

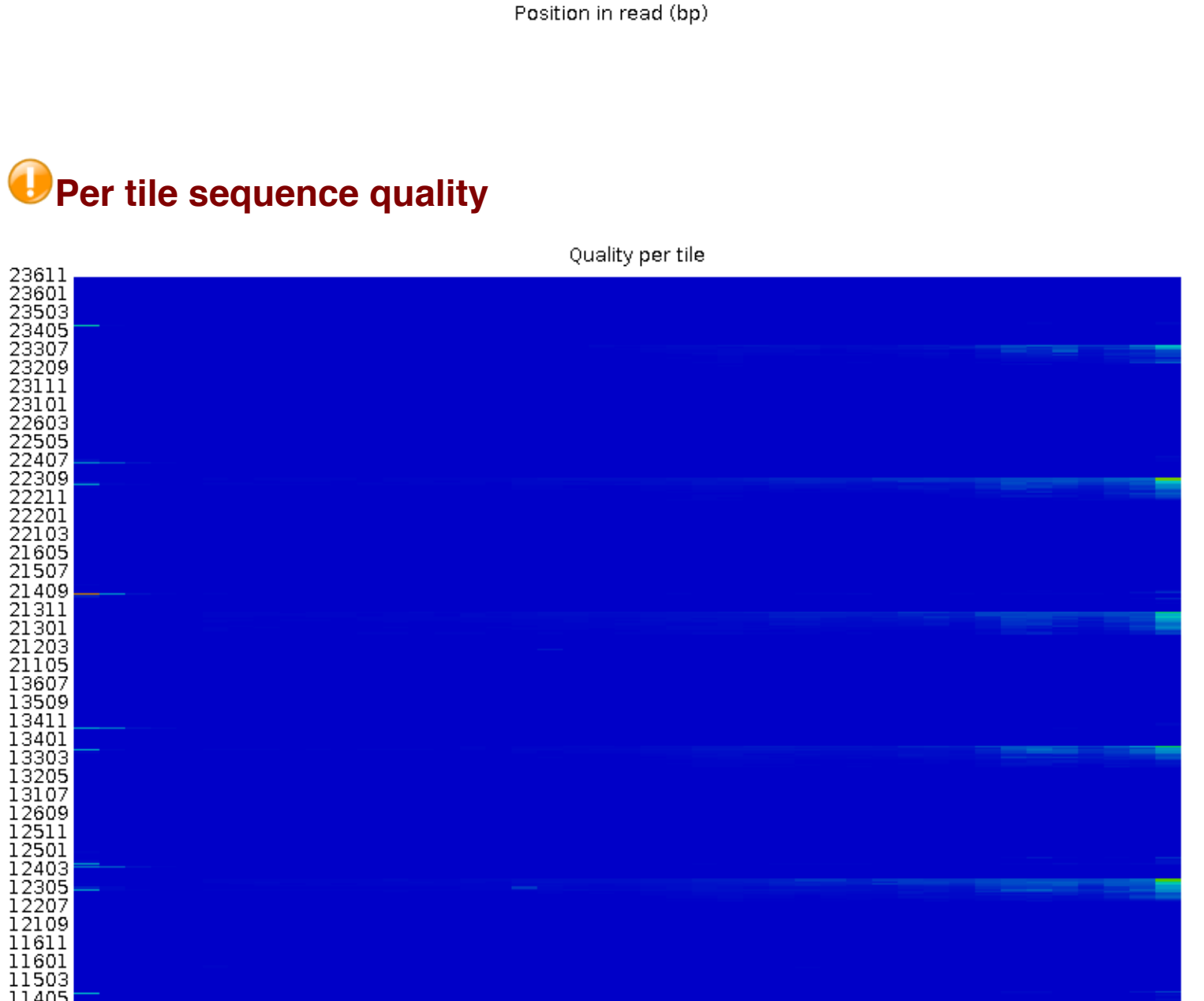
Summary

- ✔ Basic Statistics
- ✔ Per base sequence quality
- ! Per file 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

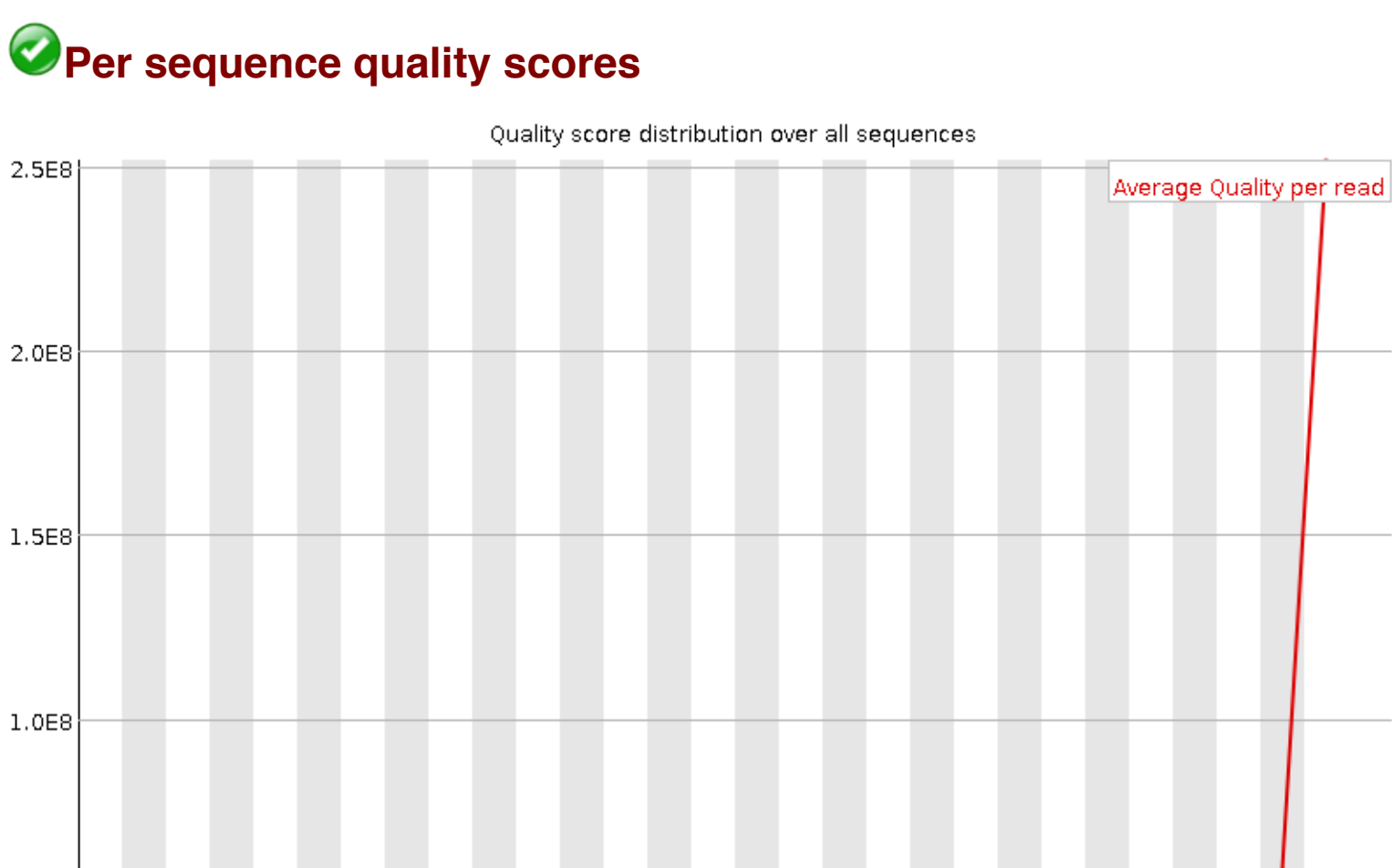
Basic Statistics

Measure	Value
Filename	jurkat_chx.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	388812515
Sequences flagged as poor quality	0
Sequence length	76
%GC	53

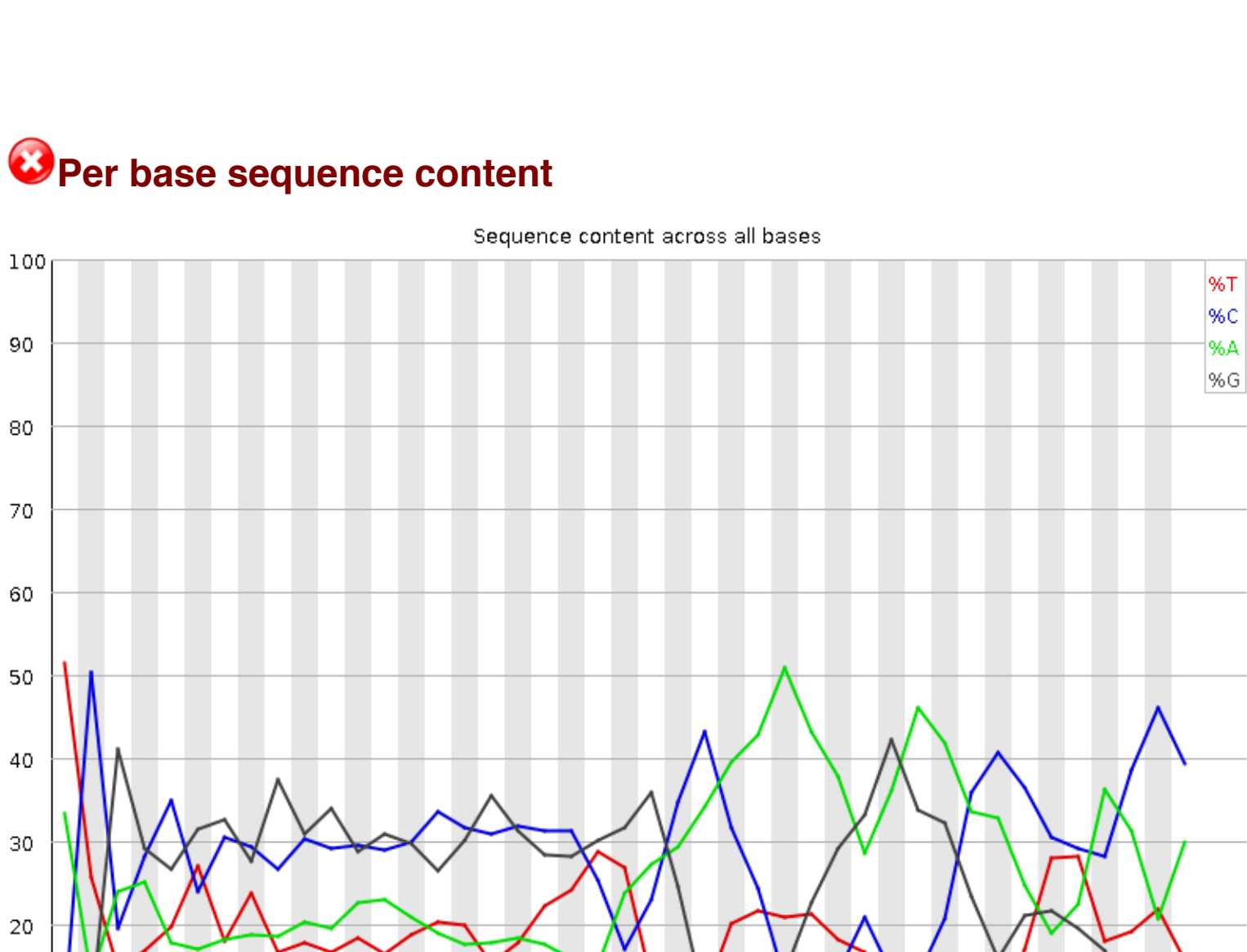
Per base sequence quality



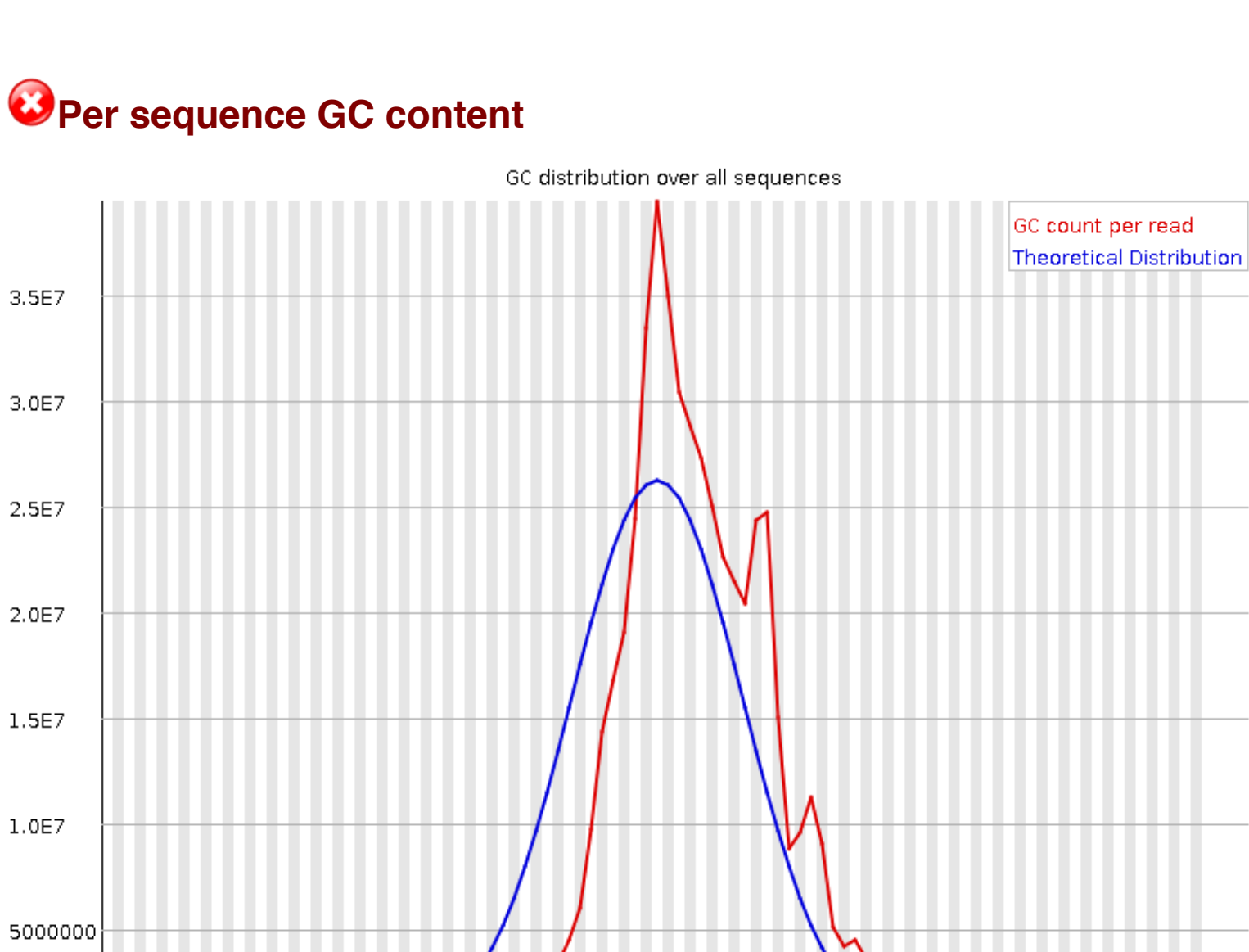
Per file sequence quality



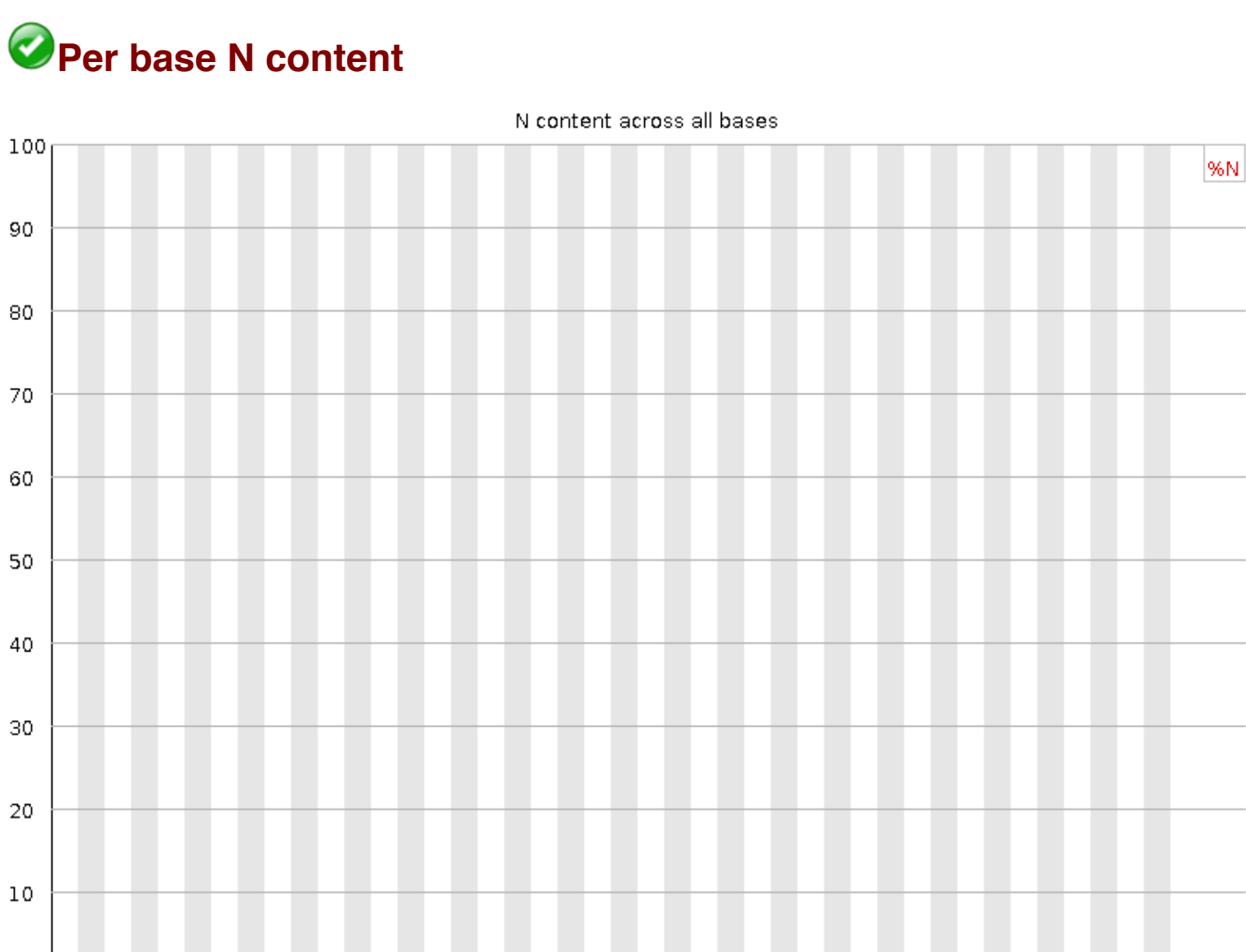
Per sequence quality scores



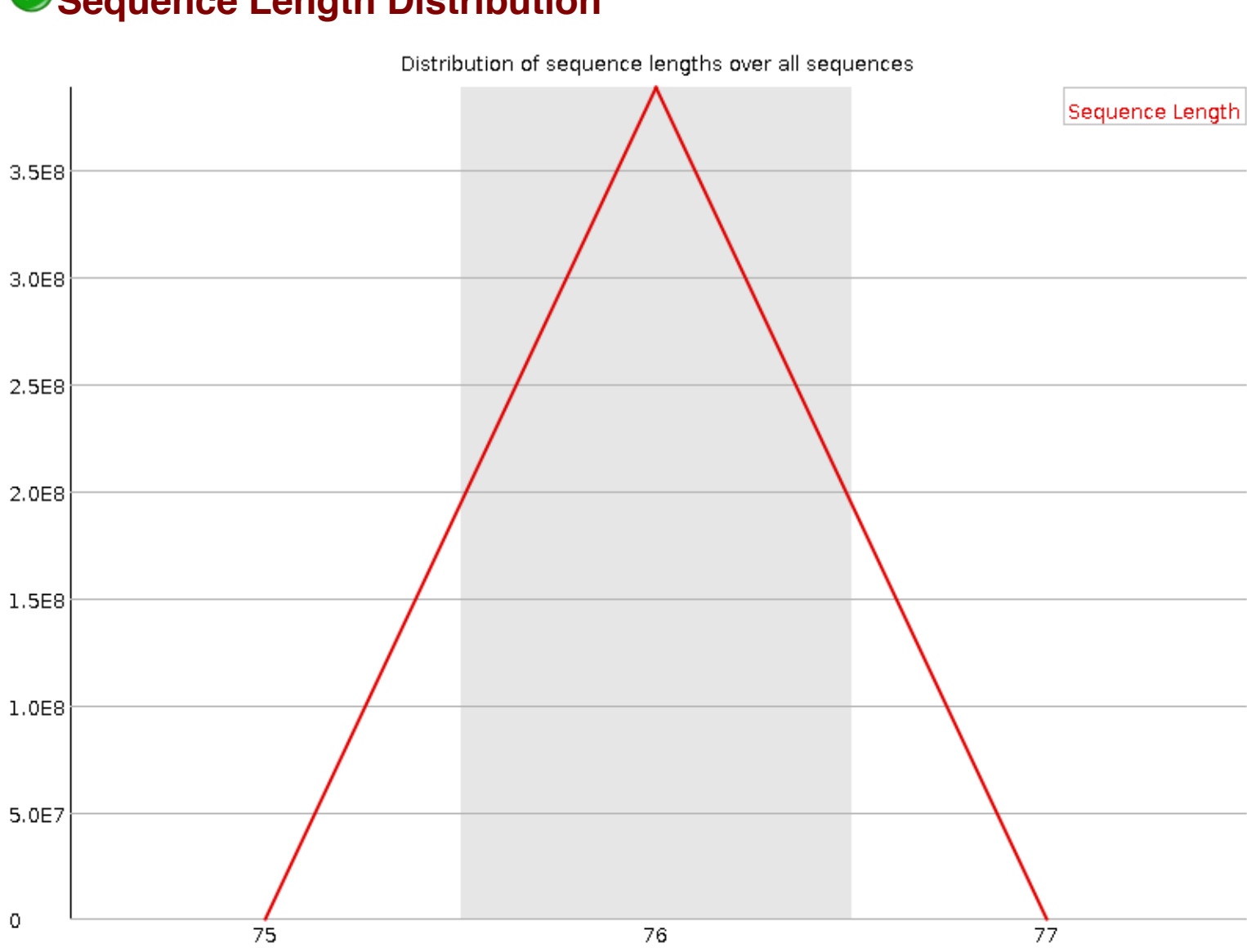
Per base sequence content



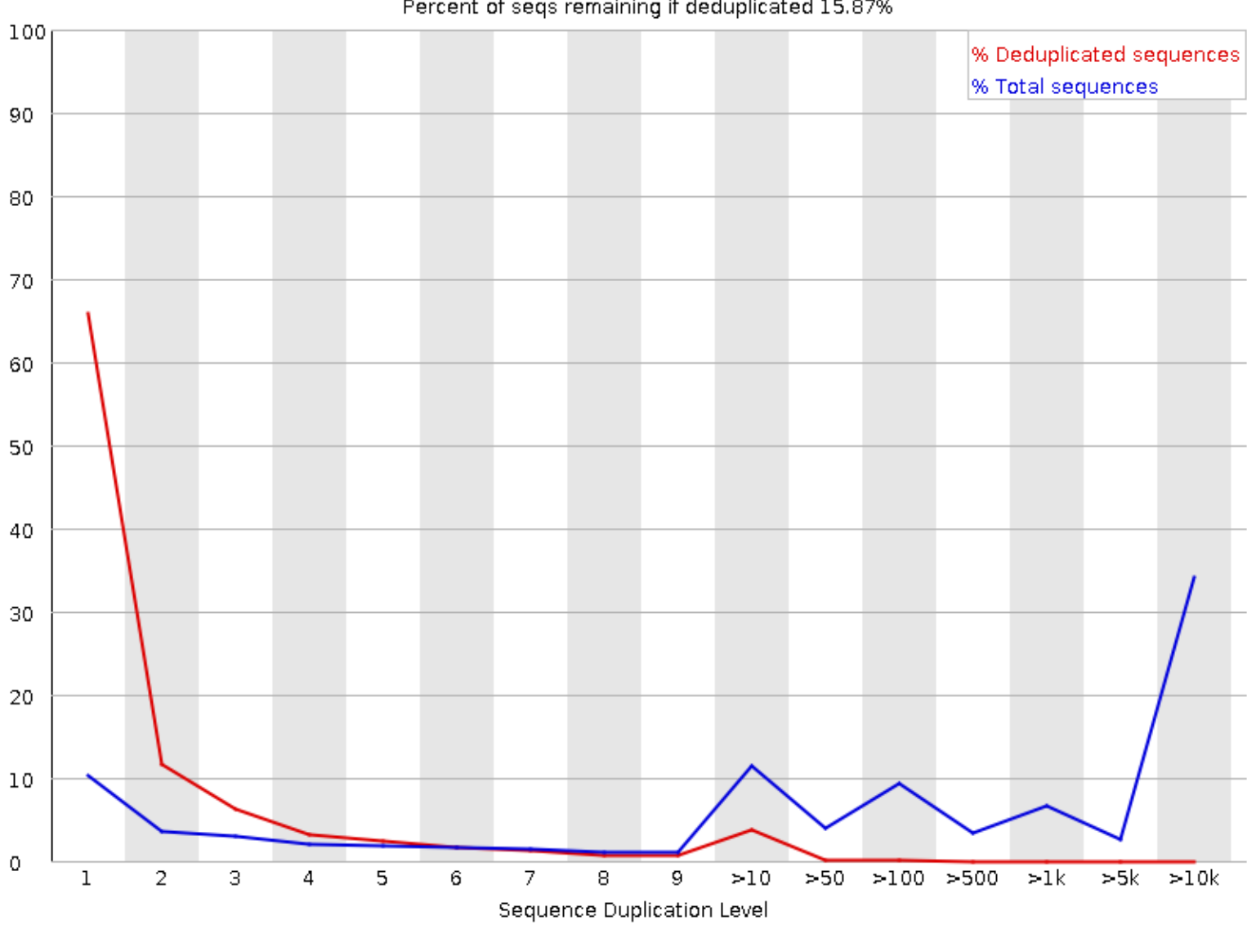
Per sequence GC content



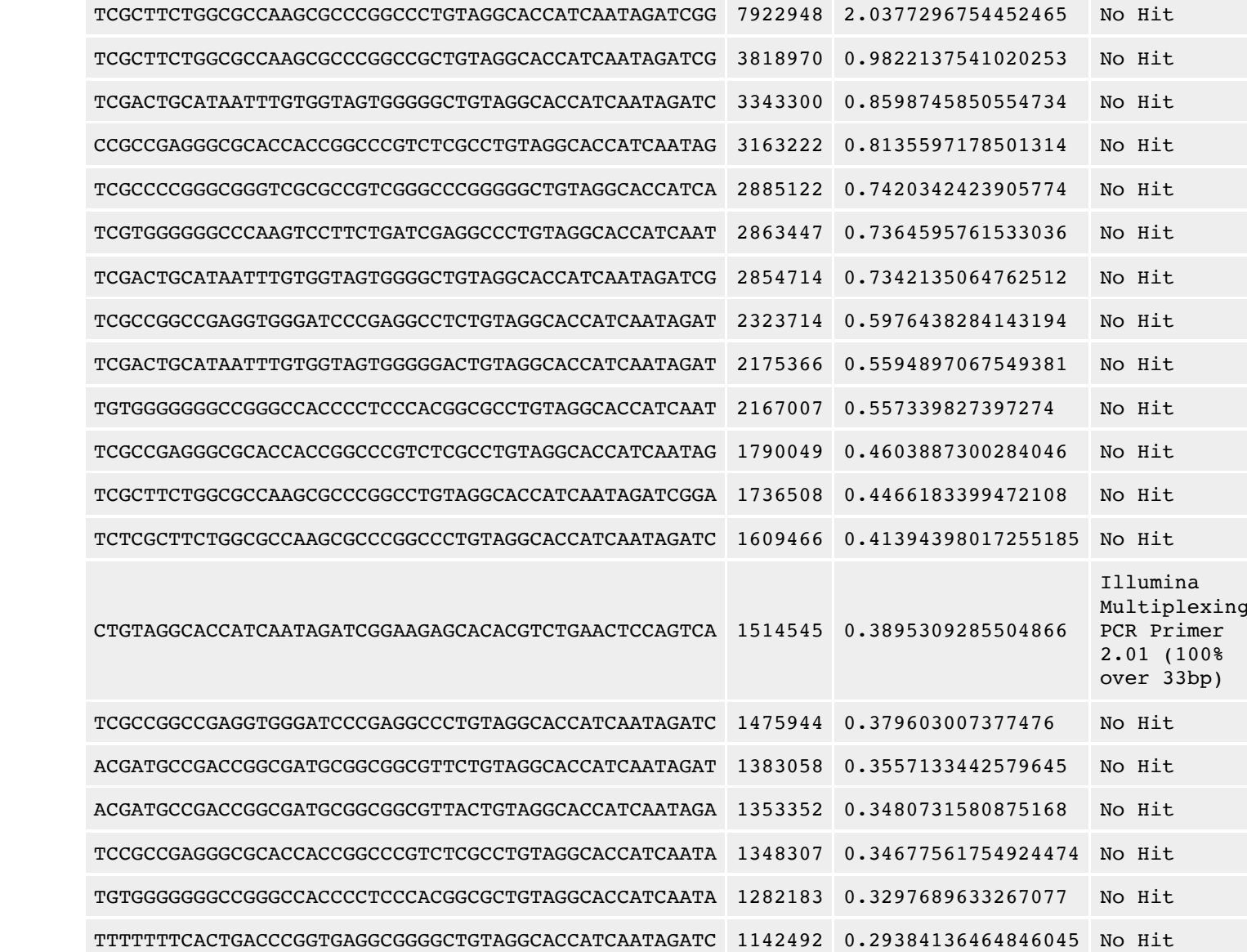
Per base N content



Sequence Length Distribution



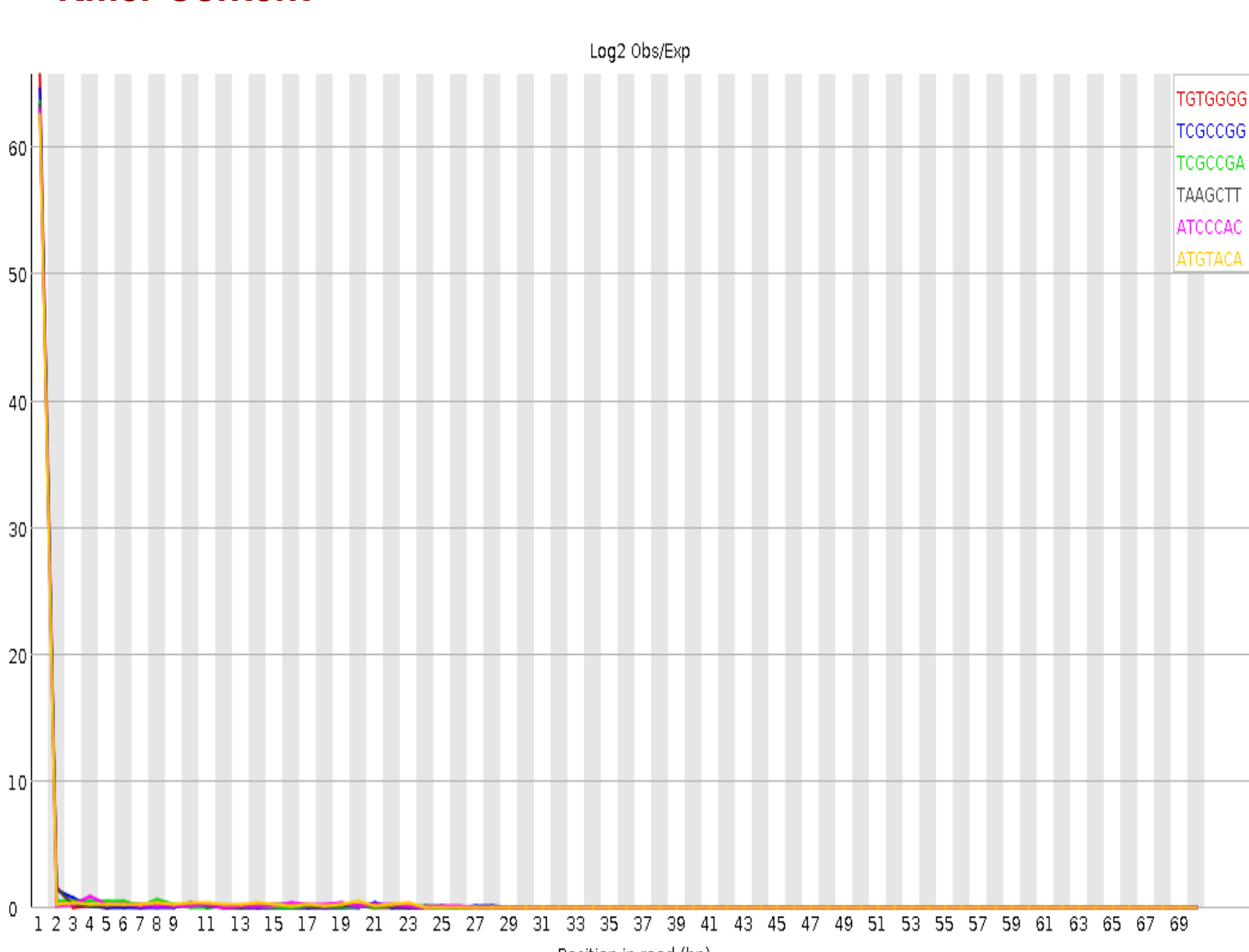
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATCG	7922948	2.0377296754452465	No Hit
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATCG	3818970	0.9822137541020253	No Hit
TCGACTGCATAATTTGTGTAGTGGGGCTGTAGGCACCATCAATAGATC	3343300	0.859874580554734	No Hit
CCGCCAGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	3163222	0.8135597178501314	No Hit
TCGCCCGGGCCGAGTCCGCTCGCGCCCTGTAGGCACCATCAATAG	2885122	0.7420342423905774	No Hit
TCGTGGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	2863447	0.7364595761533036	No Hit
TCGACTGCATAATTTGTGTAGTGGGGCTGTAGGCACCATCAATAGATC	2854714	0.7342135064762512	No Hit
TCGCCCGGAGTGGGATCCGAGCCCTGTGTAGGCACCATCAATAGATC	2323714	0.5976438284143194	No Hit
TCGACTGCATAATTTGTGTAGTGGGGCTGTAGGCACCATCAATAGATC	1790049	0.4603887300284046	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	2167007	0.557339827397274	No Hit
TCGCCAGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	1736508	0.4466183399472108	No Hit
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	1609466	0.41394398017255185	No Hit
CTGTAGGCACCATCAATAGATCGGAAGAGCACACGCTGAACTCCAGTCA	1514545	0.3895309285504866	Illumina Multiplexing PCR Primer 2.01 (100% over 33bp)
TCGCCCGGAGTGGGATCCGAGCCCTGTAGGCACCATCAATAGATC	1475944	0.379603007377476	No Hit
ACGATCCCGACCGGATCGCGCCCTGTGTAGGCACCATCAATAGATC	1383058	0.3557133442579645	No Hit
ACGATCCCGACCGGATCGCGCCCTGTGTAGGCACCATCAATAGATC	1353352	0.3480731580875168	No Hit
TCGCCAGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	1348307	0.3467561754924474	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	1282183	0.3297689632267077	No Hit
TTTTTCACTGACCCGCTGAGGGGGCTGTAGGCACCATCAATAGATC	1142492	0.29384136464846045	No Hit
ACCCCTCCACGGCCCTGTAGGCACCATCAATAGATC	1048951	0.2697832387333586	No Hit
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	990848	0.2548395336502993	No Hit
ATCCCACTGCTCCACCATCTGTAGGCACCATCAATAGATC	932440	0.23981738345022152	No Hit
ATCCCACTGCTCCACCATCTGTAGGCACCATCAATAGATC	799872	0.20572177312759596	No Hit
CGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	747664	0.19227879020303654	No Hit
CCGCCAGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	648573	0.16938767956067465	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	733694	0.1887012304622221	No Hit
TCGAGGGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	708202	0.18214485714277998	No Hit
TCAGTCCCGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	706480	0.18170197016420625	No Hit
TCTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	631139	0.1623247646748202	No Hit
TTTTTCACTGACCCGCTGAGGGGGCTGTAGGCACCATCAATAGATC	629930	0.16201381789369615	No Hit
ATCCCACTGCTCCACCATCTGTAGGCACCATCAATAGATC	621572	0.1598641957293993	No Hit
ATCCCACTGCTCCACCATCTGTAGGCACCATCAATAGATC	569447	0.14645799145637067	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	559081	0.1437919250104385	No Hit
ATGTACACGGGATCGAGCCACCTGTAGGCACCATCAATAGATC	555159	0.14278321262369859	No Hit
TTCTCGCTTGTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	533066	0.13710103955887326	No Hit
TCTCGCTTGTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	512245	0.1317460164573149	No Hit
CTGACTGCATAATTTGTGTAGTGGGGCTGTAGGCACCATCAATAGATC	499959	0.1287689632267077	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	497011	0.12782793269913137	No Hit
TCGAGGGGGCCCAAGTCTCTGTATCGAGGCCCTGTAGGCACCATCAATAG	484515	0.12461404438074736	No Hit
ATGTACACGGGATCGAGCCACCTGTAGGCACCATCAATAGATC	479331	0.12328075396441393	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	468573	0.12052387671848123	No Hit
ACCCCACTGCTGACCATCTGTAGGCACCATCAATAGATC	466932	0.12009181340266273	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	465096	0.1196196063802113	No Hit
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	456749	0.11747281334295528	No Hit
GTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	452176	0.11629666807407164	No Hit
TCTCCGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	448218	0.1152786972610719	No Hit
ACAAGCTTGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	435164	0.1129129450874286	No Hit
TGTGGGGGGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	426281	0.10963664526598818	No Hit
CAGTCCCGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	414252	0.10654286681075582	No Hit
TCAGTCCCGCCGAGCCACCTCCACGGCCCTGTAGGCACCATCAATAG	406699	0.10460028530717433	No Hit
CGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	402856	0.10361189119645493	No Hit
TCGCTTCTGGCCCAAGCCCGCCCTGTAGGCACCATCAATAGATC	398032	0.10237119039236686	No Hit
AACGATCCCGACCGGATCGCGCCCTGTGTAGGCACCATCAATAGATC	391376	0.10065931133929679	No Hit

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TGTGGGG	624565	0.0	65.62087	1
TCGCCGG	655100	0.0	64.59275	1
TCGCCGA	315085	0.0	63.509754	1
TAGCCTT	112160	0.0	63.26144	1
ATGCCAC	398715	0.0	63.0085	1
ATGFACA	170575	0.0	62.56173	1
TGTACAC	171295	0.0	61.695644	2
TTGGGGG	229240	0.0	60.81116	1
TCGTGGG	516245	0.0	60.462112	1
TACACGG	177535	0.0	59.757473	4
ACCCCGT	244590	0.0	59.39103	12
TGAAATAC	164600	0.0	59.0104	1
CCCACTT	139300	0.0	59.001675	3
ACGCTCC	247665	0.0	58.77864	1
GTACAGC	181135	0.0	58.13455	3
TGACACC	242565	0.0	58.121563	11
TTCCGCT	106905	0.0	57.910954	1
CTGACAC	248320	0.0	57.574	10
TCCCACT	248200	0.0	57.50503	2