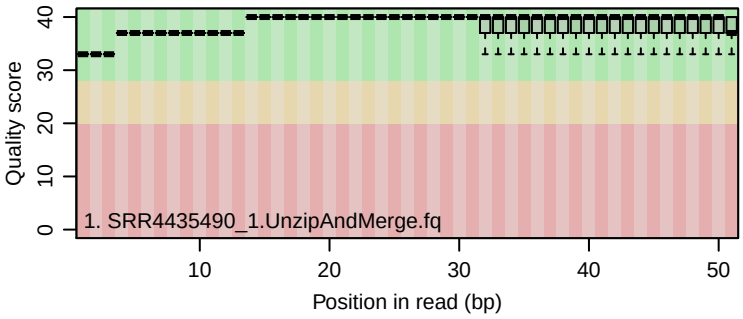
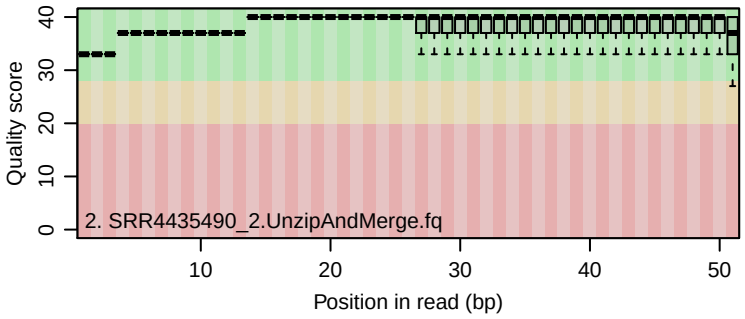
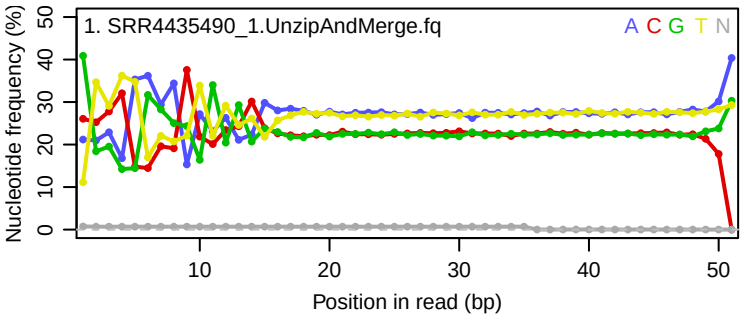
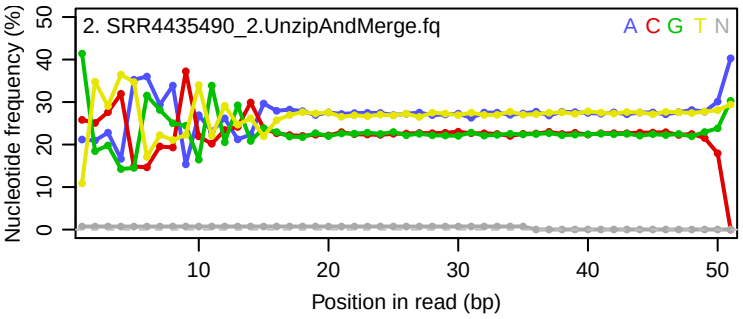
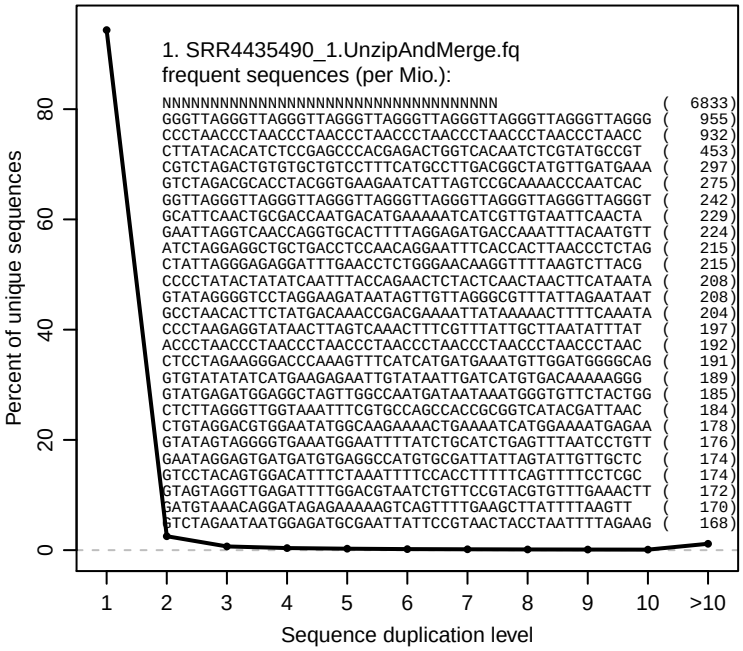

Quality score
0
10
20
30
40
1. SRR4435490_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR4435490_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR4435490_1.UnzipAndMerge.fq
A C G T N
Nucleotide frequency (%)
0
10
20
30
40
50
10
20
30
40
50
Position in read (bp)


2. SRR4435490_2.UnzipAndMerge.fq
A C G T N
Nucleotide frequency (%)
0
10
20
30
40
50
10
20
30
40
50
Position in read (bp)


1. SRR4435490_1.unzipAndMerge.fq
frequent sequences (per Mio.):
NNNN