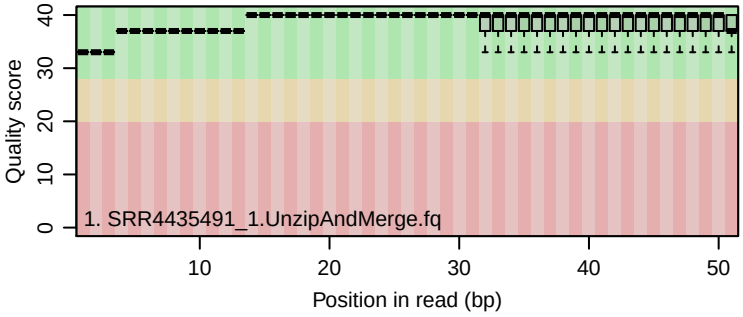
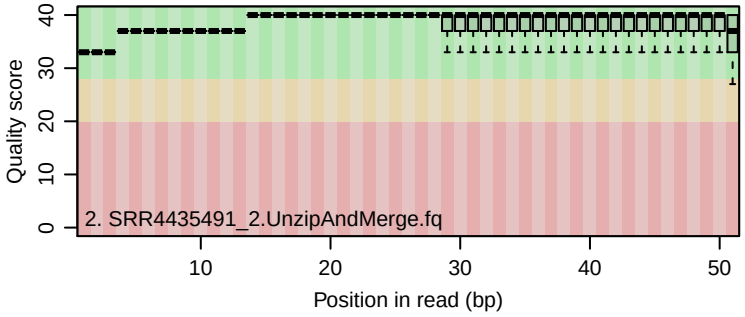
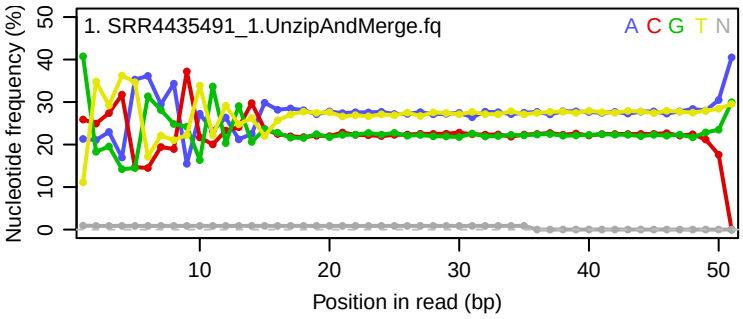
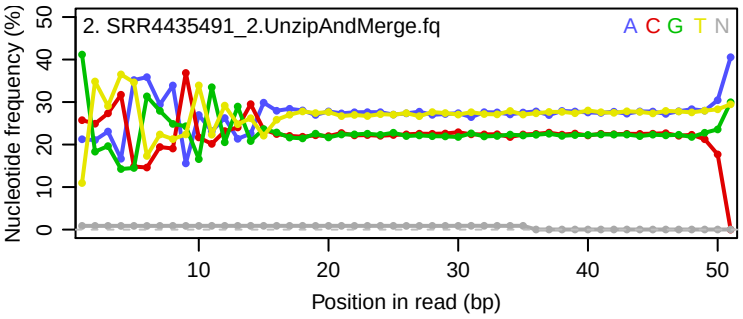
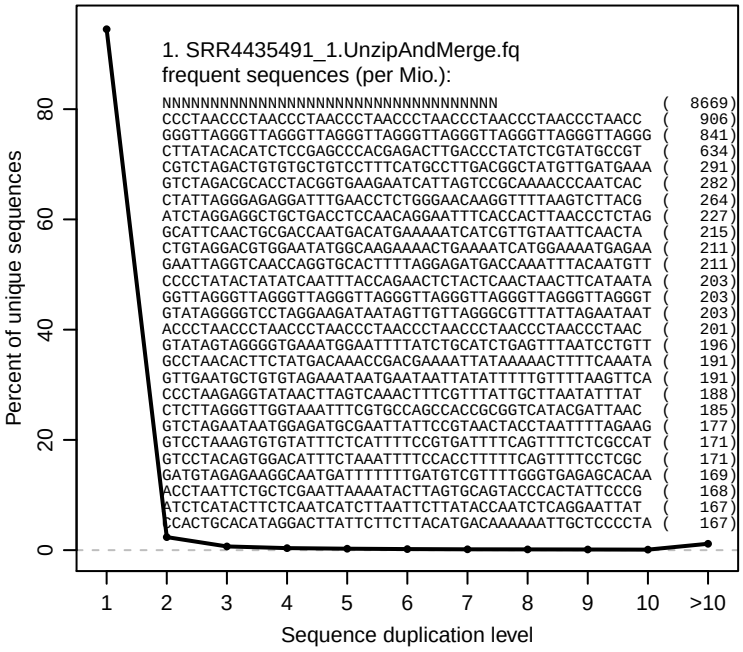
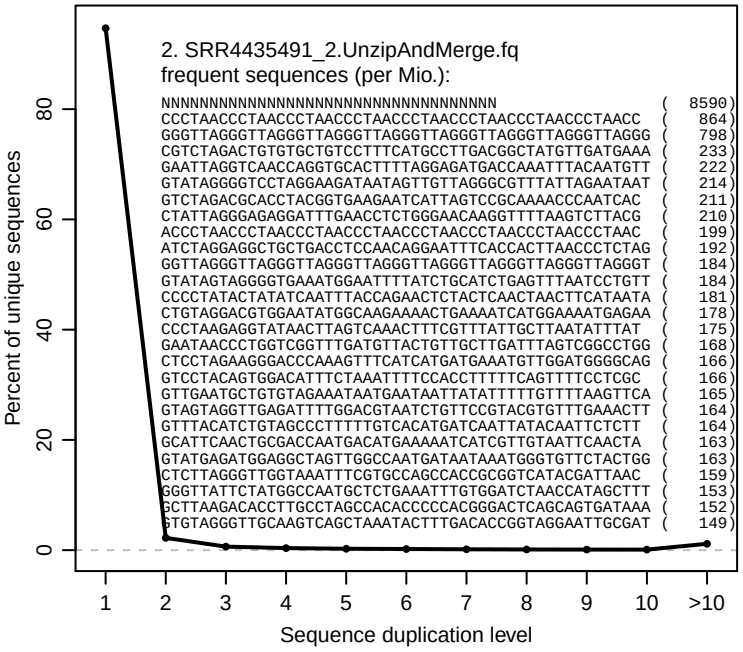

Quality score
0
10
20
30
40
1. SRR4435491_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR4435491_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR4435491_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. SRR4435491_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. SRR4435491_1.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (8669)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (906)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (841)
CTTATACACATCTCCGAGCCCACGAGACTTGACCCTATCTCGTATGCCGT (634)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (291)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (282)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (264)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (227)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (215)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (211)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (211)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (203)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (203)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (203)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (201)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (196)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (191)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (191)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (188)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (185)
GTCTAGAATAATGGAGATGCGAATTATTCCGTAACTACCTAATTTTAGAAG (177)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (171)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (171)
GATGTAGAGAAGGCAATGATTTTTTTGATGTCGTTTTGGGTGAGAGCACAA (169)
ACCTAATTCTGCTCGAATTAAAATACTTAGTGCAGTACCCACTATTCCCG (168)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (167)
CCACTGCACATAGGACTTATTCTTCTTACATGACAAAAAATTGCTCCCCTA (167)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR4435491_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (8590)
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GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (798)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (233)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (222)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (214)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (211)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (210)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (199)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (192)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (184)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (184)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (181)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (178)
CCCTAAGAGGTATAACTTAGTCAAACTTTCGTTTATTGCTTAATATTTAT (175)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (168)
CTCCTAGAAGGGACCCAAAGTTTCATCATGATGAAATGTTGGATGGGGCAG (166)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (166)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (165)
GTAGTAGGTTGAGATTTTGGACGTAATCTGTTCCGTACGTGTTTGAAACTT (164)
GTTTACATCTGTAGCCCTTTTTGTCACATGATCAATTATACAATTCTCTT (164)
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GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (163)
CTCTTAGGGTTGGTAAATTTCGTGCCAGCCACCGCGGTCATACGATTAAC (159)
GGGTTATTCTATGGCCAATGCTCTGAAATTTGTGGATCTAACCATAGCTTT (153)
GCTTAAGACACCTTGCCTAGCCACACCCCCACGGGACTCAGCAGTGATAAA (152)
GTGTAGGGTTGCAAGTCAGCTAAATACTTTGACACCGGTAGGAATTGCGAT (149)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level