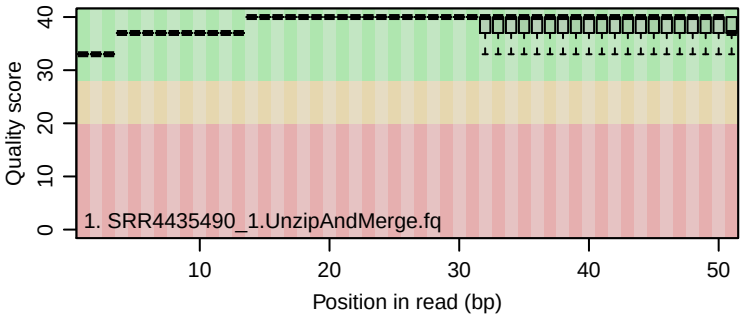
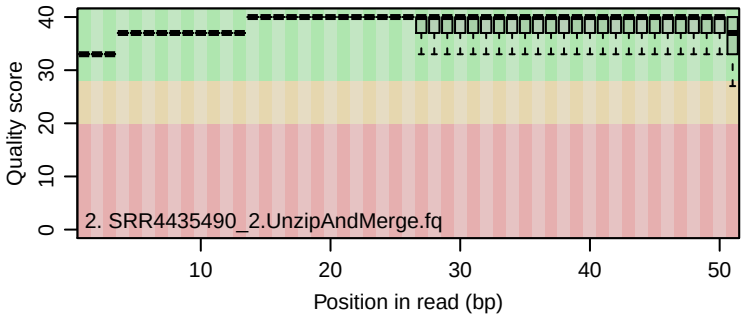
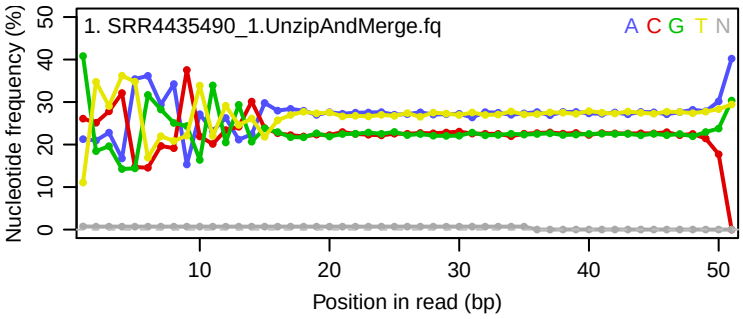
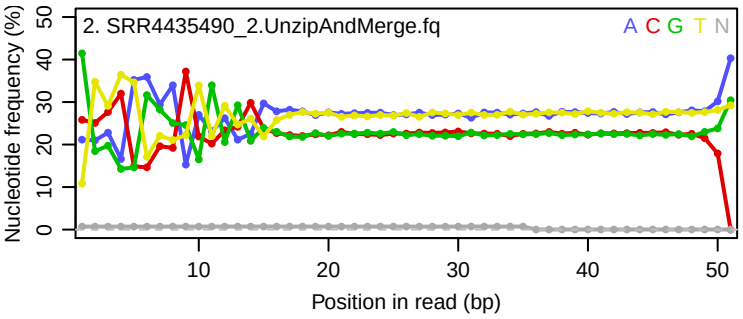
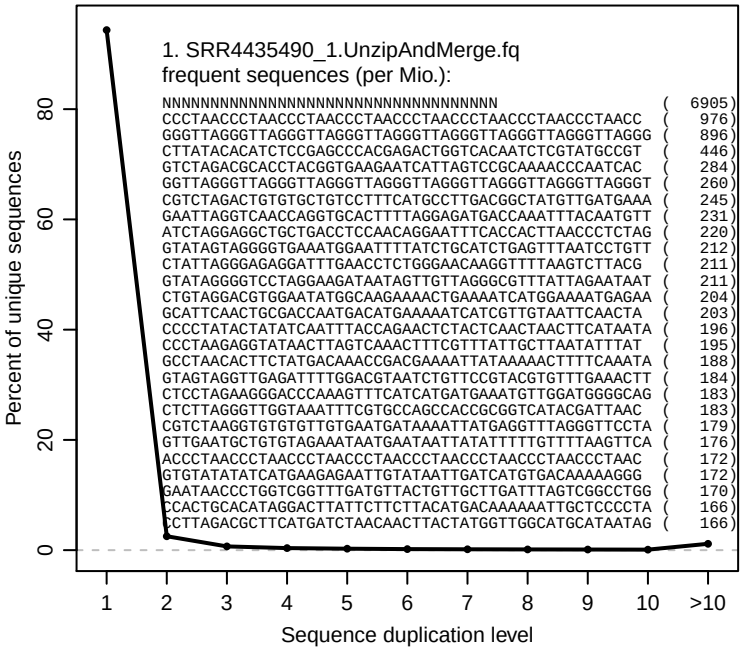
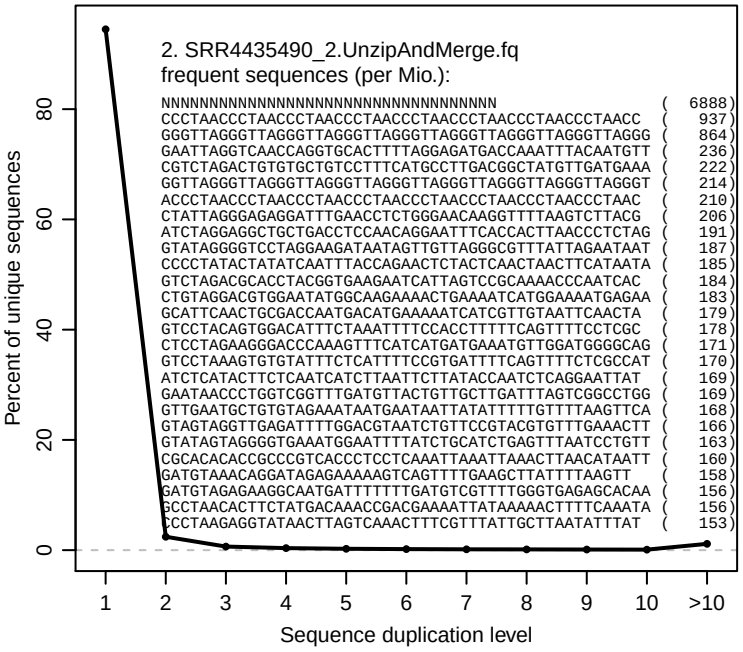

Quality score
0
10
20
30
40
1. SRR4435490_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


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.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (6905)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (976)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (896)
CTTATACACATCTCCGAGCCCACGAGACTGGTCACAATCTCGTATGCCGT (446)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (284)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (260)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (245)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (231)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (220)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (212)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (211)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (211)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (204)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (203)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (196)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (195)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (188)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (184)
CTCCTAGAAGGGACCCAAAGTTTCATCATGATGAAATGTTGGATGGGGCAG (183)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (183)
CGTCTAAGGTGTGTGTTGTGAATGATAAAATTATGAGGTTTAGGGTTCCTA (179)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (176)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (172)
GTGTATATATCATGAAGAGAATTGTATAATTGATCATGTGACAAAAAGGG (172)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (170)
CCACTGCACATAGGACTTATTCTTCTTACATGACAAAAAATTGCTCCCCTA (166)
CCTTAGACGCTTCATGATCTAACAACTTACTATGGTTGGCATGCATAATAG (166)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR4435490_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (6888)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (937)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (864)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (236)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (222)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (214)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (210)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (206)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (191)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (187)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (185)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (184)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (183)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (179)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (178)
CTCCTAGAAGGGACCCAAAGTTTCATCATGATGAAATGTTGGATGGGGCAG (171)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (170)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (169)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (169)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (168)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (166)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (163)
CGCACACACCGCCCGTCACCCTCCTCAAATTAAATTAAACTTAACATAATT (160)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (158)
GATGTAGAGAAGGCAATGATTTTTTTGATGTCGTTTTGGGTGAGAGCACAA (156)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (156)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (153)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level