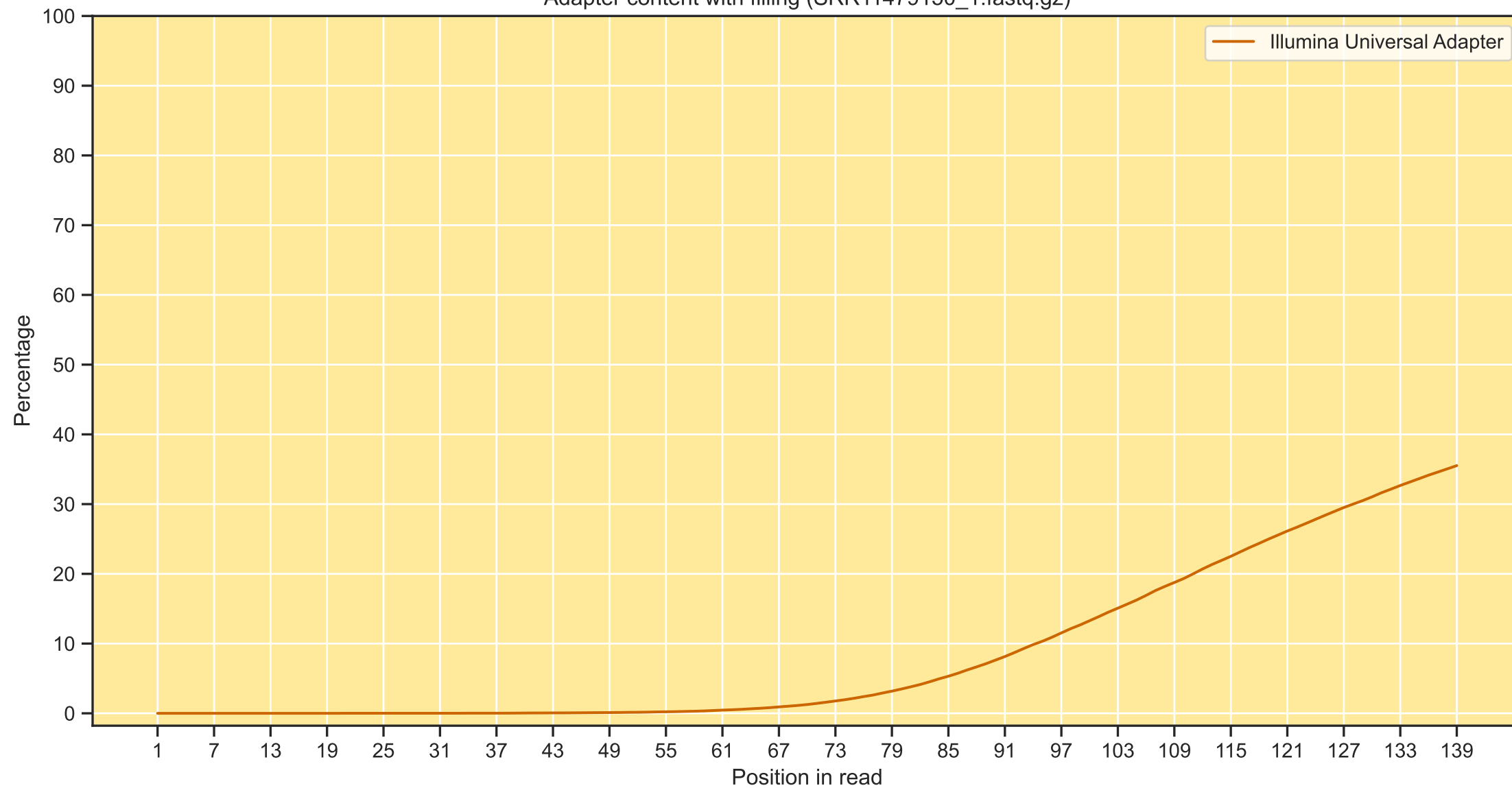
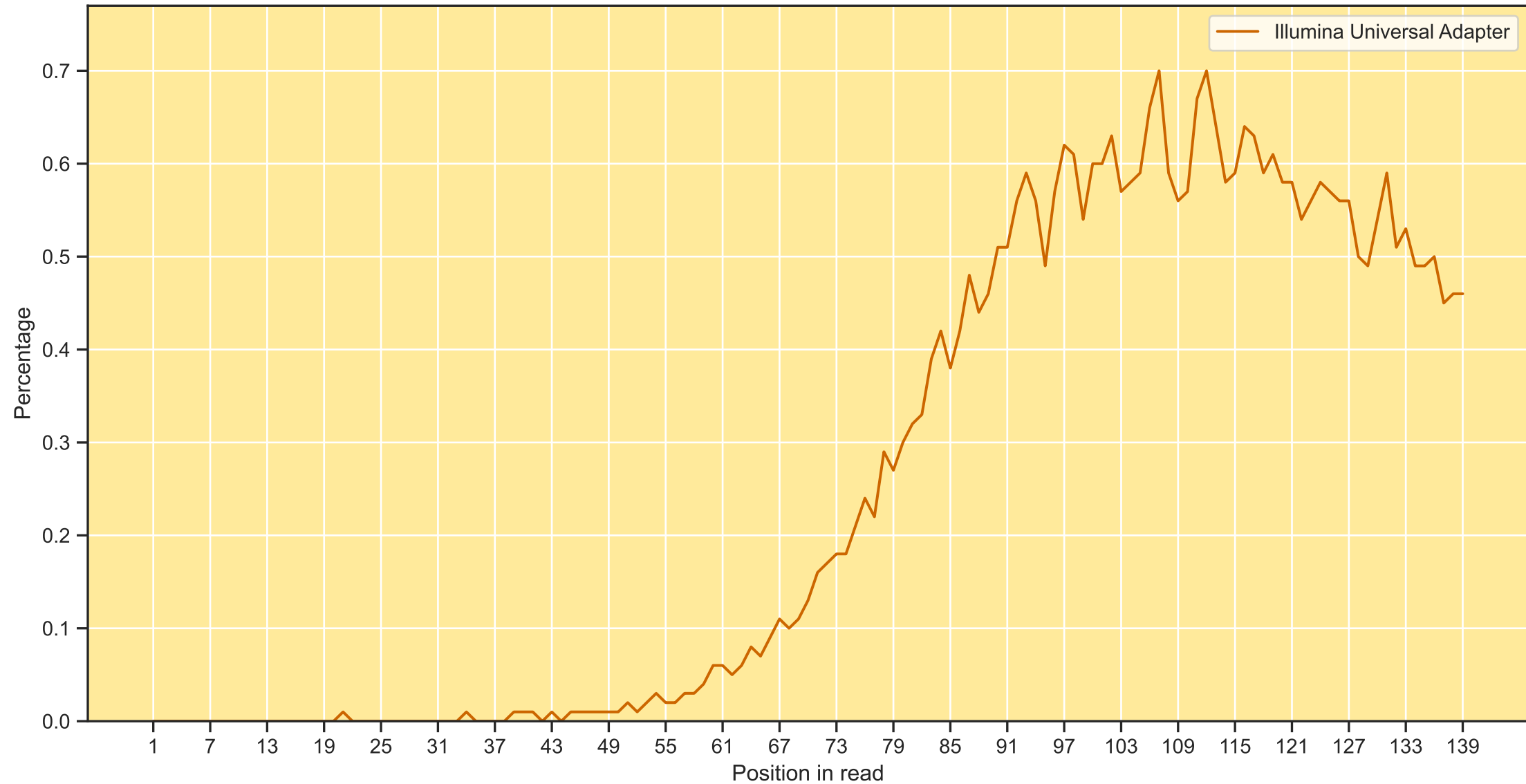
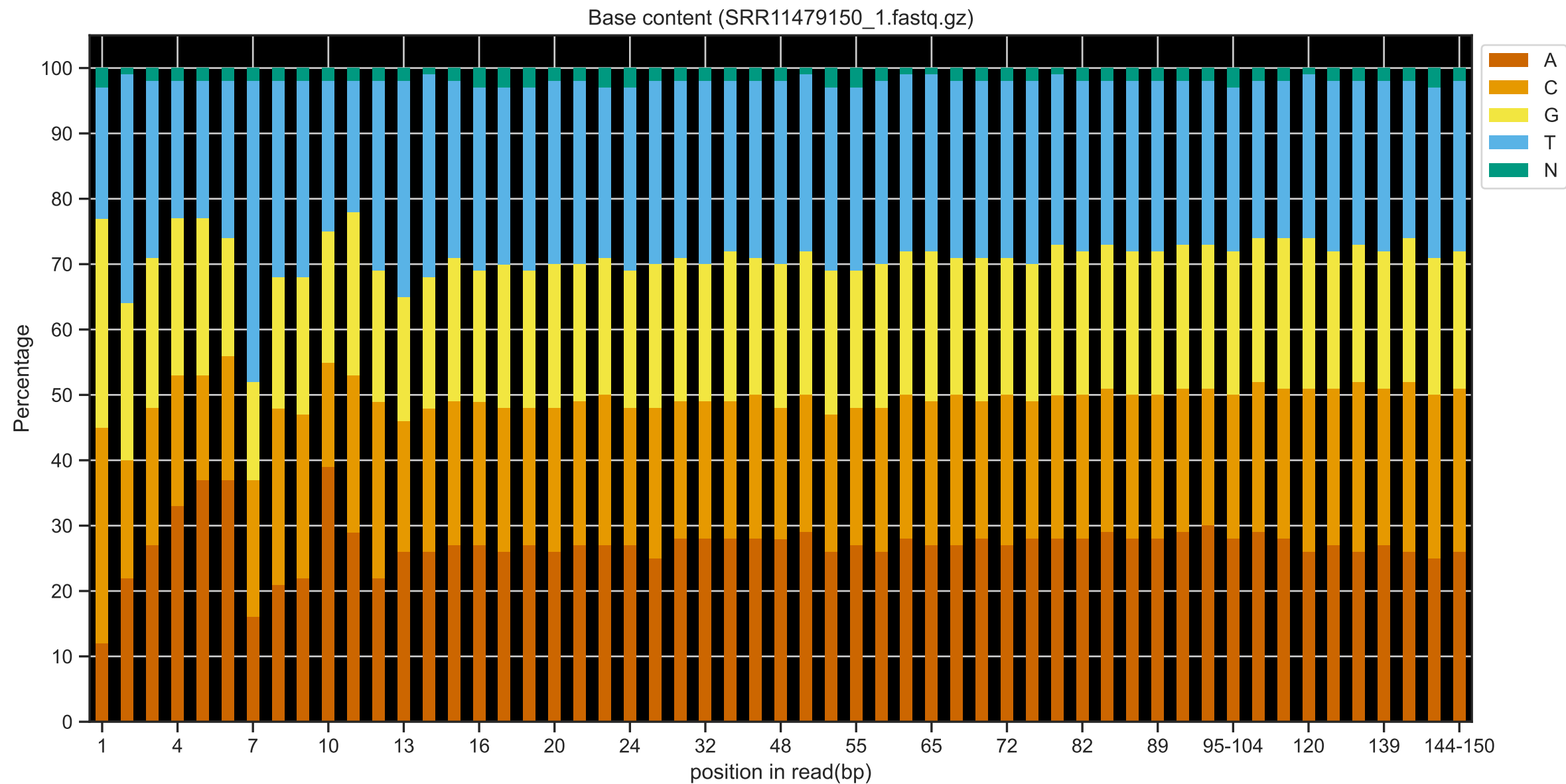


Adapter content with filling (SRR11479150_1.fastq.gz)

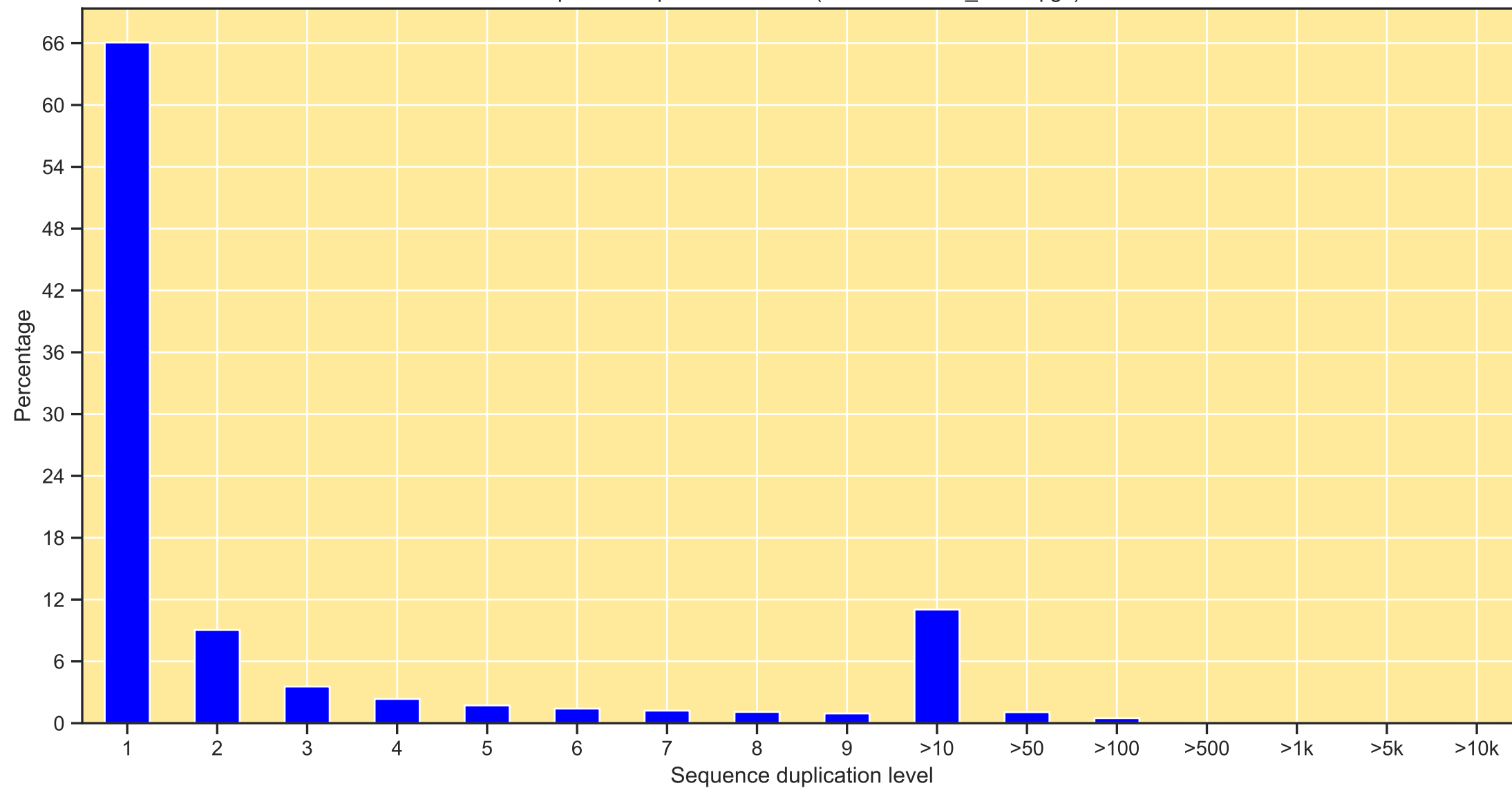


Adapter content without filling (SRR11479150_1.fastq.gz)

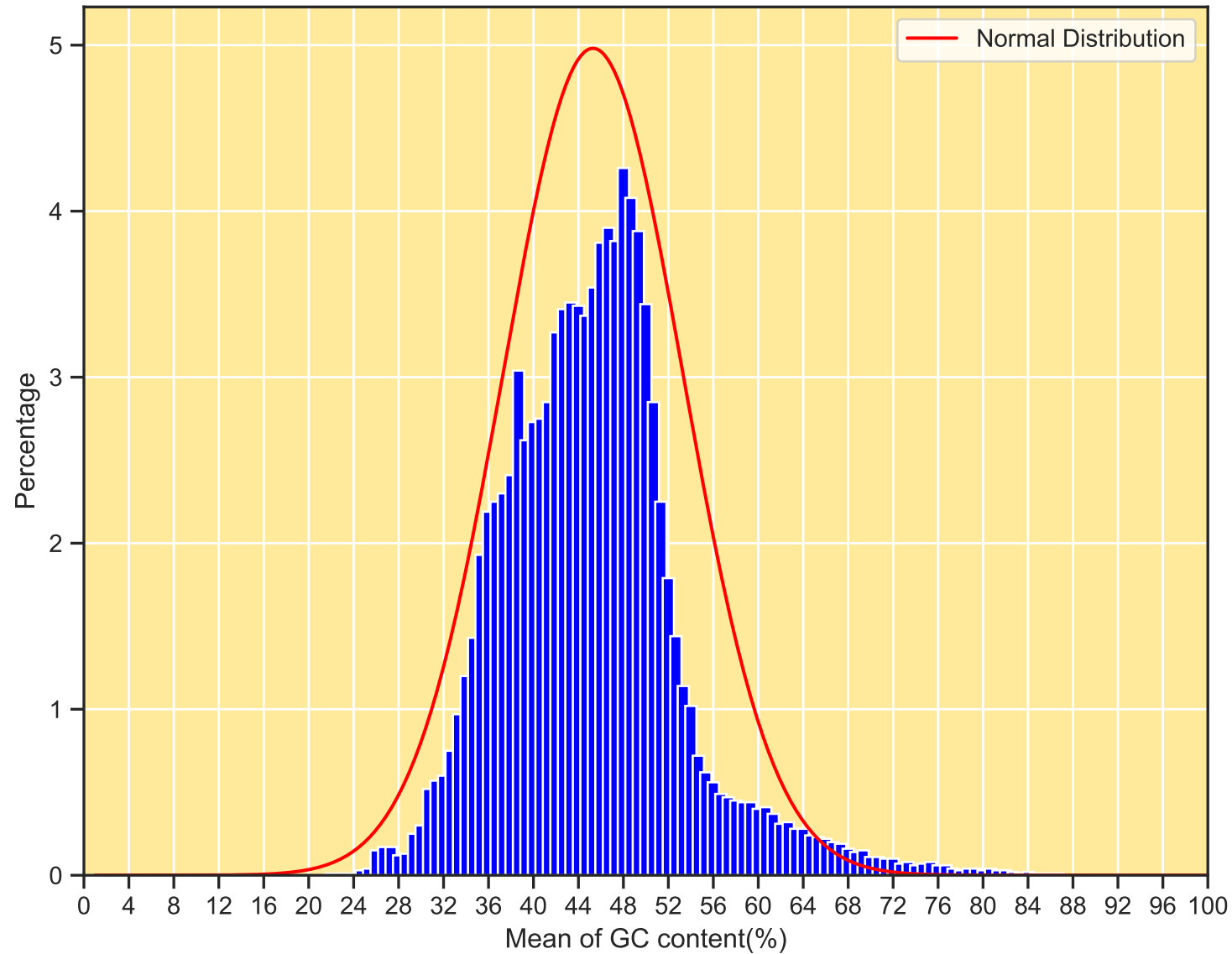




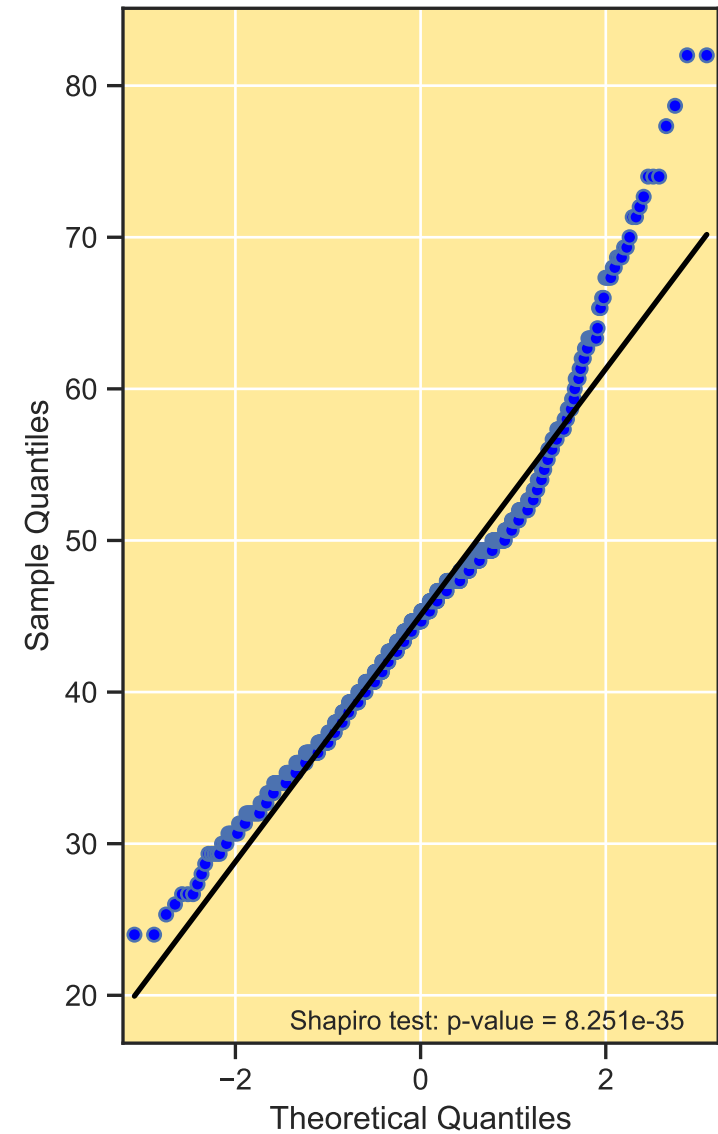
Sequence Duplication Levels (SRR11479150_1.fastq.gz)



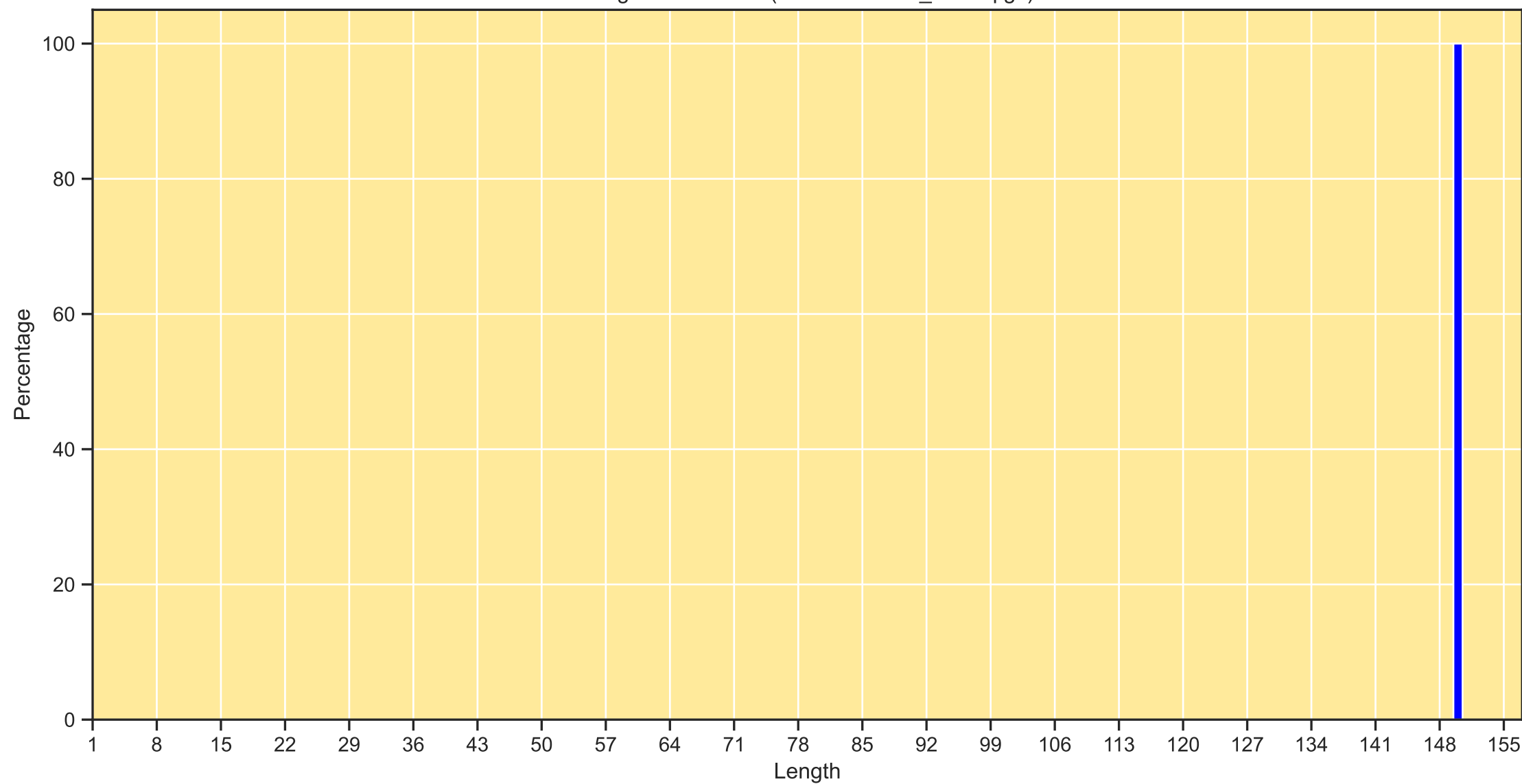
GC distribution over all sequences (SRR11479150_1.fastq.gz)



GC Q-Q Plot (SRR11479150_1.fastq.gz)



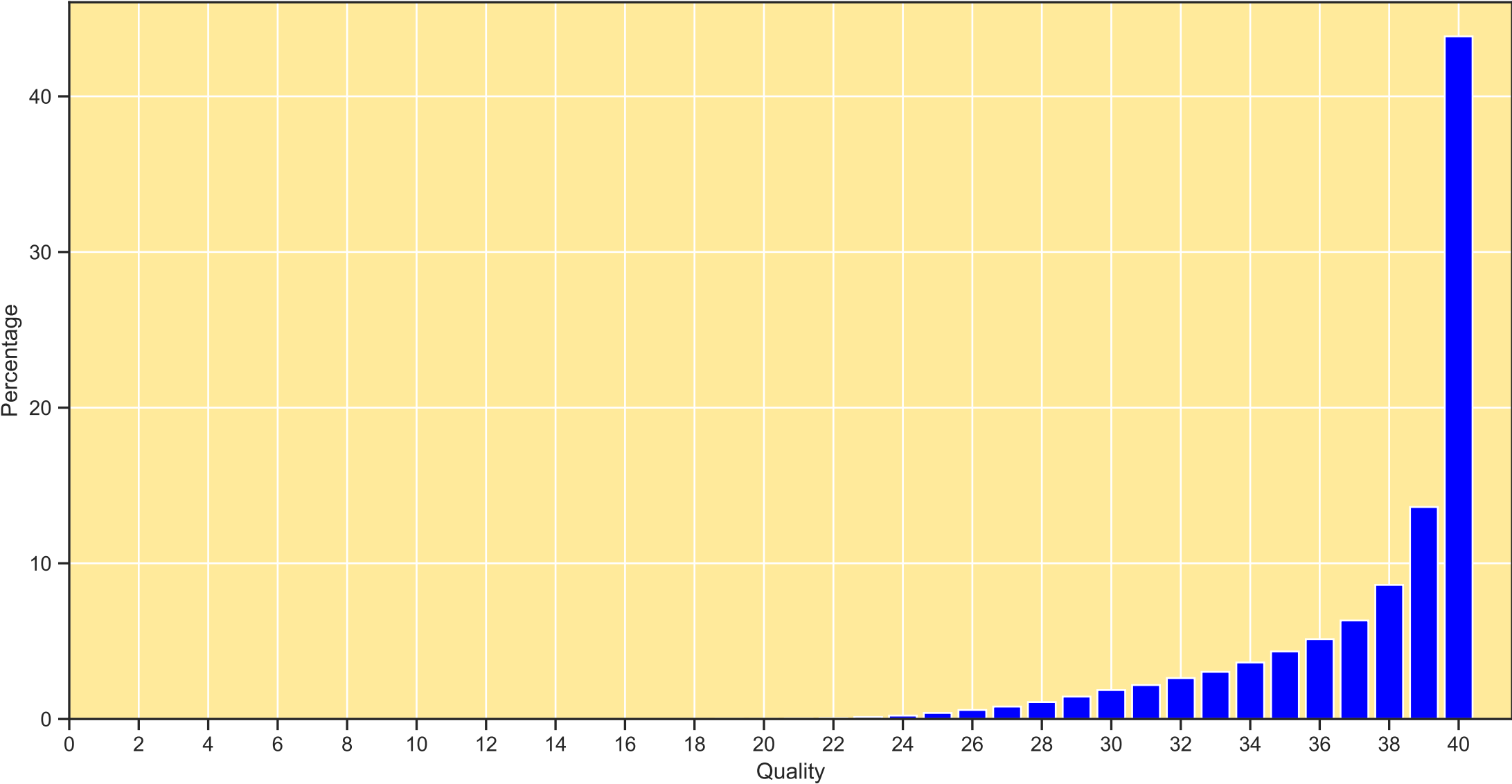
Length Distribution (SRR11479150_1.fastq.gz)



Overrepresented sequences (SRR11479150_1.fastq.gz)

Sequence	Percentage(%)
GGCAAATTGTGCAATTTGCGGCCAATGTTTGTAAATCAGTTCCTTGTCTGAT	0.385
CTGGAGTTGAATTTCTTGAAGTGTGCGACTACGTGATGAGGAACGAGAAG	0.264
GTGAGATTAAAGTTAACTACATCTACTTGTGCTATGTAGTTACGAGAATTC	0.245
CACGATTGCAGCATTGTTAGCAGGATTGCGGGTGCCAATGTGATCTTTTGG	0.235
CGGTGATGCTGCTCTTGCTTTGCTGCTGCTTGACAGATTGAACCAGCTTGA	0.228
CGAGAATTCATTCTGCACAAGAGTAGACTATATATCGTAAACGGAAAAGCG	0.197
CAAAGATCCAAATTTCAAAGATCAAGTCATTTTGCTGAATAAGCATATTGA	0.183
TAACAAACCAACCAACTTTTCGATCTCTTGTAGATCTGTTCTCTAAACGAAC	0.179
TGATTTTCTAGCTCCTACTCTAATATAACCATTTAGAATAGAAGTGAATAGG	0.175
GTTTTGTATGCGTCAATATGCTTATTCAGCAAAATGACTTGATCTTTGAAA	0.169
AGGTAACAAACCAACCAACTTTTCGATCTCTTGTAGATCTGTTCTCTAAACG	0.154
GCCAATTTGGTCATCTGGACTGCTATTGGTGTTAATTGGAACGCCTTGTC	0.143
CAAACATTGGCCGCAAATTGCACAATTTGCCCCAGCGCTTCAGCGTTCTT	0.143
CTTGAATACACCAAAAGATCACATTGGCACCCGCAATCCTGCTAACAATGC	0.139
GAAAGATCTCAGTCCAAGATGGTATTTCTACTACCTAGGAACTGGGCCAGA	0.138
CTCGTAACTACATAGCACAAAGTAGATGTAGTTAACTTTAATCTCACATAGC	0.136
AAGAAATTCAACTCCAGGCAGCAGTAGGGGAAGTTCTCCTGCTAGAATGGC	0.133
CTCAGATTCAACTGGCAGTAACCAGAATGGAGAACGCAGTGGGGCGCGATC	0.126
GCCATGTTGAGTGAGAGCGGTGAACCAAGACGCAGTATTATTGGGTAAACC	0.119
GTTTAGGCCTGAGTTGAGTCAGCACTGCTCATGGATTGTTGCAATTGTTTG	0.118
TGAAACTCAAGCCTTACCGCAGAGACAGAAGAAACAGCAAAGTGTGACTCT	0.116
CCCAGGTAACAAACCAACCAACTTTTCGATCTCTTGTAGATCTGTTCTCTAA	0.114
CCTGTGTAGGTCAACCACGTTCCCGAAGGTGTGACTTCCATGCCAATGCGC	0.114
TGTCATTCTCCTAAGAAGCTATTAAAATCACATGGGGATAGCACTACTAAA	0.109
CGCGCATTGGCATGGAAGTCACACCTTCGGGAACGTGGTTGACCTACACAG	0.107
GTTGAATCTGAGGGTCCACCAAACGTAATGCGGGGTGCATTCGCTGATTT	0.107
CGGTGATCCAATTTATTCTGTAAACAGCAGCAAGCACAAAACAAGCTAAAG	0.106
CTGGACTGCTATTGGTGTTAATTGGAACGCCTTGTCTCGAGGGAATTTAA	0.104
CTAAAATTAAAGTTCCAAACAGAAAACTAATATAATATTTAGTTCGTTTA	0.104
GGGTCATCAACTACATATGGTTGATGTTGAGTACATGACTGTAAACTACAT	0.103
GGAAGTTGTAGCACGATTGCAGCATTGTTAGCAGGATTGCGGGTGCCAATG	0.102
CGGCATCATATGGGTTGCAACTGAGGGAGCCTTGAATACACCAAAAGATCA	0.102
TGGGAATGTTTTGTATGCGTCAATATGCTTATTCAGCAAAATGACTTGATC	0.102
CTTTAATCTCACATAGCAATCTTTAATCAGTGTGTAACATTAGGGAGGACT	0.101
GCAAAACCTGAGTCACCTGCTACACGCTGCGAAGCTCCCAATTTGTAATAA	0.101
GGAATGTTTTGTATGCGTCAATATGCTTATTCAGCAAAATGACTTGATCTT	0.1
GATCGGAAGAGCACACGTCTGAACTCCAGTCACTCTCGCGCATCTCGTATG	0.1

Per sequence quality scores (SRR11479150_1.fastq.gz)



Quality scores across all bases (SRR11479150_1.fastq.gz)

