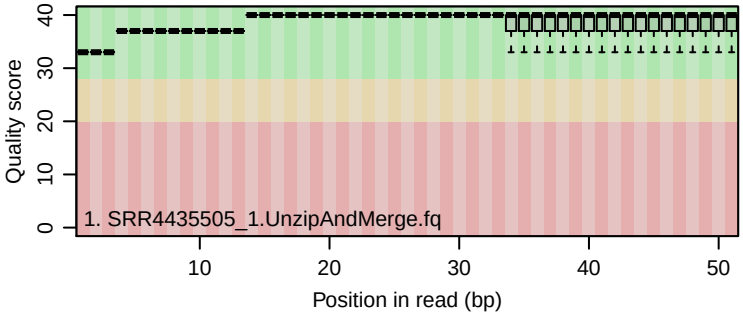
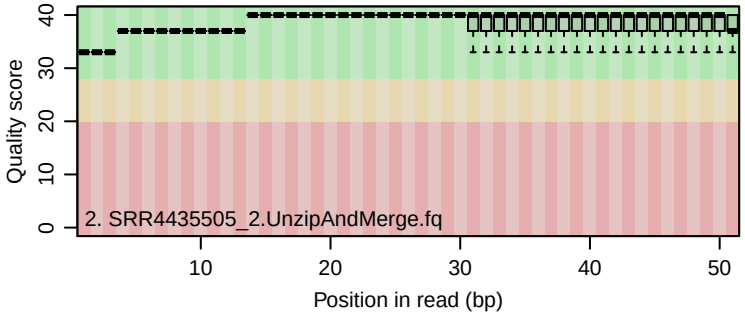
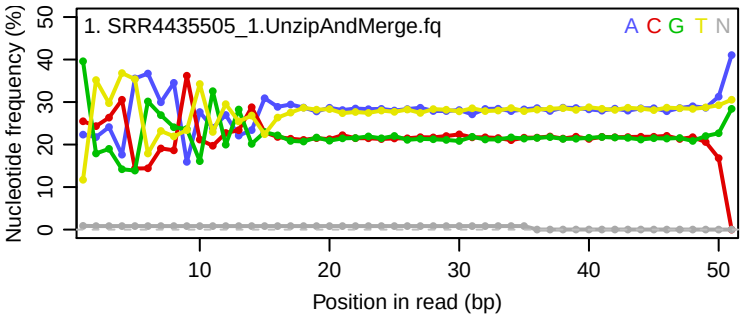
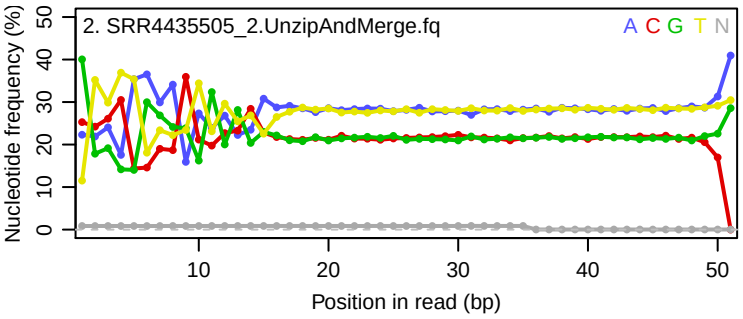
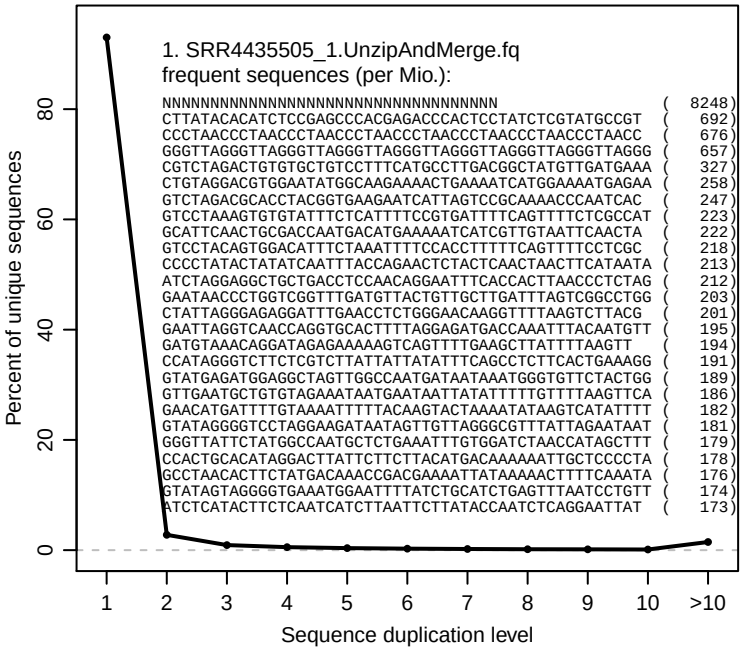

Quality score
0
10
20
30
40
1. SRR4435505_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
0
10
20
30
40
2. SRR4435505_2.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


1. SRR4435505_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. SRR4435505_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. SRR4435505_1.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (8248)
CTTATACACATCTCCGAGCCCACGAGACCCACTCCTATCTCGTATGCCGT (692)
CCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACC (676)
GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (657)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (327)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (258)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (247)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (223)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (222)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (218)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (213)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (212)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (203)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (201)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (195)
GATGTAAACAGGATAGAGAAAAAGTCAGTTTTGAAGCTTATTTTAAGTT (194)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG (191)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (189)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (186)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT (182)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (181)
GGGTTATTCTATGGCCAATGCTCTGAAATTTGTGGATCTAACCATAGCTTT (179)
CCACTGCACATAGGACTTATTCTTCTTACATGACAAAAAATTGCTCCCCTA (178)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (176)
GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (174)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (173)
Percent of unique sequences
0
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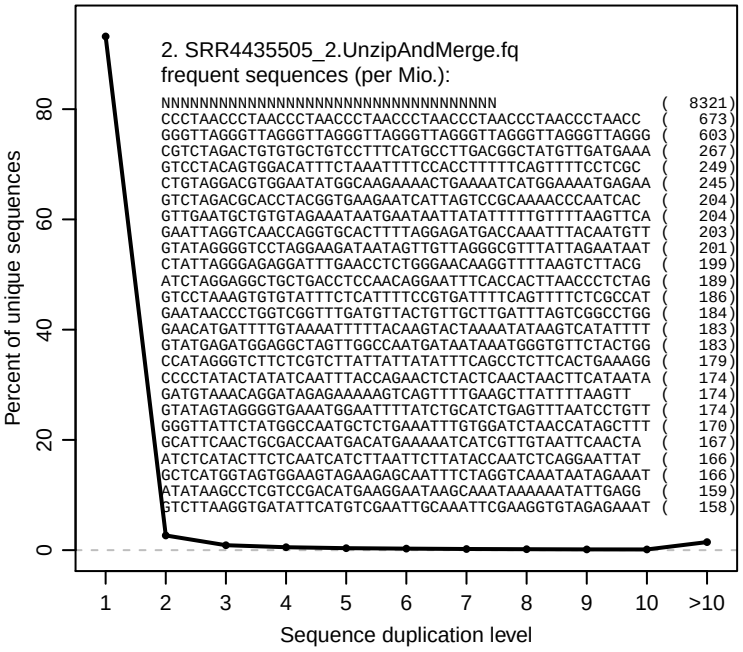
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level


2. SRR4435505_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN (8321)
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GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (603)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (267)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (249)
CTGTAGGACGTGGAATATGGCAAGAAAACTGAAAATCATGGAAAATGAGAA (245)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (204)
GTTGAATGCTGTGTAGAAATAATGAATAATTATATTTTTGTTTTAAGTTCA (204)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (203)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (201)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (199)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (189)
GTCCTAAAGTGTGTATTTCTCATTTTCCGTGATTTTCAGTTTTCTCGCCAT (186)
GAATAACCCTGGTCGGTTTGATGTTACTGTTGCTTGATTTAGTCGGCCTGG (184)
GAACATGATTTTGTAAAATTTTTACAAGTACTAAAATATAAGTCATATTTT (183)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (183)
CCATAGGGTCTTCTCGTCTTATTATTATATTTCAGCCTCTTCACTGAAAGG (179)
CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (174)
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GTATAGTAGGGGTGAAATGGAATTTTATCTGCATCTGAGTTTAATCCTGTT (174)
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GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (167)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (166)
GCTCATGGTAGTGGAAGTAGAAGAGCAATTTCTAGGTCAAATAATAGAAAT (166)
ATATAAGCCTCGTCCGACATGAAGGAATAAGCAAATAAAAAATATTGAGG (159)
GTCTTAAGGTGATATTCATGTCGAATTGCAAATTCGAAGGTGTAGAGAAAT (158)
Percent of unique sequences
0
20
40
60
80
1
2
3
4
5
6
7
8
9
10
>10
Sequence duplication level