FastQC Report

Sun 1 Feb 2015
C_cutadapt_2nd.fastq.gz

Summary

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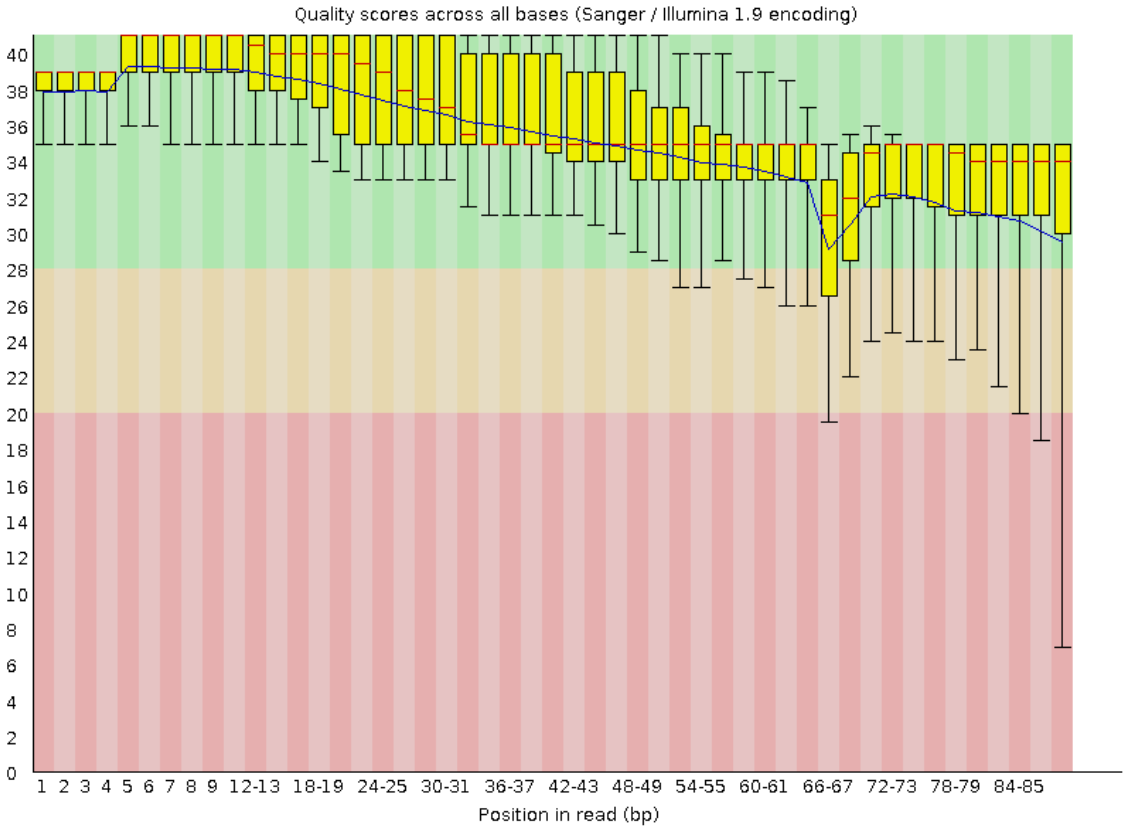
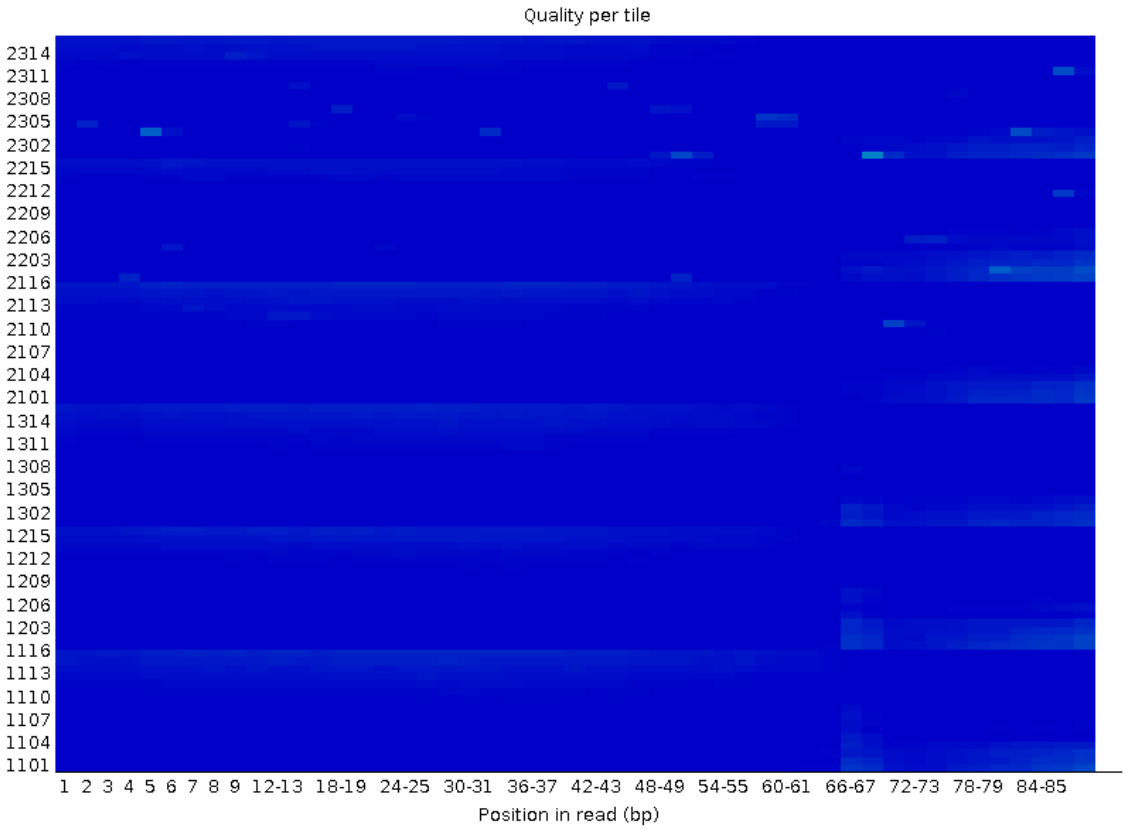
Basic Statistics

Measure	Value
Filename	C_cutadapt_2nd.fastq.gz
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	24600690
Sequences flagged as poor quality	0
Sequence length	6-88
%GC	64

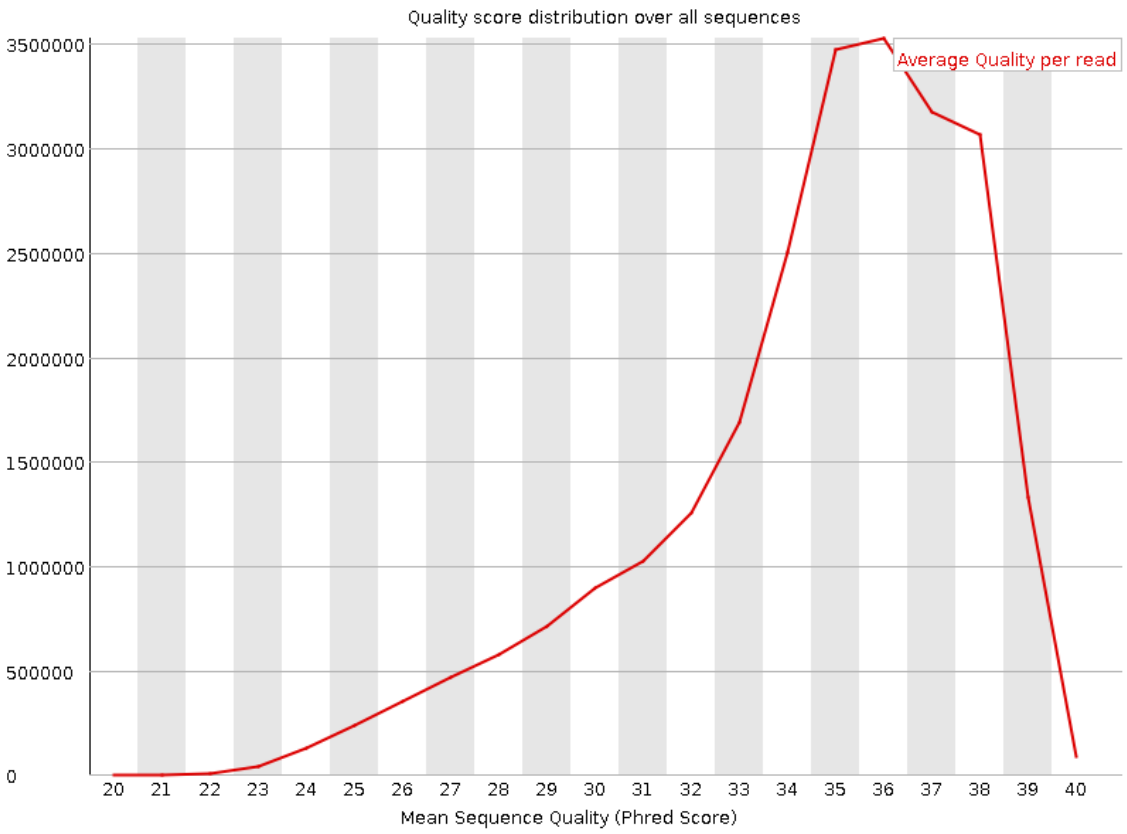
Per base sequence quality



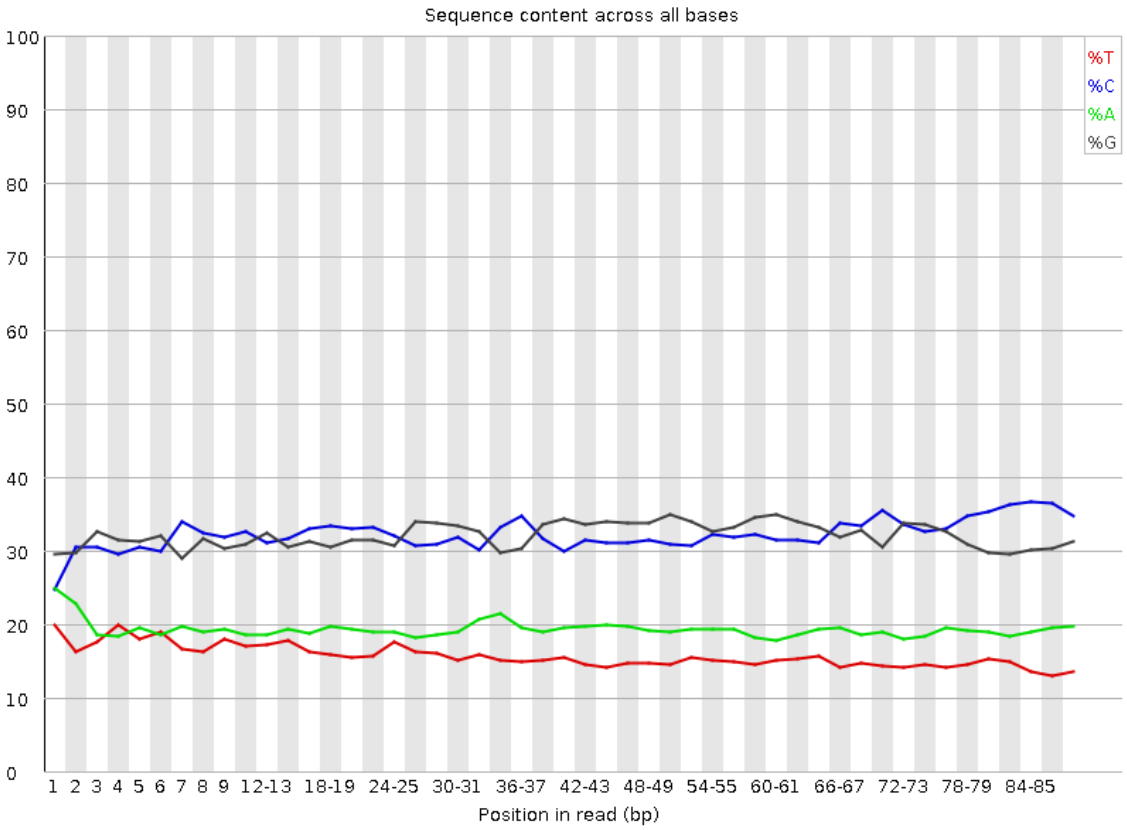
Per tile sequence quality



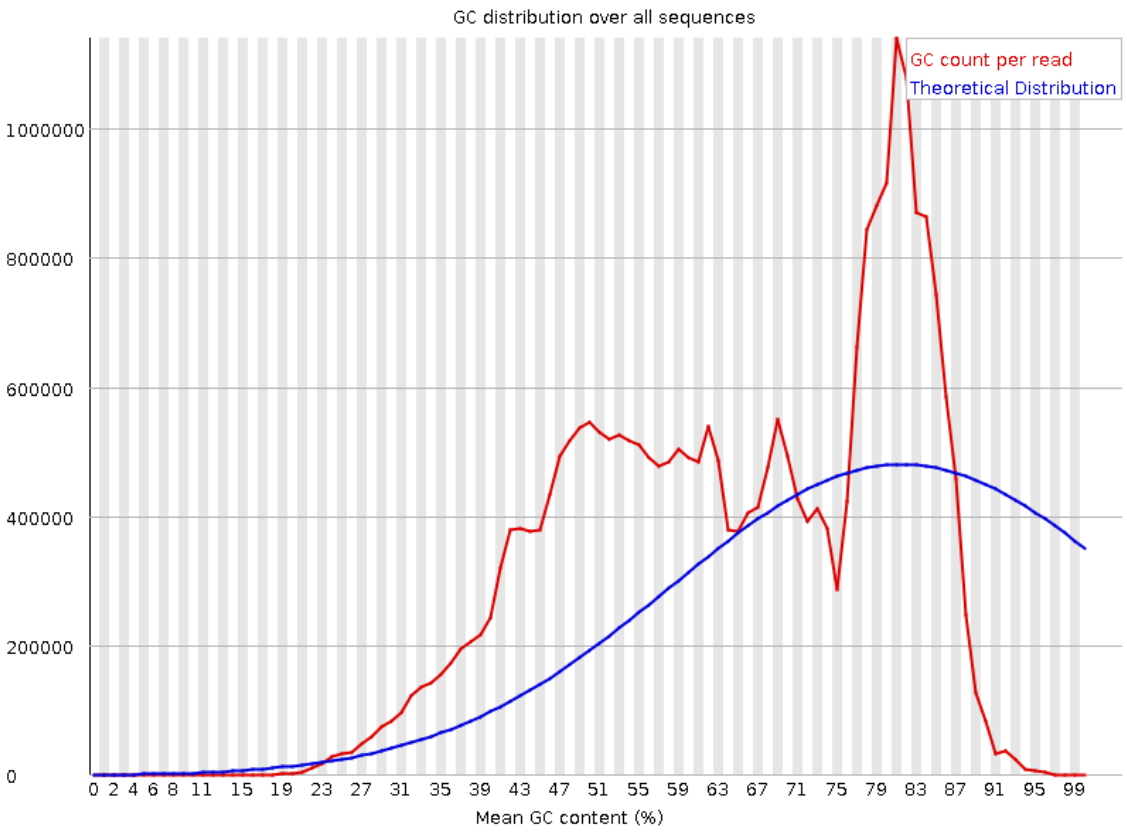
Per sequence quality scores



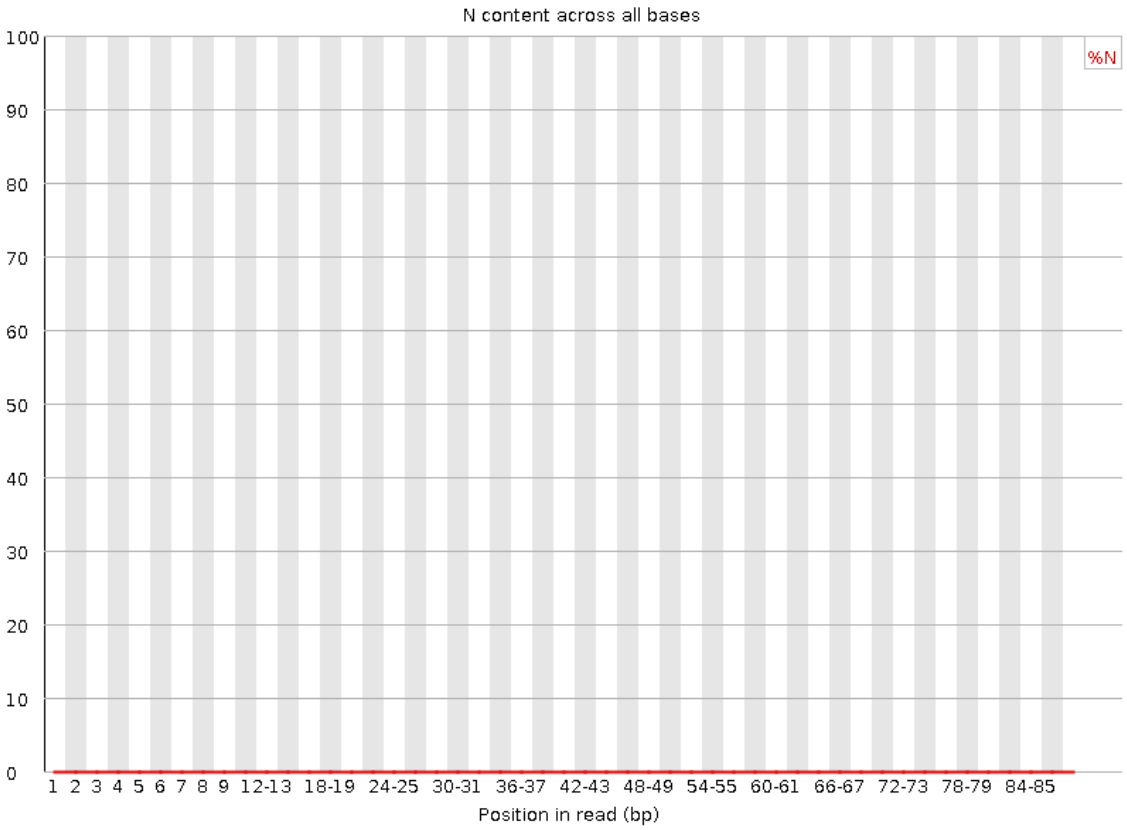
Per base sequence content



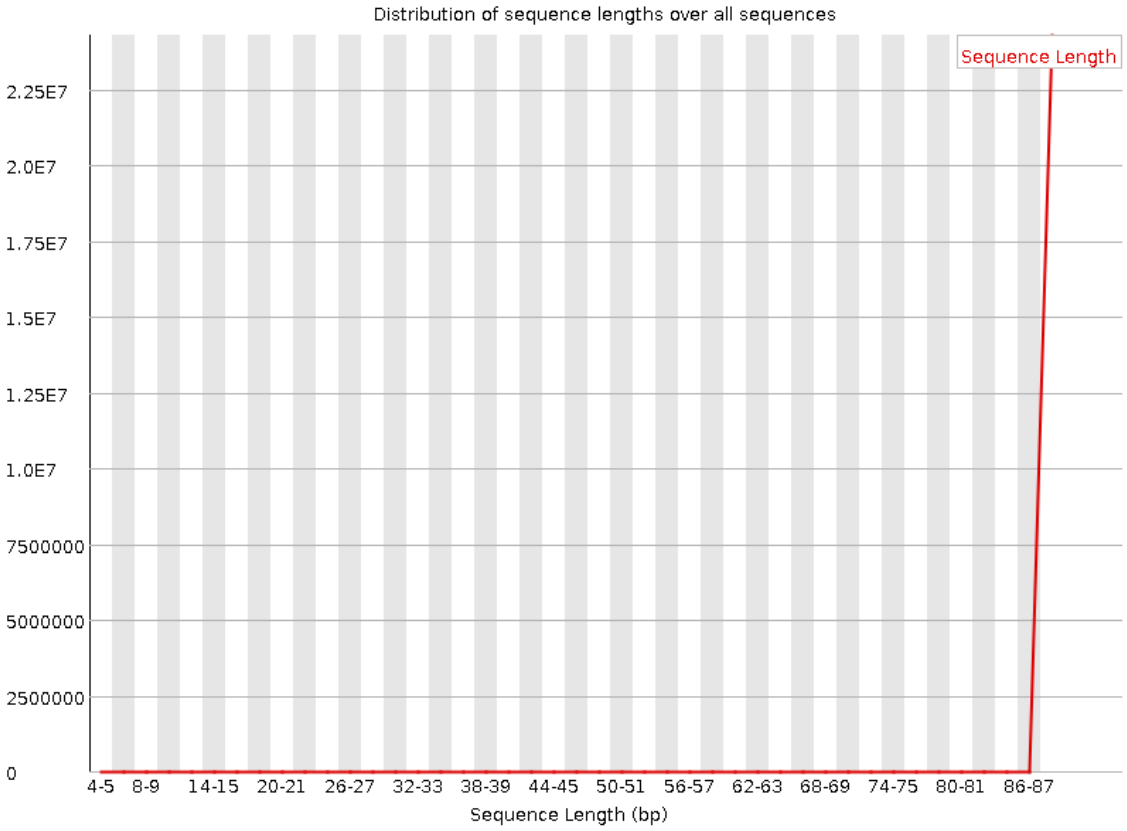
Per sequence GC content



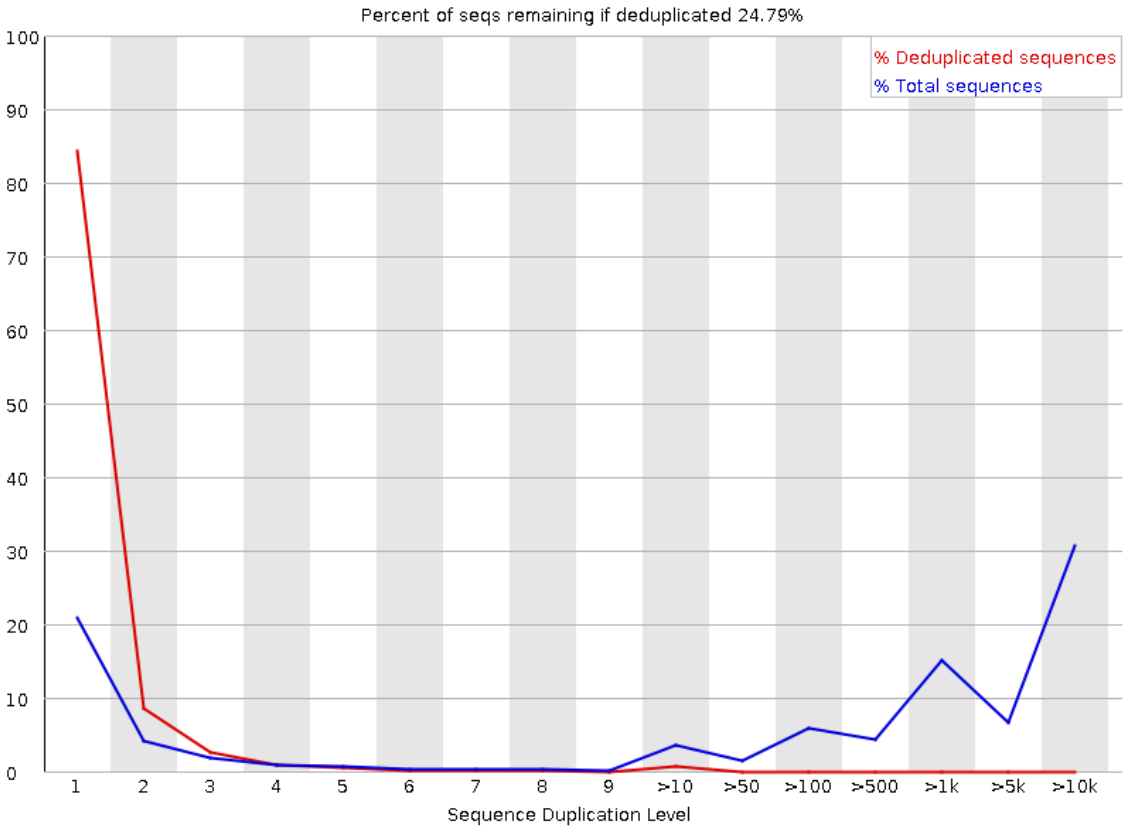
Per base N content



Sequence Length Distribution



Sequence Duplication Levels

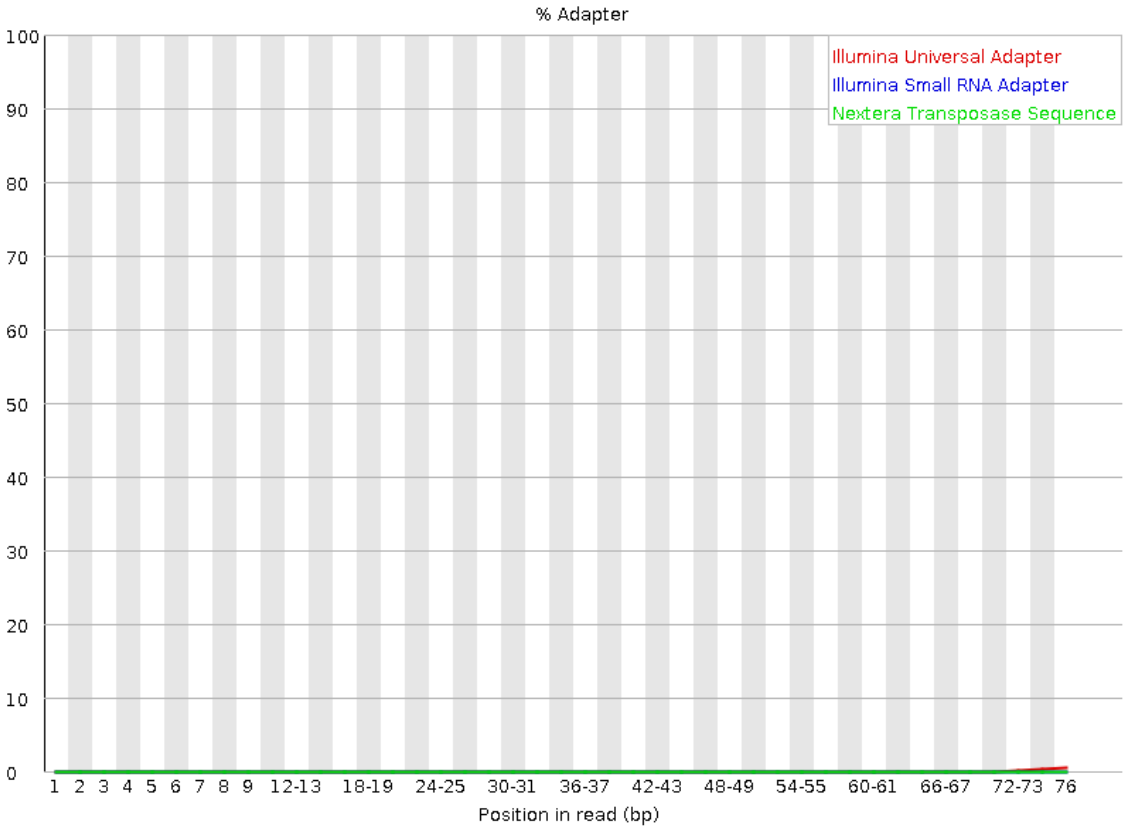


Overrepresented sequences

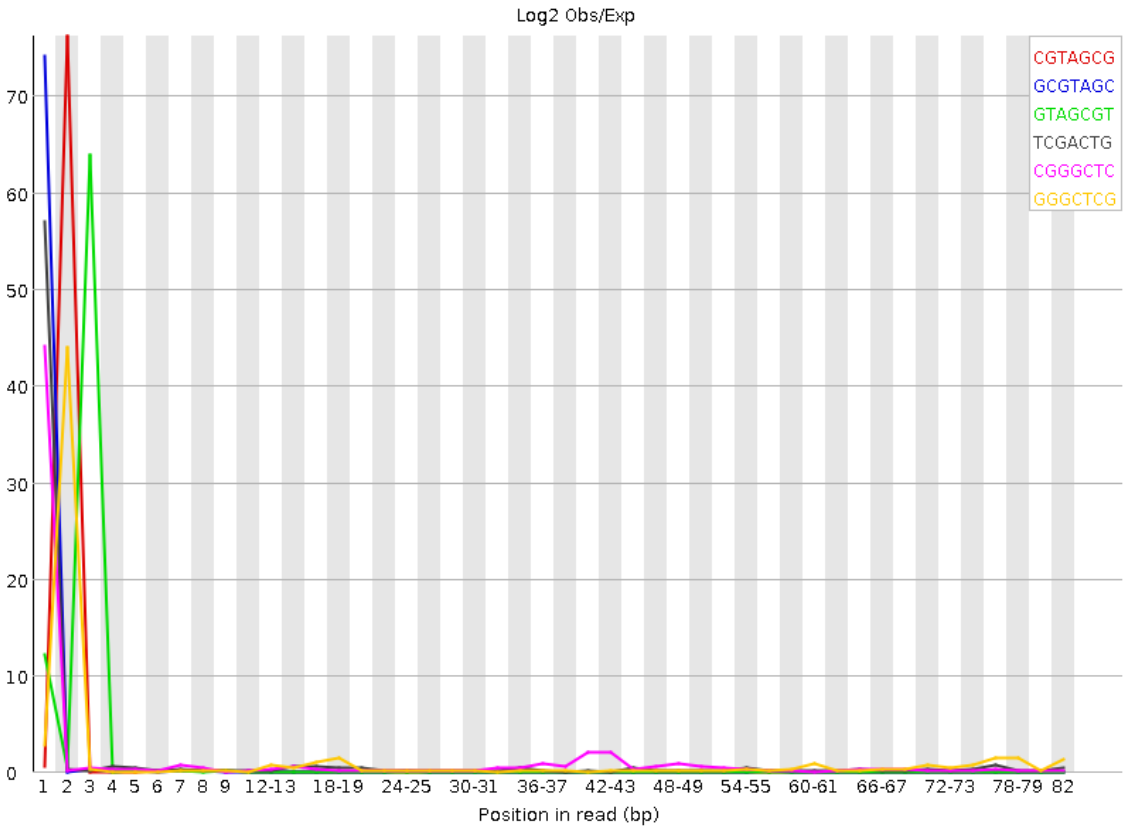
Sequence	Count	Percentage	Possible Source
TAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGGGGGG	231674	0.9417378130450812	No Hit
TAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAGG	203234	0.8261312995692396	No Hit
GGCGGCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGAAGGGCCCGG	184047	0.7481375522393885	No Hit
GTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACGA	177028	0.7196058321941377	No Hit
GTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGC	143987	0.5852965912744723	No Hit
GCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGG	141495	0.5751667941021167	No Hit
GACGGGCGAGAGGGCGGCCCCCTTTCCGGCCGCACCCCGTTTCCCAAGAC	138738	0.5639597913717054	No Hit
AAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGC	125388	0.509693020805514	No Hit
GCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCG	120773	0.49093338438881184	No Hit
TCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGAGGGCTGTAACACTCGG	114058	0.46363740204034926	No Hit
AGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAGG	113698	0.46217402845204747	No Hit
CGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGC	109668	0.4457923741163358	No Hit
GAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAG	106388	0.43245941475625277	No Hit
AACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACC	99735	0.4054154578591088	No Hit
ACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCG	92228	0.3749000536163823	No Hit
AGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAA	91811	0.37320497920993273	No Hit
TCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGG	89594	0.3641930368619742	No Hit
CGCCGCCGCCGCCGGCCCCCCCGAGTGTCCGGGCCCCCCGCCCCACCGGG	87532	0.3558111581423123	No Hit
ACCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACCCCGCGCCGCCGCG	84577	0.3437992999383351	No Hit
CCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGA	81783	0.33244189492245946	No Hit
AGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGT	78416	0.31875528694520355	No Hit
CGGGCTCGCCCCCCCGCCTCACCGGGTCAGTGAAAAAACGATGAGAGTAG	76276	0.3100563439480763	No Hit
TAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCG	74348	0.3022191653973933	No Hit
CCTCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGAGGGCTGTAACACTC	72494	0.2946827914176391	No Hit
GGCTTCCTCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGAGGGCTGTAA	72285	0.2938332217510972	No Hit
GGCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTGATGCCGAA	71477	0.29054876103068655	No Hit
GGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGGGGGGCG	59624	0.24236718563585008	No Hit
TGGGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGA	58785	0.23895671218978004	No Hit
TCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAAC	58644	0.23838355753436186	No Hit
GGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAGGG	56908	0.23132684489743988	No Hit
GCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGGGGGGCGG	56242	0.22861960375908152	No Hit
GTTTAGCGCCAGGTTCCACACGAACGTGCGTTCAACGTGACGGGCGAGAG	56203	0.22846107162034887	No Hit
AGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGA	55723	0.2265099068359465	No Hit
CCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCG	54612	0.22199377334538176	No Hit
TTGCCCAGGCTGGAGTGCAGTGGCTATTCACAGGCGCGATCCCACTACTG	54079	0.2198271674493683	No Hit
ATGTATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGAGAGGAGCGAG	52756	0.2144492695123592	No Hit
GTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGC	52548	0.2136037647724515	No Hit
CGACCTGGGCCGGTTCACCCCTCCTTAGGCAACCTGGTGGTCCCCCGCTC	52292	0.21256314355410358	No Hit
GCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAGGGG	50700	0.2060917803525023	No Hit
CACACGAACGTGCGTTCAACGTGACGGGCGAGAGGGCGGCCCCCTTTCCG	49447	0.20099842727988523	No Hit
CGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCC	47321	0.1923563932556363	No Hit
TCGAATGGGTCGTCGCCGCCACGGGGGGCGTGCGATCGGCCCGAGGTTAT	45137	0.18347859348660545	No Hit
AGGCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTGATGCCGA	45094	0.18330380164133608	No Hit
CGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGC	44626	0.18140141597654375	No Hit
GGTCGCGGCGCACCGCCACGGTGGAAGTGCGCCCGGCGGCGGCCGGTCGC	44589	0.1812510136910794	No Hit
GTGTTTCAAGACGGGTCGGGTGGGTAGCCGACATCGCCGCCGACCCCGTG	43201	0.17560889552284917	No Hit
CAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGGG	42643	0.1733406664609814	No Hit
GCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTGATGCCGAAC	40755	0.16566608497566532	No Hit
GCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGGGGGGCGGAC	40749	0.16564169541586027	No Hit
AGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCG	39145	0.15912155309464895	No Hit
GCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGAAGGGCCCGGCTCG	37859	0.15389405744310425	No Hit
AGGGGGGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGG	37726	0.15335342220075943	No Hit

Sequence	Count	Percentage	Possible Source
GCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGC	37464	0.15228841142260643	No Hit
GCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAGGGCGGGCCCGGGCG	37320	0.15170306198728573	No Hit
GCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGGT	36333	0.14769097939935832	No Hit
AGAGTCGCCGCCGCCGCCGGCCCCCCCGAGTGTCCGGGCCCCCCGCCCCA	36274	0.14745114872794218	No Hit
CGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACG	36107	0.14677230598003552	No Hit
CCGACCTGGGCCGGTTCACCCCTCCTTAGGCAACCTGGTGGTCCCCCGCT	35785	0.14546339960383226	No Hit
CCGGGCCCCCCGCCCCACCGGGGGCCCGCTGGTTCCTCCCGCTCCGGAAC	35108	0.14271144427249804	No Hit
GCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCG	33917	0.1378701166511996	No Hit
TCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGAC	33612	0.13663031402777726	No Hit
CGGCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGAAGGGCCCGGCT	33390	0.13572790031499116	No Hit
ACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACCC	33217	0.13502466800727947	No Hit
CCGCCAGGCCGTGGGCCGACCCCGGCGGGGCCGATCCGAGGGCCTCACTA	32867	0.13360194368531939	No Hit
ACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTGATGCCGAACTTA	32771	0.1332117107284389	No Hit
CCAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGG	32563	0.13236620598853122	No Hit
CGACGGCGCGACCCGCCCGGGGCGCACTGGGGACAGTCCGCCCCGCCCCC	32417	0.13177272669994217	No Hit
GGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACG	32286	0.13124022131086566	No Hit
CCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACCCCGCGCCGCCGCGG	32261	0.1311385981450114	No Hit
ACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAGGGCGGGCCCGGG	32079	0.13039878149759213	No Hit
CACAGGCGCGATCCCACTACTGATCAGCACGGGAGTTTTGACCTGCTCCG	31640	0.1286142787051908	No Hit
CGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGG	31518	0.12811835765582186	No Hit
CGGACCCGGCGGGGGAACACCGACGCGGAGGTTCCCCCCACACGCGCGGG	30507	0.12400871682867433	No Hit
CTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGG	30454	0.12379327571706321	No Hit
CGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACGACGCCCGGGG	30079	0.12226892822924885	No Hit
TATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGAGAGGAGCGAGCGA	29874	0.12143561826924366	No Hit
CCACACGAACGTGCGTTCAACGTGACGGGCGAGAGGGCGGCCCCCTTTCC	29508	0.11994785512113686	No Hit
CAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTGATGCCGAACT	29421	0.11959420650396392	No Hit
GAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACGACGCCC	29353	0.11931779149284025	No Hit
GGCTCGCCCCCCCGCCTCACCGGGTCAGTGAAAAAACGATGAGAGTAGTG	29253	0.11891129882942307	No Hit
GGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACGACGCC	29209	0.11873244205751954	No Hit
CTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACC	28568	0.1161268240850155	No Hit
ACGCGTGACCGACGGTCCCCCCGGGACCCGACGGCGCGACGACGCCCGGG	28096	0.11420817871368649	No Hit
GCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAGGGGAGGCGGGGGAC	27674	0.11249277967406605	No Hit
ATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGAC	27656	0.11241961099465096	No Hit
CCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGGTC	27242	0.1107367313681039	No Hit
GTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAG	27138	0.11031397899815006	No Hit
ACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCG	26942	0.10951725337785241	No Hit
CGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGAC	26793	0.10891157930936085	No Hit
CTCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACG	24623	0.10009068851320838	No Hit

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CGTAGCG	15975	0.0	76.11031	2
GCGTAGC	16410	0.0	74.197815	1
GTAGCGT	19035	0.0	63.896618	3

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGACTG	2300	0.0	57.04888	1
CGGGCTC	15660	0.0	44.157978	1
GGGCTCG	15755	0.0	44.0435	2
TAGCGTC	39575	0.0	42.24737	1
AGCGTCC	41160	0.0	40.557964	2
TTGCCCA	12440	0.0	37.89938	1
GTCCGCA	32375	0.0	37.533318	1
GGTCCGC	18010	0.0	37.17182	5
GCGTCCG	45370	0.0	36.740677	3
GGCCGCG	44730	0.0	36.656185	4
TCGTGCG	445	0.0	36.628494	1
CGTCCGC	49440	0.0	33.716248	4
CCCTGGT	20065	0.0	33.529495	1
TCCGCGG	50005	0.0	33.490456	6
CCGCGAC	49660	0.0	32.377476	6
GCCGCGA	49840	0.0	32.366627	5
CGCCTAG	6660	0.0	29.692919	82

Produced by FastQC (version 0.11.2)