGGTGTCCTA   | 3542 | 0.13140053606373409 | No Hit |
| GAAGTTTCCCTCAGGATAGCTGGATCTCAGGCAGTTATATTCGGTAAAGC   | 3342 | 0.12398096880999415 | No Hit |
| TGGGAGTCTTCGGACGACAGTGAAATACCACCACTTTCATCGACTCTTTA   | 3228 | 0.1197518154753624  | No Hit |
| AAGCATTAAGCGGAGCCATTTTATGGCACCGTGACTCTCCTCGAAGACAG   | 3170 | 0.11760014097177782 | No Hit |
| GGACAAACCGGGGGGCATTTCGTATCATTACGCGAGAGGTGAAATTCGTGG  | 2971 | 0.1102176715543066  | No Hit |
| CCAGTGCTCTGAATGTTAAATCGTAGTAATTCGAGTAAGCGCGGGTAAAC   | 2820 | 0.10461589827773295 | No Hit |
| GTGATAAACTTCATCTAAGGCTAAATATCGACTCGATTGCGATAGCGAAC   | 2794 | 0.10365135453474676 | No Hit |
| ACATGTGCGTTGTCTAGCGCCAGGTCGTAACGAGTAGGAAGGTCGTGGCG   | 2775 | 0.10294649564564146 | No Hit |
| TAAGGGAAGTCGGCAAAC TAGATCCGTAACCTTCGGGAAAAGGATTGGCTC | 2768 | 0.10268681079176056 | No Hit |
| AGAGAGAGTTCAAGAGAACGTGAAATCGCTGGAGTGGAACCGGAGACAGT   | 2764 | 0.10253841944668578 | No Hit |

## ! Kmer Content



| Sequence | Count  | Obs/Exp Overall | Obs/Exp Max | Max Obs/Exp Position |
|----------|--------|-----------------|-------------|----------------------|
| GCTTG    | 968885 | 2.9515345       | 6.106902    | 300-349              |
| CGAAA    | 876190 | 2.6261063       | 7.5916796   | 4                    |
| CCAAG    | 701735 | 2.5151176       | 38.079727   | 3                    |
| ATTCG    | 788830 | 2.4308336       | 11.042055   | 15-19                |
| GCCAA    | 640685 | 2.296306        | 38.377346   | 2                    |
| GTTGA    | 899505 | 2.2914374       | 6.0845246   | 7                    |
| TCTTC    | 604830 | 2.2861323       | 8.037179    | 90-99                |
| TCTCG    | 604890 | 2.2290478       | 10.642368   | 8                    |
| GAAAG    | 898800 | 2.226946        | 9.331886    | 1                    |
| AGAGG    | 899060 | 2.2021105       | 10.348968   | 1                    |
| GACTC    | 604050 | 2.195265        | 9.688371    | 7                    |
| CAAAC    | 597965 | 2.1679893       | 46.93244    | 4                    |

|       |        |           |           |         |
|-------|--------|-----------|-----------|---------|
| TTGAT | 827205 | 2.161438  | 12.480903 | 8       |
| GCTCA | 580530 | 2.1097875 | 5.009564  | 25–29   |
| AAAGC | 691630 | 2.0729456 | 10.670861 | 2       |
| TCGTA | 660450 | 2.0352218 | 10.715128 | 15–19   |
| ACCGT | 552690 | 2.0086102 | 8.092911  | 4       |
| TCAAC | 546010 | 2.0072935 | 7.7186193 | 3       |
| CCAAC | 454735 | 1.9715642 | 8.431394  | 60–69   |
| TTCGG | 645965 | 1.9678166 | 5.098487  | 9       |
| CAGTT | 635315 | 1.9577667 | 5.656981  | 300–349 |
| TGGTT | 754725 | 1.9494948 | 5.117994  | 3       |
| GCGAA | 657595 | 1.9483919 | 5.8201027 | 70–79   |
| TGATT | 744825 | 1.9461832 | 13.684332 | 5       |
| CAACT | 527170 | 1.9380322 | 21.202312 | 5       |
| AGGTG | 772605 | 1.9188317 | 8.310038  | 35–39   |
| ATCCG | 527940 | 1.9186628 | 5.194099  | 200–249 |
| AGCAG | 643835 | 1.9076223 | 8.183675  | 3       |
| AAGGC | 643810 | 1.9075483 | 29.028828 | 5       |
| TGAAA | 741210 | 1.8837053 | 8.607549  | 35–39   |
| CGCCC | 366495 | 1.8784322 | 8.835066  | 60–69   |
| CTCAA | 504245 | 1.8537531 | 8.264539  | 2       |
| TGCCC | 425100 | 1.8474653 | 5.89307   | 9       |
| TTTTT | 671885 | 1.8259063 | 12.547928 | 300–349 |
| TCGAT | 591875 | 1.8239033 | 5.0384216 | 15–19   |
| AACTT | 581970 | 1.8141309 | 6.8515267 | 300–349 |
| TTGAC | 588670 | 1.8140271 | 8.39119   | 300–349 |
| AAACG | 604250 | 1.8110511 | 5.78167   | 9       |
| AAGAA | 721520 | 1.8083863 | 5.6953034 | 300–349 |
| CGTTG | 591810 | 1.8028431 | 6.789306  | 6       |
| TCATT | 569625 | 1.8004701 | 10.148149 | 20–24   |
| GAGAC | 606130 | 1.7959061 | 7.437911  | 300–349 |
| TATCC | 480020 | 1.7893633 | 5.580461  | 200–249 |
| CAAGA | 596015 | 1.7863693 | 5.8644967 | 80–89   |
| AGACC | 495975 | 1.7776448 | 13.110057 | 300–349 |
| ATCTC | 476870 | 1.777621  | 11.277019 | 7       |
| AAGCA | 581375 | 1.7424903 | 8.9051    | 2       |
| CTGAA | 573315 | 1.7423532 | 12.969076 | 300–349 |
| CTATC | 466555 | 1.7391698 | 5.269792  | 200–249 |
| GAGCT | 574750 | 1.726735  | 6.1092896 | 2       |
| GTTGC | 566655 | 1.7262126 | 10.978951 | 300–349 |

|       |        |           |           |         |
|-------|--------|-----------|-----------|---------|
| CAAGG | 581040 | 1.7215669 | 28.857468 | 4       |
| TTGCG | 561655 | 1.7109812 | 11.385581 | 300-349 |
| TGCCA | 470605 | 1.7102932 | 6.6741443 | 80-89   |
| GTGAA | 680740 | 1.710239  | 9.485092  | 35-39   |
| TGAAC | 559465 | 1.700262  | 6.6717973 | 3       |
| TTGCC | 461300 | 1.6999121 | 7.230737  | 80-89   |
| CTTCG | 460890 | 1.6984011 | 5.4078927 | 8       |
| AGCCA | 473840 | 1.6983099 | 12.838793 | 2       |
| AAGCG | 568020 | 1.6829897 | 10.406347 | 6       |
| AACGA | 561265 | 1.682217  | 7.393668  | 2       |
| TCGTG | 551035 | 1.6786294 | 8.861659  | 40-44   |
| AATTC | 534810 | 1.6671226 | 10.268858 | 40-44   |
| CTTCA | 445960 | 1.6623983 | 7.682185  | 90-99   |
| CGGAC | 463410 | 1.641929  | 8.784098  | 5       |
| ACCAC | 377035 | 1.6346856 | 13.889459 | 300-349 |
| GAGAG | 667100 | 1.6339599 | 8.366394  | 30-34   |
| GCCAT | 447530 | 1.6264331 | 6.8703423 | 7       |
| CGTGG | 546880 | 1.6242113 | 10.372867 | 6       |
| GAAAT | 635060 | 1.6139368 | 7.4383616 | 35-39   |
| AACAG | 535620 | 1.605354  | 5.3414497 | 60-69   |
| GCAAA | 535170 | 1.6040052 | 5.884453  | 250-299 |
| ATCGA | 525190 | 1.5960975 | 9.138597  | 300-349 |
| AGTTT | 610710 | 1.595749  | 6.231976  | 3       |
| CCCAA | 367150 | 1.5918278 | 7.758268  | 60-69   |
| CGAGA | 531855 | 1.5758362 | 9.930964  | 30-34   |
| TGTCT | 502855 | 1.5712433 | 5.9076433 | 90-99   |
| TCCGG | 437035 | 1.5701246 | 5.588552  | 200-249 |
| CAAGC | 437815 | 1.5691912 | 12.243247 | 5       |
| TATCA | 501225 | 1.5624306 | 10.662072 | 20-24   |
| CTCGT | 423310 | 1.5599172 | 8.974655  | 9       |
| CGTAG | 518975 | 1.5591688 | 5.396004  | 50-59   |
| AAGTC | 512335 | 1.55703   | 8.494568  | 8       |
| CATTT | 491340 | 1.553027  | 6.5481286 | 9       |
| GTATC | 502630 | 1.5488886 | 9.09094   | 20-24   |
| GGAGT | 622870 | 1.5469518 | 5.2084317 | 1       |
| GACCG | 429605 | 1.522153  | 10.040043 | 45-49   |
| ACGCC | 354510 | 1.5194445 | 7.962619  | 60-69   |
| CTCTC | 340615 | 1.5183578 | 8.183202  | 300-349 |
| GCCCA | 354075 | 1.5175799 | 8.19896   | 60-69   |

|       |        |           |           |         |
|-------|--------|-----------|-----------|---------|
| CGGGG | 521085 | 1.508808  | 59.61389  | 9       |
| AACGT | 495630 | 1.5062621 | 5.5789933 | 300–349 |
| GACAG | 507900 | 1.5048598 | 5.811361  | 4       |
| GCATT | 487605 | 1.5025882 | 9.255508  | 10–14   |
| ATGCC | 413105 | 1.5013244 | 5.7136493 | 8       |
| AAACC | 414040 | 1.5011487 | 46.595684 | 5       |
| TCACC | 339265 | 1.4914905 | 8.070387  | 300–349 |
| ACAGC | 413470 | 1.4819353 | 6.4242415 | 60–69   |
| GATTG | 580350 | 1.4784085 | 12.981962 | 6       |
| GAGGT | 593435 | 1.4738474 | 8.206051  | 30–34   |
| TCGGT | 483365 | 1.4724848 | 5.592275  | 300–349 |
| TTCGT | 470945 | 1.471536  | 10.456918 | 15–19   |
| CAACA | 404305 | 1.4658532 | 6.462569  | 60–69   |
| CGCGA | 411435 | 1.457774  | 10.062308 | 25–29   |
| TGAGA | 579445 | 1.4557531 | 5.2484565 | 50–59   |
| TGGCC | 403505 | 1.4496622 | 11.810475 | 8       |
| CATTA | 461585 | 1.4388639 | 8.730351  | 20–24   |
| AACCG | 400360 | 1.4349471 | 585.5826  | 350–354 |
| ATGTC | 465195 | 1.4335302 | 5.079678  | 90–99   |
| CCAAA | 392085 | 1.4215481 | 7.4641156 | 7       |
| CAGCC | 331625 | 1.4213585 | 14.176265 | 1       |
| AACTA | 462335 | 1.4213332 | 17.720568 | 6       |
| CCCCA | 274035 | 1.4207895 | 6.739046  | 10–14   |
| GGCGG | 490030 | 1.4188881 | 24.67766  | 7       |
| CACCA | 326220 | 1.4143704 | 7.92943   | 300–349 |
| ACTCA | 382970 | 1.4079105 | 10.018402 | 8       |
| ATCAT | 451265 | 1.4066942 | 10.228944 | 20–24   |
| CCGTA | 385745 | 1.4018914 | 6.275145  | 50–59   |
| TTTGC | 448265 | 1.4006691 | 5.5794554 | 80–89   |
| ACCAA | 384135 | 1.3927246 | 7.482563  | 6       |
| TAACT | 444760 | 1.3864164 | 6.2490396 | 300–349 |
| GTGGA | 555510 | 1.3796573 | 7.905152  | 45–49   |
| AGGCG | 470900 | 1.379273  | 27.666239 | 6       |
| TGGAA | 547490 | 1.375472  | 5.497108  | 3       |
| CCTAT | 365840 | 1.3637362 | 5.39883   | 10–14   |
| GGCCA | 382520 | 1.355324  | 35.70709  | 1       |
| TTCAT | 426640 | 1.3485234 | 5.9781337 | 90–99   |
| AGAGA | 544225 | 1.3484199 | 6.434042  | 300–349 |
| AGCTT | 436980 | 1.3465837 | 5.656981  | 300–349 |

|       |        |           |           |         |
|-------|--------|-----------|-----------|---------|
| GGAAC | 453975 | 1.3450851 | 7.06127   | 4       |
| CCGGG | 381660 | 1.3368093 | 286.13156 | 350–354 |
| TTGAA | 515480 | 1.32835   | 5.852842  | 8       |
| GAAGG | 542290 | 1.3282568 | 5.7363954 | 1       |
| GCGAG | 453020 | 1.3269023 | 8.316932  | 30–34   |
| GTGGC | 445940 | 1.3244236 | 10.438263 | 7       |
| ACGAG | 446115 | 1.3217967 | 7.2983217 | 3       |
| CTCAG | 355890 | 1.2933911 | 10.736562 | 9       |
| AGGGA | 526850 | 1.290439  | 7.281838  | 3       |
| GACGC | 363915 | 1.2894038 | 5.463123  | 60–69   |
| ACTGA | 423160 | 1.2860196 | 6.4489136 | 1       |
| CCTGA | 350835 | 1.27502   | 18.8093   | 3       |
| GCGGG | 433685 | 1.2557403 | 24.494944 | 8       |
| AAATT | 479150 | 1.249017  | 7.9237256 | 40–44   |
| ACGGC | 352375 | 1.2485158 | 6.50432   | 300–349 |
| CAACC | 285875 | 1.2394493 | 17.007582 | 4       |
| GCTGG | 414730 | 1.2317312 | 6.539401  | 9       |
| TTTCG | 393770 | 1.2303916 | 6.2639174 | 300–349 |
| TGCAA | 403010 | 1.2247818 | 18.51783  | 3       |
| TCTCC | 272645 | 1.2153683 | 6.531883  | 300–349 |
| TAGTG | 475460 | 1.2112072 | 6.207004  | 1       |
| ACCCC | 233435 | 1.2102907 | 6.6282043 | 10–14   |
| ATGAA | 472735 | 1.2014052 | 5.6423516 | 2       |
| GCGGT | 401580 | 1.1926762 | 5.452095  | 300–349 |
| CCTTT | 313835 | 1.1862315 | 5.3816853 | 300–349 |
| GAACC | 329035 | 1.179308  | 7.42521   | 4       |
| GGACT | 390325 | 1.1726626 | 8.100775  | 6       |
| AACCA | 323400 | 1.172523  | 7.3002987 | 5       |
| AAGAC | 390395 | 1.1700872 | 5.5020804 | 300–349 |
| AGGAA | 470335 | 1.1653435 | 5.0665874 | 9       |
| CTAAT | 371365 | 1.1576278 | 5.7224355 | 300–349 |
| CATTC | 308600 | 1.1503636 | 10.449873 | 15–19   |
| GAATC | 376475 | 1.1441398 | 5.7564845 | 9       |
| CTGAT | 366910 | 1.1306583 | 15.735959 | 4       |
| TAAAC | 367270 | 1.1290796 | 6.5142145 | 1       |
| ATTGA | 436600 | 1.1250825 | 11.979472 | 7       |
| GGTGA | 449695 | 1.1168567 | 9.179128  | 35–39   |
| GACAA | 371765 | 1.1142497 | 45.448345 | 2       |
| TCCAA | 303060 | 1.1141378 | 6.7487483 | 300–349 |

|       |        |            |           |         |
|-------|--------|------------|-----------|---------|
| TTTCC | 293915 | 1.1109381  | 8.17945   | 300–349 |
| TCTCA | 297850 | 1.1102909  | 7.5147223 | 1       |
| GTCTT | 354915 | 1.1089834  | 5.7023516 | 90–99   |
| ACAAG | 369645 | 1.1078956  | 10.377434 | 300–349 |
| CAAGT | 364510 | 1.1077771  | 7.3487215 | 7       |
| TTACG | 358530 | 1.1048347  | 10.095685 | 25–29   |
| TTCCC | 247535 | 1.1034355  | 7.028275  | 300–349 |
| CAGTG | 361885 | 1.0872197  | 5.5151796 | 300–349 |
| GGGGC | 374000 | 1.0829217  | 11.524038 | 10–14   |
| ACAAC | 298250 | 1.0813389  | 7.715494  | 3       |
| GTTTT | 407205 | 1.078876   | 5.733428  | 300–349 |
| ATGCT | 348975 | 1.0753903  | 5.0190287 | 25–29   |
| CGGGT | 359250 | 1.0669578  | 194.09459 | 350–354 |
| ACCGG | 298020 | 1.0559282  | 385.923   | 350–354 |
| TATTG | 403680 | 1.0547919  | 5.3296657 | 300–349 |
| GCAGA | 355980 | 1.0547352  | 5.8580527 | 4       |
| AAAAA | 413535 | 1.0484588  | 7.2831736 | 300–349 |
| TCCGA | 287950 | 1.0464805  | 6.671554  | 300–349 |
| ATGGC | 347635 | 1.0444081  | 7.801605  | 300–349 |
| CAGAA | 348050 | 1.0431713  | 5.4000707 | 5       |
| TTTTC | 324635 | 1.0404499  | 5.2298136 | 300–349 |
| TACCC | 235245 | 1.0341936  | 5.733118  | 10–14   |
| GAAGC | 348605 | 1.0328838  | 8.670349  | 1       |
| CGAGT | 336725 | 1.0116309  | 7.4768233 | 4       |
| AGCGT | 334680 | 1.005487   | 9.791252  | 4       |
| TAACG | 330395 | 1.0040988  | 6.2112927 | 1       |
| TTGCA | 325410 | 1.0027733  | 8.990561  | 300–349 |
| AGCAT | 329285 | 1.0007253  | 5.247261  | 70–79   |
| TGGAC | 331155 | 0.9948969  | 9.438597  | 45–49   |
| CGTAT | 322495 | 0.9937904  | 8.696886  | 15–19   |
| AACCT | 269235 | 0.98978716 | 7.218856  | 5       |
| GGCCT | 275390 | 0.98938674 | 10.967323 | 9       |
| CTGAC | 270890 | 0.98448026 | 5.8615227 | 2       |
| AGAGC | 331845 | 0.98322546 | 6.8673186 | 1       |
| CAGGA | 327780 | 0.9711812  | 5.5599422 | 2       |
| TTACC | 259540 | 0.9674833  | 6.843087  | 300–349 |
| ATGGT | 379095 | 0.96572286 | 7.6602163 | 300–349 |
| GTCTG | 316480 | 0.96409947 | 5.5922747 | 300–349 |
| CAAAG | 320430 | 0.960389   | 6.001044  | 300–349 |

|       |        |            |           |         |
|-------|--------|------------|-----------|---------|
| GGCAA | 324045 | 0.9601149  | 7.222942  | 5       |
| ACGGA | 323720 | 0.9591518  | 7.431215  | 4       |
| AATTG | 367060 | 0.9458837  | 5.1595693 | 300–349 |
| CATGC | 260075 | 0.945176   | 20.895306 | 1       |
| CCATT | 253505 | 0.9449867  | 6.89925   | 8       |
| ACAAA | 311350 | 0.94397205 | 39.56267  | 3       |
| AGCTG | 313455 | 0.94172037 | 8.765197  | 300–349 |
| GCACC | 219085 | 0.9390073  | 5.22582   | 300–349 |
| AATTT | 355175 | 0.93878937 | 5.809585  | 300–349 |
| GAATT | 362475 | 0.93406844 | 5.50354   | 300–349 |
| TCAGG | 310105 | 0.93165576 | 7.7699966 | 1       |
| CCACC | 178975 | 0.92793185 | 5.196836  | 300–349 |
| TCCGT | 251565 | 0.9270288  | 6.764815  | 300–349 |
| TGCAG | 307825 | 0.9248059  | 6.022711  | 300–349 |
| GGACC | 260670 | 0.92359173 | 10.473639 | 45–49   |
| AGCTA | 303230 | 0.921542   | 5.5789933 | 300–349 |
| GATGA | 365745 | 0.91886973 | 6.1914797 | 1       |
| CGAGC | 258155 | 0.9146807  | 6.50432   | 300–349 |
| AGTGG | 366565 | 0.91039604 | 7.3324485 | 1       |
| ATTTT | 287460 | 0.9086033  | 5.2897944 | 300–349 |
| CGTCC | 208120 | 0.90448016 | 13.383253 | 9       |
| AGACA | 300645 | 0.9010896  | 5.5020804 | 300–349 |
| AGTGC | 299570 | 0.9000053  | 5.0349298 | 3       |
| CCACA | 207105 | 0.89793134 | 11.258739 | 300–349 |
| GGGCA | 303130 | 0.8878724  | 9.810323  | 10–14   |
| GAGTA | 352345 | 0.8852046  | 5.9715943 | 5       |
| AAAAC | 291525 | 0.88386524 | 6.6639175 | 300–349 |
| AGTGT | 346475 | 0.8826253  | 6.051057  | 2       |
| TACGC | 241690 | 0.87836045 | 11.591636 | 25–29   |
| ATTAC | 279030 | 0.869799   | 8.183178  | 25–29   |
| ACGCG | 243685 | 0.8634114  | 10.859822 | 25–29   |
| GGACA | 288600 | 0.8550946  | 44.813564 | 1       |
| ACCTG | 232230 | 0.84398055 | 19.036184 | 2       |
| CGAAT | 274000 | 0.8327094  | 5.5581756 | 300–349 |
| GCAAG | 278835 | 0.8261618  | 7.333478  | 6       |
| CCGTT | 220125 | 0.8111709  | 8.117556  | 5       |
| GGGGG | 337655 | 0.8082232  | 8.942189  | 10–14   |
| GCAAC | 221020 | 0.792167   | 20.259657 | 4       |
| TATCG | 255310 | 0.7867552  | 5.656981  | 300–349 |

|       |        |            |           |         |
|-------|--------|------------|-----------|---------|
| GTGGG | 320435 | 0.7867252  | 5.2292137 | 3       |
| GCGTC | 218380 | 0.7845683  | 11.158664 | 8       |
| AAGTG | 310560 | 0.7802271  | 6.6467805 | 1       |
| GAGGG | 322180 | 0.7801047  | 8.027737  | 2       |
| ACTAT | 250155 | 0.7797892  | 17.10049  | 7       |
| AGTCT | 249485 | 0.7688051  | 7.4914927 | 9       |
| CTAAC | 208555 | 0.76670957 | 13.497495 | 300-349 |
| AACAC | 208345 | 0.75537825 | 6.6557093 | 300-349 |
| ATGCA | 247680 | 0.7527208  | 18.595196 | 2       |
| CCGAG | 207095 | 0.7337676  | 6.48005   | 300-349 |
| GTACG | 239290 | 0.71890455 | 7.8810744 | 2       |
| GGCAT | 233490 | 0.70147955 | 9.504646  | 10-14   |
| AATGC | 227425 | 0.6911641  | 5.5789933 | 300-349 |
| ACCCG | 159500 | 0.6836236  | 5.02417   | 1       |
| TATGG | 265545 | 0.67646074 | 9.352923  | 300-349 |
| CACAA | 186205 | 0.6751072  | 10.618455 | 300-349 |
| CAGGT | 224705 | 0.6750865  | 5.515179  | 300-349 |
| TGTGA | 264935 | 0.67490673 | 9.352922  | 300-349 |
| GCTGA | 212560 | 0.63859904 | 8.804502  | 300-349 |
| CATTG | 205790 | 0.634156   | 5.656981  | 300-349 |
| GGTAC | 208835 | 0.62740797 | 7.158159  | 1       |
| TGCAT | 203550 | 0.6272532  | 5.65698   | 300-349 |
| GTGTA | 243015 | 0.61906683 | 5.8827577 | 3       |
| TGTAT | 235635 | 0.6157003  | 6.010254  | 4       |
| ACCTA | 166735 | 0.612967   | 5.3868937 | 300-349 |
| CTCCC | 114620 | 0.6025776  | 9.614839  | 300-349 |
| GCGTG | 188920 | 0.5610847  | 9.423927  | 5       |
| TGACG | 185275 | 0.556626   | 5.774717  | 300-349 |
| TACGG | 178700 | 0.5368727  | 7.1690845 | 3       |
| TATCT | 167730 | 0.53016084 | 7.335055  | 6       |
| GACCT | 145005 | 0.52698356 | 9.702096  | 300-349 |
| TACCT | 140575 | 0.5240193  | 18.847809 | 1       |
| TAGCT | 167105 | 0.5149455  | 5.06197   | 7       |
| GGCGT | 172555 | 0.5124814  | 9.0487    | 300-349 |
| TATAC | 161025 | 0.501951   | 16.484423 | 9       |
| GGCAC | 135130 | 0.47878528 | 5.9296756 | 300-349 |
| CAGGG | 161375 | 0.47266978 | 5.3467736 | 5       |
| TCCCG | 107625 | 0.46773344 | 5.2988715 | 300-349 |
| CTATA | 145310 | 0.45296377 | 16.499441 | 8       |

|       |        |            |           |         |
|-------|--------|------------|-----------|---------|
| TCCCC | 85405  | 0.4489892  | 8.578533  | 300-349 |
| AGGGC | 144050 | 0.42192465 | 7.497116  | 3       |
| TACTC | 110075 | 0.4103249  | 6.843087  | 300-349 |
| ACATG | 124040 | 0.3769682  | 11.157987 | 300-349 |
| CCCCC | 60500  | 0.37510276 | 10.376162 | 300-349 |
| GGCCG | 103550 | 0.36269614 | 6.4299226 | 300-349 |
| GGGCC | 95225  | 0.33353683 | 6.632642  | 5       |
| TGGGC | 107830 | 0.3202507  | 5.506574  | 4       |
| CGGTC | 45315  | 0.16280206 | 6.595243  | 300-349 |
| TAACC | 37285  | 0.13707063 | 1201.2771 | 350-354 |

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