FastQC Report

Tue 13 Jan 2015
stdin

Summary

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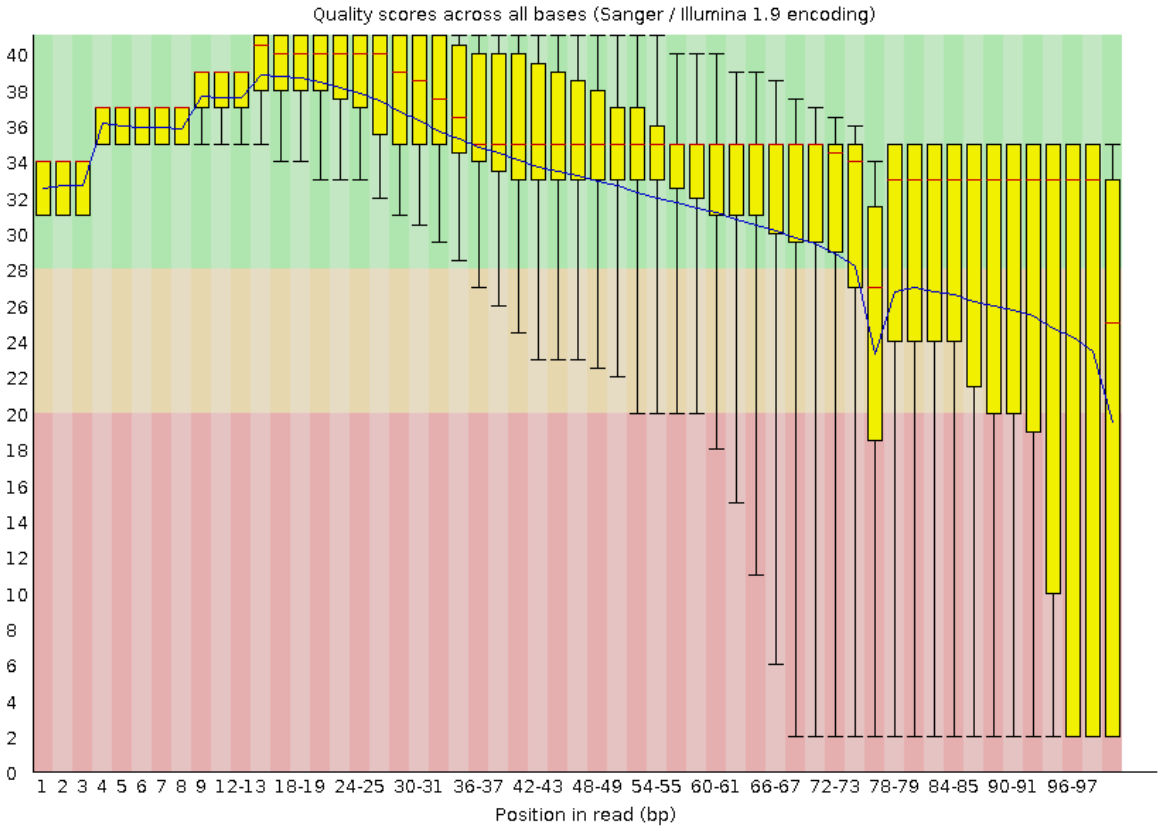
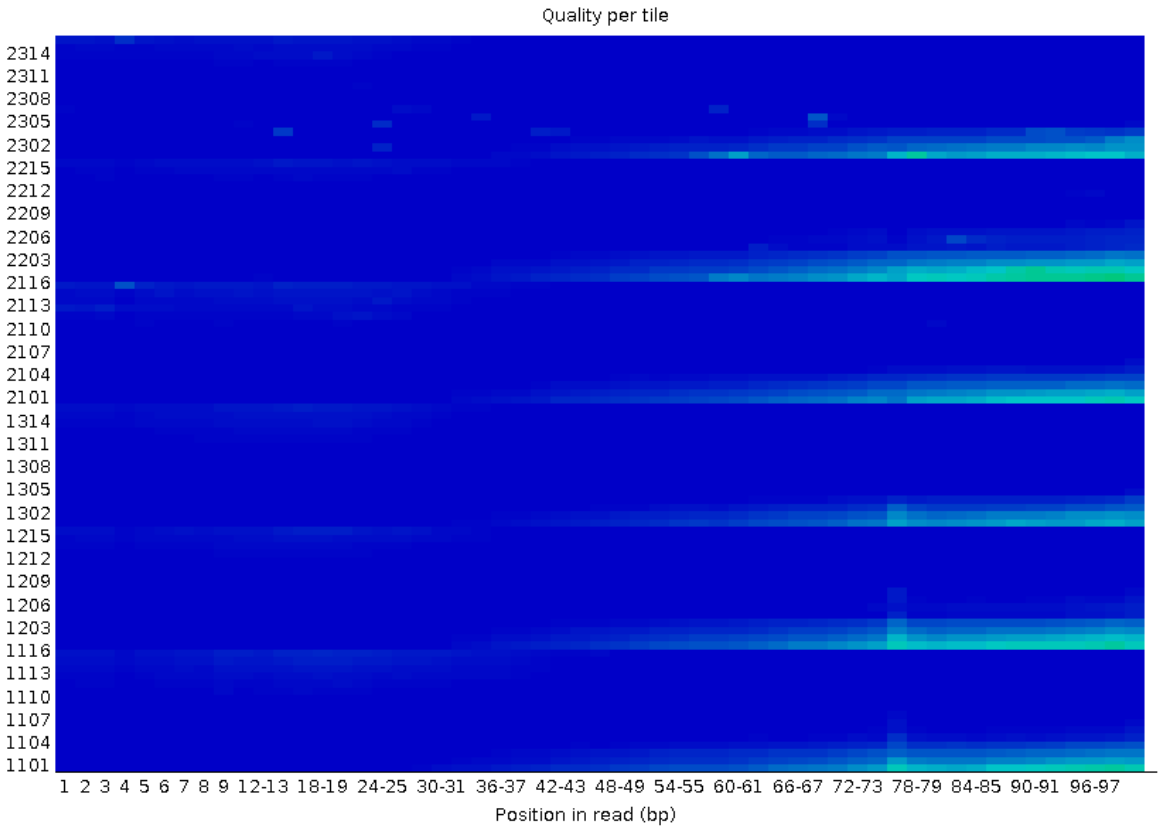
Basic Statistics

Measure	Value
Filename	stdin
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36473676
Sequences flagged as poor quality	0
Sequence length	15-100
%GC	69

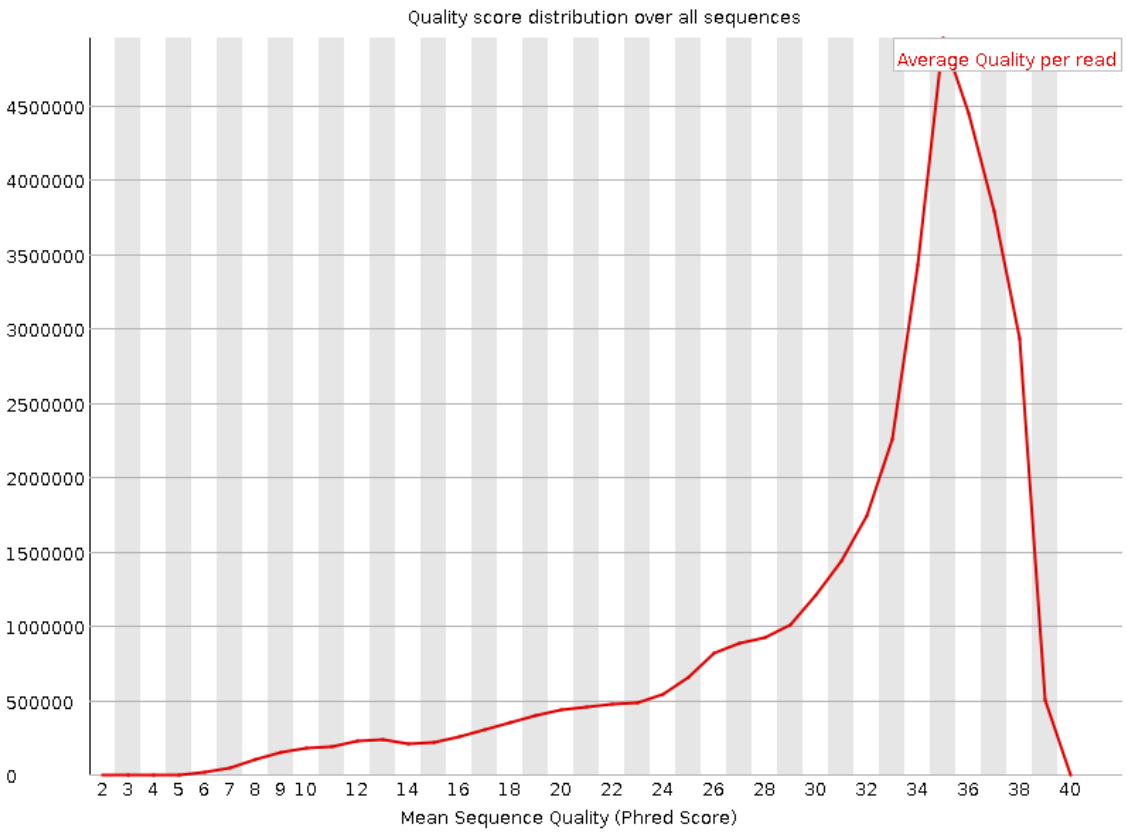
Per base sequence quality



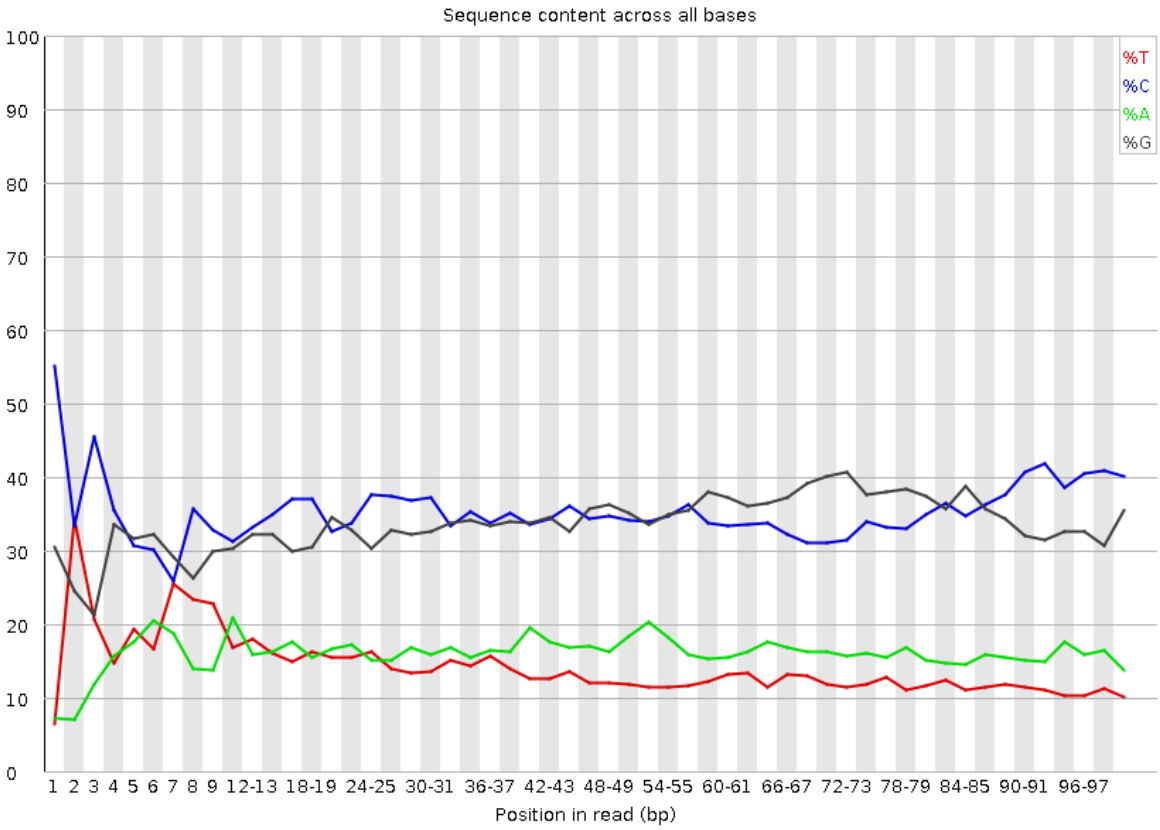
Per tile sequence quality



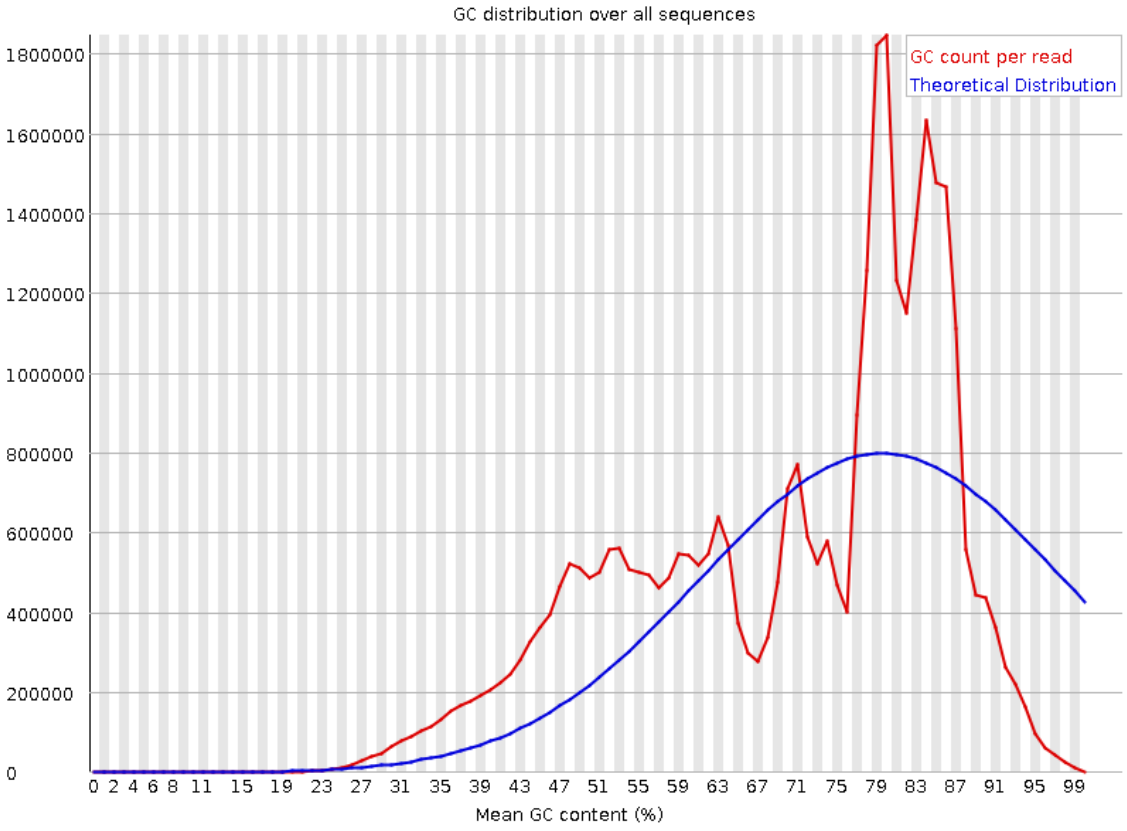
Per sequence quality scores



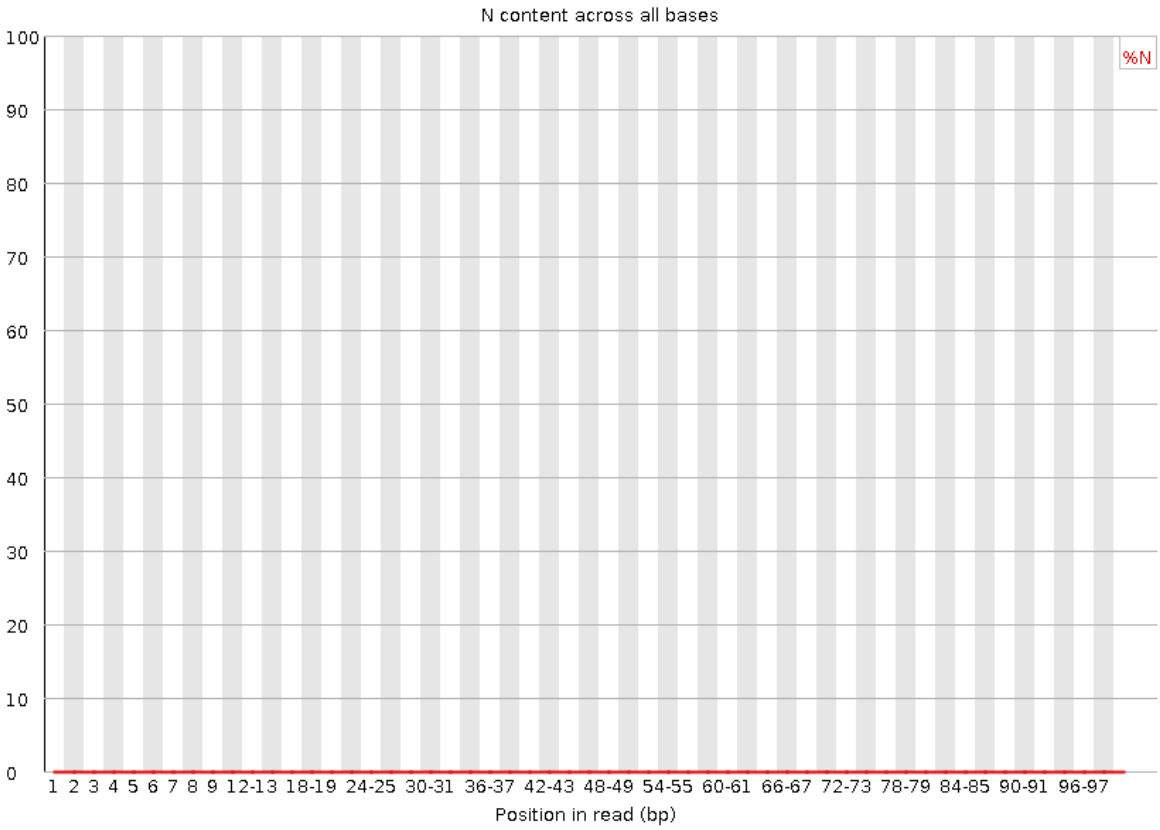
Per base sequence content



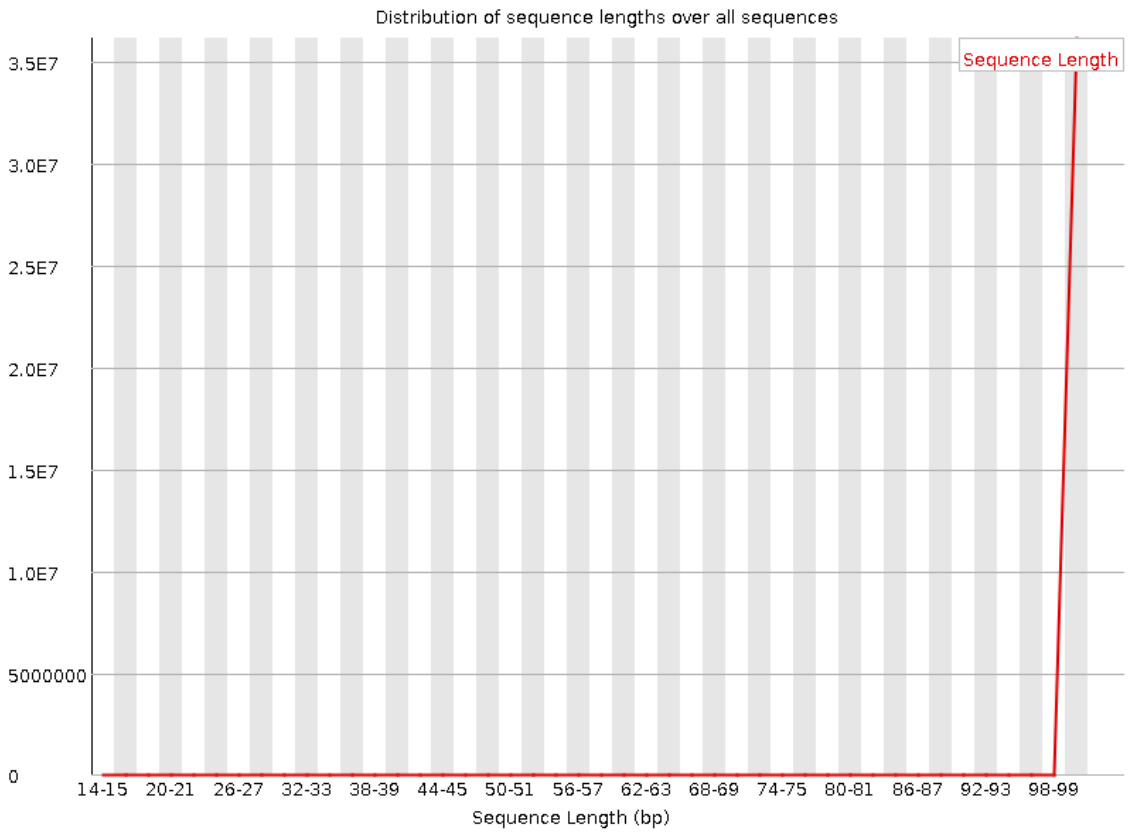
Per sequence GC content



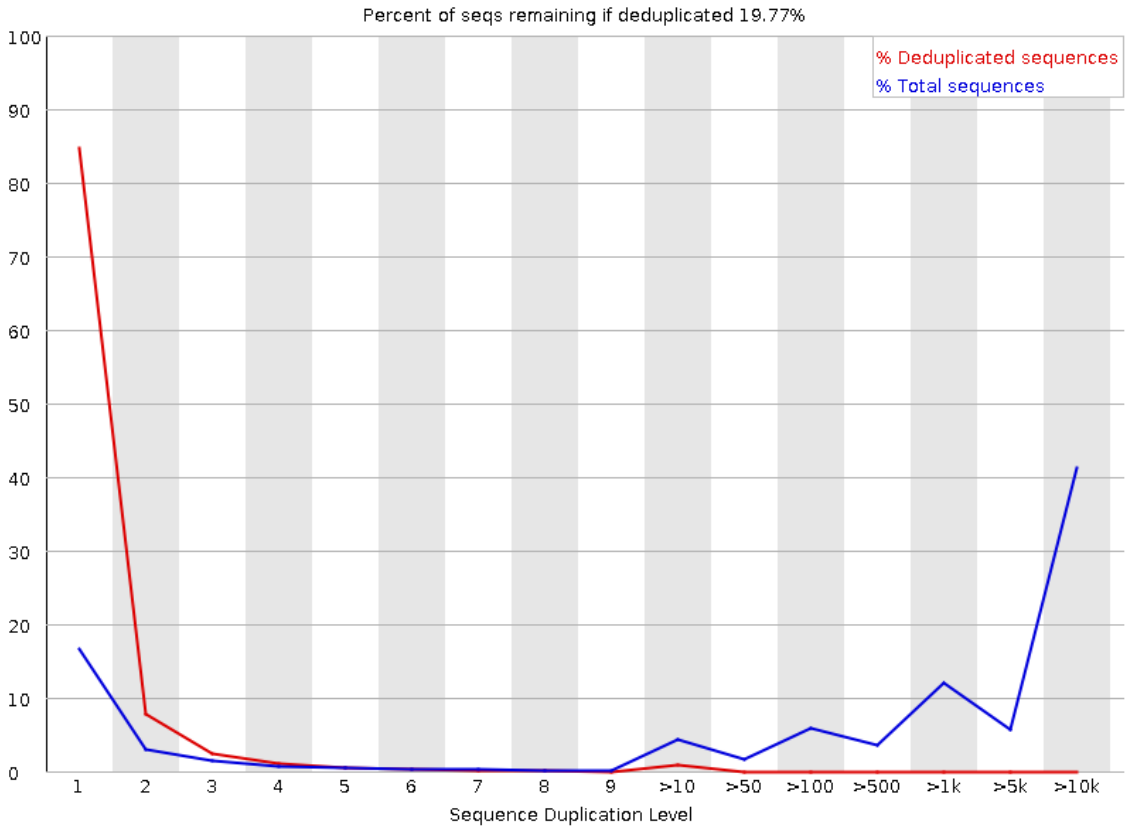
Per base N content



Sequence Length Distribution



Sequence Duplication Levels



Overrepresented sequences

Sequence	Count	Percentage	Possible Source
CCTGCGGCGGCCTCCACCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCG	978357	2.6823646730864197	No Hit
CTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCG	733976	2.0123444645393023	No Hit
GTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGC	375576	1.029717980715736	No Hit
CCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGG	322252	0.8835193908066739	No Hit
CTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCC	288144	0.7900053726419021	No Hit
GTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGG	276132	0.7570720318950028	No Hit
CCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGC	266920	0.7318154605529753	No Hit
GTCCAGAGTCGCCGCCGCCGCCGGCCCCCCCGAGTGTCCGGGCCCCCCGC	255959	0.7017636500362617	No Hit
CCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAA	245494	0.6730717243855542	No Hit
CTCCCCGGGGGCGGCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGA	212872	0.583631877412082	No Hit
GGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGC	202505	0.5552086386905449	No Hit
CTCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACCCGACG	198852	0.5451931963205463	No Hit
CTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAA	187880	0.5151112270668852	No Hit
GCTACTACCACCAAGATCTGCACCTGCGGCGGCTCCACCCGGGCCCGCGC	152153	0.4171583911640823	No Hit
ATTCCCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAG	151533	0.41545853508157504	No Hit
GTTCAACGTGACGGGCGAGAGGGCGGCCCCCTTTCCGGCCGCACCCCGTT	145544	0.3990384736652264	No Hit
CTAGGCTTCAAGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGC	141810	0.38880095332315834	No Hit
CCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGA	141275	0.38733414202615607	No Hit
CTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCC	139040	0.3812064350190532	No Hit
CTGCGGCGGCCTCCACCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCGC	137769	0.3777217300499133	No Hit
CCCAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGG	126283	0.34623052526978637	No Hit
CAAGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGG	125151	0.34312691706753107	No Hit
CCCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCG	124775	0.3420960366045912	No Hit
CTGGCTTCCTCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGAGGGCTGT	124089	0.34021522810039767	No Hit
GGGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAA	114516	0.3139689018458134	No Hit
CTTCAAGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCG	112823	0.309327198059225	No Hit
GGGGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGA	107207	0.29392979199573965	No Hit
ACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCG	106564	0.292166876735978	No Hit
GTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAGGGGAG	105878	0.2902860682317845	No Hit
CCCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGG	105405	0.288989242543033	No Hit
GGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGG	103448	0.28362372906969946	No Hit
GGGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGAC	100637	0.2759168009278801	No Hit
GCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACCCCGC	99139	0.27180972929627384	No Hit
CTCGCGTCCAGAGTCGCCGCCGCCGCCGGCCCCCCCGAGTGTCCGGGCCC	98715	0.2706472470721076	No Hit
CGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGC	95344	0.26140496504931393	No Hit
AGAGCCCCTCGGGCTCGCCCCCCCGCCTCACCGGGTCAGTGAAAAAACGA	94317	0.25858923569974135	No Hit
CTACCACCAAGATCTGCACCTGCGGCGGCTCCACCCGGGCCCGCGCCCTA	94181	0.2582163640429333	No Hit
GTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGC	93915	0.2574870709494705	No Hit
AGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGG	87168	0.23898879838708884	No Hit
GCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGG	85686	0.23492559400922464	No Hit
GTCGGATTCCCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGG	82042	0.224934826969456	No Hit
GCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCC	81046	0.2222040904240088	No Hit
CGGGTGGGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGG	80908	0.22182573536048297	No Hit
CGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCC	74618	0.2045804212331107	No Hit
CGGGTATCTGGCTTCCTCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGA	74044	0.20300668350511203	No Hit
CACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGC	72331	0.19831014565134591	No Hit
CTACTACCACCAAGATCTGCACCTGCGGCGGCTCCACCCGGGCCCGCGCC	71324	0.19554925036895104	No Hit
GGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCC	70033	0.19200971133263345	No Hit
CTCCTTGGTCCGTGTTTCAAGACGGGTCGGGTGGGTAGCCGACATCGCCG	69494	0.19053193322219564	No Hit
TCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGA	68639	0.18818777685035093	No Hit
ATCTGGCTTCCTCGGCCCCGGGATTCGGCGAAAGCTGCGGCCGGAGGGCT	67967	0.18634535219318174	No Hit
CCCTCCTTAGGCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATT	67368	0.184703071881211	No Hit

Sequence	Count	Percentage	Possible Source
CGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGC	62331	0.17089311206251873	No Hit
CGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGC	61913	0.16974708005850575	No Hit
CGGGTCGGGTGGGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTC	61613	0.16892456905084094	No Hit
CACCAAGATCTGCACCTGCGGCGGCTCCACCCGGGCCCGCGCCCTAGGCT	61444	0.16846122118318976	No Hit
CCCGGAGCCGGTCGCGGCGCACCGCCACGGTGGAAGTGCGCCCGGCGGCG	59651	0.16354534706071305	No Hit
CCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCGCAGCGGCCCTCCTACT	58565	0.1605678572129664	No Hit
GGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAG	57938	0.15884880920694697	No Hit
CTACGAATGGTTTAGCGCCAGGTTCCACACGAACGTGCGTTCAACGTGAC	56833	0.15581922699538156	No Hit
CTCCACCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCGCAGCGGCCCTC	56577	0.15511735093550758	No Hit
CACCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCGCAGCGGCCCTCCTA	56362	0.1545278847133478	No Hit
CCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACG	55830	0.15306929852642218	No Hit
TTCAAGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGC	54420	0.14920349679039754	No Hit
GTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAA	54301	0.1488772340906905	No Hit
CCCGTTTCCCAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACGC	54053	0.14819729165768758	No Hit
CGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGG	53975	0.14798343879569473	No Hit
CTCGCTATGTTGCCCAGGCTGGAGTGCAGTGGCTATTCACAGGCGCGATC	53766	0.14741042279368824	No Hit
GTCGGGTGGGTAGCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTC	53400	0.14640695936433717	No Hit
GGGGGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGGGCCCCGCGGGG	53388	0.1463740589240306	No Hit
TCCCCTGGTCCGCACCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGC	52907	0.145055299608408	No Hit
CCGTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGA	52444	0.1437858909532453	No Hit
CTCCGTTTCCGACCTGGGCCGGTTCACCCCTCCTTAGGCAACCTGGTGGT	51841	0.14213264382783902	No Hit
CCAGAGTCGCCGCCGCCGCCGGCCCCCCCGAGTGTCCGGGCCCCCCGCCC	51319	0.14070147467450225	No Hit
CGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGACGCCGCGG	51094	0.14008459141875362	No Hit
CTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACCGCGGCCCGG	50980	0.139772037235841	No Hit
CTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAACC	50477	0.138392960446323	No Hit
CCCGTCGGCATGTATTAGCTCTAGAATTACCACAGTTATCCAAGTAGGAG	50046	0.13721128629864454	No Hit
CTCGTTTGAATATTTGCTACTACCACCAAGATCTGCACCTGCGGCGGCTC	48231	0.1322350947022724	No Hit
GCCAGGTTCCACACGAACGTGCGTTCAACGTGACGGGCGAGAGGGCGGCC	47544	0.13035154449471997	No Hit
GGCAGACGTTCGAATGGGTCGTCGCCGCCACGGGGGGCGTGCGATCGGCC	46765	0.12821575757815035	No Hit
CCTTGGTCCGTGTTTCAAGACGGGTCGGGTGGGTAGCCGACATCGCCGCC	45886	0.12580580032569244	No Hit
GGCCTCCACCCGGGCCCGCGCCCTAGGCTTCAAGGCTCACCGCAGCGGCC	44482	0.1219564488098211	No Hit
CCCCGGGCCCGACGGCGCGACCCGCCCGGGGCGCACTGGGGACAGTCCGC	43915	0.12040190300533458	No Hit
GTGCGCTCGGCTTCGTCGGGAGACGCGTGACCGACGGTCCCCCCGGGACC	43400	0.11898992577551	No Hit
CACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGA	43121	0.1182249905383817	No Hit
CCGGGGGCGGCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGAAGGG	42667	0.11698025721344894	No Hit
CCAGTTCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGG	42632	0.11688429759588806	No Hit
CCAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGG	42070	0.11534346030819596	No Hit
GCCGACATCGCCGCCGACCCCGTGCGCTCGGCTTCGTCGGGAGACGCGTG	42036	0.11525024239399395	No Hit
CCCCGTTTCCCAAGACGAACGGCTCTCCGCACCGGACCCCGGTCCCGACG	40635	0.11140911598819926	No Hit
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ACCGCAGCGGCCCTCCTACTCGTCGCGGCGTAGCGTCCGCGGGGCCCGAC	40390	0.110737398665273	No Hit
CCTCCTTAGGCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATATTG	39732	0.10893335785512819	No Hit
TCTAAGTCGGCTGCTAGGCGCCGGCCGAGGCGAGGCGCCGCGCGGAAAAC	39638	0.1086756377393932	No Hit
CTCTCCGCACCGGACCCCGGTCCCGACGCCCGGCGGGGGGAGACCCCGCG	39578	0.10851113553786024	No Hit
CCCCGGGGGCGGCCGCGACGCCCGCCGCAGCTGGGGCGATCCACGGGAAG	38832	0.10646582483213372	No Hit
GGCGACGACGCGGGGGACGACGGGGCCCCGCGGGGAAGAGGGGAGGGCGG	38703	0.10611214509883785	No Hit
CCCCTCCTTAGGCAACCTGGTGGTCCCCCGCTCCCGGGAGGTCACCATAT	38663	0.10600247696448255	No Hit
CCCGGGGGGCGGACCCGGCGGGGGAACACCGACGCGGAGGTTCCCCCCAC	37535	0.10290983557566284	No Hit
GGCCCGGCTCGCGTCCAGAGTCGCCGCCGCCGGCCCCCCCGAGTGTC	37510	0.10284129299169079	No Hit
GGAAGAAGGAGGGGGGGAAGAGAGGTGGCGACGACGCGGGGGACGACGGG	37310	0.10229295231991423	No Hit
CCGCGGGGCCCGACGCCGCGGGGGCGAAACCCGGCGCGCGGAGGGGAGGC	37308	0.10228746891319646	No Hit
CCCGAGTGTCCGGGCCCCCCGCCCCACCGGGGGCCCGCTGGTTCCTCCCG	37229	0.10207087434784473	No Hit

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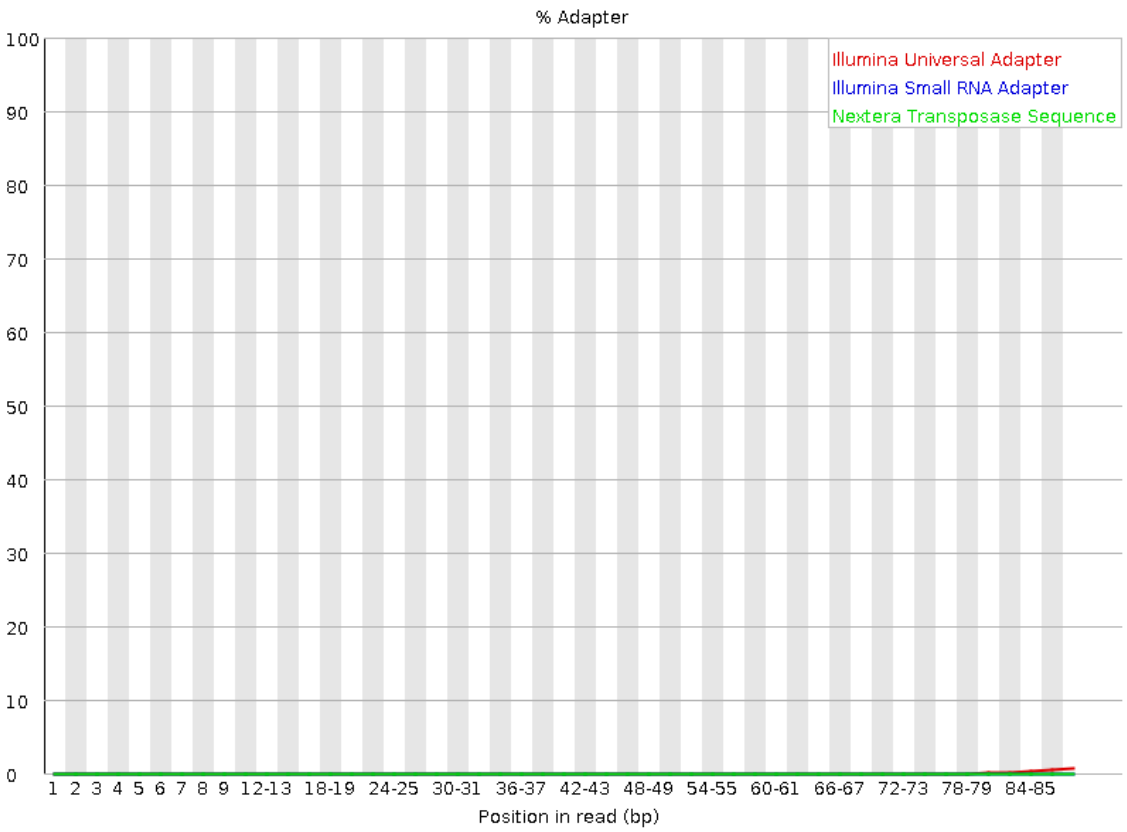
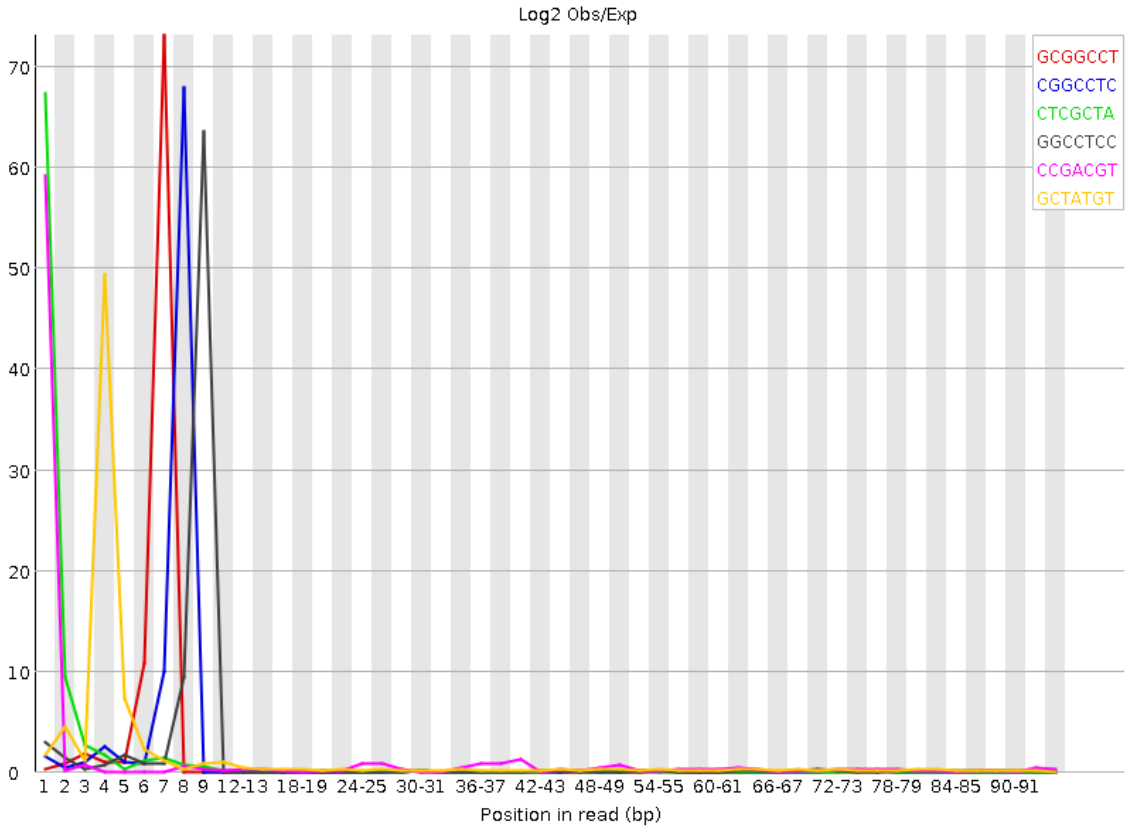
CCCTAGGCTTCAAGGCTCACCGCAGCGGCCCTCCTACTCGTCGCGGCGTA	37132	0.10180492912203311	No Hit

Adapter Content



Kmer Content



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CGGCCTC	143540	0.0	67.82219	8
CTCGCTA	7890	0.0	67.26186	1
GGCCTCC	153070	0.0	63.533405	9
CCGACGT	6745	0.0	59.218464	1
GCTATGT	10820	0.0	49.380222	4
CTATGTT	10805	0.0	49.16838	5
ATGTTGC	11035	0.0	48.441692	7
CCTGCGG	207950	0.0	47.359226	1
GTCGGAT	17245	0.0	45.86183	1
TCGGATT	18020	0.0	44.290833	2
TGCGGCG	225640	0.0	43.73714	3
TGTTGCC	12280	0.0	43.492107	8
GTTGCCC	12675	0.0	41.9897	9
TGTTACG	3415	0.0	41.969387	3
TCGGGCT	24115	0.0	41.364376	9
GTTCGCG	1135	0.0	40.892044	1
TATGTTG	13225	0.0	40.31279	6
TCGCTAT	13685	0.0	39.86228	2
GTTACGA	3645	0.0	39.439877	4

Produced by FastQC (version 0.11.2)