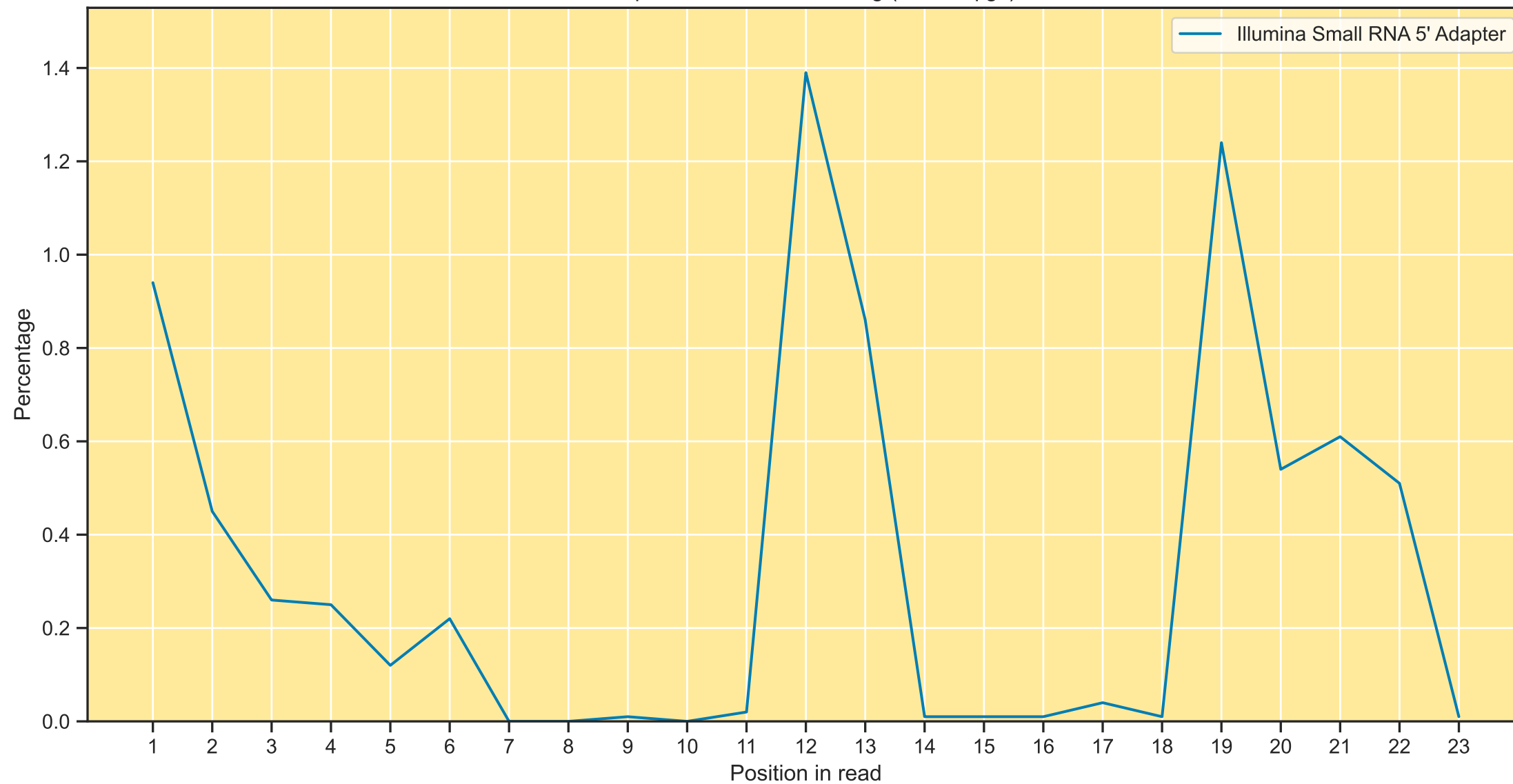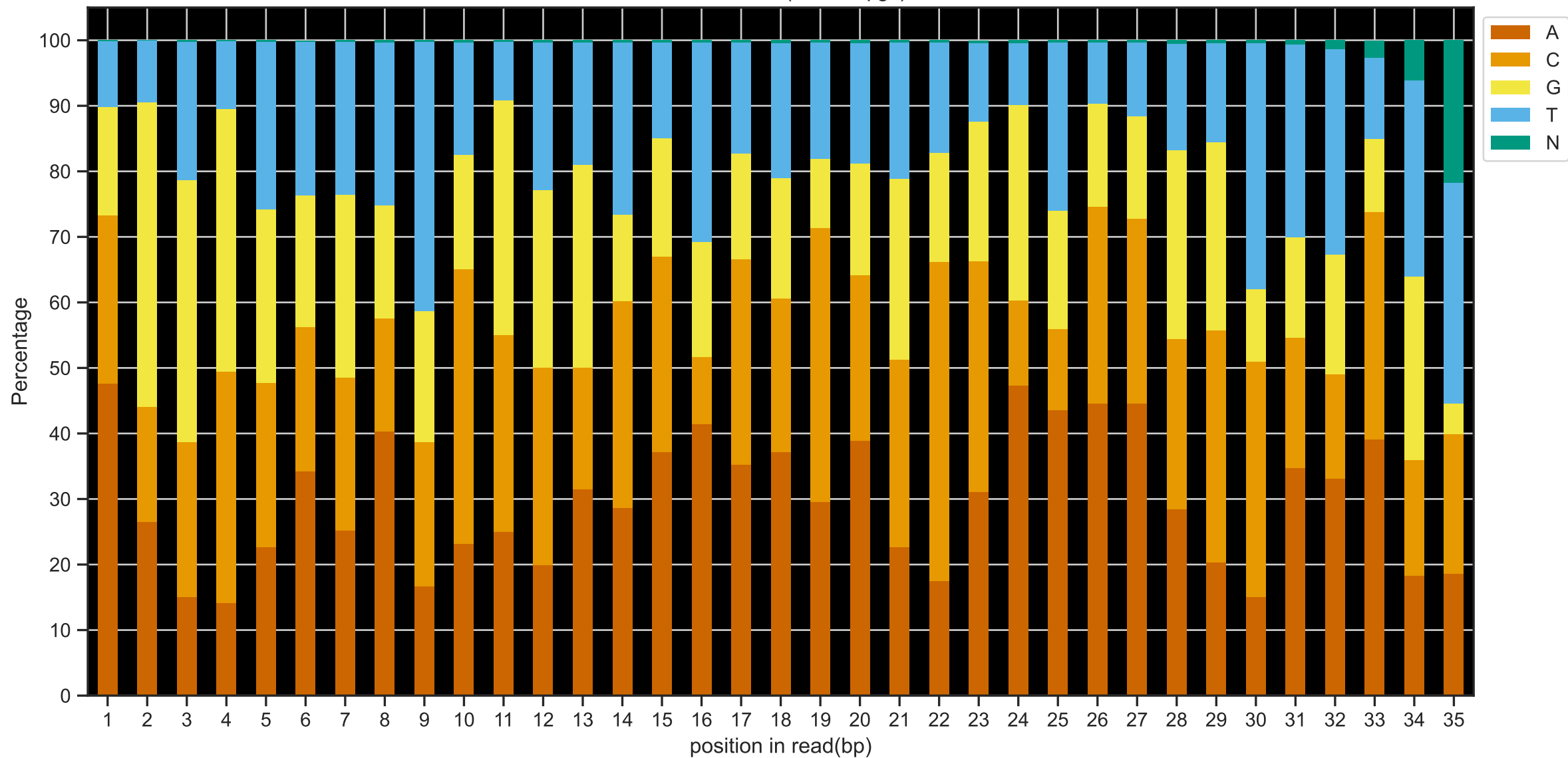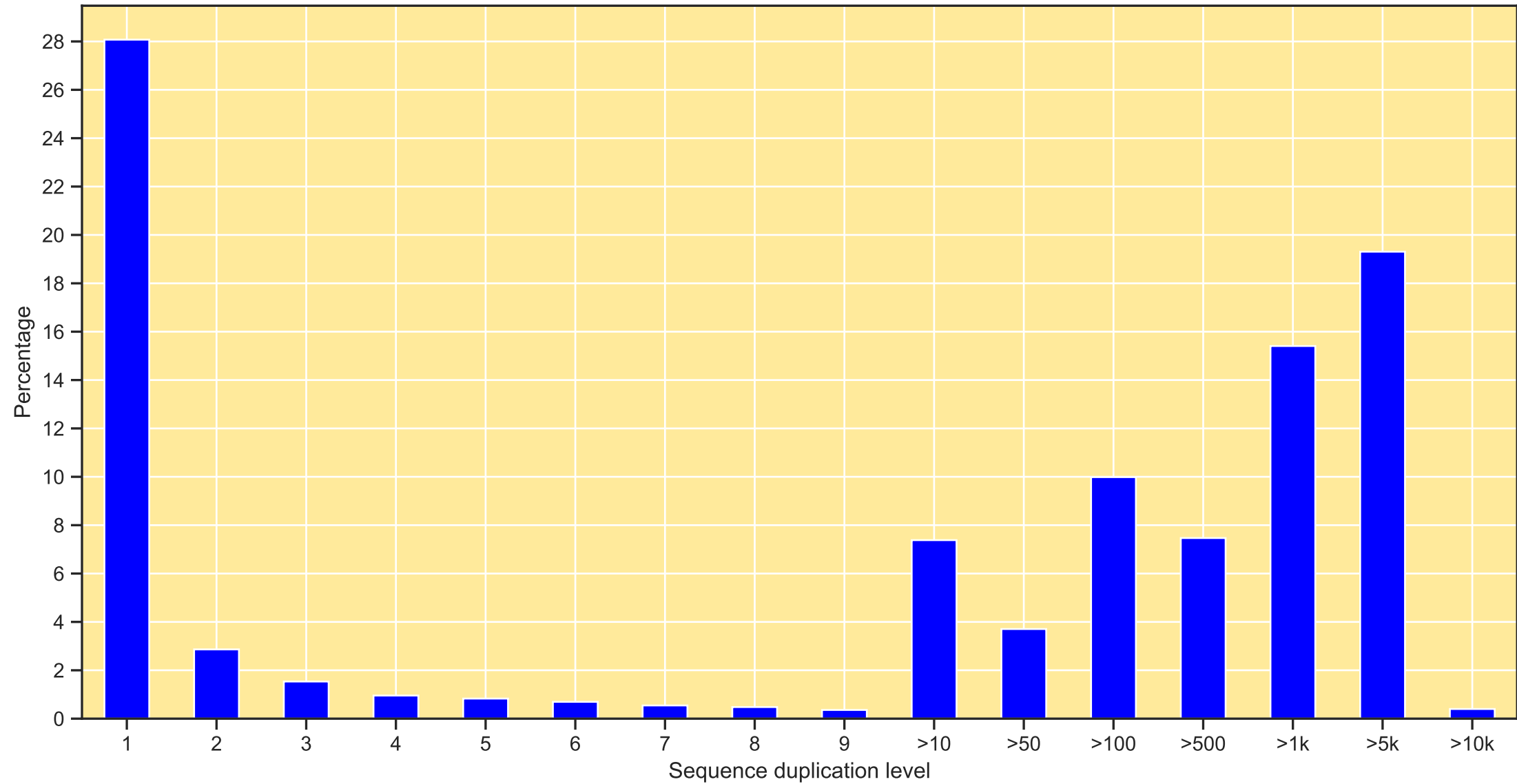Adapter content with filling (file.fastq.gz)

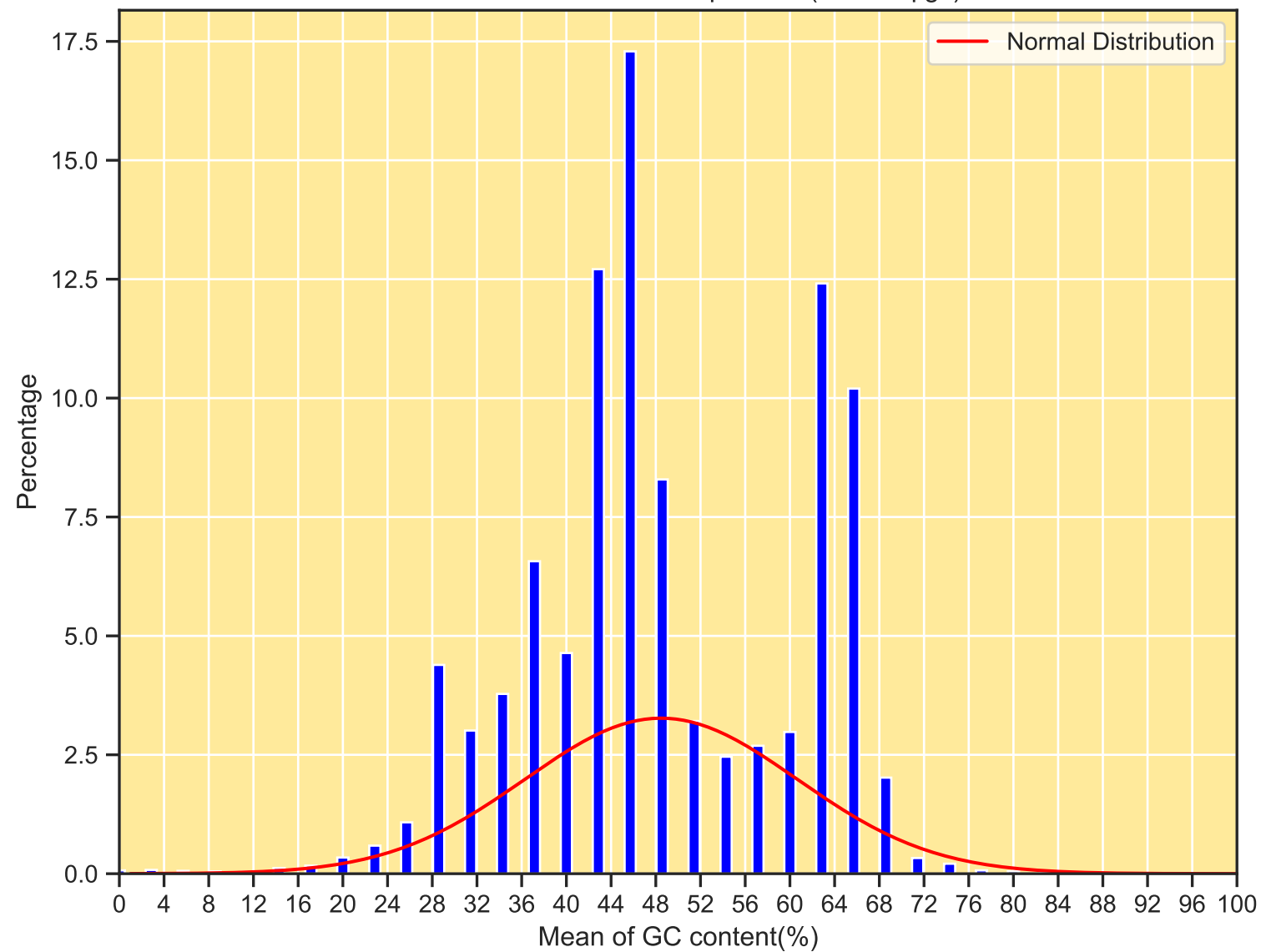Adapter content without filling (file.fastq.gz)
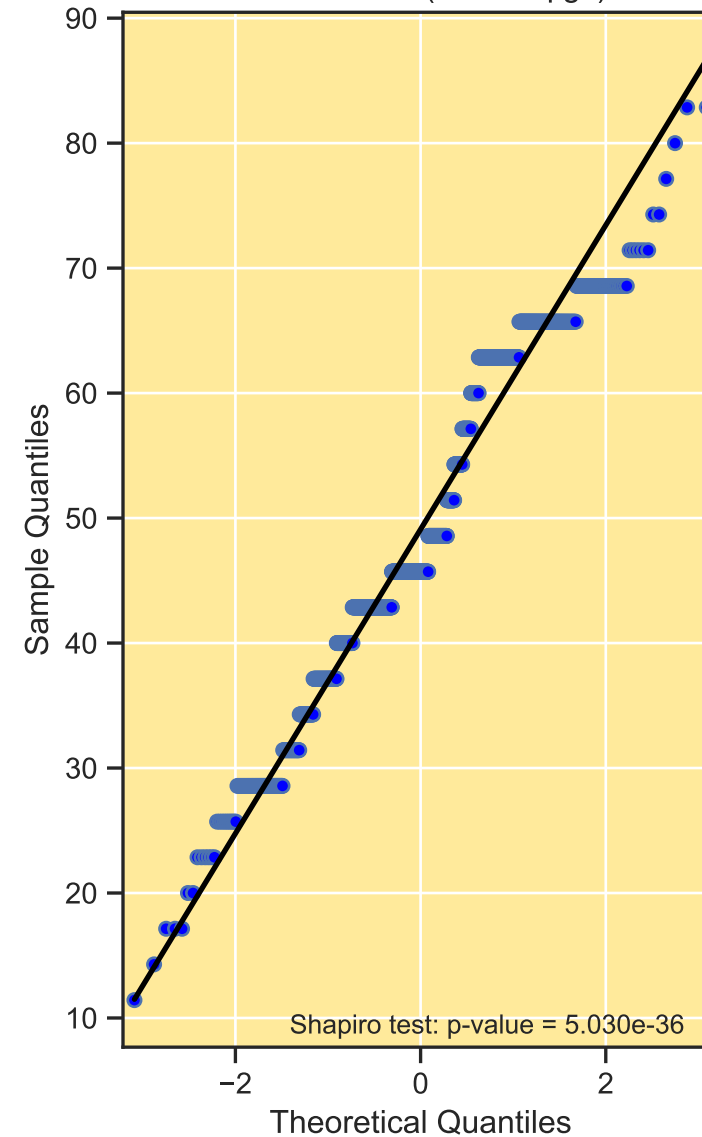
Base content (file.fastq.gz)

Sequence Duplication Levels (file.fastq.gz)

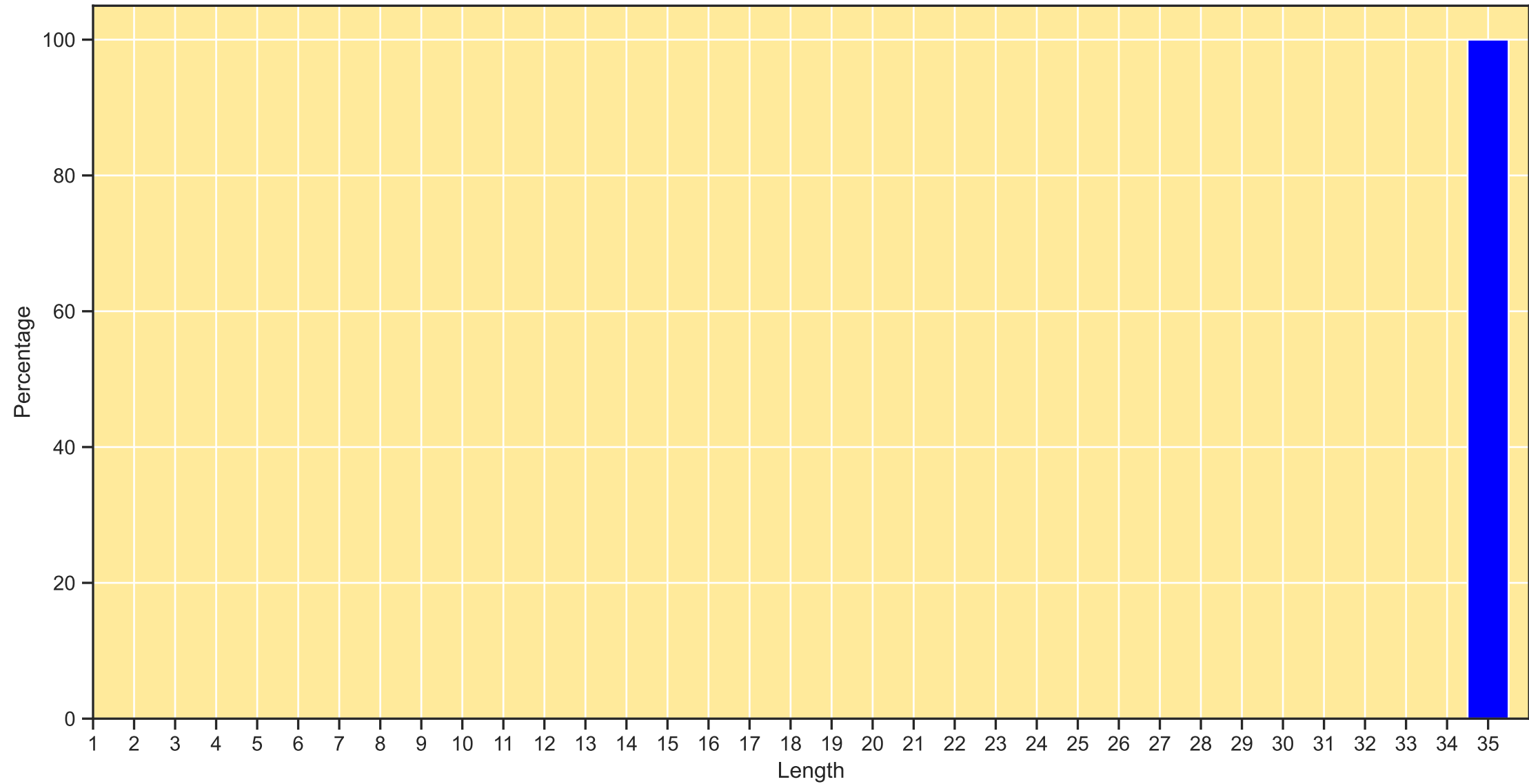GC distribution over all sequences (file.fastq.gz)
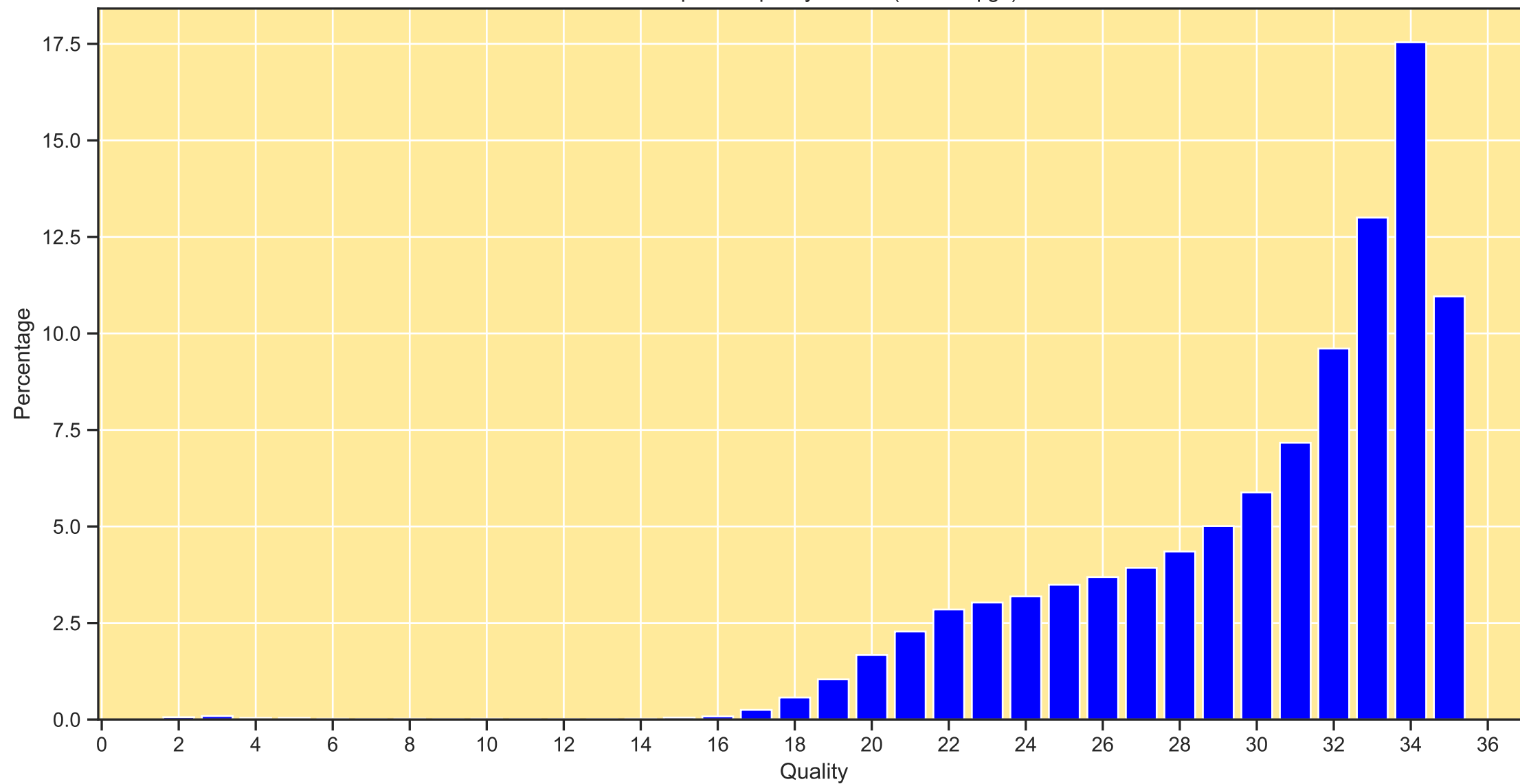
GC Q-Q Plot (file.fastq.gz)

Shapiro test: p-value = 5.030e-36

Length Distribution (file.fastq.gz)

Overrepresented sequences (file.fastq.gz)

Sequence	Percentage(%)
CGGGCAGATCGCAACTCCCAGGCATCCCGCAAAGT	8.297
AGGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTN	5.7
ACTCAGAGTTGTTCCTCTCCACGGAAATCTTTAGT	5.311
AGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCC	4.844
AGCCTTGCCAAAGCAAGGCCTCAAAAAATTGGGTT	2.678
AGGGGCTTTCCGGTAAAAAGCCAGAAAGCCTACTN	2.193
CAGGGGAAAGCGCGAACGCAGTCCCCCACTACCAC	1.975
AGCCTTGTCGGAACAAGGCCTCAAAAAATTAGCTT	1.674
GTATCAGATATTAAACTGATAAGAACAGATACTAC	1.043
TAGCTTAAGACTCAGAGTTGTTCCTCTCCACGGAA	1.001
ACAGCACCCGGTATTCCCAGGCGGTCTCCCATCCA	0.993
AAGGGCGCCGGGACCAACGATCACCAGCTGCCCAA	0.865
CTCGGATAGAGGACGTATCAGATATTAAACTGATA	0.752
ACGTATCAGATATTAAACTGATAAGAACAGATACT	0.745
CATTTAATATATTGTCCTCGGATAGAGGACGTATC	0.645
GATAAGAACAGATACTACACTTGATCTTAGCCAAA	0.606
GAAGAGAAACCAGAGTATGATCGTCGGACTGTAGA	0.6
GGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTNN	0.589
ACCACTCAGACCGCGTTCTCTCCCTCTCACTCCCC	0.566
AAGGGGCTTTCCGGTAAAAAACCAGAAAGCCTACT	0.562
GATCGTCGGACTGTAGAACTCTGAACGTGTAGATC	0.545
AATATTGTCCTCGGATAGAGGACGTATCAGATATT	0.444
TAAACTGATAAGAACAGATACTACACTTGATCTTN	0.443
CAGAGTTGTTCCTCTCCACGGAAATCTTTAGTAAA	0.42
TGGGCAGATCGCAACTCCCAGGCATCCCGCAAAGT	0.41
GGGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTN	0.362
CGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCC	0.333
GGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCC	0.325
AGCCTTGCCTAGGCAAGACTTCAAAAAATTTAACC	0.322
TGCACCGTTCCTGGAGGTACTGCAATACCAGGTCG	0.297
CGGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTN	0.277
GCTCAGAGTTGTTCCTCTCCACGGAAATCTTTAGT	0.271
CGGATAGAGGACGTATCAGATATTAAACTGATANN	0.269
GGGGCTTTCCGGTAAAAAGCCAGAAAGCCTACTNN	0.256
GAGGACGTATCAGATATTAAACTGATAAGAACNNN	0.248
TGTTCCTCTCCACGGAAATCTTTAGTAAAAGGCGA	0.244
CTGATAAGAACAGATACTACACTTGATCTTAGCCA	0.227
AATTGTCCTCGGATAGAGGACGTATCAGATATTAA	0.227
GGATCGTCGGACTGTAGAACTCTGAACGTGTNNNN	0.214
GACGTATCAGATATTAAACTGATAAGAACAGATAC	0.208
GCGCGAACGCAGTCCCCCACTACCACAAATTATGC	0.192
ATCCATTTAATATATTGTCCTCGGATAGAGGACGT	0.191
AAGGGGCTTTCCGGTAAAAAGCCAGAAAGCCTACT	0.191
TGCCTACAGCACCCGGTATTCCCAGGCGGTCTCCC	0.188
TCTCTCCACGGAAATCTTTAGTAAAAGGCGAANNN	0.188
CCTCAGAGTTGTTCCTCTCCACGGAAATCTTTAGT	0.176
AAAATTGTCCTCGGATAGAGGACGTATCAGATATT	0.168
GTTTCTCTCCACGGAAATCTTTAGTAAAAGGCGAA	0.166
CGTTCCTCTCCACGGAAATCTTTAGTAAAAGGCGA	0.159
TGGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTN	0.154
AGATATTAAACTGATAAGAACAGATACTACACTTG	0.153
CTCCACGGAAATCTTTAGTAAAAGGCGAAAGATTT	0.145
CACAAATTATGCAGTCGAGTTTCCCACATTTGGGG	0.144
GGCCTTGCCAAAGCAAGGCCTCAAAAAATTGGGTT	0.141
ACTGATAAGAACAGATACTACACTTGATCTTAGCC	0.141
GTTCCTCTCCACGGAAATCTTTAGTAAAAGGCGAA	0.141
GGGGGCTTTCCGGTAAAAAGCCAGAAAGCCTACTN	0.138
TGTCAGACTCTTATGTTTCACTCATAAAAGGAGTG	0.136
ATTTAATATATTGTCCTCGGATAGAGGACGTATCN	0.134
TGGATCGTCGGACTGTAGAACTCTGAACGTGTNNN	0.12
ATCCGGAGTGCAATGGATAAGCCTCGCCCTGGGAA	0.119
CTCCAAAAATCCATTTAATATATTGTCCTCGGATN	0.117
AAGGGCTTTCCGGTAAAAAACCAGAAAGCCTACTN	0.117
ACTCAGAGTAGTTCCTCTCCACGGAAATCTTTAGT	0.116
TGATCGTCGGACTGTAGAACTCTGAACGTGTNNNN	0.116
TAGGGGAAAGCGCGAACGCAGTCCCCCACTACCAC	0.114
AGCCAACAGCACCCGGTATTCCCAGGCGGTCTCCC	0.11
CGGGGCTTTCCGGTAAAAAGCCAGAAAGCCTACTN	0.108
GGCCTTGTCGGAACAAGGCCTCAAAAAATTAGCTT	0.107

Per sequence quality scores (file.fastq.gz)

Quality scores across all bases (file.fastq.gz)