

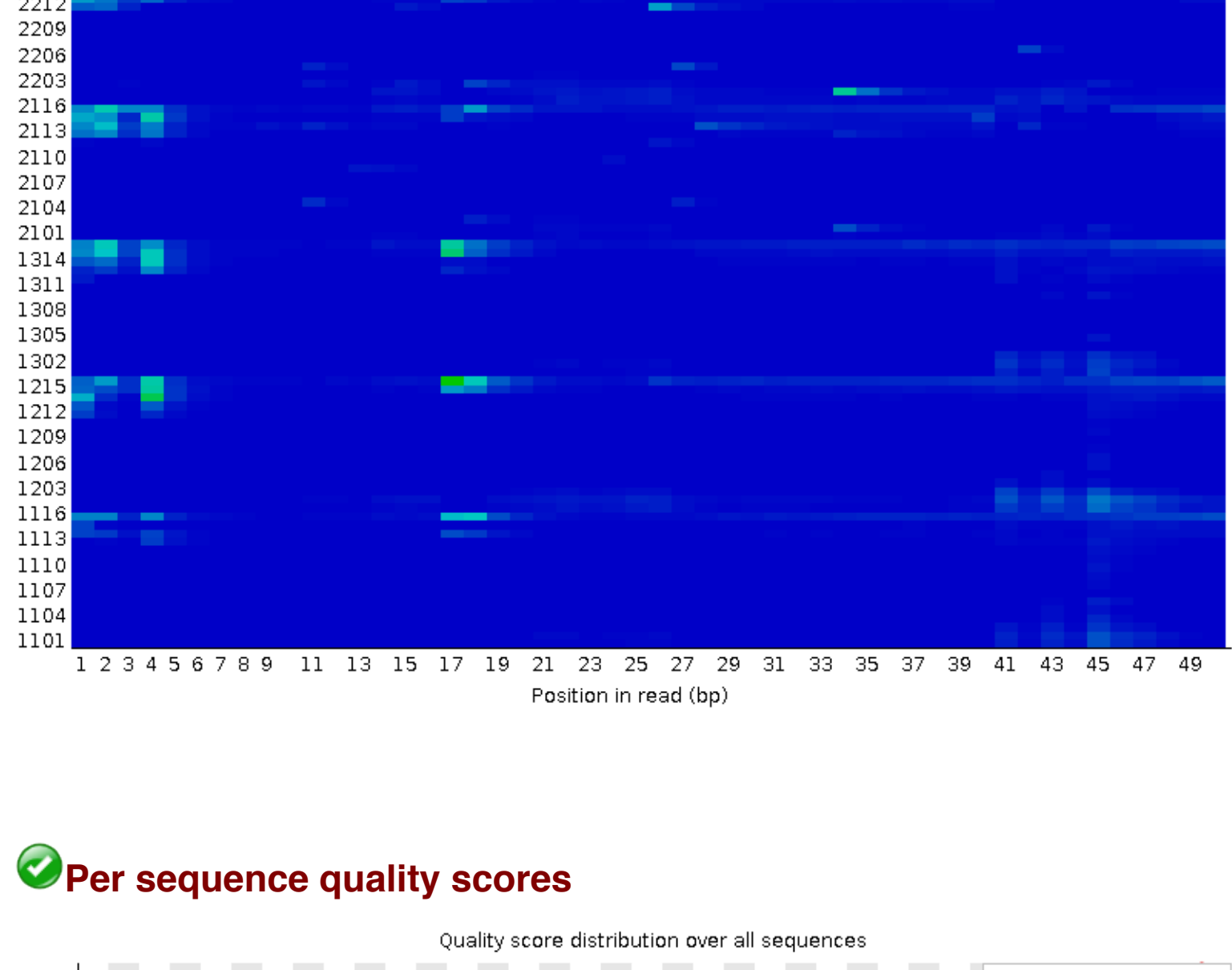
Summary

- 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

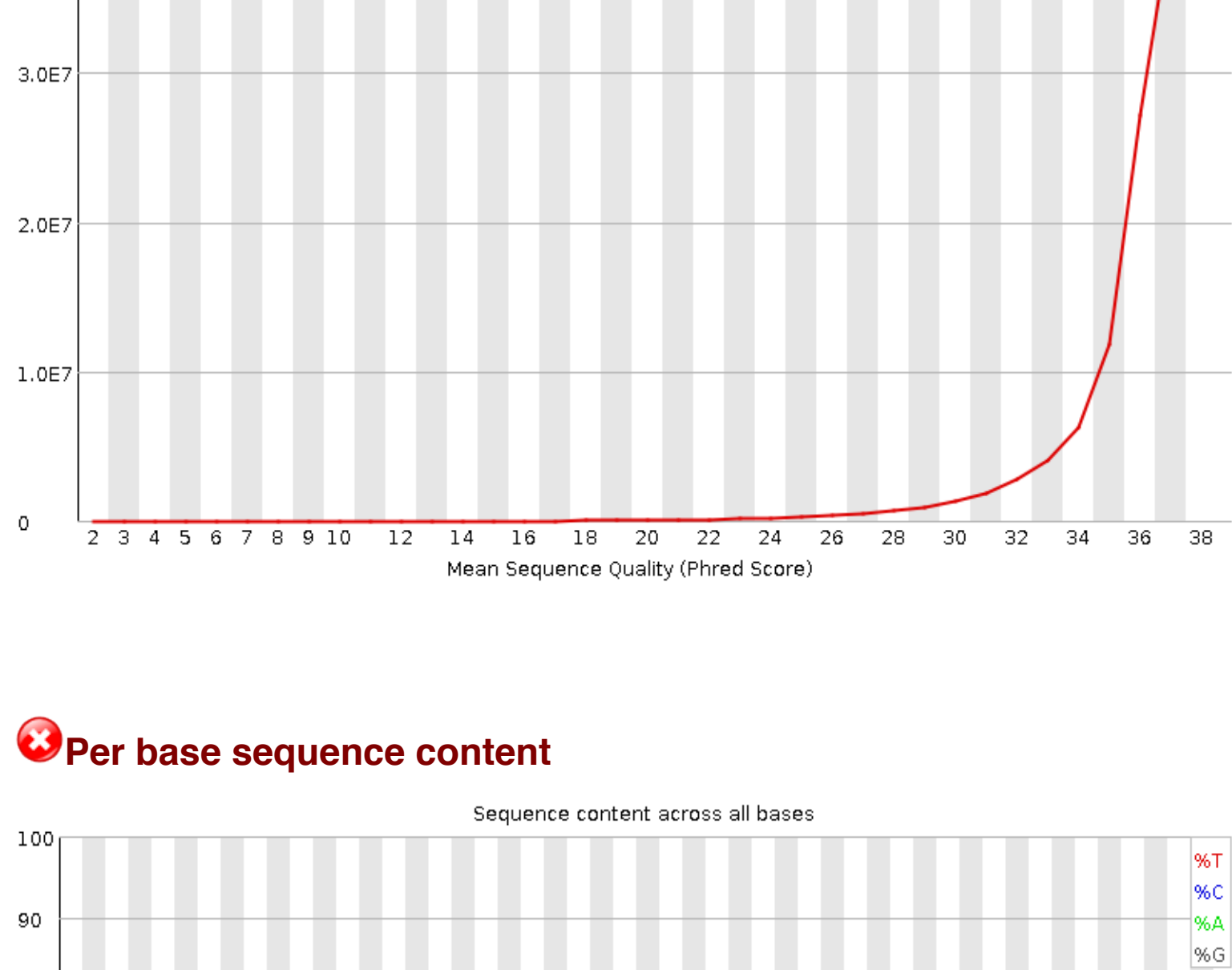
Basic Statistics

Measure	Value
Filename	HCT116_CHX.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	15506923
Sequences flagged as poor quality	0
Sequence length	50
%GC	57

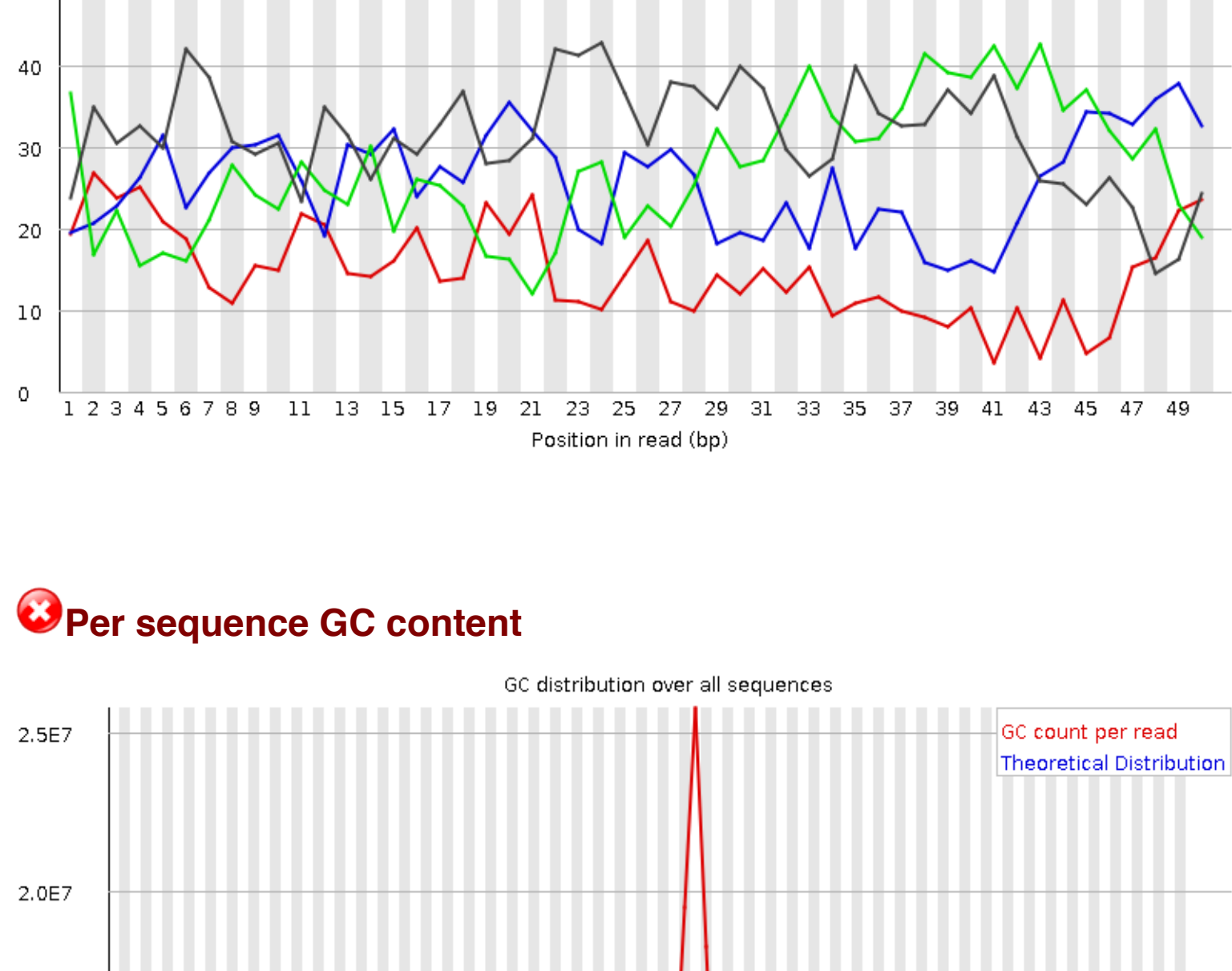
Per base sequence quality



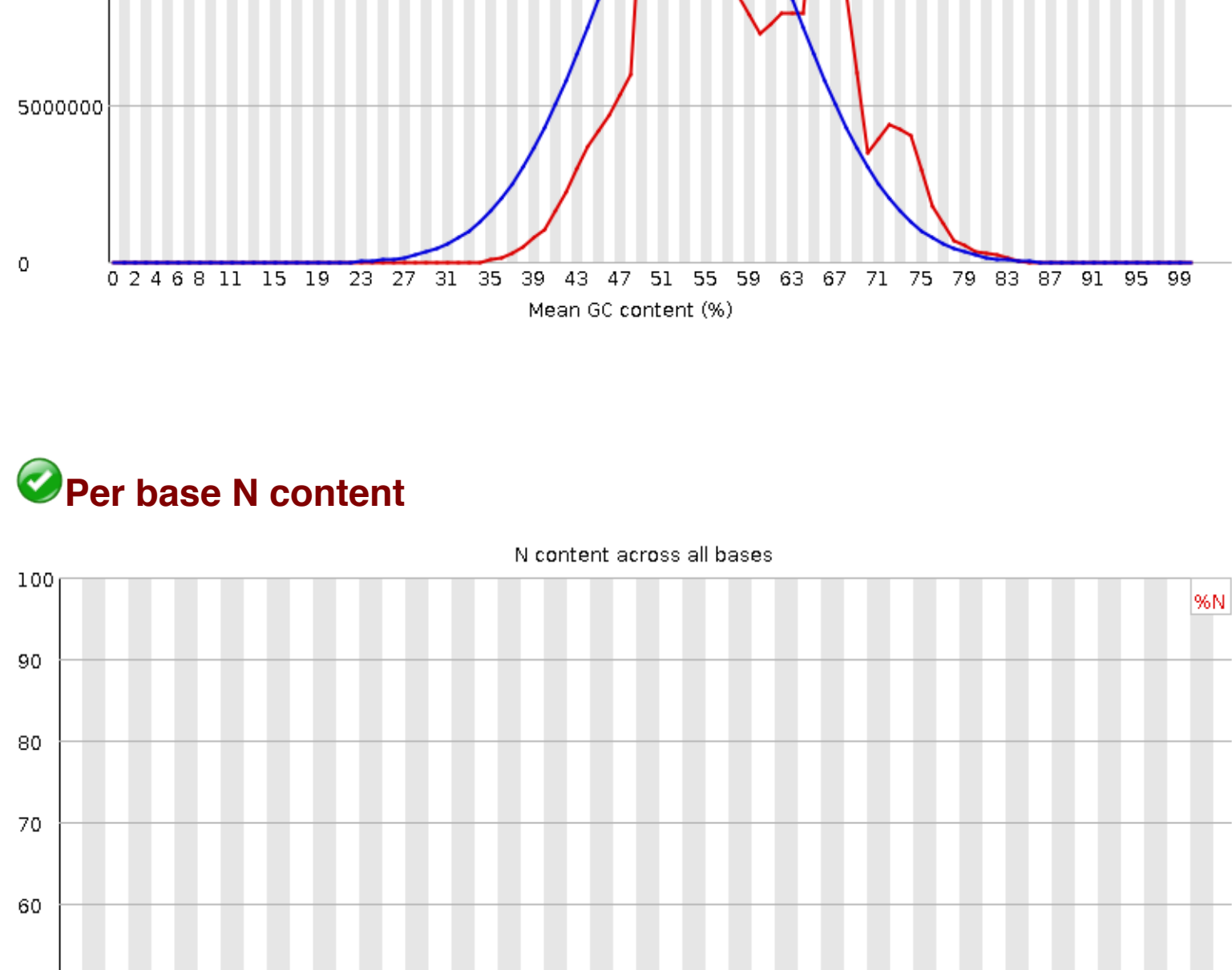
Per tile sequence quality



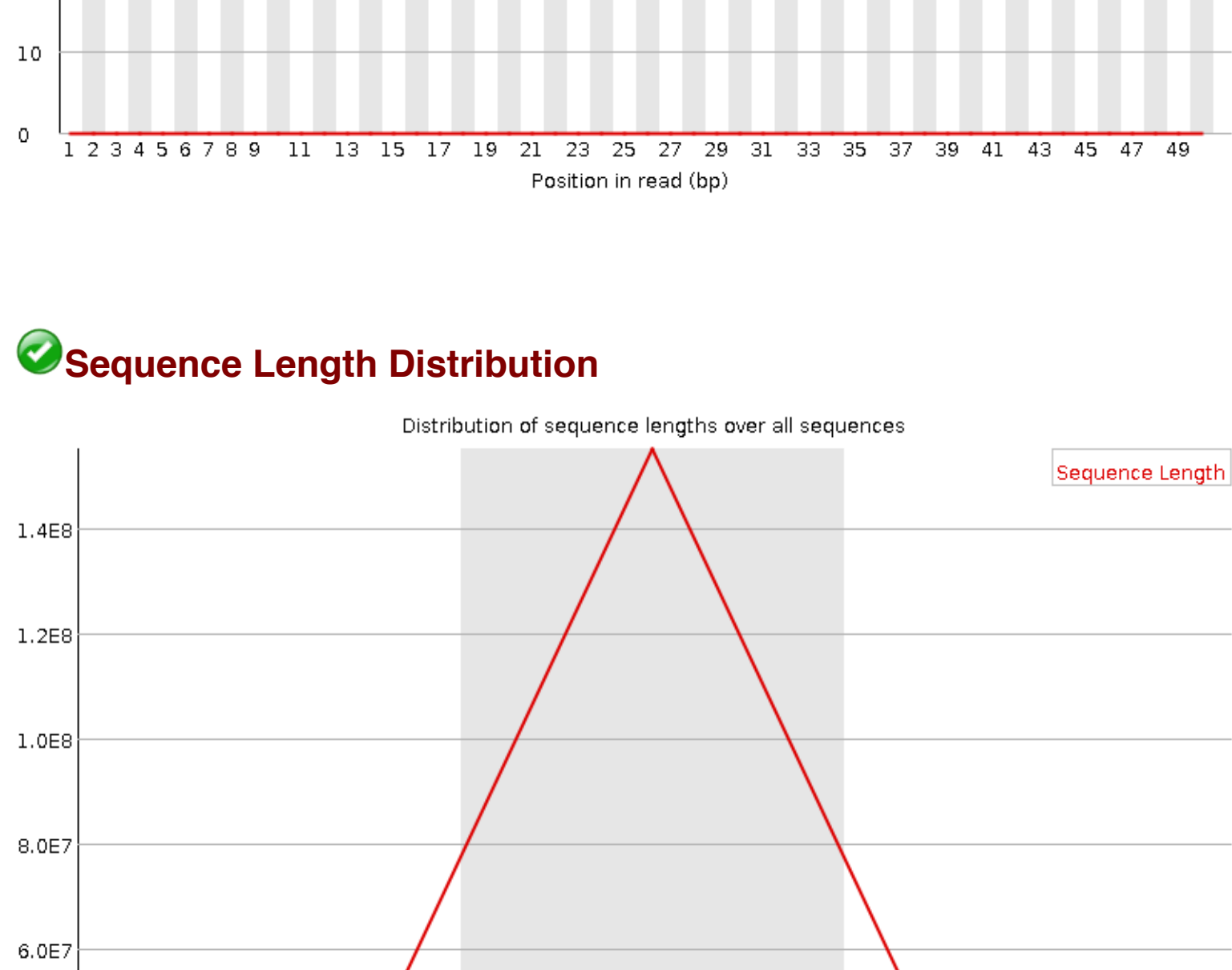
Per sequence quality scores



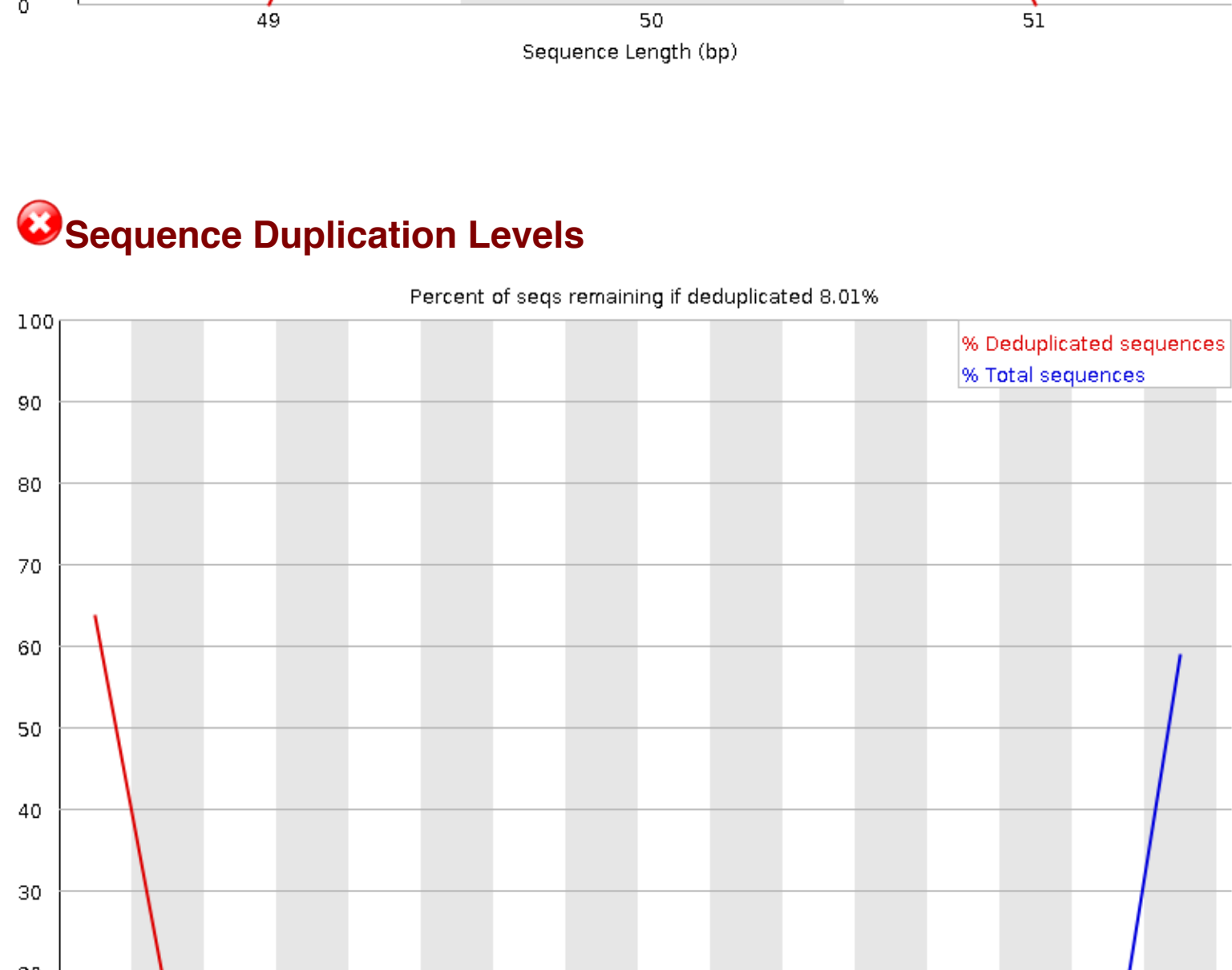
Per base sequence content



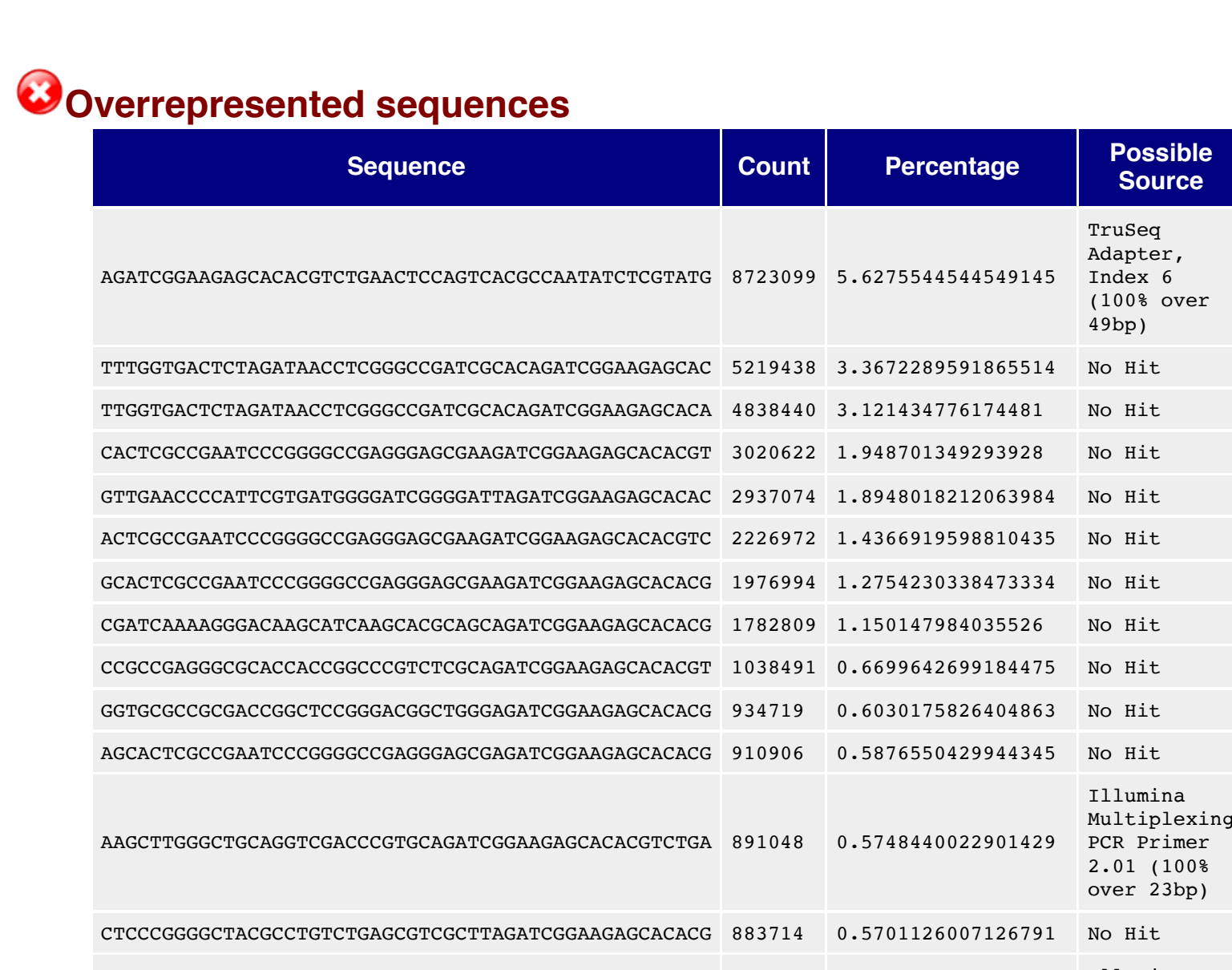
Per sequence GC content



Per base N content



Sequence Length Distribution



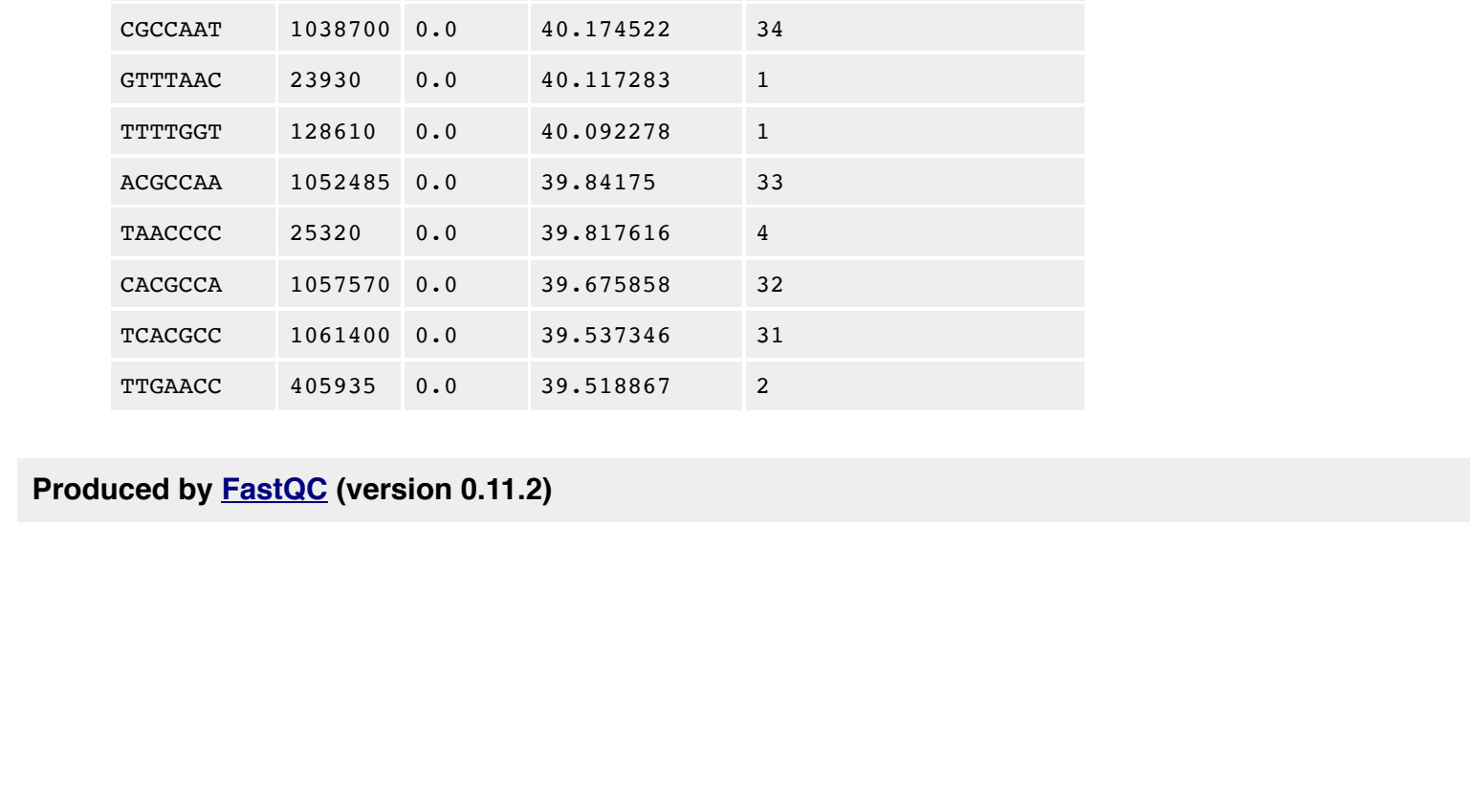
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGATCGGAGAGCACACGCTGTGAACCTCCAGTCAGCCCAATATCTCTGATG	8723099	5.6275544544549145	TruSeq Adapter, Index 6 (100% over 49bp)
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	5219438	3.3672289591865514	No Hit
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	4838440	3.121434776174481	No Hit
CACCTCCCGAATCCCGGGCCGAGGGAGGAGGATCGGAAGAGCACACCT	3020622	1.948701349293928	No Hit
GTGAAACCCCAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	2937074	1.8948018211063984	No Hit
ACTCCGCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	2226972	1.4366919598810435	No Hit
CGATCCGCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	1976994	1.2754230338473334	No Hit
GGTGAACCCCAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	1782809	1.150147984035526	No Hit
CCGCGGAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	1038491	0.6699642699184475	No Hit
AGTCCGCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	934719	0.6030178582640863	No Hit
AGCACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	910906	0.5876550422994345	No Hit
AAGCTTGGCTGCGAGTCCGACCCCTCCAGTCAGCCGGAAGAGCACACCTGA	891048	0.5748440022901429	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
CTCCCGGGCTACGCCCTGTGAGGCTCGCTGTAGATCGGAAGAGCACACG	883714	0.5701126007126791	No Hit
AGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTCTGAAGTC	880452	0.5680081785766433	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
ACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCTCT	810069	0.522601819532925	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
AGCCCTGGACGGTGTGAGCCGGTGTAGCGGAGGAGCACACCTCTGAAC	785886	0.5070005808708299	Illumina Multiplexing PCR Primer 2.01 (100% over 25bp)
TTTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCAC	727536	0.4693571009083252	No Hit
AGCACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	700082	0.451646339174481	No Hit
CGTGGGGCCCAAGCTCTCTGATCGAGGAGGATCGGAAGAGCACAC	631091	0.4071329928049723	No Hit
CCTGAAAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	590633	0.3810625295748758	No Hit
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	587725	0.3791604843352706	No Hit
GCCGCTCGATACCCGAGCTAGGATAATAGATAGATCGGAAGAGCACAC	565888	0.3719756439523672	No Hit
TTTGTGACTCTAGATAAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCAC	578189	0.3665571628818424	No Hit
AGCATCAAAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	551090	0.3555260560846047	No Hit
AGCACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	544436	0.35123334459068	No Hit
TTTGTGACTCTAGATAAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCAC	474517	0.3061263270157295	No Hit
TTTGTGACTCTAGATAAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	472376	0.30474509838505726	No Hit
ACTCTGGTGGATCCGAGTCCGACCCCTCCAGTCAGCCGGAAGAGCACAC	464101	0.2994066271787264	No Hit
TTTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	451188	0.29107603148796135	No Hit
AGCCCTGGACGGTGTGAGCCGCTGAGCCGCCCGGAGGATCGGAAGAGCAC	431635	0.2784617235134716	No Hit
CGGAGGAGGAGAGCACCGAAGAGGATCGGAAGAGCACACCTCTG	391892	0.2528222562033568	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
AGCCCTGGACGGTGTGAGCCGGTGTAGCGGAGGATCGGAAGAGCACACCTCT	391158	0.2523487289661249	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
ACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCTCTG	388235	0.2504630663393829	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCT	387053	0.24970046015299588	No Hit
AGCACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	374849	0.24182726341842165	No Hit
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	368522	0.23774551024408117	No Hit
GAATACAAGCTTGGATCCGAGGATCGCAGATCGGAAGAGCACACCT	350919	0.2263892427207021	No Hit
TTTGTGACTCTAGATAAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	349551	0.2255067020458177	No Hit
ACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	333393	0.21508265150195904	No Hit
CGTGGGGCCCAAGCTCTCTGATCGAGGAGGATCGGAAGAGCACACCT	328940	0.2122098765872011	No Hit
GCATCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	306214	0.1975485954238897	No Hit
CGGCGGAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	290034	0.1871103524840629	No Hit
GCATCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	276186	0.17817655795928547	No Hit
AGGCGAAGGAGGAGGATCGCAGGAGGATCGGAAGAGCACACCT	275772	0.1779094731143073	No Hit
TCCCGGGCCGATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	271890	0.17540560884328	No Hit
ATGTGGCTACGAGAGACCCGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	267332	0.17246455501861682	No Hit
TGATATACTGGTAATCTTAGAGCTAATACAAGATCGGAAGAGCACACCT	262846	0.1695704907322107	No Hit
ATGTGGCTACGAGAGACCCGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	255954	0.1651242377904736	No Hit
TAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTCTGAAGTC	248271	0.1601678489753197	Illumina Multiplexing PCR Primer 2.01 (100% over 26bp)
ACTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCTCTGA	245921	0.1586516235794191	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
CTTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	239179	0.15430214042762463	No Hit
AGCCCTGGACGGTGTGAGCCGGTGTAGCGGAGGAGCACACCTCTGAAC	236193	0.1523757748549036	No Hit
CTCCCGGGCCCAAGCTCTCTGATCGAGGAGGATCGGAAGAGCACAC	231865	0.1504785813832057	No Hit
CTCTGAGTCTAGATAAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	228660	0.1477289142928255	No Hit
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACAC	222030	0.1471289124292855	No Hit
CCGCTTGGATCCCGACCTAGGATAATAGATAGATCGGAAGAGCACAC	222398	0.14347617235134716	No Hit
TTTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTGA	210443	0.1357661360324532	Illumina Multiplexing PCR Primer 2.01 (100% over 24bp)
GC0CCGATCTCTCTGATCTCGGAGATAGCAGATCGGAAGAGCACAC	206405	0.13315856866599435	No Hit
CGTGGGGCCCAAGCTCTCTGATCGAGGAGGATCGGAAGAGCACAC	203632	0.13310502267050356	No Hit
GGCACTAGATCAAGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	202917	0.1315547906622208	No Hit
AAGCTTGGCTGCGAGTCCGACCCCTCCAGTCAGCCGGAAGAGCACACCT	200712	0.12948582948130646	No Hit
GGTGAACCCCAATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	194225	0.12530085511083916	No Hit
AGCATCAAAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	187013	0.121478949077463	No Hit
AGGATTCACCCCGGGCCGCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	185422	0.11962175392643591	No Hit
GGGAGGAGGAGGATCGCAGGAGGATCGGAAGAGCACACCT	184777	0.1192484814216492	No Hit
CGGCGGAGGAGCACACCTCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	182023	0.1174289486412462	No Hit
ATGGAATCGGATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	181265	0.11693993822456561	No Hit
AOTGAAAGGAGGATCAAGAGGATCGGAAGAGCACACCT	179133	0.1155641576617556	No Hit
CGGCGGAGGAGGATCGCAGGAGGATCGGAAGAGCACACCT	178463	0.11513227702739444	No Hit
AATCGTAGTAGGACGGCCGCTGTGACAGATCGGAAGAGCACACCTCT	176803	0.11406135711757855	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
GAACGGAAGGAGGAGGATCGGAGGATCGGAAGAGCACACCTCT	174960	0.1128723796469259	No Hit
TTTGTGACTCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTG	170037	0.10969639078636506	Illumina Multiplexing PCR Primer 2.01 (100% over 25bp)
AACCTCCGGCCGATCGCAGATCGGAAGAGCACACCTCTGAAGTC	169263	0.10919705825010151	Illumina Multiplexing PCR Primer 2.01 (100% over 31bp)
CGTGAACCCCAATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	169126	0.10910867510091792	No Hit
AGACCCGAGAAAGCTGTGGTTGATATAGACAGATCGGAAGAGCACAC	167994	0.10837838513832057	No Hit
GAGCCCGCCGCGCTGAACTCGGGAGGAGGATCGGAAGAGCACACCT	165515	0.10677910173083044	No Hit
CACCTCCCGAATCCCGGGCCGAGGGAGGATCGGAAGAGCACACCT	164268	0.10597462153351693	No Hit
CTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTCTG	163432	0.10543529078375423	Illumina Multiplexing PCR Primer 2.01 (100% over 25bp)
GTTGAACCCCAATCCCGGGCCGAGGGAGGATCGGAAGAGCACAC	160422	0.10349344203161816	No Hit
AAGCTTGGCTGCGAGTCCGACCCGATCGGAAGAGCACACCTCTGAAGTC	160056	0.10325732354547802	Illumina Multiplexing PCR Primer 2.01 (100% over 26bp)
TCTAGATAAAGCTCCGGCCGATCGCAGATCGGAAGAGCACACCTCTGA	159115	0.10265025388575709	Illumina Multiplexing PCR Primer 2.01 (100% over 14bp)
CGGCGTGGCCGAGGAGGATCGGAGGATCGGAAGAGCACAC	155862	0.10055163794200339	No Hit
GGCGTGGCCGAGGAGGATCGGAGGATCGGAAGAGCACAC	155556	0.10035422740441084	No Hit

Adapter Content



Kmer Content

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGCCCGT	252340	0.0	43.198402	1
TCGTATG	1021035	0.0	40.989896	44
CTCGTAT	1026905	0.0	40.760822	43
TATCTCG	1023860	0.0	40.665688	40
TCTCGTA	1028820	0.0	40.630993	42
ATATCTC	1026925	0.0	40.536816	37
CAATATC	1031575	0.0	40.402164	39
AATATCT	1030865	0.0	40.323355	38
GAATACA	99360	0.0	40.354996	1
CCAAATAT	1034500	0.0	40.327698	36
GTACAGT	22465	0.0	40.323986	1
GCCCAATA	1038695	0.0	40.226597	35
CGCCAAT	1038700	0.0	40.174522	34
GTTTAAC	23930	0.0	40.117283	1
TTTTGGT	128610	0.0	40.092278	1
AGCCCAA	1052485	0.0	39.84175	33
TAAACCC	25320	0.0	39.817616	4
CACGCCA	1057570	0.0	39.675588	32
TCAAGCC	1061400	0.0	39.533346	31
TTGAACC	405935	0.0	39.518867	2