













FastQC Report

Summary

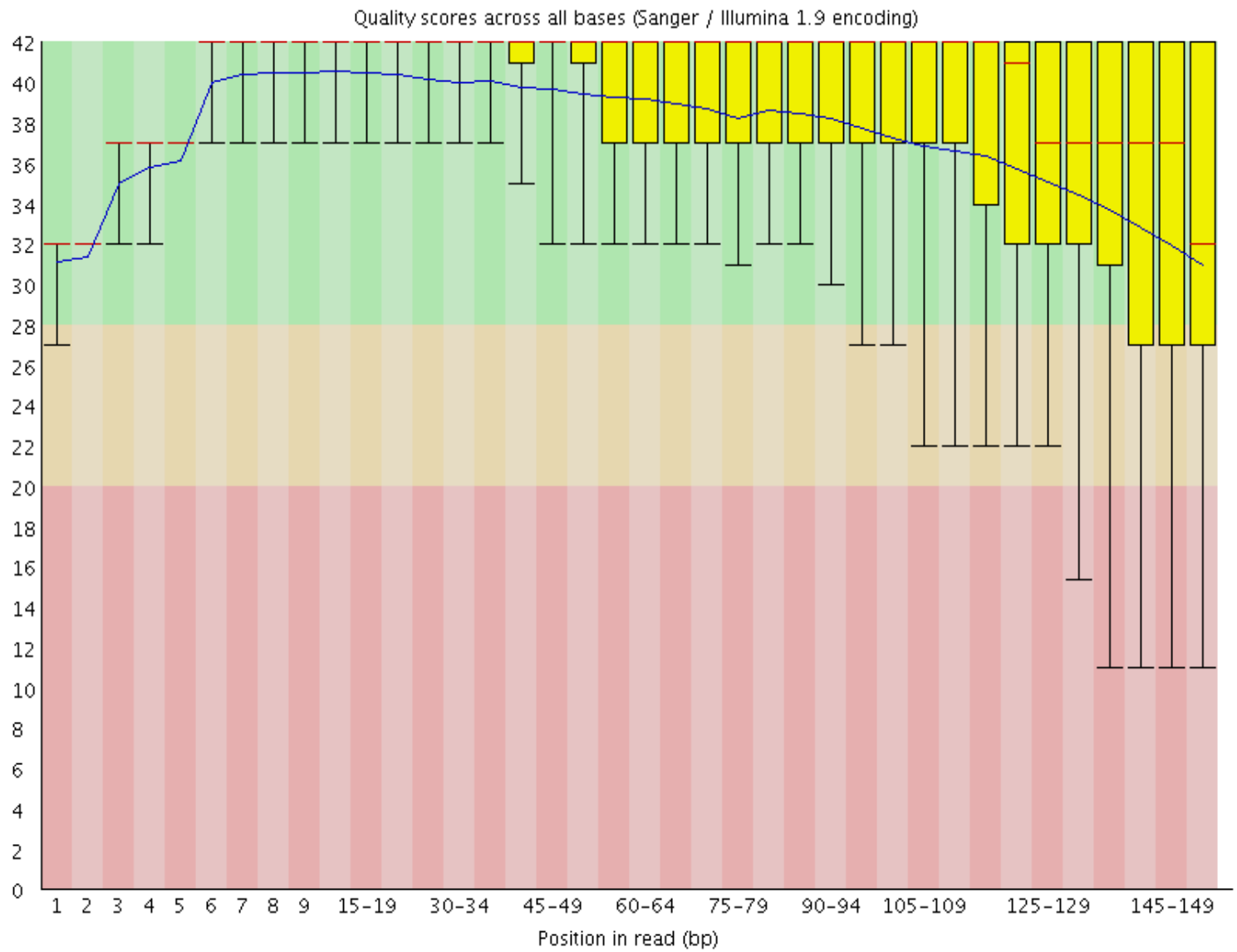
Wed 11 Apr 2018
PBA_S37_L007_R1_001.fastq

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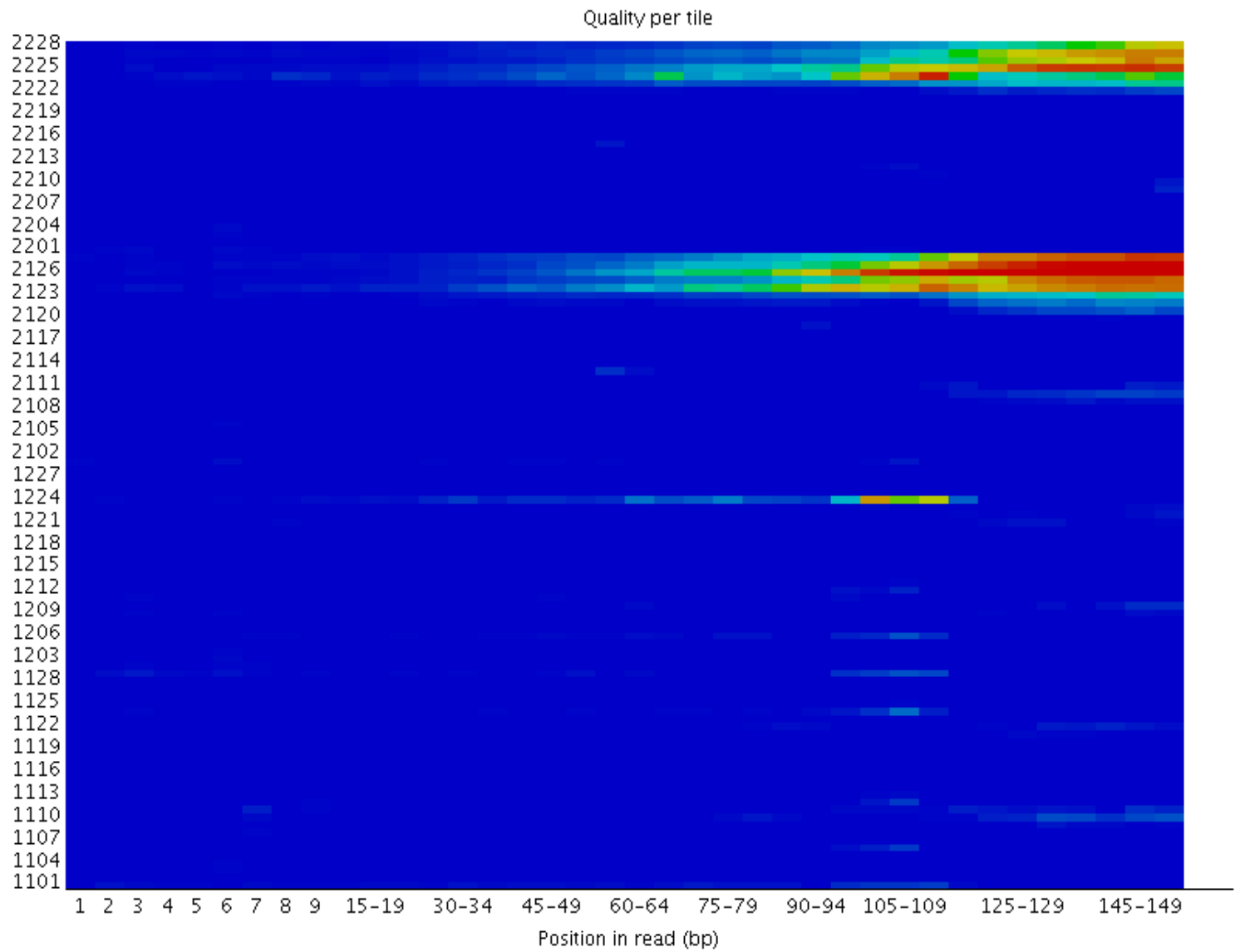
Basic Statistics

Measure	Value
Filename	PBA_S37_L007_R1_001.fastq
File type	Conventional base calls
Encoding	Sanger / Illumina 1.9
Total Sequences	32319223
Sequences flagged as poor quality	0
Sequence length	151
%GC	42

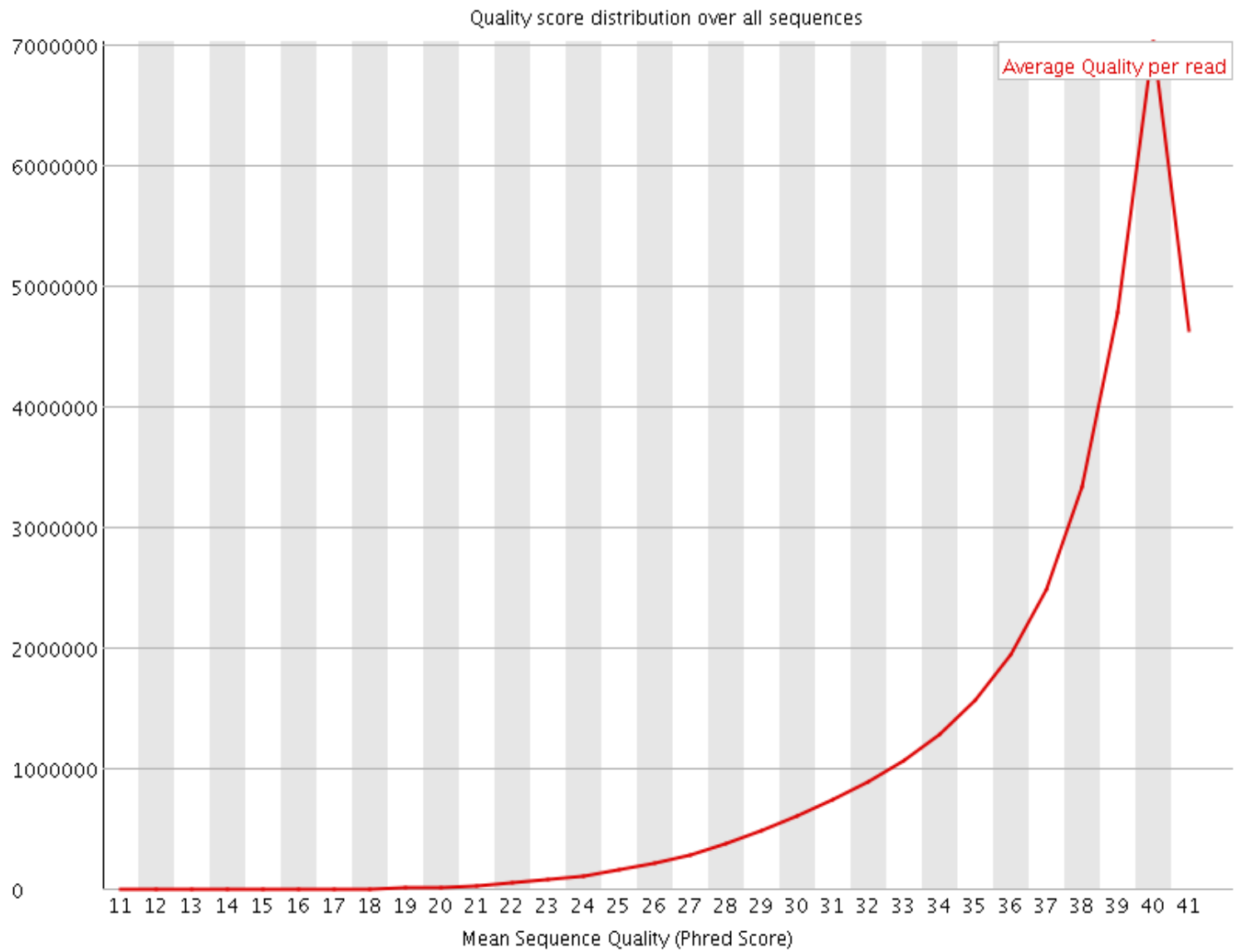
Per base sequence quality



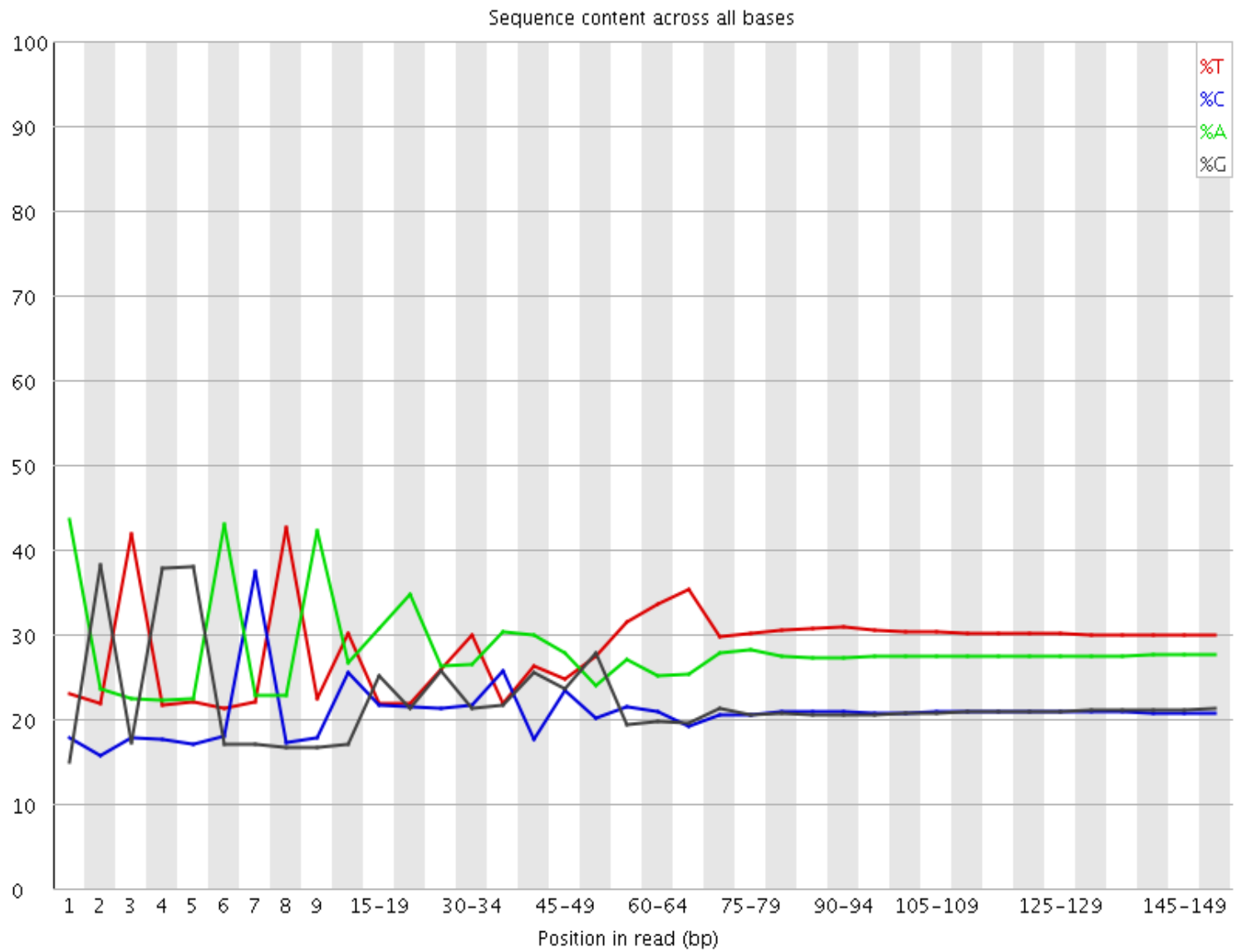
✖ Per tile sequence quality



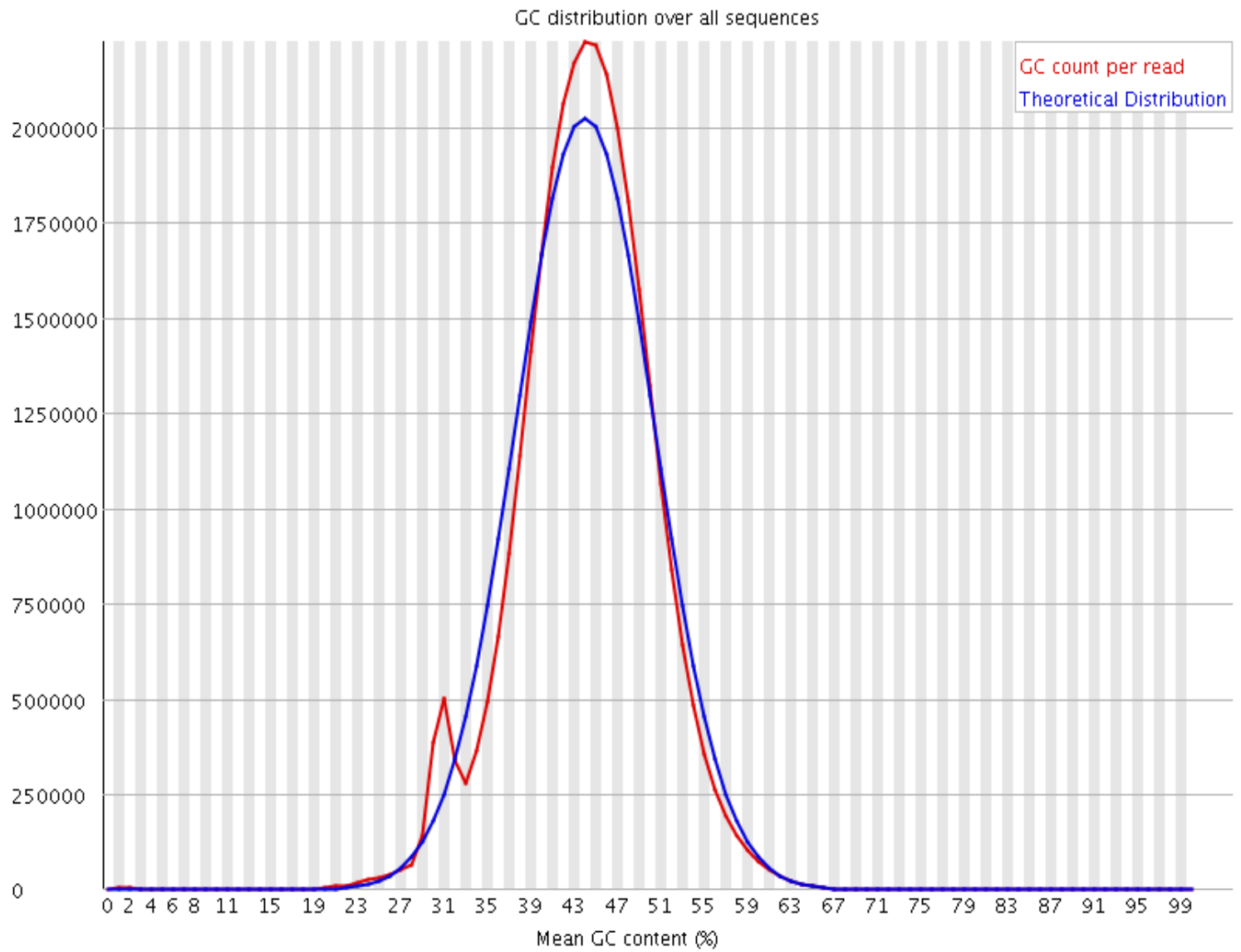
Per sequence quality scores



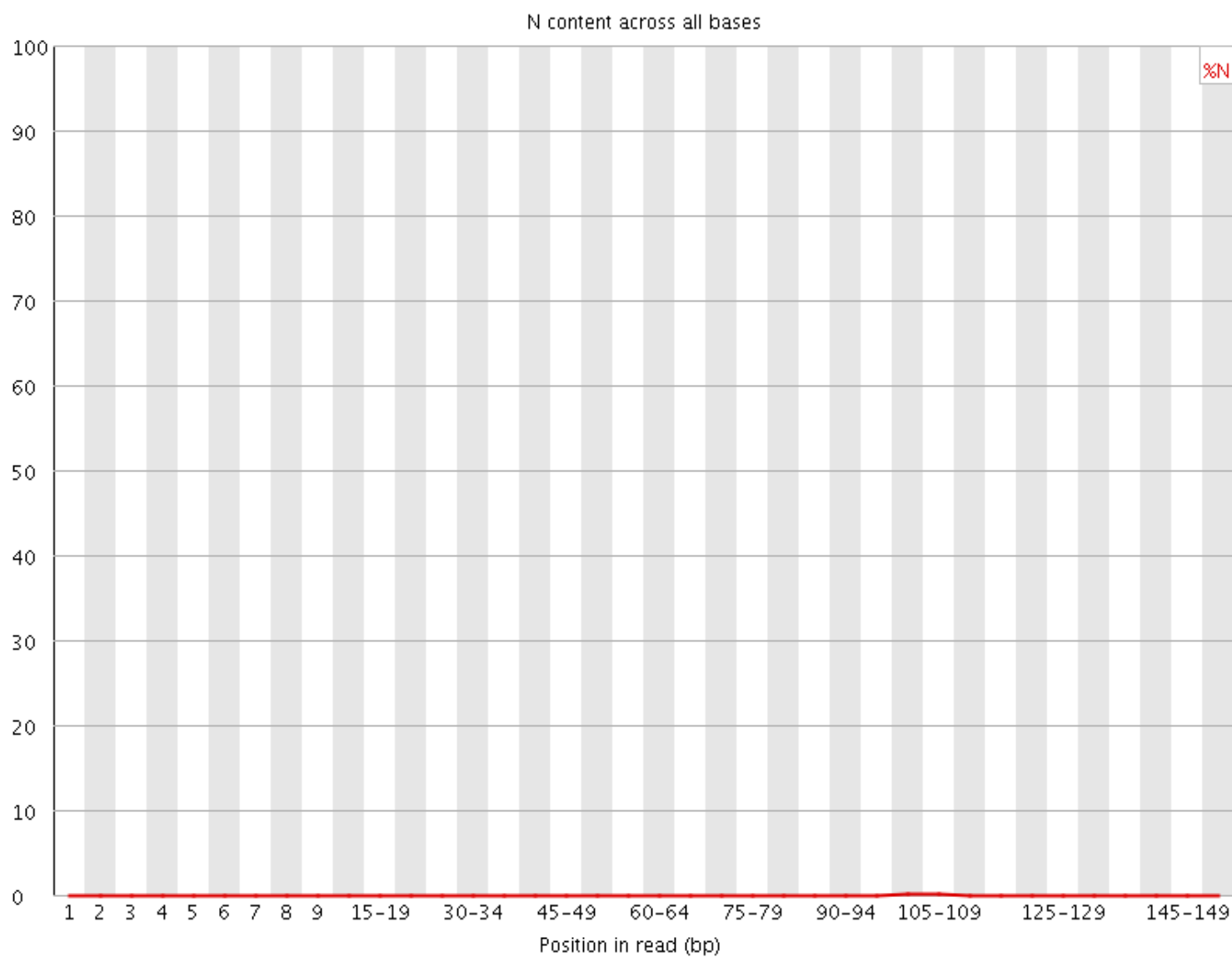
✖ Per base sequence content



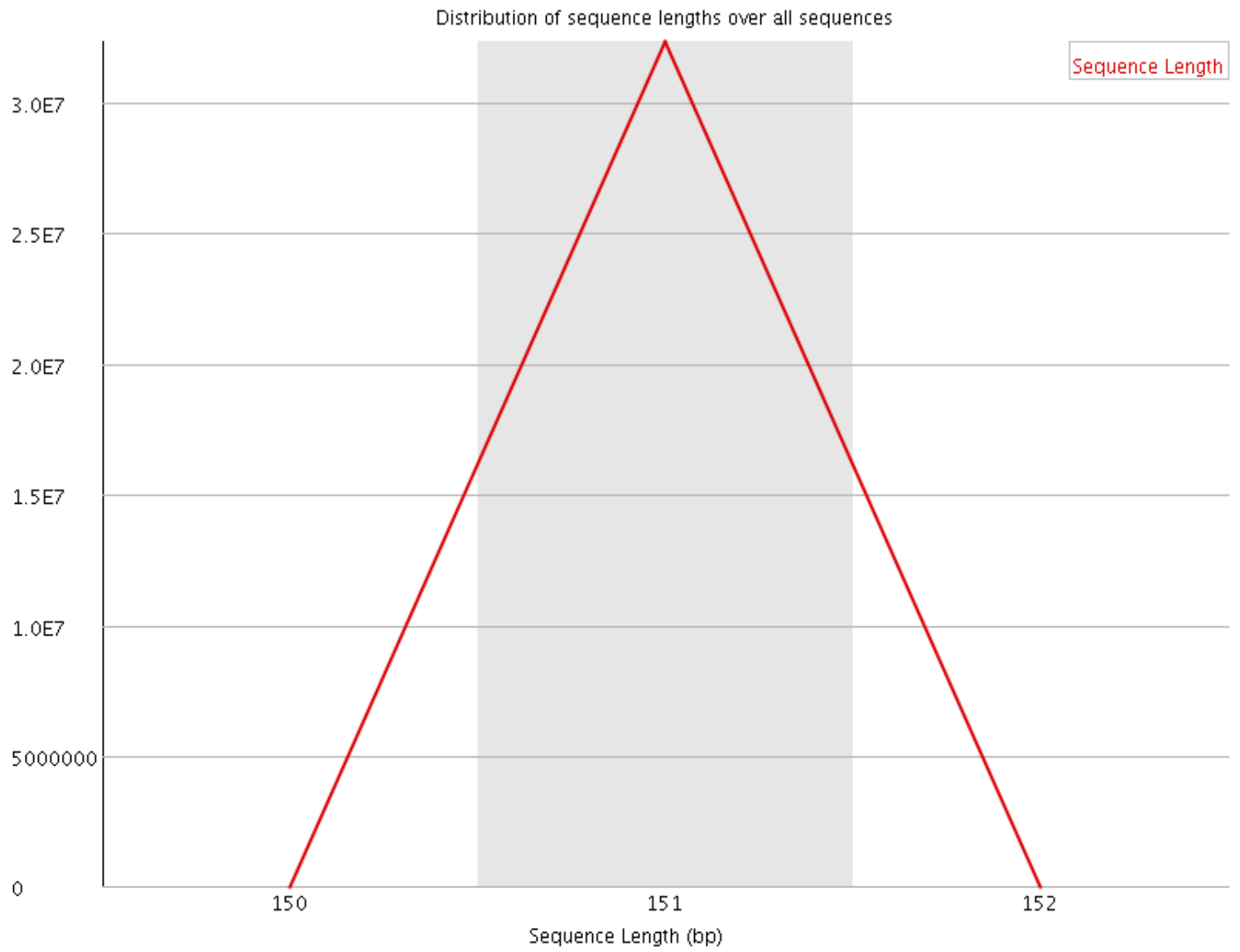
Per sequence GC content



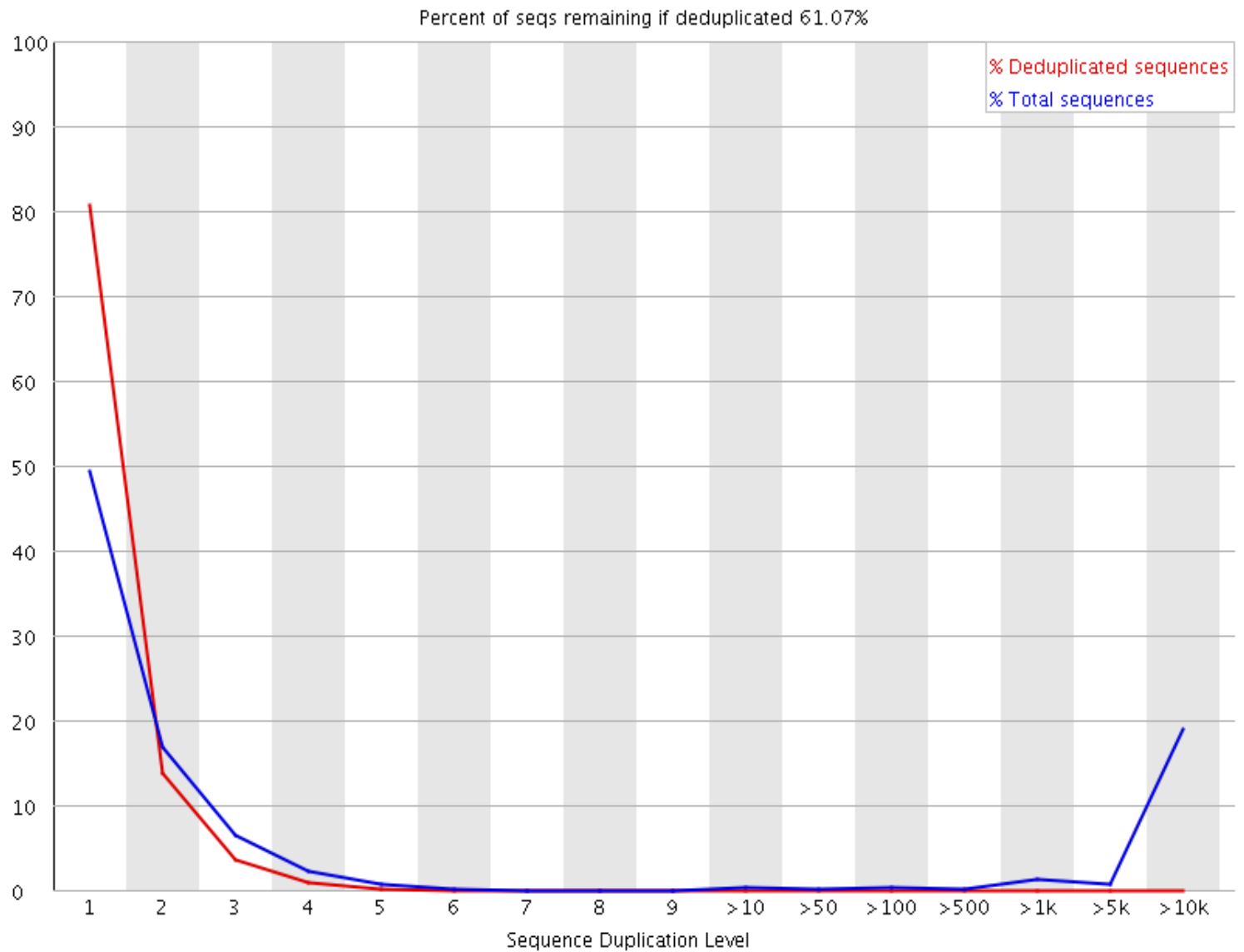
Per base N content



Sequence Length Distribution



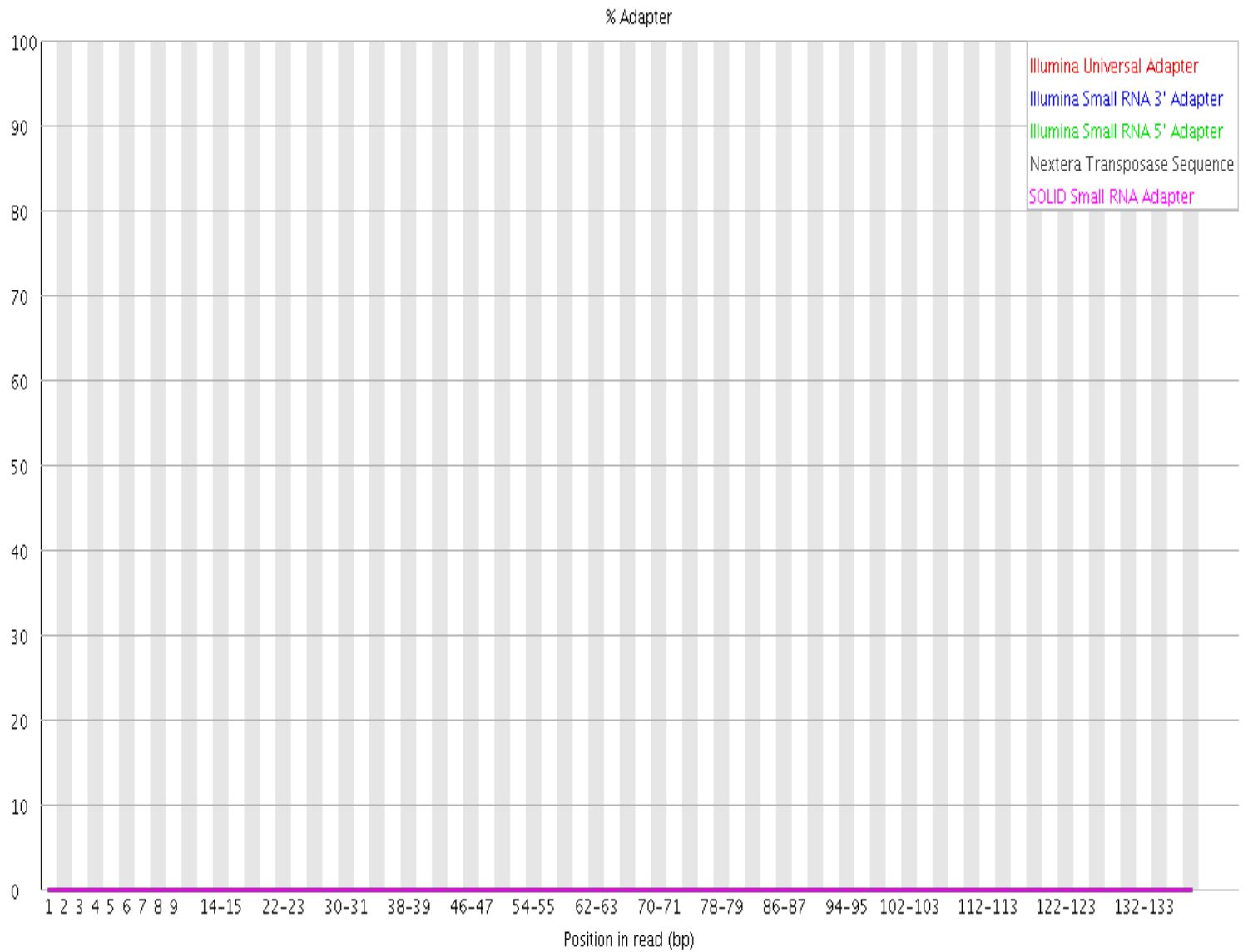
⚠ Sequence Duplication Levels



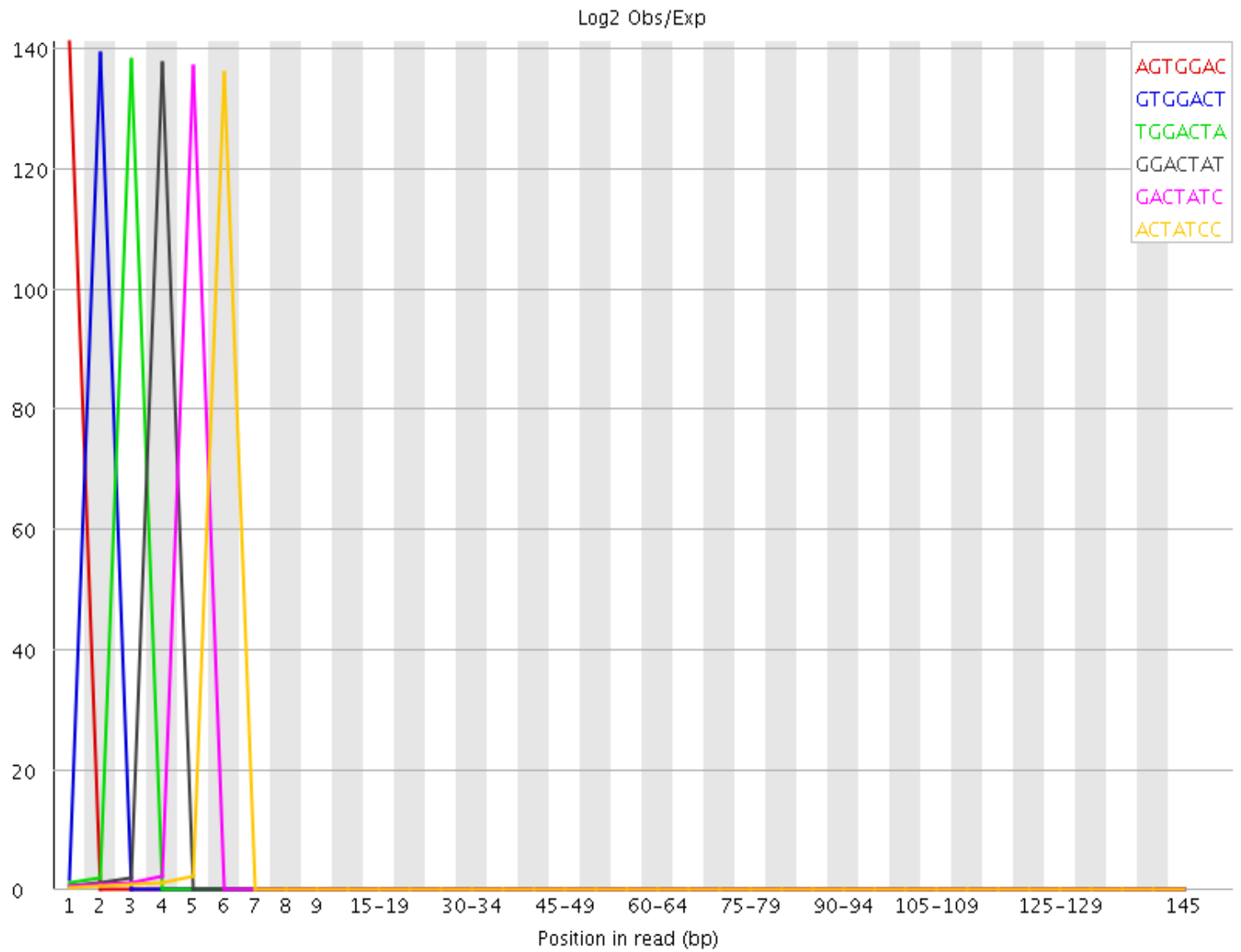
✖ Overrepresented sequences

Sequence	Count	Percentage	Possible Source
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGAGTCGCAGT	2708214	8.379576452070028	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGAGTACATGG	2556333	7.909636317680039	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGATTACATGG	59591	0.18438252677052291	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGATTTCGCAGT	55387	0.17137478831096897	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCGAGTCGCAGTC	53770	0.16637157397007965	No Hit
TCCATGAACGCAAAGCAGTGGTATCAACGCAGAGTCGCAGTCGGTACTTT	43411	0.1343194420237145	No Hit
AGTGGACTATCCATGAACGCAAAGCAGTGGTATCAACGCAGGTCGCAGTC	42608	0.1318348525891232	No Hit
AACGCAAAGCAGTGGTATCAACGCAGAGTCGCAGTCGGTACTTTTTTCTT	33102	0.10242201676692536	No Hit

✓ Adapter Content



✗ Kmer Content



Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGTGGAC	682455	0.0	140.96655	1
GTGGACT	690820	0.0	139.17679	2
TGGACTA	695585	0.0	138.04778	3
GGACTAT	698225	0.0	137.46384	4
GACTATC	701065	0.0	136.92143	5
ACTATCC	704325	0.0	135.91628	6
CTATCCA	713755	0.0	133.9967	7
TATCCAT	730620	0.0	130.76498	8
ATCCATG	738775	0.0	129.07259	9
TGAACGC	732160	0.0	26.995125	10-14
ATGAACG	733365	0.0	26.911045	10-14
CATGAAC	753715	0.0	26.08274	10-14
CGCAAAG	756970	0.0	25.967342	15-19

Sequence	Count	PValue	Obs/Exp Max	Max Obs/Exp Position
AGTGGAC	682455	0.0	140.96655	1
GTGGACT	690820	0.0	139.17679	2
TGGACTA	695585	0.0	138.04778	3
GGACTAT	698225	0.0	137.46384	4
GACTATC	701065	0.0	136.92143	5
ACTATCC	704325	0.0	135.91628	6
CTATCCA	713755	0.0	133.9967	7
TATCCAT	730620	0.0	130.76498	8
ATCCATG	738775	0.0	129.07259	9
TGAACGC	732160	0.0	26.995125	10-14
ATGAACG	733365	0.0	26.911045	10-14
CATGAAC	753715	0.0	26.08274	10-14
CGCAAAG	756970	0.0	25.967342	15-19

ACGCAA	754595	0.0	25.94555	15-19
AACGCA	756540	0.0	25.713528	15-19
GAACGCA	737690	0.0	25.699472	15-19
TCAACGC	761495	0.0	25.695671	30-34
CCATGAA	759045	0.0	25.645454	10-14
CAACGCA	749495	0.0	25.613003	30-34
GTCGGTA	368700	0.0	25.501919	45-49

Produced by [FastQC](#) (version 0.11.5)