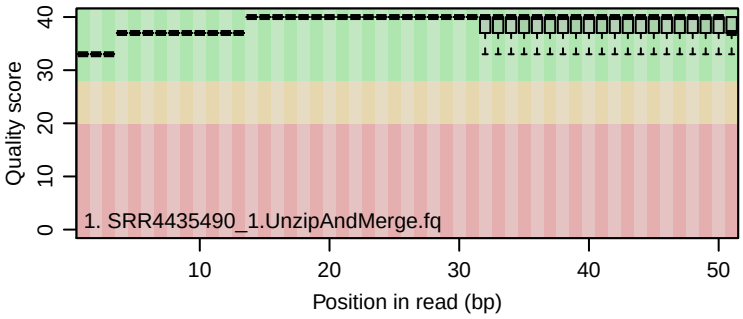
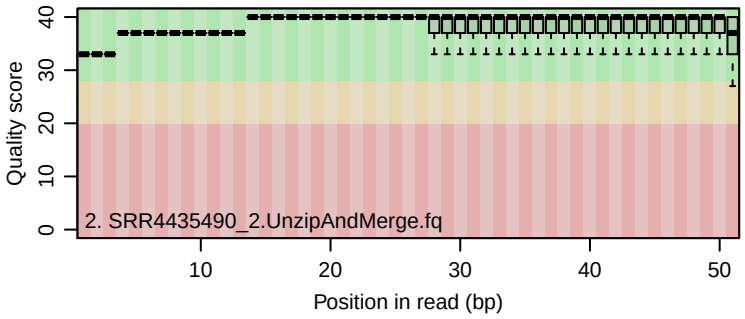

Quality score
0
10
20
30
40
1. SRR4435490_1.UnzipAndMerge.fq
10
20
30
40
50
Position in read (bp)


Quality score
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2. SRR4435490_2.UnzipAndMerge.fq
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30
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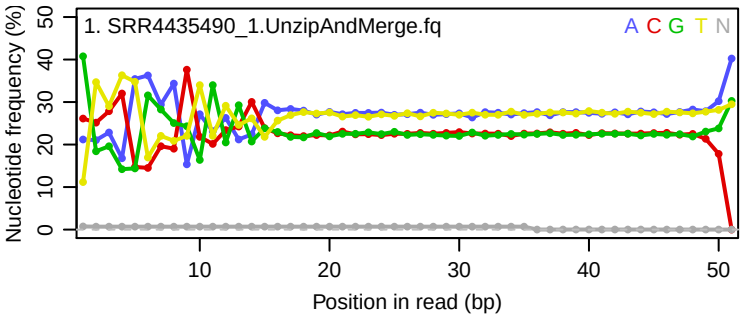
50
Position in read (bp)


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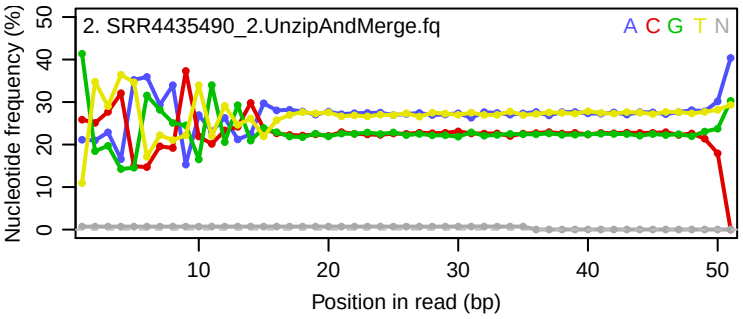
Position in read (bp)


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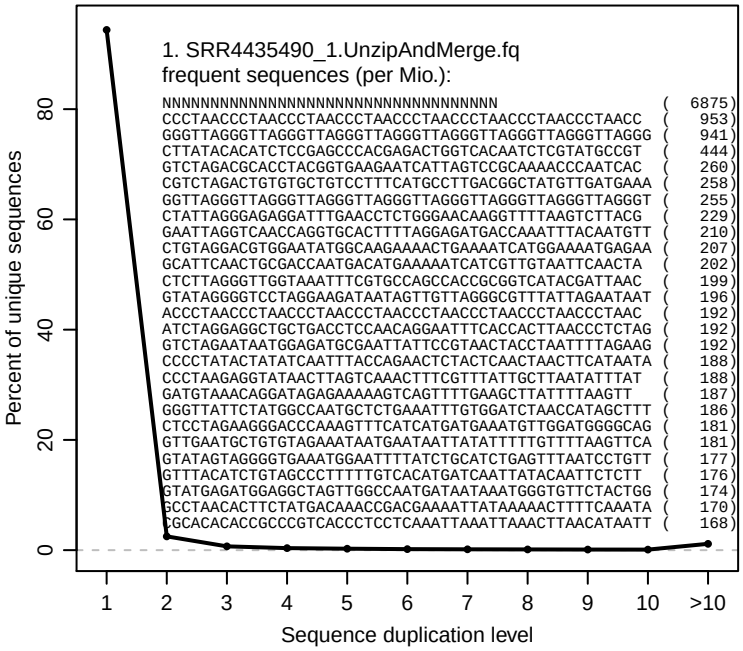
Position in read (bp)


1. SRR4435490_1.UnzipAndMerge.fq
frequent sequences (per Mio.):
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GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG (941)
CTTATACACATCTCCGAGCCCACGAGACTGGTCACAATCTCGTATGCCGT (444)
GTCTAGACGCACCTACGGTGAAGAATCATTAGTCCGCAAAACCCAATCAC (260)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (258)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (255)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (229)
GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (210)
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CTCCTAGAAGGGACCCAAAGTTTCATCATGATGAAATGTTGGATGGGGCAG (181)
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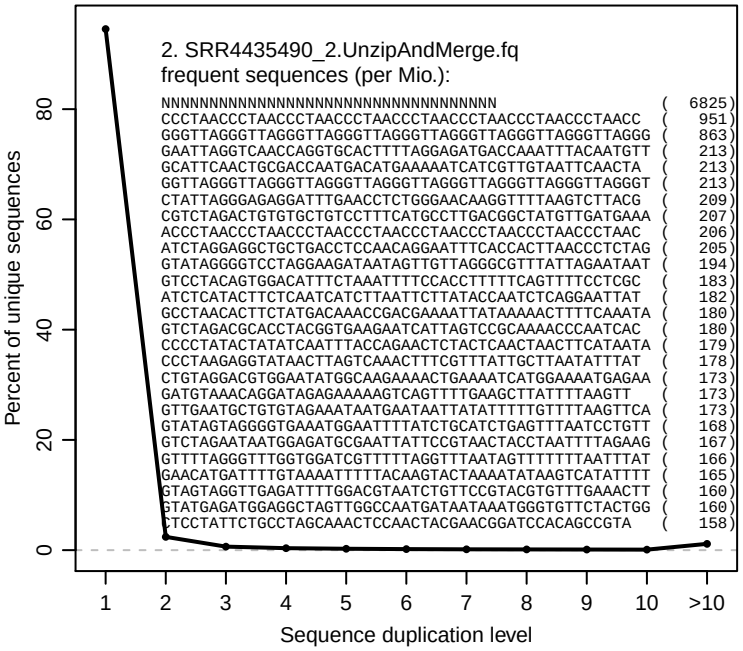
GTTTACATCTGTAGCCCTTTTTGTCACATGATCAATTATACAATTCTCTT (176)
GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (174)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (170)
CGCACACACCGCCCGTCACCCTCCTCAAATTAAATTAAACTTAACATAATT (168)
Percent of unique sequences
Sequence duplication level


2. SRR4435490_2.UnzipAndMerge.fq
frequent sequences (per Mio.):
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GAATTAGGTCAACCAGGTGCACTTTTAGGAGATGACCAAATTTACAATGTT (213)
GCATTCAACTGCGACCAATGACATGAAAAATCATCGTTGTAATTCAACTA (213)
GGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT (213)
CTATTAGGGAGAGGATTTGAACCTCTGGGAACAAGGTTTTAAGTCTTACG (209)
CGTCTAGACTGTGTGCTGTCCTTTCATGCCTTGACGGCTATGTTGATGAAA (207)
ACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAAC (206)
ATCTAGGAGGCTGCTGACCTCCAACAGGAATTTCACCACTTAACCCTCTAG (205)
GTATAGGGGTCCTAGGAAGATAATAGTTGTTAGGGCGTTTATTAGAATAAT (194)
GTCCTACAGTGGACATTTCTAAATTTTCCACCTTTTTCAGTTTTCCTCGC (183)
ATCTCATACTTCTCAATCATCTTAATTCTTATACCAATCTCAGGAATTAT (182)
GCCTAACACTTCTATGACAAACCGACGAAAATTATAAAAACTTTTCAAATA (180)
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CCCCTATACTATATCAATTTACCAGAACTCTACTCAACTAACTTCATAATA (179)
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GTATGAGATGGAGGCTAGTTGGCCAATGATAATAAATGGGTGTTCTACTGG (160)
CTCCTATTCTGCCTAGCAAACTCCAACTACGAACGGATCCACAGCCGTA (158)
Percent of unique sequences
Sequence duplication level