

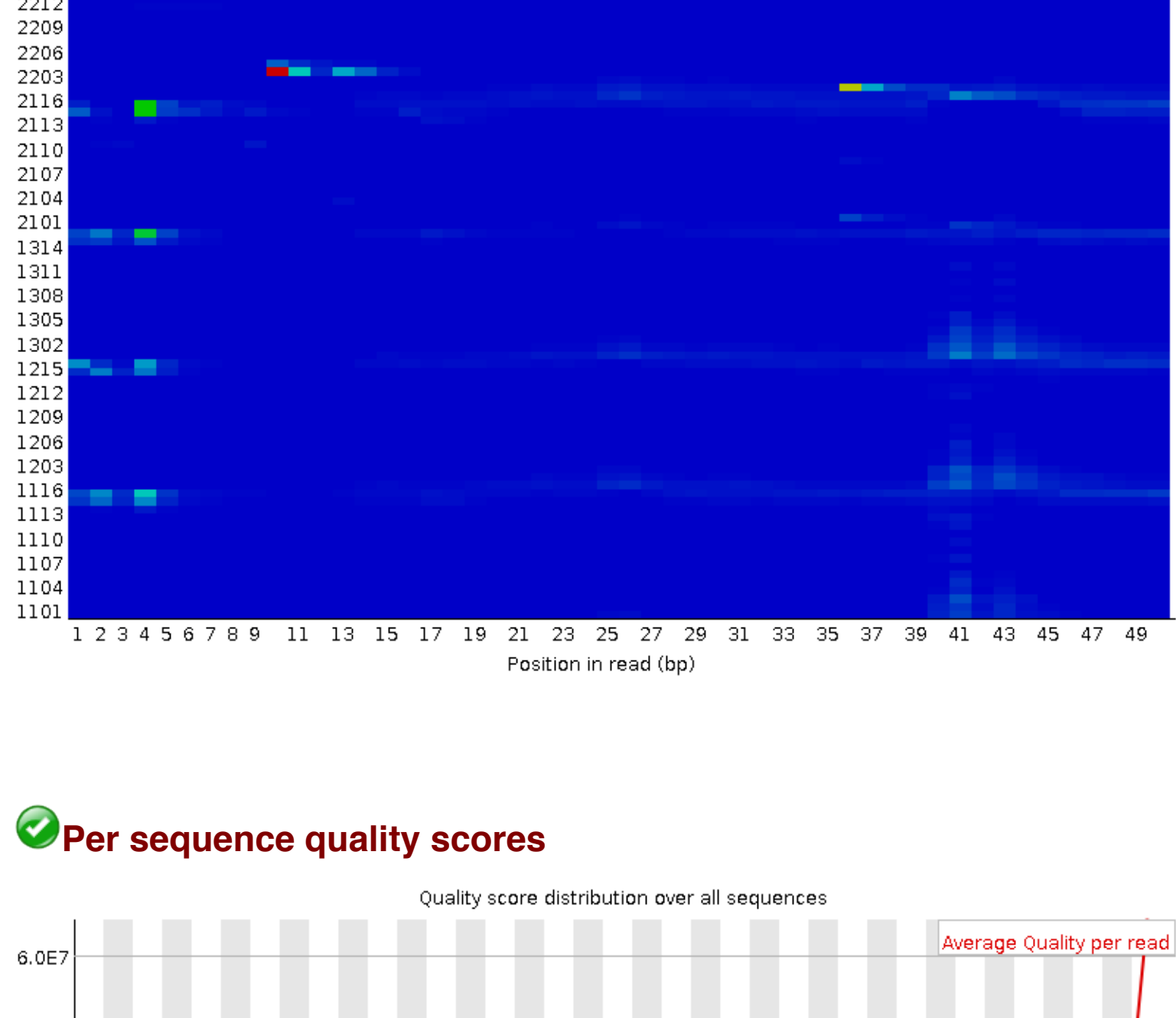
Summary

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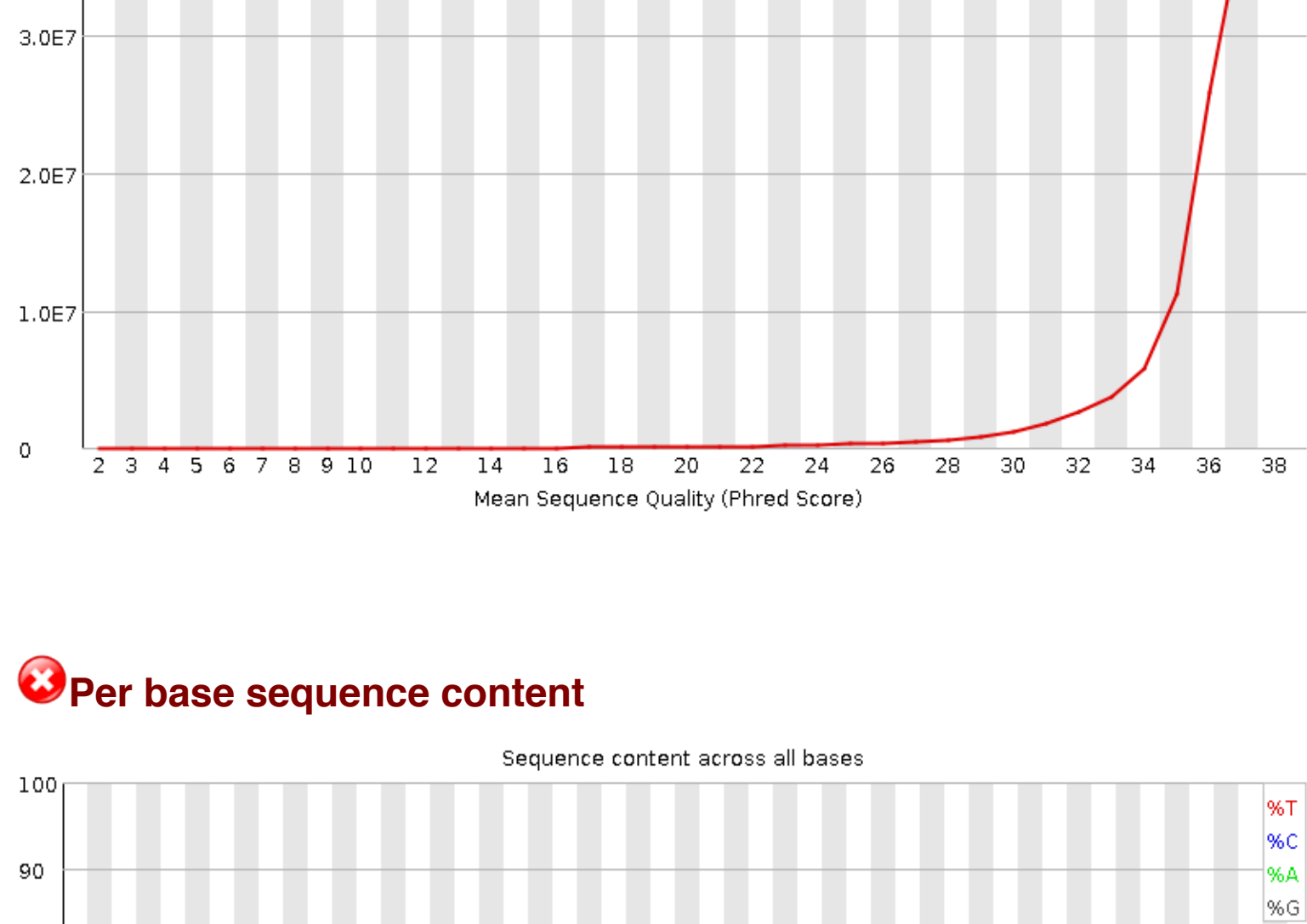
Basic Statistics

Measure	Value
Filename	HCT116_LTM.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	158957695
Sequences flagged as poor quality	0
Sequence length	50
%GC	57

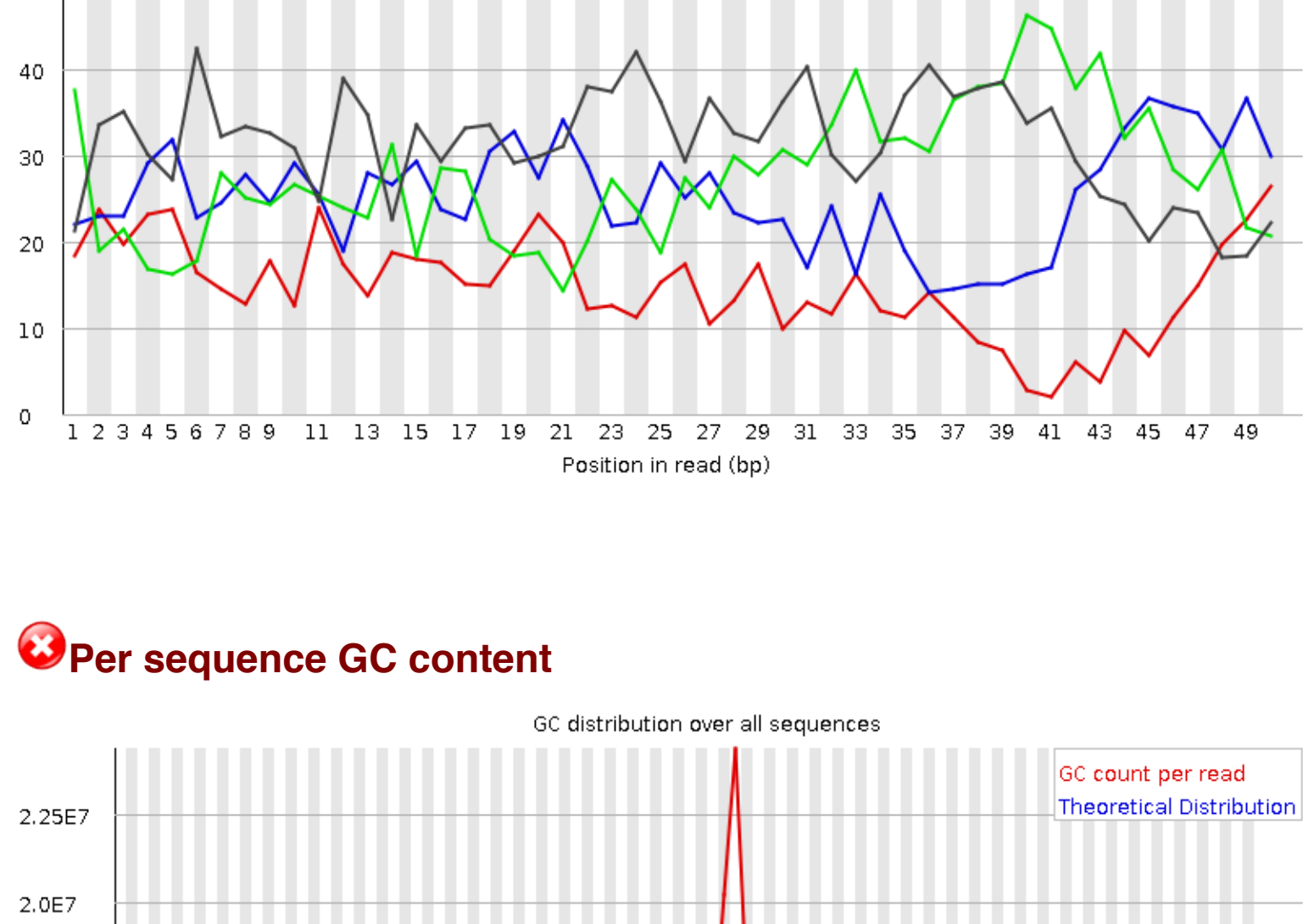
Per base sequence quality



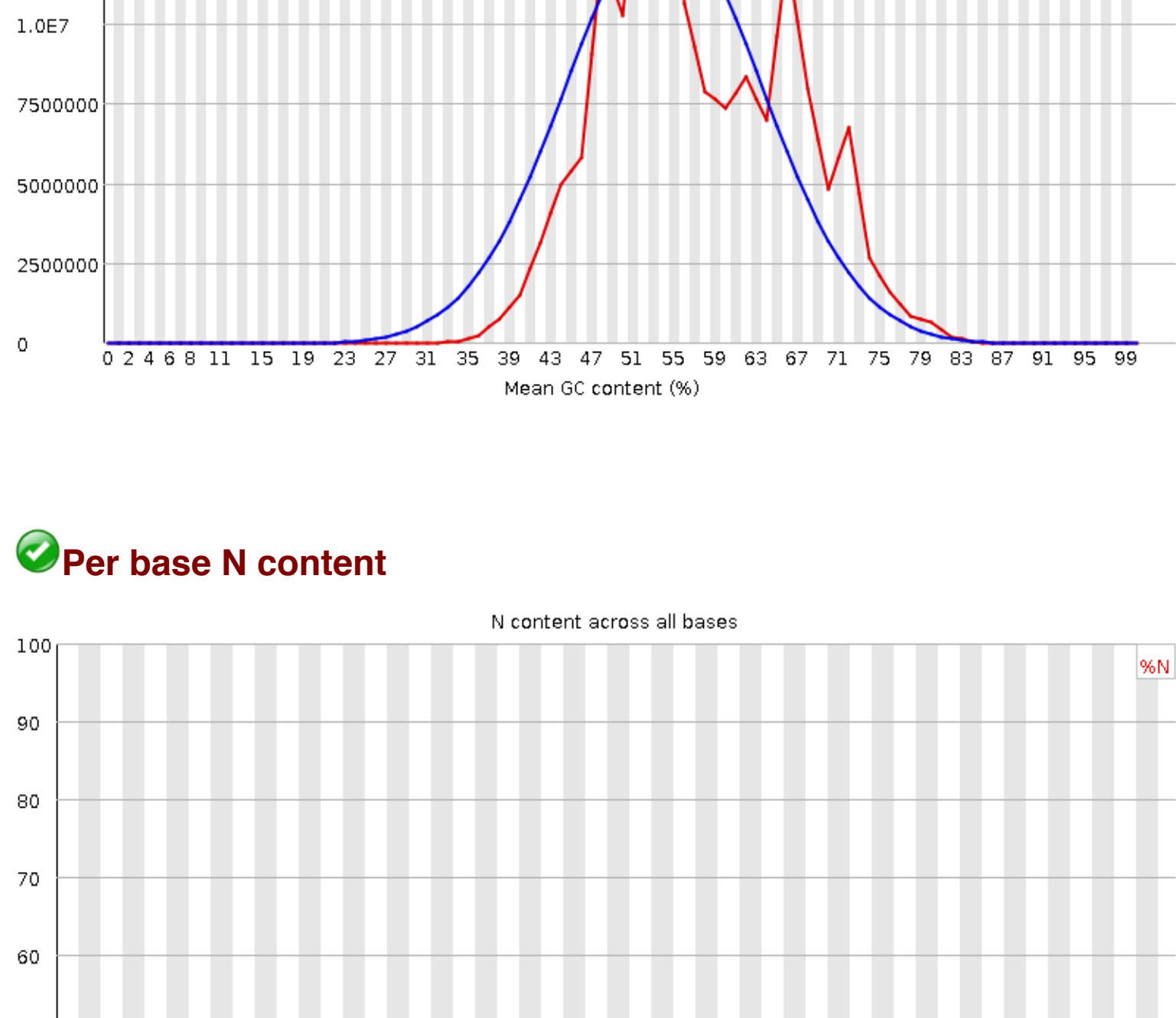
Per tile sequence quality



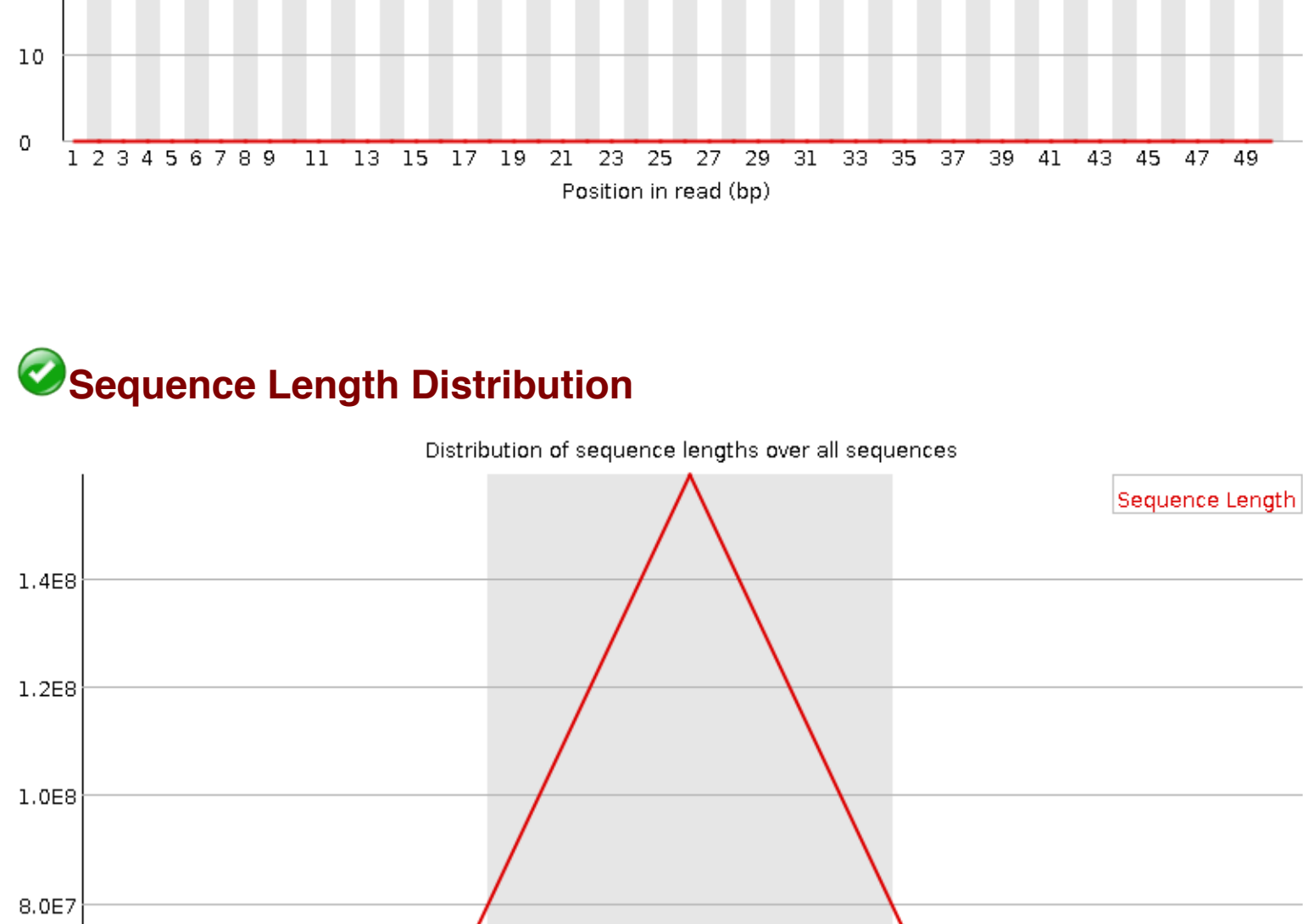
Per sequence quality scores



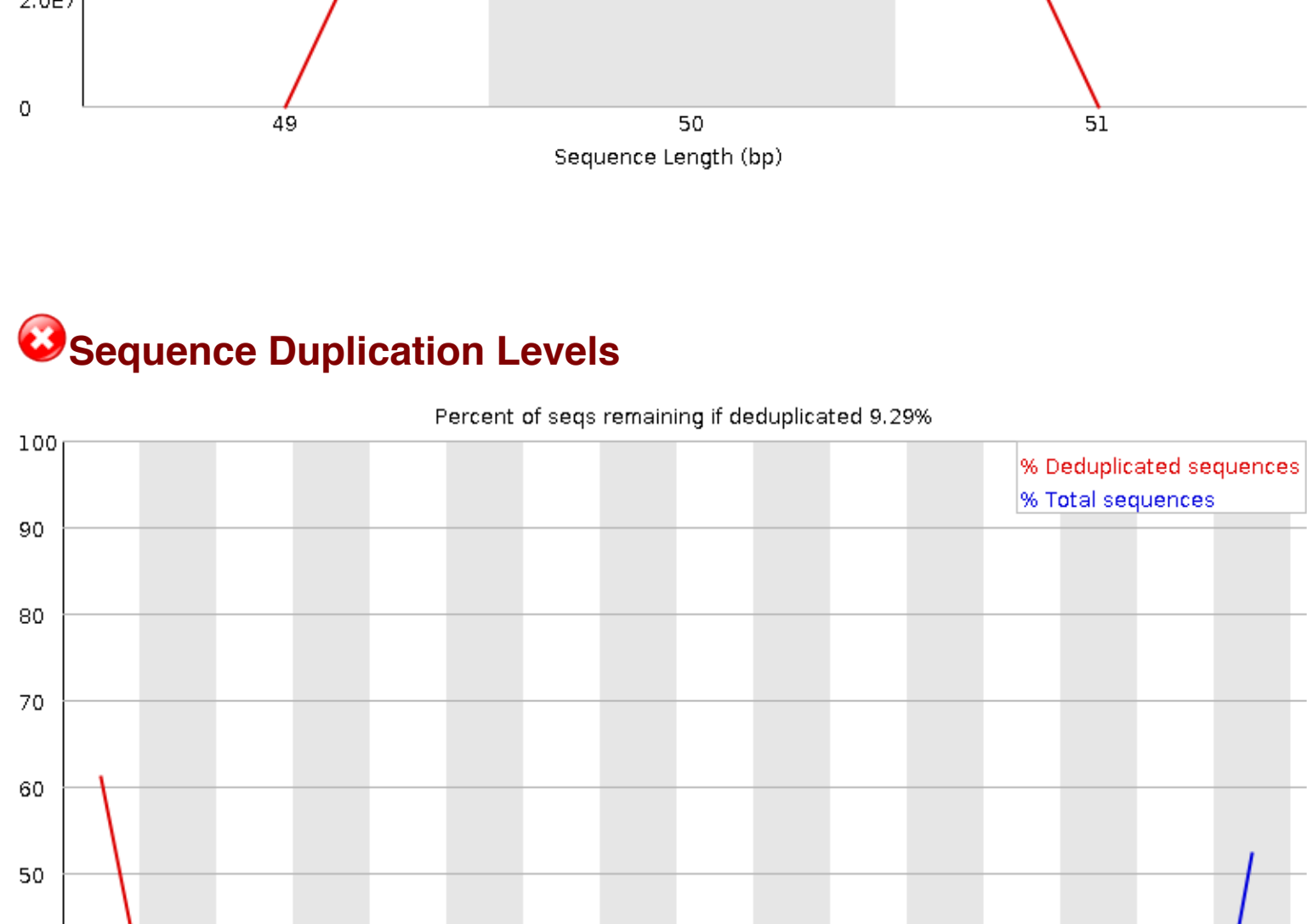
Per base sequence content



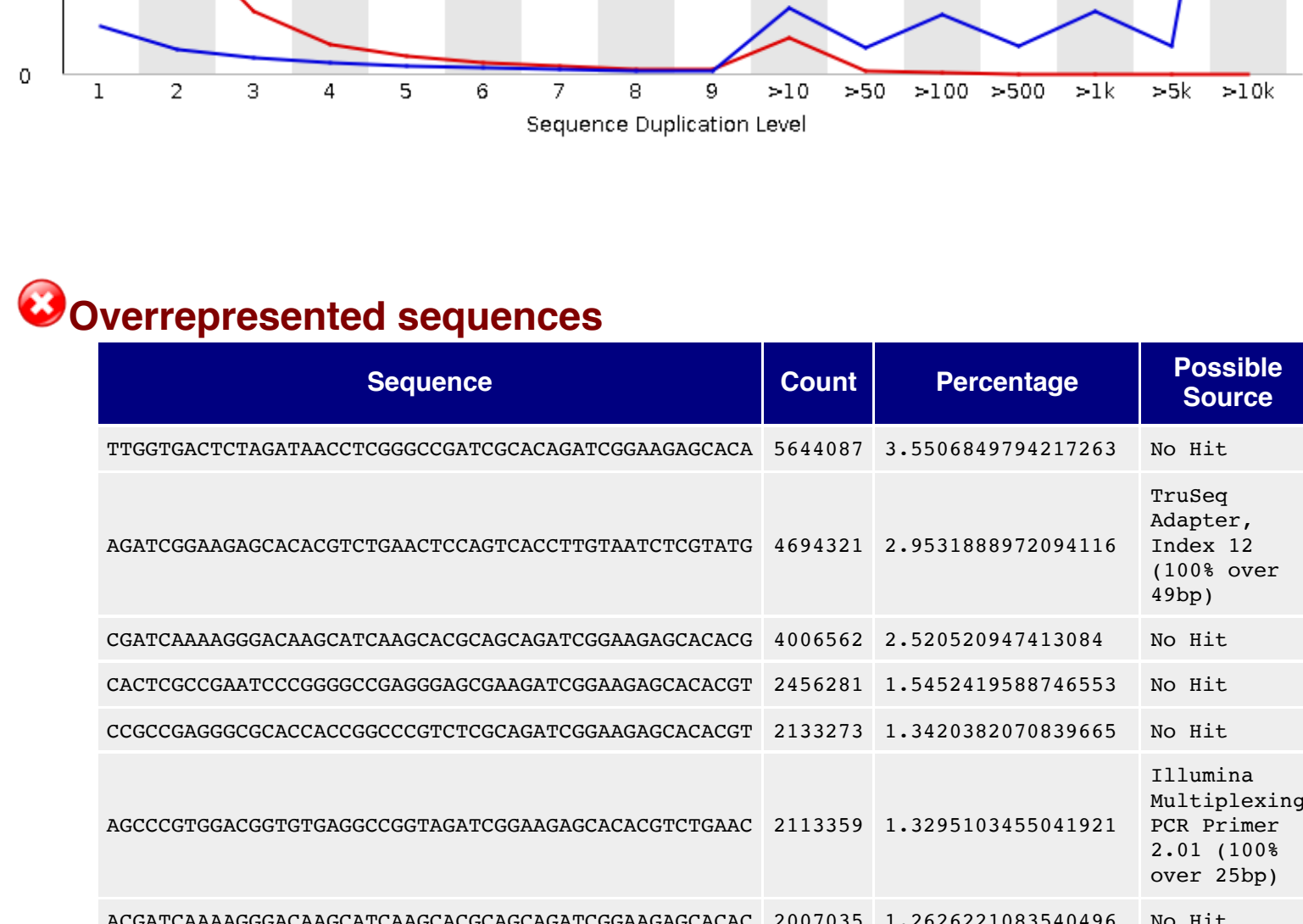
Per sequence GC content



Per base N content



Sequence Length Distribution



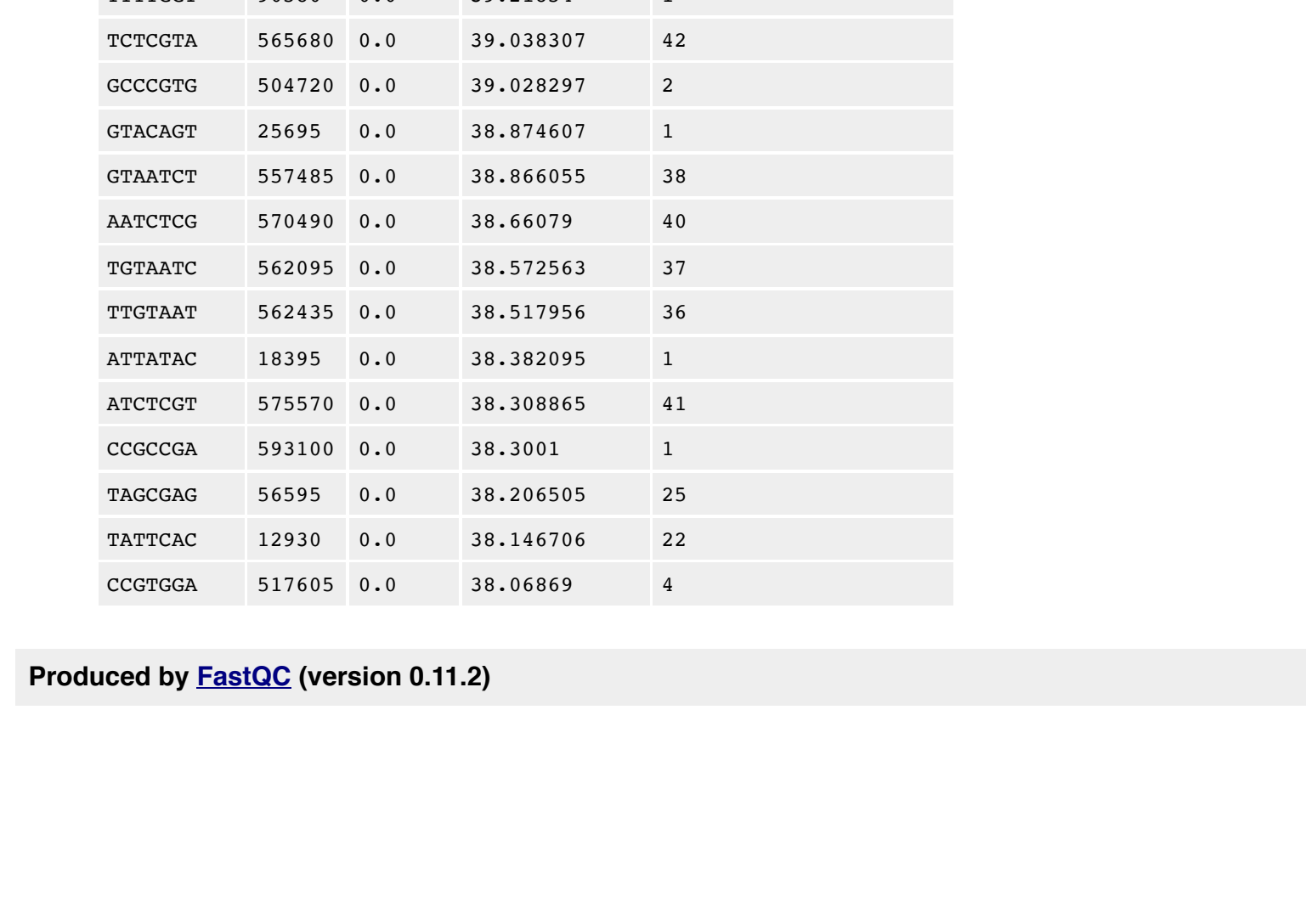
Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TTGGTGA	5644087	3.5506849794217263	No Hit
AGATCGG	4694321	2.9531888972094116	TruSeq Adapter, Index 12 (10% over 49bp)
CGATCAA	4006562	2.520520947413084	No Hit
CCCTCCG	2456281	1.5452419588746553	No Hit
CCCTCGG	2133273	1.3420382070839665	No Hit
AGCCCTG	2113359	1.3295103455041921	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
AGCTCAA	2007035	1.2626221083540496	No Hit
ACTCCCG	1924034	1.2104063285517572	No Hit
TTTGTGA	1633735	1.0277794798258892	No Hit
AAGCTTG	1534784	0.9655298537135935	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
CCGCGGG	1514450	0.9527377708892923	No Hit
GTTAAAC	1405248	0.8840389891594066	No Hit
GCACCTC	958134	0.6027603759604089	No Hit
ACTCCCG	915225	0.5757664012427961	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
CACCTCG	846841	0.5327461498482348	No Hit
TTGGTGA	831586	0.5231492567881033	No Hit
AGCCCTG	766687	0.48232141262491257	No Hit
AGATAAC	692679	0.4357631129464981	Illumina Multiplexing PCR Primer 2.01 (100% over 27bp)
CTGTGGG	669041	0.4208924896652534	No Hit
TTGGTGA	574247	0.3612577547795709	No Hit
GTGGGGG	569769	0.3584406530303505	No Hit
AAAAGGG	510505	0.3211577723123123	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
AGCACTC	501475	0.3154770204739066	No Hit
GTGCGCC	488672	0.30742262700505967	No Hit
AGCACTC	465855	0.2930685425253507	No Hit
TTGGTGA	461229	0.2901583342662335	Illumina Multiplexing PCR Primer 2.01 (100% over 25bp)
AGCCCTG	439232	0.2763200611332468	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
TGGATAA	437180	0.2750291516242734	No Hit
ACTCCCG	430893	0.27107401123298874	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
GTGGAGG	430195	0.27063490068851307	No Hit
CCCTCCG	408209	0.2568035476357404	No Hit
CTCCGGG	378181	0.2379129868484819	No Hit
TTTGTGA	349199	0.23591119637209132	No Hit
ACTCTCG	370756	0.2332419327041701	No Hit
TTGGTGA	369496	0.232442962897058993	No Hit
GAATACA	364880	0.22954535167360096	No Hit
AGCACTC	359940	0.22643760655940565	No Hit
CCGCGGG	354689	0.2231342119046203	No Hit
GTTAAAC	349199	0.21968046277973519	No Hit
TTTGTGA	342806	0.21565863797911766	No Hit
TTTGTGA	337140	0.21209416757081181	No Hit
TTTGTGA	334786	0.2104063285517572	No Hit
GCACCTC	322439	0.20284579491417512	No Hit
ACTCCCG	304359	0.19147169943550074	No Hit
ACCCCTC	285432	0.17956475778036413	Illumina Multiplexing PCR Primer 2.01 (100% over 26bp)
TGTTGAC	284389	0.17890860835645608	No Hit
CCGCGGG	258678	0.1627338645040116	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
CTCCGGG	257689	0.16211168638297127	No Hit
AGCCCTG	257030	0.1616971106683448	No Hit
TAGATAA	255912	0.1609937788793427	Illumina Multiplexing PCR Primer 2.01 (100% over 26bp)
ACTCCCG	255142	0.16050937326437703	Illumina Multiplexing PCR Primer 2.01 (100% over 23bp)
COTGGGG	246058	0.15479464520418468	No Hit
CGTCCCG	246035	0.15478017594555582	No Hit
GGACGTG	244426	0.15376795693973797	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
AAGCTTG	242093	0.15230027083621211	Illumina Multiplexing PCR Primer 2.01 (100% over 26bp)
AGCACTC	239256	0.1505155192392542	No Hit
CGATCAA	224280	0.1410941445727257	Illumina Multiplexing PCR Primer 2.01 (100% over 21bp)
GTCCGGG	218155	0.13724091809459116	No Hit
COTGGGG	215977	0.1358707422122597	No Hit
GCACCTC	215070	0.1353001501437222	No Hit
AGCCCTG	212063	0.1334084518525511	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
ACCGGGG	206182	0.12970872533097563	No Hit
GAATACA	203331	0.12791516635920017	No Hit
TTTGTGA	199640	0.12559316489837125	Illumina Multiplexing PCR Primer 2.01 (100% over 24bp)
CCGCGGG	189011	0.11890648011742125	No Hit
CCGCGGG	187382	0.1178816791473983	No Hit
TCCCGGG	183964	0.11573142149551174	No Hit
ATGTGGG	183822	0.11564208959593366	No Hit
CTGCTCG	177973	0.11196249417179836	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
GTGGGGG	175001	0.11009281431767114	No Hit
GCACCTC	173160	0.1098751539206706	No Hit
AGTAAAA	173403	0.1089346445291623	No Hit
ATGTGGG	172037	0.10822816724915393	No Hit
CCGCGGG	170557	0.1072910191129783	Illumina Multiplexing PCR Primer 2.01 (100% over 22bp)
GTTAAAC	169073	0.10636352018063674	No Hit
GGTGAAC	160309	0.10085010354484569	No Hit

Adapter Content



Kmer Content

Sequence	Count	PValue	Obs/Exp Max	max Obs/Exp Position
AGCCCT	458350	0.0	42.801205	1
CCCTGG	495835	0.0	40.03166	3
GAATACA	123555	0.0	39.647346	1
GGCTAGC	28265	0.0	39.21346	5
TCGTATG	559910	0.0	39.45886	44
CTCGTAT	561620	0.0	39.32058	43
TTTTTGT	90580	0.0	39.21854	1
TCTCGTA	565680	0.0	39.03807	42
GCCTCGT	504720	0.0	39.02897	2
GTCACGT	25695	0.0	38.874607	1
GTAATCT	557485	0.0	38.866055	38
AATCTCG	570490	0.0	38.66079	40
TGTAATC	562095	0.0	38.572563	37
TTGTAA	562435	0.0	38.517956	36
ATTATAC	18395	0.0	38.382095	1
ATCTCGT	575570	0.0	38.308865	41
CCGCCGA	593100	0.0	38.3001	1
TAGCGAG	56595	0.0	38.206505	25
TATTACG	12930	0.0	38.146706	22
CCGTGGA	517605	0.0	38.08669	4