

FastQC Report

Summary

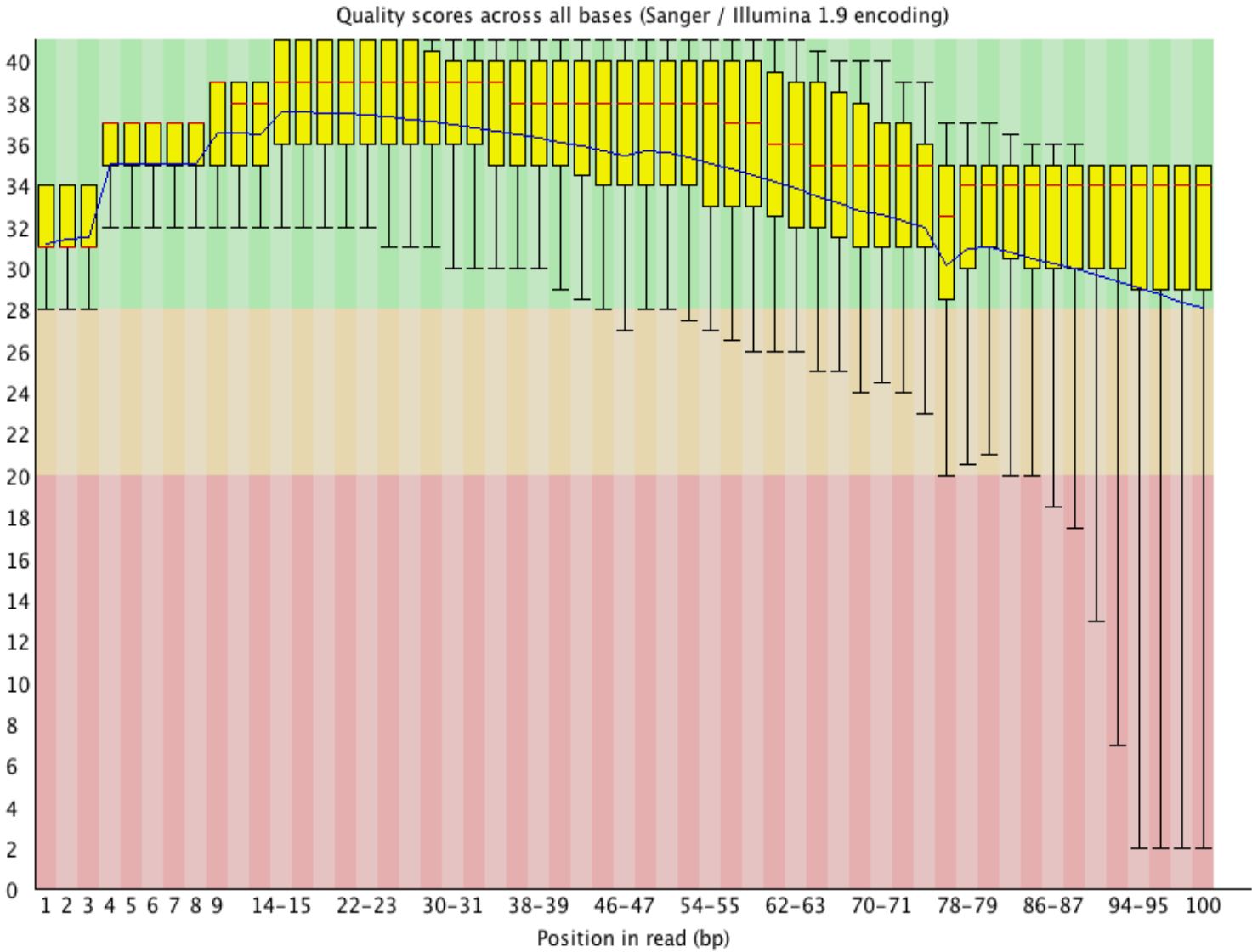
Mon 2 Mar 2015
1A_ATCACG_L001_R1_001.fastq

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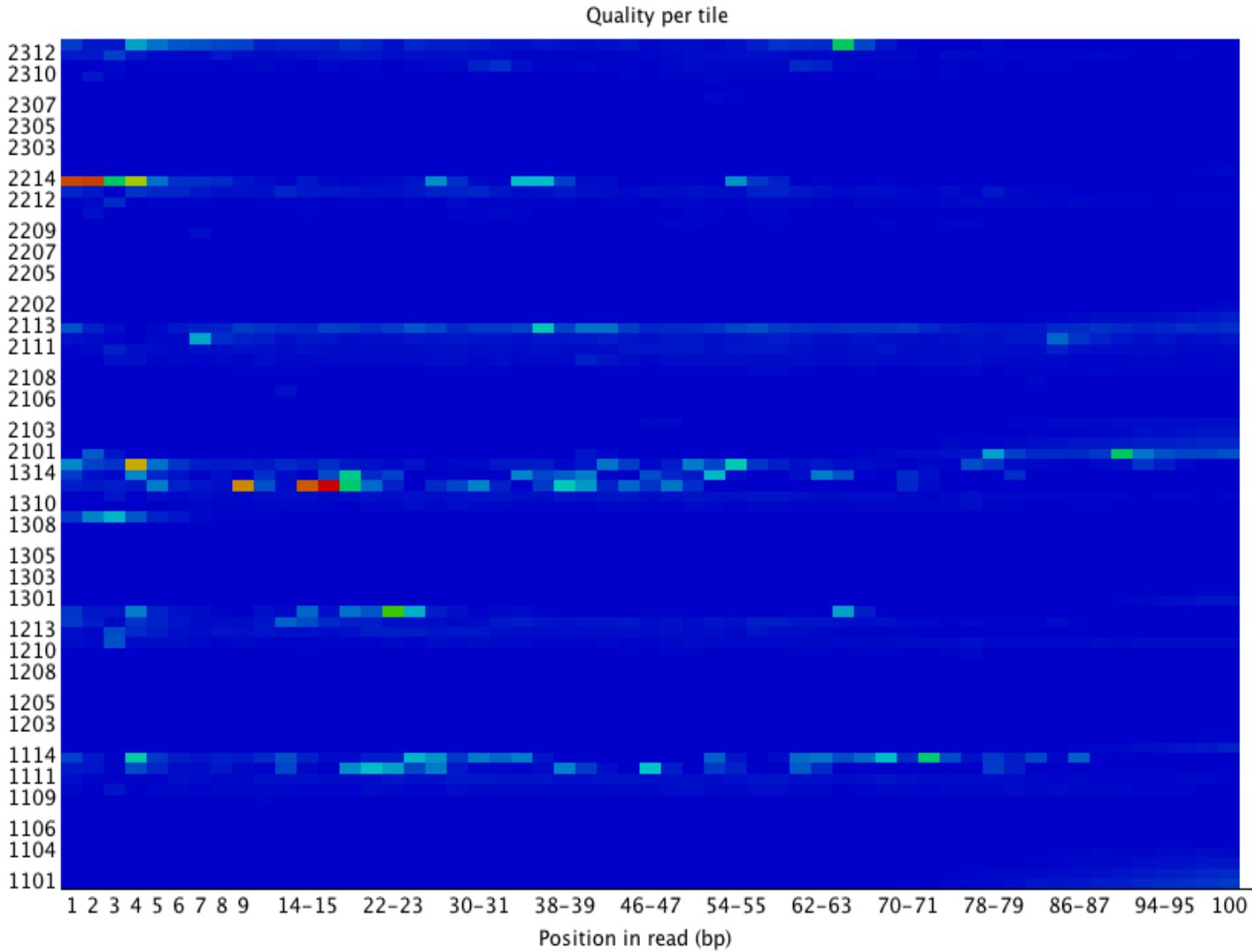
Basic Statistics

Measure	Value
Filename	1A_ATCACG_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	37098362
Sequences flagged as poor quality	0
Sequence length	100
%GC	41

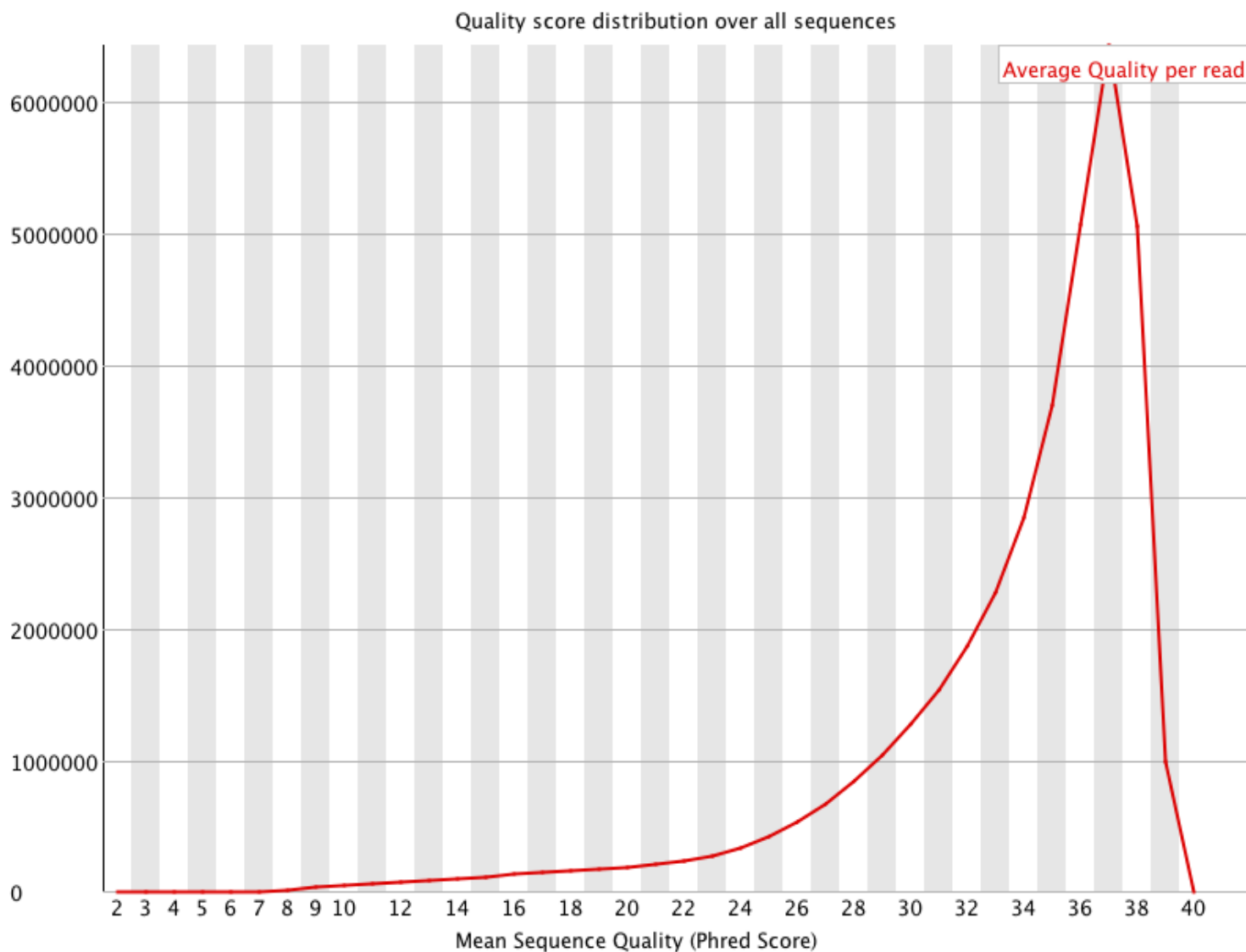
Per base sequence quality



 Per tile sequence quality

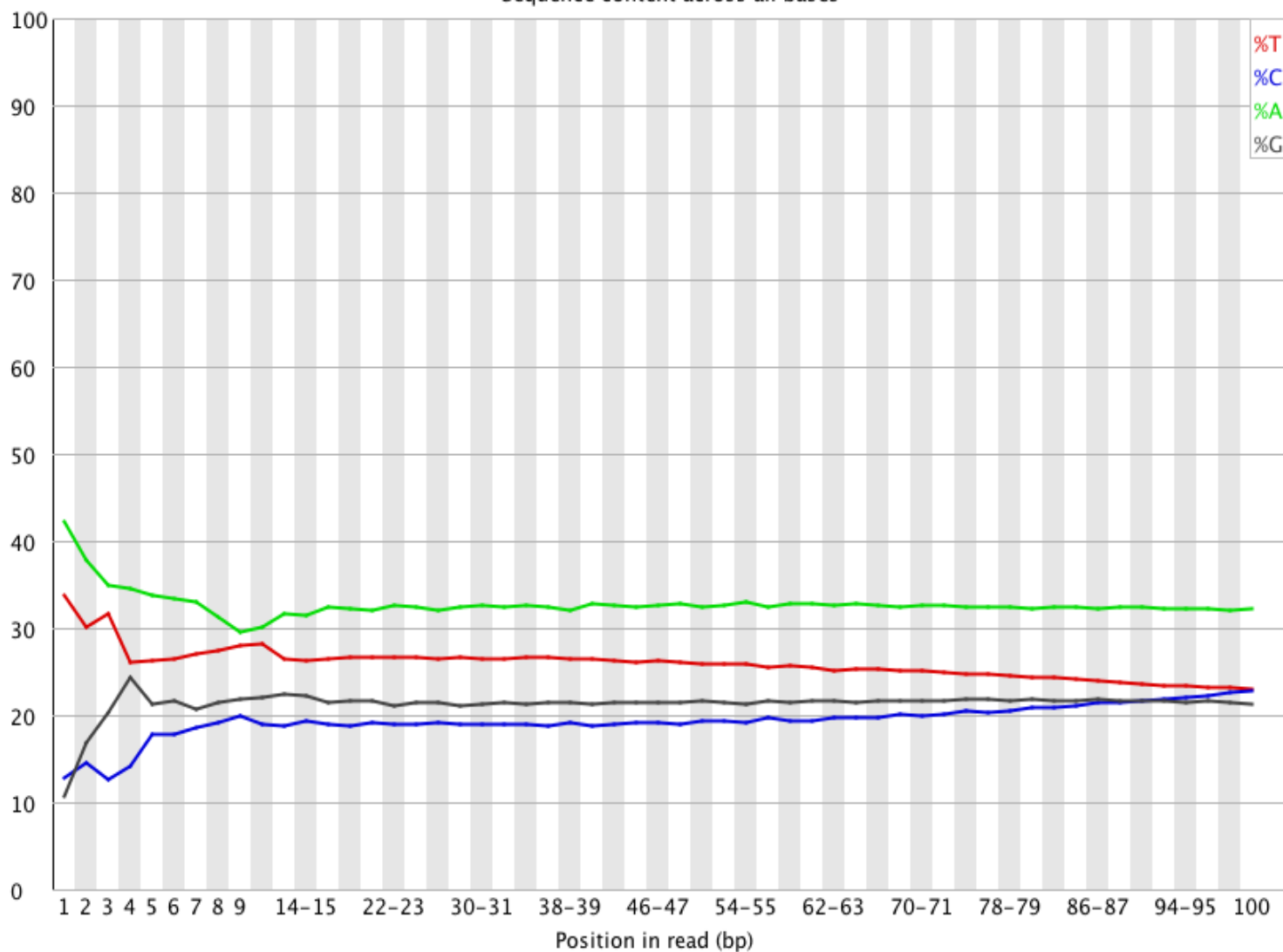


 Per sequence quality scores

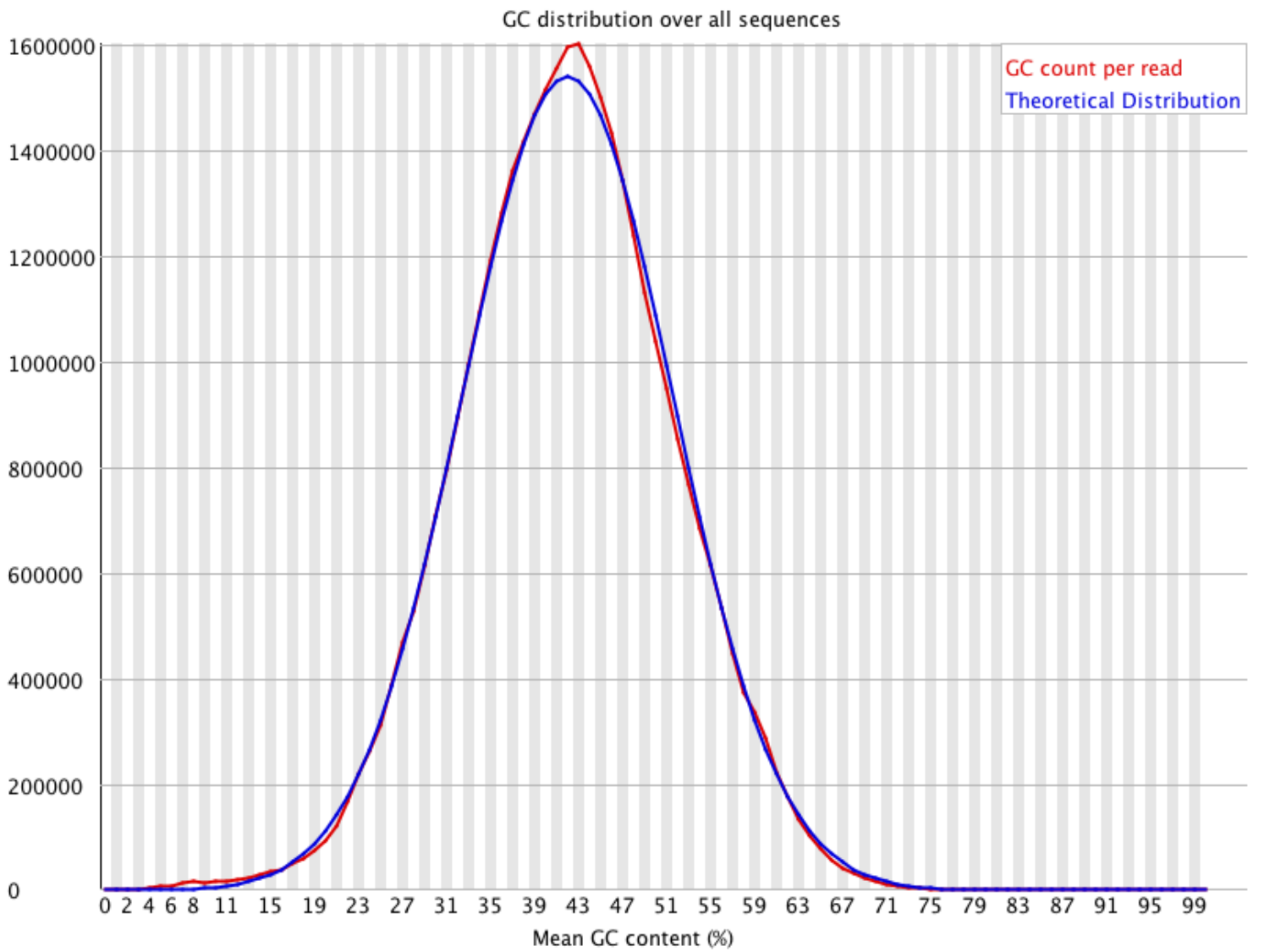


✖ Per base sequence content

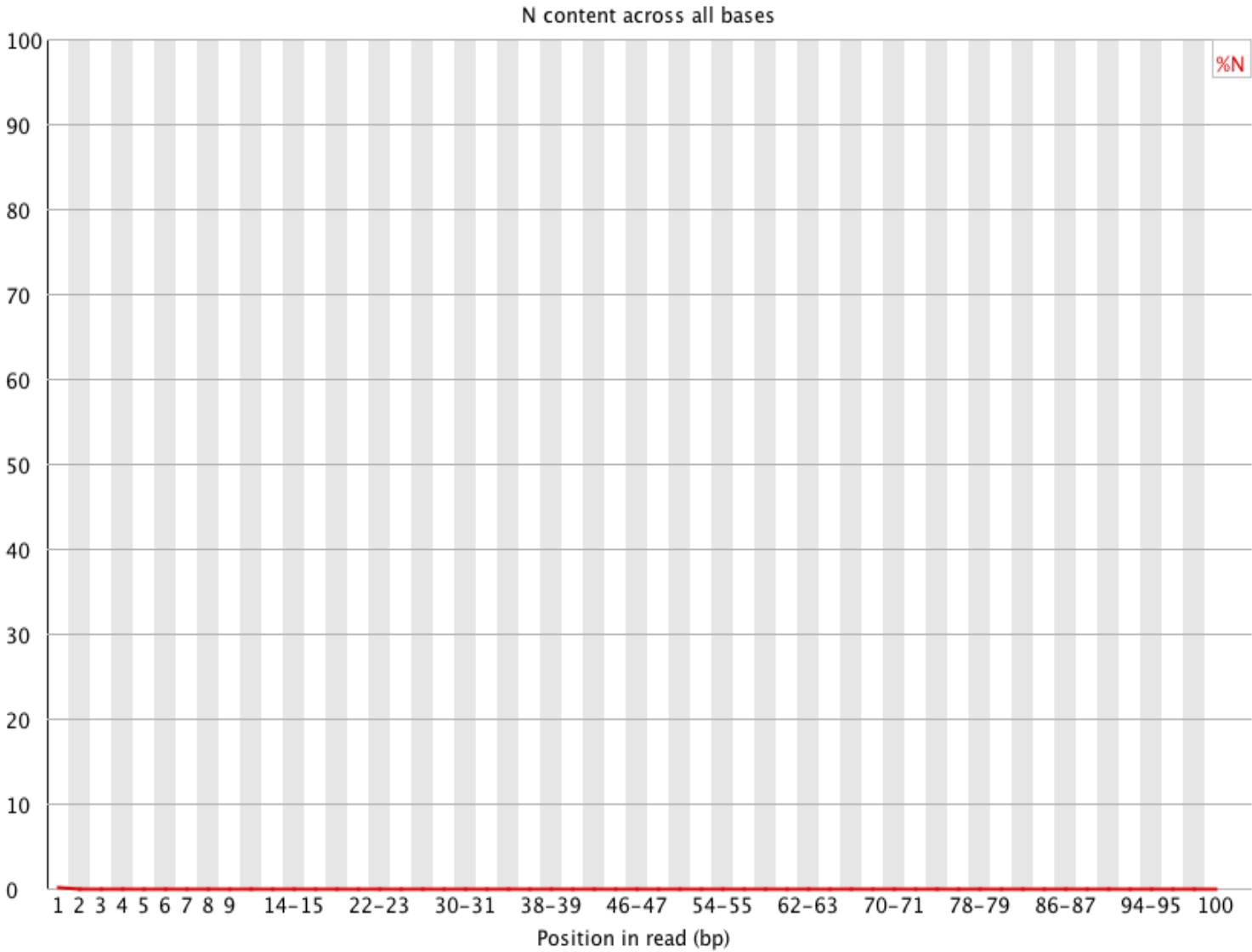
Sequence content across all bases



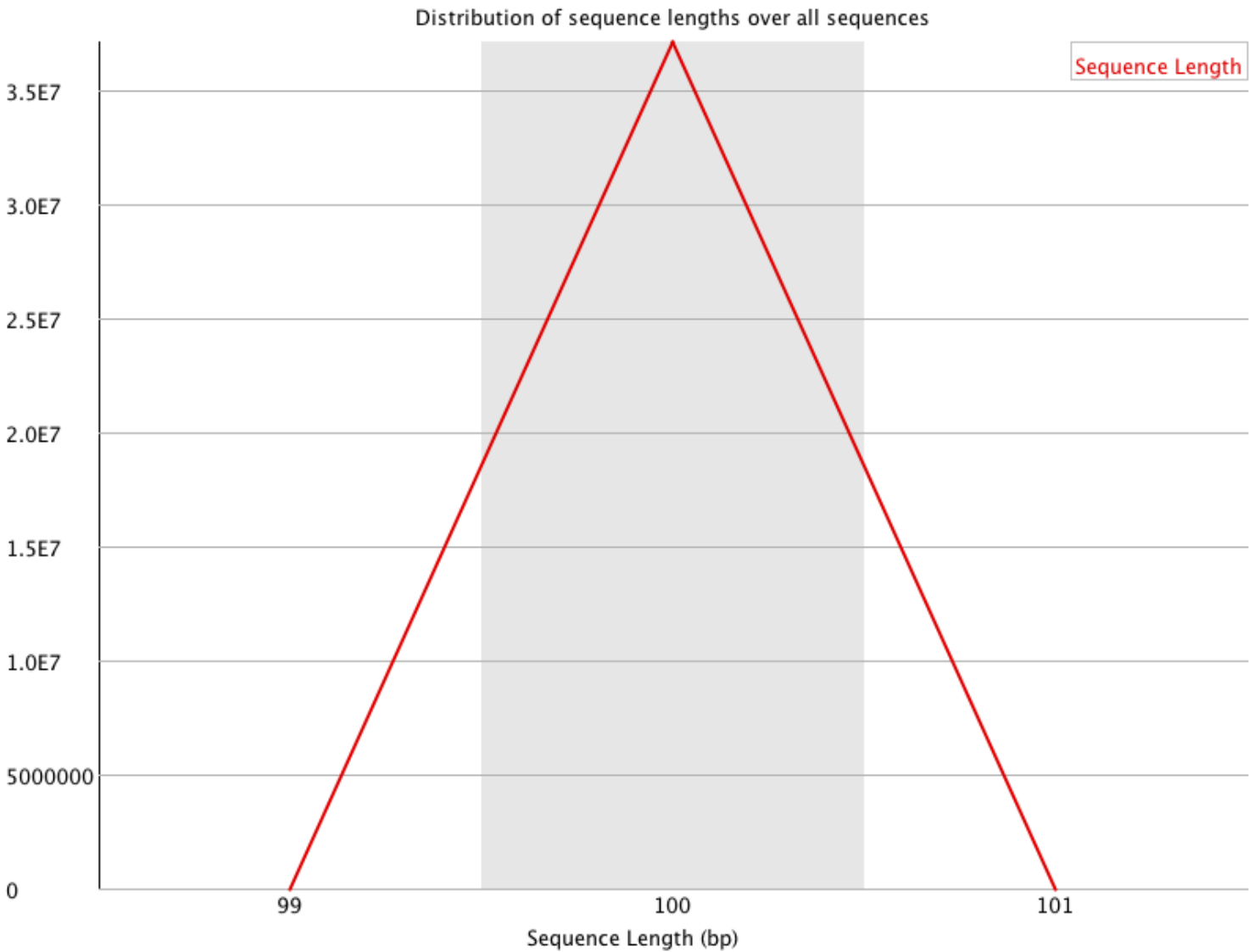
Per sequence GC content



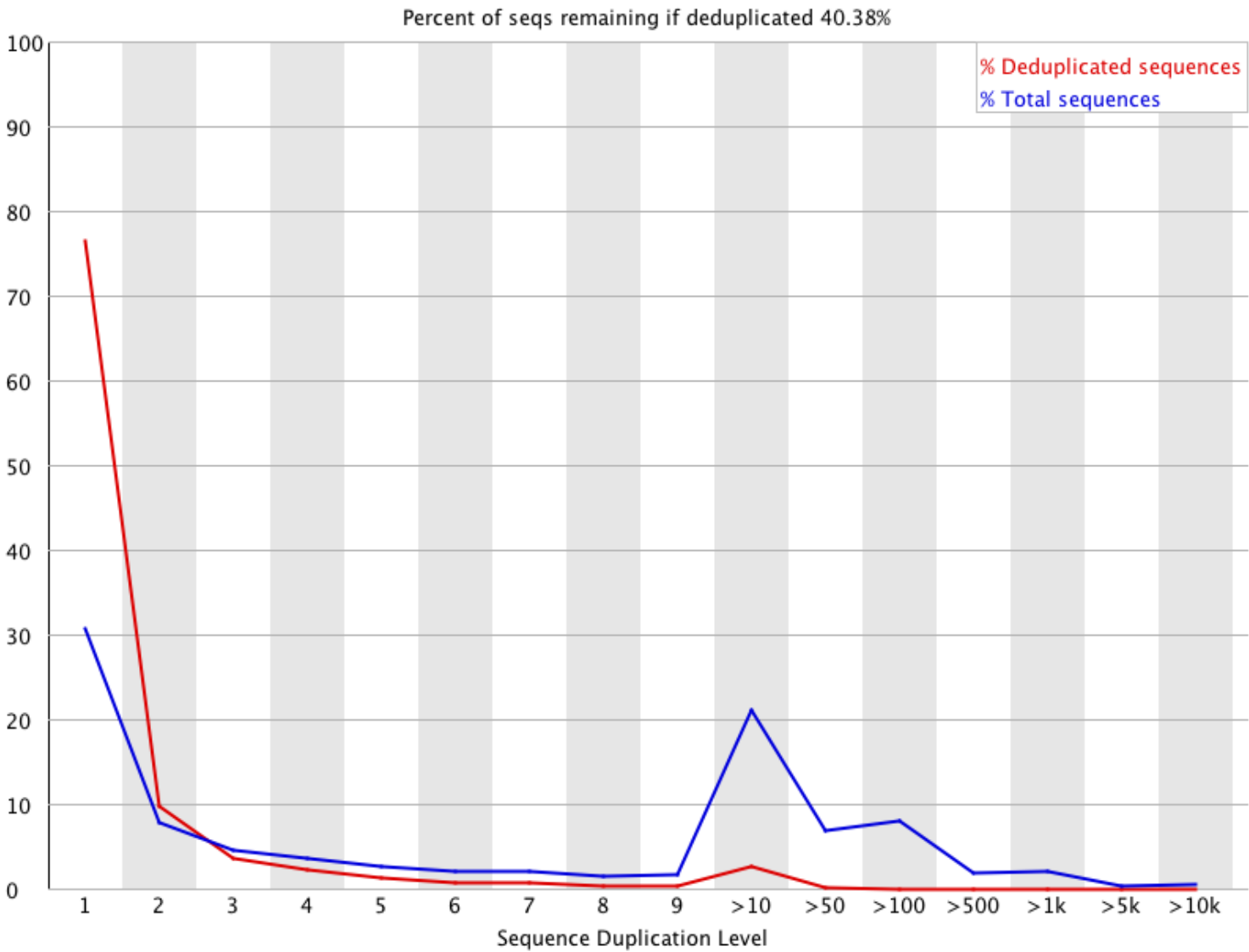
 Per base N content



 Sequence Length Distribution



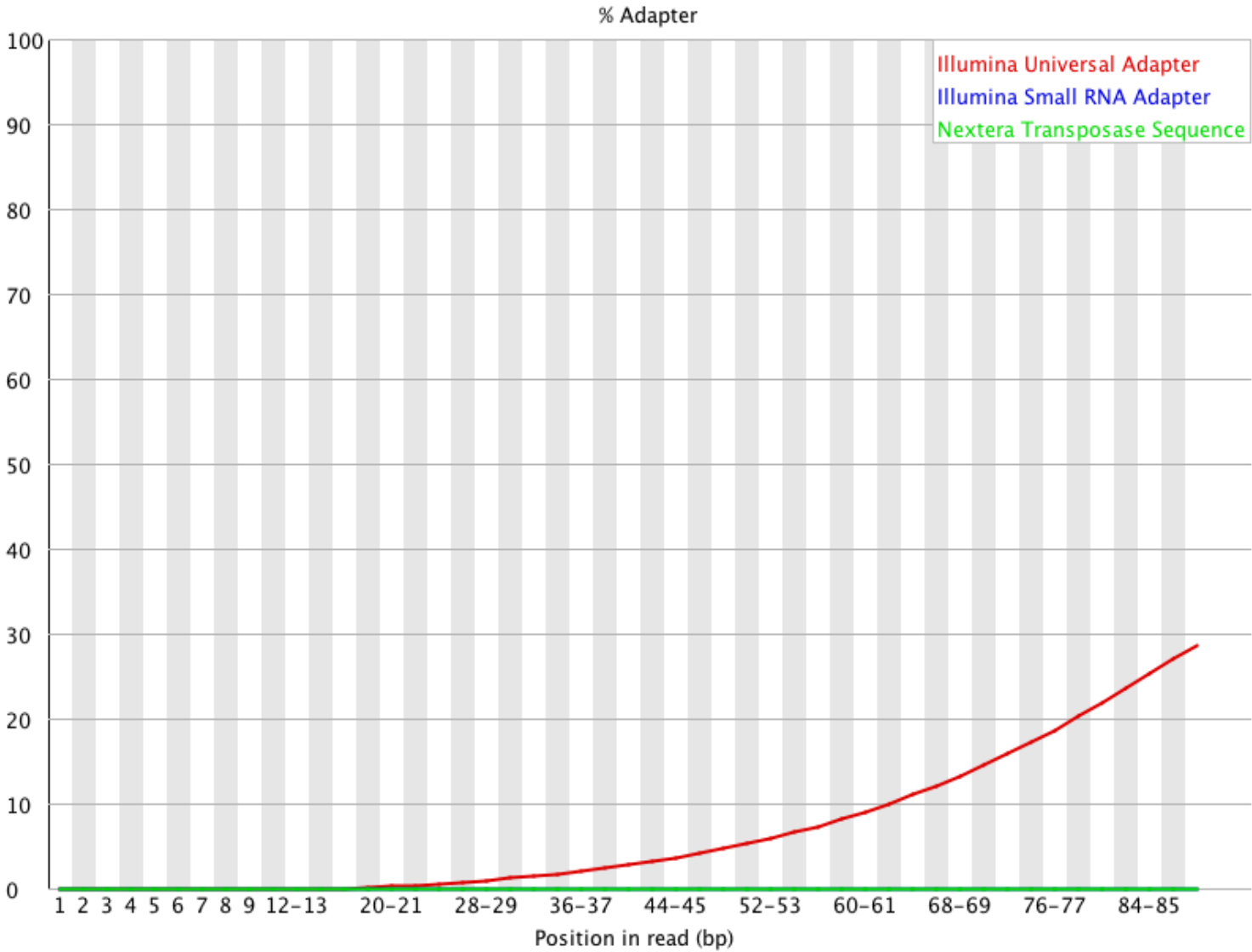
 Sequence Duplication Levels



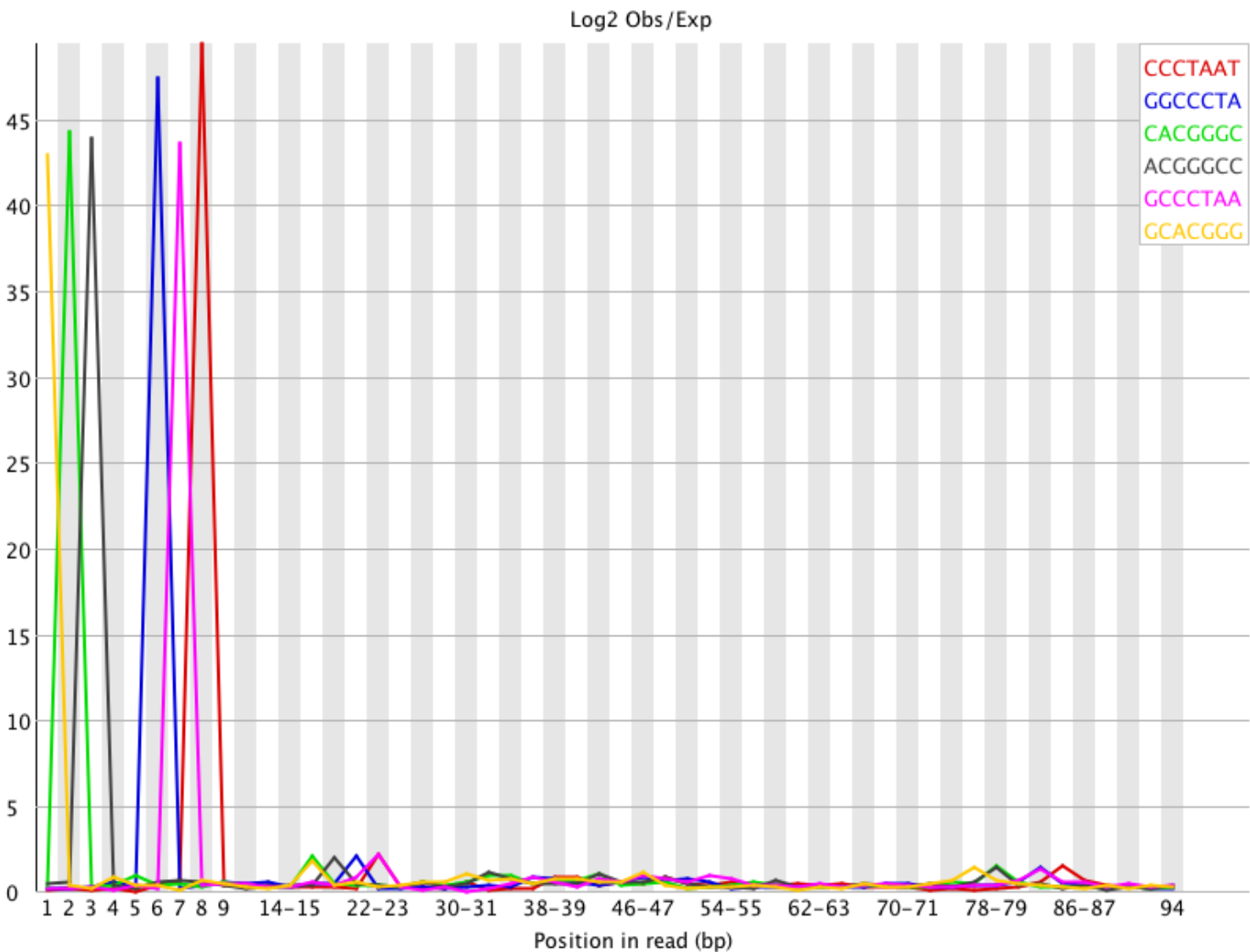
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCACGGGCCCTAATTGCCGTACGGAGTCGCGGATCCTGCTTCGGGATCTT	42834	0.1154606233019129	No Hit

✖ Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCCTAAT	10760	0.0	49.404648	8
GGCCCTA	11240	0.0	47.420288	6
CACGGGC	12090	0.0	44.353592	2
ACGGGCC	12095	0.0	43.912685	3
GCCCTAA	12195	0.0	43.668224	7
GCACGGG	12370	0.0	42.96169	1
CACACCC	11460	0.0	35.766506	1
CCTAATT	15920	0.0	33.59825	9
TCGGGCG	13180	0.0	31.524942	9
ACCGGTC	13470	0.0	30.91602	4
CGGGCCC	17400	0.0	30.659428	4
CACCCGT	13790	0.0	30.300858	3
GGGCCCT	17750	0.0	30.10784	5

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTCGGGC	14790	0.0	28.538137	8
ACACCCG	14915	0.0	27.69715	2
CTAGCGG	9355	0.0	26.326632	70–71
CCGTCGG	16670	0.0	25.545242	6
CCGGTTC	12180	0.0	25.196218	24–25
CCCGGCA	12300	0.0	25.046059	42–43
ATCCGGT	12440	0.0	24.59405	22–23

Produced by [FastQC](#) (version 0.11.2)

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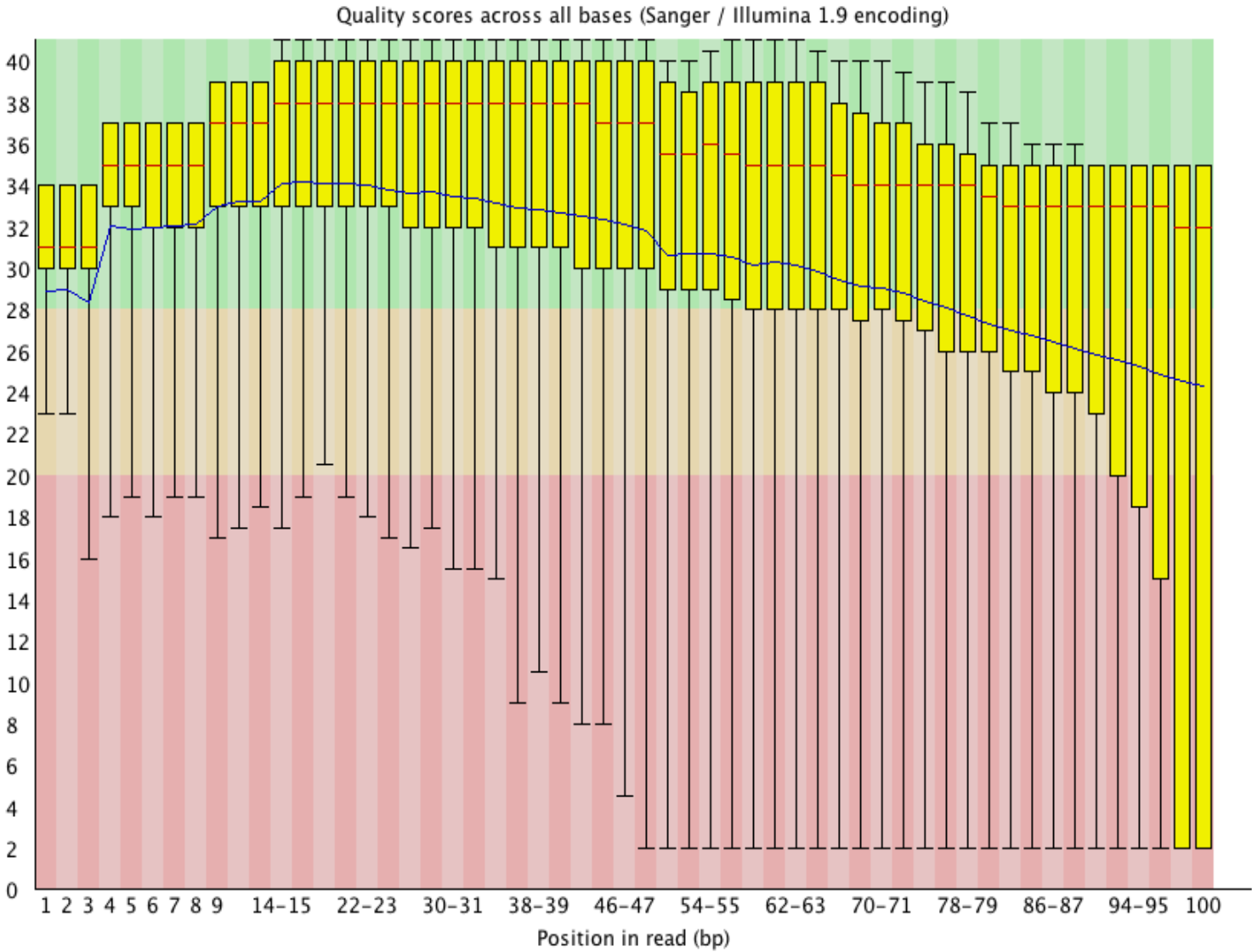
Fri 20 Mar 2015
1A_ATCACG_L001_R2_001.fastq

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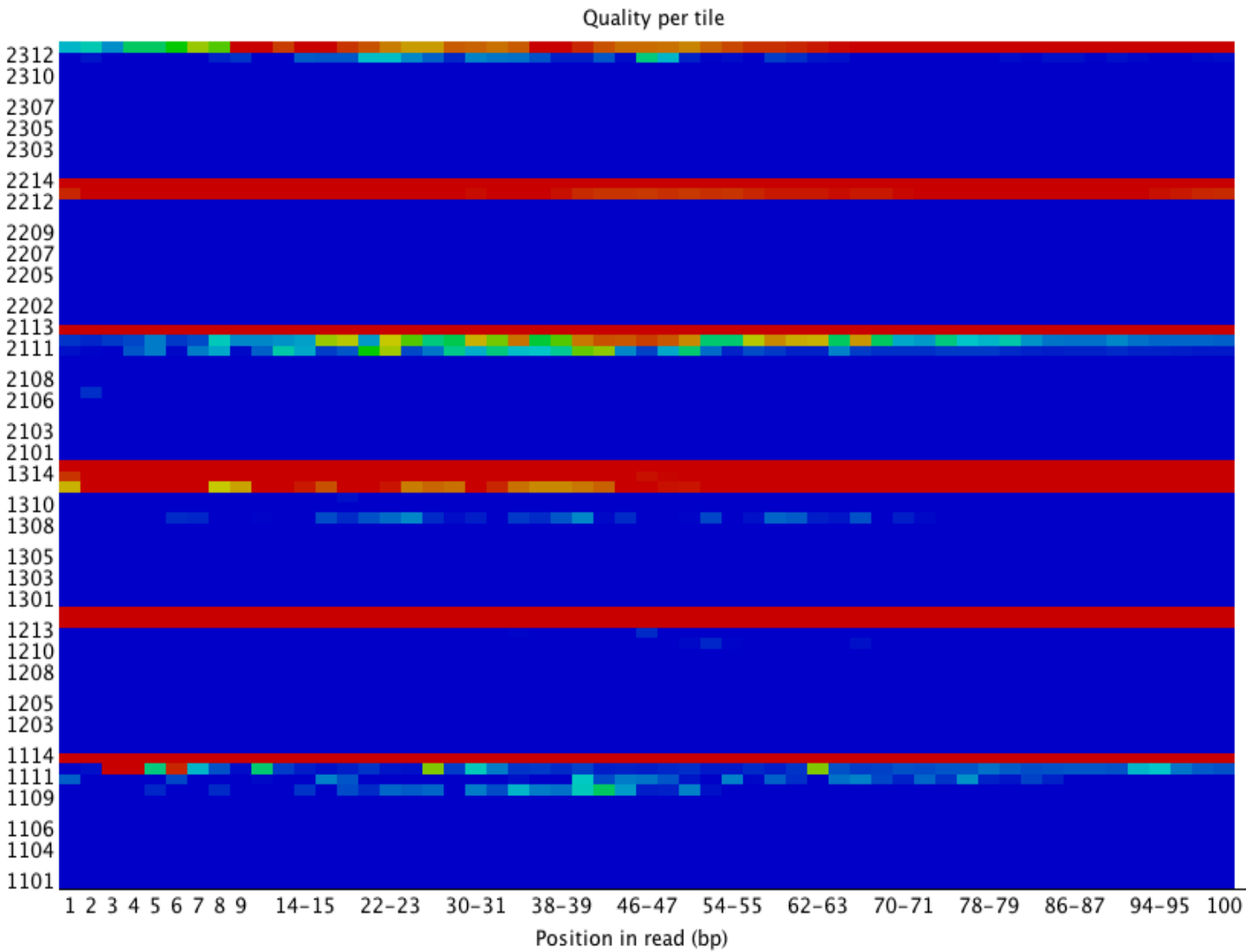
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Measure	Value
Filename	1A_ATCACG_L001_R2_001.fastq
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Total Sequences	37098362
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Sequence length	100
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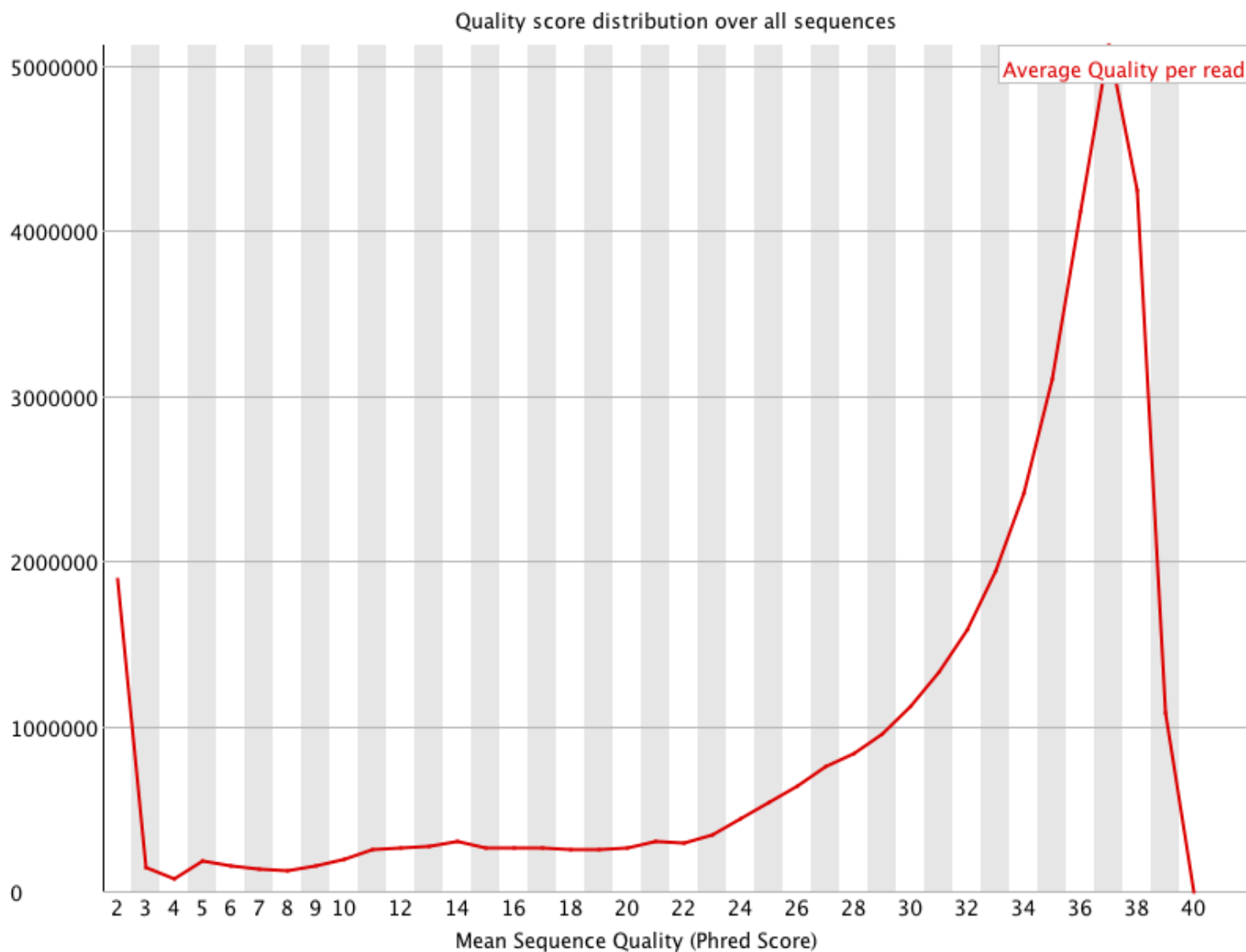
Per base sequence quality



✖ Per tile sequence quality

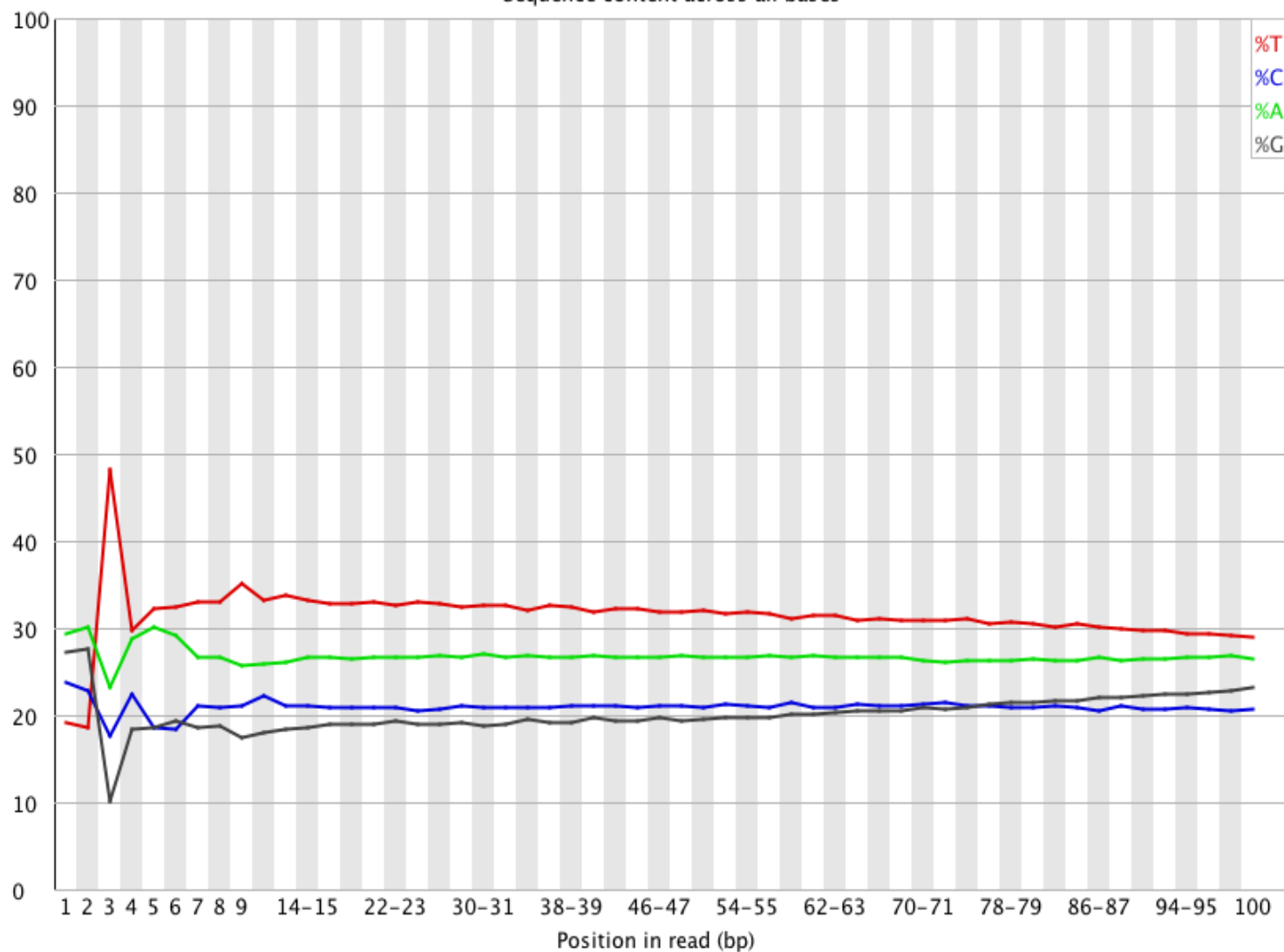


 Per sequence quality scores

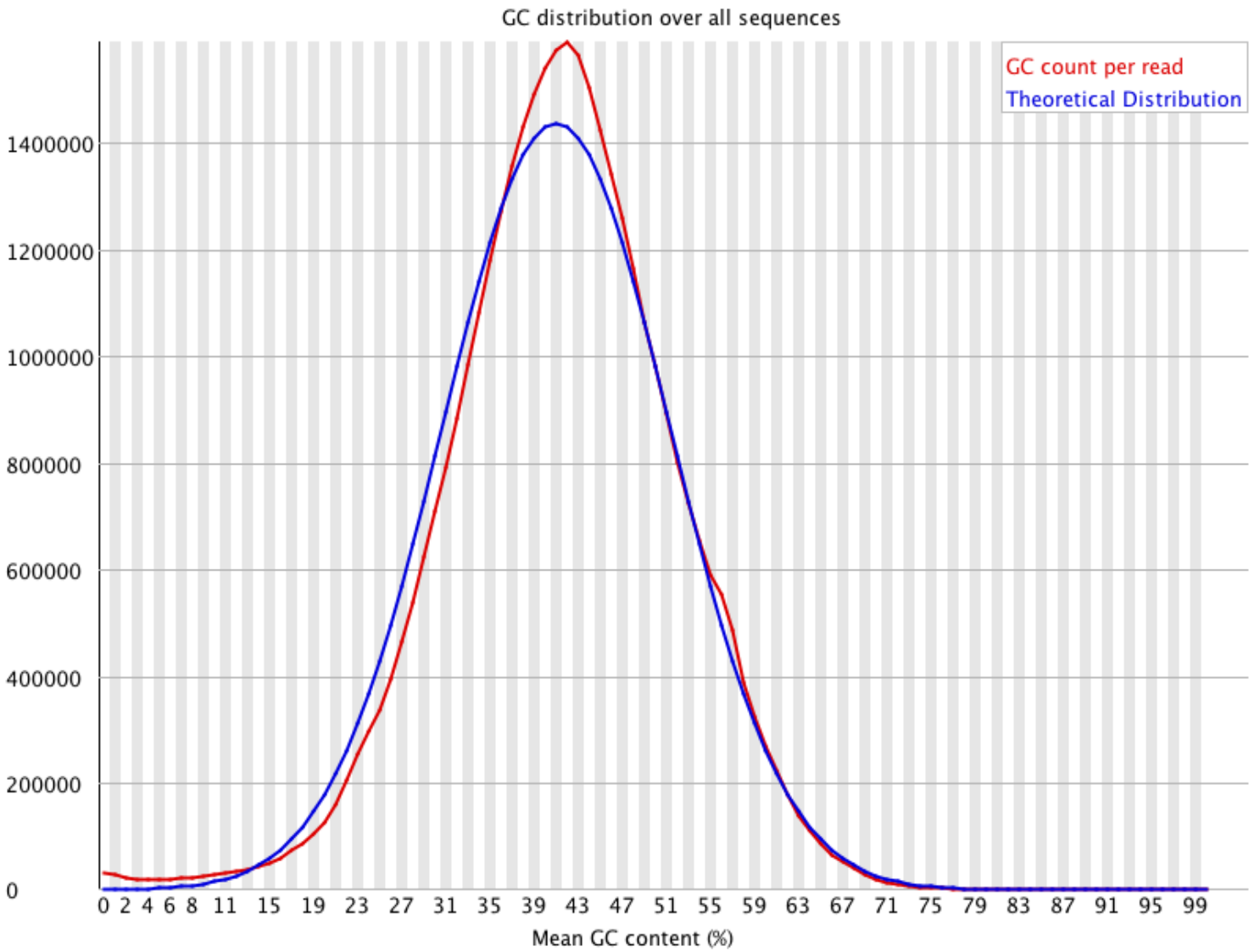


✖ Per base sequence content

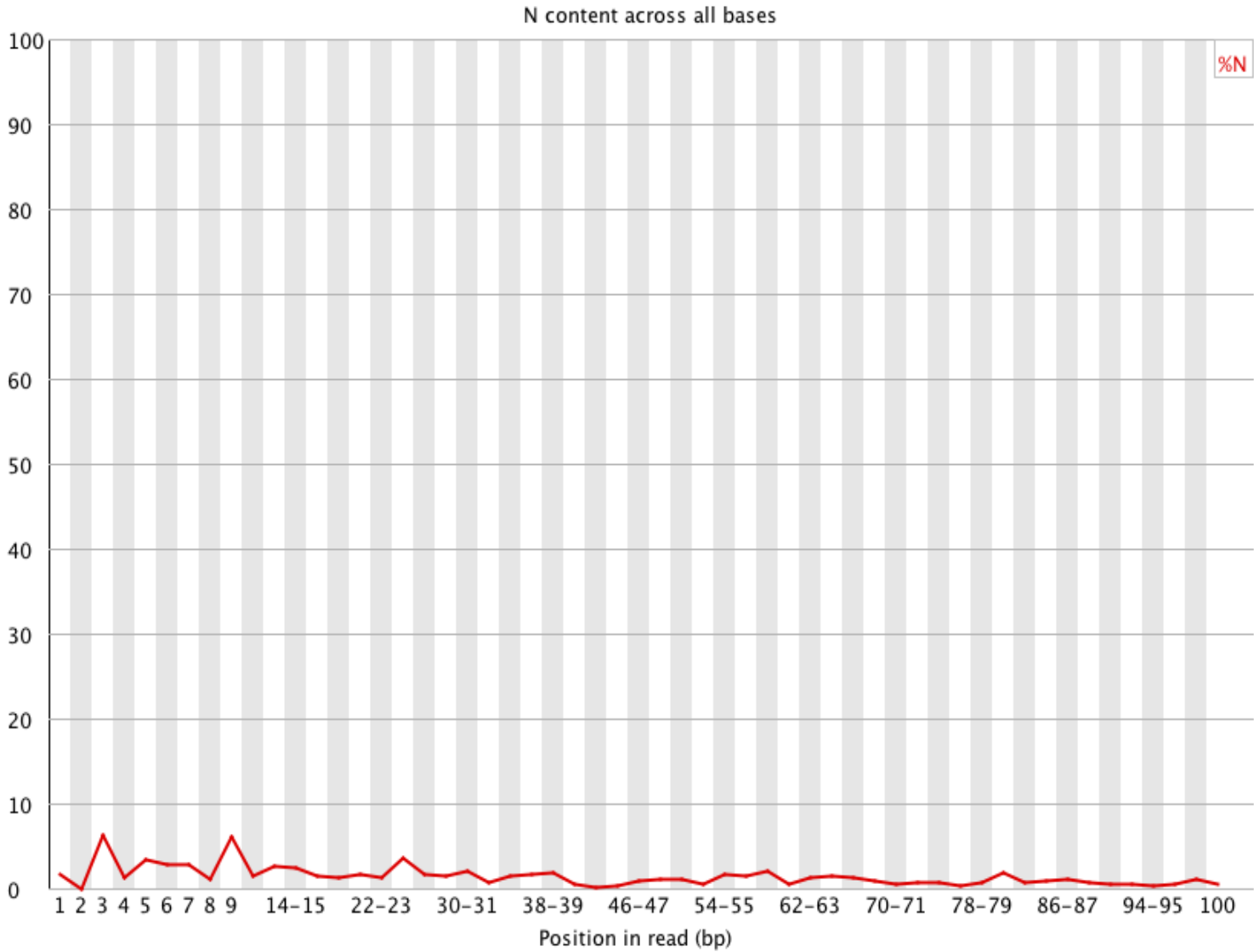
Sequence content across all bases



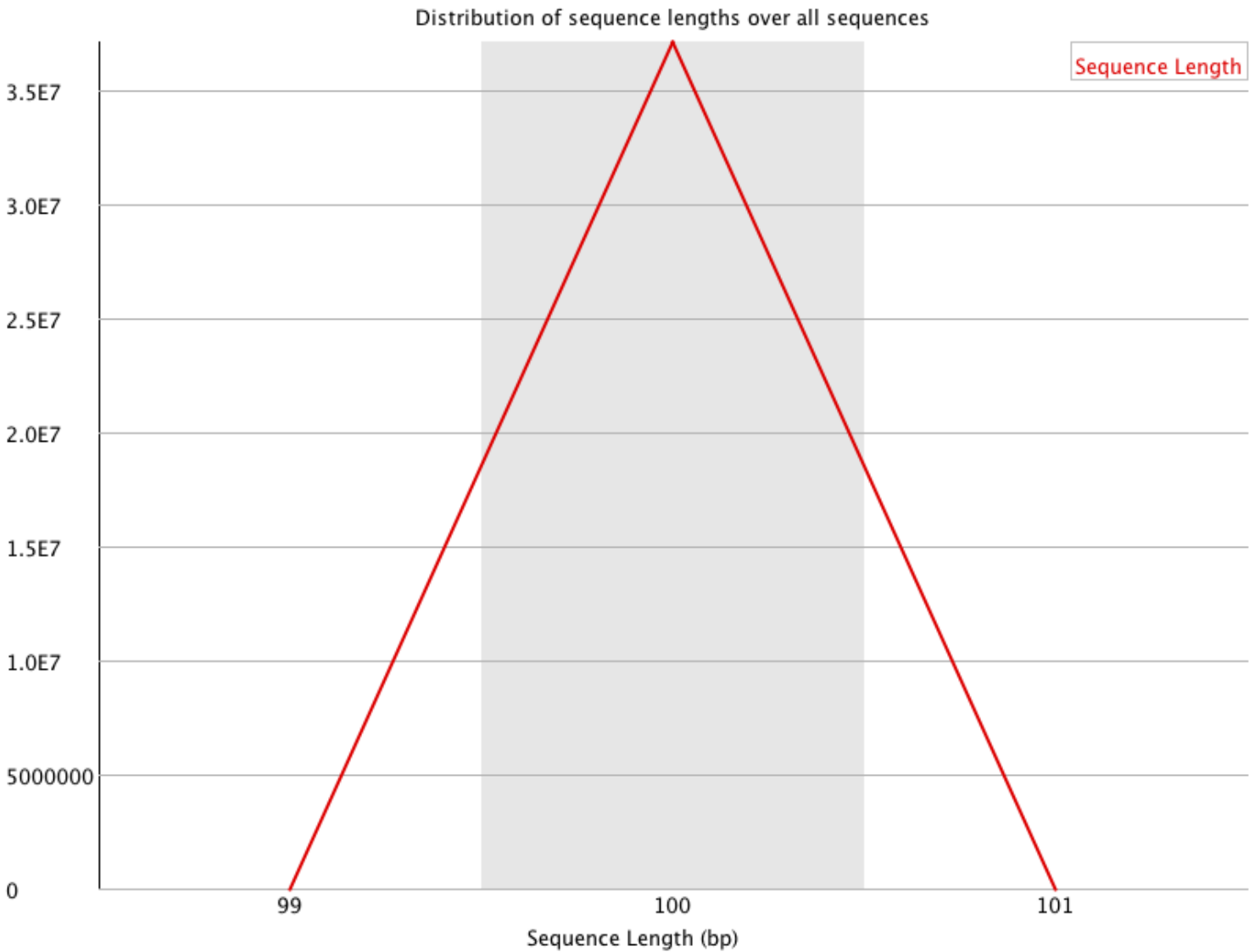
Per sequence GC content



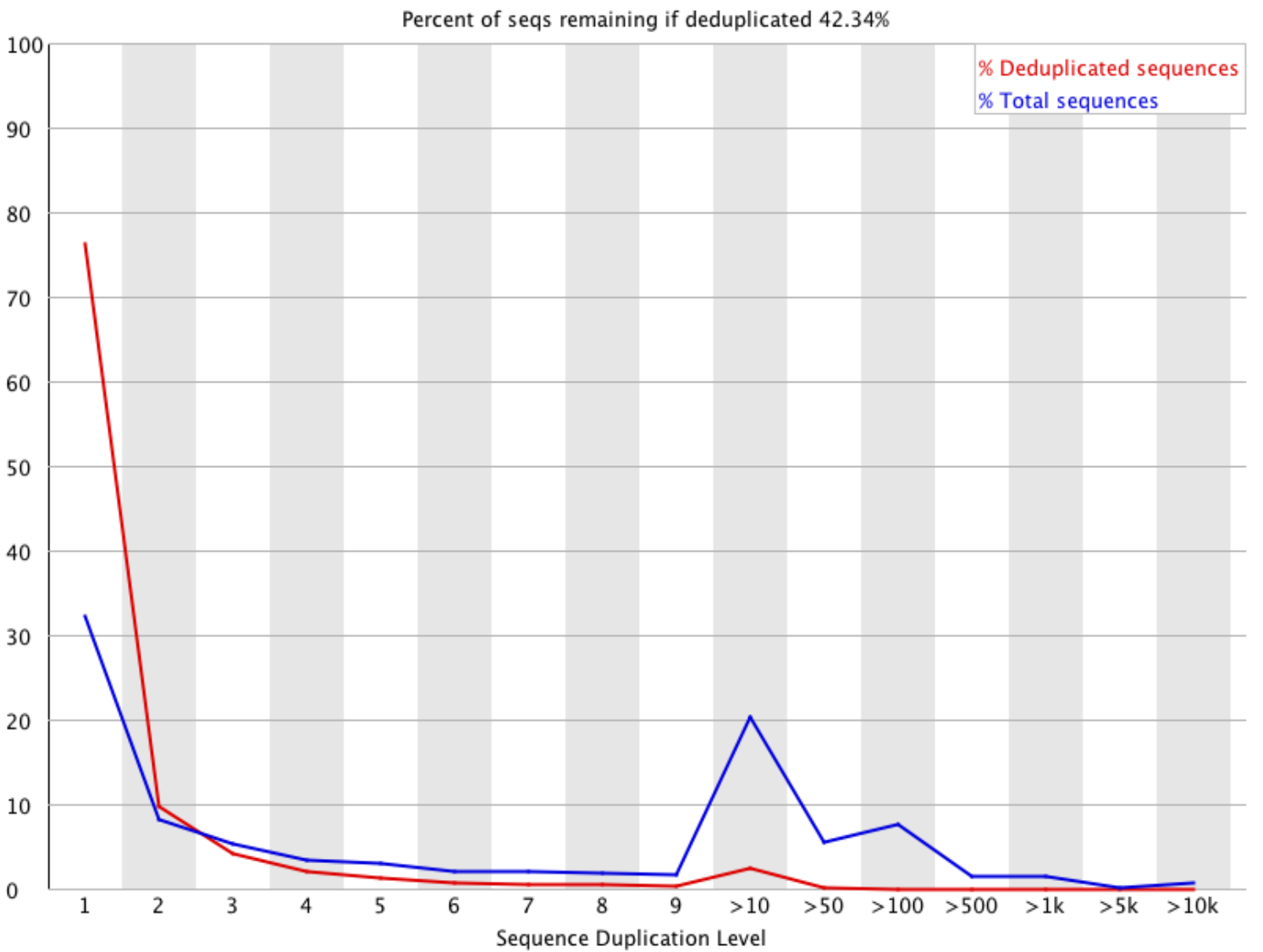
 Per base N content



 Sequence Length Distribution



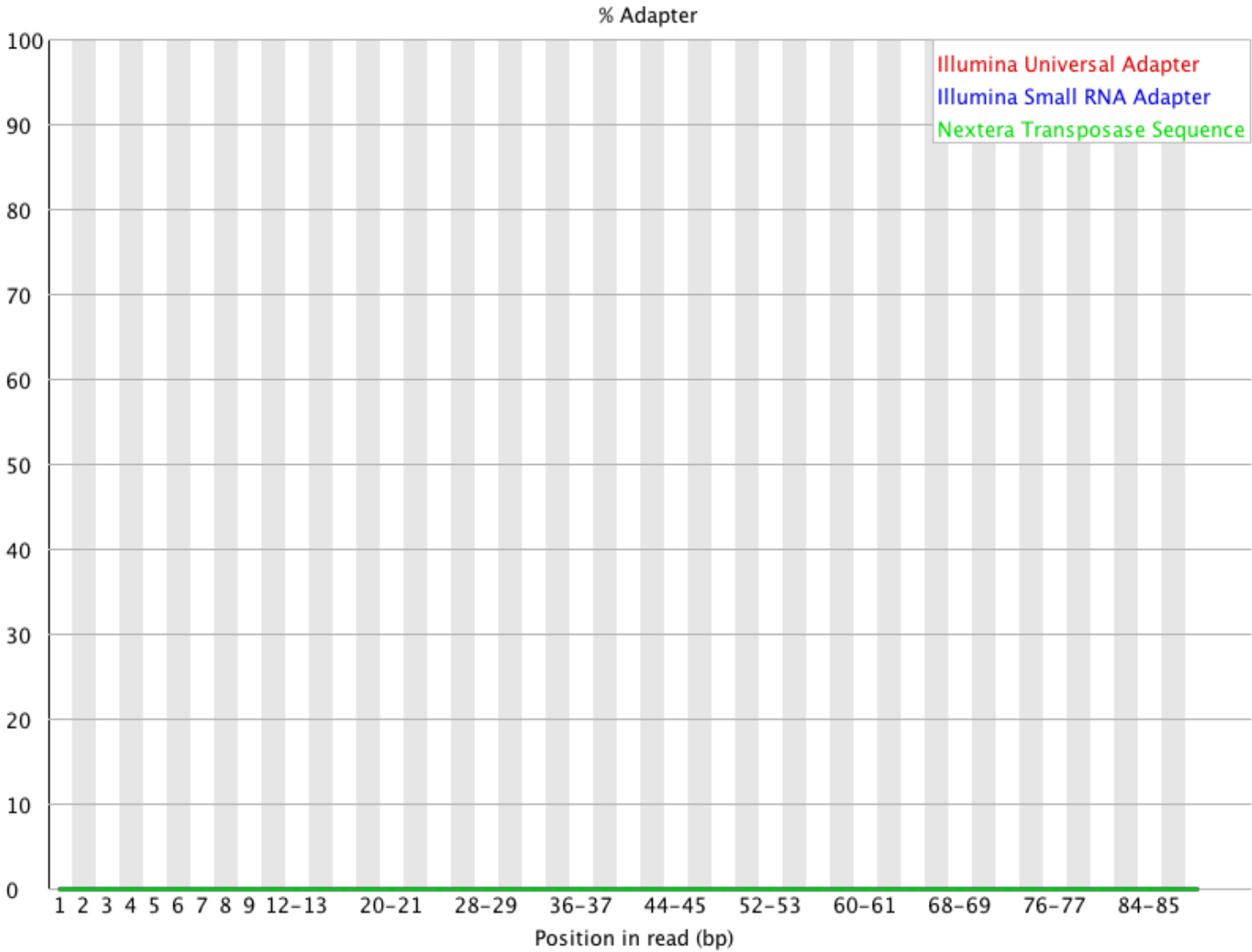
 Sequence Duplication Levels



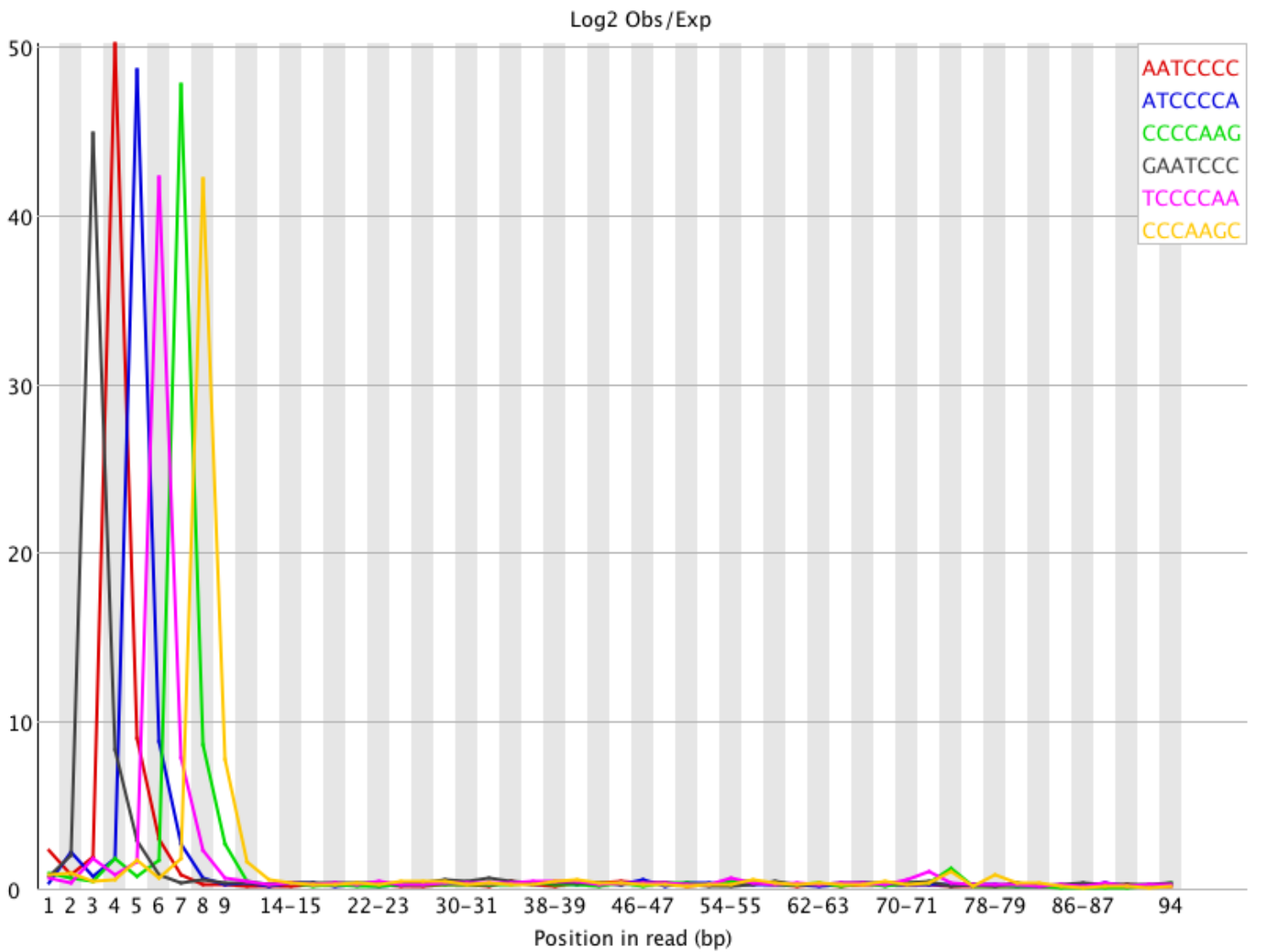
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TT	117257	0.3160705585869263	No Hit
ACGAATCCCCAAGCCAAGGGCTGAGTCTCAACAGATCGCAGCGTGGTAAC	70463	0.18993560955602298	No Hit

✓ Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AATCCCC	17650	0.0	50.187508	4
ATCCCCA	18220	0.0	48.69699	5
CCCCAAG	18580	0.0	47.830517	7
GAATCCC	19685	0.0	44.945415	3
TCCCCAA	20885	0.0	42.36745	6
CCCAAGC	21070	0.0	42.201084	8
CCAAGCC	24210	0.0	36.88949	9
ACAGACG	23930	0.0	35.151043	94
CGAATCC	26580	0.0	33.678135	2
ACGAATC	28560	0.0	30.817095	1
CACCCCG	17015	0.0	28.971367	68–69
CCAAGGG	18880	0.0	27.339907	14–15
GGGCTGA	19825	0.0	26.304056	18–19

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACCCCGC	16660	0.0	26.248932	68-69
CCCCGCC	19355	0.0	25.68085	70-71
CGTGGTA	19070	0.0	25.499357	42-43
AGCGTGG	19970	0.0	25.017275	40-41
ACACCCC	17405	0.0	24.993465	66-67
AAGGGCT	21045	0.0	24.622795	16-17
AACACCC	20300	0.0	24.465876	66-67

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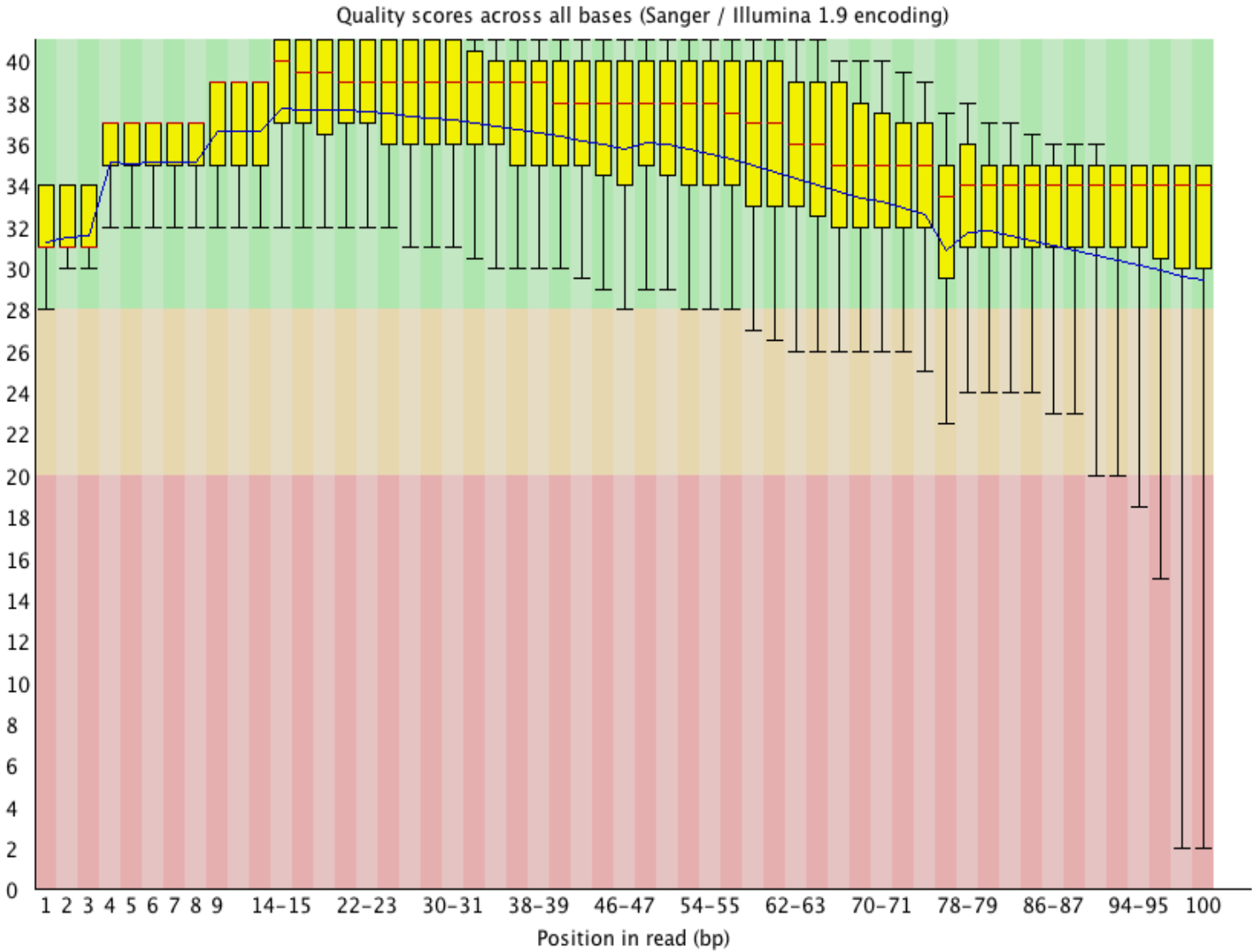
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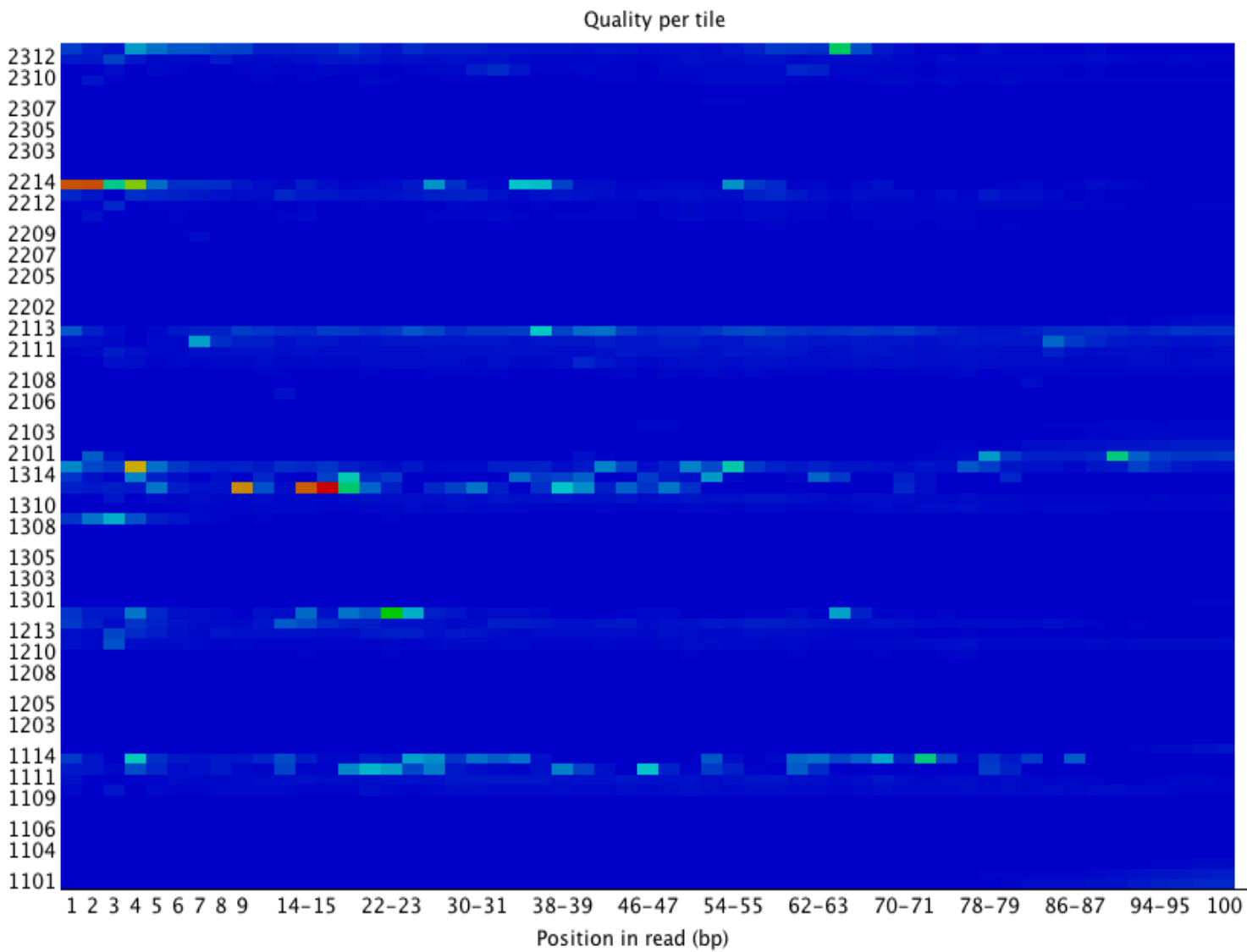
Basic Statistics

Measure	Value
Filename	1P_CGATGT_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	38608557
Sequences flagged as poor quality	0
Sequence length	100
%GC	40

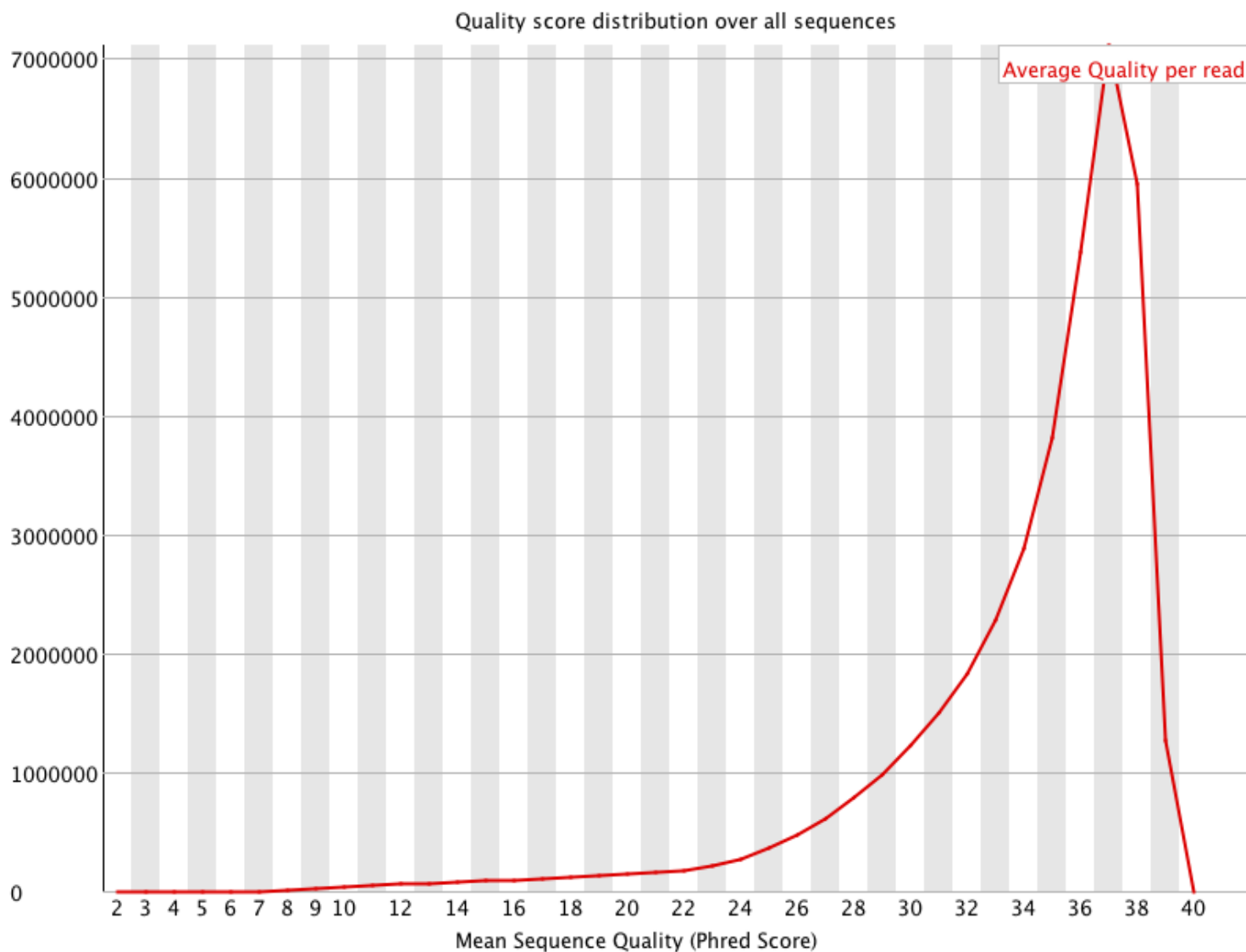
Per base sequence quality



 **Per tile sequence quality**

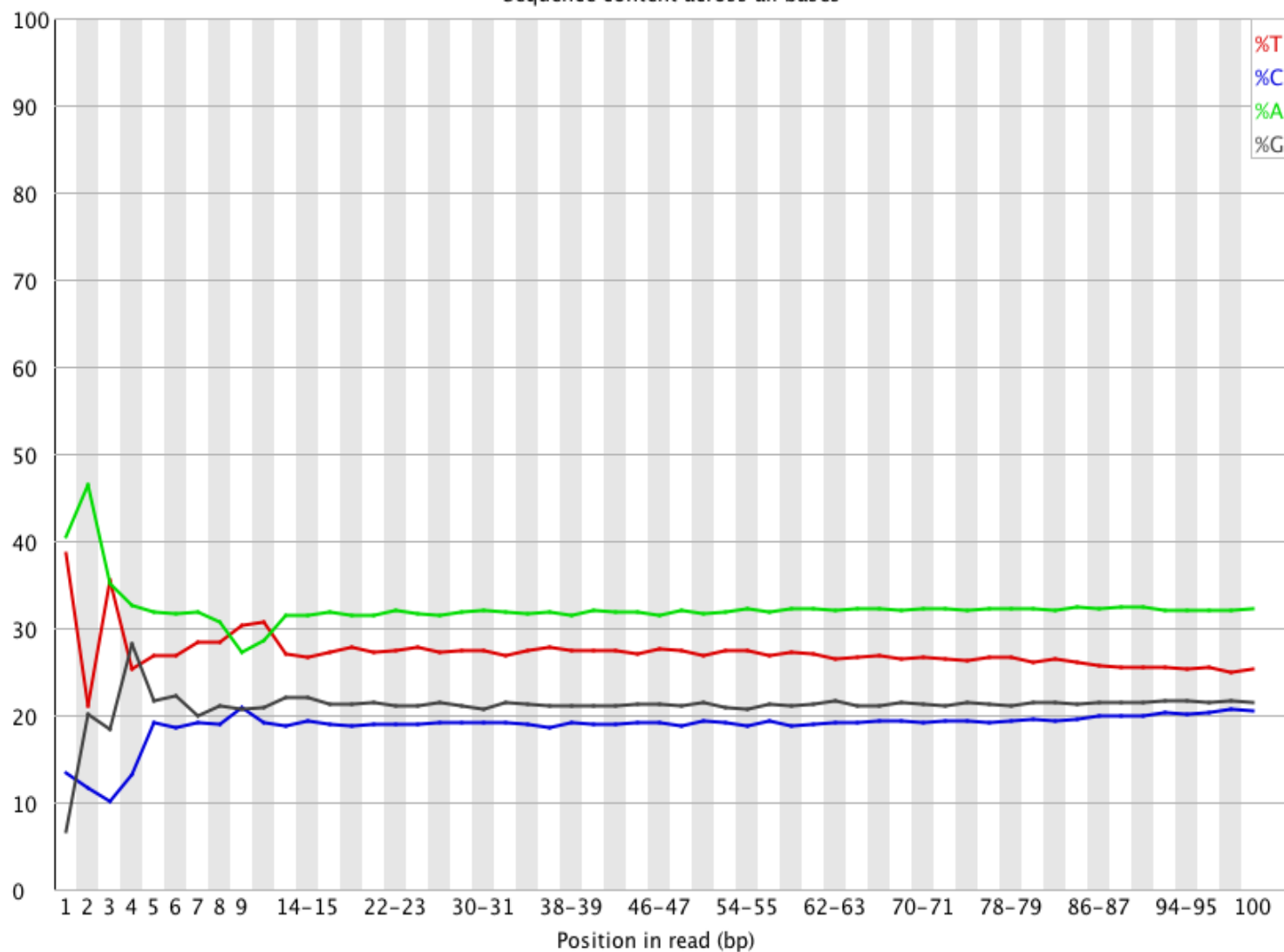


 Per sequence quality scores

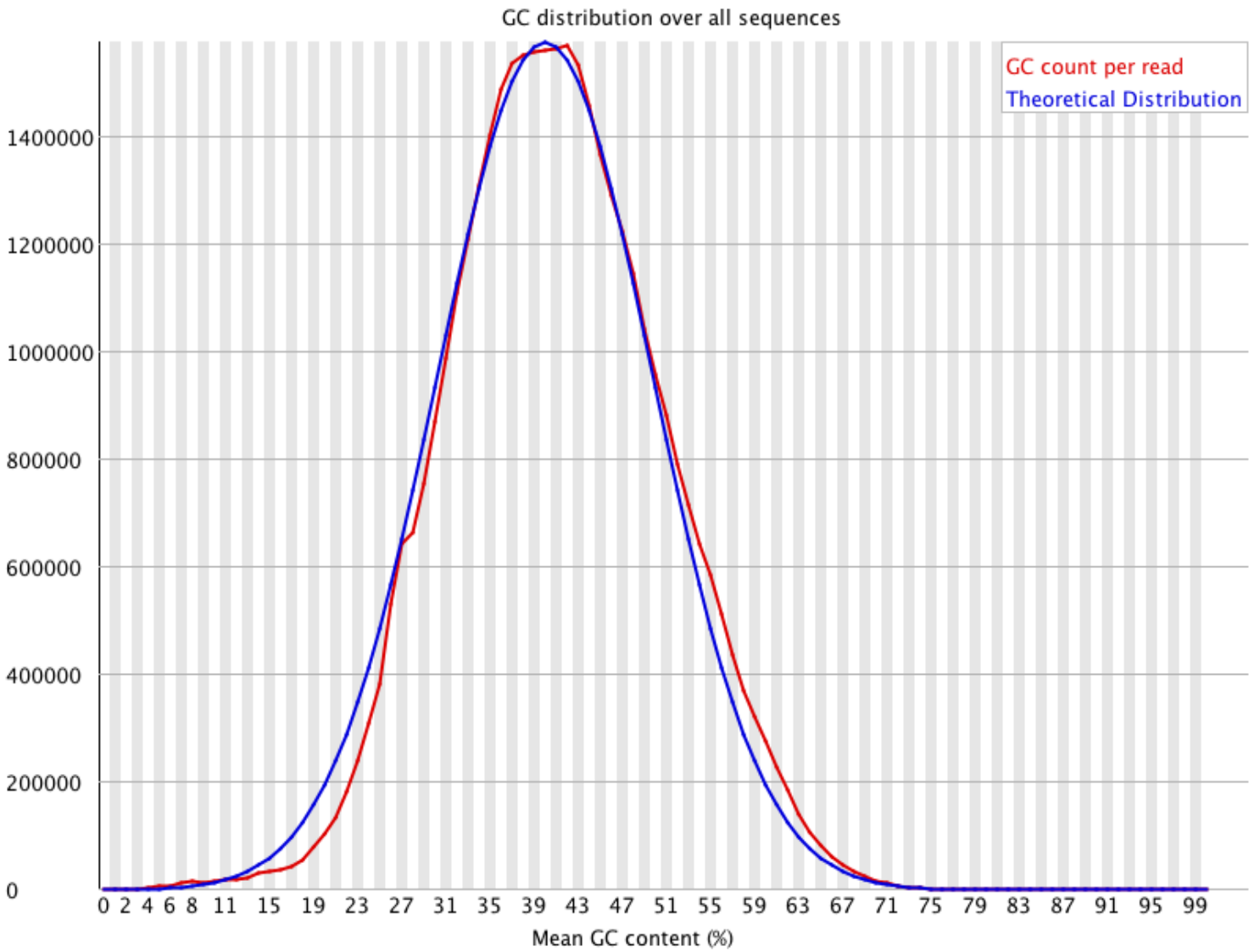


✖ Per base sequence content

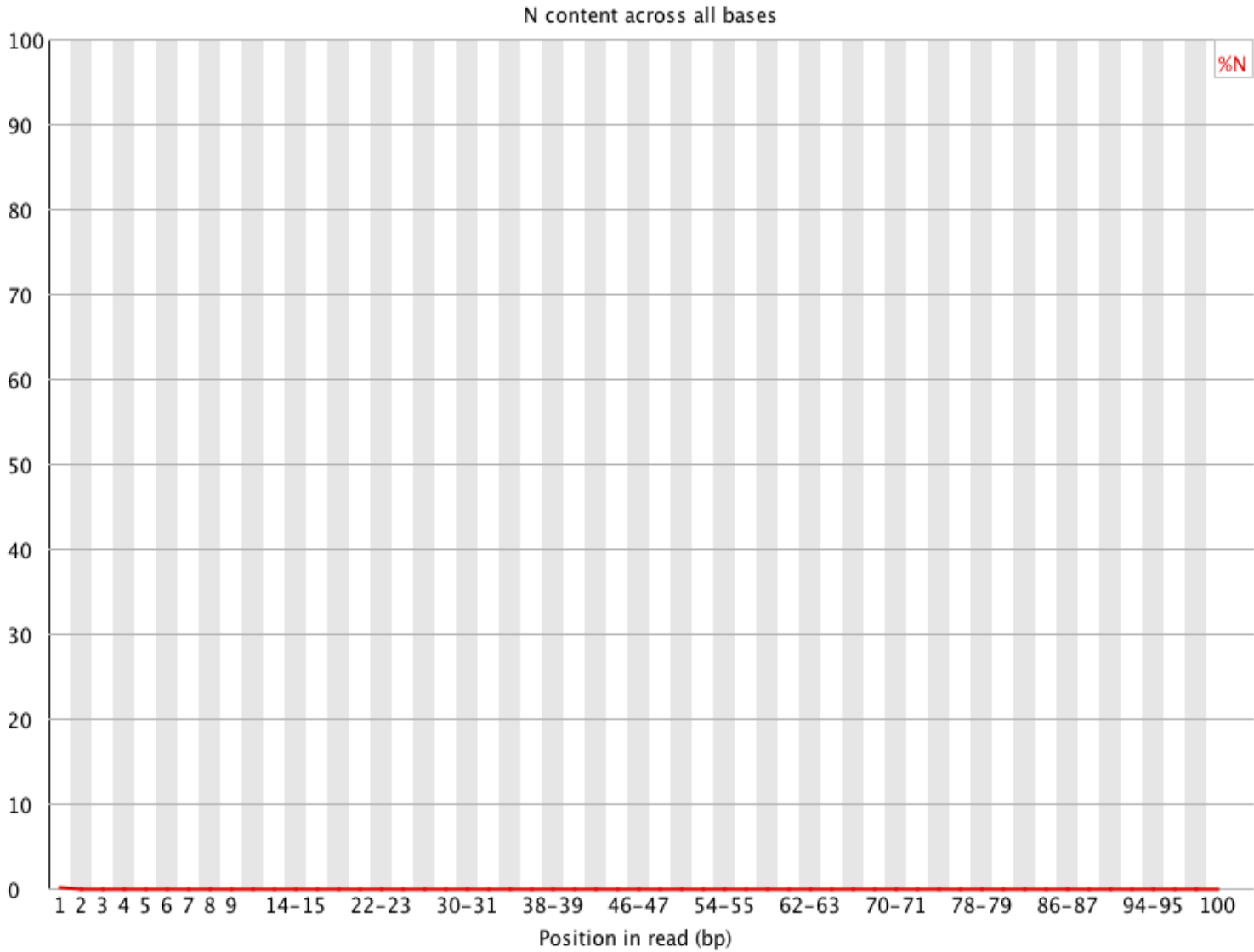
Sequence content across all bases



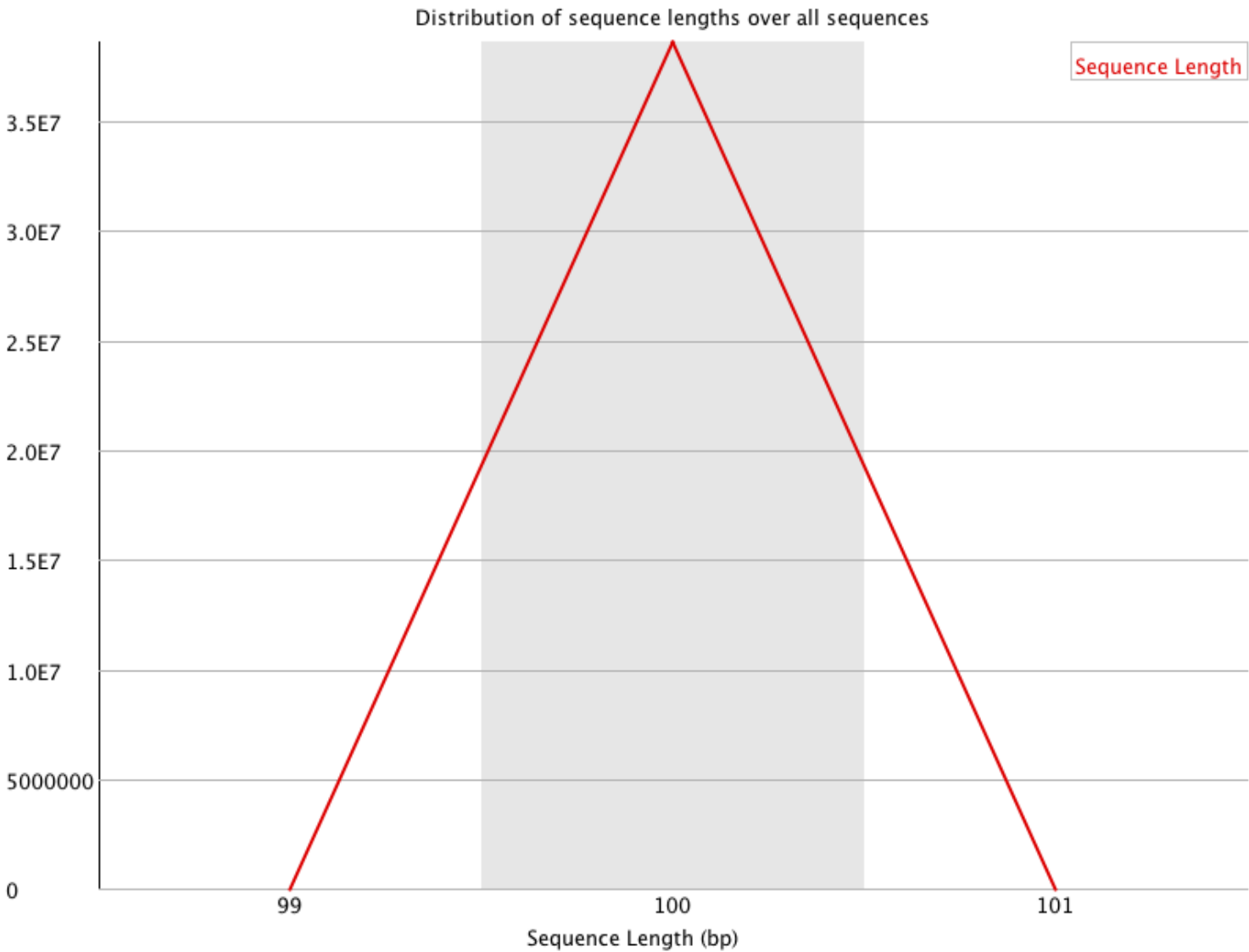
Per sequence GC content



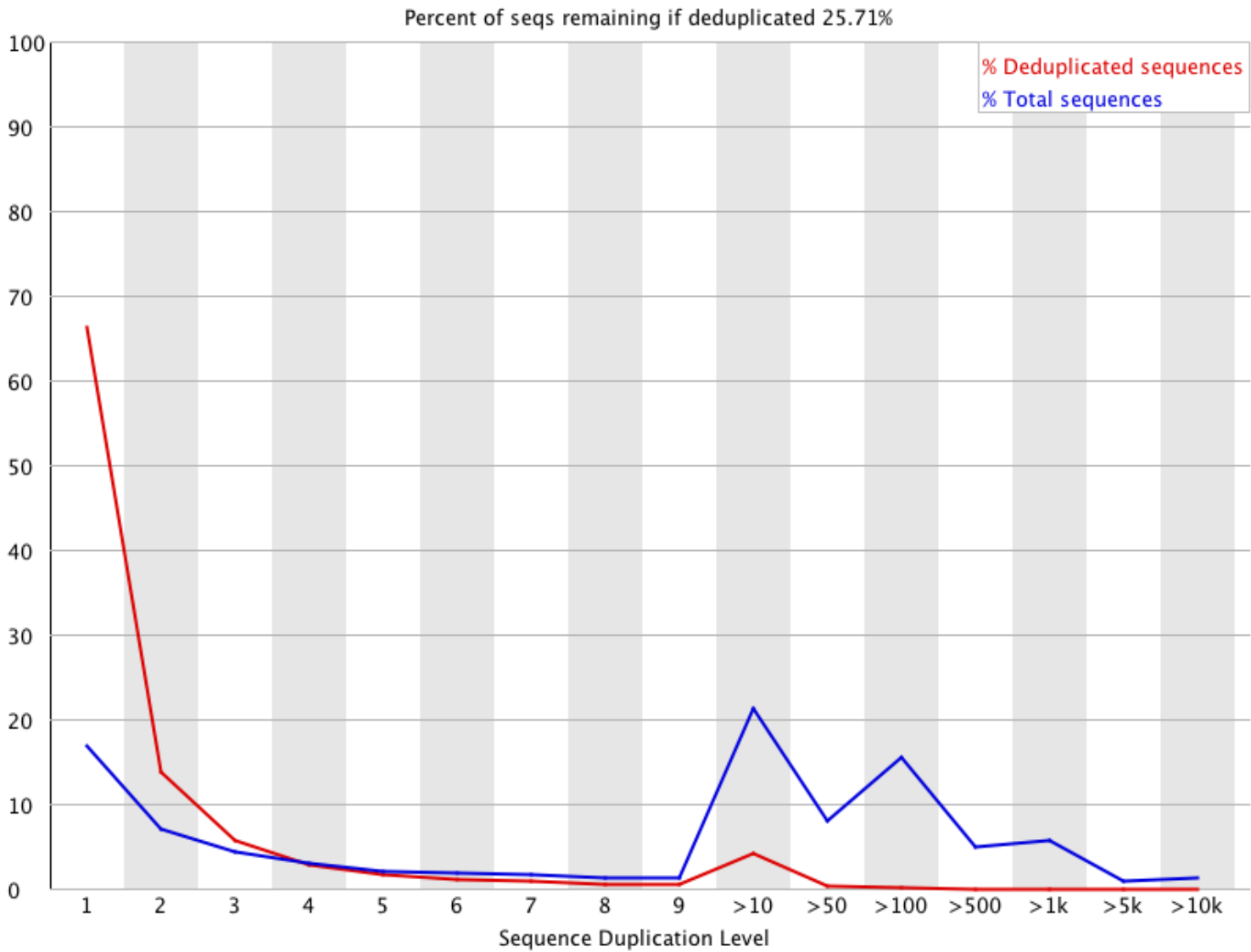
 Per base N content



✔ Sequence Length Distribution



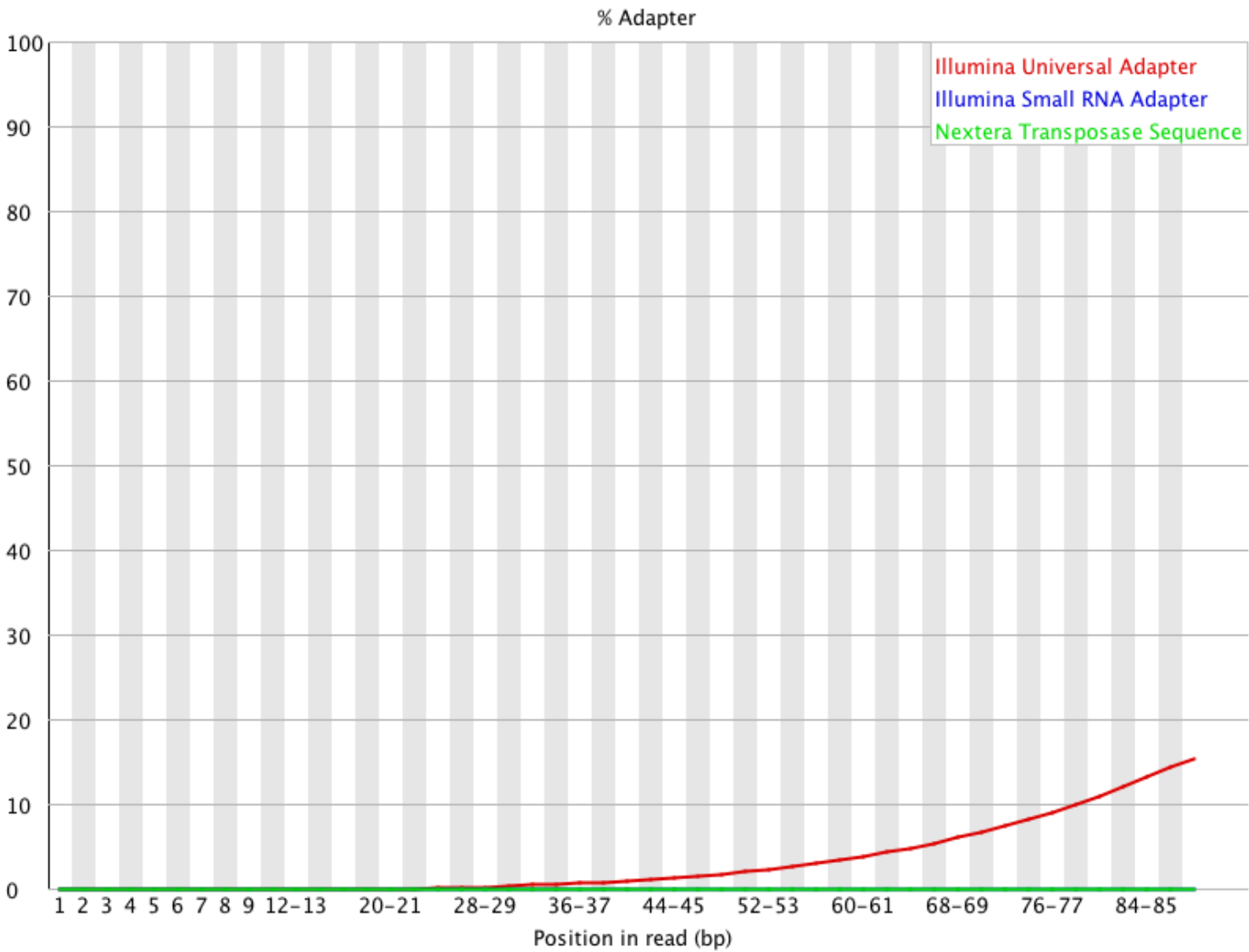
 Sequence Duplication Levels



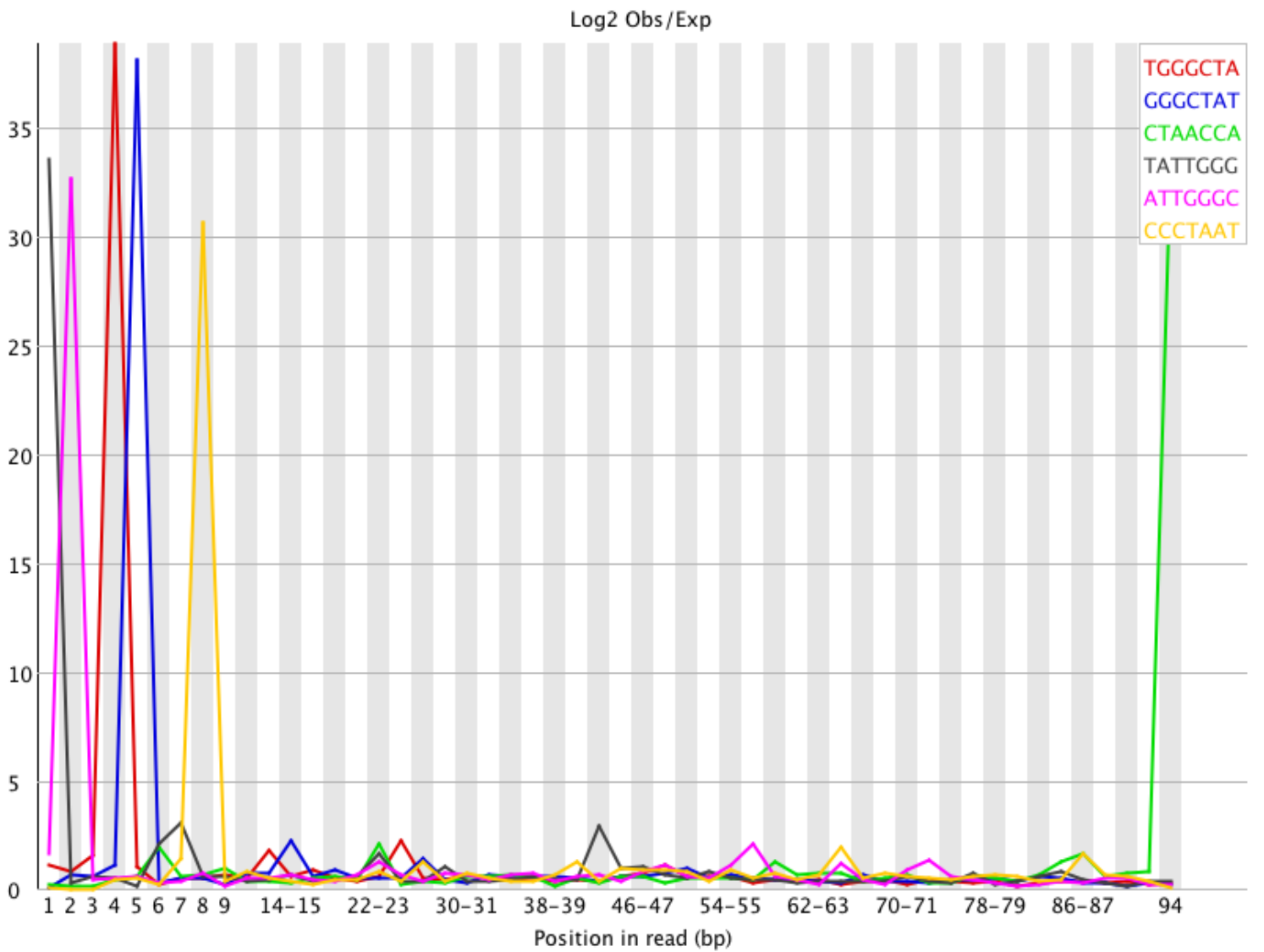
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TATTGGGCTATTAGGATTTATTGTTTGGGCTCATCATATATTTACTGTAG	59513	0.1541445850980652	No Hit
TTTAAATAGCTGCAGTATTTTGAAGGTACAAAGGTAGCATAATCAATTGT	47011	0.12176316250306894	No Hit
AGACGGACAGAAGCGAAAGCATTTCGCCAAAAATGTTTTTCATTAATCAAGA	44502	0.11526460312930109	No Hit

✖ Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TGGGCTA	16045	0.0	38.844067	4
GGGCTAT	16540	0.0	38.107822	5
CTAACCA	13255	0.0	34.003162	94
TATTGGG	18690	0.0	33.555275	1
ATTGGGC	19410	0.0	32.711643	2
CCCTAAT	6415	0.0	30.700031	8
GGCCCTA	6480	0.0	30.392044	6
GGCTATT	21180	0.0	29.959097	6
CTATTAG	22340	0.0	28.403511	8
CACACCC	9610	0.0	28.14366	1
GCCCTAG	8375	0.0	27.076963	84-85
ACCCGTC	10075	0.0	26.91855	4
CCCTAGT	8455	0.0	26.903326	86-87

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GTCGGGC	10710	0.0	26.858603	8
CGCCCTA	8625	0.0	26.564579	84-85
TATTAGG	24460	0.0	26.133883	9
TCGGGCG	10505	0.0	26.085186	9
ACGGGCC	7760	0.0	25.742346	3
CACCCGT	10615	0.0	25.504887	3
CACGGGC	7665	0.0	25.384035	2

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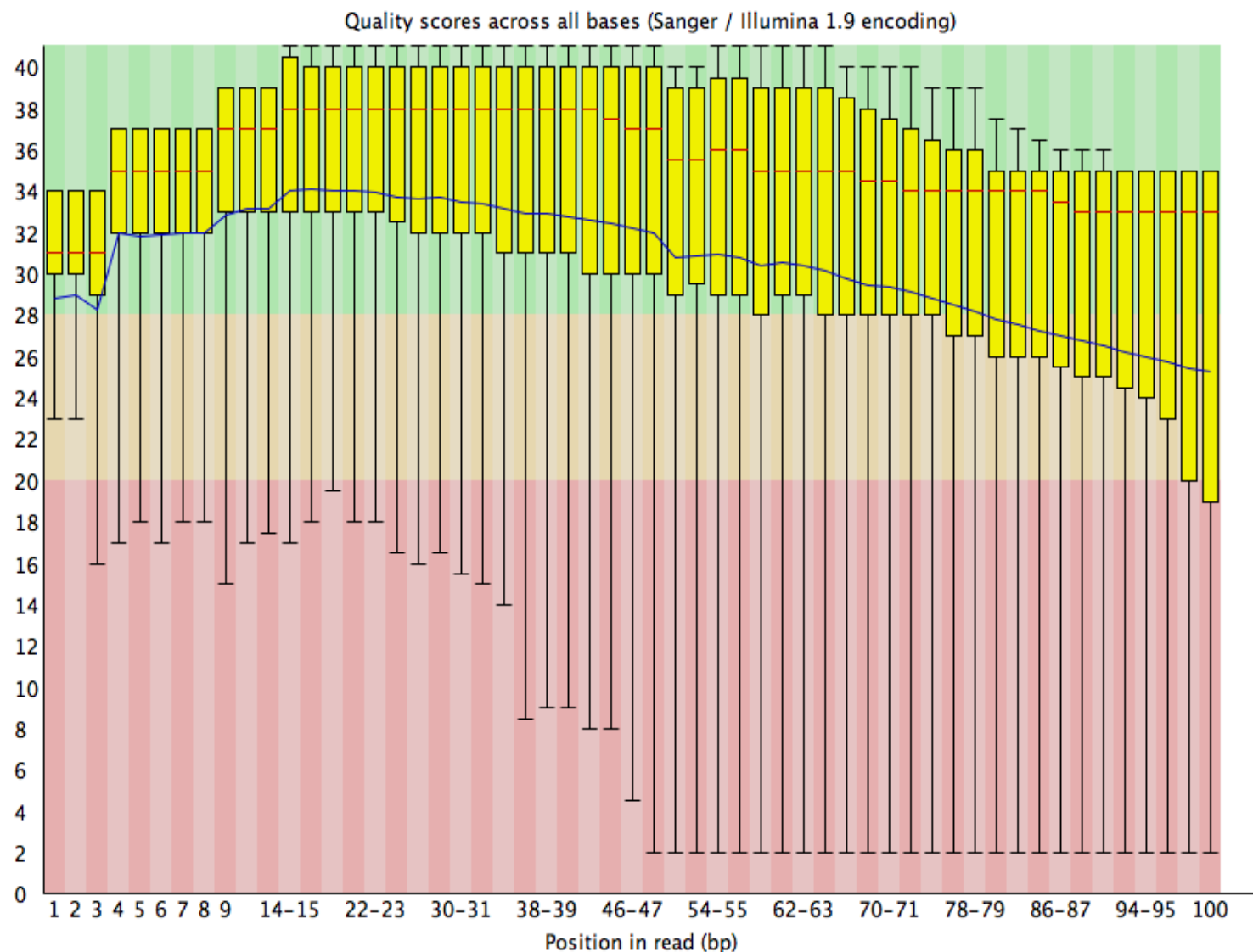
Thu 20 Dec 2018
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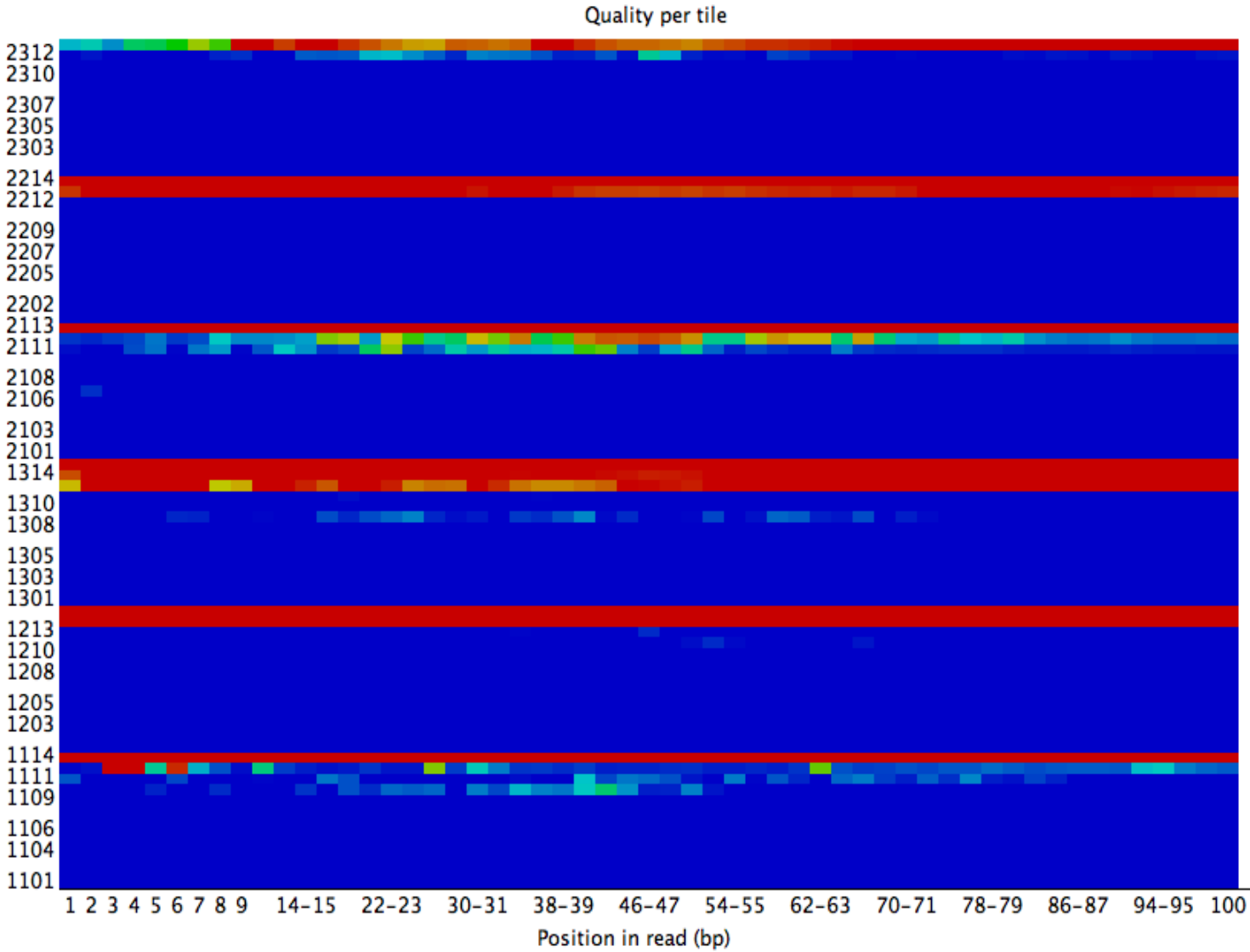
Basic Statistics

Measure	Value
Filename	1P_CGATGT_L001_R2_001.fastq
File type	Conventional base calls
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Total Sequences	38608557
Sequences flagged as poor quality	0
Sequence length	100
%GC	40

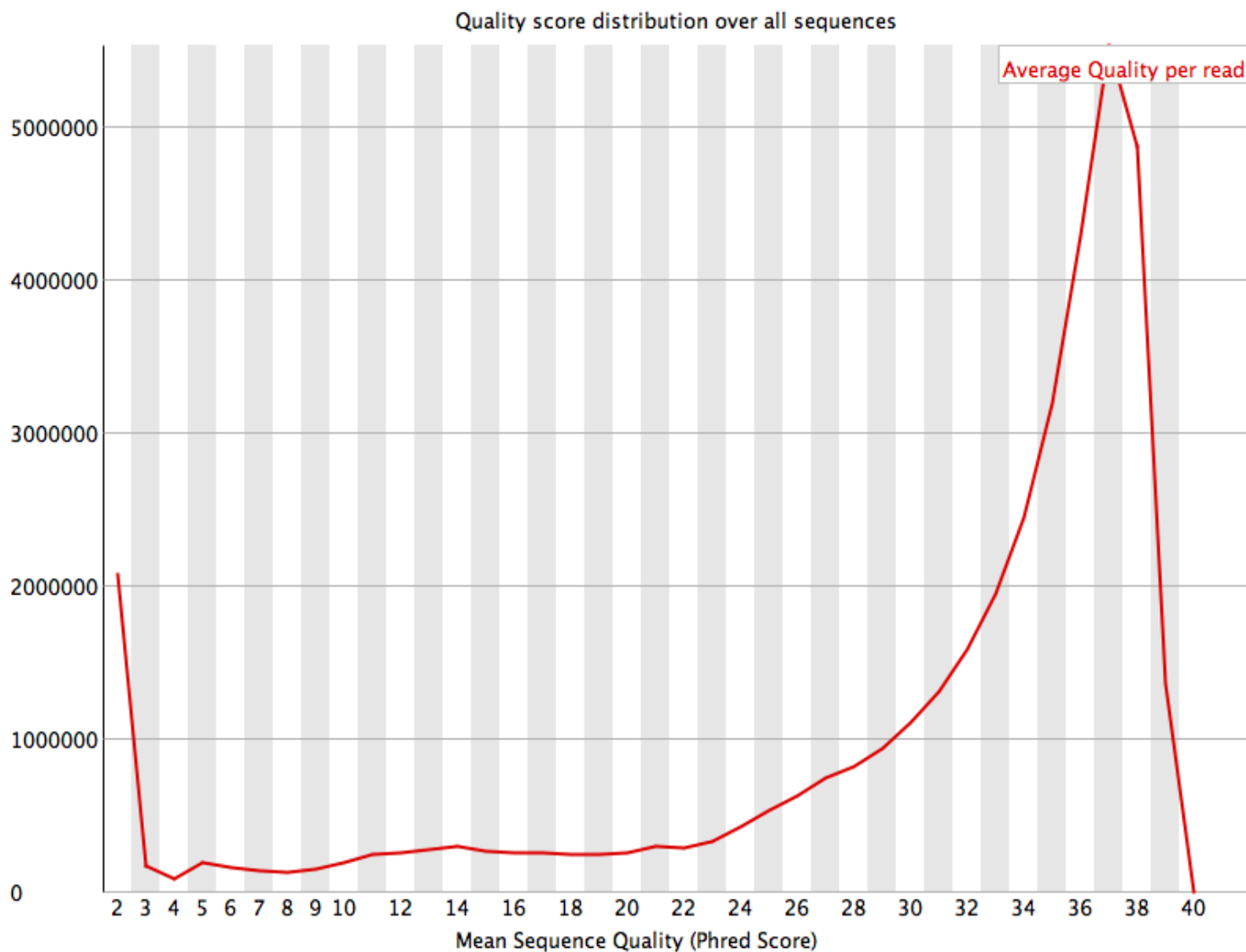
Per base sequence quality



✖ Per tile sequence quality

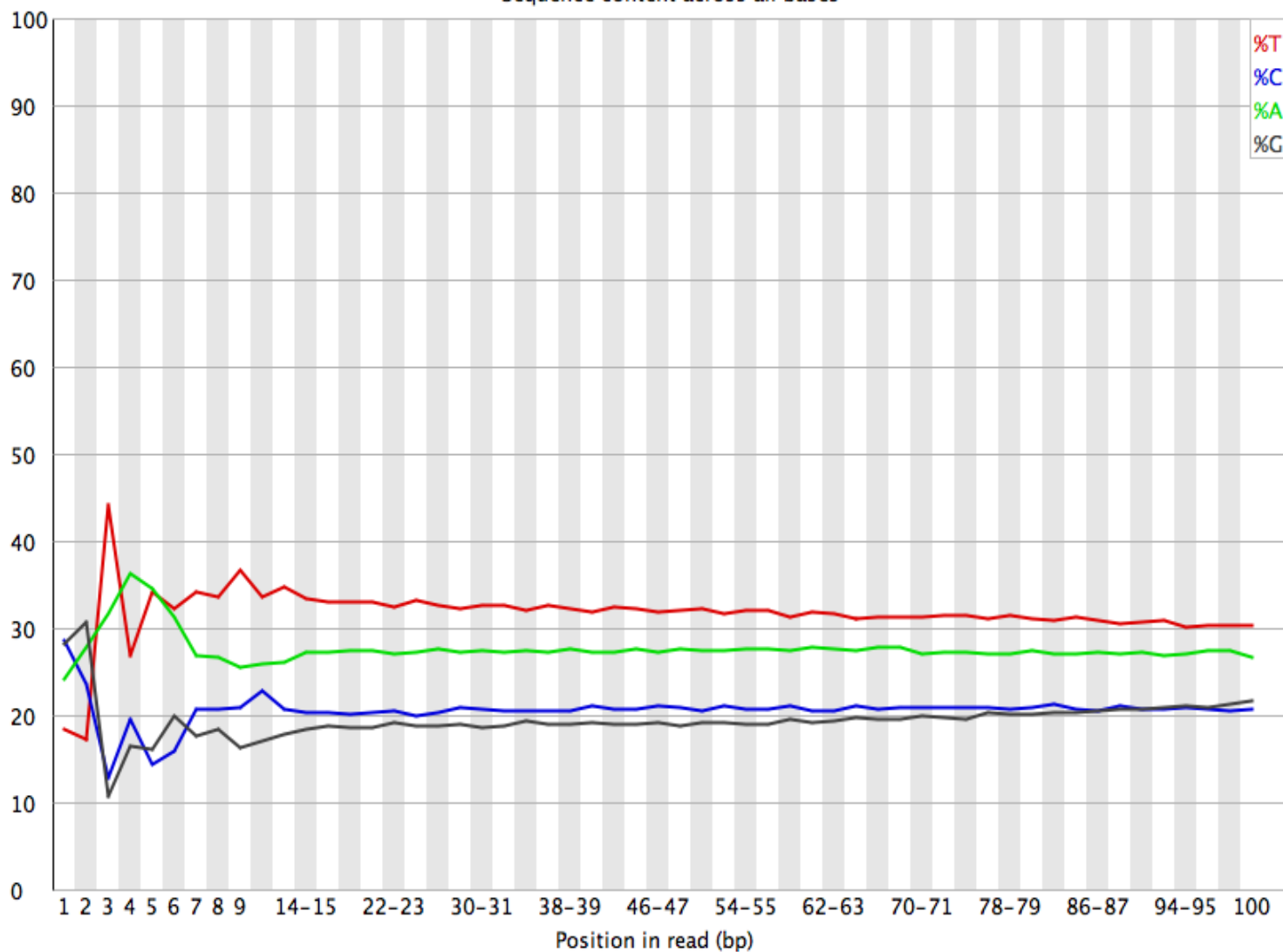


 Per sequence quality scores

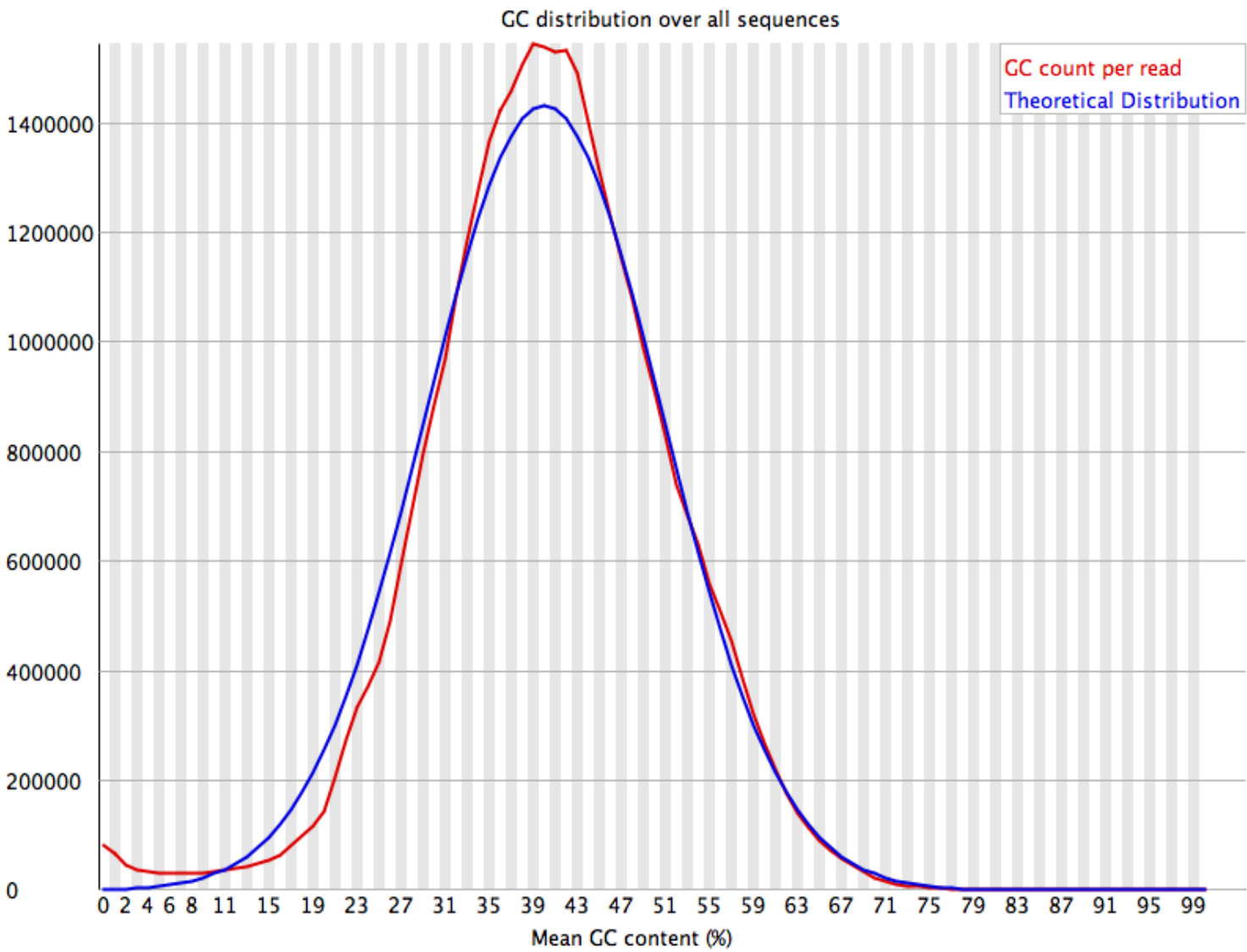


✖ Per base sequence content

Sequence content across all bases

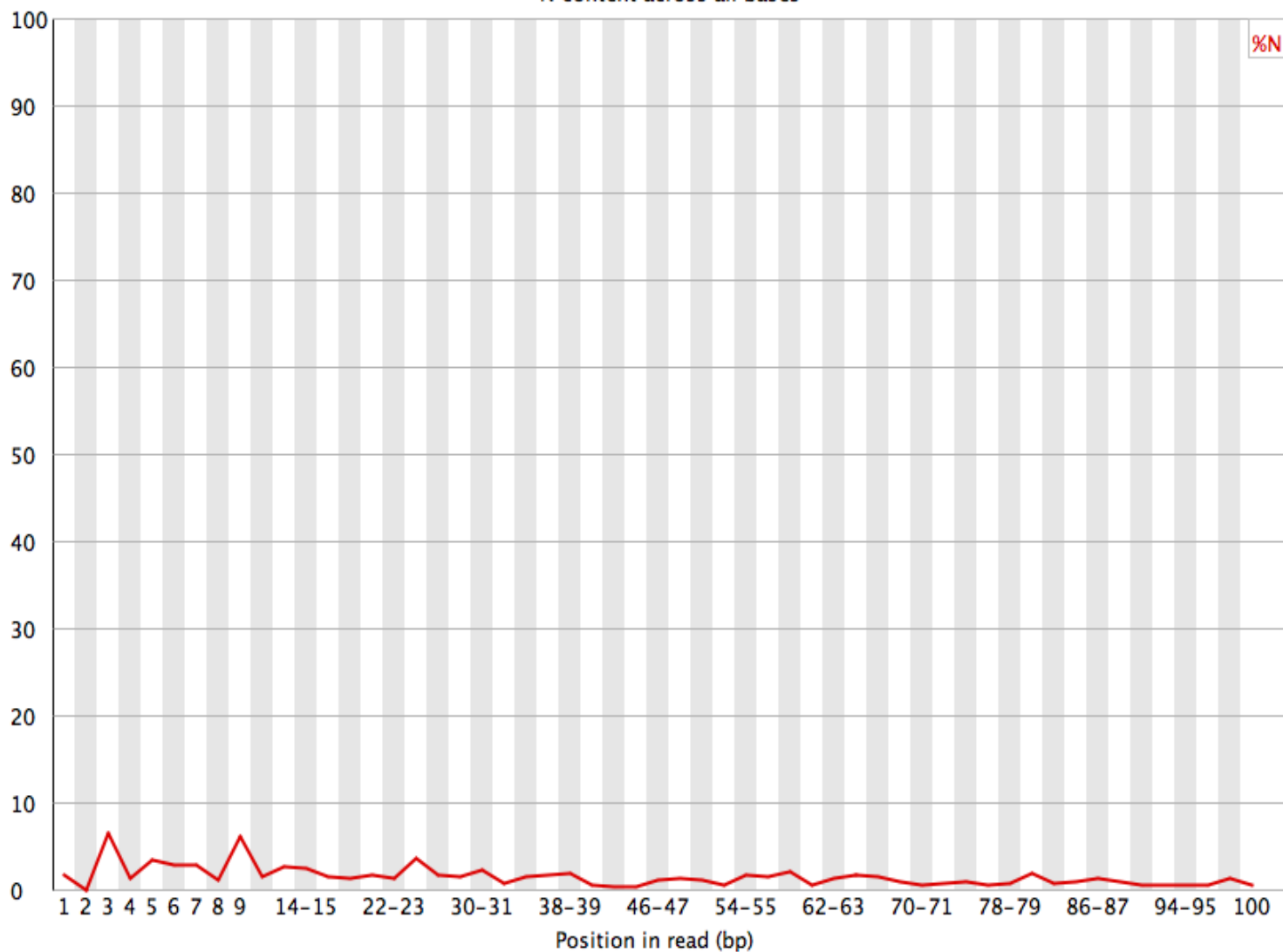


Per sequence GC content

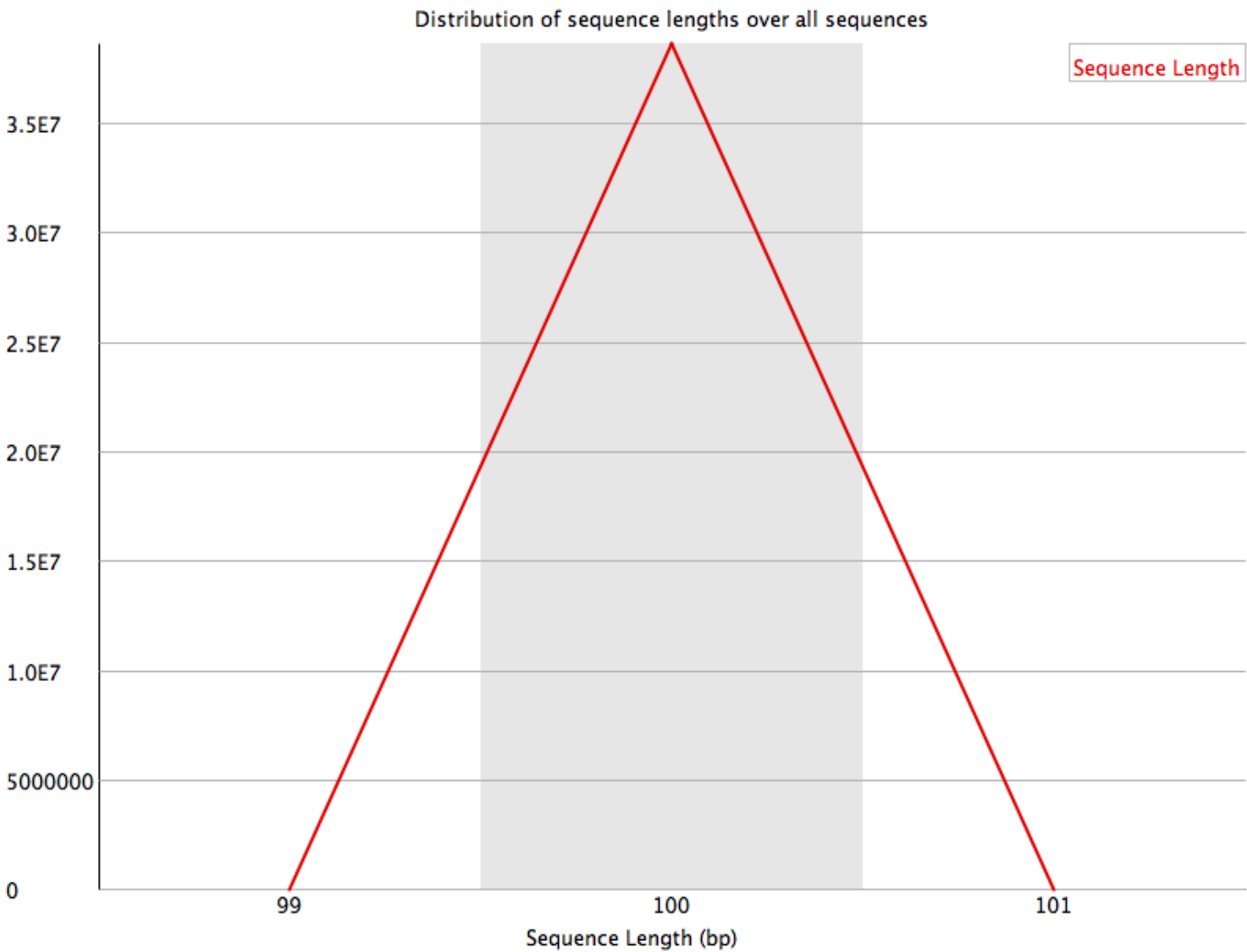


! Per base N content

N content across all bases



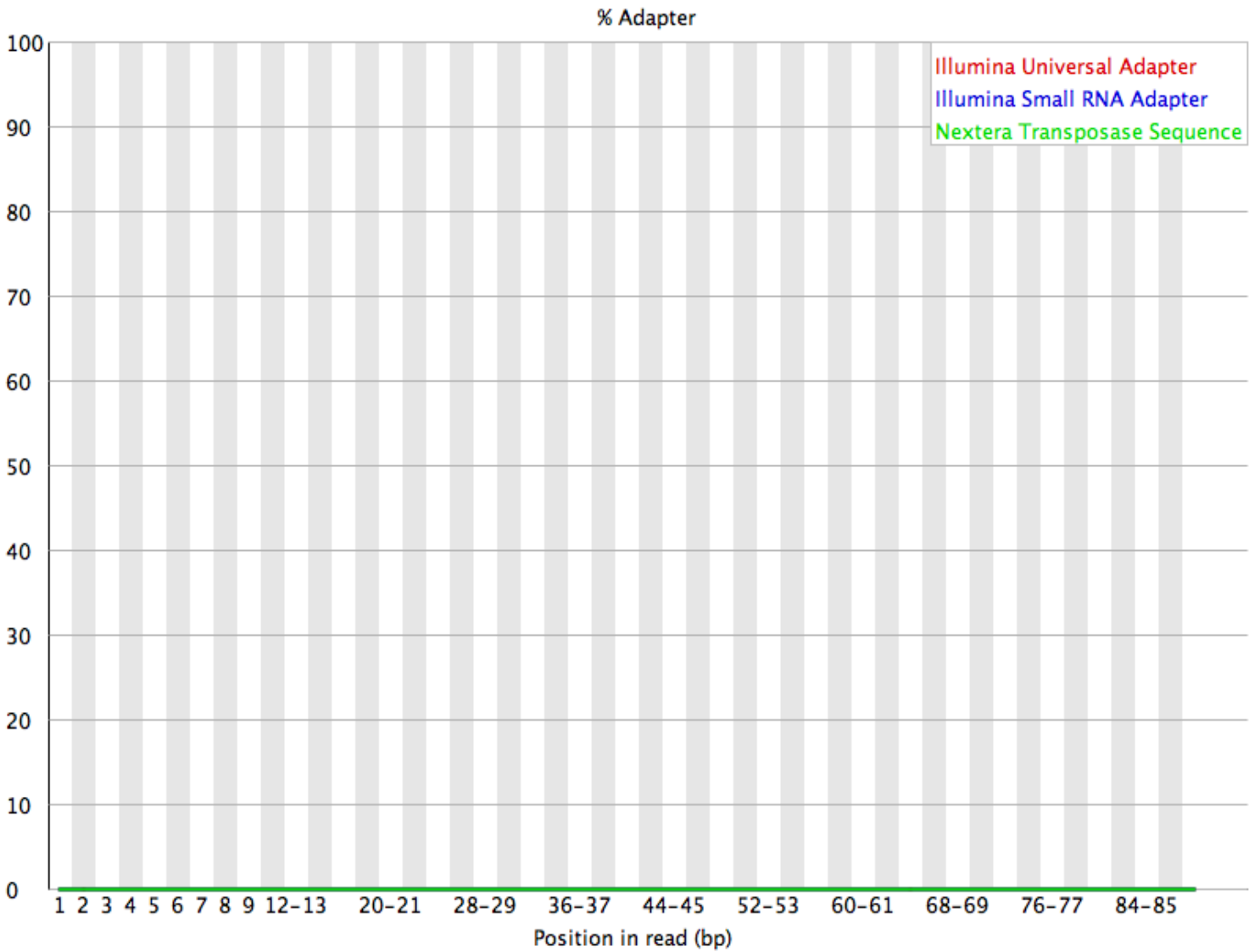
Sequence Length Distribution



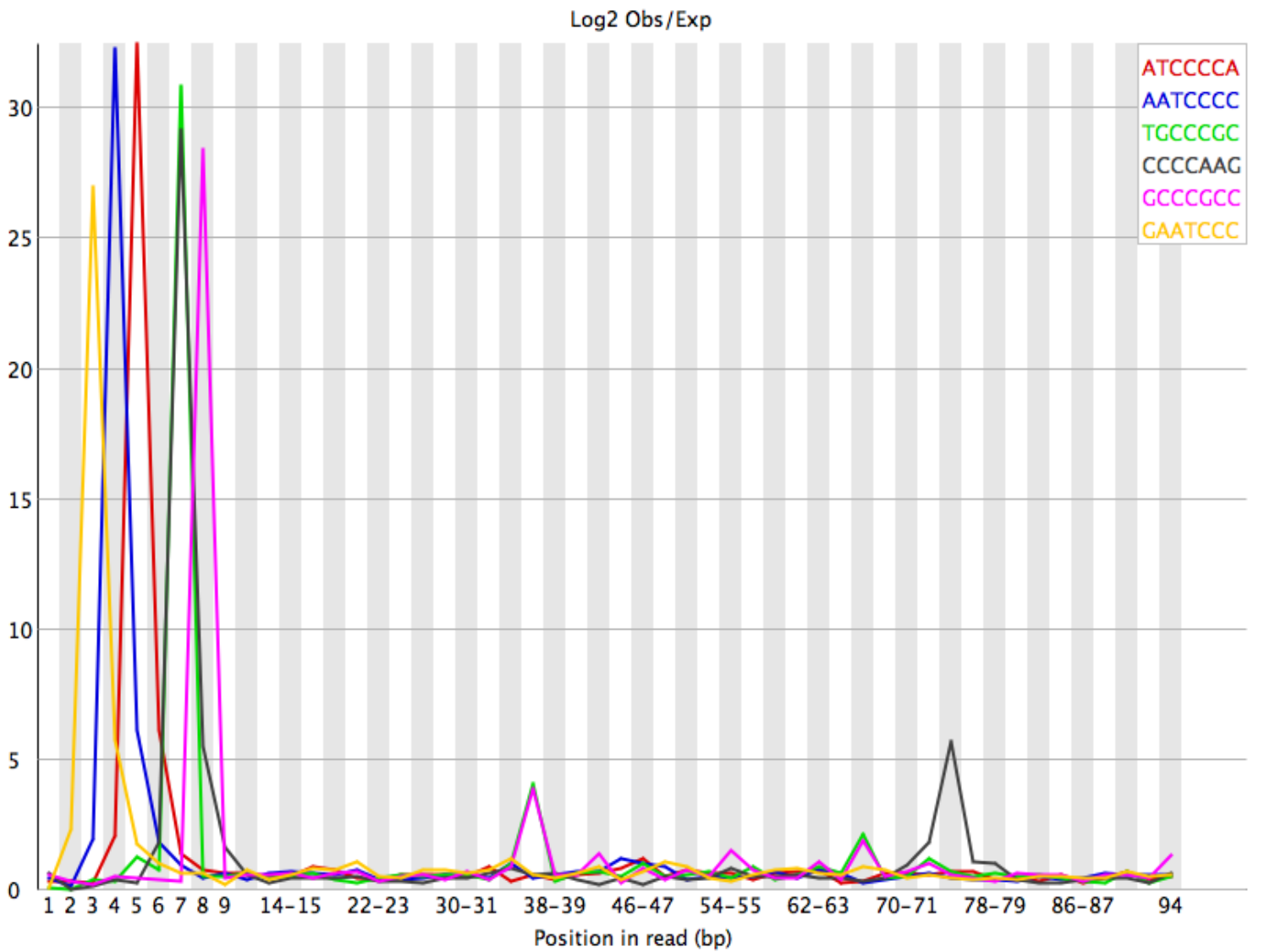
 Sequence Duplication Levels



Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCCCA	10810	0.0	32.41173	5
AATCCCC	11215	0.0	32.232372	4
TGCCCGC	8690	0.0	30.80844	7
CCCCAAG	11875	0.0	29.137959	7
GCCCGCC	9400	0.0	28.378794	8
GAATCCC	13410	0.0	26.953484	3
CTGCCCCG	9955	0.0	26.797136	6
CCCGCCG	10585	0.0	25.294903	9
TAGATGC	15375	0.0	23.82933	1
CACCCCG	8525	0.0	22.445795	68–69
TCCCCAA	15710	0.0	22.240917	6
GATGCTA	16565	0.0	22.202164	3
CCCAAGC	15890	0.0	21.866924	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACAGACG	14925	0.0	21.77182	94
GCTGCCC	12355	0.0	21.630789	5
ACCCCGC	8165	0.0	21.18474	68–69
CCAAGCC	16560	0.0	21.129654	9
CGAATCC	18590	0.0	20.332567	2
GCTAATC	18320	0.0	20.206629	6
GGAGAGC	13705	0.0	19.557308	1

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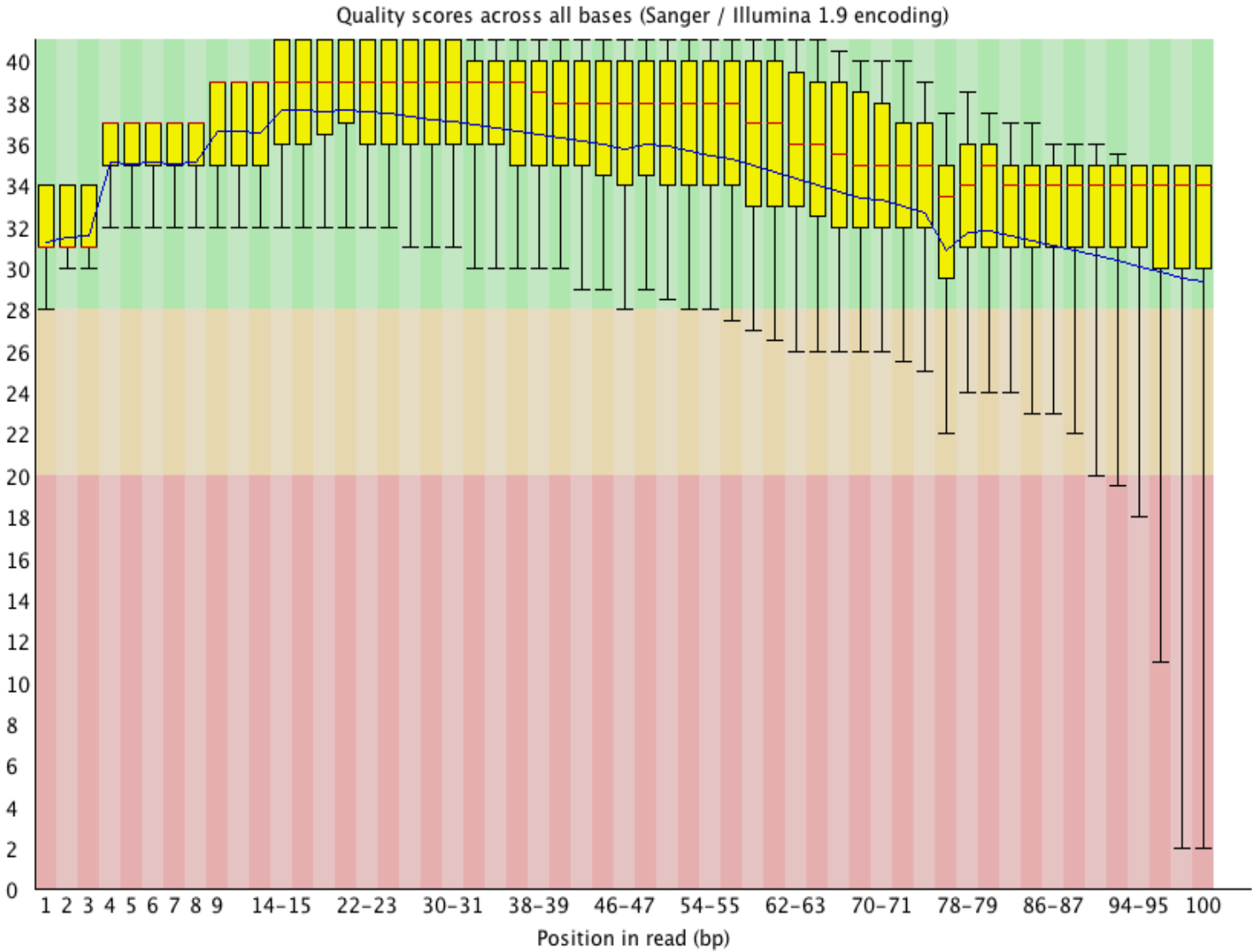
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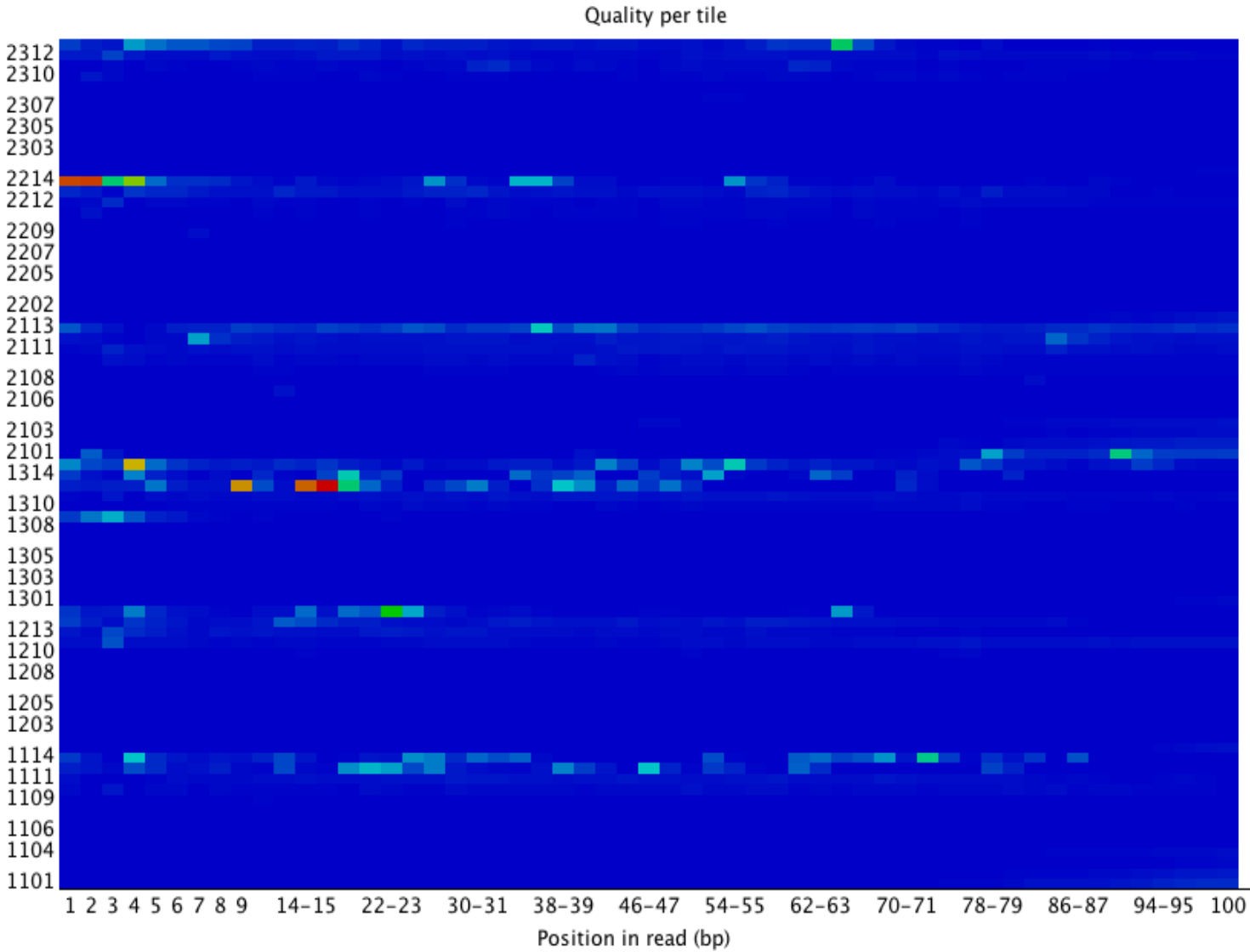
Basic Statistics

Measure	Value
Filename	2A_TTAGGC_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36863703
Sequences flagged as poor quality	0
Sequence length	100
%GC	39

Per base sequence quality

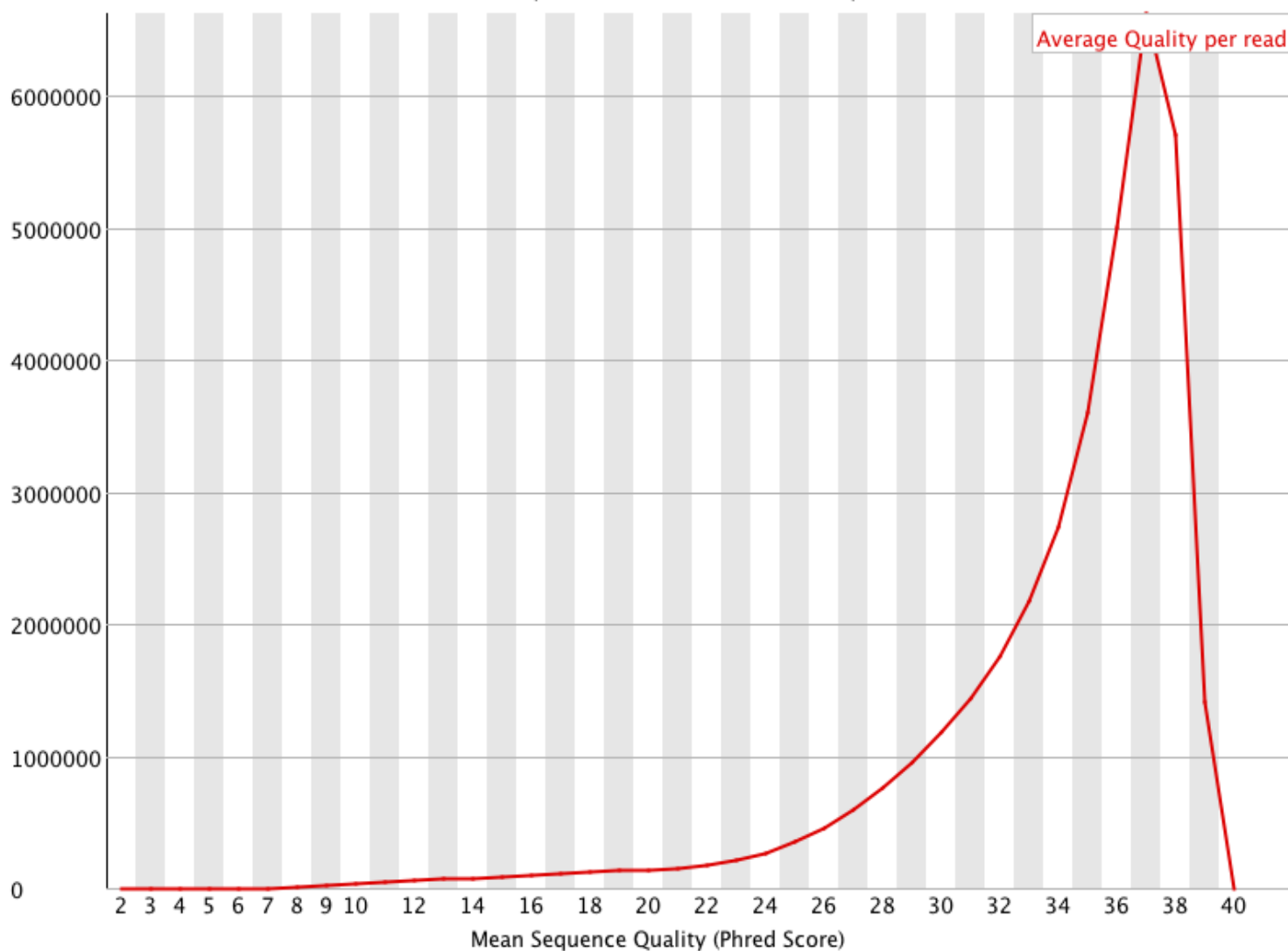


 **Per tile sequence quality**



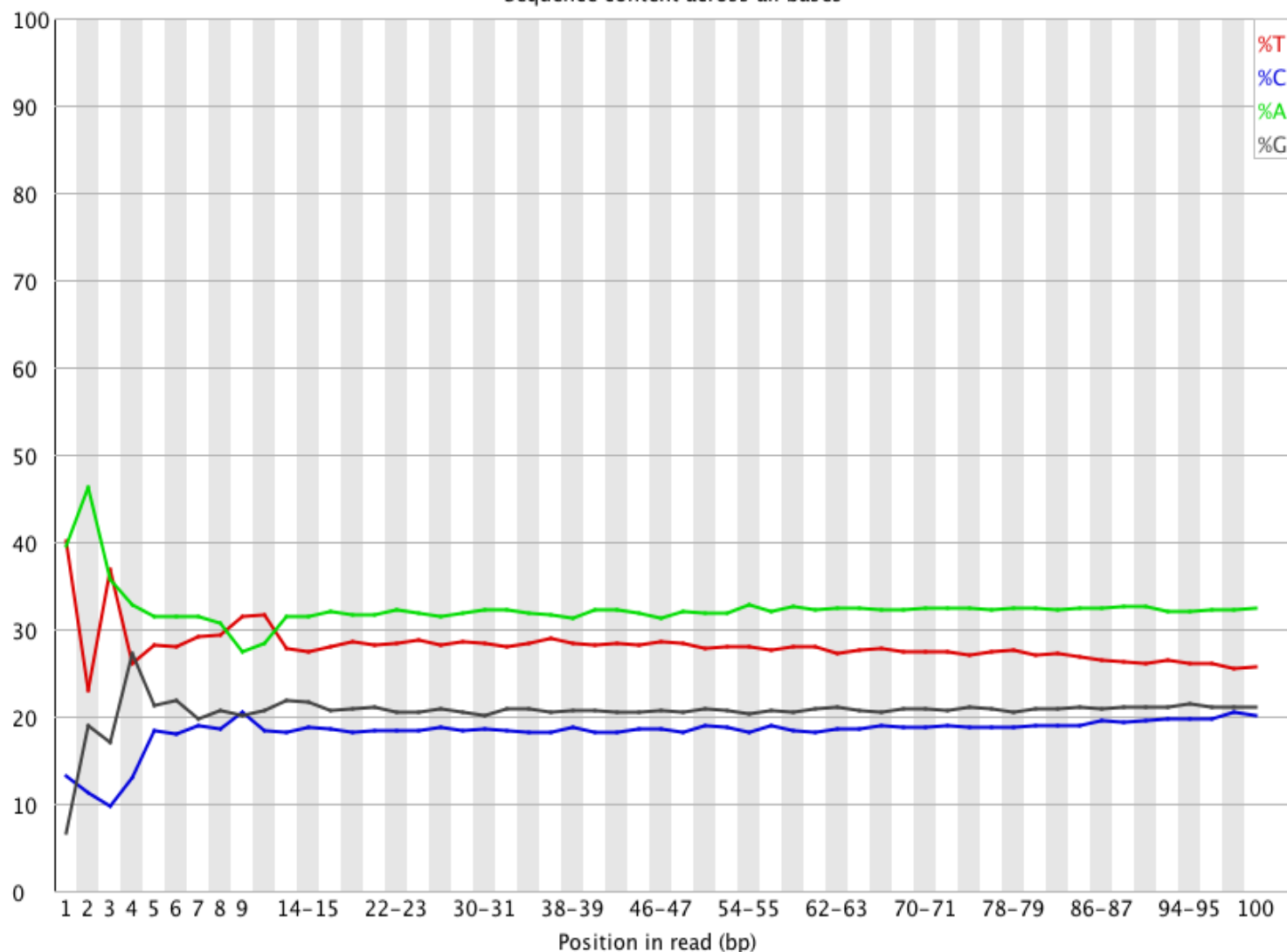
 Per sequence quality scores

Quality score distribution over all sequences



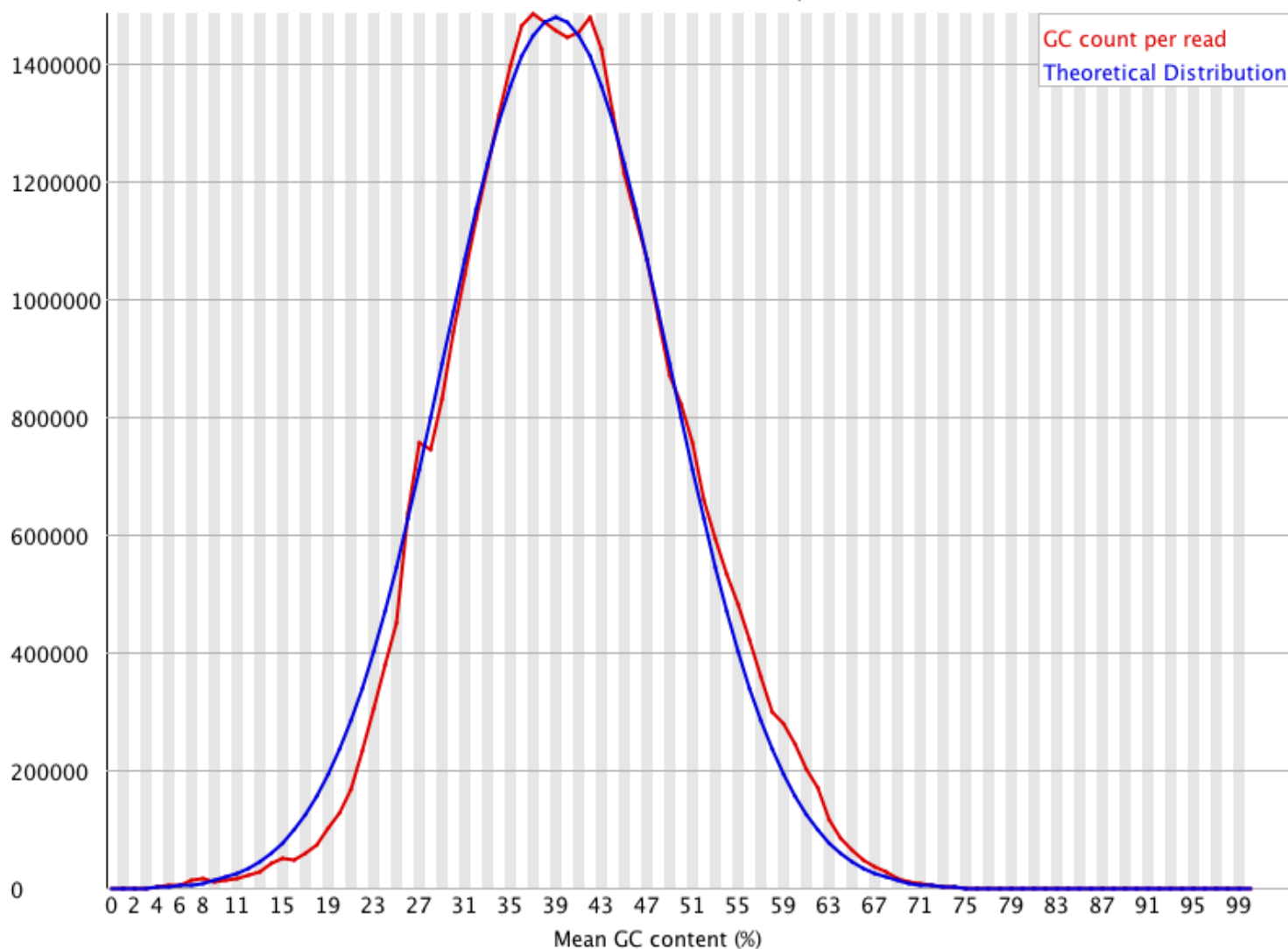
✖ Per base sequence content

Sequence content across all bases

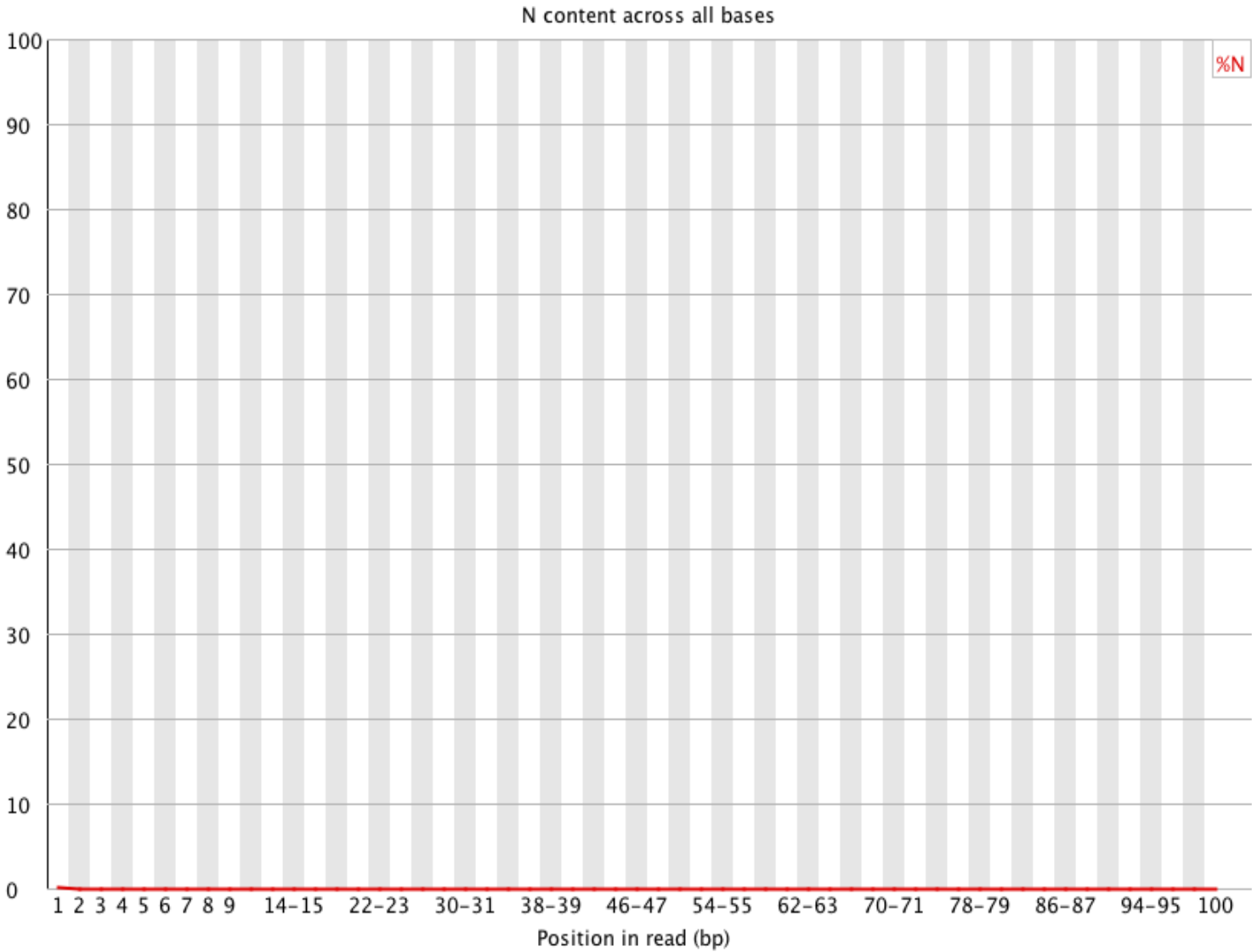


Per sequence GC content

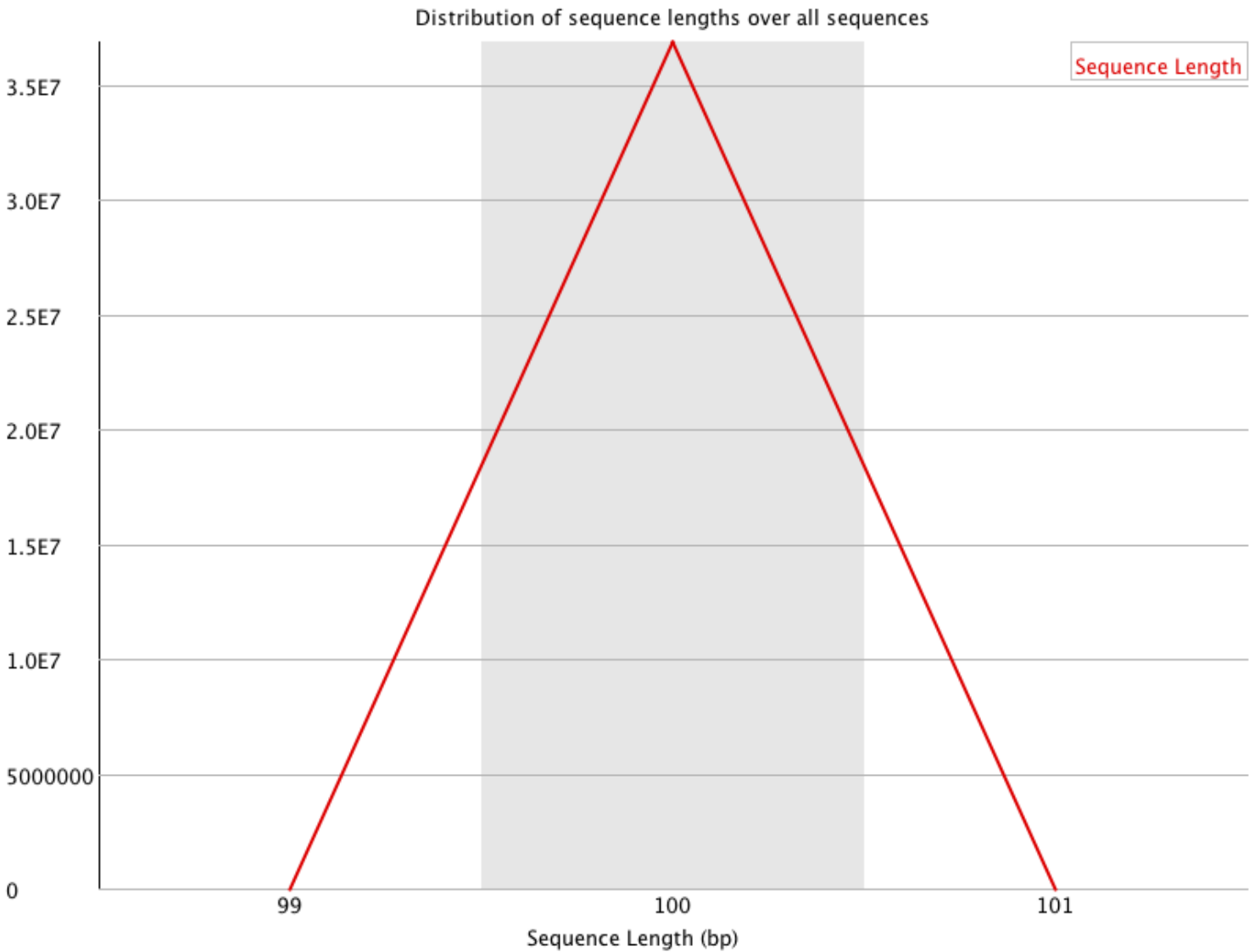
GC distribution over all sequences



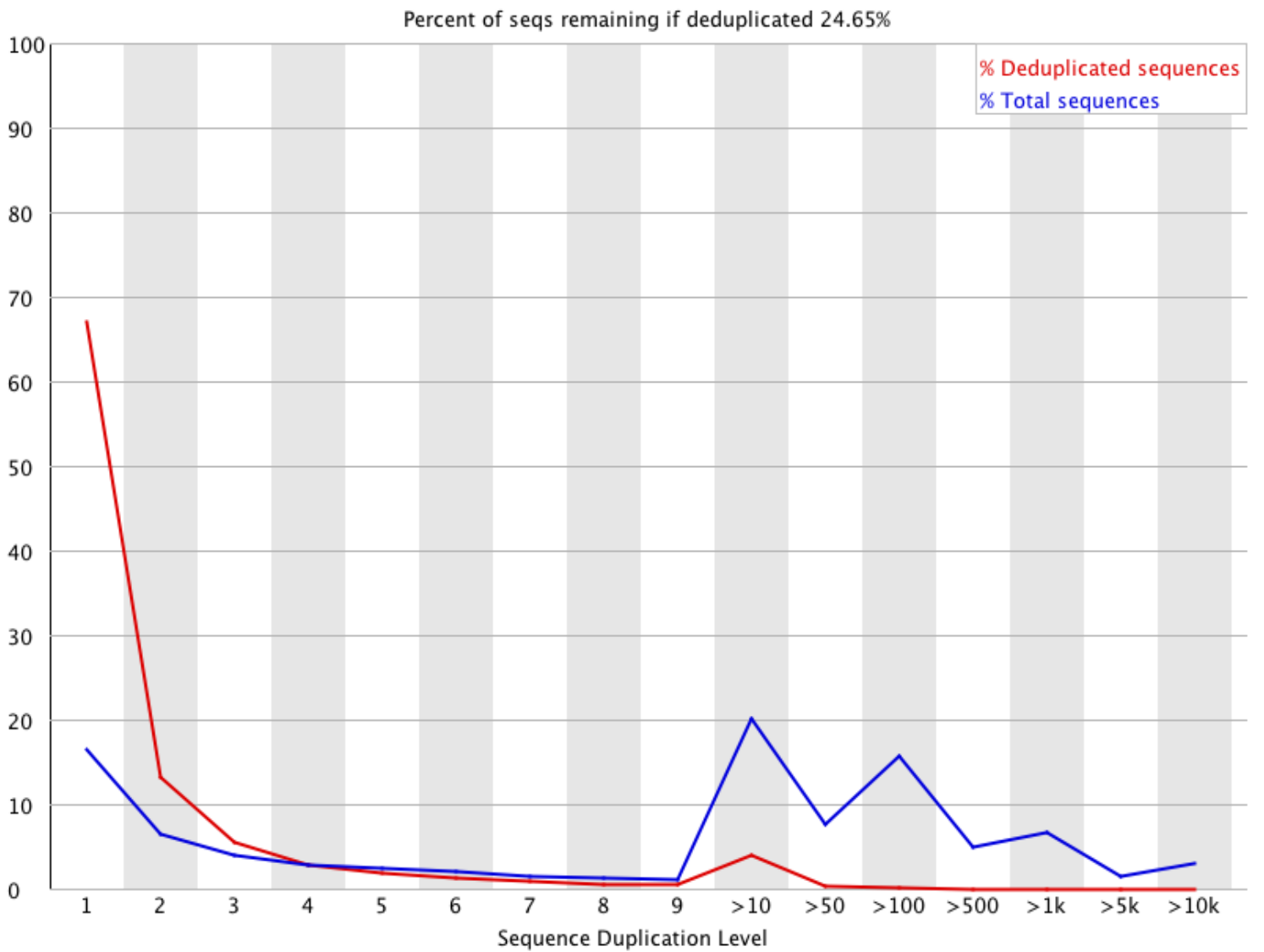
Per base N content



✔ Sequence Length Distribution



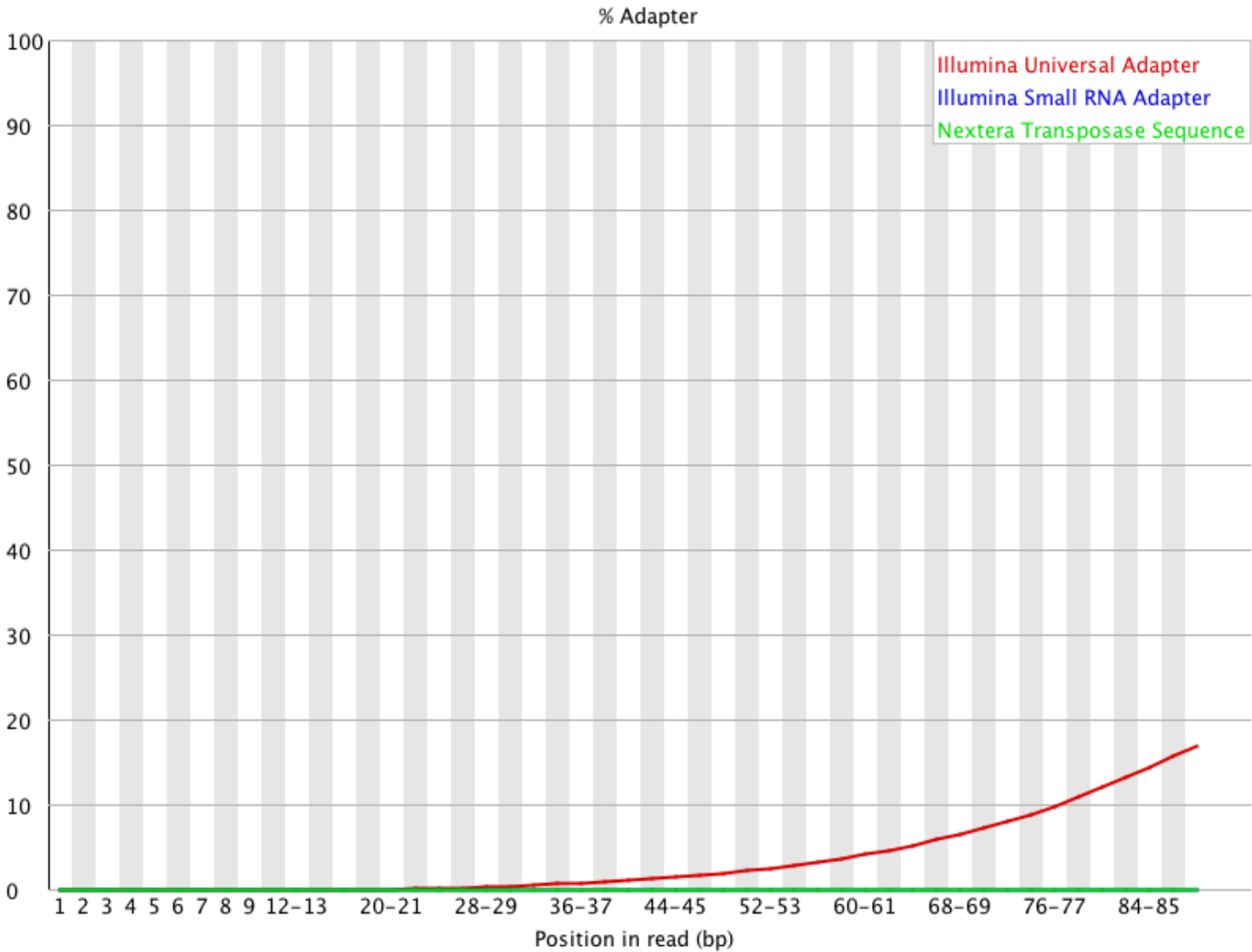
 Sequence Duplication Levels



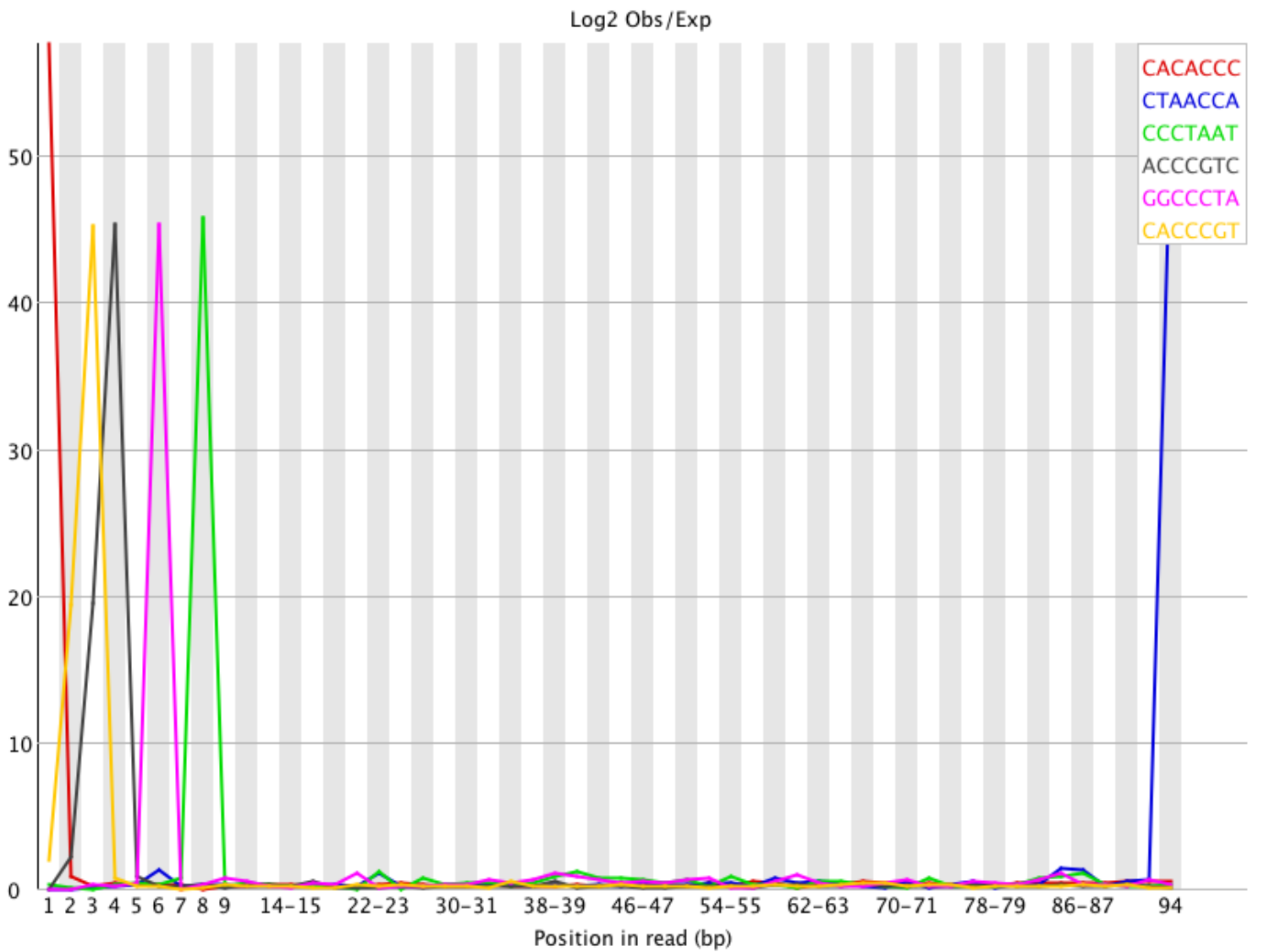
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGACGGACAGAAGCGAAAGCATTGCCCCAAATGTTTTCATTAATCAAGA	98852	0.26815537223702135	No Hit
CACACCCGTCGGGCGAAAGGGAATCCGGTTCCTATTCCGGAACCCGGCAG	71942	0.19515673723825303	No Hit
AATAAATCAATTCTGCTCAATGAATTTATTTAAATAGCTGCAGTATTTTG	68638	0.18619399141751983	No Hit
TAAATCAATTCTGCTCAATGAATTTATTTAAATAGCTGCAGTATTTTGAC	67267	0.18247488593319017	No Hit
TATTGGGCTATTAGGATTTATTGTTTGGGCTCATCATATATTTACTGTAG	58511	0.15872252443006066	No Hit
TTTAAATAGCTGCAGTATTTTGACTGTACAAAGGTAGCATAATCAATTGT	42992	0.11662420348818457	No Hit
GCACGGGCCCTAATTGCCGTACGGAGTCGCGGATCCTGCTTCGGGATCTT	38216	0.103668369941023	No Hit

✖ Adapter Content



✖ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CACACCC	13730	0.0	57.58284	1
CTAACCA	18280	0.0	52.654995	94
CCCTAAT	9200	0.0	45.826588	8
ACCCGTC	17570	0.0	45.31625	4
GGCCCTA	9350	0.0	45.29242	6
CACCCGT	17525	0.0	45.191235	3
CACGGGC	9490	0.0	44.372276	2
GTCGGGC	18320	0.0	43.845955	8
TCGGGCG	18845	0.0	42.59951	9
TGGGCTA	15045	0.0	41.643795	4
ACGGGCC	10255	0.0	41.616207	3
ACACCCG	19040	0.0	41.4926	2
CCGTCGG	20545	0.0	39.21182	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCACGGG	10705	0.0	38.995876	1
CGGACAG	28860	0.0	38.84225	4
GCCCTAA	11280	0.0	37.70959	7
GGGCTAT	16945	0.0	37.25176	5
GCCCTAG	14270	0.0	34.417873	84–85
CCCTAGT	14330	0.0	34.370853	86–87
GACGGAC	33245	0.0	34.35183	2

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FastQC Report

Summary

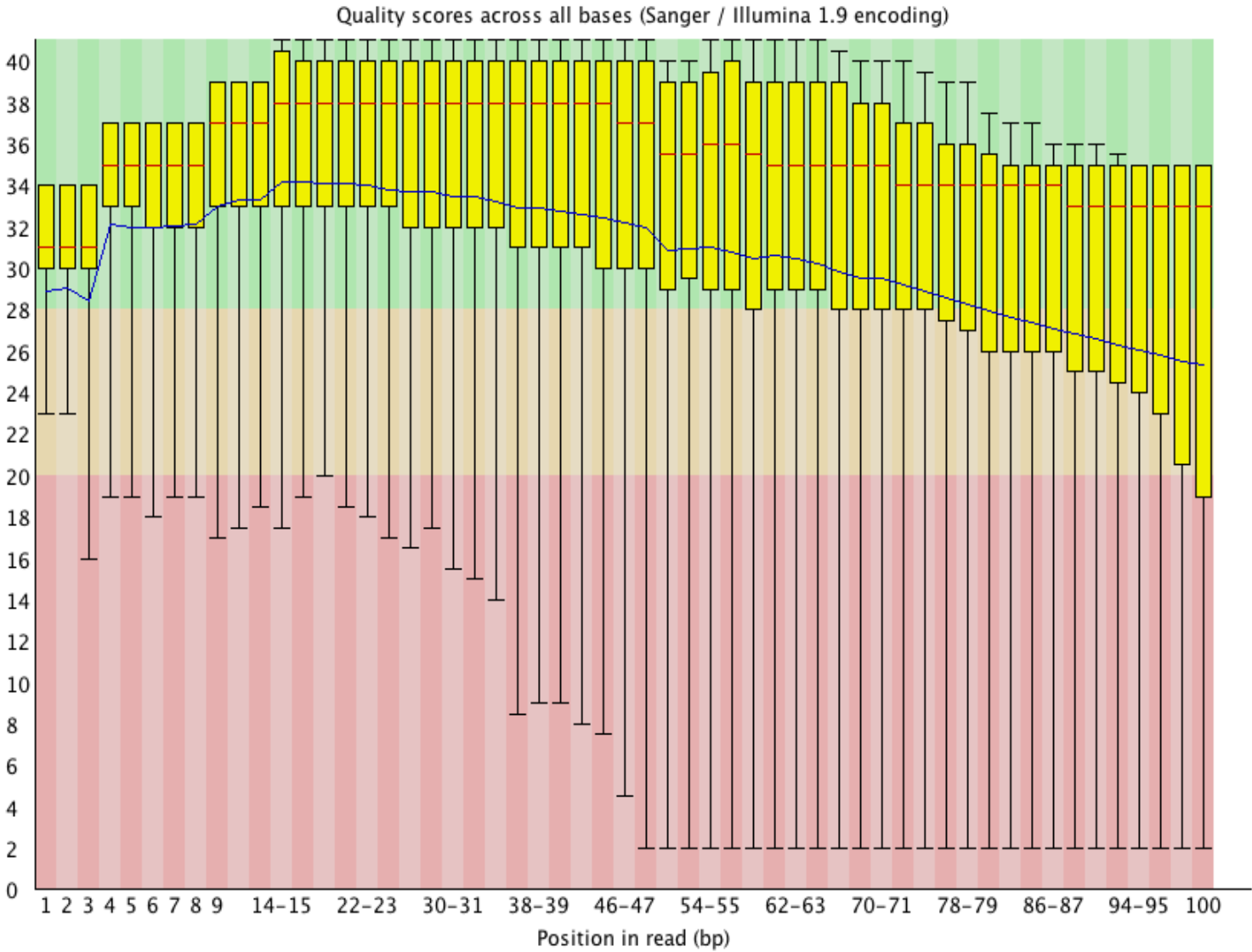
Fri 20 Mar 2015
2A_TTAGGC_L001_R2_001.fastq

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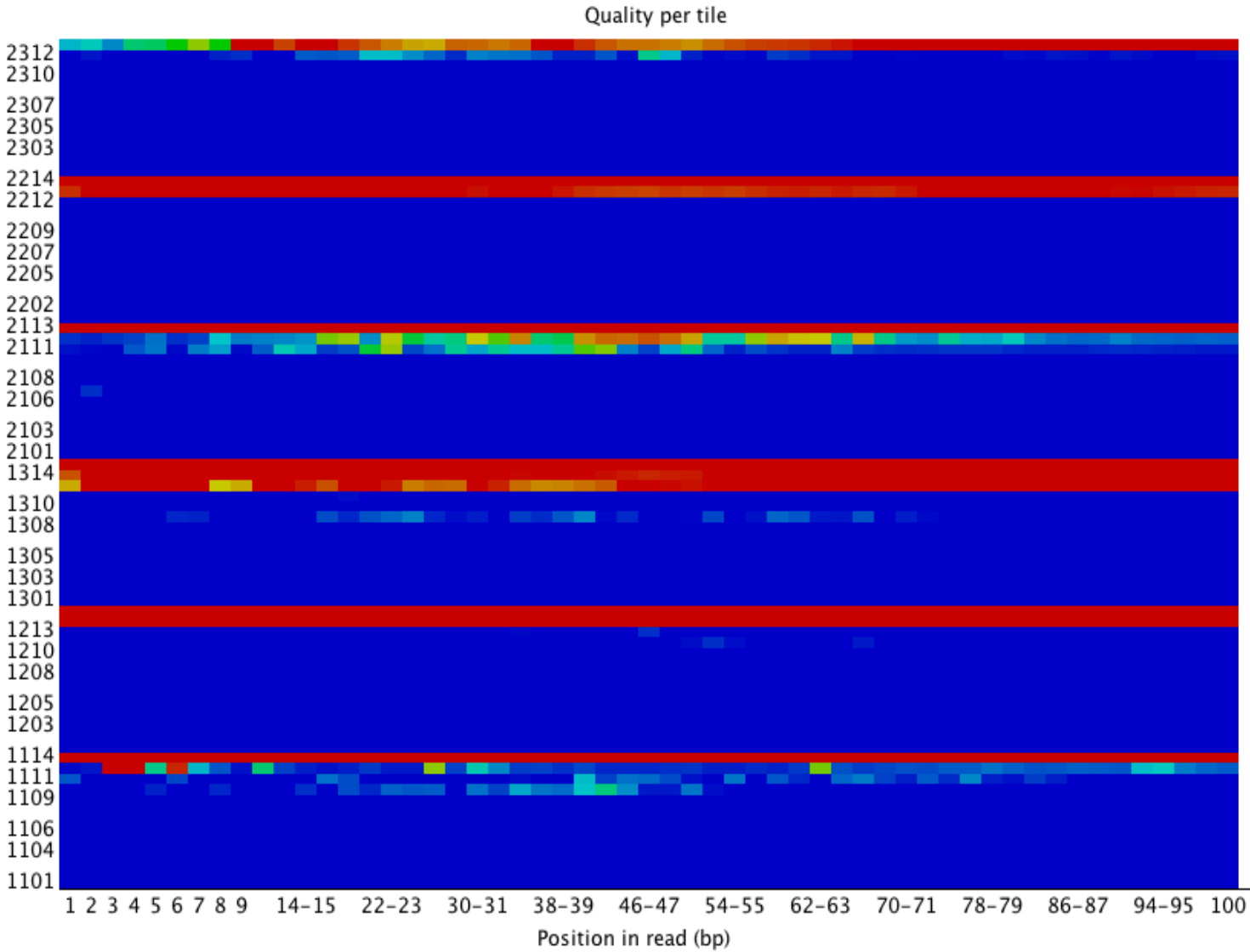
Basic Statistics

Measure	Value
Filename	2A_TTAGGC_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	36863703
Sequences flagged as poor quality	0
Sequence length	100
%GC	39

Per base sequence quality

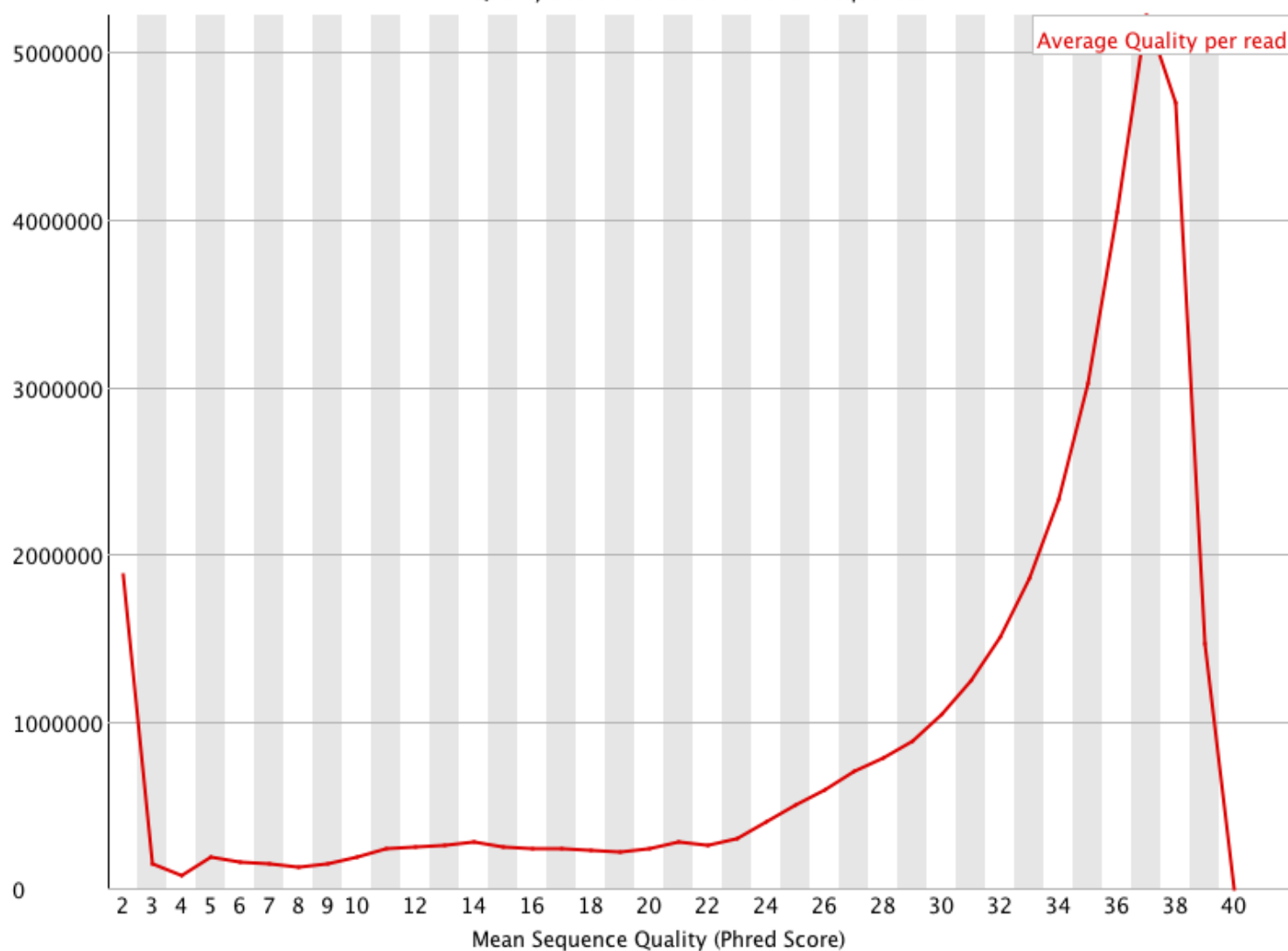


✖ Per tile sequence quality



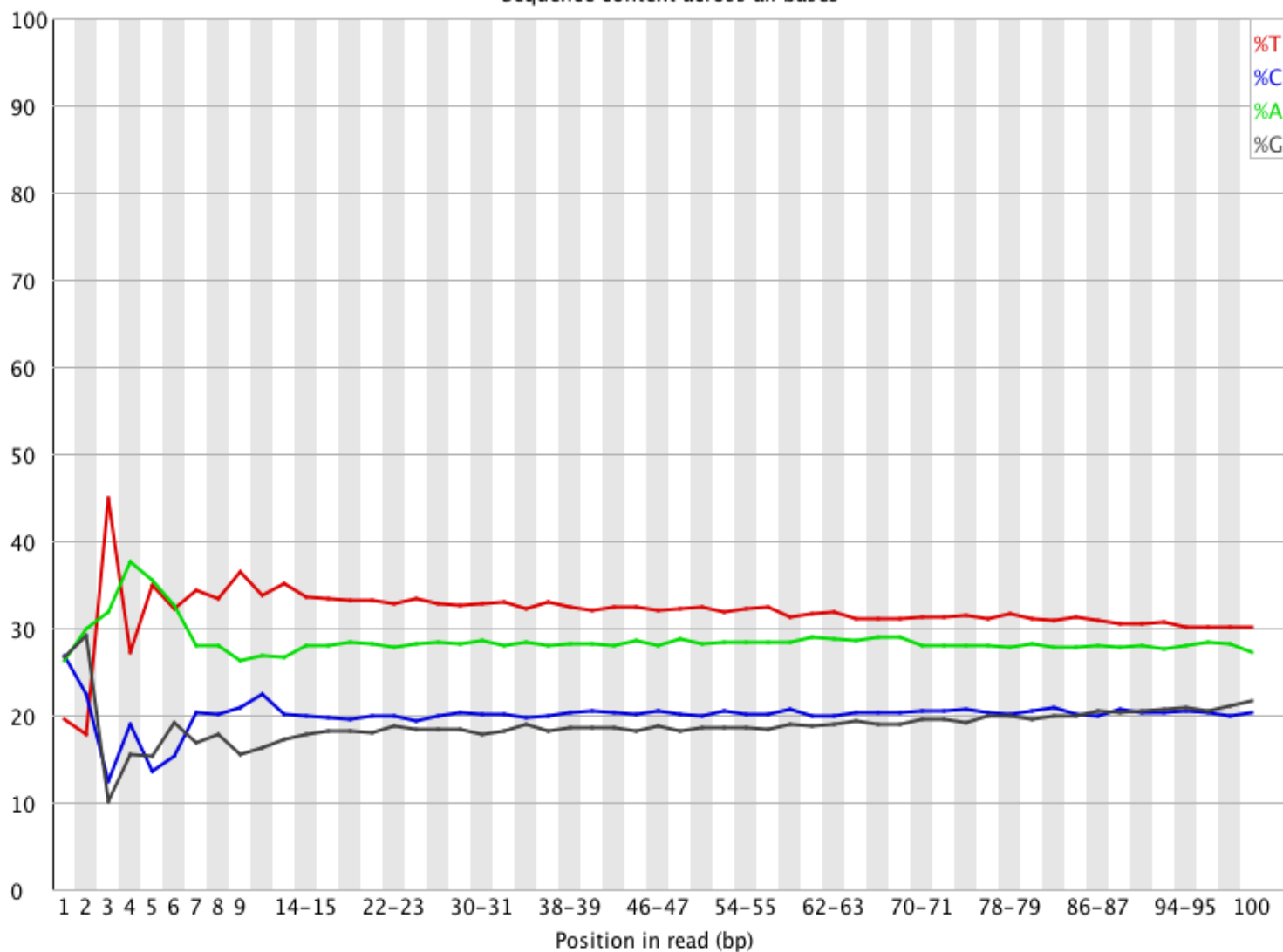
 Per sequence quality scores

Quality score distribution over all sequences



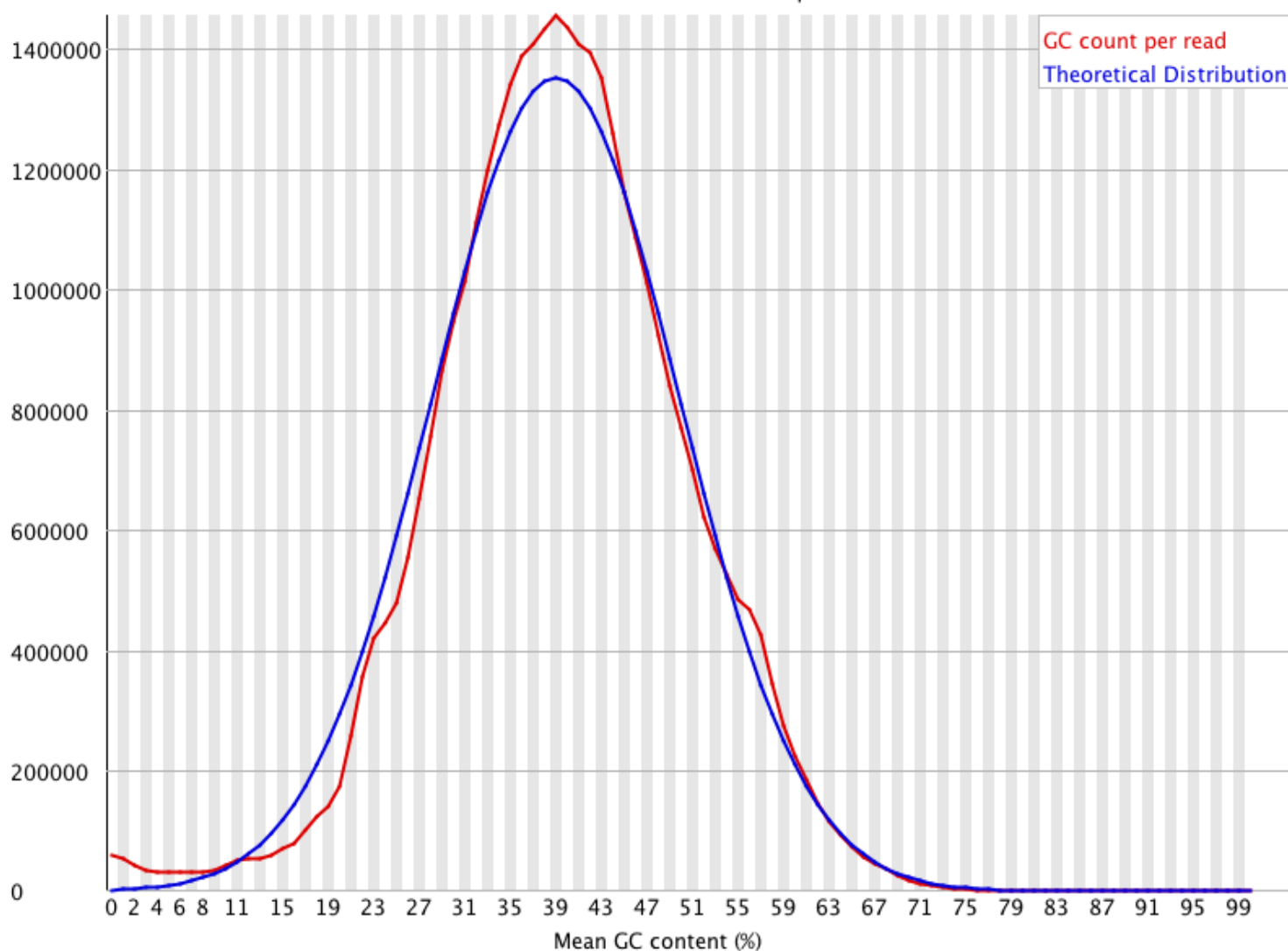
Per base sequence content

Sequence content across all bases

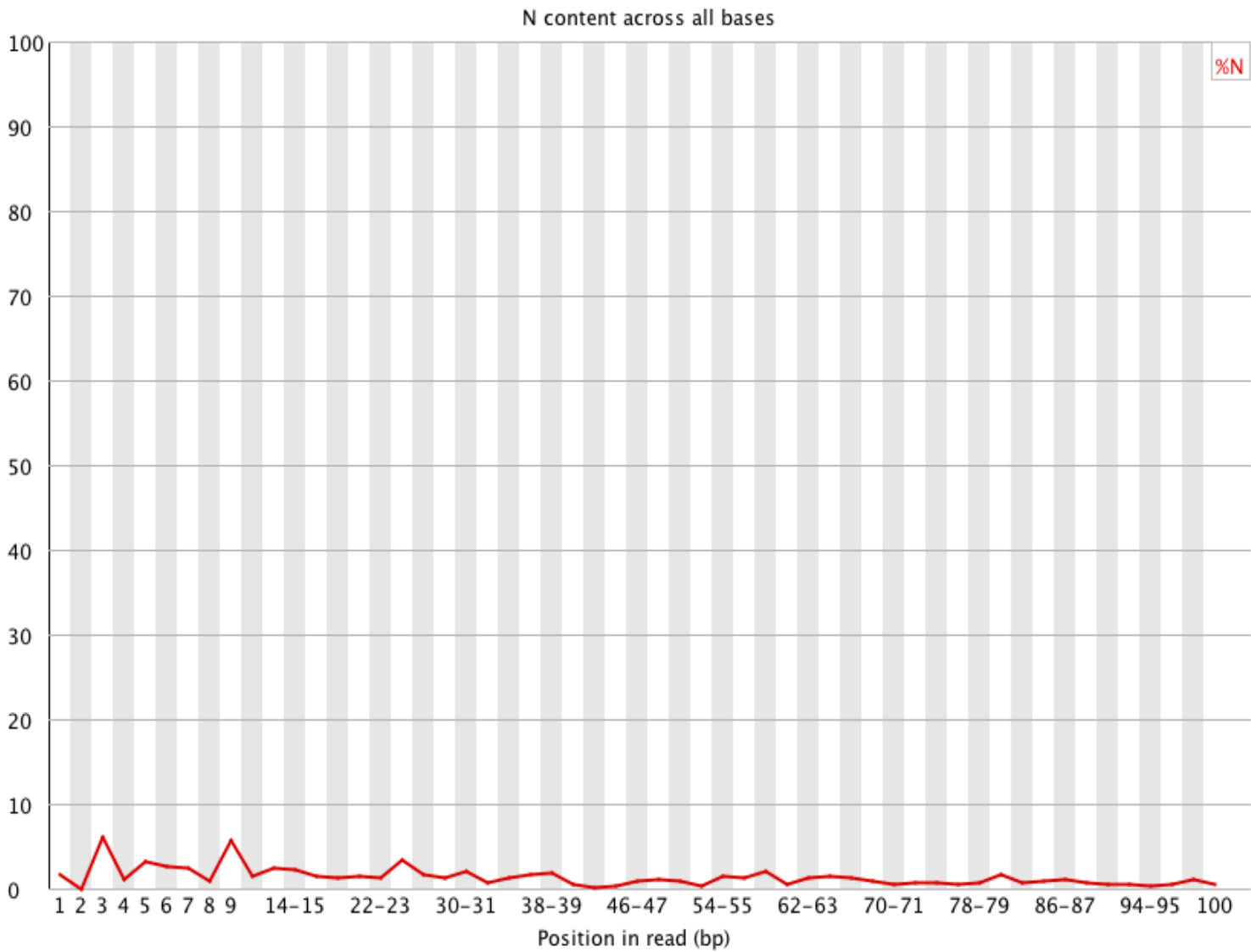


Per sequence GC content

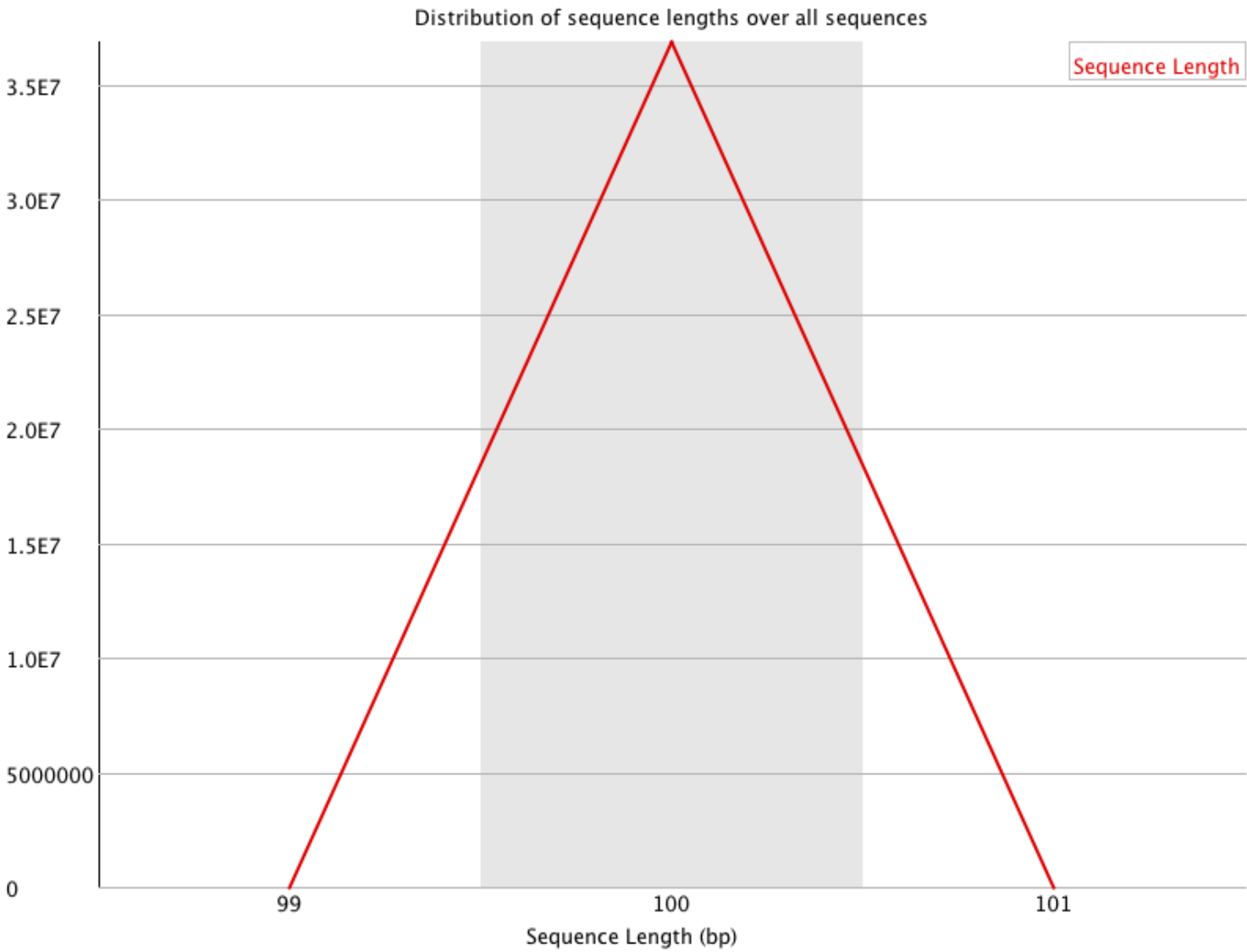
GC distribution over all sequences



! Per base N content



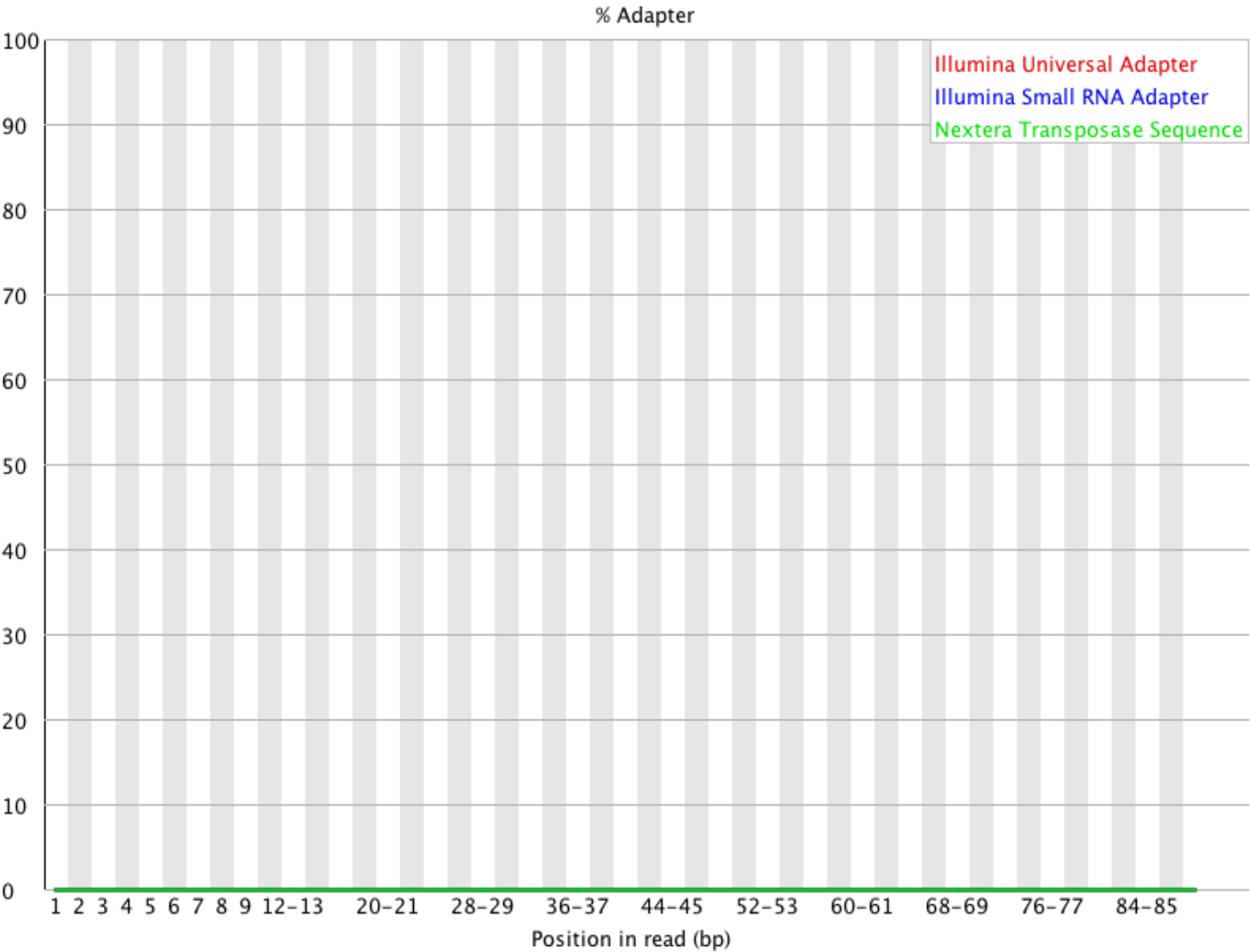
✔ Sequence Length Distribution



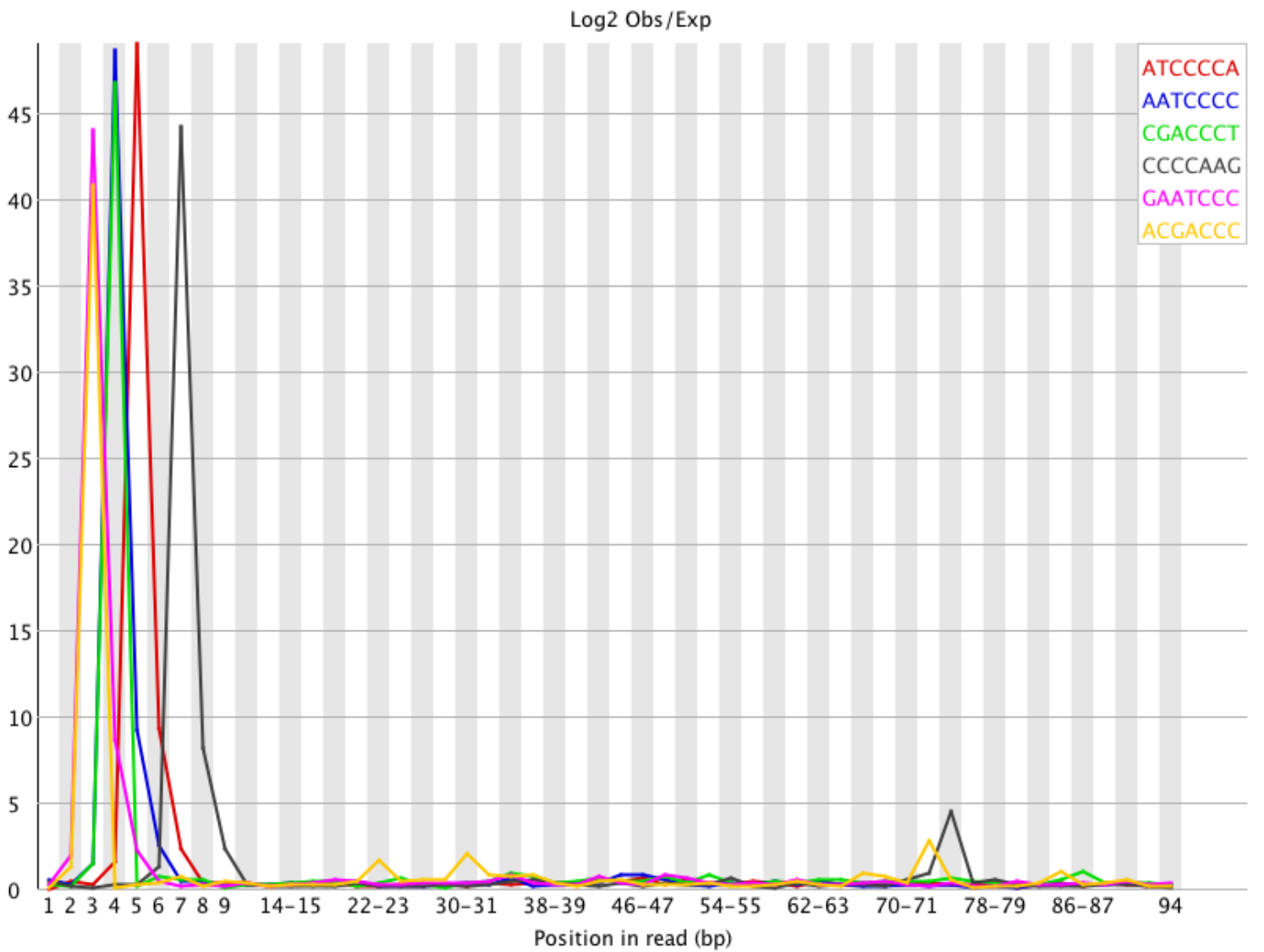
 Sequence Duplication Levels

[illegible]

 Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCCCA	16205	0.0	49.04256	5
AATCCCC	16480	0.0	48.75123	4
CGACCCT	9720	0.0	46.863453	4
CCCCAAG	17985	0.0	44.24119	7
GAATCCC	18240	0.0	44.114334	3
ACGACCC	11235	0.0	40.894535	3
GACCCTC	11215	0.0	40.745464	5
CCCTCAG	11350	0.0	40.72736	7
ACCCTCA	11330	0.0	40.37448	6
CCAAGCC	20385	0.0	39.012012	9
CCCAAGC	20630	0.0	38.33546	8
TGCCCCG	12390	0.0	37.386646	7
TCCCCAA	21380	0.0	37.19444	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GCCCGCC	12660	0.0	37.047043	8
CGAATCC	23000	0.0	35.412266	2
ACAGACG	20385	0.0	35.091846	94
CTGCCCC	13445	0.0	34.741062	6
CCCGCCG	14265	0.0	32.779617	9
CACCCCG	14015	0.0	30.611841	68-69
GCTGCCC	15390	0.0	30.507229	5

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FastQC Report

Summary

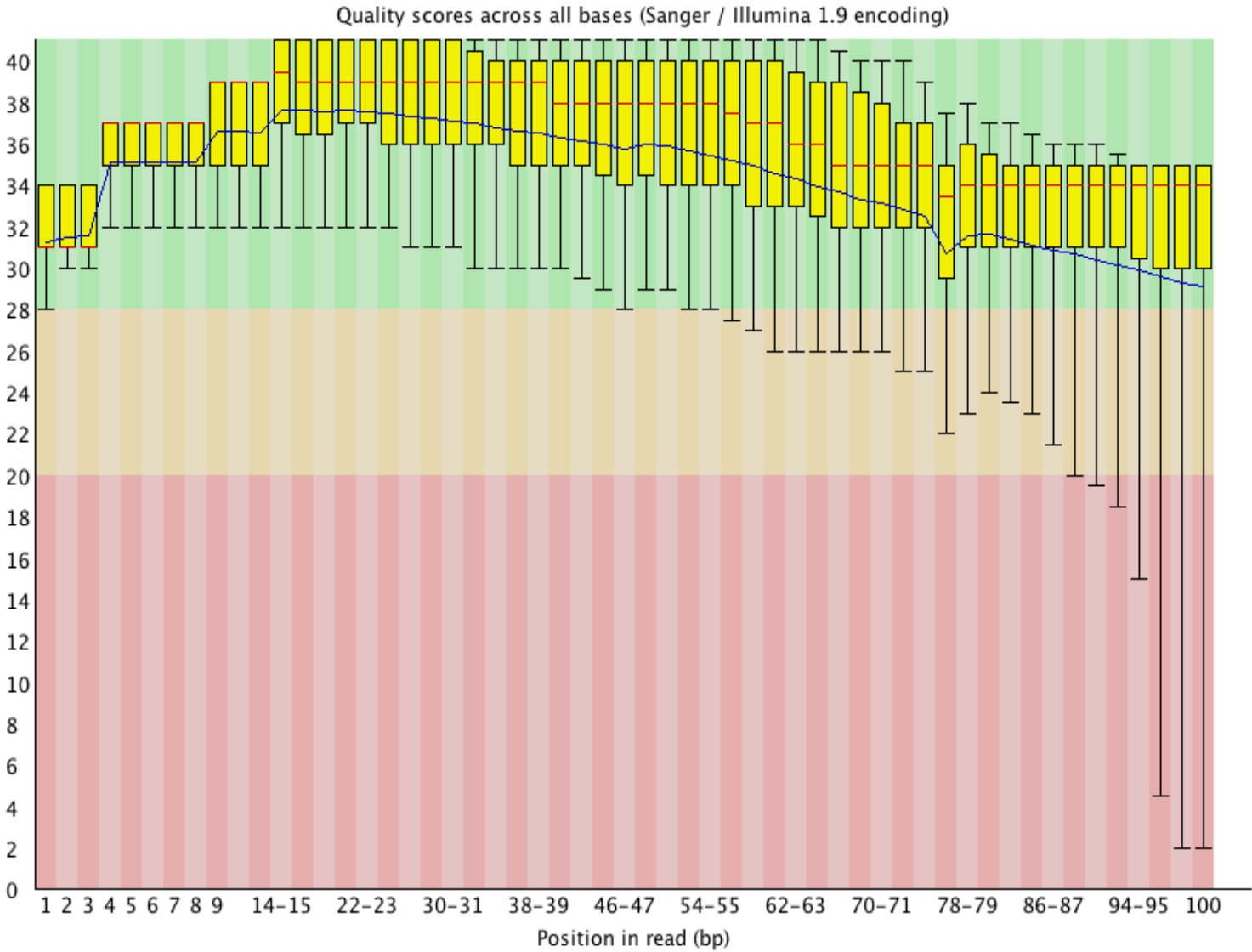
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2P_TGACCA_L001_R1_001.fastq

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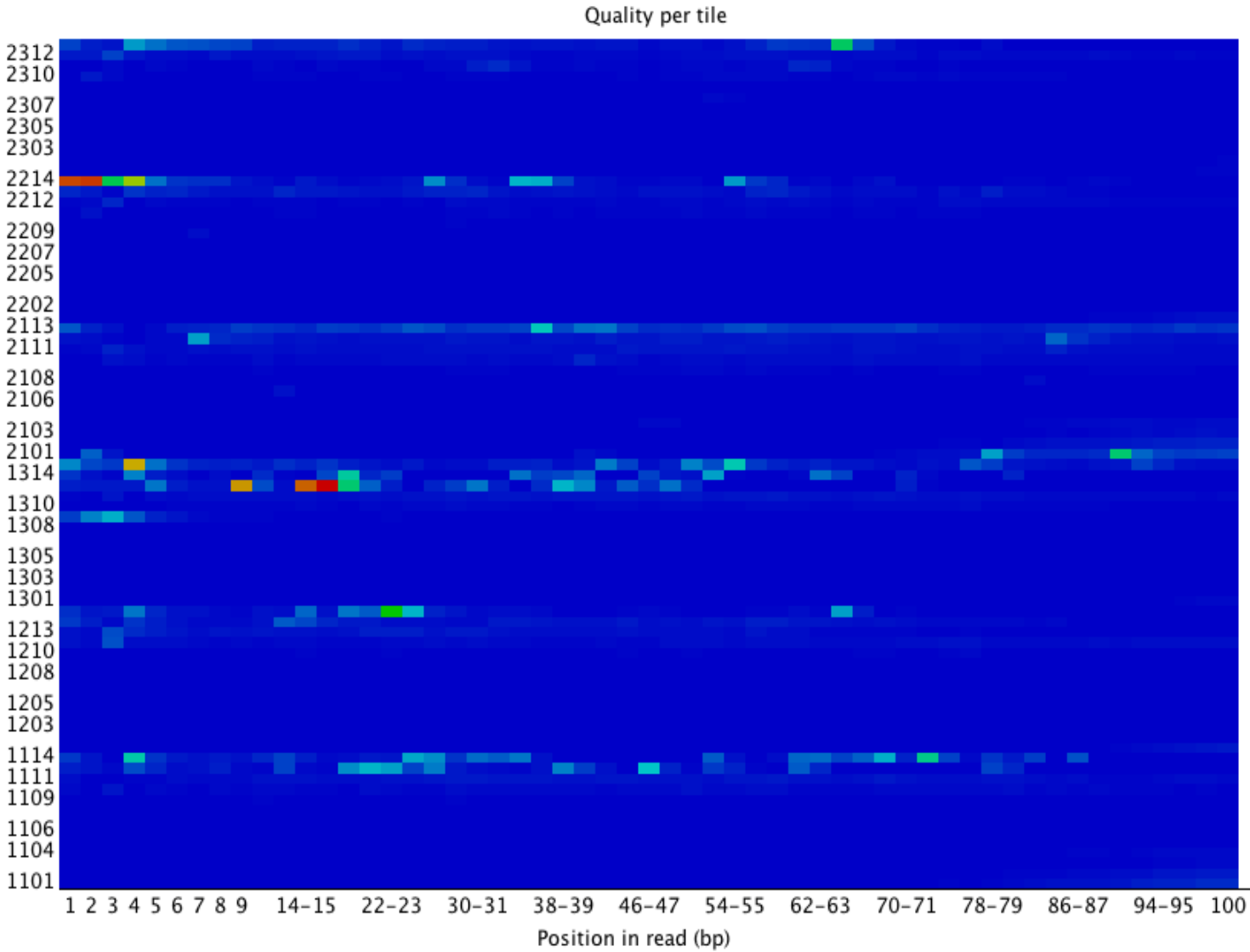
Basic Statistics

Measure	Value
Filename	2P_TGACCA_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	35860572
Sequences flagged as poor quality	0
Sequence length	100
%GC	39

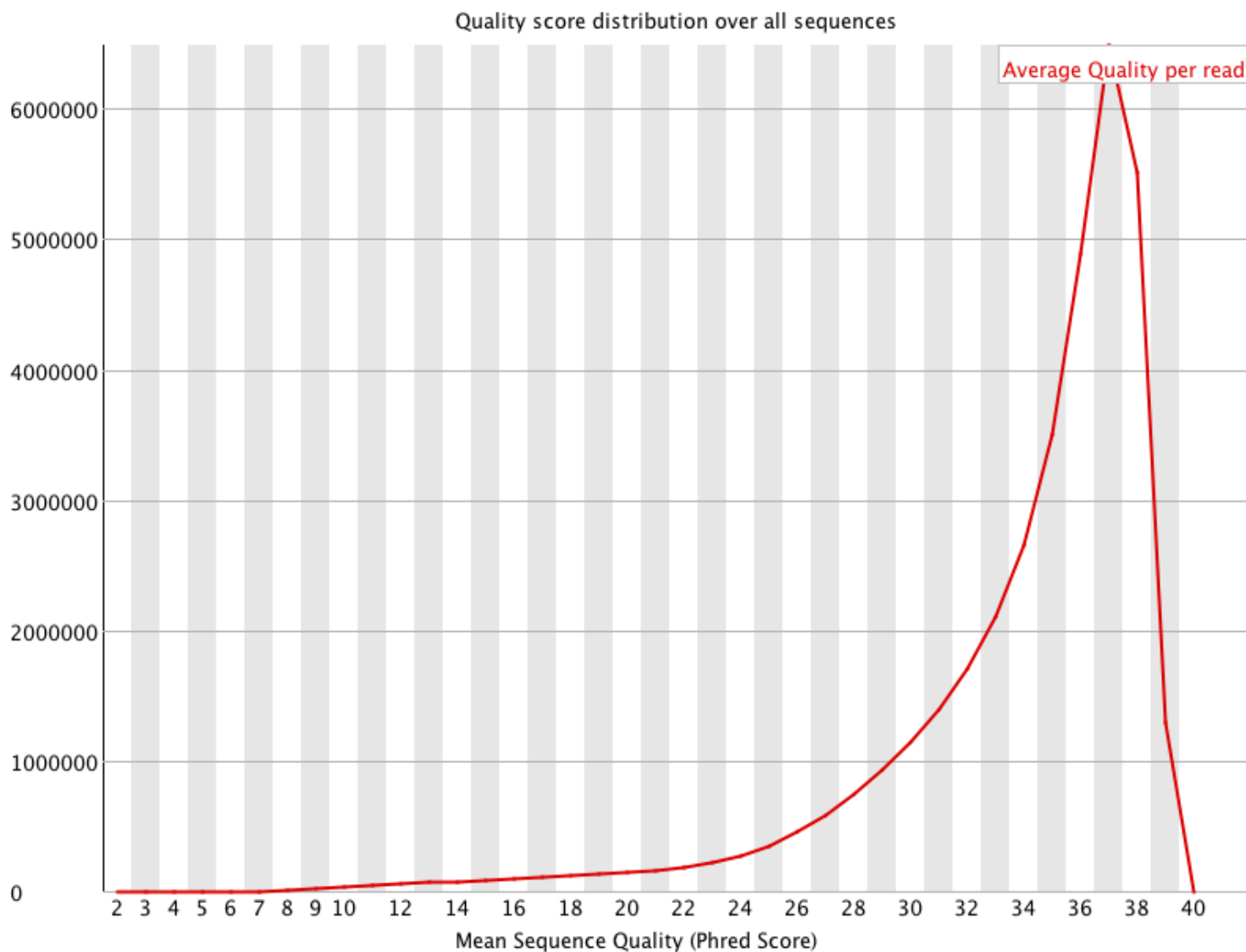
Per base sequence quality



✖ Per tile sequence quality

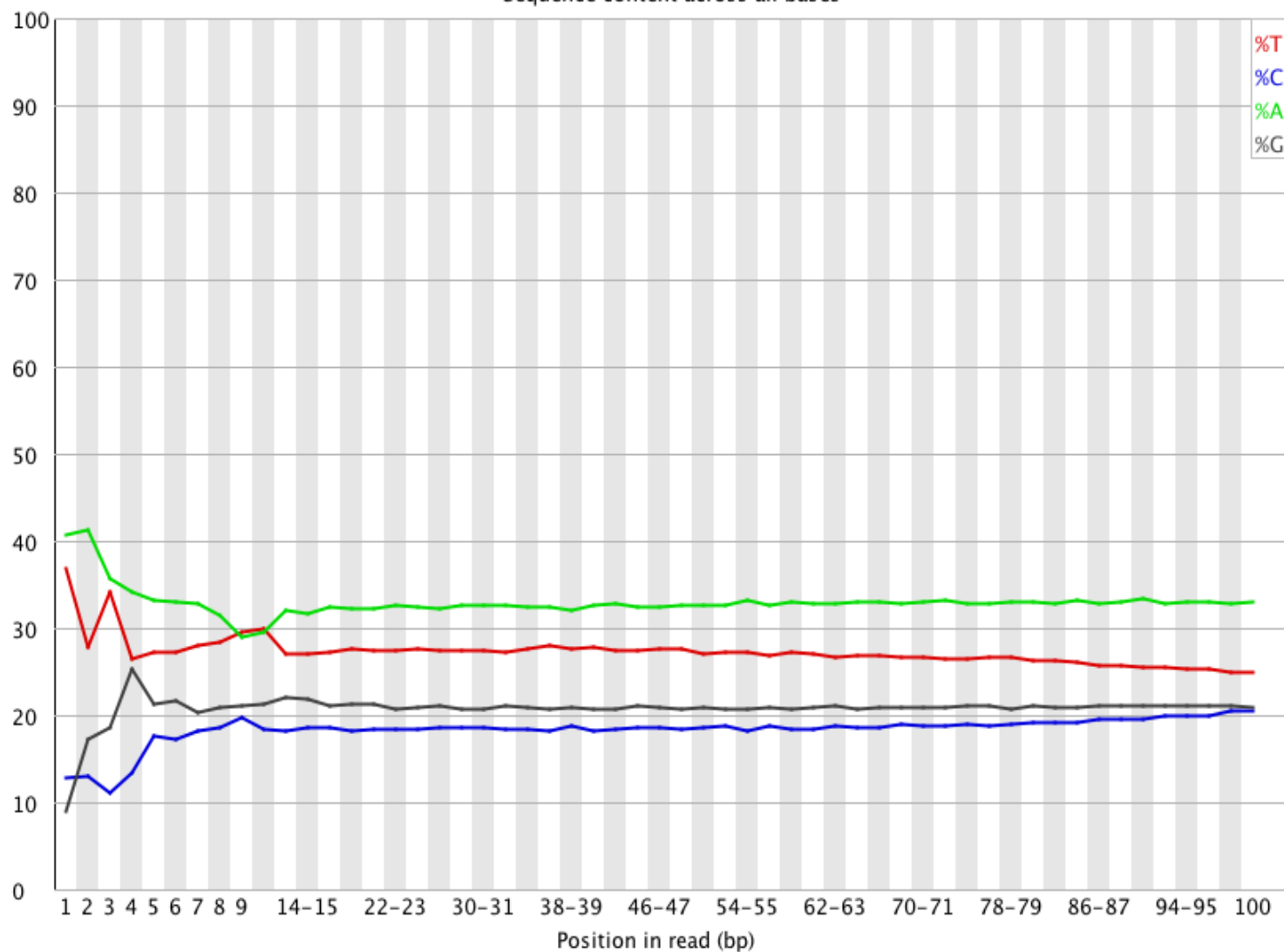


 Per sequence quality scores

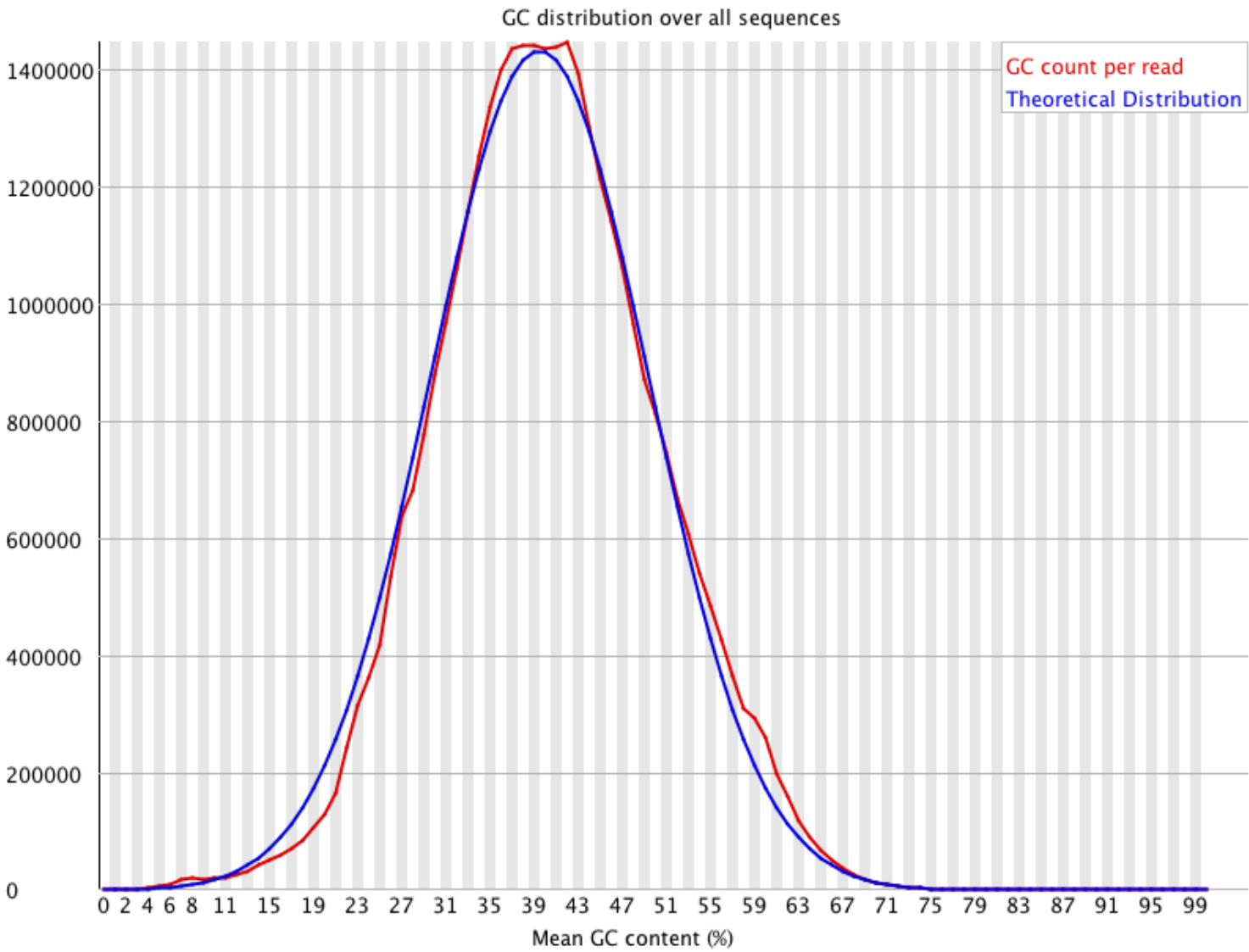


✖ Per base sequence content

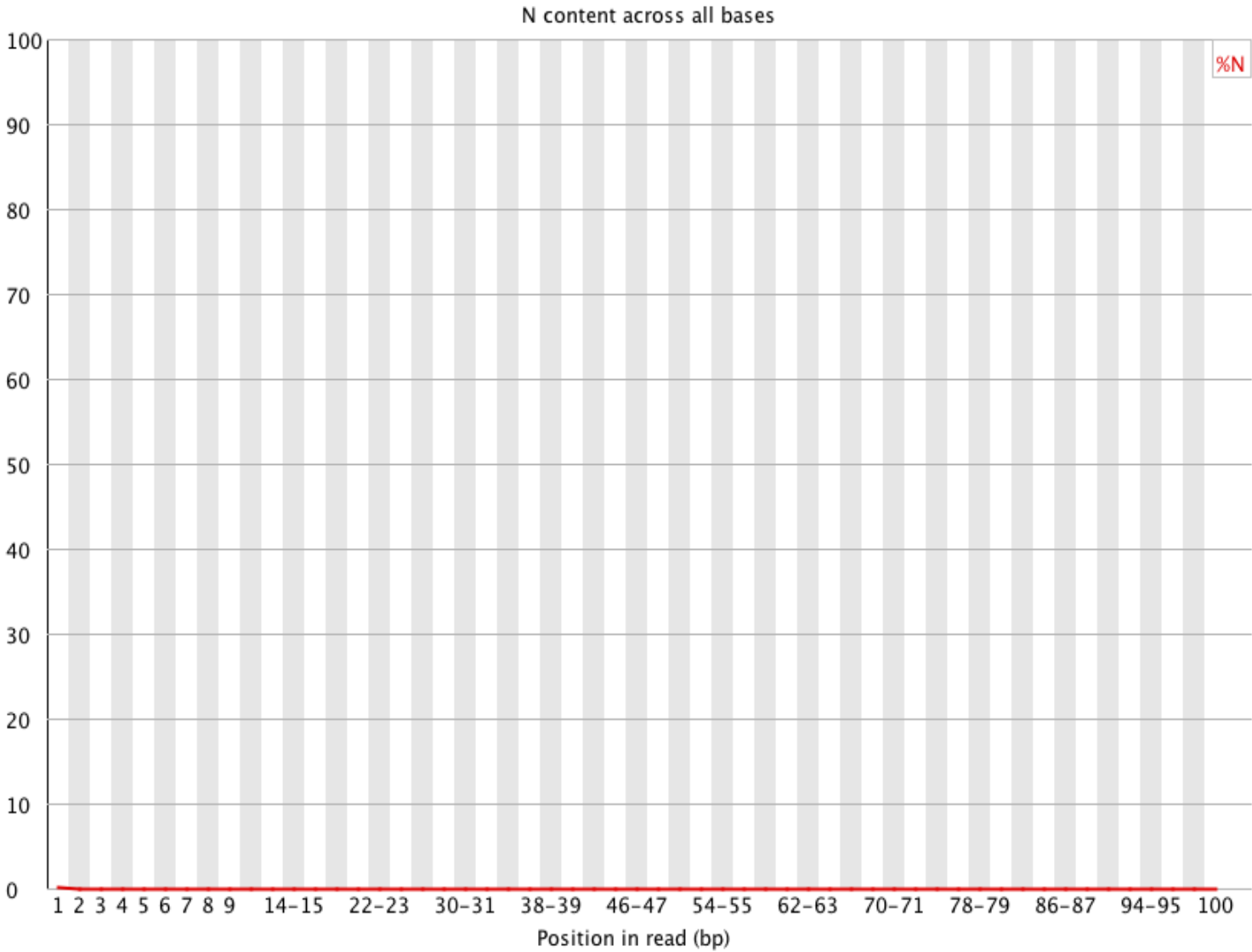
Sequence content across all bases



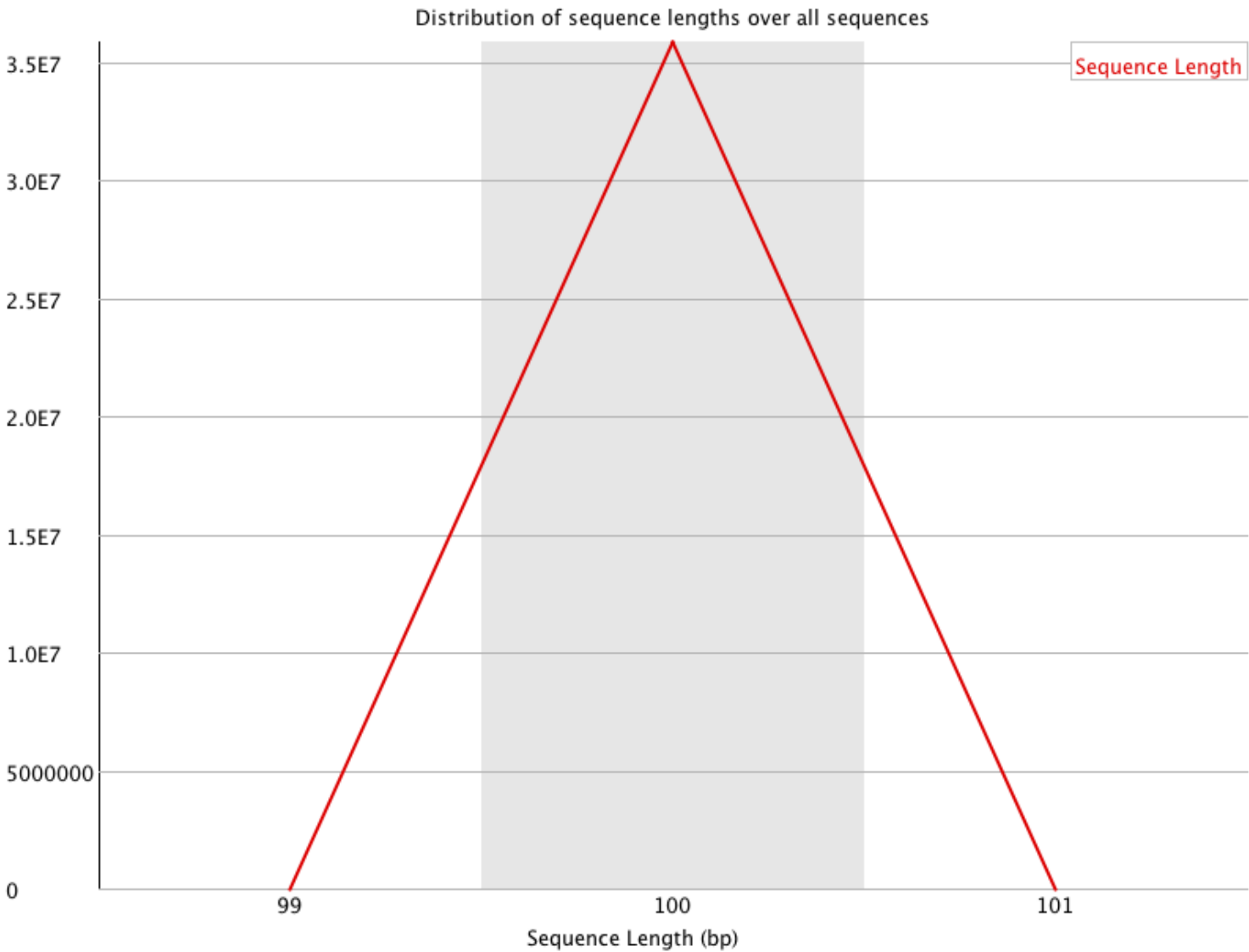
Per sequence GC content



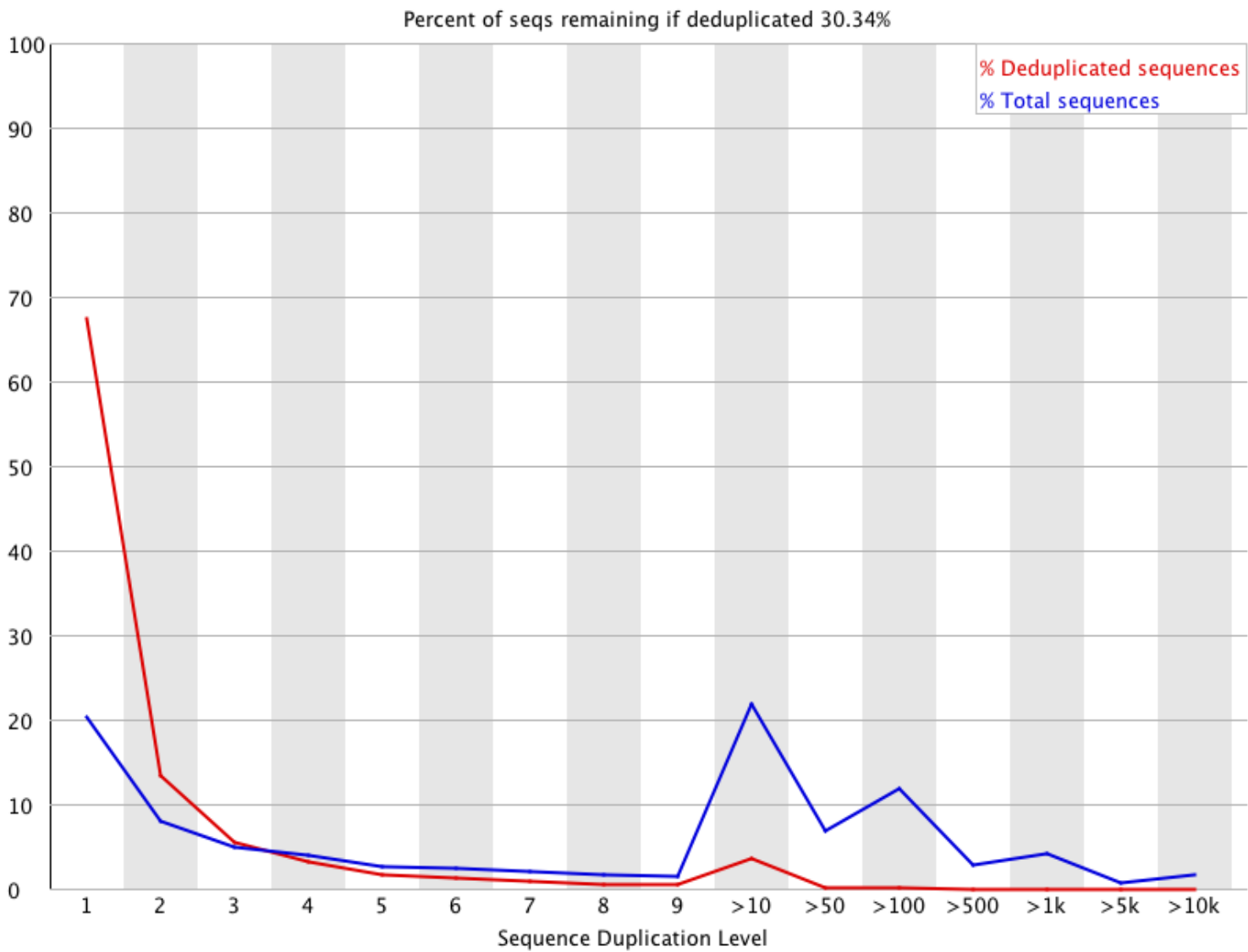
✔ Per base N content



 Sequence Length Distribution



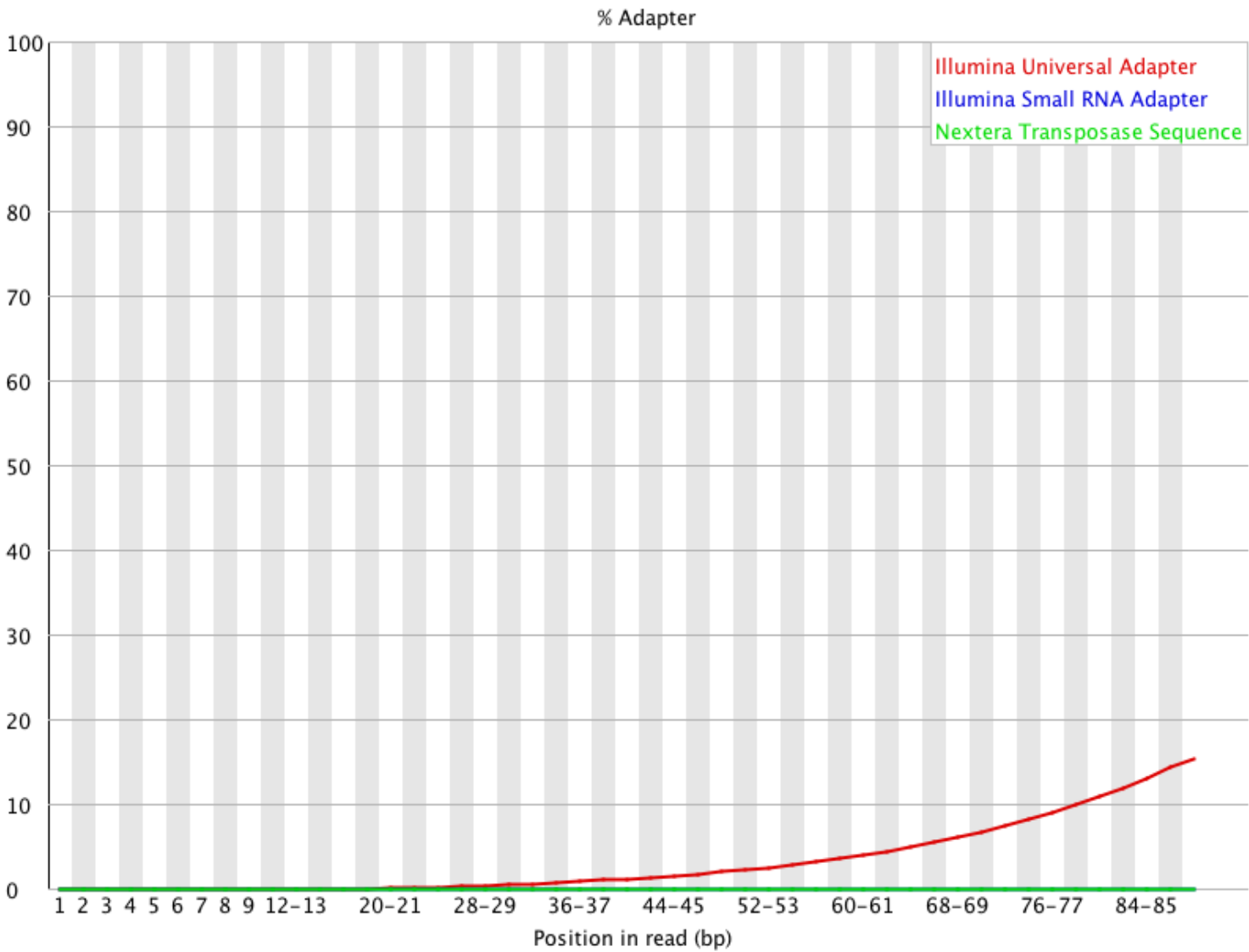
 Sequence Duplication Levels



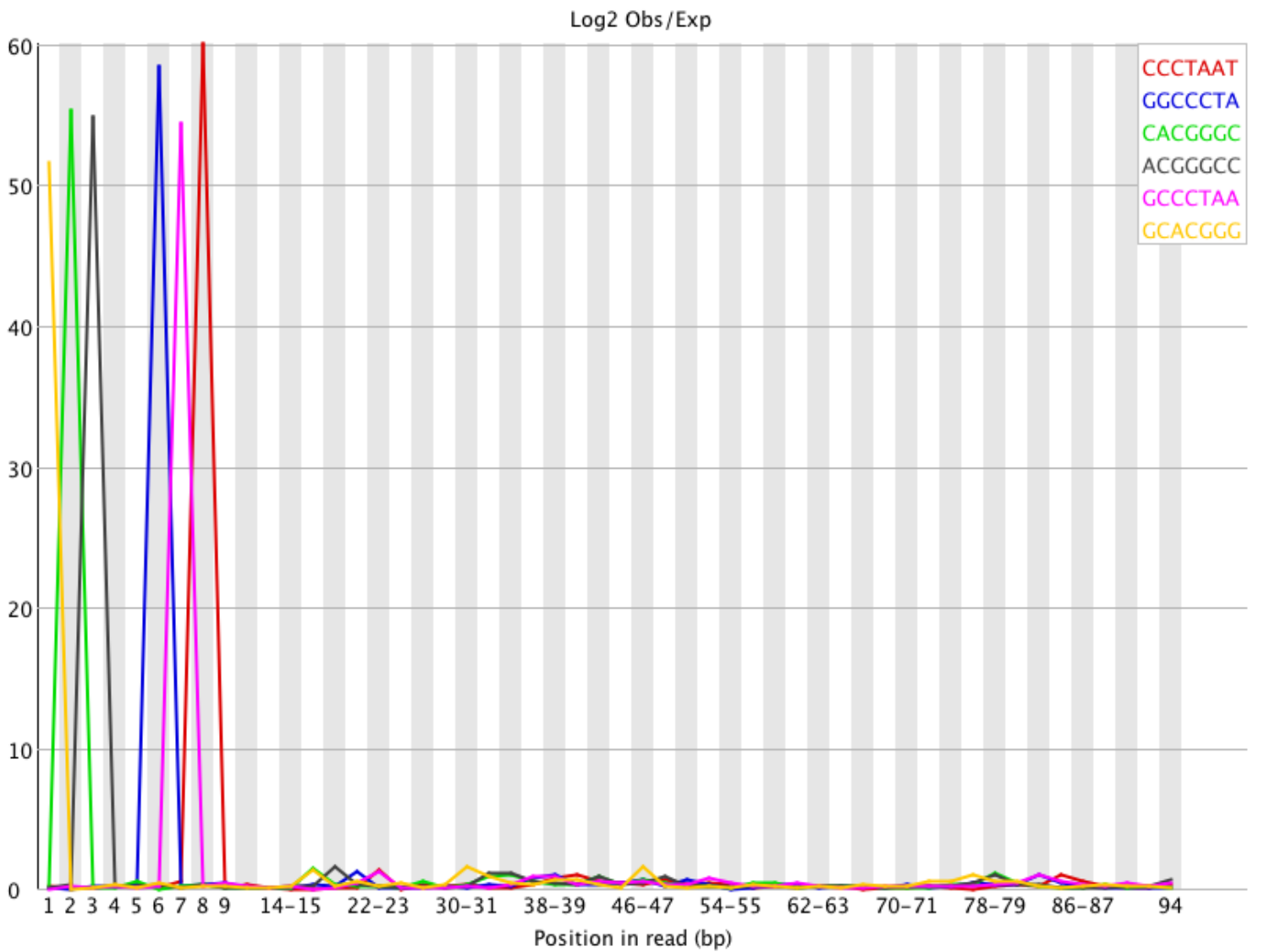
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
GCACGGGCCCTAATTGCCGTACGGAGTCGCGGATCCTGCTTCGGGATCTT	74619	0.20808089731530216	No Hit
AGACGGACAGAAGCGAAAGCATTTCGCCAAAAATGTTTTTCATTAATCAAGA	56798	0.1583856498440683	No Hit
CACACCCGTCGGGCGAAAGGGAATCCGGTTCCTATTCCGGAACCCGGCAG	43497	0.12129477466226696	No Hit

✖ Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCCTAAT	14465	0.0	60.016346	8
GGCCCTA	14865	0.0	58.43299	6
CACGGGC	15595	0.0	55.360043	2
ACGGGCC	15775	0.0	54.853645	3
GCCCTAA	15985	0.0	54.368248	7
GCACGGG	16670	0.0	51.6651	1
CCTAATT	20070	0.0	43.302265	9
CACACCC	11490	0.0	41.29202	1
CGGGCCC	21745	0.0	39.923496	4
CTAACCA	13860	0.0	39.368942	94
GGGCCCT	22365	0.0	38.92182	5
ACCCGTC	12665	0.0	38.336834	4
TCGGGCG	13155	0.0	37.051773	9

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CACCCGT	13020	0.0	36.713947	3
GTCGGGC	14205	0.0	34.809326	8
ACACCCG	14650	0.0	32.72165	2
CCGTCGG	15145	0.0	32.462616	6
CTAGCGG	12660	0.0	32.00157	70–71
GCCCTAG	9050	0.0	31.081621	84–85
CCCTAGT	9050	0.0	31.054766	86–87

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Summary

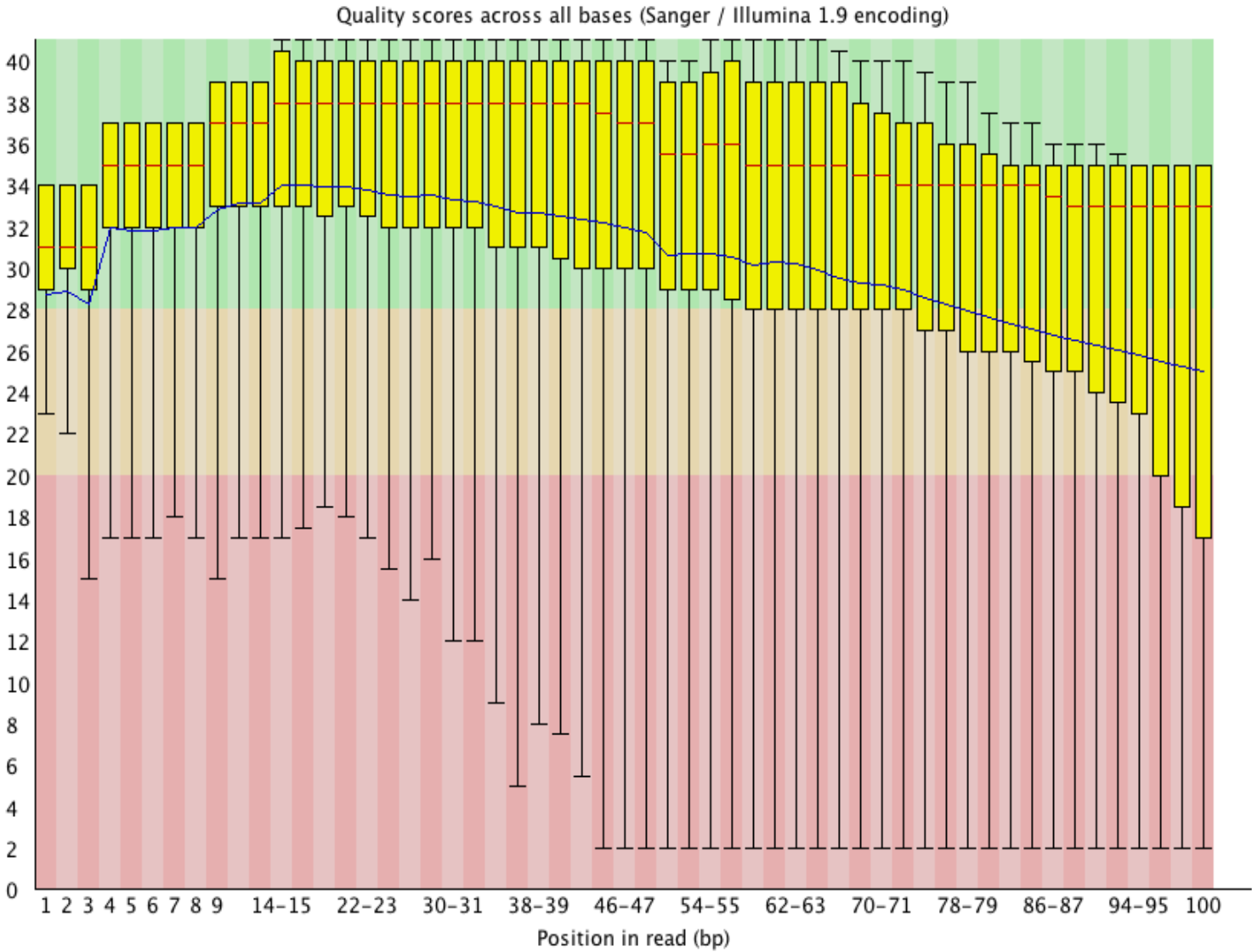
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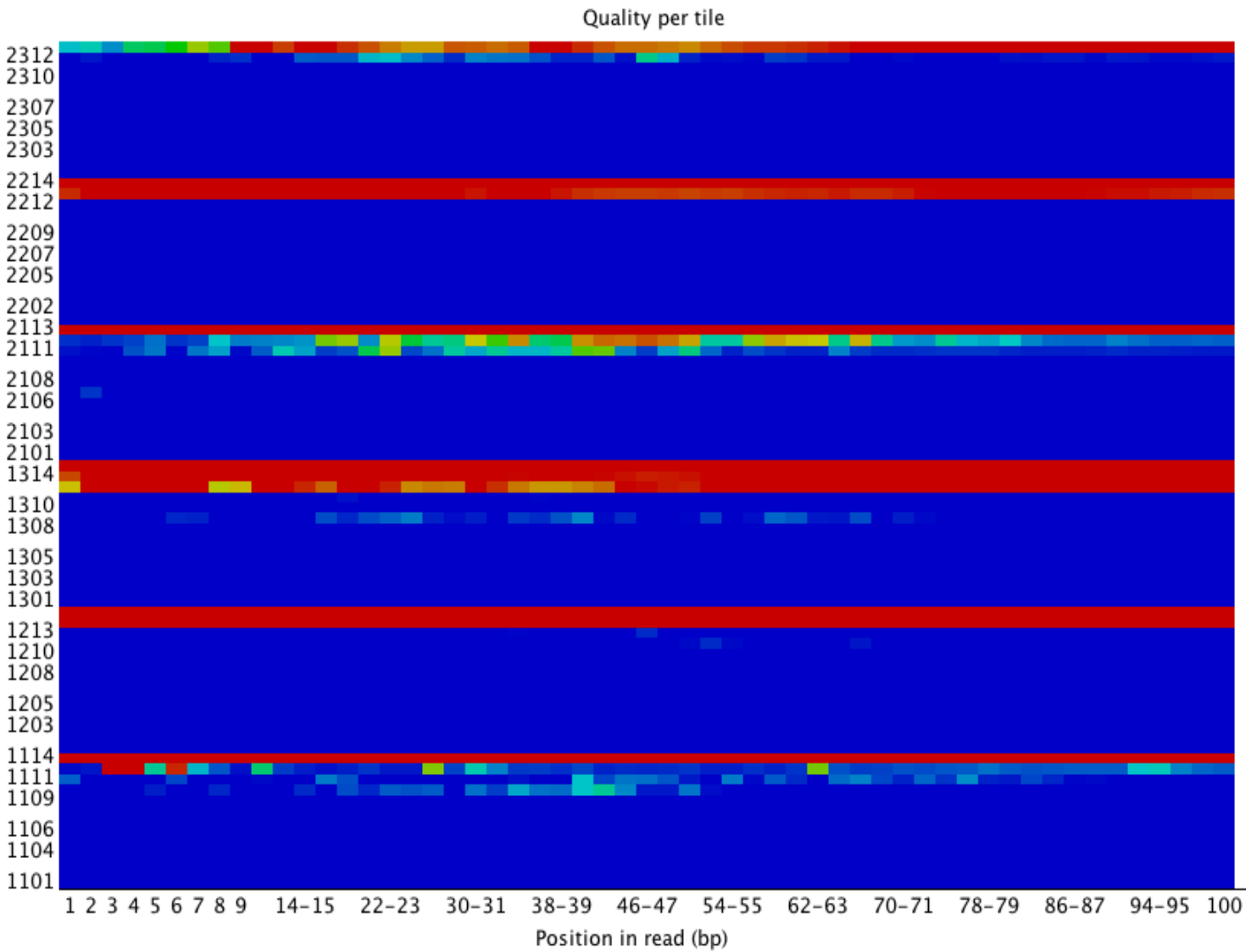
Basic Statistics

Measure	Value
Filename	2P_TGACCA_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	35860572
Sequences flagged as poor quality	0
Sequence length	100
%GC	39

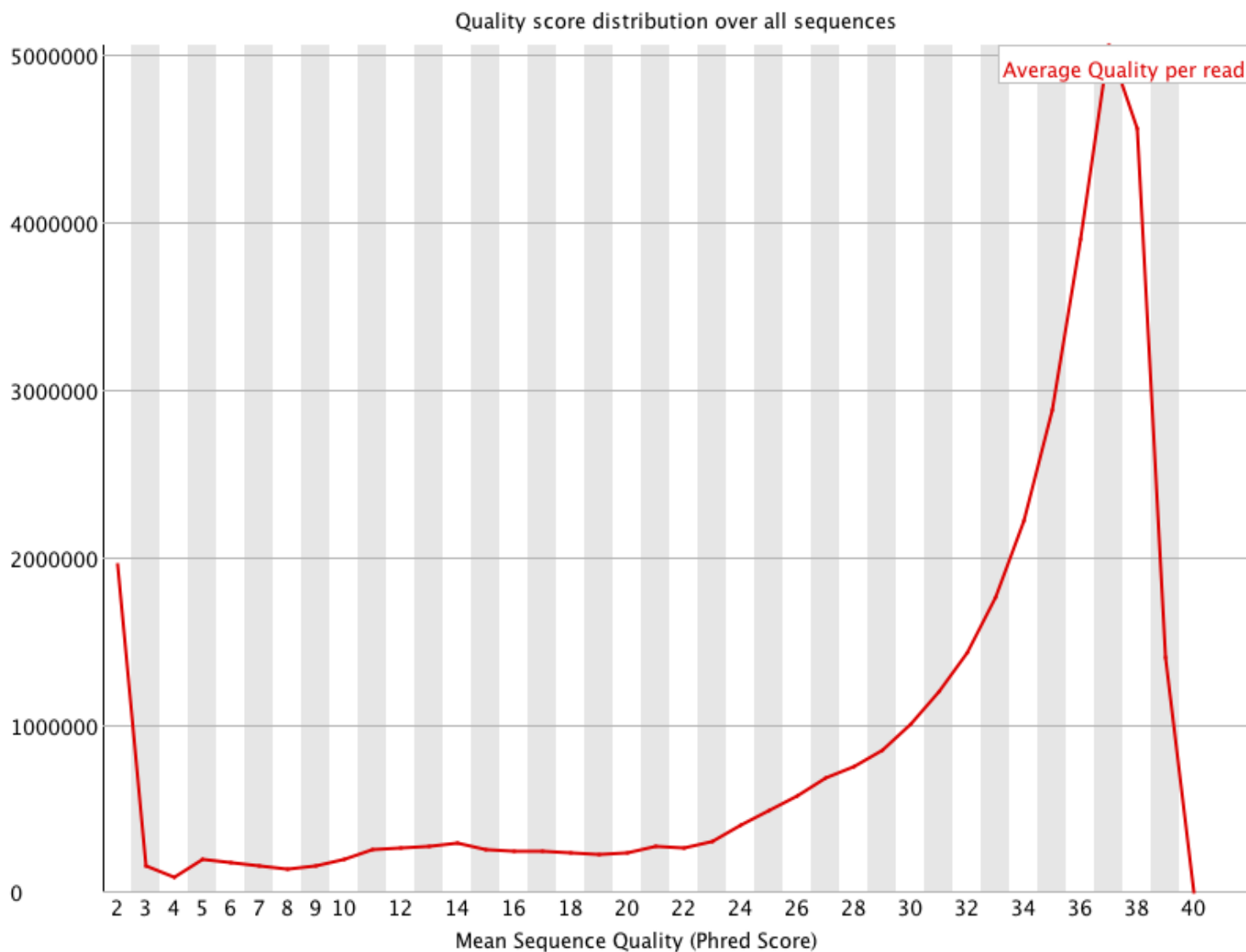
Per base sequence quality



✖ Per tile sequence quality

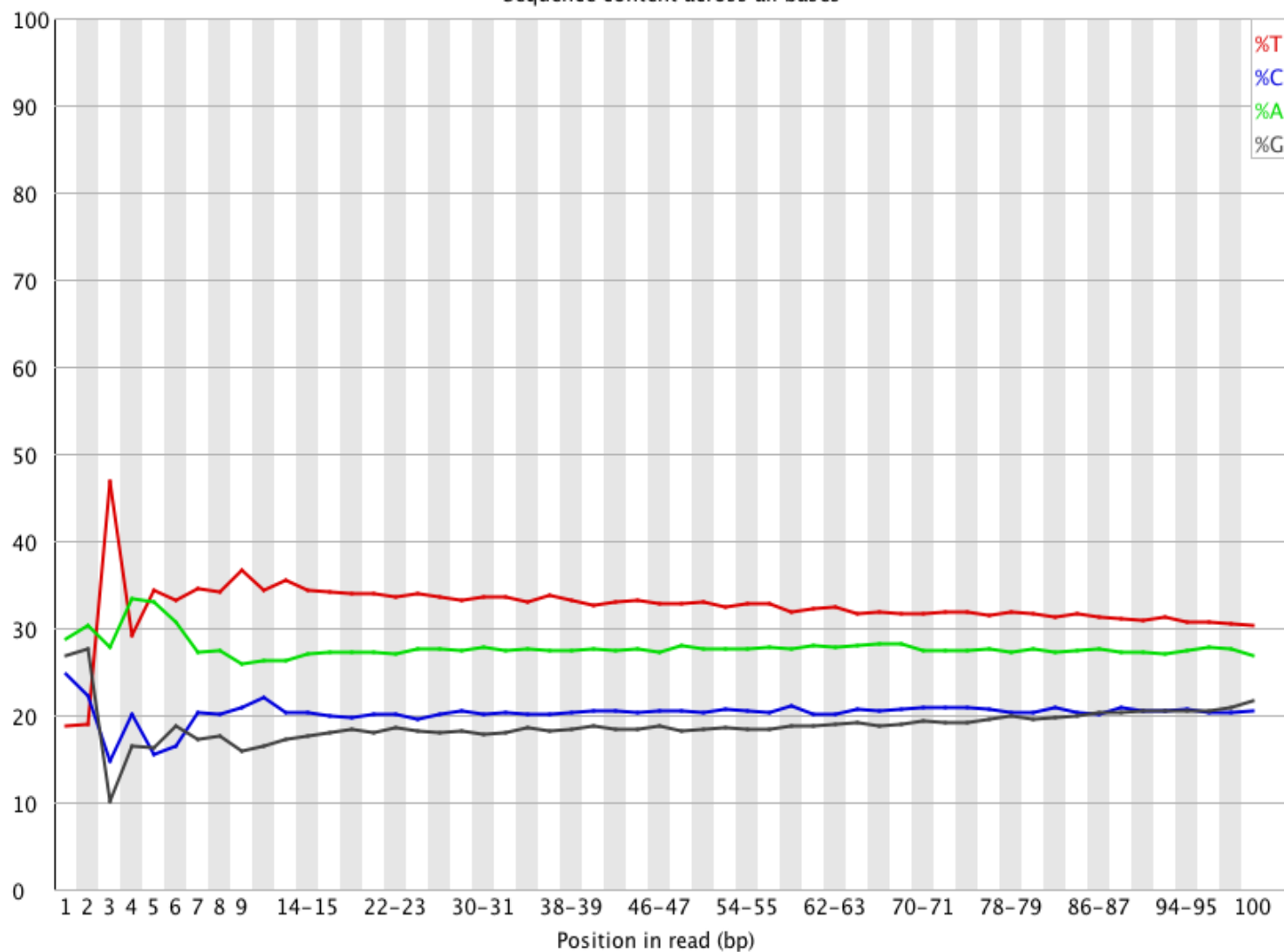


 Per sequence quality scores

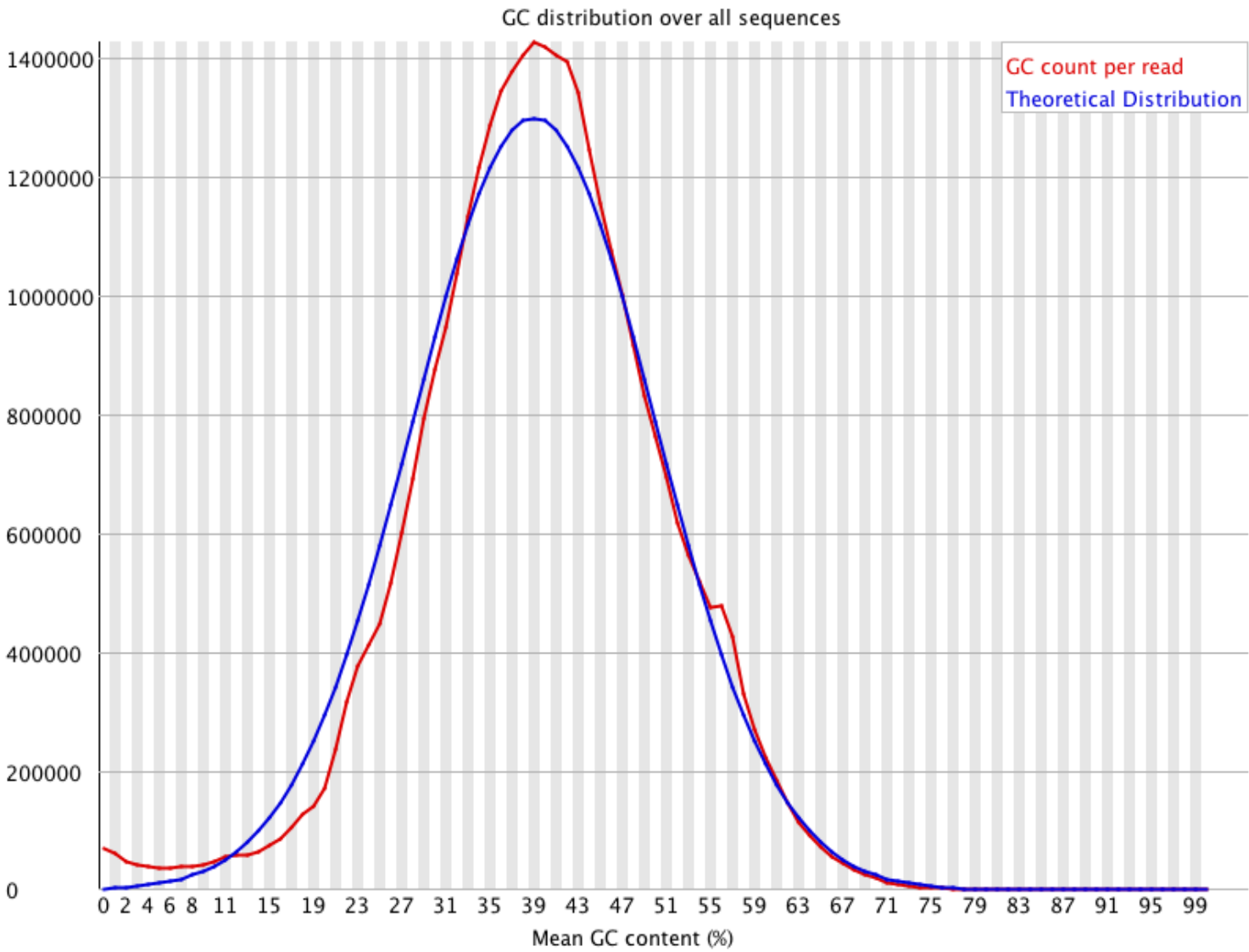


✖ Per base sequence content

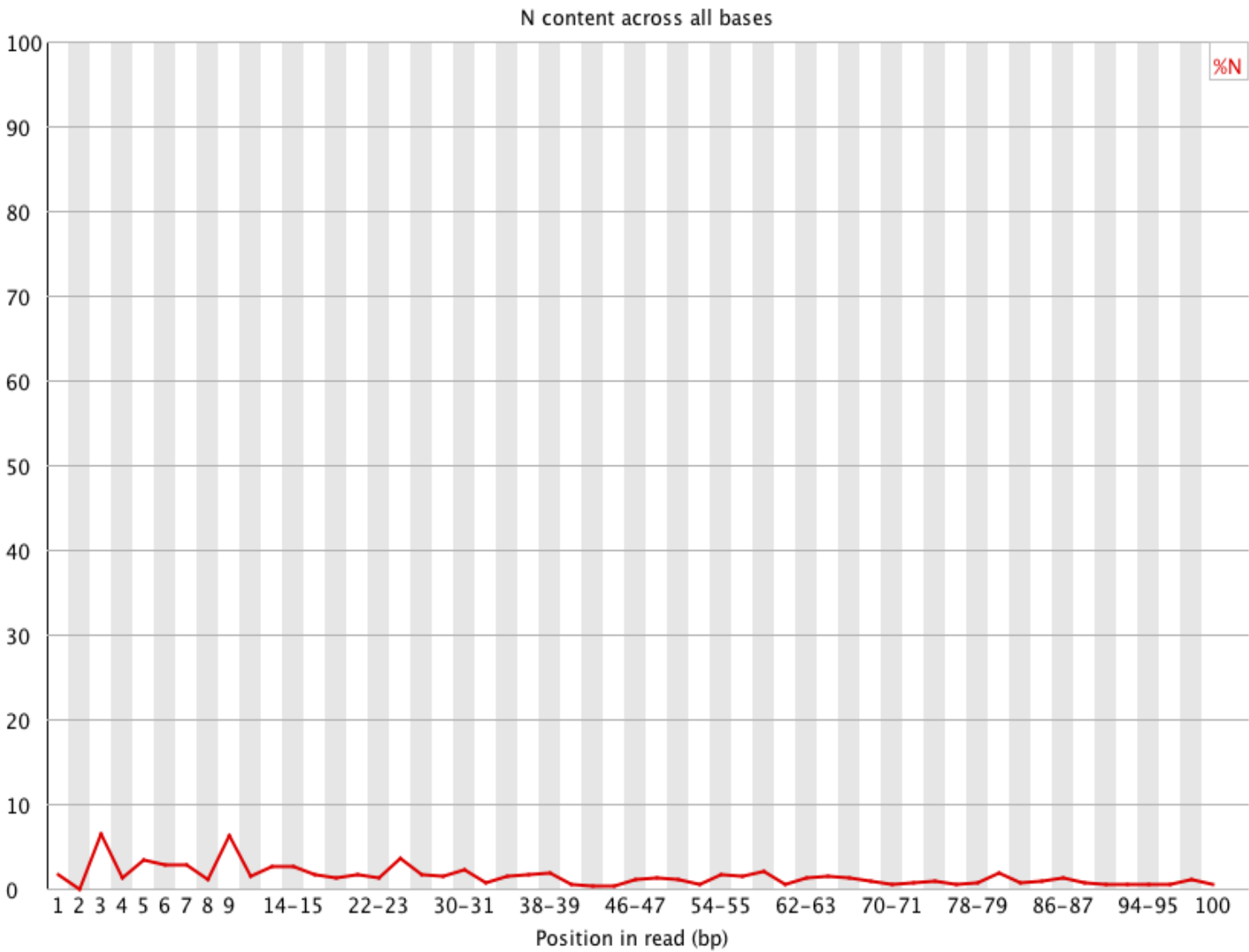
Sequence content across all bases



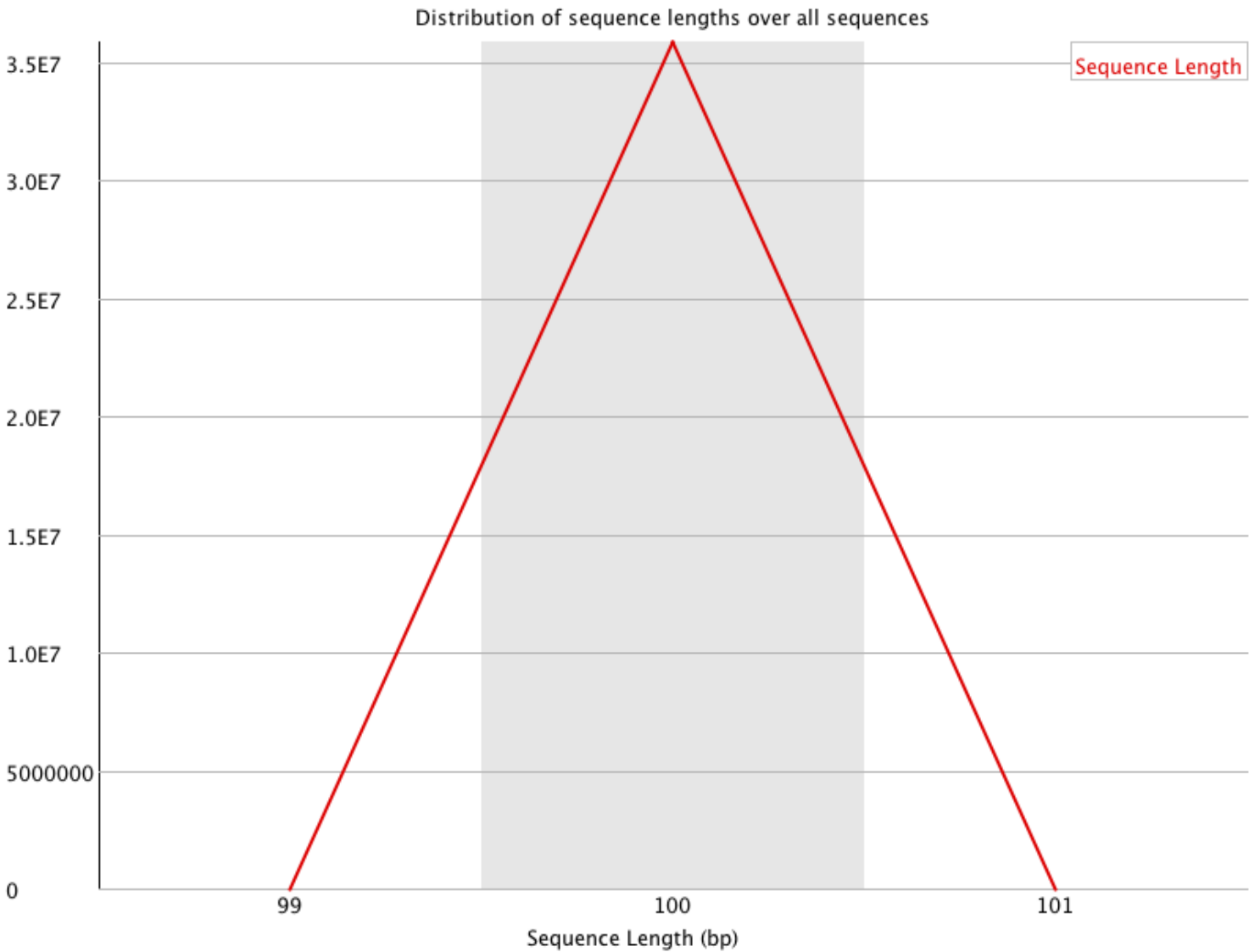
Per sequence GC content



! Per base N content



Sequence Length Distribution

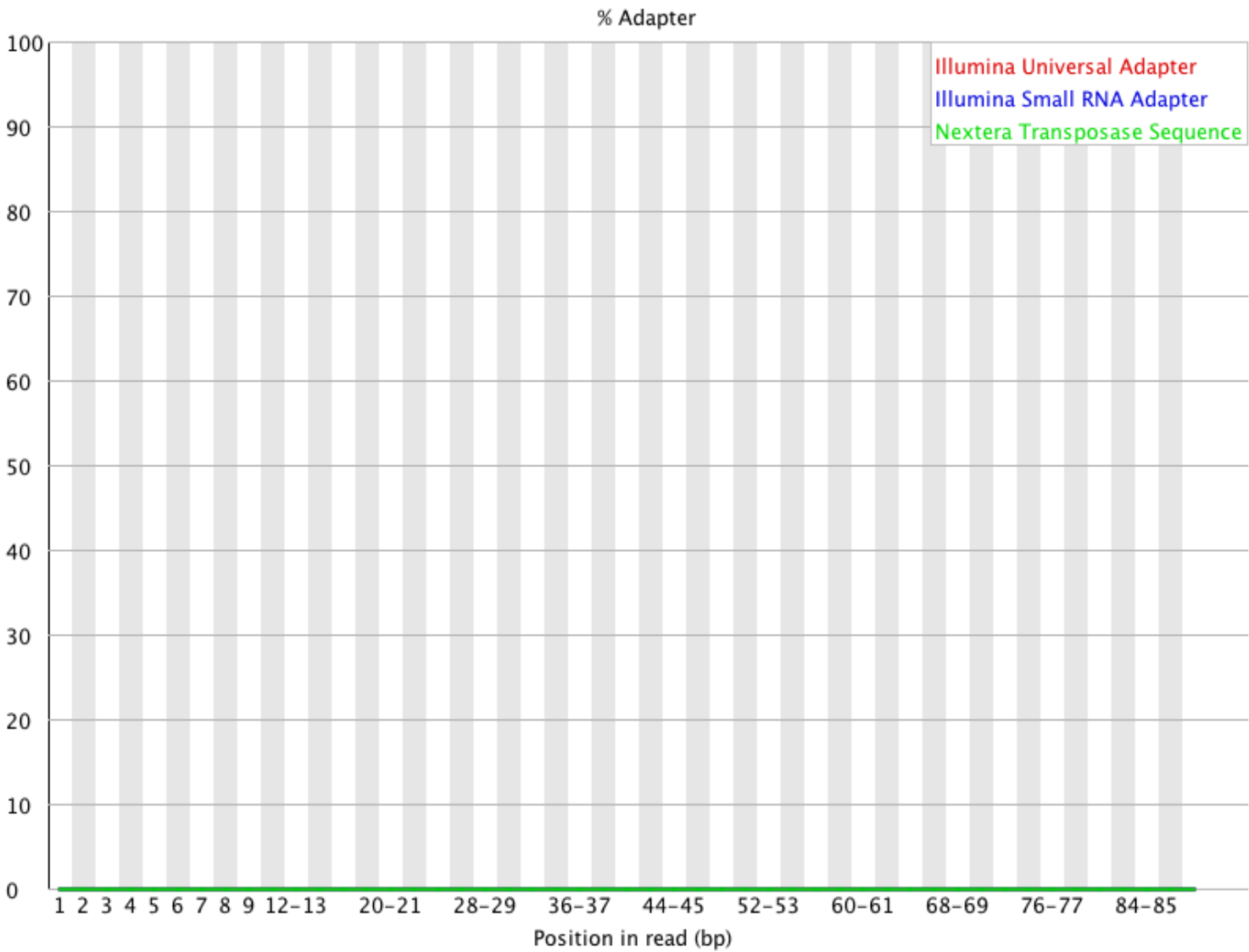


 Sequence Duplication Levels

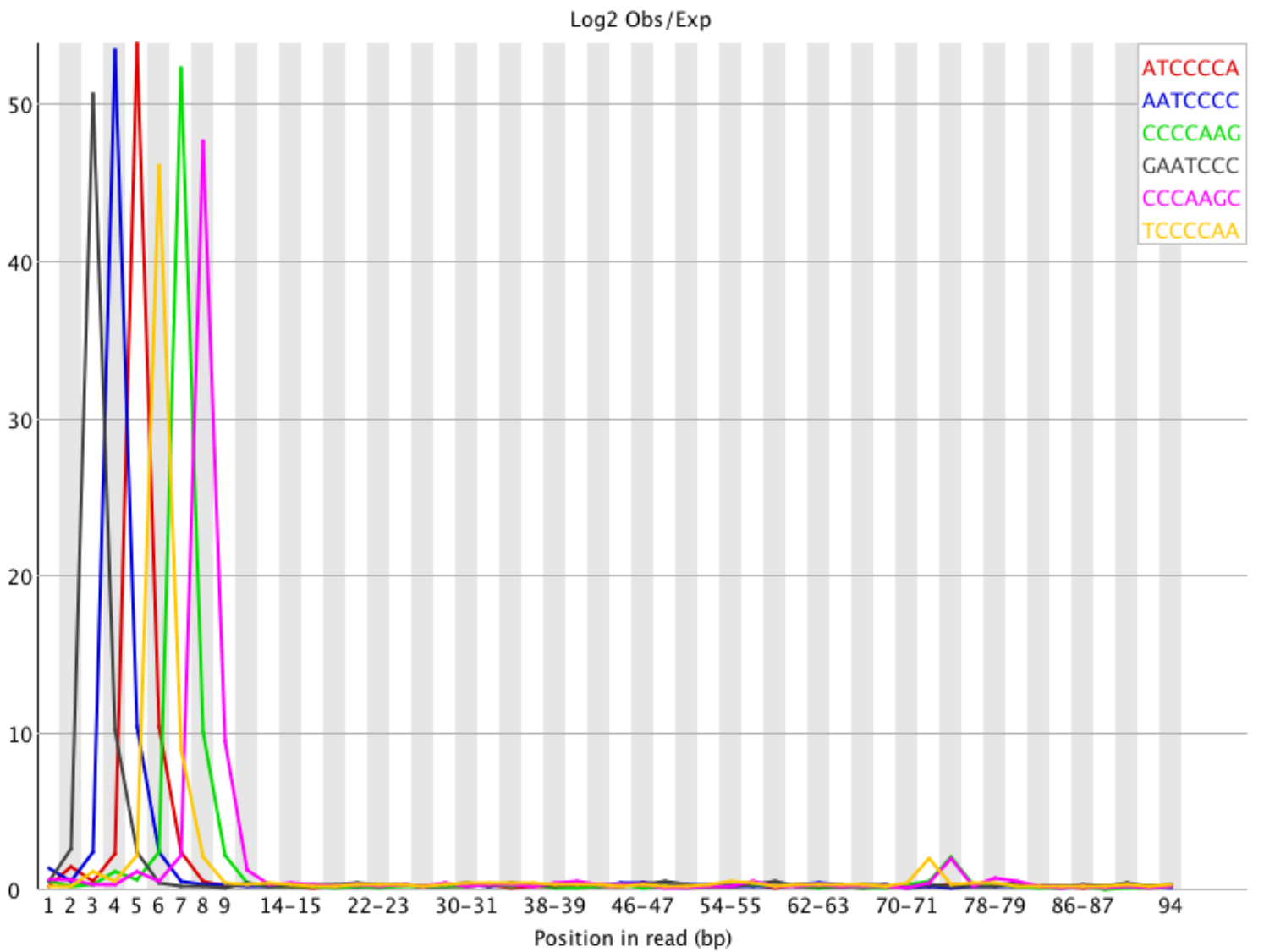


Sequence	Count	Percentage	Possible Source
TTT	175065	0.4881823970905985	No Hit
ACGAATCCCCAAGCCAAGGGCTGAGTCTCAACAGATCGCAGCGTGGTAAC	94646	0.26392774772248473	No Hit
AAATTTAAAATTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTTT	57346	0.15991379055526497	No Hit
AAAAATTTAAAATTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTTT	52601	0.14668198822930098	No Hit
AATTTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTTTCATTCTAG	37041	0.10329171548072351	No Hit

Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCCCA	22050	0.0	53.815372	5
AATCCCC	22310	0.0	53.49152	4
CCCCAAG	22740	0.0	52.3514	7
GAATCCC	23545	0.0	50.632523	3
CCCAAGC	25070	0.0	47.65946	8
TCCCCAA	25760	0.0	46.08355	6
ACAGACG	25335	0.0	45.366226	94
CCAAGCC	26730	0.0	44.973953	9
CGAATCC	28790	0.0	41.87306	2
ACGAATC	32325	0.0	36.84329	1
CACCCCG	20795	0.0	32.56856	68-69
AAGCCCC	7295	0.0	31.605053	6
CCAAGGG	22435	0.0	31.485128	14-15

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGGCTGA	22465	0.0	31.397612	18–19
CGACCCT	7425	0.0	30.856403	4
AGCCCCG	7570	0.0	30.264729	7
GCCCCGA	7685	0.0	29.937674	8
CGTGGTA	22060	0.0	29.573511	42–43
AAGGGCT	23675	0.0	29.531504	16–17
AGCGTGG	22780	0.0	29.461538	40–41

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FastQC Report

Summary

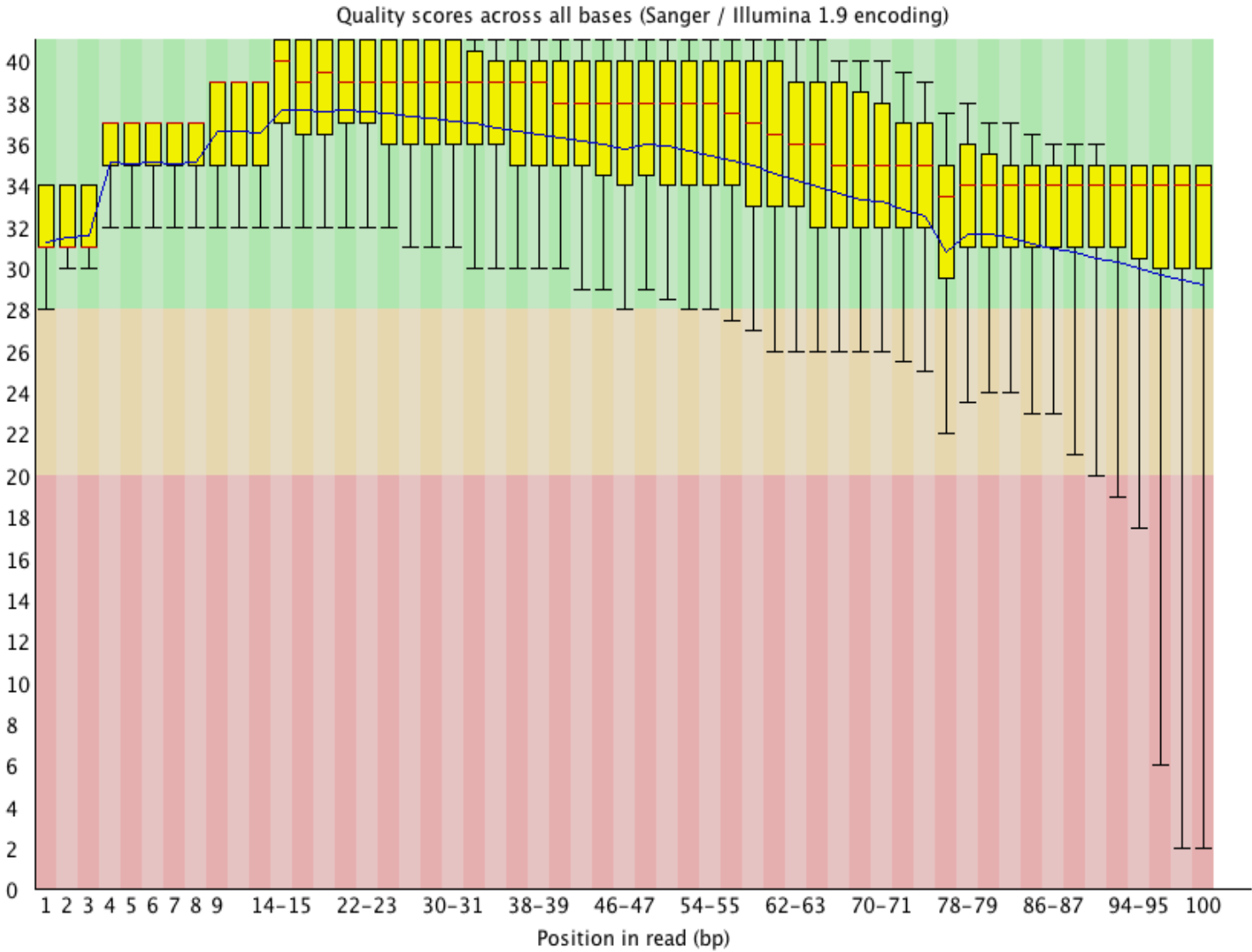
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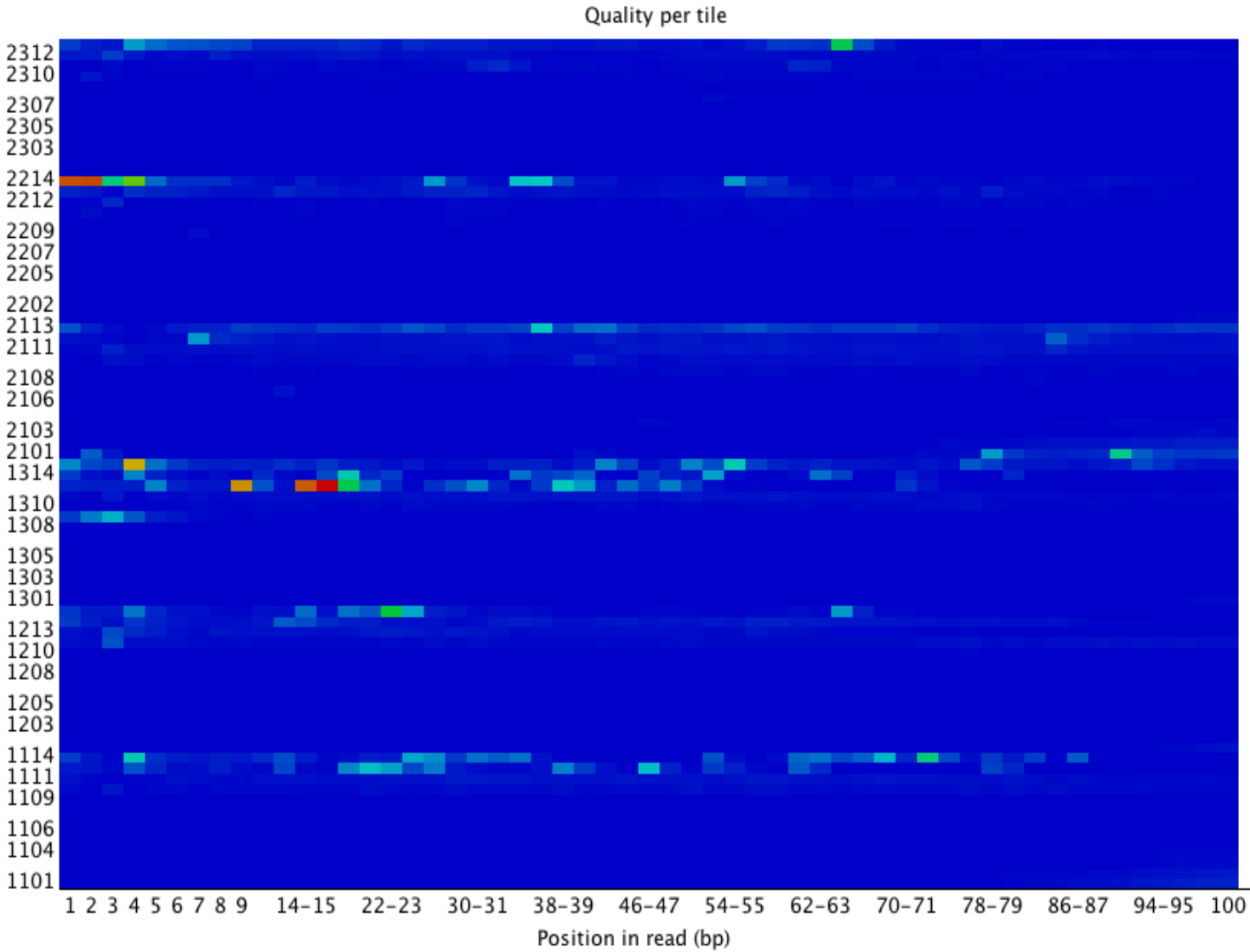
Basic Statistics

Measure	Value
Filename	3A_ACAGTG_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	37154642
Sequences flagged as poor quality	0
Sequence length	100
%GC	40

Per base sequence quality

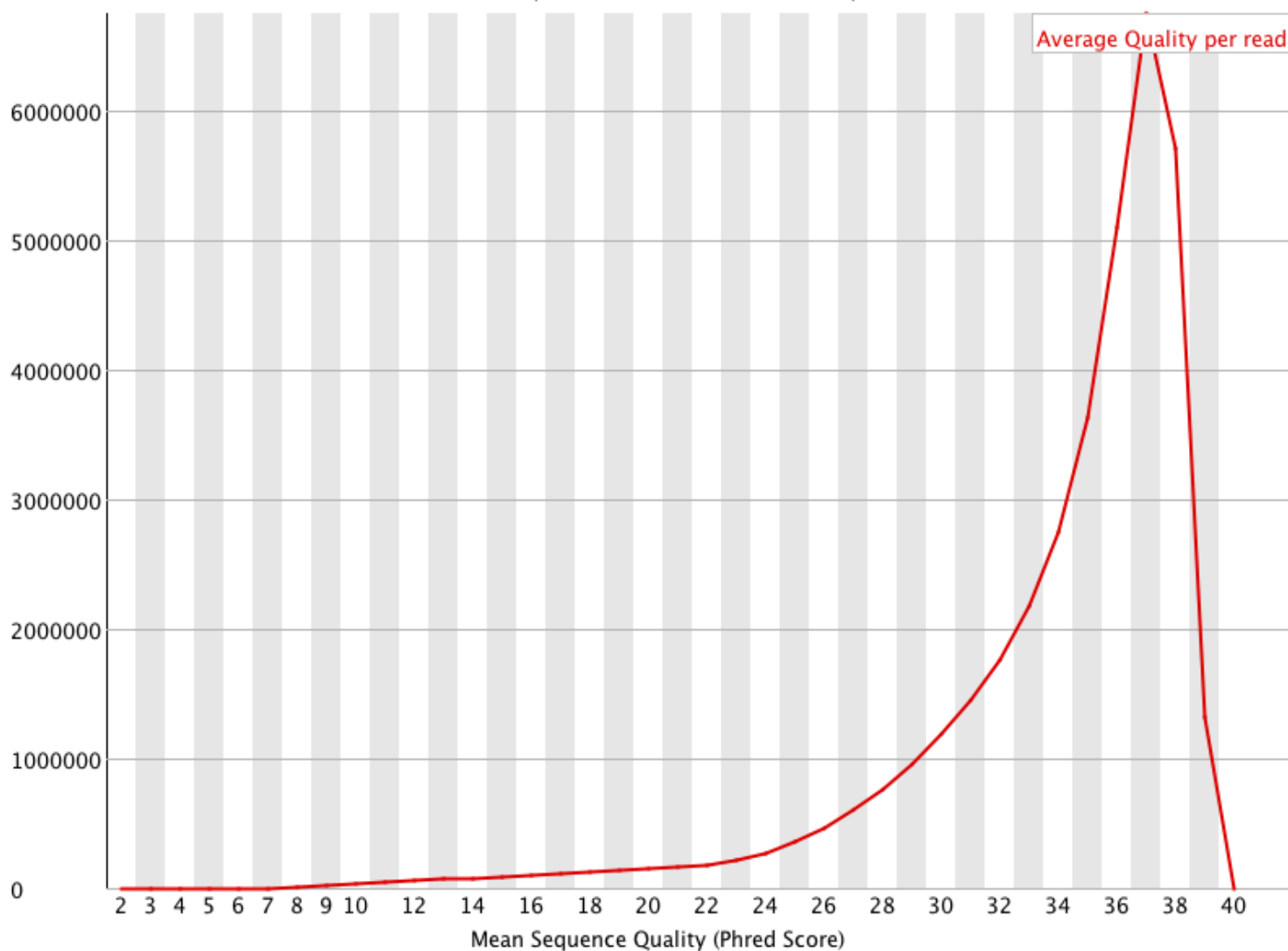


✖ Per tile sequence quality



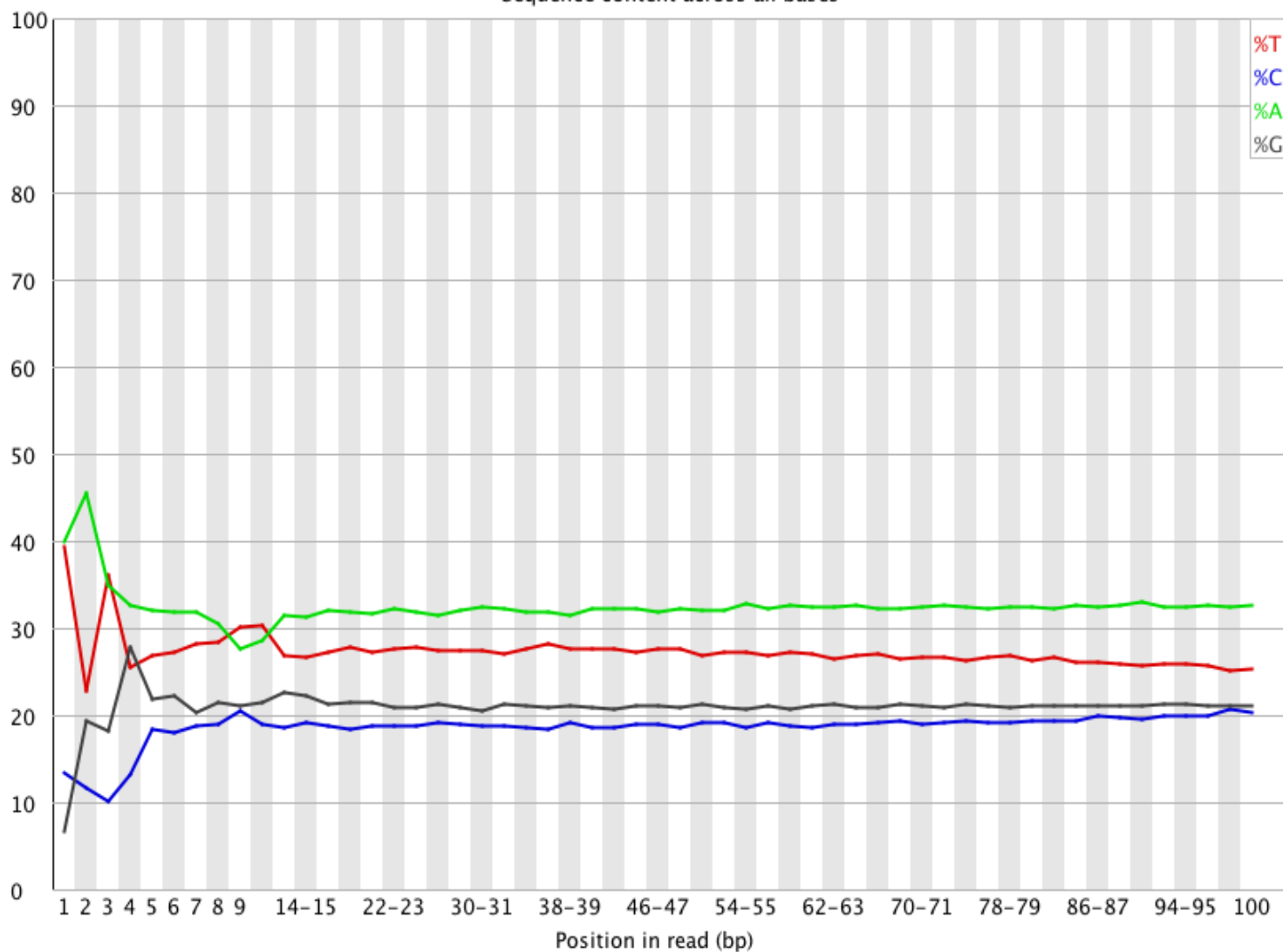
 Per sequence quality scores

Quality score distribution over all sequences



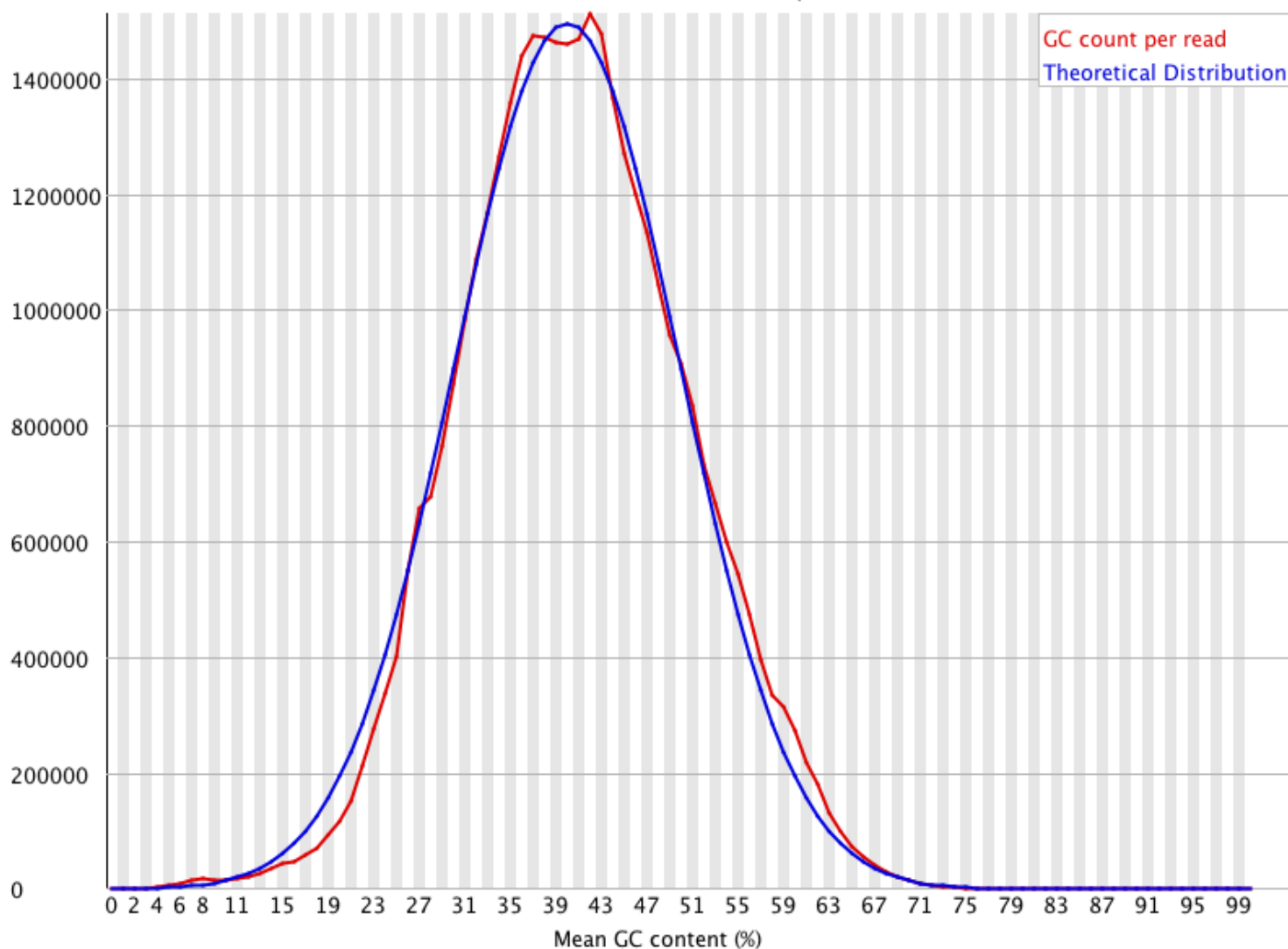
✖ Per base sequence content

Sequence content across all bases

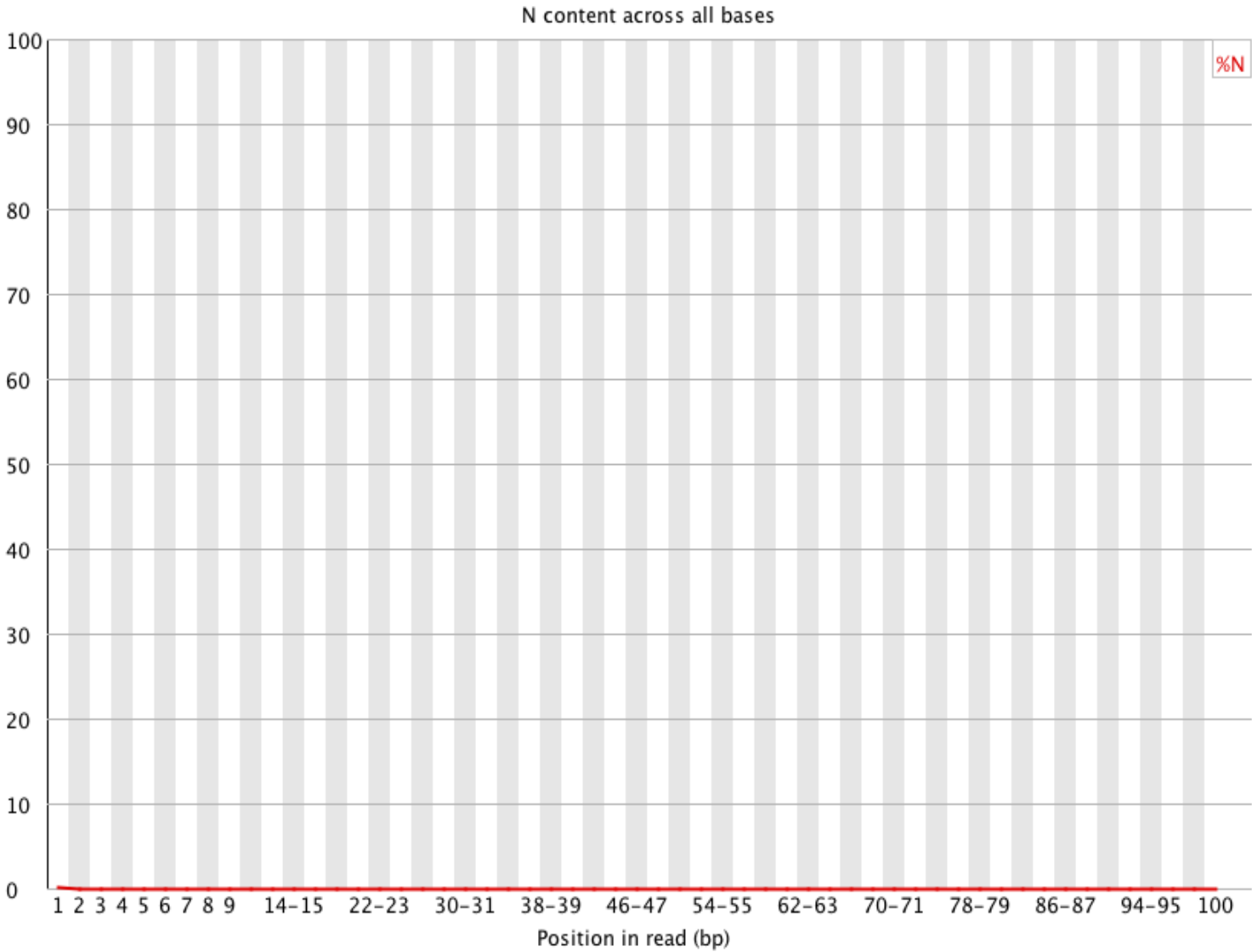


Per sequence GC content

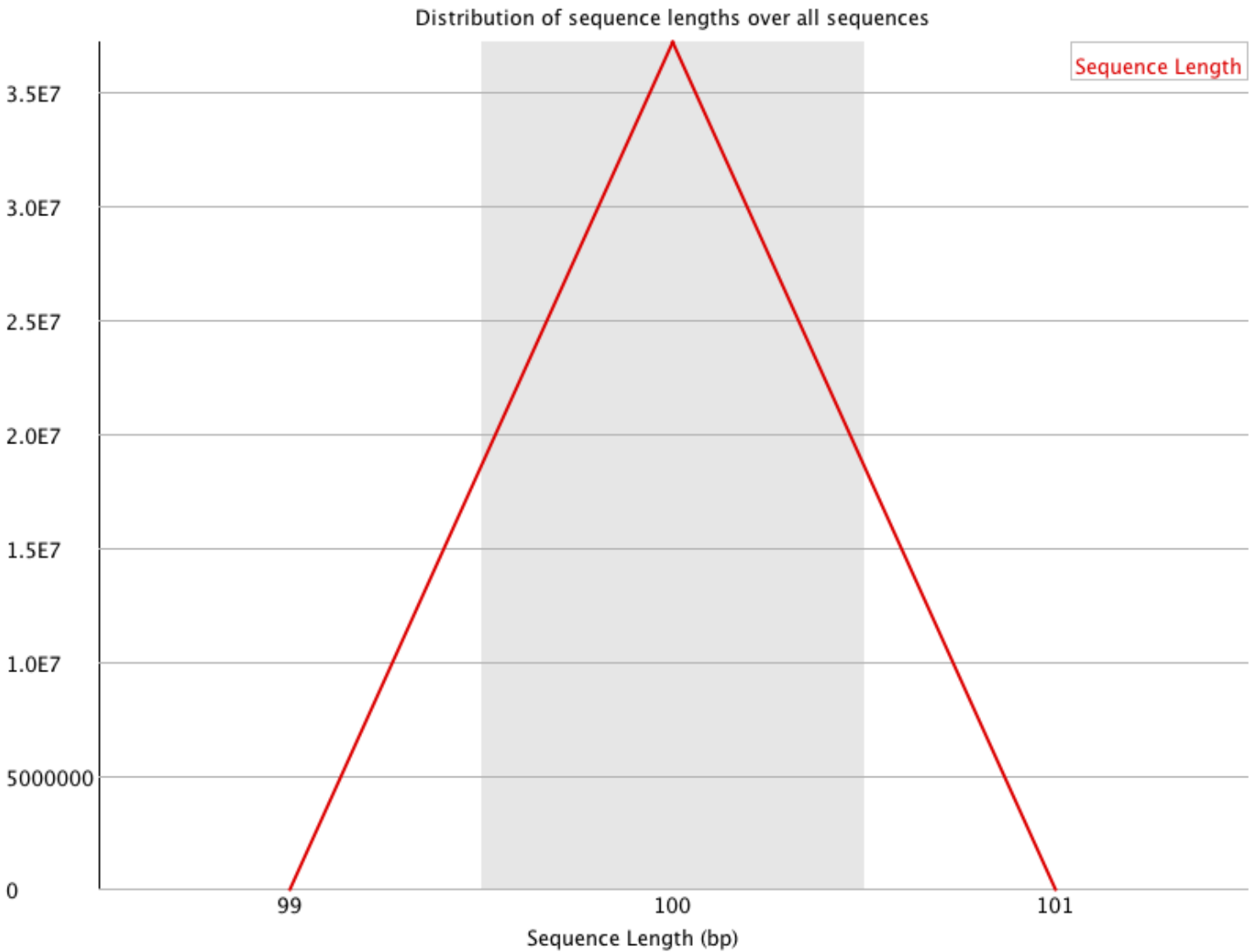
GC distribution over all sequences



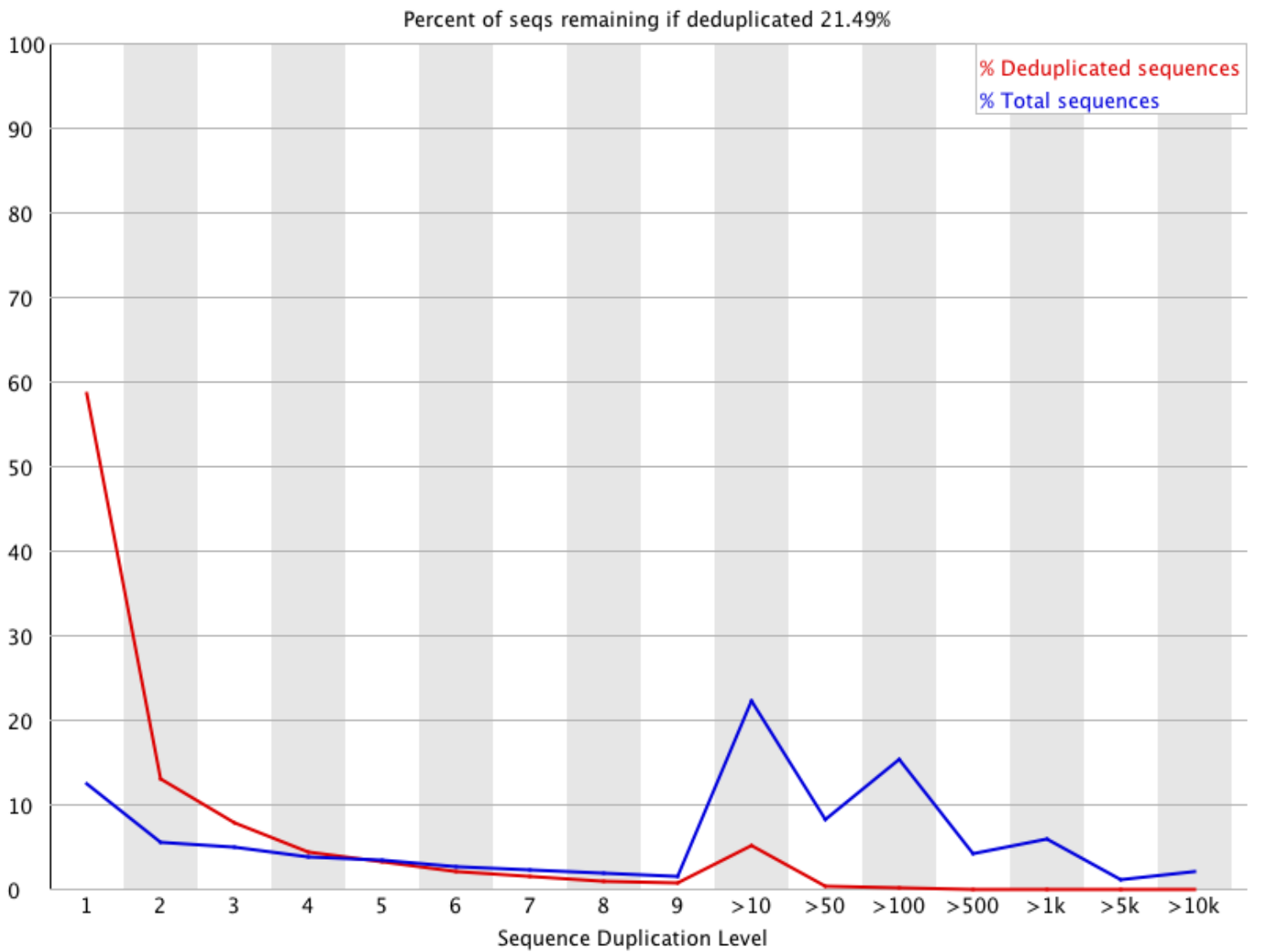
Per base N content



✔ Sequence Length Distribution



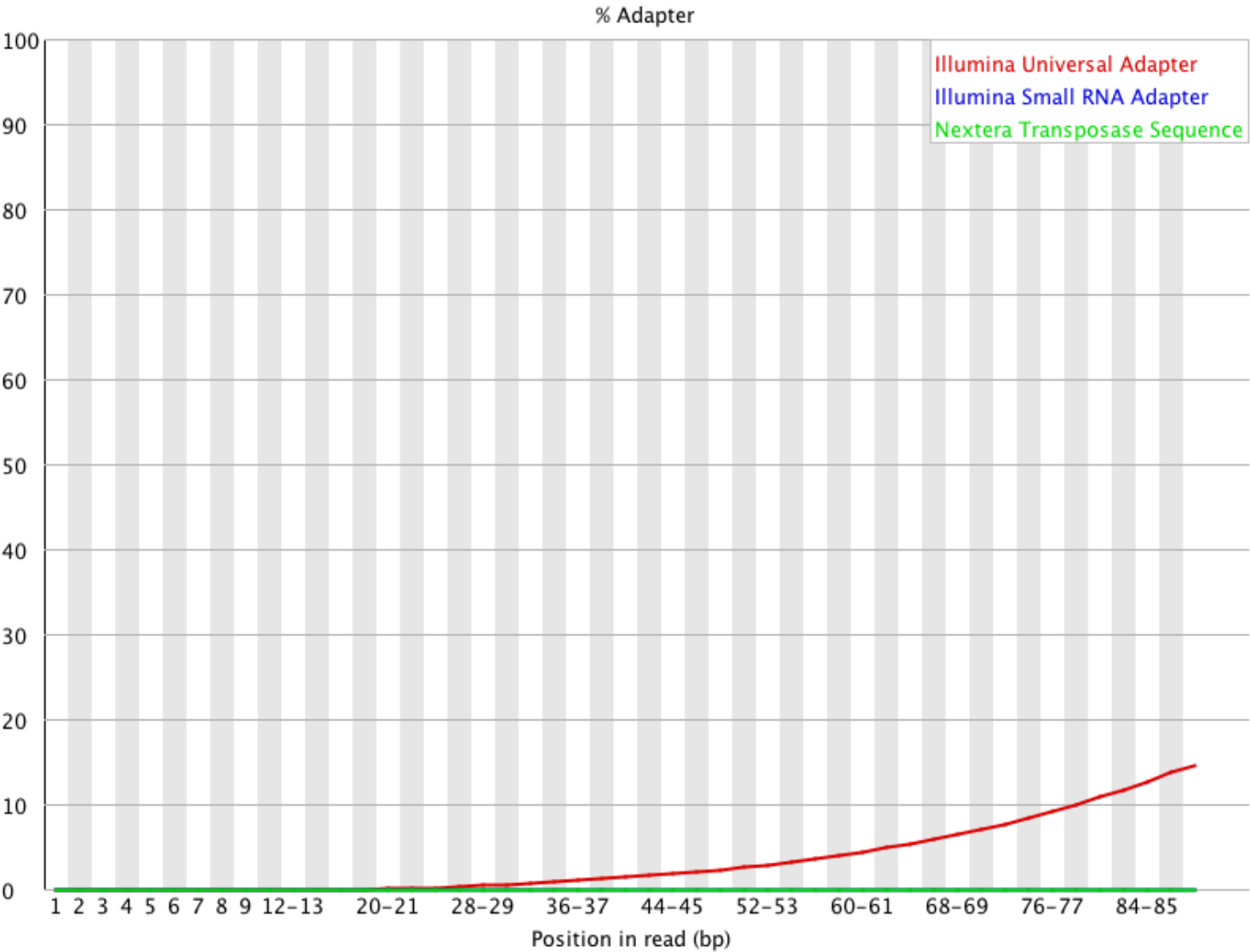
 Sequence Duplication Levels



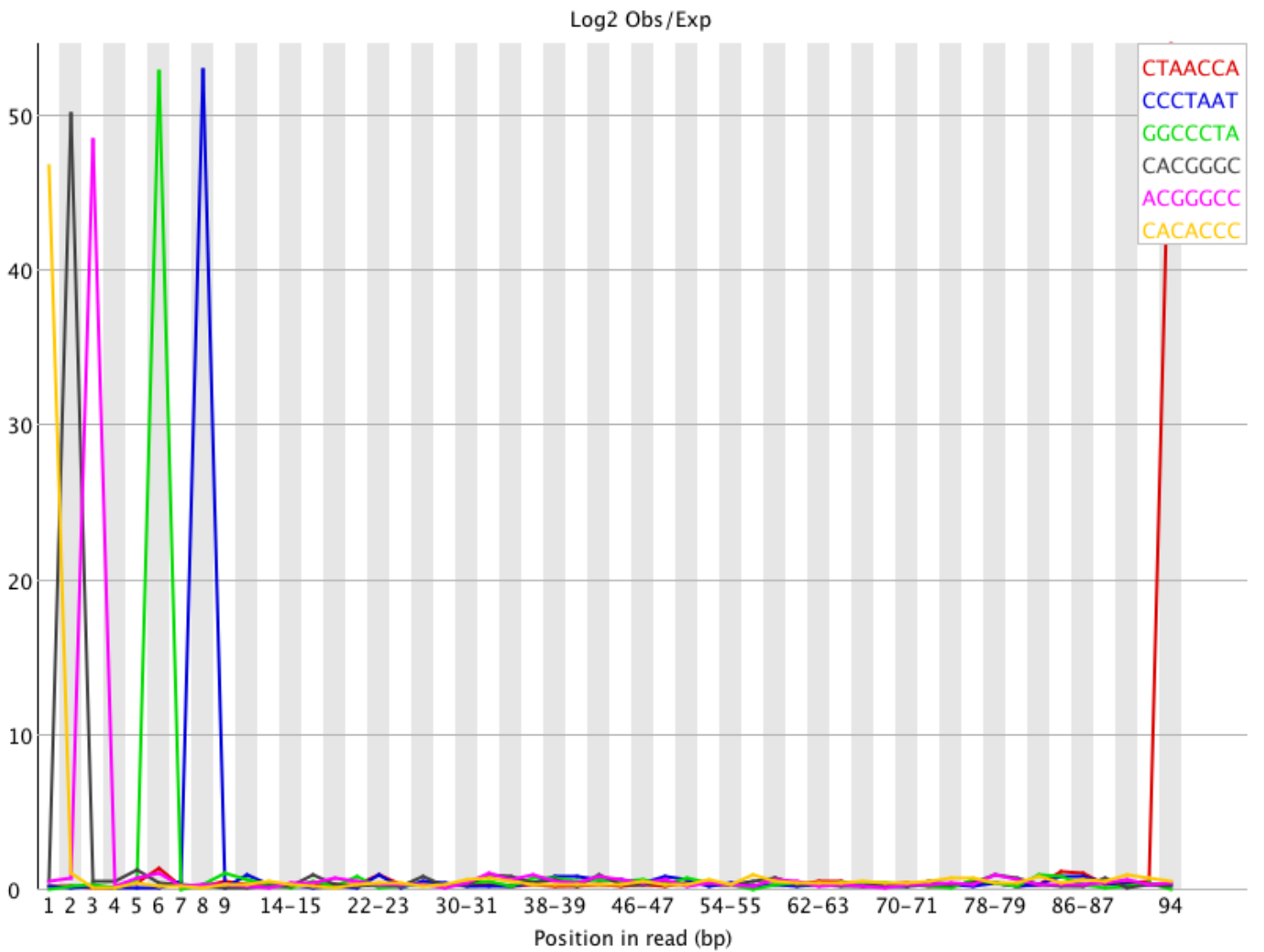
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGACGGACAGAAGCGAAAGCATTTCGCCAAAAATGTTTTTCATTAATCAAGA	106328	0.28617689278233394	No Hit
TATTGGGCTATTAGGATTTATTGTTTGGGCTCATCATATATTTACTGTAG	57198	0.15394577075994972	No Hit
GCACGGGCCCTAATTGCCGTACGGAGTCGCGGATCCTGCTTCGGGATCTT	55627	0.14971749694156655	No Hit
CACACCCGTCGGGCGAAAGGGAATCCGGTTCCTATTCCGGAACCCGGCAG	52830	0.14218950084352852	No Hit
TTTAAATAGCTGCAGTATTTTGACTGTACAAAGGTAGCATAATCAATTGT	46732	0.12577701596478846	No Hit
AATAAATCAATTCTGCTCAATGAATTTATTTAAATAGCTGCAGTATTTTG	41037	0.11044918694143252	No Hit

 Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CTAACCA	19475	0.0	54.53984	94
CCCTAAT	11745	0.0	52.904606	8
GGCCCTA	11895	0.0	52.790657	6
CACGGGC	12370	0.0	50.036545	2
ACGGGCC	12875	0.0	48.407352	3
CACACCC	12665	0.0	46.688747	1
GCCCTAA	13635	0.0	45.916008	7
GCACGGG	13500	0.0	45.790325	1
TGGGCTA	14930	0.0	41.681488	4
ACCCGTC	14790	0.0	40.169266	4
GGGCTAT	15970	0.0	39.231983	5
CACCCGT	15060	0.0	39.137005	3
GTCGGGC	15385	0.0	38.67686	8

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
TCGGGCG	15475	0.0	38.421555	9
CGGACAG	32555	0.0	37.032646	4
CCTAATT	17165	0.0	36.856686	9
ACACCCG	16045	0.0	36.847847	2
TATTGGG	17850	0.0	34.948093	1
CCGTCGG	17190	0.0	34.861763	6
GACGGAC	35965	0.0	34.07993	2

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FastQC Report

Summary

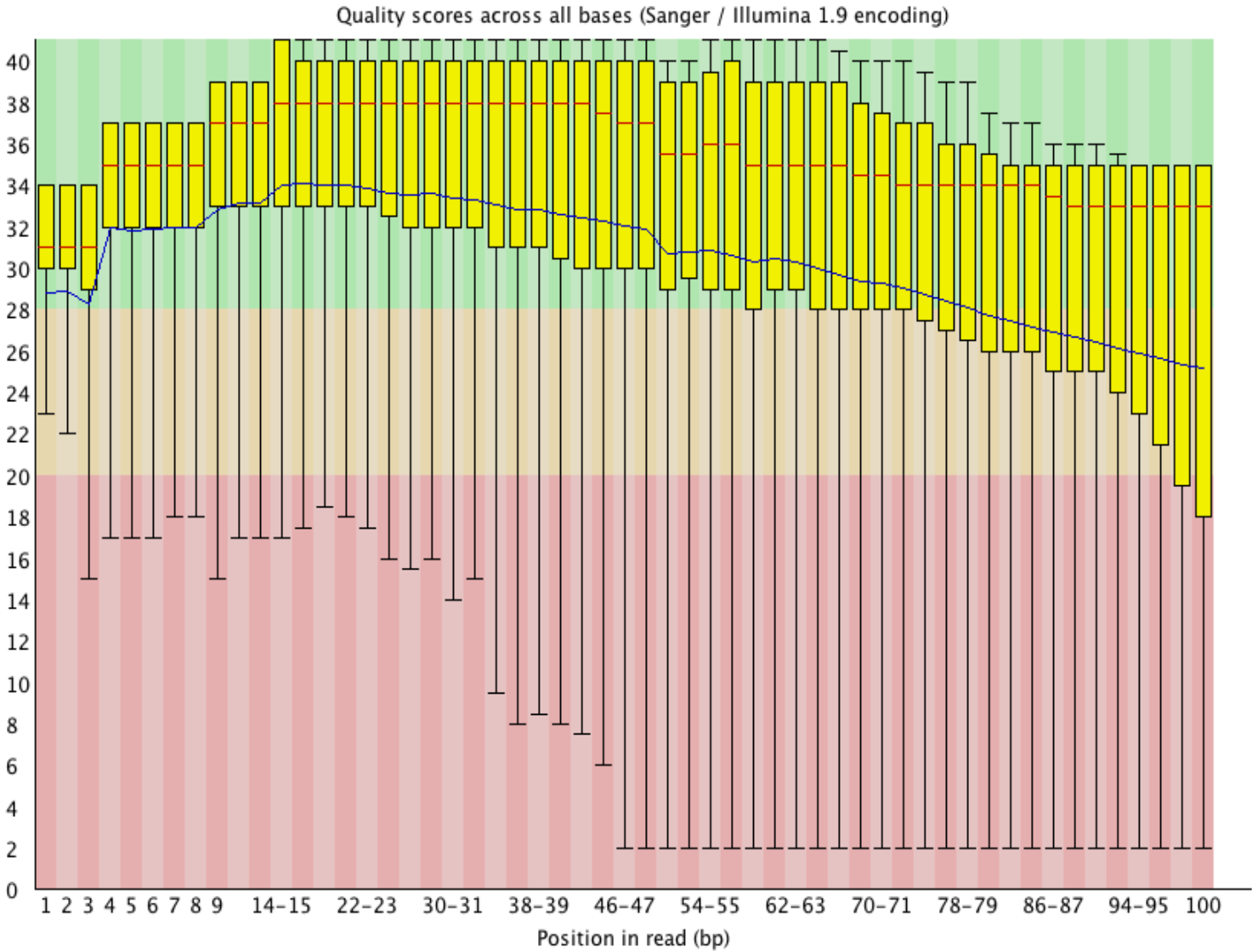
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3A_ACAGTG_L001_R2_001.fastq

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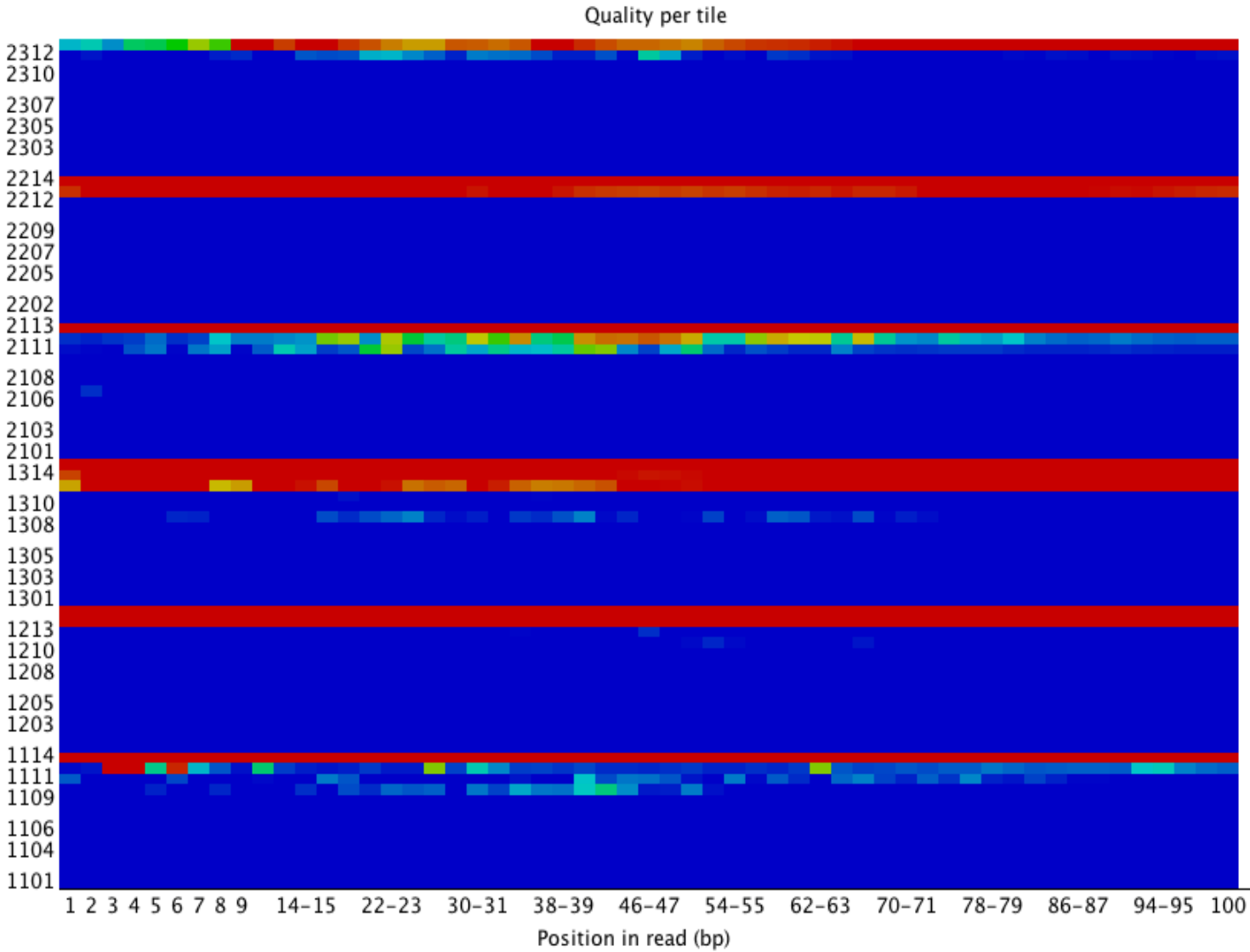
Basic Statistics

Measure	Value
Filename	3A_ACAGTG_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	37154642
Sequences flagged as poor quality	0
Sequence length	100
%GC	40

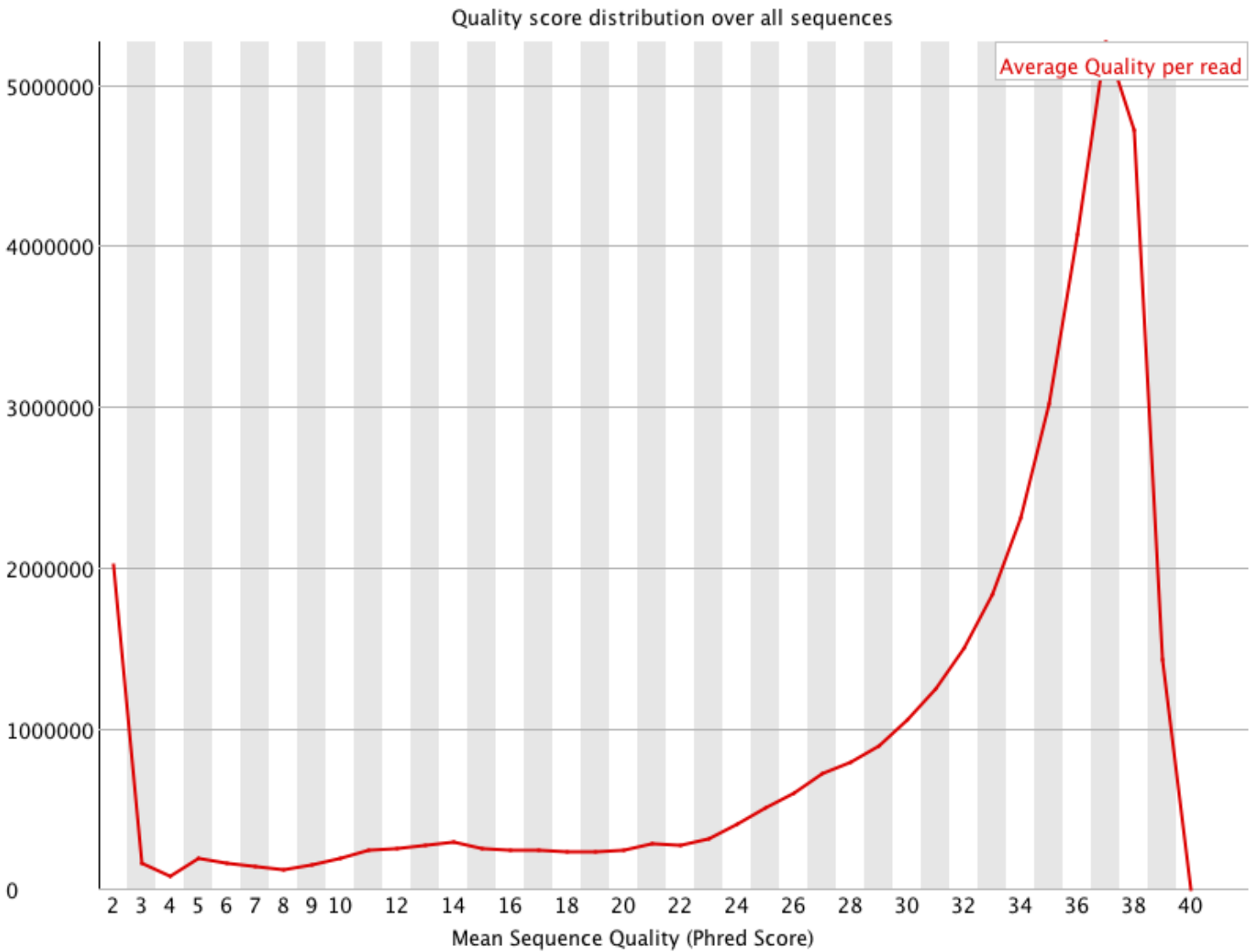
Per base sequence quality



 **Per tile sequence quality**

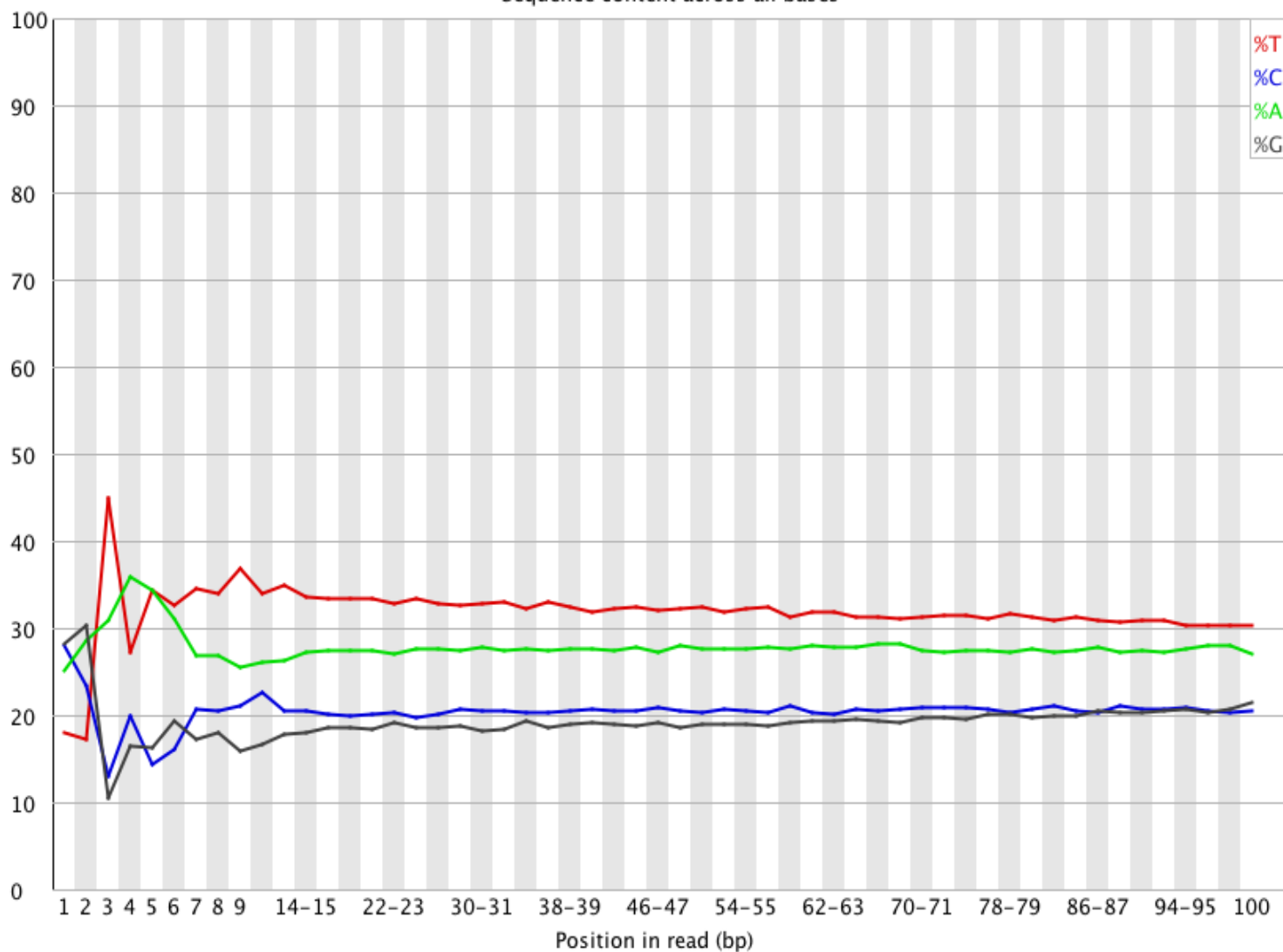


 Per sequence quality scores

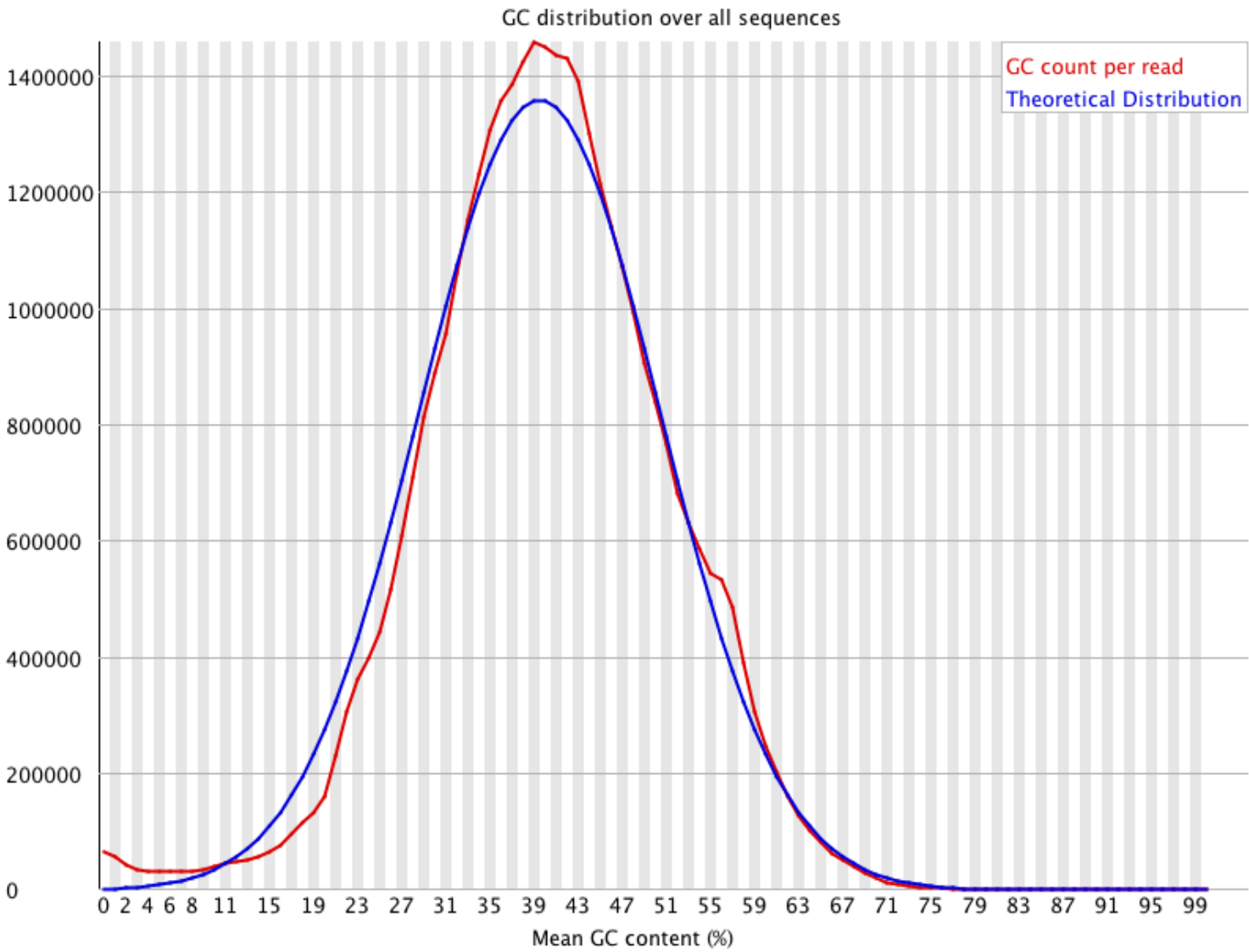


✖ Per base sequence content

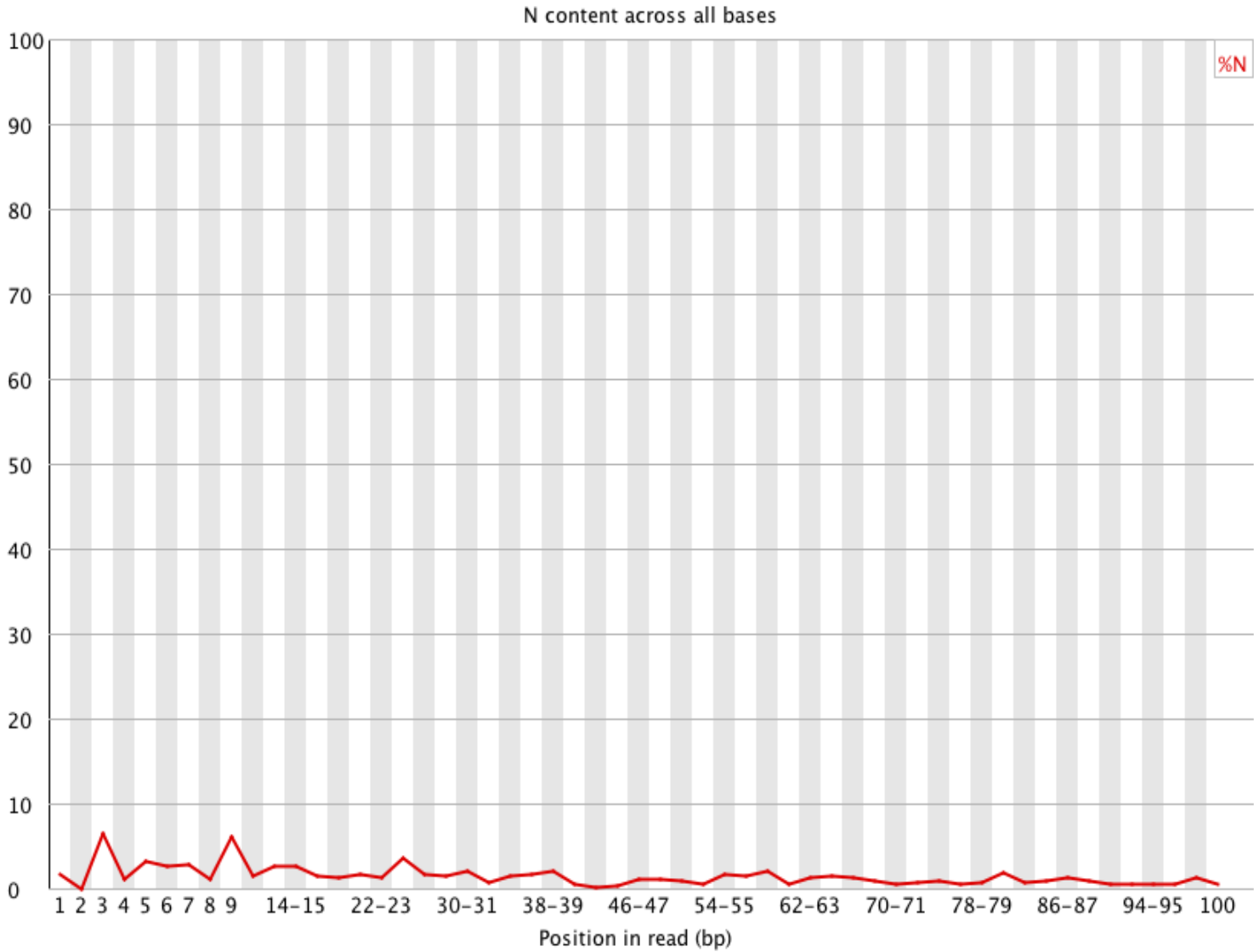
Sequence content across all bases



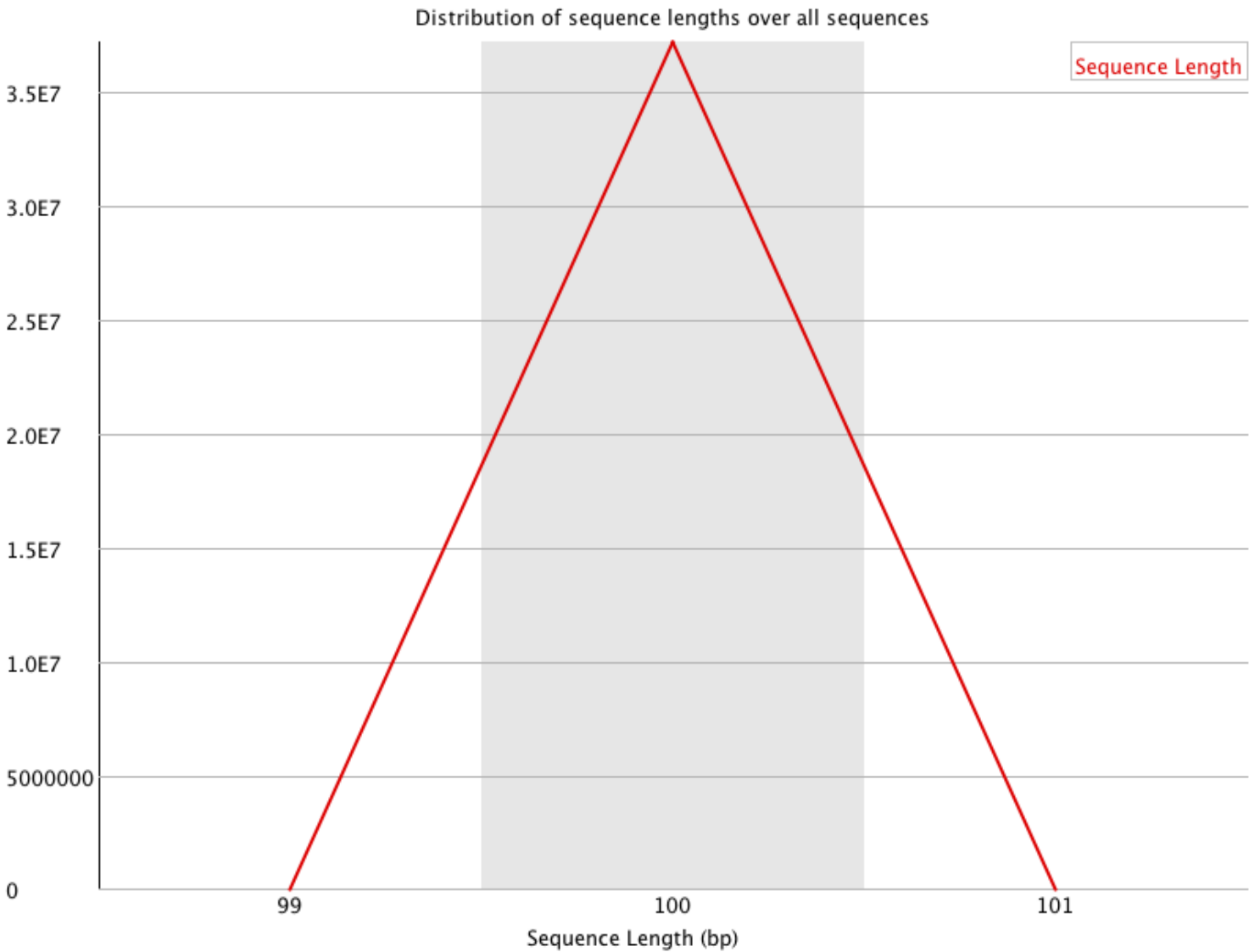
Per sequence GC content



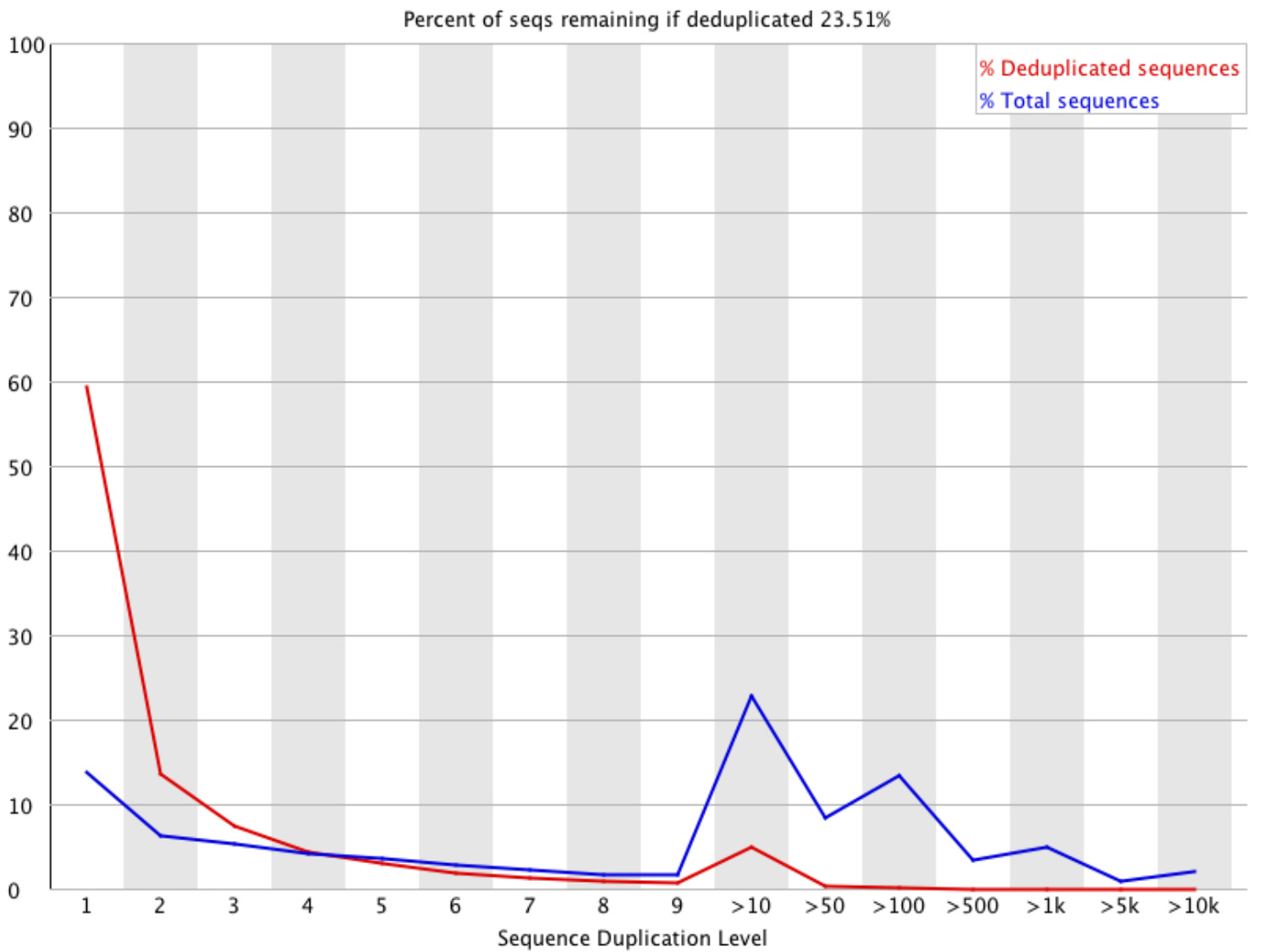
! Per base N content



✔ Sequence Length Distribution



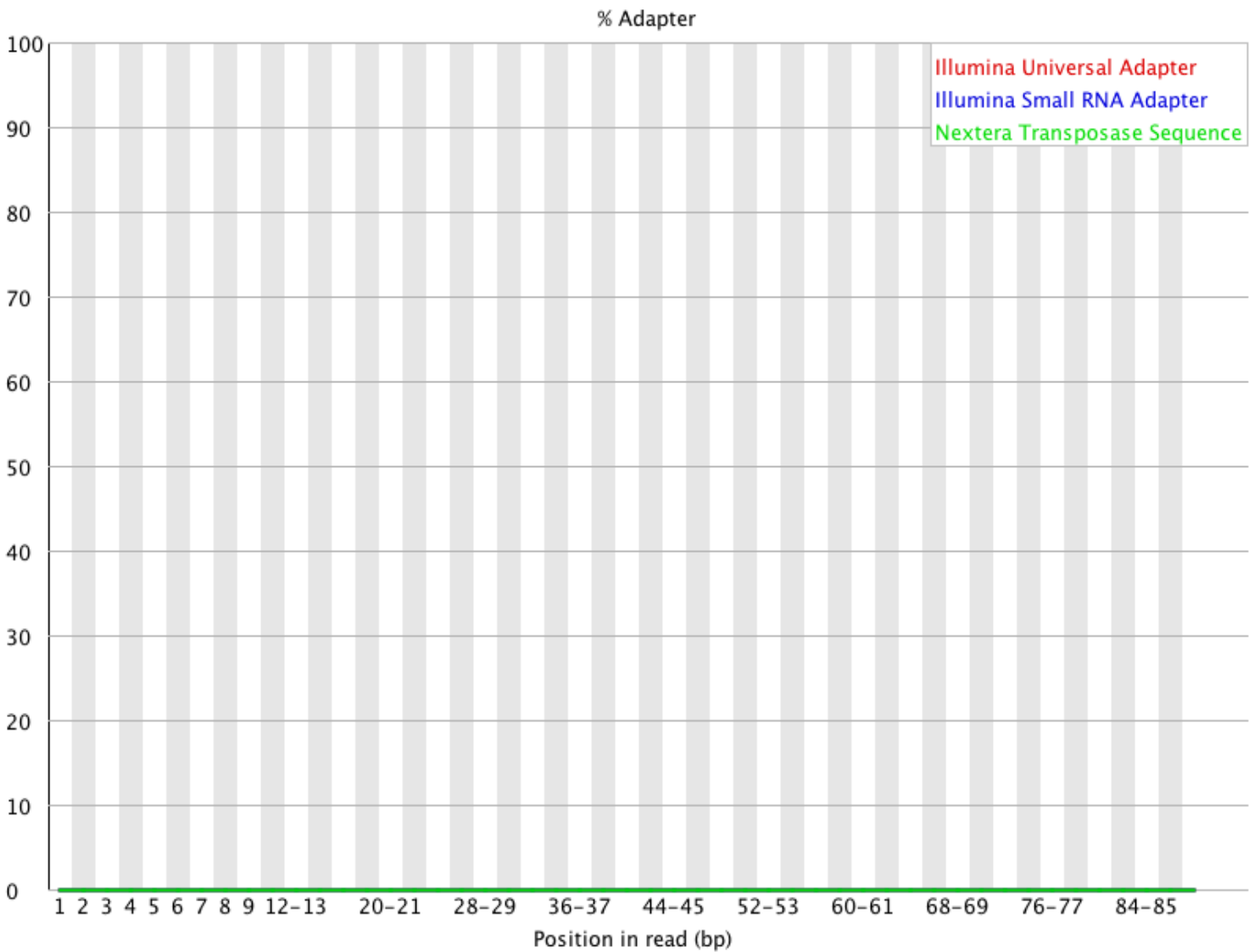
 Sequence Duplication Levels



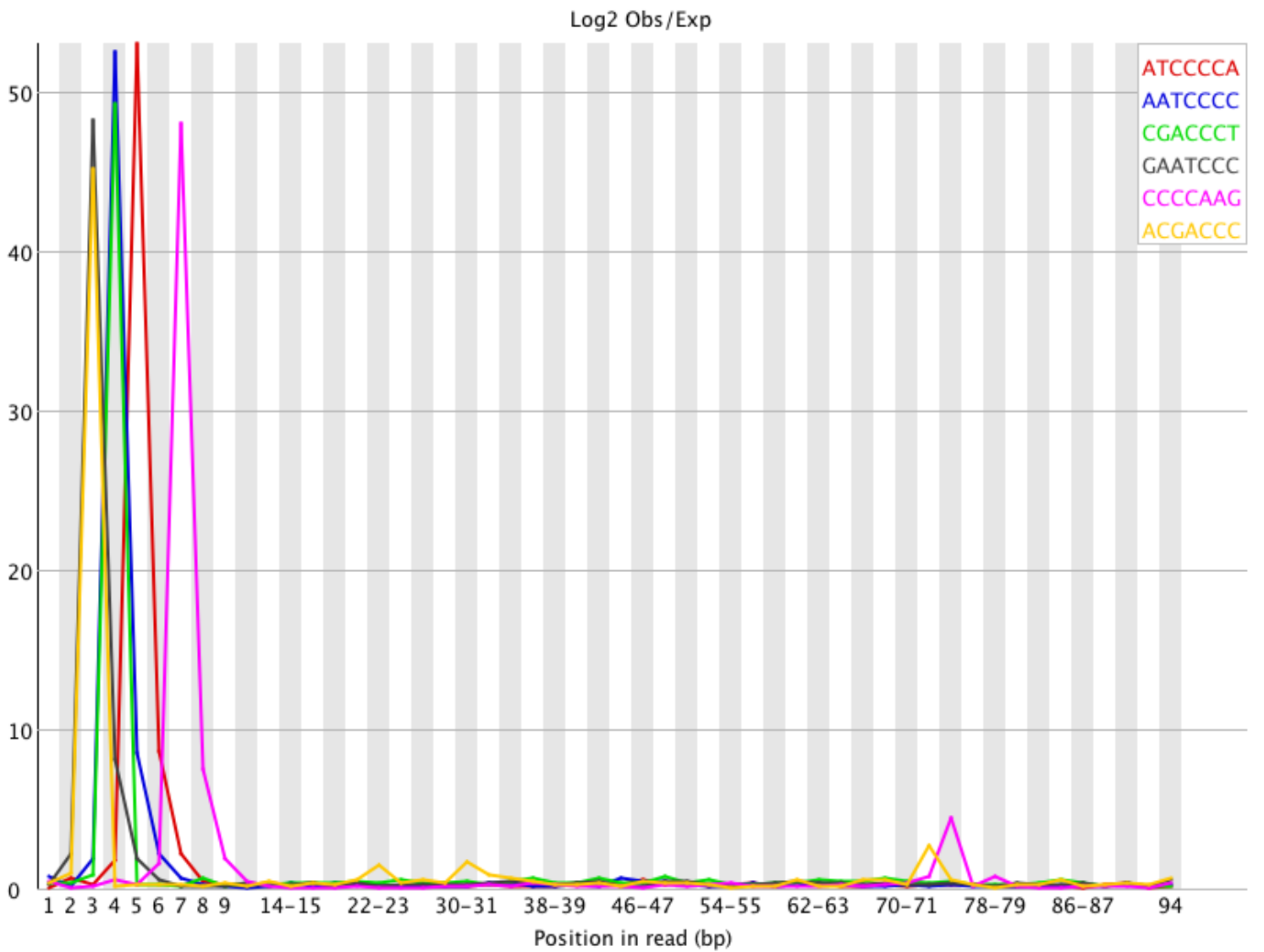
! Overrepresented sequences

Sequence	Count	Percentage	Possible Source
TT	157688	0.42440995663475917	No Hit
ACGAATCCCCAAGCCAAGGGCTGAGTCTCAACAGATCGCAGCGTGGTAAC	80797	0.2174613874627025	No Hit
GGAAGCTGCCCGCCGAGTCATCGGAGGAAC TTCGGCGGATCGCTAGCTGG	53122	0.14297540533427827	No Hit
AAATTTAAAATTTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTTT	51186	0.13776475090245788	No Hit
GAACGACCCTCAGCCAGGCGTGGTCCGGGAATCGTATCCGAGGACCGCAA	47139	0.12687243763511433	No Hit
AATTTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTTTTCATTCTAG	40185	0.10815606835883387	No Hit
AAAATTTAAAATTTATTTATTCTGAGACAGTTTTTATTTTCATTATTTCTT	39881	0.10733786642325877	No Hit

Adapter Content



Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ATCCCCA	19140	0.0	52.971115	5
AATCCCC	19390	0.0	52.537373	4
CGACCCT	10830	0.0	49.262466	4
GAATCCC	21115	0.0	48.215786	3
CCCCAAG	21255	0.0	48.062977	7
ACGACCC	11760	0.0	45.19095	3
CCCAAGC	23420	0.0	43.578968	8
TGCCCCG	15630	0.0	43.501266	7
TCCCCAA	23720	0.0	42.743134	6
GCCCGCC	16225	0.0	42.144577	8
CCAAGCC	24685	0.0	41.58378	9
ACAGACG	22975	0.0	41.325306	94
CTGCCCC	16860	0.0	40.29984	6

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GACCCTC	13415	0.0	40.130085	5
CGAATCC	26385	0.0	39.688347	2
CCCTCAG	13685	0.0	39.125664	7
ACCCTCA	13890	0.0	38.792538	6
CCCGCCG	18225	0.0	37.44292	9
GCTGCCC	18965	0.0	36.005173	5
ACGAATC	30215	0.0	33.872917	1

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FastQC Report

Summary

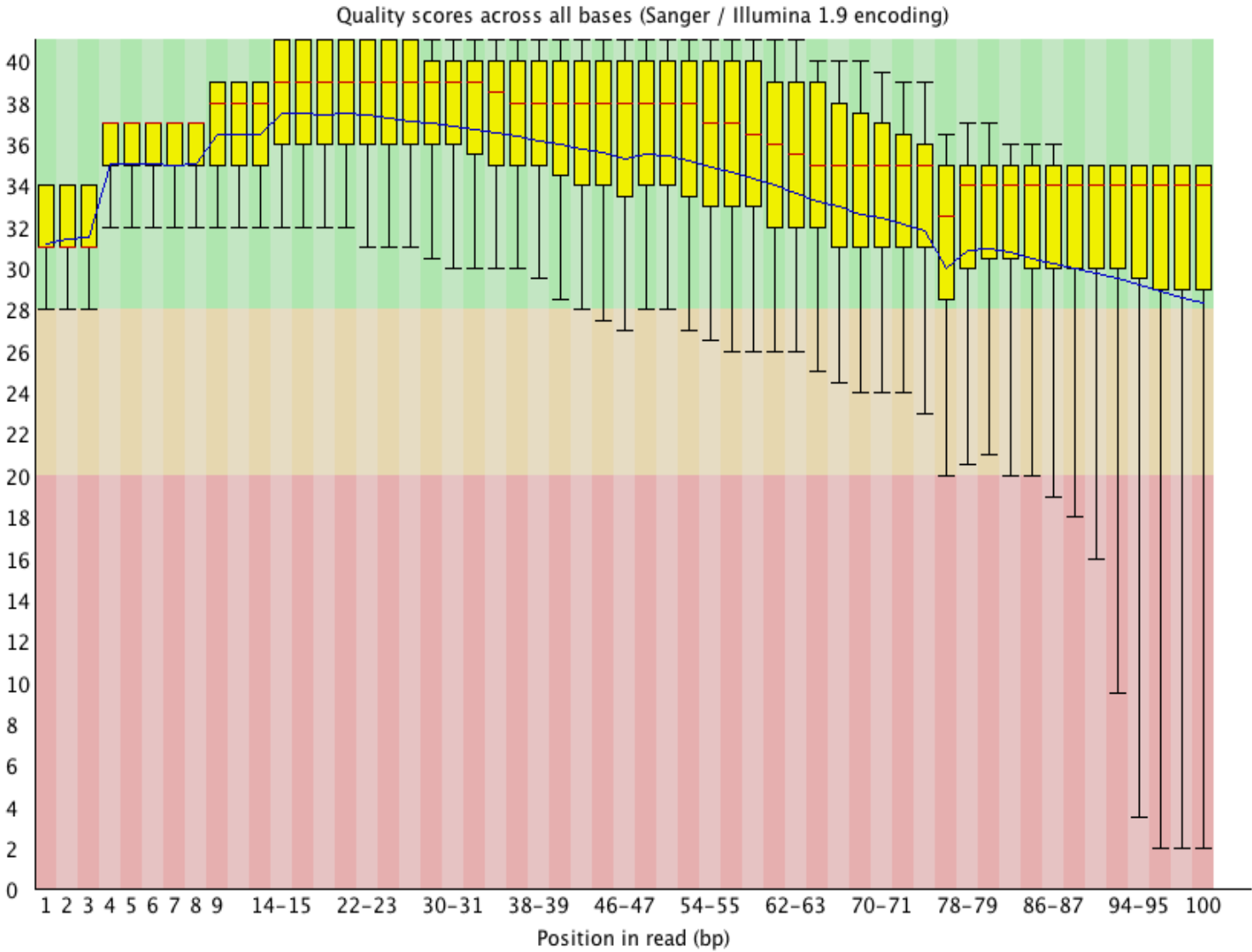
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-  [Sequence Length Distribution](#)
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-  [Overrepresented sequences](#)
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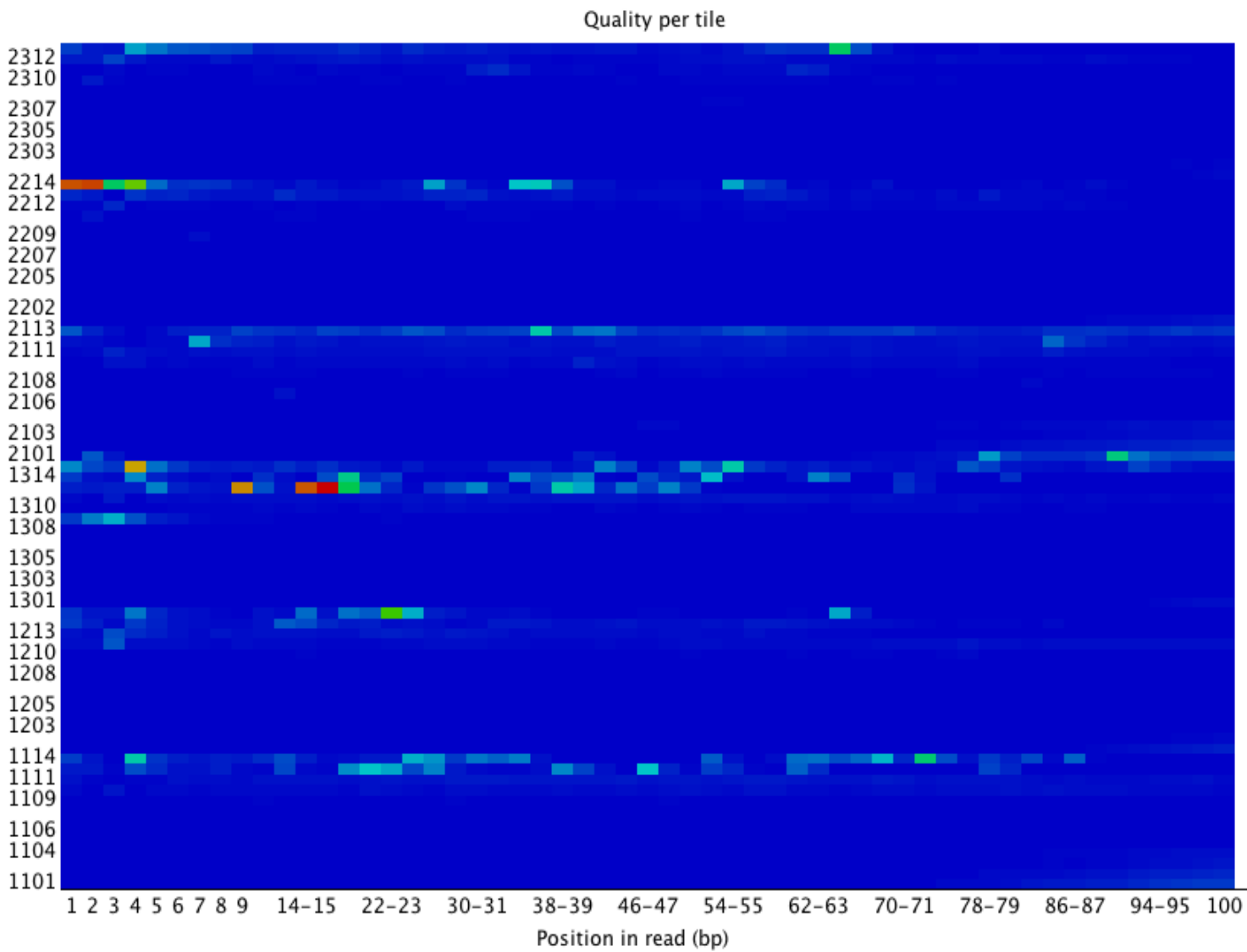
Basic Statistics

Measure	Value
Filename	3P_GCCAAT_L001_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	42848501
Sequences flagged as poor quality	0
Sequence length	100
%GC	42

Per base sequence quality

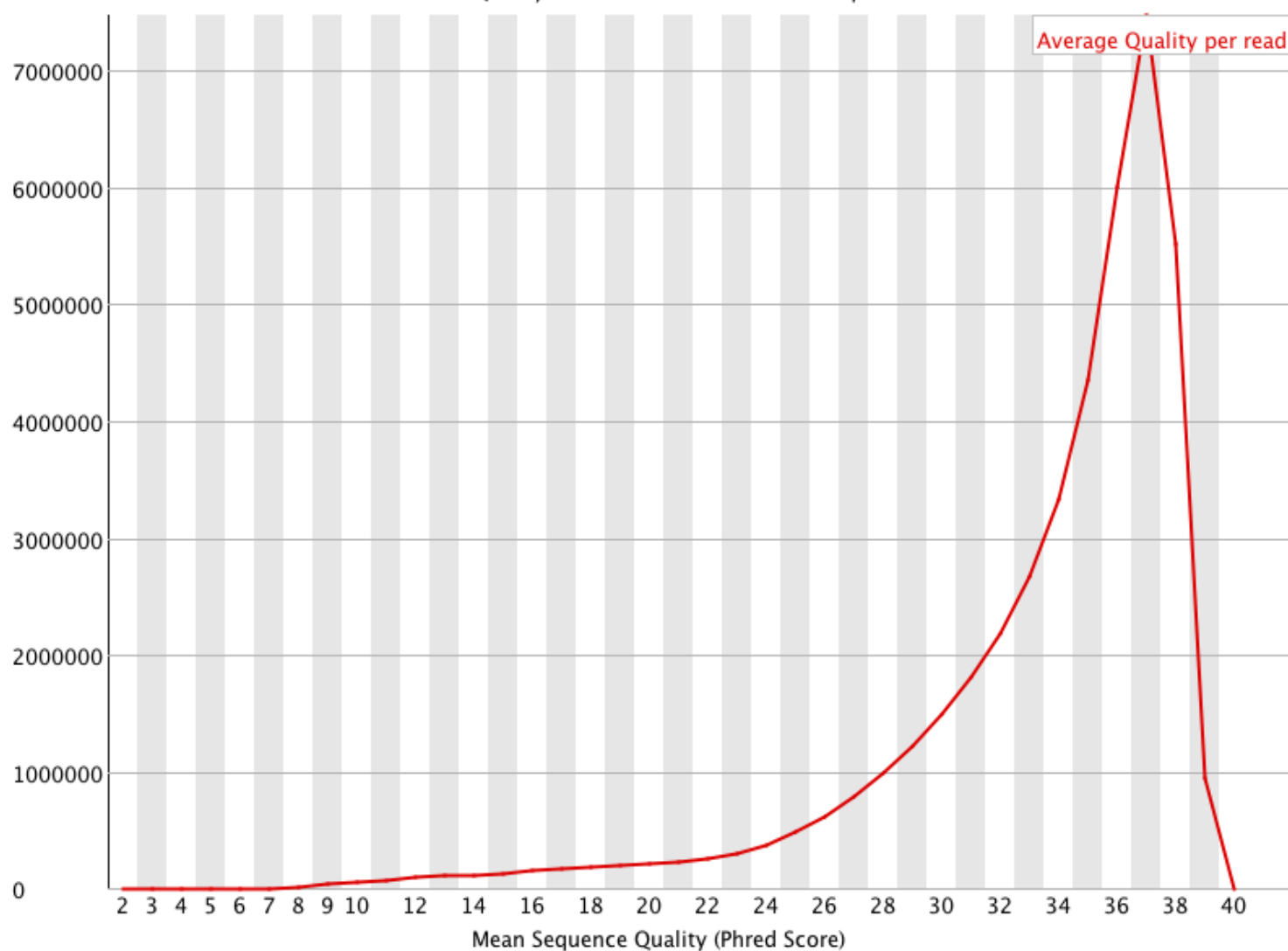


 Per tile sequence quality



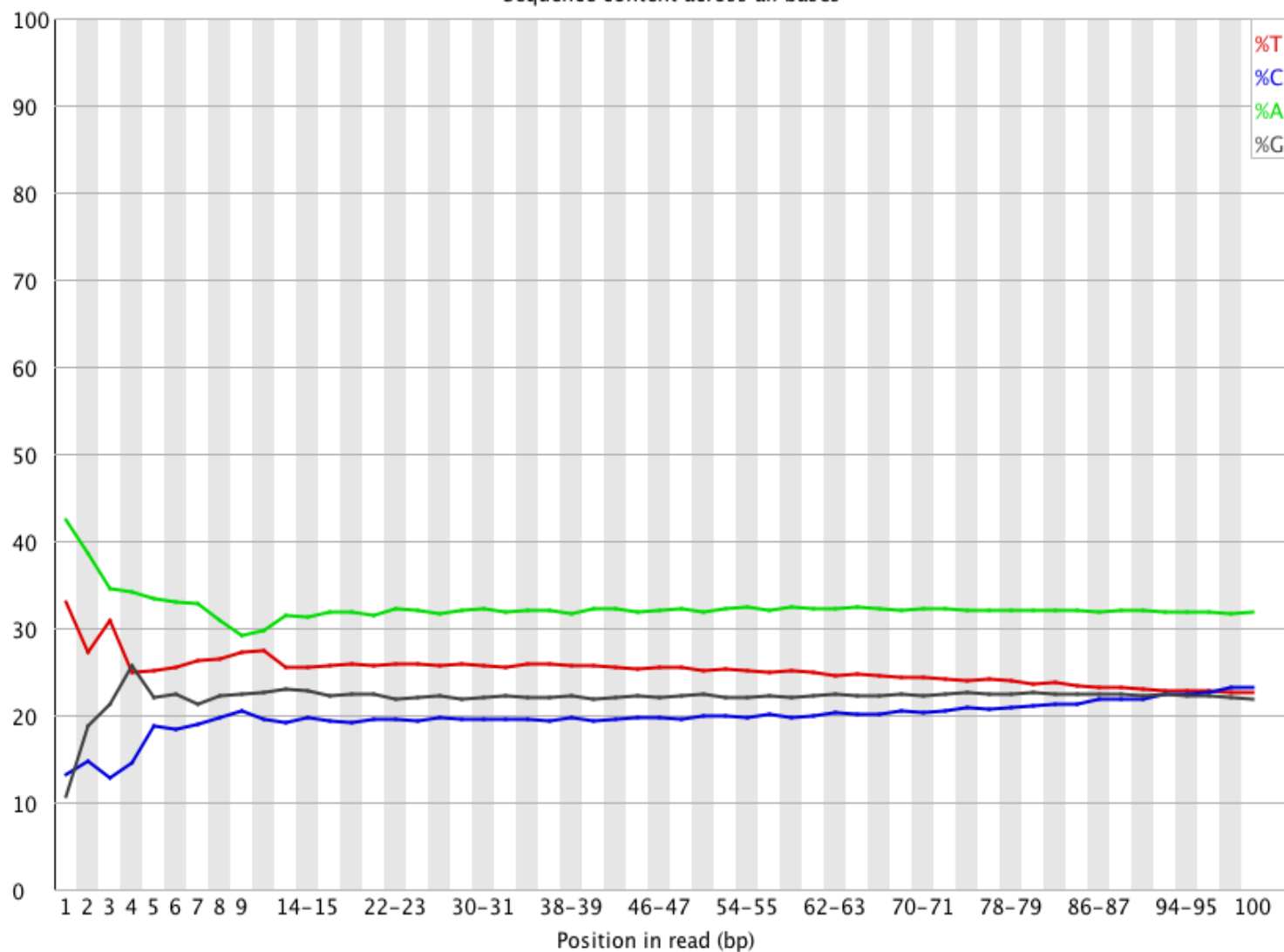
 Per sequence quality scores

Quality score distribution over all sequences

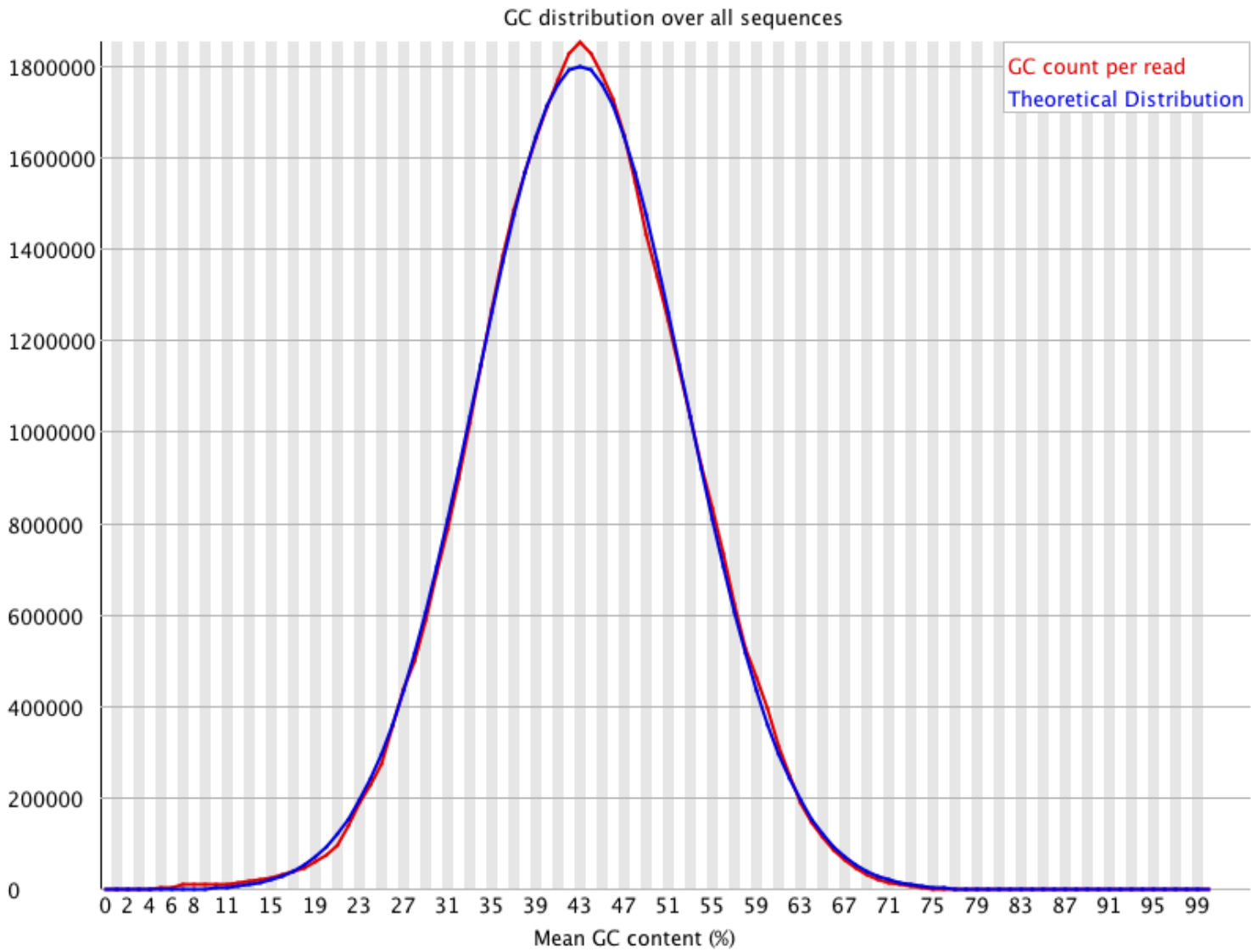


✖ Per base sequence content

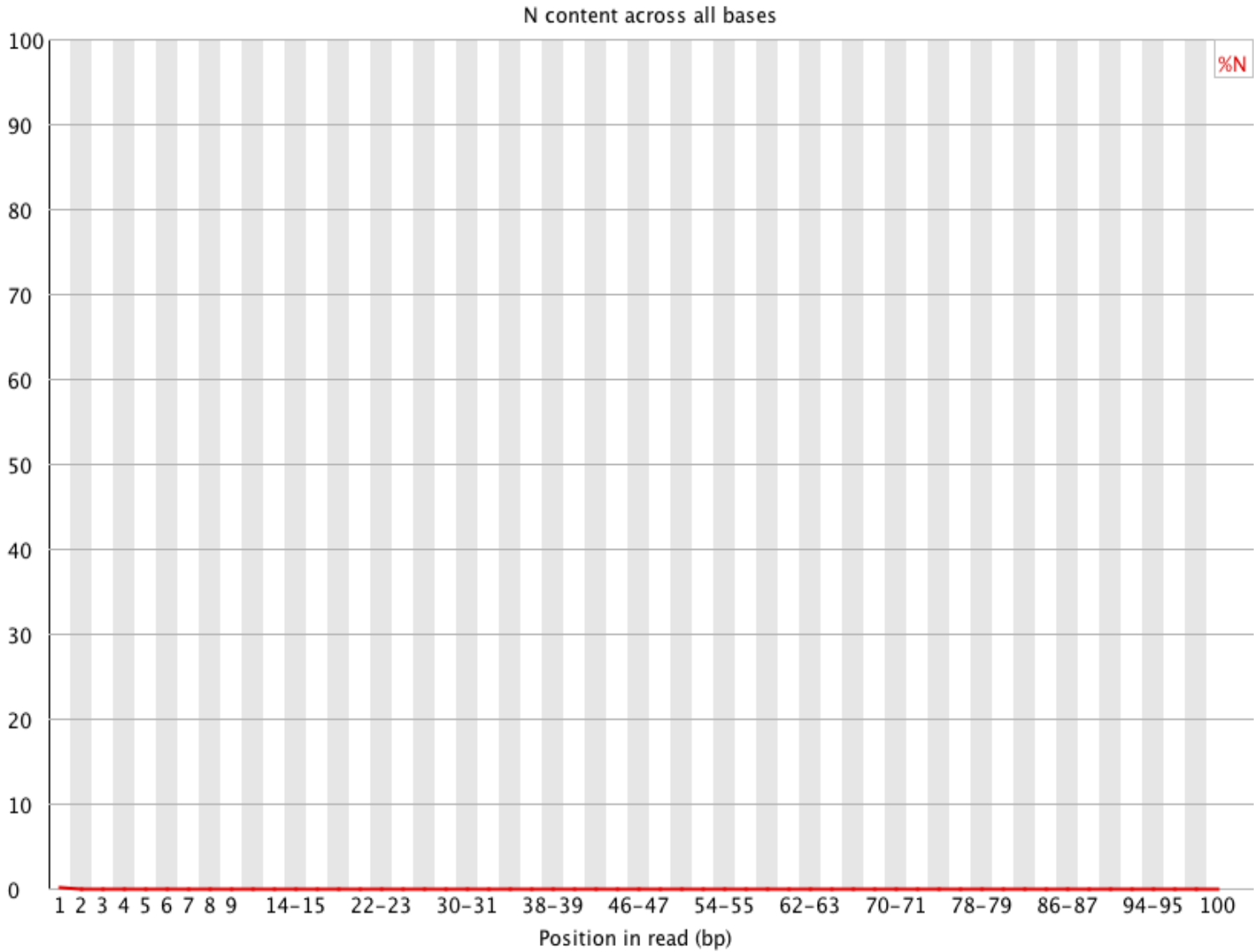
Sequence content across all bases



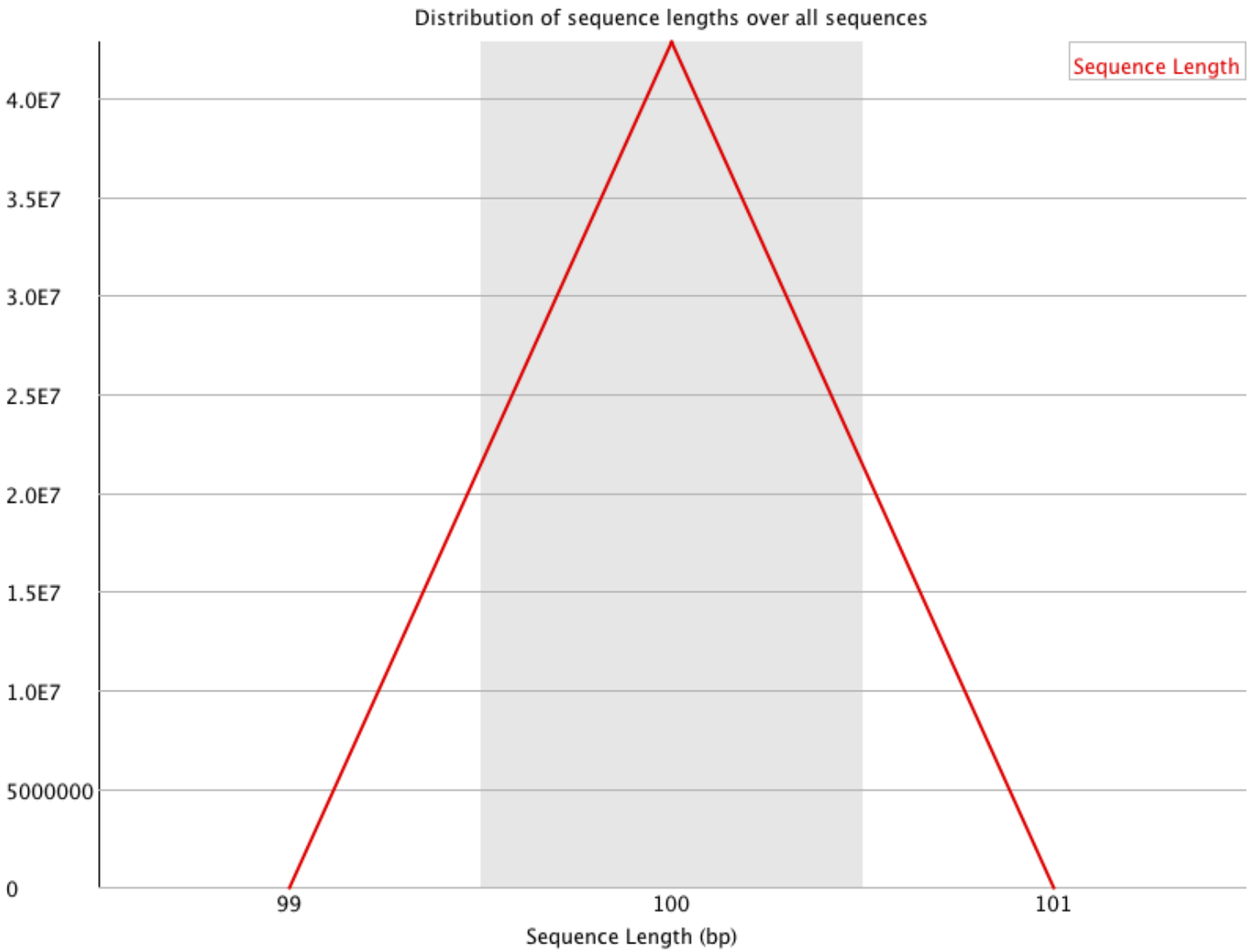
Per sequence GC content



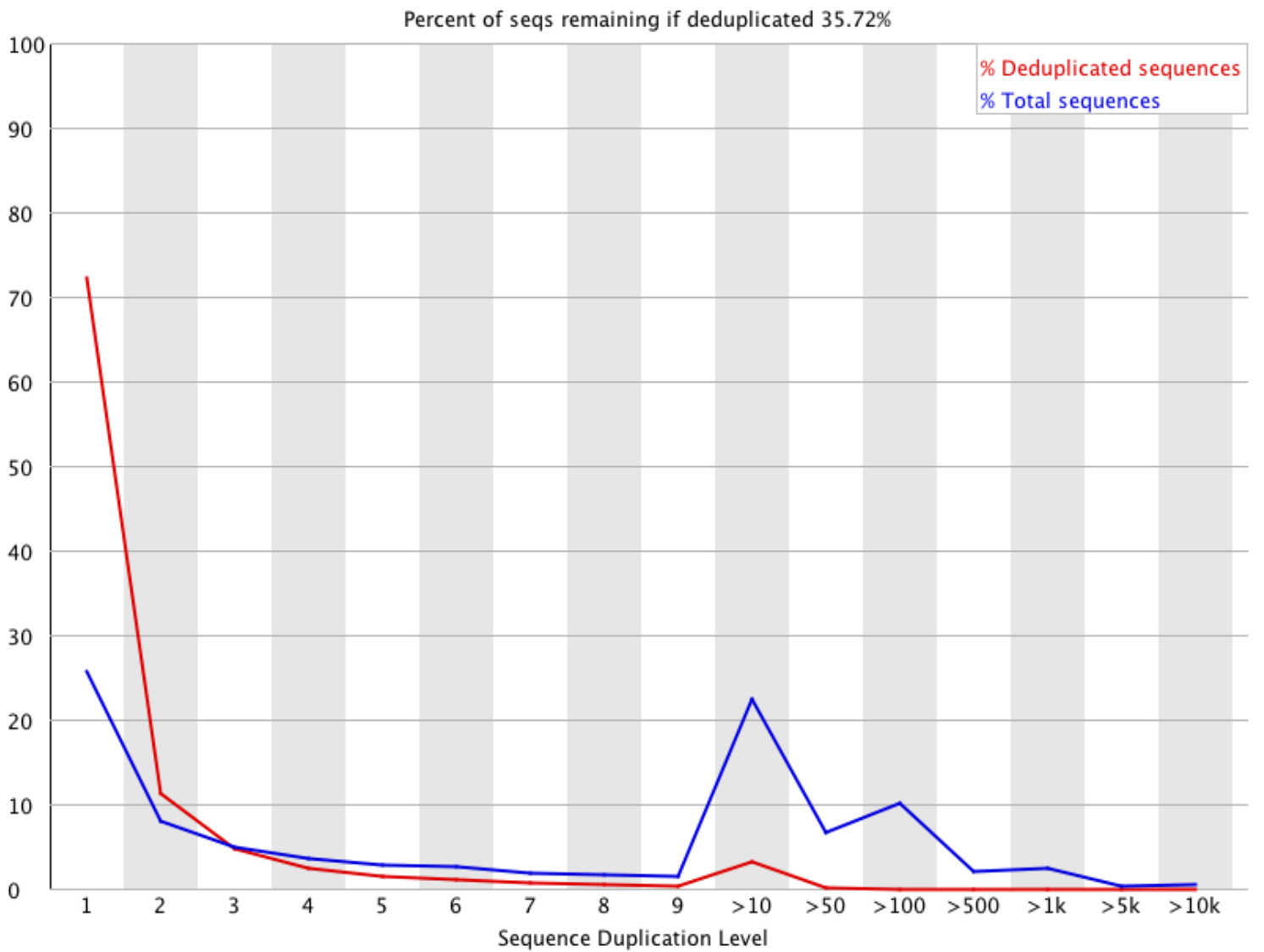
 Per base N content



✔ Sequence Length Distribution

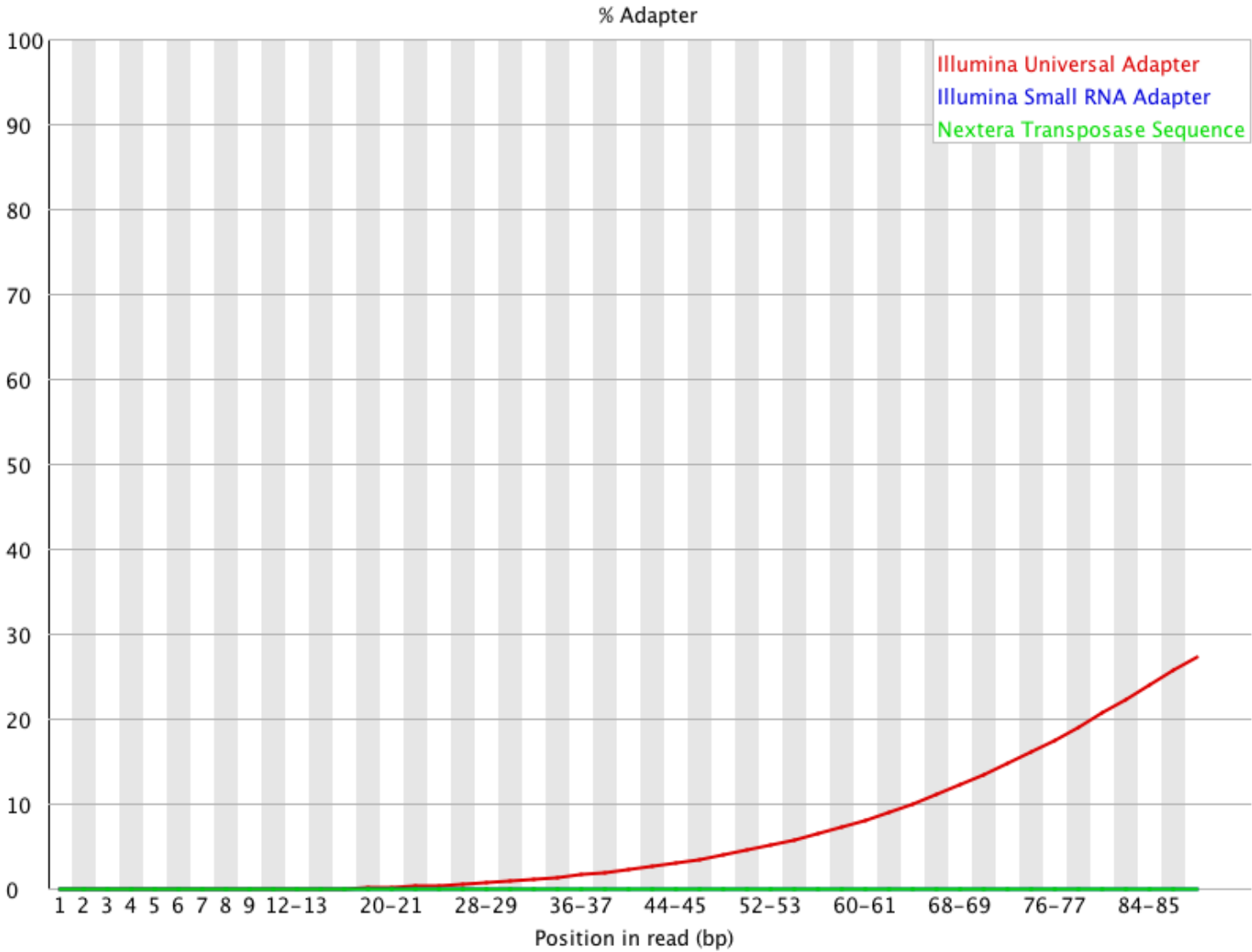


 Sequence Duplication Levels

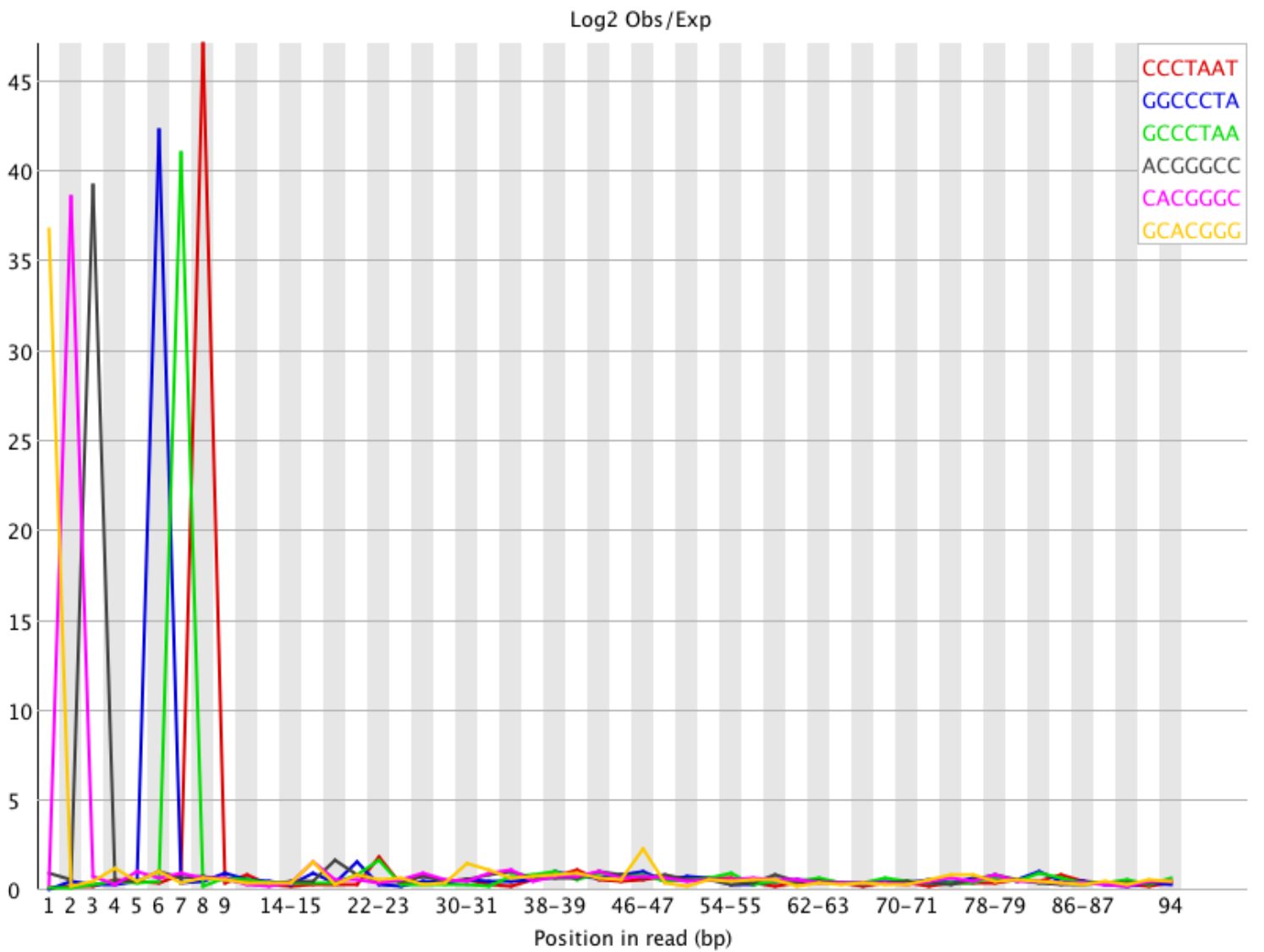


 **Overrepresented sequences**
No overrepresented sequences

 **Adapter Content**



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
CCCTAAT	10330	0.0	47.00213	8
GGCCCTA	11435	0.0	42.29575	6
GCCCTAA	11815	0.0	41.014977	7
ACGGGCC	12250	0.0	39.213207	3
CACGGGC	12430	0.0	38.527687	2
GCACGGG	12965	0.0	36.773525	1
CCTAATT	15465	0.0	31.669073	9
CACACCC	13245	0.0	29.237967	1
ACCCGTC	13545	0.0	28.975105	4
CACCCGT	13595	0.0	28.799393	3
TCGGGCG	13755	0.0	28.635246	9
GGGCCCT	17780	0.0	27.36063	5
CGGGCCC	17735	0.0	27.350548	4

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
ACACCCG	15610	0.0	25.10921	2
GTCGGGC	16590	0.0	24.535166	8
CTAGCGG	9895	0.0	22.752075	70–71
CCGTCGG	18140	0.0	22.075972	6
CCGGTTC	12365	0.0	21.398565	24–25
ATCCGGT	12865	0.0	20.658224	22–23
CTTCGGG	11955	0.0	20.206142	38–39

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FastQC Report

Summary

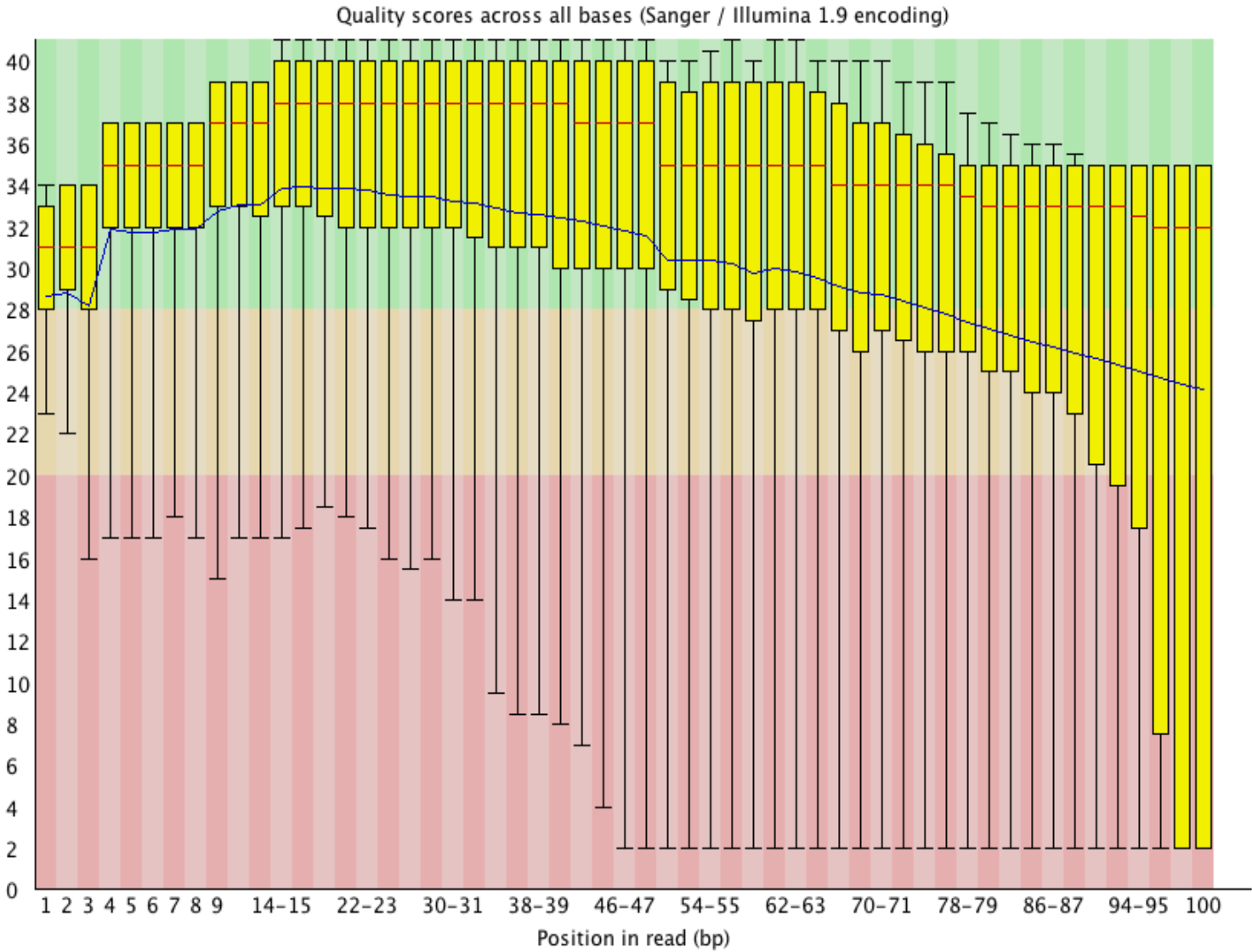
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-  [Sequence Length Distribution](#)
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-  [Adapter Content](#)
-  [Kmer Content](#)

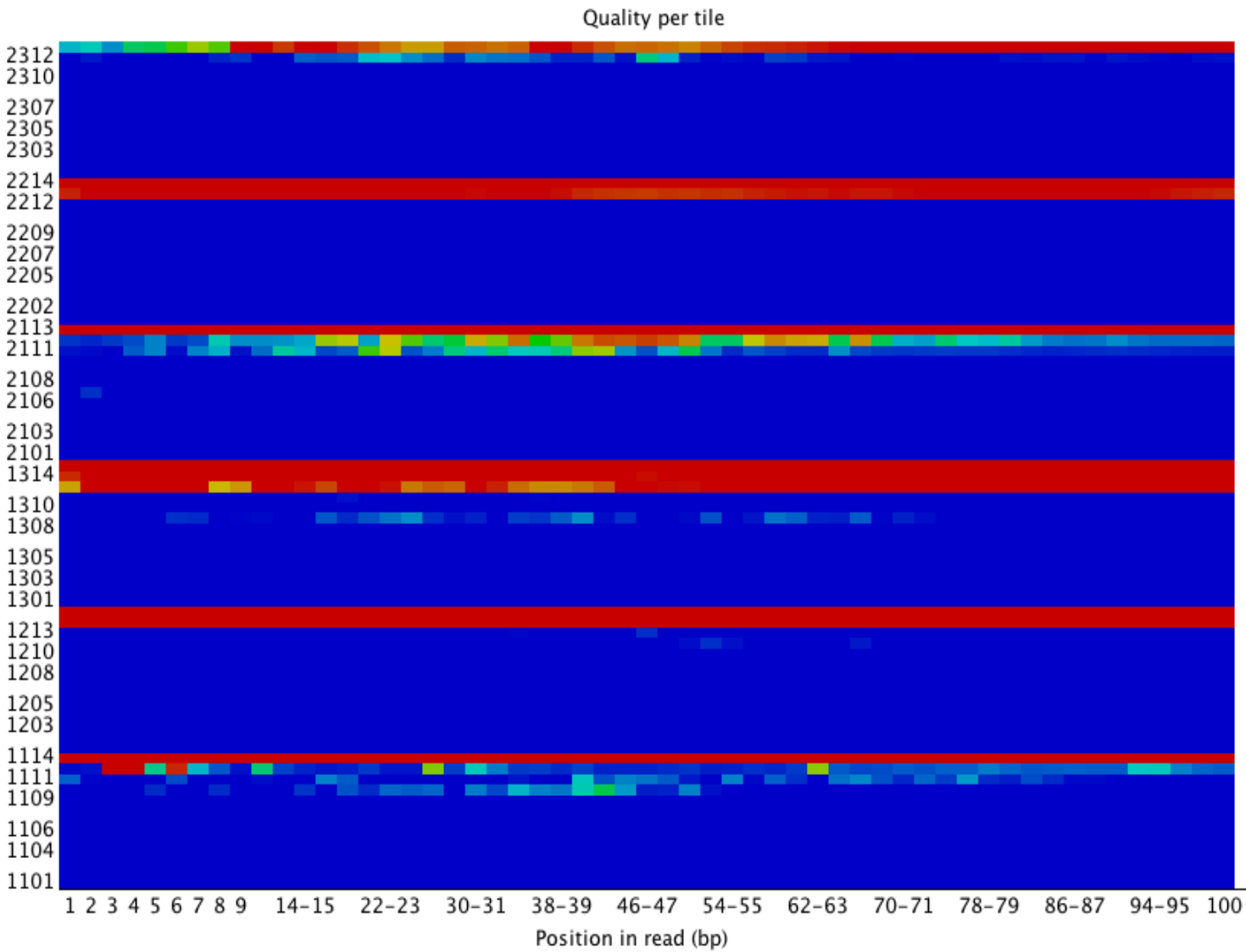
Basic Statistics

Measure	Value
Filename	3P_GCCAAT_L001_R2_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	42848501
Sequences flagged as poor quality	0
Sequence length	100
%GC	42

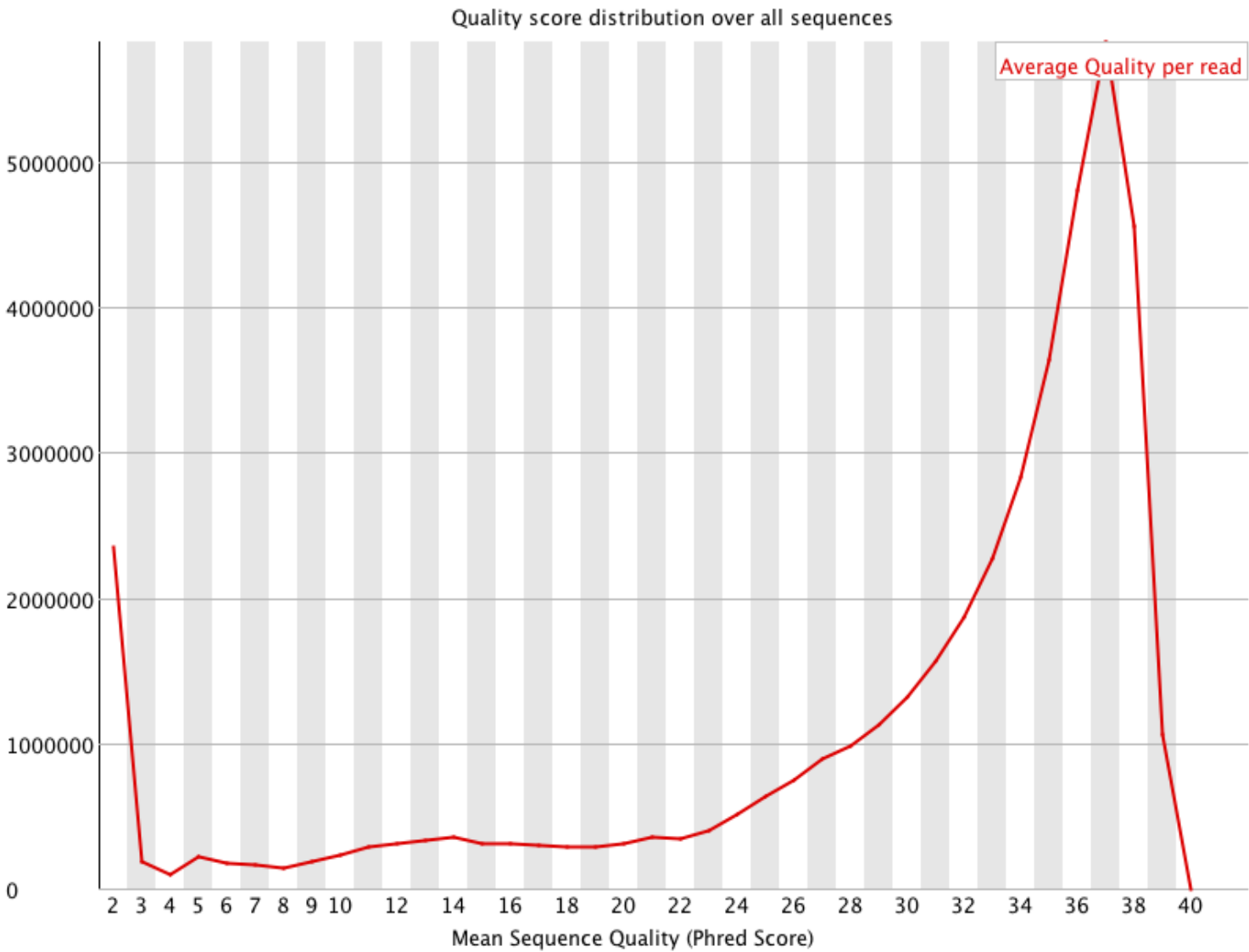
Per base sequence quality



✖ Per tile sequence quality

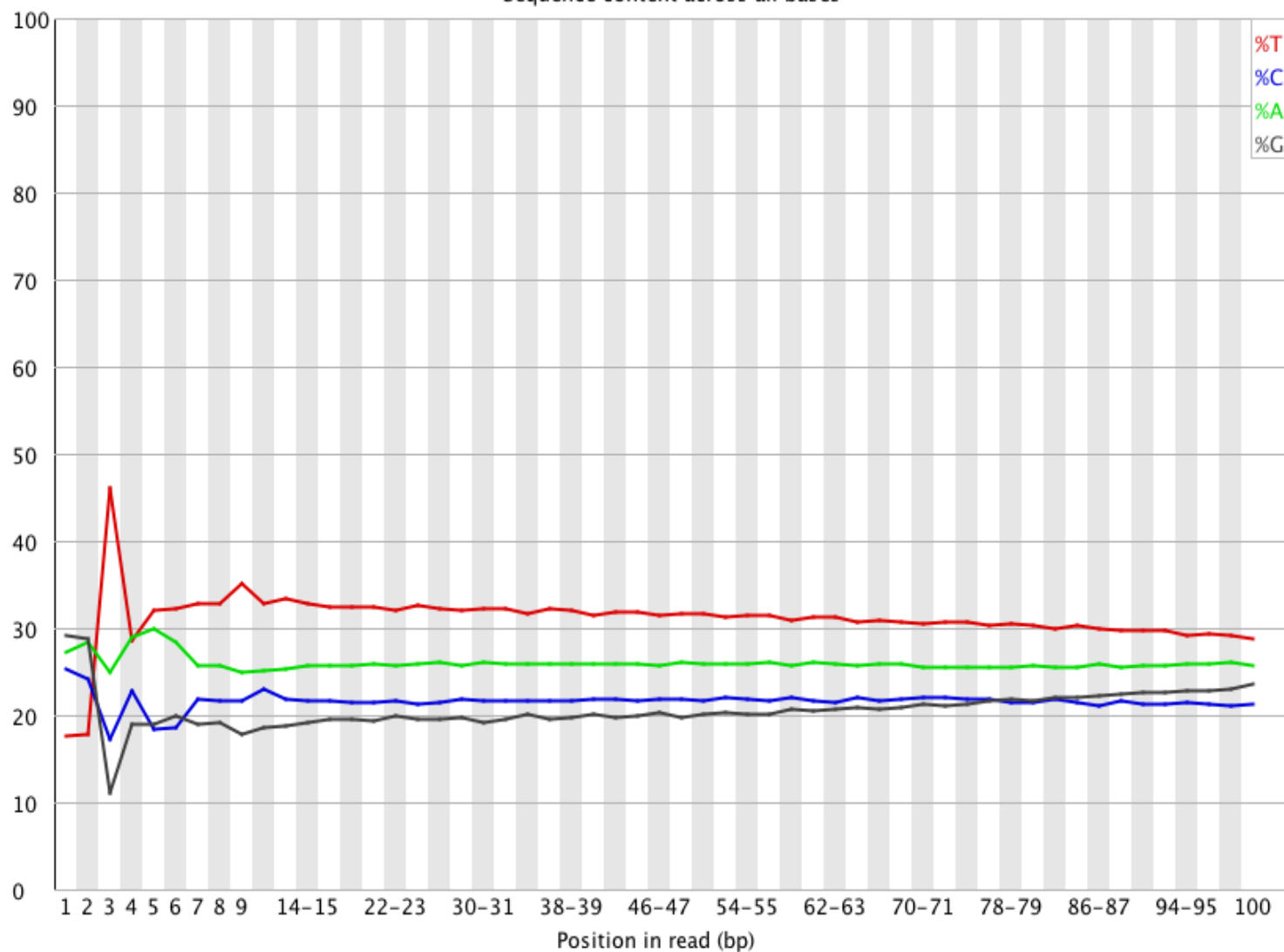


 Per sequence quality scores



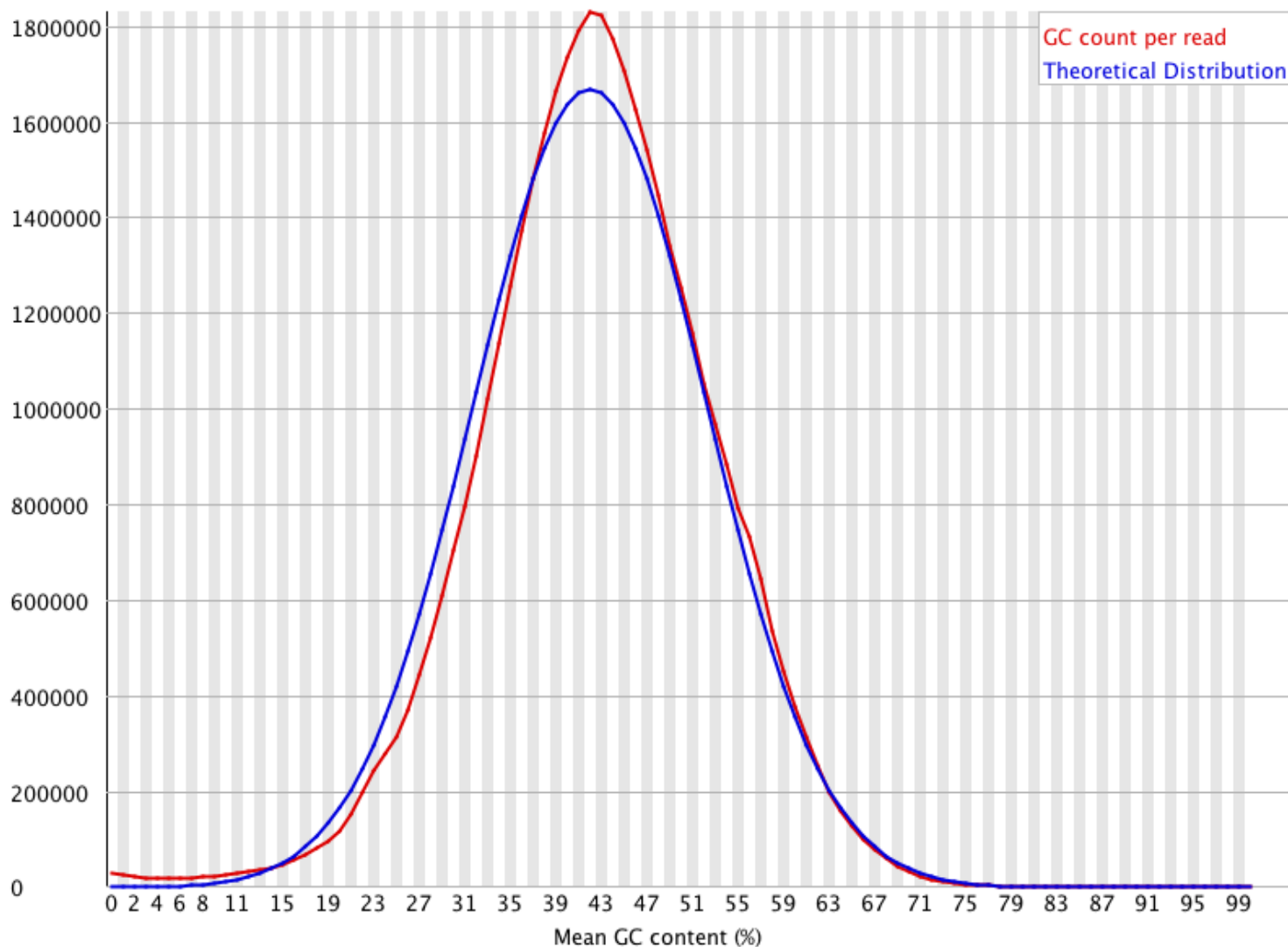
✖ Per base sequence content

Sequence content across all bases

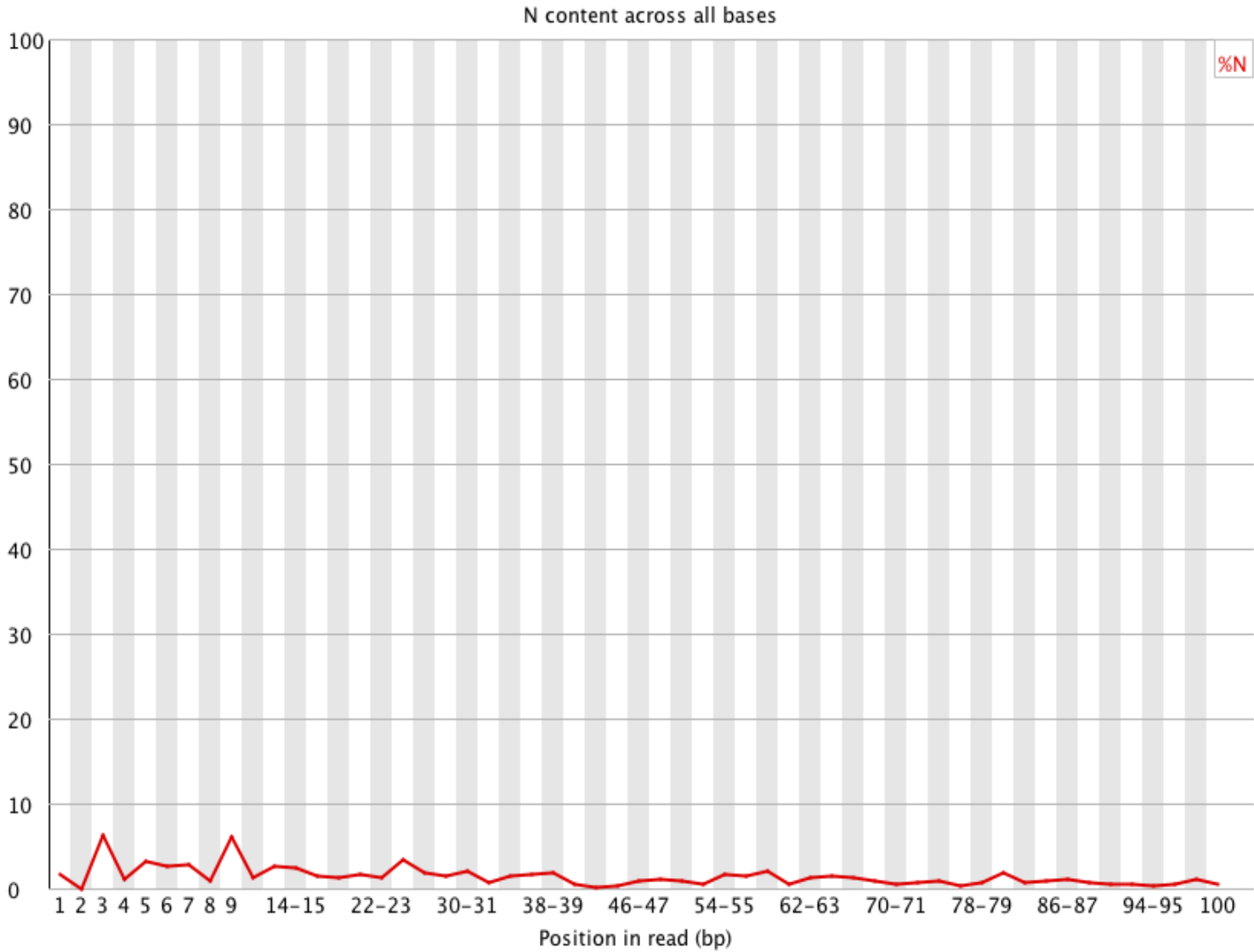


Per sequence GC content

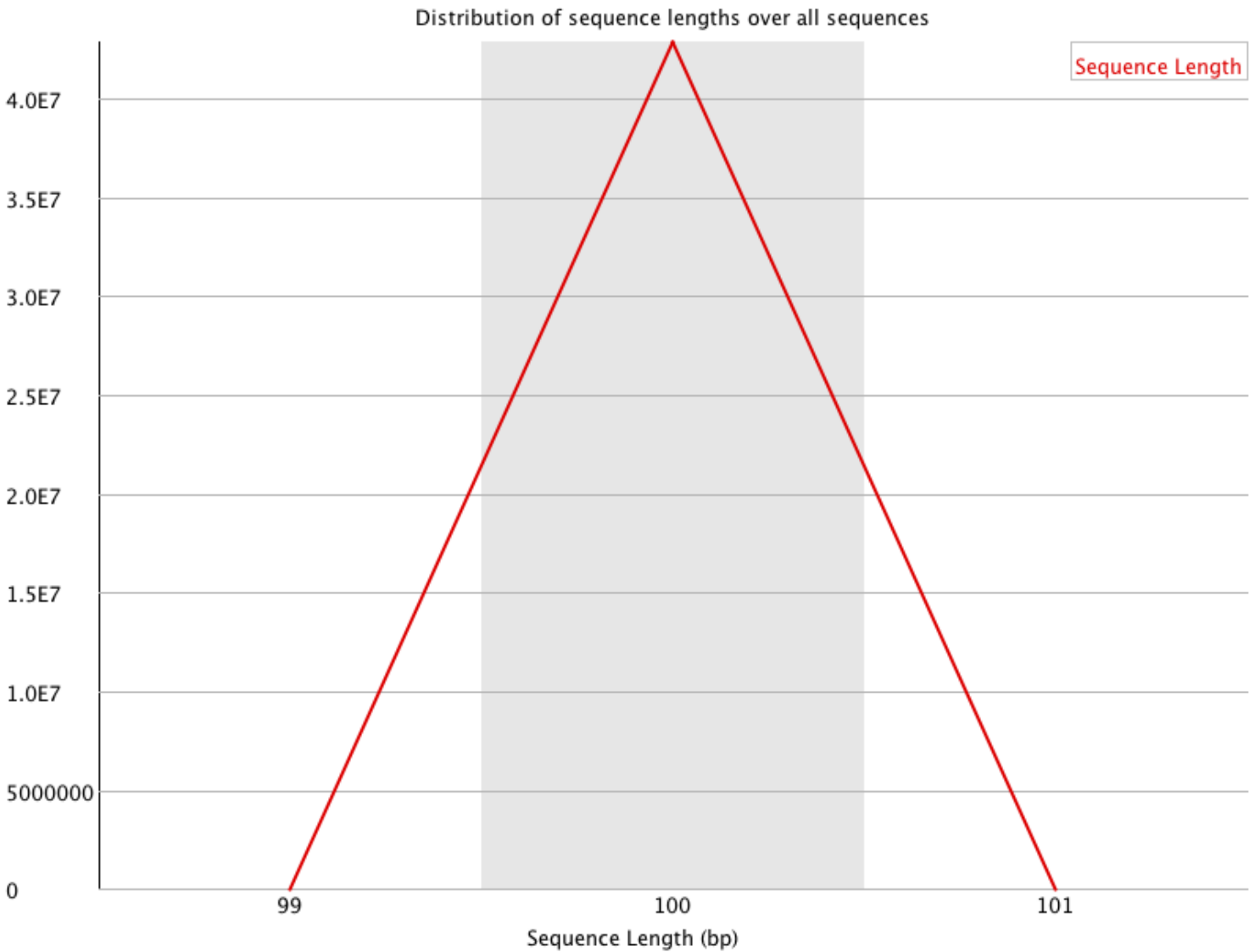
GC distribution over all sequences



! Per base N content



✔ Sequence Length Distribution

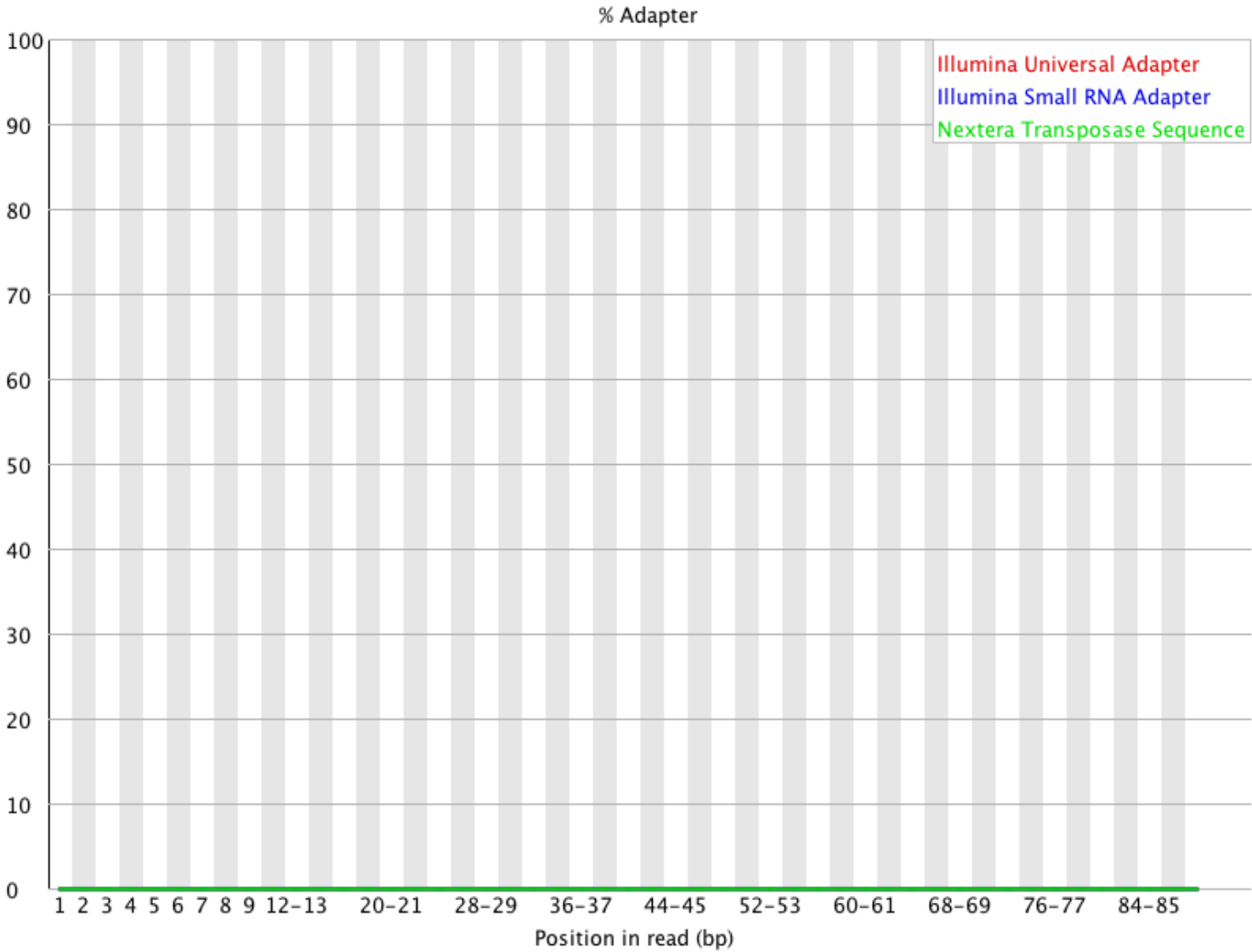


 Sequence Duplication Levels

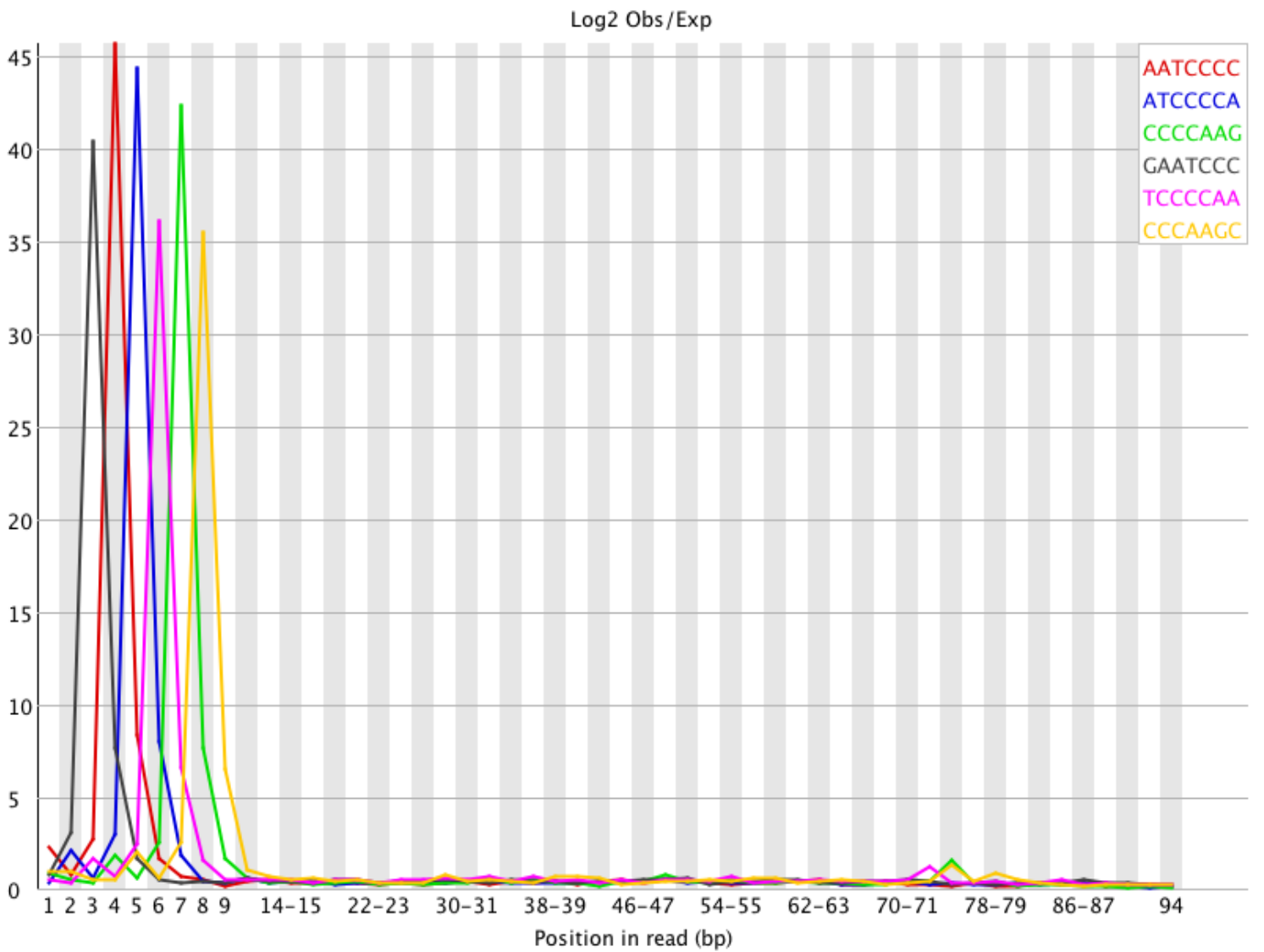


Sequence	Count	Percentage	Possible Source
TTT	104372	0.24358378371276043	No Hit
ACGAATCCCCAAGCCAAGGGCTGAGTCTCAACAGATCGCAGCGTGGTAAC	60232	0.14056967827182568	No Hit

Adapter Content



 Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AATCCCC	17115	0.0	45.679775	4
ATCCCCA	17430	0.0	44.38296	5
CCCCAAG	18345	0.0	42.37875	7
GAATCCC	19540	0.0	40.439472	3
TCCCCAA	21485	0.0	36.118732	6
CCCAAGC	21870	0.0	35.570786	8
ACAGACG	23670	0.0	30.795156	94
CCAAGCC	25420	0.0	30.775688	9
CGAATCC	28160	0.0	28.837755	2
ACGAATC	29475	0.0	26.927872	1
CACCCCG	16435	0.0	25.804176	68–69
CCAAGGG	18620	0.0	24.44364	14–15
ACCCCGC	15830	0.0	24.202917	68–69

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
GGGCTGA	19790	0.0	23.130438	18-19
ACACCCC	17050	0.0	22.705233	66-67
CGTGGTA	18475	0.0	22.692219	42-43
AGCGTGG	19450	0.0	22.312975	40-41
AAGGGCT	20925	0.0	21.771658	16-17
CCCCGCC	19865	0.0	21.428267	70-71
CAAGGGC	19785	0.0	21.12618	14-15

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